AS23056_3134858_Ion_V2_RBC2_BC37_rawlib.basecaller

Overall QC Status: PASS
Sample QC Status: PASS
Fusion QC Status: PASS
Variations QC Status: PASS
Job: 20231116_AS23056_S1662 [3512]
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: 16-Nov-2023 3:06
Report Creator: mpvghtpe@gmail.com
Report Date: 16-Nov-2023 23:21

Statistics

Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
3,500,000	3,217,419	3,080,233

Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	3,064,348 / 100.0	3,064,348 / 100.0	100.0	98.2
Unique Fragments	715,788 / 23.4	715,788 / 100.0	100.0	97.9

DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	222,468.0 / 7.4	2,331,717.0 / 77.5	455,507.0 / 15.1
Molecular Bins	65,238.0 / 9.3	479,464.0 / 68.4	155,960.0 / 22.3
Average Molecular Bins per GSP2	60.07	441.5	143.61
Unique Start Sites	29,085.0 / 27.0	66,924.0 / 62.1	27,220.0 / 25.3
Average Unique Start Sites per GSP2	27.83	83.62	29.06
Average Unique Start Sites per GSP2 Control	29.0	174.92	27.5

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
56.52	174.92

Miscellaneous Statistics

On Target Deduplication Ratio
4.30:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
137.0	150.3	137.0	147.0

Reportable Variants

NP_001895.1:p.Ser45Pr o	
Gene: CTNNB1	**Location:** chr3:41266136
Ref./ Mutation: T / C (. PRESENT)	**Depth:** 2531
Allele Fraction: 0.4887	**Clinical Sig.** Pathogenic
Mutation Classification: Undefined	**Disease:** Hepatocellular_carcinoma
Is Artifact: no	**HGVSp:** NP_001895.1
	Sift: deleterious(0)
	PolyPhen: possibly_damaging(0.905)
NP_002515.1:p.Gln61Le u	
Gene: NRAS	**Location:** chr1:115256529
Ref./ Mutation: T / A (. PRESENT)	**Depth:** 839
Allele Fraction: 0.4958	**Clinical Sig.** Pathogenic
Mutation Classification: Undefined	**Disease:** Thyroid_cancer\x2c_folli cular
Is Artifact: no	**HGVSp:** NP_002515.1
	Sift: deleterious(0)
	PolyPhen: possibly_damaging(0.861)

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: SS18 → SSX2		
Filters: ✔ 🗄 **GSP2:** SS18_chr18_23612369_25_-_A1_GSP2 **Mutation Classification:** Undefined **Is Artifact:** no	**Reads**: 507 (17.17%) **Start Sites:** 181	**Segments** chr18:23612496→23612363 SS18(-) NM_005637.3, exon:9 chrX:52729628→52729493 SSX2(-) NM_003147.5, exon:6