



Supplemental Figure S1. Schematic of our current study. We analyzed all 723 RNA-seq data uniformly. For each gene in a tissue/cell type, we computed a t -statistic to measure its expression specificity in this particular tissue/cell type using a previously published method (Finucane et al. 2018). We determined tissue-specific highly expressed genes by ranking t -statistics, then taking the top 3, 5, and 10% of genes, respectively. We performed bioinformatics analyses with other data sources to provide novel biological insights into the tissue-specific genes, such as, biological functions, promoter DNA methylation and evolution features. We integrated tissue-specific genes (after adding 10, 20 and 50kb upstream and downstream sequences to include the *cis*-regulatory regions) with the largest-scale GWAS in cattle to date to detect the trait-relevant tissues/cell types. We also incorporated tissue-specific genes into genomic prediction models to improve prediction accuracy compared to the null model based on all genes.