AS23041_29060900_Ion_V2_RBC1_BC6_rawlib.basecaller

Overall QC Status: PASS
Sample QC Status: PASS
Fusion QC Status: PASS
Variations QC Status: PASS
Job: 20230804_AS23036_AS23037_AS23038_AS23040_AS23041 [3486]
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: 03-Aug-2023 20:42
Report Creator: mpvghtpe@gmail.com
Report Date: 04-Aug-2023 0:00

Statistics

Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
1,413,016	1,298,045	1,207,302

Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	1,201,925 / 100.0	1,201,925 / 100.0	100.0	99.0
Unique Fragments	497,530 / 41.4	497,530 / 100.0	100.0	99.1

DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	114,659.0 / 9.6	897,715.0 / 75.4	177,839.0 / 14.9
Molecular Bins	53,138.0 / 10.8	348,623.0 / 70.7	91,331.0 / 18.5
Average Molecular Bins per GSP2	80.63	529.02	138.59
Unique Start Sites	19,501.0 / 32.2	35,842.0 / 59.2	14,672.0 / 24.2
Average Unique Start Sites per GSP2	30.79	73.78	25.45

Average Unique Start Sites per GSP2 Control	23.08	118.83	16.42

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
55.83	118.83

Miscellaneous Statistics

On Target Deduplication Ratio
2.41:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
129.0	140.1	126.0	131.8

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: EWSR1 → WT1		
Filters: **GSP2:** EWSR1_chr22_29683087_28_+_A1_GSP 2 **Mutation Classification:** Undefined **Is Artifact:** no	**Reads**: 27 (1.38%) **Start Sites:** 22	**Segments** chr22:29683088→29683123 EWSR1(+) NM_005243.3, exon:7 chr11:32414301→32414212 WT1(-) NM_000378.4, exon:7