

Data Sheet

Product Name: Paraffin Tissue Section - Human Tumor: Breast, Visium-Characterized

Catalog No.: T2235086-SV

Lot No.: C706408

Species: Human Mouse Rat Monkey (Rh) Guinea Pig Porcine
 Bovine Hamster Dog Monkey (Cy) Rabbit Plant

Tissue Type: Normal Adult Fetal Tumor Disease Cell line

Tissue Name: Breast

Tumor Size: N/A

Donor Information: H50538T, Race: Caucasian

Male: _____ year(s) old

Female: 58 year(s) old

Pathological Diagnosis: Invasive carcinoma, Stage IIA T1cN1aM0

Location: Breast

Visium Characterization:

C706408:



Summary	
Number of Spots Under Tissue	3,075
Mean Reads per Spot	57,359
Median Genes per Spot	4,358
Sequencing	
Number of Reads	176,378,225
Valid Barcodes	98.6%
Valid UMIs	100.0%
Sequencing Saturation	80.2%
Q30 Bases in Barcode	96.4%
Q30 Bases in Probe Read	69.0%
Q30 Bases in UMI	96.3%
Mapping	
Reads Mapped to Probe Set	98.7%
Reads Mapped Confidently to Probe Set	98.3%
Reads Mapped Confidently to the Filtered Probe Set	83.4%
Spots	
Fraction Reads in Spots Under Tissue	95.9%
Mean Reads per Spot	57,359
Mean Reads Under Tissue per Spot	54,256
Median UMI Counts per Spot	9,670
Median Genes per Spot	4,358
Genes Detected	16,422

Summary Legend

Column Header	Definition
Number of Reads	Total number of read pairs that were assigned to this library in demultiplexing.
Valid Barcodes	Fraction of reads with barcodes that match the whitelist after barcode correction.
Valid UMIs	Fraction of reads with valid UMIs; i.e. UMI sequences that do not contain Ns and that are not homopolymers.
Sequencing Saturation	The fraction of reads originating from an already-observed UMI. This is a function of library complexity and sequencing depth. More specifically, this is the fraction of confidently mapped, valid spot-barcode, valid UMI reads that had a non-unique spot-barcode/UMI/gene combination.
Q30 Bases in Barcode	Fraction of spot barcode bases with Q-score ≥ 30 , excluding very low quality/no-call ($Q \leq 2$) bases from the denominator.
Q30 Bases in Probe Read	Fraction of RNA read bases with Q-score ≥ 30 , excluding very low quality/no-call ($Q \leq 2$) bases from the denominator. This is Read 2 for the Visium v1 chemistry.
Q30 Bases in UMI	Fraction of UMI bases with Q-score ≥ 30 , excluding very low quality/no-call ($Q \leq 2$) bases from the denominator.
Reads Mapped to Probe Set	Fraction of reads that mapped to the probe set.
Reads Mapped Confidently to Probe Set	Fraction of reads that mapped uniquely to a probe in the probe set.
Reads Mapped Confidently to the Filtered Probe Set	Fraction of reads from probes that map to a unique gene. These reads are considered for UMI counting by default. This metric will be None when probe filtering is disabled.
Fraction Reads in Spots Under Tissue	The fraction of valid-barcode, confidently-mapped-to-transcriptome reads with tissue-associated barcodes.
Mean Reads per Spot	The number of reads, both under and outside of tissue, divided by the number of barcodes associated with a spot under tissue.
Mean Reads Under Tissue per Spot	The number of reads under tissue divided by the number of barcodes associated with a spot under tissue.
Median UMI Counts per Spot	The median number of UMI counts per tissue covered spot.
Median Genes per Spot	The median number of genes detected per spot under tissue-associated barcode. Detection is defined as the presence of at least 1 UMI count.
Genes Detected	The number of unique genes from the filtered probe set with at least one UMI count in any tissue covered spot.

Components:

1. 5 slides per package
2. Certificate of Analysis

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APPROVED BY: _____

