AS23046_46243509_Ion_V2_RBC1_BC2_rawlib.basecaller

Overall QC Status: PASS
Sample QC Status: PASS
Fusion QC Status: PASS
Variations QC Status: PASS
Job: 20230824_AS23046 [3493]
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: 24-Aug-2023 2:28
Report Creator: mpvghtpe@gmail.com
Report Date: 24-Aug-2023 3:08

Statistics

Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
3,500,000	3,316,027	3,197,868

Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	3,187,443 / 100.0	3,187,443 / 100.0	100.0	99.2
Unique Fragments	64,878 / 2.0	64,878 / 100.0	100.0	98.1

DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	361,128.0 / 11.4	2,361,599.0 / 74.7	439,459.0 / 13.9
Molecular Bins	7,000.0 / 11.0	39,084.0 / 61.4	17,546.0 / 27.6
Average Molecular Bins per GSP2	10.62	59.31	26.63
Unique Start Sites	3,981.0 / 21.3	11,397.0 / 60.9	5,147.0 / 27.5
Average Unique Start Sites per GSP2	6.11	18.89	8.3
Average Unique Start Sites per GSP2 Control	5.42	36.5	5.17

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
14.38	36.5

Miscellaneous Statistics

On Target Deduplication Ratio
49.70:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
94.0	102.6	91.0	96.5

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		
Filters: ☑ ◎ **GSP2:** SS18_chr18_23612369_25_-_A1_GSP2 **Mutation Classification:** Undefined **Is Artifact:** no	**Reads**: 149 (51.74%) **Start Sites:** 39	**Segments** chr18:23612430→23612363 SS18(-) NM_005637.3, exon:9 chrX:48123217→48123352 SSX1(+) NM_005635.3, exon:6