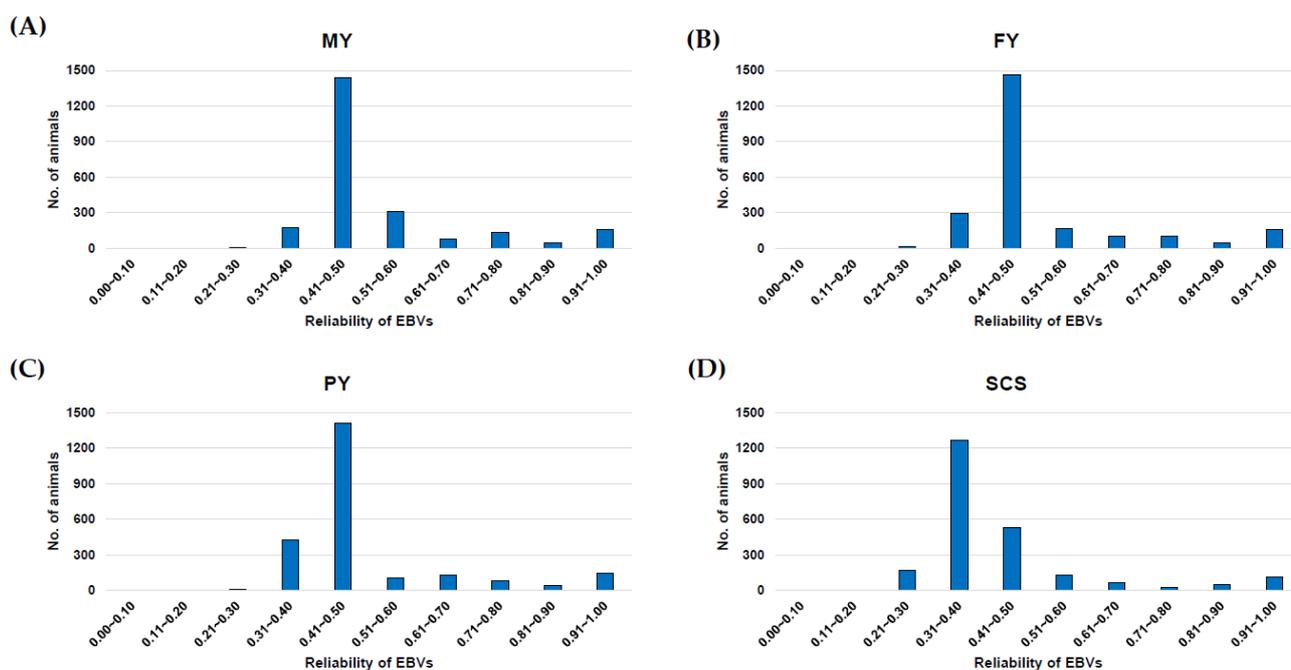
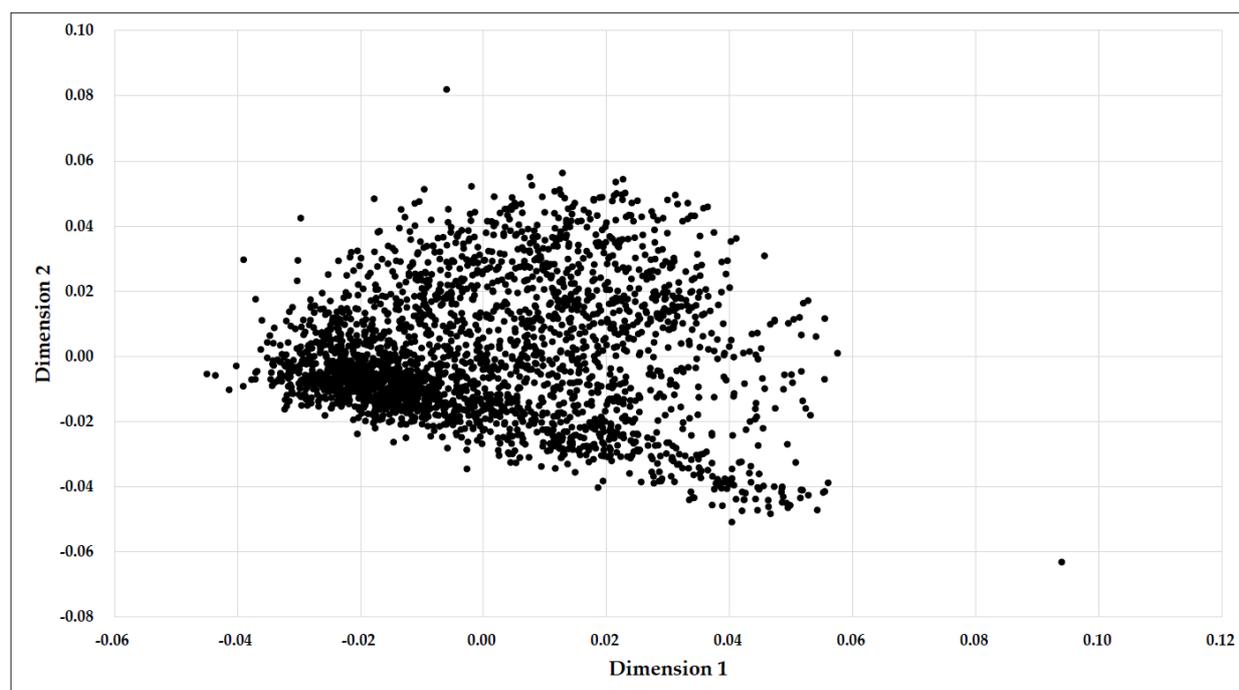


# Genome-Wide Identification of Candidate Genes for Milk Production Traits in Korean Holstein Cattle

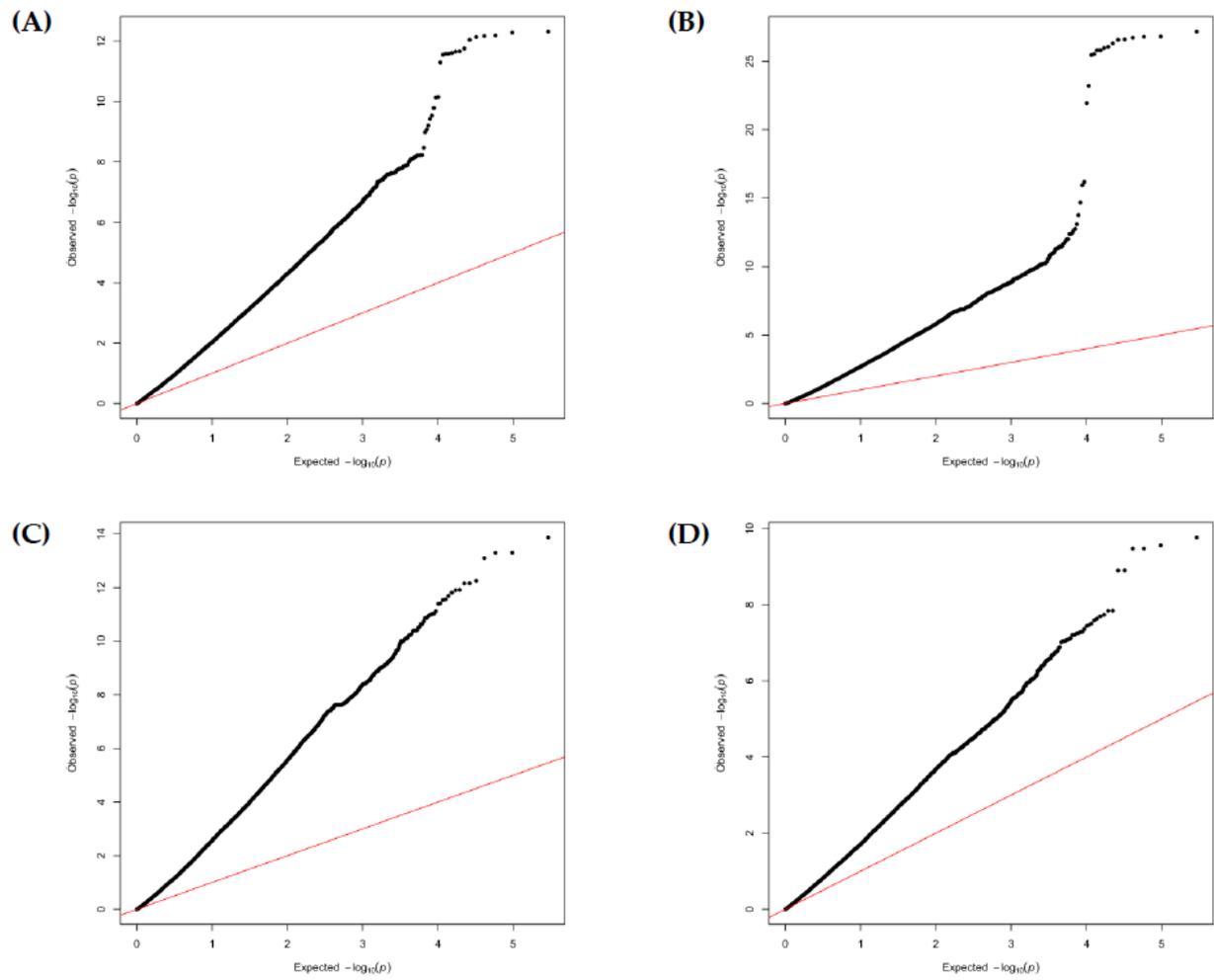
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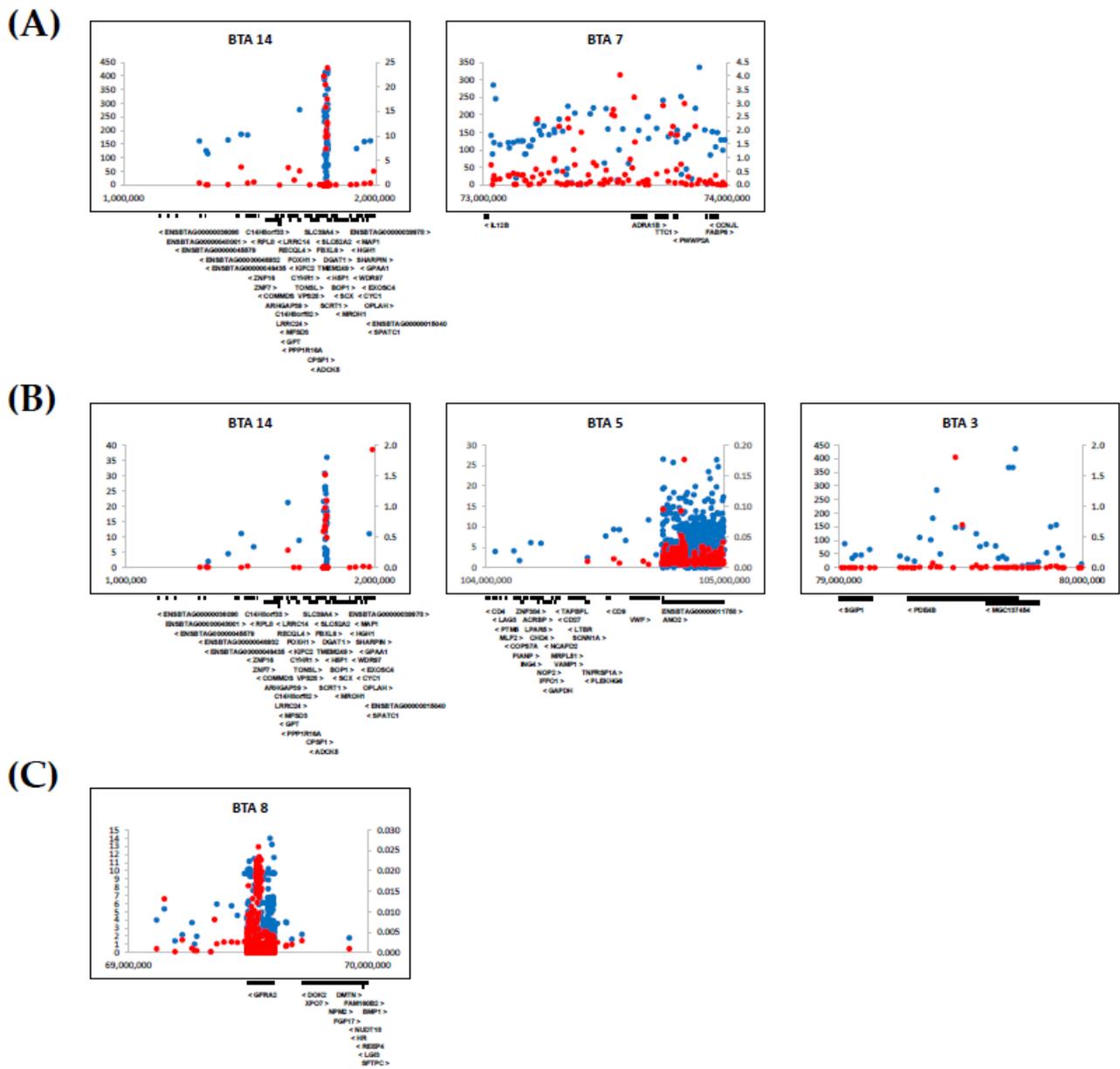
**Figure S1.** The distribution for reliabilities of EBVs in each phenotype: (A) MY, (B) FY, (C) PY, and (D) SCS.



**Figure S2.** Multidimensional scaling (MDS) plot based on SNPs for Korean Holstein population.



**Figure S3.** Quantile-Quantile (Q-Q) plots for 4 milk production phenotypes based on single marker regression (SMR). **(A)** Q-Q plot for MY. **(B)** Q-Q plot for FY. **(C)** Q-Q plot for PY. **(D)** Q-Q plot for SCS.



**Figure S4.** Visualization of the fine mapping in common significant regions by genome-wide association studies (GWAS) based on single marker regression (SMR) and Bayesian C (BayesC). **(A)** Common significant regions for MY. **(B)** Common significant regions for FY. **(C)** Common significant region for PY. Left Y- and Right Y-axis present effect ( $\beta$ , blue) in SMR and 1-Mb window genetic variance (red) in BayesC, respectively. Genes included in 1-Mb windows were annotated.