



**Overall QC Status:** PASS  
**Sample QC Status:** PASS  
**Fusion QC Status:** PASS  
**Variations QC Status:** PASS  
**Job:** [3448] 20230118\_AS23003 [3449]  
**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:** 18-Jan-2023 1:39  
**Report Creator:** mpvghtpe@gmail.com  
**Report Date:** 19-Jun-2023 2:43

## Statistics

### Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
3,500,000	3,290,909	3,074,072

### Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	3,056,553 / 100.0	3,056,553 / 100.0	100.0	97.8
Unique Fragments	631,212 / 20.7	631,212 / 100.0	100.0	97.9

### DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	209,434.0 / 7.0	2,291,037.0 / 76.7	487,377.0 / 16.3
Molecular Bins	57,156.0 / 9.2	420,830.0 / 68.1	139,938.0 / 22.6
Average Molecular Bins per GSP2	86.73	638.59	212.35
Unique Start Sites	21,963.0 / 31.6	42,145.0 / 60.6	17,016.0 / 24.4
Average Unique Start Sites per GSP2	34.76	90.98	30.57
Average Unique Start Sites per GSP2 Control	33.67	181.5	37.08

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
64.78	181.5

Miscellaneous Statistics

On Target Deduplication Ratio
4.84:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
137.0	147.4	131.0	138.6

**Reportable Variants**

*None Found*

# Reportable Isoforms

None Found