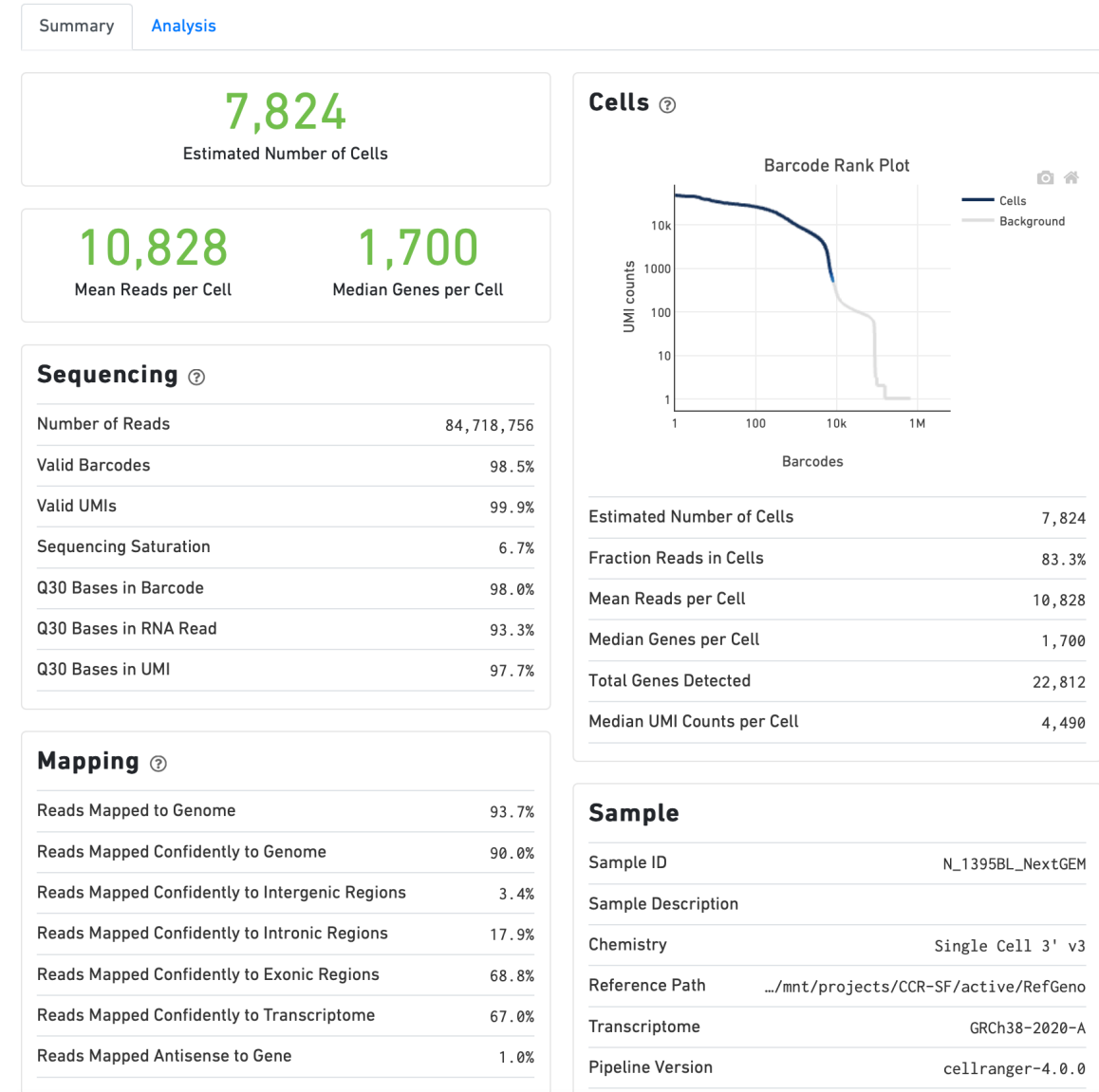
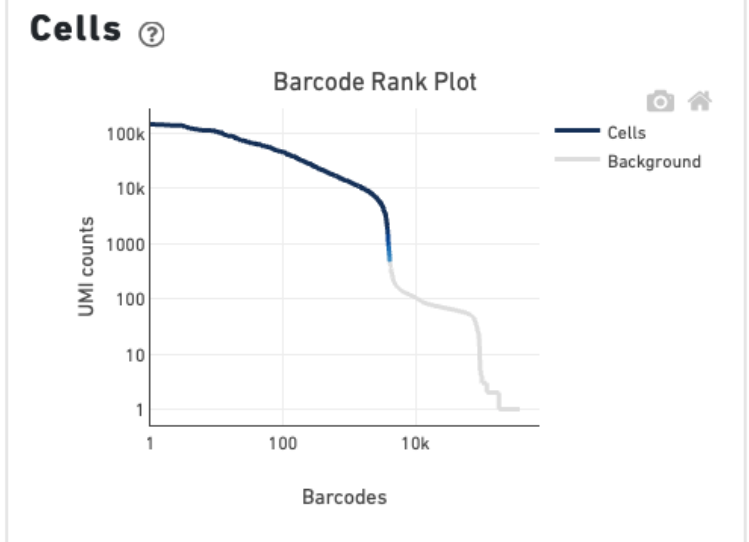
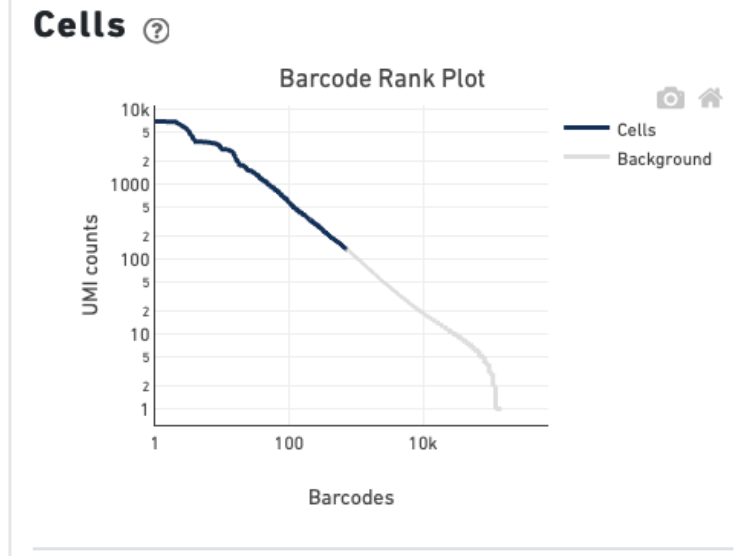


10X Cell Ranger and Basic Quality Control

- Count **function**
- Used to process **FASTQ** files for **10X** samples
- Generates **UMI** expression matrices, basic sample statistics, and interactive analysis platform
- Can only detect genes that are included in the reference genome used



- **Barcode Rank Plot (Knee plot) can be used to determine sample quality**
- **Cell Ranger increased sensitivity for low UMI cell populations**



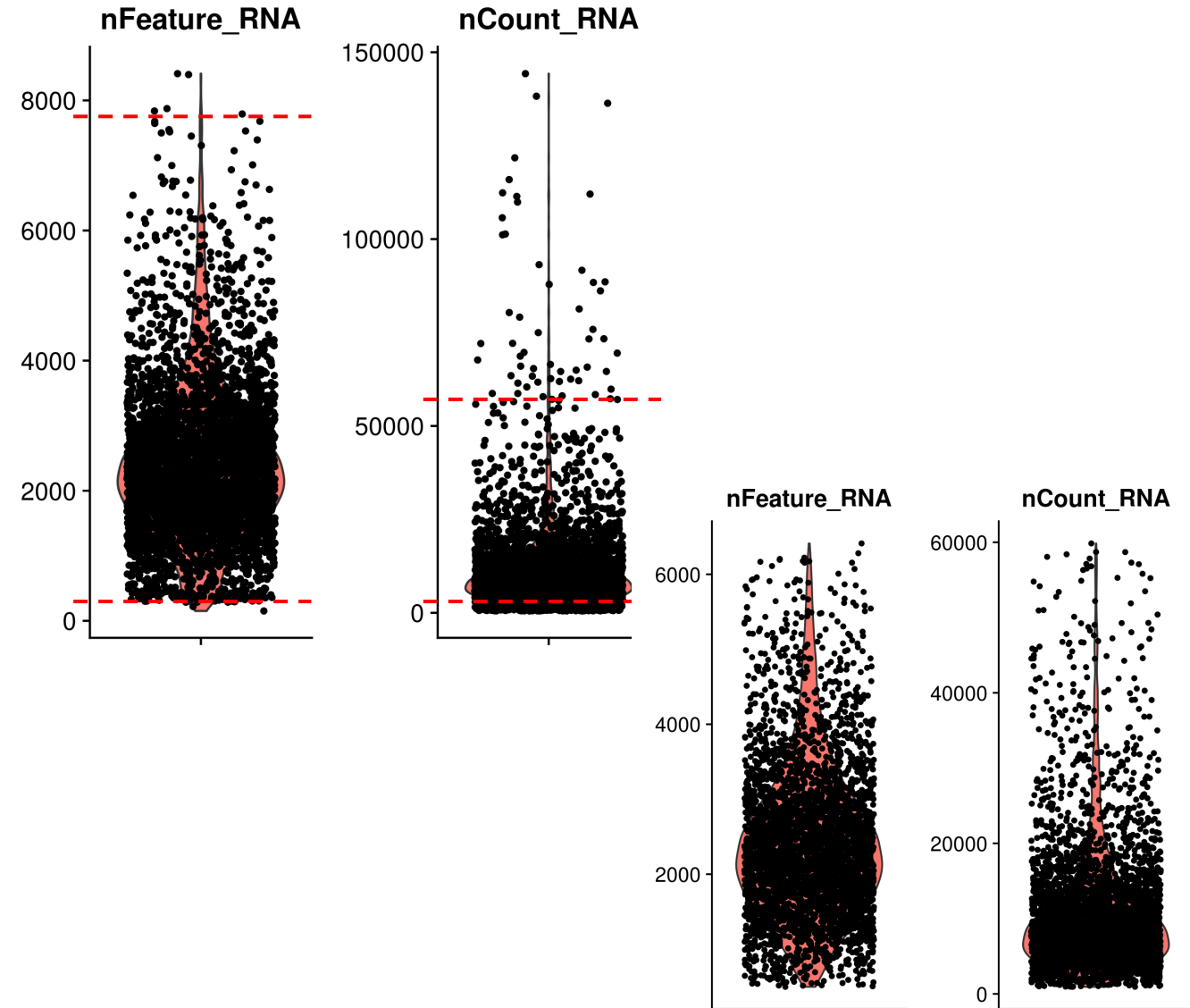
Filtering Data

- **Data can contain values present due to noise, low quality cells, or doublets/multiplets**
- **Filtering is used to remove the excess noise to have a clean analysis**
- **Genes or cells with very sparse amounts of data usually excluded for downstream analysis**
 - When a gene only shows up in a few cells, or a cell only contains a few genes this can be due to noise and have not enough data for analysis

- **Low quality cells include dying cells or cells with broken membranes**
 - Contains lower amounts of genes
 - Has a higher expression of mitochondrial genes
- **Doublet/Multiplets are when more than one cell is captured and labeled with the same cell barcode**
- **Stringent filters risk losing useful data**
- **Loose filters risk leaving in noise**

Cell Filtering

- Different cell types have different expression levels
- Filtering based on UMI count, gene count, and mitochondrial gene expression
- Cut-offs used for one cell type may not be appropriate for others
- Distributions and statistical methods can be used to find cut-offs



Cell Filtering

- Filtering based on UMI count, gene count, and mitochondrial gene expression
- Mitochondrial fraction is linked to cell death, which may influence normalization
- Different cell types have different expression levels
- Cut-offs used for one cell type may not be appropriate for others
- Distributions and statistical methods can be used to find cut-offs

