

Table 5. Single marker transmission and conditional analyses in SLE trios from the US and UK

Marker	Position ¹	Allele ²	T ³	U ³	T/U ³	χ^2	P^4	P^5 conditional on Group 1 variants (rs2070197)	P conditional on Group 1 (rs2070197) and Group 2 (rs2004640) variants	P conditional on Group 1 (rs2070197), Group 2 (rs2004640), and Group 3 (rs10954213) variants
rs7780972	128,113,113	C	88	73	1.2	1.4	0.237	0.03	0.14	0.25
rs9656375	128,115,191	G	213	210	1.0	0.0	0.884	0.87	0.65	0.58
rs4731523	128,124,227	A	241	211	1.1	2.0	0.158	0.36	0.32	0.40
rs6948542	128,141,463	G	184	166	1.1	0.9	0.336	0.29	0.27	0.37
rs1495461	128,145,691	G	260	220	1.2	3.3	0.068	0.37	0.59	0.45
rs960633	128,154,711	T	257	209	1.2	4.9	0.026	0.54	0.75	0.56
rs6968225	128,157,557	G	106	105	1.0	0.0	0.945	0.48	0.08	0.19
rs729302	128,162,910	A	270	195	1.4	12.1	5.0×10^{-4}	0.0024	0.56	0.82
rs4728142	128,167,917	A	363	257	1.4	18.1	2.1×10^{-5}	0.0054	0.0096	0.20
rs3807135	128,171,568	C	298	241	1.2	6.0	0.0141	0.28	0.0008	0.31
rs2004640	128,172,251	T	344	233	1.5	21.4	3.8×10^{-6}	0.0019	-	-
rs752637	128,173,371	G	297	238	1.2	6.5	0.011	0.28	0.0010	0.14
rs1874328	128,179,054	T	280	275	1.0	0.0	0.832	0.47	0.04	0.94
Exon 6 indel	128,181,324-54	A	337	294	1.1	2.9	0.087	0.25	0.01	NA
rs2070197	128,182,950	C	205	111	1.8	28.0	1.2×10^{-7}	-	-	-
rs10954213	128,183,377	A	282	226	1.2	6.2	0.013	0.14	0.0089	-
rs11770589	128,183,438	G	338	288	1.2	4.0	0.046	0.16	0.01	NA
rs10954214	128,183,583	T	281	232	1.2	4.7	0.031	0.14	0.02	NA
rs10488630	128,187,899	G	280	263	1.1	0.5	0.466	0.42	0.11	0.90
rs10488631	128,188,133	C	223	125	1.8	27.6	1.5×10^{-7}	1.00	NA ⁶	NA
rs2280714	128,188,675	A	268	219	1.2	4.9	0.026	0.18	0.0078	NA
rs3847098	128,189,099	G	211	199	1.1	0.4	0.553	0.28	0.06	0.83
rs11761242	128,189,556	T	25	20	1.3	0.6	0.456	0.03	0.06	0.06
rs12539741	128,190,755	T	222	125	1.8	27.1	1.9×10^{-7}	1.00	NA	NA
rs17166351	128,191,754	C	336	290	1.2	3.4	0.066	0.17	0.005	NA
rs696612	128,192,475	C	153	124	1.2	3.0	0.081	0.0078	0.825	0.29

¹ Position in the HG17 assembly of the Human Genome.² The overtransmitted allele.³ Number of transmitted alleles (T), untransmitted alleles (U), and transmitted to untransmitted allele ratio (T/U).⁴ Nominal P value for association to SLE.⁵ P value for the association to SLE under the model that the indicated markers fully explain the association to SLE, as determined by conditional logistic regression.⁶ NA indicates that the association to SLE cannot be calculated because it is statistically indistinguishable from the proposed model.