# AS22030_Ion_V2_RBC1_BC4_rawlib.basecaller

**Overall QC Status:** PASS
**Sample QC Status:** PASS
**Fusion QC Status:** PASS
**Variations QC Status:** PASS
**Job:** 20221006_AS22030 [4745]
**Type:** RNA FusionRNA SNP/InDel Targeted Mutations: Archer Comprehensive Targets NIH v1.3.1 2 Include Non-Targeted Variants: No
**Software Version:** Suite_Analysis_v6.2.7
**Analysis Date:** 06-Oct-2022 1:41
**Report Creator:** mpvghtpe@gmail.com
**Report Date:** 20-Jun-2023 20:51

## Statistics

### Molecular Barcode Statistics

| Total Fragments | Fragments with Complete Adapter | Number of Reads After Trimming Adapters |
|---|---|---|
| 3,500,000 | 3,284,181 | 3,093,925 |

### Read Statistics

| Type | Total Fragments (# / %) | Mapped (# / %) | Pass Alignment Filter (%) | On Target (%) |
|---|---|---|---|---|
| All Fragments | 3,087,210 / 100.0 | 3,087,210 / 100.0 | 100.0 | 99.4 |
| Unique Fragments | 90,502 / 2.9 | 90,502 / 100.0 | 100.0 | 97.8 |

### DNA/RNA Statistics

| Type | DNA Reads (# / %) | RNA Reads (# / %) | Ambiguous Reads (# / %) |
|---|---|---|---|
| All Fragments | 319,948.0 / 10.4 | 2,263,192.0 / 73.8 | 484,388.0 / 15.8 |
| Molecular Bins | 9,366.0 / 10.6 | 54,954.0 / 62.1 | 24,196.0 / 27.3 |
| Average Molecular Bins per GSP2 | 14.21 | 83.39 | 36.72 |
| Unique Start Sites | 5,339.0 / 22.0 | 15,606.0 / 64.2 | 6,311.0 / 26.0 |
| Average Unique Start Sites per GSP2 | 8.3 | 27.55 | 10.56 |
| Average Unique Start Sites per GSP2 Control | 9.42 | 68.33 | 7.08 |

## QC Statistics

| Avg. Unique DNA And Ambiguous Start Sites Per GSP2 | Avg. Unique RNA Start Sites Per GSP2 Control |
|---|---|
| 18.76 | 68.33 |

## Miscellaneous Statistics

| On Target Deduplication Ratio |
|---|
| 34.66:1 |

## DNA/RNA Fragment Lengths

| DNA Median Fragment Length | DNA Mean Fragment Length | RNA Median Fragment Length | RNA Mean Fragment Length |
|---|---|---|---|
| 105.0 | 121.1 | 118.0 | 124.2 |

## 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 → SSX2 | | |
|---|---|---|
| **Filters:** ✔ 🗄<br><br>**GSP2:**<br>SS18_chr18_23612369_25_-_A1_GSP2<br><br>**Mutation Classification:** Undefined<br><br>**Is Artifact:** no | **Reads**: 34 (13.93%)<br><br>**Start Sites:** 27 | **Segments**<br><br>chr18:23612394→23612363<br>SS18(-) NM_005637.3, exon:9<br><br>chrX:52729628→52729493<br>SSX2(-) NM_003147.5, exon:6 |