Supplementary Table 1: Markers and primers used for finemapping

Chr	Marker	Gen pos [*]	Phys pos [†]	Forward primer sequence	Reverse primer sequence
2p	D2S2584	1.95	0.17	TGCAGATTAGACCTCTGTAACACAC	TTCTAGATCTCCCCAGAAAATACCT
2p	D2S323	4.52	2.11	TACAGAAAAGGTTGTCTGCTACACC	CCATAGTGACTTCAGACCATTGATT
2p	D2S319	7.60	3.43	CAGACCATGACAGGCTATGTGTA	GGTTTGAGAGATGTTAGTCAAAGGA
2p	D2S304	10.64	4.67	TGTCCAGAGAACAGAAGCAAGA	CCCAGTCTCCATAATCACATCA
2p	D2S281	15.19	6.66	CTGTGCACCTTGTTCTATTCCTAAT	CTACCCTTCATAATCACAGGAGCTA
2p	D2S1329	19.11	7.85	CTCAAATACCAGGAATCTCATTCAG	TAGAGTGGAAGTCTTGCTGTTTTTC
2p	D2S2164	20.00	8.23	AACCACTCTCCTCTGTCTCTGTCT	AGAGAGCCATTACAGATTCACTGAC
2p	D2S2326	22.73	8.76	AGTCCTTGTCACATTGATGAACC	TCTCTTGGATTTAAGGAAGGAGGT
2p	D2S423	25.44	9.94	GTTCCACTCAAGCATAGATGAGC	TGCCTGAATTTCTCCCATTC
2p	D2S2377	29.66	11.80	GCCATATATTACGTAACACCCTTAGC	ACAGTAATTCAGGTCAGCAAGAATG
2p	D2S262	30.23	11.90	GTGGTAATGCTATCCAGTTATGAGC	GTTCACTTGTTTATCTGCTGACCTT
2p	D2S2267	34.47	13.74	TGATGTGTCCTTTCTGAAGCTG	CTCATAGCTTTACTTAATGGGCAAG
2q	Clen55	159.79	150.03	CCTGGACCCAGCTATGCTCATT	AAGGAAGATGAAAGGACAAAGAGGT
2q	Clen53	168.10	160.45	GGGTCCTGTTTAGACTAGAGATACA	CCGCCTTCTATCTTTCTTAATTGCT
2q	Clen46	177.43	171.39	GAGGCAGAGTGCAGTCTTTTGTGTT	TGTGAAAGGGTAAACCAACCTGGAT
2q	Clen45	179.52	173.38	ATCGATTTAGGGTTAGAGATGAACA	AAAAACAGGACCTTCTCTCTCCCTT
2q	D2S2310	186.57	181.87	GACTGCTTTAATAGCTAGAGAACCA	TTATTCAACCCTCGACTTGAGTAGA
2q [‡]	D2S118	190.98	191.31		
2q [‡]	D2S117	194.63	195.33		
2q	D2S115	196.51	198.68	CAAGAACAGCCATATTGACTTGAAC	GGGTACAGCCCATGTGTGAG
2q	D2S309	198.66	201.64	GCTCTAGTAGGCTGGTTACATAA	TTCCAAGAATAATGCAATCTCAG
2q	D2S2309	199.20	202.33	TGTCAGGCACTTCGCTA	TGCTTCTTATTGTACCCAAA
2q	D2S2214	199.28	202.44	GTCTTGCCACAATCACCC	AGCAAACAGTTTTGAGGACAT
2q	D2S346	199.77	202.67	TCAGGATGGGAGCAGA	CTGTGAGAATTAAATGAGTTACAA
2q	D2S105	200.83	204.50	CTCTACAGTTTATAACCAGC	TACACTGGATTCATATTCCC
2q	D2S1271	200.93	204.68	GGAAGGTCCAGATTAGAAG	AAGGGAAATAAAGAGAAGCAT
2q	D2S2237	202.01	205.34	CAGAATGCCTGTCCTGTCCA	GGCAAGTTGGCTACCTGACC
2q [‡]	D2S2358	204.25	207.24		
2q [‡]	D2S2382	213.82	216.76		
2q [‡]	D2S163	221.36	220.50		

2q[‡]	D2S133	227.17	224.34		
2q	D2S401	230.67	227.97	GAAGTTGCAGAACCATATAAACTCA	TATGTCTGCTGCAGCTTGTGGTAGT
2q	D2S341	235.25	230.58	TTAATCCTTCCCAGAACCTTAGTGT	CAGCAGTAAACCTTTTTGTATCCTG
2q	D2S1279	240.25	233.95	GGGCTTCTAGTAAAGGTCTGTTTGT	GAGAATCACTTGAACCCAGGAG
3q	D3S1303	126.07	119.64	GGTATCATATCACACACCAGATCAA	GCTGAGCAAAAGAGGTCTTAGAATA
3q	D3S1589	133.17	127.43	TGTGACACCTCAGCACTATACACTT	GCCCTCCCCTTTATAGAGATACAT
3q	D3S1238	142.60	135.40	TACATAATAAAGCTGAGTGCGGTGT	TGTGTATGGGCTCTTGAAATTG
3q	D3S1576	144.46	138.90	CAACTGTAGCAACTGTCTCTGTCTC	GAGAGGAAAAGGGGTATAACAAGAA
3q	D3S1557	152.31	146.65	GACGTGCTGATAATAAATTCACTCC	AGACGTGAAGAAGGAAGACAATAAG
3q	D3S3705	157.53	150.53	CCTAGGCAATTTTGAAATCTCTTCC	CGTTGCTTTATTTAGTACTGTGTCC
3q	D3S1237	161.34	153.64	TTATAGACCTTCTGCAAGTTTCCTG	CTATGGAGCTTGCTAAAACAGTACC
3q	D3S3579	166.45	162.06	GAGAGGGCAGTCTTACATAGGAGAT	CTCACTGGGGATTTGACAGTATTAG
3q	D3S3668	167.47	165.83	TCTATCCTGTCTCTTCTAAACATGG	CATTTGCCCAATTTCCAAAC
3q	D3S1243	169.98	169.84	TTGTTACCAATGTTTTTGCTTGA	TCAGGAATCCATATCTCCACTCTTA
3q	D3S3725	174.44	173.29	AATATTACTCACAGTGCCCTGACTT	CTATTTGAGGCAATCTAAAGCCATC
3q	D3S2412	183.07	178.55	ATGCTTCTCACCCTCCACAA	AGAAATAAGCAGGTAGATCCCAGAC
3q	D3S3583	190.37	185.77	CTCTCCCAGTAACTCTTCCTCTACC	CCCTGACATGGTGTAAGTATCAAT
7q	D7S666	111.42	101.54	TAGTGCTAAACTCTTTCTGCCTTCT	ACTCCCTGATATGTGAGGTAATGAA
7q	D7S2459	117.72	107.12	CTTATCTTCCCAACACAGAAAGAAC	GCCTTAGTAAAACCCATTTGAAGAC
7q	D7S3052	118.93	109.17	ATCTATTCCTCAGCCTCATTGACT	AAAGTGAGACTAGCAGATGTACTTGG
7q	D7S2554	121.75	114.24	TGTGATAGGGATGGGATGGT	GCTACACCATGTATTGTTTATGCAC
7q	D7S685	125.46	121.08	ATGTTTGCATCTACGCTCATCA	TCCCTAACTTAATCAATGAGACCAG
7q	D7S648	127.02	123.64	AGACTCTCTCCTCTTTCTGTGTATG	TCATAGGGTTTCTATATCGATGGAC
7q	D7S2501	129.10	127.30	TGCTCTTCTCACTCTTCACCTATTT	GATCGCAGACAGTAAACTTCTTACC
8p	D8S1786	39.17	22.43	CCTTGTTTGCAGACTGTTTTGA	TGAGCCCAAAGAGGAGAATAAAC
8p	D8S1725	43.74	25.10	GGTCAGGCTTAGAGATCTAGGTTTT	AAACACAAACACCTACCAAGGACT
8p	D8S1048	46.42	26.81	ACTACAGGCTGAATGACAGAATGA	GTTGCAGCCAAATTGTGACTAA
8p	D8S1809	47.81	28.19	TGGGCACTTTAGGATGTTTACTG	CAGATCAGAATCCTGTCGAGTTAGT
8p	D8S339	52.12	30.36	GACAACTAAGTGCTGTGTGATTCTG	CCTATATACCCTTTGCACAGATTTC
8p	D8S1777	54.57	35.35	CTTGCGATTTTAGACATATCTAGCC	TACCTATATCCCTCACTCAGTTCCA
8q	D8S531	62.26	49.02	TGGAGTCTTCTTATGTTGTTTAGGC	CTACAGATTCACAGAGGAATGATTG
8q	D8S285	68.31	57.07	TCACACAGAATCTTTGCTACCTACA	TCTGCATCTGAAAAACGTATGG
8q	D8S1763	71.87	60.10	GCTCAAAGATTACTCAAAGGACTTG	ATGAAAGCCTTTATCTACAGGTGTG

8q	D8S543	79.78	70.01	TGTCATTGCTTTCTAGTCTGTCTCA	GTGGATATAGAAAAAGATGCACAGG
8q	D8S1807	83.68	72.55	TTATCGCCTGTCCCTAGTTCTTT	GAGGACCCTACACTGCTGCTAATA
8q	D8S1805	89.45	78.09	TTTGTATCAATCTTAGCTCCACCTC	GAATTTACATCTCTGGCTCTCACAG
9q	D9S1879	65.58	70.65	TCATCCCCTCTCATTCCCTA	ACCCTCTCATCCATCCCTTC
9q	D9S1876	68.30	74.42	CAGTGGTAATCTCCAGGAAGC	CTCTGTCCCTCTAGAAATCACACAT
9q	D9S1674	74.35	79.11	TATTTCTGTTGTGTTAGGGTTCTCC	ACCCTGTAGACTGACTTTGAACTTG
9q	D9S933	78.26	82.83	TCCCCACATCACTCAAAGATACTAA	TTGTCAACCTCTGTCTGTCTATATGTC
9q	D9S1790	84.06	87.10	GGGGATCTTAAGCAAGTCATTTTAC	GAATGCATAACTTGTAGCAAGGAAG
9q	D9S1781	95.32	93.46	AAATTTCTTGGTGAGGTTACTCCTG	TGTATAGTAGTGGAGTCTGGGCTTC
9q	D9S1809	98.70	97.60	AGGCAAGAGTGGAGCATATGTGTA	CGAATTAAGGTTTGTGCTTCCT
9q	D9S176	102.68	101.10	GGAAACTAGATGACTGCTCAGTGTAA	ATCATAGGCTCTACATCCCTTCAG
9q	D9S1162	109.77	109.19	GAGCCACAGTAAACCAACTAGAGAC	GAAGTGTGAGGGACTGAGGAAG
9q	D9S1683	115.35	112.90	CACAAGATAGTCAAGCAAGATGAAG	TGGTCTAGCTGCAGTAAGTTTTCTC
9q	D9S51	121.49	116.90	AGTTGAGAAAACCAAGGTTGAGTG	GGGTACCAATTCCAACTAGAAAAGT

[*] deCODE genetic map position in cM [37]

[†] Physical position in Mb

[‡] Primers from ABI Prism Linkage Mapping Set v2.5 (Applied Biosystems); primer sequences not available

Supplementary Table 2: Details of families and results for finemapping at 2q24.3-q37.1

Family	No. affected	Genotyped		Max Aff only LOD	Location (cM)	Max NPL	Location (cM)	Location of segregating haplotype (cM)	Affecteds sharing haplotype
		Affected	Total						
1	9	8	32	1.53	179-240	2.15	168-240	168-235	8/9
2a*	5	4	6	0.13	179-201	0.42	177-202	168-202	3/3[†,‡]
2b*	11	9	25	0.47	181-190	0.87	180-214	-	-
3	11	10	19	1.11	220-240	1.45	214-240	214-240	9/10[‡]
4	8	8	21	-ve	-	0.38	227-240	-	-
5	9	8	20	1.43	181-226	1.19	180-231	180-227	8/9
6	4	4	13	0.41	192-235	1.22	191-235	191-240	4/4
7	6	4	15	0.01	187-201	0.92	180-201	-	-
8	5	5	15	0.72	181-240	1.83	186-240	180-240	5/5
9	7	7	19	-ve	-	1.55	197-199	-	-
10	7	6	11	0.33 0.18	160-210 225-229	0.80 0.90	160-214 221-231	160-214	6/7
11	6	6	10	0.04	198-203	0.95	177-214	195-214	5/6
Total	88	79	206						

[*] Includes 5 individuals (4 affected, 1 unaffected, all genotyped) who were counted as part of both Family 2a and Family 2b

[†] Haplotypes could not be assigned for one affected individual

[‡] Affected spouses excluded