

## Legends for supplementary material

- Table S1 (file S1\_SNP\_markers.csv): matrix of genotypes, one row per sample, one column per SNP marker. Column names indicate the position on the genome. The first column indicates the sample. Values in 0/1/2.
- Table S2 (file S2\_phenotypes.csv): matrix of phenotypes. One row per sample, one column per measured trait, either in BLUE or BLUP form. The first column indicates the sample. One extra column reports the cross to which the sample belongs.
- Table S3 (file S3\_kinship.csv): square matrix of kinships computed using Astle & Balding method. One row/column per sample.
- Table S4 (file S4\_DPCA.csv): the first seven components resulting from DPCA after clustering with K=17