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Towards fully automated genotyping: use of an X linked recessive spastic paraplegia family to test alternative analysis methods

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In the above article there was a mistake in Table 4 on p. 488. The recombination fraction between DXS425 and HPRT should read 0.10. The entire table is correctly printed below.

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Table 4 Markers used for linkage analysis, intermarker recombination fractions, support for local order, maximum two-point lod scores between each marker and the disease locus and corresponding recombination fractions. (Markers are ordered p-ter to q-ter.)

Locus	Recombination fraction	Support for order ^a	Two-point	
			$\hat{Z}_{\max}$	$\hat{\theta}$
DXS1060			0.13	0.00
DXS987	0.16	10.0	0.50	0.50
DXS999	0.03	2.6	0.00	0.50
DXS997	0.20	13.9	0.03	0.50
DXS1068	0.08	3.5	1.03	0.50
DXS993	0.10	7.7	0.00	0.50
DXS1003	0.11	11.8	0.07	0.34
DXS991	0.10	14.2	0.07	0.34
DXS983	0.06	8.0	0.13	0.00
DXS986	0.03	2.2	0.00	0.50
DXS990	0.09	7.2	0.05	0.17
DXS1106	0.10	5.5	1.08	0.00
DXS456	0.07	2.7	1.68	0.00
DXS287	0.03	1.8	1.03	0.00
DXS1001	0.19	14.0	0.43	0.14
DXS425	0.04	1.5	0.43	0.15
HPRT	0.10	8.6	0.09	0.50
DXS984	0.10	5.5	0.43	0.50
DXS998	0.19	4.9	0.11	0.38

^a Difference in $\log_{10}$ likelihood between the most likely order and inversion of each pair of adjacent markers