



**Overall QC Status:** PASS  
**Sample QC Status:** PASS  
**Fusion QC Status:** PASS  
**Variations QC Status:** PASS  
**Job:** 20230615\_AS23026\_28 [3477]  
**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:** 15-Jun-2023 4:11  
**Report Creator:** mpvghtpe@gmail.com  
**Report Date:** 15-Jun-2023 18:51

## Statistics

### Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
3,500,000	3,289,194	3,101,316

### Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	3,083,952 / 100.0	3,083,952 / 100.0	100.0	98.5
Unique Fragments	634,351 / 20.6	634,351 / 100.0	100.0	98.9

### DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	249,581.0 / 8.2	2,257,438.0 / 74.3	529,750.0 / 17.4
Molecular Bins	62,216.0 / 9.9	419,324.0 / 66.9	145,588.0 / 23.2
Average Molecular Bins per GSP2	57.29	386.12	134.06
Unique Start Sites	28,050.0 / 27.8	60,855.0 / 60.3	25,556.0 / 25.3
Average Unique Start Sites per GSP2	26.53	72.41	26.96
Average Unique Start Sites per GSP2 Control	38.75	175.58	33.83

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
53.18	175.58

Miscellaneous Statistics

On Target Deduplication Ratio
4.84:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
128.0	139.0	130.0	137.0

**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: EWSR1 → NR4A3		
<div>Filters:  </div> <div>GSP2: NR4A3_chr9_102587978_20_-_A1_GSP 2</div> <div>Mutation Classification: Undefined</div> <div>Is Artifact: no</div>	<div>Reads: 965 (24.44%)</div> <div>Start Sites: 234</div>	<div>Segments</div> <div>chr22:29682913→29683123 EWSR1(+) NM_005243.3, exon:7</div> <div>chr9:102587941→102588114 NR4A3(+) NM_006981.3, exon:2</div>

Fusion: EWSR1 → NR4A3		
<div>Filters:  </div> <div>GSP2: EWSR1_chr22_29683087_28+_A1_GSP 2</div> <div>Mutation Classification: Undefined</div> <div>Is Artifact: no</div>	<div>Reads: 11 (0.28%)</div> <div>Start Sites: 8</div>	<div>Segments</div> <div>chr22:29683088→29683123 EWSR1(+) NM_005243.3, exon:7</div> <div>chr9:102587944→102588088 NR4A3(+) NM_006981.3, exon:2</div>