

Supplementary Table 2 LOD scores and target genes.

(a) LOD scores on chromosome 1q23 as calculated for model 1 and 2 in the genome wide linkage analysis. For further details see text and **Supplementary Methods** online.

Marker	Genetic(cM)	Sequence(Mb)	θ						
			0.0	0.01	0.03	0.05	0.07	0.1	0.15
D1S551	113.7	82.6	-	0.63	1.02	1.15	1.21	1.22	1.15
GATA124C08	129.4	?	-	0.75	1.12	1.23	1.27	1.26	1.16
GATA133A08	137.6	106.0	0.04	0.04	0.05	0.06	0.06	0.05	0.04
D1S534	151.9	119.3	-	-1.14	-0.68	-0.48	-0.35	-0.23	-0.11
D1S442	154.7	143.1	0.00	0.00	0.00	0.00	0.00	0.00	0.00
D1S498	155.9	148.1	2.67	2.63	2.54	2.45	2.35	2.20	1.94
D1S2346	158.8	150.0	2.02	1.97	1.88	1.78	1.69	1.55	1.33
D1S305	159.3	151.0	2.80	2.75	2.65	2.55	2.45	2.29	2.01
D1S1153	161.1	152.1	2.80	2.75	2.65	2.55	2.45	2.29	2.01
D1S2624	162.6	153.4	-	0.46	0.86	1.00	1.07	1.10	1.05
D1S2635	165.6	156.0	-	1.05	1.42	1.54	1.58	1.57	1.46
D1S1679	170.8	159.1	-	0.93	1.31	1.44	1.49	1.49	1.40
D1S1589	192.0	171.0	0.89	0.88	0.85	0.82	0.79	0.74	0.65
D1S518	202.2	184.2	-	-4.28	-2.66	-1.92	-1.45	-0.98	-0.52

For model 1 (assumes no common ancestor for the parents)

Marker	Genetic(cM)	Sequence(Mb)	θ						
			0.0	0.01	0.03	0.05	0.07	0.1	0.15
D1S551	113.7	82.6	-	-0.32	0.35	0.63	0.79	0.91	0.95
GATA124C08	129.4	?	-	0.22	0.44	0.71	0.85	0.95	0.96
GATA133A08	137.6	106.0	-1.25	-0.94	-0.64	-0.47	-0.36	-0.25	-0.13
D1S534	151.9	119.3	-	-2.08	-1.33	-0.98	-0.75	-0.52	-0.29
D1S442	154.7	143.1	-1.25	-0.94	-0.65	-0.50	-0.39	-0.29	-0.18
D1S498	155.9	148.1	3.12	3.06	2.94	2.81	2.69	2.50	2.17
D1S2346	158.8	150.0	2.47	2.40	2.28	2.15	2.03	1.85	1.56
D1S305	159.3	151.0	3.38	3.32	3.18	3.04	2.90	2.69	2.33
D1S1153	161.1	152.1	3.38	3.32	3.18	3.04	2.90	2.69	2.33
D1S2624	162.6	153.4	-	1.02	1.39	1.49	1.52	1.50	1.38
D1S2635	165.6	156.0	-	1.61	1.95	2.03	2.04	1.98	1.79
D1S1679	170.8	159.1	-	-0.01	0.66	0.94	1.09	1.20	1.22
D1S1589	192.0	171.0	1.34	1.31	1.25	1.18	1.12	1.03	0.88
D1S518	202.2	184.2	-	-5.24	-3.34	-2.44	-1.86	-1.29	-0.72

For model 2 (assumes parents are second degree cousins)

(b) List of target genes that were sequenced without evidence of mutations leading to altered protein sequences.

Sequenced genes	GenBank accession number
<i>VPS45A</i>	NM_007259
<i>S100A1</i>	NM_001007636
<i>S100A2</i>	NM_005978
<i>S100A3</i>	NM_002960
<i>S100A4</i>	NM_019554, NM_002961
<i>S100A5</i>	NM_002962
<i>S100A6</i>	NM_014624
<i>S100A7</i>	NM_002963
<i>S100A8</i>	NM_002964
<i>S100A9</i>	NM_002965
<i>S100A10</i>	NM_002966
<i>S100A11</i>	NM_005620
<i>S100A12</i>	NM_005621
<i>IL6R</i>	NM_000565
<i>PIAS3</i>	NM_006099
<i>PBXIP1 (HPIP)</i>	AF221521
<i>Rab13</i>	NM_002870
<i>Rab25</i>	NM_020387
<i>SNAPAP</i>	NM_012437