

1.1. Methods M5

Average fold change values for select individual genes were calculated based on their $\log_2$ fold change from the average TCPS control value for that gene as:

$$f = \log_2 \frac{A}{B} = \log_2 A - \log_2 B$$

Where, A is the average fluorescence intensity value of the gene of interest and B is the average fluorescence intensity value of TCPS. Standard deviation in fold change was calculated as

$$\sigma_f^2 = \sigma_A^2 \left[\frac{1}{A \ln 2} \right]^2 + \sigma_B^2 \left[\frac{1}{B \ln 2} \right]^2$$

in order to compensate for error propagation in the fold change calculation [34].