



Supplemental Figure S14. Genomic prediction incorporating clustered tissue-specific genes. **A** Clustering of 91 tissues and cell types into 20 categories based on t -statistics of gene expression. We determine category-specific genes as the uniquely combination of specific genes for each tissue in the corresponding category. **B** Three Barplots for prediction accuracy of the 20 two-component models with corresponding category-specific genes and the remaining genome across fat yield (left), milk yield (middle) and protein yield (right), respectively. The black dashed line is the prediction accuracy for the null model with two genetic components: one is for all 24,616 genes and the other for the remaining genome.