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1 **Role of epigenetic therapy in the modulation of tumor growth and migration in human**
2 **castration resistance prostate cancer cells with neuroendocrine differentiation.**

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27 **Short Title:** epigenetic therapy in prostate cancer cells with neuroendocrine differentiation.

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32 **Keywords:** epigenetic drugs, castration resistance prostate cancer, apoptosis, migration, DNA
33 methylation

34 **ABSTRACT**

35 INTRODUCTION: Neuroendocrine transdifferentiation (NED) of prostate cancer cells is associated
36 with the development of resistance to anti-androgen therapy and poor prognosis in patients with
37 castration resistance prostate cancer (CRPC). Many of the molecular events, involved in NED, appear
38 to be mediated by epigenetic mechanisms. In this study, we evaluated the antitumor activity and
39 epigenetic modulation of two epigenetic drugs, such as the demethylating agent 5-aza-2'-
40 deoxycytidine (AZA) and the methyl donor S-adenosylmethionine (SAM), in two human CRPC cell
41 lines with NED (DU-145 and PC-3). METHODS: The effects of AZA and SAM on cell viability, cell
42 cycle, apoptosis, migration and genome-wide DNA methylation profiling have been evaluated.
43 RESULTS: Both drugs showed a prominent antitumor activity in DU-145 and PC-3 cells, through
44 perturbation of cell cycle progression, induction of apoptosis and inhibition of cell migration. AZA
45 and SAM reversed NED in DU-145 and PC-3, respectively. Moreover, AZA treatment modified
46 DNA methylation pattern in DU-145 cells, sustaining a pervasive hypomethylation of the genome,
47 with a relevant effect on several pathways involved in the regulation of cell proliferation, apoptosis
48 and cell migration, in particular Wnt/ β -catenin. CONCLUSIONS: A relevant antitumor activity of
49 these epigenetic drugs on CRPC cell lines with NED opens a new scenario in the therapy of this lethal
50 variant of prostate cancer.

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68 INTRODUCTION

69 Prostate cancer (PC) represents a leading cause of cancer-related deaths in men in developed
70 countries. Androgen deprivation is the cornerstone of treatment for advanced PC. However, this
71 therapy is rarely curative and beneficial effects are often temporary with the development of drug-
72 resistance in Castration-Resistant Prostate Cancer (CRPC) [1]. A relevant factor contributing to the
73 progression of PC from a hormone-sensitive to castration-resistant state is the neuroendocrine
74 transdifferentiation (NED), characterized by a loss of differentiation towards an
75 epithelial/mesenchymal transition and a cellular transdifferentiation harboring neuroendocrine
76 features [2-4]. Neuroendocrine-like cells lack the expression of androgen receptor and prostate
77 specific antigens and are resistant to androgen deprivation. Moreover, neuroendocrine-like cells
78 produce several growth factors [5] that support the growth of surrounding tumor cells in a paracrine
79 manner. DU-145 and PC-3 are immortalized CRPC cell lines [6] with NED, as confirmed by the
80 expression of several neuroendocrine cell markers in both cells [7, 8] and non-functional AR signaling
81 [9]. Indeed, they are unresponsive to the stimulation with dihydrotestosterone [6] and represent a
82 good model to study NED in PC [7].

83 Most of the molecular events, involved in the development of drug-resistance and NED, appear to be
84 mediated by epigenetic mechanisms, in particular DNA methylation [10, 11]. This leads to silencing
85 of tumor suppressor genes or activation of oncogenes, but “reversibility” of DNA methylation makes
86 this process a potential therapeutic target for epigenetic drugs, such as 5-aza-2'-deoxycytidine (AZA)
87 and S-adenosylmethionine (SAM). The first one is a demethylating agent approved by FDA for the
88 treatment of patients with myelodysplastic syndromes and acute lymphoblastic leukemia [12],
89 whereas SAM is a methyl donor regulating DNA methylation, distributed as a dietary supplement
90 [13]. Both compounds showed a relevant antitumor activity both *in vitro* and *in vivo* for several
91 tumors [14]. In PC AZA induced tumor growth delay and increased expression of androgen receptor
92 [15, 16], while SAM reduced tumor cell invasiveness and proliferation [17]. However, the role of
93 epigenetic therapy in PC with NED is not well defined.

94 The aim of the present study was to evaluate the antitumor activity and epigenetic modulation of AZA
95 and SAM in two human CRPC cell lines with NED (DU-145 and PC-3).

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97

98 MATERIAL AND METHODS

99 Drug preparation and cell line cultures

100 AZA was provided by Sigma-Aldrich (St. Louis, USA and diluted in DMSO at concentration of 10^{-3} M, whereas SAM was purchased by New England Biolabs, Inc (Massachusetts, USA). Human PC
101 cell lines, DU-145 and PC-3 were provided by ATCC and maintained as previously described [18]
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103

104 Cell viability assay

105 In order to measure the cellular metabolic activity, as an indicator of cell viability, we performed a
106 colorimetric assay, such as 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT).
107 DU-145 and PC-3 cells were seeded in 96 well plates at a density of 2×10^3 cells/well. The day after
108 cell culture medium was replaced with medium containing vehicle (control), or different
109 concentrations of AZA and SAM. For experiments of long-term incubation, medium was replaced
110 with new one containing vehicle or drugs after 3 days of incubation. After 3 and 6 days of treatment
111 cells were harvested for MTT assay, as previously described [18].
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113 Wound-healing assay

114 This method is used to study in vitro cell migration creating a “wound” in a cell monolayer. DU-145
115 and PC-3 cells were seeded in 6-well plates (4×10^5 cells/well) and cultured as monolayer to
116 confluence. Cells were washed with Phosphate-Buffered Saline (PBS), supplemented with assay
117 medium containing vehicle (control), AZA (10^{-5} M) or SAM (2.5×10^{-4} M). Images were captured
118 immediately (T_0) and at 72 hours (T_{72}) after wounding by phase microscopy (10x magnification).
119 Wound-healing area was used to estimate migration ability and calculated with Image J program.
120 Data were reported as percentage wound healing using equation % wound healing = $100 \times (1 - [\text{wound}$
121 $\text{area at } T_{72} / \text{wound area at } T_0])$.
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122

123 Flow cytometric analysis of cell cycle and apoptosis

124 DU-145 and PC-3 cells were plated in duplicates in 6-well plates at density of 3×10^5 cells/well.
125 Following day, cell culture medium was replaced with medium containing vehicle (control), AZA
126 (10^{-5} M) or SAM (2.5×10^{-4} M). After 3 days, cells were harvested by gentle trypsinization, washed
127 with cold PBS and collected by centrifugation. Flow cytometry techniques in analysis of cell cycle
128 and apoptosis were applied after staining of tumor cells with propidium iodide (PI) and Annexin-V-
129 fluorescein isothiocyanate/PI, respectively, as previously described [18]. After staining with PI,
130 10,000 cells for each tube were immediately measured and fluorescence was collected as FL1-A
131 through a FACScalibur flow cytometer (Becton Dickinson, Erembodegem, Belgium). Cell cycle

132 distribution was expressed as percentage of cells in G₀/G₁, S, and G₂/M phases compared to control.
133 By staining cells with a combination of Annexin-V-fluorescein isothiocyanate and PI, we identified
134 viable cells (Annexin-V⁻/PI⁻), early apoptotic cells (Annexin-V⁺/PI⁻) and late apoptotic/necrotic cells
135 (Annexin-V⁺/PI⁺). Data were analyzed using Cell Quest Pro Software, as previously reported [18].

136

137 **Western blot analysis**

138 We performed western blot analyses of protein extracts from cell lysates. DU-145 and PC-3 cells
139 were plated and following day, cell culture medium was replaced with medium containing vehicle
140 (control), AZA (10⁻⁵ M) or SAM (2.5*10⁻⁴ M). After 3 days, cells were scraped, washed twice in cold
141 PBS and resuspended in lysis radioimmunoprecipitation assay buffer containing protease and
142 phosphatase inhibitors. Proteins were then separated and quantified, as previously described [18].
143 Primary specific antibodies were anti-caspase-3, anti-cleaved caspase-3, anti-neuron specific enolase
144 (NSE), anti-β catenin, anti PARP and anti-cleaved PARP (Cell Signaling Technology, Beverly, MA,
145 USA) at dilution 1:1000 and HRP conjugated mouse and rabbit as secondary antibodies (dilution
146 1:5000 for anti-caspase- 3 and 1: 10,000 for all other antibodies). Results were normalized against
147 level of actin expression in each sample. Intensities of the bands were expressed as arbitrary units
148 when compared to controls.

149

150 **DNA extraction and bisulphite treatment**

151 DU-145 cells were plated in 6-well plates and treated with vehicle (control), AZA (10⁻⁵ M) or SAM
152 (2.5*10⁻⁴ M). After 3 days, total DNA was extracted using DNeasy Blood & Tissue Kit (Qiagen,
153 Germany). Quality control and quantification of DNA were performed before and after bisulphite
154 conversion. One microgram of genomic DNA was bisulfite-treated using the EZ DNA Methylation-
155 Gold Kit (Zymo Research).

156

157 **Genome-wide DNA methylation analysis**

158 The Infinium HumanMethylation 450K BeadChip was used to assess genome-wide DNA
159 methylation. This microarray allows to estimate DNA methylation of more than 480000 CpG sites
160 widespread across the genome at single base resolution. Four microliters of bisulfite-converted DNA
161 were used for hybridization on Infinium HumanMethylation 450K BeadChip, according to Illumina's
162 standard protocol. Arrays were scanned by HiScan (Illumina). Raw data were extracted using *minfi*
163 R package and normalized using *preprocessFunnorm* function. Probes having a detection p-value
164 >0.05 in more than 1% of the samples (1187 probes) were removed, leaving 484325 probes for
165 differential analysis.

166

167 **Statistical Analyses**

168 All **the** experiments were carried out at least 3 times and **showed** comparable results. For statistical
169 analysis GraphPad Prism 5.0 (GraphPad Software, San Diego, CA) was used. **We have firstly**
170 **compared several groups by analysis of variance (ANOVA). When ANOVA suggested significant**
171 **differences between groups, individual means were compared by the Newman-Keuls (experiments of**
172 **dose curve responses) and Bonferroni's Multiple Comparison Test (protein expression analysis).**
173 Unpaired Student's t test was used to analyze effects of AZA and SAM on cell cycle modulation,
174 apoptosis and migration. $p < 0.05$ was considered statistically significant. **Figures reported values as**
175 **mean \pm Standard Error of the Mean (S.E.M).**

176 **To analyze genome-wide DNA methylation data, we applied an analytical pipeline [19] that allows**
177 **to identify both differentially methylated probes (DMPs) and differentially methylated regions**
178 **(DMRs), *i.e.* groups of differentially methylated CpG sites which are physically adjacent along the**
179 **chromosome. Briefly, ANOVA was used to identify DMPs. For DMRs analysis, we focused on**
180 **probes in CpG islands and CpG islands-surrounding sequences (shores and shelves) that map in genic**
181 **regions. Probes mapping in the same island, shore or shelf were grouped (block of probes, BOPs) and**
182 **multivariate analysis of variance (MANOVA) was performed on BOPs including at least 3 CpGs**
183 **(31418 BOPs) to compare different experimental conditions. For both DMPs and DMRs analyses, p-**
184 **values were corrected using Benjamini Hochberg method and a significance threshold of 0.05 was**
185 **used. Fisher exact test was calculated using fisher test function implemented in R software. Kyoto**
186 **Encyclopedia of Genes and Genomes (KEGG) pathways enrichment analysis was performed by**
187 **WebGestalt [20], using default settings and a user-defined background list of genes derived from**
188 **Infinium 450k annotation.**

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190

191 **RESULTS**

192 **Epigenetic drugs reduced **viability** of human **CRPC cell lines with NED****

193 We performed dose-response curves after 3 and 6 days of incubation with **AZA and SAM** in DU-145
194 and PC-3 cell lines. **Both compounds significantly inhibited viability of both human cell lines in a**
195 **dose-dependent manner (Figure 1A, B). SAM exerted a prominent and early effect on cell viability**
196 **after 3 days of incubation (Figure 1B), while AZA showed a later effect after 6 days (Figure 1A).** For
197 further experiments, **we selected** submaximal concentrations of AZA (10^{-5} M) and SAM ($2.5 \cdot 10^{-4}$
198 M).

199

200 **Epigenetic drugs decreased NED features of human CRPC cell lines with NED**

201 After 3 days of incubation, AZA and SAM significantly suppressed the expression of NSE ($p < 0.05$
202 vs CTR), a marker of NED, in DU-145 and PC-3 cells, respectively (Figure 1 C, D).

203

204 **Epigenetic drugs modulated migration of human CRPC cell lines with NED**

205 In both cell lines, we observed a significant decrease in cell migration (-32.3% in DU-145 and -44.5%
206 in PC-3 compared to controls, both $p < 0.001$) (Figure 2 A-D) with a concomitant suppression in β -
207 catenin expression (Figure 2 E-H) after 3 days of incubation with AZA compared to controls ($p < 0.01$
208 and $p < 0.001$, in DU-145 and PC-3, respectively). Otherwise, we did not observe any significant effect
209 on cell migration and β -catenin expression after incubation with SAM compared to controls (Figure
210 2).

211

212 **Epigenetic drugs induced cell cycle perturbations in human CRPC cell lines with NED**

213 AZA significantly increased the percentage of DU-145 cells in G_0/G_1 (+54.4%, $p < 0.05$) and in S
214 phase (+62%, $p < 0.01$) and decreased cell population in G_2/M phase (-27.5%, $p < 0.01$) compared to
215 controls (Figure 3A). In PC-3, AZA significantly decreased cell population in S phase (-43.3%,
216 $p < 0.01$) and increased cell number in G_2/M phase (+26.6%, $p < 0.01$) compared to untreated cells
217 (Figure 3 B).

218 After SAM incubation, we observed a prominent induction of both cell lines in pre- G_1 phase (Figure
219 3 A, B). In DU-145 (Figure 3A) SAM decreased cells in G_0/G_1 (-33.2%, $p < 0.05$), S (-52.3%, $p < 0.01$)
220 and G_2/M (-65%, $p < 0.01$) phases compared to controls. SAM induced a significant increase of PC-3
221 cells in both G_0/G_1 (+71%, $p < 0.01$) and S phases (+66.6 %, $p < 0.01$) and a decrease in G_2/M phase (-
222 50.6%, $p < 0.01$) compared to controls (Figure 3 B).

223

224 **Epigenetic drugs induced apoptosis in human CRPC cell lines with NED**

225 No significant change in early apoptosis was observed after incubation with both epigenetic drugs in
226 DU-145 and PC-3 cells. AZA induced an increase of both cell lines in late apoptosis/necrosis (+83.6%
227 in DU-145 and +137.8% in PC-3, $p < 0.05$ and $p < 0.01$, respectively) compared to controls (Figure 3
228 C, D). SAM induced a very prominent increase in the population of late apoptotic/necrotic cells
229 (+2534.3% in DU-145 and +1438.7% in PC-3, both $p < 0.001$) compared to controls (Figure 3 C, D).
230 Moreover, after 3 days of incubation, AZA and SAM (Figure 4) significantly stimulated expression
231 of cleaved PARP (both drugs $p < 0.001$ in DU-145 and $p < 0.05$ in PC-3) and cleaved caspase-3 (both
232 drugs $p < 0.001$ in DU-145 and $p < 0.01$ in PC-3 cells) in human CRPC cell lines with NED.

233

234 **Modulation of DNA methylation status by AZA and SAM in DU-145 cells**

235 To elucidate cellular signaling perturbed by epigenetic modulators, we evaluated changes in
236 epigenome-wide DNA methylation profiling through Infinium450k microarray after incubation of
237 DU-145 cells with AZA (10^{-5} M) or SAM (2.5×10^{-4} M) compared to controls (Figure 5). As a first
238 step, we evaluated global DNA methylation patterns of treated and **vehicle control cells** by **principal**
239 **component analysis**. The first component explained 63% of the variance, while the second component
240 explained 76% of the remaining variance. Cells treated with SAM **clustered with controls**, while cells
241 treated with AZA clearly **separated** along the first component (Figure 5 A), indicating that **AZA**
242 **intensely modified DNA methylation patterns**. To identify CpG sites, whose DNA methylation level
243 was affected by epigenetic modulators (differentially methylated probes, DMPs), we compared
244 **control** and treated cells by ANOVA. Treatment with SAM did not significantly **modify** DNA
245 methylation profile **in** DU-145 cells (no probes with q-value <0.05 ; Figure 5 C), while a widespread
246 hypomethylation was observed in cells treated with AZA (Figure 5 B, E), with 9666 DMPs (q-value
247 <0.05 ; Table 1 and Supplementary file 1). As expected, vast majority (99%) of DMPs was
248 hypomethylated after AZA treatment, with only 73 hypermethylated probes. Probes with highest
249 methylation values in control cells (>0.8) were more affected by the treatment, underlying relevant
250 hypomethylation effect (Figure 5 D). Interestingly, DMPs were significantly enriched (**$p < 0.01$**) in
251 CpG islands (**odds ratio = 1.31**) and open sea (regions not CpG-rich and not associated to a gene,
252 **odds ratio = 1.06**). **The** number of DMPs mapping in shores and shelves was less than expected
253 (Figure 5 E, **$p < 0.01$; odds ratio ranging from 0.68 to 0.9**), despite these regions tended to have
254 relatively high DNA methylation levels in control cells (Figure 5 F). Moreover, DMPs were
255 particularly enriched on chromosomes X and Y (**$p < 0.01$, odds ratio=2.4 and 4.3, respectively**). We
256 found that chromosome Y hosted several of the few probes that got hypermethylated after AZA
257 treatment (Figure 5 D, black dots).

258 As a second step of the analysis, we **used MANOVA to search** for DMRs, *i.e.* regions containing
259 **multiple adjacent** CpG probes **that** are concomitantly affected by the treatment. No DMRs were found
260 when we compared untreated cells with cells treated with SAM. In the comparison between **control**
261 **cells** and cells treated with AZA we identified 54 DMRs, all hypomethylated in treated cells (**q-**
262 **value <0.05** ; Supplementary file 2). We selected top 20 genes and analyzed their involvement in PC
263 with NED. A Pubmed search of top 20 genes using query “gene name AND prostate cancer AND
264 neuroendocrine [title/abstract]”, revealed that most of these genes appear to be involved in
265 tumorigenesis of this cancer (Table 2).

266 Finally, we investigated pathways affected by AZA treatment in DU-145 cells. We used WebGestalt
267 to identify KEGG pathways and gene ontologies enriched in the lists of 9666 DMPs and 54 DMRs.
268 Analysis on DMRs did not return any significant result (using a q-value threshold of 0.05). Ten
269 pathways and 10 gene ontologies were enriched in the DMPs list (Tables 3 and 4, respectively). The
270 most enriched pathway was Wnt/ β -catenin signaling pathway (q-value: 0.0006). Other significantly
271 enriched KEGG pathways included biological processes involved in cell migration, cell proliferation,
272 apoptosis and related to development, synaptic organization and axon guidance.

273

274

275 DISCUSSION

276 **Castration resistance prostate cancer** is the most aggressive form of PC that becomes unresponsive to
277 androgen ablation therapy. **The NED of PC appears to be involved in the development of resistance**
278 **to anti-androgen therapy and associated with poor prognosis in patients with CRPC.** Epigenetic
279 modifications, such as hyper or hypo-methylation of gene promoters linked to drug metabolism,
280 apoptosis, cell cycle control, **play** an important role in NED [3, 21]. In the last years, FDA approved
281 a variety of epigenetic drugs, like demethylating drug AZA or methylating agent SAM. In several
282 neuroendocrine neoplasms AZA induced growth inhibition through induction in apoptosis and
283 improving expression of target receptors [22, 23]. Whereas the effect of SAM is poorly known in
284 neuroendocrine neoplasms and in CRPC with NED.

285 In the present study, we evaluated *in vitro* the antitumor activity of AZA and SAM in **CRPC cell lines**
286 **with NED.** These two epigenetic drugs induced a prominent anti-proliferative effect through cell
287 cycle modulation and induction in apoptosis. Moreover, AZA and SAM reverted **NED** toward a less
288 aggressive subtype, as shown by a decrease in NSE expression in DU-145 and PC-3, respectively.
289 Interestingly, only AZA decreased the migration of both cell lines in a wound healing assay, probably
290 due to the inhibition of Wnt/ β -catenin pathway, as suggested by the concomitant decrease in β -catenin
291 expression. This signalling, modulated by epigenetic mechanisms [24], is involved in invasive
292 phenotype, by inducing cell mobility and tumor invasion [25], and in NED of PC [26]. **Previous**
293 **reports showed that PC with NED exhibited distinctive DNA methylation patterns [10, 11]. Beltran**
294 **and co-workers reported marked epigenetic differences between CRPC with NED and CRPC**
295 **adenocarcinoma [2]. They identified several epigenetically deregulated pathways involved in**
296 **neuronal and developmental processes, cell-cell adhesion, stem cell programs and epithelial-**
297 **mesenchymal transition. The authors suggested that this DNA methylation remodelling was**
298 **associated to transition to neuroendocrine PC subtype [2]. Accordingly, using a xenograft model of**

299 CRPC, Peter et al demonstrated that DNA methylation progressively changes from the castration
300 naïve state to the treatment-induced NED state. These epigenetic alterations were likely able to affect
301 gene expression of genes related to neurodevelopmental and morphogenic pathways [27].

302 In our study, DNA methylation landscape of DU-145 cells was not significantly altered by SAM. On
303 the contrary, AZA profoundly modified DNA methylation pattern, sustaining a pervasive
304 hypomethylation of the genome. Pathways analysis on the list of DMPs identified several biological
305 processes associated with NED in previous studies [2, 11, 27], such as neural functions and axonal
306 guidance, but also others involved in regulation of cell migration, proliferation and apoptosis. In
307 particular, the most enriched pathway was Wnt/ β -catenin signaling. Moreover, it is interesting to
308 observe that sex chromosomes were enriched in DMPs after AZA treatment. A role of chromosome
309 Y in PC onset and progression has been recently proposed [28] and expression of some genes on the
310 non-recombining Y regions is dependent on epigenetic regulation [29]. The methylation of
311 cg05163709 on Y chromosome has been proposed as biomarker of PC [30], but this probe is not
312 included in our DMPs list. Further studies should better investigate the DNA methylation pattern on
313 Y chromosome and its responsiveness to epigenetic drugs.

314 Finally, we found that most of the top 20 genes correlated with DMRs have implications for PC
315 carcinogenesis and progression (table 2). *LRPAP1*, a lipid transporter, and *ELOVL7*, a fatty acid
316 elongase 7, have been recently associated with PC disease progression [31, 32]. *PML* and *FAM46B*
317 are tumor suppressors, that have been found to be aberrantly down regulated in PC and considered as
318 unfavorable prognostic markers [33-37]. They are both involved in the modulation of Wnt/beta-
319 catenin pathway [37, 38] together with *DNAJB6*, *ELAVL1* and *NOS1AP*, the latter through activation
320 of tumor suppressor Scribble promoting neurogenesis [39-42]. *ERN2*, *ELAVL1*, *KLK15*, *RRBP1*,
321 *FOXD2*, *HOXD8* *FAM20C* genes are directly involved in PC tumorigenesis, as well as, indirectly,
322 *SIKE1* and *NOS1AP* [43, 44] and some of them have been suggested as prognostic biomarkers for PC
323 [45-56].

324 The main limitation of this study derives from the use of in vitro and in silico models, that may not
325 completely recapitulate the complex scenario occurring in cancer patients. In addition, epigenetic
326 drugs, currently used in clinical practice, lack locus specificity. This property induces unintended off-
327 target effects with high toxicity.

328 In conclusion, both AZA and SAM showed a relevant antitumor activity on CRPC cell lines with
329 NED, bringing back NED to a less aggressive phenotype. AZA strongly modified DNA methylation
330 pattern affecting several pathways involved in the regulation of cell proliferation, apoptosis and cell
331 migration, in particular Wnt/ β -catenin signaling. This opens a new scenario in the therapy of this

332 lethal variant of PC. Future efforts should focus on the development of more specific epigenetic drugs
333 with negligible toxicity.

334

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336 None

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339 **Statement of Ethics**

340 The study was approved by the Institutional Ethics Committee (Istituto Auxologico Italiano, approval
341 number 2012_02_21_16)

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343

344 **Conflict of Interest Statement:** The authors declare that they have no conflict of interest.

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346

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352 **Author Contributions**

353 A.D., D.S., M.C.C., G.G. performed and analyzed the in vitro experiments, whereas G.G. and E.S.G.
354 executed Western blot analyses. M.G.B. performed the statistical analysis and discussed the data with
355 P.G. and C.F. M.O.B. performed FACS analysis of cell cycle and apoptosis. A.D., G.G., M.G.B. and
356 G.V. designed the experiments and analyzed the data. A.D., M.G.B., D.G., A.M.D.B., L.P. and G.V.
357 wrote the manuscript. All authors critically revised the manuscript and approved final version.

358

359 **Data Availability statements**

360 The authors confirm that the data supporting the findings of this study are available within the article
361 and its supplementary materials. Further enquiries can be directed to the corresponding author.

362 DNA methylation data are available at the NCBI Gene Expression Omnibus (GEO) database
363 (<http://www.ncbi.nlm.nih.gov/geo/>) under accession number GSE164249.

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365

366

367 **Abbreviations:** NED: Neuroendocrine transdifferentiation; CRPC: castration resistance prostate
368 cancer; AZA: 5-aza-2'-deoxycytidine; SAM: S-adenosylmethionine; PC: Prostate cancer; MTT: 3-
369 (4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide; PI: propidium iodide; NSE: neuron
370 specific enolase; PARP: Poly (ADP-ribose) polymerase; ANOVA: Analysis of Variance; DMPs:
371 differentially methylated probes; DMRs: differentially methylated regions; BOPs: block of probes;
372 MANOVA: multivariate analysis of variance; PBS: Phosphate-Buffered Saline; KEGG: Kyoto
373 Encyclopedia of Genes and Genomes; DMSO: Dimethyl sulfoxide.

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Table legends

Table 1. Top 20 DMPs emerged in the comparison between untreated DU-145 cells and cells treated with AZA. For each DMP, the table reports its genomic location and, when present, the name of the CpG island and gene in which the probe maps. Finally, the Benjamini Hochberg corrected p-value of ANOVA test is reported. *DMPs*: differentially methylated probes; *Chr*: chromosome; *Position*: coordinates of the probes in the chromosome, according to GRCh37/hg19 assembly; *UCSC CpG_island_name*: name of the CpG island according to UCSC Genome Browser; *Relation to UCSC CpG island*: position of the CpG probe according to the CpG island (Island: within the CpG island; N-Shore: shore at the 5' of the CpG island; S-Shore: shore at the 3' of the CpG island; N-Shelf: shelf at the 5' of the CpG island; Shores are defined as the 2000 bp upstream and downstream the CpG islands; Shelves are defined as the regions at 2000-4000 bp upstream and downstream the islands); *UCSC RefGene name*: name of the Gene according to UCSC Genome Browser; *q-value*: Benjamini Hochberg corrected p-value.

Table 2. Top 20 DMRs emerged in the comparison between untreated DU-145 cells and cells treated with AZA. For each DMR, the table reports its genomic location, the name of the gene mapping in the DMR, the Benjamini Hochberg corrected p-value of MANOVA test and Pubmed references resulted from the query “gene name AND prostate cancer or neuroendocrine [title/abstract]”. *DMRs*: differentially methylated regions, defined on the basis of the *UCSC CpG Island name* and *Relation to UCSC CpG island* information. *UCSC RefGene name*: name of the Gene according to UCSC Genome Browser; *q-value*: Benjamini Hochberg corrected p-value.

Table 3. Pathways significantly enriched after AZA treatment in DU-145 cells. *Gene Set*: name of the KEGG pathway; *Description*: description of the pathway; *Ratio*: enrichment ratio; *q-value*: Benjamini Hochberg corrected p-value

581 **Table 4.** Gene ontologies significantly enriched after AZA treatment in DU-145 cells. *Gene Set*: name
582 of the Gene Ontology; *Description*: description of the gene ontology; *Ratio*: enrichment ratio; *q-*
583 *value*: Benjamini Hochberg corrected p-value.

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588 **Figure legends**

589

590 **Fig. 1** Effect of AZA (A) and SAM (B) on cell **viability** in DU-145 (□) and PC-3 (■) cell lines. Dose-
591 response curves were measured by MTT assay after 6 days of AZA and 3 days of SAM treatment,
592 and are expressed as nonlinear regression (curve fit) of log (concentration drug) versus the percentage
593 of **vehicle-treated control (CTR) cells**. Representative Western blot analysis of the NSE protein and
594 relative quantifications, from at least 3 independent experiments, after 3 days of incubation with **AZA**
595 **(10⁻⁵ M) or SAM (2.5*10⁻⁴ M)** in DU-145 (C) and PC-3 (D), compared to vehicle CTR. For western
596 blot analysis actin was used as a loading control. **The intensities of the bands were expressed as**
597 **arbitrary units when compared to those of the CTR**. Values represent the mean and S.E.M. of at least
598 3 independent experiments. *p<0.05; *** p<0.001.

599

600 **Fig. 2** Effects of **AZA (10⁻⁵ M) or SAM (2.5*10⁻⁴ M)** on cell migration (A-D) and beta-catenin
601 expression (E-H). Representative wound healing assay in DU-145 (A) and PC-3 (B) cells. The area
602 of wound was recorded at 0 and 72 h and percentage of wound healing with respect to T0 was
603 calculated using the equation **% wound healing = 100x (1- [wound area at T72 /wound area at T0]**
604 **for DU-145 (C) and PC-3 (D) cells**. Representative Western blot analysis and quantification of the
605 beta-catenin protein expression after 3 days of incubation with AZA and SAM in DU-145 (E, G) and
606 PC-3 (F, H) cells compared to **vehicle-treated control (CTR) cells**. **Expression of the house-keeping**
607 **protein actin was used as loading control. The intensities of the bands were expressed as arbitrary**
608 **units when compared to those of the CTR. Values represent** the mean ± SEM of at least 3 independent
609 experiments. ** p<0.01 ***p<0.001. Scale bar 500 μm.

610

611 **Fig. 3** Effects of **AZA (10⁻⁵ M) or SAM (2.5*10⁻⁴ M)** on cell cycle (A, B) and cell death (C, D) in
612 DU-145 (A, C) and PC-3 (B, D) cells, after 3 days of incubation. **Cell cycle distribution is expressed**
613 **as percentage of cells in G₀/G₁, S, and G₂/M phases compared to vehicle control (CTR) cells**. CTR
614 values have been set to 100%. The proportions of early apoptotic cells (EA) and late

615 apoptotic/necrotic cells (A/N) are expressed as percentage compared with the CTR and represent the
616 mean and SEM of at least 3 independent experiments. *p<0.05; ** p<0.01; ***p<0.001.

617

618 **Fig. 4** Representative Western blot images (A-D) and relative quantifications for the expression of
619 the total (E, G) and cleaved PARP (F, H), the total (I, K) and cleaved caspase 3 (J, L), after 3 days of
620 incubation with AZA (10^{-5} M) or SAM (2.5×10^{-4} M) compared to vehicle-control (CTR) in DU-145
621 (A, B, E, F, I, J) and PC-3 (C, D, G, H, K, L). Actin was used as a loading control. The intensities of
622 the bands were expressed as arbitrary units when compared to those of the CTR. Values represent
623 means \pm S.E.M from at least 3 independent experiments. *p<0.05; ** p<0.01; ***p<0.001.

624

625 **Fig. 5** Genome-wide DNA methylation analysis in DU-145 cells treated with AZA (10^{-5} M) or SAM
626 (2.5×10^{-4} M) and characterization of DMPs resulted from the comparison between vehicle-treated
627 control (CTR) cells and cells treated with AZA. (A) Principal component (PC) analysis plot,
628 calculated using all the Infinium450k probes retained after quality checks. (B-C) Volcano plots of the
629 ANOVA comparison of untreated cells with cells treated with AZA (B) or SAM (C). In each plot,
630 the y-axis reports the $-\log_{10}(q\text{-value})$ of each probe, while the x-axis reports the methylation
631 difference between control and treated cells. Dots highlighted in grey have a q-value <0.05. (D)
632 Relationship between DNA methylation level in control cells (x axis) and the change in DNA
633 methylation after AZA treatment (Mean CTR – Mean AZA; y axis). Dark grey and black dots
634 represent probes on X and Y chromosomes, respectively. (E) Odds ratio resulted from Fisher's exact
635 test for enrichment in the different functional genomic regions. (F) Boxplots of DNA methylation
636 values of the probes, divided according to functional genomic regions, in control cells. (G) Odds ratio
637 resulted from Fisher's exact test for enrichment in the different chromosomes. (H) Boxplots of DNA
638 methylation values of the probes, divided according to chromosome, in control cells.

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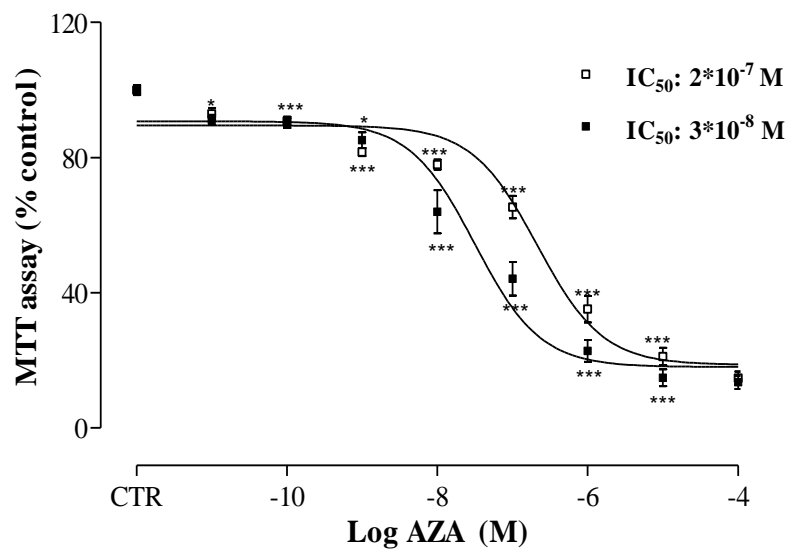
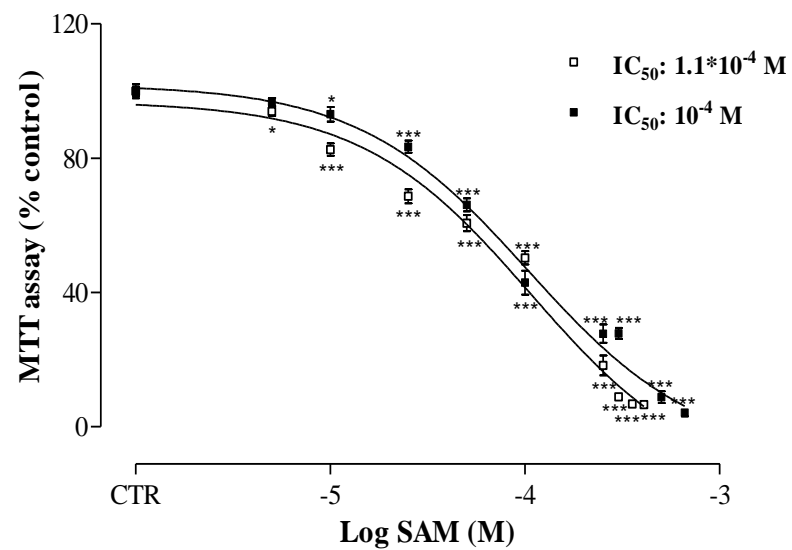
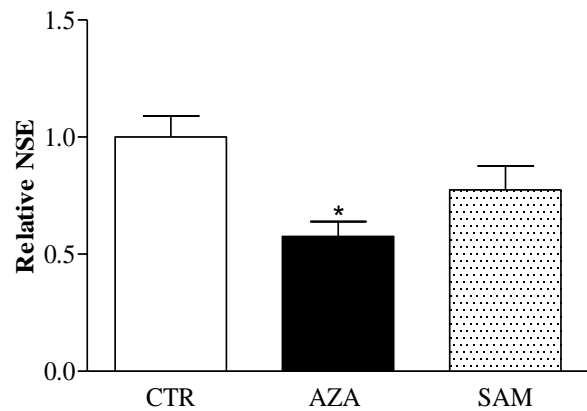
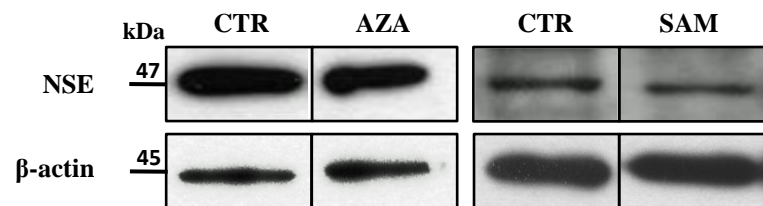
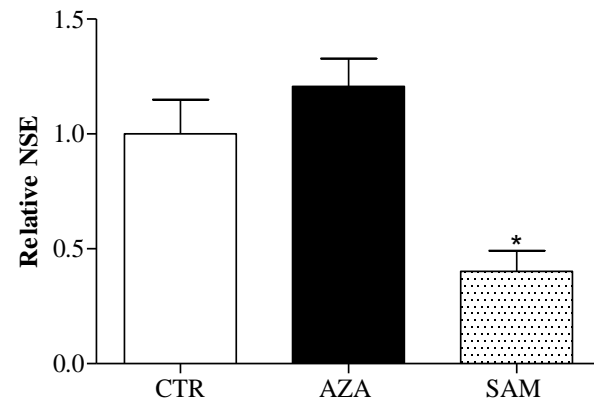
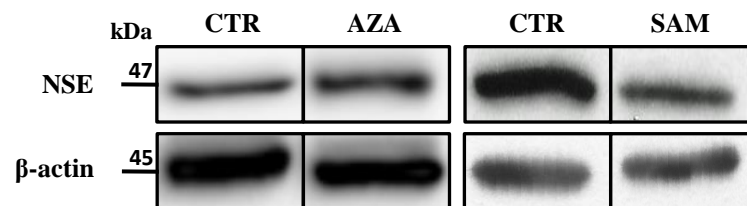
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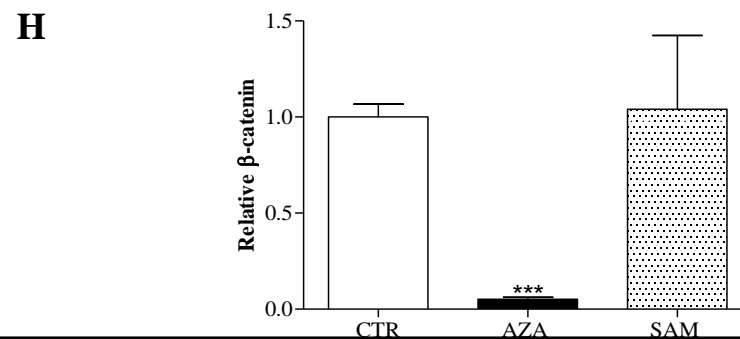
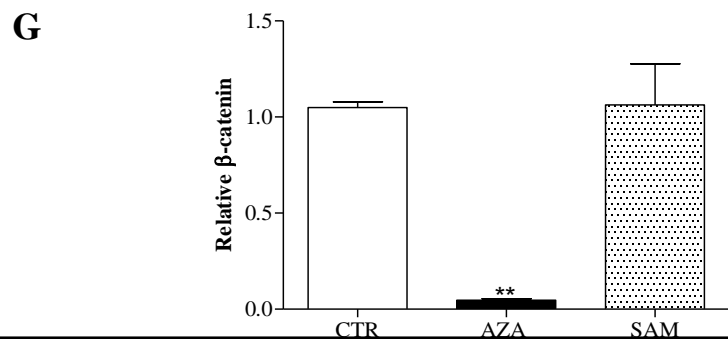
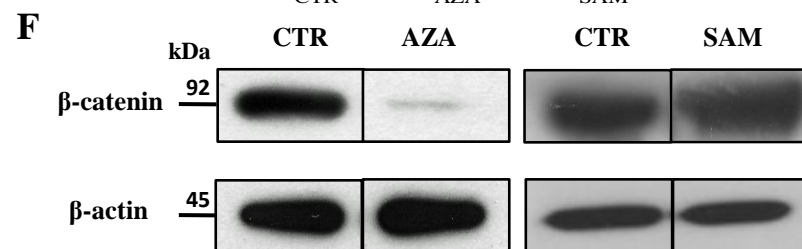
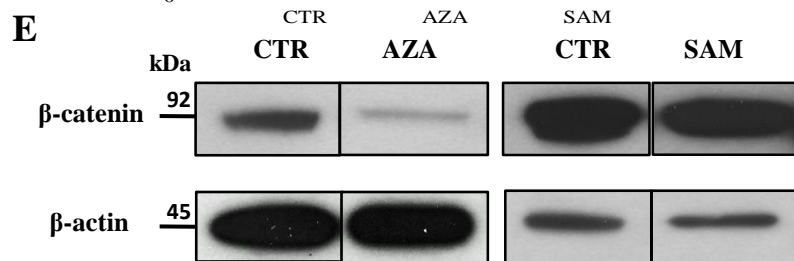
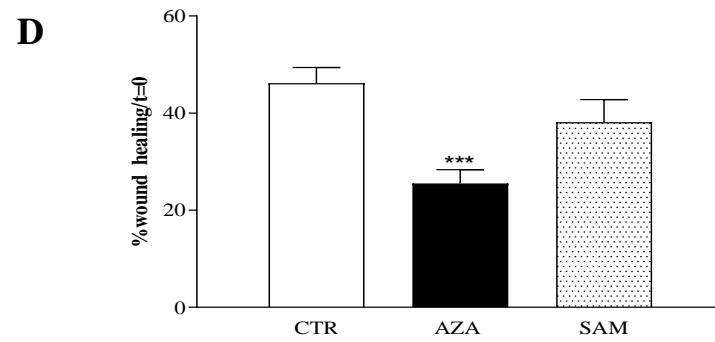
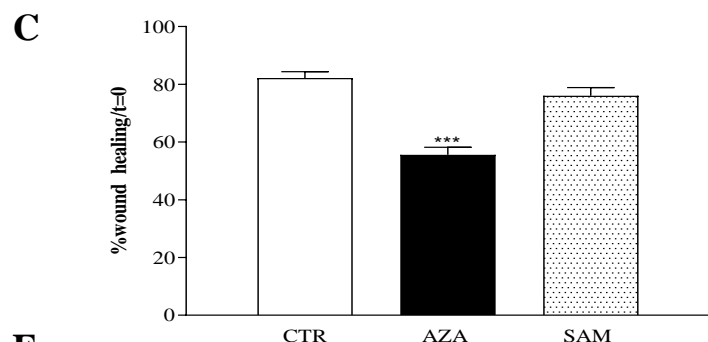
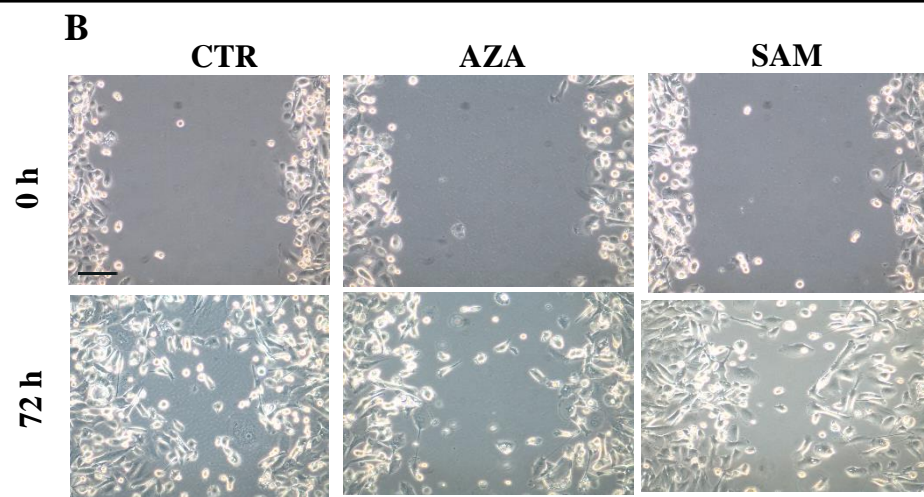
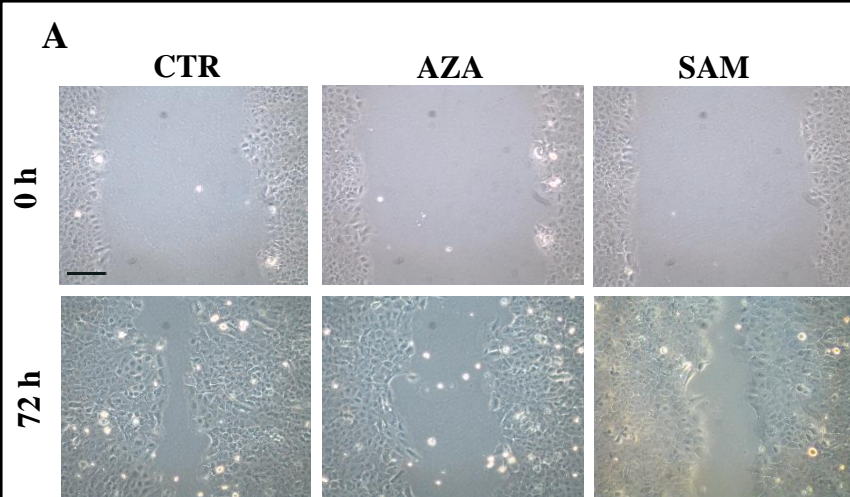
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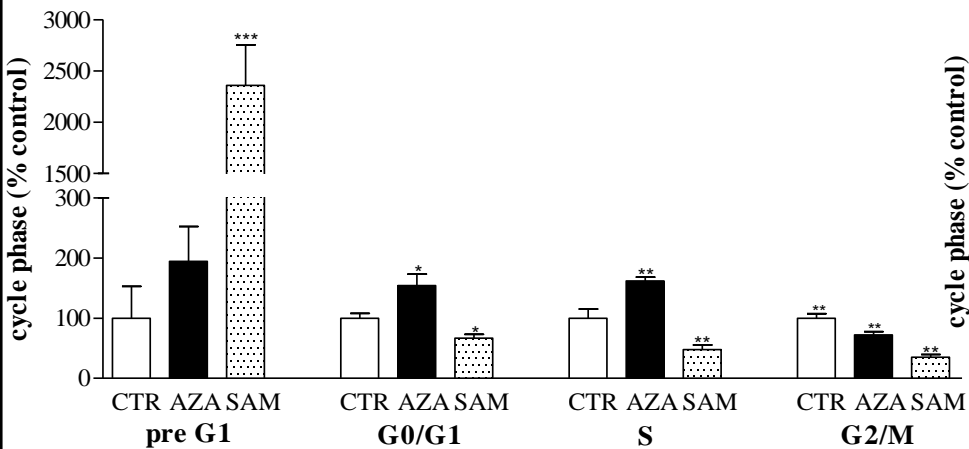
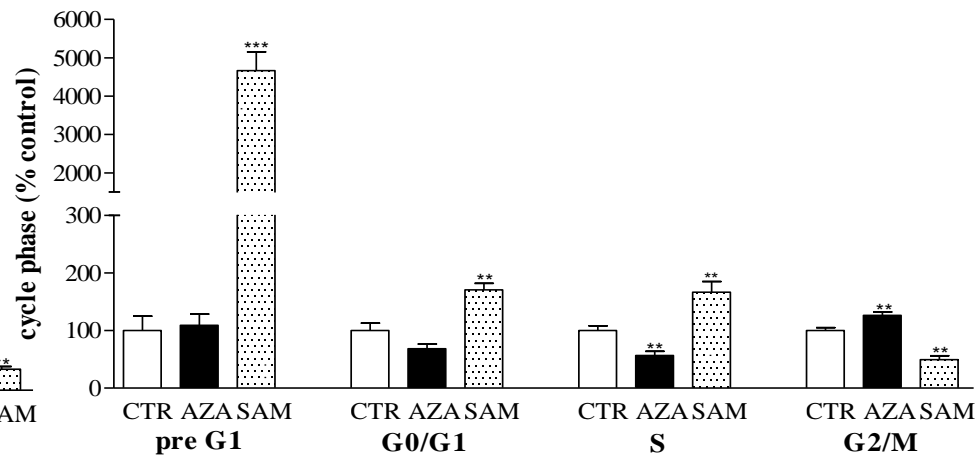
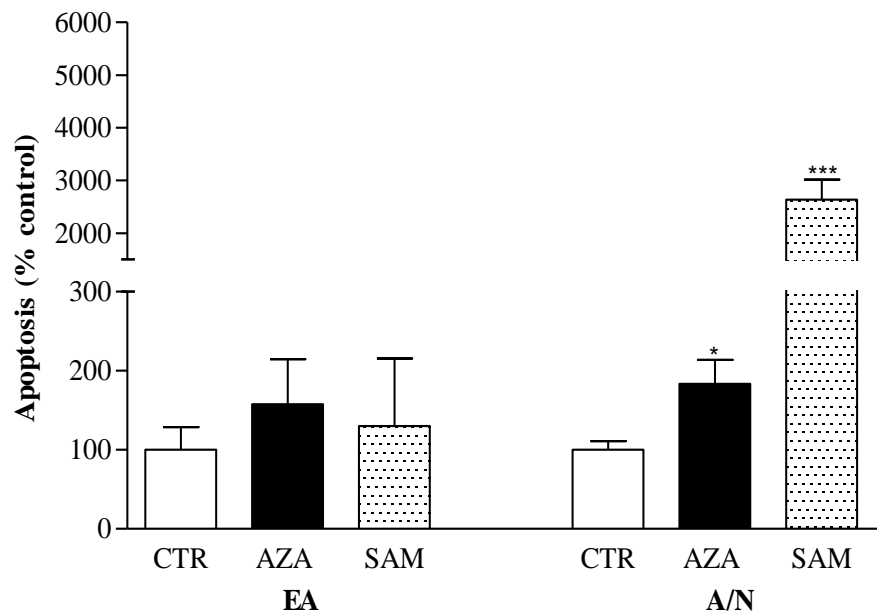
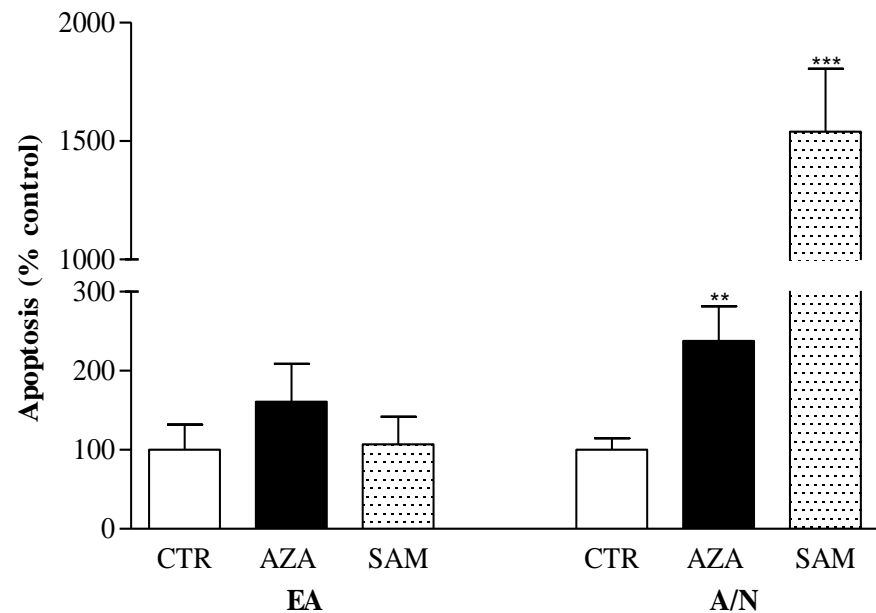
642 **Supplementary File 1.** DMPs identified in the comparison between untreated cells and cells treated
643 with AZA

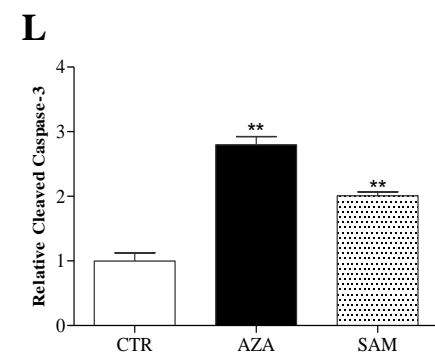
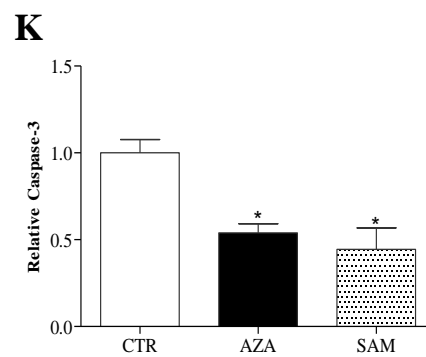
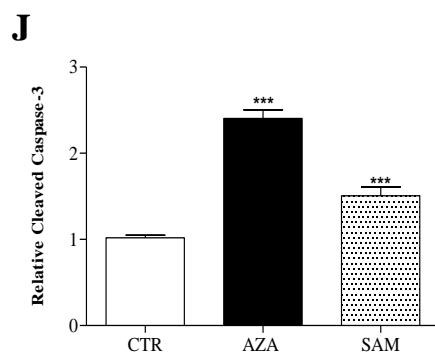
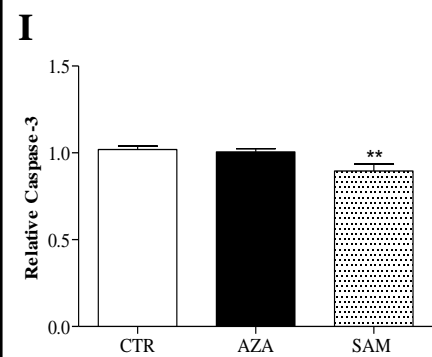
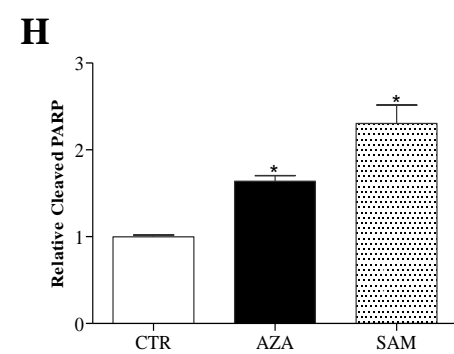
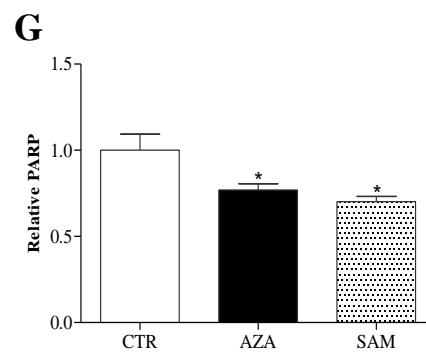
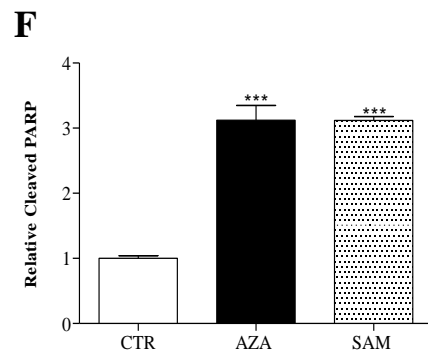
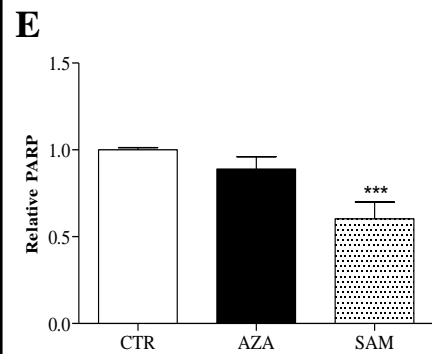
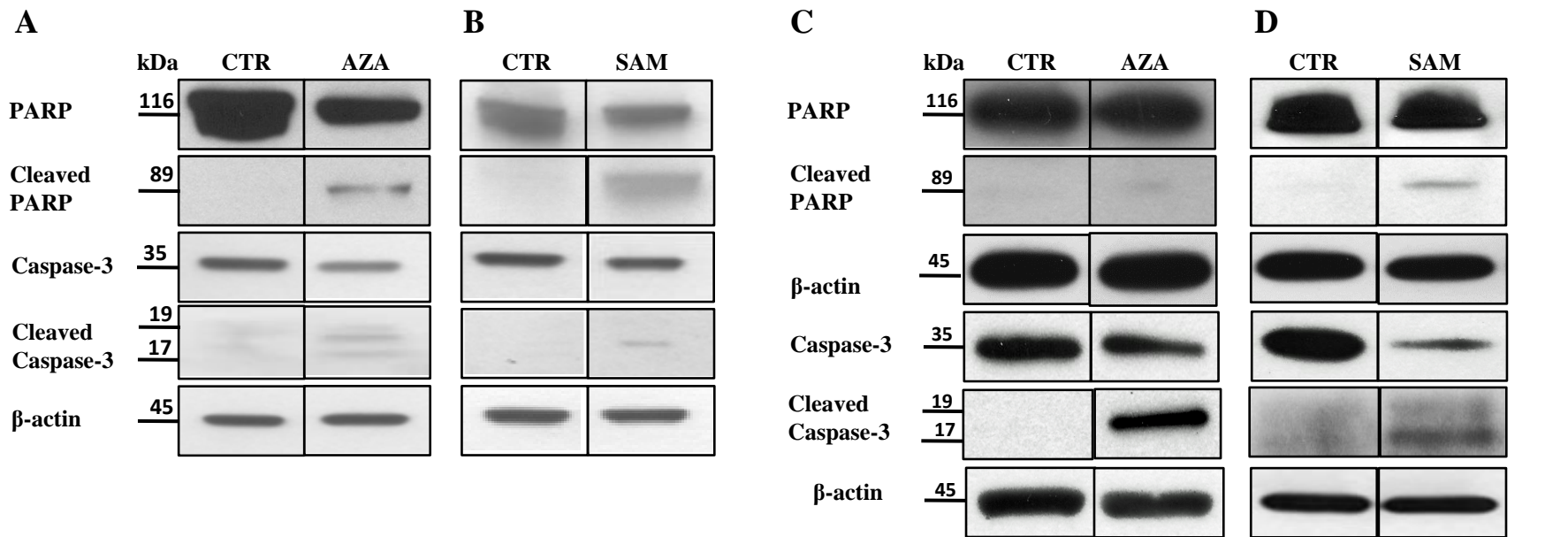
644

645 **Supplementary File 2.** DMRs identified in the comparison between untreated cells and cells treated
646 with AZA

A**B****C****D**



A**B****C****D**



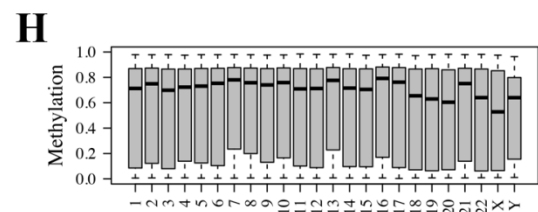
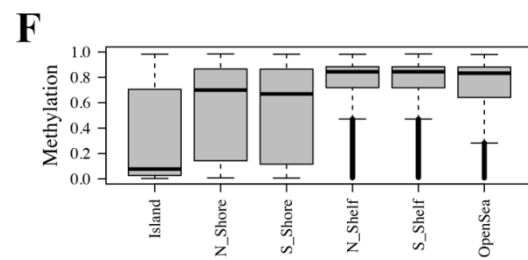
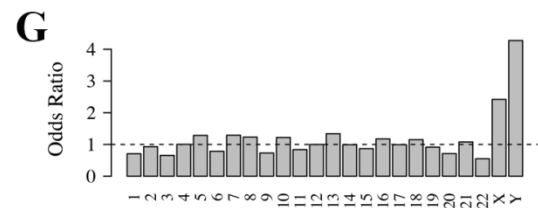
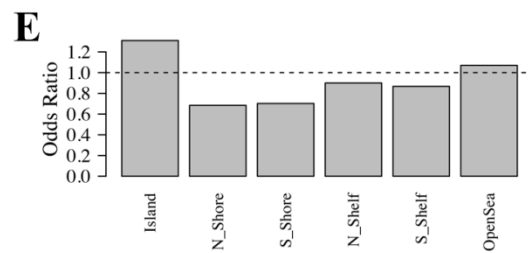
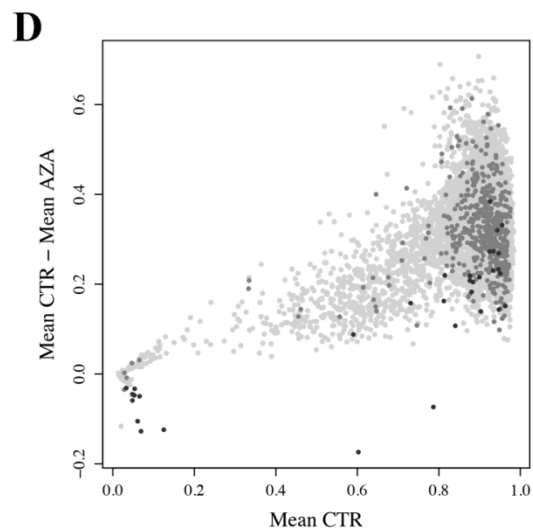
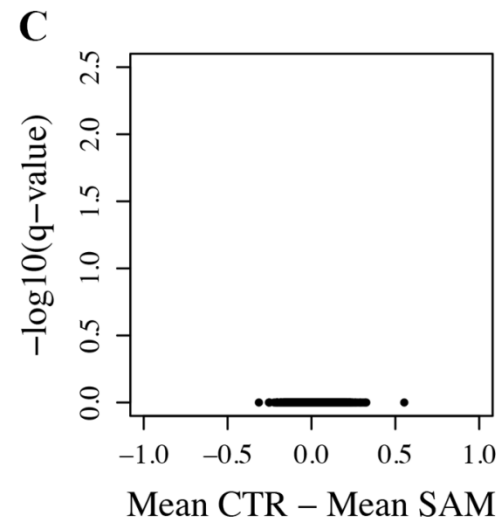
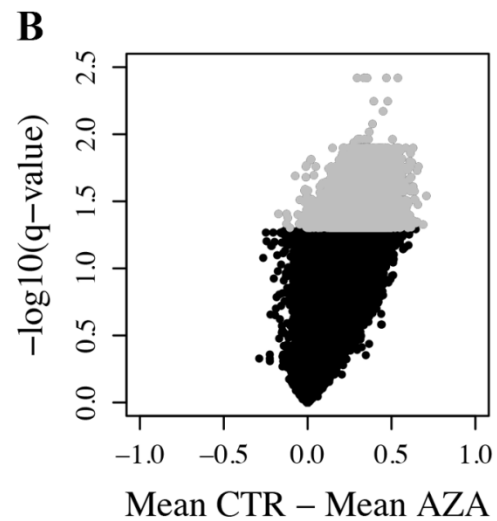
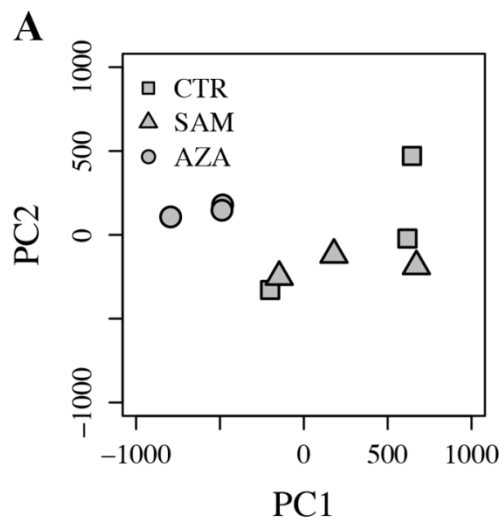


Table 1

DMPs	Chr	Position	UCSC CpG island name	Relation to UCSC CpG island	UCSC RefGene name	q-value
cg19410378	7	152551811	-	-	ACTR3B	0.0038
cg00824714	X	49189225	chrX:49187974-49188588	S-Shore	GAGE2E;GAGE13;GAGE8	0.0038
cg08656053	19	53602096	chr19:53606059-53606784	N-Shelf	ZNF160	0.0038
cg05138918	3	197225707	chr3:197225631-197226150	Island	-	0.0038
cg14531093	14	102973717	chr14:102973317-102976666	Island	ANKRD9	0.0038
cg13021479	17	8380298	chr17:8380172-8380539	Island	MYH10	0.0038
cg25104118	12	125621344	-	-	AACS	0.0057
cg00525828	16	88094415	-	-	BANP	0.0057
cg18694169	6	28227079	chr6:28226979-28227483	Island	NKAPL	0.0068
cg10451760	X	136649093	chrX:136647526-136650178	Island	ZIC3	0.0083
cg18023771	7	24874132	-	-	OSBPL3	0.0096
cg08520423	16	68013968	chr16:68013967-68014545	Island	DPEP3	0.0109
cg04196933	5	178195556	-	-	AACSL	0.0109
cg09205538	15	37783062	chr15:37782884-37783121	Island	-	0.0109
cg15816181	X	82763261	chrX:82763571-82764462	N-Shore	POU3F4	0.0109
cg23719132	13	113525257	-	-	ATP11A	0.0109
cg27532331	8	51404106	-	-	SNTG1	0.0109
cg26738106	X	3265038	chrX:3263353-3265347	Island	MXRA5	0.0115
cg24304658	2	26950770	chr2:26950538-26951474	Island	KCNK3	0.0126
cg15672234	1	11716015	chr1:11714217-11715304	S-Shore	FBXO44;FBXO2	0.0126

Table 2

DMRs	UCSC RefGene name	q-value	Function in PC	References
chr4:3516456-3516844 Island	LRPAP1	0.0337	Lipid transporter: associated with PC progression.	Tousignant et al. 2019
chr7:157208794-157209008 Island	DNAJB6	0.0337	-	-
chr16:23724270-23724775 S-Shore	ERN2	0.0337	Endoplasmic reticulum protein: PC cells escape apoptosis through down-regulation of ERN2.	So et al. 2009
chr19:8649787-8650524 Island	ADAMTS10	0.0337	-	-
chr7:206451-207365 Island	FAM20C	0.0340	Member of the family of secreted protein kinases: involved in the development of bone metastasis in PC.	Quiroz-Munoz et al. 2019
chr15:74290344-74290760 Island	PML	0.0363	Nuclear protein: involved in the regulation of transcription, apoptosis, and cell cycle progression; aberrant down-regulation in PC plays a crucial role in tumor development.	Zhang AY et al. 2019 Birch et al. 2014 Gurrieri et al. 2004 Zhang H et al. 2003
chr19:8028515-8028820 Island	ELAVL1	0.0363	RNA binding protein: involved in translation control, its accumulation is a predictor of adverse clinical behavior in PC.	Melling et al. 2016 Ahadi et al. 2016 Barbisan et al. 2009 Niesporek et al. 2008
chr19:51330212-51330470 Island	KLK15	0.0419	Serine proteases: unfavorable prognostic marker in PC.	Filippou et al. 2018 Mavridis et al. 2013 Rabien et al 2007, 2010
chr20:17595271-17595483 Island	RRBP1	0.0448	Endoplasmic reticulum membrane protein: unfavorable prognostic marker in PC.	Li et al. 2019
chr22:50632707-50633041 Island	TRABD	0.0448	-	-
chr1:27332593-27332982 Island	FAM46B	0.0499	Family with sequence similarity 46 member B: tumor suppressor gene in PC, through ubiquitination of beta-catenin.	Liang et al. 2018
chr1:32713918-32714186 Island	FAM167B	0.0499	-	-
chr1:47902793-47905518 N-Shore	FOXD2	0.0499	Forkhead transcription factor D2: highly expressed in PC.	van der Heul-Nieuwenhuijsen et al. 2009
chr1:115323075-115323462 S-Shore	SIKE1	0.0499	Suppressor of IKBKE 1: IKBKE is over-expressed in PC and may be involved in tumor progression.	Seo et al. 2009
chr1:147380138-147380482 Island	GJA8	0.0499	-	-

chr1:162336876-162337321 N-Shore	NOS1AP	0.0499	Nitric oxide synthase 1 adaptor protein: tumor suppressor gene in PC through Hippo signaling.	Zhang et al. 2015
chr2:176993479-176995557 N-Shore	HOXD8	0.0499	Homeobox D8: transcription factor, epigenetic biomarker that predicts PC progression.	Zhao et al. 2017
chr4:128651419-128651977 Island	SLC25A31	0.0499	-	-
chr5:662283-663402 Island	TPPP	0.0499	-	-
chr5:60139359-60140155 N-Shore	ELOVL7	0.0499	Fatty acid elongase 7: expression reduced the growth of CRPC tumors.	Tolkach et al. 2015

Table 3

Gene Set	Description	Ratio	q-value
hsa04310	Wnt signaling pathway	1.8464	0.00060000
hsa04072	Phospholipase D signaling pathway	1.8102	0.00060000
hsa04390	Hippo signaling pathway	1.7795	0.00060000
hsa05032	Morphine addiction	2.0334	0.00060000
hsa05200	Pathways in cancer	1.3817	0.00060000
hsa05033	Nicotine addiction	2.6369	0.00060000
hsa04550	Signaling pathways regulating pluripotency of stem cells	1.7897	0.00060000
hsa04015	Rap1 signaling pathway	1.6157	0.00070000
hsa04360	Axon guidance	1.6754	0.00070000
hsa04724	Glutamatergic synapse	1.8455	0.00070000

Table 4

Gene Set	Description	Ratio	q-value
GO:0098742	cell-cell adhesion via plasma-membrane adhesion molecules	2.1537	0
GO:0048736	appendage development	2.2451	7.3608e-12
GO:0050808	synapse organization	1.7927	2.5379e-10
GO:0048705	skeletal system morphogenesis	1.9193	3.6902e-9
GO:0007389	pattern specification process	1.6374	1.9951e-8
GO:0061564	axon development	1.5925	2.9000e-8
GO:0097485	neuron projection guidance	1.8207	2.9000e-8
GO:0048568	embryonic organ development	1.6262	2.9000e-8
GO:0048706	embryonic skeletal system development	2.1642	8.0038e-8
GO:0060348	bone development	1.8611	5.4849e-7

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DMPs	Chr	Position	UCSC CpG island name
cg19410378	7	152551811	
cg00824714	X	49189225	chrX:49187974-4918858
cg08656053	19	53602096	chr19:53606059-536067
cg05138918	3	197225707	chr3:197225631-197226
cg14531093	14	102973717	chr14:102973317-10297
cg13021479	17	8380298	chr17:8380172-8380539
cg25104118	12	125621344	
cg00525828	16	88094415	
cg18694169	6	28227079	chr6:28226979-2822748
cg10451760	X	136649093	chrX:136647526-136650
cg18023771	7	24874132	
cg08520423	16	68013968	chr16:68013967-680145
cg04196933	5	178195556	
cg09205538	15	37783062	chr15:37782884-377831
cg15816181	X	82763261	chrX:82763571-8276446
cg23719132	13	113525257	
cg27532331	8	51404106	
cg26738106	X	3265038	chrX:3263353-3265347
cg24304658	2	26950770	chr2:26950538-2695147
cg15672234	1	11716015	chr1:11714217-1171530
cg07225966	10	94820376	chr10:94820026-948232
cg18023065	11	94278603	chr11:94276894-942789
cg21789510	2	91873084	chr2:91873047-9187452
cg19320476	11	82443592	chr11:82443435-824449
cg13307142	X	74743056	chrX:74742765-7474311
cg18202521	1	19600702	chr1:19600249-1960094
cg11781335	10	30818581	
cg21725496	7	5372402	chr7:5372280-5372717
cg23012683	14	105187498	chr14:105186698-10518
cg10023749	12	132303409	
cg11140305	1	249106302	chr1:249106095-249106
cg23363832	3	139258939	chr3:139257712-139257
cg09868359	21	43230669	chr21:43230458-432307
cg25137968	1	120905306	chr1:120905971-120906
cg07532183	8	120684968	
cg18509722	X	24331994	chrX:24331643-2433234
cg10336039	17	76834989	chr17:76836060-768374
cg18481342	11	1782709	chr11:1784805-1785553
cg01299774	5	565934	chr5:561826-565967
cg23260105	5	1218653	chr5:1218487-1218704
cg16732616	1	50886782	chr1:50884228-5089147
cg13515842	9	127215440	chr9:127215291-127216
cg27198114	12	133132130	chr12:133131896-13313
cg20078054	3	127339608	
cg18092028	20	59827212	chr20:59826977-598289
cg00913953	1	6189040	chr1:6188873-6189120
cg14880205	X	34150470	chrX:34148740-3414895
cg20019985	11	32008961	chr11:32008802-320090
cg20141398	1	2928616	chr1:2929155-2929376
cg06279276	16	67184164	chr16:67183208-671849
cg15717258	5	140537705	chr5:140536896-140537
cg23688334	7	1946397	chr7:1950279-1950482

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cg11667387	10	104835919	
cg09121928	16	75271179	chr16:75269028-752698
cg01224510	16	88034065	chr16:88032156-880349
cg10482495	X	71351314	chrX:71350941-7135213
cg24492446	8	141572291	
cg00610508	16	4013337	chr16:4015001-4015232
cg00879606	19	8028761	chr19:8028515-8028820
cg10544018	14	101535442	chr14:101531643-10153
cg08538682	3	158390336	
cg07911905	12	105096644	
cg06291428	11	57559063	
cg13473894	10	13771383	
cg03524083	18	70534316	chr18:70533965-705368
cg21131796	12	124829443	chr12:124829153-12482
cg08187983	16	87670386	
cg08437789	10	135085344	chr10:135083739-13508
cg26316452	X	40692474	chrX:40691960-4069244
cg26144456	X	108779006	chrX:108780054-108780
cg19989295	14	24641077	chr14:24641053-246422
cg10421979	17	48546321	chr17:48545570-485469
cg21887309	5	140209490	chr5:140208753-140209
cg13440244	X	52896774	
cg15412228	14	104718313	
cg10547527	2	198650123	chr2:198649751-198651
cg17025688	1	2107410	
cg08582182	7	101478535	
cg05583608	16	51147536	chr16:51147490-511479
cg00148867	7	66751227	chr7:66751106-6675133
cg25994622	19	15582775	chr19:15582605-155829
cg21232767	7	157619282	chr7:157618856-157619
cg06702718	12	132921327	chr12:132922117-13292
cg02008936	14	105187362	chr14:105186698-10518
cg11762838	17	80863711	chr17:80863327-808637
cg03018369	11	71187445	
cg03540794	5	2112109	chr5:2111836-2112484
cg04498198	17	27899966	chr17:27899511-279000
cg13132307	17	10533415	
cg13742952	10	131567801	
cg17268992	X	72666981	chrX:72667157-7266759
cg26804360	2	239982769	
cg25987871	8	141231538	
cg15295597	Y	4868368	chrY:4867956-4868586
cg09648313	6	736838	
cg25572565	7	155142756	chr7:155142688-155143
cg27471304	X	124339778	chrX:124338904-124339
cg06293719	7	889564	chr7:886803-887535
cg14388804	6	15521099	chr6:15517282-1551755
cg20984994	X	40064789	chrX:40064743-4006499
cg08402381	10	34587560	
cg19123465	12	133131971	chr12:133131896-13313
cg15427886	8	55379663	chr8:55378928-5538018
cg14073057	17	78796363	chr17:78796078-787963
cg06674527	15	65369928	chr15:65369126-653704
cg07475957	5	140590251	chr5:140589744-140590
cg18297751	5	140798971	chr5:140798757-140799

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cg08548396	6	30095549	chr6:30095173-3009561
cg22596411	17	80976941	chr17:80975646-809762
cg11834106	6	31747010	
cg12116395	X	40441216	chrX:40439739-4044070
cg19351954	7	156259207	
cg15051239	2	131583886	
cg12857407	X	151903194	
cg26799656	16	88458669	chr16:88459515-884597
cg04640920	15	37180889	chr15:37179516-371797
cg09350919	Y	9365070	chrY:9365289-9365809
cg20844384	X	69282289	chrX:69282384-6928328
cg25721452	12	102133339	chr12:102132753-10213
cg03991547	13	112815119	chr13:112817816-11281
cg16706374	14	100793650	chr14:100795072-10079
cg06750897	1	164545553	chr1:164545540-164545
cg07602740	6	32025960	
cg05656763	12	133118770	
cg06153873	16	4056360	
cg09169456	16	84695433	chr16:84695169-846956
cg11761622	6	25726956	chr6:25726454-2572672
cg27325462	11	129903118	chr11:129902811-12990
cg20108119	19	1393304	chr19:1393155-1393470
cg25921813	3	194797138	
cg18401451	21	46376494	chr21:46378278-463786
cg13352750	7	27225123	chr7:27225050-2722562
cg17882374	17	78041429	chr17:78039291-780395
cg27576434	3	122840254	
cg10554639	7	793518	chr7:793118-793767
cg12309653	15	37170454	chr15:37172473-371730
cg06426011	16	12798592	
cg08384999	X	40004346	chrX:40004305-4000453
cg15241633	7	86415945	chr7:86415620-8641611
cg12661256	15	31745916	chr15:31745466-317457
cg23311252	12	132835050	chr12:132834178-13283
cg26521404	7	27204981	chr7:27203915-2720646
cg03370193	X	31284813	chrX:31284504-3128501
cg23930711	5	140734758	chr5:140734720-140735
cg16306898	1	1475675	chr1:1476093-1476669
cg22010791	X	31090296	chrX:31089886-3109033
cg22821947	11	133837401	
cg11227064	8	6479776	
cg06878303	X	151903174	
cg20707679	19	3434945	chr19:3434929-3435417
cg19878627	2	54087184	chr2:54086776-5408726
cg05909343	10	133051487	
cg17426146	20	62126289	chr20:62125930-621264
cg24569831	15	93617168	chr15:93615622-936171
cg11859529	X	70150922	chrX:70150675-7015100
cg13955432	7	117864720	
cg06846819	11	68850022	chr11:68849897-688505
cg15488660	2	242519181	chr2:242519162-242519
cg10215339	13	112905729	
cg09525227	X	103500030	chrX:103498706-103499
cg22152229	5	140208954	chr5:140208753-140209
cg25490145	17	80358850	chr17:80361614-803621

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cg24122498	17	4648682	
cg17694851	8	1707553	chr8:1711234-1712654
cg04906467	16	50092519	
cg11130778	5	176296658	chr5:176296541-176296
cg09293286	X	3235329	chrX:3235151-3235731
cg11554566	21	47398596	chr21:47401108-474014
cg22078907	17	20920756	
cg20600051	4	22636672	
cg01472951	12	5603816	chr12:5603587-5603990
cg19737787	13	28492265	chr13:28491488-284925
cg10505163	10	73466728	
cg26763877	8	4851751	chr8:4848968-4852635
cg24408776	1	203098067	chr1:203097233-203097
cg18406033	2	223159869	chr2:223159725-223160
cg02238387	17	77964734	chr17:77965805-779662
cg00104845	5	140892370	chr5:140892913-140893
cg23217622	1	156405438	chr1:156405160-156406
cg21104965	6	117869453	chr6:117869097-117869
cg09051235	8	7429853	
cg21811204	5	132158625	chr5:132158542-132159
cg11024341	5	2041368	chr5:2038527-2038949
cg06538774	22	24584247	chr22:24584178-245843
cg21445553	20	23969237	chr20:23969149-239694
cg17807479	17	11145042	chr17:11143487-111454
cg15812020	13	25506235	chr13:25506113-255063
cg12485020	X	110039269	chrX:110038946-110039
cg02777670	13	24797637	
cg18921306	7	75596055	
cg00593773	18	77336201	chr18:77336081-773362
cg01688536	7	35296968	chr7:35296921-3529821
cg21842944	7	98985712	
cg22053108	8	144885612	chr8:144885269-144886
cg08484668	6	157472027	
cg17400113	15	93617146	chr15:93615622-936171
cg04676446	X	152954816	
cg06234730	12	132199443	chr12:132195034-13219
cg13174084	2	84517877	chr2:84517714-8451795
cg00221747	11	2152428	chr11:2154033-2154387
cg26917697	16	1160677	
cg27096032	16	12210910	chr16:12210655-122112
cg08980987	12	25054905	chr12:25055599-250562
cg19539224	3	125439871	
cg03469578	4	3735986	
cg11551464	8	49595738	
cg21006325	21	44480624	chr21:44480559-444807
cg17540192	7	97875259	
cg05050072	14	96707554	
cg10208897	5	178548229	chr5:178547421-178548
cg24691854	X	139593162	chrX:139593105-139593
cg17341113	11	69237570	
cg12415455	1	2846998	chr1:2847056-2847288
cg14193007	17	77953016	chr17:77951845-779522
cg12667021	8	1588618	chr8:1590038-1592282
cg09263516	12	115107338	chr12:115104848-11510
cg12712747	13	110900663	

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cg26298294	5	6755150	chr5:6755104-6755387
cg01340310	17	536443	
cg26897717	19	39691363	chr19:39690976-396913
cg20210482	11	126286493	chr11:126286451-12628
cg05114100	X	114524286	
cg01082498	11	68608225	chr11:68608155-686094
cg10737412	13	114174980	
cg10346077	X	145701720	chrX:145700793-145702
cg05369327	14	95826853	chr14:95826675-958269
cg03590420	11	132662963	
cg02737268	20	3780182	chr20:3776198-3776419
cg02864619	17	78933961	chr17:78935043-789353
cg14050824	9	140683797	chr9:140683120-140683
cg17091049	1	1860127	chr1:1859246-1859523
cg19289355	7	127260012	
cg06594404	4	380396	chr4:379899-380399
cg07002602	17	17124752	chr17:17124698-171249
cg22718140	17	15217411	
cg21382589	2	8785969	chr2:8785459-8786072
cg03769817	X	99666219	chrX:99666131-9966638
cg20202246	X	118407296	chrX:118406941-118407
cg10447827	8	142178476	
cg24391203	11	49837274	chr11:49839280-498395
cg05777400	1	147380398	chr1:147380138-147380
cg24296761	19	42408458	chr19:42408315-424085
cg17331904	7	23749977	
cg17582546	X	49592789	
cg04382920	4	128651526	chr4:128651419-128651
cg11599887	5	1552064	chr5:1553035-1553269
cg16537589	16	88044443	chr16:88044296-880445
cg08863777	11	94278457	chr11:94276894-942789
cg00531246	13	114174973	
cg24637044	6	30039013	chr6:30038881-3003947
cg21897676	13	113428161	chr13:113429177-11342
cg26681770	20	56247302	chr20:56247249-562476
cg06501366	5	78365687	chr5:78365298-7836571
cg21040726	12	109985255	
cg23832787	X	3264728	chrX:3263353-3265347
cg06743060	21	47166624	chr21:47165786-471669
cg09642925	2	114261793	chr2:114260095-114261
cg09869144	16	83948818	
cg02722214	10	121578137	chr10:121577529-12157
cg18496502	19	42880157	chr19:42879637-428802
cg02375347	2	236648327	
cg25283432	12	125282561	
cg25512107	17	78831167	chr17:78831505-788318
cg25793425	19	6007842	chr19:6007829-6008225
cg04383154	17	80968667	chr17:80969748-809701
cg11467141	2	132348705	chr2:132348566-132348
cg06638980	22	22471930	chr22:22471899-224727
cg07137955	5	42992774	chr5:42992033-4299295
cg06442865	17	48913413	
cg08767743	7	158673942	chr7:158669800-158670
cg03548062	14	101158251	
cg09769113	6	30131719	

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cg10061374	8	5909945	
cg27250236	6	48036617	chr6:48036137-4803641
cg06332339	15	73889528	
cg13482308	9	37002685	chr9:37002489-3700295
cg18005337	2	98340655	chr2:98340397-9834095
cg02057688	6	2697758	
cg09579361	1	2116287	chr1:2116432-2116801
cg26750548	10	88441152	
cg08699341	13	114193224	chr13:114195709-11419
cg04920535	2	233321738	chr2:233323380-233323
cg18344811	7	822633	chr7:821689-822634
cg25596655	19	38185862	chr19:38182793-381833
cg08464831	16	5951274	
cg02714462	X	30265188	chrX:30265172-3026555
cg26038441	X	2836027	chrX:2835949-2836236
cg23138608	14	91770145	chr14:91770110-917704
cg19937061	13	25320133	chr13:25319668-253222
cg19572849	13	49076914	
cg00401797	1	3315193	
cg09348504	2	209025539	
cg19580937	15	70740429	
cg27224718	8	135614730	
cg19924619	1	165323692	chr1:165323486-165323
cg20457193	1	32645180	chr1:32645154-3264581
cg00501869	7	157690732	chr7:157690559-157690
cg04530981	16	1786516	chr16:1790363-1790708
cg08200869	5	140807666	chr5:140807339-140807
cg12793123	22	24823554	chr22:24819537-248208
cg16649298	7	158664174	
cg18476631	X	152954833	
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cg15956049	8	1850864	
cg08083988	19	38040340	chr19:38039561-380403
cg00976097	5	421733	chr5:421224-421751
cg17137424	1	231299352	chr1:231297812-231299
cg01367666	16	2052269	chr16:2052209-2052718
cg13031882	3	195701118	
cg02920514	3	195610120	chr3:195613588-195613
cg19716727	7	4794309	chr7:4794117-4794525
cg18807030	7	931980	chr7:931767-932014
cg22153345	8	651449	chr8:651163-651453
cg08760128	16	4723507	
cg16733705	12	85667616	
cg06963308	16	84252035	
cg22346429	12	132504721	
cg10632969	11	134023334	
cg08266619	22	19776364	chr22:19776196-197764
cg11409998	X	139587372	chrX:139585867-139588
cg00325125	11	58736081	
cg21154964	7	43484715	chr7:43484390-4348512
cg01622930	4	3960266	chr4:3956663-3958275
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cg07590638	5	38631548	
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cg05397886	7	139992453	chr7:139992321-139992
cg09795422	X	44703298	chrX:44703485-4470389
cg21331812	X	102319001	chrX:102318601-102319
cg18468394	5	170736021	chr5:170735169-170739
cg04757806	11	94278595	chr11:94276894-942789
cg04484550	1	2980163	chr1:2979275-2980758
cg08589821	5	55033950	chr5:55033694-5503399
cg15693780	8	117543400	
cg04549333	11	44325823	chr11:44325657-443265
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cg17346246	12	123214864	
cg08380311	19	3435252	chr19:3434929-3435417
cg02973171	11	82443614	chr11:82443435-824449
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cg11993252	11	2721961	chr11:2720410-2722087
cg08560074	5	169532686	chr5:169533080-169533
cg15705062	19	5110748	chr19:5110587-5110853
cg18322023	17	7141420	chr17:7141121-7143071
cg09667606	6	158507930	chr6:158507719-158508
cg22189618	X	92928608	chrX:92928546-9292878
cg13325231	5	1342170	chr5:1344545-1345469
cg01277910	14	91795105	
cg21595968	X	150396241	chrX:150396220-150396
cg23238709	7	155574363	chr7:155573602-155573
cg10701252	3	55508585	chr3:55508336-5550870
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cg04623837	6	29943414	chr6:29944402-2994516
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cg19437757	7	157697057	chr7:157695025-157695
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cg09425262	X	147062672	chrX:147062671-147062
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cg05928290	14	54418728	chr14:54418677-544188
cg01220680	20	866011	chr20:865828-866064
cg19426459	12	132554069	
cg21480420	X	119445407	chrX:119444859-119445
cg01590076	8	70246362	
cg18943033	6	168993309	
cg02894810	X	118284617	chrX:118284519-118285
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cg02264195	16	3724381	chr16:3724344-3724849
cg22942245	6	32036179	
cg05829046	7	2557446	chr7:2558371-2559967
cg07400057	11	7111072	chr11:7110132-7111376
cg03440272	X	51139066	chrX:51138953-5113925
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cg06857845	16	88909425	chr16:88908433-889086
cg24641901	11	93212232	
cg12337622	7	158050413	
cg20009378	13	114325829	
cg21726327	17	6018	
cg08502383	19	1377233	chr19:1376554-1377568
cg17825572	X	64626582	chrX:64626743-6462804
cg10652674	10	62023665	
cg01800442	17	74086473	
cg10024484	20	20435885	chr20:20433105-204333
cg21356851	13	114180126	
cg24352349	22	45597767	chr22:45598721-455990
cg05191217	5	154070325	chr5:154070260-154070
cg10433678	8	144943023	chr8:144942911-144943
cg14899145	4	1333483	chr4:1333378-1333676
cg04242349	17	79082840	chr17:79084336-790845
cg05214685	2	223177493	chr2:223176493-223177
cg01206697	11	45420355	
cg03307425	4	866811	chr4:866098-866344
cg11801727	1	228659093	chr1:228658937-228659
cg05212510	18	77623544	chr18:77623265-776242
cg24039697	10	8094534	chr10:8091374-8098329
cg19961545	2	54087066	chr2:54086776-5408726
cg12782180	7	127880932	chr7:127880750-127881
cg27350602	X	136630265	chrX:136629544-136630
cg23495279	8	4849827	chr8:4848968-4852635
cg04717534	10	75633052	chr10:75633600-756347
cg27241044	13	23499838	chr13:23500589-235013
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cg07116631	16	3345463	chr16:3345145-3345605
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cg23808182	11	1306868	chr11:1302772-1302982
cg26638505	2	31806183	chr2:31805293-3180640
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cg24667575	5	172097064	chr5:172096731-172097
cg11526462	6	30309578	chr6:30312837-3031341
cg09832244	12	6729600	chr12:6729248-6730310
cg07630035	6	93354486	
cg00636427	18	77190089	chr18:77193463-771937
cg24669311	17	20747058	chr17:20746783-207476
cg05667401	16	31073266	chr16:31072988-310736
cg19048532	7	27148002	chr7:27147589-2714838
cg24118521	13	47472330	
cg17949813	7	1801521	
cg01176947	6	10385279	chr6:10384965-1038549
cg05934015	12	129280265	chr12:129280256-12928
cg23257934	1	234858982	
cg26966828	8	10208257	

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cg06255006	16	86653215	
cg26248373	2	1572462	chr2:1571951-1573123
cg24033503	14	101005128	chr14:101004067-10100
cg19163067	1	36042438	chr1:36042432-3604344
cg21047695	8	63614552	
cg05827468	13	90015633	chr13:90015412-900157
cg05075473	2	1843120	chr2:1842846-1843137
cg05346688	15	92459525	chr15:92459266-924596
cg13485703	17	21730179	chr17:21729786-217302
cg10533694	14	105181370	chr14:105181017-10518
cg10664842	4	7710280	
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cg26365014	10	134622019	chr10:134622423-13462
cg22548831	19	398562	chr19:401970-402280
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cg24944959	8	142445786	
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cg01013491	X	135180748	chrX:135180417-135180
cg10693767	17	78773124	chr17:78775591-787758
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cg15876513	10	1149726	chr10:1147967-1148271
cg05845376	5	140683632	chr5:140683195-140683
cg20215769	2	36706722	
cg20429954	7	126446875	
cg12544191	5	172671754	chr5:172670829-172671
cg18490269	7	1849928	
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cg15391375	7	150110226	
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cg25630506	8	1510176	chr8:1509850-1511735
cg15067764	12	84405423	
cg13301423	5	177986696	
cg16178603	2	66667101	
cg13474414	1	205500676	chr1:205498003-205498
cg27097992	14	104800950	chr14:104800444-10480
cg02155398	2	45160490	chr2:45161427-4516305
cg00249621	8	98290359	chr8:98289604-9829040
cg23239891	19	8808017	chr19:8807813-8808794
cg20611882	1	68696709	chr1:68696639-6869762
cg16743903	16	89593216	chr16:89593169-895933
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cg27198013	17	17714293	chr17:17712911-177144
cg15057747	10	1205673	chr10:1205562-1205859
cg03439958	2	101612331	
cg14343513	17	78753273	
cg00422714	16	1814418	chr16:1814084-1814482
cg25074317	8	144812633	chr8:144808221-144810
cg26423041	6	4794490	
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cg02867242	6	31832445	chr6:31830299-3183094
cg06672737	4	778827	chr4:778661-780592
cg25297146	10	679399	chr10:678262-679515
cg26904215	21	47823096	chr21:47823082-478241
cg25519281	7	63028277	chr7:63028071-6302833
cg14751199	7	1991939	chr7:1991914-1992122
cg18983789	10	133457589	chr10:133458017-13345
cg02823457	17	47583920	chr17:47583606-475840
cg19625524	4	1803148	chr4:1803076-1805672
cg21167716	12	132896743	chr12:132896299-13289
cg02477603	10	125034296	
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cg12517318	4	529948	chr4:529848-530049
cg04964672	Y	7428198	chrY:7428179-7428424
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cg09653758	16	19883256	
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cg06625916	X	41332957	chrX:41332738-4133412
cg18422972	X	40029227	chrX:40028925-4002931
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cg13447295	6	887704	chr6:887605-887908
cg04142643	17	75478263	
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cg20387695	8	711085	
cg17380661	6	100912946	chr6:100912071-100913
cg01706334	8	72872845	
cg09731745	10	134473515	chr10:134477298-13447
cg10067723	13	113807384	chr13:113807288-11380
cg20081453	X	51138790	chrX:51138953-5113925
cg09105442	10	1228439	chr10:1230813-1231214
cg19306958	22	46782343	chr22:46785171-467853
cg15035437	X	63005077	
cg05694921	1	29587117	chr1:29587087-2958741
cg14474302	15	101093778	chr15:101094520-10109
cg06406458	10	128810499	
cg06951122	5	140222653	chr5:140222122-140223
cg11576274	1	146552552	chr1:146552328-146552

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cg09657173	6	30923593	chr6:30923208-3092362
cg05972308	16	31476161	chr16:31475788-314762
cg05642789	1	1564482	chr1:1564421-1570006
cg06535952	19	56126775	chr19:56125349-561281
cg18623351	7	114813677	
cg16615154	6	40567553	chr6:40567266-4056758
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cg12465250	6	163521043	chr6:163520984-163521
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cg11070172	14	23586812	
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cg19001199	10	133955570	chr10:133953845-13395
cg08701047	10	130085199	
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cg23949969	5	180219412	chr5:180219007-180219
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cg20606821	10	134719971	chr10:134719934-13472
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cg05141695	6	341180	
cg26923547	14	104640527	chr14:104640469-10464
cg05495790	10	743286	chr10:743240-743479
cg21350392	13	30079047	chr13:30077245-300774
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cg19346371	12	115120789	chr12:115120774-11512
cg15611336	15	75248496	chr15:75248277-752499
cg00729564	8	1857241	
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cg23811942	11	128813470	
cg10072464	13	114064536	chr13:114066946-11406
cg05703749	16	88027707	
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cg23615262	1	166766052	
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cg15475285	6	26247246	chr6:26246815-2624710
cg21283340	5	16701575	chr5:16701071-1670177
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cg15935877	Y	9303715	chrY:9303622-9303934
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cg09998941	X	27826007	
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cg10125522	21	47344376	chr21:47343715-473451
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cg13618741	9	137535210	chr9:137533359-137534
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cg15281205	Y	21100472	
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cg26785230	16	66969735	chr16:66969499-669698
cg16850623	10	48413758	chr10:48413741-484139
cg03401726	11	2721248	chr11:2720410-2722087
cg23076870	10	135174003	chr10:135170645-13517
cg17211612	12	124330647	
cg25249207	19	56125145	chr19:56125349-561281
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cg16208053	10	135379215	chr10:135378883-13537
cg21497990	7	155255122	chr7:155255098-155255
cg12057563	X	135230841	chrX:135228947-135230
cg18114166	X	36982033	chrX:36981567-3698211
cg26394771	5	140531420	chr5:140531157-140532
cg06058235	X	154113543	chrX:154113124-154113
cg19182279	4	892011	chr4:893911-894186
cg05302825	6	170024559	
cg27096779	7	15726466	
cg04995493	1	2572909	chr1:2574030-2574864
cg16326123	2	240015886	
cg14730445	12	101603581	chr12:101603387-10160
cg00723997	X	48690473	chrX:48689589-4869082
cg07910065	10	4230752	
cg06910254	16	3185002	chr16:3184276-3185312
cg27041022	X	151935162	chrX:151938000-151938
cg18004371	11	5950357	
cg02893344	16	85517269	chr16:85519109-855193
cg22397926	8	83290913	

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cg16272981	5	1489889	chr5:1489799-1490071
cg09017434	5	16179660	chr5:16179064-1618042
cg07094915	7	27279101	chr7:27278945-2727946
cg05123368	X	37026697	chrX:37026348-3702670
cg09568556	13	113140301	chr13:113140124-11314
cg04494136	10	126703576	
cg04492929	16	2155436	chr16:2155867-2156884
cg21127068	3	147124417	chr3:147126988-147128
cg13078134	4	165109478	chr4:165109389-165109
cg02061626	2	233274167	chr2:233274080-233274
cg07452164	7	72993570	chr7:72992434-7299339
cg14601621	9	97848457	chr9:97848140-9784852
cg00436476	6	26240505	chr6:26240697-2624095
cg14451382	5	1876397	chr5:1874907-1879032
cg18850127	7	39170497	
cg00647217	1	165086866	chr1:165086756-165087
cg08442149	10	1767484	
cg19599827	6	596273	
cg00445126	2	63276010	chr2:63274475-6327943
cg19717586	11	131781257	chr11:131780328-13178
cg05437476	16	88233989	chr16:88233988-882341
cg26703128	11	69199398	
cg09608716	16	88455742	chr16:88453549-884539
cg12026967	18	19780728	chr18:19780619-197808
cg13506244	X	62647814	
cg02656891	1	34642519	chr1:34642382-3464302
cg05487769	7	23530633	chr7:23530434-2353069
cg13918058	1	179556346	chr1:179555401-179555
cg27036347	14	69341603	chr14:69341427-693418
cg09687738	X	113818934	chrX:113818519-113819
cg10399970	7	12510772	
cg06293983	X	135863104	
cg20741134	1	181382639	chr1:181382290-181382
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cg01849466	14	104193079	chr14:104193901-10419
cg12836313	7	156733574	chr7:156733539-156734
cg18700416	10	133938970	chr10:133937695-13393
cg19046826	17	48546297	chr17:48545570-485469
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cg23510258	17	80840821	
cg02089929	16	84812726	
cg20215598	4	763475	
cg21167532	1	33231272	
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cg13682598	10	135195405	chr10:135191594-13519
cg20462129	17	78607095	
cg26191724	10	133876051	chr10:133879005-13387
cg11091909	13	33640726	
cg11469098	8	49647809	chr8:49647702-4964798
cg14211055	21	47704251	chr21:47705627-477064

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cg08409113	17	40937365	chr17:40937258-409374
cg25397840	17	78073434	chr17:78074902-780757
cg00346501	1	16073336	chr1:16073318-1607352
cg02066716	1	2112006	
cg01451203	15	22955743	
cg01447429	16	29222265	
cg23542274	11	45718455	
cg20959907	7	111368847	chr7:111368366-111368
cg06938654	X	21875563	chrX:21875378-2187563
cg10155891	16	88941576	chr16:88943427-889436
cg17943757	3	10417161	
cg25529393	6	27858380	chr6:27858166-2785856
cg05740106	6	169273346	
cg10666224	6	29768246	chr6:29768025-2976833
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cg21216268	3	169847102	
cg14899164	7	4823857	chr7:4823506-4824097
cg00767000	16	87525307	
cg08829140	7	101559608	chr7:101559402-101559
cg11524400	11	1778524	chr11:1774588-1775040
cg02833016	8	139890086	chr8:139889881-139890
cg21697794	6	30095269	chr6:30095173-3009561
cg04591032	17	46827458	chr17:46827435-468276
cg27238852	16	58192174	
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cg13746854	9	34370894	chr9:34370773-3437290
cg09848445	10	43601862	chr10:43600146-436011
cg27457201	17	78854232	chr17:78857630-788578
cg13754915	9	140174272	chr9:140172613-140176
cg13215995	17	43222258	chr17:43221927-432223
cg06360427	18	74962672	chr18:74961556-749638
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cg23987846	8	651301	chr8:651163-651453
cg27363741	6	6005349	chr6:6006689-6007043
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cg12200038	14	38091470	chr14:38091469-380921
cg14045327	19	387968	chr19:387964-388350
cg27006650	14	29236034	chr14:29236835-292378
cg19054524	20	21686273	chr20:21686199-216876
cg13802506	9	95888884	
cg11153505	13	113378377	
cg05835309	4	3748554	chr4:3748224-3748581
cg24789467	5	132159003	chr5:132158542-132159
cg20503077	X	49236806	chrX:49235589-4923620
cg04086189	10	102642531	
cg23618269	11	1215457	chr11:1215375-1215986
cg14068146	5	176940708	chr5:176943525-176944
cg24748548	10	135153961	chr10:135148196-13515
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cg02128981	11	58904901	
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cg09396068	15	22940794	
cg17785250	5	140554081	chr5:140553681-140554
cg19053358	X	110039078	chrX:110038946-110039
cg21270593	7	94293250	chr7:94293609-9429386
cg06670039	16	12530246	
cg08381537	19	310296	chr19:310258-310582
cg06587955	Y	9368165	chrY:9364545-9364859
cg00381974	18	44260357	chr18:44259905-442604
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cg24005260	7	1138185	chr7:1141229-1141545
cg21526172	19	18980110	chr19:18979351-189812
cg06424138	8	102701376	
cg04667538	2	105372176	
cg07721276	19	18119064	chr19:18118741-181195
cg18209323	7	92672878	chr7:92672789-9267301
cg15044957	11	30038672	chr11:30038522-300388
cg01272937	16	84812514	
cg23306089	7	1885248	chr7:1885033-1885402
cg26343001	12	115104274	chr12:115104848-11510
cg20113888	7	100732273	chr7:100732088-100732
cg23476456	X	110039192	chrX:110038946-110039
cg07984614	10	126314798	
cg14925024	1	228291705	chr1:228289669-228291
cg22198853	6	1594411	
cg05732750	7	6704045	chr7:6703503-6704075
cg20484507	X	21392617	chrX:21391835-2139340
cg24169503	2	159723831	
cg13848087	12	89893700	
cg17279652	5	180622276	chr5:180622178-180622
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cg05209525	19	18255980	chr19:18255822-182560
cg18863595	3	6902845	chr3:6902823-6903516
cg14223613	15	80884071	
cg19073447	10	134024191	
cg06063209	3	195602274	chr3:195600845-195602
cg11413039	11	125774447	chr11:125774292-12577
cg18293441	11	134534264	chr11:134534242-13453
cg26969786	8	50891848	
cg23618440	6	48036605	chr6:48036137-4803641
cg07820332	12	127101141	
cg17649599	3	84175248	
cg09787554	1	19209892	chr1:19209626-1920991
cg25424856	X	50557036	chrX:50556224-5055717
cg06756931	17	78820893	chr17:78818440-788186
cg10917426	6	31867698	chr6:31867691-3186795
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cg02349468	5	1093661	chr5:1093579-1093837
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cg00731608	14	103593907	chr14:103593234-10359
cg06011441	16	88328938	
cg14839905	11	68183723	chr11:68181086-681812
cg23244790	5	140811102	chr5:140810494-140812
cg00530568	5	135587383	
cg05435315	10	133872448	
cg24478926	11	69237550	
cg25260137	8	65282185	chr8:65281903-6528304
cg14951132	X	105067038	chrX:105066349-105067
cg22816462	8	6633067	
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cg10938556	14	105126275	chr14:105126190-10512
cg05742082	12	129636122	
cg17055721	4	749157	chr4:752029-753788
cg14480594	9	111625292	
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cg11670605	5	41510851	chr5:41509783-4151016
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cg01995289	8	145939351	chr8:145938492-145939
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cg12072028	14	92981227	chr14:92979726-929812
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cg05616550	17	54675154	chr17:54674873-546752
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cg17240275	15	75500943	chr15:75500858-755011
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cg16870351	X	136651271	chrX:136651178-136651
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cg09228536	7	16708976	
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cg10331100	16	88966509	chr16:88966202-889665
cg24359671	11	64030212	chr11:64025913-640267
cg11418477	2	175199741	chr2:175199463-175202
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cg07036799	16	85667676	chr16:85667565-856678
cg09639931	17	38024394	chr17:38024145-380246
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cg21026426	7	156754584	
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cg23782833	7	218121	chr7:218309-218951
cg26027669	1	92952467	chr1:92945907-9295260
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cg18336674	5	170735264	chr5:170735169-170739
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cg10067182	2	239974554	chr2:239974439-239974
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cg13373361	7	98885594	
cg22627940	8	49390241	
cg17742293	5	14461138	chr5:14461130-1446146
cg02632809	7	5336811	chr7:5336513-5336894
cg12332083	11	1296469	chr11:1298009-1298476
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cg03730428	11	32009004	chr11:32008802-320090
cg27665489	X	51075530	chrX:51075272-5107633
cg23023126	19	308808	chr19:308413-308930
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cg00318897	16	88268362	chr16:88268113-882683
cg13770495	X	37404519	chrX:37404358-3740461
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cg07237653	8	28950303	
cg02387803	3	147123457	chr3:147126988-147128
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cg05505758	16	425399	chr16:426038-426290
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cg13777717	5	76250527	chr5:76249435-7625052
cg20594982	1	976707	chr1:975496-980305
cg03707183	7	4901449	chr7:4901336-4901753
cg16906092	8	125183790	
cg00021786	X	31090306	chrX:31089886-3109033
cg07616879	10	134631386	
cg15358931	X	114546538	chrX:114546353-114546
cg07136998	5	168728081	chr5:168727429-168728
cg22884541	7	97841864	chr7:97841636-9784200
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cg01275664	X	34405983	chrX:34405907-3440637
cg06178754	8	145617776	chr8:145616814-145619
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cg03986562	16	7703893	chr16:7703811-7704090
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cg04143909	1	234367322	chr1:234367135-234367
cg15324978	12	129298759	
cg07838270	16	86861522	
cg09996902	6	26598600	chr6:26598524-2659875
cg20442599	6	108479500	chr6:108478523-108479
cg13729816	19	52954722	chr19:52954461-529548
cg19968619	21	42676391	chr21:42676113-426764
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cg27546241	19	7701753	chr19:7701661-7702336
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cg05770241	12	117593501	chr12:117593353-11759
cg13671128	19	1612344	chr19:1614308-1614599
cg10718425	10	134754754	chr10:134755663-13475
cg23871388	19	56609854	chr19:56609803-566102
cg16463880	6	31867707	chr6:31867691-3186795
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cg24265865	X	47497341	chrX:47497182-4749739
cg08235947	7	158039076	chr7:158037708-158038
cg15221831	19	42408464	chr19:42408315-424085
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cg18873674	11	4158576	
cg02434121	7	4901798	chr7:4901336-4901753
cg24740515	1	2229140	chr1:2232310-2232617
cg21819984	15	101084507	chr15:101084428-10108
cg15607387	2	231714575	chr2:231712775-231712
cg01933329	14	104639768	chr14:104639242-10463
cg13608733	11	8228022	
cg27034819	15	88799526	chr15:88799522-888010
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cg03935709	16	2125759	chr16:2125659-2125995
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cg07994386	X	12156284	chrX:12156604-1215727
cg10788674	12	133214645	
cg25122402	14	101531901	chr14:101531643-10153
cg00077281	15	58840596	
cg14122138	17	36719737	chr17:36719544-367199
cg25251442	6	24476581	
cg03269218	10	96990700	
cg19239040	7	35298664	chr7:35296921-3529821
cg01723606	7	101944275	chr7:101943785-101944
cg06959657	20	60518853	chr20:60518033-605238
cg17991430	13	114083000	chr13:114085423-11408
cg09259182	1	248597493	
cg05625103	10	2543513	chr10:2543463-2544121
cg04341461	1	2410006	chr1:2409757-2410049
cg00869989	19	2774197	chr19:2774196-2774550
cg13914990	12	121174878	chr12:121177115-12117
cg21921996	20	55685638	chr20:55685276-556858
cg24140841	18	77642911	chr18:77642685-776433
cg00400827	16	29230046	chr16:29229952-292301

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cg22934785	22	30950930	chr22:30950862-309520
cg03454357	2	42565216	
cg12854762	7	138554496	chr7:138554231-138554
cg12607413	11	66062536	chr11:66061831-660630
cg12515402	8	144918044	chr8:144917878-144918
cg24096540	17	12695725	chr17:12692737-126936
cg09473364	13	112927190	
cg06376520	12	81110776	chr12:81110725-811111
cg11886880	14	104376135	
cg19497523	19	2425476	chr19:2424005-2427983
cg04900999	17	40610958	chr17:40610746-406110
cg11098525	4	1320231	chr4:1320098-1320301
cg06444891	8	141348866	chr8:141348840-141349
cg21229570	12	115124768	chr12:115124729-11512
cg22923523	19	47549464	chr19:47548451-475494
cg05766948	2	136783356	
cg20258934	7	4119142	
cg01000236	16	1262174	chr16:1265151-1265661
cg09064314	10	131742209	
cg26477549	12	106642937	chr12:106640880-10664
cg18561899	14	53162556	chr14:53161838-531627
cg14751679	8	4504999	
cg10108612	1	19203999	chr1:19203874-1920423
cg05000748	21	36399146	chr21:36398960-363992
cg26809488	16	87991343	chr16:87991287-879915
cg07040161	21	48084674	chr21:48087200-480881
cg12452813	2	68675892	
cg12579995	X	102755696	
cg09163516	1	147997372	chr1:147997265-147997
cg03816625	16	12192430	
cg19741660	14	100631897	
cg16151651	2	1609119	
cg09438742	5	1777602	
cg06934654	16	89180742	
cg23268197	19	17932244	chr19:17931951-179323
cg22991320	20	56725871	chr20:56725857-567261
cg06720669	X	108868282	chrX:108867762-108868
cg20945085	2	74875227	chr2:74875128-7487556
cg05506209	11	123480969	
cg07550554	14	73395778	chr14:73392696-733936
cg20761810	8	140723642	
cg06674436	5	1278864	chr5:1277467-1277713
cg22367191	6	10425648	chr6:10426200-1042663
cg06560300	5	1278791	chr5:1277467-1277713
cg14204266	7	100490184	chr7:100489981-100490
cg15624160	11	70644185	
cg09529821	11	1669581	
cg25482900	5	167956911	chr5:167956219-167957
cg22629111	1	166135208	chr1:166134258-166136
cg24404878	7	3082168	
cg11754374	11	131707651	
cg08398691	10	131217895	

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cg01246390	12	9392651	chr12:9392459-9392686
cg19937979	14	70039915	chr14:70038108-700403
cg10100767	14	105246561	
cg20511548	11	3178322	chr11:3181574-3182120
cg27462497	7	2633190	chr7:2632171-2632372
cg15732221	3	183675117	
cg02558205	16	87916134	chr16:87916188-879164
cg12798157	1	19600719	chr1:19600249-1960094
cg02049865	X	117973548	chrX:117973316-117973
cg17757848	1	166958583	chr1:166958220-166958
cg25071634	Y	9172441	chrY:9174129-9174443
cg23191009	21	26734384	chr21:26734108-267344
cg24357770	8	7868012	
cg18988498	11	31824262	chr11:31825743-318269
cg20764358	17	800100	
cg13462935	15	73617719	
cg22753661	15	79092743	chr15:79092538-790928
cg02688393	13	111109497	chr13:111109139-11110
cg02430183	9	95947766	chr9:95946147-9594783
cg15369608	2	239975220	chr2:239974439-239974
cg12772435	13	110385518	
cg08945711	15	77852711	
cg09447786	4	1594089	chr4:1595293-1595539
cg25881804	20	21081901	chr20:21080929-210828
cg20761204	7	106433397	
cg27179375	22	22987126	chr22:22986928-229872
cg13086574	8	135490821	chr8:135490786-135491
cg00077898	6	1081144	
cg00804073	14	59704022	
cg24668061	17	43318760	chr17:43318429-433192
cg15216232	5	158754684	chr5:158758474-158758
cg14337844	14	99740585	chr14:99739801-997409
cg11316510	17	38510570	
cg23299641	X	108868237	chrX:108867762-108868
cg18390621	1	3553628	chr1:3556963-3557201
cg25745379	13	27333481	chr13:27334226-273352
cg03051577	14	103366987	
cg06263395	10	46195640	chr10:46195451-461956
cg18206027	7	49813486	chr7:49813008-4981575
cg00078759	16	1600969	chr16:1598952-1599157
cg04389917	X	3238486	chrX:3235151-3235731
cg21627187	3	196751186	chr3:196754626-196754
cg08609445	5	1729137	chr5:1729073-1729282
cg16515500	18	13826508	chr18:13826186-138265
cg20438820	5	1641593	chr5:1645124-1645712
cg15850390	X	72668487	chrX:72667157-7266759
cg07696033	11	44326410	chr11:44325657-443265
cg24885442	8	1740059	
cg06775073	17	17603749	chr17:17603583-176041
cg04456029	12	113496126	chr12:113494389-11349
cg19093689	12	49783097	chr12:49782965-497831

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cg25873934	X	11446095	chrX:11445527-1144618
cg26919100	16	67695516	chr16:67693451-676955
cg05224126	14	101528671	chr14:101531643-10153
cg06838090	6	170566002	chr6:170564873-170565
cg26965669	10	128830556	
cg11372818	10	131989849	chr10:131988211-13198
cg18558237	10	81444220	chr10:81444163-814444
cg27465357	8	51404066	
cg21725374	8	145171334	chr8:145170253-145171
cg03163982	13	22058128	chr13:22057995-220582
cg01816775	22	36682843	
cg22111009	5	173416274	chr5:173415924-173416
cg27032056	7	155674731	chr7:155674717-155674
cg02390319	1	3310268	chr1:3310102-3311035
cg07529210	12	122019110	chr12:122016170-12201
cg14169163	15	20500279	chr15:20499875-205008
cg27311866	5	55033877	chr5:55033694-5503399
cg16228356	17	43848958	
cg17602198	6	170201785	
cg27598340	7	55145727	
cg14617041	5	72415687	chr5:72415611-7241676
cg20590175	12	132530165	
cg17165158	1	2182612	
cg23178550	7	27127576	chr7:27127500-2712836
cg22694548	19	5455843	chr19:5455481-5456262
cg04873833	12	129417818	
cg13225272	1	83729633	
cg24986058	14	100812247	
cg06621094	13	75149963	
cg01909845	11	119535897	chr11:119535559-11953
cg20519277	X	118207533	chrX:118207507-118207
cg15036160	6	168628425	chr6:168630046-168630
cg17441377	17	3906640	chr17:3907378-3907703
cg12216208	12	6756377	chr12:6756001-6756679
cg26716902	17	40835920	chr17:40835731-408362
cg26963271	1	66259081	chr1:66258440-6625891
cg02692313	6	33048444	chr6:33048416-3304881
cg26996458	8	141636297	
cg25361175	10	134736163	chr10:134735972-13473
cg13023870	14	37124018	chr14:37125219-371256
cg13446474	9	14349430	chr9:14349307-1434951
cg26793903	X	136629762	chrX:136629544-136630
cg02259232	14	47121002	chr14:47120868-471211
cg07382347	6	30039408	chr6:30038881-3003947
cg03709091	6	48036409	chr6:48036137-4803641
cg26037170	1	228504579	chr1:228503556-228504
cg04624564	X	73325368	chrX:73325164-7332552
cg04630982	X	139006339	
cg07413956	X	55101460	
cg08613153	16	622765	chr16:619805-620195
cg09802835	11	71952131	chr11:71952112-719525
cg18155407	19	33210662	chr19:33210453-332110
cg00214873	5	42813896	
cg14192207	21	33672816	chr21:33672605-336732

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cg07179816	8	49647907	chr8:49647702-4964798
cg23314972	11	1977533	chr11:1977523-1977765
cg05417729	2	3307997	
cg24234651	12	75728471	
cg13418007	17	42476521	
cg18026225	17	43198423	chr17:43198277-431987
cg19115205	5	5062128	
cg07088555	16	89315186	chr16:89315019-893153
cg23525438	6	17016226	
cg07569018	7	157202818	chr7:157202370-157203
cg21824017	2	15804594	
cg18147067	X	11445818	chrX:11445527-1144618
cg15046299	7	27309073	
cg19463665	13	113492776	chr13:113492486-11349
cg15193953	15	72581722	chr15:72581710-725823
cg14007179	14	106015750	chr14:106012960-10601
cg06323896	16	85410525	chr16:85407314-854075
cg16681268	7	117067616	chr7:117067403-117067
cg01764713	17	34839287	chr17:34838512-348391
cg12783819	17	75369657	chr17:75368688-753705
cg27103642	7	158272547	
cg21010435	7	157208882	chr7:157208794-157209
cg09861971	5	3536279	chr5:3535630-3536355
cg24980551	11	64599054	chr11:64596975-645975
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cg06959457	10	82363384	
cg25773262	1	156616855	chr1:156616553-156616
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cg16577724	5	428068	
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cg10792227	8	116226967	
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cg14795528	7	157451260	chr7:157453774-157454
cg12230728	12	58021569	chr12:58021294-580220
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cg11327565	15	90892795	chr15:90895472-908959
cg10709771	X	25027268	chrX:25025211-2502571
cg06324707	17	105824	
cg00243187	11	128746214	
cg15508809	14	29231309	chr14:29234889-292359
cg18843192	5	126905427	
cg01416563	5	140237151	chr5:140236862-140237
cg27613976	5	1020718	
cg03844838	10	661087	
cg02864732	X	130192365	chrX:130192131-130192
cg15762348	11	66458829	chr11:66458783-664591
cg24459953	19	56466500	
cg07200487	X	124339462	chrX:124338904-124339
cg05157140	7	1272545	chr7:1269165-1282864

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cg04074536	4	798711	chr4:798538-798984
cg23112651	1	90459291	chr1:90460399-9046123
cg11354472	22	17589511	chr22:17589440-175902
cg23779626	6	33864747	
cg04917181	8	98290229	chr8:98289604-9829040
cg05026346	7	23057327	chr7:23052971-2305400
cg07698121	16	85659946	chr16:85658742-856589
cg17561243	8	179176	chr8:179001-179288
cg20638675	10	45374906	
cg13470333	7	1908714	chr7:1908539-1908803
cg08584759	10	11912126	chr10:11911554-119124
cg02559817	16	78466533	
cg13944175	19	52222698	chr19:52222423-522232
cg09301410	7	157951964	chr7:157951254-157951
cg03353885	13	113489392	chr13:113492486-11349
cg08612137	7	42533206	chr7:42533076-4253328
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cg05952909	7	158713084	chr7:158712559-158713
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cg24033224	12	131438016	
cg25085925	X	66763691	chrX:66763684-6676407
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cg13601079	X	48216275	
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cg14301348	8	20109523	chr8:20107432-2010765
cg05375100	16	565623	chr16:565420-565781
cg09981013	16	88008551	
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cg15765801	X	114969816	chrX:114959730-115005
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cg11295942	19	6707296	chr19:6707112-6707567
cg09955012	13	22477006	
cg25735398	19	2717293	chr19:2717060-2717800
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cg06956805	11	485055	chr11:484870-485620
cg22935551	19	35550654	chr19:35550550-355508
cg13980392	9	132123345	
cg13943560	X	40004481	chrX:40004305-4000453
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cg23098168	1	109801427	chr1:109801054-109801
cg23366234	21	45713704	chr21:45713509-457138
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cg17824363	5	7826845	
cg09738481	16	89653835	chr16:89654041-896546
cg25740208	7	1001911	
cg26510723	7	157464230	
cg17625535	7	4807525	chr7:4806860-4807086
cg23868757	6	31747257	
cg02111786	14	80328189	chr14:80328014-803283
cg08214957	X	139866495	
cg16181848	18	2913135	chr18:2913059-2913307
cg18411237	11	70653173	
cg09909417	7	158934031	chr7:158936507-158938
cg22459755	8	49293005	chr8:49293201-4929354
cg00947782	6	30039142	chr6:30038881-3003947
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cg26983317	4	128651500	chr4:128651419-128651
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cg22992730	19	4784940	chr19:4785250-4785490
cg14213394	8	38508585	chr8:38508299-3850874
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cg27477504	17	22191976	chr17:22191801-221920
cg08368654	6	1378868	chr6:1378445-1379318
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cg01135961	3	107416903	
cg27169819	17	79388690	chr17:79388434-793889
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cg11969813	17	79816559	chr17:79818230-798192
cg05465955	17	40715236	chr17:40714087-407152
cg13421439	18	21199515	chr18:21199431-211997
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cg13618137	X	124454138	chrX:124453902-124454
cg12708841	18	76463655	chr18:76463363-764636
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cg22885136	7	63041232	chr7:63041128-6304136
cg12275871	13	114096262	chr13:114096050-11409
cg16942223	4	6050460	
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cg19567689	14	97059467	chr14:97058943-970595
cg25937114	17	12899453	
cg17403512	15	28700396	chr15:28699850-287006
cg04340895	4	47463168	chr4:47465510-4746581
cg20392203	7	636590	
cg21042749	8	145676033	chr8:145675351-145676
cg24480695	11	18727628	chr11:18727320-187277

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cg14644204	12	123518833	
cg08629836	4	3617256	
cg03308399	7	27146237	chr7:27146069-2714660
cg12950231	X	129197768	chrX:129194007-129194
cg04141164	2	11809681	chr2:11809606-1181043
cg08407014	19	2541104	chr19:2540906-2541138
cg26096090	8	986000	chr8:983687-986272
cg12301347	22	46285638	chr22:46285477-462859
cg23536372	2	80136875	
cg07618159	19	306671	chr19:306214-306681
cg03079698	17	78410017	
cg25076272	11	60923776	
cg27459435	13	30056312	chr13:30054342-300545
cg21880624	21	40194678	chr21:40194644-401948
cg05714748	17	80856238	chr17:80856874-808573
cg16781264	2	101087575	
cg14225031	9	129387848	chr9:129386112-129389
cg14507337	14	60978161	chr14:60975732-609781
cg17291521	5	50260045	
cg08327705	5	6756273	chr5:6755104-6755387
cg07584805	17	56738915	chr17:56738847-567390
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cg16080125	7	2774654	chr7:2774444-2774655
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cg22796363	1	214477063	
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cg26791879	10	131005696	
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cg07251141	10	127914071	
cg20390450	1	228403247	chr1:228403232-228403
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cg17288397	5	72715731	chr5:72715407-7271599
cg26422851	6	424272	chr6:423846-424313
cg24684816	18	12093809	chr18:12093607-120938
cg06911187	17	80988709	chr17:80989059-809893
cg18761221	20	60518478	chr20:60518033-605238
cg09806671	1	165324679	chr1:165324191-165326
cg20348895	7	76163353	
cg19637330	1	19110922	chr1:19110720-1911093
cg16388071	6	169726476	

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cg20861422	X	152585214	chrX:152584949-152585
cg14783646	7	4800873	chr7:4800616-4800919
cg27080348	5	140182129	chr5:140181888-140183
cg17498856	1	1457042	chr1:1456829-1457074
cg03167389	4	42154927	chr4:42152766-4215498
cg08165875	12	132603220	chr12:132603367-13260
cg21206277	19	4048075	chr19:4047754-4048428
cg19841653	10	71160897	
cg22984587	7	64043119	
cg01961086	1	3086487	
cg26719943	19	3531956	chr19:3531568-3532102
cg20565727	17	77461480	chr17:77460245-774606
cg09614506	X	80259692	chrX:80259089-8025949
cg22220310	1	1168541	chr1:1167001-1168985
cg04583842	16	88103117	chr16:88101473-881019
cg25340432	8	3974225	
cg02846841	6	28945341	
cg01382105	13	113406866	chr13:113410004-11341
cg08373573	11	1028291	chr11:1029083-1029390
cg04176488	16	88738398	
cg26910936	5	173661962	
cg19590511	17	957402	
cg00016481	8	77768353	
cg17509220	19	13617012	chr19:13616752-136172
cg02360155	4	3511597	chr4:3510934-3511598
cg10471356	13	113382760	chr13:113382598-11338
cg06304546	20	32448765	chr20:32450500-324507
cg20119495	11	792013	chr11:791953-792400
cg22123804	X	123467129	chrX:123466685-123467
cg23916284	4	26358537	chr4:26361172-2636141
cg04510420	16	88102758	chr16:88101473-881019
cg09142414	10	3145966	chr10:3145919-3146206
cg27052113	19	47951305	chr19:47950869-479515
cg07469546	16	86927990	
cg11953513	13	42618810	chr13:42621745-426230
cg19755813	17	650208	
cg17207346	2	3289626	chr2:3289426-3289731
cg11474468	8	144940301	chr8:144940233-144940
cg25350986	7	4762844	chr7:4764684-4765252
cg08873424	6	28945492	
cg24062526	2	86255804	
cg08689075	X	153523851	chrX:153523741-153524
cg17039011	10	694058	
cg05039004	1	29586299	chr1:29585897-2958659
cg17470251	8	19459996	chr8:19459905-1946013
cg22053765	2	24433938	
cg09269945	20	55837692	chr20:55839287-558397
cg03943293	1	143275393	
cg03044471	11	1321009	chr11:1315467-1317115
cg07855447	2	168401353	
cg14654471	1	5937169	chr1:5937157-5937392
cg14094409	12	122712093	chr12:122710054-12271
cg24127965	11	67653560	
cg03136712	5	140053068	chr5:140052059-140053
cg07628855	7	25100356	

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cg13935315	19	12547760	chr19:12551471-125518
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cg14630369	13	100803190	
cg22375826	15	101606897	
cg11937033	7	155150681	
cg13423098	15	23807234	
cg15145174	5	6755386	chr5:6755104-6755387
cg02951883	7	2050386	chr7:2054060-2054386
cg26472802	21	45713719	chr21:45713509-457138
cg15731655	12	54357604	chr12:54359658-543599
cg11437063	10	1715848	
cg10962762	1	228075749	chr1:228075377-228075
cg10464529	16	58030730	chr16:58030214-580316
cg20201270	2	45397874	chr2:45395869-4539818
cg02523640	10	129534613	chr10:129534410-12953
cg27295850	16	3414983	chr16:3414964-3415167
cg19451167	7	96655981	chr7:96653467-9665419
cg06590120	20	60520027	chr20:60518033-605238
cg07143083	7	70597921	chr7:70596228-7059838
cg19472956	5	179743769	chr5:179740710-179741
cg03043709	7	2046920	chr7:2044583-2044788
cg02287939	15	26026283	
cg27197524	12	133249278	chr12:133249979-13325
cg14525402	9	5233806	
cg01953317	2	55642894	chr2:55646621-5564732
cg03636188	5	36591815	
cg15459605	22	20716864	chr22:20708651-207165
cg17647597	12	20935799	
cg20072442	2	80530255	chr2:80529677-8053084
cg10034364	13	28491590	chr13:28491488-284925
cg09410317	10	3168669	
cg19275261	18	5630072	chr18:5628324-5630785
cg05411980	X	68345134	chrX:68348399-6834877
cg07907386	4	41749443	chr4:41749184-4174981
cg17514558	5	140621375	chr5:140620864-140621
cg00794209	8	255189	chr8:253718-255462
cg26976412	17	17626127	chr17:17625605-176285
cg15452135	10	105233106	chr10:105232921-10523
cg22591964	10	98144438	chr10:98144299-981445
cg07159469	16	89355005	chr16:89352528-893528
cg12712184	7	155790801	
cg11300369	6	33391259	chr6:33393592-3339390
cg27112666	6	100050791	chr6:100051018-100051
cg26923863	4	1221838	chr4:1221837-1222050
cg23972431	5	26237674	
cg00046625	1	66258760	chr1:66258440-6625891
cg27325224	16	87946544	chr16:87948518-879487
cg03408945	16	8738531	
cg25284710	18	14998834	chr18:14997380-150005
cg16729832	8	21645078	chr8:21644908-2164784
cg14238959	12	114885270	chr12:114885105-11488

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cg09771054	12	130918514	
cg08626605	16	1363957	chr16:1363813-1364496
cg05678789	16	85529938	chr16:85529839-855301
cg17817067	5	14713179	
cg07166654	12	52652220	chr12:52652018-526527
cg24748746	7	155738916	
cg17602885	1	9804627	
cg24686380	17	62971592	chr17:62971515-629722
cg16238815	14	36741794	
cg23575603	13	50707753	chr13:50707585-507080
cg15101633	14	101293726	chr14:101293427-10129
cg26967100	14	61104032	chr14:61103978-611046
cg02304824	1	100943261	
cg08783090	X	151143125	chrX:151142680-151143
cg09921371	2	1670073	chr2:1669991-1670203
cg17863743	10	100993587	chr10:100993820-10099
cg04861869	15	101728611	
cg06616729	8	55379248	chr8:55378928-5538018
cg00436996	2	77962212	
cg14454796	2	242031694	
cg12070987	11	67804055	chr11:67806251-678066
cg21135483	21	42830710	
cg01016191	12	130707332	
cg12739617	X	70979239	chrX:70981816-7098382
cg00833479	7	62528852	chr7:62528466-6252897
cg23008352	13	110951025	
cg19241352	1	166958389	chr1:166958220-166958
cg02890566	17	71434142	chr17:71431621-714318
cg07276358	13	114263342	chr13:114260191-11426
cg13413387	2	10534660	
cg02583740	7	612613	chr7:612540-613739
cg12149986	19	50059027	chr19:50058876-500592
cg11059561	2	3428786	
cg15694580	1	149261176	chr1:149261001-149261
cg15793573	8	27779514	chr8:27779081-2777976
cg02556155	3	114052269	
cg16108684	X	125300035	chrX:125299245-125300
cg19623624	10	135278901	chr10:135278716-13527
cg04880091	8	43132451	chr8:43132045-4313247
cg05821633	1	10837632	
cg12437197	5	482948	chr5:481639-482225
cg02056918	10	324049	
cg15492820	11	61323113	chr11:61322732-613232
cg02447239	2	235936137	
cg24137774	11	19372014	chr11:19366653-193682
cg01198024	21	33672713	chr21:33672605-336732
cg19437626	17	40171883	chr17:40171931-401722
cg07280731	16	2867773	chr16:2867245-2868002
cg07521193	15	27819422	
cg17002993	11	119044331	
cg02734891	5	104728427	
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cg06491573	3	126062601	chr3:126062535-126062
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cg13735557	3	184290720	chr3:184290593-184290
cg06878649	16	84336112	
cg26360697	5	1673409	
cg06900650	2	130956219	chr2:130955619-130956
cg25896901	X	125300481	chrX:125299245-125300
cg09582314	5	176295891	chr5:176296541-176296
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cg22762844	2	95692424	chr2:95690857-9569243
cg26258226	10	134684054	chr10:134682700-13468
cg22932313	11	34535189	
cg25837719	1	61547969	chr1:61548753-6154956
cg23712018	6	30039132	chr6:30038881-3003947
cg01913196	X	125687041	chrX:125685711-125686
cg25821416	X	47431407	chrX:47433414-4743412
cg09085220	16	8736433	
cg18486102	12	50297777	chr12:50297580-502979
cg17512474	5	149546335	chr5:149546027-149546
cg08795535	10	2777128	
cg08516516	5	115152492	chr5:115151348-115152
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cg19923393	4	7252587	
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cg16766914	17	55962703	chr17:55962573-559632
cg15781397	7	23695266	chr7:23695159-2369537
cg01828427	11	134794919	
cg06620390	8	10192943	chr8:10191940-1019262
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cg18601714	17	25485531	
cg13916459	12	85673221	chr12:85673878-856747
cg26310429	17	71024449	
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cg19759366	2	236715747	
cg26273958	1	228509696	chr1:228509553-228509
cg24425807	13	109741176	
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cg21045312	X	151080969	
cg16491960	7	56297490	chr7:56297432-5629766
cg25315312	7	2020528	chr7:2019763-2020100
cg15713103	1	933685	chr1:933387-937410
cg22423294	13	114286133	chr13:114287533-11428
cg06577450	5	1710235	
cg13750214	19	1302619	chr19:1302530-1302811
cg10017105	6	31832428	chr6:31830299-3183094
cg09544149	10	80588828	
cg22432760	17	80829718	chr17:80829533-808298
cg06626847	1	149333142	chr1:149332993-149333
cg15122993	5	140256817	chr5:140256273-140257

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cg26161643	5	24645024	
cg17807393	4	132651902	chr4:132651811-132652
cg06379192	1	3157287	chr1:3157509-3158300
cg07230107	1	224804396	chr1:224803637-224805
cg00164462	1	25234549	chr1:25234428-2523480
cg15422579	Y	22737424	chrY:22737825-2273805
cg15479073	15	59499039	chr15:59498959-594993
cg07933790	X	41333435	chrX:41332738-4133412
cg00219792	12	83053315	
cg25105415	17	79913327	chr17:79913240-799134
cg08556938	17	58512855	
cg23983671	18	76755310	chr18:76751939-767555
cg13483099	2	43216931	
cg00936349	X	106690556	chrX:106692681-106693
cg15182939	3	67701995	chr3:67704628-6770505
cg01062937	16	88537260	chr16:88536936-885373
cg26415787	12	133414334	chr12:133414254-13341
cg20634940	10	465975	chr10:465928-466396
cg06407371	16	85074868	
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cg15571686	13	113411162	chr13:113410004-11341
cg20778411	X	37003920	chrX:37003510-3700454
cg22358067	17	16797159	
cg04452731	7	158953370	chr7:158954897-158955
cg17296858	X	40482886	chrX:40482374-4048321
cg08706312	X	30265243	chrX:30265172-3026555
cg13894250	20	60927156	chr20:60926764-609271
cg10192483	7	76632239	chr7:76629263-7662948
cg01157126	2	219849189	chr2:219848919-219850
cg01328500	3	197639792	
cg16752925	8	145235335	chr8:145235202-145235
cg27087423	11	14542224	chr11:14541600-145422
cg09897374	6	28584076	chr6:28583934-2858428
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cg17677524	7	150069026	chr7:150068756-150070
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cg07856667	10	94455710	chr10:94455524-944558
cg20858622	6	32015651	
cg13434842	8	11567896	chr8:11565217-1156721
cg14156842	9	140611316	chr9:140612441-140612
cg08473240	5	1227100	chr5:1226976-1227305
cg19008266	12	51346506	
cg17242353	18	76189809	chr18:76189718-761901
cg03240752	X	68058033	chrX:68060178-6806055
cg03224572	8	97172012	chr8:97171805-9717202
cg01620164	2	164590272	chr2:164592917-164593
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cg09332484	11	18433887	
cg27583010	16	30198505	chr16:30194747-301953
cg18867200	2	71116698	chr2:71114733-7111547
cg00529958	13	100624288	chr13:100620241-10062

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cg12359503	4	3566794	chr4:3565311-3567185
cg00995209	8	144881704	chr8:144885269-144886
cg20170147	12	24712933	chr12:24714956-247162
cg18582965	2	241401686	chr2:241401561-241401
cg19265480	1	147781887	chr1:147782066-147782
cg07348339	7	2609259	
cg07299736	8	135490787	chr8:135490786-135491
cg26410635	12	96350720	chr12:96350518-963507
cg22257374	3	15139756	chr3:15140035-1514089
cg09187505	6	106434429	chr6:106433984-106434
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cg16224521	5	205606	
cg17485838	7	27138712	chr7:27135342-2713673
cg26510975	7	5347588	chr7:5347663-5347956
cg12738008	8	2037954	chr8:2037706-2037986
cg21944491	19	41119829	chr19:41119031-411203
cg07964958	6	83899780	chr6:83902606-8390377
cg10530883	5	3596207	chr5:3594467-3603054
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cg00335252	2	161245200	
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cg00683655	10	839865	chr10:839608-840210
cg25654262	6	100841682	
cg15969606	8	1733475	chr8:1733267-1733929
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cg15837100	1	22647529	
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cg26628435	X	102319088	chrX:102318601-102319
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cg18492257	8	2548901	
cg04023872	5	310073	chr5:309705-310136
cg11699517	17	79419796	chr17:79420144-794204
cg18577618	17	60500856	chr17:60501111-605017
cg26722684	10	45799357	
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cg17956530	17	78667699	
cg18451114	1	38511677	chr1:38510102-3851364
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cg07222124	12	132429633	chr12:132429528-13242
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cg23064157	10	85324925	chr10:85324699-853250
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cg19594666	7	127881280	chr7:127880750-127881
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cg07104230	1	120909060	chr1:120904698-120905
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cg21385480	3	66454763	
cg14420357	6	158464617	
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cg02667487	16	67920036	chr16:67918679-679189
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cg01144764	10	121633063	chr10:121631654-12163
cg21587238	5	42953590	chr5:42951076-4295241
cg01816814	16	959883	chr16:959714-959977
cg07281948	12	57601935	
cg12229632	17	2607906	chr17:2607735-2608005
cg22386646	1	112524496	chr1:112524468-112525
cg19506677	2	242878672	chr2:242878602-242879

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cg06773963	1	9416303	chr1:9416126-9416404
cg25594100	7	4786943	chr7:4786761-4786987
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cg22699044	1	228633460	chr1:228633382-228634
cg15240033	6	3623985	
cg17181598	1	118165662	
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cg25924823	8	145113480	chr8:145113210-145113
cg01854776	2	235904366	
cg19809791	1	17027832	chr1:17025923-1702794
cg17334762	7	4862349	
cg24024505	6	28829401	chr6:28831682-2883213
cg05481991	12	66216880	chr12:66217627-662201
cg03146219	11	71189514	
cg13138954	15	22546672	chr15:22545218-225472
cg25632105	7	136553728	chr7:136553854-136556
cg05803790	9	80765939	chr9:80765851-8076612
cg11841704	17	75539913	
cg23231268	3	46792462	chr3:46791861-4679251
cg25545503	6	160680162	chr6:160679377-160679
cg02761960	18	77507709	chr18:77507538-775078
cg11999331	17	81016852	chr17:81016044-810162
cg02775417	19	643457	chr19:643092-643720
cg02749215	6	100675273	chr6:100676823-100677
cg20182983	12	123470916	chr12:123470553-12347
cg26465317	4	8398823	
cg14930335	2	236619767	
cg10831684	11	66807539	
cg20648847	11	66326767	chr11:66326639-663268
cg08463820	7	157453872	chr7:157453774-157454
cg18279094	1	63790044	chr1:63782394-6379047
cg13412514	13	114175012	
cg14314744	6	100897445	chr6:100897080-100897
cg01968402	6	137817775	chr6:137818167-137819
cg20032789	10	30336565	
cg12582028	1	151736699	chr1:151735445-151736
cg13900349	7	158109559	chr7:158109334-158109
cg04102734	1	209406725	chr1:209404845-209405
cg12193929	5	140237485	chr5:140236862-140237
cg02699898	13	113424938	chr13:113424898-11342
cg09235562	19	384251	chr19:384250-384464
cg25145765	4	46391392	chr4:46391903-4639257
cg24839386	10	73004576	
cg05971966	5	40681137	chr5:40679502-4068208
cg09193347	15	79381867	chr15:79381804-793842
cg27202779	7	3020536	
cg15074033	12	52652462	chr12:52652018-526527
cg02571204	10	114591733	
cg20024953	12	57584802	
cg18219878	12	19459468	chr12:19459257-194597
cg09854734	16	66613273	chr16:66612749-666134

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cg25225517	22	49812267	chr22:49811997-498124
cg01939453	6	166077483	chr6:166073882-166077
cg13627598	11	65387073	chr11:65382824-653838
cg08104023	16	34777881	chr16:34777874-347781
cg06658637	5	466542	chr5:464887-465666
cg03913921	7	120496827	chr7:120497120-120498
cg15452747	X	68726029	chrX:68723731-6872605
cg17619311	3	42947565	chr3:42947480-4294817
cg09965557	17	1381989	chr17:1381746-1382043
cg04415798	14	37128586	chr14:37126786-371282
cg19731612	5	176559334	chr5:176558852-176561
cg23475278	4	128651543	chr4:128651419-128651
cg00551957	X	45017137	chrX:45016977-4501717
cg14326416	4	25892942	
cg27636925	5	266909	
cg10984692	X	103294682	chrX:103294657-103294
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cg01206993	16	87450718	chr16:87446632-874471
cg13031251	5	77268734	chr5:77268350-7726878
cg18198730	1	247681584	chr1:247681399-247681
cg16501560	21	46078007	
cg00563824	1	209405064	chr1:209404845-209405
cg02004499	7	4244250	
cg22830844	3	44283343	chr3:44283239-4428383
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cg05453337	10	106075736	chr10:106075559-10607
cg14796474	22	24647469	chr22:24647367-246476
cg04970158	17	43208740	chr17:43209347-432107
cg25535708	19	15289906	chr19:15288314-152889
cg00510025	19	3453955	chr19:3453363-3453956
cg25587069	5	151066484	
cg23839556	1	53905233	chr1:53904140-5390524
cg26996656	16	880371	
cg18646521	2	111875858	chr2:111875206-111880
cg10203588	13	112255534	
cg10032110	7	1718541	
cg18965659	17	80624885	chr17:80621841-806220
cg10126205	7	19158664	chr7:19156050-1915804
cg07291317	5	16701194	chr5:16701071-1670177
cg13008301	20	54978749	chr20:54978524-549787
cg01888044	17	19617307	chr17:19617083-196174
cg12206403	6	32017229	
cg25942789	2	241696788	
cg02515233	9	72658837	chr9:72658836-7265927
cg20591136	17	58119926	chr17:58119752-581204
cg18297437	3	147131332	chr3:147131066-147131
cg04392554	22	46685472	chr22:46685379-466857
cg19592502	7	80520597	
cg20387387	8	144511212	chr8:144510850-144513
cg19407410	X	99665951	chrX:99666131-9966638
cg20806427	1	149718671	chr1:149718542-149718

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cg13645530	12	116756948	
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cg04671971	11	130271905	
cg03680250	13	111567502	chr13:111566486-11156
cg13909661	12	26386833	
cg07009376	6	28793219	
cg11633007	X	56310955	
cg22115465	7	2170343	
cg12382229	7	145058067	
cg23090607	11	60135537	
cg08166513	1	233120048	chr1:233121927-233122
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cg12528056	11	60619955	chr11:60619924-606211
cg12337683	4	847411	chr4:843317-843936
cg04015433	8	8820844	chr8:8820766-8821112
cg20607798	8	58055168	chr8:58054945-5805560
cg06783533	16	56388908	
cg03335262	5	140536920	chr5:140536896-140537
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cg23253914	1	15895370	
cg11490865	8	143425585	chr8:143429001-143429
cg15874144	3	157614907	
cg27155168	11	68207327	chr11:68205925-682061
cg01858089	4	125448037	
cg20594345	6	28973520	
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cg11872186	7	152236239	
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cg24923931	19	40904691	chr19:40904444-409049
cg27179622	1	226127290	chr1:226127112-226127
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cg01420688	6	99271924	chr6:99272394-9927301
cg25899306	7	63088618	chr7:63088056-6308873
cg20487366	17	75136973	chr17:75136325-751377
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cg05360371	2	121746437	chr2:121745840-121746
cg18844144	14	23528430	chr14:23528360-235285
cg12283393	11	1874445	
cg07831918	16	84690554	chr16:84690432-846914
cg00412239	19	5044006	chr19:5043658-5044441
cg14241370	9	104499850	chr9:104499849-104501
cg16438722	14	101517458	
cg10386298	1	221050491	chr1:221050448-221050
cg06831576	16	62070086	chr16:62069121-620706
cg22603247	10	124907553	chr10:124907283-12491
cg26844246	5	170736277	chr5:170735169-170739
cg17589890	1	210857205	chr1:210857059-210857
cg12528981	5	170919715	
cg19882663	3	180308459	
cg16857641	7	1492452	chr7:1491773-1491975
cg03117053	19	34263644	chr19:34262943-342639
cg06998119	5	51813680	
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cg24680632	12	116044032	
cg16310579	5	178808980	
cg14535167	8	30589108	chr8:30584790-3058565
cg18966232	1	3183165	chr1:3182821-3183216
cg27568550	10	127461233	chr10:127462230-12746
cg01091156	16	87991122	chr16:87991287-879915
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cg09887059	12	113916664	chr12:113916433-11391
cg11610925	10	134978049	chr10:134977930-13497
cg27100806	3	180630217	chr3:180630152-180630
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cg13613450	X	136657310	chrX:136655909-136657
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cg05227111	16	75512979	chr16:75512545-755137
cg04968132	16	27560915	chr16:27560979-275615
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cg25016190	1	88108838	
cg17947175	5	1003134	chr5:1003937-1005687
cg06809074	8	976415	chr8:976015-976416
cg09265315	6	29572317	
cg21164369	8	86840929	chr8:86838850-8684067
cg16990945	18	74832261	chr18:74832039-748322
cg11033688	7	1902804	chr7:1902762-1903059
cg21944972	8	2020566	
cg15546282	1	1903425	
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cg03107179	6	167065376	
cg14811319	6	88757392	chr6:88757292-8875787
cg15221604	11	124738735	chr11:124738712-12473
cg18288532	6	90597356	chr6:90597207-9059765
cg08073280	19	55035609	chr19:55038204-550385
cg10991514	X	125300111	chrX:125299245-125300
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cg06654051	X	153409667	
cg19182035	12	3393005	
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cg04137490	8	25176732	
cg04752989	13	111972854	
cg17733714	X	68114285	chrX:68114440-6811471
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cg13352717	19	17405195	chr19:17404959-174053
cg12638737	1	204120607	chr1:204120398-204121
cg05208399	16	1815968	chr16:1814084-1814482
cg20422052	8	143474721	chr8:143471631-143472
cg25379549	10	1707569	
cg11162118	11	31837104	chr11:31831620-318390
cg08818092	X	24665074	
cg10679301	6	50818268	chr6:50818180-5081843
cg10716768	7	6370368	
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cg14304073	14	91691190	
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cg01718733	15	29409410	chr15:29407695-294082
cg14326989	17	46799479	chr17:46800533-468007
cg09074755	12	29650711	
cg06372919	7	4153868	chr7:4153645-4153898
cg22898362	19	51506358	chr19:51505914-515063
cg07881817	3	170904870	
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cg01233948	15	31318495	chr15:31318285-313185
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cg20760609	5	3962310	chr5:3962286-3962512
cg20638467	19	34302382	chr19:34302168-343025
cg21367866	4	187563992	
cg22407879	X	99194407	chrX:99194334-9919459
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cg27367235	16	88568705	chr16:88569267-885694
cg22951728	X	153664905	chrX:153664761-153666
cg23956190	7	1514455	chr7:1514354-1514578
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cg16068263	13	36729231	chr13:36728962-367292
cg23194712	12	132401025	
cg16874494	7	210873	chr7:206451-207365
cg22475974	4	3748341	chr4:3748224-3748581
cg08960448	16	4838658	
cg07103129	6	50787964	chr6:50787286-5078809
cg18511011	10	115348546	
cg17522332	10	1707523	
cg17181956	9	136879298	chr9:136877009-136879
cg16762300	7	2625332	
cg26267430	15	96894509	chr15:96895306-968957
cg10746936	14	95240143	chr14:95240083-952403
cg13192239	6	15512657	
cg20208523	11	118764491	
cg20512947	2	242889340	
cg24540732	7	139256534	
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cg07912402	1	989305	chr1:990274-990694
cg03455316	15	62516405	chr15:62516324-625168
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cg08539872	10	73004610	
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cg26968501	X	82765734	chrX:82765442-8276577
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cg05166248	11	134252845	chr11:134253449-13425
cg24060874	10	134460304	chr10:134460274-13446
cg14160518	20	50418952	chr20:50417312-504190
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cg03701266	5	10649678	chr5:10649367-1065035
cg10299941	8	145009137	chr8:145008908-145009
cg26090107	11	60718882	chr11:60718428-607188
cg06636203	6	31867788	chr6:31867691-3186795
cg19517476	19	14591301	chr19:14591032-145913
cg23460285	12	133076687	chr12:133073397-13307
cg18161890	12	52995250	chr12:52994772-529953
cg18315976	7	936456	chr7:936385-936592

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cg07478240	16	87174203	
cg18811550	7	27198311	chr7:27198182-2719851
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cg26327984	X	42637506	chrX:42637008-4263738
cg09264619	17	80180166	chr17:80179930-801801
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cg14590644	9	127528498	chr9:127532040-127533
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cg19222397	12	7129898	chr12:7125534-7126356
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cg04833819	17	927551	chr17:926234-926439
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cg24440302	11	406829	chr11:406491-407871
cg04947680	2	132587079	chr2:132585112-132588
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cg04449523	11	1247948	chr11:1247830-1248140
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cg24324584	10	133892464	
cg02162286	5	5887361	chr5:5887062-5887528
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cg06732825	12	132916669	
cg09434222	8	1185201	chr8:1185092-1185445
cg18556834	14	24641070	chr14:24641053-246422
cg00628919	16	87702703	chr16:87702493-877027
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cg03536686	14	106066568	chr14:106066400-10606
cg09749862	12	57584720	
cg11442732	X	133118088	chrX:133118081-133118
cg26673975	16	66420974	
cg13691247	12	54071090	chr12:54071053-540712
cg06218787	10	14575319	
cg14088196	11	70211408	
cg05771369	12	58021713	chr12:58021294-580220
cg00160667	1	29587357	chr1:29587087-2958741
cg24144440	1	119526882	chr1:119526782-119527
cg21620087	17	41570101	
cg19769301	1	149147625	chr1:149148145-149148
cg17203063	12	75601711	chr12:75601081-756017
cg05836951	8	77594834	chr8:77594255-7759486
cg17560598	17	612456	
cg10333959	10	131354940	
cg17814335	X	74143945	chrX:74143852-7414517
cg03426194	16	27500918	
cg10193870	14	73138006	
cg09474101	2	105279258	chr2:105275588-105275
cg14072515	10	125732604	chr10:125732220-12573
cg10074727	6	10883105	chr6:10882926-1088314
cg27607136	11	1857442	
cg07128900	16	70714357	chr16:70713461-707143
cg23755933	12	133349383	chr12:133349663-13334
cg06934023	16	587828	chr16:587567-588172
cg07055259	2	236300855	
cg25679378	17	73274392	
cg02542872	11	70269505	
cg23911852	1	2409853	chr1:2409757-2410049
cg12753558	1	247464072	chr1:247463848-247464
cg18444868	X	30265251	chrX:30265172-3026555
cg15275758	12	133412815	chr12:133412394-13341
cg25096313	1	895141	chr1:894313-902654
cg10420161	10	102899983	chr10:102899822-10290
cg14419975	1	91196332	chr1:91190489-9119280
cg18070818	14	76905770	chr14:76905703-769060
cg26004810	11	70048845	chr11:70049099-700498
cg20384632	7	106508080	chr7:106508057-106508
cg22223709	X	42637305	chrX:42637008-4263738
cg15254559	7	27292145	chr7:27291119-2729219
cg13388615	2	242878809	chr2:242878602-242879
cg07708613	10	42737139	chr10:42737286-427391
cg03848676	22	38528943	chr22:38528820-385290
cg12778183	17	56769387	chr17:56769865-567702
cg03484267	2	207988651	
cg13603142	8	7867451	
cg05063999	3	64253605	chr3:64253533-6425381
cg14023573	8	140971379	chr8:140971270-140971
cg09020928	7	98552952	chr7:98552746-9855296
cg01435564	5	132150904	chr5:132148854-132150

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cg00522555	19	10602587	chr19:10602280-106028
cg02654411	16	1652552	
cg04012618	16	21548169	
cg05134013	20	61288351	chr20:61287997-612884
cg10434881	7	6884098	
cg06367102	7	1192688	
cg01696784	2	235904501	
cg07355262	7	5347698	chr7:5347663-5347956
cg02809746	16	49312033	chr16:49311413-493123
cg13285593	8	1246442	chr8:1245671-1246464
cg06712559	1	968395	chr1:967966-970238
cg13629132	9	22863277	
cg16755924	X	25041099	chrX:25040878-2504136
cg11168432	4	1333422	chr4:1333378-1333676
cg07508942	7	5267994	chr7:5267748-5268110
cg08123749	16	30544067	chr16:30543867-305443
cg16588297	7	128765024	chr7:128766335-128767
cg18935349	X	75004943	
cg19873496	3	197105397	
cg19149132	10	130854436	
cg15105326	3	147108916	chr3:147108511-147111
cg02399044	12	2500229	
cg20071744	8	141057329	chr8:141057284-141057
cg04800768	17	80545544	chr17:80545433-805456
cg06077670	3	99629837	
cg11647481	7	4781704	chr7:4784820-4785058
cg06070578	X	102602857	
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cg24885650	10	11069298	
cg01971880	12	34474637	
cg19058262	19	1231292	chr19:1230974-1231323
cg02529544	16	87690083	
cg09402276	10	50887472	chr10:50887565-508878
cg05973772	4	154178277	
cg00678709	3	14584745	
cg23476877	5	176543964	chr5:176543900-176544
cg10239600	14	103411866	
cg16007456	1	101004638	chr1:101004471-101005
cg20930366	5	113698847	chr5:113696516-113699
cg15212354	10	422330	chr10:422180-422411
cg19550490	7	157915530	chr7:157918704-157919
cg18401298	4	40890484	
cg18057887	11	133800913	chr11:133800684-13380
cg18602928	17	80747240	
cg09953988	X	41334352	chrX:41332738-4133412
cg01763090	15	31775406	chr15:31775540-317769
cg20319634	17	72903450	
cg02691002	5	233697	
cg24810473	5	139090314	chr5:139088812-139091
cg26340737	6	32145373	
cg07973026	4	103553119	

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cg13200474	4	189602236	
cg10300188	11	2890577	chr11:2890388-2891337
cg16648494	15	32606571	chr15:32604647-326078
cg21173317	1	1478665	chr1:1476093-1476669
cg10318197	8	141294172	
cg13925890	5	170863162	
cg20324110	X	119249449	chrX:119249439-119249
cg12474748	18	77465527	chr18:77465403-774656
cg19388016	19	3435350	chr19:3434929-3435417
cg03045635	4	9783198	chr4:9783035-9784960
cg18651470	6	114662697	chr6:114663328-114664
cg01907476	1	148929710	
cg02158292	6	31868842	chr6:31868781-3187031
cg06179765	7	23287352	chr7:23287221-2328750
cg20859099	2	240082138	
cg00144817	8	17503298	
cg01405040	2	176964137	chr2:176964062-176965
cg01624004	7	150745494	chr7:150746002-150746
cg00682090	17	3733468	
cg13571576	15	101587971	
cg26586384	17	12526632	
cg19812706	11	33060549	chr11:33060699-330618
cg06096175	20	60701350	chr20:60696561-606983
cg22069286	4	140781209	chr4:140781109-140781
cg04083533	6	4062956	
cg19273694	2	24233923	chr2:24232680-2423326
cg10069394	11	119453007	chr11:119455153-11945
cg08828621	13	112679081	
cg26652079	19	5707316	chr19:5707315-5707524
cg03889767	4	987672	chr4:984926-985695
cg26249873	10	25465430	chr10:25463756-254656
cg26548311	15	52821789	chr15:52820333-528216
cg16986571	13	114872102	chr13:114875198-11487
cg10980329	7	32532231	chr7:32535086-3253554
cg06286796	3	64008041	chr3:64008883-6400929
cg12176022	X	102864314	chrX:102862719-102863
cg05406088	15	66947617	chr15:66947360-669475
cg13251533	12	132286017	chr12:132285972-13228
cg12139873	2	151397889	
cg01005322	20	25059984	chr20:25061761-250629
cg07949720	13	112856747	
cg04453552	16	57394387	
cg24107899	6	161771136	
cg18456140	11	67810268	chr11:67806251-678066
cg24462702	X	135730445	
cg23468699	14	101526893	
cg10109731	16	88472541	
cg00854242	18	74961724	chr18:74961556-749638
cg16145071	2	101727897	
cg27349909	4	746564	
cg25763393	19	52956832	chr19:52956656-529572
cg18461733	7	26188268	chr7:26191794-2619275
cg15487867	1	1475742	chr1:1476093-1476669

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cg26961332	19	18420631	chr19:18420489-184207
cg25848652	11	17591822	
cg11492063	17	5990345	
cg18142615	11	128563618	chr11:128562671-12856
cg21297493	1	156357905	chr1:156358050-156358
cg02796278	19	885898	chr19:885746-886200
cg11521434	1	38227381	chr1:38227079-3822774
cg17098995	11	34492984	
cg14330479	8	1808270	
cg07375964	7	16439254	
cg23221544	X	152907546	chrX:152907595-152908
cg06720768	2	7464944	
cg15558969	2	748534	
cg16304950	18	5543945	chr18:5543437-5544241
cg18124063	1	168106719	chr1:168105316-168106
cg07940971	10	568540	
cg23207280	3	152147674	
cg00034336	2	8684126	
cg09093150	5	32709301	chr5:32709910-3271445
cg27630540	4	1347166	
cg27054514	1	2252995	chr1:2253723-2254758
cg20450471	6	28584061	chr6:28583934-2858428
cg24090908	12	12605470	
cg19339021	7	2697963	chr7:2697934-2698204
cg06018666	4	10079364	chr4:10079335-1007955
cg18342462	11	111385659	chr11:111385337-11138
cg24709681	3	140771372	chr3:140769886-140771
cg10205045	15	69087809	
cg11825249	17	10651577	
cg22011370	5	112770203	
cg12262378	17	6899522	chr17:6898820-6900427
cg01290478	17	80890438	chr17:80889046-808894
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cg00502209	15	101626824	chr15:101626334-10162
cg22117143	9	13251431	
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cg16221651	7	16438465	
cg01225086	12	121175417	chr12:121177115-12117
cg20294752	8	143414639	
cg11557492	19	56002240	chr19:56002140-560024
cg18894028	11	68156978	chr11:68158059-681583
cg14871932	7	44185323	chr7:44184770-4418569
cg01962727	16	46603059	
cg19552441	22	18275800	chr22:18275679-182759
cg00159780	8	86574469	chr8:86573421-8657524
cg23972301	1	117504011	
cg09595415	Y	2655942	chrY:2657802-2658099
cg03183215	10	1252341	chr10:1252141-1252505
cg23180593	13	111301487	chr13:111301316-11130
cg15077087	2	241070823	chr2:241069198-241069
cg07489488	10	400897	chr10:396943-397228
cg01833044	8	1759492	

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cg07041681	16	87737091	chr16:87738617-877388
cg11880242	11	102282062	
cg14299483	14	101967780	
cg24519526	22	39483689	
cg13896891	9	136741139	
cg22087053	5	140751506	chr5:140751298-140751
cg12557114	6	112375870	
cg22795586	1	170629555	chr1:170630456-170630
cg13677149	7	27284789	chr7:27284639-2728623
cg23969380	12	131708174	
cg22461434	19	41640676	chr19:41640631-416408
cg05307865	X	152482021	
cg20957182	X	70823865	chrX:70823513-7082410
cg23996846	8	10383156	
cg08785317	16	86604854	chr16:86599355-866026
cg06562372	7	87230196	chr7:87230059-8723026
cg04061482	X	117629338	chrX:117629130-117629
cg15393676	8	134251264	
cg20139338	11	64120656	
cg16550477	X	8769499	chrX:8769177-8769559
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cg19830849	3	48677553	chr3:48677529-4867787
cg15996284	7	156296906	
cg11885221	13	25620993	chr13:25620937-256215
cg04848693	7	2078786	
cg17738743	22	20710577	chr22:20708651-207165
cg11218432	10	3150898	chr10:3148406-3148625
cg10523198	13	100605441	chr13:100608122-10060
cg06008531	7	90233961	
cg02584537	10	131569018	
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cg06106265	7	2195912	chr7:2195683-2195983
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cg21555471	15	41060201	chr15:41055396-410567
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cg13023646	4	165898835	
cg18439861	5	140807423	chr5:140807339-140807
cg12427264	6	144508349	chr6:144507826-144508
cg20787969	3	3221595	chr3:3221083-3221617
cg20311673	2	1746207	chr2:1746833-1748971
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cg13030539	X	55290965	
cg25024074	2	182322501	chr2:182321761-182323
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cg12645284	15	79092878	chr15:79092538-790928
cg11637968	4	159732036	
cg10876737	5	1052223	chr5:1053544-1053807
cg27414909	4	1201492	chr4:1202956-1203200
cg17019070	10	73466639	
cg14036303	3	125876217	
cg15821544	1	43473840	chr1:43472867-4347333
cg12877723	8	57358312	chr8:57358126-5735941

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cg02666566	6	2510173	
cg26827394	16	1362626	chr16:1363813-1364496
cg20588703	7	156371613	
cg19327049	12	133306772	chr12:133308488-13331
cg17263026	2	121453143	
cg10199770	8	143152889	
cg18136895	15	74290733	chr15:74290344-742907
cg14214635	9	138816622	
cg14079463	6	127796989	chr6:127796286-127797
cg17943995	1	18617630	
cg26531551	13	113702436	chr13:113701833-11370
cg09427369	3	32210781	
cg03998866	16	88935317	chr16:88937055-889373
cg12600174	7	27205230	chr7:27203915-2720646
cg04206025	1	16975443	chr1:16973485-1697504
cg14482308	2	18059109	chr2:18059038-1805924
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cg25614269	11	5949877	
cg12640180	8	144208685	
cg03383508	2	119591097	chr2:119592602-119593
cg01125608	5	646071	chr5:646055-646291
cg19843760	16	90160979	chr16:90160332-901610
cg02716147	3	126733173	chr3:126732968-126733
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cg20467755	19	49183887	chr19:49183498-491841
cg18958339	11	129788450	
cg14224196	9	134183545	chr9:134183330-134183
cg24080008	1	38600199	
cg16644803	10	133458190	chr10:133458017-13345
cg00312872	18	44557732	chr18:44554879-445566
cg11094040	10	128973797	chr10:128973590-12897
cg03360001	X	53453272	chrX:53448968-5344977
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cg00081019	1	243658800	
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cg10140906	15	83240578	
cg03108070	6	33245490	chr6:33244677-3324555
cg11344566	2	124782885	chr2:124782252-124783
cg04029366	X	45017072	chrX:45016977-4501717
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cg26792116	3	168865089	chr3:168864030-168864
cg23852781	11	1258213	chr11:1257584-1257806
cg05902834	4	189024495	chr4:189027609-189028
cg19033943	7	1140782	chr7:1141229-1141545
cg04320956	16	69143512	chr16:69143499-691439
cg14325184	22	21025079	chr22:21024739-210254
cg01315092	2	120980375	chr2:120980332-120981
cg26709693	4	1305780	chr4:1303490-1303835
cg13662851	12	48723821	chr12:48723323-487238
cg03631459	10	54631369	chr10:54631211-546314
cg06706159	19	18260350	chr19:18260252-182605
cg10576499	2	80101315	
cg04440717	10	133938266	chr10:133937695-13393
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cg01140660	11	133233200	chr11:133230884-13323
cg09380415	19	40380319	chr19:40380216-403804
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cg00169354	20	54922827	chr20:54919036-549193
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cg00594866	2	237478577	chr2:237476311-237477
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cg03421195	10	7517215	
cg14606117	17	35870413	chr17:35872722-358730
cg09606452	X	18239054	chrX:18238232-1823907
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cg02332456	X	37026473	chrX:37026348-3702670
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cg09070855	12	133302174	chr12:133303808-13330
cg19349861	11	133402246	
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cg08973950	7	1083309	chr7:1084387-1084595
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cg16654419	10	135379580	chr10:135378883-13537
cg27519455	7	157323034	chr7:157320462-157320
cg09788778	6	31867822	chr6:31867691-3186795
cg19721065	12	113549986	chr12:113549885-11355
cg14918358	X	49158640	
cg02597199	15	101098829	chr15:101094520-10109
cg21728844	2	233749736	
cg17543488	5	172672959	chr5:172672311-172672
cg18912470	4	57848125	chr4:57844857-5784520
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cg18592195	1	227963171	
cg01953429	4	1367848	chr4:1366462-1366688
cg18137598	14	104205122	chr14:104205070-10420
cg27609342	X	74145250	chrX:74143852-7414517
cg08934126	1	9942543	
cg03983213	7	157475737	chr7:157476886-157486
cg03897412	12	57599056	chr12:57596968-575973
cg01904634	16	2160904	chr16:2157862-2162139
cg10640168	8	141360745	chr8:141359155-141359
cg00144180	2	240294362	
cg13011976	X	55101289	
cg02968407	7	1660685	chr7:1660480-1660781
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cg14437072	8	144461130	chr8:144461972-144462
cg22679316	12	54396990	chr12:54399412-543996
cg06966660	10	123923066	chr10:123922850-12392
cg02602423	7	105255065	
cg10964472	11	1241885	
cg02088166	5	142488	
cg08579577	X	8751402	chrX:8751285-8751608
cg26307355	7	73938543	
cg03595123	11	63452694	chr11:63448704-634493
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cg27483767	11	1098080	chr11:1096272-1096519
cg09304136	11	17905750	chr11:17905443-179059
cg11380881	2	2829731	
cg26863085	19	10747328	chr19:10747141-107474
cg02817925	19	1046325	chr19:1046249-1047701
cg20715048	10	44680954	
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cg25900280	17	59534847	chr17:59531723-595352
cg16378215	1	149885265	
cg18725375	11	86142478	chr11:86142379-861426
cg12215609	20	36031618	chr20:36031537-360318
cg02723291	12	22777465	chr12:22777988-227783
cg03054424	16	14965269	
cg02677286	8	1051703	chr8:1051641-1051896
cg21929771	1	29586580	chr1:29585897-2958659
cg17693669	2	8711075	
cg10692693	7	101688648	
cg25454298	7	150815445	chr7:150817005-150817
cg12866103	14	20020762	
cg03218198	16	588562	chr16:590093-590368
cg11889692	14	77591661	chr14:77591159-775918
cg06532268	6	25732817	chr6:25732692-2573295
cg26092675	6	26225258	chr6:26225386-2622579
cg17546196	8	143398481	chr8:143398358-143398
cg09807356	16	88905700	chr16:88905509-889057
cg01623282	16	89252924	
cg26316511	12	96709972	
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cg26127778	15	93617141	chr15:93615622-936171
cg11567723	7	152163944	chr7:152161034-152162
cg22022973	19	21933745	chr19:21933434-219338
cg07475394	17	79466438	chr17:79465815-794662
cg06060868	5	231934	
cg00675891	13	113698994	chr13:113701833-11370
cg11553045	5	178687826	chr5:178684326-178684
cg21293831	6	170591802	chr6:170592384-170593
cg15320905	12	114162813	
cg24859945	7	155832992	
cg03374231	16	86903449	
cg18786873	1	110610899	chr1:110610265-110613
cg07509935	14	24780167	chr14:24779874-247809
cg04094210	2	136343909	
cg18002126	7	3221373	
cg13790727	20	36148738	chr20:36148603-361501
cg16232530	7	1097131	chr7:1097405-1097953
cg24946911	12	2788654	chr12:2788614-2788879
cg24452821	11	113953812	chr11:113953620-11395
cg25791773	11	129910324	chr11:129910305-12991
cg06282524	X	139593371	chrX:139593105-139593
cg05213048	Y	14100276	chrY:14100002-1410059
cg17296120	8	9705580	
cg26301689	3	142681704	chr3:142681137-142683
cg20278383	13	96086098	chr13:96086047-960862
cg16251986	15	101869516	
cg23527409	19	44956065	chr19:44952416-449528
cg12906880	6	34294802	
cg20333904	2	240724165	
cg14305701	10	134527922	chr10:134527742-13452
cg12028762	19	3496671	chr19:3500416-3500840
cg24530787	X	91034390	chrX:91033993-9103462
cg26639864	11	2569788	
cg04578774	11	44332664	chr11:44332314-443327
cg25537993	19	58545182	chr19:58545115-585458
cg09432136	19	1818466	chr19:1818465-1818781
cg24975842	20	57416221	chr20:57415135-574171
cg22136672	3	12581830	
cg24630516	11	75852389	
cg07727134	12	120222632	
cg18516158	5	76939772	chr5:76941395-7694188
cg26350007	11	2013524	chr11:2013333-2013617
cg15889703	7	97937000	
cg07194832	7	97978655	
cg02690148	3	17375660	
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cg04027548	12	21926447	
cg06002687	8	80783997	
cg06489433	16	89491229	chr16:89487760-894881
cg01573747	19	17008740	chr19:17007101-170088
cg08310581	2	131797438	chr2:131797362-131798

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cg03093076	19	1390962	chr19:1390693-1391304
cg05882680	17	48042605	chr17:48041282-480430
cg00426425	16	87677927	chr16:87677885-876786
cg22705131	X	26210609	
cg25900085	8	65291513	chr8:65290108-6529094
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cg25188395	7	27204052	chr7:27203915-2720646
cg21928406	5	140802669	chr5:140802399-140802
cg02052242	12	3281658	
cg06363968	16	84629008	
cg20382601	13	110571583	
cg09510128	7	1132036	chr7:1131625-1133187
cg05456652	X	34960884	chrX:34961430-3496170
cg06633543	14	100151561	chr14:100149727-10015
cg18085033	14	101198783	chr14:101200617-10120
cg11002258	12	130976515	
cg02645450	16	3532570	chr16:3534833-3535066
cg18128887	1	24861708	chr1:24861702-2486192
cg12371263	12	132522852	chr12:132520325-13252
cg11186850	8	39695788	
cg07425646	1	4221616	chr1:4221387-4221672
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cg21768014	8	2060983	
cg18204334	2	2864572	
cg07452997	X	118893383	chrX:118891923-118893
cg26707398	19	50713914	chr19:50713630-507140
cg11464436	7	792090	chr7:791984-792238
cg22902939	2	201355148	
cg22156300	3	175338899	
cg04078658	7	2054064	chr7:2054060-2054386
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cg20745910	18	34340791	chr18:34340584-343408
cg14820221	19	5593932	chr19:5593709-5594194
cg19417588	11	68529067	
cg00719108	2	220080756	chr2:220082991-220084
cg25783361	7	47783949	
cg17994840	10	134572417	
cg11875917	8	4980497	chr8:4980317-4980946
cg15785868	12	110156356	chr12:110156267-11015
cg06986584	1	180904677	chr1:180904316-180904
cg22335155	1	179100500	
cg08718490	4	52943099	chr4:52942978-5294324
cg20538951	7	5360801	chr7:5360640-5360869
cg03333893	7	211878	
cg13889508	3	11059010	chr3:11058818-1105905
cg11753771	1	214638070	
cg14564616	5	1876337	chr5:1874907-1879032
cg15257681	4	727544	chr4:724335-726070
cg02607059	15	101632053	chr15:101629128-10162
cg10294252	15	74912474	chr15:74906938-749085
cg12036553	10	1148121	chr10:1147967-1148271

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cg08330572	5	620259	chr5:623167-623555
cg25399267	21	45926600	chr21:45926531-459267
cg06038944	2	181010312	
cg20057198	2	731561	chr2:732036-733096
cg11897433	7	156880681	
cg17913405	17	25290204	chr17:25289487-252904
cg06135495	18	47338985	chr18:47339411-473409
cg05837235	17	77043815	chr17:77043741-770444
cg12109260	8	144850435	chr8:144852777-144854
cg20461275	2	205466396	
cg26402417	11	94841384	
cg10525574	12	95228036	
cg23569120	2	25470883	chr2:25470765-2547097
cg27534671	13	52979688	chr13:52979999-529805
cg19625388	13	113977418	chr13:113975893-11397
cg10204707	19	53794711	chr19:53794411-537947
cg14508093	9	98862825	
cg20894884	6	7247534	chr6:7246665-7247572
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cg00701051	1	145385391	chr1:145385289-145385
cg01407576	7	55515199	chr7:55516871-5551724
cg17980283	2	45156642	chr2:45155195-4515704
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cg25416334	5	1725184	chr5:1725183-1725420
cg03159877	12	118199247	chr12:118198767-11819
cg27411547	8	142287226	
cg23558227	7	97586426	
cg04223956	1	198201614	
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cg12650985	1	223289931	
cg16115627	7	154684433	chr7:154684402-154684
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cg11611320	6	28827692	chr6:28831682-2883213
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cg13579167	11	2772852	
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cg25009498	17	80562120	chr17:80559025-805594
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cg23586121	10	134586462	chr10:134586170-13458
cg18403285	11	1317034	chr11:1315467-1317115
cg11263997	11	70257280	chr11:70257279-702575
cg07503662	16	87761121	
cg19305545	1	3548894	
cg23170483	X	54508656	
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cg09815793	X	82763239	chrX:82763571-8276446

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cg05592035	17	72462984	
cg26158897	15	53083135	chr15:53080458-530836
cg01831771	13	113428172	chr13:113429177-11342
cg05014291	2	11780446	
cg16925682	X	49032012	chrX:49032261-4903256
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cg16659657	3	185288478	
cg03206660	11	134021905	
cg23936587	19	10406145	chr19:10405924-104063
cg01408363	12	125033903	
cg21239572	9	111617595	chr9:111617320-111618
cg26365690	6	142410061	chr6:142409473-142410
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cg05950018	10	134605986	chr10:134605584-13460
cg12135598	4	717040	chr4:716281-716977
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cg06874656	11	131780353	chr11:131780328-13178
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cg21104449	3	196485278	
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cg17099815	15	31217407	
cg11536851	7	4832359	chr7:4832111-4832481
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cg13095991	4	160789746	
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cg22304543	8	82530924	
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cg02250241	15	75648987	chr15:75648404-756487
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cg27309282	4	1016081	chr4:1017524-1018938
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cg02074191	5	140779461	chr5:140779013-140779
cg24131141	5	1270787	chr5:1270778-1271101
cg26075905	14	102391388	chr14:102394772-10239
cg10012722	2	237085763	chr2:237086727-237088
cg17916447	3	197356641	chr3:197354106-197355
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cg06413196	7	640338	chr7:644181-644461
cg08642538	13	22058122	chr13:22057995-220582
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cg12062672	19	643555	chr19:643092-643720
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cg14433037	7	824325	chr7:821689-822634
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cg07514703	2	45155774	chr2:45155195-4515704
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cg13667655	9	77707358	chr9:77702885-7770381
cg06048662	5	1216726	chr5:1216639-1217081
cg00031896	12	122020205	chr12:122018170-12201
cg00245896	4	8034100	
cg11441553	12	57614120	chr12:57609976-576111
cg20699960	11	64135904	chr11:64135815-641363
cg18485070	2	132203745	chr2:132202265-132203
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cg02023345	10	63212226	chr10:63212495-632130
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cg05223249	X	55020520	

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cg00139317	X	24665544	
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cg10489284	5	1088244	chr5:1088243-1088464
cg07860213	8	70982039	chr8:70981873-7098488
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cg13998712	17	34062321	chr17:34062168-340624
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cg04716580	10	134546291	chr10:134549623-13454
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cg17713751	7	101723568	
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cg15798163	13	113933520	
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cg10692302	3	51747227	chr3:51749754-5175006
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cg27255454	16	1841732	chr16:1840623-1842688

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cg03002835	6	168476648	chr6:168476320-168476
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cg27452062	X	110039414	chrX:110038946-110039
cg16607197	16	968643	chr16:967241-967619
cg25916993	5	134880580	chr5:134879443-134879
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cg26796518	12	6184516	
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cg04200026	16	89345595	chr16:89345463-893485
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cg16331358	10	1147675	chr10:1147967-1148271
cg11770080	5	78408179	
cg02515033	7	2205283	
cg26010182	1	146713493	chr1:146714089-146715
cg04723401	14	29229249	
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cg12434747	15	70740470	
cg16904899	3	13860638	chr3:13860434-1386088
cg06027112	8	49890360	chr8:49890386-4989087
cg13544966	10	640085	
cg06503255	5	140053350	chr5:140052059-140053
cg03700135	17	707059	chr17:708319-708598
cg04159903	5	42949799	chr5:42951076-4295241
cg09962925	16	86228639	
cg15002761	11	133816097	
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cg22242857	18	76751952	chr18:76751939-767555
cg04292660	4	155661234	chr4:155661678-155661
cg18245268	14	95109786	
cg23950714	5	176935364	chr5:176931110-176931
cg26809926	7	138139745	
cg25967745	14	100118974	chr14:100118877-10011
cg14241609	11	128781826	
cg23282561	4	1229392	chr4:1229249-1229501
cg10372920	17	5800501	
cg08190858	12	54321346	chr12:54321301-543217
cg01275006	19	38876250	chr19:38876070-388763
cg12637786	2	220355222	
cg21502629	X	49196412	chrX:49197477-4919809
cg04428718	6	171021519	chr6:171021489-171022
cg01783070	20	21686293	chr20:21686199-216876
cg26305504	19	947612	chr19:947547-947981
cg19660531	12	5937409	chr12:5936876-5937085
cg09824721	3	170588815	chr3:170587936-170588
cg00414384	11	68518048	chr11:68517667-685181
cg07278332	7	94294290	chr7:94293609-9429386
cg01993818	14	34270437	chr14:34268946-342704
cg12062220	15	53087232	chr15:53087211-530874
cg12314682	17	77952463	chr17:77951845-779522
cg11951433	11	130078236	chr11:130078173-13007
cg24376548	1	207588998	
cg02743895	17	77394015	
cg02602182	X	40026844	chrX:40026592-4002837
cg06911753	11	47611236	chr11:47611138-476124
cg03310874	7	4850260	chr7:4848251-4849204
cg18144692	8	107095959	
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cg07572348	19	5997117	chr19:5997031-5997435
cg02288564	19	49934404	chr19:49934316-499348
cg03097114	7	155679586	
cg24373369	15	65320737	chr15:65321431-653219
cg05337594	7	21081930	
cg07176677	10	101771161	
cg18927067	11	71827947	chr11:71823668-718239
cg07855471	3	29782270	
cg13172627	X	26576336	chrX:26575758-2657617
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cg05477246	16	601244	chr16:604801-605348
cg00435469	11	1495117	chr11:1491197-1491525
cg18890615	13	112161629	
cg05706189	1	228504454	chr1:228503556-228504
cg03372659	22	49698771	chr22:49698417-496987
cg03537537	8	88886262	chr8:88886171-8888644
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cg11942622	15	79298659	
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cg07244043	3	112725993	
cg12317217	5	140203603	chr5:140202573-140203
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cg17219656	1	236924443	
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cg05999195	5	4866602	chr5:4866317-4866630
cg00661320	10	73848825	chr10:73846806-738482
cg10590657	3	192538384	
cg21548869	14	105834472	chr14:105836031-10583
cg08840616	5	1036426	chr5:1037964-1038426
cg17813310	4	87974092	
cg17555660	7	38253299	
cg14689317	11	64128973	chr11:64126430-641269
cg22031783	1	3128606	
cg09251492	1	3701070	chr1:3703672-3703908
cg14212850	17	77460269	chr17:77460245-774606
cg18929217	12	42326707	
cg19679397	11	70048852	chr11:70049099-700498
cg27257566	X	3265053	chrX:3263353-3265347
cg20391058	2	2295451	
cg21665850	2	731073	chr2:732036-733096
cg01787821	3	10400481	chr3:10400381-1040058
cg22717323	7	2094977	
cg05177065	10	133204297	
cg17020497	7	63028201	chr7:63028071-6302833
cg15966877	19	17758119	chr19:17758055-177583
cg21171954	9	94495731	chr9:94495366-9449576
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cg04418647	8	50653901	
cg08268734	8	756400	
cg24675998	3	134369661	chr3:134369464-134370
cg27341926	10	118032905	chr10:118030732-11803
cg07771477	13	111142065	
cg01788773	8	1113662	chr8:1113058-1114073
cg26473833	10	129063066	
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cg27181199	12	31945286	chr12:31944806-319452
cg23468479	12	53509381	
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cg02212575	3	156838403	chr3:156837983-156838
cg02008951	19	5703619	chr19:5707315-5707524
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cg25729907	3	146263345	chr3:146262126-146262
cg21385821	17	50237844	chr17:50235175-502364
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cg00823843	1	244094885	chr1:244094755-244095
cg14063817	6	537496	chr6:537144-537522
cg01567115	16	989564	
cg04558386	6	13815568	chr6:13813943-1381494
cg21545862	5	174159294	chr5:174158680-174159
cg05364058	7	27498008	
cg07154754	12	132514292	chr12:132514283-13251
cg11244095	X	135382675	chrX:135382457-135382
cg23322383	X	67916187	chrX:67913299-6791413
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cg18075761	7	75617028	
cg13059335	8	24242109	
cg09340639	1	157789662	
cg23245063	14	100154773	chr14:100149727-10015
cg07544187	19	19651235	chr19:19650683-196512
cg01473128	6	31828335	chr6:31830299-3183094
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cg02194243	16	54324597	chr16:54317821-543246
cg05355225	8	86350568	chr8:86350765-8635119
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cg07478662	19	5047466	chr19:5047451-5047830
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cg11336860	13	112575966	chr13:112575723-11257
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cg15598789	1	5955929	
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cg22731271	2	66667059	
cg09491828	5	115367063	
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cg01340347	5	173415630	chr5:173415924-173416
cg24847996	12	123340818	
cg14496282	7	544525	
cg15577180	7	611487	chr7:611232-611602
cg05374412	16	82660727	chr16:82660651-826618
cg21399703	1	247681439	chr1:247681399-247681
cg10946263	5	36243704	chr5:36241003-3624266
cg04826882	13	114838756	chr13:114838658-11483
cg12467143	X	11684543	chrX:11682333-1168454
cg17401837	X	30261250	chrX:30265172-3026555
cg05242402	7	1491921	chr7:1491773-1491975
cg09561365	22	45676755	chr22:45680644-456810
cg13910651	5	3962477	chr5:3962286-3962512
cg16139202	5	134662788	chr5:134662721-134663

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cg17698295	8	145106299	chr8:145103285-145108
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cg09387992	8	103497121	
cg26912592	17	37074981	chr17:37074860-370750
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cg06615999	16	89178870	
cg12299795	1	64982093	
cg16570917	1	43996062	chr1:43996724-4399759
cg10604258	15	93588851	chr15:93588102-935885
cg22599477	4	25507245	chr4:25506581-2550807
cg24346858	6	41738686	
cg08446143	X	47049440	chrX:47050088-4705034
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cg00448752	1	101775370	
cg19155932	20	56725873	chr20:56725857-567261
cg03316628	16	368066	
cg22326973	4	39771745	chr4:39771679-3977194
cg06906472	2	107502801	chr2:107502353-107504
cg27635110	2	1926436	
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cg16198416	4	155669266	chr4:155664819-155665
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cg25995995	2	240927173	
cg23069923	19	19626251	chr19:19624954-196272
cg03705912	5	16179210	chr5:16179064-1618042
cg13252710	13	20134915	chr13:20135399-201360
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cg24641302	1	165087025	chr1:165086756-165087
cg11806178	20	39319929	chr20:39316550-393199
cg14020326	14	105821532	chr14:105821482-10582
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cg14635160	9	82526898	
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cg16477196	17	20516820	
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cg27058166	11	2285989	
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cg04554240	3	138170552	chr3:138170508-138171
cg01883989	2	208019901	
cg23419170	18	12067067	chr18:12067145-120685
cg10534507	15	82336761	chr15:82335472-823399
cg26264232	7	27138751	chr7:27135342-2713673
cg23828814	12	131747277	
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cg16195332	6	158937358	chr6:158937285-158937
cg08136772	13	53420933	chr13:53419897-534228
cg19619585	15	101170019	
cg05418779	X	138771271	chrX:138773796-138774
cg13917662	13	100548513	chr13:100547633-10054
cg10838844	21	44480699	chr21:44480559-444807
cg19140429	17	48858746	chr17:48858635-488589
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cg09720205	16	57508738	
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cg01036050	6	157472067	
cg17676994	2	241405196	chr2:241403950-241404
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cg13226924	17	2275664	chr17:2275525-2275753
cg14364844	9	37830047	
cg12140144	1	2984275	chr1:2983925-2987962
cg12467264	5	175200071	chr5:175200315-175200
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cg23928118	5	140215201	chr5:140215200-140216
cg24980040	10	1714535	
cg23514016	5	78407564	
cg11599864	6	38145464	
cg22656750	5	167689454	chr5:167689227-167689
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cg13629201	9	5111420	chr9:5110784-5112274
cg20398123	21	45926961	chr21:45926531-459267
cg11842944	20	32378867	chr20:32378837-323791
cg25193157	7	791962	chr7:791984-792238
cg18748888	17	76102450	chr17:76100679-761011
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cg14654363	6	28601443	chr6:28602853-2860329
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cg16602369	5	10564338	chr5:10562816-1056568
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cg22659681	17	7318433	chr17:7320371-7320945
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cg00181849	16	920856	chr16:919858-920117
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cg23189410	3	147125712	chr3:147126988-147128
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cg09895223	X	110039197	chrX:110038946-110039
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cg27177195	17	34945903	chr17:34948053-349489
cg14044640	7	27187560	chr7:27186927-2718769
cg16246200	18	77222022	chr18:77221855-772221
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cg11640008	19	42914542	chr19:42914500-429148
cg01538344	X	100546291	chrX:100546063-100546
cg15279616	6	168467854	
cg25018208	6	37338607	
cg05760937	10	134552168	chr10:134555113-13455
cg10084644	7	99775521	chr7:99774733-9977558
cg09593727	4	132273830	
cg13549321	19	33697274	chr19:33696189-336972
cg02082613	3	180588094	
cg16697214	7	50343361	chr7:50342895-5034345
cg09159452	7	2609861	
cg03102386	11	128746438	
cg12205555	12	28837108	
cg27617132	10	134543871	chr10:134539817-13454
cg14440640	14	61578115	
cg16721321	4	1202696	chr4:1202956-1203200
cg04998671	14	104000505	chr14:104000887-10400
cg13782301	6	32116875	chr6:32116590-3211722
cg27608806	12	125509780	chr12:125509569-12550
cg09592155	17	8029700	chr17:8029673-8030090
cg13059719	1	179712027	chr1:179711947-179713
cg00553149	7	99775558	chr7:99774733-9977558
cg03769088	Y	8120126	
cg20823730	8	790768	chr8:789923-790798
cg06459454	8	146033798	chr8:146032710-146033
cg19934382	11	94145963	
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cg00364644	16	88234627	chr16:88233988-882341
cg22622667	10	134790769	chr10:134790715-13479
cg22881266	7	157543942	
cg14852134	20	13200748	chr20:13200670-132026
cg12183594	7	148802155	chr7:148801209-148802
cg15442155	14	104674859	
cg12737854	7	42005612	chr7:42005067-4200612
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cg06755155	1	5955966	
cg00907473	1	90459283	chr1:90460399-9046123
cg06662140	1	18809297	chr1:18808873-1880966
cg15615586	6	32730040	chr6:32729342-3272987
cg07728485	5	1279582	chr5:1277467-1277713
cg12225220	4	87281434	
cg04632887	20	3065559	chr20:3063005-3064146
cg12029639	13	36050993	chr13:36052553-360531
cg11829626	17	18811532	
cg00360761	2	43398079	chr2:43398040-4339827
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cg11769925	8	80301560	
cg08840280	5	6749347	
cg09555153	4	186544662	chr4:186544754-186545
cg22500428	12	4381882	chr12:4378366-4382222
cg04652943	2	3750565	chr2:3750828-3751927
cg12984349	7	1519886	chr7:1518997-1519444
cg20304727	7	98255916	

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cg04371585	X	3264725	chrX:3263353-3265347
cg00097518	6	139115476	chr6:139116946-139117
cg01084500	1	244973602	
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cg22523852	15	27112049	chr15:27112030-271134
cg20065718	12	133430224	chr12:133429925-13343
cg13625631	15	70340707	
cg06412320	10	1789454	
cg18498090	8	1340584	chr8:1341220-1342166
cg08072507	7	133897858	
cg23402097	14	104640581	chr14:104640469-10464
cg14604568	7	32110523	chr7:32110063-3211091
cg17103088	19	3600595	chr19:3599914-3600566
cg03449456	1	3191219	
cg23845400	6	36343668	
cg15911153	5	138730783	chr5:138727710-138730
cg11743671	1	5956021	
cg01069311	X	47373245	chrX:47372476-4737304
cg08979319	6	100896055	chr6:100895773-100896
cg21538208	4	4864488	chr4:4864456-4864834
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cg01000954	5	140821244	chr5:140821228-140821
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cg01600921	2	97649526	chr2:97651764-9765244
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cg03971454	1	43770557	chr1:43770522-4377088
cg15928392	2	81694446	chr2:81694322-8169468
cg23530031	11	7541099	
cg08561856	19	44324945	chr19:44324436-443250
cg08223945	7	151829665	chr7:151828355-151828
cg24281668	12	113661270	chr12:113659038-11365
cg26109154	1	245411604	
cg19067392	12	131291630	
cg00475112	12	9444815	
cg24996161	5	140735397	chr5:140736821-140737
cg08037985	21	47287206	chr21:47287012-472874
cg14799696	7	157571491	chr7:157568163-157568
cg11781718	6	26204333	chr6:26204764-2620521
cg25207052	1	2736859	
cg24033491	1	181382830	chr1:181382290-181382
cg00054971	10	129796937	
cg02909018	13	113696937	
cg24932788	17	70118912	chr17:70116274-701199
cg15149712	19	38956783	chr19:38956756-389570
cg24891660	8	145003653	chr8:145003589-145004
cg03700001	12	133073220	chr12:133073397-13307
cg07238832	11	27681475	
cg10372921	15	74218733	chr15:74218696-742203
cg26154851	12	101961257	
cg04031507	1	35334359	chr1:35334304-3533450
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cg14033944	8	11627058	chr8:11627091-1162766
cg01636873	13	111281479	chr13:111277412-11127
cg13437581	18	44777799	chr18:44777632-447780
cg00146249	17	79042364	chr17:79045454-790456
cg06377362	13	113500867	chr13:113497296-11349
cg20030796	17	72356254	chr17:72356096-723563
cg06593910	16	88709927	chr16:88709525-887100
cg16420310	14	50828728	
cg26674943	15	76627788	chr15:76627523-766278
cg25290992	4	183778479	
cg20695297	19	3178844	chr19:3178741-3179986
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cg22657475	X	20135285	chrX:20134203-2013535
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cg19840493	8	142242910	
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cg01544903	16	56697229	chr16:56696892-566972
cg00037314	19	14274039	chr19:14273429-142741
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cg04849508	7	2801959	chr7:2802440-2802698
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cg14178383	9	91347716	
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cg18097155	6	7246900	chr6:7246665-7247572
cg10011015	15	28473421	
cg06379722	20	50804300	chr20:50807798-508088
cg11724984	12	121890864	chr12:121890758-12189
cg18664438	7	155580862	chr7:155579868-155580
cg08092588	14	105041452	chr14:105041307-10504
cg04243901	12	125441307	
cg27589003	7	130132286	chr7:130130739-130133
cg20656975	2	3507718	chr2:3504282-3504628
cg24618413	X	40007471	chrX:40005040-4000706
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cg02452944	5	140810109	chr5:140810494-140812
cg15822010	7	206484	chr7:206451-207365
cg06436667	17	78058704	
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cg21621910	2	102486284	
cg07533148	1	248020812	chr1:248020330-248021
cg07676300	19	11285258	chr19:11285122-112853
cg12044749	8	144995682	chr8:144990270-145002
cg02577387	2	231855524	chr2:231854997-231855
cg13327545	10	22623548	chr10:22623350-226258
cg08452671	8	145451919	chr8:145447159-145448
cg24123311	19	48675164	chr19:48675065-486753
cg17057098	15	89386741	

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cg24069602	17	62045522	
cg25305259	10	51911889	chr10:51912613-519129
cg00440195	16	86652360	
cg01923549	6	41774024	chr6:41773954-4177442
cg00435606	17	16257223	chr17:16255618-162571
cg20356136	4	7802238	chr4:7802191-7802440
cg06912824	11	126078631	chr11:126081369-12608
cg05859395	5	203595	
cg11145055	1	244624752	chr1:244624501-244624
cg18471471	15	100537686	
cg21724239	8	58056113	chr8:58055960-5805624
cg17712694	5	16180068	chr5:16179064-1618042
cg03984347	1	45190262	chr1:45189705-4519055
cg01533689	16	11000899	chr16:11000779-110010
cg16016063	1	165586560	
cg15313740	2	171625337	chr2:171627225-171628
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cg07957458	20	33862215	chr20:33865333-338655
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cg16430402	1	5947386	chr1:5950824-5951029
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cg07343187	15	89390622	
cg21214566	9	138549731	
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cg23664334	1	149288143	chr1:149286812-149287
cg09642408	15	101208028	
cg17827271	4	189191535	
cg21914290	1	170635960	chr1:170633274-170634
cg16962008	7	48075950	chr7:48074838-4807598
cg18402987	7	1209562	
cg04025150	1	34642862	chr1:34642382-3464302
cg06246999	6	100904689	chr6:100905444-100905
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cg15888279	X	30327778	chrX:30326439-3032766
cg17114200	7	4822807	chr7:4823506-4824097
cg07300060	16	54323335	chr16:54317821-543246
cg03877767	2	11680057	
cg07699237	10	134489106	
cg10091798	12	46654629	
cg00865724	19	17346507	chr19:17346165-173468
cg07202869	5	171723771	chr5:171723742-171724

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cg10666926	5	173945243	
cg14469749	14	52127507	
cg21009935	11	68158312	chr11:68158059-681583
cg04745820	2	33249103	
cg10620659	Y	22737391	chrY:22737825-2273805
cg12301921	5	1122879	
cg07548495	2	81421272	chr2:81421204-8142253
cg07792636	1	27878409	chr1:27874417-2787463
cg20860472	13	112598541	
cg19953427	6	166078843	chr6:166073882-166077
cg16103203	1	32041507	
cg15699226	13	78492678	chr13:78492425-784933
cg00945486	8	139890004	chr8:139889881-139890
cg02984614	17	31618409	chr17:31618345-316204
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cg21087160	19	2269166	chr19:2269115-2271364
cg00937691	6	29796105	chr6:29795553-2979659
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cg10526374	11	2292525	chr11:2290104-2292932
cg05289897	10	3904141	
cg08257257	11	68517804	chr11:68517667-685181
cg02586212	1	192544902	
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cg22685807	6	28945189	
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cg17849156	17	79255961	chr17:79255960-792563
cg16886329	20	6100495	chr20:6103436-6103970
cg20664445	17	80969547	chr17:80969748-809701
cg11458217	X	134125022	chrX:134124938-134125
cg25631414	6	169641941	chr6:169641803-169642
cg26492368	10	22634733	chr10:22634000-226348
cg03224901	2	85086620	
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cg19304273	11	49070231	chr11:49069720-490707
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cg15992532	8	142229932	chr8:142229701-142229
cg18697160	10	134184523	
cg10132287	10	131584334	
cg23300732	4	5053496	chr4:5053230-5054092
cg13924635	1	1168432	chr1:1167001-1168985
cg09723184	8	101159106	chr8:101157647-101158

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cg21113768	6	144386848	chr6:144384894-144385
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cg22132026	5	83590	chr5:83428-85530
cg10642957	19	56114094	chr19:56113827-561142
cg13079528	7	4027346	
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cg09822538	1	107682798	chr1:107682889-107684
cg01904812	1	17746340	chr1:17746200-1774654
cg02108196	2	3322515	chr2:3321063-3321293
cg20723473	12	132520836	chr12:132520325-13252
cg06657917	19	613111	chr19:612989-614068
cg05154546	4	3373555	chr4:3374733-3374998
cg21667061	15	60772094	chr15:60771068-607715
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cg06528267	7	49815642	chr7:49813008-4981575
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cg22143064	2	162948592	
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cg10462048	5	140774660	chr5:140772385-140772
cg13832135	15	29442040	
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cg27393146	18	77495563	chr18:77495021-774959
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cg13656404	2	106959384	chr2:106959115-106959
cg17137182	7	82792284	chr7:82791674-8279241
cg19893751	2	45029285	chr2:45028955-4502931
cg16708264	7	157336976	
cg17146473	6	32052428	chr6:32055067-3205560
cg27594095	6	31095276	
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cg13728069	9	140352318	chr9:140352818-140354
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cg27600813	17	9808167	chr17:9808067-9808339
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cg19761682	10	124402817	chr10:124402658-12440
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cg01572549	20	60926800	chr20:60926764-609271
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cg11488401	16	77468373	chr16:77468309-774690
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cg11740194	10	466232	chr10:465928-466396
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cg21699044	8	65281689	chr8:65281903-6528304
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cg14568830	10	23463243	chr10:23462224-234638
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cg11712105	1	113741631	chr1:113741473-113741
cg10414881	14	22993036	
cg15518542	10	1444784	
cg03798045	10	133195086	
cg03691170	6	25727107	chr6:25726454-2572672
cg04983687	16	88558223	chr16:88558051-885583
cg08545132	19	15348803	chr19:15348678-153490
cg08959039	13	111062266	
cg17324588	14	106743777	chr14:106743602-10674
cg03248767	17	9676174	chr17:9674854-9675265
cg08569517	19	2424793	chr19:2424005-2427983
cg03570498	10	131566727	
cg25352836	19	19625264	chr19:19624954-196272
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cg07540917	16	87742602	chr16:87742556-877431
cg22138002	18	44237002	chr18:44236839-442370
cg21486834	17	74477542	chr17:74475239-744754
cg24864576	18	74499573	chr18:74499316-744996
cg26777760	X	132092564	chrX:132090363-132092
cg15710681	11	30348418	chr11:30344536-303449
cg22255690	13	49076999	
cg14711067	22	37975975	
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cg17081408	1	7778321	
cg11105358	5	176758052	chr5:176759071-176759
cg18404559	7	151322523	
cg05453358	8	47529280	chr8:47528989-4752937
cg09030685	16	88943641	chr16:88943427-889436
cg26982271	19	36365679	chr19:36365453-363658
cg04101050	21	40984700	
cg20087519	10	135379242	chr10:135378883-13537
cg01393985	6	89927651	
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cg20373036	X	82763706	chrX:82763571-8276446
cg17339956	3	44283355	chr3:44283239-4428383
cg18592294	19	2790475	chr19:2790376-2790717
cg01301117	7	1953969	chr7:1950279-1950482
cg16434156	14	94497084	chr14:94492639-944932
cg10249705	11	106890150	chr11:106888323-10689
cg03352106	12	21926476	
cg04058752	11	76751369	chr11:76750692-767517
cg07037371	4	112709384	
cg13190540	X	71289504	
cg15527356	1	2276565	chr1:2276358-2276657
cg25494480	6	45387917	chr6:45387346-4538816
cg08417748	11	10002835	
cg23732138	1	175014924	
cg01824933	17	75539901	
cg25086136	8	50823124	chr8:50822270-5082286
cg08269974	19	853054	chr19:852855-853495
cg05348668	2	190686969	chr2:190686740-190687
cg07481380	19	3834519	chr19:3834515-3834903
cg19268477	7	157951471	chr7:157951254-157951
cg00748218	11	19372553	
cg19761271	4	5446052	
cg09825979	7	27179432	chr7:27179062-2717951
cg24395452	4	52943197	chr4:52942978-5294324
cg20275528	17	75369484	chr17:75368688-753705
cg02001099	2	240449715	chr2:240449074-240449
cg09121543	17	61774794	chr17:61776890-617787
cg02229261	19	52222431	chr19:52222423-522232
cg20773479	5	619994	chr5:623167-623555
cg22561647	17	60747596	chr17:60744507-607448
cg16653700	2	1232428	
cg00430613	17	406426	chr17:406197-406502
cg14012082	17	56274407	chr17:56274392-562745
cg11724750	6	163558823	
cg26428731	1	35334352	chr1:35334304-3533450
cg08701479	19	5135291	chr19:5135285-5135545
cg05809668	7	35301188	chr7:35301150-3530173
cg00699997	1	121485059	
cg07856071	5	15928114	chr5:15928088-1592851
cg06144920	16	52503197	
cg23748172	11	66633713	chr11:66631254-666314
cg02521750	16	81712054	chr16:81711864-817122
cg23602489	7	101508949	
cg10288921	2	3289711	chr2:3289426-3289731
cg15001959	2	54483431	chr2:54482924-5448343
cg03753331	2	115919006	chr2:115918737-115920
cg20049422	15	26044289	
cg05516128	8	42269324	chr8:42268436-4226875
cg09870004	16	88050251	chr16:88052061-880523
cg06482904	11	61537000	
cg09788161	X	34148765	chrX:34148740-3414895
cg18942464	2	204106998	chr2:204103464-204104
cg08821656	5	76373091	chr5:76372882-7637372

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cg23238315	7	156259194	
cg27215236	7	878040	
cg21927637	8	48746197	chr8:48743841-4874417
cg01158161	6	26214630	chr6:26217211-2621752
cg14157019	2	65541214	chr2:65540761-6554131
cg05080790	6	54001868	
cg01382281	19	56104340	chr19:56103728-561049
cg09860935	12	21572311	
cg08734740	5	50679149	chr5:50678632-5067937
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cg18599162	15	31217417	
cg23960088	5	34006894	chr5:34007796-3400810
cg18877361	14	105973846	
cg03067362	5	140051861	chr5:140052059-140053
cg02767633	5	2253242	
cg21480464	17	17457767	
cg18058689	13	93879670	chr13:93879245-938808
cg16497431	13	19582812	
cg10450108	5	140208893	chr5:140208753-140209
cg06732667	8	141312916	
cg20035319	17	76102438	chr17:76100679-761011
cg08347626	5	1850140	chr5:1851342-1851564
cg22489321	13	100643388	chr13:100641334-10064
cg25368917	12	124788627	chr12:124788559-12478
cg11324832	3	181441806	chr3:181444409-181445
cg02288552	7	1152401	chr7:1155303-1157445
cg19571721	8	1456819	
cg02753511	11	69468378	chr11:69468810-694691
cg06769094	8	41151382	
cg11546537	10	121508846	
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cg16570314	5	1003099	chr5:1003937-1005687
cg08756121	8	8820884	chr8:8820766-8821112
cg06074994	7	116964789	chr7:116962841-116964
cg08811309	5	87968749	chr5:87968635-8796890
cg03822746	5	257618	chr5:258801-262401
cg13789881	2	86094755	
cg06655810	7	27260102	chr7:27260101-2726046
cg25976563	3	179169592	chr3:179168735-179169
cg25530944	X	130964695	
cg06781532	22	42077939	chr22:42078060-420785
cg21913319	1	86622628	chr1:86621278-8662287
cg18805870	3	23867300	
cg01119718	10	134567309	chr10:134566441-13456
cg25242556	15	91423375	chr15:91423329-914235
cg16103507	8	144569981	chr8:144568915-144570
cg20815084	6	31633626	chr6:31632815-3163409
cg10709708	10	133458170	chr10:133458017-13345
cg14736058	4	16085606	chr4:16084195-1608573
cg16675054	5	171616574	chr5:171614430-171615

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cg22862734	13	39263555	chr13:39261236-392622
cg04629247	13	25494305	chr13:25496588-254972
cg16723800	X	100546517	chrX:100546063-100546
cg25028189	17	2898878	
cg13311886	15	22979752	chr15:22982192-229824
cg18358621	15	32933704	
cg11405200	6	14212128	chr6:14211081-1421174
cg14138275	X	23018057	
cg08519949	5	309765	chr5:309705-310136
cg14563129	8	141290188	
cg09498014	6	161575585	
cg05412045	2	3337680	
cg16873973	7	5920535	
cg15880760	17	48546290	chr17:48545570-485469
cg03576530	14	105167973	chr14:105167663-10516
cg22985016	5	497397	chr5:498111-498430
cg10576257	2	75428132	chr2:75426592-7542803
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cg20978766	1	197704881	
cg04610450	19	18280601	chr19:18279514-182801
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cg14328601	9	140209339	chr9:140210552-140211
cg13425135	9	137330570	chr9:137331316-137331
cg05687091	18	77218862	chr18:77218227-772188
cg26200347	10	15254612	chr10:15254598-152548
cg12178445	6	8436263	chr6:8435314-8436141
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cg01048749	2	8724685	chr2:8723855-8724093
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cg10709704	X	47518846	chrX:47518015-4751885
cg17093212	7	15726473	
cg24680284	X	9863586	chrX:9863527-9863822
cg18196463	5	1069235	chr5:1068746-1069000
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cg03647436	10	134477441	chr10:134477298-13447
cg16835101	17	406380	chr17:406197-406502
cg25851597	15	89248474	
cg02305377	12	103355958	chr12:103359248-10335
cg03254534	18	56343105	chr18:56338211-563392

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cg23489390	2	36712570	
cg17953764	4	48492845	chr4:48492117-4849358
cg02450725	17	75502873	
cg26579578	11	69707303	chr11:69706778-697070
cg23279522	2	66659348	chr2:66660452-6666079
cg15848031	4	4864293	chr4:4864456-4864834
cg02007567	16	10912696	chr16:10912159-109127
cg19064601	11	68142605	
cg00492957	16	980633	chr16:979422-979663
cg09009881	5	170910013	
cg07999738	8	140744386	chr8:140744199-140744
cg20447301	7	155572037	chr7:155573602-155573
cg00042611	16	57760115	chr16:57759991-577602
cg25995133	11	407183	chr11:406491-407871
cg02720091	1	10699958	chr1:10699394-1070009
cg27644733	16	9857216	
cg27520104	10	3172590	
cg06427821	16	899090	chr16:898972-899173
cg15413702	11	34124180	chr11:34126828-341275
cg09778919	12	40019907	
cg10136166	8	144777909	chr8:144776009-144776
cg15708405	20	23337156	chr20:23336868-233372
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cg15178807	22	17178585	chr22:17178519-171788
cg08627327	17	79216928	chr17:79212416-792137
cg21333208	4	3475372	chr4:3475058-3475360
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cg13379983	2	198649727	chr2:198649751-198651
cg00013993	19	7533810	chr19:7531810-7532669
cg14040034	9	140970188	
cg12504641	X	122696254	
cg14650175	8	141545624	chr8:141545521-141545
cg19456953	5	95768418	chr5:95768874-9576908
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cg10699312	3	10203470	chr3:10206449-1020702
cg26814635	7	883024	chr7:886803-887535
cg07758529	X	103813150	chrX:103811550-103812
cg01277542	16	55689901	chr16:55689598-556908
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cg21244745	2	242665522	chr2:242663547-242663
cg23390118	12	2339513	chr12:2339162-2339615
cg02881531	X	62647796	
cg00986824	12	75601465	chr12:75601081-756017
cg25437005	X	22051050	
cg02951880	1	160389175	chr1:160389103-160389
cg07140289	8	142299684	chr8:142295218-142295
cg15951798	17	103504	chr17:99719-100301
cg02695704	16	1250494	chr16:1250277-1250687
cg18726518	12	132924516	chr12:132922117-13292
cg24377062	20	23965921	chr20:23969149-239694
cg16421619	2	240305693	
cg16725948	14	90167635	chr14:90167782-901683
cg07796597	10	11379739	
cg16157016	22	38470264	chr22:38470263-384704
cg03351894	X	48686200	chrX:48684837-4868606
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cg11234637	10	94820945	chr10:94820026-948232
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cg17892150	10	133769511	
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cg27441045	X	100446383	chrX:100446240-100446
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cg08150784	6	99280513	chr6:99279317-9928384
cg04399728	6	170441291	
cg27209278	19	5455482	chr19:5455481-5456262
cg03258315	Y	14077975	chrY:14077836-1407804
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cg27178922	1	213476578	
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cg14919130	6	129250687	chr6:129251113-129251
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cg18881778	12	120241287	chr12:120241921-12024
cg20078624	15	22922301	
cg23716449	8	21608280	chr8:21608078-2160833
cg07312676	16	47338451	
cg07077277	6	25726912	chr6:25726454-2572672
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cg24060527	17	9066156	chr17:9066152-9066388
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cg04276099	7	157503503	chr7:157503469-157504
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cg13180787	1	24127146	chr1:24126799-2412754
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cg10165842	11	1155095	chr11:1155476-1155861
cg08094291	1	44883137	chr1:44883136-4488427
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cg06127256	16	73206588	
cg24755459	14	101908865	chr14:101908781-10190
cg07397481	16	81927366	
cg22268467	19	4361713	chr19:4361470-4361842
cg20892245	6	15244618	chr6:15244877-1524616

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cg00595030	19	10398582	chr19:10397603-103987
cg23397523	15	74315331	chr15:74315178-743157
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cg11062418	2	26395859	chr2:26396102-2639720
cg11468711	15	90545745	chr15:90545272-905459
cg27324804	7	101509161	
cg01226963	8	1051814	chr8:1051641-1051896
cg11712459	18	14146627	chr18:14146394-141466
cg22887949	10	134683495	chr10:134682700-13468
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cg12804283	1	240569726	chr1:240569320-240569
cg21528273	1	44056889	chr1:44056755-4405717
cg23405351	7	7863142	
cg27309229	22	49085091	chr22:49088758-490889
cg08419582	6	166068543	
cg25258098	11	396794	chr11:396685-397462
cg16746539	X	147062784	chrX:147062671-147062
cg07888193	5	1865662	
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cg12111295	21	32253584	
cg27364766	7	22705331	chr7:22704823-2270542
cg14418633	1	2005489	chr1:2005179-2005565
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cg03048372	12	124929991	chr12:124929872-12493
cg07483726	17	790664	
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cg17972105	7	22485718	
cg25216538	4	6925470	chr4:6925211-6925591
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cg09681877	5	113391671	chr5:113391071-113392
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cg25017250	19	45445693	
cg02493904	16	2570404	chr16:2569559-2571071
cg00594917	1	203020566	
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cg05233128	19	3659669	chr19:3659641-3659949
cg27320005	5	140683767	chr5:140683195-140683
cg15825856	5	59992788	chr5:59995374-5999633
cg05716724	8	56362167	chr8:56361856-5636216
cg22841286	19	56709228	chr19:56709055-567092
cg26346230	X	152162720	chrX:152162552-152162
cg03041174	17	20949598	chr17:20945386-209456

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cg10034481	16	87864431	
cg07185695	1	220959586	chr1:220960016-220960
cg18008467	2	236586710	
cg14742937	8	39172097	
cg14597280	7	158198692	chr7:158198545-158198
cg10259701	15	31645503	
cg16507755	21	36164414	chr21:36164144-361649
cg12435415	3	186490344	chr3:186490602-186490
cg06568401	4	42089384	
cg16363447	4	25678113	chr4:25677808-2567813
cg15409097	12	58003925	chr12:58003880-580042
cg03710196	10	126257103	
cg06038358	2	128176007	chr2:128173475-128173
cg27602981	16	89385820	
cg20336172	7	2773782	chr7:2774444-2774655
cg08383338	6	46703225	chr6:46702736-4670331
cg03321020	1	11958326	
cg00415665	8	123875036	
cg17420036	1	22182143	
cg23207244	11	69813323	chr11:69813249-698134
cg15828044	13	25940053	
cg03727554	7	2214778	
cg05316463	14	95786663	chr14:95785752-957861
cg20786909	8	145235410	chr8:145235202-145235
cg24154839	4	46995741	chr4:46995128-4699587
cg11303795	3	122783668	chr3:122785734-122786
cg04635735	7	44259819	chr7:44259669-4425992
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cg07868599	16	3079708	chr16:3079536-3079954
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cg19690494	13	74182598	
cg05470468	3	44620074	chr3:44619873-4462026
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cg21831937	15	57519802	
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cg22811668	19	2046303	chr19:2046074-2046437
cg13732857	2	45029729	chr2:45029728-4503003
cg17295225	6	137814971	chr6:137814355-137815
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cg03625952	5	159625457	
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cg26097051	12	120242090	chr12:120241921-12024
cg15116677	18	48190513	chr18:48190434-481906
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cg07039149	14	105182455	chr14:105181017-10518
cg24035447	6	48036613	chr6:48036137-4803641
cg15649474	8	41507852	chr8:41507516-4150786
cg03241502	19	7505149	chr19:7504923-7505186
cg27628340	8	133906156	
cg09138524	22	19776431	chr22:19776196-197764
cg07805642	6	132890602	
cg14226755	2	236923322	
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cg25686891	4	854566	
cg03900355	11	64521088	
cg13649681	12	130931884	chr12:130935712-13093
cg07794230	4	93104334	chr4:93103617-9310395
cg09168980	X	24380413	chrX:24380305-2438066
cg02650705	13	111145564	
cg05886546	17	40936498	chr17:40936445-409366
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cg13053914	7	75511260	chr7:75508166-7550875
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cg12658387	17	81033543	chr17:81032582-810329
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cg26701785	6	158448455	
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cg19999682	4	14864863	chr4:14864508-1486480
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cg21764101	6	117194158	chr6:117198089-117198
cg06844454	5	77568105	
cg10423587	10	632914	chr10:630309-630950
cg26593722	16	87376314	
cg07587893	7	153446726	chr7:153445164-153446
cg26365299	7	27205381	chr7:27203915-2720646
cg26358634	5	62365115	
cg25459300	8	20375578	
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cg18421360	5	90415181	
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cg17912803	17	671921	
cg26750188	16	735814	chr16:729438-735815
cg02537309	16	30680763	
cg03947979	6	78176785	chr6:78172231-7817408
cg20509119	X	39378476	
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cg25544164	19	5824159	chr19:5824103-5824334
cg12280664	10	11317787	
cg19693869	12	132330383	chr12:132329177-13233
cg13725913	9	140675929	chr9:140675454-140675
cg13509363	9	139739661	chr9:139738276-139744
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cg23246666	2	236672684	chr2:236673303-236673
cg02455203	18	76782895	chr18:76782657-767828
cg01489441	16	1764111	
cg07828380	X	11683977	chrX:11682333-1168454
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cg06535849	16	81925084	
cg23946858	19	18779305	chr19:18778485-187800
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cg04610375	13	36924539	chr13:36919737-369210
cg02281662	14	104643907	chr14:104643173-10464
cg01970383	5	177729224	chr5:177729223-177729
cg17379325	17	7555411	chr17:7554139-7555338
cg26920294	14	20137365	chr14:20136633-201369
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cg14115325	10	128275008	
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cg16097069	5	178552097	chr5:178551777-178552
cg00214611	Y	15815688	chrY:15815488-1581577
cg05904283	16	716021	chr16:717931-719064
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cg17918270	2	1983484	
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cg04622775	15	89442186	chr15:89438176-894388
cg08144675	16	73097057	chr16:73096888-730971
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cg25186055	13	112598514	
cg16963144	20	22566976	chr20:22566821-225670

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cg06123976	22	17489752	chr22:17488274-174891
cg00350519	1	53905742	chr1:53904140-5390524
cg06317989	4	186847142	
cg17764715	19	33622953	chr19:33622910-336232
cg21658616	19	5214593	chr19:5210564-5210864
cg00436722	10	5666842	
cg18424634	3	147127097	chr3:147126988-147128
cg02634861	1	10757954	chr1:10757891-1075825
cg14894848	22	48884945	chr22:48884884-488870
cg09414987	19	392121	chr19:387964-388350
cg04517903	16	1557605	chr16:1559965-1560194
cg13629903	9	15236855	chr9:15232687-1523293
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cg12170314	11	15136505	chr11:15136058-151365
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cg14756202	13	113529568	
cg21762523	6	108497717	chr6:108497595-108497
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cg18143098	13	100731095	
cg08238677	11	125753051	
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cg24274272	17	72278023	
cg12061019	1	3417208	
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cg03248761	13	81228965	chr13:81229047-812294
cg24391931	4	1234067	chr4:1233872-1234420
cg13204538	X	119445300	chrX:119444859-119445
cg15379185	7	27282987	chr7:27282086-2728313
cg10818901	4	739607	chr4:738424-741517
cg22869726	21	34398265	chr21:34395128-344002
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cg17689721	10	102976904	chr10:102975969-10297
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cg07113136	14	96343419	chr14:96342209-963435
cg18447950	17	79073781	chr17:79077317-790775
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cg16993043	1	200008026	chr1:200008392-200009
cg10181414	19	2546598	chr19:2546620-2546983
cg24544320	1	226825435	
cg14190344	10	133729189	
cg24856050	19	3192433	chr19:3192416-3192705
cg01145140	6	166077613	chr6:166073882-166077
cg20498859	3	154145810	chr3:154146347-154146
cg10701490	X	75005131	
cg03340135	16	88788543	chr16:88788033-887894
cg13472192	1	41350014	chr1:41349740-4135029
cg16140952	X	110039485	chrX:110038946-110039
cg23952578	1	116371871	chr1:116370810-116371
cg20071884	X	118284647	chrX:118284519-118285
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cg27290624	3	194208441	chr3:194207385-194208
cg20840426	12	117800609	chr12:117798076-11779
cg16709294	14	70235567	chr14:70233570-702346
cg07135032	1	165322099	chr1:165321703-165322
cg08799778	16	1017338	chr16:1020219-1021303
cg13244241	10	102491731	chr10:102489343-10249
cg05279806	3	175128616	
cg21531040	14	106743603	chr14:106743602-10674
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cg11521470	6	170531259	chr6:170529588-170530
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cg01992935	X	108868271	chrX:108867762-108868
cg26492446	20	61638574	chr20:61636171-616390
cg08160891	16	15252968	chr16:15247870-152491
cg08505883	5	162860583	chr5:162864384-162865
cg06733925	14	65746397	chr14:65746329-657469
cg19183743	7	27188020	chr7:27186927-2718769
cg12031275	15	101093834	chr15:101094520-10109
cg18319941	7	64894861	
cg00017826	2	30644955	

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cg18971175	11	129183160	
cg22697239	11	44626708	
cg07608562	16	111658	chr16:110995-113162
cg01990910	16	12207648	chr16:12210655-122112
cg11597902	17	75096239	
cg04296903	1	1203256	chr1:1203166-1203597
cg12656653	10	13771427	
cg24660635	15	28437148	
cg14662585	7	16890769	chr7:16890768-1689108
cg00050294	1	2886818	chr1:2886589-2886923
cg21445918	3	43405550	chr3:43405419-4340562
cg22016513	8	3855577	
cg05987823	12	54428592	chr12:54427025-544287
cg22444338	7	1054449	chr7:1052387-1052736
cg13257878	10	133747771	chr10:133751399-13375
cg08106487	16	67980202	
cg15769475	17	3960566	
cg01525669	13	107211833	
cg14554716	5	115185209	
cg13546414	14	37053664	chr14:37053134-370536
cg11241133	10	134072078	chr10:134071971-13407
cg08888203	3	10149979	chr3:10149750-1015006
cg02336762	12	118313990	
cg09951320	11	123448238	chr11:123448093-12344
cg17238412	11	116450919	chr11:116450659-11645
cg21165595	8	67046248	
cg19109397	10	61828511	
cg05650453	1	7432644	
cg13393809	2	239974467	chr2:239974439-239974
cg21341928	13	25670327	chr13:25670041-256705
cg06912227	16	4053409	
cg15566393	15	78190123	
cg11504646	3	186913950	chr3:186917411-186917
cg20818528	17	4510743	chr17:4510554-4510777
cg23874934	8	143473852	chr8:143471631-143472
cg24631834	4	85205711	
cg24317190	7	54900936	chr7:54900736-5490126
cg13088465	1	227170628	
cg03664916	16	89674560	
cg09862509	1	181069576	
cg03148084	18	72201665	
cg06517965	16	30845736	chr16:30845650-308461
cg06009497	8	37695050	chr8:37698846-3769993
cg11237215	1	244806055	
cg27297104	16	1414480	chr16:1414417-1414851
cg25402979	12	58068659	chr12:58068473-580687
cg11204987	1	49723190	
cg14332120	8	97657097	chr8:97657174-9765794
cg18612255	12	1770715	chr12:1770701-1771476
cg04158367	1	92952440	chr1:92945907-9295260
cg25354915	4	165850972	
cg20957776	2	1482963	chr2:1480758-1481631
cg11992783	19	50734287	chr19:50733984-507342
cg18834544	13	101182535	chr13:101184396-10118
cg18740289	6	2437142	

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cg04977376	1	246457244	
cg25612391	19	19216451	
cg23445461	5	140864733	chr5:140864527-140864
cg04104579	1	170627558	chr1:170630456-170630
cg26506940	7	16682697	chr7:16684239-1668450
cg03528486	13	111090669	chr13:111090637-11109
cg17823234	19	38180021	chr19:38182793-381833
cg19927328	15	28016955	chr15:28015346-280157
cg05294276	10	112618918	
cg09618998	8	1950965	chr8:1949245-1951390
cg06794034	4	7301854	
cg02857643	17	48696108	
cg21871608	14	93409468	
cg09667289	15	33165563	
cg12209693	7	73894884	chr7:73894815-7389511
cg05783727	1	149232994	chr1:149230771-149231
cg15287403	3	51746779	chr3:51749754-5175006
cg11569374	7	148142969	
cg10191248	10	134441085	
cg21035402	19	36435543	chr19:36435457-364357
cg26401825	X	99666164	chrX:99666131-9966638
cg02820072	19	33210552	chr19:33210453-332110
cg22529900	1	8044553	
cg09532726	13	36516270	
cg07051704	16	71658155	chr16:71659829-716607
cg07553213	11	79210331	
cg10900641	11	1767793	chr11:1768979-1770712
cg22710391	X	34960893	chrX:34961430-3496170
cg23542414	11	22674391	
cg05288071	19	7712539	chr19:7712037-7712355
cg06425919	11	17741925	chr11:17740789-177437
cg10607675	X	21674415	chrX:21674018-2167706
cg21569714	5	153798362	
cg21098557	5	43191993	chr5:43191974-4319315
cg25597531	8	54507339	chr8:54507107-5450735
cg08844966	1	18435244	chr1:18435566-1843590
cg01244571	10	368451	chr10:367469-369416
cg11274148	17	78876656	chr17:78880030-788802
cg06845706	22	23733812	chr22:23730282-237305
cg04917446	17	46699073	chr17:46698880-466990
cg17227257	4	1202694	chr4:1202956-1203200
cg06904356	5	1849983	chr5:1851342-1851564
cg18606700	22	25756156	chr22:25755941-257561
cg20106601	4	163483332	
cg00707406	5	140167620	chr5:140167091-140168
cg02910208	7	54610022	chr7:54609734-5461014
cg27046920	5	538702	chr5:537303-537522
cg02301128	7	127792165	
cg15470261	19	1698699	chr19:1698698-1698960
cg20872809	6	1481524	
cg03556869	6	149358767	
cg14068702	5	106946646	
cg05067926	11	134231915	chr11:134231727-13423

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cg22580292	10	133758839	
cg12939425	5	130344188	
cg05079049	16	55364843	chr16:55364823-553654
cg14044707	9	132628998	chr9:132630324-132630
cg00990635	19	19745667	chr19:19745475-197457
cg18147865	19	5507344	chr19:5507247-5507523
cg24671235	10	45448095	
cg03190433	4	54791006	
cg06635625	11	18994080	
cg00590639	19	10464771	chr19:10464666-104649
cg23935616	8	2112392	
cg10890925	8	1899468	
cg20824977	15	59978600	chr15:59981234-599817
cg05523267	16	341185	chr16:341081-341421
cg16953816	12	123349952	chr12:123351641-12335
cg10958086	17	952903	chr17:951746-952265
cg19913626	8	49533357	
cg17016355	13	32601953	chr13:32605320-326059
cg22643760	19	36746845	chr19:36746712-367469
cg18175606	21	42543209	chr21:42539367-425408
cg18896032	11	57097718	
cg26537561	19	57335060	
cg23517116	8	65499841	chr8:65499748-6550014
cg18948877	2	242904738	
cg09424526	2	223163809	chr2:223162946-223163
cg16007508	17	14027721	
cg16159925	X	139866657	
cg08527195	1	161442697	chr1:161410142-161442
cg06904408	5	1289828	chr5:1289275-1295970
cg19035075	7	4736276	
cg09480515	2	237033375	chr2:237032557-237032
cg12918457	11	115630748	chr11:115630398-11563
cg22547978	3	55589874	
cg25404678	5	1089260	chr5:1088821-1089276
cg09095924	16	1722278	
cg10546562	7	5390491	chr7:5391323-5391572
cg11331678	20	44540794	chr20:44540445-445409
cg05929865	X	70128121	
cg21330272	3	16922923	chr3:16925381-1692684
cg11709150	1	2440438	chr1:2440126-2440478
cg05064106	22	50528213	chr22:50528201-505290
cg23352492	17	80823397	
cg09024126	4	16085603	chr4:16084195-1608573
cg27398283	7	785029	
cg17657179	19	52227309	
cg10838500	5	1393877	
cg22514112	5	1859764	chr5:1856773-1858444
cg22242926	17	73627717	chr17:73627542-736278
cg20390711	6	127796683	chr6:127796286-127797
cg04740264	16	3632588	
cg17519899	22	36682868	
cg12318152	13	52435351	

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cg25734842	1	228657381	chr1:228657327-228657
cg00738309	13	114748624	chr13:114748541-11474
cg13621679	17	37761692	chr17:37761691-377635
cg05445331	X	133119028	chrX:133118960-133119
cg11488864	4	8379238	chr4:8375042-8375342
cg13928485	9	136726359	chr9:136728386-136728
cg09971069	17	70592090	chr17:70587771-705890
cg06808021	12	80643719	
cg00329618	12	113515439	chr12:113515164-11351
cg07702888	1	156338793	chr1:156338758-156339
cg06856329	3	71247442	
cg18049569	6	3154105	chr6:3154104-3154746
cg15731035	1	6106539	
cg15770585	7	4762742	chr7:4764684-4765252
cg27444290	11	2356831	
cg16856213	8	588810	
cg10261003	X	88001657	
cg18114708	11	66460719	chr11:66458783-664591
cg20487025	17	61613121	chr17:61613060-616133
cg06462703	12	133430564	chr12:133429925-13343
cg00931124	16	967929	chr16:967241-967619
cg11131351	Y	2802287	chrY:2802964-2804283
cg26488985	16	89584852	chr16:89588816-895890
cg00666903	12	2861589	chr12:2861782-2862472
cg18424208	5	149546337	chr5:149546027-149546
cg00922825	10	98946790	chr10:98945062-989462
cg26973953	16	1412266	chr16:1411892-1412368
cg01453281	2	105475049	chr2:105468851-105473
cg18588835	8	141381180	
cg19426572	20	61919450	chr20:61919024-619198
cg21491340	19	18092572	chr19:18092430-180929
cg10271315	10	393842	chr10:391382-394008
cg09789939	16	88532245	
cg22975920	8	144398248	chr8:144399189-144399
cg01979600	7	57715349	
cg22616881	7	96642096	chr7:96645786-9664659
cg03565777	12	125028339	chr12:125028132-12502
cg22929280	15	81134497	
cg00321775	10	48416391	chr10:48413741-484139
cg23245663	8	1298579	chr8:1298338-1300481
cg08567279	13	53313529	chr13:53313127-533140
cg08833670	11	124746754	chr11:124745909-12474
cg19635580	1	220441596	chr1:220445480-220445
cg12159023	19	613818	chr19:612989-614068
cg08144588	3	3080327	
cg16569937	5	57174377	
cg15188908	5	1840272	
cg19888509	12	125145641	chr12:125145445-12514
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cg08484479	5	887419	

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cg26369916	X	139587279	chrX:139585867-139588
cg03456971	2	194955432	
cg09597710	7	1121124	chr7:1119980-1120248
cg07206202	6	28297279	
cg14256977	11	95636491	
cg23937078	1	31246279	chr1:31246010-3124628
cg07342618	10	3300407	
cg07206010	X	152710312	chrX:152710204-152710
cg11380051	10	135087462	chr10:135089969-13509
cg16617141	11	72408186	chr11:72408050-724085
cg26113809	12	54132180	chr12:54132148-541323
cg00059240	10	3155604	
cg16525277	5	171190008	
cg06697929	19	48945130	chr19:48945800-489476
cg05983723	16	70432258	
cg08369368	5	176559881	chr5:176558852-176561
cg01873334	11	2721632	chr11:2720410-2722087
cg21544698	12	130935962	chr12:130935712-13093
cg08206657	10	14575436	
cg09185797	2	163008822	
cg06088782	11	70563839	chr11:70563664-705638
cg22506548	1	2996949	chr1:2997272-2997473
cg15506446	20	60948875	chr20:60948494-609489
cg01102311	19	36644751	chr19:36642327-366435
cg07120174	8	41351213	chr8:41347794-4134858
cg18145652	4	49323237	
cg16596103	2	233749413	
cg26272220	12	81471884	chr12:81471569-814721
cg23441673	11	134831429	chr11:134831329-13483
cg22106265	1	147955332	
cg01774705	17	4447783	
cg19901956	11	77921274	chr11:77921113-779213
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cg13749070	15	99451935	
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cg15326755	17	25620596	chr17:25620999-256217
cg02152290	7	551601	chr7:550450-550681
cg09375892	17	708413	chr17:708319-708598
cg27658314	7	157968629	
cg17498717	2	241372344	chr2:241374410-241376
cg17911539	3	126260814	chr3:126260488-126261
cg04821387	16	1143016	chr16:1142315-1144087
cg10509185	10	134504666	chr10:134504420-13450
cg22417032	7	157350867	chr7:157352995-157353
cg24676071	7	45613410	chr7:45613386-4561550
cg14131835	6	154858688	
cg25494665	13	42623369	chr13:42623339-426235
cg24079672	17	73739840	chr17:73738579-737388
cg25312876	19	5151581	chr19:5151332-5151730
cg10505415	1	161993970	chr1:161993022-161994
cg25103726	12	130892289	
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cg15371801	2	232348684	chr2:232348216-232348
cg14206962	15	29406153	chr15:29405951-294062
cg13341982	17	38708603	
cg25691775	17	2699122	
cg05551825	7	5735129	
cg00434991	10	134504552	chr10:134504420-13450
cg03134653	6	31600558	chr6:31599519-3159976
cg23727927	2	3665303	
cg04627702	6	170047692	
cg08889009	15	59157123	chr15:59157045-591575
cg03647899	X	79829286	chrX:79830094-7983053
cg05877788	17	27899874	chr17:27899511-279000
cg00773093	10	135246653	chr10:135246474-13524
cg00542775	1	4188710	chr1:4192633-4193243
cg11462099	13	113540512	chr13:113540350-11354
cg06765373	17	568565	
cg15140703	7	99775532	chr7:99774733-9977558
cg27496299	7	157171202	
cg00638202	21	37259424	chr21:37259191-372596
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cg04928692	2	176042976	chr2:176045969-176046
cg04919489	11	120283690	
cg18811130	10	131268886	chr10:131264948-13126
cg26169783	13	34371837	
cg18417954	19	55672513	chr19:55672023-556732
cg16061777	16	76269192	chr16:76268977-762691
cg14976190	1	1615736	
cg24540877	7	106661281	
cg21745537	11	121233743	chr11:121233742-12123
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cg16855440	19	45842723	chr19:45843870-458444
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cg26010218	4	78977223	chr4:78978365-7897925
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cg16661234	17	10541620	chr17:10541481-105417
cg11268385	5	75377922	chr5:75377898-7537818
cg05505912	1	210001218	chr1:210001129-210001
cg20499506	2	3173204	
cg10634728	19	418906	chr19:418898-419191
cg07016060	10	134505029	chr10:134504420-13450
cg03395651	16	88107091	chr16:88106774-881073
cg02457461	8	9913680	chr8:9911629-9912633
cg21949830	17	1510041	chr17:1509882-1510101
cg07710266	6	134436740	
cg12208258	18	25757438	chr18:25755414-257581
cg08307311	11	2079875	
cg01633149	16	16208885	
cg12817154	4	864995	chr4:866098-866344
cg11214430	8	42268294	chr8:42268436-4226875

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cg21602882	8	140937410	
cg26987690	7	907797	chr7:905608-905886
cg03966099	22	16157595	chr22:16155753-161580
cg27571057	4	1646179	chr4:1645886-1646324
cg20442586	15	45444606	chr15:45444487-454447
cg08878662	19	2444048	chr19:2444300-2444522
cg10593459	1	44447478	chr1:44444635-4444562
cg01203579	7	79880295	
cg16262034	5	628091	
cg17743085	19	18557182	chr19:18557038-185572
cg25043633	6	170061104	chr6:170062622-170063
cg15810747	7	54765501	chr7:54765426-5476563
cg05886469	17	66205079	chr17:66201166-662021
cg16583193	19	3652060	chr19:3651790-3652134
cg20147645	13	28023563	chr13:28024165-280252
cg06018095	13	46550134	
cg03011594	16	56370697	
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cg17158149	10	32213946	chr10:32216901-322171
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cg26703617	20	29551422	chr20:29550849-295518
cg05123067	1	203455873	chr1:203455815-203456
cg25074809	2	16086016	chr2:16079801-1608303
cg06873401	5	77792105	
cg02223323	X	20134399	chrX:20134203-2013535
cg12879381	18	12326166	chr18:12325040-123260
cg01959025	15	93749169	
cg17227967	20	9496556	chr20:9496471-9496893
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cg23857725	X	135180640	chrX:135180417-135180
cg15653910	1	20799948	
cg04254159	8	66701461	
cg19164621	12	19794901	
cg05187422	16	89597159	chr16:89593169-895933
cg11049634	X	40016121	chrX:40010919-4001620
cg05800450	9	115818372	chr9:115818836-115819
cg06795722	8	143429730	chr8:143429001-143429
cg08504510	10	7501433	
cg09646197	7	149462836	chr7:149461653-149463
cg15215612	19	51231736	chr19:51231632-512319
cg08307850	5	150460163	chr5:150460086-150460
cg15375704	14	106134972	chr14:106138654-10613
cg02322843	12	129285402	
cg17089511	4	2438721	
cg07167423	1	36042986	chr1:36042432-3604344
cg07772128	15	75095447	chr15:75095349-750955
cg04645150	6	28584172	chr6:28583934-2858428
cg22135566	12	124416315	
cg20275928	17	79283959	chr17:79283863-792841
cg15119027	11	69634363	chr11:69632033-696347
cg03217800	7	56439703	chr7:56436287-5643655

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cg27175491	12	70425656	
cg01233786	13	113498450	chr13:113497296-11349
cg24995657	14	67879126	chr14:67878534-678791
cg17541025	3	72978020	chr3:72977999-7297832
cg13082295	15	20564078	chr15:20563982-205642
cg02184535	7	55409237	chr7:55411965-5541277
cg15042811	4	144621971	chr4:144620822-144622
cg20801778	7	130125200	chr7:130126017-130126
cg13189008	10	2370970	
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cg09937438	7	1095005	chr7:1097405-1097953
cg14891209	15	37170381	chr15:37172473-371730
cg11351958	11	75277791	chr11:75277366-752780
cg14932408	10	133985911	
cg02537382	20	61697965	chr20:61697208-616974
cg03336586	1	3732904	chr1:3731458-3732015
cg26584771	X	74145551	chrX:74143852-7414517
cg13101963	17	74913881	
cg24391773	10	75491947	chr10:75492493-754934
cg13372862	8	145235328	chr8:145235202-145235
cg14981422	11	1300358	chr11:1298009-1298476
cg25133533	7	100611097	chr7:100608736-100609
cg13579574	15	75975227	chr15:75975005-759753
cg27393769	19	15512265	chr19:15512025-155123
cg10616776	2	232479924	chr2:232478359-232479
cg06485995	7	27547647	
cg18365383	7	33725819	
cg19300401	6	16962712	
cg19512693	13	29025833	
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cg19602374	1	15833485	
cg20746793	X	9858615	chrX:9858608-9858930
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cg00874494	22	26828939	chr22:26829718-268301
cg22782070	13	114085586	chr13:114085423-11408
cg09984392	8	126011784	chr8:126010436-126011
cg16088894	X	44169621	chrX:44169510-4416976
cg25595641	18	77208991	chr18:77208691-772090
cg15684329	8	118825173	
cg07827796	19	33622959	chr19:33622910-336232
cg18627235	14	96342747	chr14:96342209-963435
cg11832804	5	1279449	chr5:1277467-1277713
cg13766489	9	131670359	chr9:131669882-131671
cg02622601	16	85537527	
cg04218880	1	40388264	
cg22662808	7	143045023	chr7:143042508-143042
cg11050793	12	124876650	chr12:124873241-12487
cg04752574	X	75005102	
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cg12327866	10	1939663	
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cg27560182	1	26511621	
cg07690734	10	134188661	
cg19230048	19	22702156	chr19:22700396-227012
cg15266705	12	115136096	chr12:115135925-11513
cg16594581	5	140531865	chr5:140531157-140532
cg02847216	18	19997803	
cg04508964	12	106977389	chr12:106977388-10697
cg02803486	16	29171518	chr16:29169898-291704
cg00150520	1	45082905	chr1:45082739-4508328
cg21177558	8	27677755	
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cg01798341	17	80842262	
cg14992035	2	241819352	
cg01821906	X	103268245	chrX:103267755-103268
cg06724305	1	50887944	chr1:50884228-5089147
cg05346286	1	2980598	chr1:2979275-2980758
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cg04899361	7	1597412	
cg25937854	12	120150414	
cg27598661	4	184404666	chr4:184404501-184404
cg03467014	1	1158648	chr1:1159168-1159528
cg12081253	17	71431773	chr17:71431621-714318
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cg25372296	1	98510328	chr1:98510966-9851171
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cg03897436	16	1425469	chr16:1425047-1425604
cg16440299	16	56779141	
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cg26675182	7	2405750	
cg02104967	17	1386368	chr17:1388686-1389730
cg17517128	X	13397532	chrX:13396888-1339749
cg20402382	3	49711530	chr3:49710968-4971227
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cg13296578	17	79410560	chr17:79412470-794127
cg20192747	18	44774846	chr18:44772992-447755
cg14398860	10	134491205	
cg20842253	2	27529788	chr2:27529083-2753146
cg21735031	12	34455187	
cg01181584	3	187439427	
cg26573772	8	1245943	chr8:1245671-1246464
cg00228689	1	53742112	chr1:53742297-5374284
cg02950608	18	75400720	chr18:75402320-754025
cg21288259	6	150238164	
cg02250553	10	134511404	
cg23275764	17	21561942	
cg05626376	6	31938847	chr6:31939730-3194055
cg00570000	1	118728226	chr1:118727816-118728

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cg25601889	12	57630456	chr12:57630106-576304
cg20474425	12	54746067	
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cg16846645	2	14773973	chr2:14772377-1477580
cg11645417	6	163731815	
cg10248981	10	126157948	
cg19076702	17	55193605	
cg17396852	7	106508336	chr7:106508057-106508
cg13523236	12	129277140	chr12:129280256-12928
cg07416427	X	10085204	chrX:10085183-1008575
cg14308265	X	51361547	chrX:51360851-5136177
cg11013726	15	65116557	chr15:65116013-651165
cg27309098	2	236619748	
cg24101492	14	96343119	chr14:96342209-963435
cg23548151	12	130823838	chr12:130823502-13082
cg21033440	11	65409861	chr11:65409636-654101
cg17526887	2	223918000	chr2:223917576-223918
cg19037143	4	187524750	
cg05148217	3	108836878	chr3:108836795-108837
cg23011324	6	32803482	chr6:32806284-3280666
cg02762561	7	154792046	chr7:154794017-154795
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cg10837116	12	53069933	
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cg07001421	6	32130375	
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cg10204951	7	910479	
cg14314071	17	15165812	chr17:15165796-151665
cg03726437	17	3474461	chr17:3474582-3474897
cg09128429	5	126073744	
cg12395689	10	133777125	
cg24328125	12	126168546	chr12:126168440-12616
cg08934799	5	135188205	chr5:135188169-135188
cg09862845	4	530437	chr4:530297-530600

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cg05656442	1	111175082	
cg03905369	2	120824615	
cg12883629	6	25042497	
cg00713400	7	22233206	
cg01920090	1	3791310	chr1:3790864-3791611
cg00439392	17	35060323	chr17:35060322-350606
cg26583560	16	896768	chr16:896563-897148
cg12934366	8	1960466	chr8:1956926-1957177
cg17692753	14	99642476	chr14:99640360-996427
cg00005740	13	24079418	
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cg06498313	10	387473	chr10:387294-387544
cg18668041	19	41190396	chr19:41190249-411904
cg24399349	7	55517045	chr7:55516871-5551724
cg05705212	3	45984743	
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cg09268800	1	153914384	chr1:153914343-153914
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cg14166284	1	221055719	chr1:221055492-221055
cg03224459	7	2318251	chr7:2318238-2319079
cg16658412	7	1883420	chr7:1885033-1885402
cg26109145	17	79045877	chr17:79045454-790456
cg03048889	20	20433168	chr20:20433105-204333
cg18488266	4	3752338	chr4:3748224-3748581
cg19248302	1	7745081	chr1:7740143-7741117
cg24242823	7	24323675	chr7:24323558-2432508
cg11755933	11	67266128	chr11:67260413-672627
cg14642045	12	109538736	chr12:109535264-10953
cg08990626	10	685091	chr10:685033-685407
cg24286789	6	10417726	chr6:10417384-1041784
cg22901100	6	41774260	chr6:41773954-4177442

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cg07588430	6	41561444	chr6:41561221-4156147
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cg24652615	6	44243304	chr6:44243085-4424448
cg13443168	9	471920	chr9:470108-470324
cg13054523	17	81055722	chr17:81057525-810578
cg10078688	8	107290576	
cg02198562	11	134582289	chr11:134582296-13458
cg05675373	1	110754257	chr1:110752256-110754
cg19831031	19	54619140	chr19:54618652-546191
cg17086759	4	6303693	chr4:6303533-6304210
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cg12161132	10	134054189	
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cg10153214	16	71571146	
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cg12308164	11	1315468	chr11:1315467-1317115
cg19440264	17	7350413	chr17:7348274-7348830
cg13486406	7	113727612	chr7:113724924-113727
cg24701320	8	2033423	
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cg21087137	12	75728469	
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cg22243109	17	75789365	chr17:75789326-757895
cg16267012	4	132899460	chr4:132898749-132899
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cg22472290	19	52391480	chr19:52390841-523913
cg21907914	19	53757677	chr19:53757819-537581
cg26477488	5	153858936	chr5:153857038-153859
cg11641840	17	71431640	chr17:71431621-714318
cg10799668	10	131631816	
cg06702850	6	166876890	
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cg03272020	11	39868461	
cg22995959	14	59931024	chr14:59930634-599322
cg21961890	7	12510665	
cg04136185	5	565937	chr5:561826-565967

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cg11982471	6	31130267	chr6:31125894-3112656
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cg25532627	17	77997833	chr17:77997723-779979
cg24398479	7	27192061	chr7:27190274-2719111
cg07925619	17	39913753	chr17:39913716-399140
cg08021833	19	5785663	chr19:5785399-5785819
cg08925169	11	5664261	
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cg07806886	3	120626899	chr3:120626880-120627
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cg10551631	X	43832862	
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cg04697482	19	16989084	chr19:16989009-169897
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cg04171554	19	2761892	chr19:2761665-2761909
cg20073313	8	52322009	chr8:52321162-5232222
cg12850546	22	42539477	chr22:42538474-425395
cg10084932	X	134571153	chrX:134570079-134571
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cg26619296	10	1585286	chr10:1585174-1585421
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cg14655360	10	2374371	
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cg22891278	19	50713660	chr19:50713630-507140
cg25447872	13	113492708	chr13:113492486-11349
cg17681524	5	21802422	
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cg09049334	X	24380401	chrX:24380305-2438066
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cg14045872	7	49813065	chr7:49813008-4981575
cg16226962	6	10415687	chr6:10417384-1041784
cg06844526	2	192169585	
cg19504661	2	239542427	chr2:239542238-239542
cg22451265	5	43104902	
cg01055099	16	3516099	
cg26549114	12	19260747	
cg12986628	11	119204915	chr11:119205023-11920
cg02862100	3	175734212	
cg13611347	18	31739207	chr18:31739047-317395
cg02527886	7	2968316	chr7:2968234-2968596
cg05707116	2	88924001	chr2:88926237-8892729
cg18869061	15	100272053	chr15:100272901-10027
cg18249580	8	65281496	chr8:65281903-6528304
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cg08358166	17	18538271	chr17:18538247-185388
cg14607286	6	38673615	chr6:38670576-3867097
cg07745707	16	88496476	chr16:88496201-884977
cg03201165	X	152584950	chrX:152584949-152585
cg07537147	12	110271031	chr12:110271000-11027
cg01610632	3	147127579	chr3:147126988-147128
cg06992285	8	99952047	chr8:99952020-9995468
cg11572844	5	129239273	chr5:129239553-129241
cg17965019	6	27858545	chr6:27858166-2785856
cg17330061	7	98630634	chr7:98633091-9863330
cg08398005	7	47344608	
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cg15247169	8	47057504	
cg07544045	6	158592420	chr6:158588887-158589
cg05652090	12	118293169	
cg23570034	X	149396133	
cg09559189	8	25898412	chr8:25899335-2589969
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cg09456829	6	166228306	
cg17336584	6	12750256	chr6:12749877-1275049
cg11843948	7	5410861	chr7:5410672-5410989
cg12306853	6	143833173	chr6:143832389-143832
cg27083466	6	168417061	
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cg08313939	20	37353117	chr20:37352130-373573
cg24860092	19	36195363	chr19:36195267-361954
cg08861369	16	85671714	chr16:85670134-856703
cg12688781	12	125570079	chr12:125569828-12557
cg05402634	11	70644141	
cg21879791	6	29594830	chr6:29595298-2959579
cg09321400	16	55690443	chr16:55689598-556908
cg01424241	9	705143	chr9:707021-707420

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cg27562682	1	243053865	chr1:243053597-243054
cg26931862	12	54349169	chr12:54348695-543493
cg07979747	6	30860136	
cg22337169	7	100218717	chr7:100218511-100218
cg18229521	14	92790285	chr14:92789494-927907
cg20286344	3	29280399	
cg08784238	15	28511044	
cg19275838	7	45115588	
cg00954996	1	2193454	
cg22705204	19	2246901	chr19:2246820-2247035
cg21282669	8	128328563	chr8:128327887-128328
cg04735509	12	63545783	chr12:63543636-635449
cg19760898	7	123673583	chr7:123672063-123673
cg20076070	8	1639573	chr8:1639891-1640612
cg26393393	6	158093249	chr6:158093810-158094
cg14805347	15	58357879	chr15:58357309-583587
cg24825937	2	128639118	chr2:128642787-128644
cg21961506	13	20235918	
cg23326301	1	120439812	chr1:120439013-120439
cg13139630	21	46438065	chr21:46438140-464393
cg17008486	8	25543184	
cg03834023	2	27356128	chr2:27356980-2735765
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cg04652961	6	121758242	
cg00391044	X	136510091	chrX:136510308-136510
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cg01935942	12	132043560	chr12:132045105-13204
cg23231666	1	10699975	chr1:10699394-1070009
cg00028598	15	27128633	chr15:27128249-271289
cg23449696	3	147125942	chr3:147126988-147128
cg00172812	1	23279685	chr1:23279553-2328056
cg20228495	2	74945369	chr2:74942324-7494281
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cg24498587	11	123596947	
cg14132916	2	237993322	chr2:237994004-237994
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cg04352272	17	3289798	chr17:3289362-3290072
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cg14610776	9	140605874	
cg05845533	17	64672205	
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cg23423423	22	37603155	chr22:37603001-376037
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cg02524346	8	600233	chr8:599904-600309
cg02361027	2	170217401	chr2:170218314-170219
cg03400811	22	19554366	chr22:19554014-195544
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cg13050504	21	43913111	chr21:43916278-439169
cg02194398	4	142556368	chr4:142557388-142558
cg13489054	X	134653741	chrX:134655102-134655

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cg12923994	22	18277981	chr22:18275679-182759
cg17818471	2	177012640	chr2:177012371-177012
cg14249008	6	34231076	chr6:34231093-3423150
cg19728345	5	1394320	
cg01598250	5	145722855	chr5:145722467-145722
cg01422370	2	73384389	
cg05068156	6	29408587	
cg22770294	4	3308933	chr4:3310005-3310235
cg04399647	8	143379069	chr8:143378961-143379
cg09645993	5	77289836	
cg01867395	11	31839628	chr11:31839363-318398
cg16884847	2	46121488	
cg12164713	19	12969204	chr19:12969200-129695
cg10443532	X	136657084	chrX:136655909-136657
cg01362762	13	114805400	chr13:114805719-11480
cg13745678	4	109253949	
cg09527270	2	25390385	chr2:25391072-2539187
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cg07686528	10	65198176	
cg18795127	10	135212911	chr10:135216526-13521
cg20297979	17	73552110	
cg09111484	12	80749651	
cg15318814	2	98351769	chr2:98351659-9835201
cg22155080	5	56368149	
cg21609106	5	38259214	chr5:38257825-3825913
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cg06369532	7	2155044	chr7:2154677-2155252
cg26396721	2	214171	chr2:214011-214245
cg03205103	5	38257541	chr5:38257825-3825913
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cg10942690	14	95538480	
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cg16811771	16	1482952	chr16:1482551-1483201
cg01761453	X	140983037	
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cg03547366	12	132490709	
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cg17094363	1	1065864	
cg26859186	7	157351708	chr7:157352995-157353
cg18954144	2	5896473	
cg14703002	6	26018058	chr6:26020671-2602112
cg18841634	18	49868236	chr18:49868377-498687
cg14477263	1	1168550	chr1:1167001-1168985
cg15021292	5	67521596	
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cg05350360	19	4475274	chr19:4472119-4473123
cg23220012	11	69355713	
cg11363615	8	41507621	chr8:41507516-4150786

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cg06980013	1	1945959	
cg04498913	7	1135747	chr7:1135744-1135992
cg03460534	11	63839528	
cg13643764	5	1028233	chr5:1025330-1025629
cg23053516	4	1388811	chr4:1388614-1389430
cg20786173	X	20135761	chrX:20134203-2013535
cg25806370	19	2790585	chr19:2790376-2790717
cg21002224	11	66488919	
cg23024824	15	70349890	
cg04271677	7	156754681	
cg22452170	7	157427295	
cg16893488	8	71154701	
cg01274643	11	1283946	
cg06303238	20	50418959	chr20:50417312-504190
cg21906444	11	67432774	chr11:67432755-674330
cg13762887	9	131517731	
cg14370961	14	105767520	chr14:105766558-10576
cg08616061	5	140753570	chr5:140753654-140753
cg24322366	4	190567721	chr4:190566549-190567
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cg14537605	6	6952892	
cg25859141	7	155168238	chr7:155164557-155167
cg12521678	X	153197865	chrX:153199952-153200
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cg20008148	14	37053169	chr14:37053134-370536
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cg20017132	10	105233022	chr10:105232921-10523
cg03964851	5	93905427	
cg13692426	9	79625269	chr9:79628910-7962939
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cg17463145	7	79084011	chr7:79082174-7908242
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cg14448086	10	3151088	chr10:3148406-3148625
cg06948435	17	123982	chr17:122796-123426
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cg23546474	2	223163033	chr2:223162946-223163
cg08374687	4	123300658	chr4:123300407-123300
cg07209141	11	68171070	
cg02089452	16	89500152	chr16:89500025-895002
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cg03825670	13	78234875	
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cg22711741	19	57742444	chr19:57741955-577424
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cg19912337	19	51529628	
cg13649087	19	3871442	chr19:3870788-3871043
cg15067806	1	149146748	chr1:149148145-149148
cg25372722	10	134540624	chr10:134539817-13454
cg09890269	X	51239014	chrX:51238706-5124010
cg21674010	15	58844583	
cg23865240	7	27134109	chr7:27134097-2713430
cg10345724	7	1120465	chr7:1119980-1120248
cg21163717	8	21769903	chr8:21769694-2177008
cg12061099	X	15804193	chrX:15808190-1580882
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cg00116172	2	3389717	chr2:3391402-3392500
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cg05144642	3	75720199	chr3:75721294-7572190
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cg17129809	2	23840282	
cg00561891	13	113745525	chr13:113745161-11374
cg04682087	2	875946	
cg18423110	X	72347359	
cg04858155	11	44332369	chr11:44332314-443327
cg18395189	1	152189015	chr1:152188860-152189
cg06437256	8	81178033	chr8:81177941-8117819
cg03513066	6	32586134	
cg19780614	8	28932339	chr8:28928996-2892971
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cg25088009	14	74188055	chr14:74185482-741859
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cg10606029	5	37952598	
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cg19402876	3	71119415	
cg10765171	13	23270757	chr13:23270580-232709
cg23623622	6	30139880	chr6:30139718-3014026
cg00041872	1	46632690	chr1:46632689-4663293
cg03631743	11	68519694	chr11:68517667-685181
cg02725313	20	30071913	chr20:30071912-300723
cg19617948	20	30135124	chr20:30135076-301352
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cg24803719	17	45855879	chr17:45855552-458560
cg25717351	17	744675	chr17:744617-744907
cg01555397	6	107808378	chr6:107810066-107812
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cg13729210	5	3606561	chr5:3606488-3607135
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cg26914616	6	127980151	
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cg15637415	19	11560140	chr19:11560045-115602
cg05336198	7	50853341	chr7:50849752-5085087
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cg13071306	1	6314113	chr1:6313761-6314139
cg17144164	17	78896700	chr17:78896436-788968
cg14318489	14	100759310	chr14:100758608-10075
cg04450456	4	17643702	
cg26151355	3	183226025	
cg15924566	4	57969541	
cg21683105	1	228494821	
cg22625953	7	138555959	chr7:138554231-138554
cg26916576	14	91700557	chr14:91700081-917012
cg09926389	19	41837123	chr19:41837014-418372
cg25463483	6	30530544	
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cg16619049	1	805541	chr1:805198-805628
cg04459447	8	135487401	chr8:135490786-135491
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cg17016890	18	45556172	chr18:45555644-455562
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cg11183535	7	157654985	
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cg18630125	6	14677373	
cg17171920	15	37349117	
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cg23523659	10	2125911	
cg11959894	12	132886529	chr12:132885388-13288
cg18060965	12	30903750	chr12:30907359-309082
cg08328513	5	78365691	chr5:78365298-7836571
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cg06566039	6	22569785	chr6:22569584-2257070
cg16588852	4	4034611	
cg03480001	13	114287656	chr13:114287533-11428
cg07252731	15	88799999	chr15:88799522-888010
cg06817368	5	112315632	chr5:112312387-112313
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cg18457159	17	73489129	
cg17159890	10	105233093	chr10:105232921-10523
cg19159759	13	20989818	chr13:20989007-209898
cg15121276	5	1318882	
cg08796240	16	70733832	
cg18973586	4	963968	chr4:963804-964115
cg01940490	16	10934608	
cg26811411	1	111685877	chr1:111682227-111683
cg22238104	1	42049046	
cg05393726	3	133615119	chr3:133613566-133615
cg24726783	10	29759454	
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cg20116804	6	48036212	chr6:48036137-4803641

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cg04873169	22	47021767	chr22:47022457-470226
cg17037406	12	133294835	chr12:133294088-13329
cg17664577	20	44642114	chr20:44642094-446424
cg01881136	16	89438758	chr16:89438503-894388
cg23887396	17	26699551	chr17:26698359-266995
cg22132788	7	45002486	chr7:45002111-4500284
cg24590093	10	8125599	
cg08314208	16	67682810	chr16:67681975-676839
cg04990989	5	10291308	
cg05549854	16	30798770	chr16:30797744-307987
cg21540460	4	187894584	chr4:187880885-187894
cg18395355	17	46796556	chr17:46796234-467972
cg03653137	6	33263805	chr6:33266302-3326758
cg22860181	1	182922502	chr1:182921819-182922
cg03567028	13	44544293	chr13:44544202-445445
cg17561241	12	54070294	chr12:54071053-540712
cg06339396	16	57736130	
cg14053639	6	32046840	chr6:32046815-3204709
cg02974491	1	1162280	chr1:1161959-1162281
cg00814985	13	114801132	chr13:114803616-11480
cg03534846	19	1999322	chr19:1998800-1999332
cg00561736	8	7434441	
cg05215994	13	23310203	
cg05065989	7	27205200	chr7:27203915-2720646
cg23531285	22	16288696	chr22:16288314-162885
cg16084014	7	114585003	
cg23395165	19	4483111	chr19:4483031-4483646
cg02093176	2	3660939	
cg02910299	17	78796166	chr17:78796078-787963
cg00386101	2	11621399	chr2:11622000-1162329
cg21969566	19	11447922	chr19:11450016-114504
cg25129716	7	150330422	
cg07180988	12	59325286	
cg23924306	1	55271927	chr1:55271665-5527197
cg04173432	X	114423864	chrX:114423906-114427
cg12930896	2	34719719	
cg09579704	6	30166164	
cg05265234	22	38884016	
cg19565305	2	178973019	
cg14621053	10	128077315	chr10:128076155-12807
cg15555527	4	80885981	chr4:80885844-8088614
cg12798492	10	3627893	
cg02724404	15	100274248	chr15:100272901-10027
cg23574802	14	89017726	chr14:89017660-890179
cg09831562	3	181327125	
cg14396995	7	42278089	chr7:42276003-4227785
cg17054449	X	118284808	chrX:118284519-118285
cg19515081	14	105268492	chr14:105268485-10526
cg04380800	7	100491337	chr7:100492217-100494
cg14973204	12	133052753	chr12:133052680-13305
cg12218406	19	18120692	chr19:18120613-181208
cg00143362	10	15000025	chr10:15001272-150018

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cg23911372	19	42546731	chr19:42546647-425468
cg16377923	3	197279261	chr3:197281605-197283
cg20606759	6	170047995	
cg23373850	11	75898132	
cg20541925	5	818218	
cg11432069	21	47702262	chr21:47705627-477064
cg25347419	2	177043501	chr2:177042751-177043
cg03740666	16	75597830	chr16:75600006-756008
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cg14048463	19	11145635	chr19:11145589-111457
cg19587904	13	28492425	chr13:28491488-284925
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cg13474692	10	131441327	
cg11832717	11	2434218	chr11:2435295-2436651
cg13579926	4	103131830	
cg13636543	7	158200291	chr7:158198545-158198
cg01147107	1	47696505	chr1:47696504-4769819
cg08995871	10	76803361	chr10:76803360-768038
cg06402589	8	142439259	chr8:142439683-142440
cg14350800	9	136816077	
cg09614210	2	1546715	chr2:1544272-1544489
cg02675550	18	77208807	chr18:77208691-772090
cg08143701	19	1957871	chr19:1957774-1958038
cg07352757	13	113495579	chr13:113495320-11349
cg14601038	2	1481097	chr2:1480758-1481631
cg09819081	X	135382647	chrX:135382457-135382
cg18581191	8	145770785	chr8:145770743-145771
cg12028326	19	523360	chr19:523165-523661
cg04842146	8	85097056	chr8:85096759-8509724
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cg18273840	5	45695643	chr5:45695394-4569651
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cg03217915	21	44840965	chr21:44840119-448404
cg02336104	3	71481486	
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cg03742890	19	13910592	chr19:13905810-139066
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cg01687680	16	49312238	chr16:49311413-493123
cg23430209	11	1521257	
cg11337790	10	29932431	
cg26905258	13	77898407	chr13:77900504-779011
cg08605347	10	533359	chr10:530713-531099
cg18247055	10	22634226	chr10:22634000-226348
cg08985853	5	166802258	
cg15865827	18	23713838	chr18:23713728-237139
cg03788230	10	125816412	chr10:125816267-12581
cg09377855	19	4446336	chr19:4446011-4446629
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cg21557875	19	42348686	chr19:42348675-423489
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cg00053135	6	167032403	chr6:167032330-167032
cg08369295	22	25759225	chr22:25755941-257561
cg00464927	11	68139121	
cg27382860	7	151300485	chr7:151300169-151300
cg06305891	3	195897904	
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cg09240436	19	57630594	chr19:57630339-576306
cg07690326	8	145019032	chr8:145018815-145019
cg05238769	21	34399260	chr21:34395128-344002
cg03515494	12	8068627	
cg26526983	16	12136938	chr16:12136720-121369
cg01454947	2	99223011	chr2:99224681-9922532
cg18869404	5	76937348	chr5:76936126-7693698
cg11174855	10	134598352	chr10:134597357-13460
cg12726906	8	104362929	
cg11170552	11	69307431	
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cg15915602	2	114737459	chr2:114736853-114737
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cg09847820	7	42261049	
cg27533534	2	149859227	
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cg10383396	14	105119708	chr14:105119773-10512
cg13028630	6	31964754	
cg21646955	6	35108921	chr6:35108801-3510949
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cg05540617	16	3714372	
cg23314866	19	48016020	chr19:48017717-480187
cg27462820	7	636583	
cg16171858	3	58472734	
cg23529677	18	52499934	chr18:52495604-524960
cg11722816	13	100966268	
cg02931762	16	54325015	chr16:54325040-543257
cg20386580	10	105344807	chr10:105344173-10534
cg23968456	10	73521631	
cg25950377	X	27481481	
cg04771838	13	110993474	
cg10218605	7	158379132	chr7:158379328-158381
cg27406070	6	29575566	
cg02991338	14	29236017	chr14:29236835-292378
cg06835018	8	12272982	
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cg23247945	5	140530410	chr5:140531157-140532
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cg08355301	17	62009651	
cg13661832	9	98495510	chr9:98491389-9849169
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cg23785882	18	32824104	chr18:32820785-328212
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cg10092265	17	7311742	chr17:7311672-7312063
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cg24912415	20	33585435	chr20:33585039-335854
cg00004883	16	75148460	chr16:75148398-751488
cg16334004	10	134722168	chr10:134722046-13472
cg05132905	2	38600367	chr2:38603569-3860451
cg02257048	17	78880031	chr17:78880030-788802
cg00710180	2	95723453	
cg02260098	21	44782434	chr21:44782248-447826
cg26656258	4	54969688	chr4:54966163-5496806
cg19123356	8	130898833	
cg27303983	7	73153259	chr7:73152564-7315371
cg03758150	19	30866192	chr19:30865683-308664
cg10823473	15	76630514	chr15:76630029-766309
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cg01305849	7	76610047	
cg23723163	6	169781435	
cg19780250	11	45420388	
cg07559615	X	47497286	chrX:47497182-4749739
cg11203616	7	47576580	chr7:47576519-4757721
cg10888031	1	2938799	chr1:2938633-2939043
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cg10850215	6	33048469	chr6:33048416-3304881
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cg23157290	7	138602695	
cg14636113	2	240742128	chr2:240738027-240738
cg24203192	X	34149344	chrX:34149264-3414948
cg27548655	X	55247168	
cg04511195	19	3523009	
cg10755235	14	60974039	chr14:60973772-609741
cg21635870	6	101847058	chr6:101846766-101847
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cg07494987	X	15664840	chrX:15664741-1566517
cg15010372	1	175832735	
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cg19241689	6	33245516	chr6:33244677-3324555
cg15625675	5	114957464	chr5:114961329-114961
cg02368812	6	3019900	
cg25711997	10	106075710	chr10:106075559-10607
cg18613238	19	49214363	chr19:49217245-492178

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cg20291436	4	111539352	chr4:111539228-111539
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cg03515372	3	79551514	
cg10375964	13	112815146	chr13:112817816-11281
cg11295761	12	124430049	
cg26970905	8	8175877	chr8:8175699-8176775
cg19204189	12	1973208	chr12:1973739-1974958
cg27143703	17	77961719	
cg01256987	12	42539512	chr12:42538125-425389
cg19294448	17	6900799	chr17:6898820-6900427
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cg12934371	8	1579180	chr8:1579038-1579241
cg09046445	16	87703364	chr16:87702493-877027
cg02279071	3	37034154	chr3:37034228-3703535
cg11276053	19	46307734	chr19:46307477-463079
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cg07996594	1	25257505	chr1:25255527-2525900
cg06566239	10	131361472	
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cg08194879	6	123317569	chr6:123317164-123317
cg02272334	2	10114151	
cg05923687	1	63795711	chr1:63795363-6379614
cg21869704	6	32134622	chr6:32134460-3213519
cg04691270	10	2371195	
cg17326555	1	119535693	chr1:119535666-119535
cg26076724	6	15090163	
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cg09286493	11	78387387	chr11:78387189-783874
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cg05989423	18	44561188	chr18:44561025-445618
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cg14343091	17	6351011	chr17:6347465-6348111
cg09834706	2	39470743	chr2:39470742-3947120
cg20181323	7	158243369	
cg08104981	2	133343149	chr2:133343114-133343
cg03566814	6	169019307	
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cg06962177	1	63785946	chr1:63782394-6379047
cg02958004	18	19997969	
cg21021052	8	43055930	chr8:43059755-4305997
cg10262747	6	16742123	
cg24949049	13	61013241	
cg01554064	9	106855171	chr9:106855962-106856
cg06332111	10	71812321	chr10:71812318-718136
cg13375589	17	4487125	chr17:4487398-4488482
cg05272827	17	79380706	chr17:79380359-793807
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cg08337835	19	43918868	chr19:43918854-439191
cg04799838	5	63256926	chr5:63256548-6325788
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cg05436760	6	32149143	
cg22519233	4	1806633	chr4:1806488-1806696
cg09469566	13	112717244	chr13:112717125-11271
cg16041981	13	114057379	chr13:114056100-11405
cg16712866	16	12359297	chr16:12355013-123559
cg06679270	15	101084980	chr15:101084428-10108
cg05348188	21	45877268	chr21:45875391-458773

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cg09785512	17	21934840	chr17:21934703-219350
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cg01942790	4	1211419	chr4:1209765-1210193
cg08107208	1	62901199	chr1:62901651-6290366
cg16233515	7	73408058	
cg09287096	10	86998622	
cg09359351	3	122509111	chr3:122512485-122512
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cg10830145	5	87440121	chr5:87437095-8743750
cg03727313	17	8661774	
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cg27196194	19	4054253	chr19:4053879-4055289
cg00356769	7	23455115	chr7:23454792-2345519
cg07258474	2	11809858	chr2:11809606-1181043
cg27573031	7	150554420	chr7:150554419-150554
cg05939956	2	70437536	
cg08021120	3	195498017	
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cg23575668	22	21800832	chr22:21800412-218010
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cg25956966	7	157213519	chr7:157215001-157215
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cg21010753	22	50898040	chr22:50897713-508980
cg02862087	2	1711134	
cg13089599	11	70023060	chr11:70023057-700233
cg24095120	5	106838352	
cg27173971	19	463914	chr19:463853-464103
cg13715901	8	1145806	
cg02368274	5	176692739	chr5:176693340-176693
cg02156870	17	36717733	chr17:36717727-367185
cg25923345	7	100304669	chr7:100303014-100304
cg05380821	6	108491108	chr6:108491033-108491
cg12465520	5	14733886	
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cg09192801	12	77156412	chr12:77157518-771584
cg02920176	7	36404389	chr7:36406370-3640701
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cg02045428	11	34120275	
cg05163268	5	180116385	
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cg10733317	13	41161439	
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cg16734795	19	47839187	
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cg01327147	9	34371380	chr9:34370773-3437290
cg19771575	12	132358037	
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cg09786329	16	88821445	chr16:88821117-888216
cg23987345	X	51076387	chrX:51075272-5107633
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cg23074601	7	157985748	
cg15153068	2	2009035	
cg19009471	14	101908998	chr14:101908781-10190
cg10476962	16	3724846	chr16:3724344-3724849
cg05034702	13	61989701	
cg02828802	16	2983208	
cg08103988	17	6558365	chr17:6558221-6558441
cg03154665	3	180324050	chr3:180319823-180320
cg00189061	16	20709548	
cg07348982	5	58479549	
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cg07516702	19	5240224	chr19:5238767-5239060
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cg08523848	16	88532266	
cg24366168	19	3097712	chr19:3097564-3097793
cg19161124	7	153583563	chr7:153583317-153585
cg13166748	15	28437159	
cg16400647	7	150069707	chr7:150068756-150070
cg22935533	4	184441284	
cg23192255	4	1309340	chr4:1309204-1309417
cg16053281	3	196387058	chr3:196386796-196387
cg06351643	11	69624649	chr11:69625108-696254
cg27324527	3	40657289	chr3:40657159-4065739
cg12651286	11	102473828	
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cg01101873	1	3269478	
cg26105731	3	110607964	
cg05194481	10	403383	
cg25104105	1	14925198	chr1:14924610-1492599
cg27065869	12	118583229	
cg02752243	7	76610035	
cg20934323	2	87161889	chr2:87157803-8715800
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cg21206233	3	53844068	
cg22186831	5	176544048	chr5:176543900-176544
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cg00171578	1	147789747	chr1:147789652-147790
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cg14584961	7	157533065	
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cg06942742	19	38713242	chr19:38713166-387134
cg01716084	8	142367700	chr8:142367050-142367
cg11691038	12	40019919	
cg12009398	7	158854856	chr7:158854446-158854
cg22956811	4	544333	
cg06657050	15	53083587	chr15:53080458-530836
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cg09571369	3	150996563	
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cg15363314	11	1283970	
cg10703936	11	68549447	chr11:68550231-685505
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cg00095018	6	36101338	chr6:36098039-3609862
cg19409583	6	169273973	
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cg02268620	9	97847913	chr9:97848140-9784852
cg17093867	6	112668571	
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cg18377044	4	6568049	chr4:6564751-6565185
cg19559668	19	36105986	chr19:36103554-361038
cg10571993	X	124453998	chrX:124453902-124454
cg00237026	5	10065651	
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cg11907729	6	55443757	chr6:55443732-5544409
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cg16211990	12	91763848	
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cg08155591	8	86099504	
cg13973436	16	67428898	chr16:67427284-674289
cg10218510	16	88453688	chr16:88453549-884539
cg17387694	19	32833011	chr19:32836353-328368
cg20000220	8	144800997	chr8:144800957-144801
cg14420349	2	240100930	chr2:240101503-240101

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cg03298716	6	168196351	chr6:168197142-168198
cg25206725	X	49593930	
cg16343302	5	10649157	chr5:10649367-1065035
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cg02582391	17	74005445	chr17:74003179-740054
cg24710938	13	36788861	chr13:36788414-367890
cg20382675	3	71591429	
cg14623735	3	42265667	
cg10140536	19	57630596	chr19:57630339-576306
cg17971113	4	47706142	chr4:47708443-4770871
cg18194483	1	44064515	chr1:44063469-4406375
cg12748499	1	244374172	
cg00957684	16	88962800	chr16:88962670-889634
cg16563255	16	72995177	chr16:72993103-729938
cg22868225	1	2015815	
cg15711521	3	167767619	
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cg02858606	16	62068447	chr16:62069121-620706
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cg01963754	13	111977248	chr13:111978588-11197
cg26663742	5	70906136	
cg05950157	12	130603995	
cg16163981	2	11052885	chr2:11051858-1105347
cg08264507	17	53827753	chr17:53828422-538287

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cg00788028	2	114049041	chr2:114048828-114049
cg13993183	9	134699541	chr9:134699141-134699
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cg15250771	6	149020047	
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cg08150250	17	36739017	chr17:36734659-367352
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cg03904534	16	78466521	
cg08017189	16	85680248	chr16:85684107-856844
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cg00232735	11	132934139	chr11:132934059-13293
cg06215798	1	164743113	
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cg24298476	6	32729808	chr6:32729342-3272987
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cg04653469	4	1232739	chr4:1233872-1234420
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cg03220124	17	54756137	
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cg17879912	5	118626530	
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cg25537125	2	108993602	
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cg05928369	7	2185971	chr7:2185771-2186205
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cg24652379	7	141477912	
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cg23989768	X	84189001	chrX:84189065-8418959
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cg16227623	5	3605783	chr5:3606488-3607135
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cg15491461	15	89959984	chr15:89959742-899599
cg24806294	8	145554322	chr8:14555342-145562
cg09828310	1	2452844	chr1:2452795-2453007
cg05979020	2	176981336	chr2:176980765-176981
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cg16259171	11	73660510	
cg18361730	7	44047039	
cg11715095	19	19737444	chr19:19737385-197379
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cg06819605	1	977003	chr1:975496-980305
cg00071984	3	60617504	
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cg16467854	17	21496239	chr17:21496106-214963
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cg08502239	17	9808122	chr17:9808067-9808339
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cg22282405	6	50810682	chr6:50810642-5081099
cg12372745	20	62187666	chr20:62187125-621878
cg06567373	10	102483843	chr10:102484200-10248
cg19303162	2	236506727	chr2:236506378-236506
cg19867914	2	144234430	
cg02578162	16	3927429	chr16:3929483-3929769
cg19380303	15	90172193	chr15:90171665-901719
cg27543431	16	27499592	
cg00170236	7	99691604	
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cg20654468	11	58342997	chr11:58345673-583473
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cg03255182	12	54423566	chr12:54423427-544237
cg19245612	12	133295328	chr12:133296223-13329
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cg19471462	X	39871053	chrX:39871532-3987476
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cg18581669	8	619965	chr8:619097-619607
cg20660269	22	24823514	chr22:24819537-248208
cg11447335	5	865350	chr5:865317-865642
cg23016129	10	22634224	chr10:22634000-226348
cg07527105	16	88053339	chr16:88052773-880533
cg12563935	17	63163128	
cg10475468	5	646259	chr5:646055-646291
cg04342202	7	1961968	
cg25180759	12	116609750	
cg03242964	19	3381991	chr19:3381525-3382275
cg00551398	6	88298474	chr6:88299620-8829994
cg25840378	2	235585914	
cg11801842	22	48025368	chr22:48027586-480278
cg07876450	8	1740065	
cg16918684	12	52056579	
cg27339188	3	20195067	
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cg12059309	12	70686336	
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cg05965188	21	45078342	chr21:45077671-450798
cg24973591	4	10079421	chr4:10079335-1007955
cg03857384	11	3187777	chr11:3186131-3186768
cg00100564	6	170041760	
cg23367107	12	115136287	chr12:115135925-11513
cg00944166	5	101834675	chr5:101834354-101834
cg20999347	6	30095517	chr6:30095173-3009561
cg20197694	11	70440363	
cg17686260	10	131412764	
cg18469713	9	32954332	chr9:32955651-3295627
cg25757115	1	46913787	chr1:46913786-4691434
cg17291887	8	37397163	
cg20348298	2	3193239	
cg17350552	19	7143108	chr19:7142907-7143109
cg03090436	6	71121859	chr6:71122892-7112382
cg03790189	16	89977815	chr16:89977562-899778
cg25403721	12	114885372	chr12:114885105-11488
cg08389497	10	73820491	
cg04860563	3	189524470	
cg13960334	21	43990142	chr21:43989948-439901
cg25439798	21	47456315	chr21:47456271-474565
cg12368065	9	79379372	
cg12058390	7	4885521	
cg16419441	8	105478683	chr8:105478672-105479
cg08684663	12	10325221	
cg04175399	5	80383034	
cg10977643	14	97082103	
cg13490403	9	124982413	chr9:124981535-124982
cg01179256	12	105141965	
cg07812459	19	57920371	chr19:57922440-579230
cg08575049	4	126238838	chr4:126235895-126238
cg27532732	6	35480036	chr6:35479872-3548015
cg12903574	15	37326903	
cg11893698	8	143463667	
cg17719126	6	33383819	chr6:33385678-3338626
cg23288099	11	115860986	
cg00417291	8	114389356	
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cg13398027	18	46447840	chr18:46447718-464480
cg07387286	8	39172120	
cg19143282	18	77507733	chr18:77507538-775078
cg17552368	10	133741156	
cg09072859	11	132934128	chr11:132934059-13293
cg16241684	14	101711890	
cg02808397	6	159656576	chr6:159653233-159655
cg21056036	13	19755954	
cg18457613	5	77945739	chr5:77943868-7794522
cg00032884	2	48540671	chr2:48541252-4854258
cg21385746	2	105118572	
cg02614024	15	93652766	chr15:93652755-936530
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cg12799689	18	67067893	chr18:67067509-670691
cg22245494	15	99669982	
cg16689238	16	34649152	
cg21582112	12	54421335	chr12:54423427-544237
cg08439022	17	80709573	chr17:80709052-807108
cg25406442	8	94750120	chr8:94752975-9475349
cg21851351	13	28368087	chr13:28366549-283685
cg06341731	14	99641017	chr14:99640360-996427
cg02711397	19	39360313	chr19:39359916-393611
cg05394800	13	50707050	chr13:50707585-507080
cg21511395	8	144942223	chr8:144942165-144942
cg14797402	11	58673453	chr11:58672851-586732
cg20325921	8	142368332	chr8:142367050-142367
cg01358993	5	87968315	chr5:87968635-8796890
cg14315232	17	13313251	
cg22022927	1	58343668	
cg00495740	19	34291318	chr19:34286184-342891
cg20929387	4	7774510	chr4:7774495-7774769
cg18322739	2	242841490	chr2:242843760-242844
cg22006392	17	927457	chr17:926234-926439
cg04661194	5	90042723	
cg17335657	19	29583995	chr19:29583946-295842
cg02470697	2	48844916	chr2:48844751-4884498
cg20160197	4	1222037	chr4:1221837-1222050
cg04101699	17	722997	
cg06184979	X	107225589	
cg18715665	19	48675166	chr19:48675065-486753
cg18480168	10	120796676	
cg02455836	8	141557701	chr8:141559164-141559
cg21548955	5	140794993	chr5:140794358-140795
cg25629913	X	150248149	chrX:150250877-150251
cg12814550	X	119134684	chrX:119133851-119134
cg05283184	6	79620031	chr6:79620330-7962071
cg27331241	7	751830	chr7:751712-752150
cg16060330	2	173369204	
cg26728517	20	39319540	chr20:39316550-393199
cg00737801	16	1516140	chr16:1514412-1514859
cg09055743	5	152069274	
cg13474004	8	1783980	
cg09295799	6	5994235	chr6:5994909-5995203
cg04850875	16	85698376	
cg20069688	6	31941049	chr6:31939730-3194055
cg00348891	13	46251914	
cg04905477	11	68153835	chr11:68153809-681541
cg16927040	3	187388128	chr3:187387914-187388
cg23270423	14	55966172	
cg12271981	13	88326752	chr13:88326600-883269
cg19214916	X	73642734	chrX:73642494-7364276
cg00185004	17	55752472	
cg25968206	4	125875296	
cg18768238	10	49892829	

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cg15501281	20	19193060	chr20:19192459-191939
cg11337053	1	232651485	
cg12385599	7	56184153	chr7:56183577-5618416
cg10883542	10	118594572	
cg26470641	6	30691760	chr6:30687941-3068821
cg01882666	Y	17571429	chrY:17567579-1756861
cg00587834	3	51749959	chr3:51749754-5175006
cg11642199	7	780367	chr7:780239-780601
cg14420245	2	148601095	chr2:148601280-148602
cg01872122	5	16940481	chr5:16936753-1693695
cg11005562	14	65746824	chr14:65746329-657469
cg23482427	2	26785120	chr2:26785114-2678568
cg20611680	1	16554171	chr1:16553326-1655366
cg22702772	3	48699012	chr3:48698335-4870166
cg12730468	17	63274652	
cg04810284	4	79971177	
cg16439118	18	54814548	
cg21768956	17	927652	chr17:926234-926439
cg08848003	3	98299487	
cg17059185	13	79352486	
cg16451995	16	8942340	
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cg09666541	X	26576330	chrX:26575758-2657617
cg25005357	15	57426631	
cg12279076	6	68595425	
cg19463975	3	15905683	chr3:15900497-1590199
cg13654344	Y	2654978	chrY:2657802-2658099
cg22306015	11	66454625	
cg13035254	15	75015138	chr15:75018186-750193
cg21910355	8	55366152	chr8:55366180-5536762
cg14136893	17	872770	
cg13824665	14	76183993	
cg03717503	16	86734176	
cg12658929	13	111281384	chr13:111277412-11127
cg20299151	14	100758864	chr14:100758608-10075
cg17002518	6	30315468	chr6:30312837-3031341
cg16177058	17	79862475	chr17:79859808-798609
cg01926972	6	168476576	chr6:168476320-168476
cg06673178	X	50557022	chrX:50556224-5055717
cg18711081	17	55123653	chr17:55122795-551240
cg23081488	2	210616647	
cg25146976	3	9550667	
cg13357416	17	707032	chr17:708319-708598
cg05065603	3	195989296	
cg05740024	16	18480523	chr16:18478279-184825
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cg00994032	14	50315768	chr14:50319426-503196
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cg14386951	6	5999186	chr6:5999149-5999787
cg19200589	21	36041605	chr21:36041305-360432
cg07138854	18	77678609	chr18:77678372-776787
cg21058973	20	43029997	
cg00914384	2	5593580	
cg26568402	19	40996346	chr19:40995880-409961
cg16038510	21	15443107	chr21:15442956-154431
cg10711475	6	170473165	chr6:170474406-170475
cg26595256	5	14380529	
cg12720965	1	245397981	
cg00812438	12	127940086	chr12:127940451-12794
cg16202259	14	104625420	chr14:104625248-10462
cg23676577	14	37049565	chr14:37049333-370517
cg08928753	1	43770707	chr1:43770522-4377088
cg27473895	10	102497354	chr10:102497154-10249
cg06036563	10	134040367	chr10:134040198-13404
cg20501527	X	5470290	
cg15528091	19	18119069	chr19:18118741-181195
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cg14880527	10	81921745	
cg02235663	3	160825607	chr3:160822494-160823
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cg10176510	6	97337802	
cg03050981	1	65906670	
cg00094063	16	66913816	chr16:66914167-669147
cg03146079	4	2929622	chr4:2928053-2928271
cg13371767	13	113473689	chr13:113474080-11347
cg17603288	5	14405747	
cg24242968	3	196387120	chr3:196386796-196387
cg11945845	8	8998699	
cg22829375	2	233764831	chr2:233765849-233766
cg24918705	5	140501321	chr5:140502890-140503
cg05922723	7	100285650	chr7:100284888-100285
cg14157445	Y	14774019	
cg04658846	4	528022	chr4:529166-529556
cg01544807	8	42195539	chr8:42195860-4219622
cg25145023	6	35348742	
cg06875227	5	50683378	chr5:50683285-5068361
cg22219795	3	126911763	
cg08825223	10	81146193	chr10:81145958-811461
cg08318732	19	53192577	chr19:53193139-531939
cg07697428	17	4079341	
cg20731110	18	580228	chr18:580179-580899
cg13458561	10	134558389	chr10:134555113-13455
cg02261780	19	3097728	chr19:3097564-3097793
cg11247129	6	97457431	
cg06875060	7	128096171	chr7:128095678-128096
cg00688681	X	53030043	chrX:53029708-5303009
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cg03554196	6	29404667	
cg13959595	9	139910220	chr9:139909878-139910
cg16564271	X	138769193	
cg06260964	7	2473003	chr7:2472245-2473567
cg17184161	17	80873120	chr17:80871287-808715
cg24747427	2	204292883	
cg09450771	17	79073095	
cg24330088	1	67613911	
cg13437146	19	3575538	chr19:3576628-3578314
cg04777541	X	71263427	
cg02088470	10	1551251	
cg06832985	1	248651841	
cg02765496	9	71393662	chr9:71394793-7139549
cg11382963	8	72754469	chr8:72753874-7275475
cg02710004	1	165910731	chr1:165910640-165910
cg14544505	18	12325956	chr18:12325040-123260
cg21454362	7	2609875	
cg05821634	1	16164109	chr1:16163752-1616412
cg16626314	16	30780252	
cg18899802	10	9226457	
cg06103624	15	66998926	chr15:66993543-669965
cg07605143	19	48827843	chr19:48824529-488254
cg04142323	5	87981449	chr5:87980878-8798127
cg06377543	18	23713657	chr18:23713728-237139
cg02309431	20	31618931	
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cg06672093	X	103502294	chrX:103498706-103499
cg01131241	10	54166783	chr10:54170771-541709
cg16733946	X	102809791	
cg04606550	5	14226569	
cg04045327	4	905805	chr4:907653-907967
cg07817967	1	184721222	chr1:184723252-184724
cg22814042	19	7688694	chr19:7688620-7688832
cg06962628	6	170441311	
cg14098153	5	72533169	chr5:72529099-7252997
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cg03599658	7	4803508	chr7:4801841-4802219
cg22621686	1	35260256	chr1:35258564-3525879
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cg16903885	10	134795548	chr10:134791449-13479
cg14102880	17	915634	chr17:915736-915979
cg07821909	11	103765434	
cg06916239	2	223162881	chr2:223162946-223163
cg20525449	10	1416224	chr10:1415976-1416249
cg04388767	16	89177789	chr16:89173704-891739
cg04168670	2	124782817	chr2:124782252-124783
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cg16771467	18	55315872	chr18:55315730-553159
cg04403442	8	24287082	
cg01006880	16	89146961	chr16:89146936-891471
cg07221258	10	30276523	
cg06722022	16	87641631	
cg15824707	15	45403733	chr15:45403248-454042
cg17494897	2	3200012	
cg24280439	17	80763859	chr17:80764626-807648
cg02441015	19	5244038	chr19:5243869-5244393
cg04411337	1	231133412	
cg09007841	16	29230149	chr16:29229952-292301
cg07093674	X	40693703	chrX:40691960-4069244
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cg26630902	16	15692851	
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cg13911828	1	149147566	chr1:149148145-149148
cg05493945	13	107163855	
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cg22702334	5	155061	
cg10838270	11	119549290	
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cg26769118	10	394632	chr10:395170-395404
cg08575950	X	20135450	chrX:20134203-2013535
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cg10158886	6	7728986	chr6:7728885-7729108
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cg05285352	16	87598762	
cg09859040	15	80743325	
cg19277182	17	80560098	chr17:80559025-805594
cg00097146	2	45171818	chr2:45169505-4517188
cg10744200	4	24844162	
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cg03784363	12	38938054	
cg20648501	8	61626832	chr8:61626645-6162707
cg09394681	6	4482990	
cg02090762	17	79503859	chr17:79503586-795041
cg23224752	5	176693109	chr5:176693340-176693
cg24748448	17	3493352	
cg05340339	1	23111011	chr1:23110904-2311156
cg01186595	11	89954679	chr11:89955742-899563
cg04874825	1	246139168	chr1:246137775-246139
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cg13625187	12	27736287	
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cg19509303	14	101318703	
cg02552292	2	133343308	chr2:133343114-133343
cg25819846	12	131443445	
cg17177455	2	176969218	chr2:176969217-176969
cg10665891	12	117042917	
cg25341268	2	37734390	
cg14279898	9	99687244	chr9:99687155-9968758
cg22254103	8	989193	chr8:989167-990699
cg20000541	X	8769269	chrX:8769177-8769559
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cg09216670	10	22999381	chr10:23002155-230037
cg10741333	14	72400168	chr14:72398664-723995
cg27282922	7	158799041	chr7:158798591-158799
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cg24932662	8	145700268	chr8:145700238-145700
cg10976732	13	113525143	
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cg15641339	6	22569638	chr6:22569584-2257070
cg26240231	7	1148101	chr7:1149179-1150306
cg25305174	7	44279680	chr7:44279048-4427932
cg17916835	7	96655044	chr7:96653467-9665419
cg11570508	1	230492846	chr1:230492716-230492
cg14683055	6	14480474	
cg00074086	7	4901785	chr7:4901336-4901753
cg15061647	7	158249209	chr7:158247888-158249
cg26848724	13	31326405	
cg26132774	13	79170146	chr13:79170114-791712
cg19989242	9	96069142	chr9:96069141-9606938
cg20482145	17	8525165	
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cg09582738	5	171664436	
cg13800349	17	80971527	chr17:80969748-809701
cg10573143	11	70628992	
cg07832006	1	115397374	chr1:115397448-115397
cg27284833	13	114112018	
cg09741851	10	30692665	
cg00044950	6	31855393	chr6:31856896-3185710
cg24359323	11	69634372	chr11:69632033-696347
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cg16677019	17	44847268	chr17:44847139-448474
cg22887748	X	47497392	chrX:47497182-4749739
cg07365741	6	170478434	chr6:170474406-170475
cg08777771	2	233278	
cg15541987	11	2077307	
cg08986016	7	866214	chr7:862515-862800
cg24841511	1	44069648	chr1:44070892-4407114
cg14765818	20	36148954	chr20:36148603-361501
cg25102206	14	75897342	chr14:75894308-758954
cg12309703	2	218621258	chr2:218621279-218621
cg21193180	X	2800457	
cg19951766	6	170060988	chr6:170062622-170063
cg09775121	11	69199466	
cg24766840	12	124824871	chr12:124821019-12482
cg20697188	5	82360356	
cg13630560	10	468051	chr10:465928-466396
cg11867671	19	51128350	chr19:51128325-511287
cg00012529	12	132896897	chr12:132896299-13289
cg08146698	7	178613	chr7:178517-179127
cg15720064	X	13062833	
cg22572661	5	28404717	
cg03582787	20	60492176	chr20:60494768-604954
cg00815484	7	1878297	chr7:1881181-1881391
cg14134006	19	36961371	
cg04517429	4	155413618	chr4:155410623-155413
cg16572603	5	140725235	chr5:140725051-140725
cg04121561	21	44007550	chr21:44007475-440104
cg02286008	16	30133247	chr16:30134220-301344
cg19050484	5	467021	chr5:464887-465666
cg27041096	8	120079173	
cg26847490	7	95115289	
cg23489384	14	21199099	
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cg01967073	7	48147130	
cg16385941	7	1579643	chr7:1575736-1575993
cg20090283	17	36718549	chr17:36717727-367185
cg03738979	19	11145704	chr19:11145589-111457
cg14840848	13	112927276	
cg18082337	3	147113726	chr3:147113608-147114
cg07080653	4	54374249	
cg16455945	5	16777377	
cg25881591	11	131779935	chr11:131780328-13178

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cg13855924	6	39281183	chr6:39281135-3928221
cg17570188	5	33985937	
cg02057305	16	83974834	
cg02706018	7	27168780	chr7:27169572-2717063
cg14386202	X	139521779	chrX:139521561-139521
cg25010832	5	178634615	
cg03078006	22	37493737	chr22:37493704-374941
cg18242760	15	48429733	
cg10977770	1	217309906	chr1:217310749-217311
cg13263691	18	77568018	chr18:77567283-775700
cg19369363	18	76557159	chr18:76556716-765573
cg16581905	5	137681158	chr5:137681061-137681
cg26518327	12	74565563	chr12:74564752-745651
cg08093097	2	209054740	
cg19143209	9	19789287	chr9:19788215-1978928
cg15138339	17	40715222	chr17:40714087-407152
cg08290675	11	23425026	chr11:23426952-234273
cg20935368	5	178288625	chr5:178286874-178287
cg04600831	4	15616578	
cg10203922	4	145566200	chr4:145566242-145567
cg24152857	X	48326650	
cg01394199	12	121416547	chr12:121416485-12141
cg16919675	3	124237310	
cg09944697	14	105685660	chr14:105685452-10568
cg19419739	11	1902923	chr11:1903078-1903334
cg13330559	17	11144043	chr17:11143487-111454
cg01081718	3	112278508	chr3:112280022-112280
cg14321042	3	189915550	
cg05689415	2	234386055	chr2:234385358-234385
cg14480343	15	89876619	chr15:89876390-898769
cg17718302	6	27858637	chr6:27858166-2785856
cg23801396	1	246415165	chr1:246414748-246415
cg17608440	10	114912149	
cg01720475	1	4542769	
cg18935396	17	4089136	
cg15594578	X	71800011	
cg26153483	2	24838522	
cg24363858	6	138752062	
cg16929692	11	117389301	chr11:117389186-11738
cg00623015	16	89177293	chr16:89173704-891739
cg02997735	19	44096738	chr19:44096223-440975
cg06234970	16	88679642	
cg06732989	4	1135181	chr4:1137998-1139821
cg02462912	2	198318262	chr2:198317967-198318
cg12281152	1	11821573	chr1:11822139-1182236
cg06460652	5	176519331	chr5:176520157-176520
cg13312403	8	71246470	
cg16418817	21	40198485	chr21:40194644-401948
cg20496568	10	128021322	
cg05027597	19	47935656	chr19:47935483-479357
cg20079298	15	40572326	chr15:40572078-405727
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cg27286614	7	2050401	chr7:2054060-2054386
cg22819672	1	218497739	

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cg15423357	2	25149977	
cg03309978	13	113748255	chr13:113750486-11375
cg22707397	19	49020528	chr19:49016737-490172
cg10742917	7	56242801	chr7:56242406-5624329
cg15484532	1	4714171	chr1:4713989-4716555
cg05152874	X	50557122	chrX:50556224-5055717
cg04787888	16	86547322	chr16:86549069-865505
cg22762091	8	132052843	chr8:132052203-132054
cg02107461	Y	14103651	chrY:14107137-1410748
cg23442198	4	187126114	
cg16341737	13	113634407	chr13:113635654-11363
cg06653292	2	208286307	
cg19687650	X	71289025	
cg18559579	2	209224676	chr2:209224972-209225
cg18350497	11	93476777	chr11:93474085-934750
cg20864707	17	21496299	chr17:21496106-214963
cg04593880	2	225298537	
cg12917058	7	7229837	
cg15775218	2	3286338	chr2:3286324-3286530
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cg00992145	20	36891623	chr20:36888891-368894
cg10539616	8	17102212	chr8:17103890-1710486
cg14462432	9	127572501	chr9:127572126-127572
cg13051197	7	116597218	chr7:116593880-116594
cg21561701	13	114193150	chr13:114195709-11419
cg16904399	10	22902615	
cg18383668	19	45594410	chr19:45594397-455950
cg26815611	19	13919905	chr19:13919665-139200
cg25720578	19	38993211	chr19:38993163-389933
cg04035353	16	89335133	chr16:89334574-893350
cg09154414	12	89118099	
cg13485481	7	2186344	chr7:2185771-2186205
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cg25809434	19	8201264	chr19:8201068-8201350
cg11139095	12	9395304	chr12:9392459-9392686
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cg15104644	1	231297103	chr1:231296559-231297
cg15481429	15	94945799	
cg26889367	15	64673792	
cg11325970	5	87979642	chr5:87980878-8798127
cg08747034	5	6348534	
cg14353137	8	67873799	chr8:67873388-6787560
cg00562871	8	144190362	
cg04662649	15	41191689	
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cg05860371	4	152931291	
cg23677882	7	157281167	
cg14699932	13	114748340	chr13:114748541-11474
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cg07564690	14	32597733	

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cg04143011	1	160639836	
cg02825171	6	168720183	chr6:168719681-168720
cg02129382	1	171307312	
cg11221635	17	74878301	chr17:74878245-748784
cg06325540	16	1183618	chr16:1179618-1179942
cg04004744	6	22190121	
cg01369276	17	67312371	
cg01794156	11	397077	chr11:396685-397462
cg16057826	21	36041334	chr21:36041305-360432
cg02203513	16	1369140	chr16:1369053-1369525
cg08438385	10	59081346	
cg17842918	13	113540400	chr13:113540350-11354
cg09700984	3	176838579	
cg09254350	11	2574026	
cg14075645	21	47552343	chr21:47551837-475526
cg00040923	X	100806880	chrX:100807793-100808
cg20229989	X	153409212	
cg10701000	10	79541025	
cg16252322	19	50789296	chr19:50789768-507899
cg22736807	5	92938149	chr5:92939795-9294021
cg02249577	10	52434778	chr10:52434646-524348
cg27369325	13	98962075	
cg14615553	5	147093466	
cg03784302	7	157916077	chr7:157918704-157919
cg26576398	10	18550135	
cg02744699	17	80197898	chr17:80200604-802008
cg19391276	6	100055785	chr6:100055641-100055
cg01736389	4	7706665	
cg16125397	14	35021983	chr14:35025181-350253
cg03357803	15	28272345	
cg27468941	7	158933383	chr7:158936507-158938
cg01892567	7	156760930	chr7:156760878-156761
cg15516728	X	74524038	
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cg10700934	6	30296700	chr6:30294169-3029507
cg13380624	19	7735426	chr19:7735081-7735456
cg11948766	8	49494499	
cg04845915	5	140802804	chr5:140802399-140802
cg00231361	3	5017589	chr3:5019876-5022223
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cg15537455	19	56739749	chr19:56739524-567397
cg07213616	5	60725347	
cg22772691	5	1104195	chr5:1099943-1100764
cg08134592	11	1007447	chr11:1007921-1008343
cg17537307	4	36284867	
cg01386335	7	17704951	
cg14833008	1	3731826	chr1:3731458-3732015
cg03766449	15	89920918	chr15:89920793-899227
cg02970775	9	140483477	chr9:140484219-140485
cg00954931	7	80342707	
cg19938149	1	215993110	

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cg10434261	1	156358059	chr1:156358050-156358
cg06824013	15	53097247	chr15:53097561-530984
cg24952158	18	34338496	chr18:34340584-343408
cg06912356	2	127815206	chr2:127817994-127818
cg14751552	8	74209522	chr8:74206223-7420817
cg03829216	X	47497456	chrX:47497182-4749739
cg22254463	11	108422663	
cg23331981	10	7574780	
cg01412654	3	12328084	chr3:12328994-1232922
cg12147994	2	262754	chr2:263400-265238
cg27136844	3	147142355	chr3:147142181-147142
cg15722389	3	11888434	chr3:11887799-1188853
cg06349165	1	215586699	
cg20894522	6	17919097	
cg17286244	15	69222592	chr15:69222589-692233
cg06173833	10	82172659	chr10:82168064-821689
cg24630419	1	217311608	chr1:217311467-217311
cg21433558	17	40837037	chr17:40837022-408375
cg19206010	X	47518849	chrX:47518015-4751885
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cg18653560	13	113718453	chr13:113721520-11372
cg15961716	21	47532167	chr21:47531899-475328
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cg16625916	2	80085213	
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cg14266287	2	239334506	chr2:239335160-239336
cg11231069	2	240225142	
cg08658810	6	28832727	chr6:28831682-2883213
cg04312413	1	186340995	chr1:186344124-186344
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cg23851359	20	30602775	chr20:30605744-306059
cg17259265	11	125753373	chr11:125757055-12575
cg04971812	14	105236654	chr14:105239263-10523
cg15848561	14	101924186	chr14:101923575-10192
cg19766102	10	111683738	chr10:111682775-11168
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cg04825491	16	51130058	
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cg08624068	18	51881278	chr18:51883947-518849
cg20992503	17	59668589	
cg24743200	10	1451381	
cg26815748	8	101730502	chr8:101733213-101735
cg18865832	5	140566476	chr5:140568216-140569

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cg17136073	13	23310675	
cg25633284	19	603853	chr19:603638-603945
cg02087067	5	176225592	
cg17649671	10	89298596	
cg06759629	4	25090198	chr4:25090106-2509051
cg26746037	19	3821359	chr19:3821059-3821446
cg01105362	7	1059627	chr7:1059528-1059877
cg05730385	10	1939683	
cg04065832	X	72667191	chrX:72667157-7266759
cg05746523	6	108437684	chr6:108437998-108441
cg15485560	20	21000369	chr20:21000765-210012
cg01834160	16	70713567	chr16:70713461-707143
cg22049485	12	120534798	chr12:120534552-12053
cg09816855	16	54211588	
cg01288350	16	2136783	chr16:2139803-2142170
cg25409554	1	234871422	
cg10442056	8	120865430	chr8:120867785-120868
cg15793688	7	158512671	
cg13343549	17	80983747	chr17:80983038-809835
cg09368074	X	124339119	chrX:124338904-124339
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cg01530024	4	5458553	
cg19768607	11	68768879	chr11:68772796-687731
cg03662997	11	15963027	chr11:15962882-159632
cg13501371	X	110039194	chrX:110038946-110039
cg02304465	2	176931543	chr2:176931575-176932
cg24231854	2	9235924	
cg05981335	12	81102562	chr12:81102034-811027
cg12877223	5	177980691	
cg03339668	12	120241957	chr12:120241921-12024
cg08639389	4	26995889	
cg04340595	1	9789174	chr1:9790292-9790704
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cg10809560	10	79936959	
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cg00609645	6	26205074	chr6:26204764-2620521
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cg16481556	8	2196764	
cg09541794	8	144872852	chr8:144872530-144873
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cg10920817	13	34702716	
cg17799946	1	91301962	chr1:91300979-9130189
cg26734215	20	62616301	chr20:62612300-626127
cg22802167	1	533950	chr1:533219-534114
cg08848154	10	6278954	
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cg12818656	11	1031856	chr11:1033084-1033356
cg11142013	13	24441476	
cg02391400	1	237032112	
cg02255242	15	33420912	
cg11067696	12	132328378	chr12:132329177-13233
cg25061755	2	48808114	
cg02050847	Y	22918038	
cg23850637	12	132937910	chr12:132938326-13293
cg19705853	2	1804642	chr2:1801618-1802060
cg24388153	X	37364728	chrX:37364322-3736482
cg00400448	15	60285691	chr15:60287107-602876
cg13393851	5	140731930	chr5:140731239-140731
cg25601674	3	122380355	
cg13494037	12	24737079	
cg03841065	20	35274627	
cg11967457	1	226128626	chr1:226127112-226127
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cg18228933	2	240170936	
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cg22151179	7	63867800	
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cg11123583	17	744766	chr17:744617-744907
cg23348270	2	176969612	chr2:176969217-176969
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cg22528270	7	151505116	
cg19743270	X	2746333	chrX:2746553-2748235
cg07924013	16	2048236	chr16:2048194-2048754
cg05235248	10	35503876	chr10:35503808-355040
cg07112091	14	106936070	chr14:106936174-10693
cg12062819	1	156358231	chr1:156358050-156358
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cg19522930	11	133837711	
cg19726408	10	105428651	chr10:105428505-10542
cg10003032	7	6200116	chr7:6198495-6198731
cg03515871	12	132913728	chr12:132910476-13291
cg16028694	3	105246298	
cg02991118	7	4823955	chr7:4823506-4824097
cg23055199	8	603425	chr8:599904-600309
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cg07903472	2	168846657	
cg03457729	15	89953295	chr15:89954603-899551
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cg21375017	3	31988082	
cg25155053	12	8596201	
cg06496454	7	4807062	chr7:4806860-4807086
cg04946721	17	62131780	
cg06064297	16	14581967	
cg20119080	6	114183715	chr6:114179734-114181
cg13873902	6	118042761	
cg24259244	13	100624279	chr13:100620241-10062
cg20497631	8	8647440	
cg19446385	12	34458462	
cg26967566	16	85743863	chr16:85743485-857440
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cg09796544	X	152913595	chrX:152912491-152913
cg00499201	7	152600590	chr7:152600496-152600
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cg01940439	12	132252573	
cg02595770	19	45867304	chr19:45866930-458673
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cg20186067	7	129422439	chr7:129418286-129422
cg03682112	18	77623598	chr18:77623265-776242
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cg23158189	12	132845336	chr12:132845758-13284
cg01414185	2	177017449	chr2:177017266-177017
cg00034650	17	76987444	chr17:76989642-769900
cg00142402	17	75956190	chr17:75953890-759559
cg19015955	17	41287434	
cg24476033	19	6710658	chr19:6710625-6710828
cg15202738	19	53636108	chr19:53635625-536362
cg01078565	X	30233575	
cg21889472	5	42992555	chr5:42992033-4299295
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cg03829559	2	54681906	chr2:54682899-5468437
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cg26558363	4	14482701	
cg02283353	19	622406	chr19:615691-623505
cg16290006	14	101908561	chr14:101908781-10190
cg09178970	12	123351798	chr12:123351641-12335
cg19814400	7	158936632	chr7:158936507-158938
cg08696931	12	123754071	chr12:123754049-12375
cg26463500	10	38739478	chr10:38739405-387397
cg03155755	Y	9385861	chrY:9385471-9385777
cg05652828	X	47445107	
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cg22603628	8	1642625	chr8:1639891-1640612
cg02362620	8	109144230	
cg24836679	19	56017564	chr19:56014811-560153
cg02760300	11	78780772	chr11:78780676-787810
cg09451092	1	159869223	chr1:159869901-159870
cg00567298	1	166818939	
cg12869262	3	195528619	
cg25135457	17	40715244	chr17:40714087-407152
cg18398125	14	94291069	
cg26351354	X	53283877	chrX:53283829-5328403
cg13585334	7	31235174	chr7:31232677-3123290
cg26170257	20	23345093	chr20:23346034-233466
cg26870771	16	67197640	chr16:67196792-671999
cg21120892	14	60725731	
cg20300093	3	123138250	
cg26226576	1	234721577	
cg02295369	X	117959263	chrX:117957615-117957
cg06957447	14	95242007	chr14:95240083-952403
cg19652433	10	48899772	chr10:48901419-489016
cg06181508	3	147102840	
cg02689072	4	802844	chr4:798538-798984
cg09451320	12	132639764	chr12:132639460-13263
cg17614939	5	140720426	chr5:140720138-140720
cg06077821	5	180048893	chr5:180045789-180048
cg01239666	3	195601381	chr3:195600845-195602
cg02237629	14	57264095	chr14:57264638-572655
cg14635199	12	95841289	
cg00623498	6	540351	chr6:537144-537522
cg07729303	15	22940817	
cg21873741	7	45762358	
cg02731159	12	65559832	chr12:65563195-655643
cg01336260	6	130473404	
cg20139706	2	237068750	chr2:237068071-237068
cg27496267	7	90895466	chr7:90893567-9089668
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cg19938791	4	6423283	
cg16136096	X	119744207	
cg17367836	4	7716106	
cg01042202	5	140242159	chr5:140242073-140243
cg06062984	3	22413960	chr3:22413492-2241436
cg02639793	X	70273113	chrX:70273009-7027325
cg05409047	21	37259564	chr21:37259191-372596
cg09623712	10	134731415	chr10:134731433-13473
cg03611733	15	45585637	
cg16776524	16	19420745	chr16:19421816-194224
cg07485775	5	172110569	chr5:172110282-172111
cg23368787	19	36049342	chr19:36048556-360496
cg21241989	9	839126	chr9:841374-843364
cg20977769	8	49737422	
cg27345924	5	2727758	
cg08201673	17	18167551	chr17:18167174-181677
cg21300993	2	237123218	chr2:237123015-237123

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cg25670229	5	140236873	chr5:140236862-140237
cg20718350	12	103352294	chr12:103351579-10335
cg05014727	10	6214016	
cg05369582	1	228404763	chr1:228404717-228405
cg11173579	21	33247885	chr21:33244910-332466
cg24140200	10	63422254	chr10:63422538-634231
cg10925417	11	64875148	chr11:64875134-648762
cg24474622	7	1103876	chr7:1105259-1105974
cg13481374	9	34318769	chr9:34318282-3431894
cg01624768	16	85465657	chr16:85465046-854652
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cg14897298	14	96750481	
cg03292206	2	111424914	
cg07066860	12	11932089	
cg05257260	4	114561619	
cg09580249	17	96503	chr17:99719-100301
cg01679060	3	31893876	
cg08260959	6	26240920	chr6:26240697-2624095
cg09890687	1	36641984	chr1:36641756-3664246
cg00370293	5	43397113	chr5:43396897-4339736
cg25699218	13	96583970	
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cg03531984	17	3500374	
cg08214693	8	144885540	chr8:144885269-144886
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cg04192258	21	43999785	
cg03685886	16	86912525	chr16:86912403-869126
cg07382920	1	3567646	chr1:3566445-3569636
cg23081357	2	231710048	chr2:231712775-231712
cg07071449	2	238777806	
cg09616857	3	169122917	
cg13188915	12	25622615	
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cg09185350	X	50556361	chrX:50556224-5055717
cg22030839	5	306838	chr5:307286-307592
cg25923609	5	3607092	chr5:3606488-3607135
cg26048897	10	51632982	
cg27215131	6	34753792	
cg15096958	19	58334700	chr19:58331004-583314
cg09629753	16	29323721	
cg19608824	6	80778561	
cg08200856	8	144338584	chr8:144337536-144338
cg18543993	8	88886320	chr8:88886171-8888644
cg05976247	10	77600354	
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cg10782633	1	1027572	chr1:1027509-1027730
cg25778262	12	69327449	chr12:69327021-693275
cg09894268	13	98973904	
cg02096887	1	10699831	chr1:10699394-1070009
cg17127816	1	154544538	chr1:154543818-154544
cg12671565	12	1904730	chr12:1905277-1906765
cg04923020	12	46005007	
cg11946503	5	134870514	chr5:134870740-134872
cg27175943	16	85334190	
cg06969979	1	3557200	chr1:3556963-3557201
cg24228819	7	136553868	chr7:136553854-136556
cg15243034	11	77907656	chr11:77907211-779080
cg20621200	11	94883516	chr11:94883335-948835
cg20410537	1	33612991	chr1:33612976-3361332
cg16540238	17	56089241	chr17:56083750-560853
cg27009703	7	27204894	chr7:27203915-2720646
cg01934296	15	29429225	
cg16191360	5	466529	chr5:464887-465666
cg10426234	12	132939776	chr12:132938326-13293
cg20631820	13	95086158	
cg06120404	1	111888935	chr1:111889138-111889
cg13715001	5	1019448	
cg03969956	4	11884	
cg26147269	3	13520256	chr3:13520912-1352131
cg00059161	3	164907027	
cg26467717	7	122342889	
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cg25522232	5	195132	chr5:195087-195323
cg27138293	17	79503701	chr17:79503586-795041
cg03710719	19	36389795	chr19:36389545-363899
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cg04029483	12	15943686	chr12:15941718-159427
cg20168823	18	34916738	chr18:34916712-349169
cg10863922	6	2892150	chr6:2891929-2892182
cg13709271	10	45966142	
cg19573236	10	65733388	chr10:65733267-657335
cg10791023	3	122005090	
cg01486146	10	102415311	chr10:102414425-10241
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cg24637364	1	66259084	chr1:66258440-6625891
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cg26894575	1	153518054	
cg11256278	8	2243209	chr8:2241982-2242312
cg02933100	7	50658454	
cg21624165	5	178411451	chr5:178413296-178413
cg21127362	17	78168238	chr17:78172176-781724
cg21598190	7	2099404	chr7:2099668-2100358
cg20673840	5	54281362	
cg09250149	16	85684353	chr16:85684107-856844
cg04863758	4	1303710	chr4:1303490-1303835
cg08617970	6	30881112	chr6:30881533-3088229
cg11001470	X	24170765	chrX:24167563-2416878
cg14340500	X	142723216	chrX:142721410-142722
cg26527263	1	53875972	
cg02501086	8	26717875	chr8:26721642-2672456
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cg13300273	1	200842890	chr1:200842196-200843
cg07584200	17	44185029	
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cg02504716	11	124071642	
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cg06826760	1	193076307	chr1:193074174-193074
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cg03369668	7	2578307	chr7:2578020-2578366
cg22766368	14	105119774	chr14:105119773-10512
cg21863110	1	116380417	chr1:116380359-116382
cg02400611	3	194783274	chr3:194785977-194786
cg26497399	12	48215165	chr12:48213109-482141
cg26479374	4	1243980	chr4:1241412-1244111
cg19033906	3	53532972	chr3:53527927-5353010
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cg06730409	7	50202657	chr7:50198771-5019898
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cg19759135	5	179221059	chr5:179222608-179223
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cg23946462	11	890331	chr11:890191-890506
cg01256365	16	85517170	chr16:85519109-855193
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cg10409230	17	40318360	
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cg06331359	17	78190755	chr17:78188803-781890
cg23249922	10	134231549	
cg22084487	5	662614	chr5:662283-663402
cg06390041	7	140111776	
cg18546622	11	44325029	chr11:44324875-443250
cg10727171	14	33407334	chr14:33402094-334040
cg19360685	11	113188759	chr11:113185332-11318
cg22467232	5	1816093	
cg06236737	16	89950219	chr16:89945514-899463
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cg15993027	7	43484421	chr7:43484390-4348512
cg07862744	7	2100161	chr7:2099668-2100358
cg02818910	2	1941247	chr2:1941068-1941560
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cg14992633	7	129962562	
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cg18064631	13	28496413	chr13:28498226-284990
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cg06900311	14	106333919	chr14:106333492-10633
cg14716990	10	129533731	chr10:129534410-12953
cg12031031	12	103980882	
cg18151262	19	1254251	chr19:1254024-1254454
cg15829073	19	50826823	chr19:50826780-508270
cg21477861	17	43196290	chr17:43198277-431987
cg08901578	4	187885870	chr4:187880885-187894
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cg01856162	2	233350940	chr2:233350278-233352
cg01243072	2	43398171	chr2:43398040-4339827
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cg26335620	19	48215149	chr19:48216486-482168
cg19629631	7	2060116	chr7:2059907-2060131
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cg13413955	9	842914	chr9:841374-843364
cg06393563	6	133564066	chr6:133562086-133563
cg10362842	10	123353578	chr10:123356616-12335
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cg20441048	5	6447257	chr5:6448753-6449629
cg24435704	7	139763773	chr7:139762255-139763
cg02840092	6	168748530	
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cg19934476	18	76262286	chr18:76262285-762630
cg19736654	19	6746221	chr19:6746023-6746292
cg05897008	3	138647715	chr3:138647671-138648
cg03350163	8	143207661	
cg10899301	6	10416007	chr6:10417384-1041784
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cg02724608	17	884373	chr17:881733-883381
cg08722200	20	55960520	chr20:55964272-559646
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cg09413529	12	115112225	chr12:115112014-11511
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cg13323391	7	157579745	chr7:157577685-157577
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cg06883126	5	140457585	
cg04021098	11	59482698	
cg03732020	11	47282968	
cg26402169	7	1883139	chr7:1885033-1885402
cg23591125	1	178481898	
cg09771916	12	132673274	chr12:132673993-13267
cg06077305	16	2903246	chr16:2902829-2903362
cg19861147	1	13881542	chr1:13881410-1388161
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cg00922420	1	55529158	
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cg01040782	1	12704481	
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cg01160695	7	862799	chr7:862515-862800
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cg16264642	5	11384581	chr5:11384681-1138552
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cg09381737	9	140173549	chr9:140172613-140176
cg24735165	X	153218313	chrX:153218818-153219
cg22842717	12	57939823	chr12:57940563-579409
cg18894878	1	166958221	chr1:166958220-166958
cg20301593	X	153882028	
cg27108388	21	46929959	chr21:46929225-469302
cg03352153	6	64030429	

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cg03168501	19	33211891	chr19:33211781-332120
cg16956686	7	4304779	chr7:4303079-4305062
cg04621795	5	876076	
cg22495848	1	2425173	
cg11135724	1	147309347	
cg13994196	6	117737102	
cg09796094	14	105350432	chr14:105350177-10535
cg01289769	3	125077434	chr3:125075915-125076
cg18575438	6	151811868	chr6:151814980-151815
cg02972640	10	1415977	chr10:1415976-1416249
cg25010500	5	140619586	chr5:140620864-140621
cg17491365	5	109962391	
cg03987818	2	186988953	
cg07236912	4	95429383	
cg11205981	8	144790410	chr8:144788491-144791
cg00371368	1	239550378	chr1:239550108-239551
cg08561895	11	75905850	chr11:75905717-759059
cg12596096	X	119252099	chrX:119249439-119249
cg04270085	2	12223636	
cg17129028	17	74304023	chr17:74303478-743044
cg10406676	16	3494094	chr16:3493098-3493569
cg19754520	10	101825118	chr10:101824961-10182
cg09103423	6	4665238	
cg10246871	16	84256036	chr16:84256189-842564
cg14329045	2	106694419	
cg09211372	6	168490623	
cg07912144	18	77247106	chr18:77246356-772478
cg20790648	3	151619923	
cg04826673	5	180272367	
cg23481243	6	30112493	
cg22165106	7	1782220	chr7:1784027-1786934
cg20927547	3	31494215	
cg23281527	1	18809531	chr1:18808873-1880966
cg04413547	11	43905825	chr11:43902254-439025
cg16300329	18	9535889	
cg05632866	7	63764120	chr7:63767750-6376799
cg03793937	11	95625728	
cg19597652	1	6154558	
cg21790626	19	58220494	chr19:58220189-582205
cg16530760	2	120121136	chr2:120124241-120125
cg18907098	4	512994	
cg01357745	2	148264586	
cg26986928	5	3059243	
cg12035880	5	6447235	chr5:6448753-6449629
cg12614283	X	140991045	
cg08500704	6	100060453	chr6:100060979-100062
cg07123608	7	93198461	
cg08423879	12	103437918	
cg03531326	19	39443344	chr19:39440404-394410
cg08071472	13	98984334	
cg18300285	10	118434728	
cg05937392	2	18736132	
cg16534163	3	146213718	
cg10359157	13	51418020	chr13:51417371-514181
cg08926436	8	12235070	

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cg22038249	6	30706320	chr6:30710307-3071244
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cg11403739	15	22923741	
cg13850380	1	1475143	chr1:1474962-1475220
cg11665991	1	50893469	chr1:50893468-5089374
cg14576258	9	88513789	
cg12347757	7	139779027	
cg07214164	2	105480254	chr2:105480197-105480
cg15978880	1	204954591	chr1:204950982-204951
cg17258703	2	237022779	
cg05810363	17	74475270	chr17:74475239-744754
cg10690003	7	96622311	
cg13293535	8	11597251	
cg17968668	6	30038859	chr6:30038881-3003947
cg06428196	2	19338174	
cg13154057	6	4894381	
cg07841762	7	99704525	
cg06948294	14	25518624	chr14:25518424-255196
cg20768313	5	179267916	
cg10016575	19	40398384	chr19:40397965-403985
cg03702675	13	113174184	
cg08171351	22	17600844	chr22:17600563-176026
cg01740135	X	42638571	chrX:42637008-4263738
cg19903927	15	23811369	
cg26328483	1	156823867	
cg26857370	16	34442283	chr16:34441786-344423
cg26039141	11	75113160	chr11:75110493-751109
cg13600420	5	177614205	chr5:177614102-177614
cg06702884	10	73096492	
cg16958467	15	57655799	
cg04406200	1	240568125	chr1:240569320-240569
cg00240875	6	32817673	chr6:32820849-3282237
cg18009127	22	28010359	chr22:28010273-280105
cg22754206	20	61151391	chr20:61151586-611519
cg01854967	2	863946	chr2:863930-865091
cg24884444	8	49572044	
cg11397581	15	22955729	
cg04612869	4	89841012	
cg08194989	8	41655154	chr8:41654875-4165598
cg07123769	5	1809881	
cg25362652	6	106429769	chr6:106429111-106429
cg18586758	2	241294011	chr2:241293841-241294
cg24942747	5	140856971	chr5:140857864-140858
cg05372365	2	74687608	chr2:74684565-7468578
cg16198103	8	53471884	
cg15738084	16	88890280	chr16:88889857-888902
cg23610752	1	170522223	
cg06411322	16	71838776	chr16:71841923-718431
cg07424785	1	3204078	chr1:3203765-3204453
cg20636351	8	55087400	
cg13101431	1	188826823	
cg24496563	1	67842041	
cg09080432	17	75558493	
cg08842508	2	147346362	chr2:147344801-147345

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cg13644282	12	132616666	chr12:132619197-13262
cg12163646	6	30529027	chr6:30523775-3052518
cg14721708	22	43606235	chr22:43605965-436062
cg11339341	5	87969330	chr5:87969960-8797207
cg15686782	7	2143886	
cg15229245	10	131744460	
cg09340386	2	1605954	
cg11874730	8	108178488	
cg09817171	X	2836084	chrX:2835949-2836236
cg06074123	4	56660460	chr4:56659626-5666014
cg27319216	8	6693540	chr8:6691833-6693135
cg05245430	14	91755524	chr14:91755280-917555
cg27181148	12	45819307	
cg25967031	7	27171203	chr7:27169572-2717063
cg09391761	2	238230401	
cg16182936	3	13060741	
cg24004780	3	113683598	
cg18028999	15	81426610	chr15:81426499-814267
cg04826345	13	22615334	
cg01316378	10	63629580	
cg13889085	11	4389408	
cg13453904	10	133484610	
cg03509094	19	7928546	chr19:7926590-7928752
cg24671891	X	12601783	chrX:12601482-1260183
cg18959207	10	18549686	
cg11613559	10	121577971	chr10:121577529-12157
cg21913159	12	57588171	
cg04597449	5	94955575	chr5:94955630-9495724
cg17846796	5	153868992	chr5:153872839-153873
cg05259332	6	25627764	
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cg08084788	2	1587102	
cg15968932	11	19860035	
cg26974276	8	660494	chr8:663998-664794
cg20242781	7	29111255	
cg03640426	4	76559064	chr4:76555366-7655607
cg15811530	6	68595695	
cg23111106	5	38772401	
cg16860882	8	142285145	
cg13763287	9	97856079	
cg04461926	3	20026603	
cg10252138	17	58120427	chr17:58119752-581204
cg20312205	13	84456308	chr13:84453664-844538
cg21036096	14	54417114	chr14:54418677-544188
cg07062130	14	47121033	chr14:47120868-471211
cg08237348	6	38684210	chr6:38682949-3868326
cg15467577	19	35547085	chr19:35550550-355508
cg23029635	19	57904254	chr19:57901091-579015
cg11171672	14	104395485	chr14:104394529-10439
cg17795586	3	151047735	
cg16201038	13	28544760	chr13:28544524-285448
cg06097213	6	29717651	chr6:29716468-2971715
cg01317226	3	194666543	
cg01029568	5	83860878	
cg06694119	6	114385144	

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cg16844333	10	89167457	
cg15520955	1	245844133	
cg18651659	7	158550241	
cg23627301	14	32673368	chr14:32672536-326729
cg26080331	13	113613318	
cg14755019	4	41749810	chr4:41749184-4174981
cg14018339	7	74564032	
cg13367929	5	176077110	chr5:176074138-176074
cg04215055	17	74911520	
cg13256546	22	39472544	
cg04879750	12	130590529	
cg22642498	19	54312855	
cg13675721	7	140227273	
cg16549153	20	18297604	
cg14503165	17	2202686	chr17:2206517-2207248
cg24070990	1	228634724	chr1:228633382-228634
cg22280238	17	79251323	chr17:79254407-792546
cg03311134	10	134807208	chr10:134807176-13480
cg19366770	19	35713391	chr19:35715623-357161
cg25350011	8	6419483	
cg00034559	2	39892124	chr2:39893121-3989349
cg07056645	19	6230546	chr19:6230458-6230666
cg22654940	2	54856752	chr2:54856098-5485648
cg22184136	6	30038720	chr6:30038881-3003947
cg22927076	12	131849082	
cg12097883	17	62774939	chr17:62774366-627777
cg05308391	19	7614864	chr19:7614785-7615998
cg21040569	X	137793665	chrX:137793095-137794
cg24425342	19	3114929	chr19:3114752-3115094
cg08844325	2	9459368	chr2:9459243-9459454
cg07223937	6	134313583	
cg06100967	12	38545214	
cg01699919	7	43963083	chr7:43965806-4396640
cg15963551	17	77669222	
cg04601296	1	149718651	chr1:149718542-149718
cg00876266	19	5915133	chr19:5915007-5915301
cg18469036	10	504497	
cg23186825	X	136112821	chrX:136113583-136114
cg07347645	20	58507171	chr20:58507755-585095
cg16782719	12	129280334	chr12:129280256-12928
cg03325726	3	152999960	
cg13347354	8	42269559	chr8:42268436-4226875
cg16399855	1	2318621	chr1:2316353-2316749
cg09347582	1	233497916	chr1:233497707-233497
cg17815669	1	2003198	chr1:2005179-2005565
cg17716699	7	907864	chr7:905608-905886
cg04020211	5	179763432	
cg18930892	X	119250427	chrX:119249439-119249
cg27430402	1	245223499	
cg05047401	1	156131213	
cg20460554	21	43917260	chr21:43917046-439172
cg10817497	2	234261386	
cg18781383	5	150089452	

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cg19726343	1	7515595	
cg14794043	19	22193759	chr19:22193330-221935
cg06529996	2	3469212	
cg05138138	2	106764528	
cg14472390	5	140740387	chr5:140741174-140741
cg03526459	1	146549940	chr1:146549850-146550
cg07198150	1	86623101	chr1:86621278-8662287
cg26869506	10	133775762	
cg23004031	10	131323903	
cg22942804	6	26183572	chr6:26184036-2618433
cg02054697	4	90360897	
cg10077239	14	30397686	chr14:30396210-303974
cg12266049	11	69461334	chr11:69461060-694613
cg17339414	4	1334513	chr4:1333378-1333676
cg22778435	7	24882838	
cg16582214	1	153914492	chr1:153914343-153914
cg09356193	14	105816327	chr14:105817303-10581
cg19276014	10	133598638	
cg24764310	7	157512201	
cg20738735	5	13810195	chr5:13810126-1381033
cg20164253	1	92951487	chr1:92945907-9295260
cg13126790	6	160010346	
cg11453174	6	136512768	
cg21806832	17	21262831	
cg08222618	4	941054	chr4:940613-941057
cg09322899	2	240280217	
cg07365623	2	46656259	
cg01659483	8	77220647	
cg21617218	19	46805820	chr19:46806998-468076
cg19359398	12	108523056	chr12:108522950-10852
cg15997512	8	21608254	chr8:21608078-2160833
cg04684152	2	72012863	chr2:72012850-7201307
cg18477943	3	66002958	
cg05073880	7	149251163	
cg06845639	16	77747526	
cg01240056	7	1263927	chr7:1263496-1264364
cg00015930	1	46921746	
cg03422757	1	20129806	chr1:20126029-2012678
cg18648122	4	105412473	chr4:105412655-105412
cg12496673	6	170891169	chr6:170893259-170893
cg25587058	X	147581919	chrX:147581861-147582
cg15262728	2	231733948	chr2:231729631-231730
cg06601473	11	33694151	
cg14598943	8	32504504	
cg13912702	13	113520917	
cg13147090	12	247963	chr12:247455-248501
cg18335316	11	43668018	
cg09121378	21	45883590	chr21:45883589-458839
cg01895333	3	109035405	
cg04644817	10	48949616	chr10:48952215-489528
cg08236045	14	103449947	
cg21410293	18	46386361	chr18:46386266-463864
cg12089490	17	234536	chr17:234438-236162
cg10028823	7	1952561	chr7:1950279-1950482

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cg14074878	13	113696482	
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cg26982030	X	151307018	
cg14622996	6	32109801	
cg13718418	12	85672285	chr12:85673878-856747
cg03197110	X	71096923	chrX:71092472-7109319
cg03625300	17	79294196	
cg17744605	6	111368770	
cg02083080	6	169104434	
cg10118784	14	65209977	chr14:65209843-652100
cg04916416	3	30651317	chr3:30647987-3064888
cg10500716	1	111993148	chr1:111991304-111992
cg01361049	9	136876905	chr9:136877009-136879
cg22583981	17	13504472	chr17:13503829-135055
cg09814487	16	86598824	chr16:86599355-866026
cg07464571	7	127881001	chr7:127880750-127881
cg18884557	7	101847700	
cg07020453	2	3313364	
cg13451153	14	99736489	chr14:99736040-997375
cg25605277	1	169859761	chr1:169862455-169862
cg08491487	6	30039130	chr6:30038881-3003947
cg23032536	3	183209993	chr3:183209667-183209
cg14426371	9	113714986	
cg11153057	1	147380334	chr1:147380138-147380
cg18979623	20	62434140	chr20:62433937-624342
cg05005343	11	121970285	
cg12173558	8	69244734	chr8:69242920-6924380
cg03031726	19	19672779	
cg25582295	18	31158105	
cg20237074	4	187985452	chr4:187985216-187985
cg26651303	7	158533204	
cg23575858	2	237712268	
cg10787409	8	144462631	chr8:144462630-144462
cg11271430	4	187984718	chr4:187984505-187984
cg13532854	7	155898355	chr7:155898140-155898
cg03837726	12	119633116	
cg03311232	1	46951291	chr1:46951168-4695179
cg08195491	16	50746063	
cg00017221	1	149719536	chr1:149719314-149719
cg07679203	4	1993400	chr4:1994662-1994872
cg22653345	11	69307400	
cg24519441	17	40941337	chr17:40937258-409374
cg07585610	6	46656612	chr6:46655262-4665673
cg04627891	7	157053650	
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cg09249800	1	6341287	chr1:6341136-6341412
cg12573705	13	36050889	chr13:36052553-360531
cg11385631	8	6321006	
cg01129958	8	19458710	chr8:19459905-1946013
cg04203950	17	4443191	chr17:4439300-4439705
cg19438375	17	48249792	
cg23475109	2	97530683	chr2:97530558-9753080
cg01707795	14	69341738	chr14:69341427-693418

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cg04733222	X	68757663	chrX:68758191-6875864
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cg15310492	11	30038677	chr11:30038522-300388
cg13197308	6	32135083	chr6:32134460-3213519
cg21637392	7	5735123	
cg20575173	3	101228308	chr3:101231610-101232
cg01615861	16	85513978	
cg02300154	7	70597058	chr7:70596228-7059838
cg00012123	5	667619	chr5:667947-668589
cg18737081	10	80999807	chr10:81002109-810036
cg16359406	15	41696062	chr15:41694493-416947
cg01566965	4	174447847	chr4:174448333-174448
cg21376090	6	106201547	
cg16759218	3	99371838	
cg24919342	3	127399204	
cg15013257	7	2205278	
cg27570249	15	65688530	chr15:65688039-656885
cg11381843	3	142681401	chr3:142681137-142683
cg05603527	2	71131629	chr2:71131200-7113225
cg06276864	4	190802469	
cg08605656	X	73642885	chrX:73641647-7364201
cg07292251	5	176829198	chr5:176829339-176829
cg14222630	9	127961717	chr9:127962543-127963
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cg17676806	11	1302836	chr11:1302772-1302982
cg20417128	2	1690625	
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cg05136804	18	32849113	chr18:32847284-328481
cg00766188	15	89953370	chr15:89954603-899551
cg04915780	12	59989742	chr12:59989651-599905
cg18652319	4	154625489	
cg23256140	7	1991534	chr7:1991914-1992122
cg27492220	X	55101327	
cg23986474	6	30309773	chr6:30312837-3031341
cg14098468	19	53140973	chr19:53141175-531418
cg20840456	X	75391688	
cg02087416	1	200182788	
cg22813950	12	130645566	chr12:130645327-13064
cg25428929	2	242606353	chr2:242606078-242606
cg11534240	1	183442651	chr1:183440351-183442
cg15934634	11	68920095	
cg21364615	10	1222689	chr10:1219146-1219427
cg13740185	10	73486801	
cg19678392	7	94953810	chr7:94953769-9495397
cg27472937	2	3683119	chr2:3683029-3683290
cg22853963	13	112200308	chr13:112200212-11220
cg08519853	4	143767621	chr4:143766940-143768
cg25030467	14	94417495	
cg10940055	12	132910456	chr12:132910476-13291
cg21560819	11	1539711	chr11:1536729-1536953
cg26819718	10	77872170	chr10:77872083-778723
cg04869514	16	87705841	chr16:87702493-877027
cg11555666	17	78172397	chr17:78172176-781724
cg04172848	22	20712476	chr22:20708651-207165

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cg00895196	6	22147182	
cg04438129	6	164241373	
cg10766942	2	30682532	
cg26124560	17	78064152	
cg14154131	1	8748155	
cg14191654	20	44829602	chr20:44829506-448298
cg19678538	5	140605042	chr5:140604453-140605
cg16143654	5	140176361	chr5:140175666-140176
cg04999824	17	76967757	
cg09859456	12	72234313	chr12:72233323-722336
cg03293206	16	46603015	
cg09201525	16	111871	chr16:110995-113162
cg02112608	2	104914302	
cg17736997	6	163851615	
cg00327072	5	172110477	chr5:172110282-172111
cg03490460	13	114840698	chr13:114840918-11484
cg14777507	4	93103772	chr4:93103617-9310395
cg03181524	19	39048014	chr19:39051804-390522
cg12460765	7	2415105	
cg03950599	19	48698419	chr19:48697900-486986
cg08941716	15	35384864	chr15:35385071-353853
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cg10068793	21	17442467	
cg05892817	10	131638672	chr10:131638564-13163
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cg19007731	8	93107394	
cg09273212	2	128331593	
cg04807864	2	130750050	chr2:130750104-130750
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cg12815355	2	75894077	
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cg16010385	19	1558732	chr19:1555539-1556866
cg03079818	13	110324798	
cg05338976	7	114561850	chr7:114562170-114563
cg05710479	1	7120104	chr1:7122519-7122727
cg04309194	5	1201629	chr5:1201443-1202138
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cg15819404	15	101998962	
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cg07490070	2	97505464	chr2:97505219-9750560
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cg24171152	12	90051243	
cg03859792	16	58121049	
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cg01877524	11	117651359	chr11:117651216-11765
cg11679069	13	43596577	chr13:43597504-435978
cg15361590	5	140864701	chr5:140864527-140864
cg20595621	6	114707054	
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cg02096220	4	129212177	chr4:129208297-129209
cg25142283	18	51684211	
cg26154353	13	112573558	chr13:112575723-11257
cg11491407	12	1973872	chr12:1973739-1974958
cg19968916	10	135087441	chr10:135089969-13509
cg17397823	7	150095084	chr7:150093636-150095
cg16976047	22	31556225	chr22:31556124-315564
cg08362144	6	161558085	
cg11001739	7	1983918	
cg14176930	6	10884891	chr6:10882926-1088314
cg02578944	6	28227392	chr6:28226979-2822748
cg18115040	2	176981328	chr2:176980765-176981
cg02017074	12	117425053	
cg06876404	16	30941527	chr16:30941430-309419
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cg05661282	19	58220370	chr19:58220189-582205
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cg24054774	12	19750334	
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cg05269938	20	62461294	chr20:62461266-624620
cg16284395	14	94431626	
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cg19586199	19	14225172	chr19:14228461-142292
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cg23740897	7	2195739	chr7:2195683-2195983
cg22152887	11	72849944	chr11:72852176-728541
cg01090565	10	81704187	
cg21061994	2	866867	chr2:863930-865091
cg04440724	16	4920505	
cg25722796	19	51142008	chr19:51142284-511429
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cg22827524	1	222910746	
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cg20217938	19	3958344	chr19:3958492-3959812
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cg19065773	10	98469552	
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cg18514850	14	94413936	
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cg15425276	14	69341905	chr14:69341427-693418
cg09658576	7	139477957	chr7:139477406-139478
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cg13165778	7	1952518	chr7:1950279-1950482
cg22481882	8	145161551	chr8:145163068-145165
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cg04047221	13	112723477	chr13:112720564-11272
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cg24694549	12	67072769	
cg01816880	1	228404896	chr1:228404717-228405
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cg14341771	9	133266694	
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cg05390968	16	86598792	chr16:86599355-866026
cg22877524	10	73553138	
cg16200879	19	4326975	chr19:4326878-4327380
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cg27176628	6	168476656	chr6:168476320-168476
cg00526336	1	230415902	chr1:230415342-230415
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cg15573040	15	92938295	chr15:92936677-929385
cg24963147	5	135529341	chr5:135527056-135528
cg24274347	12	132497611	
cg14105458	9	139917436	chr9:139917178-139917
cg07042077	5	75014259	chr5:75012962-7501351
cg09813769	10	94980851	
cg09448677	11	70672740	chr11:70672834-706730
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cg10985320	11	96124636	chr11:96122536-961235
cg17630294	4	7985238	
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cg10098021	6	30653732	chr6:30654392-3065493
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cg03407747	17	6899364	chr17:6898820-6900427
cg16991858	1	244612113	chr1:244614522-244615
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cg18245976	7	158708271	
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cg11462939	13	99606117	
cg18879590	1	236306640	chr1:236305534-236306
cg21197336	3	193587490	chr3:193587352-193587
cg12206571	1	32052538	chr1:32052471-3205277
cg16927285	3	62128744	
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cg10147348	2	101584913	
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cg25356719	10	1638893	
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cg26132449	12	113704034	
cg02259324	15	78111196	chr15:78110841-781128
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cg26621704	13	25081296	
cg02222844	3	48694451	chr3:48693118-4869476
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cg06374962	4	111531926	chr4:111532647-111533
cg21454386	13	114292018	chr13:114292551-11429
cg24569492	2	66808811	chr2:66808568-6680940
cg07608848	2	1647185	
cg19534769	4	3451126	chr4:3449650-3449995
cg26502105	11	117701909	
cg20582976	14	90301560	
cg08256781	19	6135510	
cg25940874	2	206804293	
cg21387117	17	3288348	chr17:3289362-3290072
cg02365967	15	28473380	

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cg14466580	Y	10037020	chrY:10036737-1003717
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cg21657087	3	147139485	chr3:147138916-147139
cg19734801	5	131281112	chr5:131280907-131281
cg09612655	2	23642945	
cg27320983	19	1230171	chr19:1227531-1230256
cg25606639	15	35371640	
cg01682070	16	29996774	chr16:29997636-299978
cg07482296	2	306606	chr2:306675-307167
cg00685229	X	118828778	chrX:118826452-118827
cg13617192	12	34534365	
cg09879526	1	243652762	chr1:243652413-243652
cg09506081	7	154684327	chr7:154684402-154684
cg10576232	1	220132097	
cg13541578	17	77419374	
cg12414174	12	89748895	chr12:89745168-897481
cg06636831	3	45077369	chr3:45077069-4507769
cg17694351	7	27252737	chr7:27252681-2725383
cg11977919	1	8263776	
cg21530267	5	140481267	chr5:140481546-140482
cg10158774	7	30015780	
cg01191815	15	63084959	
cg19729116	6	26501981	chr6:26501725-2650210
cg16361966	10	124905786	chr10:124905634-12490
cg10412286	16	89977652	chr16:89977562-899778
cg13764652	3	148688774	
cg24885631	10	133751448	chr10:133751399-13375
cg25405821	13	111531992	
cg24445165	12	113549832	chr12:113549885-11355
cg18133875	5	179228635	chr5:179228283-179229
cg05981033	16	86588144	chr16:86588435-865895
cg16861845	17	15652329	chr17:15652534-156531
cg16841189	8	1799411	chr8:1797406-1798775
cg06119016	17	80373277	chr17:80373276-803734
cg03683166	13	113611729	
cg16793173	4	170173209	
cg09038962	17	77899679	chr17:77901065-779013
cg20165604	8	134686291	
cg23912081	2	4156091	chr2:4156090-4156444
cg00904483	10	131354873	
cg18537454	10	22623213	chr10:22623350-226258
cg22995724	8	144639363	chr8:144640396-144640
cg11295178	12	114918693	
cg02084758	17	77536754	
cg08710238	X	47082076	chrX:47077163-4707863
cg14754787	17	35299600	chr17:35291899-353008
cg23212642	8	73007331	
cg13646106	X	34149301	chrX:34149264-3414948
cg27030541	8	86568090	chr8:86566584-8656841
cg18331135	7	127232254	chr7:127227758-127229
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cg25019989	4	54961835	chr4:54957979-5495854
cg10052504	11	121243886	

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cg06329547	7	1937739	chr7:1937738-1937946
cg12043732	20	61284223	chr20:61287997-612884
cg10381888	6	30228243	chr6:30227320-3022825
cg08076924	15	101988075	
cg06916310	X	76709238	
cg27365342	6	12881417	
cg02933362	2	102091607	chr2:102090370-102091
cg01342411	16	75263551	chr16:75263495-752638
cg06383124	16	85171295	chr16:85171019-851713
cg08642843	10	134303159	chr10:134304307-13430
cg09745958	11	117670977	chr11:117666634-11766
cg21566513	13	24913084	chr13:24914548-249151
cg06495529	17	33332004	
cg13107169	4	40098238	
cg25371169	8	38757772	chr8:38758457-3875938
cg07529658	21	46845160	chr21:46847505-468477
cg24346464	1	164872273	
cg11751810	17	88286	chr17:85009-85414
cg14172108	21	34405553	chr21:34405577-344065
cg14603778	12	132896466	chr12:132896299-13289
cg14020052	2	240174659	
cg06726820	3	139259742	chr3:139257712-139257
cg01441421	7	36909953	
cg25149125	12	52914037	
cg07217710	8	141348919	chr8:141348840-141349
cg16292773	12	66211550	
cg25065723	10	132892405	chr10:132893428-13289
cg12315032	17	72585012	
cg22836359	12	6933548	chr12:6933276-6933605
cg19920134	7	38227870	
cg16619721	3	160942782	chr3:160938961-160939
cg02963556	12	132588637	
cg07498975	1	101338750	
cg25384089	1	1961628	chr1:1961407-1961850
cg25712567	4	715872	chr4:716281-716977
cg07189222	6	32847527	chr6:32847498-3284784
cg09282497	2	18059200	chr2:18059038-1805924
cg21047206	1	145076221	chr1:145075483-145075
cg09227934	3	107805635	chr3:107809375-107810
cg26751406	13	21951631	chr13:21951293-219517
cg19538674	3	39186541	chr3:39186524-3918673
cg09535924	2	66671659	chr2:66672431-6667363
cg02423659	4	871439	chr4:871276-871630
cg16237262	2	103095386	
cg14039230	6	168121534	chr6:168120634-168120
cg06190807	1	62660188	chr1:62660555-6266094
cg03000848	16	396164	
cg02229344	X	130216380	chrX:130216330-130216
cg06651311	4	37246230	chr4:37245250-3724697
cg13480578	3	194836414	
cg12012871	21	43180048	chr21:43176662-431768
cg15138109	2	24713234	chr2:24713710-2471516

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cg12378888	4	4867102	chr4:4867386-4867673
cg20523947	4	53744073	
cg22490861	12	13154718	chr12:13154088-131548
cg16396948	3	111603394	
cg15766996	18	33081389	chr18:33077545-330780
cg22825635	X	37351069	chrX:37350984-3735149
cg00805577	12	123333205	
cg13385744	2	200245183	
cg10961099	8	2046910	chr8:2046691-2046963
cg00271964	2	144693693	chr2:144694666-144695
cg01577514	X	152954919	
cg01139553	3	193493033	
cg17265576	5	1509299	
cg10000492	8	15496541	
cg17067226	3	157211395	
cg17299712	X	30233762	
cg10021924	12	131401275	
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cg16154713	8	131368433	chr8:131370087-131371
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cg26968008	3	40657160	chr3:40657159-4065739
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cg22066065	6	170444432	
cg05145233	16	89169858	chr16:89167763-891679
cg07962934	8	144809621	chr8:144808221-144810
cg07501063	X	3628424	chrX:3630406-3630620
cg03171770	10	43393728	chr10:43393476-433944
cg18972998	1	55266296	chr1:55266277-5526705
cg12481389	1	14107831	
cg23347501	21	10884969	chr21:10884732-108850
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cg06669405	11	2926361	chr11:2930289-2931093
cg04696808	16	34257170	chr16:34256748-342577
cg07405259	10	134072130	chr10:134071971-13407
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cg24894318	3	104914755	
cg09784347	3	158786963	
cg06324507	6	32051999	chr6:32055067-3205560
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cg14603453	2	149631830	chr2:149632682-149633
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cg08840551	5	56718349	
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cg24083378	2	169079247	
cg22624278	12	131237708	
cg14158690	7	151826540	chr7:151825925-151826
cg21892685	4	77168991	chr4:77172587-7717306
cg17054691	17	79813439	
cg24195359	8	6418978	
cg21748138	2	174251551	

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cg07121021	10	37414597	chr10:37414145-374147
cg04298224	13	113707471	chr13:113705500-11370
cg18101249	18	29599776	chr18:29598566-295994
cg22985122	17	73566478	chr17:73569163-735694
cg14385008	2	3469154	
cg13519953	9	140025662	chr9:140023747-140025
cg11710659	1	153762434	
cg10941835	20	50419348	chr20:50417312-504190
cg05404005	11	8053420	chr11:8053245-8053490
cg04603166	11	133808092	
cg27075786	22	23438059	chr22:23437921-234384
cg07797370	12	44316362	
cg02909136	20	44941542	chr20:44941342-449415
cg11014582	13	76333727	
cg17281810	X	40007949	chrX:40005040-4000706
cg02522760	10	103530178	
cg12106728	12	115136258	chr12:115135925-11513
cg22597733	4	158142891	chr4:158143296-158144
cg21042032	X	37404389	chrX:37404358-3740461
cg20906291	6	10382103	chr6:10381558-1038235
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cg15819808	12	122631519	
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cg22974100	15	22650394	chr15:22646571-226473
cg00557236	5	115782227	chr5:115783075-115783
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cg07969419	15	100880411	chr15:100880957-10088
cg02128085	20	61567056	chr20:61568678-615699
cg27405128	15	58540402	
cg24620436	7	4918906	chr7:4922707-4923576
cg09796739	1	227924055	chr1:227922643-227923
cg02225797	5	140534890	chr5:140536896-140537
cg24621972	2	223160175	chr2:223159725-223160
cg22337509	1	204093899	
cg17702455	7	28058989	
cg24720571	6	6004328	chr6:6002471-6005125
cg20160299	1	152733395	chr1:152732958-152733
cg01844642	3	51989764	chr3:51989763-5199063
cg08107689	15	29033901	chr15:29033878-290347
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cg11471802	8	47529015	chr8:47528989-4752937
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cg16648603	1	234361804	
cg14211117	1	246016737	
cg17988709	1	117889680	

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cg26641275	2	239971554	chr2:239974439-239974
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cg18588930	19	52617816	
cg14151372	10	108045557	
cg06730678	12	6166943	chr12:6166873-6167258
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cg06638913	2	235883680	
cg17868052	6	18307649	
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cg19404500	2	9343124	chr2:9346383-9347944
cg13004897	5	177225404	
cg17506621	6	160023581	
cg02559274	2	72606914	
cg16480662	2	220413933	chr2:220412341-220412
cg18976177	7	75160019	chr7:75156588-7515752
cg27254482	21	34398085	chr21:34395128-344002
cg24784730	12	125225655	chr12:125223520-12522
cg21050416	5	159411100	chr5:159414046-159414
cg12894883	22	22288473	chr22:22288346-222885
cg23888047	12	8274843	
cg15414028	10	14644188	chr10:14645752-146467
cg14499933	2	444769	
cg15189790	4	73970976	
cg27225130	1	208218009	
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cg14173587	9	139907691	chr9:139905818-139906
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cg02314166	17	60767131	
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cg19814159	6	28719517	
cg10509850	7	158817404	chr7:158817175-158817
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cg13681781	9	139102396	
cg21144493	1	7130061	
cg20181262	12	132283956	chr12:132284454-13228
cg01218896	15	96911988	chr15:96909815-969100
cg00163462	1	76723043	
cg15627457	8	141535348	
cg17412258	14	101193017	chr14:101192851-10119
cg08800710	13	113488053	chr13:113486835-11348
cg04118950	1	53897039	
cg24075745	2	241827864	chr2:241827777-241828
cg02938320	2	223168178	chr2:223168653-223169
cg13390484	9	80765924	chr9:80765851-8076612
cg09973514	11	58830424	chr11:58830063-588307
cg17306279	5	139056667	chr5:139056577-139056

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cg13931663	10	90983647	
cg00954167	7	46699167	
cg18121066	17	80794274	chr17:80790368-807905
cg19690879	15	102189763	chr15:102192165-10219
cg20994660	2	162272299	chr2:162273294-162273
cg17087698	6	158881629	
cg02741056	16	84347783	chr16:84346476-843469
cg14034782	12	133123459	chr12:133125659-13312
cg03533979	22	47097306	chr22:47097188-470976
cg01776495	12	6858115	chr12:6857973-6858257
cg01023593	19	58962093	chr19:58962740-589633
cg24545495	1	6149049	
cg06020238	10	35928558	chr10:35928501-359318
cg16559361	16	88543440	chr16:88539860-885405
cg04707255	16	1005605	chr16:1005902-1006281
cg04577715	5	147211181	
cg17741977	6	33985139	
cg23023044	1	110765955	chr1:110765665-110766
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cg21759280	19	6534936	chr19:6534759-6535079
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cg12882389	14	68082575	chr14:68086277-680869
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cg07165288	3	114261297	
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cg08285151	7	18534872	
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cg16596604	16	21294947	chr16:21294980-212954
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cg14666369	12	121164371	chr12:121163472-12116
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cg23410056	X	111624323	chrX:111623831-111624
cg08411833	5	180876320	chr5:180875827-180878
cg03749724	11	108467652	chr11:108463598-10846
cg09732851	17	291224	chr17:291016-291264
cg26525375	10	1174817	
cg04539057	11	1031985	chr11:1033084-1033356
cg13916816	1	1953059	chr1:1950411-1951479
cg19414591	1	91190582	chr1:91190489-9119280
cg11549132	2	99061257	chr2:99061174-9906184
cg15450098	1	221057561	chr1:221057463-221057
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cg11883358	17	36631561	chr17:36633823-366341
cg11905611	12	14720974	chr12:14720248-147210
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cg01863042	13	23309892	
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cg13849454	9	14348844	chr9:14348684-1434907
cg07017998	4	733617	chr4:730282-731005
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cg09583036	11	87846644	
cg13494126	7	1908745	chr7:1908539-1908803
cg07230999	7	116863357	
cg02046017	11	70707406	
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cg12326299	5	122369268	chr5:122371569-122372

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cg14621323	5	176827161	chr5:176827081-176827
cg15190754	5	55033695	chr5:55033694-5503399
cg27116577	16	1012601	chr16:1010335-1012198
cg20961939	12	120536939	chr12:120536640-12053
cg26058289	22	47054148	chr22:47054031-470542
cg02081087	3	197832709	chr3:197831806-197832
cg20559816	18	76985797	chr18:76985514-769859
cg07805940	12	130909013	chr12:130908777-13090
cg08680868	5	205319	
cg00105628	20	21087165	chr20:21086139-210871
cg13499155	12	72376553	
cg26896760	11	93922202	
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cg08993681	13	107132340	
cg22749736	11	1306759	chr11:1302772-1302982
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cg18744777	4	41646567	chr4:41646292-4164658
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cg05790989	1	167197743	
cg13150094	6	29714824	chr6:29716468-2971715
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cg06817802	5	1291319	chr5:1289275-1295970
cg10349844	8	144519187	chr8:144521358-144521

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cg07581811	3	184491461	
cg07540421	2	71115680	chr2:71115927-7111641
cg08001952	8	140974696	chr8:140971270-140971
cg00341885	19	4323034	chr19:4322974-4323201
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cg21672758	2	48340131	
cg27264322	1	1992046	chr1:1990779-1991171
cg20602628	2	138156475	
cg20827077	15	33171339	
cg10690919	17	48912545	
cg15193133	17	19883474	chr17:19883325-198836
cg05479662	8	47347811	
cg24232053	12	121177221	chr12:121177115-12117
cg04080530	1	2886868	chr1:2886589-2886923
cg13768953	17	7114967	chr17:7117596-7118085
cg16777106	4	158281194	
cg06922248	10	135153972	chr10:135148196-13515
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cg03869448	4	10086483	
cg10408178	14	72219272	
cg01147665	3	32146075	chr3:32147826-3214887
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cg18877252	5	75380987	chr5:75378974-7538079
cg08848903	1	92352293	chr1:92350913-9235208
cg01357135	3	160475128	chr3:160472310-160474
cg05509190	2	177503639	chr2:177502240-177502
cg15386350	1	11591766	chr1:11589838-1159004
cg19160887	20	13370609	
cg23918315	5	140479025	chr5:140481546-140482
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cg11617144	8	145729772	chr8:145730390-145732
cg21179492	9	138393651	chr9:138391394-138393
cg07646362	16	34208469	chr16:34208200-342092
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cg09829263	13	49066969	
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cg01554357	1	164750454	
cg05329180	19	10629000	chr19:10627980-106284
cg19344806	7	130132298	chr7:130130739-130133
cg02072002	16	4736795	chr16:4732830-4733184
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cg23912877	11	2926337	chr11:2930289-2931093

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cg05740465	6	169825927	
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cg15674997	5	178421314	chr5:178421225-178422
cg25620125	11	61106775	chr11:61106710-611069
cg02096663	4	178650141	
cg00677217	4	3747401	chr4:3748224-3748581
cg13114125	14	105738426	chr14:105738159-10573
cg22656126	17	1637206	chr17:1637053-1637492
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cg02421172	7	1938701	chr7:1937738-1937946
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cg04842426	7	136555777	chr7:136553854-136556
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cg05632020	6	30885310	chr6:30881533-3088229
cg17653955	2	236676029	chr2:236673303-236673
cg06907680	14	91580129	
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cg09831105	12	99287469	chr12:99288222-992893
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cg03615235	20	36148779	chr20:36148603-361501
cg17672209	5	133856845	chr5:133859942-133863
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cg09570807	4	74125882	chr4:74124405-7412513
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cg08460041	1	165325136	chr1:165324191-165326
cg25230902	2	239709312	
cg15547241	7	66751257	chr7:66751106-6675133
cg10195415	17	73887371	chr17:73887196-738873
cg05940236	Y	15017297	chrY:15016544-1501729
cg20462242	1	3227744	
cg20494444	14	70013519	chr14:70014543-700149
cg25596754	6	32026610	
cg14457691	X	100740937	chrX:100740221-100740
cg09259595	8	1779056	chr8:1779620-1779821
cg16184737	7	2679971	
cg25626079	4	1333948	chr4:1333929-1334140
cg06794323	X	43518105	chrX:43514030-4351479
cg25000021	2	2735969	
cg03062544	13	113440521	chr13:113440233-11344
cg26562786	8	56361901	chr8:56361856-5636216
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cg07149609	1	170630734	chr1:170630456-170630
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cg18148349	10	131404694	
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cg00270521	1	228503273	chr1:228503556-228504
cg19563062	17	34097075	chr17:34097100-340973
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cg24179734	5	891290	chr5:892522-893479
cg02699671	17	850251	chr17:850207-850500
cg15065854	19	861829	chr19:860517-862123

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cg09555414	11	57520668	chr11:57520333-575207
cg10285526	16	34787199	chr16:34787169-347876
cg00075620	2	137180506	chr2:137181061-137181
cg06530270	17	76988329	chr17:76989642-769900
cg06369624	20	43727355	chr20:43726297-437273
cg00035636	13	21900591	chr13:21900425-219006
cg24361198	1	242002464	
cg22804352	17	57249951	
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cg00422230	2	187454414	chr2:187454399-187455
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cg19699893	19	11473353	chr19:11473094-114733
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cg21663666	2	232220549	
cg21341645	7	155091523	chr7:155088705-155090
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cg26561082	10	410363	chr10:409201-409523
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cg18593708	18	21853454	chr18:21851399-218521
cg12175172	15	67073649	chr15:67073306-670739
cg21450888	1	172114047	
cg21516614	5	1084110	chr5:1083878-1084169
cg27565067	17	149484	chr17:152117-152438
cg20999651	X	135230594	chrX:135228947-135230
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cg02809075	2	171567027	chr2:171568322-171568
cg14825116	X	100547490	chrX:100546063-100546
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cg15322230	X	40015467	chrX:40010919-4001620
cg05289873	17	40321636	
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cg19857840	8	141551367	
cg17022362	20	62084833	chr20:62084467-620849
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cg15938260	17	80804078	
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cg26298533	4	106633699	chr4:106629575-106630
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cg03816707	20	43726544	chr20:43726297-437273
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cg08291433	11	69813290	chr11:69813249-698134
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cg27560831	19	56610209	chr19:56609803-566102
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cg05661042	12	109796925	
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cg24478034	4	155433727	
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cg27234648	15	91077406	chr15:91072689-910739
cg22918949	10	78389455	
cg20782252	7	2153774	chr7:2154677-2155252
cg06352932	12	11185058	
cg04723449	16	23420567	
cg05262755	8	143645073	chr8:143645072-143645
cg16600733	1	2266362	chr1:2266007-2266432
cg08726248	11	637032	chr11:636906-640628
cg12178287	19	17631836	chr19:17631780-176319
cg25697357	20	13979928	chr20:13975768-139762
cg18675847	4	87865779	
cg05890279	17	6337357	
cg16953753	13	25135360	
cg21214613	1	16344536	
cg07976064	11	120435056	chr11:120434822-12043
cg09148348	16	84092912	
cg21356535	6	137311287	
cg21025349	11	126477878	
cg05119931	7	38469273	
cg23385838	12	1755068	chr12:1754997-1755243
cg01495521	16	978040	chr16:979422-979663

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cg23412777	15	55881706	chr15:55879792-558812
cg25823085	7	87105416	chr7:87104723-8710530
cg07676709	17	46673442	chr17:46673532-466741
cg19802390	1	2840177	
cg06506768	11	16848251	
cg21226965	6	169852806	chr6:169852315-169852
cg12437157	9	86433764	chr9:86431954-8643309
cg23961530	19	14077705	chr19:14072665-140748
cg20967028	12	14996272	
cg14557288	10	72454026	
cg15076217	1	207975699	
cg10798164	1	35442778	chr1:35442237-3544293
cg03230133	2	60812640	chr2:60812527-6081275
cg19984681	3	64479957	
cg09291131	14	101521809	
cg04282125	14	23912113	
cg20559405	3	61580543	
cg10201400	13	44359601	chr13:44359858-443616
cg24140037	4	56499522	chr4:56501912-5650252
cg04422985	7	9765993	chr7:9765661-9766215
cg02920045	3	73434063	chr3:73432739-7343407
cg17038902	20	60926987	chr20:60926764-609271
cg24908166	5	1268800	chr5:1270778-1271101
cg13019568	14	95826830	chr14:95826675-958269
cg08862210	6	29364963	
cg00885843	2	131058072	
cg03969079	10	63759909	
cg05376267	1	226075388	chr1:226075150-226075
cg05124242	4	47845589	
cg02921923	11	92651425	chr11:92648683-926491
cg14543508	9	123631308	chr9:123631106-123631
cg26116969	14	101526807	
cg18594482	1	27480543	chr1:27481345-2748174
cg16851758	2	84517782	chr2:84517714-8451795
cg13793681	10	3313302	
cg08645225	7	779089	chr7:780239-780601
cg20277740	1	5947484	chr1:5950824-5951029
cg08137669	8	143868023	
cg03326215	2	2328391	
cg19030737	1	226927988	chr1:226924560-226926
cg23528142	14	101123536	chr14:101121008-10112
cg00359423	11	95526151	chr11:95522460-955240
cg27452185	11	92648753	chr11:92648683-926491
cg27093403	12	25083077	
cg18708460	6	100051339	chr6:100051018-100051
cg08995327	16	66070379	
cg16243195	4	7252323	
cg00893348	3	139353025	
cg26313511	3	125053815	
cg22994830	7	623846	
cg14755417	21	47823560	chr21:47823082-478241
cg03963174	1	184558493	
cg17380795	3	122379686	
cg23710823	14	20020657	
cg24015037	17	709242	chr17:710581-710912

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cg04927341	1	86576497	
cg10694252	X	12601729	chrX:12601482-1260183
cg13915179	7	158038007	chr7:158037708-158038
cg15996592	13	113472632	chr13:113472423-11347
cg05797732	10	28908752	
cg14365564	9	124133079	chr9:124132057-124133
cg13115376	7	63391680	chr7:63391462-6339217
cg07549656	11	134025554	
cg04311686	5	1179328	
cg27553638	X	140786627	
cg09056876	6	156718398	chr6:156718071-156718
cg26405128	3	31655265	
cg12076692	1	1718852	
cg04397547	3	165636576	
cg18676053	9	124133094	chr9:124132057-124133
cg23338408	14	31289523	
cg14769962	2	9514994	chr2:9514723-9514995
cg26140836	X	108870738	chrX:108867762-108868
cg10601761	19	4930780	chr19:4930738-4930951
cg26679004	10	88023135	chr10:88022640-880232
cg06383163	8	139509073	chr8:139508795-139509
cg23726178	11	1847307	chr11:1847156-1847381
cg17130982	1	1946008	
cg18447471	2	242766082	chr2:242766046-242766
cg17169243	12	58219112	
cg23068797	19	10928549	
cg27281030	19	54312881	
cg16760712	2	242616758	chr2:242616820-242617
cg27513667	16	89408403	chr16:89408237-894084
cg24335149	1	20397074	
cg18597643	10	57388341	chr10:57388068-573885
cg00867406	16	89997889	chr16:90000351-900006
cg03327643	1	245836835	chr1:245836323-245836
cg24639754	4	8651092	
cg12459514	2	23914071	chr2:23913308-2391356
cg14875327	3	197081654	
cg20827346	4	22588665	
cg19094333	7	93697091	
cg12510203	2	144915087	
cg16258076	18	61615564	
cg03502812	19	36435729	chr19:36435457-364357
cg12271800	19	59028764	chr19:59028352-590289
cg08162124	13	113428094	chr13:113429177-11342
cg20458353	7	21260293	
cg25057157	8	1385462	chr8:1385205-1385432
cg08858210	8	98290361	chr8:98289604-9829040
cg03176434	18	77835972	chr18:77835862-778361
cg21751684	15	89920887	chr15:89920793-899227
cg25049295	2	131116527	chr2:131113090-131114
cg18624900	10	91295643	chr10:91294947-912959
cg26965151	7	2303844	
cg02941923	16	1005077	chr16:1005902-1006281
cg22662844	7	2116648	chr7:2116367-2116781
cg25718735	10	132959070	
cg12436377	5	87440296	chr5:87437095-8743750

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cg04290528	13	24958583	
cg02849754	20	40627977	chr20:40627224-406280
cg16761390	7	27290724	chr7:27291119-2729219
cg16526509	5	1439208	
cg12377139	10	22634218	chr10:22634000-226348
cg11025256	4	144604203	
cg23513175	15	20373649	chr15:20373594-203740
cg01691989	3	121712109	chr3:121712057-121712
cg24169669	14	38092080	chr14:38091469-380921
cg21518974	3	85553266	
cg09248345	1	165325553	chr1:165324191-165326
cg10244525	2	237146748	chr2:237145613-237146
cg01929367	2	241069288	chr2:241069198-241069
cg04004561	12	102626348	
cg19423543	5	172655948	chr5:172655840-172656
cg02217586	13	96654416	
cg09762648	4	189258068	
cg15140334	20	51588780	chr20:51589707-515900
cg02909176	13	113426343	chr13:113424898-11342
cg23776522	6	32010333	
cg13646020	4	41750390	chr4:41752280-4175250
cg04128303	X	122318829	chrX:122318752-122319
cg17546052	8	140717285	chr8:140714585-140718
cg10910267	17	61086239	
cg26783160	8	140871183	
cg15611809	5	67483833	
cg02466749	9	98054877	chr9:98054676-9805491
cg24680497	1	3343694	chr1:3342012-3342806
cg10513161	3	183705727	
cg15150472	9	140711975	chr9:140712931-140714
cg24047810	11	2162341	chr11:2158951-2162484
cg25617137	5	61684420	
cg02606988	Y	9216456	chrY:9215484-9216005
cg23624808	18	32847789	chr18:32847284-328481
cg10101862	11	95900850	
cg02923300	X	68759322	chrX:68758191-6875864
cg23071808	14	103021642	chr14:103021331-10302
cg19935909	5	178759017	
cg26699341	X	103088089	chrX:103087020-103087
cg25298683	7	101063331	
cg10601287	11	119293861	chr11:119293320-11929
cg03396005	18	10474524	chr18:10471656-104718
cg08791424	2	208795653	chr2:208795525-208795
cg10517202	3	177187243	

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Relation to UCSC CpG island	UCSC RefGene name	p-value	q-value
	ACTR3B;ACTR3B	1.41984313212921e-08	0.00381849156212571
S_Shore	GAGE2E;GAGE13;GAGE14	2.23202597608368e-08	0.00381849156212571
N_Shelf	ZNF160;ZNF160;ZNF160	3.29067447972275e-08	0.00381849156212571
Island		3.63267734660883e-08	0.00381849156212571
Island	ANKRD9	4.22081812113364e-08	0.00381849156212571
Island	MYH10	4.73049075987287e-08	0.00381849156212571
	AACS	9.15433401010201e-08	0.00565333771818927
	BANP;BANP	9.33808945346908e-08	0.00565333771818927
Island	NKAPL	1.25776835051739e-07	0.00676854062627037
Island	ZIC3	1.72229819507686e-07	0.00834152073330599
	OSBPL3;OSBPL3;OSBPL3	2.18144401937134e-07	0.00960479886074567
Island	DPEP3;DPEP3	2.80127078334808e-07	0.01085349291088
	AACSL	2.91323817357023e-07	0.01085349291088
Island		3.57940816715894e-07	0.0109083898257026
N_Shore	POU3F4	3.63328581752835e-07	0.0109083898257026
	ATP11A;ATP11A	3.63936202400637e-07	0.0109083898257026
	SNTG1	3.82888818534959e-07	0.0109083898257026
Island	MXRA5	4.29087945110604e-07	0.0115454455008719
Island	KCNK3	5.58578071505832e-07	0.0126020082697882
S_Shore	FBXO44;FBXO44;FBXO44	5.60342418752014e-07	0.0126020082697882
Island	CYP26C1	6.91891870886049e-07	0.0126020082697882
Island	FUT4	6.9920466461151e-07	0.0126020082697882
Island		7.05022396819582e-07	0.0126020082697882
Island	FAM181B	7.72115880887004e-07	0.0126020082697882
Island	ZDHHC15;ZDHHC15;ZDHHC15	8.16697508696092e-07	0.0126020082697882
Island	AKR7L;AKR7L	8.22251157985032e-07	0.0126020082697882
		8.69437709029915e-07	0.0126020082697882
Island	TNRC18	9.17815881199408e-07	0.0126020082697882
Island		9.59025146205292e-07	0.0126020082697882
		9.87539156000862e-07	0.0126020082697882
Island	SH3BP5L	1.03547298126649e-06	0.0126020082697882
S_Shore	RBP1;RBP1;RBP1	1.06077136236733e-06	0.0126020082697882
Island	PRDM15;PRDM15	1.08094049524996e-06	0.0126020082697882
N_Shore	HIST2H2BA	1.11556105718318e-06	0.0126020082697882
		1.16071217104728e-06	0.0126020082697882
Island	FAM48B2	1.17607087690565e-06	0.0126020082697882
N_Shore	USP36	1.18034779168658e-06	0.0126020082697882
N_Shelf	HCCA2;CTSD	1.19155314637197e-06	0.0126020082697882
Island		1.19501138164556e-06	0.0126020082697882
Island	SLC6A19	1.25295006065052e-06	0.0126020082697882
Island	DMRTA2	1.2585773078251e-06	0.0126020082697882
Island	GPR144	1.29515480003444e-06	0.0126020082697882
Island	FBRSL1	1.31171618349321e-06	0.0126020082697882
	MCM2	1.33219210236312e-06	0.0126020082697882
Island	CDH4	1.35759293966053e-06	0.0126020082697882
Island	CHD5	1.36683829514928e-06	0.0126020082697882
S_Shore	FAM47A	1.37013347590443e-06	0.0126020082697882
Island		1.39340244250907e-06	0.0126020082697882
N_Shore		1.41188702689746e-06	0.0126020082697882
Island	B3GNT9	1.44898950411219e-06	0.0126020082697882
Island	PCDHB17	1.49118533530339e-06	0.0126020082697882
N_Shelf	MAD1L1;MAD1L1;MAD1L1	1.50653235425064e-06	0.0126020082697882

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	CNNM2;CNNM2	1.56288474042354e-06	0.0126020082697882
S_Shore	BCAR1;BCAR1;BCAR1;	1.58830986317851e-06	0.0126020082697882
Island	BANP;BANP	1.59353077993085e-06	0.0126020082697882
Island	NHSL2;RGAG4	1.6352485963211e-06	0.0126020082697882
	EIF2C2;EIF2C2	1.63990913553099e-06	0.0126020082697882
N_Shore	ADCY9	1.70504442056347e-06	0.0126020082697882
Island	ELAVL1	1.71559944082769e-06	0.0126020082697882
S_Shelf		1.79834305166728e-06	0.0126020082697882
	LXN;LXN;GFM1	1.83122019902199e-06	0.0126020082697882
	CHST11	1.91280218338518e-06	0.0126020082697882
	CTNND1;CTNND1;CTN	1.91451697907586e-06	0.0126020082697882
	FRMD4A	1.95165539982249e-06	0.0126020082697882
Island	NETO1;NETO1;NETO1	1.99024525846211e-06	0.0126020082697882
Island	NCOR2;NCOR2	1.99125818807372e-06	0.0126020082697882
	JPH3	2.00222897094188e-06	0.0126020082697882
S_Shore	ADAM8;ADAM8;ADAM8	2.02701430176056e-06	0.0126020082697882
S_Shore	LOC100132831	2.05141259867952e-06	0.0126020082697882
N_Shore	NXT2	2.0574425375056e-06	0.0126020082697882
Island	REC8;REC8	2.06756223473952e-06	0.0126020082697882
Island	CHAD;ACSF2	2.07904493474359e-06	0.0126020082697882
Island	PCDHA6;PCDHA2;PCD	2.10717055949996e-06	0.0126020082697882
	XAGE3;XAGE3	2.11490462380259e-06	0.0126020082697882
		2.11580291601588e-06	0.0126020082697882
Island	BOLL;BOLL	2.13501307249122e-06	0.0126020082697882
	PRKCZ;PRKCZ;PRKCZ	2.13621026416896e-06	0.0126020082697882
	CUX1;CUX1;CUX1	2.15002884247611e-06	0.0126020082697882
Island		2.17074200563418e-06	0.0126020082697882
Island		2.22104997644416e-06	0.0126020082697882
Island	PGLYRP2	2.23798864056794e-06	0.0126020082697882
Island	PTPRN2;PTPRN2;PTPR	2.31698265183798e-06	0.0126020082697882
N_Shore		2.32270206526637e-06	0.0126020082697882
Island		2.35934832912372e-06	0.0126020082697882
Island	TBCD	2.38774880332714e-06	0.0126020082697882
	NADSYN1	2.4050133384321e-06	0.0126020082697882
Island		2.43868205008041e-06	0.0126020082697882
Island	TP53I13	2.44449997041171e-06	0.0126020082697882
	MYH3	2.45591974776712e-06	0.0126020082697882
		2.46008705009129e-06	0.0126020082697882
N_Shore	CDX4	2.47284722785571e-06	0.0126020082697882
	HDAC4	2.47341764831667e-06	0.0126020082697882
	TRAPPC9;TRAPPC9	2.50501532131565e-06	0.0126020082697882
Island	PCDH11Y;PCDH11Y	2.50619338328748e-06	0.0126020082697882
		2.52840662828106e-06	0.0126020082697882
Island		2.54357505875022e-06	0.0126020082697882
Island		2.54712484330603e-06	0.0126020082697882
S_Shelf	UNC84A;UNC84A	2.54993405345429e-06	0.0126020082697882
S_Shelf	JARID2	2.59186294158518e-06	0.012631976621048
Island		2.60816117711205e-06	0.012631976621048
	PARD3	2.68148238911631e-06	0.0128585045357303
Island	FBRSL1	2.72551714157618e-06	0.0128638357109266
Island		2.73571481593029e-06	0.0128638357109266
Island	RPTOR;RPTOR	2.79934134060387e-06	0.0130364518729612
Island	LOC390594	2.87833404944049e-06	0.0130526608532985
Island	PCDHB12	2.90484907606093e-06	0.0130526608532985
Island	PCDHGA4;PCDHGA9;P	2.92227977387101e-06	0.0130526608532985

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Island		2.93208636196692e-06	0.0130526608532985
S_Shore	B3GNTL1	2.94002177946516e-06	0.0130526608532985
	VARS	2.96956538564692e-06	0.0130526608532985
S_Shore	ATP6AP2	2.99147340053917e-06	0.0130526608532985
		3.06804072422258e-06	0.0131922625464865
		3.09354299470468e-06	0.0131922625464865
	MAGEA12;MAGEA12;M	3.10518335890044e-06	0.0131922625464865
N_Shore		3.16612290458112e-06	0.0133341954414022
S_Shore		3.2171138590614e-06	0.0133438271233556
N_Shore	TSPY3;TSPY4	3.24233714527327e-06	0.0133438271233556
N_Shore	OTUD6A	3.25106405937327e-06	0.0133438271233556
Island	SYCP3	3.33453106177529e-06	0.0134651751862956
N_Shelf		3.33651551382547e-06	0.0134651751862956
N_Shore	C14orf68	3.36403488884895e-06	0.0134651751862956
Island	PBX1	3.48269142051253e-06	0.0135088085781154
	TNXB	3.49942333740548e-06	0.0135088085781154
	FBRSL1	3.50137226968586e-06	0.0135088085781154
	ADCY9	3.51503234079085e-06	0.0135088085781154
Island	KLHL36	3.57075794582741e-06	0.0135088085781154
S_Shore	HIST1H2AA;HIST1H2B/A	3.57556689824917e-06	0.0135088085781154
Island		3.62993547167516e-06	0.0135088085781154
Island	NDUFS7	3.63869331109122e-06	0.0135088085781154
	C3orf21	3.66213656494428e-06	0.0135088085781154
N_Shore	C21orf70	3.68176095342019e-06	0.0135088085781154
Island	HOXA11AS;HOXA11	3.69588743167505e-06	0.0135088085781154
S_Shore	CCDC40	3.74856214748322e-06	0.0135088085781154
	PDIA5;PDIA5	3.78408882893096e-06	0.0135088085781154
Island	HEATR2	3.79122057240249e-06	0.0135088085781154
N_Shelf	LOC145845	3.79331640246467e-06	0.0135088085781154
	CPPED1;CPPED1	3.9001366726306e-06	0.013787837182276
Island	BCOR;BCOR	4.03782569430193e-06	0.0138253033589677
Island	GRM3	4.0515216368776e-06	0.0138253033589677
S_Shore		4.08849317828043e-06	0.0138253033589677
S_Shore	GALNT9	4.12458473709086e-06	0.0138253033589677
Island	HOXA9	4.17565243326477e-06	0.0138253033589677
Island	DMD;DMD;DMD;DMD;D	4.18094341050908e-06	0.0138253033589677
Island	PCDHGA4;PCDHGA4;P	4.19453458976749e-06	0.0138253033589677
N_Shore	C1orf70	4.20336002240863e-06	0.0138253033589677
Island	FTHL17	4.21804552076161e-06	0.0138253033589677
		4.25678503010301e-06	0.0138253033589677
	MCPH1	4.25916566052687e-06	0.0138253033589677
	MAGEA12;MAGEA12;M	4.26716843503948e-06	0.0138253033589677
Island	NFIC;NFIC	4.28874966631664e-06	0.0138253033589677
Island	LOC100302652;GPR75	4.31037176937826e-06	0.0138253033589677
	TCERG1L	4.45586137312287e-06	0.0141979280232746
Island	EEF1A2	4.58913014355409e-06	0.0144471673489737
Island	RGMA;RGMA;RGMA;R	4.59876491989812e-06	0.0144471673489737
Island	SLC7A3;SLC7A3;SLC7A	4.70605532751545e-06	0.0144471673489737
	ANKRD7;ANKRD7	4.70645504343492e-06	0.0144471673489737
Island	TPCN2	4.73381591628569e-06	0.0144471673489737
Island		4.73520291556532e-06	0.0144471673489737
		4.78390628350072e-06	0.0144471673489737
S_Shore	ESX1	4.8358169903496e-06	0.0144471673489737
Island	PCDHA6;PCDHA2;PCD	4.84287858153951e-06	0.0144471673489737
N_Shelf	C17orf101;C17orf101	4.914045287587e-06	0.0144471673489737

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	ZMYND15;ZMYND15	4.94192189898252e-06	0.0144471673489737
N_Shelf		4.96037188154938e-06	0.0144471673489737
		4.96081530340239e-06	0.0144471673489737
Island	UNC5A	5.02761059256561e-06	0.0144471673489737
Island	MXRA5	5.02791615863684e-06	0.0144471673489737
N_Shelf		5.06937631285162e-06	0.0144471673489737
	USP22	5.07412288673978e-06	0.0144471673489737
		5.10692220243726e-06	0.0144471673489737
Island	NTF3;NTF3	5.12538313724351e-06	0.0144471673489737
Island		5.13067213962417e-06	0.0144471673489737
	CDH23	5.1821612455564e-06	0.0145078048858619
Island	CSMD1	5.21274552371386e-06	0.0145095573320271
S_Shore	ADORA1;ADORA1	5.27713983335321e-06	0.0145315041391207
Island	PAX3;PAX3;PAX3;PAX3	5.31630114850142e-06	0.0145315041391207
N_Shore	TBC1D16	5.34211304219609e-06	0.0145315041391207
N_Shore	PCDHGB5;PCDHGC3;PCDHGC3	5.36187753968295e-06	0.0145315041391207
Island		5.37064830620474e-06	0.0145315041391207
Island	DCBLD1	5.40087674459832e-06	0.0145321090518199
	FAM90A7	5.4462115038898e-06	0.0145731292078532
Island	SHROOM1	5.50971257769703e-06	0.0146620414516105
S_Shelf		5.63041267927602e-06	0.0147152061834552
Island	SUSD2	5.633313124837e-06	0.0147152061834552
Island	GGTLC1	5.63995973654033e-06	0.0147152061834552
Island	SHISA6	5.6622723017624e-06	0.0147152061834552
Island	LOC646405	5.69943062819061e-06	0.0147152061834552
Island	CHRDL1;CHRDL1;CHRDL1	5.71198836006726e-06	0.0147152061834552
	SPATA13;SPATA13	5.77070445194163e-06	0.0147389730014001
	POR	5.79539980287698e-06	0.0147389730014001
Island		5.81250987099039e-06	0.0147389730014001
Island		5.94546719058704e-06	0.0149884639419616
	ARPC1B	5.97279417911236e-06	0.0149884639419616
Island	SCRIB;SCRIB	6.02671263513126e-06	0.0150397426307683
	ARID1B;ARID1B;ARID1B	6.0587010360997e-06	0.0150397426307683
Island	RGMA;RGMA;RGMA;RGMA	6.09947030491033e-06	0.0150397426307683
	SLC6A8;SLC6A8;SLC6A8	6.11744035154359e-06	0.0150397426307683
S_Shelf	SFRS8	6.21862789097021e-06	0.0151567505292647
Island	LOC388965	6.24476317141491e-06	0.0151567505292647
N_Shore	INS-IGF2;IGF2;IGF2;IGF2	6.27003276161522e-06	0.0151567505292647
		6.29663443328333e-06	0.0151567505292647
Island	SNX29	6.32150644074014e-06	0.0151567505292647
N_Shore	BCAT1	6.35696827059904e-06	0.0151666928948664
		6.42780011690413e-06	0.0152184366223255
		6.48336707984788e-06	0.0152184366223255
		6.50617307977384e-06	0.0152184366223255
Island	CBS	6.63337684529122e-06	0.0152184366223255
	TECPR1	6.64775214773754e-06	0.0152184366223255
	BDKRB2	6.65393439584655e-06	0.0152184366223255
Island	ADAMTS2	6.66650237607488e-06	0.0152184366223255
Island		6.6783750200843e-06	0.0152184366223255
		6.68070882502978e-06	0.0152184366223255
N_Shore		6.79296575128115e-06	0.0152184366223255
S_Shore	TBC1D16	6.81013356403908e-06	0.0152184366223255
N_Shore	DLGAP2	6.87229287906245e-06	0.0152184366223255
S_Shore		6.888294031991e-06	0.0152184366223255
	COL4A1	6.90724489011681e-06	0.0152184366223255

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Island	POLS	6.94085892486996e-06	0.0152184366223255
	VPS53;VPS53	6.95518140785349e-06	0.0152184366223255
Island	NCCRP1	6.97399989864988e-06	0.0152184366223255
Island		6.97418427587707e-06	0.0152184366223255
	LUZP4	6.97567321562228e-06	0.0152184366223255
Island	CPT1A;CPT1A	7.08298720127773e-06	0.0153672915451134
	TMCO3	7.1112847773324e-06	0.0153672915451134
Island		7.14273405707794e-06	0.0153672915451134
Island		7.1708210172831e-06	0.0153672915451134
	OPCML;OPCML	7.2455733991637e-06	0.0154008350901313
S_Shelf	CDC25B;CDC25B;CDC25B	7.25007051163978e-06	0.0154008350901313
N_Shore	RPTOR;RPTOR	7.28637844498702e-06	0.0154103722286827
S_Shore	EHMT1	7.38045638372733e-06	0.0155414762523858
S_Shore		7.47005046478917e-06	0.0155572307193827
		7.49404954591378e-06	0.0155572307193827
Island		7.51298726534925e-06	0.0155572307193827
Island	FLCN;FLCN	7.51642386483364e-06	0.0155572307193827
	TEKT3	7.64261172192287e-06	0.0155640440976558
Island		7.67327601186096e-06	0.0155640440976558
Island	PCDH19;PCDH19	7.68101105584453e-06	0.0155640440976558
Island		7.70363611295085e-06	0.0155640440976558
	DENND3	7.71470342009493e-06	0.0155640440976558
N_Shelf		7.73234477902986e-06	0.0155640440976558
Island	GJA8	7.76664827655979e-06	0.0155640440976558
Island	ARHGEF1;ARHGEF1;ARHGEF1	7.77680002401838e-06	0.0155640440976558
	STK31;STK31;STK31	7.90615982953334e-06	0.0155663928045783
	PAGE4	7.92457030011703e-06	0.0155663928045783
Island	SLC25A31	7.98533760706892e-06	0.0155663928045783
N_Shore		7.99258609833445e-06	0.0155663928045783
Island	BANP;BANP	8.12457852199028e-06	0.0155663928045783
Island	FUT4	8.13424732351034e-06	0.0155663928045783
	TMCO3	8.14540242107803e-06	0.0155663928045783
Island	RNF39;RNF39	8.18167662306717e-06	0.0155663928045783
N_Shore	ATP11A;ATP11A	8.1828986651869e-06	0.0155663928045783
Island	PMEPA1;PMEPA1;PMEPA1	8.21737872314626e-06	0.0155663928045783
Island	BHMT2;DMGDH	8.25815810212016e-06	0.0155663928045783
		8.28756931507738e-06	0.0155663928045783
Island	MXRA5	8.31036773201349e-06	0.0155663928045783
Island		8.33732435886312e-06	0.0155663928045783
Island		8.37073312233688e-06	0.0155663928045783
	MLYCD	8.42844680518304e-06	0.0155663928045783
Island	INPP5F;INPP5F	8.46915689919752e-06	0.0155663928045783
Island	MEGF8	8.47357503921162e-06	0.0155663928045783
	AGAP1;AGAP1	8.50068008148033e-06	0.0155663928045783
	SCARB1;SCARB1	8.50133168081624e-06	0.0155663928045783
N_Shore	RPTOR;RPTOR	8.52107035013538e-06	0.0155663928045783
Island	RFX2;RFX2	8.52134783780381e-06	0.0155663928045783
N_Shore	B3GNTL1	8.53418930278198e-06	0.0155663928045783
Island		8.55802273543542e-06	0.0155663928045783
Island		8.58148325777609e-06	0.0155663928045783
Island		8.64581470710055e-06	0.0155682506603787
	WFIKKN2	8.64752217947082e-06	0.0155682506603787
S_Shelf	WDR60	8.67894012966964e-06	0.0155682506603787
		8.74855667352729e-06	0.0155845120450175
	TRIM15	8.75236107209985e-06	0.0155845120450175

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Island	AGAP1;AGAP1	8.95100440402078e-06	0.0158333851444568
		8.95751309468054e-06	0.0158333851444568
S_Shore	C6orf138	8.99595663865588e-06	0.0158428233018591
	NPTN;NPTN;NPTN;NPTN	9.04553942739848e-06	0.0158428233018591
Island	PAX5	9.0609860209879e-06	0.0158428233018591
Island	ZAP70	9.13567240670616e-06	0.0158844672375306
	MYLK4	9.1805402923212e-06	0.0158844672375306
N_Shore	C1orf86;PRKCZ;PRKCZ	9.18319481032068e-06	0.0158844672375306
	LDB3;LDB3;LDB3;LDB3	9.41384272867816e-06	0.0162128594880758
N_Shelf	TMCO3	9.43999664613093e-06	0.0162128594880758
N_Shore	ALPI	9.47504026161038e-06	0.0162155437268708
Island	HEATR2	9.54159828744816e-06	0.0162719527836913
S_Shelf		9.61723921778979e-06	0.0163434013479159
		9.84186847074416e-06	0.0166087933111035
Island	MAGEB1;MAGEB1;MAGEB1	9.84199386834605e-06	0.0166087933111035
Island	ARSD;ARSD	9.91505766519755e-06	0.0166335235087987
Island	CCDC88C	9.92533586753279e-06	0.0166335235087987
Island		9.99187344455745e-06	0.0166872900208113
	RCBTB2	1.00855020367745e-05	0.0167419814936059
	PRDM16;PRDM16	1.0093756457199e-05	0.0167419814936059
	CRYGA	1.01461550191183e-05	0.0167714557325408
		1.02094860947602e-05	0.0168187392953902
	ZFAT;ZFAT;ZFAT	1.02469466666532e-05	0.0168232286248366
Island	LMX1A	1.03284191631701e-05	0.0168997013891971
Island	TXLNA	1.05109653144535e-05	0.0169869378063318
Island	PTPRN2;PTPRN2;PTPRN2	1.06505321168912e-05	0.0169869378063318
N_Shelf	MAPK8IP3;MAPK8IP3	1.06523799460186e-05	0.0169869378063318
Island	PCDHGA4;PCDHGA11;PCDHGA11	1.07143642585423e-05	0.0169869378063318
S_Shelf	ADORA2A;ADORA2A	1.07227670566476e-05	0.0169869378063318
	WDR60	1.07428232428455e-05	0.0169869378063318
	SLC6A8;SLC6A8;SLC6A8	1.07567281615218e-05	0.0169869378063318
	SLC6A8;SLC6A8;SLC6A8	1.07809366185199e-05	0.0169869378063318
	ARHGEF10	1.07884022029126e-05	0.0169869378063318
Island		1.07971516437396e-05	0.0169869378063318
Island	AHRR	1.08051500934239e-05	0.0169869378063318
Island	TRIM67	1.08567278416182e-05	0.0169869378063318
Island	ZNF598	1.0857203114048e-05	0.0169869378063318
	SDHAP1	1.09159335394649e-05	0.0169869378063318
N_Shelf	TNK2;TNK2	1.09883471174105e-05	0.0169869378063318
Island	FO XK1	1.09933523504764e-05	0.0169869378063318
Island	C7orf20	1.09977254142856e-05	0.0169869378063318
Island	ERICH1	1.1013056256002e-05	0.0169869378063318
	MGRN1;MGRN1;MGRN1	1.11526042276283e-05	0.0171135470207175
		1.11658098560816e-05	0.0171135470207175
		1.13070164033669e-05	0.0172753019544501
	EP400	1.14944998961224e-05	0.0173575231165894
	NCAPD3	1.15170885694737e-05	0.0173575231165894
Island	GNB1L	1.1586327440125e-05	0.0173575231165894
Island	SOX3	1.16463604636213e-05	0.0173575231165894
		1.16637160083143e-05	0.0173575231165894
Island	HECW1	1.17038067531941e-05	0.0173575231165894
S_Shore		1.17164052197904e-05	0.0173575231165894
Island	POM121L1P	1.17293284897003e-05	0.0173575231165894
		1.17678415620218e-05	0.0173575231165894
Island	FAM83H	1.17822747737297e-05	0.0173575231165894

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S_Shore	CARS2	1.17891436006792e-05	0.0173575231165894
	PRAGMIN	1.18150665529045e-05	0.0173575231165894
	COL6A3;COL6A3;COL6	1.18529482509814e-05	0.0173575231165894
Island	PNCK;PNCK	1.19413336833399e-05	0.0173575231165894
		1.1976064476892e-05	0.0173575231165894
Island		1.20436908891278e-05	0.0173575231165894
N_Shore	DUSP21;DUSP21	1.21234909713995e-05	0.0173575231165894
Island	BEX1	1.21281285211022e-05	0.0173575231165894
Island	TLX3	1.21901885916129e-05	0.0173575231165894
Island	FUT4	1.22169403623377e-05	0.0173575231165894
Island	FLJ42875	1.22212355349593e-05	0.0173575231165894
Island	DDX4;DDX4;DDX4	1.231367741363e-05	0.0173575231165894
		1.23138077726015e-05	0.0173575231165894
Island	ALX4	1.25110187441723e-05	0.0173575231165894
Island		1.25289664937659e-05	0.0173575231165894
	GPR81	1.25433930751846e-05	0.0173575231165894
Island	NFIC;NFIC	1.2649316926984e-05	0.0173575231165894
Island	FAM181B	1.26540593172362e-05	0.0173575231165894
		1.26714149941629e-05	0.0173575231165894
Island	KCNQ1OT1;KCNQ1;KC	1.26935049602379e-05	0.0173575231165894
N_Shore	FOX11;FOX11	1.27440192219555e-05	0.0173575231165894
Island	KDM4B	1.27820315740677e-05	0.0173575231165894
Island	PHF23	1.27943282440985e-05	0.0173575231165894
Island	SYNJ2	1.27969617841391e-05	0.0173575231165894
Island	FAM133A;FAM133A;NA	1.29162075004598e-05	0.0173575231165894
N_Shelf	CLPTM1L	1.29179648195551e-05	0.0173575231165894
	CCDC88C	1.29226626243648e-05	0.0173575231165894
Island		1.29257528402969e-05	0.0173575231165894
S_Shore		1.29482131566032e-05	0.0173575231165894
Island	WNT5A	1.29651318880246e-05	0.0173575231165894
Island	NKAPL	1.29676356904858e-05	0.0173575231165894
Island	CHST7	1.2985269431519e-05	0.0173575231165894
	CUX1;CUX1;CUX1	1.29985772854288e-05	0.0173575231165894
N_Shore	HCG9	1.30127320814142e-05	0.0173575231165894
		1.31481940528072e-05	0.0173575231165894
	SPDYE1;POLR2J4	1.31648813261953e-05	0.0173575231165894
Island	CYP2F1	1.31826600734346e-05	0.0173575231165894
S_Shore	PTPRN2;PTPRN2;PTPF	1.33177897454549e-05	0.0173575231165894
		1.33471116436426e-05	0.0173575231165894
Island	FMR1NB	1.33662310333965e-05	0.0173575231165894
Island	C15orf39	1.33673233504217e-05	0.0173575231165894
Island	BMP4;BMP4;BMP4	1.34967992774938e-05	0.0173575231165894
Island	ANGPT4	1.35137016442792e-05	0.0173575231165894
	EP400	1.35761973572534e-05	0.0173575231165894
S_Shore	FAM70A;FAM70A;FAM7	1.35989123818517e-05	0.0173575231165894
		1.37802480622567e-05	0.0173575231165894
	SMOC2;SMOC2	1.3782339334502e-05	0.0173575231165894
Island	KIAA1210	1.37940519832986e-05	0.0173575231165894
Island	HEATR2	1.38201409692974e-05	0.0173575231165894
Island	TRAP1	1.3879203691368e-05	0.0173575231165894
	TNXB	1.39186099201523e-05	0.0173575231165894
N_Shore	LFNG;LFNG	1.3938381079818e-05	0.0173575231165894
Island	RBMXL2	1.39386885228887e-05	0.0173575231165894
Island		1.39617079352671e-05	0.0173575231165894
	CCDC62;CCDC62;CCD	1.39765801173965e-05	0.0173575231165894

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Island	TLL2	1.39788620764808e-05	0.0173575231165894
Island		1.39803171621266e-05	0.0173575231165894
	TIMP2	1.40453645943298e-05	0.0173575231165894
Island	BCL11B;BCL11B	1.40826529513183e-05	0.0173575231165894
S_Shore	GALNS	1.41148281206199e-05	0.0173575231165894
	C11orf75	1.42083938803946e-05	0.0173575231165894
	PTPRN2;PTPRN2;PTPRN2	1.42380836688654e-05	0.0173575231165894
	GRK1	1.4255656884394e-05	0.0173575231165894
	DOC2B	1.428540409303e-05	0.0173575231165894
Island	MUM1;MUM1	1.43026944574705e-05	0.0173575231165894
N_Shore		1.43084168259866e-05	0.0173575231165894
	ANK3	1.43200115394669e-05	0.0173575231165894
	EXOC7;EXOC7;EXOC7	1.43295477413281e-05	0.0173575231165894
S_Shelf	RALGAPA2	1.43542703660891e-05	0.0173575231165894
	TMCO3	1.43663466994936e-05	0.0173575231165894
N_Shore	C22orf9;C22orf9;MIR124	1.44284368439252e-05	0.0173575231165894
Island		1.44285360134536e-05	0.0173575231165894
Island	EPPK1	1.44621657192629e-05	0.0173575231165894
Island	MAEA;MAEA	1.45097096247059e-05	0.0173575231165894
N_Shore	BAIAP2;BAIAP2;BAIAP2	1.45595650423141e-05	0.0173575231165894
Island		1.4606238373667e-05	0.0173575231165894
		1.46077894231604e-05	0.0173575231165894
S_Shore	GAK	1.48093587488653e-05	0.0173575231165894
Island		1.48207429243695e-05	0.0173575231165894
Island	KCNG2	1.48392382457962e-05	0.0173575231165894
Island	FLJ45983;FLJ45983	1.48570128284915e-05	0.0173575231165894
Island	GPR75;LOC100302652	1.48675119094596e-05	0.0173575231165894
Island	LEP	1.487586174126e-05	0.0173575231165894
Island		1.48808125384742e-05	0.0173575231165894
Island	CSMD1	1.49057487927863e-05	0.0173575231165894
N_Shore	CAMK2G;CAMK2G;CAMK2G	1.49636213645061e-05	0.0173575231165894
N_Shore		1.49708163632471e-05	0.0173575231165894
Island	HDGFL1	1.50177021504726e-05	0.0173575231165894
Island		1.50489034878219e-05	0.0173575231165894
		1.507930417254e-05	0.0173575231165894
Island	ZNF672	1.50814798224399e-05	0.0173575231165894
Island		1.5118815646501e-05	0.0173575231165894
S_Shelf	TOLLIP	1.51483044912628e-05	0.0173575231165894
Island	SRD5A2	1.51507301786488e-05	0.0173575231165894
Island	ADAMTS10	1.51588656018585e-05	0.0173575231165894
	ARHGAP10	1.51597218361995e-05	0.0173575231165894
Island	NEURL1B	1.52712854626368e-05	0.0173865744373808
N_Shelf	TRIM39;TRIM39	1.53058913625245e-05	0.0173865744373808
Island	LPAR5;LPAR5	1.53890214826919e-05	0.0173865744373808
		1.53906219750499e-05	0.0173865744373808
N_Shelf	NFATC1;NFATC1;NFATC1	1.54157015405344e-05	0.0173865744373808
Island		1.54831453761491e-05	0.0173865744373808
Island	ZNF668	1.54965001848772e-05	0.0173865744373808
Island	HOXA3;HOXA3;HOXA3	1.55049832708419e-05	0.0173865744373808
	HTR2A;HTR2A	1.55150462372887e-05	0.0173865744373808
		1.5558956695156e-05	0.0173865744373808
Island		1.5579978951785e-05	0.0173865744373808
Island	SLC15A4	1.56417609262332e-05	0.0174032388001948
		1.56667777151394e-05	0.0174032388001948
	MSRA;MSRA;MSRA	1.57265115078152e-05	0.0174296171304865

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N_Shore		1.58229562743754e-05	0.0174607542745202
Island	ZNF517	1.58440829938984e-05	0.0174607542745202
	AGAP1;AGAP1	1.58908487533507e-05	0.0174607542745202
		1.59336480488768e-05	0.0174607542745202
Island		1.59535885284859e-05	0.0174607542745202
Island	BEGAIN;BEGAIN	1.5970916520131e-05	0.0174607542745202
Island	TFAP2E	1.6100768531211e-05	0.0174961470272239
	NKAIN3	1.61027954724355e-05	0.0174961470272239
Island		1.6111663808686e-05	0.0174961470272239
Island	MYT1L	1.61642618343488e-05	0.0175139957783468
Island	SLCO3A1;SLCO3A1	1.62463306880036e-05	0.0175309035245858
Island		1.6260153486637e-05	0.0175309035245858
Island	INF2;INF2	1.63233293928216e-05	0.0175309035245858
	SORCS2	1.63313810632354e-05	0.0175309035245858
Island		1.63840540974467e-05	0.0175309035245858
		1.64166332393255e-05	0.0175309035245858
N_Shore		1.64332425544045e-05	0.0175309035245858
N_Shelf		1.64985254101052e-05	0.0175443631370081
		1.65183081411773e-05	0.0175443631370081
	FLJ43860	1.67126918311874e-05	0.0176693211086308
S_Shelf	PTPN18;PTPN18	1.67484826173626e-05	0.0176693211086308
Island		1.67777787659016e-05	0.0176693211086308
N_Shelf	RPTOR;RPTOR	1.67818875960773e-05	0.0176693211086308
	TUBGCP2	1.68837055842641e-05	0.0177299474900604
N_Shore	GDNF;GDNF;GDNF	1.6912684128236e-05	0.0177299474900604
S_Shore	WDR37	1.69822066822199e-05	0.0177607183818163
Island	SLC25A2	1.70153787831781e-05	0.0177607183818163
	CRIM1	1.70570699491744e-05	0.0177659471035137
	GRM8;GRM8;GRM8	1.72510528980479e-05	0.0179294338945216
Island		1.73992884856772e-05	0.0180447760081919
		1.74903884455768e-05	0.0180603206801213
Island	ZNF707;ZNF707;ZNF707	1.75221681127248e-05	0.0180603206801213
N_Shore		1.75514252719138e-05	0.0180603206801213
Island		1.7579358530006e-05	0.0180603206801213
Island	CDH22	1.76351693621995e-05	0.0180603206801213
Island		1.76380151379702e-05	0.0180603206801213
N_Shore	C12orf23	1.77130253911407e-05	0.0180604481792505
N_Shelf	STK32C	1.77358964489353e-05	0.0180604481792505
N_Shore	KLHL34;KLHL34	1.77714657964839e-05	0.0180604481792505
S_Shelf	CORO1B;CORO1B;PTP	1.78701206151605e-05	0.0180604481792505
	FRMD4A	1.78848935042702e-05	0.0180604481792505
		1.78958952261783e-05	0.0180604481792505
N_Shore	PPT2;PRRT1;PPT2	1.78991692067109e-05	0.0180604481792505
Island	DLGAP2	1.79808680169917e-05	0.0180686333273726
		1.79818949337606e-05	0.0180686333273726
	COL23A1	1.81003144246866e-05	0.0181499684963486
	MEIS1	1.81885732260281e-05	0.0182007866274712
S_Shelf	CDK18;CDK18;CDK18	1.82546785324753e-05	0.0182292725365796
Island		1.84927740172555e-05	0.018429038633554
N_Shore		1.86510852315563e-05	0.0185486383054897
Island	TSPYL5	1.87476902394989e-05	0.018549107912511
Island	ACTL9	1.87980977193317e-05	0.018549107912511
Island	GPR177;GPR177	1.88679334756135e-05	0.018549107912511
Island	SPG7;SPG7	1.88826034100524e-05	0.018549107912511
	CHD3;CHD3;CHD3	1.88935527784028e-05	0.018549107912511

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	USP18	1.89261256013152e-05	0.018549107912511
	ZNF19	1.89569307980283e-05	0.018549107912511
Island	FAM47C	1.90887803631719e-05	0.018549107912511
	COG5;COG5;COG5	1.91207720402539e-05	0.018549107912511
Island	RAI1	1.91837487528572e-05	0.018549107912511
Island	NCRNA00200	1.91852902950712e-05	0.018549107912511
	NPAS2	1.91889936627476e-05	0.018549107912511
	RPTOR;RPTOR	1.91997429093567e-05	0.018549107912511
Island	MAPK8IP3;MAPK8IP3	1.92197904705984e-05	0.018549107912511
S_Shore	FAM83H	1.92578086570102e-05	0.018549107912511
	CDYL;CDYL	1.92837325669827e-05	0.018549107912511
	DLGAP2	1.93392908392064e-05	0.018549107912511
S_Shore	SLC44A4	1.93765847792775e-05	0.018549107912511
Island	CPLX1	1.94232029536367e-05	0.018549107912511
Island	DIP2C	1.94494401594738e-05	0.018549107912511
Island	PCNT	1.94588700578724e-05	0.018549107912511
Island		1.94941329220422e-05	0.018549107912511
Island	MAD1L1;MAD1L1;MAD1	1.95513375595595e-05	0.0185670618892817
N_Shore		1.96414767808271e-05	0.0185698586772443
Island	NGFR	1.97685384872427e-05	0.0185698586772443
Island	FGFR3;FGFR3;FGFR3	1.97983526738736e-05	0.0185698586772443
S_Shore	GALNT9	1.98228252341584e-05	0.0185698586772443
		1.98279863962748e-05	0.0185698586772443
	RASA3	1.98339442531057e-05	0.0185698586772443
	GEMIN4	1.9878495487625e-05	0.0185698586772443
	MACROD1	1.98947295462717e-05	0.0185698586772443
N_Shore	HTR2C	1.98993581861142e-05	0.0185698586772443
Island		2.01149257124612e-05	0.0187176452553484
Island	PIGG;PIGG	2.01804951651335e-05	0.0187176452553484
Island		2.02238509147223e-05	0.0187176452553484
S_Shore		2.02558627503474e-05	0.0187176452553484
	GPRC5B	2.02721964938532e-05	0.0187176452553484
Island	TBCD	2.03202774269413e-05	0.0187176452553484
Island	NYX	2.03606474598259e-05	0.0187176452553484
Island	BCOR;BCOR	2.03958778190783e-05	0.0187176452553484
	RNF144A	2.04762199885502e-05	0.0187176452553484
Island		2.05202467895259e-05	0.0187176452553484
	SEPT9;SEPT9;SEPT9;S	2.05392047597848e-05	0.0187176452553484
Island	ARMCX1	2.0559204573846e-05	0.0187176452553484
Island		2.05601347769481e-05	0.0187176452553484
Island	CCDC8	2.07154946872527e-05	0.0188236997455979
		2.08250436516416e-05	0.0188650075390804
Island	SIM1	2.08388562089671e-05	0.0188650075390804
		2.08844543688069e-05	0.0188710137353963
N_Shelf	INPP5A	2.09416084874995e-05	0.0188874199826969
Island		2.10122270745259e-05	0.0188987504624714
N_Shore		2.1032212872084e-05	0.0188987504624714
N_Shelf	ADARB2	2.11842640213741e-05	0.0190001271706519
N_Shelf	CELSR1	2.14242580623516e-05	0.0191737163751549
		2.14569850314024e-05	0.0191737163751549
Island	PTPRU;PTPRU;PTPRU	2.1621587412358e-05	0.0192852215902215
N_Shore		2.16749490470027e-05	0.0192972788551279
	DOCK1	2.17620647577542e-05	0.0193037006138894
Island	PCDHA6;PCDHA2;PCD	2.181478316988e-05	0.0193037006138894
Island		2.18364682150471e-05	0.0193037006138894

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Island	CXorf67	2.18885358223778e-05	0.0193037006138894
	LRSAM1;LRSAM1;LRSAM1	2.18962073143413e-05	0.0193037006138894
		2.1921303541298e-05	0.0193037006138894
Island		2.20482668980298e-05	0.0193802665433544
Island	ARMC5;ARMC5	2.22033823168584e-05	0.0194812556895153
Island	MIB2;MIB2;MIB2;MIB2;MIB2	2.22755767722072e-05	0.0195092562752247
Island		2.23522027351139e-05	0.0195285566614002
		2.24346057297357e-05	0.0195285566614002
Island		2.25078924570776e-05	0.0195285566614002
N_Shore	EXD3	2.25434814785553e-05	0.0195285566614002
Island	ZBED4	2.25566298939846e-05	0.0195285566614002
Island	PACRG;PACRG;PACRG	2.26083175354847e-05	0.0195285566614002
Island	SRCIN1	2.26135421147921e-05	0.0195285566614002
	CEBPE	2.2660243200201e-05	0.0195285566614002
Island	LOC404266;LOC404266	2.26605045036017e-05	0.0195285566614002
		2.27932816830017e-05	0.0195946720259268
	MRPS31	2.28181386932797e-05	0.0195946720259268
Island	SLC6A18	2.28735730490113e-05	0.0196075102070131
	MAD1L1;MAD1L1;MAD1L1	2.32423948362429e-05	0.0197766600666206
S_Shelf	FBRS1	2.32732408663642e-05	0.0197766600666206
Island	RUNX1	2.32771999089114e-05	0.0197766600666206
Island	PLEKHF1	2.3277915611146e-05	0.0197766600666206
	C3orf67	2.32930335508785e-05	0.0197766600666206
Island	C10orf41;C10orf41	2.33158992371659e-05	0.0197766600666206
		2.34579168980548e-05	0.0198623349679203
		2.3553855534578e-05	0.0198641222784576
		2.35782916922669e-05	0.0198641222784576
	CATSPER4	2.36477341770047e-05	0.0198641222784576
		2.36620153200043e-05	0.0198641222784576
	TSPAN18	2.36650979294277e-05	0.0198641222784576
N_Shore	C9orf91	2.37637565786413e-05	0.0198824122208757
Island	AP3D1;AP3D1	2.37851381428255e-05	0.0198824122208757
S_Shore	JAKMIP3	2.38100430250511e-05	0.0198824122208757
		2.39206624551823e-05	0.0199379369021949
Island	FBXL18	2.39914015598192e-05	0.0199379369021949
Island	MGAT1;MGAT1;MGAT1	2.40078797445193e-05	0.0199379369021949
Island		2.40412019839608e-05	0.0199379369021949
N_Shelf	SEMA4D;SEMA4D	2.41071760383564e-05	0.019958475273123
Island		2.41844808679115e-05	0.0199883083555481
S_Shore		2.43056484577932e-05	0.0200542303054867
Island		2.43826503025323e-05	0.0200626976163426
		2.44386493297729e-05	0.0200626976163426
		2.44904872956051e-05	0.0200626976163426
		2.44906564841093e-05	0.0200626976163426
	CACNA1G;CACNA1G;CACNA1G	2.45518221919165e-05	0.0200626976163426
Island		2.45644550384374e-05	0.0200626976163426
	DUSP22	2.46235937016372e-05	0.0200771414470462
Island	KIF26A	2.47609639827533e-05	0.0201552166066336
Island		2.4877819364419e-05	0.0201553073842376
S_Shore	MTUS2;MTUS2	2.4917542935308e-05	0.0201553073842376
Island	RPS6KA4;MIR1237;RPS6KA4	2.4922907805257e-05	0.0201553073842376
Island	TBX3;TBX3	2.49275365160962e-05	0.0201553073842376
Island	RPP25	2.50239713700512e-05	0.0201995582230001
	ARHGEF10	2.50953452481303e-05	0.0202234660354421
N_Shore	IFNGR2	2.51440667135109e-05	0.0202290699518624

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Island	ARPC1B	2.52429422478191e-05	0.0202537453336703
Island	USP29	2.52594597897489e-05	0.0202537453336703
	ENGASE	2.53040831662425e-05	0.0202537453336703
N_Shore	NKX2-1;NKX2-1	2.53420114018566e-05	0.0202537453336703
	TP53AIP1	2.54382403843321e-05	0.0202718358563424
N_Shelf		2.54989672365868e-05	0.0202718358563424
	BANP;BANP	2.55190098105166e-05	0.0202718358563424
N_Shore	ADAM23	2.55320701437442e-05	0.0202718358563424
		2.56275674947295e-05	0.020314356181481
Island	MS4A13;MS4A13;MS4A	2.57436195532119e-05	0.0203324411655978
S_Shore	HIST1H4G	2.58606629327193e-05	0.0203324411655978
Island	MYO10	2.5921781714886e-05	0.0203324411655978
	H2AFY2	2.59304523168655e-05	0.0203324411655978
	THBS4	2.59797702292979e-05	0.0203324411655978
Island	TSPY1;TSPY4	2.60122762986318e-05	0.0203324411655978
S_Shore	UHRF1;UHRF1	2.60123017887043e-05	0.0203324411655978
	MAGEB10	2.6024905641164e-05	0.0203324411655978
Island	YWHAG	2.60282114750852e-05	0.0203324411655978
N_Shore		2.61273510654564e-05	0.0203450297894817
Island		2.61283405338515e-05	0.0203450297894817
	HORMAD1	2.6220607929619e-05	0.0203841026252211
	AGAP1;AGAP1	2.63276585294157e-05	0.0204287460806288
Island	PCBP3;PCBP3	2.63623936414453e-05	0.0204287460806288
	MAD1L1;MAD1L1;MAD1	2.642912186023e-05	0.0204477387299615
S_Shore	COL5A1	2.65362786867606e-05	0.0204978998005827
Island	PCGF3	2.65923495364514e-05	0.0205085026898755
	TTY14	2.66893038397514e-05	0.0205505517999803
Island	PHLDB3	2.69499350331413e-05	0.0206374982476685
		2.69681415149096e-05	0.0206374982476685
Island	FAM96B;CES2;FAM96B	2.70293377294172e-05	0.0206374982476685
Island	GDF2	2.70823928365222e-05	0.0206374982476685
Island	KCNQ1OT1;KCNQ1;KC	2.70980241093235e-05	0.0206374982476685
S_Shelf		2.71045444614334e-05	0.0206374982476685
	DNAH10	2.71445822862574e-05	0.0206374982476685
N_Shore		2.72136166652291e-05	0.0206374982476685
Island	WDR27	2.72153308525021e-05	0.0206374982476685
Island	SYCE1;SYCE1;SYCE1	2.72467782072927e-05	0.0206374982476685
Island	EN2	2.72709417818776e-05	0.0206374982476685
S_Shore	FHL1;FHL1;FHL1;FHL1;	2.74904665139384e-05	0.0207711703500206
Island		2.75449878745174e-05	0.020779947433529
Island	PCDHB6	2.76122125998702e-05	0.02079030097675
Island	F8;H2AFB1;F8A3;F8A1;	2.76445647633862e-05	0.02079030097675
N_Shore	GAK	2.77109653638394e-05	0.0208079275966535
	WDR27	2.77568493033117e-05	0.0208101177071617
	MEOX2	2.7846421418571e-05	0.0208317235719359
N_Shore		2.79032002047378e-05	0.0208317235719359
	HDAC4	2.79147031398057e-05	0.0208317235719359
Island	SLC5A8	2.79834186397086e-05	0.0208508757425798
Island	PCSK1N	2.80359203351707e-05	0.0208579064766998
		2.81317973224008e-05	0.0208710193251713
Island	ZNF213;ZNF213	2.81580124085017e-05	0.0208710193251713
N_Shelf	MAGEA3	2.81828248359305e-05	0.0208710193251713
		2.82464744803173e-05	0.0208824814482906
N_Shore		2.82845358593479e-05	0.0208824814482906
		2.83968897973281e-05	0.0209035751735576

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	ITFG3	2.83994269637143e-05	0.0209035751735576
		2.85944818727096e-05	0.0210009832405122
S_Shore		2.8618487459326e-05	0.0210009832405122
	APLP2;APLP2;APLP2;A	2.86633159315654e-05	0.0210020582277692
Island	LPCAT1	2.87264154346274e-05	0.0210021000277799
Island		2.8750100280634e-05	0.0210021000277799
Island		2.88162027569647e-05	0.0210186858437755
Island	FAM47C	2.88981127825061e-05	0.021046734546447
Island	TUBGCP3	2.90276943296879e-05	0.0210820963705035
	CTBP2;CTBP2;CTBP2	2.90337237993617e-05	0.0210820963705035
N_Shore	PKD1;PKD1	2.91863699393498e-05	0.0211612105102928
N_Shelf	ZIC4;ZIC4	2.92655747137981e-05	0.0211869199899257
Island		2.94984363633945e-05	0.0213236271517926
Island	ALPPL2	2.95540546608207e-05	0.0213276067870764
S_Shore	TBL2	2.9592013133568e-05	0.0213276067870764
Island	C9orf3	2.96591979585871e-05	0.0213442660494691
N_Shore	HIST1H4F	2.97826498084213e-05	0.0213964083083024
Island		2.98200084821228e-05	0.0213964083083024
	POU6F2;POU6F2	3.00056622529654e-05	0.0214977697790939
Island		3.01439044975362e-05	0.0215649136569708
	ADARB2	3.022736133764e-05	0.0215657885490157
	EXOC2	3.02341824699978e-05	0.0215657885490157
Island	LOC100132215	3.04334951548888e-05	0.0216760331483699
Island	NTM;NTM;NTM;NTM;N	3.05062207772906e-05	0.0216894249078091
Island		3.05835687065946e-05	0.0216894249078091
		3.0586917993915e-05	0.0216894249078091
S_Shore		3.06540256460658e-05	0.0216894249078091
Island	GATA6	3.07308222395019e-05	0.0216894249078091
	LOC92249	3.07478324113217e-05	0.0216894249078091
Island	C1orf94;C1orf94	3.08067324035344e-05	0.0216894249078091
Island	RPS2P32	3.08105597203792e-05	0.0216894249078091
S_Shore		3.09800934796275e-05	0.0217367208971467
Island	ACTN1;ACTN1;ACTN1	3.0994508475658e-05	0.0217367208971467
Island	HTR2C;HTR2C	3.10123865997592e-05	0.0217367208971467
		3.11777347107634e-05	0.0217883934234967
	ARHGEF6;ARHGEF6	3.12088132120307e-05	0.0217883934234967
Island		3.12871004189577e-05	0.0217883934234967
	DIP2C	3.13238116514406e-05	0.0217883934234967
N_Shore	ZFYVE21	3.13469542324493e-05	0.0217883934234967
Island		3.13560320367052e-05	0.0217883934234967
S_Shore	JAKMIP3	3.14578314486695e-05	0.0218278140635771
Island	CHAD;ACSF2	3.15083518171483e-05	0.0218309459728992
	CHRN3	3.15524950829081e-05	0.0218309459728992
	MIR202	3.16840405099601e-05	0.0218618047160539
	TBCD	3.16873729637534e-05	0.0218618047160539
	USP10	3.1814205424387e-05	0.0218924334702966
	PCGF3	3.18221713995536e-05	0.0218924334702966
	KIAA1522	3.20432552725749e-05	0.0219881267942619
Island	ST14	3.20813580908146e-05	0.0219881267942619
S_Shelf	PAOX;PAOX;PAOX	3.20974668735728e-05	0.0219881267942619
	RPTOR;RPTOR	3.2177393778972e-05	0.0220117461045207
N_Shelf		3.24002598615166e-05	0.0221329419709859
		3.24621053982526e-05	0.0221439566155052
Island	EFCAB1;EFCAB1;EFCAB	3.25680084419278e-05	0.022184951742105
N_Shore	MCM3AP	3.2697737476865e-05	0.0222137782747303

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Island	BANP;BANP	3.27071817412658e-05	0.0222137782747303
Island	GRIK2;GRIK2;GRIK2	3.27893615224122e-05	0.0222137782747303
		3.27937881927056e-05	0.0222137782747303
S_Shore		3.28572921180336e-05	0.022225709504283
Island	WNK4	3.30423667408037e-05	0.0222709828484291
N_Shore	CCDC40	3.30531629125366e-05	0.0222709828484291
Island	TMEM82	3.3062172442101e-05	0.0222709828484291
	PRKCZ;PRKCZ;PRKCZ	3.32126055393634e-05	0.022332594963413
	CYFIP1;CYFIP1	3.32935874328375e-05	0.022332594963413
		3.33374332132762e-05	0.022332594963413
		3.33781831903728e-05	0.022332594963413
S_Shore	DOCK4	3.33841919238343e-05	0.022332594963413
Island	YY2;MBTPS2	3.35427446968249e-05	0.0224077101038479
N_Shore	CBFA2T3;CBFA2T3	3.36244217866436e-05	0.0224313334460278
	ATP2B2;ATP2B2	3.36960250099338e-05	0.0224481806230209
Island	HIST1H3J	3.38587936709822e-05	0.0224704368517408
		3.38721335771792e-05	0.0224704368517408
Island		3.38843073883544e-05	0.0224704368517408
S_Shore		3.39150143779952e-05	0.0224704368517408
	PHC3	3.40948355296482e-05	0.0225587175107881
Island	KIAA0415	3.41836587097719e-05	0.0225866309749117
	ZCCHC14	3.44332612627349e-05	0.0227110460716487
Island	CUX1;CUX1;CUX1	3.44746317959851e-05	0.0227110460716487
S_Shelf	HCCA2;CTSD	3.45126307928219e-05	0.0227110460716487
Island	COL22A1	3.46342648720979e-05	0.0227297275786092
Island		3.46414840263772e-05	0.0227297275786092
Island		3.46925705456936e-05	0.0227297275786092
	CSNK2A2	3.47287429064591e-05	0.0227297275786092
Island		3.4875272934234e-05	0.0227413367999621
Island	KIAA1161	3.48774113858697e-05	0.0227413367999621
S_Shore	RET;RET	3.49184405641776e-05	0.0227413367999621
N_Shelf	RPTOR;RPTOR	3.49786699866192e-05	0.0227413367999621
Island	C9orf167	3.50340495058916e-05	0.0227413367999621
Island		3.50620584625716e-05	0.0227413367999621
Island	GALR1	3.51485624417479e-05	0.0227413367999621
Island		3.52082636940821e-05	0.0227413367999621
Island	ERICH1	3.52898574989102e-05	0.0227413367999621
N_Shore	NRN1	3.5293832678096e-05	0.0227413367999621
		3.53531166558702e-05	0.0227413367999621
Island		3.53641551416003e-05	0.0227413367999621
Island	HDAC4	3.53683981865321e-05	0.0227413367999621
Island		3.54038464815392e-05	0.0227413367999621
Island		3.54805215400066e-05	0.0227449629201969
N_Shore	FOXG1	3.55034160278095e-05	0.0227449629201969
Island	PAX1	3.5712905068859e-05	0.0228337449692146
	NINJ1	3.58437881803064e-05	0.0228337449692146
	ATP11A;ATP11A	3.58477855167814e-05	0.0228337449692146
Island		3.58565032525891e-05	0.0228337449692146
Island	SHROOM1	3.59032838994161e-05	0.0228337449692146
S_Shore	GAGE2A;GAGE2C;GAGE2D	3.59248720725578e-05	0.0228337449692146
		3.61240924181533e-05	0.0228885939890791
Island		3.61512966154266e-05	0.0228885939890791
N_Shelf	DDX41	3.61529435846704e-05	0.0228885939890791
S_Shelf		3.6260819910228e-05	0.0229048577967506
Island	C7orf20	3.62732172200644e-05	0.0229048577967506

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N_Shore	MRPL12	3.6378938445158e-05	0.022941704899025
Island	LDHAL6B;LDHAL6B;MY	3.64355445374127e-05	0.0229475228973764
Island		3.65851711675908e-05	0.0230118350983681
Island	DLX1;DLX1	3.66407069804544e-05	0.0230168747189476
		3.68408846588831e-05	0.0230887682752552
		3.68504988938673e-05	0.0230887682752552
N_Shelf	KPTN	3.69745088761761e-05	0.023136536190509
	CYFIP1	3.71248833401953e-05	0.0231575586860859
Island	PCDHB7	3.71568787019086e-05	0.0231575586860859
Island	CHRD1;CHRD1;CHR	3.72004700905959e-05	0.0231575586860859
N_Shore	PEG10;PEG10	3.73143721168472e-05	0.0231575586860859
	SNX29	3.73654803952666e-05	0.0231575586860859
Island	MIER2	3.73913011176834e-05	0.0231575586860859
S_Shelf	TSPY4	3.74551828790088e-05	0.0231575586860859
Island	ST8SIA5	3.75299742592526e-05	0.0231575586860859
Island	FAM101A	3.75410353237886e-05	0.0231575586860859
N_Shelf	C7orf50;C7orf50;C7orf50	3.75470428857615e-05	0.0231575586860859
Island	GDF1;LASS1	3.76058076214712e-05	0.0231575586860859
	NCALD;NCALD;NCALD	3.76234846056135e-05	0.0231575586860859
		3.76771295986326e-05	0.0231575586860859
Island	ARRDC2;ARRDC2;ARR	3.7677502182699e-05	0.0231575586860859
Island		3.77515555790312e-05	0.0231736655967228
Island	KCNA4	3.78600264757576e-05	0.0232108320542674
	USP10	3.8074271860809e-05	0.0233083051456234
Island	MAD1L1;MAD1L1;MAD1	3.82700886397956e-05	0.0233083051456234
N_Shore		3.83297034310744e-05	0.0233083051456234
Island	TRIM56	3.84743418227707e-05	0.0233083051456234
Island	CHRD1;CHRD1;CHR	3.85078513620689e-05	0.0233083051456234
	FAM53B	3.8512537240451e-05	0.0233083051456234
S_Shore	C1orf35	3.8527540568883e-05	0.0233083051456234
		3.85968148089226e-05	0.0233083051456234
Island		3.86237354777369e-05	0.0233083051456234
Island	CNKSR2;CNKSR2;CNK	3.87439531589689e-05	0.0233083051456234
		3.87445202058096e-05	0.0233083051456234
	WDR51B	3.87526907729024e-05	0.0233083051456234
Island	TRIM7;TRIM7;TRIM7;TF	3.87693830090432e-05	0.0233083051456234
Island	INS-IGF2;INS-IGF2	3.87793196867654e-05	0.0233083051456234
Island	MAST3	3.87806674892211e-05	0.0233083051456234
Island	GRM7;GRM7;GRM7;GR	3.87890237905796e-05	0.0233083051456234
	ARNT2	3.89274068938126e-05	0.0233366095096254
	STK32C	3.89324946756359e-05	0.0233366095096254
Island	TNK2;TNK2	3.91356631605131e-05	0.0234293943883999
Island	PUS3;DDX25	3.93281802334834e-05	0.0234449370624163
Island		3.9335364901579e-05	0.0234449370624163
	SNTG1	3.93475490456395e-05	0.0234449370624163
S_Shore	C6orf138	3.9355254904753e-05	0.0234449370624163
		3.94183040905122e-05	0.0234536488066798
		3.94909020986128e-05	0.0234567930165892
Island	ALDH4A1;ALDH4A1;AL	3.95204523853544e-05	0.0234567930165892
Island	SHROOM4;SHROOM4;	3.97043460793477e-05	0.0234778740365381
S_Shelf	RPTOR;RPTOR	3.97419296293053e-05	0.0234778740365381
Island	ZBTB12	3.9769245216043e-05	0.0234778740365381
		3.9802909164874e-05	0.0234778740365381
Island	SLC12A7	3.98292690486236e-05	0.0234778740365381
N_Shelf		3.98468228111998e-05	0.0234778740365381

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	RERE;RERE;RERE	4.00037926663951e-05	0.0235348937064652
N_Shelf	PTPRN2;PTPRN2;PTPRN2	4.00407833874513e-05	0.0235348937064652
Island	PTBP1;PTBP1;PTBP1;PTBP1	4.01201795394737e-05	0.0235472264586945
Island	AGAP4	4.02015358435152e-05	0.0235472264586945
	CPZ;CPZ;CPZ	4.02076214965991e-05	0.0235472264586945
	ANKRD26P1	4.03866506384288e-05	0.0235767724599625
Island	TNFAIP2	4.03904343581333e-05	0.0235767724599625
		4.04041111686758e-05	0.0235767724599625
S_Shelf	LRP5	4.04927683934357e-05	0.0236000722649227
Island	PCDHGA4;PCDHGA11;PCDHGA11	4.07403145675443e-05	0.023715808717459
	TRPC7;TRPC7;TRPC7	4.08085507053352e-05	0.0237270123893895
		4.0886900664607e-05	0.0237440625472252
		4.11180406832131e-05	0.023849694675326
Island		4.11995905368904e-05	0.0238684111085878
Island	NRK	4.13351283130847e-05	0.0238798333573322
		4.13626546703246e-05	0.0238798333573322
	TTC15	4.13672228086547e-05	0.0238798333573322
Island		4.15093722431664e-05	0.0238947445378406
	TMEM132D	4.1590075159173e-05	0.0238947445378406
N_Shelf	PCGF3	4.15902516760353e-05	0.0238947445378406
	ACTL7A	4.16849709716758e-05	0.0238947445378406
	P2RY6;P2RY6;P2RY6;P2RY6	4.18060686512043e-05	0.0238947445378406
S_Shore	PLCXD3	4.18476767901699e-05	0.0238947445378406
		4.18772731485741e-05	0.0238947445378406
	TBX22;TBX22;TBX22	4.19695827276084e-05	0.0238947445378406
Island	APOA5;APOA5	4.2039581207227e-05	0.0238947445378406
S_Shore		4.21040123449657e-05	0.0238947445378406
	NFIA;NFIA;NFIA;NFIA	4.21098340793701e-05	0.0238947445378406
N_Shelf	MAEA;MAEA	4.21188177198366e-05	0.0238947445378406
Island	NHSL1;NHSL1	4.21376298539486e-05	0.0238947445378406
	XKR4;SBF1P1	4.21401790746104e-05	0.0238947445378406
Island		4.21532878424719e-05	0.0238947445378406
		4.22119781162811e-05	0.0238947445378406
Island	HPSE2;HPSE2;HPSE2;HPSE2	4.22317685942116e-05	0.0238947445378406
Island	FGFRL1;FGFRL1;FGFRL1	4.23770761434482e-05	0.0239364904508935
Island	NFYA;NFYA;LOC22144	4.24043954098315e-05	0.0239364904508935
		4.2543459827475e-05	0.0239563481333401
Island	DAK	4.25586302121359e-05	0.0239563481333401
N_Shore	MED25	4.25879641620932e-05	0.0239563481333401
		4.26384457912727e-05	0.0239569202527357
Island		4.27697886493615e-05	0.0240028712486698
Island	RIN3	4.29796831848005e-05	0.0240569677688434
	XKR6	4.29989060060768e-05	0.0240569677688434
Island	LOC134466	4.30418466366937e-05	0.0240569677688434
Island	RUNDC2A	4.3184388081213e-05	0.0240569677688434
Island	ZSCAN18;ZSCAN18	4.32381011480438e-05	0.0240569677688434
Island		4.33363873110788e-05	0.0240569677688434
Island	LRRC4B	4.33510705776056e-05	0.0240569677688434
Island	C15orf39	4.33835063816875e-05	0.0240569677688434
	TNXB	4.33906800129361e-05	0.0240569677688434
Island	ZIC3	4.33990541826119e-05	0.0240569677688434
		4.34125635264938e-05	0.0240569677688434
	ALLC	4.35378465563566e-05	0.0240988200381799
Island	KCNQ1DN	4.36187926433328e-05	0.0241160636381075
		4.37691356902289e-05	0.02416700066689

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Island		4.38107192185608e-05	0.02416700066689
	SPDYE1;POLR2J4	4.38853916575379e-05	0.0241806510973118
Island		4.39851031944694e-05	0.024208051255297
	BZW2;BZW2;BZW2	4.41472918451418e-05	0.0242564038621642
	DMKN;DMKN;DMKN;DMKN	4.41731238454113e-05	0.0242564038621642
Island	CBFA2T3;CBFA2T3	4.46307059884148e-05	0.0244601985093922
S_Shelf	PLCB3	4.46452598612558e-05	0.0244601985093922
Island	SP9	4.47373380721705e-05	0.0244829505783096
N_Shelf		4.48413342002376e-05	0.0245121661247518
Island	KIAA0182;KIAA0182	4.49071091998333e-05	0.0245125994989148
Island	ZPBP2;ZPBP2	4.49433507562821e-05	0.0245125994989148
	COL23A1	4.50713511704531e-05	0.0245547605800109
	NOM1	4.53432042429967e-05	0.0245984279468257
	C4A;C4B	4.53954845668935e-05	0.0245984279468257
	GPR133	4.54013528922239e-05	0.0245984279468257
S_Shore	EDAR	4.54111494868246e-05	0.0245984279468257
	GEMIN8;GEMIN8;GEMIN8	4.55001553144277e-05	0.0245984279468257
N_Shore		4.55256298549857e-05	0.0245984279468257
	CYP26B1	4.55662739867775e-05	0.0245984279468257
Island	AGAP1;AGAP1	4.55701983761911e-05	0.0245984279468257
		4.56086064032406e-05	0.0245984279468257
	CCNB1IP1;CCNB1IP1;CCNB1IP1	4.57344742353719e-05	0.0246388756774711
		4.58310553357459e-05	0.0246634731949835
N_Shore	FAM20C	4.59043024235509e-05	0.0246754731090858
Island	GFI1;GFI1	4.60326469085007e-05	0.0246799891893358
Island	SSTR1	4.60848386634116e-05	0.0246799891893358
Island	TLX3	4.61947329799951e-05	0.0246799891893358
		4.62857674579598e-05	0.0246799891893358
		4.63060444914218e-05	0.0246799891893358
Island	HDAC4	4.63534390049561e-05	0.0246799891893358
	C7orf60	4.63627630375351e-05	0.0246799891893358
	MYH16	4.64088452386684e-05	0.0246799891893358
		4.6515320989259e-05	0.0246799891893358
Island	TRIO	4.65365581866648e-05	0.0246799891893358
Island	SLC29A4;SLC29A4	4.65631171481373e-05	0.0246799891893358
N_Shore	TOLLIP	4.68158799990368e-05	0.0246799891893358
	ADD3;ADD3;ADD3	4.68526847727193e-05	0.0246799891893358
N_Shelf	SPATA2L	4.69317146398706e-05	0.0246799891893358
Island		4.69661027689664e-05	0.0246799891893358
Island	NUDT10	4.69961567938659e-05	0.0246799891893358
Island	MIER2	4.70667845721406e-05	0.0246799891893358
Island		4.70841753012817e-05	0.0246799891893358
Island	DYSF;DYSF;DYSF;DYSF	4.70932294624612e-05	0.0246799891893358
Island		4.71458290574716e-05	0.0246799891893358
Island		4.7185087522851e-05	0.0246799891893358
Island		4.72164076934538e-05	0.0246799891893358
Island		4.72183901242938e-05	0.0246799891893358
	KIF13B	4.73058479789099e-05	0.0246799891893358
N_Shelf	ZIC4;ZIC4;ZIC4	4.73408711916926e-05	0.0246799891893358
Island	VWCE	4.74379025634494e-05	0.0246799891893358
	ATP9A	4.74513642071205e-05	0.0246799891893358
	PTPRN2;PTPRN2;PTPRN2	4.74877739414496e-05	0.0246799891893358
Island	PDZD4	4.7549786587459e-05	0.0246799891893358
N_Shore	TMEM8A	4.76152373407255e-05	0.0246799891893358
	MGMT	4.7646285572035e-05	0.0246799891893358

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Island	RAGE	4.76871616612121e-05	0.0246799891893358
S_Shore		4.7689705441734e-05	0.0246799891893358
N_Shore	HEATR2	4.77057000846878e-05	0.0246799891893358
Island	CRHBP	4.7735406119952e-05	0.0246799891893358
Island	AGRN	4.78071008256914e-05	0.0246799891893358
Island	PAPOLB;RADIL;PAPOL	4.79179748562701e-05	0.0246799891893358
		4.79730252657109e-05	0.0246799891893358
Island	FTHL17	4.79945585633173e-05	0.0246799891893358
		4.80159768644429e-05	0.0246799891893358
Island		4.80184610754659e-05	0.0246799891893358
Island	SLIT3;SLIT3	4.81932908628534e-05	0.0246799891893358
Island	BHLHA15	4.81997544086809e-05	0.0246799891893358
Island	LRBA;MAB21L2;MAB21	4.82305762901845e-05	0.0246799891893358
Island	MEI1	4.82945151251389e-05	0.0246799891893358
Island		4.83714237670808e-05	0.0246799891893358
Island	ADCK5	4.83907545547402e-05	0.0246799891893358
		4.84180620174457e-05	0.0246799891893358
N_Shore	PPT2;PRRT1;PPT2	4.84516517932638e-05	0.0246799891893358
Island	A2BP1;A2BP1;A2BP1;A	4.85293021991566e-05	0.0246799891893358
N_Shelf		4.85864425598229e-05	0.0246799891893358
	NDUFA10	4.86375848008334e-05	0.0246799891893358
	AGPAT3	4.865389766635e-05	0.0246799891893358
Island	PCDH11X	4.8664408559987e-05	0.0246799891893358
Island	RPTOR;RPTOR	4.87272204592963e-05	0.024685994821076
Island		4.88709905940852e-05	0.0246895443938076
	FAT1	4.8872145821283e-05	0.0246895443938076
Island	LOC645323	4.89607347226636e-05	0.0246895443938076
N_Shore	GOLGA3	4.89643101228433e-05	0.0246895443938076
Island	ARHGAP23	4.90334302115851e-05	0.0246895443938076
	MAGEB2	4.90686297134052e-05	0.0246895443938076
Island	NCRNA00200	4.91352884136965e-05	0.0246895443938076
Island	CLEC3B	4.91420446923668e-05	0.0246895443938076
Island		4.93411235107727e-05	0.0247638752791243
N_Shore	GALNS	4.9427906802534e-05	0.024781750478403
Island	CLDN10;CLDN10	4.95459864304299e-05	0.0248041613917176
Island	SYDE1	4.957503376283e-05	0.0248041613917176
Island	INPP5A	4.97560775748622e-05	0.0248690529117081
Island		4.98299545242877e-05	0.0248803017783254
Island	HOXB4	4.99564422651335e-05	0.0249063868219787
	MSI2;MSI2	5.0007835039975e-05	0.0249063868219787
S_Shore	ADAP1	5.00537178474435e-05	0.0249063868219787
		5.01054291152714e-05	0.0249063868219787
	LMF1	5.01393220490977e-05	0.0249063868219787
Island		5.02469131064423e-05	0.024934258391678
N_Shore	SLC12A6;SLC12A6;SLC	5.04328541254497e-05	0.0249638585738724
Island	ANKRD30A	5.04342663480292e-05	0.0249638585738724
		5.04859523705464e-05	0.0249638585738724
Island	SLC35F3	5.05127371132916e-05	0.0249638585738724
	SLC15A4;MGC16384	5.05859428429612e-05	0.0249745532797321
		5.06460606464075e-05	0.0249787712042478
Island	ABT1	5.07432586411661e-05	0.0250012499912337
Island		5.0833289223787e-05	0.0250201552879173
Island		5.09524309786536e-05	0.0250533361763822
Island		5.10632053577563e-05	0.0250823396905632
N_Shore	BICD2;BICD2	5.12567659778858e-05	0.0250975370098509

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Island	TFAP2E	5.12936239099943e-05	0.0250975370098509
		5.13577553964319e-05	0.0250975370098509
	TBC1D14;TBC1D14;TB	5.13983005787849e-05	0.0250975370098509
		5.15364304933546e-05	0.0250975370098509
N_Shelf	C17orf101;C17orf101	5.15670763543058e-05	0.0250975370098509
		5.1590885289645e-05	0.0250975370098509
S_Shore	GSPT2	5.16237628704005e-05	0.0250975370098509
S_Shelf	FAM90A1	5.16434260934541e-05	0.0250975370098509
Island	STXBP2;STXBP2	5.16602534572702e-05	0.0250975370098509
Island	MIR596	5.16641602205572e-05	0.0250975370098509
Island	FBXO21;FBXO21	5.17571557564524e-05	0.0251175195007453
N_Shore	TCF3;TCF3	5.19275027001681e-05	0.0251712383093673
N_Shore	C10orf93	5.19926624232355e-05	0.0251712383093673
Island	ZNF787	5.20265473323119e-05	0.0251712383093673
Island	ZBTB12	5.20874144760764e-05	0.0251712383093673
Island	WNT7B	5.21277076844999e-05	0.0251712383093673
Island	ELK1;ELK1	5.23202043682697e-05	0.0252116911963067
S_Shore	PTPRN2;PTPRN2;PTPF	5.23578814270342e-05	0.0252116911963067
Island	ARHGEF1;ARHGEF1;A	5.23676484663905e-05	0.0252116911963067
Island		5.24477277730219e-05	0.0252251695667019
	RIMBP2	5.26313320464275e-05	0.0252789344057338
	TAP2;TAP2	5.26639029894913e-05	0.0252789344057338
Island	PDZRN4;PDZRN4	5.28211626994763e-05	0.0253293164598256
	RRM1	5.30495513008239e-05	0.0253920593207507
S_Shore	PAPOLB;RADIL	5.30788040562753e-05	0.0253920593207507
N_Shelf	SKI	5.31214594724241e-05	0.0253920593207507
Island	LASS3	5.32077018095811e-05	0.0253920593207507
S_Shore		5.32141438302008e-05	0.0253920593207507
Island	KIF26A	5.33797496414564e-05	0.0254255192304032
		5.33892593967274e-05	0.0254255192304032
Island	NTRK3;NTRK3;NTRK3;	5.35103214107467e-05	0.0254410748490556
Island	LRP5	5.35269814095651e-05	0.0254410748490556
Island	TSC2;TSC2;TSC2	5.38381757707678e-05	0.0255631738443119
	EXOC7;EXOC7;EXOC7	5.38932378760729e-05	0.0255631738443119
	DOCK1	5.39422158032039e-05	0.0255631738443119
		5.40069590104719e-05	0.0255688371678854
N_Shore	FRMPD4	5.43504797239855e-05	0.0255979076339981
	POLE	5.4369059597113e-05	0.0255979076339981
Island	MIR369;MIR410;MIR656	5.43837361027118e-05	0.0255979076339981
	LIPC	5.4472229438745e-05	0.0255979076339981
Island	SRCIN1	5.44928485964874e-05	0.0255979076339981
	GPLD1;GPLD1	5.45425189067926e-05	0.0255979076339981
		5.4727956663162e-05	0.0255979076339981
S_Shore		5.4729456551163e-05	0.0255979076339981
Island	SH2B2	5.47385136157448e-05	0.0255979076339981
Island		5.47587663703391e-05	0.0255979076339981
N_Shelf	ADPRHL1;ADPRHL1	5.47801556050873e-05	0.0255979076339981
		5.49131511593476e-05	0.0255979076339981
Island		5.49167347935089e-05	0.0255979076339981
Island	PLCH2	5.49170470448088e-05	0.0255979076339981
Island	SGTA	5.49857435223479e-05	0.0255979076339981
N_Shelf	ACADS	5.49994830889858e-05	0.0255979076339981
Island		5.50350165516141e-05	0.0255979076339981
Island	KCNG2	5.51042262204913e-05	0.0255979076339981
Island		5.51444750267372e-05	0.0255979076339981

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Island		5.51462905166607e-05	0.0255979076339981
Island	TRRAP	5.51782699011903e-05	0.0255979076339981
N_Shore	TSNARE1	5.52919650140198e-05	0.0256172736870166
Island	GAL3ST1	5.53258003956422e-05	0.0256172736870166
		5.54537163302699e-05	0.0256519781868749
Island	KIAA1549;KIAA1549	5.5540997112709e-05	0.0256541567719248
Island	TMEM151A	5.55673177966957e-05	0.0256541567719248
Island	NRBP2	5.56211633498721e-05	0.0256541567719248
S_Shelf	RICH2	5.56703014861776e-05	0.0256541567719248
		5.58583124569444e-05	0.0257163281185452
Island	MYF5;MYF5	5.60758457933256e-05	0.0257564178777466
		5.60950065543782e-05	0.0257564178777466
Island	TMPRSS9	5.61169390743126e-05	0.0257564178777466
Island	ATP6V0A1;ATP6V0A1;A	5.61581113485787e-05	0.0257564178777466
Island	MAEA;MAEA	5.63182362604316e-05	0.0258054207917063
Island	TRAPPC9;TRAPPC9	5.64883049849581e-05	0.0258292510716287
Island		5.64902953893716e-05	0.0258292510716287
Island	TMEM160	5.6530235143605e-05	0.0258292510716287
		5.68000800849027e-05	0.0259280855675028
	SDK1	5.68769952842464e-05	0.0259341717102339
N_Shelf	CACNA1H;CACNA1H	5.69417923386077e-05	0.0259341717102339
	EBF3	5.69740539920277e-05	0.0259341717102339
S_Shore	CKAP4	5.7070956408818e-05	0.0259538882278881
Island	ERO1L	5.71957276338096e-05	0.0259862296306237
	CSMD1	5.73785929064133e-05	0.0260448800462967
Island	ALDH4A1;ALDH4A1;AL	5.75588957998558e-05	0.0260882231178095
Island	RUNX1	5.75818107942773e-05	0.0260882231178095
Island	BANP;BANP	5.77042985950801e-05	0.0260996458740357
N_Shelf	PRMT2;PRMT2	5.77729815759653e-05	0.0260996458740357
		5.77775274075971e-05	0.0260996458740357
	RAB40A	5.78549997217906e-05	0.0260996458740357
Island		5.78764665642168e-05	0.0260996458740357
	SNX29	5.80253355406181e-05	0.0261424378006603
		5.82261959640605e-05	0.0261440641217451
		5.82650062610855e-05	0.0261440641217451
		5.85181511686875e-05	0.0261440641217451
	ACSF3;ACSF3;ACSF3	5.85856195019009e-05	0.0261440641217451
Island	INSL3	5.86052214487592e-05	0.0261440641217451
Island	C20orf85	5.86528417166237e-05	0.0261440641217451
Island	KCNE1L;KCNE1L	5.8657012173089e-05	0.0261440641217451
Island	C2orf65	5.86914987464786e-05	0.0261440641217451
	GRAMD1B	5.87102544633524e-05	0.0261440641217451
S_Shelf	DCAF4;DCAF4;DCAF4;	5.87400858291402e-05	0.0261440641217451
		5.87470862428765e-05	0.0261440641217451
S_Shore	TERT;TERT	5.88307347138788e-05	0.0261440641217451
N_Shore		5.88988393970553e-05	0.0261440641217451
S_Shore	TERT;TERT	5.8935163339451e-05	0.0261440641217451
Island	ACHE;ACHE	5.8970627790074e-05	0.0261440641217451
	SHANK2	5.90772618149202e-05	0.0261440641217451
	HCCA2	5.9083643489517e-05	0.0261440641217451
Island	FBL1	5.90896119482546e-05	0.0261440641217451
Island	FAM78B	5.90901842256753e-05	0.0261440641217451
	CARD11	5.91085535813987e-05	0.0261440641217451
	NTM	5.93387662802169e-05	0.0262219415863741
		5.94290393110591e-05	0.0262378937687591

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Island		5.95631439521806e-05	0.026264129381109
N_Shore	GTF2A1;GTF2A1	5.9640279475004e-05	0.026264129381109
	CD276;CD276	5.96511481323902e-05	0.026264129381109
Island	WDR60	5.97171743109936e-05	0.0262693192081489
Island		5.98862616194306e-05	0.0263197946087393
Island		6.00292515622468e-05	0.0263587191866593
	AKT1;AKT1;AKT1	6.02523784859295e-05	0.0264213733459586
N_Shelf	OSBPL5;OSBPL5;OSBPL5	6.03277199229506e-05	0.0264213733459586
S_Shore	IQCE;IQCE	6.03650527870594e-05	0.0264213733459586
	ABCC5	6.04524686079553e-05	0.0264213733459586
N_Shore		6.04548612250762e-05	0.0264213733459586
Island	AKR7L;AKR7L	6.04992578137988e-05	0.0264213733459586
Island		6.06298749300178e-05	0.0264545623202531
Island	MAEL;MAEL	6.07616826267613e-05	0.0264882105654421
N_Shore	TTY20	6.10766332702046e-05	0.026528148483246
Island		6.11143453846679e-05	0.026528148483246
		6.133355360571e-05	0.026528148483246
N_Shore	PAX6;PAX6;PAX6	6.14816587252367e-05	0.026528148483246
	NXN	6.14952199144713e-05	0.026528148483246
	HCN4	6.16010661635462e-05	0.026528148483246
Island	ADAMTS7	6.16060814090558e-05	0.026528148483246
Island	COL4A2	6.16695509533029e-05	0.026528148483246
Island	WNK2	6.17954255119882e-05	0.026528148483246
S_Shore	HDAC4	6.18096362409541e-05	0.026528148483246
		6.18235335930325e-05	0.026528148483246
		6.18249662125746e-05	0.026528148483246
N_Shore		6.19055146777524e-05	0.026528148483246
Island		6.1988772114202e-05	0.026528148483246
		6.20148389279014e-05	0.026528148483246
Island	POM121L1P	6.2131603442229e-05	0.026528148483246
Island	ZFAT;ZFAT	6.21575375334423e-05	0.026528148483246
	LOC285768;LOC285768	6.21591595121854e-05	0.026528148483246
	DAAM1	6.22630768529249e-05	0.026528148483246
Island	FMNL1	6.23098754361144e-05	0.026528148483246
N_Shelf	IL12B	6.23227441995668e-05	0.026528148483246
Island		6.23718615333178e-05	0.026528148483246
	RARA;RARA;RARA;RARA	6.2382636690084e-05	0.026528148483246
Island	KCNE1L	6.25572694604985e-05	0.026528148483246
N_Shelf	WDR8	6.26834769748289e-05	0.026528148483246
N_Shore	GPR12	6.27476092351854e-05	0.026528148483246
	TRAF3;TRAF3;TRAF3	6.27533973615917e-05	0.026528148483246
Island		6.27567003086567e-05	0.026528148483246
Island	VWC2;VWC2	6.27709390920156e-05	0.026528148483246
S_Shore	IFT140;TMEM204	6.28134125291259e-05	0.026528148483246
S_Shelf	MXRA5	6.28275421852327e-05	0.026528148483246
N_Shelf	MFI2;MFI2	6.28521824919221e-05	0.026528148483246
Island		6.29047822046541e-05	0.026528148483246
Island	MC5R	6.29166678467133e-05	0.026528148483246
N_Shelf		6.29442773369185e-05	0.026528148483246
S_Shore	CDX4	6.29603937894089e-05	0.026528148483246
Island	ALX4	6.30678052060304e-05	0.026528148483246
		6.31103437057442e-05	0.026528148483246
Island	RAI1	6.31568732494714e-05	0.026528148483246
S_Shore	DTX1	6.32380457506167e-05	0.026528148483246
Island	SPATS2	6.32553667778058e-05	0.026528148483246

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S_Shore	ZNF354C	6.33667757176197e-05	0.026528148483246
Island	ARHGAP6;ARHGAP6	6.33691938190467e-05	0.026528148483246
Island	PARD6A;ACD;ACD;PAF	6.33899504047608e-05	0.026528148483246
N_Shelf		6.34015317182088e-05	0.026528148483246
S_Shore	LOC154449	6.34146851221274e-05	0.026528148483246
	DOCK1	6.34276486730993e-05	0.026528148483246
S_Shore		6.36355103114175e-05	0.0265391345201277
Island	LOC650623	6.36557039151871e-05	0.0265391345201277
	SNTG1	6.36605790217233e-05	0.0265391345201277
Island	KIAA1875	6.36838554095359e-05	0.0265391345201277
Island		6.37352006031734e-05	0.0265391345201277
	MYH9	6.38138250866986e-05	0.0265391345201277
Island	C5orf47	6.39615073395553e-05	0.0265391345201277
Island		6.40639029486898e-05	0.0265391345201277
Island	PRDM16;PRDM16	6.42139119552839e-05	0.0265391345201277
S_Shore	KDM2B;KDM2B	6.43328648496729e-05	0.0265391345201277
Island		6.43536827245785e-05	0.0265391345201277
Island	DDX4;DDX4;DDX4;DDX4	6.44205491630438e-05	0.0265391345201277
		6.44600915451517e-05	0.0265391345201277
	C6orf208	6.45110521414382e-05	0.0265391345201277
	EGFR;EGFR;EGFR;EGFR	6.45205283185926e-05	0.0265391345201277
Island	TMEM171;TMEM171	6.45727511760824e-05	0.0265391345201277
	EP400	6.45928137222808e-05	0.0265391345201277
	SKI	6.4680801233025e-05	0.0265391345201277
Island		6.47094352051687e-05	0.0265391345201277
Island	ZNRF4	6.47186211915169e-05	0.0265391345201277
	GLT1D1	6.47382187069938e-05	0.0265391345201277
		6.47601476914372e-05	0.0265391345201277
	WARS;WARS;WARS;WARS	6.48325043569023e-05	0.0265391345201277
		6.48448748581734e-05	0.0265391345201277
Island	PVRL1;PVRL1	6.48750010903535e-05	0.0265391345201277
Island		6.49498568468811e-05	0.0265391345201277
N_Shore		6.49703141535391e-05	0.0265391345201277
N_Shore		6.5030094391717e-05	0.0265391345201277
Island	ACRBP	6.50430035108482e-05	0.0265391345201277
Island	CNTNAP1	6.51980348109924e-05	0.0265653601198635
S_Shore	PDE4B;PDE4B	6.52206242211783e-05	0.0265653601198635
Island	HLA-DPB1	6.53405905660978e-05	0.0265653601198635
	EIF2C2;EIF2C2	6.53486815224906e-05	0.0265653601198635
Island		6.54283522509473e-05	0.0265653601198635
N_Shore		6.54721971582557e-05	0.0265653601198635
Island		6.55167389014123e-05	0.0265653601198635
Island		6.56066192996116e-05	0.0265653601198635
Island	RPL10L;RPL10L	6.56943720983973e-05	0.0265653601198635
Island	RNF39;RNF39	6.57437994538087e-05	0.0265653601198635
Island	C6orf138;C6orf138	6.58231626114177e-05	0.0265653601198635
Island	OBSCN;OBSCN	6.58580797306875e-05	0.0265653601198635
Island	NCRNA00182	6.58873798532744e-05	0.0265653601198635
	MIR505	6.59063093992055e-05	0.0265653601198635
	PAGE2B	6.59934213108354e-05	0.0265653601198635
S_Shelf	PIGQ;PIGQ	6.60040983404435e-05	0.0265653601198635
Island	PHOX2A	6.60719937457885e-05	0.0265653601198635
Island	TDRD12	6.60945830680545e-05	0.0265653601198635
		6.61645581286975e-05	0.0265714341755235
Island	MRAP;MRAP	6.62914244408597e-05	0.0265731672408382

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N_Shore	PCDHGA4;PCDHGA2;P	6.63085284560069e-05	0.0265731672408382
Island	C7orf72	6.64406117237593e-05	0.0265731672408382
N_Shore		6.64804840228421e-05	0.0265731672408382
Island	PTPRT;PTPRT	6.64883389512033e-05	0.0265731672408382
Island	EFCAB1;EFCAB1;EFCA	6.64980719473409e-05	0.0265731672408382
Island	MRPL23	6.65807465476564e-05	0.0265842704630616
	TSSC1	6.66547272806947e-05	0.0265855659271745
	GLIPR1L1;GLIPR1L1	6.6693775050879e-05	0.0265855659271745
	GPATCH8	6.67820951408958e-05	0.026598880122627
Island	PLCD3	6.69440056721672e-05	0.0266153952304662
	LOC340094	6.69463186176111e-05	0.0266153952304662
Island		6.69884205563172e-05	0.0266153952304662
		6.70879036485204e-05	0.0266330728971882
Island	DNAJB6	6.74732953278321e-05	0.0267137329186344
		6.75174914850603e-05	0.0267137329186344
Island	ARHGAP6;ARHGAP6	6.75363887156314e-05	0.0267137329186344
		6.75617442369352e-05	0.0267137329186344
Island	ATP11A;ATP11A	6.75936790778612e-05	0.0267137329186344
Island	BRUNOL6	6.76220235549388e-05	0.0267137329186344
S_Shelf		6.78165931711644e-05	0.0267687624186016
S_Shelf		6.79188235100992e-05	0.0267712222450865
Island	ASZ1;ASZ1	6.79333756035952e-05	0.0267712222450865
S_Shore		6.81293655163223e-05	0.0268266300436527
Island	SEPT9;SEPT9;SEPT9;S	6.83720920123535e-05	0.026834256308086
	PTPRN2;PTPRN2;PTPF	6.83867637198191e-05	0.026834256308086
Island	DNAJB6	6.83986949422283e-05	0.026834256308086
Island		6.84084542982264e-05	0.026834256308086
S_Shore	CDC42BPG	6.84504002467369e-05	0.026834256308086
	SLC16A14	6.85334989097377e-05	0.026834256308086
	SH2D4B;SH2D4B	6.86829492781189e-05	0.026834256308086
Island	BCAN;BCAN	6.87072379617972e-05	0.026834256308086
	IFT140	6.87458482417504e-05	0.026834256308086
	AHRR	6.87474338896391e-05	0.026834256308086
N_Shelf	MUC4;MUC4;MUC4	6.87650521019432e-05	0.026834256308086
		6.89527804913125e-05	0.026834256308086
Island	TAF7L;TAF7L	6.89600955593954e-05	0.026834256308086
	AGAP1;AGAP1	6.89668476167967e-05	0.026834256308086
Island	C6orf174	6.89798154205691e-05	0.026834256308086
N_Shelf	PTPRN2;PTPRN2;PTPF	6.90820470028132e-05	0.0268524577966593
Island	B4GALNT1	6.9366932291716e-05	0.0269415713570051
S_Shore		6.94273009981728e-05	0.0269434115031571
N_Shelf	GABARAPL3	6.96180178467403e-05	0.026995793829962
S_Shore	ARX	6.97030108520805e-05	0.0270071285847471
	RPH3AL	6.99151898913778e-05	0.0270676853270516
		7.00854743307964e-05	0.0271100023159421
N_Shelf		7.01393748480815e-05	0.0271100023159421
		7.02684425183403e-05	0.0271100023159421
Island	PCDHA6;PCDHA2;PCD	7.02883523615274e-05	0.0271100023159421
	NKD2	7.04910676534747e-05	0.0271100023159421
	DIP2C	7.05230713854063e-05	0.0271100023159421
Island	FLJ30058;FLJ30058	7.05253901657392e-05	0.0271100023159421
Island	SPTBN2	7.05801194243489e-05	0.0271100023159421
	NLRP8	7.05801901734997e-05	0.0271100023159421
Island		7.06396192577027e-05	0.0271100023159421
Island	UNCX	7.06402166370079e-05	0.0271100023159421

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	DOC2A	7.09041357418333e-05	0.027189743106226
N_Shore		7.10339605253492e-05	0.027199960540888
Island		7.10431013972504e-05	0.027199960540888
Island	CPLX1	7.12250703027492e-05	0.0272211672875768
N_Shore	ZNF326;LOC492303;ZNF	7.12331276886922e-05	0.0272211672875768
Island	IL17RA	7.12806910771537e-05	0.0272211672875768
		7.1323308290786e-05	0.0272211672875768
Island	TSPYL5	7.15038021833665e-05	0.027265965203984
S_Shelf		7.15532788401664e-05	0.027265965203984
S_Shore	KIAA0182;KIAA0182	7.17027982339407e-05	0.0273014604989413
Island	RPL23AP53	7.18114291762453e-05	0.0273213436259113
		7.19024888624092e-05	0.0273345156344477
Island	MAD1L1;MAD1L1;MAD1	7.21630276687489e-05	0.0273942691707269
Island	C10orf47	7.21875571632239e-05	0.0273942691707269
	WVOX	7.2273691180063e-05	0.0273942691707269
Island	HAS1	7.22964026391283e-05	0.0273942691707269
S_Shore	PTPRN2;PTPRN2;PTPR	7.2413445140226e-05	0.0273942691707269
N_Shelf	ATP11A;ATP11A	7.24482817960536e-05	0.0273942691707269
Island		7.24556006972614e-05	0.0273942691707269
	DIP2C	7.2579020638819e-05	0.0274195274343963
		7.27342459457336e-05	0.0274567526638094
Island	WDR60	7.29136823798969e-05	0.0275030523509685
	LGR4	7.33641764696453e-05	0.0276514433997361
		7.34762834426977e-05	0.0276608132574265
	EBF3	7.35307349918904e-05	0.0276608132574265
	SKAP2	7.35603726331809e-05	0.0276608132574265
Island	LRP3	7.37887932524271e-05	0.0277096647600796
	GPR133	7.3840090124268e-05	0.0277096647600796
Island	AR	7.38990642537161e-05	0.0277096647600796
	AP2A2	7.391913873953e-05	0.0277096647600796
	SSX3;SSX3	7.40235249709885e-05	0.0277273346725244
Island	GALNS	7.40980227125684e-05	0.0277336956345719
S_Shore	LZTS1	7.41550319450175e-05	0.0277336956345719
Island	RAB11FIP3;RAB11FIP3	7.42608445895539e-05	0.0277518391634535
	BANP;BANP	7.44828942012343e-05	0.0277655247292394
	HDAC4	7.45817535380734e-05	0.0277655247292394
Island	TSPY4	7.46557628511869e-05	0.0277655247292394
S_Shore	LOXHD1	7.47072078540306e-05	0.0277655247292394
		7.48946145507999e-05	0.0277655247292394
N_Shore		7.50281516064547e-05	0.0277655247292394
Island		7.50649367232021e-05	0.0277655247292394
N_Shore	INPP5A	7.51157046827549e-05	0.0277655247292394
Island	C3	7.51771540626141e-05	0.0277655247292394
		7.51822040571564e-05	0.0277655247292394
Island	DIRAS1	7.51933067066274e-05	0.0277655247292394
Island	C18orf1;C18orf1	7.52315092478836e-05	0.0277655247292394
Island	PTDSS2	7.52519839508285e-05	0.0277655247292394
Island	LOC100128675;HPN;HPN	7.52884713421017e-05	0.0277655247292394
		7.53846540984253e-05	0.0277655247292394
Island	BCOR;BCOR	7.54764851416153e-05	0.0277655247292394
	AHRR	7.55077707475296e-05	0.0277655247292394
Island	CELSR2	7.55203400998218e-05	0.0277655247292394
Island	AIRE;AIRE	7.55227430896415e-05	0.0277655247292394
Island	EGFLAM	7.55465804260722e-05	0.0277655247292394
		7.55635869264658e-05	0.0277655247292394

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S_Shore	MSRA;MSRA;MSRA	7.55713335863524e-05	0.0277655247292394
N_Shore	IQSEC1;IQSEC1	7.56160163482511e-05	0.0277655247292394
		7.58017968421389e-05	0.0278126554966431
Island	FMR1NB	7.59039791041626e-05	0.0278290648596696
	ADCY2	7.59887991940361e-05	0.0278390886305987
N_Shore	CPNE7;CPNE7	7.62696402470989e-05	0.0279011034797078
		7.63082859801742e-05	0.0279011034797078
	PTPRN2;PTPRN2;PTPF	7.63425563481817e-05	0.0279011034797078
S_Shore	FOXK1	7.63885060942394e-05	0.0279011034797078
	VARS	7.67311371885051e-05	0.0280051303834384
Island	NRXN3;NRXN3;NRXN3	7.70598809722021e-05	0.0280260645879384
	CDR1	7.70746497669522e-05	0.0280260645879384
Island	EMILIN2	7.71470609559726e-05	0.0280260645879384
	SHANK2	7.71575778523575e-05	0.0280260645879384
N_Shelf	VIPR2	7.7255544585082e-05	0.0280260645879384
N_Shore		7.7325560392015e-05	0.0280260645879384
Island	RNF39;RNF39	7.73258226100785e-05	0.0280260645879384
Island	MAPK8IP3;MAPK8IP3	7.73276457487622e-05	0.0280260645879384
	DENND1A;DENND1A	7.73423386382557e-05	0.0280260645879384
	CLEC16A	7.73671570826896e-05	0.0280260645879384
Island	TF	7.74299060928601e-05	0.0280278320391812
Island		7.75646533587118e-05	0.0280498763186519
Island	SLC25A31	7.76066365911186e-05	0.0280498763186519
	TRAPPC9;TRAPPC9	7.77312383455555e-05	0.0280739612317011
N_Shore		7.78223950688547e-05	0.0280859400087355
Island		7.79711522462903e-05	0.0281186733519617
	ZNF645	7.80840589914894e-05	0.0281384388921526
Island		7.81584986070504e-05	0.0281443232995239
Island		7.82433758789034e-05	0.0281517004062262
		7.83684012081875e-05	0.0281517004062262
	BBX;BBX	7.84090946157576e-05	0.0281517004062262
Island	BAHCC1	7.84372643945669e-05	0.0281517004062262
N_Shelf	ABCA17P	7.85544049393375e-05	0.0281517004062262
	PACSIN1	7.85880393139411e-05	0.0281517004062262
Island	ZNF219;ZNF219;ZNF21	7.86623944396767e-05	0.0281517004062262
Island	FZD9	7.86634203817432e-05	0.0281517004062262
Island		7.8702116037847e-05	0.0281517004062262
N_Shore	P4HB	7.88126070671676e-05	0.0281704176515173
Island	COASY;COASY;COASY	7.8905721512037e-05	0.0281829008638033
Island	ANKRD29	7.90316876409291e-05	0.0282070907271135
Island	KCNAB3	7.9102260428786e-05	0.0282114891621294
Island		7.9211647913793e-05	0.0282297140366798
Island		7.93207995075494e-05	0.0282478281040396
	CARD11	7.95095570594461e-05	0.0282751262184578
Island		7.95142144418304e-05	0.0282751262184578
Island	ADPRHL1;ADPRHL1	7.99319616064039e-05	0.0283896517570105
	JAKMIP1	7.99535126135597e-05	0.0283896517570105
S_Shore	PHLDA3	8.00392578602301e-05	0.0283964789846733
Island		8.00900021536442e-05	0.0283964789846733
	ELAC2;ELAC2;ELAC2	8.02990485509065e-05	0.0284375975054406
Island		8.03367921885722e-05	0.0284375975054406
N_Shelf	COMMD8	8.03821214782392e-05	0.0284375975054406
	PRKAR1B;PRKAR1B;PR	8.05136610749052e-05	0.0284501955495021
Island	CYHR1	8.05352151930365e-05	0.0284501955495021
Island	IGSF22	8.07378270400672e-05	0.0285009825664581

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Island	MAGEB1;MAGEB1;MAG	8.07988722076445e-05	0.0285017580349362
S_Shore	MAZ;MAZ	8.09623218498271e-05	0.0285304815439535
Island		8.10253557759321e-05	0.0285304815439535
	PITPNM2	8.11719271113562e-05	0.0285304815439535
		8.11726135378441e-05	0.0285304815439535
Island	HOXA3;HOXA3;HOXA3	8.12150859382438e-05	0.0285304815439535
S_Shelf		8.12345455138038e-05	0.0285304815439535
Island	NTSR2	8.12926537565803e-05	0.0285304815439535
Island	GNG7	8.15286342643811e-05	0.0285925820348272
Island		8.16709034370363e-05	0.0286155166942497
Island		8.17121965377532e-05	0.0286155166942497
	CTNNA2;CTNNA2	8.1786336714291e-05	0.0286207857869573
Island	MIER2	8.19930136102601e-05	0.0286602145117307
	FLJ35220;FLJ35220	8.20173588257033e-05	0.0286602145117307
	VPS37C	8.21640859453548e-05	0.0286907865360375
S_Shore	MTUS2;MTUS2	8.22869017023611e-05	0.0287129709416398
Island	ETS2	8.23824729665858e-05	0.0287256236281797
N_Shore	TBCD	8.26176040288065e-05	0.0287813305538336
	NMS	8.26610866678006e-05	0.0287813305538336
Island	LMX1B	8.27473725219486e-05	0.0287831113691705
Island	SIX6	8.27850599024509e-05	0.0287831113691705
		8.29660137213092e-05	0.028791399115048
S_Shore	POLS	8.29881060840173e-05	0.028791399115048
Island	TEX14;TEX14	8.30156691200595e-05	0.028791399115048
Island		8.30466826278265e-05	0.028791399115048
N_Shelf	ABCB6	8.31370299657765e-05	0.0288021044622136
		8.33464637963177e-05	0.0288356151157503
Island	GNA12	8.33838014641984e-05	0.0288356151157503
		8.34596777763577e-05	0.0288356151157503
	ANKRD33B	8.34934847697543e-05	0.0288356151157503
Island	ZFYVE28	8.3606335966858e-05	0.0288356151157503
	SMYD2	8.36901686456939e-05	0.0288356151157503
Island	CACNG2	8.36974427766671e-05	0.0288356151157503
		8.37100600892891e-05	0.0288356151157503
	MSI2;MSI2	8.38882161832447e-05	0.0288567956699201
		8.38907103768078e-05	0.0288567956699201
Island	GGT7	8.41030803451561e-05	0.0289093146828728
	RBM25	8.43322794120845e-05	0.0289675398767786
S_Shore	GALNS	8.44287068552099e-05	0.0289801087509919
	CRISP2;CRISP2;CRISP	8.46629875690961e-05	0.0290201815105119
	ADAM12;ADAM12	8.46652897834168e-05	0.0290201815105119
Island	OBSCN;OBSCN	8.4761073211219e-05	0.0290246606390673
Island	SMOC2;SMOC2	8.48146651232275e-05	0.0290246606390673
	PLK1	8.48581416712317e-05	0.0290246606390673
Island	PCDHGA2;PCDHGA3;P	8.49706308366566e-05	0.0290361411030824
	MAD1L1;MAD1L1;MAD	8.50116101464324e-05	0.0290361411030824
Island		8.51731043416039e-05	0.0290411099867653
Island		8.52747425777423e-05	0.0290411099867653
Island		8.5280498091692e-05	0.0290411099867653
N_Shore	B3GNTL1	8.53927745429675e-05	0.0290411099867653
Island		8.53965804077772e-05	0.0290411099867653
Island	LMX1A	8.5447483469675e-05	0.0290411099867653
		8.54700081294473e-05	0.0290411099867653
Island		8.55058542117944e-05	0.0290411099867653
		8.56279105485345e-05	0.0290621848468248

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Island		8.57206302756879e-05	0.029073280292908
Island	FOXK1	8.59446129569286e-05	0.0291213146788124
Island	PCDHA2;PCDHA1;PCD	8.59825117239494e-05	0.0291213146788124
Island	ATAD3A;ATAD3A;ATAD	8.60441034528633e-05	0.0291218102060154
Island	BEND4;BEND4	8.61126485775347e-05	0.0291246567893258
N_Shore	EP400NL	8.61948658037732e-05	0.0291321202933792
Island	ZBTB7A	8.64382553797261e-05	0.0291884080855053
	HK1;HK1;HK1;HK1;HK1	8.64819400251898e-05	0.0291884080855053
	LOC641746	8.65757414657162e-05	0.0291907787235626
	PRDM16;PRDM16	8.66501831515887e-05	0.0291907787235626
Island	FZR1;FZR1;FZR1	8.67194991611321e-05	0.0291907787235626
S_Shore	HRNBP3	8.6773640858566e-05	0.0291907787235626
S_Shore		8.67916166986726e-05	0.0291907787235626
Island	SDF4;SDF4;B3GALT6	8.68505902867987e-05	0.0291907787235626
S_Shore	BANP;BANP	8.70283919453388e-05	0.0292233059669421
	CSMD1	8.7068542453092e-05	0.0292233059669421
		8.71283824214411e-05	0.0292233059669421
N_Shelf	ATP11A;ATP11A	8.73753164361413e-05	0.0292637788526227
N_Shore	MUC6	8.73821151553185e-05	0.0292637788526227
	MGC23284;MGC23284	8.74303164192332e-05	0.0292637788526227
		8.7581680374312e-05	0.02928245035904
	ABR;ABR;ABR	8.77112550078113e-05	0.02928245035904
	ZFH4	8.77284651153934e-05	0.02928245035904
Island	CACNA1A;CACNA1A	8.77378176384144e-05	0.02928245035904
Island		8.77987242514162e-05	0.02928245035904
Island	ATP11A;ATP11A	8.78488625854234e-05	0.02928245035904
N_Shore		8.80424972271618e-05	0.0293268105017504
Island	SLC25A22	8.82964255396103e-05	0.0293469978791288
Island		8.83659933014081e-05	0.0293469978791288
N_Shelf	RBPJ;RBPJ;RBPJ;RBPJ	8.83996393965658e-05	0.0293469978791288
S_Shore	BANP;BANP	8.84038809332956e-05	0.0293469978791288
Island	PFKP	8.84752726464484e-05	0.0293469978791288
Island	SLC8A2	8.85254949326962e-05	0.0293469978791288
		8.85978416591328e-05	0.0293469978791288
N_Shelf		8.86717464799378e-05	0.0293469978791288
	GEMIN4	8.86976426032462e-05	0.0293469978791288
Island	TSSC1	8.87090381356416e-05	0.0293469978791288
Island	EPPK1	8.89291543946342e-05	0.0293513550239258
N_Shore	FOXK1	8.89695986777307e-05	0.0293513550239258
		8.90296091327615e-05	0.0293513550239258
	POLR1A	8.90666764839392e-05	0.0293513550239258
Island	TEX28;TKTL1;TKTL1	8.91177927314997e-05	0.0293513550239258
	DIP2C	8.91179978235131e-05	0.0293513550239258
Island	PTPRU;PTPRU;PTPRU	8.91608367496738e-05	0.0293513550239258
Island	CSGALNACT1;CSGALN	8.92132879970335e-05	0.0293513550239258
	ITSN2;ITSN2	8.9326949356042e-05	0.0293513550239258
N_Shore	BMP7	8.93342805051984e-05	0.0293513550239258
		8.93888373721996e-05	0.0293513550239258
S_Shelf	TOLLIP	8.96142659823394e-05	0.0294054399538595
		8.96787374752757e-05	0.0294066719889729
Island	NPHP4	8.99540968256621e-05	0.0294770080819275
S_Shore	DIABLO;DIABLO;DIABL	9.02905813518647e-05	0.0295672655938079
		9.03730854771105e-05	0.0295672655938079
Island	DND1	9.04172854114379e-05	0.0295672655938079
		9.05160187526499e-05	0.0295672655938079

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	DPP6;DPP6;DPP6	9.06239339049885e-05	0.0295676299688941
	TRAPPC9;TRAPPC9	9.06476963683298e-05	0.0295676299688941
Island	BID;BID;BID	9.07909926294975e-05	0.0295676299688941
	MAGEC1	9.08232776934735e-05	0.0295676299688941
N_Shelf	ZNF443	9.08550760322762e-05	0.0295676299688941
Island	HLX	9.09078366828102e-05	0.0295676299688941
	PCCA;PCCA	9.09338949647799e-05	0.0295676299688941
	LRRK1	9.09943688648839e-05	0.0295676299688941
		9.10875269914286e-05	0.0295676299688941
		9.10975818493901e-05	0.0295676299688941
Island	POLS	9.11771622945608e-05	0.0295676299688941
N_Shelf	MAD1L1;MAD1L1;MAD1	9.1227284120777e-05	0.0295676299688941
Island	AIRE;AIRE	9.13150062731494e-05	0.0295676299688941
N_Shelf	HOTAIR	9.1329529620535e-05	0.0295676299688941
	ADARB2	9.15188246816386e-05	0.0295803155574887
Island		9.15301411380458e-05	0.0295803155574887
Island	ZNF319	9.162610093195e-05	0.0295803155574887
Island		9.16420364058787e-05	0.0295803155574887
Island	FOXI2	9.17015644584032e-05	0.0295803155574887
Island		9.17351653690147e-05	0.0295803155574887
S_Shore		9.20000099001877e-05	0.0296459779074573
Island		9.21087176089456e-05	0.0296574970722315
Island	WBSCR17	9.2168835018102e-05	0.0296574970722315
S_Shelf	GFPT2	9.22283916984064e-05	0.0296574970722315
S_Shelf	MAD1L1;MAD1L1;MAD1	9.22806959951538e-05	0.0296574970722315
	ATP10A	9.24113458437092e-05	0.0296797911642934
N_Shore	POLE	9.26971355210678e-05	0.0297350283998843
	INSL4	9.27061227147583e-05	0.0297350283998843
N_Shelf	CCDC88A;CCDC88A	9.30094659009442e-05	0.0297952493342599
		9.31053695099171e-05	0.0297952493342599
S_Shore		9.31088042641837e-05	0.0297952493342599
		9.31399524948526e-05	0.0297952493342599
Island	CTNNA2;LRRTM1;CTN	9.34332391993844e-05	0.029869342293889
Island		9.36196456867644e-05	0.0299040943181313
	PFKP	9.37315239052334e-05	0.0299040943181313
Island		9.37635182101923e-05	0.0299040943181313
N_Shelf		9.37892342401141e-05	0.0299040943181313
Island	PHOX2B	9.3872752149276e-05	0.0299040943181313
Island	PCDHB19P	9.39124089358958e-05	0.0299040943181313
Island		9.40436360218624e-05	0.0299148831907406
Island	RAI1	9.40698231549021e-05	0.0299148831907406
Island	CALHM3	9.41693808983762e-05	0.0299268933094528
Island	TLL2	9.44456002688813e-05	0.0299682913096527
S_Shelf	ANKRD11	9.44704950532789e-05	0.0299682913096527
		9.44852750319304e-05	0.0299682913096527
N_Shelf	SYNGAP1	9.46193889177234e-05	0.0299911881790421
N_Shore		9.46819842390545e-05	0.0299914009264749
Island	CTBP1;CTBP1	9.4827459623562e-05	0.029997092212182
		9.48299566749539e-05	0.029997092212182
Island	PDE4B;PDE4B	9.4946970062969e-05	0.029997092212182
N_Shore	CA5A	9.49476949595313e-05	0.029997092212182
	C16orf68	9.51587627418727e-05	0.0300441771609892
Island		9.52534340414269e-05	0.030054475206589
Island	GFRA2;GFRA2;GFRA2	9.53681582825964e-05	0.0300710828517048
Island		9.55970519867274e-05	0.0301236448949068

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		9.58599517237056e-05	0.030177075720659
N_Shore	POU3F4	9.58912291004889e-05	0.030177075720659
		9.63429333028291e-05	0.0302321762055044
	RIMBP2	9.64012506677254e-05	0.0302321762055044
Island	UBE2I;UBE2I;UBE2I;UB	9.64278172666787e-05	0.0302321762055044
Island		9.6435968610263e-05	0.0302321762055044
	ANKH	9.64545588398102e-05	0.0302321762055044
Island		9.6475137583768e-05	0.0302321762055044
		9.65032662235271e-05	0.0302321762055044
	CLSTN1;CLSTN1	9.6703463001001e-05	0.0302546108681212
Island	FLJ32065	9.68601473071965e-05	0.0302546108681212
		9.69200912680342e-05	0.0302546108681212
Island		9.69279661086615e-05	0.0302546108681212
Island	MEG3;MEG3;MEG3	9.70109092312328e-05	0.0302546108681212
Island		9.71191930614705e-05	0.0302546108681212
	CDC14A;CDC14A;CDC	9.71858739436284e-05	0.0302546108681212
Island	GABRE;GABRE	9.71991168424902e-05	0.0302546108681212
Island	PXDN	9.7258439678717e-05	0.0302546108681212
N_Shore	HPSE2;HPSE2;HPSE2;H	9.72630421035072e-05	0.0302546108681212
	CHSY1	9.73356794117378e-05	0.0302546108681212
Island		9.7363392229242e-05	0.0302546108681212
		9.7533102249993e-05	0.0302546108681212
	MTERFD2;MTERFD2;S	9.75488363030724e-05	0.0302546108681212
N_Shelf	NDUFS8	9.76075031482877e-05	0.0302546108681212
	MX1;MX1	9.76261487956916e-05	0.0302546108681212
		9.76368281358043e-05	0.0302546108681212
N_Shelf		9.78901603549722e-05	0.0303137160574948
Island		9.80817091084795e-05	0.0303499325623202
	COL4A1	9.81324408044051e-05	0.0303499325623202
Island	MAEL	9.8318688890284e-05	0.0303862690268626
S_Shelf	SDK2	9.8375408731989e-05	0.0303862690268626
S_Shelf	TFDP1;TFDP1	9.85953614487336e-05	0.0303942421482839
	HPCAL1;HPCAL1	9.86189187791654e-05	0.0303942421482839
Island	PRKAR1B;PRKAR1B;P	9.87446532733522e-05	0.0303942421482839
Island	NOSIP	9.88200067169973e-05	0.0303942421482839
	TTC15	9.89129971653432e-05	0.0303942421482839
Island		9.89405565669183e-05	0.0303942421482839
Island	SCARA5	9.89934684967881e-05	0.0303942421482839
		9.90526445420633e-05	0.0303942421482839
Island	DCAF12L2	9.90613855692306e-05	0.0303942421482839
Island	LOC619207	9.90654963243112e-05	0.0303942421482839
Island		9.90915363694632e-05	0.0303942421482839
	CASZ1;CASZ1	9.9179455485589e-05	0.0303998497046882
S_Shore	SLC9A3	9.9235353085453e-05	0.0303998497046882
	DIP2C	9.92988936724821e-05	0.0304000863956542
Island	SYT7	0.00010000356488515	0.0305585626015426
	SH3BP4	0.000100081029783216	0.0305585626015426
S_Shelf	NAV2	0.000100091420042348	0.0305585626015426
Island	MRAP;MRAP	0.000100113226279027	0.0305585626015426
N_Shore	NKIRAS2;NKIRAS2;NKI	0.000100132016411806	0.0305585626015426
Island	PRSS21;PRSS21;PRSS	0.000100266353810126	0.0305655214458365
		0.000100299744623608	0.0305655214458365
	NLRX1;NLRX1	0.000100466635123345	0.0305655214458365
		0.000100551956571825	0.0305655214458365
	MAP2K5;MAP2K5	0.000100570493822174	0.0305655214458365

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		0.000100583637105836	0.0305655214458365
Island	SOX11;SOX11	0.00010059658531908	0.0305655214458365
	SEPT9;SEPT9;SEPT9;S	0.000100702752634047	0.0305785960310251
		0.000100885032594313	0.0306147515108023
Island	KLF15	0.000100978703545887	0.0306205832975149
	TNXB;TNXB	0.000101030696555885	0.0306205832975149
Island	EPHB3	0.000101184448790528	0.0306412909918087
	WFDC1	0.000101225552236399	0.0306412909918087
		0.000101337403422896	0.0306559887025572
Island	TUBA3E	0.000101422378744621	0.0306625428124147
S_Shore	DCAF12L2	0.000101555054090719	0.0306835006690501
N_Shore	UNC5A	0.000101724644658682	0.03070856328679
Island	SRRM4	0.000101796172704887	0.03070856328679
Island	MAL;MAL;MAL;MAL	0.000101955021877603	0.03070856328679
S_Shore		0.000101957975034575	0.03070856328679
	ELF5	0.000101973504298448	0.03070856328679
N_Shore	NFIA;NFIA;NFIA;NFIA	0.000102018434581005	0.03070856328679
Island	RNF39;RNF39	0.000102200505627428	0.030721123804475
S_Shore	DCAF12L1	0.000102292691081137	0.030721123804475
N_Shelf	SYN1;SYN1	0.000102314646199521	0.030721123804475
	C16orf68	0.000102349657007498	0.030721123804475
Island	FAIM2	0.000102424365780235	0.030721123804475
Island	CDX1	0.000102577663506645	0.030721123804475
		0.000102622053745443	0.030721123804475
Island	CDO1	0.000102670449822904	0.030721123804475
Island		0.000102904484161066	0.030721123804475
Island		0.000102974712023888	0.030721123804475
	SORCS2	0.000102975757114297	0.030721123804475
Island	CACNA2D2;CACNA2D2	0.00010297825655994	0.030721123804475
		0.000103060583831247	0.030721123804475
Island	CUEDC1	0.000103061831485592	0.030721123804475
Island		0.000103101058845326	0.030721123804475
		0.000103114599378347	0.030721123804475
S_Shore	MSRA;MSRA;MSRA	0.000103138486153051	0.030721123804475
	C2orf39	0.000103365568436951	0.0307414723961054
		0.000103380378507377	0.0307414723961054
N_Shore	ALX1	0.000103397219910712	0.0307414723961054
	SLC39A11;SLC39A11	0.000103597012412533	0.0307634552499442
	C14orf159;C14orf159;C	0.000103598194420398	0.0307634552499442
	AGAP1;AGAP1	0.0001037312236342	0.03076757311199
Island	OBSCN;OBSCN	0.000103790704504159	0.03076757311199
	MYO16	0.000103802641748808	0.03076757311199
	KDM2B;KDM2B	0.00010393817207922	0.0307889022582679
	MAGEA4	0.000104130504585334	0.0308179897733005
Island		0.000104359226927966	0.0308179897733005
S_Shore	MAD1L1;MAD1L1;MAD1	0.000104414478971675	0.0308179897733005
Island		0.000104439058505521	0.0308179897733005
N_Shore	TFDP1;TFDP1	0.000104514220919445	0.0308179897733005
		0.000104574956753283	0.0308179897733005
Island		0.000104576916290595	0.0308179897733005
S_Shore	SLC44A4	0.000104599788840183	0.0308179897733005
		0.00010461115564798	0.0308179897733005
Island	TBCD	0.000104777972332054	0.0308179897733005
Island		0.000104843705505896	0.0308179897733005
Island	PCDHA7;PCDHA6;PCD	0.000104863034079691	0.0308179897733005

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N_Shore		0.000104863567122076	0.0308179897733005
Island	SLC32A1	0.000105029682844371	0.030823492640696
Island	ZNF286A;ZNF286A	0.000105056661168402	0.030823492640696
	CDH10	0.000105073218086593	0.030823492640696
Island		0.000105439544843037	0.0309122321768182
N_Shore	PRDM16;PRDM16	0.000105558666683926	0.0309279586107117
Island	CNIH3;CNIH3	0.000105620902373648	0.0309279586107117
Island	RUNX3;RUNX3	0.000105774474642932	0.0309371192489188
N_Shore	EIF1AY	0.000105871967175112	0.0309371192489188
Island	LDHAL6B;MYO1E	0.000105979698507665	0.0309371192489188
Island	NYX	0.000106104946756028	0.0309371192489188
		0.000106131661256858	0.0309371192489188
Island	NOTUM	0.000106180468484134	0.0309371192489188
		0.000106204715787369	0.0309371192489188
Island	SALL3	0.000106212078601466	0.0309371192489188
		0.000106262583355189	0.0309371192489188
N_Shelf		0.000106290954276985	0.0309371192489188
N_Shelf	SUCLG2	0.000106363531998596	0.0309396502313633
Island	ZFPM1	0.000106449079777991	0.0309459487175724
Island		0.000106643113681383	0.0309519814007549
Island	DIP2C	0.000106760354167056	0.0309519814007549
	KIAA0513	0.000106784606361482	0.0309519814007549
Island	FGF18	0.000106837577518645	0.0309519814007549
	FAM40B;FAM40B	0.000106849364126057	0.0309519814007549
S_Shore	ATP11A;ATP11A	0.000106853276006942	0.0309519814007549
Island		0.00010695980816642	0.0309614507461519
		0.000107091938821116	0.0309614507461519
N_Shore		0.00010717007692081	0.0309614507461519
Island		0.000107191258356018	0.0309614507461519
Island	MAGEB1;MAGEB1;MAG	0.000107205601406693	0.0309614507461519
Island	LAMA5	0.000107347443554937	0.0309655848056137
S_Shelf	PMS2L11	0.000107347786896455	0.0309655848056137
Island	FEV	0.00010765943712568	0.0310139111352504
	IQCG;IQCG	0.000107700656929905	0.0310139111352504
Island	HEATR7A;HEATR7A;HE	0.000107707424827319	0.0310139111352504
Island	PSMA1;PSMA1;PSMA1	0.000107808712339774	0.031023240732223
Island		0.000107948714352429	0.031023240732223
	AFAP1;AFAP1;LOC8474	0.000108029723670828	0.031023240732223
Island	REPIN1;REPIN1;REPIN	0.000108040504573265	0.031023240732223
Island	CACNA1I;CACNA1I	0.000108091040349523	0.031023240732223
Island		0.000108124152905575	0.031023240732223
	TNXB	0.000108398756135495	0.0310412861312003
S_Shore	GATA4	0.000108494080443271	0.0310412861312003
N_Shore	EHMT1;EHMT1	0.000108536780665627	0.0310412861312003
Island	SLC6A18	0.000108596441551473	0.0310412861312003
	HIGD1C	0.000108614447609116	0.0310412861312003
Island		0.000108684273616061	0.0310412861312003
N_Shelf	EFNB1	0.000108695730849909	0.0310412861312003
Island	GDF6	0.000108718229247791	0.0310412861312003
N_Shelf	FIGN	0.00010876387253321	0.0310412861312003
		0.00010904887892224	0.0310785489981711
	LDHC;LDHC;LDHC;LDF	0.000109057317864442	0.0310785489981711
S_Shelf	CORO1A;LOC606724	0.000109112177007701	0.0310785489981711
S_Shore		0.000109151111022328	0.0310785489981711
Island	ZIC5	0.00010923012616375	0.031082773709905

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Island	PTPRN2;PTPRN2;PTPF	0.000109431899281656	0.031108494530988
	AGAP1;AGAP1	0.000109448974719049	0.031108494530988
Island	RSPH6A	0.000109632040224346	0.0311398257100021
Island	ZBTB12	0.00010970562938929	0.0311398257100021
Island		0.000109794649512289	0.0311398257100021
N_Shelf	SCRIB;SCRIB	0.000109851531963953	0.0311398257100021
N_Shelf	SOX5	0.000109896829128414	0.0311398257100021
Island	GPC1	0.0001099449790205	0.0311398257100021
N_Shore		0.000110446758159011	0.0312578022310419
	IQCE;IQCE	0.000110515231352157	0.0312578022310419
Island	ZFAT;ZFAT	0.000110608711189757	0.0312578022310419
Island	AMDHD1	0.000110627166401345	0.0312578022310419
N_Shore	ZFYVE20	0.000110684211688921	0.0312578022310419
Island		0.000110918943566008	0.0312946333783903
	C3orf26;FILIP1L;FILIP1L	0.000110995650729031	0.0312946333783903
	VCX3A	0.000111008476011097	0.0312946333783903
	TTC15	0.000111191076924403	0.0313052476506774
	CCDC127	0.000111223775948859	0.0313052476506774
S_Shore		0.000111268237684606	0.0313052476506774
N_Shore	TNRC18	0.000111379837919453	0.0313052476506774
Island	MYOM2	0.000111425075808467	0.0313052476506774
Island	LTBP4;LTBP4;LTBP4	0.00011147217064728	0.0313052476506774
N_Shelf	PGM3	0.000111557152851317	0.0313052476506774
Island	IRX1;IRX1	0.000111618838007811	0.0313052476506774
Island	NRBP2	0.000111705126826776	0.0313052476506774
Island	IRX1	0.000111717688526612	0.0313052476506774
	PACRG;PACRG;PACRG	0.000111757132479267	0.0313052476506774
	WHSC1L1;WHSC1L1	0.000112063178769599	0.0313728318251943
N_Shore	PCDH19;PCDH19	0.000112195035828922	0.0313864282231862
Island	DSC3;DSC3	0.000112245957883534	0.0313864282231862
Island		0.000112306158283759	0.0313864282231862
		0.000112388586614364	0.0313913507566332
Island	HOXB3	0.000112616178896403	0.0314004223633841
		0.000112638010637182	0.0314004223633841
N_Shore	ZNF625	0.000112661749718911	0.0314004223633841
	MRAP2	0.000112681097879631	0.0314004223633841
		0.000112745232003149	0.0314004223633841
		0.000112890180763899	0.0314027764382525
	ACSF3;ACSF3;ACSF3	0.000112944643453405	0.0314027764382525
S_Shelf	PLCB3	0.000112999690163617	0.0314027764382525
	SDK1;SDK1	0.000113013037385793	0.0314027764382525
	SPATA13;SPATA13	0.000113126095281691	0.0314161674869869
	PLXNA4	0.00011328386472606	0.0314419528844981
Island		0.000113420850008624	0.0314619434023063
	LOC100128288	0.000113558161222729	0.031482001393359
	SCN8A	0.000113681455236719	0.0314911993618101
	RBMS1;RBMS1	0.000113837881951111	0.0314911993618101
Island		0.00011387296415822	0.0314911993618101
Island		0.00011402083828576	0.0314911993618101
	SIM1	0.000114058875474879	0.0314911993618101
Island	CLN8	0.000114073933254738	0.0314911993618101
	NXN	0.000114130994321439	0.0314911993618101
Island	GREB1	0.000114159348472666	0.0314911993618101
		0.000114176526256828	0.0314911993618101
	SPG7	0.000114313929657176	0.0315067494299093

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Island	C22orf34	0.000114434249502534	0.0315067494299093
S_Shelf	C20orf20	0.000114517043295781	0.0315067494299093
N_Shelf	NCOR2;NCOR2	0.000114621685165582	0.0315067494299093
Island	BEX1;BEX1	0.000114718918004436	0.0315067494299093
S_Shelf		0.00011487635577397	0.0315067494299093
		0.000114920061602932	0.0315067494299093
Island	AHRR;PDCD6	0.000114930015560495	0.0315067494299093
N_Shore	BAHCC1	0.000114972921086293	0.0315067494299093
N_Shore	METTL2A	0.000115007064660508	0.0315067494299093
	OR13A1	0.000115031323050159	0.0315067494299093
Island	DEF8;DEF8	0.000115083458417246	0.0315067494299093
Island		0.000115101387385431	0.0315067494299093
N_Shore		0.000115284062105288	0.0315067494299093
	RPTOR;RPTOR	0.000115312749040414	0.0315067494299093
Island	POU3F1	0.000115322638244127	0.0315067494299093
	FAM184B	0.000115383340588277	0.0315067494299093
		0.000115403857923211	0.0315067494299093
Island		0.000115695609273712	0.0315516362394275
Island		0.000115755019701569	0.0315516362394275
Island		0.000115829909139541	0.0315516362394275
Island		0.000115955383080492	0.0315516362394275
	IRF8	0.000116038797483698	0.0315516362394275
Island	NR5A2;NR5A2	0.000116091383507058	0.0315516362394275
N_Shore	METRNL	0.000116111487410817	0.0315516362394275
	ITM2A;ITM2A	0.000116167477832357	0.0315516362394275
		0.000116214207614987	0.0315516362394275
N_Shore	GAK	0.000116317182176053	0.0315516362394275
Island		0.00011633698891822	0.0315516362394275
	TTC24	0.000116421064904122	0.0315516362394275
		0.000116431549417362	0.0315516362394275
	TNIP2;TNIP2	0.000116485640037228	0.0315516362394275
		0.000116629196387042	0.0315516362394275
		0.000116777667767828	0.0315516362394275
Island	LEP	0.000116808532710812	0.0315516362394275
	MYO15A	0.000116838664690119	0.0315516362394275
S_Shelf	HIST2H2BA	0.000116863380509921	0.0315516362394275
	ATP11A;ATP11A	0.000116871182395154	0.0315516362394275
		0.000117145868076618	0.0315973005622163
	LRIG1	0.000117246808219406	0.0315973005622163
	SYNJ2	0.000117262283366952	0.0315973005622163
		0.000117349583415795	0.0315973005622163
S_Shore	NRN1L	0.000117366528078103	0.0315973005622163
		0.000117563338017257	0.0316152697238829
	RUNX3;RUNX3	0.00011759364655696	0.0316152697238829
		0.000117629104511303	0.0316152697238829
	AGAP1;AGAP1	0.000117794549799054	0.0316275235148056
N_Shore	SLC16A2	0.000117850023593044	0.0316275235148056
		0.00011793544908847	0.0316275235148056
Island	C10orf119	0.000118066652805479	0.0316275235148056
S_Shore		0.000118190896863193	0.0316275235148056
Island	LMF1	0.000118262068772034	0.0316275235148056
	LRP1	0.000118278038993552	0.0316275235148056
Island	KIAA0664	0.000118360786340213	0.0316275235148056
Island	KCND3;KCND3	0.000118412497659	0.0316275235148056
Island		0.000118536669526897	0.0316275235148056

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Island		0.000118562227005294	0.0316275235148056
	TP73;TP73;TP73;TP73	0.000118571903397298	0.0316275235148056
Island	MORC1	0.000118576439888088	0.0316275235148056
	SRPX2	0.000118684282906075	0.0316275235148056
Island	SPSB1	0.000118751219845695	0.0316275235148056
Island	FOXK1	0.000118796209323675	0.0316275235148056
Island	ZNF444	0.000118885229876406	0.0316275235148056
Island		0.000118984573472832	0.0316275235148056
		0.000119012067664079	0.0316275235148056
	FAM46C	0.000119128680556082	0.0316275235148056
Island		0.000119230555753375	0.0316275235148056
Island	OPLAH	0.00011923691177519	0.0316275235148056
	SH3BP4	0.000119404756950531	0.0316275235148056
Island	ESPNP	0.000119442978437211	0.0316275235148056
	RADIL	0.000119470323931878	0.0316275235148056
N_Shelf		0.000119571154047051	0.0316275235148056
N_Shore	HMGA2;RPSAP52;HMG	0.000119733083414634	0.0316275235148056
	NADSYN1	0.000119750084387757	0.0316275235148056
Island		0.000119887278758506	0.0316275235148056
N_Shore	CHRM2;CHRM2;CHRM2	0.000119901416460669	0.0316275235148056
Island		0.000119911327325207	0.0316275235148056
		0.000119956418262337	0.0316275235148056
Island		0.000120040737961916	0.0316275235148056
S_Shore	SLC22A2	0.000120043002124235	0.0316275235148056
Island	CTDP1;CTDP1	0.000120062873777155	0.0316275235148056
S_Shore		0.0001202373959624	0.0316275235148056
Island	FGF22	0.000120272059820063	0.0316275235148056
N_Shore		0.000120345129713608	0.0316275235148056
Island	PITPNM2	0.00012041042858952	0.0316275235148056
	ACOX3;ACOX3	0.000120464930522947	0.0316275235148056
	AGAP1;AGAP1	0.00012049592571941	0.0316275235148056
	SYT12	0.000120562247870034	0.0316275235148056
Island	ACTN3	0.000120580565524363	0.0316275235148056
Island	PTPRN2;PTPRN2;PTPRN2	0.000120741981244826	0.0316275235148056
Island	FOXD3	0.000120769625013463	0.0316275235148056
	TMCO3	0.000120780484216453	0.0316275235148056
Island	SIM1	0.000120871461578123	0.0316275235148056
N_Shore		0.000121037349891455	0.0316275235148056
	KIAA1462	0.000121124290320812	0.0316275235148056
S_Shore	OAZ3;MRPL9	0.000121132272600001	0.0316275235148056
Island	PTPRN2;PTPRN2;PTPRN2	0.000121144027429567	0.0316275235148056
S_Shore		0.00012127634471449	0.0316275235148056
Island	PCDHA6;PCDHA2;PCDHA2	0.00012146018821386	0.0316275235148056
Island	ATP11A;ATP11A	0.000121471355711327	0.0316275235148056
Island		0.000121496809394008	0.0316275235148056
N_Shore	GABRA2;GABRA2;GABRA2	0.000121516548125214	0.0316275235148056
	UNC5B	0.000121525849398774	0.0316275235148056
Island	PTGER4	0.000121595156415163	0.0316275235148056
Island	RASGRF1;RASGRF1	0.000121612705363407	0.0316275235148056
	CARD11	0.000121650860031004	0.0316275235148056
Island		0.000121672980997106	0.0316275235148056
		0.000121723437426517	0.0316275235148056
	LRP1	0.000121898861922253	0.031656121340748
Island	PLEKHA5;PLEKHA5	0.000121975484120063	0.0316590441299302
Island	CMTM2	0.000122180075092357	0.0316776740637935

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Island	KLK15;KLK15;KLK15	0.000122218097221035	0.0316776740637935
	PDE11A;PDE11A;PDE11A	0.000122320899979607	0.0316776740637935
Island		0.000122353497998097	0.0316776740637935
	CARD11	0.000122374290349162	0.0316776740637935
Island		0.000122517625671459	0.0316882836782787
Island		0.000122697019587707	0.0316882836782787
S_Shelf	PCNXL3	0.000122715649565186	0.0316882836782787
Island		0.0001227181857867	0.0316882836782787
S_Shore	EXOC3	0.000122742415073454	0.0316882836782787
N_Shore	TSPAN12	0.000122993740600905	0.0317242739445291
Island	FAM155B	0.000123012824999382	0.0317242739445291
Island	ZNF662;ZNF662;ZNF662	0.000123109284597522	0.0317322534660429
Island	MYO1C;MYO1C;MYO1C	0.000123328229531032	0.0317450282347314
S_Shore	PAX9	0.000123450955424563	0.0317450282347314
Island	NSD1;NSD1	0.000123451431658062	0.0317450282347314
Island	SLC25A31	0.000123529593962091	0.0317450282347314
Island	CXorf36	0.000123543634343443	0.0317450282347314
		0.000123552115258285	0.0317450282347314
		0.000123792770215787	0.0317686734390576
Island	H2BFM;MIR1256	0.000123834896912467	0.0317686734390576
	KLHDC4	0.00012384092386918	0.0317686734390576
S_Shelf	ZCCHC14	0.000123968369476708	0.0317845317876159
Island		0.000124059273805098	0.0317910094103989
Island		0.000124228422290297	0.0317932972783304
	KRTAP12-3;C21orf29	0.000124240432154758	0.0317932972783304
Island		0.000124265135493479	0.0317932972783304
	SDK1;SDK1	0.000124545375510378	0.0318200218625373
Island	C3orf77	0.000124565821757674	0.0318200218625373
	CRB1	0.00012456880887152	0.0318200218625373
Island	ITPRIP	0.000124632388320308	0.0318200218625373
Island	POM121L9P	0.000124759360556644	0.0318356571662785
N_Shore	PLCD3;ACBD4	0.000124906153068246	0.0318389942836083
S_Shore	NOTCH3	0.000124934530582966	0.0318389942836083
Island	NFIC;NFIC	0.000125038569378561	0.0318389942836083
	SPARC;SPARC	0.000125075308868976	0.0318389942836083
Island	FLJ40434	0.000125101132755292	0.0318389942836083
		0.000125202900045343	0.0318481589099059
Island		0.000125432604030958	0.0318898403922802
		0.000125570246807163	0.0319080848818884
		0.000125830097279163	0.0319389765308082
S_Shelf	RAB40B	0.000125965140753179	0.0319389765308082
S_Shore	TWIST1	0.000126003248900493	0.0319389765308082
Island	MYO10	0.000126394337988242	0.0319389765308082
Island	CSTF1;CSTF1;CSTF1	0.000126441634907781	0.0319389765308082
Island	SLC47A2;SLC47A2	0.00012652345784271	0.0319389765308082
	TNXB	0.00012684241389818	0.0319389765308082
	KIF1A	0.000127094783946364	0.0319389765308082
Island	MAMDC2;MAMDC2	0.000127107885232675	0.0319389765308082
Island		0.000127110282037258	0.0319389765308082
Island	ZIC1	0.000127117917669247	0.0319389765308082
Island	TTC38	0.000127118884719522	0.0319389765308082
	SEMA3C	0.00012713857364442	0.0319389765308082
Island		0.000127152564711182	0.0319389765308082
N_Shore	PCDH19;PCDH19	0.000127173736084415	0.0319389765308082
Island		0.000127206610934048	0.0319389765308082

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	DSCAML1	0.000127215308901535	0.0319389765308082
	PTPRN2;PTPRN2;PTPF	0.000127332097052791	0.0319389765308082
Island	SHROOM4;SHROOM4	0.00012738162905252	0.0319389765308082
	MGMT	0.00012743621643934	0.0319389765308082
N_Shore	FLJ12825;LOC1002407	0.000127537215083694	0.0319389765308082
Island		0.000127593043760595	0.0319389765308082
		0.000127621349809749	0.0319389765308082
Island	ANKRD43	0.000127766661410558	0.0319389765308082
		0.000127858984577742	0.0319389765308082
Island	ANKRD10	0.000127907145375268	0.0319389765308082
	SSPN;SSPN	0.00012796151379832	0.0319389765308082
		0.000127982644619261	0.0319389765308082
	KLF8;KLF8	0.000127997402873922	0.0319389765308082
	MAD1L1;MAD1L1;MAD1	0.000128020096903686	0.0319389765308082
		0.000128060477064651	0.0319389765308082
		0.000128210517831292	0.0319389765308082
N_Shore	PCNXL2	0.000128217573156974	0.0319389765308082
	TRAPPC9;TRAPPC9	0.000128291038032514	0.0319389765308082
Island	GPR44	0.000128309056439546	0.0319389765308082
S_Shelf	GAK	0.000128315943354386	0.0319389765308082
Island		0.000128325337907599	0.0319389765308082
Island		0.000128394705370768	0.0319389765308082
	GNAO1	0.000128427945836943	0.0319389765308082
Island	PCDHB17	0.000128441297632804	0.0319389765308082
		0.000128531706265431	0.0319389765308082
	DNAJC16	0.000128686998590751	0.0319389765308082
N_Shelf	TSNARE1	0.000128748892329402	0.0319389765308082
		0.000128865978952009	0.0319389765308082
S_Shore	LRP5	0.000128911211602606	0.0319389765308082
		0.0001289560040684	0.0319389765308082
	ZNF311	0.000129033650909084	0.0319389765308082
Island	GTF2A1L;STON1-GTF2	0.000129055639136616	0.0319389765308082
	SURF4	0.000129079978969924	0.0319389765308082
Island	FBRS1	0.000129099616258363	0.0319389765308082
Island	SHROOM2	0.000129317302792472	0.0319389765308082
Island	SECTM1	0.000129323088703102	0.0319389765308082
	VIPR2	0.000129342154679211	0.0319389765308082
		0.000129383157711895	0.0319389765308082
Island		0.000129399975221265	0.0319389765308082
	RAP1GAP2;RAP1GAP2	0.000129413379998097	0.0319389765308082
Island	PDE9A;PDE9A;PDE9A;P	0.000129450701347187	0.0319389765308082
Island	OBSCN;OBSCN	0.000129574058899738	0.0319531344585618
	MYO10	0.000129743295089186	0.0319636554154251
	ZC3H18	0.000129890011100887	0.0319636554154251
Island	ZNF362	0.000129958156405728	0.0319636554154251
N_Shore	PPP1R11	0.000129988110302209	0.0319636554154251
		0.000130017950282059	0.0319636554154251
Island		0.000130063820193689	0.0319636554154251
Island	PRX;PRX	0.000130078696792036	0.0319636554154251
Island	LEFTY2	0.00013028069113368	0.0319970566598984
Island		0.000130522777221396	0.0320402656248114
N_Shore		0.000130646996502114	0.0320545119457377
Island		0.000130739175069792	0.0320608865648997
Island	SEC14L1;SEC14L1;SEC	0.000130856166690562	0.0320687902567958
		0.000130903831802375	0.0320687902567958

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Island	MAGI1;MAGI1;MAGI1	0.000130971501684127	0.0320691468923987
		0.000131166475675307	0.0320870611752403
Island	GNAS;GNAS;GNAS	0.000131220798817316	0.0320870611752403
Island	PDZRN3	0.00013124341751541	0.0320870611752403
Island	GLI2	0.000131487648566747	0.0321207612703753
Island	ACIN1;ACIN1;ACIN1;AC	0.000131513899962121	0.0321207612703753
	LSP1	0.000131712212239573	0.0321398612283824
Island	KLHL36	0.000131796377695347	0.0321398612283824
Island	KDM4B	0.000131843001651165	0.0321398612283824
Island	GRIN3A	0.000131893617467531	0.0321398612283824
	MIR487A	0.000131923902590253	0.0321398612283824
Island		0.000132068196292836	0.0321485787150686
Island	CDH8	0.000132092441321399	0.0321485787150686
Island	HMX2	0.00013226897006379	0.0321487533095096
Island	TLX3	0.000132316739649113	0.0321487533095096
Island	KCNH1;KCNH1	0.000132420973159656	0.0321487533095096
		0.000132512022422316	0.0321487533095096
		0.000132548633513814	0.0321487533095096
S_Shore	MICALL2	0.000132709446997809	0.0321487533095096
Island	CHST8;CHST8;CHST8	0.000132749534742854	0.0321487533095096
		0.000132753650910645	0.0321487533095096
S_Shelf	GIT1;GIT1	0.000132755195813388	0.0321487533095096
Island	REXO1L2P;REXO1L1	0.000133076837119741	0.0321487533095096
Island	BANP;BANP	0.000133162368877552	0.0321487533095096
	FARP1;FARP1	0.000133225061138642	0.0321487533095096
		0.000133270096308817	0.0321487533095096
		0.00013328337680584	0.0321487533095096
S_Shelf		0.000133305440409026	0.0321487533095096
Island	PRDM16;PRDM16	0.000133329305806171	0.0321487533095096
N_Shore	MMP21	0.000133368612301638	0.0321487533095096
N_Shore	BANP;BANP	0.000133438472122844	0.0321487533095096
Island	RPS6KA3	0.000133517536861087	0.0321487533095096
Island		0.000133622477787995	0.0321487533095096
Island	KNDC1	0.000133668725892656	0.0321487533095096
Island	FXR1;FXR1;FXR1	0.000133805651702854	0.0321487533095096
Island	KCNQ1DN	0.000133808394339665	0.0321487533095096
N_Shore	RBM15B	0.000133854671253144	0.0321487533095096
S_Shore		0.000133911815740674	0.0321487533095096
	LHFP	0.000133950473267807	0.0321487533095096
	CD200R1;CD200R1;CD	0.000133969475856351	0.0321487533095096
Island	RTBDN;RTBDN	0.000133979234998593	0.0321487533095096
Island	CHST6	0.000134044730314694	0.0321487533095096
N_Shore	GTF3C1;KIAA0556	0.00013408451284821	0.0321487533095096
	ZNF276;ZNF276	0.000134498723634377	0.0321672562253593
Island	COL2A1;COL2A1	0.000134584660604248	0.0321672562253593
		0.000134744327921003	0.0321672562253593
N_Shore		0.000135072999228147	0.0321672562253593
Island		0.000135083591753159	0.0321672562253593
	GABBR1;GABBR1;GAB	0.000135170196134968	0.0321672562253593
S_Shore	REXO1L2P	0.000135201181825693	0.0321672562253593
Island	MBP;MBP	0.000135334155858891	0.0321672562253593
Island	MAD1L1;MAD1L1;MAD1	0.000135339867445803	0.0321672562253593
	MYOM2	0.000135372331724254	0.0321672562253593
	KIAA1751	0.000135465025349602	0.0321672562253593
Island	ATP5G2;ATP5G2	0.000135554329869704	0.0321672562253593

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S_Shore	CCDC127	0.000135688538661248	0.0321672562253593
	GRID1	0.000135691243629517	0.0321672562253593
	FYTTD1;FYTTD1;FYTT	0.000135715863055624	0.0321672562253593
N_Shelf	BTBD12	0.000135830377807983	0.0321672562253593
S_Shelf	RPH3AL	0.000135855748364576	0.0321672562253593
	RPS6KA2	0.000135891569823289	0.0321672562253593
Island	SPACA1	0.000135917891719457	0.0321672562253593
Island	ROBO3	0.000135979533346185	0.0321672562253593
Island		0.000135991076533312	0.0321672562253593
N_Shelf		0.000136025267805287	0.0321672562253593
Island	DCAF12L2	0.000136038702705039	0.0321672562253593
	EBF2	0.000136044132322241	0.0321672562253593
	OPN1LW	0.000136050806407873	0.0321672562253593
	TSPAN9;TSPAN9	0.0001360742875664	0.0321672562253593
Island	PFKP	0.000136219685785508	0.0321672562253593
	DOCK5	0.000136230072636668	0.0321672562253593
	C13orf16	0.000136320310350154	0.0321672562253593
N_Shore		0.000136358570620154	0.0321672562253593
N_Shore	PHYHIPL	0.000136398681192911	0.0321672562253593
Island	ABHD8	0.000136406451468845	0.0321672562253593
Island	ETNK2	0.000136427033129607	0.0321672562253593
S_Shore	MAPK8IP3;MAPK8IP3	0.000136451810696087	0.0321672562253593
S_Shelf	TSNARE1	0.000136673514297226	0.0321672562253593
	ADARB2	0.000136750950996056	0.0321672562253593
Island	PAX6	0.000136844987462529	0.0321672562253593
	PCYT1B;PCYT1B;PCYT	0.000136847888527154	0.0321672562253593
Island		0.000136958275436197	0.0321672562253593
	C7orf70	0.000136989847905266	0.0321672562253593
Island	EPN1;EPN1;EPN1	0.000137061109371228	0.0321672562253593
	C14orf159;C14orf159;C	0.000137209919840817	0.0321672562253593
Island	HLA-DQB2	0.000137270825034773	0.0321672562253593
S_Shore	APBA2;APBA2	0.000137534927958164	0.0321672562253593
N_Shore	C17orf93;PRAC	0.000137647082885691	0.0321672562253593
	OVCH1	0.000137768347251141	0.0321672562253593
Island	SDK1	0.00013779083178513	0.0321672562253593
Island	KLK9;KLK8;KLK8;KLK8;	0.000137855318420022	0.0321672562253593
	TNIK;TNIK;TNIK;TNIK;T	0.000137862140097833	0.0321672562253593
Island	CUX1;CUX1;CUX1	0.000137884261666604	0.0321672562253593
Island	TRPM1	0.000138059859839167	0.0321672562253593
Island	VAX1;VAX1	0.0001380920732896	0.0321672562253593
N_Shore	TMEM8A	0.000138092366883927	0.0321672562253593
Island	ZCCHC24	0.000138093505308427	0.0321672562253593
S_Shelf		0.000138102203682323	0.0321672562253593
S_Shore		0.000138135058661029	0.0321672562253593
Island		0.000138360823893329	0.0321672562253593
Island	KCTD15;KCTD15;KCTD	0.000138378923470575	0.0321672562253593
	FAT1	0.00013843481315022	0.0321672562253593
Island	LOC442459	0.000138483672115331	0.0321672562253593
S_Shelf	SFRS8	0.0001384893365684	0.0321672562253593
N_Shore	ZFPM1	0.00013849780052662	0.0321672562253593
Island	GDI1	0.000138609167828001	0.0321672562253593
Island	INTS1	0.000138736604681069	0.0321672562253593
Island	ODZ4	0.000138870616255068	0.0321672562253593
		0.000138982664735014	0.0321672562253593
Island	LOC642006	0.000138988044601079	0.0321672562253593

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	MCF2;MCF2;MCF2	0.000139011916375265	0.0321672562253593
N_Shore		0.000139021767936334	0.0321672562253593
Island	ZNF444	0.000139022803777142	0.0321672562253593
Island	MAD1L1;MAD1L1;MAD1	0.000139075003486505	0.0321672562253593
Island		0.000139189319950727	0.0321672562253593
	ULK1	0.000139273736028221	0.0321672562253593
S_Shelf	FAM20C	0.000139315274029628	0.0321672562253593
Island		0.000139331851764049	0.0321672562253593
	SEPT12;SEPT12;LOC4	0.000139429883949918	0.0321672562253593
Island	TFAP2B	0.000139462869549338	0.0321672562253593
	HABP2	0.000139517873189886	0.0321672562253593
	ADARB2	0.000139543201530355	0.0321672562253593
Island		0.000139580381281735	0.0321672562253593
	IQCE;IQCE	0.000139658194602445	0.0321672562253593
N_Shore		0.000139713456461852	0.0321672562253593
Island		0.000139793655009265	0.0321672562253593
	JARID2	0.00013979825473221	0.0321672562253593
	CXCR5;CXCR5	0.000139807101335635	0.0321672562253593
		0.000139937854511677	0.0321820519403457
	HIPK2;HIPK2	0.000140455046117706	0.0322783172911177
	C4orf44	0.000140665965987656	0.0322783172911177
Island	TBCB	0.00014071016384637	0.0322783172911177
N_Shore	AGRN	0.000140711548927521	0.0322783172911177
Island		0.000140725355917071	0.0322783172911177
	MAD1L1;MAD1L1;MAD1	0.000140766151426446	0.0322783172911177
Island	HLA-DOA	0.000140919245282544	0.0322783172911177
S_Shelf		0.000141004661212651	0.0322783172911177
	UNC5B	0.000141082089541057	0.0322783172911177
S_Shore	ABHD14A	0.000141140272261627	0.0322783172911177
	MAEA;MAEA	0.000141189736839821	0.0322783172911177
Island	MCF2L;MCF2L	0.000141300100966191	0.0322783172911177
Island		0.000141385589663765	0.0322783172911177
		0.000141391014567342	0.0322783172911177
Island	PAX1	0.000141412974564662	0.0322783172911177
N_Shore	B3GAT1;B3GAT1	0.000141432355383334	0.0322783172911177
Island	INPP5A	0.000141489428811321	0.0322783172911177
Island	SALL4;SALL4	0.000141710490852304	0.0322904841731988
Island	DPF1;DPF1;DPF1	0.000141787740268173	0.0322904841731988
Island	NUSAP1;NUSAP1;OIP5	0.000141795275090111	0.0322904841731988
N_Shore	NACC1	0.000141809445798573	0.0322904841731988
Island		0.000141970156162841	0.0323118871633308
Island		0.000142093359811495	0.0323234131613615
Island		0.000142191898092875	0.0323234131613615
N_Shore	GALR1	0.00014231637028993	0.0323234131613615
S_Shore	EBF3	0.000142440568054351	0.0323234131613615
S_Shelf	HPD	0.00014245283424626	0.0323234131613615
Island	CLCN4	0.000142477913947909	0.0323234131613615
Island	ANKRD33B	0.000142487972125137	0.0323234131613615
Island	PLEC1;PLEC1;PLEC1;P	0.000142661577327544	0.0323238118746976
Island	SLC15A3;SLC15A3	0.000142683604396715	0.0323238118746976
Island	ZBTB12	0.000142714011777794	0.0323238118746976
Island	GIPC1;GIPC1;GIPC1;G	0.000142756689413055	0.0323238118746976
S_Shelf	FBRS1	0.000142946776315252	0.0323369767208418
Island	KRT72;KRT72;KRT72;K	0.000142948365579564	0.0323369767208418
Island		0.000143166948608384	0.0323713036343396

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	PCID2;PCID2;PCID2	0.000143296944030189	0.0323749049955231
S_Shelf	ARMCX5;ARMCX5;ARM	0.000143316566996132	0.0323749049955231
Island	MAD1L1;MAD1L1;MAD1	0.000143461214192005	0.0323924720575956
		0.000143828712801107	0.0324422287351685
Island		0.000143881387040755	0.0324422287351685
	ETV6	0.000143929789230301	0.0324422287351685
S_Shore	MIR596	0.000144004024283853	0.0324422287351685
Island		0.000144016500863289	0.0324422287351685
N_Shore	POMT1;POMT1;POMT1	0.000144128350787826	0.0324523307742045
S_Shore	PPP1R2P9	0.000144213129604961	0.032456330853124
Island		0.000144328619653931	0.032460431089746
		0.000144451012831391	0.032460431089746
N_Shelf	NR6A1;NR6A1	0.000144475083508336	0.032460431089746
Island	HOXA11AS;HOXA11	0.00014461437574231	0.032460431089746
S_Shelf		0.000144640644802984	0.032460431089746
Island		0.00014468699699605	0.032460431089746
Island		0.000144700502189153	0.032460431089746
	DCUN1D2	0.0001449131646549	0.0324930872553168
Island	TOLLIP	0.000145019590610305	0.0325019033884016
	TMC2	0.000145361799712377	0.0325635308259467
Island	TNK1	0.000145832804400822	0.0326377461839804
Island	AQP2	0.00014589937740386	0.0326377461839804
S_Shore	ABR;ABR;ABR	0.000145917539150382	0.0326377461839804
	C3orf21	0.000145986454808894	0.0326377461839804
N_Shore	STRN3;STRN3;AP4S1;A	0.000146126918255177	0.0326377461839804
Island	HDAC4	0.000146129034771666	0.0326377461839804
N_Shore		0.000146212704369637	0.0326377461839804
S_Shore		0.000146232197840783	0.0326377461839804
Island	SIGIRR;SIGIRR;SIGIRR	0.000146412695396036	0.0326451969842593
Island		0.00014644307021754	0.0326451969842593
	RUNX3	0.000146467791352491	0.0326451969842593
	ZC3H3	0.000146546366269656	0.0326476857606031
Island	PAK7;PAK7	0.000146950819097983	0.0327227381423589
Island	DIP2C	0.000147094750181465	0.0327397356992821
Island	RUNX3;RUNX3	0.000147424375463659	0.0327932439851091
N_Shelf		0.000147470573271187	0.0327932439851091
Island	WTIP	0.000147730347328941	0.0328179221055797
Island	BARHL1	0.000147813210031619	0.0328179221055797
Island	BRD3	0.000147849300903702	0.0328179221055797
N_Shore	ADRA2C	0.000147852590790017	0.0328179221055797
	COL4A2	0.000147945700464046	0.0328235462103752
Island	MUC5B	0.000148092797748259	0.0328411374860007
S_Shelf	LRGUK	0.00014822633573308	0.0328557071185006
Island	SLC37A4;SLC37A4;SLC	0.000148319071577163	0.0328612233950638
		0.000148441080412089	0.0328667218323513
Island		0.000148517692449647	0.0328667218323513
N_Shore	MRPL12	0.000148547725315735	0.0328667218323513
		0.00014866733595956	0.0328667218323513
		0.000148683193175412	0.0328667218323513
Island		0.000148821909800725	0.0328687415693858
Island	REC8;REC8	0.000148834798211281	0.0328687415693858
Island	JPH3	0.000149127277661607	0.0328687415693858
	PSAP;PSAP;PSAP	0.000149195068606084	0.0328687415693858
	CCDC92	0.000149228902297408	0.0328687415693858
N_Shore		0.00014929226561849	0.0328687415693858

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	CPEB3	0.000149293512152736	0.0328687415693858
S_Shore	HLTF;HLTF	0.000149489882982793	0.0328687415693858
Island	ZSCAN5A	0.000149507873565625	0.0328687415693858
Island	FAIM2	0.000149600581171633	0.0328687415693858
Island		0.000149610812258881	0.0328687415693858
	LRP1	0.000149658514742968	0.0328687415693858
Island	GPC3;GPC3;GPC3;GPC3	0.000149739963058215	0.0328687415693858
	CDH5	0.000149771374893838	0.0328687415693858
Island	ATP5G2;ATP5G2	0.000149788487483547	0.0328687415693858
	FAM107B	0.000149795416063572	0.0328687415693858
	PPFIA1;PPFIA1	0.000149846035998976	0.0328687415693858
Island	B4GALNT1	0.000149981953400495	0.0328836621008125
Island	PTPRU;PTPRU;PTPRU	0.000150206421567849	0.0329080180091953
Island	TBX15	0.000150320834924976	0.0329080180091953
	DHX8	0.000150362450106893	0.0329080180091953
N_Shore		0.000150470761961724	0.0329080180091953
Island	KCNC2;KCNC2;KCNC2	0.000150496234170475	0.0329080180091953
Island	ZFH4;LOC100192378	0.000150500717267058	0.0329080180091953
	VPS53;VPS53	0.000150953683544907	0.0329921673207973
	MGMT	0.000151138139849722	0.0330175821302286
Island	KIAA2022	0.000151312953404446	0.0330189201454346
	GTF3C1	0.000151346254577762	0.0330189201454346
	DPF3	0.000151348790012625	0.0330189201454346
S_Shelf		0.000151630872607447	0.0330655661303925
Island		0.000151702174458824	0.0330662266628127
Island	GCM2	0.000152206862535685	0.0331489437842027
	SYT8	0.000152253137756429	0.0331489437842027
Island	MTSS1L	0.000152286997201984	0.0331489437842027
N_Shore	GOLGA3	0.000152643398780206	0.0332023336905174
Island	SOLH	0.000152669379298575	0.0332023336905174
		0.00015295628601017	0.0332484843079365
	SLC25A19;SLC25A19;S	0.000153093163204008	0.0332484843079365
	CTTN;CTTN	0.000153131829783192	0.0332484843079365
Island	PLCH2	0.000153231903707502	0.0332484843079365
Island	ZNF496	0.000153236612189934	0.0332484843079365
Island	MAGEB1;MAGEB1;MAG	0.000153293481566349	0.0332484843079365
Island		0.00015345009290588	0.0332675542733395
Island	KLHL17;NOC2L	0.00015370459762599	0.0332785987690793
Island		0.000153737818321433	0.0332785987690793
S_Shelf		0.000153836780893814	0.0332785987690793
Island	ESRRB	0.000153955836026911	0.0332785987690793
N_Shore	FADD	0.000153988000382761	0.0332785987690793
Island	PIK3CG	0.000154002620556517	0.0332785987690793
Island	PPP1R2P9	0.000154052606846097	0.0332785987690793
Island		0.000154084199551087	0.0332785987690793
Island		0.000154119438474258	0.0332785987690793
N_Shore		0.000154403087325079	0.0333196401772041
Island	PLA2G6;PLA2G6	0.000154449459640248	0.0333196401772041
N_Shore	TEX14;TEX14;RAD51C	0.00015451589704847	0.0333196401772041
	KLF7	0.000154617156330258	0.0333266374008244
		0.000154791129545908	0.0333434012023816
Island		0.000154832621285616	0.0333434012023816
Island	TRAPPC9;TRAPPC9	0.000154924843135844	0.0333484331785634
Island	TRRAP	0.00015503843943912	0.0333512629561604
Island	ANKRD43	0.000155129198978647	0.0333512629561604

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	FCRL5	0.000155144573251906	0.0333512629561604
	DIP2C	0.000155444119391672	0.0333556733219309
	FBRSL1	0.000155533132262524	0.0333556733219309
Island	C2orf84	0.000155567554406406	0.0333556733219309
Island	KEAP1;KEAP1	0.000155632675141254	0.0333556733219309
	IFT140	0.000155640053049867	0.0333556733219309
		0.000155648104638438	0.0333556733219309
Island	SLCO4A1	0.000155657999225309	0.0333556733219309
		0.000155723510848326	0.0333556733219309
	ZFAND2A	0.00015578492345885	0.0333556733219309
	SH3BP4	0.000156067675854327	0.0333897374114683
Island	TNRC18	0.000156081898517657	0.0333897374114683
Island		0.000156150842815735	0.0333897381663271
Island		0.000156352036392978	0.0334180053071619
Island	AGRN	0.000156496356352553	0.0334340969521174
		0.000156614645217494	0.0334446155401071
Island		0.00015676403466799	0.0334617633717824
Island	MAEA;MAEA	0.000157282814387703	0.0335469844188627
Island	WIPI2;WIPI2;WIPI2;WIF	0.000157395041630838	0.0335469844188627
Island	ZNF747	0.000157466137485971	0.0335469844188627
N_Shore	LOC407835	0.000157546837310752	0.0335469844188627
	MAGEE2;MAGEE2	0.000157589989437468	0.0335469844188627
		0.000157602225594452	0.0335469844188627
		0.000157778180578447	0.0335469844188627
Island	ZIC4;ZIC4;ZIC4;ZIC4;ZIC	0.000157869290304623	0.0335469844188627
	CACNA1C;CACNA1C;C	0.000157972045355015	0.0335469844188627
Island	TRAPPC9;TRAPPC9	0.000157997975997176	0.0335469844188627
Island	FOXK2	0.000158015640939884	0.0335469844188627
	C3orf26;FILIP1L;MIR548	0.000158038161909895	0.0335469844188627
N_Shelf	FOXK1	0.000158129531509774	0.0335469844188627
		0.000158133000419684	0.0335469844188627
Island	DRD4	0.000158205960237832	0.0335477678161944
	CUGBP2;CUGBP2	0.000158492494630234	0.0335658300673617
		0.000158493810143284	0.0335658300673617
Island	C19orf26	0.000158521608102376	0.0335658300673617
	JPH3	0.000158568356360137	0.0335658300673617
N_Shore	C10orf53;C10orf53	0.000158764001820707	0.033592562333689
	TRIM2;TRIM2	0.00015883712009838	0.0335933572889293
	GRIP2	0.000159172390214713	0.0336387783173972
Island		0.000159192751836788	0.0336387783173972
	CDC42BPB	0.000159452125591115	0.0336387783173972
Island	GPR88	0.000159465115098217	0.0336387783173972
Island	KCNN2	0.000159477741399392	0.0336387783173972
Island	DIP2C	0.00015948105984032	0.0336387783173972
N_Shelf	PTPRN2;PTPRN2;PTPF	0.000159620170112937	0.0336387783173972
	APBB2;APBB2;APBB2	0.000159725730838894	0.0336387783173972
Island	IGSF9B	0.000159944805713204	0.0336387783173972
	TBCD	0.000160003330063673	0.0336387783173972
S_Shore	NYX	0.000160355206963064	0.0336387783173972
N_Shore	OTUD7A	0.000160418791029798	0.0336387783173972
		0.000160550894022279	0.0336387783173972
	SDHA	0.000160596568653489	0.0336387783173972
Island		0.000160658561335514	0.0336387783173972
	RNF5P1;RNF5;AGPAT1	0.000160666483092223	0.0336387783173972
	MANBA	0.000160682149118235	0.0336387783173972

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Island	ULBP1	0.000161027859194571	0.0336387783173972
Island	ADAMTS14;ADAMTS14	0.000161037195557507	0.0336387783173972
		0.000161049484941725	0.0336387783173972
Island	KCNQ1DN	0.000161082409106778	0.0336387783173972
Island		0.000161083342447577	0.0336387783173972
S_Shore	SSU72	0.000161169545665584	0.0336387783173972
	TRAPPC9;TRAPPC9	0.000161240792302019	0.0336387783173972
	FGF18	0.000161289612048903	0.0336387783173972
Island	RHOXF1	0.000161330801184385	0.0336387783173972
Island	CTDP1;CTDP1	0.000161394750753608	0.0336387783173972
Island	NFIC;NFIC	0.000161410020224277	0.0336387783173972
Island	DRD5	0.000161469082130416	0.0336387783173972
N_Shore		0.000161489475506203	0.0336387783173972
	LOC645166;LOC645166	0.000161491358795671	0.0336387783173972
Island	ZBTB12	0.000161551412211003	0.0336387783173972
Island	GPNMB;GPNMB	0.000161638285864067	0.0336387783173972
	HDAC4	0.000161652925037952	0.0336387783173972
	MTUS1;MTUS1;MTUS1	0.000161680985440112	0.0336387783173972
Island	HOXD12	0.000161689769268917	0.0336387783173972
N_Shore	ACCN3;ACCN3;ACCN3	0.000161724969116024	0.0336387783173972
	C17orf85;C17orf85	0.00016176328187275	0.0336387783173972
	LRRK1	0.000161882128622617	0.0336387783173972
		0.00016188689212723	0.0336387783173972
N_Shore	TCP11L1;TCP11L1	0.000161899534935948	0.0336387783173972
S_Shelf	LSM14B	0.000162022598141714	0.0336499120261516
Island	MAML3	0.000162180277255928	0.0336593836349509
	PRPF4B	0.000162207198480309	0.0336593836349509
S_Shore	MFSD2B	0.000162384662593398	0.0336817780344957
N_Shelf		0.000162703661088133	0.033733497712547
		0.000162819207830913	0.0337430093421937
Island	LONP1	0.000163154139746215	0.03377353514352
S_Shore	IDUA;SLC26A1;SLC26A1	0.000163370366720623	0.03377353514352
Island	LOC100128811;GPR158	0.000163383746737792	0.03377353514352
S_Shore	MYO5A;MYO5A	0.000163386502260715	0.03377353514352
N_Shelf	RASA3	0.000163425396443262	0.03377353514352
N_Shelf	LSM5;LSM5	0.000163495362674535	0.03377353514352
N_Shore	PSMD6	0.00016350549397089	0.03377353514352
S_Shore	TCEAL3;TCEAL3	0.000163524368784503	0.03377353514352
S_Shore		0.000163739166554892	0.0338032014249742
Island		0.000163807595611241	0.0338032014249742
		0.00016393295518865	0.0338143452974072
N_Shore	VSX1;VSX1	0.000164001232857295	0.0338143452974072
		0.000164194608931649	0.0338280560452715
	CCL22	0.000164261070837805	0.0338280560452715
	PARK2;PARK2;PARK2	0.000164277267988393	0.0338280560452715
S_Shelf	TCIRG1;TCIRG1	0.000164488513429954	0.0338399266754566
	CD40LG	0.000164514383095604	0.0338399266754566
	MIR496;MIR377	0.000164544525516338	0.0338399266754566
		0.000164726891246583	0.0338630524630735
Island	GALR1	0.000164823121578511	0.0338684592102301
	TBC1D8	0.000165202186712228	0.033911322104062
	PCGF3	0.000165325154327034	0.033911322104062
Island	ZNF578;ZNF578	0.000165388546006063	0.033911322104062
N_Shelf		0.000165404464044258	0.033911322104062
N_Shore	C1orf70	0.0001654453817812	0.033911322104062

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	REPER;REPER	0.000165451822912091	0.033911322104062
Island	B3GNTL1	0.000165570149327019	0.0339184374357557
Island	LSM4	0.000165634240736763	0.0339184374357557
		0.000165696635467915	0.0339184374357557
	WSCD1	0.000166092816330328	0.0339823761669917
Island	FLI1;FLI1	0.000166150926316418	0.0339823761669917
N_Shore		0.000166219478944104	0.0339823761669917
Island	MED16	0.000166310366803699	0.0339852289876837
Island	EPHA10;EPHA10	0.00016653021332867	0.0339852289876837
	CAT	0.000166555770561505	0.0339852289876837
	ARHGEF10	0.000166579530660764	0.0339852289876837
	ISPD;ISPD	0.000166860845199889	0.0339852289876837
N_Shore	DUSP9	0.000166921117498969	0.0339852289876837
		0.000166957383401048	0.0339852289876837
		0.000166967113552065	0.0339852289876837
Island	EPB41L3;EPB41L3	0.000167028568529769	0.0339852289876837
S_Shore	GPR161	0.000167067375447143	0.0339852289876837
	DIP2C	0.000167072342829681	0.0339852289876837
	MBNL1;MBNL1;MBNL1;	0.000167090173596764	0.0339852289876837
		0.000167145646928535	0.0339852289876837
N_Shore		0.000167294903585176	0.0339855646661964
	KIAA1530	0.00016746341249031	0.0339855646661964
N_Shore	MORN1	0.000167626216509687	0.0339855646661964
Island		0.000167631746242171	0.0339855646661964
	LOH12CR1	0.000167670309266762	0.0339855646661964
Island	TTYH3	0.000167681674126573	0.0339855646661964
Island	WDR1;WDR1	0.000167791221879302	0.0339855646661964
Island	C11orf88;C11orf88	0.000167797234922906	0.0339855646661964
S_Shore	SPSB4	0.000167944303755449	0.0339855646661964
	ANP32A	0.000168013663572578	0.0339855646661964
		0.000168070330261636	0.0339855646661964
	TSSK1B;MCC	0.000168111616931024	0.0339855646661964
Island	ALOX12	0.000168157067484326	0.0339855646661964
S_Shore	TBCD	0.000168166796941497	0.0339855646661964
	MAD1L1;MAD1L1;MAD1	0.000168241279960201	0.0339855646661964
Island		0.00016827003369543	0.0339855646661964
	MPDZ	0.000168385755758545	0.0339947607993986
	CWC22	0.000168795657141221	0.0340353832854632
Island	APCDD1L	0.000168796670634277	0.0340353832854632
	ISPD;ISPD	0.000168797792085237	0.0340353832854632
N_Shore	ACADS	0.000168972517020382	0.034050854089799
	TSNARE1	0.000169015130814797	0.034050854089799
Island	SSC5D	0.000169100496995723	0.0340538869885462
N_Shore	LRP5	0.000169262093957306	0.0340722625336128
Island	GCK;GCK;GCK	0.000169762705448216	0.0341146672509317
	ANKRD26P1	0.000169824076783936	0.0341146672509317
Island	MICAL3	0.000169909680413887	0.0341146672509317
Island	REXO1L2P;REXO1L1	0.000169926240510836	0.0341146672509317
	PTGFRN	0.000169970600839216	0.0341146672509317
N_Shore	SRY	0.000170012644082695	0.0341146672509317
Island	ADARB2	0.000170043282040456	0.0341146672509317
Island	CARS2	0.000170105604567351	0.0341146672509317
S_Shore	MYEOV2;MYEOV2	0.00017010668747432	0.0341146672509317
S_Shelf	DIP2C	0.000170501611954604	0.0341797157325801
		0.000171058491531534	0.0342771633889161

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Island	MAG;MAG	0.000171149734483832	0.0342812635045004
		0.000171297018925365	0.0342865813384797
Island	DMRTA2	0.000171317868867229	0.0342865813384797
N_Shore	LOC100129637	0.000171436545514421	0.0342961606386914
	TMEM123	0.000171546829320536	0.0343040537203421
		0.000171713149303575	0.0343096480836288
	APOBEC3G	0.000171716485737297	0.0343096480836288
	VAV2;VAV2	0.000172132948581366	0.0343459261489263
Island	PCDHGA4;PCDHGB3;P	0.000172186039019724	0.0343459261489263
	WISP3;WISP3	0.000172201749222359	0.0343459261489263
N_Shore		0.000172305232646152	0.0343459261489263
Island	EVX1	0.000172413708495604	0.0343459261489263
		0.000172427444272958	0.0343459261489263
Island		0.000172455041293042	0.0343459261489263
	MAGEA1	0.000172465374271798	0.0343459261489263
Island	ACRC;BCYRN1	0.000172901727365443	0.0344162062126709
	T-SP1	0.000173097335068184	0.0344162062126709
S_Shelf		0.000173117204188594	0.0344162062126709
Island	ABCB1	0.00017312956134489	0.0344162062126709
Island	DOCK11	0.000173324212636166	0.0344162062126709
	NDRG1;NDRG1	0.000173343306751335	0.0344162062126709
	CCDC88B	0.000173375192367582	0.0344162062126709
Island	FAM9A;FAM9A	0.00017344243773635	0.0344162062126709
Island	AZ11;AZ11	0.000173519840571544	0.0344162062126709
Island	CELSR3	0.000173591295977358	0.0344162062126709
		0.000173599941728292	0.0344162062126709
Island		0.000173773757856807	0.0344182968384439
	MAD1L1;MAD1L1;MAD1	0.000173806047911324	0.0344182968384439
Island		0.000173827310296601	0.0344182968384439
S_Shelf	PFKP	0.000173894744982547	0.0344182968384439
N_Shelf		0.000174077995467759	0.0344329540410636
		0.000174165906065889	0.0344329540410636
		0.000174191855405277	0.0344329540410636
	ABCC5	0.000174293180256956	0.0344329540410636
Island	MAD1L1;MAD1L1;MAD1	0.000174324272562201	0.0344329540410636
Island	KCNAB2;KCNAB2	0.000174570370651931	0.0344675070387266
S_Shelf	DNAJC17	0.000174688694655203	0.0344768141967732
Island	ASPHD1	0.00017533002765193	0.0345628221847307
	TRIM61	0.000175400600624778	0.0345628221847307
Island	PCDHGA4;PCDHGA11;	0.000175446153133046	0.0345628221847307
Island	STX11	0.000175476620548537	0.0345628221847307
Island	CRBN	0.000175490985663431	0.0345628221847307
N_Shore	PXDN	0.000175636662956771	0.0345628221847307
		0.000175690485731728	0.0345628221847307
	PAGE3	0.000175801349810703	0.0345628221847307
Island	ITGA4	0.000175866223542457	0.0345628221847307
		0.000175891965662113	0.0345628221847307
Island	ADAMTS7	0.000175923606218543	0.0345628221847307
	FNIP2	0.000175980838295661	0.0345628221847307
N_Shore	SLC12A7	0.000176063001509384	0.0345649425237262
N_Shore	LOC100130872;LOC100	0.000176172916247229	0.0345658481109544
	CDH23	0.000176277409280192	0.0345658481109544
	ALDH1L1	0.000176319325558414	0.0345658481109544
S_Shore		0.000176353090759652	0.0345658481109544
Island	PENK;PENK	0.000176605102894855	0.0345808956833663

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	REEP5	0.000176638983554262	0.0345808956833663
Island	C5orf58	0.000176651009216547	0.0345808956833663
N_Shore	G0S2	0.000176752805576663	0.0345808956833663
		0.000176845114870291	0.0345808956833663
N_Shore	UBE2I;UBE2I;UBE2I;UB	0.000176858263785058	0.0345808956833663
		0.000177309317392	0.0346434125612538
N_Shore	ANKLE2	0.000177433598106964	0.0346434125612538
		0.000177459712846281	0.0346434125612538
		0.000177543485548519	0.0346434125612538
Island	PML;PML;PML;PML;PM	0.000177615136684441	0.0346434125612538
		0.000177656727060656	0.0346434125612538
Island	C6orf174	0.000177678700876796	0.0346434125612538
	IGSF21	0.000177817555425779	0.0346565342179438
S_Shore	MCF2L;MCF2L	0.000177942218985384	0.0346579401481122
		0.000177967887572095	0.0346579401481122
N_Shore		0.00017816590064608	0.0346825562019344
Island	HOXA9	0.000178299552726684	0.0346836807992386
S_Shore	MST1P2	0.000178325923054264	0.0346836807992386
Island	KCNS3	0.000178386514986638	0.0346836807992386
	XKR6	0.000178508905418554	0.0346935496054741
		0.000178618334887806	0.0347008925168618
		0.000178869540683209	0.0347191871423432
N_Shore		0.000178898588809716	0.0347191871423432
Island	CEP72	0.000178955769959115	0.0347191871423432
Island		0.00017899924698174	0.0347191871423432
Island	PLXNA1	0.000179091174051609	0.034723111638329
Island	GDF1;LASS1	0.000179266534807422	0.0347292718545816
Island	SEC1	0.00017940042808707	0.0347292718545816
	PRDM10;PRDM10;PRD	0.000179432302680475	0.0347292718545816
Island	PPAPDC3	0.000179550086512398	0.0347292718545816
		0.0001795522602195	0.0347292718545816
Island		0.000179553185823305	0.0347292718545816
S_Shore	TCEB3C;KATNAL2	0.000179825567096951	0.0347556570875138
Island	DOCK1;FAM196A	0.000179833121687523	0.0347556570875138
S_Shelf	RIBC1;RIBC1	0.000179958739679962	0.0347660616655356
N_Shore	CASKIN2;CASKIN2	0.000180458288031772	0.0348486684015103
	SDCCAG8;AKT3	0.000180533371556643	0.0348492726899845
N_Shore		0.000180670708043834	0.034861888714474
	GPR119	0.000180868898400808	0.0348669492941082
N_Shore	EXD3	0.000180894044412204	0.0348669492941082
		0.000180912906779733	0.0348669492941082
N_Shore	PRF1;PRF1	0.000181430133990656	0.0349504457499446
Island		0.000181490468303537	0.0349504457499446
Island		0.000181646899587019	0.0349616718200019
S_Shelf	DGKH;DGKH	0.000181718295872498	0.0349616718200019
	NFASC;NFASC;NFASC	0.000181765322134444	0.0349616718200019
S_Shore	KIAA0182;KIAA0182	0.000181909221655443	0.0349700418719149
Island	EVC2;EVC2	0.00018201373466657	0.0349700418719149
S_Shelf		0.000182025448942544	0.0349700418719149
		0.00018219795460653	0.0349770220166088
	CPEB1;CPEB1;CPEB1;C	0.000182246796046102	0.0349770220166088
Island	B3GALT4	0.000182278436111951	0.0349770220166088
Island	CNTNAP5;CNTNAP5	0.00018235729066428	0.0349782949706841
Island	CXorf36	0.000182429683755737	0.0349783280225643
Island		0.000182787842691621	0.0349957564047601

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	ACTR3C;ACTR3C	0.000182794206362415	0.0349957564047601
Island	PCDHGA2;PCDHGA1;P	0.00018282196331267	0.0349957564047601
Island		0.000182868857918506	0.0349957564047601
S_Shore	MECOM;MECOM;MECC	0.000182893040688974	0.0349957564047601
S_Shore	MUC5B	0.000182995174086716	0.0349957564047601
N_Shelf	TRIML2	0.00018302637892584	0.0349957564047601
N_Shore	C7orf50;C7orf50;C7orf5	0.000183300117769346	0.0350255039095175
Island	HAS3;HAS3	0.00018335376436547	0.0350255039095175
Island		0.000183483576573466	0.0350255039095175
Island	TMEM185B	0.000183569223968726	0.0350255039095175
S_Shore	MAEA;MAEA	0.000183577185114176	0.0350255039095175
Island	H1FNT	0.000183626429294992	0.0350255039095175
Island		0.000183695843708814	0.0350255039095175
Island	MAST3	0.000183930291643598	0.0350255039095175
	CTNNA2;CTNNA2	0.000184240971324605	0.0350255039095175
Island	JAKMIP3	0.000184253492180428	0.0350255039095175
		0.000184302442056761	0.0350255039095175
Island		0.000184317261716368	0.0350255039095175
		0.000184376501410319	0.0350255039095175
S_Shore	OPCML	0.000184378905751781	0.0350255039095175
Island	FCGBP	0.000184433525777115	0.0350255039095175
Island		0.000184511040256022	0.0350255039095175
S_Shelf		0.000184511352565578	0.0350255039095175
	VPS37A;VPS37A	0.000184606968179791	0.0350255039095175
S_Shore	CXCR7	0.000184634028898526	0.0350255039095175
N_Shore	DDX51	0.000184788251487273	0.0350255039095175
		0.000184851150847908	0.0350255039095175
N_Shelf	DUSP14	0.000184861108220803	0.0350255039095175
Island	BEND2	0.000184914077413247	0.0350255039095175
	TRAPPC9;TRAPPC9	0.000184981723587125	0.0350255039095175
Island	FAM47C;FAM47C	0.000184989911733951	0.0350255039095175
Island	EEF1A2	0.000185110667230898	0.0350283396796757
	TXNDC5;TXNDC5	0.000185149537149579	0.0350283396796757
Island		0.000185337835594022	0.0350369748174582
S_Shore	PPFIA2	0.000185467625896875	0.0350369748174582
N_Shore		0.000185474376295699	0.0350369748174582
	OPCML;OPCML	0.00018554432866917	0.0350369748174582
	MUC15;MUC15;ANO3;M	0.000185556889292893	0.0350369748174582
Island	CBFA2T3;CBFA2T3	0.000185677549935608	0.0350460948451144
	ATP2B4;ATP2B4	0.000186063967638081	0.0350850937443134
	TNXB;TNXB	0.000186072003915225	0.0350850937443134
Island		0.000186101493478844	0.0350850937443134
N_Shore	C7orf50;C7orf50;C7orf5	0.000186307191204875	0.0351007055807362
Island	LMX1A	0.000186387301675203	0.0351007055807362
S_Shore	CYP2E1	0.000186401723540296	0.0351007055807362
Island	SYCE1;SYCE1;SYCE1	0.000186577932295827	0.0351022315777481
S_Shelf		0.000186578419947088	0.0351022315777481
Island	ZBTB12	0.000186627257136636	0.0351022315777481
Island	RASAL1	0.000186700427363391	0.0351023619886546
	GAGE10	0.000186885257905672	0.0351077826819109
Island		0.000186921943505325	0.0351077826819109
	NGEF;NGEF	0.000187018557219333	0.0351077826819109
Island		0.000187019210900387	0.0351077826819109
S_Shelf	POLR2B	0.000187191018095561	0.0351264199299235
	SNX8	0.000187340699007866	0.035140892349723

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	DIAPH2;DIAPH2;RPA4;f	0.000187572054075518	0.0351469971895795
S_Shore		0.000187655042572009	0.0351469971895795
Island	FLJ30058	0.000187794678992751	0.0351469971895795
Island	DNAH9	0.000187870019251928	0.0351469971895795
	SNAP47	0.000187880379191965	0.0351469971895795
S_Shore	KIAA1530	0.000187972405291727	0.0351469971895795
Island	PPP1R13B	0.000187976815427536	0.0351469971895795
S_Shore	KIAA2022;KIAA2022	0.00018800158863956	0.0351469971895795
	CTNNBIP1;CTNNBIP1	0.000188048948395437	0.0351469971895795
N_Shore	PTPRN2;PTPRN2;PTPF	0.000188113661730197	0.0351469971895795
S_Shore	LRP1	0.000188171504078005	0.0351469971895795
Island	PKD1;PKD1	0.000188408780921659	0.0351777497378113
S_Shore	TRAPPC9;TRAPPC9	0.000188684039959898	0.0352155674965616
	HDAC4	0.00018882845764149	0.0352252962936938
	PAGE2B	0.000188961560900843	0.0352252962936938
Island		0.00018897464813956	0.0352252962936938
Island		0.000189084556055061	0.0352252962936938
N_Shore	RHPN1	0.000189203308583615	0.0352252962936938
N_Shelf	HOXC9	0.000189216758428679	0.0352252962936938
Island	TACC2;TACC2;TACC2;	0.000189281772099355	0.0352252962936938
	ATXN7L1;ATXN7L1	0.000189318012187033	0.0352252962936938
		0.000189556562104942	0.0352359837994256
	PLEKHG4B	0.000189661617384598	0.0352359837994256
Island		0.000189667634469594	0.0352359837994256
	GTF2IRD1;GTF2IRD1	0.000189691016069715	0.0352359837994256
S_Shelf	RTN3;RTN3;RTN3;RTN	0.000189752949091961	0.0352359837994256
S_Shelf		0.000189811968683635	0.0352359837994256
S_Shore	MUC2	0.000190264523304426	0.0352899849265288
Island	SERGEF	0.000190303022214284	0.0352899849265288
		0.000190321458995702	0.0352899849265288
Island	SLC44A2;SLC44A2	0.000190498696982891	0.0353014209033211
Island	ABCA7	0.000190528909804948	0.0353014209033211
		0.000190692374460107	0.0353095373343692
	ZCCHC14	0.000190739887229673	0.0353095373343692
Island	TBX4	0.000190850886568502	0.0353095373343692
	SV2A	0.000190864334365103	0.0353095373343692
Island		0.000191055178205788	0.0353203103284049
Island	SRC;SRC	0.000191068421123049	0.0353203103284049
N_Shore	ETNK1;ETNK1	0.000191202301362183	0.0353315736769321
	NOMO1	0.000191412886842003	0.0353464549114348
Island		0.000191481674787242	0.0353464549114348
Island	PTPRU;PTPRU;PTPRU	0.000191509848717618	0.0353464549114348
		0.000191574756914296	0.0353464549114348
	CUX1;CUX1;CUX1	0.00019177056908538	0.0353506349831072
N_Shore	AGAP3;AGAP3	0.000191823712924583	0.0353506349831072
	P704P	0.000191857487602692	0.0353506349831072
N_Shore	SOLH	0.00019195992682242	0.0353506349831072
Island		0.000191962359997052	0.0353506349831072
Island		0.000192100679806045	0.035352147272607
N_Shore	HIST1H3E	0.000192188242028176	0.035352147272607
Island	TSNARE1	0.000192339636323558	0.035352147272607
Island	GALNS	0.000192403297078321	0.035352147272607
	CDH15	0.000192457782728356	0.035352147272607
	CDK17;CDK17	0.000192473101152308	0.035352147272607
	PCSK6;PCSK6;PCSK6;f	0.00019257298144853	0.035352147272607

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N_Shore		0.000192592739957264	0.035352147272607
		0.000192639488917575	0.035352147272607
	TTC7B	0.00019277103386865	0.035352147272607
	CUX2	0.000192816647362395	0.035352147272607
Island	RGMA;RGMA;RGMA;R	0.000193176027647102	0.035352147272607
S_Shore		0.000193220286537227	0.035352147272607
Island	LOC641367;ZNF100	0.000193244233833699	0.035352147272607
S_Shore		0.000193263796243196	0.035352147272607
	SDHA	0.000193273824324218	0.035352147272607
N_Shelf	MCF2L;MCF2L	0.000193312133126365	0.035352147272607
S_Shelf	ADAMTS2;ADAMTS2	0.000193437813112336	0.035352147272607
N_Shore	DLL1	0.000193462121388968	0.035352147272607
		0.000193544374567193	0.035352147272607
		0.000193634288310858	0.035352147272607
		0.000193647480382242	0.035352147272607
Island	ALX3	0.000193649402187016	0.035352147272607
Island	LTB4R2;LTB4R2;LTB4R	0.000193724878979407	0.0353526006072725
	R3HDM1	0.000194241383435795	0.0354243286889755
		0.00019437132425691	0.0354243286889755
Island	BLCAP;BLCAP;BLCAP;f	0.000194401540181182	0.0354243286889755
N_Shore	C7orf50;C7orf50;GPR14	0.00019441050050131	0.0354243286889755
Island	CACNA1C;CACNA1C;C	0.00019458021272846	0.0354419185895868
Island	ZBTB16;ZBTB16	0.000194734082374594	0.0354529354353578
Island		0.000194787097906338	0.0354529354353578
Island		0.000195101409896394	0.0354552124459884
Island		0.000195136298607029	0.0354552124459884
		0.000195139502248581	0.0354552124459884
Island	PAQR9	0.000195179539401234	0.0354552124459884
Island	CLDN10;CLDN10	0.000195219864269182	0.0354552124459884
	PCSK6;PCSK6;PCSK6;f	0.00019523884084747	0.0354552124459884
S_Shelf		0.000195391892129553	0.0354633854394048
	NUDT3	0.000195430291101577	0.0354633854394048
		0.0001956420985817	0.0354885241181954
Island	INPP5A	0.000195882675625748	0.035508563447496
N_Shelf	DOHH;DOHH	0.000195929422176277	0.035508563447496
Island	PCDH11X;PCDH11X	0.000195972518649991	0.035508563447496
	KCNQ1;KCNQ1	0.000196117356313481	0.0355215177997482
Island	ALX4	0.000196614618199619	0.0355982710129086
Island	ZSCAN1	0.00019680492232927	0.0356055022563913
Island	REXO1	0.000196832351097277	0.0356055022563913
Island	GNASAS;GNAS	0.000196875104614909	0.0356055022563913
		0.00019713887950721	0.0356398984013921
	UVRAG	0.000197307195310493	0.0356570176749084
	CIT	0.00019750028511961	0.0356622234504365
N_Shore		0.000197582932245291	0.0356622234504365
Island		0.000197611917176469	0.0356622234504365
	BAIAP2L1	0.000197694014361317	0.0356622234504365
	BAIAP2L1	0.000197704165517828	0.0356622234504365
	TBC1D5;TBC1D5;TBC1	0.000197845397823879	0.0356744126213887
Island	ADARB1;ADARB1;ADA	0.000198033794678069	0.0356950940109623
	KCNJ8	0.000198411504348653	0.0357498704775527
		0.000198659208858271	0.0357732133878189
S_Shelf	ANKRD11	0.000198726617873975	0.0357732133878189
Island	CPAMD8	0.000198836069761942	0.0357732133878189
Island	ARHGEF4;ARHGEF4	0.000198841056852956	0.0357732133878189

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Island	KCND2	0.000198910367322348	0.0357732133878189
Island	DUOX2	0.000199029175967067	0.0357809791069339
N_Shore	SLC9A3	0.00019911188468443	0.0357809791069339
Island		0.000199175181277641	0.0357809791069339
Island	NDUFS7	0.00019926989577552	0.0357847209015495
Island		0.000199546685145682	0.0357988157197039
Island	JPH3	0.000199771639432108	0.0357988157197039
	MAGEB6;MAGEB6	0.000199784798163681	0.0357988157197039
S_Shore	MIR124-2	0.000199798286166496	0.0357988157197039
Island	TBCD	0.000199837400507926	0.0357988157197039
Island	HOXA9	0.000199839081782929	0.0357988157197039
Island	PCDHGA4;PCDHGA9;P	0.00019994389810361	0.0357988157197039
	TSPAN9;TSPAN9	0.000199973169229808	0.0357988157197039
	COTL1	0.000200074391680424	0.0357988157197039
		0.000200095543858261	0.0357988157197039
Island	GPER;GPER;C7orf50;C	0.000200179137080272	0.0357988157197039
N_Shore	FAM47B	0.000200236941856529	0.0357988157197039
S_Shore	CYP46A1	0.000200412864927584	0.0357988157197039
N_Shore	DLK1	0.000200457306994494	0.0357988157197039
	RIMBP2	0.000200667597702333	0.0357988157197039
N_Shelf	NAT15;NAT15;NAT15	0.000200703117059633	0.0357988157197039
Island	RCAN3	0.000200919362731001	0.0357988157197039
S_Shore	EP400	0.000200922983176155	0.0357988157197039
	ADAM2	0.000200933484311273	0.0357988157197039
Island		0.000200991683038059	0.0357988157197039
	CORO1B;CORO1B	0.000201048800361683	0.0357988157197039
	MYOM2	0.000201149328281942	0.0357988157197039
		0.000201163011016414	0.0357988157197039
Island	ANKRD58	0.000201192583241364	0.0357988157197039
Island	MYH14;MYH14;MYH14	0.000201196255384368	0.0357988157197039
Island	HEATR2	0.000201312630273692	0.03580256852756
	KCTD18	0.000201365192110821	0.03580256852756
	NAALADL2	0.000201913648671617	0.0358746154021839
Island	MAD1L1;MAD1L1;MAD1	0.000201918549705989	0.0358746154021839
Island	PCDHA1;PCDHA1;PCD	0.00020221815039205	0.035879311362486
Island	FHOD3	0.000202291012501736	0.035879311362486
Island	SAFB2	0.000202295697486415	0.035879311362486
	CPT1A;CPT1A	0.000202303118152247	0.035879311362486
N_Shelf	ABCB6	0.000202315386013419	0.035879311362486
		0.000202912566039736	0.0359490772066336
	INPP5A	0.000202964113021297	0.0359490772066336
Island		0.000202988800368719	0.0359490772066336
Island	C12orf34	0.000203005680400852	0.0359490772066336
Island	KIAA1614	0.000203343196728108	0.0359830970572443
	ABL2;ABL2;ABL2;ABL2;	0.000203346382378935	0.0359830970572443
Island	SPATA18	0.000203431237034986	0.0359849648929765
Island	TNRC18	0.000203628960126252	0.0360038588682946
	FAM20C	0.000203686725440824	0.0360038588682946
Island	SLC6A1	0.000203764031102255	0.0360043832045238
	PTPN14	0.000203897484603198	0.0360116754536583
Island		0.000204005132682184	0.0360116754536583
S_Shore	PCGF3	0.000204028364104348	0.0360116754536583
S_Shelf		0.000204234417606997	0.0360135212408787
S_Shelf	CLK3;CLK3	0.000204264888930085	0.0360135212408787
Island	WDR37	0.000204268175979485	0.0360135212408787

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Island	CPLX1	0.000204336254312568	0.0360135212408787
	ST18	0.000204488948333439	0.0360198972155542
Island	KCNV2	0.000204549408249188	0.0360198972155542
	ZC3H12C	0.000204608563906624	0.0360198972155542
Island	EPHB4	0.00020471324671046	0.0360198972155542
N_Shelf	CEP72	0.000204744287481383	0.0360198972155542
Island	C21orf29	0.000204874933239358	0.0360297937694815
		0.000205054464028168	0.0360400980474096
N_Shore		0.000205143976850443	0.0360400980474096
		0.000205280170845047	0.0360400980474096
Island		0.000205282031464233	0.0360400980474096
N_Shore	ACAA2;SCARNA17	0.000205305591313277	0.0360400980474096
Island	C1QTNF1;C1QTNF1;C1	0.000205468453351941	0.0360527902742562
N_Shelf		0.000205705831898771	0.0360527902742562
	PARD3B;PARD3B;PAR	0.000205790413486974	0.0360527902742562
	ENDOD1	0.00020581325092785	0.0360527902742562
	MIR492	0.000205827662154344	0.0360527902742562
Island	DNMT3A;DNMT3A;DNM	0.000205903636952497	0.0360527902742562
N_Shore	THSD1;THSD1	0.000205970894816151	0.0360527902742562
S_Shore	LAMP1	0.000206096799371182	0.0360527902742562
Island	BIRC8;BIRC8	0.000206103517472736	0.0360527902742562
		0.000206122286211563	0.0360527902742562
Island	RREB1;RREB1;RREB1;	0.00020629601877537	0.0360701513694516
	CUX1;CUX1;CUX1	0.00020645373579477	0.0360707471385404
Island		0.000206473027166612	0.0360707471385404
N_Shore		0.000206522855138951	0.0360707471385404
Island		0.000206837069844419	0.0361126041284781
N_Shore		0.000207044794322941	0.0361220563366765
Island		0.000207110587135684	0.0361220563366765
Island	KSR2	0.000207114954724515	0.0361220563366765
		0.000207297082633028	0.0361293868724026
		0.000207306181011525	0.0361293868724026
	NEK7	0.000207518432557884	0.0361420168697636
N_Shelf	ADAM8;ADAM8;ADAM8	0.00020757390752066	0.0361420168697636
N_Shelf		0.000207602520893372	0.0361420168697636
S_Shelf	ARSD	0.000207709841651079	0.0361477071712752
Island	MIR124-3	0.000207802694988377	0.0361508765266688
	TLR5	0.000208057445839726	0.0361630503883265
Island	DPP6;DPP6;DPP6	0.000208156297192044	0.0361630503883265
N_Shore	C1orf70	0.000208203068504221	0.0361630503883265
N_Shelf		0.000208208214155428	0.0361630503883265
Island		0.000208296548352667	0.0361630503883265
	KCNQ1;KCNQ1	0.000208320674306367	0.0361630503883265
Island	GALR1	0.000208504743940144	0.0361686950991363
Island		0.000208565172777234	0.0361686950991363
S_Shelf	FO XK2	0.000208600863220773	0.0361686950991363
Island	CDH2	0.000208654729702693	0.0361686950991363
Island	INPP5A	0.000208771763537052	0.0361686950991363
Island	TOLLIP	0.000208827783187028	0.0361686950991363
Island	CTTN;CTTN	0.000208875941139285	0.0361686950991363
	KLHDC4	0.00020933614558084	0.0362252308385906
	WDR8	0.000209474248269167	0.0362252308385906
	FGD1	0.000209475311969526	0.0362252308385906
Island	CANT1;CANT1;CANT1	0.000209501618910633	0.0362252308385906
N_Shore	POU3F4	0.000209674663827593	0.0362411019715748

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Island	MIR124-2	0.000209743062667267	0.0362411019715748
Island	PCDH19;PCDH19	0.000209830146528331	0.0362432188720878
Island	ALX4	0.000210151206176448	0.0362857336653862
	CD300A	0.000210338711413323	0.0362956563438736
Island	ONECUT1	0.000210358555427147	0.0362956563438736
N_Shore	ATP11A;ATP11A	0.000210500154019698	0.036304986124974
	GREB1	0.000210690117578596	0.036304986124974
N_Shore	PRICKLE3	0.000210778268094201	0.036304986124974
N_Shore	ELANE	0.000210792122356539	0.036304986124974
		0.000210851631562838	0.036304986124974
		0.000210898620634521	0.036304986124974
Island	ICAM5	0.000210976539483902	0.036304986124974
		0.000211122677884759	0.036304986124974
Island	ACTL7B	0.000211127409984443	0.036304986124974
Island	NMBR	0.000211188056516967	0.036304986124974
N_Shore	NYX	0.000211270865782202	0.036304986124974
	WDR37	0.000211386393579853	0.036304986124974
S_Shelf	NFATC4;NFATC4	0.000211387107567081	0.036304986124974
Island		0.000211497842462914	0.0363111281640733
S_Shore	PCGF3	0.000211741565561672	0.036337348346451
	BTF3L1	0.00021186792504449	0.036337348346451
Island	TRAPPC9;TRAPPC9	0.000211949362016385	0.036337348346451
Island	ZNRF4;ZNRF4	0.000212137212864248	0.036337348346451
Island	NTM;NTM;NTM;NTM	0.000212172564744585	0.036337348346451
N_Shore	RAB40B	0.000212202625150778	0.036337348346451
Island	NEURL1B	0.000212213810875968	0.036337348346451
Island	PCDHB5	0.000212250778861529	0.036337348346451
	PAK2	0.000212402264165747	0.0363384908877909
Island	KIAA0562	0.000212407510872526	0.0363384908877909
	MTMR15	0.000212590465650129	0.0363509028854424
Island		0.00021265169384582	0.0363509028854424
		0.000212705226402403	0.0363509028854424
	ARHGEF10	0.000212797754888069	0.0363538880550843
Island	MOBKL2A	0.000212895324273948	0.0363548892441914
S_Shelf	CCDC99	0.000212953741363281	0.0363548892441914
Island	CNPY1	0.000213135913642411	0.0363645102401371
Island		0.000213160263401124	0.0363645102401371
Island	AURKC;AURKC;AURKC	0.000213388238611955	0.0363782454306649
	MGMT	0.000213465914895735	0.0363782454306649
		0.00021346610956269	0.0363782454306649
Island	DRD1	0.000213558263639304	0.0363811487995448
	MTMR2;MTMR2;MTMR2	0.000213895608215398	0.036425602160489
S_Shore	ZFYVE28	0.000213969624005763	0.036425602160489
S_Shelf	C21orf70	0.000214249155335169	0.0364485898573335
N_Shelf	MLLT1	0.000214306788346585	0.0364485898573335
Island	C7orf50;C7orf50;C7orf50	0.000214330426704559	0.0364485898573335
		0.000214515929978299	0.0364580221525351
N_Shore		0.000214536443782016	0.0364580221525351
	CTTNBP2NL	0.000214623926071002	0.0364600957538892
		0.000215019473927865	0.0365024890418493
S_Shore	SIX3	0.000215041403707313	0.0365024890418493
		0.000215123612453351	0.0365024890418493
N_Shelf		0.000215215819389684	0.0365024890418493
S_Shore	MAN2C1	0.000215250314775247	0.0365024890418493
Island		0.000215389995534965	0.0365106218228505

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		0.000215512527328807	0.0365106218228505
Island		0.000215585624210716	0.0365106218228505
		0.000215599810898369	0.0365106218228505
	MGC14436;MGC14436;	0.000215954557016209	0.0365384173072629
Island	TUBGCP2	0.000215965309577974	0.0365384173072629
Island	CLVS2;CLVS2	0.000216000842668431	0.0365384173072629
N_Shore	FGFRL1;FGFRL1;FGFR	0.00021606571448511	0.0365384173072629
Island	SSBP4;SSBP4	0.00021619381133196	0.0365462098499778
Island	PCDHGA4;PCDHGB5;P	0.000216305684617013	0.0365462098499778
Island	TERT;TERT	0.000216447763285766	0.0365462098499778
N_Shelf	PPP2R5C;PPP2R5C;PP	0.000216450317909721	0.0365462098499778
N_Shore		0.000216518176659802	0.0365462098499778
S_Shore		0.000216733767654723	0.0365462098499778
S_Shore	FTSJ1;FTSJ1;FTSJ1	0.000216751646078126	0.0365462098499778
Island	MYO7A;MYO7A;MYO7A	0.000216751882938149	0.0365462098499778
S_Shelf		0.000216910568360045	0.0365462098499778
Island	MC1R	0.000217009767001221	0.0365462098499778
Island	OLFML2A	0.000217013935636946	0.0365462098499778
Island	TRIM74;TRIM73	0.000217187760755485	0.0365462098499778
Island		0.000217233798681375	0.0365462098499778
N_Shelf	PRKAR1B;PRKAR1B;PF	0.000217295059165334	0.0365462098499778
Island		0.000217357104915639	0.0365462098499778
	RUNDC2C	0.000217384391106958	0.0365462098499778
		0.000217394581278658	0.0365462098499778
S_Shelf	LOC100130872;LOC100	0.000217566798995052	0.0365496750001729
Island	SLC9A3	0.000217632263707258	0.0365496750001729
Island	FGF22	0.000217641589223143	0.0365496750001729
S_Shelf	NCOR2;NCOR2	0.000217824436907371	0.0365535896691341
S_Shore	HEATR2	0.000217950743337223	0.0365535896691341
	ADARB2	0.00021798646140415	0.0365535896691341
Island	WNT5B;WNT5B	0.000217993827368205	0.0365535896691341
Island	GSC	0.000218088323296058	0.0365535896691341
Island	KCNQ2;KCNQ2;KCNQ2	0.00021811773941836	0.0365535896691341
Island	APOB48R	0.000218455228042488	0.0365974847186711
Island		0.000218618844642229	0.0366035826417548
Island	KLHL35	0.000218642780328491	0.0366035826417548
Island	HDGF2;HDGF2	0.000218965557961609	0.0366429256207838
Island		0.000219029101682071	0.0366429256207838
Island	INPP5A	0.000219115583633749	0.036644735857533
	RASGRF1;RASGRF1;R	0.000219297124422945	0.0366550717443136
Island	KIF26A	0.000219328752211884	0.0366550717443136
N_Shelf	FIBCD1;FIBCD1	0.000219519786911596	0.0366695490578367
Island	EGLN3	0.000219611744981224	0.0366695490578367
S_Shelf	OSTF1	0.00021964251652668	0.0366695490578367
Island	SLC6A19	0.00021986358963196	0.0366834159552603
S_Shore	KDM2B	0.000220048714720227	0.0366834159552603
	ABLIM2;ABLIM2;ABLIM2	0.000220164744558505	0.0366834159552603
S_Shelf	NXPH4	0.0002202857698415	0.0366834159552603
Island	RPS6KA4;MIR1237;RPS	0.000220379792496484	0.0366834159552603
S_Shore	LOC401010	0.000220431924846825	0.0366834159552603
		0.000220432273810471	0.0366834159552603
N_Shore	TMEM26	0.000220464202501211	0.0366834159552603
	DOK4	0.000220494563295915	0.0366834159552603
Island		0.000220499068316868	0.0366834159552603
	PFKFB1	0.000220558730731881	0.0366834159552603

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Island		0.000220754980884241	0.036703452151308
N_Shelf	ZFPM1	0.000220843685823331	0.0367055999095349
Island	ZCCHC13	0.000221305698267077	0.03675363413845
	PCYT1B;PCYT1B;PCYT	0.00022135604610829	0.03675363413845
Island	DPY19L2P4	0.000221360348488843	0.03675363413845
Island	SLC12A7	0.000221575445774229	0.0367561209711746
Island	PRDM14	0.000221625278194683	0.0367561209711746
Island	SLC13A3;SLC13A3	0.00022164256363243	0.0367561209711746
Island	RASL10B	0.000221803957544897	0.0367561209711746
N_Shore		0.000221857947053096	0.0367561209711746
	CTAGE1	0.000221894748550346	0.0367561209711746
S_Shore	PFKP	0.000221906566292705	0.0367561209711746
	KCNK10;KCNK10;KCNK	0.000222074790725543	0.0367689901888803
Island	TBX20;TBX20	0.000222136097233601	0.0367689901888803
Island	PLEC1;PLEC1;PLEC1;P	0.000222457016977985	0.0368037246075225
N_Shore		0.000222596993351563	0.0368037246075225
		0.000222639922656054	0.0368037246075225
S_Shelf	TFAP2C	0.00022264990058337	0.0368037246075225
S_Shore	CYFIP1	0.000222849350797286	0.0368051690410946
S_Shore	SMOC1;SMOC1	0.000223153094960135	0.0368051690410946
Island		0.000223177052534953	0.0368051690410946
		0.000223207332415369	0.0368051690410946
	PAK3;PAK3;PAK3;PAK3	0.000223223144725701	0.0368051690410946
Island	RREB1;RREB1;RREB1;	0.000223244810272566	0.0368051690410946
Island	AMDHD2;ATP6V0C;AM	0.000223299188200362	0.0368051690410946
Island		0.000223328179105935	0.0368051690410946
		0.000223342573296396	0.0368051690410946
N_Shore	PJA1;PJA1;PJA1	0.000223560918919242	0.0368146670131594
Island	HSPG2	0.000223626595296877	0.0368146670131594
N_Shelf	INPP5A	0.000223628676086959	0.0368146670131594
	PRDM16;PRDM16	0.000223730820385082	0.0368146670131594
	C5orf45;C5orf45	0.000223798592735402	0.0368146670131594
N_Shelf		0.00022385628318537	0.0368146670131594
N_Shore	ALX1	0.000224014807366523	0.0368187536282928
	PASD1	0.000224033173886499	0.0368187536282928
S_Shore	DNAH17	0.000224379398076264	0.0368549639591136
N_Shelf	TUT1	0.000224434936340599	0.0368549639591136
Island	PCDHGA4;PCDHGA2;P	0.000224504875237161	0.0368549639591136
	TMCO3	0.000224635702704234	0.0368549639591136
N_Shelf	INPP5A	0.000224637106419384	0.0368549639591136
	CUX1;CUX1;CUX1	0.000224777068709816	0.0368549639591136
N_Shelf	TELO2	0.000224786173613218	0.0368549639591136
	ADAM5P	0.000224934445019993	0.0368667935987506
	LPCAT1	0.000225077791813783	0.0368778083627234
		0.000225754277846425	0.0369761381866655
		0.000225903962598697	0.0369881462764076
	IGF1R	0.000226156817304319	0.0369909255820865
Island	FLJ42875	0.000226360574231601	0.0369909255820865
Island	AURKC;AURKC;AURKC	0.000226397246039664	0.0369909255820865
Island	NONO;NONO;NONO;NO	0.000226420432985955	0.0369909255820865
N_Shelf	GRM2;GRM2	0.000226533998887708	0.0369909255820865
N_Shore	ERICH1	0.000226636841495899	0.0369909255820865
	ZSCAN21	0.000226691269478757	0.0369909255820865
	ACAN;ACAN	0.000226840692450475	0.0369909255820865
Island	IGFALS;IGFALS;IGFALS	0.000226886564873983	0.0369909255820865

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Island	SERPINB9	0.000227039612409482	0.0369909255820865
N_Shore	RARG;RARG	0.000227119076935325	0.0369909255820865
	RADIL	0.000227304927270816	0.0369909255820865
S_Shore	JAKMIP3	0.000227490033053248	0.0369909255820865
Island	C21orf99	0.000227502822964933	0.0369909255820865
Island	FRMD1;FRMD1	0.000227526554502085	0.0369909255820865
	TUBGCP2	0.000227551474536579	0.0369909255820865
S_Shore	CHRD1;CHRD1;CHR	0.000227600905464881	0.0369909255820865
S_Shore	LMF1	0.000227673712247954	0.0369909255820865
S_Shore		0.000227705287728801	0.0369909255820865
N_Shelf	HIST1H1A	0.000227791968515534	0.0369909255820865
Island	CLYBL	0.000227842792991519	0.0369909255820865
	VWF	0.000227920756604407	0.0369909255820865
	NSUN5B;NSUN5B;NSU	0.000227978869585219	0.0369909255820865
Island	ANKRD11	0.000228196049652758	0.0369909255820865
Island	IGLN5	0.000228405499894406	0.0369909255820865
Island	KCNF1	0.00022841299169644	0.0369909255820865
	PION	0.000228431518098645	0.0369909255820865
Island	CHRD1;CHRD1;CHR	0.000228469363013085	0.0369909255820865
Island	GALNT9	0.000228527100413532	0.0369909255820865
		0.000228581022734316	0.0369909255820865
N_Shore	NXN	0.000228604459026071	0.0369909255820865
	SH3BP4	0.000228618243216543	0.0369909255820865
Island	LRPAP1	0.000228641326402056	0.0369909255820865
N_Shore	MDGA1	0.000228657613026124	0.0369909255820865
	DLC1;DLC1	0.000228705153109035	0.0369909255820865
		0.000228722493304149	0.0369909255820865
Island		0.000228800566897481	0.0369909255820865
	DNAH10	0.000228849549758058	0.0369909255820865
		0.000228899610735587	0.0369909255820865
Island	POLM	0.000229206976175421	0.037008575011603
Island	NOTCH3	0.000229334922300461	0.037008575011603
Island	DLX4;DLX4;DLX4	0.000229385871389626	0.037008575011603
N_Shore		0.000229543822414687	0.037008575011603
	RUNDC2C	0.000229655988716969	0.037008575011603
Island	NCOR2;NCOR2	0.000229720890489742	0.037008575011603
N_Shore	WDR37	0.000229746627784104	0.037008575011603
	BHMT	0.000229834437970829	0.037008575011603
	MAD1L1;MAD1L1;MAD1	0.000229847356317948	0.037008575011603
N_Shore	CHD1L	0.000229890363523701	0.037008575011603
		0.000229901835547372	0.037008575011603
	CBFA2T3;CBFA2T3	0.000229964513242531	0.037008575011603
		0.000230002190233676	0.037008575011603
Island	WNT7A	0.000230089323476531	0.0370102994330026
N_Shore		0.000230262575504815	0.0370258704785424
	DIP2C	0.000230435756631938	0.037041275847068
Island	DND1	0.000230561775958513	0.037041275847068
N_Shore	NXN	0.000230587821563846	0.037041275847068
N_Shore		0.00023069514903827	0.0370462294621883
		0.000230940516270418	0.0370733395898807
	IGSF9B	0.00023115626904778	0.0370913167132692
		0.00023120566800673	0.0370913167132692
		0.000231503549650203	0.0371268068491174
Island	EPB41L3	0.00023159284866816	0.0371288336415778
Island	GIPC3	0.000231806658427122	0.0371329239902869

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Island		0.000231927472153867	0.0371329239902869
	KIAA1598;KIAA1598	0.000231932473988879	0.0371329239902869
Island	KCNQ1DN	0.0002320360182373	0.0371329239902869
Island	SALL3	0.000232041917107099	0.0371329239902869
N_Shore		0.000232226769679212	0.0371329239902869
	SERPINA13	0.00023227578817939	0.0371329239902869
S_Shelf	DOK3;DOK3;DOK3	0.000232302375992078	0.0371329239902869
		0.000232308387323738	0.0371329239902869
Island	HHIPL1;HHIPL1	0.000232611464971332	0.037169101871409
	KCNJ5	0.000232692368314539	0.0371697662545972
Island	CTBP1;CTBP1	0.000233420309140761	0.0372737524644244
		0.000233601264456106	0.0372903534633169
Island		0.000233802711880253	0.0372965372982741
Island	GGN	0.00023390480411287	0.0372965372982741
	SPEG	0.000233927557406531	0.0372965372982741
N_Shore	GAGE2D;GAGE8;GAGE	0.000234004143729817	0.0372965372982741
Island		0.00023402503866093	0.0372965372982741
Island	PAX1	0.00023411741314701	0.0372989855665874
Island	ARID3A	0.000234315306330427	0.037313393194119
S_Shore	ANO2	0.000234368635548758	0.037313393194119
S_Shore	RPL22L1	0.000234459515145397	0.037313393194119
Island	MTL5;MTL5	0.00023451601483074	0.037313393194119
S_Shore	PEG10;PEG10	0.000234600767502479	0.037314619612689
Island	NPAS3;NPAS3;NPAS3;N	0.000234745378180418	0.0373253628651448
Island		0.000234851912629238	0.0373300467949313
S_Shore	TBC1D16	0.000235172972970149	0.0373611566139491
Island	ST14	0.000235201913004554	0.0373611566139491
		0.000235424131627061	0.0373841942787791
	HRNBP3	0.00023570261819572	0.0374114532240526
Island	BCOR;BCOR	0.000235831278516939	0.0374114532240526
Island	C1QTNF4	0.000235861434511585	0.0374114532240526
S_Shore	RADIL	0.000235904770858941	0.0374114532240526
		0.000236071039960835	0.0374255667525471
N_Shelf	RAB37;RAB37;RAB37;R	0.000236154469191561	0.0374265423073307
Island	RFX2;RFX2	0.000236459955969884	0.0374479091350354
Island	SLC17A7	0.000236555941581809	0.0374479091350354
		0.000236569176841127	0.0374479091350354
N_Shore	MTFMT	0.000236665182498502	0.0374479091350354
		0.000236675888839815	0.0374479091350354
	DNMBP	0.000237087374371839	0.0374928366040601
S_Shelf		0.000237114661680145	0.0374928366040601
	RBMS3;RBMS3;RBMS3	0.000237368145777994	0.0375191967086657
S_Shore	VENTXP1	0.000237461977953184	0.0375191967086657
N_Shore	RPTOR;RPTOR	0.000237553525961123	0.0375191967086657
	SDK1	0.000237591237919739	0.0375191967086657
Island	ZNF837;ZNF837	0.000237686878134018	0.0375220655972158
N_Shelf	SOLH	0.000237934529780041	0.0375489218428539
S_Shelf	HCCA2	0.000238184690105052	0.0375761563632343
		0.000238263194382961	0.0375763014065541
Island	OBSCN;OBSCN	0.000238411788902868	0.0375874966342388
Island		0.00023878395699736	0.0376168437813695
Island	DCAF4L2;DCAF4L2	0.000238807007413149	0.0376168437813695
Island		0.000238830939199321	0.0376168437813695
	RASGRF1;RASGRF1;R	0.000238933671669826	0.0376207901597817
Island	FGF13;FGF13;FGF13;F	0.000239390684451621	0.0376659596905678

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	ADAMDEC1;ADAMDEC	0.000239411445039909	0.0376659596905678
N_Shelf	RNASEH1	0.000239470413760378	0.0376659596905678
Island	DIRAS1	0.000239630036071178	0.0376659596905678
Island		0.000239649668481413	0.0376659596905678
	C3orf17;C3orf17;C3orf1	0.000239687168257534	0.0376659596905678
Island	PCDHA2;PCDHA1;PCD	0.000239929779812718	0.0376902903804753
	LTA;LTA	0.000240070766138905	0.0376902903804753
	ACTN2	0.000240118676498273	0.0376902903804753
	ATP11A;ATP11A	0.000240398264594957	0.0376902903804753
Island		0.000240400060775992	0.0376902903804753
S_Shore	SPOCK2;SPOCK2	0.000240405529359449	0.0376902903804753
	C3orf59	0.00024052363122184	0.0376902903804753
N_Shore	PACS2;PACS2	0.000240608291647463	0.0376902903804753
N_Shore	NKD2	0.000240738969292212	0.0376902903804753
	AFF1;AFF1	0.000240778976936879	0.0376902903804753
	STARD3NL	0.000240783971168022	0.0376902903804753
S_Shelf	RPS6KA4;RPS6KA4	0.000240802217858851	0.0376902903804753
	PRDM16;PRDM16	0.000240945178487861	0.0376902903804753
N_Shelf	LRRC47	0.000240996816407122	0.0376902903804753
Island	HRNBP3	0.00024100930017722	0.0376902903804753
		0.000241125302732623	0.0376962596016713
N_Shore	FADD	0.000241655763953439	0.0377499275729863
Island	MXRA5	0.00024176229587711	0.0377499275729863
	MYT1L	0.000241776463070074	0.0377499275729863
N_Shore		0.000241780365108973	0.0377499275729863
Island	ATP2B2;ATP2B2	0.000241874428184308	0.0377524435805236
	MAD1L1;MAD1L1;MAD1	0.000241972507344595	0.0377555846068528
		0.00024206766371868	0.0377582677071014
Island		0.000242189863802666	0.0377651660612448
Island	UNC13A	0.000242488282710429	0.03779952929634
Island	ROR2	0.000242626638626307	0.0378035601770713
		0.000242670249502946	0.0378035601770713
N_Shore	GPRASP1;GPRASP1;G	0.000243134591315119	0.0378637173436319
Island	SIX6;SIX6	0.000243323871397163	0.0378685114161829
		0.000243338140026579	0.0378685114161829
		0.000243485981840482	0.0378685114161829
Island	KY	0.000243606092139842	0.0378685114161829
Island	GFRA1;GFRA1;GFRA1;	0.000243754008029008	0.0378685114161829
	COL4A2	0.000243778496330782	0.0378685114161829
Island		0.00024379069027026	0.0378685114161829
	DOCK1	0.000243797080705701	0.0378685114161829
Island	KEAP1;KEAP1	0.000243897884759539	0.0378685114161829
	ELMO1	0.000243947257768008	0.0378685114161829
Island	IRF4	0.000244571136468095	0.0379099586642301
	MAPRE1	0.000244581408433476	0.0379099586642301
	CUX1;CUX1;CUX1	0.000244642215255101	0.0379099586642301
S_Shore	H3F3C	0.000244664754517609	0.0379099586642301
	SOAT2	0.000245033375172379	0.0379099586642301
Island		0.000245098892467077	0.0379099586642301
S_Shore		0.000245122574916024	0.0379099586642301
N_Shelf	LONP1	0.000245139464084077	0.0379099586642301
N_Shore	CHST8;CHST8;CHST8	0.000245146998881451	0.0379099586642301
S_Shore	PLSCR1	0.000245199723658725	0.0379099586642301
S_Shore	CA10;CA10	0.00024526869373985	0.0379099586642301
		0.00024532882200179	0.0379099586642301

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N_Shore	ZNF275	0.000245338393979377	0.0379099586642301
	ERN1	0.000245346479837517	0.0379099586642301
Island	ITGAX	0.000245430991385952	0.0379099586642301
	NSMCE2	0.000245466639903011	0.0379099586642301
Island		0.000245924905676981	0.0379507045537032
Island	EXOC2	0.000245937743625543	0.0379507045537032
	LMF1	0.000245965542959943	0.0379507045537032
S_Shore	CCDC90A	0.000246163065684114	0.0379690849641587
Island		0.000246402590631619	0.0379856971343751
		0.00024642762689559	0.0379856971343751
Island	SNORA49;EP400	0.000246689335226012	0.0380024516980254
Island	GPR112	0.000246697796070196	0.0380024516980254
S_Shelf	STARD8;STARD8;STAF	0.000246771714427894	0.0380024516980254
	SYCP2	0.000246928352792786	0.0380084479739188
	TMEM120A	0.000246990334870206	0.0380084479739188
	ADAMDEC1;ADAMDEC	0.000247046083150563	0.0380084479739188
	FCRL1;FCRL1;FCRL1	0.000247190714386965	0.0380186226565471
S_Shelf	CYP46A1	0.000247374103242365	0.0380306693522019
Island	CILP2	0.000247426086055413	0.0380306693522019
N_Shore	NEU1	0.000247544129935734	0.0380367419832248
Island	ANKRD20B	0.000247911211933193	0.0380583298877308
Island		0.000248036122035257	0.0380583298877308
N_Shore	CA3	0.000248038820696911	0.0380583298877308
		0.000248124952866605	0.0380583298877308
	DIP2C	0.000248151511430284	0.0380583298877308
S_Shelf	TNS3	0.000248321897373313	0.0380583298877308
		0.000248345854382592	0.0380583298877308
Island	KDM4B	0.000248568164191782	0.0380583298877308
		0.000248598841205742	0.0380583298877308
	HDAC4	0.000248629947635151	0.0380583298877308
Island		0.000248640858746404	0.0380583298877308
		0.000248723078728768	0.0380583298877308
	HDAC9;HDAC9;HDAC9	0.000248744716103195	0.0380583298877308
	NPHP4	0.000248784746656803	0.0380583298877308
S_Shore		0.000248867307566095	0.0380589386602301
N_Shelf		0.000249405271651019	0.0381196888365382
		0.000249445751150502	0.0381196888365382
Island	WSCD1	0.00024950067333263	0.0381196888365382
	MEIS1	0.000250116499539451	0.0381956002630691
		0.000250155255323295	0.0381956002630691
Island	PLEKHF1	0.000250396758124406	0.0382033156397298
N_Shore	C5orf47	0.000250409167806941	0.0382033156397298
	HIP1R	0.000250444210408517	0.0382033156397298
	PDGFA;PDGFA	0.000250577513090458	0.0382033156397298
Island	PRKAR1B;PRKAR1B;PF	0.000250656158871725	0.0382033156397298
Island	CDH13	0.000250679062825708	0.0382033156397298
Island		0.000250863278485843	0.0382042105945791
S_Shore	C5orf33	0.000250894426855312	0.0382042105945791
Island	RASA3	0.000250923555778664	0.0382042105945791
Island	ARHGAP6;ARHGAP6	0.000251000460665773	0.0382042105945791
N_Shelf	MAGEB1;MAGEB1;MAG	0.000251276438046788	0.0382070875089467
Island	MICALL2	0.000251294026601243	0.0382070875089467
N_Shelf		0.000251313375241958	0.0382070875089467
Island		0.000251495401342551	0.0382070875089467
Island		0.000251525209129073	0.0382070875089467

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N_Shelf	RPTOR;RPTOR	0.00025161250142478	0.0382070875089467
Island		0.000251631470395949	0.0382070875089467
Island		0.000251650460235461	0.0382070875089467
S_Shelf		0.000251893396117682	0.0382319865480089
Island	OPLAH	0.000252122212203353	0.0382547275768762
N_Shore	C3orf38	0.00025222123463233	0.0382577668222058
		0.000252623392140058	0.0383067703187958
		0.000252755874920425	0.0383148635745961
Island	LASP1	0.000252864018276334	0.0383192633453334
		0.000253143892328558	0.038349676462943
	ACSF3;ACSF3;ACSF3	0.000253345606575933	0.0383682335537489
	CACHD1	0.000253460893165662	0.0383736939926412
N_Shore	PTPRF;PTPRF	0.000253568115246094	0.0383779304426764
S_Shore	RGMA;RGMA;RGMA;R	0.000253745253047065	0.0383802414730418
Island		0.000253780771284433	0.0383802414730418
	FRS3	0.000253894828295861	0.0383802414730418
N_Shore	UBA1	0.000253972414633498	0.0383802414730418
		0.000254176350940115	0.0383802414730418
		0.000254294523923639	0.0383802414730418
Island	C20orf85	0.000254320030187174	0.0383802414730418
	AXIN1;AXIN1	0.000254493441305939	0.0383802414730418
Island	UBE2K;UBE2K;UBE2K	0.000254581713900159	0.0383802414730418
Island	ST6GAL2;ST6GAL2;ST6	0.000254610130501723	0.0383802414730418
	MYT1L	0.000254645573957597	0.0383802414730418
	KIAA1211	0.000254746753155001	0.0383802414730418
	MAGEB2	0.000254832749977329	0.0383802414730418
S_Shelf	LRAT	0.000254928666027332	0.0383802414730418
N_Shore		0.000254960433515044	0.0383802414730418
	NDUFA10	0.000254968481368502	0.0383802414730418
Island	TSSK6;NDUFA13;TSSK	0.000255013639597019	0.0383802414730418
Island		0.000255161682285556	0.0383802414730418
N_Shore		0.000255177981117009	0.0383802414730418
S_Shore	CAPS2	0.000255245623502089	0.0383802414730418
	POLE	0.000255247525493558	0.0383802414730418
	NCBP2;NCBP2	0.000255482030671125	0.0383954249066804
	WSCD1	0.000255645304292673	0.0383954249066804
		0.000255687221825549	0.0383954249066804
Island	ABHD8	0.000255747517922434	0.0383954249066804
S_Shelf	PRKAR2B	0.000255880286396651	0.0383954249066804
	PIWIL4;PIWIL4	0.000255919653880802	0.0383954249066804
Island		0.000255957744515278	0.0383954249066804
Island		0.00025598271207076	0.0383954249066804
Island	PACS2;PACS2	0.000256491420867575	0.038431001982123
	ICK;ICK	0.000256545076499896	0.038431001982123
		0.000256608911937746	0.038431001982123
		0.000256614984214695	0.038431001982123
Island		0.000256637699545459	0.038431001982123
	POTEC	0.000256758144691419	0.038431001982123
		0.000256820984112638	0.038431001982123
	GPR133	0.000256926321918757	0.038431001982123
N_Shore		0.00025708224295541	0.038431001982123
Island	PTPRS;PTPRS;PTPRS;	0.000257090310576278	0.038431001982123
		0.000257092750574673	0.038431001982123
		0.000257380982422577	0.0384483991215472
Island	CHST5	0.000257389263630769	0.0384483991215472

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N_Shore	DIDO1;DIDO1;DIDO1;D	0.000257447289219383	0.0384483991215472
Island	HOXA6	0.000257836949599633	0.038494722754267
		0.000257979636177934	0.0384956854376386
	MIR220A	0.000258002363971661	0.0384956854376386
S_Shelf	ASB18	0.000258258691332251	0.0385115097666474
		0.000258316635464079	0.0385115097666474
Island	PRDM11	0.000258346967907577	0.0385115097666474
		0.000258461156077785	0.038514179543538
Island	TBX4	0.000258523920293278	0.038514179543538
	GULP1	0.000258650276804826	0.0385211547704481
Island	ESYT3	0.000258790383459066	0.0385301729077197
	KLF7	0.000259196376055116	0.0385684923440126
N_Shore		0.000259207025406	0.0385684923440126
Island	MEX3B	0.000259400011120196	0.0385853533125888
S_Shelf		0.000259625437145797	0.0385866394671001
		0.000259658452221359	0.0385866394671001
		0.000259757732822111	0.0385866394671001
Island		0.000259784668105275	0.0385866394671001
Island	PCDH8;PCDH8	0.000260127955682879	0.0385866394671001
	ASB7;ASB7	0.000260144538362983	0.0385866394671001
N_Shelf	MCF2	0.000260213097863003	0.0385866394671001
Island	CLYBL	0.000260221045450467	0.0385866394671001
Island	CBS	0.000260322566742096	0.0385866394671001
Island		0.000260378573287354	0.0385866394671001
	PACS2;PACS2	0.000260399527639719	0.0385866394671001
		0.000260428360071401	0.0385866394671001
	TOX3;TOX3	0.00026044438015372	0.0385866394671001
Island	VPS28;VPS28	0.000260793042673438	0.0386264802424505
Island	AGAP1;AGAP1	0.000261093638438832	0.0386591795893877
Island	DRD5	0.000261211380577246	0.0386644974791273
	DLEU7	0.00026135415885603	0.0386644974791273
	ATP11A;ATP11A	0.000261369049185284	0.0386644974791273
S_Shore	PCDHB9	0.000261508326393494	0.0386672227131646
Island	THBS2	0.000261547146251644	0.0386672227131646
Island	ESPNL	0.000261675382169862	0.0386743757917053
S_Shelf		0.000261819131430914	0.0386838166047216
Island	DIP2C	0.00026203600786167	0.0387015309646154
N_Shore	PYROXD1	0.000262186306640051	0.0387015309646154
	KCND3;KCND3	0.000262251213137133	0.0387015309646154
	UBE2E3;UBE2E3	0.000262329877602766	0.0387015309646154
N_Shore	CDK2AP1	0.000262429442535839	0.0387015309646154
	DOK4	0.000262445365108457	0.0387015309646154
	FLJ35220;FLJ35220	0.000262505216532845	0.0387015309646154
	ZBTB16;ZBTB16	0.000262666427988994	0.0387015309646154
Island		0.000262684240661006	0.0387015309646154
	ARID1B;ARID1B;ARID1	0.000262767628093264	0.0387015309646154
S_Shore	GPC1	0.000262818015470232	0.0387015309646154
	SLC22A23;SLC22A23	0.000262926820955344	0.0387057849724004
Island	SGSM2;SGSM2	0.000263086065388119	0.0387174593190825
	DCAF10	0.000263329307218895	0.0387211550644234
Island	FLJ42875;PRDM16;FLJ	0.000263476692033931	0.0387211550644234
N_Shore		0.000263480351886146	0.0387211550644234
	LRRK1	0.000263482873390682	0.0387211550644234
Island	EXTL3	0.000263585918291464	0.0387211550644234
N_Shore		0.000263615560465746	0.0387211550644234

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N_Shore	KDM2B;KDM2B	0.000263670818979958	0.0387211550644234
	MAGED2;SNORA11;MA	0.000263974473027396	0.0387539971655027
N_Shelf	KIAA1191;KIAA1191;KIA	0.000264060830156181	0.0387549277470886
Island	LASP1	0.000264291774974217	0.0387644689485911
Island	PCDHA6;PCDHA2;PCD	0.000264415877644017	0.0387644689485911
	ADARB2	0.000264423237831726	0.0387644689485911
	BHMT	0.000264476057834659	0.0387644689485911
	BTBD9;BTBD9;BTBD9	0.000264526030816277	0.0387644689485911
Island	ODZ2	0.000264628664183022	0.0387677791229408
	CUX1;CUX1;CUX1	0.000264740487265824	0.0387724331705535
	ANKH	0.000264906598770666	0.0387771263397912
	SOAT2	0.000265102283195847	0.0387771263397912
Island	PRDM13	0.000265176185572842	0.0387771263397912
	C12orf51	0.00026519815959554	0.0387771263397912
	LARP1	0.00026521146919813	0.0387771263397912
		0.000265252918110212	0.0387771263397912
Island	DAB2IP	0.000265339648134454	0.0387781005077608
N_Shelf	MBP;MBP	0.00026561864822099	0.0387794364418641
S_Shelf		0.00026568650040978	0.0387794364418641
Island	JAK2	0.000265775034450992	0.0387794364418641
S_Shore	C21orf29	0.0002658229884432	0.0387794364418641
Island	ZNF341	0.000265843529254444	0.0387794364418641
N_Shore	HEATR2	0.000265865954551376	0.0387794364418641
S_Shore	TNRC6C;TNRC6C	0.000266005048283906	0.0387794364418641
	TRIM15	0.000266065232663264	0.0387794364418641
N_Shore		0.000266069410615422	0.0387794364418641
S_Shelf	LRRFIP1;LRRFIP1;LRR	0.000266272024071545	0.0387873142320963
	FARP1	0.000266316992585352	0.0387873142320963
Island		0.000266385610750779	0.0387873142320963
	CCDC6	0.000266556344274774	0.0387873142320963
		0.000266574049257205	0.0387873142320963
N_Shore	MCTP1	0.000266662738547995	0.0387873142320963
	GPX5;GPX5	0.000266840003459599	0.0387873142320963
Island	CHST12	0.000266859813755403	0.0387873142320963
Island	KIAA1751	0.000266967891426678	0.0387873142320963
Island		0.00026716299854074	0.0387873142320963
		0.000267335663374482	0.0387873142320963
S_Shore	FAM38A	0.000267381699936383	0.0387873142320963
N_Shore	LOC440925	0.00026742020712227	0.0387873142320963
Island		0.000267464312728553	0.0387873142320963
	HERC2	0.000267614942472554	0.0387873142320963
Island	CHST7	0.000267665178407457	0.0387873142320963
		0.000267691455056964	0.0387873142320963
Island		0.000267707129202085	0.0387873142320963
Island	COL6A1	0.000267795672197171	0.0387873142320963
Island	ANKRD33B	0.000268039686093865	0.0387873142320963
Island	LOC100132215;EHBP1;	0.000268278010353212	0.0387873142320963
Island	NKAPL;NKAPL	0.000268373057292391	0.0387873142320963
S_Shore	FASN	0.000268492181540937	0.0387873142320963
	NXNL1	0.00026856132874336	0.0387873142320963
Island	C9orf69	0.000268586362367429	0.0387873142320963
	LARP1;LARP1	0.000268598776190882	0.0387873142320963
N_Shelf	RPTOR;RPTOR	0.000268674475259306	0.0387873142320963
	MAGEA10;MAGEA10	0.000268686371860988	0.0387873142320963
S_Shore		0.000268736387924576	0.0387873142320963

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	PTPRN2;PTPRN2;PTPF	0.000268760284606622	0.0387873142320963
	DENND1A;DENND1A	0.000268808311077322	0.0387873142320963
Island	ELANE	0.000268852833734465	0.0387873142320963
	CRMP1;CRMP1	0.000268947388083752	0.0387873142320963
Island		0.000268950242775995	0.0387873142320963
N_Shelf		0.000268957459530734	0.0387873142320963
N_Shore	MON1B	0.00026910025671765	0.0387873142320963
Island	ANK1;ANK1;ANK1;ANK	0.000269184885353716	0.0387873142320963
N_Shore	NLGN2	0.000269196177033796	0.0387873142320963
Island	SLITRK4	0.000269265547942248	0.0387873142320963
N_Shelf	C7orf50;C7orf50;C7orf5	0.000269378151350951	0.0387873142320963
	SUGT1P1;AQP7	0.000269460835018784	0.0387873142320963
N_Shore	ZC3H3	0.000269508983066749	0.0387873142320963
		0.000269567128901536	0.0387873142320963
S_Shore	FAM38A	0.000269967455002808	0.0388083761967615
	GRB10;GRB10;GRB10;	0.000269969632574807	0.0388083761967615
		0.000269977100326191	0.0388083761967615
Island	SCN8A	0.000270034022160917	0.0388083761967615
Island	LRPAP1	0.000270194490067142	0.038819918837665
		0.000270423554807178	0.0388413072900316
		0.000270664334268322	0.0388502011431583
Island		0.000270685695737804	0.0388502011431583
S_Shore	LMF1	0.000270797377321751	0.0388502011431583
S_Shelf	SMAD6;SMAD6	0.000270808653890676	0.0388502011431583
N_Shore	SIX2	0.000270920903849217	0.0388502011431583
		0.000270966767070849	0.0388502011431583
	ERGIC1	0.00027136504672049	0.0388626050821276
N_Shelf	PACS2;PACS2	0.000271386862338753	0.0388626050821276
Island	C17orf93;PRAC	0.000271448308082059	0.0388626050821276
Island	RNF39;RNF39	0.000271507876150097	0.0388626050821276
	DIP2C	0.000271511708780882	0.0388626050821276
	DRD2;DRD2	0.000271688881499444	0.0388626050821276
		0.000271769838856618	0.0388626050821276
Island		0.000271835788802494	0.0388626050821276
N_Shore	ZIC4;ZIC1	0.00027190620305894	0.0388626050821276
Island	DGKQ	0.000271913053435561	0.0388626050821276
Island		0.000271935928608539	0.0388626050821276
Island	FAM5B	0.000272378672309	0.0389143954177158
	PAGE2	0.000272701649827559	0.0389332842508779
	PCSK6;PCSK6;PCSK6;	0.000272834408503846	0.0389332842508779
S_Shore	STK10	0.000272954683947215	0.0389332842508779
Island		0.000272980501574101	0.0389332842508779
Island	CHRD1;CHRD1;CHR	0.000273115066420418	0.0389332842508779
Island	ALPK1;ALPK1	0.000273173716956291	0.0389332842508779
		0.00027320179806184	0.0389332842508779
Island		0.000273202977007574	0.0389332842508779
Island	DAB2IP;DAB2IP	0.000273378792760337	0.0389332842508779
N_Shelf	GGNBP2	0.000273391299388072	0.0389332842508779
Island	HOXA6	0.000273452337531426	0.0389332842508779
Island	NFATC1;NFATC1;NFAT	0.000273475523711323	0.0389332842508779
N_Shore		0.000273697591662576	0.0389534487458058
	GFRA1;GFRA1;GFRA1	0.000274094635186077	0.0389835670721249
S_Shelf	CLCN5;CLCN5	0.000274102604309058	0.0389835670721249
	ATP8B3	0.00027415068280113	0.0389835670721249
	UNC80;UNC80	0.000274422220777833	0.0390029569340934

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	CAPS2	0.000274506373097667	0.0390029569340934
Island		0.000274608015188949	0.0390029569340934
Island	LIPE	0.000274684288986009	0.0390029569340934
Island	TAF7L;TAF7L;TAF7L	0.000274805823942083	0.0390029569340934
	FRMD1;FRMD1	0.000274875730946627	0.0390029569340934
	RNF8;RNF8	0.000274894746970638	0.0390029569340934
N_Shelf	INPP5A	0.00027493128575439	0.0390029569340934
Island	STAG3;GPC2	0.000275050638392002	0.0390064654667573
		0.000275192240704261	0.0390064654667573
Island	LRP3	0.000275243859726436	0.0390064654667573
		0.00027537034343846	0.0390064654667573
Island	IKZF1	0.000275425561469844	0.0390064654667573
	IQCE;IQCE	0.000275443579478087	0.0390064654667573
		0.000275519781885669	0.0390064654667573
		0.00027568539302225	0.0390185061296029
S_Shelf	INPP5A	0.000276090048794238	0.0390587004557598
		0.00027644187467302	0.0390587004557598
N_Shore	LOC100130872-SPON2	0.000276541351717794	0.0390587004557598
N_Shore	TRMT61A	0.000276565917924931	0.0390587004557598
Island	PRRT1	0.000276637253799462	0.0390587004557598
Island	BRI3BP	0.000276685721565855	0.0390587004557598
Island		0.000276686945671121	0.0390587004557598
Island	FAM163A	0.000276868667342929	0.0390587004557598
Island	STAG3;STAG3;GPC2	0.000276980823236064	0.0390587004557598
		0.000276990615326811	0.0390587004557598
Island		0.000277006204354311	0.0390587004557598
Island	ZNF517	0.000277054027130679	0.0390587004557598
		0.000277113159641522	0.0390587004557598
N_Shore		0.000277140854796308	0.0390587004557598
S_Shore		0.000277179070802553	0.0390587004557598
Island		0.000277404819730377	0.039064361020285
	PTPRN2;PTPRN2;PTPRN2	0.000277438703224748	0.039064361020285
Island		0.000277512871154108	0.039064361020285
S_Shore	ZNF425	0.000277541870171477	0.039064361020285
		0.000277734974602987	0.0390801834905845
Island	GLI3	0.000277916712808698	0.0390943978887809
Island	ZSCAN1	0.000278048806307591	0.0390970390479716
	NPHP4	0.000278096938048339	0.0390970390479716
N_Shore	ZNF326;LOC492303;ZNF326	0.000278629626969114	0.0391222991940379
Island	KLHDC7A	0.000278751642458143	0.0391222991940379
S_Shore	HLA-DQB2	0.000278781182446209	0.0391222991940379
S_Shore	TERT;TERT	0.000278870309053521	0.0391222991940379
	MAPK10;MAPK10;MAPK10	0.000278929699880526	0.0391222991940379
S_Shore	AVP	0.000278940932811732	0.0391222991940379
N_Shore	MIR548F5;NBEA;MAB2	0.000279064871408677	0.0391222991940379
	PRPSAP2	0.000279067739633931	0.0391222991940379
Island		0.000279195650480035	0.0391222991940379
		0.000279343849545958	0.0391222991940379
		0.000279390160152357	0.0391222991940379
	POLS	0.000279536431242921	0.0391222991940379
N_Shore	SORBS2;SORBS2;SORBS2	0.000279591606320563	0.0391222991940379
Island	CCND2	0.000279633470547775	0.0391222991940379
N_Shore		0.000279652787761488	0.0391222991940379
S_Shore	INTS1	0.000279712870562125	0.0391222991940379
	NPTX2	0.000279713867953604	0.0391222991940379

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	MBNL3;MBNL3;MBNL3	0.000279851558619529	0.0391222991940379
S_Shore	NUP155;NUP155	0.000279870188719205	0.0391222991940379
Island	EBF2	0.000279892152392177	0.0391222991940379
Island	MXRA5	0.000279981840303054	0.0391235443752962
N_Shore		0.00028013613023695	0.0391320370055423
		0.000280204210675106	0.0391320370055423
		0.000280458267705965	0.039153476341718
	USP43	0.000280562462507633	0.039153476341718
Island	GABRA5;GABRA5;GAB	0.000280600250621181	0.039153476341718
Island	CHFR;CHFR;CHFR;CH	0.000280818873352075	0.0391726960933882
	TLE3;TLE3;TLE3	0.000281021385327693	0.0391896580618585
		0.000281218761694108	0.0392058942882841
N_Shore		0.000281326092789648	0.0392095711914666
	LRGUK	0.00028144082538712	0.0392142772599588
Island	KIF26A	0.000281657274732686	0.0392286613537311
Island	PDE1C	0.000281713263172477	0.0392286613537311
S_Shore	TBXA2R;TBXA2R	0.000281787049707594	0.0392286613537311
	PRDM16;PRDM16	0.000282165413298981	0.0392644314032864
	ETV7	0.000282273082048322	0.0392644314032864
Island	LOC389333;LOC389333	0.00028231071884897	0.0392644314032864
	NPHP4	0.000282368274562838	0.0392644314032864
S_Shore		0.000282636922817054	0.0392849296318768
Island	SIM1	0.000282832944448585	0.0392849296318768
Island	MSX1	0.000282848604643499	0.0392849296318768
Island	MVP;MVP	0.000282991304557018	0.0392849296318768
Island	PCDHGA4;PCDHGA12;	0.000283530793775034	0.0392849296318768
Island	XKR7	0.000283564962668084	0.0392849296318768
N_Shelf	FAM178B	0.000283567438038842	0.0392849296318768
N_Shore	KDM6B	0.000283575110275098	0.0392849296318768
Island	TIE1	0.000283654355089623	0.0392849296318768
Island		0.000283780405277899	0.0392849296318768
	PPFIBP2	0.000283869779960898	0.0392849296318768
Island	LYPD5	0.000284048620640848	0.0392849296318768
S_Shore		0.000284190648721408	0.0392849296318768
S_Shore	TPCN1;TPCN1	0.000284295081270766	0.0392849296318768
	KIF26B	0.000284353052114478	0.0392849296318768
	STX2;STX2	0.000284360841969809	0.0392849296318768
	LOC642846	0.000284377152520385	0.0392849296318768
N_Shore	PCDHGA2;PCDHGA4;P	0.000284412651859999	0.0392849296318768
Island	PCBP3;PCBP3	0.000284603466288696	0.0392849296318768
S_Shelf	PTPRN2;PTPRN2;PTP	0.00028464299756893	0.0392849296318768
N_Shore	HIST1H4E	0.000284650417550927	0.0392849296318768
		0.000284681790902617	0.0392849296318768
Island		0.000284682631804779	0.0392849296318768
	PTPRE	0.000284755649545083	0.0392849296318768
	MCF2L;MCF2L	0.000284942028463118	0.0392849296318768
Island	SOX9	0.000285114324554385	0.0392849296318768
Island	RYR1;RYR1	0.000285174522493074	0.0392849296318768
Island	PLEC1;PLEC1;PLEC1;P	0.000285241370800678	0.0392849296318768
N_Shore	FBRSL1	0.000285251451666492	0.0392849296318768
	BDNF;BDNF;BDNF;BDN	0.00028525904571206	0.0392849296318768
Island	LOXL1	0.00028536107722681	0.0392849296318768
		0.000285489206431287	0.0392849296318768
Island	DLGAP3	0.000285508184972304	0.0392849296318768
Island		0.00028551239913253	0.0392849296318768

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		0.00028552872466987	0.0392849296318768
Island	NLRP4	0.00028570876765807	0.0392849296318768
	PRAMEF11	0.000285778953211447	0.0392849296318768
Island	MAD1L1;MAD1L1;MAD1	0.000285871814747438	0.0392849296318768
	HRNBP3	0.000285972103005248	0.0392849296318768
N_Shore	NEIL2;NEIL2;NEIL2;NEI	0.000286105485178673	0.0392849296318768
S_Shelf	CARKD	0.000286242895774951	0.0392849296318768
Island		0.000286257850354778	0.0392849296318768
N_Shelf	BAIAP2;BAIAP2;BAIAP2	0.000286265634327905	0.0392849296318768
S_Shelf	ATP11A;ATP11A	0.000286272990657735	0.0392849296318768
Island	BTBD17	0.000286380633529021	0.0392849296318768
Island	CYBA	0.000286409281813415	0.0392849296318768
	CDKL1	0.000286546102176185	0.0392849296318768
Island	ISL2	0.00028660523095304	0.0392849296318768
		0.000286719950312671	0.0392849296318768
Island	S1PR4	0.000286769283367035	0.0392849296318768
S_Shore	PRCD	0.000286790018697787	0.0392849296318768
Island	MAP7D2;MAP7D2;MAP7	0.000286792757406763	0.0392849296318768
		0.000286814662010667	0.0392849296318768
		0.000287147411594313	0.0393193865197669
Island	NEURL	0.00028739098745316	0.0393330323151192
Island		0.000287602981981141	0.0393330323151192
Island	LPHN1;LPHN1	0.000287731697472818	0.0393330323151192
	EVL	0.000287734578570562	0.0393330323151192
N_Shore	GNA12	0.000287746636604619	0.0393330323151192
	FOXN3	0.000287806847768413	0.0393330323151192
		0.000287832821835482	0.0393330323151192
		0.000287896762622408	0.0393330323151192
		0.000288069492529333	0.0393455321402338
N_Shore		0.000288228103023283	0.0393544091646361
Island	RREB1;RREB1;RREB1;	0.000288380986749525	0.0393544091646361
	HERC2	0.000288523359727223	0.0393544091646361
N_Shelf	ZFP64;ZFP64;ZFP64;ZF	0.000288589971707337	0.0393544091646361
Island	KDM2B;KDM2B	0.000288785959933475	0.0393544091646361
S_Shore		0.000288799647323107	0.0393544091646361
Island		0.000288807751505335	0.0393544091646361
	DHX37	0.000288825204230496	0.0393544091646361
Island	MEST;MEST;MESTIT1;	0.000288948708089215	0.0393544091646361
S_Shelf	ADI1	0.000289019686014044	0.0393544091646361
S_Shore	BCOR;BCOR	0.000289028304131752	0.0393544091646361
		0.000289143409721298	0.0393590168390297
S_Shore		0.000289243686402897	0.0393616039384892
N_Shore	PCDHGA4;PCDHGA11;	0.000289461913140178	0.0393802362588812
Island	FAM20C	0.000289569099454727	0.0393837557128365
	CCDC40	0.000289706624196041	0.0393911908894548
N_Shore	MAEA;MAEA	0.000289813800797273	0.0393911908894548
	MAP4K4;MAP4K4;MAP4	0.000289920145980794	0.0393911908894548
Island	TRIM58	0.000290062353362604	0.0393911908894548
Island	KANK2;KANK2	0.000290099938082357	0.0393911908894548
Island	PLEC1;PLEC1;PLEC1;P	0.000290209308105866	0.0393911908894548
Island		0.000290310258979701	0.0393911908894548
Island		0.000290340017453484	0.0393911908894548
S_Shelf		0.00029051641466753	0.0393911908894548
Island		0.000290519784642964	0.0393911908894548
	ACAN;ACAN	0.000290702391335739	0.0393911908894548

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	ZC3H13	0.00029074258144268	0.0393911908894548
S_Shore	TSSC1	0.000290841815905967	0.0393911908894548
	ZFAND3	0.000290911907666378	0.0393911908894548
N_Shore		0.000291035677858919	0.0393911908894548
	SCN4A	0.000291063403748616	0.0393911908894548
N_Shore		0.00029109151986326	0.0393911908894548
		0.000291163783065922	0.0393911908894548
Island	USP49	0.000291169077343206	0.0393911908894548
S_Shore	CENPV	0.000291297484772142	0.0393923952280793
Island	AFAP1;AFAP1	0.000291340648752346	0.0393923952280793
N_Shelf	RPUSD4;RPUSD4	0.000291514117949595	0.0394009066371697
		0.00029161798554522	0.0394009066371697
Island	C1orf101;C1orf101	0.000291715047941231	0.0394009066371697
	ADAMTS17	0.000291764029994522	0.0394009066371697
Island		0.000291861058434804	0.0394009066371697
Island		0.000292106378488259	0.0394009066371697
Island	C1orf228	0.000292451012187897	0.0394009066371697
Island	CIITA	0.000292473205718932	0.0394009066371697
		0.000292487252295214	0.0394009066371697
N_Shore		0.000292510971673661	0.0394009066371697
Island	ZSCAN1	0.000292521246501739	0.0394009066371697
N_Shelf	MMP24	0.000292534652103603	0.0394009066371697
	DCAF8L1;DCAF8L1	0.000292575535642928	0.0394009066371697
		0.0002926619311392	0.0394009066371697
	RPS6KA2;RPS6KA2	0.000292893488399286	0.0394009066371697
	SNRNP35;SNRNP35;SNRNP35	0.00029292631112579	0.0394009066371697
N_Shelf	NPHP4	0.000293071211269051	0.0394009066371697
Island	CAND2;CAND2	0.00029308108621265	0.0394009066371697
		0.000293097484986273	0.0394009066371697
	ACAN;ACAN	0.000293122216218346	0.0394009066371697
		0.000293158349145426	0.0394009066371697
S_Shelf	DIP2C	0.000293240306081771	0.0394009066371697
	CTTN;CTTN	0.000293274698656887	0.0394009066371697
	RIMS1	0.000293469666793201	0.0394161664918517
	MYH3	0.000293589398902146	0.0394213156704413
Island	KDM4B	0.000293779334086443	0.0394246346603142
S_Shore		0.000293959392977109	0.0394246346603142
S_Shore	LOC388692	0.000293981117698076	0.0394246346603142
		0.000294007428893205	0.0394246346603142
		0.000294021122991906	0.0394246346603142
S_Shore	PRRX1;PRRX1	0.00029462348031973	0.0394818038292638
Island	C7orf57	0.000294681133963948	0.0394818038292638
		0.000294692037047001	0.0394818038292638
Island	C1orf94;C1orf94;C1orf94	0.000294860018913466	0.0394933845852501
N_Shore	SIM1	0.000294985830846139	0.0394993122821554
Island	USP36	0.000295101963900255	0.0395039410353761
Island	LRP5	0.00029521965691021	0.0395087759969709
S_Shore	NR0B1	0.000295514268601006	0.039537278491763
N_Shore	KIAA0415	0.000295849155227573	0.0395646096988746
Island		0.000295881931201825	0.0395646096988746
	GREB1;GREB1	0.000296066185823101	0.0395783205765315
	INPP5A	0.000296166284673728	0.0395807769935439
	SLC38A1;SLC38A1	0.000296400453880576	0.0395948533792
Island	NR2F6	0.000296435117644101	0.0395948533792
Island		0.000296841060351686	0.0396271709273964

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		0.000296939670352257	0.0396271709273964
Island		0.000296958816944367	0.0396271709273964
N_Shelf		0.000297018916440831	0.0396271709273964
	COL4A1	0.000297086166597587	0.0396271709273964
		0.000297264952115629	0.0396313471143028
	FRMD6;FRMD6	0.000297435327524786	0.0396313471143028
Island	LRP5	0.000297447173770963	0.0396313471143028
	LTBP1	0.000297460242442794	0.0396313471143028
N_Shore	EIF1AY	0.000297601809099639	0.0396313471143028
		0.000297647686173428	0.0396313471143028
Island		0.00029769027161892	0.0396313471143028
S_Shelf	AHDC1	0.000297854640685253	0.0396423327424801
		0.00029798369094031	0.0396486129435895
S_Shore		0.000298112046538441	0.0396505382611095
	TINAGL1	0.000298196532067923	0.0396505382611095
Island	EDNRB;EDNRB;EDNRB	0.00029824376376446	0.0396505382611095
Island	COL22A1	0.000298402714705609	0.0396553343177995
Island	ACCN1;ACCN1	0.000298543175817068	0.0396553343177995
	C8orf74	0.000298600004999557	0.0396553343177995
		0.00029866700358473	0.0396553343177995
Island	OAZ1	0.000298933301997879	0.0396553343177995
Island	HLA-G	0.000299086340523695	0.0396553343177995
		0.000299111994758158	0.0396553343177995
Island	BCL11B;BCL11B	0.000299261099470173	0.0396553343177995
	RAD51L1	0.000299277836728897	0.0396553343177995
		0.000299300383103387	0.0396553343177995
Island	ASCL2	0.000299301235798991	0.0396553343177995
		0.000299326993318595	0.0396553343177995
Island	MTL5;MTL5	0.000299359150439317	0.0396553343177995
	RGS1;RGS1	0.000299556077338005	0.0396553343177995
Island	CYP26A1;CYP26A1	0.000299570722966858	0.0396553343177995
	SPANXN3	0.00029989206049911	0.0396553343177995
Island	PCDH7;PCDH7;PCDH7	0.000299894768449977	0.0396553343177995
S_Shore	UCKL1	0.000299972976169358	0.0396553343177995
		0.000299975579068619	0.0396553343177995
		0.000299998348642398	0.0396553343177995
Island		0.00030005121319838	0.0396553343177995
Island	SLC38A10;SLC38A10	0.000300081144427265	0.0396553343177995
N_Shelf	FERMT1	0.000300173884405539	0.0396567693848097
N_Shore	B3GNTL1	0.000300324715230226	0.0396652826382139
Island	LOC644538;LOC644538	0.00030040211989257	0.0396652826382139
Island	THBS2	0.000300738861334929	0.039697055887805
Island	SPAG6;SPAG6	0.000300876281373011	0.039697055887805
	C2orf89	0.000300901614529899	0.039697055887805
	ARMCX3;ARMCX3;ARM	0.000301014921105936	0.039697055887805
N_Shelf		0.000301114791688768	0.039697055887805
Island		0.000301141681713759	0.039697055887805
	ANGPT2;ANGPT2;ANG	0.000301229580122235	0.039697055887805
Island	CAPS2	0.000301412243527862	0.039697055887805
Island	SLC45A4	0.000301497427662984	0.039697055887805
	LRRC27;LRRC27	0.000301511989584647	0.039697055887805
		0.00030168716324138	0.039697055887805
Island	STK32B	0.000301884410353888	0.039697055887805
Island	SDF4;SDF4;B3GALT6	0.000301928548474907	0.039697055887805
S_Shore	FBXO43;FBXO43	0.000302046229591984	0.039697055887805

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	SPDYE5	0.000302049571563972	0.039697055887805
Island	C5orf42	0.000302086486602609	0.039697055887805
		0.000302252595520754	0.039697055887805
Island		0.000302259653671477	0.039697055887805
	C17orf54	0.000302322071695035	0.039697055887805
S_Shore	PLAGL1;PLAGL1	0.000302356433609272	0.039697055887805
Island	POM121L1P	0.000302364684093472	0.039697055887805
Island		0.000302445953081093	0.039697055887805
Island	ZNF524	0.000302551125067357	0.0397001012322535
	SDK1	0.000302699048895822	0.0397045138794511
	GPM6B;GPM6B;GPM6B	0.000302842597345892	0.0397045138794511
Island	C1orf228	0.000302916853201187	0.0397045138794511
Island	RGS7;RGS7	0.000302979170481141	0.0397045138794511
S_Shelf	CHFR;CHFR;CHFR;CHFR	0.00030300067554027	0.0397045138794511
S_Shore	PHKG2	0.000303076627909628	0.0397045138794511
N_Shore	NTNG1;NTNG1;NTNG1	0.000303299331140036	0.0397229444441314
Island	RCC2;RCC2	0.000303497940671142	0.0397333619467574
S_Shore	TSSC1	0.000303542949884896	0.0397333619467574
Island	EP400	0.000303903820843261	0.0397638938911772
Island	HCN2	0.000303940401972101	0.0397638938911772
N_Shore	RGS12;RGS12;RGS12	0.000304223958081395	0.0397902426405
S_Shore	NARG2;NARG2	0.000304491904177786	0.0398145360396615
N_Shelf	RAB40C	0.000304818099241436	0.0398305058092565
Island	XAB2	0.000304823189622483	0.0398305058092565
N_Shore	SHANK2;SHANK2	0.000304873513093058	0.0398305058092565
S_Shore	TMSB15B;MIR1256	0.000304942993941513	0.0398305058092565
Island	PLA2G4C;PLA2G4C;PLA2G4C	0.000305205176669892	0.0398438524442435
		0.000305209709530054	0.0398438524442435
N_Shore	AGAP1;AGAP1	0.000305426025248182	0.0398510941920053
	GNAO1;GNAO1	0.000305429745812675	0.0398510941920053
Island		0.000305593832500445	0.0398617648601611
	FLJ36000	0.000305770979959163	0.0398703686253769
Island	HSF4;HSF4;FBXL8	0.000305824434921334	0.0398703686253769
S_Shelf	GOLGA3	0.000306182380910893	0.0399011355013549
Island	MYO7A;MYO7A;MYO7A	0.000306225201380346	0.0399011355013549
Island	SNX18;SNX18;SNX18	0.000306380515169415	0.0399106355592864
S_Shore	CTNNA2;CTNNA2;LRRK1	0.000306658824066211	0.0399321024842555
Island	ZNF574	0.000306710207487597	0.0399321024842555
	CACNB2;CACNB2;CACNB2	0.000306875407578071	0.0399428733607228
		0.00030704431211649	0.0399469517327797
	TRIM39;TRIM39	0.000307150857181619	0.0399469517327797
S_Shore	BLCAP;BLCAP;BLCAP;BLCAP	0.000307205370342123	0.0399469517327797
N_Shore	CEP78;CEP78	0.000307297049013675	0.0399469517327797
S_Shelf	HCG27	0.000307319139330691	0.0399469517327797
	ERN1	0.000307486035098447	0.0399476739198901
		0.000307560166224356	0.0399476739198901
Island	VWC2	0.000307572138640934	0.0399476739198901
	NID1	0.000307726044894276	0.0399569481751797
		0.000307979147938108	0.0399757859956081
N_Shelf	SRM	0.0003080362015911	0.0399757859956081
S_Shore	PCDHGA4;PCDHGA6;PCDHGA6	0.000308268325142324	0.0399843963369833
	FAM189A1	0.000308323557316688	0.0399843963369833
Island	RNU5E;RNU5D;ACOT1	0.000308350220035374	0.0399843963369833
Island	CTDP1;CTDP1	0.00030848038829555	0.0399866455257394
		0.000308537165005809	0.0399866455257394

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Island	ZEB2;ZEB2	0.000308701831238854	0.0399866455257394
		0.000308739276719846	0.0399866455257394
	CFB	0.000308799454938204	0.0399866455257394
Island	PCDH10;PCDH10	0.000308862934830519	0.0399866455257394
Island		0.000309104300705008	0.0400071994759361
Island		0.000309231538620766	0.0400117509033991
Island	PCLO;PCLO	0.000309417235369584	0.0400117509033991
Island		0.000309493881623301	0.0400117509033991
	PTPRN2;PTPRN2;PTPF	0.000309549756530479	0.0400117509033991
N_Shelf	TNXB	0.000309602104583159	0.0400117509033991
	PSORS1C1	0.000309635146618365	0.0400117509033991
		0.000309904016594989	0.0400261232708085
S_Shore	MIR1229;MGAT4B;MGA	0.000309936301903857	0.0400261232708085
		0.00030999429802055	0.0400261232708085
S_Shelf	KCNT1	0.0003101061469396	0.0400298932879855
N_Shore	C4orf31	0.000310208645749503	0.0400324546636366
N_Shore	NELF;NELF;NELF;NELF	0.000310633652326186	0.040062356558508
	TRIO	0.000310643602855067	0.040062356558508
	PLCG2	0.000310688507167204	0.040062356558508
		0.000310772140798791	0.0400624746053698
N_Shore	NCOR2;NCOR2	0.000311030692293618	0.0400851357224871
		0.000311242910308828	0.0400926379911756
	AGL;AGL;AGL;AGL;AGL	0.000311254465176938	0.0400926379911756
		0.000311478532871584	0.0401108323406089
	SPHAR;RAB4A;SPHAR	0.000311821680425147	0.0401406741314998
Island	SREBF1;SREBF1	0.000311876026958826	0.0401406741314998
Island	CTDP1;CTDP1	0.000312020613719376	0.0401414896929923
S_Shore	KATNAL2;TCEB3B	0.000312146901450459	0.0401414896929923
	JUP;JUP	0.000312245132615623	0.0401414896929923
S_Shore	CACNB1	0.000312289965481636	0.0401414896929923
S_Shore	INTS1	0.000312296770068023	0.0401414896929923
N_Shore	ADCY9	0.00031253094921411	0.0401553360688787
	ITPK1;ITPK1;ITPK1	0.000312719306346573	0.0401553360688787
	SYT1;SYT1;SYT1	0.000312784036141065	0.0401553360688787
Island	PITRM1	0.000312789501385195	0.0401553360688787
Island		0.000312819042972961	0.0401553360688787
	BCL11B;BCL11B	0.000313209064315738	0.040172633567839
S_Shore	ZNF696	0.00031323200691402	0.040172633567839
S_Shelf		0.000313268142468745	0.040172633567839
		0.00031328557680427	0.040172633567839
Island	RCVRN	0.00031357282833408	0.0401769491579709
	ARHGAP15	0.000313621175600248	0.0401769491579709
Island	DMBT1;DMBT1;DMBT1	0.00031367988604347	0.0401769491579709
N_Shore	NEUROG1;NEUROG1	0.00031369581364843	0.0401769491579709
	MUC4;MUC4;MUC4	0.00031373400447106	0.0401769491579709
Island	PCSK1N	0.000314161758791097	0.0402138090765901
		0.000314325069263079	0.0402138090765901
N_Shore	ERICH1	0.00031456247384183	0.0402138090765901
		0.000314643950614756	0.0402138090765901
N_Shore	C4orf38	0.000314727370553418	0.0402138090765901
		0.000314784027806914	0.0402138090765901
Island		0.000314859709730933	0.0402138090765901
	NLRX1;NLRX1	0.000314909602787776	0.0402138090765901
	AFF3;AFF3	0.000314910148096799	0.0402138090765901
S_Shore		0.000315008451194827	0.0402138090765901

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	EYS	0.000315018147739107	0.0402138090765901
Island	ZBTB12	0.00031503826714112	0.0402138090765901
	PDE4D	0.0003151012345959	0.0402138090765901
Island	RPH3AL	0.000315617180447292	0.0402378639734722
Island		0.000315618504349058	0.0402378639734722
N_Shelf	SLC22A18AS;SLC22A18	0.000315635647440687	0.0402378639734722
Island	ZNF334;ZNF334	0.000315666879835757	0.0402378639734722
S_Shore	ASZ1;ASZ1	0.000315737280714635	0.0402378639734722
Island	LAMA5	0.000315829641356566	0.0402378639734722
		0.000315900799811136	0.0402378639734722
Island	ADAMTS18	0.000316025563292287	0.0402378639734722
	FAM82A1;FAM82A1;FA	0.000316118854656401	0.0402378639734722
Island	DIP2C	0.000316188033380765	0.0402378639734722
Island	EPN1;EPN1;EPN1	0.000316247800457269	0.0402378639734722
N_Shore		0.000316286683832155	0.0402378639734722
Island	HOXA9	0.000316510716732746	0.0402504050527438
Island	CTU1	0.000316682367258509	0.0402504050527438
Island		0.00031681036610369	0.0402504050527438
	GATA2;GATA2;GATA2	0.000316839583226501	0.0402504050527438
		0.000316866327589732	0.0402504050527438
		0.000316922782787529	0.0402504050527438
Island		0.000316967005360378	0.0402504050527438
		0.000317100214042182	0.0402536978681797
	ADARB2	0.000317177048319805	0.0402536978681797
		0.000317352834956308	0.0402536978681797
S_Shore	HIST1H2AA;HIST1H2BA	0.000317517156914913	0.0402536978681797
Island	ZFPM1	0.000317525970275487	0.0402536978681797
Island	BRD4	0.000317580341150169	0.0402536978681797
	COL4A2	0.000317860887071992	0.0402536978681797
Island		0.000317959898062006	0.0402536978681797
S_Shore	DHRS7C	0.000317972830567385	0.0402536978681797
Island	TMPRSS9	0.000317981688606001	0.0402536978681797
		0.000317990368070211	0.0402536978681797
Island	TSSK6;TSSK6	0.000318092892571892	0.0402536978681797
		0.000318121563702094	0.0402536978681797
Island	ODZ4	0.00031815651770896	0.0402536978681797
Island	KLHDC4	0.000318281558668369	0.040259001280245
Island	LOXHD1	0.000318464677692206	0.0402647471528348
S_Shelf	RHBDF2;RHBDF2	0.000318497894517649	0.0402647471528348
Island		0.000318618942677327	0.0402647471528348
Island	HS6ST2;HS6ST2	0.000318659527872433	0.0402647471528348
S_Shelf	C11orf46	0.000318837649246613	0.0402767460801684
	RCBTB2	0.000319049039407888	0.0402929402897589
	LGALS2;LGALS2	0.000319270061573097	0.0403089339350412
N_Shore	PNLDC1	0.00031934213494813	0.0403089339350412
	CAMTA1	0.000319679694478999	0.0403410286681973
N_Shore		0.000319870919220851	0.040354645207512
	PRKAG2;PRKAG2;PRK	0.000320053729339275	0.0403563615374887
Island		0.000320256420968642	0.0403563615374887
Island	CBFA2T3;CBFA2T3	0.000320291955071228	0.0403563615374887
Island	APLP1;APLP1	0.000320596092029773	0.0403563615374887
	C21orf88;C21orf88	0.000320613114843119	0.0403563615374887
Island	SYCE1;SYCE1;SYCE1	0.000320660474536022	0.0403563615374887
	GABRR1	0.000320737612805818	0.0403563615374887
	IFT140	0.000320814212528038	0.0403563615374887

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S_Shore		0.000320818983959225	0.0403563615374887
Island	RPTOR;RPTOR	0.000320909187697531	0.0403563615374887
Island	POU3F4	0.00032118761176817	0.0403563615374887
Island	C3orf77	0.000321222483057255	0.0403563615374887
Island	THOP1	0.000321243090953287	0.0403563615374887
S_Shelf	MAD1L1;MAD1L1;MAD1	0.000321527856035801	0.0403563615374887
S_Shelf	OTUB2	0.000321631244280262	0.0403563615374887
Island	GUCY1A2	0.000321682880052706	0.0403563615374887
	KCNJ8	0.000321689144817472	0.0403563615374887
Island	B3GNT6	0.000321695425580527	0.0403563615374887
		0.000321741575361396	0.0403563615374887
	NHSL2	0.000321773440914359	0.0403563615374887
Island	MORN1	0.000321777960593939	0.0403563615374887
Island	RUNX2;RUNX2	0.000321926769188327	0.0403563615374887
	SBF2	0.000321932448413054	0.0403563615374887
		0.000321947183874512	0.0403563615374887
		0.00032203332677754	0.0403563615374887
S_Shore	SNTG1	0.000322109704115046	0.0403563615374887
Island	ELANE	0.000322175623309243	0.0403563615374887
Island	PMS1;PMS1;PMS1	0.000322287808005359	0.0403563615374887
Island	ZFR2	0.000322341303132944	0.0403563615374887
Island	PTPRN2;PTPRN2;PTPF	0.000322384272520609	0.0403563615374887
	NAV2	0.000322623870341128	0.0403590972164488
	STK32B	0.000322643437420512	0.0403590972164488
Island		0.000322762742079758	0.0403590972164488
Island	SPATA18	0.000322813821580375	0.0403590972164488
Island	SEPT9;SEPT9;SEPT9;S	0.000322887029199301	0.0403590972164488
Island		0.000323009787613498	0.0403590972164488
N_Shelf	LIMD2	0.000323064388072513	0.0403590972164488
Island	HAS1	0.000323212495703783	0.0403590972164488
N_Shelf	CEP72	0.000323420044658861	0.0403590972164488
S_Shelf	MRC2	0.00032348788072043	0.0403590972164488
	SNTG2	0.000323501067973704	0.0403590972164488
Island		0.000323581968351912	0.0403590972164488
Island	EPX	0.000323929033905816	0.0403590972164488
	PACRG;PACRG;PACRC	0.000324033680764148	0.0403590972164488
Island	DLGAP3	0.000324038128387206	0.0403590972164488
Island	KDM4B	0.000324150108295193	0.0403590972164488
Island		0.000324164597501867	0.0403590972164488
		0.000324175377906174	0.0403590972164488
Island	FBXL7	0.000324234373473852	0.0403590972164488
	TOX3;TOX3	0.000324259918182529	0.0403590972164488
S_Shelf	PC;PC;PC	0.000324279431023608	0.0403590972164488
Island	CMIP;CMIP	0.000324379349234648	0.0403590972164488
	CUX1;CUX1;CUX1	0.000324404880594221	0.0403590972164488
Island	TSSC1	0.000324642129631585	0.0403590972164488
Island	TSPYL6;ACYP2	0.000324648479320944	0.0403590972164488
Island	DPP10;DPP10	0.000324664734592946	0.0403590972164488
	ATP10A	0.000324731959050689	0.0403590972164488
S_Shore		0.000324739383373769	0.0403590972164488
N_Shore	BANP;BANP	0.000325092092833028	0.0403826942182473
	C11orf9;C11orf9	0.000325103951042043	0.0403826942182473
Island	FAM47A	0.000325237812326923	0.0403826942182473
S_Shelf	CYP20A1	0.000325262768069752	0.0403826942182473
Island	ZBED3	0.000325771883177033	0.0404314046577185

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N_Shelf		0.000325972118011104	0.0404314046577185
	MEIS1	0.000326008712040274	0.0404314046577185
	KCNJ5	0.000326043818725392	0.0404314046577185
Island	OPA3;OPA3	0.000326072506257262	0.0404314046577185
S_Shore	INPP5A	0.000326247778491552	0.0404427835469468
		0.000326335529234402	0.0404433099274441
	UNC84A;UNC84A	0.000326554697125941	0.0404462474235554
S_Shelf	PRKDC;PRKDC	0.00032660616916125	0.0404462474235554
N_Shelf		0.000326916948115474	0.0404462474235554
Island	SPRED2;SPRED2	0.000326934173369067	0.0404462474235554
	C6orf142	0.000327160068926511	0.0404462474235554
Island	FIZ1	0.000327176678335997	0.0404462474235554
		0.000327191481002953	0.0404462474235554
Island	ISL1;ISL1	0.000327281972811161	0.0404462474235554
		0.000327283030795101	0.0404462474235554
	MTMR15	0.000327318893841702	0.0404462474235554
N_Shore	AMACR;AMACR;AMACR	0.000327378681482107	0.0404462474235554
		0.000327581520699182	0.0404462474235554
N_Shore	DND1	0.000327596392951116	0.0404462474235554
		0.000328011006566693	0.0404462474235554
	PENT;PENT;PENT	0.000328040009931826	0.0404462474235554
Island	GPC6;GPC6	0.00032806644181898	0.0404462474235554
	LOC348021	0.000328104690778483	0.0404462474235554
Island	PCDHA6;PCDHA2;PCDHA6	0.000328131168239191	0.0404462474235554
	TRAPPC9;TRAPPC9	0.000328467291850663	0.0404462474235554
S_Shore	TNRC6C;TNRC6C	0.000328491424116387	0.0404462474235554
N_Shore		0.000328525955417934	0.0404462474235554
S_Shore		0.00032853907446076	0.0404462474235554
Island	FAM101A	0.000328570647331203	0.0404462474235554
N_Shelf	SOX2OT	0.000328616926271427	0.0404462474235554
N_Shelf	C7orf50;C7orf50;C7orf50	0.000328632397061021	0.0404462474235554
	DLGAP2	0.000328646113724427	0.0404462474235554
N_Shore	CCND1	0.000328803826848182	0.0404462474235554
	SFRP1	0.000328806338495996	0.0404462474235554
	INPP5F;INPP5F	0.000328813931972111	0.0404462474235554
	STXBP5;STXBP5	0.000328870304562722	0.0404462474235554
N_Shore		0.000329036892677769	0.0404462474235554
Island		0.000329101006814932	0.0404462474235554
Island	WNT2;WNT2	0.000329219583697446	0.0404462474235554
Island	LOC645323;LOC645323	0.00032927642322754	0.0404462474235554
N_Shore		0.000329357874540575	0.0404462474235554
	ST3GAL5;ST3GAL5;ST3GAL5	0.000329365611600686	0.0404462474235554
Island		0.000329529374025328	0.0404551897166607
Island	GNB4	0.000329605489334524	0.0404551897166607
	LOC286467	0.000330462163385846	0.0405317867894375
N_Shore	NHP2L1;NHP2L1	0.000330472675024302	0.0405317867894375
Island	COL24A1	0.000330522817413402	0.0405317867894375
	UBE2E1;UBE2E1	0.000330743324715205	0.0405317867894375
S_Shore	INPP5A	0.000330889377372967	0.0405317867894375
Island	FURIN	0.000330988185591044	0.0405317867894375
Island	ZC3H3	0.000331032157426612	0.0405317867894375
Island	BAT4;CSNK2B	0.000331173806333228	0.0405317867894375
Island		0.000331252648336252	0.0405317867894375
Island	PROM1;PROM1;PROM1	0.00033142891136146	0.0405317867894375
S_Shore	STK10	0.0003315226365284	0.0405317867894375

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Island	CNP	0.000331549986651663	0.0405317867894375
		0.000331638806584918	0.0405317867894375
	DTHD1;DTHD1	0.000331681572859704	0.0405317867894375
S_Shore	FREM2	0.000331700794598332	0.0405317867894375
N_Shelf	CENPJ	0.000331743693494071	0.0405317867894375
Island	TAF7L;TAF7L	0.000331867501728729	0.0405317867894375
	RAP1GAP2;RAP1GAP2	0.000331932568734745	0.0405317867894375
N_Shelf	CYFIP1;CYFIP1	0.000331977528121745	0.0405317867894375
	SCG5;SCG5	0.000332015153953715	0.0405317867894375
S_Shore		0.000332230718795239	0.0405317867894375
	DDX53	0.000332245886812212	0.0405317867894375
Island	AHRR;PDCD6	0.000332304939195701	0.0405317867894375
	TRAPPC9;TRAPPC9	0.000332464268980736	0.0405317867894375
	AGPAT4	0.000332495920321467	0.0405317867894375
	TSSC1	0.000332668549816104	0.0405317867894375
	OCM	0.000332825218064259	0.0405317867894375
Island	CHAD;ACSF2	0.000332917366636727	0.0405317867894375
Island	INF2;INF2;INF2	0.000333045483286081	0.0405317867894375
N_Shore	SLC9A3	0.000333098481365017	0.0405317867894375
S_Shore	TACR1;TACR1	0.0003331032347174	0.0405317867894375
Island		0.000333171623121677	0.0405317867894375
	PITRM1	0.000333220643476623	0.0405317867894375
		0.000333304771581824	0.0405317867894375
	DENND1B;DENND1B	0.000333317826463096	0.0405317867894375
S_Shore	PIK3R2	0.000333317955893573	0.0405317867894375
	SLC12A1	0.000333325983135972	0.0405317867894375
	PACRG;PACRG;LOC28	0.000333411112670554	0.0405319621345799
	SCOC;SCOC;SCOC;SCOC	0.000333654238266151	0.0405513397611678
S_Shelf	RIMBP2	0.000333801699771062	0.0405590838538935
N_Shore	EXD3	0.000334001018219648	0.0405678222882595
N_Shore	RXRA	0.000334122410524882	0.0405678222882595
Island	NFATC1;NFATC1;NFATC1	0.000334147651518752	0.0405678222882595
Island	FAM171A1	0.000334464121578719	0.0405678222882595
S_Shore	SLC35B3;SLC35B3;SLC35B3	0.00033454334976293	0.0405678222882595
		0.000334586921226018	0.0405678222882595
		0.00033461674366595	0.0405678222882595
S_Shore		0.000334626188968151	0.0405678222882595
Island	TSNARE1	0.000334627471308722	0.0405678222882595
Island	PRKCZ;PRKCZ;PRKCZ	0.0003348971762492	0.0405903590808042
Island	MYOCD;MYOCD	0.00033509273297162	0.0406038998990443
Island	GPR143	0.000335362223348986	0.0406263904010749
	MGMT	0.00033547588330887	0.0406299967950908
Island	NOTCH1	0.000335692654858254	0.040646086266056
		0.000335957072254777	0.0406481461722872
	SLC12A4;SLC12A4;SLC12A4	0.000336023730402268	0.0406481461722872
Island	LOC100133957;UXT;LOC100133957	0.000336031990246554	0.0406481461722872
	MEOX2	0.00033610563475043	0.0406481461722872
Island	SHROOM2	0.000336129304537264	0.0406481461722872
S_Shore	SLC12A7	0.000336272738305323	0.0406553404842051
	KIAA1244	0.000336370777054034	0.040657044321611
Island	INPP5A	0.000336687806999655	0.0406852101110548
Island		0.000336970200902929	0.0406950035595657
		0.000337162932147426	0.0406950035595657
N_Shelf		0.000337301288494257	0.0406950035595657
S_Shelf	MALT1;MALT1	0.000337444715195272	0.0406950035595657

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Island	FAT3	0.000337466334003948	0.0406950035595657
S_Shelf		0.000337470382437462	0.0406950035595657
	NPHP4	0.000337524964714232	0.0406950035595657
	CRIM1	0.000337568960969069	0.0406950035595657
Island	ZAR1	0.000337637199786286	0.0406950035595657
		0.000337821179696035	0.0406950035595657
S_Shore		0.000337831528199985	0.0406950035595657
N_Shore		0.000337847449274786	0.0406950035595657
N_Shore	MSX1	0.000337861166185957	0.0406950035595657
Island	FAM18A	0.000338207616781416	0.0407266046737094
	LRP5	0.00033837586420325	0.0407314256544427
S_Shore	LMF1	0.000338418286785062	0.0407314256544427
		0.00033849994994917	0.0407314256544427
Island	TRAPPC9;TRAPPC9	0.000338677589677456	0.0407426784949165
N_Shore	RBM33	0.000338788193086534	0.0407440445149281
Island	CCDC135	0.000338879695906014	0.0407440445149281
Island	SIGIRR;SIGIRR;SIGIRR	0.000339073100466856	0.0407440445149281
Island	CASZ1	0.000339077104973148	0.0407440445149281
	GRIN2A;GRIN2A;GRIN2	0.000339113555280153	0.0407440445149281
	PFKP	0.000339242293501943	0.0407440445149281
Island		0.000339277822802261	0.0407440445149281
N_Shelf		0.000339483607026566	0.0407550456765242
	C12orf40	0.000339537726329996	0.0407550456765242
S_Shore	BREA2	0.000339695525780631	0.0407635692458108
Island		0.00033980033070988	0.0407635692458108
	TTY19	0.000339861234944684	0.0407635692458108
N_Shore	LOC645323	0.000340017010276903	0.040764892278657
Island	KCTD1;KCTD1	0.000340040602499921	0.040764892278657
N_Shore	TMEM18	0.000340257931239894	0.040775433682967
Island		0.000340412624678389	0.040775433682967
S_Shelf		0.000340454478797916	0.040775433682967
S_Shore	DOK7;DOK7	0.000340465294613986	0.040775433682967
Island	PDIA3P	0.000340552269484348	0.0407757670996309
Island	TMCO3	0.000340836455171929	0.0407771308003556
		0.000340864870329267	0.0407771308003556
Island	PAX6;PAX6;PAX6	0.000340875860363626	0.0407771308003556
Island	KCTD1;KCTD1;KCTD1	0.000340900433821586	0.0407771308003556
S_Shore		0.000341100959234067	0.0407790515890222
Island		0.000341111694645226	0.0407790515890222
Island	NCRNA00200	0.000341264158288139	0.0407790515890222
	CLEC3A	0.000341320793487031	0.0407790515890222
Island	ARRDC2;ARRDC2	0.000341469830459788	0.0407790515890222
		0.000341600270182721	0.0407790515890222
N_Shelf		0.000341632927711451	0.0407790515890222
S_Shore	SGSH	0.000341648112483395	0.0407790515890222
	RAC1;RAC1	0.000341674271095343	0.0407790515890222
N_Shore	DPYSL3	0.000341969362370607	0.0407964865167276
N_Shelf	KDSR	0.000341988820023567	0.0407964865167276
N_Shore	BOLL;BOLL	0.000342202893168855	0.0408019888023637
S_Shore	ARHGEF18;ARHGEF18	0.000342208749733254	0.0408019888023637
	CACNA1B	0.000342287679768758	0.0408019888023637
	MIR220A	0.000342444168231851	0.0408040823737804
Island	EIF2C2;EIF2C2	0.000342549831005781	0.0408040823737804
N_Shore	PCSK1	0.000342557990877595	0.0408040823737804
Island		0.000342659308163297	0.0408061149314454

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N_Shore	MAD1L1;MAD1L1;MAD1	0.000342916001554329	0.0408112401853548
	OTUD4;OTUD4;OTUD4	0.000342963254502096	0.0408112401853548
Island		0.000342980566110475	0.0408112401853548
N_Shelf		0.000343039402869105	0.0408112401853548
N_Shelf	UNC84A;UNC84A	0.000343539478516607	0.0408606969382504
S_Shore	IL1RAPL2	0.000343842693629041	0.0408793721008298
Island	SLC6A2	0.000343865301065979	0.0408793721008298
N_Shore	TGFBRAP1;TGFBRAP1	0.000344027997516658	0.0408886772754
S_Shore	ING5	0.000344192052193699	0.0408981392734821
Island	CACNA1C;CACNA1C;C	0.000344309037515071	0.0408987290534518
	LOC92249	0.000344677540463145	0.0408987290534518
Island	KCNC2;KCNC2;KCNC2	0.000344858759798865	0.0408987290534518
	PHEX;PHEX	0.000345032491190638	0.0408987290534518
Island	VANGL2	0.000345240786268078	0.0408987290534518
S_Shelf		0.000345277316935494	0.0408987290534518
S_Shelf	RPH3AL	0.000345278746863598	0.0408987290534518
Island	CACNA1H;CACNA1H	0.000345339905250132	0.0408987290534518
S_Shelf		0.000345344416352125	0.0408987290534518
N_Shelf	GGTLC1;GGTLC1	0.000345370373273696	0.0408987290534518
	HDAC4	0.000345404436513269	0.0408987290534518
N_Shore		0.000345460726234131	0.0408987290534518
		0.000345603041641307	0.0408987290534518
Island	PICK1;PICK1;PICK1	0.000345749448159613	0.0408987290534518
S_Shore	ERAS	0.000345786936476208	0.0408987290534518
Island	ADAMTS16	0.00034589582260133	0.0408987290534518
		0.000345916250096299	0.0408987290534518
S_Shore	POP7	0.000345920629846563	0.0408987290534518
Island		0.00034595834269525	0.0408987290534518
Island	CYP26C1	0.000346045923415673	0.0408987290534518
	NLRC4	0.000346054201272937	0.0408987290534518
	PPP2R2D;PPP2R2D;PP	0.000346142753478273	0.0408987290534518
S_Shelf	CDH23	0.000346189955795201	0.0408987290534518
		0.000346388262106008	0.0408987290534518
N_Shore	ZNF763	0.000346432458808869	0.0408987290534518
N_Shore	TBCD	0.000346501430265881	0.0408987290534518
	DNM3;DNM3	0.000346612507845797	0.0408987290534518
Island	SYN1;SYN1	0.000346618347231043	0.0408987290534518
		0.000346645914962927	0.0408987290534518
	CUL4A;CUL4A	0.000346927345108236	0.0409219645444584
Island	TMEM132E	0.00034730257440029	0.0409277358431547
	CYP26B1	0.000347622794628919	0.0409277358431547
Island	SLCO3A1;SLCO3A1	0.000347748050532349	0.0409277358431547
Island	ZNF135;ZNF135;ZNF13	0.000347756472616609	0.0409277358431547
Island		0.000348040586243144	0.0409277358431547
Island	TMCO3	0.000348041291295087	0.0409277358431547
		0.000348108219615158	0.0409277358431547
		0.000348135251747625	0.0409277358431547
	OPN5;OPN5	0.000348161465677864	0.0409277358431547
Island		0.000348199594769221	0.0409277358431547
		0.000348210343521669	0.0409277358431547
Island	ZNRF4;ZNRF4	0.000348227615277612	0.0409277358431547
Island		0.000348237215991121	0.0409277358431547
		0.000348239340042197	0.0409277358431547
N_Shore	CNPY1	0.000348243843306954	0.0409277358431547
		0.000348795686864472	0.0409778605380018

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	RPTOR;RPTOR	0.000348839558144183	0.0409778605380018
	CAPRIN1;CAPRIN1	0.000349359373894506	0.0410174810457339
S_Shore	RPS16	0.000349481770617992	0.0410174810457339
Island		0.000349563927285909	0.0410174810457339
S_Shore	GLI3	0.000349593545693199	0.0410174810457339
	MGMT	0.000349600292689391	0.0410174810457339
		0.000349770953024543	0.0410207824394823
	FNIP2	0.000349835404647009	0.0410207824394823
	KIAA0586	0.0003498825215661	0.0410207824394823
N_Shore	LAMA2;LAMA2	0.000349987205730842	0.0410214173079781
Island	UGT1A10;UGT1A6;UGT1A9	0.000350057332852679	0.0410214173079781
N_Shore	CIT	0.000350310900523783	0.041030461751998
	CYFIP1	0.000350506576055933	0.041030461751998
Island	GFRA2;GFRA2;GFRA2	0.000350520138121284	0.041030461751998
	ITFG1	0.000350547814452469	0.041030461751998
S_Shore	HIST1H2AA;HIST1H2BA	0.000350729558088886	0.041030461751998
		0.000350855977556937	0.041030461751998
Island	MGST2	0.000350873901272274	0.041030461751998
Island	NTN1	0.000350890571951436	0.041030461751998
	GALNT14	0.000350896965006506	0.041030461751998
S_Shore	GNA11	0.000351251287261025	0.0410619791703345
	ZMIZ2;ZMIZ2	0.000351397367325297	0.041063188116947
		0.000351523162903505	0.041063188116947
N_Shore	LMF1	0.000351586331646569	0.041063188116947
Island	MVD	0.00035181120931646	0.041063188116947
N_Shore		0.00035183111176296	0.041063188116947
	KLHL13;KLHL13;KLHL13	0.00035184841192213	0.041063188116947
	NCRNA00189	0.000351938547011923	0.041063188116947
	PVRL1	0.000351939903728791	0.041063188116947
N_Shelf	HPCA	0.000352068801997831	0.0410675216366264
Island		0.000352165218609001	0.0410675216366264
	PID1;PID1	0.000352265770744305	0.0410675216366264
Island	KCNT1	0.00035231621824226	0.0410675216366264
		0.000352749674294771	0.0411001086629163
Island	PTPRN2;PTPRN2;PTPRN2	0.000352799788484815	0.0411001086629163
S_Shelf	ERICH1	0.000352850362505355	0.0411001086629163
	STK32C	0.000353215996209677	0.0411251313937836
Island	RBM44	0.000353302160663708	0.0411251313937836
Island	FKRP;FKRP	0.000353319923046577	0.0411251313937836
		0.000353482440482322	0.0411303232477064
N_Shore	LOC728661;CDK11B;CDK11B	0.000353534373984828	0.0411303232477064
Island	PITX1	0.000353741457097004	0.0411445319905155
Island	KIF5C	0.000353887660079893	0.0411454281379392
Island	NOTCH3	0.000353977244131494	0.0411454281379392
Island	GALE;GALE;GALE	0.000354078611770002	0.0411454281379392
	BPTF;BPTF	0.000354137663682263	0.0411454281379392
N_Shore	RASA3	0.000354212310069571	0.0411454281379392
N_Shore		0.000354258886770674	0.0411454281379392
Island	RNF220	0.000354486915740678	0.0411620415886128
S_Shore	SORCS2	0.000354597242971125	0.0411649831500456
		0.00035471931015302	0.041169285859061
Island		0.000354896653847381	0.0411791200283705
	PLCG2	0.000354974089957047	0.0411791200283705
Island	SH3GL1	0.00035513917584204	0.0411811738515188
N_Shore		0.000355226425406845	0.0411811738515188

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Island	BCOR;BCOR	0.000355246878339226	0.0411811738515188
Island	KCNS1	0.000355485375654345	0.0411945627921556
Island	ICAM4;ICAM4;ICAM4	0.000355570093336501	0.0411945627921556
Island	PML;PML;PML;PML;PM	0.000355639593015959	0.0411945627921556
N_Shore	MBP;MBP	0.000355774395889956	0.0411945627921556
N_Shore	FAM59B	0.000355787655313244	0.0411945627921556
Island	ZNF710	0.000356142732166903	0.0412142140765425
	CUX1;CUX1;CUX1	0.000356147067472557	0.0412142140765425
Island		0.000356292332460246	0.0412142140765425
Island		0.000356297763564721	0.0412142140765425
S_Shore		0.000356557679807342	0.041218338150291
N_Shore	MYBPC3	0.000356656904306196	0.041218338150291
Island	KIAA0182;KIAA0182	0.00035675041171925	0.041218338150291
S_Shore	FMN2	0.000356783195953386	0.041218338150291
Island	PTPRF;PTPRF	0.000356791320114958	0.041218338150291
		0.000356844044524173	0.041218338150291
N_Shelf	FAM19A5;FAM19A5	0.000357092157086027	0.041237162370217
	PDE10A;PDE10A	0.000357195847792009	0.0412384345167639
Island	PKP3	0.000357356331162329	0.0412384345167639
Island	FMR1NB	0.000357378349315123	0.0412384345167639
		0.000357443758016569	0.0412384345167639
N_Shore	GALNS	0.000357841210536055	0.0412744568451714
	KRTAP11-1	0.000358099864154429	0.0412944563587128
Island		0.000358198894752814	0.0412960437279593
Island	PRKCZ;PRKCZ	0.00035840887625236	0.0413009084222159
Island	XKR7	0.000358526815144166	0.0413009084222159
Island	TUBB4;MIR220B	0.000358529389689117	0.0413009084222159
N_Shore	SLC43A2	0.000358582191535473	0.0413009084222159
Island	NCOR2;NCOR2	0.000358715663782199	0.0413028623694499
	NXN	0.000358769714526972	0.0413028623694499
Island	MAGIX;MAGIX;MAGIX;M	0.000359441466827915	0.0413618790829228
		0.00035950436911921	0.0413618790829228
S_Shelf		0.000359547797022812	0.0413618790829228
Island	GRM5;GRM5	0.000359687972993598	0.0413618790829228
	MGC87042;MGC87042	0.000359783311874351	0.0413618790829228
Island	TBC1D14;TBC1D14	0.000359794758842417	0.0413618790829228
		0.000359967069957178	0.0413657296178775
		0.000360164004947616	0.0413657296178775
	FAM66A;DEFB109P1	0.000360178427067657	0.0413657296178775
S_Shore	VSIG8;C1orf204	0.000360250632764385	0.0413657296178775
Island		0.00036025529866971	0.0413657296178775
Island	SSC5D	0.000360441836445009	0.0413698574648846
	WWTR1;WWTR1;WWTR1	0.000360535776561976	0.0413698574648846
N_Shelf		0.000360547500870857	0.0413698574648846
	APOC4	0.000360793922615209	0.0413883269944602
Island	AMDHD2;AMDHD2;AMDH	0.000361077012443186	0.0413946941443629
	PPFIA4;PPFIA4	0.0003610905042427	0.0413946941443629
		0.000361401294587792	0.0413946941443629
Island	PIP5K1C	0.000361472753158744	0.0413946941443629
Island	SLC25A2	0.000361660414968453	0.0413946941443629
N_Shelf	DEPDC1B;DEPDC1B	0.00036168425006739	0.0413946941443629
Island	XKR4;SBF1P1	0.000361726425776443	0.0413946941443629
Island		0.000361756598246759	0.0413946941443629
Island		0.000361915354802571	0.0413946941443629
S_Shelf		0.000361919816312357	0.0413946941443629

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N_Shore	SLC45A4	0.000361943224981871	0.0413946941443629
N_Shelf	KIAA1522	0.000362024032001546	0.0413946941443629
	SLC7A5	0.000362026880198056	0.0413946941443629
N_Shore	MOSC1	0.000362045990596234	0.0413946941443629
	AGAP1;AGAP1	0.000362155326999218	0.0413974224094634
	ADAM5P	0.000362369636891102	0.041412145914885
Island	PTPRN2;PTPRN2;PTPF	0.000362625960199183	0.0414270190907775
	KLF13	0.000362670853135594	0.0414270190907775
Island	RUNX1;RUNX1	0.000362880639309865	0.0414412085908395
N_Shore		0.000363014892441986	0.0414467675110714
	SLC30A9	0.000363147474901114	0.0414479845038414
Island	SLC34A2	0.000363196709305328	0.0414479845038414
Island	GEFT;GEFT	0.00036350904155912	0.0414652664791593
	LHPP;LHPP	0.000363617293548678	0.0414652664791593
S_Shelf	PROC;PROC	0.00036366688006458	0.0414652664791593
	ANKRD11	0.000363690604456653	0.0414652664791593
N_Shore	GNA12	0.000363899356640414	0.0414721406567112
Island	PLA2G7;PLA2G7	0.000363922155145868	0.0414721406567112
		0.000364067142303784	0.0414789034806587
	ZHX2	0.000364184993612032	0.0414797883232353
	HSPG2	0.000364246197777773	0.0414797883232353
Island		0.000364431138052068	0.0414910933091367
		0.000364890028790523	0.0414986171700438
	MAD1L1;MAD1L1;MAD1	0.000364921497068211	0.0414986171700438
S_Shore	CLMN	0.00036516094548728	0.0414986171700438
Island	HEATR7A;HEATR7A;HE	0.000365189640794545	0.0414986171700438
Island	GABRA4	0.000365229830322467	0.0414986171700438
N_Shelf		0.000365285299224238	0.0414986171700438
Island	CAMK2B;CAMK2B;CAM	0.000365351773677714	0.0414986171700438
	USP49	0.000365368715387786	0.0414986171700438
Island	CCDC64B	0.000365384662248915	0.0414986171700438
Island		0.000365552305394674	0.0414986171700438
Island	MFHAS1	0.000365638145844079	0.0414986171700438
		0.000365646661730866	0.0414986171700438
S_Shore	HOXB13	0.000365966831323798	0.0414986171700438
	RPTOR;RPTOR	0.000366071109305915	0.0414986171700438
		0.000366156255429865	0.0414986171700438
S_Shelf	PDE8B;PDE8B;PDE8B;P	0.000366158225635108	0.0414986171700438
Island		0.000366263716185898	0.0414986171700438
		0.000366268285471909	0.0414986171700438
Island	ZNF167	0.000366271373968702	0.0414986171700438
Island	MBP;MBP	0.000366300997024358	0.0414986171700438
	TCF12;TCF12;TCF12;TC	0.000366346658574606	0.0414986171700438
Island	PCGF3	0.00036647024600017	0.0414986171700438
S_Shore	PLEKHG6;PLEKHG6;PL	0.00036655229956892	0.0414986171700438
		0.000366553624639338	0.0414986171700438
	CDH4	0.00036671132783064	0.0415067688365447
Island	PHOX2B	0.000366859553859104	0.041513844257666
		0.000367014855841822	0.0415197501998063
Island	MKNK2;MKNK2	0.000367083198999784	0.0415197501998063
Island		0.000367288986358553	0.0415242894791479
Island	OLIG3	0.000367769315517182	0.0415242894791479
	CCDC3	0.000367814998153367	0.0415242894791479
		0.000367873052031086	0.0415242894791479
N_Shore		0.000367906963077263	0.0415242894791479

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	ANKS3	0.000368003391240122	0.0415242894791479
	ZBTB5	0.000368177652864061	0.0415242894791479
Island	GALR2	0.000368221337023481	0.0415242894791479
		0.00036824627508322	0.0415242894791479
S_Shore	BMP7	0.000368291552765456	0.0415242894791479
	GMDS	0.000368351478436357	0.0415242894791479
	FABP6;FABP6	0.000368381267314022	0.0415242894791479
S_Shelf	CDK16;CDK16;CDK16	0.00036850359209099	0.0415242894791479
Island	CIT	0.000368547652331035	0.0415242894791479
Island	MAPK4	0.000368566084348482	0.0415242894791479
	SLC20A2	0.000368571289829022	0.0415242894791479
S_Shore	INF2;INF2	0.000368751571917496	0.0415242894791479
S_Shore	C6orf138	0.00036876586560625	0.0415242894791479
Island		0.000368819674098494	0.0415242894791479
Island	ARHGEF18;ARHGEF18	0.000368887533357566	0.0415242894791479
	TG	0.000368986280829779	0.0415242894791479
Island	GNB1L	0.000369305611685593	0.0415242894791479
	TAAR6	0.000369404038923339	0.0415242894791479
	AGAP1;AGAP1	0.000369470629344997	0.0415242894791479
Island	SLC25A31	0.000369552446754322	0.0415242894791479
	GAK	0.000369587195035092	0.0415242894791479
	PYGM;PYGM	0.000369623491014537	0.0415242894791479
N_Shelf	RIMBP2	0.00036963487868999	0.0415242894791479
S_Shore		0.000369752313953222	0.0415242894791479
Island	FAM48B1	0.000369760195377922	0.0415242894791479
	COL4A2	0.000369781160426501	0.0415242894791479
Island	WNK4	0.000370320153265598	0.0415751757603989
N_Shelf	NTM	0.00037052839632715	0.0415889143803353
S_Shelf	RHBDD2;RHBDD2	0.000370871816459636	0.041615796047711
	HRNBP3	0.000370939744051966	0.041615796047711
S_Shore		0.000371116761611655	0.0416167403158269
Island	PTPRN2;PTPRN2;PTPRN2	0.000371205401612236	0.0416167403158269
Island		0.000371205942630201	0.0416167403158269
Island		0.000371523063488633	0.0416398697488493
Island	ACOX3;ACOX3	0.000371584198739538	0.0416398697488493
	UBAC1	0.000371806132502026	0.0416551018098644
N_Shore	COL4A2	0.000371982275534295	0.0416587589586875
		0.000372010803688274	0.0416587589586875
S_Shelf	CORO1B;CORO1B;PTPRN2	0.000372156360106179	0.0416614962983445
	ADARB2	0.0003722072874267	0.0416614962983445
	SYNJ2	0.000372464239956685	0.0416617884923579
N_Shore		0.000372558739191721	0.0416617884923579
		0.000372572445186221	0.0416617884923579
		0.000372600833098446	0.0416617884923579
S_Shore		0.000372639999481535	0.0416617884923579
Island	HSD17B8	0.000372733593606334	0.0416626350619404
N_Shelf		0.000373073406976609	0.0416877551824558
	AP3B1	0.000373135663907488	0.0416877551824558
S_Shore	DIP2C	0.000373315066623603	0.0416877551824558
	FBXO31;FBXO31	0.000373466600179458	0.0416877551824558
Island		0.000373555032610705	0.0416877551824558
Island	HOXA9	0.000373557517924727	0.0416877551824558
		0.000373681887991295	0.0416877551824558
		0.000373814973843942	0.0416877551824558
Island	TMCO3	0.000373858071468124	0.0416877551824558

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	MAGEC2	0.000373867956348332	0.0416877551824558
S_Shore	DCTPP1	0.000373905143266584	0.0416877551824558
Island	EPS8L1;EPS8L1	0.000374396595249442	0.041724613161137
Island	CSDAP1	0.000374457573744386	0.041724613161137
	WHSC1L1;WHSC1L1	0.000374494179345404	0.041724613161137
	GPR98;GPR98	0.00037458286179154	0.0417248952477432
	ERICH1	0.000374721896224851	0.0417307846376411
	GLOD4	0.000374862090603682	0.041736800467041
Island	JMJD8;WDR24	0.000374999778425204	0.0417391672346809
	FBR5	0.000375151284992539	0.0417391672346809
S_Shelf		0.00037535150943727	0.0417391672346809
		0.00037539163393793	0.0417391672346809
S_Shore	MTMR6	0.000375427595030613	0.0417391672346809
Island	NRTN;NRTN	0.000375650527472003	0.0417391672346809
	CUGBP2;CUGBP2;CUG	0.000375692503662906	0.0417391672346809
S_Shore	MMP17	0.00037569370552821	0.0417391672346809
S_Shore	EHMT1;EHMT1	0.000375879062630739	0.0417391672346809
Island	C9orf172	0.000375945680660562	0.0417391672346809
Island	KIF26A	0.000376043184278575	0.0417391672346809
N_Shore	AGAP1;AGAP1	0.000376135406335376	0.0417391672346809
Island		0.000376180090458953	0.0417391672346809
	MAPK8IP3;MAPK8IP3	0.000376215196477695	0.0417391672346809
Island	ARHGAP6;ARHGAP6	0.000376241725223	0.0417391672346809
	SLC9A9	0.000376336454808104	0.0417391672346809
	PLCG2	0.000376458582778113	0.0417391672346809
Island	KLHL26	0.000376467289555705	0.0417391672346809
S_Shelf		0.000376520769417893	0.0417391672346809
S_Shore	TMTC4;TMTC4	0.000376890163774549	0.0417651575299755
	LASS6	0.000376954266829814	0.0417651575299755
S_Shelf	SPG20	0.000377275969489444	0.0417651575299755
Island	KIF26A	0.00037727738395271	0.0417651575299755
Island	COL23A1	0.000377314573427074	0.0417651575299755
S_Shore	ATP1B2	0.000377330533725835	0.0417651575299755
S_Shore		0.000377358858929795	0.0417651575299755
		0.000377639786048336	0.0417782975438644
	SPTBN2	0.000377660073611518	0.0417782975438644
Island	RD3;RD3	0.000377736364929711	0.0417782975438644
Island		0.000378218347480144	0.0418216929068516
		0.000378325516378628	0.0418216929068516
	IDH3A	0.000378447329573511	0.0418216929068516
S_Shore	KBTBD11	0.000378474123802675	0.0418216929068516
Island	HSPB6	0.00037874014319942	0.0418415419377415
Island	DPP10;DPP10	0.000378957042676179	0.0418559566007161
		0.000379147995016565	0.0418586420524846
Island	ADAMTS2	0.00037915420984721	0.0418586420524846
Island	TMSB4Y;TMSB4Y	0.000379308303846296	0.0418630773005522
N_Shore	WDR90	0.000379388641975315	0.0418630773005522
Island		0.000379700541186445	0.0418630773005522
	MYT1L	0.000379743945926626	0.0418630773005522
S_Shelf	COL18A1;COL18A1;CO	0.000379830209466133	0.0418630773005522
S_Shelf	MFGE8;MFGE8	0.000379845425473588	0.0418630773005522
Island		0.000379978695068995	0.0418630773005522
Island		0.000380071899850765	0.0418630773005522
		0.000380121659866448	0.0418630773005522
Island	FOXA2	0.000380230379276737	0.0418630773005522

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Island	BOP1	0.000380315518719507	0.0418630773005522
S_Shore		0.000380359906398797	0.0418630773005522
	RCVRN	0.000380444084098956	0.0418630773005522
Island	SLC12A7	0.000380452490114726	0.0418630773005522
	MAGEC2	0.000380490922989791	0.0418630773005522
Island	SPG7;SPG7	0.000380664878304988	0.0418672792166767
S_Shore	GAB4	0.000380702003138892	0.0418672792166767
S_Shore	FLJ40434	0.000380810948340791	0.0418674989916291
	SORBS2	0.000381003577855255	0.0418674989916291
Island	WDR88	0.000381059072845424	0.0418674989916291
S_Shelf	PTPRS;PTPRS;PTPRS;	0.000381086231077989	0.0418674989916291
		0.000381219005730711	0.0418674989916291
Island	ZIC1	0.00038137911739485	0.0418674989916291
Island	CASZ1;CASZ1	0.000381426552657735	0.0418674989916291
Island	FAM19A5	0.000381486789417384	0.0418674989916291
S_Shelf		0.000381533118055184	0.0418674989916291
N_Shelf	TELO2	0.000381568452070513	0.0418674989916291
S_Shelf	TTC39B;TTC39B;TTC39	0.00038174521015121	0.0418717761681902
Island		0.000381780340801585	0.0418717761681902
N_Shore	HOXC4;HOXC5;HOXC6	0.000382017773258954	0.0418793371360209
		0.000382022219515698	0.0418793371360209
S_Shore	CXXC5	0.000382298918575672	0.0418994645993809
S_Shore	C6orf108;C6orf108	0.000382378843812034	0.0418994645993809
Island	BLCAP;BLCAP;BLCAP;	0.00038248651216951	0.0419017824036412
Island		0.000383105743094099	0.0419305277321454
Island	MOBKL2C;MOBKL2C	0.000383323794726421	0.0419305277321454
		0.000383368468226722	0.0419305277321454
	FRMD4A	0.000383427499896352	0.0419305277321454
		0.000383545728424143	0.0419305277321454
Island	INSC;INSC;INSC	0.000383670570624732	0.0419305277321454
	PFKP	0.000383786688592154	0.0419305277321454
N_Shore	ATP11A;ATP11A	0.000383803209286563	0.0419305277321454
Island		0.000383809338749637	0.0419305277321454
S_Shelf	TH1L	0.000383930208619422	0.0419305277321454
Island	LOC100132215	0.000383930454651341	0.0419305277321454
N_Shore	ANAPC2	0.000383953287124102	0.0419305277321454
	EPHA6	0.000383980572160864	0.0419305277321454
Island	NKX2-6	0.000384042012664629	0.0419305277321454
	IL22RA1	0.000384047532173225	0.0419305277321454
Island	SLC35F1	0.000384275401294743	0.0419459508073195
S_Shelf	SYNE2;SYNE2	0.000384609162787553	0.0419547259935411
Island	GRIN2C	0.000384681957262098	0.0419547259935411
	EIF4E3;EIF4E3;EIF4E3;	0.000384791112473711	0.0419547259935411
N_Shelf	RGS16	0.000385248610945489	0.0419547259935411
Island		0.000385369124757983	0.0419547259935411
Island	GPRIN1	0.000385471231948822	0.0419547259935411
N_Shore	TCERG1;TCERG1	0.000385487853823806	0.0419547259935411
N_Shore	SCRIB;SCRIB	0.000385501688763369	0.0419547259935411
	SMAD9;SMAD9	0.000385744734178061	0.0419547259935411
	USP43	0.000385807422193355	0.0419547259935411
N_Shore	VAV2;VAV2	0.000385930416219173	0.0419547259935411
Island	TSNARE1	0.000385979773188928	0.0419547259935411
	ATP11A;ATP11A	0.0003859948109105	0.0419547259935411
Island	NR2E1	0.000386104408599542	0.0419547259935411
Island		0.000386119262870615	0.0419547259935411

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	STXBP5;STXBP5	0.000386293422895982	0.0419547259935411
N_Shore		0.000386323475116599	0.0419547259935411
Island	HIST1H2BH;HIST1H3F	0.000386339775303858	0.0419547259935411
		0.000386375261137206	0.0419547259935411
	HYLS1	0.000386529281883835	0.0419547259935411
Island		0.000386559414436024	0.0419547259935411
	DNAI2	0.000386693855245249	0.0419547259935411
	MEGF6	0.000386822590589425	0.0419547259935411
		0.00038683077416613	0.0419547259935411
N_Shore		0.000386937506959242	0.0419547259935411
N_Shore		0.000386981130616011	0.0419547259935411
Island	CTBP1;CTBP1	0.000387459992186661	0.0419547259935411
S_Shore	FAM70A;FAM70A;FAM7	0.000387590828568567	0.0419547259935411
Island	EVX1	0.0003878804766064	0.0419547259935411
Island	PCGF3	0.000387959305710166	0.0419547259935411
Island	OLIG2;OLIG2	0.000388099774367579	0.0419547259935411
	TANC2	0.000388119222628447	0.0419547259935411
N_Shelf	PTPRN2;PTPRN2;PTPF	0.000388134599365323	0.0419547259935411
Island	SH3D20	0.000388148752392166	0.0419547259935411
		0.000388309176602909	0.0419547259935411
	UBE4B;UBE4B	0.000388373922923083	0.0419547259935411
		0.000388392712684588	0.0419547259935411
S_Shelf		0.000388435914165422	0.0419547259935411
Island	KLF15	0.00038845856823122	0.0419547259935411
	RASA3	0.00038853508564209	0.0419547259935411
	MAP3K15	0.000388578584716292	0.0419547259935411
N_Shore	PCGF3	0.000388634242406138	0.0419547259935411
Island	PRDM16;PRDM16	0.000389071306477685	0.0419547259935411
Island		0.000389084146106697	0.0419547259935411
Island	NT5C1B;NT5C1B	0.000389174205773079	0.0419547259935411
Island		0.00038926172586767	0.0419547259935411
N_Shelf	BAIAP2;BAIAP2;BAIAP2	0.000389268000982556	0.0419547259935411
Island		0.000389280625883538	0.0419547259935411
	HECW1	0.000389523613722429	0.0419547259935411
Island	TFAP2E	0.000389546332186467	0.0419547259935411
	EHMT1;EHMT1	0.000389575269315168	0.0419547259935411
S_Shore	TSNARE1	0.000389690393927152	0.0419547259935411
	UGT2B4	0.000389699100071707	0.0419547259935411
		0.000389714145605002	0.0419547259935411
Island	PCDHA6;PCDHA2;PCD	0.000389736798033889	0.0419547259935411
S_Shore	SP5	0.000389761910628694	0.0419547259935411
N_Shore	NR5A2;NR5A2	0.000389895946094242	0.0419547259935411
N_Shore	GNG7	0.000389909097322688	0.0419547259935411
	ITPKB	0.000389987359222929	0.0419547259935411
		0.000390025246747254	0.0419547259935411
Island	NCLN	0.000390055795118371	0.0419547259935411
Island		0.000390095722720672	0.0419547259935411
N_Shore	GPR149	0.000390144664777405	0.0419547259935411
	MAGEE2	0.000390145343232925	0.0419547259935411
Island	FAM38A	0.000390222512106203	0.0419547259935411
Island		0.000390296656502122	0.0419547259935411
S_Shore	CHRDL1;CHRDL1;CHR	0.000390317790855884	0.0419547259935411
S_Shore		0.00039033582575756	0.0419547259935411
Island	KIAA1210	0.00039033781880048	0.0419547259935411
S_Shore		0.000390419553095318	0.0419547259935411

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		0.000390595111379078	0.0419642806829352
Island	NOM1	0.00039074856389796	0.0419670020209005
N_Shore	LTBP4;LTBP4;LTBP4	0.000390861336999726	0.0419670020209005
N_Shelf	ZNF43	0.000391031820059323	0.0419670020209005
		0.000391115793534542	0.0419670020209005
		0.000391143672400934	0.0419670020209005
	ADARB2	0.000391158702400772	0.0419670020209005
Island	OBSL1	0.000391409216682655	0.0419670020209005
Island	IL17RA	0.000391684680589753	0.0419670020209005
Island		0.000391750953119593	0.0419670020209005
		0.000391755623223138	0.0419670020209005
	SLC22A8	0.000391797980182413	0.0419670020209005
		0.000391847801809447	0.0419670020209005
	FNDC1	0.000391927812657311	0.0419670020209005
Island	ADAD2;ADAD2	0.000391950726377604	0.0419670020209005
Island	SLC8A2	0.000391958351777305	0.0419670020209005
Island	CPEB2;CPEB2	0.000392006849001299	0.0419670020209005
Island	CUEDC1	0.000392114632548191	0.0419692639577685
S_Shore		0.000392264255991259	0.0419760021615039
Island		0.000392557114077948	0.0419823461980778
S_Shore	FBLN7;FBLN7	0.000392571818928872	0.0419823461980778
N_Shore	ZNF586	0.000392660876515132	0.0419823461980778
		0.000392745765412917	0.0419823461980778
	HRNBP3	0.000392783887594112	0.0419823461980778
	BCAT1	0.000392843633860917	0.0419823461980778
	SNED1	0.000393056001852378	0.0419919183105208
N_Shelf		0.000393162023793218	0.0419919183105208
	DENND3	0.000393193309323722	0.0419919183105208
	ANK3;ANK3	0.000393611613497616	0.0420195612008884
Island	TUBB1	0.000393688620800342	0.0420195612008884
	PLA2G2C	0.00039371242188537	0.0420195612008884
	CDC42BPB	0.000394031181219162	0.042044316334869
	DIP2C	0.000394188183956045	0.0420518043661233
	ARHGEF10	0.000394275008778332	0.0420518043661233
	BMPR1A	0.000394483526769705	0.042053046747196
	OLA1;OLA1	0.000394534025480862	0.042053046747196
Island	ANO8	0.000394547141731809	0.042053046747196
	INPP5A	0.000394721571115873	0.0420623817229252
N_Shelf	CCDC42B	0.00039489899096633	0.0420639101888057
N_Shore	GPT	0.000394909615709492	0.0420639101888057
Island	CCDC17	0.000395081678798777	0.0420729846271366
S_Shelf	PRDM16;PRDM16	0.00039558088293197	0.0421009569742537
S_Shore		0.000395581549241021	0.0421009569742537
Island	NNAT;NNAT;BLCAP;NN	0.000395615274965381	0.0421009569742537
		0.000395742992473638	0.0421009569742537
	DIP2C	0.000395853267636242	0.0421009569742537
S_Shore		0.000395870959313955	0.0421009569742537
		0.000396068104774369	0.0421009569742537
N_Shore	NEXN	0.000396121898042122	0.0421009569742537
Island	AGAP1;AGAP1	0.000396230298450057	0.0421009569742537
Island	ZNF711	0.000396396173983076	0.0421009569742537
		0.000396408077675921	0.0421009569742537
N_Shelf		0.000396503268528344	0.0421009569742537
	OSMR;OSMR	0.000396551146702495	0.0421009569742537
		0.000396561329100388	0.0421009569742537

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Island	SIX6	0.00039687120380576	0.0421161711470157
Island		0.00039699223049443	0.0421161711470157
		0.000397044343913068	0.0421161711470157
S_Shelf	FAM91A1	0.000397136993226519	0.0421161711470157
Island	PAPOLB;RADIL	0.000397167230690447	0.0421161711470157
Island		0.000397226386826135	0.0421161711470157
S_Shore	NOS1	0.000397438031941437	0.0421163750704651
S_Shore	SFRS5;SFRS5;LOC100	0.000397462599991174	0.0421163750704651
Island	LMX1A	0.000397489186903621	0.0421163750704651
N_Shelf	LMF1	0.000397599651133894	0.0421188650558669
S_Shore		0.000397917360586449	0.0421406452264124
	NAALADL2	0.000398129030335835	0.0421406452264124
Island		0.000398143394736089	0.0421406452264124
	LPTM4B	0.000398168962944085	0.0421406452264124
N_Shore	ADAMTS2;ADAMTS2	0.000398276094757977	0.0421406452264124
	TIMP2	0.000398327308824685	0.0421406452264124
S_Shore	RPTOR;RPTOR	0.000398561814544398	0.0421562460863104
	PHLPP1	0.000398844964513554	0.0421581716779296
Island	TRIM3;TRIM3	0.00039887718986735	0.0421581716779296
Island	GPR25	0.000398893670555927	0.0421581716779296
		0.000398928200691584	0.0421581716779296
		0.000399084833292543	0.0421653177808929
Island	PCDHGA4;PCDHGA12;	0.000399183842073715	0.0421653177808929
Island	NCOR2;NCOR2	0.000399327132598895	0.0421653177808929
N_Shore		0.000399383686568872	0.0421653177808929
Island	SLC38A3	0.000399431121620268	0.0421653177808929
Island	HNRNPUL1;HNRNPUL1	0.000399664034946523	0.0421769856214433
N_Shelf	ASB1	0.000399831211263635	0.0421769856214433
		0.000399921657811326	0.0421769856214433
N_Shore	CA3	0.000400202670499649	0.0421769856214433
	ABCC2	0.000400207295504979	0.0421769856214433
		0.000400318598575061	0.0421769856214433
N_Shelf		0.000400336504716403	0.0421769856214433
N_Shore	HIST1H4F	0.000400396815686699	0.0421769856214433
	HNRNPC;HNRNPC;HNF	0.000400427319550663	0.0421769856214433
Island		0.00040047496151528	0.0421769856214433
S_Shore		0.000400529491095144	0.0421769856214433
S_Shelf	NCOR2;NCOR2	0.000400595496472109	0.0421769856214433
		0.000400713428801019	0.0421769856214433
Island	SMTN;SMTN;SMTN	0.000400773053554837	0.0421769856214433
	DGKI	0.000400894743692774	0.0421769856214433
	MXD4	0.00040093499571801	0.0421769856214433
Island	C4orf22	0.000401133670948719	0.0421887220808335
	ESM1;ESM1	0.000401310973397082	0.0421982060769739
Island	NFYA;NFYA;LOC22144	0.000401612157145346	0.0422207093573735
Island	SHANK2;SHANK2	0.000401830513552097	0.0422251781803897
Island	KCNE1L;KCNE1L	0.000401925579765595	0.0422251781803897
Island	BHLHE23	0.000401985690307005	0.0422251781803897
S_Shelf		0.000402003399762095	0.0422251781803897
N_Shelf		0.000402187971964995	0.0422294092856696
Island		0.000402219483269887	0.0422294092856696
S_Shore	HOXA6	0.00040230525874997	0.0422294092856696
N_Shore		0.000402778316664216	0.0422527010896874
		0.000402910133329236	0.0422527010896874
		0.000402923141197334	0.0422527010896874

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		0.000402979892784597	0.0422527010896874
	CD82;CD82	0.000403013640594265	0.0422527010896874
Island	RHBDF1	0.000403050594196781	0.0422527010896874
N_Shelf	SNX29	0.000403140192982959	0.0422529482723375
		0.000403241778973607	0.0422544514498901
Island	UBE2J2;UBE2J2;UBE2J	0.000403546687902881	0.0422548717410966
	FRMD4A	0.000403548410711761	0.0422548717410966
	HERC2	0.00040356294768563	0.0422548717410966
Island		0.000403594769368322	0.0422548717410966
Island		0.000403696353760987	0.0422563727113227
Island		0.000403823967672282	0.0422575510529927
	CSDM1	0.000403960548663936	0.0422575510529927
Island	HOXC4;HOXC5;HOXC5	0.000403969362257484	0.0422575510529927
S_Shore	C7orf50;C7orf50;C7orf5	0.000404208548637434	0.0422716085759593
N_Shelf	PPP2R2D;PPP2R2D;PP	0.000404499763062398	0.0422716085759593
	SLC12A4;SLC12A4;SLC	0.00040452126812455	0.0422716085759593
	ZZEF1	0.000404541067125139	0.0422716085759593
	ARGLU1	0.000404690805071709	0.0422716085759593
	AP3S1	0.000404708417371647	0.0422716085759593
Island		0.000404753811223288	0.0422716085759593
Island	STK32C	0.000404930812572388	0.0422716085759593
Island	C3orf24;C3orf24	0.000405004799311177	0.0422716085759593
	KSR2	0.000405055150375781	0.0422716085759593
Island	GRAMD1B	0.000405127304434391	0.0422716085759593
Island		0.000405216890982346	0.0422716085759593
	TRIM55;TRIM55;TRIM5	0.000405309067686922	0.0422716085759593
	ANK3;ANK3	0.000405370248123675	0.0422716085759593
	CAMTA1	0.000405412939318291	0.0422716085759593
Island	HDAC4	0.000405708437287235	0.0422832292402036
Island	PABPC3;PABPC3	0.000405746640760395	0.0422832292402036
	ADCY9	0.000405786299506461	0.0422832292402036
		0.000406141860634244	0.042306816537231
N_Shelf	RTP1	0.000406187367776027	0.042306816537231
Island	SMTNL2;SMTNL2	0.000406445336968596	0.0423245834932951
S_Shore	TSNARE1	0.000406677422955517	0.0423360026200876
		0.00040676622883008	0.0423360026200876
Island		0.000406817232630749	0.0423360026200876
	CABC1	0.00040749118705323	0.0423970288226758
		0.000407596242300792	0.0423988509562567
		0.000407736067468603	0.0424042883566096
	CNDP1	0.000408018452511185	0.0424078228566489
Island		0.000408035519800782	0.0424078228566489
N_Shelf	GPR124	0.000408141920149883	0.0424078228566489
		0.000408189313602829	0.0424078228566489
Island	UNKL	0.000408414424163051	0.0424078228566489
Island		0.000408506882576568	0.0424078228566489
	AGBL4	0.000408574695005117	0.0424078228566489
N_Shore	PGCP	0.000408579425384974	0.0424078228566489
Island		0.000408655264680931	0.0424078228566489
Island	GFI1;GFI1	0.000408659035901239	0.0424078228566489
		0.000408733220657279	0.0424078228566489
S_Shore	TPO;TPO;TPO;TPO	0.000408927667417682	0.0424128895967879
Island	MYH14;MYH14;MYH14	0.000408982403893871	0.0424128895967879
N_Shore	PCCA;PCCA	0.000409044768092905	0.0424128895967879
		0.000409179953742312	0.0424178255771073

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	CLDN14;CLDN14	0.000409441981659898	0.0424300615790515
N_Shore	EPHX4	0.000409473200475893	0.0424300615790515
	SMYD3;SMYD3	0.000409665026257594	0.0424376694919331
	SLC25A42	0.000409766699048611	0.0424376694919331
Island	PCDHGA4;PCDHGC3;P	0.00040991652829007	0.0424376694919331
N_Shelf		0.000409970073738888	0.0424376694919331
N_Shore	ANKMY2	0.000409984732468394	0.0424376694919331
Island	COL4A2	0.000410295123495673	0.0424461270117215
N_Shelf	ZNF781	0.000410436205183293	0.0424461270117215
S_Shore	OCA2	0.000410717109129901	0.0424461270117215
		0.00041096915884276	0.0424461270117215
Island	KBTBD11	0.000411005679696393	0.0424461270117215
	SORCS2	0.00041110840122736	0.0424461270117215
	CACNA1G;CACNA1G;C	0.000411174647803065	0.0424461270117215
	ITPK1;ITPK1;ITPK1	0.000411259710235396	0.0424461270117215
	FMN1	0.00041126397541568	0.0424461270117215
Island	GTF2IRD1;GTF2IRD1	0.000411281538984554	0.0424461270117215
S_Shore		0.000411308909168177	0.0424461270117215
N_Shelf	GRM2;GRM2	0.00041131721610222	0.0424461270117215
		0.000411351846606544	0.0424461270117215
	INPP5A	0.000411360181201613	0.0424461270117215
Island	LRFN3	0.00041138103586026	0.0424461270117215
Island	PCDH19;PCDH19	0.000411516939748203	0.0424475651833229
Island	TDRD12	0.000411652584542554	0.0424475651833229
	PARK7;PARK7	0.000411672262884763	0.0424475651833229
	MIR548F5;DCLK1	0.000411792576886473	0.0424475651833229
N_Shore		0.000411983229202108	0.0424475651833229
		0.000411984962972107	0.0424475651833229
N_Shore	HCCA2;LOC402778	0.000412070038946723	0.0424475651833229
N_Shore	FAM47B	0.000412096116227707	0.0424475651833229
		0.00041234958328638	0.0424492206542519
S_Shore	STXBP2;STXBP2	0.000412437387925897	0.0424492206542519
Island	MYOD1	0.000412479951810172	0.0424492206542519
Island	KLHL34	0.000412541991204484	0.0424492206542519
	GALNT10;GALNT10	0.00041260867529932	0.0424492206542519
Island	MGC42105	0.000412685759272064	0.0424492206542519
Island		0.00041303135619483	0.0424492206542519
N_Shore	IGSF21	0.000413042440854718	0.0424492206542519
Island	DIP2C	0.000413107820306603	0.0424492206542519
N_Shelf	RPTOR;RPTOR	0.000413388124869946	0.0424492206542519
S_Shelf	ZDHC8P	0.00041348683771481	0.0424492206542519
Island	HOXB9	0.000413677079509457	0.0424492206542519
N_Shore	LOC100130872-SPON2	0.000413741116833995	0.0424492206542519
N_Shore		0.000413803532830729	0.0424492206542519
Island	LRP5L;LRP5L;LRP5L	0.00041380479339138	0.0424492206542519
		0.000413817816111753	0.0424492206542519
Island	PCDHA1;PCDHA1;PCD	0.000413970314112338	0.0424492206542519
Island	VSTM2A;VSTM2A	0.000413990971699967	0.0424492206542519
S_Shore		0.000413994434832439	0.0424492206542519
		0.000414033915860311	0.0424492206542519
Island		0.000414177530496142	0.0424492206542519
		0.000414240512603639	0.0424492206542519
	UST	0.000414409449599193	0.0424492206542519
	EFNA5	0.000414435368825349	0.0424492206542519
Island	GLB1L2	0.000414574608590905	0.0424492206542519

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	MAGI1;MAGI1;MAGI1	0.000414656732158864	0.0424492206542519
	USP9Y	0.000414838747576167	0.0424492206542519
Island	RPTOR;RPTOR	0.000414856059096098	0.0424492206542519
	PPP2R2D;PPP2R2D;PPP2R2D	0.000414965888193075	0.0424492206542519
		0.000414969650407991	0.0424492206542519
Island		0.000414989681400735	0.0424492206542519
N_Shore	USP20;USP20;USP20	0.000415070088742538	0.0424492206542519
Island	GMIP	0.000415254574462353	0.0424492206542519
Island		0.000415293389992785	0.0424492206542519
		0.000415358531222964	0.0424492206542519
		0.000415399995350918	0.0424492206542519
		0.000415500303466943	0.0424492206542519
Island	TYK2	0.000415566096711813	0.0424492206542519
		0.000415584706963469	0.0424492206542519
	ARHGEF10	0.00041561803405247	0.0424492206542519
N_Shelf	BNIP2	0.000415863238675873	0.0424653095238651
Island	AXIN1;AXIN1	0.000416356289435206	0.0425066947471977
N_Shore	VPS37B	0.0004164738311581	0.0425097340939192
S_Shore	ABR;ABR;ABR	0.000416686770168546	0.0425225073665995
		0.000416865507383576	0.0425299274643309
N_Shelf		0.000416976851888717	0.0425299274643309
Island		0.000417222526021913	0.0425299274643309
S_Shelf	BACE2;BACE2;BACE2	0.000417333717289693	0.0425299274643309
	SSRP1	0.000417337540680907	0.0425299274643309
	PEG3;PEG3;PEG3;PEG3	0.000417375818105646	0.0425299274643309
Island		0.000417452231183533	0.0425299274643309
		0.00041748888157216	0.0425299274643309
Island	PAX3;PAX3;PAX3;CCDC70	0.000417549796299785	0.0425299274643309
	COX10	0.000417811814230716	0.0425476675625087
	CDR1;CDR1	0.00041794234008961	0.042552012584381
S_Shore		0.000418071755492694	0.0425562427446404
Island	TERT;TERT	0.000418351173740189	0.0425695768715929
	FOXK1	0.000418419603387101	0.0425695768715929
S_Shore	AGAP1;AGAP1	0.00041846643366676	0.0425695768715929
Island		0.000418757333800746	0.0425902237910639
	ERC2	0.00041891464121061	0.0425917608983699
Island	SLC12A7	0.000418948327919959	0.0425917608983699
	CRAMP1L	0.000419050586720167	0.0425932162462214
N_Shore	TNRC18	0.000419187741583527	0.0425945028623457
Island	PLTP;PLTP	0.000419320999021168	0.0425945028623457
	TEX11;TEX11	0.00041941824466167	0.0425945028623457
N_Shelf		0.000419430349946077	0.0425945028623457
Island	PANK4	0.000419502975591574	0.0425945028623457
Island	MOV10L1;MOV10L1;MOV10L1	0.000419875344116012	0.0426233758203705
	TBCD	0.000419987134112222	0.0426257897587808
Island	PROM1;PROM1;PROM1	0.000420090281673927	0.0426260752783881
	HEATR2	0.000420165969914881	0.0426260752783881
	HAS1	0.000420390979908602	0.0426345296217619
	SLC6A3	0.000420425362047251	0.0426345296217619
S_Shore		0.000420532211998043	0.0426364378429877
Island	RECQL5	0.000420723182889792	0.0426468722379863
Island	C6orf174	0.00042103475819509	0.0426598230764019
	BTBD12	0.000421108117462357	0.0426598230764019
	MYH9	0.000421115189445677	0.0426598230764019
	CCDC70	0.000421208557406638	0.0426603585457904

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Island	SRRM4	0.000421493650514999	0.0426803078163657
	PAGE2	0.000421742749915937	0.0426875307150269
		0.000421893307646937	0.0426875307150269
Island		0.000421916495244724	0.0426875307150269
Island	RASA3	0.000421917533748689	0.0426875307150269
Island	NEUROD2	0.000422208434677099	0.0426974829992619
Island	GPC3;GPC3;GPC3;GPC3	0.00042220865939093	0.0426974829992619
S_Shelf	ACOX3;ACOX3	0.000422398837786578	0.0426974829992619
N_Shelf	VAV2;VAV2	0.000422432690450869	0.0426974829992619
S_Shelf		0.000422467970753689	0.0426974829992619
		0.000422544853178057	0.0426974829992619
Island	DTX1	0.000422645695113815	0.0426987643483518
Island	RHBG;RHBG	0.000422869044515156	0.0427093077789892
	FOXP1;FOXP1	0.000422926423595793	0.0427093077789892
Island	TUBB2A	0.000423113535363345	0.0427129594182961
	KCNAB2;KCNAB2	0.000423182307022322	0.0427129594182961
N_Shore	FOXK1	0.000423227155832143	0.0427129594182961
		0.000423339484409105	0.0427151274722534
		0.000423430865835519	0.0427151274722534
	CPXCR1	0.000423513223809964	0.0427151274722534
S_Shore	SPTBN2	0.000423609799891219	0.0427159725863658
Island	KCNH6;KCNH6	0.000423850726695844	0.0427252156585678
Island	CHFR;CHFR;CHFR;CHFR	0.000423877894470486	0.0427252156585678
S_Shore	LMF1	0.000424122981393639	0.0427410243369693
N_Shore	ZFY;ZFY;ZFY	0.0004244427990267	0.0427618988181287
N_Shelf	SPG7;SPG7	0.000424506704212178	0.0427618988181287
N_Shore		0.000424644121332684	0.0427645551665514
Island	CDX1	0.000424709668819723	0.0427645551665514
S_Shore	SLIT1	0.000425112702275633	0.0427962397692051
Island	GNPTG	0.000425207400515947	0.0427968774428275
S_Shore		0.000425336017760224	0.0428006536742956
	TRAPPC9;TRAPPC9	0.000425571593548495	0.0428006536742956
Island	ARFGAP1;ARFGAP1	0.000425579888930152	0.0428006536742956
Island	KCNN1	0.000425653554795088	0.0428006536742956
Island	DIP2C	0.00042568677798809	0.0428006536742956
	ZFPM1	0.000425978803072073	0.0428141552089337
N_Shore	TOP1MT	0.000426268489133618	0.0428141552089337
		0.00042628118544548	0.0428141552089337
N_Shelf	DLX6AS	0.000426290642931568	0.0428141552089337
Island		0.000426297924556019	0.0428141552089337
	MIR549;KIAA1199	0.000426351459397486	0.0428141552089337
S_Shelf	GDF2	0.000426515524157699	0.0428198675299736
Island		0.000426585166638358	0.0428198675299736
Island	LECT1;LECT1	0.000426894881627954	0.0428381667872517
Island	ROBO3	0.000426944368104195	0.0428381667872517
N_Shelf	RAB3GAP2;AURKAPS1	0.000427073221955405	0.0428422200131631
Island	HCN2	0.000427401590149728	0.0428545133308584
	CNTN4;CNTN4;CNTN4	0.000427417989253671	0.0428545133308584
		0.000427461216954271	0.0428545133308584
		0.000427610229310197	0.0428605803623057
Island		0.00042778327143034	0.0428609207368329
	ZFPM2	0.000427918092876386	0.0428609207368329
S_Shelf	KIAA1712;KIAA1712	0.000427953649281768	0.0428609207368329
Island	MEIS2;MEIS2;MEIS2;MEIS2	0.000427967609938211	0.0428609207368329
	BRD9;BRD9;BRD9	0.000428246141498725	0.0428628265770344

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	MAD1L1;MAD1L1;MAD1	0.000428274779878294	0.0428628265770344
Island		0.000428343241211642	0.0428628265770344
Island	RECQL4	0.000428459903206607	0.0428628265770344
Island	SOX3	0.000428475659793381	0.0428628265770344
		0.000428517640604967	0.0428628265770344
S_Shore	C7orf50;C7orf50;C7orf50	0.000428642424531062	0.0428660322688812
	ZNF323;ZNF323;ZNF323	0.000428726702752202	0.0428660322688812
	MTMR2;MTMR2;MTMR2	0.000428925033037211	0.042877010655469
Island		0.000429069937634291	0.042877618450979
		0.000429153925388742	0.042877618450979
Island	TREX2	0.000429196705208995	0.042877618450979
N_Shelf	ADAM8;ADAM8;ADAM8	0.00042943062431468	0.0428921400538683
Island	ARAP1;ARAP1;ARAP1	0.00042960810584923	0.0429010197660676
Island		0.000430028526214125	0.042933215186355
	PFKP	0.000430107799688628	0.042933215186355
		0.000430311382411597	0.0429347660073208
N_Shore	GRIN2D	0.000430324001551131	0.0429347660073208
	ST3GAL2	0.000430389281919253	0.0429347660073208
Island	NSD1;NSD1	0.000430726459794059	0.0429595536737557
Island	KCNQ1OT1;KCNQ1;KCNQ1	0.000431033716953328	0.0429813475321022
Island	RIMBP2	0.000431224750522825	0.0429862790067231
	FAM107B	0.000431260681760527	0.0429862790067231
	GCG	0.000431687504954712	0.043019969308064
Island	SHANK2	0.000431928919655058	0.0430351726006863
N_Shore	PRDM16;PRDM16	0.000432214008815847	0.043045581355426
Island		0.000432362516222464	0.043045581355426
S_Shore	COX7A1	0.000432395856772977	0.043045581355426
S_Shelf	GOLGA7;GOLGA7	0.000432490241357478	0.043045581355426
		0.000432526760434908	0.043045581355426
	NGEF;NGEF	0.000432566653500972	0.043045581355426
Island	ACSS3;ACSS3	0.00043290037688258	0.043052002299952
Island		0.000432982825682911	0.043052002299952
	PPIAL4A;PPIAL4B	0.000433029660835085	0.043052002299952
	MYBBP1A;MYBBP1A	0.000433053054632786	0.043052002299952
Island	USP35	0.000433422666458574	0.043052002299952
		0.000433562201927885	0.043052002299952
	IGF1R	0.000433600895815994	0.043052002299952
		0.000434134447929905	0.043052002299952
N_Shore	WSB1;WSB1	0.000434323063367659	0.043052002299952
S_Shore	PDGFA;PDGFA	0.000434508577056775	0.043052002299952
Island	NXN	0.00043451400815806	0.043052002299952
	PTPRN2;PTPRN2;PTPRN2	0.000434533802978994	0.043052002299952
N_Shelf		0.000434622642286974	0.043052002299952
Island	CHST13	0.000434960077603614	0.043052002299952
Island	C1QTNF8	0.000434970876509016	0.043052002299952
Island	INPP5A	0.000434999125955516	0.043052002299952
N_Shelf	PTPRN2;PTPRN2;PTPRN2	0.000435085730143307	0.043052002299952
Island	ADCY1	0.000435090298214884	0.043052002299952
		0.000435100083804109	0.043052002299952
Island	DGKH;DGKH	0.00043521332668074	0.043052002299952
S_Shore	ITGB4;ITGB4;ITGB4	0.000435250572293786	0.043052002299952
Island	KDM4B	0.0004352886418353	0.043052002299952
Island	OLFML2B	0.000435419728762846	0.043052002299952
	RIMBP2	0.000435522584425501	0.043052002299952
N_Shelf		0.000435545069412407	0.043052002299952

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Island	TRIM50;FKBP6;FKBP6	0.000435768569848688	0.043052002299952
		0.000435905213280291	0.043052002299952
		0.000435938276229763	0.043052002299952
	PTPRG	0.000436130895635217	0.043052002299952
Island		0.00043615273852939	0.043052002299952
Island	APBA2;APBA2	0.000436187473078078	0.043052002299952
		0.000436190716163897	0.043052002299952
	RAP1GAP2;RAP1GAP2	0.000436249211230926	0.043052002299952
	RNF216;RNF216	0.000436275767956253	0.043052002299952
Island	INPP5A	0.000436278490129757	0.043052002299952
S_Shore	BAT2	0.000436318059083466	0.043052002299952
	COLEC11;COLEC11	0.000436484530590009	0.043052002299952
	WDR27	0.000436584013790038	0.043052002299952
Island		0.000436618142576227	0.043052002299952
N_Shore		0.000436703875625601	0.043052002299952
Island	TP53I13	0.000436721598482838	0.043052002299952
Island		0.000436762001271595	0.043052002299952
N_Shelf		0.00043687747801384	0.043052002299952
Island	ATP11A;ATP11A	0.000436887611786436	0.043052002299952
	VPS53;VPS53	0.000437001412851532	0.043052002299952
Island	STAG3;GPC2	0.000437035065876788	0.043052002299952
	DNAJB6;DNAJB6	0.00043705437843254	0.043052002299952
Island		0.000437091552849727	0.043052002299952
Island	KLB	0.000437158775619355	0.043052002299952
N_Shelf	ATP5G3;ATP5G3	0.000437623268726692	0.043052002299952
	ARHGEF12	0.000437644763173007	0.043052002299952
S_Shelf	MGMT	0.000437702985265256	0.043052002299952
		0.000437833099942396	0.043052002299952
Island	C19orf51	0.000437971007354465	0.043052002299952
Island		0.000437979724116535	0.043052002299952
	CDK11B;CDK11B;CDK11B	0.000438091782712235	0.043052002299952
		0.000438114218498227	0.043052002299952
Island		0.00043813036465235	0.043052002299952
S_Shore	SLC6A18	0.000438141523042352	0.043052002299952
	ANKRD11	0.000438444276864623	0.043052002299952
	INTS4L2	0.000438457598954751	0.043052002299952
N_Shore	KLC3	0.000438459284438659	0.043052002299952
		0.00043847875303816	0.043052002299952
N_Shore	FRAS1;FRAS1	0.000438503581555071	0.043052002299952
		0.000438532240426565	0.043052002299952
Island	MYH3	0.000438552014048127	0.043052002299952
Island	SV2C	0.000438586856651965	0.043052002299952
Island	C1orf107	0.000438884082376063	0.0430677759567457
		0.000438993109733901	0.0430677759567457
Island	SHC2	0.000439139302212845	0.0430677759567457
Island	INPP5A	0.000439251037578573	0.0430677759567457
Island	BANP;BANP	0.000439295333335704	0.0430677759567457
S_Shore	MSRA;MSRA	0.000439334479167586	0.0430677759567457
Island	SLC43A2	0.000439375600526247	0.0430677759567457
		0.000439460482477214	0.0430677759567457
Island	CDH2;CDH2	0.000439555165178511	0.0430677759567457
		0.000439636781768751	0.0430677759567457
	ABCC1;ABCC1;ABCC1;	0.000439909060650313	0.0430845468155801
N_Shore	GAK	0.000440005222145648	0.0430845468155801
N_Shore		0.000440074852829556	0.0430845468155801

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	PLXND1	0.000440448660340972	0.043112428742854
N_Shore	FAM197Y2;TSPY4	0.000440773795738386	0.0431355361933712
Island	KCNQ1DN	0.000440992879404099	0.0431399093758032
N_Shelf	B3GNTL1	0.000441128402557975	0.0431399093758032
	TRAPPC9;TRAPPC9	0.000441149259622139	0.0431399093758032
S_Shore	UNC84A;UNC84A	0.000441376976033456	0.0431399093758032
Island		0.000441445398739215	0.0431399093758032
Island	FAM53A	0.000441450157007237	0.0431399093758032
Island	DUOX1;DUOX1	0.000441522642613973	0.0431399093758032
N_Shore	LMNB2	0.000441607267296067	0.0431399093758032
S_Shore	B4GALT2;B4GALT2	0.000441620132525127	0.0431399093758032
		0.000441744101520843	0.043143317598121
	CEP72	0.000441946833684655	0.0431544153678066
Island	ELL	0.00044232272574038	0.0431824136553537
N_Shore	WDR27	0.000442484968651592	0.0431870884313119
Island		0.000442655901789134	0.0431870884313119
S_Shelf		0.000442792989256437	0.0431870884313119
Island	PIP5K1C	0.000442893270881104	0.0431870884313119
N_Shore	MTIF3;MTIF3;MTIF3;MTIF3	0.000442908056905346	0.0431870884313119
	ZC3H13	0.000443011725506821	0.0431870884313119
	GNAO1;GNAO1	0.000443078682602417	0.0431870884313119
		0.000443130507538536	0.0431870884313119
N_Shelf	ARHGAP12	0.000443233135209837	0.0431870884313119
S_Shore	GABRB2;GABRB2	0.000443262306492648	0.0431870884313119
Island		0.000443466294141946	0.0431982729103576
Island	PRELP;PRELP	0.000444280375809355	0.0432496560027396
S_Shelf	MYCN	0.000444392046767047	0.0432496560027396
	LHFPL2	0.000444429983561555	0.0432496560027396
Island	MAP7D2;MAP7D2;MAP7D2	0.000444603960223835	0.0432496560027396
S_Shore	TUBB6	0.000444721894881044	0.0432496560027396
		0.000444788528128151	0.0432496560027396
Island	C20orf103	0.000444811472235312	0.0432496560027396
		0.000445316443658907	0.0432496560027396
Island		0.000445355406258142	0.0432496560027396
		0.000445358757030932	0.0432496560027396
	PDE7A;PDE7A	0.000445370910106341	0.0432496560027396
		0.000445371211592439	0.0432496560027396
S_Shelf	SPG7;SPG7	0.000445376646797467	0.0432496560027396
Island	BCOR;BCOR	0.000445399768587497	0.0432496560027396
N_Shore	ZFP37	0.000445520226422949	0.0432496560027396
S_Shore	TSNARE1	0.000445642760026657	0.0432496560027396
		0.000445680629183857	0.0432496560027396
Island	ZNF467	0.000445680941279189	0.0432496560027396
Island		0.000445690462209618	0.0432496560027396
Island	TNIP1	0.000445991229390821	0.0432701727112799
N_Shelf		0.000446222172659617	0.0432833909627518
	SLC15A4	0.000446484720766647	0.0432833909627518
		0.00044650477015422	0.0432833909627518
Island	TFAP2E	0.000446546843865156	0.0432833909627518
Island	CSK;CSK	0.000446679229079563	0.0432833909627518
Island		0.000446697211438073	0.0432833909627518
	DNAH10	0.00044687690785819	0.0432833909627518
Island	C17orf55	0.000446931771250935	0.0432833909627518
Island	FGF3	0.000446936127677997	0.0432833909627518
S_Shelf		0.000447088143058224	0.0432833909627518

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S_Shore	SLITRK4	0.000447110524929845	0.0432833909627518
	CUX2	0.00044730286269745	0.0432850429408874
		0.000447306333390062	0.0432850429408874
S_Shore	ATP11A;ATP11A	0.000447395961507503	0.0432850677301481
Island	PLEK2	0.000447486859471849	0.0432852153412629
Island	GXYLT2	0.00044768855035232	0.0432932143718156
Island		0.000447901222159298	0.0432932143718156
N_Shelf		0.000447908320429843	0.0432932143718156
Island	FREM3	0.000447994703338986	0.0432932143718156
N_Shore	MEST	0.000448016498077819	0.0432932143718156
		0.000448558451307385	0.0433243118206633
		0.00044870551905771	0.0433243118206633
	OTUD4;OTUD4;OTUD4	0.000448708677695861	0.0433243118206633
N_Shelf	C7orf50;C7orf50;C7orf50	0.000448772258715372	0.0433243118206633
N_Shelf	LOC145845	0.000448872725789002	0.0433243118206633
Island	SERPINH1	0.000449010124946334	0.0433243118206633
	JAKMIP3	0.000449045354501191	0.0433243118206633
S_Shore		0.000449105078729498	0.0433243118206633
S_Shore	KIAA0562	0.000449178740865546	0.0433243118206633
S_Shore	KIAA2022	0.00044923283737856	0.0433243118206633
	MGAT5B;MGAT5B	0.000449347836543299	0.0433267750216669
N_Shore		0.000449810338519212	0.0433374379687139
Island	HEATR7A;HEATR7A;HEATR7A	0.000449985134241491	0.0433374379687139
S_Shore	TOLLIP	0.000450005768772072	0.0433374379687139
S_Shore		0.000450173254426877	0.0433374379687139
Island	CSPG4	0.000450247351749179	0.0433374379687139
Island	AKAP8L	0.000450383545970207	0.0433374379687139
Island		0.00045048693500302	0.0433374379687139
		0.000450487609784082	0.0433374379687139
		0.00045056961068424	0.0433374379687139
		0.00045073511924603	0.0433374379687139
	FLT1;FLT1;FLT1;FLT1	0.00045079245818443	0.0433374379687139
Island	INS-IGF2;INS-IGF2	0.000450820603592669	0.0433374379687139
	CASP9;CASP9	0.000450874142066147	0.0433374379687139
Island	SHROOM2	0.000450990225226208	0.0433374379687139
	SBNO2;SBNO2	0.000451183749450093	0.0433374379687139
Island		0.000451399675996722	0.0433374379687139
N_Shore	ASPHD2	0.000451659424871708	0.0433374379687139
Island	ADPRHL1;ADPRHL1	0.000451772996789733	0.0433374379687139
S_Shore	SQLE	0.000451882322741993	0.0433374379687139
Island	EFHC2	0.000452012552891706	0.0433374379687139
Island	NFATC1;NFATC1;NFATC1	0.000452021489184457	0.0433374379687139
	EXT1	0.000452094688830259	0.0433374379687139
Island	WDR88	0.00045212655652786	0.0433374379687139
Island		0.000452210325719049	0.0433374379687139
S_Shore	TERT;TERT	0.000452319193685994	0.0433374379687139
Island	LRRRC8A;LRRRC8A;LRRRC8A	0.000452521042176257	0.0433374379687139
		0.000452525171434253	0.0433374379687139
		0.000452533878015455	0.0433374379687139
S_Shelf	CLCN1	0.000452663272685765	0.0433374379687139
S_Shelf	NCOR2;NCOR2	0.000452672776951857	0.0433374379687139
	MAGEE2	0.000452776797936048	0.0433374379687139
Island	AATK	0.000452798332887693	0.0433374379687139
		0.00045314234603825	0.0433374379687139
N_Shore	TMEM175	0.000453186063236344	0.0433374379687139

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	KLHDC5	0.000453323314266561	0.0433374379687139
Island		0.000453445302627318	0.0433374379687139
	NXN	0.000453577294277648	0.0433374379687139
Island	IL17RE;IL17RE;IL17RC;	0.000453694738007201	0.0433374379687139
S_Shore	LOC440356;LOC440356	0.000453696562691424	0.0433374379687139
	CNKSR1;CNKSR1	0.000454004823965289	0.0433374379687139
	LRRC27;LRRC27	0.000454119635695355	0.0433374379687139
S_Shore		0.000454463560946379	0.0433374379687139
Island		0.000454515628516538	0.0433374379687139
Island	PCDHB6	0.000454553028622572	0.0433374379687139
	CTAGE1;CTAGE1	0.000454632106146935	0.0433374379687139
Island	RFX4	0.000454643841401086	0.0433374379687139
S_Shore		0.000454674626145849	0.0433374379687139
Island	RNF220	0.000454718114091389	0.0433374379687139
	PBK	0.000454896397656018	0.0433374379687139
N_Shore	FAM47B	0.000454906266108273	0.0433374379687139
	TBCD	0.000454962219661893	0.0433374379687139
		0.000455024509609964	0.0433374379687139
Island	H2BFWT;MIR1256;H2B	0.000455133196802625	0.0433374379687139
Island	DMRTA2	0.000455220937077996	0.0433374379687139
Island	FLJ42875	0.000455327428144709	0.0433374379687139
	DCTD;DCTD	0.000455344728865624	0.0433374379687139
	TMEM184A	0.000455449049877674	0.0433374379687139
	CIT	0.000455478391213387	0.0433374379687139
Island		0.000455485869486936	0.0433374379687139
N_Shore	SDF4;SDF4	0.000455533729832871	0.0433374379687139
Island	SDK2	0.000455569721595087	0.0433374379687139
	C3orf21	0.000455593473019428	0.0433374379687139
N_Shore	CWF19L2	0.000455640169268279	0.0433374379687139
N_Shore		0.000455907608140949	0.0433374379687139
N_Shore		0.000455933373321812	0.0433374379687139
Island	UNKL	0.000455945740171562	0.0433374379687139
	NUP93	0.000456070932775104	0.0433374379687139
		0.000456193083750518	0.0433374379687139
N_Shore	BRD4	0.000456466362040348	0.0433374379687139
	FAAH2	0.000456545438655623	0.0433374379687139
	EIF3B;EIF3B	0.000456580465783292	0.0433374379687139
N_Shelf	MYO1C;MYO1C;MYO1C	0.000456612852424813	0.0433374379687139
S_Shore		0.000456759233392741	0.0433374379687139
Island	APEH;APEH	0.00045680025968896	0.0433374379687139
		0.000456896490444943	0.0433374379687139
N_Shore	BAHCC1	0.000456902747188725	0.0433374379687139
Island		0.000457153605913258	0.0433374379687139
	INPP5A	0.000457222586516122	0.0433374379687139
Island	TRIM54;TRIM54	0.000457355204522839	0.0433374379687139
		0.000457395741734329	0.0433374379687139
	BCL6;BCL6;BCL6	0.000457572218079365	0.0433374379687139
Island		0.000457595450439345	0.0433374379687139
N_Shore	LRP8;LRP8;LRP8;LRP8	0.000457679917828173	0.0433374379687139
N_Shore		0.000457825972566015	0.0433374379687139
	RAET1G	0.000457865185621081	0.0433374379687139
	INPP5A	0.000458094753139075	0.0433374379687139
		0.000458125166627596	0.0433374379687139
N_Shore	STK19;STK19;STK19;D	0.000458364745661039	0.0433374379687139
S_Shore	SPAG17	0.000458463150231007	0.0433374379687139

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Island		0.000458485248062847	0.0433374379687139
Island	FAM83H	0.000458487072681776	0.0433374379687139
	KIF13A;KIF13A;KIF13A;	0.000458617059682902	0.0433374379687139
N_Shelf	NINJ2	0.000458725981961666	0.0433374379687139
N_Shelf	SHANK1	0.000458804499478121	0.0433374379687139
Island	NDUFA4L2	0.00045882241579973	0.0433374379687139
		0.00045890116218789	0.0433374379687139
N_Shore	CYTH3	0.000458944956505296	0.0433374379687139
Island		0.000459055154298521	0.0433374379687139
Island	FAM84A	0.000459079636382115	0.0433374379687139
	PACRG;PACRG;LOC28	0.000459131874251609	0.0433374379687139
	LHPP;LHPP	0.000459289568136821	0.0433374379687139
	AKAP1	0.000459318654986312	0.0433374379687139
Island	PIK3CG	0.000459398141444378	0.0433374379687139
N_Shelf		0.00045947360872652	0.0433374379687139
Island	WWC3	0.000459575288781241	0.0433374379687139
Island		0.00045959329391016	0.0433374379687139
Island	PIF1	0.000459628678944254	0.0433374379687139
	AGAP1;AGAP1	0.000459740258486797	0.0433374379687139
Island		0.000459778367625995	0.0433374379687139
Island	PIWIL1	0.000459862417632475	0.0433374379687139
Island	SIPA1;SIPA1	0.000459932586284391	0.0433374379687139
Island	KCNE4	0.000459955495135886	0.0433374379687139
	FAT1	0.000460087593759012	0.0433374379687139
Island	MORC1	0.000460151854536054	0.0433374379687139
N_Shelf	TAP2;TAP2	0.0004601809538393	0.0433374379687139
N_Shore	PAXIP1	0.000460218102353481	0.0433374379687139
Island		0.000460366752998552	0.0433374379687139
		0.000460384752819539	0.0433374379687139
Island	STX16;STX16;STX16;S	0.000460418890192793	0.0433374379687139
	KRT1	0.000460573705264264	0.0433374379687139
S_Shore	SH3RF1	0.00046068183651972	0.0433374379687139
Island		0.000460689713744433	0.0433374379687139
	CXCR7	0.000460715081571374	0.0433374379687139
S_Shore	FAM70A;FAM70A;FAM7	0.000460765845050432	0.0433374379687139
		0.000460963903045305	0.0433374379687139
Island		0.000461191954440464	0.0433374379687139
N_Shore		0.000461236669446204	0.0433374379687139
	SPARCL1;SPARCL1	0.000461313534453574	0.0433374379687139
Island	GAL3ST2	0.000461398246317564	0.0433374379687139
N_Shelf	RPTOR;RPTOR	0.000461484626649455	0.0433374379687139
	PPT2;PPT2	0.000461507256953373	0.0433374379687139
N_Shore	TOLLIP	0.000461614513846846	0.0433374379687139
Island	MEX3D	0.000461660827720776	0.0433374379687139
	KLHL29	0.000461665696466449	0.0433374379687139
Island	AKAP8	0.000461817692621754	0.0433374379687139
Island	LYPD5	0.000461828129758057	0.0433374379687139
	UNC84A;UNC84A	0.000461839703928603	0.0433374379687139
Island	PMP22;PMP22;PMP22	0.000461894417018031	0.0433374379687139
N_Shore	TRPV1;TRPV1;TRPV1;	0.000461896154017449	0.0433374379687139
		0.000462160251646037	0.0433462554683147
		0.000462237471312586	0.0433462554683147
Island		0.00046230109464982	0.0433462554683147
Island	LOC153328	0.000462348125224412	0.0433462554683147
Island	PIGG;PIGG	0.000462477339510975	0.043349978219209

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N_Shore		0.00046323831909563	0.0434129061331252
S_Shore	CARKD	0.000464071805850923	0.0434562484964703
N_Shore	EXOSC2	0.000464110748724727	0.0434562484964703
Island	HLTF;HLTF	0.000464152270228211	0.0434562484964703
		0.000464185949401776	0.0434562484964703
	EPB41L5	0.000464229565752252	0.0434562484964703
		0.000464383295621633	0.0434562484964703
	RAPGEF5	0.000464417997189749	0.0434562484964703
Island	DFFB	0.000464498877594894	0.0434562484964703
Island		0.000464548315643179	0.0434562484964703
Island		0.000464598058565474	0.0434562484964703
S_Shelf		0.000464960720423913	0.0434637129909063
Island	BCL11B;BCL11B	0.000464993523754577	0.0434637129909063
		0.000465115265777019	0.0434637129909063
Island	KIAA1210	0.000465223274546872	0.0434637129909063
Island	DIP2C	0.000465305537830325	0.0434637129909063
Island	NUMBL	0.000465306435887725	0.0434637129909063
Island		0.000465389626631047	0.0434637129909063
	CXCR6;FYCO1	0.000465395789130935	0.0434637129909063
Island	SOX30;SOX30	0.000465533582548927	0.0434671883631163
N_Shore		0.000465749553963508	0.0434671883631163
N_Shelf	DNMT3A;DNMT3A	0.000465762970474762	0.0434671883631163
Island		0.000465927816426728	0.0434671883631163
N_Shore	TBCD	0.000466161896214616	0.0434671883631163
		0.000466170522206402	0.0434671883631163
Island	FCGBP	0.00046621303748439	0.0434671883631163
	LOC148696	0.000466213041135282	0.0434671883631163
Island	LOC645323	0.000466378733595934	0.0434671883631163
Island		0.000466520516123896	0.0434671883631163
Island	DENND4B	0.000466535319796681	0.0434671883631163
Island		0.000466677399614988	0.0434671883631163
	DGCR9	0.000466814364092761	0.0434671883631163
S_Shore	RAB5C;RAB5C	0.000466828881045955	0.0434671883631163
Island	RUNX3;RUNX3	0.000466870251324056	0.0434671883631163
S_Shelf		0.000467068731188396	0.0434671883631163
Island	CACNA1H;CACNA1H	0.000467099309100104	0.0434671883631163
	ADSSL1;ADSSL1	0.000467144861285816	0.0434671883631163
N_Shelf	TPPP	0.000467159725635738	0.0434671883631163
N_Shore	ZNF442	0.000467280312887152	0.0434671883631163
Island	RASL10B	0.000467320394570612	0.0434671883631163
	AGAP5	0.000467407457791998	0.0434671883631163
N_Shore	FLJ26850	0.000467900114915152	0.0434919605251673
Island	HLX	0.000467932292806075	0.0434919605251673
Island	SNX8	0.000467943232946156	0.0434919605251673
N_Shore	MAD1L1;MAD1L1;MAD1	0.000468560396649597	0.0435161182238882
S_Shore	BAIAP2;BAIAP2;BAIAP2	0.000468572152283664	0.0435161182238882
Island	RALGAPA2	0.000468693364887166	0.0435161182238882
S_Shelf		0.000468711693321094	0.0435161182238882
S_Shelf	CAMTA1	0.000468738047809892	0.0435161182238882
Island	NPY	0.000468742246991224	0.0435161182238882
S_Shelf	PITPNM1;PITPNM1	0.000469092891719088	0.0435275037469145
S_Shelf	UNG;UNG	0.000469127035609766	0.0435275037469145
Island	DIP2C	0.000469173986870976	0.0435275037469145
Island	TFAP2A	0.000469233684776968	0.0435275037469145
Island	USP49	0.000469314250898441	0.0435275037469145

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Island	RPTOR;RPTOR	0.000469651517418445	0.0435337452087785
Island		0.000469922503098518	0.0435337452087785
	EIF2C2;EIF2C2	0.000469948481167014	0.0435337452087785
	AXIN1;AXIN1	0.000470022834459856	0.0435337452087785
Island	MYOM1;MYOM1	0.000470107627060913	0.0435337452087785
Island	FOXP4;FOXP4;FOXP4	0.000470194222712066	0.0435337452087785
N_Shore	PIP5K1C	0.000470239735985164	0.0435337452087785
Island	TMEM151B	0.000470243805682337	0.0435337452087785
S_Shore		0.000470325410092468	0.0435337452087785
N_Shore		0.000470429555171937	0.0435337452087785
	OXR1	0.000470448945820345	0.0435337452087785
N_Shore		0.000470460171213021	0.0435337452087785
Island	KCNC4;KCNC4;KCNC4	0.000470569500867876	0.043535544127571
Island	PRPF31;TFPT;PRPF31	0.000470772254737147	0.0435444303661048
Island	WFS1;WFS1	0.000470891279596387	0.0435444303661048
	CYSLTR2	0.000471098575212446	0.0435444303661048
	STK32C	0.000471180617447061	0.0435444303661048
	VPS53;VPS53	0.000471201905858889	0.0435444303661048
	CHST4;CHST4	0.000471261020734038	0.0435444303661048
Island		0.000471294903172708	0.0435444303661048
Island	TOLLIP	0.000471637626775555	0.0435582437075171
S_Shore	CHRN1	0.00047164330103794	0.0435582437075171
Island		0.000471714217201109	0.0435582437075171
	MYOM2	0.000471822084625602	0.0435598991872464
Island	KDM2B;KDM2B	0.000472044202541738	0.0435675905752496
		0.000472128226851852	0.0435675905752496
	ATP11A;ATP11A	0.000472175260268384	0.0435675905752496
	ZMYM2;ZMYM2	0.00047237233885455	0.0435774729553772
S_Shelf	DDX20	0.000472827986788594	0.0435973182693413
Island		0.000472856826020441	0.0435973182693413
		0.000472889755164873	0.0435973182693413
Island	MAFG;MAFG	0.000472947525292148	0.0435973182693413
	SATB2	0.000473054947234279	0.0435989224204076
		0.000473177440467899	0.0436019147364184
	PTPN21	0.000473333430082978	0.043607991920285
N_Shore	RBMY1F;RBMY2FP	0.000473599306447549	0.0436241886829991
Island	UNC13A	0.00047402640361768	0.0436301183281783
	GLIPR1L1;GLIPR1L1	0.000474112722702156	0.0436301183281783
S_Shore	AGAP1;AGAP1	0.000474127805398357	0.0436301183281783
		0.000474157984639797	0.0436301183281783
Island		0.000474198471455601	0.0436301183281783
S_Shore		0.000474204187022207	0.0436301183281783
N_Shore	VASH1	0.000474736982425954	0.0436427799882875
S_Shore	ZNF577;ZNF577;ZNF577	0.000474789285388871	0.0436427799882875
N_Shore	ZNF677	0.000474817131531888	0.0436427799882875
Island	HAND1	0.000474840662306414	0.0436427799882875
Island	SDK2	0.000474856479500989	0.0436427799882875
		0.000474882466398131	0.0436427799882875
	RPS6KA2;RPS6KA2	0.000475290537015903	0.0436688972249243
		0.000475433612541993	0.0436688972249243
Island	NCOA4;NCOA4;NCOA4	0.000475465786279983	0.0436688972249243
		0.000475575110326158	0.0436688972249243
Island	GPR135	0.000475830226613653	0.0436688972249243
		0.000475916283580377	0.0436688972249243
Island		0.000475961875194116	0.0436688972249243

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	DOCK1	0.000476028899731019	0.0436688972249243
	GSN;GSN;GSN;GSN;GS	0.000476031110296806	0.0436688972249243
Island	ASCL1	0.000476233641886396	0.0436688972249243
S_Shelf		0.000476416050824808	0.0436688972249243
S_Shelf	TCF19;TCF19	0.000476455615915579	0.0436688972249243
Island	SLC12A7	0.000476488346829414	0.0436688972249243
Island	TBC1D16	0.000476505438130554	0.0436688972249243
S_Shore		0.000476519118017292	0.0436688972249243
Island	JUP;JUP	0.000477034831922842	0.0437046605072052
Island	PRR22;DUS3L;DUS3L;P	0.000477114602505934	0.0437046605072052
	TRIM34;TRIM78P;TRIM	0.000477201960262786	0.0437046605072052
N_Shore		0.000477391976182177	0.0437046605072052
		0.000477431264703071	0.0437046605072052
Island		0.000477517359261666	0.0437046605072052
S_Shore	EPDR1	0.000477641068850482	0.0437046605072052
Island	STXBP5L	0.000477661046691334	0.0437046605072052
Island	FBLL1	0.000477721514943776	0.0437046605072052
		0.000478240770068982	0.0437402796785019
	PDLIM5;PDLIM5;PDLIM	0.000478361276242944	0.0437402796785019
	C4orf23	0.000478381792096267	0.0437402796785019
	HFM1	0.000478926762837477	0.0437737463014077
	LOC389705	0.000479001026952934	0.0437737463014077
Island	AJAP1;AJAP1	0.000479018955035278	0.0437737463014077
		0.000479239550011118	0.0437787321536936
S_Shore	VENTXP1	0.000479254298000069	0.0437787321536936
N_Shelf	ACOX3;ACOX3	0.000479540325624543	0.0437959348503294
S_Shore	TBL2	0.000479640323526959	0.0437959348503294
	NDUFS6	0.000479713899511686	0.0437959348503294
	DCUN1D2	0.000479897497985254	0.0438044394481169
Island	HTATSF1;HTATSF1	0.000480232028344865	0.0438190261361483
	FILIP1	0.000480436751457671	0.0438190261361483
S_Shore	ADAMTS7	0.000480538851881133	0.0438190261361483
Island	APBA1	0.000480572577493545	0.0438190261361483
	ASAP2;ASAP2	0.00048060774662883	0.0438190261361483
	OBSCN;OBSCN	0.000480671937513054	0.0438190261361483
Island	ZNF232	0.000480751218500806	0.0438190261361483
		0.000480781097171305	0.0438190261361483
	TULP4;TULP4	0.000481009244058113	0.0438256125875624
	RPTOR;RPTOR	0.000481101369566538	0.0438256125875624
	C12orf67	0.000481124827601444	0.0438256125875624
	FLJ22536	0.000481674180435019	0.0438542057450825
Island	TAC1;TAC1;TAC1;TAC1	0.000481675819339887	0.0438542057450825
	DENND3	0.000481710369202165	0.0438542057450825
S_Shore	SLC15A4	0.000481960590690667	0.0438553401083373
N_Shore		0.000482206472003499	0.0438553401083373
	RAB27A;RAB27A	0.000482303320566682	0.0438553401083373
	P704P	0.000482449499438247	0.0438553401083373
	RXRG;RXRG	0.000482664950306947	0.0438553401083373
	NID1	0.000482666151843585	0.0438553401083373
S_Shore	GLB1L2	0.000482873731273489	0.0438553401083373
N_Shelf		0.000482916920182196	0.0438553401083373
	NDP;NDP	0.000482996173133092	0.0438553401083373
Island	TLL2	0.000483161441087625	0.0438553401083373
S_Shore	PSPN	0.000483307708621854	0.0438553401083373
	OLA1;OLA1	0.000483460994795435	0.0438553401083373

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	MAP3K13	0.000483463064323251	0.0438553401083373
S_Shore	LAMP1	0.000483539706047882	0.0438553401083373
Island	TESSP1	0.000483667466728376	0.0438553401083373
		0.000483859635595018	0.0438553401083373
Island		0.000483898706532158	0.0438553401083373
Island	SIN3B	0.000483899281429404	0.0438553401083373
S_Shore	DTNB;DTNB;DTNB;DTN	0.000484023501629352	0.0438553401083373
Island	EBF3	0.000484105810279439	0.0438553401083373
Island	SGTA	0.000484228706823786	0.0438553401083373
Island	PXDNL	0.00048427660550659	0.0438553401083373
Island	CYP2D7P1	0.000484412727823669	0.0438553401083373
Island		0.000484689816993153	0.0438553401083373
	CHD7	0.000484782763170205	0.0438553401083373
N_Shore	TAP1	0.00048482322938414	0.0438553401083373
Island	PTRF	0.00048493708337443	0.0438553401083373
	BRF1;BRF1	0.000484946640736403	0.0438553401083373
		0.000484947907467708	0.0438553401083373
	PAGE2B	0.000485027870072737	0.0438553401083373
	FBP1;FBP1	0.000485152544070822	0.0438553401083373
Island	HOXC4	0.000485158068906756	0.0438553401083373
	PTPRN2;PTPRN2;PTPF	0.000485187816679011	0.0438553401083373
S_Shelf		0.000485263961966639	0.0438553401083373
N_Shore	MTNR1B	0.000485266481625632	0.0438553401083373
Island	ADARB2	0.000485316980075379	0.0438553401083373
Island	PKD1;MIR1225;PKD1	0.000485329251932264	0.0438553401083373
Island	DDX3X;DDX3X	0.000485355818232036	0.0438553401083373
Island	SLC2A14	0.000485462055802979	0.0438553401083373
		0.000485471500313947	0.0438553401083373
N_Shore	ACTR8	0.000485497333089447	0.0438553401083373
	AGAP1;AGAP1	0.000485525904425551	0.0438553401083373
S_Shore	TSNARE1	0.000485623071928163	0.0438554306906202
	RERE;RERE	0.000485708006451219	0.0438554306906202
	PGGT1B	0.000486052521648578	0.0438672709011861
S_Shore	HIST1H2AJ;HIST1H2BM	0.000486053686900851	0.0438672709011861
Island	SUGT1L1	0.000486134963662218	0.0438672709011861
Island		0.000486278566893443	0.0438672709011861
	RPTOR;RPTOR	0.00048629200943265	0.0438672709011861
Island		0.00048644462790941	0.0438728667434311
	CDYL;CDYL	0.000486631241849494	0.0438815260116842
		0.000486891512993342	0.0438968227904877
N_Shore	PCDHB3	0.000487196483013592	0.0439062928833062
	SOBP	0.000487282250448072	0.0439062928833062
N_Shore	ADRA1A;ADRA1A;ADR	0.000487342196019504	0.0439062928833062
		0.000487364571185793	0.0439062928833062
Island	STARD10	0.000487449825702859	0.0439062928833062
		0.000487544288793608	0.0439066358627676
		0.000487668451127103	0.0439090309435163
	RASA3	0.000487752204565359	0.0439090309435163
Island	MYH14;MYH14;MYH14	0.00048785570685036	0.0439101868091991
Island	ATP11A;ATP11A	0.000488107476433746	0.043924684787026
	CDH12	0.000488379175398013	0.0439352525471581
	KIRREL3;KIRREL3	0.000488552374343522	0.0439352525471581
Island	FAM48B1	0.000488578362917876	0.0439352525471581
	HDAC4	0.000488587766931283	0.0439352525471581
Island	PLEC1;PLEC1;PLEC1;P	0.000488901487177088	0.0439503579616

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Island	EGFL8	0.000488957344511968	0.0439503579616
	FBXW8;FBXW8	0.000489027985454111	0.0439503579616
Island		0.000489182126922481	0.0439560544752747
		0.000489580386150391	0.0439746861774975
Island	VWC2	0.000489606160567906	0.0439746861774975
N_Shore	TFAP2A;TFAP2A	0.000489661864564587	0.0439746861774975
	MYO1B;MYO1B;MYO1B	0.000489889738620477	0.0439794404835532
Island		0.000489896415441634	0.0439794404835532
		0.000490014613292311	0.0439818991072644
	NAT15;NAT15;NAT15	0.000490384752958156	0.0439990617346426
		0.000490427908291501	0.0439990617346426
N_Shore	RNF26	0.000490478365364859	0.0439990617346426
		0.000490709305549171	0.0439992681223853
Island	NOL4	0.00049077144201426	0.0439992681223853
Island	CARD11	0.00049090913886051	0.0439992681223853
N_Shelf	EIF2AK3	0.000490915286458168	0.0439992681223853
N_Shore	LYSMD4	0.000491009652155189	0.0439992681223853
N_Shore		0.000491108318568425	0.0439992681223853
Island	SLC12A7	0.00049123358434076	0.0439992681223853
	ERCC8	0.000491296379167075	0.0439992681223853
	CCDC40	0.000491298285254446	0.0439992681223853
Island	HRNBP3	0.000491540229085025	0.044010507981048
Island		0.000491660163769295	0.044010507981048
S_Shelf		0.00049176987277219	0.044010507981048
Island	ZNF469	0.000491793124097955	0.044010507981048
Island		0.000491906093886971	0.044010507981048
Island	TRPV4;TRPV4	0.000492000258119611	0.044010507981048
Island	ZIC1;ZIC1	0.000492236543655988	0.044010507981048
Island		0.000492272137724195	0.044010507981048
N_Shore	CHSY3	0.000492301283633551	0.044010507981048
Island	HIST1H3J	0.000492458247803861	0.044010507981048
N_Shelf	SMURF1;SMURF1	0.000492509355815936	0.044010507981048
	TNS3	0.000492541482930932	0.044010507981048
N_Shelf		0.000492658068798362	0.044010507981048
		0.000492695967115558	0.044010507981048
S_Shelf	GTF2H5	0.000492866651193434	0.0440176361495961
	KSR2	0.000493218935774008	0.0440256528567769
	MIR2114	0.000493223914656386	0.0440256528567769
N_Shore	EBF2	0.000493313693022652	0.0440256528567769
N_Shore	KIAA0802	0.000493320018693497	0.0440256528567769
		0.000493467754054537	0.0440307240203507
Island	PHACTR1	0.000493644542017294	0.0440383851192717
Island	TNRC18	0.000493936293003842	0.0440472412466039
S_Shore	FUCA2	0.000494271979093585	0.0440472412466039
	KIF25;KIF25	0.000494442436703655	0.0440472412466039
S_Shore	BANP;BANP	0.000494443226439537	0.0440472412466039
Island	MCF2L;MCF2L	0.000494527063664035	0.0440472412466039
Island	SLC32A1;SLC32A1	0.000494551206364141	0.0440472412466039
Island		0.000494682381750133	0.0440472412466039
S_Shore	KIAA0182;KIAA0182	0.00049469629936699	0.0440472412466039
Island	AACS	0.000494800691320331	0.0440472412466039
	SHANK2	0.000494922149393806	0.0440472412466039
N_Shore	GABBR1;GABBR1;GAB	0.000494995695598224	0.0440472412466039
Island	SLC6A2	0.000495111615231136	0.0440472412466039
N_Shore	KANK1	0.000495241885509186	0.0440472412466039

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Island	PM20D1	0.000495403459495143	0.0440472412466039
		0.000495591920608246	0.0440472412466039
Island	DLX5	0.000495726044250077	0.0440472412466039
Island		0.00049575237579549	0.0440472412466039
Island	HOXC12	0.000495787575251628	0.0440472412466039
	DDR1;DDR1;DDR1	0.000495842042007755	0.0440472412466039
Island	TFR2	0.000496021248540527	0.0440472412466039
Island	SLC24A4;SLC24A4;SLC	0.000496051586997443	0.0440472412466039
		0.0004960695471994	0.0440472412466039
	HERC2	0.00049614885576814	0.0440472412466039
	CCM2;CCM2;CCM2;CC	0.000496173359992195	0.0440472412466039
	SKI	0.000496179367717949	0.0440472412466039
Island	SF3A2	0.000496182494574587	0.0440472412466039
S_Shore		0.000496236780350776	0.0440472412466039
S_Shore	AVPR1A;AVPR1A	0.000496290291607324	0.0440472412466039
Island	TMEM229A	0.000496551460316158	0.0440558944629264
N_Shore	DLGAP2	0.000496585642795453	0.0440558944629264
N_Shore	ZDHHC14;ZDHHC14	0.000496660679848404	0.0440558944629264
Island	ALDH1A2;ALDH1A2;AL	0.000497075225689253	0.0440845923241069
N_Shelf	AMMECR1L	0.000497191694031003	0.044086848628994
	MPHOSPH8	0.000497780446407977	0.0441189133595541
S_Shore	ADAM30	0.000497970781390292	0.0441189133595541
N_Shore		0.000498200813635725	0.0441189133595541
		0.000498239910803957	0.0441189133595541
N_Shore	PREB	0.000498320094149927	0.0441189133595541
	CRISP2;CRISP2;CRISP	0.000498429906024438	0.0441189133595541
	GJA1	0.000498492538733529	0.0441189133595541
N_Shore		0.000498697433865609	0.0441189133595541
Island		0.00049876594759113	0.0441189133595541
N_Shore		0.000498774265454401	0.0441189133595541
Island	CASZ1	0.00049880511808012	0.0441189133595541
Island	GABRA5;GABRA5	0.000498865033053295	0.0441189133595541
N_Shore	ZIC1	0.000499070573190557	0.0441189133595541
Island		0.000499129979021202	0.0441189133595541
S_Shelf		0.000499197466962403	0.0441189133595541
	SKAP2	0.000499272707818448	0.0441189133595541
	ZNF202	0.000499360809928568	0.0441189133595541
N_Shore	COPS8;COPS8	0.000499452573154685	0.0441189133595541
N_Shelf	MAPK8IP3;MAPK8IP3	0.000499648438236949	0.0441189133595541
Island		0.000499694075333599	0.0441189133595541
	DIP2C	0.000499732309293724	0.0441189133595541
		0.000499758050311893	0.0441189133595541
	NLRP5	0.000499780003364909	0.0441189133595541
	EHMT1;EHMT1	0.000499811572470709	0.0441189133595541
	PRKCA	0.000499830645958547	0.0441189133595541
	RUNX1T1;RUNX1T1;RU	0.000499997645110006	0.0441256121479416
Island	SSTR3	0.000500121107502518	0.0441284670051297
Island	PCDHGA2;PCDHGA3;P	0.000500478232824558	0.0441519344467676
Island		0.00050069958869777	0.0441606323702711
N_Shore	LRP2	0.000500800164197282	0.0441606323702711
Island	LOC150185	0.000500850366200174	0.0441606323702711
Island	COL4A2	0.000501369754701782	0.0441790171635576
N_Shelf	RSPH1	0.000501403016040653	0.0441790171635576
N_Shore	IL15;IL15	0.000501408664085412	0.0441790171635576
N_Shore	DDX26B	0.000501501407209911	0.0441790171635576

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Island	ULBP1	0.000501514966944179	0.0441790171635576
Island	PFKL;PFKL	0.000501655727783156	0.0441810349305107
S_Shelf	MICAL3	0.00050172031614682	0.0441810349305107
Island		0.000502008800629095	0.0441900629277718
N_Shore		0.000502273520306289	0.0441900629277718
	SLC6A3	0.000502284487320565	0.0441900629277718
Island		0.000502297155743365	0.0441900629277718
		0.000502328566903528	0.0441900629277718
	OR10C1	0.000502370281278711	0.0441900629277718
N_Shore		0.000502743427312687	0.0442022757314694
Island	TSNARE1	0.000502771513770347	0.0442022757314694
		0.000502876879778004	0.0442022757314694
Island	PAX6	0.000503034656592863	0.0442022757314694
	PRKCE	0.000503039793626253	0.0442022757314694
Island	MAST1	0.000503056715700943	0.0442022757314694
Island		0.000503148774437379	0.044202345398038
N_Shore	RASA3	0.000503364862614845	0.0442036605856858
		0.00050342131164273	0.0442036605856858
N_Shore	POMC;POMC	0.000503531016043333	0.0442036605856858
N_Shelf	PPP2R5C;PPP2R5C;PP	0.000503627742657879	0.0442036605856858
	JMJD1C	0.000503675810117039	0.0442036605856858
N_Shelf	MTG1	0.000503836519542959	0.0442036605856858
	LLGL2;LLGL2;LLGL2	0.000503854900228568	0.0442036605856858
		0.000503893893756406	0.0442036605856858
Island	ZAP70;ZAP70	0.000504118577145113	0.0442074585622918
		0.000504199732723177	0.0442074585622918
S_Shore	EGFLAM	0.000504273001788077	0.0442074585622918
Island	RP1	0.000504302294031203	0.0442074585622918
Island	MAD1L1;MAD1L1;MAD1	0.000504514385429687	0.0442180473621486
Island		0.000505022343996615	0.0442450677961588
N_Shore	EGFLAM	0.000505045891862688	0.0442450677961588
		0.000505297251712723	0.0442450677961588
N_Shelf	C7orf50;C7orf50;C7orf50	0.00050539923603886	0.0442450677961588
		0.000505467075669429	0.0442450677961588
		0.000505545680452029	0.0442450677961588
Island		0.000505548566587213	0.0442450677961588
	MAGEC3;MAGEC3	0.000505653872009334	0.0442450677961588
N_Shore	GALNT9	0.000505723338451396	0.0442450677961588
		0.000505768185047455	0.0442450677961588
Island	TLN2	0.000506074689997126	0.0442450677961588
		0.000506515126895336	0.0442450677961588
	UST	0.00050653833233062	0.0442450677961588
	EP400	0.000506544968705759	0.0442450677961588
	C4orf10;NOP14	0.000506555764905341	0.0442450677961588
		0.000506681594352318	0.0442450677961588
N_Shore	PTPRN2;PTPRN2;PTPR	0.000506736181286069	0.0442450677961588
		0.00050680960522324	0.0442450677961588
N_Shelf	HIST1H1A	0.000506915124435906	0.0442450677961588
N_Shore	DCC	0.000506963848694726	0.0442450677961588
Island	SDF4;SDF4;B3GALT6	0.000507034233050659	0.0442450677961588
	PIK3R1	0.000507087510412138	0.0442450677961588
	IGHMBP2	0.000507199507754033	0.0442450677961588
S_Shelf	HDGF2;HDGF2	0.000507288884356555	0.0442450677961588
		0.00050732654262113	0.0442450677961588
Island		0.000507414781992835	0.0442450677961588

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N_Shore	DDX25;PUS3	0.000507496913648082	0.0442450677961588
S_Shelf	SLC4A8;SLC4A8	0.000507633144181327	0.0442450677961588
	MAPT;MAPT;MAPT;MA	0.000507646586573994	0.0442450677961588
N_Shelf	B4GALT4;B4GALT4	0.000507659500530004	0.0442450677961588
	FRMD4A	0.000507846479577357	0.0442450677961588
		0.000508057351639046	0.0442450677961588
		0.000508064031805325	0.0442450677961588
Island	C7orf50;C7orf50;C7orf50	0.00050811644155508	0.0442450677961588
	MACROD1	0.00050811721568783	0.0442450677961588
S_Shelf	NKD2	0.000508147624318928	0.0442450677961588
Island	CRIPAK	0.000508284414737204	0.0442450677961588
S_Shore	MAP7D2;MAP7D2;MAP	0.000508294135586285	0.0442450677961588
Island	THOP1	0.000508521328569953	0.0442526985092029
	SPTBN2	0.000508621393849169	0.0442526985092029
	TLE3;TLE3;TLE3	0.000508786939130562	0.0442526985092029
	NOM1	0.000509058490273664	0.0442526985092029
	PTPRN2;PTPRN2;PTP	0.000509074259551454	0.0442526985092029
	NCOA2	0.000509257804467443	0.0442526985092029
		0.000509299700703498	0.0442526985092029
Island	SALL4;SALL4	0.000509474381373505	0.0442526985092029
Island	ALDH3B2;ALDH3B2	0.000509592087471966	0.0442526985092029
	ZER1	0.000509594133547636	0.0442526985092029
Island	BRF1	0.000509627910515307	0.0442526985092029
N_Shore	PCDHGA4;PCDHGA1;P	0.000509642853929635	0.0442526985092029
Island		0.000509771491192902	0.0442526985092029
Island		0.000509806896105528	0.0442526985092029
	NKD2	0.000510006045570325	0.0442526985092029
	TNFRSF19;TNFRSF19	0.000510074966914879	0.0442526985092029
		0.000510092584201248	0.0442526985092029
		0.000510128954030884	0.0442526985092029
S_Shore		0.000510229185512305	0.0442526985092029
N_Shelf	NAA10	0.000510259409829161	0.0442526985092029
	TRRAP	0.000510300565062506	0.0442526985092029
	METTL8	0.00051050107342727	0.0442565025593876
S_Shore	COL5A1	0.000510527186908169	0.0442565025593876
S_Shore	INPP5A	0.000510673999463025	0.0442597925403994
Island	NKX2-8	0.000510833714247952	0.0442597925403994
	IGF1R	0.000511185105713428	0.0442597925403994
	RNF44	0.000511221357714427	0.0442597925403994
Island	CALHM3	0.00051146679193967	0.0442597925403994
	MIR1974;C5orf36;C5orf	0.000511491058797697	0.0442597925403994
N_Shelf		0.000511544528562219	0.0442597925403994
		0.000511614536695904	0.0442597925403994
	AGAP3	0.000511655364117404	0.0442597925403994
S_Shore	MAGI2	0.000511825920311334	0.0442597925403994
N_Shelf		0.000511887208678983	0.0442597925403994
N_Shore	MSC	0.000512040095941613	0.0442597925403994
Island	BAHCC1	0.000512224246588574	0.0442597925403994
S_Shore	INPP5A	0.000512254136123543	0.0442597925403994
Island	C20orf195	0.000512296287588894	0.0442597925403994
S_Shore	KIF13A;KIF13A;KIF13A;	0.00051231023904229	0.0442597925403994
S_Shore		0.000512488453262648	0.0442597925403994
S_Shelf	PFKP	0.000512535262917065	0.0442597925403994
S_Shore	RPH3AL	0.000512554032892307	0.0442597925403994
Island	KIAA1543;KIAA1543	0.000512625733738292	0.0442597925403994

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		0.000512647509006611	0.0442597925403994
Island	NTM;NTM;NTM;NTM	0.0005127196753325	0.0442597925403994
		0.000512811099569534	0.0442597925403994
Island	JPH1	0.000512838763017756	0.0442597925403994
	EFR3A	0.000512890096910959	0.0442597925403994
Island		0.000512947803180729	0.0442597925403994
		0.000513092771258027	0.0442597925403994
Island	TTLL10	0.000513123904639121	0.0442597925403994
Island	PAX3;PAX3;PAX3;CCD	0.000513261977202679	0.0442638189296096
Island	ADAD1;ADAD1;ADAD1;	0.000513458594665483	0.0442658384629785
	LRP5	0.000513473245174085	0.0442658384629785
Island	ANKRD11	0.000513618382487579	0.0442658384629785
S_Shore		0.000513675677488982	0.0442658384629785
Island	CNR1;CNR1;CNR1;CNF	0.000513820741347845	0.0442658384629785
Island	ITGAL;ITGAL	0.000513833776573303	0.0442658384629785
		0.000514453555035435	0.0442947030985482
	SSTR3	0.00051449885164278	0.0442947030985482
Island	AURKC;AURKC;AURKC	0.000514542297231506	0.0442947030985482
Island		0.000514580351731795	0.0442947030985482
	KLK11;KLK11;KLK11;KL	0.00051462611745322	0.0442947030985482
S_Shore		0.000514863215686165	0.0443021488328614
N_Shore		0.000514895567604763	0.0443021488328614
S_Shore	INPP5A	0.000515086463683926	0.0443107018692216
Island	NUDT11	0.000515348572624318	0.0443253769199561
	LIPC	0.000515579731394712	0.0443305272066034
Island	HOXA1;HOXA1	0.000515681369729759	0.0443305272066034
S_Shore	C7orf50;C7orf50;C7orf5	0.000515683043993193	0.0443305272066034
Island	DOK2	0.000516233741501374	0.044369992342973
N_Shelf	CA5B;INE2	0.000516768700837366	0.0444080343125377
Island	SLC9A3	0.000516859731419553	0.0444080343125377
N_Shore	TTC15	0.000517019659995417	0.0444138845039029
Island	PWWP2B;PWWP2B	0.000517207642444946	0.0444138845039029
S_Shelf	COX10	0.000517269601131827	0.0444138845039029
	SORD	0.000517586591201236	0.0444138845039029
	PART1;PART1;PDE4D;P	0.000517616465408167	0.0444138845039029
		0.000517675354971576	0.0444138845039029
Island	ACER3	0.000517720517784435	0.0444138845039029
	TTC15	0.000517806772394915	0.0444138845039029
	NCK2;NCK2	0.000517814110521044	0.0444138845039029
		0.000517844847558023	0.0444138845039029
Island	SHANK2	0.000518040535983899	0.044422801450142
	PMS2L11	0.000518326562886901	0.0444394605364132
		0.000518588296032022	0.0444540312346388
S_Shore	OXR1	0.000519013728942145	0.044463494993909
Island	EGFL8	0.000519050776189606	0.044463494993909
		0.000519089486720231	0.044463494993909
	PRKCZ;PRKCZ;PRKCZ	0.000519145362751775	0.044463494993909
		0.000519157722997069	0.044463494993909
	CLPTM1L	0.000519619265574241	0.0444951557282963
		0.000519829884186037	0.0445020262007793
Island	ZNF768	0.000519958497006041	0.0445020262007793
		0.000519975153605968	0.0445020262007793
N_Shore		0.000520118038971521	0.0445044991095692
		0.000520187827304539	0.0445044991095692
Island	PRMT8	0.000520572583413563	0.0445222619694573

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Island	SIM1	0.000520579300124992	0.0445222619694573
Island	PCDHB9	0.000520674318321099	0.0445225263454919
S_Shelf		0.000520791484898611	0.044523063069619
	KLHL29	0.000520941366472094	0.044523063069619
Island	MCF2L;MCF2L	0.000521058244034584	0.044523063069619
		0.000521100721786192	0.044523063069619
	NAP1L6	0.000521445181113312	0.044523063069619
Island	ALX4	0.000521476897821669	0.044523063069619
Island	HRNR	0.000521485193244811	0.044523063069619
Island		0.000521563528830436	0.044523063069619
		0.00052176087673365	0.044523063069619
S_Shelf	KIF13B	0.000521837146762848	0.044523063069619
	CREBBP;CREBBP	0.000521967025168492	0.044523063069619
	CD96;CD96	0.000521990406391228	0.044523063069619
S_Shelf	C14orf43;C14orf43	0.000522297280151515	0.044523063069619
Island	RBM44	0.000522333620496024	0.044523063069619
		0.000522643707393183	0.044523063069619
Island	ARHGAP22	0.000522830622846721	0.044523063069619
	FOXP1	0.000522862739076796	0.044523063069619
Island		0.000522913542007023	0.044523063069619
Island	TRIM15	0.000522941061822863	0.044523063069619
Island		0.00052304185665286	0.044523063069619
S_Shore	MTL5;MTL5	0.000523051242317319	0.044523063069619
Island	REM1	0.000523146889063212	0.044523063069619
Island	HM13;HM13;HM13;PSIN	0.000523172265918636	0.044523063069619
	UNC5C	0.000523174880334664	0.044523063069619
Island		0.000523248560993406	0.044523063069619
Island	NXN	0.000523304922619771	0.044523063069619
N_Shore		0.000523704605800344	0.044523063069619
Island	PDE9A;PDE9A;PDE9A;P	0.00052374004402563	0.044523063069619
Island		0.000523835641082074	0.044523063069619
N_Shore		0.000523847261428194	0.044523063069619
S_Shelf	RGL2;RGL2	0.000523918267172724	0.044523063069619
	AKT1;AKT1;AKT1	0.000523995934984922	0.044523063069619
		0.000524038229590157	0.044523063069619
	MGMT	0.000524148165762049	0.044523063069619
		0.000524158570394621	0.044523063069619
Island	ADAM12;ADAM12	0.000524296636968344	0.044523063069619
S_Shelf	FAM155B	0.000524305245996661	0.044523063069619
		0.000524315688206376	0.044523063069619
		0.000524326345855372	0.044523063069619
		0.000524358395470392	0.044523063069619
S_Shore		0.000524449646027309	0.044523063069619
Island	TNRC18	0.000524570064540628	0.0445254813369505
Island	PRKCSH;PRKCSH	0.000524768849495335	0.0445345493309669
S_Shelf	GRB10	0.000524914771539838	0.0445391287186461
		0.000525269474375067	0.0445410391520769
		0.000525421579811819	0.0445410391520769
	PBX1	0.000525513435175721	0.0445410391520769
	TEX11;TEX11	0.000525751340270584	0.0445410391520769
	ALPL;ALPL	0.000525823230669828	0.0445410391520769
N_Shore	ELAVL3;ELAVL3	0.000525918377158621	0.0445410391520769
	ATG10;ATG10	0.000525925825060306	0.0445410391520769
Island		0.000525966092290474	0.0445410391520769
Island	SLCO5A1;SLCO5A1;SL	0.000526014937735663	0.0445410391520769

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S_Shore	SH2D3A	0.000526028065482217	0.0445410391520769
Island	ZNF136	0.000526039234001962	0.0445410391520769
Island		0.000526046799337413	0.0445410391520769
S_Shore	CHRD1;CHRD1;CHR	0.000526132834334449	0.0445410391520769
Island	GPR153	0.000526493192438136	0.0445551607031434
Island	RPTOR;RPTOR	0.00052653720333745	0.0445551607031434
Island	SLC25A29	0.000526632303233881	0.0445551607031434
	FAM184B	0.000526778783336129	0.0445551607031434
	KLHL6	0.000526843326588456	0.0445551607031434
	IGFBP7	0.000526851608624173	0.0445551607031434
	OBSCN;OBSCN	0.000527008306201572	0.0445553526377157
S_Shore	KIAA1549;KIAA1549	0.000527051046327835	0.0445553526377157
Island	GPR68	0.00052712986241493	0.0445553526377157
Island	TGFB1	0.000527317446723568	0.0445634308819389
	PRR3;PRR3	0.000527479677800778	0.0445693640877289
Island	CSNK1A1P	0.000527655311370165	0.044574822987184
		0.000527728353912173	0.044574822987184
Island	KRT12	0.00052789905577307	0.0445814664668338
Island	MGC16121	0.000528163158135855	0.0445850997082153
N_Shore	SLC39A14;SLC39A14;S	0.000528443347666275	0.0445850997082153
Island	FAM41C	0.000528472056662288	0.0445850997082153
N_Shelf		0.000528558918989634	0.0445850997082153
Island	ODZ4	0.000528598268959318	0.0445850997082153
N_Shore	C7orf51	0.000528771051462543	0.0445850997082153
S_Shore	LOC100129637	0.000528946402441287	0.0445850997082153
Island	ZBTB7C	0.000528958051287936	0.0445850997082153
Island	BCOR;BCOR;BCOR;BC	0.000528970326848959	0.0445850997082153
		0.00052906440760436	0.0445850997082153
S_Shore	TRAP1	0.00052932429617117	0.0445850997082153
	CUL1	0.000529342057131966	0.0445850997082153
		0.000529360510241931	0.0445850997082153
Island		0.00052941293443113	0.0445850997082153
Island	FAM187B	0.000529436582457894	0.0445850997082153
	SLC1A3;SLC1A3;SLC1A	0.000529583588628546	0.0445850997082153
	ABCC1;ABCC1;ABCC1;	0.000529727192503503	0.0445850997082153
	BANP;BANP	0.000529819001145865	0.0445850997082153
		0.00052996145091668	0.0445850997082153
		0.000529997728521955	0.0445850997082153
		0.00053000765129409	0.0445850997082153
N_Shore	B3GNTL1	0.000530040697187645	0.0445850997082153
Island	ZNF274;ZNF274;ZNF27	0.000530196852741188	0.0445850997082153
Island	FGF3	0.000530316257528387	0.0445850997082153
N_Shore		0.00053033278501937	0.0445850997082153
	CHRM1	0.000530335537952879	0.0445850997082153
Island	CDGAP	0.000530483869956198	0.0445898299751016
	DLG4;DLG4	0.00053062754357598	0.0445941671078321
	TXNDC3	0.000530786248293073	0.0445971009309055
N_Shore	NXT2	0.000530846615117266	0.0445971009309055
	FBN1	0.000531072861205613	0.0446083703613265
	TNFRSF21	0.000531550523794442	0.0446346195577226
	ST6GAL1;ST6GAL1	0.000531569680708086	0.0446346195577226
Island		0.000531801620049499	0.0446463545901323
	SYT7	0.000531952969245021	0.0446513209410043
Island		0.000532134260697014	0.0446587984425717
N_Shelf	CRYL1	0.000532453626319681	0.0446778590726402

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N_Shore	CCDC67	0.000533104684869383	0.0447247404294758
Island		0.000533380333281159	0.0447401160229299
Island	SRGAP3;SRGAP3	0.000533611042187406	0.0447517174038815
Island	CYP26C1	0.000533833831754996	0.044762650721042
	PTPRN2;PTPRN2;PTPF	0.000534049191909096	0.0447693762391264
Island	POFUT2;POFUT2;POFU	0.000534098912733541	0.0447693762391264
	CARD11	0.000534209784247425	0.04477092122437
		0.000534384285417504	0.0447777974108707
	MEIS2;MEIS2;MEIS2;M	0.000534507929552932	0.044780410479281
Island	CHDH	0.000535153509490453	0.0448267422144524
		0.000535350340140948	0.0448297621637265
S_Shore	GALNT9	0.000535658234563801	0.0448297621637265
N_Shelf	CAPRN2;CAPRN2;CA	0.000535661413289015	0.0448297621637265
Island	BHMT2;DMGDH	0.000535676674499991	0.0448297621637265
S_Shore	TESC;TESC;TESC	0.000535700619404927	0.0448297621637265
	MEIS1	0.000535744930374539	0.0448297621637265
	SCAND3	0.000535994616154603	0.044835287809094
N_Shore	MMP21	0.000536308960698502	0.044835287809094
S_Shelf	SEC11C	0.000536358382958539	0.044835287809094
	WNT11	0.000536382875486341	0.044835287809094
N_Shore	MAPK8IP3;MAPK8IP3	0.000536496464912317	0.044835287809094
N_Shore	CCDC57	0.000536588246412552	0.044835287809094
Island	ZNF516	0.000536682138639381	0.044835287809094
		0.000536753348905624	0.044835287809094
Island	EGR2;EGR2;EGR2;EGF	0.000536831444253504	0.044835287809094
	FBN1	0.000536923008137591	0.044835287809094
Island	ASCL1	0.00053694954569633	0.044835287809094
N_Shore		0.000537023343920349	0.044835287809094
Island		0.000537239926979066	0.044835287809094
	VOPP1	0.000537319786080526	0.044835287809094
S_Shelf	MYO3A	0.00053737582002962	0.044835287809094
Island	PCDHB9	0.000537425149076837	0.044835287809094
	TRAPPC9;TRAPPC9	0.000537433923648671	0.044835287809094
	MMP12	0.000537477274597841	0.044835287809094
Island		0.000537925600914854	0.0448411426091427
		0.000537952905254057	0.0448411426091427
Island	HDGFL1;HDGFL1	0.000537962253115127	0.0448411426091427
		0.000537985324978408	0.0448411426091427
Island	TFDP1;TFDP1	0.00053801038497234	0.0448411426091427
Island	NTRK3;NTRK3;NTRK3	0.000538255150649295	0.0448487215716156
S_Shelf	DCP2	0.000538286519373977	0.0448487215716156
N_Shore	CSNK1D;CSNK1D	0.000538558206239464	0.0448541245961758
	KIAA0195	0.00053874794092283	0.0448541245961758
Island	CALHM3	0.000538792070421845	0.0448541245961758
Island	CRYL1	0.000538837607173766	0.0448541245961758
	CLPTM1L	0.000538950299161216	0.0448541245961758
	VAC14	0.000538969124211232	0.0448541245961758
Island	DGKQ	0.000538999649305204	0.0448541245961758
		0.000539805742875018	0.0449134884758535
S_Shelf	CEPT1;CEPT1	0.000540076227599794	0.044928275323303
	HIVEP3;HIVEP3	0.000540514731404745	0.0449334627735962
Island	RAB6B	0.000540546080861396	0.0449334627735962
	SVIL;SVIL	0.000540591057947695	0.0449334627735962
	SH3TC1	0.000540846754495196	0.0449334627735962
Island	C6orf138	0.000540853283786262	0.0449334627735962

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	SNORD116-2	0.000540971826205956	0.0449334627735962
Island	PPP1R2P9	0.000541094038918681	0.0449334627735962
Island	GDF11	0.000541103022729517	0.0449334627735962
N_Shore	GRAMD4	0.000541113347769861	0.0449334627735962
Island	PGAM5;PGAM5;PGAM5	0.000541173871519599	0.0449334627735962
Island	MMP9	0.0005412369720915	0.0449334627735962
Island	ANKRD11	0.000541332741375976	0.0449334627735962
Island	SARM1	0.000541596056433824	0.0449334627735962
Island	MYO1G	0.0005416240623943	0.0449334627735962
		0.000541628521745173	0.0449334627735962
Island	RLTPR	0.000541775041848663	0.0449334627735962
	CMBL	0.000541782588214435	0.0449334627735962
Island	ZNF629	0.000541927281590371	0.0449334627735962
S_Shore		0.000541938471855527	0.0449334627735962
Island		0.000542145317685731	0.0449334627735962
N_Shelf	RGL2;RGL2	0.000542188800904737	0.0449334627735962
Island	C1orf14;C1orf14	0.000542190463105923	0.0449334627735962
Island		0.000542310229570475	0.0449334627735962
N_Shore	ATP5G2;ATP5G2;ATP5	0.000542365195631949	0.0449334627735962
	CCDC135	0.000542466113190189	0.0449341372106787
Island	TNXB	0.000542577246208088	0.0449356574503646
Island	SDF4;SDF4	0.000542960008735726	0.0449550994457045
N_Shelf	RASA3	0.000542997639513491	0.0449550994457045
Island	BTBD2	0.000543242666507978	0.0449675969387176
	FAM90A7	0.000543394095949602	0.0449675969387176
		0.000543427130299518	0.0449675969387176
Island	HOXA9	0.000543606644270834	0.0449692797700913
S_Shore	POTEH	0.000543704752473066	0.0449692797700913
	MDFIC;MDFIC	0.000543885355464125	0.0449692797700913
Island	HDGF2;HDGF2	0.000543900592078012	0.0449692797700913
	COLEC11;COLEC11	0.000544032399486243	0.0449692797700913
Island	RPTOR;RPTOR	0.000544039021768062	0.0449692797700913
N_Shore		0.000544097412796645	0.0449692797700913
N_Shelf	RAB3D	0.000544282672406119	0.0449769161087005
	GIMAP6;GIMAP6	0.000544530830724349	0.0449799256379728
		0.000544574426672109	0.0449799256379728
Island	C1orf177;C1orf177	0.000545005289911778	0.0449799256379728
N_Shore	RBMXL3;LRCH2	0.000545080260130699	0.0449799256379728
		0.000545099428162869	0.0449799256379728
	TRIM26	0.000545158233039569	0.0449799256379728
	DDX17;DDX17;DDX17;[0.000545191351090521	0.0449799256379728
	PDE11A;PDE11A	0.000545219951927725	0.0449799256379728
Island	ADAM12;ADAM12	0.000545291441725828	0.0449799256379728
Island	ANTXR2	0.000545389100697042	0.0449799256379728
		0.000545455234967727	0.0449799256379728
S_Shore	LYSMD4	0.000545487824040654	0.0449799256379728
Island	PTPN21	0.000545526419650963	0.0449799256379728
	SOX2OT	0.000545833748620984	0.0449921258677452
S_Shore	GLI3	0.000545866952848354	0.0449921258677452
Island	KIAA1210	0.000545953076394442	0.0449921258677452
Island	ZBTB42	0.000546111508246357	0.0449931913425512
N_Shore	ACHE;ACHE	0.00054626749797115	0.0449931913425512
Island		0.00054637055485913	0.0449931913425512
Island	ARRDC2;ARRDC2	0.000546491561649519	0.0449931913425512
N_Shore	MEIG1	0.000546499121314519	0.0449931913425512

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		0.000546539108103401	0.0449931913425512
	NCRNA00171	0.000546682438111187	0.0449931913425512
Island		0.000546709195376893	0.0449931913425512
Island		0.000547136732042809	0.0450153012129053
Island	GRIK5	0.000547351432456798	0.0450153012129053
N_Shelf	BDH1;BDH1;BDH1	0.000547517211020489	0.0450153012129053
	WDR27	0.000547526787400361	0.0450153012129053
	WNT11	0.000547546692693908	0.0450153012129053
	ZDHHC11	0.000547917601754681	0.0450153012129053
N_Shelf	MCM3AP	0.000548003584357416	0.0450153012129053
S_Shore		0.000548277955942193	0.0450153012129053
N_Shelf		0.000548282753586768	0.0450153012129053
	ALAS2;ALAS2;ALAS2	0.000548310145100237	0.0450153012129053
Island	SMARCA4;SMARCA4;S	0.000548327208391954	0.0450153012129053
Island		0.000548405381641904	0.0450153012129053
		0.000548430861167953	0.0450153012129053
	STOX2	0.000548629307600417	0.0450153012129053
	MGMT	0.000548688030744941	0.0450153012129053
N_Shore	TRPM5	0.000548731857220404	0.0450153012129053
		0.000548748746269885	0.0450153012129053
S_Shore	PTPRN2;PTPRN2;PTPF	0.000548768762304034	0.0450153012129053
Island	TAL1	0.000548951326848183	0.0450153012129053
Island	DUPD1	0.000548975690220145	0.0450153012129053
N_Shore	PTP4A3;PTP4A3	0.000548977523223493	0.0450153012129053
	VAV2;VAV2	0.000549100322796405	0.0450153012129053
S_Shelf		0.00054918646951302	0.0450153012129053
Island	NFATC1;NFATC1;NFAT	0.000549208516733717	0.0450153012129053
Island	CSNK1G2	0.000549365418693144	0.0450205425395189
Island	ATP11A;ATP11A	0.00054966886361669	0.0450238527008013
Island	TPO;TPO;TPO;TPO	0.000549771389621595	0.0450238527008013
Island	GPR112	0.000549840898352273	0.0450238527008013
Island	KIAA1688	0.000550065910863185	0.0450238527008013
Island		0.000550073975614493	0.0450238527008013
Island	RALYL;RALYL;RALYL;R	0.000550109378519142	0.0450238527008013
Island		0.000550277175352547	0.0450238527008013
Island	HCN1	0.000550332490335985	0.0450238527008013
	DIO2;DIO2;DIO2	0.00055035844390589	0.0450238527008013
N_Shore		0.00055041986734907	0.0450238527008013
S_Shore	SIK1	0.000550428393829442	0.0450238527008013
	FOXP1;FOXP1	0.000550593844613361	0.0450294524149089
N_Shore	ELOVL5	0.000550719884268368	0.0450294524149089
	ZC3H12C	0.000550897717515105	0.0450294524149089
S_Shelf	ZSWIM4	0.000550904897172449	0.0450294524149089
N_Shelf		0.000550961719941672	0.0450294524149089
Island	CBLN1	0.000551170901849816	0.0450326853150408
	HCCA2	0.000551260922052649	0.0450326853150408
	SVIL	0.0005512802172774	0.0450326853150408
N_Shelf	MYCBP2	0.000551385336443072	0.0450336767407742
S_Shelf	DIP2C	0.000551484835337941	0.0450342088813097
Island	SPAG6;SPAG6	0.000551724657136738	0.045046197668198
	ODZ2	0.000551874793559712	0.0450484482958785
Island	PSMA8;PSMA8;PSMA8;	0.000551938248464859	0.0450484482958785
Island		0.000552392154050741	0.0450777653112578
Island	UBXN6;UBXN6	0.000552483590332166	0.0450777653112578
	NAALADL2	0.000552742909639572	0.0450913272210183

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	ZDHHC14;ZDHHC14	0.000553015302405707	0.0451059508820552
		0.000553257443888511	0.0451061170458313
	IGSF11;C3orf30;IGSF11	0.000553285514973827	0.0451061170458313
Island	ZNF366	0.000553296735393142	0.0451061170458313
Island	GATAD2A	0.000553450893123077	0.045111091183412
Island	LYPD4;DMRTC2	0.000553664112452492	0.0451155761769152
Island	GPR83	0.00055369222071044	0.0451155761769152
Island	RPS6KA2;RPS6KA2	0.000553872735660311	0.0451215332172791
S_Shelf	LRP5L;LRP5L	0.000554030173689407	0.0451215332172791
	LRP5	0.000554044821231939	0.0451215332172791
Island	PRKAG2;PRKAG2;PRK	0.000554162485655909	0.0451235282221416
		0.000554284444848765	0.0451258722056444
Island	FLJ30058	0.000554495437932982	0.0451301883920596
Island	USP29	0.000554523824128729	0.0451301883920596
Island	PLEC1;PLEC1;PLEC1;P	0.000554716092018791	0.0451382512209343
Island	OLIG2	0.000555071221425499	0.0451595614508492
		0.000555287135491434	0.0451695401237636
Island	RUNDC2A	0.000555663896620371	0.045182714150138
N_Shore	C2orf64	0.000555701462861466	0.045182714150138
S_Shore		0.000555857060206207	0.045182714150138
Island	NKX6-2	0.000555905296170112	0.045182714150138
		0.000556052353514054	0.045182714150138
		0.000556088524829106	0.045182714150138
Island	NOC4L	0.00055618221561594	0.045182714150138
		0.000556195409617763	0.045182714150138
	BAT2L2	0.00055667108886754	0.0451987914568103
	IL1F6	0.000556699851536623	0.0451987914568103
Island	CCDC48	0.000556706438307381	0.0451987914568103
Island		0.00055676661297957	0.0451987914568103
	CALD1;CALD1;CALD1;C	0.000556928660199031	0.0452043695912344
	HK1;HK1;HK1;HK1;HK1	0.000557157654856913	0.045215378885485
Island	ODZ4	0.000557298464218285	0.0452173451157262
	GLI3	0.000557380807741748	0.0452173451157262
	KIF5C	0.000557461968071028	0.0452173451157262
Island		0.000557754171173251	0.0452316887609132
N_Shore		0.000558302569551915	0.0452316887609132
	C4B;C4A	0.000558450600691763	0.0452316887609132
Island	TCP11;TCP11	0.000558568131951274	0.0452316887609132
Island	WT1;WT1;WT1;WT1	0.000558747888640954	0.0452316887609132
	TRAP1	0.000558801156215425	0.0452316887609132
N_Shore	NAPA	0.00055882262477427	0.0452316887609132
	PRKAR1B;PRKAR1B;PF	0.000558844842494392	0.0452316887609132
		0.000558849617878404	0.0452316887609132
S_Shelf	RAB27B	0.000559031212369829	0.0452316887609132
	PCCA;PCCA	0.000559261251706346	0.0452316887609132
N_Shore		0.000559289338160761	0.0452316887609132
Island	NEURL	0.000559359423649086	0.0452316887609132
	CDH23;C10orf54	0.000559452884272015	0.0452316887609132
	SMEK3P	0.000559553094602665	0.0452316887609132
	COL4A2	0.000559604868043772	0.0452316887609132
N_Shore	PTPRN2;PTPRN2;PTPR	0.000559756422047787	0.0452316887609132
	GABBR1;GABBR1;GAB	0.000559934756950261	0.0452316887609132
N_Shore	FOXG1	0.000560082983663623	0.0452316887609132
		0.000560236893280816	0.0452316887609132
	TPH2	0.000560264238789971	0.0452316887609132

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S_Shore		0.000560264615469967	0.0452316887609132
	AGAP1;AGAP1	0.000560361675085089	0.0452316887609132
	MBL1P	0.000560595958399515	0.0452316887609132
		0.00056087818043108	0.0452316887609132
S_Shore	C17orf28	0.000560941217735915	0.0452316887609132
N_Shore	PCDHB6	0.00056106823940292	0.0452316887609132
	SASH3	0.000561095837656597	0.0452316887609132
	CD79B;CD79B;CD79B;C	0.00056116590089396	0.0452316887609132
S_Shelf		0.000561272709967352	0.0452316887609132
	ZDHHC14;ZDHHC14	0.000561419261681233	0.0452316887609132
S_Shelf	ZNF397;ZNF397	0.000561449209676735	0.0452316887609132
N_Shore	LPPR4;LPPR4	0.000561511279752995	0.0452316887609132
Island	NLGN2	0.000561554172795634	0.0452316887609132
	IMMT;IMMT;IMMT	0.00056156966191869	0.0452316887609132
Island	MYH7B	0.000561587201184823	0.0452316887609132
Island	LDHD;LDHD	0.00056173116680023	0.0452316887609132
Island		0.000561853911762785	0.0452316887609132
N_Shelf	ATL2;ATL2;ATL2	0.000561861253095686	0.0452316887609132
Island	RPTOR;RPTOR	0.000561870166656093	0.0452316887609132
		0.000562124504573683	0.0452316887609132
Island		0.000562135668796035	0.0452316887609132
S_Shore		0.000562164695908852	0.0452316887609132
	FAM49B	0.000562225423999197	0.0452316887609132
Island	ABHD11;ABHD11;ABHD	0.000562408494862319	0.0452316887609132
Island	ZNF536	0.000562414222970551	0.0452316887609132
Island	ISL2	0.000562431034816003	0.0452316887609132
N_Shelf	COL4A2	0.000562490521448943	0.0452316887609132
	PMS2L11	0.000562519100316963	0.0452316887609132
		0.000562520293106156	0.0452316887609132
		0.00056253143002243	0.0452316887609132
Island	ELK1;ELK1	0.000562751246322289	0.0452316887609132
Island	TNS3	0.000562782120956054	0.0452316887609132
Island	ACTRT2	0.000562802767211745	0.0452316887609132
Island		0.000562907200686963	0.0452316887609132
Island	HLA-DPB1	0.000563373734245077	0.0452316887609132
Island	ARAP1	0.000563550460544592	0.0452316887609132
		0.000563599437525348	0.0452316887609132
	KIAA1549;KIAA1549	0.000563623727681174	0.0452316887609132
S_Shelf		0.000563655478817996	0.0452316887609132
Island	FAM47A	0.000563657464453136	0.0452316887609132
	PAGE5;PAGE5	0.000563658121713988	0.0452316887609132
	FZR1;FZR1;FZR1	0.000563689764938039	0.0452316887609132
Island		0.000563706009459092	0.0452316887609132
Island	GRIK2;GRIK2;GRIK2;Gf	0.000563736751522988	0.0452316887609132
		0.000563971763435069	0.0452316887609132
	HEYL	0.000564164958033315	0.0452316887609132
Island	TMEM27	0.000564306782089139	0.0452316887609132
		0.000564434909644283	0.0452316887609132
	AGAP1;AGAP1	0.000564437053142046	0.0452316887609132
Island	PTRF	0.000564444209743337	0.0452316887609132
Island	B3GALT4	0.000564523583495558	0.0452316887609132
N_Shelf	TMED7-TICAM2;TMED7	0.000564557589561867	0.0452316887609132
	NQO2	0.000564575860573078	0.0452316887609132
Island	ITPRIP	0.000564643143030984	0.0452316887609132
N_Shelf		0.000564788765500809	0.0452358721434065

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S_Shore	BMP4;BMP4	0.0005649887117249	0.045244404399167
S_Shore	KCNJ4	0.000565262183264555	0.0452476137436252
	CCNY;CCNY	0.000565391727142796	0.0452476137436252
Island	PITX2;PITX2;PITX2	0.000565469721458916	0.0452476137436252
Island	KIF26A	0.000565494267691467	0.0452476137436252
	ROBO1	0.000565569680716959	0.0452476137436252
N_Shelf		0.000565640683168923	0.0452476137436252
	CCDC92	0.000565682756862955	0.0452476137436252
Island	PRAGMIN	0.000565841413352426	0.0452496618624824
N_Shore	CACNA2D4	0.0005658969984723	0.0452496618624824
	TBC1D16	0.00056598864721606	0.0452496618624824
S_Shore	GXYLT1;GXYLT1	0.000566198084452689	0.0452525271404374
S_Shore	ALOX12	0.000566211354918805	0.0452525271404374
		0.000566399396739589	0.0452600870856132
		0.000567151291034459	0.0453126936704494
		0.000567273442940055	0.0453149777753492
	LOXL2	0.000567489564950702	0.0453247664156907
Island	DLGAP2	0.000567652150637461	0.0453292916977216
S_Shore	JPH3	0.000567771529244463	0.0453292916977216
N_Shore	MLH1;MLH1;MLH1;EPM	0.000567832794935249	0.0453292916977216
Island	RSPH6A	0.000567920594686986	0.0453292916977216
	SEMA6A	0.000568044377695993	0.0453317009767032
Island		0.000568238850708952	0.0453376135041102
		0.000568380793312672	0.0453376135041102
	MYOM2	0.000568440101580914	0.0453376135041102
Island	B3GNTL1	0.000568492906231273	0.0453376135041102
Island		0.00056875556128911	0.0453462893327755
S_Shore	RASA3	0.000568788948942572	0.0453462893327755
Island	RUNX3;RUNX3	0.00056902481637456	0.0453474805833835
	MGMT	0.000569082370543142	0.0453474805833835
	CBFA2T3	0.000569084781883663	0.0453474805833835
S_Shore		0.000569284440003495	0.0453538058285251
S_Shelf		0.000569351446729845	0.0453538058285251
S_Shelf	WNT3A	0.000569504749193216	0.0453585574170374
		0.000569644974922318	0.0453622661097092
	BTRC;BTRC	0.000570270207667831	0.0453970617527408
Island	KHDRBS2;KHDRBS2	0.000570310156271976	0.0453970617527408
Island	CLVS2	0.000570598415540187	0.0453970617527408
	GRHL1	0.000570599890828022	0.0453970617527408
Island		0.000570736030774187	0.0453970617527408
Island	EGFL8	0.000570922832657245	0.0453970617527408
		0.00057109583092606	0.0453970617527408
Island		0.000571264581502586	0.0453970617527408
		0.000571277842667144	0.0453970617527408
	FAM53B	0.000571291108873182	0.0453970617527408
Island	ODZ4	0.000571311299417257	0.0453970617527408
Island	B3GAT1;B3GAT1	0.000571448291316607	0.0453970617527408
Island	TCEB3B;KATNAL2	0.000571488249687748	0.0453970617527408
	PIGG;PIGG	0.000571568944252188	0.0453970617527408
S_Shelf	FAM64A	0.000571605443555346	0.0453970617527408
Island		0.00057168510804064	0.0453970617527408
	PTPRN2;PTPRN2;PTPRN2	0.000571803572830188	0.0453970617527408
Island	GPR39	0.000571940290808088	0.0453970617527408
	SMOC2;SMOC2	0.000571957964630259	0.0453970617527408
Island		0.000571976973850279	0.0453970617527408

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N_Shore		0.000572104900504634	0.0453970617527408
Island	C8orf73	0.000572144045710483	0.0453970617527408
Island	GABRE	0.000572245315149501	0.045397659665812
Island		0.000572566538861418	0.045415704050779
Island		0.0005730433346559	0.0454435430692632
	CTAGE1	0.000573105169188169	0.0454435430692632
N_Shelf	HGSNAT	0.000573672575949978	0.0454810886146625
	ATXN1;ATXN1	0.000574198633699131	0.0455153442334422
	TDRD3;TDRD3;TDRD3	0.000574747522239162	0.0455380513577032
N_Shore	SMC2;SMC2	0.000574758277244841	0.0455380513577032
Island	H2AFY2	0.000574767166571289	0.0455380513577032
N_Shore	SMTNL2;SMTNL2	0.000574959061655692	0.0455392687581862
Island	BAHCC1	0.000575007869945585	0.0455392687581862
		0.000575064611005145	0.0455392687581862
	HECW2	0.000575292005520381	0.0455455769785129
	RP1L1	0.000575399195039777	0.0455455769785129
Island	JARID2	0.000575426985699163	0.0455455769785129
	DCUN1D2	0.000575520427622978	0.0455455769785129
Island	HOXD3	0.00057566917452228	0.0455499057262708
N_Shore	PCDHGB4;PCDHGA4;P	0.000575985402961467	0.0455639216802578
Island	ZNF177	0.000576034465386297	0.0455639216802578
Island	TEX101;TEX101	0.000576135761332547	0.0455644925877508
Island	HTR1A	0.00057653257021621	0.0455743417858003
	RNF44	0.000576578098058882	0.0455743417858003
N_Shore	TMEM26	0.000576645855594953	0.0455743417858003
Island	FN3K	0.000576869544643195	0.0455743417858003
Island	DNAH17	0.000576872093554672	0.0455743417858003
Island	LOC100130872;LOC100	0.0005769110127049	0.0455743417858003
	CSRP3;CSRP3	0.00057691898929178	0.0455743417858003
	LOC285830;LOC285830	0.000577070279059466	0.045578233310991
	RPTOR;RPTOR	0.000577156464969407	0.045578233310991
Island	XKR7	0.0005772622240684	0.0455790168050608
N_Shelf	IBTK	0.000577466763629071	0.0455790168050608
		0.000577508945410272	0.0455790168050608
	LOC150622	0.000577685909999234	0.0455790168050608
	BFSP2	0.000577785800988509	0.0455790168050608
Island	CRB2	0.000577798425559161	0.0455790168050608
Island	RIPPLY2	0.000577859762582632	0.0455790168050608
Island	KCNG2	0.000578090788314784	0.0455790168050608
N_Shore	STBD1	0.000578100081311092	0.0455790168050608
		0.000578376397437061	0.0455790168050608
S_Shore		0.000578407741687611	0.0455790168050608
S_Shelf		0.000578550232512312	0.0455790168050608
Island	BRSK2	0.000578653566914628	0.0455790168050608
	PCSK6;PCSK6	0.000578663272006014	0.0455790168050608
	BPTF;BPTF	0.000578741635551538	0.0455790168050608
Island		0.000578853077611233	0.0455790168050608
S_Shore	C1orf59	0.000578880776389607	0.0455790168050608
	AGER;AGER	0.000578893961650021	0.0455790168050608
Island	FGFR3;FGFR3;FGFR3	0.000578970986543441	0.0455790168050608
Island		0.000579056641036615	0.0455790168050608
S_Shore		0.000579142661267422	0.0455790168050608
S_Shelf	SNX29	0.00057931070819227	0.0455847347969346
Island	LASS3	0.000579403556310183	0.0455847347969346
Island	LRRC3	0.000579591370651556	0.0455855155457096

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N_Shore	C6orf136;C6orf136;C6orf136	0.000579601723492447	0.0455855155457096
Island	PER3	0.00057974230931214	0.0455891693387891
S_Shelf	HSF2BP	0.000579904023947043	0.0455944831815181
	WARS2;WARS2	0.000580273439782092	0.0456161229869278
Island		0.000580470698220308	0.0456190528802121
	TTN;TTN;TTN;MIR548N	0.000580515648958104	0.0456190528802121
	MYO10	0.000580593283339963	0.0456190528802121
	ACYP2	0.00058071282787237	0.0456210446649287
N_Shelf	HGS	0.000580887419067057	0.0456273595912508
	OR6X1	0.00058112012033305	0.0456354402569685
		0.000581215585812502	0.0456354402569685
Island	ELFN1	0.00058151547727496	0.0456354402569685
	ANKRD26P1	0.000581517618798712	0.0456354402569685
Island	SLC25A2	0.00058159122744151	0.0456354402569685
	TNXB	0.000581610176119633	0.0456354402569685
	BPGM;BPGM	0.000581894346017889	0.0456354402569685
N_Shore		0.000582005067360756	0.0456354402569685
	RBM47;RBM47	0.00058201412065471	0.0456354402569685
	MAD1L1;MAD1L1;MAD1L1	0.000582089119925748	0.0456354402569685
N_Shore	DNAH10	0.000582188634931609	0.0456354402569685
N_Shelf		0.000582252778405789	0.0456354402569685
S_Shore	CARD14;CARD14	0.000582477120511087	0.0456354402569685
	FAM92B	0.000582481220782704	0.0456354402569685
S_Shore	TOLLIP	0.000582489211469149	0.0456354402569685
Island		0.000582497892259494	0.0456354402569685
		0.000582751637382941	0.0456479357553765
Island	MRC2	0.00058300265487676	0.0456602135871906
N_Shelf	FBXL22	0.000583232065537557	0.0456663078434335
		0.000583391667515659	0.0456663078434335
Island		0.000583501469992976	0.0456663078434335
Island		0.000583652707761924	0.0456663078434335
N_Shelf	DIP2C	0.000583834818814629	0.0456663078434335
Island	VCPIP1;VCPIP1	0.000583924526229214	0.0456663078434335
Island	ZNF787	0.000583976907272317	0.0456663078434335
	ZBTB16;ZBTB16	0.000584139755154282	0.0456663078434335
S_Shore	CTBP1;CTBP1	0.000584147967322104	0.0456663078434335
N_Shore	USP1;USP1;USP1	0.000584186718504184	0.0456663078434335
		0.000584283117577173	0.0456663078434335
		0.00058429410403171	0.0456663078434335
N_Shelf	HSPBAP1	0.000584322684546323	0.0456663078434335
Island	SLC24A3	0.000584414576051262	0.0456663078434335
S_Shelf		0.000584559178220805	0.0456663078434335
	SPDYE4;SPDYE4	0.000584951675578355	0.0456663078434335
Island		0.000585076603252208	0.0456663078434335
Island	ZBTB7A	0.000585120491168712	0.0456663078434335
Island	IGF2BP3	0.000585169254715705	0.0456663078434335
Island	NTSR2	0.000585212186878882	0.0456663078434335
Island	ABP1	0.000585237860809954	0.0456663078434335
	TIA1;TIA1	0.000585356628258034	0.0456663078434335
	MUC4;MUC4;MUC4	0.000585544953762082	0.0456663078434335
	PAPLN	0.000585626431465683	0.0456663078434335
Island	GRIN2A;GRIN2A;GRIN2A	0.000585657841333674	0.0456663078434335
Island	HIC2	0.000585660884293172	0.0456663078434335
Island	PAK7;PAK7	0.000585745490540759	0.0456663078434335
	GJA5	0.000585769146694829	0.0456663078434335

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	HK1;HK1;HK1;HK1;HK1	0.00058608810198392	0.0456663078434335
Island		0.000586101094390736	0.0456663078434335
	SRRM4	0.000586224509013646	0.0456663078434335
Island		0.000586240269806953	0.0456663078434335
N_Shore		0.000586251688080988	0.0456663078434335
		0.000586352762368264	0.0456663078434335
N_Shore	SNAR-F	0.000586380567755769	0.0456663078434335
Island	KIAA1409;COX8C;COX8C	0.000586530854446793	0.0456706681800552
Island	FGF4	0.000586992383998386	0.0456776095730559
Island	SBF1	0.000587180477761746	0.0456776095730559
	PXDN	0.000587307289870098	0.0456776095730559
Island	ANO1;ANO1	0.000587483488498093	0.0456776095730559
	EFNA5	0.000587484946461531	0.0456776095730559
Island	ODF3L2	0.000587508667223246	0.0456776095730559
		0.000587743773270726	0.0456776095730559
N_Shore	NSD1;NSD1	0.000587876351923708	0.0456776095730559
Island	SRCIN1	0.000587902960150825	0.0456776095730559
S_Shore	POP7	0.000587909987426432	0.0456776095730559
Island	NR2E1	0.000588152825223266	0.0456776095730559
	ANKH	0.00058839575926787	0.0456776095730559
Island		0.000588449656590703	0.0456776095730559
	CUX2	0.000588581627993537	0.0456776095730559
N_Shore	ZDHC17	0.000588589242009427	0.0456776095730559
N_Shore	KIAA0895;KIAA0895	0.000588643418134278	0.0456776095730559
	NGDN;NGDN	0.000588651350652919	0.0456776095730559
	CHST15	0.000588653531821604	0.0456776095730559
	AGAP1;AGAP1	0.000588663871126892	0.0456776095730559
	CAPRIN1;CAPRIN1	0.000588845361573764	0.0456776095730559
		0.000588933321235213	0.0456776095730559
N_Shelf	HIST1H1A	0.00058895918104879	0.0456776095730559
	PTPRN2;PTPRN2;PTPRN2	0.000588968412025624	0.0456776095730559
	FOXO1	0.00058906473685518	0.0456776095730559
S_Shore	CNR2	0.000589067009779047	0.0456776095730559
S_Shore	DDX52;DDX52	0.000589072109416832	0.0456776095730559
	GPR77	0.000589462663008847	0.0456984593011649
	THSD7A	0.000589529703636357	0.0456984593011649
Island	KIAA0182;KIAA0182	0.000589799238572149	0.0457120365212763
Island	KIAA1161	0.000589972506860431	0.0457181419119132
		0.000590172309487839	0.0457181419119132
	ZC3H13	0.000590298817267546	0.0457181419119132
N_Shore	ZC3H3	0.0005903189471583	0.0457181419119132
Island	FAM38A	0.000590349991260218	0.0457181419119132
S_Shore	NUDT10	0.000590449610990516	0.0457185464177429
	BCL2	0.000590584980819553	0.0457217184839242
	PTPRN2;PTPRN2;PTPRN2	0.000591014931778279	0.0457476916786823
	MYT1L	0.000591234570186204	0.04575737986664
Island		0.000591355869980387	0.0457594554606568
Island	TRAP1	0.000591578397107622	0.0457652581681974
	PCDH20	0.000591633976167252	0.0457652581681974
	FLYWCH1;FLYWCH1	0.000591755253905756	0.0457652581681974
Island		0.000592249257464201	0.0457652581681974
S_Shelf	TTC14;TTC14	0.000592431644914665	0.0457652581681974
		0.000592451895144088	0.0457652581681974
	PDE4D;PDE4D;PDE4D	0.000592486736317854	0.0457652581681974
N_Shore	KIAA0664	0.000592706635986729	0.0457652581681974

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	TGFBR2;TGFBR2	0.000592941092800377	0.0457652581681974
N_Shelf	ANXA11;ANXA11;ANXA	0.000593043636680382	0.0457652581681974
	AGAP1;AGAP1	0.000593052729315355	0.0457652581681974
N_Shelf	RNPS1;RNPS1	0.000593131567332271	0.0457652581681974
	LGR6;LGR6;LGR6	0.000593241234544122	0.0457652581681974
S_Shore	PTPRS;PTPRS;PTPRS;	0.000593306657147706	0.0457652581681974
N_Shelf		0.000593376831329339	0.0457652581681974
	ZFPM1	0.000593388870197987	0.0457652581681974
Island	GNA11	0.000593394307653506	0.0457652581681974
Island	DPP6	0.000593468049992549	0.0457652581681974
	HERC2	0.000593483356558821	0.0457652581681974
Island	REPIN1;REPIN1;REPIN	0.000593520203343193	0.0457652581681974
		0.000593560623684655	0.0457652581681974
Island	MAEA;MAEA	0.00059356880740329	0.0457652581681974
Island	LRRC33	0.000593697618562389	0.0457652581681974
N_Shore		0.000593775298466988	0.0457652581681974
Island		0.000593793180878444	0.0457652581681974
	MMP20	0.000593936668132033	0.0457673733737708
S_Shore		0.00059421585679507	0.0457673733737708
Island		0.000594242580770051	0.0457673733737708
	PRDM16;PRDM16	0.000594365824451934	0.0457673733737708
		0.000594406095163322	0.0457673733737708
	DIP2C	0.000594409415957651	0.0457673733737708
Island	KIAA1026;KIAA1026	0.000594482105805795	0.0457673733737708
	PEBP1	0.000594912875120979	0.0457932578262823
	PMS2L11	0.000595110076174385	0.0457963151989616
S_Shelf	RGPD1;RGPD2	0.000595141708279078	0.0457963151989616
Island	CDH4	0.000595338229094875	0.0458010566826967
	CACNA1D;CACNA1D;C	0.000595468874299433	0.0458010566826967
Island		0.000595487026131092	0.0458010566826967
		0.000595844349484289	0.0458120042236843
	ACTC1	0.000595907515967794	0.0458120042236843
	CUX1;CUX1;CUX1	0.000595913129838871	0.0458120042236843
		0.000596211023562745	0.0458179688832823
S_Shore		0.000596322630952731	0.0458179688832823
S_Shore	PCDHGB4;PCDHGA4;P	0.000596345357931503	0.0458179688832823
	JUP;JUP	0.000596397210221212	0.0458179688832823
S_Shore	FOXK2	0.000596519201332769	0.0458179688832823
Island		0.000596558327110883	0.0458179688832823
	TNXB	0.000596785978861848	0.0458281860174829
S_Shore	WDR60	0.000596909586129401	0.0458304114302667
	PTPRN2;PTPRN2;PTPF	0.000597100554032207	0.0458351519058159
S_Shelf	HECW1	0.00059716060192164	0.0458351519058159
	UCK2	0.000597352527098187	0.0458354108830816
N_Shore	PXDNL	0.000597477729271328	0.0458354108830816
Island		0.00059755583042587	0.0458354108830816
Island	DPF1;DPF1;DPF1	0.000597675009556721	0.0458354108830816
Island	GPR20	0.000597706646959906	0.0458354108830816
	C12orf40	0.000597731802276454	0.0458354108830816
Island	VIPR2	0.000597850402279348	0.0458372480740771
		0.000597989048393768	0.0458381273843614
Island	ONECUT1	0.000598108372395412	0.0458381273843614
Island	MDFI	0.000598156028699292	0.0458381273843614
	MED12L;P2RY14	0.00059824044432261	0.0458381273843614
N_Shelf	KIFC1	0.000598367040390297	0.0458388984177276

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	ZKSCAN3	0.000598546793595932	0.0458388984177276
Island	C2orf54;C2orf54	0.000598703951779001	0.0458388984177276
N_Shore	DOK7;DOK7	0.000598709399727043	0.0458388984177276
N_Shore	EIF3B;EIF3B	0.000598741831566367	0.0458388984177276
		0.000598920965347937	0.0458388984177276
	DLG5	0.000598922966393848	0.0458388984177276
Island		0.0005991904539674	0.0458388984177276
Island	C1QL3	0.000599221485887823	0.0458388984177276
		0.000599240476896874	0.0458388984177276
N_Shore	CPT1A;CPT1A	0.000599291601261656	0.0458388984177276
	PPP1R12B;PPP1R12B;PPP1R12B	0.000599515271089645	0.045845197627717
	MYT1L	0.000599563272129169	0.045845197627717
		0.000599848224663011	0.0458466944382317
	TRAF5;TRAF5;TRAF5	0.000599848689151281	0.0458466944382317
	ZNF645	0.000599866830444586	0.0458466944382317
S_Shelf	MAPK13	0.000600166833181634	0.0458623858442245
		0.000600475826117198	0.0458787591866559
N_Shore	EGFLAM	0.0006006588015443	0.0458855006400541
Island		0.00060097968082712	0.0459008577057768
N_Shore	MIR24-1;C9orf3	0.000601049377112551	0.0459008577057768
	RFPL4B;RFPL4B	0.000601378911098184	0.0459097896368808
	PXDN	0.000601501618307677	0.0459097896368808
S_Shelf		0.000601536489355634	0.0459097896368808
S_Shelf	HAUS5	0.000601619867039524	0.0459097896368808
Island		0.000601722992108254	0.0459097896368808
		0.000601735084116904	0.0459097896368808
		0.0006018306309037	0.0459098472692446
	AFG3L1;AFG3L1;AFG3L1	0.000602177121856217	0.0459160127134104
S_Shore		0.000602264003444009	0.0459160127134104
Island	HLA-DQB2	0.000602427331058437	0.0459160127134104
Island	ARRDC2;ARRDC2	0.000602578376999625	0.0459160127134104
S_Shore	CIDEA;CIDEA	0.00060272819670151	0.0459160127134104
Island		0.000602801175805649	0.0459160127134104
		0.000602852084074361	0.0459160127134104
	ZNF677	0.000602918030885246	0.0459160127134104
		0.000603037611890566	0.0459160127134104
	SALL1;SALL1	0.000603132716833351	0.0459160127134104
N_Shore		0.000603162872104241	0.0459160127134104
	CA5A	0.000603221252648819	0.0459160127134104
	ZC3H3	0.000603521854350064	0.0459160127134104
		0.000603553493341706	0.0459160127134104
	NADSYN1	0.000603563772054976	0.0459160127134104
		0.000603644161935471	0.0459160127134104
Island	NTRK3;NTRK3;NTRK3;NTRK3	0.000603871969779157	0.0459160127134104
Island	HMGCLL1;HMGCLL1	0.000603945897313613	0.0459160127134104
Island	FKRP;FKRP	0.000603980602401797	0.0459160127134104
		0.000604054300264728	0.0459160127134104
S_Shore	NRG3;NRG3;NRG3	0.000604147068063479	0.0459160127134104
S_Shelf	TNK2;TNK2	0.000604228590098465	0.0459160127134104
	E2F5;E2F5;E2F5	0.000604324648781988	0.0459160127134104
Island	ZDHHC1;TPPP3;TPPP3	0.000604425985620042	0.0459160127134104
Island		0.000604621872159319	0.0459160127134104
N_Shelf		0.000604835843767842	0.0459160127134104
Island	MAPK15	0.000604906455605232	0.0459160127134104
N_Shore	HDAC4	0.000604961681501137	0.0459160127134104

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	TRIM22	0.00060498055721562	0.0459160127134104
Island	TCF3;TCF3	0.000605000533639824	0.0459160127134104
	CENPF	0.000605010717232137	0.0459160127134104
Island		0.000605059201671437	0.0459160127134104
Island	WNT3A	0.000605093297292915	0.0459160127134104
N_Shore	C6orf123	0.000605211232099157	0.0459160127134104
	PAGE4;PAGE4	0.000605287538954713	0.0459160127134104
N_Shore	ANKRD33B	0.000605422161660147	0.0459160127134104
	PTPRR;PTPRR	0.000605585224590179	0.0459160127134104
Island	EVPL	0.00060563236594512	0.0459160127134104
Island	SOHLH2	0.000605696258845529	0.0459160127134104
	FOXP1;MIR1284;FOXP	0.000605703618904617	0.0459160127134104
	TRAK1	0.000605832717935924	0.0459176183561803
Island	USP29	0.000605914414730497	0.0459176183561803
N_Shelf	CORIN	0.000606164333087179	0.0459293711862403
S_Shore	PTPRF;PTPRF	0.000606474470946199	0.0459452471833135
		0.000606563589511396	0.0459452471833135
Island	CBFA2T3;CBFA2T3	0.000606766453987433	0.0459534265562882
S_Shore	ZFH3;ZFH3	0.000606947041755151	0.0459538482594758
	PRKCZ;PRKCZ	0.00060711790711156	0.0459538482594758
	GOLIM4	0.000607122419488104	0.0459538482594758
	TSNARE1	0.000607151551153431	0.0459538482594758
N_Shore	CDH8	0.000607249759096738	0.04595409993352
Island	ABO	0.000607430018526128	0.0459605598691872
Island	EIF2C2;EIF2C2	0.00060754613716187	0.0459621653984572
	BTBD11	0.000607843447999752	0.0459774758632641
N_Shelf	ADAM8;ADAM8;ADAM8	0.000608172531402063	0.0459915559730664
Island	ACSF3;ACSF3;ACSF3	0.000608219513771724	0.0459915559730664
		0.000608626491754959	0.046015146053578
Island	VASH1	0.000608776081583564	0.0460188867305006
	MAD1L1;MAD1L1;MAD1	0.00060886600148464	0.0460188867305006
N_Shore	TERT;TERT	0.000609410679500913	0.0460468594352919
Island	KCND2	0.000609564282911112	0.0460468594352919
	CPXM2	0.000609574952840227	0.0460468594352919
	LRIG1	0.000609627272300921	0.0460468594352919
Island	ZIC4;ZIC4;ZIC4	0.000609733329569099	0.0460468594352919
S_Shelf	ACSF3;ACSF3;ACSF3	0.000609806548119469	0.0460468594352919
	NLRP8;NLRP8	0.000609993731096363	0.0460538135328521
		0.00061029541152966	0.0460646743617472
Island	MAML3	0.00061046068184664	0.0460646743617472
Island		0.000610494683824441	0.0460646743617472
N_Shore		0.000610518029686791	0.0460646743617472
Island	SNRPF	0.00061069425698165	0.0460707937714389
S_Shore	BAI1	0.000610906144908844	0.0460796010953085
N_Shore	MTNR1B	0.000611027976342404	0.0460816139274423
	JAKMIP1;JAKMIP1	0.000611237527634107	0.0460902406307627
	ADARB2	0.000611824960267831	0.0461011840324197
		0.000611960494486473	0.0461011840324197
S_Shelf	CARKD	0.000611975462171695	0.0461011840324197
S_Shelf	MUC2	0.000612002583985158	0.0461011840324197
N_Shore	C13orf16	0.000612070581933726	0.0461011840324197
	MCCC2	0.000612162742840257	0.0461011840324197
		0.000612180979909441	0.0461011840324197
Island	KCNF1	0.000612215749112877	0.0461011840324197
N_Shore	PCTP;PCTP	0.000612239334530581	0.0461011840324197

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N_Shelf	INPP5A	0.000612647292183146	0.0461247318182189
	CLEC9A;CLEC9A	0.000612762699643126	0.0461262503115724
	SND1	0.000613009857667469	0.0461329311223856
	ZFP30	0.000613041954686778	0.0461329311223856
N_Shore	PABPC1L2B;PABPC1L2	0.000613386230664244	0.0461433910119678
Island	HDAC4	0.000613399719432619	0.0461433910119678
	C15orf33	0.000613558080187504	0.0461433910119678
	CREB5;CREB5;CREB5;	0.000613684881759421	0.0461433910119678
	SYNM;SYNM	0.00061371609911331	0.0461433910119678
Island	LOC440839	0.000613819802450351	0.0461433910119678
S_Shore		0.000614048381090596	0.0461433910119678
		0.000614162699470027	0.0461433910119678
	SMYD3;SMYD3	0.000614346101070704	0.0461433910119678
		0.000614461519118418	0.0461433910119678
	ANKRD17;ANKRD17	0.000614489042179141	0.0461433910119678
		0.000614543355358565	0.0461433910119678
		0.000614568491736831	0.0461433910119678
N_Shore	F10	0.000614590371023635	0.0461433910119678
	MYT1L	0.0006146575479268	0.0461433910119678
	NOTCH4	0.000614944777854499	0.0461433910119678
	BMPR1A	0.000615181472031157	0.0461433910119678
S_Shelf	SRCIN1	0.000615205476848595	0.0461433910119678
	FAM198B;FAM198B;FA	0.000615225821484996	0.0461433910119678
	WVOX	0.000615420506779757	0.0461433910119678
N_Shelf	KIAA0182;KIAA0182	0.000615493812638648	0.0461433910119678
N_Shelf	RPH3AL	0.000615519414593147	0.0461433910119678
	PCSK9	0.000615734730833692	0.0461433910119678
N_Shelf	CUL4A;CUL4A	0.000615755387867809	0.0461433910119678
		0.00061595567214425	0.0461433910119678
Island	LOC642006	0.000616032114390963	0.0461433910119678
	CD247;CD247	0.00061637900958333	0.0461433910119678
Island	COL4A1	0.00061646927511189	0.0461433910119678
Island	CXorf36	0.000616489657653135	0.0461433910119678
	TMEM86B;SAPS1	0.000616541281776572	0.0461433910119678
S_Shore	CPSF1	0.000616606149236516	0.0461433910119678
Island		0.00061662410260084	0.0461433910119678
Island	OPCML	0.000616637488140152	0.0461433910119678
	PBX1	0.000616758505610733	0.0461433910119678
		0.000616843507553907	0.0461433910119678
	SLC7A9;SLC7A9;SLC7A	0.000616900573579692	0.0461433910119678
	CUX1;CUX1;CUX1	0.000616904242208828	0.0461433910119678
S_Shelf		0.00061690578684899	0.0461433910119678
		0.00061694861260865	0.0461433910119678
	ANKH	0.000617067988586095	0.0461433910119678
	UBR3	0.000617144116117142	0.0461433910119678
N_Shelf	INPP5A	0.000617182443556553	0.0461433910119678
S_Shore	L3MBTL3;L3MBTL3	0.000617720269800102	0.0461764731703865
Island	HLA-DQB2	0.000617892920328001	0.0461822513330029
	NXN	0.000618569656741758	0.0462045541085238
Island	KCNQ2;KCNQ2;KCNQ2	0.000618711836752334	0.0462045541085238
Island	KDM2B;KDM2B	0.000618733661859854	0.0462045541085238
N_Shore	CTBP1;CTBP1	0.000618827946826755	0.0462045541085238
S_Shelf	PRICKLE3	0.000618928553221737	0.0462045541085238
		0.000619082181868973	0.0462045541085238
Island	MAGEE1	0.000619084638077657	0.0462045541085238

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	CD80	0.00061918691771716	0.0462045541085238
Island	CNGB1	0.000619276037879314	0.0462045541085238
	CDK13;CDK13	0.000619280466038399	0.0462045541085238
S_Shelf	FGF5;FGF5	0.000619357812282396	0.0462045541085238
		0.000619445785167944	0.0462045541085238
Island	C20orf135	0.000619666664960671	0.0462045541085238
	TNFAIP8	0.000619722315383282	0.0462045541085238
N_Shore	CPA1	0.000619763911426181	0.0462045541085238
	SULT1C4	0.000619852478947742	0.0462045541085238
N_Shelf	PRDM11	0.000619889348918642	0.0462045541085238
	TRERF1	0.000619908517208874	0.0462045541085238
		0.000620584387413906	0.0462400105759211
	HDLBP;HDLBP	0.000620704087540525	0.0462400105759211
S_Shore	TIGD2;TIGD2	0.000620719880091291	0.0462400105759211
	AGAP1;AGAP1	0.000620766115242118	0.0462400105759211
		0.000620905217045087	0.0462432599177859
N_Shore	MIR127;RTL1	0.000621118982195392	0.0462520681198929
N_Shore	PCDHB18	0.000621360027842892	0.0462533844162262
N_Shelf		0.000621428720731748	0.0462533844162262
S_Shore	PIWIL1	0.000621472559489562	0.0462533844162262
Island	MAD1L1;MAD1L1;MAD1	0.000621518661602849	0.0462533844162262
	WFDC1	0.000621630848081529	0.0462546259789655
	ANKH	0.000622280515976012	0.0462833873347381
Island		0.00062231031490078	0.0462833873347381
S_Shore	FANCM	0.000622349195018997	0.0462833873347381
	TRAF3IP2;TRAF3IP2;TRAF3IP2	0.000622410045844687	0.0462833873347381
		0.000622618470947108	0.0462833873347381
Island	NLGN4X;NLGN4X	0.000622724702051907	0.0462833873347381
Island	KIAA1549;KIAA1549	0.000622741180689698	0.0462833873347381
	AKAP6	0.00062278188253856	0.0462833873347381
	FAM46C	0.000622959969549685	0.0462834610587069
		0.000623094197703091	0.0462834610587069
	FLJ22536	0.000623178757626776	0.0462834610587069
Island	AHRR	0.000623313048887791	0.0462834610587069
Island		0.000623411427789642	0.0462834610587069
Island	CCDC40	0.00062346886986348	0.0462834610587069
	DOCK1	0.000623585704238546	0.0462834610587069
S_Shore	DKK2	0.000623684054279414	0.0462834610587069
	TRIM39;TRIM39	0.000623771819058212	0.0462834610587069
N_Shelf	ZNF415;ZNF415;ZNF415	0.000623857082103003	0.0462834610587069
S_Shelf	NCOR2;NCOR2	0.000624046501230588	0.0462834610587069
	TAS2R4	0.000624058697892214	0.0462834610587069
	TGFBR3	0.00062409087364216	0.0462834610587069
Island	TOP1MT	0.000624154118016166	0.0462834610587069
S_Shelf	PLXNA3	0.000624216316802713	0.0462834610587069
Island	UNKL	0.000624396952091975	0.0462897679200897
Island		0.000624849835388523	0.0463162529116233
N_Shore	UBE2DNL	0.000625039136550777	0.0463231950742089
S_Shelf		0.000625173971949899	0.046326099137796
		0.00062534750483641	0.0463283309973098
	C10orf108;C10orf108;D	0.000625516140551852	0.0463283309973098
N_Shore		0.000625626739537487	0.0463283309973098
		0.000625832723275353	0.0463283309973098
		0.00062594559632981	0.0463283309973098
Island		0.00062610473321152	0.0463283309973098

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Island	LOC642006	0.000626178517904685	0.0463283309973098
	WDR27	0.00062629020091694	0.0463283309973098
Island		0.000626332674215661	0.0463283309973098
Island	RASD2	0.000626358191206224	0.0463283309973098
	MYH6	0.000626395439809542	0.0463283309973098
Island		0.000626407676549402	0.0463283309973098
N_Shore		0.000626447612040224	0.0463283309973098
Island	PANK4	0.000626565771695851	0.0463299950193272
Island	HOXD10	0.000626991161224266	0.0463434744457148
	SNTG2	0.000627032671369422	0.0463434744457148
	DNAJB13	0.000627035127327248	0.0463434744457148
	SPDYE1;POLR2J4	0.000627192126726632	0.0463480053062063
Island	LPAR2	0.000627442452676556	0.0463581244310731
Island		0.000627524620926405	0.0463581244310731
Island	ZNF668	0.000627616212036435	0.0463581244310731
N_Shore	PRICKLE1;PRICKLE1;P	0.000628140135473035	0.0463782916373376
Island	AGRN	0.00062818446590552	0.0463782916373376
	FHIT;FHIT	0.00062836835845667	0.0463782916373376
S_Shore	ZPBP;ZPBP	0.000628386313734392	0.0463782916373376
	ADAMTS9	0.000628479176421667	0.0463782916373376
Island	DBP	0.000628499767415292	0.0463782916373376
Island	TBX3;TBX3	0.000628589978392987	0.0463782916373376
Island		0.000628802463800588	0.0463782916373376
	RBM4B	0.000629003786486602	0.0463782916373376
S_Shore	WDR8	0.000629020476659876	0.0463782916373376
Island		0.000629033037832058	0.0463782916373376
		0.000629136770218926	0.0463782916373376
		0.000629282143357475	0.0463782916373376
Island	NELF;NELF;NELF;NELF	0.000629512272287213	0.0463782916373376
S_Shelf	C18orf1;C18orf1	0.000629556105803363	0.0463782916373376
Island	ZIC5	0.00062964159339245	0.0463782916373376
		0.000629678917611735	0.0463782916373376
N_Shore	PCDHGA4;PCDHGC3;P	0.000629743733352806	0.0463782916373376
Island	NFKBIL2	0.000629762708885489	0.0463782916373376
	UBE2QL1	0.00062981890529713	0.0463782916373376
Island	CACNA1H;CACNA1H	0.000629900175275707	0.0463782916373376
	FRYL	0.000630056557774685	0.0463827545742855
	DDX54;DDX54	0.000630170482960563	0.0463840910577317
Island	SPSB4	0.000630411963165241	0.0463911591719564
Island	NHSL2;RGAG4	0.000630583007960623	0.0463911591719564
S_Shore	PEG3;PEG3;ZIM2;ZIM2	0.000630647118857013	0.0463911591719564
Island	RBM24;RBM24	0.000630795987702423	0.0463911591719564
Island		0.000631003730394423	0.0463911591719564
	ECE1;ECE1;ECE1;ECE	0.000631151979903826	0.0463911591719564
Island	RCVRN	0.000631195686719501	0.0463911591719564
	C9orf46	0.000631446265658358	0.0463911591719564
	CUX2	0.000631463434825869	0.0463911591719564
Island	RALGAPB	0.000631474048411393	0.0463911591719564
	MEF2C;MEF2C	0.000631574005892342	0.0463911591719564
	FBXO18;FBXO18	0.000631629822997483	0.0463911591719564
	HEATR2	0.000631718437436649	0.0463911591719564
		0.0006317671168109	0.0463911591719564
N_Shelf	SFRS8	0.000631782402409049	0.0463911591719564
	C14orf143	0.000631799072726422	0.0463911591719564
	PDE4DIP;PDE4DIP;PDE	0.00063196438293888	0.0463933596114943

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	BMP3	0.00063202061986608	0.0463933596114943
	KLHL29	0.000632159677912471	0.0463965352333622
	RASSF4	0.000632447508444733	0.0464091340114133
	ATF6B;ATF6B	0.000632549775112473	0.0464091340114133
S_Shore	FAM66B	0.000632672061591961	0.0464091340114133
	MAGEC1	0.000632818285499604	0.0464091340114133
Island	TFAP2B	0.000632861896418964	0.0464091340114133
Island	C20orf195	0.000633065640131972	0.0464091340114133
N_Shore		0.000633422262417659	0.0464091340114133
Island	AGAP1;AGAP1	0.000633625949267365	0.0464091340114133
	ARHGAP15	0.000633682535873741	0.0464091340114133
N_Shelf	CREBBP;CREBBP	0.000633766699219139	0.0464091340114133
S_Shore	KIF7	0.00063379518311308	0.0464091340114133
	GTF3C1	0.000634036167892604	0.0464091340114133
	MIR25;MCM7;MCM7;MI	0.000634047895578667	0.0464091340114133
	KLHL29	0.000634147807815234	0.0464091340114133
Island	BCOR;BCOR	0.000634158986126117	0.0464091340114133
	IGSF9B	0.000634164664308159	0.0464091340114133
N_Shelf	LPXN;LPXN	0.00063433463491419	0.0464091340114133
N_Shore	DHFR;MSH3	0.000634481805349267	0.0464091340114133
N_Shore	SMYD3;SMYD3	0.000634673996111575	0.0464091340114133
Island	HOXC4;HOXC6;HOXC5	0.000634725829589856	0.0464091340114133
N_Shore	PGAM5;PGAM5;PGAM5	0.000634778885229543	0.0464091340114133
Island		0.000634783744802273	0.0464091340114133
N_Shore		0.000634800835767307	0.0464091340114133
Island	MIR548F5;NBEA	0.00063484561223895	0.0464091340114133
N_Shore		0.000634897109204859	0.0464091340114133
	OPCML	0.000634948031965066	0.0464091340114133
	CRAMP1L	0.000634975229460887	0.0464091340114133
		0.000635014362450082	0.0464091340114133
	PTPRN2;PTPRN2;PTPR	0.000635258542461491	0.0464199748910171
	PCP4	0.000635530385833248	0.0464283386550806
	ARL1	0.000635597842216492	0.0464283386550806
S_Shore	SLC6A15;SLC6A15;SLC	0.000635732323529788	0.0464283386550806
N_Shore	ACOX3;ACOX3	0.000635756448584101	0.0464283386550806
	ST5;ST5;ST5	0.00063596372672316	0.0464364739854055
		0.000636452963660859	0.0464513677638376
Island	PLXNA3	0.000636495534858934	0.0464513677638376
S_Shore	ERICH1	0.000636513015879502	0.0464513677638376
S_Shelf	ADORA2A	0.000636657271306433	0.0464513677638376
Island	BRD9;BRD9;BRD9	0.000636766840263033	0.0464513677638376
Island	SPAG6;SPAG6	0.000636815583711304	0.0464513677638376
Island	BANP;BANP	0.000636905884347191	0.0464513677638376
	RGS9;RGS9;RGS9	0.000636934978206051	0.0464513677638376
Island	CEP72	0.000637149055800745	0.0464570261376557
	MAD1L1;MAD1L1;MAD1	0.000637204407438078	0.0464570261376557
	MED13L	0.00063741340546711	0.0464652690552164
Island	NFIC;NFIC	0.00063777802532358	0.0464742195064277
N_Shore	RARS2;ORC3L;ORC3L	0.000637840733748274	0.0464742195064277
		0.000637935518720609	0.0464742195064277
N_Shelf		0.000638115550126537	0.0464742195064277
		0.000638267599044155	0.0464742195064277
	SCN8A	0.000638321523426357	0.0464742195064277
	KAT2B	0.000638336809481444	0.0464742195064277
		0.000638478453305392	0.0464742195064277

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		0.000638490730684638	0.0464742195064277
		0.0006387156626679	0.0464742195064277
	CNOT2	0.000638791371779528	0.0464742195064277
	SPSB1	0.000638915353076335	0.0464742195064277
Island	RRP1B;HSF2BP	0.000638957626852172	0.0464742195064277
Island	WDR1;WDR1	0.000638962783155444	0.0464742195064277
S_Shore	OSBPL5;OSBPL5;OSBF	0.000639022700421614	0.0464742195064277
	WDR27	0.000639147617555493	0.0464742195064277
Island		0.000639368430928281	0.0464742195064277
Island	SLCO6A1;SLCO6A1	0.000639401772913232	0.0464742195064277
Island		0.000639439680050868	0.0464742195064277
	SHANK2;SHANK2	0.000639469389362397	0.0464742195064277
	MGMT	0.000639551278604947	0.0464742195064277
N_Shore		0.000639652410435486	0.0464745955121762
Island		0.000639790445984422	0.0464776522800967
		0.000640135220974395	0.0464786401988291
	TSSC1	0.000640271181816966	0.0464786401988291
Island	INSR;INSR	0.000640273857772891	0.0464786401988291
N_Shore	FAM135A;FAM135A	0.000640336963107271	0.0464786401988291
Island		0.000640343859446268	0.0464786401988291
Island		0.000640431472844577	0.0464786401988291
	SPOCK2	0.000640545929589531	0.0464786401988291
	TP63;TP63;TP63;TP63;	0.000640615338875208	0.0464786401988291
Island	SLC37A1	0.000640667737505565	0.0464786401988291
Island		0.000640960393654886	0.0464825113064015
	PRUNE2;PCA3	0.00064101215718605	0.0464825113064015
	RADIL	0.000641232768068996	0.0464825113064015
Island	DPYS	0.00064124877598731	0.0464825113064015
	OLR1	0.000641270144805433	0.0464825113064015
	RASGRF2	0.000641375657242568	0.0464825113064015
		0.000641396731022764	0.0464825113064015
Island	LHX6;LHX6	0.000641488887775745	0.0464825113064015
	CHST11	0.000641782967529579	0.046496863986352
N_Shelf		0.00064192214357964	0.0464999913534563
Island	FAT4	0.000642039940479897	0.0465012767382878
Island	TULP1	0.000642356574129579	0.0465012767382878
	MEIS2;MEIS2;MEIS2;M	0.000642422345425876	0.0465012767382878
	TSNARE1	0.000642530175888049	0.0465012767382878
N_Shore	PHF1;PHF1;PHF1	0.000642612200709311	0.0465012767382878
		0.000642653809853601	0.0465012767382878
	CSMD3;CSMD3;CSMD3	0.00064267810333749	0.0465012767382878
N_Shelf		0.000642707988408813	0.0465012767382878
Island	SMAD7	0.000642888378850506	0.0465026310104496
	ADAM5P	0.000643054586526412	0.0465026310104496
Island	CTDP1;CTDP1	0.000643083757094555	0.0465026310104496
		0.000643146087900356	0.0465026310104496
Island	OPCML	0.000643206782922629	0.0465026310104496
		0.000643380443990096	0.0465082438112692
S_Shore	FNDC1	0.000643544595803073	0.0465131676409974
	TUBA3C	0.000643748341474765	0.0465209512809259
S_Shore	LHFPL2	0.000643878055930495	0.0465233834758372
N_Shore	FOXN2	0.000644317943470324	0.0465482231460717
	LOC150568	0.000644659210416054	0.0465549211215754
Island		0.000644741664880487	0.0465549211215754
	C3orf59	0.000644897156335521	0.0465549211215754

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	CUX1;CUX1;CUX1	0.000645080947366306	0.0465549211215754
Island	PDE4D;PDE4D	0.000645412956993668	0.0465549211215754
Island	MAD1L1;MAD1L1;MAD1	0.000645543809920653	0.0465549211215754
	GH1;GH1;GH1;GH1;GH1	0.000645584995071513	0.0465549211215754
Island	DOK6	0.000645589480855814	0.0465549211215754
	SYNM;SYNM	0.000645617109910479	0.0465549211215754
		0.000645634379708904	0.0465549211215754
N_Shelf	HOXC4;HOXC5;HOXC6	0.000645648288249044	0.0465549211215754
Island	TBCD	0.000645779350239453	0.0465549211215754
N_Shelf	RBM12B	0.000646078084480476	0.0465549211215754
Island	GSX1	0.000646445462636687	0.0465549211215754
Island	BCL11B;BCL11B	0.000646463666647177	0.0465549211215754
Island	RINL	0.00064650645051981	0.0465549211215754
N_Shore		0.000646520295802723	0.0465549211215754
Island	EPPK1	0.000646697464415141	0.0465549211215754
S_Shore		0.000646704053884001	0.0465549211215754
S_Shore	GPR20	0.000646814118234962	0.0465549211215754
N_Shore	LOC645323;LOC645323	0.00064685943532883	0.0465549211215754
		0.000647090198325283	0.0465549211215754
	DAB1	0.000647117027570229	0.0465549211215754
S_Shelf	KCTD15;KCTD15;KCTD	0.000647119346304185	0.0465549211215754
Island	AFAP1;AFAP1;LOC8474	0.000647131813820379	0.0465549211215754
N_Shelf		0.000647236051016477	0.0465549211215754
S_Shore	ABR;ABR;ABR	0.000647266821476501	0.0465549211215754
	GPR98;GPR98	0.000647293938867354	0.0465549211215754
Island		0.000647343856326819	0.0465549211215754
Island	GTF2A1L;STON1-GTF2	0.000647389579525239	0.0465549211215754
Island	CTBP1;CTBP1	0.000647390479025057	0.0465549211215754
	NXN	0.000647658227220425	0.0465605435506205
	TEX13B;TEX13B	0.00064774655297433	0.0465605435506205
Island		0.00064805621224195	0.0465605435506205
	EIF3A	0.000648064971555652	0.0465605435506205
N_Shore	EIF2C2;EIF2C2	0.000648092793722421	0.0465605435506205
Island	PCDHGA4;PCDHGA6;P	0.000648182085540749	0.0465605435506205
N_Shelf		0.00064823443126055	0.0465605435506205
S_Shore		0.000648282118620982	0.0465605435506205
N_Shore		0.000648361283704062	0.0465605435506205
Island	PRKAR1B;PRKAR1B;P	0.000648647455188928	0.0465605435506205
	ITGA6;ITGA6	0.000648739858527168	0.0465605435506205
Island		0.000649339508515523	0.0465605435506205
S_Shore	CLCN7;CLCN7	0.000649503392041194	0.0465605435506205
		0.000649638463347952	0.0465605435506205
	ARHGEF10	0.000649805233578814	0.0465605435506205
N_Shore		0.000649819272552391	0.0465605435506205
	KIAA0182;KIAA0182	0.000649981772950229	0.0465605435506205
S_Shore	STK19;STK19;DOM3Z;S	0.000650033446770507	0.0465605435506205
		0.000650076622304224	0.0465605435506205
Island	LRP5	0.000650092673229651	0.0465605435506205
Island	SST;SST	0.000650103360494307	0.0465605435506205
		0.000650136752617075	0.0465605435506205
Island	SLITRK5	0.000650210138956636	0.0465605435506205
Island	SLC16A2	0.000650213132499419	0.0465605435506205
	MSI2	0.000650397810381855	0.0465605435506205
		0.000650458575475502	0.0465605435506205
	WDFY4	0.000650465740132544	0.0465605435506205

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		0.000650524509502592	0.0465605435506205
S_Shelf	MPZL1;MPZL1;MPZL1	0.000650597472414376	0.0465605435506205
Island	TRIM7;TRIM7;TRIM7;TRIM7	0.000650686996985336	0.0465605435506205
	CLRN2	0.000650708834858198	0.0465605435506205
Island	SLC24A3	0.000650760921526066	0.0465605435506205
	SIPA1L2	0.000650775280451323	0.0465605435506205
Island	LOC389493	0.000650826630027124	0.0465605435506205
		0.000650901866405455	0.0465605435506205
S_Shelf	TUBB	0.00065102340544206	0.0465605435506205
S_Shelf		0.000651025656170551	0.0465605435506205
Island	GRM2;GRM2	0.000651218518202752	0.0465643997168208
Island	HEATR2	0.000651271860180135	0.0465643997168208
N_Shore	ACVR2A	0.000651455816118953	0.0465706772165036
S_Shelf		0.000651806979084633	0.0465748458229961
Island		0.00065187920771655	0.0465748458229961
Island	C2orf70	0.000652096133456972	0.0465748458229961
S_Shore		0.00065211988587835	0.0465748458229961
Island	CELSR3	0.000652228888044427	0.0465748458229961
		0.000652284181717972	0.0465748458229961
		0.000652305041266907	0.0465748458229961
		0.000652437190899374	0.0465748458229961
S_Shore	ABR;ABR;ABR	0.000652450388731103	0.0465748458229961
	CPOX	0.000652475773311369	0.0465748458229961
		0.000653010817113337	0.0466059310900471
	PMM2	0.000653103709922365	0.0466059310900471
S_Shore	OSBPL5;OSBPL5;OSBPL5	0.000653354757677605	0.0466169774620221
		0.000653466335563185	0.0466180708457268
S_Shore	VENTXP1	0.000653575740498349	0.0466190089126455
	TCF12;TCF12;TCF12;TCF12	0.000653680631608986	0.0466196247833931
		0.000653858981641189	0.0466254786930755
S_Shelf		0.000654069324883961	0.0466272056088027
N_Shelf	SRY;SRY	0.000654079351061542	0.0466272056088027
	SPTBN2	0.000654197946411295	0.0466272056088027
N_Shelf	CYP1A1	0.000654268289511017	0.0466272056088027
N_Shore		0.000654617720857065	0.0466440009767414
	NXN	0.000654696574902985	0.0466440009767414
	TTL5	0.00065482181453223	0.0466444499700033
		0.000654895493307226	0.0466444499700033
S_Shelf	CARKD	0.000655105481737487	0.0466464209664163
Island	SLC25A29	0.000655320376924092	0.0466464209664163
S_Shelf		0.000655535809498728	0.0466464209664163
S_Shore	PCYT2	0.000655646903999601	0.0466464209664163
Island	FRMD1;FRMD1	0.000655682839278248	0.0466464209664163
Island	SHROOM4;SHROOM4;SHROOM4	0.000655699172228083	0.0466464209664163
Island	RNF126P1	0.000655749959947535	0.0466464209664163
		0.000655792113801308	0.0466464209664163
	LHFPL4	0.000655845819439279	0.0466464209664163
N_Shore	NXN	0.000655886288713767	0.0466464209664163
	PCYT1A	0.000656169139226401	0.0466546766620807
Island		0.000656195029003446	0.0466546766620807
		0.000656316893606468	0.046654686235893
	NXN	0.000656479741121869	0.046654686235893
	OR11L1	0.000656484151546194	0.046654686235893
N_Shelf	SDCCAG1	0.000656894709699985	0.0466770144183458
		0.000657238459541225	0.0466801217179992

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N_Shore	WDR16;WDR16	0.000657302033767727	0.0466801217179992
	MIR1185-2;MIR1185-1	0.000657376630285439	0.0466801217179992
S_Shore		0.000657415246022381	0.0466801217179992
Island		0.000657463188204949	0.0466801217179992
Island	NRN1	0.000657516730212545	0.0466801217179992
Island	CLIC6	0.000657733365512541	0.0466886578120858
Island	PQLC1;PQLC1;PQLC1	0.000657999295575501	0.0466965809793171
	HNF4A;HNF4A;HNF4A;	0.000658037815896019	0.0466965809793171
		0.000658162046048282	0.0466985544905265
S_Shore	SPTBN4	0.000658472893018762	0.0467137665023161
Island		0.000658589818055149	0.0467152187506678
N_Shore		0.000658695324350428	0.046715860735982
	TRIO	0.000659056682949626	0.0467238581715115
	KIF26B	0.000659063713023332	0.0467238581715115
N_Shore		0.000659112555807932	0.0467238581715115
Island	KIF26A	0.000659193976949235	0.0467238581715115
Island	NKX2-8	0.000659380439855269	0.0467302358110775
Island	TIE1	0.000659546886089318	0.0467351932121739
Island		0.000659673933893435	0.046737357816404
Island	STK32C	0.00065980224826908	0.0467396115098614
		0.00065995805382597	0.0467412598519276
Island	ARRDC2;ARRDC2;ARR	0.000660029547335761	0.0467412598519276
	CALN1	0.000660115041319743	0.0467412598519276
	ANXA11;ANXA11;ANXA	0.00066038721308696	0.046751657692104
S_Shelf		0.000660620777965027	0.046751657692104
	SFRS18;SFRS18	0.000660633623227916	0.046751657692104
	NDUFAF4	0.000660661922880035	0.046751657692104
	LEPR;LEPR;LEPR	0.000661378091728149	0.046751657692104
N_Shore	PDP2	0.000661382468624569	0.046751657692104
S_Shore	ADD1;ADD1;ADD1;ADD	0.000661412168547589	0.046751657692104
N_Shore	ATP11A;ATP11A	0.000661431023384129	0.046751657692104
	TRIO	0.000661434107976981	0.046751657692104
Island	LRRC33	0.000661523060242749	0.046751657692104
	PPP1R3B	0.000661562453469252	0.046751657692104
N_Shore	NGEF;NGEF	0.000661631569830507	0.046751657692104
N_Shore	PCDHB4	0.000661731269715534	0.046751657692104
S_Shore	GIGYF1	0.000661765127857554	0.046751657692104
	TTY15	0.000661779316280441	0.046751657692104
N_Shore	PIGG;PIGG	0.00066180635964913	0.046751657692104
N_Shore	POLB	0.000662065418524734	0.0467603579871366
	PPARD;PPARD	0.000662198883876687	0.0467603579871366
Island	ISL1	0.000662219161583173	0.0467603579871366
		0.00066233537189784	0.0467617462090993
Island	ZCCHC24	0.000662810772711896	0.0467783024377536
N_Shore	ZNF83	0.000663053666843761	0.0467783024377536
	ANKFY1	0.000663063808144462	0.0467783024377536
Island	CETN1	0.000663191773259664	0.0467783024377536
S_Shelf	INPP5A	0.000663199766150272	0.0467783024377536
Island	GNA11	0.000663278423568863	0.0467783024377536
	KLHL32	0.000663310168481016	0.0467783024377536
Island	C7orf68;C7orf68	0.00066334255126721	0.0467783024377536
Island		0.000663560641604932	0.046786869667391
	VAR5	0.000663920442626527	0.0467970978236616
	DKC1;SNORA36A;DKC	0.000663994226017215	0.0467970978236616
	PHF14;PHF14	0.000664093323018475	0.0467970978236616

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		0.00066412654008083	0.0467970978236616
Island	MAP1LC3A;MAP1LC3A	0.000664262138910909	0.0467970978236616
Island	PCDHGA4;PCDHGA2;P	0.000664476670956343	0.0467970978236616
	ANTXR1;ANTXR1;ANTX	0.000664494715625019	0.0467970978236616
	PRPF40B;PRPF40B	0.000664572106841933	0.0467970978236616
		0.000664575313748299	0.0467970978236616
Island	ABCA2;ABCA2	0.000664878362395923	0.0467978725300959
	MCF2	0.000665033019903588	0.0467978725300959
Island	CHST12	0.000665083481725408	0.0467978725300959
S_Shore	TBCD	0.000665109004941589	0.0467978725300959
	ABI2	0.000665256803102208	0.0467978725300959
	BAIAP2;BAIAP2;BAIAP2	0.000665276997539404	0.0467978725300959
		0.000665325951388122	0.0467978725300959
N_Shore	HMG20B	0.000665359315010045	0.0467978725300959
	NHSL2;RPS26P11	0.000665465625923275	0.0467985536917802
	ADARB2	0.00066600505733262	0.0468076642948195
	OR2T5	0.000666028926817791	0.0468076642948195
N_Shore	FAM122A;PIP5K1B	0.00066608945177974	0.0468076642948195
Island	MSC	0.000666154206403848	0.0468076642948195
Island		0.000666161523799165	0.0468076642948195
Island	TUBB6	0.000666175047714223	0.0468076642948195
	IQCE;IQCE	0.000666298605091792	0.046809554962443
Island	FLJ37453	0.000666420920478062	0.046811357840542
	RNF40	0.000666542117329067	0.0468130816379641
		0.000666695135944301	0.0468170395412822
S_Shelf	SMAD6;SMAD6	0.000666845585684701	0.0468208159302323
S_Shelf	EMP3	0.000667063577819441	0.0468243968723097
S_Shore	LOC645323	0.000667089946665848	0.0468243968723097
N_Shore	PSMA8;PSMA8;PSMA8	0.000667347620617796	0.0468315945595135
	BPIL3	0.000667455918647291	0.0468315945595135
	SERPINE2;SERPINE2;S	0.000667482573157119	0.0468315945595135
S_Shelf		0.000667771554437077	0.0468386005334764
N_Shelf		0.000667869746948582	0.0468386005334764
		0.000667872555173051	0.0468386005334764
	TRIO	0.00066802038140599	0.0468421849173963
N_Shore	GAK	0.000668251117858449	0.0468515811605086
N_Shelf	EDEM3	0.000668572840035362	0.0468517000185243
Island	XAB2	0.000668596919367028	0.0468517000185243
		0.000668645692076557	0.0468517000185243
S_Shelf		0.000668741795487772	0.0468517000185243
N_Shelf	WDR8	0.00066891815830173	0.0468517000185243
S_Shore	FOXK1	0.00066895380138334	0.0468517000185243
S_Shore	GJA4	0.000669041793228293	0.0468517000185243
N_Shelf	DZIP1L;DZIP1L	0.00066906865159646	0.0468517000185243
	AGAP3	0.000669123437832308	0.0468517000185243
		0.000669369865209462	0.0468583221510784
N_Shelf	PTPRN2;PTPRN2;PTPF	0.000669550544014224	0.0468583221510784
S_Shelf		0.000669576871768709	0.0468583221510784
N_Shore	ABR;ABR;ABR	0.00066970538945996	0.0468583221510784
		0.000669742450280687	0.0468583221510784
N_Shore	PAX3;PAX3;PAX3;CCD	0.000670076919228809	0.0468583221510784
Island	ADARB2	0.000670181331599354	0.0468583221510784
S_Shelf	ACSF3;ACSF3;ACSF3	0.00067018507078131	0.0468583221510784
Island	CNTNAP5	0.000670197835353329	0.0468583221510784
N_Shelf		0.000670289077654844	0.0468583221510784

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S_Shore	FGF20;FGF20	0.000670375047510006	0.0468583221510784
		0.000670553558785858	0.0468583221510784
		0.00067063976617918	0.0468583221510784
Island	C18orf1;C18orf1	0.00067079046690222	0.0468583221510784
Island	ATP8B1	0.000670824933417341	0.0468583221510784
		0.000670879343847152	0.0468583221510784
Island		0.000670978546610371	0.0468583221510784
		0.000671040634902236	0.0468583221510784
	JPH3	0.000671088895775653	0.0468583221510784
Island	DUOX2	0.000671330750574952	0.0468583221510784
	TSSC1	0.000671374329673513	0.0468583221510784
N_Shore	TBCD	0.000671484899907667	0.0468583221510784
Island	PTPRS;PTPRS;PTPRS;	0.000671507293404694	0.0468583221510784
	ARV1	0.000671597989760211	0.0468583221510784
Island		0.000671636757080031	0.0468583221510784
S_Shore	LOC100132831	0.000672047113849349	0.0468771118495367
		0.000672203755991084	0.0468771118495367
	KIAA0430	0.000672417317616782	0.0468771118495367
	NOL10	0.000672420302575846	0.0468771118495367
N_Shore	PHOX2B	0.000672630925552829	0.0468771118495367
		0.000672706185079957	0.0468771118495367
N_Shore		0.000672878445857639	0.0468771118495367
	EFNB2	0.000673114052127059	0.0468771118495367
	JDP2;JDP2;JDP2;JDP2	0.000673188777787165	0.0468771118495367
	PLEKHG4B	0.000673240295977048	0.0468771118495367
	PVRL1;PVRL1;PVRL1	0.000673464618406885	0.0468771118495367
	MMP27	0.000673479737431948	0.0468771118495367
N_Shelf		0.000673550677475309	0.0468771118495367
		0.000673586644459236	0.0468771118495367
Island		0.000673610741704126	0.0468771118495367
Island	GRIN3B	0.000673631012880596	0.0468771118495367
N_Shore	DIP2C	0.000673705916262473	0.0468771118495367
S_Shore	MAP7D2;MAP7D2;MAP	0.000673708134563433	0.0468771118495367
	N6AMT2	0.00067374505876142	0.0468771118495367
	C13orf30	0.000673908792082378	0.04688176899243
	C1orf162	0.000674138709475772	0.0468884995559696
Island		0.000674199165658953	0.0468884995559696
	NXF2B;NXF2;NXF2	0.000674772620518771	0.0469043520752432
	PEX14	0.000674929029774627	0.0469043520752432
Island	CCDC105;CCDC105	0.00067495647000162	0.0469043520752432
		0.000674976074104927	0.0469043520752432
Island		0.000675003672850191	0.0469043520752432
		0.000675128494731413	0.0469043520752432
Island	BMP6	0.000675147514616941	0.0469043520752432
	UXS1	0.000675322652326405	0.0469043520752432
Island	ATP5G2;ATP5G2	0.000675489154765822	0.0469043520752432
		0.000675562414458849	0.0469043520752432
	ARNT2	0.000675582427857578	0.0469043520752432
S_Shore	FOXK2	0.000675793293215658	0.0469043520752432
Island	SIX3	0.000675818355922043	0.0469043520752432
	CCDC149;CCDC149	0.000675843476868938	0.0469043520752432
	C3orf21	0.000675879777284101	0.0469043520752432
N_Shelf	TRAPPC9;TRAPPC9	0.000676160985378898	0.0469171445907786
		0.000676346453365086	0.0469232912227539
S_Shore	KCNG2	0.000676554812071901	0.0469310239697398

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Island	MYT1	0.000676982137902606	0.0469326596389177
	ANK2;ANK2;ANK2	0.000677164430332331	0.0469326596389177
N_Shore		0.000677278557753502	0.0469326596389177
		0.000677337779691877	0.0469326596389177
Island	CHD7	0.00067737189688641	0.0469326596389177
		0.000677385831408042	0.0469326596389177
Island	FSCN2;FSCN2	0.000677411155520908	0.0469326596389177
N_Shore	NSD1;NSD1	0.000677429110876382	0.0469326596389177
	TRPV1;TRPV1;TRPV1;T	0.000677450520901613	0.0469326596389177
Island	EPHB2;EPHB2	0.000677603757423068	0.0469365617582848
N_Shore	CHORDC1;CHORDC1	0.000677904959747348	0.0469507106577484
Island	SMYD3;SMYD3	0.000678010806235601	0.0469513273849095
	DST;DST;DST;DST;DS	0.00067818792942583	0.0469560081521636
	DDX54;DDX54;CCDC42	0.000678343121987526	0.0469560081521636
	PPFIBP1;PPFIBP1	0.000678398351177929	0.0469560081521636
	CCDC88C	0.00067863560056206	0.0469560081521636
	MIR770;MEG3;MEG3;M	0.000678653955218144	0.0469560081521636
Island	GPR39	0.000678660108532793	0.0469560081521636
	GPR133	0.000679102137172346	0.0469798803865157
Island		0.000679531553249852	0.0470028733972772
		0.000679687900012083	0.0470069744642799
		0.000679828264148591	0.047007046514856
Island		0.000679892262569501	0.047007046514856
Island		0.000679980112286339	0.047007046514856
Island	FAM9A;FAM9A	0.00068050117280002	0.0470215141296183
N_Shore	MTNR1B	0.000680526878217428	0.0470215141296183
N_Shelf	PIP4K2A	0.000680720379690216	0.0470215141296183
S_Shore	RGS6	0.000680733766096273	0.0470215141296183
Island		0.000680812051729325	0.0470215141296183
	MCTP2;MCTP2	0.000681088513129673	0.0470215141296183
	C4orf50	0.000681342707701202	0.0470215141296183
Island	ELL	0.000681395952876554	0.0470215141296183
Island		0.000681416965298298	0.0470215141296183
	NCKAP1;NCKAP1	0.000681505110618975	0.0470215141296183
		0.000681518942730616	0.0470215141296183
		0.000681710871289828	0.0470215141296183
Island	FOXH1	0.000681771376389649	0.0470215141296183
	ATP11A;ATP11A	0.000681808340473047	0.0470215141296183
	ST3GAL4	0.000681873317737701	0.0470215141296183
		0.000681912274731088	0.0470215141296183
	SGCG	0.000682007273474765	0.0470215141296183
Island	HDGFL1	0.000682082768844892	0.0470215141296183
N_Shore	C7orf50;C7orf50;C7orf50	0.000682438374763698	0.0470215141296183
S_Shore	CAMK2B;CAMK2B;CAM	0.000682507390938211	0.0470215141296183
S_Shore	DLX5	0.00068277443717633	0.0470215141296183
Island	PGBD5	0.000682810706897815	0.0470215141296183
		0.000682822108942484	0.0470215141296183
S_Shore	PAPOLB;RADIL	0.000682947956584387	0.0470215141296183
Island	PTPRN2;PTPRN2;PTPR	0.000683099371979342	0.0470215141296183
	ALOX5AP	0.000683290716140111	0.0470215141296183
Island		0.00068333494838209	0.0470215141296183
Island	WNK2	0.000683493644420203	0.0470215141296183
	MYH10	0.000683504364961041	0.0470215141296183
		0.000683569672803442	0.0470215141296183
	NAGPA	0.000683755468531246	0.0470215141296183

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Island	KDR	0.000683764735194621	0.0470215141296183
	GALK2;GALK2	0.000683799818089976	0.0470215141296183
	PAPSS1	0.000683899662215773	0.0470215141296183
	RBM20	0.00068392117681776	0.0470215141296183
	UBTD2	0.000684021317556938	0.0470215141296183
S_Shore	B3GNTL1	0.000684085820170957	0.0470215141296183
	SHANK2	0.000684090491050863	0.0470215141296183
N_Shore	SYCP1	0.00068423326725404	0.0470215141296183
	DCUN1D2	0.000684347474348649	0.0470215141296183
		0.000684564523175546	0.0470215141296183
N_Shore	EHMT2;EHMT2	0.000684587186615735	0.0470215141296183
Island	FGF3	0.00068464811891089	0.0470215141296183
S_Shore	TSSC1	0.000684707122375437	0.0470215141296183
Island	WNT3	0.000684733804275728	0.0470215141296183
Island	ELK1;ELK1	0.000684737661873543	0.0470215141296183
S_Shelf		0.000684795892317993	0.0470215141296183
	SH3YL1;SH3YL1	0.000684958948817245	0.0470215141296183
		0.000685084770174133	0.0470215141296183
S_Shelf	UNC84A;UNC84A	0.00068522937838987	0.0470215141296183
N_Shore	PTPRF;PTPRF	0.000685269494378753	0.0470215141296183
Island	BLCAP;BLCAP;BLCAP;P	0.000685381111229839	0.0470215141296183
S_Shore	JDP2;JDP2;JDP2;JDP2	0.000685391524259329	0.0470215141296183
N_Shore	DIRC3	0.00068543207506345	0.0470215141296183
	GYG2;GYG2	0.000686007908665805	0.0470402077185587
N_Shore	WDR27	0.000686025382936571	0.0470402077185587
		0.000686249709260353	0.0470402077185587
S_Shelf	NCOR2;NCOR2	0.000686421823107903	0.0470402077185587
	TMEM167A;SCARNA18	0.000686441115579111	0.0470402077185587
S_Shore	DIP2C	0.000686546766771393	0.0470402077185587
Island	SYT3;SYT3;SYT3	0.000686638033902532	0.0470402077185587
S_Shore	GALNT9	0.000686928374966232	0.0470402077185587
Island		0.000686938343957939	0.0470402077185587
	FAM9C	0.000687049114243216	0.0470402077185587
		0.000687111605380323	0.0470402077185587
N_Shelf	CDH4	0.000687230553875322	0.0470402077185587
N_Shelf	MAD1L1;MAD1L1;MAD1	0.000687282516871642	0.0470402077185587
	ZNF566;ZNF566;ZNF56	0.000687380672225892	0.0470402077185587
S_Shore	DCHS2;DCHS2	0.000687389847478858	0.0470402077185587
Island	PCDHGA2;PCDHGA3;P	0.000687407529504522	0.0470402077185587
Island		0.000687479582614099	0.0470402077185587
N_Shore	MAPK3;MAPK3;MAPK3	0.000687571953447325	0.0470402077185587
S_Shore	EXOC3	0.000687600348753494	0.0470402077185587
	COLEC10	0.00068764766425114	0.0470402077185587
	ASB4;ASB4	0.000687829659483134	0.0470402077185587
		0.000687841327750649	0.0470402077185587
N_Shelf		0.000687995511494279	0.0470432590846909
	UPP1;UPP1	0.000688121435386488	0.0470432590846909
S_Shelf	MAFK	0.000688177340866226	0.0470432590846909
Island	SRCIN1	0.000688667416878442	0.0470620010687896
Island	SMARCA4;SMARCA4;S	0.000688852178698006	0.0470620010687896
		0.000688902748842497	0.0470620010687896
Island	ZIC4;ZIC4;ZIC4	0.000688903370263675	0.0470620010687896
	LNX1;LNX1	0.000689001140654502	0.0470620010687896
	MYO10	0.000689034531727222	0.0470620010687896
N_Shore	NTM;NTM;NTM;NTM	0.000689247599132569	0.0470640471053223

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N_Shore	CCKBR	0.000689326632533772	0.0470640471053223
Island	KCNK17;KCNK17	0.000689360812504066	0.0470640471053223
	SLC45A2;SLC45A2	0.000689453185799333	0.0470640471053223
		0.000689835838236064	0.0470784583192669
N_Shore	HOXA4	0.000690083191225309	0.0470784583192669
Island		0.000690218853422564	0.0470784583192669
	ADAMTS2;ADAMTS2	0.000690225591779401	0.0470784583192669
Island	TMPRSS6	0.00069025078814565	0.0470784583192669
	SLC24A5	0.000690309744855577	0.0470784583192669
N_Shore	ESRRG	0.00069034472922817	0.0470784583192669
Island		0.000690495046441107	0.0470820798771771
Island		0.000690618788136711	0.0470838885929494
Island	FAM53C;FAM53C	0.000690721748343915	0.0470842801923528
S_Shore		0.000690899566558458	0.0470897737930517
	C2orf80;C2orf80	0.000691107260753986	0.0470973018242119
Island		0.000691329618605429	0.0470994911359494
Island	COASY;COASY;COASY	0.000691333882177183	0.0470994911359494
N_Shore		0.000691608749455048	0.047102162680316
S_Shore	ZNF354B	0.000691674955783683	0.047102162680316
	FBXL5;FBXL5	0.000691784744812474	0.047102162680316
N_Shore	HHIP	0.000691819461408699	0.047102162680316
	SLC38A5	0.000691859361601752	0.047102162680316
Island	HNF1A	0.000692058157677913	0.0471032097888204
	KALRN;KALRN	0.00069206925278944	0.0471032097888204
Island	BRF1;BRF1	0.000692489059363424	0.0471251599938444
N_Shore	LSP1;LSP1;LSP1;LSP1	0.000693023139691071	0.0471433918286925
Island	SHISA6	0.000693150468140477	0.0471433918286925
N_Shore	ATG3	0.00069324956744885	0.0471433918286925
		0.000693255568088664	0.0471433918286925
S_Shore	USP40	0.000693298718821034	0.0471433918286925
Island	POLG;POLG	0.000693341000352608	0.0471433918286925
S_Shore	HIST1H3J	0.000693844663983958	0.0471485112540416
Island	SMYD3;SMYD3	0.000693868620284937	0.0471485112540416
	TCF7L2;TCF7L2;TCF7L	0.000693906199425127	0.0471485112540416
		0.00069395329134691	0.0471485112540416
	ANKFY1	0.000694056934756382	0.0471485112540416
	PHKA1;PHKA1	0.000694060412979718	0.0471485112540416
	NCOA1;NCOA1;NCOA1	0.000694097734457889	0.0471485112540416
	NHSL1;NHSL1	0.000694309203999343	0.0471562621269081
Island	DSCAML1	0.000694426782831385	0.0471576348282124
S_Shelf	ACSF3;ACSF3;ACSF3	0.000694585506060585	0.0471612465410563
Island	IRGQ	0.000694674718058939	0.0471612465410563
	ZC3H18	0.000695062890488736	0.0471742287653817
N_Shelf		0.000695395251146739	0.0471742287653817
Island	COQ10B;COQ10B	0.000695403276974469	0.0471742287653817
N_Shore		0.00069554481287546	0.0471742287653817
N_Shore	FGFR4;FGFR4;FGFR4	0.00069558975833236	0.0471742287653817
	NCOA2	0.000695592215099289	0.0471742287653817
S_Shelf		0.000695670460693173	0.0471742287653817
	ADAM12;ADAM12	0.000695701121971281	0.0471742287653817
Island	SLC8A2	0.000695958252704403	0.0471742287653817
Island		0.000695994148409756	0.0471742287653817
Island	ADCY5	0.000696083498839101	0.0471742287653817
N_Shelf	MAD1L1;MAD1L1;MAD1	0.000696115544276437	0.0471742287653817
	RRP15	0.000696132169485745	0.0471742287653817

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Island	DPP6	0.000696272117363066	0.0471750390360849
		0.000696338933709743	0.0471750390360849
Island	C19orf28;C19orf28;C19d	0.000696549361589922	0.0471774081129469
N_Shore	MSX1	0.000696568720209949	0.0471774081129469
		0.000696709997775536	0.0471803788692165
N_Shelf	MCF2L;MCF2L	0.000696845446196808	0.0471829541072654
S_Shelf		0.000697011194118113	0.0471875798981346
Island		0.000697302871619155	0.0471987923678005
Island	AJAP1;AJAP1	0.00069744320318448	0.0471987923678005
Island	SHROOM4;SHROOM4	0.000697469172510913	0.0471987923678005
N_Shore	FOXF1	0.000697646434649267	0.0472041924366452
Island	ADCY8	0.000697797678625801	0.0472053321842014
N_Shelf		0.000698016528395647	0.0472053321842014
	CYP4V2	0.00069806393312653	0.0472053321842014
N_Shore	MCF2L;MCF2L	0.000698269645342838	0.0472053321842014
		0.000698286347456649	0.0472053321842014
	NHSL2	0.000698331440709316	0.0472053321842014
N_Shore		0.000698430971136276	0.0472053321842014
S_Shore	C11orf54	0.000698443009202473	0.0472053321842014
Island		0.000698554865521269	0.0472063046244717
		0.000698807779207926	0.0472151831756831
	C1GALT1	0.000698881222704737	0.0472151831756831
Island	TSSC1	0.000699080457220115	0.0472196629059709
		0.000699142523509456	0.0472196629059709
S_Shelf		0.000699654004641518	0.0472451643649169
N_Shore	CNOT7;CNOT7	0.00069974628031275	0.0472451643649169
Island	OLFML2A	0.000699885699481147	0.0472451643649169
S_Shelf	ST7;ST7;ST7OT4	0.000699923949115035	0.0472451643649169
N_Shelf	TMCO3	0.000700007844902996	0.0472451643649169
	PIP4K2A	0.000700224384951956	0.0472531942652719
Island	GEMIN7;GEMIN7;GEMI	0.000700475127870276	0.0472635297166023
Island	ZSWIM4	0.000701004632548891	0.047265241087153
Island	RYR1;RYR1	0.000701005293249896	0.047265241087153
S_Shore	ANKRD11	0.000701030731064809	0.047265241087153
		0.000701049642039767	0.047265241087153
S_Shore	MAD1L1;MAD1L1;MAD1	0.000701049945753752	0.047265241087153
N_Shore	ADI1	0.000701086031012455	0.047265241087153
Island	FBN3	0.000701281711027584	0.0472718531236513
S_Shelf		0.000701470437048463	0.0472776732679253
		0.000701652986867079	0.0472776732679253
Island		0.000701660900118406	0.0472776732679253
	MCTP2;MCTP2;MCTP2	0.000701788890770807	0.0472797196442581
	KIAA0101;KIAA0101	0.000702024884898754	0.0472823903457421
N_Shore	LOC645323	0.000702149320750614	0.0472823903457421
		0.00070221515773529	0.0472823903457421
Island		0.000702219034237181	0.0472823903457421
		0.000702475962368636	0.0472858460109655
	VPS18	0.000702759458452136	0.0472858460109655
Island	TACR1;TACR1	0.000702801698905396	0.0472858460109655
N_Shore	OXA1L	0.000702803467977459	0.0472858460109655
		0.000702879994030203	0.0472858460109655
		0.000703105709640276	0.0472858460109655
N_Shore	RASA3	0.000703111666051054	0.0472858460109655
	ERI3	0.000703140502546956	0.0472858460109655
	ARHGAP5;ARHGAP5	0.000703149048616061	0.0472858460109655

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	TBXAS1;TBXAS1	0.000703325542189694	0.0472906948644747
N_Shelf	LRIG1	0.000703416436904302	0.0472906948644747
Island	PIF1	0.000703661735211258	0.0473006203894785
		0.000703817832260438	0.0473045478225835
Island	DACT2	0.000704074964550754	0.0473073649442569
	TOP1P1;FMO4	0.000704087890648947	0.0473073649442569
Island	MGAT5B;MGAT5B	0.000704236166502012	0.0473073649442569
S_Shelf		0.000704267281673748	0.0473073649442569
	FLJ22536	0.000704462481658566	0.0473073649442569
	ABCA5;ABCA5	0.000704604831663264	0.0473073649442569
Island	PKP3	0.000704626061737555	0.0473073649442569
Island	CLIC6	0.000704646912932454	0.0473073649442569
Island	UBE2I;UBE2I;UBE2I;UB	0.00070473883874013	0.0473073649442569
		0.000704919719508608	0.0473129494388867
Island	ATP11A;ATP11A	0.000705429744123645	0.0473406208705396
	TBL1XR1	0.000705770368159417	0.0473551261781437
	KCNQ1;KCNQ1	0.000706111188706507	0.0473551261781437
Island	COL6A2	0.000706111199825393	0.0473551261781437
N_Shore	ARMCX1	0.000706200968621158	0.0473551261781437
	OPN1LW	0.000706208244812973	0.0473551261781437
		0.000706232542992272	0.0473551261781437
N_Shore	MYH14;MYH14;MYH14	0.000706420882241599	0.0473611979224339
N_Shore		0.000706529009398491	0.0473618910002663
Island		0.000706832129610221	0.0473737823019882
	FARP1	0.000706915498221692	0.0473737823019882
	JAKMIP2	0.000707091176718669	0.0473737823019882
N_Shelf	PTPRN2;PTPRN2;PTPR	0.000707209486536683	0.0473737823019882
	CACNB2;CACNB2;CAC	0.000707230508258075	0.0473737823019882
N_Shelf		0.000707399178844136	0.0473737823019882
Island	PRDM13	0.000707756261929444	0.0473737823019882
	SORCS2	0.000707778078940714	0.0473737823019882
N_Shelf		0.000707799774408291	0.0473737823019882
	OCA2	0.000707871906730448	0.0473737823019882
N_Shelf	VIPR2	0.000708121766762534	0.0473737823019882
Island	NOM1	0.000708226808916481	0.0473737823019882
	UPRT;UPRT	0.000708270404709818	0.0473737823019882
Island		0.000708341700106909	0.0473737823019882
Island	NFATC1;NFATC1;NFAT	0.000708521343302268	0.0473737823019882
S_Shore	TRIM39;TRIM39	0.000708748276526769	0.0473737823019882
Island		0.000708863543149973	0.0473737823019882
		0.000709154522894028	0.0473737823019882
Island	PCDHGA4;PCDHGA11;	0.000709220289336959	0.0473737823019882
N_Shelf		0.000709255780637088	0.0473737823019882
		0.000709350287864979	0.0473737823019882
Island	ZSCAN5A	0.000709351658306656	0.0473737823019882
	ZSWIM6	0.000709363299892971	0.0473737823019882
S_Shelf	SLC12A7	0.000709549443968153	0.0473737823019882
N_Shore	AP2A2	0.00070966117686749	0.0473737823019882
	DTHD1;DTHD1	0.000709702117572439	0.0473737823019882
		0.000709750662640663	0.0473737823019882
Island	KIAA0562	0.000709811362710456	0.0473737823019882
Island	LOC254559	0.000709897094091321	0.0473737823019882
N_Shore	ZMYND19	0.000709942794812628	0.0473737823019882
		0.000710055033657058	0.0473737823019882
	USH2A	0.000710118771058635	0.0473737823019882

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Island	RCAN3	0.000710423265180627	0.0473737823019882
		0.000710494303275867	0.0473737823019882
S_Shore	MALAT1	0.00071067182983892	0.0473737823019882
Island		0.000710892881252791	0.0473737823019882
N_Shore		0.000710949083305992	0.0473737823019882
N_Shelf	FHOD3	0.000711158177049147	0.0473737823019882
N_Shelf	BIN1;BIN1;BIN1;BIN1;B	0.000711194845988211	0.0473737823019882
S_Shore	RDH10	0.00071125344917497	0.0473737823019882
S_Shore	ELK1;ELK1	0.00071133637166284	0.0473737823019882
	EXPH5;EXPH5	0.000711339546931506	0.0473737823019882
		0.000711360381296988	0.0473737823019882
N_Shore	PPARG;PPARG	0.000711812760773008	0.0473737823019882
N_Shore	SH3YL1;SH3YL1	0.000711822405104795	0.0473737823019882
Island		0.0007118634489406	0.0473737823019882
Island	C3orf31	0.000711893590010404	0.0473737823019882
		0.000711962006456299	0.0473737823019882
	KIF13A;KIF13A;KIF13A;	0.000712045717039557	0.0473737823019882
Island	MIR548H4;SPESP1;NO	0.000712088430627706	0.0473737823019882
S_Shelf	C10orf58;C10orf58	0.00071224455047227	0.0473737823019882
Island	ESRRG	0.000712304139665009	0.0473737823019882
Island	CNTNAP1	0.000712418411486021	0.0473737823019882
Island	LOC100133957;UXT;LO	0.000712492806861924	0.0473737823019882
Island	SLC9A3	0.000712601183762936	0.0473737823019882
N_Shelf	MCF2L;MCF2L	0.000712613389134052	0.0473737823019882
Island	COL6A2;COL6A2;COL6	0.000712630998585502	0.0473737823019882
		0.00071263454483261	0.0473737823019882
	LPIN1	0.000712732766787975	0.0473737823019882
	CTNNA2;CTNNA2	0.000712740954245216	0.0473737823019882
	ODZ4	0.000712756013929951	0.0473737823019882
N_Shore	ASB1	0.000712921613901236	0.0473737823019882
	HDAC4	0.000712935835896238	0.0473737823019882
S_Shore		0.000712966498114267	0.0473737823019882
N_Shelf	TPR;MIR548F1	0.000713218957048164	0.0473840564296779
	PTPRN2;PTPRN2;PTPR	0.000713532238534495	0.0473927131699442
	JAKMIP3	0.000713944608293441	0.0473927131699442
N_Shelf	C20orf160	0.000713950805323164	0.0473927131699442
N_Shelf	HYLS1	0.000713980450447238	0.0473927131699442
N_Shelf	AKT1;AKT1;AKT1	0.00071398929570034	0.0473927131699442
Island		0.000713991741341187	0.0473927131699442
S_Shore	XPNPEP1;XPNPEP1;XF	0.000714171755402039	0.0473927131699442
		0.000714344124561623	0.0473927131699442
		0.000714425814910752	0.0473927131699442
	MAPK8IP3;MAPK8IP3	0.000714551844554259	0.0473927131699442
		0.000714774488996348	0.0473927131699442
		0.000714882624441556	0.0473927131699442
Island	LANCL3;LANCL3;LANC	0.000714884275052007	0.0473927131699442
N_Shelf	GREB1;GREB1	0.000714902709469523	0.0473927131699442
		0.000715017223660302	0.0473927131699442
		0.000715082559192566	0.0473927131699442
		0.000715185869233264	0.0473927131699442
N_Shelf	STARD6	0.000715224899429863	0.0473927131699442
	NACA2	0.000715274186151935	0.0473927131699442
	ADARB2	0.000715306319666117	0.0473927131699442
N_Shelf	PABPC1	0.000715507714526966	0.0473930912449246
N_Shore	PCDHB9	0.000715507733821068	0.0473930912449246

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	SLC6A3	0.00071566829093995	0.0473931345563312
Island	TBX4	0.00071570409568989	0.0473931345563312
		0.000716041581259496	0.0474069088109092
Island	HCN2	0.000716107871492513	0.0474069088109092
		0.000716494277389309	0.0474127882931395
	MINPP1	0.000716566646307621	0.0474127882931395
Island		0.000716720842205818	0.0474127882931395
Island	ZFR2	0.00071687422439391	0.0474127882931395
Island	C7orf50;C7orf50;C7orf50	0.000716932335677584	0.0474127882931395
		0.000716984976203167	0.0474127882931395
Island	CDX4	0.000716985036028502	0.0474127882931395
N_Shore		0.000717052061219256	0.0474127882931395
N_Shore		0.000717077735502497	0.0474127882931395
Island	MTSS1L	0.000717242673454728	0.0474172205597817
Island	RAB35;RAB35	0.000717585112217851	0.0474333846697026
		0.000717793114866997	0.0474352631290474
N_Shelf	TSC2;TSC2;TSC2	0.000717809412012158	0.0474352631290474
		0.000717971640007496	0.0474395108522006
N_Shelf	DSCC1	0.000718214678218897	0.0474490961708317
		0.000718558856377798	0.0474653598083984
S_Shore	B3GNTL1	0.000718732467894746	0.0474660191711247
Island		0.00071876484716054	0.0474660191711247
		0.000719270750502353	0.0474747362705544
	STK32B	0.000719330053924238	0.0474747362705544
N_Shelf		0.000719529958856782	0.0474747362705544
Island		0.00071956427087112	0.0474747362705544
Island	CHRD1;CHRD1;CHR	0.000719678129627242	0.0474747362705544
N_Shore		0.000719729674065223	0.0474747362705544
		0.000719820749643546	0.0474747362705544
Island	MYF6	0.000719864955662186	0.0474747362705544
	COL23A1	0.000719903220340895	0.0474747362705544
Island	CIT	0.000720056075486399	0.0474747362705544
	STIM2;STIM2;STIM2	0.000720103719638039	0.0474747362705544
N_Shore	CLSTN1;CLSTN1	0.000720143604208487	0.0474747362705544
Island	ZBTB12	0.000720200762875344	0.0474747362705544
Island		0.00072026916247568	0.0474747362705544
Island	FOXK2	0.000720796977593297	0.0474979357514973
		0.00072087915262467	0.0474979357514973
	RAD51L1;RAD51L1;RA	0.00072096770820771	0.0474979357514973
	NXN	0.000721013417942515	0.0474979357514973
	NDUFS6	0.000721402643501148	0.0475088733197351
N_Shore	FAM20B	0.00072153337355634	0.0475088733197351
N_Shelf	IPP;IPP	0.000721555977580774	0.0475088733197351
Island	HIST1H4E	0.000721641314896513	0.0475088733197351
Island	VGLL2;VGLL2;VGLL2;V	0.000721674791028839	0.0475088733197351
	ZNF17	0.000721831169005049	0.0475088733197351
		0.000721898701558478	0.0475088733197351
Island		0.000722034761601219	0.0475088733197351
	RPL31P11	0.000722069630576696	0.0475088733197351
		0.000722176339942229	0.0475088733197351
S_Shore		0.000722440698698933	0.0475088733197351
S_Shelf	PRPF6	0.000722692648058452	0.0475088733197351
Island		0.000722694257275863	0.0475088733197351
		0.000722889532506272	0.0475088733197351
	TMEM163	0.000722906291538452	0.0475088733197351

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Island	FAM167B	0.000723032763713937	0.0475088733197351
Island	LOC100132831	0.000723098502145208	0.0475088733197351
		0.00072311263489516	0.0475088733197351
Island	PAX6	0.000723144544012204	0.0475088733197351
N_Shore	MUC6	0.000723220497164671	0.0475088733197351
	MIPEP	0.000723239401200447	0.0475088733197351
	MTR	0.000723367063319367	0.0475108154247562
		0.000723647701534756	0.0475228031248571
N_Shore	MMP17	0.000723798645586134	0.0475243294115905
	STON1-GTF2A1L;STON	0.000723867192627477	0.0475243294115905
	RPS4Y2;RPS4Y2	0.000724608774360346	0.0475665688048353
N_Shore		0.000725180858449638	0.047576269029839
S_Shelf	MYT1L	0.000725206376489717	0.047576269029839
Island		0.000725329484219151	0.047576269029839
N_Shore		0.000725393729627753	0.047576269029839
Island	PCDHGB1;PCDHGA2;P	0.000725400315034037	0.047576269029839
		0.00072561135319379	0.047576269029839
	C12orf67	0.00072569471131379	0.047576269029839
	SLA2;SLA2	0.000725765253668353	0.047576269029839
S_Shore	LEFTY2	0.000725803651226985	0.047576269029839
N_Shelf	SOLH	0.000725951802730168	0.047576269029839
		0.000725996225307517	0.047576269029839
Island	FZD2	0.000726021692679975	0.047576269029839
	HDAC4	0.000726116355920956	0.047576269029839
Island	PLXNB3;PLXNB3	0.000726233287424465	0.047576269029839
		0.000726404845334226	0.047576269029839
Island		0.000726587450707472	0.047576269029839
Island	MAPK4	0.000726703214947323	0.047576269029839
	GK2	0.000726796370312269	0.047576269029839
Island	BCL11A;BCL11A;BCL11	0.000726898668540607	0.047576269029839
Island	NXN	0.000727020893012352	0.047576269029839
Island		0.00072704034991597	0.047576269029839
		0.000727065812017977	0.047576269029839
N_Shore	GPRASP2;GPRASP2	0.000727071270819844	0.047576269029839
	PRKAG2;PRKAG2	0.000727114114197838	0.047576269029839
N_Shore	GYG2;GYG2	0.000727365419428369	0.0475862835019107
Island	ZNF598	0.000727963415065418	0.0476103265657115
Island		0.000728256349948571	0.0476103265657115
N_Shore		0.000728359614270666	0.0476103265657115
Island		0.000728385513906275	0.0476103265657115
	PTPRN2;PTPRN2;PTPF	0.000728413079760176	0.0476103265657115
	DDX53;DDX53	0.000728542940261525	0.0476103265657115
Island	IGF2BP1;IGF2BP1	0.000728602607584501	0.0476103265657115
Island		0.000728752113872447	0.0476103265657115
Island	SIPA1;SIPA1	0.00072894571125772	0.0476103265657115
		0.00072914674771649	0.0476103265657115
Island	SH3PXD2A	0.000729206613756619	0.0476103265657115
S_Shore	USP42	0.000729336110326552	0.0476103265657115
S_Shelf		0.00072952222204226	0.0476103265657115
	ALCAM	0.000729574001268352	0.0476103265657115
Island	KIAA0415	0.00072960039043187	0.0476103265657115
S_Shelf		0.000729741911505537	0.0476103265657115
	C7orf60	0.000729830220982196	0.0476103265657115
Island		0.000729833524789599	0.0476103265657115
	CLU;CLU;CLU	0.000729868124607093	0.0476103265657115

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Island		0.000729880778406139	0.0476103265657115
Island	SLC25A24;SLC25A24	0.000729885273819923	0.0476103265657115
S_Shore		0.000729948077583982	0.0476103265657115
	STK39	0.000730009309815098	0.0476103265657115
N_Shore		0.000730092180671119	0.0476103265657115
		0.000730600570786319	0.0476260762526136
	OSBPL10	0.000730822662147527	0.0476260762526136
		0.000730828739598285	0.0476260762526136
Island	FOXK1	0.00073085768768551	0.0476260762526136
	ERN1	0.000730901335616242	0.0476260762526136
	PARN;PARN	0.000730923707811237	0.0476260762526136
S_Shelf	MARCKS	0.000731023917895469	0.0476261984173693
		0.00073114740874737	0.047627837086963
Island	ZIC5	0.000731417958520745	0.0476312732895622
	MFHAS1	0.000731507013260255	0.0476312732895622
		0.000731516269342185	0.0476312732895622
Island	C16orf74	0.000731954139289443	0.0476312732895622
S_Shore		0.000732098890230809	0.0476312732895622
Island	DUSP9	0.000732109111805383	0.0476312732895622
Island		0.000732119654046037	0.0476312732895622
Island	FAM133A;FAM133A;NA	0.000732240746221137	0.0476312732895622
	OCA2	0.000732329966186199	0.0476312732895622
		0.000732443802762188	0.0476312732895622
		0.000732528463528018	0.0476312732895622
	USP10	0.000732539404972565	0.0476312732895622
Island		0.000732683073389101	0.0476312732895622
	SFRS8	0.00073274812635275	0.0476312732895622
Island	ERCC2;ERCC2	0.000733096858683145	0.0476312732895622
S_Shelf	IMP4	0.000733117006323827	0.0476312732895622
Island		0.000733277453459112	0.0476312732895622
Island	KCNG2	0.000733277617459804	0.0476312732895622
	MAGI1;MAGI1;MAGI1	0.000733325715587517	0.0476312732895622
S_Shore		0.00073340954566961	0.0476312732895622
N_Shore	GALNT9	0.000733581580790088	0.0476312732895622
Island	HOXD4	0.000733670525175417	0.0476312732895622
N_Shelf		0.000733715461011332	0.0476312732895622
S_Shore		0.000733723557613133	0.0476312732895622
	NBR2	0.000733750916452037	0.0476312732895622
Island	C3	0.000733814346990049	0.0476312732895622
Island	ZNF415;ZNF415;ZNF41	0.000733880280803885	0.0476312732895622
	MAGEB2	0.000734094238337497	0.0476312732895622
Island		0.000734146479257548	0.0476312732895622
N_Shelf		0.000734150529306936	0.0476312732895622
N_Shore		0.000734378258581124	0.0476350835791227
	SORCS2	0.000734408603434559	0.0476350835791227
		0.000734528771333975	0.0476350835791227
Island	POLRMT	0.000734772529804487	0.0476350835791227
N_Shore		0.000734931240561619	0.0476350835791227
Island	VPS37B	0.000735039307264389	0.0476350835791227
Island	VIPR2	0.000735047421690694	0.0476350835791227
Island	CDK2AP1	0.000735086583008975	0.0476350835791227
Island	LOC399744	0.000735464534272338	0.0476350835791227
S_Shore		0.000735561508006037	0.0476350835791227
	TIMP1;SYN1;SYN1	0.00073558470622381	0.0476350835791227
	ABCC1;ABCC1;ABCC1;	0.000735655462553629	0.0476350835791227

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		0.000735675928485908	0.0476350835791227
N_Shore	PCDHB13	0.000735682177521723	0.0476350835791227
		0.000735707486486168	0.0476350835791227
S_Shelf	DLGAP2	0.000735782914892721	0.0476350835791227
		0.000735992045821845	0.0476393844207071
S_Shelf	SSC5D	0.000736061871366759	0.0476393844207071
Island	ODZ4	0.000736234150325795	0.0476393844207071
N_Shore	CCDC19	0.000736242796446585	0.0476393844207071
	POGK	0.000736595174210148	0.047650490953415
	MUC4;MUC4;MUC4	0.000736693071102817	0.047650490953415
Island	COASY;COASY;COASY	0.000736714913110752	0.047650490953415
		0.000736911624199229	0.047650490953415
Island	IQSEC2;IQSEC2	0.000736989446908051	0.047650490953415
S_Shelf		0.000737058274945485	0.047650490953415
N_Shore	GZF1	0.00073723161438708	0.047650490953415
Island	HSF4;HSF4;HSF4;HSF4	0.000737344836951173	0.047650490953415
	PPM1A;PPM1A;PPM1A	0.00073743101485151	0.047650490953415
	ADCY5	0.00073755920984718	0.047650490953415
		0.000737611041498136	0.047650490953415
S_Shore	ZCCHC12	0.000737736678938377	0.047650490953415
S_Shore		0.000737814018790668	0.047650490953415
N_Shore		0.000737888118741599	0.047650490953415
		0.000737926946290915	0.047650490953415
S_Shelf	CPLX1	0.00073798860814859	0.047650490953415
Island		0.000738132489168604	0.0476533783854669
Island	PCDHGA2;PCDHGA1;P	0.000738496049941127	0.0476533783854669
Island	FLT4;FLT4	0.000738509633011969	0.0476533783854669
Island	TNK2;TNK2	0.000738705690361081	0.0476533783854669
N_Shore		0.000738787803765362	0.0476533783854669
		0.000738902965078738	0.0476533783854669
S_Shelf	EXOC2	0.00073896299353442	0.0476533783854669
	CYFIP1	0.000739184322357916	0.0476533783854669
	ADCY1	0.000739358250215041	0.0476533783854669
N_Shelf		0.000739430470587781	0.0476533783854669
	SAMD3	0.000739532170833028	0.0476533783854669
Island		0.000739626367882113	0.0476533783854669
Island	FZD1	0.000739692502215088	0.0476533783854669
	DSCR8;DSCR8;DSCR8	0.000739807715786585	0.0476533783854669
	PPP2R2C	0.000739882649198411	0.0476533783854669
	MCTS1;MCTS1	0.000739931352231676	0.0476533783854669
	SORCS2	0.000740061388196399	0.0476533783854669
Island	PCDHA6;PCDHA2;PCD	0.000740138320741783	0.0476533783854669
Island		0.000740210740324314	0.0476533783854669
Island		0.000740318352453045	0.0476533783854669
Island		0.000740401191270383	0.0476533783854669
N_Shore		0.000740551912241259	0.0476533783854669
		0.000740662626036816	0.0476533783854669
N_Shore	TMC5;TMC5	0.00074084589186438	0.0476533783854669
Island	NEURL1B	0.000740967103851337	0.0476533783854669
Island	ATP4A	0.000741132894848014	0.0476533783854669
N_Shelf		0.000741249461512103	0.0476533783854669
		0.000741325971321245	0.0476533783854669
		0.00074149930915174	0.0476533783854669
Island	SMCR7;SMCR7;SMCR7	0.000741553170586393	0.0476533783854669
Island	ASB18	0.000741654063966311	0.0476533783854669

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S_Shelf	TMCO3	0.000741704496417394	0.0476533783854669
Island	MEST;MEST;MESTIT1;	0.000741887949965283	0.0476533783854669
		0.00074189959346412	0.0476533783854669
Island	PCDHA6;PCDHA2;PCD	0.000742108470475461	0.0476533783854669
Island	ASCL1	0.000742130674303986	0.0476533783854669
	PFKFB3	0.000742135245551472	0.0476533783854669
Island	OBSCN;OBSCN	0.000742240424478178	0.0476533783854669
S_Shore	HUNK	0.00074227746158327	0.0476533783854669
N_Shore	C10orf107	0.000742329114431582	0.0476533783854669
Island	C11orf2	0.000742376946213184	0.0476533783854669
N_Shore	C7orf50;C7orf50;C7orf50	0.000742518434525386	0.0476533783854669
Island	KIF24	0.000742536744392125	0.0476533783854669
S_Shore		0.000742668894215458	0.0476533783854669
	TBC1D22B	0.000742881503528152	0.0476533783854669
		0.000742938620018866	0.0476533783854669
	ATG2B	0.000743024498347311	0.0476533783854669
	BUB1	0.000743148533865101	0.0476533783854669
	ETV6	0.0007432615829704	0.0476533783854669
	CAMK2D;CAMK2D;CAM	0.000743364055754467	0.0476533783854669
N_Shelf	RPH3AL	0.000743498451213196	0.0476533783854669
	OSBPL10	0.000743524647374811	0.0476533783854669
Island	HIST1H4F	0.000743658656305997	0.0476533783854669
Island	MAP7D1	0.000743673333742377	0.0476533783854669
Island	CCL28	0.000743701214105359	0.0476533783854669
	UGGT2	0.000743748177409332	0.0476533783854669
Island		0.000743814761453557	0.0476533783854669
	TRPV1;TRPV1;TRPV1	0.000743838332933223	0.0476533783854669
Island	SCRIB;SCRIB	0.000743991759582762	0.0476533783854669
N_Shore	IFNGR2	0.000744053533430163	0.0476533783854669
	ZNF621;ZNF621	0.000744063308884275	0.0476533783854669
	PTPRE	0.000744338620773738	0.0476533783854669
	ADAMTS2;ADAMTS2	0.000744353240695663	0.0476533783854669
Island	DPP10	0.000744387760739956	0.0476533783854669
S_Shore	PTPRN2;PTPRN2;PTPR	0.000744506034714535	0.0476533783854669
Island	ZCCHC14	0.000744527154788268	0.0476533783854669
	SLC37A1	0.000744810188451534	0.0476609889676382
Island		0.000744844089866244	0.0476609889676382
Island	TP73;WDR8	0.000745027332904502	0.0476609889676382
N_Shelf		0.000745039689204541	0.0476609889676382
	RAMP1	0.000745274638748148	0.047663653004887
	MECOM	0.000745296683359884	0.047663653004887
		0.000745460014776831	0.047663653004887
N_Shore	SYP	0.000745474983765073	0.047663653004887
Island	SHROOM4;SHROOM4	0.000745714377477784	0.0476726657697898
N_Shore	AHRR;PDCD6	0.000746117698093509	0.0476921544317195
Island		0.0007463595957871	0.0477013210912625
		0.000746547762857619	0.0477016094512192
		0.000746566456244367	0.0477016094512192
S_Shelf		0.000746659580343144	0.0477016094512192
	RUNDC2C	0.000746991149691659	0.0477164980973902
		0.000747166382555003	0.0477205283684864
Island	ZFP41	0.000747251302630673	0.0477205283684864
Island	DCAF4L2	0.000747502576558459	0.0477302815282367
	C10orf11	0.000747890824251638	0.0477306197632147
	SH3TC1	0.000747937569490256	0.0477306197632147

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N_Shore	SEMA6B	0.000748108969691484	0.0477306197632147
	DHX37	0.000748167602527335	0.0477306197632147
S_Shelf	KIAA1467	0.000748251381635619	0.0477306197632147
		0.000748376915987166	0.0477306197632147
		0.000748591060529514	0.0477306197632147
	MTOR	0.000748602736676191	0.0477306197632147
	C17orf54	0.000748659293258857	0.0477306197632147
	SH3RF3	0.000748688350293871	0.0477306197632147
Island	C1orf159	0.000748751073040103	0.0477306197632147
Island	CPM;CPM;CPM	0.000748754553377615	0.0477306197632147
	FARP1	0.000748810261653172	0.0477306197632147
Island	CASZ1	0.000748933452268465	0.0477306197632147
Island	CHRN2	0.000749030923453542	0.0477306197632147
N_Shore	CACNA2D4	0.000749084686564177	0.0477306197632147
		0.000749265977814519	0.0477358911740354
N_Shore	NEUROG1;NEUROG1	0.000749721354325447	0.0477471622725375
		0.00074974656658067	0.0477471622725375
Island	WDR8	0.000749750304974286	0.0477471622725375
Island	CHRM2;CHRM2;CHRM2	0.000749900962449195	0.0477471622725375
Island	USP35	0.000749965307717311	0.0477471622725375
Island		0.000750202134354649	0.0477471622725375
Island	TRIM62	0.000750380154837413	0.0477471622725375
S_Shelf		0.000750422619388188	0.0477471622725375
Island	HOXA9	0.000750472491947642	0.0477471622725375
	FAM189A1	0.00075052398659604	0.0477471622725375
S_Shore	EXOC3	0.000750527324381	0.0477471622725375
S_Shore		0.000750936902679726	0.0477515734170116
		0.000750975491709123	0.0477515734170116
N_Shore	C1orf88	0.000751110901407517	0.0477515734170116
	NKD2	0.00075122869977002	0.0477515734170116
		0.000751382137910425	0.0477515734170116
N_Shore	HDAC11	0.000751592410664321	0.0477515734170116
	SLITRK3	0.000751604907494993	0.0477515734170116
	CADPS2;CADPS2;RNF1	0.000751646410200872	0.0477515734170116
N_Shore	TIGD4	0.000751718591439077	0.0477515734170116
		0.000751980752314829	0.0477515734170116
	ZFAND3	0.000752004544740169	0.0477515734170116
		0.000752164041057425	0.0477515734170116
S_Shore	SYPL1;SYPL1	0.000752175666402984	0.0477515734170116
		0.000752186096152207	0.0477515734170116
Island	LRRC14B	0.00075232342368577	0.0477515734170116
Island	FSCN2;FSCN2	0.00075236361024789	0.0477515734170116
Island	NFKBID	0.000752404205819453	0.0477515734170116
S_Shore	C4orf44;C4orf44	0.000752422456812207	0.0477515734170116
S_Shore	PLAGL1;PLAGL1;PLAG	0.000752469949555841	0.0477515734170116
S_Shore	EPS8	0.000752634233056221	0.0477557415072651
Island	BRUNOL4;BRUNOL4;B	0.000753682931588195	0.047793893832098
Island	SERPINB9	0.000754001372914336	0.047793893832098
	MARCH8;MARCH8;MA	0.000754047042581483	0.047793893832098
Island		0.000754090533996426	0.047793893832098
	CASR	0.000754174011071742	0.047793893832098
Island		0.000754338994390114	0.047793893832098
N_Shore		0.000754379697681133	0.047793893832098
S_Shore	PDE4B;PDE4B	0.000754511504476585	0.047793893832098
	FAM82A1;FAM82A1;FA	0.000754779886147929	0.047793893832098

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Island		0.000754978084234769	0.047793893832098
	POLI	0.000755206706487717	0.047793893832098
S_Shore	CXorf67	0.000755272827447453	0.047793893832098
	MED12L	0.00075546671627761	0.047793893832098
	S100A4;S100A4	0.000755761741350815	0.047793893832098
S_Shore		0.0007558452368765	0.047793893832098
	GRB10;GRB10;GRB10;	0.000755949988169623	0.047793893832098
N_Shore	GRM6	0.000755990475165837	0.047793893832098
N_Shelf	CARD14;CARD14	0.00075613767441686	0.047793893832098
N_Shore	MAD1L1;MAD1L1;MAD1	0.00075614380479369	0.047793893832098
	ESM1;ESM1;ESM1;ESM	0.000756146730647522	0.047793893832098
Island	KIAA0182;KIAA0182	0.000756197059383938	0.047793893832098
Island	MAEA;MAEA	0.000756268717286514	0.047793893832098
N_Shore	VAR2;VAR2;VAR2;	0.000756368566862054	0.047793893832098
S_Shore	ZFX	0.000756473558575632	0.047793893832098
S_Shore	SLITRK4	0.000756604637258546	0.047793893832098
		0.000756719382684304	0.047793893832098
N_Shelf	ADRA1A;ADRA1A;ADR	0.00075674023323725	0.047793893832098
Island	GFRA2;GFRA2;GFRA2	0.000756925018272673	0.047793893832098
Island	GPR25	0.000756971112781462	0.047793893832098
	KIAA1267	0.000757026875959366	0.047793893832098
N_Shelf		0.000757035338208302	0.047793893832098
		0.00075703919409394	0.047793893832098
		0.000757130290226113	0.047793893832098
S_Shelf		0.000757175118569818	0.047793893832098
	TCF25	0.000757264266027543	0.047793893832098
S_Shore	GLRX2	0.000757301671802802	0.047793893832098
	GK2	0.000757494502596799	0.047793893832098
Island	C7orf27	0.000757601032903022	0.047793893832098
Island		0.000757635670434203	0.047793893832098
Island	NHLH2;NHLH2	0.000757636613782597	0.047793893832098
N_Shelf		0.000757679526265637	0.047793893832098
S_Shore	HDAC7;HDAC7	0.00075770790978848	0.047793893832098
Island	CTBP1;CTBP1;C4orf42	0.000757771433066206	0.047793893832098
S_Shelf	CACNA1D;CACNA1D;C	0.000757837578861626	0.047793893832098
S_Shore	DCLK1	0.000757924534444979	0.047793893832098
Island	TMPRSS6	0.000757955068407955	0.047793893832098
		0.000758275875987721	0.047793893832098
		0.000758516495053182	0.047793893832098
	EFR3A	0.000758579144808537	0.047793893832098
Island	KIAA1543;KIAA1543	0.000758625251902632	0.047793893832098
N_Shelf		0.000758630973003106	0.047793893832098
Island	HMGA1;HMGA1;HMGA	0.000758677510145157	0.047793893832098
Island	TCF21;TCF21	0.000758694062472187	0.047793893832098
N_Shelf		0.000758720108484563	0.047793893832098
	DLGAP2	0.000758784585580663	0.047793893832098
S_Shelf		0.000758926583563521	0.047793893832098
N_Shelf		0.000759029711701299	0.047793893832098
N_Shore	LTC4S;LTC4S	0.000759055583352589	0.047793893832098
	KIAA1244;PBOV1	0.000759092628732535	0.047793893832098
	ESM1;ESM1	0.000759236712604901	0.047793893832098
Island		0.000759255085209647	0.047793893832098
Island	CHID1;CHID1;CHID1;C	0.000759428055629603	0.0477985695962063
N_Shore		0.000759762017938043	0.0478108020608458
N_Shelf	SHFM1	0.00075984387543344	0.0478108020608458

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N_Shore		0.000760125647168959	0.0478108020608458
Island	LOC154822	0.000760189725180615	0.0478108020608458
Island	REXO1	0.000760202464882281	0.0478108020608458
	UPP1;UPP1	0.000760349806947686	0.0478108020608458
	KCNH4	0.000760408242884175	0.0478108020608458
		0.000760432414336073	0.0478108020608458
N_Shelf	ZC3H8	0.000760510853407849	0.0478108020608458
S_Shore	SGSH	0.000760832360783623	0.0478176138921783
		0.000760860180347504	0.0478176138921783
Island	TPPP	0.000760937055803942	0.0478176138921783
	RAB19	0.000761051353423188	0.0478176138921783
Island	ALX4	0.000761112859123114	0.0478176138921783
S_Shelf	NPAS3;NPAS3;NPAS3;NPAS3	0.000761248484939041	0.0478199315782232
S_Shelf	TTC12	0.00076184153013409	0.047850979001711
	NDUFS6	0.000762119195155464	0.0478622120323742
S_Shelf	TCF25	0.000762354419150636	0.0478707771366695
	ANKRD55	0.000762654628478124	0.0478820523844703
	SMAP1;SMAP1	0.000762840091952672	0.0478820523844703
		0.000763007863108621	0.0478820523844703
S_Shelf	PARVB	0.000763081757240175	0.0478820523844703
Island	HECW1	0.000763194559105827	0.0478820523844703
Island	MAD1L1;MAD1L1;MAD1L1	0.000763326261945004	0.0478820523844703
Island	MYT1L	0.000763405921539667	0.0478820523844703
	PLD1;PLD1	0.000763503802009465	0.0478820523844703
Island	SH3D20	0.000763666895585768	0.0478820523844703
S_Shore	C1orf223	0.000763836719124609	0.0478820523844703
S_Shore	UGT8	0.000763839948881982	0.0478820523844703
N_Shelf	TAF13	0.000763847897235987	0.0478820523844703
	SLC8A2	0.000763977745976095	0.0478820523844703
		0.000764066044115756	0.0478820523844703
	KIF14	0.000764070763375883	0.0478820523844703
Island	PLXNA3	0.00076442169812701	0.0478820523844703
		0.000764518389252161	0.0478820523844703
	CPA4;CPA4	0.000764548217979628	0.0478820523844703
N_Shelf	TMCO3	0.000764568038054501	0.0478820523844703
N_Shore	RBMXL3;LRCH2	0.000764569527112553	0.0478820523844703
N_Shore	RGS10	0.000764616148880781	0.0478820523844703
N_Shore	PDX1	0.000764842837466874	0.0478820523844703
Island		0.000764947458035924	0.0478820523844703
	SNAR-I	0.000765144855076188	0.0478820523844703
N_Shore		0.000765280181334054	0.0478820523844703
		0.000765341077633074	0.0478820523844703
S_Shore	FAM119B;FAM119B	0.000765455272646354	0.0478820523844703
	C5orf47	0.000765491882143369	0.0478820523844703
		0.000765534981452377	0.0478820523844703
Island		0.000765591001483881	0.0478820523844703
	AMZ1	0.000765615944773641	0.0478820523844703
Island		0.000765697611557781	0.0478820523844703
N_Shore		0.000765851193062456	0.047884617220017
	STAB2	0.00076593636422541	0.047884617220017
Island	MIDN	0.000766050564144454	0.0478849668763803
Island	KCNC3	0.000766225823131943	0.0478849668763803
N_Shore	PLCD3	0.000766238565615954	0.0478849668763803
Island		0.000766452113478172	0.0478921326100265
Island	ADAMTS15	0.000766629120266203	0.0478970135026998

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Island	ESX1	0.000766803680091387	0.0479017402760558
		0.000766918196158484	0.0479027154184237
S_Shelf	ECT2	0.000767031807913163	0.047903254555221
N_Shore	ADAMTS17	0.00076726240637215	0.047903254555221
Island	ECEL1	0.000767282586546545	0.047903254555221
Island		0.000767322456696235	0.047903254555221
Island	NCOR2;NCOR2	0.000767567888451242	0.0479124007699636
N_Shore	EHD2	0.000767804838342859	0.0479210152487635
Island	MAD1L1;MAD1L1;MAD1	0.000767935700768846	0.047921475050576
S_Shelf	CABP2;CABP2	0.000768142936279176	0.047921475050576
Island	DMRT1	0.000768241900058426	0.047921475050576
S_Shore	EYA4;EYA4;EYA4	0.000768331303997891	0.047921475050576
N_Shelf	FGFR2;FGFR2;FGFR2;	0.000768390788944938	0.047921475050576
Island	KCNIP4	0.000768619840464405	0.047921475050576
N_Shore	UBE2QL1	0.000768819207783771	0.047921475050576
S_Shore	PARP12	0.000768832494569037	0.047921475050576
		0.000768842570181745	0.047921475050576
Island	DMRTA2	0.000768847651634666	0.047921475050576
Island	WNT5A	0.000768967376799642	0.047921475050576
Island	SMARCA4;SMARCA4;S	0.000768999543887012	0.047921475050576
	EXT1	0.000769134898707592	0.0479237437046899
Island		0.000769325943533609	0.0479253350429539
S_Shore	RPTOR;RPTOR	0.000769451026541651	0.0479253350429539
Island		0.00076945729684408	0.0479253350429539
Island	TRIP10	0.000769605719600413	0.0479284158602893
Island		0.000770695340558037	0.047954046199396
		0.000770753684510442	0.047954046199396
N_Shore	TFAP2A;TFAP2A	0.00077081636180718	0.047954046199396
	BANK1;BANK1;BANK1	0.00077082998942862	0.047954046199396
	RPH3AL	0.000770900458584241	0.047954046199396
	FGF1;FGF1;FGF1;FGF1	0.00077095308717288	0.047954046199396
Island		0.000770970189529857	0.047954046199396
Island	C17orf28	0.000771035406795606	0.047954046199396
S_Shore		0.000771104872945663	0.047954046199396
	HDAC4	0.000771192896554267	0.047954046199396
Island	UTF1	0.000771266662939276	0.047954046199396
	GTDC1;GTDC1;GTDC1	0.000771367496028779	0.047954046199396
	LRRFIP1;LRRFIP1;LRR	0.000771376984163693	0.047954046199396
N_Shelf		0.00077152885811842	0.047954046199396
N_Shelf	CRYM;CRYM	0.000771585515934197	0.047954046199396
	FBXO21;FBXO21	0.000771780427236042	0.047954046199396
S_Shore	NEURL	0.000771789803754454	0.047954046199396
N_Shelf	GABBR1;GABBR1;GAB	0.000771977792289137	0.047954046199396
		0.000771992793724668	0.047954046199396
	USP22	0.000772177031820291	0.047954046199396
	SIAH1	0.000772188482752424	0.047954046199396
S_Shore	TIGD2	0.000772195542887708	0.047954046199396
S_Shore	NXN	0.000772419581684863	0.0479548601002278
N_Shelf		0.000772440056156031	0.0479548601002278
Island	OTX1	0.000772517437054971	0.0479548601002278
Island	TBX3;TBX3	0.000772750168655623	0.0479548601002278
	EMP2	0.000772983581652489	0.0479548601002278
N_Shore		0.000773160090402693	0.0479548601002278
	ADARB2	0.000773195953328853	0.0479548601002278
	TRAPPC9;TRAPPC9	0.00077322000199773	0.0479548601002278

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		0.000773248062616	0.0479548601002278
	EML1;EML1	0.000773367071638985	0.0479548601002278
	NCOA1;NCOA1;NCOA1	0.0007736160996698	0.0479548601002278
	GAPT	0.000773664940321654	0.0479548601002278
S_Shelf	SOCS5;SOCS5	0.000773810212651187	0.0479548601002278
N_Shore	TBC1D22A	0.000773883796062867	0.0479548601002278
S_Shore	PTPRN2;PTPRN2;PTPRN2	0.000773900327330455	0.0479548601002278
		0.00077403590640985	0.0479548601002278
		0.000774309522085778	0.0479548601002278
	OR10V1	0.000774311837385976	0.0479548601002278
	NR1H3;NR1H3;NR1H3	0.000774335824995281	0.0479548601002278
N_Shore	MAD1L1;MAD1L1;MAD1L1	0.000774376117250052	0.0479548601002278
	C1orf49;C1orf49;C1orf49	0.000774440733000527	0.0479548601002278
N_Shore		0.000774515804386652	0.0479548601002278
Island	PRSS22	0.000774672074036221	0.0479548601002278
Island		0.000774682882273537	0.0479548601002278
Island	TRPS1	0.000774683994062215	0.0479548601002278
	FRMD6	0.000774852713897789	0.0479591745250539
Island	LOC254559	0.0007750182570335	0.0479632912519486
Island	CTNNA2;LRRTM1;LRRTM1	0.000775132509601071	0.0479642331305147
	VTI1A	0.000775336336728066	0.0479704681714569
Island	PRDM15;PRDM15	0.000775431363886514	0.0479704681714569
S_Shore	ANTXR2	0.000775563867368586	0.0479725376836897
S_Shore	REM1	0.000775707256502271	0.0479752799138631
	PCSK9	0.000775858219338411	0.0479784872561803
S_Shore	SLCO6A1	0.000775957240856162	0.0479784872561803
Island	SPHK2	0.000776168693421176	0.0479820333535402
	AADA4L4	0.000776212731791643	0.0479820333535402
S_Shelf	ITPR3	0.00077672266110503	0.0480037266130994
S_Shore	MFSD2B	0.000776761896385403	0.0480037266130994
		0.000777192632116443	0.0480101298040455
Island	MSX1	0.000777269992396582	0.0480101298040455
	ANKRD35	0.00077736207403947	0.0480101298040455
	ANK3	0.000777455017975766	0.0480101298040455
		0.000777625320744201	0.0480101298040455
		0.000777644876617397	0.0480101298040455
N_Shelf	ADAM8;ADAM8;ADAM8	0.000777803604033635	0.0480101298040455
Island	UNC84A;UNC84A	0.000777826139782887	0.0480101298040455
N_Shore		0.000777897783880207	0.0480101298040455
Island	PCDHB15	0.000777938079208454	0.0480101298040455
Island	GPC3;GPC3;GPC3;GPC3	0.000778027940405385	0.0480101298040455
N_Shore	CTNND2	0.000778055043270434	0.0480101298040455
		0.00077838936859333	0.0480104591490592
Island	HTRA1	0.000778576039823987	0.0480104591490592
	C5orf25	0.000778665233169448	0.0480104591490592
S_Shelf	BRE;BRE;BRE;BRE;BRE	0.000778672395672	0.0480104591490592
	RRP15	0.0007787113167164	0.0480104591490592
	FARP1	0.000778786868428734	0.0480104591490592
Island	C9orf167	0.000778789298288346	0.0480104591490592
N_Shore	HCFC1	0.000778943519298218	0.0480104591490592
N_Shore	DCTN2	0.000778952538054628	0.0480104591490592
Island	MAEL	0.000779114337825492	0.0480143213726087
	CTAG2;CTAG2	0.000779362148273009	0.0480153395060755
Island	COL18A1;COL18A1;COL18A1	0.00077948375132458	0.0480153395060755
	LGSN;LGSN	0.000779506638919927	0.0480153395060755

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Island	TDRD12	0.00077960843920484	0.0480153395060755
Island	SDK1;SDK1	0.000779626552161828	0.0480153395060755
	BRD9;BRD9;BRD9	0.000780168431248549	0.0480426033648384
	PLCH2	0.000780356869701059	0.0480466118426407
		0.000780594038839408	0.0480466118426407
	ROS1	0.00078079373301127	0.0480466118426407
Island	KIAA0284;KIAA0284	0.000780819070095931	0.0480466118426407
S_Shore	ZNF148	0.000780911057171887	0.0480466118426407
N_Shelf		0.000780952255345447	0.0480466118426407
Island	ADARB2	0.000780973603726069	0.0480466118426407
N_Shore	PCDHB19P	0.000781301137860221	0.0480466118426407
	TMEM232	0.000781310698077845	0.0480466118426407
		0.000781325332243995	0.0480466118426407
	PDLIM5;PDLIM5;PDLIM	0.00078137038284642	0.0480466118426407
Island	LOC100130274	0.000781491545980096	0.0480466118426407
Island		0.000781523167493571	0.0480466118426407
Island	WNT11	0.00078184834707608	0.0480471442809979
S_Shelf		0.000781864463938094	0.0480471442809979
		0.000781972419391439	0.0480471442809979
Island	QRICH2	0.000782027759958218	0.0480471442809979
S_Shore	NAT15;ZNF597	0.000782035532985075	0.0480471442809979
Island	CPN1	0.000782127054171037	0.0480471442809979
		0.000782455309701414	0.0480579247503876
N_Shore	KCNG4	0.000782512046651442	0.0480579247503876
	C2orf40	0.000782600221971419	0.0480579247503876
		0.000782857659529551	0.0480641090513667
Island	NFATC1;NFATC1;NFAT	0.000782899409087352	0.0480641090513667
		0.000783234907232759	0.0480786117167942
		0.000783528545752664	0.0480905414930502
	TRIM40	0.000783769954958328	0.0480992629796239
N_Shore	ELFN1	0.000784101004239403	0.0481087970855793
		0.000784123975003485	0.0481087970855793
Island	KLHDC7A	0.000784227770249212	0.0481090709089233
S_Shelf	ALKBH3	0.000784460795692964	0.0481138555210866
	RALBP1	0.000784811545233546	0.0481138555210866
N_Shelf		0.00078481496491116	0.0481138555210866
	MTMR2;MTMR2;MTMR	0.000784839180487563	0.0481138555210866
	KCNAB2;KCNAB2	0.000784927274684583	0.0481138555210866
Island	ZNF154;ZNF154	0.00078494242170497	0.0481138555210866
N_Shelf	C2orf76	0.000785001158989575	0.0481138555210866
	PIGG;PIGG	0.000785304335797431	0.0481159876570915
		0.000785319569396997	0.0481159876570915
		0.0007853339852977	0.0481159876570915
N_Shore	UBE2QL1	0.000785614285733767	0.0481187783147154
	MAGEC1	0.000785646156167456	0.0481187783147154
N_Shore	PRDM13	0.000785773664904855	0.0481187783147154
	CALCR;CALCR	0.000785776942530499	0.0481187783147154
		0.000786456691786069	0.0481531809194818
S_Shelf	FBXO17;FBXO17	0.000786537581694153	0.0481531809194818
	FARP1	0.000786677921927204	0.0481556856088717
	HSPA12A	0.000786984950939254	0.0481585611052088
	RDH14	0.000787000495645228	0.0481585611052088
	PLSCR2;PLSCR2	0.000787027130119023	0.0481585611052088
Island	DLEU7	0.000787245024170511	0.0481585611052088
	FAM66A	0.000787289408856268	0.0481585611052088

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	CELA1	0.000787321502774053	0.0481585611052088
N_Shelf	FLOT1	0.00078774269737072	0.0481641484049342
		0.000787965899424461	0.0481641484049342
	CYFIP1	0.00078821424421804	0.0481641484049342
Island	C1orf70	0.000788264575071309	0.0481641484049342
Island		0.000788292962925214	0.0481641484049342
		0.000788427840421116	0.0481641484049342
		0.00078847044778719	0.0481641484049342
Island		0.000788603502868078	0.0481641484049342
S_Shelf	NFASC;NFASC;NFASC	0.000788728363088781	0.0481641484049342
	AGAP1;AGAP1	0.000788997987783561	0.0481641484049342
Island	RHBDF2;RHBDF2	0.00078913047392242	0.0481641484049342
	DLX6AS	0.000789140912005679	0.0481641484049342
	GATA4	0.000789341389842929	0.0481641484049342
N_Shore	RNF39;RNF39	0.000789548540759065	0.0481641484049342
		0.000789584278753912	0.0481641484049342
	CDYL;CDYL;CDYL;CDYL	0.000789607641404489	0.0481641484049342
	AP4M1	0.000789608781370701	0.0481641484049342
Island	STXBP6;STXBP6	0.000789626497647913	0.0481641484049342
	C5orf45;C5orf45	0.000789755386688569	0.0481641484049342
Island	FCGBP	0.000789783229226148	0.0481641484049342
	TUBGCP3	0.000789905579417595	0.0481641484049342
Island	CECR6;CECR6	0.000790034306847871	0.0481641484049342
S_Shore	PPP1R2P9	0.000790179961056318	0.0481641484049342
	MKRN3	0.00079020314049188	0.0481641484049342
	NTRK1;INSRR	0.000790329596605145	0.0481641484049342
Island		0.000790562892432237	0.0481641484049342
S_Shelf	RPS3	0.000790718467418997	0.0481641484049342
Island	GMCL1L	0.000790746299848432	0.0481641484049342
	SLC29A3	0.000790782710585642	0.0481641484049342
		0.000791046204945947	0.0481641484049342
N_Shore	FMN2	0.000791079812401166	0.0481641484049342
N_Shelf	TAP1	0.000791194040982888	0.0481641484049342
Island		0.000791217145018413	0.0481641484049342
N_Shore	C20orf166;MIR1-1	0.000791462114365595	0.0481641484049342
Island		0.000791471969769753	0.0481641484049342
		0.000791663019190877	0.0481641484049342
	CYFIP1;CYFIP1	0.000791795361184164	0.0481641484049342
	FAM13A	0.000791874854031968	0.0481641484049342
Island	ANK1;ANK1;ANK1;ANK1	0.00079194750062296	0.0481641484049342
	NDUFS6	0.000791996371200293	0.0481641484049342
Island		0.000792130704854215	0.0481641484049342
Island		0.000792226512624786	0.0481641484049342
N_Shore	PCDHGA4;PCDHGA12;	0.000792302122496383	0.0481641484049342
S_Shore	WBP1	0.000792371690711511	0.0481641484049342
	FAM150A	0.000792402685441402	0.0481641484049342
Island	GALNS	0.000792409227228274	0.0481641484049342
	GORAB;GORAB	0.000792419415255829	0.0481641484049342
N_Shelf	AP1G1;AP1G1	0.000792518429374987	0.0481641484049342
Island	PRDM16;PRDM16	0.00079260242059765	0.0481641484049342
		0.000792646321824451	0.0481641484049342
		0.000792653755809299	0.0481641484049342
	IL12RB2	0.000792659096836386	0.0481641484049342
		0.000792880938388904	0.0481641484049342
S_Shore	PABPC1P2	0.000792884279024662	0.0481641484049342

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N_Shelf		0.000792923668713024	0.0481641484049342
S_Shelf	PRR3;PRR3	0.000792981818780664	0.0481641484049342
Island	SCUBE1	0.000793399420142861	0.0481747740359864
N_Shore	LOC645323;LOC645323	0.000793425407078099	0.0481747740359864
	MAD1L1;MAD1L1;MAD1L1	0.000793455164373228	0.0481747740359864
	EBF3	0.00079372113180774	0.0481800308581062
		0.000794056918121032	0.0481800308581062
		0.000794075458850525	0.0481800308581062
Island	ARSD;ARSD	0.000794155701453548	0.0481800308581062
S_Shore		0.00079416332736645	0.0481800308581062
S_Shore	XKR5	0.000794222419586252	0.0481800308581062
Island	CCDC88C	0.000794238097085882	0.0481800308581062
	ANO6;ANO6;ANO6;ANO6	0.000794441751509054	0.0481863495678926
S_Shore	HOXA4	0.000794823472279949	0.0482034658417213
		0.000795417463434439	0.0482247723987624
	IQSEC1	0.00079542187238488	0.0482247723987624
	KIAA1407	0.000795473507858799	0.0482247723987624
Island	C15orf26	0.000795595153236874	0.0482261104620086
		0.000795920874380164	0.0482318962191679
		0.000795958826056172	0.0482318962191679
	OR52B4	0.000795989359376057	0.0482318962191679
		0.000796110118727615	0.0482331790408747
Island	EVI5L;EVI5L	0.000796424411814072	0.0482364178297423
Island	FRMPD4	0.000796469025357209	0.0482364178297423
	CACNB2;CACNB2;CACNB2	0.000796488576692701	0.0482364178297423
Island	INPP5F;INPP5F	0.000796586299155928	0.0482364178297423
	LRP1;MIR1228	0.000796748666285433	0.0482364178297423
N_Shore	GPR150	0.000796761147241911	0.0482364178297423
N_Shelf		0.000797306491908766	0.0482544520316246
		0.000797328165573278	0.0482544520316246
	MAD1L1;MAD1L1;MAD1L1	0.000797357930334159	0.0482544520316246
		0.000797600783702078	0.0482604086073946
	NAV2;NAV2;NAV2	0.000797694319474699	0.0482604086073946
N_Shelf	ERICH1	0.000797755290994272	0.0482604086073946
	CPVL;CPVL	0.000797886932415159	0.0482623440167318
S_Shelf		0.000798312792197346	0.0482733581825252
		0.000798330309898638	0.0482733581825252
		0.000798368036013063	0.0482733581825252
		0.000798709399265788	0.0482738061799325
		0.00079881977228323	0.0482738061799325
	RAB5A;C3orf48	0.000798867377535018	0.0482738061799325
Island		0.000798941283113912	0.0482738061799325
S_Shelf	SLITRK1;SLITRK1	0.00079906658554136	0.0482738061799325
N_Shore	BMP4;BMP4;BMP4	0.000799093544593565	0.0482738061799325
Island	RPL10L	0.000799115392849084	0.0482738061799325
S_Shore		0.000799218032615992	0.0482738061799325
N_Shelf	HPN;HPN	0.000799347197406	0.0482738061799325
S_Shelf	ZNF548	0.000799404408269048	0.0482738061799325
S_Shore	TDRD9	0.000799514405619537	0.0482738061799325
	MED12L;P2RY13	0.00079960408535384	0.0482738061799325
Island	CDX2	0.000799813028533571	0.0482738061799325
S_Shore	LOC285830;LOC285830	0.000799837816064515	0.0482738061799325
		0.000799870530313237	0.0482738061799325
		0.000800070767143502	0.0482744195852587
	HS3ST5	0.000800080041317032	0.0482744195852587

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Island		0.000800232066669703	0.0482775779384409
Island	GIMAP1	0.000800859355176853	0.0482997845526487
		0.000800904288863838	0.0482997845526487
	KIF26B	0.000800942529578031	0.0482997845526487
	ESYT2	0.000801001044145429	0.0482997845526487
S_Shore		0.000801120736867167	0.0482997845526487
		0.000801198511528374	0.0482997845526487
Island	PHOX2B	0.000801488298757927	0.0483074212411069
	GTF2IRD2B	0.000801524672675445	0.0483074212411069
S_Shelf	TSPAN17;TSPAN17;TS	0.000801804531021258	0.0483118458250112
	MGAT5B;MGAT5B	0.000801840016606459	0.0483118458250112
	APOBEC3G	0.00080201217007933	0.0483118458250112
		0.000802070131031016	0.0483118458250112
	NLRP12;NLRP12	0.00080209811944067	0.0483118458250112
	DENND2A	0.000802196591389542	0.0483118458250112
	ZNF133;ZNF133	0.000802368671939238	0.0483130035439811
N_Shelf	SMG6;SMG6	0.000802415321339563	0.0483130035439811
S_Shore		0.000802992815225797	0.048330610548552
N_Shelf	SLC38A10;SLC38A10	0.000802998855768152	0.048330610548552
Island		0.000803024828531523	0.048330610548552
N_Shelf		0.00080310690898621	0.048330610548552
	ANGPT2;ANGPT2;ANG	0.000803377537356735	0.0483363539584513
N_Shore	TMEM178;TMEM178	0.00080340194985915	0.0483363539584513
Island	MLLT1	0.000803924000153447	0.0483613164204196
S_Shore	SPTBN1;SPTBN1	0.000804310370810933	0.0483613164204196
N_Shore	RNF39;RNF39	0.000804340626518236	0.0483613164204196
		0.00080442210189864	0.0483613164204196
Island	LOC146880;LOC146880	0.00080453605469253	0.0483613164204196
Island	PNPLA6;PNPLA6;PNPL	0.000804672715098964	0.0483613164204196
Island	FGF13;FGF13;FGF13;F	0.000804764512909424	0.0483613164204196
Island	GNA11	0.000804859891125491	0.0483613164204196
Island	ASAP2;ASAP2	0.000804869952785588	0.0483613164204196
	SLC2A12	0.000804892605334478	0.0483613164204196
		0.000804937168484195	0.0483613164204196
N_Shelf	URGCP	0.000805211635224557	0.0483613164204196
		0.000805250537658038	0.0483613164204196
Island		0.000805311534357379	0.0483613164204196
Island	CAPS;CAPS	0.000805314648078633	0.0483613164204196
	DIP2C	0.00080542338414518	0.0483618498048741
N_Shore	GPR101	0.000805552172393279	0.0483635869461231
N_Shore	SYCP2;SYCP2	0.000805888319339296	0.0483777714754592
Island	SLC15A4	0.000806080757589461	0.0483833266723901
		0.000806360546539562	0.0483941228875803
S_Shore		0.000806632591987393	0.0484044517549615
S_Shore	MORN1	0.000806859618174234	0.048412076879613
Island	KIAA1804	0.000806987889077144	0.0484137754709882
N_Shore	PRKCZ	0.000807122366766196	0.0484158459603713
S_Shore	UNC84A;UNC84A	0.000807344241417743	0.0484173821248158
	GFPT2	0.000807411128418126	0.0484173821248158
S_Shore	RHOXF1	0.000807447881943194	0.0484173821248158
	EFCAB2;EFCAB2;EFCAB	0.000807646893335152	0.048419314546343
	SEMA4A	0.000807866724433056	0.048419314546343
Island	RSPH1	0.000807885038539843	0.048419314546343
		0.000807902154901404	0.048419314546343
	DCTN4;DCTN4;DCTN4	0.000807979972463829	0.048419314546343

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S_Shore		0.000808410715743638	0.0484215702728401
	CAMTA1	0.000808656168296498	0.0484215702728401
S_Shore	ZNF208	0.000808741229554344	0.0484215702728401
	TTC15	0.000808754911066601	0.0484215702728401
	UXS1	0.000808827199553896	0.0484215702728401
N_Shore	PCDHGA4;PCDHGA2;P	0.000808890803767897	0.0484215702728401
Island		0.000808952389042383	0.0484215702728401
S_Shore	COL24A1	0.000809064894516246	0.0484215702728401
		0.000809065134727294	0.0484215702728401
	MGMT	0.000809110289317254	0.0484215702728401
N_Shore	HIST1H2BE	0.000809117365855769	0.0484215702728401
		0.000809505070027621	0.0484387871313476
S_Shore	PRKD1	0.000809629031467918	0.0484402199710561
Island	CCND1	0.000809770073375089	0.0484426742573357
S_Shore		0.000810048008585487	0.0484533162601168
	OSBPL3;OSBPL3;OSBF	0.00081054231757211	0.0484745434660017
Island	DENND4B	0.000810603061025442	0.0484745434660017
N_Shore	PACS2;PACS2	0.000810727267820779	0.0484759856774443
		0.000810888838804029	0.0484796613817752
	PTPRN2;PTPRN2;PTPF	0.000811495107116206	0.0484914274562245
Island	DNAH5	0.000811519587364163	0.0484914274562245
Island	GFI1;GFI1	0.000811550597756915	0.0484914274562245
		0.000811632924121326	0.0484914274562245
	PDE7B	0.000811646477744336	0.0484914274562245
		0.000811686372554817	0.0484914274562245
Island	TMEM175	0.000811822467577381	0.0484935762961785
	HDAC4	0.000812095441784496	0.0485037793795654
		0.000812267943479261	0.0485037793795654
		0.000812507323362587	0.0485037793795654
N_Shore	HIF3A;HIF3A;HIF3A	0.000812540061511322	0.0485037793795654
Island	WSCD2	0.000812588550189066	0.0485037793795654
Island	GFRA2;GFRA2;GFRA2	0.000812797423148354	0.0485037793795654
Island		0.000812846859248843	0.0485037793795654
	MAGI1;MAGI1;MAGI1	0.000813138683254835	0.0485037793795654
	ZNF767;ZNF767	0.000813217787749958	0.0485037793795654
		0.000813244296557263	0.0485037793795654
Island		0.000813280235308114	0.0485037793795654
		0.000813397164906839	0.0485037793795654
S_Shelf		0.000813461194547187	0.0485037793795654
N_Shore	CXXC4	0.000813497376052502	0.0485037793795654
N_Shelf	PDCD2;PDCD2	0.000813571926926776	0.0485037793795654
Island	AFF2;AFF2;AFF2;AFF2;	0.00081359563037132	0.0485037793795654
S_Shelf	ITM2C;ITM2C;ITM2C	0.000814022998566008	0.0485143817522055
	C11orf41	0.000814060204291963	0.0485143817522055
	NRG1;NRG1;NRG1;NRG1	0.000814222658321206	0.0485143817522055
	ATP11A;ATP11A	0.00081424409496111	0.0485143817522055
Island	IQSEC3;IQSEC3	0.000814352295223609	0.0485143817522055
		0.000814681935138764	0.0485143817522055
Island		0.000814690638184003	0.0485143817522055
	DPPA2	0.000814891204485124	0.0485143817522055
N_Shelf	BMS1P1;BMS1P5	0.000814919076735223	0.0485143817522055
	CDC42BPB	0.000815000891165471	0.0485143817522055
Island	KIAA0427;KIAA0427	0.000815014241246354	0.0485143817522055
Island		0.00081509362211341	0.0485143817522055
S_Shelf	MAD1L1;MAD1L1;MAD1	0.000815306213719185	0.0485143817522055

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		0.000815317056727396	0.0485143817522055
Island	RAP1GAP;RAP1GAP;R	0.000815464226352133	0.0485143817522055
	MCF2L;MCF2L	0.000815528949719079	0.0485143817522055
		0.000815568730333956	0.0485143817522055
	MAGEA10;MAGEA10;M	0.000815576516236942	0.0485143817522055
		0.000815780860088383	0.0485186870414753
N_Shore		0.000815849248471119	0.0485186870414753
S_Shelf		0.000816221465669578	0.0485348632732251
	TMEM105	0.000816442337855924	0.0485420372307968
	LOC442245	0.000816852163978347	0.0485438051122701
		0.000817137781150051	0.0485438051122701
Island	PLEKHG3	0.000817148899235786	0.0485438051122701
S_Shelf	TGFBR2;TGFBR2	0.000817152248359958	0.0485438051122701
S_Shore	WDR77;ATP5F1	0.000817213758412743	0.0485438051122701
N_Shore		0.000817381234402681	0.0485438051122701
Island	HS3ST3A1;HS3ST3A1	0.000817443941828807	0.0485438051122701
N_Shore		0.000817758412148772	0.0485438051122701
Island	LEP	0.000817997207062027	0.0485438051122701
	CUX1;CUX1;CUX1	0.000818203424301205	0.0485438051122701
	TSSC1	0.000818363568514522	0.0485438051122701
Island	BCL11B;BCL11B	0.000818405784331579	0.0485438051122701
N_Shelf	SCYL3;SCYL3	0.000818439972852741	0.0485438051122701
Island	RNF39;RNF39	0.000818449118213001	0.0485438051122701
S_Shore	KLHL6	0.0008185445249051	0.0485438051122701
	LPAR1;LPAR1	0.000818602467680837	0.0485438051122701
Island	GJA8	0.000818675996428593	0.0485438051122701
Island	ZBTB46	0.000818834292827244	0.0485438051122701
	LOC399959	0.000818870347403383	0.0485438051122701
S_Shore		0.000818896114514454	0.0485438051122701
	PBX4	0.000819174053949301	0.0485438051122701
	ASXL3	0.000819253563008768	0.0485438051122701
Island		0.00081927047001554	0.0485438051122701
	ESYT2	0.000819493013959296	0.0485438051122701
		0.00081951309386397	0.0485438051122701
Island	RHPN1	0.000819777612596377	0.0485438051122701
Island		0.000819830637254991	0.0485438051122701
Island		0.000819841758934505	0.0485438051122701
		0.00081990996763205	0.0485438051122701
Island		0.000820004237760127	0.0485438051122701
	NOD2	0.000820100087256513	0.0485438051122701
Island		0.00082031899525693	0.0485438051122701
N_Shore	WHSC2	0.000820401244925297	0.0485438051122701
		0.000820487733580011	0.0485438051122701
S_Shelf	WNK4	0.000820501151562227	0.0485438051122701
Island	TDRD6;TDRD6	0.000820610204811695	0.0485438051122701
	UBE3C	0.000821048479079639	0.0485438051122701
	ZNF699	0.000821150025936411	0.0485438051122701
Island	ACOT7;ACOT7;ACOT7;	0.000821258281687196	0.0485438051122701
N_Shore	MIR548F5;NBEA;MAB2	0.000821328137844688	0.0485438051122701
	MCPH1	0.00082145075488147	0.0485438051122701
N_Shore	CSGALNACT1;CSGALN	0.000821705850196755	0.0485438051122701
S_Shelf	SPNS2;MYBBP1A;MYB	0.000821747211975826	0.0485438051122701
	HILS1;HILS1;SGCA;SG	0.000821755064886664	0.0485438051122701
Island	SEMA4C	0.000821929568472603	0.0485438051122701
Island	ACTN1;ACTN1;ACTN1	0.000822017720938107	0.0485438051122701

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S_Shelf		0.000822204303275539	0.0485438051122701
N_Shore		0.000822380833748122	0.0485438051122701
Island	F10	0.000822407455298452	0.0485438051122701
Island	KCNA4	0.000822572187089564	0.0485438051122701
Island	EGFL8	0.000822573526296481	0.0485438051122701
	RNF216;RNF216	0.00082263410349545	0.0485438051122701
N_Shelf	SENP7;SENP7	0.000823010151314356	0.0485438051122701
		0.000823234079286213	0.0485438051122701
Island	WBSCR17	0.000823348983972211	0.0485438051122701
N_Shore	TPPP	0.000823447207773674	0.0485438051122701
N_Shelf	ZMIZ1	0.000823549222539398	0.0485438051122701
S_Shore	NDUFAF1	0.000823555356237269	0.0485438051122701
N_Shore	HAND2	0.000823614057269537	0.0485438051122701
		0.000823767096481561	0.0485438051122701
	COL8A1;MIR548G;COL	0.000823877458205189	0.0485438051122701
	ABTB1;ABTB1;ABTB1	0.000823884878401269	0.0485438051122701
	MAD1L1;MAD1L1;MAD1	0.00082390884057215	0.0485438051122701
Island	IGDCC4	0.000823924038414225	0.0485438051122701
Island	PAQR9	0.000823957568055961	0.0485438051122701
Island	VAX2	0.00082400437035542	0.0485438051122701
		0.00082408798604402	0.0485438051122701
S_Shore	SLC16A2	0.000824129012677517	0.0485438051122701
N_Shore	F12	0.000824207771066444	0.0485438051122701
N_Shore	RABEPK	0.000824218111803644	0.0485438051122701
	HIPK3;HIPK3	0.00082425909028607	0.0485438051122701
Island	TOLLIP	0.000824393042833011	0.0485438051122701
	PXDN	0.000824398124355126	0.0485438051122701
S_Shore	PHYHIPL;PHYHIPL	0.000824487871765077	0.0485438051122701
S_Shore	ZNF397OS;ZNF397OS	0.000824562169310827	0.0485438051122701
N_Shore		0.00082470989090605	0.0485438051122701
Island		0.000824744778800025	0.0485438051122701
	TLR2	0.000824877376077941	0.0485438051122701
N_Shore	MAD1L1;MAD1L1;MAD1	0.000824922780641927	0.0485438051122701
	PAGE2B	0.000824930009328581	0.0485438051122701
N_Shelf	TRIM39;TRIM39	0.000824956487986549	0.0485438051122701
N_Shore	ZNF83;ZNF83;ZNF83;Z	0.000824963294952211	0.0485438051122701
	CXorf26	0.000824985269190006	0.0485438051122701
	FAM58B	0.000825246496945519	0.0485438051122701
Island	FZD10	0.000825492340862971	0.0485438051122701
Island	ATG4B;ATG4B	0.000825555074653772	0.0485438051122701
S_Shore	SMG7;SMG7;SMG7	0.000825652058334096	0.0485438051122701
		0.000825683971489852	0.0485438051122701
S_Shelf		0.000825709631095333	0.0485438051122701
	C10orf105;CDH23	0.000825791348424442	0.0485438051122701
Island	PON1;PON1	0.000825890077182973	0.0485438051122701
Island	COLEC11;COLEC11	0.000825901872371828	0.0485438051122701
Island		0.000826358918856785	0.0485438051122701
Island	INPP4B;INPP4B	0.000826370765566054	0.0485438051122701
	ASB2	0.000826395973953321	0.0485438051122701
N_Shore		0.00082655655318533	0.0485438051122701
S_Shelf	HCCA2	0.000826590580871844	0.0485438051122701
Island	C10orf11	0.000826825341030073	0.0485438051122701
S_Shelf	JPH3	0.00082686522677212	0.0485438051122701
Island	CARD14;CARD14	0.000826905605274936	0.0485438051122701
Island		0.000827057403064129	0.0485438051122701

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Island		0.000827076673367626	0.0485438051122701
		0.000827173006869537	0.0485438051122701
		0.000827399990471006	0.0485438051122701
	FLJ22536	0.000827672561769658	0.0485438051122701
		0.000827811010531326	0.0485438051122701
	LCLAT1;LCLAT1	0.00082789665706296	0.0485438051122701
	CCDC40	0.000827908037067647	0.0485438051122701
	RERE;RERE	0.000827995843447674	0.0485438051122701
Island	CDH22	0.00082818954571159	0.0485438051122701
Island	PCDHB14	0.000828249761337362	0.0485438051122701
Island	PCDHA1;PCDHA1;PCD	0.000828489596140981	0.0485438051122701
	LGALS3BP	0.000828511785637742	0.0485438051122701
S_Shore	TBC1D15;TBC1D15;TB	0.000828524678492041	0.0485438051122701
	ANKRD26P1	0.000828622755599517	0.0485438051122701
Island	RHBDF1	0.000828697458720383	0.0485438051122701
		0.000828704274303436	0.0485438051122701
	QKI;QKI;QKI;QKI	0.000828766109586122	0.0485438051122701
Island	NEURL1B	0.000828768163258371	0.0485438051122701
N_Shore	RASA3	0.000828828156657442	0.0485438051122701
Island		0.000828893140466994	0.0485438051122701
N_Shelf	RYR1;RYR1	0.00082902012750662	0.0485438051122701
	EIF3B;EIF3B	0.000829220137173637	0.0485438051122701
Island		0.00082922641504312	0.0485438051122701
N_Shore		0.000829258113050034	0.0485438051122701
S_Shore	ESCO2	0.000829275235871062	0.0485438051122701
		0.000829365838058291	0.0485438051122701
S_Shelf	C13orf15	0.000829538820719347	0.0485438051122701
Island		0.000829671413220106	0.0485438051122701
	C21orf34	0.000829760927222416	0.0485438051122701
Island	EBF3	0.000829818149218348	0.0485438051122701
	TBCK;TBCK;TBCK;TBC	0.000829910397418805	0.0485438051122701
	RUNX1T1;RUNX1T1	0.000830089149122612	0.0485438051122701
	MYO7B	0.000830168188078003	0.0485438051122701
N_Shore		0.000830170976254328	0.0485438051122701
Island	SPTBN2	0.00083017604523677	0.0485438051122701
	C2orf3	0.000830297195757241	0.0485438051122701
S_Shore	TRRAP	0.000830312395525301	0.0485438051122701
S_Shore	MEX3D	0.0008304583557162	0.0485438051122701
		0.00083052966533585	0.0485438051122701
N_Shore	MDFIC;MDFIC;MDFIC	0.000830604476261564	0.0485438051122701
N_Shelf	CAMTA1	0.000830768171364066	0.048543914873731
Island	SLC6A19	0.000830806814408417	0.048543914873731
Island	RPL13AP3	0.000830965696240626	0.0485473414754814
Island	NXN	0.000831314411947078	0.0485521987247525
N_Shore	GNA12	0.000831330744277489	0.0485521987247525
Island	GCM2	0.000831363909971645	0.0485521987247525
Island	PITPNB;LOC284900;PI	0.000831472970075815	0.0485521987247525
	PCSK6;PCSK6;PCSK6;P	0.000831550071587926	0.0485521987247525
Island	ZNF703	0.00083191279405665	0.0485666083868036
N_Shelf	GRAMD2	0.000832269445591612	0.0485666083868036
	RNU5E;RNU5D;CKMT2	0.000832355894146494	0.0485666083868036
Island		0.000832363634437234	0.0485666083868036
	CECR1;CECR1	0.000832586426609818	0.0485666083868036
Island	FLI1;FLI1	0.000832806932795273	0.0485666083868036
	LCP1	0.000832987565804288	0.0485666083868036

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Island	RALGAPA2	0.000833127776411993	0.0485666083868036
	CLRN1;CLRN1OS	0.000833148568320986	0.0485666083868036
	RALB	0.000833183903167301	0.0485666083868036
		0.000833270895691037	0.0485666083868036
Island	ANKRD23	0.000833281047866238	0.0485666083868036
	EPB42;EPB42	0.000833328707622155	0.0485666083868036
	ATP2B1;ATP2B1	0.000833337412035434	0.0485666083868036
		0.000833474058148092	0.0485666083868036
Island	RNF39;RNF39	0.000833595249351191	0.0485666083868036
Island	DSCAML1	0.000833632184641534	0.0485666083868036
N_Shore	DNAJC15	0.00083373461602559	0.0485666083868036
Island	PCDHGA4;PCDHGC3;P	0.000833755578164298	0.0485666083868036
		0.000833809031880165	0.0485666083868036
Island	ESPNL	0.000833902679697845	0.0485666083868036
N_Shore		0.000834171787167204	0.0485764399206151
S_Shelf		0.000834279769190115	0.0485768873783364
	MBD2	0.000834806105764884	0.0485804795856582
N_Shelf		0.000834809607175333	0.0485804795856582
Island	CACNA2D4	0.000834873602947431	0.0485804795856582
N_Shelf	ADAM8;ADAM8;ADAM8	0.00083503600482659	0.0485804795856582
Island	ZNF775	0.000835108968968663	0.0485804795856582
Island	RNF185;RNF185;RNF18	0.000835145010539624	0.0485804795856582
	AGPAT4	0.000835166702632452	0.0485804795856582
	MAD1L1;MAD1L1;MAD1	0.000835258837371008	0.0485804795856582
S_Shore		0.000835628534681297	0.0485804795856582
Island	NKAPL	0.000835649070721629	0.0485804795856582
Island	HOXD10	0.000835837420694554	0.0485804795856582
	FBXW8;FBXW8	0.000835891008128714	0.0485804795856582
Island	FBXL19	0.000836070575872786	0.0485804795856582
Island	CBLN2	0.000836081019591343	0.0485804795856582
	ODZ2	0.000836085256112425	0.0485804795856582
Island		0.000836419444769738	0.0485804795856582
	C7orf28B	0.000836450139064379	0.0485804795856582
N_Shelf	BANP;BANP	0.000836458727736934	0.0485804795856582
		0.000836481778925965	0.0485804795856582
Island	ACOX3;ACOX3	0.000836984123026867	0.0485804795856582
Island		0.000837053424086289	0.0485804795856582
Island	ZNF154;ZNF154	0.00083714077274751	0.0485804795856582
	DIP2C	0.000837151704786318	0.0485804795856582
S_Shore	MIR124-2	0.000837312381382799	0.0485804795856582
Island	HS3ST3B1;MGC12916	0.000837454327194448	0.0485804795856582
	TRIO	0.000837523922803398	0.0485804795856582
S_Shelf	MGC23270	0.000837526331487978	0.0485804795856582
N_Shelf		0.00083756532127232	0.0485804795856582
		0.000837604488245962	0.0485804795856582
N_Shore	COL4A2	0.000837771334098759	0.0485804795856582
	SMYD3;SMYD3	0.000837803967727938	0.0485804795856582
	LOC643837	0.000837812094053428	0.0485804795856582
	MEOX2	0.000837821281531456	0.0485804795856582
	KLHL5;KLHL5	0.000837983936126299	0.0485804795856582
Island		0.00083804517588948	0.0485804795856582
Island		0.000838059215829226	0.0485804795856582
		0.000838136639596324	0.0485804795856582
	MGMT	0.000838193542666083	0.0485804795856582
Island	SHC2	0.000838313813871757	0.0485804795856582

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		0.000838353684771448	0.0485804795856582
S_Shore		0.000838524512192903	0.0485845656619007
		0.000838980303712929	0.0486011057318784
Island	LAYN;LAYN	0.000839010674700325	0.0486011057318784
	CRTAC1	0.00083912157686291	0.0486017170191496
	PDE7B	0.000839321142072586	0.0486061298174959
N_Shelf	PRKACA;PRKACA	0.000839459469366372	0.0486061298174959
	RNF144A	0.000839700790781739	0.0486061298174959
Island	MAD1L1;MAD1L1;MAD1	0.000839814389400959	0.0486061298174959
N_Shelf	FCHSD2	0.000839900920247454	0.0486061298174959
	SFTPD	0.000839974508978906	0.0486061298174959
S_Shore		0.000839991969805017	0.0486061298174959
	UBN1;UBN1	0.00084000063298909	0.0486061298174959
N_Shore	SYT3;SYT3;SYT3	0.000840201949393172	0.0486118449269946
Island	PXDN	0.000840300140873997	0.0486118449269946
N_Shelf	TBCD	0.000840790720636938	0.0486303335380903
Island	PMEPA1;PMEPA1;PME	0.000840888781637685	0.0486303335380903
	MLPH;MLPH	0.000840920958822085	0.0486303335380903
	TEX12;TEX12	0.000841229664446611	0.0486309066014384
S_Shore	ADAMTS2;ADAMTS2	0.000841411904977519	0.0486309066014384
	DEAF1	0.000841420368076298	0.0486309066014384
		0.000841457504902625	0.0486309066014384
Island	OSR1	0.000841770052728168	0.0486309066014384
Island		0.000841780871187699	0.0486309066014384
Island	CIT	0.000841821553952049	0.0486309066014384
	FAM177B	0.000841839027874071	0.0486309066014384
N_Shelf	ZNF704	0.000841994910760616	0.0486309066014384
	ADCY5	0.000842010730839158	0.0486309066014384
Island	C19orf41	0.000842076604981062	0.0486309066014384
	C10orf11	0.000842135784166136	0.0486309066014384
	NKD1	0.000842565356118026	0.048649912506183
Island	C3orf59	0.000842912970658785	0.0486594193973921
N_Shore		0.000842930942536767	0.0486594193973921
		0.000843258374653406	0.0486725196405685
Island	OR2L13;OR2L13	0.000843592649916919	0.0486851810439212
N_Shore	GABRG3	0.000843678778716009	0.0486851810439212
		0.000843806378216243	0.0486867434035718
Island	SOX14	0.000844470397313306	0.0487142492942018
		0.000844484255560044	0.0487142492942018
	TRRAP	0.000844585835760643	0.0487143068839792
S_Shelf	TTC31;TTC31	0.000844736532455146	0.0487171970804166
N_Shelf	WNT9A	0.000845178635714697	0.048734107049012
	PIK3AP1	0.000845284355553634	0.048734107049012
S_Shore	DLX6AS;DLX6	0.000845331612695503	0.048734107049012
	ASB2	0.000845775424707377	0.048753863488144
S_Shore	SLC35F3	0.000845875630807565	0.048753863488144
	DYNC1H1	0.000846125623957166	0.0487624693982692
S_Shelf		0.000846264129696078	0.0487646489726416
Island	MYO9B;MYO9B	0.000846574774870645	0.0487763954604748
S_Shore	ACTN1;ACTN1;ACTN1	0.000846764808736638	0.0487763954604748
Island	TBXAS1;TBXAS1;HIPK2	0.000846857758181995	0.0487763954604748
Island	SLFNL1;SLFNL1	0.000846870819030883	0.0487763954604748
S_Shelf	MAD1L1;MAD1L1;MAD1	0.000847082916449862	0.0487828101676075
N_Shore	KIAA1875;MAF1	0.000847222265788219	0.0487850343452478
N_Shore	MACROD1	0.000847532329821172	0.0487866588228051

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N_Shore		0.000847716968131698	0.0487866588228051
N_Shelf		0.000847721841576666	0.0487866588228051
N_Shelf		0.000847906741657122	0.0487866588228051
		0.000847922229291435	0.0487866588228051
		0.000847927698282347	0.0487866588228051
	TMEM132D	0.000848025057608962	0.0487866588228051
Island	SOX1;SOX1	0.000848056327113397	0.0487866588228051
N_Shore	LOC641518;LEF1;LEF1	0.000848385027774384	0.0487980747857704
	GRIP1;GRIP1	0.000848488049104828	0.0487980747857704
Island	OBSCN;OBSCN	0.000848557034730312	0.0487980747857704
	UPK1B	0.000849166953049396	0.0488273518384956
		0.000849299235274037	0.0488284709651115
	CBFA2T3	0.000849452332072539	0.0488284709651115
	PSD3;PSD3	0.000849570159779157	0.0488284709651115
N_Shore	NSUN2	0.000849589686311865	0.0488284709651115
		0.000850069294393025	0.0488440430853593
		0.000850129073592734	0.0488440430853593
Island	BNIP3	0.000850297067538661	0.0488440430853593
N_Shore		0.000850319400754219	0.0488440430853593
	CDH23	0.00085039169061972	0.0488440430853593
Island	STAP2;STAP2	0.000850475473309132	0.0488440430853593
	CLMN	0.000850566581080721	0.0488440430853593
		0.000850756667881121	0.0488491669438677
Island	ZBTB46	0.000850948729229644	0.0488511981553746
		0.000850993772439777	0.0488511981553746
S_Shore		0.000851389240665865	0.0488624789882376
	PCNXL2	0.000851491985036202	0.0488624789882376
	H2AFY2	0.000851505232246413	0.0488624789882376
	RASA3	0.000851751682313936	0.0488624789882376
		0.000851821972368922	0.0488624789882376
S_Shelf	ZFP3	0.000851888624368346	0.0488624789882376
S_Shore	PPIL1	0.000851896500442221	0.0488624789882376
Island	FRMD1;FRMD1	0.000852232676419949	0.0488759728842027
S_Shore	GALNT2	0.000852494555744141	0.048882691075944
Island		0.000852551678146904	0.048882691075944
S_Shore	GRP;GRP;GRP	0.000852843951091098	0.0488931786955718
N_Shelf	TMCO4	0.000852936492642102	0.0488931786955718
N_Shelf	TERT;TERT	0.000853168587549426	0.0489004424946734
Island		0.000853265141222289	0.0489004424946734
		0.000853415975119841	0.0489028221465653
	MIR487A	0.000853508606008189	0.0489028221465653
Island	TMCC2	0.000853736285187738	0.0489100811832921
	DPP6;DPP6;DPP6	0.000854019753393499	0.0489205342474638
Island	CD1D	0.000854302017140296	0.048929274173167
Island		0.000854437967728811	0.048929274173167
	TTC12	0.000854500706453002	0.048929274173167
Island		0.0008545899334304	0.048929274173167
Island	BRF1	0.000854677457296223	0.048929274173167
	ATXN1;ATXN1	0.000855090088575162	0.0489471111156087
	C22orf9;C22orf9	0.000855241917890429	0.0489500167669915
	ADAM18	0.000855572131533921	0.048961688631791
N_Shore	ZIC1	0.000855995706366839	0.048961688631791
Island		0.000856186909681602	0.048961688631791
	C7orf16;C7orf16	0.000856187862674308	0.048961688631791
S_Shore		0.00085636156767146	0.048961688631791

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	PPP2R2D;PPP2R2D;PPP2R2D	0.000856425101480384	0.048961688631791
Island	DUOX1;DUOX1	0.000856508341002866	0.048961688631791
Island	ADAD1;ADAD1;ADAD1	0.000856552552436295	0.048961688631791
S_Shelf	TRIM3;TRIM3	0.00085659751313902	0.048961688631791
Island	INPP5A	0.000856618703771659	0.048961688631791
Island	ST8SIA2	0.000856793497123224	0.048961688631791
S_Shore	LOC389332	0.000856821182203032	0.048961688631791
	EP400	0.000856850365541884	0.048961688631791
Island	ABCA2;ABCA2	0.000856861142503609	0.048961688631791
S_Shore	C5orf37	0.000857050986932411	0.0489667593778507
		0.000857252024183862	0.0489689474062291
N_Shore	SHANK2	0.000857418755633458	0.0489689474062291
Island		0.000857489352255613	0.0489689474062291
Island		0.000857493713833126	0.0489689474062291
S_Shore	JRKL	0.00085772126473039	0.0489746779378094
	ABLIM2;ABLIM2;ABLIM2	0.00085779629989457	0.0489746779378094
N_Shelf		0.000858049579177527	0.048975865407432
Island	CSRNP2	0.000858160794607742	0.048975865407432
N_Shore	KIAA1949;KIAA1949	0.000858215241759212	0.048975865407432
N_Shelf		0.000858249740228422	0.048975865407432
Island	ALOX12	0.00085840801906253	0.048975865407432
N_Shelf	ADSS	0.000858423829956518	0.048975865407432
N_Shelf	ARHGEF9	0.0008585697680583	0.0489784220158818
Island		0.000858744604665086	0.0489799457289298
N_Shelf		0.000858798738718985	0.0489799457289298
Island	TCL1A;TCL1A	0.000859124775749885	0.048986655997366
	LOC100128023	0.000859171546249631	0.048986655997366
S_Shore	EBF3	0.000859266197283283	0.048986655997366
	CDKAL1	0.000859320971152886	0.048986655997366
	UROC1;UROC1	0.000859560962268607	0.0489904218766669
	PRKCQ	0.000859589335896176	0.0489904218766669
S_Shelf	BAIAP2;BAIAP2;BAIAP2	0.00086010343203432	0.0490019373382383
S_Shore		0.000860169271898314	0.0490019373382383
S_Shore	LMTK2	0.000860226788033215	0.0490019373382383
		0.000860240050717809	0.0490019373382383
S_Shore		0.000860310716688908	0.0490019373382383
S_Shelf	PIK3CD	0.000860398441386215	0.0490019373382383
	GCNT2;GCNT2;GCNT2	0.000860565460954672	0.049004613124455
Island		0.000860647786582594	0.049004613124455
	HDAC4	0.000860759518190293	0.0490052137824748
	RAD52	0.000861131543625196	0.0490191009276998
	TMEM132D	0.000861309555399114	0.0490191009276998
Island	ROR2	0.000861463246049098	0.0490191009276998
		0.000861469775595718	0.0490191009276998
		0.000861509496921655	0.0490191009276998
	C12orf59;C12orf59	0.000861651744566202	0.049021435591099
S_Shore		0.000861881894418194	0.049028228113189
	ZNF443	0.000862144402276237	0.049028228113189
S_Shore		0.000862330292782134	0.049028228113189
N_Shelf	BAIAP2;BAIAP2;BAIAP2	0.000862338356891537	0.049028228113189
Island	SLC7A9;SLC7A9	0.000862379938860357	0.049028228113189
N_Shelf	F8;F8	0.000862731304975935	0.049028228113189
Island	GABRD	0.000862772205640998	0.049028228113189
	WDR60	0.000862812941585102	0.049028228113189
S_Shore	PTHLH;PTHLH;PTHLH	0.000863093331615004	0.049028228113189

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Island		0.000863114789922893	0.049028228113189
	ADCY9	0.000863171052046894	0.049028228113189
	CHRFAM7A;CHRFAM7A	0.000863295124357536	0.049028228113189
S_Shore	RGPD3	0.000863462424492758	0.049028228113189
		0.000863496751989126	0.049028228113189
	NACA2;NACA2	0.000863504088911654	0.049028228113189
	KLRC4	0.000863650725329515	0.049028228113189
Island	MGAT4B;MGAT4B	0.000863659572277425	0.049028228113189
	ZNHIT1	0.000863712345604005	0.049028228113189
N_Shore	INPP5E	0.000863760850541767	0.049028228113189
S_Shore	RGPD8;RGPD5	0.000863795737345464	0.049028228113189
	DOCK9;DOCK9;DOCK9	0.000863939431624219	0.0490294120916875
Island	GPR137B	0.000864271610535487	0.0490294120916875
Island		0.000864280532047187	0.0490294120916875
Island	TINAGL1	0.000864536371466254	0.0490294120916875
	PTPRG	0.000864546604376026	0.0490294120916875
N_Shore	POU3F4;POU3F4	0.000864607201766918	0.0490294120916875
Island		0.000864832263912486	0.0490294120916875
N_Shelf	TMEM64;TMEM64	0.00086485472417084	0.0490294120916875
	C2orf66	0.000864889955517977	0.0490294120916875
	NPPA	0.000864921043278173	0.0490294120916875
		0.000864930154155532	0.0490294120916875
Island	BPHL;BPHL;BPHL;BPHL	0.000865277732215696	0.0490407018552507
S_Shore	BCOR;BCOR;BCOR;BCOR	0.000865370954910078	0.0490407018552507
	SEMA3A	0.000865511013740315	0.0490407018552507
Island	KCNIP2;KCNIP2;KCNIP2	0.000865534340491784	0.0490407018552507
	GTSF1	0.000865670056915629	0.0490426541485158
Island	SIM2;SIM2	0.000865853537683087	0.0490473116536095
	PDXDC1	0.00086630745410138	0.0490563416350102
Island		0.000866378082882869	0.0490563416350102
N_Shore	THAP4	0.000866512246152958	0.0490563416350102
Island		0.000866716578211754	0.0490563416350102
	PWWP2A	0.000866756026398005	0.0490563416350102
N_Shore		0.000866765326458751	0.0490563416350102
	NRG1	0.000866849232054878	0.0490563416350102
N_Shore	KIAA0415	0.000867026476702637	0.0490563416350102
		0.000867060510028391	0.0490563416350102
Island	TCF23	0.000867106056544495	0.0490563416350102
N_Shore		0.00086712711657941	0.0490563416350102
		0.00086762482708087	0.0490648459918944
Island	PAX1	0.000867643808856497	0.0490648459918944
	ATP10A	0.000867679461754491	0.0490648459918944
Island	ATP11A;ATP11A	0.000867682663336758	0.0490648459918944
S_Shelf	TMEM171;TMEM171	0.00086796525032976	0.0490701635501335
Island	MCHR2;MCHR2	0.000867979334401474	0.0490701635501335
N_Shelf	CCHCR1;CCHCR1;CCHCR1	0.000868328696030529	0.0490831422754288
Island	KRBA1	0.000868411595846072	0.0490831422754288
	PRR4;PRR4	0.000868628882280869	0.0490892263527366
	PARD3	0.00086874895561879	0.0490892263527366
Island	MATN4;MATN4;MATN4	0.000868877175435086	0.0490892263527366
S_Shelf	PPM1B;PPM1B;PPM1B	0.000868937841798946	0.0490892263527366
	NPAS2	0.000869120166949794	0.0490892263527366
Island	PTPRN2;PTPRN2;PTPRN2	0.000869127375160721	0.0490892263527366
	ADARB2	0.000869377667714471	0.0490913676382185
S_Shore	VANGL2	0.000869400955653466	0.0490913676382185

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Island	PTPRS;PTPRS;PTPRS;	0.000869471118874052	0.0490913676382185
	KLRAQ1;KLRAQ1;KLRAQ1;	0.000869683939164621	0.0490913676382185
	FAM49A	0.000870126488237463	0.0490913676382185
		0.000870174835523335	0.0490913676382185
Island	WDR88;WDR88	0.000870378036927106	0.0490913676382185
N_Shelf		0.000870513112029703	0.0490913676382185
N_Shore		0.0008705526942028	0.0490913676382185
Island	KLHL29	0.000870571688397227	0.0490913676382185
	TRAPPC9;TRAPPC9	0.000870658177332188	0.0490913676382185
S_Shelf	ALDH1B1	0.000870723586206455	0.0490913676382185
	GABRR2	0.000870756553173502	0.0490913676382185
		0.000871034177014442	0.0490913676382185
	GNA12	0.000871067516984252	0.0490913676382185
Island	SLC45A4	0.000871655191536268	0.0490913676382185
S_Shelf	KIAA0913	0.000871848249921014	0.0490913676382185
S_Shore	MTG1	0.000871865389865332	0.0490913676382185
Island		0.000871887603143678	0.0490913676382185
N_Shore	GUSBL1	0.000871926977643318	0.0490913676382185
	EIF2C2;EIF2C2	0.000871959981445491	0.0490913676382185
	PRAGMIN	0.000872008229562303	0.0490913676382185
N_Shelf		0.000872084421537226	0.0490913676382185
		0.000872203889834642	0.0490913676382185
	RPIA	0.000872258203723338	0.0490913676382185
S_Shore	TAPBP;TAPBP	0.000872375055166732	0.0490913676382185
	TMPRSS11F	0.000872564845329791	0.0490913676382185
		0.000872667168774655	0.0490913676382185
	RNF213;LOC100294362	0.000872814516936313	0.0490913676382185
		0.000872820351076118	0.0490913676382185
Island	KIAA0907	0.000872872758953232	0.0490913676382185
Island		0.000872911526648061	0.0490913676382185
	SLC6A9;SLC6A9;SLC6A9	0.000872952872815466	0.0490913676382185
S_Shelf	UNC84A;UNC84A	0.000873093714112404	0.0490913676382185
	CD48	0.000873126774975612	0.0490913676382185
Island	PQLC3	0.000873171697002339	0.0490913676382185
Island		0.000873362674392253	0.0490913676382185
Island		0.0008733664671174	0.0490913676382185
Island	CTBP2;CTBP2;CTBP2	0.000873407534617819	0.0490913676382185
		0.000873504869373372	0.0490913676382185
N_Shelf		0.000873608676127493	0.0490913676382185
N_Shelf	USP28	0.000873613981593656	0.0490913676382185
Island	PLXNB2	0.00087362566963963	0.0490913676382185
		0.000873805613288273	0.0490913676382185
	ARL15	0.000873854390025409	0.0490913676382185
		0.000873989423540222	0.0490913676382185
	CXCR6;FYCO1	0.000874131242709928	0.0490913676382185
Island	KSR2	0.000874348017592261	0.0490913676382185
		0.000874505570497308	0.0490913676382185
	DPYSL5	0.000874509137945107	0.0490913676382185
N_Shelf		0.00087454040050275	0.0490913676382185
	BBX;BBX	0.000874559713153203	0.0490913676382185
	ZNF398;ZNF398	0.000874570829272396	0.0490913676382185
	GABBR1;GABBR1;GABBR1	0.000874754208804363	0.0490913676382185
Island	PCDHB10	0.000874779093004648	0.0490913676382185
Island	GRM7;GRM7	0.000874841468198965	0.0490913676382185
N_Shelf	FAM70A;FAM70A;FAM70A	0.000875122231913658	0.0491014336157996

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N_Shore	EIF2C2;EIF2C2	0.000875783833155837	0.0491154139466454
S_Shore	C4orf49	0.00087599499764078	0.0491154139466454
S_Shelf	ANKRD44	0.000876003716904755	0.0491154139466454
Island		0.000876162259972042	0.0491154139466454
N_Shore		0.000876310507784707	0.0491154139466454
		0.000876432967424496	0.0491154139466454
	TPCN1;TPCN1	0.000876511678946821	0.0491154139466454
Island		0.000876514695361099	0.0491154139466454
Island		0.0008771443325831	0.0491154139466454
		0.000877176563800089	0.0491154139466454
	PARP4	0.000877203445326971	0.0491154139466454
Island	CELSR3	0.000877235774871359	0.0491154139466454
Island	PQLC1;PQLC1;PQLC1	0.000877291743728194	0.0491154139466454
	JAKMIP3	0.000877782733435608	0.0491154139466454
Island	IL1RAPL2	0.000877800393434434	0.0491154139466454
	IL16;IL16;IL16	0.000877803161679429	0.0491154139466454
Island		0.000877853714746832	0.0491154139466454
N_Shore		0.00087786396410147	0.0491154139466454
		0.000877896498070702	0.0491154139466454
Island		0.000877961169590836	0.0491154139466454
		0.000877997191234074	0.0491154139466454
N_Shelf	B3GNTL1	0.00087804609489089	0.0491154139466454
S_Shelf		0.000878144841434392	0.0491154139466454
		0.000878323581478186	0.0491154139466454
	PPPDE1	0.000878345697978991	0.0491154139466454
N_Shore		0.000878445260095808	0.0491154139466454
		0.000878509238627205	0.0491154139466454
Island	KDM4B	0.000878773649889126	0.0491154139466454
	TMX3	0.000878826357386578	0.0491154139466454
	PLXNA4	0.000879002795390034	0.0491154139466454
	NUP93	0.000879254480853773	0.0491154139466454
Island	ANO7	0.000879332638467489	0.0491154139466454
Island	NDUFS7	0.000879343582286234	0.0491154139466454
Island	IRX1	0.00087935300660337	0.0491154139466454
S_Shore	LRRC6	0.000879379832205813	0.0491154139466454
N_Shore	GALNT9	0.000879651358687551	0.0491154139466454
N_Shore	HOXC13	0.000879779965518508	0.0491154139466454
Island	CHST7	0.00087981645033942	0.0491154139466454
N_Shelf	UXS1	0.000879857418221392	0.0491154139466454
N_Shelf		0.00087995482142772	0.0491154139466454
	FOXK1	0.000880103601361519	0.0491154139466454
		0.000880184667340255	0.0491154139466454
Island		0.000880434036421144	0.0491154139466454
	MIR145;LOC728264	0.000880470991472048	0.0491154139466454
N_Shore		0.000880609902321448	0.0491154139466454
N_Shore	TFDP1;TFDP1	0.000880629856292318	0.0491154139466454
Island		0.00088075004469613	0.0491154139466454
	PXDN	0.000880763494666438	0.0491154139466454
S_Shore	HGFAC	0.000880804827220171	0.0491154139466454
		0.000880820460223262	0.0491154139466454
	C14orf143	0.000880948205913782	0.0491154139466454
	ACSBG2	0.000881094332650248	0.0491154139466454
		0.00088112564909098	0.0491154139466454
N_Shore		0.000881157188078666	0.0491154139466454
	HERC2	0.000881274383467063	0.0491154139466454

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Island		0.000881455218634487	0.0491154139466454
	MAGI2	0.000881516885600294	0.0491154139466454
	FAP	0.000881568712082636	0.0491154139466454
Island	TMEM90B	0.000881625100657458	0.0491154139466454
Island		0.000881816886627402	0.0491154139466454
Island		0.000882007136553158	0.0491154139466454
	KLHL29	0.000882015659184861	0.0491154139466454
Island	C19orf26	0.000882092352943669	0.0491154139466454
		0.000882103433135627	0.0491154139466454
N_Shore	TAOK2;TAOK2	0.000882124369788607	0.0491154139466454
N_Shore		0.000882133139306411	0.0491154139466454
S_Shore	SEPT6;SEPT6;SEPT6;S	0.000882165871928701	0.0491154139466454
		0.000882574049484735	0.0491309826142552
Island	SDCCAG8;AKT3	0.000882648386365838	0.0491309826142552
N_Shore	DPP6;DPP6;DPP6	0.00088275177389562	0.0491310908862326
		0.00088307532784666	0.049136546564515
	HRNBP3	0.000883206313147119	0.049136546564515
S_Shore		0.000883237096778627	0.049136546564515
Island	CLEC3B	0.000883255612224576	0.049136546564515
Island		0.000883637628086939	0.0491441273402821
		0.000883677150827209	0.0491441273402821
N_Shore	PCDHB3	0.000883751833783006	0.0491441273402821
	SCRN1;SCRN1;SCRN1	0.000883821309260583	0.0491441273402821
	TLN2	0.000883899227298193	0.0491441273402821
Island	BTN1A1	0.000884661623038129	0.049159402781004
Island		0.000884681358808196	0.049159402781004
Island	TCF25	0.000884773134535033	0.049159402781004
		0.000884799180104686	0.049159402781004
Island	PPP2R2D;PPP2R2D;PP	0.000885005714969184	0.049159402781004
	ANKRD10	0.00088512762120646	0.049159402781004
N_Shore	RASAL1	0.000885145224962836	0.049159402781004
Island	MGAT4B;MGAT4B	0.000885239582196601	0.049159402781004
N_Shore	MTHFSD;MTHFSD;MTH	0.000885269494860775	0.049159402781004
N_Shore		0.00088529475076049	0.049159402781004
S_Shore	ARHGEF10	0.000885423740965353	0.049159402781004
Island	C17orf101;C17orf101	0.000885510360727615	0.049159402781004
		0.000885595583062543	0.049159402781004
	SH3RF1	0.000885685321495185	0.049159402781004
N_Shore		0.000885833795963712	0.049159402781004
		0.000886060816845314	0.049159402781004
Island		0.000886289564877433	0.049159402781004
	MGMT	0.00088629190703143	0.049159402781004
N_Shore		0.000886309136796372	0.049159402781004
N_Shore	GSDMD;GSDMD	0.00088637164185499	0.049159402781004
		0.000886600278575196	0.049159402781004
		0.00088665195441045	0.049159402781004
S_Shelf	CDK16;CDK16;CDK16	0.000886760669535734	0.049159402781004
Island	LHX1	0.000886896645733191	0.049159402781004
		0.000887187745107593	0.049159402781004
Island	FAM47A	0.000887196205113316	0.049159402781004
Island	REXO1L2P	0.000887269342506911	0.049159402781004
S_Shelf	FSCN3	0.000887330478403103	0.049159402781004
S_Shore	RFX2;RFX2	0.000887430921746939	0.049159402781004
S_Shelf		0.00088772791654325	0.049159402781004
		0.000887731118798782	0.049159402781004

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	CRTAM	0.000887998104734551	0.049159402781004
Island		0.000888156188902013	0.049159402781004
Island		0.000888255134791223	0.049159402781004
Island	MAD1L1;MAD1L1;MAD1	0.000888273264572421	0.049159402781004
N_Shelf	SLCO4A1	0.000888281159360814	0.049159402781004
Island	HLA-L	0.000888314289120481	0.049159402781004
	PCSK6;PCSK6;PCSK6;P	0.000888680200446999	0.049159402781004
	FGF16	0.000888832429649209	0.049159402781004
	PHACTR1	0.000888918981872104	0.049159402781004
S_Shore	RFX8	0.000889101616216968	0.049159402781004
Island	BCAR1;BCAR1;BCAR1;	0.000889151506398346	0.049159402781004
Island		0.000889215670077717	0.049159402781004
N_Shore		0.000889239598748392	0.049159402781004
S_Shelf		0.00088932053489653	0.049159402781004
N_Shore		0.000889383455932184	0.049159402781004
	LIG3	0.000889563990525872	0.049159402781004
	N4BP2	0.000889575758424136	0.049159402781004
N_Shore	PLEKHA2	0.000889673677892448	0.049159402781004
N_Shelf	NCRNA00175;NCRNA0	0.000889824429272404	0.049159402781004
		0.000889849723469115	0.049159402781004
S_Shelf	RPH3AL	0.000889968081287236	0.049159402781004
N_Shore		0.000889980796425118	0.049159402781004
Island	GALNT9	0.000890169748369903	0.049159402781004
	HDAC4	0.000890315226758759	0.049159402781004
S_Shore	RBP1;RBP1;RBP1	0.000890423411160932	0.049159402781004
	ELMO1;ELMO1;ELMO1	0.000890435947806164	0.049159402781004
	KRT5	0.000890454058182299	0.049159402781004
Island	TRAPPC9;TRAPPC9	0.000890634210935889	0.049159402781004
	RPSAP52	0.000890643483988687	0.049159402781004
N_Shore	TCERG1L	0.000890728885967883	0.049159402781004
	C17orf77;CD300LD	0.000890831321838794	0.049159402781004
Island	GPR162;GPR162	0.000890979274059664	0.049159402781004
	STARD3NL	0.000891003183256429	0.049159402781004
S_Shelf	NMD3	0.000891062883661685	0.049159402781004
	EP400NL	0.00089111843887587	0.049159402781004
	EXTL2;EXTL2	0.000891143196678264	0.049159402781004
Island	GABRD	0.000891151832473223	0.049159402781004
N_Shore	PCGF3	0.000891177528348144	0.049159402781004
Island	PPP1R2P1	0.000891757662039532	0.0491762051310097
Island	KCNS3	0.000891814120769902	0.0491762051310097
S_Shore	PDE4DIP	0.000891843670554091	0.0491762051310097
N_Shelf	CD47;CD47;CD47	0.000891910430620614	0.0491762051310097
Island	ZDHHC20	0.000891989804523658	0.0491762051310097
Island	CSRNP1	0.000892150825462231	0.0491794842410647
N_Shore	MEIS1	0.000892296055894658	0.0491818922580153
Island	GAK	0.000892440618905935	0.049183759047596
	SLC9A4	0.000892622812867227	0.049183759047596
S_Shore		0.000892634578079532	0.049183759047596
N_Shore	L1TD1;L1TD1	0.000892809764396934	0.0491854674378625
	AXIN1;AXIN1	0.000892868692951401	0.0491854674378625
Island	FLJ30058	0.000893037577080552	0.0491887935215506
Island	KIAA1239	0.000893260526177024	0.0491887935215506
	C3orf21	0.000893291590450346	0.0491887935215506
S_Shelf	RIPK4	0.000893624216154327	0.0491887935215506
N_Shore		0.000893756158749968	0.0491887935215506

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	SHANK2	0.00089398139733513	0.0491887935215506
Island	TPPP3;TPPP3;ZDHC1	0.000894064979288286	0.0491887935215506
	CNGB1;CNGB1	0.000894074174629777	0.0491887935215506
	PELI2	0.000894075404996488	0.0491887935215506
N_Shore		0.000894114916140712	0.0491887935215506
	SCFD2	0.000894216374298521	0.0491887935215506
Island	HTR7P;HEBP1	0.000894216807607081	0.0491887935215506
	PHLDB2;PHLDB2;PHLD	0.000894249371717862	0.0491887935215506
S_Shelf		0.000894370151736623	0.0491898505268953
Island		0.000894583159959985	0.0491905371509732
	HIP1R	0.000894676882949334	0.0491905371509732
	SATB2	0.000894687331364111	0.0491905371509732
Island	MYOM2	0.00089502083844808	0.0491939431059389
N_Shore		0.000895083625753965	0.0491939431059389
	SLC6A8;SLC6A8;SLC6A	0.000895128157497208	0.0491939431059389
		0.000895242405848874	0.0491939431059389
	LPCAT1	0.0008953015863645	0.0491939431059389
	TUSC3;TUSC3	0.000895658001381873	0.0491939431059389
	VEPH1;VEPH1;VEPH1;V	0.000895832535423579	0.0491939431059389
	MAGEB2;MAGEB2	0.000895870858717479	0.0491939431059389
		0.000895892000938237	0.0491939431059389
	SLC38A4;SLC38A4	0.000896114838337084	0.0491939431059389
N_Shore	ASAP1	0.000896332290298784	0.0491939431059389
	PRPF8	0.00089650208836075	0.0491939431059389
Island		0.000896516230584513	0.0491939431059389
		0.000896588534376043	0.0491939431059389
		0.000896668648824353	0.0491939431059389
S_Shore	ACSF3;ACSF3;ACSF3	0.000896773472978101	0.0491939431059389
Island	FAM83H	0.000896868028632884	0.0491939431059389
N_Shore	PRKX	0.000896879045549621	0.0491939431059389
Island		0.000896943419449278	0.0491939431059389
Island	TTC22;TTC22	0.000897088856394782	0.0491939431059389
	PRDM2;PRDM2;PRDM2	0.000897109500793333	0.0491939431059389
Island		0.000897144758399071	0.0491939431059389
	DOC2A	0.000897198169240098	0.0491939431059389
N_Shelf	SLC22A18;SLC22A18;S	0.000897300470400732	0.0491939431059389
Island		0.000897551585289568	0.0491939431059389
Island	STK32C	0.000897555733232842	0.0491939431059389
		0.000897611178937179	0.0491939431059389
	FAT1	0.000897646524330137	0.0491939431059389
		0.000897758490109406	0.0491939431059389
	IQCJ;IQCJ	0.000897796444770339	0.0491939431059389
N_Shelf	TNXB	0.000898053785666864	0.049202477346505
	YWHAQ	0.000898510504038265	0.0492202731063809
N_Shore	KIF5C	0.000898581850630506	0.0492202731063809
N_Shore		0.000898869591660581	0.0492275389170132
		0.000898987543422072	0.0492275389170132
Island	ZFYVE28	0.000899019422332075	0.0492275389170132
	STK39	0.000899399425860599	0.0492406021139753
		0.000899461326386908	0.0492406021139753
Island		0.000899601839006912	0.0492409791377771
N_Shelf		0.000899840562616104	0.0492409791377771
	P4HB	0.000899873319179015	0.0492409791377771
	ANGPT2;ANGPT2;ANG	0.000899874890514562	0.0492409791377771
		0.000900224278509672	0.0492447234784685

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Island		0.000900253693929196	0.0492447234784685
S_Shelf	ALDH1B1	0.000900361148335742	0.0492447234784685
Island		0.00090045167896696	0.0492447234784685
Island	ANKRD30A	0.000900453978467135	0.0492447234784685
S_Shore	MCF2L;MCF2L	0.000900681947551527	0.0492447234784685
S_Shore	RNF125	0.000900692834061127	0.0492447234784685
N_Shelf	LLGL2;LLGL2	0.000900926564775731	0.0492447234784685
	TTC15	0.00090101660265295	0.0492447234784685
S_Shore		0.000901063241153058	0.0492447234784685
		0.000901138243339797	0.0492447234784685
S_Shore	SALL4	0.00090116344229529	0.0492447234784685
Island		0.00090141089422144	0.0492526885541289
	IGSF9B	0.000901621626285886	0.049256823679043
Island	RTDR1;GNAZ	0.000901746021516771	0.049256823679043
	TMEM117	0.000901791680301604	0.049256823679043
Island		0.000901950927586363	0.0492585075005299
	LMO7;LMO7	0.000902025918592268	0.0492585075005299
S_Shore	BCOR;BCOR	0.000902284372812768	0.0492633217926504
	FGF8;FGF8;FGF8;FGF8	0.000902463491349264	0.0492633217926504
Island		0.000902518170750816	0.0492633217926504
N_Shore	GRIA2;GRIA2;GRIA2	0.000902582372668923	0.0492633217926504
Island		0.000902627934231024	0.0492633217926504
Island		0.000902886671278878	0.0492633217926504
	CD22	0.000903144943987353	0.0492633217926504
	FGF12;FGF12	0.0009032291542622	0.0492633217926504
		0.000903265320462048	0.0492633217926504
		0.000903380596332872	0.0492633217926504
Island		0.00090338223178255	0.0492633217926504
	TMTC1	0.000903462808330329	0.0492633217926504
Island	TMEM74	0.000903552467650848	0.0492633217926504
S_Shore		0.000903699069288313	0.0492633217926504
		0.000903738323479597	0.0492633217926504
S_Shelf	LOC400043	0.000903741525066224	0.0492633217926504
S_Shelf		0.000903876754646383	0.0492646817691709
N_Shore	SEMA6A	0.000903969910458105	0.0492646817691709
	DACH1;DACH1;DACH1	0.000904072073515983	0.0492647060087341
N_Shore	ADAMTS17	0.000904181895383632	0.0492651475398445
N_Shore	DIDO1;DIDO1;DIDO1	0.000904325251307252	0.0492674158986935
		0.000904571776171203	0.049270762294511
N_Shelf	RADIL	0.000904657260752974	0.049270762294511
S_Shore	JMJD4;SNAP47;JMJD4	0.000904777621105512	0.049270762294511
N_Shelf	PCDHB17	0.000904923462185158	0.049270762294511
Island	PAX3;PAX3;PAX3;PAX3	0.000904925688477372	0.049270762294511
	SOX13	0.000905108299659007	0.049270762294511
	JAZF1	0.00090554852140037	0.049270762294511
Island	NRN1	0.000905596804438852	0.049270762294511
S_Shore	KPRP	0.000905628892214035	0.049270762294511
Island	GPR62	0.000905647950234413	0.049270762294511
Island		0.00090580647087106	0.049270762294511
	MAEA;MAEA	0.000905810030240408	0.049270762294511
Island		0.000905838735752076	0.049270762294511
	IKZF4;IKZF4	0.000905876020844314	0.049270762294511
	SLC35F3	0.000906272723065057	0.049270762294511
	SMYD3;SMYD3	0.000906601608774672	0.049270762294511
		0.000906606080465856	0.049270762294511

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Island	FERD3L	0.000906718973770224	0.049270762294511
S_Shore	ETV1;ETV1	0.000906758158166083	0.049270762294511
Island	HCN1	0.0009069201071614	0.049270762294511
N_Shelf	HDAC4	0.000906981871600245	0.049270762294511
	KIF2B	0.000907115397982809	0.049270762294511
	EXOC2	0.000907260793879429	0.049270762294511
	ZNF616	0.000907414699781232	0.049270762294511
		0.000907418118668161	0.049270762294511
Island	VWF	0.00090742788873181	0.049270762294511
		0.000907790995565838	0.049270762294511
	CYFIP1;CYFIP1	0.000907976023580758	0.049270762294511
	SH3BP4	0.000907981090603704	0.049270762294511
		0.000908018070565692	0.049270762294511
S_Shore	TSPYL2	0.000908061708335637	0.049270762294511
N_Shelf		0.000908173138088624	0.049270762294511
		0.000908181334057813	0.049270762294511
		0.000908186823391532	0.049270762294511
	EXOC6B	0.000908245456761872	0.049270762294511
S_Shore	TMEM198	0.000908374745018326	0.049270762294511
S_Shelf		0.000908378972413034	0.049270762294511
Island	OLIG2	0.000908570010034884	0.049270762294511
S_Shore		0.00090885841065659	0.049270762294511
N_Shelf		0.000909077745689049	0.049270762294511
Island	PPM1F	0.000909167607850618	0.049270762294511
	CLEC4A;CLEC4A;CLEC4E	0.000909208888565792	0.049270762294511
N_Shore	FAM107B	0.000909289098780528	0.049270762294511
		0.000909383311690804	0.049270762294511
	ANKRD17;ANKRD17	0.000909528818588604	0.049270762294511
	PLXNA2	0.000909551459013005	0.049270762294511
		0.000909581105084896	0.049270762294511
S_Shore	ABCA2;ABCA2	0.000909584624346852	0.049270762294511
Island	SLC32A1	0.000909620045179444	0.049270762294511
	MRC2	0.000909690538845861	0.049270762294511
N_Shore	RASA3	0.000909769531643452	0.049270762294511
S_Shelf		0.000909792663460727	0.049270762294511
		0.000909792753927027	0.049270762294511
Island	LOC154822	0.000910033549932075	0.049270762294511
	XAGE3;XAGE3	0.000910113227673547	0.049270762294511
		0.000910485911053297	0.049270762294511
	GTF3C1	0.000910797233933455	0.049270762294511
		0.000910809010437561	0.049270762294511
	QSOX2	0.000910879793617416	0.049270762294511
	CAMTA1	0.000910882950785282	0.049270762294511
N_Shore	SFRS8	0.00091109375992043	0.049270762294511
S_Shore		0.000911137613993236	0.049270762294511
	ST6GALNAC3;ST6GALNAC3	0.000911138860967405	0.049270762294511
		0.000911241868060725	0.049270762294511
Island	DLK1	0.000911341722189677	0.049270762294511
S_Shore	ATP11A;ATP11A	0.00091137972874237	0.049270762294511
		0.00091139700272817	0.049270762294511
Island	C2orf54;C2orf54	0.000911500370829061	0.049270762294511
N_Shore	CCDC140	0.000911540531511641	0.049270762294511
Island		0.00091154425589052	0.049270762294511
Island		0.000911609561598334	0.049270762294511
Island	CXXC5	0.000912064756394593	0.0492865731006237

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N_Shore	ZFPM1	0.000912194444636081	0.0492865731006237
Island		0.000912207384037559	0.0492865731006237
		0.000912395568590613	0.0492912419138481
	LIPA;LIPA	0.00091258917419537	0.0492962025197605
		0.000912969145186412	0.0493112279739499
S_Shelf	TBCD;ZNF750	0.000913526102397914	0.049315997150574
N_Shelf	TM2D3;TM2D3	0.000913532244447556	0.049315997150574
N_Shore	TBR1	0.000913696375493976	0.049315997150574
	TULP4;TULP4	0.000913875322758639	0.049315997150574
S_Shore	WFDC1	0.000914115870421209	0.049315997150574
N_Shelf	FBRSL1	0.000914132048011052	0.049315997150574
Island	CERK	0.000914166608665901	0.049315997150574
Island	MLF2;MLF2	0.00091424084903151	0.049315997150574
N_Shore	ZNF324B	0.000914303365227304	0.049315997150574
	KCNAB2;KCNAB2	0.000914425977089579	0.049315997150574
Island	FZD8	0.000914475974551618	0.049315997150574
S_Shelf	ZFPM1	0.000914522703367551	0.049315997150574
N_Shore	LMF1	0.000914615894968647	0.049315997150574
	SPINK1;SPINK1	0.000914674564195169	0.049315997150574
		0.000914759560448661	0.049315997150574
Island	KCNC4;KCNC4;KCNC4	0.000914794698871446	0.049315997150574
	SEPT9;SEPT9;SEPT9;S	0.00091491782639343	0.049315997150574
Island	TNFSF9	0.000914987668625779	0.049315997150574
	ZFAT;ZFAT	0.000915080490140846	0.049315997150574
	SH3PXD2A	0.000915143439686783	0.049315997150574
Island	NR5A2;NR5A2	0.00091520262864393	0.049315997150574
Island		0.00091529757577352	0.049315997150574
N_Shelf		0.0009154335139388	0.0493178349987107
	PDE6B;PDE6B	0.000915986433437834	0.0493421342870403
Island	RIN3	0.000916347547746252	0.0493560972044266
		0.000916609307907872	0.0493595840185338
Island		0.000916672757479852	0.0493595840185338
S_Shore	TP73;TP73;TP73;TP73	0.000916797359250461	0.0493595840185338
S_Shore		0.000917021131996796	0.0493595840185338
N_Shore	PARD3	0.000917058409192858	0.0493595840185338
Island	SBNO2;SBNO2	0.000917066805980343	0.0493595840185338
	DOC2B	0.000917165172358198	0.0493595840185338
		0.000917227597515727	0.0493595840185338
S_Shelf		0.000917411734065733	0.0493604696651114
	USP12	0.000917447887111615	0.0493604696651114
	ZBTB20;ZBTB20;ZBTB2	0.000917651443471642	0.0493659375052097
Island	GIPC2	0.000917901140708287	0.0493707080786469
Island	RYR1;RYR1	0.000917943996795984	0.0493707080786469
S_Shore	MKX	0.000918237408852421	0.0493810052234564
N_Shore		0.000918477930271119	0.0493862177428285
		0.000918558285839862	0.0493862177428285
	VASN;CORO7	0.000918731500641948	0.0493862177428285
		0.000918742212074299	0.0493862177428285
S_Shore	PTPRN2;PTPRN2;PTPR	0.000919064108279077	0.0493974052749033
	HDAC9;HDAC9;HDAC9	0.000919244121333558	0.0493974052749033
S_Shore	MTA1	0.000919297689731122	0.0493974052749033
N_Shore	CRYM	0.000919438021098539	0.0493974052749033
	GPR137B	0.000919460297430968	0.0493974052749033
N_Shore	CRCT1	0.000919575983524049	0.0493981408851248
Island	PCDHAC2;PCDHA7;PC	0.000919784376687753	0.0494035056972719

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	LLGL2;LLGL2;LLGL2	0.000919972322240431	0.0494035056972719
	TGIF2LY	0.000920214406984801	0.0494035056972719
N_Shelf	CCT8	0.000920391653665065	0.0494035056972719
		0.000920394138714833	0.0494035056972719
S_Shore	ACADS	0.000920451785088294	0.0494035056972719
		0.000920484472725895	0.0494035056972719
S_Shore	ZCCHC16	0.000920521646869549	0.0494035056972719
Island		0.000920650697516848	0.0494035056972719
S_Shelf		0.00092069590135462	0.0494035056972719
Island	FAM101B	0.000921067263851157	0.0494129721407461
	WDR37	0.00092107636914604	0.0494129721407461
N_Shore	MUC6	0.000921363888483532	0.0494229222826212
S_Shore	GABRD	0.000921621962794412	0.0494312909335995
Island		0.000921810625916618	0.0494359352670874
Island	INPP4A;INPP4A;INPP4A	0.000921961001849586	0.0494385254894598
Island	HLX	0.000922571979454228	0.0494650731814852
	ROBO1	0.000922780719709545	0.0494650731814852
		0.000923067624322074	0.0494650731814852
	PTPRN2;PTPRN2;PTPRN2	0.000923101873519105	0.0494650731814852
		0.000923219689480528	0.0494650731814852
Island		0.000923220457331569	0.0494650731814852
	MYH9	0.000923351304692448	0.0494650731814852
		0.000923436962573283	0.0494650731814852
Island		0.000923772140656984	0.0494650731814852
Island	NEURL	0.000923803771521043	0.0494650731814852
	ATP6V1C2;ATP6V1C2	0.000923817415880045	0.0494650731814852
S_Shelf	SLC17A9	0.000924017573510556	0.0494650731814852
	HTR2A;HTR2A	0.000924155671276287	0.0494650731814852
N_Shore		0.000924172064351382	0.0494650731814852
S_Shore	ASRGL1;ASRGL1	0.000924452807748985	0.0494650731814852
Island		0.000924509465477544	0.0494650731814852
N_Shelf	ARHGAP23	0.000924650477398281	0.0494650731814852
Island	PLBD1	0.000924734867933751	0.0494650731814852
		0.000924770338444238	0.0494650731814852
		0.000924788150165758	0.0494650731814852
	KSR1	0.000924888494470619	0.0494650731814852
		0.000924893356074258	0.0494650731814852
S_Shelf		0.0009249012345614	0.0494650731814852
		0.000924958567585726	0.0494650731814852
	KIAA1530	0.000925009379661822	0.0494650731814852
	NUDT15	0.000925262869114085	0.0494688828939558
Island	TMEM104	0.00092542927699248	0.0494688828939558
	ZNF280A	0.000925471751557798	0.0494688828939558
Island		0.000925529767604405	0.0494688828939558
Island		0.000925735378514456	0.0494688828939558
Island		0.000925740989180157	0.0494688828939558
S_Shelf	PCGF3	0.000925795601199226	0.0494688828939558
Island		0.000926109079598955	0.049479284099733
N_Shore	BRD3	0.000926209606457029	0.049479284099733
	RAB38	0.000926296740685035	0.049479284099733
Island	MAD1L1;MAD1L1;MAD1L1	0.000926879957188745	0.0495049774223025
	ST7;ST7	0.000927155147423555	0.049508137563003
	SHANK2	0.00092733662702517	0.049508137563003
	PSD3;PSD3	0.000927725505686158	0.049508137563003
N_Shelf	PPIC	0.000927850974979397	0.049508137563003

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Island	PCDHA7;PCDHA6;PCD	0.000927899907185269	0.049508137563003
		0.000927936796848121	0.049508137563003
	DTHD1;DTHD1	0.000927944256630125	0.049508137563003
		0.000927957725493315	0.049508137563003
Island	PFN3;PFN3	0.000927997603876352	0.049508137563003
Island	DDX4;DDX4;DDX4	0.000928040906593876	0.049508137563003
S_Shore	LMF1	0.000928197316082902	0.049508137563003
Island	RAB35;RAB35	0.000928252478117205	0.049508137563003
Island	GRAMD4	0.000928267996096899	0.049508137563003
Island		0.000928749036517672	0.0495256846681273
Island	ATP9B	0.000928853458217275	0.0495256846681273
Island	RIMBP2	0.000928963482737076	0.0495256846681273
	CCDC127	0.00092910418141117	0.0495256846681273
Island		0.000929179922201918	0.0495256846681273
	TPH2	0.000929299642675777	0.0495256846681273
		0.000929445883862307	0.0495256846681273
N_Shore		0.000929449430332303	0.0495256846681273
		0.00092952124562397	0.0495256846681273
S_Shelf	TOLLIP	0.000929656772840465	0.0495256846681273
	IPCEF1;IPCEF1;IPCEF1	0.000929721829355522	0.0495256846681273
N_Shore		0.000929971246619037	0.0495292939358535
N_Shelf		0.000930102587879325	0.0495292939358535
	TUBA3C;TUBA3C	0.00093012588269739	0.0495292939358535
N_Shore	SFRP2	0.000930507970298815	0.0495292939358535
Island	NCRNA00111	0.000930578277464175	0.0495292939358535
Island	LIMCH1;LIMCH1;LIMCH1	0.000930871430170188	0.0495292939358535
Island	RAB11B	0.000930939860328323	0.0495292939358535
Island	GDF6	0.000930947003272512	0.0495292939358535
		0.000930966716649634	0.0495292939358535
S_Shore	TBC1D16	0.000931044954149056	0.0495292939358535
S_Shore	USP29	0.000931188077422831	0.0495292939358535
	CLDN1	0.000931209397837535	0.0495292939358535
N_Shore	MYH10	0.000931321747415187	0.0495292939358535
N_Shore	FAM194A	0.000931332455423749	0.0495292939358535
N_Shore		0.000931426082587126	0.0495292939358535
S_Shore	CPLX1	0.000931490712790091	0.0495292939358535
Island	BMP8A	0.000931661708275033	0.0495292939358535
S_Shelf	NCOA4;NCOA4;NCOA4	0.000931969230574132	0.0495292939358535
	ISG20	0.000932039628825511	0.0495292939358535
Island	DPP9	0.000932088095573817	0.0495292939358535
N_Shelf		0.000932177827930608	0.0495292939358535
	PLEC1;PLEC1	0.000932207737189168	0.0495292939358535
Island		0.000932247577098361	0.0495292939358535
		0.000932322061970353	0.0495292939358535
N_Shore	DNMT3A;DNMT3A;DNMT3A	0.000932415414389817	0.0495292939358535
	LOC440839	0.000932448463546405	0.0495292939358535
Island		0.000932697563416393	0.0495368881824427
		0.000932795994887476	0.0495368881824427
	POU2F1	0.000933095403772642	0.0495473557101398
N_Shore	LOC285830;LOC285830	0.00093346573126407	0.0495615863072211
		0.000933983184773087	0.0495656386125314
Island	ODZ4	0.000934008849312111	0.0495656386125314
Island	SOX14	0.000934080337880429	0.0495656386125314
Island	TERT;TERT	0.000934086577056061	0.0495656386125314
N_Shelf		0.000934087907580688	0.0495656386125314

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Island		0.000934156091994397	0.0495656386125314
N_Shore	WDR90	0.000934271299309005	0.0495663212879652
N_Shore	TSSC1	0.000934525942632493	0.0495744005657702
		0.000934895263689195	0.0495885607913996
N_Shore		0.000935301238519089	0.049597821951585
S_Shelf	TRAPPC9;TRAPPC9	0.000935312595389843	0.049597821951585
Island	FSD1	0.000935405129294652	0.049597821951585
		0.000935479489036761	0.049597821951585
		0.000935661172699684	0.0496004969484885
S_Shore	PRKCZ	0.000935847986205396	0.0496004969484885
	THSD7B	0.000935867816986692	0.0496004969484885
	FMN1	0.000936093333045715	0.0496004969484885
	WFIKKN2	0.000936273990944319	0.0496004969484885
Island		0.000936387010190636	0.0496004969484885
		0.000936439984448479	0.0496004969484885
Island	ACADS	0.000936521073855762	0.0496004969484885
Island		0.000936661001944238	0.0496004969484885
N_Shelf	DLG4;DLG4	0.000936691755734973	0.0496004969484885
	GRIA2;GRIA2;GRIA2	0.000936719300576237	0.0496004969484885
S_Shelf		0.000936783511443118	0.0496004969484885
N_Shore		0.000937090094945958	0.0496004969484885
	WDR1;WDR1	0.000937210758326893	0.0496004969484885
		0.000937227135183674	0.0496004969484885
N_Shore		0.00093736078546495	0.0496004969484885
N_Shelf	FOXK1	0.000937383384846825	0.0496004969484885
S_Shore	SV2C	0.000937417291859631	0.0496004969484885
S_Shore	TGFBR3	0.000937475763312783	0.0496004969484885
S_Shore	PPM1L	0.000937646598216995	0.0496041167319985
S_Shore		0.00093779150287179	0.0496063640922215
S_Shore	PTCHD2	0.000938157846561757	0.0496068728180618
	TASP1	0.0009381767705618	0.0496068728180618
N_Shelf	PCDHB3	0.000938286081767692	0.0496068728180618
	MAD1L1;MAD1L1;MAD1	0.000938295859815546	0.0496068728180618
Island		0.000938313243971019	0.0496068728180618
N_Shelf		0.000938623340149489	0.0496125946299011
N_Shore	GPT	0.000938626345106661	0.0496125946299011
S_Shore	MRPS2	0.000938941781997332	0.0496234522670091
Island		0.000939036679971379	0.0496234522670091
		0.000939265854819034	0.049627524873159
S_Shelf		0.000939318681695657	0.049627524873159
	RCBTB2	0.000939595693215228	0.0496367456497017
Island	TNFSF9	0.000940080412692407	0.0496477971014554
		0.000940327886840341	0.0496477971014554
	PBX1	0.00094038207585552	0.0496477971014554
S_Shore	S1PR5;S1PR5	0.000940456143775726	0.0496477971014554
Island	MEST;MEST;MESTIT1;	0.000940495866087948	0.0496477971014554
S_Shelf	MGRN1;MGRN1;MGRN	0.000940497992147833	0.0496477971014554
Island	DOCK4	0.000940623231194957	0.0496477971014554
	C6orf204;BRD7P3;C6orf	0.000940624965060557	0.0496477971014554
Island	ZNF783	0.000940728224592485	0.0496478366978048
	LOC399753	0.000940916034616118	0.049652338032845
	LPAR6;LPAR6;RB1	0.000941336028860708	0.0496690894626825
	ARHGAP10	0.000941567829429951	0.0496709605178597
Island	RPTOR;RPTOR	0.000941641878113353	0.0496709605178597
N_Shelf	SLC22A18;SLC22A18;S	0.000941679160635912	0.0496709605178597

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		0.000942051977245931	0.0496790244317384
		0.000942093080789284	0.0496790244317384
Island	JARID2	0.000942139760296325	0.0496790244317384
Island	LMTK2	0.000942296944966519	0.0496819037525484
		0.000942454612999936	0.0496827710789019
		0.000942597607745001	0.0496827710789019
		0.000942621139614989	0.0496827710789019
Island	GRM6	0.000942877831692546	0.0496835297857878
Island	DAK	0.000943103694023425	0.0496835297857878
	LOC285501	0.000943147564758513	0.0496835297857878
N_Shore		0.000943228796587552	0.0496835297857878
Island	BRF1	0.000943416028697264	0.0496835297857878
Island	WDR81;WDR81;WDR81	0.000943710948133127	0.0496835297857878
	RCOR1	0.000943712209628599	0.0496835297857878
		0.000943745247137748	0.0496835297857878
S_Shore	MAD1L1;MAD1L1;MAD1L1	0.000943913202290925	0.0496835297857878
N_Shelf	ARMCX1	0.000943921044010254	0.0496835297857878
Island	PITX2;PITX2;PITX2	0.000943967600928761	0.0496835297857878
	GALK2;GALK2	0.000944065981778011	0.0496835297857878
Island	CHRM2;CHRM2;CHRM2	0.000944414590485018	0.0496835297857878
	TERT;TERT	0.000944425196861779	0.0496835297857878
	RAGE	0.000944515572305415	0.0496835297857878
Island		0.000944712523601163	0.0496835297857878
	OR52H1	0.000944821127423057	0.0496835297857878
N_Shore	PCSK2;PCSK2	0.000945034288918965	0.0496835297857878
	AGAP1;AGAP1	0.000945055617714617	0.0496835297857878
S_Shelf	VAR2;VAR2;VAR2	0.000945200989690273	0.0496835297857878
S_Shelf	AGAP1;AGAP1	0.000945236469598256	0.0496835297857878
	C14orf159;C14orf159;C14orf159	0.00094534976683554	0.0496835297857878
	SMYD3;SMYD3	0.000945351083787722	0.0496835297857878
N_Shore	ANKS1B;ANKS1B;ANKS1B	0.000945402963824647	0.0496835297857878
Island	STAG3;GPC2	0.000945405759915528	0.0496835297857878
	HDAC4	0.000945439833292517	0.0496835297857878
	PCDH24	0.000945545029817629	0.0496835297857878
S_Shore		0.000945687312553382	0.0496835297857878
Island	BLCAP;BLCAP;BLCAP	0.000945764158669606	0.0496835297857878
N_Shelf		0.00094576487041401	0.0496835297857878
N_Shelf	MMP15	0.000945891712951483	0.0496835297857878
	RGS3;RGS3;RGS3	0.000945979989939389	0.0496835297857878
N_Shore	SLC20A2	0.000946196566257986	0.0496835297857878
	HNMT;HNMT	0.00094624309844618	0.0496835297857878
S_Shore	ANKRD17;ANKRD17	0.00094629116615562	0.0496835297857878
Island	MAD1L1;MAD1L1;MAD1L1	0.000946438592831477	0.0496835297857878
		0.000946521252376544	0.0496835297857878
N_Shore	CENPJ	0.000946582321628236	0.0496835297857878
	USP22	0.000946714493836521	0.0496835297857878
	SLC22A2	0.000946860767439042	0.0496835297857878
N_Shore		0.000946921472542969	0.0496835297857878
Island		0.000947103164494977	0.0496835297857878
	PAPPA	0.000947174911311576	0.0496835297857878
		0.000947232747484438	0.0496835297857878
		0.000947405428374278	0.0496835297857878
	GATSL1	0.000947557008004112	0.0496835297857878
	LOC399959	0.000947645325066648	0.0496835297857878
Island		0.000947803177637629	0.0496835297857878

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	SETD3;SETD3	0.000947828461733454	0.0496835297857878
N_Shore		0.000947930132645829	0.0496835297857878
N_Shelf	NCOR2;NCOR2	0.000948019067982639	0.0496835297857878
	C17orf69;C17orf69	0.000948248695453569	0.0496835297857878
Island	LMX1A	0.000948407204217735	0.0496835297857878
		0.000948452881508432	0.0496835297857878
Island		0.000948508327624936	0.0496835297857878
Island	TRIM65	0.000948825626892884	0.0496835297857878
Island	DDX3Y;DDX3Y	0.00094891719225733	0.0496835297857878
	PRDM16;PRDM16	0.000948996829618766	0.0496835297857878
N_Shore		0.000949002134579537	0.0496835297857878
	TNXB	0.000949269881824188	0.0496835297857878
S_Shore	ARMCX4	0.000949360577815525	0.0496835297857878
N_Shore	ARHGEF10	0.000949456864880364	0.0496835297857878
	TTYH3	0.000949490059007892	0.0496835297857878
Island		0.000949577771585412	0.0496835297857878
S_Shelf	MAOA	0.000949606944716825	0.0496835297857878
		0.000949623952857223	0.0496835297857878
Island	ATP11A;ATP11A	0.000949625480395891	0.0496835297857878
Island	XKR4;SBF1P1	0.000949687025244239	0.0496835297857878
	AHRR	0.000949868694034225	0.0496835297857878
	SFRS8	0.000950020950699066	0.0496835297857878
		0.000950087663216486	0.0496835297857878
Island		0.000950185883321152	0.0496835297857878
		0.000950221609491576	0.0496835297857878
	MGMT	0.000950264469541023	0.0496835297857878
Island	TMEM196	0.000950329262242375	0.0496835297857878
S_Shore		0.000950454038240302	0.0496846899158914
N_Shore	OBSCN;OBSCN	0.000950852212886435	0.0496911106473009
N_Shore	MMP28	0.000950998025447609	0.0496911106473009
N_Shore	TTL11;TTL11	0.00095109697868433	0.0496911106473009
S_Shelf	KDM4B	0.000951102154246927	0.0496911106473009
N_Shelf	KLK13	0.000951187225166257	0.0496911106473009
	SORBS2;SORBS2;SOR	0.000951258370602867	0.0496911106473009
S_Shelf	PCNXL3	0.000951419211451371	0.0496911106473009
	MBNL1;MBNL1;MBNL1;	0.000951470474854932	0.0496911106473009
	ARHGAP25;ARHGAP25	0.000951500253224732	0.0496911106473009
Island		0.000951766607941016	0.0496948716728709
Island	C3orf39	0.00095179757813538	0.0496948716728709
	AFF3;AFF3	0.00095201384601509	0.0496948716728709
Island		0.000952026369383195	0.0496948716728709
	SCD5	0.000952085302746233	0.0496948716728709
Island	CENPB	0.000952696375311784	0.0497116417441991
Island	PRPH	0.000952713444409051	0.0497116417441991
		0.000952845944463868	0.0497116417441991
S_Shore	MAP7D2;MAP7D2;MAP	0.000952917600772327	0.0497116417441991
		0.000952987147712777	0.0497116417441991
Island		0.000953684690708671	0.0497116417441991
		0.000953707995009472	0.0497116417441991
	CNTNAP2	0.000953755129986094	0.0497116417441991
Island	TPO;TPO;TPO;TPO	0.000953859923347798	0.0497116417441991
N_Shelf	ZFR2	0.000953867008422427	0.0497116417441991
N_Shore	BRD9;BRD9;BRD9	0.00095387219555754	0.0497116417441991
Island	NXN	0.000953901206710352	0.0497116417441991
Island	CFD	0.000954030471220343	0.0497116417441991

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S_Shelf	KIFC1	0.000954177416811901	0.0497116417441991
	C3orf21	0.000954325583010556	0.0497116417441991
N_Shelf	DENND3	0.000954401891333833	0.0497116417441991
S_Shelf	MRGPRF;MRGPRF	0.000954507195208323	0.0497116417441991
S_Shelf		0.000954543484834903	0.0497116417441991
Island		0.000954777675302443	0.0497116417441991
Island	BTBD18	0.00095484285202052	0.0497116417441991
Island		0.000954856936514306	0.0497116417441991
N_Shore		0.000954886242175817	0.0497116417441991
N_Shore	CANT1;CANT1;CANT1	0.000954946792573582	0.0497116417441991
Island	KCNS1	0.000954967409728645	0.0497116417441991
Island		0.000955017059484013	0.0497116417441991
		0.000955156197405945	0.0497116417441991
	PRR11	0.000955177903415097	0.0497116417441991
N_Shore	RUSC1;FDPS;FDPS;RU	0.000955461172402297	0.0497158803906464
	RFTN1	0.000955464646004514	0.0497158803906464
	SPATS1;SPATS1	0.000955694497666852	0.0497224983975183
N_Shore	H6PD	0.000956108630922121	0.0497354183696647
	TJP1;TJP1	0.000956177785416939	0.0497354183696647
		0.000956550030352557	0.0497354183696647
Island	RECQL5	0.000956565006326773	0.0497354183696647
	KCNMA1;KCNMA1;KCN	0.000956643289476584	0.0497354183696647
	SPDYE1;POLR2J4	0.000956650878419492	0.0497354183696647
S_Shelf	B3GNTL1	0.000956661658043249	0.0497354183696647
Island		0.00095682438693103	0.0497385393582023
	CPN1	0.000957154685341723	0.0497461514086764
Island	ITGAV;ITGAV	0.000957176245243288	0.0497461514086764
	COL6A6	0.000957279269860197	0.0497461676368069
	A2ML1	0.000957443565566123	0.0497489108413873
Island	POLS	0.000957537494169025	0.0497489108413873
Island	PABPC5;PABPC5	0.000957695938809994	0.049751805809734
N_Shore	HSBP1L1	0.000958158076223484	0.0497606478571182
Island		0.000958163859386163	0.0497606478571182
N_Shelf		0.000958292073374394	0.0497606478571182
Island	PCDHA6;PCDHA2;PCD	0.000958312995392185	0.0497606478571182
Island	TRPM8	0.000958379854872656	0.0497606478571182
Island		0.000958622895724694	0.0497655735885419
N_Shore	INPP5A	0.000958680228320024	0.0497655735885419
Island	LPPR2;LPPR2	0.000958797218441787	0.0497663125947721
	ORC5L	0.000958971185026132	0.0497700084856174
N_Shelf	GRM6	0.000959112517880534	0.0497704849703115
S_Shelf		0.000959341084919524	0.0497704849703115
		0.000959560446019991	0.0497704849703115
S_Shore	INSIG1;INSIG1;INSIG1	0.000959651577594982	0.0497704849703115
S_Shore	SLC6A18	0.000959855219777332	0.0497704849703115
S_Shore	DIP2C	0.000959979342175397	0.0497704849703115
	SEMA3E	0.000960002813974252	0.0497704849703115
		0.000960022580109131	0.0497704849703115
S_Shore	OSBPL1A;OSBPL1A	0.000960059721730881	0.0497704849703115
Island	SMAD6;SMAD6;SMAD6	0.000960074798797496	0.0497704849703115
	DNM3;DNM3;MIR199A2	0.000960110754302627	0.0497704849703115
Island	SLC12A7	0.000960272384289583	0.0497716225653537
N_Shelf	RPH3AL	0.000960338229232912	0.0497716225653537
S_Shore	FHL1;FHL1;FHL1;FHL1;	0.000960533834616415	0.0497764337096721
Island		0.000960693114126463	0.0497793615597838

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	TNIK;TNIK;TNIK;TNIK;T	0.000961106891862622	0.0497954744759696
N_Shelf	EPHB3	0.00096133724014627	0.0497963076005873
Island	C7orf50;C7orf50;C7orf50	0.000961438498875531	0.0497963076005873
	DYRK2;DYRK2	0.000961641008252625	0.0497963076005873
N_Shore	GPR155;GPR155	0.000961710526853112	0.0497963076005873
N_Shore		0.000961860747172994	0.0497963076005873
S_Shore	TAF7L;TAF7L	0.000961968218288994	0.0497963076005873
	PIK3AP1	0.000962035077005	0.0497963076005873
N_Shelf		0.000962183702541312	0.0497963076005873
Island	BCOR;BCOR	0.000962198322890985	0.0497963076005873
	KCNH4	0.000962283065354281	0.0497963076005873
S_Shelf	POLI	0.000962284830348169	0.0497963076005873
	EIF2C2;EIF2C2	0.000962356762796669	0.0497963076005873
Island	KCNQ2;KCNQ2;KCNQ2	0.000962822510937563	0.0498088833966383
	WDR20;WDR20;WDR20	0.000962891449544559	0.0498088833966383
	TBCD	0.00096304804300879	0.0498088833966383
S_Shore		0.00096310628462724	0.0498088833966383
S_Shelf	GSTCD;GSTCD	0.000963214480349532	0.0498088833966383
		0.000963295746289145	0.0498088833966383
S_Shore	TRPC3;TRPC3	0.00096349915045681	0.0498088833966383
Island		0.000963594492751423	0.0498088833966383
Island		0.000963649437337646	0.0498088833966383
		0.000963766261022396	0.0498088833966383
		0.000963805803292506	0.0498088833966383
N_Shelf	C7orf50;C7orf50;C7orf50	0.000964075883180937	0.0498088833966383
		0.00096409018427212	0.0498088833966383
	SH3BP4	0.00096413618625145	0.0498088833966383
	AHRR	0.000964142428830814	0.0498088833966383
	CLPTM1L	0.000964290062350848	0.0498111971467656
	MIR299	0.000964497143744535	0.049811624967829
	FAM155A	0.000964583326363797	0.049811624967829
Island		0.000964695905123143	0.049811624967829
		0.000964803112388908	0.049811624967829
Island	CIRBP;CIRBP;C19orf24	0.000964812582095089	0.049811624967829
	DHX8	0.000964937911447972	0.0498127855427456
	MYLK4	0.00096516682869384	0.0498188982939481
		0.00096529895324637	0.0498188982939481
Island	IGDCC3	0.000965419506095884	0.0498188982939481
N_Shelf	EHMT2;EHMT2	0.000965467773472351	0.0498188982939481
Island	PPP2R2B;PPP2R2B;PPP2R2B	0.000965721007448919	0.0498208209050278
N_Shore	ZNF483;ZNF483	0.000965795393752446	0.0498208209050278
	PLN;C6orf204;C6orf204	0.000965854969981245	0.0498208209050278
	C6orf35	0.000965916498834897	0.0498208209050278
	ATG2A	0.000966308161178174	0.0498217548103089
N_Shore		0.000966318132089232	0.0498217548103089
Island	MYO1F	0.000966444712986715	0.0498217548103089
Island	TAS1R2	0.000966529810917113	0.0498217548103089
Island	GREM2	0.000966571700457007	0.0498217548103089
S_Shore	RPTOR;RPTOR	0.000966645293036929	0.0498217548103089
Island	PCDHA6;PCDHA2;PCDHA2	0.000966654684256383	0.0498217548103089
S_Shelf	CHCHD5	0.000966786890195692	0.0498232667156872
		0.000967044070542165	0.0498274266563426
Island	FAM47B	0.000967086764360634	0.0498274266563426
		0.000967329393369372	0.0498274266563426
	SSH1	0.00096734893134785	0.0498274266563426

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Island	PREX2;PREX2	0.000967557756500332	0.0498274266563426
N_Shore	RNF39;RNF39	0.000967873612154032	0.0498274266563426
Island	RASA3	0.000967914333888724	0.0498274266563426
S_Shelf		0.000968079728264184	0.0498274266563426
Island	VIPR2	0.000968133829138154	0.0498274266563426
Island	PDE4D;PDE4D	0.000968425484931328	0.0498274266563426
		0.000968593632029122	0.0498274266563426
	GPR158	0.000968622008728916	0.0498274266563426
Island		0.000968903217512485	0.0498274266563426
S_Shelf		0.000968966422893921	0.0498274266563426
	C3orf21	0.000969062670661511	0.0498274266563426
Island	KCNS1	0.00096933918800711	0.0498274266563426
	MGC15885;TLN2	0.000969345061766119	0.0498274266563426
Island		0.000969535062419524	0.0498274266563426
Island	ARSI	0.000969593157958678	0.0498274266563426
Island	ZNF787	0.000969616645645214	0.0498274266563426
Island	CELSR1	0.000969626883050663	0.0498274266563426
	SNRPN;SNRPN;SNRPN	0.000969654074135189	0.0498274266563426
Island	ERICH1	0.00096968488765753	0.0498274266563426
Island		0.000969832127934686	0.0498274266563426
	CSNK2A2	0.000969847654398852	0.0498274266563426
		0.000969884402426328	0.0498274266563426
		0.000969888874753806	0.0498274266563426
Island	ZNF238	0.000969898064005505	0.0498274266563426
N_Shore	PTPRN2;PTPRN2;PTPRN2	0.000969998008556579	0.0498274266563426
S_Shore		0.000970056519290288	0.0498274266563426
Island	PCDH19;PCDH19	0.000970056895561151	0.0498274266563426
N_Shore	KCNQ1;KCNQ1	0.000970215980431651	0.0498303133321908
S_Shore	ZFYVE28	0.000970458118545946	0.049837464559937
	SLC25A21;SLC25A21	0.000970585673262124	0.0498387305134307
	FAM172A;FAM172A;FAM172A	0.000970938059986577	0.0498464523058898
	GCNT2;GCNT2;GCNT2	0.00097094189037065	0.0498464523058898
N_Shelf		0.000971344222239887	0.0498618219858329
S_Shore	ENO3;ENO3	0.000971696279802933	0.0498746079605294
	MAMLD1;MAMLD1	0.000972083804900197	0.0498892114875795
Island	MOBKL2C;MOBKL2C	0.000972242638436907	0.0498920762726165
	NMT1	0.000972354700298129	0.0498921117671417
	NTNG1;NTNG1;NTNG1	0.000972472298591736	0.0498921117671417
	NR1H4	0.000972574415291107	0.0498921117671417
		0.000972736539407282	0.0498921117671417
	CAMTA1	0.00097275839863133	0.0498921117671417
Island		0.000973054237024749	0.0498923240413735
	ZNF407;ZNF407;ZNF407	0.000973113424831262	0.0498923240413735
Island	HLA-DQB2	0.000973181950719125	0.0498923240413735
Island	NFIX	0.000973330578580789	0.0498923240413735
Island	COL6A1	0.000973460506391428	0.0498923240413735
	RAI14;RAI14;RAI14;RAI14	0.000973472408140279	0.0498923240413735
		0.000973571161926922	0.0498923240413735
Island	C2CD4C	0.000973826440053381	0.0498923240413735
Island		0.000973856146625045	0.0498923240413735
Island		0.000973938358497048	0.0498923240413735
		0.00097412340093339	0.0498923240413735
Island	REEP6	0.000974418746708687	0.0498923240413735
		0.000974848661325656	0.0498923240413735
N_Shore	MMP17	0.000974864678820305	0.0498923240413735

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Island	NFYA;NFYA;LOC22144;	0.00097492981971074	0.0498923240413735
N_Shelf	MCF2L;MCF2L	0.000974958342073583	0.0498923240413735
Island	MIR127;RTL1	0.00097499941358763	0.0498923240413735
	MARCH8;MARCH8;MAF	0.000975016587330756	0.0498923240413735
N_Shore		0.000975073975269745	0.0498923240413735
Island		0.000975182401910786	0.0498923240413735
		0.000975186701779329	0.0498923240413735
		0.000975195955716979	0.0498923240413735
		0.000975208415414511	0.0498923240413735
Island		0.000975321517484983	0.0498923240413735
N_Shore	MMP15	0.000975419244067346	0.0498923240413735
Island	VWA1;VWA1	0.000975440905069459	0.0498923240413735
	CCDC85C	0.000975589959366417	0.0498946786768891
Island		0.000975796619343258	0.0498999786361972
		0.000975999800411187	0.0499034499292667
	TMOD1;TMOD1	0.000976070574882451	0.0499034499292667
	ST6GAL1;ST6GAL1	0.000976310370694514	0.0499040203525333
Island	FLJ42709;FLJ42709;FL	0.000976360864289134	0.0499040203525333
Island	FASN	0.000976492604716823	0.0499040203525333
Island		0.000976551784569766	0.0499040203525333
Island		0.000976645143244086	0.0499040203525333
Island	CPT1A;CPT1A	0.000976783296057984	0.0499040203525333
S_Shore		0.000976802999931895	0.0499040203525333
S_Shelf	KRBA1	0.000976918833476727	0.0499046739820289
	TRIM39;TRIM39	0.000977095389691555	0.0499084290879944
S_Shelf	VANGL2	0.000977375089133132	0.0499159468591598
	UNC80;UNC80	0.000977493501663436	0.0499159468591598
Island	PACS2;PACS2	0.000977651457330888	0.0499159468591598
N_Shore		0.00097765482249727	0.0499159468591598
Island	TMEM47;TMEM47	0.000977820452646984	0.0499175034745041
	SYCE1L	0.000978103892901546	0.0499175034745041
Island	PTPRS;PTPRS;PTPRS;	0.000978159512576684	0.0499175034745041
Island		0.000978226471623741	0.0499175034745041
S_Shelf	PKD1;PKD1	0.000978262964210008	0.0499175034745041
S_Shelf	CRTC3;CRTC3	0.000978335845891397	0.0499175034745041
		0.000978406773310211	0.0499175034745041
N_Shore	MAD1L1;MAD1L1;MAD1	0.000978746979211291	0.0499247329197757
	TAS2R31;PRR4;PRH1	0.000978765803123261	0.0499247329197757
	COG7	0.000978857717041636	0.0499247329197757
Island		0.000978979548180018	0.0499256891304925
Island	MORN1	0.000979095925287273	0.0499263670261906
Island	DRD4	0.000979254557417361	0.049929199233726
Island	PGLS	0.000979728450037581	0.0499422453754434
S_Shelf	MACROD2	0.000979856764566412	0.0499422453754434
	AFF1	0.00097993993482404	0.0499422453754434
	AIPL1;AIPL1;AIPL1	0.000979992144906252	0.0499422453754434
		0.00098010159997601	0.0499422453754434
	HSPB7;HSPB7	0.000980129132903709	0.0499422453754434
Island		0.000980270207723452	0.0499431366590028
	MBTPS1	0.000980352862679275	0.0499431366590028
	NHEG1	0.000980594228890758	0.0499501787870757
	KIRREL3;KIRREL3	0.00098102921495815	0.0499611675837317
	AMPH;AMPH	0.000981031208884515	0.0499611675837317
Island	WNT5B;WNT5B	0.000981126958919316	0.0499611675837317
N_Shore	LMF1	0.000981293264358365	0.0499611675837317

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S_Shore	PYGO1	0.000981325736280472	0.0499611675837317
S_Shore	ABCB4;ABCB4;ABCB4	0.000981578967944948	0.0499615667199427
N_Shore	LOC404266;LOC404266	0.000981584820172221	0.0499615667199427
		0.000981748868889199	0.0499615667199427
	PLEKHA7	0.000981831561397293	0.0499615667199427
S_Shore		0.000982131781804913	0.0499615667199427
S_Shore	GKAP1;GKAP1	0.00098220998625923	0.0499615667199427
S_Shelf	RFX1	0.000982258363535446	0.0499615667199427
	ART4;ART4	0.000982269034806925	0.0499615667199427
	ADAMTS14;ADAMTS14	0.000982299494010458	0.0499615667199427
	MIR29C	0.000982365147109925	0.0499615667199427
Island		0.000982511470616171	0.0499637618654113
Island		0.000982756243730844	0.0499709233404892
		0.000982914490879397	0.0499709233404892
	MIR453;MIR485	0.000982961826593384	0.0499709233404892
		0.000983397378070576	0.0499813645044668
	PTPRG	0.000983510128541069	0.0499813645044668
N_Shore	ENOX1	0.000983602766652652	0.0499813645044668
N_Shelf	NMU	0.000983622264331718	0.0499813645044668
Island		0.000983786281481022	0.0499813645044668
Island	PDZRN3	0.000983858044692309	0.0499813645044668
Island	LAMA5	0.000983889597244798	0.0499813645044668
N_Shore	TERT;TERT	0.000983997942561479	0.049981625960261
Island		0.000984206128338515	0.0499844154325098
	OR12D2	0.000984357581926314	0.0499844154325098
		0.00098436247229707	0.0499844154325098
	ARID5B	0.000984567111434383	0.0499858265705359
Island	LEFTY1	0.000984654833177871	0.0499858265705359
		0.000984699883981795	0.0499858265705359
S_Shelf		0.000984942738673266	0.0499860457883939
Island	PHF19	0.000985228189551258	0.0499860457883939
	MIR496	0.000985294110315738	0.0499860457883939
N_Shore	SLC9A1	0.000985368237006476	0.0499860457883939
Island	LOC388965	0.000985526640125521	0.0499860457883939
		0.000985667543907307	0.0499860457883939
N_Shore	HEATR2	0.000985755854915122	0.0499860457883939
N_Shelf	NPHP4	0.00098579957515993	0.0499860457883939
	LY6D	0.000986171271451435	0.0499860457883939
	MYT1L;LOC730811	0.000986490773095464	0.0499860457883939
S_Shore	ITPKB	0.000986519603059645	0.0499860457883939
S_Shelf	C14orf70	0.000986703952331247	0.0499860457883939
S_Shelf	CEP57	0.000986754664827716	0.0499860457883939
Island		0.000986797839110595	0.0499860457883939
	BCAT1	0.000987016592823528	0.0499860457883939
Island		0.00098709814260523	0.0499860457883939
		0.000987216337369546	0.0499860457883939
	SORCS2	0.000987362795604956	0.0499860457883939
	NMNAT3	0.000987421030919667	0.0499860457883939
	ZNF148	0.000987544445680115	0.0499860457883939
	PRKAR1B;PRKAR1B;PRKAR1B	0.000987596161067242	0.0499860457883939
Island	PCNT	0.000987606786802851	0.0499860457883939
	C1orf21	0.000987707467796745	0.0499860457883939
		0.000987781233940178	0.0499860457883939
	P704P	0.000987813786556855	0.0499860457883939
N_Shore	NXN	0.000987840129412924	0.0499860457883939

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	COL24A1	0.000987956652024775	0.0499860457883939
Island	FRMPD4	0.000988078746499771	0.0499860457883939
Island	PTPRN2;PTPRN2;PTPF	0.000988094867511419	0.0499860457883939
Island	ATP11A;ATP11A	0.000988154147615532	0.0499860457883939
	WAC;WAC;WAC	0.000988246229997411	0.0499860457883939
Island	STOM;STOM	0.000988257900518808	0.0499860457883939
Island		0.000988423561192363	0.0499860457883939
	NCAPD3	0.000988623582900786	0.0499860457883939
		0.000988760959701766	0.0499860457883939
	SPANXD;SPANXE;SPA	0.00098901092442823	0.0499860457883939
Island		0.00098903185657923	0.0499860457883939
	STT3B	0.000989348048064597	0.0499860457883939
	GNB1	0.000989351239115059	0.0499860457883939
		0.000989367060735093	0.0499860457883939
Island	STOM;STOM	0.000989384809149326	0.0499860457883939
		0.000989452846276676	0.0499860457883939
Island	ASAP2;ASAP2	0.000989601753018909	0.0499860457883939
S_Shelf		0.000989725334328404	0.0499860457883939
Island	UHRF1;UHRF1	0.000989743725182967	0.0499860457883939
Island	GRID1	0.000990049503506447	0.0499860457883939
Island	FAM135B	0.000990060466428023	0.0499860457883939
Island		0.000990137494270363	0.0499860457883939
		0.000990177660694947	0.0499860457883939
Island		0.00099019475329404	0.0499860457883939
	CTDSP2;MIR26A2	0.000990536262017394	0.0499860457883939
	DNM2;MIR199A1;DNM2	0.000990622028851771	0.0499860457883939
	NLRP12;NLRP12	0.000990710304233364	0.0499860457883939
N_Shore	DTYMK;DTYMK;DTYMK	0.000990811947319126	0.0499860457883939
Island	ANKRD11	0.000990881800758505	0.0499860457883939
	PLA2G5	0.000990898941191073	0.0499860457883939
Island		0.00099090192127723	0.0499860457883939
N_Shelf	TUBB3	0.000991031625514941	0.0499860457883939
S_Shore	KIF26B	0.000991131938762503	0.0499860457883939
		0.000991162636268241	0.0499860457883939
S_Shore	KLHL29	0.000991177334399065	0.0499860457883939
		0.000991197620860415	0.0499860457883939
		0.000991206284523275	0.0499860457883939
		0.000991471942852432	0.0499873957323203
	GTDC1;GTDC1;GTDC1	0.000991783109729847	0.0499873957323203
	HMSD	0.000991901067945061	0.0499873957323203
Island	LRFN3	0.000991961763562224	0.0499873957323203
Island	ZBTB45	0.000992001275476975	0.0499873957323203
N_Shore	ATP11A;ATP11A	0.000992272340045724	0.0499873957323203
		0.00099229287698126	0.0499873957323203
S_Shore		0.000992323499146019	0.0499873957323203
Island	TSPYL5	0.000992360204240744	0.0499873957323203
Island		0.000992465791007902	0.0499873957323203
Island	LOC254559	0.000992498994254645	0.0499873957323203
S_Shelf	PTPN18;PTPN18	0.000992563513088151	0.0499873957323203
Island	SLC16A12	0.00099262982859015	0.0499873957323203
	SNX8	0.00099267799959419	0.0499873957323203
N_Shore	LMF1	0.000992976895374887	0.0499883428582168
Island	MAD1L1;MAD1L1;MAD1	0.000992989873627512	0.0499883428582168
	TCERG1L	0.000993047570524218	0.0499883428582168
S_Shelf		0.00099332622476823	0.0499883428582168

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		0.000993596909696155	0.0499883428582168
Island		0.000993647998703155	0.0499883428582168
N_Shore		0.000993834445517239	0.0499883428582168
	SLC6A3	0.00099395096106533	0.0499883428582168
Island	SPAG6;SPAG6	0.000994008843800286	0.0499883428582168
	FREM3	0.000994153825444829	0.0499883428582168
Island		0.000994174539093332	0.0499883428582168
Island	ILDR1	0.000994424416046361	0.0499883428582168
Island		0.000994717573765564	0.0499883428582168
	CADM2;CADM2	0.000994865586037868	0.0499883428582168
Island	LMX1A	0.000994884122586571	0.0499883428582168
S_Shore	ASB18	0.000994907117849621	0.0499883428582168
Island	MYEOV2	0.000994953360090296	0.0499883428582168
		0.000995114031336638	0.0499883428582168
Island		0.000995222033267092	0.0499883428582168
	UGGT2	0.000995265725735244	0.0499883428582168
		0.000995386444192929	0.0499883428582168
N_Shore	TSHZ2	0.000995497748812976	0.0499883428582168
S_Shore	ATP11A;ATP11A	0.000995711902010536	0.0499883428582168
	TNXB;TNXB	0.000996013665585297	0.0499883428582168
N_Shore	PHOX2B	0.000996024537550808	0.0499883428582168
Island	GRIA3;GRIA3	0.00099617991915586	0.0499883428582168
Island		0.000996289631431428	0.0499883428582168
	TANC2	0.000996290681063747	0.0499883428582168
	TRAPPC9;TRAPPC9	0.000996352179489095	0.0499883428582168
		0.000996423251225618	0.0499883428582168
Island	FANCC	0.000996492152717227	0.0499883428582168
S_Shore	PRDM16;PRDM16	0.000996570198733279	0.0499883428582168
	ABCC5;ABCC5	0.000996591553450653	0.0499883428582168
N_Shore	EHMT1	0.000996716845757376	0.0499883428582168
Island	IGF2AS;INS-IGF2;IGF2;	0.000996860089764986	0.0499883428582168
	DIMT1L	0.000996869372215856	0.0499883428582168
S_Shore	TSPY4;TSPY4	0.000996905153882137	0.0499883428582168
Island	ZNF397OS;ZNF397OS	0.000996953832639278	0.0499883428582168
	MAML2	0.000997020373313093	0.0499883428582168
S_Shore		0.000997030714326457	0.0499883428582168
Island		0.000997099883642133	0.0499883428582168
	ADAMTS2;ADAMTS2	0.000997182090635569	0.0499883428582168
S_Shore	RAB9B	0.000997223607366719	0.0499883428582168
	EMID2	0.000997342908593972	0.0499883428582168
Island	THY1;THY1	0.000997437381942926	0.0499883428582168
S_Shelf	APCDD1	0.000997444578293104	0.0499883428582168
Island	PLEKHM3	0.000997717742804011	0.0499949956818149
		0.000997783777959889	0.0499949956818149

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AZA mean	CTR mean	AZA standard deviation	CTR standard deviation
0.495273520234946	0.96356372376575	0.0045170675351305	0.00340656412212613
0.612821240068696	0.967325292790617	0.00331483081810784	0.0034658040165051
0.678675197049996	0.97244978841402	0.00162049273961764	0.00406852635778175
0.642125325361991	0.978370417751167	0.00399981002454139	0.00322494720983804
0.635888905949974	0.973685745812602	0.00128047700493853	0.00520383098766756
0.410477502295641	0.949612542413162	0.00806655761871726	0.00351863939638357
0.57058137672898	0.963592347732367	0.00638836307160351	0.00405564679105446
0.496353637424788	0.972814403132032	0.00219414619647157	0.00895454579114758
0.502225012286342	0.950931885750431	0.00333958726486249	0.00873737465736776
0.577884261346975	0.965553018878828	0.00544059353078846	0.00684327757916519
0.600000601985829	0.968002426139942	0.00867930684819486	0.00147853105658128
0.656663876101867	0.964577290227823	0.00510820229001526	0.00595053298490267
0.667160355535432	0.964820802029311	0.00279526925117799	0.00712738434735899
0.62133567065505	0.958731384366516	0.00706591614518205	0.00579250743559594
0.613221970878526	0.975059700321075	0.00914171917673817	0.00362809076348607
0.448691347894623	0.955115279577807	0.0080351936246242	0.0111839849661405
0.643644915236706	0.959382459791059	0.0040700790343633	0.00768427718770342
0.690843844929909	0.966025831686684	0.00675067075566242	0.00390312608454215
0.63171300008853	0.976875389699282	0.00273457172473375	0.0100839155387614
0.555753758830294	0.96823961092747	0.0122745777700546	0.00234126873487394
0.611041437789697	0.966010427457763	0.00992870066245308	0.00547092725548968
0.56090586557168	0.968167091051376	0.0106898502286502	0.00746871372290885
0.649217265338883	0.976922631283775	0.0100614061262644	0.00305472167580961
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0.556704674598233	0.963052316083477	0.0111784281251788	0.00761733486594504
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0.425313504227697	0.942856923673216	0.0150462760734183	0.00893774880172466
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0.597757552856401	0.969937236404593	0.0127568942404482	0.00246545875480983
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0.52043385032584	0.973784241858525	0.0141160461131258	0.00792555990107903
0.53263232555417	0.682328960796387	0.00409358911624299	0.0035031586283102
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0.536576677169782	0.965156589268714	0.0132510384348157	0.00919081096632675
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0.615947007986149	0.972402839459151	0.00439852462018846	0.0128313157230518
0.663451555643083	0.967230719440924	0.0111976016948166	0.0030210473690961
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0.537099478913939	0.97892213922351	0.0101027533881451	0.0137974474071821
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0.422955855156756	0.938872738749484	0.00844154313339571	0.0183568301044502
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0.64656019329421	0.975878592061884	0.0120419019758231	0.00578261986248275
0.275847055813742	0.523473553458931	0.00148963307653504	0.00997976468268695
0.566602268198456	0.969964688585009	0.0151896446913599	0.00673716658687256
0.616640099362545	0.968249422920022	0.0131078352543519	0.00617135358444238
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0.415665764441073	0.960136706678324	0.0216924082113965	0.00765550542762506
0.59247272160921	0.963628894024704	0.0125413567833267	0.00947256563107126
0.673588153933686	0.973905240071031	0.0100202291547416	0.00783344532087505
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0.668868738973436	0.9722424367245	0.00801828766495436	0.0101998685647982
0.713957117032244	0.969194185552032	0.00596843441508704	0.00916417681141421
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0.430615067352169	0.934704754853128	0.00449675878966683	0.0229390715066539
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0.392334601664829	0.946047996745156	0.0203865140057881	0.0157377743391731
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0.686289670368479	0.979504807686653	0.00969200308050719	0.0104229569377077
0.550063967502082	0.962967848982604	0.0113504372525377	0.0165421863753506
0.380518063410836	0.927523074439866	0.0156512902532066	0.0215968619271552
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0.430008793502882	0.943253982260585	0.0148568455805212	0.0202268113400155
0.54345701855447	0.951998240731216	0.018476992036492	0.00760200163407727
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0.598809388180892	0.920798166883943	0.0114502461599212	0.0111689063306802
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0.546664630354098	0.945350618974423	0.018367805910503	0.00757235177713015
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0.676039192767224	0.968034400273263	0.00513614141824125	0.0137817401436425
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Supplementary file 1

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Supplementary file 1

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Supplementary file 1

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Supplementary file 1

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Supplementary file 1

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Supplementary file 1

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Supplementary file 1

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Supplementary file 1

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Supplementary file 2

DMRs	UCSC CpG island name	Relation to UCSC CpG island
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chr4:3516456-3516844*Island	chr4:3516456-3516844	Island
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chr7:157208794-157209008*Island	chr7:157208794-157209008	Island
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chr16:23724270-23724775*S_Shore	chr16:23724270-23724775	S_Shore
chr16:23724270-23724775*S_Shore	chr16:23724270-23724775	S_Shore
chr16:23724270-23724775*S_Shore	chr16:23724270-23724775	S_Shore
chr16:23724270-23724775*S_Shore	chr16:23724270-23724775	S_Shore
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chr19:8649787-8650524*Island	chr19:8649787-8650524	Island
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Supplementary file 2

chr1:47902793-47905518*N_S	chr1:47902793-47905518	N_Shore
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chr1:115323075-115323462*S	chr1:115323075-115323462	S_Shore
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chr1:147380138-147380482*Is	chr1:147380138-147380482	Island
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chr1:147380138-147380482*Is	chr1:147380138-147380482	Island
chr1:147380138-147380482*Is	chr1:147380138-147380482	Island
chr1:162336876-162337321*N	chr1:162336876-162337321	N_Shore
chr1:162336876-162337321*N	chr1:162336876-162337321	N_Shore
chr1:162336876-162337321*N	chr1:162336876-162337321	N_Shore
chr2:176993479-176995557*N	chr2:176993479-176995557	N_Shore
chr2:176993479-176995557*N	chr2:176993479-176995557	N_Shore
chr2:176993479-176995557*N	chr2:176993479-176995557	N_Shore
chr4:128651419-128651977*Is	chr4:128651419-128651977	Island
chr4:128651419-128651977*Is	chr4:128651419-128651977	Island
chr4:128651419-128651977*Is	chr4:128651419-128651977	Island
chr4:128651419-128651977*Is	chr4:128651419-128651977	Island
chr4:128651419-128651977*Is	chr4:128651419-128651977	Island
chr4:128651419-128651977*Is	chr4:128651419-128651977	Island
chr4:128651419-128651977*Is	chr4:128651419-128651977	Island
chr4:128651419-128651977*Is	chr4:128651419-128651977	Island
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chr4:128651419-128651977*Is	chr4:128651419-128651977	Island
chr4:128651419-128651977*Is	chr4:128651419-128651977	Island
chr5:662283-663402*Island	chr5:662283-663402	Island
chr5:662283-663402*Island	chr5:662283-663402	Island
chr5:662283-663402*Island	chr5:662283-663402	Island
chr5:60139359-60140155*N_S	chr5:60139359-60140155	N_Shore
chr5:60139359-60140155*N_S	chr5:60139359-60140155	N_Shore
chr5:60139359-60140155*N_S	chr5:60139359-60140155	N_Shore
chr5:60139359-60140155*N_S	chr5:60139359-60140155	N_Shore
chr5:60139359-60140155*N_S	chr5:60139359-60140155	N_Shore
chr5:60139359-60140155*N_S	chr5:60139359-60140155	N_Shore
chr5:140589744-140590657*Is	chr5:140589744-140590657	Island
chr5:140589744-140590657*Is	chr5:140589744-140590657	Island
chr5:140589744-140590657*Is	chr5:140589744-140590657	Island
chr7:599089-599327*N_Shore	chr7:599089-599327	N_Shore
chr7:599089-599327*N_Shore	chr7:599089-599327	N_Shore
chr7:599089-599327*N_Shore	chr7:599089-599327	N_Shore
chr7:599089-599327*N_Shore	chr7:599089-599327	N_Shore
chr7:599089-599327*N_Shore	chr7:599089-599327	N_Shore
chr7:599089-599327*N_Shore	chr7:599089-599327	N_Shore
chr7:599089-599327*N_Shore	chr7:599089-599327	N_Shore
chr7:599089-599327*N_Shore	chr7:599089-599327	N_Shore
chr7:2107080-2107381*S_Sho	chr7:2107080-2107381	S_Shore
chr7:2107080-2107381*S_Sho	chr7:2107080-2107381	S_Shore
chr7:2107080-2107381*S_Sho	chr7:2107080-2107381	S_Shore
chr7:2107080-2107381*S_Sho	chr7:2107080-2107381	S_Shore
chr7:4169481-4169753*N_Sho	chr7:4169481-4169753	N_Shore
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chr7:4169481-4169753*N_Sho	chr7:4169481-4169753	N_Shore
chr7:4169481-4169753*N_Sho	chr7:4169481-4169753	N_Shore
chr7:4169481-4169753*N_Sho	chr7:4169481-4169753	N_Shore
chr7:4169481-4169753*N_Sho	chr7:4169481-4169753	N_Shore
chr7:4169481-4169753*N_Sho	chr7:4169481-4169753	N_Shore
chr7:4169481-4169753*N_Sho	chr7:4169481-4169753	N_Shore
chr7:4823506-4824097*N_Sho	chr7:4823506-4824097	N_Shore

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chr7:4823506-4824097*N_Shore	chr7:4823506-4824097	N_Shore
chr7:4823506-4824097*N_Shore	chr7:4823506-4824097	N_Shore
chr7:4823506-4824097*N_Shore	chr7:4823506-4824097	N_Shore
chr7:4823506-4824097*N_Shore	chr7:4823506-4824097	N_Shore
chr7:98552746-98552962*Island	chr7:98552746-98552962	Island
chr7:98552746-98552962*Island	chr7:98552746-98552962	Island
chr7:98552746-98552962*Island	chr7:98552746-98552962	Island
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chr7:100489981-100490365*Island	chr7:100489981-100490365	Island
chr7:100489981-100490365*Island	chr7:100489981-100490365	Island
chr7:100489981-100490365*Island	chr7:100489981-100490365	Island
chr7:148922909-148923195*N_Shore	chr7:148922909-148923195	N_Shore
chr7:148922909-148923195*N_Shore	chr7:148922909-148923195	N_Shore
chr7:148922909-148923195*N_Shore	chr7:148922909-148923195	N_Shore
chr8:1579038-1579241*Island	chr8:1579038-1579241	Island
chr8:1579038-1579241*Island	chr8:1579038-1579241	Island
chr8:1579038-1579241*Island	chr8:1579038-1579241	Island
chr8:1579038-1579241*Island	chr8:1579038-1579241	Island
chr8:140744199-140744498*Island	chr8:140744199-140744498	Island
chr8:140744199-140744498*Island	chr8:140744199-140744498	Island
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chr8:140744199-140744498*Island	chr8:140744199-140744498	Island
chr9:139294086-139294813*N_Shore	chr9:139294086-139294813	N_Shore
chr9:139294086-139294813*N_Shore	chr9:139294086-139294813	N_Shore
chr9:139294086-139294813*N_Shore	chr9:139294086-139294813	N_Shore
chr9:139294086-139294813*N_Shore	chr9:139294086-139294813	N_Shore
chr10:99473520-99474664*S_Shelf	chr10:99473520-99474664	S_Shelf
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chr10:99473520-99474664*S_Shelf	chr10:99473520-99474664	S_Shelf
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chr10:99473520-99474664*S_Shelf	chr10:99473520-99474664	S_Shelf
chr11:1302772-1302982*S_Shelf	chr11:1302772-1302982	S_Shelf
chr11:1302772-1302982*S_Shelf	chr11:1302772-1302982	S_Shelf
chr11:1302772-1302982*S_Shelf	chr11:1302772-1302982	S_Shelf
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chr11:130078173-130078667*Island	chr11:130078173-130078667	Island
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chr12:58021294-58022037*Island	chr12:58021294-58022037	Island
chr12:63195657-63195909*Island	chr12:63195657-63195909	Island
chr12:63195657-63195909*Island	chr12:63195657-63195909	Island
chr12:63195657-63195909*Island	chr12:63195657-63195909	Island
chr12:124831133-124831430*S_Shore	chr12:124831133-124831430	S_Shore
chr12:124831133-124831430*S_Shore	chr12:124831133-124831430	S_Shore
chr12:124831133-124831430*S_Shore	chr12:124831133-124831430	S_Shore

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chr12:124831133-124831430*	chr12:124831133-124831430	S_Shore
chr13:20766208-20767779*N	chr13:20766208-20767779	N_Shelf
chr13:20766208-20767779*N	chr13:20766208-20767779	N_Shelf
chr13:20766208-20767779*N	chr13:20766208-20767779	N_Shelf
chr13:20766208-20767779*N	chr13:20766208-20767779	N_Shelf
chr13:20766208-20767779*N	chr13:20766208-20767779	N_Shelf
chr13:113540350-113540558*	chr13:113540350-113540558	Island
chr13:113540350-113540558*	chr13:113540350-113540558	Island
chr13:113540350-113540558*	chr13:113540350-113540558	Island
chr13:113540350-113540558*	chr13:113540350-113540558	Island
chr15:22945002-22945206*Island	chr15:22945002-22945206	Island
chr15:22945002-22945206*Island	chr15:22945002-22945206	Island
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chr15:37387386-37387614*Island	chr15:37387386-37387614	Island
chr15:37387386-37387614*Island	chr15:37387386-37387614	Island
chr15:37387386-37387614*Island	chr15:37387386-37387614	Island
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chr15:72104191-72104418*N	chr15:72104191-72104418	N_Shore
chr15:72104191-72104418*N	chr15:72104191-72104418	N_Shore
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chr15:72104191-72104418*N	chr15:72104191-72104418	N_Shore
chr16:88044296-88044502*Island	chr16:88044296-88044502	Island
chr16:88044296-88044502*Island	chr16:88044296-88044502	Island
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chr16:88044296-88044502*Island	chr16:88044296-88044502	Island
chr17:43138229-43138857*S	chr17:43138229-43138857	S_Shore
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chr17:80975646-80976250*S	chr17:80975646-80976250	S_Shore
chr18:46287906-46288140*Island	chr18:46287906-46288140	Island
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chr18:77465403-77465674*Island	chr18:77465403-77465674	Island
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chr19:603638-603945*Island	chr19:603638-603945	Island
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chr19:5110587-5110853*Island	chr19:5110587-5110853	Island
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chr19:5110587-5110853*Island	chr19:5110587-5110853	Island
chr19:19737385-19737923*Island	chr19:19737385-19737923	Island
chr19:19737385-19737923*Island	chr19:19737385-19737923	Island
chr19:19737385-19737923*Island	chr19:19737385-19737923	Island

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chr20:54978524-54978771*Isl	chr20:54978524-54978771	Island
chr20:54978524-54978771*Isl	chr20:54978524-54978771	Island
chr20:54978524-54978771*Isl	chr20:54978524-54978771	Island
chr21:44480559-44480772*Isl	chr21:44480559-44480772	Island
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chrX:3263353-3265347*Islan	chrX:3263353-3265347	Island
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chrX:99194334-99194598*Isl	chrX:99194334-99194598	Island
chrX:99194334-99194598*Isl	chrX:99194334-99194598	Island
chrX:99194334-99194598*Isl	chrX:99194334-99194598	Island
chrY:4867956-4868586*Islan	chrY:4867956-4868586	Island
chrY:4867956-4868586*Islan	chrY:4867956-4868586	Island
chrY:4867956-4868586*Islan	chrY:4867956-4868586	Island
chrY:4867956-4868586*Islan	chrY:4867956-4868586	Island
chr21:33672605-33673215*Isl	chr21:33672605-33673215	Island
chr21:33672605-33673215*Isl	chr21:33672605-33673215	Island
chr21:33672605-33673215*Isl	chr21:33672605-33673215	Island

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Manova p-value	Manova q-value	CpG probe
1.31852984682002e-06	0.033679225897872	cg26401028
1.31852984682002e-06	0.033679225897872	cg04857395
1.31852984682002e-06	0.033679225897872	cg27321949
1.31852984682002e-06	0.033679225897872	cg08297640
6.31839898031855e-06	0.033679225897872	cg21010435
6.31839898031855e-06	0.033679225897872	cg03559568
6.31839898031855e-06	0.033679225897872	cg22412150
1.17815062103678e-06	0.033679225897872	cg03596167
1.17815062103678e-06	0.033679225897872	cg16786481
1.17815062103678e-06	0.033679225897872	cg26952936
1.17815062103678e-06	0.033679225897872	cg07841477
1.17815062103678e-06	0.033679225897872	cg03645571
1.17815062103678e-06	0.033679225897872	cg09979356
1.95412701359194e-06	0.033679225897872	cg26523264
1.95412701359194e-06	0.033679225897872	cg21676617
1.95412701359194e-06	0.033679225897872	cg19640789
1.95412701359194e-06	0.033679225897872	cg19662846
1.95412701359194e-06	0.033679225897872	cg12845177
7.43928598266404e-06	0.0339890981134245	cg15822010
7.43928598266404e-06	0.0339890981134245	cg17613810
7.43928598266404e-06	0.0339890981134245	cg19882119
1.05965055847791e-05	0.0363105363642129	cg15038331
1.05965055847791e-05	0.0363105363642129	cg01180441
1.05965055847791e-05	0.0363105363642129	cg18136895
4.88634037474236e-06	0.0363105363642129	cg26278134
4.88634037474236e-06	0.0363105363642129	cg19590914
4.88634037474236e-06	0.0363105363642129	cg00879606
4.88634037474236e-06	0.0363105363642129	cg09689465
6.99441887372125e-06	0.0419429070786287	cg15116481
6.99441887372125e-06	0.0419429070786287	cg18254983
6.99441887372125e-06	0.0419429070786287	cg01773685
6.99441887372125e-06	0.0419429070786287	cg14307477
1.81992559628238e-05	0.0447731732646163	cg12632411
1.81992559628238e-05	0.0447731732646163	cg26161708
1.81992559628238e-05	0.0447731732646163	cg02451508
9.06586325345132e-06	0.0447731732646163	cg00210133
9.06586325345132e-06	0.0447731732646163	cg05335030
9.06586325345132e-06	0.0447731732646163	cg01149940
9.06586325345132e-06	0.0447731732646163	cg02410870
8.92438239802565e-05	0.0498607010085873	cg18267790
8.92438239802565e-05	0.0498607010085873	cg13362782
8.92438239802565e-05	0.0498607010085873	cg06177967
3.83954321469039e-05	0.0498607010085873	cg01070065
3.83954321469039e-05	0.0498607010085873	cg11286035
3.83954321469039e-05	0.0498607010085873	cg14258143
3.83954321469039e-05	0.0498607010085873	cg19776942
9.56982161196554e-06	0.0498607010085873	cg26518431
9.56982161196554e-06	0.0498607010085873	cg23659056
9.56982161196554e-06	0.0498607010085873	cg24114899
9.56982161196554e-06	0.0498607010085873	cg16342298
9.56982161196554e-06	0.0498607010085873	cg14106085
9.56982161196554e-06	0.0498607010085873	cg00914781

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9.56982161196554e-06	0.0498607010085873	cg26366304
9.56982161196554e-06	0.0498607010085873	cg16657448
3.75358381359208e-05	0.0498607010085873	cg20986076
3.75358381359208e-05	0.0498607010085873	cg20153160
3.75358381359208e-05	0.0498607010085873	cg14272177
3.75358381359208e-05	0.0498607010085873	cg06313880
6.27810202880468e-05	0.0498607010085873	cg05161602
6.27810202880468e-05	0.0498607010085873	cg11153057
6.27810202880468e-05	0.0498607010085873	cg05777400
6.27810202880468e-05	0.0498607010085873	cg06531250
6.37101681610227e-05	0.0498607010085873	cg03391436
6.37101681610227e-05	0.0498607010085873	cg18383680
6.37101681610227e-05	0.0498607010085873	cg23225572
5.84173424106843e-05	0.0498607010085873	cg25423004
5.84173424106843e-05	0.0498607010085873	cg23901857
5.84173424106843e-05	0.0498607010085873	cg14601868
1.55200616910341e-05	0.0498607010085873	cg26983317
1.55200616910341e-05	0.0498607010085873	cg09796800
1.55200616910341e-05	0.0498607010085873	cg04382920
1.55200616910341e-05	0.0498607010085873	cg07641839
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Chr	Position	UCSC RefGene name
4	3516534	LRPAP1
4	3516637	LRPAP1
4	3516692	LRPAP1
4	3516758	LRPAP1
7	157208882	DNAJB6
7	157208968	DNAJB6
7	157208980	DNAJB6
16	23724821	ERN2
16	23724835	ERN2
16	23724854	ERN2
16	23724901	ERN2
16	23724943	ERN2
16	23725375	ERN2
19	8649844	ADAMTS10
19	8649942	ADAMTS10
19	8650112	ADAMTS10
19	8650410	ADAMTS10
19	8650523	ADAMTS10
7	206484	FAM20C
7	206977	FAM20C
7	207069	FAM20C
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15	74290493	PML;PML;PML;PML;PML;PML
15	74290733	PML;PML;PML;PML;PML;PML
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19	8028642	ELAVL1
19	8028761	ELAVL1
19	8028819	ELAVL1
19	51330265	KLK15;KLK15;KLK15
19	51330299	KLK15;KLK15;KLK15
19	51330453	KLK15;KLK15;KLK15
19	51330469	KLK15;KLK15;KLK15
20	17595355	RRBP1;RRBP1
20	17595448	RRBP1;RRBP1
20	17595472	RRBP1;RRBP1
22	50632714	TRABD
22	50632819	TRABD
22	50632967	TRABD
22	50633040	TRABD
1	27332632	FAM46B
1	27332751	FAM46B
1	27332971	FAM46B
1	32714023	FAM167B
1	32714038	FAM167B
1	32714146	FAM167B
1	32714164	FAM167B
1	47901555	MGC12982;FOXD2
1	47901632	MGC12982;FOXD2
1	47901721	MGC12982;FOXD2;FOXD2
1	47902085	FOXD2;FOXD2
1	47902269	FOXD2;FOXD2
1	47902275	FOXD2;FOXD2

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1	47902310	FOXD2;FOXD2
1	47902371	FOXD2;FOXD2
1	115324213	SIKE1;SIKE1
1	115324285	SIKE1;SIKE1
1	115324450	SIKE1;SIKE1
1	115324617	SIKE1;SIKE1
1	147380211	GJA8
1	147380334	GJA8
1	147380398	GJA8
1	147380445	GJA8
1	162335175	NOS1AP;NOS1AP;NOS1AP
1	162335231	NOS1AP;NOS1AP;NOS1AP
1	162335982	NOS1AP;NOS1AP;NOS1AP
2	176993211	HOXD8
2	176993221	HOXD8
2	176993320	HOXD8
4	128651500	SLC25A31
4	128651518	SLC25A31
4	128651526	SLC25A31
4	128651532	SLC25A31
4	128651543	SLC25A31
4	128651564	SLC25A31;SLC25A31
4	128651707	SLC25A31
4	128651936	SLC25A31
5	662284	TPPP
5	662614	TPPP
5	662907	TPPP
5	60137757	ELOVL7;ELOVL7
5	60138761	ELOVL7;ELOVL7
5	60138838	ELOVL7;ELOVL7
5	60138883	ELOVL7;ELOVL7
5	60139131	ELOVL7;ELOVL7
5	60139293	ELOVL7;ELOVL7
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5	140590251	PCDHB12
5	140590533	PCDHB12
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7	597568	PRKAR1B;PRKAR1B;PRKAR1
7	597575	PRKAR1B;PRKAR1B;PRKAR1
7	597596	PRKAR1B;PRKAR1B;PRKAR1
7	598459	PRKAR1B;PRKAR1B;PRKAR1
7	598729	PRKAR1B;PRKAR1B;PRKAR1
7	598979	PRKAR1B;PRKAR1B;PRKAR1
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7	2107835	MAD1L1;MAD1L1;MAD1L1
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7	2109353	MAD1L1;MAD1L1;MAD1L1
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7	4167809	SDK1
7	4167882	SDK1;SDK1
7	4167943	SDK1;SDK1
7	4168039	SDK1;SDK1
7	4169306	SDK1;SDK1
7	4169314	SDK1;SDK1
7	4822006	KIAA0415

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7	4822807	KIAA0415
7	4822924	KIAA0415
7	4823045	KIAA0415
7	4823097	KIAA0415
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7	98552884	TRRAP
7	98552952	TRRAP
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7	100490061	ACHE;ACHE
7	100490184	ACHE;ACHE
7	100490250	ACHE;ACHE
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7	148922355	ZNF282
8	1579039	DLGAP2
8	1579108	DLGAP2
8	1579180	DLGAP2
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8	140744326	TRAPPC9;TRAPPC9
8	140744338	TRAPPC9;TRAPPC9
8	140744386	TRAPPC9;TRAPPC9
8	140744488	TRAPPC9;TRAPPC9
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9	139292811	SNAPC4
9	139293044	SNAPC4
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12	49783097	SPATS2
12	49783192	SPATS2
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12	63195796	PPM1H
12	63195908	PPM1H
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12	124832556	NCOR2;NCOR2
12	124832755	NCOR2;NCOR2

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13	20763293	GJB2
13	20763366	GJB2
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13	20763734	GJB2
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13	113540421	ATP11A;ATP11A
13	113540512	ATP11A;ATP11A
13	113540557	ATP11A;ATP11A
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15	22945077	CYFIP1
15	22945134	CYFIP1
15	22945189	CYFIP1
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15	37387523	MEIS2;MEIS2;MEIS2;MEIS2;M
15	37387525	MEIS2;MEIS2;MEIS2;MEIS2;M
15	37387577	MEIS2;MEIS2;MEIS2;MEIS2;M
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15	72102874	NR2E3;NR2E3
15	72102890	NR2E3;NR2E3
15	72103133	NR2E3;NR2E3
15	72103457	NR2E3;NR2E3
15	72103854	NR2E3;NR2E3
15	72103908	NR2E3;NR2E3
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16	88044443	BANP;BANP
16	88044501	BANP;BANP
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17	43139021	NMT1;DCAKD
17	43139717	NMT1;DCAKD
17	43139826	NMT1;DCAKD
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17	80976941	B3GNTL1
17	80977010	B3GNTL1
17	80977389	B3GNTL1
17	80977450	B3GNTL1
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18	46288005	KIAA0427;KIAA0427
18	46288073	KIAA0427;KIAA0427
18	77465430	CTDP1;CTDP1
18	77465527	CTDP1;CTDP1
18	77465673	CTDP1;CTDP1
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19	603718	HCN2
19	603777	HCN2
19	603853	HCN2
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19	5110798	KDM4B
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19	19737740	LPAR2
19	19737909	LPAR2

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21	44480699	CBS
21	44480711	CBS
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X	3264432	MXRA5
X	3264517	MXRA5
X	3264695	MXRA5
X	3264711	MXRA5
X	3264725	MXRA5
X	3264728	MXRA5
X	3264853	MXRA5
X	3264864	MXRA5
X	3265038	MXRA5
X	3265053	MXRA5
X	3265089	MXRA5
X	3265318	MXRA5
X	99194407	LOC442459
X	99194477	LOC442459
X	99194597	LOC442459
Y	4867963	PCDH11Y
Y	4867968	PCDH11Y
Y	4868368	PCDH11Y;PCDH11Y
Y	4868397	PCDH11Y;PCDH11Y
21	33672713	MRAP;MRAP
21	33672816	MRAP;MRAP
21	33673209	MRAP;MRAP

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Anova p-value	Anova q-value	AZA mean
0.00606011880800479	0.0787362110038292	0.578825227419358
0.00220198663586455	0.0625434605579219	0.513552118121408
0.0169026013089813	0.108269385932534	0.583866062647235
0.00669105097786095	0.0804902220389716	0.684015039661277
6.83986949422283e-05	0.0231251482467374	0.648600503137449
0.056067993032531	0.200458326855687	0.778537412245537
0.0245052105177395	0.127355682275819	0.767879533853671
0.0133793682224243	0.0989171152740298	0.707128000621888
0.00569866083073868	0.0776156877090003	0.624933113641008
0.0198650990654393	0.115643405935906	0.678419245928472
0.00812387650673648	0.0843343868307763	0.61929839957348
0.195169715867099	0.433732580369549	0.671857478155475
0.307295277198665	0.565207232238459	0.342063507775587
0.00955547022263228	0.0886422905301568	0.595150212040373
0.00175240676322019	0.0599638245585635	0.676777939348679
1.51588656018585e-05	0.013774454860224	0.807897697249631
0.0177098702210806	0.110144058869095	0.687436452864975
0.00869326712908663	0.0861835304781304	0.676009683991241
0.000289569099454727	0.0366133100269894	0.559466015485115
0.0496369797570338	0.18667932735309	0.746862350763183
0.00659838265274749	0.0802302202577869	0.645722348707883
0.00424881303630408	0.0725373139533809	0.596092384787339
0.0230953488212935	0.123779820020547	0.611347301304106
0.000177615136684441	0.0313951392897332	0.659542070554043
0.0177541456245387	0.110245405679674	0.712113438576721
0.0175301842136226	0.109733465916021	0.70771232257678
1.71559944082769e-06	0.00889756237565692	0.612592517362726
0.00601106688882753	0.0785929050275658	0.684857979866272
0.000122218097221035	0.0284598260281295	0.65373180720441
0.00724054352195875	0.0819319717841555	0.635015360956168
0.0162493019605178	0.106650727801925	0.665492608385155
0.00162537306408325	0.0590612101351777	0.672001975739163
0.250471662857195	0.502740586895734	0.797369811213578
0.00268221359723185	0.0652283823638008	0.649350746241311
0.00746315089181331	0.08254773716811	0.585323145839177
0.0322825705012921	0.146564675820803	0.671167391422683
0.0017388598310062	0.0598554596996823	0.624734587848625
0.0309426903197217	0.143252062313495	0.673953158678301
0.208485472261372	0.451238065829049	0.694179662305598
0.00154927876542349	0.058195691564666	0.712141301219957
0.0528630997351362	0.19372838956447	0.71064202666392
0.0244621602043888	0.127256889137551	0.60955133886774
0.433021971573656	0.677977361767865	0.25004179596437
0.306322377537709	0.564236321352656	0.289340345320093
0.000723032763713937	0.0471400229761967	0.633721922858223
0.0349126721128667	0.152911026462614	0.748967718653701
0.0045797136508076	0.0737342311429749	0.514305771175867
0.200392909957563	0.440748790299892	0.531577074363794
0.0579571574367019	0.204556178242079	0.632763247876758
0.0203535205673062	0.116922457451249	0.605687898133514
0.152814821490208	0.373244341951237	0.0407174937726322
0.65321687201602	0.828576758361304	0.0369349686750471

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0.918653606985973	0.965486422201252	0.0238359176764757
0.621181409135066	0.810017484467243	0.0375982605637646
0.00656012467795266	0.0800799517279868	0.646972325433734
0.485021158647811	0.718147523249486	0.412700521968168
0.0180098248971005	0.110905982450961	0.574953336688995
0.0654917836708827	0.220356104505769	0.696016743825594
0.0052899432773981	0.0763021481777836	0.665464039637725
0.000818675996428593	0.0489189757531773	0.502515948805382
7.76664827655979e-06	0.0125010889594614	0.631336867582751
0.00156633377795662	0.0583867905667342	0.609782977394541
0.00192158797872587	0.0607851676261338	0.486169290528872
0.012703068209328	0.0972486839612048	0.666346490161343
0.0345467114227819	0.152092081316458	0.643494738090964
0.0171123220407057	0.108754570362273	0.530509868061101
0.0584382177328343	0.205584762900837	0.54676862712518
0.00143595818583169	0.0573329489734659	0.51114645329558
7.76066365911186e-05	0.0242937890844093	0.544293390234834
0.000369552446754322	0.0390286157378769	0.494102020959401
7.98533760706892e-06	0.0125010889594614	0.549300971281558
0.00300452486205397	0.0671527525223524	0.507253242833982
0.000123529593962091	0.0284598260281295	0.474847062083489
0.0839572883522691	0.256707914028165	0.732811669160517
0.00410738023736462	0.0721902737230603	0.533477157132728
0.0299150771907217	0.140549518700438	0.730039825640686
0.125910666566109	0.330737176236448	0.739759105937578
0.000760937055803942	0.0477221477529966	0.60351748841463
0.0134227220637223	0.0990316037622284	0.604695014342769
0.0141347340929076	0.100894334507169	0.569597807295134
0.0624264090975059	0.213989433628771	0.5279207388394
0.00590251293910876	0.0783261410971321	0.390938555284465
0.0594617333869506	0.207783338494637	0.636975582818936
0.243239982318016	0.494148731030719	0.183232550862386
0.116697055740376	0.315205040952085	0.0264768350870744
0.31358969818603	0.571775361442696	0.61789243512676
2.90484907606093e-06	0.00972701136732981	0.63484517165399
0.0223209012373082	0.121981304518331	0.665970899413384
0.035165227567514	0.153532203832511	0.672958896326279
0.0416891099440722	0.16889188073675	0.61703277700516
0.0260880921953876	0.131162946722491	0.614549572568488
0.0299637585046193	0.140685583486626	0.612253198399973
0.00860137066402383	0.0859851442498303	0.642175077380604
0.00161213374144456	0.0590222824889451	0.699577653503412
0.0279478833760024	0.13568403232931	0.788232334320317
0.0442711662826922	0.174482885277301	0.760821598807258
0.0179364778460863	0.110678069549206	0.639495006745743
0.00319169082863542	0.0680410552715125	0.579304197149621
0.0072589791882569	0.0820341598582446	0.626018780736125
0.0291107228208605	0.13861785234719	0.520255847303152
0.00199386423109916	0.0612366509337516	0.54124204088222
0.00102204855364428	0.052141299978039	0.425545530399413
0.0215118989977797	0.119936118382298	0.402969195589797
0.00273234552303999	0.0656789737075272	0.470960218690212
0.00754880684625638	0.0827035439519882	0.636277294330894
0.0196086652980054	0.11494808264235	0.6692569364965
0.00750437945026944	0.0825921059423678	0.659937152070975

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0.000295849155227573	0.0369362954423744	0.721501709907336
0.051648681776351	0.191093902583136	0.641802601662168
0.00754406832123628	0.0826937825325345	0.723922574930979
0.538335234615661	0.756177942046164	0.812267246505537
0.0665448128985501	0.222547381975852	0.761168743149106
0.00269089063591938	0.0652527857244428	0.562359511121638
0.00015503843943912	0.0300383978308886	0.387565557707414
0.0093880353157319	0.0881292469141902	0.680177106649853
0.0236555700283212	0.12517319299877	0.692369314347126
5.8970627790074e-05	0.0224978841893518	0.537389287221586
0.0143306679850049	0.101420621122085	0.504654838731295
0.0171974699825554	0.108941532744372	0.636838084052039
0.015151495204398	0.10357488930791	0.654128611582192
0.00254448104644461	0.0644135628479225	0.687862305628218
0.0772394426668715	0.243721098108728	0.599852515879944
0.00149560005010448	0.0577917206634411	0.66821658193827
0.000567652150637461	0.0437492648557508	0.541126607232436
0.0196490337430852	0.115052251404495	0.587103194644647
0.00103332348847227	0.0522756591164406	0.658827138565529
0.00382074009096551	0.0712219098865831	0.626684055312784
0.0140522282202866	0.100669823535179	0.617081502420927
0.000338677589677456	0.0382967532828178	0.735722921452092
0.0527832851938949	0.193550479876686	0.458777135969029
0.00780411208841739	0.0834566806102647	0.616598390170748
0.010836124436102	0.0920869130353123	0.725221502195643
0.053190747926532	0.194361211103838	0.711495354468965
0.266107168658121	0.520451930719594	0.432715776432528
0.0833544765749507	0.255664948270193	0.659524977662446
0.154271030572429	0.375515343615755	0.773392087675019
0.0206375297470451	0.117666296001307	0.589412441573385
0.341780678829301	0.599113711719304	0.240286649366236
0.418580325469218	0.666635259774246	0.0532288905027135
0.0349985811207459	0.153112499023887	0.663678287456524
0.000929656772840465	0.0509154395313376	0.462259167347772
0.00424460430150274	0.0725276342599587	0.573492405148063
1.51483044912628e-05	0.013774454860224	0.54584922872949
0.000235201913004554	0.0341144108014134	0.53193411701037
0.00563264313553864	0.0774137457242562	0.595068218882099
0.00292477861394882	0.0668781718050365	0.615766233422118
0.149326264244958	0.367789956340565	0.635682062603382
0.00448672088172238	0.0733361025072804	0.696875673510492
6.32553667778058e-05	0.0227453659017856	0.762749045857795
0.191620913765439	0.428761675155113	0.758909885860651
0.0965587281761747	0.280341184015519	0.793735235019231
0.0797397138815401	0.248758972804157	0.729458867316513
6.9366932291716e-05	0.0231898246887142	0.614181032950608
0.000149981953400495	0.0296508045562733	0.712754256168929
0.00110265316007375	0.0533147117736393	0.633971406484503
0.0149203510958015	0.102929187479415	0.60724591951505
0.071855763993616	0.233056356302193	0.750151236399065
0.00198418292249294	0.061130389787535	0.538309485268773
0.0140712786496873	0.100737419886801	0.592410030562239
0.00228938693535567	0.0629824649476412	0.68471103992039
0.0710782375941029	0.231528854801199	0.657525443441728
0.00162237370762643	0.0590612101351777	0.542079199552351

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0.00988984069555192	0.0894462605811778	0.531933264934002
0.0674729931536169	0.224467807462316	0.609549102537317
0.0176544092900105	0.110022275517712	0.780264898269861
0.00170977590314355	0.059472101409626	0.585529174400077
0.0329432573130853	0.147976299913918	0.437031870960934
0.0153894442110893	0.104162506738893	0.678106484613548
0.000705429744123645	0.0467909866779725	0.548088018602382
0.0565180878055119	0.201351681611773	0.586759630849142
0.000436887611786436	0.0411817730835293	0.600524967150598
0.0807938691607376	0.250799895514054	0.688683290767109
0.0149967307367537	0.103132691378572	0.686052510684661
0.0307625662047345	0.142778909220151	0.655737181709604
0.00146092555617184	0.057493308449221	0.69977626060315
0.0837197685811506	0.256271596359337	0.716577910809415
0.0103889993077506	0.09081015215791	0.772774914573444
0.000427967609938211	0.0409185653244959	0.575894417853322
0.0601617005204333	0.209212146265444	0.601239586617442
0.0247476752616271	0.127839168879131	0.708916546057262
0.277094173162497	0.532882077242867	0.129058449547215
0.0537503894665176	0.195445961675648	0.681838761116658
0.0132905496174162	0.0987118023916022	0.654827429806401
0.0259259838686801	0.130755595472266	0.623700576879604
0.00478141967180185	0.0741638506861119	0.562246955364056
0.00134498535308942	0.0562662343562486	0.573760087743715
0.132678550937528	0.34167413909067	0.721652459600047
0.00257705842538185	0.0645556070354123	0.582784898384848
0.00604724989368826	0.0787106361263396	0.648426300763091
8.12457852199028e-06	0.0125010889594614	0.571309059034619
0.00407401102631958	0.0720838003249462	0.558501194973094
0.0771815362188132	0.243596396391067	0.0319881672292623
0.0933014921488539	0.274215891456206	0.0492442152521605
0.155935345500377	0.378089362297869	0.490022972402651
0.0122295424463917	0.0960693176764976	0.547448991697216
0.019256507891035	0.11400497663926	0.605552931636887
2.94002177946516e-06	0.00972701136732981	0.469685737539934
0.00843228263903939	0.0853630288599661	0.578030341578457
0.0616222530588482	0.21230432024018	0.678633230978364
0.0904253886022437	0.268825967067796	0.657481253231528
0.0307471992918583	0.142729245887882	0.700188730437833
0.0975135154123282	0.282101332702695	0.679649370596756
0.00871566043758043	0.0862424780604601	0.638464817962667
0.0820223227943766	0.253179531259282	0.660263316373714
0.000161394750753608	0.0303359997787019	0.624352814384089
0.00674175693559646	0.0805664429239766	0.615673135252651
0.0122458125990465	0.0961054137358894	0.678692823250887
0.00377940122359071	0.0710205315086523	0.613942868238676
0.00937302643337506	0.0881109483345519	0.567337760134805
0.000716107871492513	0.0469635583309779	0.591051217986273
0.0172206849722691	0.109002948352969	0.764893891472051
0.0361379729682927	0.155843792865461	0.738998207408622
1.27820315740677e-05	0.013774454860224	0.609015877257759
0.0149075353782936	0.102889500370877	0.746577636765605
0.000627442452676556	0.0453784966692146	0.705397493878218
0.00294551300079616	0.0669930521214623	0.547962046980464
0.0426881372999004	0.1710092073809	0.816232369494016

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0.00504468374477806	0.0752920974378017	0.675954748698227
0.0114527645746398	0.0938285196764356	0.613600848477212
0.000126441634907781	0.0287663973606081	0.536223250096905
6.63337684529122e-06	0.0117362245316492	0.602774546151074
0.000260322566742096	0.0357579226752143	0.571382820328544
0.00768949416093341	0.0832140995674393	0.566125514841948
0.0263019572728902	0.131609974255661	0.747038310498614
0.0109783663244248	0.0923690414939453	0.694101619258618
0.211502860871501	0.455062711343954	0.188388515668888
0.679172336915605	0.844315093227684	0.279918748833919
0.00690402970737521	0.081004467661733	0.593923088532828
0.00963791300755848	0.0887533960278638	0.563790851742958
0.0108644673140979	0.0921514547503931	0.37362445813309
0.000279981840303054	0.0363752710219591	0.442247243703734
8.31036773201349e-06	0.0125010889594614	0.533089095810143
0.192452512981788	0.429905058837305	0.746090317961151
0.0162041670152905	0.106528144742818	0.488216077602076
4.29087945110604e-07	0.00889756237565692	0.690843844929909
0.00024176229587711	0.0344571401433877	0.317193087296674
0.0086891409488651	0.0861685147214285	0.572820224152987
0.264652819149195	0.518937277338496	0.776394842674767
0.000138483672115331	0.0290080223576439	0.701676862359303
0.00399702251330323	0.0717268468264388	0.671380232271605
0.00768119006994983	0.0831711389743152	0.676814969033857
0.517931121784139	0.74172132653762	0.732349994480077
0.0594867871612333	0.207822859776489	0.628919410624697
2.50619338328748e-06	0.00956457237666659	0.651948677410433
0.00398919915715469	0.0717268468264388	0.469529196161315
0.000100113226279027	0.0268719429683417	0.288800488649572
6.62914244408597e-05	0.0228272773204278	0.615617976564356
0.0448778819682435	0.175878329520672	0.449048887098698

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CTR mean	AZA standard deviation	CTR standard deviation
0.899155384200925	0.0124133990505322	0.103814954153554
0.894160375751116	0.0221377955510347	0.0916532691025804
0.862839643383445	0.0461155425282762	0.113503076399514
0.929784729307943	0.00297047238451651	0.0824195813618
0.963152776255525	0.0109526998593376	0.0298937803595035
0.909871219351395	0.0495977315252611	0.0694490280871908
0.932190974000364	0.0685635558308677	0.0429559730824173
0.921161004179309	0.0618278162370675	0.0621385771581971
0.879006024105354	0.0194730032409269	0.0791596444745774
0.852187802153832	0.0448149100312637	0.0664609032001519
0.902594987210978	0.0295658105880843	0.0959701583347774
0.8227604473388	0.0498374654278863	0.160648633349023
0.488782089251379	0.0681799104708385	0.2064060474531
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Supplementary file 2

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Supplementary file 2

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Supplementary file 2

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Supplementary file 2

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Supplementary file 2

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