AS22027_S111-29147E_Ion_V2_RBC2_BC32_rawlib.basecaller

Overall QC Status: PASS
Sample QC Status: PASS
Fusion QC Status: PASS
Variations QC Status: PASS
Job: 20230208_AS22027_AS23006 [4766]
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: 08-Feb-2023 6:38
Report Creator: mpvghtpe@gmail.com
Report Date: 09-Feb-2023 1:37

Statistics

Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
3,500,000	3,312,174	3,120,875

Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	3,103,312 / 100.0	3,103,312 / 100.0	100.0	98.7
Unique Fragments	413,647 / 13.3	413,647 / 100.0	100.0	99.1

DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	259,703.0 / 8.5	2,393,239.0 / 78.1	411,302.0 / 13.4
Molecular Bins	38,291.0 / 9.3	282,594.0 / 69.0	88,868.0 / 21.7
Average Molecular Bins per GSP2	35.26	260.22	81.83
Unique Start Sites	18,736.0 / 24.8	47,763.0 / 63.1	18,462.0 / 24.4
Average Unique Start Sites per GSP2	17.66	54.49	18.93
Average Unique Start Sites per GSP2 Control	19.17	121.83	17.67

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
36.37	121.83

Miscellaneous Statistics

On Target Deduplication Ratio
7.48:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
114.0	126.5	112.0	121.0

Reportable Variants

None Found

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: PPM1D → PRKCA		
Filters: ☑ **GSP2:** PRKCA_chr17_64637480_26_-_A1_GSP 2 **Mutation Classification:** Undefined **Is Artifact:** no	**Reads**: 34 (13.39%) **Start Sites:** 24	**Segments** chr17:58725326→58725443 PPM1D(+) NM_003620.3, exon:4 chr17:64492319→64492401 PRKCA(+) NM_002737.2, exon:3