

Single-cell QC report

public 10x PBMC 3k dataset (example run) · generated 2026-08-01 · OMICSDESK

2,700

cells / barcodes

32,738

genes

817

median genes/cell

2,197

median UMIs/cell

2.03%

median mitochondrial

6.6%

removed by suggestion

Suggested thresholds for this dataset

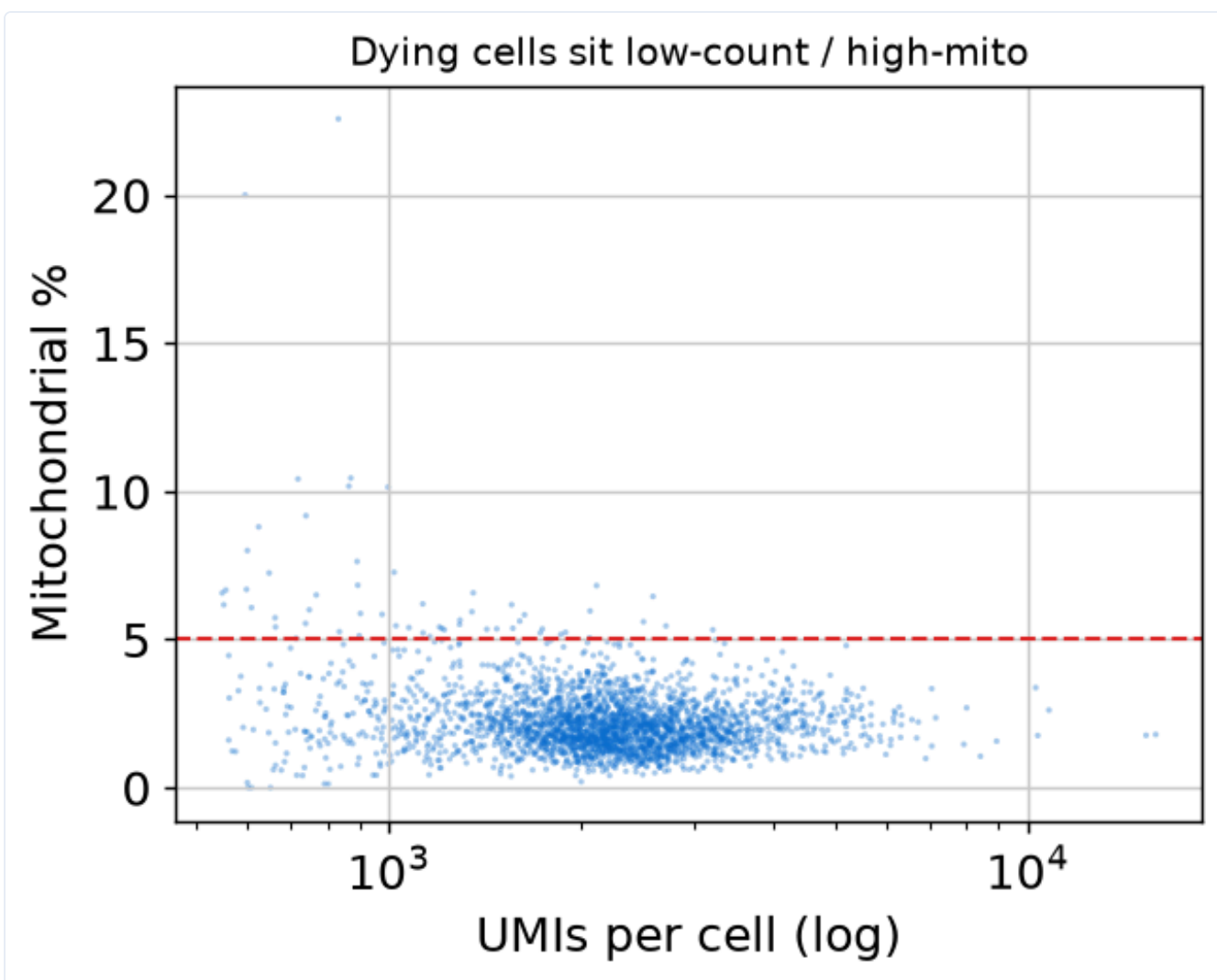
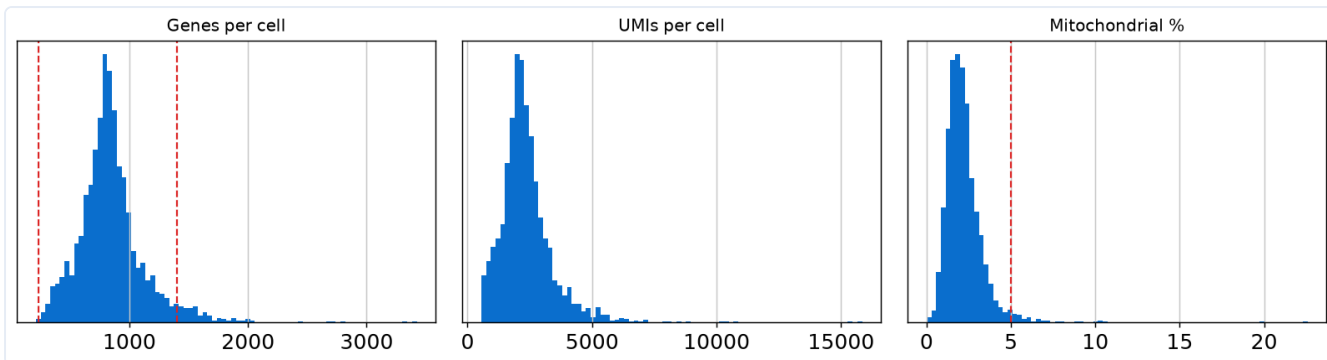
FILTER	SUGGESTED	COMMON TUTORIAL DEFAULT
Minimum genes per cell	232	200
Maximum genes per cell	1,402	2,500
Maximum mitochondrial %	5.0%	5%
Cells retained	2,523 of 2,700	

Thresholds are median $\pm$ 3 MAD of this dataset's own distributions, floored at 200 genes. They are a starting point, not a verdict — tissue biology beats any formula. A 5% mitochondrial cut-off, for example, deletes real cells in heart, liver and muscle.

Things worth a second look

No structural problems detected in these metrics.

Distributions

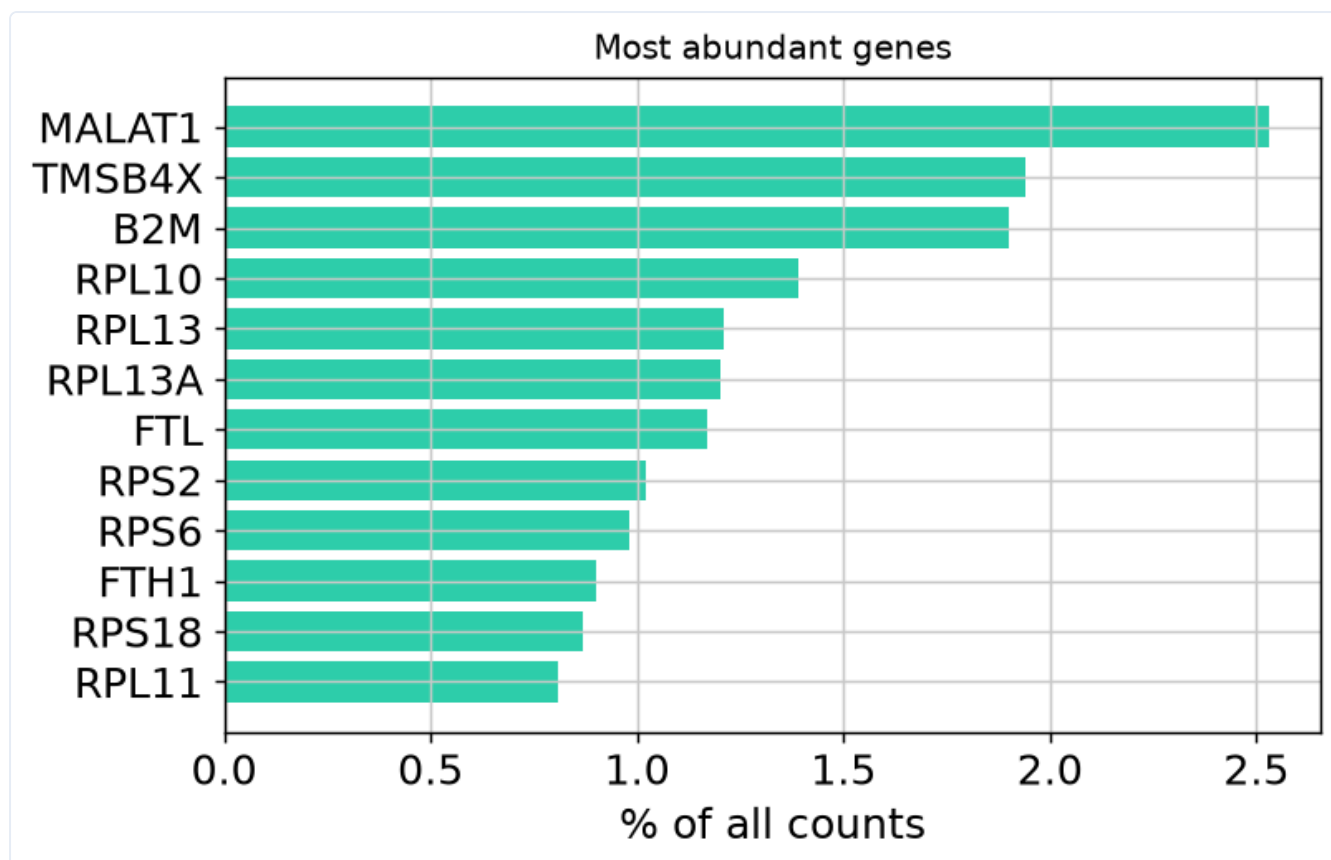


[Barcode rank](#)



Most abundant genes

The top 10 genes carry **14.2%** of all counts. A high share, or haemoglobin and mitochondrial genes at the top, usually indicates ambient RNA rather than biology.



GENE	% OF COUNTS
MALAT1	2.53%
TMSB4X	1.94%
B2M	1.9%
RPL10	1.39%
RPL13	1.21%
RPL13A	1.2%
FTL	1.17%
RPS2	1.02%
RPS6	0.98%
FTH1	0.9%

What comes next

Quality control is the first step. A full analysis continues with empty-droplet removal, ambient-RNA correction, doublet detection (expect roughly 58 doublets at this cell count on a droplet platform), normalisation, integration where needed, clustering, annotation verified against an independent reference, and differential testing at the level of subjects rather than cells.