



Overall QC Status: PASS
Sample QC Status: PASS
Fusion QC Status: PASS
Variations QC Status: PASS
Job: 20211006 AS21003 [3439]
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: 06-Oct-2021 6:30
Report Creator: mpvghtpe@gmail.com
Report Date: 19-Jun-2023 2:32

Statistics

Molecular Barcode Statistics

| Total Fragments | Fragments with Complete Adapter | Number of Reads After Trimming Adapters |
|-----------------|---------------------------------|---|
| 3,500,000 | 3,198,120 | 2,946,136 |

Read Statistics

| Type | Total Fragments (# / %) | Mapped (# / %) | Pass Alignment Filter (%) | On Target (%) |
|------------------|-------------------------|-------------------|---------------------------|---------------|
| All Fragments | 2,924,299 / 100.0 | 2,924,299 / 100.0 | 100.0 | 99.1 |
| Unique Fragments | 757,640 / 25.9 | 757,640 / 100.0 | 100.0 | 99.3 |

DNA/RNA Statistics

| Type | DNA Reads (# / %) | RNA Reads (# / %) | Ambiguous Reads (# / %) |
|---|-------------------|--------------------|-------------------------|
| All Fragments | 251,061.0 / 8.7 | 1,806,484.0 / 62.3 | 840,527.0 / 29.0 |
| Molecular Bins | 76,359.0 / 10.2 | 419,107.0 / 55.7 | 256,659.0 / 34.1 |
| Average Molecular Bins per GSP2 | 130.08 | 713.98 | 437.24 |
| Unique Start Sites | 21,656.0 / 33.1 | 38,832.0 / 59.3 | 15,967.0 / 24.4 |
| Average Unique Start Sites per GSP2 | 38.64 | 89.97 | 33.85 |
| Average Unique Start Sites per GSP2 Control | 36.0 | 144.17 | 21.08 |

QC Statistics

| Avg. Unique DNA And Ambiguous Start Sites Per GSP2 | Avg. Unique RNA Start Sites Per GSP2 Control |
|--|--|
| 71.83 | 144.17 |

Miscellaneous Statistics

| On Target Deduplication Ratio |
|-------------------------------|
| 3.85:1 |

DNA/RNA Fragment Lengths

| DNA Median Fragment Length | DNA Mean Fragment Length | RNA Median Fragment Length | RNA Mean Fragment Length |
|----------------------------|--------------------------|----------------------------|--------------------------|
| 112.0 | 127.8 | 118.0 | 125.5 |

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: SS18 → SSX1 | | |
|--|---|---|
| <div>Filters:  </div> <div>GSP2: SS18_chr18_23614979_21_-_A1_GSP2</div> <div>Mutation Classification: Undefined</div> <div>Is Artifact: no</div> | <div>Reads: 1082 (20.29%)</div> <div>Start Sites: 257</div> | <div>Segments</div> <div>chr18:23615091→23614969 SS18(-) NM_001007559.2, exon:9</div> <div>chrX:48121201→48121234 SSX1(+) NM_005635.3, exon:5</div> |

| Fusion: SS18 → SSX2 | | |
|--|--|--|
| <div>Filters:  </div> <div>GSP2: SS18_chr18_23614979_21_-_A1_GSP2</div> <div>Mutation Classification: Undefined</div> <div>Is Artifact: no</div> | <div>Reads: 361 (8.68%)</div> <div>Start Sites: 84</div> | <div>Segments</div> <div>chr18:23612496→23612496 SS18(-) NM_001007559.2, exon:10</div> <div>chrX:52731680→52731631 SSX2(-) NM_003147.5, exon:5</div> |

| Fusion: SS18 → SSX2 | | |
|--|--|---|
| <div>Filters:  </div> <div>GSP2: SS18_chr18_23614979_21_-_A1_GSP2</div> <div>Mutation Classification: Undefined</div> <div>Is Artifact: no</div> | <div>Reads: 310 (5.95%)</div> <div>Start Sites: 75</div> | <div>Segments</div> <div>chr18:23615091→23614969 SS18(-) NM_001007559.2, exon:9</div> <div>chrX:52731680→52731631 SSX2(-) NM_003147.5, exon:5</div> |