AS23007_49170481_Ion_V2_RBC2_BC35_rawlib.basecaller

Overall QC Status: PASS
Sample QC Status: PASS
Fusion QC Status: PASS
Variations QC Status: PASS
Job: 20230215_AS23003_AS23007 [4767]
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: 15-Feb-2023 7:37
Report Creator: mpvghtpe@gmail.com
Report Date: 15-Feb-2023 17:26

Statistics

Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
3,500,000	3,303,690	3,110,467

Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	3,091,799 / 100.0	3,091,799 / 100.0	100.0	98.3
Unique Fragments	647,369 / 20.9	647,369 / 100.0	100.0	98.6

DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	212,129.0 / 7.0	2,306,451.0 / 75.9	519,602.0 / 17.1
Molecular Bins	54,211.0 / 8.5	431,677.0 / 67.6	152,451.0 / 23.9
Average Molecular Bins per GSP2	49.92	397.49	140.38
Unique Start Sites	22,007.0 / 24.4	57,925.0 / 64.3	23,454.0 / 26.0
Average Unique Start Sites per GSP2	20.86	70.58	25.02
Average Unique Start Sites per GSP2 Control	28.08	174.75	35.92

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
45.57	174.75

Miscellaneous Statistics

On Target Deduplication Ratio
4.76:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
122.0	138.1	130.0	138.7

Reportable Variants

None Found

Reportable Isoforms

☑ Passed all strong-evidence filters   ☰ Known fusion partners in Archer Quiver™   ✦ Intronic fusion
◄ Likely off-target mispriming event   ⇅ Percent GSP2 reads below threshold   ↓≡ Not enough unique start sites
◎ Exact breakpoint known   ⚖ Fusion expression imbalance   ○ Transcriptional readthrough event
✕ Cross contamination   ↳ Low confidence   ⊓ Known ensembl paralogue
✗ User-annotated false positive   ⌂ User-annotated true positive

Fusion: EML4 → ALK		
Filters: ☑ ◎ **GSP2:** ALK_chr2_29446355_20_+_A1_GSP2 **Mutation Classification:** Undefined **Is Artifact:** no	**Reads**: 184 (90.20%) **Start Sites:** 66	**Segments** chr2:42472645→42472827 EML4(+) NM_019063.4, exon:2 chr2:29446394→29446208 ALK(-) NM_004304.4, exon:20

Fusion: EML4 → ALK		
Filters: ☰ ✦ **GSP2:** ALK_chr2_29446473_24_+_A1_GSP2 **Mutation Classification:** Undefined **Is Artifact:** no	**Reads**: 13 (100.00%) **Start Sites:** 13	**Segments** chr2:42475070→42475134 EML4(+) NM_019063.4, intron:2 chr2:29446701→29446474 ALK(-) XM_024452779.1, exon:2