Supplemental Data

A Multi-tissue Transcriptome Analysis of Human

Metabolites Guides Interpretability of Associations

Based on Multi-SNP Models for Gene Expression

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SUPPLEMENTAL FIGURES
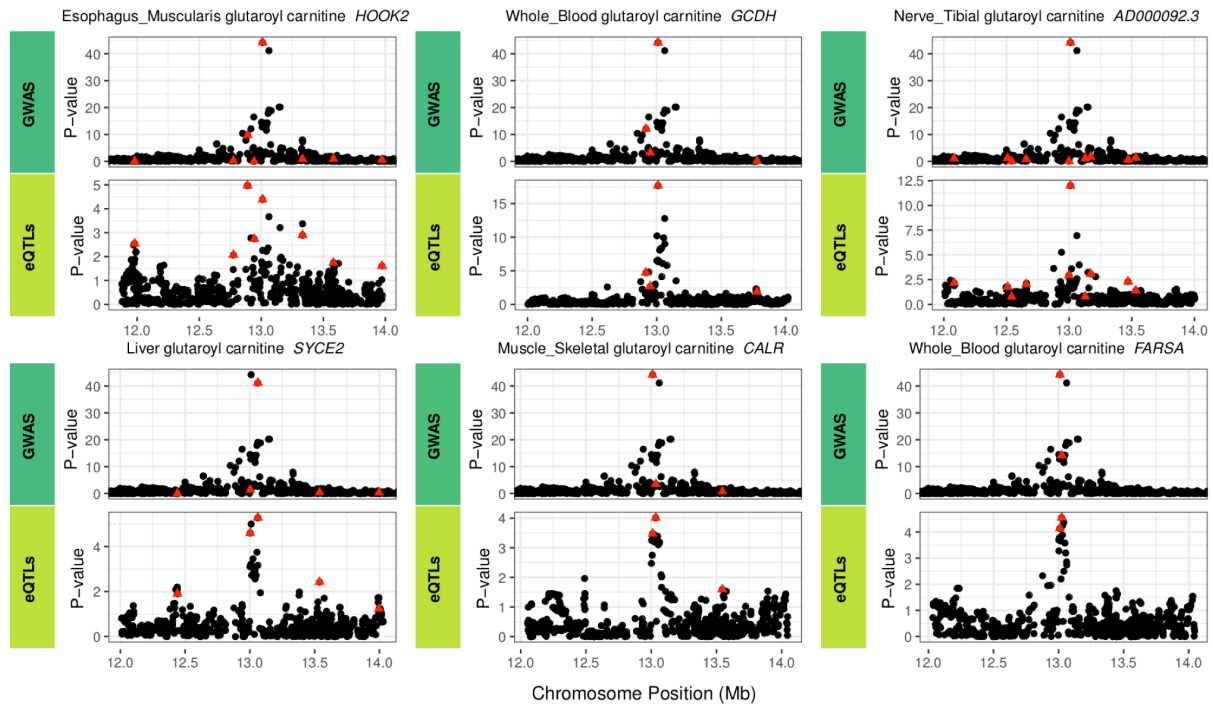
Figure S1. Gene expression co-regulation at the *GCDH* locus. Six genes at the *GCDH* locus whose predicted expression significantly mediated glutarylcarnitine levels. The multi-SNP models for all six genes included the *cis*-eQTL rs8012 that regulates the expression for all the genes. *GCDH* is the true causal gene influencing metabolite levels at this locus.
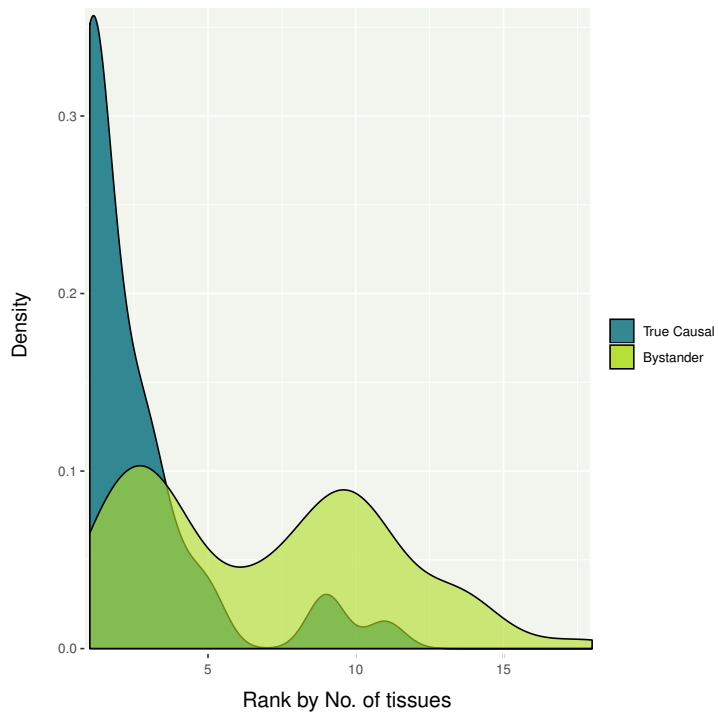
Figure S2. Causal and bystander gene ranks by number of tissues. Comparison of ranks by tissue counts for true causal genes and bystander genes at each locus. True causal genes ranked higher (significant in a more tissues) than bystander genes at the same locus.