



**Overall QC Status:** PASS  
**Sample QC Status:** PASS  
**Fusion QC Status:** PASS  
**Variations QC Status:** PASS  
**Job:** 20240614\_AS24010 [3539]  
**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:** 14-Jun-2024 4:07  
**Report Creator:** mpvghtpe@gmail.com  
**Report Date:** 16-Jun-2024 18:34

## Statistics

### Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
3,500,000	3,173,017	2,944,921

### Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	2,932,005 / 100.0	2,932,005 / 100.0	100.0	98.8
Unique Fragments	938,403 / 32.0	938,403 / 100.0	100.0	99.0

### DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	226,010.0 / 7.8	2,241,675.0 / 77.4	429,320.0 / 14.8
Molecular Bins	91,357.0 / 9.8	645,659.0 / 69.5	192,026.0 / 20.7
Average Molecular Bins per GSP2	84.12	594.53	176.82
Unique Start Sites	34,639.0 / 30.7	68,648.0 / 60.7	28,428.0 / 25.2
Average Unique Start Sites per GSP2	33.65	88.32	30.21
Average Unique Start Sites per GSP2 Control	28.42	148.58	23.17

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
63.38	148.58

Miscellaneous Statistics

On Target Deduplication Ratio
3.12:1










DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
138.0	149.7	138.0	147.1

**Reportable Variants**

*None Found*

# Reportable Isoforms

- ☒ Passed all strong-evidence filters
- ☒ Likely off-target mispriming event
- ☒ Exact breakpoint known
- ☒ Cross contamination
- ☒ User-annotated false positive
-  Known fusion partners in Archer Quiver™
-  Percent GSP2 reads below threshold
-  Fusion expression imbalance
-  Low confidence
-  User-annotated true positive
-  Intronic fusion
-  Not enough unique start sites
-  Transcriptional readthrough event
-  Known ensembl paralogue

Fusion: BCOR → MAML1		
<div>Filters: <input checked="" type="checkbox"/></div> <div>GSP2: BCOR_chrX_39911402_21_-_A1_GSP2</div> <div>Mutation Classification: Undefined</div> <div>Is Artifact: no</div>	<div>Reads: 5564 (99.02%)</div> <div>Start Sites: 144</div>	<div>Segments</div> <div>chrX:39911606→39911368 BCOR(-) NM_017745.5, exon:15</div> <div>chr5:179160237→179160287 MAML1(+) NM_014757.4, exon:1</div>