

Table SV. Heterogeneity test using the invariance weighted method.

Gene	Q	Q_df	Q_P-value
CACNA2D2	2.306334356	11	0.99709757
ADRB1	4.911347921	3	0.178404979
CALCRL	1.651071699	11	0.999394453
PAFAH1B3	1.257179677	5	0.93927556
SEMA6A	1.71651647	4	0.787715245
NDRG4	1.251691449	3	0.740635101
PRX	21.61367933	14	0.086908472
CNFN	0.345458324	3	0.951264036
RASIP1	4.269884736	2	0.118251405
CAV2	31.74308518	29	0.331262742
FOLR3	67.01659229	56	0.148778805
TNNC1	0.371810323	5	0.996070599
TEK	8.606662208	19	0.979457286
FOSB	3.660601709	4	0.453882085
LRRC32	2.842725069	2	0.241384897
ACVRL1	1.660643518	8	0.989708547
IGSF10	0.271365646	2	0.873119522
AGRP	0.576390081	12	0.999999378
LOXHD1	7.435045384	9	0.591921389
DPEP2	24.37296201	19	0.182232787
CA4	12.37517558	12	0.416038438
TMEM88	2.790916944	6	0.834594195
TNXB	5.082480647	6	0.533278782
FRMD3	17.89085401	22	0.712439614
PPP1R14B	0.261002715	2	0.877655302
THBD	26.10061695	23	0.296139269
ITLN1	7.734870732	14	0.902676194
KRT79	2.013440828	4	0.733286599
PLAC9	19.44044862	11	0.053631201

UPK3B	12.49417202	16	0.709319444
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df, degrees of freedom.

Table SVI. Level multivariate test.

Gene	Egger_intercept	SE	P-value
CACNA2D2	-0.003430314	0.026220891	0.898509188
ADRB1	-0.046545432	0.045382961	0.412916165
CALCRL	0.007430228	0.01611443	0.654598562
PAFAH1B3	-0.0256069	0.046950845	0.614467209
SEMA6A	0.137725254	0.145357506	0.413288369
NDRG4	0.04986073	0.057129208	0.474817978
PRX	-0.008876909	0.047704002	0.85525185
CNFN	-0.011018094	0.051501987	0.850426634
RASIP1	-0.037487269	0.073551733	0.699925865
CAV2	-0.012843413	0.007986318	0.119015618
FOLR3	-0.009574396	0.013229844	0.472318823
TNNC1	0.017226882	0.042135606	0.703596742
TEK	-0.008094403	0.013056024	0.543044141
FOSB	0.147481196	0.110269324	0.273430718
LRRC32	-0.050577158	0.030871324	0.348878754
ACVRL1	-0.005894877	0.016788016	0.735817254
IGSF10	-0.000518804	0.023106198	0.985708367
AGRP	0.006319676	0.077790051	0.936710288
LOXHD1	0.017627814	0.013790056	0.236981783
DPEP2	0.011083192	0.013245576	0.413706328
CA4	-0.017972896	0.010208107	0.106034927
TMEM88	0.006375943	0.053905767	0.910451097
TNXB	-0.005904022	0.026509432	0.832570211
FRMD3	-0.010223375	0.00712695	0.166164053
PPP1R14B	-0.033013041	0.064678808	0.699550517
THBD	-0.008926826	0.014176998	0.535395963
ITLN1	0.013193141	0.010753204	0.241615718
KRT79	-0.003114749	0.020320358	0.887905678
PLAC9	0.005564567	0.024712114	0.826377496
UPK3B	-0.010334232	0.010664024	0.347875206

SE, standard error.

Table SVII. Steiger directionality test.

Gene	ENSEMBL	SNP	Steiger directionality	Steiger_P-value
CACNA2D 2	eqtl-a- ENSG00000007402	rs13073141	TRUE	2.58×10^{-12}
ADRB1	eqtl-a- ENSG00000043591	rs540609	TRUE	2.33×10^{-27}
CALCRL	eqtl-a- ENSG00000064989	rs13430665	TRUE	2.86×10^{-70}
PAFAH1B 3	eqtl-a- ENSG00000079462	rs75439367	TRUE	4.74×10^{-16}
SEMA6A	eqtl-a- ENSG00000092421	rs154607	TRUE	2.73×10^{-13}
NDRG4	eqtl-a- ENSG00000103034	rs67742851	TRUE	2.48×10^{-30}
PRX	eqtl-a- ENSG00000105227	rs13344213	TRUE	1.69×10^{-07}
CNFN	eqtl-a- ENSG00000105427	rs75665308	TRUE	4.39×10^{-10}
RASIP1	eqtl-a- ENSG00000105538	rs4911259	TRUE	2.93×10^{-06}
CAV2	eqtl-a- ENSG00000105971	rs19327863 4	TRUE	7.40×10^{-10}
FOLR3	eqtl-a- ENSG00000110203	rs7121292	TRUE	4.97×10^{-23}
TNNC1	eqtl-a- ENSG00000114854	rs34131802	TRUE	5.21×10^{-09}
TEK	eqtl-a- ENSG00000120156	rs10812363	TRUE	3.86×10^{-07}
FOSB	eqtl-a- ENSG00000125740	rs17696736	TRUE	1.72×10^{-06}

LRRC32	eqtl-a- ENSG00000137507	rs7943302	TRUE	2.21×10^{-18}
ACVRL1	eqtl-a- ENSG00000139567	rs18337395 3	TRUE	3.65×10^{-07}
IGSF10	eqtl-a- ENSG00000152580	rs4076581	TRUE	6.76×10^{-07}
AGRP	eqtl-a- ENSG00000159723	rs11698814 8	TRUE	4.89×10^{-18}
LOXHD1	eqtl-a- ENSG00000167210	rs79906843	TRUE	5.62×10^{-06}
DPEP2	eqtl-a- ENSG00000167261	rs8056803	TRUE	3.22×10^{-16}
CA4	eqtl-a- ENSG00000167434	rs56388170	TRUE	1.46×10^{-17}
TMEM88	eqtl-a- ENSG00000167874	rs78180894	TRUE	6.66×10^{-07}
TNXB	eqtl-a- ENSG00000168477	rs2269426	TRUE	1.07×10^{-104}
FRMD3	eqtl-a- ENSG00000172159	rs329121	TRUE	7.83×10^{-06}
PPP1R14B	eqtl-a- ENSG00000173457	rs1058735	TRUE	1.13×10^{-15}
THBD	eqtl-a- ENSG00000178726	rs14399019 9	TRUE	5.84×10^{-28}
ITLN1	eqtl-a- ENSG00000179914	rs73660574	TRUE	4.88×10^{-17}
KRT79	eqtl-a- ENSG00000185640	rs902771	TRUE	1.45×10^{-38}
PLAC9	eqtl-a- ENSG00000189129	rs75714675	TRUE	2.04×10^{-06}
UPK3B	eqtl-a- ENSG00000243566	rs10156094	TRUE	2.24×10^{-161}

SNP, single nucleotide polymorphism.