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Supplemental Data

Identification of a Kir3.4 Mutation

in Congenital Long QT Syndrome

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Table S1. Two-Point LOD Score of the Genome-wide Scan

Chr	Number of markers	Density range of markers (mean) (cM)	Peak LOD score	Genetic position of markers with peak LOD score (cM) ^a	Markers with positive LOD scores
1	31	3.8-15.9 (9.25)	0.21	266.27	D1S2785
2	30	5.0-12.9 (9.11)	0.11	152.04	D2S151
3	23	4.5 -13.9 (9.87)	-1.43	207.73	
4	22	4.2-13.9 (9.91)	-∞		
5	22	2.2-22.4 (9.50)	-∞		
6	20	4.7-25.9 (9.97)	-1.14	18.22	
7	22	3.5-12.4 (8.45)	0.69	53.50	D7S484, D7S517, D7S630
8	14	7.1-24.5 (10.92)	-1.05	71.00	
9	20	2.8-14.6 (8.18)	-∞		
10	20	2.6-12.6 (9.13)	-0.18	40.36	
11	18	4.4-13.5 (8.38)	1.74	127.33	D11S4151, D11S898
12	19	3.8-12.6 (9.22)	-1.44	147.17	
13	14	4.9-11.8 (8.24)	-1.29	25.08	
14	14	5.2-18.2 (9.88)	-1.77	117.30	
15	15	0.8-12.8 (7.58)	0.28	14.58	D15S1002, D15S28
16	13	5.3-18.7 (10.09)	-2.28	125.82	
17	15	0-13.7 (9.23)	0.26	36.14	D17S921
18	14	4.3-14.7 (9.83)	-1.91	52.86	
19	12	4.7-13.1 (8.09)	0.27	92.56	D19S418
20	13	2-11.9 (7.69)	-∞		
21	5	7.2-12.1 (9.63)	-0.98	35.45	
22	7	6.6-10.4 (8.18)	-∞		

^aGenetic position is the relative position from pter to qter in cM and based on the data from the Center for Medical Genetics, Marshfield Medical Research Foundation, database.