SUPPLEMENTAL MATERIAL

Table S1. Information on Genotyped SNPs of SCNN1A, SCNN1B, and SCNN1G
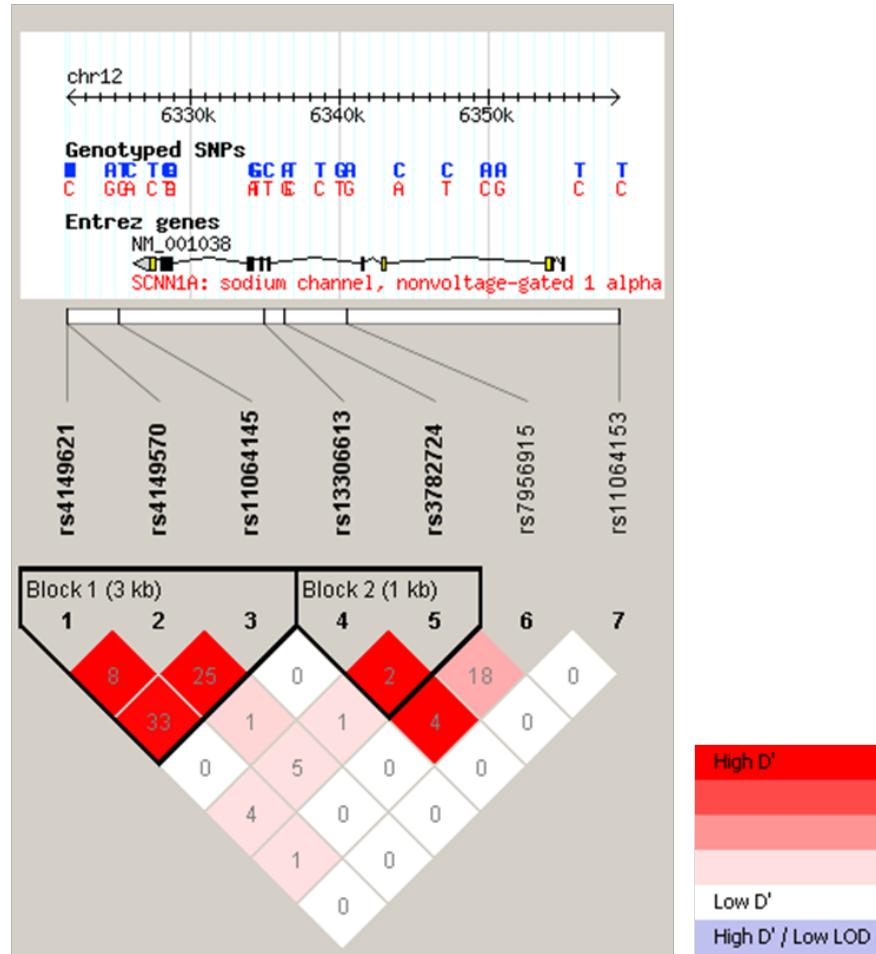
Gene	Chr	SNP	Position	Region in Gene	MAF	Alleles*	HW p-values
SCNN1A	12	rs4149621	6321822	3' Flanking	0.08	T:C	0.48
		rs4149570	6321851	3' Flanking	0.50	C:A	0.63
		rs11064145	6325359	3' Flanking	0.21	T:G	0.33
		rs13306613	6335070	Intron	0.06	C:T	0.26
		rs3782724	6336342	Intron	0.24	A:G	0.90
		rs7956915	6340521	Intron	0.40	C:T	0.40
		rs11064153	6358711	5' Flanking	0.35	G:A	0.05
SCNN1B	16	rs1004749	23222352	Intron	0.34	A:C	0.22
		rs3785368	23228281	Intron	0.35	G:A	0.32
		rs11074555	23231527	Intron	0.30	A:G	0.18
		rs7205273	23232350	Intron	0.26	C:T	0.20
		rs239345	23253439	Intron	0.28	T:A	0.10
		rs7190829	23254805	Intron	0.18	A:G	0.70
		rs8055868	23255752	Intron	0.20	G:A	0.88
		rs12447134	23258170	Intron	0.08	A:C	0.39
		rs239349	23260349	Intron	0.48	G:A	0.04
		rs238547	23267700	Exon (syn)	0.03	C:T	1
		rs8044970	23269331	Intron	0.38	T:G	0.33
		rs8044984	23269354	Intron	0.31	A:C	0.11
		rs152733	23270179	Intron	0.45	A:G	0.46
		rs3785361	23270900	Intron	0.29	T:A	0.49
		rs63982	23271582	Intron	0.38	G:T	1

		rs238551	23283422	Intron	0.50	A:G	0.32
		rs239350	23286980	Intron	0.13	G:A	0.02
		rs889299	23289415	Intron	0.34	G:A	0.63
		rs12596831	23292758	Intron	0.13	C:T	0.04
		rs4967999	23295036	Intron	0.45	C:T	0.92
		rs168748	23295756	Intron	0.45	G:A	0.29
		rs2303153	23297702	Intron	0.11	G:C	0.76
		rs250567	23301900	3' Flanking	0.10	G:A	0.29
		rs181835	23304614	3' Flanking	0.33	A:G	0.76
SCNN1G	16	rs4421986	23098751	5' Flanking	0.06	C:T	0.04
		rs4073930	23103147	Intron	0.16	T:C	0.03
		rs4073291	23103494	Intron	0.16	T:G	0.02
		rs7404408	23104239	Intron	0.16	C:T	0.01
		rs4967948	23106745	Intron	0.01	G:A	1
		rs5735	23108349	Exon (syn)	0.17	T:C	0.09
		rs4247210	23113158	Intron	0.16	G:C	0.57
		rs13331086	23115618	Intron	0.06	A:C	0.59
		rs4299163	23119520	Intron	0.10	G:C	0.35
		rs4401050	23124903	Intron	0.09	C:T	0.85
		rs4499238	23128880	Intron	0.10	G:A	0.25
		rs4297681	23132542	Intron	0.06	C:A	1
		rs5723	23134288	Exon (syn)	0.06	C:G	0.62
		rs5728	23134863	3' UTR	0.19	A:G	1
		rs9930846	23136036	3' Flanking	0.06	T:C	0.53
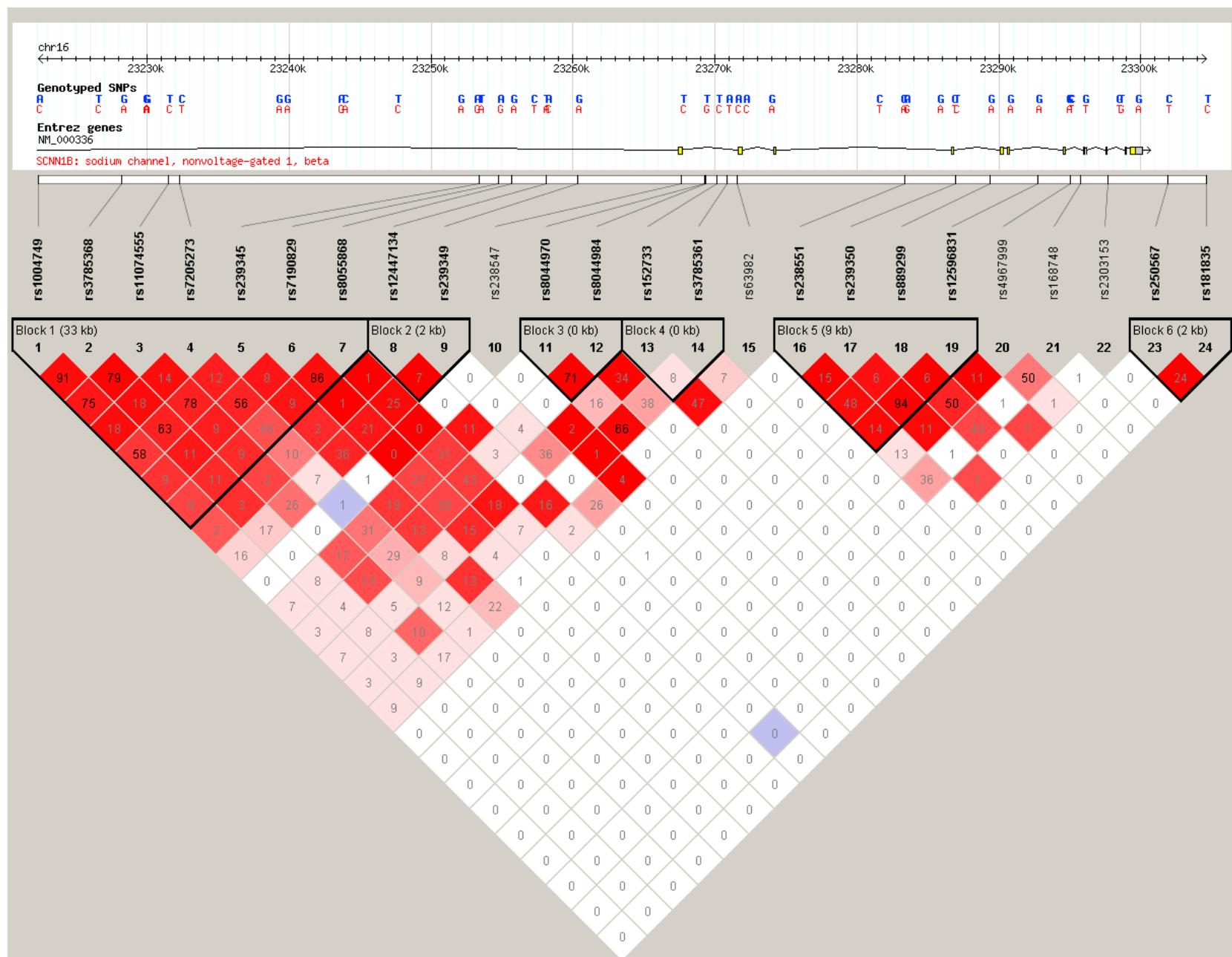
*Major allele: minor allele.

Figure S1. Linkage disequilibrium structure of the SCNN1A (a), SCNN1B (b), and SCNN1G (c) genes. The D' color scheme of Haploview was applied and $r^2 \times 100$ are shown in each cell (r^2 values of 1.0 are not shown).
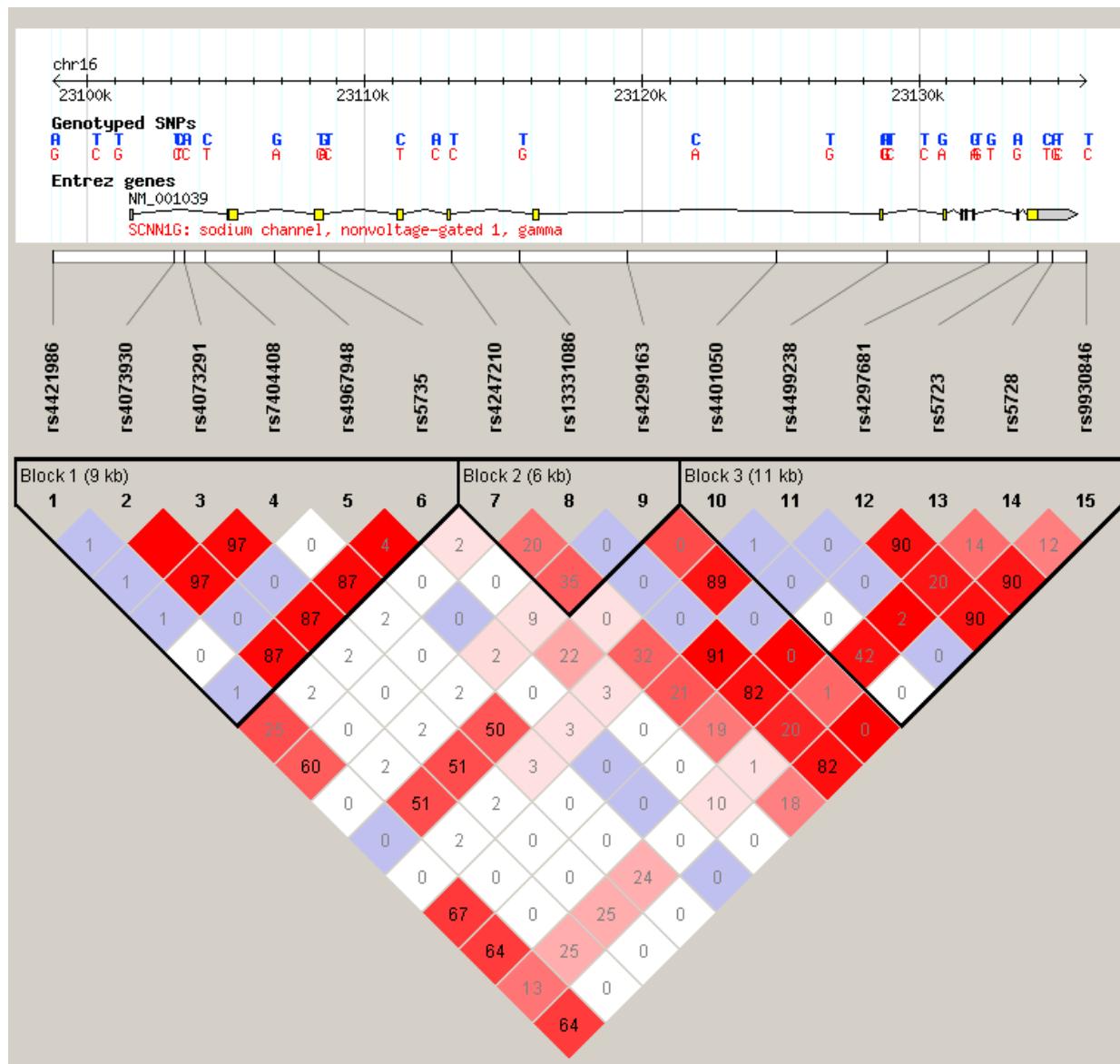
a.

b.

C.

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