Table S2. eQTL/LDL colocalisation

Chr	Region	Signal	PP.H3.abf	PP.H4.abf	Tesl	Biom pval	Biom SNP	eQTL pval	eQTL SNP	Best Causal
1	109618271:110144587	CELSR2	2	98	Y	9.70E-171	rs629301	1.50E-120	rs646776	rs629301
		PSRC1	7	93	Y	9.70E-171	rs629301	1.10E-299	rs7528419	rs629301
		SORT1	7	93	Y	9.70E-171	rs629301	1.10E-299	rs7528419	rs629301
		PSMA5	7	93	Y	9.70E-171	rs629301	1.50E-17	rs599839	rs629301
1	150767063:151167122	ANXA9	3	97	N	6.50E-08	rs267733	6.10E-08	rs267734	rs267733
1	25626305:26026364	TMEM57	10	90	Y	1.20E-10	rs12027135	2.10E-31	rs873308	rs12027135
2	120908798:121308857	INHBB	7	77	N	3.80E-07	rs2030746	4.90E-21	rs17050272	rs17050272
8	59158506:59558565	UBXN2B	13	87	N	3.90E-09	rs1030431	3.50E-10	rs11996829	rs13263105
8	8795514:9392282	PPP1R3B	4	96	Y	7.40E-15	rs2126259	6.20E-17	rs2126259	rs2126259
		ENSG00000254235	13	87	N	7.40E-15	rs2126259	4.00E-13	rs4841133	rs9987289
9	2454062:2854121	VLDLR	1	91	N	8.00E-06	rs3780181	1.40E-07	rs3780181	rs3780181
11	126084467:126484526	ST3GAL4	15	85	Y	1.20E-15	rs11220462	7.20E-25	rs4307732	rs4307732
11	18429356:18829415	SPTY2D1	6	93	N	2.90E-07	rs10128711	7.20E-17	rs10832963	rs10832963
11	61367291:61767350	FADS1	17	83	Y	1.20E-21	rs174583	2.90E-20	rs102275	rs102275
12	111508189:111908248	CUX2	2	98	N	1.50E-09	rs11065987	1.00E-17	rs4378452	rs3184504
14	24688259:25088318	NYNRIN	5	95	Y	4.40E-11	rs2332328	1.10E-78	rs6573778	rs6573778
16	71894416:72310900	HP	1	97	N	1.80E-22	rs2000999	1.30E-05	rs2000999	rs2000999
		HPR	1	99	N	1.80E-22	rs2000999	4.20E-08	rs2000999	rs2000999
17	45562645:45962704	KPNB1	16	83	N	1.10E-07	rs8072100	3.10E-09	rs4794048	rs8072100
20	12947054:13347113	SPTLC3	4	86	N	4.20E-06	rs364585	2.30E-41	rs168622	rs364585

Positive (PP4 $> 75\%$) eQTL/LDL colocalisation results between the liver eQTL dataset and the Teslovich meta-analysis using the most stringent prior for the probability that one SNP is associated with both traits, $p_{12} = 10^{-6}$. The column **Signal** includes genes that are part of overlapping regions and that colocalise at PP4 $> 75\%$; the column **Region** represents the genomic coordinates for the start and stop of the signal; in the column **Tesl**, “Y” indicates that this signal with any of the genes included has been reported to be an intermediate for any of the four lipid biomarker associations by Teslovich et al. ; the columns **Biom pval** and **eQTL pval** report the lowest p-value found for LDL association and for the expression association respectively, with the corresponding SNP name (**Biom SNP** and **eQTL SNP**); the column **Best Causal** reports the SNP within the region with the highest posterior probability to be the true causal variant. The probabilities have been rounded to 1 significant figure.