

Additional file 1

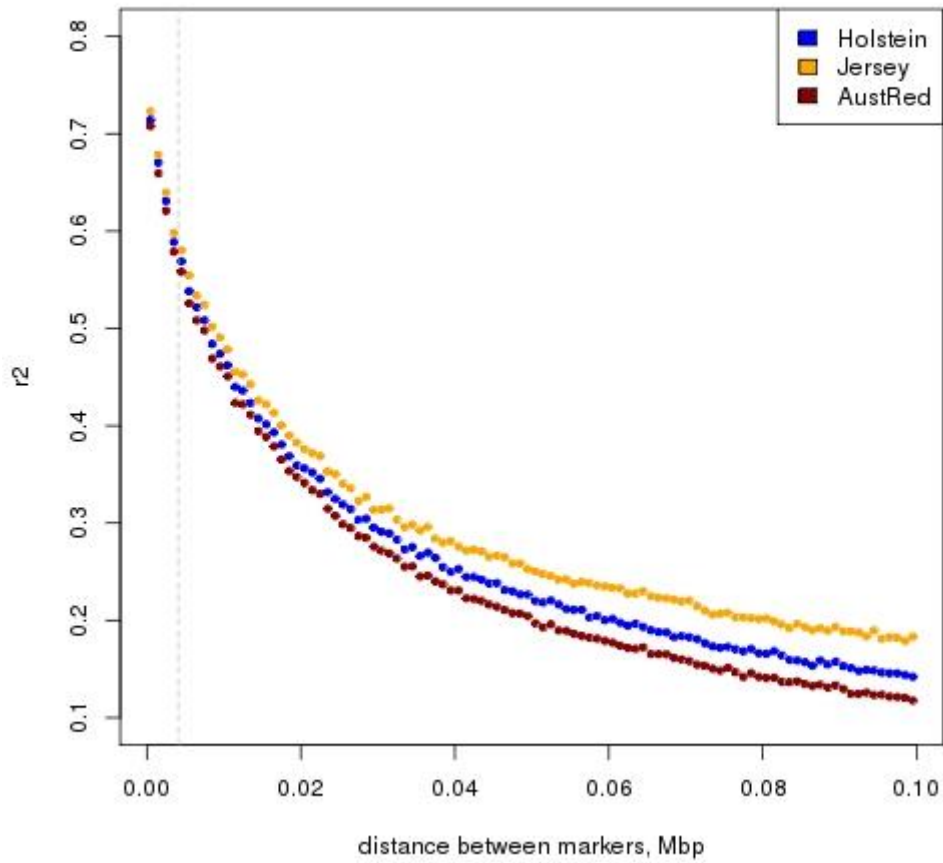


Figure S1 Linkage disequilibrium in Holstein, Jersey and Australian Red dairy cattle

Shown is the average r^2 (correlation) between SNP pairs and the average distance between adjacent SNP (vertical grey line) on BTA1.

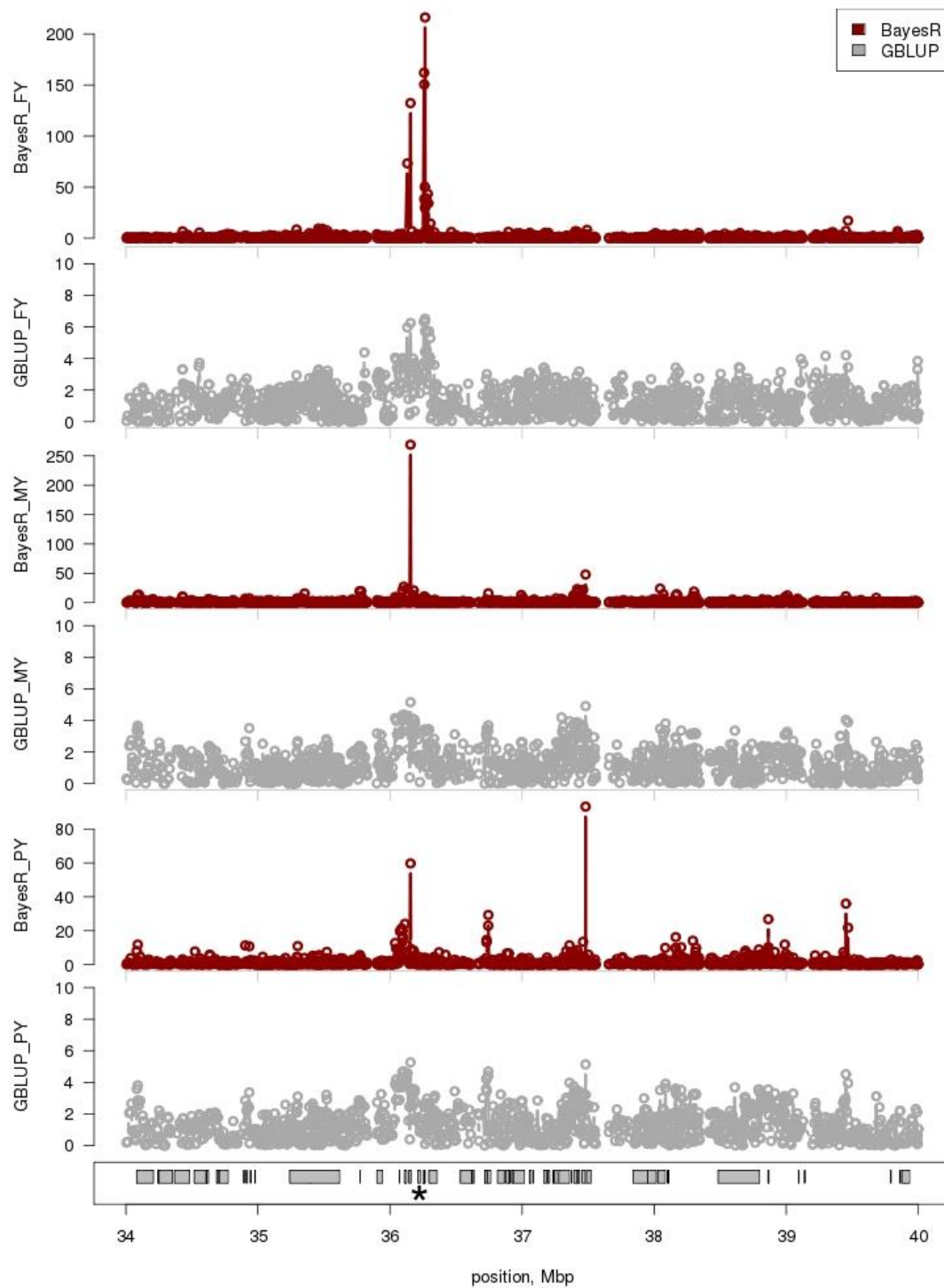


Figure S2 SNP effects estimated by BayesR and GBLUP for FY, MY and PY near AGPAT6

Shown is the (mean corrected) absolute SNP effect for Holstein and Jersey animals from the bull and cow, multi-breed reference population. Traits are FY = fat yield, MY = milk yield and PY = protein yield. The position of AGPAT6 on BTA27 is marked (*). Note the changed y-axis scale for each graph.

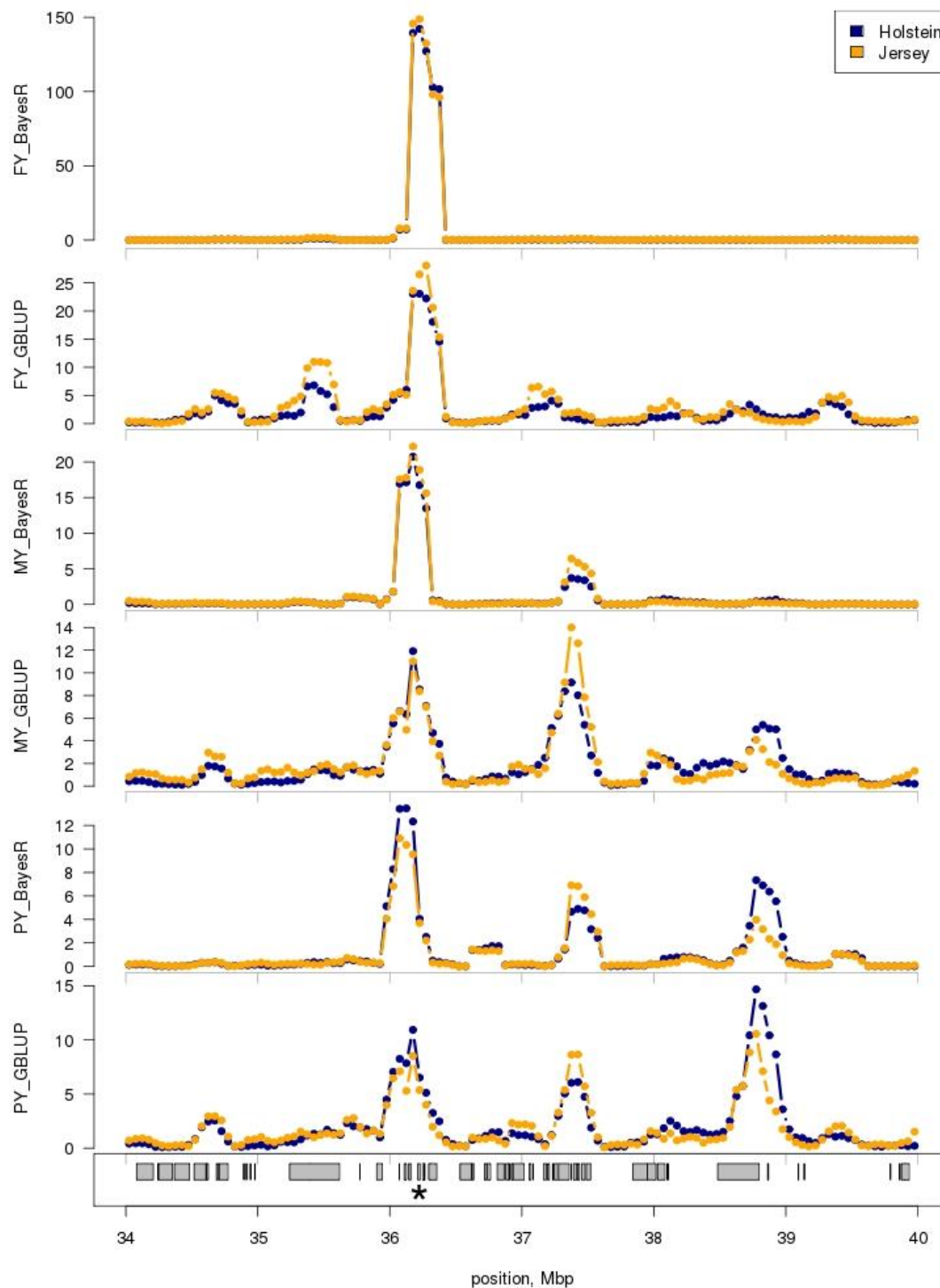


Figure S3 Local GEBV variance near AGPAT6 for FY, MY and PY using BayesR and GBLUP

Shown is the (mean corrected) GEBV variance in 250kb windows for Holstein and Jersey animals from the bull and cow, multi-breed reference population. Traits are FY = fat yield, MY = milk yield and PY = protein yield. The position of AGPAT6 on BTA27 is marked (*). Note the changed y-axis scale for each graph

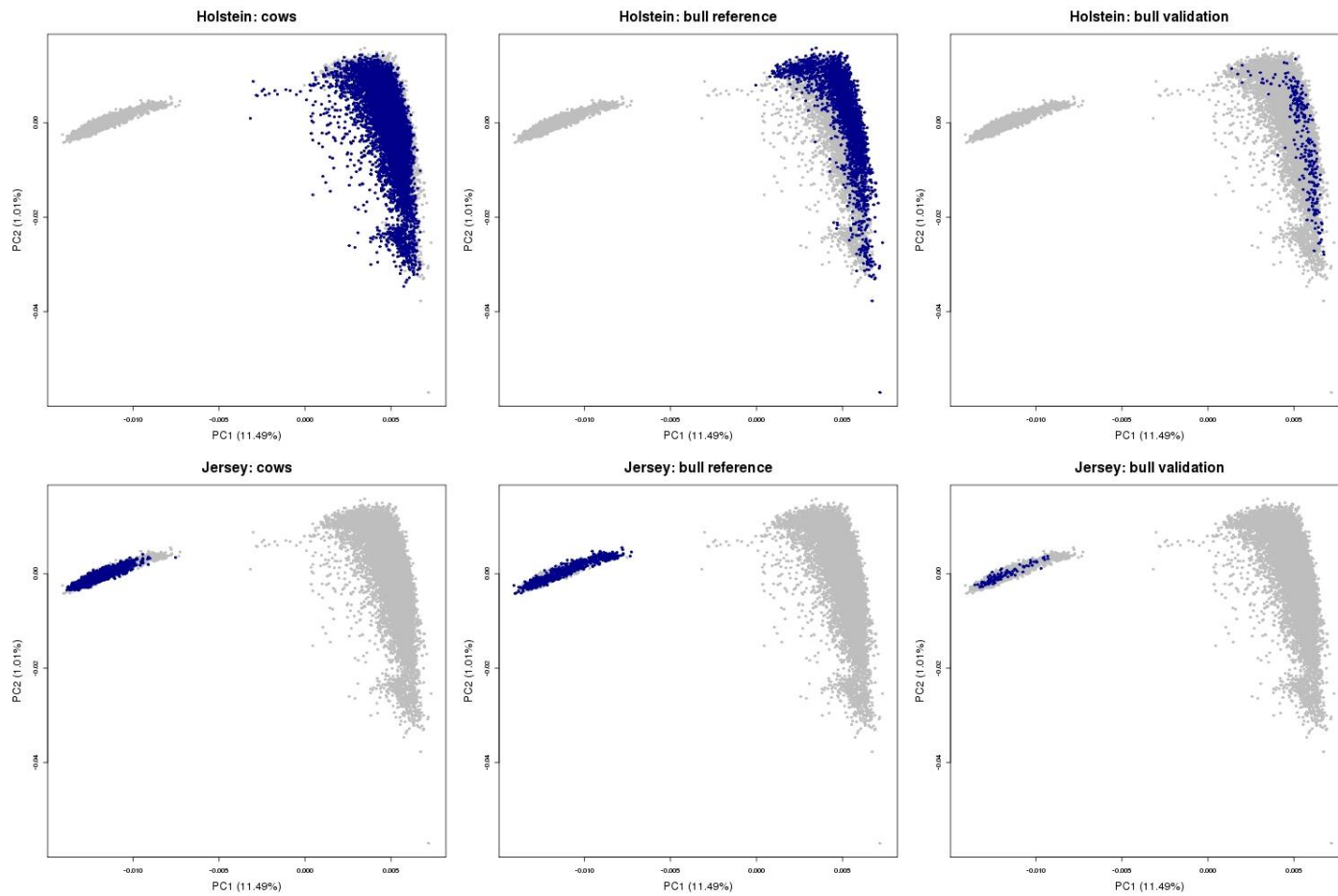


Figure S4 Relationship between Holstein and Jersey cows and bulls in the reference and validation datasets

Principle components from the G matrix using the `eigen()` function in R [51]. The named subset (i.e. Holstein cows, top left) is highlighted in blue for each panel.