

Blood Gene Expression Signatures Associated with Heart Failure Outcomes- data supplement

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Table 1 Genes Associated with Survival Time in Heart Failure Patients.

Gene Title	Gene Symbol	Entrez Gene	Survival Analysis			Ctrl vs NYHA I-II		Ctrl vs NYHA III-IV		Pathways
			p, longrank test	q-value	hr (95% CI)	p	fold change	p	fold change	
5'-nucleotidase, ecto	NT5E	4907	9.45E-05	4.39E-02	0.1 (0.1, 0.4)	3.1E-02	0.77	3.3E-04	0.62	
acidic repeat containing	ACRC	93953	6.25E-05	3.94E-02	7.9 (2.7, 22.8)	7.6E-02	0.89	3.5E-01	1.13	
acyl-CoA synthetase family member 3	ACSF3	197322	2.43E-03	1.98E-01	6.4 (1.7, 25.0)	8.2E-01	1.00	5.3E-02	1.09	
adaptor-related protein complex 3, beta 1 subunit	AP3B1	8546	1.34E-04	5.37E-02	18.4 (4.0, 85.0)	1.9E-01	1.05	5.3E-03	1.15	
adenylate kinase 5	AK5	26289	1.42E-03	1.50E-01	0.1 (0.0, 0.4)	2.6E-01	1.06	4.8E-01	0.97	
alanine-glyoxylate aminotransferase 2-like 2	AGXT2L2	85007	1.52E-03	1.56E-01	302.8 (10.4, 8,840.5)	7.5E-01	1.00	5.8E-02	1.08	
amyloid beta precursor protein-binding, family A, member 2	APBA2	321	9.95E-04	1.32E-01	0.1 (0.0, 0.5)	3.3E-02	0.88	6.7E-04	0.80	
ankylosis, progressive homolog	ANKH	56172	4.88E-04	9.94E-02	0.3 (0.1, 0.6)	4.8E-01	0.95	3.2E-04	0.70	
ankyrin 1, erythrocytic	ANK1	286	1.31E-04	5.37E-02	3.9 (1.6, 9.2)	2.7E-01	0.98	3.0E-01	1.10	
ankyrin 3, node of Ranvier	ANK3	288	5.28E-04	1.04E-01	0.4 (0.3, 0.7)	6.8E-01	0.91	7.5E-03	0.59	
AP2 associated kinase 1	AAK1	22848	7.52E-04	1.21E-01	0.3 (0.1, 0.6)	4.2E-01	0.95	7.4E-05	0.76	
aquaporin 3	AQP3	360	1.86E-05	2.26E-02	0.4 (0.2, 0.6)	9.2E-01	1.01	2.8E-02	0.68	
ATPase, class V, type 10A	ATP10A	57194	1.75E-03	1.69E-01	0.2 (0.1, 0.6)	8.1E-01	1.00	1.8E-02	0.87	

B-cell CLL/lymphoma 11B	BCL11B	64919	1.97E-03	1.81E-01	0.4 (0.3, 0.8)	6.3E-01	0.89	3.3E-03	0.59	
Bcl2 modifying factor	BMF	90427	4.27E-04	9.19E-02	2.7 (1.5, 4.9)	1.5E-01	1.10	2.4E-02	1.33	
BRCA2 and CDKN1A interacting protein	BCCIP	56647	1.49E-03	1.55E-01	11.7 (2.5, 55.8)	6.0E-02	1.09	2.8E-02	1.13	
Bruton agammaglobulinemia tyrosine kinase	BTK	695	1.40E-04	5.45E-02	14.5 (3.7, 57.3)	8.3E-02	1.11	1.1E-03	1.29	1, 2, 3, 7
BTB domain containing 11	BTBD11	121551	4.37E-05	3.40E-02	0.4 (0.3, 0.6)	3.6E-01	0.83	9.3E-03	0.61	
calmodulin 1	CALM1	801	2.42E-03	1.98E-01	0.1 (0.0, 0.4)	2.3E-02	0.88	1.1E-03	0.83	1, 7, 9, 11
cannabinoid receptor 2	CNR2	1269	2.17E-04	6.61E-02	4.2 (1.9, 9.2)	2.0E-01	1.09	2.8E-01	1.19	
carbonyl reductase 3	CBR3	874	2.29E-04	6.73E-02	0.1 (0.0, 0.3)	3.4E-01	1.09	1.5E-01	0.93	
casein kinase 1, epsilon	CSNK1E	1454	1.19E-03	1.40E-01	6.6 (2.0, 21.4)	8.0E-01	1.02	2.9E-01	1.10	
cathepsin K	CTSK	1513	2.86E-04	7.75E-02	29.5 (4.7, 185.3)	5.9E-01	1.05	3.6E-02	1.18	
CD200 receptor 1	CD200R1	131450	6.17E-04	1.09E-01	0.1 (0.0, 0.3)	6.4E-02	1.13	1.7E-01	0.94	
CD22 molecule	CD22	933	2.25E-03	1.93E-01	21.6 (2.3, 207.3)	3.5E-01	0.96	8.8E-01	0.99	7
CD28 molecule	CD28	940	8.63E-05	4.23E-02	0.5 (0.3, 0.7)	8.5E-01	1.01	1.5E-02	0.58	1
CD3d molecule, delta	CD3D	915	1.66E-03	1.63E-01	0.3 (0.2, 0.7)	5.9E-01	0.95	7.1E-03	0.75	1, 8
CD3e molecule, epsilon	CD3E	916	7.88E-04	1.23E-01	0.3 (0.2, 0.6)	7.9E-01	0.96	1.5E-03	0.68	1, 8
CD3g molecule, gamma	CD3G	917	2.00E-03	1.81E-01	0.4 (0.2, 0.7)	4.8E-01	0.90	3.4E-03	0.68	1, 8
CD7 molecule	CD7	924	9.90E-04	1.32E-01	0.3 (0.2, 0.7)	9.0E-02	0.82	1.3E-03	0.67	
CDC14 cell division cycle 14 homolog A	CDC14A	8556	1.30E-03	1.45E-01	0.2 (0.1, 0.5)	4.2E-01	1.08	1.5E-03	0.77	
cerebellar degeneration-related protein 2, 62kDa	CDR2	1039	2.32E-03	1.94E-01	0.2 (0.1, 0.6)	8.7E-01	1.03	4.3E-03	0.78	
choline kinase alpha	CHKA	1119	9.74E-04	1.32E-01	19.8 (3.4, 115.1)	3.5E-01	1.05	8.2E-02	1.12	
chromosome 1 open reading frame 113	C1orf113	79729	9.52E-04	1.32E-01	5.5 (1.8, 16.7)	7.8E-02	1.07	4.5E-02	1.10	
chromosome 10 open reading frame 58	C10orf58	84293	1.55E-03	1.56E-01	0.2 (0.1, 0.6)	5.7E-01	1.03	3.5E-02	0.87	
chromosome 14 open reading frame 64	C14orf64	388011	5.90E-04	1.07E-01	0.3 (0.1, 0.6)	7.6E-01	0.94	4.1E-04	0.59	
chromosome 17 open reading frame 56	C17orf56	146705	1.40E-03	1.49E-01	47.8 (4.3, 528.3)	3.6E-01	0.94	6.8E-01	1.02	
Chromosome 18 open reading frame 50	C18orf50	619463	1.81E-03	1.73E-01	0.4 (0.2, 0.7)	7.8E-01	0.93	3.2E-02	0.71	
chromosome 20 open reading frame 72	C20orf72	92667	5.77E-05	3.82E-02	24.7 (5.8, 105.8)	9.4E-01	1.02	1.8E-01	1.11	
Chromosome 3 open reading frame 37	C3orf37	56941	2.25E-04	6.70E-02	0.1 (0.0, 0.3)	1.4E-01	0.90	1.0E-03	0.77	
chromosome 4 open reading frame 34	C4orf34	201895	1.72E-05	2.26E-02	4.3 (2.0, 9.4)	1.3E-01	0.95	2.3E-01	1.20	
chromosome 9 open reading frame 52	C9orf52	158219	1.98E-03	1.81E-01	0.1 (0.0, 0.5)	3.7E-01	0.92	2.7E-02	0.83	
coiled-coil domain containing 104	CCDC104	112942	8.43E-04	1.26E-01	0.3 (0.2, 0.6)	9.2E-01	0.99	3.9E-03	0.71	
coiled-coil domain containing 65	CCDC65	85478	2.13E-03	1.86E-01	0.2 (0.1, 0.5)	3.7E-01	1.08	3.7E-02	0.87	

coiled-coil domain containing 88A	CCDC88A	55704	9.84E-05	4.49E-02	4.3 (2.1, 8.8)	3.4E-02	1.24	6.0E-04	1.65	
cold shock domain protein A	CSDA	8531	5.63E-04	1.04E-01	2.6 (1.5, 4.4)	7.7E-01	0.98	1.1E-02	1.60	
core-binding factor, runt domain, alpha subunit 2; translocated to, 3	CBFA2T3	863	4.47E-04	9.46E-02	12.0 (2.8, 51.3)	5.7E-01	1.04	3.5E-02	1.20	
cryptochrome 1	CRY1	1407	3.43E-04	8.25E-02	0.4 (0.2, 0.7)	1.7E-01	0.92	7.5E-05	0.72	
cyclin-dependent kinase 2	CDK2	1017	1.55E-04	5.64E-02	0.0 (0.0, 0.1)	3.1E-01	0.95	1.7E-01	0.94	6
cyclin-dependent kinase inhibitor 2A	CDKN2A	1029	1.55E-04	5.64E-02	8.8 (2.5, 30.6)	1.4E-01	1.04	2.0E-02	1.12	6
cyclin-dependent kinase-like 3	CDKL3	51265	9.96E-04	1.32E-01	7.9 (2.2, 28.8)	5.9E-01	1.03	7.9E-01	1.05	
cytochrome P450, family 2, subfamily B, polypeptide 7 pseudogene 1	CYP2B7P1	1556	9.71E-04	1.32E-01	0.0 (0.0, 0.2)	7.1E-01	1.01	8.1E-01	1.00	
DCN1, defective in cullin neddylation 1, domain containing 4	DCUN1D4	23142	2.06E-03	1.84E-01	0.1 (0.0, 0.4)	4.7E-01	0.96	9.7E-02	0.90	
dedicator of cytokinesis 9	DOCK9	23348	1.63E-03	1.61E-01	0.3 (0.1, 0.7)	3.7E-01	0.93	8.7E-05	0.64	
dehydrogenase E1 and transketolase domain containing 1	DHTKD1	55526	2.29E-03	1.94E-01	36.6 (3.4, 396.4)	6.9E-01	0.98	9.7E-01	1.01	
dehydrogenase/reductase member 3	DHRS3	9249	2.70E-04	7.52E-02	0.2 (0.1, 0.5)	4.7E-01	0.94	9.0E-03	0.79	
DIP2 disco-interacting protein 2 homolog C	DIP2C	22982	6.94E-05	4.00E-02	9.3 (2.2, 38.5)	9.1E-01	1.00	4.1E-01	1.06	
dipeptidyl-peptidase 4	DPP4	1803	2.57E-05	2.52E-02	0.3 (0.2, 0.5)	7.0E-01	1.06	2.7E-03	0.78	
dynamin binding protein	DNMBP	23268	3.36E-06	8.09E-03	3.3 (1.9, 5.7)	9.3E-01	1.01	1.0E-01	1.32	
EGFR-coamplified and overexpressed protein	ECOP	81552	2.88E-04	7.75E-02	3.5 (1.7, 7.1)	9.4E-01	1.00	5.4E-02	1.25	
EPH receptor A1	EPHA1	2041	4.69E-05	3.53E-02	0.1 (0.0, 0.3)	3.9E-01	1.03	3.2E-02	0.94	
Epstein-Barr virus induced gene 2	EBI2	1880	1.35E-03	1.46E-01	0.3 (0.2, 0.7)	8.4E-01	1.00	4.2E-03	0.66	
family with sequence similarity 134, member B	FAM134B	54463	1.88E-05	2.26E-02	0.2 (0.1, 0.4)	2.1E-01	0.93	1.0E-04	0.73	
family with sequence similarity 65, member A	FAM65A	79567	1.22E-03	1.41E-01	41.1 (4.5, 378.5)	2.3E-01	1.06	1.4E-03	1.18	
family with sequence similarity 84, member B	FAM84B	157638	3.36E-04	8.25E-02	0.4 (0.2, 0.7)	3.0E-02	0.82	5.9E-07	0.56	
FGFR1 oncogene partner 2	FGFR1OP2	26127	2.33E-03	1.94E-01	0.0 (0.0, 0.2)	9.0E-01	1.00	2.1E-02	0.92	
fragile histidine triad gene	FHIT	2272	1.63E-03	1.61E-01	0.6 (0.4, 0.8)	6.6E-01	0.91	2.3E-02	0.61	
G protein-coupled receptor kinase interactor 2	GIT2	9815	1.15E-03	1.37E-01	52.3 (4.4, 619.7)	2.9E-01	0.94	9.3E-02	1.09	
galactose-3-O-sulfotransferase 4	GAL3ST4	79690	1.08E-03	1.36E-01	0.0 (0.0, 0.3)	7.7E-01	1.02	3.4E-02	0.91	
gametocyte specific factor 1	GTSF1	121355	8.07E-05	4.19E-02	4.8 (2.1, 11.1)	3.1E-01	1.07	8.5E-02	1.26	
gametocyte specific factor 1-like	GTSF1L	149699	5.04E-04	1.00E-01	4.7 (1.9, 11.3)	9.2E-01	0.98	4.0E-01	1.15	
GATA binding protein 3	GATA3	2625	1.32E-03	1.45E-01	0.4 (0.2, 0.7)	4.6E-01	0.93	5.1E-05	0.55	
glycosyltransferase 25 domain containing 1	GLT25D1	79709	5.68E-04	1.04E-01	25.9 (4.2, 160.0)	3.9E-01	1.04	1.3E-04	1.17	

GrpE-like 2, mitochondrial	GRPEL2	134266	2.34E-03	1.94E-01	0.2 (0.0, 0.5)	9.5E-01	1.01	4.9E-01	0.95	
HEAT repeat containing 6	HEATR6	63897	4.40E-04	9.40E-02	6.8 (2.0, 22.5)	5.4E-01	0.98	2.2E-01	1.09	
Heat shock 70kDa protein 4	HSPA4	3308	4.64E-04	9.67E-02	2.9 (1.5, 5.7)	9.1E-01	1.00	7.1E-02	1.29	8
heat shock transcription factor 2	HSF2	3298	3.64E-04	8.66E-02	0.2 (0.1, 0.4)	1.0E-01	0.88	2.8E-04	0.72	
HERPUD family member 2	HERPUD2	64224	2.07E-03	1.84E-01	0.0 (0.0, 0.2)	2.4E-01	0.95	4.1E-03	0.87	
hypothetical gene supported by AY007155	LOC439949	439949	1.48E-04	5.60E-02	0.4 (0.3, 0.7)	8.7E-01	1.00	6.1E-03	0.67	
hypothetical protein FLJ25791	FLJ25791	222521	7.39E-04	1.20E-01	7.2 (2.1, 24.2)	9.1E-01	1.01	2.0E-01	1.07	
hypothetical protein LOC129293	LOC129293	129293	9.47E-04	1.32E-01	0.4 (0.2, 0.7)	6.9E-01	0.88	1.3E-02	0.60	
hypothetical protein LOC641518	LOC641518	641518	3.11E-05	2.84E-02	0.0 (0.0, 0.2)	7.3E-01	0.98	8.8E-03	0.77	
IL2-inducible T-cell kinase	ITK	3702	5.47E-04	1.04E-01	0.3 (0.2, 0.6)	9.7E-01	1.00	2.9E-03	0.71	1, 3
inositol 1,4,5-triphosphate receptor, type 2	ITPR2	3709	1.52E-03	1.56E-01	38.6 (3.9, 379.0)	3.0E-02	1.12	1.8E-02	1.12	9
Integrator complex subunit 9	INTS9	55756	7.51E-04	1.21E-01	97.5 (6.7, 1,428.0)	6.5E-02	1.05	9.8E-03	1.09	
integrin, alpha 4	ITGA4	3676	9.70E-04	1.32E-01	0.2 (0.1, 0.5)	2.3E-01	1.10	7.5E-01	0.98	3
integrin, alpha 6	ITGA6	3655	1.63E-04	5.69E-02	0.3 (0.1, 0.5)	5.7E-01	0.96	1.3E-04	0.64	
Interferon, alpha-inducible protein 6	IFI6	2537	3.96E-04	9.00E-02	0.3 (0.2, 0.6)	2.1E-02	0.71	5.8E-03	0.73	
interleukin 23, alpha subunit p19	IL23A	51561	1.71E-03	1.66E-01	0.1 (0.0, 0.4)	1.8E-01	0.62	2.0E-02	0.49	
interleukin 7 receptor	IL7R	3575	8.62E-05	4.23E-02	0.4 (0.2, 0.6)	9.5E-01	1.00	2.0E-03	0.68	
KIAA0040	KIAA0040	9674	2.33E-03	1.94E-01	6.0 (1.8, 19.8)	3.7E-01	0.93	5.2E-02	1.20	
KIAA0888	KIAA0888	26049	1.32E-03	1.45E-01	0.4 (0.2, 0.7)	1.1E-01	0.85	1.6E-05	0.57	
KIAA0922	KIAA0922	23240	1.32E-04	5.37E-02	31.3 (5.3, 186.4)	8.8E-01	1.00	4.9E-01	1.05	
KIAA1012	KIAA1012	22878	1.86E-03	1.75E-01	1,778.2 (17.6, 179,866.3)	6.5E-01	0.99	5.4E-01	1.02	
KIAA1407	KIAA1407	57577	6.42E-04	1.11E-01	1.9 (1.2, 2.8)	1.4E-01	1.08	3.5E-01	1.54	
lactate dehydrogenase B	LDHB	3945	1.28E-03	1.45E-01	0.2 (0.1, 0.6)	9.8E-01	0.99	2.5E-02	0.79	
latrophilin 1	LPHN1	22859	4.59E-06	9.35E-03	0.1 (0.0, 0.2)	2.1E-01	1.07	4.0E-03	0.87	
leptin receptor overlapping transcript-like 1	LEPROTL1	23484	7.03E-04	1.17E-01	0.1 (0.0, 0.4)	3.0E-01	0.92	5.9E-03	0.79	
leucine rich repeat neuronal 3	LRRN3	54674	1.35E-03	1.46E-01	0.5 (0.3, 0.8)	8.5E-01	1.33	7.9E-03	0.57	
LIM domain only 4	LMO4	8543	1.13E-03	1.37E-01	16.3 (3.1, 86.7)	9.2E-01	1.02	9.5E-04	1.21	
linker for activation of T cells	LAT	27040	8.25E-04	1.26E-01	0.2 (0.1, 0.5)	4.9E-01	0.96	1.7E-03	0.77	1, 2, 4
lipin 2	LPIN2	9663	1.99E-03	1.81E-01	0.1 (0.0, 0.5)	3.0E-01	0.93	3.2E-02	0.86	
Lix1 homolog-like	LIX1L	128077	6.08E-04	1.09E-01	0.3 (0.2, 0.6)	2.7E-01	0.92	4.3E-01	0.97	

low density lipoprotein receptor adaptor protein 1	LDLRAP1	26119	7.74E-04	1.23E-01	0.3 (0.1, 0.6)	3.0E-01	0.89	1.8E-03	0.65	
low density lipoprotein receptor-related protein 5-like	LRP5L	91355	2.01E-04	6.26E-02	6.4 (2.0, 20.3)	7.3E-01	0.99	8.1E-02	1.13	
lysosomal associated multispinning membrane protein 5	LAPTM5	7805	1.70E-03	1.66E-01	3,553.7 (22.8, 554,931.3)	9.9E-01	1.00	1.4E-02	1.05	
mal, T-cell differentiation protein	MAL	4118	4.01E-04	9.00E-02	0.5 (0.4, 0.8)	9.2E-01	0.97	1.1E-01	0.71	
mannosidase, alpha, class 1C, member 1	MAN1C1	57134	9.87E-04	1.32E-01	0.5 (0.4, 0.8)	1.0E+00	0.90	1.6E-01	0.66	
mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A	MGAT4A	11320	6.45E-05	3.97E-02	0.2 (0.1, 0.5)	2.2E-01	0.93	2.2E-04	0.76	
mitogen-activated protein kinase 8 interacting protein 3	MAPK8IP3	23162	9.37E-04	1.32E-01	108.3 (6.5, 1,816.3)	6.9E-01	1.02	3.3E-01	1.05	
mucolin 2	MCOLN2	255231	6.79E-04	1.15E-01	1.8 (1.2, 2.7)	4.4E-01	0.89	5.1E-01	1.59	
myeloid/lymphoid or mixed-lineage leukemia; translocated to, 3	MLLT3	4300	8.50E-05	4.23E-02	0.2 (0.1, 0.5)	7.6E-01	0.98	2.7E-03	0.69	
NEL-like 2	NELL2	4753	1.15E-04	4.98E-02	0.4 (0.2, 0.7)	7.1E-01	0.91	3.4E-03	0.57	
neuronal pentraxin 1	NPTX1	4884	1.73E-06	5.09E-03	2.7 (1.5, 4.9)	6.5E-01	1.02	2.5E-01	1.44	
N-myristoyltransferase 2	NMT2	9397	5.36E-04	1.04E-01	0.5 (0.3, 0.7)	6.4E-01	0.94	2.8E-04	0.55	
nuclear receptor coactivator 3	NCOA3	8202	8.34E-04	1.26E-01	5.0 (1.7, 14.4)	4.4E-01	0.98	5.3E-01	1.07	8
nuclear receptor subfamily 3, group C, member 2	NR3C2	4306	5.28E-04	1.04E-01	0.3 (0.1, 0.6)	1.7E-01	0.82	4.8E-05	0.50	
nucleosome assembly protein 1-like 3	NAP1L3	4675	5.59E-04	1.04E-01	0.4 (0.2, 0.7)	1.9E-01	0.84	9.7E-04	0.60	
oxidoreductase NAD-binding domain containing 1	OXNAD1	92106	3.37E-04	8.25E-02	0.2 (0.1, 0.5)	7.5E-01	0.98	2.3E-02	0.79	
phosphatidylinositol transfer protein, cytoplasmic 1	PITPNC1	26207	2.24E-03	1.92E-01	0.4 (0.2, 0.8)	2.1E-01	0.90	4.9E-04	0.70	
phosphodiesterase 3B, cGMP-inhibited	PDE3B	5140	2.22E-04	6.67E-02	0.3 (0.2, 0.6)	2.5E-03	0.80	7.9E-05	0.72	
Phosphoglucomutase 2-like 1	PGM2L1	283209	1.83E-03	1.74E-01	0.0 (0.0, 0.2)	2.9E-01	1.03	3.3E-01	0.98	
phospholipase C, gamma 2	PLCG2	5336	8.92E-04	1.31E-01	27.7 (4.0, 191.5)	1.5E-01	0.94	3.0E-01	1.06	2, 3, 4, 5, 7, 10, 11
phospholysine phosphohistidine inorganic pyrophosphate phosphatase	LHPP	64077	1.55E-03	1.56E-01	12.7 (3.0, 53.5)	2.9E-01	1.06	5.7E-01	1.06	
pleckstrin homology domain containing, family A member 2	PLEKHA2	59339	1.52E-04	5.64E-02	6.0 (2.1, 17.2)	3.9E-01	0.97	2.7E-01	1.11	
poly(A) binding protein, cytoplasmic 1-like	PABPC1L	80336	5.94E-04	1.07E-01	9.7 (2.6, 36.0)	4.9E-01	1.05	2.1E-02	1.29	
PR domain containing 2, with ZNF domain	PRDM2	7799	1.73E-04	5.77E-02	12.0 (3.2, 45.2)	6.1E-02	0.93	5.8E-01	0.99	
prickle homolog 1	PRICKLE1	144165	2.11E-03	1.85E-01	2.6 (1.4, 4.7)	6.3E-02	1.12	2.7E-01	1.45	
programmed cell death 4	PDCD4	27250	1.47E-03	1.54E-01	0.1 (0.0, 0.4)	4.1E-02	0.88	1.8E-03	0.81	
Proprotein convertase subtilisin/kexin type 5	PCSK5	5125	4.14E-04	9.00E-02	0.2 (0.1, 0.5)	5.4E-01	1.06	9.3E-01	1.02	

protein inhibitor of activated STAT, 2	PIAS2	9063	9.93E-04	1.32E-01	2.3 (1.3, 3.8)	3.6E-01	0.81	1.7E-01	1.31	
protein inhibitor of activated STAT, 2	PIAS2	9063	1.04E-03	1.35E-01	2.4 (1.4, 4.3)	1.4E-01	0.77	1.7E-01	1.30	
protein kinase C, alpha	PRKCA	5578	1.52E-03	1.56E-01	0.4 (0.2, 0.7)	9.1E-01	0.98	6.2E-02	0.74	2, 3, 4, 5, 9, 10, 11
protein kinase C, beta 1	PRKCB1	5579	1.45E-05	2.26E-02	29.1 (7.3, 117.0)	4.2E-01	1.04	3.6E-01	1.08	2, 3, 4, 5, 7, 9, 10, 11
protein kinase C, eta	PRKCH	5583	6.39E-04	1.11E-01	0.2 (0.1, 0.5)	6.2E-02	0.91	7.3E-04	0.82	2, 3, 4, 5, 9
protein tyrosine phosphatase, non-receptor type 2	PTPN2	5771	3.35E-04	8.25E-02	18.0 (3.7, 86.9)	8.3E-02	1.06	5.0E-03	1.15	
PRP18 pre-mRNA processing factor 18 homolog	PRPF18	8559	1.73E-03	1.68E-01	12.2 (2.6, 57.4)	7.3E-01	0.96	7.1E-01	1.01	
Rap guanine nucleotide exchange factor 6	RAPGEF6	51735	1.31E-03	1.45E-01	0.1 (0.0, 0.5)	1.4E-01	0.95	4.7E-05	0.82	
RAS p21 protein activator 4	RASA4	10156	5.45E-04	1.04E-01	0.3 (0.2, 0.6)	6.0E-01	1.06	5.5E-02	0.75	
Ras protein-specific guanine nucleotide-releasing factor 2	RASGRF2	5924	1.18E-04	5.05E-02	0.3 (0.1, 0.5)	2.6E-01	0.84	3.4E-04	0.54	
RCAN family member 3	RCAN3	11123	4.77E-04	9.87E-02	0.3 (0.2, 0.6)	5.5E-01	0.94	3.1E-02	0.73	
reversion-inducing-cysteine-rich protein with kazal motifs	RECK	8434	1.59E-03	1.59E-01	0.3 (0.1, 0.6)	4.0E-01	0.93	7.5E-03	0.77	
Rho GTPase activating protein 24	ARHGAP24	83478	1.99E-04	6.26E-02	2.8 (1.6, 4.9)	2.8E-01	0.76	2.0E-01	1.24	
Rho guanine nucleotide exchange factor 7	ARHGEF7	8874	2.92E-04	7.75E-02	18.9 (4.8, 73.7)	3.3E-01	1.04	6.3E-01	1.06	
Rho-related BTB domain containing 2	RHOBTB2	23221	1.11E-06	4.84E-03	5.0 (2.0, 12.8)	1.3E-01	1.04	2.8E-01	1.14	
Rho-type GTPase-activating protein RICH2	RICH2	9912	6.81E-05	4.00E-02	5.2 (2.1, 12.5)	4.7E-01	1.03	6.8E-01	1.11	
ribosome binding protein 1 homolog 180kDa	RRBP1	6238	1.93E-03	1.79E-01	11.7 (2.5, 55.6)	8.5E-01	0.99	6.0E-02	1.14	
ring finger protein 144A	RNF144A	9781	1.65E-03	1.63E-01	0.4 (0.2, 0.7)	1.8E-01	0.88	2.4E-04	0.67	
SATB homeobox 1	SATB1	6304	3.17E-04	8.09E-02	0.1 (0.0, 0.4)	4.6E-01	0.95	3.1E-04	0.74	
sema domain, immunoglobulin domain, transmembrane domain and short cytoplasmic domain, 4C	SEMA4C	54910	1.02E-03	1.33E-01	0.2 (0.1, 0.5)	6.1E-02	0.88	1.8E-04	0.75	
SET domain containing 8	SETD8	387893	1.21E-03	1.40E-01	8.2 (2.2, 30.9)	3.9E-01	0.93	2.0E-01	1.12	
sex comb on midleg-like 1	SCML1	6322	1.23E-06	4.84E-03	0.4 (0.2, 0.6)	2.9E-01	0.86	1.2E-03	0.56	
sex comb on midleg-like 4	SCML4	256380	1.37E-03	1.48E-01	0.3 (0.2, 0.7)	3.6E-01	0.95	2.6E-02	0.86	
SH3-domain binding protein 5	SH3BP5	9467	1.15E-03	1.37E-01	5.4 (2.0, 14.5)	7.8E-01	0.97	5.4E-01	1.09	
signal-regulatory protein gamma	SIRPG	55423	6.80E-04	1.15E-01	0.2 (0.1, 0.5)	6.4E-01	0.96	3.7E-03	0.75	
similar to protein immuno-reactive with anti-PTH polyclonal antibodies	FLJ40330	645784	1.75E-04	5.77E-02	2.3 (1.4, 3.8)	9.3E-01	0.86	8.8E-01	1.36	
single-stranded DNA binding protein 2	SSBP2	23635	2.37E-03	1.95E-01	0.1 (0.0, 0.5)	6.6E-01	0.96	1.7E-01	0.90	
SMAD family member 3	SMAD3	4088	2.24E-03	1.92E-01	0.1 (0.0, 0.4)	5.4E-01	0.94	4.0E-01	0.95	6

SMEK homolog 2, suppressor of mek1	SMEK2	57223	5.72E-04	1.04E-01	0.1 (0.0, 0.3)	5.1E-01	0.98	3.0E-01	0.96	
solute carrier family 25 member 15	SLC25A15	10166	9.35E-04	1.32E-01	0.1 (0.0, 0.4)	2.3E-01	0.92	8.3E-03	0.82	
Spleen tyrosine kinase	SYK	6850	3.98E-05	3.24E-02	75.5 (10.2, 556.2)	6.5E-01	1.02	1.9E-02	1.13	2, 4, 7
Src-like-adaptor 2	SLA2	84174	7.79E-04	1.23E-01	0.2 (0.1, 0.5)	8.9E-02	0.87	7.4E-03	0.79	
suppressor of variegation 4-20 homolog 1	SUV420H1	51111	2.03E-03	1.84E-01	85.1 (6.9, 1,043.4)	7.6E-01	1.01	7.1E-01	1.03	
T cell receptor alpha	TRA@	6955	8.33E-04	1.26E-01	0.3 (0.1, 0.6)	5.0E-01	0.98	1.1E-04	0.61	1
T cell receptor associated transmembrane adaptor 1	TRAT1	50852	9.39E-04	1.32E-01	0.4 (0.2, 0.7)	6.6E-01	1.06	1.2E-01	0.80	
tandem C2 domains, nuclear	TC2N	123036	4.08E-04	9.00E-02	0.2 (0.1, 0.5)	7.3E-01	0.96	1.5E-03	0.69	
TBC1 domain family, member 4	TBC1D4	9882	6.45E-04	1.11E-01	0.4 (0.2, 0.7)	9.8E-01	1.00	5.8E-03	0.67	
TBC1 domain family, member 5	TBC1D5	9779	1.79E-03	1.72E-01	16.1 (3.7, 69.9)	6.7E-01	0.99	2.9E-01	1.11	
T-cell activation NFKB-like protein	TA-NFKBH	84807	2.34E-04	6.73E-02	7.0 (2.3, 20.8)	2.8E-01	1.05	4.6E-02	1.17	
Tetraspanin 18	TSPAN18	90139	1.06E-03	1.36E-01	0.3 (0.2, 0.6)	7.6E-01	0.94	8.2E-02	0.78	
thioesterase superfamily member 4	THEM4	117145	1.20E-03	1.40E-01	0.2 (0.1, 0.6)	2.4E-01	0.89	3.2E-04	0.65	
TRAF2 and NCK interacting kinase	TNIK	23043	9.37E-04	1.32E-01	0.2 (0.1, 0.6)	3.5E-01	1.08	3.1E-01	0.90	
trafficking protein, kinesin binding 1	TRAK1	22906	2.11E-03	1.85E-01	3.1 (1.4, 7.1)	8.9E-01	1.01	3.4E-01	1.10	
transcription factor 3	TCF3	6929	1.54E-03	1.56E-01	4.1 (1.7, 10.1)	6.6E-01	1.02	9.7E-01	1.05	
transcription factor 7	TCF7	6932	8.99E-04	1.31E-01	0.5 (0.3, 0.7)	5.2E-01	0.82	1.0E-02	0.54	
transcription factor EB	TFEB	7942	7.64E-05	4.05E-02	56.5 (7.0, 454.9)	7.6E-01	1.02	2.8E-02	1.16	
transketolase-like 1	TKTL1	8277	7.13E-04	1.18E-01	0.3 (0.2, 0.6)	3.2E-01	0.70	7.7E-02	0.60	
transmembrane and immunoglobulin domain containing 2	TMIGD2	126259	5.03E-04	1.00E-01	0.0 (0.0, 0.1)	1.1E-01	0.93	7.7E-02	0.93	
Transmembrane emp24 protein transport domain containing 8	TMED8	283578	4.55E-04	9.56E-02	3.5 (1.7, 7.2)	7.8E-01	0.92	3.2E-02	1.27	
transmembrane protein 204	TMEM204	79652	1.76E-04	5.77E-02	0.4 (0.2, 0.7)	5.2E-01	0.91	3.9E-03	0.65	
transmembrane protein 66	TMEM66	51669	1.29E-03	1.45E-01	0.0 (0.0, 0.2)	2.0E-01	0.96	4.3E-04	0.87	
tribbles homolog 2	TRIB2	28951	3.96E-04	9.00E-02	0.3 (0.1, 0.6)	6.7E-01	0.95	2.2E-03	0.69	
TSC22 domain family, member 1	TSC22D1	8848	2.30E-03	1.94E-01	0.3 (0.1, 0.6)	7.8E-01	0.99	1.2E-02	0.86	
tumor necrosis factor receptor superfamily, member 13B	TNFRSF13B	23495	2.08E-04	6.40E-02	19.9 (3.4, 115.6)	8.5E-01	1.01	9.6E-01	1.02	
tumor necrosis factor receptor superfamily, member 25	TNFRSF25	8718	5.57E-04	1.04E-01	0.1 (0.0, 0.3)	3.6E-01	0.93	1.2E-02	0.83	
TXK tyrosine kinase	TXK	7294	1.54E-03	1.56E-01	0.6 (0.4, 0.8)	3.7E-01	0.92	1.3E-03	0.61	1, 3
ubiquitin associated and SH3 domain containing, B	UBASH3B	84959	7.88E-04	1.23E-01	6.0 (2.1, 17.1)	3.8E-01	1.06	8.5E-02	1.20	
UDP-glucose ceramide glucosyltransferase-like 2	UGCGL2	55757	2.50E-05	2.52E-02	26.5 (4.8, 145.9)	9.5E-01	1.00	1.9E-02	1.08	

uncoupling protein 3	UCP3	7352	1.19E-03	1.40E-01	377.1 (14.1, 10,100.0)	1.7E-01	1.03	1.6E-01	1.04	
v-myc myelocytomatosis viral oncogene homolog	MYC	4609	8.89E-04	1.31E-01	0.3 (0.2, 0.6)	8.3E-01	1.03	3.6E-01	0.90	5, 6, 10
WAS protein family, member 2	WASF2	10163	1.24E-03	1.42E-01	127.5 (6.5, 2,514.9)	6.3E-01	1.02	8.1E-01	1.00	
WD repeat domain 91	WDR91	29062	1.08E-04	4.77E-02	7.6 (2.7, 21.4)	2.5E-02	0.85	8.4E-01	1.02	
zinc finger protein 793	ZNF793	390927	2.67E-04	7.52E-02	5.5 (2.1, 14.4)	5.6E-01	1.04	8.3E-03	1.25	
Zinc finger protein 80	ZNF80	7634	3.73E-04	8.75E-02	3.7 (1.7, 8.0)	4.5E-01	1.04	8.8E-01	1.11	
zinc finger, CCHC domain containing 14	ZCCHC14	23174	6.88E-05	4.00E-02	0.4 (0.3, 0.7)	5.6E-02	0.89	8.1E-05	0.73	
zinc finger, DHHC-type containing 19	ZDHHC19	131540	2.83E-06	7.50E-03	2.5 (1.6, 4.1)	4.4E-01	0.94	1.7E-01	1.43	
zinc finger, DHHC-type containing 21	ZDHHC21	340481	1.88E-03	1.76E-01	3.5 (1.5, 8.1)	3.1E-01	1.05	1.6E-01	1.20	

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12 *hr.* hazard ratio; 1. T cell receptor signaling; 2. Fc Epsilon RI signaling; 3. Leukocyte extravasation signaling; 4. Natural killer cell

13 signaling; 5. Neuregulin signaling; 6. Cell cycle: G1/S; 7. B cell receptor signaling; 8. Glucocorticoid receptor signaling; 9. Synaptic long

14 term potentiation; 10. PDGF signaling; 11. Chemokin signalling