

Supplementary Table 1 Alternate Allele Frequencies of the Most Significant Markers from a Series of Conditional GWAS in Sub-populations

Step	Marker	Gene	Ref allele	Alt allele	African (n=379)	Asian (n=2,017)	Caucasian (n=4,631)	Native American (n=189)	Caucasian and Native American (n=939)	Caucasian, African and Native American (n=2,282)	Total (n=10,542)
1	rs72728755	8q24	T	A	0.15	0.03	0.23	0.04	0.06	0.19	0.16
2	rs7552	FAM49A	A	G	0.68	0.74	0.34	0.73	0.63	0.52	0.50
3	rs2235370	TRAF3IP3	C	A	-	0.18	0.04	0.40	0.35	0.18	0.13
4	rs16957821	NTN1	C	G	0.41	0.18	0.19	0.35	0.37	0.30	0.24
5	rs12600562	LRRC37A2	G	T	0.48	0.38	0.59	0.46	0.52	0.55	0.53
6	rs12543318		C	A	0.68	0.44	0.62	0.49	0.48	0.49	0.55
7	rs3845903	LRIG1	C	T	0.80	0.94	-	0.99	0.98	0.97	0.97
8	rs10778143	CHPT1	A	C	0.63	0.59	0.25	0.20	0.21	0.25	0.33
9	rs6929507	GMDS	T	C	0.15	0.002	-	-	0.007	0.02	0.01
10	rs138322543	TRMO	CCACC A	C	0.77	0.91	0.66	0.66	0.67	0.72	0.73

Supplementary Table 2 Results with suggestive evidence of association from the gene-based association study

Gene	Ensembl Transcript ID	Chr; Pos	Beta (S.E.)	z	p-value
<i>Whole Blood</i>					
<i>IRGM</i>	ENSG00000237693.4	5; 150,846,523-150,900,736	-3.1560 (0.7636)	-4.1328	3.58E-05
<i>OSBPL11</i>	ENSG00000144909.7	3; 125,528,858-125,595,090	-2.0234 (0.4949)	-4.0887	4.34E-05
<i>SYCE3</i>	ENSG00000217442.3	22; 50,551,112-50,562,905	3.3258 (0.8238)	4.0371	5.41E-05
<i>ALDH5A1</i>	ENSG00000112294.8	6; 24,494,852-24,537,207	-1.8371 (0.4635)	-3.9633	7.39E-05
<i>PRSS45</i>	ENSG00000188086.8	3; 46,742,092-46,744,755	2.9393 (0.7508)	3.9150	9.04E-05
<i>Skeletal Muscle</i>					
<i>ATP6V1D</i>	ENSG00000100554.7	14; 67,294,371-67,360,265	2.4795 (0.5800)	4.2750	1.91E-05
<i>HSD17B12</i>	ENSG00000149084.7	11; 43,680,558-43,856,617	-0.4123 (0.0991)	-4.1609	3.17E-05
<i>MIF-AS1</i>	ENSG00000218537.1	22; 23,894,426-23,898,930	0.7923 (0.1948)	4.0666	4.77E-05
<i>CD151</i>	ENSG00000177697.13	11; 832,843-839,831	-0.718 (0.1769)	-4.0581	4.95E-05
<i>SQOR</i>	ENSG00000137767.9	15; 45,631,148-45,691,294	-2.9416 (0.7321)	-4.0179	5.87E-05
<i>LYSMD1</i>	ENSG00000163155.7	1; 151,159,748-151,165,948	1.7668 (0.4436)	3.9829	6.81E-05
<i>DHX30</i>	ENSG00000132153.10	3; 47,802,909-47,850,195	6.5430 (1.6673)	3.9242	8.70E-05
<i>Adipose (Subcutaneous)</i>					
<i>ALX4</i>	ENSG00000052850.5	11; 44,260,444-44,310,166	-0.9276 (0.2179)	-4.2564	2.08E-05
<i>KDM1B</i>	ENSG00000165097.9	6; 18,155,329-18,223,853	-1.4586 (0.3619)	-4.0300	5.58E-05
<i>SFSWAP</i>	ENSG00000061936.5	12; 131,711,081-131,799,737	-2.0699 (0.5166)	-4.0065	6.16E-05
<i>GSTT2B</i>	ENSG00000133433.6	22; 23,957,414-23,961,186	-1.0478 (0.2674)	-3.9185	8.91E-05
<i>Adipose (Visceral)</i>					
<i>MX2</i>	ENSG00000183486.8	21; 41,361,943-41,409,390	-2.0284 (0.4610)	-4.4001	1.08E-05
<i>GSTP1</i>	ENSG00000084207.11	11; 67,583,595-67,586,656	1.8047 (0.4145)	4.3535	1.34E-05
<i>ADAMTS13</i>	ENSG00000160323.14	9; 33,414,358-133,459,402	-1.2160 (0.3068)	-3.9634	7.39E-05
<i>HSD17B12</i>	ENSG00000149084.7	11; 43,680,558-43,856,617	-0.3960 (0.1005)	-3.9410	8.11E-05
<i>CNTNAP1</i>	ENSG00000108797.7	17; 42,682,613-42,699,814	-1.1957 (0.3065)	-3.9012	9.57E-05

Chr: Chromosome, Pos: Position (basepair; bp)

Supplementary Table 3 Candidate Genes in the GTEx database

Gene	Locus	Phenotype	Study Type	Reference
<i>ARHGAP29</i>	1p22.1	CL/P	GWAS	[15, 17, 19]
<i>GRHL3</i>	1p36.11	CP	GWAS, GWAS replication	[14, 18]
<i>IRF6</i>	1q32.2	CL/P	Linkage, GWAS, GWAS replication	[8, 9, 11–15, 17, 19, 23]
<i>TGFA</i>	2p13	CL/P	Linkage	[9]
<i>THADA</i>	2p21	CL/P	GWAS meta-analysis	[16]
<i>FAM49A</i>	2p24	CL/P	GWAS	[17, 19]
<i>COL8A1</i>	3q12	CL/P	GWAS, GWAS replication, GWAS meta-analysis	[14, 19, 23]
<i>TP63</i>	3q27–28	CL/P	Linkage, GWAS	[9, 19]
<i>SHROOM3</i>	4q21.1	CL/P	GWAS meta-analysis	[19]
<i>PIK3R1</i>	5q13.1	CL/P	GWAS meta-analysis	[19]
<i>NRG1</i>	8p12	CL/P	GWAS meta-analysis	[19]
<i>BAALC</i>	8q22.3	CP & multivitamins	GWAS X E	[20]
<i>SMC2</i>	9q31.1	CP & maternal alcohol	GWAS X E	[20]
<i>TBK1</i>	12q14	CP & maternal smoking	GWAS X E	[20]
<i>KRT18</i>	12q13.13	CL/P	GWAS meta-analysis	[19]
<i>PAX9</i> <i>TGFB3</i>	14q21–24	CL/P	Linkage	[8, 9]
<i>TPM1</i>	15q22	CL/P	GWAS meta-analysis	[16]
<i>ARID3B</i>	15q24	CL/P	GWAS	[17, 19]
<i>CREBBP</i>	16p13	CL/P	GWAS	[27]
<i>CRISPLD2</i>	16q24	CL/P	Linkage	[9]
<i>WNT9B</i> <i>GOSR2</i>	17q21.32	CP	GWAS meta-analysis	[19]
<i>TANC2</i>	17q23.2	CL/P	GWAS	[17]
<i>ZNF236</i>	18q22	CP & maternal smoking	GWAS X E	[20]
<i>RHPN2</i>	19q13.11	CL/P	GWAS	[17]
<i>MAFB</i>	20q12	CL/P	GWAS	[15, 17, 19]

Supplementary Table 4 Candidate Gene Study Using Predicted Expression Levels

Gene	Transcript ID	Chr; Pos	Beta (SE)	z	p
Whole Blood					
<i>ARID3B</i>	ENSG00000179361	15;74,541,177-74,598,131	-1.54 (0.59)	-2.61	0.0090
<i>CRISPLD2</i>	ENSG00000103196	16;84,819,984-84,920,768	0.64 (0.51)	1.27	0.2033
<i>TBK1</i>	ENSG00000183735	12;64,451,880-64,502,108	-0.48 (0.41)	-1.16	0.2448
<i>IRF6</i>	ENSG00000117595	1;209,785,623-209,806,175	0.17 (0.16)	1.07	0.2858
<i>SMC2</i>	ENSG00000136824	9;104,094,260-104,141,417	0.44 (0.46)	0.96	0.3348
<i>BAALC</i>	ENSG00000164929	8;103,140,710-103,230,305	0.40 (0.43)	0.92	0.3509
<i>TGFB3</i>	ENSG00000119699	14;75,958,099-75,982,991	-0.27 (0.36)	-0.73	0.4658
<i>TGFA</i>	ENSG00000163235	2;70,447,280-70,554,193	0.27 (0.37)	0.73	0.4662
<i>KRT18</i>	ENSG00000111057	12;52,948,871-52,952,901	-2.99(10.41)	-0.29	0.7743
<i>TANC2</i>	ENSG00000170921	17;63,009,556-63,427,699	1.94 (8.53)	0.23	0.8200
<i>NRG1</i>	ENSG00000157168	8;31,639,386-32,767,959	-0.02 (0.22)	-0.11	0.9104
<i>ZNF236</i>	ENSG00000130856	18;76,822,607-76,970,727	-0.02 (0.49)	-0.05	0.9578
Skeletal Muscle					
<i>RHPN2</i>	ENSG00000131941	19; 32,978,593-33,064,888	-1.9960 (0.64)	-3.11	0.0019*
<i>SHROOM3</i>	ENSG00000138771	4; 76,435,100-76,783,253	0.6720 (0.27)	2.46	0.0138
<i>PIK3R1</i>	ENSG00000145675	5; 68,215,720-68,301,821	1.2415 (0.51)	2.45	0.0143
<i>TBK1</i>	ENSG00000183735	12; 64,451,880-64,502,108	-0.5811 (0.37)	-1.56	0.1193
<i>COL8A1</i>	ENSG00000144810	3; 99,638,475-99,799,226	0.2524 (0.25)	0.99	0.3205
<i>TGFA</i>	ENSG00000163235	2; 70,447,280-70,554,193	0.3384 (0.37)	0.91	0.3613
<i>TANC2</i>	ENSG00000170921	17; 63,009,556-63,427,699	-0.3166 (0.58)	-0.57	0.5701
<i>ZNF236</i>	ENSG00000130856	18; 76,822,607-76,970,727	-0.4588 (0.84)	-0.54	0.5866
<i>GOSR2</i>	ENSG00000108433	17; 46,923,075-46,975,524	-0.1294 (0.26)	-0.51	0.6119
<i>SMC2</i>	ENSG00000136824	9; 104,094,260-104,141,417	-0.4881 (1.05)	-0.46	0.6431
<i>MAFB</i>	ENSG00000204103	20; 40,685,848-40,689,240	0.1451 (0.65)	0.23	0.8237
Adipose (Subcutaneous)					
<i>RHPN2</i>	ENSG00000131941	19; 32,978,593-33,064,888	-0.61 (0.19)	-3.19	0.0014*
<i>IRF6</i>	ENSG00000117595	1; 209,785,623-209,806,175	0.34 (0.20)	1.69	0.0910
<i>TP63</i>	ENSG00000073282	3; 189,631,416-189,897,279	-0.36 (0.39)	-0.94	0.3497
<i>THADA</i>	ENSG00000115970	2; 43,230,836-43,596,046	0.32 (0.48)	0.67	0.5014
<i>TGFB3</i>	ENSG00000119699	14; 75,958,099-75,982,991	-0.18 (0.42)	-0.44	0.6582
<i>TPM1</i>	ENSG00000140416	15; 63,042,632-63,071,915	0.07 (0.22)	0.34	0.7336
<i>KRT18</i>	ENSG00000111057	12; 52,948,871-52,952,901	-261.49 (2.18)	3.43	NA
Adipose (Visceral)					
<i>SHROOM3</i>	ENSG00000138771	4; 76,435,100-76,783,253	-1.28 (0.58)	-2.22	0.0262
<i>ARHGAP29</i>	ENSG00000137962	1; 94,148,988-94,275,068	0.29 (0.22)	1.34	0.1808
<i>ZNF236</i>	ENSG00000130856	18; 76,822,607-76,970,727	-0.45 (0.39)	-1.15	0.2495
<i>TPM1</i>	ENSG00000140416	15; 63,042,632-63,071,915	-0.11 (0.41)	-0.27	0.7847
<i>THADA</i>	ENSG00000115970	2; 43,230,836-43,596,046	-0.14 (0.51)	-0.27	0.7885
<i>IRF6</i>	ENSG00000117595	1; 209,785,623-209,806,175	0.04 (0.27)	0.16	0.8708
<i>COL8A1</i>	ENSG00000144810	3; 99,638,475-99,799,226	-0.0064 (0.31)	-0.02	0.9836
<i>SHROOM3</i>	ENSG00000138771	4; 76,435,100-76,783,253	-1.28 (0.58)	-2.22	0.0262

Chr: Chromosome, Pos: Position (basepair; bp)