

Table S1 Differential gene expression analysis identified 14 downregulated and 53 upregulated IFN- β -associated genes.

gene	conMean	treatMean	logFC	pValue	fd
CD63	30.10657	313.0741	3.378354	0.000172	0.002036
CD70	0.555679	2.200962	1.98581	0.000832	0.002797
E2F1	3.505146	10.48335	1.580554	0.007463	0.013579
FTL	651.6117	3210.001	2.300489	0.000599	0.002369
GAPDH	512.1522	1157.601	1.176493	0.001146	0.00318
GSTP1	32.61208	108.6335	1.735991	0.000337	0.002036
LGALS1	17.39993	328.6125	4.239234	0.000206	0.002036
MNT	6.166503	3.011482	-1.03398	0.000325	0.002036
NDUFB3	20.31884	32.20039	0.66426	0.021104	0.033464
NFKBIA	10.93926	56.22313	2.361648	0.000779	0.002703
PIN1	27.5438	14.49285	-0.92639	0.001473	0.003803
PRDX1	83.12447	162.8397	0.970107	0.00152	0.003833
PRDX6	34.97637	82.92948	1.245504	0.000619	0.002369
RPLP1	42.436	203.9833	2.26509	0.000149	0.002036
RPS2	14.01768	276.6118	4.302543	0.000144	0.002036
S100A2	0.755174	2.902967	1.942647	0.000237	0.002036
SEC61B	12.62775	46.94838	1.894478	0.000144	0.002036
SHC1	3.090129	19.56899	2.66283	0.000206	0.002036
TMSB10	662.5164	1667.381	1.331555	0.003943	0.007816
TP53I3	1.08063	8.602309	2.992851	0.000144	0.002036
TPM2	3.217674	18.44204	2.518909	0.000916	0.002906
TRAF3	5.798808	3.876128	-0.58114	0.002193	0.00507
TSHR	0.52064	1.21914	1.227504	0.008086	0.014477
TXN	42.52225	70.3807	0.726962	0.01964	0.031595
XRCC5	24.69804	41.33577	0.742994	0.000373	0.002072
AKT1	5.828089	11.30404	0.955743	0.001341	0.003545
AMPD2	17.22854	9.199601	-0.90516	0.007264	0.013439
BCL2L2	41.065	8.016368	-2.35689	0.000144	0.002036
BCL3	1.536024	7.403995	2.269103	0.000507	0.002369
CASP7	1.701272	4.602387	1.435769	0.000428	0.002262
CASP9	3.27981	4.734607	0.529632	0.022131	0.034119
CHST15	7.984939	5.270313	-0.59939	0.025479	0.038742
CLK2	5.013503	9.431446	0.91166	0.002328	0.005274
CXCL9	0.522583	2.959908	2.50182	0.000303	0.002036
DDIT3	10.53898	39.86037	1.91922	0.004295	0.008364
DNAJA1	81.49636	57.45116	-0.5044	0.016566	0.027444
DST	11.587	4.898513	-1.24209	0.000619	0.002369
ENO3	1.078342	1.936191	0.844407	0.002866	0.006118
ETV4	0.449016	5.842307	3.7017	0.000524	0.002369
FAS	1.211993	5.397376	2.154877	0.000619	0.002369
FGF9	2.489786	1.05976	-1.23228	0.002193	0.00507
HLA-B	13.25433	323.677	4.610019	0.000185	0.002036
HLA-C	21.08252	260.7631	3.62862	0.000214	0.002036
HRK	4.302541	1.496812	-1.5233	0.000887	0.002896
HSP90B1	53.99334	105.0129	0.959713	0.002193	0.00507
IFITM3	37.89578	210.6592	2.474802	0.001146	0.00318
IGFBP5	15.80209	156.8898	3.311564	0.001075	0.00318
IL15RA	0.909774	1.710014	0.910427	0.000337	0.002036
IL18	1.533749	6.167387	2.007597	0.00111	0.00318
IRF1	1.646495	5.161978	1.648526	0.001146	0.00318
KDM5A	2.286764	3.631279	0.66717	0.001943	0.004792
MAP3K14	1.968346	4.329348	1.137166	0.000348	0.002036
MAPK1	37.5546	15.92404	-1.23778	0.00126	0.003411
MAPK10	16.65285	4.83445	-1.78434	0.000683	0.002529
MC4R	1.741701	0.887979	-0.9719	0.000328	0.002036
MMP7	0.39799	4.360563	3.453711	0.003039	0.006247
NFKB1	3.08316	5.389852	0.805836	0.002546	0.005653
PER2	4.063261	2.574965	-0.65809	0.006518	0.012263
PTPRZ1	9.053498	136.0179	3.909177	0.000542	0.002369
RPGR	1.267263	2.035992	0.684016	0.002952	0.006181
STAT1	11.88487	29.58109	1.315548	0.002866	0.006118
TIMP3	1.351658	2.491341	0.882192	0.014275	0.024759
TLX1	0.606327	1.01475	0.742957	0.000764	0.002703
TNFSF14	0.682826	1.188035	0.798987	0.003129	0.006316
TP53	1.339876	18.70788	3.803475	0.000179	0.002036
TRAIIP	1.100777	2.933994	1.414344	0.000314	0.002036
VCAM1	0.722361	10.0756	3.802003	0.000619	0.002369

Table S2 Univariate Cox regression model found 5 survival-related genes

id	HR	HR.95L	HR.95H	pvalue
PRDX1	1.002986	1.000224	1.005755	0.034085
SEC61B	1.018342	1.005051	1.03181	0.006698
TXN	1.007272	1.000557	1.014032	0.03375
XRCC5	1.025477	1.005747	1.045595	0.011145
BCL2L2	0.944842	0.894724	0.997768	0.041319

Table S3 Lasso-penalized Cox analysis identified 5 genes to construct the prognostic model

id	ftime	fustat	PRDX1	SEC61B	TXN	XRCC5	BCL2L2	riskScore	risk
TCGA-19-5960	0.013699	0	140.3251	29.66717	42.88298	69.56536	8.375261	1.564664	high
TCGA-06-5418	0.019178	0	118.8639	39.67598	64.92846	33.20539	12.76465	0.848628	low
TCGA-12-1597	0.054795	0	142.8102	49.3957	51.56646	40.8878	6.976729	1.180437	low
TCGA-32-4213	0.071233	0	138.0042	40.21844	32.29656	40.58741	5.224391	1.129728	low
TCGA-14-0871	0.076712	0	98.02954	84.35446	76.9631	69.41546	6.750546	1.831538	high
TCGA-14-0790	0.093151	0	173.3056	56.72675	67.44097	35.26562	3.706071	1.260257	high
TCGA-32-2616	0.123288	0	136.5546	37.67904	84.84546	41.9269	7.657441	1.167249	low
TCGA-28-2509	0.128767	0	167.6415	46.34816	100.2417	33.30769	5.840747	1.168708	low
TCGA-06-2558	0.134247	0	206.7004	54.56901	64.06912	50.17674	9.021406	1.468887	high
TCGA-27-1831	0.147945	0	224.5134	85.01386	76.92627	30.65479	1.804257	1.459245	high
TCGA-19-4065	0.156164	0	111.5957	80.26543	175.2979	37.46402	16.77551	1.189536	high
TCGA-76-4928	0.186301	0	126.2451	59.36295	101.6404	43.99712	7.968783	1.308979	high
TCGA-02-2483	0.224658	0	103.1318	78.0226	221.6511	82.41142	6.414456	2.271565	high
TCGA-06-2565	0.257534	0	134.3475	34.55243	41.9556	39.66919	9.606255	1.002286	low
TCGA-06-0221	0.263014	0	109.8401	20.9592	35.09466	45.88823	22.92124	0.718923	low
TCGA-19-2620	0.268493	0	171.5653	34.255	45.71353	24.66921	13.49417	0.719022	low
TCGA-08-0386	0.268493	0	157.493	41.18219	81.36895	60.2722	11.21148	1.479606	high
TCGA-28-5208	0.271233	0	233.758	52.12235	82.99764	57.8433	7.005562	1.717449	high
TCGA-19-1787	0.273973	0	134.0508	38.18114	62.76541	51.43739	5.878342	1.343401	high
TCGA-06-5412	0.279452	0	158.7072	41.60444	49.7972	36.22516	9.70667	1.027343	low
TCGA-19-1389	0.284932	0	143.523	45.00921	147.8676	42.3617	8.237626	1.305182	high
TCGA-26-5134	0.287671	0	143.8337	71.34361	87.63025	42.11121	4.609562	1.41316	high
TCGA-06-2561	0.30137	0	129.4165	26.95697	27.06816	35.69237	9.664078	0.860468	low
TCGA-06-0174	0.309589	0	135.2137	42.86477	42.50185	58.87772	5.421822	1.428654	high
TCGA-27-2524	0.312329	0	154.5816	100.9761	166.88	43.40007	6.635765	1.674917	high
TCGA-32-5222	0.315068	0	249.77	52.27965	88.19906	50.01179	4.78742	1.657946	high
TCGA-41-5651	0.326027	0	152.466	40.48911	116.6978	60.24457	10.65221	1.530896	high
TCGA-06-0158	0.331507	0	120.1098	32.92711	39.32712	32.09478	10.14526	0.814416	low
TCGA-06-0138	0.345205	0	152.6425	54.89752	85.10129	28.5542	2.827759	1.135179	low
TCGA-14-2554	0.347945	0	168.2275	63.95563	73.87036	35.23214	5.07638	1.266138	high
TCGA-28-5204	0.350685	0	127.6719	28.99288	71.11637	44.76476	9.008068	1.112678	low
TCGA-19-1390	0.356164	0	48.07005	36.19385	27.43887	37.05623	5.534106	0.866978	low
TCGA-06-0646	0.364384	0	99.09356	35.56775	46.89974	43.21746	4.947798	1.111174	low
TCGA-12-0618	0.364384	0	67.443	54.4239	120.9357	59.02999	9.576032	1.448237	high
TCGA-28-5209	0.369863	0	229.5587	38.23931	69.0032	45.6831	7.450065	1.390104	high
TCGA-26-5136	0.372603	0	192.7499	71.43491	108.2516	49.15737	12.54333	1.498292	high
TCGA-12-5295	0.389041	0	301.1052	63.88231	125.8404	46.04834	2.670659	1.835403	high
TCGA-32-1970	0.394521	0	108.0138	22.59641	25.95279	37.36755	9.544778	0.831774	low
TCGA-28-2499	0.39726	0	287.5934	24.36353	31.9343	35.21199	3.168737	1.271774	high
TCGA-02-2485	0.4	0	122.7897	37.32248	42.40419	64.6278	6.116927	1.525002	high
TCGA-06-5413	0.4	0	235.1694	60.04048	59.99449	60.03172	5.626302	1.792517	high
TCGA-06-0139	0.405479	0	180.1379	62.03357	101.702	28.21095	3.903835	1.216003	high
TCGA-06-0744	0.413699	0	142.3851	54.56737	29.33902	31.89612	7.657043	0.992391	low
TCGA-06-5411	0.419178	0	174.0267	48.40504	97.56886	39.33645	16.05117	1.084493	low
TCGA-06-0686	0.421918	0	193.3583	52.96145	57.03175	39.39186	7.497999	1.260213	high
TCGA-06-0129	0.430137	1	64.39262	28.57973	30.56102	47.85222	9.750011	0.975217	low
TCGA-06-2567	0.438356	1	171.171	34.98164	61.42383	57.83904	6.989487	1.488365	high
TCGA-06-5408	0.452055	1	180.6637	52.13031	74.65464	54.80463	5.087023	1.591817	high
TCGA-76-4927	0.487671	1	195.3624	54.4249	56.66848	39.63224	9.78166	1.227297	high
TCGA-06-0878	0.487671	1	195.2847	50.80717	92.53551	49.44408	5.464186	1.532894	high
TCGA-06-0644	0.490411	1	176.7468	77.41673	173.0849	52.90885	4.969178	1.820638	high
TCGA-14-0789	0.512329	1	85.53151	30.52127	53.45421	32.2351	9.854335	0.769117	low
TCGA-27-1837	0.512329	1	170.7995	39.68927	45.59562	28.03151	8.16817	0.915896	low
TCGA-12-5299	0.517808	1	201.5399	71.76869	99.38701	43.24753	5.812191	1.53445	high
TCGA-76-4929	0.545205	1	132.1505	47.63228	72.17132	59.83373	4.660162	1.578536	high
TCGA-06-0210	0.558904	1	132.6637	23.60292	30.64785	36.9697	10.20039	0.867921	low
TCGA-32-2638	0.578082	1	138.0039	35.93231	54.23497	31.32749	8.398541	0.906184	low
TCGA-76-4931	0.59726	1	206.52	46.3373	45.81722	44.76383	11.05181	1.260377	high
TCGA-15-0742	0.613699	1	140.2915	51.77297	51.50417	39.23977	7.642791	1.143086	low
TCGA-06-0211	0.632877	1	137.4622	40.34184	37.00743	43.08321	7.17278	1.141582	low
TCGA-16-1045	0.632877	1	189.5629	21.41512	33.77338	35.13166	6.343518	1.012997	low
TCGA-06-0750	0.635616	1	214.1866	67.80955	105.8879	28.75555	5.671292	1.285691	high
TCGA-27-2519	0.635616	1	246.4598	54.09209	75.02524	41.32633	3.477736	1.508975	high
TCGA-28-2513	0.643836	1	92.4272	46.08829	59.67444	31.23411	6.011135	0.927367	low
TCGA-02-2486	0.649315	1	202.8742	51.72237	134.1644	42.58534	9.683138	1.399915	high
TCGA-28-5207	0.660274	1	249.7809	36.48221	56.77898	45.59285	8.330949	1.380562	high
TCGA-26-5139	0.663014	1	142.0489	42.97583	59.73121	31.55857	9.442725	0.938152	low
TCGA-27-1834	0.668493	1	173.8029	40.20974	64.40529	39.56591	7.562747	1.175947	low
TCGA-41-3915	0.70137	1	110.5389	50.78608	65.69816	35.63073	4.583821	1.102399	low
TCGA-06-0219	0.70137	1	284.344	71.72125	116.4953	35.94176	3.115479	1.633877	high
TCGA-14-1034	0.717808	1	78.00486	36.94946	44.68549	69.12016	13.87659	1.365421	high
TCGA-28-5216	0.745205	1	233.103	68.47629	126.0057	43.57916	7.246914	1.592525	high
TCGA-06-0130	0.758904	1	151.6874	59.51141	153.388	37.89631	5.606221	1.370916	high
TCGA-32-1980	0.764384	1	179.2239	34.27197	96.54481	28.55438	23.48885	0.672392	low
TCGA-32-2634	0.772603	1	162.9924	51.91409	74.72735	77.57591	6.695917	1.942323	high
TCGA-27-2523	0.772603	1	306.2665	52.58156	49.13376	49.97735	8.001871	1.637298	high
TCGA-26-5133	0.780822	1	107.9234	52.95517	90.52421	50.55217	11.62783	1.272051	high
TCGA-12-0821	0.783562	1	213.9815	41.63904	49.7821	51.27075	4.013296	1.523024	high
TCGA-06-0743	0.786301	1	132.5178	47.62646	57.33837	20.91613	4.887153	0.83911	low
TCGA-26-5135	0.794521	1	97.98138	51.72713	38.20319	28.82615	11.2631	0.779261	low
TCGA-06-0745	0.810959	1	200.6202	70.09513	73.81489	34.8811	3.279742	1.385898	high
TCGA-19-2629	0.816438	1	149.4207	47.73915	59.70498	57.72573	5.361791	1.538915	high
TCGA-06-0649	0.821918	1	184.1714	42.66877	55.02432	26.83747	3.84453	1.036828	low
TCGA-19-2625	0.835616	1	168.2398	42.77317	56.27156	27.66384	4.121188	1.019349	low
TCGA-14-1823	0.841096	1	244.1291	57.43299	142.4175	42.67542	2.630909	1.663639	high
TCGA-14-0817	0.876712	1	292.8486	82.6027	139.8963	46.5586	2.909204	1.935509	high
TCGA-06-0125	0.882192	1	98.89503	26.41783	54.53219	34.74653	7.94453	0.861279	low
TCGA-12-3653	0.89589	1	150.4582	26.95858	15.78032	44.80021	3.654312	1.174116	low
TCGA-06-5859	0.89589	1	184.9683	39.76688	65.82692	47.17211	6.482991	1.358275	high
TCGA-27-1835	0.89863	1	199.1631	40.6902	57.34481	29.29569	4.377708	1.092263	low
TCGA-16-0846	0.90137	1	194.5448	39.89706	53.27018	30.62852	12.18135	0.936065	low
TCGA-06-2557	0.936986	1	202.47	28.04383	47.36417	47.15006	9.956309	1.233923	high
TCGA-06-5417	0.947945	1	153.9124	48.00988	39.71992	73.74442	4.761712	1.824675	high
TCGA-06-5416	0.950685	1	221.3037	63.22576	139.8653	46.6906	3.720026	1.6967	high
TCGA-14-1825	0.961644	1	256.05	58.68413	56.40678	56.05472	3.89726	1.782033	high
TCGA-28-1753	0.980822	1	171.5687	40.83743	52.40134	40.02558	7.762524	1.161219	low
TCGA-41-2571	0.986301	1	157.2702	51.18373	155.181	31.91235	10.95407	1.122988	low
TCGA-06-5414	1.019178	1	110.792	36.88267	27.16114	37.16333	8.885071	0.917248	low
TCGA-27-2526	1.049315	1	464.1159	74.75511	96.82345	29.17577	2.742156	1.832725	high
TCGA-12-0619	1.054795	1	145.8938	39.38512	88.58783	50.39442	13.92942</		

Table S4 The result is validated on the GEO datasets (GSE83300)

id	futime	fustat	PRDX1	SEC61B	TXN	XRCC5	BCL2L2	riskScore	risk
GSM2198606	1.421096	1	158.5011	47.44586	70.23023	43.02052	6.151619	1.283959	high
GSM2198621	1.089041	1	158.6632	45.31044	67.63565	40.81352	8.719337	1.176295	low
GSM2198638	1.248493	1	159.0652	46.06398	68.78135	43.68051	8.227831	1.245121	high
GSM2198650	0.810411	1	162.2663	47.31064	71.20021	43.43334	10.75034	1.203611	high
GSM2198635	1.431781	1	160.879	43.46473	70.48607	36.49387	14.22017	0.98221	low
GSM2198625	0.961644	1	161.0721	44.92775	70.02774	36.63123	13.75186	1.00116	low
GSM2198647	0.507945	1	162.0038	48.29496	70.6601	41.88264	4.096471	1.316984	high
GSM2198631	1.132603	1	160.2842	46.93892	70.90604	41.20961	5.462799	1.266941	high
GSM2198649	1.596986	1	158.1686	47.78961	71.58481	43.75235	5.911007	1.305436	high
GSM2198640	0.756986	0	161.1215	43.29883	70.36428	35.91489	15.40181	0.946496	low
GSM2198628	0.656712	1	160.5564	45.56183	69.81504	43.22226	9.63876	1.209254	high
GSM2198626	2.232329	1	161.9134	47.65329	72.82851	42.19876	10.42718	1.191133	high
GSM2198634	1.44	1	161.1763	46.13161	71.83742	41.25074	8.545298	1.20275	high
GSM2198623	0.877808	1	160.6083	46.54484	66.71349	43.80434	9.330568	1.226516	high
GSM2198617	3.523562	0	162.1622	44.61726	66.11918	41.6441	2.917961	1.312973	high
GSM2198619	2.870137	0	162.0734	44.65216	70.37382	36.59659	13.43372	1.00817	low
GSM2198622	0.535068	1	164.6226	44.88713	67.61092	41.70163	8.282754	1.210514	high
GSM2198610	1.116164	1	161.8135	43.3809	68.12242	40.0803	15.26726	1.023949	low
GSM2198632	2.134521	0	159.6826	43.17884	68.49758	40.88172	8.584207	1.173276	low
GSM2198636	1.296986	0	161.6886	45.27234	66.87629	39.81109	5.099265	1.237431	high
GSM2198624	2.767397	1	158.7431	44.7161	66.01263	42.6376	5.592995	1.2696	high
GSM2198633	1.578082	1	160.4605	44.80295	68.14713	41.38813	3.651932	1.293815	high
GSM2198608	1.029863	1	158.9377	46.65563	69.46389	42.53322	9.629252	1.198582	high
GSM2198645	1.60274	1	158.2679	44.48455	67.56667	39.879	8.103859	1.167172	low
GSM2198616	1.496712	1	161.0128	48.33633	70.8353	41.24672	9.134263	1.199222	high
GSM2198613	2.599726	0	161.6886	47.2491	69.88271	40.11478	7.669721	1.203527	high
GSM2198651	1.762192	0	160.6083	47.52619	69.13951	41.60163	7.064177	1.241606	high
GSM2198627	1.807397	0	160.4605	46.42049	69.98005	42.1178	9.307213	1.2001	high
GSM2198629	1.070137	1	160.474	45.08372	69.32687	39.7867	11.17931	1.111084	low
GSM2198612	3.802192	1	159.6018	47.04356	72.87525	45.81499	4.9017	1.365196	high
GSM2198620	1.343014	1	161.8791	46.79922	67.10441	39.72549	5.935078	1.226505	high
GSM2198648	0.908219	1	162.2194	47.8651	71.32424	41.72115	10.87167	1.172471	low
GSM2198639	3.488219	0	158.7135	43.76471	68.71442	36.12018	13.30507	0.989212	low
GSM2198641	1.52137	1	159.1846	47.14843	69.2003	39.60023	5.552775	1.232018	high
GSM2198655	0.77589	1	158.8376	47.70972	69.35851	41.88617	6.496708	1.256579	high
GSM2198630	2.942466	1	162.7697	45.57526	67.29524	40.61352	4.543426	1.267757	high
GSM2198614	0.367397	1	159.4361	45.881	71.25549	39.31793	8.740576	1.158004	low
GSM2198637	0.759452	1	160.773	46.15948	68.38086	42.90547	6.849474	1.262572	high
GSM2198611	2.1	1	160.9429	47.59477	73.38612	42.10188	8.165656	1.235151	high
GSM2198607	3.510411	0	161.8217	44.73034	70.06024	37.67286	12.52959	1.04614	low
GSM2198653	0.913151	1	160.2465	43.58849	70.04769	38.88511	14.75297	1.013733	low
GSM2198609	0.683836	1	161.0047	47.56048	70.99878	42.42731	7.386254	1.253707	high
GSM2198644	1.483562	1	157.1923	46.75535	70.47631	39.39552	8.940903	1.154179	low
GSM2198652	2.610411	1	158.0662	43.4521	69.93959	37.25537	15.00604	0.973787	low
GSM2198615	1.367671	1	160.5731	43.20611	69.4625	37.36482	15.62775	0.965573	low
GSM2198646	1.875616	0	161.0646	45.08518	68.30957	40.04181	9.239542	1.155666	low
GSM2198643	0.980548	1	160.9683	45.93237	69.55838	42.18097	7.952068	1.227394	high
GSM2198642	1.527123	1	153.4301	46.47485	69.59679	38.71802	10.58431	1.098029	low
GSM2198654	1.043014	1	162.6299	47.85886	68.13601	42.66464	7.174759	1.262597	high
GSM2198618	1.034795	1	158.1369	47.51073	68.69376	45.02126	7.87105	1.282224	high