



Overall QC Status: PASS  
 Sample QC Status: PASS  
 Fusion QC Status: PASS  
 Variations QC Status: PASS

Job:  
 20230804\_AS23036\_AS23037\_AS23038\_AS23040\_AS23041  
 [3486]

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: 03-Aug-2023 20:42

Report Creator: mpvghtpe@gmail.com

Report Date: 03-Aug-2023 23:38

## Statistics

### Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
1,407,410	1,315,202	1,228,169

### Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	1,223,835 / 100.0	1,223,835 / 100.0	100.0	99.1
Unique Fragments	314,946 / 25.7	314,946 / 100.0	100.0	98.9

### DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	131,274.0 / 10.8	719,269.0 / 59.3	362,558.0 / 29.9
Molecular Bins	34,898.0 / 11.2	159,960.0 / 51.3	116,670.0 / 37.5
Average Molecular Bins per GSP2	52.96	242.73	177.04
Unique Start Sites	12,729.0 / 27.9	26,788.0 / 58.8	11,700.0 / 25.7
Average Unique Start Sites per GSP2	19.79	49.8	21.5

Average Unique Start Sites per GSP2 Control	19.75	100.08	13.17
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QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
40.96	100.08

Miscellaneous Statistics

On Target Deduplication Ratio
3.89:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
115.0	126.6	122.0	127.0

**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: PAX3 → FOXO1		
<div>Filters: <input checked="" type="checkbox"/> <input checked="" type="checkbox"/></div> <div>GSP2: PAX3_chr2_223084865_21_-_A1_GSP2</div> <div>Mutation Classification: Undefined</div> <div>Is Artifact: no</div>	<div>Reads: 121 (11.68%)</div> <div>Start Sites: 74</div>	<div>Segments</div> <div>chr2:223085073→223084859 PAX3(-) NM_181457.3, exon:7</div> <div>chr13:41134997→41134821 FOXO1(-) NM_002015.3, exon:2</div>