

Duke Molecular Genomics Core

10x Genomics Visium HD Data Analysis

BASIC (10x Genomics Space Ranger)

- Conversion of raw sequencing data to Fastq format
- Alignment of sequencing reads to reference transcriptome and tissue / fiducial alignment to input slide
- Segmentation and conversion of bins to cells
- Generation of count matrix and alignment files for each sample
- Deliverable files include the following: Count matrix files, Alignment files , Loupe Browser slide image, fastq files.

ADVANCED (Seurat, Banksy, SingleR)

- Quality control filtering
- Dimensional reduction and cell clustering with Banksy
- Conserved gene marker identification per cell cluster
- Differentially expressed gene identification between samples by cluster
- Plotting initial genes of interest (up to 30)
- Celltype annotation using relevant single-cell reference with SingleR/Celltypist
- Deliverable files include the following: Results from Seurat, Banksy, and SingleR/Celltypist analyses (.csv, .png, .pdf, .rds files)

OTHER ANALYSES charged per hour

- Gene Set Enrichment Analysis (GSEA) between the identified clusters or between the samples
- Cell-cell communication with COMMOT
- Spatially variable gene expression (per slide basis) with SpaceXR
- Spatial Trajectory Analysis with spaTrack
- Deliverable files include the following: Results from GSEA, COMMOT, SpaceXR, and spaTrack analyses (.csv, .png, .pdf, files)

IMPORTANT!

- It is your responsibility to store your data long term. We will delete data 90 days after transfer.
- You will receive a link with your raw sequencing data. You must download it by the deadline listed in the email.
- Basic analysis results will be shared either via Duke OneDrive, 10X cloud or using sftp download option from temp directory. Advanced analysis and other analysis results would be shared via Duke Box or email. You must download your files within two weeks of receipt.
- Any analysis requested after initial basic and advanced analysis requires submission of a new service request.