

Supplementary

An online human blood transcript correlation browser for easy access to the blood cell interactome

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Table S1. Associations with CREB1

Gene Symbol	Gene Title	NM number	Oslo cohort		Framingham cohort		Comparison	Presence of CREB1 promoter element
			Estimate	P-value ¹	Estimate	P-value ¹		
<i>PKN2</i>	protein kinase N2	NM 006256	0,92	1,3E-38	0,64	1,3E-135	Significant in both cohorts	Yes
<i>SPAG9</i>	sperm associated antigen 9	NM 001130528	0,91	8,4E-36	0,43	6,2E-53	Significant in both cohorts	Yes
<i>JMJD1C</i>	jumonji domain containing 1C	NM 004241	0,9	9,9E-36	NA	NA	Not in Framingham data	Yes
<i>BRWD3</i>	bromodomain and WD repeat domain containing 3	NM 153252	0,9	1,1E-35	0,38	5,3E-40	Significant in both cohorts	Yes
<i>STX7</i>	syntaxin 7	NM 003569	0,9	1,5E-35	0,55	6,4E-92	Significant in both cohorts	Yes
<i>SETX</i>	senataxin	NM 015046	0,9	1,5E-35	0,37	1,3E-38	Significant in both cohorts	Yes
<i>CREBRF</i>	CREB3 regulatory factor	NM 153607	0,9	1,8E-35	0,57	3,5E-101	Significant in both cohorts	Yes
<i>PICALM</i>	phosphatidylinositol binding clathrin assembly protein	NM 007166	0,9	2,1E-35	0,26	2,2E-17	Significant in both cohorts	Yes
<i>BRGX</i>	BRO1 domain and CAAX motif containing	NM 144695	0,9	5,0E-35	NA	NA	Not in Framingham data	Yes
<i>SOS2</i>	SOS Ras/Rho guanine nucleotide exchange factor 2	NM 006939	0,9	5,9E-35	0,32	1,5E-27	Significant in both cohorts	Yes
<i>KIAA0232</i>	KIAA0232	NM 014743	0,9	1,2E-34	0,2	6,0E-10	Significant in both cohorts	Yes
<i>AGTPBP1</i>	ATP/GTP binding protein 1	NM 015239	0,9	1,6E-34	0,29	5,2E-23	Significant in both cohorts	Yes
<i>MARCH7</i>	membrane associated ring finger 7	NM 022826	0,9	2,3E-34	0,56	2,0E-98	Significant in both cohorts	Yes
<i>PAN3</i>	PAN3 poly(A) specific ribonuclease subunit	NM 175854	0,9	8,7E-34	0,27	5,3E-20	Significant in both cohorts	Yes
<i>MGEA5</i>	meningioma expressed antigen 5 (hyaluronidase)	NM 012215	0,89	1,3E-33	0,19	7,2E-09	Significant in both cohorts	Yes
<i>VPS8</i>	vacuolar protein sorting 8 homolog (S. cerevisiae)	NM 001009921	0,89	1,3E-33	0,37	3,6E-38	Significant in both cohorts	Yes
<i>MED13</i>	mediator complex subunit 13	NM 005121	0,89	1,5E-33	0,29	1,6E-22	Significant in both cohorts	Yes
<i>MTMR10</i>	myotubularin related protein 10	NM 017762	0,89	3,5E-33	0,28	1,9E-20	Significant in both cohorts	Yes
<i>UBR2</i>	ubiquitin protein ligase E3 component n-recognin 2	NM 015255	0,89	3,7E-33	0,56	3,9E-98	Significant in both cohorts	Yes
<i>MAP3K2</i>	mitogen-activated protein kinase kinase kinase 2	NM 006609	0,89	4,9E-33	0,5	5,2E-76	Significant in both cohorts	No
<i>NIN</i>	ninein (GSK3B interacting protein)	NM 020921	0,89	5,8E-33	0,32	1,5E-28	Significant in both cohorts	Yes
<i>VPS13B</i>	vacuolar protein sorting 13 homolog B (yeast)	NM 017890	0,89	6,1E-33	0,55	4,9E-93	Significant in both cohorts	Yes
<i>IVNS1ABP</i>	influenza virus NS1A binding protein	NM 006469	0,89	8,8E-33	0,4	2,1E-46	Significant in both cohorts	Yes
<i>ATP7A</i>	ATPase, Cu++ transporting, alpha polypeptide	NM 000052	0,89	9,1E-33	0,2	1,9E-10	Significant in both cohorts	Yes
<i>HBP1</i>	HMG-box transcription factor 1	NM 012257	0,89	9,3E-33	0,5	1,3E-74	Significant in both cohorts	Yes
<i>TMEM71</i>	transmembrane protein 71	NM 144649	0,89	1,5E-32	0,29	3,0E-22	Significant in both cohorts	No
<i>SHOC2</i>	SHOC2 leucine-rich repeat scaffold protein	NM 007373	0,89	1,5E-32	0,39	1,5E-43	Significant in both cohorts	Yes
<i>APC</i>	adenomatous polyposis coli	NM 001127511	0,89	1,6E-32	0,49	4,5E-73	Significant in both cohorts	Yes
<i>CYB5R4</i>	cytochrome b5 reductase 4	NM 016230	0,89	1,7E-32	0,45	3,1E-60	Significant in both cohorts	Yes
<i>CFLAR</i>	CASP8 and FADD like apoptosis regulator	NM 003879	0,89	2,2E-32	0,11	4,5E-02	Significant in both cohorts	Yes
<i>RAD21</i>	RAD21 cohesin complex component	NM 006265	0,89	2,4E-32	0,38	3,2E-41	Significant in both cohorts	Yes
<i>USP9X</i>	ubiquitin specific peptidase 9, X-linked	NM 001039590	0,89	3,5E-32	0,33	1,9E-29	Significant in both cohorts	Yes
<i>FNIP1</i>	folliculin interacting protein 1	NM 133372	0,89	3,6E-32	NA	NA	Not in Framingham data	Yes
<i>NUFIP2</i>	nuclear fragile X mental retardation protein interacting	NM 020772	0,89	4,9E-32	0,33	1,2E-29	Significant in both cohorts	Yes
<i>CASP8</i>	caspase 8, apoptosis-related cysteine peptidase	NM 001228	0,89	5,6E-32	0,48	3,7E-67	Significant in both cohorts	Yes
<i>NR3C1</i>	nuclear receptor subfamily 3, group C, member 1	NM 000176	0,89	7,5E-32	0,48	1,5E-68	Significant in both cohorts	Yes
<i>ZFC3H1</i>	zinc finger, C3H1-type containing	NM 144982	0,89	7,9E-32	0,32	4,8E-27	Significant in both cohorts	Yes
<i>RBM39</i>	RNA binding motif protein 39	NM 184234	0,89	7,9E-32	0,27	1,7E-19	Significant in both cohorts	Yes
<i>RICTOR</i>	RPTOR independent companion of MTOR, complex 2	NM 152756	0,89	9,0E-32	0,55	1,0E-93	Significant in both cohorts	Yes
<i>DOCK11</i>	dedicator of cytokinesis 11	NM 144658	0,89	9,4E-32	0,37	7,0E-39	Significant in both cohorts	Yes
<i>KIAA1109</i>	KIAA1109	NM 015312	0,88	1,1E-31	0,31	1,2E-25	Significant in both cohorts	No
<i>ANTXR2</i>	anthrax toxin receptor 2	NM 058172	0,88	1,2E-31	0,54	2,4E-89	Significant in both cohorts	Yes
<i>RRM2B</i>	ribonucleotide reductase M2 B (TP53 inducible)	NM 015713	0,88	1,3E-31	0,35	1,2E-34	Significant in both cohorts	Yes
<i>ITCH</i>	itchy E3 ubiquitin protein ligase	NM 031483	0,88	1,7E-31	0,29	3,2E-22	Significant in both cohorts	Yes
<i>KIDINS220</i>	kinase D-interacting substrate 220kDa	NM 020738	0,88	2,0E-31	NA	NA	Not in Framingham data	Yes
<i>SPOPL</i>	speckle-type POZ protein-like	NM 001001664	0,88	2,0E-31	0,57	1,3E-100	Significant in both cohorts	Yes
<i>KMT2E</i>	lysine (K)-specific methyltransferase 2E	NM 182931	0,88	2,7E-31	0,54	1,6E-91	Significant in both cohorts	Yes
<i>HIPK3</i>	homeodomain interacting protein kinase 3	NM 005734	0,88	3,2E-31	0,37	1,1E-38	Significant in both cohorts	Yes
<i>AKAP10</i>	A kinase (PRKA) anchor protein 10	NM 007202	0,88	4,6E-31	0,23	3,9E-14	Significant in both cohorts	Yes
<i>DDX3X</i>	DEAD (Asp-Glu-Ala-Asp) box helicase 3, X-linked	NM 001356	0,88	4,7E-31	0,26	1,7E-17	Significant in both cohorts	Yes
<i>CEP350</i>	centrosomal protein 350kDa	NM 014810	0,88	4,7E-31	0,47	7,2E-64	Significant in both cohorts	Yes
<i>AHCTF1</i>	AT hook containing transcription factor 1	NM 015446	0,88	4,9E-31	0	1,0E+00	Significant in Oslo only	Yes
<i>TRIM33</i>	tripartite motif containing 33	NM 015906	0,88	5,7E-31	0,57	1,9E-101	Significant in both cohorts	Yes
<i>PTPN12</i>	protein tyrosine phosphatase, non-receptor type 12	NM 002835	0,88	7,8E-31	0,5	1,5E-73	Significant in both cohorts	Yes
<i>LRMP</i>	lymphoid-restricted membrane protein	NM 006152	0,88	8,4E-31	0,4	4,9E-45	Significant in both cohorts	Yes
<i>OSBPL11</i>	oxysterol binding protein-like 11	NM 022776	0,88	9,1E-31	0,56	1,5E-99	Significant in both cohorts	Yes
<i>CUL3</i>	cullin 3	NM 003590	0,88	1,0E-30	0,57	6,3E-102	Significant in both cohorts	Yes
<i>STK4</i>	serine/threonine kinase 4	NM 006282	0,88	1,2E-30	0,32	1,4E-28	Significant in both cohorts	Yes
<i>KBTBD2</i>	kelch repeat and BTB (POZ) domain containing 2	NM 015483	0,88	1,3E-30	0,41	6,1E-48	Significant in both cohorts	Yes
<i>PAPOLA</i>	poly(A) polymerase alpha	NM 032632	0,88	1,3E-30	0,35	3,8E-34	Significant in both cohorts	Yes
<i>UBR5</i>	ubiquitin protein ligase E3 component n-recognin 5	NM 015902	0,88	1,7E-30	0,21	3,9E-11	Significant in both cohorts	Yes
<i>PIK3CA</i>	phosphatidylinositol 4,5-bisphosphate 3-kinase, catalytic	NM 006218	0,88	1,8E-30	0,47	9,0E-65	Significant in both cohorts	Yes
<i>TRAPPC8</i>	trafficking protein particle complex 8	NM 014939	0,88	2,0E-30	0,34	3,4E-32	Significant in both cohorts	Yes
<i>AMD1</i>	adenosylmethionine decarboxylase 1	NM 001634	0,88	2,3E-30	0,52	1,3E-80	Significant in both cohorts	Yes
<i>MKLN1</i>	muskelin 1, intracellular mediator containing kelch motifs	NM 013255	0,88	2,9E-30	0,5	1,6E-73	Significant in both cohorts	Yes
<i>PIK3C3</i>	phosphatidylinositol 3-kinase, catalytic subunit type 3	NM 002647	0,88	3,4E-30	0,31	1,4E-26	Significant in both cohorts	Yes
<i>NIPBL</i>	Nipped-B homolog (Drosophila)	NM 015384	0,88	4,9E-30	0,49	2,6E-71	Significant in both cohorts	Yes
<i>GSK3B</i>	glycogen synthase kinase 3 beta	NM 002093	0,88	5,1E-30	0,38	3,4E-40	Significant in both cohorts	Yes
<i>PHIP</i>	pleckstrin homology domain interacting protein	NM 017934	0,87	7,1E-30	0,46	7,8E-61	Significant in both cohorts	Yes
<i>PUM2</i>	pumilio RNA binding family member 2	NM 015317	0,87	7,8E-30	0,54	5,8E-88	Significant in both cohorts	No
<i>SNX13</i>	sorting nexin 13	NM 015132	0,87	8,9E-30	0,49	6,4E-72	Significant in both cohorts	Yes
<i>ELF2</i>	E74-like factor 2 (ets domain transcription factor)	NM 201999	0,87	1,0E-29	0,4	7,9E-45	Significant in both cohorts	No
<i>BOD1L1</i>	biorientation of chromosomes in cell division 1-like 1	NM 148894	0,87	1,0E-29	0,51	1,9E-77	Significant in both cohorts	Yes
<i>NFAT5</i>	nuclear factor of activated T-cells 5, tonicity-responsive	NM 138714	0,87	1,1E-29	0,33	3,5E-29	Significant in both cohorts	Yes
<i>STXBPS</i>	syntaxin binding protein 5 (tomosyn)	NM 001127715	0,87	1,2E-29	0,42	2,1E-51	Significant in both cohorts	Yes
<i>ARID4B</i>	AT rich interactive domain 4B (RBP1-like)	NM 016374	0,87	1,3E-29	0,48	3,8E-69	Significant in both cohorts	Yes
<i>SRPK2</i>	SRSF protein kinase 2	NM 182691	0,87	1,4E-29	0,51	4,2E-79	Significant in both cohorts	Yes
<i>PHF20L1</i>	PHD finger protein 20-like 1	NM 016018	0,87	1,6E-29	0,53	3,5E-87	Significant in both cohorts	Yes
<i>ITSN2</i>	intersectin 2	NM 006277	0,87	1,6E-29	0,45	1,2E-57	Significant in both cohorts	Yes
<i>STRN</i>	striatin, calmodulin binding protein	NM 003162	0,87	1,8E-29	0,5	2,8E-75	Significant in both cohorts	Yes
<i>PTPRC</i>	protein tyrosine phosphatase, receptor type, C	NM 002838	0,87	1,9E-29	0,5	2,8E-73	Significant in both cohorts	Yes
<i>VPS4B</i>	vacuolar protein sorting 4 homolog B (S. cerevisiae)	NM 004869	0,87	1,9E-29	0,4	3,7E-44	Significant in both cohorts	Yes
<i>ANKRD44</i>	ankyrin repeat domain 44	NM 153697	0,87	1,9E-29	0,37	1,9E-38	Significant in both cohorts	Yes
<i>APAF1</i>	apoptotic peptidase activating factor 1	NM 181861	0,87	2,1E-29	0,32	1,4E-27	Significant in both cohorts	Yes
<i>EXOC1</i>	exocyst complex component 1	NM 001024924	0,87	2,1E-29	0,5	3,1E-75	Significant in both cohorts	Yes
<i>ABI1</i>	abl-interactor 1	NM 005470	0,87	2,4E-29	0,29	3,4E-22	Significant in both cohorts	Yes
<i>USP15</i>	ubiquitin specific peptidase 15	NM 006313	0,87	2,8E-29	0,12	6,0E-03	Significant in both cohorts	Yes
<i>LPGAT1</i>	lysophosphatidylglycerol acyltransferase 1	NM 014873	0,87	2,9E-29	0,42	4,8E-50	Significant in both cohorts	Yes
<i>VPS41</i>	vacuolar protein sorting 41 homolog (S. cerevisiae)	NM 014396	0,87	4,1E-29	0,54	3,8E-90	Significant in both cohorts	Yes
<i>PDS5B</i>	PDS5 cohesin associated factor B	NM 015032	0,87	5,1E-29	0,35	9,1E-33	Significant in both cohorts	Yes
<i>RFWD2</i>	ring finger and WD repeat domain 2, E3 ubiquitin protein	NM 022457	0,87	5,2E-29	0,42	1,2E-50	Significant in both cohorts	Yes
<i>TPR</i>	translocated promoter region, nuclear basket protein	NM 003292	0,87	5,8E-29	0,41	9,1E-49	Significant in both cohorts	Yes
<i>CHD2</i>	chromodomain helicase DNA binding protein 2	NM 001271	0,87	6,4E-29	0,3	5,6E-25	Significant in both cohorts	Yes
<i>OGFRL1</i>	opioid growth factor receptor-like 1	NM 024576	0,87	6,8E-29	0,47	2,0E-63	Significant in both cohorts	Yes
<i>CCPG1</i>	cell cycle progression 1	NM 004748	0,87	6,9E-29	0,29	2,3E-22	Significant in both cohorts	Yes
<i>ADAM10</i>	ADAM metallopeptidase domain 10	NM 001110	0,87	7,8E-29	0,35	6,4E-34	Significant in both cohorts	Yes
<i>DNAJC13</i>	DnaJ (Hsp40) homolog, subfamily C, member 13	NM 015268	0,87	7,9E-29	0,45	2,4E-57	Significant in both cohorts	Yes
<i>PPP1R12A</i>	protein phosphatase 1, regulatory subunit 12A	NM 001143885	0,87	8,4E-29	NA	NA	Not in Framingham data	Yes
<i>TET2</i>	tet methylcytosine dioxygenase 2	NM 017628	0,87	9,5E-29	0,49	1,5E-71	Significant in both cohorts	Yes
<i>RPS6KA5</i>	ribosomal protein S6 kinase, 90kDa, polypeptide 5	NM 004755	0,87	9,6E-29	0,39	8,3E-44	Significant in both cohorts	Yes
<i>ZFYVE16</i>	zinc finger, FYVE domain containing 16	NM 014733	0,87	9,9E-29	NA	NA	Not in Framingham data	No
<i>KIF5B</i>	kinesin family member 5B	NM 004521	0,87	1,0E-28	0,35	2,0E-34	Significant in both cohorts	Yes
<i>LYST</i>	lysosomal trafficking regulator	NM_000081	0,87	1,2E-28	0,54	4,3E-88	Significant in both cohorts	Yes

MAP3K5	mitogen-activated protein kinase kinase kinase 5	NM_005923	0,87	1,2E-28	0,45	5,4E-60	Significant in both cohorts	Yes
STXBP3	syntaxin binding protein 3	NM_007269	0,87	1,3E-28	0,56	8,2E-100	Significant in both cohorts	Yes
PPP3CA	protein phosphatase 3, catalytic subunit, alpha isozyme	NM_000944	0,87	1,3E-28	0,52	1,4E-80	Significant in both cohorts	Yes
AFTPH	aftiphilin	NM_203437	0,87	1,3E-28	0,53	4,7E-87	Significant in both cohorts	Yes
CTBS	chitobiase, di-N-acetyl-	NM_004388	0,87	1,3E-28	0,5	1,1E-73	Significant in both cohorts	Yes
BAZ1A	bromodomain adjacent to zinc finger domain 1A	NM_013448	0,87	1,4E-28	0,33	1,6E-29	Significant in both cohorts	Yes
NTSC2	5-nucleotidase, cytosolic II	NM_012229	0,87	1,5E-28	0,21	3,9E-11	Significant in both cohorts	Yes
CARD8	caspase recruitment domain family, member 8	NM_014959	0,87	1,6E-28	0,07	1,0E+00	Significant in Oslo only	Yes
HERC4	HECT and RLD domain containing E3 ubiquitin protein ligase	NM_022079	0,87	1,7E-28	0,27	4,7E-19	Significant in both cohorts	Yes
GOLGB1	golgin B1	NM_004487	0,87	1,8E-28	0,46	1,2E-61	Significant in both cohorts	Yes
DICER1	dicer 1, ribonuclease type III	NM_177438	0,87	1,8E-28	0,43	4,9E-53	Significant in both cohorts	Yes
RNF169	ring finger protein 169	NM_001098638	0,87	1,8E-28	NA	NA	Not in Framingham data	Yes
LRRFIP1	leucine rich repeat (in FLII) interacting protein 1	NM_001137552	0,87	1,9E-28	NA	NA	Not in Framingham data	Yes
TIPARP	TCDD-inducible poly(ADP-ribose) polymerase	NM_015508	0,87	2,0E-28	0,47	2,2E-65	Significant in both cohorts	Yes
IFNAR1	interferon (alpha, beta and omega) receptor 1	NM_000629	0,86	2,4E-28	0,23	2,4E-13	Significant in both cohorts	Yes
CRLF3	cytokine receptor-like factor 3	NM_015986	0,86	2,9E-28	0,13	5,9E-04	Significant in both cohorts	Yes
NPEPPS	aminopeptidase puromycin sensitive	NM_006310	0,86	3,0E-28	0,22	3,7E-12	Significant in both cohorts	Yes
ST8SIA4	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	NM_005668	0,86	3,4E-28	0,55	2,4E-92	Significant in both cohorts	Yes
KDM5A	lysine (K)-specific demethylase 5A	NM_005056	0,86	3,6E-28	0,1	1,7E-01	Significant in Oslo only	Yes
PCF11	PCF11 cleavage and polyadenylation factor subunit	NM_015885	0,86	3,8E-28	0,31	3,7E-25	Significant in both cohorts	Yes
PIK3CB	phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic	NM_006219	0,86	3,9E-28	0,42	2,1E-51	Significant in both cohorts	No
RP2	retinitis pigmentosa 2 (X-linked recessive)	NM_006915	0,86	4,1E-28	0,18	2,2E-08	Significant in both cohorts	Yes
RC3H1	ring finger and CCH-type domains 1	NM_172071	0,86	4,7E-28	NA	NA	Not in Framingham data	No
FBXO38	F-box protein 38	NM_205836	0,86	5,4E-28	NA	NA	Not in Framingham data	Yes
RNASEL	ribonuclease L (2,5-oligoadenylate synthetase-dependent)	NM_021133	0,86	6,0E-28	0,29	2,2E-22	Significant in both cohorts	Yes
NEK7	NIMA-related kinase 7	NM_133494	0,86	6,0E-28	0,41	6,0E-48	Significant in both cohorts	Yes
RAB27A	RAB27A, member RAS oncogene family	NM_004580	0,86	6,5E-28	0,07	1,0E+00	Significant in Oslo only	Yes
SCAF11	SR-related CTD-associated factor 11	NM_004719	0,86	8,6E-28	0,34	3,2E-32	Significant in both cohorts	Yes
IFNAR2	interferon (alpha, beta and omega) receptor 2	NM_207585	0,86	8,7E-28	-0,04	1,0E+00	Significant in Oslo only	Yes
CASC4	cancer susceptibility candidate 4	NM_138423	0,86	1,1E-27	0,17	2,6E-07	Significant in both cohorts	Yes
UPF2	UPF2 regulator of nonsense transcripts homolog (yeast)	NM_080599	0,86	1,2E-27	0,32	1,5E-27	Significant in both cohorts	Yes
UBXN4	UBX domain protein 4	NM_014607	0,86	1,3E-27	0,49	3,5E-70	Significant in both cohorts	Yes
IRAK4	interleukin 1 receptor associated kinase 4	NM_001114182	0,86	1,3E-27	0,28	2,7E-21	Significant in both cohorts	Yes
ATF6	activating transcription factor 6	NM_007348	0,86	1,3E-27	0,31	9,0E-27	Significant in both cohorts	Yes
BAZ2B	bromodomain adjacent to zinc finger domain 2B	NM_013450	0,86	1,3E-27	0,49	2,6E-71	Significant in both cohorts	Yes
RAB21	RAB21, member RAS oncogene family	NM_014999	0,86	1,4E-27	0,19	5,3E-09	Significant in both cohorts	Yes
AP3B1	adaptor-related protein complex 3, beta 1 subunit	NM_003664	0,86	1,5E-27	0,57	4,0E-101	Significant in both cohorts	Yes
ZNF217	zinc finger protein 217	NM_006526	0,86	1,8E-27	0,11	1,7E-02	Significant in both cohorts	No
FAM49B	family with sequence similarity 49, member B	BC017297	0,86	1,9E-27	0,23	1,9E-13	Significant in both cohorts	Yes
ELF1	E74-like factor 1 (ets domain transcription factor)	NM_172373	0,86	1,9E-27	0,29	2,9E-23	Significant in both cohorts	No
CD46	CD46 molecule, complement regulatory protein	NM_002389	0,86	1,9E-27	0,46	7,3E-62	Significant in both cohorts	Yes
TLK2	tousled-like kinase 2	NM_006852	0,86	2,1E-27	0,11	1,7E-02	Significant in both cohorts	Yes
PIK3CG	phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic	NM_002649	0,86	2,2E-27	0,27	8,5E-20	Significant in both cohorts	No
HSDL2	hydroxysteroid dehydrogenase like 2	NM_032303	0,86	2,5E-27	0,33	3,3E-30	Significant in both cohorts	Yes
SP1	Sp1 transcription factor	NM_138473	0,86	2,7E-27	-0,13	6,8E-04	Significant in both cohorts	Yes
TAOK1	TAO kinase 1	NM_020791	0,86	2,9E-27	0,28	1,9E-20	Significant in both cohorts	Yes
MORC3	MORC family CW-type zinc finger 3	NM_015358	0,86	3,5E-27	0,22	2,0E-12	Significant in both cohorts	Yes
RB1	retinoblastoma 1	NM_000321	0,86	3,6E-27	0,27	1,4E-18	Significant in both cohorts	Yes
STK38L	serine/threonine kinase 38 like	NM_015000	0,86	3,9E-27	0,31	2,9E-26	Significant in both cohorts	Yes
NGLY1	N-glycanase 1	NM_018297	0,86	3,9E-27	0,42	7,5E-51	Significant in both cohorts	Yes
TAOK3	TAO kinase 3	NM_016281	0,86	3,9E-27	0,27	1,2E-18	Significant in both cohorts	Yes
OSTF1	osteoclast stimulating factor 1	NM_012383	0,86	4,3E-27	0,09	3,8E-01	Significant in Oslo only	Yes
USP34	ubiquitin specific peptidase 34	NM_014709	0,86	5,2E-27	0,5	1,8E-73	Significant in both cohorts	Yes
ZFX	zinc finger protein, X-linked	NM_003410	0,86	5,6E-27	0,28	1,5E-21	Significant in both cohorts	Yes
CSGALNACT	chondroitin sulfate N-acetylgalactosaminyltransferase 2	NM_018590	0,86	5,7E-27	0,19	9,0E-09	Significant in both cohorts	Yes
PAK2	p21 protein (Cdc42/Rac)-activated kinase 2	NM_002577	0,86	6,4E-27	0,44	5,7E-57	Significant in both cohorts	Yes
RLF	rearranged L-myc fusion	NM_012421	0,86	6,4E-27	0,41	1,4E-46	Significant in both cohorts	Yes
DCP2	decapping mRNA 2	NM_152624	0,85	6,8E-27	0,43	4,5E-54	Significant in both cohorts	Yes
PPTC7	PTC7 protein phosphatase homolog	NM_139283	0,85	7,1E-27	0,15	3,7E-05	Significant in both cohorts	Yes
SLC35F5	solute carrier family 35, member F5	NM_025181	0,85	7,2E-27	0,37	3,0E-38	Significant in both cohorts	Yes
FBXL5	F-box and leucine-rich repeat protein 5	NM_033535	0,85	7,2E-27	0,35	2,0E-34	Significant in both cohorts	Yes
CSNK1A1	casein kinase 1, alpha 1	NM_001025105	0,85	7,2E-27	0,43	1,9E-53	Significant in both cohorts	Yes
CACUL1	CDK2-associated, cullin domain 1	NM_153810	0,85	7,3E-27	0,19	3,1E-09	Significant in both cohorts	Yes
ARIH1	ariadne RBR E3 ubiquitin protein ligase 1	NM_005744	0,85	8,1E-27	0,2	1,8E-10	Significant in both cohorts	Yes
WHSC1L1	Wolf-Hirschhorn syndrome candidate 1-like 1	NM_023034	0,85	8,2E-27	0,37	2,2E-38	Significant in both cohorts	Yes
SYNJ1	synaptojanin 1	NM_003895	0,85	9,0E-27	0,2	1,8E-10	Significant in both cohorts	Yes
KDM7A	lysine (K)-specific demethylase 7A	NM_030647	0,85	9,9E-27	NA	NA	Not in Framingham data	Yes
NUP58	nucleoporin 58kDa	NM_014089	0,85	1,0E-26	0,23	1,2E-13	Significant in both cohorts	No
SEL1L	sel-1 suppressor of lin-12-like (C. elegans)	NM_005065	0,85	1,0E-26	0,26	8,3E-18	Significant in both cohorts	Yes
NRDC	nardilysin convertase	NM_002525	0,85	1,0E-26	0,52	3,9E-83	Significant in both cohorts	No
RPS6KA3	ribosomal protein S6 kinase, 90kDa, polypeptide 3	NM_004586	0,85	1,1E-26	0,2	1,7E-10	Significant in both cohorts	Yes
GDAP2	ganglioside induced differentiation associated protein 2	NM_001135589	0,85	1,1E-26	NA	NA	Not in Framingham data	Yes
VAV3	vav 3 guanine nucleotide exchange factor	NM_006113	0,85	1,3E-26	0,49	3,1E-70	Significant in both cohorts	No
ATG3	autophagy related 3	NM_022488	0,85	1,4E-26	0,45	1,4E-58	Significant in both cohorts	Yes
CLK1	CDC like kinase 1	NR_027856	0,85	1,4E-26	NA	NA	Not in Framingham data	Yes
FBXL3	F-box and leucine-rich repeat protein 3	NM_012158	0,85	1,5E-26	0,33	1,4E-30	Significant in both cohorts	No
SPG11	spastic paraplegia 11 (autosomal recessive)	NM_025137	0,85	1,6E-26	0,24	2,2E-14	Significant in both cohorts	Yes
USP48	ubiquitin specific peptidase 48	NM_032236	0,85	1,9E-26	0,48	4,1E-67	Significant in both cohorts	Yes
PTBP3	polypyrimidine tract binding protein 3	NM_005156	0,85	2,1E-26	0,2	1,2E-09	Significant in both cohorts	Yes
RBM5	RNA binding motif protein 5	NM_005778	0,85	2,2E-26	0,24	1,3E-14	Significant in both cohorts	Yes
CHIC2	cysteine rich hydrophobic domain 2	NM_012110	0,85	2,2E-26	0,26	2,3E-17	Significant in both cohorts	Yes
CLTC	clathrin, heavy chain (Hc)	NM_004859	0,85	2,4E-26	0,32	2,9E-28	Significant in both cohorts	Yes
SNAP23	synaptosome associated protein 23kDa	NM_003825	0,85	2,5E-26	0,13	5,1E-04	Significant in both cohorts	Yes
ERBB2IP	erb2 interacting protein	NM_018695	0,85	2,6E-26	0,54	3,2E-89	Significant in both cohorts	Yes
TMOD3	tropomodulin 3 (ubiquitous)	NM_014547	0,85	2,7E-26	0,23	3,3E-14	Significant in both cohorts	Yes
CCNL1	cyclin L1	NM_020307	0,85	2,8E-26	0,46	7,0E-61	Significant in both cohorts	Yes
YTHDF3	YTH N(6)-methyladenosine RNA binding protein 3	NM_152758	0,85	2,8E-26	0,49	6,0E-71	Significant in both cohorts	Yes
CHD1	chromodomain helicase DNA binding protein 1	NM_001270	0,85	3,1E-26	0,43	6,4E-53	Significant in both cohorts	Yes
SBNO1	strawberry notch homolog 1 (Drosophila)	NM_018183	0,85	3,1E-26	0,26	2,4E-18	Significant in both cohorts	No
N4BP2L2	NEDD4 binding protein 2-like 2	NM_014887	0,85	3,2E-26	0,21	7,3E-11	Significant in both cohorts	Yes
MCL1	myeloid cell leukemia 1	NM_021960	0,85	3,3E-26	0,31	9,4E-26	Significant in both cohorts	Yes
RBM25	RNA binding motif protein 25	NM_021239	0,85	3,4E-26	0,2	9,2E-10	Significant in both cohorts	Yes
MFSD14A	major facilitator superfamily domain containing 14A	NM_033055	0,85	3,6E-26	0,36	3,4E-35	Significant in both cohorts	No
STAG1	stromal antigen 1	NM_005862	0,85	3,7E-26	0,51	3,8E-77	Significant in both cohorts	Yes
---	---	ENST00000459345	0,85	4,0E-26	NA	NA	Not in Framingham data	NA
MOSPD2	motile sperm domain containing 2	NM_152581	0,85	4,0E-26	0,35	4,8E-34	Significant in both cohorts	Yes
RBPJ	recombination signal binding protein for immunoglobulin	NM_005349	0,85	4,3E-26	0,48	4,6E-68	Significant in both cohorts	Yes

¹P-values are Bonferroni corrected; NA: not applicable (did not reach detection level in the Framingham cohort); significant correlations are shaded

Table S2. Associations with GATA1

Gene Symbol	Gene Title	NM number	Oslo cohort		Framingham cohort		Comparison	Presence of GATA1 promoter element
			Estimate	P-value ¹	Estimate	P-value ¹		
<i>SPTB</i>	spectrin, beta, erythrocytic	NM_001024858	0,86	5,3E-27	0,61	3,3E-119	Significant in both cohorts	Yes
<i>SHARPIN</i>	SHANK-associated RH domain interactor	NM_030974	0,85	1,9E-26	0,47	2,2E-64	Significant in both cohorts	Yes
<i>ST6GALNAC4</i>	ST6 (alpha-N-acetyl-neuraminy-2,3-beta-galactosyl-1,3)-N-	NM_175039	0,84	2,9E-25	0,48	2,3E-67	Significant in both cohorts	Yes
<i>DMTN (EPB49)</i>	dematin actin binding protein	NM_001978	0,84	2,9E-24	0,6	3,3E-118	Significant in both cohorts	Yes
<i>RILP</i>	Rab interacting lysosomal protein	NM_031430	0,83	2,7E-23	0,57	3,8E-101	Significant in both cohorts	Yes
<i>SLC6A10PB (SLC6A8)</i>	solute carrier family 6 (neurotransmitter transporter),	NM_005629	0,83	3,6E-23	0,57	1,5E-103	Significant in both cohorts	Yes
<i>ANK1</i>	ankyrin 1, erythrocytic	NM_020476	0,83	3,7E-23	0,59	6,4E-110	Significant in both cohorts	No
<i>SLC25A39</i>	solute carrier family 25, member 39	NM_001143780	0,82	9,2E-23	NA	NA	Not in Framingham data	Yes
<i>CARM1</i>	coactivator-associated arginine methyltransferase 1	NM_199141	0,82	3,1E-22	0,62	9,7E-129	Significant in both cohorts	Yes
<i>FKBP8</i>	FK506 binding protein 8	NM_012181	0,82	4,5E-22	0,5	2,7E-73	Significant in both cohorts	Yes
<i>TNS1</i>	tensin 1	NM_022648	0,81	7,4E-22	0,52	4,3E-83	Significant in both cohorts	No
<i>CDC34</i>	cell division cycle 34	NM_004359	0,81	8,2E-22	0,61	8,3E-120	Significant in both cohorts	Yes
<i>DNAJB2</i>	DnaJ (Hsp40) homolog, subfamily B, member 2	NM_006736	0,81	2,0E-21	0,51	5,3E-80	Significant in both cohorts	Yes
<i>HAGH</i>	hydroxyacylglutathione hydrolase	NM_005326	0,8	2,1E-20	NA	NA	Not in Framingham data	Yes
<i>HBM</i>	hemoglobin, mu	NM_001003938	0,8	4,8E-20	0,47	9,9E-66	Significant in both cohorts	Yes
<i>PRR5</i>	proline rich 5 (renal)	NM_181333	0,79	7,6E-20	NA	NA	Not in Framingham data	No
<i>ATP6VOC</i>	ATPase, H+ transporting, lysosomal 16kDa, VO subunit c	NM_001694	0,79	1,0E-19	NA	NA	Not in Framingham data	Yes
<i>MAF1</i>	MAF1 homolog, negative regulator of RNA polymerase III	NM_032272	0,79	1,1E-19	0,49	1,5E-70	Significant in both cohorts	Yes
<i>FIX</i>	nuclear factor I/X (CCAAT-binding transcription factor)	NM_002501	0,79	3,6E-19	0,55	6,2E-92	Significant in both cohorts	Yes
<i>FAM210B (C20orf108)</i>	family with sequence similarity 210, member B	NM_080821	0,79	3,8E-19	0,4	4,6E-45	Significant in both cohorts	Yes
<i>SLC7A5</i>	solute carrier family 7 (amino acid transporter light chain, L	NM_003486	0,78	9,2E-19	0,53	5,4E-86	Significant in both cohorts	Yes
<i>GUCD1 (C22ORF13)</i>	guanylyl cyclase domain containing 1	NM_031444	0,78	2,7E-18	0,63	6,7E-132	Significant in both cohorts	Yes
<i>HDGF</i>	hepatoma-derived growth factor	NM_004494	0,78	3,0E-18	0,55	1,6E-93	Significant in both cohorts	Yes
<i>AP2A1</i>	adaptor-related protein complex 2, alpha 1 subunit	NM_014203	0,78	3,3E-18	0,58	1,1E-104	Significant in both cohorts	Yes
<i>TMEM63B</i>	transmembrane protein 63B	NM_018426	0,78	3,7E-18	NA	NA	Not in Framingham data	Yes
<i>MCOLN1</i>	mucolipin 1	NM_020533	0,77	6,1E-18	0,61	2,2E-120	Significant in both cohorts	No
<i>RBM38</i>	RNA binding motif protein 38	NM_017495	0,77	1,2E-17	0,57	1,2E-102	Significant in both cohorts	Yes
<i>ZER1</i>	zyg-11 related, cell cycle regulator	NM_006336	0,77	1,5E-17	0,64	2,0E-139	Significant in both cohorts	No
<i>UBXN6</i>	UBX domain protein 6	NM_025241	0,77	1,9E-17	0,59	1,6E-112	Significant in both cohorts	No
<i>POLL</i>	polymerase (DNA directed), lambda	NM_013274	0,77	2,0E-17	0,51	8,4E-79	Significant in both cohorts	Yes
<i>ADIPOR1</i>	adiponectin receptor 1	NM_015999	0,77	2,7E-17	NA	NA	Not in Framingham data	Yes
<i>RNF10</i>	ring finger protein 10	NM_014868	0,77	2,8E-17	0,59	3,1E-110	Significant in both cohorts	Yes
<i>IGF2BP2</i>	insulin-like growth factor 2 mRNA binding protein 2	NM_006548	0,76	3,8E-17	0,34	1,6E-31	Significant in both cohorts	No
<i>MXI1</i>	MAX interactor 1, dimerization protein	NM_005962	0,76	5,2E-17	0,38	8,9E-40	Significant in both cohorts	No
<i>MFSD2B</i>	major facilitator superfamily domain containing 2B	NM_001080473	0,76	5,4E-17	NA	NA	Not in Framingham data	Yes
<i>GLRX5</i>	glutaredoxin 5	NM_016417	0,76	6,9E-17	0,5	1,3E-74	Significant in both cohorts	Yes
<i>MARCH2</i>	membrane associated ring finger 2	NM_016496	0,76	8,4E-17	0,04	1,0E+00	Significant in Oslo only	No
<i>RNF123</i>	ring finger protein 123	NM_022064	0,76	1,1E-16	0,55	7,6E-95	Significant in both cohorts	Yes
<i>OSBP2</i>	oxysterol binding protein 2	NM_030758	0,76	1,7E-16	0,51	1,9E-77	Significant in both cohorts	No
<i>KLF1</i>	Kruppel-like factor 1 (erythroid)	NM_006563	0,76	2,1E-16	0,46	3,2E-63	Significant in both cohorts	Yes
<i>E2F2</i>	E2F transcription factor 2	NM_004091	0,75	2,8E-16	0,49	6,3E-70	Significant in both cohorts	Yes
<i>TMOD1</i>	tropomodulin 1	NM_003275	0,75	2,9E-16	0,46	5,1E-63	Significant in both cohorts	Yes
<i>HPS1</i>	Hermansky-Pudlak syndrome 1	NM_000195	0,75	3,0E-16	0,51	2,3E-79	Significant in both cohorts	No
<i>GPR146</i>	G protein-coupled receptor 146	NM_138445	0,75	3,6E-16	0,49	4,0E-72	Significant in both cohorts	Yes
<i>TMEM86B</i>	transmembrane protein 86B	NM_173804	0,75	3,7E-16	0,42	6,7E-50	Significant in both cohorts	Yes
<i>SOX6</i>	SRY box 6	NM_017508	0,75	4,4E-16	0,42	5,0E-50	Significant in both cohorts	Yes
<i>SLC4A1</i>	solute carrier family 4 (anion exchanger), member 1 (Diego	NM_000342	0,75	4,7E-16	0,61	1,8E-122	Significant in both cohorts	Yes
<i>SlAH2</i>	siah E3 ubiquitin protein ligase 2	NM_005067	0,75	4,8E-16	0,46	2,0E-62	Significant in both cohorts	Yes
<i>XK</i>	X-linked Kx blood group	NM_021083	0,75	5,8E-16	0,46	5,9E-61	Significant in both cohorts	Yes
<i>GMPR</i>	guanosine monophosphate reductase	NM_006877	0,75	6,9E-16	0,58	4,4E-105	Significant in both cohorts	Yes
<i>LYL1</i>	lymphoblastic leukemia associated hematopoiesis	NM_005583	0,75	1,0E-15	0,13	1,1E-03	Significant in both cohorts	Yes
<i>ELOF1</i>	ELF1 homolog, elongation factor 1	NM_032377	0,74	1,7E-15	0,41	9,0E-47	Significant in both cohorts	Yes
<i>FAM117A</i>	family with sequence similarity 117, member A	NM_030802	0,74	3,7E-15	0,55	1,1E-95	Significant in both cohorts	Yes
<i>MAP2K3</i>	mitogen-activated protein kinase kinase 3	NM_002756	0,74	4,0E-15	0,54	6,3E-91	Significant in both cohorts	Yes
<i>CDH1</i>	cadherin 1, type 1	NM_004360	0,74	4,5E-15	0,44	2,0E-56	Significant in both cohorts	Yes
<i>R3HDM4 (C19orf22)</i>	R3H domain containing 4	NM_138774	0,74	5,4E-15	0,46	1,5E-60	Significant in both cohorts	Yes
<i>TRIM58</i>	tripartite motif containing 58	NM_015431	0,74	6,5E-15	0,53	7,9E-86	Significant in both cohorts	Yes
<i>SELENBP1</i>	selenium binding protein 1	NM_003944	0,74	6,9E-15	0,6	2,2E-117	Significant in both cohorts	Yes
<i>GUK1</i>	guanylate kinase 1	NM_000858	0,74	7,2E-15	0,52	1,9E-81	Significant in both cohorts	Yes
<i>ROGDI</i>	rogdi homolog	NM_024589	0,73	8,4E-15	0,41	1,3E-46	Significant in both cohorts	Yes
<i>BCL2L1</i>	BCL2-like 1	NM_138578	0,73	8,6E-15	0,55	1,0E-93	Significant in both cohorts	Yes
<i>RANBP10</i>	RAN binding protein 10	NM_020850	0,73	1,0E-14	0,55	8,3E-96	Significant in both cohorts	Yes
<i>TBC1D22B</i>	TBC1 domain family, member 22B	NM_017772	0,73	1,1E-14	0,5	2,8E-73	Significant in both cohorts	Yes
<i>GYPC</i>	glycophorin C (Gerbich blood group)	NM_002101	0,73	1,1E-14	0,53	4,5E-84	Significant in both cohorts	Yes
<i>DPM2</i>	dolichyl-phosphate mannosyltransferase polypeptide 2,	NM_003863	0,73	1,1E-14	0,56	1,1E-99	Significant in both cohorts	Yes
<i>UBE2O</i>	ubiquitin-conjugating enzyme E2O	NM_022066	0,73	1,2E-14	0,51	3,4E-80	Significant in both cohorts	No
<i>CNPPD1 (C2orf24)</i>	cyclin Pas1/PHO80 domain containing 1	NM_015680	0,73	1,2E-14	0,51	1,9E-78	Significant in both cohorts	Yes
<i>FAM214B (KIAA1539)</i>	family with sequence similarity 214, member B	BC004406	0,73	2,1E-14	0,45	5,7E-59	Significant in both cohorts	Yes
<i>RNF187</i>	ring finger protein 187	NM_001010858	0,73	2,1E-14	NA	NA	Not in Framingham data	Yes
<i>FOXO4</i>	forkhead box O4	NM_005938	0,73	2,5E-14	0,47	9,1E-64	Significant in both cohorts	Yes
---	---	ENST00000434251	0,73	3,0E-14	NA	NA	Not in Framingham data	NA
<i>YBX3 (CSDA)</i>	Y box binding protein 3	NM_003651	0,73	3,4E-14	0,41	1,3E-47	Significant in both cohorts	Yes
<i>AHSP</i>	alpha hemoglobin stabilizing protein	NM_016633	0,73	3,5E-14	0,53	1,1E-85	Significant in both cohorts	Yes
<i>CAPN5</i>	calpain 5	NM_004055	0,72	3,9E-14	0,49	4,1E-70	Significant in both cohorts	Yes
<i>RAB11B</i>	RAB11B, member RAS oncogene family	NM_004218	0,72	4,0E-14	0,45	4,1E-59	Significant in both cohorts	No
<i>FURIN</i>	furin (paired basic amino acid cleaving enzyme)	NM_002569	0,72	4,4E-14	0,53	2,4E-86	Significant in both cohorts	Yes
<i>KEL</i>	Kell blood group, metallo-endorpeptidase	NM_000420	0,72	4,9E-14	0,44	1,9E-56	Significant in both cohorts	Yes
<i>EPB42</i>	erythrocyte membrane protein band 4.2	NM_000119	0,72	7,2E-14	0,62	9,0E-129	Significant in both cohorts	Yes
<i>MYL4</i>	myosin light chain 4	NM_001002841	0,72	8,0E-14	0,52	5,9E-82	Significant in both cohorts	Yes
<i>TGM2</i>	transglutaminase 2	NM_004613	0,72	9,8E-14	0,55	1,7E-92	Significant in both cohorts	Yes
<i>KLC3</i>	kinesin light chain 3	NM_177417	0,72	1,0E-13	0,52	9,2E-82	Significant in both cohorts	No
---	---	ENST00000444706	0,72	1,1E-13	NA	NA	Not in Framingham data	NA
<i>HMBS</i>	hydroxymethylbilane synthase	NM_000190	0,72	1,2E-13	0,5	9,8E-76	Significant in both cohorts	Yes
<i>TESC</i>	tescalcin	NM_017899	0,72	1,4E-13	0,56	1,5E-97	Significant in both cohorts	No
<i>TRIM10</i>	tripartite motif containing 10	NM_006778	0,71	2,4E-13	0,48	5,3E-69	Significant in both cohorts	No
<i>SLC38A5</i>	solute carrier family 38, member 5	NM_033518	0,71	2,4E-13	0,49	7,5E-73	Significant in both cohorts	Yes
<i>DCAF12</i>	DDB1 and CUL4 associated factor 12	NM_015397	0,71	2,6E-13	0,57	9,2E-103	Significant in both cohorts	Yes
<i>NFIA</i>	nuclear factor I/A	NM_001134673	0,71	5,0E-13	0,37	1,7E-38	Significant in both cohorts	Yes
<i>GRINA</i>	glutamate receptor, ionotropic, N-methyl D-aspartate-	NM_000837	0,71	5,2E-13	0,47	9,7E-66	Significant in both cohorts	Yes
<i>SLC48A1</i>	solute carrier family 48 (heme transporter), member 1	NM_017842	0,71	5,4E-13	0,39	1,1E-42	Significant in both cohorts	Yes
<i>TANGO2 (C22orf25)</i>	transport and golgi organization 2 homolog	NM_152906	0,71	5,8E-13	0,61	5,5E-122	Significant in both cohorts	Yes
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<i>AK1</i>	adenylate kinase 1	NM_000476	0,71	7,2E-13	0,48	2,8E-67	Significant in both cohorts	Yes
<i>PPP2R5B</i>	protein phosphatase 2, regulatory subunit B, beta	NM_006244	0,7	1,3E-12	0,47	1,1E-64	Significant in both cohorts	Yes
<i>TAL1</i>	T-cell acute lymphocytic leukemia 1	NM_003189	0,7	1,4E-12	0,41	1,7E-47	Significant in both cohorts	Yes
<i>FAM46C</i>	family with sequence similarity 46, member C	NM_017709	0,7	1,5E-12	0,45	1,8E-59	Significant in both cohorts	Yes
<i>KRTAP4-7 (KRTAP4-9)</i>	keratin associated protein 4-7	NM_001146041	0,7	1,7E-12	NA	NA	Not in Framingham data	No
<i>SLC1A5</i>	solute carrier family 1 (neutral amino acid transporter),	NM_005628	0,7	1,7E-12	0,54	3,4E-90	Significant in both cohorts	Yes
<i>TCEB2</i>	transcription elongation factor B (SIII), polypeptide 2	NM_007108	0,7	1,8E-12	0,13	1,7E-03	Significant in both cohorts	Yes
<i>TPGS2 (C18orf10)</i>	tubulin polyglutamylase complex subunit 2	NM_015476	0,7	1,8E-12	0,47	1,0E-63	Significant in both cohorts	No
<i>mar.08</i>	membrane associated ring finger 8	NM_001002265	0,7	2,1E-12	0,46	1,3E-62	Significant in both cohorts	Yes
<i>ALAS2</i>	5-aminolevulinate synthase 2	NM_000032	0,7	2,1E-12	0,52	1,9E-83	Significant in both cohorts	Yes
<i>BLVRB</i>	biliverdin reductase B	NM_000713	0,7	2,3E-12	0,57	9,8E-104	Significant in both cohorts	Yes

PSMF1	proteasome inhibitor subunit 1	NM 178578	0,7	2,4E-12	0,57	3,5E-103	Significant in both cohorts	Yes
HMGN1	high mobility group nucleosome binding domain 1	ENST00000380748	0,7	2,5E-12	NA	NA	Not in Framingham data	Yes
STK11	serine/threonine kinase 11	NM 000455	0,7	3,3E-12	0,48	6,2E-68	Significant in both cohorts	Yes
PTMS	parathymosin	NM 002824	0,69	3,5E-12	0,41	2,2E-48	Significant in both cohorts	Yes
PLEK2	pleckstrin 2	NM 016445	0,69	4,4E-12	0,47	5,6E-65	Significant in both cohorts	Yes
RAD23A	RAD23 homolog A, nucleotide excision repair protein	NM 005053	0,69	6,0E-12	0,56	1,3E-96	Significant in both cohorts	Yes
---	---	ENST00000363109	0,69	6,2E-12	NA	NA	Not in Framingham data	Yes
DNAJC6	DnaJ (Hsp40) homolog, subfamily C, member 6	NM 014787	0,69	7,1E-12	0,38	3,3E-40	Significant in both cohorts	Yes
PHOSPHO1	phosphatase, orphan 1	NM 001143804	0,69	7,5E-12	NA	NA	Not in Framingham data	Yes
ATP1B2	ATPase, Na+/K+ transporting, beta 2 polypeptide	NM 001678	0,69	7,8E-12	0,51	2,2E-79	Significant in both cohorts	Yes
TRAPPC5	trafficking protein particle complex 5	NM 174894	0,69	8,4E-12	0,32	6,0E-28	Significant in both cohorts	Yes
PINK1	PTEN induced putative kinase 1	NM 032409	0,69	1,1E-11	0,57	6,3E-103	Significant in both cohorts	
SNCA	synuclein alpha	NM 000345	0,68	1,4E-11	0,38	1,7E-41	Significant in both cohorts	Yes
RUNDC3A	RUN domain containing 3A	NM 006695	0,68	1,5E-11	0,48	8,2E-67	Significant in both cohorts	No
PNPLA2	patatin-like phospholipase domain containing 2	NM 020376	0,68	1,5E-11	0,44	1,4E-54	Significant in both cohorts	No
SLC6A9	solute carrier family 6 (neurotransmitter transporter,	NM 201649	0,68	1,6E-11	0,43	6,1E-54	Significant in both cohorts	Yes
VWCE	von Willebrand factor C and EGF domains	NM 152718	0,68	2,4E-11	0,47	9,2E-65	Significant in both cohorts	Yes
CCDC124	coiled-coil domain containing 124	NM 138442	0,68	3,4E-11	0,25	8,2E-17	Significant in both cohorts	No
FECH	ferrochelatase	NM 001012515	0,68	3,7E-11	0,47	2,4E-64	Significant in both cohorts	Yes
SEC14L4	SEC14-like lipid binding 4	NM 174977	0,67	5,1E-11	0,37	8,0E-39	Significant in both cohorts	Yes
SPTA1	spectrin, alpha, erythrocytic 1	NM 003126	0,67	5,1E-11	0,39	1,1E-41	Significant in both cohorts	Yes
HBD	hemoglobin, delta	NM 000519	0,67	5,2E-11	0,5	1,8E-73	Significant in both cohorts	Yes
SMIM24 (C19orf77)	small integral membrane protein 24	NM 001136503	0,67	6,4E-11	NA	NA	Not in Framingham data	Yes
NEDD4L	neural precursor cell expressed, developmentally down-	NM 001144967	0,67	1,1E-10	NA	NA	Not in Framingham data	Yes
TSPAN5	tetraspanin 5	NM 005723	0,67	1,2E-10	0,52	1,5E-81	Significant in both cohorts	Yes
PBX1	pre-B-cell leukemia homeobox 1	NM 002585	0,67	1,5E-10	0,42	5,5E-50	Significant in both cohorts	
INPP5K	inositol polyphosphate-5-phosphatase K	NM 130766	0,67	1,7E-10	NA	NA	Not in Framingham data	Yes
SLC25A37	solute carrier family 25 (mitochondrial iron transporter),	NM 016612	0,67	1,8E-10	0,5	6,7E-75	Significant in both cohorts	Yes
---	---	NA	0,66	2,4E-10	NA	NA	Not in Framingham data	NA
SFRP2	secreted frizzled-related protein 2	NM 003013	0,66	2,5E-10	0,3	2,5E-24	Significant in both cohorts	No
PPDPF	pancreatic progenitor cell differentiation and proliferation	NM 024299	0,66	2,5E-10	NA	NA	Not in Framingham data	Yes
ARHGEF12	Rho guanine nucleotide exchange factor (GEF) 12	NM 015313	0,66	2,8E-10	0,41	5,6E-49	Significant in both cohorts	Yes
BABAM1 (C19orf62)	BRISC and BRCA1 A complex member 1	NM 001033549	0,66	3,7E-10	0,53	1,9E-84	Significant in both cohorts	Yes
---	---	NA	0,66	4,3E-10	NA	NA	Not in Framingham data	NA
ASCC2	activating signal cointegrator 1 complex subunit 2	NM 032204	0,66	5,1E-10	0,58	6,2E-107	Significant in both cohorts	Yes
MKRN1	makorin ring finger protein 1	NM 013446	0,65	7,0E-10	0,41	1,3E-48	Significant in both cohorts	Yes
PLVAP	plasmalemma vesicle associated protein	NM 031310	0,65	7,2E-10	0,42	1,6E-51	Significant in both cohorts	Yes
NA	NA	NM 004639	0,65	8,5E-10	0,51	7,6E-77	Significant in both cohorts	Yes
MICAL2	microtubule associated monooxygenase, calponin and LIM	NM 014632	0,65	8,7E-10	0,51	8,0E-77	Significant in both cohorts	No
E2F4	E2F transcription factor 4, p107/p130-binding	NM 001950	0,65	9,6E-10	0,3	1,6E-24	Significant in both cohorts	No
SERF2	small EDRK-rich factor 2	NM 001018108	0,65	1,1E-09	0,28	5,8E-21	Significant in both cohorts	Yes
---	---	ENST00000410622	0,65	1,1E-09	NA	NA	Not in Framingham data	
TSTA3	tissue specific transplantation antigen P35B	NM 003313	0,65	1,4E-09	0,49	5,7E-70	Significant in both cohorts	Yes
HES3	hes family bHLH transcription factor 3	NM 001024598	0,65	1,5E-09	NA	NA	Not in Framingham data	No
YOD1	YOD1 deubiquitinase	NM 018566	0,64	2,2E-09	NA	NA	Not in Framingham data	Yes
PIM1	Pim-1 proto-oncogene, serine/threonine kinase	NM 002648	0,64	2,3E-09	0,48	1,7E-68	Significant in both cohorts	Yes
YPEL3	yippee like 3	NM 031477	0,64	3,0E-09	0,45	5,4E-59	Significant in both cohorts	Yes
SLC14A1	solute carrier family 14 (urea transporter), member 1 (Kidd	NM 001128588	0,64	3,1E-09	0,49	1,6E-70	Significant in both cohorts	Yes
MPP1	membrane protein, palmitoylated 1	NM 002436	0,64	4,0E-09	NA	NA	Not in Framingham data	Yes
SH3GLB2	SH3-domain GRB2-like endophilin B2	NM 020145	0,64	4,5E-09	0,25	6,9E-16	Significant in both cohorts	Yes
PIGQ	phosphatidylinositol glycan anchor biosynthesis class Q	NM 004204	0,64	4,8E-09	0,28	5,8E-21	Significant in both cohorts	Yes
SMOX	spermine oxidase	NM 175839	0,63	6,1E-09	0,47	2,2E-65	Significant in both cohorts	Yes
---	---	ENST00000410524	0,63	6,4E-09	NA	NA	Not in Framingham data	NA
---	---	NA	0,63	6,8E-09	NA	NA	Not in Framingham data	NA
PQLC1	PQ loop repeat containing 1	NM 025078	0,63	7,0E-09	0,22	8,0E-13	Significant in both cohorts	No
MYBL2	v-myb avian myeloblastosis viral oncogene homolog-like 2	NM 002466	0,63	7,1E-09	0,26	1,6E-18	Significant in both cohorts	Yes
---	---	NA	0,63	1,1E-08	NA	NA	Not in Framingham data	
UBL7	ubiquitin-like 7	NM 032907	0,63	1,1E-08	0,43	4,6E-53	Significant in both cohorts	Yes
ERMAP	erythroblast membrane-associated protein (Scianna blood	NM 001017922	0,63	1,1E-08	0,31	1,1E-26	Significant in both cohorts	Yes
---	---	ENST00000410779	0,63	1,2E-08	NA	NA	Not in Framingham data	
MED25	mediator complex subunit 25	NM 030973	0,63	1,2E-08	0,34	1,2E-31	Significant in both cohorts	Yes
YIPF2	Yip1 domain family member 2	NM 024029	0,63	1,4E-08	0,29	1,1E-22	Significant in both cohorts	Yes
BSG	basigin (Ok blood group)	NM 001728	0,63	1,6E-08	0,55	2,8E-93	Significant in both cohorts	Yes
HNRNPU	heterogeneous nuclear ribonucleoprotein U (scaffold	NM 031844	-0,62	1,9E-08	-0,26	1,7E-17	Significant in both cohorts	Yes
SRSF5	serine/arginine-rich splicing factor 5	NM 001039465	-0,62	2,1E-08	-0,13	8,5E-04	Significant in both cohorts	Yes
---	---	ENST00000410468	0,62	2,2E-08	NA	NA	Not in Framingham data	
PDXP	pyridoxal (pyridoxine, vitamin B6) phosphatase	NM 020315	0,62	2,2E-08	0,04	1,0E+00	Significant in Oslo only	No
ANKRD9	ankyrin repeat domain 9	NM 152326	0,62	2,3E-08	0,2	3,8E-10	Significant in both cohorts	Yes
SMIM5 (LOC643008)	small integral membrane protein 5	NM 001162995	0,62	2,3E-08	NA	NA	Not in Framingham data	Yes
SMG1P1	SMG1 pseudogene 1	NM 015092	-0,62	2,6E-08	-0,2	5,1E-10	Significant in both cohorts	No
SRRD	SRR1 domain containing	NM 001013694	0,62	3,0E-08	0,57	9,3E-103	Significant in both cohorts	Yes
---	---	NA	0,62	3,3E-08	NA	NA	Not in Framingham data	NA
H1FO	H1 histone family, member 0	NM 005318	0,62	3,8E-08	0,27	4,1E-19	Significant in both cohorts	Yes
---	---	NA	0,62	4,1E-08	NA	NA	Not in Framingham data	NA
SARAF (TMEM66)	store-operated calcium entry-associated regulatory factor	NM 016127	-0,62	4,2E-08	-0,01	1,0E+00	Significant in Oslo only	Yes
---	---	ENST00000411152	0,62	4,5E-08	NA	NA	Not in Framingham data	NA
---	---	ENST00000411252	0,62	4,8E-08	NA	NA	Not in Framingham data	NA
KANK2	KN motif and ankyrin repeat domains 2	NM 001136191	0,61	5,3E-08	NA	NA	Not in Framingham data	No
CA1	carbonic anhydrase I	NM 001738	0,61	6,3E-08	NA	NA	Not in Framingham data	Yes
NPRL3	NPR3-like, GATOR1 complex subunit	NM 001077350	0,61	6,6E-08	0,45	2,0E-58	Significant in both cohorts	Yes
---	---	NA	0,61	7,2E-08	NA	NA	Not in Framingham data	NA
---	---	NA	0,61	7,3E-08	NA	NA	Not in Framingham data	NA
DNAJA4	DnaJ (Hsp40) homolog, subfamily A, member 4	NM 018602	0,61	7,6E-08	0,46	1,6E-60	Significant in both cohorts	Yes
MRC2	mannose receptor, C type 2	NM 006039	0,61	7,7E-08	0,3	1,1E-23	Significant in both cohorts	No
CRAT	carnitine O-acetyltransferase	NM 000755	0,61	8,1E-08	0,36	9,2E-36	Significant in both cohorts	Yes
MAP2K7	mitogen-activated protein kinase kinase 7	NM 145185	0,61	8,2E-08	0,28	1,6E-20	Significant in both cohorts	Yes
GNAS	GNAS complex locus	NM 000516	0,61	1,0E-07	NA	NA	Not in Framingham data	No
---	---	ENST00000410359	0,61	1,1E-07	NA	NA	Not in Framingham data	NA
ZBED3	zinc finger, BED-type containing 3	NM 032367	0,61	1,2E-07	0,06	1,0E+00	Significant in Oslo only	Yes
GID4 (C17orf39)	GID complex subunit 4 homolog	NM 024052	0,61	1,2E-07	0,41	4,2E-47	Significant in both cohorts	Yes
GSK3A	glycogen synthase kinase 3 alpha	NM 019884	0,61	1,3E-07	0,48	1,2E-67	Significant in both cohorts	Yes
ALDH5A1	aldehyde dehydrogenase 5 family, member A1	NM 170740	0,61	1,4E-07	0,35	8,2E-34	Significant in both cohorts	Yes
HGH1 (C8orf30A)	HGH1 homolog	NM 016458	0,61	1,4E-07	NA	NA	Not in Framingham data	No
SH3GL1	SH3-domain GRB2-like 1	NM 003025	0,6	1,4E-07	0,34	6,9E-31	Significant in both cohorts	No
CYB5R3	cytochrome b5 reductase 3	NM 000398	0,6	2,0E-07	NA	NA	Not in Framingham data	Yes
TM7SF2	transmembrane 7 superfamily member 2	NM 003273	0,6	2,1E-07	0,25	2,2E-16	Significant in both cohorts	No
CISD2	CDGSH iron sulfur domain 2	NM 001008388	0,6	2,3E-07	0,29	3,3E-22	Significant in both cohorts	Yes

¹P-values are Bonferroni corrected; NA: not applicable (did not reach detection level in the Framingham cohort); significant correlations are shaded

Table S3. Associations with NR3C1/GR

Gene Symbol	Gene Title	NM number	Oslo cohort		Framingham cohort		Comparison	Presence of GR promoter element
			Estimate	P-value ¹	Estimate	P-value ¹		
<i>ERBB2IP</i>	erbb2 interacting protein	NM_018695	0,92	7,7E-41	0,4	4,1E-46	Significant in both cohorts	Yes
<i>SBNO1</i>	strawberry notch homolog 1 (Drosophila)	NM_018183	0,92	2,9E-40	0,29	3,0E-22	Significant in both cohorts	No
<i>PIK3CA</i>	phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic	NM_006218	0,92	3,1E-40	0,41	6,1E-48	Significant in both cohorts	No
<i>MARCH7</i>	membrane associated ring finger 7	NM_022826	0,92	9,5E-40	0,52	1,9E-80	Significant in both cohorts	Yes
<i>PUM2</i>	pumilio RNA binding family member 2	NM_015317	0,92	1,1E-39	0,49	1,0E-70	Significant in both cohorts	No
<i>CUL3</i>	cullin 3	NM_003590	0,92	1,6E-38	0,46	3,4E-61	Significant in both cohorts	Yes
<i>FBXL3</i>	F-box and leucine-rich repeat protein 3	NM_012158	0,92	2,0E-38	0,23	4,6E-14	Significant in both cohorts	No
<i>HERC4</i>	HECT and RLD domain containing E3 ubiquitin protein ligase 4	NM_022079	0,91	4,5E-38	0,2	6,6E-10	Significant in both cohorts	Yes
<i>DOCK11</i>	dedicator of cytokinesis 11	NM_144658	0,91	5,0E-38	0,32	1,2E-27	Significant in both cohorts	No
<i>CSNK1A1</i>	casein kinase 1, alpha 1	NM_001025105	0,91	3,3E-37	0,4	9,3E-46	Significant in both cohorts	Yes
<i>PAN3</i>	PAN3 poly(A) specific ribonuclease subunit	NM_175854	0,91	3,5E-37	0,23	9,8E-14	Significant in both cohorts	Yes
<i>COPB2</i>	coatomer protein complex subunit beta 2 (beta prime)	NR_023350	0,91	3,9E-37	0,56	3,7E-97	Significant in both cohorts	No
<i>KIF5B</i>	kinesin family member 5B	NM_004521	0,91	9,1E-37	0,28	1,3E-21	Significant in both cohorts	No
<i>USP34</i>	ubiquitin specific peptidase 34	NM_014709	0,91	1,1E-36	0,43	1,3E-53	Significant in both cohorts	Yes
<i>YTHDF3</i>	YTH N(6)-methyladenosine RNA binding protein 3	NM_152758	0,91	1,7E-36	0,36	3,0E-35	Significant in both cohorts	Yes
<i>NIPBL</i>	Nipped-B homolog (Drosophila)	NM_015384	0,91	2,0E-36	0,44	2,1E-55	Significant in both cohorts	Yes
<i>ARIH1</i>	ariadne RBR E3 ubiquitin protein ligase 1	NM_005744	0,91	3,1E-36	0,22	4,4E-12	Significant in both cohorts	Yes
<i>ADAM10</i>	ADAM metallopeptidase domain 10	NM_001110	0,91	3,1E-36	0,34	2,2E-32	Significant in both cohorts	No
<i>MKLN1</i>	muskelin 1, intracellular mediator containing kelch motifs	NM_013255	0,91	3,3E-36	0,44	9,6E-56	Significant in both cohorts	Yes
<i>NEK7</i>	NIMA-related kinase 7	NM_133494	0,91	3,8E-36	0,42	1,9E-51	Significant in both cohorts	No
<i>CEP350</i>	centrosomal protein 350kDa	NM_014810	0,91	4,2E-36	0,47	1,8E-65	Significant in both cohorts	Yes
<i>NUFIP2</i>	nuclear fragile X mental retardation protein interacting	NM_020772	0,91	4,2E-36	0,39	2,8E-42	Significant in both cohorts	Yes
<i>UBR5</i>	ubiquitin protein ligase E3 component n-recognin 5	NM_015902	0,91	6,0E-36	0,3	2,8E-24	Significant in both cohorts	Yes
<i>PCF11</i>	PCF11 cleavage and polyadenylation factor subunit	NM_015885	0,91	8,1E-36	0,2	1,5E-09	Significant in both cohorts	No
<i>PPP3CA</i>	protein phosphatase 3, catalytic subunit, alpha isozyme	NM_000944	0,9	1,1E-35	0,51	1,4E-78	Significant in both cohorts	No
<i>ZFC3H1</i>	zinc finger, C3H1-type containing	NM_144982	0,9	1,4E-35	0,23	4,7E-13	Significant in both cohorts	No
<i>TRAPP8</i>	trafficking protein particle complex 8	NM_014939	0,9	1,6E-35	0,27	6,7E-20	Significant in both cohorts	Yes
<i>ARFGEF1</i>	ADP-ribosylation factor guanine nucleotide-exchange factor 1	NM_006421	0,9	1,6E-35	0,31	1,2E-25	Significant in both cohorts	No
<i>GDAP2</i>	ganglioside induced differentiation associated protein 2	NM_001135589	0,9	3,4E-35	NA	NA	Not in Framingham data	No
<i>TPR</i>	translocated promoter region, nuclear basket protein	NM_003292	0,9	3,5E-35	0,37	8,6E-39	Significant in both cohorts	No
<i>DDX3X</i>	DEAD (Asp-Glu-Ala-Asp) box helicase 3, X-linked	NM_001356	0,9	3,8E-35	0,22	1,9E-12	Significant in both cohorts	Yes
<i>MED13</i>	mediator complex subunit 13	NM_005121	0,9	4,0E-35	0,28	4,5E-21	Significant in both cohorts	No
<i>ATP7A</i>	ATPase, Cu++ transporting, alpha polypeptide	NM_000052	0,9	4,3E-35	0,13	2,4E-03	Significant in both cohorts	No
<i>CDC73</i>	cell division cycle 73	NM_024529	0,9	6,9E-35	0,43	2,1E-52	Significant in both cohorts	Yes
<i>PDS5B</i>	PDS5 cohesin associated factor B	NM_015032	0,9	8,8E-35	0,23	4,9E-14	Significant in both cohorts	No
<i>MAP3K2</i>	mitogen-activated protein kinase kinase kinase 2	NM_006609	0,9	9,6E-35	0,54	3,7E-91	Significant in both cohorts	No
<i>WAPL (WAPAL)</i>	WAPL cohesin release factor	NM_015045	0,9	9,8E-35	0,27	1,3E-18	Significant in both cohorts	No
<i>VPS8</i>	vacuolar protein sorting 8 homolog (S. cerevisiae)	NM_001009921	0,9	1,1E-34	0,34	2,1E-32	Significant in both cohorts	No
<i>ITCH</i>	itchy E3 ubiquitin protein ligase	NM_031483	0,9	1,1E-34	0,34	1,2E-32	Significant in both cohorts	No
<i>RBSN1L</i>	round spermatid basic protein 1-like	NM_198467	0,9	2,0E-34	0,38	1,0E-40	Significant in both cohorts	No
<i>BCLAF1</i>	BCL2-associated transcription factor 1	NM_014739	0,9	3,4E-34	0,34	5,2E-32	Significant in both cohorts	No
<i>GNAI3</i>	guanine nucleotide binding protein (G protein), alpha	NM_006496	0,9	3,7E-34	0,52	1,4E-80	Significant in both cohorts	No
<i>RBM39</i>	RNA binding motif protein 39	NM_184234	0,9	4,4E-34	0,26	4,0E-17	Significant in both cohorts	Yes
<i>KIDINS220</i>	kinase D-interacting substrate 220kDa	NM_020738	0,9	6,6E-34	NA	NA	Not in Framingham data	No
<i>PHIP</i>	pleckstrin homology domain interacting protein	NM_017934	0,9	6,8E-34	0,39	6,8E-43	Significant in both cohorts	No
<i>IVNS1ABP</i>	influenza virus NS1A binding protein	NM_006469	0,9	6,9E-34	0,38	7,3E-41	Significant in both cohorts	Yes
<i>TNKS2</i>	tankyrase, TRF1-interacting ankyrin-related ADP-ribose	NM_025235	0,9	7,7E-34	0,3	1,7E-24	Significant in both cohorts	No
<i>RAB18</i>	RAB18, member RAS oncogene family	NM_021252	0,9	8,0E-34	0,19	6,8E-09	Significant in both cohorts	No
<i>MON2</i>	MON2 homolog, regulator of endosome-to-Golgi trafficking	NM_015026	0,9	8,3E-34	0,23	5,2E-14	Significant in both cohorts	No
<i>SNX13</i>	sorting nexin 13	NM_015132	0,9	1,0E-33	0,37	9,3E-38	Significant in both cohorts	No
<i>PIK3C3</i>	phosphatidylinositol 3-kinase, catalytic subunit type 3	NM_002647	0,89	1,4E-33	0,3	5,1E-24	Significant in both cohorts	No
<i>KDM5A</i>	lysine (K)-specific demethylase 5A	NM_005056	0,89	1,6E-33	0,13	5,6E-04	Significant in both cohorts	Yes
<i>RAD21</i>	RAD21 cohesin complex component	NM_006265	0,89	1,7E-33	0,35	7,1E-33	Significant in both cohorts	Yes
<i>ZFX</i>	zinc finger protein, X-linked	NM_003410	0,89	2,5E-33	0,25	1,2E-15	Significant in both cohorts	Yes
<i>SYNJ1</i>	synaptojanin 1	NM_003895	0,89	2,7E-33	0,26	2,9E-17	Significant in both cohorts	Yes
<i>SETX</i>	senataxin	NM_015046	0,89	2,8E-33	0,35	2,1E-33	Significant in both cohorts	No
<i>BRWD3</i>	bromodomain and WD repeat domain containing 3	NM_153252	0,89	2,9E-33	0,33	1,8E-30	Significant in both cohorts	No
<i>MED23</i>	mediator complex subunit 23	NM_004830	0,89	3,4E-33	0,41	5,1E-49	Significant in both cohorts	Yes
<i>STAG1</i>	stromal antigen 1	NM_005862	0,89	3,8E-33	0,47	9,5E-64	Significant in both cohorts	No
<i>CRLF3</i>	cytokine receptor-like factor 3	NM_015986	0,89	3,9E-33	0,14	2,5E-04	Significant in both cohorts	No
<i>AMD1</i>	adenosylmethionine decarboxylase 1	NM_001634	0,89	4,8E-33	0,41	1,6E-47	Significant in both cohorts	No
<i>KDM6A</i>	lysine (K)-specific demethylase 6A	NM_021140	0,89	5,6E-33	0,15	2,9E-05	Significant in both cohorts	Yes
<i>RLF</i>	rearranged L-myc fusion	NM_012421	0,89	5,6E-33	0,49	9,9E-72	Significant in both cohorts	Yes
<i>RNF19A</i>	ring finger protein 19A, RBR E3 ubiquitin protein ligase	NM_183419	0,89	5,9E-33	0,25	1,2E-15	Significant in both cohorts	Yes
<i>PKN2</i>	protein kinase N2	NM_006256	0,89	6,8E-33	0,44	3,8E-56	Significant in both cohorts	Yes
<i>SF3B1</i>	splicing factor 3b, subunit 1, 155kDa	NM_012433	0,89	8,0E-33	0,52	2,9E-80	Significant in both cohorts	No
<i>PTPN12</i>	protein tyrosine phosphatase, non-receptor type 12	NM_002835	0,89	1,1E-32	0,44	5,3E-56	Significant in both cohorts	Yes
<i>RAB21</i>	RAB21, member RAS oncogene family	NM_014999	0,89	1,2E-32	0,21	5,8E-11	Significant in both cohorts	No
<i>CLK1</i>	CDC like kinase 1	NR_027856	0,89	1,5E-32	NA	NA	Not in Framingham data	No
<i>RPS6KA3</i>	ribosomal protein S6 kinase, 90kDa, polypeptide 3	NM_004586	0,89	1,6E-32	0,27	1,7E-19	Significant in both cohorts	No
<i>EXOC1</i>	exocyst complex component 1	NM_001024924	0,89	1,6E-32	0,42	2,5E-51	Significant in both cohorts	No
<i>XRCC5</i>	X-ray repair complementing defective repair in Chinese	NM_021141	0,89	2,1E-32	0,63	1,1E-132	Significant in both cohorts	No
<i>STXBP5</i>	syntaxin binding protein 5 (tomosyn)	NM_001127715	0,89	2,4E-32	0,44	2,9E-55	Significant in both cohorts	No
<i>SLC35F5</i>	solute carrier family 35, member F5	NM_025181	0,89	2,6E-32	0,25	1,0E-16	Significant in both cohorts	No
<i>PRKAA1</i>	protein kinase, AMP-activated, alpha 1 catalytic subunit	NM_206907	0,89	2,9E-32	0,48	1,1E-69	Significant in both cohorts	No
<i>ZMYM2</i>	zinc finger, MYM-type 2	NM_003453	0,89	3,0E-32	0,28	7,6E-21	Significant in both cohorts	Yes
<i>AHCTF1</i>	AT hook containing transcription factor 1	NM_015446	0,89	3,3E-32	-0,02	1,0E+00	Significant in Oslo only	No
<i>CLPX</i>	caseinolytic mitochondrial matrix peptidase chaperone	NM_006660	0,89	3,6E-32	0,22	8,4E-12	Significant in both cohorts	No
<i>USP9X</i>	ubiquitin specific peptidase 9, X-linked	NM_001039590	0,89	3,7E-32	0,27	4,2E-19	Significant in both cohorts	Yes
<i>FBXO38</i>	F-box protein 38	NM_205836	0,89	4,0E-32	NA	NA	Not in Framingham data	No
<i>PAPOLA</i>	poly(A) polymerase alpha	NM_032632	0,89	4,1E-32	0,21	5,0E-11	Significant in both cohorts	No
<i>USO1</i>	USO1 vesicle transport factor	NM_003715	0,89	4,8E-32	0,35	3,3E-34	Significant in both cohorts	No
<i>PTPRC</i>	protein tyrosine phosphatase, receptor type, C	NM_002838	0,89	5,0E-32	0,44	1,7E-55	Significant in both cohorts	No
<i>STAG2</i>	stromal antigen 2	NM_001042750	0,89	5,1E-32	0,3	7,0E-25	Significant in both cohorts	Yes
<i>AGTPBP1</i>	ATP/GTP binding protein 1	NM_015239	0,89	5,8E-32	0,24	2,0E-15	Significant in both cohorts	Yes
<i>CREB1</i>	cAMP responsive element binding protein 1	NM_004379	0,89	7,5E-32	0,48	1,5E-68	Significant in both cohorts	Yes
<i>POLR2B</i>	polymerase (RNA) II (DNA directed) polypeptide B, 140kDa	NM_000938	0,89	7,9E-32	0,51	6,5E-78	Significant in both cohorts	No
<i>VPS4B</i>	vacuolar protein sorting 4 homolog B (S. cerevisiae)	NM_004869	0,89	8,6E-32	0,35	2,5E-34	Significant in both cohorts	No
<i>PAFAH1B1</i>	platelet-activating factor acetylhydrolase 1b, regulatory	NM_000430	0,88	9,9E-32	NA	NA	Not in Framingham data	Yes
<i>CLTC</i>	clathrin, heavy chain (Hc)	NM_004859	0,88	1,0E-31	0,37	4,8E-39	Significant in both cohorts	Yes
<i>KBTBD2</i>	kelch repeat and BTB (POZ) domain containing 2	NM_015483	0,88	1,3E-31	0,41	6,2E-49	Significant in both cohorts	Yes
<i>TRIP12</i>	thyroid hormone receptor interactor 12	NM_004238	0,88	1,6E-31	0,45	2,6E-58	Significant in both cohorts	Yes
<i>COL4A3BP</i>	collagen, type IV, alpha 3 (Goodpasture antigen) binding	NM_005713	0,88	1,7E-31	0,62	1,6E-124	Significant in both cohorts	No
<i>TAOK3</i>	TAO kinase 3	NM_016281	0,88	1,8E-31	0,36	2,1E-36	Significant in both cohorts	No
<i>GSK3B</i>	glycogen synthase kinase 3 beta	NM_002093	0,88	2,0E-31	0,39	9,1E-43	Significant in both cohorts	No
<i>IRAK4</i>	interleukin 1 receptor associated kinase 4	NM_001114182	0,88	2,0E-31	0,32	5,7E-27	Significant in both cohorts	No
<i>SPAST</i>	spastin	NM_014946	0,88	2,2E-31	0,4	2,5E-46	Significant in both cohorts	No
<i>ABI1</i>	abl-interactor 1	NM_005470	0,88	2,9E-31	0,19	8,5E-09	Significant in both cohorts	No
<i>SHOC2</i>	SHOC2 leucine-rich repeat scaffold protein	NM_007373	0,88	3,4E-31	0,27	5,7E-19	Significant in both cohorts	No
<i>APPBP2</i>	amyloid beta precursor protein (cytoplasmic tail) binding	NM_006380	0,88	3,4E-31	0,23	7,7E-14	Significant in both cohorts	No

<i>PRPF38B</i>	pre-mRNA processing factor 38B	NM_018061	0,88	4,3E-31	0,37	3,5E-37	Significant in both cohorts	Yes
<i>HECTD1</i>	HECT domain containing E3 ubiquitin protein ligase 1	NM_015382	0,88	6,0E-31	0,26	3,9E-18	Significant in both cohorts	Yes
<i>TMOD3</i>	tropomodulin 3 (ubiquitous)	NM_014547	0,88	8,3E-31	0,25	3,5E-16	Significant in both cohorts	Yes
<i>STK4</i>	serine/threonine kinase 4	NM_006282	0,88	1,1E-30	0,35	1,1E-33	Significant in both cohorts	No
<i>NIN</i>	ninein (GSK3B interacting protein)	NM_020921	0,88	1,2E-30	0,39	9,8E-42	Significant in both cohorts	No
<i>TRIM33</i>	tripartite motif containing 33	NM_015906	0,88	1,3E-30	0,48	3,3E-69	Significant in both cohorts	No
<i>FXR1</i>	fragile X mental retardation, autosomal homolog 1	NM_001013439	0,88	1,4E-30	0,39	6,0E-43	Significant in both cohorts	No
<i>STX7</i>	syntaxin 7	NM_003569	0,88	1,6E-30	0,42	2,1E-50	Significant in both cohorts	No
<i>BROX (C1orf58)</i>	BRO1 domain and CAAX motif containing	NM_144695	0,88	1,6E-30	NA	NA	Not in Framingham data	No
<i>SLC39A9</i>	solute carrier family 39, member 9	NM_018375	0,88	1,7E-30	0,07	1,0E+00	Significant in Oslo only	No
<i>ATP13A3</i>	ATPase type 13A3	NM_024524	0,88	1,9E-30	0,33	1,6E-30	Significant in both cohorts	No
<i>MORC3</i>	MORC family CW-type zinc finger 3	NM_015358	0,88	1,9E-30	0,13	1,3E-03	Significant in both cohorts	Yes
<i>SEL1L</i>	sel-1 suppressor of lin-12-like (C. elegans)	NM_005065	0,88	2,0E-30	0,34	5,9E-31	Significant in both cohorts	No
<i>KIAA1429</i>	KIAA1429	NM_015496	0,88	2,1E-30	0,3	6,0E-25	Significant in both cohorts	Yes
<i>STRN</i>	striatin, calmodulin binding protein	NM_003162	0,88	2,4E-30	0,56	1,3E-98	Significant in both cohorts	Yes
<i>DNAJC13</i>	DnaJ (Hsp40) homolog, subfamily C, member 13	NM_015268	0,88	2,4E-30	0,44	2,4E-56	Significant in both cohorts	No
<i>BLZ1 (BZW1L1)</i>	basic leucine zipper and W2 domains 1	NR_026584	0,88	2,5E-30	NA	NA	Not in Framingham data	No
<i>CLK4</i>	CDC like kinase 4	NM_020666	0,88	2,5E-30	0,33	2,2E-29	Significant in both cohorts	No
<i>USP48</i>	ubiquitin specific peptidase 48	NM_032236	0,88	2,9E-30	0,48	8,3E-69	Significant in both cohorts	No
<i>AFTPH</i>	aftiphilin	NM_203437	0,88	3,1E-30	0,52	1,2E-83	Significant in both cohorts	No
<i>AQR</i>	aquarius intron-binding spliceosomal factor	NM_014691	0,88	3,4E-30	0,25	1,0E-15	Significant in both cohorts	No
<i>FAM91A1</i>	family with sequence similarity 91, member A1	NM_144963	0,88	3,5E-30	0,44	8,0E-55	Significant in both cohorts	No
<i>USP15</i>	ubiquitin specific peptidase 15	NM_006313	0,88	3,7E-30	0,21	3,2E-11	Significant in both cohorts	Yes
<i>AZIN1</i>	antizyme inhibitor 1	NM_015878	0,88	4,1E-30	0,09	2,4E-01	Significant in Oslo only	No
<i>CAB39</i>	calcium binding protein 39	NM_016289	0,88	4,3E-30	0,54	1,0E-89	Significant in both cohorts	No
<i>TOPBP1</i>	topoisomerase (DNA) II binding protein 1	NM_007027	0,87	5,6E-30	0,49	1,6E-70	Significant in both cohorts	No
<i>VPS41</i>	vacuolar protein sorting 41 homolog (S. cerevisiae)	NM_014396	0,87	5,8E-30	0,51	1,6E-79	Significant in both cohorts	No
<i>SIRT1</i>	sirtuin 1	NM_012238	0,87	6,1E-30	0,21	2,2E-11	Significant in both cohorts	No
<i>DCP2</i>	decapping mRNA 2	NM_152624	0,87	7,4E-30	0,48	4,1E-67	Significant in both cohorts	No
<i>PIK3CG</i>	phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic	NM_002649	0,87	7,5E-30	0,42	3,6E-49	Significant in both cohorts	No
<i>ANKRD44</i>	ankyrin repeat domain 44	NM_153697	0,87	7,6E-30	0,46	2,9E-61	Significant in both cohorts	No
<i>STXBP3</i>	syntaxin binding protein 3	NM_007269	0,87	9,2E-30	0,43	7,8E-52	Significant in both cohorts	Yes
<i>PPP1R12A</i>	protein phosphatase 1, regulatory subunit 12A	NM_001143885	0,87	9,7E-30	NA	NA	Not in Framingham data	No
<i>RSF1</i>	remodeling and spacing factor 1	NM_016578	0,87	1,0E-29	0,25	5,4E-16	Significant in both cohorts	Yes
<i>RICTOR</i>	RPTOR independent companion of MTOR, complex 2	NM_152756	0,87	1,1E-29	0,42	2,1E-50	Significant in both cohorts	Yes
<i>ATRX</i>	alpha thalassemia/mental retardation syndrome X-linked	NM_000489	0,87	1,2E-29	0,21	5,2E-11	Significant in both cohorts	No
<i>HOOK3</i>	hook microtubule-tethering protein 3	NM_032410	0,87	1,3E-29	0,42	3,8E-49	Significant in both cohorts	No
<i>RAP1A</i>	RAP1A, member of RAS oncogene family	NM_001010935	0,87	1,4E-29	0,41	8,2E-49	Significant in both cohorts	Yes
<i>NDUFS1</i>	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa	NM_005006	0,87	1,4E-29	0,39	2,8E-42	Significant in both cohorts	No
<i>TMEM30A</i>	transmembrane protein 30A	NM_018247	0,87	1,5E-29	0,4	4,8E-45	Significant in both cohorts	No
<i>ACAP2</i>	ArfGAP with coiled-coil, ankyrin repeat and PH domains 2	NM_012287	0,87	1,6E-29	0,6	4,9E-115	Significant in both cohorts	No
<i>AGO3 (EIF2C3)</i>	argonaute RISC catalytic component 3	NM_024852	0,87	1,7E-29	0,38	2,3E-39	Significant in both cohorts	No
<i>SOS2</i>	SOS Ras/Rho guanine nucleotide exchange factor 2	NM_006939	0,87	1,8E-29	0,29	2,0E-22	Significant in both cohorts	Yes
<i>KIAA0232</i>	KIAA0232	NM_014743	0,87	1,8E-29	0,11	1,3E-02	Significant in both cohorts	Yes
<i>KIAA1109</i>	KIAA1109	NM_015312	0,87	1,9E-29	0,37	1,1E-37	Significant in both cohorts	No
<i>LTN1</i>	listerin E3 ubiquitin protein ligase 1	NM_015565	0,87	2,0E-29	0,23	4,0E-13	Significant in both cohorts	No
<i>VPS35</i>	VPS35 retromer complex component	NM_018206	0,87	2,0E-29	0,33	1,8E-30	Significant in both cohorts	No
<i>FRYL</i>	FRY like transcription coactivator	NM_015030	0,87	2,1E-29	0,43	2,1E-53	Significant in both cohorts	No
<i>GGNBP2</i>	gametogenetin binding protein 2	NM_024835	0,87	2,2E-29	0,18	6,3E-08	Significant in both cohorts	Yes
<i>SMAD2</i>	SMAD family member 2	NM_005901	0,87	2,2E-29	0,19	4,9E-09	Significant in both cohorts	Yes
<i>CYB5R4</i>	cytochrome b5 reductase 4	NM_016230	0,87	2,3E-29	0,45	7,0E-59	Significant in both cohorts	No
<i>RARS2</i>	arginyl-tRNA synthetase 2, mitochondrial	NM_020320	0,87	2,4E-29	0,4	2,4E-44	Significant in both cohorts	No
<i>CSGALNACT2</i>	chondroitin sulfate N-acetylgalactosaminyltransferase 2	NM_018590	0,87	2,4E-29	0,2	1,6E-10	Significant in both cohorts	No
<i>CCNH</i>	cyclin H	NM_001239	0,87	2,6E-29	0,33	2,1E-30	Significant in both cohorts	Yes
<i>UBXN4</i>	UBX domain protein 4	NM_014607	0,87	2,8E-29	0,47	1,4E-65	Significant in both cohorts	No
<i>MGEA5</i>	meningioma expressed antigen 5 (hyaluronidase)	NM_012215	0,87	2,8E-29	0,24	1,5E-15	Significant in both cohorts	Yes
<i>GOLGB1</i>	golgin B1	NM_004487	0,87	3,0E-29	0,47	3,3E-66	Significant in both cohorts	No
<i>ZNF638</i>	zinc finger protein 638	NM_014497	0,87	3,4E-29	0,37	3,6E-37	Significant in both cohorts	No
<i>BRWD1</i>	bromodomain and WD repeat domain containing 1	NM_033656	0,87	3,7E-29	0,22	6,3E-12	Significant in both cohorts	Yes
<i>FAM214A</i>	family with sequence similarity 214, member A	NM_019600	0,87	3,9E-29	NA	NA	Not in Framingham data	No
<i>FAR1</i>	fatty acyl CoA reductase 1	NM_032228	0,87	4,1E-29	0,25	1,0E-15	Significant in both cohorts	No
<i>UPF2</i>	UPF2 regulator of nonsense transcripts homolog (yeast)	NM_080599	0,87	4,2E-29	0,3	1,7E-24	Significant in both cohorts	Yes
<i>MTM1</i>	myotubularin 1	NM_000252	0,87	4,2E-29	0,26	4,4E-17	Significant in both cohorts	No
<i>sep.07</i>	septin 7	NM_001788	0,87	4,6E-29	0,17	2,4E-07	Significant in both cohorts	Yes
<i>FNIP1</i>	folliculin interacting protein 1	NM_133372	0,87	4,7E-29	NA	NA	Not in Framingham data	No
<i>NAA50</i>	N(alpha)-acetyltransferase 50, NatE catalytic subunit	NM_025146	0,87	4,8E-29	0,39	1,2E-43	Significant in both cohorts	No
<i>UGP2</i>	UDP-glucose pyrophosphorylase 2	NM_001001521	0,87	5,4E-29	0,42	1,7E-50	Significant in both cohorts	Yes
<i>MIR632 (ZNF207)</i>	microRNA 632	NM_001098507	0,87	5,4E-29	0,09	5,0E-01	Significant in Oslo only	No
<i>ATP2C1</i>	ATPase, Ca++ transporting, type 2C, member 1	NM_014382	0,87	5,9E-29	0,34	4,2E-31	Significant in both cohorts	No
<i>UBXN7</i>	UBX domain protein 7	NM_015562	0,87	6,4E-29	0,33	1,8E-29	Significant in both cohorts	No
<i>SLMAP</i>	sarcolemma associated protein	NM_007159	0,87	6,5E-29	0,49	1,6E-70	Significant in both cohorts	Yes
<i>AKAP10</i>	A kinase (PRKA) anchor protein 10	NM_007202	0,87	6,5E-29	0,26	3,4E-17	Significant in both cohorts	Yes
<i>RB1</i>	retinoblastoma 1	NM_000321	0,87	6,6E-29	0,16	1,2E-05	Significant in both cohorts	No
<i>ARID4B</i>	AT rich interactive domain 4B (RBP1-like)	NM_016374	0,87	6,9E-29	0,41	1,5E-46	Significant in both cohorts	No
<i>VPS13B</i>	vacuolar protein sorting 13 homolog B (yeast)	NM_017890	0,87	7,2E-29	0,54	3,9E-89	Significant in both cohorts	Yes
<i>NEMF (SDCCAG1)</i>	nuclear export mediator factor	NM_004713	0,87	7,4E-29	0,17	5,5E-07	Significant in both cohorts	No
<i>PHF3</i>	PHD finger protein 3	NM_015153	0,87	7,8E-29	0,39	1,0E-41	Significant in both cohorts	No
<i>SPAG9</i>	sperm associated antigen 9	NM_001130528	0,87	8,4E-29	0,43	7,9E-52	Significant in both cohorts	Yes
<i>PAK2</i>	p21 protein (Cdc42/Rac)-activated kinase 2	NM_002577	0,87	8,6E-29	0,54	3,2E-89	Significant in both cohorts	No
<i>CHD2</i>	chromodomain helicase DNA binding protein 2	NM_001271	0,87	8,9E-29	0,26	3,6E-17	Significant in both cohorts	No
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<i>OSBPL11</i>	oxysterol binding protein-like 11	NM_022776	0,87	1,0E-28	0,57	2,3E-101	Significant in both cohorts	Yes
<i>HIPK3</i>	homeodomain interacting protein kinase 3	NM_005734	0,87	1,1E-28	0,38	2,8E-40	Significant in both cohorts	Yes
<i>ARID4A</i>	AT rich interactive domain 4A (RBP1-like)	NM_002892	0,87	1,2E-28	0,26	2,5E-18	Significant in both cohorts	No
<i>YME1L1</i>	YME1-like 1 ATPase	NM_139312	0,87	1,3E-28	0,27	7,1E-19	Significant in both cohorts	No
<i>ANKHD1</i>	ankyrin repeat and KH domain containing 1	NM_020690	0,87	1,4E-28	0,56	5,3E-100	Significant in both cohorts	Yes
<i>SENP5</i>	SUMO1/sentrin specific peptidase 5	NM_152699	0,87	1,5E-28	0,01	1,0E+00	Significant in Oslo only	Yes
<i>RAB27A</i>	RAB27A, member RAS oncogene family	NM_004580	0,87	1,5E-28	0,22	1,5E-12	Significant in both cohorts	No
<i>ZNF292</i>	zinc finger protein 292	NM_015021	0,87	1,5E-28	NA	NA	Not in Framingham data	Yes
<i>ITSN2</i>	intersectin 2	NM_006277	0,87	1,5E-28	0,47	1,8E-66	Significant in both cohorts	Yes
<i>RBM25</i>	RNA binding motif protein 25	NM_021239	0,87	1,6E-28	0,17	5,0E-07	Significant in both cohorts	No
<i>IREB2</i>	iron responsive element binding protein 2	NM_004136	0,87	1,7E-28	0,19	5,7E-09	Significant in both cohorts	Yes
<i>CTBS</i>	chitobiase, di-N-acetyl-	NM_004388	0,87	1,8E-28	0,41	1,3E-46	Significant in both cohorts	No
<i>ZFYVE16</i>	zinc finger, FYVE domain containing 16	NM_014733	0,87	1,8E-28	NA	NA	Not in Framingham data	No
<i>ARCN1</i>	archain 1	NM_001655	0,87	1,8E-28	0,19	2,1E-09	Significant in both cohorts	No
<i>UBR3</i>	ubiquitin protein ligase E3 component n-recognin 3 (putative)	NM_172070	0,87	1,9E-28	0,42	5,0E-51	Significant in both cohorts	No
<i>ANGEL2</i>	angel homolog 2 (Drosophila)	NM_144567	0,87	1,9E-28	0,2	2,9E-10	Significant in both cohorts	No
<i>PIK3CB</i>	phosphatidylinositol-4,5-bisphosphate 3-kinase, catalytic	NM_006219	0,87	2,1E-28	0,5	4,6E-74	Significant in both cohorts	No
<i>SCYL3</i>	SCY1-like, kinase-like 3	NM_181093	0,87	2,1E-28	0,28	1,8E-21	Significant in both cohorts	Yes
<i>USP7</i>	ubiquitin specific peptidase 7 (herpes virus-associated)	NM_003470	0,87	2,2E-28	0,17	2,1E-07	Significant in both cohorts	No

¹P-values are Bonferroni corrected; NA: not applicable (did not reach detection level in the Framingham cohort); significant correlations are shaded

Table S4. Verified associations for top 10 blood expressed miRNAs (verification in all cell lines and tissues)

Column	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC	AD	AE	AF	AG	AH	AI	AJ	AK	AL	AM	AN
	hsa-miR-223-3p (hsa-miR-223)				hsa-miR-484				hsa-miR-191-5p (hsa-miR-191)				hsa-miR-19b-3p (hsa-miR-19b)				hsa-miR-150-5p (hsa-miR-150)				hsa-miR-16-5p (hsa-miR-16)				hsa-miR-92a-3p (hsa-miR-92a)				hsa-miR-30c-5p (hsa-miR-30c)				hsa-miR-30b-5p (hsa-miR-30b)				hsa-miR-486-5p			
	TarBase v.8		Correlation browser scores		TarBase v.8		Correlation browser scores		TarBase v.8		Correlation browser scores		TarBase v.8		Correlation browser scores		TarBase v.8		Correlation browser scores		TarBase v.8		Correlation browser scores		TarBase v.8		Correlation browser scores		TarBase v.8		Correlation browser scores		TarBase v.8		Correlation browser scores		TarBase v.8		Correlation browser scores	
Gene	pred. score	r	p-value		Gene	pred. score	r	p-value	Gene	pred. score	r	p-value	Gene	pred. score	r	p-value	Gene	pred. score	r	p-value	Gene	pred. score	r	p-value	Gene	pred. score	r	p-value	Gene	pred. score	r	p-value	Gene	pred. score	r	p-value	Gene	pred. score	r	p-value
SCAR81	0.90	-0.22	2,58E-02		AVL9	1.00	0.24	1,40E-02	FUBP3	0.90	NA		PATL1	1.00	-0.04	7,14E-01	MTCH2	0.99	0.05	5,95E-01	PRDM4	1.00	0.00	9,99E-01	UBE2W	1.00	-0.10	3,22E-01	SNAI1	1.00	na		ERLIN1	1.00	0.15	1,34E-01	SRSF3	1.00	-0.23	1,91E-02
RASGRP1	0.90	-0.01	8,97E-01		PCDH19	1.00	NA		AMMECR1L	0.89	0.05	5,94E-01	SNIDA1	1.00	na		LDLR	0.98	0.06	5,37E-01	FBXW7	1.00	-0.06	5,70E-01	MIAX3	1.00	0.18	7,37E-02	ERUN1	1.00	0.15	1,31E-01	PFR2	1.00	na		BTAF1	0.99	-0.04	6,92E-01
DDIT4	0.82	0.04	6,56E-01		SLC20A2	1.00	-0.02	8,33E-01	TMOD2	0.88	-0.05	6,05E-01	RNF111	1.00	0.04	6,87E-01	PDE7A	0.98	0.25	1,14E-02	ASH1L	1.00	-0.21	3,22E-02	ERGIC2	1.00	-0.08	4,42E-01	PFN2	1.00	na		PDE7A	1.00	0.39	3,08E-05	TANC1	0.99	na	
GFPT1	0.74	0.14	1,47E-01		SNRNP200	0.99	0.25	1,03E-02	TPP1	0.84	na		ELOV15	1.00	0.09	3,42E-01	MDM4	0.93	-0.02	8,55E-01	TSPYL2	1.00	0.00	9,61E-01	FBXW7	1.00	-0.01	9,01E-01	PLAGL2	1.00	-0.04	7,13E-01	PLAGL2	1.00	-0.03	7,94E-01	PLAGL2	0.99	0.21	3,16E-02
RGS1	0.73	NA			DCBLD2	0.99	NA		ZBTB34	0.82	-0.10	2,97E-01	SMARCA2	1.00	0.09	7,32E-01	PERP	0.93	0.06	5,14E-01	PLAG1	1.00	na		FNIP2	1.00	0.19	5,17E-02	PDE7A	1.00	0.43	4,95E-06	PIP4K2A	1.00	-0.24	1,42E-02	PTEN	0.99	-0.27	5,04E-03
MECP2	0.70	-0.21	3,59E-02		SNN	0.99	0.09	3,76E-01	TLX3	0.82	0.05	6,14E-01	ATXN1	1.00	-0.01	9,01E-01	SMC3	0.89	-0.02	8,58E-01	FGF2	1.00	0.16	1,03E-01	CD69	1.00	-0.13	1,74E-01	SYNGR3	1.00	-0.21	3,54E-02	R3HDM1	1.00	0.18	6,18E-02	STGGALNAC6	0.99	0.19	5,80E-02
MT1E	0.68	-0.01	9,52E-01		ANAPC7	0.98	0.18	7,33E-02	DTD2	0.81	na		PCDH10	1.00	na		SAR1A	0.88	0.00	9,66E-01	PAPPA	1.00	na		KLHDC10	1.00	-0.05	6,30E-01	R3HDM1	1.00	0.28	3,52E-03	SYNGR3	1.00	-0.17	7,47E-02	CREBL2	0.96	-0.17	8,82E-02
TTBK2	0.67	-0.24	1,24E-02		KCNJ2	0.98	0.13	1,98E-01	CRKL	0.78	0.02	8,69E-01	SLCSA6	1.00	0.17	9,06E-02	SP1	0.88	-0.09	3,71E-01	ZBTB34	1.00	-0.04	7,03E-01	PTAR1	1.00	0.10	2,96E-01	TLE1	1.00	-0.12	2,36E-01	TLE1	1.00	-0.17	9,22E-02	ZNF367	0.93	0.11	2,58E-01
WDR7	0.65	0.30	2,09E-03		C10orf2	0.97	-0.06	5,35E-01	CDK6	0.77	0.16	9,73E-02	HBP1	1.00	0.38	7,13E-05	CHD2	0.85	-0.09	3,64E-01	USP25	1.00	-0.20	4,01E-02	MAN2A1	1.00	0.04	6,55E-01	TBC1D108	1.00	-0.13	1,96E-01	GLCC1	1.00	0.11	2,70E-01	RBM12	0.93	na	
FADS1	0.59	-0.01	9,20E-01		ACVR1B	0.96	0.06	5,52E-01	CEBPB	0.75	-0.03	7,42E-01	ZBTB10	1.00	0.07	5,10E-01	SP1	0.83	-0.13	1,86E-01	CTTNBP2	1.00	na		PPP1R37	1.00	na		GLCC1	1.00	0.20	4,60E-02	MTDH	1.00	0.23	1,90E-02	EMPI	0.91	na	
GD1I	0.57	-0.12	2,09E-01		IFNAR1	0.96	0.21	3,50E-02	WWP1	0.73	0.05	6,16E-01	SIN3B	1.00	-0.38	5,65E-05	VTI1A	0.80	-0.05	6,45E-01	CACUL1	1.00	na		DKK3	1.00	-0.05	5,93E-01	MTDH	1.00	0.27	5,99E-03	PPARGC1B	1.00	-0.31	1,16E-03	PYCR2	0.86	0.14	1,48E-01
CHUK	0.57	0.34	3,99E-04		FAM212B	0.96	NA		WIZ	0.73	0.01	9,17E-01	FBXO32	1.00	-0.07	4,91E-01	FAM46C	0.76	-0.03	7,85E-01	WIP1	1.00	0.06	5,59E-01	ARRDC3	1.00	-0.01	9,01E-01	SETD7	1.00	0.12	2,16E-01	GALNT1	1.00	0.39	3,06E-05	NR2F1	0.83	-0.06	5,65E-01
SOK5	0.56	NA			KMT2A	0.96	NA		EIF3B	0.72	0.04	6,65E-01	PRICKLE2	1.00	na		NBEAL1	0.75	0.05	5,89E-01	SLIT2	1.00	na		MAP2K4	1.00	-0.05	6,38E-01	PPARGC1B	1.00	-0.34	3,71E-04	DCUN1D3	1.00	0.07	4,81E-01	ITGB8	0.82	na	
SERINC1	0.55	0.35	2,45E-04		NOL9	0.95	0.28	4,40E-03	HLTF	0.71	0.12	2,27E-01	ADSS	1.00	0.24	1,57E-02	MESDC2	0.73	0.15	1,15E-01	SREK1	1.00	na		ITGA5	1.00	0.36	2,00E-04	CCNE2	1.00	na		CCNE2	1.00	na		TFAM	0.81	-0.29	2,98E-03
TMEM69	0.51	0.13	1,76E-01		HIPK1	0.95	0.27	5,82E-03	DCAF15	0.69	0.15	1,35E-01	ZBTB18	1.00	na		CDKN18	0.72	-0.11	2,53E-01	LSM11	1.00	na		KLF4	1.00	0.16	9,56E-02	GALNT7	1.00	0.36	1,88E-04	BRWD3	1.00	0.36	1,94E-04	G3BP2	0.81	-0.10	3,28E-01
CPEB4	0.49	0.20	4,62E-02		HOXA5	0.95	NA		PWWP2A	0.68	-0.12	2,24E-01	RAPGEF2	1.00	0.14	1,58E-01	ATP9A	0.71	-0.12	2,07E-01	CDC37L1	1.00	0.14	1,69E-01	TEF	1.00	-0.05	5,96E-01	MEX3B	1.00	-0.25	8,78E-03	MEX3B	1.00	-0.22	2,31E-02	GXYLT1	0.80	-0.22	2,62E-02
RNF213	0.49	-0.10	2,96E-01		SCARB1	0.90	-0.18	6,62E-02	B4GALT6	0.66	na		PNRC1	1.00	0.21	3,07E-02	LSM8	0.70	na		GOLGA1	1.00	0.00	9,90E-01	GRAMD1B	1.00	0.12	2,31E-01	DCUN1D3	1.00	0.01	8,81E-01	KLHL20	1.00	0.24	1,35E-02	RBM12B	0.78	-0.21	3,44E-02
COX7A2L	0.45	-0.01	9,17E-01		TCHP	0.90	-0.06	5,71E-01	EGRI	0.66	-0.02	8,53E-01	MYLIP	1.00	0.17	8,09E-02	ALDH6A1	0.69	0.20	4,39E-02	WNT3A	1.00	0.11	2,57E-01	FMN2	1.00	na		PIP4K2A	1.00	-0.20	4,18E-02	DES2	1.00	na		G3BP1	0.78	-0.01	0,92
					RASGRP1	0.90	0.23	2,00E-02	SIN3B	0.64	0.15	1,23E-01	RORA	1.00	-0.01	9,05E-01	ZNF395	0.67	0.25	1,17E-02	SLC20A2	1.00	-0.16	1,01E-01	LHFPL2	1.00	0.03	7,35E-01	BRWD3	1.00	0.33	6,79E-04	ZNRF1	1.00	-0.21	2,90E-02	C7orf13	0.77	-0.06	5,30E-01
					RTN3	0.90	0.02	8,42E-01	BLOC155-TXNDC5	0.64	na		TUB	1.00	na		ZNF625	0.66	0.10	3,20E-01	CD2AP	1.00	-0.03	7,69E-01	JMY	1.00	0.16	1,10E-01	LCLAT1	1.00	0.28	3,61E-03	MAML1	1.00	-0.35	2,15E-04	PITPNA	0.75	-0.08	4,39E-01

The ten toppmost expressed peripheral blood miRNAs was identified based on PCR ct-values. Then regulation of/by other genes was identified from TarBase 8.0 using DIANA Tools as described below, thereby identifying experimentally verified interactions (considering all cell lines and tissues) as prediction score (column k, p, u.....).

The 20 miRNAs/gene pairs with topmost TarBase prediction scores (column B, F, J.....) were then compared as indicated with Pearson correlation r and p values (columns C+D, G+H, K+L,.....) from the peripheral blood correlation browser.

Assesment of gene regulation using TarBase

TarBase v.8 prediction score was assessed using the function TarBase v.8 in DIANA tools (http://carolina.imis.athena-innovation.gr/diana_tools/web/index.php?r=tarbasev8%2Findex)

with the following setting:

Species: Homo sapiens

(All other settings remained un-ticked)

Table S5. Topmost verified peripheral blood mRNA/miRNA interactions versus associations in the Oslo cohort

Output from TarBase v.8							Corresponding output from the Correlation browser	
Gene name	miRNA	Experiments throughput	Publications	Cell lines	Tissues	Pred. Score	r	p-value
ITCH	hsa-miR-146a-5p	low: 0 high: 1	1	1	1	0,94	-0,31	1,54E-03
PTAR1	hsa-miR-146a-5p	low: 0 high: 2	1	1	1	0,89	-0,22	2,54E-02
RBL1	hsa-miR-146a-5p	low: 0 high: 1	1	1	1	0,85	-0,17	8,00E-02
BACH1	hsa-miR-20a-3p	low: 1 high: 0	1	1	1	0,83	0,09	3,59E-01
BACH1	hsa-miR-17-3p	low: 1 high: 0	1	1	1	0,80	0,08	4,39E-01
PELI1	hsa-miR-106b-5p	low: 1 high: 0	1	1	1	0,79	0,15	1,38E-01
PELI1	hsa-miR-20a-5p	low: 1 high: 0	1	1	1	0,78	0,07	4,93E-01
SRSF1	hsa-miR-146a-5p	low: 0 high: 1	1	1	1	0,76	-0,26	7,53E-03
CLIC4	hsa-miR-25-3p	low: 1 high: 0	1	1	1	0,73	-0,04	6,72E-01
LY75	hsa-miR-146a-5p	low: 1 high: 0	1	1	1	0,72	-0,17	7,50E-02
TNIK	hsa-miR-146a-5p	low: 0 high: 1	1	1	1	0,72	-0,02	8,11E-01
SESTD1	hsa-miR-146a-5p	low: 0 high: 1	1	1	1	0,72	-0,24	1,23E-02
DAZAP2	hsa-miR-17-5p	low: 1 high: 0	1	1	1	0,70	-0,05	6,04E-01
DAZAP2	hsa-miR-93-5p	low: 1 high: 0	1	1	1	0,69	0,05	6,27E-01
LY75	hsa-miR-20a-5p	low: 1 high: 0	1	1	1	0,67	-0,07	4,63E-01
LY75	hsa-miR-106b-5p	low: 1 high: 0	1	1	1	0,67	0,09	3,73E-01
BACH1	hsa-miR-25-3p	low: 1 high: 0	1	1	1	0,66	0,08	3,94E-01
WDR36	hsa-miR-146a-5p	low: 0 high: 1	1	1	1	0,65	-0,22	2,41E-02
BACH1	hsa-miR-146a-5p	low: 1 high: 0	1	1	1	0,64	-0,36	1,59E-04
SPEN	hsa-miR-146a-5p	low: 0 high: 1	1	1	1	0,63	-0,30	1,92E-03
PELI1	hsa-miR-25-3p	low: 1 high: 0	1	1	1	0,62	0,13	1,97E-01
GIMAP4	hsa-miR-146a-5p	low: 0 high: 1	1	1	1	0,62	-0,25	1,05E-02
PDS5A	hsa-miR-146a-5p	low: 0 high: 1	1	1	1	0,60	-0,22	2,30E-02
MED13	hsa-miR-146a-5p	low: 0 high: 1	1	1	1	0,60	-0,26	6,72E-03
SUPT16H	hsa-miR-146a-5p	low: 0 high: 1	1	1	1	0,60	-0,27	4,79E-03
DAZAP2	hsa-miR-20a-5p	low: 1 high: 0	1	1	1	0,59	0,00	9,68E-01
KBTBD6	hsa-miR-146a-5p	low: 0 high: 1	1	1	1	0,59	0,14	1,55E-01
DAZAP2	hsa-miR-106b-5p	low: 1 high: 0	1	1	1	0,59	0,04	7,09E-01
LNPEP	hsa-miR-146a-5p	low: 0 high: 1	1	1	1	0,59	-0,24	1,50E-02
HOXB8	hsa-miR-146a-5p	low: 0 high: 1	1	1	1	0,59	0,22	2,59E-02

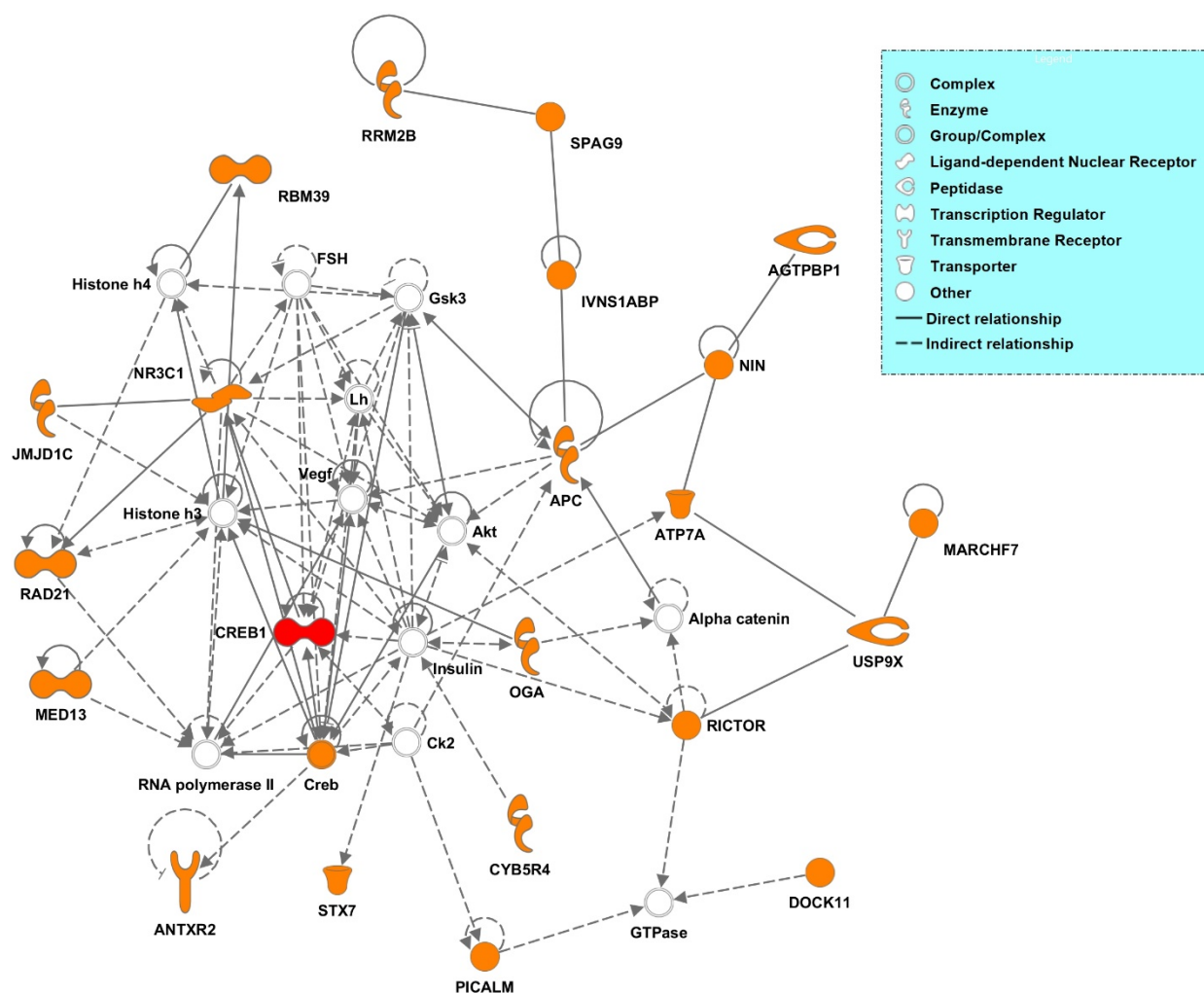
The topmost peripheral blood experimentally verified miRNA/mRNA interactions with highest predictive score were identified using the function TarBase v.8 in DIANA tools (leftmost panel). The corresponding miRNAs/gene pairs with Pearson r and p values, calculated in the correlation browser, are shown in the rightmost panel. Nominally significant associations ($p < 0.05$) are shaded.

Table S6. Results from Ingenuity Pathway Analysis within the category “Physiological System Development and Function” for the transcripts associated with transcription factors CREB1, GATA1 and GR

Name	p-value range	# Molecules
CREB1		
Embryonic Development	4.30E-03 - 9.11E-06	18
Hematological System Development and Function	4.47E-03 - 9.11E-06	17
Hematopoiesis	4.30E-03 - 9.11E-06	13
Lymphoid Tissue Structure and Development	4.30E-03 - 9.11E-06	17
Organ Development	4.30E-03 - 9.11E-06	17
GATA1		
Hematological System Development and Function	3.30E-02 - 1.18E-09	15
Hematopoiesis	3.30E-02 - 1.18E-09	10
Tissue Morphology	3.42E-02 - 1.18E-09	20
Connective Tissue Development and Function	3.52E-02 - 1.22E-04	16
Organismal Development	3.52E-02 - 1.22E-04	22
GR		
Organismal Survival	2.24E-03 - 1.29E-06	23
Embryonic Development	4.47E-03 - 3.31E-05	12
Organismal Development	4.47E-03 - 3.31E-05	18
Tissue Morphology	4.47E-03 - 3.31E-05	13
Nervous System Development and Function	4.47E-03 - 1.36E-04	5

The indicated transcription factors and respective 50 topmost associated genes (Table 1, 2 or 3) were subjected to «core analysis» including direct and indirect relationships and default settings/filters.

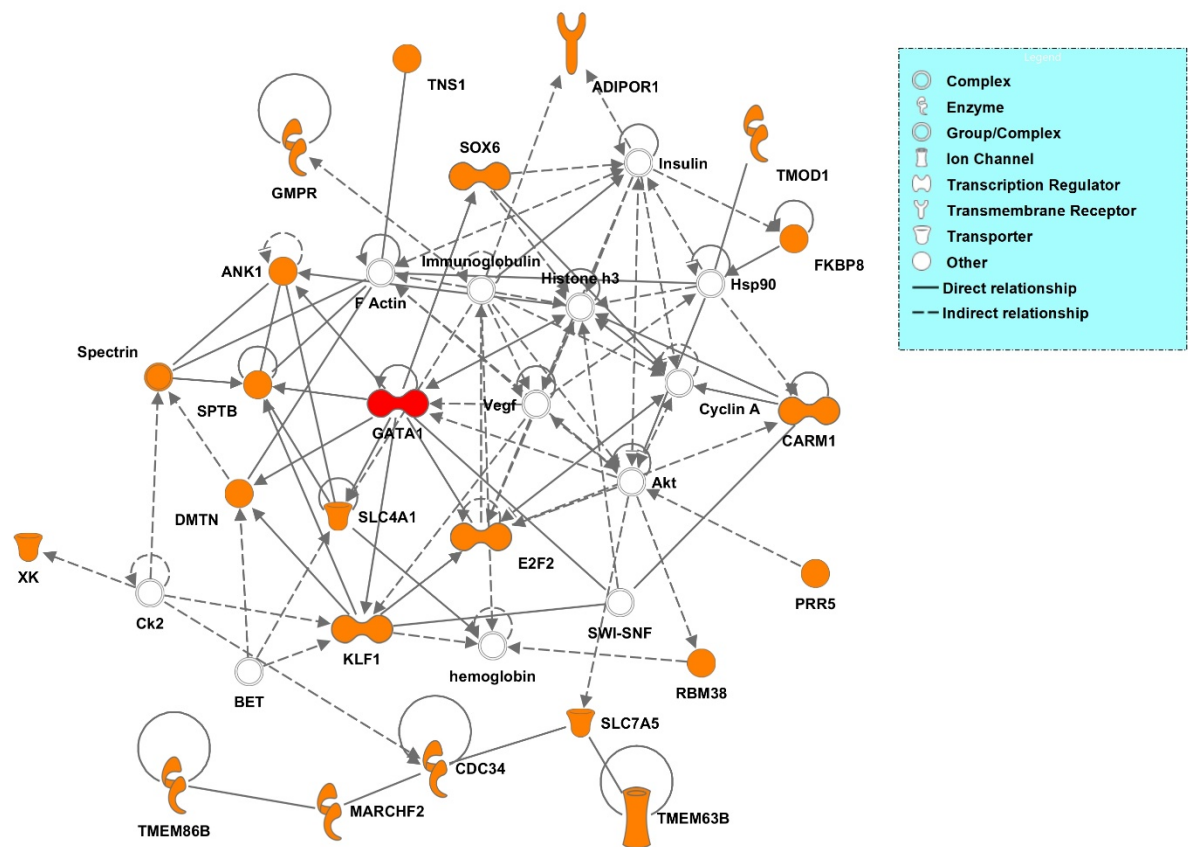
CREB1



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Figure S1. Top network calculated by IPA when CREB1 and its 50 topmost associated genes were subjected to «core analysis» including direct and indirect relationships and default settings/filters. Orange symbols indicate genes among the 50 topmost CREB1 associated.

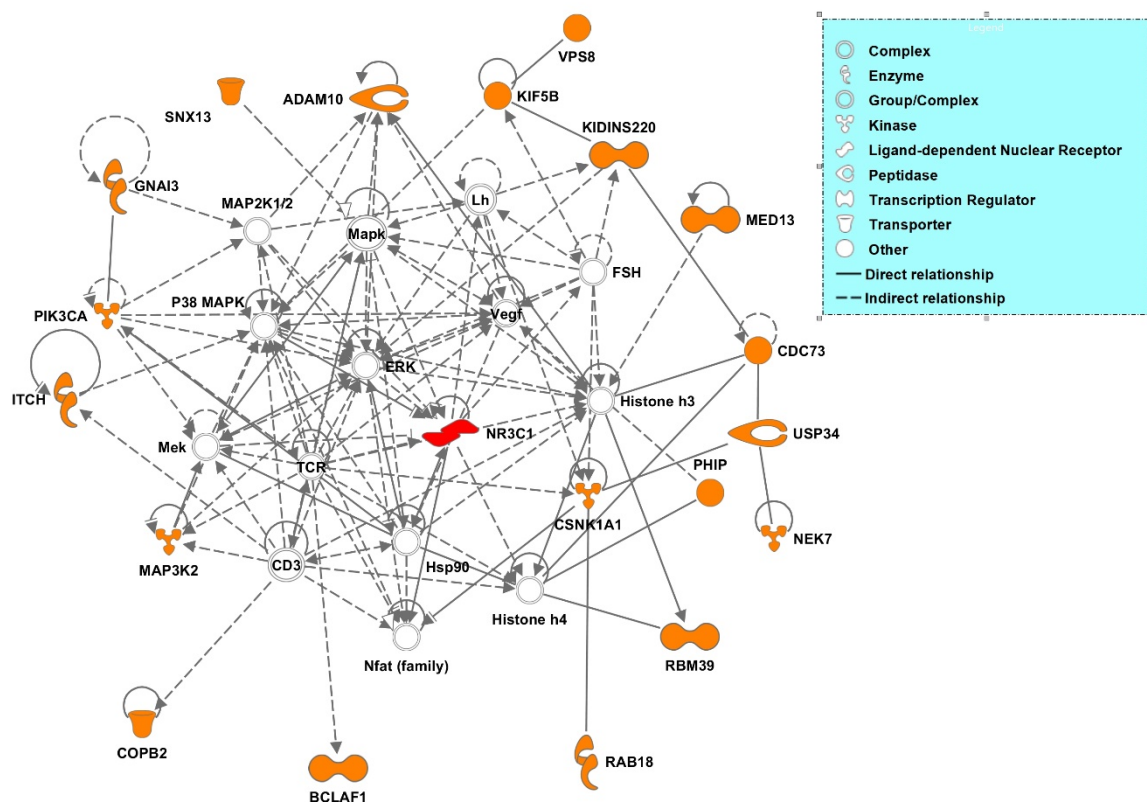
GATA1



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Figure S2. Top network calculated by IPA when GATA1 and its 50 topmost associated genes were subjected to «core analysis» including direct and indirect relationships and default settings/filters. Orange symbols indicate genes among the 50 topmost GATA1 associated.

NR3C1



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Figure S3. Top network calculated by IPA when GR (NR3C1) and its 50 topmost associated genes were subjected to «core analysis» including direct and indirect relationships and default settings/filters. Orange symbols indicate genes among the 50 topmost GR associated.