Explore Prostate Cancer Datasets

Data Input | Gene Profile | Survival | Gene Correlation | Heatmap | Copy Number | Quick Analysis

You can select which gene to display the results for

Gene to plot

UBE2C ▼

Output options

What to call the output files

UBE2C-survival

File format for plots

◉ pdf
○ png

PDF can be imported into Illustrator (or similar) for editing. PNG plots are suitable for presentation

PDF dimensions are measured in inches, and PNG dimensions are measured in pixels

Width of plot

12

Height of plot

6.3

⬇ Export K-M plot....

⬇ Download R script....

A recursive partitioning (RP) analysis [1] is performed to determine if the samples can be split into groups based on the expression data from your chosen gene(s). An RP p-value < 0.05 indicates a significant split. The p-value from RP and cut-off corresponding to a split are shown in the table below

If no cut-off can be found with RP, the samples will be divided according to median expression level in the plots below

Show 25 ▼ entries   Search:

	Gene	RP_p.value	RP_Cut.off
1	ACOT7	0.4900	
2	AURKA	0.0110	6.84
3	AURKB	0.0120	6.71
4	BUB1	0.0110	6.26
5	CCNE2	0.3000	
6	CDC2	0.0037	7.13
7	CDC20	0.0014	7.40
8	CENPM	0.0074	7.88
9	KIAA0101	0.1900	
10	MCM4	0.0300	7.24
11	MELK	0.0240	6.97
12	NCAPG	0.0270	6.63
13	NUSAP1	0.0099	7.10

A histogram of expression level will be shown with a line to indicate the median expression level or RP cut-off

Partitioning using cut-off found by RP
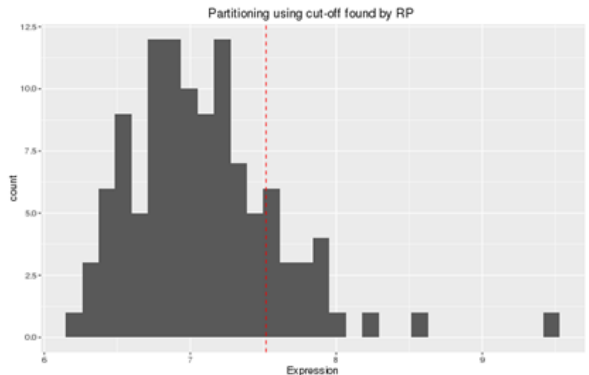
The grouping of samples found by RP, or using median expression level, is used to construct a Kaplan-Meier plot

UBE2C , p= 0.0018

UBE2C > 7.52 n= 19
UBE2C <= 7.52 n=92