

Technical Overview mapper				
	Cell Ranger	STARsolo	Alevin	Kallisto
Mapping scheme	Exact alignment	Exact alignment	Pseudo mapping	Pseudo mapping
Internal Mapper	Star	Star	Salmon	Kallisto
Reference	Genome	Genome	Transcriptome + Genome	Transcriptome
Supported sequence technology	10X Chromium v1 – v3	10X Chromium v2;v3, Smart-seq, Drop-seq, inDrop	10x Chromium v2;v3, Drop-seq, Cel-seq, Cel-seq2, Quartz-seq2	10x Chromium v1 – v3, Cel-seq, Cel-seq2, Drop-seq, inDrops v1-v3, SCRB-Seq, SureCell
Barcode correction	1-Hamming distance based	1-Hamming distance based	Edit distance calculation	1-Hamming distance based
Whitelisting	Whitelist based	Whitelist based	Frequency based, no whitelist needed	Whitelist based
Alternative Splicing detection	no	yes	no	no
UMI correction	Two round correction by barcode, read count and annotation	Two round correction by barcode, read count and annotation	graph based correction	NA
Index	Suffix array	Suffix array	Colored De-Bruijn Graph	Colored De-Bruijn Graph
Handling of multimapped reads	discarded	discarded	Distributing read count between genes by EM-algorithm	discarded
Output	Matrix + Bam-File and summary file as html-file with primary results as well as clustering and DEG analysis	Gene count matrix and primary results summary	Gene count matrix ready for analysis	External software required to create gene count matrix