

scPipe workflow

Fastq reformat
(sc_trim_barcode)

Reads alignment
(Rsubread::align)

Exon mapping
(sc_exon_mapping)

Barcode demultiplex
(sc_demultiplex)

Gene count
(sc_gene_counting)

Gene counting
matrix

An SCDData object for quality control
and further downstream analysis

Quality control metrics collected at each step

Number of
Removed reads

Alignment rate

Number of
reads mapped to
intron/exon

Reads per
cell;
unmatched
barcodes

Number of
corrected
UMI & filtered
genes

Quality control
information matrix