***CCR-Sequencing Facility Illumina Sequencing Report***

***Principal Investigator:*** {PI}

***PI Laboratory Contact:*** {LC}

***Bioinformatics Contact:*** {BC}

***Project Title:*** {PT}

***NAS Order ID:*** {CSAC}

***Samples Total in project:*** {STIP}

***Samples in This Report:*** {SITR}

***Completion of NAS:*** Yes

***Report Date:*** {DATE}

***Immediate data access:*** Data are available for via the following link. We recommend that you review the results as soon as possible and contact us at CCRSF\_IFX@nih.gov if you have any questions.

{DMELINK}

***Long-term data access:*** Data are being uploaded for long-term storage on your behalf to the NCI Data Vault and will be available via the DME interface, therefore you do not need to take any additional steps to back up this data or transfer it to another drive for storage. Additional details about the NCI Data Vault are provided at the end of this report.

***Data Integrity:*** To ensure the integrity of the files, we recommend verifying them against the MD5 information provided on DME. If you encounter any issues, please contact us at [CCRSF\_IFX@nih.gov](mailto:CCRSF_IFX@nih.gov).

***Sequencing Details***

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Flowcell IDs: |  | H7JY5BGXB | Sequence Control: |  | PhiX |
| Instrument: |  | NextSeq 500 | Control Result: |  | Pass |
| Flowcell Type: |  | scRNA | Library Protocol: |  | Chromium 3’ RNA-seq library prep, catalog number:  PN120237 |
| Sequencing Type: |  | scRNA | Reference Genome: |  | hg38 - 3.0.0 |
| Read Length: |  | R1: 26bp, R2: 57bp |  |  |  |
|  |  |  |  |  |  |

***Run Comments***

PLACEHOLDER

|  |
| --- |
| ***Note:*** *Residual samples will be retained up to* ***90 days*** *of the delivery of this report. To avoid shipping charges, please contact SFILLUMINALAB@mail.nih.gov to arrange pickup samples prior to this time.* |

***Analysis Workflow***



***Software and Parameters***

|  |  |  |
| --- | --- | --- |
| **Analysis Step** | **Software** | **Software Parameters / Notes** |
| Basecalling | RTA {RTAVERSION} | Illumina instrument run time analysis software |
| Demultiplexing | Bcl2fastq 2.20 | Barcode demultiplexed allowing 1 mismatch |
| Alignment, tagging,  gene and transcript counting,  clustering analysis | Cellranger {VERSION} | cellranger run --id=sample\_ID --transcriptome=reference\_dir --  fastqs=fastq\_path --cells=estimated\_input\_cells |

***Samples Data Statistics***

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| ***Sample*** | ***Estimated Number of Cells*** | ***Mean Reads per Cell*** | ***Median Genes per Cell*** | ***Total Genes Detected*** | ***Median UMI Counts per Cell*** |

***Notes***

***Accessing Data from NCI Data Vault Repository***

Data have been uploaded for long-term storage on your behalf to NCI’s most secure storage tier, the NCI Data Vault. You therefore do not need to take any additional steps to back up this data or transfer it to another drive for storage. However, we do recommend that you check the project data files as soon as you can using the immediate access link shown at the top of this report.

How to access your project data via DME in the NCI Data Vault:

• Navigate the DME link on the first page to the master copy of this dataset.

• Click the download icon from the icon bar. If you need further assistance with downloading or transferring data via the DME interface, please email ncidatavault@mail.nih.gov.

• The DME tutorial <https://wiki.nci.nih.gov/display/DMEdoc>

• You can analyze data stored in the NCI Data Vault using the genomics analysis tools hosted in NIDAP by logging into your NIDAP Account.

• Note that master copies stored on your behalf in the NCI Data Vault cannot be overwritten or accidentally deleted without your approval and are intended for long-term retention. Any copies you download may be regarded as temporary and can be deleted when no longer in active use or when space on your storage drive becomes limiting.