AS21007_Ion_V2_RBC1_BC17_rawlib.basecaller

Overall QC Status: PASS
Sample QC Status: PASS
Fusion QC Status: PASS
Variations QC Status: PASS
Job: 20211119 AS21007 AS21008 AS21009 AS21010 [4712]
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: 19-Nov-2021 8:33
Report Creator: mpvghtpe@gmail.com
Report Date: 19-Jun-2023 2:49

Statistics

Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
3,500,000	3,254,946	3,077,839

Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	3,065,072 / 100.0	3,065,072 / 100.0	100.0	99.3
Unique Fragments	104,203 / 3.4	104,203 / 100.0	100.0	98.7

DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	312,297.0 / 10.3	1,737,486.0 / 57.1	994,612.0 / 32.7
Molecular Bins	10,223.0 / 9.9	52,022.0 / 50.6	40,603.0 / 39.5
Average Molecular Bins per GSP2	17.42	88.62	69.17
Unique Start Sites	4,058.0 / 18.9	13,340.0 / 62.3	6,111.0 / 28.5
Average Unique Start Sites per GSP2	6.98	25.68	11.76
Average Unique Start Sites per GSP2 Control	8.08	66.25	8.42

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
18.72	66.25

Miscellaneous Statistics

On Target Deduplication Ratio
29.60:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
90.0	101.9	95.0	101.0

Reportable Variants

NP_001895.1:p.Ser45Ph e	
Gene: CTNNB1	**Location:** chr3:41266137
Ref./ Mutation: C / T (. PRESENT)	**Depth:** 450
Allele Fraction: 0.4244	**Clinical Sig.** Pathogenic
Mutation Classification: Undefined	**Disease:** Hepatocellular_carcinoma
Is Artifact: no	**HGVSp:** NP_001895.1
	Sift: deleterious(0)
	PolyPhen: probably_damaging(0.928)

Reportable Isoforms

None Found