



**Overall QC Status:** PASS

**Sample QC Status:** PASS

**Fusion QC Status:** PASS

**Variations QC Status:** PASS

**Job:** 20231221\_AS23064\_AS23065\_AS23066 [3520]

**Type:** RNA FusionRNA SNP/InDel Targeted Mutations: Archer

Comprehensive Targets NIH v1.3.1 Include Non-Targeted

Variants: No

**Software Version:** Suite\_Analysis\_v6.2.7

**Analysis Date:** 21-Dec-2023 5:14

**Report Creator:** mpvghtpe@gmail.com

**Report Date:** 21-Dec-2023 19:01

## Statistics

### Molecular Barcode Statistics

| Total Fragments | Fragments with Complete Adapter | Number of Reads After Trimming Adapters |
|-----------------|---------------------------------|---|
| 3,500,000       | 3,321,912                       | 3,146,844                               |

### Read Statistics

| Type             | Total Fragments (# / %) | Mapped (# / %)    | Pass Alignment Filter (%) | On Target (%) |
|------------------|-------------------------|-------------------|---------------------------|---------------|
| All Fragments    | 3,126,656 / 100.0       | 3,126,656 / 100.0 | 100.0                     | 98.8          |
| Unique Fragments | 682,266 / 21.8          | 682,266 / 100.0   | 100.0                     | 98.7          |

### DNA/RNA Statistics

| Type  | DNA Reads (# / %) | RNA Reads (# / %)  | Ambiguous Reads (# / %) |
|---|-------------------|--------------------|-------------------------|
| All Fragments                               | 311,467.0 / 10.1  | 2,419,464.0 / 78.3 | 358,210.0 / 11.6        |
| Molecular Bins                              | 77,548.0 / 11.5   | 470,727.0 / 69.9   | 125,190.0 / 18.6        |
| Average Molecular Bins per GSP2             | 71.41             | 433.45             | 115.28                  |
| Unique Start Sites                          | 30,351.0 / 30.0   | 61,018.0 / 60.4    | 24,384.0 / 24.1         |
| Average Unique Start Sites per GSP2         | 28.93             | 73.8               | 25.51                   |
| Average Unique Start Sites per GSP2 Control | 54.75             | 212.42             | 42.33                   |

QC Statistics

| Avg. Unique DNA And Ambiguous Start Sites Per GSP2 | Avg. Unique RNA Start Sites Per GSP2 Control |
|--|--|
| 54.01  | 212.42                                       |

Miscellaneous Statistics

| On Target Deduplication Ratio |
|-------------------------------|
| 4.59:1                        |

DNA/RNA Fragment Lengths

| DNA Median Fragment Length | DNA Mean Fragment Length | RNA Median Fragment Length | RNA Mean Fragment Length |
|----------------------------|--------------------------|----------------------------|--------------------------|
| 128.0                      | 140.2                    | 131.0                      | 138.6                    |

**Reportable Variants**

*None Found*

# Reportable Isoforms

None Found