

Table S7. Known SNPs contributing to the calculation of BMI, LDLc, and CRP allelic scores in ALSPAC. The first seven columns refer to results from published meta-analyses, whereas the last three columns refer to association in the ALSPAC cohort

Variable	SNP	Chromosome	Position	Putative Gene	Effect Allele	Effect size	ALSPAC RQSR ³	ALSPAC pvalue	ALSPAC RSQ ⁴
BMI	rs2815752	1	72585028	<i>NEGR1</i>	A	0.13	0.9964	0.049	0.07%
BMI	rs1514175	1	74764232	<i>TNNI3K</i>	A	0.07	0.9984	1.3x10 ⁻⁴	0.25%
BMI	rs1555543	1	96717385	<i>PTBP2</i>	C	0.06	0.996	0.94	0%
BMI	rs543874	1	176156103	<i>SEC16B</i>	G	0.22	0.9965	3.2x10 ⁻⁵	0.30%
BMI	rs2867125	2	612827	<i>TMEM18</i>	C	0.31	0.9997	2.5x10 ⁻⁵	0.30%
BMI	rs713586	2	25011512	<i>RBJ/ADCY3/POMC</i>	C	0.14	0.9993	1.3x10 ⁻⁷	0.48%
BMI	rs887912	2	59156381	<i>FANCL</i>	T	0.1	0.9972	0.42	0%
BMI	rs2890652	2	142676401	<i>LRP1B</i>	C	0.09	0.9888	0.42	0%
BMI	rs13078807	3	85966840	<i>CADM2</i>	G	0.1	0.9966	9.9x10 ⁻³	0.01%
BMI	rs9816226	3	187317193	<i>ETV5</i>	T	0.14	0.9556	0.042	0.07%
BMI	rs10938397	4	44877284	<i>GNPDA2</i>	G	0.18	0.9881	0.012	0.11%
BMI	rs13107325	4	103407732	<i>SLC39A8</i>	T	0.19	0.9972	6.9x10 ⁻⁴	0.20%
BMI	rs2112347	5	75050998	<i>FLJ35779/HMGCR</i>	T	0.1	0.9945	0.064	0.06%
BMI	rs4836133	5	124360002	<i>ZNF608</i>	A	0.07	0.9429	0.83	0%
BMI	rs206936	6	34410847	<i>HMGAI</i>	G	0.06	0.9875	0.83	0%
BMI	rs987237	6	50911009	<i>TFAP2B</i>	G	0.13	0.9994	4.2x10 ⁻³	0.14%
BMI	rs10968576	9	28404339	<i>LRRN6C</i>	G	0.11	0.9995	0.94	0%
BMI	rs4929949	11	8561169	<i>RPL27A</i>	C	0.06	0.9671	0.64	0%
BMI	rs10767664	11	27682562	<i>BDNF</i>	A	0.19	0.9965	0.018	0.10%
BMI	rs3817334	11	47607569	<i>MTCH2</i>	T	0.06	0.9984	0.017	0.10%
BMI	rs7138803	12	48533735	<i>FAIM2</i>	A	0.12	0.998	2.0x10 ⁻⁴	0.24%
BMI	rs4771122	13	26918180	<i>MTIF3</i>	G	0.09	0.9313	0.48	0%
BMI	rs11847697	14	29584863	<i>PRKD1</i>	T	0.17	0.9688	2.5x10 ⁻³	0.16%
BMI	rs10150332	14	79006717	<i>NRXN3</i>	C	0.13	0.9963	0.82	0%

BMI	rs2241423	15	65873892	<i>MAP2K5</i>	G	0.13	0.9997	0.17	0.03%
BMI	rs12444979	16	19841101	<i>GPRC5B</i>	C	0.17	0.9975	5.7×10^{-4}	0.20%
BMI	rs7359397	16	28793160	<i>SH2B1</i>	T	0.15	0.9988	0.14	0.04%
BMI	rs1558902	16	52361075	<i>FTO</i>	A	0.39	0.9967	1.5×10^{-9}	0.63%
BMI	rs571312	18	55990749	<i>MC4R</i>	A	0.23	0.9995	5.2×10^{-8}	0.51%
BMI	rs29941	19	39001372	<i>KCTD15</i>	G	0.06	0.9999	0.32	0.02%
BMI	rs2287019	19	50894012	<i>QPCTL/GIPR</i>	C	0.15	0.9991	0.57	0%
BMI	rs3810291	19	52260843	<i>TMEM160</i>	A	0.09	0.7652	0.026	0.08%
CRP	rs12037222	1	39837548	<i>PABPC4</i>	A	0.045	0.9823	0.65	0%
CRP	rs4420065	1	65934049	<i>LEPR</i>	C	0.09	0.9859	4.5×10^{-23}	2.3%
CRP	rs4129267	1	152692888	<i>IL6R</i>	C	0.079	0.9997	2.7×10^{-6}	0.52%
CRP	rs2794520	1	157945440	<i>CRP</i>	C	0.16	0.9986	5.2×10^{-24}	2.4%
CRP	rs12239046	1	245668218	<i>NLRP3</i>	C	0.047	0.9918	0.29	0.03%
CRP	rs1260326	2	27584444	<i>GCKR</i>	T	0.072	0.9976	0.38	0.02%
CRP	rs6734238	2	113557501	<i>IL1F10</i>	G	0.05	0.9994	0.71	0%
CRP	rs4705952	5	131867517	<i>IRF1</i>	G	0.042	0.9101	0.44	0.01%
CRP	rs6901250	6	117220718	<i>GPRC6A</i>	A	0.035	0.9750	0.53	0.01%
CRP	rs13233571	7	72609167	<i>BCL7B</i>	C	0.054	0.9833	0.063	0.08%
CRP	rs9987289	8	9220768	<i>PPP1R3B</i>	A	0.069	0.9902	0.62	0%
CRP	rs10745954	12	102007224	<i>ASCL1</i>	A	0.039	0.9968	0.081	0.7%
CRP	rs1183910	12	119905190	<i>HNF1A</i>	G	0.149	0.9918	1.6×10^{-7}	0.64%
CRP	rs340029	15	58682257	<i>RORA</i>	T	0.032	0.9945	0.097	0.06%
CRP	rs10521222	16	49716211	<i>SALL1</i>	C	0.104	0.9829	0.11	0.06%
CRP	rs2847281	18	12811593	<i>PTPN2</i>	A	0.031	0.9624	0.40	0.02%
CRP	rs4420638	19	50114786	<i>APOC1</i>	A	0.236	0.5938	2.7×10^{-7}	0.62%
CRP	rs1800961	20	42475778	<i>HNF4A</i>	C	0.088	0.9918	0.14	0.05%
LDLc	rs12027135	1	25648320	<i>LDLRAP1</i>	T	NA	0.9736	0.011	0.15%

LDLc	rs2479409	1	55277238	<i>PCSK9</i>	G	NA	0.6897	9.5x10 ⁻³	0.16%
LDLc	rs2131925	1	62798530	<i>ANGPTL3</i>	T	NA	0.9966	2.6x10 ⁻³	0.21%
LDLc	rs629301	1	109619829	<i>SORT1</i>	T	NA	0.9976	6.2x10 ⁻¹²	1.1%
LDLc	rs2642442	1	219040186	<i>MOSC1</i>	T	NA	0.8834	0.25	0.03%
LDLc	rs514230	1	232925220	<i>IRF2BP2</i>	T	NA	0.9914	0.99	0%
LDLc	rs1367117	2	21117405	<i>APOB</i>	A	NA	0.8927	3.5x10 ⁻⁶	0.51%
LDLc	rs4299376	2	43926080	<i>ABCG5/8</i>	G	NA	0.9972	0.011	0.15%
LDLc	rs12916	5	74692295	<i>HMGCR</i>	C	NA	0.9644	2.7x10 ⁻⁵	0.41%
LDLc	rs6882076	5	156322875	<i>TIMD4</i>	C	NA	0.9439	0.81	0%
LDLc	rs3757354	6	16235386	<i>MYLIP</i>	C	NA	0.9981	3.8x10 ⁻⁴	0.30%
LDLc	rs1800562	6	26201120	<i>HFE</i>	G	NA	0.9965	0.12	0.06%
LDLc	rs3177928 ¹	6	32520413	<i>HLA</i>	A	NA	0.9919	0.38	0.01%
LDLc	rs9488822	6	116419586	<i>FRK</i>	A	NA	0.9252	0.038	0.10%
LDLc	rs1564348	6	160498850	<i>LPA</i>	C	NA	0.9986	0.013	0.15%
LDLc	rs12670798	7	21573877	<i>DNAH11</i>	C	NA	0.9994	0.34	0.02%
LDLc	rs2072183	7	44545705	<i>NPC1L1</i>	C	NA	0.7527	3.6x10 ⁻³	0.20%
LDLc	rs9987289	8	9220768	<i>PPP1R3B</i>	G	NA	0.9902	0.25	0.03%
LDLc	rs2081687	8	59551119	<i>CYP7A1</i>	T	NA	0.9977	0.54	0%
LDLc	rs2954029	8	126560154	<i>TRIB1</i>	A	NA	0.991	0.36	0.02%
LDLc	rs11136341	8	145115531	<i>PLEC1</i>	G	NA	0.9173	0.37	0.02%
LDLc	rs9411489 ²	9	135144821	<i>ABO</i>	T	NA	NA	NA	NA
LDLc	rs2255141	10	113923876	<i>GPAM</i>	A	NA	0.9989	0.072	0.08%
LDLc	rs174546	11	61326406	<i>FADS1-2-3</i>	C	NA	0.9999	2.4x10 ⁻⁷	0.63%
LDLc	rs964184	11	116154127	<i>APOA1</i>	G	NA	0.999	0.071	0.08%
LDLc	rs11220462	11	125749162	<i>ST3GAL4</i>	A	NA	0.9996	0.46	0.01%
LDLc	rs11065987	12	110556807	<i>BRAP</i>	A	NA	0.9994	7.0x10 ⁻³	0.17%
LDLc	rs1169288	12	119901033	<i>HNF1A</i>	C	NA	0.9675	0.094	0.07%
LDLc	rs8017377	14	23953727	<i>NYNRIN</i>	A	NA	0.9991	0.64	0%
LDLc	rs3764261	16	55550825	<i>CETP</i>	C	NA	0.9332	8.7x10 ⁻⁷	0.57%

LDLc	rs2000999	16	70665594	<i>HPR</i>	A	NA	0.9922	7.9×10^{-3}	0.17%
LDLc	rs7206971	17	42780114	<i>OSBPL7</i>	A	NA	0.99	5.3×10^{-3}	0.18%
LDLc	rs6511720	19	11063306	<i>LDLR</i>	G	NA	0.9972	1.3×10^{-3}	0.24%
LDLc	rs10401969	19	19268718	<i>CILP2</i>	T	NA	0.852	1.1×10^{-20}	2.0%
LDLc	rs4420638	19	50114786	<i>APOE</i>	G	NA	0.5938	1.7×10^{-25}	2.5%
LDLc	rs2902940	20	38524901	<i>MAFB</i>	A	NA	0.9967	0.25	0.03%
LDLc	rs6029526	20	39106032	<i>TOP1</i>	A	NA	0.993	0.44	0.01%

¹ Variants +/- 2 MB around this region were excluded from the calculations excluding known regions because of the high linkage disequilibrium in this part of the genome

² This SNP could not be imputed and so did not contribute to the allelic score for LDLc consisting of known variants only, but variants +/- 1 MB around it were still excluded from the calculations involving excluding known regions

³ RSQR imputation accuracy as calculated by MACH in the ALSPAC cohort

⁴ Proportion of variance explained (adjusted R²) in the ALSPAC cohort