



**Overall QC Status:** PASS

**Sample QC Status:** PASS

**Fusion QC Status:** PASS

**Variations QC Status:** PASS

**Job:** 23230608\_AS23024\_AS23021-1 [3474]

**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:** 08-Jun-2023 3:03

**Report Creator:** mpvghtpe@gmail.com

**Report Date:** 08-Jun-2023 18:59

## Statistics

### Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
3,500,000	3,259,552	3,059,906

### Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	3,046,680 / 100.0	3,046,680 / 100.0	100.0	99.0
Unique Fragments	198,674 / 6.5	198,674 / 100.0	100.0	98.0

### DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	718,533.0 / 23.8	1,640,286.0 / 54.4	658,597.0 / 21.8
Molecular Bins	46,076.0 / 23.7	95,633.0 / 49.1	53,044.0 / 27.2
Average Molecular Bins per GSP2	69.92	145.12	80.49
Unique Start Sites	23,618.0 / 45.8	19,602.0 / 38.0	11,731.0 / 22.8
Average Unique Start Sites per GSP2	36.68	35.04	19.71
Average Unique Start Sites per GSP2 Control	27.5	53.25	5.58

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
56.33	53.25

Miscellaneous Statistics

On Target Deduplication Ratio
15.49:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
102.0	111.2	96.0	103.4

**Reportable Variants**

*None Found*

# Reportable Isoforms

None Found