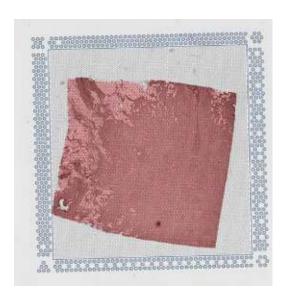


C706408:

Tel: 1-888-762-2568 Fax: 1-510-783-5386 Email: info@biochain.com

## **Data Sheet**

Product Name: Paraffin Tissue Section -	· Human Tumor:	Breast, Visium-	-Characterize
Catalog No.: <u>T2235086-SV</u>	Lot No.: C706408		
Species: ■ Human □ Mouse □ Rat □ Bovine □ Hamster □ Dog	• , ,	•	
Tissue Type: □ Normal □ Adult □ Feta Tissue Name: Breast Tumor Size: N/A	al ■Tumor	□ Disease □ C	ell line
Donor Information: H50538T, Race: Cau Male: year(s) old Female: <u>58</u> year(s) old	casian		
Pathological Diagnosis: Invasive carcine	oma, Stage IIA T	1cN1aM0	
Location: Breast			
Visium Characterization:			





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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



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## **Summary Legend**

Column Header	Definition
	Total number of read pairs that were assigned to this library in
Number of Reads	demultiplexing.
	Fraction of reads with barcodes that match the whitelist after barcode
Valid Barcodes	correction.
	Fraction of reads with valid UMIs; i.e. UMI sequences that do not contain
Valid UMIs	Ns and that are not homopolymers.
	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
Sequencing Saturation	that had a non-unique spot-barcode/UMI/gene combination.
On Bases in Barranda	Fraction of spot barcode bases with Q-score >= 30, excluding very low
Q30 Bases in Barcode	quality/no-call (Q <= 2) bases from the denominator.
	Fraction of RNA read bases with Q-score >= 30, excluding very low
Q30 Bases in Probe Read	quality/no-call (Q <= 2) bases from the denominator. This is Read 2 for the Visium v1 chemistry.
Q30 Bases III Probe nead	Fraction of UMI bases with Q-score >= 30, excluding very low quality/no-
Q30 Bases in UMI	call (Q <= 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 roads that manned uniqualy to a probe in the probe set
Sei	Fraction of reads that mapped uniquely to a probe in the probe set.
Reads Mapped Confidently to the	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
Filtered Probe Set	probe filtering is disabled.
Fraction Reads in Spots Under	The fraction of valid-barcode, confidently-mapped-to-transcriptome reads
Tissue	with tissue-associated barcodes.
1.0000	The number of reads, both under and outside of tissue, divided by the
Mean Reads per Spot	number of barcodes associated with a spot under tissue.
	The number of reads under tissue divided by the number of barcodes
Mean Reads Under Tissue per Spot	associated with a spot under tissue.
Median UMI Counts per Spot	The median number of UMI counts per tissue covered spot.
	The median number of genes detected per spot under tissue-associated
Median Genes per Spot	barcode. Detection is defined as the presence of at least 1 UMI count.
	The number of unique genes from the filtered probe set with at least one
Genes Detected	UMI count in any tissue covered spot.

## Components:

- 1. 5 slides per package
- 2. Certificate of Analysis

APPROVED BY: