Correlation analyses - Legend to figures

Correlation analysis between two genes.

Plotted values correspond to the $\log_2$-normalized gene expression values (fluorescence intensity or RSEM-UQ) for two genes (in X and Y-axis) for each patient in the indicated dataset. Black line represents linear regression, grey area indicates the limits of the confidence intervals and R and p indicate Pearson´s or Spearman's correlation coefficient (depending on the analysis selected) and statistical significance, respectively.

Heatmap. Visual grid representation of the correlation values between the gene expression of one gene and other one or more genes (rows) in the indicated datasets (columns).

In every cell, the corresponding R and p-values of the analysis are shown. The color of each cell represents its correlation R value, being red towards 1 and blue towards -1. Correlations with p-value<=0.05 and $|R| >= 0.2$ are indicated with (*). In case of NA, the cell is colored in grey and with no data. On the left side, the coherence among data sets is shown for each pair of genes.

Note

- All the graphs generated with CANCERTOOL are produced in PNG (600 ppp) and PDF, which can be edited for example with *__Inkscape__* or *__GIMP__*.
- All the p-values shown on the figures are non-adjusted. Adjusted p-values, calculated using Benjamini & Hochberg (BH) method, are only provided in the Statistical Results table when custom analyses are requested.