Supplemental on-line Table 1. Polymorphisms with the lowest P-values for association with sensory peripheral neuropathy in White, Black, and Hispanic patients, considering the entire genome.

	White					Black					Hispanic				
	Ca/Co[b]	**Gene**	**SNP**	**OR**	**P**	**Ca/Co[b]**	**Gene**	**SNP**	**OR**	**P**	**Ca/Co[b]**	**Gene**	**SNP**	**OR**	**P**
Grade ≥1	40/85	*Intergenic*	rs7244245	5.365	1.1E-06	37/49	*NFE2L3*	rs4722585	0.2	5.1E-06	13/30	*HIF3A*	rs3826795	12.8	3.0E-06
		MAP2K6	rs817565	3.779	2.7E-06		*HPSE2*	rs11189867	26.8	7.4E-06		*ADCK1*[a]	rs4899685	14.0	3.6E-06
		MAP2K6	rs12451722	3.722	3.8E-06		*FAM19A2*	rs10784285	4.1	9.2E-06		*RSP04*[a]	rs502716	14.0	3.6E-06
		CALD1	rs17169635	3.526	5.6E-06		*FSHR*[a]	rs9636436	4.7	1.0E-05		*STXBP5L*	rs11707293	14.2	5.2E-06
		Intergenic	rs10216322	4.776	7.8E-06		*CAMTA1*	rs2412148	8.7	1.7E-05		*HIF3A*	rs17801257	NA	6.4E-06
Grade ≥2	19/85	*GPC6*	rs7985891	38.2	2.4E-07	30/49	*NFE2L3*[a]	rs4722585	0.2	5.4E-06	9/30	*RSP04*[a]	rs502716	28.0	3.2E-08
		KIF20B[a]	rs10509586	9.3	3.8E-07		*FAM49A*[a]	rs1346751	0.1	8.3E-06		*LINCOO443*[a]	rs1330950	17.5	8.4E-07
		Intergenic	rs6637197	14.9	1.0E-06		*MRPL45P1*	rs11684168	11.5	9.5E-06		*FBX031*	rs1062746	15.6	2.1E-06
		IL37[a]	rs2708973	31.7	2.6E-06		*FSIP1*	rs16969786	9.3	1.3E-05		*GLIS3*	rs717423	14.1	4.1E-06
		WDHD1	rs28489712	31.7	2.6E-06		*FSIP1*	rs12324408	9.3	1.3E-05		*IL6R*	rs8192282	23.2	4.7E-06
Grade 3	8/85	*IL2RA*	rs12722486	38.2	1.5E-09	12/49	*ZNF648*	rs7554182	48.5	5.7E-08	3/30	*TANK*	rs7568498	NA	2.1E-08
		CXCL12[a]	rs266095	56.3	7.8E-09		*LRIG1*	rs9827908	48.5	5.7E-08		*Intergenic*	rs801350	NA	2.1E-08
		CXCL12	rs266092	56.3	7.8E-09		*Intergenic*	rs9636436	11.1	2.2E-07		*Intergenic*	rs801378	NA	2.1E-08
		Intergenic	rs9501753	NA	1.3E-08		*CHST9*[a]	rs1514687	16.8	2.2E-07		*HDAC9*	rs213273	NA	2.1E-08
		PTPRB	rs17108344	25.3	2.7E-08		*FSHR*[a]	rs10495970	10.3	5.0E-07		*HDAC9*	rs213276	NA	2.1E-08

[a] These polymorphisms are within 100 kb of the named gene.
[b] Ca/Co indicates cases/controls.

Supplemental on-line Table 2. Polymorphisms with the lowest P-values for association with sensory peripheral neuropathy in White, Black, and Hispanic patients, considering neuropathy-associated genes[a]

	White					Black					Hispanic				
	Ca/Co[b]	**Gene**	**SNP**	**OR**	**P**	**Ca/Co[b]**	**Gene**	**SNP**	**OR**	**P**	**Ca/Co[b]**	**Gene**	**SNP**	**OR**	**P**
Grade ≥1	40/85	*KIF1A*	rs11886288	0.1	4.6E-04	37/49	*CCDC19*	rs2501325	0.2	1.3E-03	13/30	*NEFL*[c]	rs6557786	12.9	2.7E-04
		SPTLC2[c]	rs7145386	3.5	8.9E-04		*LITAF*[c]	rs13333308	13.4	2.0E-03		Intergenic	rs32147	5.0	1.3E-03
		SPTLC2[c]	rs11159273	0.3	9.4E-04		*KIF1B*	rs4475756	2.8	2.0E-03		*GDAP1*	rs3780014	0.2	1.7E-03
		SPTLC1[c]	rs7045602	3.6	1.3E-03		*KIF1B*	rs8019	2.6	2.6E-03		*SBF2*	rs12808226	5.6	1.8E-03
		SH3TC2	rs3763022	2.3	2.1E-03		*GAN*[c]	rs8044853	2.6	3.0E-03		*NEFL*[c]	rs17763685	NA	1.9E-03
Grade ≥2	19/85	*SPTLC1*[c]	rs7045602	5.2	2.4E-04	30/49	*LITAF*[c]	rs13333308	17.1	4.6E-04	9/30	*NEFL*[c]	rs6557786	23.2	4.7E-06
		SBF2	rs4243951	0.2	2.9E-04		*FAM134B*	rs162848	0.2	1.2E-03		*NEFL*[c]	rs17830286	11.2	9.8E-05
		NEFL[c]	rs3757985	0.1	1.1E-03		*GAN*[c]	rs8044853	2.9	1.7E-03		*NEFL*[c]	rs17763685	NA	1.8E-04
		SH3TC2[c]	rs10045726	3.2	1.2E-03		*FAM134B*[c]	rs149511	0.3	2.0E-03		*MFN2*[c]	rs12759042	6.5	9.5E-04
		SH3TC2	rs6580590	3.2	1.2E-03		*NEFL*[c]	rs3757985	2.9	2.3E-03		*PMP22*[c]	rs230930	6.1	1.3E-03
Grade 3	8/85	*KIF1A*[c]	rs10199388	5.3	8.4E-04	12/49	*LITAF*[c]	rs13333308	32.3	6.0E-06	3/30	*NEFL*[c]	rs17763685	NA	5.6E-06
		SPTLC2[c]	rs7145386	5.5	2.3E-03		*HMCN2*	rs914977	6.5	1.0E-04		*BSCL2*	rs575134	NA	5.6E-06
		SH3TC2	rs10477401	12.0	2.8E-03		*HMCN2*	rs2039463	6.8	1.2E-04		*NEFL*[c]	rs6557786	29.0	3.8E-05
		KIF1A[c]	rs6437363	4.5	2.8E-03		*FAM134B*	rs256880	0.2	2.7E-03		*ZNF622*	rs10520840	14.0	1.0E-03
		PMP22[c]	rs230924	4.2	4.6E-03		*WDR54*[c]	rs2268424	4.4	4.2E-03		*NEFL*[c]	rs17830286	14.0	1.0E-03

[a] The neuropathy-associated genes from the Inherited Peripheral Neuropathies Mutation Database[7] plus *DNMT1* and *KIF1A*.

[b] Ca/Co indicates cases/controls.

[c] These polymorphisms are within 100 kb of the named gene.

Supplemental On-line Table 3: Neuropathy-associated genes

Chromosome	Start Position[a]	Stop Position	Gene
1	10143350	10414248	KIF1B
1	154301084	154426502	LMNA
1	11912824	12046159	MFN2
1	159491148	159596386	MPZ
1	115778537	115930857	NGFB
1	155002165	155168266	NTRK1
1	6398738	6552656	PLEKHG5
1	32963426	33106220	YARS
2	74391789	74511472	DCTN1
2	241251856	241458297	KIF1A
3	129877668	130066331	RAB7A
5	10253281	10369501	CCT5
5	16476146	16720118	FAM134B
5	148291905	148472930	SH3TC2
6	110069116	110303327	FIG4
7	30550705	30690173	GARS
7	75719858	75821548	HSPB1
8	1709555	1944214	ARHGEF10
8	75375172	75491890	GDAP1
8	134268595	134428680	NDRG1
8	24814385	24920043	NEFL
9	110619620	110786429	IKBKAP
9	134076647	134270193	SETX
9	93783247	93967511	SPTLC1
10	64191762	64296133	EGR2
11	62164322	62281446	BSCL2
11	68377894	68514645	IGHMBP2
11	95155693	95347019	MTMR2
11	9706789	10322330	SBF2
12	32496360	32734940	FGD4
12	118050977	118166934	HSPB8
12	682485	940879	WNK1
14	50949800	51149786	ATL1
14	76993022	77202863	SPTLC2
15	32259488	32467557	SLC12A6
16	79856075	80021441	GAN
16	11499356	11637730	LITAF
17	15023820	15159369	PMP22
17	72739086	73058273	SEPT9
18	75490788	75665495	CTDP1
19	10639754	10853579	DNM2
19	10055021	10216811	DNMT1
19	45541510	45661111	PRX
22	36648264	36760485	SOX10
X	70301786	70411777	GJB1
X	106708309	106830912	PRPS1

[a] Chromosome start and stop positions span the regions included in genetic analyses for each gene, and are based one genomic build 37.