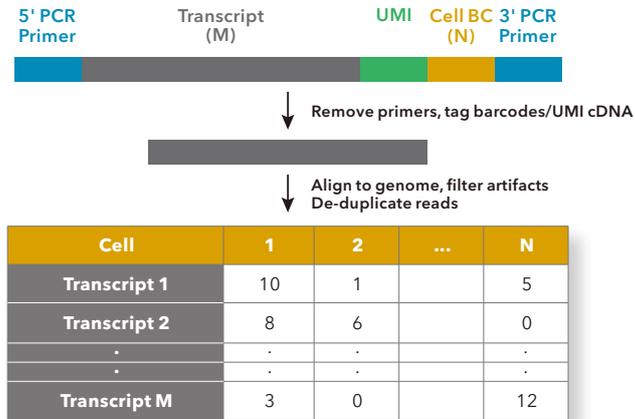


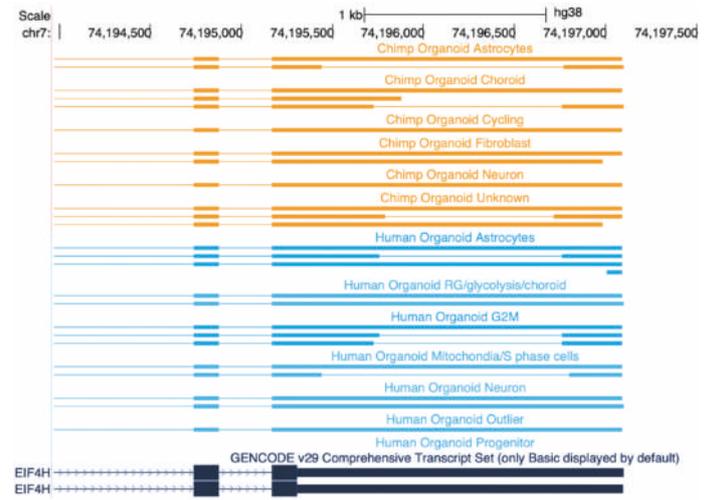
DATA ANALYSIS SOLUTIONS

- Analyze HiFi reads which allow accurate single-cell barcode and UMI identification⁸
- Use the single-cell Iso-Seq analysis tools on GitHub⁸ to output high-quality, full-length transcript FASTA sequences per UMI, with no assembly required, to characterize transcript variants for each cell



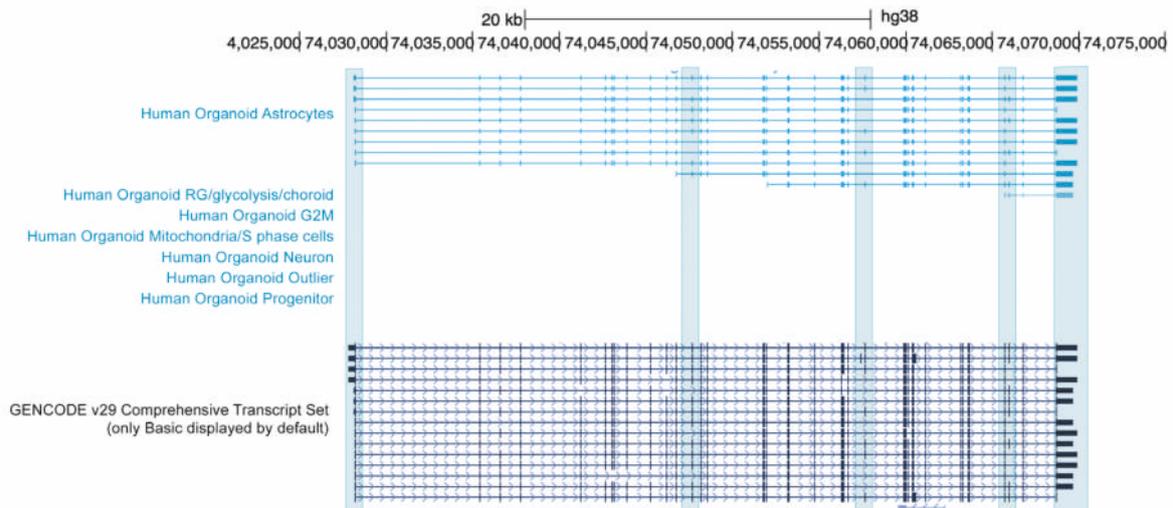
From gene count matrix to isoform count matrix.

COMPARE ALTERNATIVE GENE-SPLICING EVENTS BETWEEN SPECIES



Assessment of post-transcriptional gene regulation for the EIF4H gene, reveals isoform heterogeneity between cell types.

ASSIGN ALTERNATIVE ISOFORMS TO CORRECT CELL TYPE



The GENCODE database catalogs the numerous alternatively spliced Tropoelastin isoforms. Single-cell RNA sequencing assigned isoforms to individual cell types with multiple isoforms expressed in astrocytes and absent in other brain-specific cell types. The blue boxes also indicate new alternative splicing events compared to the reference.

KEY REFERENCES

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7. Macaulay et al. (2015) [G&T-seq: parallel sequencing of single-cell genomes and transcriptomes](#). *Nature Methods* 12: 519
8. [Data Analysis Procedure on PacBio GitHub](#)



Single-Cell
RNA Sequencing