CELLX analysis

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2020-03-14

Data from CELLX

- Go to http://54.149.52.246/cgi-bin/RPPA/cellx.cgi
- Select "Expression" tab out of "CNV"/"Expression"/"Mutation"/"Other" tabs
- Select "RSEM-barplot" option on the sidebar. Read more about RSEM selected_gene expression measures at https://deweylab.github.io/RSEM/
- Select any cancer-associated selected_gene from http://cancer.sanger.ac.uk/census, e.g., "ERBB2". Alternatively, use any selected_gene name you may find biologically interesting
- Enter lower-case selected_gene name into the "HUGO" textbox at the bottom of the page
- Click "Submit" - the page will refresh in ~20 sec
- Save the tab-separated data using "Download table" link into `data/RSEM_expression_GENESYMBOL.data.tsv`
- Import the downloaded data into R

Gene IGFBP3 analysis

CCLE expression

Top 15 cell lines with the *highest* log2(RSEM) expression of IGFBP3

cell	IGFBP3	CCLE_ID
SNU349	18.87	NA
RCC10RGB	18.64	NA
TUHR14TKB	17.7	TUHR14TKB_KIDNEY
RS5	17.67	NA
OSRC2	17.17	NA
HS742T	17.17	HS742T_FIBROBLAST
TUHR10TKB	16.79	TUHR10TKB_KIDNEY
647V	16.75	NA
HS255T	16.67	NA
HS688AT	16.67	HS688AT_FIBROBLAST
KMRC1	16.64	KMRC1_KIDNEY
SNU466	16.6	NA
TUHR4TKB	16.53	NA
MKN1	16.36	MKN1_STOMACH
HS819T	16.36	NA

Top 15 cell lines with the *lowest* log2(RSEM) expression of IGFBP3

cell	IGFBP3	CCLE_ID
NCIH510	4.649	NCIH510_LUNG
NCIH1963	4.632	NCIH1963_LUNG
BCP1	4.6	BCP1_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE
EOL1	4.58	NA
GA10	4.5	NA
CA46	4.411	CA46_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE
HCC1428	4.387	NA
EM2	4.285	NA
DAUDI	4.211	NA
GRANTA519	4.194	GRANTA519_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE
NCIH1092	4.178	NA
COLO684	4.095	NA
CL11	4.09	CL11_LARGE_INTESTINE
BV173	4.071	NA
NCIH2171	3.661	NA
MOLT3	0	MOLT3_HAEMATOPOIETIC_AND_LYMPHOID_TISSUE

Cancer vs. normal IGFBP3 log2(RSEM) expression boxplots, all cancers
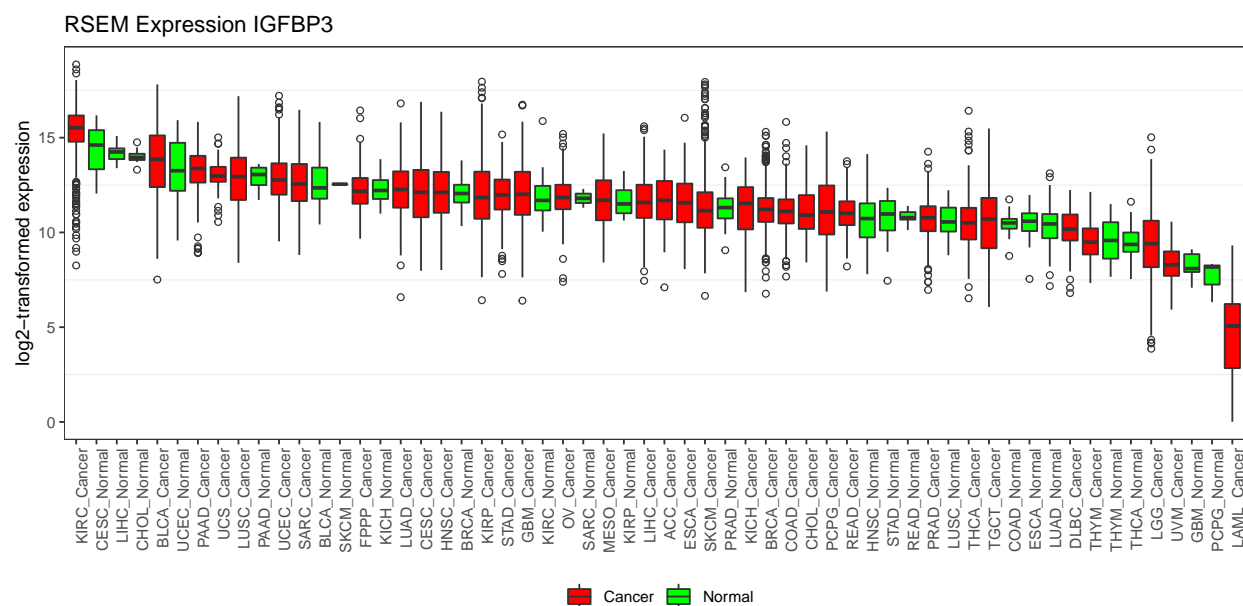
Differential expression of selected_gene IGFBP3 between tumor and normal tissues

The table below displays differential expression statistics comparing the expression levels of IGFBP3 in normal versus cancer tissues (where at least 12 normal samples are available) by Welch two-sample t-test.

The table is sorted by "p_value" column, from most to least significant. Positive/negative log2 Fold change indicate the gene is up/down in cancer samples, respectively.

TCGA ID	Description	log2 Fold change	p-value	Mean log2(RSEM) normal	Mean log2(RSEM) cancer
LIHC	Liver hepatocellular carcinoma	-2.53	4.17e-81	14.18	11.65
KIRC	Kidney renal clear cell carcinoma	3.443	3.11e-53	11.86	15.3
LUSC	Lung squamous cell carcinoma	2.258	1.22e-28	10.61	12.86
BRCA	Breast invasive carcinoma	-0.8166	9.74e-24	12.04	11.23
LUAD	Lung adenocarcinoma	1.943	9.28e-21	10.31	12.26
THCA	Thyroid carcinoma	1.112	4.85e-16	9.455	10.57
COAD	Colon adenocarcinoma	0.6466	4.01e-09	10.45	11.1
HNSC	Head and Neck squamous cell carcinoma	1.315	2.29e-07	10.82	12.14
STAD	Stomach adenocarcinoma	1.179	8.67e-07	10.82	12
PRAD	Prostate adenocarcinoma	-0.5576	1.47e-05	11.27	10.72
KICH	Kidney Chromophobe	-1.065	6.80e-05	12.32	11.25
BLCA	Bladder urothelial carcinoma	1.052	3.57e-03	12.56	13.61
KIRP	Kidney renal papillary cell carcinoma	0.3413	5.19e-02	11.69	12.03
UCEC	Uterine Corpus Endometrial Carcinoma	-0.4331	1.53e-01	13.29	12.86

Cancer vs. normal IGFBP3 log2(RSEM) expression boxplots, individual cancers

The figure below is a plot that highlights the differences in IGFBP3 expression distribution in normal and cancer tissues for each cancer type (where at least 12 normal samples are available).

RSEM Expression IGFBP3