Table S9 KEGG pathways with enrichment of genes showing differential expression between genotype groups in the eQTL analysis of *cis*-mQTL-SNPs

Pathway (total number of genes in pathway)	Observed number of genes	Expected number of genes	Ratio of enrichment	Raw *P*-value	Adjusted *P*-value	Observed genes
Glutathione metabolism (45)	3	0.08	35.56	8.09×10^{-5}	0.0003	*GSTT1, GSTM3, GPX7*
Drug metabolism - cytochrome P450 (53)	2	0.10	20.13	0.0044	0.0059	*GSTT1, GSTM3*
Metabolism of xenobiotics by cytochrome P450 (53)	2	0.10	20.13	0.0044	0.0059	*GSTT1, GSTM3*

P-values have been adjusted for multiple testing using Benjamini-Hochberg