AS23060_49945837_Ion_V2_RBC1_BC20_rawlib.basecaller

Overall QC Status: PASS
Sample QC Status: PASS
Fusion QC Status: PASS
Variations QC Status: PASS
Job: 20231207_AS23060 [3516]
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: 07-Dec-2023 3:39
Report Creator: mpvghtpe@gmail.com
Report Date: 07-Dec-2023 17:48

Statistics

Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
3,500,000	3,300,492	3,146,959

Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	3,133,323 / 100.0	3,133,323 / 100.0	100.0	98.7
Unique Fragments	230,431 / 7.4	230,431 / 100.0	100.0	97.3

DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	314,234.0 / 10.2	2,444,810.0 / 79.1	333,533.0 / 10.8
Molecular Bins	26,927.0 / 12.0	151,700.0 / 67.7	45,481.0 / 20.3
Average Molecular Bins per GSP2	40.86	230.2	69.02
Unique Start Sites	11,745.0 / 27.2	27,341.0 / 63.4	9,607.0 / 22.3
Average Unique Start Sites per GSP2	18.39	53.8	16.13
Average Unique Start Sites per GSP2 Control	23.33	133.08	17.25

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
34.28	133.08

Miscellaneous Statistics

On Target Deduplication Ratio
13.80:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
128.0	141.6	131.0	138.2

Reportable Variants

NP_001895.1:p.Thr41Al a	
Gene: CTNNB1	**Location:** chr3:41266124
Ref./ Mutation: A / G (. PRESENT)	**Depth:** 2368
Allele Fraction: 0.4637	**Clinical Sig.** Pathogenic
Mutation Classification: Undefined	**Disease:** Hepatoblastoma
Is Artifact: no	**HGVSp:** NP_001895.1
	Sift: deleterious(0)
	PolyPhen: possibly_damaging(0.694)

Reportable Isoforms

None Found