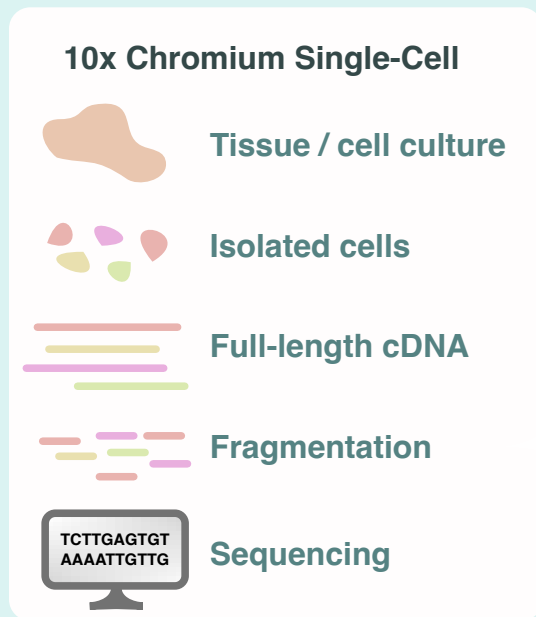


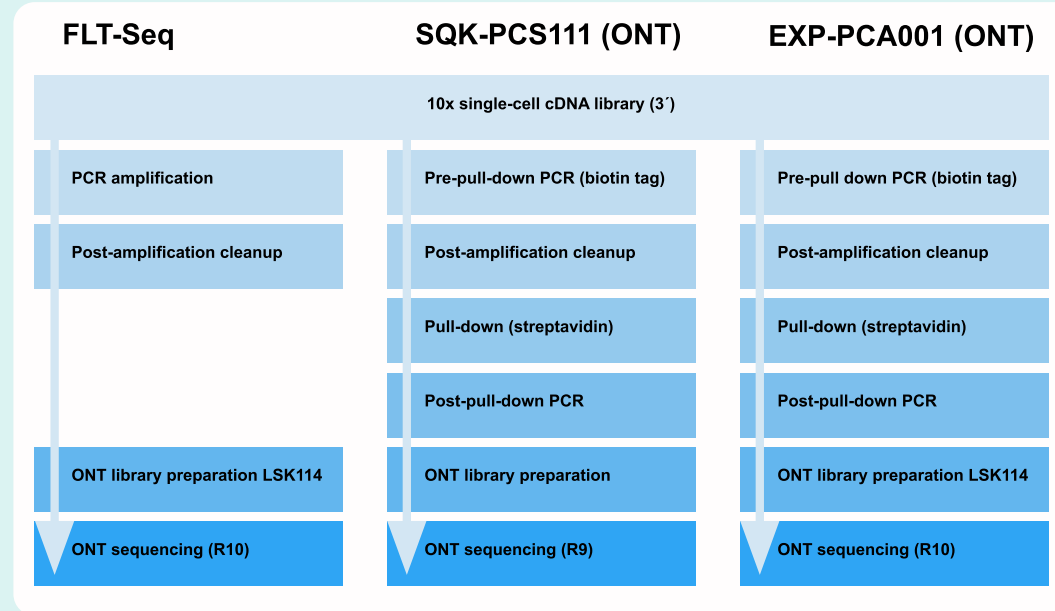
Isoform-Level Analysis of 10x Genomics Single-Cell cDNA Libraries from Cultured K562 Cells Using Long-Read Sequencing

Short reads can miss the bigger picture



Fragmentation erases the variation of full-length mRNA. To fully analyze this complexity of mRNA isoforms, long-read sequencing of unfragmented mRNA is necessary.

Evaluate three methods for mRNA isoform seq



Result

All three methods performed similarly well and are suitable for mRNA isoform analysis. The “FLT-seq” method was preferred for its simpler protocol and cost-effectiveness.