

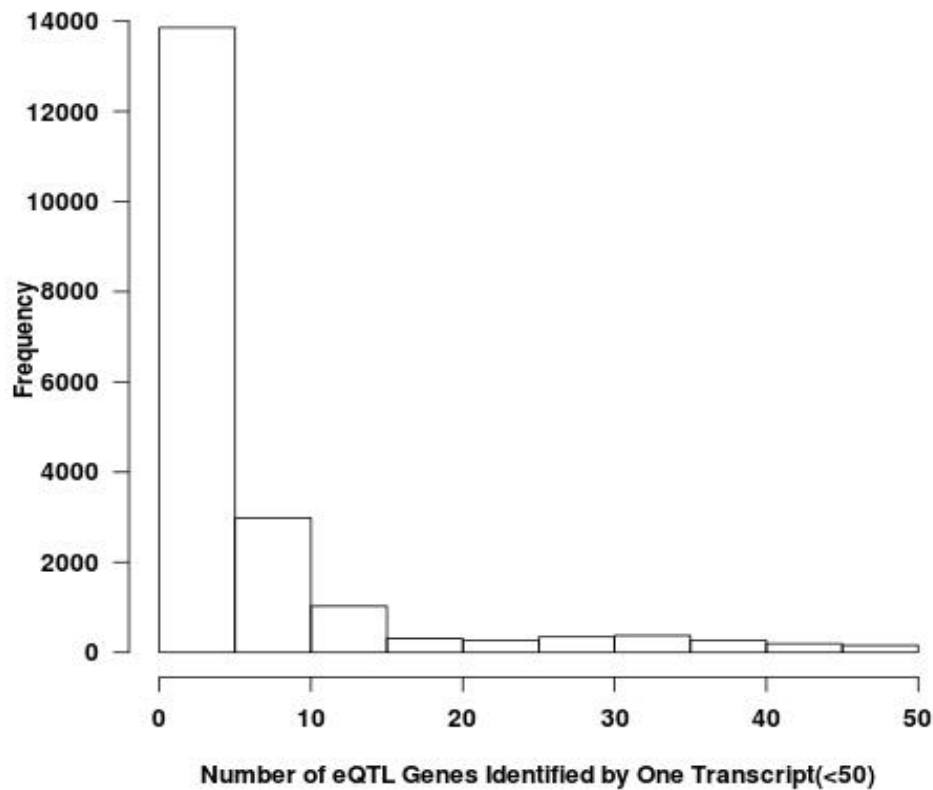


Figure S1. Distribution of number of eQTL identified for each transcript (<50)
Histogram showing the distribution of the numbers of eQTL associated with each phenotypic transcript in LIMIX results. The X-axis shows the number of eQTL genes identified for one transcript. The Y-axis shows the number of transcripts. For each transcript, significant eQTL that are located within 20kb of each other are counted once. This plot only shows transcripts with less than 50 eQTL genes.

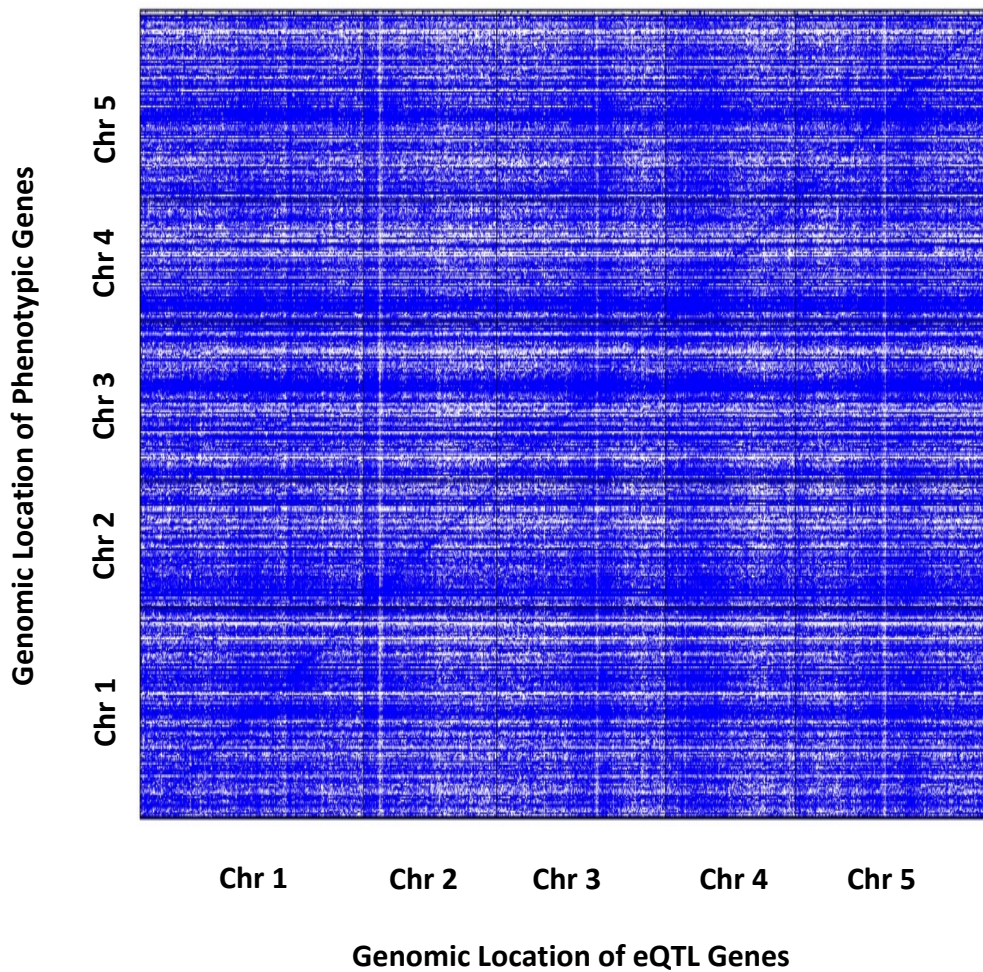


Figure S2. Genomic distribution of eQTL-LIMIX

Dot plot showing the genome-wide distribution of the identified eQTL using LIMIX. The X-axis represents the genomic location of eQTL genes. The Y-axis represents the genomic location of phenotypic genes. Each dot in the plot represents a significant association between a transcript (Y-axis) and a gene unit (X-axis). The plot features a diagonal line across all transcripts and all chromosome regions. The diagonal line represents the overall enrichment of local eQTL identified throughout the genome.

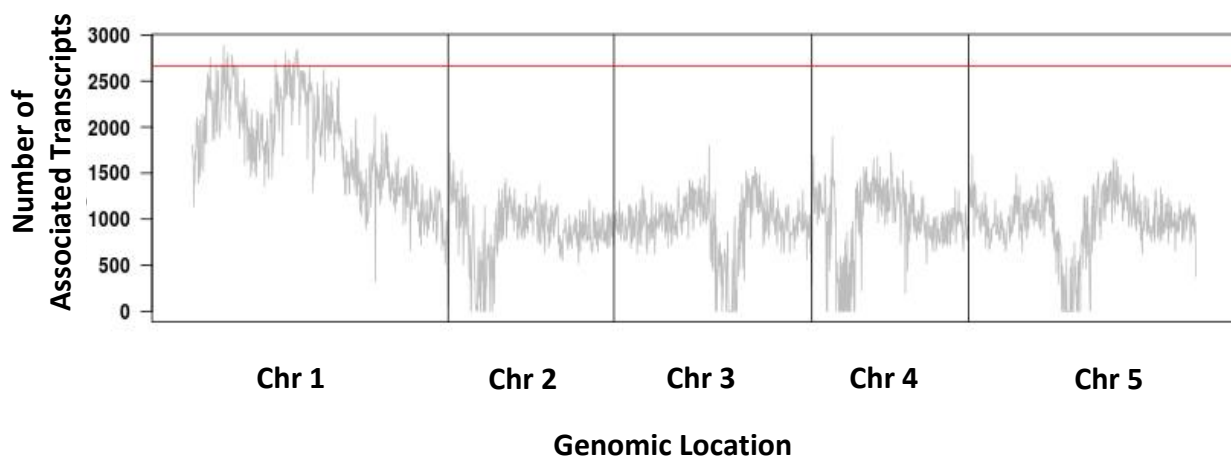


Figure S3. Quantitative distribution of significant associations- LIMIX

The Arabidopsis genome is divided into 50kb windows. The X-axis represent the genomic location of each genomic window. The Y-axis represents the number of associated transcripts with eQTL in each genomic window. The red line indicates the 99% percentile of the number of transcripts associated with eQTL genes in all the 50 kb genomic windows.

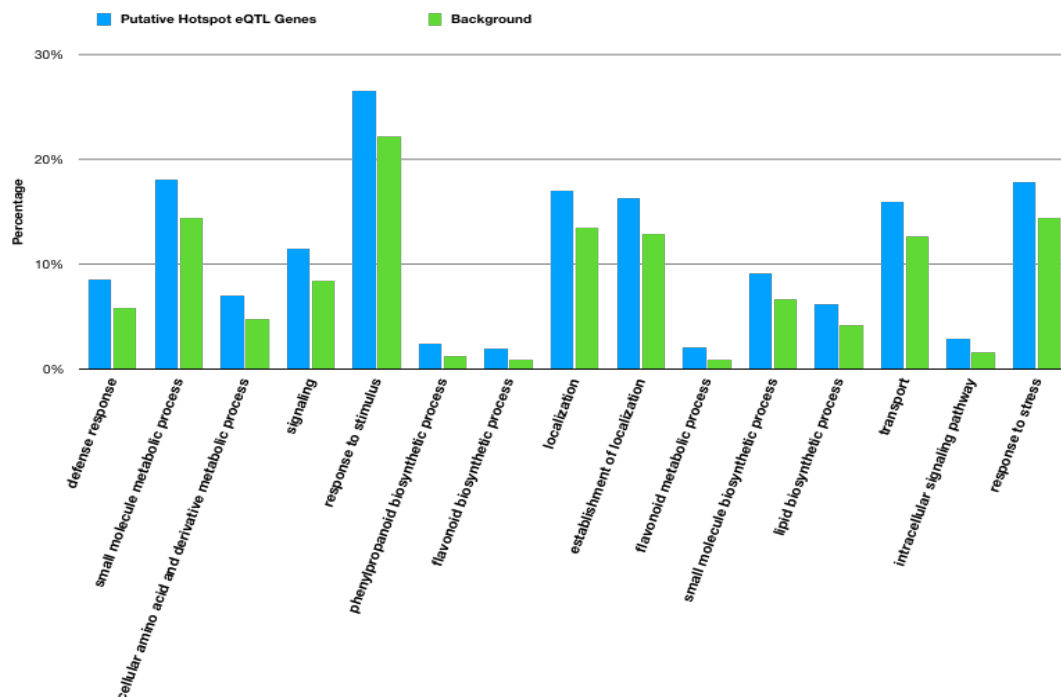


Figure S4. Gene ontology enrichment of putative hotspot eQTL genes- LIMIX.

Bar-chart showing the enriched gene ontology of the top 1000 eQTL genes with the largest number of associated transcripts. The X-axis shows the enriched GO terms. The Y-axis shows the percentage of genes with each GO term. Enriched GO with $FDR < 0.15$ were shown. (There is no significant GO in biological process with $FDR < 0.1$.)