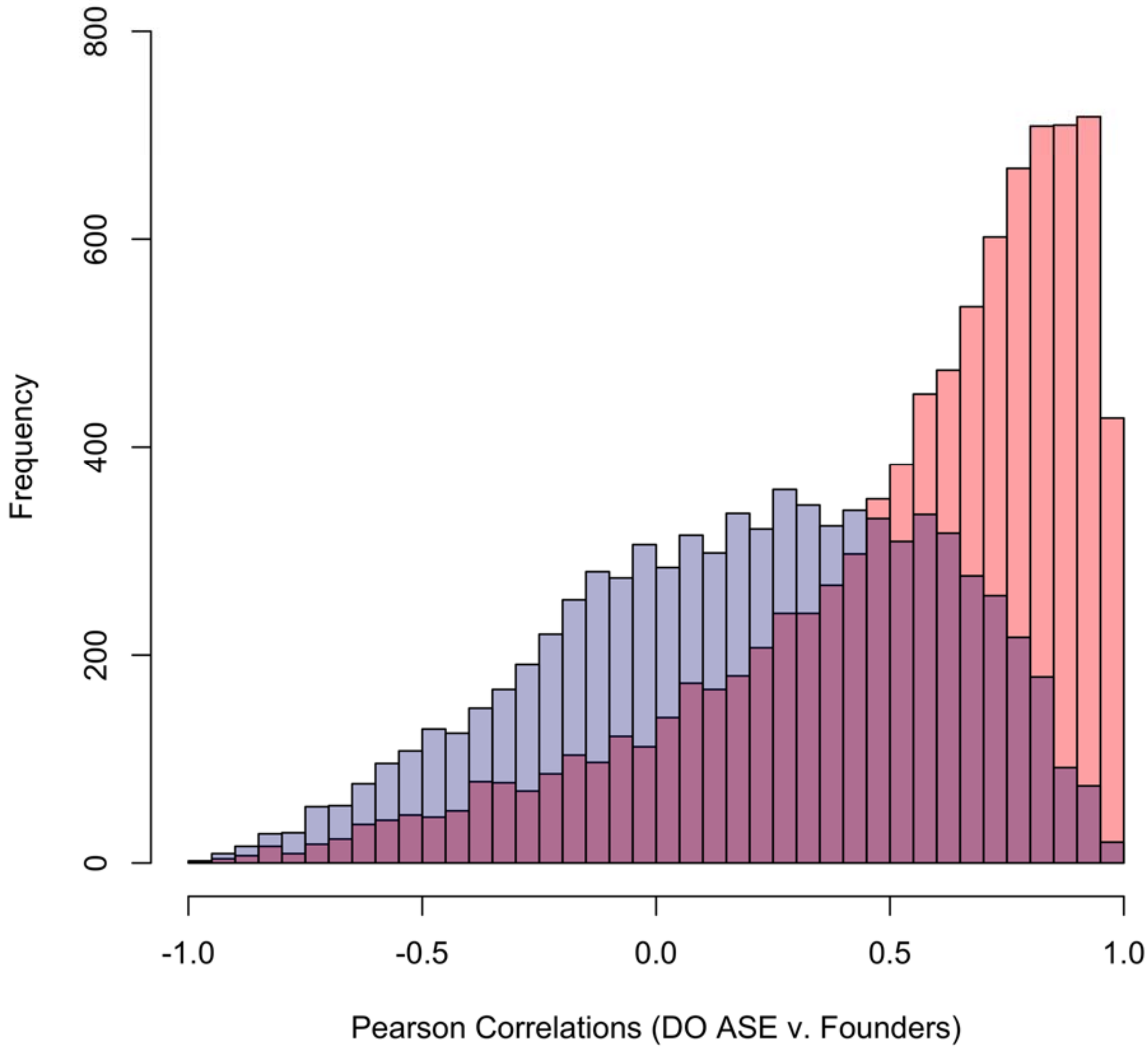

Figure S3 Comparison of gene-level expression in Founder strain samples and founder allele-level estimates in the DO samples for genes with and without significant local eQTL after alignment to individualized genomes. Pearson correlations between founder strain expression and founder allele estimates in the DO population are plotted as a histogram above. Founder allele estimates for genes with significant local eQTL (n=8,981 genes, shown in pink) exhibit higher concordance to gene-level liver expression in Founder strain samples compared to genes that do not have significant local eQTL (n=7,893 genes, shown in blue).