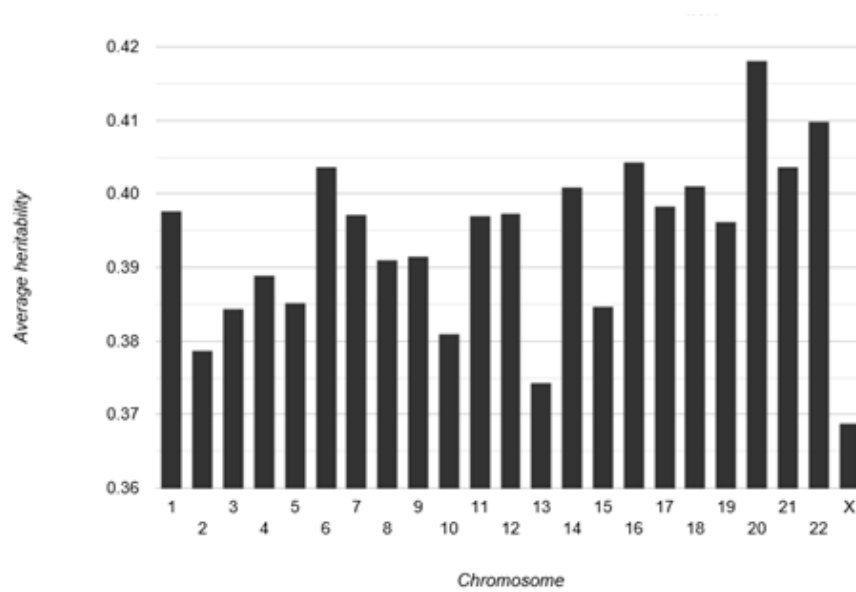
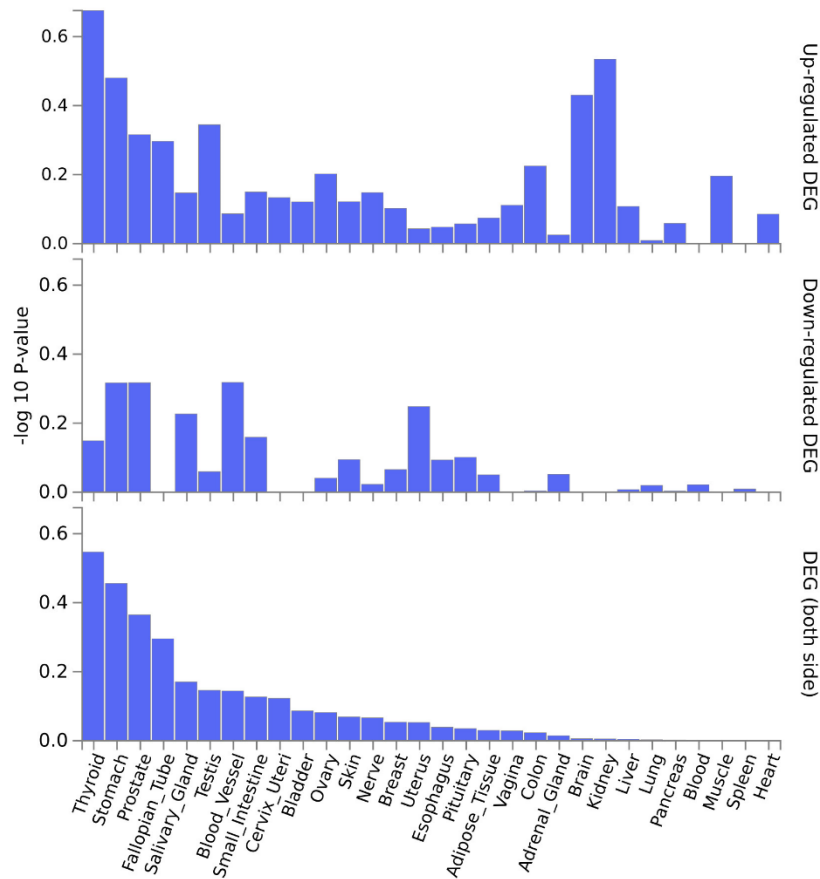


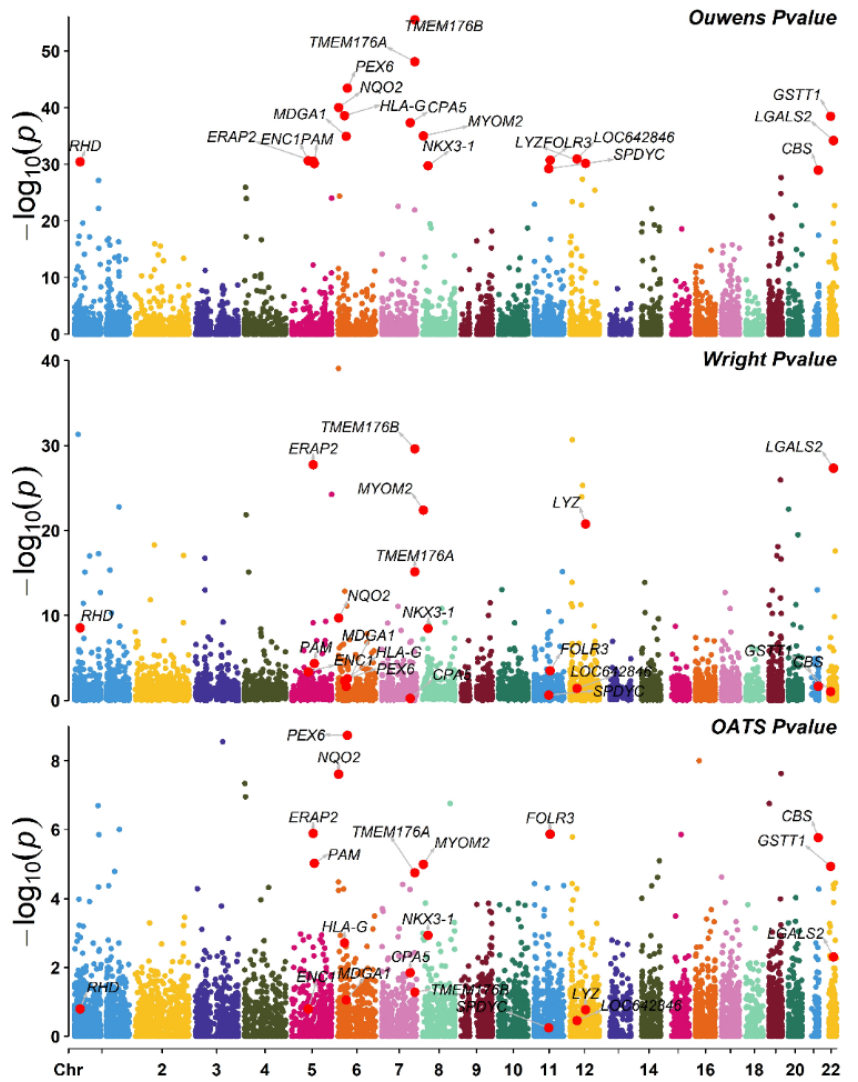
Supplementary Figures:



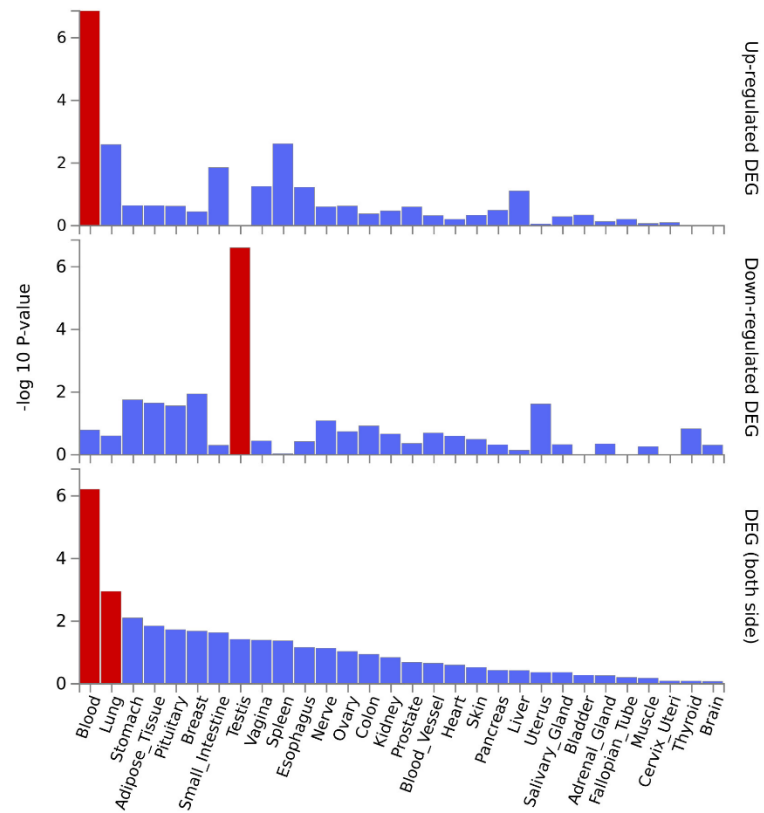
Supplementary Figure 1: Average Heritability of Gene Expression across Chromosomes for the OATS cohort.



Supplementary Figure 2: Upregulation and downregulation of the non-heritable gene set (n=100) for OATS across 30 different tissues using data from FUMA, showing that these genes are not significantly up or down regulated in any of the regions studied. Blue indicates the changes in gene expression are non-significant.



Supplementary Figure 3: Manhattan plots for gene expression heritability for each of the three studies (OATS, Ouwens et al., 2020; Wright et al., 2014) using only the genes common to all cohorts (N= 9479). The y axis shows $-\log_{10}(q\text{-value})$. Gene names for Top 20 FDR significant genes displayed.



Supplementary Figure 4: Tissue- specific gene expression levels of the FDR significant overlapping genes across the three studies (n=38) across 30 different tissues using FUMA (GTEx). Red indicates significant in gene expression, blue is not significant.