

cell_count_output_1

Alerts

The analysis detected ⚠ 1 warning and ⓘ 1 informational notice.

Alert	Detail
⚠ Unsupported workflow used	Multiome Gene Expression only analysis is not a supported workflow. Results may vary.
 ⓘ Automated cell type annotation is now available for Cell Ranger!	For details on how to run cell type annotation and which species we have it available for, visit our support page .

Summary Gene Expression

3,011

Estimated Number of Cells

56,560

Mean Reads per Cell

1,528

Median Genes per Cell

Run Summary

Sample ID	cell_count_output_1
Sample Description	
Chemistry	Single Cell Multiome ATAC + Gene Expression v1
Include introns	True
Transcriptome	GRCh38-2024-A
Pipeline Version	10.0.0

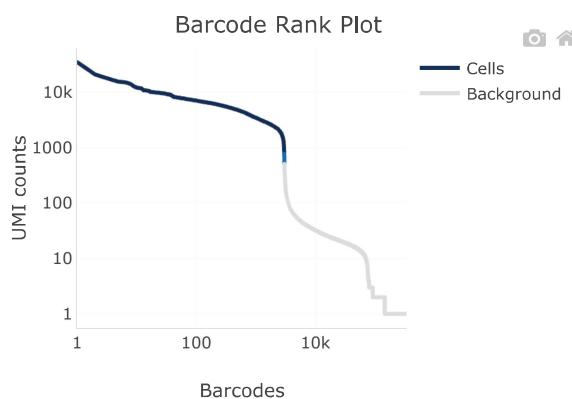
Sequencing ⓘ

Number of Reads	170,301,081
Number of Short Reads Skipped	0
Valid Barcodes	95.2%
Valid UMI Sequences	100.0%
Sequencing Saturation	89.0%
Q30 Bases in Barcode	93.0%
Q30 Bases in RNA Read	88.7%
Q30 Bases in UMI	92.4%

Mapping ?

Reads Mapped to Genome	96.0%
Reads Mapped Confidently to Genome	90.6%
Reads Mapped Confidently to Intergenic Regions	6.1%
Reads Mapped Confidently to Intronic Regions	40.8%
Reads Mapped Confidently to Exonic Regions	43.7%
Reads Mapped Confidently to Transcriptome	65.6%
Reads Mapped Antisense to Gene	18.3%

Cells ?



Estimated Number of Cells	3,011
Fraction Reads in Cells	87.4%
Mean Reads per Cell	56,560
Median UMI Counts per Cell	2,837
Median Genes per Cell	1,528
Total Genes Detected	27,315

Command Line Arguments Hide

```
cellranger-10.0.0/bin/cellranger count --id cell_count_output_1 --transcriptome  
human_reference_genome/refdata-gex-GRCh38-2024-A/ --fastqs pbmc_unsorted_3k/gex/ --sample  
-chemistry ARC-v1 --create-bam false
```

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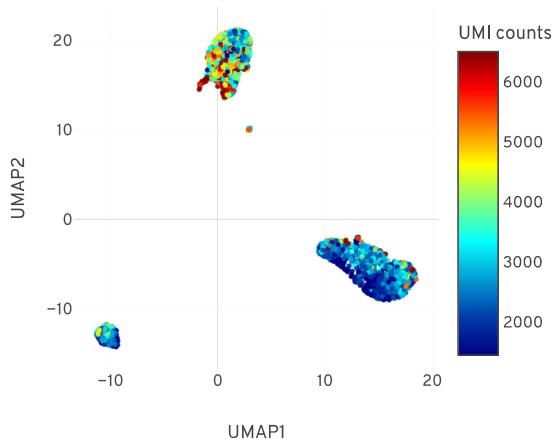
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[Summary](#) [Gene Expression](#)

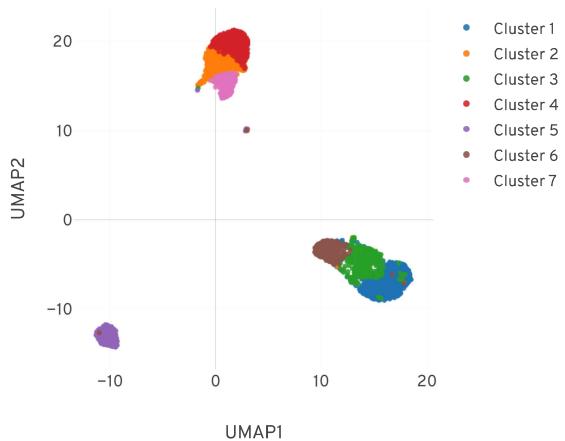
UMAP Projection ⓘ

Clustering Type: Graph-based ⓘ

UMAP Projection of Cells Colored by UMI Count ⓘ camera home



UMAP Projection of Cells by Clustering ⓘ ⓘ



Top Features by Cluster (Log2 fold-change, p-value) ⓘ

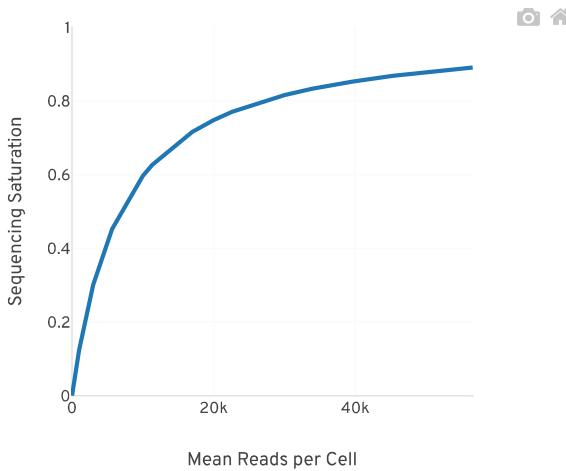
Feature		Cluster 1		Cluster 2		L
ID	Name	L2FC	p-value	L2FC	p-value	L
ENSG00000184613	NELL2	4.04	5e-37	-4.17	2e-16	L
ENSG00000138795	LEF1	3.69	2e-35	-4.31	1e-19	L
ENSG0000034053	APBA2	3.45	1e-27	-3.66	5e-14	L
ENSG0000091409	ITGA6	3.40	1e-26	-4.17	7e-16	L
ENSG00000126353	CCR7	3.37	1e-27	-3.45	1e-13	L
ENSG00000113319	RASGRF2	3.30	4e-25	-3.84	2e-14	L
ENSG00000290067	ENSG00...	3.04	6e-21	-2.67	2e-8	L
ENSG0000074966	TXK	2.96	3e-22	-3.22	2e-13	L
ENSG0000081059	TCF7	2.91	2e-21	-3.69	8e-16	L
ENSG00000152495	CAMK4	2.83	9e-21	-4.17	2e-19	L

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Sequencing Saturation ?



Median Genes per Cell ?

