

CELLX analysis

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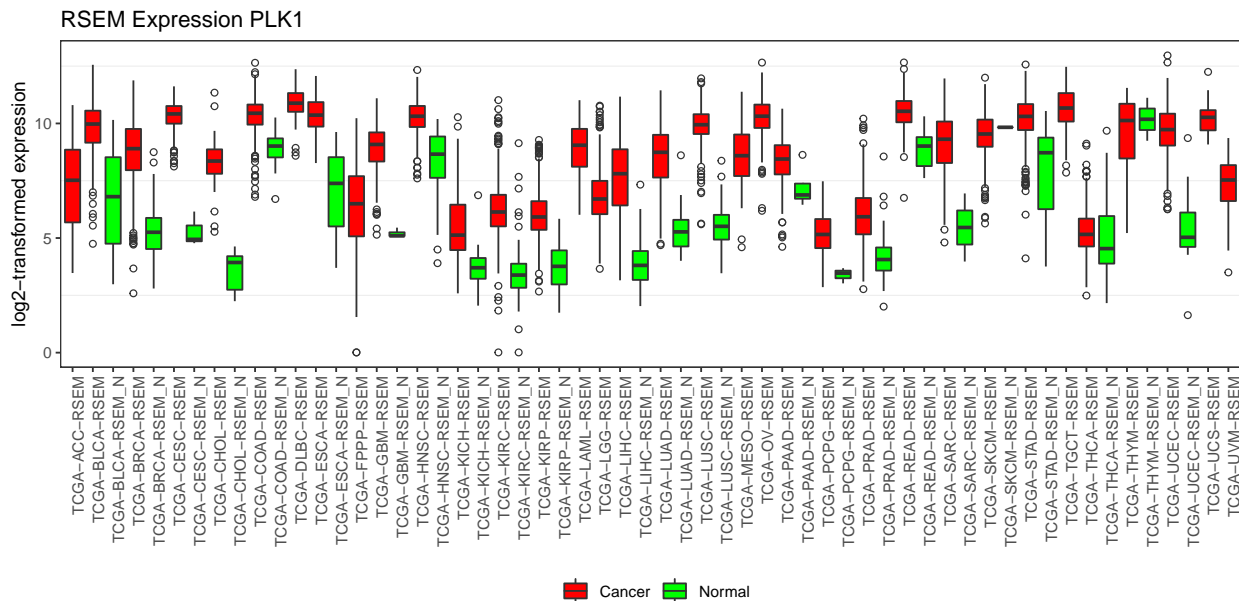
Data from CELLX

- 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 gene expression measures at <https://deweylab.github.io/RSEM/>
- Select any cancer-associated gene from <http://cancer.sanger.ac.uk/census>, e.g., “ERBB2”. Alternatively, use any gene name you may find biologically interesting
- Enter lower-case 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 PLK1 analysis

There are 11188 unique samples from 59 tissue sources ($N_{\text{cancer}} = 35$, $N_{\text{normal}} = 24$) indexing expression of the gene *PLK1*. The graph below shows the expression in of *PLK1* in normal versus cancerous tissues.

Cancer vs. normal expression boxplots, all cancers



Differential expression of gene *PLK1* between tumor and normal tissues

The table below displays differential expression statistics comparing the expression levels of *PLK1* in normal versus cancer tissues (where normal comparison tissues are available) by Welch two-sample t-test.

Column names: “Cancer.Name”, “Acronym” - cancer type, “Fold_change” - fold change (positive/negative - upregulated/downregulated in cancer), “p_value”, “t_statistic” - results of Welch two-sample t-test, “Normal”, “Cancer” - number of samples.

The table is sorted by “p_value” column, from most to least significant.

	Cancer.Name	Acronym	Fold_change	p_value	Normal	Cancer	t_statistic
1	Breast invasive carcinoma	BRCA	11.29410	1.70e-67	114	1116	31.370
2	Lung adenocarcinoma	LUAD	9.66185	1.05e-45	59	530	26.635
3	Lung squamous cell carcinoma	LUSC	21.29730	3.43e-35	51	502	29.023
4	Liver hepatocellular carcinoma	LIHC	12.53940	1.06e-34	50	374	20.704
5	Kidney renal clear cell carcinoma	KIRC	6.59878	4.68e-28	72	538	16.170
6	Uterine Corpus Endometrial Carcinoma	UCEC	18.95750	3.15e-20	35	550	18.532
8	Colon adenocarcinoma	COAD	2.72244	3.49e-17	41	475	12.701
9	Kidney renal papillary cell carcinoma	KIRP	5.06443	1.56e-16	32	291	12.988
10	Prostate adenocarcinoma	PRAD	3.35288	4.46e-16	52	502	10.821
11	Head and Neck squamous cell carcinoma	HNSC	4.21403	2.35e-11	44	522	8.838
13	Kidney Chromophobe	KICH	3.46871	3.71e-09	25	66	6.658
14	Stomach adenocarcinoma	STAD	4.90958	2.93e-07	35	415	6.308
15	Bladder urothelial carcinoma	BLCA	9.33597	6.68e-06	19	411	6.204
21	Thyroid carcinoma	THCA	1.19119	2.37e-01	59	513	1.193

Cancer vs. normal expression boxplots, individual cancers

The figure below is a plot that highlights the differences in *PLK1* expression distribution in normal and cancer tissues for each cancer type.

RSEM Expression PLK1

