



**Overall QC Status:** PASS  
**Sample QC Status:** PASS  
**Fusion QC Status:** PASS  
**Variations QC Status:** PASS  
**Job:** 20240301\_AS24003 [3527]  
**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:** 01-Mar-2024 2:29  
**Report Creator:** mpvghtpe@gmail.com  
**Report Date:** 03-Mar-2024 17:40

## Statistics

### Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
3,500,000	3,334,039	3,160,915

### Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	3,145,614 / 100.0	3,145,614 / 100.0	100.0	98.6
Unique Fragments	377,994 / 12.0	377,994 / 100.0	100.0	97.8

### DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	294,160.0 / 9.5	2,338,019.0 / 75.4	470,550.0 / 15.2
Molecular Bins	40,261.0 / 10.9	238,876.0 / 64.6	90,452.0 / 24.5
Average Molecular Bins per GSP2	37.07	219.96	83.29
Unique Start Sites	18,056.0 / 25.7	43,169.0 / 61.5	17,109.0 / 24.4
Average Unique Start Sites per GSP2	17.0	49.07	17.87
Average Unique Start Sites per GSP2 Control	27.58	127.33	23.08

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
34.72	127.33

Miscellaneous Statistics

On Target Deduplication Ratio
8.40:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
109.0	121.4	113.0	121.8

**Reportable Variants**

*None Found*

# Reportable Isoforms

None Found