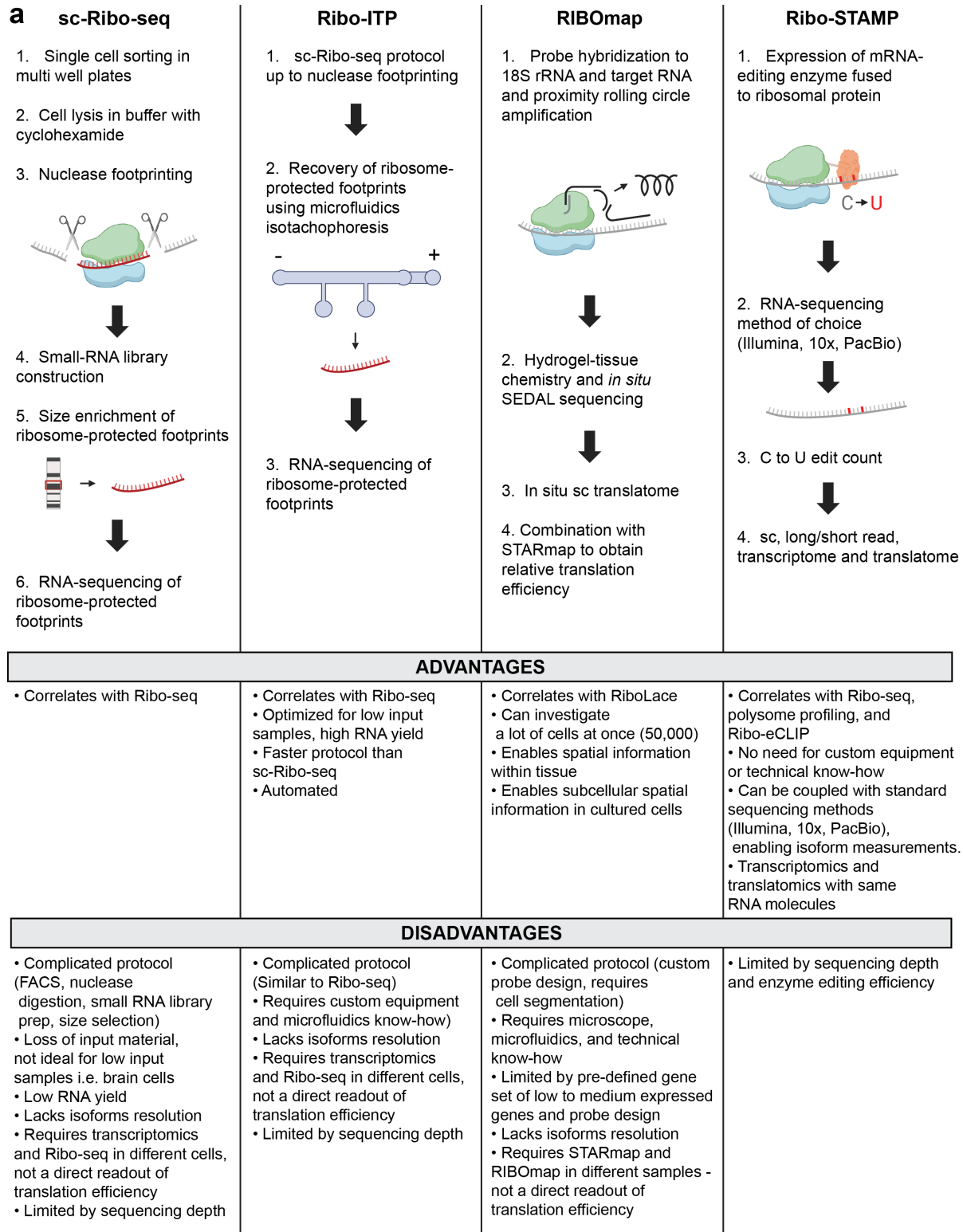

Supplementary information

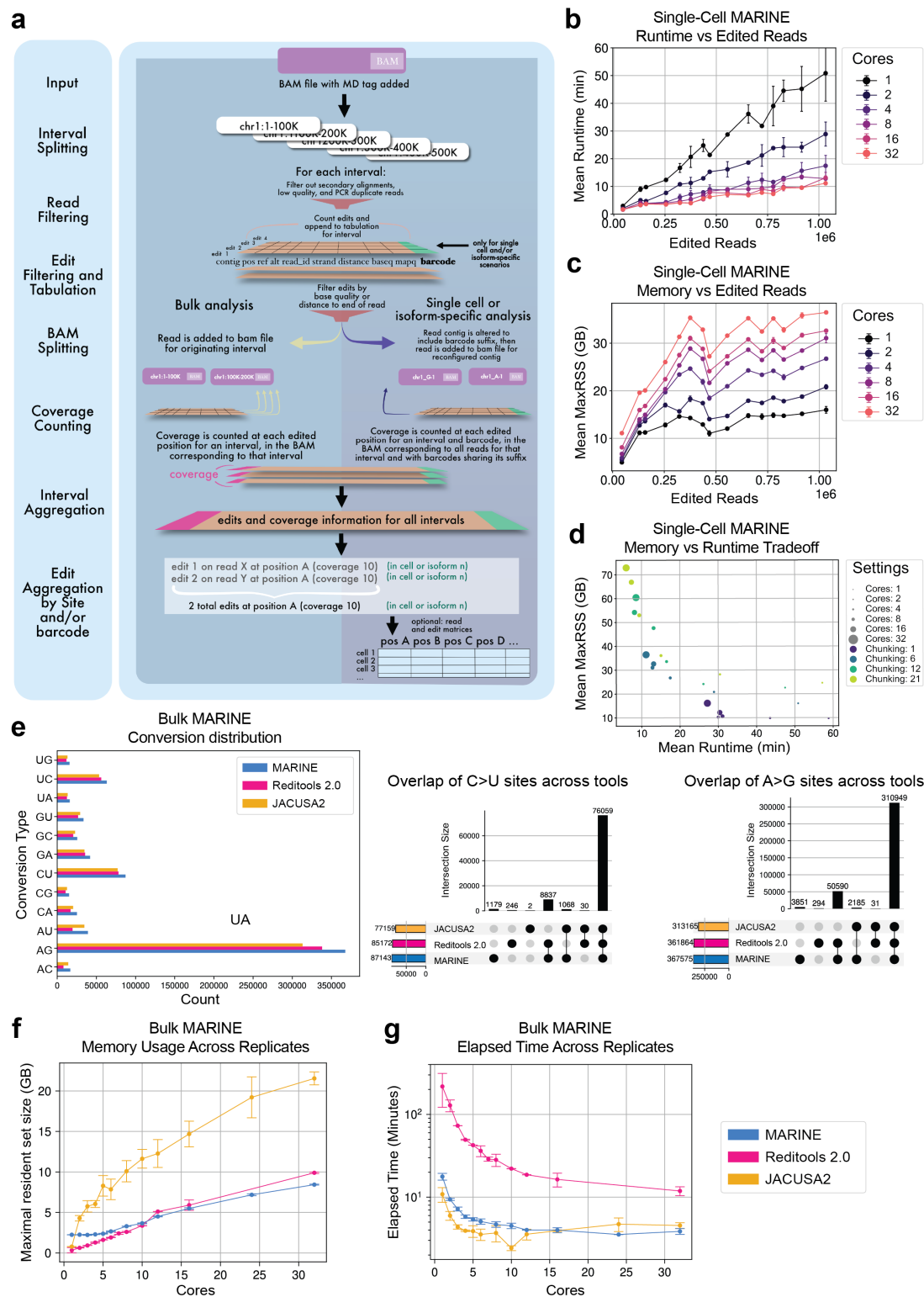
**Single-cell and isoform-specific
translational profiling of the mouse brain**

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Supplementary Information Fig.1. Schematic of sc translational profiling techniques. a, Schematic (top), advantages (middle), and disadvantages (bottom) of the four sc translational profiling techniques (sc-Ribo-seq, Ribo-ITP, RIBOmap, and Ribo-STAMP). Briefly, scRibo-seq

is restricted by loss of input material, Ribo-ITP is better suited for low cell numbers but requires custom microfluidics, and RIBOmap requires a pre-selected list of genes for analysis, hindering unbiased discovery. Figure created in BioRender.



Supplementary Information Fig. 2. MARINE is a new computational tool that enables efficient analysis of RNA editing at single-cell resolution. a, Flowchart depicting MARINE's workflow for calling RNA edits of all types in bulk and single-cell samples. **b**, MARINE runs on

single-cell data with $O(n)$ time complexity, and runs faster with more cores. **c**, MARINE runs on single-cell data with $O(c)$ memory complexity, depending on RAM available. **d**, By throttling the number of contigs simultaneously processed, users can find an optimal trade-off between memory and runtime for their runtime environment. **e**, Edit conversion distributions from MARINE, Reditools2.0 and JACUSA2 are comparable, with concordant site discovery across all three tools. **f**, MARINE runs on bulk data with $O(n)$ time complexity with regard to edited reads; example runs using 32 cores. **g**, MARINE runs on bulk data in with $O(c)$ memory complexity, which can be adjusted by modifying processed genomic interval size; example runs using 32 cores. **(b,f,g)** bars represent standard deviation.