



Overall QC Status: PASS
Sample QC Status: PASS
Fusion QC Status: PASS
Variations QC Status: PASS
Job: 20240530_AS24009 [3536]
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: 30-May-2024 2:59
Report Creator: mpvghtpe@gmail.com
Report Date: 30-May-2024 18:13

Statistics

Molecular Barcode Statistics

| Total Fragments | Fragments with Complete Adapter | Number of Reads After Trimming Adapters |
|-----------------|---------------------------------|---|
| 3,500,000 | 3,324,509 | 3,195,072 |

Read Statistics

| Type | Total Fragments (# / %) | Mapped (# / %) | Pass Alignment Filter (%) | On Target (%) |
|------------------|-------------------------|-------------------|---------------------------|---------------|
| All Fragments | 3,183,314 / 100.0 | 3,183,314 / 100.0 | 100.0 | 99.2 |
| Unique Fragments | 166,410 / 5.2 | 166,410 / 100.0 | 100.0 | 98.3 |

DNA/RNA Statistics

| Type | DNA Reads (# / %) | RNA Reads (# / %) | Ambiguous Reads (# / %) |
|---|-------------------|--------------------|-------------------------|
| All Fragments | 366,736.0 / 11.6 | 1,877,389.0 / 59.4 | 914,772.0 / 29.0 |
| Molecular Bins | 21,590.0 / 13.2 | 85,403.0 / 52.2 | 56,649.0 / 34.6 |
| Average Molecular Bins per GSP2 | 19.88 | 78.64 | 52.16 |
| Unique Start Sites | 10,829.0 / 24.2 | 26,587.0 / 59.5 | 11,201.0 / 25.1 |
| Average Unique Start Sites per GSP2 | 10.22 | 27.79 | 12.1 |
| Average Unique Start Sites per GSP2 Control | 12.42 | 59.92 | 5.83 |

QC Statistics

| Avg. Unique DNA And Ambiguous Start Sites Per GSP2 | Avg. Unique RNA Start Sites Per GSP2 Control |
|--|--|
| 22.25 | 59.92 |

Miscellaneous Statistics

| On Target Deduplication Ratio |
|-------------------------------|
| 19.30:1 |

DNA/RNA Fragment Lengths

| DNA Median Fragment Length | DNA Mean Fragment Length | RNA Median Fragment Length | RNA Mean Fragment Length |
|----------------------------|--------------------------|----------------------------|--------------------------|
| 113.0 | 127.9 | 120.0 | 129.6 |

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: 172 (36.06%)</div> <div>Start Sites: 97</div> | <div>Segments</div> <div>chr2:223085053→223084859 PAX3(-) NM_181457.3, exon:7</div> <div>chr13:41134997→41134805 FOXO1(-) NM_002015.3, exon:2</div> |