

## UhOVC2

Summary

Analysis

3,258

Number of Spots Under Tissue

31,432

Mean Reads per Spot

1,000

Median Genes per Spot

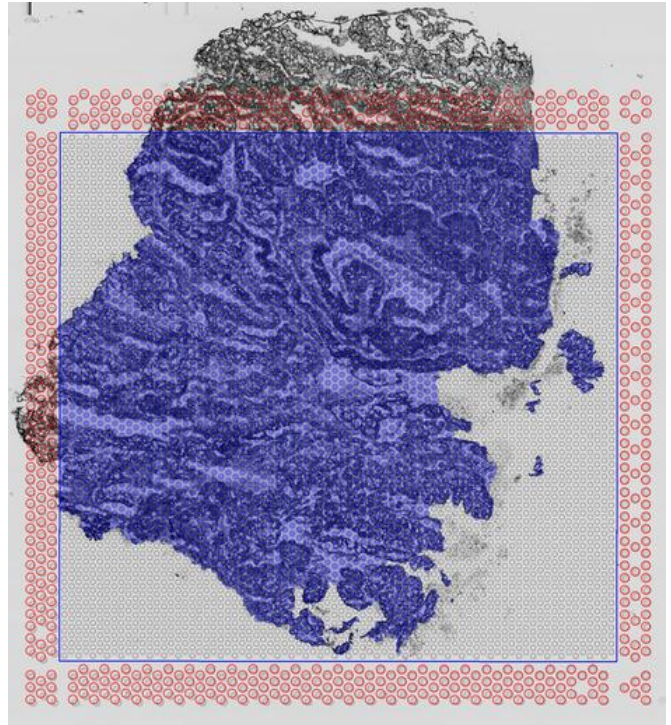
## Sequencing ?

Number of Reads	102,404,930
Valid Barcodes	97.3%
Valid UMIs	99.9%
Sequencing Saturation	78.8%
Q30 Bases in Barcode	97.5%
Q30 Bases in RNA Read	91.1%
Q30 Bases in UMI	97.1%

## Mapping ?

Reads Mapped to Genome	46.4%
Reads Mapped Confidently to Genome	44.3%
Reads Mapped Confidently to Intergenic Regions	2.1%
Reads Mapped Confidently to Intronic Regions	1.8%
Reads Mapped Confidently to Exonic Regions	40.4%
Reads Mapped Confidently to Transcriptome	39.0%
Reads Mapped Antisense to Gene	0.8%

## Spots ?



Fraction Reads in Spots Under Tissue	62.7%
Mean Reads per Spot	31,432
Median Genes per Spot	1,000
Total Genes Detected	21,393
Median UMI Counts per Spot	1,277

## Sample

Sample ID	UhOVC2
Sample Description	
Chemistry	Spatial 3' v1
Slide Serial Number	V19N11-090-B1
Reference Path	...fdata-gex-GRCh38-2020-A
Transcriptome	GRCh38-2020-A
Pipeline Version	spaceranger-1.1.0