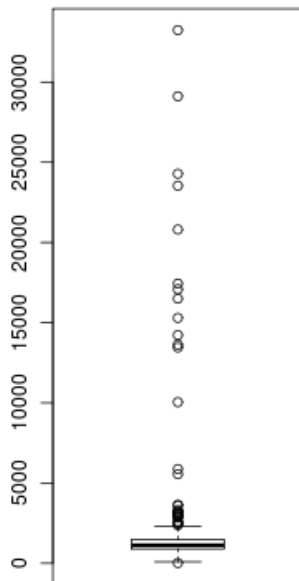


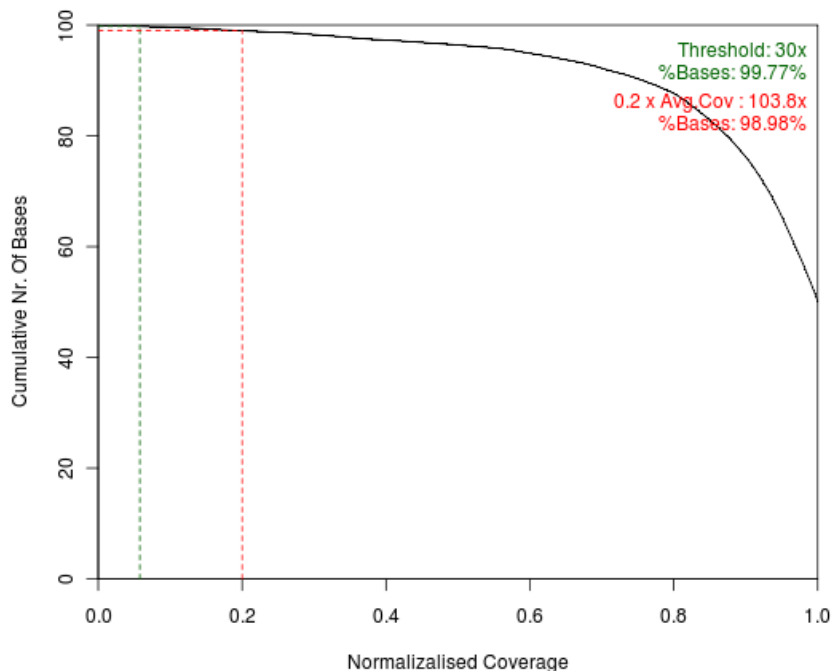
Coverage Report for "Sample_5"

Overall Summary

Target Region Coverage



Cumulative Normalised Base-Coverage Plot



Samtools Flagstat Summary

In total (QC-passed reads)	934147
Duplicates	0
Mapped (99.93%)	933507
Paired in sequencing	932753
Read1	466245
Read2	466508
Properly paired (98.71%)	920678
With itself and mate mapped	932085
Singletons (0.02%)	190
With mate mapped to a different chr	9568
With mate mapped to a different chr (mapQ≥5)	8018

Target Region Coverage

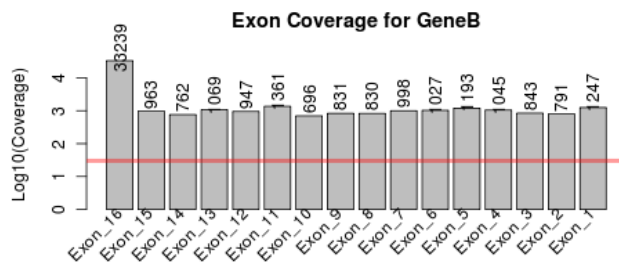
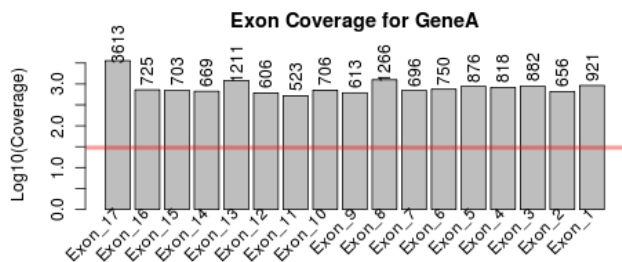
Number of Target Regions	360
Minimal Region Coverage	15
25% Region Coverage	904
50% (Median) Region Coverage	1124.5
75% Region Coverage	1489
Maximal Region Coverage	33239
Average Region Coverage	1907
Mapped On Target	73.6
<u>Target Base Coverage</u>	
Number of Target Bases	153387
Average Base Coverage	519
Non-Covered Bases	33

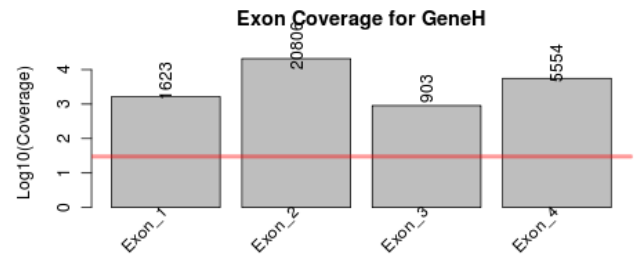
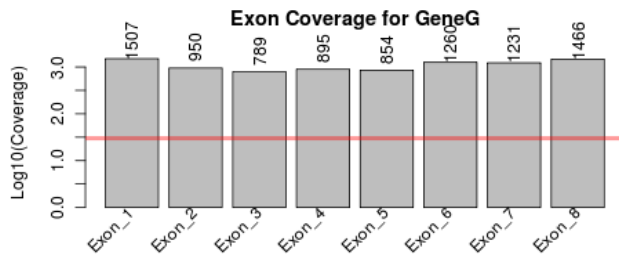
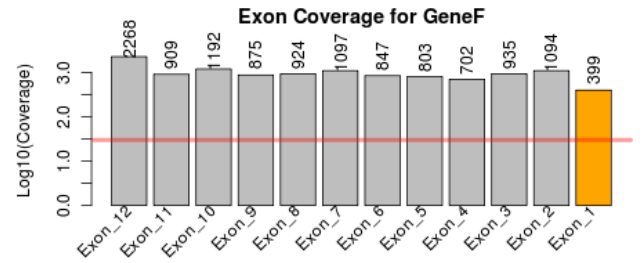
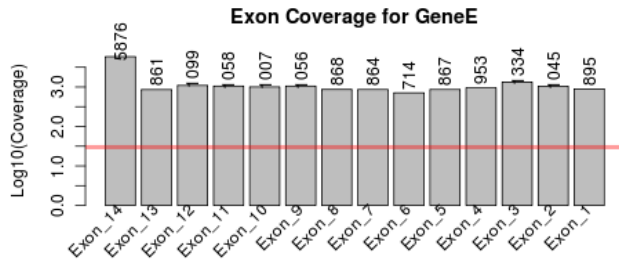
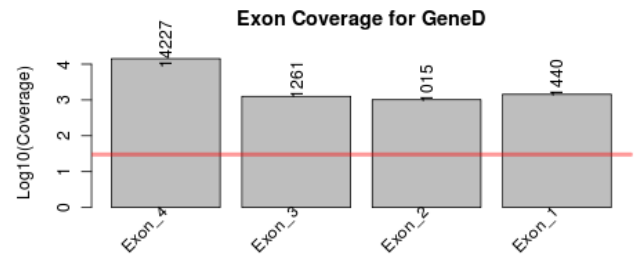
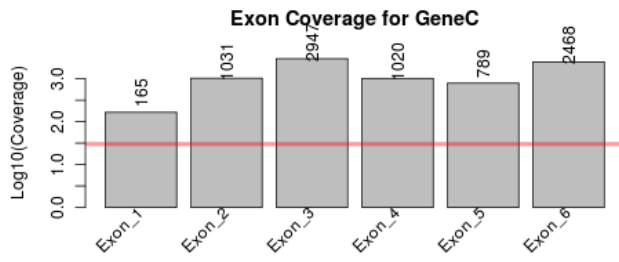
Gene Summaries

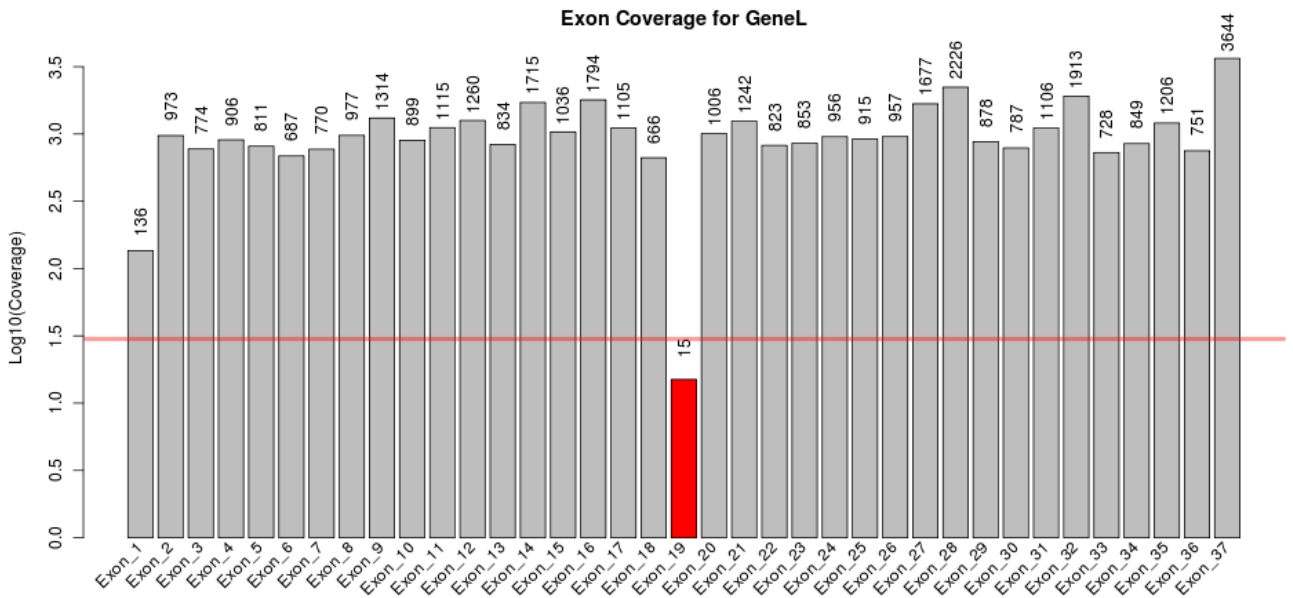
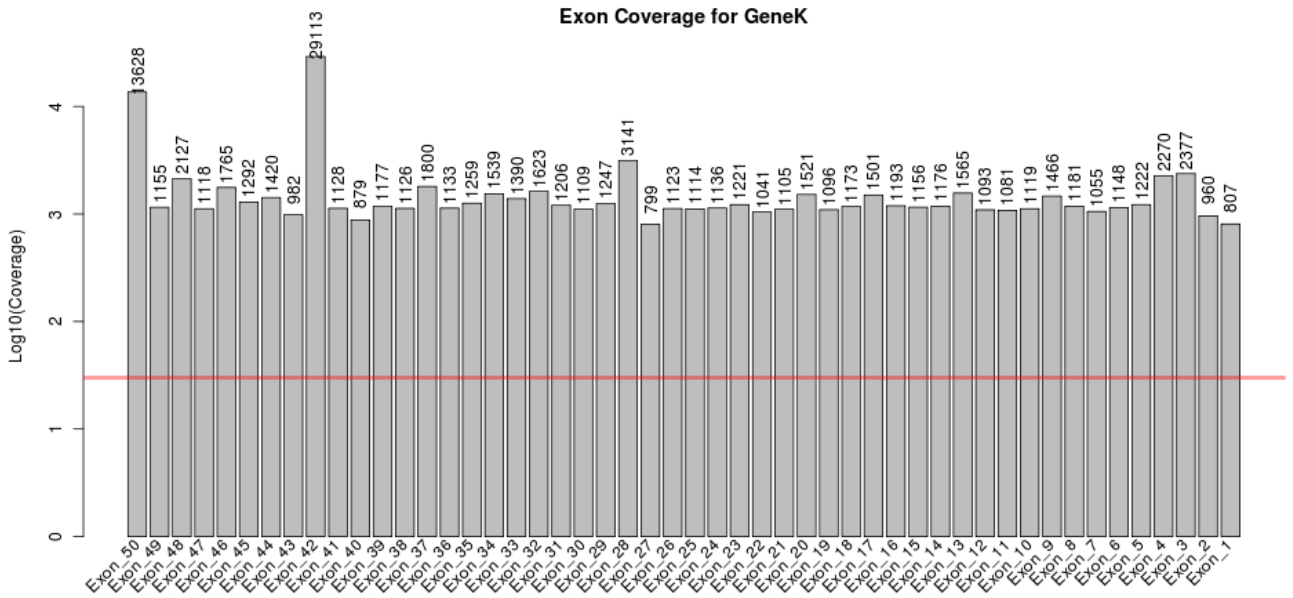
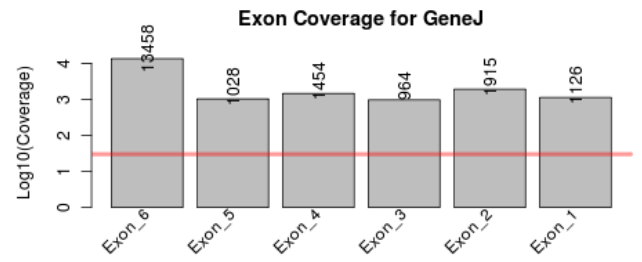
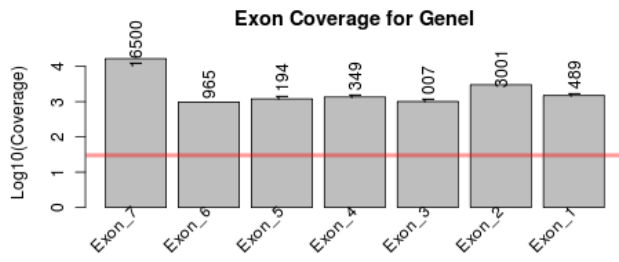
Legend:

RED: Coverage did not reach set threshold of 30

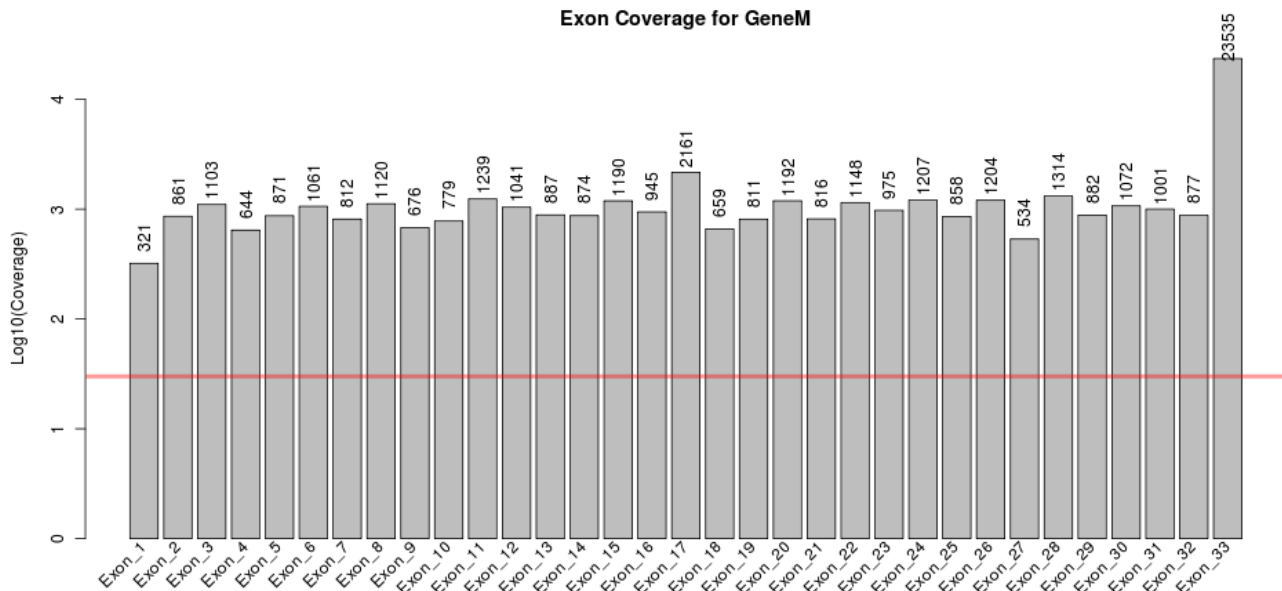
ORANGE: Coverage was incomplete for the exon. Overruled by red.



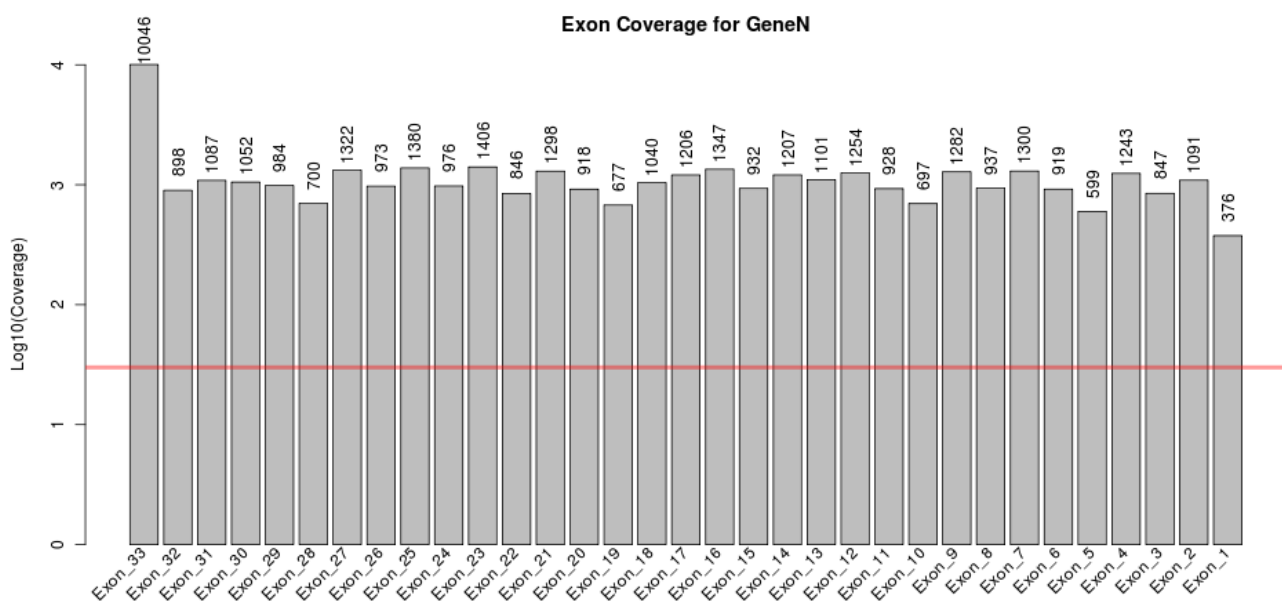


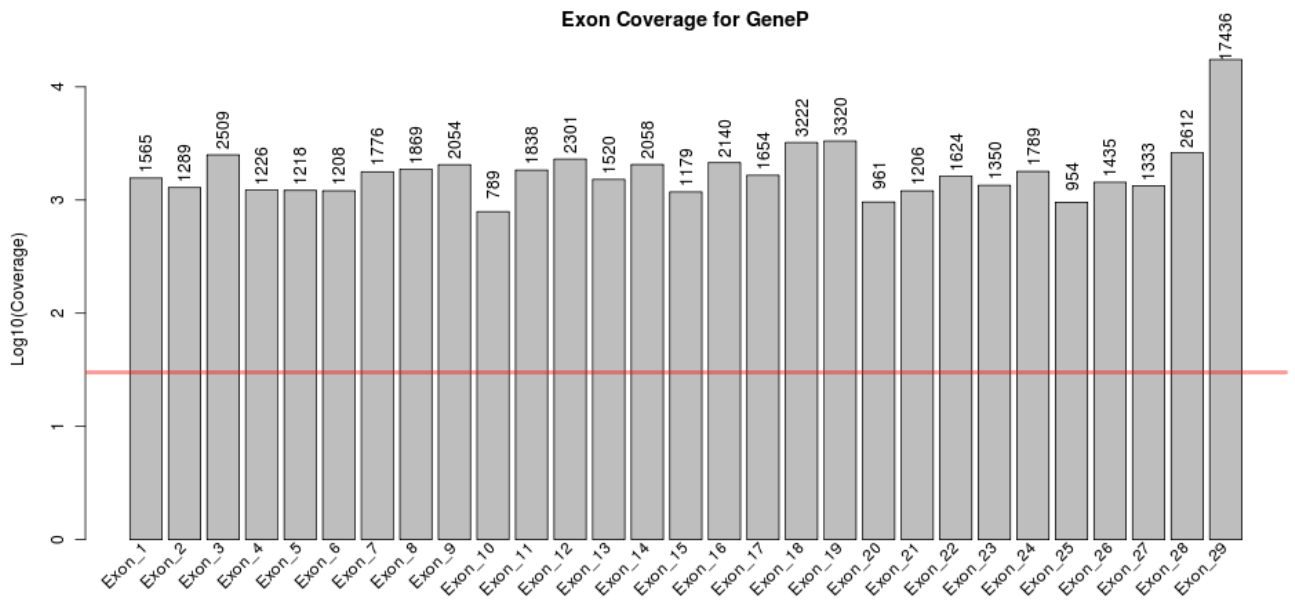
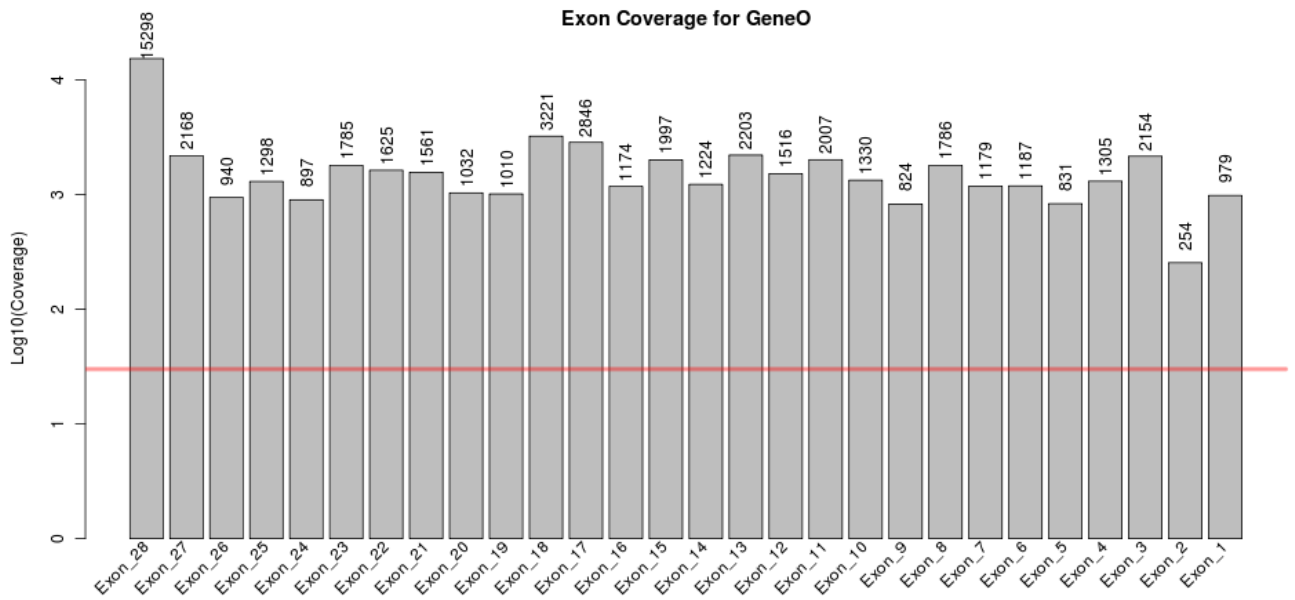


Exon Coverage for GeneM

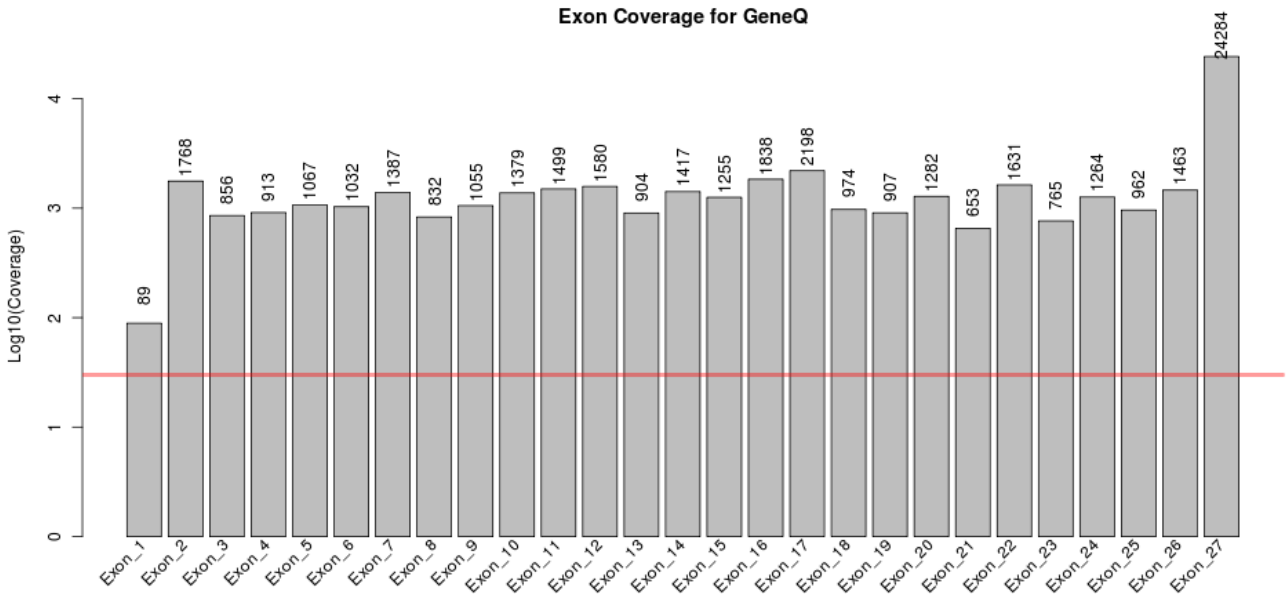


Exon Coverage for GeneN

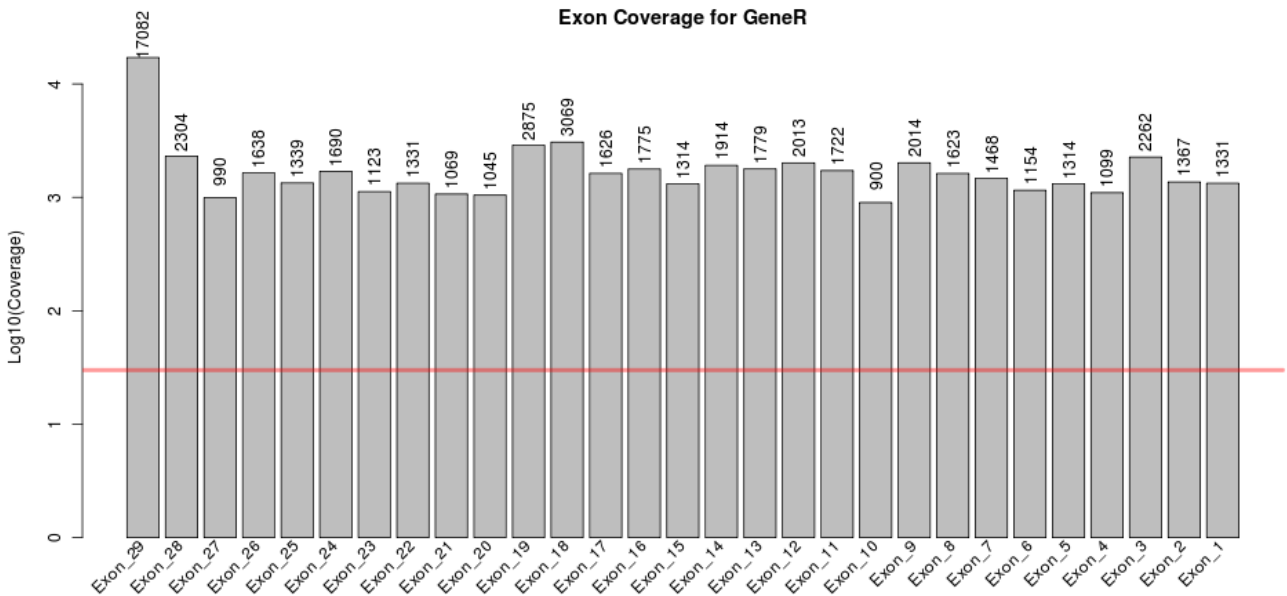




Exon Coverage for GeneQ



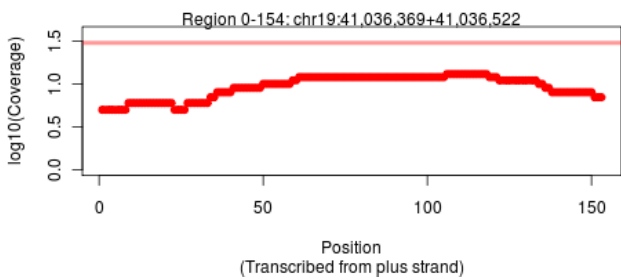
Exon Coverage for GeneR



Failed Exon Plots

NOTE: ALL exons were tested for local coverage <30

Coverage for GeneL Exon 19



Coverage for GeneN Exon 1

