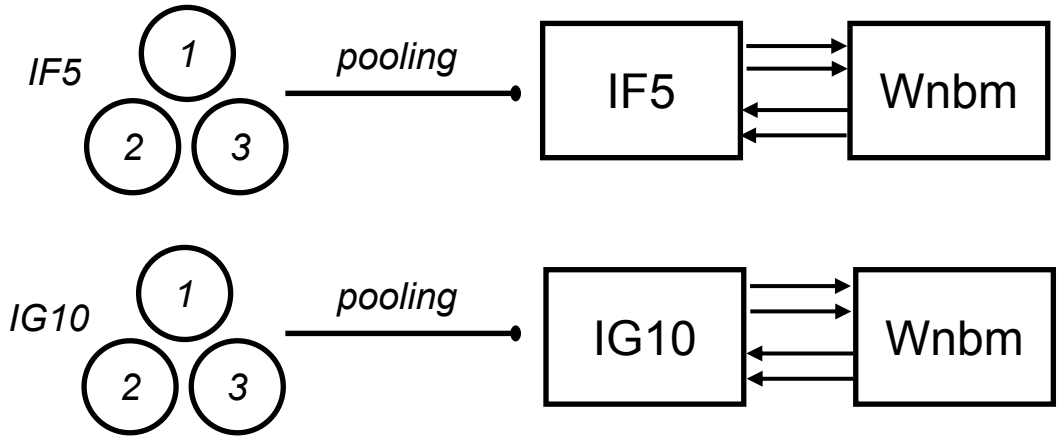
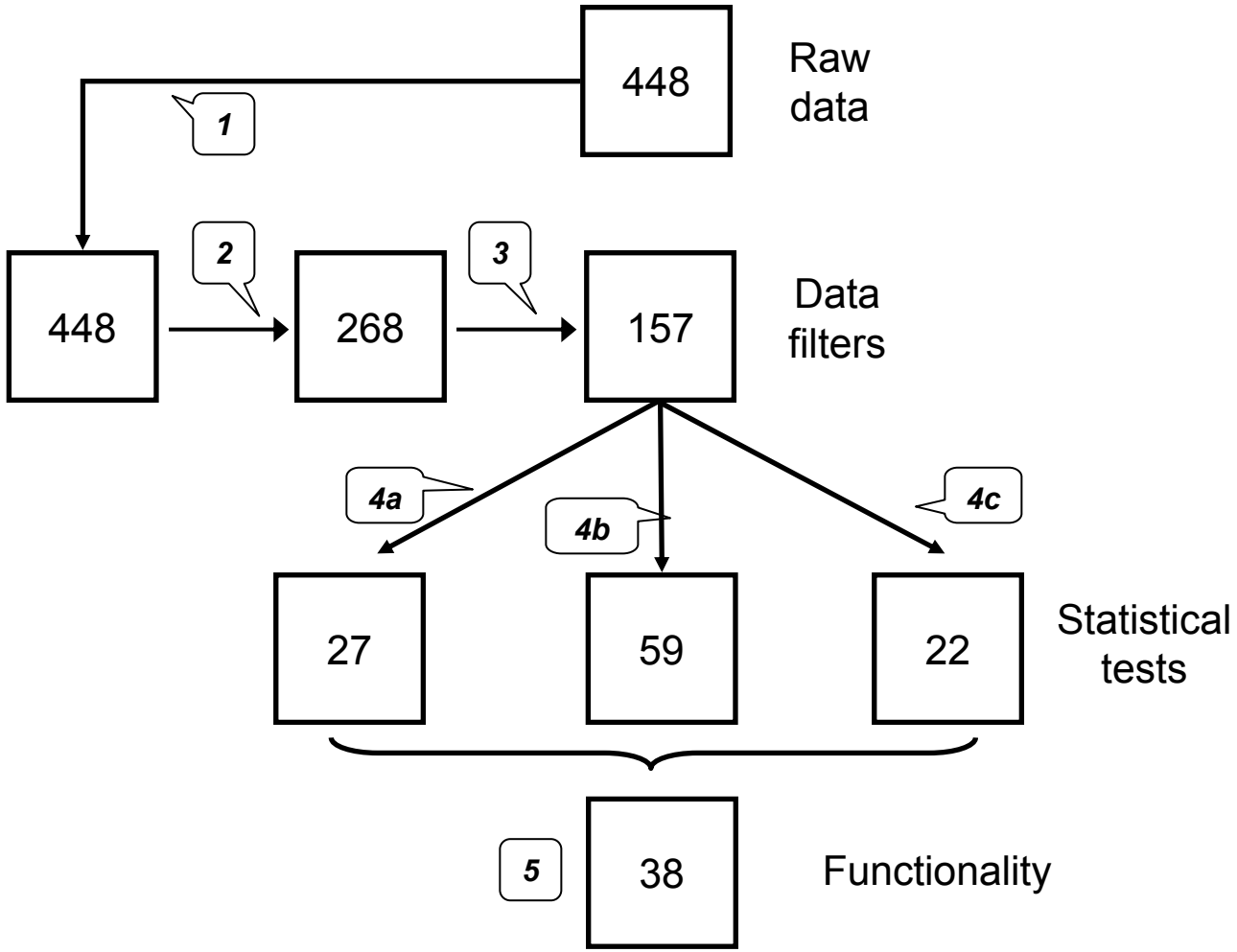


Supplementary Figure 1, Urzua et al

Supplementary figure 1. Experimental design

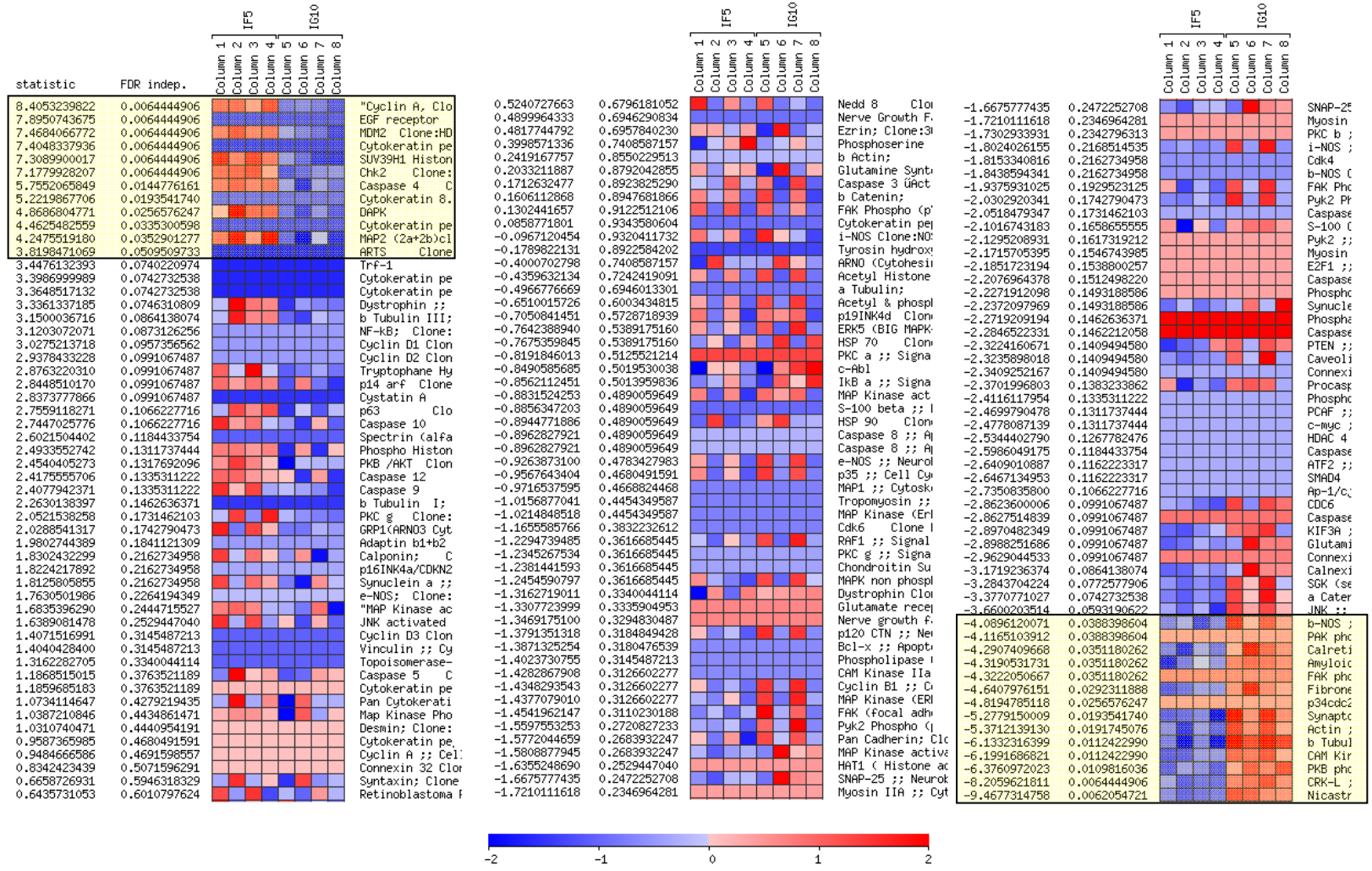
Numbers 1, 2 and 3 in circles depict culture replicates. Double forward and reverse arrows indicate repeated Cyanine-3/Cyanine-5 dye-swap experiments. The sample “Wnbm” is the common reference sample (see main text).



Supplementary Figure 2, Urzua et al

Supplementary figure 2. Data analysis workflow

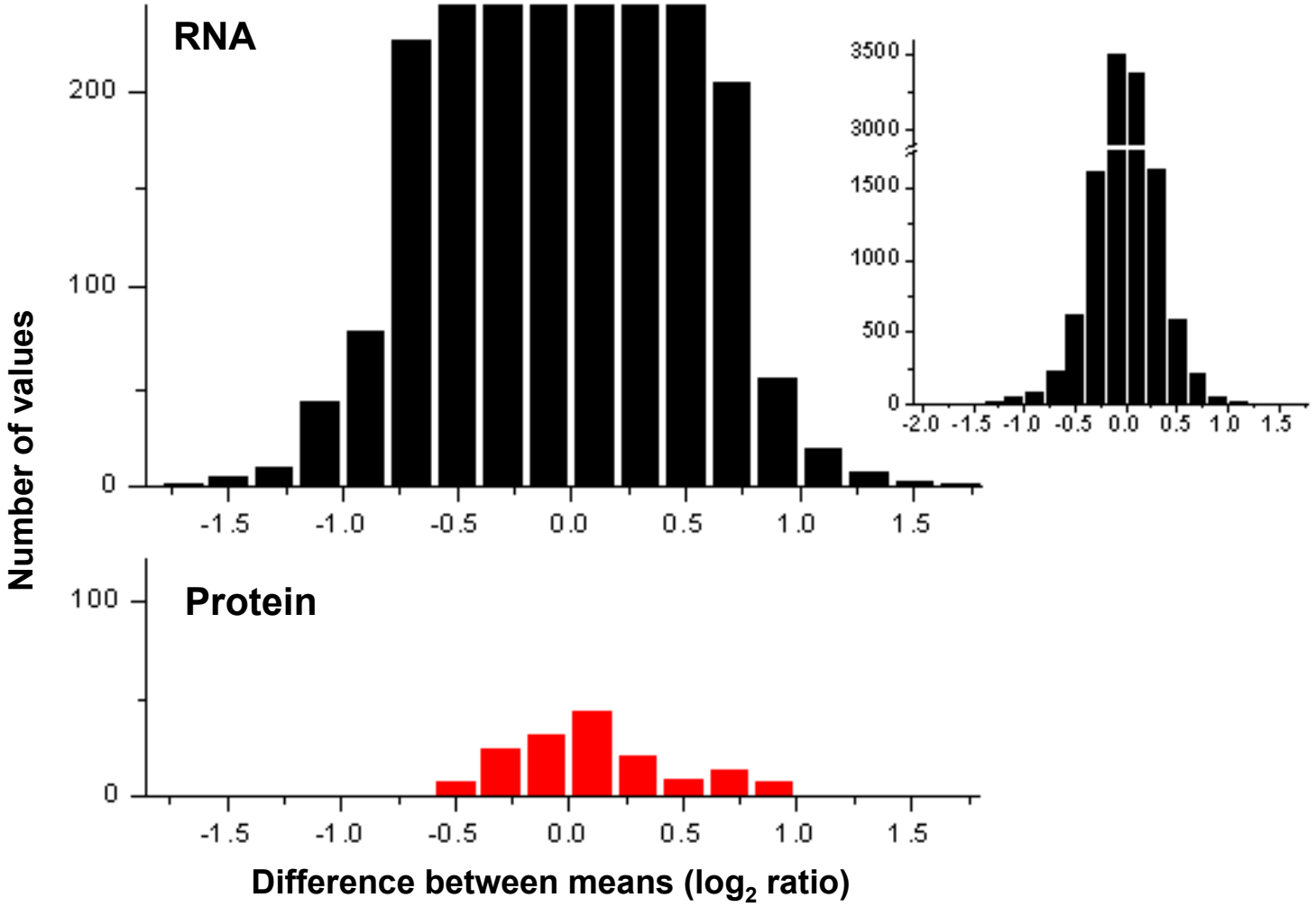
Steps of numerical analysis were: 1 = Lowess normalization; 2 = Dye-swap consistency; 3 = resolution of repeats; 4 = two classes tests, a) t-test, b) SAM, c) Clear; 5 = data mining and interpretation.



Supplementary Figure 3, Urzua et al

Supplementary figure 3. Sample output of a 2-class statistical test

Graphical representation of t-test results as generated by the T-rex tool. The original image was split in 3 parts with top-leftmost corresponding to proteins upregulated in IF5 and bottom-rightmost, proteins upregulated in IG10. Yellow boxes highlight statistical significance $p<0.05$ (FDR indep).



Supplementary Figure 4, Urzua et al

Supplementary figure 4. Microarray RNA and protein data distribution

The difference between mean log2-ratios between IG10 minus IF5 mRNA data and IG10 minus IF5 protein data obtained from two-color DNA and antibody microarray platforms respectively, is shown in the same scale of number of values. Total mRNA values were 11,970 and total protein values were 146. The inset shows the overall mRNA data distribution. Axes legends are the same as major plots.