

**Table S13. RegulomeDB scores and functional assignments of 153 SCARB1 variants.**

SNP Name <sup>a</sup>	SNP ID <sup>b</sup>	Chr12 Position <sup>c</sup>	Location	Amino Acid Change	Indels	Major/Minor Alleles	MAF	Assoc Trait(s) <sup>d</sup>	RegDB Score <sup>e</sup>	RegDB Functional Assignments
p972	rs181338950	125348548	5' flanking-promoter			C/T	0.048		2a	Motifs Footprinting SP1, Motifs PWM Zfp410, Motifs PWM SP1, Motifs PWM KROX, Motifs Footprinting Sp1, Motifs Footprinting SP4, Motifs PWM UF1H3BETA, Motifs Footprinting KROX, Motifs Footprinting Klf4, Motifs PWM Bcl6b, Motifs Footprinting UF1H3BETA, Motifs PWM Klf4, Motifs PWM Sp1, Motifs PWM SP4, Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq GATA1, Protein_Binding ChIP-seq GABPA, Protein_Binding ChIP-seq EGR1, Protein_Binding ChIP-seq TFAP2C, Protein_Binding ChIP-seq TFAP2A, Protein_Binding ChIP-seq MYC, Protein_Binding ChIP-seq MAX, Protein_Binding ChIP-seq IRF1, Protein_Binding ChIP-seq ELF1, Protein_Binding ChIP-seq SP1, Protein_Binding ChIP-seq CCNT2, Protein_Binding ChIP-seq TBP, Protein_Binding ChIP-seq YY1, Protein_Binding ChIP-seq POLR2A, Protein_Binding ChIP-seq TAF1, Protein_Binding ChIP-seq ZBTB7A, Protein_Binding ChIP-seq CTCF
p1048 insC (1048_1049)		125348472	Exon 1-5' UTR		insC	[-/C]	0.0079		2a	Motifs PWM HIC1, Motifs Footprinting AP-2gamma, Motifs Footprinting TFAP2A, Motifs Footprinting AP-2alpha, Motifs Footprinting HIC1, Motifs PWM AP-2alpha, Motifs PWM AP-2gamma, Motifs PWM AP-2, Motifs PWM TFAP2A, Motifs Footprinting AP-2, Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq GATA1, Protein_Binding ChIP-seq SIN3A, Protein_Binding ChIP-seq HEY1, Protein_Binding ChIP-seq EGR1, Protein_Binding ChIP-seq TFAP2C, Protein_Binding ChIP-seq TFAP2A, Protein_Binding ChIP-seq IRF1, Protein_Binding ChIP-seq RAD21, Protein_Binding ChIP-seq SMC3, Protein_Binding ChIP-seq SP1, Protein_Binding ChIP-seq CCNT2, Protein_Binding ChIP-seq TBP, Protein_Binding ChIP-seq POLR2A, Protein_Binding ChIP-seq TAF1, Protein_Binding ChIP-seq CTCF, Protein_Binding ChIP-seq CTCF, Protein_Binding ChIP-seq EBF1, Protein_Binding ChIP-seq CDX2
p1257	rs4238001	125348263	Exon 1	Gly2Ser		G/A	0.032		4	Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq GATA1, Protein_Binding ChIP-seq MXI1, Protein_Binding ChIP-seq TFAP2C, Protein_Binding ChIP-seq TFAP2A, Protein_Binding ChIP-seq POU2F2, Protein_Binding ChIP-seq RAD21, Protein_Binding ChIP-seq CCNT2, Protein_Binding ChIP-seq E2F6, Protein_Binding ChIP-seq POLR2A, Protein_Binding ChIP-seq TAF1, Protein_Binding ChIP-seq CDX2
p1265	rs2070242	125348255	Exon 1	Ser4Ser		C/T	0.1284		2b	Motifs PWM E2F-1, Motifs Footprinting E2F-1, Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq,

									Protein_Binding ChIP-seq GATA1, Protein_Binding ChIP-seq MXI1, Protein_Binding ChIP-seq TFAP2A, Protein_Binding ChIP-seq POU2F2, Protein_Binding ChIP-seq RAD21, Protein_Binding ChIP-seq E2F6, Protein_Binding ChIP-seq POLR2A, Protein_Binding ChIP-seq TAF1, Protein_Binding ChIP-seq CDX2
									Motifs Footprinting NRSF, Motifs PWM REST, Motifs PWM NRSF, Motifs PWM Osr2, Motifs Footprinting REST, Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq GATA1, Protein_Binding ChIP-seq MXI1, Protein_Binding ChIP-seq E2F6, Protein_Binding ChIP-seq CDX2
p1316	rs10396208	125348204	Exon 1	Cys21Cys	C/T	0.0476		2b	
p1419	rs201717369	125348101	Intron 1		G/A	0.0121		4	Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq GATA1, Protein_Binding ChIP-seq E2F6, Protein_Binding ChIP-seq ZBTB7A, Protein_Binding ChIP-seq E2F1
p4072	rs7139401	125345448	Intron 1		T/C	0.4386		3b	Motifs PWM Mafk, Motifs PWM Dlx3, Motifs PWM Dlx4, Protein_Binding ChIP-seq MAFK
p5055	rs11057869	125344465	Intron 1		G/A	0.0740		7	No data
p6600	rs12831105	125342920	Intron 1		C/T	0.1188		7	No data
p7650	rs11615630	125341870	Intron 1		G/A	0.0436		5	Chromatin_Structure DNase-seq
p10292	rs4765181	125339228	Intron 1		G/T	0.2490		5	Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq
p10991	rs10773112	125338529	Intron 1		G/A	0.3534		4	Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq FOXA1, Protein_Binding ChIP-seq RXRA, Protein_Binding ChIP-seq HDAC2
p13570	rs11057864	125335950	Intron 1		G/T	0.1180		4	Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq HNF4A
p16565	rs10773111	125332955	Intron 1		G/A	0.1928		6	Single_Nucleotides SCARB1 eQTL
p20207	rs11057853	125329313	Intron 1		G/A	0.4484	HDL-C	5	Motifs PWM HNF4, Motifs PWM HNF4A, Motifs PWM HNF4directrepeat1, Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq
p20694	rs11057852	125328826	Intron 1		G/A	0.1050		7	No data
p20741	rs11057851	125328779	Intron 1		C/T	0.3237	HDL-C (best SNP), ApoA-I	5	Chromatin_Structure DNase-seq
p21145	rs3924313	125328375	Intron 1		C/T	0.1772		6	Motifs PWM TFIIA
p22116	rs12370382	125327404	Intron 1		G/A	0.0645		1f	Single_Nucleotides SCARB1 eQTL, Chromatin_Structure DNase-seq
p22168	rs7137797	125327352	Intron 1		T/C	0.3977		2b	Motifs PWM Staf, Motifs Footprinting Staf, Motifs Footprinting zfn143, Motifs PWM zfn143, Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq GATA1
p22331	rs6488944	125327189	Intron 1		T/G	0.1474		4	Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq GATA1, Protein_Binding ChIP-seq EP300, Protein_Binding ChIP-seq GATA2
p22675	rs12425134	125326845	Intron 1		G/T	0.0526		4	Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq GATA1
p28137	rs12229555	125321383	Intron 1		A/G	0.3896		7	No data
p28692	rs4765622	125320828	Intron 1		C/T	0.2565		5	Chromatin_Structure DNase-seq
p28957	rs11057844	125320563	Intron 1		G/A	0.2362		5	Motifs PWM HTF, Motifs Footprinting HTF, Protein_Binding ChIP-seq GATA1
p29749	rs10846751	125319771	Intron 1		C/T	0.4492		7	No data
p31072	rs10846749	125318448	Intron 1		C/G	0.4461		4	Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq EP300, Protein_Binding ChIP-seq MAX, Protein_Binding ChIP-seq NANOG, Protein_Binding ChIP-seq USF1, Protein_Binding ChIP-seq TCF4,

								Protein_Binding ChIP-seq SP1, Protein_Binding ChIP-seq JUND, Protein_Binding ChIP-seq TCF12, Protein_Binding ChIP-seq RXRA
p31938	rs10744182	125317582	Intron 1	G/A	0.1837	5		Chromatin_Structure DNase-seq
p32129	rs10773107	125317391	Intron 1	G/T	0.1009	7		No data
p32273	rs12580803	125317247	Intron 1	T/C	0.1006	5		Chromatin_Structure DNase-seq Motifs Footprinting AR, Motifs PWM AR, Chromatin_Structure DNase-seq
p32290	rs10744181	125317230	Intron 1	T/C	0.1238	5		Motifs PWM E2F-1, Chromatin_Structure DNase-seq
p32395	rs12581963	125317125	Intron 1	C/T	0.1314	5		
p32750	rs7967521	125316770	Intron 1	A/G	0.3425	7		No data
p32777	rs11057841	125316743	Intron 1	G/A	0.2805	7		No data
p32860	rs7967406	125316660	Intron 1	A/C	0.0991	6		Motifs PWM Hbp1, Motifs PWM Rfx3
p33531	rs11057838	125315989	Intron 1	C/A	0.2278	7		No data Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq HNF4A, Protein_Binding ChIP-seq TFAP2C, Protein_Binding ChIP-seq TFAP2A, Protein_Binding ChIP-seq STAT1, Protein_Binding ChIP-seq GTF2F1, Protein_Binding ChIP-seq TBP, Protein_Binding ChIP-seq NR3C1, Protein_Binding ChIP-seq STAT3, Protein_Binding ChIP-seq ESR1, Protein_Binding ChIP-seq POLR2A, Protein_Binding ChIP-seq CDX2
p36094	rs11608336	125313426	Intron 1	G/A	0.1543	4		Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq HNF4A, Protein_Binding ChIP-seq TFAP2A, Protein_Binding ChIP-seq NR3C1, Protein_Binding ChIP-seq ESR1
p36461	rs4765178	125313059	Intron 1	C/T	0.1671	4		Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq HNF4A, Protein_Binding ChIP-seq EP300, Protein_Binding ChIP-seq TFAP2C, Protein_Binding ChIP-seq AR, Protein_Binding ChIP-seq FOXA1, Protein_Binding ChIP-seq CDX2
p36908	rs10846745	125312612	Intron 1	C/G	0.3257	4		Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq HNF4A, Protein_Binding ChIP-seq EP300, Protein_Binding ChIP-seq TFAP2C, Protein_Binding ChIP-seq MAX, Protein_Binding ChIP-seq AR, Protein_Binding ChIP-seq ESR1, Protein_Binding ChIP-seq FOXA1, Protein_Binding ChIP-seq CDX2, Protein_Binding ChIP-seq GATA3
p37095	rs10846744	125312425	Intron 1	C/G	0.3056	4		
p41632	rs6488943	125307888	Intron 1	A/C	0.2954	5		Chromatin_Structure DNase-seq
p42467	rs11057830	125307053	Intron 1	C/T	0.1523	7		No data
p45516	rs1902569	125304004	Intron 1	G/A	0.1544	5	HDL-C	Chromatin_Structure DNase-seq
p45627	rs12297372	125303893	Intron 1	A/G	0.0487	5		Chromatin_Structure DNase-seq
p46964	rs114061302	125302556	Intron 1	G/A	0.0388	4		Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq IKZF1
p48969	rs2343394	125300551	Intron 2	C/T	0.1898	5		Chromatin_Structure DNase-seq
p49537	rs7305310	125299983	Intron 2	C/T	0.1007	5		Chromatin_Structure DNase-seq Motifs PWM Asc2, Motifs PWM E47, Motifs Footprinting E47, Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq
p49570 delC	rs145376237	125299950	Intron 2	delC	[C/-]	0.2276		
p49690	rs4765615	125299830	Intron 2	G/A	0.4426	5	HDL-C, ApoA-I	Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq Motifs PWM Gm397, Motifs PWM Zscan4, Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq
p49759	rs146272788	125299761	Intron 2	C/T	0.0020	5		Motifs Footprinting Pax-3, Motifs PWM Pax-3, Chromatin_Structure DNase-seq
p49978	rs5891	125299542	Exon 3	Val135Ile	G/A	0.0058		Chromatin_Structure DNase-seq

p50024	rs368880622	125299496	Intron 3		G/T	0.0026	5	Chromatin_Structure DNase-seq
p50118	rs58710319	125299402	Intron 3		C/T	0.0208	5	Chromatin_Structure DNase-seq
p50151	rs2278986	125299369	Intron 3		T/C	0.1933	5	Chromatin_Structure DNase-seq
p50380	rs141748317	125299140	Intron 3		A/G	0.0112	2b	Motifs Footprinting HEN1, Motifs PWM HEN1, Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq IKZF1
p50489	rs61320152	125299031	Intron 3		G/T	0.0257	4	Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq IKZF1
p50954		125298566	Intron 4		T/C	0.0007	5	Chromatin_Structure DNase-seq
p51888	rs7138304	125297632	Intron 4		C/T	0.1079	2b	Motifs Footprinting TRF1, Motifs PWM TRF1, Motifs Footprinting IRF-1, Motifs PWM IRF-1, Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq NFYB, Protein_Binding ChIP-seq USF2, Protein_Binding ChIP-seq USF1, Protein_Binding ChIP-seq IKZF1
p52096	rs10846739	125297424	Intron 4		A/G	0.4693	3a	Motifs PWM Tbp, Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq IKZF1
p52556	rs11057820	125296964	Intron 4		G/A	0.1000	5	Chromatin_Structure DNase-seq
p52610	rs10846738	125296910	Intron 4		C/T	0.1349	4	Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq SPI1
p52919		125296601	Intron 4		G/T	0.0013	5	Motifs PWM Zfp281, Motifs PWM MZF1_5-13, Motifs Footprinting MZF1_5-13, Motifs PWM Gabpa, Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq
p52956	rs77740046	125296564	Intron 4		C/T	0.0546	5	Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq
p52995	rs113910315	125296525	Intron 4- splice site		T/G	0.0020	5	Motifs PWM Zic3, Motifs PWM Zic2, Motifs PWM Zic1, Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq
p53128	rs372212527	125296392	Intron 5		C/T	0.005	5	Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq
p53159	rs59809936	125296361	Intron 5		G/A	0.049	5	Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq
p53359	rs112371713	125296161	Intron 5		G/A	0.1243	5	Chromatin_Structure DNase-seq
p53372	rs115604379	125296148	Intron 5		C/T	0.0066	5	Chromatin_Structure DNase-seq
p53481	rs143611171	125296039	Intron 5		C/T	0.099	6	Motifs Footprinting ARP-1(COUP-TF2), Motifs PWM ARP-1(COUP-TF2)
p53790	rs4765614	125295730	Intron 5		G/A	0.2653	5	Chromatin_Structure DNase-seq
p54445	rs60910935	125295075	Intron 5		A/G	0.0418	4	Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq RFX3
p54475	rs60227139	125295045	Intron 5		C/T	0.0437	4	Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq RFX3
p54492	rs61762481	125295028	Intron 5		G/A	0.1005	4	Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq RFX3
p54611		125294909	Intron 5		T/C	0.0007	4	Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq RFX3
p54627		125294893	Intron 5		G/C	0.0020	4	Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq RFX3
p54856		125294664	Intron 6		C/T	0.0007	4	Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq RFX3, Protein_Binding ChIP-seq STAT3
p55923	rs838900	125293597	Intron 6		G/A	0.3921	7	No data
p55963	rs7134858	125293557	Intron 6		C/T	0.1560	6	ApoA-I (best SNP) Motifs PWM STAT1
p56845	rs838902	125292675	Intron 6		A/G	0.4249	5	Motifs PWM Bbx, Chromatin_Structure DNase-seq
p57004	rs187562853	125292516	Intron 6		G/A	0.0098	4	Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq GATA1
p57107	rs5892	125292413	Exon 7	Phe301Phe	C/T	0.0589	4	Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq GATA1, Protein_Binding ChIP-seq NR3C1
p57508	rs71458866	125292012	Intron 7		G/A	0.1130	4	Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq GATA1
p57592	rs838903	125291928	Intron 7		G/A	0.3763	4	Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq GATA1

p58514	rs838905	125291006	Intron 7		T/C	0.4329	4	Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq CEBPB
p58664	rs865716	125290856	Intron 7		A/T	0.2708	5	Chromatin_Structure DNase-seq
p60255	rs3782287	125289265	Intron 7		C/T	0.2831	5	Chromatin_Structure DNase-seq
p61872	rs838909	125287648	Intron 7		C/T	0.2199	4	Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq RFX3
p62140	rs838910	125287380	Intron 7		G/T	0.3047	5	Chromatin_Structure FAIRE, Protein_Binding ChIP-seq RFX3
p62409	rs838911	125287111	Intron 7		C/T	0.4211	5	Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq
p62615	rs7138386	125286905	Intron 7		T/C	0.1137	5	Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq
p63483	rs838912	125286037	Intron 7		G/A	0.0867	7	No data
p64772	rs5888	125284748	Exon 8	Ala350Ala	C/T	0.0961	3a	Motifs PWM Nr2f2, Motifs PWM Rara, Motifs PWM PPARalpha:RXRalpha, Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq RFX3, Protein_Binding ChIP-seq GATA2
p64923	rs838915	125284597	Intron 8		C/A	0.1435	5	Motifs PWM AP-2, Chromatin_Structure DNase-seq
p65999	rs12819677	125283521	Intron 8		G/A	0.2813	6	Motifs PWM PPARG
p67439	rs961170	125282081	Intron 8		G/A	0.0893	4	Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq SPI1
p67700	rs1726374	125281820	Intron 8		G/A	0.1933	7	No data
p69013	rs7135117	125280507	Intron 8		A/G	0.2901	7	No data
p69699	rs10396210	125279821	Intron 8- splice site		G/A	0.1511	4	Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq NFKB1, Protein_Binding ChIP-seq TCF12, Protein_Binding ChIP-seq POLR2A, Protein_Binding ChIP-seq EBF1, Motifs PWM RREB-1, Motifs PWM GR, Chromatin_Structure DNase-seq
p69994	rs188094006	125279526	Intron 9		C/T	<u>0.005</u>	5	Motifs PWM RREB-1, Motifs PWM GR, Chromatin_Structure DNase-seq
p69995 delC	rs5801571	125279525	Intron 9	delC	[C/-]	0.2761	5	Motifs PWM RREB-1, Motifs PWM GR, Chromatin_Structure DNase-seq
p70088	rs117585141	125279432	Intron 9		G/A	0.158	7	No data
p70129	rs1814575	125279391	Intron 9		C/T	0.047	7	No data
p70148	rs183061101	125279372	Intron 9		T/C	<u>0.011</u>	6	Motifs PWM Nrf-2, Motifs PWM LUN-1
p70201		125279319	Intron 9		T/C	0.0010	6	Motifs PWM MEF2A
p70292	rs150388176	125279228	Intron 9		C/T	<u>0.016</u>	5	Chromatin_Structure DNase-seq, Motifs PWM EWSR1-FLI1, Motifs Footprinting EWSR1-FLI1, Chromatin_Structure DNase-seq
p71867	rs7954022	125277653	Intron 9		C/T	0.1323	5	Chromatin_Structure DNase-seq
p72197	rs838861	125277323	Intron 9		A/G	0.3777	7	No data
p72777	rs838862	125276743	Intron 9		C/T	0.0887	5	Chromatin_Structure DNase-seq
p75766	rs838866	125273754	Intron 9		T/C	0.2116	6	Single_Nucleotides SCARB1 eQTL
p75778	rs7301120	125273742	Intron 9		C/T	0.1135	6	Single_Nucleotides SCARB1 eQTL
p76204	rs866793	125273316	Intron 9		A/G	0.0520	7	No data
p76757	rs9919713	125272763	Intron 9		A/T	0.4390	6	Motifs PWM FOXJ2, Motifs PWM Alx-4, Motifs Footprinting FOXJ2, Motifs Footprinting Alx-4
p77181	rs146246031	125272339	Intron 9		T/C	0.0053	7	No data
p77250	rs201901986	125272270	Intron 9		G/T	<u>0.095</u>	6	Motifs PWM Srf, Motifs PWM Mtf1, Motifs PWM Tcfap2e
p77251	rs34339961	125272269	Intron 9		A/T	0.1177	6	Motifs PWM Srf, Motifs PWM Mtf1, Motifs PWM Tcfap2e
p77381	rs138499966	125272139	Intron 9		T/C	0.0046	6	Motifs PWM Foxo1, Motifs PWM Freac-2, Motifs PWM Foxj3, Motifs PWM FOXO3, Motifs PWM HFH8(FOXF1A), Motifs PWM FOXJ2, Motifs PWM Freac-4, Motifs Footprinting Foxq1, Motifs PWM Foxa2, Motifs PWM HFH1(FOXQ1), Motifs PWM Foxk1,

									Motifs Footprinting HFH1(FOXQ1), Motifs PWM Foxq1, Motifs PWM HNF3
p77620	rs377124254	125271900	Intron 10		G/A	0.0007	5	Chromatin_Structure DNase-seq	
p77682	rs150082885	125271838	Intron 10		A/G	0.0106	5	Chromatin_Structure DNase-seq	
p77704		125271816	Intron 10		C/A	0.0040	5	Chromatin_Structure DNase-seq	
p77842	rs2272310	125271678	Intron 10		G/A	0.0807	5	Chromatin_Structure DNase-seq	
p78255	rs184052375	125271265	Intron 10		A/G	0.0072	4	Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq SIX5, Protein_Binding ChIP-seq MAX, Protein_Binding ChIP-seq NANOG, Protein_Binding ChIP-seq USF2, Protein_Binding ChIP-seq USF1, Protein_Binding ChIP-seq ATF3, Protein_Binding ChIP-seq YY1, Protein_Binding ChIP-seq TBP, Protein_Binding ChIP-seq POLR2A, Protein_Binding ChIP-seq TAF1	
p78402	rs838898	125271118	Intron 10		G/A	0.0714	5	Motifs PWM Hic1, Motifs PWM Eomes, Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq	
p78430	rs838897	125271090	Intron 10		C/G	0.3830	5	Motifs PWM RNF96, Motifs PWM AP-2, Motifs Footprinting AP-2, Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq	
p78747	rs2293440	125270773	Intron 11		T/C	0.4112	5	Chromatin_Structure DNase-seq	
p78791	rs75289200	125270729	Intron 11		T/C	0.0321	5	Chromatin_Structure DNase-seq	
p79721	rs838896	125269799	Intron 11		G/C	0.3104	5	ApoA-I Chromatin_Structure DNase-seq	
p79828	rs838895	125269692	Intron 11		C/G	0.3171	5	Motifs PWM Pax-5, Chromatin_Structure DNase-seq	
p80045	rs838893	125269475	Intron 11		G/A	0.3244	5	Chromatin_Structure DNase-seq	
p81863	rs185445624	125267657	Intron 11		G/A	0.0020	5	Motifs PWM ESR1, Motifs PWM Rfx3, Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq	
p82019	rs838890	125267501	Intron 11		C/T	0.0320	5	Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq	
p82264	rs141545424	125267256	Exon 12	Gly501Gly	C/A	0.0007	5	Chromatin_Structure DNase-seq	
p82340	rs77483223	125267180	Intron 12		G/A	0.0231	5	Motifs PWM Arid3a, Chromatin_Structure DNase-seq	
p82369	rs75446635	125267151	Intron 12		G/A	0.0059	5	Chromatin_Structure DNase-seq	
p82434	rs838889	125267086	Intron 12		T/C	0.0315	5	Motifs PWM FOXP1, Motifs Footprinting HFH3(FOX11), Motifs PWM MRF-2, Motifs Footprinting MRF-2, Motifs PWM HFH3(FOX11), Chromatin_Structure DNase-seq	
p83547	rs838887	125265973	Intron 12		C/G	0.4564	5	Chromatin_Structure DNase-seq	
p83884	rs7011106	125265636	Intron 12		C/T	0.2597	5	ApoA-I Chromatin_Structure DNase-seq	
p86245	rs188375019	125263275	Intron 12		C/T	0.0341	4	Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq BATF Motifs PWM NGFI-C, Motifs Footprinting NGFI-C, Motifs Footprinting Sp3, Motifs PWM Sp3, Motifs PWM KROX, Motifs PWM UF1H3BETA, Motifs Footprinting KROX, Motifs Footprinting UF1H3BETA, Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq	
p86276	rs7471155	125263244	Intron 12		C/T	0.1495	2b	Protein_Binding ChIP-seq BATF Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq EGR1, Protein_Binding ChIP-seq BATF	
p86316	rs7011104	125263204	Intron 12		G/T	0.0487	4		
p86481	rs7011103	125263039	Exon 13-3' UTR	Gly499Arg (isoform 2)	G/A	0.2451	5	Chromatin_Structure DNase-seq	
p86967	rs187492239	125262553	Exon 13-3' UTR		A/G	0.0355	4	Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq HNF4A, Protein_Binding ChIP-seq HEY1, Protein_Binding ChIP-seq TCF4,	

							Protein_Binding ChIP-seq JUND, Protein_Binding ChIP-seq POLR2A, Protein_Binding ChIP-seq HNF4G, Protein_Binding ChIP-seq FOSL2, Protein_Binding ChIP-seq HDAC2
							Motifs PWM HNF4alpha1, Motifs Footprinting HNF4alpha1, Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq HNF4A, Protein_Binding ChIP-seq HEY1, Protein_Binding ChIP-seq TCF4, Protein_Binding ChIP-seq JUND, Protein_Binding ChIP-seq POLR2A, Protein_Binding ChIP-seq HNF4G, Protein_Binding ChIP-seq FOSL2, Protein_Binding ChIP-seq HDAC2
p87011	rs58032386	125262509	Exon 13-3' UTR	C/T	0.1417	2a	Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq TCF4
p87195	rs10396211	125262325	Exon 13-3' UTR	G/C	<u>0.122</u>	4	Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq ELF1
p87266	rs150512235	125262254	Exon 13-3' UTR	T/C	0.0057	4	Motifs PWM DEAF1, Motifs Footprinting DEAF1, Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq CEBPB, Protein_Binding ChIP-seq ELF1, Protein_Binding ChIP-seq FOXA2, Protein_Binding ChIP-seq JUND, Protein_Binding ChIP-seq FOSL2, Protein_Binding ChIP-seq FOXA1
p87416	rs838884	125262104	3' flanking	C/T	<u>0.301</u>	2b	Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq CEBPB, Protein_Binding ChIP-seq ELF1, Protein_Binding ChIP-seq FOXA2, Protein_Binding ChIP-seq JUND, Protein_Binding ChIP-seq FOSL2, Protein_Binding ChIP-seq FOXA1
p87459		125262061	3' flanking	C/T	<u>0.005</u>	4	Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq CEBPB, Protein_Binding ChIP-seq ELF1, Protein_Binding ChIP-seq FOXA2, Protein_Binding ChIP-seq JUND, Protein_Binding ChIP-seq FOSL2, Protein_Binding ChIP-seq FOXA1
p87611	rs190688220	125261909	3' flanking	C/T	0.0316	4	Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq, Motifs PWM TP53, Motifs PWM p53, Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq
p87681	rs838883	125261839	3' flanking	G/A	0.0459	5	No data
p87694		125261826	3' flanking	C/T	0.0020	5	Motifs PWM NFIL3, Motifs Footprinting NFIL3, Motifs PWM TFIIA, Chromatin_Structure FAIRE
p87707	rs838882	125261813	3' flanking	G/A	<u>0.303</u>	7	No data
p87723	rs838881	125261797	3' flanking	C/T	0.3183	6	No data
p87749	rs76465225	125261771	3' flanking	G/A	0.0844	7	No data
p87927	rs838880	125261593	3' flanking	G/A	<u>0.2414</u>	5	Chromatin_Structure DNase-seq

ApoA-I, apolipoprotein A-I; HDL-C, high-density lipoprotein cholesterol; del, deletion; eQTL, expression quantitative trait loci; Indels, insertion and deletion variations; ins, insertion; MAF, minor allele frequency; RegDB, RegulomeDB score; SNP, single nucleotide polymorphism; UTR, untranslated region.

All alleles on the reverse strand. Splice site is defined as  $\pm 20$  bp from the start or end of an exon.

A list of 83 variants identified by sequencing is shown in Additional file 3 Table S3.

A list of 68 common HapMap-YRI tagSNPs successfully genotyped in our entire sample is shown in Additional file 7 Table S5.

A list of 138 genotyped variants in our entire sample is shown in Additional file 9 Table S6.

Underlined MAFs are based on our sequencing data/sample due to genotyping failure (Additional file 3 Table S3).

Double underlined MAFs are identified in our sequencing stage but not selected for genotyping based on the linkage disequilibrium plot (Additional file 3 Table S3; Additional file 5 Figure S1 and Additional file 6 Figure S2).

All 10 novel variants identified in this study have been submitted to dbSNP database (batch ID: SCARB1\_AB): [http://www.ncbi.nlm.nih.gov/SNP/snp\\_viewTable.cgi?handle=KAMBOH](http://www.ncbi.nlm.nih.gov/SNP/snp_viewTable.cgi?handle=KAMBOH).

<sup>a,c</sup> RefSeq of SCARB1: hg19, NM\_005505 (CHIP Bioinformatics).

<sup>b</sup> dbSNP build 139: GRCh37.p10.

<sup>d</sup> Evidence is based on SNPs with MAF  $\geq 5\%$  exhibiting nominally significant association with either HDL-C or ApoA-I ( $P < 0.05$ ; Additional file 14 Table S9 and Additional file 15 Table S10) in single-site analysis observed in the current study.

<sup>e</sup> The RegulomeDB (version 1.0) scoring scheme is described at the footnote of Additional file 17 Table S12 or can be seen at <http://regulome.stanford.edu/help>.

<sup>f</sup> Close to a miRNA-145 seed site based on TargetScanHuman (version 6.2, <http://www.targetscan.org/>).