

# Supplementary Information for “UMI or not UMI, that is the question for scRNAseq zero-inflation”

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Table 1. Overview of analyzed data sets<sup>1</sup>

Data	Method	Cells	Genes	Measurements	percentage of genes over $x$ percentage points away from expected fraction			
					1 percentage point	5 percentage points	10 percentage points	20 percentage points
Cortex	10xChromium	5720	23313	reads	72.17%	59.31%	52.78%	43.95%
				UMIs	9.62%	2.69%	1.25%	0.24%
	DroNc-seq	3087	22864	reads	72.07%	57.72%	49.07%	36.09%
				UMIs	15.82%	1.89%	0.50%	0.06%
	Sci-RNA-seq	5792	23493	reads	74.05%	59.61%	51.80%	41.49%
				UMIs	8.19%	1.60%	0.37%	0.08%
PBMC	Seq-Well	5676	22978	reads	54.24%	37.97%	28.26%	15.51%
				UMIs	5.17%	1.58%	0.91%	0.54%
	Drop-seq	11052	25015	reads	57.97%	44.28%	38.06%	29.96%
				UMIs	7.88%	0.52%	0.18%	0.05%
	inDrops	11350	21514	reads	63.53%	50.24%	43.25%	32.57%
				UMIs	3.29%	0.67%	0.21%	0.06%
	CEL-Seq2	560	22730	reads	86.03%	75.22%	69.34%	61.77%
				UMIs	17.70%	2.26%	0.73%	0.17%
	10xChromiumv3	4027	22499	reads	62.61%	48.07%	41.13%	31.68%
				UMIs	13.01%	3.26%	1.28%	0.45%
	10xChromiumv2	11768	24968	reads	57.83%	44.52%	37.94%	29.11%
				UMIs	5.03%	1.18%	0.44%	0.18%

Table shows results for data sets<sup>1</sup> for heterogeneous cells from cortex (top) and PMBCs (bottom), including scRNAseq method, cells and genes analyzed, and percentage of genes over  $x = 1, 5, 10, 20$  percentage points away from expected fraction for a negative binomial model without zero-inflation. Percentages are reported for both read counts and UMI counts. 10xChromium: Chromium Single Cell 3' Reagent; DroNc-seq: single nucleus RNA-seq with Drop-seq; Sci-RNA-seq: single-cell combinatorial-indexing RNA-seq; Seq-Well; Drop-seq: Droplet-Sequencing; inDrops: indexing droplets; CEL-seq2: improved version of CEL-seq; 10xChromiumv3 / v2: Chromium Single Cell 3' Reagent (version 3 / version 2, respectively).

## References

1. Ding, J. *et al.* *BioRxiv* 632216 (2019).

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**URN:** urn:nbn:de:hbz:465-20230912-163113-2

Authors Accepted Manuscript.

Supplementary Information for: Cao, Y., Kitanovski, S., Küppers, R. et al. UMI or not UMI, that is the question for scRNA-seq zeroinflation. *Nat Biotechnol* 39, 158-159 (2021).

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