Supplementary Table S1. Detailed information on the selected candidate prognostic genes.

Gene	Cox model in NSCLC tumor RNA-seq data (GSE81089)				Results of *t*-tests in NSCLC tumor microarray data (GSE28582)	
	Cutoff Point	*p*-value	HR	95%CI	Fold Change (short-survival/long-survival)	*p*-value
ADCY2	0.421	0.016	0.598	[0.3928, 0.9092]	0.929	0.013
ARGLU1	66.804	0.00085	0.491	[0.3238, 0.7459]	0.977	0.044
ARNTL2	11.982	0.0045	1.852	[1.2105, 2.8333]	1.084	0.0099
EXOC4	27.970	0.025	1.731	[1.0724, 2.7928]	1.018	0.028
FAM118A	32.030	0.026	0.621	[0.409, 0.944]	0.965	0.047
FGF5	0.179	0.015	1.762	[1.118, 2.779]	1.024	0.012
HRH1	5.977	9.02E-05	2.262	[1.503, 3.403]	1.051	0.0097
KRR1	76.966	0.021	1.917	[1.102, 3.336]	1.026	0.034
LONRF2	0.696	0.011	0.588	[0.390, 0.886]	0.918	0.048
MAP4	43.202	0.0043	2.731	[1.371, 5.440]	1.019	0.017
MAP4K4	52.814	0.0013	1.977	[1.305, 2.996]	1.025	0.039
PTBP3	41.805	0.012	1.696	[1.121, 2.565]	1.015	0.035
RSL24D1	53.082	0.027	1.622	[1.057, 2.490]	1.019	0.050
TP53INP1	20.588	0.0049	0.521	[0.331, 0.820]	0.966	0.022
TRIM38	11.492	0.026	0.533	[0.307, 0.926]	0.975	0.024
TSPYL2	18.323	0.0016	0.501	[0.326, 0.770]	0.979	0.012
UBL5	205.301	0.0061	0.887	[0.482, 1.631]	0.986	0.025
WDR5B	3.354	0.0028	0.466	[0.283, 0.769]	0.970	0.019

Supplementary Table S2. Biological context of network edges in Figure 1A (Precision Threshold: 0.7704, Scope Threshold: 0.1462; *p*-value < 0.00005; one-tailed *z*-tests).

Biological context	Precision	Scope
The up-regulation of ACTR3 implies the up-regulation of RPL37.	0.869388	0.159505
The up-regulation of ANAPC5 implies the up-regulation of ITPRIPL2.	0.794872	0.152344
The up-regulation of APOC1P1 implies the up-regulation of PNPT1.	0.847619	0.205078
The up-regulation of APOC1P1 implies the up-regulation of RPL37.	0.934694	0.159505
The up-regulation of ARCN1 implies the up-regulation of LOC100505876.	0.788235	0.147569
The up-regulation of ARCN1 implies the up-regulation of ORC6.	0.782805	0.19184
The up-regulation of ARCN1 implies the up-regulation of PNPT1.	0.87451	0.166016
The up-regulation of ARCN1 implies the up-regulation of RPP30.	0.823529	0.177083
The up-regulation of ARGLU1 implies the up-regulation of EEF2.	0.896104	0.200521
The up-regulation of ARGLU1 implies the up-regulation of KMT2E.	0.857708	0.219618
The up-regulation of ARGLU1 implies the up-regulation of RPL27.	0.875325	0.167101
The up-regulation of ARGLU1 implies the up-regulation of RPL37.	0.937662	0.167101
The up-regulation of ARGLU1 implies the up-regulation of RPL37A.	1	0.162326
The up-regulation of ARGLU1 implies the up-regulation of RPS21.	0.945455	0.190972
The up-regulation of ARGLU1 implies the up-regulation of RPS29.	0.937662	0.167101
The up-regulation of ARNTL2 implies the up-regulation of ITPRIPL2.	0.776224	0.186198
The up-regulation of ARNTL2 implies the up-regulation of PNPT1.	0.870707	0.161133
The up-regulation of BLK implies the up-regulation of EEF2.	0.832753	0.186849

The up-regulation of BLK implies the up-regulation of RPL27.	0.933101	0.155707
The up-regulation of BLK implies the up-regulation of RPL37.	1	0.155707
The up-regulation of BLK implies the up-regulation of RPL37A.	0.931133	0.151259
The up-regulation of BLK implies the up-regulation of RPS21.	0.941463	0.177951
The up-regulation of BLK implies the up-regulation of RPS29.	0.933101	0.155707
The up-regulation of BLK implies the up-regulation of SON.	0.804878	0.213542
The up-regulation of CCT3 implies the up-regulation of PNPT1.	0.793548	0.151367
The up-regulation of CES2 implies the up-regulation of PNPT1.	0.80155	0.209961
The up-regulation of CES2 implies the up-regulation of RPL37.	0.808638	0.163303
The up-regulation of CNOT1 implies the up-regulation of EEF2.	0.850932	0.209635
The up-regulation of CNOT1 implies the up-regulation of RPL27.	0.940373	0.174696
The up-regulation of CNOT1 implies the up-regulation of RPL37.	0.880745	0.174696
The up-regulation of CNOT1 implies the up-regulation of RPL37A.	0.877238	0.169705
The up-regulation of CNOT1 implies the up-regulation of RPS21.	0.843478	0.199653
The up-regulation of CNOT1 implies the up-regulation of RPS29.	0.821118	0.174696
The up-regulation of DDX3X implies the up-regulation of EEF2.	0.805471	0.214193
The up-regulation of DDX3X implies the up-regulation of RPL37.	0.883283	0.178494
The up-regulation of DDX3X implies the up-regulation of RPL37A.	0.87985	0.173394
The up-regulation of DDX3X implies the up-regulation of RPS21.	0.846809	0.203993
The up-regulation of DDX3X implies the up-regulation of RPS29.	0.883283	0.178494
The up-regulation of DDX46 implies the up-regulation of RPL37.	0.859341	0.148112
The up-regulation of DDX46 implies the up-regulation of RPS29.	0.789011	0.148112
The up-regulation of DDX6 implies the up-regulation of EEF2.	0.900621	0.209635
The up-regulation of DDX6 implies the up-regulation of RPL27.	1	0.174696
The up-regulation of DDX6 implies the up-regulation of RPL37.	1	0.174696
The up-regulation of DDX6 implies the up-regulation of RPL37A.	1	0.169705
The up-regulation of DDX6 implies the up-regulation of RPS21.	0.947826	0.199653
The up-regulation of DDX6 implies the up-regulation of RPS29.	1	0.174696
The up-regulation of EEF2 implies the up-regulation of RPL27.	0.847619	0.205078
The up-regulation of EEF2 implies the up-regulation of RPL37.	0.949206	0.205078
The up-regulation of EEF2 implies the up-regulation of RPL37A.	0.895425	0.199219
The up-regulation of EEF2 implies the up-regulation of RPS21.	0.822222	0.234375
The up-regulation of EEF2 implies the up-regulation of RPS29.	0.898413	0.205078
The up-regulation of EIF2S3 implies the up-regulation of RPL27.	0.776093	0.186089
The up-regulation of EIF2S3 implies the up-regulation of RPL37.	0.776093	0.186089
The up-regulation of EIF3E implies the up-regulation of RPL27.	0.866202	0.155707
The up-regulation of EIF3E implies the up-regulation of RPL37.	0.933101	0.155707
The up-regulation of EIF3E implies the up-regulation of RPL37A.	0.7934	0.151259
The up-regulation of EIF3E implies the up-regulation of RPS29.	0.799303	0.155707
The up-regulation of EIF3H implies the up-regulation of RPL27.	0.808638	0.163303
The up-regulation of EIF3H implies the up-regulation of RPL37.	0.808638	0.163303
The up-regulation of EIF3H implies the up-regulation of RPL37A.	0.80301	0.158637
The up-regulation of EIF3H implies the up-regulation of RPS21.	0.82558	0.186632
The up-regulation of EIF3H implies the up-regulation of RPS29.	0.808638	0.163303
The up-regulation of EIF4E implies the up-regulation of CES2.	0.792992	0.20128

The up-regulation of EIF4E implies the up-regulation of LOC100505876.	0.794286	0.15191
The up-regulation of EWSR1 implies the up-regulation of EEF2.	0.832753	0.186849
The up-regulation of EWSR1 implies the up-regulation of PNPT1.	0.843902	0.200195
The up-regulation of EWSR1 implies the up-regulation of RPL27.	0.866202	0.155707
The up-regulation of EWSR1 implies the up-regulation of RPL37.	1	0.155707
The up-regulation of EWSR1 implies the up-regulation of RPL37A.	0.931133	0.151259
The up-regulation of EWSR1 implies the up-regulation of RPS29.	0.933101	0.155707
The up-regulation of EXOC4 implies the up-regulation of ARGLU1.	0.872679	0.163628
The up-regulation of EXOC4 implies the up-regulation of WDR5B.	0.805274	0.160482
The up-regulation of FAM118A implies the up-regulation of CES2.	0.791001	0.149523
The up-regulation of HNRNPU implies the up-regulation of EEF2.	0.819549	0.173177
The up-regulation of HRH1 implies the up-regulation of LINC00907.	0.868132	0.157986
The up-regulation of HUWE1 implies the up-regulation of RPS21.	0.810526	0.164931
The up-regulation of ITPRIPL2 implies the up-regulation of PNPT1.	0.90303	0.214844
The up-regulation of ITPRIPL2 implies the up-regulation of RPL37.	0.812987	0.167101
The up-regulation of KMT2E implies the up-regulation of RPL27.	0.945143	0.189887
The up-regulation of KMT2E implies the up-regulation of RPL37.	0.890286	0.189887
The up-regulation of KMT2E implies the up-regulation of RPL37A.	0.943529	0.184462
The up-regulation of KMT2E implies the up-regulation of RPS21.	0.904	0.217014
The up-regulation of KMT2E implies the up-regulation of RPS29.	0.945143	0.189887
The up-regulation of KRR1 implies the up-regulation of NCL.	0.928994	0.146701
The up-regulation of LINC00907 implies the up-regulation of RPL37.	0.812987	0.167101
The up-regulation of LONRF2 implies the up-regulation of LOC100505876.	0.776744	0.186632
The up-regulation of MAP4 implies the up-regulation of LOC100505876.	0.87027	0.16059
The up-regulation of MAP4 implies the up-regulation of RPP30.	0.783784	0.192708
The up-regulation of MAP4K4 implies the up-regulation of TRIM22.	0.786667	0.146484
The up-regulation of MDN1 implies the up-regulation of EIF3E.	0.831085	0.185004
The up-regulation of NAA50 implies the up-regulation of PNPT1.	0.796825	0.205078
The up-regulation of NAA50 implies the up-regulation of RPL37.	0.804082	0.159505
The up-regulation of NCL implies the up-regulation of RPL27.	0.812987	0.167101
The up-regulation of NCL implies the up-regulation of RPL37.	0.937662	0.167101
The up-regulation of NCL implies the up-regulation of RPL37A.	0.871658	0.162326
The up-regulation of NCL implies the up-regulation of RPS21.	0.836364	0.190972
The up-regulation of NCL implies the up-regulation of RPS29.	0.875325	0.167101
The up-regulation of NCL implies the up-regulation of SON.	0.772727	0.229167
The up-regulation of NUP98 implies the up-regulation of EEF2.	0.819549	0.173177
The up-regulation of PNPT1 implies the up-regulation of RPL37.	0.892437	0.193685
The up-regulation of PPP2R1A implies the up-regulation of ACTR3.	0.857778	0.146484
The up-regulation of PSMA3 implies the up-regulation of EEF2.	0.792208	0.150391
The up-regulation of PTBP3 implies the up-regulation of ORC6.	0.794872	0.152344
The up-regulation of RPL37 implies the up-regulation of RPS29, and the nonup-regulation of RPL37 implies the nonup-regulation of RPS29.	0.775176	0.185124
The up-regulation of RPL37A implies the up-regulation of RPL27, and the nonup-regulation of RPL37A implies the nonup-regulation of RPL27.	0.796418	0.1535
The up-regulation of RPL37A implies the up-regulation of RPS29, and the nonup-regulation of RPL37A implies the nonup-regulation of RPS29.	0.796418	0.1535

The up-regulation of RPP30 implies the up-regulation of LOC100505876.	0.8	0.208333
The up-regulation of RPS21 implies the up-regulation of RPL27.	0.902041	0.212674
The up-regulation of RPS21 implies the up-regulation of RPL37.	0.804082	0.212674
The up-regulation of RPS21 implies the up-regulation of RPL37A.	0.94958	0.206597
The up-regulation of RPS21 implies the up-regulation of RPS29.	0.853061	0.212674
The up-regulation of RSL24D1 implies the up-regulation of DDX3X.	0.797326	0.154188
The up-regulation of SF3A3 implies the up-regulation of APOC1P1.	0.816092	0.169922
The up-regulation of SF3B1 implies the up-regulation of RPS29.	0.828571	0.182292
The up-regulation of SON implies the up-regulation of EEF2.	0.809524	0.21875
The up-regulation of SON implies the up-regulation of RPL27.	0.828571	0.182292
The up-regulation of SON implies the up-regulation of RPL37.	1	0.182292
The up-regulation of SON implies the up-regulation of RPL37A.	0.882353	0.177083
The up-regulation of SON implies the up-regulation of RPS21.	0.85	0.208333
The up-regulation of SON implies the up-regulation of RPS29.	0.942857	0.182292
The up-regulation of SRSF1 implies the up-regulation of ARGLU1.	0.794872	0.152344
The up-regulation of SUPT5H implies the up-regulation of ARGLU1.	0.857988	0.146701
The up-regulation of TP53INP1 implies the up-regulation of KMT2E.	0.804348	0.159722
The up-regulation of TRIM22 implies the up-regulation of EEF2.	0.782313	0.191406
The up-regulation of TRIM22 implies the up-regulation of RPL27.	0.804082	0.159505
The up-regulation of TRIM22 implies the up-regulation of RPL37.	0.869388	0.159505
The up-regulation of TRIM22 implies the up-regulation of RPL37A.	0.865546	0.154948
The up-regulation of TRIM22 implies the up-regulation of RPS21.	0.885714	0.182292
The up-regulation of TRIM22 implies the up-regulation of RPS29.	0.869388	0.159505
The up-regulation of TRIM38 implies the up-regulation of RPL37.	0.872425	0.163303
The up-regulation of TSPYL2 implies the up-regulation of BLK.	0.790545	0.149197
The up-regulation of TUBA1B implies the up-regulation of DDX6.	0.82	0.173611
The up-regulation of UBA1 implies the up-regulation of NCL.	0.815385	0.169271
The up-regulation of UBA1 implies the up-regulation of PNPT1.	0.786667	0.146484
The up-regulation of UBA1 implies the up-regulation of SON.	0.933333	0.15625
The up-regulation of UBE2I implies the up-regulation of LOC100505876.	0.805405	0.16059
The up-regulation of UBL5 implies the up-regulation of EEF2.	0.930736	0.150391
The up-regulation of URB1 implies the up-regulation of CES2.	0.798742	0.155273
The up-regulation of VCP implies the up-regulation of NCL.	0.794872	0.152344
The up-regulation of WBP11 implies the up-regulation of DDX6.	0.786667	0.146484
The up-regulation of WDR5B implies the up-regulation of LOC100505876.	0.84	0.195312
The up-regulation of WDR5B implies the up-regulation of RPL37.	0.817143	0.170898
The up-regulation of ZNF207 implies the up-regulation of KMT2E.	0.804348	0.159722
The up-regulation of ZNF207 implies the up-regulation of PNPT1.	0.8	0.15625

Supplementary Table S3. Significantly enriched pathways in the ToppGene enrichment analysis of the B-cell network in Figure 1A.

ID	Name	Source	*p*-value	*q*-value Bonferroni	*q*-value FDR B&H	*q*-value FDR B&Y	Hit Count in Query List	Hit Count in Genome	Hit in Query List
1269649	Gene Expression	BioSystems: REACTOME	2.20E-10	1.80E-07	5.62E-08	4.09E-07	25	1844	RPL27,PPP2R1A,WBP11,EEF2,DDX46,RPL37,RPL37A,SRSF1,SF3B1,TP53INP1,UBE2I,SUPT5H,EIF2S3,PSMA3,EIF4E,RPP30,EIF3E,NUP98,SF3A3,RPS21,EIF3H,RPS29,KRR1,CNOT1,HNRNPU
1268678	Translation	BioSystems: REACTOME	2.27E-10	1.86E-07	5.62E-08	4.09E-07	10	165	RPL27,EEF2,RPL37,RPL37A,EIF2S3,EIF4E,EIF3E,RPS21,EIF3H,RPS29
1268686	GTP hydrolysis and joining of the 60S ribosomal subunit	BioSystems: REACTOME	2.74E-10	2.25E-07	5.62E-08	4.09E-07	9	119	RPL27,RPL37,RPL37A,EIF2S3,EIF4E,EIF3E,RPS21,EIF3H,RPS29
1268688	L13a-mediated translational silencing of Ceruloplasmin expression	BioSystems: REACTOME	2.74E-10	2.25E-07	5.62E-08	4.09E-07	9	119	RPL27,RPL37,RPL37A,EIF2S3,EIF4E,EIF3E,RPS21,EIF3H,RPS29
1268680	Cap-dependent Translation Initiation	BioSystems: REACTOME	4.92E-10	4.03E-07	6.72E-08	4.90E-07	9	127	RPL27,RPL37,RPL37A,EIF2S3,EIF4E,EIF3E,RPS21,EIF3H,RPS29
1268679	Eukaryotic Translation Initiation	BioSystems: REACTOME	4.92E-10	4.03E-07	6.72E-08	4.90E-07	9	127	RPL27,RPL37,RPL37A,EIF2S3,EIF4E,EIF3E,RPS21,EIF3H,RPS29
1268685	Ribosomal scanning and start codon recognition	BioSystems: REACTOME	8.08E-08	6.61E-05	8.00E-06	5.83E-05	6	63	EIF2S3,EIF4E,EIF3E,RPS21,EIF3H,RPS29
1268681	Formation of a pool of free 40S subunits	BioSystems: REACTOME	8.53E-08	6.99E-05	8.00E-06	5.83E-05	7	107	RPL27,RPL37,RPL37A,EIF3E,RPS21,EIF3H,RPS29
1268684	Translation initiation complex formation	BioSystems: REACTOME	8.89E-08	7.28E-05	8.00E-06	5.83E-05	6	64	EIF2S3,EIF4E,EIF3E,RPS21,EIF3H,RPS29
1268683	Activation of the mRNA upon binding of the cap-binding complex and eIFs, and subsequent binding to 43S	BioSystems: REACTOME	9.76E-08	8.00E-05	8.00E-06	5.83E-05	6	65	EIF2S3,EIF4E,EIF3E,RPS21,EIF3H,RPS29
1268677	Metabolism of proteins	BioSystems: REACTOME	1.95E-07	1.60E-04	1.46E-05	1.06E-04	20	1631	TUBA1B,RPL27,EEF2,UBA1,RPL37,RPL37A,UBE2I,CCT3,EIF2S3,PSMA3,EIF4E,TSPYL2,EIF3E,NUP98,RPS21,EIF3H,RPS29,ARCN1,VCP,EXOC4
M189	Ribosome	MSigDB C2 BIOCARTA (v7.3)	6.03E-07	4.94E-04	4.11E-05	3.00E-04	6	88	RPL27,RPL37,RPL37A,RPS21,RPS29,RSL24D1
1268691	Peptide chain elongation	BioSystems: REACTOME	8.37E-07	6.85E-04	5.27E-05	3.84E-04	6	93	RPL27,EEF2,RPL37,RPL37A,RPS21,RPS29
M39423	Translation Factors	MSigDB C2 BIOCARTA (v7.3)	1.11E-06	9.07E-04	6.23E-05	4.54E-04	5	53	EEF2,EIF2S3,EIF4E,EIF3E,EIF3H
1268690	Eukaryotic Translation Elongation	BioSystems: REACTOME	1.14E-06	9.34E-04	6.23E-05	4.54E-04	6	98	RPL27,EEF2,RPL37,RPL37A,RPS21,RPS29

1268682	Formation of the ternary complex, and subsequently, the 43S complex	BioSystems: REACTOME	1.34E-06	1.09E-03	6.83E-05	4.98E-04	5	55	EIF2S3,EIF3E,RPS21,EIF3H,RPS29
177876	RNA transport	BioSystems: KEGG	2.07E-06	1.70E-03	9.85E-05	7.17E-04	7	171	UBE2I,EIF2S3,EIF4E,RPP30,EIF3E,NUP98,EIF3H
1269688	Processing of Capped Intron-Containing Pre-mRNA	BioSystems: REACTOME	2.16E-06	1.77E-03	9.85E-05	7.17E-04	8	248	WBP11,DDX46,SRSF1,SF3B1,EIF4E,NUP98,SF3A3,HNRNPU
1383086	Major pathway of rRNA processing in the nucleolus and cytosol	BioSystems: REACTOME	3.02E-06	2.47E-03	1.30E-04	9.49E-04	7	181	RPL27,RPL37,RPL37A,RPP30,RPS21,RPS29,KRR1
1269716	Nonsense-Mediated Decay (NMD)	BioSystems: REACTOME	3.92E-06	3.21E-03	1.53E-04	1.11E-03	6	121	RPL27,PPP2R1A,RPL37,RPL37A,RPS21,RPS29
1269717	Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC)	BioSystems: REACTOME	3.92E-06	3.21E-03	1.53E-04	1.11E-03	6	121	RPL27,PPP2R1A,RPL37,RPL37A,RPS21,RPS29
1427846	rRNA processing in the nucleus and cytosol	BioSystems: REACTOME	4.62E-06	3.79E-03	1.72E-04	1.25E-03	7	193	RPL27,RPL37,RPL37A,RPP30,RPS21,RPS29,KRR1
M2044	Spliceosome	MSigDB C2 BIOCARTA (v7.3)	5.19E-06	4.25E-03	1.85E-04	1.35E-03	6	127	WBP11,DDX46,SRSF1,SF3B1,SF3A3,HNRNPU
1383085	rRNA processing	BioSystems: REACTOME	6.45E-06	5.28E-03	2.20E-04	1.60E-03	7	203	RPL27,RPL37,RPL37A,RPP30,RPS21,RPS29,KRR1
125136	Spliceosome	BioSystems: KEGG	7.07E-06	5.79E-03	2.32E-04	1.69E-03	6	134	WBP11,DDX46,SRSF1,SF3B1,SF3A3,HNRNPU
1269056	Infectious disease	BioSystems: REACTOME	7.80E-06	6.39E-03	2.46E-04	1.79E-03	9	393	RPL27,EEF2,RPL37,RPL37A,SUPT5H,PSMA3,NUP98,RPS21,RPS29
1269115	Influenza Viral RNA Transcription and Replication	BioSystems: REACTOME	8.37E-06	6.86E-03	2.54E-04	1.85E-03	6	138	RPL27,RPL37,RPL37A,NUP98,RPS21,RPS29
1269109	Influenza Life Cycle	BioSystems: REACTOME	1.20E-05	9.85E-03	3.52E-04	2.56E-03	6	147	RPL27,RPL37,RPL37A,NUP98,RPS21,RPS29
M39495	Cytoplasmic Ribosomal Proteins	MSigDB C2 BIOCARTA (v7.3)	1.54E-05	1.26E-02	4.28E-04	3.12E-03	5	90	RPL27,RPL37,RPL37A,RPS21,RPS29
83036	Ribosome	BioSystems: KEGG	1.57E-05	1.28E-02	4.28E-04	3.12E-03	6	154	RPL27,RPL37,RPL37A,RPS21,RPS29,RSL24D1
1269120	Viral mRNA Translation	BioSystems: REACTOME	1.81E-05	1.48E-02	4.64E-04	3.38E-03	5	93	RPL27,RPL37,RPL37A,RPS21,RPS29
1269108	Influenza Infection	BioSystems: REACTOME	1.81E-05	1.49E-02	4.64E-04	3.38E-03	6	158	RPL27,RPL37,RPL37A,NUP98,RPS21,RPS29
1339156	Selenocysteine synthesis	BioSystems: REACTOME	2.11E-05	1.73E-02	5.21E-04	3.79E-03	5	96	RPL27,RPL37,RPL37A,RPS21,RPS29
1268692	Eukaryotic Translation Termination	BioSystems: REACTOME	2.21E-05	1.81E-02	5.21E-04	3.79E-03	5	97	RPL27,RPL37,RPL37A,RPS21,RPS29
M7721	Eukaryotic protein translation	MSigDB C2 BIOCARTA (v7.3)	2.23E-05	1.82E-02	5.21E-04	3.79E-03	3	16	EEF2,EIF2S3,EIF4E

1269718	Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)	BioSystems: REACTOME	2.57E-05	2.10E-02	5.84E-04	4.25E-03	5	100	RPL27,RPL37,RPL37A,RPS21,RPS29
M40040	nsp1 from SARS-CoV-2 inhibits translation initiation in the host cell	MSigDB C2 BIOCARTA (v7.3)	2.70E-05	2.21E-02	5.97E-04	4.35E-03	3	17	EIF2S3,EIF3E,EIF3H
1268854	Disease	BioSystems: REACTOME	3.37E-05	2.76E-02	7.26E-04	5.29E-03	12	867	RPL27,PPP2R1A,EEF2,RPL37,RPL37A,SUPT5H,PSMA3,NUP98,FGF5,RPS21,RPS29,VCP
1269690	mRNA Splicing - Major Pathway	BioSystems: REACTOME	4.83E-05	3.95E-02	1.01E-03	7.39E-03	6	188	WBP11,DDX46,SRSF1,SF3B1,SF3A3,HNRNPU
1268689	SRP-dependent cotranslational protein targeting to membrane	BioSystems: REACTOME	5.24E-05	4.29E-02	1.07E-03	7.82E-03	5	116	RPL27,RPL37,RPL37A,RPS21,RPS29
1269689	mRNA Splicing	BioSystems: REACTOME	6.09E-05	4.99E-02	1.22E-03	8.86E-03	6	196	WBP11,DDX46,SRSF1,SF3B1,SF3A3,HNRNPU
1339149	Selenoamino acid metabolism	BioSystems: REACTOME	6.93E-05	5.68E-02	1.35E-03	9.85E-03	5	123	RPL27,RPL37,RPL37A,RPS21,RPS29
M39406	mRNA Processing	MSigDB C2 BIOCARTA (v7.3)	1.01E-04	8.23E-02	1.91E-03	1.39E-02	5	133	SRSF1,SF3B1,SUPT5H,SF3A3,HNRNPU
M5374	SARS Coronavirus Protease	MSigDB C2 BIOCARTA (v7.3)	2.52E-04	2.07E-01	4.70E-03	3.42E-02	2	7	EIF4E,NCL
M15247	Ubiquitin mediated proteolysis	MSigDB C2 BIOCARTA (v7.3)	1.28E-03	1.00E+00	2.33E-02	1.70E-01	4	135	UBA1,UBE2I,HUWE1,ANAPC5
83056	Ubiquitin mediated proteolysis	BioSystems: KEGG	1.35E-03	1.00E+00	2.41E-02	1.75E-01	4	137	UBA1,UBE2I,HUWE1,ANAPC5
1270158	Metabolism of amino acids and derivatives	BioSystems: REACTOME	1.73E-03	1.00E+00	3.02E-02	2.20E-01	6	367	RPL27,RPL37,RPL37A,PSMA3,RPS21,RPS29
1470929	Protein methylation	BioSystems: REACTOME	2.00E-03	1.00E+00	3.28E-02	2.39E-01	2	19	EEF2,VCP
M194	Proteasome Complex	MSigDB C2 BIOCARTA (v7.3)	2.00E-03	1.00E+00	3.28E-02	2.39E-01	2	19	UBA1,PSMA3
M16991	Skeletal muscle hypertrophy is regulated via AKT/mTOR pathway	MSigDB C2 BIOCARTA (v7.3)	2.00E-03	1.00E+00	3.28E-02	2.39E-01	2	19	EIF2S3,EIF4E

Supplementary Table S4. The cutoff values to stratify high expression and low expression of genes in Figure 3B-C.

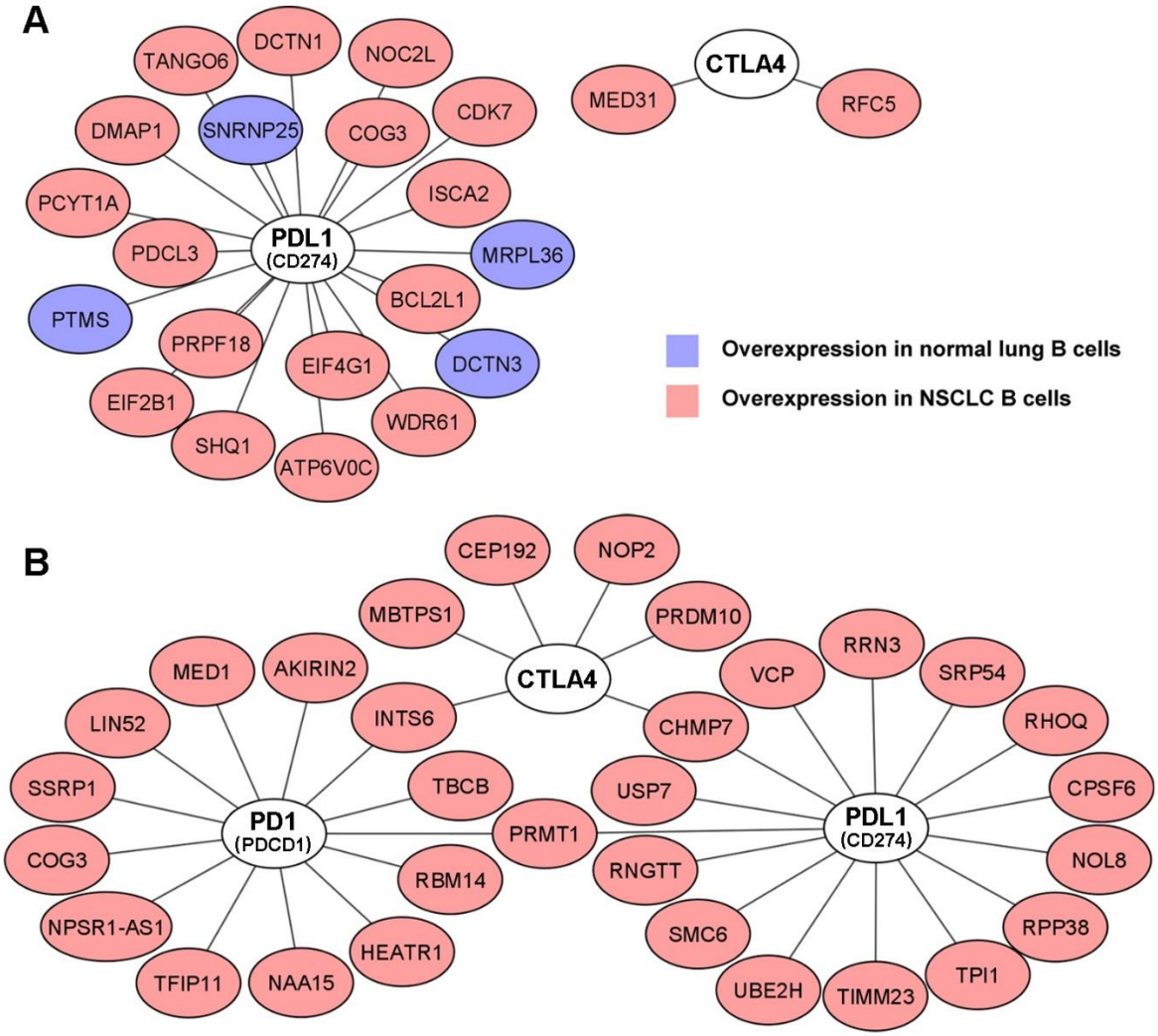
gene	TCGA-LUAD & TCGA-LUSC	LUAD Proteomic
HLA-DRA	15.76	8.87
HLA-DRB1	13.36	7.76
OAS1	11.44	6.88
CD74	16.55	7.95

Supplementary Table S5. Detailed information of CMap input gene lists (Figure 5A).

	gene	category
up gene list	CCND2	Drug sensitive gene
	CD24	Epithelial gene
	CDH1	Epithelial gene
	CLDN7	Epithelial gene
	DDR1	Epithelial gene
	EPCAM	Epithelial gene
	ESRP1	Epithelial gene
	ESRP2	Epithelial gene
	IL2RA	Drug sensitive gene
	KRT19	Epithelial gene
	RAB25	Epithelial gene
	TIGIT	Drug sensitive gene
	TSC22D3	Drug sensitive gene
down gene list	ARCN1	Proliferation gene
	CDK7	Drug resistant gene
	EEF2	Proliferation gene
	FN1	Mesenchymal gene
	HLA-DRB1	Drug resistant gene
	HRH1	Hazard gene in the 9-gene model
	MAP4	Hazard gene in the 9-gene model / Drug resistant gene
	PPP2R1A	Hazard gene in the 9-gene model
	PSMA3	Proliferation gene
	SF3B1	Proliferation gene
	SRSF1	Proliferation gene
	TUBA1B	Hazard gene in the 9-gene model
	VCP	Hazard gene in the 9-gene model / Proliferation gene
	VIM	Mesenchymal gene
	ZEB1	Mesenchymal gene

Supplementary Table S6. The significant ($p < 0.05$, connectivity score > 0.9) compounds from CMap.

src_set_id	cell_iname	pert_type	compounds
CALCINEURIN_INHIBITOR	A549	TRT_CP	INCA-6, tacrolimus, cyclosporin-a, tacrolimus
CORTICOSTEROID_AGONIST	HCC515	TRT_CP	dexamethasone, diflorasone, fluocinolone, hydrocortisone, triamcinolone
CP_BCL_INHIBITOR	HCC515	TRT_CP	BH3I-1, BCL2-inhibitor, gossypol, ABT-737, navitoclax, TW-37, obatoclax, HA-14-1
CP_FGFR_INHIBITOR	A549	TRT_CP	PD-173074, dovitinib, brivanib, orantinib
CP_JAK_INHIBITOR	HCC515	TRT_CP	JAK3-inhibitor-I, JAK3-Inhibitor-II, JAK3-inhibitor-VI, TG-101348, lestaurtinib
CP_T_TYPE_CALCIUM_CHANNEL_BLOCKER	A549	TRT_CP	dichlorobenzamil, KB-R7943, mibefradil, NNC-55-0396, penfluridol
GROWTH_FACTOR_RECEPTOR_INHIBITOR	HCC515	TRT_CP	GW-441756, danusertib, lestaurtinib
LEUCINE_RICH_REPEAT_KINASE_INHIBITOR	A549	TRT_CP	GW-5074, indirubin, XMD-1150, XMD-885



Supplementary Figure S1. Tumor-specific B-cell proliferation networks involving *PD1 (PDCD1), PDL1 (CD274),* and *CTLA4* in NSCLC. (A) Proliferation networks ($p < 0.05$, one-tailed *z*-tests) involving *PD1*, *PDL1*, and *CTLA4* present only in normal lung B cells. **(B)** Proliferation networks ($p < 0.05$, one-tailed *z*-tests) involving *PD1*, *PDL1*, and *CTLA4* present only in NSCLC tumor B cells. Each gene associated with the three immune checkpoint inhibitors was significantly differentially expressed in NSCLC tumor-associated B cells vs. normal lung B cells. Each gene had a significant impact (dependency score < –0.5) on proliferation in CRISPR-Cas9 or RNAi assays in more than 50% of the tested human NSCLC cell lines.

Supplementary Table S7. Biological context of edges in Supplementary Figure 1A network (Precision Threshold: 0.6179, Scope Threshold: 0.0278; *p*-value < 0.05; one-tailed *z*-tests).

Biological context	Precision	Scope
The up-regulation of PDL1 (CD274) implies the up-regulation of ATP6V0C.	0.652174	0.029948
The up-regulation of PDL1 (CD274) implies the up-regulation of BCL2L1.	0.652174	0.029948
The up-regulation of PDL1 (CD274) implies the up-regulation of CDK7.	0.652174	0.029948
The up-regulation of PDL1 (CD274) implies the up-regulation of COG3.	0.627907	0.027995
The up-regulation of PDL1 (CD274) implies the up-regulation of DCTN1.	0.627907	0.027995
The up-regulation of PDL1 (CD274) implies the up-regulation of DCTN3.	0.627907	0.027995
The up-regulation of PDL1 (CD274) implies the up-regulation of DMAP1.	0.640449	0.028971
The up-regulation of PDL1 (CD274) implies the up-regulation of EIF2B1.	0.627907	0.027995
The up-regulation of PDL1 (CD274) implies the up-regulation of EIF4G1.	0.648352	0.029622
The up-regulation of PDL1 (CD274) implies the up-regulation of ISCA2.	0.644444	0.029297
The up-regulation of PDL1 (CD274) implies the up-regulation of MRPL36.	0.636364	0.028646
The up-regulation of PDL1 (CD274) implies the up-regulation of NOC2L.	0.636364	0.028646
The up-regulation of PDL1 (CD274) implies the up-regulation of PCYT1A.	0.632184	0.02832
The up-regulation of PDL1 (CD274) implies the up-regulation of PDCL3.	0.648352	0.029622
The up-regulation of PDL1 (CD274) implies the up-regulation of PRPF18.	0.632184	0.02832
The up-regulation of PDL1 (CD274) implies the up-regulation of PTMS.	0.636364	0.028646
The up-regulation of PDL1 (CD274) implies the up-regulation of SHQ1.	0.640449	0.028971
The up-regulation of PDL1 (CD274) implies the up-regulation of SNRNP25.	0.640449	0.028971
The up-regulation of PDL1 (CD274) implies the up-regulation of TANGO6.	0.632184	0.02832
The up-regulation of PDL1 (CD274) implies the up-regulation of WDR61.	0.636364	0.028646
The up-regulation of CTLA4 implies the up-regulation of MED31.	0.632184	0.02832
The up-regulation of CTLA4 implies the up-regulation of RFC5.	0.632184	0.02832

Supplementary Table S8. Biological context of edges in Supplementary Figure 1B network (Precision Threshold: 0.6179, Scope Threshold: 0.0278; *p*-value < 0.05; one-tailed *z*-tests).

Biological context	Precision	Scope
The up-regulation of PDL1 (CD274) implies the up-regulation of CHMP7.	0.725714	0.037977
The up-regulation of PDL1 (CD274) implies the up-regulation of CPSF6.	0.695238	0.03418
The up-regulation of PDL1 (CD274) implies the up-regulation of NOL8.	0.709091	0.035807
The up-regulation of PDL1 (CD274) implies the up-regulation of PRMT1.	0.704615	0.035265
The up-regulation of PDL1 (CD274) implies the up-regulation of RHOQ.	0.657143	0.030382
The up-regulation of PDL1 (CD274) implies the up-regulation of RNGTT.	1	0.029839
The up-regulation of PDL1 (CD274) implies the up-regulation of RPP38.	0.704615	0.035265
The up-regulation of PDL1 (CD274) implies the up-regulation of RRN3.	0.685246	0.033095
The up-regulation of PDL1 (CD274) implies the up-regulation of SMC6.	0.690323	0.033637
The up-regulation of PDL1 (CD274) implies the up-regulation of SRP54.	1	0.028212
The up-regulation of PDL1 (CD274) implies the up-regulation of TIMM23.	0.690323	0.033637
The up-regulation of PDL1 (CD274) implies the up-regulation of TPI1.	0.650909	0.029839
The up-regulation of PDL1 (CD274) implies the up-regulation of UBE2H.	1	0.032552
The up-regulation of PDL1 (CD274) implies the up-regulation of USP7.	0.668966	0.031467
The up-regulation of PDL1 (CD274) implies the up-regulation of VCP.	0.657143	0.030382

The up-regulation of CTLA4 implies the up-regulation of CEP192.	0.661972	0.030816
The up-regulation of CTLA4 implies the up-regulation of CHMP7.	0.657143	0.030382
The up-regulation of CTLA4 implies the up-regulation of INTS6.	0.630769	0.028212
The up-regulation of CTLA4 implies the up-regulation of MBTPS1.	0.641791	0.02908
The up-regulation of CTLA4 implies the up-regulation of NOP2.	0.671233	0.031684
The up-regulation of CTLA4 implies the up-regulation of PRDM10.	0.688312	0.03342
The up-regulation of PD1 (PDCD1) implies the up-regulation of AKIRIN2.	0.661972	0.030816
The up-regulation of PD1 (PDCD1) implies the up-regulation of COG3.	0.671233	0.031684
The up-regulation of PD1 (PDCD1) implies the up-regulation of HEATR1.	0.7	0.034722
The up-regulation of PD1 (PDCD1) implies the up-regulation of INTS6.	0.630769	0.028212
The up-regulation of PD1 (PDCD1) implies the up-regulation of LIN52.	1	0.028212
The up-regulation of PD1 (PDCD1) implies the up-regulation of MED1.	0.652174	0.029948
The up-regulation of PD1 (PDCD1) implies the up-regulation of NAA15.	0.630769	0.028212
The up-regulation of PD1 (PDCD1) implies the up-regulation of NPSR1-AS1.	0.666667	0.03125
The up-regulation of PD1 (PDCD1) implies the up-regulation of PRMT1.	0.630769	0.028212
The up-regulation of PD1 (PDCD1) implies the up-regulation of RBM14.	1	0.032552
The up-regulation of PD1 (PDCD1) implies the up-regulation of SSRP1.	0.7	0.034722
The up-regulation of PD1 (PDCD1) implies the up-regulation of TBCB.	0.652174	0.029948
The up-regulation of PD1 (PDCD1) implies the up-regulation of TFIP11.	0.7	0.034722