

# Data Sheet

**Product Name: Matched Pair - Paraffin Tissue Section - Human Primary Tumor and Normal (PP): Colon, Visium-Characterized**

**Catalog No.: T8235090-PP-SV**

**Lot No.: C706403**

**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: Colon**

**Tumor Size: N/A**

**Donor Information: H50533T, Race: Caucasian**

**Male:** 53 year(s) old

**Female:** \_\_\_\_\_ year(s) old

**Pathological Diagnosis: Adenocarcinoma, Stage IIIB T3N2aM0**

**Location: Colon**

**Visium Characterization:**

**C706403-PN:**



<b>Summary</b>	
Number of Spots Under Tissue	2,193
Mean Reads per Spot	51,240
Median Genes per Spot	2,812
<b>Sequencing</b>	
Number of Reads	112,368,451
Valid Barcodes	98.6%
Valid UMIs	100.0%
Sequencing Saturation	77.4%
Q30 Bases in Barcode	96.4%
Q30 Bases in Probe Read	69.0%
Q30 Bases in UMI	96.3%
<b>Mapping</b>	
Reads Mapped to Probe Set	98.3%
Reads Mapped Confidently to Probe Set	96.6%
Reads Mapped Confidently to the Filtered Probe Set	77.8%
<b>Spots</b>	
Fraction Reads in Spots Under Tissue	81.1%
Mean Reads per Spot	51,240
Mean Reads Under Tissue per Spot	40,815
Median UMI Counts per Spot	5,633
Median Genes per Spot	2,812
Genes Detected	16,590

**C706403-PT:**



<b>Summary</b>	
Number of Spots Under Tissue	2,008
Mean Reads per Spot	53,298
Median Genes per Spot	5,618
<b>Sequencing</b>	
Number of Reads	107,021,920
Valid Barcodes	98.6%
Valid UMIs	100.0%
Sequencing Saturation	55.3%
Q30 Bases in Barcode	96.3%
Q30 Bases in Probe Read	68.8%
Q30 Bases in UMI	96.2%
<b>Mapping</b>	
Reads Mapped to Probe Set	98.6%
Reads Mapped Confidently to Probe Set	97.9%
Reads Mapped Confidently to the Filtered Probe Set	81.3%
<b>Spots</b>	
Fraction Reads in Spots Under Tissue	82.1%
Mean Reads per Spot	53,298
Mean Reads Under Tissue per Spot	43,069
Median UMI Counts per Spot	15,985
Median Genes per Spot	5,618
Genes Detected	16,805

## Summary Legend

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

