



Overall QC Status: PASS  
Sample QC Status: PASS  
Fusion QC Status: PASS  
Variations QC Status: PASS  
Job: 20230106\_AS23001 [4759]  
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: 06-Jan-2023 3:51  
Report Creator: mpvghtpe@gmail.com  
Report Date: 19-Jun-2023 2:55

## Statistics

### Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
3,279,572	3,054,300	2,846,613

### Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	2,827,761 / 100.0	2,827,761 / 100.0	100.0	98.3
Unique Fragments	508,433 / 18.0	508,433 / 100.0	100.0	98.3

### DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	168,197.0 / 6.1	2,308,554.0 / 83.1	302,518.0 / 10.9
Molecular Bins	37,443.0 / 7.5	370,877.0 / 74.2	91,193.0 / 18.3
Average Molecular Bins per GSP2	56.82	562.79	138.38
Unique Start Sites	17,288.0 / 26.6	42,479.0 / 65.3	16,239.0 / 25.0
Average Unique Start Sites per GSP2	27.04	90.99	28.49
Average Unique Start Sites per GSP2 Control	26.42	191.42	39.83

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
55.08	191.42

Miscellaneous Statistics

On Target Deduplication Ratio
5.56:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
129.0	142.2	131.0	138.9

**Reportable Variants**

*None Found*

# Reportable Isoforms

None Found