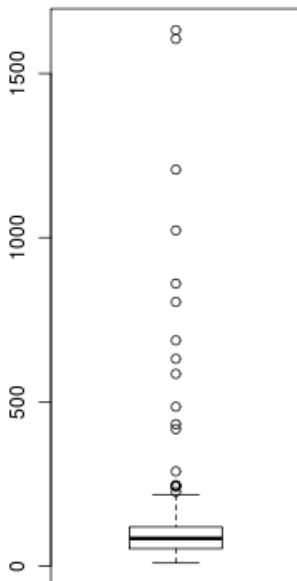


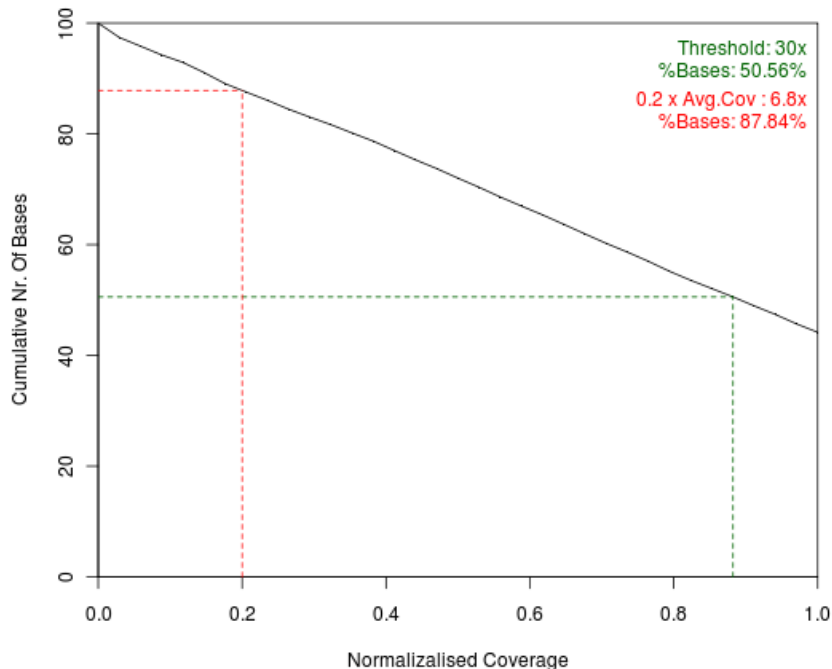
Coverage Report for "Demo_Report"

Overall Summary

Target Region Coverage



Cumulative Normalised Base-Coverage Plot



Samtools Flagstat Summary

In total (QC-passed reads)	32696429
Duplicates	0
Mapped (99.90%)	32664148
Paired in sequencing	32417869
Read1	16329073
Read2	16088796
Properly paired (98.09%)	31798118
With itself and mate mapped	32370992
Singletons (0.05%)	14596
With mate mapped to a different chr	267886
With mate mapped to a different chr (mapQ≥5)	245525

Target Region Coverage

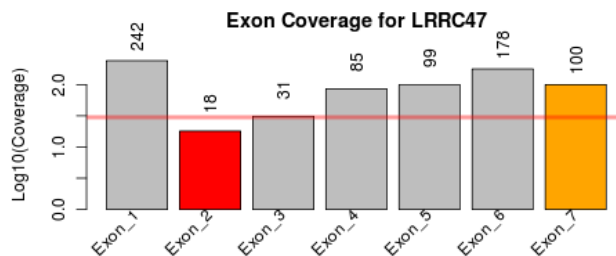
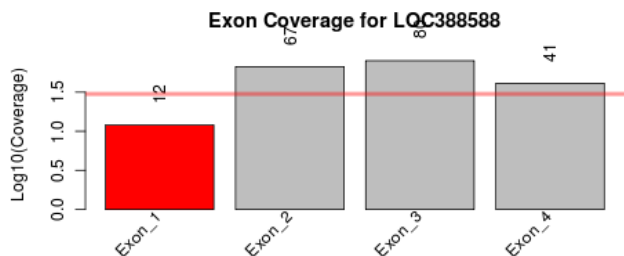
Number of Target Regions	249
Minimal Region Coverage	9
25% Region Coverage	53
50% (Median) Region Coverage	84
75% Region Coverage	119
Maximal Region Coverage	1632
Average Region Coverage	126
Mapped On Target	0.1
<u>Target Base Coverage</u>	
Number of Target Bases	70631
Average Base Coverage	33
Non-Covered Bases	1839

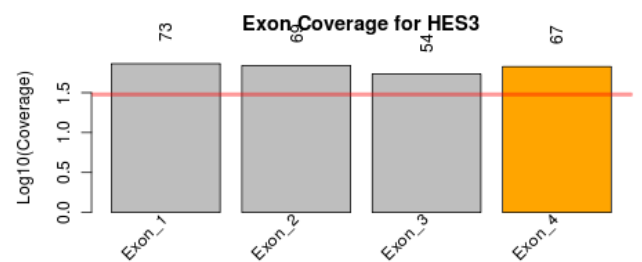
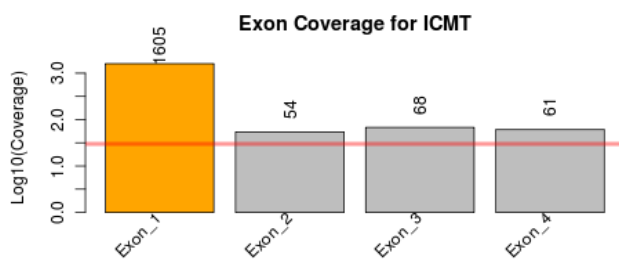
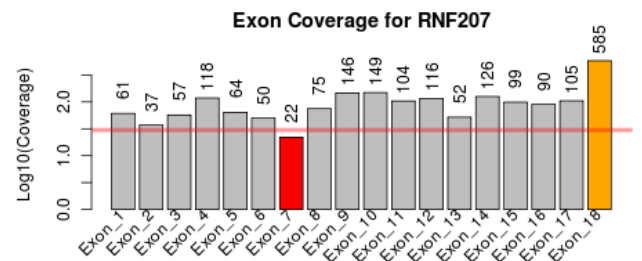
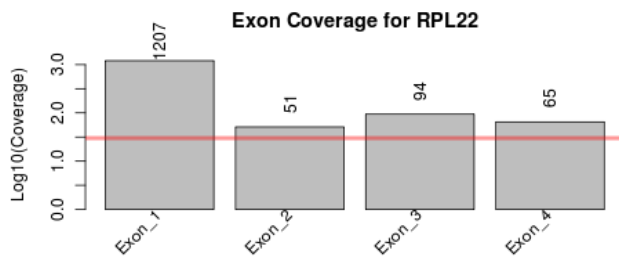
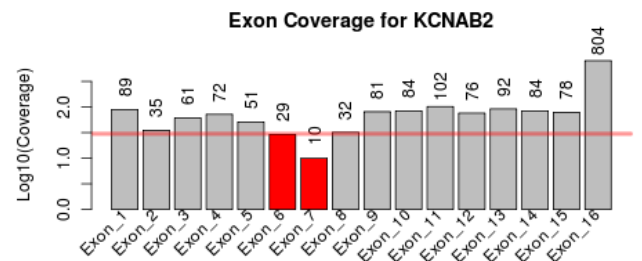
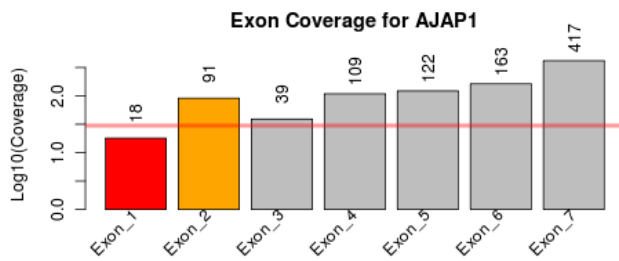
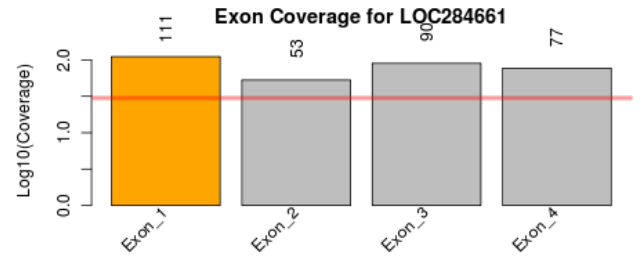
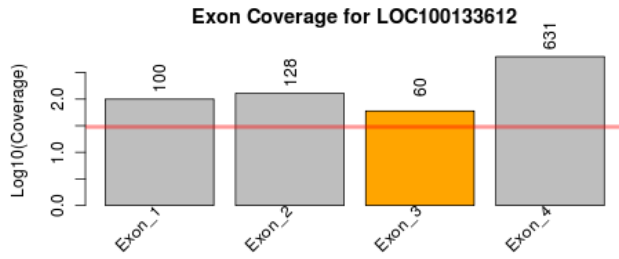
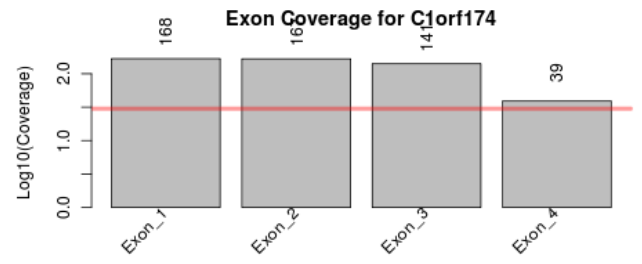
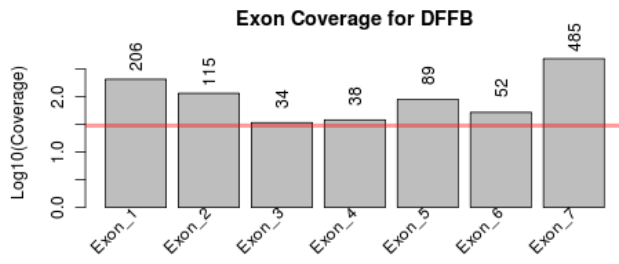
Gene Summaries

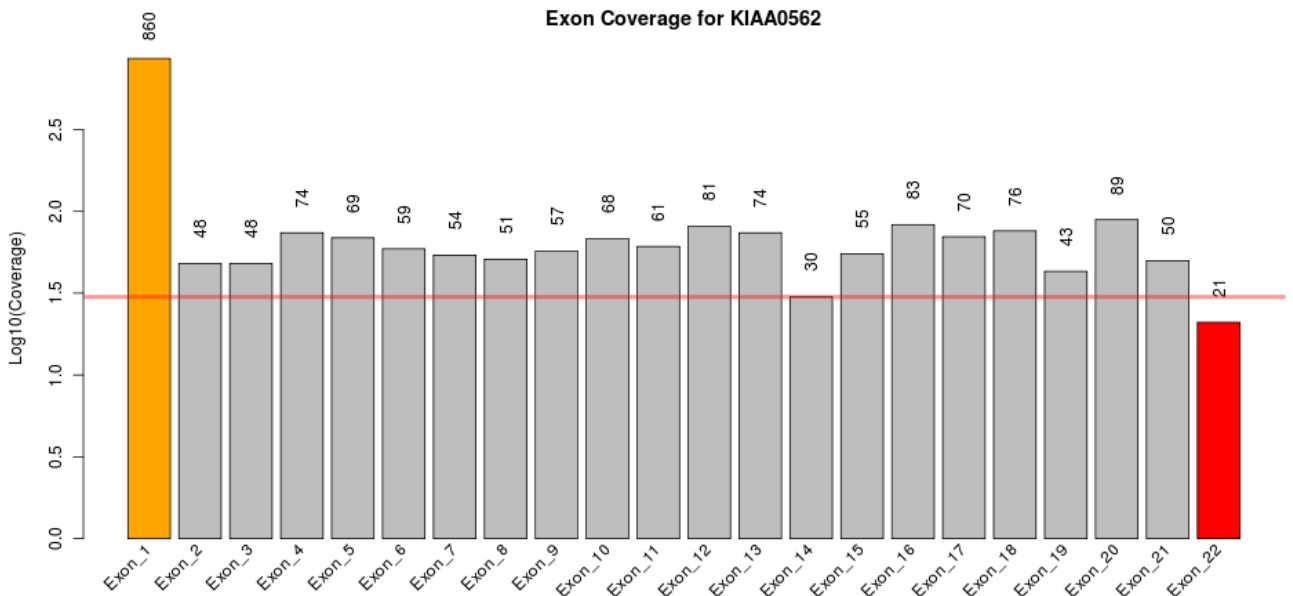
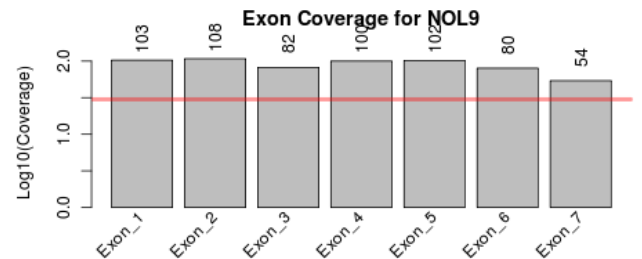
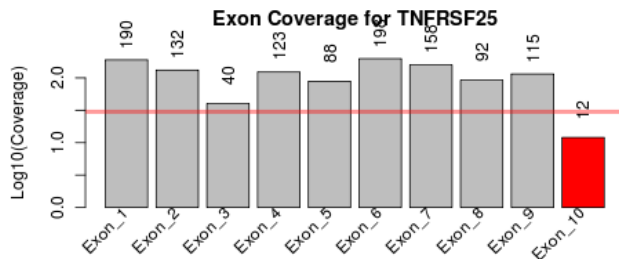
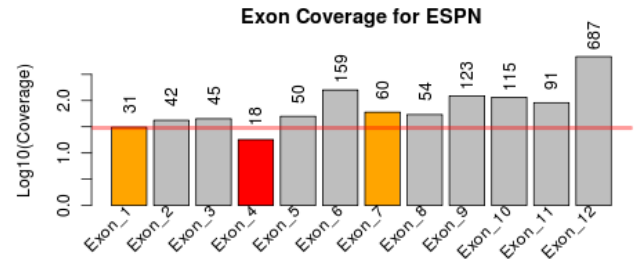
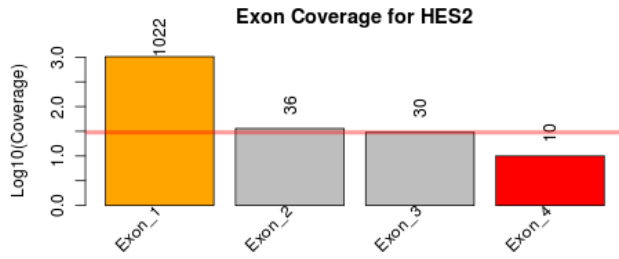
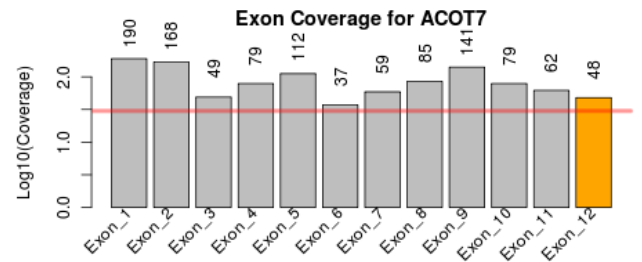
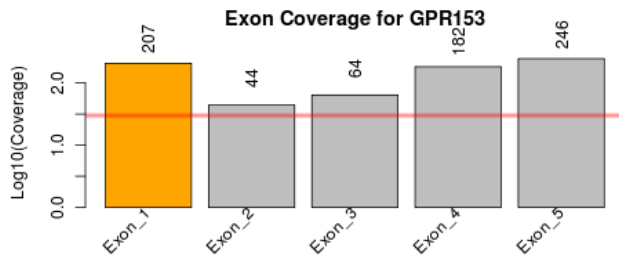
Legend:

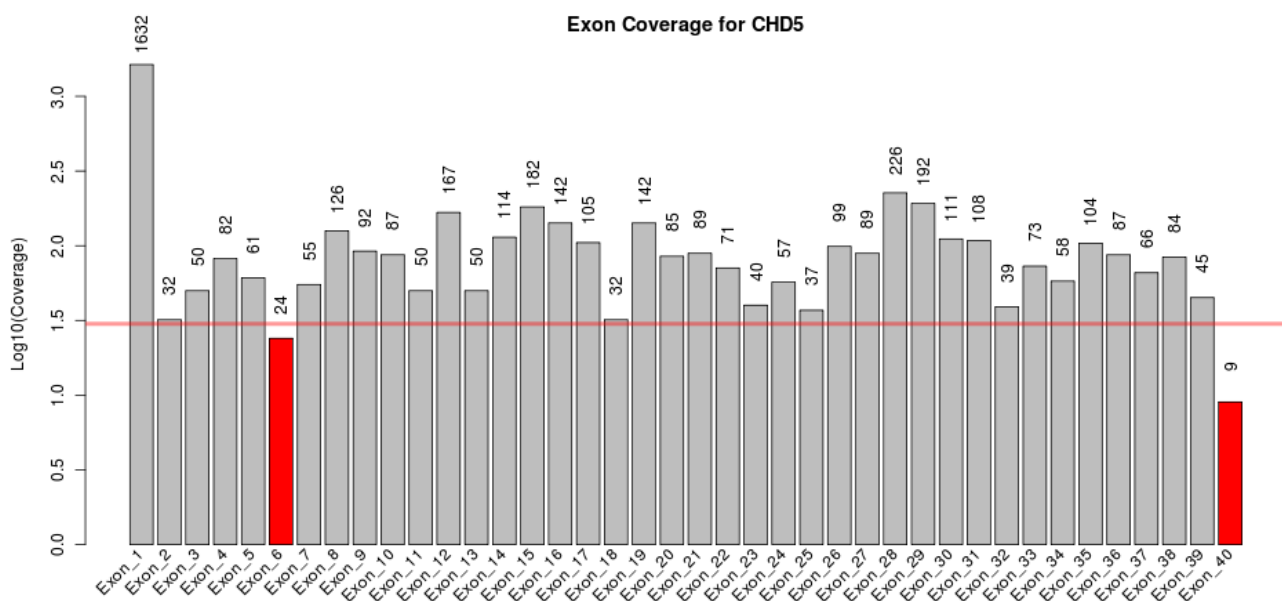
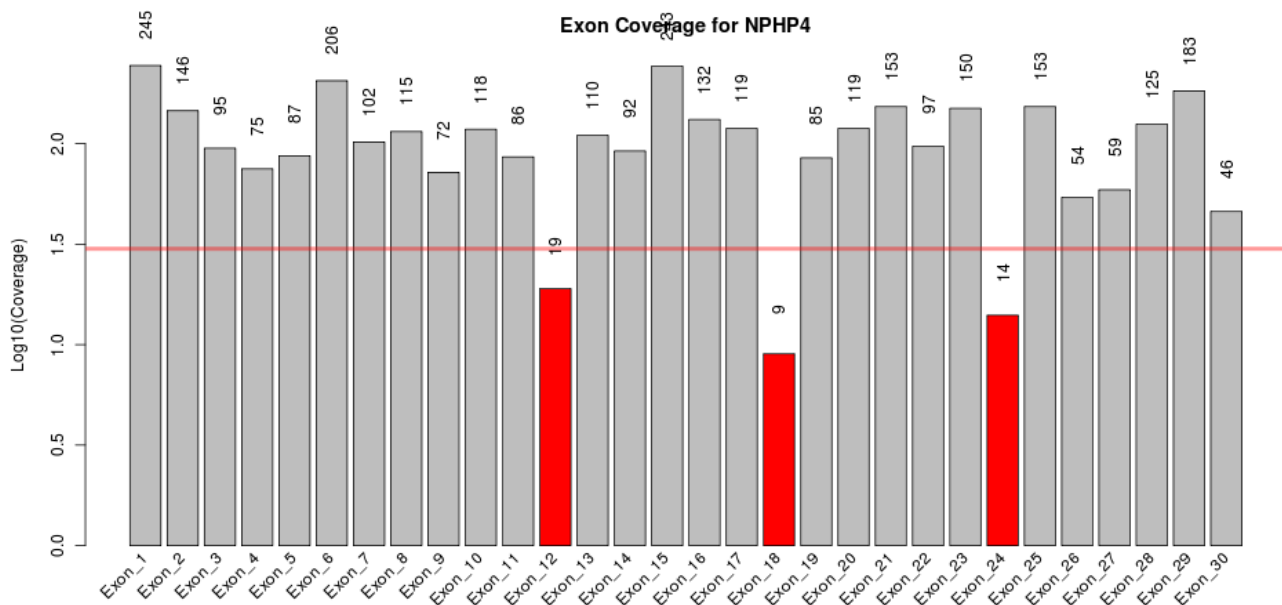
RED: Coverage did not reach set threshold of 30

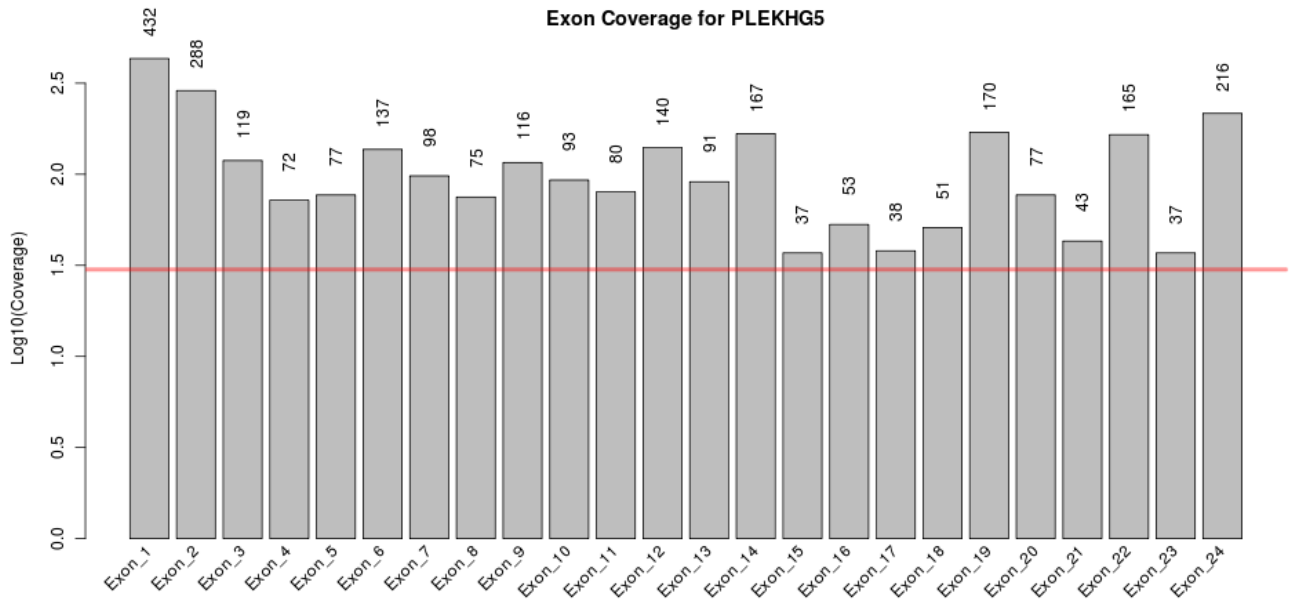
ORANGE: Coverage was incomplete for the exon. Overruled by red.











Failed Exon Plots

NOTE: ALL exons are plotted, regardless of coverage

