haematologica
Journal of The Ferrata Storti Foundation

DIS3 depletion in multiple myeloma causes extensive perturbation in cell cycle progression and centrosome amplification

by Vanessa K. Favasuli, Domenica Ronchetti, Ilaria Silvestris, Noemi Puccio, Giuseppina Fabbiano, Valentina Traini, Katia Todoerti, Silvia Erratico, Alessia Ciarrocchi, Valentina Fragliasso, Domenica Giannandrea, Francesca Tumiatti, Raffaella Chiaramonte, Yvan Torrente, Palma Finelli, Eugenio Morelli, Nikhil C. Munshi, Niccolò Bolli, Antonino Neri, and Elisa Taìana

Received: April 4, 2023.
Accepted: July 5, 2023.

Citation: Vanessa K. Favasuli, Domenica Ronchetti, Ilaria Silvestris, Noemi Puccio, Giuseppina Fabbiano, Valentina Traini, Katia Todoerti, Silvia Erratico, Alessia Ciarrocchi, Valentina Fragliasso, Domenica Giannandrea, Francesca Tumiatti, Raffaella Chiaramonte, Yvan Torrente, Palma Finelli, Eugenio Morelli, Nikhil C. Munshi, Niccolò Bolli, Antonino Neri, and Elisa Taìana. DIS3 depletion in multiple myeloma causes extensive perturbation in cell cycle progression and centrosome amplification. Haematologica. 2023 July 13. doi: 10.3324/haematol.2023.283274 [Epub ahead of print]

DIS3 depletion in multiple myeloma causes extensive perturbation in cell cycle progression and centrosome amplification

*****Vanessa K. Favasuli,[1,2] *Domenica Ronchetti,[1] Ilaria Silvestris,[1] Noemi Puccio,[3,4] Giuseppina Fabbiano,[5] Valentina Traini,[5] Katia Todoerti,[6] Silvia Erratico,[7,8] Alessia Ciarrocchi,[3] Valentina Fragliasso,[3] Domenica Giannandrea,[9] Francesca Tumiatti,[10] Raffaella Chiaramonte,[9] Yvan Torrente,[7] Palma Finelli,[10,11] Eugenio Morelli,[2] Nikhil C. Munshi,[2] Niccolò Bolli,[1,5] Antonino Neri[12] and Elisa Taìana[5]

*VKF and DR contributed equally as co-first authors

[1]Department of Oncology and Hemato-oncology, University of Milan, Italy.
[2]Department of Medical Oncology, Jerome Lipper Multiple Myeloma Center, Dana-Farber Cancer Institute, Boston, MA.
[3]Laboratory of Translational Research, Azienda USL-IRCCS Reggio Emilia, 42123 Reggio Emilia, Italy
[4]Clinical and Experimental Medicine PhD Program, University of Modena and Reggio Emilia, Modena, 41121, Italy.
[5]Hematology, Fondazione IRCCS Ca' Granda Ospedale Maggiore Policlinico, 20122 Milan, Italy.
[6]Department of Pathology and Laboratory Medicine, Fondazione IRCCS Istituto Nazionale dei Tumori, Milan, Italy.
[7]Stem Cell Laboratory, Department of Pathophysiology and Transplantation, University of Milan, Centro Dino Ferrari, Unit of Neurology, Fondazione IRCCS Cà Granda Ospedale Maggiore Policlinico, 20122 Milan, Italy.
[8]Novystem Spa, Milan, Italy.
[9]Department of Health Sciences, University of Milan, 20142 Milan, Italy.
[10]Medical Genetics Laboratory, Fondazione IRCCS Ca' Granda Ospedale Maggiore Policlinico, 20122 Milan, Italy.
[11]Department of Medical Biotechnology and Translational Medicine, University of Milan, Segrate, 20090 Milan, Italy.
[12]Scientific Directorate, Azienda USL-IRCCS Reggio Emilia, 42123 Reggio Emilia, Italy.

Running heads: *DIS3* affects centrosome duplication in myeloma

Correspondence
Prof. Antonino Neri
Azienda USL-IRCCS Reggio Emilia, viale Umberto 1, 502, 42123 Reggio Emilia, Italy
Phone: 0522 296979; Fax: 0522 295622;
mail: antonino.neri@ausl.re.it

Author Contributions VKF, ET, IS, GF, VT, NP, FT, KT, VF and DR performed experiments and analyzed the data; VKF, ET, DG and IS performed cytofluorimetric experiments; ET, VKF and SE performed confocal analysis; NB, NM, EM AC, RC, PF and YT provided critical evaluation of experimental data and of the manuscript. DR, VKF, ET and AN conceived the study and wrote the manuscript.

Disclosures. The authors declare no conflicts of interest

Data-sharing statement: Data are available from the corresponding author upon reasonable request.

Word counts text: 3688
Word counts abstract: 243
Figure/table number: 7
Reference count: 45
Supplementary data file: 1

Funding. This work was financially supported by grants from Associazione Italiana Ricerca sul Cancro (AIRC) to AN (IG24365), to ET (MFAG 2022-ID.27606) and to RC (IG20614). NB is funded by the European Research Council under the European Union’s Horizon 2020 research and innovation program (grant agreement no. 817997) and by Associazione Italiana Ricerca sul Cancro (IG25739). YT acknowledges support by “Piattaforme cellulari per la Ricerca e lo Sviluppo di Terapie Avanzate in Life Science” - Fondo Europeo di Sviluppo Regionale 2014-2020. POR FESR 2014-2020. VKF received a fellowship by the PhD program in Experimental Medicine of the University of Milan. NP received a fellowship by the PhD program in Clinical and Experimental Medicine of University of Modena and Reggio Emilia. The work was partially founded by Italian Ministry of Health (Current Research IRCCS).

ABSTRACT

DIS3 gene mutations occur in approximately 10% of patients with multiple myeloma (MM); furthermore, *DIS3* expression can be affected by monosomy 13 and del(13q), found in roughly 40% of MM cases. Despite the high incidence of *DIS3* mutations and deletions, the biological significance of *DIS3* and its contribution to MM pathogenesis remains poorly understood. Herein, we investigated the functional role of *DIS3* in MM, by exploiting a loss of function approach in human MM cell lines. We found that *DIS3* knockdown inhibits proliferation in MM cell lines and largely affects MM plasma cells (PC) cell cycle progression, finally inducing a significant increase of the percentage of cells in the G0/G1 phase and a decrease in the S and G2/M phases. *DIS3* plays an important role not only in the control of MM PCs cell cycle, but also in the centrosome duplication cycle, which are strictly coregulated in physiological condition in the G1 phase. Indeed, *DIS3* silencing leads to the formation of supernumerary centrosomes accompanied by the assembing of multipolar spindles during mitosis. In MM, centrosome amplification is present in about a third of patients and may represent a mechanism leading to genomic instability. These findings strongly prompt further studies investigating the relevance of *DIS3* in the centrosome duplication process; indeed, a combination of *DIS3* defects and deficient spindle-assembly checkpoint, can allow cells to progress through the cell cycle without proper chromosome segregation generating aneuploid cells which finally lead to the development of MM.

Keywords: *DIS3*, Multiple Myeloma, cell cycle, centrosome amplification

INTRODUCTION

Multiple myeloma (MM) is a hematological malignancy still incurable despite the recent introduction of a large array of innovative therapies.[1] MM is characterized by the abnormal proliferation of plasma cells (PC) in the bone marrow (BM) and presents different clinical course and a highly heterogeneous genetic background with both structural chromosomal alterations and specific gene mutations affecting the expression and the activity of both putative oncogenes and tumor suppressor genes.[2]

Among frequently mutated genes in MM, *DIS3* has been reported to be mutated in roughly 10% of patients with a significant impact in clinical outcome.[3–6] Despite the detailed overview of *DIS3* mutations, their functional consequences on MM pathogenesis remain largely unknown, to the point that it is still unclear whether *DIS3* behaves as an oncogene or a tumor suppressor gene.[7,8] Aberrant expression of *DIS3* has been reported in different tumor types;[7,9,10] notably, monosomy 13 and del(13q), which occur in approximately 40% of MM cases, could affect *DIS3* expression.[11,12] *DIS3* encodes for a highly conserved ribonuclease[13–15] that endowes the catalytic activity to the exosome, a multi-subunit complex that processes and degrades RNA for gene expression regulation, mRNA quality control, and small RNA processing.[16,17] Moreover, studies in *Schizosaccharomyces pombe* have revealed functions of *DIS3* in chromosome segregation,[18,19] cell cycle progression,[20,21] and spindle assembly.[22] *DIS3* involvement in cell cycle regulation has been demonstrated also in *Drosophila melanogaster*; in addition, *DIS3* is required for the development of a multicellular organism participating in cell type-specific RNA turnover.[23] In humans, *DIS3* has been described to shape the RNA polymerase II transcriptome by degrading a variety of unwanted transcripts.[24] Data concerning the functional role of *DIS3* in myeloma are limited to a recent study reporting that *DIS3* depletion in different cell types including malignant PCs causes a pervasive accumulation of DNA:RNA hybrids that induces genomic DNA double-strand breaks, eventually leading to genomic instability by increasing mutational load.[25]

In this study, we aimed to expand our knowledge on the biological role of *DIS3* in the disease by investigating the functional consequences of its depletion in myeloma cells. Our data indicate that DIS3 silencing causes a marked perturbation in cell cycle progression and mitotic process.

METHODS

Full details of quantitative real-time PCR, cell cycle analysis and apoptosis, immunofluorescence, gapmeR design and gymnotic delivery, proteomic assays, and gene expression analysis are provided in Supplementary Methods.

Multi-Omics Data in CoMMpass Study

Multi-omics data about BM MM samples at baseline (BM_1) were freely accessible from the MMRF CoMMpass Study (https://research.themmrf.org/) including more than 1000 MM patients from several worldwide sites and retrieved from the Interim Analysis 15a (MMRF_CoMMpass_IA15a, accessed on 16 October 2020). Details about the molecular and clinical data of the CoMMpass cohort selected for the present study are described in Supplementary Methods.

Statistical and Survival Analyses

Wilcoxon rank-sum and Kruskal-Wallis tests were applied to assess differential expression patterns between two or multiple molecular groups. Dunn's test was used for pairwise comparisons. *P*-values were corrected using the Benjamini-Hochberg (BH) method, and adjusted *p*-values <0.05 were considered significant. Survival analyses were performed as described in Supplementary Methods.

MM Cell Lines and Drugs

AMO-1 was kindly provided by Dr. C. Driessen (University of Tubingen, Germany). NCI-H929 and U266 were purchased from DSMZ, which certified authentication performed by short tandem repeat DNA typing. All human MM cell lines (HMCLs) were immediately frozen and used from the original stock within 6 months. HMCLs were cultured in RPMI-1640 medium (Gibco®, Life Technologies, Carlsbad, CA, USA) supplemented with 10% fetal bovine serum (FBS), 50 U/ml penicillin, and 50 μg/ml streptomycin (Gibco®) at 37°C in 5% CO_2 atmosphere, and routinely tested to rule out mycoplasma contamination.

For cell cycle analyses, cells were synchronized with Synchroset kit (EuroClone, Milan, Italy). For mitotic analyses, cells were synchronized with RO-3306 and MG-132 (Selleckchem, Aurogene, Rome, Italy).

Primary Patient Cells

$CD138^+$ cells were isolated from the BM aspirates of MM patients by Ficoll-Hypaque (Lonza Group, Basel, Switzerland) density gradient sedimentation, followed by antibody-mediated positive selection using anti-CD138 magnetic activated cell separation microbeads (Miltenyi Biotech, Gladbach, Germany). The purity of immunoselected cells was assessed by flow-cytometry analysis using a phycoerythrin-conjugated CD138 monoclonal antibody by standard procedures. $CD138^+$

cells from MM patients were seeded and cultured in RPMI-1640 medium (Gibco®, Life Technologies) supplemented with 20% fetal bovine serum (Lonza Group Ltd) and 1% penicillin/streptomycin (Gibco®, Life Technologies).

Ethics approval and consent to participate

Written informed consent was obtained from all patients in accordance with the declaration of Helsinki. The study was approved by the Ethical Committee of the Fondazione IRCCS Ca' Granda Ospedale Maggiore Policlinico (N°575, 03/29/2018).

RESULTS

DIS3 expression in MM correlates with molecular subtypes

To gain insight into the role of *DIS3* in MM, we start exploring its expression in pathological sample compared to the normal controls. In detail, we investigated *DIS3* expression levels in a proprietary, publicly available, RNA dataset profiled by microarrays that includes four healthy donors, 130 MM, 24 primary plasma cell leukemia (pPCL), and 12 secondary PCL (sPCL) patients (GSE66293). Considering that *DIS3* expression levels could be affected by the presence of chromosome 13 deletion (del13), we stratified patients based on the presence of this molecular lesion. We found that MM, pPCL and sPCL patients without del13 showed *DIS3* expression levels significantly higher than normal controls; conversely, pathological samples with del13 displayed *DIS3* expression levels comparable to normal controls (Figure 1A).

Next, we focused on the expression pattern of *DIS3* in MM by taking advantage of a large cohort of MM patients enrolled in the Multiple Myeloma Research Foundation (MMRF) CoMMpass study. To this end, we evaluated MM PC expression levels from 774 MM patients included in the CoMMpass dataset (Figure 1B). In detail, *DIS3* expression spanned a limited range of estimated values (3.3-43.2; median: 13.16) of transcripts per million (TPM). In addition, MM with t(11;14) chromosomal translocation showed *DIS3* expression levels significantly higher than patients with other translocations (namely t(4;14), MAF translocations, MYC, double translocations) or negative for any translocations.

To assess *DIS3* expression profiles in relation to major molecular aberrations in MM, we investigated 660 MM patients of the CoMMpass cohort for which expression, Non-Synonymous (NS) somatic mutations, and Copy Number Alterations (CNAs) data were available by RNA-sequencing (RNA-seq), Whole Exome Sequencing (WES) and next generation sequencing (NGS)-based FISH (FISH-WES), respectively (Supplementary Table S1).

We observed that the presence of del13 is associated with a reduction of *DIS3* expression levels. Interestingly, significantly higher *DIS3* expression levels were observed in MM patients carrying t(11;14), in particular in those without del13 alteration (Supplementary Figures S1A and S2A). Significantly higher *DIS3* expression levels were also found in MM patients carrying NS somatic mutations in the *RAS/BRAF* or *FAM46C* genes, whereas lower expression levels were evidenced in samples with 1q-gain, del13, t(4;14), or *DIS3* gene mutation (Supplementary Figure S1A). However, concerning patients with *DIS3* mutations, we observed that samples with *DIS3* hot-spot mutations display *DIS3* expression levels higher than MM patients carryng not hot-spot *DIS3* mutations (Supplementary Figure S2B). No significant differences in *DIS3* expression levels were observed in relation to del(17p)/TP53, t(6;14), MYC or MAF translocations, del(1p), the occurrence of NS somatic mutations in *TRAF3* or *TP53* genes, or hyperdiploid (HD) cases (Supplementary Figure S1B).

Finally, in order to investigate the relevance of *DIS3* expression levels in clinical outcome, we considered 767 MM patients of the CoMMpass dataset with available clinical data. High versus low expression groups were determined according to the median cut-off value for *DIS3* expression level across the entire dataset. Our data showed that *DIS3* expression levels did not affect clinical outcome either in terms of overall survival (OS) or progression free survival (PFS) (Supplementary Figure S3).

DIS3 **knockdown inhibits proliferation in MM cell lines and affects cell cycle progression and distribution**

To investigate the functional role of *DIS3* in MM, we exploited a loss of function approach by using LNA-gapmeR anti-sense oligonucleotide (ASO) that triggers RNAse-H-dependent degradation of transcripts. Specifically, we designed three “in-house” sequences (g*DIS3*#2/13/15) able to recognize all three *DIS3* isoforms (Supplementary Figure S4A) and tested them in the AMO-1 HMCL by using electroporation. Among them, the g*DIS3*#13 gapmeR showed the strongest silencing efficiency (nearly 70%) after 24hr (Supplementary Figure S4B). To achieve a more pronounced and prolonged knockdown (KD) effect, we optimized its gymnotic delivery;[26] the strikingly downregulation of *DIS3* at both the transcriptional and protein level obtained in different HMCLs, AMO-1, NCI-H929 and U266 (Figure 2A and B), suggested this strategy as valuable tool for subsequent investigations.

In particular, we found that in AMO-1, NCI-H929 and U266 cells *DIS3*-KD was associated with a significant reduction of the cell growth and an increase in apoptosis at 6 days after g*DIS3*#13 delivery (Figure 3A-B). Notably, HMCLs showed the same phenotype at 48hr post electroporation by using an RNA interference strategy (Supplementary Figure S5). Furthermore, *DIS3*-KD dramatically reduced (fold change 5-10) the clonogenic potential of MM cells (Figure 3C). Finally, we evaluated the biological effects of g*DIS3*#13 *ex-vivo* on primary CD138$^+$ tumor cells purified from the BM of four MM patients. *DIS3*-KD leads to an important alteration of cell morphology, causing cytoplasmic vacuolization, which suggests a suffering cell phenotype, and affecting the cell membrane integrity to one typical of apoptotic cells (Figure 3D), in agreement with the reduced viability of g*DIS3*#13 treated primary cells (Supplementary Table S2).

To inspect whether the inhibitory effects on proliferative potential of *DIS3* silencing are associated with specific changes in cell cycle progression, we analysed AMO-1 and NCI-H929 cells silenced with g*DIS3* for 4 days. *DIS3*-KD in HMCLs caused a significant increase in the number of cells in the G0/G1 phase of the cell cycle, and a decrease of the percentage of cells distributed in the S and G2/M phases, indicating G0/G1 cell cycle arrest (Supplementary Figure S6). To investigate more in detail the alterations in cell cycle progression, we synchronized HMCLs by using the Synchroset reagent, and followed cell cycle progression at different time points (Supplementary Figure S7) by collecting samples before block, during and after release (Supplementary Figures S8-S10). In agreement with previous results, we found that AMO-1, NCI-H929 and U266 exhibited a modulation of cell cycle phases distribution after *DIS3*-KD, with a significant increased percentage of G0/G1 phase events and a decrease of the S and G2/M phases (Figure 4A-B).

To further confirm that *DIS3*-KD results in a perturbation of cell cycle progression in HMCLs, we investigated proteins that are reported as associated with the different cell cycle checkpoints (Figure 5). In line with cytofluorimetric analysis showing a cell cycle arrest in G0/G1 phase, *DIS3*-KD cells showed a slight increase of CCNE1 protein levels, whereas there was a decrease in the expression levels of the cyclin A protein (CCNA2), whose accumulation creates a decision window to enter in S phase and to initiate DNA replication. In agreement with a reduced G2/M phase of the cell cycle, *DIS3*-KD cells displayed a reduction of both cyclin B (CCNB1) total protein and its phosphorylated fraction (pCCNB1), whose accumulation in the cyclin A/B-CDK1 complex creates a second decision window.[27,28] CCNB1 expression changes during the different cell cycle phases, reaching its maximum in G2/M transition. Cell entry into mitosis depends on the binding of CCNB1 to CDK1 to form the mitosis-promoting factor (MPF); CCNB1 phosphorylation promotes nuclear translocation of MPF and is important for the decisiveness and irreversibility of mitotic entry. However, MPF remains in the inactive state until phosphorylation of CDK1 (pCDK1). In our experimental condition, gDIS3-treated NCI-H929 and U266 showed a consistent reduction of the pCDK1 fraction; pCDK1 was not affected in gDIS3-treated AMO-1 cell line, which, however, reduces the total amount of CDK1 protein. Furthermore, we investigated CDC20 that is a critical checkpoint effector of mitosis and its overexpression is associated with several cancer type, including MM.[29,30] In our experiments, we observed an important decrease in the expression level of CDC20 protein but not of its phosphorylated fraction (pCDC20) in *DIS3*-KD cells. pCDC20 is important in the early steps of mitosis; in late anaphase and G1 phase, CDC20 is dephosphorylated and targeted for degradation by the proteasome; it will not be expressed again until S phase. Finally, we observed a strong down-modulation of histone H3 variant CENP-A in all *DIS3* depleted cells tested; this protein plays a fundamental role in defining centromere identity and structure and is a critical protein for the proper formation of the mitotic spindle.[31]

Transcriptional signature associated with *DIS3* silencing in NCI-H929 cell line

In order to identify *DIS3* downstream-related pathway in MM, we investigated gene expression profiling of synchronized NCI-H929 cells after five days of g*DIS3*#13 gymnotic delivery. Out of 55540 globally analyzed genes, the expression of 4032 genes resulted significantly modulated (FDR < 10%) by SAM analysis. They were virtually all down-regulated (3995 genes, 99%) in *DIS3*-silenced cells, principally involving protein coding genes (2608 genes, 65%) and to a lesser extent long non-coding RNAs (464 lncRNAs, 12%) (Supplementary Table S3). As expected based on previous biologic results, chromosome organization, chromatin and histone modification, and cell cycle checkpoint were recognized among the top 20 most significantly enriched GO Biological Process terms (Supplementary Figure S11A). In addition, genes involved in serine/threonine protein kinase activity, with helicase function, catalytic activity on RNA, or with tubulin binding function were evidenced in the top 20 remarkably enriched GO Molecular Function terms under *DIS3* silencing (Supplementary Figure S11B). In particular, numerous protein coding genes that were significantly enriched in multiple annotation categories were linked to complex interactions, regarding chromosome organization and nuclear division, or molecular activities on nucleic acids and tubulin, resulted globally down-regulated in *DIS3*-silenced cells (Supplementary Figure S12).

Finally, to find possible molecular subsets of genes that were coordinately modulated in *DIS3*-silenced cells in comparison to control NCI-H929 cells, Gene Set Enrichment Analysis (GSEA) was performed on global annotated protein coding gene expression profiles and the most significant gene sets were selected under stringent conditions (nominal p-value < 0.05 and FDR q-value <5%) (Supplementary Table S4). Among the most significantly up-regulated gene sets in *DIS3*-silenced NCI-H929 cells, some were involved in degradation of extracellular matrix and DNA and histone epigenetic modifications, whereas cell cycle checkpoint, chromosome organization, RNA processing and degradation, DNA recombination and repair, regulation of TP53 activity and numerous cell signaling pathways resulted among the most significant under-expressed gene sets in *DIS3* silenced cells (Figure 6 and Supplementary Table S4).

Based on our evidence that *DIS3* can regulate cell cycle, chromosome organization and DNA repair processes, we validated the expression of some genes involved in these processes by means of qRT-PCR in *DIS3* silenced AMO-1, NCI-H929, and U266 cell lines. In particular, we considered *RAD51B* and *ARID5B* involved in Homologous Recombination (HR) and DNA repair process; in addition, we investigated *CCNB1*, *CDC20*, the microtubule motor protein *KIF14*, the DNA topoisomerase *TOP2A* and the RNA polymerase *POLR2H*, all of them involved in cell cycle process. All these genes resulted down-regulated upon *DIS3* silencing in all cell lines, (Figure 7A). The down-regulation of these genes was also validated *ex-vivo* in *DIS3*-depleted primary CD138+

tumor cells, except for *CCNB1* and *CDC20*, likely because purified PCs hardly duplicate (Figure 7B).

DIS3 depletion affects mitotic spindle organization and geometry of MM cells

Considering previously reported data in yeast and drosophila indicating that *DIS3*-KD can impact chromosome segregation and spindle assembly, and based on our evidence that *DIS3*-KD in HMCLs leads to a decrease of CENP-A, which is fundamental for the proper formation of the mitotic spindle, we investigated whether *DIS3* depletion could affect mitotic spindle formation also in MM PCs.

To obtain a significant number of mitotic cells to analyze, *DIS3*-KD cells were synchronized at the M phases of the cell cycle (Figure 8A). In detail, cells were immunostained for *DIS3*, centrosomes (γ-tubulin), mitotic spindle fibers (α-tubulin), and nuclei were counterstained with DAPI. Notably, we found that *DIS3* silencing leads to the formation of supernumerary centrosomes accompanied by important changes in mitotic spindle organization and geometry in HMCLs. Hence, in contrast to control cells which displayed normal spindle localization and physiological bipolar cell division, *DIS3*-KD cells showed the presence of multipolar spindles during mitosis (Figure 8B-C and Supplementary Figure S13).

DISCUSSION

DIS3 aberrant expression has been described in different tumors types, including MM. Of note, the frequent and almost specific occurrence of *DIS3* mutations observed in MM impacts the clinical outcome of the patients.[3] However, to date, *DIS3* expression pattern and its functional and pathogenic role in plasma cell malignancies has not yet been clarified. In this study, we investigated the effects of *DIS3* depletion in myeloma cells providing insights into its putative role in the pathobiology of the disease.

First of all, we explored *DIS3* expression in patients affected by MM or PCL and we found that pathological samples expressed *DIS3* transcript levels higher than normal controls; indeed, even in patients carrying del13, despite their loss of heterozygosity, the amount of *DIS3* transcript did not fall below the levels of normal controls. Our analysis showed that *DIS3* expression levels do not impact MM clinical outcome in patients included in the CoMMpass data set; however, this result could be affected by the fact that the group with low *DIS3* expression level is largely enriched in cases with del13 and/or t(4;14), whereas the group with higher *DIS3* expression level is enriched in patients with t(11;14) and/or hotspot *DIS3* mutations (Supplementary Figure S2). Overall, these data suggest that the co-occurrence of different molecular alterations in MM patients could mask the specific oncogenic function of *DIS3* expression in the disease[32].

Hence, the biological role of *DIS3* was investigated *in vitro* by exploiting a loss of function approach in HMCLs. Our experiments revealed that *DIS3*-KD largely affects cell cycle progression in MM cells, leading to a decrease in the fraction of cells distributed in S and G2/M phases, and a consistent increase of cells in the G0/G1 phase. These findings strongly suggest an important role of *DIS3* in the control of the G1 phase of the cell cycle. In agreement with this idea, we found that in the CoMMpass dataset, MM patients with t(11;14) and high expression levels of CCND1, which is necessary for the transition from the G1 to the S phase of the cell cycle, are those significantly associated with the highest *DIS3* expression levels (Supplementary Figure S1).

The prominent role of *DIS3* in the G1 phase is also suggested by the fact that in different cell types, including HMCLs, *DIS3*-KD gives rise to a pervasive accumulation of DNA:RNA hybrids.[25] R-loops are three-stranded structures generated by the annealing of nascent transcripts to the template DNA strand playing important roles in physiological processes; however, uncontrolled hybrids production or lack of their immediate resolution through protein complexes, including RNases, helicases, and topoisomerases can induce DNA damage and genome instability.[33] Importantly, the inhibition of the key homologous recombination factor RAD51 leads to DNA:RNA hybrids accumulation in the early G1 phase of the cell cycle,[34] indicating that R-loops metabolism mainly occurs in the G1 phase.

Our results showed that *DIS3* plays an important role not only in the control of cell cycle in MM cells, but also in the centrosome duplication cycle, which are strictly coregulated in physiological condition in the G1 phase of the cell cycle.[35,36] Indeed, for the first time we identified that *DIS3*-KD leads to the formation of supernumerary centrosomes that finally results in altered and multipolar mitotic spindles in the M phase of the cell cycle of MM cells. The requirement of *DIS3* RNase activity for proper mitotic cell division and correct chromosome condensation has been already described in yeast and *Drosophila melanogaster* models.[21,22,37–39] In addition, *S. pombe DIS3* mutants have been shown to have elongated metaphase spindles and a block in metaphase to anaphase transition.[22] Smith et al. provide further evidence that *DIS3* is involved in mitotic progression by demonstrating that perturbation of *DIS3* in *S. cerevisiae* affects microtubule localization and structure.[21] In MM PCs, we found that DIS3 could impact mitotic spindles formation by affecting centrosome duplication.

Numerical and/or structural centrosome amplification (CA) is a hallmark of solid tumors and hematological malignancies that is often associated with the aberrant tumor karyotypes and poor clinical outcomes.[40,41] In MM, CA is present in about a third of patients and may represent a mechanism leading to genomic instability.[42] However, CA clinical impact in MM is still debated and existing contradictory results may be explained by the clonal heterogeneity of MM in which each myeloma subclones with CA may be potentially associated with different clinical behavior influenced by complex processes including mitotic dysregulation, apoptotic failure and chromosome instability.[43,44]

The molecular mechanism by which *DIS3*-KD could induce formation of supernumerary centrosomes remains to be elucidated. These mechanisms might involve consecutive rounds of centrosome reproduction, or concurrent formation of daughter centrioles around the existing centrioles, or via de novo centrosome assembly independent of pre-existing centrioles,[40] Our transcriptional analysis revealed that genes involved in cell cycle checkpoint and chromosome organization resulted among the most significant under-expressed ones in *DIS3* silenced cells (Figure 6 and Supplementary Table S4). Moreover, genes involved in serine/threonine protein kinase activity, with helicase function, catalytic activity on RNA, or with tubulin binding function were evidenced in the top 20 remarkably enriched GO Molecular Function terms upon *DIS3* silencing (Supplementary Figure S11B). In particular, several protein coding genes that were significantly enriched in multiple annotation categories linked in complex interactions, regarding chromosome organization and nuclear division, or molecular activities on nucleic acids and tubulin, resulted globally down-regulated in *DIS3*-silenced cells. Specifically, the downregulation of *KIF14*, *TOP2A* and *POLR2H*, all of them involved in cell cycle processes, have been validated *in vitro* and *ex-vivo*.

Our transcriptomic analysis also showed that genes involved in DNA methylation are over-expressed in *DIS3* silenced cells. This data is in agreement with the observation that most of mRNA expression level is reduced after *DIS3* knockdown despite *DIS3* has ribonuclease activity, overall suggesting that global gene downregulation may be a secondary effect of *DIS3* deficiency on DNA methylation.

Overall, our data prompt further studies to clarify the role of DIS3 in the centrosome duplication process; indeed a combination of *DIS3* defects and deficient spindle-assembly checkpoint, already described in MM,[45] can allow cells to progress through the cell cycle without proper chromosome segregation, thus generating aneuploid cells which may lead to the development of MM.

References

1. Munshi NC, Anderson KC. New strategies in the treatment of multiple myeloma. Clin Cancer Res. 2013;19(13):3337-3344.

2. Morgan GJ, Walker BA, Davies FE. The genetic architecture of multiple myeloma. Nat Rev Cancer. 2012;12(5):335-348.

3. Todoerti K, Ronchetti D, Favasuli V, et al. DIS3 mutations in multiple myeloma impact the transcriptional signature and clinical outcome. Haematologica. 2022;107(4):921-932.

4. Lionetti M, Barbieri M, Todoerti K, et al. A compendium of DIS3 mutations and associated transcriptional signatures in plasma cell dyscrasias. Oncotarget. 2015;6(28):26129-26141.

5. Boyle EM, Ashby C, Tytarenko RG, et al. BRAF and DIS3 Mutations Associate with Adverse Outcome in a Long-term Follow-up of Patients with Multiple Myeloma. Clin Cancer Res. 2020;26(10):2422-2432.

6. Bolli N, Avet-Loiseau H, Wedge DC, et al. Heterogeneity of genomic evolution and mutational profiles in multiple myeloma. Nat Commun. 2014;5:2997.

7. de Groen FLM, Krijgsman O, Tijssen M, et al. Gene-dosage dependent overexpression at the 13q amplicon identifies DIS3 as candidate oncogene in colorectal cancer progression. Genes Chromosomes Cancer. 2014;53(4):339-348.

8. Weißbach S, Langer C, Puppe B, et al. The molecular spectrum and clinical impact of DIS3 mutations in multiple myeloma. Br J Haematol. 2015;169(1):57-70.

9. Ng D, Toure O, Wei MH, et al. Identification of a novel chromosome region, 13q21.33-q22.2, for susceptibility genes in familial chronic lymphocytic leukemia. Blood. 2007;109(3):916-925.

10. Rose AE, Poliseno L, Wang J, et al. Integrative genomics identifies molecular alterations that challenge the linear model of melanoma progression. Cancer Res. 2011;71(7):2561-2571.

11. Binder M, Rajkumar SV, Ketterling RP, et al. Prognostic implications of abnormalities of chromosome 13 and the presence of multiple cytogenetic high-risk abnormalities in newly diagnosed multiple myeloma. Blood Cancer J. 2017;7(9):e600.

12. Chiecchio L, Dagrada GP, Ibrahim AH, et al. Timing of acquisition of deletion 13 in plasma cell dyscrasias is dependent on genetic context. Haematologica. 2009;94(12):1708-1713.

13. Tomecki R, Kristiansen MS, Lykke-Andersen S, et al. The human core exosome interacts with differentially localized processive RNases: hDIS3 and hDIS3L. EMBO J. 2010;29(14):2342-2357.

14. Schneider C, Leung E, Brown J, Tollervey D. The N-terminal PIN domain of the exosome subunit Rrp44 harbors endonuclease activity and tethers Rrp44 to the yeast core exosome. Nucleic Acids Res. 2009;37(4):1127-1140.

15. Tomecki R, Drazkowska K, Kucinski I, et al. Multiple myeloma-associated hDIS3 mutations cause perturbations in cellular RNA metabolism and suggest hDIS3 PIN domain as a potential drug target. Nucleic Acids Res. 2014;42(2):1270-1290.

16. Mitchell P, Petfalski E, Shevchenko A, Mann M, Tollervey D. The Exosome: A Conserved Eukaryotic RNA Processing Complex Containing Multiple 3′→5′ Exoribonucleases. Cell. 1997;91(4):457-466.

17. Wasmuth EV, Lima CD. Exo- and endoribonucleolytic activities of yeast cytoplasmic and nuclear RNA exosomes are dependent on the noncatalytic core and central channel. Mol Cell. 2012;48(1):133-144.

18. Kinoshita N, Goebl M, Yanagida M. The fission yeast dis3+ gene encodes a 110-kDa essential protein implicated in mitotic control. Mol Cell Biol. 1991;11(12):5839-5847.

19. Ohkura H, Adachi Y, Kinoshita N, Niwa O, Toda T, Yanagida M. Cold-sensitive and caffeine-supersensitive mutants of the Schizosaccharomyces pombe dis genes implicated in sister chromatid separation during mitosis. EMBO J. 1988;7(5):1465-1473.

20. Noguchi E, Hayashi N, Azuma Y, et al. Dis3, implicated in mitotic control, binds directly to Ran and enhances the GEF activity of RCC1. EMBO J. 1996;15(20):5595-5605.

21. Smith SB, Kiss DL, Turk E, Tartakoff AM, Andrulis ED. Pronounced and extensive microtubule defects in a Saccharomyces cerevisiae DIS3 mutant. Yeast Chichester Engl. 2011;28(11):755-769.

22. Murakami H, Goto DB, Toda T, et al. Ribonuclease activity of Dis3 is required for mitotic progression and provides a possible link between heterochromatin and kinetochore function. PloS One. 2007;2(3):e317.

23. Hou D, Ruiz M, Andrulis ED. The ribonuclease Dis3 is an essential regulator of the developmental transcriptome. BMC Genomics. 2012;13:359.

24. Szczepińska T, Kalisiak K, Tomecki R, et al. DIS3 shapes the RNA polymerase II transcriptome in humans by degrading a variety of unwanted transcripts. Genome Res. 2015;25(11):1622-1633.

25. Gritti I, Basso V, Rinchai D, et al. Loss of ribonuclease DIS3 hampers genome integrity in myeloma by disrupting DNA:RNA hybrid metabolism. EMBO J. 2022;41(22):e108040.

26. Taiana E, Favasuli V, Ronchetti D, et al. Long non-coding RNA NEAT1 targeting impairs the DNA repair machinery and triggers anti-tumor activity in multiple myeloma. Leukemia. 2020;34(1):234-244.

27. Matthews HK, Bertoli C, de Bruin RAM. Cell cycle control in cancer. Nat Rev Mol Cell Biol. 2022;23(1):74-88.

28. Musacchio A, Salmon ED. The spindle-assembly checkpoint in space and time. Nat Rev Mol Cell Biol. 2007;8(5):379-393.

29. Bruno S, Ghelli Luserna di Rorà A, Napolitano R, Soverini S, Martinelli G, Simonetti G. CDC20 in and out of mitosis: a prognostic factor and therapeutic target in hematological malignancies. J Exp Clin Cancer Res CR. 2022;41(1):159.

30. Lub S, Maes A, Maes K, et al. Inhibiting the anaphase promoting complex/cyclosome induces a metaphase arrest and cell death in multiple myeloma cells. Oncotarget. 2016;7(4):4062-4076.

31. Pesenti ME, Raisch T, Conti D, et al. Structure of the human inner kinetochore CCAN complex and its significance for human centromere organization. Mol Cell. 2022;82(11):2113-2131.

32. Bolli N, Biancon G, Moarii M, et al. Analysis of the genomic landscape of multiple myeloma highlights novel prognostic markers and disease subgroups. Leukemia. 2018;32(12):2604-2616.

33. Santos-Pereira JM, Aguilera A. R loops: new modulators of genome dynamics and function. Nat Rev Genet. 2015;16(10):583-597.

34. Nascakova Z, Boleslavska B, Urban V, et al. RAD51 Inhibition Induces R-Loop Formation in Early G1 Phase of the Cell Cycle. Int J Mol Sci. 2021;22(7):3740.

35. Prigent C, Uzbekov R. Duplication and Segregation of Centrosomes during Cell Division. Cells. 2022;11(15):2445.

36. Lin M, Xie SS, Chan KY. An updated view on the centrosome as a cell cycle regulator. Cell Div. 2022;17(1):1.

37. Graham AC, Kiss DL, Andrulis ED. Core exosome-independent roles for Rrp6 in cell cycle progression. Mol Biol Cell. 2009;20(8):2242-2253.

38. Robinson SR, Oliver AW, Chevassut TJ, Newbury SF. The 3’ to 5’ Exoribonuclease DIS3: From Structure and Mechanisms to Biological Functions and Role in Human Disease. Biomolecules. 2015;5(3):1515-1539.

39. Snee MJ, Wilson WC, Zhu Y, et al. Collaborative Control of Cell Cycle Progression by the RNA Exonuclease Dis3 and Ras Is Conserved Across Species. Genetics. 2016;203(2):749-762.

40. Mittal K, Kaur J, Jaczko M, et al. Centrosome amplification: a quantifiable cancer cell trait with prognostic value in solid malignancies. Cancer Metastasis Rev. 2021;40(1):319-339.

41. Krämer A, Neben K, Ho AD. Centrosome aberrations in hematological malignancies. Cell Biol Int. 2005;29(5):375-383.

42. Chng WJ, Fonseca R. Centrosomes and myeloma; aneuploidy and proliferation. Environ Mol Mutagen. 2009;50(8):697-707.

43. Dementyeva E, Kryukov F, Kubiczkova L, et al. Clinical implication of centrosome amplification and expression of centrosomal functional genes in multiple myeloma. J Transl Med. 2013;11:77.

44. Kryukova E, Kryukov F, Hajek R. Centrosome amplification and clonal evolution in multiple myeloma: Short review. Crit Rev Oncol Hematol. 2016;98:116-121.

45. Díaz-Rodríguez E, Álvarez-Fernández S, Chen X, et al. Deficient spindle assembly checkpoint in multiple myeloma. PloS One. 2011;6(11):e27583.

LEGEND TO FIGURES

Figure 1. *DIS3* expression analysis in plasma cell dyscrasias. (A) Box plot of *DIS3* expression level in healthy donors (N) and PC dyscrasias (proprietary dataset, GSE66293). The 4 N are RNA samples from bone marrow PCs purified (>90%) from normal individuals and purchased from Voden (Medical Instruments IT). Total RNA samples from highly purified BM CD138+ plasma cells were profiled by Gene 1.0 ST array. (B) Box plot of *DIS3* expression level in main IgH translocation groups in 774 cases of the CoMMpass cohort; trx.MAF: MAF translocation, trx.MYC: MYC translocation, double.trx: presense of 2 translocations, trx.neg: absence of the considered translocations. Kruskal-Wallis test was applied to assess differences in expression levels between groups. The pairwise comparison were performed by the Dunn's test; significant results are marked red-bold in the tables.

Figure 2. ***DIS3* expression analysis in *DIS3*-depleted cells.** (A) qRT-PCR of *DIS3* mRNA in AMO-1, NCI-H929 and U266 at the indicated time point; *DIS3* mRNA expression was expressed as $2^{-\Delta\Delta Ct}$ relative to the housekeeping *GAPDH* gene and the scramble condition at the same time point used as calibrator. (B) WB analyses of *DIS3*-KD in AMO-1, NCI-H929 and U266 cells. WB results are quantified and plotted in histogram.

Figure 3. **Functional impact of *DIS3* depletion in MM cells.** (A) Growth curves of AMO-1, NCI-H929 and U266 following *DIS3* silencing. (B) Flow cytometry analyses of apoptosis in AMO-1, NCI-H929 and U266 6 days after treatment with g*DIS3* (5µM). (C) Colony formation assay performed on AMO-1, NCI-H929 and U266 treated for 21 days with g*DIS3*; representative pictures of colonies at day 21 are also shown, $^{**}p < 0.01$, $^{***}p < 0.001$, Student's t test. (D) Rappresentative images of May-Grunwald Giemsa staining of two CD138+ primary tumors treated for 6 days with g*DIS3* (50x magnification).

Figure 4. Cell cycle analysis in *DIS3*-depleted cells. (A) Cell cycle progression in synchronized AMO-1, NCI-H929, and U266 cells was monitored by PI staining and FACS analysis of the DNA content of cells at 6 hrs after release. Percentage of cell cycle distribution is represented in the histogram (B); standard deviation of three replicates are reported, $^{*}p < 0.05$, $^{**}p < 0.01$, $^{***}p < 0.001$, Student's t test.

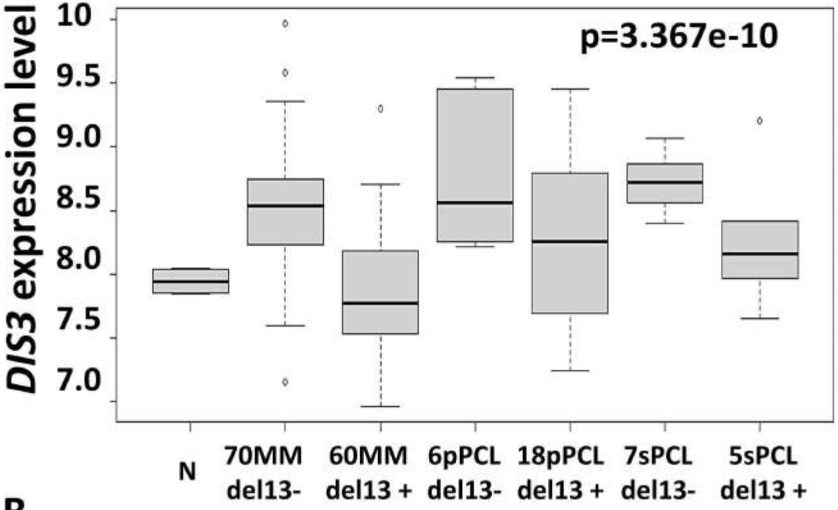
Figure 5. WB analyses of cell cycle check point proteins. (A) Analysis performed in synchronized AMO-1, NCI-H929 and U266 6 hr after release. For NCI-H929 cells, the evaluation of pCDC20, CDC20 and CENP-A have been performed on the same blot, thus having the same GAPDH control; to improve the overall symmetry of the figure and its comprehension, the same GAPDH panel has been reported twice. (B) WB results are quantified and plotted in histogram. (C) Histogram of the modulation of the phosphorylated protein fraction upon g*DIS3* treatment, calculated as ratio of phosphorylated protein to total protein in gDIS3-treated cells compared to the ratio of phosphorylated protein to total protein in scramble-treated ones.

Figure 6. Transcriptomic analyses in *DIS3*-depleted cells. Enrichment plots of selected GSEA gene sets significantly modulated in *DIS3*-silenced cells in comparison to scramble NCI-H929 cells; GSEA was performed on global annotated protein coding gene expression profiles (19.048 genes) and most significant gene sets were selected under stringent conditions (nominal p-value < 0.05 and FDR q-value < 5%). Enrichment Score (NES) and nominal p-value are reported for each plot.

Figure 7. Molecular validation of transcriptomic analysis. (A) qRT-PCR validation of the indicated genes in *DIS3*-depleted AMO-1, NCI-H929, and U266 HMCLs; gene expression was expressed as $2^{-\Delta\Delta Ct}$ relative to the housekeeping *GAPDH* gene and the scramble condition used as calibrator. (B) *Ex-vivo* validation of the indicated genes in *DIS3*-depleted primary CD138+ tumor cells purified from 4 MM patients.

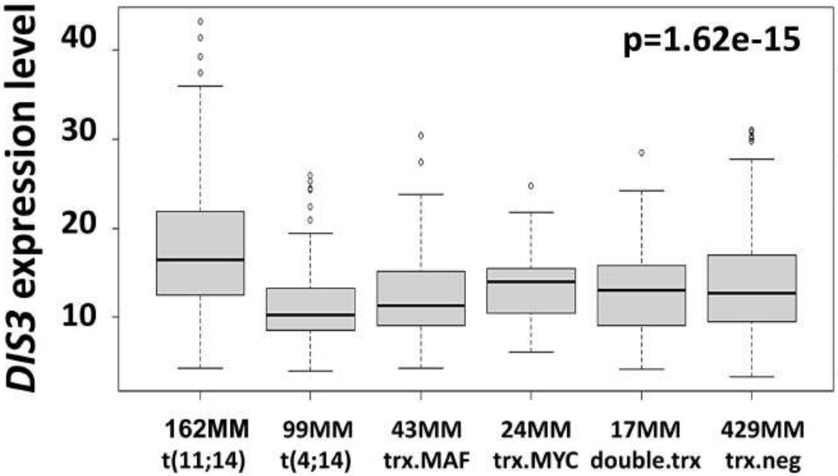
Figure 8. Images of metaphase spindles in NCI-H929 and AMO-1 cells treated with g*DIS3* or scramble. (A) Schematic representation of the experimental setup used to synchronize cells. (B) Representative images of multipolar spindles in both cell lines following *DIS3*-KD (right panel for each cell line). Scale bar, 5µm. (C) Percentage of mitotic cells with defective spindles in NCI-H929 and AMO-1 cells treated with g*DIS3* versus scramble.

A

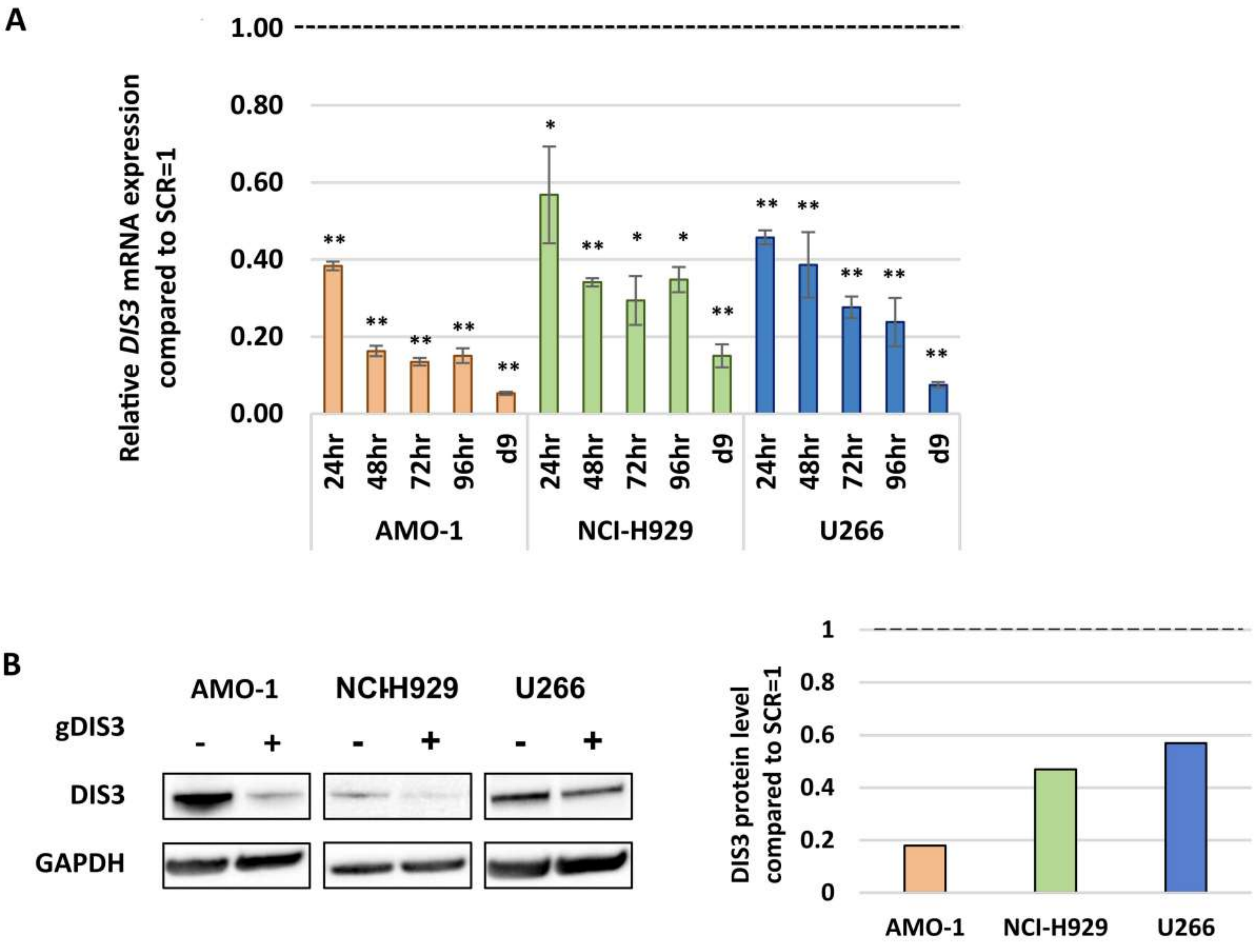


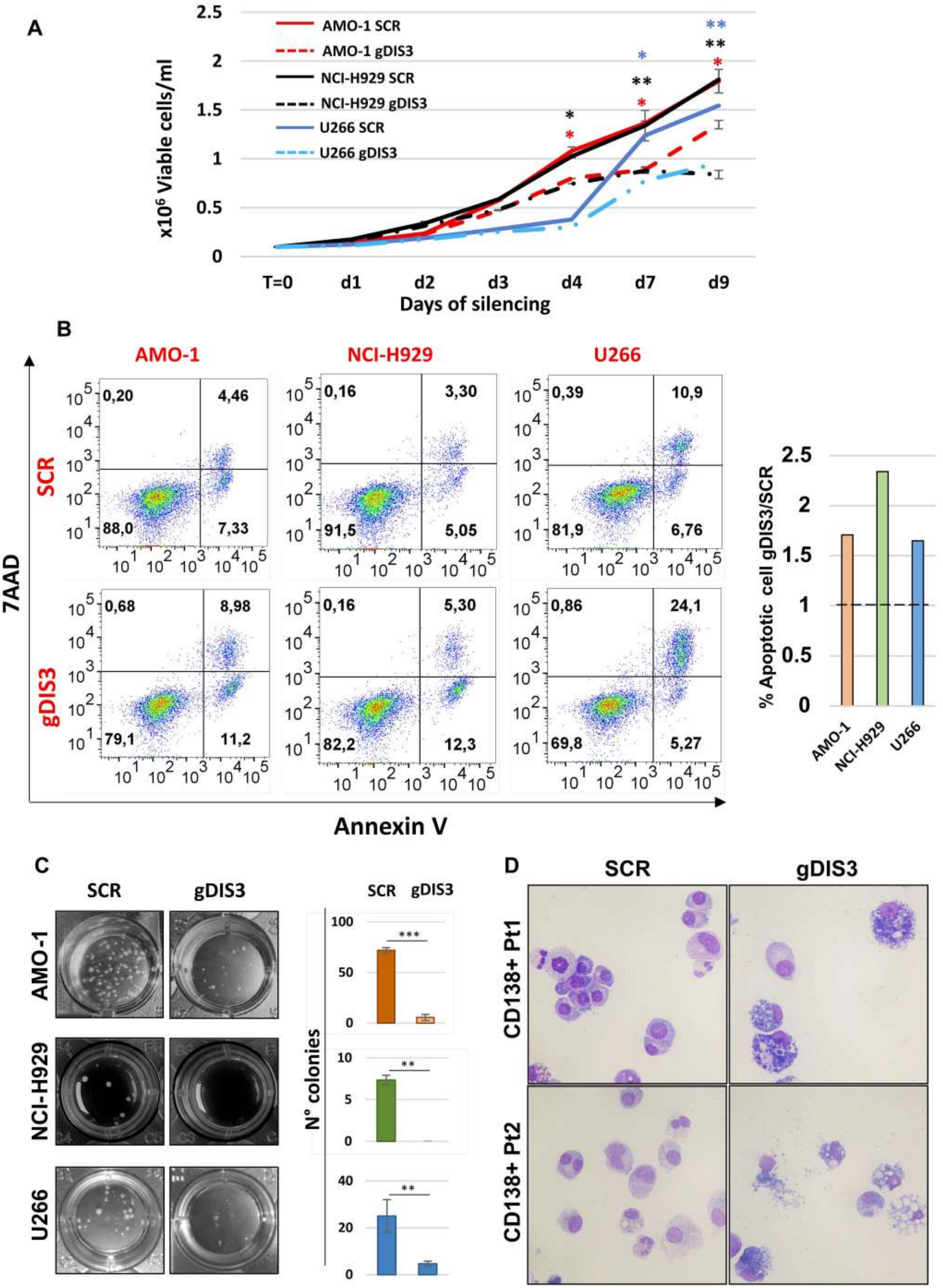
	N	MM del13-	MM del13+	pPCL del13-	pPCL del13	sPCL del13-
MM del13-	**0.018**					
MMdel13+	0.43	0				
pPCL del13-	**0.018**	0.26	**0.0004**			
pPCL del13+	0.13	**0.037**	**0.0048**	0.059		
sPCL del13-	**0.006**	0.1	0	0.34	**0.015**	
sPCL del13+	0.18	0.14	0.07	0.1	0.48	**0.047**

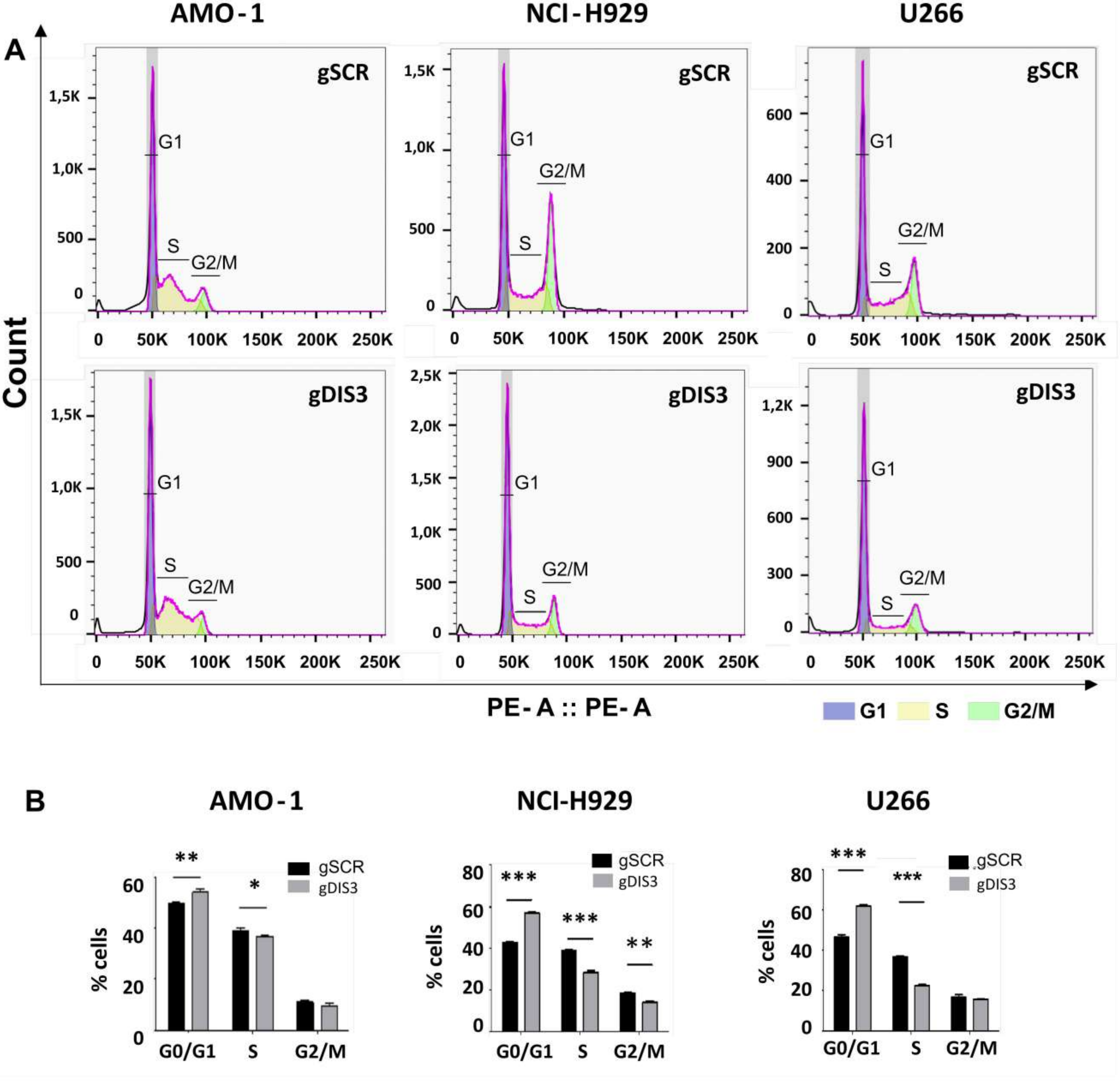
B

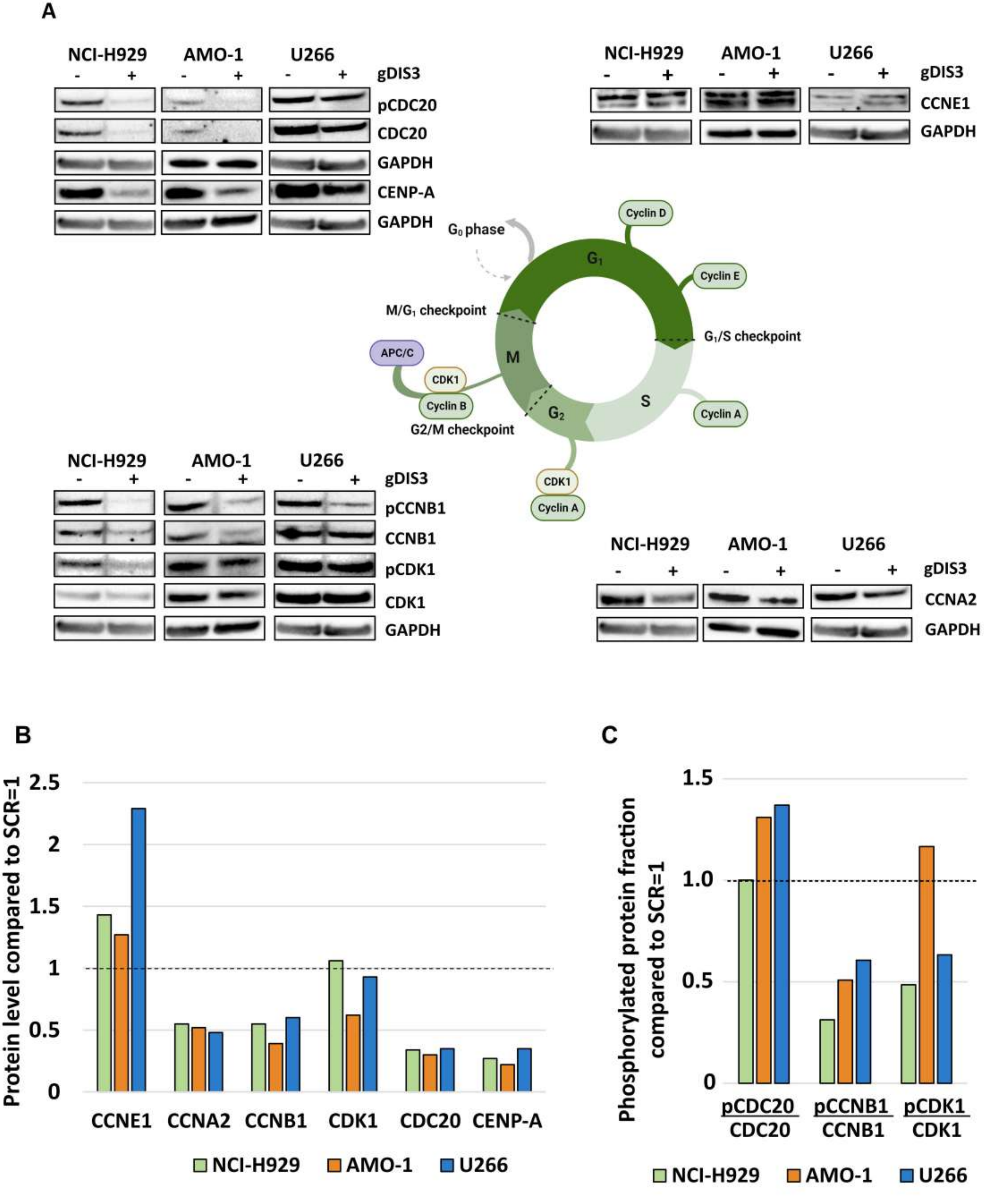


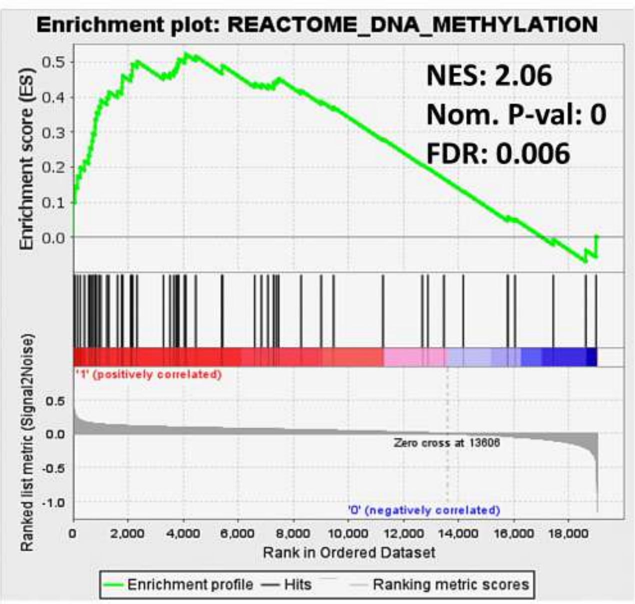
	t(11;14)	t(4;14)	Trx.MAF	Trx.MYC	Double Trx
t(4;14)	**0.0000**				
Trx.MAF	**0.0000**	0.0590			
Trx.MYC	**0.0059**	**0.0120**	0.1800		
Double Trx	**0.0068**	0.0500	0.3000	0.4000	
Trx NEG	**0.0000**	**0.0000**	0.1500	0.3800	0.4700

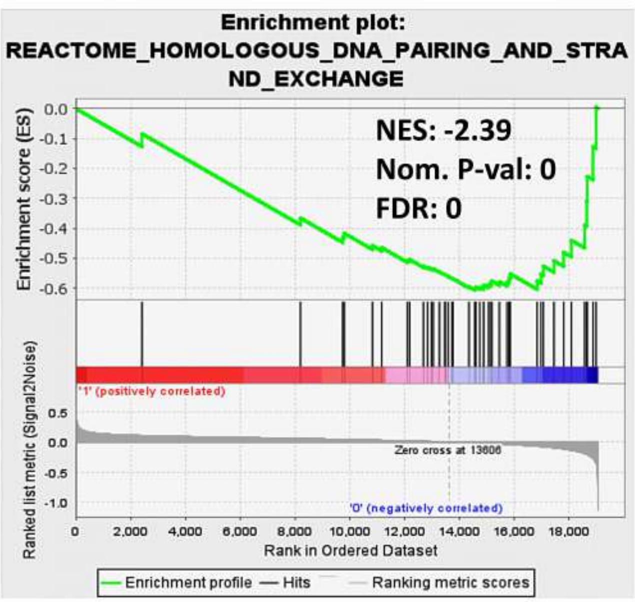

A
Relative *DIS3* mRNA expression compared to SCR=1
1.00
0.80
0.60
0.40
0.20
0.00
**
**
**
**
**
*
**
*
*
**
**
**
**
**
**
24hr
48hr
72hr
96hr
d9
24hr
48hr
72hr
96hr
d9
24hr
48hr
72hr
96hr
d9
AMO-1
NCI-H929
U266
B
AMO-1
NCI-H929
U266
gDIS3
-
+
-
+
-
+
DIS3
GAPDH
DIS3 protein level compared to SCR=1
1
0.8
0.6
0.4
0.2
0
AMO-1
NCI-H929
U266

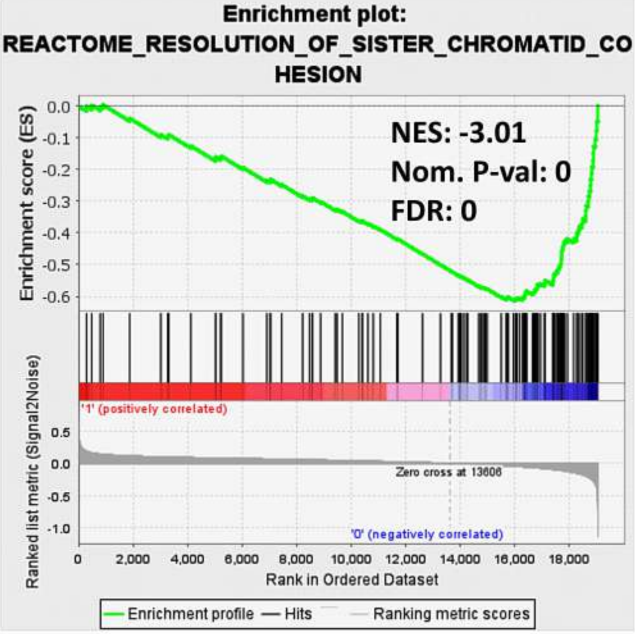

A
2.5
2
1.5
1
0.5
0
x10^6 Viable cells/ml
AMO-1 SCR
AMO-1 gDIS3
NCI-H929 SCR
NCI-H929 gDIS3
U266 SCR
U266 gDIS3
*
*
*
**
*
**
**
*
T=0
d1
d2
d3
d4
d7
d9
Days of silencing
B
AMO-1
NCI-H929
U266
SCR
gDIS3
7AAD
Annexin V
0,20
4,46
88,0
7,33
0,16
3,30
91,5
5,05
0,39
10,9
81,9
6,76
0,68
8,98
79,1
11,2
0,16
5,30
82,2
12,3
0,86
24,1
69,8
5,27
% Apoptotic cell gDIS3/SCR
2.5
2
1.5
1
0.5
0
AMO-1
NCI-H929
U266
C
SCR
gDIS3
AMO-1
NCI-H929
U266
SCR
gDIS3
N° colonies
100
50
0
***
10
5
0
**
40
20
0
**
D
SCR
gDIS3
CD138+ Pt1
CD138+ Pt2

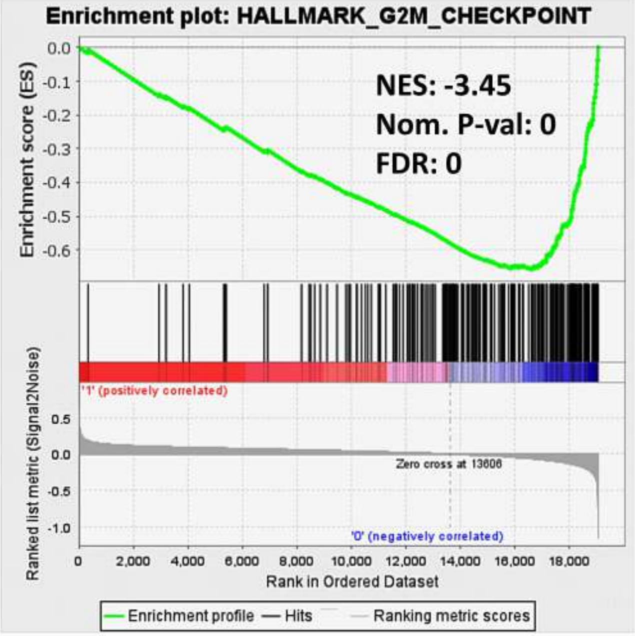

A
AMO-1
NCI-H929
U266
gSCR
gDIS3
G1
S
G2/M
Count
0
500
1,0K
1,5K
2,0K
2,5K
200
400
600
300
900
1,2K
0
50K
100K
150K
200K
250K
PE-A :: PE-A
G1
S
G2/M
B
AMO-1
NCI-H929
U266
% cells
0
20
40
60
80
gSCR
gDIS3
G0/G1
S
G2/M
*
**
***

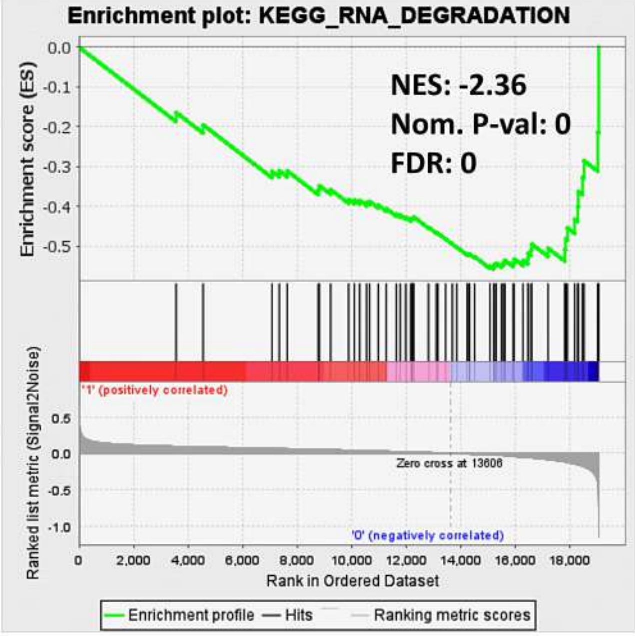

A
NCI-H929
AMO-1
U266
-
+
gDIS3
pCDC20
CDC20
GAPDH
CENP-A
GAPDH
CCNE1
GAPDH
pCCNB1
CCNB1
pCDK1
CDK1
GAPDH
CCNA2
GAPDH
G₀ phase
Cyclin D
G₁
Cyclin E
M/G₁ checkpoint
G₁/S checkpoint
APC/C
M
CDK1
Cyclin B
S
G₂
Cyclin A
G2/M checkpoint
CDK1
Cyclin A
B
Protein level compared to SCR=1
2.5
2
1.5
1
0.5
0
CCNE1
CCNA2
CCNB1
CDK1
CDC20
CENP-A
NCI-H929
AMO-1
U266
C
Phosphorylated protein fraction compared to SCR=1
1.5
1.0
0.5
0
pCDC20 / CDC20
pCCNB1 / CCNB1
pCDK1 / CDK1
NCI-H929
AMO-1
U266

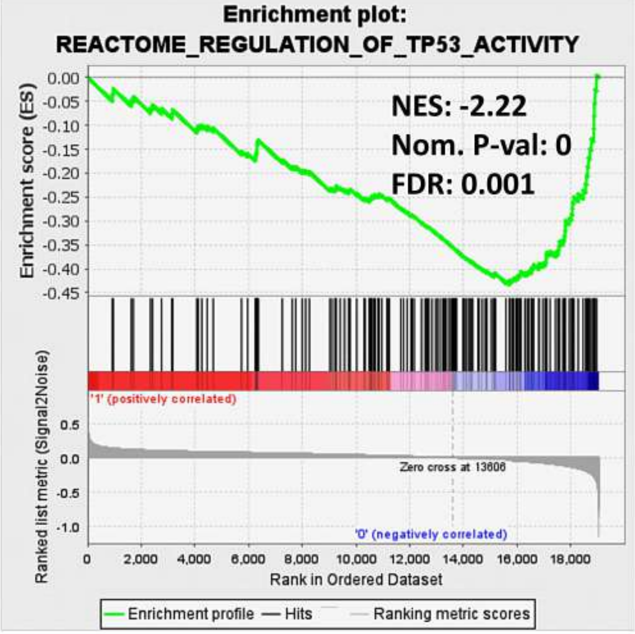

Enrichment plot: REACTOME_DNA_METHYLATION
NES: 2.06
Nom. P-val: 0
FDR: 0.006
Enrichment score (ES)
0.5
0.4
0.3
0.2
0.1
0.0
'1' (positively correlated)
Ranked list metric (Signal2Noise)
0.5
0.0
-0.5
-1.0
Zero cross at 13606
'0' (negatively correlated)
0
2,000
4,000
6,000
8,000
10,000
12,000
14,000
16,000
18,000
Rank in Ordered Dataset
Enrichment profile
Hits
Ranking metric scores

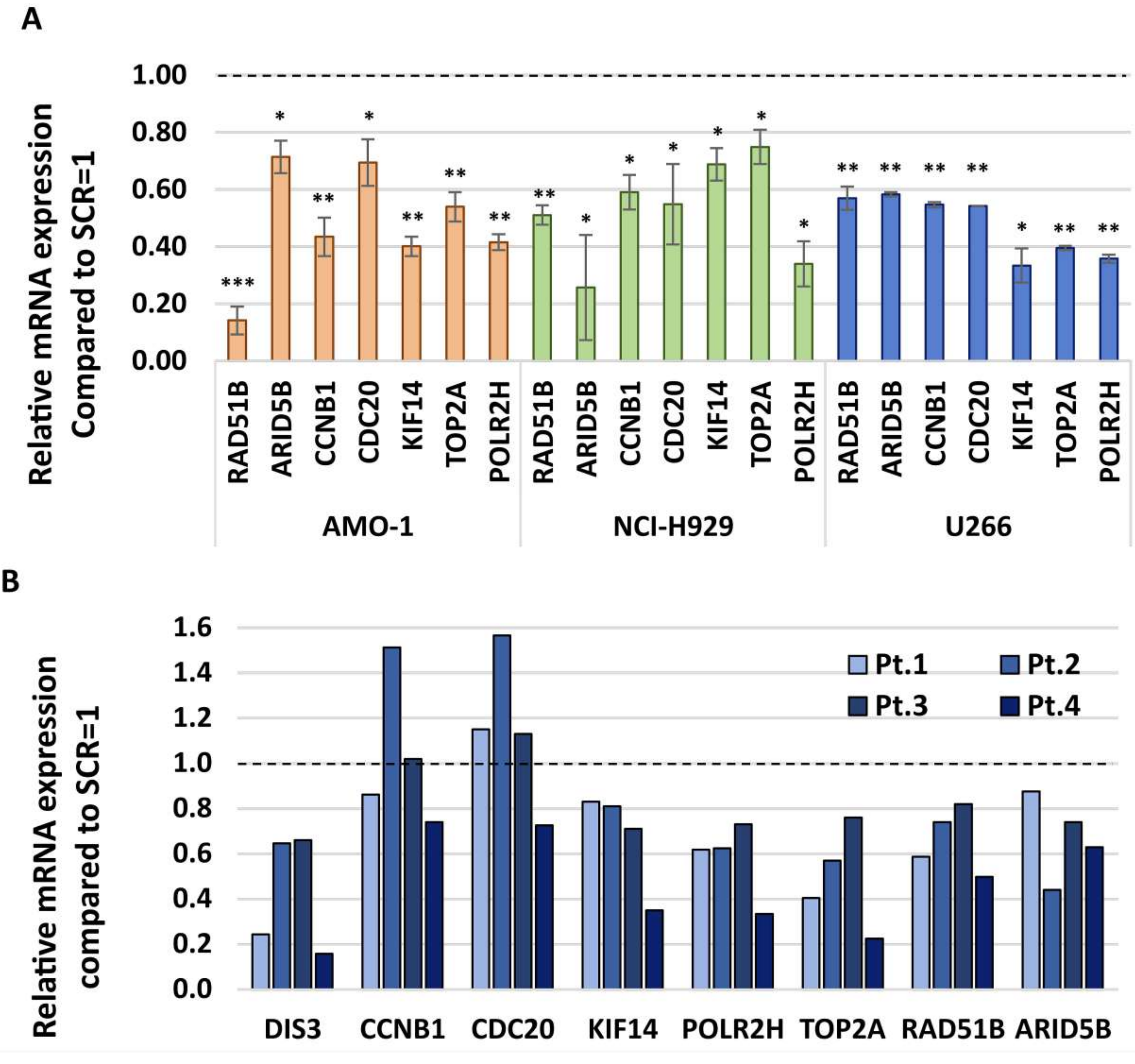

Enrichment plot: REACTOME_HOMOLOGOUS_DNA_PAIRING_AND_STRAND_EXCHANGE
NES: -2.39
Nom. P-val: 0
FDR: 0
Enrichment score (ES)
0.0
-0.1
-0.2
-0.3
-0.4
-0.5
-0.6
'1' (positively correlated)
Ranked list metric (Signal2Noise)
0.5
0.0
-0.5
-1.0
Zero cross at 13606
'0' (negatively correlated)
0
2,000
4,000
6,000
8,000
10,000
12,000
14,000
16,000
18,000
Rank in Ordered Dataset
Enrichment profile
Hits
Ranking metric scores

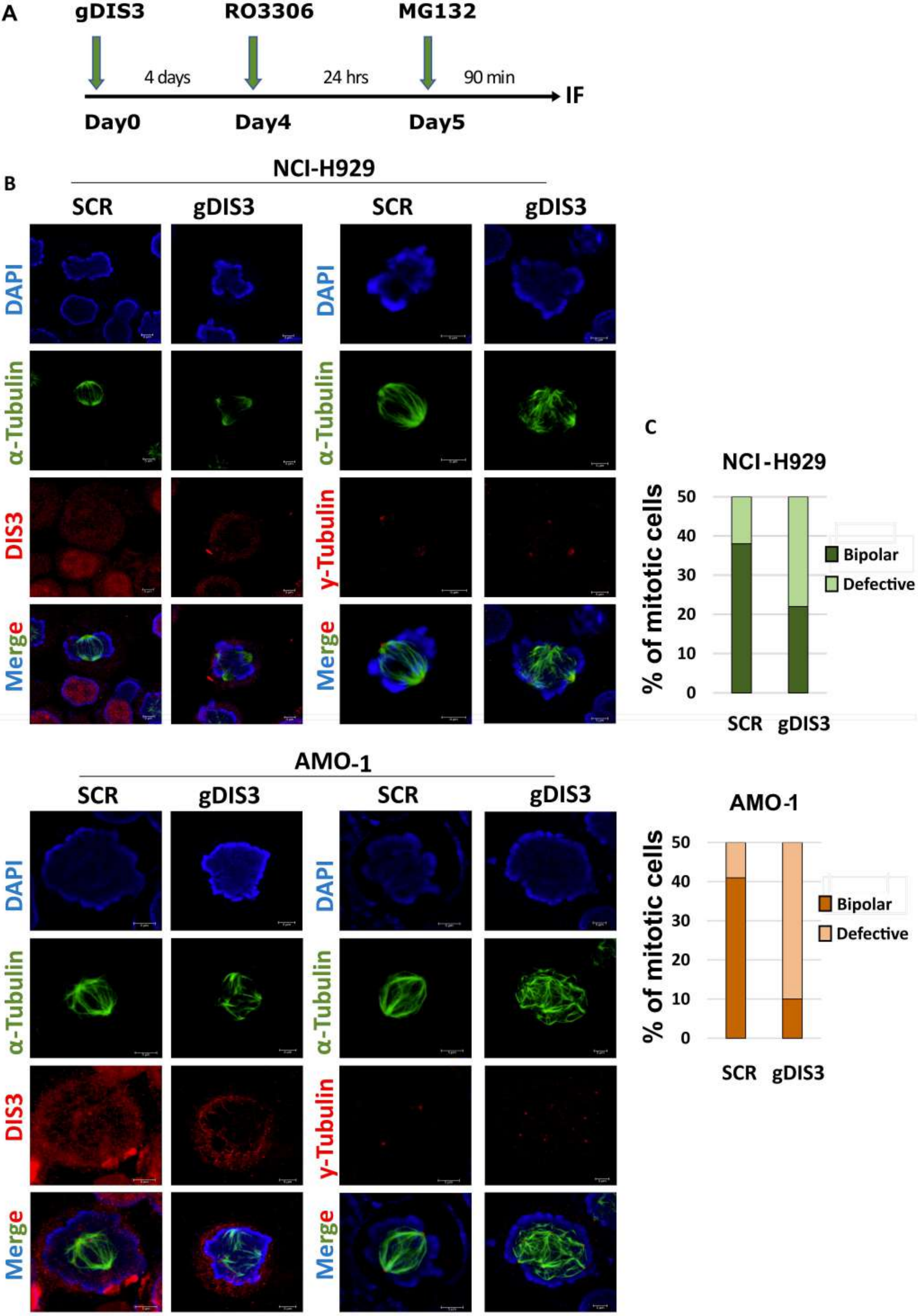

Enrichment plot: REACTOME_RESOLUTION_OF_SISTER_CHROMATID_COHESION
NES: -3.01
Nom. P-val: 0
FDR: 0
Enrichment score (ES)
0.0
-0.1
-0.2
-0.3
-0.4
-0.5
-0.6
'1' (positively correlated)
Ranked list metric (Signal2Noise)
0.5
0.0
-0.5
-1.0
Zero cross at 13606
'0' (negatively correlated)
0
2,000
4,000
6,000
8,000
10,000
12,000
14,000
16,000
18,000
Rank in Ordered Dataset
Enrichment profile
Hits
Ranking metric scores


Enrichment plot: HALLMARK_G2M_CHECKPOINT
NES: -3.45
Nom. P-val: 0
FDR: 0
Enrichment score (ES)
0.0
-0.1
-0.2
-0.3
-0.4
-0.5
-0.6
'1' (positively correlated)
Ranked list metric (Signal2Noise)
0.5
0.0
-0.5
-1.0
Zero cross at 13606
'0' (negatively correlated)
0
2,000
4,000
6,000
8,000
10,000
12,000
14,000
16,000
18,000
Rank in Ordered Dataset
Enrichment profile
Hits
Ranking metric scores


Enrichment plot: KEGG_RNA_DEGRADATION
NES: -2.36
Nom. P-val: 0
FDR: 0
Enrichment score (ES)
0.0
-0.1
-0.2
-0.3
-0.4
-0.5
'1' (positively correlated)
Ranked list metric (Signal2Noise)
0.5
0.0
-0.5
-1.0
Zero cross at 13606
'0' (negatively correlated)
0
2,000
4,000
6,000
8,000
10,000
12,000
14,000
16,000
18,000
Rank in Ordered Dataset
Enrichment profile
Hits
Ranking metric scores


Enrichment plot: REACTOME_REGULATION_OF_TP53_ACTIVITY
NES: -2.22
Nom. P-val: 0
FDR: 0.001
Enrichment score (ES)
0.00
-0.05
-0.10
-0.15
-0.20
-0.25
-0.30
-0.35
-0.40
-0.45
'1' (positively correlated)
Ranked list metric (Signal2Noise)
0.5
0.0
-0.5
-1.0
Zero cross at 13606
'0' (negatively correlated)
0
2,000
4,000
6,000
8,000
10,000
12,000
14,000
16,000
18,000
Rank in Ordered Dataset
Enrichment profile
Hits
Ranking metric scores


A
Relative mRNA expression Compared to SCR=1
1.00
0.80
0.60
0.40
0.20
0.00
***
*
**
*
**
**
**
**
*
*
*
*
*
*
**
**
**
**
*
**
**
RAD51B
ARID5B
CCNB1
CDC20
KIF14
TOP2A
POLR2H
RAD51B
ARID5B
CCNB1
CDC20
KIF14
TOP2A
POLR2H
RAD51B
ARID5B
CCNB1
CDC20
KIF14
TOP2A
POLR2H
AMO-1
NCI-H929
U266
B
Relative mRNA expression compared to SCR=1
1.6
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
Pt.1
Pt.2
Pt.3
Pt.4
DIS3
CCNB1
CDC20
KIF14
POLR2H
TOP2A
RAD51B
ARID5B


A
gDIS3
RO3306
MG132
4 days
24 hrs
90 min
IF
Day0
Day4
Day5
B
NCI-H929
SCR
gDIS3
SCR
gDIS3
DAPI
α-Tubulin
DIS3
γ-Tubulin
Merge
C
NCI-H929
% of mitotic cells
50
40
30
20
10
0
Bipolar
Defective
SCR
gDIS3
AMO-1
SCR
gDIS3
SCR
gDIS3
DAPI
α-Tubulin
DIS3
γ-Tubulin
Merge
AMO-1
% of mitotic cells
50
40
30
20
10
0
Bipolar
Defective
SCR
gDIS3

SUPPLEMENTARY DATA

Supplementary methods

Multi-Omics Data in CoMMpass Study

Multi-omics data about bone marrow MM samples at baseline (BM_1) were freely available from MMRF CoMMpass Study (https://research.themmrf.org/) and obtained from the Interim Analysis 15a (MMRF_CoMMpass_IA15a).

Transcript per Million (TPM) reads values of the *DIS3* transcript were retrieved using Salmon gene expression quantification data (MMRF_CoMMpass_IA15a_E74GTF_Salmon_V7.2_Filtered_Gene_TPM) in 774 BM_1 MM patients. Clinical data regarding Overall Survival (OS) and Progression free Survival (PFS) were considered in 767 MM patients for which both RNA-seq expression and survival data were available. Non-synonymous (NS) somatic mutation variants and counts data were obtained from whole exome sequencing (WES) analyses, main IgH translocations were inferred from RNA-seq spike expression estimates of known target genes and Copy Number Alteration (CNA) data were retrieved by means of Next generation Sequencing (NGS)-based fluorescence in situ hybridization (FISH) [1] in 660 MM cases for which all data were available [2]. The presence of a specific CNA was considered when occurring in at least one of the investigated cytoband at a 20% cut-off for each considered chromosomal aberration, as previously reported [2].

Survival analysis

Survival analyses were performed using survival [3-4] and survminer [5] packages in R Bioconductor (version 4.0.0). Kaplan-Meier analysis was applied on OS and PFS data in *DIS3* high/low expression groups according to median *DIS3* expression level, using survminer package. Log-Rank test p-value was calculated to measure the global difference between survival curves.

siRNA and *in vitro* HMCLs transfection

DIS3 silencing was obtained by using ON-TARGETplus siRNAs targeting *DIS3* and a non-silencing negative control siRNA (siSCR) (Dharmacon). NCI-H929 and AMO-1 cells were seeded at 0.1×10^6 cells/0.5mL), and transfected by Neon Transfection System (Invitrogen, CA, US), with the following electroporation conditions: 1100 V, 30 ms, 2 pulse. siRNA was used at 200 nM concentration. The transfection efficiency was evaluated by comparative qRT-PCR. Cells were incubated at 37° C and collected at 24-48 hrs after transfection to assess the downregulation of *DIS3* by qRT-PCR and then by Western blot analysis.

Design of GapmeRs and *in vitro* transfection of HMCLs

LNA gampeR oligonucleotides were provided by Exiqon (QIAGEN). LNA gapmeRs were in house-designed and purified by HPLC followed by Na^+-salt exchange and lyophilization.

NAME	DESIGN ID	SEQUENCE 5'-3'	Mw. calc. (Da)
g*DIS3*#2	339511-1	ACTTAATGGTAATAGA	5351.29
g*DIS3*#13	339511-2	GAGTCGAGACACCATG	5268.21
g*DIS3*#15	339511-3	TTCTATGCGACAAGGG	5302.21

HMCLs were transfected through the use of Neon Transfection System, with the following electroporation conditions: 1100 V, 30 ms, 2 pulse. LNA gapmeRs were used at 100 nM. The transfection efficiency was evaluated by comparative qRT-PCR.

Gymnosis

Cells were seeded at low plating density (5 x 10^4/mL) to reach confluence on the final day of the experiments (day 6). Cells were treated with the naked gDIS3g#13 and the scrambled g#SCR, at the same time of the seeding at a final concentration of 5 µM.

Cell viability and growth assessment

Cell viability was evaluated by counting the number of viable cells after trypan blue staining.

Colony-formation assay

For colony-forming assay, SCR and g*DIS3* silenced cells were suspended in RPMI-1640 medium with 10% fetal bovine serum (FBS) and plated on methylcellulose-based media (MethoCult TM STEMCELL Technologies) containing 1% methylcellulose in RPMI-1640 medium, 10% FBS. Colonies were scored by an inverted microscope after a 21-day incubation at 37 °C in a fully humidified atmosphere at 5% CO^2. Each condition was evaluated twice in triplicates.

Cell cycle analysis and apoptosis

Cell cycle distribution of *DIS3* silenced and relative SCR HMCLs was assessed using BD FACSVerse™ flow cytometer (BD Bioscience, Italy). Samples for cell cycle analysis were fixed in 70% ethanol at 4 °C for at least 2 hrs and incubated with FxCycle™ PI/RNase Staining Solution (Life Technologies) for 30 min in the dark, according to the manufacturer's instructions. Fluorescent emissions were collected through a 575 nm band-pass filter. Flow cytometry analysis was performed by using FlowJo™ Software (BD Bioscience, Italy). To detect apoptosis, scramble and *DIS3*-silenced cells were stained using a PE Annexin V Apoptosis Detection Kit (BD Biosciences), followed by BD FACSVerse™ flow cytometry (BD Biosciences) to analyze apoptotic distribution.

RNA extraction, RT-PCR and qPCR

Total RNA was extracted using TRIzol® Reagent (Invitrogen, Life Technologies) according to manufacturer's instructions. The purity and concentration of total RNA was determined by the NanoDrop One spectrophotometer (Thermo Fisher Scientific). The ratios of absorption (260 nm/280 nm) of all samples were between 1.8 and 2.0. cDNA was synthesized from 500 ng of total RNA with random primers using the High-Capacity cDNA Reverse Transcriptase Kit (Invitrogen, Life Technologies) according to the manufacturer`s instructions. mRNA expression was performed by real-time quantitative PCR (q-RT-PCR) reaction using SYBR green PCR Master Mix (Applied Biosystems) after optimization of the primer conditions. 10 ng of reverse-transcribed RNAs were mixed with 300 nM of specific forward and reverse primers in a final volume of 10 µl. Q-RT-PCR was performed on an Applied Biosystems StepOnePlus Real-Time PCR system for 40 cycles. The relative expression level was calculated with the $2^{-\Delta\Delta Ct}$ method and expressed as a fold change: normalization of data was performed on house-keeping gene (GAPDH) expression. To determine RNA levels by q-RT-PCR, the following primers were used:

Primer Name	**Sequence (5'-3')**
GAPDH FW	5'-ACAGTCAGCCGCATCTTCTT-3'
GAPDH RW	5'-AATGAAGGGGTCATTGATGG-3'
***DIS3* FW**	5'-GCGATTCGAGTAGCAGCAAA-3'
***DIS3* RW**	5'-TGAGTTCGGGGTTAGCAGTT-3'
RAD51B FW	5'-CATGTTAGGAGCGCTGGAAC-3'
RAD51B RW	5'-TGGCCCTGGTCTTCTTTTCT-3'
ARID5B FW	5'-GGCAGAAATAGCGACCATGG -3'
ARID5B RW	5'-CCCAAGGCCTCAGTTTTCAC -3'
CCNB1 FW	5'-TTTCTGCTGGGTGTAGGTCC-3'
CCNB1 RW	5'-GCCATGTTGATCTTCGCCTT-3'
CDC20 FW	5'-CGTTCGAGAGTGACCTGCA-3'
CDC20 RW	5'-CCAGGTTTGCTAGGAGTGGT-3'
KIF14 RW	5'-TGCCATGGGATTGATTAGATCTC -3'
KIF14 RW	5'-TGGAGCACGATTAACCATCCT-3'
TOP2A FW	5'-ACATATTTTGCTCCGCCCAG-3'

TOP2A RW	5’-CTTTGTTTGTTGTCCGCAGC-3’
POLR2H FW	5’-CTCGACTGCATTGTGAGAGTG-3’
POLR2H RW	5’-AAGGCCTATCATCAGTGGGG-3’

Protein detection by Western blots

Cells were homogenized in lysis buffer M-PER® Mammalian Protein Extraction Reagent (Thermo Scientific, Italy) and Halt Protease and Phosphatase inhibitor cocktail, EDTA-free, 100X, (Thermo Scientific). Whole cell lysates (40 µg per cell line) from cell lines were separated using Bolt™ 4-12% Bis-Tris Plus Acrylamide Gels (Invitrogen), electro-transferred onto nitrocellulose membranes (Bio-Rad, Hercules, CA, USA), and immunoblotted with specific primary antibody (listed below). Membranes were washed three times in PBST solution and then incubated with a secondary antibody conjugated with horseradish peroxidase (HRP) in BSA 2% - PBST for 2 hrs at RT. Chemiluminescence was developed using Clarity ECL Western Blot Substrate Kit (BIO-RAD) and signal intensity was detected by the use of ChemiDoc MP System (Bio-Rad). The experiments were repeated at least three times.

Ab	**Company**	**Code**	**Dilution**	**Secondary Ab**
Anti-CCNE1	Cell Signaling Technology	#20808	1:1000 BSA 5%-PBS TW 0,1%	Rabbit: 1:2000 BSA 2%-PBS TW 0,1%
Anti-CCNA2	Cell Signaling Technology	#4656	1:1000 BSA 5%-PBS TW 0,1%	Mouse: 1:2000 BSA 2%-PBS TW 0,1%
Anti-pCCNB1 Ser133	Cell Signaling Technology	#4133	1:1000 BSA 5%-PBS TW 0,1%	Rabbit: 1:2000 BSA 2%-PBS TW 0,1%
Anti-CCNB1	Cell Signaling Technology	#4138	1:1000 BSA 5%-PBS TW 0,1%	Rabbit: 1:2000 BSA 2%-PBS TW 0,1%
Anti-pCDK1 Thr161	Cell Signaling Technology	#9114	1:1000 BSA 5%-PBS TW 0,1%	Rabbit: 1:2000 BSA 2%-PBS TW 0,1%
Anti-CDK1	Cell Signaling Technology	#77055	1:1000 BSA 5%-PBS TW 0,1%	Rabbit: 1:2000 BSA 2%-PBS TW 0,1%
Anti-pCDC20 Ser51	Cell Signaling Technology	#8038	1:1000 BSA 5%-PBS TW 0,1%	Rabbit: 1:2000 BSA 2%-PBS TW 0,1%
Anti-CDC20	Cell Signaling Technology	#4823	1:1000 BSA 5%-PBS TW 0,1%	Rabbit: 1:2000 BSA 2%-PBS TW 0,1%
Anti-CENP-A	Cell Signaling Technology	#2186	1:1000 BSA 5%-PBS TW 0,1%	Rabbit: 1:2000 BSA 2%-PBS TW 0,1%

Anti-GAPDH	Santa Cruz	Sc-7899	1:2000 BSA 5%-PBS TW 0,1%	Mouse: 1:2000 BSA 2%-PBS TW 0,1%
Anti-*DIS3*	Proteintech	14689-1-AP	1:1000 BSA 5%-PBS TW 0,1%	Rabbit: 1:2000 BSA 2%-PBS TW 0,1%

Immunofluorescence

0.050 x 10^{6} cells were harvested, centrifuged onto glass slides (Cytospin 4, Thermo Scientific), then fixed in 4% paraformaldehyde in PBS1X for 6 min at 22°C, followed by three 5-min washes in PBS. Cells were permeabilized (0.5% Triton X-100 in PBS, 15-min), washed in PBS (3X, 5 min each), blocked 1 h at 22° C with 5% BSA Triton X-100 0.1% in PBS, and then incubated 1 hr at 22°C with *DIS3* antibody (#14689-1-AP; Proteintech; 1:100) or γ-Tubulin (#5886; Cell Signaling Technology; 1:100) to detect centriole. Thereafter, slides were washed in PBS (3X, 5 min each) and incubated 1 h at 22°C in the dark, with Alexa Fluor 555 Anti-Rabbit IgG secondary Antibody (Cell Signaling Technology, 1:500).

Anti-α-Tubulin Alexa Fluor 488 (Abcam; #185031, 1:100) was used to detect microtubule. After three PBS washes, cells were mounted under coverslips with DAPI-containing Vectashield (Vector Laboratories). Images were acquired by Leica TCS SP8 confocal laser scanning microscope (DMi8); acquisitions were performed with 40X and 63X immersion oil objectives. Conversion of imaged z-stacks into average intensity projections was processed by Leica Microsystem software (Leica Application Suite X - LAS X).

Gene expression profiling

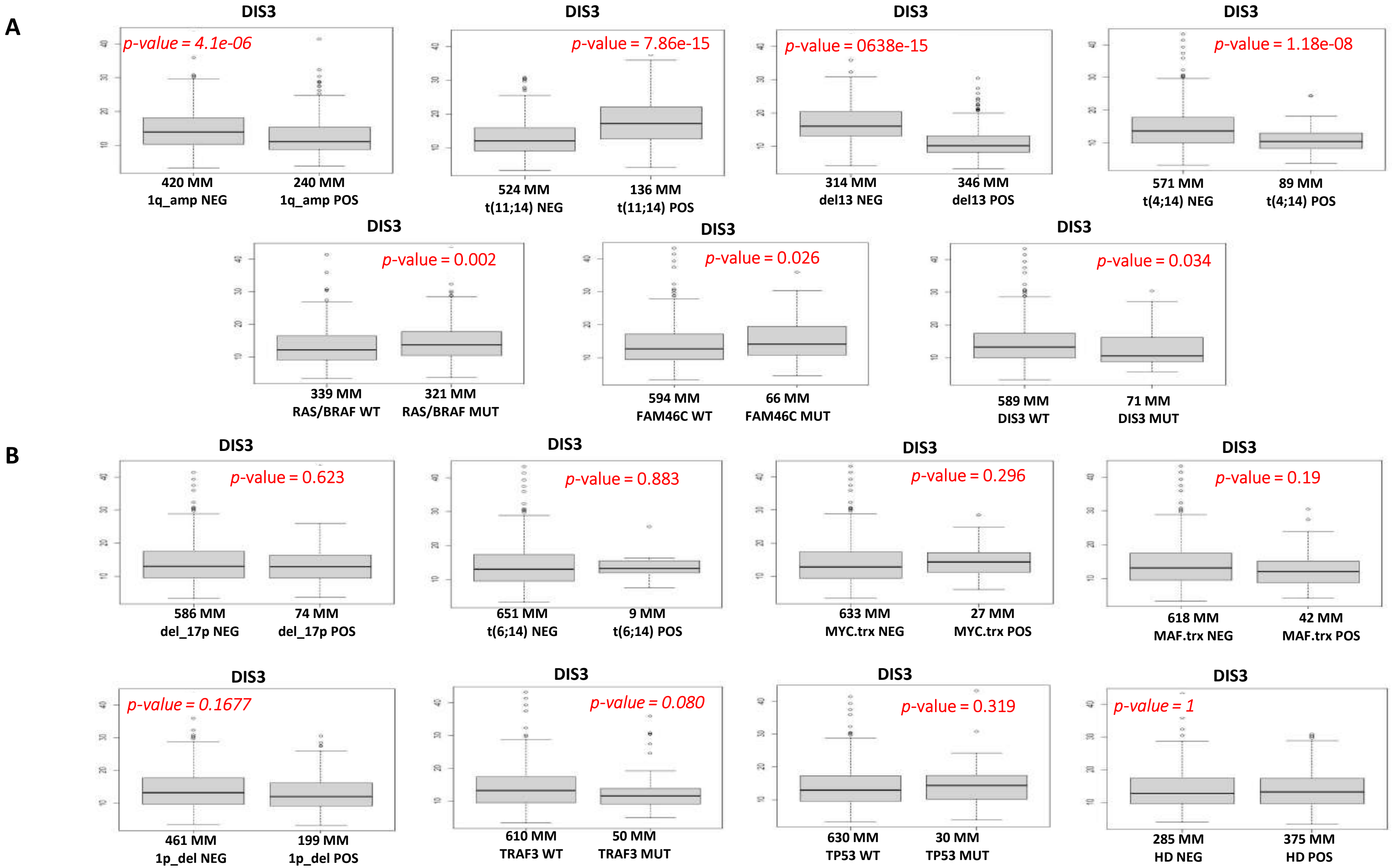
Total RNA samples were processed using WT PLUS Reagent Kit in accordance with the manufacturer's protocols (Thermo Fisher Scientific, Waltham, MA, USA). Global gene expression profiles were obtained using Clariom D array (Thermo Fisher Scientific, Waltham, MA, USA) in triplicates NCI-H929 *DIS3*-KD and controls. Robust Multichip Average (RMA) normalization was applied on raw data and a custom annotation pipeline was applied using the Chip Definition File (CDF) version 25 for GENECODE transcript annotations, freely available: at http://brainarray.mbni.med.umich.edu/Brainarray/Database/CustomCDF/25.0.0/gencodet.asp.

Therefore, the expression levels of Ensembl genes specific for 19241 protein coding were obtained.

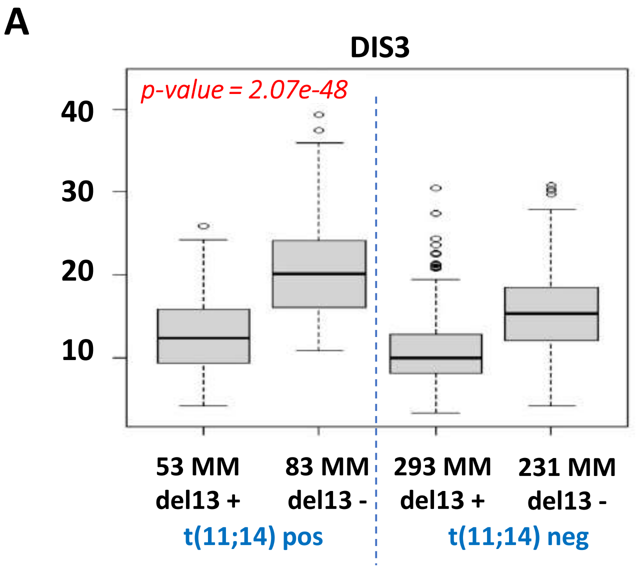
Genes differentially expressed in gymnotic *DIS3*-KD and SCR NCI-H929 triplicates were evaluated by means of Significance analysis of Microarrays (SAM) analysis [6] applying 500 permutations and default analysis conditions. Specific transcriptional patterns were defined using a 10% cut-off on FDR q-value.

Functional enrichment analysis was performed using clusterProfiler package (version 3.18.1) (Guangchuang Y et al., A Journal of Integrative Biology. 2012) in R 4.0.0 environment, on Gene Ontology (GO) Biological Process (BP) and Molecular Function (MF) terms. Barplot charts of the top 20 most significant annotation category terms were depicted using the global differentially expressed (DE) gene list ranked by Fold Change (FC) and setting p-value < 0.05 and q-value < 0.10 cut-off. Network interactions between the top five GO-BP or GO-MF annotation terms were visualized by using the cnetplot function. Gene Set Enrichment Analysis (GSEA) [7] was achieved on global annotated protein coding genes gene expression profiles. Significant Hallmark, KEGG and Reactome gene sets (version 7.4) were selected on the base of nominal p-value <0.05 and FDR q-value < 5%.

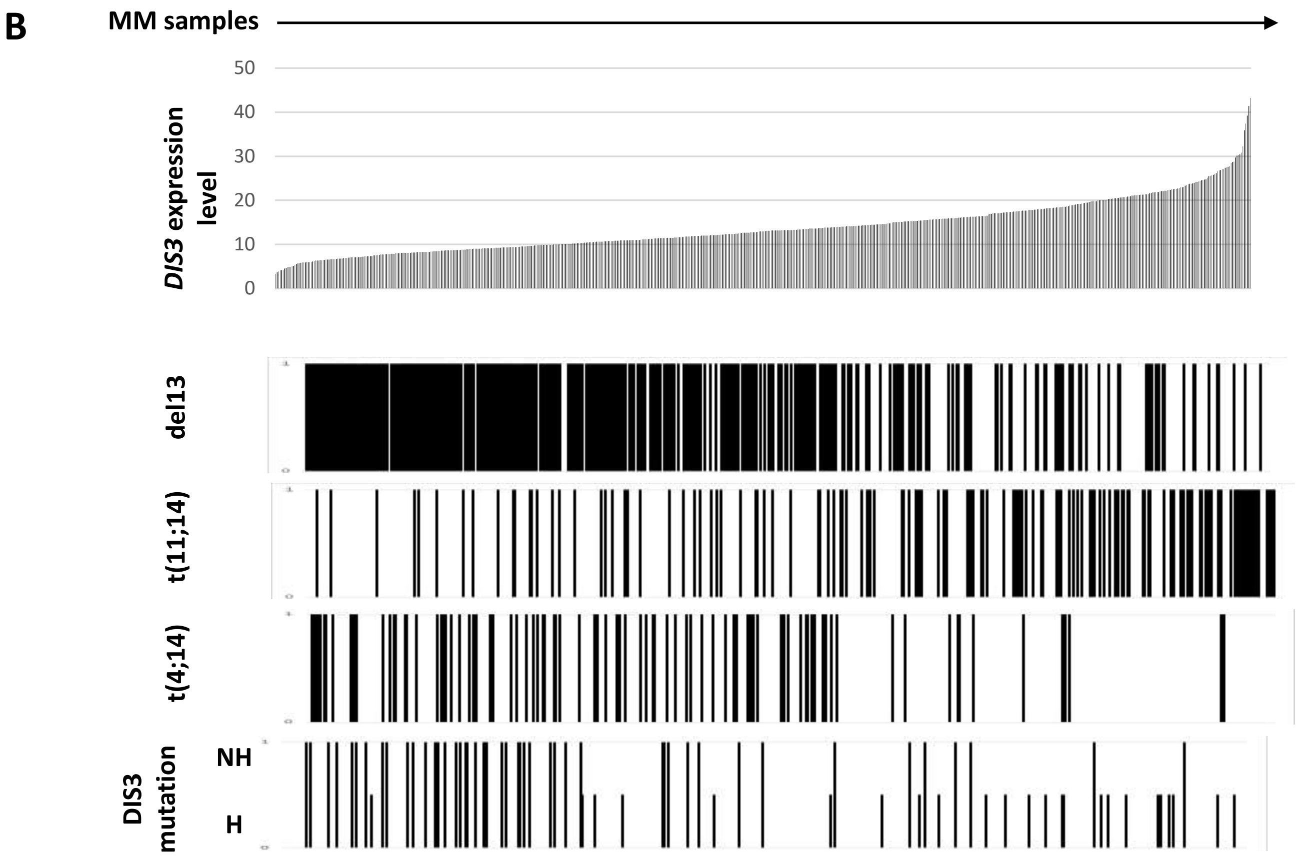
1. Miller, C. et al. A comparison of clinical FISH and sequencing based FISH estimates in multiple myeloma: An MMRF CoMMpass analysis. In: Hematology TASo, editor. The American Society of Hematology; 2016: Blood; 2016. p. 374.
2. Todoerti K, Ronchetti D, Favasuli V, Maura F, Morabito F, Bolli N, Taiana E, Neri A. *DIS3* mutations in multiple myeloma impact the transcriptional signature and clinical outcome. Haematologica. 2021.
3. Therneau T (2021). A Package for Survival Analysis in R_. R package version 3.2-11, <URL: https://CRAN.R-project.org/package=survival>.
4. Terry M. Therneau, Patricia M. Grambsch (2000). _Modeling Survival Data: Extending the Cox Model_. Springer, New York. ISBN 0-387-98784-3.
5. Alboukadel Kassambara, Marcin Kosinski and Przemyslaw Biecek (2021). survminer: Drawing Survival Curves using 'ggplot2'. R package version 0.4.9. https://CRAN.R-project.org/package=survminer
6. Tusher VG, Tibshirani R, Chu G. Significance analysis of microarrays applied to the ionizing radiation response. Proc Natl Acad Sci U.S.A. 2001; 98:5116-5121
7. Subramanian A, Tamayo P, Mootha VK, et al. Gene set enrichment analysis: a knowledge-based approach for interpreting genome-wide expression profiles. PNAS. 2005; 102(43):15545-50.



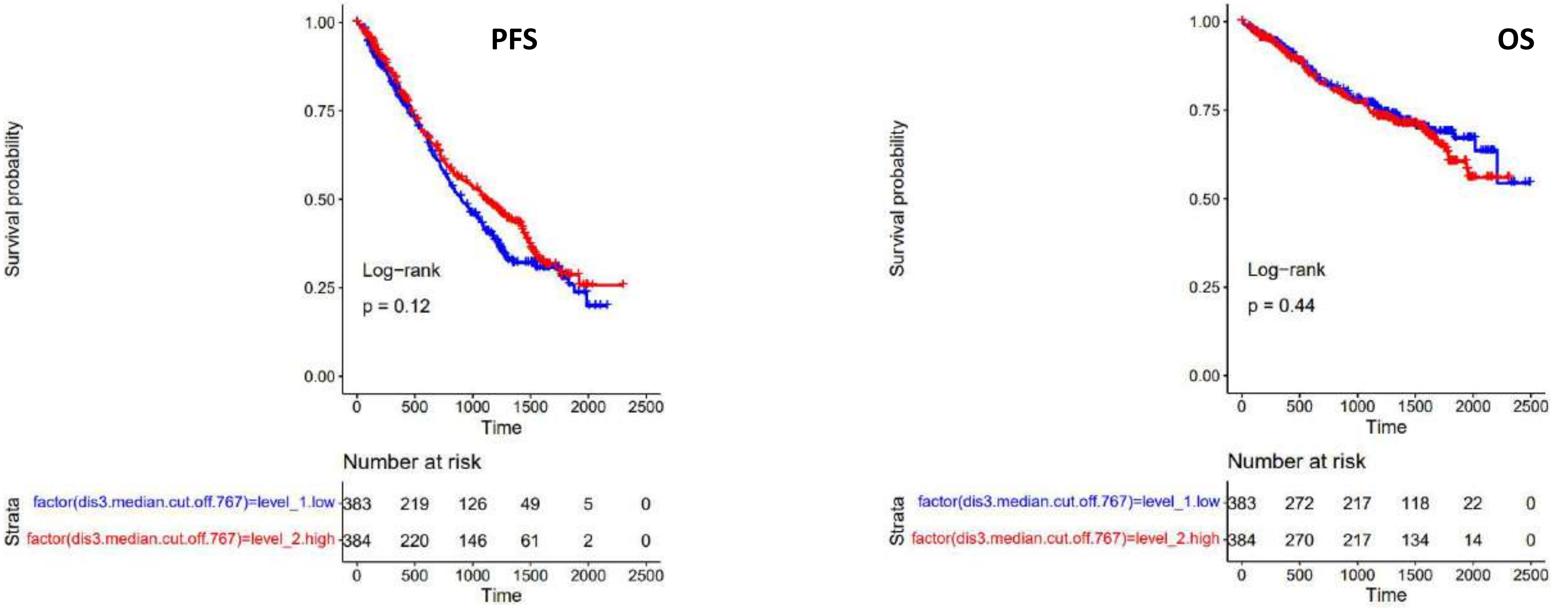
Supplementary Figure S1 (A) Significant differences in *DIS3* expression levels as shown by box plots of 660 MM cases stratified according to the presence of 1q-gain, t(11;14), del(13q), t(4;14), or the occurrence of NS somatic mutations in *RAS/BRAF*, *FAM46C*, or *DIS3* genes. **(B)** Not-significant differences in *DIS3* expression level as shown by box plots in 660 MM cases stratified according to the presence of del(17p)/TP53, t(6;14), MYC translocations, MAF translocations, del(1p), the occurrence of NS somatic mutations in *TRAF3* or *TP53* genes, or hyperdiploidy (HD). For each plot, differential expression was tested by Wilcoxon rank-sum test with continuity correction. P-values were corrected by BH adjustment.



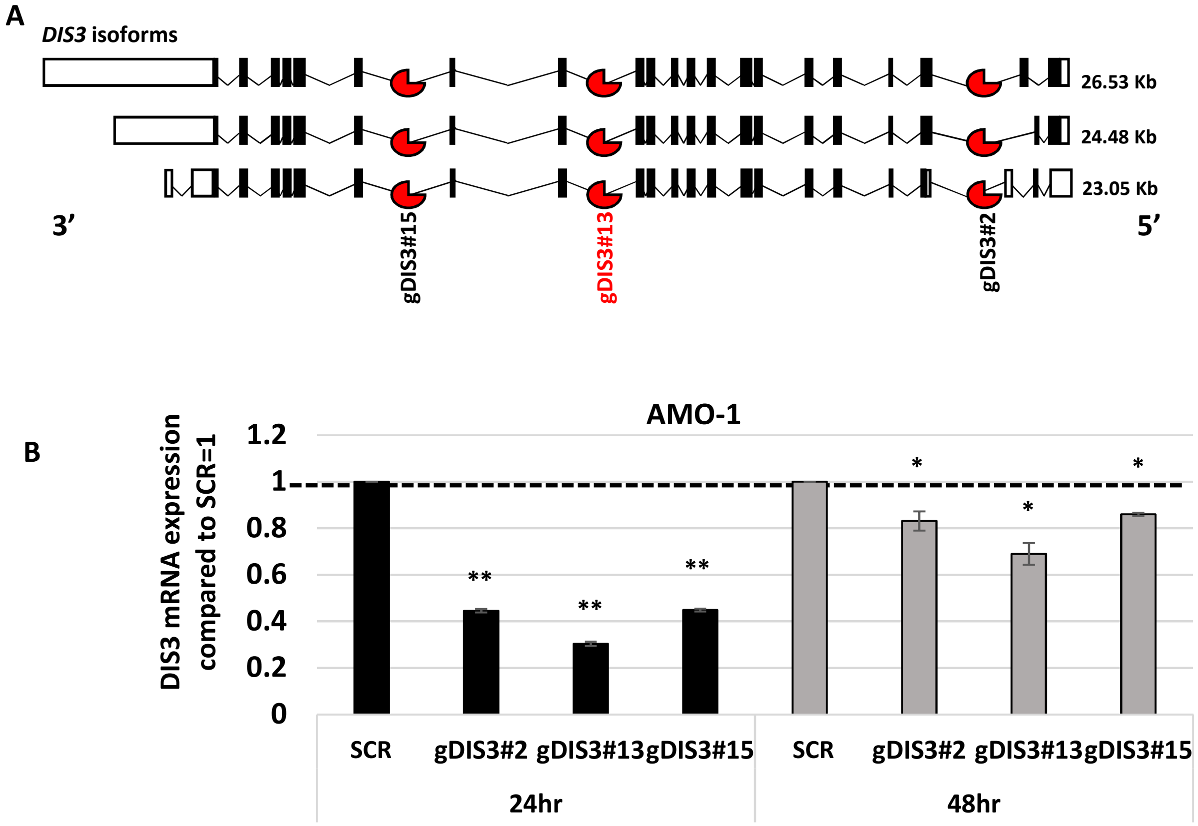
	t(11;14) + del13 pos	t(11;14) + del13 neg	t(11;14) - del13 pos
t(11;14) + del13 neg	**0.0000***		
t(11;14) - del13 pos	**0.0014***	**0.0000***	
t(11;14) - del13 neg	**0.0004***	**0.0000***	**0.0000***



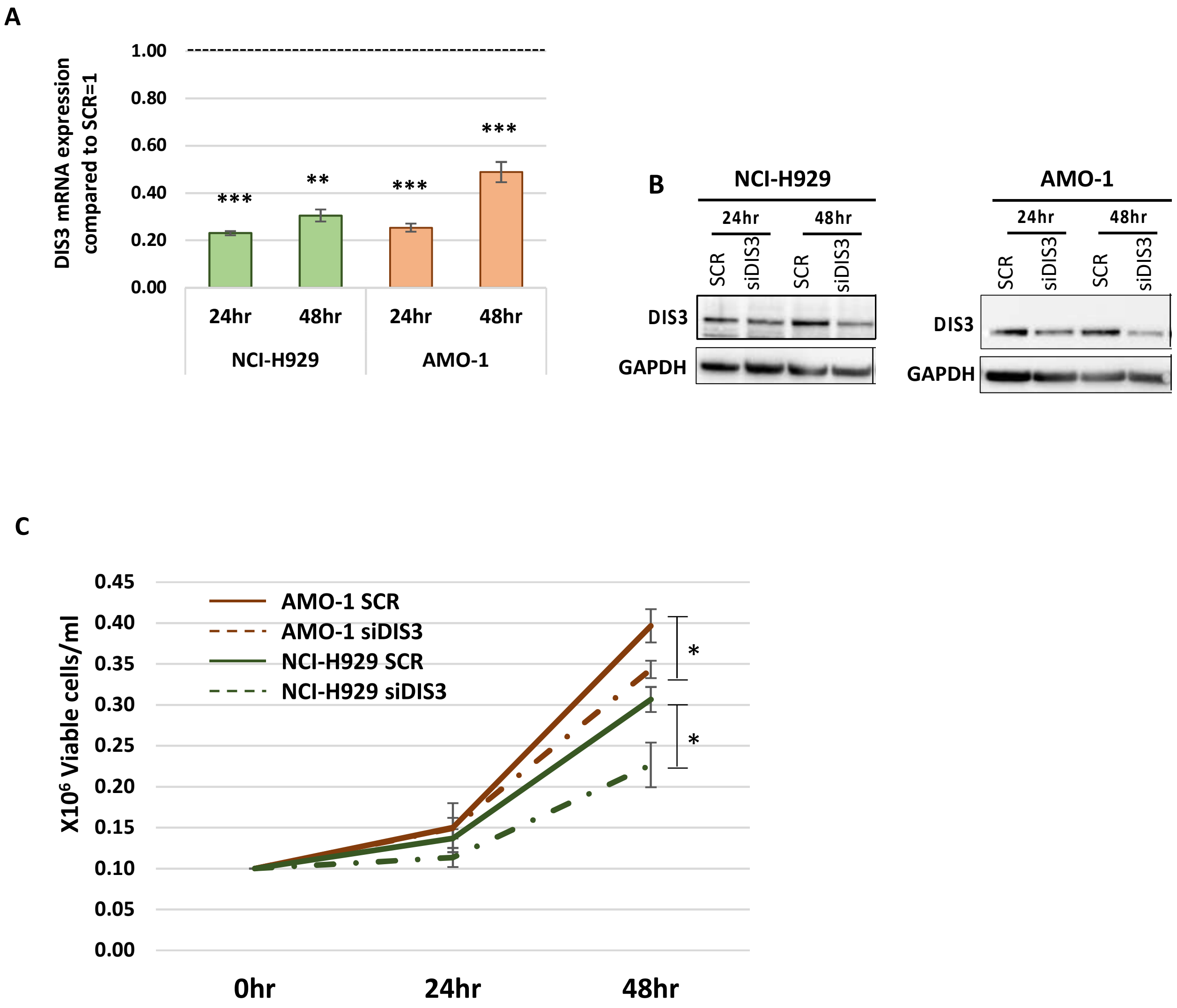
Supplementary Figure S2 (A) Significant differences in *DIS3* expression level as shown by box plots of 660 MM cases stratified according to the presence of t(11;14) and del13. Kruskal-Wallis test was applied to assess differences in expression levels between groups. The significant pairwise comparison performed by the Dunn's test are marked red-bold in the table. **(B)** Representation of the distribution of del13, t(11;14, t(4;14), and *DIS3* gene mutation in the cohort of 660 CoMMpass samples ordered based on increasing *DIS3* expression levels. For *DIS3* mutation, the high bar in the histogram indicates the presence of not-hotspot *DIS3* mutations (NH) in the patients, the shorter bar indicates hotspot (H) *DIS3* mutations.



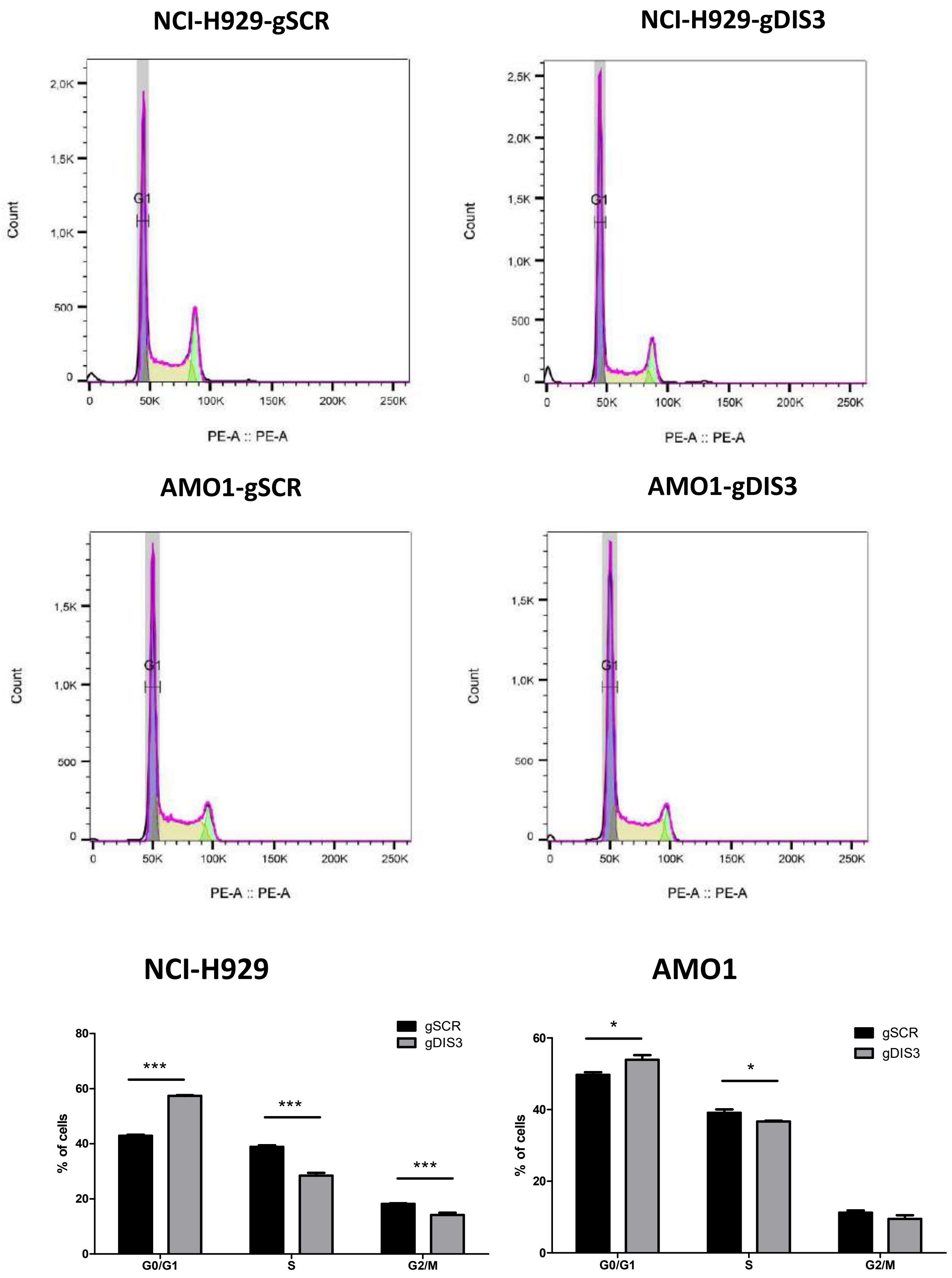
Supplementary Figure S3 Kaplan-Meier survival curves (PFS=Progression Free Survival; OS= Overall Survival) in the CoMMpass global dataset including 767 MM. MM cases were stratified in high and low *DIS3* expression groups, according to the median expression level across the dataset. Log-rank test p-value measuring the global difference between survival curves and number of samples at risk in each group across time are reported.



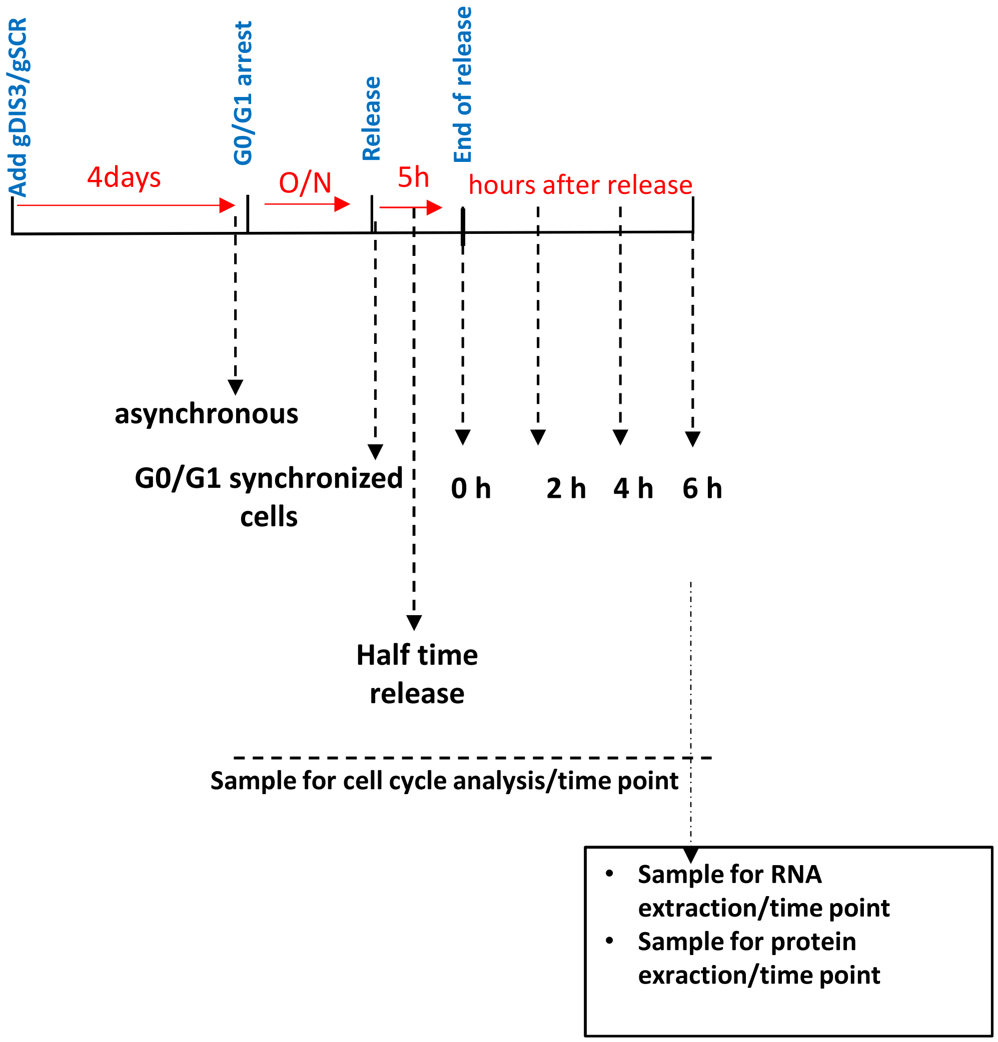
Supplementary Figure S4. (A) Schematic rapresentation of DIS3 protein coding isoforms together with all the tested gapmeRs; the gapmer selected for following experiments is marked in red. (**B**) *DIS3* expression in AMO-1 24 hr and 48 hr after each LNA-gampeR transfection using Neon Transfection System.



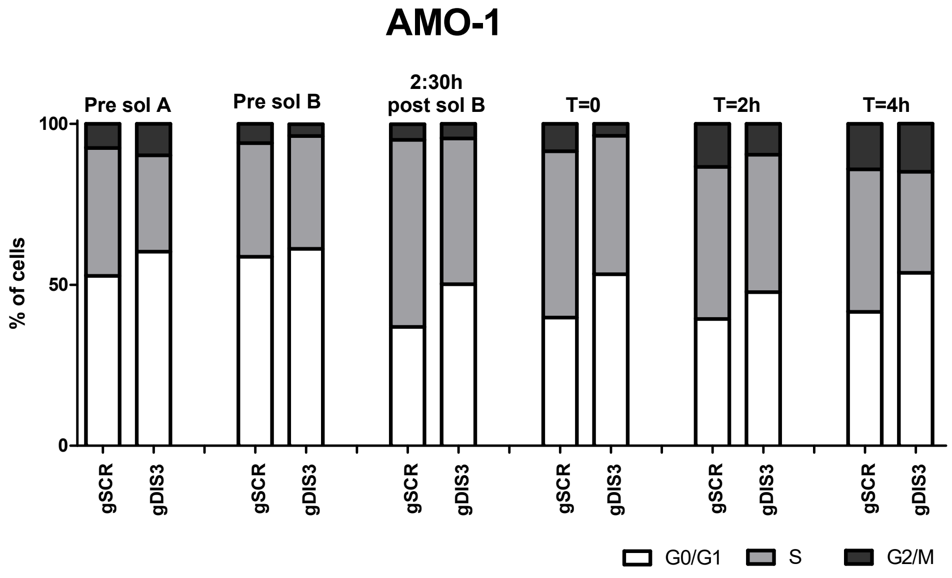
Supplementary Figure S5. (A) Quantitative real-time PCR (qRT-PCR) of *DIS3* in NCI-H929 and AMO-1 cells at the indicated time points using RNA interference strategy; *DIS3* expression was expressed as $2^{-\Delta\Delta Ct}$ relative to the scramble siRNA at the same time point. (**B)** WB of DIS3 in NCI-H929 and AMO-1 cells 24-48 hrs after siRNA delivery (200 nM). **C** Growth curves of AMO-1 and NCI-H929 cells after siRNA delivery. *p < 0.05, Student's t test.



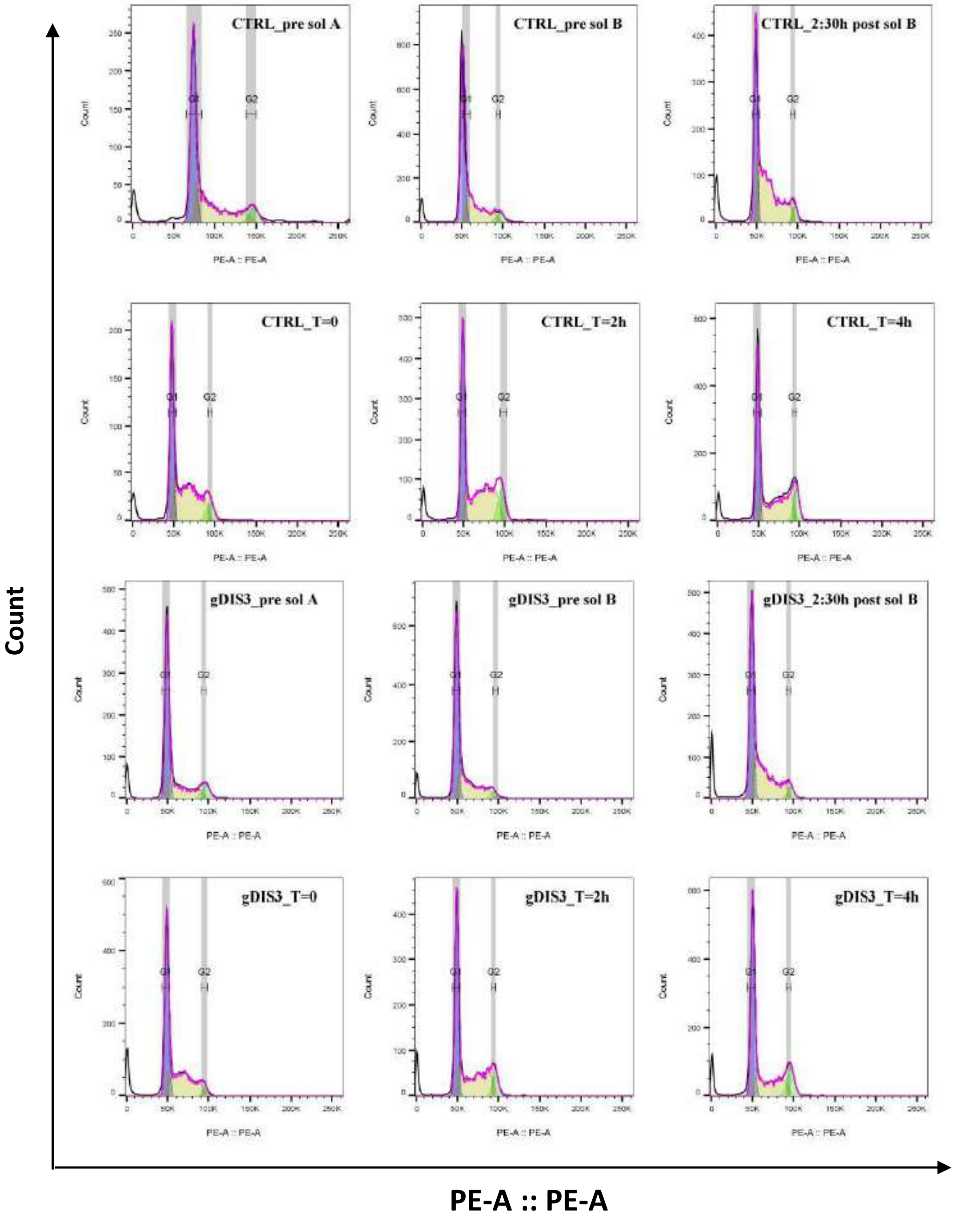
Supplementary Figure S6. Cell cycle analysis by flow cytometry of NCI-H929 and AMO-1 cells treated with gDIS3 or scramble (gSCR) gapmeR (5µM) for 4 days. Standard deviation of three replicates are reported, *p < 0.05, **p < 0.01, ***p < 0.001, Student's t test.

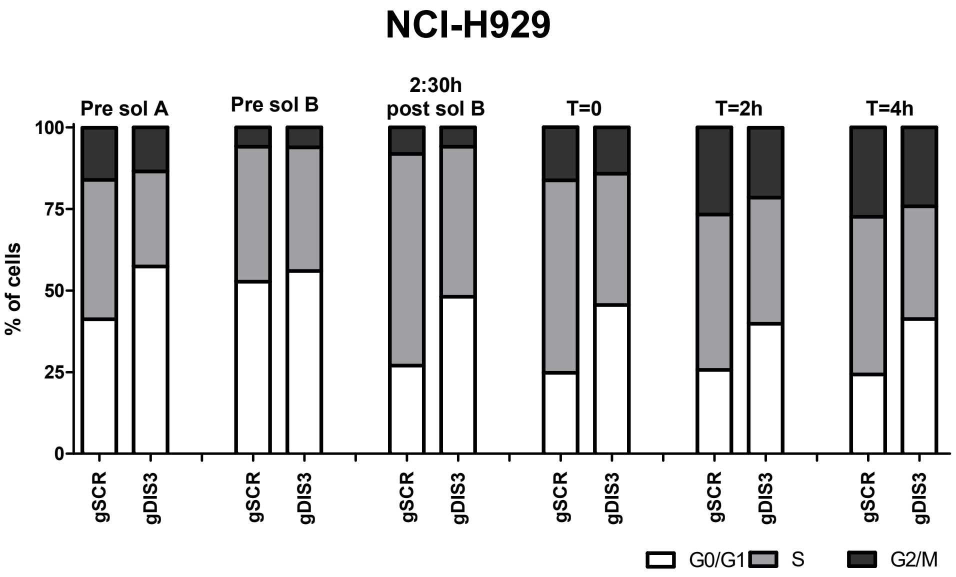


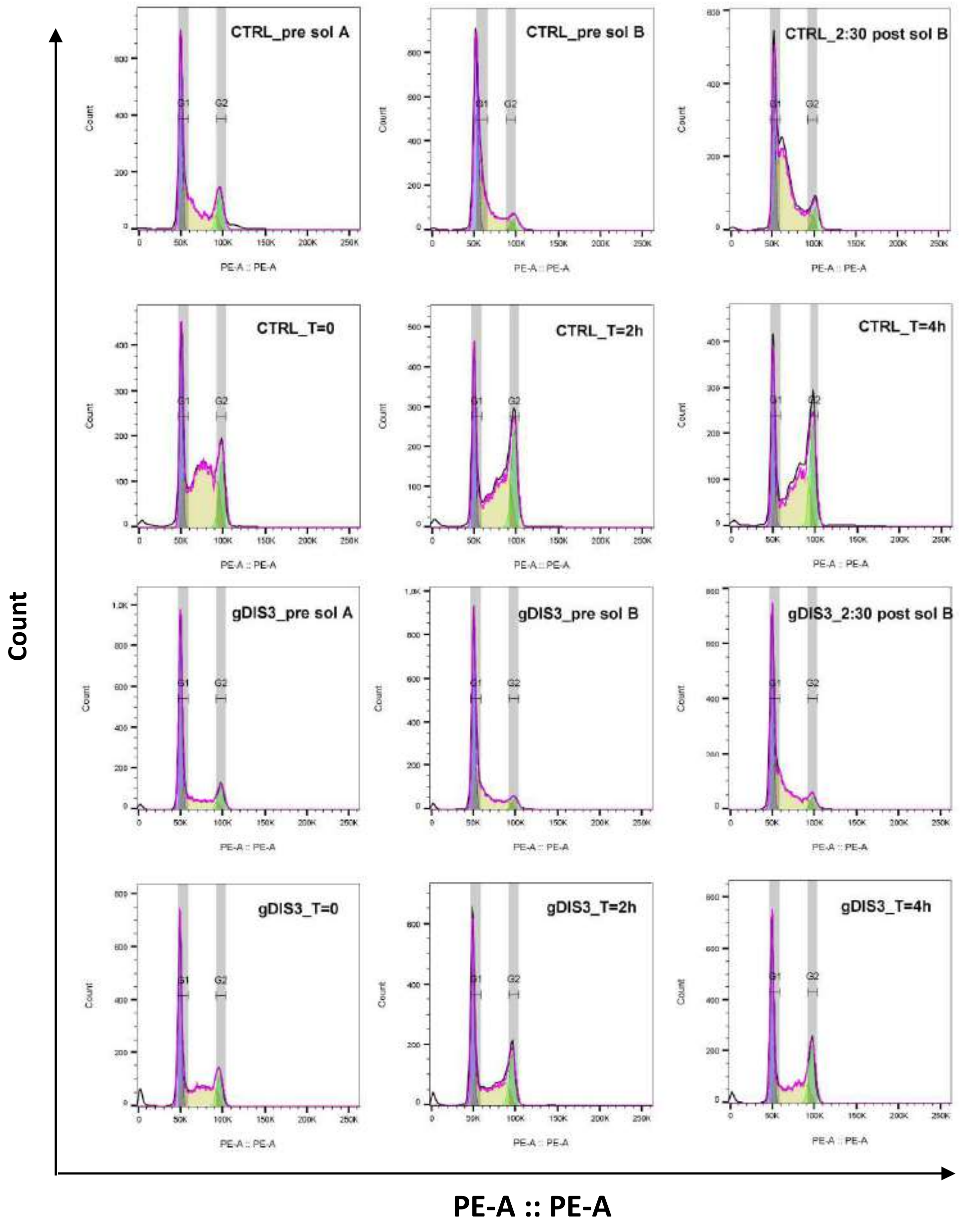
Supplementary Figure S7. Schematic representation of Synchroset protocol for cell synchronization. At time 0 cells were seeded and gDIS3 was added. At day 4, solution A was added and cells were incubated overnight. At day 5, solution B was added and cells were incubated for 5 hrs for release. Then, samples were collected for RNA, proteins and cell cycle analysis.



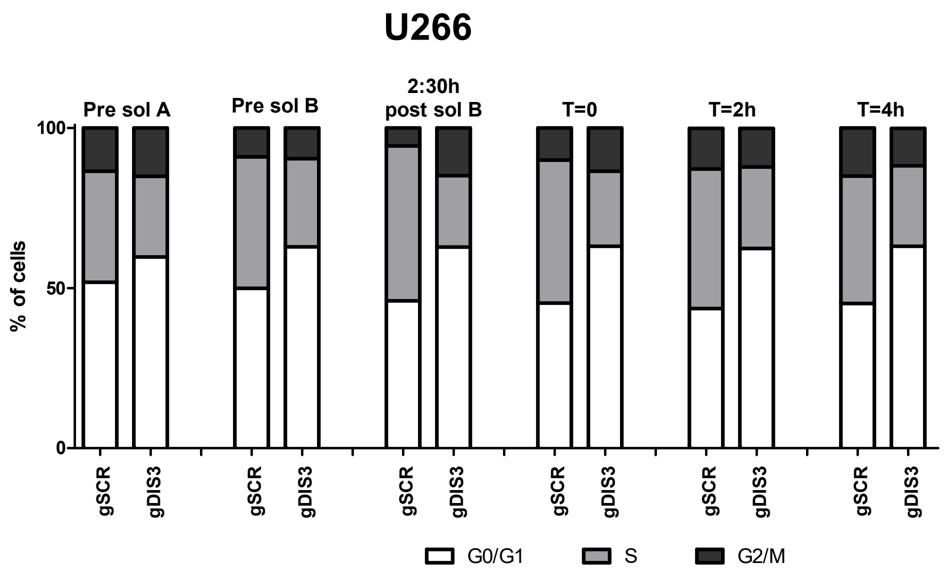
Supplementary Figure S8. AMO-1 cells were synchronized by synchroset protocol. Cell cycle progression was monitored by PI staining and FACS analysis of the DNA content of cells before synchronization (asynchronous cells), and at different time points after synchronization and after release.

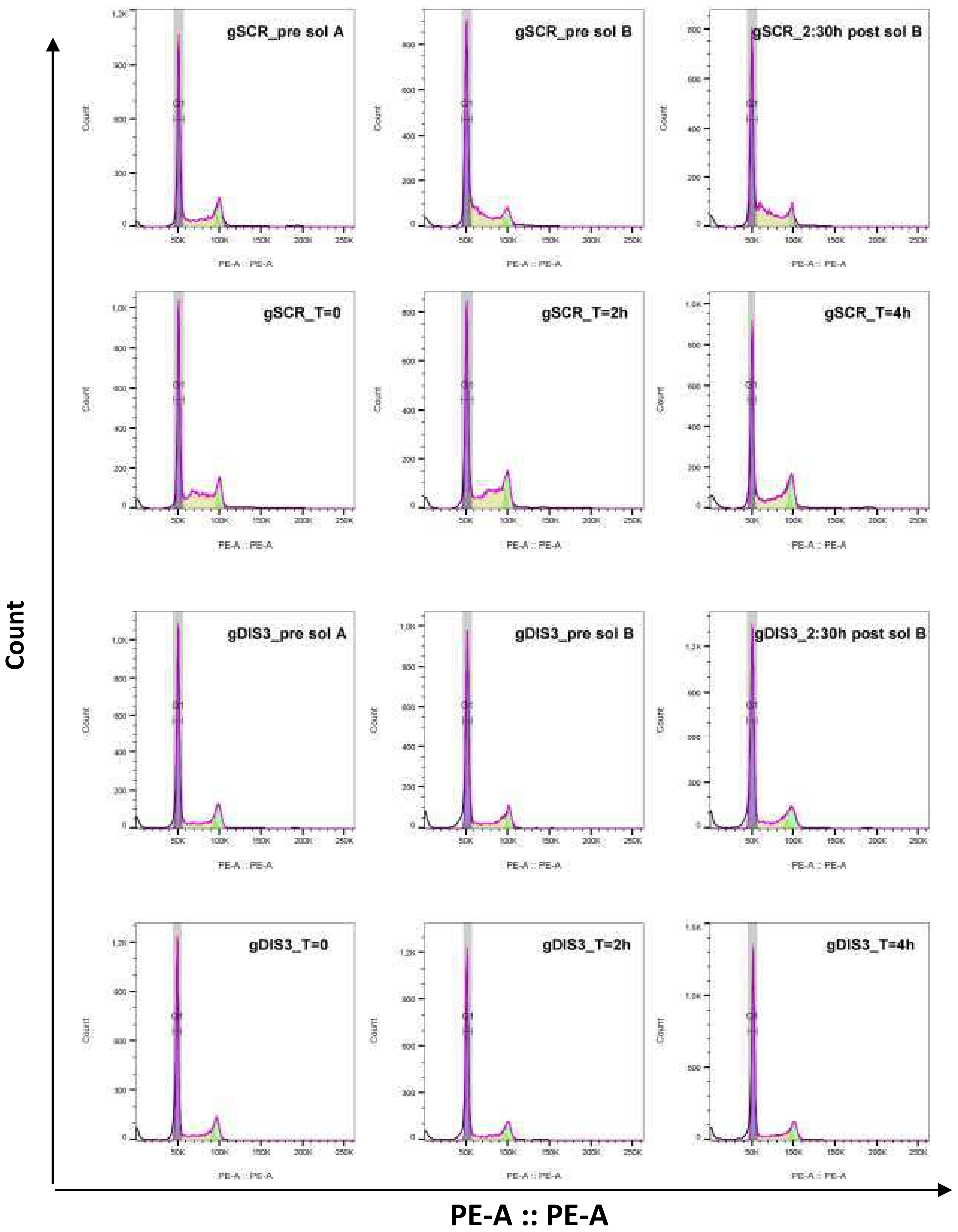




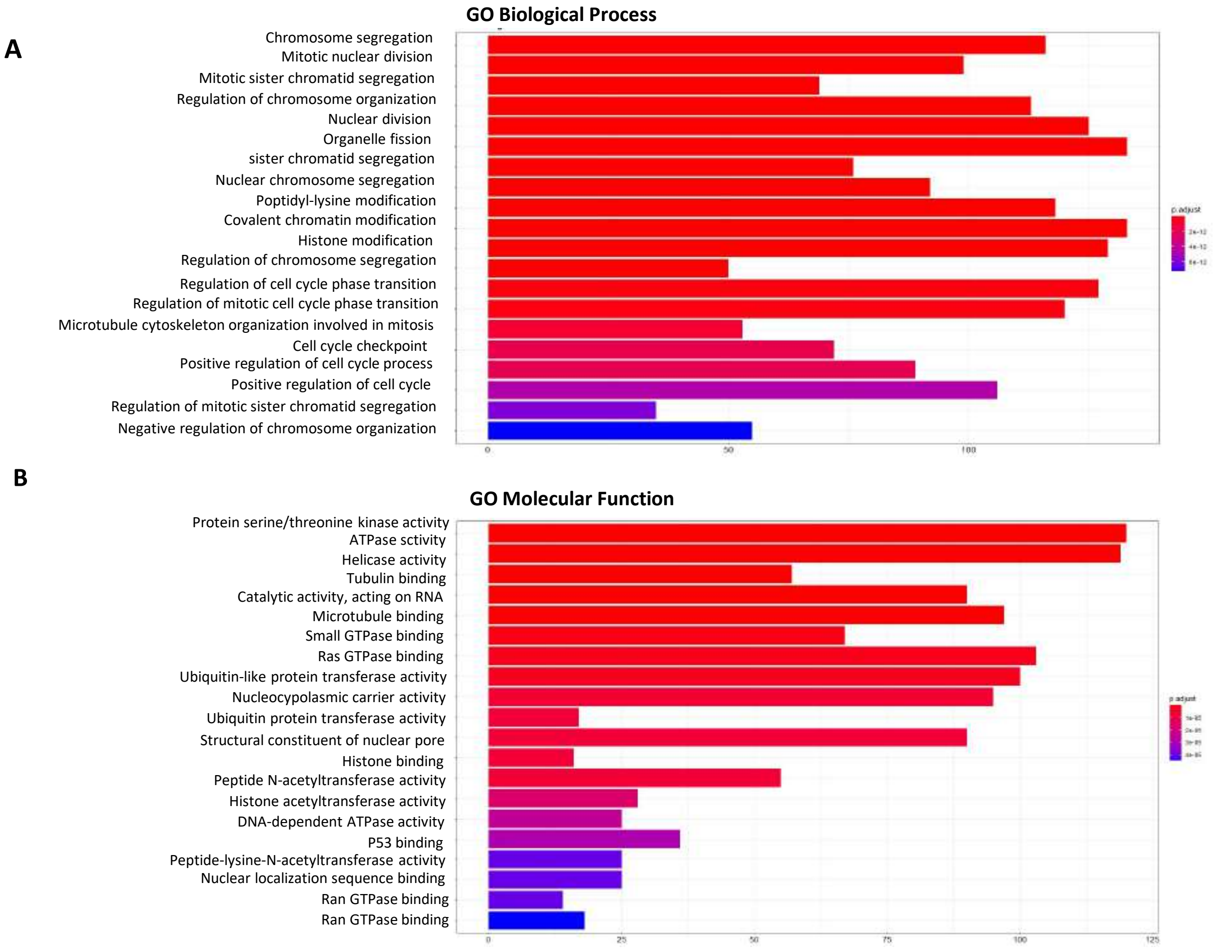


Supplementary Figure S9. NCI-H929 cells were synchronized by Synchroset protocol. Cell cycle progression was monitored by PI staining and FACS analysis of the DNA content of cells before synchronization (asynchronous cells), and at different time points after synchronization and after release.

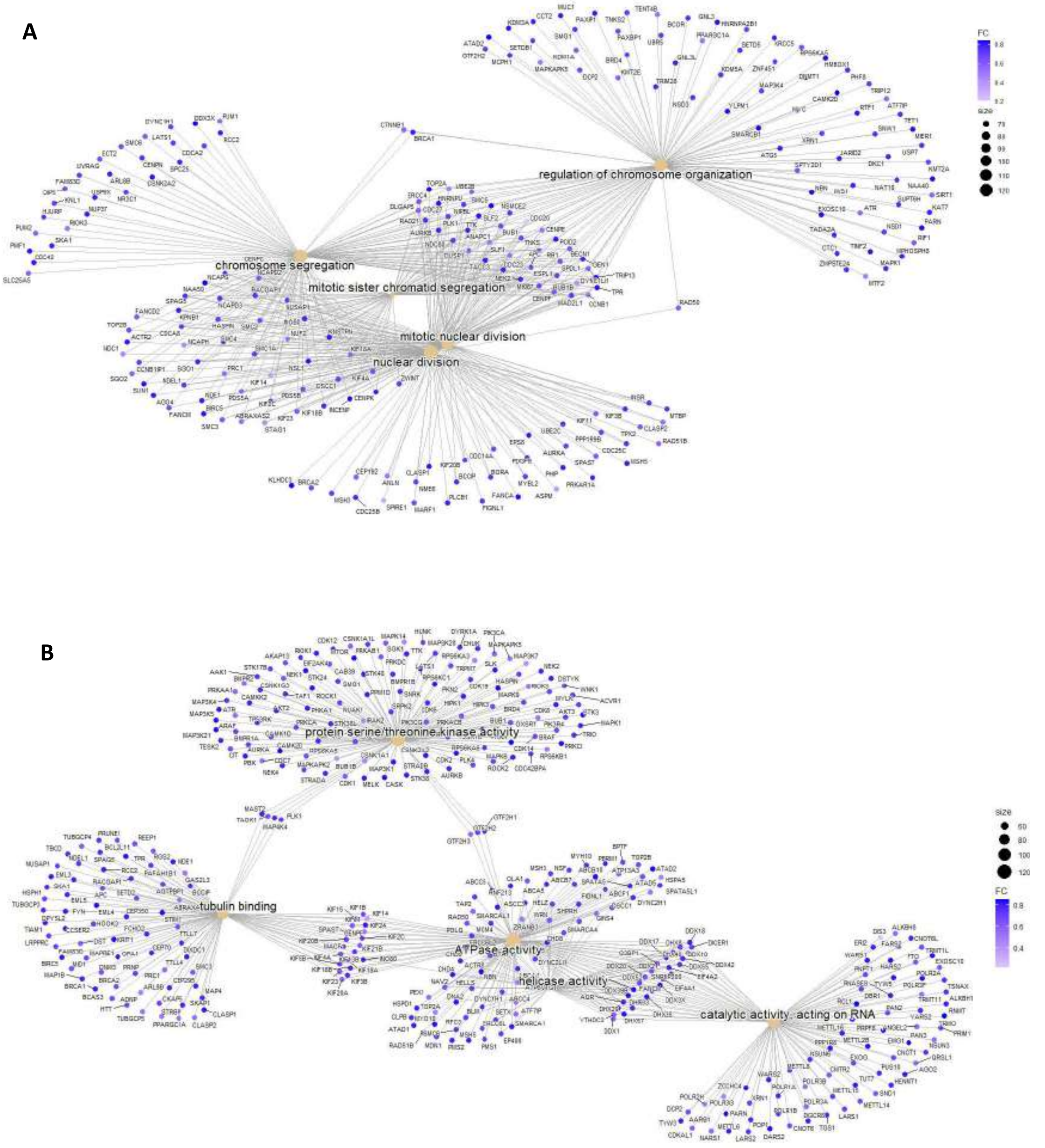




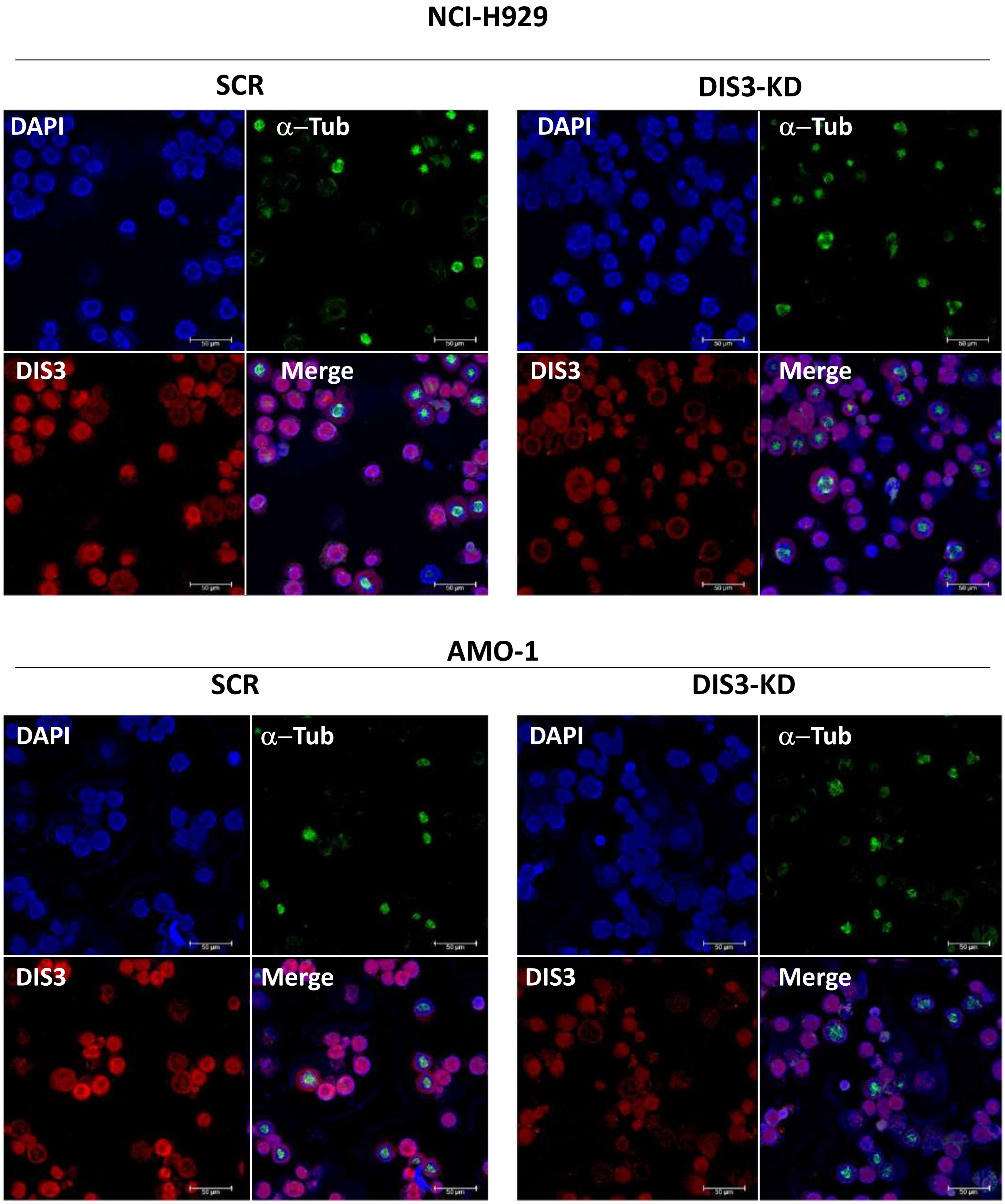
Supplementary Figure S10. U266 cells were synchronized by Synchroset protocol. Cell cycle progression was monitored by PI staining and FACS analysis of the DNA content of cells before synchronization (asynchronous cells), and at different time points after synchronization and after release.



Supplementary Figure S11. Top 20 most significantly enriched GO Biological Process **(A)** and GO Molecular function **(B)** terms for 2595 differentially expressed protein coding genes with annotated gene symbols.



Supplementary Figure S12. Network interactions between the top five GO-BP **(A)** or GO-MF **(B)** annotation terms were visualized by using the cnetplot function.



Supplementary Figure S13. Representative images of multipolar spindles in NCI-H929 and AMO-1 cells upon *DIS3* silencing. Scale bar 50 µm.

Supplementary Table S1. Number and relative frequency of main IgH translocations (trx), copy number alterations (CNAs) and non-synonymous (NS) somatic mutations, in 660 BM-1 MM cases of MMRF_CoMMpass_IA15a cohort with available data about DIS3 expression by RNA sequencing (RNA-seq), IgH trx by RNA-seq, NS somatic mutations by Whole Exome sequencing (WES) and CNAs by next generation sequencing (NGS)-based FISH (FISH-WES).

IgH trx (RNA-seq)	**N (%)**
t(11;14)/CCND1	136 (20.6%)
t(6;14)/CCND3	9 (1.4%)
t(4;14)/WHSC1/FGFR3	89 (13.5%)
t(14;16)/MAF;t(14;20)/MAFB; t(8;16)/MAFA	42 (6.4%)
t(8;14)/MYC	27 (4.1%)
CNA (FISH-WES)	**N (%)**
del(13)(q14)/(q34)/RB1_20%	346 (52.4%)
1q21 gain_20%	240 (36.4%)
del(1)(p22)/CDKN2C_20%	199 (30.2%)
del(17)(p13)/TP53_20%	74 (11.2%)
HD	375 (56.8%)
NS Somatic Mutation (WES)	**N (%)**
DIS3	71 (10.8%)
N-RAS	146 (22.1%)
H-RAS	0 (0%)
K-RAS	160 (24.2%)
BRAF	51 (7.7%)
TP53	30 (4.5%)
FAM46C	66 (10%)
TRAF3	50 (7.6%)

Supplementary Table S2. Percentage of cell viability in *ex-vivo* primary CD138+ tumor cells purified from the BM of four MM patients after treatment with gSCR or gDIS3.

	gSCR	**g*DIS3***
Patient N°1	87%	79%
Patient N°2	79%	67%
Patient N°3	81%	79%
Patient N°4	66%	59%

Supplementary Table S3. List of significant differentially expressed genes between NCI-H929 *DIS3*-KD and NCI-H929 control, by SAM analysis at q-value =0. 37 up- and 3995 down-regulated transcripts in *DIS3*-KD vs control are respectively ordered according to score(d). Fold change (FC), q-value and score(d) statistics parameters are reported for each transcript.

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000112078	**KCTD20**	protein_coding	-12.509	0.143	0
ENSG00000083520	**DIS3**	protein_coding	-9.625	0.21	0
ENSG00000117399	**CDC20**	protein_coding	-9.115	0.2	0
ENSG00000100216	**TOMM22**	protein_coding	-7.3	0.287	0
ENSG00000139921	**TMX1**	protein_coding	-7.272	0.316	0
ENSG00000134278	**SPIRE1**	protein_coding	-7.145	0.304	0
ENSG00000253352	**TUG1**	protein_coding	-7.124	0.348	0
ENSG00000231007	**CDC20P1**	processed_pseudogene	-6.783	0.239	0
ENSG00000177646	**ACAD9**	protein_coding	-6.6	0.281	0
ENSG00000165970	**SLC6A5**	protein_coding	-6.552	0.268	0
ENSG00000187323	**DCC**	protein_coding	-6.353	0.338	0
ENSG00000170540	**ARL6IP1**	protein_coding	-6.284	0.348	0
ENSG00000102531	**FNDC3A**	protein_coding	-6.252	0.323	0
ENSG00000156970	**BUB1B**	protein_coding	-6.248	0.386	0
ENSG00000148110	**MFSD14B**	protein_coding	-6.235	0.386	0
ENSG00000006576	**PHTF2**	protein_coding	-5.95	0.329	0
ENSG00000184371	**CSF1**	protein_coding	-5.949	0.405	0
ENSG00000135341	**MAP3K7**	protein_coding	-5.846	0.4	0
ENSG00000118007	**STAG1**	protein_coding	-5.725	0.417	0
ENSG00000106415	**GLCCI1**	protein_coding	-5.689	0.431	0
ENSG00000138459	**SLC35A5**	protein_coding	-5.679	0.368	0
ENSG00000068650	**ATP11A**	protein_coding	-5.669	0.35	0
ENSG00000164305	**CASP3**	protein_coding	-5.633	0.42	0
ENSG00000019995	**ZRANB1**	protein_coding	-5.59	0.413	0
ENSG00000139117	**CPNE8**	protein_coding	-5.546	0.365	0
ENSG00000118193	**KIF14**	protein_coding	-5.436	0.35	0
ENSG00000197043	**ANXA6**	protein_coding	-5.404	0.405	0
ENSG00000138709	**LARP1B**	protein_coding	-5.298	0.444	0
ENSG00000178982	**EIF3K**	protein_coding	-5.286	0.371	0
ENSG00000145386	**CCNA2**	protein_coding	-5.265	0.428	0
ENSG00000111912	**NCOA7**	protein_coding	-5.221	0.406	0
ENSG00000113712	**CSNK1A1**	protein_coding	-5.191	0.444	0
ENSG00000112062	**MAPK14**	protein_coding	-5.162	0.441	0
ENSG00000120690	**ELF1**	protein_coding	-5.153	0.431	0
ENSG00000134070	**IRAK2**	protein_coding	-5.106	0.427	0
ENSG00000100461	**RBM23**	protein_coding	-5.072	0.432	0
ENSG00000080802	**CNOT4**	protein_coding	-5.054	0.394	0
ENSG00000121152	**NCAPH**	protein_coding	-5.044	0.428	0
ENSG00000110108	**TMEM109**	protein_coding	-5.032	0.401	0
ENSG00000066279	**ASPM**	protein_coding	-4.995	0.366	0
ENSG00000068489	**PRR11**	protein_coding	-4.992	0.443	0
ENSG00000144711	**IQSEC1**	protein_coding	-4.928	0.405	0
ENSG00000173706	**HEG1**	protein_coding	-4.913	0.461	0
ENSG00000072571	**HMMR**	protein_coding	-4.905	0.372	0

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000198755	**RPL10A**	protein_coding	-4.869	0.416	0
ENSG00000163882	**POLR2H**	protein_coding	-4.846	0.449	0
ENSG00000044574	**HSPA5**	protein_coding	-4.842	0.456	0
ENSG00000143033	**MTF2**	protein_coding	-4.839	0.465	0
ENSG00000196757	**ZNF700**	protein_coding	-4.838	0.377	0
ENSG00000119285	**HEATR1**	protein_coding	-4.83	0.442	0
ENSG00000236015	**ENSG00000236015**	processed_pseudogene	-4.778	0.365	0
ENSG00000058804	**NDC1**	protein_coding	-4.709	0.427	0
ENSG00000122068	**FYTTD1**	protein_coding	-4.696	0.383	0
ENSG00000101126	**ADNP**	protein_coding	-4.694	0.455	0
ENSG00000005020	**SKAP2**	protein_coding	-4.692	0.447	0
ENSG00000119537	**KDSR**	protein_coding	-4.678	0.438	0
ENSG00000161547	**SRSF2**	protein_coding	-4.655	0.461	0
ENSG00000165650	**PDZD8**	protein_coding	-4.649	0.468	0
ENSG00000127081	**ZNF484**	protein_coding	-4.632	0.4	0
ENSG00000089022	**MAPKAPK5**	protein_coding	-4.6	0.481	0
ENSG00000113356	**POLR3G**	protein_coding	-4.593	0.457	0
ENSG00000110075	**PPP6R3**	protein_coding	-4.564	0.485	0
ENSG00000136888	**ATP6V1G1**	protein_coding	-4.546	0.454	0
ENSG00000138018	**SELENOI**	protein_coding	-4.532	0.492	0
ENSG00000152683	**SLC30A6**	protein_coding	-4.525	0.374	0
ENSG00000101557	**USP14**	protein_coding	-4.51	0.451	0
ENSG00000111707	**SUDS3**	protein_coding	-4.507	0.509	0
ENSG00000164941	**INTS8**	protein_coding	-4.471	0.461	0
ENSG00000131747	**TOP2A**	protein_coding	-4.464	0.466	0
ENSG00000197142	**ACSL5**	protein_coding	-4.458	0.443	0
ENSG00000152767	**FARP1**	protein_coding	-4.45	0.491	0
ENSG00000124406	**ATP8A1**	protein_coding	-4.44	0.488	0
ENSG00000030066	**NUP160**	protein_coding	-4.386	0.497	0
ENSG00000163660	**CCNL1**	protein_coding	-4.378	0.477	0
ENSG00000140386	**SCAPER**	protein_coding	-4.37	0.502	0
ENSG00000105778	**AVL9**	protein_coding	-4.369	0.486	0
ENSG00000198589	**LRBA**	protein_coding	-4.368	0.477	0
ENSG00000139278	**GLIPR1**	protein_coding	-4.355	0.478	0
ENSG00000138363	**ATIC**	protein_coding	-4.354	0.469	0
ENSG00000150347	**ARID5B**	protein_coding	-4.33	0.434	0
ENSG00000178105	**DDX10**	protein_coding	-4.265	0.531	0
ENSG00000172939	**OXSR1**	protein_coding	-4.262	0.514	0
ENSG00000275835	**TUBGCP5**	protein_coding	-4.261	0.502	0
ENSG00000134057	**CCNB1**	protein_coding	-4.25	0.49	0
ENSG00000095139	**ARCN1**	protein_coding	-4.223	0.509	0
ENSG00000114480	**GBE1**	protein_coding	-4.219	0.452	0
ENSG00000153107	**ANAPC1**	protein_coding	-4.216	0.494	0
ENSG00000164983	**TMEM65**	protein_coding	-4.21	0.472	0
ENSG00000080298	**RFX3**	protein_coding	-4.192	0.522	0
ENSG00000139505	**MTMR6**	protein_coding	-4.176	0.525	0
ENSG00000163539	**CLASP2**	protein_coding	-4.158	0.529	0
ENSG00000011426	**ANLN**	protein_coding	-4.154	0.499	0
ENSG00000130348	**QRSL1**	protein_coding	-4.148	0.527	0

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000204217	**BMPR2**	protein_coding	-4.146	0.548	0
ENSG00000069275	**NUCKS1**	protein_coding	-4.133	0.526	0
ENSG00000121274	**TENT4B**	protein_coding	-4.132	0.509	0
ENSG00000173334	**TRIB1**	protein_coding	-4.129	0.51	0
ENSG00000226360	**RPL10AP6**	processed_pseudogene	-4.124	0.396	0
ENSG00000198431	**TXNRD1**	protein_coding	-4.113	0.547	0
ENSG00000145780	**FEM1C**	protein_coding	-4.112	0.503	0
ENSG00000202411	**RNA5SP259**	rRNA_pseudogene	-4.101	0.377	0
ENSG00000155495	**MAGEC1**	protein_coding	-4.097	0.464	0
ENSG00000189308	**LIN54**	protein_coding	-4.09	0.524	0
ENSG00000136021	**SCYL2**	protein_coding	-4.089	0.473	0
ENSG00000108443	**RPS6KB1**	protein_coding	-4.068	0.495	0
ENSG00000101752	**MIB1**	protein_coding	-4.048	0.53	0
ENSG00000141384	**TAF4B**	protein_coding	-4.046	0.527	0
ENSG00000125257	**ABCC4**	protein_coding	-4.032	0.523	0
ENSG00000110172	**CHORDC1**	protein_coding	-4.028	0.499	0
ENSG00000280433	**ENSG00000280433**	protein_coding	-4.023	0.463	0
ENSG00000136010	**ALDH1L2**	protein_coding	-4.02	0.495	0
ENSG00000075223	**SEMA3C**	protein_coding	-4.017	0.491	0
ENSG00000152520	**PAN3**	protein_coding	-4.007	0.551	0
ENSG00000143702	**CEP170**	protein_coding	-3.97	0.488	0
ENSG00000177189	**RPS6KA3**	protein_coding	-3.956	0.471	0
ENSG00000162378	**ZYG11B**	protein_coding	-3.943	0.469	0
ENSG00000109819	**PPARGC1A**	protein_coding	-3.939	0.525	0
ENSG00000163629	**PTPN13**	protein_coding	-3.923	0.528	0
ENSG00000106066	**CPVL**	protein_coding	-3.913	0.5	0
ENSG00000171241	**SHCBP1**	protein_coding	-3.911	0.506	0
ENSG00000093144	**ECHDC1**	protein_coding	-3.91	0.534	0
ENSG00000196083	**IL1RAP**	protein_coding	-3.886	0.492	0
ENSG00000121039	**RDH10**	protein_coding	-3.885	0.533	0
ENSG00000140199	**SLC12A6**	protein_coding	-3.884	0.514	0
ENSG00000121988	**ZRANB3**	protein_coding	-3.878	0.501	0
ENSG00000147853	**AK3**	protein_coding	-3.876	0.519	0
ENSG00000182923	**CEP63**	protein_coding	-3.868	0.487	0
ENSG00000183475	**ASB7**	protein_coding	-3.865	0.534	0
ENSG00000134644	**PUM1**	protein_coding	-3.863	0.547	0
ENSG00000101782	**RIOK3**	protein_coding	-3.845	0.518	0
ENSG00000198901	**PRC1**	protein_coding	-3.838	0.554	0
ENSG00000146433	**TMEM181**	protein_coding	-3.831	0.492	0
ENSG00000133302	**SLF1**	protein_coding	-3.826	0.52	0
ENSG00000173757	**STAT5B**	protein_coding	-3.817	0.544	0
ENSG00000097046	**CDC7**	protein_coding	-3.813	0.525	0
ENSG00000172243	**CLEC7A**	protein_coding	-3.811	0.514	0
ENSG00000119314	**PTBP3**	protein_coding	-3.809	0.501	0
ENSG00000198879	**SFMBT2**	protein_coding	-3.807	0.513	0
ENSG00000157741	**UBN2**	protein_coding	-3.805	0.559	0
ENSG00000187988	**KCTD9P3**	processed_pseudogene	-3.799	0.413	0
ENSG00000134243	**SORT1**	protein_coding	-3.792	0.536	0
ENSG00000055917	**PUM2**	protein_coding	-3.789	0.575	0

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000276966	**H4C5**	protein_coding	-3.784	0.506	0
ENSG00000113594	**LIFR**	protein_coding	-3.784	0.493	0
ENSG00000173852	**DPY19L1**	protein_coding	-3.78	0.51	0
ENSG00000164211	**STARD4**	protein_coding	-3.78	0.456	0
ENSG00000176986	**SEC24C**	protein_coding	-3.777	0.547	0
ENSG00000187257	**RSBN1L**	protein_coding	-3.773	0.54	0
ENSG00000112699	**GMDS**	protein_coding	-3.76	0.531	0
ENSG00000173120	**KDM2A**	protein_coding	-3.759	0.573	0
ENSG00000197329	**PELI1**	protein_coding	-3.751	0.454	0
ENSG00000198125	**MB**	protein_coding	-3.748	0.524	0
ENSG00000137776	**SLTM**	protein_coding	-3.741	0.563	0
ENSG00000134440	**NARS1**	protein_coding	-3.739	0.545	0
ENSG00000165209	**STRBP**	protein_coding	-3.739	0.508	0
ENSG00000143815	**LBR**	protein_coding	-3.737	0.565	0
ENSG00000248216	**KCTD9P5**	processed_pseudogene	-3.735	0.39	0
ENSG00000164808	**SPIDR**	protein_coding	-3.734	0.565	0
ENSG00000115761	**NOL10**	protein_coding	-3.731	0.533	0
ENSG00000080839	**RBL1**	protein_coding	-3.711	0.476	0
ENSG00000124789	**NUP153**	protein_coding	-3.704	0.546	0
ENSG00000115970	**THADA**	protein_coding	-3.699	0.564	0
ENSG00000104970	**KIR3DX1**	transcribed_unprocessed	-3.687	0.549	0
ENSG00000106460	**TMEM106B**	protein_coding	-3.687	0.511	0
ENSG00000165660	**ABRAXAS2**	protein_coding	-3.674	0.525	0
ENSG00000187240	**DYNC2H1**	protein_coding	-3.672	0.495	0
ENSG00000196586	**MYO6**	protein_coding	-3.661	0.557	0
ENSG00000101191	**DIDO1**	protein_coding	-3.659	0.584	0
ENSG00000121892	**PDS5A**	protein_coding	-3.658	0.566	0
ENSG00000127980	**PEX1**	protein_coding	-3.653	0.526	0
ENSG00000115840	**SLC25A12**	protein_coding	-3.651	0.55	0
ENSG00000165934	**CPSF2**	protein_coding	-3.632	0.51	0
ENSG00000120800	**UTP20**	protein_coding	-3.628	0.534	0
ENSG00000243156	**MICAL3**	protein_coding	-3.618	0.585	0
ENSG00000115464	**USP34**	protein_coding	-3.614	0.542	0
ENSG00000280098	**ENSG00000280098**	TEC	-3.611	0.476	0
ENSG00000206560	**ANKRD28**	protein_coding	-3.607	0.541	0
ENSG00000155380	**SLC16A1**	protein_coding	-3.594	0.573	0
ENSG00000185274	**GALNT17**	protein_coding	-3.59	0.53	0
ENSG00000124275	**MTRR**	protein_coding	-3.584	0.559	0
ENSG00000147251	**DOCK11**	protein_coding	-3.573	0.541	0
ENSG00000147874	**HAUS6**	protein_coding	-3.573	0.498	0
ENSG00000167193	**CRK**	protein_coding	-3.557	0.551	0
ENSG00000151806	**GUF1**	protein_coding	-3.552	0.545	0
ENSG00000005483	**KMT2E**	protein_coding	-3.552	0.572	0
ENSG00000156103	**MMP16**	protein_coding	-3.55	0.517	0
ENSG00000060339	**CCAR1**	protein_coding	-3.548	0.59	0
ENSG00000066651	**TRMT11**	protein_coding	-3.526	0.538	0
ENSG00000170965	**PLAC1**	protein_coding	-3.511	0.569	0
ENSG00000143228	**NUF2**	protein_coding	-3.507	0.522	0
ENSG00000148606	**POLR3A**	protein_coding	-3.496	0.563	0

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000278540	**ACACA**	protein_coding	-3.491	0.559	0
ENSG00000171681	**ATF7IP**	protein_coding	-3.491	0.546	0
ENSG00000159579	**RSPRY1**	protein_coding	-3.485	0.593	0
ENSG00000036549	**ZZZ3**	protein_coding	-3.482	0.572	0
ENSG00000198793	**MTOR**	protein_coding	-3.474	0.579	0
ENSG00000106692	**FKTN**	protein_coding	-3.473	0.523	0
ENSG00000107672	**NSMCE4A**	protein_coding	-3.473	0.581	0
ENSG00000145819	**ARHGAP26**	protein_coding	-3.468	0.591	0
ENSG00000224837	**GCSHP5**	processed_pseudogene	-3.458	0.289	0
ENSG00000143013	**LMO4**	protein_coding	-3.456	0.59	0
ENSG00000157483	**MYO1E**	protein_coding	-3.447	0.559	0
ENSG00000112984	**KIF20A**	protein_coding	-3.444	0.563	0
ENSG00000008869	**HEATR5B**	protein_coding	-3.442	0.556	0
ENSG00000099219	**ERMP1**	protein_coding	-3.429	0.561	0
ENSG00000013503	**POLR3B**	protein_coding	-3.423	0.543	0
ENSG00000144893	**MED12L**	protein_coding	-3.419	0.585	0
ENSG00000120685	**PROSER1**	protein_coding	-3.416	0.572	0
ENSG00000175054	**ATR**	protein_coding	-3.415	0.54	0
ENSG00000054118	**THRAP3**	protein_coding	-3.415	0.57	0
ENSG00000132356	**PRKAA1**	protein_coding	-3.405	0.568	0
ENSG00000197024	**ZNF398**	protein_coding	-3.4	0.555	0
ENSG00000224078	**SNHG14**	lncRNA	-3.397	0.585	0
ENSG00000171497	**PPID**	protein_coding	-3.383	0.578	0
ENSG00000074657	**ZNF532**	protein_coding	-3.379	0.548	0
ENSG00000187951	**ENSG00000187951**	lncRNA	-3.367	0.536	0
ENSG00000111358	**GTF2H3**	protein_coding	-3.365	0.535	0
ENSG00000269997	**ENSG00000269997**	lncRNA	-3.363	0.436	0
ENSG00000225014	**KCTD9P1**	transcribed_processed_ps	-3.361	0.356	0
ENSG00000025800	**KPNA6**	protein_coding	-3.361	0.612	0
ENSG00000095574	**IKZF5**	protein_coding	-3.352	0.543	0
ENSG00000272335	**ENSG00000272335**	lncRNA	-3.347	0.503	0
ENSG00000140396	**NCOA2**	protein_coding	-3.341	0.594	0
ENSG00000099256	**PRTFDC1**	protein_coding	-3.34	0.525	0
ENSG00000222588	**ENSG00000222588**	snoRNA	-3.334	0.523	0
ENSG00000174485	**DENND4A**	protein_coding	-3.332	0.563	0
ENSG00000116748	**AMPD1**	protein_coding	-3.329	0.546	0
ENSG00000143384	**MCL1**	protein_coding	-3.328	0.572	0
ENSG00000129003	**VPS13C**	protein_coding	-3.326	0.568	0
ENSG00000147202	**DIAPH2**	protein_coding	-3.325	0.497	0
ENSG00000117222	**RBBP5**	protein_coding	-3.321	0.604	0
ENSG00000115827	**DCAF17**	protein_coding	-3.32	0.56	0
ENSG00000201217	**Y_RNA**	misc_RNA	-3.314	0.514	0
ENSG00000121879	**PIK3CA**	protein_coding	-3.31	0.583	0
ENSG00000169756	**LIMS1**	protein_coding	-3.307	0.578	0
ENSG00000137760	**ALKBH8**	protein_coding	-3.305	0.546	0
ENSG00000166263	**STXBP4**	protein_coding	-3.301	0.561	0
ENSG00000139372	**TDG**	protein_coding	-3.298	0.533	0
ENSG00000129071	**MBD4**	protein_coding	-3.295	0.576	0
ENSG00000096717	**SIRT1**	protein_coding	-3.295	0.57	0

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000168036	**CTNNB1**	protein_coding	-3.293	0.565	0
ENSG00000101639	**CEP192**	protein_coding	-3.291	0.596	0
ENSG00000130449	**ZSWIM6**	protein_coding	-3.289	0.569	0
ENSG00000123104	**ITPR2**	protein_coding	-3.287	0.609	0
ENSG00000092140	**G2E3**	protein_coding	-3.282	0.536	0
ENSG00000200090	**Y_RNA**	misc_RNA	-3.28	0.485	0
ENSG00000139514	**SLC7A1**	protein_coding	-3.275	0.593	0
ENSG00000273797	**ENSG00000273797**	lncRNA	-3.274	0.481	0
ENSG00000197594	**ENPP1**	protein_coding	-3.273	0.562	0
ENSG00000023516	**AKAP11**	protein_coding	-3.271	0.56	0
ENSG00000196914	**ARHGEF12**	protein_coding	-3.265	0.604	0
ENSG00000166801	**FAM111A**	protein_coding	-3.264	0.575	0
ENSG00000117280	**RAB29**	protein_coding	-3.264	0.604	0
ENSG00000184575	**XPOT**	protein_coding	-3.256	0.596	0
ENSG00000124151	**NCOA3**	protein_coding	-3.25	0.61	0
ENSG00000281183	**NPTN-IT1**	lncRNA	-3.25	0.176	0
ENSG00000112624	**BICRAL**	protein_coding	-3.247	0.58	0
ENSG00000100934	**SEC23A**	protein_coding	-3.241	0.566	0
ENSG00000134970	**TMED7**	protein_coding	-3.235	0.552	0
ENSG00000182185	**RAD51B**	protein_coding	-3.234	0.578	0
ENSG00000137822	**TUBGCP4**	protein_coding	-3.233	0.605	0
ENSG00000211456	**SACM1L**	protein_coding	-3.232	0.596	0
ENSG00000079785	**DDX1**	protein_coding	-3.231	0.59	0
ENSG00000176225	**RTTN**	protein_coding	-3.23	0.562	0
ENSG00000189091	**SF3B3**	protein_coding	-3.23	0.606	0
ENSG00000113583	**C5orf15**	protein_coding	-3.229	0.574	0
ENSG00000197872	**CYRIA**	protein_coding	-3.226	0.576	0
ENSG00000251513	**LIX1-AS1**	lncRNA	-3.224	0.525	0
ENSG00000144554	**FANCD2**	protein_coding	-3.223	0.598	0
ENSG00000149294	**NCAM1**	protein_coding	-3.222	0.584	0
ENSG00000151893	**CACUL1**	protein_coding	-3.221	0.582	0
ENSG00000155849	**ELMO1**	protein_coding	-3.219	0.6	0
ENSG00000004487	**KDM1A**	protein_coding	-3.219	0.6	0
ENSG00000125686	**MED1**	protein_coding	-3.216	0.571	0
ENSG00000149485	**FADS1**	protein_coding	-3.215	0.587	0
ENSG00000164164	**OTUD4**	protein_coding	-3.215	0.624	0
ENSG00000131873	**CHSY1**	protein_coding	-3.213	0.6	0
ENSG00000174606	**ANGEL2**	protein_coding	-3.209	0.563	0
ENSG00000132549	**VPS13B**	protein_coding	-3.205	0.587	0
ENSG00000151914	**DST**	protein_coding	-3.204	0.578	0
ENSG00000113070	**HBEGF**	protein_coding	-3.202	0.608	0
ENSG00000198826	**ARHGAP11A**	protein_coding	-3.201	0.566	0
ENSG00000109911	**ELP4**	protein_coding	-3.196	0.595	0
ENSG00000023228	**NDUFS1**	protein_coding	-3.187	0.609	0.227
ENSG00000218336	**TENM3**	protein_coding	-3.182	0.571	0.227
ENSG00000163029	**SMC6**	protein_coding	-3.18	0.605	0.227
ENSG00000139354	**GAS2L3**	protein_coding	-3.179	0.509	0.227
ENSG00000155903	**RASA2**	protein_coding	-3.172	0.573	0.227
ENSG00000188033	**ZNF490**	protein_coding	-3.172	0.577	0.227

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000005022	**SLC25A5**	protein_coding	-3.168	0.579	0.227
ENSG00000242110	**AMACR**	protein_coding	-3.152	0.56	0.227
ENSG00000197563	**PIGN**	protein_coding	-3.151	0.6	0.227
ENSG00000145982	**FARS2**	protein_coding	-3.142	0.564	0.227
ENSG00000261096	**ENSG00000261096**	lncRNA	-3.137	0.505	0.227
ENSG00000146263	**MMS22L**	protein_coding	-3.136	0.584	0.227
ENSG00000266618	**MIR4742**	miRNA	-3.132	0.425	0.227
ENSG00000280365	**ENSG00000280365**	TEC	-3.127	0.496	0.227
ENSG00000138468	**SENP7**	protein_coding	-3.123	0.543	0.227
ENSG00000145703	**IQGAP2**	protein_coding	-3.12	0.596	0.227
ENSG00000259924	**ENSG00000259924**	processed_pseudogene	-3.12	0.462	0.227
ENSG00000145241	**CENPC**	protein_coding	-3.118	0.555	0.227
ENSG00000189266	**PNRC2**	protein_coding	-3.116	0.572	0.227
ENSG00000101194	**SLC17A9**	protein_coding	-3.116	0.596	0.227
ENSG00000180917	**CMTR2**	protein_coding	-3.115	0.613	0.227
ENSG00000243005	**RN7SL16P**	misc_RNA	-3.113	0.559	0.227
ENSG00000105849	**POLR1F**	protein_coding	-3.11	0.572	0.227
ENSG00000126581	**BECN1**	protein_coding	-3.106	0.609	0.227
ENSG00000149308	**NPAT**	protein_coding	-3.102	0.579	0.227
ENSG00000115808	**STRN**	protein_coding	-3.099	0.595	0.227
ENSG00000166478	**ZNF143**	protein_coding	-3.099	0.607	0.227
ENSG00000253729	**PRKDC**	protein_coding	-3.097	0.62	0.227
ENSG00000186908	**ZDHHC17**	protein_coding	-3.096	0.611	0.227
ENSG00000138778	**CENPE**	protein_coding	-3.09	0.518	0.227
ENSG00000144136	**SLC20A1**	protein_coding	-3.09	0.63	0.227
ENSG00000115165	**CYTIP**	protein_coding	-3.089	0.613	0.227
ENSG00000116852	**KIF21B**	protein_coding	-3.083	0.605	0.227
ENSG00000111731	**C2CD5**	protein_coding	-3.081	0.606	0.227
ENSG00000102384	**CENPI**	protein_coding	-3.081	0.549	0.227
ENSG00000217128	**FNIP1**	protein_coding	-3.078	0.626	0.227
ENSG00000153944	**MSI2**	protein_coding	-3.077	0.62	0.227
ENSG00000196418	**ZNF124**	protein_coding	-3.076	0.579	0.227
ENSG00000279845	**ENSG00000279845**	TEC	-3.075	0.443	0.227
ENSG00000189283	**FHIT**	protein_coding	-3.071	0.605	0.227
ENSG00000095319	**NUP188**	protein_coding	-3.066	0.621	0.227
ENSG00000035687	**ADSS2**	protein_coding	-3.065	0.61	0.227
ENSG00000047188	**YTHDC2**	protein_coding	-3.062	0.59	0.227
ENSG00000205765	**C5orf51**	protein_coding	-3.059	0.613	0.227
ENSG00000147536	**GINS4**	protein_coding	-3.055	0.569	0.227
ENSG00000105677	**TMEM147**	protein_coding	-3.053	0.589	0.227
ENSG00000197157	**SND1**	protein_coding	-3.046	0.614	0.227
ENSG00000139173	**TMEM117**	protein_coding	-3.045	0.578	0.227
ENSG00000186260	**MRTFB**	protein_coding	-3.04	0.587	0.227
ENSG00000198146	**ZNF770**	protein_coding	-3.037	0.581	0.227
ENSG00000113522	**RAD50**	protein_coding	-3.036	0.584	0.227
ENSG00000164031	**DNAJB14**	protein_coding	-3.035	0.526	0.227
ENSG00000188873	**RPL10AP2**	processed_pseudogene	-3.035	0.522	0.227
ENSG00000118515	**SGK1**	protein_coding	-3.034	0.612	0.227
ENSG00000132002	**DNAJB1**	protein_coding	-3.032	0.574	0.227

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000119446	**RBM18**	protein_coding	-3.031	0.6	0.227
ENSG00000130803	**ZNF317**	protein_coding	-3.028	0.595	0.227
ENSG00000021574	**SPAST**	protein_coding	-3.021	0.622	0.227
ENSG00000152952	**PLOD2**	protein_coding	-3.02	0.575	0.227
ENSG00000132294	**EFR3A**	protein_coding	-3.018	0.568	0.227
ENSG00000213673	**SLC25A5P3**	processed_pseudogene	-3.017	0.504	0.227
ENSG00000073712	**FERMT2**	protein_coding	-3.014	0.6	0.227
ENSG00000075151	**EIF4G3**	protein_coding	-3.013	0.632	0.227
ENSG00000200879	**SNORD14E**	snoRNA	-3.01	0.549	0.227
ENSG00000185104	**FAF1**	protein_coding	-3	0.633	0.227
ENSG00000164091	**WDR82**	protein_coding	-3	0.604	0.227
ENSG00000135919	**SERPINE2**	protein_coding	-2.99	0.606	0.227
ENSG00000175782	**SLC35E3**	protein_coding	-2.989	0.6	0.227
ENSG00000144635	**DYNC1LI1**	protein_coding	-2.982	0.562	0.227
ENSG00000066739	**ATG2B**	protein_coding	-2.98	0.622	0.227
ENSG00000166479	**TMX3**	protein_coding	-2.975	0.622	0.227
ENSG00000124120	**TTPAL**	protein_coding	-2.974	0.558	0.227
ENSG00000065183	**WDR3**	protein_coding	-2.972	0.645	0.227
ENSG00000159921	**GNE**	protein_coding	-2.971	0.604	0.227
ENSG00000181222	**POLR2A**	protein_coding	-2.969	0.624	0.227
ENSG00000125249	**RAP2A**	protein_coding	-2.966	0.631	0.227
ENSG00000226241	**ENSG00000226241**	processed_pseudogene	-2.965	0.584	0.227
ENSG00000064651	**SLC12A2**	protein_coding	-2.964	0.601	0.227
ENSG00000145996	**CDKAL1**	protein_coding	-2.956	0.578	0.227
ENSG00000168301	**KCTD6**	protein_coding	-2.954	0.506	0.227
ENSG00000004766	**VPS50**	protein_coding	-2.953	0.604	0.227
ENSG00000251194	**ENSG00000251194**	lncRNA	-2.953	0.558	0.227
ENSG00000065526	**SPEN**	protein_coding	-2.95	0.64	0.227
ENSG00000100554	**ATP6V1D**	protein_coding	-2.948	0.585	0.227
ENSG00000121621	**KIF18A**	protein_coding	-2.938	0.569	0.227
ENSG00000148943	**LIN7C**	protein_coding	-2.938	0.628	0.227
ENSG00000163596	**ICA1L**	protein_coding	-2.937	0.609	0.227
ENSG00000125869	**LAMP5**	protein_coding	-2.937	0.613	0.227
ENSG00000185607	**ACTBP7**	processed_pseudogene	-2.935	0.533	0.227
ENSG00000010292	**NCAPD2**	protein_coding	-2.933	0.614	0.227
ENSG00000160551	**TAOK1**	protein_coding	-2.931	0.62	0.227
ENSG00000204120	**GIGYF2**	protein_coding	-2.928	0.652	0.227
ENSG00000105483	**CARD8**	protein_coding	-2.926	0.615	0.227
ENSG00000103994	**ZNF106**	protein_coding	-2.924	0.621	0.227
ENSG00000196505	**GDAP2**	protein_coding	-2.923	0.578	0.227
ENSG00000183808	**RBM12B**	protein_coding	-2.918	0.606	0.227
ENSG00000132953	**XPO4**	protein_coding	-2.917	0.636	0.227
ENSG00000122741	**DCAF10**	protein_coding	-2.914	0.575	0.227
ENSG00000109861	**CTSC**	protein_coding	-2.91	0.601	0.227
ENSG00000092931	**MFSD11**	protein_coding	-2.899	0.607	0.227
ENSG00000241634	**ENSG00000241634**	processed_pseudogene	-2.899	0.355	0.227
ENSG00000242247	**ARFGAP3**	protein_coding	-2.891	0.602	0.227
ENSG00000153767	**GTF2E1**	protein_coding	-2.891	0.603	0.227
ENSG00000185420	**SMYD3**	protein_coding	-2.891	0.623	0.227

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000108588	**CCDC47**	protein_coding	-2.887	0.639	0.227
ENSG00000142875	**PRKACB**	protein_coding	-2.886	0.638	0.227
ENSG00000170275	**CRTAP**	protein_coding	-2.885	0.6	0.227
ENSG00000086200	**IPO11**	protein_coding	-2.88	0.58	0.227
ENSG00000068615	**REEP1**	protein_coding	-2.88	0.653	0.227
ENSG00000128989	**ARPP19**	protein_coding	-2.876	0.627	0.227
ENSG00000249859	**PVT1**	lncRNA	-2.873	0.623	0.227
ENSG00000088325	**TPX2**	protein_coding	-2.873	0.62	0.227
ENSG00000048052	**HDAC9**	protein_coding	-2.871	0.611	0.227
ENSG00000263790	**MIR4473**	miRNA	-2.87	0.427	0.227
ENSG00000255725	**TDGP1**	processed_pseudogene	-2.868	0.523	0.227
ENSG00000253333	**ENSG00000253333**	unprocessed_pseudogene	-2.866	0.642	0.227
ENSG00000272886	**DCP1A**	protein_coding	-2.861	0.62	0.227
ENSG00000103489	**XYLT1**	protein_coding	-2.861	0.582	0.227
ENSG00000005844	**ITGAL**	protein_coding	-2.856	0.646	0.227
ENSG00000144426	**NBEAL1**	protein_coding	-2.856	0.63	0.227
ENSG00000140718	**FTO**	protein_coding	-2.855	0.633	0.227
ENSG00000151012	**SLC7A11**	protein_coding	-2.853	0.631	0.227
ENSG00000114757	**PEX5L**	protein_coding	-2.851	0.611	0.227
ENSG00000026508	**CD44**	protein_coding	-2.849	0.651	0.227
ENSG00000143437	**ARNT**	protein_coding	-2.846	0.635	0.227
ENSG00000115163	**CENPA**	protein_coding	-2.845	0.584	0.227
ENSG00000100281	**HMGXB4**	protein_coding	-2.84	0.584	0.227
ENSG00000234857	**HNRNPUL2-BSCL2**	protein_coding	-2.84	0.571	0.227
ENSG00000158966	**CACHD1**	protein_coding	-2.839	0.61	0.227
ENSG00000170312	**CDK1**	protein_coding	-2.838	0.601	0.227
ENSG00000103091	**WDR59**	protein_coding	-2.836	0.629	0.227
ENSG00000196233	**LCOR**	protein_coding	-2.832	0.634	0.227
ENSG00000137601	**NEK1**	protein_coding	-2.832	0.629	0.227
ENSG00000160190	**SLC37A1**	protein_coding	-2.832	0.619	0.227
ENSG00000265415	**ENSG00000265415**	lncRNA	-2.826	0.59	0.227
ENSG00000241913	**RPS29P21**	processed_pseudogene	-2.821	0.566	0.227
ENSG00000240024	**LINC00888**	transcribed_unprocessed_	-2.819	0.625	0.227
ENSG00000261098	**ENSG00000261098**	lncRNA	-2.819	0.581	0.227
ENSG00000110395	**CBL**	protein_coding	-2.817	0.636	0.227
ENSG00000184634	**MED12**	protein_coding	-2.814	0.662	0.227
ENSG00000120705	**ETF1**	protein_coding	-2.812	0.635	0.227
ENSG00000104643	**MTMR9**	protein_coding	-2.811	0.669	0.227
ENSG00000170854	**RIOX2**	protein_coding	-2.81	0.625	0.227
ENSG00000081014	**AP4E1**	protein_coding	-2.808	0.626	0.227
ENSG00000118762	**PKD2**	protein_coding	-2.805	0.658	0.227
ENSG00000104147	**OIP5**	protein_coding	-2.803	0.626	0.227
ENSG00000166833	**NAV2**	protein_coding	-2.802	0.634	0.227
ENSG00000188641	**DPYD**	protein_coding	-2.799	0.636	0.227
ENSG00000024526	**DEPDC1**	protein_coding	-2.797	0.582	0.227
ENSG00000185900	**POMK**	protein_coding	-2.797	0.643	0.227
ENSG00000138074	**SLC5A6**	protein_coding	-2.797	0.631	0.227
ENSG00000108055	**SMC3**	protein_coding	-2.796	0.621	0.227
ENSG00000135932	**CAB39**	protein_coding	-2.794	0.643	0.227

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000122707	**RECK**	protein_coding	-2.794	0.65	0.227
ENSG00000090861	**AARS1**	protein_coding	-2.791	0.634	0.227
ENSG00000134987	**WDR36**	protein_coding	-2.79	0.626	0.227
ENSG00000225224	**RPS27AP12**	processed_pseudogene	-2.789	0.405	0.227
ENSG00000004897	**CDC27**	protein_coding	-2.788	0.595	0.227
ENSG00000237999	**ACTG1P19**	processed_pseudogene	-2.787	0.588	0.227
ENSG00000140262	**TCF12**	protein_coding	-2.782	0.627	0.227
ENSG00000163535	**SGO2**	protein_coding	-2.781	0.573	0.227
ENSG00000154945	**ANKRD40**	protein_coding	-2.779	0.643	0.227
ENSG00000203546	**ENSG00000203546**	protein_coding	-2.777	0.537	0.227
ENSG00000116984	**MTR**	protein_coding	-2.775	0.623	0.227
ENSG00000117724	**CENPF**	protein_coding	-2.773	0.618	0.227
ENSG00000156958	**GALK2**	protein_coding	-2.773	0.634	0.227
ENSG00000224315	**RPL7P7**	processed_pseudogene	-2.773	0.5	0.227
ENSG00000100784	**RPS6KA5**	protein_coding	-2.771	0.644	0.227
ENSG00000252343	**RNU2-34P**	snRNA	-2.769	0.375	0.227
ENSG00000197386	**HTT**	protein_coding	-2.768	0.64	0.227
ENSG00000226421	**SLC25A5P5**	processed_pseudogene	-2.765	0.531	0.227
ENSG00000266709	**ENSG00000266709**	lncRNA	-2.76	0.57	0.227
ENSG00000052795	**FNIP2**	protein_coding	-2.758	0.659	0.227
ENSG00000157456	**CCNB2**	protein_coding	-2.757	0.612	0.227
ENSG00000151532	**VTI1A**	protein_coding	-2.757	0.655	0.227
ENSG00000196712	**NF1**	protein_coding	-2.755	0.607	0.227
ENSG00000167986	**DDB1**	protein_coding	-2.754	0.648	0.227
ENSG00000103544	**VPS35L**	protein_coding	-2.753	0.633	0.227
ENSG00000157764	**BRAF**	protein_coding	-2.752	0.664	0.227
ENSG00000125648	**SLC25A23**	protein_coding	-2.751	0.616	0.227
ENSG00000180747	**SMG1P3**	transcribed_unprocessed_	-2.751	0.52	0.227
ENSG00000039319	**ZFYVE16**	protein_coding	-2.751	0.614	0.227
ENSG00000225813	**ENSG00000225813**	processed_pseudogene	-2.751	0.637	0.227
ENSG00000080345	**RIF1**	protein_coding	-2.747	0.616	0.227
ENSG00000119048	**UBE2B**	protein_coding	-2.746	0.597	0.227
ENSG00000151726	**ACSL1**	protein_coding	-2.745	0.636	0.227
ENSG00000238713	**Y_RNA**	misc_RNA	-2.745	0.49	0.227
ENSG00000033030	**ZCCHC8**	protein_coding	-2.737	0.599	0.227
ENSG00000107929	**LARP4B**	protein_coding	-2.736	0.632	0.227
ENSG00000117362	**APH1A**	protein_coding	-2.731	0.614	0.227
ENSG00000165512	**ZNF22**	protein_coding	-2.729	0.566	0.227
ENSG00000184009	**ACTG1**	protein_coding	-2.726	0.614	0.227
ENSG00000221978	**CCNL2**	protein_coding	-2.725	0.635	0.227
ENSG00000213763	**ACTBP2**	processed_pseudogene	-2.723	0.505	0.401
ENSG00000170776	**AKAP13**	protein_coding	-2.718	0.658	0.401
ENSG00000138160	**KIF11**	protein_coding	-2.718	0.613	0.401
ENSG00000123473	**STIL**	protein_coding	-2.718	0.603	0.401
ENSG00000116171	**SCP2**	protein_coding	-2.717	0.63	0.401
ENSG00000072803	**FBXW11**	protein_coding	-2.716	0.682	0.401
ENSG00000159593	**NAE1**	protein_coding	-2.715	0.613	0.401
ENSG00000235064	**SLC25A5P2**	processed_pseudogene	-2.715	0.502	0.401
ENSG00000151690	**MFSD6**	protein_coding	-2.708	0.642	0.401

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000165195	**PIGA**	protein_coding	-2.708	0.594	0.401
ENSG00000204469	**PRRC2A**	protein_coding	-2.707	0.648	0.401
ENSG00000284633	**ENSG00000284633**	lncRNA	-2.707	0.592	0.401
ENSG00000133657	**ATP13A3**	protein_coding	-2.706	0.634	0.401
ENSG00000125107	**CNOT1**	protein_coding	-2.705	0.671	0.401
ENSG00000185483	**ROR1**	protein_coding	-2.704	0.624	0.401
ENSG00000137807	**KIF23**	protein_coding	-2.701	0.61	0.401
ENSG00000212124	**TAS2R19**	protein_coding	-2.701	0.578	0.401
ENSG00000101871	**MID1**	protein_coding	-2.7	0.646	0.401
ENSG00000101166	**PRELID3B**	protein_coding	-2.7	0.618	0.401
ENSG00000163297	**ANTXR2**	protein_coding	-2.699	0.667	0.401
ENSG00000197959	**DNM3**	protein_coding	-2.698	0.642	0.401
ENSG00000125968	**ID1**	protein_coding	-2.698	0.601	0.401
ENSG00000119414	**PPP6C**	protein_coding	-2.698	0.63	0.401
ENSG00000145365	**TIFA**	protein_coding	-2.698	0.613	0.401
ENSG00000116668	**SWT1**	protein_coding	-2.696	0.605	0.401
ENSG00000075218	**GTSE1**	protein_coding	-2.695	0.635	0.401
ENSG00000251934	**RNU6-1143P**	snRNA	-2.692	0.373	0.401
ENSG00000011201	**ANOS1**	protein_coding	-2.685	0.605	0.401
ENSG00000057019	**DCBLD2**	protein_coding	-2.685	0.64	0.401
ENSG00000090530	**P3H2**	protein_coding	-2.684	0.577	0.401
ENSG00000171634	**BPTF**	protein_coding	-2.683	0.673	0.401
ENSG00000196950	**SLC39A10**	protein_coding	-2.682	0.641	0.401
ENSG00000169570	**DTWD2**	protein_coding	-2.678	0.615	0.401
ENSG00000173848	**NET1**	protein_coding	-2.678	0.662	0.401
ENSG00000136824	**SMC2**	protein_coding	-2.677	0.656	0.401
ENSG00000003989	**SLC7A2**	protein_coding	-2.669	0.622	0.401
ENSG00000090863	**GLG1**	protein_coding	-2.667	0.642	0.401
ENSG00000183049	**CAMK1D**	protein_coding	-2.665	0.662	0.401
ENSG00000064703	**DDX20**	protein_coding	-2.663	0.634	0.401
ENSG00000231952	**DPY19L1P2**	unprocessed_pseudogene	-2.663	0.624	0.401
ENSG00000138430	**OLA1**	protein_coding	-2.663	0.633	0.401
ENSG00000121964	**GTDC1**	protein_coding	-2.661	0.658	0.401
ENSG00000009413	**REV3L**	protein_coding	-2.661	0.652	0.401
ENSG00000138658	**ZGRF1**	protein_coding	-2.661	0.603	0.401
ENSG00000175455	**CCDC14**	protein_coding	-2.659	0.614	0.401
ENSG00000226468	**ENSG00000226468**	processed_pseudogene	-2.659	0.514	0.401
ENSG00000112339	**HBS1L**	protein_coding	-2.658	0.625	0.401
ENSG00000123643	**SLC36A1**	protein_coding	-2.658	0.645	0.401
ENSG00000100815	**TRIP11**	protein_coding	-2.657	0.631	0.401
ENSG00000144481	**TRPM8**	protein_coding	-2.656	0.656	0.401
ENSG00000218819	**TDRD15**	protein_coding	-2.654	0.589	0.401
ENSG00000134982	**APC**	protein_coding	-2.65	0.662	0.401
ENSG00000169826	**CSGALNACT2**	protein_coding	-2.65	0.631	0.401
ENSG00000159086	**PAXBP1**	protein_coding	-2.644	0.666	0.401
ENSG00000069869	**NEDD4**	protein_coding	-2.642	0.614	0.401
ENSG00000126787	**DLGAP5**	protein_coding	-2.639	0.63	0.401
ENSG00000136731	**UGGT1**	protein_coding	-2.638	0.66	0.401
ENSG00000108306	**FBXL20**	protein_coding	-2.636	0.602	0.401

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000263631	**MIR378D1**	miRNA	-2.636	0.602	0.401
ENSG00000213079	**SCAF8**	protein_coding	-2.632	0.67	0.401
ENSG00000109084	**TMEM97**	protein_coding	-2.632	0.628	0.401
ENSG00000127946	**HIP1**	protein_coding	-2.631	0.633	0.401
ENSG00000158079	**PTPDC1**	protein_coding	-2.628	0.652	0.401
ENSG00000177485	**ZBTB33**	protein_coding	-2.628	0.644	0.401
ENSG00000170340	**B3GNT2**	protein_coding	-2.627	0.608	0.401
ENSG00000183826	**BTBD9**	protein_coding	-2.627	0.641	0.401
ENSG00000107863	**ARHGAP21**	protein_coding	-2.622	0.625	0.401
ENSG00000164171	**ITGA2**	protein_coding	-2.622	0.669	0.401
ENSG00000168769	**TET2**	protein_coding	-2.622	0.639	0.401
ENSG00000243508	**DNAJB6P7**	processed_pseudogene	-2.62	0.445	0.401
ENSG00000144036	**EXOC6B**	protein_coding	-2.62	0.634	0.401
ENSG00000148154	**UGCG**	protein_coding	-2.62	0.626	0.401
ENSG00000271971	**ENSG00000271971**	lncRNA	-2.62	0.521	0.401
ENSG00000101544	**ADNP2**	protein_coding	-2.619	0.639	0.401
ENSG00000058668	**ATP2B4**	protein_coding	-2.617	0.653	0.401
ENSG00000165392	**WRN**	protein_coding	-2.617	0.635	0.401
ENSG00000134852	**CLOCK**	protein_coding	-2.616	0.659	0.401
ENSG00000075539	**FRYL**	protein_coding	-2.612	0.644	0.401
ENSG00000248625	**ENSG00000248625**	processed_pseudogene	-2.607	0.533	0.401
ENSG00000171100	**MTM1**	protein_coding	-2.604	0.6	0.401
ENSG00000233125	**ACTBP12**	processed_pseudogene	-2.6	0.542	0.401
ENSG00000185477	**GPRIN3**	protein_coding	-2.6	0.663	0.401
ENSG00000115084	**SLC35F5**	protein_coding	-2.6	0.64	0.401
ENSG00000236088	**COX10-AS1**	lncRNA	-2.599	0.638	0.401
ENSG00000119004	**CYP20A1**	protein_coding	-2.599	0.645	0.401
ENSG00000153253	**SCN3A**	protein_coding	-2.598	0.632	0.401
ENSG00000196396	**PTPN1**	protein_coding	-2.597	0.616	0.401
ENSG00000163026	**WDCP**	protein_coding	-2.597	0.577	0.401
ENSG00000080200	**CRYBG3**	protein_coding	-2.595	0.664	0.401
ENSG00000131844	**MCCC2**	protein_coding	-2.593	0.632	0.401
ENSG00000279957	**ENSG00000279957**	TEC	-2.584	0.64	0.401
ENSG00000005339	**CREBBP**	protein_coding	-2.582	0.652	0.401
ENSG00000285728	**ENSG00000285728**	lncRNA	-2.573	0.555	0.401
ENSG00000165891	**E2F7**	protein_coding	-2.572	0.636	0.401
ENSG00000198105	**ZNF248**	protein_coding	-2.571	0.666	0.401
ENSG00000163597	**SNHG16**	lncRNA	-2.568	0.657	0.401
ENSG00000114346	**ECT2**	protein_coding	-2.567	0.657	0.401
ENSG00000170185	**USP38**	protein_coding	-2.567	0.669	0.401
ENSG00000164074	**ABHD18**	protein_coding	-2.566	0.652	0.401
ENSG00000105851	**PIK3CG**	protein_coding	-2.566	0.638	0.401
ENSG00000040275	**SPDL1**	protein_coding	-2.566	0.643	0.401
ENSG00000140534	**TICRR**	protein_coding	-2.566	0.629	0.401
ENSG00000088451	**TGDS**	protein_coding	-2.565	0.573	0.401
ENSG00000166747	**AP1G1**	protein_coding	-2.563	0.654	0.401
ENSG00000188994	**ZNF292**	protein_coding	-2.563	0.683	0.401
ENSG00000115307	**AUP1**	protein_coding	-2.562	0.646	0.401
ENSG00000201944	**SNORA72**	snoRNA	-2.561	0.633	0.401

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000165732	**DDX21**	protein_coding	-2.56	0.658	0.401
ENSG00000060237	**WNK1**	protein_coding	-2.56	0.67	0.401
ENSG00000090989	**EXOC1**	protein_coding	-2.559	0.664	0.401
ENSG00000168610	**STAT3**	protein_coding	-2.559	0.66	0.401
ENSG00000139144	**PIK3C2G**	protein_coding	-2.558	0.626	0.401
ENSG00000064607	**SUGP2**	protein_coding	-2.558	0.666	0.401
ENSG00000181555	**SETD2**	protein_coding	-2.555	0.675	0.401
ENSG00000136051	**WASHC4**	protein_coding	-2.552	0.645	0.401
ENSG00000110066	**KMT5B**	protein_coding	-2.55	0.661	0.401
ENSG00000182670	**TTC3**	protein_coding	-2.547	0.655	0.401
ENSG00000179820	**MYADM**	protein_coding	-2.544	0.627	0.401
ENSG00000126249	**PDCD2L**	protein_coding	-2.541	0.662	0.401
ENSG00000134900	**TPP2**	protein_coding	-2.541	0.647	0.401
ENSG00000175216	**CKAP5**	protein_coding	-2.538	0.689	0.401
ENSG00000175984	**DENND2C**	protein_coding	-2.538	0.653	0.401
ENSG00000281344	**HELLPAR**	lncRNA	-2.537	0.59	0.401
ENSG00000139324	**TMTC3**	protein_coding	-2.537	0.668	0.401
ENSG00000092847	**AGO1**	protein_coding	-2.536	0.664	0.401
ENSG00000176542	**USF3**	protein_coding	-2.536	0.65	0.401
ENSG00000051382	**PIK3CB**	protein_coding	-2.535	0.635	0.401
ENSG00000152749	**GPR180**	protein_coding	-2.534	0.639	0.401
ENSG00000022267	**FHL1**	protein_coding	-2.532	0.66	0.401
ENSG00000215264	**RPL10AP3**	processed_pseudogene	-2.53	0.572	0.401
ENSG00000090889	**KIF4A**	protein_coding	-2.528	0.658	0.401
ENSG00000163947	**ARHGEF3**	protein_coding	-2.527	0.653	0.401
ENSG00000065534	**MYLK**	protein_coding	-2.525	0.69	0.401
ENSG00000103257	**SLC7A5**	protein_coding	-2.525	0.674	0.401
ENSG00000154608	**CEP170P1**	transcribed_unprocessed_	-2.523	0.561	0.401
ENSG00000179295	**PTPN11**	protein_coding	-2.523	0.682	0.401
ENSG00000189180	**ZNF33A**	protein_coding	-2.52	0.631	0.401
ENSG00000215158	**ENSG00000215158**	transcribed_unprocessed_	-2.518	0.622	0.401
ENSG00000134313	**KIDINS220**	protein_coding	-2.516	0.676	0.401
ENSG00000162894	**FCMR**	protein_coding	-2.514	0.614	0.401
ENSG00000179598	**PLD6**	protein_coding	-2.512	0.581	0.401
ENSG00000138780	**GSTCD**	protein_coding	-2.511	0.643	0.401
ENSG00000064313	**TAF2**	protein_coding	-2.51	0.626	0.401
ENSG00000155256	**ZFYVE27**	protein_coding	-2.509	0.643	0.401
ENSG00000100888	**CHD8**	protein_coding	-2.508	0.687	0.401
ENSG00000260269	**ENSG00000260269**	lncRNA	-2.508	0.463	0.401
ENSG00000136938	**ANP32B**	protein_coding	-2.507	0.64	0.401
ENSG00000120129	**DUSP1**	protein_coding	-2.506	0.588	0.401
ENSG00000153560	**UBP1**	protein_coding	-2.506	0.672	0.401
ENSG00000223559	**ENSG00000223559**	processed_pseudogene	-2.506	0.587	0.401
ENSG00000115419	**GLS**	protein_coding	-2.505	0.649	0.401
ENSG00000054523	**KIF1B**	protein_coding	-2.505	0.677	0.401
ENSG00000169855	**ROBO1**	protein_coding	-2.505	0.671	0.401
ENSG00000119866	**BCL11A**	protein_coding	-2.504	0.648	0.401
ENSG00000075624	**ACTB**	protein_coding	-2.503	0.639	0.401
ENSG00000155744	**FAM126B**	protein_coding	-2.501	0.654	0.51

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000184005	**ST6GALNAC3**	protein_coding	-2.5	0.616	0.51
ENSG00000198382	**UVRAG**	protein_coding	-2.5	0.646	0.51
ENSG00000255014	**ARL6IP1P3**	processed_pseudogene	-2.496	0.575	0.51
ENSG00000139083	**ETV6**	protein_coding	-2.495	0.633	0.51
ENSG00000166483	**WEE1**	protein_coding	-2.494	0.662	0.51
ENSG00000108582	**CPD**	protein_coding	-2.493	0.671	0.51
ENSG00000127947	**PTPN12**	protein_coding	-2.493	0.651	0.51
ENSG00000166783	**MARF1**	protein_coding	-2.491	0.651	0.51
ENSG00000198843	**SELENOT**	protein_coding	-2.49	0.68	0.51
ENSG00000196628	**TCF4**	protein_coding	-2.488	0.645	0.51
ENSG00000066557	**LRRC40**	protein_coding	-2.487	0.661	0.51
ENSG00000236105	**PRELID3BP10**	processed_pseudogene	-2.487	0.582	0.51
ENSG00000156650	**KAT6B**	protein_coding	-2.485	0.67	0.51
ENSG00000189007	**ADAT2**	protein_coding	-2.484	0.667	0.51
ENSG00000035499	**DEPDC1B**	protein_coding	-2.484	0.637	0.51
ENSG00000148773	**MKI67**	protein_coding	-2.483	0.67	0.51
ENSG00000102908	**NFAT5**	protein_coding	-2.482	0.673	0.51
ENSG00000136143	**SUCLA2**	protein_coding	-2.482	0.665	0.51
ENSG00000135049	**AGTPBP1**	protein_coding	-2.48	0.684	0.51
ENSG00000258890	**CEP95**	protein_coding	-2.479	0.657	0.51
ENSG00000178764	**ZHX2**	protein_coding	-2.478	0.605	0.51
ENSG00000225406	**ELF2P4**	processed_pseudogene	-2.477	0.556	0.51
ENSG00000106723	**SPIN1**	protein_coding	-2.477	0.661	0.51
ENSG00000109458	**GAB1**	protein_coding	-2.476	0.648	0.51
ENSG00000185480	**PARPBP**	protein_coding	-2.476	0.649	0.51
ENSG00000260404	**ENSG00000260404**	transcribed_unprocessed	-2.474	0.684	0.51
ENSG00000143458	**GABPB2**	protein_coding	-2.473	0.651	0.51
ENSG00000268785	**RPL7P50**	processed_pseudogene	-2.473	0.54	0.51
ENSG00000134802	**SLC43A3**	protein_coding	-2.469	0.669	0.51
ENSG00000158161	**EYA3**	protein_coding	-2.468	0.654	0.51
ENSG00000112159	**MDN1**	protein_coding	-2.466	0.69	0.51
ENSG00000137558	**PI15**	protein_coding	-2.466	0.636	0.51
ENSG00000175175	**PPM1E**	protein_coding	-2.464	0.607	0.51
ENSG00000144566	**RAB5A**	protein_coding	-2.464	0.665	0.51
ENSG00000252764	**RNU6-1092P**	snRNA	-2.464	0.299	0.51
ENSG00000275111	**ZNF2**	protein_coding	-2.463	0.658	0.51
ENSG00000164597	**COG5**	protein_coding	-2.461	0.652	0.51
ENSG00000075711	**DLG1**	protein_coding	-2.461	0.663	0.51
ENSG00000070610	**GBA2**	protein_coding	-2.46	0.67	0.51
ENSG00000051341	**POLQ**	protein_coding	-2.46	0.657	0.51
ENSG00000095787	**WAC**	protein_coding	-2.457	0.672	0.51
ENSG00000235146	**ENSG00000235146**	lncRNA	-2.456	0.366	0.51
ENSG00000215784	**FAM72D**	protein_coding	-2.453	0.585	0.51
ENSG00000152127	**MGAT5**	protein_coding	-2.453	0.667	0.51
ENSG00000231006	**RPL7P32**	processed_pseudogene	-2.453	0.518	0.51
ENSG00000143569	**UBAP2L**	protein_coding	-2.453	0.687	0.51
ENSG00000104177	**MYEF2**	protein_coding	-2.452	0.682	0.51
ENSG00000176087	**SLC35A4**	protein_coding	-2.451	0.609	0.51
ENSG00000122566	**HNRNPA2B1**	protein_coding	-2.449	0.684	0.51

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000233020	**CHORDC1P5**	processed_pseudogene	-2.448	0.434	0.51
ENSG00000205268	**PDE7A**	protein_coding	-2.447	0.681	0.51
ENSG00000124571	**XPO5**	protein_coding	-2.447	0.679	0.51
ENSG00000131558	**EXOC4**	protein_coding	-2.442	0.687	0.51
ENSG00000125827	**TMX4**	protein_coding	-2.442	0.697	0.51
ENSG00000083642	**PDS5B**	protein_coding	-2.44	0.652	0.51
ENSG00000110422	**HIPK3**	protein_coding	-2.438	0.662	0.51
ENSG00000198677	**TTC37**	protein_coding	-2.438	0.647	0.51
ENSG00000234129	**ENSG00000234129**	lncRNA	-2.432	0.632	0.51
ENSG00000134516	**DOCK2**	protein_coding	-2.43	0.667	0.51
ENSG00000159128	**IFNGR2**	protein_coding	-2.427	0.637	0.51
ENSG00000129691	**ASH2L**	protein_coding	-2.426	0.666	0.51
ENSG00000118058	**KMT2A**	protein_coding	-2.426	0.676	0.51
ENSG00000157600	**TMEM164**	protein_coding	-2.425	0.68	0.51
ENSG00000197045	**GMFB**	protein_coding	-2.424	0.673	0.51
ENSG00000197056	**ZMYM1**	protein_coding	-2.424	0.611	0.51
ENSG00000115966	**ATF2**	protein_coding	-2.423	0.666	0.51
ENSG00000198919	**DZIP3**	protein_coding	-2.422	0.629	0.51
ENSG00000151612	**ZNF827**	protein_coding	-2.421	0.643	0.51
ENSG00000172292	**CERS6**	protein_coding	-2.419	0.656	0.51
ENSG00000158987	**RAPGEF6**	protein_coding	-2.419	0.698	0.51
ENSG00000121486	**TRMT1L**	protein_coding	-2.419	0.659	0.51
ENSG00000183474	**GTF2H2C**	protein_coding	-2.417	0.627	0.51
ENSG00000105339	**DENND3**	protein_coding	-2.416	0.692	0.51
ENSG00000257803	**PIGAP1**	processed_pseudogene	-2.416	0.425	0.51
ENSG00000100479	**POLE2**	protein_coding	-2.416	0.667	0.51
ENSG00000273373	**ENSG00000273373**	lncRNA	-2.416	0.583	0.51
ENSG00000275490	**ENSG00000275490**	unprocessed_pseudogene	-2.412	0.489	0.51
ENSG00000173727	**ENSG00000173727**	transcribed_unprocessed_	-2.411	0.613	0.51
ENSG00000148337	**CIZ1**	protein_coding	-2.41	0.652	0.51
ENSG00000276564	**ENSG00000276564**	lncRNA	-2.408	0.658	0.51
ENSG00000115232	**ITGA4**	protein_coding	-2.407	0.679	0.51
ENSG00000035681	**NSMAF**	protein_coding	-2.404	0.651	0.51
ENSG00000122565	**CBX3**	protein_coding	-2.402	0.679	0.51
ENSG00000206622	**SNORA69**	snoRNA	-2.402	0.493	0.51
ENSG00000187231	**SESTD1**	protein_coding	-2.4	0.632	0.51
ENSG00000100731	**PCNX1**	protein_coding	-2.399	0.673	0.51
ENSG00000113448	**PDE4D**	protein_coding	-2.399	0.686	0.51
ENSG00000139746	**RBM26**	protein_coding	-2.395	0.701	0.51
ENSG00000185009	**AP3M1**	protein_coding	-2.394	0.671	0.51
ENSG00000116667	**C1orf21**	protein_coding	-2.394	0.662	0.51
ENSG00000103995	**CEP152**	protein_coding	-2.394	0.657	0.51
ENSG00000086730	**LAT2**	protein_coding	-2.394	0.619	0.51
ENSG00000119900	**OGFRL1**	protein_coding	-2.394	0.635	0.51
ENSG00000233673	**ANAPC1P1**	transcribed_unprocessed_	-2.393	0.663	0.51
ENSG00000134986	**NREP**	protein_coding	-2.393	0.692	0.51
ENSG00000166946	**CCNDBP1**	protein_coding	-2.392	0.684	0.51
ENSG00000204310	**AGPAT1**	protein_coding	-2.39	0.65	0.51
ENSG00000205659	**LIN52**	protein_coding	-2.389	0.634	0.51

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000173276	**ZBTB21**	protein_coding	-2.388	0.671	0.51
ENSG00000225507	**ENSG00000225507**	processed_pseudogene	-2.388	0.671	0.51
ENSG00000172175	**MALT1**	protein_coding	-2.387	0.66	0.51
ENSG00000139687	**RB1**	protein_coding	-2.386	0.624	0.51
ENSG00000072364	**AFF4**	protein_coding	-2.385	0.663	0.51
ENSG00000084774	**CAD**	protein_coding	-2.385	0.656	0.51
ENSG00000253132	**IGHV3-62**	IG_V_pseudogene	-2.383	0.592	0.51
ENSG00000178202	**POGLUT3**	protein_coding	-2.382	0.698	0.51
ENSG00000236901	**MIR600HG**	lncRNA	-2.381	0.597	0.51
ENSG00000142892	**PIGK**	protein_coding	-2.38	0.699	0.51
ENSG00000095564	**BTAF1**	protein_coding	-2.379	0.678	0.51
ENSG00000137992	**DBT**	protein_coding	-2.379	0.64	0.51
ENSG00000127080	**IPPK**	protein_coding	-2.379	0.652	0.51
ENSG00000133393	**CEP20**	protein_coding	-2.376	0.659	0.51
ENSG00000163249	**CCNYL1**	protein_coding	-2.374	0.624	0.51
ENSG00000206527	**HACD2**	protein_coding	-2.373	0.668	0.51
ENSG00000171295	**ZNF440**	protein_coding	-2.372	0.652	0.51
ENSG00000198312	**BMS1P9**	unprocessed_pseudogene	-2.371	0.604	0.51
ENSG00000283255	**ENSG00000283255**	lncRNA	-2.371	0.469	0.51
ENSG00000008294	**SPAG9**	protein_coding	-2.37	0.683	0.51
ENSG00000179119	**SPTY2D1**	protein_coding	-2.37	0.635	0.51
ENSG00000146842	**TMEM209**	protein_coding	-2.369	0.653	0.51
ENSG00000131467	**PSME3**	protein_coding	-2.368	0.648	0.51
ENSG00000145860	**RNF145**	protein_coding	-2.367	0.667	0.51
ENSG00000199251	**RNU6-664P**	snRNA	-2.367	0.486	0.51
ENSG00000119402	**FBXW2**	protein_coding	-2.366	0.652	0.51
ENSG00000122966	**CIT**	protein_coding	-2.364	0.657	0.51
ENSG00000137941	**TTLL7**	protein_coding	-2.364	0.652	0.51
ENSG00000109046	**WSB1**	protein_coding	-2.364	0.649	0.51
ENSG00000118217	**ATF6**	protein_coding	-2.361	0.703	0.51
ENSG00000065413	**ANKRD44**	protein_coding	-2.36	0.673	0.51
ENSG00000166851	**PLK1**	protein_coding	-2.359	0.705	0.51
ENSG00000153339	**TRAPPC8**	protein_coding	-2.359	0.668	0.51
ENSG00000162889	**MAPKAPK2**	protein_coding	-2.358	0.697	0.51
ENSG00000173542	**MOB1B**	protein_coding	-2.358	0.69	0.51
ENSG00000139618	**BRCA2**	protein_coding	-2.357	0.66	0.51
ENSG00000161405	**IKZF3**	protein_coding	-2.357	0.689	0.51
ENSG00000212424	**RNU1-119P**	snRNA	-2.357	0.452	0.51
ENSG00000240356	**RPL23AP7**	transcribed_processed_ps	-2.357	0.587	0.51
ENSG00000153201	**RANBP2**	protein_coding	-2.356	0.68	0.51
ENSG00000242931	**RPL7P49**	processed_pseudogene	-2.356	0.58	0.51
ENSG00000092439	**TRPM7**	protein_coding	-2.356	0.676	0.51
ENSG00000186106	**ANKRD46**	protein_coding	-2.353	0.699	0.51
ENSG00000117523	**PRRC2C**	protein_coding	-2.352	0.686	0.51
ENSG00000113532	**ST8SIA4**	protein_coding	-2.352	0.704	0.51
ENSG00000114166	**KAT2B**	protein_coding	-2.351	0.678	0.51
ENSG00000118922	**KLF12**	protein_coding	-2.351	0.654	0.51
ENSG00000083168	**KAT6A**	protein_coding	-2.347	0.673	0.51
ENSG00000264853	**ENSG00000264853**	lncRNA	-2.346	0.504	0.51

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000176244	**ACBD7**	protein_coding	-2.344	0.66	0.51
ENSG00000132466	**ANKRD17**	protein_coding	-2.344	0.707	0.51
ENSG00000106346	**USP42**	protein_coding	-2.344	0.667	0.51
ENSG00000237094	**ENSG00000237094**	transcribed_unprocessed	-2.344	0.668	0.51
ENSG00000154229	**PRKCA**	protein_coding	-2.343	0.689	0.51
ENSG00000271503	**CCL5**	protein_coding	-2.342	0.667	0.51
ENSG00000239115	**RNU7-67P**	snRNA	-2.341	0.571	0.51
ENSG00000254252	**RPL7P20**	processed_pseudogene	-2.341	0.626	0.51
ENSG00000177570	**SAMD12**	protein_coding	-2.341	0.661	0.51
ENSG00000056586	**RC3H2**	protein_coding	-2.339	0.666	0.51
ENSG00000168538	**TRAPPC11**	protein_coding	-2.339	0.692	0.51
ENSG00000058091	**CDK14**	protein_coding	-2.338	0.663	0.51
ENSG00000127616	**SMARCA4**	protein_coding	-2.337	0.677	0.51
ENSG00000104517	**UBR5**	protein_coding	-2.335	0.719	0.51
ENSG00000112200	**ZNF451**	protein_coding	-2.334	0.716	0.51
ENSG00000272337	**RNU6-90P**	snRNA	-2.332	0.611	0.51
ENSG00000141404	**GNAL**	protein_coding	-2.33	0.675	0.51
ENSG00000234702	**VDAC1P3**	processed_pseudogene	-2.33	0.566	0.51
ENSG00000153094	**BCL2L11**	protein_coding	-2.329	0.678	0.51
ENSG00000115760	**BIRC6**	protein_coding	-2.329	0.7	0.51
ENSG00000280347	**ENSG00000280347**	TEC	-2.329	0.611	0.51
ENSG00000157895	**C12orf43**	protein_coding	-2.328	0.617	0.51
ENSG00000135473	**PAN2**	protein_coding	-2.327	0.674	0.51
ENSG00000266079	**SNORA59B**	snoRNA	-2.327	0.536	0.51
ENSG00000271880	**ENSG00000271880**	lncRNA	-2.327	0.654	0.51
ENSG00000085721	**RRN3**	protein_coding	-2.326	0.691	0.51
ENSG00000116138	**DNAJC16**	protein_coding	-2.324	0.695	0.51
ENSG00000119927	**GPAM**	protein_coding	-2.323	0.669	0.51
ENSG00000141376	**BCAS3**	protein_coding	-2.322	0.676	0.51
ENSG00000151304	**SRFBP1**	protein_coding	-2.317	0.685	0.51
ENSG00000164494	**PDSS2**	protein_coding	-2.314	0.62	0.51
ENSG00000198780	**FAM169A**	protein_coding	-2.313	0.689	0.51
ENSG00000138095	**LRPPRC**	protein_coding	-2.31	0.697	0.51
ENSG00000113300	**CNOT6**	protein_coding	-2.309	0.653	0.51
ENSG00000138035	**PNPT1**	protein_coding	-2.309	0.683	0.51
ENSG00000172348	**RCAN2**	protein_coding	-2.309	0.661	0.51
ENSG00000165997	**ARL5B**	protein_coding	-2.308	0.71	0.51
ENSG00000235089	**ENSG00000235089**	processed_pseudogene	-2.308	0.629	0.51
ENSG00000100321	**SYNGR1**	protein_coding	-2.307	0.659	0.51
ENSG00000242999	**RN7SL239P**	misc_RNA	-2.303	0.465	0.51
ENSG00000011405	**PIK3C2A**	protein_coding	-2.302	0.651	0.51
ENSG00000111670	**GNPTAB**	protein_coding	-2.301	0.698	0.51
ENSG00000072274	**TFRC**	protein_coding	-2.301	0.693	0.51
ENSG00000225355	**ARL6IP1P2**	processed_pseudogene	-2.299	0.537	0.51
ENSG00000270640	**ENSG00000270640**	lncRNA	-2.299	0.48	0.51
ENSG00000102218	**RP2**	protein_coding	-2.298	0.681	0.51
ENSG00000126216	**TUBGCP3**	protein_coding	-2.297	0.684	0.51
ENSG00000076716	**GPC4**	protein_coding	-2.295	0.641	0.51
ENSG00000177272	**KCNA3**	protein_coding	-2.294	0.648	0.51

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000161813	**LARP4**	protein_coding	-2.294	0.684	0.51
ENSG00000157036	**EXOG**	protein_coding	-2.292	0.689	0.51
ENSG00000169679	**BUB1**	protein_coding	-2.291	0.671	0.51
ENSG00000003402	**CFLAR**	protein_coding	-2.29	0.682	0.51
ENSG00000180182	**MED14**	protein_coding	-2.29	0.7	0.51
ENSG00000135297	**MTO1**	protein_coding	-2.29	0.7	0.51
ENSG00000153250	**RBMS1**	protein_coding	-2.29	0.661	0.51
ENSG00000077097	**TOP2B**	protein_coding	-2.289	0.665	0.51
ENSG00000254590	**ENSG00000254590**	processed_pseudogene	-2.288	0.543	0.51
ENSG00000248783	**ENSG00000248783**	lncRNA	-2.287	0.631	0.779
ENSG00000176853	**FAM91A1**	protein_coding	-2.284	0.687	0.779
ENSG00000018699	**TTC27**	protein_coding	-2.283	0.648	0.779
ENSG00000137812	**KNL1**	protein_coding	-2.282	0.687	0.779
ENSG00000072849	**DERL2**	protein_coding	-2.281	0.668	0.779
ENSG00000067596	**DHX8**	protein_coding	-2.281	0.692	0.779
ENSG00000004864	**SLC25A13**	protein_coding	-2.281	0.68	0.779
ENSG00000113369	**ARRDC3**	protein_coding	-2.28	0.659	0.779
ENSG00000162852	**CNST**	protein_coding	-2.28	0.67	0.779
ENSG00000155100	**OTUD6B**	protein_coding	-2.28	0.684	0.779
ENSG00000164253	**WDR41**	protein_coding	-2.28	0.681	0.779
ENSG00000130150	**MOSPD2**	protein_coding	-2.278	0.645	0.779
ENSG00000060749	**QSER1**	protein_coding	-2.278	0.705	0.779
ENSG00000137502	**RAB30**	protein_coding	-2.277	0.719	0.779
ENSG00000136943	**CTSV**	protein_coding	-2.276	0.669	0.779
ENSG00000156931	**VPS8**	protein_coding	-2.276	0.704	0.779
ENSG00000274943	**ENSG00000274943**	lncRNA	-2.276	0.587	0.779
ENSG00000287292	**ENSG00000287292**	lncRNA	-2.274	0.623	0.779
ENSG00000079335	**CDC14A**	protein_coding	-2.273	0.68	0.779
ENSG00000068912	**ERLEC1**	protein_coding	-2.271	0.671	0.779
ENSG00000065060	**UHRF1BP1**	protein_coding	-2.271	0.699	0.779
ENSG00000155592	**ZKSCAN2**	protein_coding	-2.268	0.672	0.779
ENSG00000101367	**MAPRE1**	protein_coding	-2.266	0.679	0.779
ENSG00000204186	**ZDBF2**	protein_coding	-2.266	0.684	0.779
ENSG00000108510	**MED13**	protein_coding	-2.264	0.69	0.779
ENSG00000136040	**PLXNC1**	protein_coding	-2.262	0.684	0.779
ENSG00000092531	**SNAP23**	protein_coding	-2.262	0.705	0.779
ENSG00000168827	**GFM1**	protein_coding	-2.258	0.691	0.779
ENSG00000170759	**KIF5B**	protein_coding	-2.258	0.698	0.779
ENSG00000107518	**ATRNL1**	protein_coding	-2.257	0.693	0.779
ENSG00000206651	**Y_RNA**	misc_RNA	-2.256	0.541	0.779
ENSG00000280356	**ENSG00000280356**	lncRNA	-2.255	0.577	0.779
ENSG00000278053	**DDX52**	protein_coding	-2.254	0.687	0.779
ENSG00000185722	**ANKFY1**	protein_coding	-2.253	0.684	0.779
ENSG00000162063	**CCNF**	protein_coding	-2.253	0.676	0.779
ENSG00000230551	**ENSG00000230551**	lncRNA	-2.253	0.688	0.779
ENSG00000008311	**AASS**	protein_coding	-2.252	0.661	0.779
ENSG00000279415	**ENSG00000279415**	TEC	-2.252	0.499	0.779
ENSG00000108061	**SHOC2**	protein_coding	-2.251	0.711	0.779
ENSG00000165675	**ENOX2**	protein_coding	-2.25	0.696	0.779

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000285035	**ENSG00000285035**	transcribed_unprocessed	-2.249	0.522	0.779
ENSG00000185305	**ARL15**	protein_coding	-2.246	0.676	0.779
ENSG00000163510	**CWC22**	protein_coding	-2.246	0.707	0.779
ENSG00000147854	**UHRF2**	protein_coding	-2.246	0.719	0.779
ENSG00000103064	**SLC7A6**	protein_coding	-2.245	0.704	0.779
ENSG00000148634	**HERC4**	protein_coding	-2.244	0.682	0.779
ENSG00000107560	**RAB11FIP2**	protein_coding	-2.243	0.676	0.779
ENSG00000273449	**ENSG00000273449**	lncRNA	-2.243	0.456	0.779
ENSG00000270135	**ENSG00000270135**	lncRNA	-2.241	0.576	0.779
ENSG00000204568	**MRPS18B**	protein_coding	-2.24	0.707	0.779
ENSG00000086758	**HUWE1**	protein_coding	-2.238	0.71	0.779
ENSG00000174010	**KLHL15**	protein_coding	-2.238	0.695	0.779
ENSG00000078304	**PPP2R5C**	protein_coding	-2.238	0.703	0.779
ENSG00000270048	**ENSG00000270048**	lncRNA	-2.237	0.694	0.779
ENSG00000090905	**TNRC6A**	protein_coding	-2.236	0.701	0.779
ENSG00000130856	**ZNF236**	protein_coding	-2.236	0.7	0.779
ENSG00000254186	**ENSG00000254186**	lncRNA	-2.236	0.635	0.779
ENSG00000172795	**DCP2**	protein_coding	-2.234	0.663	0.779
ENSG00000173517	**PEAK1**	protein_coding	-2.234	0.661	0.779
ENSG00000120733	**KDM3B**	protein_coding	-2.233	0.708	0.779
ENSG00000152601	**MBNL1**	protein_coding	-2.232	0.707	0.779
ENSG00000205534	**SMG1P2**	transcribed_unprocessed	-2.231	0.607	0.779
ENSG00000135119	**RNFT2**	protein_coding	-2.229	0.683	0.779
ENSG00000280374	**ENSG00000280374**	lncRNA	-2.229	0.569	0.779
ENSG00000081320	**STK17B**	protein_coding	-2.227	0.696	0.779
ENSG00000176208	**ATAD5**	protein_coding	-2.226	0.666	0.779
ENSG00000137478	**FCHSD2**	protein_coding	-2.226	0.691	0.779
ENSG00000207984	**MIR513A2**	miRNA	-2.226	0.551	0.779
ENSG00000131023	**LATS1**	protein_coding	-2.224	0.718	0.779
ENSG00000172965	**MIR4435-2HG**	lncRNA	-2.224	0.677	0.779
ENSG00000162594	**IL23R**	protein_coding	-2.223	0.672	0.779
ENSG00000108651	**UTP6**	protein_coding	-2.222	0.685	0.779
ENSG00000185112	**FAM43A**	protein_coding	-2.22	0.674	0.779
ENSG00000173482	**PTPRM**	protein_coding	-2.22	0.7	0.779
ENSG00000197102	**DYNC1H1**	protein_coding	-2.219	0.706	0.779
ENSG00000135476	**ESPL1**	protein_coding	-2.219	0.685	0.779
ENSG00000207741	**MIR590**	miRNA	-2.219	0.56	0.779
ENSG00000160049	**DFFA**	protein_coding	-2.218	0.694	0.779
ENSG00000082805	**ERC1**	protein_coding	-2.217	0.707	0.779
ENSG00000222921	**RNA5SP104**	rRNA_pseudogene	-2.217	0.63	0.779
ENSG00000145604	**SKP2**	protein_coding	-2.216	0.687	0.779
ENSG00000212415	**ENSG00000212415**	snoRNA	-2.215	0.627	0.779
ENSG00000279384	**ENSG00000279384**	TEC	-2.215	0.503	0.779
ENSG00000103429	**BFAR**	protein_coding	-2.209	0.719	0.779
ENSG00000131263	**RLIM**	protein_coding	-2.208	0.696	0.779
ENSG00000124222	**STX16**	protein_coding	-2.208	0.69	0.779
ENSG00000104472	**CHRAC1**	protein_coding	-2.207	0.677	0.779
ENSG00000107099	**DOCK8**	protein_coding	-2.207	0.684	0.779
ENSG00000112282	**MED23**	protein_coding	-2.207	0.727	0.779

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000279608	**ENSG00000279608**	TEC	-2.207	0.673	0.779
ENSG00000163635	**ATXN7**	protein_coding	-2.205	0.706	0.779
ENSG00000215421	**ZNF407**	protein_coding	-2.205	0.671	0.779
ENSG00000141867	**BRD4**	protein_coding	-2.204	0.699	0.779
ENSG00000117318	**ID3**	protein_coding	-2.203	0.623	0.779
ENSG00000124198	**ARFGEF2**	protein_coding	-2.201	0.715	0.779
ENSG00000153827	**TRIP12**	protein_coding	-2.201	0.721	0.779
ENSG00000111328	**CDK2AP1**	protein_coding	-2.2	0.694	0.779
ENSG00000149635	**OCSTAMP**	protein_coding	-2.2	0.673	0.779
ENSG00000212168	**ENSG00000212168**	snoRNA	-2.199	0.607	0.779
ENSG00000011009	**LYPLA2**	protein_coding	-2.198	0.692	0.779
ENSG00000164654	**MIOS**	protein_coding	-2.196	0.688	0.779
ENSG00000138381	**ASNSD1**	protein_coding	-2.194	0.703	0.779
ENSG00000215895	**HSPA5P1**	processed_pseudogene	-2.193	0.574	0.779
ENSG00000104133	**SPG11**	protein_coding	-2.191	0.7	0.779
ENSG00000137135	**ARHGEF39**	protein_coding	-2.19	0.707	0.779
ENSG00000183495	**EP400**	protein_coding	-2.19	0.699	0.779
ENSG00000163681	**SLMAP**	protein_coding	-2.189	0.71	0.779
ENSG00000145907	**G3BP1**	protein_coding	-2.188	0.731	0.779
ENSG00000204802	**ENSG00000204802**	lncRNA	-2.188	0.68	0.779
ENSG00000127527	**EPS15L1**	protein_coding	-2.186	0.706	0.779
ENSG00000206887	**RNU6-1008P**	snRNA	-2.185	0.523	0.779
ENSG00000204116	**CHIC1**	protein_coding	-2.184	0.683	0.779
ENSG00000228071	**RPL7P47**	processed_pseudogene	-2.184	0.584	0.779
ENSG00000133639	**BTG1**	protein_coding	-2.183	0.704	0.779
ENSG00000051825	**MPHOSPH9**	protein_coding	-2.182	0.684	0.779
ENSG00000120254	**MTHFD1L**	protein_coding	-2.182	0.707	0.779
ENSG00000213047	**DENND1B**	protein_coding	-2.18	0.702	0.779
ENSG00000213066	**CEP43**	protein_coding	-2.177	0.697	0.779
ENSG00000181544	**FANCB**	protein_coding	-2.177	0.672	0.779
ENSG00000164327	**RICTOR**	protein_coding	-2.177	0.699	0.779
ENSG00000181804	**SLC9A9**	protein_coding	-2.177	0.681	0.779
ENSG00000111371	**SLC38A1**	protein_coding	-2.176	0.697	0.779
ENSG00000173273	**TNKS**	protein_coding	-2.176	0.692	0.779
ENSG00000213390	**ARHGAP19**	protein_coding	-2.175	0.624	0.779
ENSG00000116539	**ASH1L**	protein_coding	-2.173	0.712	0.779
ENSG00000111300	**NAA25**	protein_coding	-2.173	0.702	0.779
ENSG00000092201	**SUPT16H**	protein_coding	-2.172	0.693	0.779
ENSG00000171488	**LRRC8C**	protein_coding	-2.171	0.716	0.779
ENSG00000244754	**N4BP2L2**	protein_coding	-2.171	0.715	0.779
ENSG00000198743	**SLC5A3**	protein_coding	-2.17	0.614	0.779
ENSG00000173875	**ZNF791**	protein_coding	-2.17	0.721	0.779
ENSG00000084676	**NCOA1**	protein_coding	-2.169	0.678	0.779
ENSG00000279541	**ENSG00000279541**	TEC	-2.169	0.662	0.779
ENSG00000276573	**ENSG00000276573**	lncRNA	-2.168	0.545	0.779
ENSG00000284882	**ENSG00000284882**	lncRNA	-2.167	0.528	0.779
ENSG00000152061	**RABGAP1L**	protein_coding	-2.166	0.692	0.779
ENSG00000066422	**ZBTB11**	protein_coding	-2.166	0.698	0.779
ENSG00000162636	**FAM102B**	protein_coding	-2.164	0.69	0.779

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000124614	**RPS10**	protein_coding	-2.164	0.708	0.779
ENSG00000151320	**AKAP6**	protein_coding	-2.163	0.734	0.779
ENSG00000224389	**C4B**	protein_coding	-2.163	0.628	0.779
ENSG00000201367	**RNU6-522P**	snRNA	-2.162	0.633	0.779
ENSG00000072415	**MPP5**	protein_coding	-2.16	0.714	0.779
ENSG00000170734	**POLH**	protein_coding	-2.159	0.68	0.779
ENSG00000267249	**ENSG00000267249**	lncRNA	-2.159	0.545	0.779
ENSG00000215236	**RPL7P33**	processed_pseudogene	-2.157	0.565	0.779
ENSG00000100697	**DICER1**	protein_coding	-2.156	0.686	0.779
ENSG00000198265	**HELZ**	protein_coding	-2.156	0.71	0.779
ENSG00000114982	**KANSL3**	protein_coding	-2.155	0.701	0.779
ENSG00000199890	**Y_RNA**	misc_RNA	-2.153	0.595	0.779
ENSG00000138794	**CASP6**	protein_coding	-2.152	0.714	0.779
ENSG00000105983	**LMBR1**	protein_coding	-2.152	0.695	0.779
ENSG00000036672	**USP2**	protein_coding	-2.152	0.72	0.779
ENSG00000133706	**LARS1**	protein_coding	-2.151	0.701	0.779
ENSG00000133119	**RFC3**	protein_coding	-2.151	0.715	0.779
ENSG00000075336	**TIMM21**	protein_coding	-2.15	0.703	0.779
ENSG00000171365	**CLCN5**	protein_coding	-2.149	0.694	0.779
ENSG00000187790	**FANCM**	protein_coding	-2.145	0.661	0.779
ENSG00000085511	**MAP3K4**	protein_coding	-2.145	0.72	0.779
ENSG00000124067	**SLC12A4**	protein_coding	-2.145	0.712	0.779
ENSG00000280710	**ENSG00000280710**	lncRNA	-2.145	0.663	0.779
ENSG00000157426	**AASDH**	protein_coding	-2.142	0.685	0.779
ENSG00000179387	**ELMOD2**	protein_coding	-2.141	0.701	0.779
ENSG00000184661	**CDCA2**	protein_coding	-2.138	0.708	0.779
ENSG00000116641	**DOCK7**	protein_coding	-2.137	0.684	0.779
ENSG00000172113	**NME6**	protein_coding	-2.137	0.705	0.779
ENSG00000118705	**RPN2**	protein_coding	-2.137	0.712	0.779
ENSG00000164535	**DAGLB**	protein_coding	-2.136	0.713	0.779
ENSG00000166024	**R3HCC1L**	protein_coding	-2.134	0.697	0.779
ENSG00000139734	**DIAPH3**	protein_coding	-2.133	0.687	0.779
ENSG00000136997	**MYC**	protein_coding	-2.133	0.717	0.779
ENSG00000264932	**ENSG00000264932**	lncRNA	-2.133	0.677	0.779
ENSG00000131504	**DIAPH1**	protein_coding	-2.131	0.729	0.779
ENSG00000230449	**RPL7P4**	processed_pseudogene	-2.13	0.611	0.779
ENSG00000132485	**ZRANB2**	protein_coding	-2.129	0.724	0.779
ENSG00000207160	**RNU6-1289P**	snRNA	-2.128	0.521	0.779
ENSG00000101935	**AMMECR1**	protein_coding	-2.127	0.713	0.779
ENSG00000007168	**PAFAH1B1**	protein_coding	-2.126	0.722	0.779
ENSG00000157450	**RNF111**	protein_coding	-2.126	0.709	0.779
ENSG00000141298	**SSH2**	protein_coding	-2.125	0.722	0.779
ENSG00000172493	**AFF1**	protein_coding	-2.124	0.709	0.779
ENSG00000198000	**NOL8**	protein_coding	-2.124	0.718	0.779
ENSG00000069956	**MAPK6**	protein_coding	-2.123	0.683	0.779
ENSG00000165685	**TMEM52B**	protein_coding	-2.122	0.654	0.779
ENSG00000145632	**PLK2**	protein_coding	-2.121	0.699	0.779
ENSG00000067057	**PFKP**	protein_coding	-2.12	0.704	0.779
ENSG00000119682	**AREL1**	protein_coding	-2.119	0.693	0.779

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000249274	**PDLIM1P4**	processed_pseudogene	-2.117	0.707	0.779
ENSG00000072501	**SMC1A**	protein_coding	-2.117	0.709	0.779
ENSG00000267040	**ENSG00000267040**	lncRNA	-2.116	0.664	0.779
ENSG00000104299	**INTS9**	protein_coding	-2.114	0.673	0.779
ENSG00000005889	**ZFX**	protein_coding	-2.114	0.73	0.779
ENSG00000232707	**AP1B1P2**	unprocessed_pseudogene	-2.113	0.62	0.779
ENSG00000068878	**PSME4**	protein_coding	-2.113	0.716	0.779
ENSG00000145284	**SCD5**	protein_coding	-2.113	0.698	0.779
ENSG00000270627	**ENSG00000270627**	processed_pseudogene	-2.113	0.563	0.779
ENSG00000279078	**SND1-IT1**	lncRNA	-2.112	0.601	0.779
ENSG00000132436	**FIGNL1**	protein_coding	-2.11	0.726	0.779
ENSG00000090674	**MCOLN1**	protein_coding	-2.107	0.665	0.779
ENSG00000172954	**LCLAT1**	protein_coding	-2.106	0.703	0.779
ENSG00000101057	**MYBL2**	protein_coding	-2.106	0.71	0.779
ENSG00000107854	**TNKS2**	protein_coding	-2.106	0.702	0.779
ENSG00000142731	**PLK4**	protein_coding	-2.104	0.682	0.779
ENSG00000160746	**ANO10**	protein_coding	-2.102	0.742	0.779
ENSG00000136982	**DSCC1**	protein_coding	-2.102	0.699	0.779
ENSG00000227525	**RPL7P6**	processed_pseudogene	-2.102	0.592	0.779
ENSG00000156787	**TBC1D31**	protein_coding	-2.098	0.697	0.779
ENSG00000168803	**ADAL**	protein_coding	-2.097	0.638	0.779
ENSG00000163513	**TGFBR2**	protein_coding	-2.097	0.704	0.779
ENSG00000100393	**EP300**	protein_coding	-2.096	0.718	0.779
ENSG00000123505	**AMD1**	protein_coding	-2.095	0.713	0.779
ENSG00000258445	**MAD2L1P1**	processed_pseudogene	-2.095	0.711	0.779
ENSG00000112242	**E2F3**	protein_coding	-2.094	0.671	0.779
ENSG00000176183	**ENSG00000176183**	processed_pseudogene	-2.094	0.597	0.779
ENSG00000186073	**CDIN1**	protein_coding	-2.093	0.684	0.779
ENSG00000111364	**DDX55**	protein_coding	-2.093	0.734	0.779
ENSG00000120071	**KANSL1**	protein_coding	-2.092	0.714	0.779
ENSG00000187555	**USP7**	protein_coding	-2.091	0.744	0.779
ENSG00000198700	**IPO9**	protein_coding	-2.09	0.717	0.779
ENSG00000105639	**JAK3**	protein_coding	-2.089	0.673	0.779
ENSG00000155926	**SLA**	protein_coding	-2.089	0.724	0.779
ENSG00000040341	**STAU2**	protein_coding	-2.088	0.703	0.779
ENSG00000075568	**TMEM131**	protein_coding	-2.087	0.702	1.118
ENSG00000151148	**UBE3B**	protein_coding	-2.087	0.695	1.118
ENSG00000058056	**USP13**	protein_coding	-2.087	0.716	1.118
ENSG00000273973	**ENSG00000273973**	lncRNA	-2.087	0.613	1.118
ENSG00000102710	**SUPT20H**	protein_coding	-2.086	0.709	1.118
ENSG00000235486	**ANAPC1P6**	unprocessed_pseudogene	-2.085	0.543	1.118
ENSG00000171793	**CTPS1**	protein_coding	-2.085	0.739	1.118
ENSG00000113318	**MSH3**	protein_coding	-2.085	0.713	1.118
ENSG00000108064	**TFAM**	protein_coding	-2.085	0.701	1.118
ENSG00000203965	**EFCAB7**	protein_coding	-2.084	0.66	1.118
ENSG00000074590	**NUAK1**	protein_coding	-2.084	0.694	1.118
ENSG00000213790	**OLA1P1**	processed_pseudogene	-2.082	0.564	1.118
ENSG00000202534	**RNU6-1329P**	snRNA	-2.082	0.672	1.118
ENSG00000114770	**ABCC5**	protein_coding	-2.081	0.714	1.118

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000277253	**CICP28**	processed_pseudogene	-2.081	0.512	1.118
ENSG00000120756	**PLS1**	protein_coding	-2.081	0.708	1.118
ENSG00000151240	**DIP2C**	protein_coding	-2.08	0.691	1.118
ENSG00000274487	**NPEPPSP1**	transcribed_unprocessed	-2.08	0.469	1.118
ENSG00000033867	**SLC4A7**	protein_coding	-2.079	0.713	1.118
ENSG00000176871	**WSB2**	protein_coding	-2.077	0.696	1.118
ENSG00000125630	**POLR1B**	protein_coding	-2.076	0.712	1.118
ENSG00000144724	**PTPRG**	protein_coding	-2.075	0.714	1.118
ENSG00000100814	**CCNB1IP1**	protein_coding	-2.074	0.712	1.118
ENSG00000151276	**MAGI1**	protein_coding	-2.074	0.707	1.118
ENSG00000185760	**KCNQ5**	protein_coding	-2.073	0.726	1.118
ENSG00000181827	**RFX7**	protein_coding	-2.072	0.707	1.118
ENSG00000100426	**ZBED4**	protein_coding	-2.072	0.681	1.118
ENSG00000138433	**CIR1**	protein_coding	-2.071	0.712	1.118
ENSG00000259366	**ENSG00000259366**	lncRNA	-2.07	0.6	1.118
ENSG00000145388	**METTL14**	protein_coding	-2.069	0.67	1.118
ENSG00000269972	**ENSG00000269972**	lncRNA	-2.069	0.663	1.118
ENSG00000151743	**AMN1**	protein_coding	-2.067	0.667	1.118
ENSG00000174799	**CEP135**	protein_coding	-2.067	0.695	1.118
ENSG00000140022	**STON2**	protein_coding	-2.066	0.741	1.118
ENSG00000067365	**METTL22**	protein_coding	-2.065	0.725	1.118
ENSG00000230360	**DDX10P2**	processed_pseudogene	-2.063	0.683	1.118
ENSG00000148429	**USP6NL**	protein_coding	-2.063	0.658	1.118
ENSG00000207697	**MIR573**	miRNA	-2.06	0.705	1.118
ENSG00000072736	**NFATC3**	protein_coding	-2.06	0.721	1.118
ENSG00000168653	**NDUFS5**	protein_coding	-2.058	0.694	1.118
ENSG00000231245	**C1DP1**	processed_pseudogene	-2.056	0.459	1.118
ENSG00000135315	**CEP162**	protein_coding	-2.056	0.69	1.118
ENSG00000166086	**JAM3**	protein_coding	-2.055	0.725	1.118
ENSG00000143379	**SETDB1**	protein_coding	-2.055	0.722	1.118
ENSG00000088538	**DOCK3**	protein_coding	-2.054	0.717	1.118
ENSG00000168843	**FSTL5**	protein_coding	-2.054	0.73	1.118
ENSG00000127507	**ADGRE2**	protein_coding	-2.053	0.709	1.118
ENSG00000138376	**BARD1**	protein_coding	-2.053	0.696	1.118
ENSG00000138231	**DBR1**	protein_coding	-2.052	0.703	1.118
ENSG00000147224	**PRPS1**	protein_coding	-2.052	0.724	1.118
ENSG00000048707	**VPS13D**	protein_coding	-2.052	0.714	1.118
ENSG00000251986	**Y_RNA**	misc_RNA	-2.052	0.697	1.118
ENSG00000156017	**CARNMT1**	protein_coding	-2.051	0.702	1.118
ENSG00000121957	**GPSM2**	protein_coding	-2.051	0.7	1.118
ENSG00000113580	**NR3C1**	protein_coding	-2.051	0.713	1.118
ENSG00000143493	**INTS7**	protein_coding	-2.047	0.704	1.118
ENSG00000148700	**ADD3**	protein_coding	-2.046	0.696	1.118
ENSG00000230589	**IMP3P1**	processed_pseudogene	-2.046	0.706	1.118
ENSG00000009954	**BAZ1B**	protein_coding	-2.045	0.719	1.118
ENSG00000107104	**KANK1**	protein_coding	-2.045	0.716	1.118
ENSG00000168385	**SEPTIN2**	protein_coding	-2.045	0.734	1.118
ENSG00000172985	**SH3RF3**	protein_coding	-2.045	0.712	1.118
ENSG00000162733	**DDR2**	protein_coding	-2.044	0.682	1.118

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000215120	**SOCS6P1**	processed_pseudogene	-2.044	0.708	1.118
ENSG00000156876	**SASS6**	protein_coding	-2.043	0.699	1.118
ENSG00000163006	**CCDC138**	protein_coding	-2.04	0.663	1.118
ENSG00000123600	**METTL8**	protein_coding	-2.04	0.697	1.118
ENSG00000075945	**KIFAP3**	protein_coding	-2.039	0.655	1.118
ENSG00000066084	**DIP2B**	protein_coding	-2.038	0.744	1.118
ENSG00000185238	**PRMT3**	protein_coding	-2.038	0.71	1.118
ENSG00000138180	**CEP55**	protein_coding	-2.037	0.695	1.118
ENSG00000153904	**DDAH1**	protein_coding	-2.037	0.634	1.118
ENSG00000199514	**RNU6-235P**	snRNA	-2.033	0.559	1.118
ENSG00000100603	**SNW1**	protein_coding	-2.033	0.74	1.118
ENSG00000287697	**ENSG00000287697**	lncRNA	-2.032	0.676	1.118
ENSG00000135250	**SRPK2**	protein_coding	-2.03	0.736	1.118
ENSG00000237629	**UQCRHP2**	processed_pseudogene	-2.03	0.677	1.118
ENSG00000164291	**ARSK**	protein_coding	-2.029	0.705	1.118
ENSG00000037637	**FBXO42**	protein_coding	-2.028	0.703	1.118
ENSG00000073614	**KDM5A**	protein_coding	-2.028	0.732	1.118
ENSG00000139146	**SINHCAF**	protein_coding	-2.028	0.684	1.118
ENSG00000133065	**SLC41A1**	protein_coding	-2.028	0.731	1.118
ENSG00000196455	**PIK3R4**	protein_coding	-2.027	0.716	1.118
ENSG00000214259	**ENSG00000214259**	processed_pseudogene	-2.025	0.683	1.118
ENSG00000197894	**ADH5**	protein_coding	-2.024	0.714	1.118
ENSG00000143776	**CDC42BPA**	protein_coding	-2.024	0.722	1.118
ENSG00000120549	**KIAA1217**	protein_coding	-2.024	0.729	1.118
ENSG00000196850	**PPTC7**	protein_coding	-2.024	0.691	1.118
ENSG00000140943	**MBTPS1**	protein_coding	-2.022	0.736	1.118
ENSG00000037749	**MFAP3**	protein_coding	-2.022	0.687	1.118
ENSG00000272800	**ENSG00000272800**	lncRNA	-2.022	0.668	1.118
ENSG00000087586	**AURKA**	protein_coding	-2.021	0.693	1.118
ENSG00000104361	**NIPAL2**	protein_coding	-2.019	0.717	1.118
ENSG00000185127	**C6orf120**	protein_coding	-2.017	0.675	1.118
ENSG00000257923	**CUX1**	protein_coding	-2.017	0.711	1.118
ENSG00000117139	**KDM5B**	protein_coding	-2.017	0.74	1.118
ENSG00000278845	**MRPL45**	protein_coding	-2.017	0.638	1.118
ENSG00000055070	**SZRD1**	protein_coding	-2.017	0.692	1.118
ENSG00000180776	**ZDHHC20**	protein_coding	-2.017	0.72	1.118
ENSG00000238754	**SCARNA18B**	snoRNA	-2.014	0.633	1.118
ENSG00000178691	**SUZ12**	protein_coding	-2.014	0.723	1.118
ENSG00000163625	**WDFY3**	protein_coding	-2.014	0.711	1.118
ENSG00000220267	**ACTBP8**	processed_pseudogene	-2.013	0.632	1.118
ENSG00000165671	**NSD1**	protein_coding	-2.013	0.724	1.118
ENSG00000137509	**PRCP**	protein_coding	-2.013	0.706	1.118
ENSG00000288062	**ENSG00000288062**	lncRNA	-2.013	0.463	1.118
ENSG00000225155	**TOMM22P5**	processed_pseudogene	-2.012	0.565	1.118
ENSG00000172915	**NBEA**	protein_coding	-2.011	0.712	1.118
ENSG00000284671	**ENSG00000284671**	transcribed_unprocessed	-2.011	0.416	1.118
ENSG00000100201	**DDX17**	protein_coding	-2.01	0.74	1.118
ENSG00000114450	**GNB4**	protein_coding	-2.01	0.702	1.118
ENSG00000100519	**PSMC6**	protein_coding	-2.01	0.726	1.118

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000117020	**AKT3**	protein_coding	-2.009	0.716	1.118
ENSG00000188419	**CHM**	protein_coding	-2.009	0.735	1.118
ENSG00000204856	**FAM216A**	protein_coding	-2.009	0.702	1.118
ENSG00000276894	**RAB28P4**	processed_pseudogene	-2.009	0.612	1.118
ENSG00000181163	**NPM1**	protein_coding	-2.008	0.735	1.118
ENSG00000222365	**SNORD12B**	snoRNA	-2.008	0.488	1.118
ENSG00000241547	**ACTG1P20**	processed_pseudogene	-2.007	0.668	1.118
ENSG00000278571	**MIR7161**	miRNA	-2.007	0.632	1.118
ENSG00000252255	**RNU2-35P**	snRNA	-2.007	0.546	1.118
ENSG00000145348	**TBCK**	protein_coding	-2.006	0.7	1.118
ENSG00000100503	**NIN**	protein_coding	-2.005	0.725	1.118
ENSG00000156831	**NSMCE2**	protein_coding	-2.003	0.724	1.118
ENSG00000157106	**SMG1**	protein_coding	-2.003	0.731	1.118
ENSG00000280079	**ENSG00000280079**	TEC	-2.003	0.667	1.118
ENSG00000081386	**ZNF510**	protein_coding	-2	0.691	1.118
ENSG00000150756	**ATPSCKMT**	protein_coding	-1.998	0.738	1.118
ENSG00000148175	**STOM**	protein_coding	-1.997	0.715	1.118
ENSG00000103657	**HERC1**	protein_coding	-1.995	0.733	1.118
ENSG00000275597	**ANAPC1P5**	unprocessed_pseudogen	-1.994	0.571	1.118
ENSG00000143376	**SNX27**	protein_coding	-1.994	0.709	1.118
ENSG00000137265	**IRF4**	protein_coding	-1.993	0.732	1.118
ENSG00000261371	**PECAM1**	protein_coding	-1.993	0.74	1.118
ENSG00000083312	**TNPO1**	protein_coding	-1.993	0.728	1.118
ENSG00000105968	**H2AZ2**	protein_coding	-1.992	0.722	1.118
ENSG00000277130	**ENSG00000277130**	lncRNA	-1.992	0.565	1.118
ENSG00000174197	**MGA**	protein_coding	-1.991	0.736	1.118
ENSG00000208005	**MIR503**	miRNA	-1.991	0.714	1.118
ENSG00000140455	**USP3**	protein_coding	-1.99	0.736	1.118
ENSG00000244701	**ENSG00000244701**	lncRNA	-1.99	0.713	1.118
ENSG00000124107	**SLPI**	protein_coding	-1.989	0.607	1.118
ENSG00000254151	**NIPA2P4**	processed_pseudogene	-1.988	0.707	1.118
ENSG00000138246	**DNAJC13**	protein_coding	-1.986	0.727	1.118
ENSG00000137337	**MDC1**	protein_coding	-1.986	0.701	1.118
ENSG00000080986	**NDC80**	protein_coding	-1.986	0.717	1.118
ENSG00000100401	**RANGAP1**	protein_coding	-1.986	0.712	1.118
ENSG00000128708	**HAT1**	protein_coding	-1.985	0.689	1.118
ENSG00000142945	**KIF2C**	protein_coding	-1.985	0.706	1.118
ENSG00000256682	**ENSG00000256682**	transcribed_processed_p	-1.985	0.698	1.118
ENSG00000107951	**MTPAP**	protein_coding	-1.983	0.742	1.118
ENSG00000253668	**ENSG00000253668**	processed_pseudogene	-1.983	0.49	1.118
ENSG00000168214	**RBPJ**	protein_coding	-1.981	0.716	1.118
ENSG00000114127	**XRN1**	protein_coding	-1.981	0.7	1.118
ENSG00000110768	**GTF2H1**	protein_coding	-1.979	0.755	1.118
ENSG00000025039	**RRAGD**	protein_coding	-1.979	0.746	1.118
ENSG00000090054	**SPTLC1**	protein_coding	-1.979	0.716	1.118
ENSG00000182481	**KPNA2**	protein_coding	-1.978	0.733	1.118
ENSG00000252178	**RNU7-69P**	snRNA	-1.978	0.659	1.118
ENSG00000163257	**DCAF16**	protein_coding	-1.975	0.74	1.118
ENSG00000166446	**CDYL2**	protein_coding	-1.974	0.708	1.118

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000133943	**DGLUCY**	protein_coding	-1.974	0.75	1.118
ENSG00000029725	**RABEP1**	protein_coding	-1.974	0.722	1.118
ENSG00000165409	**TSHR**	protein_coding	-1.974	0.706	1.118
ENSG00000166579	**NDEL1**	protein_coding	-1.973	0.735	1.118
ENSG00000278266	**ENSG00000278266**	lncRNA	-1.973	0.536	1.118
ENSG00000151702	**FLI1**	protein_coding	-1.972	0.719	1.118
ENSG00000116741	**RGS2**	protein_coding	-1.97	0.614	1.118
ENSG00000117114	**ADGRL2**	protein_coding	-1.969	0.713	1.118
ENSG00000134909	**ARHGAP32**	protein_coding	-1.967	0.742	1.118
ENSG00000171105	**INSR**	protein_coding	-1.967	0.728	1.118
ENSG00000147316	**MCPH1**	protein_coding	-1.967	0.735	1.118
ENSG00000071189	**SNX13**	protein_coding	-1.967	0.736	1.118
ENSG00000164754	**RAD21**	protein_coding	-1.966	0.749	1.118
ENSG00000280104	**ENSG00000280104**	TEC	-1.966	0.705	1.118
ENSG00000237447	**CDC27P2**	processed_pseudogene	-1.965	0.672	1.118
ENSG00000250950	**ENSG00000250950**	lncRNA	-1.965	0.589	1.118
ENSG00000287097	**ENSG00000287097**	lncRNA	-1.964	0.664	1.118
ENSG00000108094	**CUL2**	protein_coding	-1.961	0.728	1.118
ENSG00000181610	**MRPS23**	protein_coding	-1.961	0.711	1.118
ENSG00000151503	**NCAPD3**	protein_coding	-1.961	0.735	1.118
ENSG00000143398	**PIP5K1A**	protein_coding	-1.96	0.718	1.118
ENSG00000143507	**DUSP10**	protein_coding	-1.959	0.709	1.118
ENSG00000129515	**SNX6**	protein_coding	-1.959	0.73	1.118
ENSG00000110400	**NECTIN1**	protein_coding	-1.958	0.701	1.118
ENSG00000157837	**SPPL3**	protein_coding	-1.957	0.708	1.118
ENSG00000242477	**ENSG00000242477**	processed_pseudogene	-1.955	0.622	1.118
ENSG00000135451	**TROAP**	protein_coding	-1.954	0.704	1.118
ENSG00000130396	**AFDN**	protein_coding	-1.953	0.744	1.118
ENSG00000168918	**INPP5D**	protein_coding	-1.953	0.701	1.118
ENSG00000173889	**PHC3**	protein_coding	-1.953	0.73	1.118
ENSG00000144028	**SNRNP200**	protein_coding	-1.953	0.73	1.118
ENSG00000250162	**CSNK1A1P3**	processed_pseudogene	-1.95	0.621	1.118
ENSG00000273014	**ENSG00000273014**	lncRNA	-1.95	0.675	1.118
ENSG00000278287	**ENSG00000278287**	misc_RNA	-1.95	0.654	1.118
ENSG00000196911	**KPNA5**	protein_coding	-1.949	0.725	1.118
ENSG00000108406	**DHX40**	protein_coding	-1.948	0.715	1.118
ENSG00000254612	**DNAJB6P1**	processed_pseudogene	-1.948	0.571	1.118
ENSG00000275927	**ENSG00000275927**	lncRNA	-1.948	0.504	1.118
ENSG00000107779	**BMPR1A**	protein_coding	-1.947	0.696	1.118
ENSG00000090857	**PDPR**	protein_coding	-1.947	0.743	1.118
ENSG00000168411	**RFWD3**	protein_coding	-1.947	0.731	1.118
ENSG00000113761	**ZNF346**	protein_coding	-1.947	0.75	1.118
ENSG00000267264	**ENSG00000267264**	processed_pseudogene	-1.947	0.674	1.118
ENSG00000153207	**AHCTF1**	protein_coding	-1.946	0.72	1.118
ENSG00000163125	**RPRD2**	protein_coding	-1.946	0.731	1.118
ENSG00000006695	**COX10**	protein_coding	-1.945	0.731	1.118
ENSG00000265733	**SNORA74C-1**	snoRNA	-1.945	0.625	1.118
ENSG00000183337	**BCOR**	protein_coding	-1.944	0.734	1.118
ENSG00000223756	**TSSC2**	transcribed_unprocessed_	-1.944	0.734	1.118

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000250874	**ENSG00000250874**	lncRNA	-1.943	0.625	1.118
ENSG00000257103	**LSM14A**	protein_coding	-1.942	0.726	1.118
ENSG00000003393	**ALS2**	protein_coding	-1.939	0.726	1.118
ENSG00000168439	**STIP1**	protein_coding	-1.939	0.745	1.118
ENSG00000123552	**USP45**	protein_coding	-1.939	0.706	1.118
ENSG00000151779	**NBAS**	protein_coding	-1.938	0.724	1.118
ENSG00000131374	**TBC1D5**	protein_coding	-1.937	0.713	1.118
ENSG00000064933	**PMS1**	protein_coding	-1.936	0.709	1.118
ENSG00000271751	**ENSG00000271751**	lncRNA	-1.936	0.6	1.118
ENSG00000198056	**PRIM1**	protein_coding	-1.935	0.703	1.118
ENSG00000216938	**RPL7P58**	processed_pseudogene	-1.935	0.652	1.118
ENSG00000183309	**ZNF623**	protein_coding	-1.935	0.703	1.118
ENSG00000279679	**ENSG00000279679**	TEC	-1.935	0.559	1.118
ENSG00000107290	**SETX**	protein_coding	-1.934	0.723	1.118
ENSG00000207981	**MIR519D**	miRNA	-1.933	0.63	1.118
ENSG00000207988	**MIR576**	miRNA	-1.933	0.68	1.118
ENSG00000197223	**C1D**	protein_coding	-1.932	0.691	1.118
ENSG00000100226	**GTPBP1**	protein_coding	-1.932	0.751	1.118
ENSG00000223482	**NUTM2A-AS1**	lncRNA	-1.931	0.737	1.118
ENSG00000134690	**CDCA8**	protein_coding	-1.929	0.719	1.118
ENSG00000233642	**GPR158-AS1**	lncRNA	-1.929	0.722	1.118
ENSG00000073969	**NSF**	protein_coding	-1.929	0.713	1.118
ENSG00000137073	**UBAP2**	protein_coding	-1.928	0.74	1.118
ENSG00000135720	**DYNC1LI2**	protein_coding	-1.927	0.726	1.118
ENSG00000256040	**PAPPA-AS1**	lncRNA	-1.926	0.669	1.118
ENSG00000279267	**ENSG00000279267**	TEC	-1.926	0.605	1.118
ENSG00000238721	**RNU7-194P**	snRNA	-1.923	0.628	1.118
ENSG00000254556	**ENSG00000254556**	lncRNA	-1.923	0.678	1.118
ENSG00000286791	**ENSG00000286791**	lncRNA	-1.923	0.73	1.118
ENSG00000264743	**DPRXP4**	processed_pseudogene	-1.921	0.343	1.118
ENSG00000105976	**MET**	protein_coding	-1.921	0.739	1.118
ENSG00000163602	**RYBP**	protein_coding	-1.921	0.668	1.118
ENSG00000168172	**HOOK3**	protein_coding	-1.92	0.702	1.118
ENSG00000115207	**GTF3C2**	protein_coding	-1.919	0.731	1.118
ENSG00000252542	**SNORD36C**	snoRNA	-1.919	0.536	1.118
ENSG00000151116	**UEVLD**	protein_coding	-1.919	0.72	1.118
ENSG00000140006	**WDR89**	protein_coding	-1.919	0.722	1.118
ENSG00000286676	**ACTBP4**	processed_pseudogene	-1.918	0.589	1.118
ENSG00000168461	**RAB31**	protein_coding	-1.917	0.73	1.118
ENSG00000224869	**ENSG00000224869**	processed_pseudogene	-1.917	0.641	1.118
ENSG00000079387	**SENP1**	protein_coding	-1.916	0.739	1.118
ENSG00000011376	**LARS2**	protein_coding	-1.915	0.725	1.118
ENSG00000110660	**SLC35F2**	protein_coding	-1.915	0.756	1.118
ENSG00000287151	**C2orf27A**	lncRNA	-1.913	0.732	1.118
ENSG00000069493	**CLEC2D**	protein_coding	-1.913	0.707	1.118
ENSG00000163002	**NUP35**	protein_coding	-1.913	0.718	1.118
ENSG00000117000	**RLF**	protein_coding	-1.913	0.715	1.118
ENSG00000152291	**TGOLN2**	protein_coding	-1.913	0.723	1.118
ENSG00000118985	**ELL2**	protein_coding	-1.912	0.728	1.118

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000104756	**KCTD9**	protein_coding	-1.911	0.713	1.118
ENSG00000226521	**ENSG00000226521**	transcribed_unprocessed_	-1.91	0.683	1.118
ENSG00000103591	**AAGAB**	protein_coding	-1.909	0.736	1.118
ENSG00000152404	**CWF19L2**	protein_coding	-1.909	0.704	1.118
ENSG00000118482	**PHF3**	protein_coding	-1.909	0.742	1.118
ENSG00000080819	**CPOX**	protein_coding	-1.908	0.723	1.118
ENSG00000102024	**PLS3**	protein_coding	-1.908	0.721	1.118
ENSG00000166068	**SPRED1**	protein_coding	-1.908	0.754	1.118
ENSG00000115977	**AAK1**	protein_coding	-1.907	0.714	1.118
ENSG00000108819	**PPP1R9B**	protein_coding	-1.906	0.702	1.118
ENSG00000238311	**SNORD13E**	snoRNA	-1.906	0.707	1.118
ENSG00000101447	**FAM83D**	protein_coding	-1.904	0.708	1.662
ENSG00000100647	**SUSD6**	protein_coding	-1.904	0.701	1.662
ENSG00000147130	**ZMYM3**	protein_coding	-1.904	0.736	1.662
ENSG00000136167	**LCP1**	protein_coding	-1.903	0.723	1.662
ENSG00000089902	**RCOR1**	protein_coding	-1.903	0.725	1.662
ENSG00000234376	**UBTFL2**	processed_pseudogene	-1.903	0.616	1.662
ENSG00000202314	**SNORD6**	snoRNA	-1.902	0.692	1.662
ENSG00000240291	**ENSG00000240291**	lncRNA	-1.902	0.692	1.662
ENSG00000116704	**SLC35D1**	protein_coding	-1.9	0.708	1.662
ENSG00000115514	**TXNDC9**	protein_coding	-1.9	0.706	1.662
ENSG00000005810	**MYCBP2**	protein_coding	-1.899	0.746	1.662
ENSG00000241458	**RPL7P19**	processed_pseudogene	-1.899	0.669	1.662
ENSG00000197323	**TRIM33**	protein_coding	-1.899	0.747	1.662
ENSG00000170113	**NIPA1**	protein_coding	-1.898	0.74	1.662
ENSG00000146676	**PURB**	protein_coding	-1.897	0.715	1.662
ENSG00000196655	**TRAPPC4**	protein_coding	-1.896	0.702	1.662
ENSG00000261249	**LINC01751**	lncRNA	-1.895	0.734	1.662
ENSG00000228649	**SNHG26**	lncRNA	-1.895	0.685	1.662
ENSG00000114120	**SLC25A36**	protein_coding	-1.894	0.737	1.662
ENSG00000103978	**TMEM87A**	protein_coding	-1.893	0.729	1.662
ENSG00000119397	**CNTRL**	protein_coding	-1.892	0.705	1.662
ENSG00000268117	**VN1R84P**	unprocessed_pseudogene	-1.892	0.608	1.662
ENSG00000259039	**ENSG00000259039**	lncRNA	-1.892	0.61	1.662
ENSG00000188786	**MTF1**	protein_coding	-1.891	0.732	1.662
ENSG00000113569	**NUP155**	protein_coding	-1.891	0.751	1.662
ENSG00000106344	**RBM28**	protein_coding	-1.891	0.731	1.662
ENSG00000267369	**TAF5LP1**	processed_pseudogene	-1.891	0.675	1.662
ENSG00000116729	**WLS**	protein_coding	-1.891	0.752	1.662
ENSG00000125484	**GTF3C4**	protein_coding	-1.89	0.717	1.662
ENSG00000174373	**RALGAPA1**	protein_coding	-1.89	0.724	1.662
ENSG00000284741	**PDE11A**	protein_coding	-1.889	0.704	1.662
ENSG00000234253	**RPL7P13**	processed_pseudogene	-1.889	0.644	1.662
ENSG00000175066	**GK5**	protein_coding	-1.887	0.716	1.662
ENSG00000137804	**NUSAP1**	protein_coding	-1.887	0.712	1.662
ENSG00000123728	**RAP2C**	protein_coding	-1.887	0.696	1.662
ENSG00000197892	**KIF13B**	protein_coding	-1.886	0.733	1.662
ENSG00000112531	**QKI**	protein_coding	-1.886	0.736	1.662
ENSG00000228599	**RPL7P52**	processed_pseudogene	-1.886	0.635	1.662

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000277693	**ENSG00000277693**	lncRNA	-1.886	0.68	1.662
ENSG00000242887	**IGHJ3**	IG_J_gene	-1.884	0.72	1.662
ENSG00000283891	**MIR628**	miRNA	-1.884	0.631	1.662
ENSG00000170537	**TMC7**	protein_coding	-1.883	0.703	1.662
ENSG00000152413	**HOMER1**	protein_coding	-1.88	0.734	1.662
ENSG00000118976	**OTUD4P1**	processed_pseudogene	-1.879	0.698	1.662
ENSG00000204267	**TAP2**	protein_coding	-1.877	0.721	1.662
ENSG00000287708	**ENSG00000287708**	lncRNA	-1.877	0.752	1.662
ENSG00000124207	**CSE1L**	protein_coding	-1.875	0.713	1.662
ENSG00000163788	**SNRK**	protein_coding	-1.875	0.759	1.662
ENSG00000181800	**CELF2-AS1**	lncRNA	-1.874	0.657	1.662
ENSG00000126003	**PLAGL2**	protein_coding	-1.874	0.724	1.662
ENSG00000131269	**ABCB7**	protein_coding	-1.873	0.736	1.662
ENSG00000213857	**ACTBP15**	processed_pseudogene	-1.873	0.646	1.662
ENSG00000092853	**CLSPN**	protein_coding	-1.873	0.736	1.662
ENSG00000088812	**ATRN**	protein_coding	-1.87	0.738	1.662
ENSG00000282508	**LINC01002**	lncRNA	-1.87	0.71	1.662
ENSG00000134250	**NOTCH2**	protein_coding	-1.87	0.731	1.662
ENSG00000109618	**SEPSECS**	protein_coding	-1.87	0.736	1.662
ENSG00000177853	**ZNF518A**	protein_coding	-1.869	0.696	1.662
ENSG00000113273	**ARSB**	protein_coding	-1.867	0.739	1.662
ENSG00000115540	**MOB4**	protein_coding	-1.867	0.714	1.662
ENSG00000141279	**NPEPPS**	protein_coding	-1.866	0.739	1.662
ENSG00000276334	**ENSG00000276334**	lncRNA	-1.865	0.635	1.662
ENSG00000131779	**PEX11B**	protein_coding	-1.864	0.69	1.662
ENSG00000165733	**BMS1**	protein_coding	-1.863	0.724	1.662
ENSG00000260413	**ENSG00000260413**	transcribed_unprocessed_	-1.863	0.686	1.662
ENSG00000259051	**HNRNPUP1**	processed_pseudogene	-1.862	0.75	1.662
ENSG00000155858	**LSM11**	protein_coding	-1.862	0.731	1.662
ENSG00000038532	**CLEC16A**	protein_coding	-1.861	0.75	1.662
ENSG00000180667	**YOD1**	protein_coding	-1.861	0.742	1.662
ENSG00000153310	**CYRIB**	protein_coding	-1.86	0.755	1.662
ENSG00000148843	**PDCD11**	protein_coding	-1.857	0.748	1.662
ENSG00000156026	**MCU**	protein_coding	-1.856	0.709	1.662
ENSG00000137504	**CREBZF**	protein_coding	-1.855	0.746	1.662
ENSG00000140299	**BNIP2**	protein_coding	-1.854	0.71	1.662
ENSG00000179912	**R3HDM2**	protein_coding	-1.854	0.709	1.662
ENSG00000147604	**RPL7**	protein_coding	-1.854	0.722	1.662
ENSG00000167978	**SRRM2**	protein_coding	-1.854	0.74	1.662
ENSG00000248503	**ENSG00000248503**	transcribed_processed_ps	-1.854	0.628	1.662
ENSG00000243806	**RPL7P18**	processed_pseudogene	-1.853	0.729	1.662
ENSG00000254240	**IGLVI-20**	IG_V_pseudogene	-1.852	0.725	1.662
ENSG00000255088	**ENSG00000255088**	processed_pseudogene	-1.852	0.614	1.662
ENSG00000083857	**FAT1**	protein_coding	-1.85	0.682	1.662
ENSG00000162441	**LZIC**	protein_coding	-1.85	0.697	1.662
ENSG00000261072	**ENSG00000261072**	processed_pseudogene	-1.85	0.617	1.662
ENSG00000181690	**PLAG1**	protein_coding	-1.849	0.737	1.662
ENSG00000101868	**POLA1**	protein_coding	-1.848	0.755	1.662
ENSG00000076382	**SPAG5**	protein_coding	-1.848	0.757	1.662

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000138036	**DYNC2LI1**	protein_coding	-1.847	0.7	1.662
ENSG00000143797	**MBOAT2**	protein_coding	-1.847	0.719	1.662
ENSG00000207168	**SNORA15**	snoRNA	-1.847	0.641	1.662
ENSG00000127362	**TAS2R3**	protein_coding	-1.847	0.696	1.662
ENSG00000221944	**TIGD1**	protein_coding	-1.847	0.671	1.662
ENSG00000128915	**ICE2**	protein_coding	-1.846	0.751	1.662
ENSG00000170345	**FOS**	protein_coding	-1.844	0.693	1.662
ENSG00000050426	**LETMD1**	protein_coding	-1.843	0.731	1.662
ENSG00000136875	**PRPF4**	protein_coding	-1.843	0.725	1.662
ENSG00000236287	**ZBED5**	protein_coding	-1.842	0.739	1.662
ENSG00000163719	**MTMR14**	protein_coding	-1.841	0.747	1.662
ENSG00000119396	**RAB14**	protein_coding	-1.841	0.727	1.662
ENSG00000271134	**IFITM3P9**	processed_pseudogene	-1.84	0.72	1.662
ENSG00000196981	**WDR5B**	protein_coding	-1.84	0.728	1.662
ENSG00000084710	**EFR3B**	protein_coding	-1.838	0.737	1.662
ENSG00000283677	**MIR3913-2**	miRNA	-1.838	0.666	1.662
ENSG00000072401	**UBE2D1**	protein_coding	-1.837	0.705	1.662
ENSG00000074356	**NCBP3**	protein_coding	-1.836	0.713	1.662
ENSG00000104738	**MCM4**	protein_coding	-1.835	0.752	1.662
ENSG00000269189	**ENSG00000269189**	lncRNA	-1.834	0.588	1.662
ENSG00000119522	**DENND1A**	protein_coding	-1.833	0.737	1.662
ENSG00000117862	**TXNDC12**	protein_coding	-1.831	0.746	1.662
ENSG00000138182	**KIF20B**	protein_coding	-1.829	0.711	1.662
ENSG00000156136	**DCK**	protein_coding	-1.828	0.703	1.662
ENSG00000160606	**TLCD1**	protein_coding	-1.828	0.703	1.662
ENSG00000275580	**ENSG00000275580**	lncRNA	-1.828	0.64	1.662
ENSG00000265102	**MIR3942**	miRNA	-1.827	0.666	1.662
ENSG00000171867	**PRNP**	protein_coding	-1.827	0.715	1.662
ENSG00000162129	**CLPB**	protein_coding	-1.826	0.746	1.662
ENSG00000235454	**HAUS6P3**	processed_pseudogene	-1.825	0.594	1.662
ENSG00000133704	**IPO8**	protein_coding	-1.825	0.743	1.662
ENSG00000166889	**PATL1**	protein_coding	-1.825	0.755	1.662
ENSG00000116750	**UCHL5**	protein_coding	-1.825	0.739	1.662
ENSG00000268565	**ENSG00000268565**	lncRNA	-1.825	0.709	1.662
ENSG00000001561	**ENPP4**	protein_coding	-1.824	0.755	1.662
ENSG00000136937	**NCBP1**	protein_coding	-1.824	0.736	1.662
ENSG00000135763	**URB2**	protein_coding	-1.824	0.74	1.662
ENSG00000284719	**ENSG00000284719**	lncRNA	-1.824	0.7	1.662
ENSG00000286085	**ENSG00000286085**	lncRNA	-1.822	0.673	1.662
ENSG00000086475	**SEPHS1**	protein_coding	-1.821	0.751	1.662
ENSG00000218418	**ENSG00000218418**	processed_pseudogene	-1.821	0.631	1.662
ENSG00000180957	**PITPNB**	protein_coding	-1.82	0.75	1.662
ENSG00000280207	**ENSG00000280207**	lncRNA	-1.82	0.665	1.662
ENSG00000123066	**MED13L**	protein_coding	-1.819	0.756	1.662
ENSG00000047644	**WWC3**	protein_coding	-1.819	0.729	1.662
ENSG00000073464	**CLCN4**	protein_coding	-1.817	0.749	1.662
ENSG00000143669	**LYST**	protein_coding	-1.817	0.765	1.662
ENSG00000147548	**NSD3**	protein_coding	-1.817	0.741	1.662
ENSG00000104356	**POP1**	protein_coding	-1.817	0.761	1.662

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000099942	**CRKL**	protein_coding	-1.816	0.719	1.662
ENSG00000279960	**ENSG00000279960**	TEC	-1.815	0.598	1.662
ENSG00000204387	**SNHG32**	lncRNA	-1.814	0.751	1.662
ENSG00000147124	**ZNF41**	protein_coding	-1.813	0.718	1.662
ENSG00000135749	**PCNX2**	protein_coding	-1.812	0.745	1.662
ENSG00000268089	**GABRQ**	protein_coding	-1.811	0.716	1.662
ENSG00000164190	**NIPBL**	protein_coding	-1.81	0.737	1.662
ENSG00000034693	**PEX3**	protein_coding	-1.81	0.756	1.662
ENSG00000142583	**SLC2A5**	protein_coding	-1.81	0.72	1.662
ENSG00000225701	**EIF4A1P13**	processed_pseudogene	-1.809	0.685	1.662
ENSG00000263001	**GTF2I**	protein_coding	-1.809	0.759	1.662
ENSG00000135679	**MDM2**	protein_coding	-1.809	0.723	1.662
ENSG00000178694	**NSUN3**	protein_coding	-1.809	0.732	1.662
ENSG00000115282	**TTC31**	protein_coding	-1.809	0.721	1.662
ENSG00000204778	**CBWD4P**	unprocessed_pseudogene	-1.808	0.295	1.662
ENSG00000135677	**GNS**	protein_coding	-1.808	0.752	1.662
ENSG00000248508	**SRP14-AS1**	lncRNA	-1.808	0.709	1.662
ENSG00000148516	**ZEB1**	protein_coding	-1.807	0.751	1.662
ENSG00000170100	**ZNF778**	protein_coding	-1.807	0.744	1.662
ENSG00000095261	**PSMD5**	protein_coding	-1.806	0.748	1.662
ENSG00000262815	**ENSG00000262815**	lncRNA	-1.806	0.574	1.662
ENSG00000185658	**BRWD1**	protein_coding	-1.804	0.737	1.662
ENSG00000184293	**CLECL1**	protein_coding	-1.804	0.696	1.662
ENSG00000214185	**XPOTP1**	processed_pseudogene	-1.804	0.665	1.662
ENSG00000273243	**ENSG00000273243**	lncRNA	-1.804	0.653	1.662
ENSG00000275576	**ENSG00000275576**	lncRNA	-1.804	0.681	1.662
ENSG00000135966	**TGFBRAP1**	protein_coding	-1.803	0.763	1.662
ENSG00000224707	**E2F3-IT1**	lncRNA	-1.802	0.686	1.662
ENSG00000141027	**NCOR1**	protein_coding	-1.802	0.742	1.662
ENSG00000206852	**RNU6-895P**	snRNA	-1.802	0.733	1.662
ENSG00000135040	**NAA35**	protein_coding	-1.801	0.721	1.662
ENSG00000162885	**B3GALNT2**	protein_coding	-1.8	0.741	1.662
ENSG00000135452	**TSPAN31**	protein_coding	-1.8	0.699	1.662
ENSG00000122952	**ZWINT**	protein_coding	-1.8	0.721	1.662
ENSG00000252840	**ENSG00000252840**	snoRNA	-1.8	0.61	1.662
ENSG00000116005	**PCYOX1**	protein_coding	-1.798	0.753	1.662
ENSG00000166233	**ARIH1**	protein_coding	-1.797	0.761	1.662
ENSG00000229752	**RPL7P10**	processed_pseudogene	-1.797	0.612	1.662
ENSG00000139597	**N4BP2L1**	protein_coding	-1.796	0.683	1.662
ENSG00000207815	**MIR563**	miRNA	-1.794	0.623	1.662
ENSG00000276712	**MIR7111**	miRNA	-1.794	0.687	1.662
ENSG00000122126	**OCRL**	protein_coding	-1.794	0.736	1.662
ENSG00000104067	**TJP1**	protein_coding	-1.793	0.736	1.662
ENSG00000204745	**ENSG00000204745**	unprocessed_pseudogene	-1.792	0.722	1.662
ENSG00000261451	**ENSG00000261451**	lncRNA	-1.792	0.723	1.662
ENSG00000155974	**GRIP1**	protein_coding	-1.79	0.749	1.662
ENSG00000071051	**NCK2**	protein_coding	-1.79	0.719	1.662
ENSG00000277687	**ENSG00000277687**	lncRNA	-1.79	0.67	1.662
ENSG00000148672	**GLUD1**	protein_coding	-1.789	0.753	1.662

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000170248	**PDCD6IP**	protein_coding	-1.789	0.721	1.662
ENSG00000156011	**PSD3**	protein_coding	-1.789	0.751	1.662
ENSG00000122042	**UBL3**	protein_coding	-1.789	0.718	1.662
ENSG00000102786	**INTS6**	protein_coding	-1.788	0.749	1.662
ENSG00000095397	**WHRN**	protein_coding	-1.788	0.745	1.662
ENSG00000165355	**FBXO33**	protein_coding	-1.786	0.69	1.662
ENSG00000140015	**KCNH5**	protein_coding	-1.784	0.683	1.662
ENSG00000141252	**VPS53**	protein_coding	-1.784	0.744	1.662
ENSG00000156384	**SFR1**	protein_coding	-1.782	0.677	1.662
ENSG00000135913	**USP37**	protein_coding	-1.782	0.733	1.662
ENSG00000250442	**EIF3KP3**	processed_pseudogene	-1.781	0.669	1.662
ENSG00000119969	**HELLS**	protein_coding	-1.781	0.709	1.662
ENSG00000091157	**WDR7**	protein_coding	-1.781	0.761	1.662
ENSG00000114744	**COMMD2**	protein_coding	-1.779	0.736	1.662
ENSG00000280069	**ENSG00000280069**	TEC	-1.779	0.67	1.662
ENSG00000124496	**TRERF1**	protein_coding	-1.778	0.756	1.662
ENSG00000273294	**C1QTNF3-AMACR**	protein_coding	-1.777	0.663	1.662
ENSG00000041880	**PARP3**	protein_coding	-1.777	0.759	1.662
ENSG00000162402	**USP24**	protein_coding	-1.777	0.755	1.662
ENSG00000259562	**ENSG00000259562**	transcribed_processed_ps	-1.777	0.653	1.662
ENSG00000273437	**ENSG00000273437**	lncRNA	-1.777	0.663	1.662
ENSG00000125962	**ARMCX5**	protein_coding	-1.776	0.674	1.662
ENSG00000082438	**COBLL1**	protein_coding	-1.775	0.734	1.662
ENSG00000137269	**LRRC1**	protein_coding	-1.775	0.757	1.662
ENSG00000015676	**NUDCD3**	protein_coding	-1.775	0.737	1.662
ENSG00000133026	**MYH10**	protein_coding	-1.774	0.741	1.662
ENSG00000158615	**PPP1R15B**	protein_coding	-1.774	0.73	1.662
ENSG00000180773	**SLC36A4**	protein_coding	-1.773	0.75	1.662
ENSG00000115993	**TRAK2**	protein_coding	-1.773	0.761	1.662
ENSG00000280206	**ENSG00000280206**	lncRNA	-1.773	0.698	1.662
ENSG00000198740	**ZNF652**	protein_coding	-1.772	0.733	1.662
ENSG00000121644	**DESI2**	protein_coding	-1.771	0.744	1.662
ENSG00000146276	**GABRR1**	protein_coding	-1.771	0.767	1.662
ENSG00000225871	**ENSG00000225871**	processed_pseudogene	-1.771	0.634	1.662
ENSG00000255521	**ENSG00000255521**	lncRNA	-1.771	0.677	1.662
ENSG00000228294	**BMS1P17**	transcribed_unprocessed_	-1.77	0.68	1.662
ENSG00000088387	**DOCK9**	protein_coding	-1.77	0.767	1.662
ENSG00000136122	**BORA**	protein_coding	-1.769	0.731	1.662
ENSG00000214354	**PAFAH1B1P1**	processed_pseudogene	-1.769	0.614	1.662
ENSG00000276688	**ENSG00000276688**	lncRNA	-1.769	0.727	1.662
ENSG00000142149	**HUNK**	protein_coding	-1.768	0.705	1.662
ENSG00000252391	**RNU6-638P**	snRNA	-1.768	0.655	1.662
ENSG00000146414	**SHPRH**	protein_coding	-1.767	0.754	1.662
ENSG00000278332	**ENSG00000278332**	processed_pseudogene	-1.767	0.729	1.662
ENSG00000188321	**ZNF559**	protein_coding	-1.766	0.709	1.662
ENSG00000237321	**ENSG00000237321**	lncRNA	-1.766	0.733	1.662
ENSG00000168137	**SETD5**	protein_coding	-1.765	0.75	1.662
ENSG00000256019	**TAS2R63P**	unprocessed_pseudogene	-1.765	0.657	1.662
ENSG00000279481	**ENSG00000279481**	TEC	-1.765	0.627	1.662

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000285603	**ENSG00000285603**	lncRNA	-1.765	0.678	1.662
ENSG00000145736	**GTF2H2**	protein_coding	-1.763	0.7	1.662
ENSG00000166451	**CENPN**	protein_coding	-1.762	0.742	1.662
ENSG00000226359	**ACTG1P24**	processed_pseudogene	-1.761	0.671	1.662
ENSG00000228816	**AK3P5**	processed_pseudogene	-1.761	0.643	1.662
ENSG00000107669	**ATE1**	protein_coding	-1.759	0.757	1.662
ENSG00000175115	**PACS1**	protein_coding	-1.758	0.759	1.662
ENSG00000168813	**ZNF507**	protein_coding	-1.758	0.744	1.662
ENSG00000280405	**ENSG00000280405**	TEC	-1.757	0.696	1.662
ENSG00000119820	**YIPF4**	protein_coding	-1.756	0.769	1.662
ENSG00000151422	**FER**	protein_coding	-1.755	0.741	1.662
ENSG00000240622	**RPL7P15**	processed_pseudogene	-1.755	0.633	1.662
ENSG00000084073	**ZMPSTE24**	protein_coding	-1.755	0.75	1.662
ENSG00000183814	**LIN9**	protein_coding	-1.754	0.766	1.662
ENSG00000197857	**ZNF44**	protein_coding	-1.754	0.748	1.662
ENSG00000206926	**RNU6-1024P**	snRNA	-1.753	0.46	1.662
ENSG00000207443	**RNU6-417P**	snRNA	-1.753	0.734	1.662
ENSG00000250432	**FAM242C**	lncRNA	-1.751	0.662	1.662
ENSG00000143363	**PRUNE1**	protein_coding	-1.749	0.744	1.662
ENSG00000084234	**APLP2**	protein_coding	-1.748	0.753	1.662
ENSG00000047621	**C12orf4**	protein_coding	-1.747	0.748	1.662
ENSG00000163808	**KIF15**	protein_coding	-1.747	0.727	1.662
ENSG00000177034	**MTX3**	protein_coding	-1.747	0.71	1.662
ENSG00000146350	**TBC1D32**	protein_coding	-1.747	0.741	1.662
ENSG00000261684	**ENSG00000261684**	lncRNA	-1.747	0.592	1.662
ENSG00000267787	**ENSG00000267787**	lncRNA	-1.746	0.667	1.662
ENSG00000201658	**RNU6-283P**	snRNA	-1.744	0.674	1.662
ENSG00000237819	**CDK6-AS1**	lncRNA	-1.743	0.741	1.662
ENSG00000241058	**NSUN6**	protein_coding	-1.743	0.743	1.662
ENSG00000206629	**RNU1-63P**	snRNA	-1.743	0.588	1.662
ENSG00000235090	**RPL7L1P3**	processed_pseudogene	-1.742	0.691	1.662
ENSG00000175063	**UBE2C**	protein_coding	-1.742	0.744	1.662
ENSG00000173275	**ZNF449**	protein_coding	-1.742	0.742	1.662
ENSG00000288098	**ENSG00000288098**	lncRNA	-1.742	0.72	1.662
ENSG00000159322	**ADPGK**	protein_coding	-1.74	0.746	1.662
ENSG00000105810	**CDK6**	protein_coding	-1.739	0.773	1.662
ENSG00000120948	**TARDBP**	protein_coding	-1.739	0.754	1.662
ENSG00000141556	**TBCD**	protein_coding	-1.739	0.757	1.662
ENSG00000170006	**TMEM154**	protein_coding	-1.739	0.702	1.662
ENSG00000169372	**CRADD**	protein_coding	-1.738	0.76	1.662
ENSG00000100528	**CNIH1**	protein_coding	-1.737	0.76	1.662
ENSG00000053254	**FOXN3**	protein_coding	-1.737	0.763	1.662
ENSG00000108883	**EFTUD2**	protein_coding	-1.736	0.762	1.662
ENSG00000135372	**NAT10**	protein_coding	-1.736	0.751	1.662
ENSG00000196367	**TRRAP**	protein_coding	-1.735	0.755	1.662
ENSG00000172943	**PHF8**	protein_coding	-1.734	0.751	1.662
ENSG00000249125	**ENSG00000249125**	lncRNA	-1.734	0.66	1.662
ENSG00000267041	**ZNF850**	protein_coding	-1.733	0.748	1.662
ENSG00000074800	**ENO1**	protein_coding	-1.732	0.766	1.662

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000213931	**HBE1**	protein_coding	-1.732	0.511	1.662
ENSG00000271601	**LIX1L**	protein_coding	-1.732	0.753	1.662
ENSG00000173039	**RELA**	protein_coding	-1.732	0.728	1.662
ENSG00000138336	**TET1**	protein_coding	-1.731	0.75	1.662
ENSG00000038382	**TRIO**	protein_coding	-1.731	0.748	1.662
ENSG00000226642	**ACTG1P12**	processed_pseudogene	-1.73	0.617	1.662
ENSG00000158169	**FANCC**	protein_coding	-1.73	0.716	1.662
ENSG00000119509	**INVS**	protein_coding	-1.73	0.78	1.662
ENSG00000164109	**MAD2L1**	protein_coding	-1.73	0.722	1.662
ENSG00000056277	**ZNF280C**	protein_coding	-1.729	0.751	1.662
ENSG00000217495	**ENSG00000217495**	processed_pseudogene	-1.728	0.646	1.662
ENSG00000287513	**ENSG00000287513**	lncRNA	-1.728	0.628	1.662
ENSG00000182150	**ERCC6L2**	protein_coding	-1.728	0.727	2.511
ENSG00000252431	**RNU6-1247P**	snRNA	-1.728	0.673	2.511
ENSG00000198231	**DDX42**	protein_coding	-1.727	0.763	2.511
ENSG00000027001	**MIPEP**	protein_coding	-1.727	0.741	2.511
ENSG00000140829	**DHX38**	protein_coding	-1.726	0.765	2.511
ENSG00000068097	**HEATR6**	protein_coding	-1.726	0.731	2.511
ENSG00000284032	**MIR29A**	miRNA	-1.726	0.606	2.511
ENSG00000260142	**ENSG00000260142**	lncRNA	-1.726	0.658	2.511
ENSG00000143207	**COP1**	protein_coding	-1.725	0.746	2.511
ENSG00000275854	**ENSG00000275854**	lncRNA	-1.725	0.614	2.511
ENSG00000241685	**ARPC1A**	protein_coding	-1.724	0.728	2.511
ENSG00000141219	**C17orf80**	protein_coding	-1.723	0.742	2.511
ENSG00000134769	**DTNA**	protein_coding	-1.723	0.768	2.511
ENSG00000085760	**MTIF2**	protein_coding	-1.723	0.733	2.511
ENSG00000171763	**SPATA5L1**	protein_coding	-1.723	0.734	2.511
ENSG00000171960	**PPIH**	protein_coding	-1.722	0.728	2.511
ENSG00000272072	**ENSG00000272072**	lncRNA	-1.722	0.569	2.511
ENSG00000276517	**ENSG00000276517**	lncRNA	-1.722	0.702	2.511
ENSG00000029364	**SLC39A9**	protein_coding	-1.721	0.767	2.511
ENSG00000048740	**CELF2**	protein_coding	-1.72	0.767	2.511
ENSG00000144840	**RABL3**	protein_coding	-1.72	0.729	2.511
ENSG00000123485	**HJURP**	protein_coding	-1.719	0.741	2.511
ENSG00000112893	**MAN2A1**	protein_coding	-1.718	0.746	2.511
ENSG00000115750	**TAF1B**	protein_coding	-1.717	0.744	2.511
ENSG00000268235	**TCP11X1**	protein_coding	-1.717	0.503	2.511
ENSG00000145375	**SPATA5**	protein_coding	-1.716	0.78	2.511
ENSG00000177410	**ZFAS1**	lncRNA	-1.716	0.764	2.511
ENSG00000287981	**ENSG00000287981**	lncRNA	-1.716	0.597	2.511
ENSG00000114098	**ARMC8**	protein_coding	-1.714	0.759	2.511
ENSG00000068654	**POLR1A**	protein_coding	-1.714	0.762	2.511
ENSG00000253467	**IGHV7-40**	IG_V_pseudogene	-1.713	0.699	2.511
ENSG00000173660	**UQCRH**	protein_coding	-1.713	0.753	2.511
ENSG00000185862	**EVI2B**	protein_coding	-1.711	0.708	2.511
ENSG00000241218	**CSP2**	processed_pseudogene	-1.71	0.741	2.511
ENSG00000162408	**NOL9**	protein_coding	-1.71	0.756	2.511
ENSG00000163406	**SLC15A2**	protein_coding	-1.71	0.76	2.511
ENSG00000127481	**UBR4**	protein_coding	-1.709	0.771	2.511

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000237666	**ENSG00000237666**	unprocessed_pseudogene	-1.709	0.529	2.511
ENSG00000177479	**ARIH2**	protein_coding	-1.708	0.757	2.511
ENSG00000182963	**GJC1**	protein_coding	-1.708	0.734	2.511
ENSG00000172167	**MTBP**	protein_coding	-1.707	0.736	2.511
ENSG00000266173	**STRADA**	protein_coding	-1.706	0.77	2.511
ENSG00000267463	**UBE2V2P2**	processed_pseudogene	-1.706	0.708	2.511
ENSG00000275004	**ZNF280B**	protein_coding	-1.706	0.756	2.511
ENSG00000227515	**C1DP4**	processed_pseudogene	-1.705	0.611	2.511
ENSG00000135052	**GOLM1**	protein_coding	-1.705	0.734	2.511
ENSG00000012174	**MBTPS2**	protein_coding	-1.705	0.757	2.511
ENSG00000156642	**NPTN**	protein_coding	-1.705	0.726	2.511
ENSG00000266365	**ENSG00000266365**	unprocessed_pseudogene	-1.705	0.585	2.511
ENSG00000065150	**IPO5**	protein_coding	-1.703	0.781	2.511
ENSG00000214846	**ENSG00000214846**	processed_pseudogene	-1.703	0.73	2.511
ENSG00000279410	**ENSG00000279410**	TEC	-1.703	0.631	2.511
ENSG00000286122	**ENSG00000286122**	lncRNA	-1.703	0.609	2.511
ENSG00000187325	**TAF9B**	protein_coding	-1.702	0.746	2.511
ENSG00000286400	**ENSG00000286400**	lncRNA	-1.702	0.659	2.511
ENSG00000189079	**ARID2**	protein_coding	-1.701	0.783	2.511
ENSG00000169905	**TOR1AIP2**	protein_coding	-1.7	0.784	2.511
ENSG00000113812	**ACTR8**	protein_coding	-1.699	0.777	2.511
ENSG00000091039	**OSBPL8**	protein_coding	-1.699	0.757	2.511
ENSG00000165312	**OTUD1**	protein_coding	-1.699	0.661	2.511
ENSG00000226823	**SUGT1P1**	unprocessed_pseudogene	-1.699	0.742	2.511
ENSG00000116127	**ALMS1**	protein_coding	-1.698	0.734	2.511
ENSG00000161960	**EIF4A1**	protein_coding	-1.698	0.769	2.511
ENSG00000177602	**HASPIN**	protein_coding	-1.698	0.706	2.511
ENSG00000161800	**RACGAP1**	protein_coding	-1.698	0.739	2.511
ENSG00000233786	**CDC27P1**	processed_pseudogene	-1.697	0.622	2.511
ENSG00000170027	**YWHAG**	protein_coding	-1.697	0.748	2.511
ENSG00000260852	**FBXL19-AS1**	lncRNA	-1.696	0.718	2.511
ENSG00000107949	**BCCIP**	protein_coding	-1.695	0.76	2.511
ENSG00000150995	**ITPR1**	protein_coding	-1.695	0.776	2.511
ENSG00000136536	**MARCHF7**	protein_coding	-1.695	0.75	2.511
ENSG00000136237	**RAPGEF5**	protein_coding	-1.695	0.764	2.511
ENSG00000222430	**Y_RNA**	misc_RNA	-1.695	0.622	2.511
ENSG00000287665	**ENSG00000287665**	lncRNA	-1.695	0.482	2.511
ENSG00000232202	**CHORDC1P1**	processed_pseudogene	-1.693	0.652	2.511
ENSG00000119707	**RBM25**	protein_coding	-1.693	0.771	2.511
ENSG00000213450	**VDAC1P7**	processed_pseudogene	-1.693	0.724	2.511
ENSG00000104219	**ZDHHC2**	protein_coding	-1.692	0.765	2.511
ENSG00000252171	**Y_RNA**	misc_RNA	-1.691	0.528	2.511
ENSG00000171466	**ZNF562**	protein_coding	-1.691	0.764	2.511
ENSG00000115170	**ACVR1**	protein_coding	-1.69	0.746	2.511
ENSG00000168297	**PXK**	protein_coding	-1.69	0.726	2.511
ENSG00000205581	**HMGN1**	protein_coding	-1.689	0.757	2.511
ENSG00000071054	**MAP4K4**	protein_coding	-1.689	0.774	2.511
ENSG00000212136	**RNU6-696P**	snRNA	-1.689	0.696	2.511
ENSG00000212539	**U3**	snoRNA	-1.688	0.718	2.511

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000243072	**ENSG00000243072**	processed_pseudogene	-1.688	0.655	2.511
ENSG00000204304	**PBX2**	protein_coding	-1.687	0.77	2.511
ENSG00000240695	**ENSG00000240695**	processed_pseudogene	-1.687	0.718	2.511
ENSG00000127483	**HP1BP3**	protein_coding	-1.686	0.764	2.511
ENSG00000171492	**LRRC8D**	protein_coding	-1.686	0.774	2.511
ENSG00000232548	**LINC01809**	lncRNA	-1.685	0.708	2.511
ENSG00000185236	**RAB11B**	protein_coding	-1.685	0.738	2.511
ENSG00000100347	**SAMM50**	protein_coding	-1.685	0.753	2.511
ENSG00000234383	**CTBP2P8**	processed_pseudogene	-1.684	0.712	2.511
ENSG00000145715	**RASA1**	protein_coding	-1.684	0.746	2.511
ENSG00000264164	**ENSG00000264164**	transcribed_processed_p	-1.684	0.713	2.511
ENSG00000131966	**ACTR10**	protein_coding	-1.683	0.739	2.511
ENSG00000124177	**CHD6**	protein_coding	-1.683	0.762	2.511
ENSG00000147133	**TAF1**	protein_coding	-1.683	0.753	2.511
ENSG00000128791	**TWSG1**	protein_coding	-1.683	0.775	2.511
ENSG00000196323	**ZBTB44**	protein_coding	-1.683	0.766	2.511
ENSG00000077943	**ITGA8**	protein_coding	-1.682	0.785	2.511
ENSG00000265342	**ENSG00000265342**	lncRNA	-1.682	0.761	2.511
ENSG00000158122	**PRXL2C**	protein_coding	-1.681	0.75	2.511
ENSG00000199313	**RNU4-82P**	snRNA	-1.681	0.613	2.511
ENSG00000203995	**ZYG11A**	protein_coding	-1.681	0.775	2.511
ENSG00000092964	**DPYSL2**	protein_coding	-1.68	0.757	2.511
ENSG00000171711	**DEFB4A**	protein_coding	-1.679	0.498	2.511
ENSG00000226112	**FCF1P4**	processed_pseudogene	-1.679	0.726	2.511
ENSG00000283409	**MIR3662**	miRNA	-1.679	0.553	2.511
ENSG00000249730	**OR10J4**	polymorphic_pseudogene	-1.679	0.75	2.511
ENSG00000272130	**ENSG00000272130**	lncRNA	-1.679	0.61	2.511
ENSG00000111145	**ELK3**	protein_coding	-1.678	0.764	2.511
ENSG00000134371	**CDC73**	protein_coding	-1.677	0.772	2.511
ENSG00000243264	**IGKV2D-29**	IG_V_gene	-1.677	0.711	2.511
ENSG00000133398	**MED10**	protein_coding	-1.677	0.74	2.511
ENSG00000158864	**NDUFS2**	protein_coding	-1.677	0.772	2.511
ENSG00000214455	**RCN1P2**	processed_pseudogene	-1.677	0.605	2.511
ENSG00000244249	**ENSG00000244249**	processed_pseudogene	-1.677	0.663	2.511
ENSG00000229001	**ACTBP14**	processed_pseudogene	-1.676	0.706	2.511
ENSG00000050405	**LIMA1**	protein_coding	-1.676	0.731	2.511
ENSG00000172197	**MBOAT1**	protein_coding	-1.676	0.71	2.511
ENSG00000145779	**TNFAIP8**	protein_coding	-1.676	0.75	2.511
ENSG00000274038	**ENSG00000274038**	lncRNA	-1.676	0.575	2.511
ENSG00000109805	**NCAPG**	protein_coding	-1.675	0.752	2.511
ENSG00000108395	**TRIM37**	protein_coding	-1.675	0.769	2.511
ENSG00000100601	**ALKBH1**	protein_coding	-1.674	0.754	2.511
ENSG00000158402	**CDC25C**	protein_coding	-1.674	0.746	2.511
ENSG00000062485	**CS**	protein_coding	-1.674	0.784	2.511
ENSG00000135905	**DOCK10**	protein_coding	-1.674	0.695	2.511
ENSG00000070018	**LRP6**	protein_coding	-1.673	0.763	2.511
ENSG00000264764	**MIR4772**	miRNA	-1.673	0.684	2.511
ENSG00000255463	**ENSG00000255463**	processed_pseudogene	-1.673	0.662	2.511
ENSG00000138688	**KIAA1109**	protein_coding	-1.672	0.752	2.511

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000185737	**NRG3**	protein_coding	-1.671	0.724	2.511
ENSG00000226479	**TMEM185B**	protein_coding	-1.671	0.742	2.511
ENSG00000064419	**TNPO3**	protein_coding	-1.671	0.758	2.511
ENSG00000154217	**PITPNC1**	protein_coding	-1.67	0.748	2.511
ENSG00000152818	**UTRN**	protein_coding	-1.67	0.755	2.511
ENSG00000175832	**ETV4**	protein_coding	-1.669	0.745	2.511
ENSG00000182022	**CHST15**	protein_coding	-1.668	0.778	2.511
ENSG00000272219	**ENSG00000272219**	lncRNA	-1.668	0.58	2.511
ENSG00000287961	**ENSG00000287961**	lncRNA	-1.668	0.594	2.511
ENSG00000277829	**ENSG00000277829**	lncRNA	-1.667	0.608	2.511
ENSG00000130826	**DKC1**	protein_coding	-1.666	0.779	2.511
ENSG00000165417	**GTF2A1**	protein_coding	-1.666	0.769	2.511
ENSG00000277172	**GAPDHP41**	processed_pseudogene	-1.665	0.691	2.511
ENSG00000286561	**ENSG00000286561**	lncRNA	-1.665	0.686	2.511
ENSG00000287669	**ENSG00000287669**	lncRNA	-1.665	0.708	2.511
ENSG00000102780	**DGKH**	protein_coding	-1.664	0.768	2.511
ENSG00000139318	**DUSP6**	protein_coding	-1.664	0.767	2.511
ENSG00000138614	**INTS14**	protein_coding	-1.664	0.767	2.511
ENSG00000283188	**MIR2052**	miRNA	-1.664	0.628	2.511
ENSG00000081913	**PHLPP1**	protein_coding	-1.664	0.76	2.511
ENSG00000091009	**RBM27**	protein_coding	-1.664	0.749	2.511
ENSG00000238998	**RNU7-187P**	snRNA	-1.663	0.683	2.511
ENSG00000066382	**MPPED2**	protein_coding	-1.662	0.739	2.511
ENSG00000241765	**RPS26P45**	processed_pseudogene	-1.662	0.747	2.511
ENSG00000164118	**CEP44**	protein_coding	-1.661	0.717	2.511
ENSG00000067141	**NEO1**	protein_coding	-1.661	0.758	2.511
ENSG00000233995	**ENSG00000233995**	unprocessed_pseudogene	-1.661	0.705	2.511
ENSG00000278643	**ENSG00000278643**	misc_RNA	-1.661	0.708	2.511
ENSG00000256525	**POLG2**	protein_coding	-1.659	0.788	2.511
ENSG00000207938	**MIR511**	miRNA	-1.658	0.734	2.511
ENSG00000285918	**ENSG00000285918**	lncRNA	-1.658	0.588	2.511
ENSG00000227344	**HAUS6P1**	processed_pseudogene	-1.657	0.659	2.511
ENSG00000154975	**CA10**	protein_coding	-1.656	0.736	2.511
ENSG00000170852	**KBTBD2**	protein_coding	-1.655	0.767	2.511
ENSG00000138594	**TMOD3**	protein_coding	-1.655	0.76	2.511
ENSG00000049618	**ARID1B**	protein_coding	-1.654	0.766	2.511
ENSG00000181007	**ZFP82**	protein_coding	-1.654	0.726	2.511
ENSG00000178295	**GEN1**	protein_coding	-1.653	0.758	2.511
ENSG00000227770	**RPL7P12**	processed_pseudogene	-1.653	0.652	2.511
ENSG00000106080	**FKBP14**	protein_coding	-1.652	0.748	2.511
ENSG00000165219	**GAPVD1**	protein_coding	-1.652	0.761	2.511
ENSG00000111897	**SERINC1**	protein_coding	-1.652	0.754	2.511
ENSG00000113739	**STC2**	protein_coding	-1.652	0.74	2.511
ENSG00000096384	**HSP90AB1**	protein_coding	-1.651	0.782	2.511
ENSG00000176349	**ENSG00000176349**	lncRNA	-1.65	0.733	2.511
ENSG00000184743	**ATL3**	protein_coding	-1.649	0.768	2.511
ENSG00000041802	**LSG1**	protein_coding	-1.649	0.771	2.511
ENSG00000154124	**OTULIN**	protein_coding	-1.649	0.767	2.511
ENSG00000144736	**SHQ1**	protein_coding	-1.648	0.752	2.511

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000222529	**Y_RNA**	misc_RNA	-1.648	0.579	2.511
ENSG00000177613	**CSTF2T**	protein_coding	-1.647	0.706	2.511
ENSG00000124813	**RUNX2**	protein_coding	-1.647	0.78	2.511
ENSG00000250615	**ENSG00000250615**	lncRNA	-1.647	0.721	2.511
ENSG00000112983	**BRD8**	protein_coding	-1.645	0.76	2.511
ENSG00000263606	**CHORDC1P4**	transcribed_processed_p	-1.644	0.625	2.511
ENSG00000028137	**TNFRSF1B**	protein_coding	-1.644	0.764	2.511
ENSG00000075340	**ADD2**	protein_coding	-1.643	0.762	2.511
ENSG00000031823	**RANBP3**	protein_coding	-1.643	0.762	2.511
ENSG00000110713	**NUP98**	protein_coding	-1.641	0.78	2.511
ENSG00000079308	**TNS1**	protein_coding	-1.641	0.742	2.511
ENSG00000120694	**HSPH1**	protein_coding	-1.64	0.765	2.511
ENSG00000204574	**ABCF1**	protein_coding	-1.639	0.765	2.511
ENSG00000175376	**EIF1AD**	protein_coding	-1.639	0.758	2.511
ENSG00000047849	**MAP4**	protein_coding	-1.639	0.762	2.511
ENSG00000172840	**PDP2**	protein_coding	-1.639	0.767	2.511
ENSG00000207518	**RNU6-59P**	snRNA	-1.639	0.675	2.511
ENSG00000021776	**AQR**	protein_coding	-1.638	0.767	2.511
ENSG00000188352	**FOCAD**	protein_coding	-1.638	0.779	2.511
ENSG00000186818	**LILRB4**	protein_coding	-1.638	0.748	2.511
ENSG00000166822	**TMEM170A**	protein_coding	-1.638	0.756	2.511
ENSG00000072133	**RPS6KA6**	protein_coding	-1.637	0.743	2.511
ENSG00000122692	**SMU1**	protein_coding	-1.637	0.74	2.511
ENSG00000288235	**FAM106C**	lncRNA	-1.636	0.606	2.511
ENSG00000164151	**ICE1**	protein_coding	-1.636	0.759	2.511
ENSG00000113441	**LNPEP**	protein_coding	-1.636	0.764	2.511
ENSG00000164180	**TMEM161B**	protein_coding	-1.636	0.742	2.511
ENSG00000082516	**GEMIN5**	protein_coding	-1.634	0.766	2.511
ENSG00000175398	**OR10P1**	protein_coding	-1.633	0.751	2.511
ENSG00000232105	**RPL32P28**	processed_pseudogene	-1.633	0.754	2.511
ENSG00000206896	**RNU6-1124P**	snRNA	-1.632	0.601	2.511
ENSG00000144161	**ZC3H8**	protein_coding	-1.632	0.757	2.511
ENSG00000150477	**KIAA1328**	protein_coding	-1.631	0.737	2.511
ENSG00000146281	**PM20D2**	protein_coding	-1.631	0.755	2.511
ENSG00000179242	**CDH4**	protein_coding	-1.63	0.733	2.511
ENSG00000128829	**EIF2AK4**	protein_coding	-1.63	0.752	2.511
ENSG00000151466	**SCLT1**	protein_coding	-1.63	0.761	2.511
ENSG00000229587	**ENSG00000229587**	lncRNA	-1.63	0.715	2.511
ENSG00000230118	**ENSG00000230118**	processed_pseudogene	-1.63	0.688	2.511
ENSG00000198018	**ENTPD7**	protein_coding	-1.629	0.764	2.511
ENSG00000166225	**FRS2**	protein_coding	-1.629	0.714	2.511
ENSG00000173226	**IQCB1**	protein_coding	-1.629	0.755	2.511
ENSG00000135842	**NIBAN1**	protein_coding	-1.629	0.779	2.511
ENSG00000126860	**EVI2A**	protein_coding	-1.628	0.707	2.511
ENSG00000253030	**MIR2116**	miRNA	-1.628	0.637	2.511
ENSG00000139496	**NUP58**	protein_coding	-1.628	0.759	2.511
ENSG00000197121	**PGAP1**	protein_coding	-1.628	0.736	2.511
ENSG00000265213	**MIR3684**	miRNA	-1.627	0.683	2.511
ENSG00000055208	**TAB2**	protein_coding	-1.627	0.744	2.511

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000115365	**LANCL1**	protein_coding	-1.626	0.745	2.511
ENSG00000150712	**MTMR12**	protein_coding	-1.626	0.783	2.511
ENSG00000121064	**SCPEP1**	protein_coding	-1.626	0.789	2.511
ENSG00000199405	**SNORA1B**	snoRNA	-1.626	0.747	2.511
ENSG00000242610	**OR5BH1P**	unprocessed_pseudogene	-1.625	0.676	2.511
ENSG00000142039	**CCDC97**	protein_coding	-1.624	0.759	2.511
ENSG00000171621	**SPSB1**	protein_coding	-1.624	0.76	2.511
ENSG00000110090	**CPT1A**	protein_coding	-1.623	0.765	2.511
ENSG00000113327	**GABRG2**	protein_coding	-1.623	0.733	2.511
ENSG00000259151	**CAP2P1**	transcribed_processed_ps	-1.622	0.695	2.511
ENSG00000173456	**RNF26**	protein_coding	-1.622	0.717	2.511
ENSG00000117597	**UTP25**	protein_coding	-1.622	0.757	2.511
ENSG00000075391	**RASAL2**	protein_coding	-1.62	0.774	2.511
ENSG00000248103	**ENSG00000248103**	lncRNA	-1.62	0.727	2.511
ENSG00000259301	**ENSG00000259301**	processed_pseudogene	-1.62	0.734	2.511
ENSG00000270130	**ENSG00000270130**	lncRNA	-1.62	0.756	2.511
ENSG00000138696	**BMPR1B**	protein_coding	-1.619	0.76	2.511
ENSG00000233560	**KRT8P39**	processed_pseudogene	-1.619	0.652	2.511
ENSG00000232036	**ENSG00000232036**	processed_pseudogene	-1.619	0.744	2.511
ENSG00000197299	**BLM**	protein_coding	-1.618	0.759	2.511
ENSG00000047346	**FAM214A**	protein_coding	-1.617	0.76	2.511
ENSG00000238271	**IFNWP19**	unprocessed_pseudogene	-1.617	0.678	2.511
ENSG00000222297	**RNU6-1156P**	snRNA	-1.617	0.661	2.511
ENSG00000279348	**ENSG00000279348**	TEC	-1.617	0.627	2.511
ENSG00000185825	**BCAP31**	protein_coding	-1.616	0.767	2.511
ENSG00000107581	**EIF3A**	protein_coding	-1.616	0.772	2.511
ENSG00000186105	**LRRC70**	protein_coding	-1.616	0.689	2.511
ENSG00000207617	**MIR3074**	miRNA	-1.616	0.693	2.511
ENSG00000188580	**NKAIN2**	protein_coding	-1.616	0.716	2.511
ENSG00000113163	**CERT1**	protein_coding	-1.615	0.769	2.511
ENSG00000184922	**FMNL1**	protein_coding	-1.614	0.747	2.511
ENSG00000213090	**SCYL2P1**	processed_pseudogene	-1.614	0.675	2.511
ENSG00000273951	**ENSG00000273951**	lncRNA	-1.614	0.706	2.511
ENSG00000104442	**ARMC1**	protein_coding	-1.613	0.782	2.511
ENSG00000163714	**U2SURP**	protein_coding	-1.613	0.772	2.511
ENSG00000166669	**ATF7IP2**	protein_coding	-1.61	0.716	2.511
ENSG00000263793	**MIR3115**	miRNA	-1.61	0.679	2.511
ENSG00000112992	**NNT**	protein_coding	-1.61	0.766	2.511
ENSG00000213341	**CHUK**	protein_coding	-1.609	0.772	2.511
ENSG00000139842	**CUL4A**	protein_coding	-1.608	0.775	2.511
ENSG00000266431	**MIR5580**	miRNA	-1.608	0.691	2.511
ENSG00000065923	**SLC9A7**	protein_coding	-1.608	0.747	2.511
ENSG00000272103	**ENSG00000272103**	lncRNA	-1.608	0.69	2.511
ENSG00000156976	**EIF4A2**	protein_coding	-1.607	0.778	2.511
ENSG00000164070	**HSPA4L**	protein_coding	-1.607	0.77	2.511
ENSG00000234803	**FAM197Y2**	transcribed_unprocessed_	-1.606	0.565	2.511
ENSG00000137574	**TGS1**	protein_coding	-1.606	0.766	2.511
ENSG00000233109	**ENSG00000233109**	processed_pseudogene	-1.606	0.771	2.511
ENSG00000257000	**ENSG00000257000**	lncRNA	-1.606	0.726	2.511

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000145734	**BDP1**	protein_coding	-1.605	0.755	2.511
ENSG00000274274	**GAGE13**	protein_coding	-1.605	0.445	2.511
ENSG00000166912	**MTMR10**	protein_coding	-1.605	0.779	2.511
ENSG00000171988	**JMJD1C**	protein_coding	-1.604	0.753	2.511
ENSG00000137944	**KYAT3**	protein_coding	-1.604	0.772	2.511
ENSG00000180385	**EMC3-AS1**	transcribed_unprocessed_	-1.603	0.774	2.511
ENSG00000197081	**IGF2R**	protein_coding	-1.603	0.781	2.511
ENSG00000132326	**PER2**	protein_coding	-1.603	0.746	2.511
ENSG00000109674	**NEIL3**	protein_coding	-1.602	0.751	2.511
ENSG00000172315	**TP53RK**	protein_coding	-1.601	0.755	2.511
ENSG00000160710	**ADAR**	protein_coding	-1.6	0.758	2.511
ENSG00000234282	**ENSG00000234282**	unprocessed_pseudogene	-1.6	0.709	2.511
ENSG00000058673	**ZC3H11A**	protein_coding	-1.598	0.743	2.511
ENSG00000168014	**C2CD3**	protein_coding	-1.597	0.775	2.511
ENSG00000162923	**WDR26**	protein_coding	-1.597	0.772	2.511
ENSG00000177311	**ZBTB38**	protein_coding	-1.596	0.766	2.511
ENSG00000261087	**ZNNT1**	lncRNA	-1.596	0.726	2.511
ENSG00000111665	**CDCA3**	protein_coding	-1.595	0.759	2.511
ENSG00000207468	**SNORA19**	snoRNA	-1.595	0.696	2.511
ENSG00000279265	**ENSG00000279265**	TEC	-1.595	0.623	2.511
ENSG00000140443	**IGF1R**	protein_coding	-1.594	0.764	2.511
ENSG00000252887	**RNU6-430P**	snRNA	-1.594	0.683	2.511
ENSG00000185278	**ZBTB37**	protein_coding	-1.594	0.751	2.511
ENSG00000259863	**SH3RF3-AS1**	lncRNA	-1.593	0.69	2.511
ENSG00000256981	**ENSG00000256981**	unprocessed_pseudogene	-1.593	0.671	2.511
ENSG00000267749	**ENSG00000267749**	lncRNA	-1.593	0.67	2.511
ENSG00000100350	**FOXRED2**	protein_coding	-1.592	0.749	2.511
ENSG00000100722	**ZC3H14**	protein_coding	-1.592	0.796	2.511
ENSG00000112031	**MTRF1L**	protein_coding	-1.591	0.748	2.511
ENSG00000151692	**RNF144A**	protein_coding	-1.591	0.763	2.511
ENSG00000207092	**Y_RNA**	misc_RNA	-1.591	0.611	2.511
ENSG00000255893	**ENSG00000255893**	lncRNA	-1.591	0.695	2.511
ENSG00000183530	**PRR14L**	protein_coding	-1.59	0.742	2.511
ENSG00000118503	**TNFAIP3**	protein_coding	-1.59	0.771	2.511
ENSG00000138768	**USO1**	protein_coding	-1.59	0.769	2.511
ENSG00000204516	**MICB**	protein_coding	-1.589	0.758	2.511
ENSG00000236229	**VEZF1P1**	processed_pseudogene	-1.589	0.706	2.511
ENSG00000188177	**ZC3H6**	protein_coding	-1.589	0.76	2.511
ENSG00000197714	**ZNF460**	protein_coding	-1.589	0.752	2.511
ENSG00000260865	**ENSG00000260865**	transcribed_processed_ps	-1.589	0.703	2.511
ENSG00000271778	**ENSG00000271778**	lncRNA	-1.588	0.617	2.511
ENSG00000275361	**ENSG00000275361**	unprocessed_pseudogene	-1.588	0.741	2.511
ENSG00000110906	**KCTD10**	protein_coding	-1.587	0.743	2.511
ENSG00000100030	**MAPK1**	protein_coding	-1.587	0.771	2.511
ENSG00000184787	**UBE2G2**	protein_coding	-1.587	0.775	2.511
ENSG00000138629	**UBL7**	protein_coding	-1.587	0.755	2.511
ENSG00000206144	**MAPK6P1**	processed_pseudogene	-1.586	0.775	2.511
ENSG00000168003	**SLC3A2**	protein_coding	-1.586	0.778	2.511
ENSG00000176142	**TMEM39A**	protein_coding	-1.586	0.783	2.511

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000118620	**ZNF430**	protein_coding	-1.586	0.733	2.511
ENSG00000213186	**TRIM59**	protein_coding	-1.585	0.764	2.511
ENSG00000123200	**ZC3H13**	protein_coding	-1.585	0.752	2.511
ENSG00000133111	**RFXAP**	protein_coding	-1.584	0.752	2.511
ENSG00000264503	**ENSG00000264503**	processed_pseudogene	-1.584	0.577	2.511
ENSG00000188312	**CENPP**	protein_coding	-1.583	0.787	2.511
ENSG00000136560	**TANK**	protein_coding	-1.583	0.749	2.511
ENSG00000105939	**ZC3HAV1**	protein_coding	-1.583	0.78	2.511
ENSG00000239969	**ENSG00000239969**	transcribed_unprocessed_	-1.583	0.522	2.511
ENSG00000225210	**DUXAP9**	transcribed_processed_ps	-1.581	0.68	2.511
ENSG00000091436	**MAP3K20**	protein_coding	-1.581	0.768	2.511
ENSG00000185619	**PCGF3**	protein_coding	-1.581	0.747	2.511
ENSG00000239653	**PSMD6-AS2**	lncRNA	-1.579	0.721	2.511
ENSG00000108963	**DPH1**	protein_coding	-1.578	0.787	2.511
ENSG00000152133	**GPATCH11**	protein_coding	-1.578	0.771	2.511
ENSG00000232077	**LINC01031**	lncRNA	-1.578	0.76	2.511
ENSG00000207444	**SNORD56B**	snoRNA	-1.578	0.686	2.511
ENSG00000142207	**URB1**	protein_coding	-1.578	0.768	2.511
ENSG00000273284	**ENSG00000273284**	lncRNA	-1.578	0.649	2.511
ENSG00000165521	**EML5**	protein_coding	-1.577	0.777	2.511
ENSG00000136925	**TSTD2**	protein_coding	-1.577	0.759	2.511
ENSG00000249006	**ENSG00000249006**	processed_pseudogene	-1.577	0.716	2.511
ENSG00000258081	**ENSG00000258081**	lncRNA	-1.577	0.775	2.511
ENSG00000097007	**ABL1**	protein_coding	-1.576	0.754	2.511
ENSG00000165813	**CCDC186**	protein_coding	-1.576	0.757	2.511
ENSG00000258065	**ENSG00000258065**	processed_pseudogene	-1.576	0.7	2.511
ENSG00000260816	**ENSG00000260816**	lncRNA	-1.576	0.595	2.511
ENSG00000279659	**ENSG00000279659**	TEC	-1.576	0.733	2.511
ENSG00000155111	**CDK19**	protein_coding	-1.575	0.749	2.511
ENSG00000108439	**PNPO**	protein_coding	-1.575	0.775	2.511
ENSG00000146112	**PPP1R18**	protein_coding	-1.575	0.727	2.511
ENSG00000116455	**WDR77**	protein_coding	-1.574	0.77	2.511
ENSG00000150764	**DIXDC1**	protein_coding	-1.573	0.773	2.511
ENSG00000280016	**ENSG00000280016**	TEC	-1.573	0.707	2.511
ENSG00000287932	**ENSG00000287932**	lncRNA	-1.573	0.75	2.511
ENSG00000136238	**RAC1**	protein_coding	-1.572	0.771	2.511
ENSG00000248774	**ENSG00000248774**	lncRNA	-1.571	0.629	2.511
ENSG00000244509	**APOBEC3C**	protein_coding	-1.57	0.777	2.511
ENSG00000146085	**MMUT**	protein_coding	-1.57	0.751	2.511
ENSG00000279235	**ENSG00000279235**	TEC	-1.57	0.698	2.511
ENSG00000156162	**DPY19L4**	protein_coding	-1.568	0.745	2.511
ENSG00000211455	**STK38L**	protein_coding	-1.568	0.777	2.511
ENSG00000078687	**TNRC6C**	protein_coding	-1.568	0.746	2.511
ENSG00000166226	**CCT2**	protein_coding	-1.567	0.797	2.511
ENSG00000276550	**HERC2P2**	transcribed_unprocessed_	-1.566	0.743	2.511
ENSG00000138600	**SPPL2A**	protein_coding	-1.565	0.759	2.511
ENSG00000280279	**LINC02887**	lncRNA	-1.564	0.735	2.511
ENSG00000163939	**PBRM1**	protein_coding	-1.564	0.799	2.511
ENSG00000162927	**PUS10**	protein_coding	-1.564	0.766	2.511

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000139131	**YARS2**	protein_coding	-1.564	0.766	2.511
ENSG00000287546	**ENSG00000287546**	lncRNA	-1.564	0.679	2.511
ENSG00000275318	**ENSG00000275318**	unprocessed_pseudogene	-1.563	0.564	2.511
ENSG00000136518	**ACTL6A**	protein_coding	-1.562	0.773	2.511
ENSG00000232827	**LINC01189**	lncRNA	-1.562	0.662	2.511
ENSG00000182199	**SHMT2**	protein_coding	-1.562	0.782	2.511
ENSG00000224162	**UQCRHP3**	processed_pseudogene	-1.562	0.682	2.511
ENSG00000163568	**AIM2**	protein_coding	-1.561	0.762	2.511
ENSG00000114302	**PRKAR2A**	protein_coding	-1.561	0.783	2.511
ENSG00000225703	**ENSG00000225703**	lncRNA	-1.561	0.609	2.511
ENSG00000286362	**ENSG00000286362**	lncRNA	-1.561	0.699	2.511
ENSG00000123570	**RAB9B**	protein_coding	-1.56	0.76	2.511
ENSG00000239473	**RPL7P38**	processed_pseudogene	-1.558	0.754	2.511
ENSG00000197860	**SGTB**	protein_coding	-1.558	0.788	4.003
ENSG00000149182	**ARFGAP2**	protein_coding	-1.557	0.774	4.003
ENSG00000155393	**HEATR3**	protein_coding	-1.557	0.786	4.003
ENSG00000109111	**SUPT6H**	protein_coding	-1.557	0.771	4.003
ENSG00000114491	**UMPS**	protein_coding	-1.557	0.781	4.003
ENSG00000081181	**ARG2**	protein_coding	-1.556	0.767	4.003
ENSG00000140525	**FANCI**	protein_coding	-1.555	0.781	4.003
ENSG00000181752	**OR8K5**	protein_coding	-1.555	0.725	4.003
ENSG00000234109	**RPL7P36**	processed_pseudogene	-1.555	0.684	4.003
ENSG00000256684	**LINC02737**	lncRNA	-1.554	0.77	4.003
ENSG00000169327	**OR5AU1**	protein_coding	-1.554	0.674	4.003
ENSG00000252644	**RNU7-30P**	snRNA	-1.554	0.451	4.003
ENSG00000269918	**ENSG00000269918**	lncRNA	-1.554	0.777	4.003
ENSG00000100473	**COCH**	protein_coding	-1.552	0.734	4.003
ENSG00000228485	**GRK5-IT1**	lncRNA	-1.552	0.709	4.003
ENSG00000003056	**M6PR**	protein_coding	-1.552	0.759	4.003
ENSG00000160199	**PKNOX1**	protein_coding	-1.552	0.792	4.003
ENSG00000131626	**PPFIA1**	protein_coding	-1.552	0.772	4.003
ENSG00000104331	**BPNT2**	protein_coding	-1.551	0.793	4.003
ENSG00000261628	**ENSG00000261628**	unprocessed_pseudogene	-1.551	0.602	4.003
ENSG00000273261	**ENSG00000273261**	lncRNA	-1.551	0.676	4.003
ENSG00000280385	**ENSG00000280385**	TEC	-1.551	0.712	4.003
ENSG00000140750	**ARHGAP17**	protein_coding	-1.55	0.786	4.003
ENSG00000282308	**DPRXP3**	processed_pseudogene	-1.55	0.646	4.003
ENSG00000180008	**SOCS4**	protein_coding	-1.55	0.778	4.003
ENSG00000130726	**TRIM28**	protein_coding	-1.55	0.762	4.003
ENSG00000120334	**CENPL**	protein_coding	-1.549	0.765	4.003
ENSG00000215796	**ENSG00000215796**	processed_pseudogene	-1.549	0.724	4.003
ENSG00000176390	**CRLF3**	protein_coding	-1.548	0.784	4.003
ENSG00000069248	**NUP133**	protein_coding	-1.548	0.783	4.003
ENSG00000203362	**POLH-AS1**	lncRNA	-1.548	0.726	4.003
ENSG00000199402	**RNA5SP308**	rRNA_pseudogene	-1.548	0.715	4.003
ENSG00000154127	**UBASH3B**	protein_coding	-1.548	0.764	4.003
ENSG00000280036	**ENSG00000280036**	lncRNA	-1.548	0.618	4.003
ENSG00000287392	**ENSG00000287392**	lncRNA	-1.548	0.716	4.003
ENSG00000265739	**ENSG00000265739**	lncRNA	-1.547	0.579	4.003

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000178631	**ACTG1P1**	processed_pseudogene	-1.546	0.658	4.003
ENSG00000119965	**C10orf88**	protein_coding	-1.545	0.717	4.003
ENSG00000031003	**FAM13B**	protein_coding	-1.545	0.771	4.003
ENSG00000118579	**MED28**	protein_coding	-1.544	0.767	4.003
ENSG00000163138	**PACRGL**	protein_coding	-1.544	0.8	4.003
ENSG00000100311	**PDGFB**	protein_coding	-1.544	0.777	4.003
ENSG00000272263	**ENSG00000272263**	lncRNA	-1.544	0.685	4.003
ENSG00000173545	**ZNF622**	protein_coding	-1.543	0.764	4.003
ENSG00000244405	**ETV5**	protein_coding	-1.542	0.749	4.003
ENSG00000073536	**NLE1**	protein_coding	-1.542	0.766	4.003
ENSG00000227105	**PARP1P1**	processed_pseudogene	-1.542	0.734	4.003
ENSG00000270620	**ENSG00000270620**	unprocessed_pseudogene	-1.542	0.7	4.003
ENSG00000134108	**ARL8B**	protein_coding	-1.541	0.789	4.003
ENSG00000230146	**SEPHS1P4**	processed_pseudogene	-1.541	0.663	4.003
ENSG00000084444	**FAM234B**	protein_coding	-1.54	0.736	4.003
ENSG00000198825	**INPP5F**	protein_coding	-1.54	0.777	4.003
ENSG00000108239	**TBC1D12**	protein_coding	-1.54	0.79	4.003
ENSG00000257267	**ZNF271P**	transcribed_unitary_pseu	-1.54	0.765	4.003
ENSG00000256591	**ENSG00000256591**	protein_coding	-1.54	0.641	4.003
ENSG00000157540	**DYRK1A**	protein_coding	-1.539	0.744	4.003
ENSG00000181104	**F2R**	protein_coding	-1.539	0.771	4.003
ENSG00000105176	**URI1**	protein_coding	-1.539	0.775	4.003
ENSG00000237350	**CDC42P6**	processed_pseudogene	-1.538	0.74	4.003
ENSG00000113649	**TCERG1**	protein_coding	-1.538	0.782	4.003
ENSG00000180357	**ZNF609**	protein_coding	-1.537	0.756	4.003
ENSG00000106689	**LHX2**	protein_coding	-1.536	0.762	4.003
ENSG00000147140	**NONO**	protein_coding	-1.536	0.787	4.003
ENSG00000131503	**ANKHD1**	protein_coding	-1.535	0.777	4.003
ENSG00000135046	**ANXA1**	protein_coding	-1.535	0.699	4.003
ENSG00000226982	**CENPCP1**	processed_pseudogene	-1.535	0.713	4.003
ENSG00000227850	**SEPTIN2P1**	processed_pseudogene	-1.535	0.751	4.003
ENSG00000252820	**Y_RNA**	misc_RNA	-1.534	0.736	4.003
ENSG00000271565	**ENSG00000271565**	processed_pseudogene	-1.534	0.699	4.003
ENSG00000266028	**SRGAP2**	protein_coding	-1.533	0.751	4.003
ENSG00000145868	**FBXO38**	protein_coding	-1.532	0.774	4.003
ENSG00000166913	**YWHAB**	protein_coding	-1.532	0.799	4.003
ENSG00000164463	**CREBRF**	protein_coding	-1.531	0.782	4.003
ENSG00000107758	**PPP3CB**	protein_coding	-1.531	0.775	4.003
ENSG00000069399	**BCL3**	protein_coding	-1.53	0.768	4.003
ENSG00000106144	**CASP2**	protein_coding	-1.53	0.768	4.003
ENSG00000233176	**OR7E157P**	unprocessed_pseudogene	-1.529	0.554	4.003
ENSG00000128059	**PPAT**	protein_coding	-1.529	0.782	4.003
ENSG00000136754	**ABI1**	protein_coding	-1.528	0.783	4.003
ENSG00000259735	**ENSG00000259735**	lncRNA	-1.528	0.707	4.003
ENSG00000124767	**GLO1**	protein_coding	-1.527	0.788	4.003
ENSG00000108622	**ICAM2**	protein_coding	-1.527	0.726	4.003
ENSG00000251542	**LINC01957**	lncRNA	-1.527	0.768	4.003
ENSG00000169519	**METTL15**	protein_coding	-1.527	0.718	4.003
ENSG00000224219	**SEC61GP1**	processed_pseudogene	-1.527	0.685	4.003

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000169902	**TPST1**	protein_coding	-1.527	0.757	4.003
ENSG00000207131	**Y_RNA**	misc_RNA	-1.527	0.766	4.003
ENSG00000241317	**ENSG00000241317**	lncRNA	-1.526	0.724	4.003
ENSG00000251844	**ENSG00000251844**	snoRNA	-1.526	0.742	4.003
ENSG00000278535	**DHRS11**	protein_coding	-1.525	0.746	4.003
ENSG00000111206	**FOXM1**	protein_coding	-1.525	0.77	4.003
ENSG00000228283	**KATNBL1P6**	transcribed_processed_ps	-1.525	0.733	4.003
ENSG00000240309	**MTCO1P6**	processed_pseudogene	-1.525	0.642	4.003
ENSG00000269952	**ENSG00000269952**	lncRNA	-1.525	0.677	4.003
ENSG00000236119	**ENSG00000236119**	lncRNA	-1.524	0.715	4.003
ENSG00000058063	**ATP11B**	protein_coding	-1.523	0.765	4.003
ENSG00000188100	**FAM25A**	protein_coding	-1.523	0.524	4.003
ENSG00000157470	**FAM81A**	protein_coding	-1.523	0.755	4.003
ENSG00000263361	**MIR378H**	miRNA	-1.523	0.733	4.003
ENSG00000166803	**PCLAF**	protein_coding	-1.523	0.684	4.003
ENSG00000274455	**GUSBP7**	unprocessed_pseudogene	-1.522	0.631	4.003
ENSG00000186185	**KIF18B**	protein_coding	-1.522	0.764	4.003
ENSG00000204138	**PHACTR4**	protein_coding	-1.521	0.772	4.003
ENSG00000255555	**ENSG00000255555**	lncRNA	-1.521	0.763	4.003
ENSG00000270108	**ENSG00000270108**	lncRNA	-1.521	0.657	4.003
ENSG00000275578	**ENSG00000275578**	unprocessed_pseudogene	-1.521	0.756	4.003
ENSG00000279880	**ENSG00000279880**	TEC	-1.521	0.636	4.003
ENSG00000133740	**E2F5**	protein_coding	-1.52	0.763	4.003
ENSG00000216636	**RPL7P25**	processed_pseudogene	-1.52	0.697	4.003
ENSG00000232838	**PET117**	protein_coding	-1.519	0.66	4.003
ENSG00000196187	**TMEM63A**	protein_coding	-1.519	0.776	4.003
ENSG00000229122	**AGBL5-IT1**	lncRNA	-1.518	0.681	4.003
ENSG00000168710	**AHCYL1**	protein_coding	-1.518	0.782	4.003
ENSG00000198369	**SPRED2**	protein_coding	-1.518	0.78	4.003
ENSG00000250485	**EXOC7P1**	processed_pseudogene	-1.517	0.71	4.003
ENSG00000005156	**LIG3**	protein_coding	-1.517	0.78	4.003
ENSG00000253586	**ENSG00000253586**	lncRNA	-1.517	0.658	4.003
ENSG00000143614	**GATAD2B**	protein_coding	-1.515	0.787	4.003
ENSG00000075188	**NUP37**	protein_coding	-1.514	0.801	4.003
ENSG00000186723	**OR10H1**	protein_coding	-1.514	0.774	4.003
ENSG00000207508	**RNU6-1237P**	snRNA	-1.514	0.705	4.003
ENSG00000144048	**DUSP11**	protein_coding	-1.513	0.796	4.003
ENSG00000006831	**ADIPOR2**	protein_coding	-1.512	0.744	4.003
ENSG00000196866	**H2AC7**	protein_coding	-1.512	0.711	4.003
ENSG00000222627	**RNU2-37P**	snRNA	-1.512	0.72	4.003
ENSG00000107864	**CPEB3**	protein_coding	-1.511	0.798	4.003
ENSG00000149262	**INTS4**	protein_coding	-1.511	0.773	4.003
ENSG00000101350	**KIF3B**	protein_coding	-1.511	0.757	4.003
ENSG00000204308	**RNF5**	protein_coding	-1.511	0.729	4.003
ENSG00000185946	**RNPC3**	protein_coding	-1.511	0.759	4.003
ENSG00000271797	**ENSG00000271797**	lncRNA	-1.511	0.694	4.003
ENSG00000150337	**FCGR1A**	protein_coding	-1.51	0.784	4.003
ENSG00000157107	**FCHO2**	protein_coding	-1.51	0.787	4.003
ENSG00000199961	**SNORD1B**	snoRNA	-1.51	0.645	4.003

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000068120	**COASY**	protein_coding	-1.509	0.779	4.003
ENSG00000086102	**NFX1**	protein_coding	-1.509	0.796	4.003
ENSG00000138771	**SHROOM3**	protein_coding	-1.509	0.797	4.003
ENSG00000221962	**TMEM14EP**	transcribed_processed_ps	-1.509	0.737	4.003
ENSG00000181472	**ZBTB2**	protein_coding	-1.509	0.748	4.003
ENSG00000228446	**ANKRD49P1**	processed_pseudogene	-1.508	0.679	4.003
ENSG00000154642	**C21orf91**	protein_coding	-1.508	0.779	4.003
ENSG00000157181	**ODR4**	protein_coding	-1.508	0.807	4.003
ENSG00000217527	**RPS16P5**	transcribed_processed_ps	-1.508	0.709	4.003
ENSG00000185811	**IKZF1**	protein_coding	-1.507	0.796	4.003
ENSG00000200822	**Y_RNA**	misc_RNA	-1.507	0.721	4.003
ENSG00000281026	**N4BP2L2-IT2**	lncRNA	-1.506	0.745	4.003
ENSG00000287568	**ENSG00000287568**	lncRNA	-1.506	0.742	4.003
ENSG00000279696	**ENSG00000279696**	TEC	-1.505	0.714	4.003
ENSG00000160216	**AGPAT3**	protein_coding	-1.504	0.781	4.003
ENSG00000116918	**TSNAX**	protein_coding	-1.503	0.748	4.003
ENSG00000197779	**ZNF81**	protein_coding	-1.503	0.797	4.003
ENSG00000247134	**ENSG00000247134**	lncRNA	-1.503	0.767	4.003
ENSG00000156735	**BAG4**	protein_coding	-1.502	0.764	4.003
ENSG00000203668	**CHML**	protein_coding	-1.502	0.765	4.003
ENSG00000104142	**VPS18**	protein_coding	-1.502	0.766	4.003
ENSG00000272407	**ENSG00000272407**	transcribed_processed_ps	-1.502	0.682	4.003
ENSG00000112249	**ASCC3**	protein_coding	-1.501	0.791	4.003
ENSG00000005100	**DHX33**	protein_coding	-1.501	0.779	4.003
ENSG00000172869	**DMXL1**	protein_coding	-1.5	0.781	4.003
ENSG00000259089	**GRAMD4P5**	unprocessed_pseudogene	-1.5	0.722	4.003
ENSG00000201809	**U8**	snoRNA	-1.5	0.722	4.003
ENSG00000199762	**Y_RNA**	misc_RNA	-1.5	0.678	4.003
ENSG00000229349	**ACTG1P9**	processed_pseudogene	-1.499	0.712	4.003
ENSG00000135837	**CEP350**	protein_coding	-1.499	0.791	4.003
ENSG00000008083	**JARID2**	protein_coding	-1.499	0.79	4.003
ENSG00000212572	**RNU6-903P**	snRNA	-1.499	0.729	4.003
ENSG00000211697	**TRGV5**	TR_V_gene	-1.499	0.701	4.003
ENSG00000274303	**7SK**	misc_RNA	-1.498	0.747	4.003
ENSG00000172269	**DPAGT1**	protein_coding	-1.498	0.748	4.003
ENSG00000134146	**DPH6**	protein_coding	-1.498	0.735	4.003
ENSG00000177733	**HNRNPA0**	protein_coding	-1.498	0.771	4.003
ENSG00000163166	**IWS1**	protein_coding	-1.498	0.791	4.003
ENSG00000231307	**RPS3P2**	processed_pseudogene	-1.498	0.75	4.003
ENSG00000184305	**CCSER1**	protein_coding	-1.497	0.782	4.003
ENSG00000198961	**PJA2**	protein_coding	-1.496	0.792	4.003
ENSG00000200041	**Y_RNA**	misc_RNA	-1.496	0.754	4.003
ENSG00000248322	**ENSG00000248322**	lncRNA	-1.496	0.641	4.003
ENSG00000252548	**RNU7-149P**	snRNA	-1.495	0.711	4.003
ENSG00000023734	**STRAP**	protein_coding	-1.495	0.79	4.003
ENSG00000279786	**ENSG00000279786**	TEC	-1.495	0.74	4.003
ENSG00000088205	**DDX18**	protein_coding	-1.494	0.792	4.003
ENSG00000147650	**LRP12**	protein_coding	-1.494	0.769	4.003
ENSG00000241293	**PPATP1**	processed_pseudogene	-1.494	0.768	4.003

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000101413	**RPRD1B**	protein_coding	-1.493	0.786	4.003
ENSG00000226619	**ENSG00000226619**	lncRNA	-1.493	0.747	4.003
ENSG00000253908	**ENSG00000253908**	processed_pseudogene	-1.493	0.653	4.003
ENSG00000273786	**ENSG00000273786**	lncRNA	-1.493	0.696	4.003
ENSG00000277911	**ENSG00000277911**	lncRNA	-1.493	0.656	4.003
ENSG00000279111	**OR10X1**	protein_coding	-1.492	0.76	4.003
ENSG00000280392	**ENSG00000280392**	TEC	-1.492	0.559	4.003
ENSG00000131711	**MAP1B**	protein_coding	-1.491	0.782	4.003
ENSG00000066933	**MYO9A**	protein_coding	-1.491	0.773	4.003
ENSG00000235631	**RNF148**	protein_coding	-1.491	0.712	4.003
ENSG00000250612	**ENSG00000250612**	processed_pseudogene	-1.491	0.774	4.003
ENSG00000183249	**NF1P3**	unprocessed_pseudogene	-1.49	0.74	4.003
ENSG00000185246	**PRPF39**	protein_coding	-1.49	0.771	4.003
ENSG00000167325	**RRM1**	protein_coding	-1.49	0.784	4.003
ENSG00000198554	**WDHD1**	protein_coding	-1.49	0.767	4.003
ENSG00000232672	**ACTG1P21**	processed_pseudogene	-1.489	0.693	4.003
ENSG00000128908	**INO80**	protein_coding	-1.489	0.783	4.003
ENSG00000251090	**OR5AC4P**	transcribed_unprocessed_	-1.489	0.734	4.003
ENSG00000254500	**RANP3**	processed_pseudogene	-1.488	0.672	4.003
ENSG00000227382	**EIF4A2P2**	processed_pseudogene	-1.487	0.797	4.003
ENSG00000113194	**FAF2**	protein_coding	-1.487	0.783	4.003
ENSG00000136381	**IREB2**	protein_coding	-1.487	0.775	4.003
ENSG00000251856	**MIR449C**	miRNA	-1.487	0.766	4.003
ENSG00000201596	**Y_RNA**	misc_RNA	-1.487	0.556	4.003
ENSG00000217512	**ENSG00000217512**	processed_pseudogene	-1.487	0.71	4.003
ENSG00000232508	**MRPL45P1**	processed_pseudogene	-1.486	0.696	4.003
ENSG00000117640	**MTFR1L**	protein_coding	-1.486	0.771	4.003
ENSG00000273454	**ENSG00000273454**	lncRNA	-1.486	0.666	4.003
ENSG00000224141	**MIR548XHG**	lncRNA	-1.485	0.762	4.003
ENSG00000274934	**ENSG00000274934**	misc_RNA	-1.484	0.69	4.003
ENSG00000162437	**RAVER2**	protein_coding	-1.483	0.777	4.003
ENSG00000038210	**PI4K2B**	protein_coding	-1.482	0.787	4.003
ENSG00000154265	**ABCA5**	protein_coding	-1.481	0.78	4.003
ENSG00000139323	**POC1B**	protein_coding	-1.481	0.786	4.003
ENSG00000240940	**RN7SL591P**	misc_RNA	-1.481	0.676	4.003
ENSG00000199601	**RNU6-562P**	snRNA	-1.481	0.579	4.003
ENSG00000141293	**SKAP1**	protein_coding	-1.481	0.776	4.003
ENSG00000286103	**ENSG00000286103**	lncRNA	-1.481	0.653	4.003
ENSG00000129226	**CD68**	protein_coding	-1.48	0.779	4.003
ENSG00000183150	**GPR19**	protein_coding	-1.48	0.764	4.003
ENSG00000101224	**CDC25B**	protein_coding	-1.479	0.767	4.003
ENSG00000231475	**IGHV4-31**	IG_V_gene	-1.479	0.668	4.003
ENSG00000114030	**KPNA1**	protein_coding	-1.479	0.8	4.003
ENSG00000248693	**LINC02100**	lncRNA	-1.479	0.706	4.003
ENSG00000237885	**ENSG00000237885**	processed_pseudogene	-1.479	0.691	4.003
ENSG00000248955	**ENSG00000248955**	processed_pseudogene	-1.479	0.735	4.003
ENSG00000180611	**MB21D2**	protein_coding	-1.478	0.676	4.003
ENSG00000163848	**ZNF148**	protein_coding	-1.478	0.773	4.003
ENSG00000219302	**ENSG00000219302**	processed_pseudogene	-1.478	0.717	4.003

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000188848	**BEND4**	protein_coding	-1.477	0.774	4.003
ENSG00000106701	**FSD1L**	protein_coding	-1.477	0.788	4.003
ENSG00000167515	**TRAPPC2L**	protein_coding	-1.477	0.773	4.003
ENSG00000109790	**KLHL5**	protein_coding	-1.476	0.778	4.003
ENSG00000237263	**MAPK6P3**	processed_pseudogene	-1.476	0.714	4.003
ENSG00000274591	**ENSG00000274591**	lncRNA	-1.476	0.685	4.003
ENSG00000279502	**ENSG00000279502**	TEC	-1.476	0.621	4.003
ENSG00000187097	**ENTPD5**	protein_coding	-1.475	0.774	4.003
ENSG00000144381	**HSPD1**	protein_coding	-1.475	0.788	4.003
ENSG00000017797	**RALBP1**	protein_coding	-1.475	0.776	4.003
ENSG00000134308	**YWHAQ**	protein_coding	-1.475	0.779	4.003
ENSG00000143322	**ABL2**	protein_coding	-1.474	0.785	4.003
ENSG00000115677	**HDLBP**	protein_coding	-1.474	0.798	4.003
ENSG00000184182	**UBE2F**	protein_coding	-1.473	0.8	4.003
ENSG00000238832	**ENSG00000238832**	snoRNA	-1.472	0.725	4.003
ENSG00000182158	**CREB3L2**	protein_coding	-1.471	0.805	4.003
ENSG00000196604	**POTEF**	protein_coding	-1.471	0.674	4.003
ENSG00000255071	**SAA2-SAA4**	protein_coding	-1.47	0.666	4.003
ENSG00000258536	**FKBP1BP1**	processed_pseudogene	-1.469	0.735	4.003
ENSG00000108424	**KPNB1**	protein_coding	-1.469	0.799	4.003
ENSG00000152217	**SETBP1**	protein_coding	-1.469	0.796	4.003
ENSG00000232542	**DPYD-IT1**	lncRNA	-1.468	0.763	4.003
ENSG00000122507	**BBS9**	protein_coding	-1.467	0.784	4.003
ENSG00000114107	**CEP70**	protein_coding	-1.467	0.792	4.003
ENSG00000271629	**ENSG00000271629**	processed_pseudogene	-1.467	0.761	4.003
ENSG00000259904	**ACTG1P15**	processed_pseudogene	-1.466	0.689	4.003
ENSG00000144369	**FAM171B**	protein_coding	-1.466	0.748	4.003
ENSG00000241549	**GUSBP2**	transcribed_unprocessed_	-1.466	0.729	4.003
ENSG00000213690	**ENSG00000213690**	processed_pseudogene	-1.466	0.7	4.003
ENSG00000258441	**LINC00641**	lncRNA	-1.465	0.703	4.003
ENSG00000213281	**NRAS**	protein_coding	-1.465	0.762	4.003
ENSG00000276234	**TADA2A**	protein_coding	-1.465	0.778	4.003
ENSG00000227809	**ENSG00000227809**	lncRNA	-1.465	0.799	4.003
ENSG00000257027	**ENSG00000257027**	lncRNA	-1.465	0.699	4.003
ENSG00000261187	**ENSG00000261187**	lncRNA	-1.465	0.685	4.003
ENSG00000177340	**FLJ13224**	lncRNA	-1.464	0.718	4.003
ENSG00000047932	**GOPC**	protein_coding	-1.464	0.807	4.003
ENSG00000061987	**MON2**	protein_coding	-1.464	0.783	4.003
ENSG00000103047	**TANGO6**	protein_coding	-1.464	0.798	4.003
ENSG00000284607	**ENSG00000284607**	lncRNA	-1.464	0.709	4.003
ENSG00000014824	**SLC30A9**	protein_coding	-1.463	0.782	4.003
ENSG00000203875	**SNHG5**	lncRNA	-1.463	0.797	4.003
ENSG00000113732	**ATP6V0E1**	protein_coding	-1.462	0.765	4.003
ENSG00000143515	**ATP8B2**	protein_coding	-1.461	0.775	4.003
ENSG00000094880	**CDC23**	protein_coding	-1.461	0.784	4.003
ENSG00000147155	**EBP**	protein_coding	-1.461	0.755	4.003
ENSG00000100330	**MTMR3**	protein_coding	-1.461	0.796	4.003
ENSG00000164951	**PDP1**	protein_coding	-1.461	0.786	4.003
ENSG00000083123	**BCKDHB**	protein_coding	-1.46	0.785	4.003

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000108506	**INTS2**	protein_coding	-1.46	0.755	4.003
ENSG00000211943	**IGHV3-15**	IG_V_gene	-1.459	0.694	4.003
ENSG00000168159	**RNF187**	protein_coding	-1.459	0.751	4.003
ENSG00000163823	**CCR1**	protein_coding	-1.458	0.8	4.003
ENSG00000089041	**P2RX7**	protein_coding	-1.458	0.78	4.003
ENSG00000231967	**ENSG00000231967**	processed_pseudogene	-1.458	0.649	4.003
ENSG00000212102	**MIR301B**	miRNA	-1.457	0.749	4.003
ENSG00000207983	**MIR613**	miRNA	-1.457	0.75	4.003
ENSG00000105887	**MTPN**	protein_coding	-1.457	0.784	4.003
ENSG00000138801	**PAPSS1**	protein_coding	-1.457	0.76	4.003
ENSG00000082146	**STRADB**	protein_coding	-1.457	0.794	4.003
ENSG00000272211	**ENSG00000272211**	lncRNA	-1.457	0.724	4.003
ENSG00000012048	**BRCA1**	protein_coding	-1.456	0.792	4.003
ENSG00000033170	**FUT8**	protein_coding	-1.456	0.775	4.003
ENSG00000135093	**USP30**	protein_coding	-1.456	0.803	4.003
ENSG00000166348	**USP54**	protein_coding	-1.456	0.803	4.003
ENSG00000275097	**ENSG00000275097**	lncRNA	-1.456	0.618	4.003
ENSG00000100167	**SEPTIN3**	protein_coding	-1.455	0.792	4.003
ENSG00000186153	**WWOX**	protein_coding	-1.455	0.791	4.003
ENSG00000073905	**VDAC1P1**	processed_pseudogene	-1.454	0.749	4.003
ENSG00000235060	**VDAC1P4**	processed_pseudogene	-1.454	0.742	4.003
ENSG00000231887	**PRH1**	protein_coding	-1.453	0.752	4.003
ENSG00000239280	**ENSG00000239280**	processed_pseudogene	-1.453	0.743	4.003
ENSG00000010539	**ZNF200**	protein_coding	-1.452	0.791	4.003
ENSG00000283971	**MIR4442**	miRNA	-1.451	0.626	4.003
ENSG00000144233	**AMMECR1L**	protein_coding	-1.45	0.764	4.003
ENSG00000248476	**BACH1-IT1**	lncRNA	-1.45	0.726	4.003
ENSG00000125149	**C16orf70**	protein_coding	-1.45	0.797	4.003
ENSG00000144283	**PKP4**	protein_coding	-1.45	0.802	4.003
ENSG00000228481	**PRKCE-AS1**	lncRNA	-1.45	0.755	4.003
ENSG00000288024	**ENSG00000288024**	lncRNA	-1.45	0.701	4.003
ENSG00000265599	**MIR4471**	miRNA	-1.449	0.764	4.003
ENSG00000113048	**MRPS27**	protein_coding	-1.448	0.774	4.003
ENSG00000157212	**PAXIP1**	protein_coding	-1.448	0.799	4.003
ENSG00000126773	**PCNX4**	protein_coding	-1.448	0.762	4.003
ENSG00000114062	**UBE3A**	protein_coding	-1.448	0.789	4.003
ENSG00000280372	**ENSG00000280372**	TEC	-1.448	0.631	4.003
ENSG00000207827	**MIR30A**	miRNA	-1.447	0.624	4.003
ENSG00000154839	**SKA1**	protein_coding	-1.447	0.783	4.003
ENSG00000272215	**U7**	snRNA	-1.447	0.653	4.003
ENSG00000263427	**ENSG00000263427**	lncRNA	-1.447	0.766	4.003
ENSG00000186871	**ERCC6L**	protein_coding	-1.446	0.682	4.003
ENSG00000101452	**DHX35**	protein_coding	-1.445	0.801	4.003
ENSG00000168906	**MAT2A**	protein_coding	-1.444	0.792	4.003
ENSG00000207416	**Y_RNA**	misc_RNA	-1.444	0.612	4.003
ENSG00000145675	**PIK3R1**	protein_coding	-1.443	0.765	4.003
ENSG00000147459	**DOCK5**	protein_coding	-1.442	0.794	4.003
ENSG00000103494	**RPGRIP1L**	protein_coding	-1.442	0.785	4.003
ENSG00000155850	**SLC26A2**	protein_coding	-1.442	0.79	4.003

Gene ID	**Gene name**	**Gene type**	**Score(d)**	**Fold Change**	**q-value(%)**
ENSG00000114316	**USP4**	protein_coding	-1.442	0.795	4.003
ENSG00000135775	**COG2**	protein_coding	-1.441	0.797	4.003
ENSG00000204406	**MBD5**	protein_coding	-1.441	0.794	4.003
ENSG00000263669	**RN7SL470P**	misc_RNA	-1.441	0.682	4.003
ENSG00000256238	**SUPT16HP1**	processed_pseudogene	-1.441	0.705	4.003
ENSG00000274104	**ENSG00000274104**	lncRNA	-1.441	0.619	4.003
ENSG00000206803	**RNU6-968P**	snRNA	-1.44	0.57	4.003
ENSG00000197969	**VPS13A**	protein_coding	-1.44	0.77	4.003
ENSG00000200522	**RNU6-957P**	snRNA	-1.439	0.629	4.003
ENSG00000236896	**ENSG00000236896**	lncRNA	-1.439	0.698	4.003
ENSG00000178971	**CTC1**	protein_coding	-1.438	0.788	4.003
ENSG00000101019	**UQCC1**	protein_coding	-1.437	0.803	4.003
ENSG00000138767	**CNOT6L**	protein_coding	-1.436	0.796	4.003
ENSG00000228612	**HK2P1**	processed_pseudogene	-1.436	0.668	4.003
ENSG00000275640	**MIR6793**	miRNA	-1.436	0.75	4.003
ENSG00000283431	**ENSG00000283431**	unprocessed_pseudogene	-1.436	0.678	4.003
ENSG00000145990	**GFOD1**	protein_coding	-1.435	0.797	4.003
ENSG00000236654	**ENSG00000236654**	processed_pseudogene	-1.435	0.586	4.003
ENSG00000110931	**CAMKK2**	protein_coding	-1.434	0.791	4.003
ENSG00000151292	**CSNK1G3**	protein_coding	-1.434	0.77	4.003
ENSG00000280190	**ENSG00000280190**	TEC	-1.434	0.592	4.003
ENSG00000165029	**ABCA1**	protein_coding	-1.433	0.776	4.003
ENSG00000150456	**EEF1AKMT1**	protein_coding	-1.433	0.756	4.003
ENSG00000128944	**KNSTRN**	protein_coding	-1.433	0.805	4.003
ENSG00000136153	**LMO7**	protein_coding	-1.433	0.787	4.003
ENSG00000207008	**SNORA54**	snoRNA	-1.433	0.764	4.003
ENSG00000271452	**ENSG00000271452**	lncRNA	-1.433	0.681	4.003
ENSG00000012983	**MAP4K5**	protein_coding	-1.432	0.779	4.003
ENSG00000166343	**MSS51**	protein_coding	-1.432	0.796	4.003
ENSG00000271429	**RPL17P51**	processed_pseudogene	-1.432	0.695	4.003
ENSG00000254936	**ENSG00000254936**	lncRNA	-1.432	0.783	4.003
ENSG00000096060	**FKBP5**	protein_coding	-1.431	0.788	4.003
ENSG00000168575	**SLC20A2**	protein_coding	-1.431	0.809	4.003
ENSG00000168939	**SPRY3**	protein_coding	-1.431	0.772	4.003
ENSG00000078124	**ACER3**	protein_coding	-1.43	0.799	4.003
ENSG00000258816	**ENSG00000258816**	unprocessed_pseudogene	-1.43	0.65	4.003
ENSG00000128731	**HERC2**	protein_coding	-1.429	0.798	4.003
ENSG00000207701	**MIR597**	miRNA	-1.429	0.721	4.003
ENSG00000254623	**DEFB108E**	unprocessed_pseudogene	-1.428	0.729	4.003
ENSG00000277556	**OR13C5**	protein_coding	-1.428	0.608	4.003
ENSG00000274963	**RN7SL600P**	misc_RNA	-1.428	0.68	4.003
ENSG00000259461	**ANP32BP3**	processed_pseudogene	-1.427	0.711	4.003
ENSG00000118412	**CASP8AP2**	protein_coding	-1.427	0.793	4.003
ENSG00000111860	**CEP85L**	protein_coding	-1.427	0.801	4.003
ENSG00000127804	**METTL16**	protein_coding	-1.427	0.802	4.003
ENSG00000230499	**ENSG00000230499**	lncRNA	-1.427	0.707	4.003
ENSG00000280310	**ENSG00000280310**	TEC	-1.427	0.577	4.003
ENSG00000280081	**LINC01667**	transcribed_processed_ps	-1.425	0.772	4.003
ENSG00000186575	**NF2**	protein_coding	-1.425	0.798	4.003

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000104447	**TRPS1**	protein_coding	-1.425	0.769	4.003
ENSG00000279594	**ENSG00000279594**	TEC	-1.425	0.762	4.003
ENSG00000248122	**APOOP4**	processed_pseudogene	-1.424	0.73	4.003
ENSG00000148019	**CEP78**	protein_coding	-1.424	0.797	4.003
ENSG00000276819	**TRBV15**	TR_V_gene	-1.424	0.7	4.003
ENSG00000256035	**ENSG00000256035**	processed_pseudogene	-1.424	0.759	4.003
ENSG00000077514	**POLD3**	protein_coding	-1.423	0.796	4.003
ENSG00000201579	**RNU6-343P**	snRNA	-1.422	0.662	4.003
ENSG00000085433	**WDR47**	protein_coding	-1.422	0.76	4.003
ENSG00000142599	**RERE**	protein_coding	-1.421	0.813	4.003
ENSG00000008277	**ADAM22**	protein_coding	-1.42	0.808	4.003
ENSG00000120647	**CCDC77**	protein_coding	-1.42	0.783	4.003
ENSG00000186001	**LRCH3**	protein_coding	-1.42	0.793	4.003
ENSG00000134318	**ROCK2**	protein_coding	-1.42	0.794	4.003
ENSG00000168078	**PBK**	protein_coding	-1.419	0.801	4.003
ENSG00000137713	**PPP2R1B**	protein_coding	-1.419	0.794	4.003
ENSG00000199781	**Y_RNA**	misc_RNA	-1.419	0.647	4.003
ENSG00000074603	**DPP8**	protein_coding	-1.418	0.794	4.003
ENSG00000116906	**GNPAT**	protein_coding	-1.418	0.792	4.003
ENSG00000078747	**ITCH**	protein_coding	-1.418	0.814	4.003
ENSG00000196199	**MPHOSPH8**	protein_coding	-1.418	0.789	4.003
ENSG00000107036	**RIC1**	protein_coding	-1.418	0.793	4.003
ENSG00000251660	**ENSG00000251660**	lncRNA	-1.418	0.642	4.003
ENSG00000136504	**KAT7**	protein_coding	-1.417	0.791	4.003
ENSG00000111224	**PARP11**	protein_coding	-1.417	0.787	4.003
ENSG00000126226	**PCID2**	protein_coding	-1.417	0.808	4.003
ENSG00000196313	**POM121**	protein_coding	-1.417	0.795	4.003
ENSG00000199326	**RNU6-1298P**	snRNA	-1.417	0.765	4.003
ENSG00000207127	**Y_RNA**	misc_RNA	-1.417	0.721	4.003
ENSG00000209482	**SNORD83A**	snoRNA	-1.416	0.719	4.003
ENSG00000270510	**ENSG00000270510**	processed_pseudogene	-1.416	0.658	4.003
ENSG00000213435	**ATP6V0CP3**	processed_pseudogene	-1.415	0.76	4.003
ENSG00000113810	**SMC4**	protein_coding	-1.415	0.781	4.003
ENSG00000048028	**USP28**	protein_coding	-1.414	0.786	4.003
ENSG00000153015	**CWC27**	protein_coding	-1.413	0.807	4.003
ENSG00000127603	**MACF1**	protein_coding	-1.413	0.804	4.003
ENSG00000250337	**PURPL**	lncRNA	-1.413	0.792	4.003
ENSG00000206615	**RNU6-338P**	snRNA	-1.413	0.582	4.003
ENSG00000169860	**P2RY1**	protein_coding	-1.412	0.701	4.003
ENSG00000119906	**SLF2**	protein_coding	-1.412	0.813	4.003
ENSG00000212306	**Y_RNA**	misc_RNA	-1.412	0.704	4.003
ENSG00000227994	**ENSG00000227994**	processed_pseudogene	-1.412	0.725	4.003
ENSG00000234584	**ENSG00000234584**	lncRNA	-1.412	0.734	4.003
ENSG00000229101	**ELOCP20**	unprocessed_pseudogen	-1.411	0.794	4.003
ENSG00000198964	**SGMS1**	protein_coding	-1.411	0.778	4.003
ENSG00000204637	**ARPP19P2**	processed_pseudogene	-1.41	0.73	4.003
ENSG00000170558	**CDH2**	protein_coding	-1.41	0.79	4.003
ENSG00000199109	**MIR411**	miRNA	-1.41	0.74	4.003
ENSG00000270601	**PRAMEF5**	protein_coding	-1.41	0.45	4.003

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000163694	**RBM47**	protein_coding	-1.41	0.801	4.003
ENSG00000134294	**SLC38A2**	protein_coding	-1.41	0.767	4.003
ENSG00000198464	**ZNF480**	protein_coding	-1.41	0.774	4.003
ENSG00000182827	**ACBD3**	protein_coding	-1.409	0.797	4.003
ENSG00000279319	**ENSG00000279319**	TEC	-1.409	0.782	4.003
ENSG00000260644	**HERC2P5**	transcribed_unprocessed	-1.408	0.745	4.003
ENSG00000138380	**CARF**	protein_coding	-1.407	0.751	4.003
ENSG00000229014	**RPL30P13**	processed_pseudogene	-1.407	0.783	4.003
ENSG00000226389	**MAPK6P6**	processed_pseudogene	-1.406	0.767	4.003
ENSG00000223695	**ENSG00000223695**	lncRNA	-1.406	0.725	4.003
ENSG00000225292	**ENSG00000225292**	lncRNA	-1.406	0.737	4.003
ENSG00000270096	**ENSG00000270096**	lncRNA	-1.406	0.739	4.003
ENSG00000278971	**ENSG00000278971**	TEC	-1.406	0.79	4.003
ENSG00000084463	**WBP11**	protein_coding	-1.405	0.793	4.003
ENSG00000223271	**Y_RNA**	misc_RNA	-1.405	0.719	4.003
ENSG00000249919	**FABP5P6**	processed_pseudogene	-1.404	0.745	4.003
ENSG00000218186	**KRT8P43**	processed_pseudogene	-1.404	0.702	4.003
ENSG00000139722	**VPS37B**	protein_coding	-1.404	0.773	4.003
ENSG00000253423	**ENSG00000253423**	processed_pseudogene	-1.404	0.692	4.003
ENSG00000115364	**MRPL19**	protein_coding	-1.403	0.807	4.003
ENSG00000163605	**PPP4R2**	protein_coding	-1.403	0.793	4.003
ENSG00000288162	**ENSG00000288162**	lncRNA	-1.403	0.519	4.003
ENSG00000123545	**NDUFAF4**	protein_coding	-1.402	0.783	4.003
ENSG00000266920	**ACTBP9**	processed_pseudogene	-1.401	0.7	4.003
ENSG00000119929	**CUTC**	protein_coding	-1.401	0.793	4.003
ENSG00000118276	**B4GALT6**	protein_coding	-1.4	0.775	4.003
ENSG00000265584	**MIR3978**	miRNA	-1.4	0.679	4.003
ENSG00000270325	**BNIP3P9**	processed_pseudogene	-1.399	0.687	4.003
ENSG00000180138	**CSNK1A1L**	protein_coding	-1.399	0.72	4.003
ENSG00000168310	**IRF2**	protein_coding	-1.399	0.808	4.003
ENSG00000174780	**SRP72**	protein_coding	-1.399	0.797	4.003
ENSG00000287021	**ENSG00000287021**	lncRNA	-1.399	0.749	4.003
ENSG00000163320	**CGGBP1**	protein_coding	-1.398	0.784	4.003
ENSG00000106459	**NRF1**	protein_coding	-1.398	0.79	4.003
ENSG00000277757	**ENSG00000277757**	lncRNA	-1.398	0.728	4.003
ENSG00000122512	**PMS2**	protein_coding	-1.398	0.789	5.863
ENSG00000173166	**RAPH1**	protein_coding	-1.398	0.797	5.863
ENSG00000151491	**EPS8**	protein_coding	-1.397	0.799	5.863
ENSG00000131389	**SLC6A6**	protein_coding	-1.397	0.782	5.863
ENSG00000144791	**LIMD1**	protein_coding	-1.396	0.786	5.863
ENSG00000139289	**PHLDA1**	protein_coding	-1.396	0.768	5.863
ENSG00000252685	**RNU6-928P**	snRNA	-1.396	0.694	5.863
ENSG00000112079	**STK38**	protein_coding	-1.396	0.805	5.863
ENSG00000183864	**TOB2**	protein_coding	-1.396	0.771	5.863
ENSG00000213856	**VDAC1P2**	processed_pseudogene	-1.396	0.73	5.863
ENSG00000269987	**ENSG00000269987**	lncRNA	-1.396	0.723	5.863
ENSG00000277755	**ENSG00000277755**	processed_pseudogene	-1.396	0.774	5.863
ENSG00000065457	**ADAT1**	protein_coding	-1.395	0.782	5.863
ENSG00000162736	**NCSTN**	protein_coding	-1.395	0.8	5.863

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000252010	**SCARNA5**	scaRNA	-1.395	0.74	5.863
ENSG00000260505	**ENSG00000260505**	lncRNA	-1.395	0.747	5.863
ENSG00000169919	**GUSB**	protein_coding	-1.393	0.785	5.863
ENSG00000129347	**KRI1**	protein_coding	-1.393	0.799	5.863
ENSG00000178177	**LCORL**	protein_coding	-1.393	0.791	5.863
ENSG00000230484	**OR51A10P**	unitary_pseudogene	-1.393	0.663	5.863
ENSG00000162735	**PEX19**	protein_coding	-1.393	0.801	5.863
ENSG00000266984	**POLR3GP2**	processed_pseudogene	-1.393	0.748	5.863
ENSG00000111602	**TIMELESS**	protein_coding	-1.393	0.817	5.863
ENSG00000184188	**ENSG00000184188**	processed_pseudogene	-1.393	0.791	5.863
ENSG00000201376	**SNORA70**	snoRNA	-1.392	0.645	5.863
ENSG00000205133	**TRIQK**	protein_coding	-1.392	0.767	5.863
ENSG00000138399	**FASTKD1**	protein_coding	-1.391	0.799	5.863
ENSG00000163607	**GTPBP8**	protein_coding	-1.391	0.777	5.863
ENSG00000170836	**PPM1D**	protein_coding	-1.391	0.803	5.863
ENSG00000124486	**USP9X**	protein_coding	-1.391	0.798	5.863
ENSG00000147905	**ZCCHC7**	protein_coding	-1.391	0.801	5.863
ENSG00000254000	**ENSG00000254000**	lncRNA	-1.391	0.783	5.863
ENSG00000257941	**ENSG00000257941**	processed_pseudogene	-1.391	0.71	5.863
ENSG00000205208	**C4orf46**	protein_coding	-1.39	0.81	5.863
ENSG00000206723	**RNU6-1056P**	snRNA	-1.39	0.685	5.863
ENSG00000233126	**ZNF736P3Y**	processed_pseudogene	-1.39	0.753	5.863
ENSG00000261542	**ENSG00000261542**	lncRNA	-1.39	0.699	5.863
ENSG00000272791	**ENSG00000272791**	lncRNA	-1.39	0.666	5.863
ENSG00000285292	**ABCF2-H2BE1**	protein_coding	-1.389	0.516	5.863
ENSG00000258290	**BRWD1P2**	processed_pseudogene	-1.389	0.731	5.863
ENSG00000124784	**RIOK1**	protein_coding	-1.389	0.797	5.863
ENSG00000111880	**RNGTT**	protein_coding	-1.389	0.788	5.863
ENSG00000207371	**Y_RNA**	misc_RNA	-1.389	0.646	5.863
ENSG00000241772	**ENSG00000241772**	lncRNA	-1.389	0.759	5.863
ENSG00000281469	**ENSG00000281469**	TEC	-1.389	0.728	5.863
ENSG00000204842	**ATXN2**	protein_coding	-1.388	0.807	5.863
ENSG00000048828	**FAM120A**	protein_coding	-1.388	0.814	5.863
ENSG00000185499	**MUC1**	protein_coding	-1.388	0.793	5.863
ENSG00000141458	**NPC1**	protein_coding	-1.388	0.777	5.863
ENSG00000196376	**SLC35F1**	protein_coding	-1.388	0.779	5.863
ENSG00000105221	**AKT2**	protein_coding	-1.387	0.794	5.863
ENSG00000140577	**CRTC3**	protein_coding	-1.387	0.797	5.863
ENSG00000235045	**RPL7P8**	processed_pseudogene	-1.387	0.63	5.863
ENSG00000272123	**ENSG00000272123**	lncRNA	-1.386	0.795	5.863
ENSG00000105186	**ANKRD27**	protein_coding	-1.385	0.805	5.863
ENSG00000015568	**RGPD5**	protein_coding	-1.385	0.732	5.863
ENSG00000143751	**SDE2**	protein_coding	-1.385	0.796	5.863
ENSG00000262663	**ENSG00000262663**	lncRNA	-1.385	0.776	5.863
ENSG00000221883	**ARIH2OS**	lncRNA	-1.384	0.66	5.863
ENSG00000231537	**MTCO3P10**	unprocessed_pseudogen	-1.384	0.718	5.863
ENSG00000214980	**ENSG00000214980**	processed_pseudogene	-1.384	0.671	5.863
ENSG00000005194	**CIAPIN1**	protein_coding	-1.383	0.795	5.863
ENSG00000188394	**GPR21**	protein_coding	-1.383	0.777	5.863

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000225484	**NUTM2B-AS1**	lncRNA	-1.383	0.754	5.863
ENSG00000114331	**ACAP2**	protein_coding	-1.382	0.795	5.863
ENSG00000178035	**IMPDH2**	protein_coding	-1.382	0.808	5.863
ENSG00000108474	**PIGL**	protein_coding	-1.382	0.791	5.863
ENSG00000271257	**ENSG00000271257**	processed_pseudogene	-1.382	0.777	5.863
ENSG00000138303	**ASCC1**	protein_coding	-1.381	0.806	5.863
ENSG00000271524	**BNIP3P17**	processed_pseudogene	-1.381	0.705	5.863
ENSG00000227295	**ELL2P1**	processed_pseudogene	-1.381	0.737	5.863
ENSG00000196678	**ERI2**	protein_coding	-1.381	0.788	5.863
ENSG00000132323	**ILKAP**	protein_coding	-1.381	0.797	5.863
ENSG00000227509	**LINC01839**	lncRNA	-1.381	0.741	5.863
ENSG00000200138	**RNY1P10**	misc_RNA	-1.381	0.779	5.863
ENSG00000254445	**HSPB2-C11orf52**	protein_coding	-1.38	0.724	5.863
ENSG00000230898	**ENSG00000230898**	lncRNA	-1.38	0.731	5.863
ENSG00000280088	**ENSG00000280088**	TEC	-1.38	0.686	5.863
ENSG00000130119	**GNL3L**	protein_coding	-1.379	0.788	5.863
ENSG00000007202	**KIAA0100**	protein_coding	-1.379	0.811	5.863
ENSG00000130227	**XPO7**	protein_coding	-1.379	0.798	5.863
ENSG00000170653	**ATF7**	protein_coding	-1.378	0.789	5.863
ENSG00000108256	**NUFIP2**	protein_coding	-1.378	0.803	5.863
ENSG00000206190	**ATP10A**	protein_coding	-1.377	0.796	5.863
ENSG00000173064	**HECTD4**	protein_coding	-1.377	0.791	5.863
ENSG00000251349	**MSANTD3-TMEFF1**	protein_coding	-1.377	0.596	5.863
ENSG00000267310	**OR4G1P**	transcribed_unprocessed	-1.377	0.73	5.863
ENSG00000256341	**ENSG00000256341**	lncRNA	-1.377	0.76	5.863
ENSG00000260123	**CARMAL**	lncRNA	-1.376	0.795	5.863
ENSG00000286741	**ENSG00000286741**	lncRNA	-1.376	0.603	5.863
ENSG00000182197	**EXT1**	protein_coding	-1.375	0.783	5.863
ENSG00000253073	**RN7SKP295**	misc_RNA	-1.375	0.774	5.863
ENSG00000202245	**RNU6-728P**	snRNA	-1.375	0.732	5.863
ENSG00000253401	**VTA1P2**	processed_pseudogene	-1.375	0.746	5.863
ENSG00000079246	**XRCC5**	protein_coding	-1.375	0.806	5.863
ENSG00000258800	**ENSG00000258800**	lncRNA	-1.375	0.693	5.863
ENSG00000262160	**ENSG00000262160**	lncRNA	-1.375	0.693	5.863
ENSG00000250853	**RNF138P1**	processed_pseudogene	-1.374	0.732	5.863
ENSG00000204713	**TRIM27**	protein_coding	-1.374	0.805	5.863
ENSG00000165490	**DDIAS**	protein_coding	-1.373	0.781	5.863
ENSG00000114867	**EIF4G1**	protein_coding	-1.373	0.804	5.863
ENSG00000089154	**GCN1**	protein_coding	-1.373	0.805	5.863
ENSG00000171208	**NETO2**	protein_coding	-1.373	0.813	5.863
ENSG00000279996	**ENSG00000279996**	TEC	-1.373	0.721	5.863
ENSG00000266992	**DHX40P1**	transcribed_unprocessed	-1.372	0.645	5.863
ENSG00000253546	**IGLVVI-22-1**	IG_V_pseudogene	-1.372	0.805	5.863
ENSG00000225801	**RABEPKP1**	processed_pseudogene	-1.372	0.76	5.863
ENSG00000255310	**ENSG00000255310**	lncRNA	-1.372	0.606	5.863
ENSG00000231340	**ACTG1P10**	processed_pseudogene	-1.371	0.766	5.863
ENSG00000136643	**RPS6KC1**	protein_coding	-1.371	0.818	5.863
ENSG00000165699	**TSC1**	protein_coding	-1.371	0.806	5.863
ENSG00000141664	**ZCCHC2**	protein_coding	-1.371	0.773	5.863

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000145332	**KLHL8**	protein_coding	-1.37	0.796	5.863
ENSG00000135912	**TTLL4**	protein_coding	-1.369	0.811	5.863
ENSG00000279648	**ENSG00000279648**	TEC	-1.369	0.744	5.863
ENSG00000163378	**EOGT**	protein_coding	-1.368	0.79	5.863
ENSG00000189362	**NEMP2**	protein_coding	-1.368	0.796	5.863
ENSG00000211845	**TRAJ44**	TR_J_gene	-1.368	0.663	5.863
ENSG00000166004	**CEP295**	protein_coding	-1.367	0.79	5.863
ENSG00000163349	**HIPK1**	protein_coding	-1.367	0.804	5.863
ENSG00000146247	**PHIP**	protein_coding	-1.367	0.797	5.863
ENSG00000227470	**RPL39P16**	processed_pseudogene	-1.367	0.705	5.863
ENSG00000264538	**SUZ12P1**	transcribed_unprocessed_	-1.367	0.758	5.863
ENSG00000054654	**SYNE2**	protein_coding	-1.367	0.804	5.863
ENSG00000116761	**CTH**	protein_coding	-1.366	0.781	5.863
ENSG00000283476	**MIR1279**	miRNA	-1.366	0.723	5.863
ENSG00000265623	**MIR3139**	miRNA	-1.366	0.73	5.863
ENSG00000006757	**PNPLA4**	protein_coding	-1.366	0.791	5.863
ENSG00000128191	**DGCR8**	protein_coding	-1.365	0.793	5.863
ENSG00000179051	**RCC2**	protein_coding	-1.365	0.795	5.863
ENSG00000180245	**RRH**	protein_coding	-1.365	0.764	5.863
ENSG00000124201	**ZNFX1**	protein_coding	-1.365	0.817	5.863
ENSG00000253118	**ENSG00000253118**	processed_pseudogene	-1.365	0.755	5.863
ENSG00000103194	**USP10**	protein_coding	-1.364	0.82	5.863
ENSG00000274378	**ENSG00000274378**	unprocessed_pseudogene	-1.364	0.477	5.863
ENSG00000213716	**FABP5P5**	processed_pseudogene	-1.363	0.736	5.863
ENSG00000134324	**LPIN1**	protein_coding	-1.363	0.816	5.863
ENSG00000155561	**NUP205**	protein_coding	-1.363	0.81	5.863
ENSG00000182621	**PLCB1**	protein_coding	-1.363	0.798	5.863
ENSG00000108423	**TUBD1**	protein_coding	-1.363	0.789	5.863
ENSG00000271511	**ENSG00000271511**	processed_pseudogene	-1.363	0.717	5.863
ENSG00000178904	**DPY19L3**	protein_coding	-1.362	0.782	5.863
ENSG00000228963	**OR7E93P**	unprocessed_pseudogene	-1.362	0.661	5.863
ENSG00000129810	**SGO1**	protein_coding	-1.362	0.782	5.863
ENSG00000208772	**SNORD94**	snoRNA	-1.362	0.784	5.863
ENSG00000123908	**AGO2**	protein_coding	-1.361	0.806	5.863
ENSG00000274099	**ABCB10P1**	processed_pseudogene	-1.361	0.718	5.863
ENSG00000070269	**TMEM260**	protein_coding	-1.361	0.776	5.863
ENSG00000285734	**ENSG00000285734**	lncRNA	-1.361	0.633	5.863
ENSG00000224032	**EPB41L4A-AS1**	lncRNA	-1.36	0.809	5.863
ENSG00000240207	**ENSG00000240207**	lncRNA	-1.36	0.774	5.863
ENSG00000248185	**ENSG00000248185**	processed_pseudogene	-1.36	0.751	5.863
ENSG00000286008	**ENSG00000286008**	lncRNA	-1.36	0.685	5.863
ENSG00000226419	**SLC16A1-AS1**	lncRNA	-1.359	0.809	5.863
ENSG00000199461	**Y_RNA**	misc_RNA	-1.359	0.685	5.863
ENSG00000231204	**ENSG00000231204**	lncRNA	-1.359	0.799	5.863
ENSG00000279551	**ENSG00000279551**	TEC	-1.359	0.64	5.863
ENSG00000074054	**CLASP1**	protein_coding	-1.358	0.813	5.863
ENSG00000253846	**PCDHGA10**	protein_coding	-1.358	0.785	5.863
ENSG00000101654	**RNMT**	protein_coding	-1.358	0.797	5.863
ENSG00000252108	**RNU6-1232P**	snRNA	-1.358	0.788	5.863

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000225159	**NPM1P39**	processed_pseudogene	-1.357	0.775	5.863
ENSG00000230622	**UQCRHP1**	processed_pseudogene	-1.357	0.722	5.863
ENSG00000163811	**WDR43**	protein_coding	-1.357	0.823	5.863
ENSG00000174442	**ZWILCH**	protein_coding	-1.357	0.793	5.863
ENSG00000279315	**ENSG00000279315**	TEC	-1.357	0.72	5.863
ENSG00000085377	**PREP**	protein_coding	-1.356	0.793	5.863
ENSG00000238882	**RNU6-329P**	snRNA	-1.356	0.72	5.863
ENSG00000141564	**RPTOR**	protein_coding	-1.356	0.811	5.863
ENSG00000139697	**SBNO1**	protein_coding	-1.356	0.825	5.863
ENSG00000100154	**TTC28**	protein_coding	-1.356	0.786	5.863
ENSG00000234844	**CDC42P2**	processed_pseudogene	-1.355	0.791	5.863
ENSG00000198563	**DDX39B**	protein_coding	-1.355	0.823	5.863
ENSG00000117262	**GPR89A**	protein_coding	-1.355	0.814	5.863
ENSG00000252017	**RNU6-1194P**	snRNA	-1.355	0.744	5.863
ENSG00000232205	**CDY18P**	unprocessed_pseudogene	-1.354	0.625	5.863
ENSG00000205683	**DPF3**	protein_coding	-1.354	0.803	5.863
ENSG00000211699	**TRGV3**	TR_V_gene	-1.354	0.771	5.863
ENSG00000229159	**TSPY23P**	unprocessed_pseudogene	-1.354	0.793	5.863
ENSG00000133059	**DSTYK**	protein_coding	-1.353	0.801	5.863
ENSG00000158711	**ELK4**	protein_coding	-1.353	0.813	5.863
ENSG00000157827	**FMNL2**	protein_coding	-1.353	0.795	5.863
ENSG00000116580	**GON4L**	protein_coding	-1.353	0.809	5.863
ENSG00000101928	**MOSPD1**	protein_coding	-1.353	0.8	5.863
ENSG00000253075	**RN7SKP92**	misc_RNA	-1.353	0.702	5.863
ENSG00000279910	**ENSG00000279910**	TEC	-1.353	0.725	5.863
ENSG00000186432	**KPNA4**	protein_coding	-1.352	0.787	5.863
ENSG00000263711	**LINC02864**	lncRNA	-1.352	0.793	5.863
ENSG00000264200	**MIR4693**	miRNA	-1.352	0.818	5.863
ENSG00000068383	**INPP5A**	protein_coding	-1.351	0.803	5.863
ENSG00000114686	**MRPL3**	protein_coding	-1.351	0.815	5.863
ENSG00000105193	**RPS16**	protein_coding	-1.351	0.802	5.863
ENSG00000170265	**ZNF282**	protein_coding	-1.351	0.793	5.863
ENSG00000248227	**LINC02513**	lncRNA	-1.35	0.716	5.863
ENSG00000221680	**MIR1278**	miRNA	-1.35	0.74	5.863
ENSG00000188050	**RNF133**	protein_coding	-1.349	0.746	5.863
ENSG00000177565	**TBL1XR1**	protein_coding	-1.349	0.8	5.863
ENSG00000152253	**SPC25**	protein_coding	-1.348	0.78	5.863
ENSG00000277462	**ZNF670**	protein_coding	-1.348	0.727	5.863
ENSG00000152223	**EPG5**	protein_coding	-1.347	0.807	5.863
ENSG00000108829	**LRRC59**	protein_coding	-1.346	0.802	5.863
ENSG00000214013	**GANC**	protein_coding	-1.345	0.789	5.863
ENSG00000267450	**OR1AB1P**	unprocessed_pseudogene	-1.345	0.751	5.863
ENSG00000268845	**ENSG00000268845**	lncRNA	-1.345	0.76	5.863
ENSG00000275409	**ENSG00000275409**	lncRNA	-1.345	0.668	5.863
ENSG00000260286	**ARMH2**	protein_coding	-1.344	0.793	5.863
ENSG00000086015	**MAST2**	protein_coding	-1.344	0.796	5.863
ENSG00000083635	**NUFIP1**	protein_coding	-1.344	0.8	5.863
ENSG00000201288	**RNU6-1047P**	snRNA	-1.344	0.799	5.863
ENSG00000228681	**ENSG00000228681**	processed_pseudogene	-1.344	0.729	5.863

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000107186	**MPDZ**	protein_coding	-1.343	0.798	5.863
ENSG00000223158	**RNY1P3**	misc_RNA	-1.343	0.713	5.863
ENSG00000122862	**SRGN**	protein_coding	-1.343	0.798	5.863
ENSG00000186660	**ZFP91**	protein_coding	-1.342	0.782	5.863
ENSG00000138138	**ATAD1**	protein_coding	-1.341	0.807	5.863
ENSG00000184156	**KCNQ3**	protein_coding	-1.341	0.79	5.863
ENSG00000279098	**ENSG00000279098**	TEC	-1.341	0.753	5.863
ENSG00000108587	**GOSR1**	protein_coding	-1.34	0.813	5.863
ENSG00000165899	**OTOGL**	protein_coding	-1.34	0.779	5.863
ENSG00000088179	**PTPN4**	protein_coding	-1.34	0.804	5.863
ENSG00000248699	**ENSG00000248699**	processed_pseudogene	-1.34	0.768	5.863
ENSG00000272183	**ENSG00000272183**	lncRNA	-1.34	0.696	5.863
ENSG00000273314	**ENSG00000273314**	lncRNA	-1.34	0.714	5.863
ENSG00000166377	**ATP9B**	protein_coding	-1.339	0.819	5.863
ENSG00000240680	**H4P1**	processed_pseudogene	-1.339	0.688	5.863
ENSG00000070882	**OSBPL3**	protein_coding	-1.339	0.804	5.863
ENSG00000116874	**WARS2**	protein_coding	-1.339	0.8	5.863
ENSG00000123219	**CENPK**	protein_coding	-1.338	0.798	5.863
ENSG00000172936	**MYD88**	protein_coding	-1.338	0.772	5.863
ENSG00000114904	**NEK4**	protein_coding	-1.338	0.787	5.863
ENSG00000151881	**TMEM267**	protein_coding	-1.337	0.803	5.863
ENSG00000274403	**ENSG00000274403**	lncRNA	-1.337	0.733	5.863
ENSG00000132842	**AP3B1**	protein_coding	-1.336	0.8	5.863
ENSG00000157224	**CLDN12**	protein_coding	-1.336	0.778	5.863
ENSG00000175749	**EIF3KP1**	processed_pseudogene	-1.336	0.706	5.863
ENSG00000201545	**RNU4-85P**	snRNA	-1.336	0.735	5.863
ENSG00000196247	**ZNF107**	protein_coding	-1.336	0.785	5.863
ENSG00000251278	**ENSG00000251278**	processed_pseudogene	-1.336	0.786	5.863
ENSG00000276570	**ENSG00000276570**	lncRNA	-1.336	0.671	5.863
ENSG00000133703	**KRAS**	protein_coding	-1.335	0.791	5.863
ENSG00000063322	**MED29**	protein_coding	-1.335	0.782	5.863
ENSG00000145725	**PPIP5K2**	protein_coding	-1.335	0.765	5.863
ENSG00000201574	**RNU1-93P**	snRNA	-1.335	0.668	5.863
ENSG00000138190	**EXOC6**	protein_coding	-1.334	0.807	5.863
ENSG00000081189	**MEF2C**	protein_coding	-1.334	0.822	5.863
ENSG00000201619	**ENSG00000201619**	snoRNA	-1.334	0.653	5.863
ENSG00000008405	**CRY1**	protein_coding	-1.333	0.821	5.863
ENSG00000178917	**ZNF852**	protein_coding	-1.333	0.799	5.863
ENSG00000252945	**ENSG00000252945**	snoRNA	-1.333	0.706	5.863
ENSG00000270387	**ENSG00000270387**	processed_pseudogene	-1.332	0.753	5.863
ENSG00000280376	**ENSG00000280376**	TEC	-1.332	0.657	5.863
ENSG00000138071	**ACTR2**	protein_coding	-1.331	0.811	5.863
ENSG00000196793	**ZNF239**	protein_coding	-1.331	0.801	5.863
ENSG00000253558	**ENSG00000253558**	transcribed_processed_ps	-1.331	0.77	5.863
ENSG00000259712	**ENSG00000259712**	lncRNA	-1.331	0.762	5.863
ENSG00000286165	**ENSG00000286165**	protein_coding	-1.331	0.697	5.863
ENSG00000167258	**CDK12**	protein_coding	-1.33	0.81	5.863
ENSG00000153046	**CDYL**	protein_coding	-1.33	0.825	5.863
ENSG00000249557	**HSPD1P15**	processed_pseudogene	-1.33	0.611	5.863

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000264757	**MIR3198-1**	miRNA	-1.33	0.697	5.863
ENSG00000163584	**RPL22L1**	protein_coding	-1.33	0.792	5.863
ENSG00000029153	**ARNTL2**	protein_coding	-1.329	0.822	5.863
ENSG00000152242	**C18orf25**	protein_coding	-1.329	0.805	5.863
ENSG00000152457	**DCLRE1C**	protein_coding	-1.329	0.775	5.863
ENSG00000160294	**MCM3AP**	protein_coding	-1.329	0.808	5.863
ENSG00000227445	**OR10R1P**	unprocessed_pseudogene	-1.329	0.737	5.863
ENSG00000137872	**SEMA6D**	protein_coding	-1.329	0.789	5.863
ENSG00000287684	**ENSG00000287684**	lncRNA	-1.329	0.699	5.863
ENSG00000057663	**ATG5**	protein_coding	-1.328	0.795	5.863
ENSG00000251363	**LINC02315**	lncRNA	-1.328	0.741	5.863
ENSG00000164930	**FZD6**	protein_coding	-1.327	0.812	5.863
ENSG00000252452	**RNU6-107P**	snRNA	-1.327	0.631	5.863
ENSG00000200645	**RNU6-1210P**	snRNA	-1.327	0.633	5.863
ENSG00000125676	**THOC2**	protein_coding	-1.327	0.809	5.863
ENSG00000225594	**ENSG00000225594**	unprocessed_pseudogene	-1.327	0.703	5.863
ENSG00000226423	**ENSG00000226423**	lncRNA	-1.327	0.773	5.863
ENSG00000068366	**ACSL4**	protein_coding	-1.326	0.804	5.863
ENSG00000198380	**GFPT1**	protein_coding	-1.326	0.816	5.863
ENSG00000263641	**MIR4777**	miRNA	-1.326	0.783	5.863
ENSG00000197381	**ADARB1**	protein_coding	-1.325	0.814	5.863
ENSG00000178999	**AURKB**	protein_coding	-1.325	0.781	5.863
ENSG00000283215	**LINC02537**	lncRNA	-1.325	0.827	5.863
ENSG00000102699	**PARP4**	protein_coding	-1.325	0.802	5.863
ENSG00000227163	**ENSG00000227163**	processed_pseudogene	-1.325	0.762	5.863
ENSG00000215311	**NPM1P12**	processed_pseudogene	-1.324	0.776	5.863
ENSG00000251715	**ENSG00000251715**	snoRNA	-1.324	0.692	5.863
ENSG00000264659	**ENSG00000264659**	lncRNA	-1.324	0.742	5.863
ENSG00000171310	**CHST11**	protein_coding	-1.323	0.795	5.863
ENSG00000257331	**RACGAP1P1**	processed_pseudogene	-1.323	0.751	5.863
ENSG00000235683	**ENSG00000235683**	processed_pseudogene	-1.323	0.66	5.863
ENSG00000253551	**ENSG00000253551**	lncRNA	-1.323	0.71	5.863
ENSG00000273451	**ENSG00000273451**	lncRNA	-1.323	0.706	5.863
ENSG00000166881	**NEMP1**	protein_coding	-1.322	0.768	5.863
ENSG00000150907	**FOXO1**	protein_coding	-1.321	0.749	5.863
ENSG00000105576	**TNPO2**	protein_coding	-1.32	0.809	5.863
ENSG00000250928	**ENSG00000250928**	processed_pseudogene	-1.32	0.73	5.863
ENSG00000186480	**INSIG1**	protein_coding	-1.319	0.808	5.863
ENSG00000143947	**RPS27A**	protein_coding	-1.319	0.807	5.863
ENSG00000230965	**SNX18P13**	processed_pseudogene	-1.319	0.672	5.863
ENSG00000213036	**ENSG00000213036**	processed_pseudogene	-1.319	0.664	5.863
ENSG00000254124	**EEF1A1P37**	processed_pseudogene	-1.318	0.819	5.863
ENSG00000175387	**SMAD2**	protein_coding	-1.318	0.816	5.863
ENSG00000095209	**TMEM38B**	protein_coding	-1.318	0.828	5.863
ENSG00000132256	**TRIM5**	protein_coding	-1.318	0.793	5.863
ENSG00000180011	**ZADH2**	protein_coding	-1.318	0.793	5.863
ENSG00000278475	**ENSG00000278475**	lncRNA	-1.318	0.777	5.863
ENSG00000177981	**ASB8**	protein_coding	-1.317	0.795	5.863
ENSG00000159267	**HLCS**	protein_coding	-1.317	0.81	5.863

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000171223	**JUNB**	protein_coding	-1.317	0.766	5.863
ENSG00000254894	**NAV2-AS1**	lncRNA	-1.317	0.728	5.863
ENSG00000136159	**NUDT15**	protein_coding	-1.317	0.78	5.863
ENSG00000258397	**BCAR1P1**	processed_pseudogene	-1.316	0.646	5.863
ENSG00000236562	**IFITM3P1**	processed_pseudogene	-1.316	0.702	5.863
ENSG00000258568	**RHOQP1**	processed_pseudogene	-1.316	0.772	5.863
ENSG00000179091	**CYC1**	protein_coding	-1.315	0.794	5.863
ENSG00000211955	**IGHV3-33**	IG_V_gene	-1.315	0.734	5.863
ENSG00000135164	**DMTF1**	protein_coding	-1.314	0.808	5.863
ENSG00000200247	**RNU6-254P**	snRNA	-1.314	0.751	5.863
ENSG00000187764	**SEMA4D**	protein_coding	-1.314	0.823	5.863
ENSG00000149970	**CNKSR2**	protein_coding	-1.313	0.81	5.863
ENSG00000070759	**TESK2**	protein_coding	-1.313	0.787	5.863
ENSG00000131725	**WDR44**	protein_coding	-1.313	0.812	5.863
ENSG00000207488	**Y_RNA**	misc_RNA	-1.313	0.751	5.863
ENSG00000232952	**ENSG00000232952**	processed_pseudogene	-1.313	0.742	5.863
ENSG00000162769	**FLVCR1**	protein_coding	-1.312	0.796	5.863
ENSG00000186566	**GPATCH8**	protein_coding	-1.311	0.808	5.863
ENSG00000011258	**MBTD1**	protein_coding	-1.311	0.813	5.863
ENSG00000119685	**TTLL5**	protein_coding	-1.311	0.803	5.863
ENSG00000166716	**ZNF592**	protein_coding	-1.311	0.814	5.863
ENSG00000250071	**ENSG00000250071**	processed_pseudogene	-1.311	0.705	5.863
ENSG00000159131	**GART**	protein_coding	-1.31	0.826	5.863
ENSG00000115290	**GRB14**	protein_coding	-1.31	0.805	5.863
ENSG00000198836	**OPA1**	protein_coding	-1.31	0.809	5.863
ENSG00000134086	**VHL**	protein_coding	-1.31	0.809	5.863
ENSG00000260743	**ENSG00000260743**	lncRNA	-1.31	0.773	5.863
ENSG00000271175	**ENSG00000271175**	processed_pseudogene	-1.31	0.733	5.863
ENSG00000181090	**EHMT1**	protein_coding	-1.309	0.812	5.863
ENSG00000264616	**MIR4755**	miRNA	-1.309	0.766	5.863
ENSG00000204410	**MSH5**	protein_coding	-1.309	0.802	5.863
ENSG00000138744	**NAAA**	protein_coding	-1.309	0.801	5.863
ENSG00000199940	**RN7SKP75**	misc_RNA	-1.309	0.744	5.863
ENSG00000197312	**DDI2**	protein_coding	-1.308	0.824	5.863
ENSG00000228523	**DNAJB6P4**	processed_pseudogene	-1.308	0.732	5.863
ENSG00000139641	**ESYT1**	protein_coding	-1.308	0.808	5.863
ENSG00000148840	**PPRC1**	protein_coding	-1.308	0.816	5.863
ENSG00000138375	**SMARCAL1**	protein_coding	-1.308	0.811	5.863
ENSG00000279145	**ENSG00000279145**	lncRNA	-1.308	0.692	5.863
ENSG00000068697	**LAPTM4A**	protein_coding	-1.307	0.808	5.863
ENSG00000268295	**POLR3GP1**	transcribed_processed_p	-1.307	0.784	5.863
ENSG00000123444	**KBTBD4**	protein_coding	-1.306	0.774	5.863
ENSG00000108946	**PRKAR1A**	protein_coding	-1.306	0.807	5.863
ENSG00000223198	**RNU2-22P**	snRNA	-1.306	0.678	5.863
ENSG00000249363	**ENSG00000249363**	processed_pseudogene	-1.306	0.729	5.863
ENSG00000270409	**ENSG00000270409**	transcribed_unprocessed_	-1.306	0.779	5.863
ENSG00000201701	**ENSG00000201701**	snoRNA	-1.305	0.762	5.863
ENSG00000267637	**ENSG00000267637**	lncRNA	-1.305	0.77	5.863
ENSG00000274021	**ENSG00000274021**	lncRNA	-1.305	0.787	5.863

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000250115	**AK3P2**	processed_pseudogene	-1.304	0.767	5.863
ENSG00000073849	**ST6GAL1**	protein_coding	-1.304	0.797	5.863
ENSG00000275046	**ENSG00000275046**	processed_pseudogene	-1.304	0.667	5.863
ENSG00000277151	**ENSG00000277151**	lncRNA	-1.304	0.717	5.863
ENSG00000150768	**DLAT**	protein_coding	-1.303	0.821	5.863
ENSG00000115109	**EPB41L5**	protein_coding	-1.303	0.806	5.863
ENSG00000122912	**SLC25A16**	protein_coding	-1.303	0.794	5.863
ENSG00000025772	**TOMM34**	protein_coding	-1.303	0.787	5.863
ENSG00000223518	**CSNK1A1P1**	transcribed_processed_p	-1.302	0.768	5.863
ENSG00000136231	**IGF2BP3**	protein_coding	-1.302	0.8	5.863
ENSG00000162623	**TYW3**	protein_coding	-1.302	0.797	5.863
ENSG00000254644	**ENSG00000254644**	processed_pseudogene	-1.302	0.767	5.863
ENSG00000286386	**ENSG00000286386**	lncRNA	-1.302	0.697	5.863
ENSG00000198130	**HIBCH**	protein_coding	-1.301	0.805	5.863
ENSG00000156504	**PABIR2**	protein_coding	-1.301	0.799	5.863
ENSG00000234835	**PHBP13**	processed_pseudogene	-1.301	0.715	5.863
ENSG00000272391	**POM121C**	protein_coding	-1.301	0.801	5.863
ENSG00000214837	**LINC01347**	transcribed_unprocessed_	-1.3	0.807	5.863
ENSG00000206562	**METTL6**	protein_coding	-1.3	0.802	5.863
ENSG00000185973	**TMLHE**	protein_coding	-1.3	0.78	5.863
ENSG00000083223	**TUT7**	protein_coding	-1.3	0.807	5.863
ENSG00000259647	**ENSG00000259647**	lncRNA	-1.3	0.671	5.863
ENSG00000183354	**KIAA2026**	protein_coding	-1.299	0.786	5.863
ENSG00000216813	**ENSG00000216813**	processed_pseudogene	-1.299	0.776	5.863
ENSG00000206149	**HERC2P9**	transcribed_unprocessed_	-1.298	0.772	5.863
ENSG00000134330	**IAH1**	protein_coding	-1.298	0.819	5.863
ENSG00000223086	**RNA5SP155**	rRNA_pseudogene	-1.298	0.714	5.863
ENSG00000124422	**USP22**	protein_coding	-1.298	0.796	5.863
ENSG00000285077	**ARHGAP11B**	protein_coding	-1.297	0.722	5.863
ENSG00000198862	**LTN1**	protein_coding	-1.297	0.81	5.863
ENSG00000113100	**CDH9**	protein_coding	-1.296	0.808	5.863
ENSG00000226658	**RPL23AP30**	processed_pseudogene	-1.296	0.779	5.863
ENSG00000267771	**ENSG00000267771**	unprocessed_pseudogen	-1.296	0.665	5.863
ENSG00000207493	**SNORA46**	snoRNA	-1.295	0.772	5.863
ENSG00000178665	**ZNF713**	protein_coding	-1.294	0.804	5.863
ENSG00000218520	**ENSG00000218520**	processed_pseudogene	-1.294	0.691	5.863
ENSG00000226380	**ENSG00000226380**	lncRNA	-1.294	0.749	5.863
ENSG00000187676	**B3GLCT**	protein_coding	-1.293	0.8	5.863
ENSG00000200102	**RNU6-252P**	snRNA	-1.293	0.713	5.863
ENSG00000285676	**ENSG00000285676**	lncRNA	-1.293	0.591	5.863
ENSG00000065809	**FAM107B**	protein_coding	-1.292	0.773	5.863
ENSG00000236121	**HAUS6P2**	processed_pseudogene	-1.292	0.707	5.863
ENSG00000143674	**MAP3K21**	protein_coding	-1.292	0.829	5.863
ENSG00000137955	**RABGGTB**	protein_coding	-1.292	0.799	5.863
ENSG00000086589	**RBM22**	protein_coding	-1.292	0.812	5.863
ENSG00000230727	**RBMY2WP**	unprocessed_pseudogen	-1.292	0.778	5.863
ENSG00000147526	**TACC1**	protein_coding	-1.292	0.806	5.863
ENSG00000013810	**TACC3**	protein_coding	-1.292	0.798	5.863
ENSG00000189042	**ZNF567**	protein_coding	-1.292	0.827	5.863

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000239407	**ENSG00000239407**	lncRNA	-1.292	0.797	5.863
ENSG00000256663	**ENSG00000256663**	processed_pseudogene	-1.292	0.792	5.863
ENSG00000082153	**BZW1**	protein_coding	-1.291	0.82	5.863
ENSG00000251787	**RNU7-47P**	snRNA	-1.291	0.665	5.863
ENSG00000225918	**RPL7P59**	processed_pseudogene	-1.291	0.698	5.863
ENSG00000036054	**TBC1D23**	protein_coding	-1.291	0.824	5.863
ENSG00000230029	**CDY11P**	unprocessed_pseudogen	-1.29	0.76	5.863
ENSG00000271123	**ELOCP5**	processed_pseudogene	-1.29	0.77	5.863
ENSG00000066583	**ISOC1**	protein_coding	-1.29	0.764	5.863
ENSG00000249915	**PDCD6**	protein_coding	-1.29	0.818	5.863
ENSG00000177181	**RIMKLA**	protein_coding	-1.29	0.822	5.863
ENSG00000152102	**FAM168B**	protein_coding	-1.289	0.812	5.863
ENSG00000147509	**RGS20**	protein_coding	-1.289	0.792	5.863
ENSG00000244088	**RPL23AP44**	processed_pseudogene	-1.289	0.789	5.863
ENSG00000198794	**SCAMP5**	protein_coding	-1.289	0.777	5.863
ENSG00000127364	**TAS2R4**	protein_coding	-1.289	0.804	5.863
ENSG00000225581	**TRIM53AP**	unprocessed_pseudogen	-1.289	0.651	5.863
ENSG00000168228	**ZCCHC4**	protein_coding	-1.289	0.821	5.863
ENSG00000256733	**ENSG00000256733**	lncRNA	-1.289	0.812	5.863
ENSG00000286855	**ENSG00000286855**	lncRNA	-1.288	0.73	5.863
ENSG00000144395	**CCDC150**	protein_coding	-1.287	0.819	5.863
ENSG00000055609	**KMT2C**	protein_coding	-1.287	0.816	5.863
ENSG00000221954	**OR4C12**	protein_coding	-1.287	0.678	5.863
ENSG00000251768	**RNA5SP217**	rRNA_pseudogene	-1.287	0.744	5.863
ENSG00000252651	**RNU6-557P**	snRNA	-1.287	0.751	5.863
ENSG00000139737	**SLAIN1**	protein_coding	-1.287	0.797	5.863
ENSG00000211820	**TRAV41**	TR_V_gene	-1.287	0.77	5.863
ENSG00000092208	**GEMIN2**	protein_coding	-1.286	0.802	5.863
ENSG00000147421	**HMBOX1**	protein_coding	-1.286	0.823	5.863
ENSG00000225723	**MTND6P15**	processed_pseudogene	-1.286	0.721	5.863
ENSG00000227663	**RPL7P2**	processed_pseudogene	-1.286	0.77	5.863
ENSG00000112742	**TTK**	protein_coding	-1.286	0.794	5.863
ENSG00000201778	**Y_RNA**	misc_RNA	-1.286	0.655	5.863
ENSG00000273064	**ENSG00000273064**	lncRNA	-1.286	0.766	5.863
ENSG00000287590	**ENSG00000287590**	lncRNA	-1.286	0.708	5.863
ENSG00000157985	**AGAP1**	protein_coding	-1.285	0.804	5.863
ENSG00000169598	**DFFB**	protein_coding	-1.285	0.816	5.863
ENSG00000163755	**HPS3**	protein_coding	-1.285	0.804	5.863
ENSG00000118961	**LDAH**	protein_coding	-1.285	0.787	5.863
ENSG00000166326	**TRIM44**	protein_coding	-1.285	0.811	5.863
ENSG00000237679	**VDAC1P11**	processed_pseudogene	-1.285	0.809	5.863
ENSG00000273139	**ENSG00000273139**	lncRNA	-1.285	0.695	5.863
ENSG00000286141	**ENSG00000286141**	lncRNA	-1.285	0.739	5.863
ENSG00000112218	**GPR63**	protein_coding	-1.284	0.785	5.863
ENSG00000249263	**PARP4P3**	transcribed_unprocessed_	-1.284	0.743	5.863
ENSG00000166439	**RNF169**	protein_coding	-1.284	0.822	5.863
ENSG00000256804	**ENSG00000256804**	processed_pseudogene	-1.284	0.698	5.863
ENSG00000261609	**GAN**	protein_coding	-1.283	0.801	5.863
ENSG00000198951	**NAGA**	protein_coding	-1.283	0.798	5.863

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000204702	**OR2J1**	protein_coding	-1.283	0.755	5.863
ENSG00000225192	**ZNF33BP1**	processed_pseudogene	-1.283	0.782	5.863
ENSG00000236159	**ENSG00000236159**	processed_pseudogene	-1.283	0.734	5.863
ENSG00000006740	**ARHGAP44**	protein_coding	-1.282	0.815	5.863
ENSG00000171456	**ASXL1**	protein_coding	-1.282	0.811	5.863
ENSG00000233080	**LINC01399**	transcribed_processed_ps	-1.282	0.811	5.863
ENSG00000151835	**SACS**	protein_coding	-1.282	0.809	5.863
ENSG00000119953	**SMNDC1**	protein_coding	-1.282	0.812	5.863
ENSG00000112320	**SOBP**	protein_coding	-1.282	0.788	5.863
ENSG00000256533	**ENSG00000256533**	processed_pseudogene	-1.282	0.69	5.863
ENSG00000268282	**ENSG00000268282**	processed_pseudogene	-1.282	0.793	5.863
ENSG00000110328	**GALNT18**	protein_coding	-1.281	0.773	5.863
ENSG00000128585	**MKLN1**	protein_coding	-1.281	0.806	5.863
ENSG00000126653	**NSRP1**	protein_coding	-1.281	0.82	5.863
ENSG00000253327	**RAD21-AS1**	lncRNA	-1.281	0.808	5.863
ENSG00000286195	**ENSG00000286195**	lncRNA	-1.281	0.685	5.863
ENSG00000087299	**L2HGDH**	protein_coding	-1.28	0.796	5.863
ENSG00000158528	**PPP1R9A**	protein_coding	-1.28	0.809	5.863
ENSG00000139998	**RAB15**	protein_coding	-1.28	0.795	5.863
ENSG00000284879	**ENSG00000284879**	lncRNA	-1.28	0.724	5.863
ENSG00000213983	**AP1G2**	protein_coding	-1.279	0.805	5.863
ENSG00000156471	**PTDSS1**	protein_coding	-1.279	0.825	5.863
ENSG00000137642	**SORL1**	protein_coding	-1.279	0.81	5.863
ENSG00000251878	**SNORD79**	snoRNA	-1.278	0.779	5.863
ENSG00000181722	**ZBTB20**	protein_coding	-1.278	0.8	5.863
ENSG00000067177	**PHKA1**	protein_coding	-1.277	0.807	5.863
ENSG00000270116	**ENSG00000270116**	lncRNA	-1.277	0.696	5.863
ENSG00000279416	**ENSG00000279416**	TEC	-1.277	0.786	5.863
ENSG00000167522	**ANKRD11**	protein_coding	-1.276	0.808	5.863
ENSG00000234741	**GAS5**	lncRNA	-1.276	0.801	5.863
ENSG00000187504	**RPL7P48**	processed_pseudogene	-1.276	0.673	5.863
ENSG00000243920	**RPS26P24**	processed_pseudogene	-1.276	0.735	5.863
ENSG00000253013	**ENSG00000253013**	snoRNA	-1.276	0.733	5.863
ENSG00000268043	**NBPF12**	protein_coding	-1.275	0.783	5.863
ENSG00000253437	**RNU6-988P**	snRNA	-1.275	0.788	5.863
ENSG00000160208	**RRP1B**	protein_coding	-1.275	0.81	5.863
ENSG00000267920	**SNX6P1**	processed_pseudogene	-1.275	0.728	5.863
ENSG00000163960	**UBXN7**	protein_coding	-1.275	0.809	5.863
ENSG00000143951	**WDPCP**	protein_coding	-1.275	0.806	5.863
ENSG00000207100	**ENSG00000207100**	snoRNA	-1.275	0.633	5.863
ENSG00000279366	**ENSG00000279366**	TEC	-1.275	0.773	5.863
ENSG00000229918	**DOCK9-AS1**	lncRNA	-1.274	0.807	5.863
ENSG00000215961	**MIR297**	miRNA	-1.274	0.78	5.863
ENSG00000117751	**PPP1R8**	protein_coding	-1.274	0.809	5.863
ENSG00000154001	**PPP2R5E**	protein_coding	-1.274	0.822	5.863
ENSG00000213585	**VDAC1**	protein_coding	-1.274	0.81	5.863
ENSG00000200448	**Y_RNA**	misc_RNA	-1.274	0.763	5.863
ENSG00000272801	**ENSG00000272801**	lncRNA	-1.274	0.684	5.863
ENSG00000286753	**ENSG00000286753**	lncRNA	-1.274	0.76	5.863

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000105926	**MPP6**	protein_coding	-1.273	0.8	5.863
ENSG00000105426	**PTPRS**	protein_coding	-1.273	0.823	5.863
ENSG00000224271	**ENSG00000224271**	lncRNA	-1.273	0.803	5.863
ENSG00000253307	**ENSG00000253307**	lncRNA	-1.273	0.789	5.863
ENSG00000272076	**ENSG00000272076**	lncRNA	-1.273	0.725	5.863
ENSG00000277227	**ENSG00000277227**	unprocessed_pseudogene	-1.273	0.733	5.863
ENSG00000153093	**ACOXL**	protein_coding	-1.272	0.809	5.863
ENSG00000102900	**NUP93**	protein_coding	-1.272	0.811	5.863
ENSG00000164430	**CGAS**	protein_coding	-1.271	0.796	5.863
ENSG00000163507	**CIP2A**	protein_coding	-1.271	0.794	5.863
ENSG00000266038	**MIR4659A**	miRNA	-1.27	0.736	5.863
ENSG00000199411	**SNORD62**	snoRNA	-1.27	0.598	5.863
ENSG00000261279	**ULK4P1**	transcribed_unprocessed_	-1.27	0.724	5.863
ENSG00000205189	**ZBTB10**	protein_coding	-1.27	0.782	5.863
ENSG00000269662	**BNIP3P39**	processed_pseudogene	-1.269	0.781	5.863
ENSG00000163938	**GNL3**	protein_coding	-1.269	0.823	5.863
ENSG00000251019	**HIGD1AP13**	processed_pseudogene	-1.269	0.705	5.863
ENSG00000078589	**P2RY10**	protein_coding	-1.269	0.809	5.863
ENSG00000251045	**SLC25A48-AS1**	lncRNA	-1.269	0.802	5.863
ENSG00000117500	**TMED5**	protein_coding	-1.269	0.827	5.863
ENSG00000279952	**ENSG00000279952**	TEC	-1.269	0.776	5.863
ENSG00000200601	**RNA5SP50**	rRNA_pseudogene	-1.268	0.795	5.863
ENSG00000116754	**SRSF11**	protein_coding	-1.268	0.833	5.863
ENSG00000212347	**ENSG00000212347**	snoRNA	-1.268	0.761	5.863
ENSG00000230506	**ENSG00000230506**	lncRNA	-1.268	0.747	5.863
ENSG00000277576	**ENSG00000277576**	unprocessed_pseudogene	-1.268	0.778	5.863
ENSG00000214252	**AZGP1P2**	unprocessed_pseudogene	-1.267	0.775	5.863
ENSG00000106560	**GIMAP2**	protein_coding	-1.267	0.738	5.863
ENSG00000265981	**MIR544B**	miRNA	-1.267	0.664	5.863
ENSG00000173821	**RNF213**	protein_coding	-1.267	0.8	5.863
ENSG00000252082	**RNU6-547P**	snRNA	-1.267	0.763	5.863
ENSG00000252743	**RNU6-850P**	snRNA	-1.267	0.813	5.863
ENSG00000255717	**SNHG1**	lncRNA	-1.267	0.819	5.863
ENSG00000225326	**USP9YP19**	unprocessed_pseudogene	-1.267	0.667	5.863
ENSG00000243081	**ENSG00000243081**	lncRNA	-1.267	0.729	5.863
ENSG00000272085	**ENSG00000272085**	lncRNA	-1.267	0.726	5.863
ENSG00000286420	**ENSG00000286420**	lncRNA	-1.266	0.8	5.863
ENSG00000091140	**DLD**	protein_coding	-1.265	0.812	5.863
ENSG00000163798	**SLC4A1AP**	protein_coding	-1.265	0.814	5.863
ENSG00000114126	**TFDP2**	protein_coding	-1.265	0.814	5.863
ENSG00000249978	**TRGV7**	TR_V_pseudogene	-1.265	0.681	5.863
ENSG00000071539	**TRIP13**	protein_coding	-1.265	0.824	5.863
ENSG00000161533	**ACOX1**	protein_coding	-1.264	0.808	5.863
ENSG00000230750	**SDAD1P2**	processed_pseudogene	-1.264	0.787	5.863
ENSG00000072858	**SIDT1**	protein_coding	-1.264	0.804	5.863
ENSG00000092330	**TINF2**	protein_coding	-1.264	0.812	5.863
ENSG00000106477	**CEP41**	protein_coding	-1.263	0.801	5.863
ENSG00000084754	**HADHA**	protein_coding	-1.263	0.807	5.863
ENSG00000283569	**MIR4773-2**	miRNA	-1.263	0.736	5.863

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000101843	**PSMD10**	protein_coding	-1.263	0.825	5.863
ENSG00000267224	**ENSG00000267224**	lncRNA	-1.263	0.798	5.863
ENSG00000267838	**ENSG00000267838**	lncRNA	-1.263	0.695	5.863
ENSG00000133019	**CHRM3**	protein_coding	-1.262	0.801	5.863
ENSG00000058262	**SEC61A1**	protein_coding	-1.262	0.823	5.863
ENSG00000183171	**ENSG00000183171**	processed_pseudogene	-1.262	0.782	5.863
ENSG00000260465	**ENSG00000260465**	lncRNA	-1.262	0.749	5.863
ENSG00000134698	**AGO4**	protein_coding	-1.261	0.809	5.863
ENSG00000163214	**DHX57**	protein_coding	-1.261	0.82	5.863
ENSG00000137942	**FNBP1L**	protein_coding	-1.261	0.813	5.863
ENSG00000100938	**GMPR2**	protein_coding	-1.261	0.799	5.863
ENSG00000230585	**PHBP12**	processed_pseudogene	-1.261	0.684	5.863
ENSG00000227581	**STAU2P1**	processed_pseudogene	-1.261	0.649	5.863
ENSG00000280325	**ENSG00000280325**	TEC	-1.261	0.736	5.863
ENSG00000207994	**MIR100**	miRNA	-1.26	0.756	5.863
ENSG00000272498	**ENSG00000272498**	lncRNA	-1.26	0.799	5.863
ENSG00000279841	**ENSG00000279841**	TEC	-1.26	0.769	5.863
ENSG00000284705	**ENSG00000284705**	lncRNA	-1.26	0.66	5.863
ENSG00000228411	**CDY4P**	processed_pseudogene	-1.259	0.815	5.863
ENSG00000214035	**ENSG00000214035**	processed_pseudogene	-1.259	0.741	5.863
ENSG00000226843	**ENSG00000226843**	processed_pseudogene	-1.259	0.807	5.863
ENSG00000122026	**RPL21**	protein_coding	-1.258	0.82	5.863
ENSG00000280369	**ENSG00000280369**	TEC	-1.258	0.636	5.863
ENSG00000285082	**ENSG00000285082**	protein_coding	-1.258	0.722	5.863
ENSG00000142002	**DPP9**	protein_coding	-1.257	0.808	5.863
ENSG00000257504	**LINC02297**	lncRNA	-1.257	0.667	5.863
ENSG00000231613	**ENSG00000231613**	lncRNA	-1.257	0.745	5.863
ENSG00000271843	**ENSG00000271843**	lncRNA	-1.257	0.758	5.863
ENSG00000286571	**ENSG00000286571**	lncRNA	-1.257	0.723	5.863
ENSG00000234147	**ENSG00000234147**	lncRNA	-1.256	0.755	5.863
ENSG00000264911	**ENSG00000264911**	processed_pseudogene	-1.256	0.813	5.863
ENSG00000259670	**ENSG00000259670**	lncRNA	-1.255	0.798	5.863
ENSG00000140526	**ABHD2**	protein_coding	-1.254	0.816	5.863
ENSG00000160783	**PMF1**	protein_coding	-1.254	0.817	5.863
ENSG00000140105	**WARS1**	protein_coding	-1.254	0.815	5.863
ENSG00000270804	**ENSG00000270804**	transcribed_processed_ps	-1.254	0.805	5.863
ENSG00000278946	**ENSG00000278946**	lncRNA	-1.254	0.789	5.863
ENSG00000109572	**CLCN3**	protein_coding	-1.253	0.808	5.863
ENSG00000117650	**NEK2**	protein_coding	-1.253	0.78	5.863
ENSG00000170605	**OR9K2**	protein_coding	-1.253	0.716	5.863
ENSG00000173431	**RNASE8**	protein_coding	-1.253	0.796	5.863
ENSG00000213853	**EMP2**	protein_coding	-1.252	0.813	5.863
ENSG00000164167	**LSM6**	protein_coding	-1.252	0.814	5.863
ENSG00000136603	**SKIL**	protein_coding	-1.252	0.824	5.863
ENSG00000164828	**SUN1**	protein_coding	-1.252	0.816	5.863
ENSG00000206573	**THUMPD3-AS1**	lncRNA	-1.252	0.812	5.863
ENSG00000271204	**ENSG00000271204**	lncRNA	-1.252	0.734	5.863
ENSG00000249286	**AMD1P3**	processed_pseudogene	-1.251	0.78	5.863
ENSG00000220871	**DNAJC19P6**	processed_pseudogene	-1.251	0.747	5.863

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000229221	**HNRNPA1P66**	processed_pseudogene	-1.251	0.746	5.863
ENSG00000278236	**ENSG00000278236**	misc_RNA	-1.251	0.553	5.863
ENSG00000112234	**FBXL4**	protein_coding	-1.25	0.799	5.863
ENSG00000095015	**MAP3K1**	protein_coding	-1.25	0.817	5.863
ENSG00000053372	**MRTO4**	protein_coding	-1.25	0.798	5.863
ENSG00000102038	**SMARCA1**	protein_coding	-1.25	0.806	5.863
ENSG00000119596	**YLPM1**	protein_coding	-1.25	0.828	5.863
ENSG00000261167	**ENSG00000261167**	lncRNA	-1.25	0.686	5.863
ENSG00000166266	**CUL5**	protein_coding	-1.249	0.817	5.863
ENSG00000246863	**GPR176-DT**	lncRNA	-1.249	0.82	5.863
ENSG00000162601	**MYSM1**	protein_coding	-1.249	0.816	5.863
ENSG00000201343	**Y_RNA**	misc_RNA	-1.249	0.773	5.863
ENSG00000001629	**ANKIB1**	protein_coding	-1.248	0.813	5.863
ENSG00000162819	**BROX**	protein_coding	-1.248	0.777	5.863
ENSG00000222445	**RN7SKP56**	misc_RNA	-1.248	0.708	5.863
ENSG00000237296	**SMG1P1**	transcribed_unprocessed_	-1.248	0.762	5.863
ENSG00000229271	**ENSG00000229271**	lncRNA	-1.248	0.826	5.863
ENSG00000160588	**MPZL3**	protein_coding	-1.247	0.8	5.863
ENSG00000241186	**TDGF1**	protein_coding	-1.247	0.765	5.863
ENSG00000261544	**ENSG00000261544**	lncRNA	-1.247	0.778	5.863
ENSG00000166147	**FBN1**	protein_coding	-1.246	0.809	5.863
ENSG00000239119	**RNU7-119P**	snRNA	-1.246	0.813	5.863
ENSG00000115268	**RPS15**	protein_coding	-1.246	0.809	5.863
ENSG00000201182	**RNU6-670P**	snRNA	-1.245	0.613	5.863
ENSG00000227236	**ENSG00000227236**	processed_pseudogene	-1.245	0.769	5.863
ENSG00000198799	**LRIG2**	protein_coding	-1.244	0.813	5.863
ENSG00000231049	**OR52B5P**	transcribed_unprocessed_	-1.244	0.778	5.863
ENSG00000273106	**PPM1B-DT**	lncRNA	-1.244	0.743	5.863
ENSG00000120594	**PLXDC2**	protein_coding	-1.243	0.791	5.863
ENSG00000206939	**RNU6-281P**	snRNA	-1.243	0.734	5.863
ENSG00000238304	**RNU7-50P**	snRNA	-1.243	0.615	5.863
ENSG00000147010	**SH3KBP1**	protein_coding	-1.243	0.812	5.863
ENSG00000143324	**XPR1**	protein_coding	-1.243	0.808	5.863
ENSG00000249993	**BFSP2-AS1**	lncRNA	-1.242	0.765	5.863
ENSG00000113161	**HMGCR**	protein_coding	-1.242	0.813	5.863
ENSG00000265503	**MIR1269B**	miRNA	-1.242	0.716	5.863
ENSG00000107263	**RAPGEF1**	protein_coding	-1.242	0.798	5.863
ENSG00000241745	**RN7SL788P**	misc_RNA	-1.242	0.797	5.863
ENSG00000283347	**ENSG00000283347**	lncRNA	-1.242	0.777	5.863
ENSG00000263020	**ENSG00000263020**	protein_coding	-1.241	0.794	5.863
ENSG00000273090	**ENSG00000273090**	lncRNA	-1.241	0.733	5.863
ENSG00000224549	**ENSG00000224549**	lncRNA	-1.241	0.753	8.482
ENSG00000070831	**CDC42**	protein_coding	-1.24	0.803	8.482
ENSG00000180229	**HERC2P3**	transcribed_unprocessed_	-1.24	0.805	8.482
ENSG00000199135	**MIR101-1**	miRNA	-1.24	0.761	8.482
ENSG00000223677	**OR2AD1P**	unprocessed_pseudogene	-1.24	0.737	8.482
ENSG00000168778	**TCTN2**	protein_coding	-1.24	0.79	8.482
ENSG00000286995	**ENSG00000286995**	lncRNA	-1.24	0.711	8.482
ENSG00000182831	**C16orf72**	protein_coding	-1.239	0.837	8.482

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000231721	**LINC-PINT**	lncRNA	-1.239	0.788	8.482
ENSG00000151576	**QTRT2**	protein_coding	-1.239	0.812	8.482
ENSG00000287871	**ENSG00000287871**	lncRNA	-1.239	0.798	8.482
ENSG00000248131	**LINC01194**	lncRNA	-1.238	0.805	8.482
ENSG00000238205	**MPC1L**	protein_coding	-1.238	0.788	8.482
ENSG00000236920	**ENSG00000236920**	lncRNA	-1.238	0.727	8.482
ENSG00000238707	**ENSG00000238707**	snoRNA	-1.238	0.823	8.482
ENSG00000286837	**ENSG00000286837**	lncRNA	-1.238	0.744	8.482
ENSG00000257594	**GALNT4**	protein_coding	-1.237	0.785	8.482
ENSG00000131351	**HAUS8**	protein_coding	-1.237	0.807	8.482
ENSG00000153187	**HNRNPU**	protein_coding	-1.237	0.814	8.482
ENSG00000163738	**MTHFD2L**	protein_coding	-1.237	0.815	8.482
ENSG00000203739	**PRDX6-AS1**	lncRNA	-1.237	0.788	8.482
ENSG00000122257	**RBBP6**	protein_coding	-1.237	0.814	8.482
ENSG00000124788	**ATXN1**	protein_coding	-1.236	0.82	8.482
ENSG00000267153	**CTBP2P3**	processed_pseudogene	-1.236	0.761	8.482
ENSG00000105993	**DNAJB6**	protein_coding	-1.236	0.821	8.482
ENSG00000235651	**G3BP1P1**	processed_pseudogene	-1.236	0.707	8.482
ENSG00000075975	**MKRN2**	protein_coding	-1.236	0.811	8.482
ENSG00000165832	**TRUB1**	protein_coding	-1.236	0.803	8.482
ENSG00000241102	**ENSG00000241102**	processed_pseudogene	-1.236	0.773	8.482
ENSG00000111832	**RWDD1**	protein_coding	-1.235	0.778	8.482
ENSG00000197961	**ZNF121**	protein_coding	-1.235	0.816	8.482
ENSG00000280060	**ENSG00000280060**	TEC	-1.235	0.639	8.482
ENSG00000287552	**ENSG00000287552**	lncRNA	-1.235	0.587	8.482
ENSG00000251595	**ABCA11P**	transcribed_processed_p	-1.234	0.726	8.482
ENSG00000132964	**CDK8**	protein_coding	-1.234	0.804	8.482
ENSG00000239650	**GUSBP4**	transcribed_unprocessed_	-1.234	0.534	8.482
ENSG00000145555	**MYO10**	protein_coding	-1.234	0.828	8.482
ENSG00000109320	**NFKB1**	protein_coding	-1.234	0.828	8.482
ENSG00000001167	**NFYA**	protein_coding	-1.234	0.794	8.482
ENSG00000112210	**RAB23**	protein_coding	-1.234	0.801	8.482
ENSG00000104635	**SLC39A14**	protein_coding	-1.234	0.818	8.482
ENSG00000164953	**TMEM67**	protein_coding	-1.234	0.807	8.482
ENSG00000132846	**ZBED3**	protein_coding	-1.234	0.777	8.482
ENSG00000175322	**ZNF519**	protein_coding	-1.234	0.816	8.482
ENSG00000215547	**DEFB115**	protein_coding	-1.233	0.764	8.482
ENSG00000252777	**ENSG00000252777**	scaRNA	-1.233	0.603	8.482
ENSG00000271578	**ENSG00000271578**	processed_pseudogene	-1.233	0.812	8.482
ENSG00000067248	**DHX29**	protein_coding	-1.232	0.795	8.482
ENSG00000181450	**ZNF678**	protein_coding	-1.232	0.807	8.482
ENSG00000149499	**EML3**	protein_coding	-1.231	0.804	8.482
ENSG00000090266	**NDUFB2**	protein_coding	-1.231	0.809	8.482
ENSG00000172575	**RASGRP1**	protein_coding	-1.231	0.812	8.482
ENSG00000117620	**SLC35A3**	protein_coding	-1.231	0.83	8.482
ENSG00000285948	**ENSG00000285948**	lncRNA	-1.231	0.71	8.482
ENSG00000224688	**E2F6P2**	processed_pseudogene	-1.23	0.701	8.482
ENSG00000230818	**MTND2P16**	processed_pseudogene	-1.23	0.797	8.482
ENSG00000174738	**NR1D2**	protein_coding	-1.23	0.789	8.482

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000244691	**RPL10AP1**	processed_pseudogene	-1.23	0.815	8.482
ENSG00000146858	**ZC3HAV1L**	protein_coding	-1.23	0.796	8.482
ENSG00000145191	**EIF2B5**	protein_coding	-1.229	0.826	8.482
ENSG00000168243	**GNG4**	protein_coding	-1.229	0.816	8.482
ENSG00000172199	**OR8U1**	protein_coding	-1.229	0.744	8.482
ENSG00000248588	**ENSG00000248588**	lncRNA	-1.229	0.778	8.482
ENSG00000270859	**ENSG00000270859**	processed_pseudogene	-1.229	0.795	8.482
ENSG00000280022	**ENSG00000280022**	TEC	-1.229	0.672	8.482
ENSG00000141428	**C18orf21**	protein_coding	-1.228	0.787	8.482
ENSG00000043093	**DCUN1D1**	protein_coding	-1.228	0.819	8.482
ENSG00000138101	**DTNB**	protein_coding	-1.228	0.812	8.482
ENSG00000171843	**MLLT3**	protein_coding	-1.228	0.835	8.482
ENSG00000186124	**OR9M1P**	transcribed_unprocessed	-1.228	0.761	8.482
ENSG00000104689	**TNFRSF10A**	protein_coding	-1.228	0.804	8.482
ENSG00000112851	**ERBIN**	protein_coding	-1.227	0.806	8.482
ENSG00000187741	**FANCA**	protein_coding	-1.227	0.822	8.482
ENSG00000128654	**MTX2**	protein_coding	-1.227	0.831	8.482
ENSG00000150776	**NKAPD1**	protein_coding	-1.227	0.813	8.482
ENSG00000125450	**NUP85**	protein_coding	-1.227	0.81	8.482
ENSG00000145246	**ATP10D**	protein_coding	-1.226	0.81	8.482
ENSG00000222057	**RNU4-62P**	snRNA	-1.226	0.644	8.482
ENSG00000065613	**SLK**	protein_coding	-1.226	0.813	8.482
ENSG00000125304	**TM9SF2**	protein_coding	-1.226	0.82	8.482
ENSG00000207231	**Y_RNA**	misc_RNA	-1.226	0.669	8.482
ENSG00000253642	**ENSG00000253642**	lncRNA	-1.226	0.795	8.482
ENSG00000259375	**ENSG00000259375**	lncRNA	-1.226	0.823	8.482
ENSG00000105393	**BABAM1**	protein_coding	-1.225	0.823	8.482
ENSG00000268997	**DNAJC19P3**	processed_pseudogene	-1.225	0.764	8.482
ENSG00000136699	**SMPD4**	protein_coding	-1.225	0.794	8.482
ENSG00000200051	**ENSG00000200051**	snoRNA	-1.225	0.796	8.482
ENSG00000272829	**ENSG00000272829**	lncRNA	-1.225	0.774	8.482
ENSG00000260427	**AGGF1P9**	processed_pseudogene	-1.224	0.797	8.482
ENSG00000175548	**ALG10B**	protein_coding	-1.224	0.776	8.482
ENSG00000227740	**LINC02803**	lncRNA	-1.224	0.768	8.482
ENSG00000279465	**ENSG00000279465**	TEC	-1.224	0.678	8.482
ENSG00000214273	**AGGF1P1**	processed_pseudogene	-1.223	0.634	8.482
ENSG00000163171	**CDC42EP3**	protein_coding	-1.223	0.801	8.482
ENSG00000252072	**RNA5SP320**	rRNA_pseudogene	-1.223	0.675	8.482
ENSG00000252026	**RNU6-1262P**	snRNA	-1.223	0.593	8.482
ENSG00000260290	**ENSG00000260290**	processed_pseudogene	-1.223	0.764	8.482
ENSG00000070770	**CSNK2A2**	protein_coding	-1.222	0.818	8.482
ENSG00000234121	**GPM6BP3**	processed_pseudogene	-1.222	0.761	8.482
ENSG00000229954	**MTND2P2**	processed_pseudogene	-1.222	0.778	8.482
ENSG00000274400	**ENSG00000274400**	lncRNA	-1.222	0.778	8.482
ENSG00000107625	**DDX50**	protein_coding	-1.221	0.823	8.482
ENSG00000010810	**FYN**	protein_coding	-1.221	0.806	8.482
ENSG00000178502	**KLHL11**	protein_coding	-1.221	0.805	8.482
ENSG00000252768	**RNU6-856P**	snRNA	-1.221	0.668	8.482
ENSG00000248652	**ENSG00000248652**	processed_pseudogene	-1.221	0.675	8.482

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000181192	**DHTKD1**	protein_coding	-1.22	0.823	8.482
ENSG00000143190	**POU2F1**	protein_coding	-1.22	0.819	8.482
ENSG00000209042	**SNORD12C**	snoRNA	-1.22	0.791	8.482
ENSG00000236498	**ENSG00000236498**	lncRNA	-1.22	0.755	8.482
ENSG00000237429	**ENSG00000237429**	lncRNA	-1.22	0.789	8.482
ENSG00000241991	**ENSG00000241991**	processed_pseudogene	-1.22	0.744	8.482
ENSG00000254212	**ENSG00000254212**	processed_pseudogene	-1.22	0.715	8.482
ENSG00000261468	**ENSG00000261468**	lncRNA	-1.22	0.738	8.482
ENSG00000280277	**ENSG00000280277**	TEC	-1.22	0.756	8.482
ENSG00000138346	**DNA2**	protein_coding	-1.219	0.821	8.482
ENSG00000117298	**ECE1**	protein_coding	-1.219	0.81	8.482
ENSG00000141179	**PCTP**	protein_coding	-1.219	0.807	8.482
ENSG00000171396	**KRTAP4-4**	protein_coding	-1.218	0.744	8.482
ENSG00000039560	**RAI14**	protein_coding	-1.218	0.821	8.482
ENSG00000253580	**TRMT10BP1**	processed_pseudogene	-1.218	0.76	8.482
ENSG00000155313	**USP25**	protein_coding	-1.218	0.801	8.482
ENSG00000176567	**OR4X1**	protein_coding	-1.217	0.76	8.482
ENSG00000233541	**RPL31P47**	processed_pseudogene	-1.217	0.788	8.482
ENSG00000212378	**ENSG00000212378**	snoRNA	-1.217	0.739	8.482
ENSG00000164687	**FABP5**	protein_coding	-1.216	0.774	8.482
ENSG00000110514	**MADD**	protein_coding	-1.216	0.821	8.482
ENSG00000202231	**ENSG00000202231**	snoRNA	-1.216	0.691	8.482
ENSG00000236073	**ENSG00000236073**	processed_pseudogene	-1.216	0.752	8.482
ENSG00000254201	**ENSG00000254201**	lncRNA	-1.216	0.738	8.482
ENSG00000269786	**ENSG00000269786**	processed_pseudogene	-1.216	0.733	8.482
ENSG00000211514	**MIR454**	miRNA	-1.215	0.673	8.482
ENSG00000173418	**NAA20**	protein_coding	-1.215	0.78	8.482
ENSG00000229512	**ENSG00000229512**	lncRNA	-1.215	0.677	8.482
ENSG00000166845	**C18orf54**	protein_coding	-1.214	0.782	8.482
ENSG00000196284	**SUPT3H**	protein_coding	-1.214	0.819	8.482
ENSG00000240240	**ENSG00000240240**	lncRNA	-1.214	0.715	8.482
ENSG00000249943	**ENSG00000249943**	processed_pseudogene	-1.214	0.716	8.482
ENSG00000261315	**LARP4P**	transcribed_processed_p	-1.213	0.717	8.482
ENSG00000213089	**PDCL3P5**	processed_pseudogene	-1.213	0.745	8.482
ENSG00000146918	**NCAPG2**	protein_coding	-1.212	0.822	8.482
ENSG00000008952	**SEC62**	protein_coding	-1.212	0.839	8.482
ENSG00000216360	**ENSG00000216360**	processed_pseudogene	-1.212	0.764	8.482
ENSG00000270491	**ENSG00000270491**	processed_pseudogene	-1.212	0.73	8.482
ENSG00000138686	**BBS7**	protein_coding	-1.211	0.827	8.482
ENSG00000174944	**P2RY14**	protein_coding	-1.211	0.806	8.482
ENSG00000207155	**RNY1P14**	misc_RNA	-1.211	0.726	8.482
ENSG00000235605	**ENSG00000235605**	processed_pseudogene	-1.211	0.817	8.482
ENSG00000279148	**ENSG00000279148**	TEC	-1.211	0.815	8.482
ENSG00000153317	**ASAP1**	protein_coding	-1.21	0.824	8.482
ENSG00000118816	**CCNI**	protein_coding	-1.21	0.808	8.482
ENSG00000203737	**GPR52**	protein_coding	-1.21	0.716	8.482
ENSG00000200806	**RNA5SP275**	rRNA_pseudogene	-1.21	0.723	8.482
ENSG00000235105	**ENSG00000235105**	processed_pseudogene	-1.21	0.657	8.482
ENSG00000236358	**ENSG00000236358**	lncRNA	-1.21	0.803	8.482

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000277350	**ENSG00000277350**	lncRNA	-1.21	0.626	8.482
ENSG00000139624	**CERS5**	protein_coding	-1.209	0.804	8.482
ENSG00000187080	**OR2AK2**	protein_coding	-1.209	0.787	8.482
ENSG00000261144	**ENSG00000261144**	processed_pseudogene	-1.209	0.789	8.482
ENSG00000270751	**FBXW7-AS1**	lncRNA	-1.208	0.776	8.482
ENSG00000130935	**NOL11**	protein_coding	-1.208	0.818	8.482
ENSG00000121314	**TAS2R8**	protein_coding	-1.208	0.747	8.482
ENSG00000248347	**ENSG00000248347**	unprocessed_pseudogene	-1.208	0.828	8.482
ENSG00000273240	**ENSG00000273240**	lncRNA	-1.208	0.754	8.482
ENSG00000278880	**ENSG00000278880**	TEC	-1.208	0.718	8.482
ENSG00000113384	**GOLPH3**	protein_coding	-1.207	0.819	8.482
ENSG00000263813	**MIR3679**	miRNA	-1.207	0.739	8.482
ENSG00000230549	**USP17L1**	protein_coding	-1.207	0.793	8.482
ENSG00000136451	**VEZF1**	protein_coding	-1.207	0.807	8.482
ENSG00000101974	**ATP11C**	protein_coding	-1.206	0.815	8.482
ENSG00000000460	**C1orf112**	protein_coding	-1.206	0.811	8.482
ENSG00000147872	**PLIN2**	protein_coding	-1.206	0.81	8.482
ENSG00000250359	**PTP4A1P4**	processed_pseudogene	-1.206	0.722	8.482
ENSG00000198918	**RPL39**	protein_coding	-1.206	0.747	8.482
ENSG00000137815	**RTF1**	protein_coding	-1.206	0.807	8.482
ENSG00000271779	**ENSG00000271779**	processed_pseudogene	-1.206	0.766	8.482
ENSG00000282386	**ENSG00000282386**	lncRNA	-1.206	0.797	8.482
ENSG00000286395	**ENSG00000286395**	lncRNA	-1.206	0.779	8.482
ENSG00000253971	**CDC42P3**	processed_pseudogene	-1.205	0.757	8.482
ENSG00000129493	**HEATR5A**	protein_coding	-1.205	0.822	8.482
ENSG00000230911	**PPIHP1**	processed_pseudogene	-1.205	0.799	8.482
ENSG00000057657	**PRDM1**	protein_coding	-1.205	0.827	8.482
ENSG00000255423	**EBLN2**	protein_coding	-1.204	0.743	8.482
ENSG00000226491	**FTOP1**	processed_pseudogene	-1.204	0.791	8.482
ENSG00000204623	**ZNRD1ASP**	transcribed_unitary_pseu	-1.204	0.836	8.482
ENSG00000253667	**ENSG00000253667**	processed_pseudogene	-1.204	0.809	8.482
ENSG00000254350	**ENSG00000254350**	lncRNA	-1.204	0.733	8.482
ENSG00000276533	**ENSG00000276533**	lncRNA	-1.204	0.749	8.482
ENSG00000280202	**ENSG00000280202**	TEC	-1.204	0.75	8.482
ENSG00000252655	**Y_RNA**	misc_RNA	-1.203	0.735	8.482
ENSG00000197123	**ZNF679**	protein_coding	-1.203	0.826	8.482
ENSG00000224132	**ENSG00000224132**	lncRNA	-1.203	0.812	8.482
ENSG00000214875	**MED28P1**	processed_pseudogene	-1.202	0.763	8.482
ENSG00000186086	**NBPF6**	protein_coding	-1.202	0.727	8.482
ENSG00000188636	**RTL6**	protein_coding	-1.202	0.803	8.482
ENSG00000248445	**SEMA6A-AS1**	lncRNA	-1.202	0.826	8.482
ENSG00000278040	**ENSG00000278040**	misc_RNA	-1.202	0.761	8.482
ENSG00000021826	**CPS1**	protein_coding	-1.201	0.823	8.482
ENSG00000165304	**MELK**	protein_coding	-1.201	0.812	8.482
ENSG00000140157	**NIPA2**	protein_coding	-1.201	0.832	8.482
ENSG00000067900	**ROCK1**	protein_coding	-1.201	0.818	8.482
ENSG00000235748	**SEPTIN14P12**	processed_pseudogene	-1.201	0.735	8.482
ENSG00000253060	**ENSG00000253060**	scaRNA	-1.201	0.792	8.482
ENSG00000285473	**ENSG00000285473**	lncRNA	-1.201	0.717	8.482

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000149187	**CELF1**	protein_coding	-1.2	0.839	8.482
ENSG00000127463	**EMC1**	protein_coding	-1.2	0.822	8.482
ENSG00000250076	**MAPRE1P2**	processed_pseudogene	-1.2	0.77	8.482
ENSG00000174231	**PRPF8**	protein_coding	-1.2	0.828	8.482
ENSG00000200571	**RNU6-1284P**	snRNA	-1.2	0.75	8.482
ENSG00000252874	**Y_RNA**	misc_RNA	-1.2	0.697	8.482
ENSG00000105497	**ZNF175**	protein_coding	-1.2	0.816	8.482
ENSG00000197782	**ZNF780A**	protein_coding	-1.2	0.764	8.482
ENSG00000233589	**ENSG00000233589**	lncRNA	-1.2	0.793	8.482
ENSG00000271653	**ENSG00000271653**	lncRNA	-1.2	0.816	8.482
ENSG00000122483	**CCDC18**	protein_coding	-1.199	0.807	8.482
ENSG00000260451	**GEMIN8P2**	processed_pseudogene	-1.199	0.783	8.482
ENSG00000100578	**KIAA0586**	protein_coding	-1.199	0.813	8.482
ENSG00000244025	**KRTAP19-3**	protein_coding	-1.199	0.805	8.482
ENSG00000232970	**POLHP1**	processed_pseudogene	-1.199	0.672	8.482
ENSG00000102572	**STK24**	protein_coding	-1.199	0.825	8.482
ENSG00000267693	**ENSG00000267693**	processed_pseudogene	-1.199	0.741	8.482
ENSG00000188996	**HUS1B**	protein_coding	-1.198	0.787	8.482
ENSG00000251604	**LINC01385**	lncRNA	-1.198	0.788	8.482
ENSG00000137821	**LRRC49**	protein_coding	-1.198	0.811	8.482
ENSG00000159459	**UBR1**	protein_coding	-1.198	0.782	8.482
ENSG00000184110	**EIF3C**	protein_coding	-1.197	0.768	8.482
ENSG00000252005	**RNU4ATAC8P**	snRNA	-1.197	0.784	8.482
ENSG00000218180	**SLC25A5P7**	processed_pseudogene	-1.197	0.722	8.482
ENSG00000223959	**AFG3L1P**	transcribed_unitary_pseu	-1.196	0.826	8.482
ENSG00000231162	**COX11P1**	processed_pseudogene	-1.196	0.813	8.482
ENSG00000171877	**FRMD5**	protein_coding	-1.196	0.816	8.482
ENSG00000233448	**PMS2P9**	transcribed_unprocessed_	-1.196	0.72	8.482
ENSG00000261284	**RBM22P13**	processed_pseudogene	-1.196	0.756	8.482
ENSG00000238694	**ENSG00000238694**	snoRNA	-1.196	0.667	8.482
ENSG00000258365	**ENSG00000258365**	lncRNA	-1.196	0.814	8.482
ENSG00000258904	**ENSG00000258904**	lncRNA	-1.196	0.808	8.482
ENSG00000286052	**ENSG00000286052**	lncRNA	-1.196	0.682	8.482
ENSG00000197548	**ATG7**	protein_coding	-1.195	0.826	8.482
ENSG00000143924	**EML4**	protein_coding	-1.195	0.831	8.482
ENSG00000207959	**MIR656**	miRNA	-1.195	0.77	8.482
ENSG00000141576	**RNF157**	protein_coding	-1.195	0.827	8.482
ENSG00000143514	**TP53BP2**	protein_coding	-1.195	0.827	8.482
ENSG00000217372	**TUBB4BP7**	processed_pseudogene	-1.195	0.779	8.482
ENSG00000279478	**ENSG00000279478**	TEC	-1.195	0.793	8.482
ENSG00000217241	**CBX3P9**	processed_pseudogene	-1.194	0.715	8.482
ENSG00000176624	**MEX3C**	protein_coding	-1.194	0.824	8.482
ENSG00000263741	**MIR548AS**	miRNA	-1.194	0.711	8.482
ENSG00000226306	**NPY6R**	transcribed_processed_ps	-1.194	0.754	8.482
ENSG00000084093	**REST**	protein_coding	-1.194	0.805	8.482
ENSG00000143344	**RGL1**	protein_coding	-1.194	0.807	8.482
ENSG00000202031	**SNORD38A**	snoRNA	-1.194	0.812	8.482
ENSG00000111642	**CHD4**	protein_coding	-1.193	0.809	8.482
ENSG00000087338	**GMCL1**	protein_coding	-1.193	0.824	8.482

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000110583	**NAA40**	protein_coding	-1.193	0.829	8.482
ENSG00000260307	**PABPC1P13**	processed_pseudogene	-1.193	0.793	8.482
ENSG00000101695	**RNF125**	protein_coding	-1.193	0.809	8.482
ENSG00000199394	**RNU6-600P**	snRNA	-1.193	0.806	8.482
ENSG00000225823	**RPL7P45**	processed_pseudogene	-1.193	0.762	8.482
ENSG00000230793	**SMARCE1P5**	processed_pseudogene	-1.193	0.812	8.482
ENSG00000023608	**SNAPC1**	protein_coding	-1.193	0.798	8.482
ENSG00000287083	**ENSG00000287083**	lncRNA	-1.193	0.786	8.482
ENSG00000169607	**CKAP2L**	protein_coding	-1.192	0.809	8.482
ENSG00000100592	**DAAM1**	protein_coding	-1.192	0.816	8.482
ENSG00000133731	**IMPA1**	protein_coding	-1.192	0.829	8.482
ENSG00000078140	**UBE2K**	protein_coding	-1.192	0.832	8.482
ENSG00000229832	**ENSG00000229832**	lncRNA	-1.192	0.791	8.482
ENSG00000249079	**ENSG00000249079**	processed_pseudogene	-1.192	0.74	8.482
ENSG00000260659	**ENSG00000260659**	lncRNA	-1.192	0.736	8.482
ENSG00000123575	**FAM199X**	protein_coding	-1.191	0.822	8.482
ENSG00000137441	**FGFBP2**	protein_coding	-1.191	0.763	8.482
ENSG00000196844	**PATE2**	protein_coding	-1.191	0.801	8.482
ENSG00000231508	**RPL34P20**	processed_pseudogene	-1.191	0.714	8.482
ENSG00000286850	**ENSG00000286850**	lncRNA	-1.191	0.801	8.482
ENSG00000287616	**ENSG00000287616**	lncRNA	-1.191	0.819	8.482
ENSG00000161692	**DBF4B**	protein_coding	-1.19	0.817	8.482
ENSG00000186205	**MTARC1**	protein_coding	-1.19	0.801	8.482
ENSG00000197713	**RPE**	protein_coding	-1.19	0.813	8.482
ENSG00000115524	**SF3B1**	protein_coding	-1.19	0.831	8.482
ENSG00000257113	**ENSG00000257113**	processed_pseudogene	-1.19	0.704	8.482
ENSG00000267448	**ENSG00000267448**	lncRNA	-1.19	0.757	8.482
ENSG00000286174	**ENSG00000286174**	lncRNA	-1.19	0.746	8.482
ENSG00000287129	**ENSG00000287129**	lncRNA	-1.19	0.667	8.482
ENSG00000229606	**LINC01718**	lncRNA	-1.189	0.774	8.482
ENSG00000215871	**ENSG00000215871**	processed_pseudogene	-1.189	0.767	8.482
ENSG00000255336	**ENSG00000255336**	unprocessed_pseudogene	-1.189	0.709	8.482
ENSG00000103351	**CLUAP1**	protein_coding	-1.188	0.823	8.482
ENSG00000166197	**NOLC1**	protein_coding	-1.188	0.819	8.482
ENSG00000152193	**OBI1**	protein_coding	-1.188	0.835	8.482
ENSG00000171863	**RPS7**	protein_coding	-1.188	0.822	8.482
ENSG00000200816	**SNORA38**	snoRNA	-1.188	0.763	8.482
ENSG00000285573	**ENSG00000285573**	lncRNA	-1.188	0.758	8.482
ENSG00000206762	**RNU6-418P**	snRNA	-1.187	0.737	8.482
ENSG00000244045	**TMEM199**	protein_coding	-1.187	0.78	8.482
ENSG00000276269	**ENSG00000276269**	lncRNA	-1.187	0.788	8.482
ENSG00000185000	**DGAT1**	protein_coding	-1.186	0.833	8.482
ENSG00000119321	**FKBP15**	protein_coding	-1.186	0.821	8.482
ENSG00000104381	**GDAP1**	protein_coding	-1.186	0.811	8.482
ENSG00000236051	**MYCBP2-AS1**	lncRNA	-1.186	0.833	8.482
ENSG00000257875	**ENSG00000257875**	processed_pseudogene	-1.186	0.71	8.482
ENSG00000165288	**BRWD3**	protein_coding	-1.185	0.818	8.482
ENSG00000136280	**CCM2**	protein_coding	-1.185	0.822	8.482
ENSG00000171824	**EXOSC10**	protein_coding	-1.185	0.828	8.482

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000241945	**PWP2**	protein_coding	-1.185	0.817	8.482
ENSG00000124216	**SNAI1**	protein_coding	-1.185	0.815	8.482
ENSG00000206850	**Y_RNA**	misc_RNA	-1.185	0.687	8.482
ENSG00000116406	**EDEM3**	protein_coding	-1.184	0.823	8.482
ENSG00000143756	**FBXO28**	protein_coding	-1.184	0.819	8.482
ENSG00000156515	**HK1**	protein_coding	-1.184	0.829	8.482
ENSG00000248704	**MTND4P2**	unprocessed_pseudogene	-1.184	0.745	8.482
ENSG00000227434	**RNF19BPX**	processed_pseudogene	-1.184	0.762	8.482
ENSG00000252884	**RNU6-1213P**	snRNA	-1.184	0.769	8.482
ENSG00000229892	**ENSG00000229892**	processed_pseudogene	-1.184	0.769	8.482
ENSG00000198019	**FCGR1B**	protein_coding	-1.183	0.77	8.482
ENSG00000065243	**PKN2**	protein_coding	-1.183	0.823	8.482
ENSG00000249028	**ENSG00000249028**	lncRNA	-1.183	0.78	8.482
ENSG00000230564	**CALM1P2**	processed_pseudogene	-1.182	0.791	8.482
ENSG00000119922	**IFIT2**	protein_coding	-1.182	0.771	8.482
ENSG00000056097	**ZFR**	protein_coding	-1.182	0.838	8.482
ENSG00000230188	**ENSG00000230188**	processed_pseudogene	-1.182	0.795	8.482
ENSG00000273221	**ENSG00000273221**	lncRNA	-1.182	0.723	8.482
ENSG00000089685	**BIRC5**	protein_coding	-1.181	0.816	8.482
ENSG00000188694	**KRTAP24-1**	protein_coding	-1.181	0.805	8.482
ENSG00000253994	**NDUFB9P3**	processed_pseudogene	-1.181	0.759	8.482
ENSG00000231556	**RSL24D1P3**	processed_pseudogene	-1.181	0.773	8.482
ENSG00000164663	**USP49**	protein_coding	-1.181	0.835	8.482
ENSG00000171940	**ZNF217**	protein_coding	-1.181	0.837	8.482
ENSG00000286784	**ENSG00000286784**	lncRNA	-1.181	0.618	8.482
ENSG00000166260	**COX11**	protein_coding	-1.18	0.816	8.482
ENSG00000260846	**FRG2HP**	unprocessed_pseudogene	-1.18	0.784	8.482
ENSG00000117569	**PTBP2**	protein_coding	-1.18	0.829	8.482
ENSG00000231650	**RFESDP1**	processed_pseudogene	-1.18	0.676	8.482
ENSG00000233979	**RPL22P21**	processed_pseudogene	-1.18	0.745	8.482
ENSG00000233145	**ENSG00000233145**	lncRNA	-1.18	0.606	8.482
ENSG00000162639	**HENMT1**	protein_coding	-1.179	0.778	8.482
ENSG00000085274	**MYNN**	protein_coding	-1.179	0.809	8.482
ENSG00000223744	**RBMY2GP**	unprocessed_pseudogene	-1.179	0.684	8.482
ENSG00000226646	**RPL7P37**	processed_pseudogene	-1.179	0.78	8.482
ENSG00000170242	**USP47**	protein_coding	-1.179	0.823	8.482
ENSG00000287725	**ENSG00000287725**	protein_coding	-1.179	0.679	8.482
ENSG00000196741	**LINC01560**	lncRNA	-1.178	0.672	8.482
ENSG00000199095	**MIR372**	miRNA	-1.178	0.739	8.482
ENSG00000250746	**ENSG00000250746**	processed_pseudogene	-1.178	0.719	8.482
ENSG00000268322	**BNIP3P25**	processed_pseudogene	-1.177	0.729	8.482
ENSG00000234197	**ETV5-AS1**	lncRNA	-1.177	0.765	8.482
ENSG00000252615	**Y_RNA**	misc_RNA	-1.177	0.798	8.482
ENSG00000145349	**CAMK2D**	protein_coding	-1.176	0.844	8.482
ENSG00000067955	**CBFB**	protein_coding	-1.176	0.827	8.482
ENSG00000130816	**DNMT1**	protein_coding	-1.176	0.831	8.482
ENSG00000261794	**GOLGA8H**	protein_coding	-1.176	0.642	8.482
ENSG00000284388	**MIR4496**	miRNA	-1.176	0.599	8.482
ENSG00000078177	**N4BP2**	protein_coding	-1.176	0.82	8.482

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000143157	**POGK**	protein_coding	-1.176	0.829	8.482
ENSG00000207083	**RNU6-22P**	snRNA	-1.176	0.489	8.482
ENSG00000252585	**Y_RNA**	misc_RNA	-1.176	0.812	8.482
ENSG00000185015	**CA13**	protein_coding	-1.175	0.823	8.482
ENSG00000112855	**HARS2**	protein_coding	-1.175	0.83	8.482
ENSG00000068885	**IFT80**	protein_coding	-1.175	0.796	8.482
ENSG00000252288	**RNU6-966P**	snRNA	-1.175	0.79	8.482
ENSG00000164548	**TRA2A**	protein_coding	-1.175	0.834	8.482
ENSG00000270503	**YTHDF2P1**	processed_pseudogene	-1.175	0.815	8.482
ENSG00000202343	**ENSG00000202343**	snoRNA	-1.175	0.75	8.482
ENSG00000259388	**ENSG00000259388**	processed_pseudogene	-1.175	0.807	8.482
ENSG00000279759	**ENSG00000279759**	TEC	-1.175	0.782	8.482
ENSG00000155846	**PPARGC1B**	protein_coding	-1.174	0.837	8.482
ENSG00000265745	**RN7SL375P**	misc_RNA	-1.174	0.752	8.482
ENSG00000133812	**SBF2**	protein_coding	-1.174	0.831	8.482
ENSG00000199938	**Y_RNA**	misc_RNA	-1.174	0.815	8.482
ENSG00000275185	**ENSG00000275185**	lncRNA	-1.174	0.776	8.482
ENSG00000276805	**ENSG00000276805**	transcribed_unprocessed_	-1.174	0.799	8.482
ENSG00000287584	**ENSG00000287584**	lncRNA	-1.174	0.799	8.482
ENSG00000018236	**CNTN1**	protein_coding	-1.173	0.829	8.482
ENSG00000175595	**ERCC4**	protein_coding	-1.173	0.829	8.482
ENSG00000257242	**LINC01619**	lncRNA	-1.173	0.815	8.482
ENSG00000222099	**RN7SKP32**	misc_RNA	-1.173	0.731	8.482
ENSG00000198963	**RORB**	protein_coding	-1.173	0.814	8.482
ENSG00000250914	**ENSG00000250914**	processed_pseudogene	-1.173	0.846	8.482
ENSG00000287902	**ENSG00000287902**	lncRNA	-1.173	0.671	8.482
ENSG00000110723	**EXPH5**	protein_coding	-1.172	0.823	8.482
ENSG00000131724	**IL13RA1**	protein_coding	-1.172	0.784	8.482
ENSG00000184967	**NOC4L**	protein_coding	-1.172	0.808	8.482
ENSG00000082898	**XPO1**	protein_coding	-1.172	0.821	8.482
ENSG00000202222	**Y_RNA**	misc_RNA	-1.172	0.768	8.482
ENSG00000261299	**C2orf69P3**	processed_pseudogene	-1.171	0.797	8.482
ENSG00000264678	**MIR3140**	miRNA	-1.171	0.744	8.482
ENSG00000223263	**RNU6-387P**	snRNA	-1.171	0.74	8.482
ENSG00000199226	**RNU6-50P**	snRNA	-1.171	0.768	8.482
ENSG00000172139	**SLC9C1**	protein_coding	-1.171	0.825	8.482
ENSG00000232204	**TET1P1**	processed_pseudogene	-1.171	0.795	8.482
ENSG00000258275	**OR7K1P**	unprocessed_pseudogene	-1.17	0.75	8.482
ENSG00000231911	**TPRKBP1**	processed_pseudogene	-1.17	0.759	8.482
ENSG00000283204	**MIR4434**	miRNA	-1.169	0.714	8.482
ENSG00000222146	**RNU4-37P**	snRNA	-1.169	0.78	8.482
ENSG00000277840	**ENSG00000277840**	lncRNA	-1.169	0.72	8.482
ENSG00000103381	**CPPED1**	protein_coding	-1.168	0.82	8.482
ENSG00000178974	**FBXO34**	protein_coding	-1.168	0.833	8.482
ENSG00000196143	**OR11H13P**	unprocessed_pseudogene	-1.168	0.794	8.482
ENSG00000176903	**PNMA1**	protein_coding	-1.168	0.834	8.482
ENSG00000204479	**PRAMEF17**	protein_coding	-1.168	0.798	8.482
ENSG00000090104	**RGS1**	protein_coding	-1.168	0.667	8.482
ENSG00000173611	**SCAI**	protein_coding	-1.168	0.822	8.482

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000283491	**ENSG00000283491**	unprocessed_pseudogene	-1.168	0.688	8.482
ENSG00000006007	**GDE1**	protein_coding	-1.167	0.819	8.482
ENSG00000124702	**KLHDC3**	protein_coding	-1.167	0.835	8.482
ENSG00000145495	**MARCHF6**	protein_coding	-1.167	0.826	8.482
ENSG00000276547	**PCDHGB5**	protein_coding	-1.167	0.797	8.482
ENSG00000182347	**PDSS1P1**	processed_pseudogene	-1.167	0.814	8.482
ENSG00000146223	**RPL7L1**	protein_coding	-1.167	0.821	8.482
ENSG00000255161	**ENSG00000255161**	processed_pseudogene	-1.167	0.721	8.482
ENSG00000279042	**ENSG00000279042**	TEC	-1.167	0.735	8.482
ENSG00000280183	**ENSG00000280183**	TEC	-1.167	0.718	8.482
ENSG00000133794	**ARNTL**	protein_coding	-1.166	0.835	8.482
ENSG00000171953	**ATPAF2**	protein_coding	-1.166	0.818	8.482
ENSG00000255531	**NDUFS5P6**	processed_pseudogene	-1.166	0.754	8.482
ENSG00000286219	**NOTCH2NLC**	protein_coding	-1.166	0.819	8.482
ENSG00000240189	**RN7SL621P**	misc_RNA	-1.166	0.789	8.482
ENSG00000200616	**Y_RNA**	misc_RNA	-1.166	0.769	8.482
ENSG00000275017	**ENSG00000275017**	processed_pseudogene	-1.166	0.75	8.482
ENSG00000214264	**KCTD9P4**	processed_pseudogene	-1.165	0.754	8.482
ENSG00000048649	**RSF1**	protein_coding	-1.165	0.835	8.482
ENSG00000276094	**SNORA70**	snoRNA	-1.165	0.669	8.482
ENSG00000187735	**TCEA1**	protein_coding	-1.165	0.819	8.482
ENSG00000233470	**ENSG00000233470**	lncRNA	-1.165	0.815	8.482
ENSG00000243445	**ENSG00000243445**	processed_pseudogene	-1.165	0.77	8.482
ENSG00000109576	**AADAT**	protein_coding	-1.164	0.784	8.482
ENSG00000151917	**BEND6**	protein_coding	-1.164	0.832	8.482
ENSG00000256721	**CACNA1C-IT3**	lncRNA	-1.164	0.797	8.482
ENSG00000221325	**MIR1200**	miRNA	-1.164	0.749	8.482
ENSG00000212493	**SNORD19**	snoRNA	-1.164	0.678	8.482
ENSG00000184277	**TM2D3**	protein_coding	-1.164	0.825	8.482
ENSG00000172888	**ZNF621**	protein_coding	-1.164	0.831	8.482
ENSG00000100439	**ABHD4**	protein_coding	-1.163	0.821	8.482
ENSG00000011114	**BTBD7**	protein_coding	-1.163	0.832	8.482
ENSG00000253578	**IGKV1-22**	IG_V_pseudogene	-1.163	0.567	8.482
ENSG00000204092	**LINC00951**	lncRNA	-1.163	0.764	8.482
ENSG00000275670	**MIR8076**	miRNA	-1.163	0.793	8.482
ENSG00000181616	**OR52H1**	protein_coding	-1.163	0.772	8.482
ENSG00000117394	**SLC2A1**	protein_coding	-1.163	0.842	8.482
ENSG00000254929	**ENSG00000254929**	lncRNA	-1.163	0.802	8.482
ENSG00000264254	**ENSG00000264254**	lncRNA	-1.163	0.783	8.482
ENSG00000279488	**ENSG00000279488**	TEC	-1.163	0.761	8.482
ENSG00000286711	**ENSG00000286711**	lncRNA	-1.163	0.734	8.482
ENSG00000120798	**NR2C1**	protein_coding	-1.162	0.833	8.482
ENSG00000240935	**PLGLA**	transcribed_unprocessed_	-1.162	0.559	8.482
ENSG00000224019	**RPL21P32**	processed_pseudogene	-1.162	0.664	8.482
ENSG00000281641	**SAMD12-AS1**	lncRNA	-1.162	0.796	8.482
ENSG00000196182	**STK40**	protein_coding	-1.162	0.827	8.482
ENSG00000163872	**YEATS2**	protein_coding	-1.162	0.834	8.482
ENSG00000202183	**ENSG00000202183**	snoRNA	-1.162	0.793	8.482
ENSG00000146416	**AIG1**	protein_coding	-1.161	0.815	8.482

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000077684	**JADE1**	protein_coding	-1.161	0.826	8.482
ENSG00000072864	**NDE1**	protein_coding	-1.161	0.808	8.482
ENSG00000205578	**POM121B**	unprocessed_pseudogene	-1.161	0.728	8.482
ENSG00000104375	**STK3**	protein_coding	-1.161	0.832	8.482
ENSG00000271482	**ENSG00000271482**	processed_pseudogene	-1.161	0.758	8.482
ENSG00000285269	**ENSG00000285269**	protein_coding	-1.161	0.793	8.482
ENSG00000146476	**ARMT1**	protein_coding	-1.16	0.835	8.482
ENSG00000256464	**YWHABP2**	processed_pseudogene	-1.16	0.692	8.482
ENSG00000248337	**ENSG00000248337**	processed_pseudogene	-1.16	0.805	8.482
ENSG00000248881	**ENSG00000248881**	lncRNA	-1.16	0.713	8.482
ENSG00000153006	**SREK1IP1**	protein_coding	-1.159	0.81	8.482
ENSG00000224324	**THAP5P1**	processed_pseudogene	-1.159	0.649	8.482
ENSG00000258184	**ENSG00000258184**	processed_pseudogene	-1.159	0.773	8.482
ENSG00000266335	**ENSG00000266335**	lncRNA	-1.159	0.78	8.482
ENSG00000253685	**MTND5P41**	unprocessed_pseudogene	-1.158	0.773	8.482
ENSG00000237929	**RPL31P3**	processed_pseudogene	-1.158	0.633	8.482
ENSG00000047410	**TPR**	protein_coding	-1.158	0.821	8.482
ENSG00000271182	**ENSG00000271182**	processed_pseudogene	-1.158	0.781	8.482
ENSG00000286132	**ENSG00000286132**	protein_coding	-1.158	0.714	8.482
ENSG00000186638	**KIF24**	protein_coding	-1.157	0.809	8.482
ENSG00000043462	**LCP2**	protein_coding	-1.157	0.83	8.482
ENSG00000258548	**LINC00645**	lncRNA	-1.157	0.827	8.482
ENSG00000212122	**TSSK1B**	protein_coding	-1.157	0.83	8.482
ENSG00000285717	**ENSG00000285717**	lncRNA	-1.157	0.72	8.482
ENSG00000144320	**LNPK**	protein_coding	-1.156	0.839	8.482
ENSG00000251759	**RN7SKP298**	misc_RNA	-1.156	0.782	8.482
ENSG00000288059	**ENSG00000288059**	lncRNA	-1.156	0.724	8.482
ENSG00000185275	**CD24P4**	processed_pseudogene	-1.155	0.452	8.482
ENSG00000115649	**CNPPD1**	protein_coding	-1.155	0.828	8.482
ENSG00000201447	**RNA5SP509**	rRNA_pseudogene	-1.155	0.76	8.482
ENSG00000206951	**Y_RNA**	misc_RNA	-1.155	0.761	8.482
ENSG00000253108	**ENSG00000253108**	lncRNA	-1.155	0.81	8.482
ENSG00000254694	**ENSG00000254694**	lncRNA	-1.155	0.805	8.482
ENSG00000286864	**ENSG00000286864**	lncRNA	-1.155	0.753	8.482
ENSG00000207956	**MIR579**	miRNA	-1.154	0.77	8.482
ENSG00000236047	**RPL13AP12**	processed_pseudogene	-1.154	0.764	8.482
ENSG00000233966	**UBE2SP1**	processed_pseudogene	-1.154	0.778	8.482
ENSG00000227585	**ENSG00000227585**	processed_pseudogene	-1.154	0.776	8.482
ENSG00000140479	**PCSK6**	protein_coding	-1.153	0.819	8.482
ENSG00000248660	**SRIP1**	processed_pseudogene	-1.153	0.783	8.482
ENSG00000237422	**ENSG00000237422**	lncRNA	-1.153	0.813	8.482
ENSG00000240040	**ENSG00000240040**	lncRNA	-1.153	0.758	8.482
ENSG00000149548	**CCDC15**	protein_coding	-1.152	0.811	8.482
ENSG00000101311	**FERMT1**	protein_coding	-1.152	0.826	8.482
ENSG00000118873	**RAB3GAP2**	protein_coding	-1.152	0.831	8.482
ENSG00000164506	**STXBP5**	protein_coding	-1.152	0.836	8.482
ENSG00000235965	**ENSG00000235965**	lncRNA	-1.152	0.79	8.482
ENSG00000172489	**OR5T3**	protein_coding	-1.151	0.791	8.482
ENSG00000090924	**PLEKHG2**	protein_coding	-1.151	0.825	8.482

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000261357	**ENSG00000261357**	lncRNA	-1.151	0.763	8.482
ENSG00000107771	**CCSER2**	protein_coding	-1.15	0.828	8.482
ENSG00000238243	**OR2W3**	protein_coding	-1.15	0.722	8.482
ENSG00000116731	**PRDM2**	protein_coding	-1.15	0.834	8.482
ENSG00000250041	**ENSG00000250041**	lncRNA	-1.15	0.797	8.482
ENSG00000120868	**APAF1**	protein_coding	-1.149	0.818	8.482
ENSG00000128928	**IVD**	protein_coding	-1.149	0.847	8.482
ENSG00000186814	**ZSCAN30**	protein_coding	-1.149	0.837	8.482
ENSG00000279766	**ENSG00000279766**	TEC	-1.149	0.757	8.482
ENSG00000281348	**ENSG00000281348**	protein_coding	-1.149	0.764	8.482
ENSG00000164284	**GRPEL2**	protein_coding	-1.148	0.837	8.482
ENSG00000198160	**MIER1**	protein_coding	-1.148	0.826	8.482
ENSG00000284609	**OR8B3**	protein_coding	-1.148	0.765	8.482
ENSG00000162924	**REL**	protein_coding	-1.148	0.819	8.482
ENSG00000136932	**TRMO**	protein_coding	-1.148	0.849	8.482
ENSG00000270084	**GAS5-AS1**	lncRNA	-1.147	0.711	8.482
ENSG00000206650	**SNORA70G**	snoRNA	-1.147	0.777	8.482
ENSG00000139291	**TMEM19**	protein_coding	-1.147	0.835	8.482
ENSG00000201483	**Y_RNA**	misc_RNA	-1.147	0.769	8.482
ENSG00000185728	**YTHDF3**	protein_coding	-1.147	0.832	8.482
ENSG00000154639	**CXADR**	protein_coding	-1.146	0.826	8.482
ENSG00000197442	**MAP3K5**	protein_coding	-1.146	0.813	8.482
ENSG00000136045	**PWP1**	protein_coding	-1.146	0.832	8.482
ENSG00000252041	**RNA5SP228**	rRNA_pseudogene	-1.146	0.795	8.482
ENSG00000050438	**SLC4A8**	protein_coding	-1.146	0.838	8.482
ENSG00000230112	**ENSG00000230112**	processed_pseudogene	-1.146	0.671	8.482
ENSG00000287999	**ENSG00000287999**	lncRNA	-1.146	0.666	8.482
ENSG00000154511	**DIPK1A**	protein_coding	-1.145	0.835	8.482
ENSG00000160767	**FAM189B**	protein_coding	-1.145	0.826	8.482
ENSG00000236719	**OVAAL**	lncRNA	-1.145	0.783	8.482
ENSG00000264907	**PRELID3BP3**	processed_pseudogene	-1.145	0.692	8.482
ENSG00000101236	**RNF24**	protein_coding	-1.145	0.841	8.482
ENSG00000252857	**RNU6-389P**	snRNA	-1.145	0.761	8.482
ENSG00000215347	**SLC25A5P1**	transcribed_processed_ps	-1.145	0.791	8.482
ENSG00000078061	**ARAF**	protein_coding	-1.144	0.822	8.482
ENSG00000137814	**HAUS2**	protein_coding	-1.144	0.824	8.482
ENSG00000270685	**IGHV1OR15-6**	IG_V_pseudogene	-1.144	0.787	8.482
ENSG00000164024	**METAP1**	protein_coding	-1.144	0.831	8.482
ENSG00000162971	**TYW5**	protein_coding	-1.144	0.819	8.482
ENSG00000279838	**ENSG00000279838**	TEC	-1.144	0.714	8.482
ENSG00000050748	**MAPK9**	protein_coding	-1.143	0.834	8.482
ENSG00000216777	**PRRC2CP1**	processed_pseudogene	-1.143	0.729	8.482
ENSG00000251850	**RNA5SP96**	rRNA_pseudogene	-1.143	0.764	8.482
ENSG00000135316	**SYNCRIP**	protein_coding	-1.143	0.834	8.482
ENSG00000177125	**ZBTB34**	protein_coding	-1.143	0.783	8.482
ENSG00000153930	**ANKFN1**	protein_coding	-1.142	0.816	8.482
ENSG00000205744	**DENND1C**	protein_coding	-1.142	0.831	8.482
ENSG00000102034	**ELF4**	protein_coding	-1.142	0.81	8.482
ENSG00000184434	**LRRC19**	protein_coding	-1.142	0.838	8.482

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000130340	**SNX9**	protein_coding	-1.142	0.824	8.482
ENSG00000270381	**ENSG00000270381**	processed_pseudogene	-1.142	0.722	8.482
ENSG00000135776	**ABCB10**	protein_coding	-1.141	0.834	8.482
ENSG00000125954	**CHURC1-FNTB**	protein_coding	-1.141	0.794	8.482
ENSG00000205730	**ITPRIPL2**	protein_coding	-1.141	0.814	8.482
ENSG00000231082	**LINC02655**	lncRNA	-1.141	0.807	8.482
ENSG00000124160	**NCOA5**	protein_coding	-1.141	0.828	8.482
ENSG00000260761	**ENSG00000260761**	lncRNA	-1.141	0.796	8.482
ENSG00000277223	**ENSG00000277223**	lncRNA	-1.141	0.777	8.482
ENSG00000100523	**DDHD1**	protein_coding	-1.14	0.845	8.482
ENSG00000267046	**E2F3P1**	processed_pseudogene	-1.14	0.723	8.482
ENSG00000207705	**MIR129-1**	miRNA	-1.14	0.661	8.482
ENSG00000175198	**PCCA**	protein_coding	-1.14	0.827	8.482
ENSG00000155158	**TTC39B**	protein_coding	-1.14	0.842	8.482
ENSG00000255470	**ENSG00000255470**	lncRNA	-1.14	0.781	8.482
ENSG00000275759	**ENSG00000275759**	lncRNA	-1.14	0.759	8.482
ENSG00000115548	**KDM3A**	protein_coding	-1.139	0.812	8.482
ENSG00000237065	**NANOGP4**	transcribed_processed_ps	-1.139	0.756	8.482
ENSG00000243302	**ENSG00000243302**	processed_pseudogene	-1.139	0.8	8.482
ENSG00000260209	**ENSG00000260209**	lncRNA	-1.139	0.785	8.482
ENSG00000271003	**ENSG00000271003**	unprocessed_pseudogene	-1.139	0.733	8.482
ENSG00000271900	**ENSG00000271900**	processed_pseudogene	-1.139	0.745	8.482
ENSG00000286000	**ENSG00000286000**	lncRNA	-1.139	0.769	8.482
ENSG00000143771	**CNIH4**	protein_coding	-1.138	0.829	8.482
ENSG00000226700	**MTND4P25**	processed_pseudogene	-1.138	0.824	8.482
ENSG00000234309	**SLC25A18P1**	processed_pseudogene	-1.138	0.779	8.482
ENSG00000271734	**ENSG00000271734**	lncRNA	-1.138	0.778	8.482
ENSG00000116133	**DHCR24**	protein_coding	-1.137	0.811	8.482
ENSG00000226157	**OR52E3P**	unprocessed_pseudogene	-1.137	0.789	8.482
ENSG00000002016	**RAD52**	protein_coding	-1.137	0.847	8.482
ENSG00000072042	**RDH11**	protein_coding	-1.137	0.824	8.482
ENSG00000233661	**SPIN4-AS1**	lncRNA	-1.137	0.831	8.482
ENSG00000258212	**ZNF75BP**	processed_pseudogene	-1.137	0.762	8.482
ENSG00000203334	**ENSG00000203334**	lncRNA	-1.137	0.773	8.482
ENSG00000268582	**ENSG00000268582**	processed_pseudogene	-1.137	0.753	8.482
ENSG00000287474	**ENSG00000287474**	lncRNA	-1.137	0.82	8.482
ENSG00000138031	**ADCY3**	protein_coding	-1.136	0.809	8.482
ENSG00000186416	**NKRF**	protein_coding	-1.136	0.82	8.482
ENSG00000102595	**UGGT2**	protein_coding	-1.136	0.816	8.482
ENSG00000266379	**ENSG00000266379**	transcribed_unprocessed_	-1.136	0.811	8.482
ENSG00000273055	**ENSG00000273055**	lncRNA	-1.136	0.608	8.482
ENSG00000121058	**COIL**	protein_coding	-1.135	0.812	8.482
ENSG00000270499	**MKI67P1**	processed_pseudogene	-1.135	0.804	8.482
ENSG00000198015	**MRPL42**	protein_coding	-1.135	0.811	8.482
ENSG00000261668	**ENSG00000261668**	lncRNA	-1.135	0.808	8.482
ENSG00000259261	**IGHV4OR15-8**	IG_V_gene	-1.134	0.624	8.482
ENSG00000149503	**INCENP**	protein_coding	-1.134	0.833	8.482
ENSG00000001461	**NIPAL3**	protein_coding	-1.134	0.813	8.482
ENSG00000232064	**USP9YP33**	unprocessed_pseudogene	-1.134	0.803	8.482

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000272094	**ENSG00000272094**	lncRNA	-1.134	0.72	8.482
ENSG00000123374	**CDK2**	protein_coding	-1.133	0.831	8.482
ENSG00000202377	**SNORA25B**	snoRNA	-1.133	0.8	8.482
ENSG00000259136	**ENSG00000259136**	processed_pseudogene	-1.133	0.778	8.482
ENSG00000260212	**ENSG00000260212**	unprocessed_pseudogene	-1.133	0.804	8.482
ENSG00000260425	**ENSG00000260425**	lncRNA	-1.133	0.688	8.482
ENSG00000267222	**ENSG00000267222**	lncRNA	-1.133	0.707	8.482
ENSG00000081791	**DELE1**	protein_coding	-1.132	0.826	8.482
ENSG00000073792	**IGF2BP2**	protein_coding	-1.132	0.83	8.482
ENSG00000139725	**RHOF**	protein_coding	-1.132	0.817	8.482
ENSG00000271789	**ENSG00000271789**	lncRNA	-1.132	0.782	8.482
ENSG00000137409	**MTCH1**	protein_coding	-1.131	0.832	8.482
ENSG00000242456	**MTCO3P38**	processed_pseudogene	-1.131	0.779	8.482
ENSG00000163558	**PRKCI**	protein_coding	-1.131	0.829	8.482
ENSG00000170921	**TANC2**	protein_coding	-1.131	0.842	8.482
ENSG00000101849	**TBL1X**	protein_coding	-1.131	0.831	8.482
ENSG00000065308	**TRAM2**	protein_coding	-1.131	0.841	8.482
ENSG00000066135	**KDM4A**	protein_coding	-1.13	0.816	8.482
ENSG00000188895	**MSL1**	protein_coding	-1.13	0.832	8.482
ENSG00000211837	**TRAJ53**	TR_J_gene	-1.13	0.802	8.482
ENSG00000258311	**ENSG00000258311**	protein_coding	-1.13	0.79	8.482
ENSG00000139436	**GIT2**	protein_coding	-1.129	0.837	8.482
ENSG00000164758	**MED30**	protein_coding	-1.129	0.809	8.482
ENSG00000136839	**OR13C9**	protein_coding	-1.129	0.814	8.482
ENSG00000121390	**PSPC1**	protein_coding	-1.129	0.843	8.482
ENSG00000222202	**RNU4-26P**	snRNA	-1.129	0.691	8.482
ENSG00000105866	**SP4**	protein_coding	-1.129	0.827	8.482
ENSG00000152455	**SUV39H2**	protein_coding	-1.129	0.828	8.482
ENSG00000271187	**ENSG00000271187**	processed_pseudogene	-1.129	0.789	8.482
ENSG00000274341	**ENSG00000274341**	lncRNA	-1.129	0.681	8.482
ENSG00000162771	**FAM71A**	protein_coding	-1.128	0.756	8.482
ENSG00000154165	**GPR15**	protein_coding	-1.128	0.79	8.482
ENSG00000251958	**RNU6-1102P**	snRNA	-1.128	0.762	8.482
ENSG00000085365	**SCAMP1**	protein_coding	-1.128	0.836	8.482
ENSG00000010803	**SCMH1**	protein_coding	-1.128	0.827	8.482
ENSG00000264456	**ENSG00000264456**	lncRNA	-1.128	0.717	8.482
ENSG00000270497	**ENSG00000270497**	processed_pseudogene	-1.128	0.754	8.482
ENSG00000285797	**ENSG00000285797**	lncRNA	-1.128	0.636	8.482
ENSG00000270500	**COX6CP4**	processed_pseudogene	-1.127	0.734	8.482
ENSG00000014641	**MDH1**	protein_coding	-1.127	0.844	8.482
ENSG00000223749	**MIR503HG**	lncRNA	-1.127	0.792	8.482
ENSG00000110911	**SLC11A2**	protein_coding	-1.127	0.831	8.482
ENSG00000097096	**SYDE2**	protein_coding	-1.127	0.839	8.482
ENSG00000213557	**ENSG00000213557**	processed_pseudogene	-1.127	0.798	8.482
ENSG00000235881	**ENSG00000235881**	lncRNA	-1.127	0.773	8.482
ENSG00000266932	**ENSG00000266932**	transcribed_processed_ps	-1.127	0.726	8.482
ENSG00000287251	**ENSG00000287251**	lncRNA	-1.127	0.715	8.482
ENSG00000088035	**ALG6**	protein_coding	-1.126	0.801	8.482
ENSG00000082196	**C1QTNF3**	protein_coding	-1.126	0.815	8.482

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000279414	**CDRT15P9**	processed_pseudogene	-1.126	0.789	8.482
ENSG00000165055	**METTL2B**	protein_coding	-1.126	0.822	8.482
ENSG00000260075	**NSFP1**	unprocessed_pseudogene	-1.126	0.773	8.482
ENSG00000252311	**RNU1-103P**	snRNA	-1.126	0.693	8.482
ENSG00000223847	**ENSG00000223847**	processed_pseudogene	-1.126	0.803	8.482
ENSG00000278879	**ENSG00000278879**	TEC	-1.126	0.699	8.482
ENSG00000280099	**ENSG00000280099**	TEC	-1.126	0.804	8.482
ENSG00000198722	**UNC13B**	protein_coding	-1.125	0.831	8.482
ENSG00000236385	**ENSG00000236385**	lncRNA	-1.125	0.792	8.482
ENSG00000001631	**KRIT1**	protein_coding	-1.124	0.833	8.482
ENSG00000176312	**OR4H12P**	unprocessed_pseudogene	-1.124	0.752	8.482
ENSG00000260322	**ENSG00000260322**	lncRNA	-1.124	0.808	8.482
ENSG00000112379	**ARFGEF3**	protein_coding	-1.123	0.833	8.482
ENSG00000162642	**C1orf52**	protein_coding	-1.123	0.814	8.482
ENSG00000253626	**EIF5AL1**	protein_coding	-1.123	0.757	8.482
ENSG00000216056	**MIR891A**	miRNA	-1.123	0.792	8.482
ENSG00000176787	**OR52E2**	protein_coding	-1.123	0.79	8.482
ENSG00000243446	**RN7SL284P**	misc_RNA	-1.123	0.765	8.482
ENSG00000252725	**RNU6-765P**	snRNA	-1.123	0.804	8.482
ENSG00000175931	**UBE2O**	protein_coding	-1.123	0.814	8.482
ENSG00000147044	**CASK**	protein_coding	-1.122	0.835	8.482
ENSG00000126749	**EMG1**	protein_coding	-1.122	0.842	8.482
ENSG00000233810	**MOB1AP2**	processed_pseudogene	-1.122	0.815	8.482
ENSG00000232102	**MTCO3P2**	processed_pseudogene	-1.122	0.739	8.482
ENSG00000223691	**ENSG00000223691**	processed_pseudogene	-1.122	0.796	8.482
ENSG00000250922	**ATP5F1EP1**	processed_pseudogene	-1.121	0.758	8.482
ENSG00000185885	**IFITM1**	protein_coding	-1.121	0.806	8.482
ENSG00000196821	**ILRUN**	protein_coding	-1.121	0.837	8.482
ENSG00000167257	**RNF214**	protein_coding	-1.121	0.84	8.482
ENSG00000228739	**ENSG00000228739**	lncRNA	-1.121	0.809	8.482
ENSG00000279829	**ENSG00000279829**	TEC	-1.121	0.737	8.482
ENSG00000286259	**ENSG00000286259**	lncRNA	-1.121	0.689	8.482
ENSG00000226481	**ACTR3BP2**	processed_pseudogene	-1.12	0.739	8.482
ENSG00000265227	**MIR4699**	miRNA	-1.12	0.741	8.482
ENSG00000258239	**MTND2P17**	unprocessed_pseudogene	-1.12	0.795	8.482
ENSG00000144802	**NFKBIZ**	protein_coding	-1.12	0.816	8.482
ENSG00000117697	**NSL1**	protein_coding	-1.12	0.809	8.482
ENSG00000219222	**RPL12P47**	processed_pseudogene	-1.12	0.711	8.482
ENSG00000236378	**ENSG00000236378**	lncRNA	-1.12	0.824	8.482
ENSG00000087008	**ACOX3**	protein_coding	-1.118	0.85	8.482
ENSG00000226469	**ADAM1B**	unitary_pseudogene	-1.118	0.81	8.482
ENSG00000219387	**ATF1P1**	processed_pseudogene	-1.118	0.817	8.482
ENSG00000230562	**FAM133DP**	processed_pseudogene	-1.118	0.735	8.482
ENSG00000281332	**LINC00997**	lncRNA	-1.118	0.683	8.482
ENSG00000215424	**MCM3AP-AS1**	lncRNA	-1.118	0.816	8.482
ENSG00000167359	**OR51I1**	protein_coding	-1.118	0.622	8.482
ENSG00000207105	**Y_RNA**	misc_RNA	-1.118	0.811	8.482
ENSG00000139154	**AEBP2**	protein_coding	-1.117	0.831	8.482
ENSG00000228928	**KPNA2P2**	processed_pseudogene	-1.117	0.812	8.482

Gene ID	**Gene name**	**Gene type**	**Score(d)**	**Fold Change**	**q-value(%)**
ENSG00000196865	**NHLRC2**	protein_coding	-1.117	0.832	8.482
ENSG00000165730	**STOX1**	protein_coding	-1.117	0.824	8.482
ENSG00000187079	**TEAD1**	protein_coding	-1.117	0.832	8.482
ENSG00000212978	**ENSG00000212978**	lncRNA	-1.117	0.808	8.482
ENSG00000107890	**ANKRD26**	protein_coding	-1.116	0.816	8.482
ENSG00000188185	**LINC00265**	lncRNA	-1.116	0.788	8.482
ENSG00000186314	**PRELID2**	protein_coding	-1.116	0.82	8.482
ENSG00000084090	**STARD7**	protein_coding	-1.116	0.843	8.482
ENSG00000107341	**UBE2R2**	protein_coding	-1.116	0.833	8.482
ENSG00000279302	**ENSG00000279302**	TEC	-1.116	0.789	8.482
ENSG00000283236	**ENSG00000283236**	transcribed_unprocessed_	-1.116	0.598	8.482
ENSG00000198042	**MAK16**	protein_coding	-1.115	0.846	8.482
ENSG00000227613	**QRSL1P2**	processed_pseudogene	-1.115	0.769	8.482
ENSG00000212308	**RNA5SP23**	rRNA_pseudogene	-1.115	0.785	8.482
ENSG00000252068	**RNU6-390P**	snRNA	-1.115	0.8	8.482
ENSG00000222533	**RNU6-705P**	snRNA	-1.115	0.724	8.482
ENSG00000201377	**RNY4P23**	misc_RNA	-1.115	0.74	8.482
ENSG00000258763	**ENSG00000258763**	lncRNA	-1.115	0.785	8.482
ENSG00000284604	**ENSG00000284604**	lncRNA	-1.115	0.794	8.482
ENSG00000143761	**ARF1**	protein_coding	-1.114	0.834	8.482
ENSG00000145782	**ATG12**	protein_coding	-1.114	0.843	8.482
ENSG00000108559	**NUP88**	protein_coding	-1.114	0.849	8.482
ENSG00000265564	**PIGPP4**	processed_pseudogene	-1.114	0.78	8.482
ENSG00000205746	**PKD1P4**	transcribed_unprocessed_	-1.114	0.738	8.482
ENSG00000220311	**RPL35AP18**	processed_pseudogene	-1.114	0.762	8.482
ENSG00000231136	**ENSG00000231136**	processed_pseudogene	-1.114	0.689	8.482
ENSG00000261680	**ENSG00000261680**	processed_pseudogene	-1.114	0.778	8.482
ENSG00000272798	**ENSG00000272798**	lncRNA	-1.114	0.758	8.482
ENSG00000188092	**GPR89B**	protein_coding	-1.113	0.828	8.482
ENSG00000207721	**MIR186**	miRNA	-1.113	0.729	8.482
ENSG00000240084	**MTND4LP10**	processed_pseudogene	-1.113	0.782	8.482
ENSG00000200217	**RNU6-839P**	snRNA	-1.113	0.635	8.482
ENSG00000221740	**SNORD93**	snoRNA	-1.113	0.798	8.482
ENSG00000153914	**SREK1**	protein_coding	-1.113	0.838	8.482
ENSG00000118965	**WDR35**	protein_coding	-1.113	0.826	8.482
ENSG00000282864	**ENSG00000282864**	TEC	-1.113	0.801	8.482
ENSG00000224117	**PTPN2P2**	processed_pseudogene	-1.112	0.747	8.482
ENSG00000034533	**ASTE1**	protein_coding	-1.111	0.84	8.482
ENSG00000183943	**PRKX**	protein_coding	-1.111	0.843	8.482
ENSG00000000457	**SCYL3**	protein_coding	-1.111	0.836	8.482
ENSG00000198887	**SMC5**	protein_coding	-1.111	0.835	8.482
ENSG00000201602	**Y_RNA**	misc_RNA	-1.111	0.81	8.482
ENSG00000140694	**PARN**	protein_coding	-1.11	0.836	8.482
ENSG00000176024	**ZNF613**	protein_coding	-1.11	0.831	8.482
ENSG00000235298	**ENSG00000235298**	lncRNA	-1.11	0.733	8.482
ENSG00000254222	**ENSG00000254222**	lncRNA	-1.11	0.81	8.482
ENSG00000215301	**DDX3X**	protein_coding	-1.109	0.84	8.482
ENSG00000196550	**FAM72A**	protein_coding	-1.109	0.792	8.482
ENSG00000230342	**FANCD2P2**	unprocessed_pseudogen	-1.109	0.834	8.482

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000230528	**NOS2P3**	transcribed_unprocessed_	-1.109	0.638	8.482
ENSG00000080608	**PUM3**	protein_coding	-1.109	0.849	8.482
ENSG00000122376	**SHLD2**	protein_coding	-1.109	0.827	8.482
ENSG00000125875	**TBC1D20**	protein_coding	-1.109	0.835	8.482
ENSG00000274070	**CASTOR2**	protein_coding	-1.108	0.833	8.482
ENSG00000132664	**POLR3F**	protein_coding	-1.108	0.831	8.482
ENSG00000099956	**SMARCB1**	protein_coding	-1.108	0.834	8.482
ENSG00000232040	**ZBED9**	protein_coding	-1.108	0.835	8.482
ENSG00000249244	**ENSG00000249244**	unprocessed_pseudogene	-1.108	0.733	8.482
ENSG00000260986	**ENSG00000260986**	lncRNA	-1.108	0.598	8.482
ENSG00000269570	**ENSG00000269570**	lncRNA	-1.108	0.766	8.482
ENSG00000277210	**ENSG00000277210**	lncRNA	-1.108	0.766	8.482
ENSG00000108578	**BLMH**	protein_coding	-1.107	0.851	8.482
ENSG00000181274	**FRAT2**	protein_coding	-1.107	0.81	8.482
ENSG00000261008	**LINC01572**	lncRNA	-1.107	0.823	8.482
ENSG00000132570	**PCBD2**	protein_coding	-1.107	0.807	8.482
ENSG00000028277	**POU2F2**	protein_coding	-1.107	0.809	8.482
ENSG00000111725	**PRKAB1**	protein_coding	-1.107	0.837	8.482
ENSG00000165632	**TAF3**	protein_coding	-1.107	0.837	8.482
ENSG00000288102	**ENSG00000288102**	lncRNA	-1.107	0.764	8.482
ENSG00000153132	**CLGN**	protein_coding	-1.106	0.839	8.482
ENSG00000168116	**KIAA1586**	protein_coding	-1.106	0.819	8.482
ENSG00000183604	**SMG1P5**	transcribed_unprocessed_	-1.106	0.703	8.482
ENSG00000143387	**CTSK**	protein_coding	-1.105	0.844	8.482
ENSG00000207923	**MIR559**	miRNA	-1.105	0.835	8.482
ENSG00000271488	**RBM11P1**	processed_pseudogene	-1.105	0.749	8.482
ENSG00000279617	**ENSG00000279617**	TEC	-1.105	0.794	8.482
ENSG00000044459	**CNTLN**	protein_coding	-1.104	0.836	8.482
ENSG00000163281	**GNPDA2**	protein_coding	-1.104	0.832	8.482
ENSG00000124155	**PIGT**	protein_coding	-1.104	0.832	8.482
ENSG00000186815	**TPCN1**	protein_coding	-1.104	0.839	8.482
ENSG00000202459	**Y_RNA**	misc_RNA	-1.104	0.777	8.482
ENSG00000156639	**ZFAND3**	protein_coding	-1.104	0.828	8.482
ENSG00000156802	**ATAD2**	protein_coding	-1.103	0.841	8.482
ENSG00000259750	**NSA2P4**	processed_pseudogene	-1.103	0.782	8.482
ENSG00000219262	**OR2E1P**	unprocessed_pseudogene	-1.103	0.731	8.482
ENSG00000252386	**RNU6-1018P**	snRNA	-1.103	0.758	8.482
ENSG00000187605	**TET3**	protein_coding	-1.103	0.827	8.482
ENSG00000134490	**TMEM241**	protein_coding	-1.103	0.825	8.482
ENSG00000260572	**ENSG00000260572**	lncRNA	-1.103	0.775	8.482
ENSG00000287918	**ENSG00000287918**	lncRNA	-1.103	0.744	8.482
ENSG00000163017	**ACTG2**	protein_coding	-1.102	0.844	8.482
ENSG00000146409	**SLC18B1**	protein_coding	-1.102	0.834	8.482
ENSG00000239893	**ZNF736P9Y**	transcribed_processed_ps	-1.102	0.801	8.482
ENSG00000179600	**GPHB5**	protein_coding	-1.101	0.82	8.482
ENSG00000204084	**INPP5B**	protein_coding	-1.101	0.827	8.482
ENSG00000229243	**LINC01981**	lncRNA	-1.101	0.786	8.482
ENSG00000215417	**MIR17HG**	lncRNA	-1.101	0.839	8.482
ENSG00000188167	**TMPPE**	protein_coding	-1.101	0.827	8.482

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000271817	**U3**	snoRNA	-1.101	0.772	8.482
ENSG00000165156	**ZHX1**	protein_coding	-1.101	0.832	8.482
ENSG00000250084	**ENSG00000250084**	unprocessed_pseudogene	-1.101	0.729	8.482
ENSG00000251487	**ENSG00000251487**	lncRNA	-1.101	0.766	8.482
ENSG00000271259	**ENSG00000271259**	lncRNA	-1.101	0.711	8.482
ENSG00000284611	**ENSG00000284611**	unprocessed_pseudogene	-1.101	0.725	8.482
ENSG00000143621	**ILF2**	protein_coding	-1.1	0.844	8.482
ENSG00000111696	**NT5DC3**	protein_coding	-1.1	0.848	8.482
ENSG00000264172	**PDLIM1P3**	processed_pseudogene	-1.1	0.745	8.482
ENSG00000101773	**RBBP8**	protein_coding	-1.1	0.845	8.482
ENSG00000120158	**RCL1**	protein_coding	-1.1	0.843	8.482
ENSG00000265334	**ENSG00000265334**	lncRNA	-1.1	0.825	8.482
ENSG00000279486	**OR2AG1**	protein_coding	-1.099	0.831	8.482
ENSG00000228577	**ENSG00000228577**	lncRNA	-1.099	0.813	8.482
ENSG00000249848	**ENSG00000249848**	processed_pseudogene	-1.099	0.805	8.482
ENSG00000253985	**ENSG00000253985**	lncRNA	-1.099	0.696	8.482
ENSG00000270352	**ENSG00000270352**	processed_pseudogene	-1.099	0.841	8.482
ENSG00000069974	**RAB27A**	protein_coding	-1.098	0.845	8.482
ENSG00000052723	**SIKE1**	protein_coding	-1.098	0.846	8.482
ENSG00000250384	**UBE2CP3**	processed_pseudogene	-1.098	0.76	8.482
ENSG00000227673	**ENSG00000227673**	lncRNA	-1.098	0.8	8.482
ENSG00000253923	**ENSG00000253923**	processed_pseudogene	-1.098	0.709	8.482
ENSG00000266002	**ENSG00000266002**	lncRNA	-1.098	0.825	8.482
ENSG00000106392	**C1GALT1**	protein_coding	-1.097	0.841	8.482
ENSG00000285106	**ENSG00000285106**	lncRNA	-1.097	0.797	8.482
ENSG00000143486	**EIF2D**	protein_coding	-1.096	0.848	8.482
ENSG00000179172	**HNRNPCL1**	protein_coding	-1.096	0.814	8.482
ENSG00000249988	**ENSG00000249988**	lncRNA	-1.096	0.842	8.482
ENSG00000279214	**ENSG00000279214**	TEC	-1.096	0.798	8.482
ENSG00000147324	**MFHAS1**	protein_coding	-1.095	0.808	8.482
ENSG00000277801	**ENSG00000277801**	lncRNA	-1.095	0.657	8.482
ENSG00000279798	**ENSG00000279798**	TEC	-1.095	0.808	8.482
ENSG00000261326	**LINC01355**	lncRNA	-1.094	0.816	8.482
ENSG00000200575	**RNU6-414P**	snRNA	-1.094	0.722	8.482
ENSG00000175606	**TMEM70**	protein_coding	-1.094	0.838	8.482
ENSG00000243314	**ENSG00000243314**	processed_pseudogene	-1.094	0.782	8.482
ENSG00000252798	**ENSG00000252798**	scaRNA	-1.094	0.77	8.482
ENSG00000266579	**ENSG00000266579**	lncRNA	-1.094	0.749	8.482
ENSG00000111790	**FGFR1OP2**	protein_coding	-1.093	0.817	8.482
ENSG00000120063	**GNA13**	protein_coding	-1.093	0.828	8.482
ENSG00000265527	**MIR5690**	miRNA	-1.093	0.805	8.482
ENSG00000101079	**NDRG3**	protein_coding	-1.093	0.843	8.482
ENSG00000205331	**OR6C72P**	unprocessed_pseudogene	-1.093	0.769	8.482
ENSG00000100302	**RASD2**	protein_coding	-1.093	0.805	8.482
ENSG00000181458	**TMEM45A**	protein_coding	-1.093	0.843	8.482
ENSG00000253976	**ENSG00000253976**	lncRNA	-1.093	0.824	8.482
ENSG00000185432	**METTL7A**	protein_coding	-1.092	0.839	8.482
ENSG00000266407	**MIR3157**	miRNA	-1.092	0.813	8.482
ENSG00000131368	**MRPS25**	protein_coding	-1.092	0.849	8.482

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000270995	**ENSG00000270995**	processed_pseudogene	-1.092	0.761	8.482
ENSG00000276934	**ENSG00000276934**	lncRNA	-1.092	0.741	8.482
ENSG00000278126	**ENSG00000278126**	lncRNA	-1.092	0.789	8.482
ENSG00000139163	**ETNK1**	protein_coding	-1.091	0.836	8.482
ENSG00000240804	**NPM1P28**	processed_pseudogene	-1.091	0.782	8.482
ENSG00000249516	**PRELID3BP6**	processed_pseudogene	-1.091	0.78	8.482
ENSG00000217878	**ENSG00000217878**	processed_pseudogene	-1.091	0.735	8.482
ENSG00000234883	**MIR155HG**	lncRNA	-1.09	0.837	8.482
ENSG00000231103	**PRAMEF30P**	unprocessed_pseudogene	-1.09	0.79	8.482
ENSG00000212549	**RNA5SP354**	rRNA_pseudogene	-1.09	0.742	8.482
ENSG00000167323	**STIM1**	protein_coding	-1.09	0.834	8.482
ENSG00000111424	**VDR**	protein_coding	-1.09	0.836	8.482
ENSG00000203414	**BTBD7P1**	processed_pseudogene	-1.089	0.754	8.482
ENSG00000117593	**DARS2**	protein_coding	-1.089	0.831	8.482
ENSG00000113212	**PCDHB7**	protein_coding	-1.089	0.837	8.482
ENSG00000111961	**SASH1**	protein_coding	-1.089	0.837	8.482
ENSG00000089006	**SNX5**	protein_coding	-1.089	0.843	8.482
ENSG00000156299	**TIAM1**	protein_coding	-1.089	0.812	8.482
ENSG00000136631	**VPS45**	protein_coding	-1.089	0.822	8.482
ENSG00000238034	**ENSG00000238034**	lncRNA	-1.089	0.805	8.482
ENSG00000286596	**ENSG00000286596**	lncRNA	-1.089	0.764	8.482
ENSG00000136068	**FLNB**	protein_coding	-1.088	0.847	8.482
ENSG00000276789	**MRGPRX8P**	processed_pseudogene	-1.088	0.807	8.482
ENSG00000243104	**MTND4LP14**	processed_pseudogene	-1.088	0.695	8.482
ENSG00000121579	**NAA50**	protein_coding	-1.088	0.841	8.482
ENSG00000104320	**NBN**	protein_coding	-1.088	0.839	8.482
ENSG00000246067	**RAB30-DT**	lncRNA	-1.088	0.834	8.482
ENSG00000227161	**ENSG00000227161**	lncRNA	-1.088	0.797	8.482
ENSG00000235279	**ENSG00000235279**	lncRNA	-1.088	0.834	8.482
ENSG00000250145	**ENSG00000250145**	processed_pseudogene	-1.088	0.759	8.482
ENSG00000258142	**ENSG00000258142**	processed_pseudogene	-1.088	0.661	8.482
ENSG00000200432	**Y_RNA**	misc_RNA	2.502	2.131	8.482
ENSG00000286070	**ENSG00000286070**	protein_coding	2.505	1.534	8.482
ENSG00000244094	**SPRR2F**	protein_coding	2.516	1.637	8.482
ENSG00000164733	**CTSB**	protein_coding	2.522	1.546	8.482
ENSG00000271130	**IGHV3OR16-8**	IG_V_gene	2.567	2.729	8.482
ENSG00000277592	**Metazoa_SRP**	misc_RNA	2.577	1.565	8.482
ENSG00000119801	**YPEL5**	protein_coding	2.619	1.477	8.482
ENSG00000206659	**Y_RNA**	misc_RNA	2.68	1.834	5.863
ENSG00000251837	**Y_RNA**	misc_RNA	2.685	2.176	5.863
ENSG00000259171	**ENSG00000259171**	protein_coding	2.693	2.055	5.863
ENSG00000214025	**ATP5PBP4**	processed_pseudogene	2.715	1.679	5.863
ENSG00000275896	**PRSS2**	protein_coding	2.715	1.513	5.863
ENSG00000163191	**S100A11**	protein_coding	2.729	1.646	5.863
ENSG00000213030	**CGB8**	protein_coding	2.734	1.974	5.863
ENSG00000200600	**Y_RNA**	misc_RNA	2.751	1.85	5.863
ENSG00000207925	**MIR516B2**	miRNA	2.768	2.02	5.863
ENSG00000199866	**Y_RNA**	misc_RNA	2.8	1.902	5.863
ENSG00000228974	**ENSG00000228974**	processed_pseudogene	2.806	1.962	5.863

Gene ID	Gene name	Gene type	Score(d)	Fold Change	q-value(%)
ENSG00000169116	**PARM1**	protein_coding	2.82	1.665	5.863
ENSG00000185339	**TCN2**	protein_coding	2.847	1.633	5.863
ENSG00000151883	**PARP8**	protein_coding	2.905	1.612	4.003
ENSG00000106733	**NMRK1**	protein_coding	2.94	1.635	4.003
ENSG00000268799	**H3Y2**	protein_coding	3.054	2.193	4.003
ENSG00000262074	**SNORD3B-2**	snoRNA	3.067	1.727	4.003
ENSG00000276216	**ENSG00000276216**	lncRNA	3.116	1.849	4.003
ENSG00000241794	**SPRR2A**	protein_coding	3.13	2.278	4.003
ENSG00000202412	**RNY3P13**	misc_RNA	3.215	2.615	2.511
ENSG00000254258	**ENSG00000254258**	lncRNA	3.233	2.664	2.511
ENSG00000065833	**ME1**	protein_coding	3.336	1.716	2.511
ENSG00000273058	**ENSG00000273058**	lncRNA	3.38	2.121	2.511
ENSG00000177409	**SAMD9L**	protein_coding	3.418	2.123	2.511
ENSG00000133321	**PLAAT4**	protein_coding	3.477	1.868	2.511
ENSG00000272068	**BCAN-AS1**	lncRNA	3.55	2.341	2.511
ENSG00000270882	**H4C14**	protein_coding	3.823	2.954	1.662
ENSG00000273372	**SFTPD-AS1**	lncRNA	3.981	2.75	1.662
ENSG00000108405	**P2RX1**	protein_coding	4.153	1.871	1.662
ENSG00000165949	**IFI27**	protein_coding	4.802	2.551	1.662

Supplementary Table S4. List of positively (red) or negatively (blue) enriched gene sets in NCI-H929 *DIS3* -KD compared to NCI-H929 control, by GSEA analysis on global annotated PC gene expression profiles. Up- and down-regulated gene sets (red and blue, respectively) of Kegg, Hallmark, Reactome collections (version 7.2) are ordered according to nominal p-value and Normalized Enrichment Score (NES). Size, Normalized Enrichment Score (NES), Nominal p-value and FDR q-value are reported for each gene set.

NAME	SIZE	NES	NOM p-val	FDR q-val
REACTOME_COLLAGEN_DEGRADATION	64	2.2476418	0	0
REACTOME_COLLAGEN_CHAIN_TRIMERIZATION	44	2.2165043	0	3.30E-04
KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	125	2.087219	0	6.50E-04
REACTOME_DEGRADATION_OF_THE_EXTRACELLULAR_MATRIX	140	2.0821471	0	0.0054064
REACTOME_DNA_METHYLATION	56	2.060171	0	0.0059864
REACTOME_ACTIVATED_PKN1_STIMULATES_TRANSCRIPTION_OF_AR_ANDROGEN_RECEPTOR_REGULATED_GENES_KLK2_AND_KLK3	58	2.02988	0	0.0076293
REACTOME_AMYLOID_FIBER_FORMATION	101	2.0293024	0	0.0064687
REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS	197	2.0025346	0	0.0079409
KEGG_ARACHIDONIC_ACID_METABOLISM	58	1.9830483	0	0.0028908
REACTOME_ERCC6_CSB_AND_EHMT2_G9A_POSITIVELY_REGULATE_RRNA_EXPRESSION	67	1.978127	0	0.0096958
REACTOME_RHO_GTPASES_ACTIVATE_PKNS	85	1.9578769	0	0.0112716
REACTOME_RECOGNITION_AND_ASSOCIATION_OF_DNA_GLYCOSYLASE_WITH_SITE_CONTAINING_AN_AFFECTED_PURINE	51	1.9446796	0	0.0115748
REACTOME_SIRT1_NEGATIVELY_REGULATES_RRNA_EXPRESSION	59	1.923329	0	0.0143552
REACTOME_ASSEMBLY_OF_COLLAGEN_FIBRILS_AND_OTHER_MULTIMERIC_STRUCTURES	61	1.9198449	0	0.013809
REACTOME_INTERFERON_ALPHA_BETA_SIGNALING	72	1.9188383	0	0.0128469
REACTOME_ARACHIDONIC_ACID_METABOLISM	59	1.9181056	0	0.0121587
REACTOME_DISEASES_OF_PROGRAMMED_CELL_DEATH	93	1.9157989	0	0.0115222
REACTOME_CLASS_A_1_RHODOPSIN_LIKE_RECEPTORS	329	1.9106088	0	0.0116522
REACTOME_CLASS_B_2_SECRETIN_FAMILY_RECEPTORS	94	1.8757987	0	0.0164025
REACTOME_TRANSCRIPTIONAL_REGULATION_OF_GRANULOPOIESIS	81	1.8488111	0	0.0196586
REACTOME_GPCR_LIGAND_BINDING	461	1.8432766	0	0.0190154
KEGG_DRUG_METABOLISM_CYTOCHROME_P450	68	1.8232737	0	0.0168424
REACTOME_MEIOTIC_RECOMBINATION	78	1.820088	0	0.0210361
REACTOME_REGULATION_OF_INSULIN_LIKE_GROWTH_FACTOR_IGF_TRANSPORT_AND_UPTAKE_BY_INSULIN_LIKE_GROWTH_FACTOR_BINDING_PROTEINS_IGFBPS	124	1.8168567	0	0.0211202
REACTOME_EXTRACELLULAR_MATRIX_ORGANIZATION	301	1.8084924	0	0.022705
REACTOME_FORMATION_OF_THE_CORNIFIED_ENVELOPE	128	1.7839274	0	0.0281481
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION	271	1.7717366	0	0.0279333
REACTOME_CROSSLINKING_OF_COLLAGEN_FIBRILS	18	1.767916	0	0.0304125
REACTOME_DNA_DAMAGE_TELOMERE_STRESS_INDUCED_SENESCENCE	75	1.7657275	0	0.0305085
REACTOME_RUNX1_REGULATES_GENES_INVOLVED_IN_MEGAKARYOCYTE_DIFFERENTIATION_AND_PLATELET_FUNCTION	85	1.7646374	0	0.0300055
REACTOME_OLFACTORY_SIGNALING_PATHWAY	378	1.7527246	0	0.033169
KEGG_OLFACTORY_TRANSDUCTION	372	1.7446207	0	0.0328102
REACTOME_HDACS_DEACETYLATE_HISTONES	87	1.869546	0.001447178	0.016675
REACTOME_DNA_DOUBLE_STRAND_BREAK_RESPONSE	76	1.7466742	0.001464129	0.0343344
REACTOME_PRE_NOTCH_EXPRESSION_AND_PROCESSING	96	1.7729299	0.001474926	0.0295902
REACTOME_COLLAGEN_FORMATION	90	1.7009022	0.001481482	0.0497045
REACTOME_TNFS_BIND_THEIR_PHYSIOLOGICAL_RECEPTORS	28	1.8370649	0.001538462	0.0196812
REACTOME_BASE_EXCISION_REPAIR_AP_SITE_FORMATION	58	1.7803034	0.001557632	0.0282116
REACTOME_PRC2_METHYLATES_HISTONES_AND_DNA	64	1.8474575	0.002915452	0.0190342
REACTOME_NONHOMOLOGOUS_END_JOINING_NHEJ	67	1.8302712	0.002980626	0.0193167
REACTOME_NCAM1_INTERACTIONS	42	1.7422339	0.003025719	0.0349414
REACTOME_SYNTHESIS_SECRETION_AND_DEACYLATION_OF_GHRELIN	19	1.8588375	0.003159558	0.0186524
REACTOME_ANCHORING_FIBRIL_FORMATION	15	1.8302757	0.003169572	0.0201216
REACTOME_NICOTINATE_METABOLISM	31	1.7397816	0.00317965	0.0349094
REACTOME_FATTY_ACIDS	15	1.804805	0.003205128	0.022991
REACTOME_CONDENSATION_OF_PROPHASE_CHROMOSOMES	65	1.7056066	0.005997002	0.0485587

NAME	SIZE	NES	NOM p-val	FDR q-val
HALLMARK_G2M_CHECKPOINT	199	-3.448332	0	0
REACTOME_MITOTIC_SPINDLE_CHECKPOINT	111	-3.26577	0	0
HALLMARK_MITOTIC_SPINDLE	199	-3.264961	0	0
REACTOME_MITOTIC_PROMETAPHASE	203	-3.149322	0	0
HALLMARK_E2F_TARGETS	200	-3.093854	0	0
REACTOME_RESOLUTION_OF_SISTER_CHROMATID_COHESION	126	-3.012712	0	0
REACTOME_RHO_GTPASES_ACTIVATE_FORMINS	140	-2.959161	0	0

NAME	SIZE	NES	NOM p-val	FDR q-val
REACTOME_SUMOYLATION_OF_DNA_REPLICATION_PROTEINS	46	-2.844179	0	0
REACTOME_SUMOYLATION_OF_UBIQUITINYLATION_PROTEINS	39	-2.708669	0	0
REACTOME_POSTMITOTIC_NUCLEAR_PORE_COMPLEX_NPC_REFORMATION	27	-2.703683	0	0
REACTOME_NUCLEAR_PORE_COMPLEX_NPC_DISASSEMBLY	36	-2.695551	0	0
REACTOME_INTERACTIONS_OF_REV_WITH_HOST_CELLULAR_PROTEINS	37	-2.692247	0	0
REACTOME_NUCLEAR_IMPORT_OF_REV_PROTEIN	34	-2.680229	0	0
REACTOME_NUCLEAR_ENVELOPE_BREAKDOWN	53	-2.63313	0	0
REACTOME_EXPORT_OF_VIRAL_RIBONUCLEOPROTEINS_FROM_NUCLEUS	33	-2.61499	0	0
KEGG_CELL_CYCLE	124	-2.556227	0	0
REACTOME_TRANSPORT_OF_MATURE_TRANSCRIPT_TO_CYTOPLASM	82	-2.555709	0	0
REACTOME_INTERACTIONS_OF_VPR_WITH_HOST_CELLULAR_PROTEINS	36	-2.55144	0	0
REACTOME_MITOTIC_METAPHASE_AND_ANAPHASE	236	-2.548557	0	0
REACTOME_AURKA_ACTIVATION_BY_TPX2	72	-2.534014	0	0
REACTOME_SUMOYLATION_OF_DNA_DAMAGE_RESPONSE_AND_REPAIR_PROTEINS	77	-2.518734	0	9.89E-05
REACTOME_SNRNP_ASSEMBLY	54	-2.500463	0	9.34E-05
REACTOME_TRANSPORT_OF_THE_SLBP_DEPENDANT_MATURE_MRNA	36	-2.493957	0	8.85E-05
REACTOME_SUMOYLATION_OF_SUMOYLATION_PROTEINS	35	-2.488801	0	8.41E-05
REACTOME_RESOLUTION_OF_D_LOOP_STRUCTURES_THROUGH_SYNTHESIS_DEPENDENT_STRAND_ANNEALING_SDSA	26	-2.463775	0	8.01E-05
REACTOME_CYCLIN_A_B1_B2_ASSOCIATED_EVENTS_DURING_G2_M_TRANSITION	24	-2.460956	0	7.65E-05
REACTOME_SEPARATION_OF_SISTER_CHROMATIDS	191	-2.459688	0	7.31E-05
REACTOME_TRANSPORT_OF_MATURE_MRNAS_DERIVED_FROM_INTRONLESS_TRANSCRIPTS	43	-2.438877	0	1.44E-04
REACTOME_REGULATION_OF_PLK1_ACTIVITY_AT_G2_M_TRANSITION	87	-2.432994	0	1.38E-04
REACTOME_DEADENYLATION_DEPENDENT_MRNA_DECAY	56	-2.432105	0	1.33E-04
REACTOME_SYNTHESIS_OF_PIPS_AT_THE_PLASMA_MEMBRANE	53	-2.406737	0	1.28E-04
REACTOME_HOMOLOGOUS_DNA_PAIRING_AND_STRAND_EXCHANGE	42	-2.394648	0	1.23E-04
REACTOME_TRNA_PROCESSING	108	-2.365639	0	1.19E-04
KEGG_RNA_DEGRADATION	57	-2.361409	0	0
REACTOME_NS1_MEDIATED_EFFECTS_ON_HOST_PATHWAYS	41	-2.360186	0	1.15E-04
REACTOME_RECRUITMENT_OF_MITOTIC_CENTROSOME_PROTEINS_AND_COMPLEXES	81	-2.360047	0	1.11E-04
REACTOME_POLO_LIKE_KINASE_MEDIATED_EVENTS	16	-2.344919	0	2.66E-04
REACTOME_REGULATION_OF_GLUCOKINASE_BY_GLUCOKINASE_REGULATORY_PROTEIN	32	-2.343129	0	2.58E-04
REACTOME_G0_AND_EARLY_G1	27	-2.304086	0	4.48E-04
REACTOME_RHOD_GTPASE_CYCLE	51	-2.294348	0	5.34E-04
REACTOME_ANCHORING_OF_THE_BASAL_BODY_TO_THE_PLASMA_MEMBRANE	97	-2.28572	0	5.05E-04
REACTOME_VIRAL_MESSENGER_RNA_SYNTHESIS	44	-2.273014	0	5.38E-04
REACTOME_REGULATION_OF_TP53_EXPRESSION_AND_DEGRADATION	37	-2.266141	0	6.53E-04
REACTOME_REGULATION_OF_TP53_ACTIVITY_THROUGH_PHOSPHORYLATION	92	-2.256921	0	7.21E-04
REACTOME_TRNA_PROCESSING_IN_THE_NUCLEUS	58	-2.246669	0	7.03E-04
REACTOME_RHOBTB2_GTPASE_CYCLE	23	-2.23624	0	7.67E-04
REACTOME_M_PHASE	408	-2.229831	0	9.14E-04
REACTOME_REGULATION_OF_TP53_ACTIVITY	160	-2.221332	0	0.001048
REACTOME_HDR_THROUGH_SINGLE_STRAND_ANNEALING_SSA	37	-2.206339	0	0.0012534
REACTOME_CELL_CYCLE_CHECKPOINTS	290	-2.197289	0	0.0012975
KEGG_PROGESTERONE_MEDIATED_OOCYTE_MATURATION	85	-2.194562	0	0.001275
REACTOME_RHOF_GTPASE_CYCLE	42	-2.180184	0	0.0014536
REACTOME_APC_CDC20_MEDIATED_DEGRADATION_OF_NEK2A	26	-2.167011	0	0.0015612
REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_CELL_CYCLE_GENES	49	-2.160232	0	0.0017292
REACTOME_DOWNSTREAM_SIGNAL_TRANSDUCTION	29	-2.139323	0	0.0021402
REACTOME_GLYCOLYSIS	72	-2.118678	0	0.0029118
KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS	133	-2.114373	0	0.0042099
KEGG_RENAL_CELL_CARCINOMA	70	-2.107637	0	0.0033679
REACTOME_SIGNALING_BY_CYTOSOLIC_FGFR1_FUSION_MUTANTS	18	-2.094039	0	0.0037453
REACTOME_INHIBITION_OF_THE_PROTEOLYTIC_ACTIVITY_OF_APC_C_REQUIRED_FOR_THE_ONSET_OF_ANAPHASE_BY_MITOTIC_SPINDLE_CHECKPOINT_COMPONENTS	21	-2.087359	0	0.0039702
REACTOME_RHOBTB_GTPASE_CYCLE	35	-2.085199	0	0.0039592
REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE_MRNA	240	-2.075233	0	0.0043706
REACTOME_HDR_THROUGH_HOMOLOGOUS_RECOMBINATION_HRR	66	-2.068582	0	0.0046092
REACTOME_RNA_POLYMERASE_II_TRANSCRIBES_SNRNA_GENES	74	-2.060139	0	0.004892
REACTOME_PI_METABOLISM	84	-2.057638	0	0.0048925
REACTOME_RNA_POLYMERASE_I_TRANSCRIPTION_INITIATION	47	-2.055108	0	0.0048949
KEGG_MTOR_SIGNALING_PATHWAY	52	-2.054594	0	0.0067734
REACTOME_RNA_POLYMERASE_III_CHAIN_ELONGATION	18	-2.052248	0	0.0050316

NAME	SIZE	NES	NOM p-val	FDR q-val
REACTOME_SIGNALING_BY_PDGFR_IN_DISEASE	20	-2.039142	0	0.0055522
REACTOME_APC_C_CDC20_MEDIATED_DEGRADATION_OF_CYCLIN_B	24	-2.035909	0	0.0056706
REACTOME_TRANSCRIPTION_OF_E2F_TARGETS_UNDER_NEGATIVE_CONTROL_BY_DREAM_COMPLEX	19	-2.027188	0	0.006034
REACTOME_TRANSCRIPTIONAL_REGULATION_BY_TP53	359	-2.025639	0	0.0060238
REACTOME_CONVERSION_FROM_APC_C_CDC20_TO_APC_C_CDH1_IN_LATE_ANAPHASE	20	-2.023654	0	0.0060589
REACTOME_GLUCOSE_METABOLISM	91	-2.011766	0	0.0069281
REACTOME_REGULATION_OF_HSF1_MEDIATED_HEAT_SHOCK_RESPONSE	82	-2.010539	0	0.0069269
REACTOME_KSRP_KHSRP_BINDS_AND_DESTABILIZES_MRNA	17	-2.001992	0	0.0072746
KEGG_OOCYTE_MEIOSIS	112	-1.997197	0	0.0094559
REACTOME_BUTYRATE_RESPONSE_FACTOR_1_BRF1_BINDS_AND_DESTABILIZES_MRNA	17	-1.993935	0	0.0076456
REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION_INITIATION_FROM_TYPE_1_PROMOTER	28	-1.981166	0	0.0084978
REACTOME_EXTENSION_OF_TELOMERES	51	-1.978882	0	0.008675
REACTOME_RHO_GTPASE_CYCLE	444	-1.973101	0	0.0088615
KEGG_LYSINE_DEGRADATION	44	-1.971127	0	0.0098348
KEGG_ADHERENS_JUNCTION	73	-1.968093	0	0.0088513
REACTOME_ACTIVATED_TAK1_MEDIATES_P38_MAPK_ACTIVATION	23	-1.964695	0	0.0093436
REACTOME_CELLULAR_RESPONSE_TO_HEAT_STRESS	101	-1.962172	0	0.0095267
REACTOME_MITOTIC_G2_G2_M_PHASES	199	-1.960824	0	0.0095746
HALLMARK_TGF_BETA_SIGNALING	54	-1.958523	0	6.85E-04
REACTOME_CIRCADIAN_CLOCK	70	-1.958177	0	0.00955
REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_DNA_REPAIR_GENES	62	-1.954595	0	0.0096766
KEGG_CHRONIC_MYELOID_LEUKEMIA	73	-1.95422	0	0.0091469
REACTOME_RHO_GTPASE_EFFECTORS	315	-1.942879	0	0.0106783
REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION_INITIATION_FROM_TYPE_3_PROMOTER	28	-1.935333	0	0.0110343
REACTOME_G1_S_SPECIFIC_TRANSCRIPTION	29	-1.934437	0	0.0109703
REACTOME_NUCLEAR_EVENTS_KINASE_AND_TRANSCRIPTION_FACTOR_ACTIVATION	61	-1.930932	0	0.0113068
REACTOME_FLT3_SIGNALING	38	-1.922324	0	0.0120206
REACTOME_TRNA_MODIFICATION_IN_THE_NUCLEUS_AND_CYTOSOL	43	-1.913744	0	0.0127484
REACTOME_RRNA_MODIFICATION_IN_THE_NUCLEUS_AND_CYTOSOL	59	-1.912338	0	0.0127753
REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLICATION_STRESS	37	-1.897458	0	0.0143036
REACTOME_RNA_POLYMERASE_I_TRANSCRIPTION_TERMINATION	31	-1.892112	0	0.0149261
HALLMARK_MTORC1_SIGNALING	200	-1.881625	0	0.0022169
HALLMARK_UV_RESPONSE_DN	144	-1.877232	0	0.0018474
REACTOME_HIV_LIFE_CYCLE	149	-1.873602	0	0.017137
REACTOME_SUMOYLATION	185	-1.861285	0	0.0184433
REACTOME_RECRUITMENT_OF_NUMA_TO_MITOTIC_CENTROSOMES	95	-1.859207	0	0.0185758
REACTOME_RHOB_GTPASE_CYCLE	70	-1.858879	0	0.0184268
REACTOME_SIGNALING_BY_NTRKS	134	-1.857606	0	0.0184276
KEGG_ERBB_SIGNALING_PATHWAY	87	-1.835436	0	0.0198822
REACTOME_RRNA_PROCESSING	202	-1.829966	0	0.0217658
REACTOME_RHOQ_GTPASE_CYCLE	59	-1.828136	0	0.0218755
REACTOME_APC_C_MEDIATED_DEGRADATION_OF_CELL_CYCLE_PROTEINS	88	-1.817919	0	0.0229084
REACTOME_REGULATION_OF_LIPID_METABOLISM_BY_PPARALPHA	120	-1.814751	0	0.023041
REACTOME_DUAL_INCISION_IN_TC_NER	65	-1.810971	0	0.023478
HALLMARK_MYC_TARGETS_V2	58	-1.804868	0	0.0029176
REACTOME_ORGANELLE_BIOGENESIS_AND_MAINTENANCE	294	-1.797109	0	0.0254641
REACTOME_SIGNALING_BY_VEGF	106	-1.792773	0	0.0257844
KEGG_NEUROTROPHIN_SIGNALING_PATHWAY	126	-1.791933	0	0.0286473
REACTOME_INTERLEUKIN_17_SIGNALING	71	-1.786459	0	0.0265697
REACTOME_FACTORS_INVOLVED_IN_MEGAKARYOCYTE_DEVELOPMENT_AND_PLATELET_PRODUCTION	165	-1.778544	0	0.0282217
REACTOME_CDC42_GTPASE_CYCLE	159	-1.767657	0	0.0303699
KEGG_AMINOACYL_TRNA_BIOSYNTHESIS	41	-1.766501	0	0.032434
HALLMARK_MYC_TARGETS_V1	200	-1.761533	0	0.0032348
REACTOME_INFLUENZA_INFECTION	156	-1.746811	0	0.0338528
REACTOME_INTRA_GOLGI_AND_RETROGRADE_GOLGI_TO_ER_TRAFFIC	203	-1.743971	0	0.0342987
REACTOME_S_PHASE	162	-1.732571	0	0.0362878
REACTOME_RAC1_GTPASE_CYCLE	184	-1.699264	0	0.0419643
REACTOME_GOLGI_TO_ER_RETROGRADE_TRANSPORT	134	-1.684535	0	0.0453251
REACTOME_CILIUM_ASSEMBLY	201	-1.673082	0	0.0484422
REACTOME_COPI_DEPENDENT_GOLGI_TO_ER_RETROGRADE_TRAFFIC	100	-1.666873	0	0.0496452

NAME	SIZE	NES	NOM p-val	FDR q-val
REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLICATION	21	-1.942032	0.00257732	0.0106487
REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION_TERMINATION	23	-1.954384	0.002724796	0.0096015
REACTOME_DEADENYLATION_OF_MRNA	25	-2.286613	0.00273224	5.19E-04
REACTOME_RETROGRADE_TRANSPORT_AT_THE_TRANS_GOLGI_NETWORK	49	-1.82421	0.002747253	0.0222518
REACTOME_TRISTETRAPROLIN_TTP_ZFP36_BINDS_AND_DESTABILIZES_MRNA	17	-2.090166	0.002754821	0.0038851
REACTOME_TRANSCRIPTION_OF_E2F_TARGETS_UNDER_NEGATIVE_CONTROL_BY_P107_RBL1_AND_P130_RBL2_IN_COMPLEX_WITH_HDAC1	16	-2.1675	0.002785515	0.001593
REACTOME_RESOLUTION_OF_D_LOOP_STRUCTURES	33	-1.94347	0.002801121	0.0107433
REACTOME_SIGNALING_BY_CTNNB1_PHOSPHO_SITE_MUTANTS	15	-1.856466	0.002801121	0.0183985
REACTOME_FORMATION_OF_TC_NER_PRE_INCISION_COMPLEX	53	-1.791453	0.002816901	0.0257683
REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION_TERMINATION	66	-1.84354	0.002857143	0.0197278
HALLMARK_PROTEIN_SECRETION	95	-1.737565	0.002890173	0.0043315
REACTOME_RHOJ_GTPASE_CYCLE	55	-2.146669	0.002898551	0.0020227
REACTOME_TRANSCRIPTIONAL_ACTIVITY_OF_SMAD2_SMAD3_SMAD4_HETEROTRIMER	44	-1.821662	0.002898551	0.022619
KEGG_COLORECTAL_CANCER	62	-1.985653	0.00295858	0.0090812
KEGG_PANCREATIC_CANCER	70	-1.731527	0.00295858	0.0370705
REACTOME_HIV_TRANSCRIPTION_INITIATION	47	-1.81057	0.002994012	0.0233633
REACTOME_RHOC_GTPASE_CYCLE	74	-1.74711	0.003076923	0.0340074
REACTOME_RNA_POLYMERASE_III_TRANSCRIPTION	41	-1.90617	0.00310559	0.0134275
REACTOME_SUMOYLATION_OF_RNA_BINDING_PROTEINS	47	-2.189043	0.003134796	0.0013737
REACTOME_NUCLEOTIDE_EXCISION_REPAIR	110	-1.724177	0.003194888	0.0376632
REACTOME_TRANSCRIPTION_OF_THE_HIV_GENOME	70	-1.669471	0.003194888	0.0494238
REACTOME_TRANSCRIPTIONAL_ACTIVATION_OF_MITOCHONDRIAL_BIOGENESIS	55	-1.958553	0.003367003	0.0096251
REACTOME_DEPOLYMERISATION_OF_THE_NUCLEAR_LAMINA	15	-1.842078	0.004950495	0.0199001
REACTOME_RND1_GTPASE_CYCLE	42	-1.725937	0.005361931	0.0375914
REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_ADDITIONAL_CELL_CYCLE_GENES_WHOSE_EXACT_ROLE_IN_THE_P53_PATHWAY_REMAIN_UNCERTAIN	21	-2.000656	0.005434783	0.0072629
REACTOME_INITIATION_OF_NUCLEAR_ENVELOPE_NE_REFORMATION	19	-1.852753	0.005555556	0.0186901
REACTOME_MRNA_CAPPING	29	-1.700105	0.005586592	0.0419851
REACTOME_MRNA_DECAY_BY_3_TO_5_EXORIBONUCLEASE	16	-1.97695	0.005649718	0.0086933
REACTOME_RORA_ACTIVATES_GENE_EXPRESSION	18	-1.819651	0.005830904	0.022721
REACTOME_TP53_REGULATES_TRANSCRIPTION_OF_GENES_INVOLVED_IN_G2_CELL_CYCLE_ARREST	18	-1.737899	0.005847953	0.0350437
KEGG_ACUTE_MYELOID_LEUKEMIA	57	-1.747843	0.005952381	0.0348875
REACTOME_REGULATION_OF_CHOLESTEROL_BIOSYNTHESIS_BY_SREBP_SREBF	55	-1.845496	0.00625	0.0195813
REACTOME_PHOSPHORYLATION_OF_THE_APC_C	20	-1.794947	0.008086253	0.0257901
REACTOME_SIGNALING_BY_KIT_IN_DISEASE	20	-1.741514	0.008086253	0.0347012
REACTOME_INTERLEUKIN_3_INTERLEUKIN_5_AND_GM_CSF_SIGNALING	46	-1.751139	0.008498584	0.0336869
KEGG_RNA_POLYMERASE	28	-1.90745	0.00867052	0.0112906
REACTOME_FLT3_SIGNALING_IN_DISEASE	28	-1.793871	0.008746356	0.0258063
REACTOME_CLASS_C_3_METABOTROPIC_GLUTAMATE_PHEROMONE_RECEPTORS	39	-1.764041	0.00882353	0.0309843
REACTOME_TRNA_AMINOACYLATION	42	-1.723369	0.009009009	0.0376981
REACTOME_SIGNALING_BY_FGFR1_IN_DISEASE	38	-1.758322	0.010498688	0.0320636
REACTOME_NUCLEOBASE_BIOSYNTHESIS	15	-1.815477	0.01055409	0.0231676
REACTOME_SIGNALING_BY_NTRK2_TRKB	25	-1.713642	0.010638298	0.0396025
REACTOME_SIGNALING_BY_ERYTHROPOIETIN	25	-1.741396	0.011111111	0.0345063
REACTOME_HEME_SIGNALING	48	-1.680134	0.011204482	0.0463533
REACTOME_CD209_DC_SIGN_SIGNALING	21	-1.750014	0.011428571	0.0336939
REACTOME_SIGNALING_BY_FLT3_FUSION_PROTEINS	19	-1.874839	0.011527377	0.0171028
HALLMARK_ANDROGEN_RESPONSE	100	-1.517484	0.011976048	0.0260975
REACTOME_CYTOSOLIC_TRNA_AMINOACYLATION	24	-1.72612	0.015060241	0.0378367
REACTOME_REGULATION_OF_SIGNALING_BY_CBL	22	-1.702208	0.015584416	0.0420281
REACTOME_TRANSCRIPTIONAL_REGULATION_BY_E2F6	34	-1.692014	0.016483517	0.0434882
REACTOME_MAPK_TARGETS_NUCLEAR_EVENTS_MEDIATED_BY_MAP_KINASES	31	-1.692111	0.018867925	0.0437206
REACTOME_BETA_CATENIN_PHOSPHORYLATION_CASCADE	17	-1.754802	0.019125683	0.0328344
REACTOME_DOWNREGULATION_OF_SMAD2_3_SMAD4_TRANSCRIPTIONAL_ACTIVITY	23	-1.712721	0.021447722	0.0395958
REACTOME_JNK_C_JUN_KINASES_PHOSPHORYLATION_AND_ACTIVATION_MEDIATED_BY_ACTIVATED_HUMAN_TAK1	22	-1.700372	0.02247191	0.0422151
REACTOME_PROCESSING_OF_INTRONLESS_PRE_MRNAS	19	-1.687169	0.02247191	0.0447464
REACTOME_PLATELET_SENSITIZATION_BY_LDL	17	-1.667652	0.02387268	0.0497264
REACTOME_TELOMERE_EXTENSION_BY_TELOMERASE	23	-1.707142	0.024096385	0.0408927