

Supplementary Table 1: SNP selection for the SNPlex genotyping assay covering 14 genes of the Transient Receptor Potential channel superfamily.

Gene	SNP_ID	Position	Allele	Control population		Case-Control <i>P</i> -value [#]			SNPs captured
				MAF	HWE(<i>P</i> -value)	MA	MO	All-migraine	
TRPA1	rs7018446	3' near gene	A/C	0.52	0.44	0.1195	0.9186	0.3568	rs4738200
	rs4738201	3' near gene	G/A	0.52	0.54	in LD with rs7018446 (r2=0.996)			singleton
	rs2044270	3' UTR	T/A	0.62	1	0.2172	0.8703	0.42813	singleton
	rs9298197	3' UTR	G/T				39.88 % missing		singleton
	rs13268757	p.C3R	A/G				39.20 % missing		singleton
	rs16937976	p.T58R	C/G	0.83	0.44	0.6123	0.6401	0.55798	singleton
	rs10091093	intron	C/T				100% missing		rs16937933, rs10104927, rs10109581, rs13266501, rs10104081, rs2305017, rs7011222, rs7011431, rs2028708
	rs920829	p.K179E	G/A	0.9	1	0.8237	0.4685	0.54274	singleton
	rs7819749	p.N186K	G/T	0.58	0.1	0.0393	0.6499	0.15489	rs4738204, rs3779755, rs920830, rs10104272, rs2383846, rs1811457, rs7010969, rs13269625, rs1384002
	rs3779754	intron	G/C				100% missing		rs10100108, rs3824152, rs10107349, rs1373302, rs4737338, rs3735942, rs3824150, rs12541196, rs12541199, rs12541200, rs12548486, rs10101155, rs12677736, rs7824377, rs1443952, rs1373297, rs4738205, rs1822571, rs1968584, rs4738206, rs10111216
	rs7836192	intron	T/G				100% missing		rs1025929, rs3735943, rs3735944, rs10504526, rs6472657
	rs1025928	intron	C/T				85% missing		rs2383844, rs4737339, rs11990722, rs1562054, rs2120474, rs1842663
	rs13259803	intron	C/T	0.69	0.69	0.6711	0.9511	0.85194	rs13255063, rs13249568, rs10504523, rs2044271, rs2044272, rs10504524, rs2120473, rs6982184, rs13252489
	rs4738202	intron	G/A	0.69	0		HWE		singleton
	rs13279503	intron	G/C	0.61	1	0.7928	0.8024	0.76052	singleton
	rs959976	p.R1018H	T/C	0.83	0.35	0.3861	0.4432	0.32434	singleton
	rs2383841	intron	G/A	0.52	0.66	0.1062	0.6791	0.25413	rs1384001, rs959974, rs2383842
	rs2587562	5' near gene	G/A	0.55	0.48	0.3963	0.907	0.60282	singleton
TRPC1	rs13094259	intron	G/T	0.8	0.34	0.3941	0.3093	0.24096	rs13081200, rs17624218,
	rs4607150	intron	C/T	0.75	0.4	0.0585	0.3785	0.68965	singleton
	rs13086677	intron	C/T	0.79	0.36	0.5511	0.5262	0.45213	singleton
	rs7639403	intron	C/T	0.79	0.02	0.8235	0.0096	0.10768	rs2049328, rs2354856, rs2177398, rs7638459, rs9836269, rs6803681, rs6440108, rs1382688, rs7621642, rs9864230, rs7637846, rs9815607, rs4643748, rs2033912, rs7641514, rs9868886, rs9849461
	rs9851381	intron	G/A	0.8	0.49	in LD with rs7639403 (r2=0.889)			rs3821647, rs4259003, rs7610200
	rs11715459	5' near gene	A/G				100% missing		singleton
TRPC3	rs6841843	3' near gene	T/C	0.71	0.35	0.691	0.093	0.35218	rs17517624
	rs906493	intron	T/C	0.66	0.63	0.5629	0.2614	0.64832	rs11726196, rs4292355
	rs884701	intron	C/T	0.72	1	0.4761	0.8172	0.81245	rs10518289, rs7672879, rs13151345, rs953691, rs13131003, rs13133876, rs13143218, rs11732666, rs3805158, rs951974, rs13127488, rs1507993, rs13141092, rs906496, rs1507991, rs3805161, rs2292232, rs4833778, rs11721457
	rs2892973	intron	T/C	0.66	0.08	0.2415	0.2291	0.84142	rs12502635
	rs4076212	5' near gene					100% missing		singleton

TRPC4	rs9547988	3' near gene	T/G	0.67	1	0.8138	0.4277	0.6795	rs9547994, rs9547996, rs9547997, rs9547998, rs9548000, rs9532093, rs9548003, rs7330679, rs7321872, rs9532095, rs7321585, rs9548026, rs11843893, rs11147662, rs9547991
	rs10161932	3' UTR	C/T	0.81	0.88	0.6669	0.9031	0.74899	singleton
	rs7332871	intron	C/T	0.59	0.86	0.6195	0.4494	0.8013	rs1570609, rs7997809, rs4943528, rs2985167, rs1570608, rs9532099
	rs7336008	intron	G/A	0.63	0.65	0.5158	0.9406	0.76633	rs12856733, rs9576329, rs9566245, rs2985170, rs9566246, rs9566247, rs9566248, rs9566249, rs9603244, rs9594224, rs9603245, rs9594226, rs9603246, rs1924289, rs2025407, rs7337477, rs7337173, rs9576328, rs7338239, rs2957218, rs2957215, rs2957214, rs4450268, rs2147124, rs9576332, rs9594225, rs4943529, rs9576335, rs9576338, rs7320775, rs4284516, rs12871022, rs7325911, rs7336516, rs7336526, rs9532096, rs9532098, rs4943532, rs9548012, rs1333353, rs9532097, rs7330896, rs4943531, rs2985164
	rs8001743	intron	A/G	0.55	0.34	0.7234	0.2202	0.29482	rs2181747, rs1924304, rs9594229
	rs17056448	intron	A/G	0.68	1	0.1643	0.5205	0.74616	singleton
	rs7317546	intron	A/T	0.59	0.06	0.9049	0.8713	0.95544	rs8002313
	rs1413002	intron	A/G	0.61	0.4	0.6647	0.6241	0.56384	rs978156
	rs1344351	intron	T/C	0.53	0.26	0.2267	0.7594	0.39557	rs1333360, rs1333362, rs9315508, rs7319926, rs7332772
	rs1360623	intron	A/C	0.57	0.54	0.578	0.1428	0.48891	singleton
	rs1360624	intron	A/G	0.52	0.93	0.5228	0.3708	0.78659	singleton
	rs1577007	intron	T/C	0.56	0.42	0.1421	0.057	0.03772	rs7997030, rs1029117, rs1556541, rs2151443, rs11616422
	rs12874552	intron	T/C	0.62	0.11	0.0899	0.1358	0.05604	rs12430948, rs11147671
	rs9548043	intron	A/G	0.67	0.33	0.5268	0.5725	0.97165	rs914862, rs9548036, rs9548039, rs1360625, rs2025404, rs763969, rs9548037
	rs9315511	intron	A/G	0.75	0.72	0.5832	0.1597	0.21084	rs4943534, rs4943538, rs8000744
	rs12869943	intron	A/G	0.73	0.83	0.3101	0.718	0.42028	singleton
	rs3904512	5' UTR	G/A	0.61	0.46	0.0318	0.0318	0.03184	rs9315514, rs9594231, rs7993498
	rs12583681	5' UTR	G/A	0.87	0.58	0.86	0.9299	0.87701	singleton
	rs2151438	intron	A/G	0.56	0.41	0.1046	0.0849	0.04071	rs1319667, rs1333373, rs9315512, rs9576350, rs1333374, rs1333376, rs9315513, rs9576351, rs9548048, rs7339215, rs933006, rs9532115, rs9532116, rs4460944, rs1556543, rs7330192, rs1855253
	rs7331005	intron	A/T	0.58	0.15	0.5616	0.3401	0.34468	rs7327037
	rs1924377	intron	G/C	0.57	0.06	0.2695	0.213	0.15168	rs1924378
	rs9576354	intron	T/C	0.62	0.52	0.0014	0.2469	0.01084	singleton
	rs1333377	intron	G/C	0.55	0.11	0.8819	0.8248	0.79694	singleton
	rs9548050	intron	A/G	0.6	0.22	0.5489	0.2483	0.62856	singleton
	rs655207	intron	T/G	0.59	0.72	0.3172	0.2471	0.79996	rs7337719, rs9635087, rs668684, rs6650469, rs639445, rs639099, rs604580, rs9566254
	rs625221	intron	C/T	0.71	0.84	0.1888	0.7633	0.35754	
	rs9548067	intron	C/T	0.79	0.51	0.4508	0.1557	0.16973	rs9532126, rs2104326, rs9548074
	rs9576388	intron	C/A	0.73	0.57	in LD with rs3812840 (r2=0.899)			rs9576388, rs3812837, rs1538144, rs1415601, rs1924379, rs1337601, rs1538146
	rs9548085	intron	T/C	0.51	0.66	0.0891	0.5102	0.62993	rs9548086, rs4144140, rs1538145, rs1538148, rs2323637
	rs12583681	5' UTR	A/G			SNPlex design			
	rs4617713	intron	G/T			SNPlex design			singleton

	rs1333358	intron	C/T				24.4% missing		rs17262400, rs12875577, rs1924301, rs2184124, rs12875518, rs12861121, rs1924300, rs12858218, rs2025402, rs11147667, rs11618049, rs12854825, rs11147670, rs12874443
	rs612308	intron	A/G				57.5% missing		rs612701, rs4943540, rs603955, rs535728
	rs7322054	intron	A/C				44.2% missing		rs9532107, rs9548033, rs9532108
	rs9532117	intron	A/G				20.99% missing		singleton
	rs1333354	intron	C/G				100% missing		singleton
	rs6563569	intron	C/T				100% missing		singleton
	rs1413005	intron	GT				57.55% missing		singleton
	rs3812840	5' near gene	T/C	0.71	0.11	0.0679	0.7804	0.23725	rs3812841
TRPC5	rs4893412	intron	A/G	0.74	0.98	0.4421	0.4267	0.33763	singleton
	rs17222608	intron	A/C	0.8	0.7	0.4035	0.8219	0.54037	singleton
	rs7056863	intron	A/G	0.87	0.32	0.619	0.6686	0.99641	rs16986725
	rs2223497	intron	G/A	0.89	0.58	0.3617	0.1355	0.13348	rs6655168, rs16986742, rs7060242, rs12011058, rs7052164, rs7888649, rs7064992, rs7060180, rs16986746, rs16986748, rs12011265, rs16986754, rs10521540, rs7892137, rs7876948, rs7054642, rs16986757, rs12014370, rs7891976, rs12014696, rs7891415, rs7061480, rs4534285, rs12011820, rs6642976
	rs4893414	intron	A/G				SNPlex design		singleton
TRPC7	rs871385	intron	G/A	0.61	0.31	0.9444	0.0177	0.11941	rs7731706, rs13173271, rs11959071, rs889012, rs13157486, rs7728953, rs3734123
	rs6596299	intron	C/A	0.54	0.93	0.3647	0.0555	0.07396	rs2194138, rs6893792, rs889010, rs10463951, rs2287746
	rs2042243	intron	G/A	0.86	0.05	0.3476	0.3106	0.84283	singleton
	rs6868895	intron	A/G	0.67	0.7	0.3428	0.7089	0.43923	rs1477322, rs17170027, rs13155582
	rs17762209	intron	T/G	0.83	0.06	0.1433	0.1439	0.07242	singleton
	rs10042289	intron	C/T	0.59	0.93	0.8313	0.2244	0.48357	rs1909544, rs344824, rs1499765, rs10477781, rs6596300, rs12515960, rs4976490
	rs11748766	intron	T/C	0.82	0.06	0.1107	0.2802	0.10998	singleton
	rs12518787	intron	G/T	0.54	0.67	0.7797	0.0865	0.1922	rs4976491, rs3777151, rs4976488, rs950715, rs7701815, rs2881486, rs3777154, rs1499775, rs17763790, rs344823, rs12515628, rs180767, rs237613, rs1392170, rs4976370, rs2017353, rs1469067, rs10055133, rs1392172, rs344828, rs171101, rs11744916, rs3777150
	rs2673931	intron	A/G	0.68	1	0.9661	0.2555	0.44865	rs4976489, rs1477323, rs2546657, rs953096, rs4976487, rs2546658, rs2546659, rs2546660, rs2649699, rs4976485, rs10070699, rs2216640, rs1303813, rs4976368, rs4976369, rs10067383, rs1499764, rs11744181, rs3822748, rs344825, rs344826, rs13157395
	rs2673930	intron	A/C	0.73	0.16	0.9917	0.5829	0.70291	rs2673926, rs7727558, rs2161382
	rs963590	intron	T/C	0.73	0.39	0.9202	0.3401	0.48047	singleton
	rs2546651	intron	A/G				37.94% missing		singleton
TRPM4	rs3745297	5' near gene	A/C	0.55	0.72	0.5002	0.0981	0.13723	singleton
	rs3745298	5' near gene	C/T	0.52	0.93	0.3755	0.1739	0.15975	singleton
	rs11667393	intron	A/G	0.75	0.65	0.4203	0.4927	0.36844	singleton
	rs12979689	intron	G/A	0.74	1	0.3227	0.8115	0.71003	singleton
	rs1175806	intron	T/C	0.67	0.01	0.0524	0.6558	0.17213	rs12981989, rs10403114, rs1175791, rs909010, rs4802586, rs3760666, rs7252170
	rs11668962	3' near gene	G/A	0.55	0.93	0.0461	0.853	0.32915	singleton

	rs3745300	5' near gene				56.91% missing			singleton
	rs12461216	intron	C/G			SNPlex design			singleton
	rs3760663	5' UTR	A/G			SNPlex design			singleton
TRPM6	rs9650767	intron	G/A	0.57	0.48	0.0606	0.0225	0.00975	singleton
	rs875034	intron	G/A	0.51	0.25	0.277	0.7894	0.43441	rs1759831
	rs12551900	intron	T/C	0.73	0.27	0.9377	0.9592	0.94011	singleton
	rs2769195	intron	T/C	0.64	0.51	0.5738	0.4973	0.87866	rs2769195, rs11144082, rs514348
	rs12339024	intron	T/C	0.58	0.33	0.6266	0.2621	0.6181	rs6560408, rs7018938
	rs13299138	intron	G/T	0.71	0.83	0.3288	0.3459	0.24004	singleton
	rs2151423	intron	A/G	0.56	0.06	0.4914	0.3485	0.30881	rs11144085
	rs7858755	intron	A/G	0.75	0.73	0.469	0.9704	0.6814	rs2151424
	rs3858116	intron	G/A	0.65	0.56	0.8904	0.4892	0.6809	singleton
	rs7859201	synonymous	A/C	0.6	1	0.8504	0.5444	0.74944	rs12336062, rs7045338, rs7859884
	rs17060550	intron	A/C	0.76	0.64	0.3674	0.4244	0.95796	rs10512038, rs17060535, rs17060538, rs12115672, rs9942942, rs4300062, rs7024831
	rs1012710	intron	T/C	0.72	0.52	0.7945	0.9856	0.88125	singleton
	rs7045949	intron	T/C	0.54	0.16	0.5597	0.8549	0.65931	rs2376269, rs6560414
	rs7867868	intron	C/T	0.61	0.07	0.3032	0.8178	0.68799	rs9650770, rs11144123
	rs4431653	intron	C/T	0.65	0.15	0.9028	0.2297	0.44672	rs6560416
	rs2184118	intron	G/A	0.67	0.33	0.472	0.1916	0.61531	rs7027629, rs10869447, rs10869452, rs17060601, rs11144108, rs2104932, rs11144113
	rs1333341	intron	G/C	0.6	0.58	0.5789	0.9693	0.73306	rs4745363, rs11144130, rs1333342
	rs1333343	intron	T/C	0.8	0.49	0.7313	0.2934	0.3724	rs10746966, rs7853685
	rs476673	intron	A/G			58.76% missing			rs546542
	rs2274924	p.E1584K	C/T			SNPlex design			
TRPM7	rs11070795	3' UTR	A/G	0.68	0.84	in LD with rs644890 (r2=0.90)			rs8035534
	rs8042919	p.T1482I	G/A	0.89	0.09	0.1467	0.1261	0.06741	singleton
	rs644890	intron	T/C	0.65	0.51	0.8274	0.2658	0.38865	rs473357, rs539383, rs567109, rs480280, rs616256, rs512708, rs493728, rs506693, rs577583, rs7163283, rs7175149, rs11635045, rs12324599, rs11636930, rs7165721, rs4775899, rs7178070, rs11636576, rs11630165, rs2292175, rs2899463, rs491907, rs8042320
	rs3848127	intron	G/A	0.75	0.1	0.9531	0.1687	0.38208	rs1060599, rs4775892, rs17520350, rs17520448, rs17598819, rs998831
	rs11636964	intron	A/G	0.52	0.07	0.7181	0.8998	0.89933	rs3101853, rs2630, rs3131580, rs3109888, rs3131578, rs3131577, rs3105590, rs3105591, rs2414060, rs3109891, rs3109892, rs3109895, rs17645523, rs11070798, rs3848129, rs3848130, rs12439744, rs3101852, rs12438305, rs12442787, rs2292174, rs8023644, rs2011064, rs3109894, rs3131576, rs874665, rs7174839, rs3105592, rs2414059, rs4775894
	rs17520378	intron	G/C	0.86	0.86	0.5579	0.8857	0.66495	singleton
	rs12593556	intron	A/T			56.57% missing			rs3848128, rs8042172, rs3131583, rs2414063
	rs2115671	intron	C/G			100% missing			singleton
	rs758275	intron	T/C	0.81	0.17	0.2358	0.6328	0.32995	rs6431648, rs7604471, rs4233636, rs4663986, rs758276, rs737636, rs10189040, rs10490012, rs6711120, rs13418652, rs2302153, rs11892538, rs11563063, rs6738979, rs1965629, rs10166942, rs2362290, rs1003540, rs10170399, rs9646720
	rs7605850	intron	T/C	0.59	0.15	0.6367	0.1321	0.45496	rs13401339, rs10171428
rs13411202	intron	A/G	0.64	0.85	0.9085	0.2724	0.50034	singleton	
rs11685673	intron	C/A	0.79	1	0.2683	0.2806	0.18395	singleton	

	rs6708995	intron	T/G	0.51	0.3	0.6359	0.2064	0.25995	rs6736916, rs11689034, rs728672, rs6718140
	rs4663994	intron	C/G	0.7	0.92	0.0495	0.1966	0.05455	rs4663992, rs4233637, rs4233638
	rs6749421	intron	A/G	0.62	0.31	0.9839	0.3258	0.50227	rs10207672
	rs12465950	intron	C/T	0.73	0.37	0.1346	0.0461	0.02963	rs11563208
	rs11563056	intron	T/G	0.64	0.05	0.6771	0.004	0.0275	singleton
	rs4663998	intron	G/T	0.56	0.86	0.1002	0.1422	0.05789	rs4663999, rs1024608, rs1024607, rs2362294
	rs6723922	intron	T/C	0.56	0.24	0.6003	0.4202	0.40474	singleton
	rs7560562	intron	T/C	0.67	0.77	0.5434	0.9069	0.8068	singleton
	rs6758653	intron	G/A	0.6	0.47	0.0822	0.0817	0.03295	rs6718140, rs12999395
	rs6712962	intron	T/C	0.6	0.66	0.9632	0.2219	0.39001	singleton
	rs11563200	intron	A/G	0.56	0.86	0.1759	0.0965	0.06144	rs10929331, rs599294, rs11675108
	rs2052029	3' UTR	C/G	0.7	0.41	0.353	0.7262	0.80413	rs6431652, rs2052030, rs6431651, rs1118259, rs28948678, rs4664001, rs2190951, rs4664000, rs6721761, rs6734618, rs1024687
	rs603217	3' near gene	G/C	0.63	0.85	0.7788	0.137	0.24337	rs7371495
	rs683719	5' near gene	A/G	0.58	0.23	0.7923	0.143	0.39405	singleton
	rs10929320	intron	T/C				44.60% missing		singleton
	rs10929321	intron	G/A				100% missing		singleton
	rs758277	intron	T/C				46.37% missing		singleton
	rs602312	5' near gene	C/G				SNPlex design		rs11675064, rs591103, rs602371
	rs6727222	intron	G/T				SNPlex design		singleton
TRPV1	rs2277679	intron	G/C				SNPlex design		singleton
	rs161376	intron	C/T				SNPlex design		singleton
	rs879207	3' near gene	C/A	0.56	0.43	0.0443	0.895	0.31319	singleton
	rs7223530	3' near gene	G/C	0.68	0.69	in LD with rs879207 (r2=0.93)			rs7406509, rs17632843
	rs4790522	3' UTR	C/A	0.56	0.43	0.0443	0.895	0.31319	singleton
	rs877610	synonymous	C/T	0.97	0		HWE		singleton
	rs8065080	p.I585V	C/T	0.6	0.59	0.618	0.6863	0.99911	rs8078936
	rs150908	intron	G/A	0.62	0.85	0.3672	0.932	0.57637	singleton
	rs3826501	intron	G/A	0.74	0.14	0.4185	0.8978	0.71661	rs17706630
	rs161393	intron	A/G	0.68	1	0.1156	0.7581	0.27844	rs224534, rs224536, rs12936340
	rs222747	p.I315M	C/G	0.79	0.52	0.1432	0.3577	0.15654	singleton
	rs222749	p.S91P	C/T	0.96	0.15	0.5399	0.911	0.67326	singleton
	rs733080	intron	T/C	0.71	0.76	0.2179	0.9388	0.4684	rs2277675, rs7217945
	rs222741	intron	T/C	0.77	0.46	0.0873	0.1159	0.04485	rs460716, rs465563
	rs182637	intron	G/A	0.55	0.07	0.0143	0.4169	0.05685	singleton
	rs224546	intron	C/T				39.73% missing		rs224547
	rs4790151	intron	A/G				100% missing		rs9902581, rs161365, rs877611, rs11655540
	rs150846	intron	A/G				100% missing		singleton
	rs161364	intron	T/C				100% missing		singleton
TRPV2	rs3813769	5' UTR	A/G	0.71	0.46	0.2757	0.7081	0.39988	singleton
	rs4792738	intron	G/A	0.71	0.83	0.3326	0.8525	0.49811	rs8079271
	rs8079010	intron	C/T	0.66	0.77	0.7174	0.2689	0.34318	singleton
	rs11078341	intron	G/C	0.62	0.78	0.8122	0.4802	0.72214	rs7222754, rs8121, rs7223205, rs4792742, rs1129235, rs7208718, rs7214366, rs4072454, rs3935801, rs9251, rs7215836
	rs12936240	intron	G/T	0.74	1	0.7628	0.8957	0.7933	singleton
	rs11871958	3' near gene	T/C	0.73	0.91	0.5452	0.7554	0.88806	singleton
	rs4561507	intron	G/C				22.42% missing		rs7217735
	rs7208811	3' UTR	A/C	0.61	0.79	0.8607	0.4619	0.68442	rs2271158
TRPV3	rs7219780	intron	T/C	0.52	0.33	0.6703	0.1791	0.50001	singleton
	rs7218756	intron	A/G	0.5	1	0.9026	0.2078	0.43178	singleton
	rs7217270	intron	G/A	0.61	0.15	0.018	0.7346	0.12683	rs7216486, rs8079054, rs7207628, rs11656938, rs925102, rs17763099, rs17175319, rs925101

	rs9906883	intron	G/A	0.7	0.76	0.2515	0.1282	0.09582	rs12944105, rs8081785
	rs11078454	intron	T/C	0.61	0.58	0.0051	0.4687	0.04371	singleton
	rs4790145	intron	A/G	0.6	0.21	0.8871	0.1742	0.32714	rs365350
	rs395357	synonymous	T/C	0.51	0.23	0.8275	0.581	0.79964	singleton
	rs322942	intron	A/G	0.5	1	0.9574	0.4369	0.57054	rs322943
	rs11078458	synonymous	G/T	0.59	1	0.9154	0.7511	0.87783	singleton
	rs322937	p.G117R	A/G	0.59	0.79	0.7785	0.6205	0.85538	singleton
	rs1039519	synonymous	A/G	0.6	0.85	0.3898	0.8344	0.53701	singleton
	rs2455858	intron	T/A	0.59	0.65	0.2539	0.8811	0.47416	singleton
	rs1699138	intron	C/T	0.72	0.91	0.7624	0.7534	0.9551	singleton
	rs4790519	intron	T/C	0.58	0.6	0.3744	0.6124	0.88898	singleton
	rs322962	intron	C/T	0.68	0.31	0.6467	0.8663	0.90143	singleton
	rs9911213	intron	A/G				100% missing		rs422159, rs661835
	rs12451131	intron	C/T				22.42% missing		singleton
	rs322964	intron	C/G				100% missing		singleton
	rs7212403	intron	A/G				100% missing		singleton
	rs4790520	5' near gene	C/T				100% missing		singleton
	rs454106	intron	T/C				41.56% missing		singleton
TRPV4	rs4766631	3' near gene	G/A	0.54	0.93	0.466	0.0615	0.38628	singleton
	rs11068274	intron	G/A	0.57	0.79	0.074	0.7326	0.22918	singleton
	rs1861810	intron	C/A	0.59	0.57	in LD with rs11068274 (r ² =0.935)			singleton
	rs10735104	intron	C/T	0.51	1	0.8161	0.1676	0.41622	singleton
	rs3825394	synonymous	C/A	0.53	0.48	0.3904	0.9821	0.65751	rs10850783, rs1861809, rs10850801
	rs7971845	intron	C/G	0.74	0.09	0.5073	0.4794	0.38997	singleton
	rs10774912	intron	T/C	0.73	0.67	0.16	0.7868	0.34413	rs10850800, rs10850781, rs10774911, rs3742031, rs10744892
	rs10850830	5' near gene	C/T	0.51	0.34	0.0411	0.9491	0.26685	singleton

MAF, Minor Allele Frequency. SNP, Single Nucleotide Polymorphism. LD, Linkage Disequilibrium. HWE, Hardy-Weinberg Equilibrium.

#SNPs were excluded from the case-control association study if did not pass through the SNPLex design pipeline (SNPLex design) were not in Hardy-Weinberg equilibrium in the control sample ($p < 0.01$) (HWE) or there was a genotyping failure, in which case the percentage of missing genotypes is indicated.