AS23022_49506481_Ion_V2_RBC2_BC44_rawlib.basecaller

Overall QC Status: PASS
Sample QC Status: PASS
Fusion QC Status: PASS
Variations QC Status: PASS
Job: 20230601_AS23020_AS23022 [4777]
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: 01-Jun-2023 4:45
Report Creator: mpvghtpe@gmail.com
Report Date: 01-Jun-2023 19:15

Statistics

Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
3,500,000	3,265,321	3,047,667

Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	3,030,422 / 100.0	3,030,422 / 100.0	100.0	98.4
Unique Fragments	442,620 / 14.6	442,620 / 100.0	100.0	98.5

DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	182,105.0 / 6.1	2,387,852.0 / 80.1	412,934.0 / 13.8
Molecular Bins	36,179.0 / 8.3	306,238.0 / 70.2	93,639.0 / 21.5
Average Molecular Bins per GSP2	54.9	464.7	142.09
Unique Start Sites	15,810.0 / 26.0	39,197.0 / 64.5	15,104.0 / 24.9
Average Unique Start Sites per GSP2	25.0	80.87	26.64
Average Unique Start Sites per GSP2 Control	21.67	171.58	31.92

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
51.22	171.58

Miscellaneous Statistics

On Target Deduplication Ratio
6.84:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
128.0	140.5	129.0	135.4

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: FBN1 → FGFR3		
Filters: ☑ **GSP2:** FGFR3_chr4_1801013_18_-_A1_GSP2 **Mutation Classification:** Undefined **Is Artifact:** no	**Reads**: 2052 (99.32%) **Start Sites:** 166	**Segments** chr15:48903023→48902925 FBN1(-) NM_000138.4, exon:4 chr4:1800981→1801035 FGFR3(+) NM_000142.4, exon:3