Single cell RNA-seq (scRNA-seq) is an emerging field for characterizing cell heterogeneity in complex tissues. However, most scRNA-seq methodologies are limited to gene count information due to short read lengths.

Here, we combine the microfluidics scRNA-seq technique, Drop-Seq, with PacBio Single Molecule, Real-Time (SMRT) Sequencing to generate full-length transcript isoforms that can be confidently assigned to individual cells.

We generated single cell Iso-Seq (scIso-Seq) libraries for chimp and human cerebral organoid samples on the Dolomite Nadia platform and sequenced each library with two SMRT Cells 8M on the PacBio Sequel II System. We developed a bioinformatics pipeline to identify, classify, and generate full-length transcript isoforms that can be used to characterize cell heterogeneity in many different species.