**Figure 3–source data 2. Microarray individual probe d3’UTR mapping and d3’UTR ratio calculation.**

- R-script to perform individual probe d3’UTR mapping and d3’UTR ratio calculation:

Microarray\_d3UTR\_hg19.R

Dependent files:

- annotation file including 3d’UTR features for microarray analysis (**Figure 1-source data 1**):

features\_hg19\_UTR\_d.csv

- Individual probe location on hg19:

HuGene-1\_0-st-v1.hg19.probe.csv

- Individual probe expression obtained from the comparison: CTR versus CLP1 sh2 KD samples (**Figure 3-source data 1**):

ST1features\_CTR\_v\_CLP1\_SH2.csv

Result file:

global\_HuGene\_CTR\_v\_CLP1\_SH2.csv

In the result file, the feat\_WTnorm and feat\_KOnorm columns correspond, for the 3UTRd features, to the d3’UTR ratios in WT and KO samples, respectively.