

SUPPORTING INFORMATION

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SI.1. CCC speed-up

Computing the Custom Correlation Coefficient (CCC) for a pair of SNPs has the asymptotically fastest computation time possible, $O(n)$, where n is the number of individuals. We have determined a method to further speed up the computation time by exploiting two properties inherent to this problem. First, the CCC metric is simple and divisible. The genotypes can be divided into subsets of the individuals and the CCC values for the entire set can be easily determined from the CCC values of the subsets with *no* loss of accuracy.

Second, assuming the SNPs are biallelic, only three different states can exist for each individual's genotype. This property allows an efficient encoding of the data. We leverage these two properties and combine divide-and-conquer, encoding, and table look-up to attain further speed-up. This combination has reduced the computation time to less than 22% of the original computation, with no loss of accuracy. Additional speed-ups can be achieved by employing a conservative early termination. While the latter has been shown to maintain high accuracy, the accuracy can't be guaranteed when this option is employed.

A divide-and-conquer approach is employed and the individuals are partitioned into subsets. Let p equal the number of individuals in each subset. For n individuals, there are $K = \lfloor n/p \rfloor$ subsets, with some remainder individuals possible. Let g_{ij} equal the number of 'a' alleles for SNP j found for individual i . Each g_{ij} must be one of three values: 0, 1, or 2. Each subset of p individuals is treated as a string of ternary values, or a base-3 number with p digits. Each of these subsets is encoded into a single value. This encoding is accomplished by making a base conversion in which each base-3 number with p digits is converted to its corresponding base-10 value. We define G_{jk} as the base-10 conversion of subset k , containing individuals $\{pk - p + 1, pk - p + 2, \dots, pk\}$, for SNP j .

At some time prior to solving any particular problem, a master table of CCC values is constructed and stored for future computations. For a given p , there is a maximum number max_p that is the base-10 conversion of a base-3 number comprised of p digits, where every digit has a value of 2. The CCC values for every pair of numbers

from 0 to max_p are pre-computed and stored in a table. Once this table has been computed, it is repeatedly used for quick look-ups of CCC values.

Given two SNPs for which we will compute the CCC values, the genotypes for each SNP in each subset of individuals are encoded. This encoding is accomplished by making a base conversion in which each base-3 number with p digits is converted to its corresponding base-10 value, as previously described. At this point, each SNP is encoded as $K = \lfloor n/p \rfloor$ base-10 values, with some remainder of individuals possible.

Encoded subsets with corresponding individuals are compared for the two SNPs. The CCC values for each subset pair is looked up in the pre-computed table. Each table look-up is a fast, constant time procedure. These values are added together and the sum is divided by K , yielding the average CCC value. If applicable, the CCC values for remainder individuals are computed and the average is adjusted accordingly. Note that the CCC values for the pair are determined with 100% accuracy.

To further speed up the computation, a conservative early termination can be employed. If this option is selected, the intermediate CCC values are checked to see if they fall below specified thresholds at three checkpoints during subset value look-up. These thresholds have been set low to minimize the likelihood of losing a meaningful correlation. None of the meaningful correlations were lost using the current thresholds in any of our trials.

We have set $p = 6$ and found good results. The pre-computed look-up table was computationally economic. There are 1,062,882 values in the look-up table, and the file containing it is a little less than 10 MB. It took about one-half second to compute the table.

We tested the speed-up technique on the Framingham SHARe GWAS data of CHD cases. This data set contains 404,467 SNPs for 129 individuals. It took over 4.5 days to compute the CCC values directly. Using

the speed-up combination, we were able to compute the CCC values in 23 hours and correctly identified every highly correlated pair.

We also investigated larger values for p , yielding larger pre-computed look-up tables. For $p = 10$, the resulting table would be over 30 GB, which is too large for our current computing resources. For $p = 8$, the table requires 89 MB of memory and 48 seconds of computation time, both of which are feasible. Surprisingly, the 8-value table required more computation time than the 6-value version for our trials. We suspect that the efficiency of the cache memory contributed to fast retrievals of encoded values and a larger cache may yield better results for the 8-value table size.

SI.2. Choice of frequency weight

The frequency factor, $F_i = 1 - \frac{f_i}{q}$, relies on a tuning parameter, q . The approach we used to determine a tentative value for q involved running a series of tests on various types of random data. We varied the value of q , and for each value, ran CCC on three different random datasets. The first dataset had minor allele frequencies (MAFs) that varied randomly, the same as the random data used in the main experiments. The second dataset had MAFs equal to 5% for all SNPs, and the third had MAFs of 50% for all SNPs. The basic idea was to create random data that represented random allele frequencies, rare alleles, and common alleles. For each weight q , we plotted a histogram of the maximum CCC_{ij} values for the three datasets. We chose $q = 1.5$ as the three histograms most closely lined up for this value. Figure S1 is a plot of these histograms. This approach was somewhat arbitrarily derived, and the value of q might be improved by further study.

SI.3. Pseudocode for breadth-first search

Pseudocode for BFS follows:

```
initialize an array visited[n] to all 0's
```

```
for each node v
    if (visited[v] = 0)
        put v in a queue
        visited[v] = 1
        while (queue is not empty)
            -remove node w from queue
            -add w to component
            -add all unvisited nodes that are incident to
              w to queue and mark as visited
        record component
```

SI.4. Hypotheses checker

The hypotheses checker (HC) is an efficient program for testing a multi-SNP pattern for variation between cases and controls, which in turn indicates synergistic interaction effects of the cluster of SNPs. It detects synergistic interaction effects of the SNP cluster by checking hypotheses for substantial association of the multi-SNP pattern with the disease status. The method can be used for clusters of SNP alleles identified by any correlation metric; however, it requires that patterns of correlated alleles, not just the SNPs, are specified.

As described in the manuscript, we have developed a strategy for identifying clusters of correlated SNP *alleles* using a network model. In this model, each SNP is represented by two nodes, one for each of its alleles (we assume biallelic SNPs). The first step is to identify pair-wise correlations between SNPs. An edge is created between each pair of alleles that exhibit a high correlation. Then a breadth-first search (BFS) identifies the alleles in each connected cluster. HC is designed to test each of these clusters for multi-SNP patterns exhibit substantial variation between cases and controls.

False positive association patterns may occur due to two properties of the described procedure. First, the subsets of individuals that are correlated within a cluster might not be consistent. For example, allele ‘A’ might be correlated with allele ‘B’, and allele ‘B’ might be correlated with allele ‘C’, but the two subsets of individuals contributing to these correlations might contain different individuals. Second, many clusters of alleles might be relatively equally common to both cases and controls.

HC will prune away the multi-SNP clusters that possess either of these two properties. The procedure involves two main steps. First, for each cluster, the number of cases and the number of controls that possess all of the alleles in the cluster are tallied. A score is also tabulated to quantify the percentage of these individuals that are homozygous for the given alleles. However, this score is not currently utilized.

In the second step, the numbers of cases and controls with all of the alleles for a cluster are compared. We used the following formula to determine which clusters in the cases network appeared to have substantial variation between the two groups:

$$\frac{(c_i - c_j)^2}{c_i} \geq \delta$$

where c_i equals the percentage of cases possessing all of the alleles, c_j is the percentage of controls possessing all of the alleles, and δ is a threshold. We also switched the groups in the formula to identify interesting clusters in the controls network that appear more frequently in controls than cases. For our experiments, we set δ to 0.15.

The output from HC contains the numbers of individuals with the cluster of alleles for cases and controls, along with their scores. For each SNP in the cluster, the relevant allele, its frequency in cases and controls, its location, and gene (if known) are printed.

HC is efficient, so a wide net can be cast and large numbers of clusters can be tested. In other trials, we have tested more than 30,000 clusters for 380,000 SNPs in less than 20 seconds. HC can be used directly on the output from BFS or applied to more refined clustering results. Clusters with low densities may be comprised of a number of smaller, denser clusters. These clusters can be broken down using a clustering algorithm prior to applying HC. Due to HC's efficiency, it can be applied to both the original BFS clusters and the results after applying a clustering method.

SI.5. Annotations for additional multi-SNP candidate association patterns

The Hypotheses Checker (HC) identified a total of 42 multi-SNP candidate association patterns from the hypertensive heart disease cases and controls networks. 22 of these are patterns appear significantly more often for controls than cases and the other 20 appear more often for the cases. The annotations for these patterns are shown for cases and controls in Tables S2 and S3, respectively.

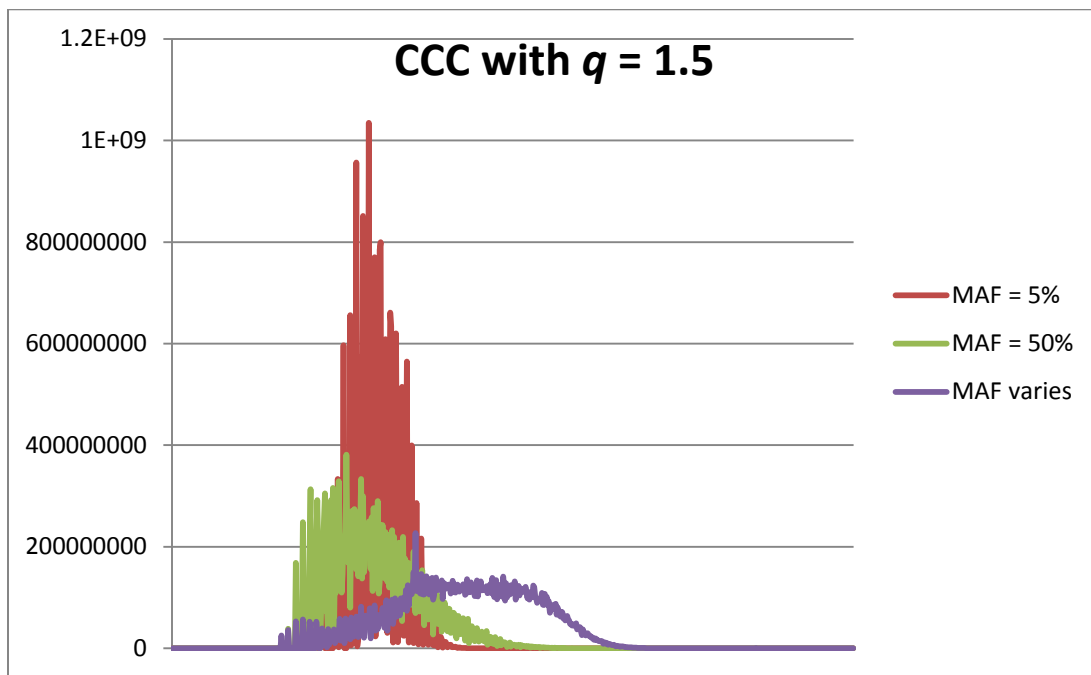


Figure S1. Histograms of maximum CCC_{ij} values for random data with minor allele frequencies (MAF) of 5% and 50%, and a variable MAF.

Table S2. 22 multi-SNP candidate association patterns from the CCC network in controls.

Number	Allele	Freq	SNP	rs.ID	Chrom	Position	Gene
Cluster 1							
18 Controls with score of 1.256							
4 Cases with score of 1.100							
26482	C	0.230	SNP_A-1929621	rs2971894	2	107051389	RGPD4
26483	G	0.230	SNP_A-1814968	rs1524288	2	107052295	ST6GAL2
184721	A	0.243	SNP_A-1939361	rs7179067	15	86143690	NTRK3
26480	T	0.230	SNP_A-4208285	rs2030675	2	107045906	ST6GAL2
184719	T	0.264	SNP_A-2193261	rs7167158	15	86121638	NTRK3
Cluster 2							
12 Controls with score of 1.472							
1 Cases with score of 1.524							
3898	A	0.392	SNP_A-1818209	rs11206455	1	55098382	DHCR24
3901	A	0.392	SNP_A-1900980	rs11206457	1	55108685	DHCR24
3902	C	0.318	SNP_A-1894765	rs608458	1	55109538	DHCR24
3903	A	0.399	SNP_A-2242907	rs7551288	1	55111267	DHCR24
82784	C	0.439	SNP_A-1804702	rs4711152	6	27488181	ZNF184
83097	A	0.291	SNP_A-2060257	rs2516662	6	30583394	HLA-E
83100	C	0.291	SNP_A-2241793	rs996588	6	30585235	HLA-E
83104	C	0.264	SNP_A-2187467	rs2252745	6	30687294	PPP1R10
139195	A	0.270	SNP_A-2156504	rs4595501	10	115481555	CASP7
139199	C	0.250	SNP_A-1923259	rs3981351	10	115505110	C10orf81
139207	C	0.203	SNP_A-2005544	rs7895170	10	115577000	DCLRE1A
3904	T	0.372	SNP_A-2066997	rs589244	1	55115517	DHCR24
3905	C	0.399	SNP_A-1917022	rs3170766	1	55126890	DHCR24
82786	C	0.574	SNP_A-2275357	rs6456785	6	27498378	ZNF184
83080	T	0.338	SNP_A-2246620	rs2516688	6	30472503	RPP21
83098	T	0.291	SNP_A-2242150	rs2844720	6	30583696	HLA-E
83099	G	0.291	SNP_A-2128828	rs996589	6	30585214	HLA-E
83101	T	0.291	SNP_A-2261029	rs2844718	6	30585255	HLA-E
83102	G	0.277	SNP_A-1912229	rs1264432	6	30670000	DDR1
139192	G	0.277	SNP_A-2111242	rs2227310	10	115479142	CASP7
139200	T	0.230	SNP_A-2290086	rs12218072	10	115530891	C10orf81
Cluster 3							
15 Controls with score of 1.467							
1 Cases with score of 1.250							
4715	A	0.459	SNP_A-4221272	rs10493310	1	61904395	TM2D1
4718	A	0.473	SNP_A-2080637	rs2172957	1	61937724	TM2D1
70051	A	0.189	SNP_A-1821787	rs17764708	5	57654406	PLK2
70039	T	0.223	SNP_A-2211249	rs17438760	5	57527405	PLK2
70049	G	0.345	SNP_A-2095725	rs37535	5	57653160	PLK2
70053	G	0.338	SNP_A-1981710	rs245491	5	57669612	PLK2
70058	T	0.250	SNP_A-1865574	rs2021394	5	57688925	PLK2
92238	G	0.216	SNP_A-2183955	rs9791224	6	153741949	unknown

Cluster 4	21 Controls with score of 1.131						
	5 Cases with score of 1.400						
23530	A	0.216	SNP_A-2229461	rs11688740	2	60391494	unknown
192398	C	0.284	SNP_A-2195412	rs11149609	16	82528341	OSGIN1
192399	C	0.155	SNP_A-2288571	rs12599670	16	82528610	OSGIN1
192397	G	0.338	SNP_A-2140361	rs11149607	16	82528087	MLYCD
Cluster 5	17 Controls with score of 1.299						
	1 Cases with score of 1.000						
49007	C	0.419	SNP_A-2074431	rs1317365	3	161761172	KPNA4
49015	C	0.568	SNP_A-2156307	rs9851063	3	161839984	KPNA4
49016	A	0.568	SNP_A-2230155	rs1920657	3	161840914	KPNA4
98379	C	0.338	SNP_A-2272377	rs11770955	7	47477102	TNS3
129158	A	0.196	SNP_A-1993141	rs2245191	10	5129815	AKR1C3
203741	C	0.358	SNP_A-4257935	rs7504278	18	65547273	DOK6
48996	G	0.466	SNP_A-2292077	rs6441314	3	161543839	IFT80
49008	T	0.541	SNP_A-2194662	rs7629423	3	161806709	ARL14
129154	T	0.257	SNP_A-2163140	rs11252920	10	5109093	unknown
129159	T	0.203	SNP_A-4225254	rs17173403	10	5136266	AKR1C3
129162	G	0.203	SNP_A-1993145	rs1937920	10	5151955	AKR1CL1
129165	T	0.405	SNP_A-2178024	rs1781937	10	5190638	AKR1CL1
129170	G	0.412	SNP_A-1993157	rs2398103	10	5196096	AKR1CL1
Cluster 6	16 Controls with score of 1.526						
	1 Cases with score of 1.059						
70200	C	0.270	SNP_A-4264923	rs7720119	5	59053824	PDE4D
203313	A	0.358	SNP_A-2293523	rs11151149	18	60529505	unknown
203314	C	0.358	SNP_A-4206321	rs12605461	18	60530557	unknown
203317	A	0.372	SNP_A-2230381	rs8091120	18	60549298	unknown
203320	C	0.372	SNP_A-4258492	rs2877891	18	60553841	unknown
203321	A	0.392	SNP_A-2291990	rs1463933	18	60558805	unknown
203322	A	0.541	SNP_A-2161625	rs17073641	18	60569424	unknown
203329	G	0.426	SNP_A-4277609	rs7241201	18	60629759	unknown
70193	G	0.162	SNP_A-2239465	rs298029	5	58975257	PDE4D
70198	T	0.203	SNP_A-4222782	rs298101	5	59048947	PDE4D
70201	G	0.270	SNP_A-4299615	rs11954036	5	59064610	PDE4D
181338	T	0.223	SNP_A-2276216	rs2460620	15	44085750	SQRDL
203316	T	0.372	SNP_A-1925704	rs9966874	18	60547550	unknown
203318	T	0.372	SNP_A-2140706	rs4374278	18	60553742	unknown
203319	G	0.372	SNP_A-4285176	rs4581804	18	60553825	unknown
203324	G	0.385	SNP_A-1800365	rs12052021	18	60570518	unknown
203326	T	0.426	SNP_A-1854524	rs1440536	18	60612151	unknown
Cluster 7	21 Controls with score of 1.349						
	6 Cases with score of 1.167						
72897	C	0.331	SNP_A-1982625	rs10478691	5	97891952	RGMB
72899	C	0.331	SNP_A-2274903	rs7709076	5	97895377	RGMB
158010	C	0.277	SNP_A-4276086	rs4758802	12	59835270	FAM19A2
21654	G	0.324	SNP_A-1838055	rs2110745	2	40354855	SLC8A1
72898	G	0.331	SNP_A-2054538	rs2112660	5	97893359	RGMB
158002	C	0.243	SNP_A-2056989	rs795401	12	59675332	FAM19A2

Cluster 8	23 Controls with score of 1.326						
	7 Cases with score of 1.286						
74535	A	0.311	SNP_A-2228555	rs4895189	5	118683369	TNFAIP8
74544	C	0.365	SNP_A-4276030	rs3813308	5	118718680	TNFAIP8
176476	T	0.345	SNP_A-2003812	rs2074562	14	68004443	RAD51L1
178544	T	0.324	SNP_A-1811451	rs7160685	14	92293743	GOLGA5
Cluster 9	16 Controls with score of 1.147						
	3 Cases with score of 1.057						
75379	C	0.331	SNP_A-4211278	rs10520083	5	129967905	HINT1
75383	A	0.196	SNP_A-2058904	rs2024309	5	130165713	HINT1
75405	A	0.189	SNP_A-2272349	rs6596024	5	130797684	RAPGEF6
75406	A	0.182	SNP_A-1948512	rs1422081	5	130803952	RAPGEF6
75413	A	0.189	SNP_A-1857968	rs4705890	5	130882899	RAPGEF6
75420	A	0.182	SNP_A-2065978	rs251015	5	131057582	FNIP1
75423	A	0.176	SNP_A-4243380	rs4705894	5	131107187	FNIP1
75424	A	0.189	SNP_A-2105433	rs11242095	5	131180474	unknown
75425	C	0.182	SNP_A-4272818	rs2896961	5	131192905	unknown
75428	C	0.189	SNP_A-4295094	rs12653237	5	131269677	unknown
75429	A	0.182	SNP_A-2026213	rs7708140	5	131280295	unknown
75432	A	0.189	SNP_A-1983483	rs667419	5	131309963	unknown
75434	A	0.169	SNP_A-1796454	rs676944	5	131316367	ACSL6
75436	C	0.182	SNP_A-2221710	rs253943	5	131348629	ACSL6
75402	G	0.392	SNP_A-2199854	rs3756295	5	130720739	CDC42SE2
75404	T	0.182	SNP_A-1951337	rs27421	5	130771670	CDC42SE2
75407	G	0.182	SNP_A-2190326	rs3776030	5	130804637	RAPGEF6
75408	G	0.182	SNP_A-2301298	rs10463887	5	130804753	RAPGEF6
75409	G	0.182	SNP_A-4211282	rs17167760	5	130810598	RAPGEF6
75410	T	0.189	SNP_A-2306489	rs31239	5	130841276	RAPGEF6
75411	G	0.182	SNP_A-2078078	rs13163091	5	130863940	RAPGEF6
75414	G	0.182	SNP_A-1799007	rs3776007	5	130902984	RAPGEF6
75417	T	0.189	SNP_A-4229115	rs10040578	5	130978131	RAPGEF6
75419	T	0.182	SNP_A-1983479	rs250888	5	131043245	FNIP1
75421	G	0.189	SNP_A-2294747	rs251012	5	131058194	FNIP1
75426	G	0.189	SNP_A-4279139	rs11954609	5	131193637	unknown
75430	T	0.189	SNP_A-1820443	rs667437	5	131303408	unknown
75433	T	0.189	SNP_A-1983484	rs477086	5	131312509	unknown
75435	G	0.182	SNP_A-1856533	rs173812	5	131347359	ACSL6
Cluster 10	12 Controls with score of 1.492						
	0 Cases with score of nan						
85565	C	0.345	SNP_A-1942424	rs2459572	6	64051334	GLULD1
85566	A	0.351	SNP_A-2143529	rs1741797	6	64116524	GLULD1
93594	A	0.257	SNP_A-2279855	rs3799630	6	166885426	RPS6KA2
93600	C	0.284	SNP_A-2152371	rs3799584	6	166939116	RPS6KA2
110909	A	0.324	SNP_A-1882856	rs4237018	8	58825543	T1560
131726	A	0.318	SNP_A-2049457	rs11007111	10	28766031	unknown
93591	G	0.405	SNP_A-1988500	rs763186	6	166875955	RPS6KA2
93592	T	0.412	SNP_A-2031888	rs6918886	6	166876885	RPS6KA2
110905	T	0.365	SNP_A-2304079	rs7836900	8	58790586	T1560
110906	T	0.365	SNP_A-1793952	rs4532583	8	58795762	T1560

Cluster 11	28 Controls with score of 1.412						
	9 Cases with score of 1.192						
89189	A	0.345	SNP_A-1961034	rs774407	6	113668957	unknown
89195	A	0.466	SNP_A-2180319	rs2637534	6	113760826	unknown
89197	A	0.297	SNP_A-2213382	rs6907063	6	113762671	unknown
89198	C	0.466	SNP_A-2157202	rs7742701	6	113767465	unknown
89199	C	0.459	SNP_A-2267895	rs9488153	6	113771077	unknown
12699	C	0.331	SNP_A-1921850	rs17545182	1	185321946	PLA2G4A
12707	T	0.446	SNP_A-1897005	rs330743	1	185496755	PLA2G4A
89192	C	0.243	SNP_A-2076092	rs2842846	6	113742923	unknown
89196	T	0.466	SNP_A-2241844	rs6905873	6	113762299	unknown
89201	G	0.466	SNP_A-1987275	rs9320441	6	113775507	unknown
89202	T	0.466	SNP_A-1895560	rs2029555	6	113778539	unknown
Cluster 12	19 Controls with score of 1.303						
	3 Cases with score of 1.333						
90948	C	0.216	SNP_A-1987801	rs4896224	6	137339819	IL20RA
154255	C	0.176	SNP_A-1837067	rs4763730	12	11924837	ETV6
172888	C	0.426	SNP_A-4274509	rs2319872	14	21118417	OR10G3
172890	A	0.331	SNP_A-2239789	rs6571924	14	21123657	OR10G3
Cluster 13	15 Controls with score of 1.300						
	2 Cases with score of 1.250						
94574	C	0.196	SNP_A-1944413	rs2192346	7	8142826	ICA1
94575	A	0.081	SNP_A-1950407	rs17330124	7	8144214	ICA1
136438	A	0.345	SNP_A-4303986	rs612715	10	85499595	unknown
54228	T	0.297	SNP_A-2146652	rs4692262	4	27533929	unknown
Cluster 14	23 Controls with score of 1.304						
	7 Cases with score of 1.257						
94800	C	0.230	SNP_A-1855176	rs3950561	7	10649386	unknown
94802	A	0.446	SNP_A-2275053	rs9986833	7	10667170	unknown
94803	A	0.203	SNP_A-2162802	rs2352452	7	10668266	unknown
94804	G	0.196	SNP_A-1952216	rs10272747	7	10669480	unknown
165475	T	0.209	SNP_A-2153472	rs1547162	13	29382862	LOC440131
Cluster 15	21 Controls with score of 1.206						
	6 Cases with score of 1.111						
104404	C	0.264	SNP_A-1915315	rs12671406	7	144337025	unknown
104406	A	0.291	SNP_A-2026176	rs13242418	7	144360489	unknown
215922	A	0.142	SNP_A-2019491	rs2837164	21	40050706	IGSF5
215923	C	0.149	SNP_A-2019494	rs744568	21	40055860	IGSF5
215931	C	0.291	SNP_A-2019508	rs1018352	21	40071715	IGSF5
215932	G	0.297	SNP_A-2019509	rs1571712	21	40074916	IGSF5
Cluster 16	13 Controls with score of 1.400						
	1 Cases with score of 1.200						
110627	A	0.209	SNP_A-2051544	rs12550655	8	55486710	unknown
174599	C	0.385	SNP_A-1837396	rs8019773	14	43961230	FSCB
110628	C	0.236	SNP_A-1902591	rs12547053	8	55496229	SOX17
124677	T	0.284	SNP_A-2239775	rs1977620	9	97515495	C9orf102
163644	G	0.311	SNP_A-1874613	rs11058803	12	125837200	unknown

Cluster 17	24 Controls with score of 1.208						
	7 Cases with score of 1.000						
115427	A	0.345	SNP_A-4235355	rs16893258	8	120953915	DEPDC6
205129	A	0.122	SNP_A-2159564	rs7256391	19	9118425	ZNF317
205131	A	0.122	SNP_A-2222986	rs16978581	19	9127296	ZNF317
205130	T	0.196	SNP_A-2059199	rs12459040	19	9121637	ZNF317
Cluster 18	15 Controls with score of 1.387						
	2 Cases with score of 1.100						
119770	A	0.176	SNP_A-1835266	rs913412	9	14455710	NFIB
150883	A	0.507	SNP_A-4297981	rs4145058	11	114146011	FAM55B
105423	T	0.311	SNP_A-1782909	rs12698117	7	157463674	PTPRN2
150879	G	0.250	SNP_A-2234596	rs12421720	11	114114318	FAM55B
150881	T	0.378	SNP_A-1946919	rs7123330	11	114120247	FAM55B
Cluster 19	16 Controls with score of 1.275						
	2 Cases with score of 1.200						
143016	C	0.203	SNP_A-2031948	rs297325	11	16346170	SOX6
143020	A	0.189	SNP_A-4283763	rs12221729	11	16389040	SOX6
143024	A	0.182	SNP_A-2008072	rs10500830	11	16441827	SOX6
143030	A	0.182	SNP_A-2070177	rs10832616	11	16462666	SOX6
143033	C	0.182	SNP_A-4243831	rs4756858	11	16626773	C11orf58
210936	A	0.196	SNP_A-2023461	rs1119803	20	36459212	unknown
210937	A	0.196	SNP_A-2142795	rs4811821	20	36462427	unknown
210939	C	0.155	SNP_A-2115876	rs1739646	20	36470998	unknown
210942	G	0.128	SNP_A-2106640	rs3752280	20	36484421	unknown
210943	G	0.162	SNP_A-1791567	rs805531	20	36508140	unknown
Cluster 20	22 Controls with score of 1.284						
	5 Cases with score of 1.150						
166060	A	0.351	SNP_A-4282482	rs9574926	13	35396356	DCLK1
51581	T	0.264	SNP_A-2232573	rs6828802	4	292934	ZNF141
166061	T	0.270	SNP_A-2125903	rs1104539	13	35413298	DCLK1
166063	T	0.169	SNP_A-1811579	rs2066448	13	35445142	DCLK1
Cluster 21	18 Controls with score of 1.278						
	4 Cases with score of 1.150						
103296	T	0.264	SNP_A-2151143	rs10228040	7	130304156	unknown
193373	T	0.284	SNP_A-1945588	rs1467138	17	6237444	AIPL1
215673	T	0.304	SNP_A-4270549	rs2835942	21	38052778	KCNJ6
215674	T	0.324	SNP_A-2019073	rs2835952	21	38067415	KCNJ6
215675	T	0.318	SNP_A-2019074	rs762145	21	38068188	DSCR4

Cluster 22	11 Controls with score of 1.455						
	0 Cases with score of nan						
21704	C	0.507	SNP_A-2306108	rs7589309	2	40794558	SLC8A1
21705	A	0.507	SNP_A-4296426	rs918013	2	40801916	SLC8A1
21707	C	0.371	SNP_A-2128224	rs1107932	2	40802672	SLC8A1
21709	A	0.486	SNP_A-4208026	rs10490262	2	40805171	SLC8A1
21712	A	0.471	SNP_A-1962895	rs12712708	2	40817419	SLC8A1
21716	A	0.329	SNP_A-4261874	rs1456587	2	40842768	SLC8A1
21719	A	0.514	SNP_A-1962896	rs7591057	2	40917895	SLC8A1
56300	A	0.443	SNP_A-2110839	rs11726451	4	59534976	unknown
108096	C	0.379	SNP_A-4280883	rs11204102	8	20137423	LZTS1
216136	C	0.293	SNP_A-2019884	rs2837941	21	41390710	unknown
21695	G	0.436	SNP_A-1940790	rs42814	2	40679386	SLC8A1
21702	T	0.386	SNP_A-2296948	rs10048831	2	40770673	SLC8A1
21703	G	0.386	SNP_A-4208023	rs10490261	2	40771068	SLC8A1
21708	T	0.436	SNP_A-2243130	rs4952645	2	40803110	SLC8A1
21711	G	0.379	SNP_A-4238930	rs12105490	2	40813313	SLC8A1
21718	T	0.414	SNP_A-2097854	rs11124763	2	40891407	SLC8A1
108095	G	0.371	SNP_A-2251200	rs13253777	8	20116050	ATP6V1B2
122444	T	0.307	SNP_A-2152050	rs7849064	9	72727974	TRPM3
122450	G	0.279	SNP_A-1881292	rs7041925	9	72775609	TRPM3
140582	T	0.343	SNP_A-2221667	rs11245048	10	128245557	C10orf90
140583	T	0.471	SNP_A-2036244	rs12264765	10	128258265	C10orf90
140585	T	0.4	SNP_A-1869292	rs10901638	10	128260689	C10orf90
140588	T	0.471	SNP_A-2207236	rs10128487	10	128263169	C10orf90
216134	G	0.3	SNP_A-2019879	rs8134934	21	41375695	unknown
216140	T	0.35	SNP_A-2019889	rs2837956	21	41401386	unknown

Table S3. 20 multi-SNP candidate association patterns from the CCC network in cases.

Number	Allele	Freq	SNP	rs.ID	Chrom	Position	Gene
Cluster 23							
1 Controls with score of 1.074							
13 Cases with score of 1.410							
18981	C	0.318	SNP_A-2151719	rs6747078	2	10094609	KLF11
34132	A	0.399	SNP_A-4278598	rs4674033	2	216388819	PECR
34133	A	0.304	SNP_A-2179890	rs10804244	2	216404561	PECR
34134	C	0.331	SNP_A-2287406	rs12052402	2	216408698	PECR
107358	A	0.493	SNP_A-2295322	rs7828061	8	14088846	SGCZ
107361	C	0.412	SNP_A-2063034	rs7016966	8	14118719	SGCZ
107369	G	0.311	SNP_A-1910098	rs17119030	8	14205514	SGCZ
167706	A	0.554	SNP_A-2128912	rs9537001	13	54669717	unknown
167708	C	0.324	SNP_A-1812593	rs9569244	13	54710213	unknown
167711	C	0.385	SNP_A-1927000	rs1436703	13	54730139	unknown
167715	C	0.385	SNP_A-2185375	rs7319488	13	54740807	unknown
167716	A	0.385	SNP_A-1926525	rs9597145	13	54744140	unknown
167717	A	0.385	SNP_A-2244658	rs12018729	13	54744575	unknown
167720	C	0.385	SNP_A-1934843	rs7989059	13	54763118	unknown
34131	G	0.405	SNP_A-2007005	rs6435922	2	216385157	PECR
34137	G	0.453	SNP_A-4302352	rs12694376	2	216455056	PECR
107364	T	0.493	SNP_A-1834171	rs7839860	8	14158131	SGCZ
107366	T	0.486	SNP_A-1992358	rs890534	8	14186652	SGCZ
167703	G	0.554	SNP_A-2139962	rs1570751	13	54597569	unknown
167705	T	0.318	SNP_A-1884601	rs9569224	13	54652498	unknown
167707	T	0.385	SNP_A-1803230	rs9597134	13	54675167	unknown
167709	G	0.385	SNP_A-2181261	rs1370079	13	54710942	unknown
167712	T	0.385	SNP_A-1843308	rs9569256	13	54739104	unknown
167713	G	0.561	SNP_A-2141111	rs2217929	13	54740159	unknown
167714	G	0.385	SNP_A-2126758	rs9563309	13	54740592	unknown
167719	T	0.324	SNP_A-2186488	rs9316780	13	54762808	unknown
167721	G	0.324	SNP_A-1937121	rs9563319	13	54783039	unknown
Cluster 24							
4 Controls with score of 1.417							
19 Cases with score of 1.184							
21005	A	0.311	SNP_A-1885588	rs11690827	2	33627243	RASGRP3
192573	C	0.243	SNP_A-1829520	rs301163	16	84371027	COX4NB
192574	A	0.297	SNP_A-1829550	rs10514609	16	84381574	COX4NB
192576	A	0.209	SNP_A-4256265	rs1800647	16	84391661	COX4I1
192577	C	0.264	SNP_A-2213307	rs2733955	16	84393792	COX4I1
192578	T	0.25	SNP_A-2174512	rs2075531	16	84396417	COX4I1

Cluster 25		2 Controls with score of 1.047					
		15 Cases with score of 1.519					
21764	A	0.345	SNP_A-2245003	rs2374232	2	41400411	SLC8A1
21772	A	0.392	SNP_A-2312953	rs4952359	2	41471265	SLC8A1
21775	C	0.392	SNP_A-1794662	rs2135999	2	41482505	SLC8A1
21778	C	0.399	SNP_A-2029610	rs6544416	2	41489442	SLC8A1
21781	C	0.378	SNP_A-1962916	rs1354982	2	41495384	SLC8A1
21793	A	0.412	SNP_A-2006319	rs6712352	2	41586291	SLC8A1
21802	A	0.412	SNP_A-2129664	rs7586603	2	41606346	SLC8A1
21817	C	0.453	SNP_A-2048778	rs12712804	2	41750576	SLC8A1
156442	A	0.331	SNP_A-4218739	rs4768224	12	38947670	LRRK2
187993	C	0.291	SNP_A-1789950	rs1985395	16	19254444	unknown
21765	T	0.331	SNP_A-1796938	rs1567236	2	41413094	SLC8A1
21767	G	0.412	SNP_A-1962914	rs2048177	2	41415124	SLC8A1
21768	T	0.358	SNP_A-2251108	rs7565096	2	41415614	SLC8A1
21770	G	0.358	SNP_A-2147161	rs4952453	2	41423389	SLC8A1
21771	T	0.405	SNP_A-1834318	rs6727419	2	41433226	SLC8A1
21773	G	0.399	SNP_A-2028580	rs1396134	2	41471675	SLC8A1
21774	T	0.399	SNP_A-2284158	rs7599534	2	41475751	SLC8A1
21776	G	0.399	SNP_A-2026941	rs4952460	2	41486576	SLC8A1
21777	G	0.399	SNP_A-1831174	rs2374240	2	41486990	SLC8A1
21779	G	0.399	SNP_A-2092418	rs4952361	2	41490131	SLC8A1
21780	T	0.378	SNP_A-1962915	rs872037	2	41494861	SLC8A1
21785	G	0.399	SNP_A-4304095	rs12468176	2	41508568	SLC8A1
21786	G	0.399	SNP_A-2207505	rs10191557	2	41511728	SLC8A1
21787	T	0.426	SNP_A-1838175	rs1508128	2	41515267	SLC8A1
21788	G	0.392	SNP_A-4208033	rs976160	2	41548646	SLC8A1
21796	G	0.412	SNP_A-2186271	rs7561570	2	41603468	SLC8A1
21797	T	0.419	SNP_A-4275074	rs7578278	2	41603584	SLC8A1
21800	T	0.419	SNP_A-1905456	rs4270392	2	41605962	SLC8A1
21801	T	0.412	SNP_A-1949725	rs4563279	2	41606116	SLC8A1
21821	T	0.392	SNP_A-4287149	rs4952497	2	41755978	SLC8A1
21822	G	0.574	SNP_A-4270895	rs6738287	2	41756046	SLC8A1
187990	G	0.345	SNP_A-1789934	rs1023442	16	19239066	unknown
Cluster 26		2 Controls with score of 1.250					
		16 Cases with score of 1.349					
38778	A	0.385	SNP_A-4239824	rs4094000	3	21935799	ZNF385D
38779	C	0.27	SNP_A-2253437	rs9821707	3	21974734	ZNF385D
38781	C	0.27	SNP_A-2130838	rs9821722	3	21974846	ZNF385D
46860	C	0.358	SNP_A-1974357	rs1881909	3	133209082	CPNE4
46864	C	0.345	SNP_A-2036598	rs1125404	3	133231863	CPNE4
46865	A	0.23	SNP_A-2245852	rs2178384	3	133239236	CPNE4
205346	C	0.291	SNP_A-1869635	rs8105884	19	14945306	CCDC105
38780	C	0.27	SNP_A-2312102	rs9821571	3	21974786	ZNF385D
38782	G	0.27	SNP_A-4263380	rs3821394	3	21975334	ZNF385D
38783	T	0.27	SNP_A-4263381	rs3821388	3	21975611	ZNF385D
46867	T	0.318	SNP_A-1934568	rs1881913	3	133249361	ACPP
205343	G	0.378	SNP_A-1821288	rs1468307	19	14886715	unknown

Cluster 27	0 Controls with score of nan						
	11 Cases with score of 1.446						
49350	A	0.426	SNP_A-4252173	rs3894957	3	166952603	SLITRK3
142464	A	0.392	SNP_A-1958578	rs3934815	11	11488870	GALNTL4
142466	A	0.372	SNP_A-2026413	rs7943562	11	11496495	GALNTL4
142481	A	0.209	SNP_A-1866874	rs10765863	11	11532033	GALNTL4
49365	G	0.331	SNP_A-2184096	rs7645596	3	167065564	BCHE
49375	T	0.365	SNP_A-1938893	rs7634954	3	167257416	BCHE
61031	T	0.378	SNP_A-1978896	rs1216415	4	129750538	PGRMC2
61032	G	0.345	SNP_A-2084663	rs17401445	4	129751887	PGRMC2
142463	G	0.378	SNP_A-1911585	rs3934816	11	11488807	GALNTL4
142472	T	0.439	SNP_A-2221700	rs10831631	11	11504723	GALNTL4
142479	G	0.318	SNP_A-2117083	rs4910382	11	11518582	GALNTL4
Cluster 28	4 Controls with score of 1.389						
	19 Cases with score of 1.351						
69871	C	0.338	SNP_A-4244238	rs6450394	5	55911470	unknown
193003	C	0.351	SNP_A-1832563	rs7225041	17	451977	VPS53
193009	A	0.507	SNP_A-2235979	rs366151	17	545061	VPS53
193011	C	0.507	SNP_A-1832649	rs2543781	17	549219	VPS53
71452	T	0.345	SNP_A-4220401	rs6870971	5	75554185	SV2C
71454	G	0.439	SNP_A-2238429	rs10066756	5	75557566	SV2C
71455	G	0.358	SNP_A-2085611	rs10036293	5	75557653	SV2C
71461	C	0.297	SNP_A-2033416	rs12654150	5	75586081	SV2C
193014	T	0.385	SNP_A-1799147	rs2740354	17	579655	FAM57A
Cluster 29	0 Controls with score of nan						
	13 Cases with score of 1.393						
76385	A	0.459	SNP_A-1983809	rs160870	5	143339639	HMHB1
76387	C	0.291	SNP_A-1983812	rs10515531	5	143346520	HMHB1
217276	A	0.378	SNP_A-1813561	rs5997062	22	25008128	SEZ6L
217278	A	0.432	SNP_A-2282101	rs137209	22	25022186	SEZ6L
217279	C	0.304	SNP_A-4263176	rs670530	22	25028892	SEZ6L
217273	G	0.236	SNP_A-2239467	rs1941120	22	24978940	SEZ6L
217280	T	0.297	SNP_A-4285971	rs2847315	22	25035391	SEZ6L
217283	G	0.284	SNP_A-4290068	rs596633	22	25046432	SEZ6L
217284	G	0.419	SNP_A-2142778	rs6005015	22	25056045	SEZ6L
Cluster 30	3 Controls with score of 1.000						
	19 Cases with score of 1.333						
78109	A	0.345	SNP_A-1822456	rs10066258	5	160346401	GABRB2
38920	T	0.25	SNP_A-1874538	rs12494751	3	23744901	UBE2E1
78111	G	0.277	SNP_A-1840984	rs1464143	5	160375458	GABRB2
Cluster 31	3 Controls with score of 1.333						
	17 Cases with score of 1.324						
92384	C	0.318	SNP_A-2072704	rs9371355	6	155300670	TIAM2
137928	C	0.331	SNP_A-2071578	rs1467616	10	102631681	PAX2
137930	G	0.453	SNP_A-2004538	rs2181834	10	102651241	PAX2
216110	A	0.277	SNP_A-2019826	rs2898425	21	41123485	unknown
216111	C	0.284	SNP_A-2019827	rs2837842	21	41124833	unknown
216112	T	0.284	SNP_A-2019830	rs2837853	21	41128454	unknown
216113	G	0.284	SNP_A-1970479	rs2837856	21	41137702	unknown
216114	G	0.318	SNP_A-2019832	rs1983527	21	41141858	unknown

Cluster 32	1 Controls with score of 1.000						
	15 Cases with score of 1.380						
108617	A	0.277	SNP_A-1871854	rs11777251	8	24956093	NEFL
108618	C	0.277	SNP_A-2108037	rs7002363	8	24956473	NEFL
108619	A	0.25	SNP_A-2269588	rs4529473	8	24971009	NEFL
108622	A	0.297	SNP_A-2028413	rs11989437	8	25003079	NEFL
213355	A	0.291	SNP_A-1940566	rs6010861	20	60785447	SLCO4A1
108616	G	0.277	SNP_A-1904325	rs6992758	8	24955439	NEFL
108623	T	0.291	SNP_A-1914737	rs17053113	8	25012277	NEFL
146632	T	0.297	SNP_A-1813576	rs2259377	11	62222652	BSCL2
146634	T	0.27	SNP_A-1861794	rs6591720	11	62262340	TTC9C
213354	T	0.432	SNP_A-2281084	rs6089848	20	60784868	RP11-93B14.6
Cluster 33	6 Controls with score of 1.167						
	22 Cases with score of 1.379						
113555	C	0.25	SNP_A-1915627	rs3134491	8	96805339	unknown
48374	T	0.257	SNP_A-1849635	rs7429509	3	152583857	MED12L
48375	T	0.446	SNP_A-1931628	rs9653953	3	152594480	MED12L
Cluster 34	2 Controls with score of 1.316						
	16 Cases with score of 1.375						
124472	A	0.223	SNP_A-1997239	rs10739944	9	94993256	WNK2
124474	C	0.372	SNP_A-2045894	rs10821099	9	95052831	WNK2
124475	C	0.372	SNP_A-2121206	rs10821101	9	95062686	WNK2
124485	C	0.223	SNP_A-2081347	rs12685091	9	95144058	C9orf129
200872	C	0.351	SNP_A-2267028	rs4627440	18	35251884	unknown
200875	A	0.453	SNP_A-2148777	rs1482967	18	35328424	unknown
200881	A	0.318	SNP_A-1931693	rs1943452	18	35437610	unknown
200882	G	0.324	SNP_A-2301682	rs2726258	18	35452192	unknown
200883	A	0.324	SNP_A-1902235	rs2852323	18	35467308	unknown
200892	C	0.385	SNP_A-4277055	rs2848791	18	35497911	unknown
200899	C	0.338	SNP_A-2271139	rs2848800	18	35575972	unknown
124471	T	0.223	SNP_A-1997238	rs10512222	9	94993162	WNK2
124476	T	0.372	SNP_A-1828522	rs10761205	9	95070213	WNK2
124482	G	0.5	SNP_A-1997241	rs3001450	9	95125191	C9orf129
200874	C	0.459	SNP_A-1829993	rs1791244	18	35323310	unknown
200876	T	0.453	SNP_A-1903940	rs1791238	18	35328700	unknown
200884	T	0.318	SNP_A-4273118	rs2852353	18	35470720	unknown
200885	T	0.318	SNP_A-4245643	rs2726242	18	35470750	unknown
200886	G	0.324	SNP_A-1793369	rs2852351	18	35472770	unknown

Cluster 35	0 Controls with score of nan						
	14 Cases with score of 1.328						
128324	G	0.351	SNP_A-4295049	rs10858294	9	136964434	FCN1
128329	C	0.392	SNP_A-1859354	rs10776918	9	136999147	FCN1
158566	A	0.385	SNP_A-2250065	rs7133554	12	66819832	DYRK2
158569	A	0.385	SNP_A-1796154	rs2193045	12	66820787	DYRK2
158572	A	0.385	SNP_A-2035254	rs2193048	12	66823141	DYRK2
158573	A	0.385	SNP_A-2070406	rs2870953	12	66830897	DYRK2
158574	A	0.473	SNP_A-2101657	rs2069718	12	66836429	IFNG
158589	A	0.365	SNP_A-4276655	rs17802036	12	66953536	IL22
158592	C	0.399	SNP_A-1858680	rs17802054	12	66966116	MDM1
158599	C	0.291	SNP_A-2041771	rs1480050	12	67011849	MDM1
158605	A	0.264	SNP_A-2081018	rs7959632	12	67030425	MDM1
15286	T	0.297	SNP_A-1918112	rs1538323	1	216467717	RRP15
15287	T	0.412	SNP_A-2291223	rs1890358	1	216479007	RRP15
15288	G	0.527	SNP_A-1849402	rs12132163	1	216483277	RRP15
15289	G	0.493	SNP_A-1903442	rs11118065	1	216484143	RRP15
128325	T	0.351	SNP_A-4302807	rs10858299	9	136980767	FCN1
128327	G	0.358	SNP_A-2112764	rs10858305	9	136998239	FCN1
158563	T	0.351	SNP_A-1856290	rs4913404	12	66796852	DYRK2
158568	T	0.473	SNP_A-2289863	rs2216164	12	66820607	IFNG
158571	T	0.446	SNP_A-4276632	rs2193047	12	66822895	DYRK2
158577	T	0.385	SNP_A-2054900	rs10878779	12	66867288	IFNG
158590	G	0.399	SNP_A-2290948	rs11615045	12	66961108	IL22
Cluster 36	8 Controls with score of 1.208						
	26 Cases with score of 1.372						
149153	A	0.345	SNP_A-1954566	rs511141	11	95523665	MAML2
210349	C	0.277	SNP_A-1786600	rs1884861	20	23595482	CST4
149154	T	0.459	SNP_A-1846632	rs515200	11	95524215	MAML2
Cluster 37	3 Controls with score of 1.370						
	19 Cases with score of 1.409						
151308	C	0.318	SNP_A-1891108	rs679327	11	117548184	SCN2B
190194	A	0.534	SNP_A-4200390	rs9934214	16	63051027	CDH11
190196	C	0.52	SNP_A-4194860	rs9302565	16	63066166	CDH11
105292	G	0.345	SNP_A-1930664	rs7786076	7	155924851	C7orf13
151312	T	0.236	SNP_A-4257114	rs7935561	11	117561932	AMICA1
151313	T	0.236	SNP_A-2175193	rs11216803	11	117562454	AMICA1
190182	G	0.432	SNP_A-2184243	rs1437160	16	62971769	CDH11
190185	T	0.392	SNP_A-1955658	rs4359464	16	62992353	CDH11
190193	T	0.534	SNP_A-2004794	rs2194332	16	63050082	CDH11
Cluster 38	4 Controls with score of 1.159						
	19 Cases with score of 1.330						
168288	A	0.277	SNP_A-1907523	rs9540083	13	63892339	unknown
168293	A	0.25	SNP_A-2205071	rs1415011	13	63963642	unknown
168295	A	0.351	SNP_A-2154513	rs9564177	13	63970921	unknown
126163	T	0.385	SNP_A-1847335	rs7043896	9	112145525	TXNDC8
126165	T	0.385	SNP_A-2165428	rs1571236	9	112154879	TXNDC8
168287	G	0.277	SNP_A-2044692	rs9528751	13	63871239	unknown
168296	T	0.399	SNP_A-4227134	rs10507711	13	63987470	unknown
168298	T	0.318	SNP_A-2148527	rs1577681	13	64041350	unknown
168300	G	0.297	SNP_A-1947671	rs12429438	13	64061932	unknown
168301	T	0.23	SNP_A-4218924	rs11618161	13	64078415	unknown
168302	G	0.351	SNP_A-2078311	rs589629	13	64079730	unknown

Cluster 39	5 Controls with score of 1.425						
	20 Cases with score of 1.388						
171438	C	0.27	SNP_A-2078243	rs1336724	13	101694501	FGF14
171439	A	0.27	SNP_A-4199874	rs1336715	13	101709465	FGF14
171441	A	0.331	SNP_A-4289112	rs1336713	13	101719560	FGF14
194045	A	0.311	SNP_A-2098440	rs11078246	17	14273233	HS3ST3B1
171424	G	0.345	SNP_A-1872850	rs554393	13	101633794	FGF14
171443	G	0.331	SNP_A-1845225	rs1415057	13	101724665	FGF14
171444	T	0.331	SNP_A-2311213	rs4772461	13	101736581	FGF14
171447	T	0.324	SNP_A-2180765	rs1336664	13	101752488	FGF14
Cluster 40	0 Controls with score of nan						
	11 Cases with score of 1.371						
185925	A	0.318	SNP_A-2226642	rs1552101	15	98494760	ADAMTS17
187435	C	0.365	SNP_A-4243755	rs709424	16	12213268	SNX29
187436	A	0.378	SNP_A-4288458	rs830735	16	12238034	SNX29
187439	C	0.345	SNP_A-1928836	rs17697005	16	12268766	SNX29
187440	C	0.358	SNP_A-1956641	rs7197417	16	12285719	SNX29
187442	A	0.365	SNP_A-4192924	rs2856771	16	12308586	SNX29
187444	A	0.358	SNP_A-2219315	rs209856	16	12314214	SNX29
187450	C	0.392	SNP_A-1786191	rs4781209	16	12357279	SNX29
187454	A	0.399	SNP_A-2253172	rs11645864	16	12360410	SNX29
187455	C	0.392	SNP_A-1788245	rs16959318	16	12364752	SNX29
187462	A	0.378	SNP_A-2114780	rs4780431	16	12406052	SNX29
187464	C	0.419	SNP_A-4291832	rs4781227	16	12408359	SNX29
187465	C	0.378	SNP_A-2170412	rs889810	16	12413226	SNX29
187467	A	0.419	SNP_A-4291967	rs6498294	16	12417372	SNX29
115976	T	0.331	SNP_A-2189127	rs1586789	8	126966068	TRIB1
187437	G	0.5	SNP_A-2155825	rs709425	16	12246546	SNX29
187438	T	0.351	SNP_A-1786130	rs11644788	16	12265421	SNX29
187441	G	0.365	SNP_A-4232162	rs11075059	16	12290830	SNX29
187443	T	0.23	SNP_A-2242665	rs1960156	16	12311517	SNX29
187445	T	0.358	SNP_A-1816964	rs209848	16	12318297	SNX29
187451	T	0.399	SNP_A-1786192	rs7190509	16	12357356	SNX29
187452	G	0.446	SNP_A-4242062	rs11075062	16	12357426	SNX29
187460	G	0.385	SNP_A-1908102	rs1974905	16	12392797	SNX29
187463	T	0.311	SNP_A-1868800	rs6498291	16	12406672	SNX29
Cluster 41	10 Controls with score of 1.125						
	34 Cases with score of 1.257						
206886	C	0.378	SNP_A-1859268	rs1233441	19	49458421	ZNF233
206889	A	0.378	SNP_A-2099239	rs892595	19	49526822	ZFP112
207153	A	0.324	SNP_A-2291792	rs10419078	19	55765344	unknown
207154	G	0.331	SNP_A-4249982	rs7255690	19	55765451	unknown
Cluster 42	5 Controls with score of 1.200						
	20 Cases with score of 1.200						
118065	A	0.23	SNP_A-2106982	rs10759043	9	911872	DMRT1
118066	C	0.324	SNP_A-2128404	rs10121226	9	912574	DMRT1
118058	G	0.264	SNP_A-1995502	rs7856502	9	894078	DMRT1
118068	T	0.236	SNP_A-1807433	rs10816055	9	915305	DMRT1