

Supplementary Table 1. Single variant association with eQTL analysis in GTEx

Trait	SNP ID (KoGES)	Proxy	Chr:Pos	Variant ID	GeneCode ID	Gene symbol	p value	NES (effect size)	Tissue
FEV <sub>1</sub>	rs7742369	rs7742369	6:34,165,721	6_34165721_A_G_b37	ENSG00000186577.7	SMIM29 (C6orf1)	0.000032	0.13	Skin
	rs7742369	rs7742369	6:34,165,721	6_34165721_A_C_b37	ENSG00000186577.7	SMIM29 (C6orf1)	0.000073	0.14	Thyroid
	rs2780226	rs2780226	6:34,199,092	6_34199092_C_T_b37	ENSG00000186577.7	SMIM29 (C6orf1)	0.000024	-0.17	Skin
	rs2780226	rs2780226	6:34,199,092	6_34199092_C_T_b37	ENSG00000186577.7	SMIM29 (C6orf1)	0.000042	-0.21	Esophagus-mucosa
	rs1150781	rs1150781	6:34,214,322	6_34214322_C_G_b37	ENSG00000186577.7	SMIM29 (C6orf1)	0.000012	-0.18	Skin
	rs1130,247,700	none	11:130,247,700	-	-	-	-	-	-
	rs1130,247,700	rs4937505	11:130,247,781	11_130247781_T_A_b37	-	-	-	-	-
	rs12110,390,979	None	12:110,390,979	-	-	-	-	-	-
	rs12110,390,979	rs11069018	12:110386611	12_110386611_G_A_b37	ENSG00000139437.16	GIT2	4.60E-07	-0.28	Artery - tibial
	rs12110,390,979	rs11069018	12:110389404	12_110389404_T_C_b37	ENSG00000139437.16	GIT2	0.000034	-0.32	Testis
rs12110,390,979	rs2292354	12:110368201	12_110368201_G_A_b37	ENSG00000139437.13	TCHP	0.000022	-0.31	Colon - sigmoid	
rs12110,390,979	rs1106939	12:110413252	12_110413252_G_C_b37	ENSG00000139437.13	TCHP	0.000055	-0.33	Colon - sigmoid	
rs114591848	rs114591848	14:21550,212	-	-	-	-	-	-	
rs114591848	rs398117960	14:21545490	14_21545490_C_CT_b37	ENSG00000165801.5	ARHGEF40	7.40E-09	-0.20	Lung	
rs114591848	rs3827911	14:21548159	14_21548159_G_A_b37	ENSG00000165801.5	ARHGEF40	1.10E-07	-0.18	Lung	
rs114591848	rs3827913	14:21548448	14_21548448_G_A_b37	ENSG00000165801.5	ARHGEF40	3.20E-08	-0.19	Lung	
rs114591848	rs1958395	14:21551058	14_21551058_G_A_b37	ENSG00000165801.5	ARHGEF40	4.30E-08	-0.19	Lung	
FEV <sub>1</sub> /FVC	rs7671167	rs7671167	4:89,883,979	4_89883979_C_T_b37	ENSG00000138640.10	FAM13A	0.000012	0.16	Lung
rs2239688	rs2239688	6:32,054,212	6_32054212_C_G_b37	-	-	-	-	-	
rs2239688	rs79770049	6:31,997,493	6_31977493_C_T_b37	ENSG00000168477.13	TNXB	3.50E-13	0.63	Adrenal gland	
rs2239688	rs2746414	6:31,996,966	6_31996966_G_A_b37	ENSG00000168477.13	TNXB	2.70E-07	0.62	Adrenal gland	
rs2239688	rs2852706	6:31,972,370	6_31972370_G_C_b37	ENSG00000168477.13	TNXB	0.000014	0.50	Adrenal gland	
rs2239688	rs76096058	6:31,997,549	6_31977548_G_A_b37	ENSG00000168477.13	TNXB	0.000027	0.54	Adrenal gland	
rs2070600	rs2070600	6:32,151,443	6_32151443_C_T_b37	ENSG00000204305.9	AGER	0.000061	-0.28	Lung	

Means that no significant eQTL were found for SNP in eQTL tissues.

eQTL, expression quantitative trait loci; GTEx, genotype-tissue expression; SNP, single nucleotide polymorphism; KoGES, Korean Genome and Epidemiology Study; Chr, chromosome; Pos, position; NES, normalized effect size; SMIM29, small integral membrane protein 29; GIT2, G protein-coupled receptor kinase interacting, Arf-GAP 2; TCHP, trichoplein keratin filament binding protein; ARHGEF40, rho guanine nucleotide exchange factor 40; FAM13A, family with sequence similarity 13 member A; TNXB, tenascin XB; AGER, advanced glycosylation end-product specific receptor.