ESM Table 1: Established HDL-C SNPs considered for the study and their MAF in Pima Indians

SNP ID	Position[a]	Proxy SNP (r2)[b]	A1	A2	Locus[c]	MAF_Pima	MAF_EUR[d]	Primary Trait[e]
rs4660293	chr1:40028180		A	G	*PABPC4*	0.03	0.23	HDL-C
rs1689800	chr1:182168885		A	G	*ZNF648*	0.16	0.35	HDL-C
rs4846914	chr1:230295691	rs10127775 (r2=1)	G	A	*GALNT2*	0.44	0.4	HDL-C
rs1042034	chr2:21225281		C	T	*APOB*	0.21	0.22	TG
rs12328675	chr2:165540800		C	T	*COBLL1*	0	0.13	HDL-C
rs2972146	chr2:227100698		G	T	*IRS1*	0.001	0.37	HDL-C
rs13107325	chr4:103188709		C	T	*SLC39A8*	0.003	0.07	HDL-C
rs6450176	chr5:53298025		G	A	*ARL15*	0.23	0.26	HDL-C
rs2814944	chr6:34552797		G	A	*C6ORF106*	0.003	0.16	HDL-C
rs605066	chr6:139829666		C	T	*CITED2*	0.27	0.42	HDL-C
rs1084651	chr6:161089817		A	G	*LPA*	0.003	0.16	HDL-C
rs17145738	chr7:72982874		C	T	*MLXIPL*	0.11	0.12	TG
rs4731702	chr7:130433384		C	T	*KLF14*	0.39	0.48	HDL-C
rs9987289	chr8:9183358		A	G	*PPP1R3B*	0.24	0.09	HDL-C
rs7016529[f]	chr8:19806631		C	T	*LPL*	0	0.01	TG
rs12678919	chr8:19844222		G	A	*LPL*	0.001	0.12	TG
rs2293889	chr8:116599199		T	G	*TRPS1*	0.24	0.41	HDL-C
rs10808546	chr8:126495818		C	T	*TRIB1*	0.33	0.44	TG
rs643531	chr9:15296034		C	A	*TTC39B*	0.004	0.14	HDL-C
rs11789603[f]	chr9:107647019		C	T	*ABCA1*	0	0.09	HDL-C
rs1883025	chr9:1076664301		C	T	*ABCA1*	0.39	0.25	HDL-C
rs2923084	chr11:10388782		A	G	*AMPD3*	0.32	0.17	HDL-C
rs3136441	chr11:46743247	rs3136457 (r2=1)	T	C	*LRP4*	0.36	0.15	HDL-C
rs174601	chr11:61623140		C	T	*FADS1-2-3*	0.009	0.36	TG
rs964184	chr11:116648917		G	C	*APOA1-C3-A4-A5*	0.42	0.13	TG
rs12225230[f]	chr11:116728630		G	C	*APOA1-C3-A4-A5*	0.26	0.14	TG
rs7115089	chr11:122530591		C	G	*UBASH3B*	0.36	0.37	TC
rs7134375	chr12:20473758		C	A	*PDE3A*	0.46	0.42	HDL-C

SNP ID	Position[a]	Proxy SNP (r2)[b]	A1	A2	Locus[c]	MAF_Pima	MAF_EUR[d]	Primary Trait[e]
rs3741414	chr12:57844049		C	T	*LRP1*	0.39	0.24	TG
rs7134594	chr12:110000193		C	T	*MVK*	0.27	0.47	HDL-C
rs11057244[f]	chr12:123773263		G	C	*ZNF664*	0.05	0.03	HDL-C
rs4759375	chr12:123796238		T	C	*SBNO1*	0	0.06	HDL-C
rs4765127	chr12:124460167		G	T	*ZNF664*	0.2	0.34	HDL-C
rs838880	chr12:125261593		C	T	*SCARB1*	0.42	0.31	HDL-C
rs1532085	chr15:58683366		A	G	*LIPC*	0.37	0.39	HDL-C
rs2070895[f]	chr15:58723939	rs1077834 (r2=1)	G	A	*LIPC*	0.14	0.21	HDL-C
rs2652834	chr15:63396867		A	G	*LACTB*	0	0.2	HDL-C
rs3764261	chr16:56993324	rs17231506 (r2=0.98)	C	A	*CETP*	0.29	0.32	HDL-C
rs9939224[f]	chr16:57002732	rs12720922 (r2=0.94)	G	T	*CETP*	0.35	0.76	HDL-C
rs16942887	chr16:67928042		G	A	*LCAT*	0.16	0.12	HDL-C
rs2925979	chr16:81534790		T	C	*CMIP*	0.05	0.3	HDL-C
rs4148008	chr17:6687294		C	G	*ABCA8*	0.25	0.32	HDL-C
rs11869286	chr17:37813856		G	C	*STARD3*	0.44	0.34	HDL-C
rs4129767	chr17:76403984		G	A	*PGS1*	0.42	0.49	HDL-C
rs7241918	chr18:47160953		G	T	*LIPG*	0	0.17	HDL-C
rs2040293[e]	chr18:47278345		G	A	*LIPG*	0.32	0.26	HDL-C
rs12967135	chr18:57849023		G	A	*MC4R*	0.005	0.23	HDL-C
rs7255436	chr19:8433196		C	A	*ANGPTL4*	0.42	0.45	HDL-C
rs737337[f]	chr19:11347493	rs56322906 (r2=1)	T	C	*LOC55908*	0.49	0.08	HDL-C
rs4420638	chr19:45422946		A	G	*APOE*	0.01	0.17	LDL-C
rs5167[e]	chr19:45448465		T	G	*APOE-C1-C2*	0.49	0.37	LDL-C
rs386000	chr19:54792761		G	C	*LILRA3*	0.21	0.2	HDL-C
rs1800961[g]	chr20:43042634		C	T	*HNF4A*	0.04	0.03	HDL-C
rs6065906	chr20:44554015		T	C	*PLTP*	0.005	0.18	HDL-C
rs181362	chr22:21932068		C	T	*UBE2L3*	0.27	0.2	HDL-C

MAF_Pima: minor allele frequency as determined by previously analyzed whole genome sequence data in 335 Pima Indians, MAF_EUR: MAF in subjects of European ancestry, A1: Reference allele, A2: Alternate allele.

[a] Position is based on genome build 37.

[b] Proxy SNP used for the actual analysis and r^2 with the GWAS index SNP.

[c] Locus based on Teslovich et al. [7].

[d] Minor allele frequency in Europeans from teslovich et al [7]

[e] Primary lipid trait at the locus based on Teslovich et al. [7].

[f] Minor allele frequency in Europeans from 1000 genome data.

[g] rs1800961 is a missense variant and was included for further analysis even though it had a MAF=0.04.