



**Overall QC Status:** PASS  
**Sample QC Status:** PASS  
**Fusion QC Status:** PASS  
**Variations QC Status:** PASS  
**Job:** 20221027\_AS22032-33 [4749]  
**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:** 27-Oct-2022 5:25  
**Report Creator:** mpvghtpe@gmail.com  
**Report Date:** 20-Jun-2023 20:56

## Statistics

### Molecular Barcode Statistics

Total Fragments	Fragments with Complete Adapter	Number of Reads After Trimming Adapters
3,500,000	3,278,053	3,126,740

### Read Statistics

Type	Total Fragments (# / %)	Mapped (# / %)	Pass Alignment Filter (%)	On Target (%)
All Fragments	3,105,798 / 100.0	3,105,798 / 100.0	100.0	98.7
Unique Fragments	33,778 / 1.1	33,778 / 100.0	100.0	93.8

### DNA/RNA Statistics

Type	DNA Reads (# / %)	RNA Reads (# / %)	Ambiguous Reads (# / %)
All Fragments	308,583.0 / 10.1	2,125,608.0 / 69.4	629,746.0 / 20.6
Molecular Bins	3,140.0 / 9.9	18,843.0 / 59.5	9,699.0 / 30.6
Average Molecular Bins per GSP2	4.76	28.59	14.72
Unique Start Sites	1,839.0 / 17.1	6,774.0 / 62.9	3,499.0 / 32.5
Average Unique Start Sites per GSP2	2.82	11.18	5.8
Average Unique Start Sites per GSP2 Control	6.67	49.67	7.5

QC Statistics

Avg. Unique DNA And Ambiguous Start Sites Per GSP2	Avg. Unique RNA Start Sites Per GSP2 Control
8.6	49.67

Miscellaneous Statistics

On Target Deduplication Ratio
96.71:1

DNA/RNA Fragment Lengths

DNA Median Fragment Length	DNA Mean Fragment Length	RNA Median Fragment Length	RNA Mean Fragment Length
97.0	112.6	112.0	116.7

# Reportable Variants

NP_006197.1:p.Pro553L eu	
<b>Gene:</b> PDGFRA	<b>Location:</b> chr4:55141012
<b>Ref./ Mutation:</b> C / T ( . PRESENT)	<b>Depth:</b> 17
<b>Allele Fraction:</b> 0.2941	<b>HGVSp:</b> NP_006197.1
<b>Mutation Classification:</b> Undefined	<b>Sift:</b> deleterious(0)
<b>Is Artifact:</b> no	<b>PolyPhen:</b> probably_damaging(0.998)

# Reportable Isoforms

None Found