



**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 19:24

## Statistics

### Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
3,500,000	3,273,561	3,096,923

### Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	3,083,656 / 100.0	3,083,656 / 100.0	100.0	99.1
Unique Fragments	127,055 / 4.1	127,055 / 100.0	100.0	98.4

### DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	358,533.0 / 11.7	2,207,547.0 / 72.2	490,394.0 / 16.0
Molecular Bins	14,675.0 / 11.7	75,741.0 / 60.6	34,545.0 / 27.6
Average Molecular Bins per GSP2	22.27	114.93	52.42
Unique Start Sites	6,519.0 / 23.4	17,307.0 / 62.0	6,899.0 / 24.7
Average Unique Start Sites per GSP2	10.13	30.62	11.52
Average Unique Start Sites per GSP2 Control	9.92	71.58	7.42

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
21.62	71.58

Miscellaneous Statistics

On Target Deduplication Ratio
24.46:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
95.0	105.8	101.0	107.8

**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: TPM3 → NTRK1		
<div>Filters:  </div> <div>GSP2: NTRK1_chr1_156844367_21_-_A1_GSP 2</div> <div>Mutation Classification: Undefined</div> <div>Is Artifact: no</div>	<div>Reads: 312 (58.21%)</div> <div>Start Sites: 81</div>	<div>Segments</div> <div>chr1:154142945→154142876 TPM3(-) NM_153649.3, exon:7</div> <div>chr1:156844363→156844418 NTRK1(+) NM_002529.3, exon:10</div>

Fusion: TPM3 → NTRK1		
<div>Filters:  </div> <div>GSP2: NTRK1_chr1_156844367_21_-_A1_GSP 2</div> <div>Mutation Classification: Undefined</div> <div>Is Artifact: no</div>	<div>Reads: 40 (8.03%)</div> <div>Start Sites: 20</div>	<div>Segments</div> <div>chr1:154141859→154141781 TPM3(-) NM_152263.3, exon:9</div> <div>chr1:156844363→156844418 NTRK1(+) NM_002529.3, exon:10</div>