

Gene name	Gene ID	Most likely model	Posterior probability of eQTL following most likely model	Most associated SNP	Minor allele frequency of most associated SNP	Marginal evidence of association ( $\log_{10}$ Bayes factor)	Genotypic effect on log fold change <sup>†</sup>	P-value from mapping log fold change
<i>C9orf5</i>	23731	GC-only	1.00	rs10816772	0.31	9.79	0.79	1.23x10 <sup>-9</sup>
<i>MFGE8</i>	4240	GC-only	1.00	rs3784752	0.15	6.18	0.90	2.16x10 <sup>-7</sup>
<i>LSG1</i>	55341	GC-only	1.00	rs898820	0.43	10.02	0.61	5.92x10 <sup>-7</sup>
<i>C1orf106</i>	55765	GC-only	1.00	rs4915463	0.51	9.21	0.63	9.86x10 <sup>-9</sup>
<i>AIRE</i>	326	GC-only	0.99	rs743479	0.19	4.17	-0.44	2.33x10 <sup>-3</sup>
<i>MS4A7</i>	58475	GC-only	0.99	rs2233252	0.40	4.59	0.66	2.44x10 <sup>-7</sup>
<i>BIRC3</i>	330	GC-only	0.98	rs11602147	0.39	4.23	0.70	2.82x10 <sup>-7</sup>
<i>TNIP1</i>	10318	GC-only	0.97	rs6870205	0.12	3.70	0.88	3.08x10 <sup>-6</sup>
<i>NQO1</i>	1728	GC-only	0.92	rs689459	0.10	12.27	1.15	1.34x10 <sup>-8</sup>
<i>LONP1</i>	9361	GC-only	0.92	rs8104044	0.24	3.34	-0.51	4.22x10 <sup>-4</sup>
<i>NLRP2</i>	55655	GC-only	0.90	rs12104320	0.03	3.82	-1.03	2.02x10 <sup>-3</sup>
<i>GSTM3</i>	2947	GC-only	0.87	rs6537874	0.10	4.23	0.75	2.18x10 <sup>-4</sup>
<i>CST7</i>	8530	GC-only	0.85	rs4610125	0.12	3.70	-1.10	3.19x10 <sup>-5</sup>
<i>HSD11B1L*</i>	374875	GC-only	0.83	rs3745640	0.25	2.88	-0.40	4.95x10 <sup>-3</sup>
<i>FAM134B</i>	54463	GC-only	0.83	rs31287	0.32	5.08	0.52	2.11x10 <sup>-5</sup>
<i>SGK1</i>	6446	GC-only	0.78	rs4429966	0.15	2.52	-0.50	0.012
<i>PDGFRL</i>	5157	GC-only	0.77	rs2517202	0.16	3.42	0.50	1.21x10 <sup>-3</sup>
<i>PANK3</i>	79646	GC-only	0.71	rs7734906	0.08	2.89	-0.73	1.44x10 <sup>-3</sup>
<i>MTIX</i>	4501	control-only	1.00	rs7195394	0.42	6.10	0.71	6.11x10 <sup>-8</sup>
<i>EDF1*</i>	8721	control-only	0.99	rs4880172	0.29	4.05	0.04	0.77
<i>FBXL6</i>	26233	control-only	0.95	rs10448143	0.14	3.48	0.63	1.26x10 <sup>-4</sup>
<i>SRD5A2</i>	6716	control-only	0.94	rs11690596	0.30	3.40	0.48	4.23x10 <sup>-4</sup>
<i>CSNK1E*</i>	1454	control-only	0.88	rs5750597	0.31	3.10	0.23	0.093
<i>SYT17</i>	51760	control-only	0.80	rs229020	0.35	3.62	-0.48	8.87x10 <sup>-4</sup>
<i>MCFD2</i>	90411	control-only	0.77	rs4953439	0.13	2.43	0.79	5.21x10 <sup>-5</sup>
<i>C12orf45</i>	121053	control-only	0.72	rs10861313	0.36	5.13	0.39	1.03x10 <sup>-3</sup>

\* eQTLs with genotypic effects in opposite directions in the YRI and TSI populations.

† Expressed in standard deviations.