Supplementary Table S1: Genome-wide Single Variant Two-point Suggestive SNPs (excluding Chromosome 11)

CHR	rsID	POS	LOD	HLOD	ALPHA	FUNCTION	GENE
8	rs10092658	130980472	2.4567	2.4567	1.00	intergenic	*FAM49B*, *MIR5194*
7	rs1882077	37436929	2.4312	2.4312	1.00	intronic	*ELMO1*
7	rs6462611	35576505	2.4145	2.4145	1.00	intergenic	*LOC401324*, *HERPUD2*
7	rs1882078	37436975	2.3921	2.3921	1.00	intronic	*ELMO1*
2	rs13420028	133188106	2.2996	2.2996	1.00	intronic	*GPR39*
10	rs12256826	67974590	2.1979	2.2933	0.85	intronic	*CTNNA3*
7	rs1962235	36972188	2.2301	2.2672	0.90	intronic	*ELMO1*
7	rs4720262	37888627	2.2539	2.2539	1.00	UTR5	*NME8*
7	rs2541090	37308230	2.0452	2.1395	0.85	intronic	*ELMO1*
7	rs1079866	41470093	2.0387	2.0916	0.85	intergenic	*LINC01449*, *INHBA*
7	rs7808629	36702492	2.0605	2.0605	1.00	intronic	*AOAH*
6	rs2842899	132859609	1.9342	2.0434	0.80	exonic	*TAAR9*
4	rs17610371	100712656	2.0262	2.0416	0.90	intergenic	*MTTP*, *DAPP1*
6	rs41265385	170068086	2.0210	2.0210	1.00	exonic	*WDR27*
7	rs1894910	36777888	1.6146	1.9841	0.70	intergenic	*AOAH, ELMO1*
7	rs4077337	36729324	1.7253	1.9793	0.80	intronic	*AOAH*
6	rs58858262	87500445	1.9766	1.9766	1.00	intergenic	*SNHG5*, *HTR1E*
1	rs61787373	110888948	1.9658	1.97366	0.95	exonic	*RBM15*
7	rs2011974	32611392	1.9375	1.9427	0.95	intronic	*AVL9*
1	rs12742611	18475260	1.9418	1.9418	1.00	intronic	*IGSF21*
4	rs2010907	189540683	1.9089	1.9105	0.95	intergenic	*LINC01060*, *LINC01262*

Table showing the genome-wide suggestive SNPs from the single variant two-point linkage analysis sorted by heterogeneity LOD score (HLOD), excluding those found on chromosome 11 (see Table 1). CHR = chromosome position, POS = position in base pairs, LOD = cumulative LOD score across all 56 families. The significance threshold is 3.3 and the suggestive threshold is 1.9, as recommended by Lander and Kruglyak. Gene annotations were performed by ANNOVAR.

Supplementary Table S2: Genome-wide Multipoint Suggestive Variants

CHR	rsID	POSITION	LOD	HLOD	ALPHA	FUNCTION	GENE
20	rs34323943	52192637	-0.2125	3.0480	0.50	intronic	*ZNF217*
20	rs2800999	51722623	-0.9340	2.8380	0.45	intronic	*TSHZ2*
20	rs6022758	52425620	-0.9170	2.7930	0.45	intronic	*ZNF217, SUMO1P1*
20	D20S480	51857207	-0.9935	2.7780	0.45	intronic	*TSHZ2*
20	rs856427	51251485	-1.3910	2.6320	0.45	intronic	*LINC01524*
20	rs6013382	50702633	-1.4470	2.5290	0.40	intronic	*ZFP64*
20	rs4809959	52785859	-1.4460	2.3880	0.40	intronic	*CYP24A1*
20	rs2022371	53196113	-1.4710	2.3750	0.40	intronic	*DOK5*
20	rs149617699	49989435	-1.5750	2.3170	0.40	intronic	*KCNG1*, *NFATC2*
20	rs6092326	55116737	-1.7410	2.3000	0.40	intronic	*FAM209B*, *TFAP2C*
20	rs2426689	55369594	-1.6940	2.2590	0.40	intronic	*TFAP2C*, *BMP7*
20	rs731803	54507813	-2.0820	2.2310	0.40	intronic	*LINC01441*, *CBLN4*
20	rs6024653	54751363	-2.0210	2.2310	0.40	intronic	*CBLN4*, *MC3R*
20	rs3852925	54067599	-2.3605	2.1500	0.40	intronic	*LINC01441*, *CBLN4*
11	rs10766542	19352288	-0.6610	2.0730	0.45	intergenic	*E2F8*, *NAV2*
11	rs874426	19569563	-0.4110	2.0070	0.45	intronic	*NAV2*

Table showing the genome-wide suggestive SNPs from the multipoint linkage analysis sorted by heterogeneity LOD score (HLOD). CHR = chromosome position, POSITION = position in base pairs, LOD = cumulative LOD score across all 56 families. The significance threshold is 3.3 and the suggestive threshold is 1.9, as recommended by Lander and Kruglyak. Gene annotations were performed by ANNOVAR.