AS23031_49545597_Ion_V2_RBC2_BC31_rawlib.basecaller

Overall QC Status: PASS
Sample QC Status: PASS
Fusion QC Status: PASS
Variations QC Status: PASS
Job: 20230628_AS23025_AS23031_AS23032 [3478]
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: 28-Jun-2023 4:07
Report Creator: mpvghtpe@gmail.com
Report Date: 29-Jun-2023 0:22

Statistics

Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
3,460,043	3,279,846	3,110,884

Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	3,090,262 / 100.0	3,090,262 / 100.0	100.0	98.5
Unique Fragments	491,230 / 15.9	491,230 / 100.0	100.0	98.6

DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	185,803.0 / 6.1	2,351,986.0 / 77.3	505,028.0 / 16.6
Molecular Bins	37,187.0 / 7.7	340,184.0 / 70.3	106,864.0 / 22.1
Average Molecular Bins per GSP2	34.24	313.24	98.4
Unique Start Sites	20,767.0 / 22.0	60,807.0 / 64.5	24,861.0 / 26.4
Average Unique Start Sites per GSP2	19.61	71.2	26.2
Average Unique Start Sites per GSP2 Control	31.0	193.92	39.5

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
45.56	193.92

Miscellaneous Statistics

On Target Deduplication Ratio
6.28:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
131.0	142.4	133.0	141.4

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: WWTR1 → CAMTA1		
Filters: ☑ ◎ **GSP2:** WWTR1_chr3_149290656_21_-_A1_GSP 2 **Mutation Classification:** Undefined **Is Artifact:** no	**Reads**: 1134 (25.78%) **Start Sites:** 249	**Segments** chr3:149290787→149290651 WWTR1(-) NM_015472.4, exon:3 chr1:7723413→7723644 CAMTA1(+) NM_015215.3, exon:9

Fusion: WWTR1 → CAMTA1		
Filters: ⛁ ⚟ **GSP2:** WWTR1_chr3_149290656_21_-_A1_GSP 2 **Mutation Classification:** Undefined **Is Artifact:** no	**Reads**: 55 (1.22%) **Start Sites:** 40	**Segments** chr3:149290787→149290651 WWTR1(-) NM_015472.4, exon:3 chr1:7730971→7731097 CAMTA1(+) NM_015215.3, exon:10