**Figure 1–source data 1. d3’UTR annotation files in mice and humans for RNA-seq and microarray analyses**

A proximal pA was validated when its genomic location from the PolyA\_DB 2 database differs from 20bp at least to the genomic location of the UCSC annotated 3’UTR distal boundary or distal pA. In case of multiple proximal pAs, the most proximal one was considered.

GFF2\_features\_hg19\_UTR\_d.gtf

GFF2\_features\_mm9\_UTR\_d.gtf

These two annotation files are GTF files to be used with intersectBed and coverageBed for RNA-seq-based d3’UTR ratio calculation.

features\_hg19\_UTR\_d.csv

features\_mm9\_UTR\_d.csv

These two annotation files are to be used with our R-implementation of PLATA (Giraud et al. 2012) for individual probe-level microarray analyses and microarray-based d3’UTR ratio calculation.