

RNA structure profiling at single-cell resolution reveals new determinants of cell identity

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The Description of Tables S1–S6

Supplementary table 1

The sequencing mappability of each sample (single-cell or mini-bulk) at different time points of batch 1 and batch 2.

Supplementary table 2

The RNA structure heterogeneity of each gene is calculated based on the cosine distance (gene level).

Supplementary table 3

Unsupervised clustering of RNA windows based on their structural heterogeneity (window level R^2).

Supplementary table 4

The well-correlated genes between RNA structure changes and their translation changes during the neurogenesis process.

Supplementary table 5

The genes that have both RNA structure changes and RNA half-life changes in hESCs and NPCs

Supplementary table 6

The sequence of benchmark genes (wildtype and their mutant) which were transfected in HEK293T cells.