Genomic retrospective evaluation of 20 years of selection in Italian Holstein bulls for feet and legs trait.

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Introduction

Under strong directional selection, allele frequencies rapidly change, allowing the identification of genomic regions carrying genes and variants that control production, functional and morphological traits. Feet and legs functionality (FLF) Estimated Breeding Values (EBV) in Italian Holstein is a summary of three Legs EBVs: rear and side view and foot angle. These traits are very important considering the growing demand of modern dairy production for functional cows.

Objectives

To identify genomic regions involved in directional selection for FLF EBV by a novel approach relying on birth date regression and allele frequencies changes analysis.

Methods

Analysis were performed on 2918 Italian Holstein bulls born between 1979 and 2011, genotyped in SELMOL, PROZOO and INNOVAGEN projects with BovineSNP50 v.1 and BovineHD SNPchips. EBVs for FLF trait were provided by the Italian Holstein association (ANAFI). SNPs positions were updated to UMD3.1 using SNPchiMp v.3. Genotypes were imputed using BEAGLE (v.3.3.4) to HD genotypes.
Genomic region identification were performed on PLUS- and MINUS-variant bulls for the target EBV over the total year range (134 bulls, group OVERALL- fig.1) and within each birth year (130 bulls, group BY_YEAR-fig.1). Were retained regions with:

- ≥ 40 SNPs with a significant linear trend;
- the highest allelic frequency difference between PLUS and MINUS (75th percentile+1.5*InterQuartile Range);
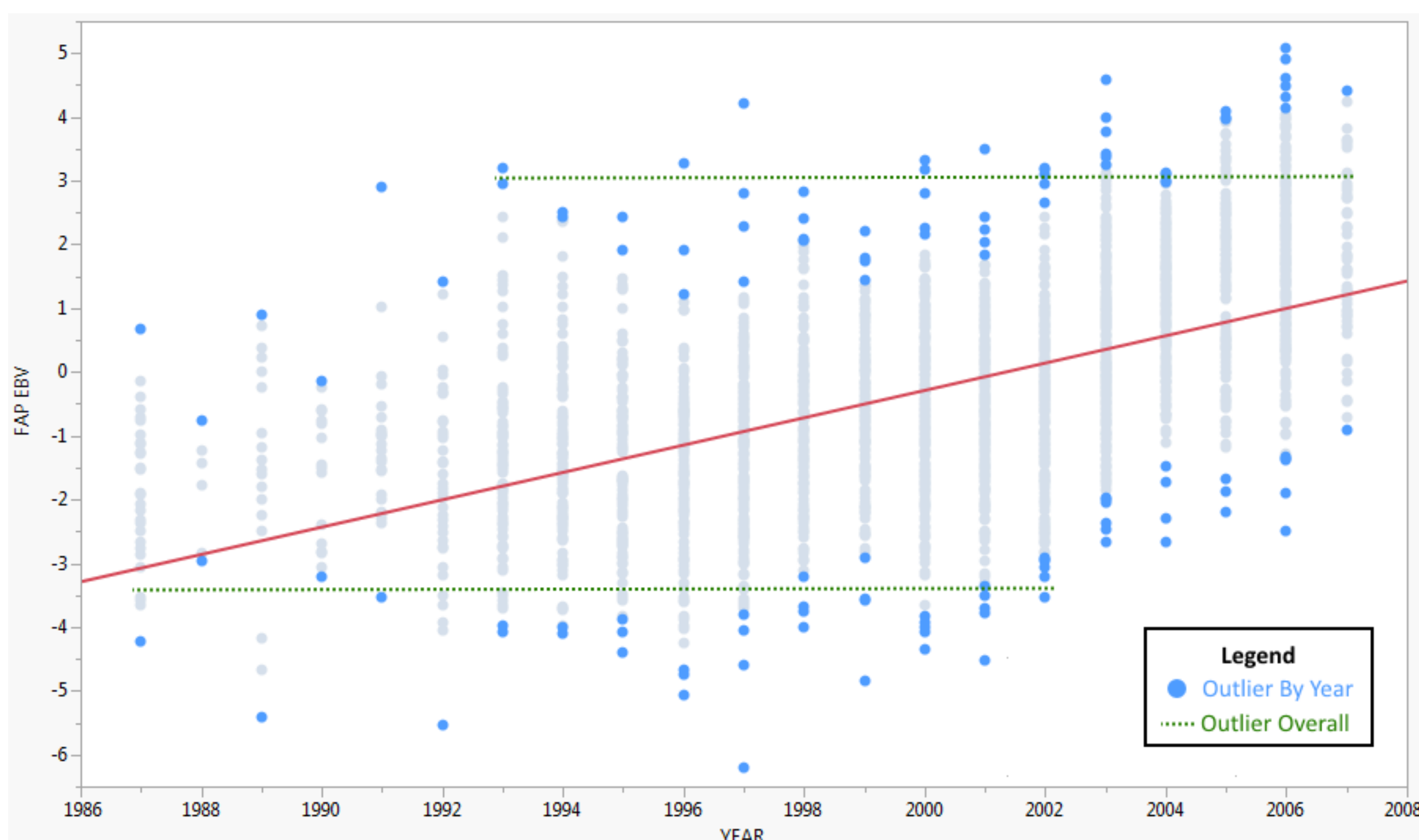- identified in both OVERALL and BY YEAR groups.

Figure 1. Positive FLF EBV linear trend in Italian Holstein Friesian bulls (red line) and plus and minus variant bulls (By YEAR and OVERALL) groups.

Results and discussion

The ~686 Kb region on BTA10 (from position 62,578 to 63,264 Kb) had the highest mean delta of allelic variation on BY YEAR group. The ~417 Kb region on BTA20 (from position 40,738 to 41,155 Kb) had the highest mean delta on OVERALL group. After linear regression evaluation, a total of 65 windows were identified. Flanking regions of 100Kb were included. These regions included 176 genes identified by StringDB. Particularly interesting are genes like PRLR, STAT5A, STAT5B, STAT3, and PIK3R1 that are involved in immune response and mammary gland and feet conformation. Windows identified include 584 unique QTLs. Among those,160 are conformation related and can be divided in 7 classes including hips, rump, legs and feet conformation traits (Fig.2). Bioinformatic analysis are underway to deepen the biological pathways involved for FLF trait.
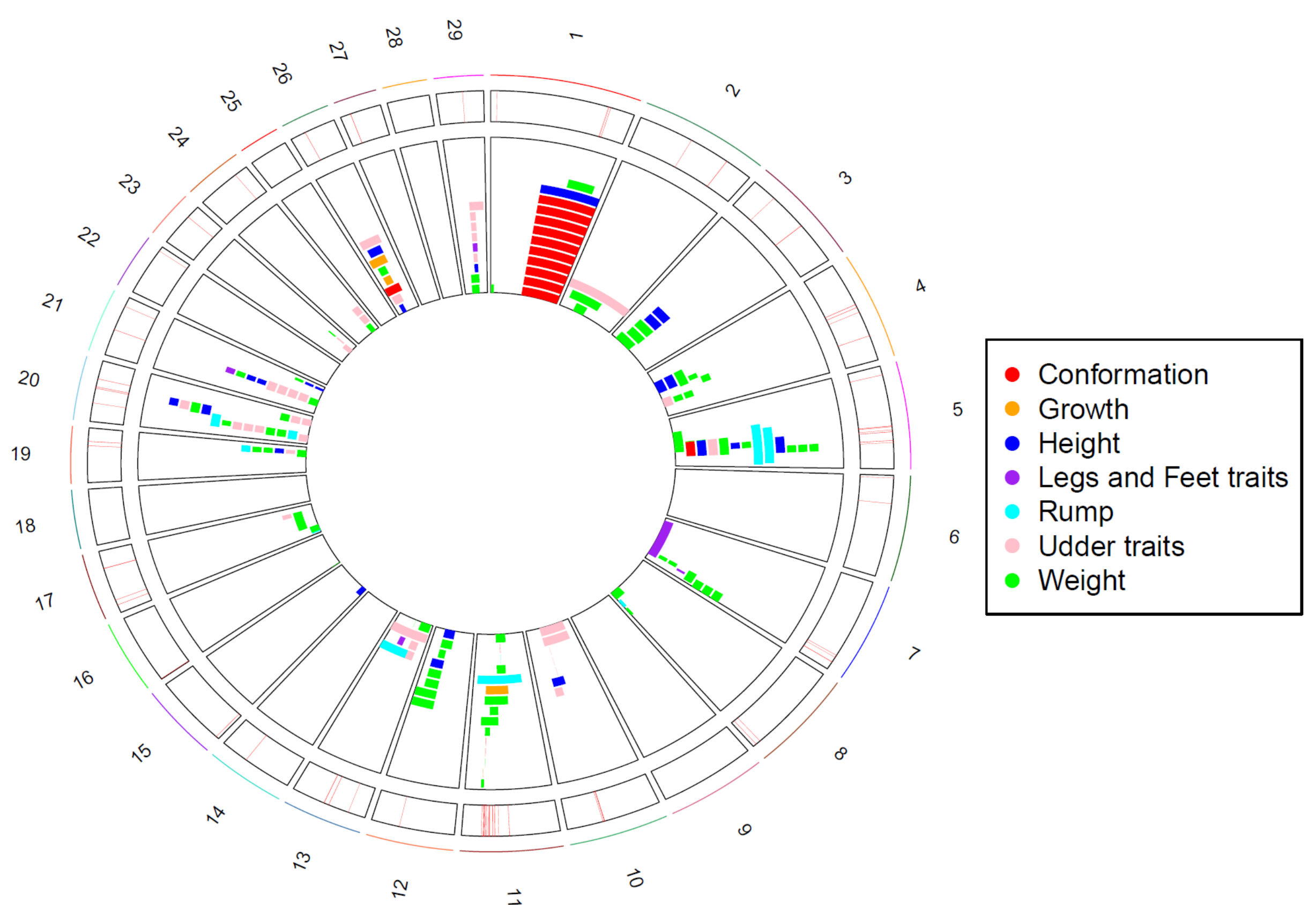

Figure 2. Identified genomic regions (outer circle) and conformation related QTL (inner circle) by chromosome.

Conclusions

This approach complements GWAS and other methods used to identify selection signature and genomic regions involved in long-term, directional selective sweeps to better identify QTLs, genes and pathways involved in phenotypic variation for interested trait.

Acknowledges