**Figure 3–source data 3. d3’UTR ratio imbalance obtained from microarray data.**

Microarray\_d3UTR\_significance.R: R-script used to perform the analysis

global\_HuGene\_CTR\_v\_CLP1\_SH2\_3dUTR.csv: This file corresponds to: global\_HuGene\_CTR\_v\_CLP1\_SH2.csv that was obtained from **Figure 3-source data 2** and restricted to the d3’UTR features.