

# UhOVC1

Summary

Analysis

## 2,652

Number of Spots Under Tissue

## 34,925

Mean Reads per Spot

## 1,810

Median Genes per Spot

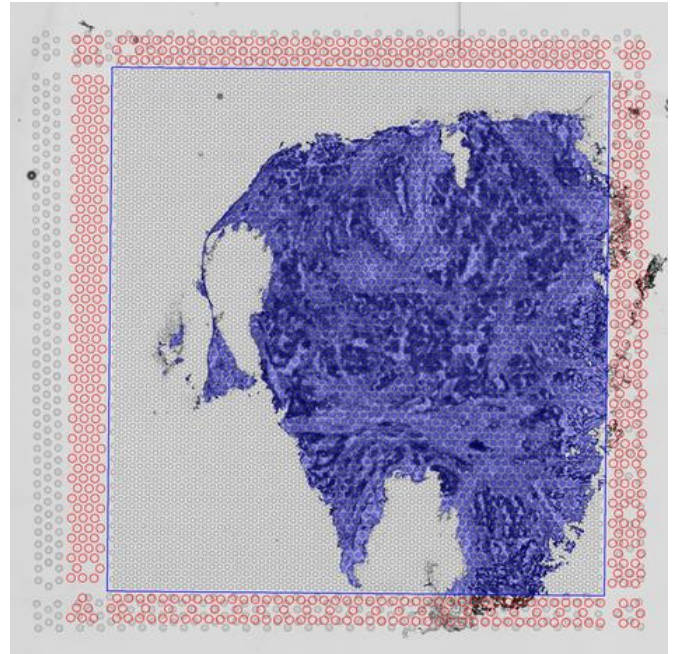
## Sequencing ?

Number of Reads	92,620,776
Valid Barcodes	97.5%
Valid UMIs	100.0%
Sequencing Saturation	73.7%
Q30 Bases in Barcode	97.4%
Q30 Bases in RNA Read	90.3%
Q30 Bases in UMI	97.0%

## Mapping ?

Reads Mapped to Genome	77.4%
Reads Mapped Confidently to Genome	74.7%
Reads Mapped Confidently to Intergenic Regions	2.4%
Reads Mapped Confidently to Intronic Regions	1.7%
Reads Mapped Confidently to Exonic Regions	70.6%
Reads Mapped Confidently to Transcriptome	68.7%
Reads Mapped Antisense to Gene	0.8%

## Spots ?



Fraction Reads in Spots Under Tissue	69.3%
Mean Reads per Spot	34,925
Median Genes per Spot	1,810
Total Genes Detected	22,668
Median UMI Counts per Spot	3,100

## Sample

Sample ID	UhOVC1
Sample Description	
Chemistry	Spatial 3' v1
Slide Serial Number	V19N11-090-A1
Reference Path	...fdata-gex-GRCh38-2020-A
Transcriptome	GRCh38-2020-A
Pipeline Version	spaceranger-1.1.0