

## **Correlation analyses - Legend to figures**

### **UPDATE** (February 2022):

- All datasets have the gene information stored with the 2021 [HGNC](#) approved nomenclature.
- Dataset normalization was performed by original authors, and no additional normalization process was applied upon download (their corresponding normalization is described in the corresponding GEO entry).
- Visit the [Datasets](#) tab to access feature information for each of the datasets.
- In microarray datasets, probes interrogating the same gene have been averaged.
- For microarray derived datasets, all probes are included. However, it is important to note that some platforms identify potentially mis-annotated or cross-hybridizing probes. We recommend users to check their genes of interest in the case of the datasets indicated with \* in the [Datasets](#) tab.

### **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  $p\text{-value} \leq 0.05$  and  $|R| \geq 0.2$  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 CANCEERTOOL 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.