

# count\_run1

## Alerts

The analysis detected 1 error.

| Alert   | Value | Detail  |
|---|-------|---|
| <span style="color: red;">1</span> Low Fraction Reads Confidently Mapped To Transcriptome | 6.3%  | Ideal > 30%. This can indicate use of the wrong reference transcriptome, a reference transcriptome with overlapping genes, poor library quality, poor sequencing quality, or reads shorter than the recommended minimum. Application performance may be affected. |

|         |          |
|---------|----------|
| Summary | Analysis |
|---------|----------|

9,731

Estimated Number of Cells

18

Mean Reads per Cell

1

Median Genes per Cell

### Sequencing ?

|                               |         |
|-------------------------------|---------|
| Number of Reads               | 178,160 |
| Number of Short Reads Skipped | 0       |
| Valid Barcodes                | 91.2%   |
| Valid UMIs                    | 99.9%   |
| Sequencing Saturation         | 0.2%    |
| Q30 Bases in Barcode          | 99.1%   |
| Q30 Bases in RNA Read         | 84.1%   |
| Q30 Bases in UMI              | 99.4%   |

### Cells ?

Barcode Rank Plot

|                            |        |
|----------------------------|--------|
| Estimated Number of Cells  | 9,731  |
| Fraction Reads in Cells    | 100.0% |
| Mean Reads per Cell        | 18     |
| Median Genes per Cell      | 1      |
| Total Genes Detected       | 5,113  |
| Median UMI Counts per Cell | 1      |

### Mapping ?

|  |       |
|--|-------|
| Reads Mapped to Genome                         | 16.9% |
| Reads Mapped Confidently to Genome             | 11.5% |
| Reads Mapped Confidently to Intergenic Regions | 4.2%  |
| Reads Mapped Confidently to Intronic Regions   | 0.4%  |
| Reads Mapped Confidently to Exonic Regions     | 6.9%  |
| Reads Mapped Confidently to Transcriptome      | 6.3%  |
| Reads Mapped Antisense to Gene                 | 0.4%  |

### Sample

|                    |                              |
|--------------------|------------------------------|
| Sample ID          | count_run1                   |
| Sample Description |                              |
| Chemistry          | Single Cell 3' v3            |
| Include introns    | False                        |
| Reference Path     | ...idopsis_thaliana.TAIR10   |
| Transcriptome      | Arabidopsis_thaliana.TAIR10- |
| Pipeline Version   | cellranger-6.0.1             |