



**Overall QC Status:** PASS  
**Sample QC Status:** PASS  
**Fusion QC Status:** PASS  
**Variations QC Status:** PASS  
**Job:** 20220210\_AS22001\_004 [4719]  
**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:** 10-Feb-2022 14:46  
**Report Creator:** mpvghtpe@gmail.com  
**Report Date:** 19-Jun-2023 3:00

## Statistics

### Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
3,500,000	3,084,663	2,866,252

### Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	2,849,813 / 100.0	2,849,813 / 100.0	100.0	98.2
Unique Fragments	702,737 / 24.7	702,737 / 100.0	100.0	98.6

### DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	210,576.0 / 7.5	1,820,734.0 / 65.1	765,947.0 / 27.4
Molecular Bins	67,250.0 / 9.7	407,821.0 / 58.9	217,478.0 / 31.4
Average Molecular Bins per GSP2	114.57	694.75	370.49
Unique Start Sites	19,829.0 / 30.2	39,003.0 / 59.4	21,508.0 / 32.7
Average Unique Start Sites per GSP2	35.01	91.52	42.99
Average Unique Start Sites per GSP2 Control	46.83	195.0	75.0

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
77.21	195.0

Miscellaneous Statistics

On Target Deduplication Ratio
4.04:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
114.0	122.5	125.0	128.9

**Reportable Variants**

*None Found*

# Reportable Isoforms

None Found