AL22002_Ion_V2_RBC2_BC48_rawlib. basecaller

Overall QC Status: PASS
Sample QC Status: PASS
Fusion QC Status: PASS
Variations QC Status: PASS
Job: 20221123_AL22001-2_F22128 [4752]
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: 23-Nov-2022 1:24
Report Creator: mpvghtpe@gmail.com
Report Date: 20-Jun-2023 21:47

Statistics

Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
518,341	484,575	459,450

Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	458,325 / 100.0	458,325 / 100.0	100.0	96.9
Unique Fragments	18,293 / 4.0	18,293 / 100.0	100.0	74.9

DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	39,290.0 / 8.8	330,208.0 / 74.3	74,758.0 / 16.8
Molecular Bins	1,363.0 / 10.0	9,049.0 / 66.1	3,282.0 / 24.0
Average Molecular Bins per GSP2	8.36	55.52	20.13
Unique Start Sites	1,054.0 / 21.3	3,157.0 / 63.8	1,145.0 / 23.2
Average Unique Start Sites per GSP2	6.52	21.37	7.2
Average Unique Start Sites per GSP2 Control	4.62	90.88	34.12

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
13.69	90.88

Miscellaneous Statistics

On Target Deduplication Ratio
32.44:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
108.0	119.5	117.0	128.8

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: SYNCRIP → BRAF		
Filters: ☑ **GSP2:** BRAF_chr7_140487350_24_+_A1_GSP2 **Mutation Classification:** Undefined **Is Artifact:** no	**Reads**: 35 (25.55%) **Start Sites:** 23	<u>**Segments**</u> chr6:86324839→86324699 SYNCRIP(-) NM_006372.4, exon:11 chr7:140487384→140487348 BRAF(-) NM_004333.4, exon:9