

**Overall QC Status:** PASS  
**Sample QC Status:** PASS  
**Fusion QC Status:** PASS  
**Variations QC Status:** PASS  
**Job:** 20221229\_AS22038\_39\_40 [4758]  
**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:** 29-Dec-2022 4:49  
**Report Creator:** mpvghtpe@gmail.com  
**Report Date:** 20-Jun-2023 21:16

## Statistics

### Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
3,500,000	3,310,173	3,111,564

### Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	3,092,812 / 100.0	3,092,812 / 100.0	100.0	98.8
Unique Fragments	180,049 / 5.8	180,049 / 100.0	100.0	98.2

### DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	229,379.0 / 7.5	2,380,740.0 / 77.9	445,716.0 / 14.6
Molecular Bins	16,248.0 / 9.2	118,567.0 / 67.1	41,974.0 / 23.7
Average Molecular Bins per GSP2	24.66	179.92	63.69
Unique Start Sites	8,168.0 / 21.6	24,473.0 / 64.9	9,486.0 / 25.1
Average Unique Start Sites per GSP2	12.62	44.59	15.88
Average Unique Start Sites per GSP2 Control	19.58	120.67	19.75

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
28.4	120.67

Miscellaneous Statistics

On Target Deduplication Ratio
17.29:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
104.0	118.6	108.0	115.6

**Reportable Variants**

*None Found*

# Reportable Isoforms

None Found