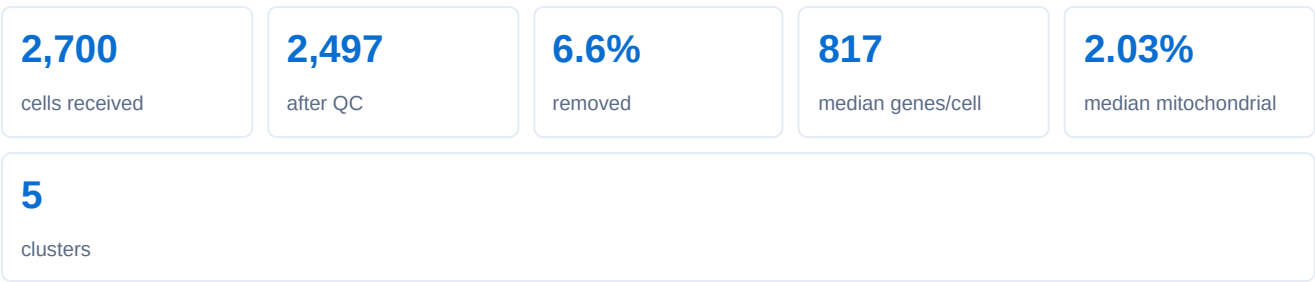


Example delivery — public PBMC 3k

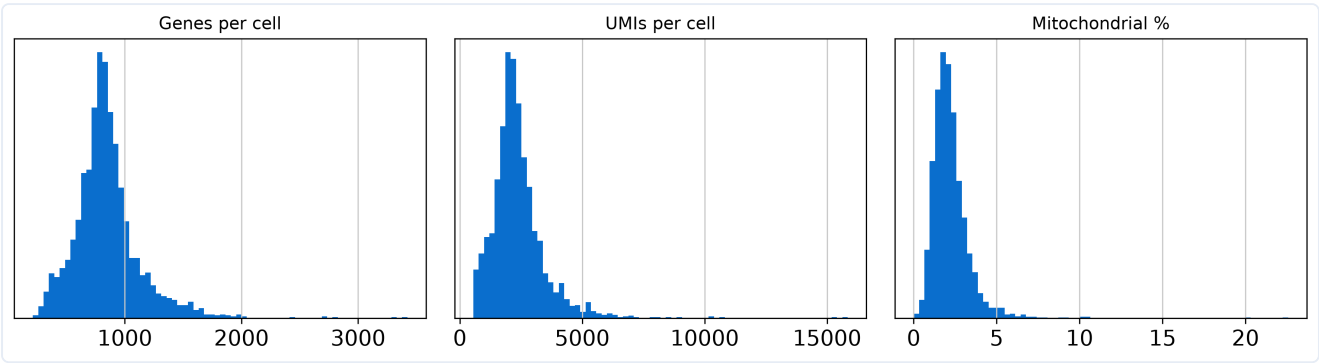
Analysis report · generated 2026-07-31 · OMICSDESK

Summary



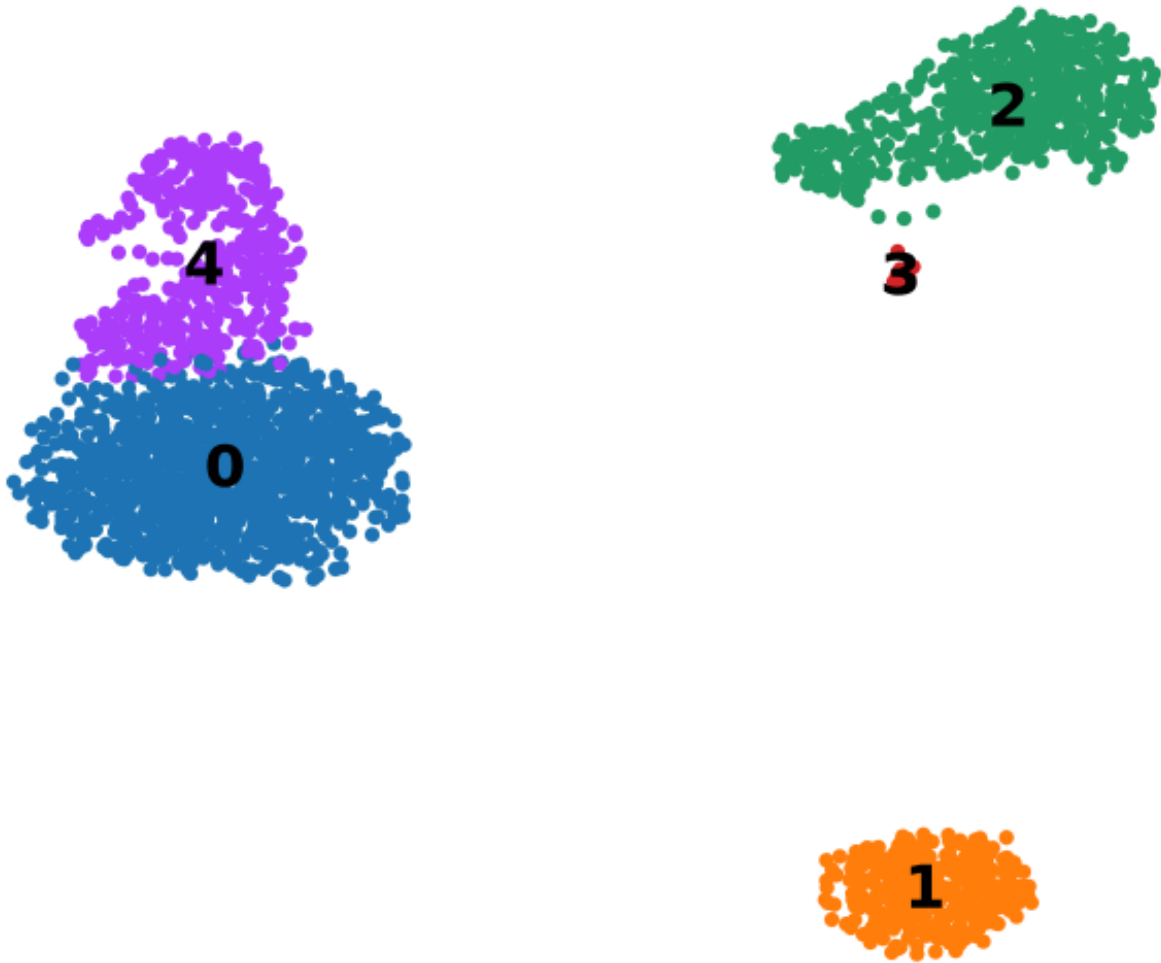
Quality control

Thresholds were derived from this dataset rather than copied from a tutorial: cells were required to have at least 200 and at most 1401 detected genes, and below 5.0% mitochondrial content (median + 3 MAD of the observed distribution).

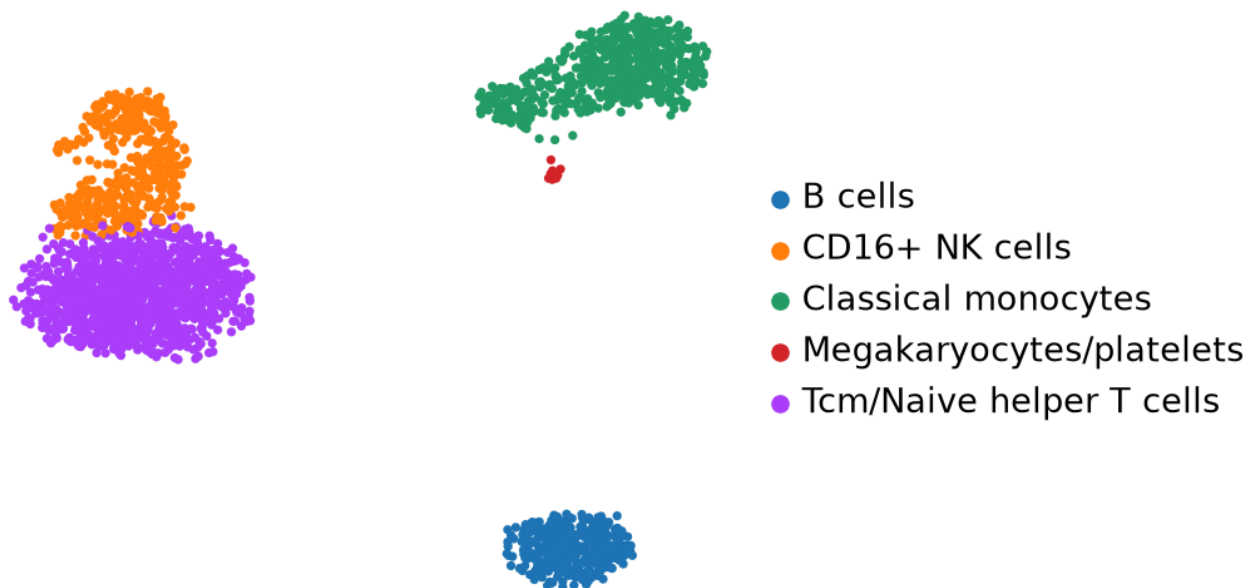


Clusters and cell types

Clusters



Cell types



CELL TYPE	CELLS	SHARE
Tcm/Naive helper T cells	1,156	46.3%
Classical monocytes	583	23.35%
CD16+ NK cells	422	16.9%
B cells	324	12.98%
Megakaryocytes/platelets	12	0.48%

Cluster markers

CLUSTER	TOP MARKERS
0	LDHB, RPS12, RPS25, RPS6, RPS27, RPS3
1	CD74, HLA-DRA, CD79A, CD79B, HLA-DPB1, HLA-DQA1
2	FTL, FTH1, CST3, TYROBP, LYZ, LST1
3	PF4, PPBP, SDPR, GNG11, GPX1, NRG1
4	NKG7, CST7, CTSW, GZMA, B2M, CCL5

Between-group testing

no group/subject columns supplied — between-group testing not performed

No subject/group information was supplied, so no between-group test was run. This is deliberate: with cells rather than subjects as the unit, group comparisons produce false positives. Send a sample sheet with a subject column and the comparison is run at subject level (pseudobulk).

Methods

Single-cell RNA-seq data were processed with Scanpy 1.12.3. Cells with fewer than 200 detected genes, more than 1401 detected genes, or more than 5.0% of counts from mitochondrial genes were removed, leaving 2,497 of 2,700 cells. Predicted doublets ($n = 26$) were removed with Scrublet. Counts were normalised to 10,000 per cell and log-transformed; highly variable genes were selected, total counts and mitochondrial fraction regressed out, and the data scaled with values clipped at 10. Principal components were computed and a neighbourhood graph built from the first 30 components ($k = 10$). Cells were embedded with UMAP and clustered with the Leiden algorithm (resolution 0.5), giving 5 clusters. Cluster markers were identified with a Wilcoxon rank-sum test. Cell types were assigned with CellTypist Immune_All_Low. no group/subject columns supplied — between-group testing not performed

Files delivered

- **figures/** — publication-resolution figures (300 dpi)
- **tables/** — cluster markers, cell-type composition, QC summary
- **processed.h5ad** — the processed object for your own downstream work
- **run_manifest.json** — inputs, parameters, software versions and per-step timings

- **report.pdf** — this document

Every number in this report is read from run_manifest.json and the delivered tables, so the document and the data cannot drift apart. Re-running the pipeline on the same input reproduces both.

OMICSDesk · omics.sinogenomics.com · pipeline run 2026-07-31T15:24:51 → 2026-07-31T15:25:55 (63.6 s) · scanpy 1.12.3 · python 3.12.13