

# Data Sheet

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

**Catalog No.: T2235152-SV**

**Lot No.: C706410**

**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: Lung**

**Tumor Size: N/A**

**Donor Information: H25823T, Race: Caucasian**

**Male: 62 year(s) old**

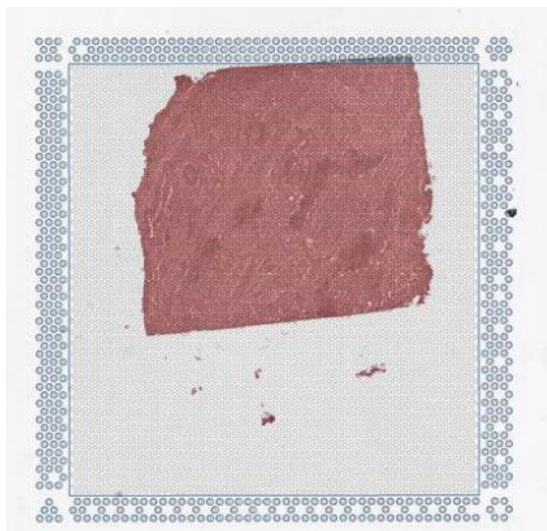
**Female: \_\_\_\_\_ year(s) old**

**Pathological Diagnosis Large cell carcinoma, Stage IIB T3N0M0**

**Location: Lung**

**Visium Characterization:**

**C706410:**



<b>Summary</b>	
Number of Spots Under Tissue	2,037
Mean Reads per Spot	61,478
Median Genes per Spot	1,300
<b>Sequencing</b>	
Number of Reads	125,230,414
Valid Barcodes	98.4%
Valid UMIs	100.0%
Sequencing Saturation	86.9%
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	97.6%
Reads Mapped Confidently to the Filtered Probe Set	81.8%
<b>Spots</b>	
Fraction Reads in Spots Under Tissue	98.6%
Mean Reads per Spot	61,478
Mean Reads Under Tissue per Spot	59,506
Median UMI Counts per Spot	2,000
Median Genes per Spot	1,300
Genes Detected	15,549

## 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:**

