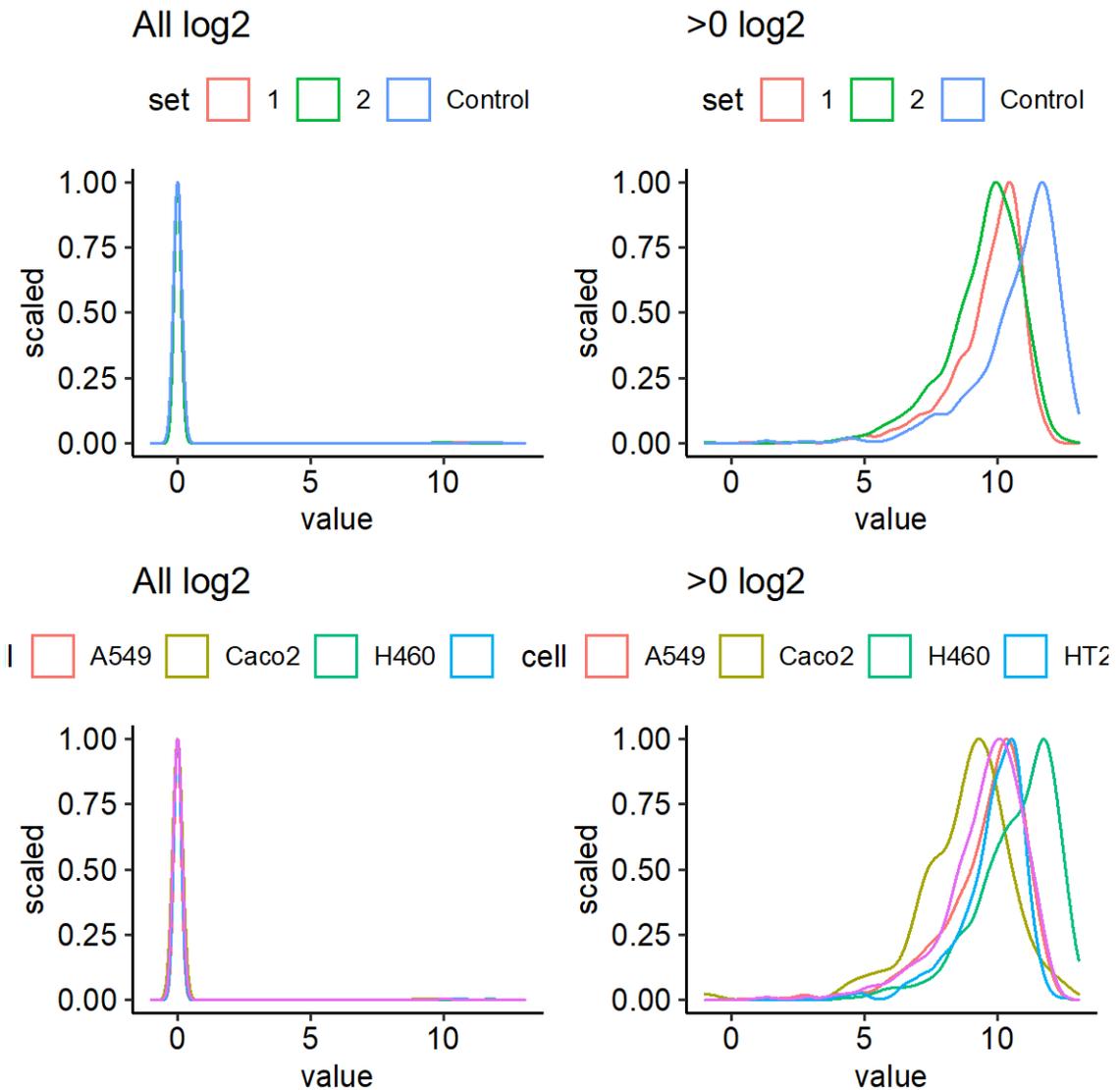


Data analysis after processing the GenePix files

Each protein analyte was evaluated in 2 biological replicates each with 3 technical replicates. Negative fluorescence signal was transformed to zero. As expected, the signal distribution was not normal and zero-inflated (DENSITY PLOTS BELOW). Therefore, non-parametric Man-Whitney test was used to compare the protein relative abundance between groups (experiment 1 or 2 Vs. Control).

Standardized effect size (Ratio) was calculated by subtracting the mean log₂ fluorescence in condition 1 or 2 and mean log₂ fluorescence in control and then dividing by the overall standard deviation of experiment and control.



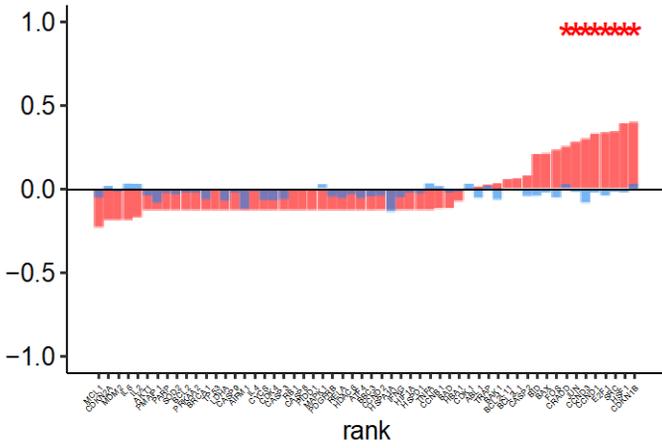
Ratio = Mean Condition X – Mean Control / SD (condition X and control)

Proteins with ratio > absolute(0.8) are transformed to -0.8 or 0.8 to fit in the scale

The order in Scale-X is the same in all the plots. Based in the rank ratio of H460 condition 2 Vs. control (red)

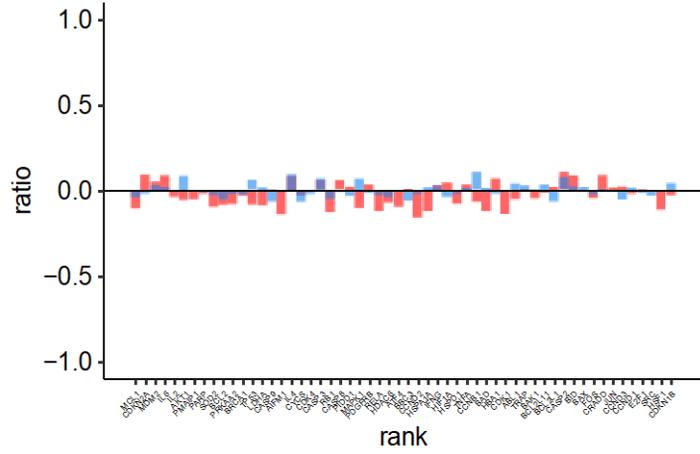
H460

set ■ 1 ■ 2



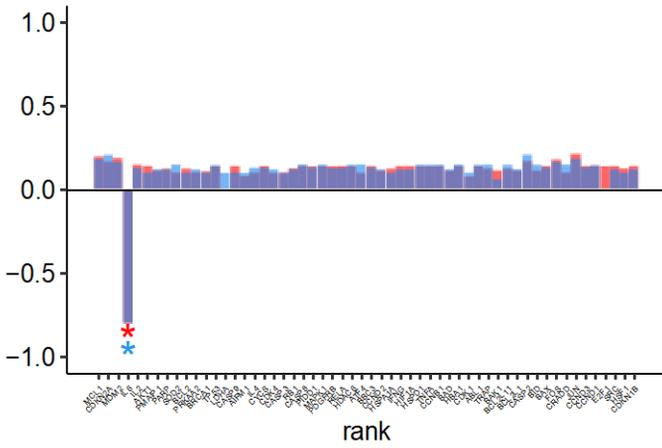
A549

set ■ 1 ■ 2



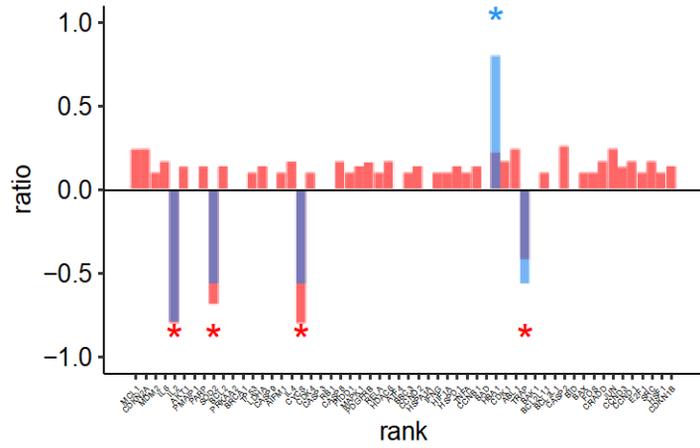
HT29

set ■ 1 ■ 2



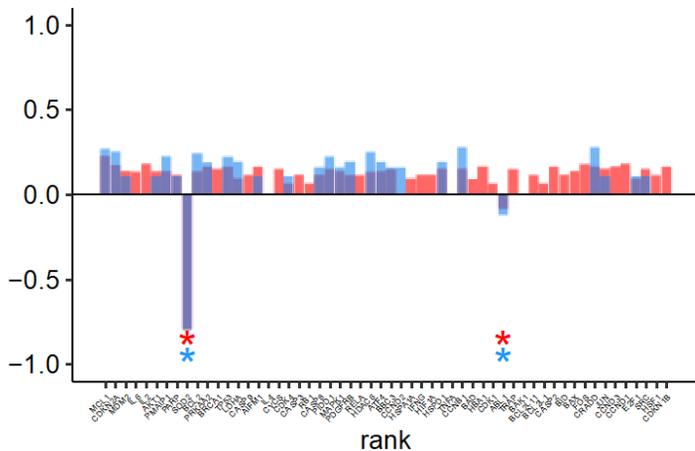
Caco2

set ■ 1 ■ 2



jurkat

set ■ 1 ■ 2



NP + Cis-Pt

Only Cis-Pt