Supplemental Figure S1. Distribution of de-regressed EBV (DRP) of Danish Holstein (HOL), Nordic Red Dairy Cattle (RDC) and Danish Jersey (JER).
Supplemental Figure S2. Imputation accuracy for whole-genome sequence variants in Danish Holstein, Nordic Red Dairy Cattle, and Danish Jersey populations plotted against minor allele frequency.
Supplemental Figure S3. Manhattan plot for association of SNP with feet and legs disorders index for Danish Holstein, obtained by efficient mixed-model association. Red line indicates genome-wide significance level ($-\log_{10}(P) = 8.48$).
Supplemental Figure S4. Q-Q plot for association of SNP with feet and legs disorders index for Danish Holstein, obtained by efficient mixed-model association.
Supplemental Figure S5. Manhattan plot for association of SNP with feet and legs disorders index for Nordic Red Dairy Cattle, obtained by efficient mixed-model association. Red line indicates genome-wide significance level (\(-\log_{10}(P) = 8.48\)).
Supplemental Figure S6. Q-Q plot for association of SNP with feet and legs disorders index for Nordic Red Dairy Cattle, obtained by efficient mixed-model association.
Supplemental Figure S7. Manhattan plot for association of SNP with feet and legs disorders index for Danish Jersey, obtained by efficient mixed-model association.
Supplemental Figure S8. Q-Q plot for association of SNP with feet and legs disorders index for Danish Jersey, obtained by efficient mixed-model association.
Supplemental Figure S9. Genome-wide plot for association of SNP with feet and legs disorders index for Danish Holstein, obtained by efficient mixed-model association (gray circles) and linear mixed model (blue triangles). Black dotted line indicates genome-wide significance level ($-\log_{10}(P) = 8.48$).
Supplemental Figure S10. Genome-wide plot for association of SNP with feet and legs disorders index for Nordic Red Dairy Cattle, obtained by efficient mixed-model association (gray circles) and linear mixed model (blue triangles). Black dotted line indicates genome-wide significance level (\(-\log_{10}(P) = 8.48\)).
Supplemental Figure S11. Genome-wide plot for association SNP with feet and legs disorders index for Danish Holstein. Gray circles were generated by efficient mixed-model association. Blue circles were generated by fixing the top SNP in the linear mixed model and including other SNP effects in a simple linear regression model. Black dotted line indicates genome-wide significance level ($-\log_{10}(P) = 8.48$). Top SNP are located on BTA2 at 64,523,865 bp, BTA5 at 105,810,028 bp, BTA10 at 49,409,318 bp, BTA11 at 78,232,488 bp, and BTA22 at 50,314,934 bp.
Supplemental Figure S12. Genome-wide plot for association SNP with feet and legs disorders index for Nordic Red Dairy Cattle. Gray circles were generated by efficient mixed-model association. Blue circles were generated by fixing the top SNP in the linear mixed model and including other SNP effects in a simple linear regression model. Black dotted line indicates genome-wide significance level (-log_{10} (P) = 8.48). Top SNP are located on BTA6 at 38,677,301 bp, BTA14 at 25,006,125 bp, and BTA22 at 31,772,891 bp.
Supplemental Figure S13. Manhattan plot for association of SNP with feet and legs disorders index for 3 breeds, Danish Holstein, Nordic Red Dairy Cattle, and Danish Jersey, obtained by meta-analysis. Red line indicates genome-wide significance level (\(-\log_{10}(P) = 8.48\)).
**Supplemental Figure S14.** Q-Q plot for association of SNP with feet and legs disorders index for 3 breeds, Danish Holstein, Nordic Red Dairy Cattle, and Danish Jersey, obtained by meta-analysis.