Supplemental Methods
Lee, Blom, *et al.,* Prioritizing candidate disease genes by network-based boosting of genome-wide association data

Inferring gene functional association from human transcript expression data

Functional associations based on mRNA co-expression patterns across multiple microarray datasets were analyzed as in (Lee et al. 2008). A total of 166 microarray datasets (spanning several thousand individual microarrays) were assembled from the Stanford Microarray Database (Gollub et al. 2003) and Gene Expression Omnibus (Barrett et al. 2005) databases. Of these sets, 21 sets (**Table S2**), composed of 1,603 total microarrays, showed significant correlations between the degree of mRNA co-expression (measured as the Pearson correlation coefficient between expression vectors) and the degree of functional association (measured as the LLS for sharing GO annotations). We assigned 21 LLS to each human gene pair based on regression models between the LLS and correlation coefficients, as well as an additional LLS derived from a similar analysis of the concatenated set of all 1,603 arrays. The resulting 22 scores were integrated into a single overall LLS (HS-CX) for co-expression using the weighted sum method of (Lee et al. 2008).

Inferring gene functional associations from genomic context of orthologs

To discover functional associations based on genomic context, we compared the human protein sequences to 31 archeaebacterial and 393 eubacterial genomes using phylogenetic profiling (Pellegrini et al. 1999) (HS-PG) and the gene neighbor method of (Bowers et al. 2004) (HS-GN), analyzing them as in (Lee et al. 2008). A subset of 184 genomes, one selected from each unique genus, maximized performance of inferred linkages by the gene neighboring method, judged by recall-precision analysis; a set of 313 genomes, one from each unique species, maximized performance by the phylogenetic profiling method. For phylogenetic profiling, we observed improved performance by considering only human proteins with fewer than two domains annotated by the InterPro database (Hunter et al. 2009), as human proteins with greater numbers of domains tended to generate promiscuous functional associations in this approach. We assigned LLS for each human gene pair based on regression models with the genomic context scores from each method.

Inferring gene functional linkages based on protein domain co-occurrence patterns

The occurrence of similar patterns of protein domains is often a good indicator of similar protein function. We therefore analyzed InterPro domains for each protein as follows: We generated a matrix of human proteins versus InterPro domains with binary scores (1 for presence and 0 for absence) indicating domain occurrences. We observed improved performance, judged by recall-precision analysis, when weighting domains according to their frequency, as rare domains are stronger indicators of shared function. We therefore multiplied each domain co-occurrence by the inverse of its frequency in the genome. The associations between protein pairs were calculated from the mutual information of these domain profiles. To minimize spurious associations, we considered only gene pairs with BLASTP scores of E < 1e − 3. We assigned

LLS (HS-DC) for each human gene pair based on regression models with the mutual information scores.

Inferring functional associations from orthologs (associalogs)

Besides human data, we incorporated datasets from yeast, fly, and worm. Within each organism, we considered previously derived functional linkages, treating each line of evidence independently and benchmarking them in the same fashion as human datasets, but with the additional step of considering gene orthology. A total of 13 linkage sets were generated from three model organisms' functional gene networks, consisting of 7 sets of linkages from YeastNet (Lee et al. 2007) derived from mRNA co-expression (SC-CX), literature curated protein interactions (SC-LC), co-citation evidence (SC-CC), genetic interactions (SC-GT), mass spectrometry (SC-MS), predicted interactions from tertiary structure (SC-TS), and yeast two-hybrid interactions (SC-YH); a set of fly PPIs derived from BIOGRID (Breitkreutz et al. 2008), IntAct (Kerrien et al. 2007), MINT (Chatr-aryamontri et al. 2007) (DM-PI); and 5 sets of functional linkages from WormNet (Lee et al. 2008) derived from mRNA co-expression (CE-CX), co-citation (CE-CC), yeast two-hybrid assays (CE-YH), genetic interactions (CE-GT), and literature curated protein interactions (CE-LC). The sets are summarized in **Table S1**. Orthologs were calculated between human and model organism genes using INPARANOID (Remm et al. 2001). Functional linkages were weighted by confidence in the orthology assignments using their INPARANOID scores, which range from 0 to 1, calculating an INPARANOID-weighted log likelihood score (IWLLS) as in (Lee et al. 2010), and fitting a regression model between the assigned IWLLS and the LLS for sharing human functional annotation.

Functional gene linkages from literature, mass spectrometry proteomics, and genome-wide Y2H screens

We incorporated human protein interactions curated from the literature by the databases HPRD Release 6 (Mishra et al. 2006), BIND (downloaded on May 2006) (Alfarano et al. 2005), BIOGRID version 2.0.24 (Breitkreutz et al. 2008), IntAct (downloaded on February 2007) (Kerrien et al. 2007), MINT (downloaded on January 2007) (Chatr-aryamontri et al. 2007), and Reactome version 20 (Vastrik et al. 2007), as well as those identified from literature by (Rual et al. 2005), in total forming the HS-LC dataset (**Table S1**).

We also inferred linkages from the approx. 6,000 reported protein interactions detected by affinity purification of human protein complexes followed by mass spectrometry (Ewing et al. 2007), and from yeast two-hybrid-based protein interactions reported in two independent studies. For each gene pair from these datasets (analyzing mass spectrometry and Y2H datasets independently), we calculated a confidence score as in (Hart et al. 2007), then fit a regression model between the confidence score and LLS for sharing functional annotation.

Functional linkages based on literature-mined protein interactions

In addition to literature curation, various large-scale text-mining algorithms have been used to retrieve protein-protein interactions (PPIs) from the scientific literature. We analyzed one such mined set of interactions generated by a Bayesian classifier-filtered co-citation analysis (Ramani

et al. 2005). Confidence scores were assigned to mined interactions using the hypergeometric probability approach of (Hart et al. 2007; Lee et al. 2007). We then calculated a LLS (HS-CC) for each gene pair based upon a regression model to the confidence scores.

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Supplemental Figure 1. Predictive power does not depend upon the number of genes associated with the phenotype, plotted for binned mouse phenotypes predicted by the Iterative Ranking method.
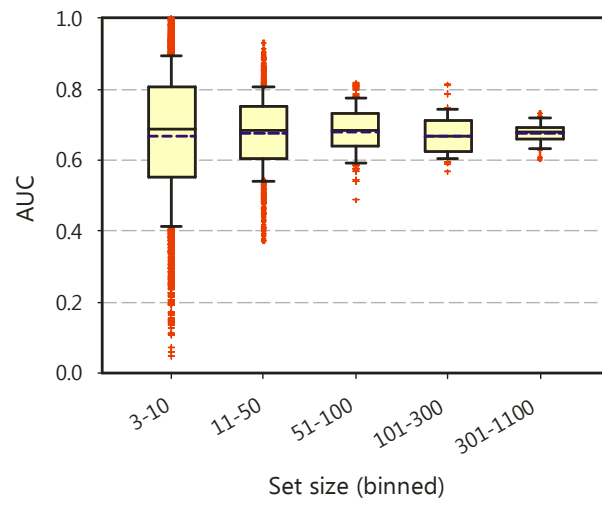
Supplemental Figure 2. While Gaussian smoothing performs better overall for associating genes with diseases, as measured by the area under a ROC curve (**Figures 2C,D**), it does not rank the withheld candidate genes as highly as *naïve* Bayes GBA for well-predicted diseases. Instead, we observe *naïve* Bayes GBA to outperform Gaussian smoothing for extremely high precision association of genes with diseases, measured as the median cross-validated rank of each withheld test gene, and evaluated in turn for each OMIM disease.
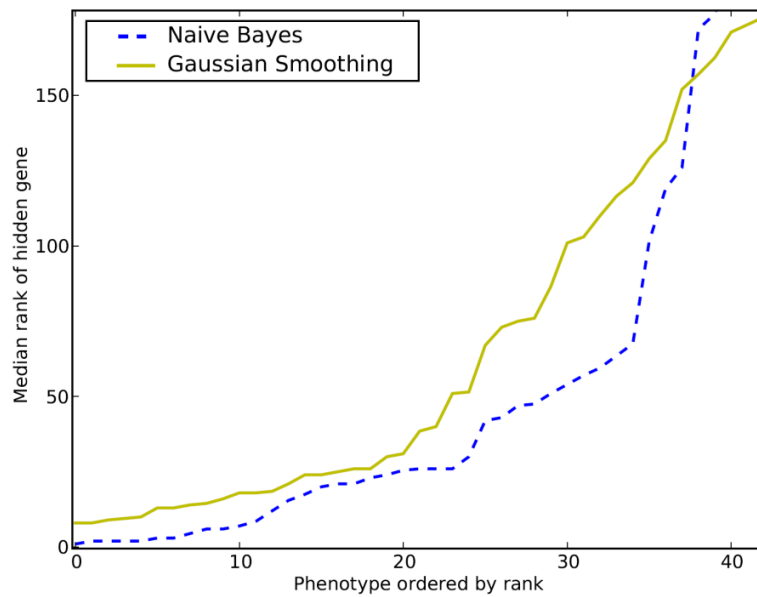
Table S1. Twenty-one different lines of evidence supporting HumanNet linkages.

Data set	Description	# genes	# gene pairs
CE-CC	Co-citation of worm genes	1,370	12,928
CE-CX	Co-expression among worm genes	2,633	41,645
CE-GT	Worm genetic interactions	1,040	5,430
CE-LC	Literature-curated worm protein physical interactions	1,402	2,640
CE-YH	High-throughput yeast 2-hybrid assays among worm genes	1,561	3,254
DM-PI	Fly protein physical interactions	4,153	15,738
HS-CC	Co-citation of human genes	3,423	6,172
HS-CX	Co-expression among human genes	11,050	156,317
HS-DC	Co-occurrence of domains among human proteins	8,737	38,797
HS-GN	Gene neighborhoods of bacterial and archaeal orthologs of human genes	3,504	36,487
HS-LC	Literature-curated linkages from protein-protein interaction DBs (HPRD, BIND, BioGRID, IntAct, MINT) and Rual *et al.*, and pathway DB (Reactome)	8,783	56,505
HS-MS	Human protein complexes from affinity purification/mass spectrometry	1,485	3,575
HS-PG	Co-inheritance of bacterial and archaeal orthologs of human genes	1,170	18,868
HS-YH	High-throughput yeast 2-hybrid assays among human genes	1,358	1,365
SC-CC	Co-citation of yeast genes	2,798	31,353
SC-CX	Co-expression among yeast genes	2,001	48,423
SC-GT	Yeast genetic interactions	2,584	17,678
SC-LC	Literature-curated yeast protein physical interactions	2,661	17,280
SC-MS	Yeast protein complexes from affinity purification/mass spectrometry	2,382	65,986
SC-TS	Yeast protein interactions inferred from tertiary structures of complexes	859	6,270
SC-YH	High-throughput yeast 2-hybrid assays among yeast genes	1,292	1,801

Table S2. Experimental microarray datasets used to derived co-expression linkages

Expression data set	Database	# experiments
Alizadeh A. A. et al. (Alizadeh et al. 2000)	SMD	133
Baird K. et al. (Baird et al. 2005)	GEO	181
Bredel M. et al. (Bredel et al. 2005)	SMD	54
Bullinger L. et al. (Bullinger et al. 2004)	SMD	119
Cario G. et al. (Cario et al. 2005)	SMD	51
Chen X. et al. (Chen et al. 2002)	SMD	207
Diehn M. et al. (Diehn et al. 2002)	SMD	68
Gilks C. B. et al. (Gilks et al. 2005)	SMD	23
Heuser M. et al. (Heuser et al. 2005)	SMD	35
Higgins J. P. et al. (Higgins et al. 2004)	SMD	34
Iacobuzio-Donahue C. A. et al. (Iacobuzio-Donahue et al. 2003)	SMD	36
Kampmann B. et al. (Kampmann et al. 2005)	SMD	16
Nielsen T. O. et al. (Nielsen et al. 2002)	SMD	46
Schaner M. E. et al. (Schaner et al. 2005)	SMD	46
Shyamsundar R. et al. (Shyamsundar et al. 2005)	SMD	123
Skotheim R. I. et al. (Skotheim et al. 2005)	GEO	30
Sorlie T. et al. (Sorlie et al. 2003)	SMD	167
Subramanian S. et al. (2004) (Subramanian et al. 2004)	SMD	26
Subramanian S. et al. (2005) (Subramanian et al. 2005)	SMD	36
Zhao H. et al. (2004) (Zhao et al. 2004)	SMD	64
Zhao H. et al. (2006) (Zhao et al. 2006)	SMD	177

SMD, Stanford Microarray Database; GEO, Gene Expression Omnibus

Table S3. Prioritization of genes for Crohn's disease using the network-assisted GWAS strategy, listing top-ranked 150 genes.

New rank	Old rank	Name	Entrez	BF	New BF	Boost weight	Major SNP
1	1	*NOD2*	64127	12.00	12.00	1.00	rs2076756
2	2	*ATG16L1*	55054	11.11	11.46	1.00	rs10210302
3	3	*IL23R*	149233	10.07	10.57	1.00	rs11805303
4	4	*CYLD*	1540	6.26	6.55	0.98	rs7342715
5	6	*PTPN2*	5771	5.42	5.92	0.95	rs2542151
6	5	*NKX2-3*	159296	5.91	5.91	0.97	rs10883365
7	17	*STAT3*	6774	3.15	4.85	0.62	rs744166
8	7	*ZNF300*	91975	4.77	4.77	0.91	rs3900064
9	9	*BSN*	8927	4.24	4.55	0.85	rs9858542
10	8	*SLC22A5*	6584	4.44	4.44	0.88	rs274547
11	10	*APEH*	327	4.24	4.38	0.85	rs9858542
12	99	*GRB2*	2885	2.01	4.14	0.15	rs16967789
13	21	*DAG1*	1605	3.02	4.03	0.58	rs1801143
14	15	*TCTA*	6988	3.16	4.01	0.62	rs9814873
15	11	*HLA-DQA2*	3118	3.69	3.69	0.76	rs9276429
16	18	*CAPN9*	10753	3.11	3.69	0.61	rs16852515
17	27	*CDK14*	5218	2.96	3.59	0.56	rs879428
18	12	*CDKAL1*	54901	3.55	3.55	0.73	rs6908425
19	13	*RSPH6A*	81492	3.48	3.48	0.71	rs8111071
20	32	*MST1*	4485	2.81	3.36	0.50	rs4855881
21	23	*CCNY*	219771	3.00	3.29	0.57	rs3936503
22	37	*USP4*	7375	2.72	3.28	0.47	rs4410472
23	45	*TRAIP*	10293	2.63	3.28	0.43	rs2352974
24	24	*FAF1*	11124	3.00	3.20	0.57	rs11205760
25	16	*AMT*	275	3.16	3.18	0.62	rs9814873
26	14	*NICN1*	84276	3.16	3.16	0.62	rs9814873
27	19	*LYRM4*	57128	3.10	3.10	0.61	rs12529198
28	65	*ERC2*	26059	2.30	3.10	0.29	rs9855289
29	125	*PPM1K*	152926	1.84	3.08	0.07	rs11733577
30	46	*APP*	351	2.62	3.08	0.43	rs2234988
31	20	*IL12RB2*	3595	3.03	3.03	0.58	rs3790567
32	22	*NFATC2*	4773	3.00	3.00	0.57	rs880324
33	25	*ZGPAT*	84619	2.99	2.99	0.57	rs2738758
34	26	*ZFHX4*	79776	2.98	2.98	0.56	rs10957818
35	42	*CREM*	1390	2.64	2.97	0.44	rs2505639
36	29	*USP7*	7874	2.90	2.95	0.54	rs2126999
37	47	*BATF*	10538	2.60	2.94	0.42	rs7161377
38	28	*GCKR*	2646	2.92	2.92	0.54	rs780094
39	44	*CAMKV*	79012	2.63	2.91	0.43	rs2352974
40	41	*C13orf31*	144811	2.67	2.89	0.45	rs3764147
41	36	*SP140*	11262	2.72	2.88	0.47	rs6743984
42	30	*C1orf106*	55765	2.87	2.87	0.53	rs7522462
43	38	*SLC22A23*	63027	2.71	2.87	0.47	rs17309827
44	31	*PGM1*	5236	2.84	2.86	0.51	rs2269252
45	33	*SBNO2*	22904	2.80	2.80	0.50	rs4807569

46	34	MDGA1	266727	2.76	2.76	0.49	rs9366943
47	35	CUL2	8453	2.73	2.73	0.47	rs17582416
48	39	TRIM15	89870	2.68	2.68	0.46	rs2517646
49	40	TRIM10	10107	2.68	2.68	0.46	rs2517646
50	57	TNFSF15	9966	2.37	2.64	0.32	rs4263839
51	43	BSG	682	2.63	2.63	0.43	rs2283573
52	48	KIFAP3	22920	2.57	2.60	0.41	rs1928887
53	73	TNFRSF6B	8771	2.22	2.57	0.25	rs2297441
54	49	DGKD	8527	2.54	2.54	0.40	rs11892545
55	106	RBMS3	27303	1.98	2.54	0.14	rs9821929
56	50	RAB3C	115827	2.51	2.51	0.38	rs2279980
57	127	NSF	4905	1.83	2.50	0.06	rs199449
58	51	TNRC6C	57690	2.47	2.49	0.37	rs4789012
59	52	SLC22A4	6583	2.47	2.47	0.37	rs3792884
60	53	ALPK2	115701	2.47	2.47	0.37	rs2003157
61	54	KIF21B	23046	2.43	2.45	0.35	rs12122721
62	327	TRAF1	7185	1.25	2.44	0.00	rs6478488
63	6125	SHC1	6464	-0.05	2.43	0.00	rs16836583
64	181	KIF23	9493	1.60	2.40	0.00	rs8030051
65	85	MAPT	4137	2.12	2.40	0.21	rs1864325
66	116	MAGI2	9863	1.89	2.39	0.10	rs10251915
67	55	CCL18	6362	2.39	2.39	0.33	rs2015070
68	169	CAMK1D	57118	1.66	2.39	0.00	rs11258009
69	56	ACSL6	23305	2.37	2.37	0.32	rs7714191
70	69	CLK3	1198	2.28	2.36	0.28	rs4073149
71	58	VWF	7450	2.35	2.35	0.31	rs12319392
72	59	SERINC5	256987	2.35	2.35	0.31	rs2289290
73	60	TNKS	8658	2.33	2.33	0.31	rs4240626
74	61	POU2F1	5451	2.33	2.33	0.31	rs12742052
75	62	IP6K1	9807	2.32	2.32	0.30	rs3749237
76	63	ZNF221	7638	2.32	2.32	0.30	rs413061
77	64	ARFRP1	10139	2.32	2.32	0.30	rs6011040
78	80	DQX1	165545	2.13	2.31	0.21	rs6546909
79	76	KCNK1	3775	2.17	2.30	0.23	rs701228
80	66	AMIGO3	386724	2.29	2.29	0.29	rs2291542
81	67	RNF123	63891	2.29	2.29	0.29	rs2291542
82	68	GMPPB	29925	2.29	2.29	0.29	rs2291542
83	347	CREBBP	1387	1.22	2.29	0.00	rs130021
84	118	PPP2R2B	5521	1.89	2.27	0.09	rs715891
85	70	DSCAM	1826	2.26	2.26	0.27	rs16999671
86	126	KCNAB1	7881	1.83	2.25	0.06	rs4680276
87	71	LYZL2	119180	2.22	2.22	0.26	rs2814637
88	72	RTEL1	51750	2.22	2.22	0.25	rs2297441
89	3139	JAK2	3717	0.12	2.21	0.00	rs10491652
90	74	IL1F10	84639	2.20	2.20	0.24	rs4849148
91	78	STX8	9482	2.13	2.18	0.21	rs9895062
92	75	CACNA1S	779	2.18	2.18	0.24	rs11583328
93	77	DPP6	1804	2.16	2.16	0.23	rs877471
94	112	N4BP1	9683	1.92	2.16	0.11	rs6500394
95	267	YWHAE	7531	1.35	2.16	0.00	rs16945811

96	79	*SEC16A*	9919	2.13	2.13	0.21	rs11145756
97	81	*TLX2*	3196	2.13	2.13	0.21	rs6546909
98	82	*AUP1*	550	2.13	2.13	0.21	rs6546909
99	83	*LRRC7*	57554	2.13	2.13	0.21	rs12035355
100	111	*DOK1*	1796	1.92	2.13	0.11	rs11126435
101	84	*OR11A1*	26531	2.12	2.12	0.21	rs2107193
102	86	*C2orf65*	130951	2.10	2.10	0.20	rs363691
103	87	*ARID3B*	10620	2.10	2.10	0.20	rs7497036
104	88	*CDH8*	1006	2.08	2.08	0.19	rs4438299
105	89	*PHACTR3*	116154	2.07	2.07	0.18	rs6027005
106	108	*PRKG1*	5592	1.96	2.06	0.13	rs11000404
107	182	*OPCML*	4978	1.60	2.06	0.00	rs1784520
108	11633	*SRC*	6714	-0.67	2.05	0.00	rs3940202
109	386	*DCTN1*	1639	1.15	2.04	0.00	rs9309484
110	90	*PROM1*	8842	2.04	2.04	0.17	rs16892888
111	621	*FOS*	2353	0.93	2.04	0.00	rs1569328
112	91	*ZNF225*	7768	2.03	2.03	0.17	rs2068061
113	92	*ZNF224*	7767	2.03	2.03	0.17	rs2068061
114	93	*CRHR1*	1394	2.03	2.03	0.16	rs8072451
115	94	*ELMO1*	9844	2.03	2.03	0.16	rs2723980
116	214	*GSN*	2934	1.49	2.02	0.00	rs10985207
117	95	*KIAA1267*	284058	2.02	2.02	0.16	rs11079729
118	96	*LDLRAD3*	143458	2.02	2.02	0.16	rs973942
119	97	*CALCB*	797	2.01	2.01	0.15	rs16924840
120	98	*USP1*	7398	2.01	2.01	0.15	rs626787
121	100	*WNT3*	7473	2.00	2.00	0.15	rs199530
122	203	*NCOA1*	8648	1.53	1.99	0.00	rs17791703
123	101	*C9orf163*	158055	1.99	1.99	0.15	rs4379550
124	228	*COL4A2*	1284	1.45	1.99	0.00	rs4773156
125	102	*MRPL53*	116540	1.99	1.99	0.14	rs1063588
126	103	*INO80B*	83444	1.99	1.99	0.14	rs1063588
127	104	*WBP1*	23559	1.99	1.99	0.14	rs1063588
128	105	*MOGS*	7841	1.99	1.99	0.14	rs1063588
129	199	*EBF1*	1879	1.54	1.98	0.00	rs6556379
130	119	*CRIP1*	1396	1.86	1.98	0.08	rs4983425
131	107	*NALCN*	259232	1.97	1.97	0.13	rs1333758
132	140	*TTC38*	55020	1.79	1.94	0.04	rs6007761
133	109	*FNDC5*	252995	1.93	1.93	0.12	rs16835198
134	110	*S100PBP*	64766	1.93	1.93	0.12	rs16835198
135	1325	*JAK1*	3716	0.54	1.91	0.00	rs17127024
136	334	*IL12B*	3593	1.24	1.91	0.00	rs2853696
137	113	*MYH3*	4621	1.90	1.90	0.10	rs2239930
138	114	*TNS4*	84951	1.90	1.90	0.10	rs8078319
139	115	*CLSTN2*	64084	1.90	1.90	0.10	rs1426036
140	222	*GRAP2*	9402	1.46	1.89	0.00	rs137954
141	117	*NKD1*	85407	1.89	1.89	0.09	rs8047222
142	290	*ANK2*	287	1.29	1.87	0.00	rs17045918
143	628	*CREB5*	9586	0.93	1.86	0.00	rs4722842
144	120	*USP3*	9960	1.86	1.86	0.08	rs8023466
145	121	*ATP8B1*	5205	1.85	1.85	0.08	rs319449

146	122	*PLD5*	200150	1.85	1.85	0.08	rs12135329
147	155	*TK1*	7083	1.69	1.85	0.00	rs1811086
148	123	*IP6K2*	51447	1.85	1.85	0.07	rs11708786
149	124	*FRMD4A*	55691	1.84	1.84	0.07	rs2797887
150	301	*CRX*	1406	1.28	1.84	0.00	rs10405809

Table S4. Prioritization of genes for type II diabetes using the network-assisted GWAS strategy, listing top-ranked 150 genes.

New rank	Old rank	Name	Entrez	BF	New BF	Boost weight	Major SNP
1	1	*TCF7L2*	6934	10.14	10.14	1.00	rs4506565
2	2	*CDKAL1*	54901	4.15	4.15	0.84	rs9465871
3	3	*TSPAN8*	7103	4.01	4.01	0.82	rs1495377
4	5	*THBS2*	7058	3.81	4.00	0.78	rs10806665
5	4	*RBMS1*	5937	3.86	3.86	0.79	rs6718526
6	6	*PDE4B*	5142	3.81	3.81	0.78	rs4655595
7	7	*KCNJ6*	3763	3.42	3.42	0.70	rs6517434
8	8	CCDC33	80125	3.30	3.30	0.66	rs2930291
9	9	ZNF239	8187	3.27	3.27	0.66	rs9326506
10	10	ANO2	57101	3.26	3.26	0.65	rs387896
11	11	ZFAND6	54469	3.24	3.24	0.65	rs2903265
12	12	NHEDC2	133308	3.17	3.17	0.63	rs1481279
13	13	PARD3B	117583	3.06	3.16	0.59	rs17248501
14	14	EBF3	253738	3.03	3.03	0.58	rs12776159
15	15	CPB1	1360	2.90	2.90	0.54	rs16861027
16	26	ISLR	3671	2.50	2.89	0.38	rs2899824
17	16	GULP1	51454	2.87	2.87	0.53	rs11688935
18	17	BEND3	57673	2.83	2.83	0.51	rs1665901
19	44	KIF23	9493	2.11	2.69	0.20	rs1504626
20	22	GTSE1	51512	2.56	2.62	0.41	rs10854854
21	18	AGBL4	84871	2.62	2.62	0.43	rs12086219
22	19	BEND5	79656	2.62	2.62	0.43	rs12086219
23	200	BACH2	60468	1.32	2.61	0.00	rs16882569
24	20	GBF1	8729	2.57	2.57	0.41	rs17780667
25	42	FAM49A	81553	2.13	2.57	0.21	rs11679606
26	21	TTC38	55020	2.56	2.56	0.41	rs10854854
27	23	HRH1	3269	2.56	2.56	0.41	rs440646
28	24	CEP110	11064	2.56	2.56	0.40	rs2057466
29	30	ANKS1A	23294	2.36	2.51	0.32	rs1996913
30	25	STRA6	64220	2.50	2.50	0.38	rs2899824
31	28	PRKG1	5592	2.41	2.44	0.34	rs11000542
32	27	DUSP16	80824	2.44	2.44	0.35	rs16908188
33	34	XYLB	9942	2.25	2.42	0.27	rs818838
34	33	ANKS1B	56899	2.26	2.40	0.27	rs11109882
35	29	TMEM108	66000	2.40	2.40	0.34	rs4600815
36	39	ATG7	10533	2.16	2.36	0.23	rs346078
37	31	PTPRT	11122	2.30	2.34	0.29	rs7262414
38	32	GALNT10	55568	2.28	2.28	0.28	rs4958711
39	35	CALCB	797	2.23	2.23	0.26	rs16924840
40	36	CREB5	9586	2.22	2.22	0.26	rs10435018
41	51	MELK	9833	2.02	2.22	0.16	rs4512469
42	65	MAGI2	9863	1.90	2.22	0.10	rs12539788
43	37	HAPLN1	1404	2.17	2.17	0.23	rs6864342
44	38	KCNIP4	80333	2.16	2.16	0.23	rs17557461
45	40	LCLAT1	253558	2.16	2.16	0.22	rs12613783
46	41	PLXNA4	91584	2.15	2.15	0.22	rs10273901

47	270	*PARD6G*	84552	1.19	2.14	0.00	rs12201
48	43	*PAQR5*	54852	2.11	2.11	0.20	rs1504626
49	45	*ANK3*	288	2.11	2.11	0.20	rs10821700
50	46	*CHST3*	9469	2.11	2.11	0.20	rs731027
51	47	*FARS2*	10667	2.09	2.09	0.19	rs9502305
52	48	*TLR5*	7100	2.08	2.08	0.19	rs1341987
53	49	*TRMU*	55687	2.08	2.08	0.19	rs6008700
54	79	*ALK*	238	1.83	2.05	0.06	rs6754787
55	50	*SEPT4*	5414	2.05	2.05	0.17	rs8182262
56	191	*CDC42*	998	1.33	2.05	0.00	rs2056975
57	66	*DYNC1H1*	1778	1.90	2.02	0.10	rs1741153
58	52	*MTHFD1L*	25902	2.02	2.02	0.16	rs12201472
59	53	*GALNT13*	114805	2.02	2.02	0.16	rs12995536
60	54	*GRIK1*	2897	2.01	2.01	0.15	rs2154490
61	55	*MCC*	4163	2.01	2.01	0.15	rs10043783
62	56	*LOH12CR1*	118426	2.00	2.00	0.15	rs3751262
63	57	*JAZF1*	221895	1.99	1.99	0.14	rs864745
64	60	*CHUK*	1147	1.93	1.98	0.11	rs11597086
65	58	*SOCS6*	9306	1.97	1.97	0.13	rs713129
66	59	*FHIT*	2272	1.94	1.94	0.12	rs9874888
67	74	*SORCS2*	57537	1.86	1.94	0.08	rs3936616
68	61	*BLNK*	29760	1.92	1.92	0.11	rs4917723
69	62	*ZKSCAN2*	342357	1.92	1.92	0.11	rs17625090
70	63	*PQLC1*	80148	1.91	1.91	0.10	rs11081573
71	64	*SMAP1*	60682	1.90	1.90	0.10	rs2347624
72	67	*PAX5*	5079	1.90	1.90	0.10	rs2297109
73	68	*GBP5*	115362	1.89	1.89	0.09	rs2209307
74	69	*TAF11*	6882	1.89	1.89	0.09	rs3734262
75	108	*XKR6*	286046	1.67	1.88	0.00	rs9657544
76	70	*FSTL4*	23105	1.88	1.88	0.09	rs17166592
77	292	*EBF1*	1879	1.16	1.87	0.00	rs10066782
78	71	*RBL2*	5934	1.87	1.87	0.08	rs8043918
79	72	*FRMD6*	122786	1.87	1.87	0.08	rs11847326
80	73	*EFCAB11*	90141	1.87	1.87	0.08	rs7158821
81	75	*MYOM2*	9172	1.85	1.85	0.08	rs1542065
82	76	*MYO3B*	140469	1.85	1.85	0.07	rs2113650
83	77	*ENOX1*	55068	1.85	1.85	0.07	rs9567136
84	78	*FLVCR2*	55640	1.85	1.85	0.07	rs8011085
85	118	*COPG*	22820	1.62	1.84	0.00	rs10934876
86	100	*ZNF532*	55205	1.72	1.84	0.01	rs6567036
87	80	*ASXL2*	55252	1.83	1.83	0.06	rs17680828
88	81	*ZPLD1*	131368	1.82	1.82	0.06	rs16845038
89	82	*CRTAC1*	55118	1.82	1.82	0.06	rs505699
90	83	*ACCN1*	40	1.82	1.82	0.06	rs317326
91	84	*SLC12A3*	6559	1.81	1.81	0.06	rs11640308
92	95	*DYRK1A*	1859	1.77	1.81	0.04	rs2835735
93	85	*GPR133*	283383	1.81	1.81	0.06	rs1195747
94	86	*KCNAB1*	7881	1.81	1.81	0.06	rs13097501
95	87	*CX3CR1*	1524	1.80	1.80	0.05	rs17038645
96	88	*ATXN1*	6310	1.80	1.80	0.05	rs1144700

97	89	*TBX15*	6913	1.80	1.80	0.05	rs12143789
98	90	*DCAKD*	79877	1.80	1.80	0.05	rs8078303
99	218	*CREM*	1390	1.28	1.79	0.00	rs2505639
100	91	*ARHGEF12*	23365	1.79	1.79	0.05	rs11217854
101	92	*SV2C*	22987	1.79	1.79	0.04	rs6896716
102	996	*PRKACB*	5567	0.59	1.79	0.00	rs11163905
103	93	*SAMD4A*	23034	1.77	1.77	0.04	rs709939
104	94	*SMYD3*	64754	1.77	1.77	0.04	rs2817506
105	140	*FOSL1*	8061	1.53	1.76	0.00	rs694994
106	96	*FRMD4A*	55691	1.75	1.75	0.02	rs6602681
107	103	*MDGA2*	161357	1.70	1.74	0.00	rs17118171
108	97	*EIF3F*	8665	1.73	1.73	0.02	rs4758263
109	101	*HIP1*	3092	1.70	1.73	0.00	rs237238
110	98	*CCL18*	6362	1.73	1.73	0.01	rs2015070
111	99	*KIAA0649*	9858	1.72	1.72	0.01	rs12238018
112	192	*LCPCAT1*	79888	1.33	1.70	0.00	rs16878933
113	102	*UBE2D3*	7323	1.70	1.70	0.00	rs223413
114	114	*EXOC4*	60412	1.64	1.69	0.00	rs6963221
115	104	*SCN11A*	11280	1.68	1.68	0.00	rs4676588
116	3099	*CTNNB1*	1499	0.08	1.68	0.00	rs13072632
117	105	*TADA2A*	6871	1.67	1.67	0.00	rs2158239
118	106	*PTPLA*	9200	1.67	1.67	0.00	rs17141401
119	125	*FEZ1*	9638	1.59	1.67	0.00	rs614910
120	107	*NTNG1*	22854	1.67	1.67	0.00	rs17018944
121	136	*MAP3K11*	4296	1.55	1.66	0.00	rs11227234
122	109	*VAV3*	10451	1.66	1.66	0.00	rs2494069
123	115	*PDE6A*	5145	1.63	1.65	0.00	rs152949
124	110	*ADAMTS3*	9508	1.65	1.65	0.00	rs13112404
125	111	*LRRTM3*	347731	1.64	1.64	0.00	rs7082306
126	112	*CTNNA3*	29119	1.64	1.64	0.00	rs7082306
127	113	*DIRC1*	116093	1.64	1.64	0.00	rs781241
128	116	*TMPRSS11A*	339967	1.63	1.63	0.00	rs17578509
129	117	*C3orf37*	56941	1.62	1.62	0.00	rs10934876
130	119	*KIAA1328*	57536	1.62	1.62	0.00	rs2046471
131	120	*FHOD3*	80206	1.62	1.62	0.00	rs507163
132	7618	*NLK*	51701	-0.09	1.61	0.00	rs11871640
133	121	*USP25*	29761	1.61	1.61	0.00	rs2026853
134	122	*NHEDC1*	150159	1.61	1.61	0.00	rs7698608
135	232	*GBE1*	2632	1.25	1.61	0.00	rs3772891
136	123	*LBH*	81606	1.60	1.60	0.00	rs4564821
137	171	*SKIV2L2*	23517	1.40	1.60	0.00	rs7730157
138	124	*CELSR1*	9620	1.60	1.60	0.00	rs6008770
139	126	*ADNP2*	22850	1.59	1.59	0.00	rs11660007
140	158	*NOX4*	50507	1.47	1.59	0.00	rs11018629
141	127	*LAMA1*	284217	1.59	1.59	0.00	rs952428
142	128	*MRPS22*	56945	1.59	1.59	0.00	rs1586861
143	138	*CCDC85B*	11007	1.53	1.58	0.00	rs694994
144	146	*WWOX*	51741	1.51	1.58	0.00	rs8055871
145	129	*PKDREJ*	10343	1.58	1.58	0.00	rs8143066
146	130	*BTBD16*	118663	1.57	1.57	0.00	rs10887122

147	143	*ZNF804A*	91752	1.53	1.57	0.00	rs6726421
148	159	*SEMA3C*	10512	1.46	1.57	0.00	rs6979288
149	131	*ZFYVE28*	57732	1.57	1.57	0.00	rs3118617
150	132	*VGLL4*	9686	1.56	1.56	0.00	rs6766610