

Table 1: Pairwise lod scores for chromosome 3 markers

Locus	Distance ^a	Lod scores at recombination fractions (θ) of:								Zmax	θ max
		0.00	0.001	0.01	0.05	0.1	0.2	0.3	0.4		
<i>D3S1263</i>		$-\infty$	-4.42	-1.47	0.40	1.02	1.28	1.08	0.6	1.28	0.18
<i>D3S1286</i>	0.12	$-\infty$	-0.39	1.59	2.81	3.04	2.69	1.94	1.01	3.04	0.10
<i>D3S2338</i>	0.01	$-\infty$	-4.68	-0.77	1.61	2.27	2.31	1.75	0.91	2.41	0.15
<i>D3S1293</i>	0.01	$-\infty$	-1.27	0.69	1.87	2.17	2.03	1.50	0.76	2.19	0.12
<i>D3S1599</i>	0.01	0.71	0.71	0.69	0.63	0.54	0.37	0.21	0.08	0.71	0.00
<i>D3S2336</i>	0.02	$-\infty$	3.55	4.50	4.89	4.71	3.87	2.70	1.32	4.89	0.05
<i>D3S1567</i>	0.03	1.50	1.49	1.47	1.37	1.23	0.94	0.62	0.31	1.50	0.00
<i>D3S1583</i>	0	-0.53	-0.53	-0.47	-0.30	-0.18	-0.05	0.01	0.02	-	-
<i>D3S2335</i>	0	$-\infty$	3.24	4.15	4.47	4.27	3.48	2.45	1.22	4.47	0.04
<i>D3S2337</i>	0	$-\infty$	3.24	4.16	4.47	4.27	3.48	2.43	1.20	4.47	0.04
<i>D3S1283</i>	0.02	$-\infty$	1.07	2.97	3.94	3.99	3.38	2.40	1.19	4.02	0.07
<i>D3S1266</i>	0	$-\infty$	1.07	2.01	2.46	2.42	1.97	1.32	0.60	2.47	0.06
<i>D3S1609</i>	0.02	2.98	2.97	2.92	2.70	2.41	1.81	1.19	0.58	2.98	0.00
<i>D3S1619</i>	0.07	$-\infty$	-3.58	-0.64	1.15	1.66	1.71	1.29	0.64	1.77	0.14
<i>D3S1277</i>	0.01	$-\infty$	-5.65	-2.70	-0.79	-0.15	0.22	0.17	0.003	-	-
<i>D3S1289</i>	0.11	$-\infty$	-11.88	-6.76	-3.05	-1.52	-0.25	0.19	0.23	-	-
<i>D3S1300</i>	0.12	$-\infty$	-6.50	-1.61	1.41	2.29	2.48	1.92	0.99	2.53	0.16
<i>D3S1261</i>	0.19	$-\infty$	-11.21	-6.21	-2.74	-1.34	-0.20	0.20	0.23	-	-
<i>D3S1284</i>	0.08	$-\infty$	-8.62	-4.64	-1.94	-0.88	-0.05	0.21	0.20	-	-
<i>D3S1274</i>	0.07	$-\infty$	-9.44	-5.46	-2.76	-1.66	-0.68	-0.24	-0.04	-	-
<i>D3S1276</i>	0.01	$-\infty$	-10.92	-5.94	-2.54	-1.18	-0.06	0.31	0.30	-	-
<i>D3S1281</i>	0.13	$-\infty$	-19.81	-11.85	-6.41	-4.18	-2.12	-1.04	-0.39	-	-

a: Distance between two adjacent markers in recombination fraction.

Table 2: Microsatellite tandem repeats localized to chromosome 3p24.2-25

Locus	Marker name	Primer sequence	Predominant allele size range (bp)
<i>D3S2338</i>	AFMa037zf5	GAAGCCAGCAGTTTCTC CTGTATTGTTTTCCAGGATAAG	191
<i>D3S2336</i>	AFM336zb5	TCCTTTAGTGGTTTTAACACA TTTACTTGGGCATGTTTG	105
<i>D3S2335</i>	AFM312yf5	GCTGAATGCTTCTGAATGTAT AAGAGATGGGGTGCTTT	166
<i>D3S2337</i>	AFM015xd7	TACTTGGCATAGCCAGTTGA AGCCTCTGTNTTGGTTGTAT	123

Legends

Figure 1:

The relative physical locations of the disease gene on the short arm of chromosome 3 and of 13 regional markers.

Figure 2:

Segregation of chromosome 3p24.2-p25 markers in the Marfan kindred.

(Note that panel A and panel B represent different parts of a single pedigree; i.e., panel B is the rightward extension of panel A). Haplotypes (top to bottom) at tel-*D3S1293*, *D3S1599*, *D3S2336*, *D3S2335*, *D3S2337*, *D3S1283* -cen markers are shown for each family member tested. Blackened symbols denote affected members, unblackened symbols denote unaffected spouses or unexamined family members, unblackened symbols with a dot in the center denote members considered unaffected, and hatched symbols denote members having an unknown phenotypic status. A slash denotes that the family member is deceased. An asterisk indicates the obligate recombinants with markers *D3S1293* (subject IV55) and *D3S1283* (subject IV54).

Figure 3:

Graph of the multipoint lod scores versus map distance in centiMorgans from locus *D3S1293*. Composite lod score curve for which marker *D3S1293* was chosen arbitrarily as origin for the map. Recombination fractions were converted into centiMorgans using Haldane map function.