



Overall QC Status: PASS  
Sample QC Status: PASS  
Fusion QC Status: PASS  
Variations QC Status: PASS  
Job: 20221221\_AS22036-37 [4755]  
Type: RNA FusionRNA SNP/InDel Targeted Mutations: Archer  
Comprehensive Targets NIH v1.3.1 2 Include Non-Targeted  
Variants: No  
Software Version: Suite\_Analysis\_v6.2.7  
Analysis Date: 21-Dec-2022 0:39  
Report Creator: mpvghtpe@gmail.com  
Report Date: 20-Jun-2023 21:11

## Statistics

### Molecular Barcode Statistics

| Total Fragments | Fragments with Complete Adapter | Number of Reads After Trimming Adapters |
|-----------------|---------------------------------|---|
| 2,409,371       | 2,190,422                       | 2,035,118                               |

### Read Statistics

| Type             | Total Fragments (# / %) | Mapped (# / %)    | Pass Alignment Filter (%) | On Target (%) |
|------------------|-------------------------|-------------------|---------------------------|---------------|
| All Fragments    | 2,021,078 / 100.0       | 2,021,078 / 100.0 | 100.0                     | 98.9          |
| Unique Fragments | 486,825 / 24.1          | 486,825 / 100.0   | 100.0                     | 98.6          |

### DNA/RNA Statistics

| Type  | DNA Reads (# / %) | RNA Reads (# / %)  | Ambiguous Reads (# / %) |
|---|-------------------|--------------------|-------------------------|
| All Fragments                               | 99,259.0 / 5.0    | 1,643,079.0 / 82.2 | 255,740.0 / 12.8        |
| Molecular Bins                              | 34,596.0 / 7.2    | 352,809.0 / 73.5   | 92,799.0 / 19.3         |
| Average Molecular Bins per GSP2             | 52.5              | 535.37             | 140.82                  |
| Unique Start Sites                          | 14,906.0 / 26.0   | 37,262.0 / 65.0    | 14,344.0 / 25.0         |
| Average Unique Start Sites per GSP2         | 23.37             | 77.24              | 25.05                   |
| Average Unique Start Sites per GSP2 Control | 25.0              | 166.25             | 33.17                   |

QC Statistics

| Avg. Unique DNA And Ambiguous Start Sites Per GSP2 | Avg. Unique RNA Start Sites Per GSP2 Control |
|--|--|
| 47.98  | 166.25                                       |

Miscellaneous Statistics

| On Target Deduplication Ratio |
|-------------------------------|
| 4.16:1                        |

DNA/RNA Fragment Lengths

| DNA Median Fragment Length | DNA Mean Fragment Length | RNA Median Fragment Length | RNA Mean Fragment Length |
|----------------------------|--------------------------|----------------------------|--------------------------|
| 139.0                      | 148.5                    | 134.0                      | 141.8                    |

**Reportable Variants**

*None Found*

# Reportable Isoforms

None Found