Supplementary Table S3: LOD Scores for Additional Candidate Genes/Genomic Locations

		Recombination Fraction/LOD Score						
Candidate gene/genomic loc.	**Marker**	**0.00**	**0.01**	**0.05**	**0.10**	**0.20**	**0.30**	**0.40**
CA4	CA4-STR-1	-16.1396	-7.2466	-3.9453	-2.4298	-1.0481	-0.4042	-0.0938
CA4	CA4-STR-2	-14.8167	-6.8893	-3.4888	-2.0404	-0.8074	-0.2853	-0.0597
FSCN2	FSCN2-STR-1	-10.2303	-5.9665	-3.1720	-1.9168	-0.7914	-0.2876	-0.0617
FSCN2	FSCN2-STR-2	-10.2030	-7.0746	-3.8230	-2.3281	-0.9728	-0.3580	-0.0779
GUCA1B	GUCA1B-STR-1	-infinity	-3.7201	-1.7379	-0.9814	-0.3766	-0.1393	-0.0343
IMPDH1	IMPDH1-STR-1	-infinity	-9.4379	-4.9140	-3.0908	-1.4227	-0.5750	-0.1367
NRL	NRL-STR-1	-infinity	-3.4476	-1.5932	-0.8507	-0.2586	-0.0553	-0.0036
PRPF3	PRPF3-STR-2	-infinity	-2.7440	-0.2259	0.6168	1.0448	0.8895	0.4306
PRPF8	PRPF8-STR-2	-infinity	-2.7662	-0.2463	0.5986	1.0314	0.8806	0.4260
PRPF31	PRPF31-STR-2	-infinity	-1.4520	-0.3146	0.1030	0.3375	0.2879	0.1168
RHO	RHO-STR-1	-infinity	-10.5476	-5.2580	-3.0978	-1.2178	-0.4109	-0.0793
ROM1	ROM1-STR-1	-infinity	-4.0436	-2.0375	-1.2449	-0.5518	-0.2238	-0.0549
RP1	RP1-STR-1	-infinity	-12.2779	-6.2395	-3.8008	-1.6446	-0.6434	-0.1521
RP9	RP9-STR-1	-infinity	-6.5735	-2.7382	-1.3473	-0.2940	-0.0082	0.0189
TOPORS	RP31-STR-1	-infinity	-10.4520	-5.0824	-2.9619	-1.1633	-0.4059	-0.0850
RP33	RP33-STR-1	-infinity	-1.4520	-0.3146	0.1030	0.3372	0.2860	0.1135
SEMA4A	SEMA4A-STR-2	-infinity	-12.3739	-6.3657	-3.8983	-1.6862	-0.6517	-0.1508

STRs for which primers were designed (Supplementary Table S2) and are not reported were not informative in the pedigree (i.e. they were homozygous in the two affected founders)