



## **DRAGEN Enrichment Sequencing Report**

**Sample: XARAR-F2-D-FEV2F2both-S54-L004**

Analysis Name: 06\_Feb\_24\_LC-189\_Target\_First\_FEV2F2both  
Report Date: 2024-02-06T10:28:28

Sample Information

Sample ID	Total PF Reads	Unique PF Reads	Percent Q30 Bases	Mean Target Coverage Depth	Percent Autosome Callability
XARAR-F2-D-FEV2F2both-S54-L004	16,221,500	2,796,304	92.39%	368.3	52.55%

Note: Percent autosome callability is the percent of non-N reference positions in the autosomes with a PASSing genotype call. The callability value for autosomes and allosomes can be found in the \*.summary.csv output file under "Percent callability".

## Enrichment Summary

Target Manifest	Total Length of Targeted Reference	Number of Targeted Regions	Padding Size
TarGT_First_v2_CDS_and_FEV2F2_GRCh37_30_Mar_23_used.bed	392,684 bp	1,254	150 bp

Note: All enrichment values are calculated without padding (sequence immediately upstream and downstream) unless otherwise stated. If any targeted region overlaps another region, the region positions will be adjusted to remove overlaps (check manifest file in the output directory for differences).

The total length of the targeted reference excludes no-call positions (Ns) in the reference sequence and might result in a smaller value than expected from the targeted regions coordinates alone.

## Read Level Enrichment

Total Aligned Reads	Percent Aligned Reads	Targeted Aligned Reads	Read Enrichment	Padded Target Aligned Reads	Padded Read Enrichment
2,727,451	97.54%	1,563,862	57.34%	1,575,572	57.77%

Note: Reads flagged as duplicates are excluded from the read level metrics.

## Base Level Enrichment

Total Aligned Bases	Percent Aligned Bases	Targeted Aligned Bases	Base Enrichment	Padded Target Aligned Bases	Padded Base Enrichment
293,685,550	96.58%	142,347,905	48.47%	169,906,068	57.85%

Note: Reads flagged as duplicates are excluded from the base level metrics.

Small Variants Summary

	SNVs	Insertions	Deletions
Total Passing	271	15	29
Het/Hom Ratio	0.000	0.000	0.000
Ts/Tv Ratio	2.110	-	-

Structural Variants Summary

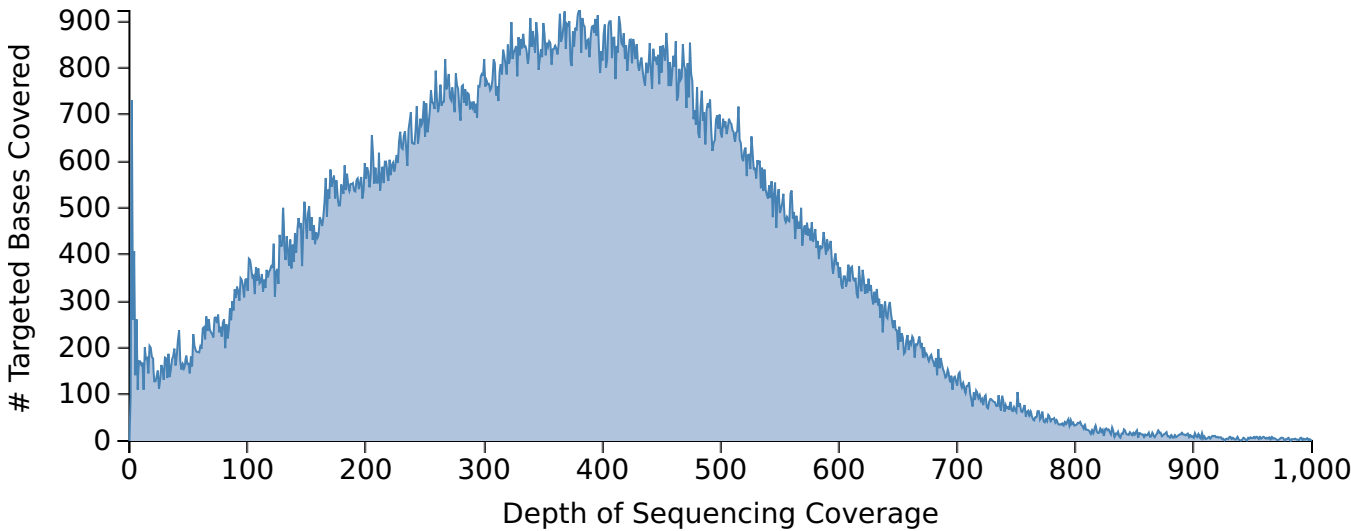
Variant Type	Total
SV Insertions	35
SV Deletions	6
SV Tandem Duplications	0
SV Breakends	170

Coverage Summary

Mean Target Coverage Depth	Uniformity of Coverage (Pct > 0.2*mean)
368.3	95.98%

Note: Uniformity of coverage is the percentage of targeted base positions in which the read depth is greater than 0.2 times the mean region target coverage depth.

Depth of Coverage in Targeted Regions



Depth of Coverage	Number of Targeted Bases Covered at Indicated Depth of Coverage	Number of Targeted Bases Covered at or Above Indicated Depth of Coverage	Target Coverage at or Above Indicated Depth of Coverage
1X	96	385,102	99.64%
10X	163	382,754	99.03%
20X	177	381,029	98.58%
30X	179	379,614	98.22%
50X	166	376,136	97.32%
100X	322	363,581	94.07%
200X	562	318,073	82.30%

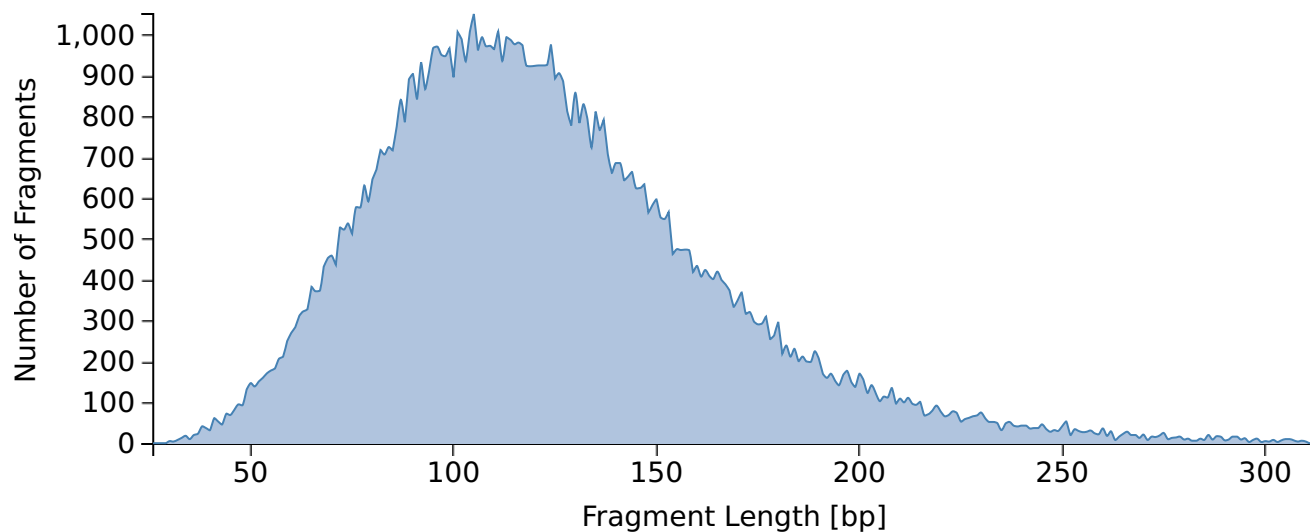
Note: Reads flagged as duplicates are excluded from the coverage statistics. The target coverage percentage is calculated for non-N reference positions in the targeted regions. Read cycles with no-calls (Ns) do not add to the target coverage.

## Fragment Length Summary

Fragment Length Median	Minimum	Maximum	Standard Deviation
118 bp	26 bp	313 bp	39 bp

Note: The minimum and maximum are calculated from values within approximately three standard deviations (excluding the lower and upper 0.15% of the data) to account for potential outliers.

## Fragment Length Distribution



## Duplicate Information

Percent Duplicate Aligned Reads
83.11%

Analysis Details

Settings

Setting Name	Value
Reference Genome	Homo sapiens (UCSC hg19-altaware)
Targeted Regions	TarGT_First_v2_CDS_and_FEV2F2_GRCh37_30_Mar_23_used.bed
Base Padding	150

Software Versions

Software	Version
DRAGEN Enrichment (BaseSpace Workflow)	3.9.5
DRAGEN Enrichment Workflow	0.15.2-O0014dragen-3.9.5-pyparsing-fix
Bam Metrics	v0.0.22
Hash Table Build (Aligner)	01.003.044.3.5.3-38-gefdaeaff-hv-8