Supplementary Table S1
One hundred twenty-six genes composing our prognostic index

Gene Symbol	Entrez ID	beta	Description
AIMP2	7965	0.00013	aminoacyl tRNA synthetase complex-interacting multifunctional protein 2
ALOX5AP	241	-0.00258	arachidonate 5-lipoxygenase-activating protein
ANKZF1	55139	0.00014	ankyrin repeat and zinc finger domain containing 1
ANXA1	301	-0.00894	annexin A1
APOL1	8542	-0.00287	apolipoprotein L
ARMCX2	9823	-0.00455	armadillo repeat containing, X-linked 2
ASCC2	84164	-0.00265	activating signal cointegrator 1 complex subunit 2
ATP5E	514	0.00071	ATP synthase, H+ transporting, mitochondrial F1 complex, epsilon subunit
ATP5J	522	0.01706	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit F6
B4GALT5*	9334	0.00971	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 5
BCL2A1	597	-0.01016	BCL2-related protein A1
BIN1	274	-0.02015	bridging integrator 1
C19orf62	29086	0.00889	chromosome 19 open reading frame 62
CCL2	6347	-0.00493	chemokine (C-C motif) ligand 2
CCL5	6352	-0.00326	chemokine (C-C motif) ligand 5
CD209	30835	-0.00919	CD209 molecule
CD38	952	-0.00500	CD38 molecule
CD8A	925	-0.00398	CD8a molecule
CDC14B	8555	0.00091	CDC14 cell division cycle 14 homolog B (S. cerevisiae)
CDK7	1022	0.01780	cyclin-dependent kinase 7
CHD8	57680	-0.01343	chromodomain helicase DNA binding protein 8
CLDN7	1366	0.01060	claudin 7
CNDP2	55748	-0.00045	CNDP dipeptidase 2 (metallopeptidase M20 family)
COL13A1	1305	0.00470	collagen, type XIII, alpha 1
COX17	10063	0.01070	COX17 cytochrome c oxidase assembly homolog (S. cerevisiae)
COX6A1	1337	0.01703	cytochrome c oxidase subunit VIa polypeptide 1
CTSH	1512	-0.02393	cathepsin H
CXCL2	2920	-0.00214	chemokine (C-X-C motif) ligand 2
CXCL9*	4283	-0.00723	chemokine (C-X-C motif) ligand 9
CXCR7	57007	0.01148	chemokine (C-X-C motif) receptor 7
DAD1	1603	-0.00500	defender against cell death 1
DNAJB1	3337	0.01212	DnaJ (Hsp40) homolog, subfamily B, member 1
DSTN	11034	0.01296	destrin (actin depolymerizing factor)
EFHA1	221154	0.04564	EF-hand domain family, member A1
EIF2B1	1967	0.00335	eukaryotic translation initiation factor 2B, subunit 1 alpha, 26kDa
EIF3K	27335	0.00034	eukaryotic translation initiation factor 3, subunit K
FAM127B	26071	-0.01210	family with sequence similarity 127, member B
FCER1G	2207	-0.00784	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide
FGL2	10875	-0.00203	fibrinogen-like 2
FKBP1B	2281	0.00577	FK506 binding protein 1B, 12.6 kDa
FNDC3A	22862	0.00892	fibronectin type III domain containing 3A

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Supplementary Table S1
Continued

Gene Symbol	Entrez ID	beta	Description
G6PD	2539	-0.00899	glucose-6-phosphate dehydrogenase
GLRX3	10539	0.00114	glutaredoxin 3
GPHN	10243	-0.00446	gephyrin
GRSF1	2926	-0.01055	G-rich RNA sequence binding factor 1
GSTM3	2947	-0.00083	glutathione S-transferase mu 3 (brain)
GTF3A	2971	0.00298	general transcription factor IIIA
HADHA	3030	0.02175	hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), alpha subunit
HDAC1	3065	0.00199	histone deacetylase 1
HK2	3099	-0.00202	hexokinase 2
HLA-DPB1	3115	-0.00185	major histocompatibility complex, class II, DP beta 1
ID4*	3400	-0.01626	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
IGSF6	10261	-0.01833	immunoglobulin superfamily, member 6
IL1B	3553	-0.00256	interleukin 1, beta
IRF1	3659	-0.00648	interferon regulatory factor 1
ITGAL	3683	-0.00731	integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide)
KANK1	23189	0.00779	KN motif and ankyrin repeat domains 1
KATNB1	10300	-0.00699	katanin p80 (WD repeat containing) subunit B 1
KIF3C	3797	0.04240	kinesin family member 3C
KIFAP3	22920	0.00243	kinesin-associated protein 3
LAPTM4A	9741	0.02578	lysosomal protein transmembrane 4 alpha
LRP12	29967	-0.00465	low density lipoprotein-related protein 12
LRRC1	55227	0.00498	leucine rich repeat containing 1
LRRC59	55379	0.00372	leucine rich repeat containing 59
MCAT	27349	-0.01881	malonyl CoA:ACP acyltransferase (mitochondrial)
MMP11	4320	0.00748	matrix metallopeptidase 11 (stromelysin 3)
MPHOSPH8	54737	0.02791	M-phase phosphoprotein 8
MRPS27	23107	0.00173	mitochondrial ribosomal protein S27
MTRF1*	9617	0.01224	mitochondrial translational release factor 1
MYST3	7994	-0.00531	MYST histone acetyltransferase (monocytic leukemia) 3
N4BP2L2	10443	0.01727	NEDD4 binding protein 2-like 2
NCKAP1L	3071	-0.01105	NCK-associated protein 1-like
NCOA1	8648	0.00937	nuclear receptor coactivator 1
NDFIP1	80762	0.00035	Nedd4 family interacting protein 1
NDUFA4	4697	0.00766	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa
NDUFB4	4710	0.00797	NDUFB4 NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa
NUCB2	4925	-0.00277	nucleobindin 2
NUP107	57122	0.00482	nucleoporin 107kDa
NUP210	23225	-0.01534	nucleoporin 210kDa
NUP98	4928	0.01535	nucleoporin 98kDa
OSR2	116039	0.00403	odd-skipped related 2 (Drosophila)
PARVA	55742	0.00441	parvin, alpha
PCYOX1L	78991	0.00031	prenylcysteine oxidase 1 like
PFDN2	5202	0.00117	prefoldin subunit 2

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Continued

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PGK1	5230	-0.00884	phosphoglycerate kinase 1
PPFIA1	8500	-0.00802	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1
PRPF18	8559	0.00351	PRP18 pre-mRNA processing factor 18 homolog (S. cerevisiae)
PRSS8	5652	0.00315	protease
PTN	5764	-0.01206	pleiotrophin
RAB25	57111	0.00231	RAB25, member RAS oncogene family
RAB3GAP2	25782	0.00072	RAB3 GTPase activating protein subunit 2 (non-catalytic)
RAD17	5884	0.01982	RAD17 homolog (S. pombe)
RAF1	5894	-0.01744	v-raf-1 murine leukemia viral oncogene homolog 1
RASGRP1	10125	-0.00647	RAS guanyl releasing protein 1 (calcium and DAG-regulated)
RBX1	9978	-0.01436	ring-box 1
RCOR3	55758	0.00619	REST corepressor 3
RNASET2	8635	-0.00647	ribonuclease T2
RNF14	9604	0.00090	ring finger protein 14
RNF146	81847	0.00507	ring finger protein 146
RPL11	6135	0.02068	ribosomal protein L11
RPS21	6227	0.00756	ribosomal protein S21
RPS7	6201	0.02085	ribosomal protein S7
RTN2	6253	0.01561	reticulon 2
SACS	26278	0.00046	spastic ataxia of Charlevoix-Saguenay (sacsin)
SCRN1	9805	0.00296	secernin 1
SERPINA1	5265	-0.00591	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1
SKIL	6498	0.01010	SKI-like oncogene
SLC7A11*	23657	-0.01056	solute carrier family 7 (anionic amino acid transporter light chain, xc- system), member 11
SMARCAL1	50485	0.00831	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a-like 1
SMYD2	56950	0.00265	SET and MYND domain containing 2
SMYD3	64754	0.00859	SET and MYND domain containing 3
SNRPD2	6633	0.00076	small nuclear ribonucleoprotein D2 polypeptide 16.5kDa
SPDEF	25803	-0.00807	SAM pointed domain containing ets transcription factor
SPTLC1	10558	0.01217	serine palmitoyltransferase, long chain base subunit 1
SRPX	8406	0.00224	sushi-repeat containing protein, X-linked
TBCB	1155	0.00450	tubulin folding cofactor B
TEAD1	7003	0.00664	TEA domain family member 1 (SV40 transcriptional enhancer factor)
TEX264	51368	-0.00258	testis expressed 264
TNIK	23043	0.00744	TRAF2 and NCK interacting kinase
TREM2	54209	-0.00029	triggering receptor expressed on myeloid cells 2
UBE2L6	9246	-0.00450	ubiquitin-conjugating enzyme E2L 6
UBL3	5412	0.00754	ubiquitin-like 3
USP16	10600	0.02525	ubiquitin specific peptidase 16
WDR73	84942	-0.01578	WD repeat domain 73
WIPI2	26100	0.00061	WD repeat domain, phosphoinositide interacting 2
WSB2	55884	0.00703	WD repeat and SOCS box-containing 2

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