

Supplementary Table 1: Overview of samples from cohort 1 used to compose the DNA pools

City	# association samples	Bad hearing pool	Average Zscore cases	Good hearing pool	Average Zscore controls	Total	Quantile
Antwerp	966	192	1.31	192	-0.52	384	19.9
Copenhagen	396	96	2.05	96	-0.66	192	24.2
Tubingen	387	96	1.78	96	-0.48	192	24.8
Gent	337	96	1.05	96	-0.79	192	28.5
Padova	327	96	1.47	96	-0.31	192	29.4
Nijmegen	273	90	1.53	90	-0.51	180	33.0
Subtotal Europe	2686	666	/	666	/	1332	/
Oulu	496	96	1.1	96	-0.82	192	19.4
Tampere	252	84	2.04	84	-0.56	168	33.0
Subtotal Finland	748	180	/	180	/	360	/
Total	3434	846	/	846	/	1692	/

Supplementary Table 2: Individual-genotyping of European samples of the 252 top-ranked SNPs

SNP	Gene	Location	Pooled		Associated	HWpval	MAF	Case,Control Frequencies	Chi square ¹	P value
			Ranking	Alleles	Allele					
rs6132107	DTD1	intron	154	A:G	A	0.3064	0.134	0.899, 0.835	24.207	8.65E-07
rs6136423	DTD1	intron	474	G:A	G	0.152	0.139	0.891, 0.832	20.822	5.04E-06
rs9942			247	C:T	C	1	0.142	0.886, 0.831	17.085	3.57E-05
rs6035106	DTD1	intron	64	C:T	T	0.9473	0.498	0.537, 0.460	16.591	4.64E-05
rs7236715			333	T:C	T	0.2652	0.299	0.737, 0.667	16.12	5.95E-05
rs9403969			282	T:G	G	0.6884	0.258	0.292, 0.226	15.686	7.48E-05
rs4813338	DTD1	intron	13	G:A	A	0.7373	0.497	0.535, 0.461	15.423	8.59E-05
rs11594945			45	T:C	T	0.7786	0.194	0.835, 0.777	14.402	1.00E-04
rs10193454	TTC15	intron	458	G:A	G	0.6564	0.143	0.883, 0.833	14.088	2.00E-04
rs17796442			302	G:C	G	0.2815	0.496	0.539, 0.469	13.675	2.00E-04
rs9565238			492	C:G	G	0.852	0.313	0.347, 0.281	14.193	2.00E-04
rs9845917	DLEC1	intron	139	T:C	C	0.693	0.345	0.378, 0.313	12.741	4.00E-04
rs562293			595	C:G	G	0.4343	0.249	0.278, 0.220	12.436	4.00E-04
rs10495177			643	T:C	T	0.8488	0.38	0.653, 0.589	12.102	5.00E-04
rs11928865	GRM7	intron	3	T:A	T	0.8713	0.259	0.769, 0.714	11.244	8.00E-04
rs2280307	RHOH	intron	79	G:A	G	0.0112	0.325	0.704, 0.646	10.837	0.001
rs3934723			17	C:G	C	1	0.388	0.642, 0.583	10.267	0.0014
rs2295956			188	T:G	T	0.0508	0.242	0.784, 0.732	9.951	0.0016
rs10229361			32	C:A	C	0.9523	0.174	0.849, 0.805	9.439	0.0021
rs11985327			186	C:T	T	0.2337	0.344	0.372, 0.318	9.257	0.0023
rs10134299	RIN3	intron	418	T:G	T	0.5452	0.123	0.896, 0.858	9.254	0.0023
rs2104237	RIN3	intron	31	A:G	A	0.5795	0.124	0.896, 0.858	9.285	0.0023
rs7163460	IQCH	intron	175	A:G	A	0.7433	0.226	0.798, 0.750	9.192	0.0024
rs13313527			293	G:A	G	0.6205	0.385	0.643, 0.587	9.135	0.0025
rs9632550			100	G:A	G	0.6702	0.125	0.894, 0.857	8.916	0.0028
rs7048135			460	T:G	T	0.6749	0.157	0.864, 0.823	8.846	0.0029
rs2056116			26	A:G	A	0.7882	0.383	0.644, 0.591	8.381	0.0038
rs6426044			127	G:A	G	0.1621	0.226	0.797, 0.752	8.376	0.0038
rs17454023			449	T:C	T	0.8409	0.456	0.572, 0.518	8.308	0.0039
rs4728377			568	T:C	T	1	0.174	0.847, 0.805	8.311	0.0039

rs11609020			103	A:G	A	0.2605	0.128	0.890, 0.854	8.268	0.004
rs4836672			325	G:A	A	0.3949	0.041	0.052, 0.030	8.306	0.004
rs9514229			190	G:C	G	0.9743	0.13	0.889, 0.852	8.249	0.0041
rs11654023			288	A:C	A	0.2739	0.157	0.863, 0.824	8.204	0.0042
rs3813948	C4BPB	intron	251	A:G	A	0.0892	0.073	0.941, 0.913	8.127	0.0044
rs6440052			218	T:C	T	0.1576	0.263	0.761, 0.714	7.731	0.0054
rs10132168	TC2N	intron	239	G:T	G	0.6611	0.029	0.980, 0.962	7.607	0.0058
rs2688388	CSMD1	intron	131	T:C	T	0.4341	0.259	0.764, 0.719	7.493	0.0062
rs1016730	ASTN2	intron	159	T:A	T	1	0.424	0.602, 0.550	7.39	0.0066
rs16899799	FGFR1OP	intron	68	A:G	A	1	0.018	0.988, 0.975	7.27	0.007
rs3794261	METAP2,USP44	coding-synonymous,intron,reference	36	G:T	G	0.3361	0.095	0.920, 0.890	7.236	0.0071
rs6768608	KCNMB2	intron	428	G:C	G	0.3462	0.387	0.638, 0.589	7.199	0.0073
rs4433032	WIPI2	intron	312	C:G	C	0.531	0.067	0.946, 0.921	7.098	0.0077
rs10157110	KIAA126	intron	388	T:G	T	0.0727	0.224	0.797, 0.756	7.052	0.0079
rs16952027			493	T:A	T	0.3957	0.092	0.923, 0.894	6.942	0.0084
rs9602899			640	C:G	G	0.9866	0.358	0.383, 0.335	6.899	0.0086
rs9972796			421	A:C	C	0.4406	0.326	0.349, 0.303	6.863	0.0088
rs10187051	LOC388963	intron	389	T:C	T	0.8408	0.137	0.880, 0.846	6.684	0.0097
rs10508823			635	G:A	G	0.2904	0.162	0.856, 0.820	6.658	0.0099
rs6023649			616	G:A	G	0.1398	0.262	0.760, 0.717	6.654	0.0099
rs6544006			519	C:T	C	0.4851	0.083	0.931, 0.904	6.591	0.0102
rs2505700			516	T:C	T	0.6084	0.121	0.895, 0.863	6.536	0.0106
rs11138851			263	A:G	A	0.3585	0.149	0.868, 0.834	6.423	0.0113
rs1425073			385	C:T	C	0.7672	0.434	0.590, 0.543	6.378	0.0116
rs11712177			404	C:G	C	0.9316	0.318	0.704, 0.660	6.375	0.0116
rs4568885			609	A:G	A	0.1247	0.04	0.970, 0.951	6.136	0.0132
rs16954288			116	T:A	T	0.4688	0.1	0.914, 0.886	6.115	0.0134
rs11104675			406	G:A	G	0.5528	0.198	0.821, 0.784	5.939	0.0148
rs1242535			187	C:T	C	0.0468	0.077	0.935, 0.910	5.898	0.0152
rs1563696			221	G:A	G	0.3057	0.347	0.675, 0.632	5.845	0.0156
rs2515800			437	T:C	T	0.6516	0.164	0.853, 0.819	5.827	0.0158
rs2733027			248	C:T	C	0.2646	0.46	0.563, 0.518	5.782	0.0162
rs9317304			442	G:A	G	0.5332	0.208	0.810, 0.774	5.608	0.0179

rs10945909			422	C:T	T	0.348	0.472	0.494, 0.450	5.594	0.018
rs17652307	FLJ3281	intron	382	A:G	A	0.7625	0.047	0.962, 0.943	5.561	0.0184
rs2983088			435	A:G	A	1	0.024	0.983, 0.970	5.439	0.0197
rs888438	RYR2	intron	151	G:T	G	0.2617	0.185	0.832, 0.799	5.304	0.0213
rs17123109	C12orf54	intron	544	A:G	A	0.759	0.055	0.955, 0.935	5.269	0.0217
rs10996614			157	T:C	T	0.7384	0.047	0.962, 0.944	5.12	0.0237
rs7920090			208	A:T	A	0.9702	0.175	0.842, 0.809	5.067	0.0244
rs6890492			1	A:G	A	0.704	0.108	0.905, 0.879	5.011	0.0252
rs2174297			2	C:T	C	0.2584	0.345	0.676, 0.636	4.968	0.0258
rs8079727	NLRP1	intron	545	A:C	A	0.1314	0.247	0.771, 0.735	4.955	0.026
rs16869623			5	T:G	T	0.3141	0.071	0.940, 0.918	4.922	0.0265
rs17716738			237	T:C	T	0.5696	0.123	0.891, 0.864	4.9	0.0269
rs489927			210	C:T	C	0.3688	0.024	0.983, 0.970	4.877	0.0272
rs7305501			439	A:G	A	0.3639	0.24	0.778, 0.742	4.829	0.028
rs6444452			409	C:T	C	0.5983	0.072	0.939, 0.917	4.788	0.0287
rs10112140			205	T:C	C	0.0846	0.477	0.498, 0.457	4.775	0.0289
rs11853442			10	G:A	G	0.8181	0.452	0.569, 0.528	4.665	0.0308
rs4584805			482	G:A	G	0.1504	0.228	0.790, 0.755	4.643	0.0312
rs9992098			123	T:C	T	0.8206	0.06	0.949, 0.930	4.558	0.0328
rs9869419			51	A:G	A	1	0.066	0.944, 0.924	4.525	0.0334
rs8181973	FAM12A	intron	104	A:G	A	0.8067	0.115	0.898, 0.873	4.405	0.0358
rs11784580			25	C:G	C	0.1688	0.334	0.685, 0.648	4.366	0.0367
rs9813040			526	A:G	A	0.5555	0.111	0.901, 0.876	4.347	0.0371
rs10483002			252	T:G	T	1	0.036	0.971, 0.957	4.115	0.0425
rs8009668			542	G:A	G	0.4844	0.222	0.795, 0.763	4.074	0.0435
rs7895344			108	T:C	T	0.3163	0.276	0.741, 0.707	4.064	0.0438
rs17127945	ATXN3	intron	129	A:G	A	0.9925	0.178	0.836, 0.807	4.001	0.0455
rs1466183			378	T:G	T	1	0.048	0.960, 0.944	3.974	0.0462
rs17284739	PFKP	intron	120	A:G	A	1	0.058	0.951, 0.933	3.962	0.0465
rs17558231			24	T:G	T	0.8931	0.059	0.950, 0.932	3.937	0.0472
rs10867852			551	C:T	C	0.574	0.071	0.939, 0.920	3.727	0.0535
rs10947914			80	T:A	A	0.0171	0.239	0.255, 0.224	3.697	0.0545
rs2952322			84	A:T	A	1	0.217	0.798, 0.768	3.68	0.0551

rs999745			606	C:T	C	0.4558	0.402	0.616, 0.580	3.673	0.0553
rs553648	ZFYVE9	intron	623	G:A	G	1	0.028	0.978, 0.966	3.658	0.0558
rs4319945	GRB14	intron	44	T:C	T	0.5735	0.284	0.732, 0.700	3.589	0.0582
rs2584991			91	G:A	G	0.2681	0.188	0.827, 0.799	3.498	0.0614
rs10514777	AFF3	intron	194	A:G	A	0.8627	0.197	0.818, 0.790	3.474	0.0623
rs7699643			600	T:C	T	0.6529	0.133	0.879, 0.856	3.451	0.0632
rs17573253	CCT4	intron	37	A:G	G	0.4717	0.241	0.256, 0.226	3.436	0.0638
rs17727615	PDE4D	intron	234	C:G	C	0.8093	0.077	0.933, 0.914	3.353	0.0671
rs982932	RORA	intron	351	T:C	C	0.5482	0.357	0.374, 0.341	3.318	0.0685
rs7187365			292	C:T	C	0.9225	0.165	0.848, 0.822	3.313	0.0687
rs4734143			166	C:T	C	0.8215	0.299	0.717, 0.685	3.302	0.0692
rs13064847	TP63	intron	124	C:G	C	0.6621	0.058	0.950, 0.934	3.281	0.0701
rs11020938	GRM5	intron	89	T:C	T	0.1806	0.019	0.985, 0.976	3.211	0.0732
rs276672			115	A:G	A	0.3219	0.196	0.818, 0.791	3.203	0.0735
rs2871238			256	A:T	T	0.9052	0.47	0.487, 0.453	3.173	0.0749
rs6836600			384	C:T	C	0.801	0.031	0.975, 0.963	3.168	0.0751
rs16852308			489	C:T	C	0.0544	0.069	0.940, 0.923	3.162	0.0754
rs12328731			39	T:G	T	1.55E-16	0.208	0.806, 0.778	3.154	0.0757
rs9299249	ASTN2	intron	355	A:G	G	0.9775	0.491	0.508, 0.474	3.132	0.0768
rs256177			359	C:G	C	0.5354	0.157	0.855, 0.831	3.123	0.0772
rs6444338			203	G:A	G	1	0.035	0.971, 0.959	3.111	0.0778
rs2169450	CDH13	intron	169	G:C	G	0.4105	0.118	0.893, 0.872	2.973	0.0847
rs6855230			570	A:G	A	0.2204	0.18	0.833, 0.808	2.948	0.086
rs1388611	PTPRG	intron	559	A:G	A	0.7843	0.222	0.791, 0.765	2.842	0.0918
rs2486027			33	C:A	C	1	0.061	0.946, 0.931	2.842	0.0918
rs8118269			109	A:G	A	0.5042	0.031	0.975, 0.964	2.832	0.0924
rs17214392	C4orf26	intron	176	A:C	A	0.309	0.228	0.786, 0.759	2.822	0.093
rs9838048			22	C:T	C	0.975	0.106	0.904, 0.884	2.802	0.0942
rs2651558			35	A:G	A	0.0827	0.14	0.871, 0.849	2.755	0.097
rs17333110			541	A:G	A	1	0.049	0.958, 0.945	2.729	0.0985
rs490144			128	T:G	T	0.613	0.045	0.962, 0.949	2.728	0.0986
rs17015175	ROBO2	intron	214	G:A	G	0.0477	0.104	0.905, 0.886	2.725	0.0988
rs4905587			202	G:T	G	1	0.11	0.900, 0.880	2.637	0.1044

rs833621			373	A:G	G	0.2258	0.368	0.382, 0.353	2.538	0.1111
rs4475756	KIF1B	intron	556	A:G	A	0.1829	0.341	0.673, 0.645	2.429	0.1191
rs17023472	RBMS3	intron	257	C:G	C	1	0.018	0.986, 0.978	2.421	0.1197
rs17120651			309	A:G	A	0.3733	0.033	0.972, 0.962	2.38	0.1229
rs4072273			142	T:G	T	0.3998	0.046	0.960, 0.948	2.378	0.123
rs8103388			555	A:G	A	0.7589	0.172	0.839, 0.817	2.343	0.1259
rs17237865			411	A:G	A	0.4192	0.144	0.866, 0.846	2.272	0.1317
rs8186775			614	G:T	G	0.098	0.044	0.962, 0.950	2.226	0.1357
rs2584622	SMARCD2	mrna-utr	72	T:C	T	0.7014	0.07	0.938, 0.923	2.153	0.1423
rs2301702	AKAP1	intron	585	C:T	C	0.5935	0.136	0.873, 0.854	2.149	0.1427
rs7119608			63	A:C	A	1.05E-13	0.079	0.929, 0.914	2.149	0.1427
rs8179740	TBC1D8	intron	66	C:T	C	0.2118	0.134	0.875, 0.857	2.037	0.1535
rs4356573			538	A:C	A	1	0.304	0.708, 0.683	2.01	0.1562
rs1269077			150	T:G	T	0.8972	0.215	0.796, 0.775	1.914	0.1665
rs806274			605	C:A	C	0.307	0.031	0.973, 0.964	1.887	0.1695
rs799718			130	G:C	G	0.9015	0.08	0.927, 0.913	1.864	0.1722
rs11048790			167	G:C	G	0.6148	0.092	0.915, 0.901	1.787	0.1814
rs7234814	FHOD3	intron	344	T:C	T	0.6583	0.038	0.967, 0.957	1.745	0.1866
rs605909			52	G:A	G	0.228	0.089	0.918, 0.904	1.725	0.189
rs11215936			177	G:A	G	0.8193	0.054	0.952, 0.941	1.653	0.1985
rs17058481			168	C:G	C	1	0.065	0.941, 0.929	1.628	0.2019
rs6090159	DIDO1	intron	138	C:G	C	0.0704	0.202	0.808, 0.789	1.622	0.2028
rs12651043			488	C:T	C	0.9329	0.147	0.861, 0.844	1.603	0.2055
rs2171504	SPATA12	intron	122	A:C	A	0.6191	0.041	0.964, 0.954	1.579	0.2089
rs4438459			98	C:T	C	0.7214	0.363	0.648, 0.625	1.575	0.2094
rs6507256			75	C:T	C	0.4746	0.113	0.894, 0.879	1.57	0.2102
rs16956753			496	T:C	T	1	0.019	0.984, 0.977	1.553	0.2127
rs815471	ERC2	intron	327	G:A	A	0.4109	0.116	0.124, 0.109	1.536	0.2152
rs6751498			30	A:C	A	0.1204	0.056	0.950, 0.939	1.526	0.2167
rs17369163			141	C:G	C	0.0544	0.13	0.878, 0.863	1.487	0.2226
rs4737369			74	C:T	C	1	0.336	0.675, 0.653	1.485	0.223
rs10513557	PPM1L	intron	14	C:T	C	0.4762	0.042	0.962, 0.953	1.418	0.2337
rs2210723			147	A:G	A	0.6223	0.08	0.926, 0.914	1.398	0.2371

rs7131977	ALDH1L2	intron	527	A:G	A	0.9509	0.034	0.970, 0.962	1.379	0.2402
rs9657021	CYP11B1	intron	86	T:C	T	0.7278	0.027	0.977, 0.970	1.324	0.2499
rs4737395			484	A:G	A	0.1848	0.115	0.892, 0.879	1.299	0.2544
rs6557093	PLEKHG1	intron	480	C:A	C	0.8746	0.148	0.859, 0.845	1.215	0.2703
rs2628235			515	C:G	C	0.9705	0.044	0.960, 0.952	1.211	0.2712
rs2077354	HIVEP3	intron	261	T:C	T	1	0.002	0.999, 0.997	1.185	0.2764
rs16904196			249	A:C	A	1	0.025	0.978, 0.972	1.123	0.2893
rs1903977	PRKG1	intron	102	A:T	A	0.5449	0.396	0.614, 0.594	1.116	0.2907
rs1025205			453	T:C	T	0.4269	0.112	0.894, 0.882	1.083	0.298
rs713971	CACNA1I	intron	637	T:C	T	0.5894	0.089	0.916, 0.905	1.051	0.3052
rs4679417			23	A:G	A	1	0.038	0.966, 0.959	1.049	0.3057
rs6736648	ZNF142	intron	342	A:G	A	0.6371	0.038	0.966, 0.959	1.003	0.3167
rs17137871			509	T:C	T	0.7254	0.083	0.922, 0.912	0.967	0.3253
rs1373978	DNAH5	intron	636	A:C	A	0.7092	0.03	0.973, 0.967	0.939	0.3326
rs6433660			625	C:T	C	0.3261	0.011	0.991, 0.987	0.933	0.3341
rs9330317			487	G:C	G	0.9034	0.085	0.920, 0.910	0.917	0.3382
rs1946643	CTNNA2	intron	508	G:A	G	0.6285	0.112	0.893, 0.882	0.916	0.3385
rs10913190	PAPPA2	intron	207	T:C	T	0.9662	0.063	0.941, 0.933	0.884	0.3471
rs17162072			588	G:A	G	0.6158	0.267	0.741, 0.726	0.859	0.3539
rs772378			307	T:C	T	0.8767	0.049	0.955, 0.947	0.829	0.3626
rs2448144			501	C:T	T	0.648	0.075	0.080, 0.071	0.793	0.3731
rs16834361			620	C:T	C	0.3404	0.04	0.964, 0.957	0.75	0.3865
rs603446	ZNF259	intron	272	C:T	C	0.9143	0.419	0.589, 0.573	0.721	0.3957
rs11039351			512	C:T	C	0.1786	0.053	0.951, 0.944	0.713	0.3984
rs12654448	SLIT3	intron	423	C:T	C	0.3938	0.068	0.936, 0.928	0.676	0.4108
rs2399681			564	G:A	G	0.6549	0.353	0.654, 0.639	0.67	0.4129
rs11668272	NLRP4	intron	246	G:A	G	0.5226	0.162	0.844, 0.832	0.665	0.4146
rs7913781			401	A:G	G	0.6446	0.064	0.068, 0.060	0.659	0.4168
rs11078697	SENP3	intron	505	C:T	C	1	0.015	0.987, 0.983	0.653	0.4192
rs1863939	KIAA947	intron	181	G:A	G	0.1059	0.044	0.959, 0.953	0.632	0.4265
rs1913453			500	A:G	A	0.8859	0.175	0.831, 0.820	0.626	0.429
rs13421576			94	C:T	T	1	0.035	0.038, 0.032	0.6	0.4385
rs1907382	MKX	intron	476	G:A	G	0.4081	0.084	0.920, 0.912	0.554	0.4566

rs988856	SPOCK1	intron	445	G:A	G	0.0325	0.158	0.847, 0.837	0.503	0.4781
rs2270603	DKFZP434B335	intron	119	C:T	C	0.7496	0.152	0.853, 0.844	0.471	0.4923
rs6744483			490	T:C	T	0.6116	0.101	0.903, 0.895	0.47	0.4932
rs2305912	UNC13D,UNK	locus-region,mrna-utr	607	T:C	T	1	0.021	0.981, 0.978	0.442	0.506
rs9309974			362	G:C	C	0.1376	0.026	0.028, 0.024	0.433	0.5106
rs2274598			43	A:G	G	0.9924	0.022	0.024, 0.020	0.422	0.5161
rs190038			262	T:A	T	0.743	0.018	0.983, 0.980	0.377	0.5393
rs11065386	HNF1A	intron	638	T:C	C	0.6195	0.028	0.030, 0.026	0.37	0.543
rs16825392			366	T:C	C	1	0.027	0.029, 0.025	0.35	0.5542
rs6834153	CPZ	intron	303	G:A	A	1	0.016	0.018, 0.015	0.345	0.557
rs548902			426	T:C	T	0.5972	0.427	0.578, 0.568	0.331	0.5652
rs10850886	KSR2	intron	456	A:C	A	0.547	0.098	0.905, 0.899	0.315	0.5745
rs10450466			372	T:C	T	1	0.019	0.983, 0.980	0.311	0.577
rs1456566			350	A:G	G	0.6214	0.119	0.122, 0.115	0.306	0.5803
rs17065005	LMO7	intron	276	C:T	T	1	0.12	0.124, 0.117	0.302	0.5823
rs920113			93	C:T	C	0.1915	0.054	0.949, 0.944	0.293	0.5883
rs4787041	A2BP1	intron	179	T:C	T	1	0.02	0.982, 0.979	0.288	0.5912
rs12626719			56	T:C	T	4.00E-04	0.031	0.971, 0.968	0.281	0.5961
rs2306936	RHOC	intron	335	C:T	C	0.6584	0.058	0.944, 0.940	0.28	0.5965
rs287539			363	A:T	T	0.4951	0.043	0.045, 0.041	0.259	0.6108
rs17215946			353	T:C	T	1	0.01	0.991, 0.990	0.241	0.6233
rs2693443			118	T:C	C	1	0.056	0.058, 0.054	0.226	0.6344
rs36359			254	A:G	A	0.9256	0.103	0.899, 0.894	0.214	0.6438
rs16969103			274	A:G	A	0.2225	0.043	0.959, 0.955	0.21	0.6465
rs5762201			161	G:A	G	0.1536	0.052	0.950, 0.946	0.203	0.6523
rs4426986			560	G:A	G	0.4582	0.078	0.924, 0.920	0.183	0.6685
rs7842019			53	A:G	A	0.2609	0.156	0.847, 0.841	0.177	0.6739
rs1544935			78	A:C	A	0.2959	0.232	0.772, 0.765	0.16	0.6892
rs16971748			213	G:A	G	0.0193	0.052	0.950, 0.947	0.149	0.6998
rs11179614			553	G:A	G	0.3039	0.093	0.909, 0.905	0.14	0.7086
rs2116714			598	G:A	A	1	0.006	0.007, 0.006	0.1	0.7512
rs11081279	ARHGAP28	intron	615	A:G	A	0.5933	0.05	0.951, 0.948	0.09	0.7644
rs769242	CCNA2	coding-nonsynonymous,reference	642	G:A	G	1	0.039	0.962, 0.960	0.085	0.7704

rs7749012			54	A:G	G	0.4137	0.033	0.034, 0.032	0.082	0.774
rs7474778			11	C:T	T	0.5918	0.293	0.295, 0.290	0.082	0.7744
rs17712680			105	T:G	G	0.6899	0.056	0.057, 0.055	0.061	0.8042
rs17037744			280	C:T	T	0.2526	0.146	0.148, 0.145	0.053	0.8186
rs6733394			529	T:G	G	0.6173	0.052	0.053, 0.051	0.049	0.8249
rs17235154			215	T:C	T	0.7908	0.054	0.947, 0.945	0.047	0.8285
rs10509685	PDLIM1	intron	478	G:A	G	0.7047	0.074	0.927, 0.925	0.039	0.8427
rs17148851	SMR3A	intron	290	C:T	T	0.2811	0.058	0.059, 0.057	0.035	0.8514
rs12230077			364	A:G	A	1	0.03	0.971, 0.970	0.031	0.86
rs2334111	CTSO	intron	394	C:T	T	1	0.021	0.022, 0.021	0.03	0.8628
rs2427016	CDH4	intron	622	C:T	T	1	0.117	0.118, 0.116	0.027	0.8691
rs1861536			61	C:T	T	0.2473	0.06	0.061, 0.059	0.019	0.8893
rs9394723			634	G:A	G	1	0.084	0.917, 0.916	0.019	0.8911
rs7024708			573	A:G	A	0.7839	0.088	0.913, 0.912	0.008	0.93
rs16953782			195	A:G	G	1	0.035	0.035, 0.035	0.002	0.9622
rs10485043			269	G:A	A	1	0.002	0.002, 0.002	0.001	0.9695
rs6494420	HERC1	intron	438	A:G	G	0.0667	0.061	0.062, 0.061	0.001	0.9724
rs10750596	FLJ3281	intron	591	A:T	A	0.0935	0.237	0.763, 0.763	0.001	0.9763
rs12638278			216	C:T	T	0.936	0.023	0.023, 0.023	0	0.9887
rs1340668	TINAG	intron	466	C:T	C	1	0.017	0.983, 0.983	0	0.9891
rs7780223			383	C:A	C	1	0.078	0.922, 0.922	0	0.9892
rs2805860	DAB1	intron	28	G:C	C	0.9237	0.021	0.021, 0.021	0	0.9908
rs7840631	FUT1	intron	574	T:T	T	1	T:T	N/A	0	1
rs7627457			224	G:A	G	1	G:A	N/A	0	1

[†]Chi-square p-values after individual-genotyping of all European samples combined.

Supplementary Table 3: Individual-genotyping of Finnish samples of the 177 top-ranked SNPs

SNP	Gene	Location	Pooled		Associated		HWpval	MAF	Case,Control Frequencies	Chi square ¹	P value
			Ranking	Alleles	Allele						
rs2839580	PDE9A	intron	124	T:G	G	0.8025	0.405	177:179, 112:246	25.176	5.23E-07	
rs10802205	KIF26B	intron	92	T:C	T	0.3878	0.487	210:144, 155:203	18.297	1.89E-05	
rs7308245			15	G:A	A	0.4795	0.329	144:212, 91:267	18.263	1.92E-05	
rs17415514	PLCE1	intron	76	T:C	T	0.3293	0.236	288:58, 244:106	17.665	2.63E-05	
rs1884869			126	T:C	T	0.7583	0.434	228:128, 175:181	16.061	6.13E-05	
rs3849811			1	A:G	A	0.3987	0.214	300:54, 258:98	15.893	6.70E-05	
rs11166358			58	T:C	T	0.7796	0.337	261:95, 211:145	15.713	7.37E-05	
rs8057489	CDH13	intron	146	C:A	A	0.2587	0.379	158:194, 109:243	14.487	1.00E-04	
rs10936200	LOC34881	intron	77	C:G	C	0.4707	0.282	277:77, 234:124	14.586	1.00E-04	
rs6086737			2	G:C	C	0.7081	0.482	193:157, 147:209	13.561	2.00E-04	
rs2022601	SLC25A21	intron	38	G:A	A	0.6349	0.37	156:200, 107:247	14.066	2.00E-04	
rs4246794			137	C:T	T	0.3607	0.363	152:202, 105:249	13.493	2.00E-04	
rs4692949	PALLD	intron	200	T:C	C	0.5352	0.409	165:179, 121:235	14.143	2.00E-04	
rs13043535			131	T:C	T	0.8393	0.413	233:123, 185:171	13.349	3.00E-04	
rs796459			59	C:T	C	0.0346	0.387	236:112, 183:153	12.841	3.00E-04	
rs10458144			41	C:T	C	0.2137	0.496	203:153, 157:201	12.381	4.00E-04	
rs4982640			112	A:T	A	0.2835	0.404	234:120, 188:166	12.413	4.00E-04	
rs17154077	COG5	intron	27	T:C	C	0.9154	0.31	132:224, 89:269	12.469	4.00E-04	
rs2520241	COG5	intron	33	T:C	C	0.9154	0.31	132:224, 89:269	12.469	4.00E-04	
rs798601			51	T:A	T	0.069	0.374	242:108, 201:157	12.766	4.00E-04	
rs1077729			13	G:A	G	0.3903	0.451	219:137, 173:185	12.548	4.00E-04	
rs179736	STRN3	intron	83	C:T	C	0.9449	0.461	215:141, 168:186	11.955	5.00E-04	
rs12626774	PDE9A	intron	12	G:C	G	0.2218	0.407	234:122, 188:168	12.311	5.00E-04	
rs1559096			180	T:C	T	0.0013	0.07	341:13, 321:37	12.102	5.00E-04	
rs11249611			139	T:C	T	1	0.33	255:93, 217:139	12.091	5.00E-04	
rs1884655			82	A:G	G	0.3157	0.249	108:246, 69:287	11.742	6.00E-04	
rs2487928	KIAA1462	intron	165	G:A	G	0.6025	0.465	210:140, 168:188	11.641	6.00E-04	
rs2250435			87	T:A	A	1	0.189	85:271, 50:308	11.433	7.00E-04	
rs10888197			32	A:G	A	1	0.441	217:131, 178:180	11.432	7.00E-04	
rs4835748	C5orf5	intron	23	C:T	T	0.3337	0.484	195:161, 148:204	11.484	7.00E-04	
rs7484197	SPON1	intron	31	A:G	A	0.1495	0.338	257:99, 216:142	11.221	8.00E-04	

rs12421865	IGSF22	intron	28	A:G	A	1	0.224	295:61, 259:99	11.359	8.00E-04
rs4810949			57	G:T	G	0.0916	0.275	275:77, 238:118	11.267	8.00E-04
rs10872897	SLC25A21	intron	105	A:T	T	0.3562	0.382	156:196, 115:243	11.185	8.00E-04
rs7213894	DNAH2	coding-nonsynonymous,reference	173	T:C	T	0.9273	0.4	234:120, 193:165	11.02	9.00E-04
rs198838			24	G:A	G	1	0.466	211:143, 168:188	10.991	9.00E-04
rs17078346			7	A:C	A	0.3402	0.092	336:20, 312:46	11.126	9.00E-04
rs3734279	EYA4	mrna-utr	42	C:T	T	0.9056	0.38	156:198, 113:241	11.085	9.00E-04
rs9532534			159	C:T	C	0.3252	0.224	293:61, 258:98	10.828	0.001
rs283730			4	T:G	T	0.3383	0.401	235:121, 193:165	10.885	0.001
rs7728933			14	G:C	C	0.3366	0.483	193:161, 151:207	10.856	0.001
rs198837			78	T:A	T	1	0.465	210:142, 170:188	10.573	0.0011
rs13421717			43	C:T	T	0.286	0.239	103:251, 66:286	10.376	0.0013
rs16916451			99	T:C	T	0.4554	0.063	344:12, 325:33	10.334	0.0013
rs17095742			36	C:A	C	1	0.279	273:79, 239:119	10.289	0.0013
rs234184			61	A:G	A	1	0.277	275:79, 238:118	10.384	0.0013
rs11192913			17	C:T	C	0.6965	0.49	203:153, 161:197	10.372	0.0013
rs4838350			63	G:A	G	0.7725	0.323	257:93, 221:135	10.398	0.0013
rs4450130	ARHGAP22	intron	34	G:A	G	0.9853	0.274	276:78, 241:117	10.147	0.0014
rs10957671			114	T:G	G	0.7205	0.471	186:164, 142:204	10.228	0.0014
rs741714			10	A:G	A	0.1841	0.399	227:117, 185:157	10.115	0.0015
rs1365203	RBM35A	intron	69	G:C	C	0.2129	0.397	162:194, 120:234	9.988	0.0016
rs11677234	CCDC128	intron	18	C:G	C	0.4596	0.312	263:91, 227:131	9.83	0.0017
rs1416079			20	T:C	T	0.3613	0.136	322:34, 295:63	9.846	0.0017
rs9503199			35	G:A	G	0.1558	0.439	218:134, 178:176	9.725	0.0018
rs11139616			170	T:A	A	0.5599	0.419	169:185, 128:226	9.75	0.0018
rs10444538	KRT8	intron	19	C:T	C	0.0711	0.062	342:12, 326:32	9.452	0.0021
rs3743566	NDRG4	mrna-utr	119	C:T	C	0.1782	0.251	283:71, 249:107	9.448	0.0021
rs2677744	MAN2A2	intron	162	G:A	G	0.3488	0.396	235:121, 195:161	9.395	0.0022
rs2178824			83	C:T	C	0.9037	0.276	276:80, 241:117	9.313	0.0023
rs1770319			140	C:G	C	0.0568	0.404	232:124, 192:164	9.329	0.0023
rs11249609			153	G:A	G	0.8853	0.276	276:80, 241:117	9.313	0.0023
rs10831750	MICAL2	intron	179	C:T	T	0.8744	0.438	176:180, 136:220	9.128	0.0025
rs4982641			6	C:T	T	0.0454	0.387	145:181, 109:221	9.058	0.0026

rs12153575			145	C:G	G	0.3445	0.27	114:242, 79:279	8.969	0.0027
rs7495407			149	T:C	T	0.1883	0.313	263:93, 226:130	8.939	0.0028
rs1532414			72	T:G	G	0.5712	0.279	116:236, 81:273	8.902	0.0028
rs8060064			118	A:G	G	0.6335	0.219	94:260, 62:296	8.873	0.0029
rs4780599	ABCC6	intron	100	T:C	T	1	0.282	272:82, 238:118	8.741	0.0031
rs17116135	ATP1A	intron	151	T:C	T	0.0688	0.074	338:16, 321:37	8.737	0.0031
rs1466113	SSTR2	intron	141	G:C	C	0.4941	0.426	171:185, 132:224	8.739	0.0031
rs6737516			120	T:C	C	0.6177	0.346	141:213, 105:253	8.68	0.0032
rs4738374			107	T:C	T	0.9038	0.436	220:136, 178:172	8.59	0.0034
rs11126997			176	A:G	A	0.3252	0.224	291:63, 260:96	8.588	0.0034
rs1703086			117	G:A	A	1	0.293	122:234, 87:271	8.567	0.0034
rs17411126			116	T:C	T	0.1364	0.265	279:77, 246:112	8.55	0.0035
rs28571682			9	C:T	C	0.5669	0.134	318:34, 295:61	8.514	0.0035
rs247651			16	A:G	A	0.7456	0.18	305:49, 277:79	8.373	0.0038
rs1446535			62	C:T	T	1	0.292	120:232, 87:271	8.235	0.0041
rs1790256	INTS4	intron	94	A:G	A	0.0235	0.364	230:104, 192:138	8.175	0.0042
rs2066300			125	A:G	A	0.7454	0.422	221:129, 188:170	8.195	0.0042
rs6019582	ARFGEF2	intron	133	C:T	C	0.9143	0.257	272:72, 245:107	8.163	0.0043
rs4415156			129	T:C	T	0.0615	0.314	262:94, 228:130	8.139	0.0043
rs6952440			88	T:C	T	0.1632	0.436	215:133, 183:175	8.16	0.0043
rs2034507	LOC1556	mrna-utr	70	A:G	A	0.1172	0.417	224:128, 189:167	8.1	0.0044
rs8077799			53	C:T	C	0.8917	0.17	308:46, 283:75	7.986	0.0047
rs10484691	KHDRBS2	intron	177	G:C	C	0.7561	0.037	20:334, 6:350	7.907	0.0049
rs906796			144	A:C	C	0.2717	0.314	129:227, 95:263	7.8	0.0052
rs8013139			37	A:G	G	0.4993	0.255	107:249, 75:283	7.794	0.0052
rs41268	FLJ23834	intron	8	A:G	A	0.1168	0.112	326:28, 306:52	7.811	0.0052
rs7693366			29	T:C	C	0.1826	0.442	175:179, 139:217	7.768	0.0053
rs11122129			135	C:G	G	0.7887	0.159	70:286, 43:313	7.668	0.0056
rs17722963			128	A:G	G	0.1443	0.18	78:276, 50:306	7.666	0.0056
rs29776	LOC153222	locus-region	106	G:C	G	0.9045	0.396	233:123, 198:160	7.674	0.0056
rs10798263	FMO2	intron	179	T:C	T	0.2152	0.277	274:82, 241:115	7.642	0.0057
rs779701	GRM7	intron	152	T:C	T	0.575	0.323	257:97, 224:132	7.608	0.0058
rs11604865			3	T:C	C	1	0.183	79:275, 51:305	7.577	0.0059

rs9953621	ARHGAP28	intron	143	G:C	C	0.9407	0.355	144:212, 109:247	7.511	0.0061
rs2631988	ALK	intron	45	C:G	G	0.7616	0.317	130:226, 96:260	7.494	0.0062
rs6134907	TASPI	intron	122	T:G	G	1	0.224	94:258, 65:293	7.462	0.0063
rs9959465			148	C:T	C	0.1611	0.362	242:110, 211:147	7.398	0.0065
rs1634997	KIAA1324L	intron	108	G:A	A	0.17	0.424	169:187, 134:224	7.368	0.0066
rs779706	GRM7	intron	86	C:G	C	0.7026	0.332	252:100, 222:136	7.34	0.0067
rs17241282	PLA2R1	intron	64	T:C	C	0.38	0.439	174:182, 138:216	7.053	0.0079
rs2538485	FLJ21986	intron	93	T:C	C	0.4687	0.197	84:272, 56:300	6.971	0.0083
rs4755436	LDLRAD3	intron	29	G:A	G	0.9986	0.41	225:127, 194:164	6.948	0.0084
rs10849147			147	A:C	C	0.4561	0.181	78:278, 51:305	6.902	0.0086
rs7700917	JMJD1B	intron	109	T:C	C	0.4967	0.359	143:209, 111:245	6.864	0.0088
rs9863323	PTPRG	intron	172	C:A	C	0.1843	0.202	298:58, 270:86	6.825	0.009
rs11646019	CDH13	intron	5	C:T	T	0.8777	0.426	168:186, 132:218	6.832	0.009
rs10515793			115	C:T	C	0.5172	0.457	206:142, 176:180	6.75	0.0094
rs761625	LOC729658,PACRG	intron,locus-region	45	G:A	G	0.366	0.309	252:90, 229:125	6.593	0.0102
rs737811	ZNF74	intron	22	G:A	G	0.3445	0.27	275:81, 246:112	6.588	0.0103
rs12138736			104	T:C	C	0.885	0.461	181:175, 146:208	6.584	0.0103
rs6743983			74	A:C	C	0.7701	0.447	176:180, 143:215	6.51	0.0107
rs6728476	RAMP1	intron	161	A:G	G	0.6596	0.334	135:221, 103:253	6.463	0.011
rs16880300			11	A:G	A	1	0.083	334:20, 319:39	6.441	0.0112
rs13259448			184	T:C	T	0.9055	0.194	297:55, 272:82	6.414	0.0113
rs2222630	CD8	intron	103	A:G	A	0.7204	0.118	325:31, 305:53	6.391	0.0115
rs12122453			178	C:G	C	0.4725	0.284	270:86, 241:117	6.374	0.0116
rs10255860			54	C:T	C	0.2655	0.411	225:129, 191:161	6.304	0.012
rs13135254	FREM3	intron	136	T:C	T	0.2446	0.354	246:110, 214:142	6.29	0.0121
rs1029089			55	G:A	G	0.2509	0.434	218:138, 186:172	6.258	0.0124
rs6474512	PLEKHA2	intron	95	C:A	A	0.2261	0.349	140:216, 109:249	6.196	0.0128
rs696518	STAG1	intron	101	A:C	C	0.5841	0.437	172:184, 140:218	6.152	0.0131
rs11808528			121	G:A	A	0.8143	0.417	163:189, 133:225	6.121	0.0134
rs696081	PCCB	intron	26	C:T	C	0.3667	0.47	205:151, 164:176	6.102	0.0135
rs8065138			127	T:C	C	0.617	0.349	137:211, 108:246	6.062	0.0138
rs1468322			151	A:G	A	0.3036	0.139	318:38, 297:61	6.055	0.0139
rs11055394			79	T:C	T	0.3777	0.192	299:55, 275:81	5.968	0.0146

rs3829881	PTGFRN	mrna-utr	59	G:A	A	0.58	0.475	184:170, 154:204	5.731	0.0167
rs9600161	KLF12	intron	181	C:G	C	0.9347	0.071	339:17, 319:33	5.705	0.0169
rs12191885			44	T:C	T	1	0.33	252:102, 221:131	5.636	0.0176
rs2248028	KRT32	locus-region	50	A:G	G	0.9472	0.24	98:254, 72:284	5.627	0.0177
rs6584410	PDZD7	intron	157	C:T	C	1	0.434	216:138, 186:170	5.558	0.0184
rs2949385	GRID1	intron	138	T:G	G	0.8928	0.346	136:214, 107:245	5.549	0.0185
rs12623398			111	A:T	A	0.9013	0.434	217:139, 186:170	5.495	0.0191
rs12534029	SEMA3C	intron	48	G:C	G	0.2258	0.148	311:41, 289:63	5.461	0.0195
rs7581601			66	A:C	A	0.7421	0.331	253:103, 225:133	5.448	0.0196
rs10516714			110	A:G	G	0.6798	0.305	123:233, 95:263	5.405	0.0201
rs169705	RAB3C	intron	133	G:A	A	0.7903	0.273	111:245, 84:274	5.353	0.0207
rs6720704			84	C:G	C	0.5477	0.273	268:82, 245:111	5.338	0.0209
rs4681202	LOC7325	intron	91	A:C	C	0.8733	0.233	94:254, 70:286	5.318	0.0211
rs7295752			156	G:A	G	0.8118	0.307	261:95, 234:124	5.307	0.0212
rs4699423	UNC5C	coding-synonymous,reference	174	A:G	A	0.592	0.483	199:157, 169:187	5.062	0.0245
rs16891378	HIST1H4D	locus-region	90	A:G	A	0.037	0.185	300:54, 280:78	5.031	0.0249
rs10468501			130	C:T	T	0.0422	0.387	149:199, 118:224	5.025	0.025
rs11059307			166	A:G	A	0.2955	0.453	206:144, 177:173	4.849	0.0277
rs188384	CCDC5	intron	75	G:C	G	0.4141	0.445	212:144, 184:174	4.804	0.0284
rs1835742			168	A:G	A	0.5791	0.274	270:84, 247:111	4.739	0.0295
rs9404214			155	A:G	A	0.067	0.329	247:101, 224:130	4.713	0.0299
rs1780542			134	T:C	T	1	0.148	303:41, 288:62	4.611	0.0318
rs2144817	CLMN	intron	150	T:C	C	0.8581	0.424	165:191, 136:218	4.571	0.0325
rs2360761			145	G:T	G	0.705	0.276	269:85, 245:111	4.564	0.0327
rs12106721			68	C:T	C	0.6991	0.301	262:94, 236:120	4.516	0.0336
rs6546923			167	T:C	T	0.7166	0.28	269:87, 245:113	4.495	0.034
rs1979803	EEA1	intron	60	A:C	A	0.2522	0.393	226:124, 201:153	4.477	0.0343
rs1465404			44	C:T	T	1	0.235	95:259, 72:284	4.313	0.0378
rs717081			81	T:C	T	0.2926	0.426	217:137, 192:166	4.281	0.0385
rs11586990			97	A:G	A	0.4215	0.258	276:80, 254:104	4.038	0.0445
rs2950694	LOC644264	intron	51	T:C	T	0.2241	0.076	334:20, 320:34	3.929	0.0475
rs13118200	ANK2	intron	169	T:A	T	0.7245	0.463	202:150, 178:178	3.884	0.0488
rs7069220	ARHGAP22	intron	33	G:A	G	0.2829	0.171	305:51, 287:71	3.82	0.0506

rs6093929			132	A:G	G	0.2324	0.494	189:167, 164:194	3.784	0.0517
rs1713421	NP	intron	113	A:C	A	0.4349	0.172	301:51, 285:71	3.693	0.0546
rs16897536	VPS13B	intron	46	A:C	A	1	0.128	319:37, 302:54	3.641	0.0564
rs13212664	LOC728275	intron	71	T:A	T	0.5066	0.268	270:84, 241:103	3.434	0.0639
rs4346412			65	T:C	T	0.0402	0.35	243:113, 221:137	3.342	0.0676
rs1921093			164	C:T	C	0.6527	0.424	216:138, 192:162	3.332	0.068
rs11241200			182	T:G	T	0.8886	0.49	193:163, 169:185	2.976	0.0845
rs4852939			171	G:C	G	0.0676	0.314	255:101, 235:123	2.971	0.0847
rs895565			102	T:C	T	0.3823	0.157	305:47, 277:61	2.879	0.0897
rs7734050			96	T:G	T	0.5554	0.241	278:76, 261:95	2.642	0.1041
rs1411944			67	T:C	T	0.684	0.309	256:100, 236:120	2.631	0.1048
rs9498995			49	A:G	A	0.9572	0.467	196:154, 179:175	2.088	0.1484
rs564370	SORBS1	intron	52	A:T	A	1	0.398	218:138, 208:144	0.34	0.5599
rs960945	NEDD9	intron	98	T:C	T	0.3252	0.186	290:66, 291:67	0.004	0.9519

¹Chi-square p-values after individual-genotyping of all Finnish samples combined.

Supplementary Table 4: GRM7 SNPs Individual-level Genotyping Results

GROUP	CHR	SNP	Position	MAF Cases	MAF Controls	CHISQ	P-value	OR	CMH P-value	N _{Cases}	N _{Controls}	N _{total}
Euro 1	3	rs11928865	7,130,702	0.23	0.29	13.34	0.00026	1.361		748	751	1499
Fin	3	rs11928865	7,130,702	0.37	0.36	0.06	0.80550	0.962		180	180	360
Euro 2	3	rs11928865	7,130,702	0.21	0.41	11.29	0.00078	2.556		63	67	130
Euro 2 + Fin	3	rs11928865	7,130,702	0.33	0.37	2.16	0.1416	1.222	0.1383	243	247	490
Euro 1 + Euro 2+ Fin	3	rs11928865	7,130,702	0.25	0.31	15.33	9.01E-05	1.323	1.02E-4	991	998	1989
Euro 1 + Fin	3	rs779701	7,493,772	0.30	0.31	0.17	0.68100	1.030	0.6761	928	931	1859
Euro 1	3	rs779701	7,493,772	0.31	0.30	0.85	0.35620	0.928		748	751	1499
Fin	3	rs779701	7,493,772	0.27	0.37	7.59	0.00587	1.560		180	180	360
Euro 1 + Fin	3	rs779706	7,499,042	0.31	0.31	0.17	0.68360	1.030	0.6798	928	931	1859
Euro 1	3	rs779706	7,499,042	0.31	0.30	0.82	0.36570	0.930		748	751	1499
Fin	3	rs779706	7,499,042	0.28	0.38	7.32	0.00680	1.542		180	180	360

MAF: Minor Allele Frequency. CMH: Cochran-Mantel-Haenszel