

a) Nextera library construction

b) Droplet capture and microfluidic barcoding

c) Final library amplification

d) Final library structure & read configuration for sequencing on illumine platforms

e) Reverse transcription with barcoded oligonucleotides

f) Tagmentation of mRNA/cDNA hybrids

g) Gap repair & Exol treatment

h) Droplet capture and microfluidic barcoding

i) Final library amplification

j) Final library structure & read configuration for sequencing on illumine platforms

a, Detailed outline with oligonucleotide sequences of the ATAC modality of SUM-seq for each step of the experimental workflow. **b**, Detailed schematic outline with oligonucleotide sequences of the RNA modality of SUM-seq. **c**, Bioanalyzer profiles of final SUM-seq snATAC- (upper panel) and snRNA-seq (lower panel) libraries. **d**, Raw recovery values (upper panel) and percentages (lower panel) of nuclei recovery before and after 10x Chromium loading.