

TCGA survival analysis

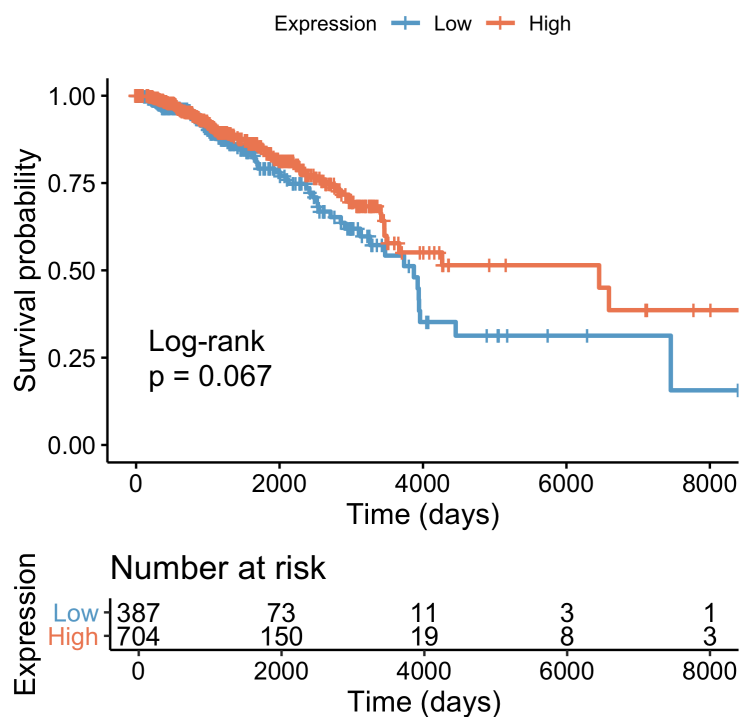
Mikhail Dozmorov

2020-03-23

Aggregation of the results generated by the survival.Rmd file

Cancer-specific analysis

Analysis 2: Survival effect of IGFBP3 in BRCA cancer



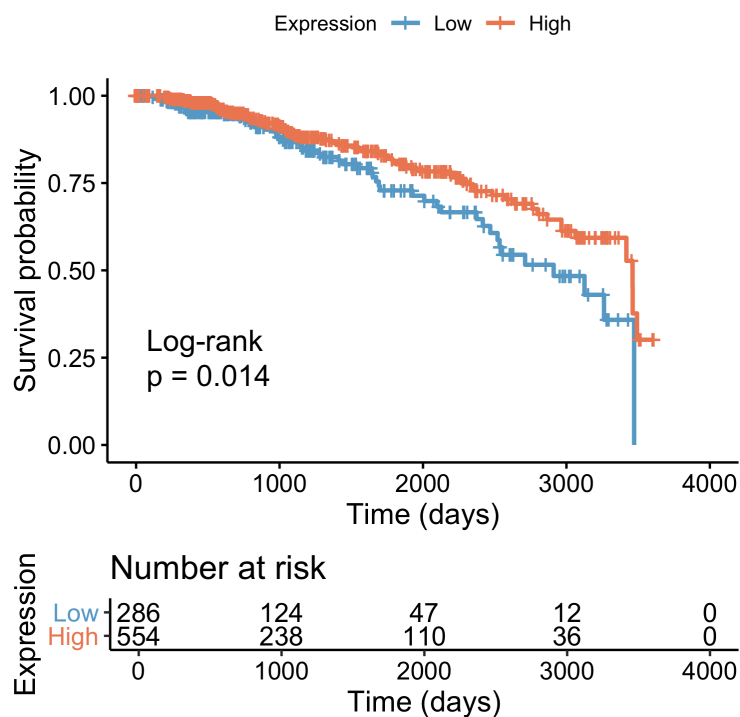
Analysis 3: Survival effect of IGFBP3 in specific clinical subtypes, BRCA cancer

The table lists clinical subtypes where the expression of IGFBP3 in BRCA most significantly affects survival. The table is sorted by increasing p-values, most significant on top. Description of clinical subtypes can be found at <https://gdc.cancer.gov/about-data/data-harmonization-and-generation/clinical-data-harmonization>

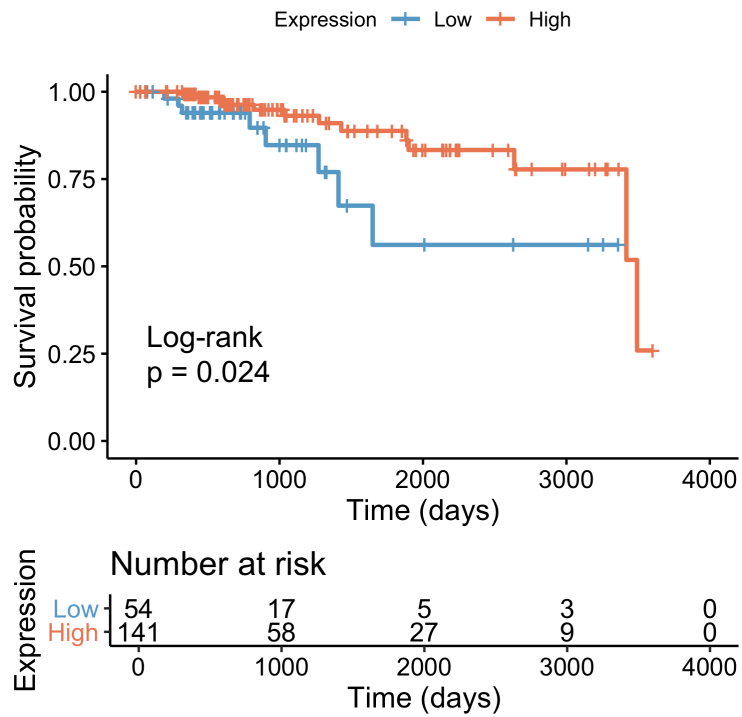
Cancer	Gene	p.value	HR	HR_left	HR_right	Min.	X1st.Qu.
BRCA-ethnicity-not hispanic or latino	IGFBP3	0.0143	0.64	0.45	0.92	6.78	10.62
BRCA-histologicaltype-infiltrating lobular carcinoma	IGFBP3	0.0239	0.36	0.14	0.91	7.96	10.84
BRCA-race-black or african american	IGFBP3	0.0284	0.42	0.19	0.93	6.78	10.54
BRCA-pathologyMstage-m0	IGFBP3	0.0400	0.67	0.46	0.98	6.78	10.58
BRCA-gender-female	IGFBP3	0.0449	0.71	0.50	0.99	6.78	10.58
BRCA-race-asian	IGFBP3	0.0767	0.15	0.01	1.68	9.25	10.79
BRCA-race-white	IGFBP3	0.0835	0.70	0.47	1.05	7.62	10.60
BRCA-radiationtherapy-no	IGFBP3	0.0860	0.61	0.35	1.08	6.78	10.50
BRCA-histologicaltype-other, specify	IGFBP3	0.1150	0.29	0.06	1.48	9.62	10.43
BRCA-pathologyMstage-mx	IGFBP3	0.1330	2.21	0.76	6.39	7.96	10.65

Top five corresponding survival plots

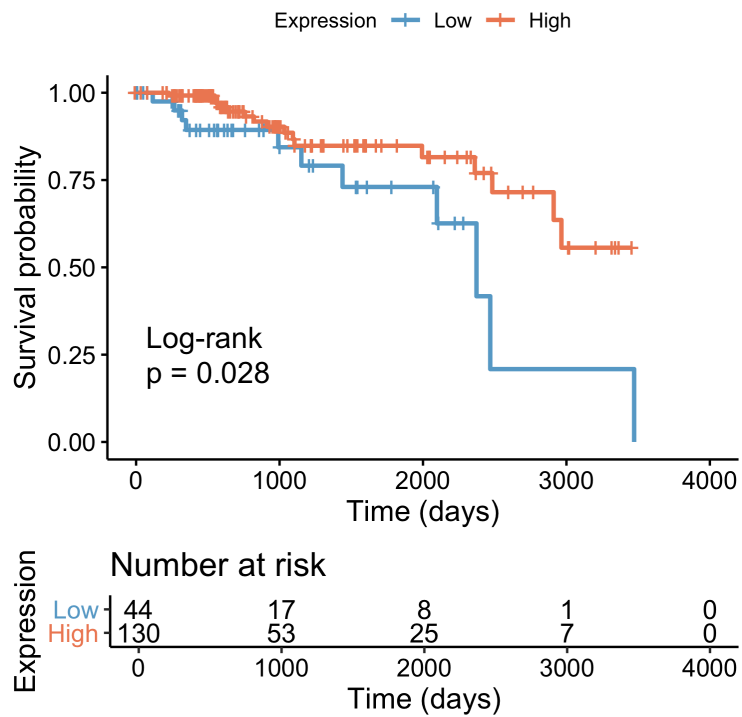
[1] "BRCA-ethnicity-not hispanic or latino"



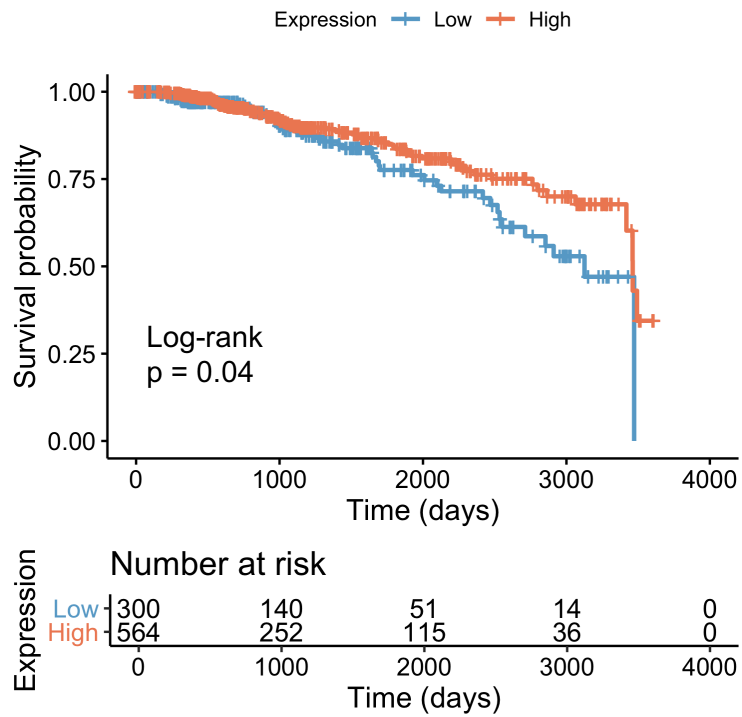
[1] "BRCA-histologicaltype-infiltrating lobular carcinoma"



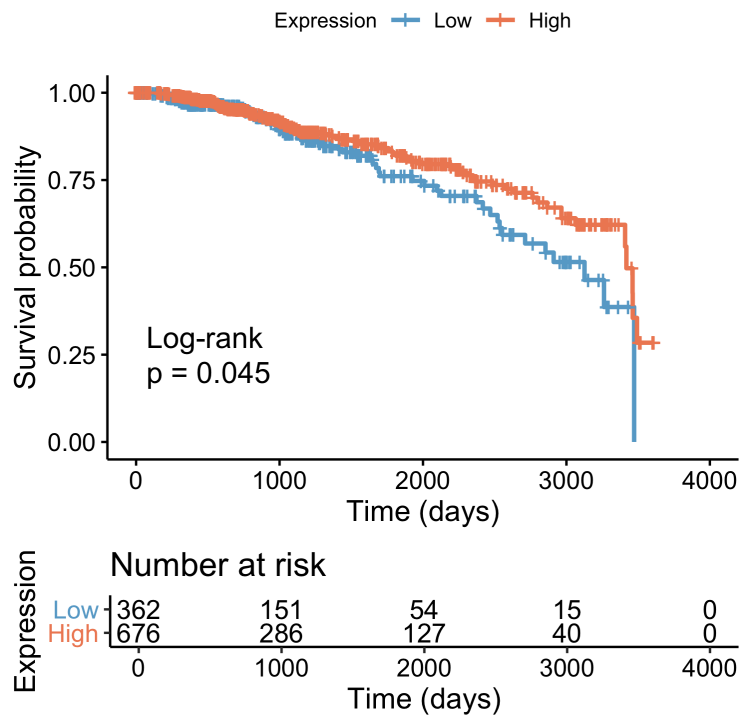
[1] "BRCA-race-black or african american"



[1] "BRCA-pathologyMstage-m0"

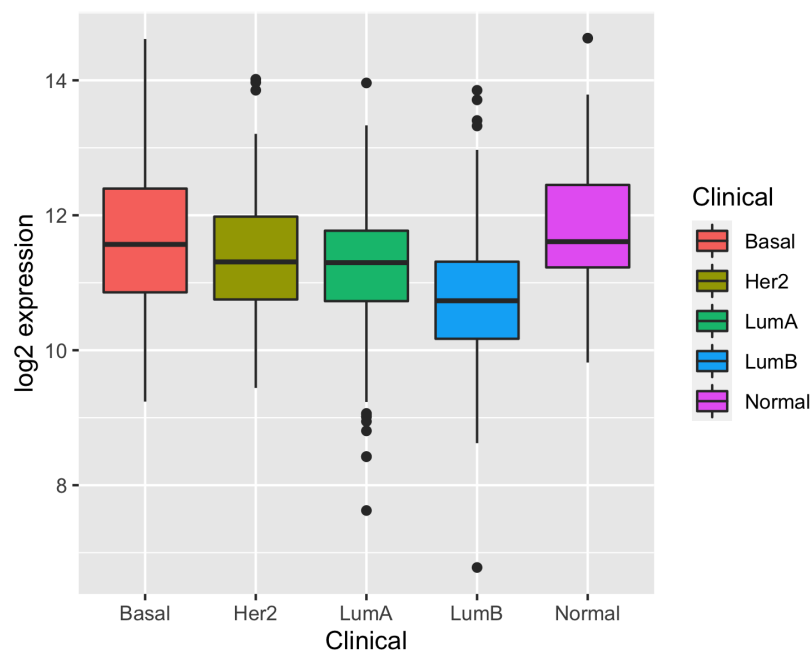


[1] "BRCA-gender-female"



Analysis 5: Clinical-centric analysis. Selected cancer, selected clinical subcategory, selected_genes expression differences across categories

Expression of IGFBP3 in selected clinical subcategories



What are the means of log2-expression per clinical subgroup?

Basal	Her2	LumA	LumB	Normal
11.65219	11.47154	11.22859	10.78419	11.87397

Is the expression of selected_genes IGFBP3 significantly different across clinical subgroups? Significant “Pr(>F)” suggests “Yes”

Analysis of Variance Table

Response: mtx_to_plot\$Gene

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
mtx_to_plot\$Clinical	4	76.37	19.0919	20.927	< 2.2e-16 ***
Residuals	835	761.79	0.9123		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Which pair of clinical categories have significant differences? “p.adj” and confidence intervals that do not cross 0 suggest significant differences in selected_genes expression between the subgroups in the corresponding pairwise comparison. Tukey HSD (Honest Significant Difference) test

	diff	lwr	upr	p adj
LumB-Basal	-0.868	-1.159	-0.5772	3.866e-13
LumB-LumA	-0.4444	-0.672	-0.2168	1.201e-06
Normal-LumB	1.09	0.5136	1.666	2.898e-06
LumB-Her2	-0.6873	-1.058	-0.3168	4.82e-06

	diff	lwr	upr	p adj
LumA-Basal	-0.4236	-0.6792	-0.168	6.589e-05
Normal-LumA	0.6454	0.08617	1.205	0.01433
LumA-Her2	-0.243	-0.5865	0.1006	0.3005
Normal-Her2	0.4024	-0.2286	1.033	0.4079
Her2-Basal	-0.1806	-0.569	0.2077	0.7088
Normal-Basal	0.2218	-0.366	0.8096	0.8408

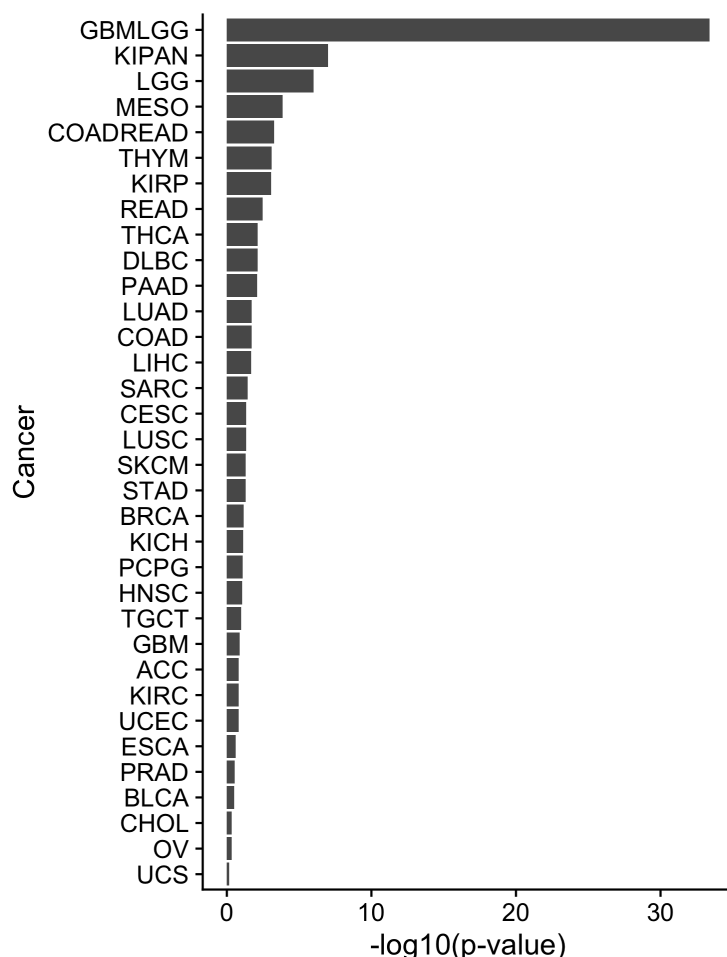
Is there a survival difference between clinical subgroups?

Cancer	Gene	p.value	HR
BRCA	PAM50Call_RNAseq-LumA-Her2	0.00536	0.44
BRCA	PAM50Call_RNAseq-LumA-LumB	0.0149	1.72
BRCA	PAM50Call_RNAseq-Basal-Her2	0.0314	2.14
BRCA	PAM50Call_RNAseq-LumB-Basal	0.0584	1.74
BRCA	PAM50Call_RNAseq-Normal-Basal	0.427	1.49
BRCA	PAM50Call_RNAseq-Normal-LumA	0.448	1.42
BRCA	PAM50Call_RNAseq-Normal-LumB	0.521	0.73
BRCA	PAM50Call_RNAseq-LumB-Her2	0.542	0.82
BRCA	PAM50Call_RNAseq-Normal-Her2	0.565	0.74
BRCA	PAM50Call_RNAseq-LumA-Basal	0.722	1.1

Global analysis

Analysis 2: Survival effect of IGFBP3 in all cancers

The bar plot shows the significance of IGFBP3 expression on survival in a given cancer. The wider (higher) the bar, the more significant survival effect the IGFBP3 has. See abbreviations of cancer types at <http://www.liuzlab.org/TCGA2STAT/CancerDataChecklist.pdf>



The same data in table format. Legend: **Cancer**, **Cancer.Name** - cancer abbreviation and description; **Gene** - selected_genes name for which survival analysis was run; **p.value** - significance of the survival effect; **HR**, **HR_left**, **HR_right** - hazard ratio, and left/right confidence interval; **Min.**, **X1st.Qu.**, **Median**, **Mean**, **X3rd.Qu.**, **Max.** - expression level of the selected_genes in a corresponding cancer; **Cutoff_type**, **Cutoff_value** - selected_genes expression cutoff best discriminating survival

Cancer	Cancer.Name	Gene	p.value	HR	HR_left	HR_right
GBMLGG	Glioma	IGFBP3	0.00e+00	4.39	3.39	5.68
KIPAN	Pan-kidney cohort (KICH+KIRC+KIRP)	IGFBP3	1.00e-07	2.73	1.86	4.01
LGG	Brain Lower Grade Glioma	IGFBP3	1.00e-06	2.36	1.65	3.36
MESO	Mesothelioma	IGFBP3	1.36e-04	2.98	1.66	5.36
COADREAD	Colorectal adenocarcinoma	IGFBP3	5.37e-04	2.20	1.39	3.48
THYM	Thymoma	IGFBP3	7.99e-04	9.16	1.90	44.21
KIRP	Kidney renal papillary cell carcinoma	IGFBP3	8.81e-04	2.67	1.46	4.87

Cancer	Cancer.Name	Gene	p.value	HR	HR_left	HR_right
READ	Rectum adenocarcinoma	IGFBP3	3.27e-03	4.22	1.49	11.95
THCA	Thyroid carcinoma	IGFBP3	7.44e-03	3.54	1.32	9.50
DLBC	Lymphoid Neoplasm Diffuse Large B-cell Lymphoma	IGFBP3	7.51e-03	0.14	0.03	0.75

Analysis 3: Survival effect of IGFBP3 in specific clinical subtypes, all cancers

Top 10 clinical subtypes across all cancers where IGFBP3 significantly (p-value < 0.05) affects survival

Cancer	Gene	p.value	HR	HR_left	HR_right	Min.	X1st.Qu.	Median
GBMLGG-race-white	IGFBP3	0e+00	4.64	3.53	6.09	3.96	8.55	
GBMLGG-ethnicity-not hispanic or latino	IGFBP3	0e+00	4.02	3.04	5.32	3.96	8.54	
GBMLGG-gender-male	IGFBP3	0e+00	4.66	3.34	6.51	3.96	8.55	
GBMLGG-radiationtherapy-yes	IGFBP3	0e+00	3.98	2.94	5.39	3.96	8.79	
GBMLGG-gender-female	IGFBP3	0e+00	3.86	2.54	5.88	4.62	8.68	
GBMLGG-karnofskyperformancescore-80	IGFBP3	0e+00	4.56	2.71	7.66	4.62	9.56	
GBMLGG-radiationtherapy-no	IGFBP3	0e+00	4.84	2.69	8.69	4.22	8.15	
LGG-race-white	IGFBP3	1e-07	2.68	1.84	3.92	3.96	8.17	
GBMLGG-tumortissuesite-central nervous system	IGFBP3	3e-07	2.52	1.75	3.64	3.96	8.19	
GBMLGG-karnofskyperformancescore-100	IGFBP3	7e-07	8.76	3.13	24.50	4.87	8.18	

Analysis 3: Cancer-specific top clinical subtypes where IGFBP3 significantly affects survival, for each cancer

Only results for cancers with clinical subtypes where IGFBP3 significantly (p-value < 0.05) affects survival are shown

Table 6: Bladder urothelial carcinoma

Cancer	Gene	p.value	HR	HR_left	HR_right	Min.	X1st.Qu.	Median	Me
BLCA-karnofskyperformancescore-90	IGFBP3	0.0101	0.31	0.12	0.80	9.29	12.45	13.80	13.
BLCA-gender-male	IGFBP3	0.0375	0.69	0.48	0.98	7.52	12.43	13.85	13.
BLCA-pathologyMstage-m0	IGFBP3	0.0473	0.62	0.38	1.00	8.61	12.58	13.86	13.

Table 7: Breast invasive carcinoma

Cancer	Gene	p.value	HR	HR_left	HR_right	Min.	X1st.Qu.	Median	Me
BRCA-ethnicity-not hispanic or latino	IGFBP3	0.0143	0.64	0.45	0.92	6.78	10.62		
BRCA-histologicalatype-infiltrating lobular carcinoma	IGFBP3	0.0239	0.36	0.14	0.91	7.96	10.84		
BRCA-race-black or african american	IGFBP3	0.0284	0.42	0.19	0.93	6.78	10.54		
BRCA-pathologyMstage-m0	IGFBP3	0.0400	0.67	0.46	0.98	6.78	10.58		
BRCA-gender-female	IGFBP3	0.0449	0.71	0.50	0.99	6.78	10.58		

Table 8: Cervical and endocervical cancers

Cancer	Gene	p.value	HR	HR_left	HR_right	Min.	X1st.Qu.	Median	Mean	X3rd
CESC-pathologyNstage-n0	IGFBP3	0.0154	4.28	1.20	15.25	8.38	11.28	12.59	12.44	1
CESC-radiationtherapy-yes	IGFBP3	0.0213	0.27	0.08	0.89	8.37	10.76	11.83	12.01	1

Table 9: Colon adenocarcinoma

Cancer	Gene	p.value	HR	HR_left	HR_right	Min.	X1st.Qu.	Me
COAD-radiationtherapy-no	IGFBP3	0.000722	2.59	1.46	4.59	8.49	10.53	1
COAD-residualtumor-r0	IGFBP3	0.001360	3.28	1.52	7.06	7.68	10.53	1
COAD-pathologyMstage-m0	IGFBP3	0.002410	3.16	1.45	6.88	8.58	10.36	1
COAD-histologicalatype-colon adenocarcinoma	IGFBP3	0.010700	2.07	1.17	3.66	7.68	10.35	1
COAD-gender-male	IGFBP3	0.011100	2.41	1.20	4.85	8.82	10.48	1
COAD-race-white	IGFBP3	0.023400	1.95	1.08	3.52	8.58	10.50	1
COAD-ethnicity-not hispanic or latino	IGFBP3	0.036900	1.86	1.03	3.38	7.68	10.39	1

Table 10: Colorectal adenocarcinoma

Cancer	Gene	p.value	HR	HR_left	HR_right	Min.	X1st.Qu.
COADREAD-radiationtherapy-no	IGFBP3	2.60e-06	3.17	1.91	5.27	8.49	10.53
COADREAD-residualtumor-r0	IGFBP3	5.40e-06	4.12	2.13	7.97	7.68	10.54
COADREAD-pathologyNstage-n1	IGFBP3	1.34e-04	5.76	2.12	15.64	9.03	10.58
COADREAD-pathologyMstage-m0	IGFBP3	2.63e-04	3.15	1.65	6.02	8.58	10.40
COADREAD-gender-male	IGFBP3	6.62e-04	2.78	1.51	5.12	8.82	10.53
COADREAD-ethnicity-not hispanic or latino	IGFBP3	1.74e-03	2.22	1.33	3.71	7.68	10.51
COADREAD-tumortissuesite-rectum	IGFBP3	4.65e-03	4.01	1.42	11.35	9.31	10.54
COADREAD-histologicalatype-rectal adenocarcinoma	IGFBP3	4.93e-03	3.98	1.41	11.24	9.31	10.54
COADREAD-tumortissuesite-colon	IGFBP3	9.22e-03	1.94	1.17	3.23	7.68	10.38
COADREAD-histologicalatype-colon adenocarcinoma	IGFBP3	1.07e-02	2.07	1.17	3.66	7.68	10.38

Table 11: Glioma

Cancer	Gene	p.value	HR	HR_left	HR_right	Min.	X1st.Qu.
GBMLGG-race-white	IGFBP3	0.00e+00	4.64	3.53	6.09	3.96	8.55
GBMLGG-ethnicity-not hispanic or latino	IGFBP3	0.00e+00	4.02	3.04	5.32	3.96	8.54
GBMLGG-gender-male	IGFBP3	0.00e+00	4.66	3.34	6.51	3.96	8.55
GBMLGG-radiationtherapy-yes	IGFBP3	0.00e+00	3.98	2.94	5.39	3.96	8.79
GBMLGG-gender-female	IGFBP3	0.00e+00	3.86	2.54	5.88	4.62	8.68
GBMLGG-karnofskyperformancescore-80	IGFBP3	0.00e+00	4.56	2.71	7.66	4.62	9.56
GBMLGG-radiationtherapy-no	IGFBP3	0.00e+00	4.84	2.69	8.69	4.22	8.15
GBMLGG-tumortissuesite-central nervous system	IGFBP3	3.00e-07	2.52	1.75	3.64	3.96	8.19
GBMLGG-karnofskyperformancescore-100	IGFBP3	7.00e-07	8.76	3.13	24.50	4.87	8.18
GBMLGG-histologicalatype-oligodendroglioma	IGFBP3	5.48e-04	3.09	1.58	6.07	3.96	8.16

Table 12: Brain Lower Grade Glioma

Cancer	Gene	p.value	HR	HR_left	HR_right	Min.	X1st.Qu.	Median
LGG-race-white	IGFBP3	1.00e-07	2.68	1.84	3.92	3.96	8.17	9.26
LGG-ethnicity-not hispanic or latino	IGFBP3	1.20e-06	2.51	1.71	3.69	3.96	8.16	9.32
LGG-gender-female	IGFBP3	1.07e-04	2.90	1.65	5.09	4.62	8.44	9.58
LGG-histologicaltype-oligodendroglioma	IGFBP3	5.48e-04	3.09	1.58	6.07	3.96	8.16	9.43
LGG-gender-male	IGFBP3	6.08e-04	2.29	1.41	3.73	3.96	8.02	9.24
LGG-histologicaltype-astrocytoma	IGFBP3	6.59e-04	2.43	1.43	4.11	4.27	8.25	9.55
LGG-radiationtherapy-no	IGFBP3	8.04e-04	3.54	1.62	7.76	4.22	7.96	9.23
LGG-radiationtherapy-yes	IGFBP3	1.14e-03	2.45	1.40	4.29	3.96	8.42	9.55
LGG-karnofskyperformancescore-80	IGFBP3	4.82e-03	3.67	1.40	9.65	4.62	8.78	9.70
LGG-histologicaltype-oligoastrocytoma	IGFBP3	1.37e-02	3.05	1.20	7.77	4.22	8.19	9.20

Table 13: Head and Neck squamous cell carcinoma

Cancer	Gene	p.value	HR	HR_left	HR_right	Min.	X1st.Qu.	Median	Mean	X3rd.
HNSC-radiationtherapy-no	IGFBP3	0.0116	1.86	1.14	3.05	8.02	10.89	11.88	11.88	1
HNSC-pathologyNstage-n1	IGFBP3	0.0247	0.34	0.13	0.91	9.20	10.98	12.11	12.15	1

Table 14: Kidney Chromophobe

Cancer	Gene	p.value	HR	HR_left	HR_right	Min.	X1st.Qu.	Median	Mean	X3rd.Qu.	Ma
KICH-race-white	IGFBP3	0.0391	3.91	0.97	15.78	6.86	10.49	11.38	11.21	12.37	13.

Table 15: Pan-kidney cohort (KICH+KIRC+KIPAN)

Cancer	Gene	p.value	HR	HR_left	HR_right	Min.
KIPAN-ethnicity-not hispanic or latino	IGFBP3	1.70e-06	2.09	1.54	2.85	6.86
KIPAN-gender-female	IGFBP3	2.00e-06	2.80	1.80	4.36	6.86
KIPAN-race-white	IGFBP3	6.50e-06	2.54	1.67	3.86	6.44
KIPAN-gender-male	IGFBP3	9.40e-06	2.78	1.74	4.47	6.44
KIPAN-pathologyNstage-nx	IGFBP3	6.34e-05	2.78	1.65	4.70	6.44
KIPAN-pathologyNstage-n0	IGFBP3	5.35e-04	2.51	1.46	4.31	6.86
KIPAN-pathologyMstage-m1	IGFBP3	6.77e-04	0.41	0.24	0.70	9.41
KIPAN-histologicaltype-kidney papillary renal cell carcinoma	IGFBP3	9.33e-04	2.66	1.46	4.87	6.44
KIPAN-pathologyMstage-mx	IGFBP3	1.63e-03	3.31	1.51	7.28	6.44
KIPAN-pathologicstage-stage ii	IGFBP3	5.10e-03	5.06	1.44	17.79	8.95

Table 16: Kidney renal clear cell carcinoma

Cancer	Gene	p.value	HR	HR_left	HR_right	Min.	X1st.Qu.	Median	Mean	X3rd.Qu.
KIRC-gender-female	IGFBP3	0.00291	2.14	1.28	3.57	8.26	14.58	15.29	15.04	15.89

Table 17: Kidney renal papillary cell carcinoma

Cancer	Gene	p.value	HR	HR_left	HR_right	Min.	X1st.Qu.	Median	M
KIRP-race-white	IGFBP3	0.000768	2.98	1.53	5.81	6.44	10.60	11.74	1
KIRP-pathologyMstage-mx	IGFBP3	0.004350	3.12	1.37	7.10	6.44	10.54	11.78	1
KIRP-gender-male	IGFBP3	0.009410	2.51	1.22	5.14	6.44	10.83	11.84	1
KIRP-pathologyNstage-nx	IGFBP3	0.010800	3.07	1.24	7.62	6.44	10.57	11.74	1
KIRP-gender-female	IGFBP3	0.012100	3.69	1.24	10.99	8.42	10.37	11.87	1
KIRP-ethnicity-not hispanic or latino	IGFBP3	0.017400	2.22	1.13	4.37	7.65	10.78	11.82	1
KIRP-radiationtherapy-no	IGFBP3	0.019100	2.41	1.13	5.17	6.44	10.65	11.82	1
KIRP-pathologicstage-stage iii	IGFBP3	0.027100	3.13	1.09	9.05	7.99	11.21	12.35	1
KIRP-race-black or african american	IGFBP3	0.043800	5.12	0.89	29.31	7.65	11.15	12.13	1

Table 18: Liver hepatocellular carcinoma

Cancer	Gene	p.value	HR	HR_left	HR_right	Min.	X1st.Qu.	Median	M
LIHC-race-asian	IGFBP3	0.00379	2.54	1.32	4.87	7.46	10.67		
LIHC-radiationtherapy-no	IGFBP3	0.00456	1.68	1.17	2.41	7.46	10.76		
LIHC-residualtumor-r0	IGFBP3	0.00896	1.65	1.13	2.40	7.46	10.76		
LIHC-histologicaltype-hepatocellular carcinoma	IGFBP3	0.01300	1.55	1.09	2.20	7.46	10.75		
LIHC-ethnicity-not hispanic or latino	IGFBP3	0.01540	1.57	1.09	2.27	7.46	10.71		
LIHC-pathologyMstage-mx	IGFBP3	0.02470	2.03	1.08	3.81	8.17	10.59		
LIHC-pathologicstage-stage iiia	IGFBP3	0.02660	2.25	1.08	4.71	8.96	10.82		
LIHC-gender-male	IGFBP3	0.04070	1.60	1.02	2.52	7.46	10.69		

Table 19: Lung adenocarcinoma

Cancer	Gene	p.value	HR	HR_left	HR_right	Min.	X1st.Qu.	Median	M
LUAD-gender-female	IGFBP3	0.00807	2.13	1.20	3.78	9.16	11.36	12.42	1
LUAD-ethnicity-not hispanic or latino	IGFBP3	0.01240	1.59	1.10	2.30	6.60	11.29	12.30	1
LUAD-gender-male	IGFBP3	0.02080	1.70	1.08	2.68	6.60	11.22	12.19	1
LUAD-pathologyTstage-t3	IGFBP3	0.04060	3.39	0.98	11.69	9.82	10.97	12.16	1
LUAD-pathologyTstage-t2	IGFBP3	0.04370	1.64	1.01	2.66	6.60	11.47	12.45	1

Table 20: Mesothelioma

Cancer	Gene	p.value	HR	HR_left	HR_right	Min.	X1st.Qu.	Median	M
MESO-pathologyMstage-m0	IGFBP3	3.26e-05	3.93	1.98	7.77	8.42	10.46		
MESO-histologicaltype-epithelioid mesothelioma	IGFBP3	9.29e-05	3.45	1.79	6.64	8.42	10.46		
MESO-race-white	IGFBP3	1.80e-04	2.94	1.63	5.29	8.42	10.61		
MESO-gender-male	IGFBP3	2.66e-04	3.44	1.71	6.93	8.42	10.63		
MESO-pathologyNstage-n0	IGFBP3	3.05e-04	4.63	1.88	11.38	8.42	10.61		
MESO-radiationtherapy-no	IGFBP3	8.80e-03	2.49	1.23	5.04	8.42	10.92		

Table 21: Pancreatic adenocarcinoma

Cancer	Gene	p.value	HR	HR_left	HR_right	Min.	X1st.Qu.	Median	Mean	X3rd.Qu.
PAAD-histologicaltype-pancreas-adenocarcinoma ductal type	IGFBP3	0.00278	1.95	1.25	3.04	9.18				
PAAD-pathologyTstage-t3	IGFBP3	0.00436	1.94	1.22	3.09	8.94				
PAAD-pathologyMstage-m0	IGFBP3	0.00909	2.30	1.21	4.36	9.27				
PAAD-ethnicity-not hispanic or latino	IGFBP3	0.01340	1.85	1.13	3.03	8.91				
PAAD-race-white	IGFBP3	0.02010	1.68	1.08	2.63	8.91				
PAAD-residualtumor-r0	IGFBP3	0.02570	1.91	1.07	3.40	8.91				
PAAD-residualtumor-r1	IGFBP3	0.02940	2.15	1.06	4.37	9.74				
PAAD-radiationtherapy-yes	IGFBP3	0.03430	2.90	1.04	8.12	9.18				
PAAD-gender-male	IGFBP3	0.03680	1.85	1.03	3.31	8.94				
PAAD-pathologyNstage-n0	IGFBP3	0.04060	2.69	1.00	7.22	8.91				

Table 22: Prostate adenocarcinoma

Cancer	Gene	p.value	HR	HR_left	HR_right	Min.	X1st.Qu.	Median	Mean	X3rd.Qu.
PRAD-pathologyTstage-t3a	IGFBP3	0.0402	0	0	Inf	7.40	10.07	10.77	10.65	11.07
PRAD-residualtumor-r0	IGFBP3	0.0455	0	0	Inf	6.98	9.89	10.56	10.54	11.07

Table 23: Rectum adenocarcinoma

Cancer	Gene	p.value	HR	HR_left	HR_right	Min.	X1st.Qu.	Median	Mean	X3rd.Qu.
READ-residualtumor-r0	IGFBP3	0.000577	7.95	1.97	32.09	9.45	10.56			
READ-radiationtherapy-no	IGFBP3	0.002390	5.39	1.60	18.15	9.45	10.53			
READ-histologicaltype-rectal adenocarcinoma	IGFBP3	0.004930	3.98	1.41	11.24	9.31	10.54			
READ-ethnicity-not hispanic or latino	IGFBP3	0.005470	4.41	1.41	13.83	9.31	10.56			
READ-pathologyMstage-m0	IGFBP3	0.005660	4.65	1.41	15.37	9.33	10.56			
READ-gender-male	IGFBP3	0.008180	7.22	1.31	39.83	9.31	10.56			

Table 24: Sarcoma

Cancer	Gene	p.value	HR	HR_left	HR_right	Min.	X1st.Qu.	Median	Mean	X3rd.Qu.
SARC-gender-female	IGFBP3	0.00399	2.67	1.33	5.34	9.3	11.65	12.45	12.48	13.07
SARC-radiationtherapy-no	IGFBP3	0.04100	1.78	1.02	3.12	9.3	11.64	12.57	12.61	13.07

Table 25: Skin Cutaneous Melanoma

Cancer	Gene	p.value	HR	HR_left	HR_right	Min.	X1st.Qu.	Median	Mean	X3rd.Qu.
SKCM-pathologyMstage-m0	IGFBP3	0.00389	5.02	1.49	16.90	8.08	9.92	10.77	10.77	11.07
SKCM-radiationtherapy-no	IGFBP3	0.01310	3.53	1.22	10.22	8.08	10.04	10.75	10.75	11.07
SKCM-ethnicity-not hispanic or latino	IGFBP3	0.01420	3.15	1.20	8.30	7.89	9.92	10.77	10.77	11.07
SKCM-melanomaprimaryknown-yes	IGFBP3	0.04800	2.41	0.98	5.93	7.89	9.96	10.75	10.75	11.07

Table 26: Stomach adenocarcinoma

Cancer	Gene	p.value	HR	HR_left	HR_right	Min.	X1st.Qu.	Median	Me
STAD-radiationtherapy=yes	IGFBP3	0.0358	2.63	1.03	6.72	9.41	11.06	12.05	12
STAD-ethnicity-not hispanic or latino	IGFBP3	0.0367	1.62	1.03	2.56	7.81	11.25	12.03	12

Table 27: Thyroid carcinoma

Cancer	Gene	p.value	HR	HR_left	HR_right	Min.	X1st.Qu.	Median	M
THCA-gender-female	IGFBP3	0.00120	6.85	1.77	26.51	6.54	9.51	10.36	1
THCA-race-white	IGFBP3	0.00274	4.59	1.54	13.72	6.54	9.62	10.46	1
THCA-radiationexposure=no	IGFBP3	0.00324	5.08	1.52	16.89	6.54	9.65	10.50	1
THCA-ethnicity-not hispanic or latino	IGFBP3	0.00342	4.14	1.47	11.65	6.54	9.57	10.50	1
THCA-multifocality-unifocal	IGFBP3	0.01460	3.45	1.20	9.95	7.12	9.60	10.61	1
THCA-pathologyNstage=n0	IGFBP3	0.04370	0.19	0.03	1.15	7.56	9.46	10.37	1

Table 28: Thymoma

Cancer	Gene	p.value	HR	HR_left	HR_right	Min.	X1st.Qu.	Median	Me
THYM-radiationtherapy=no	IGFBP3	0.000299	5.042007e+09		0.00	Inf	7.34	8.89	
THYM-ethnicity-not hispanic or latino	IGFBP3	0.001780	1.337000e+01		1.61	111.20	7.34	8.85	
THYM-tumortissuesite-thymus	IGFBP3	0.006690	7.200000e+00		1.38	37.64	7.34	8.93	
THYM-gender-male	IGFBP3	0.027300	8.440000e+00		0.87	81.48	7.76	8.90	
THYM-race-white	IGFBP3	0.033700	7.200000e+00		0.86	60.20	7.34	8.84	

Analysis 3: Survival effect of IGFBP3 in manually defined clinical subtypes, all cancers

Table 29: race-black or african american

Cancer	Gene	p.value	HR	HR_left	HR_right	Min.	X1st.Qu.	Median	Me
BRCA-race-black or african american	IGFBP3	0.0284	0.42	0.19	0.93	6.78	10.54	11.17	11
KIRP-race-black or african american	IGFBP3	0.0438	5.12	0.89	29.31	7.65	11.15	12.13	12

Table 30: race-white

Cancer	Gene	p.value	HR	HR_left	HR_right	Min.	X1st.Qu.	Median	Mean	X3rd.Qu.
GBMLGG-race-white	IGFBP3	0.00e+00	4.64	3.53	6.09	3.96	8.55	9.83	9.91	11.30
LGG-race-white	IGFBP3	1.00e-07	2.68	1.84	3.92	3.96	8.17	9.26	9.27	10.54
KIPAN-race-white	IGFBP3	6.50e-06	2.54	1.67	3.86	6.44	12.36	14.83	14.09	15.84
MESO-race-white	IGFBP3	1.80e-04	2.94	1.63	5.29	8.42	10.61	11.70	11.78	12.84
KIRP-race-white	IGFBP3	7.68e-04	2.98	1.53	5.81	6.44	10.60	11.74	11.94	13.24
THCA-race-white	IGFBP3	2.74e-03	4.59	1.54	13.72	6.54	9.62	10.46	10.54	11.30
PAAD-race-white	IGFBP3	2.01e-02	1.68	1.08	2.63	8.91	12.63	13.45	13.23	14.00
COAD-race-white	IGFBP3	2.34e-02	1.95	1.08	3.52	8.58	10.50	11.26	11.23	11.84
THYM-race-white	IGFBP3	3.37e-02	7.20	0.86	60.20	7.34	8.84	9.62	9.67	10.30

Cancer	Gene	p.value	HR	HR_left	HR_right	Min.	X1st.Qu.	Median	Mean	X3rd.Qu.
KICH-race-white	IGFBP3	3.91e-02	3.91	0.97	15.78	6.86	10.49	11.38	11.21	12.3

Methods

Survival analysis of selected_genes expression data from TCGA

Level 3 selected_genes expression data summarized as RSEM values were obtained using the TCGA2STAT R package v 1.2, along with the corresponding clinical annotations. Data for each of the 34 cancers were obtained separately. The data was log2-transformed and analyzed using Kaplan-Meier curves and Cox proportional hazard model. Each selected_genes of interest was analyzed for its effect on survival by separating patients into high/low expression subgroups. A modified approach from [1] was used to estimate the best selected_genes expression cutoff that separates high/low expression subgroups with differential survival.

We took advantage of the availability of clinical annotations. To identify if the expression of a selected_genes of interest affects survival in any specific clinical subgroup, subsets of patients annotated with specific clinical annotations were selected (e.g., “males” or “females” in the “gender” clinical annotation). Subgroups with < 40 patients were not considered.

Differential expression analysis

Samples in the selected cancer cohort were sorted by expression of the selected genes. Differentially expressed genes were detected between samples in the upper 75 percentile of the expression gradient and samples in the lower 25 percentile using limma v 3.32.6 R package [2,3]. P-values were corrected for multiple testing using the False Discovery Rate (FDR) method [4]. Genes differentially expressed at FDR < 0.01 were selected for further analysis.

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