

Supplementary Tables: Single cell transcriptome sequencing on the Nanopore platform with ScNapBar

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Table S1: Odds ratio from Fisher's test on the number of the correct and wrong barcode assignment.

	Sicelore	ScNapBar
Barcode start positions \geq 3-nt	24.797 *	0.141 *
Number of mismatches \geq 2	5.881 *	3.646 *
Number of indels \geq 2	12.607 *	7.894 *
Highest barcode occurrence in multiple matches	2.161 *	3.613 *

* p-value <0.01.

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Table S2: Cell Ranger Summary.

Number of Reads	80,860,737
Estimated Number of Cells	2,052
Mean Reads per Cell	39,405
Median Genes per Cell	4,064
Total Genes Detected	18,266
Median UMI Counts per Cell	15,791
Valid Barcodes	97.1%
Valid UMIs	93.6%
Sequencing Saturation	11.3%
Q30 Bases in Barcode	96.6%
Q30 Bases in UMI	96.5%
Q30 Bases in RNA Read	94.9%
Reads Mapped to Genome	96.1%
Fraction Reads in Cells	85.1%
