





# Correction to ‘Bias-minimized quantification of microRNA reveals widespread alternative processing and 3’ end modification’

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The authors would like to correct the name of one of the cell lines used in this study (from ‘HeLa’ to ‘HeLaT’). This change does not affect the conclusions of the article.

The authors recently became aware that the HeLa-based cell line used in this study was a ‘HeLaT’ cell line that has a defect in TUT4 (terminal uridylyl transferase) which uridylates miRNA precursors. This does not change the conclusions of the paper because TUT4 is functionally redundant to its close paralog TUT7 which remains intact in HeLaT cells and because the conclusions of the paper were derived mainly from another cell line (HEK293T).

Nevertheless, the authors performed additional experiments with the parental HeLa cells and confirmed the findings of the paper (Figures 1-3 below). Briefly, the parental HeLa and HeLaT cells show comparable miRNA profiles, with a slight increase in uridylation rate in HeLa compared with HeLaT cells, consistently with the known redundant function of TUT4 and TUT7. The new sequencing data from parental HeLa cells were deposited to the GEO repository (accession number: GSE123627).

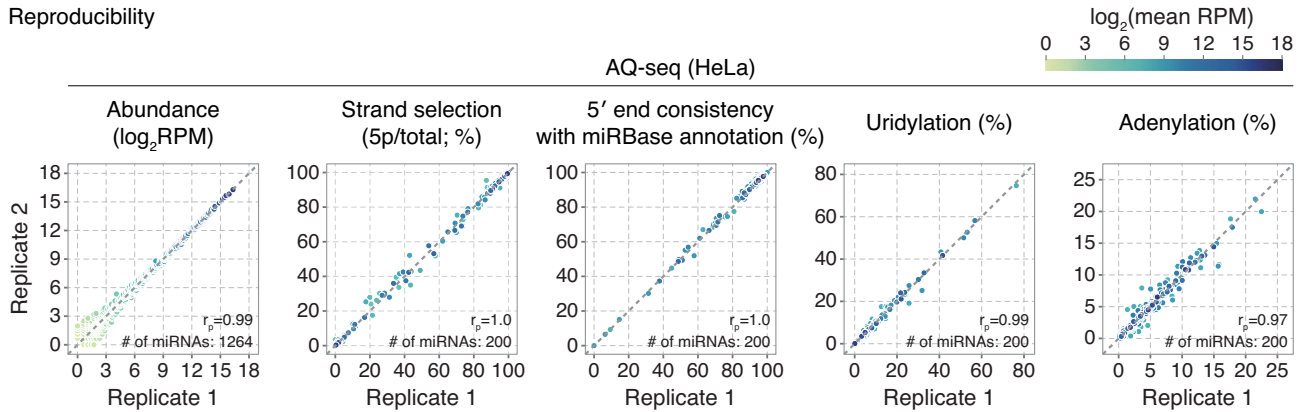
The authors apologise for this error.

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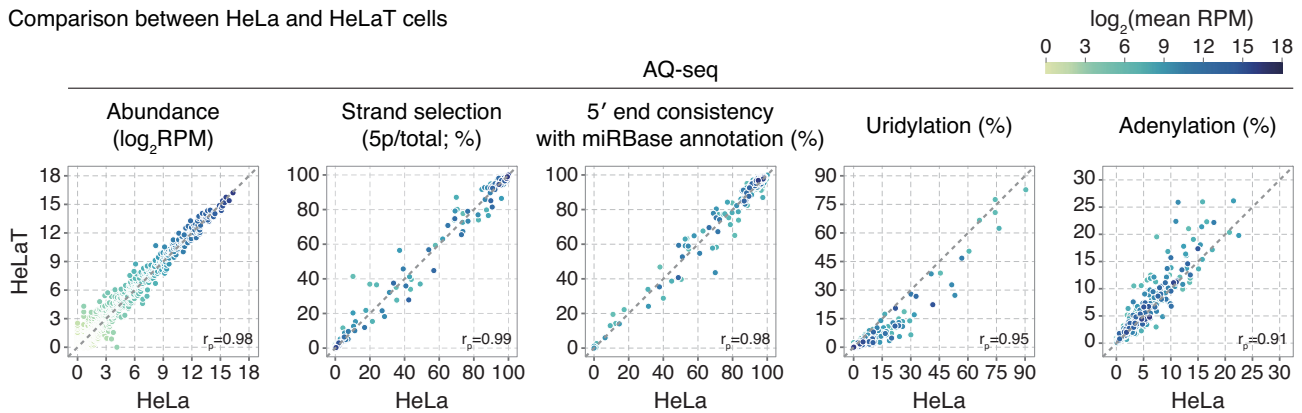
†The authors wish it to be known that, in their opinion, the first two authors should be regarded as Joint First Authors.

Reproducibility



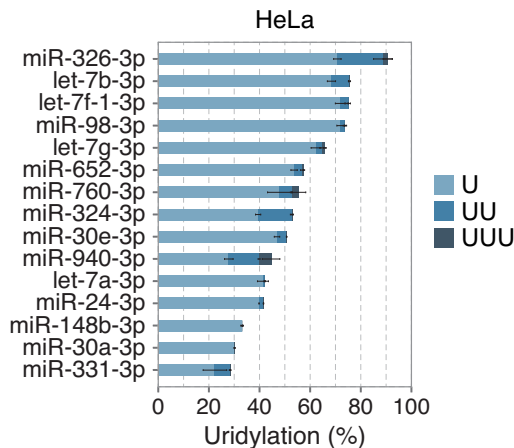
**Figure 1.** Reproducibility of AQ-seq results using parental HeLa cells (related to original Supplementary **Figure S2A**, second panel). Top 200 abundant miRNAs were included in each analysis except the expression profile to which no abundance filter was applied. RPM, reads per million.

Comparison between HeLa and HeLaT cells



**Figure 2.** Comparison of AQ-seq results between parental HeLa and HeLa T cells. Abundant miRNAs (>100 RPM) were included in each analysis except the expression profile.

Top 15 highly uridylated miRNAs



**Figure 3.** Top 15 highly uridylated miRNAs in parental HeLa cells (related to original **Figure 6A**, right panel). Abundant miRNAs (>100 RPM) were included in this analysis. The types of U-tail are indicated by different colors; light blue, blue, and navy refer to mono-uridylation (U), di-uridylation (UU), and tri-uridylation (UUU), respectively. Bars indicate mean  $\pm$  standard deviations (s.d.) (n = 2).