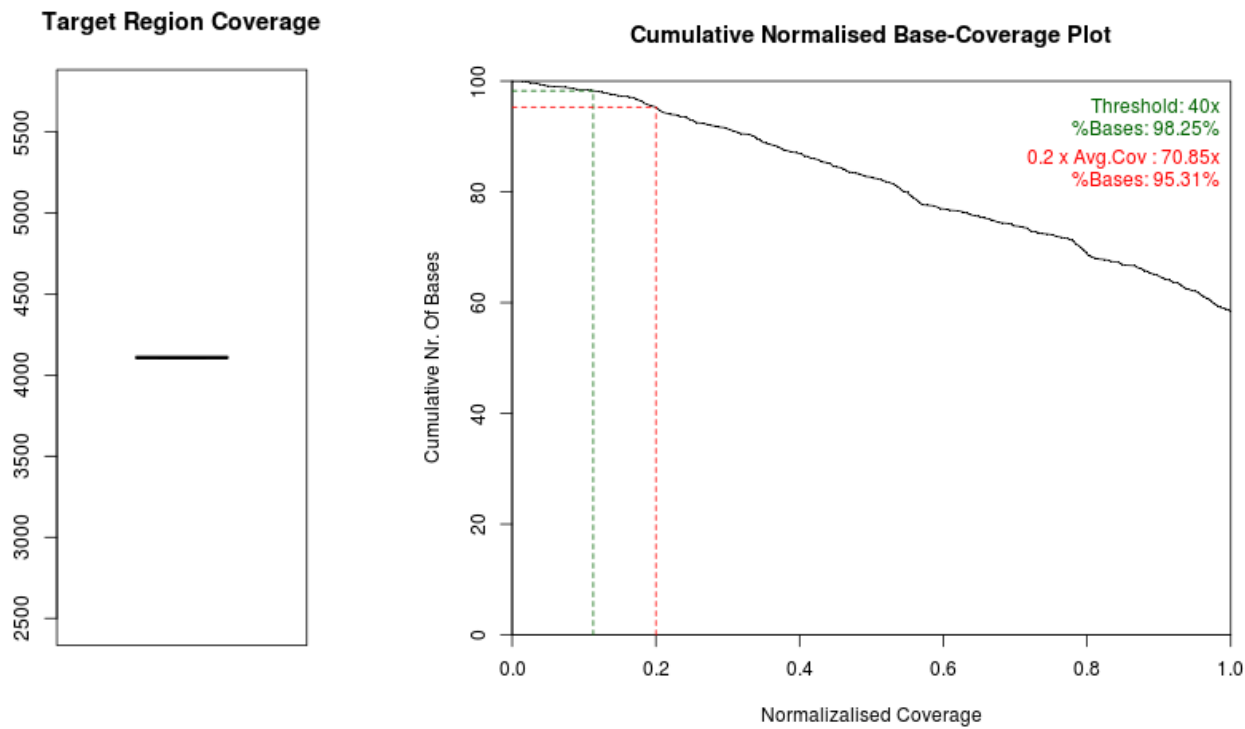


Coverage Report for “”

Overall Summary



Samtools Flagstat Summary

In total (QC-passed reads)	4108
Duplicates	0
Mapped (100.00%)	4108
Paired in sequencing	4108
Read1	2054
Read2	2054
Properly paired (100.00%)	4108
With itself and mate mapped	4108
Singletons (0.00%)	0
With mate mapped to a different chr	0
With mate mapped to a different chr (mapQ≥5)	0

Target Region Coverage

Number of Target Regions	1
Minimal Region Coverage	4108
25% Region Coverage	4108
50% (Median) Region Coverage	4108
75% Region Coverage	4108
Maximal Region Coverage	4108
Average Region Coverage	4108
Mapped On Target	100.0
<u>Target Base Coverage</u>	
Number of Target Bases	999
Average Base Coverage	354
Non-Covered Bases	0

Gene Summaries

Legend:

- RED:** Coverage did not reach set threshold of 40
- ORANGE:** Coverage was incomplete for the exon. Overruled by red.

