



**Overall QC Status:** PASS  
**Sample QC Status:** PASS  
**Fusion QC Status:** PASS  
**Variations QC Status:** PASS  
**Job:** 20230330\_AS23011 [3454]  
**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:** 29-Mar-2023 21:26  
**Report Creator:** mpvghtpe@gmail.com  
**Report Date:** 29-Mar-2023 21:58

## Statistics

### Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
3,500,000	3,233,191	3,027,933

### Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	3,011,489 / 100.0	3,011,489 / 100.0	100.0	98.8
Unique Fragments	1,043,801 / 34.7	1,043,801 / 100.0	100.0	98.9

### DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	245,327.0 / 8.2	2,312,005.0 / 77.7	419,298.0 / 14.1
Molecular Bins	110,331.0 / 10.7	722,770.0 / 70.0	198,845.0 / 19.3
Average Molecular Bins per GSP2	167.42	1,096.77	301.74
Unique Start Sites	31,985.0 / 34.9	54,127.0 / 59.0	22,460.0 / 24.5
Average Unique Start Sites per GSP2	51.4	119.68	39.59
Average Unique Start Sites per GSP2 Control	38.67	175.5	34.42

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
89.82	175.5

Miscellaneous Statistics

On Target Deduplication Ratio
2.88:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
133.0	143.9	131.0	137.5

**Reportable Variants**

*None Found*

# Reportable Isoforms

None Found