

Effect Allele Frequency

	Gene	Effect allele	Source	Effect on LDL-C	Effect on TG	NFE† (%)	FINRISK‡ (%)	FCH Affected (%)	Enrichment Ratio§	P-value in affected individuals	P-value in probands	Heterozygotes (Affected)	Homozygotes (Affected)
rs1260326	GCKR	T	T.M.T.	+	+	41	36	47	1.3	0.001	0.0097	317 (125)	132 (47)
rs12748152	PIGV-NR0B2	T	C.J.W.	+	+	7.5	7.9	15	1.9	0.0015	0.0076	125 (57)	10 (7)
rs62020698	UBR1, CAPN3	T	I.S.	+	-	12	2.7	6.5	2.4	0.0017	0.00099	52 (24)	1 (1)
rs79598313	PIGV-NR0B2	T	I.S.	+	+	2.5	3.5	8.3	2.4	0.002	0.026	59 (29)	6 (5)
rs11563251	UGT1A1	T	C.J.W.	+	+	12	10	16	1.6	0.0032	0.042	129 (54)	13 (6)
rs116843064	ANGPTL4	A	I.S.	+	-	5	2.7	0.43	0.16	0.0032		21 (2)	0 (0)
rs964184	APOA1-C3-A4-A5	G	T.M.T.	+	+	16	14	23	1.6	0.004	0.04	208 (91)	18 (8)
rs3135506	APOA5	C	J.A.K.	+	+	7.9	6.2	11	1.8	0.0041	0.0049	105 (43)	6 (5)
rs72959041	RSPO3	A	I.S.	+	+	4.8	6.6	12	1.8	0.0044	0.034	94 (45)	5 (3)
rs13702	LPL	C	J.A.K.	-	-	34	26	18	0.69	0.0044	0.004	223 (72)	27 (6)
rs72836561	CD300LG	T	I.S.	-	+	2.9	2.9	6.4	2.2	0.0048	0.015	51 (28)	1 (1)
rs438811	APOE	T	I.S.	+	+	21	24	33	1.4	0.0051	0.1	296 (110)	53 (22)
rs439401	APOE-C1-C2	T	T.M.T.	-	-	40	28	20	0.71	0.0067	0.34	231 (68)	44 (13)
rs326	LPL	G	J.A.K.	-	-	34	26	19	0.71	0.0082	0.0038	227 (73)	29 (7)
rs77697917	DUSP3	T	I.S.	-	+	4.1	2.8	5.9	2.1	0.01	0.045	44 (24)	1 (1)
rs6818397	LRPAP1	T	C.J.W.	-	+	43	27	35	1.3	0.013	0.018	284 (104)	88 (30)
rs28933094	LIPC	T	J.A.K.	+	+	0.33	1.6	4.1	2.6	0.015	0.22	45 (19)	0 (0)
rs515135	APOB	T	I.S.	-	-	19	19	13	0.67	0.026	0.06	182 (50)	21 (5)
rs3856806	PPARG	T	J.A.K.	+	-	13	20	13	0.68	0.028	0.22	155 (53)	26 (5)
rs998584	VEGFA	A	C.J.W.	+	+	50	49	57	1.2	0.03	0.015	332 (125)	186 (70)
rs2126259	PPP1R3B	T	T.M.T.	-	-	8.4	16	11	0.68	0.032	0.46	144 (48)	8 (2)
rs2169387	PPP1R3B	A	I.S.	-	+	8.3	15	10	0.69	0.033	0.62	136 (45)	8 (2)
rs115849089	LPL	A	I.S.	-	-	15	11	6.7	0.63	0.038	0.047	95 (29)	4 (1)
rs59950280	LRPAP1	A	I.S.	+	+	31	23	30	1.3	0.039	0.14	270 (92)	65 (24)
rs6831256	LRPAP1	G	C.J.W.	+	+	40	35	42	1.2	0.043	0.11	327 (113)	116 (41)

rs1801177	LPL	A	J.A.K.	+	+	1.5	0.19	1.1	5.6	0.05	0.22	8 (5)	0 (0)
rs429358	APOE	C	J.A.K.	+	+	21	19	25	1.3	0.051	0.64	237 (93)	30 (11)
rs10102164	SOX17	A	C.J.W.	+	+	17	24	29	1.2	0.061	0.32	272 (112)	48 (13)
rs41279633	NPC1L1	T	I.S.	+	-	17	21	26	1.2	0.062	0.054	229 (88)	34 (17)
rs4420638	APOE-C1-C2	G	T.M.T.	+	+	18	28	34	1.2	0.064	0.99	279 (114)	64 (23)
			J.A.K.,										
rs7412	APOE	T	C.J.W.	-	+	11	4.7	8.1	1.7	0.074	0.044	96 (34)	3 (2)
rs4810479	PLTP	C	T.M.T.	-	+	28	26	32	1.2	0.075	0.28	280 (113)	44 (18)
rs182616603	MTHFD2L	T	I.S.	+	+	0.12	2.4	4.5	1.9	0.087	0.95	27 (15)	0 (0)
rs7225700	OSBPL7	T	T.M.T.	-	+	34	32	27	0.83	0.089	0.27	296 (113)	48 (6)
rs6120974	ERGIC3	C	I.S.	-	+	16	6.2	3.7	0.6	0.09	0.41	57 (15)	3 (0)
rs7640978	CMTM6	T	C.J.W.	-	-	12	8.6	5.1	0.6	0.092	0.45	75 (24)	0 (0)
rs1883711	MAFB	C	I.S.	+	+	3.6	6.2	8.9	1.4	0.099	0.3	71 (37)	2 (1)
rs11784833	GRINA,PLEC1	C	I.S.	+	+	40	39	45	1.2	0.1	0.12	328 (114)	120 (47)
rs7206971	OSBPL7	G	I.S.	+	+	52	49	55	1.1	0.1	0.41	352 (134)	148 (39)
rs11649653	CTF1	G	T.M.T.	-	-	40	42	37	0.87	0.1	0.59	319 (102)	121 (35)
rs662799	APOA5	G	J.A.K.	+	+	8.8	8.1	12	1.4	0.11	0.65	117 (52)	5 (1)
rs2072560	APOA5	T	J.A.K.	+	+	6.7	8.1	12	1.4	0.11	0.66	117 (52)	5 (1)
rs651821	APOA5	C	J.A.K.	+	+	7.1	8.1	12	1.4	0.11	0.66	117 (52)	5 (1)
rs314253	DLG4	C	C.J.W.	-	-	32	41	47	1.1	0.11	0.18	368 (136)	112 (41)
rs4942486	BRCA2	T	C.J.W.	+	+	49	43	37	0.87	0.11	0.059	319 (102)	98 (36)
rs328	LPL	G	J.A.K.	-	-	10	8.8	5.6	0.63	0.12	0.052	89 (26)	2 (0)
rs112875651	TRIB1	A	I.S.	-	-	38	39	34	0.86	0.13	0.5	304 (100)	83 (27)
rs2479409	PCSK9	G	T.M.T.	+	+	32	29	24	0.83	0.13	0.2	270 (91)	38 (11)
rs646776	CELSR2	C	I.S.	-	+	22	21	18	0.82	0.14	0.88	212 (70)	23 (6)
rs629301	SORT1	G	T.M.T.	-	+	22	22	18	0.81	0.14	0.86	206 (70)	29 (6)
rs2266788	APOA5	G	J.A.K.	+	+	9.5	8.4	12	1.4	0.15	0.74	117 (52)	5 (1)
rs6073958	PLTP	C	I.S.	-	+	22	18	22	1.2	0.15	0.15	211 (93)	17 (5)
rs55714927	DLG4	T	I.S.	-	-	19	26	31	1.2	0.15	0.43	243 (86)	51 (19)

rs12678919	LPL	G	T.M.T.	-	-	13	8.6	5.6	0.65	0.15	0.058	88 (26)	2 (0)
rs1564348	LPA	C	T.M.T.	+	-	17	14	18	1.3	0.16	0.85	193 (76)	18 (3)
rs10889348	DOCK7	T	I.S.	-	-	32	27	22	0.84	0.16	0.92	237 (86)	33 (9)
rs2073547	NPC1L1	G	C.J.W.	+	-	17	34	38	1.1	0.17	0.16	303 (103)	92 (38)
rs7248104	INSR	A	C.J.W.	-	-	44	44	39	0.89	0.17	0.66	336 (109)	101 (37)
rs187429064	TM6SF2	G	I.S.	-	-	1.3	5.6	3.7	0.67	0.17	0.49	46 (15)	2 (0)
rs2328223	SNX5	C	C.J.W.	+	+	24	21	25	1.2	0.18	0.51	251 (86)	38 (16)
rs2131925	ANGPTL3	G	T.M.T.	-	-	32	26	22	0.85	0.18	0.77	240 (85)	30 (9)
rs9988450	DOCK7	T	I.S.	-	-	32	26	22	0.85	0.18	0.79	240 (85)	30 (9)
rs2710642	EHBP1	G	C.J.W.	-	+	38	39	44	1.1	0.19	0.29	311 (96)	132 (55)
rs217386	NPC1L1	A	T.M.T.	-	+	43	32	27	0.87	0.19	0.23	281 (102)	56 (13)
rs3850634	ANGPTL3	G	T.M.T.	-	-	30	26	22	0.85	0.19	0.77	240 (85)	30 (9)
rs11887534	ABCG5/G8	C	J.A.K.	-	-	7.7	9.1	6.2	0.68	0.19	0.22	90 (29)	0 (0)
rs114067101	HLA-area	G	I.S.	+	+	5.8	3.3	5	1.5	0.2	0.83	13 (4)	0 (0)
rs72875462	ABCG8	A	I.S.	-	-	6.4	9	6.2	0.69	0.2	0.23	89 (29)	0 (0)
rs2920503	PPARG	T	I.S.	+	+	28	32	37	1.1	0.21	0.63	293 (104)	64 (27)
rs5882	CETP	G	J.A.K.	-	-	32	38	42	1.1	0.22	0.16	329 (124)	100 (36)
rs11136341	PLEC1	G	T.M.T.	+	+	41	37	41	1.1	0.22	0.27	316 (112)	107 (41)
rs1129555	GPAM	A	T.M.T.	+	-	31	33	29	0.88	0.22	0.32	280 (105)	57 (15)
rs117492019	ZNF274	T	I.S.	-	-	20	16	13	0.82	0.22	0.022	146 (50)	13 (4)
rs56130071	DNAH11	C	I.S.	+	+	19	21	24	1.2	0.23	0.62	231 (80)	39 (15)
rs719726	RSPO3	C	C.J.W.	+	-	48	44	40	0.9	0.23	0.43	297 (98)	124 (42)
rs12670798	DNAH11	C	T.M.T.	+	+	22	24	28	1.2	0.24	0.66	260 (89)	47 (20)
rs11164654	EVI5	T	I.S.	-	-	19	22	26	1.2	0.24	0.49	223 (75)	36 (22)
rs38855	MET	G	C.J.W.	-	+	48	46	42	0.91	0.24	0.79	305 (99)	148 (48)
rs3757354	MYLIP	T	T.M.T.	-	+	20	26	29	1.1	0.25	0.13	265 (94)	50 (21)
rs2030746	LOC84931	T	C.J.W.	+	-	41	35	39	1.1	0.26	0.86	309 (108)	92 (37)
rs340839	PROX1	A	I.S.	+	-	50	38	42	1.1	0.26	0.14	330 (117)	122 (40)
rs2230806	ABCA1	T	J.A.K.	+	-	27	22	19	0.86	0.26	0.28	190 (77)	18 (6)

rs4299376	ABCG5/8	G	T.M.T.	+	+	33	21	24	1.1	0.27	0.0094	235 (94)	27 (10)
rs1495743	NAT2	G	T.M.T.	+	+	24	25	22	0.88	0.27	0.12	257 (89)	33 (7)
rs10761731	JMJD1C	T	T.M.T.	+	-	45	38	34	0.9	0.28	0.18	321 (116)	91 (22)
rs77542162	ABCA6	G	I.S.	+	-	1.7	0.54	0.21	0.39	0.28		11 (1)	0 (0)
rs138570705	FRMD5	A	I.S.	-	-	3.3	1.8	2.8	1.6	0.29	0.77	28 (13)	0 (0)
rs2954029	TRIB1	T	T.M.T.	-	-	45	46	43	0.92	0.29	0.64	327 (119)	129 (40)
rs1121980	FTO	A	C.J.W.	+	+	45	43	39	0.91	0.29	0.096	326 (107)	87 (38)
rs731839	PEPD	G	C.J.W.	-	+	33	35	31	0.89	0.29	0.95	298 (103)	64 (21)
rs7759633	LPA	A	I.S.	+	-	14	9.3	12	1.3	0.3	0.74	130 (51)	7 (2)
rs9638182	MLXIPL	G	I.S.	+	-	19	17	15	0.85	0.3	0.69	176 (50)	32 (9)
rs186696265	LPA	T	I.S.	+	-	1.1	1.6	2.5	1.6	0.31	0.67	29 (7)	1 (0)
rs3816873	MTTP	C	J.A.K.	-	+	26	19	22	1.2	0.31	0.67	198 (79)	25 (12)
rs4719841	MIR148A	G	C.J.W.	-	-	40	37	40	1.1	0.31	0.84	285 (97)	101 (45)
rs1358980	VEGFA	T	I.S.	+	+	49	47	50	1.1	0.32	0.052	348 (128)	144 (53)
rs405509	APOE	T	J.A.K.	+	-	50	45	42	0.93	0.32	0.53	326 (115)	117 (38)
rs268	LPL	G	J.A.K.	+	+	2	2.2	3.2	1.5	0.33	0.9	37 (15)	0 (0)
rs4253776	PPARA	G	C.J.W.	+	+	12	7.9	6	0.76	0.33	0.86	81 (28)	1 (0)
rs3177928	HLA	A	T.M.T.	+	+	16	21	24	1.1	0.34	0.84	240 (89)	31 (11)
rs7811265	MLXIPL	G	T.M.T.	+	-	19	17	15	0.86	0.34	0.73	175 (50)	33 (9)
rs10195252	COBLL1	C	T.M.T.	-	-	46	34	38	1.1	0.36	0.54	298 (122)	80 (27)
rs1553318	TIMD4	G	I.S.	-	-	36	32	35	1.1	0.36	0.38	291 (97)	86 (34)
rs17585887	CITED2	T	I.S.	+	+	40	50	46	0.93	0.36	0.74	309 (121)	169 (48)
rs8077889	MPP3	C	C.J.W.	+	+	26	21	23	1.1	0.38	0.77	222 (80)	42 (14)
rs645040	MSL2L1	G	T.M.T.	-	-	25	14	12	0.84	0.38	0.052	146 (52)	7 (2)
rs2954022	TRIB1	A	T.M.T.	-	-	45	47	44	0.94	0.4	0.7	331 (123)	134 (41)
rs909802	TOP1	C	T.M.T.	-	-	55	46	43	0.94	0.41	0.65	349 (129)	128 (36)
rs11613352	LRP1	T	T.M.T.	+	+	20	23	25	1.1	0.42	0.35	231 (78)	39 (20)
rs61352607	LRP1	T	I.S.	+	+	20	23	25	1.1	0.43	0.34	231 (78)	39 (20)

rs2068888	CYP26A1	A	T.M.T.	-	-	49	47	49	1.1	0.47	0.84	318 (109)	159 (61)
rs4722551	MIR148A	C	C.J.W.	+	-	18	23	21	0.91	0.48	0.83	232 (71)	41 (13)
rs11648003	HPR	G	I.S.	+	+	23	22	24	1.1	0.49	0.42	203 (83)	41 (15)
rs5763662	MTMR3	T	C.J.W.	+	-	2.4	3.1	2.4	0.75	0.49	0.12	30 (11)	1 (0)
rs1800562	HFE	A	T.M.T.	-	-	5.1	3.8	4.7	1.2	0.5	0.35	64 (22)	0 (0)
rs12027135	LDLRAP1	A	T.M.T.	-	-	47	46	49	1.1	0.5	0.23	328 (115)	142 (56)
rs1367117	APOB	A	T.M.T.	+	+	32	28	30	1.1	0.52	0.32	256 (95)	64 (22)
rs1169314	HNF1A	G	I.S.	+	+	33	31	33	1.1	0.52	0.061	284 (104)	59 (25)
rs7205804	CETP	A	T.M.T.	-	-	43	42	44	1.1	0.54	0.77	344 (120)	124 (44)
rs3890182	ABCA1	A	J.A.K.	-	-	12	11	9.4	0.89	0.55	0.23	114 (42)	5 (1)
rs193042029	TM4SF5	G	I.S.	-	-	0.37	3	2.4	0.78	0.55	0.93	37 (11)	1 (0)
rs2929282	FRMD5	T	T.M.T.	-	-	5.1	4.9	6	1.2	0.56	0.78	54 (22)	5 (3)
rs3843482	HMGCR	G	I.S.	+	+	38	44	42	0.95	0.56	0.24	342 (116)	111 (37)
rs2943645	IRS1	C	T.M.T.	+	-	37	37	39	1.1	0.57	0.55	297 (105)	101 (38)
rs2332328	NYNRIN	T	T.M.T.	+	-	51	38	40	1	0.6	0.24	316 (106)	99 (40)
rs267733	ANXA9-CERS2	G	C.J.W.	-	+	15	14	13	0.9	0.6	0.66	155 (58)	12 (1)
rs17404153	ACAD11	T	C.J.W.	-	+	12	18	16	0.92	0.61	0.3	195 (66)	19 (5)
rs1799816	INSR	T	J.A.K.	+	+	0.93	0.64	0.43	0.67	0.61		4 (2)	0 (0)
rs10822145	JMJD1C	T	I.S.	+	-	51	48	46	0.96	0.62	0.46	345 (131)	151 (42)
rs2412710	CAPN3	A	T.M.T.	-	-	3.5	0.26	0.43	1.7	0.63	0.38	5 (2)	0 (0)
rs3780181	VLDLR	G	C.J.W.	-	+	5.6	5.3	6	1.1	0.63	0.94	61 (24)	4 (2)
rs59379014	ST3GAL4	T	C.J.W.	+	-	6.3	8	7	0.88	0.63	0.55	88 (31)	1 (1)
rs3198697	PDXDC1	T	C.J.W.	+	-	42	41	42	1	0.64	0.28	308 (115)	118 (38)
rs183130	CETP	T	J.A.K.	-	-	30	28	29	1.1	0.65	0.36	274 (98)	58 (20)
rs247616	CETP	T	T.M.T.	-	-	30	28	29	1.1	0.65	0.36	274 (98)	58 (20)
rs247617	CETP	A	I.S.	-	-	30	28	29	1.1	0.65	0.37	274 (98)	58 (20)
rs821840	CETP	G	I.S.	-	-	29	28	29	1.1	0.65	0.37	274 (98)	58 (20)
rs4530754	CSNK1G3	A	C.J.W.	+	-	61	50	52	1	0.65	0.7	328 (122)	181 (52)
rs4307732	ST3GAL4	A	I.S.	+	-	9.4	16	15	0.93	0.65	0.48	176 (56)	14 (7)

rs112374545	LDLR	T	I.S.	-	-	12	11	9.8	0.92	0.65	0.64	114 (42)	5 (2)
rs6511720	LDLR	T	T.M.T.	-	-	11	11	9.8	0.92	0.65	0.64	115 (42)	5 (2)
rs6882076	TIMD4	T	T.M.T.	-	-	36	33	34	1	0.66	0.35	287 (95)	86 (33)
rs5756931	PLA2G6	C	T.M.T.	-	-	41	39	38	0.96	0.66	0.46	327 (112)	76 (32)
rs4665710	APOB	A	I.S.	-	-	22	26	27	1	0.69	0.98	271 (96)	32 (16)
rs419132	HLA-area	G	I.S.	+	+	30	16	15	0.94	0.69	0.55	174 (61)	16 (5)
rs2000999	HPR	A	T.M.T.	+	+	19	19	21	1.1	0.7	0.38	194 (72)	27 (12)
rs58542926	TM6SF2	T	I.S.	-	-	8.1	5.9	5.3	0.9	0.7	0.28	62 (25)	3 (0)
rs1042034	APOB	C	T.M.T.	-	-	21	26	27	1	0.71	0.96	273 (96)	33 (16)
rs79588679	GATA6	T	I.S.	-	+	16	17	16	0.94	0.71	0.54	174 (69)	14 (3)
rs34894639	MSL2L1,PCCB	T	I.S.	-	-	26	19	18	0.94	0.71	0.37	170 (61)	14 (6)
rs11591147	PCSK9	T	C.J.W., J.A.K.	-	-	3.5	4	3.4	0.86	0.71	0.93	49 (14)	1 (1)
rs174551	FADS1	C	I.S.	-	+	32	40	39	0.97	0.72	0.62	296 (96)	97 (36)
rs2540948	CEP68	C	I.S.	+	-	37	32	31	0.97	0.73	0.99	292 (107)	66 (18)
rs10401969	CILP2	C	T.M.T.	-	-	7.3	5.8	5.3	0.91	0.73	0.26	61 (25)	4 (0)
rs1801689	APOH-PRXCA	C	C.J.W.	+	-	3.3	0.85	1.1	1.3	0.74	0.83	16 (5)	0 (0)
rs649129	ABO	T	T.M.T.	+	-	22	20	19	0.96	0.74	0.92	132 (45)	13 (6)
rs73001065	CILP2	C	I.S.	-	-	6.4	5.8	5.3	0.92	0.74	0.27	61 (25)	3 (0)
rs12310367	ZNF664	G	T.M.T.	-	-	38	28	29	1	0.75	0.27	268 (92)	56 (21)
rs140244541	FAM117B	A	I.S.	-	-	16	13	12	0.94	0.75	0.86	129 (49)	10 (4)
rs11776767	PINX1	C	T.M.T.	-	-	41	31	30	0.97	0.76	0.74	286 (99)	61 (20)
rs3902941	MAFB	G	T.M.T.	-	-	31	26	25	0.97	0.77	0.82	267 (93)	35 (12)
rs550057	ABO	T	I.S.	+	+	28	31	30	0.97	0.78	0.94	269 (96)	53 (22)
rs11220462	ST3GAL4	A	T.M.T.	+	+	12	19	18	0.96	0.78	0.28	211 (70)	15 (8)
rs9297994	CYP7A1	G	I.S.	+	+	36	38	39	1	0.79	0.93	294 (104)	104 (39)
rs1169288	HNF1A	C	J.A.K., T.M.T.	+	+	35	39	40	1	0.8	0.09	317 (119)	84 (34)
rs586178	LDLRAP1	C	I.S.	+	+	45	47	46	0.98	0.8	0.58	265 (87)	125 (46)
rs12916	HMGCR	C	T.M.T.	+	+	40	46	45	0.98	0.8	0.29	353 (122)	122 (44)

rs2297374	LPA	T	C.J.W.	-	-	40	34	33	0.98	0.8	0.66	302 (93)	89 (30)
rs2255811	GPR85	G	I.S.	-	+	28	24	23	0.97	0.8	0.71	211 (78)	32 (14)
rs1250229	FN1	T	C.J.W.	-	-	25	20	21	1	0.81	0.35	243 (82)	23 (7)
rs174583	FADS1-2-3	T	T.M.T.	-	+	34	42	41	0.98	0.82	0.69	314 (98)	111 (47)
rs1030431	CYP7A1	A	T.M.T.	+	+	35	31	30	0.98	0.82	0.45	266 (89)	62 (24)
rs364585	SPTLC3	A	C.J.W.	-	+	37	34	33	0.98	0.83	0.58	315 (110)	64 (23)
rs442177	KLHL8	G	T.M.T.	-	-	40	48	49	1	0.84	0.56	332 (114)	157 (57)
rs1077835	LIPC	G	I.S.	+	+	22	27	27	1	0.85	0.72	257 (95)	44 (16)
rs514230	IRF2BP2	A	T.M.T.	-	-	49	43	44	1	0.87	0.61	326 (115)	147 (45)
rs174529	FADS1	C	I.S.	-	+	36	42	43	1	0.89	0.61	317 (100)	117 (50)
rs1321257	GALNT2	G	T.M.T.	+	+	39	43	43	0.99	0.89	0.51	329 (117)	132 (42)
rs769452	APOE	C	J.A.K.	+	+	0.36	0.58	0.64	1.1	0.9	0.46	6 (3)	0 (0)
rs2618568	SNX5	C	I.S.	+	+	44	37	38	1	0.9	0.15	319 (113)	88 (32)
rs9686661	MAP3K1	T	T.M.T.	+	+	20	14	15	1	0.91	0.18	150 (57)	8 (6)
rs10864728	GALNT2	A	I.S.	+	+	39	43	43	0.99	0.91	0.48	326 (116)	129 (42)
rs2807834	MOSC1	T	T.M.T.	-	-	30	29	29	1	0.92	0.86	276 (91)	69 (23)
rs8023503	LIPC	T	J.A.K.	-	+	1.4	2	1.9	0.95	0.92	0.89	22 (8)	0 (0)
rs11153594	FRK	T	T.M.T.	-	-	41	40	41	1	0.94	0.47	319 (121)	108 (34)
rs1832007	AKR1C4	G	C.J.W.	-	-	12	13	13	1	0.95	0.47	142 (47)	17 (7)
rs261342	LIPC	G	T.M.T.	+	+	22	23	23	0.99	0.96	0.83	222 (80)	39 (13)
rs10490626	INSIG2	A	C.J.W.	-	-	8.2	6.7	6.6	0.99	0.96	0.8	78 (27)	3 (2)
rs11065987	BRAP	G	T.M.T.	-	+	44	38	38	1	0.97	0.71	299 (106)	94 (35)
rs2035403	KLHL8	G	I.S.	+	+	38	40	40	1	0.98	0.94	318 (110)	108 (37)
rs11621792	NYNRIN	T	I.S.	+	-	49	36	36	1	0.98	0.22	267 (91)	79 (33)
rs12594375	LIPC	A	J.A.K.	-	+	1.2	1.9	1.9	1	0.99	0.91	25 (9)	0 (0)
rs2247056	HLA	T	T.M.T.	-	-	21	23	23	1	0.99	0.59	239 (71)	41 (19)
rs174546	FADS1-2-3	T	T.M.T.	-	+	32	42	42	1	0.99	0.54	317 (99)	113 (48)