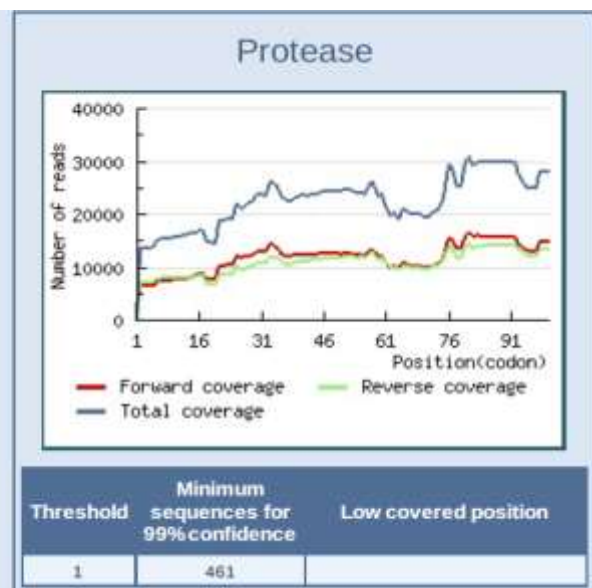
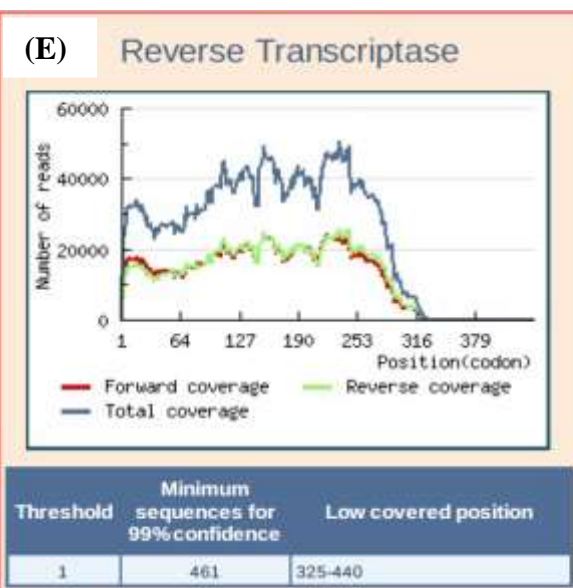
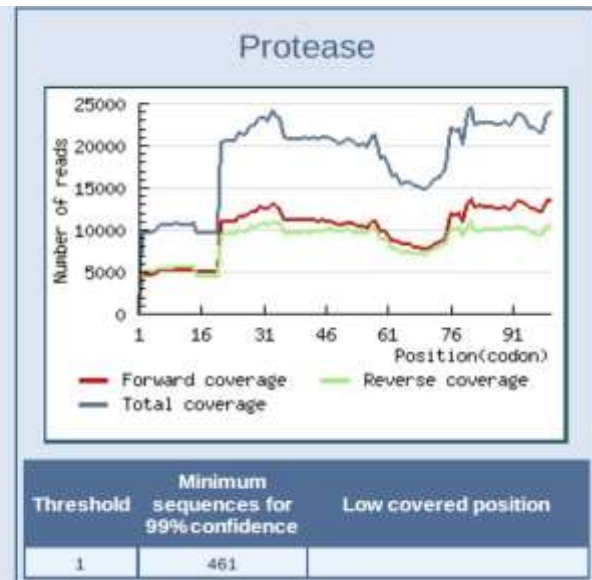
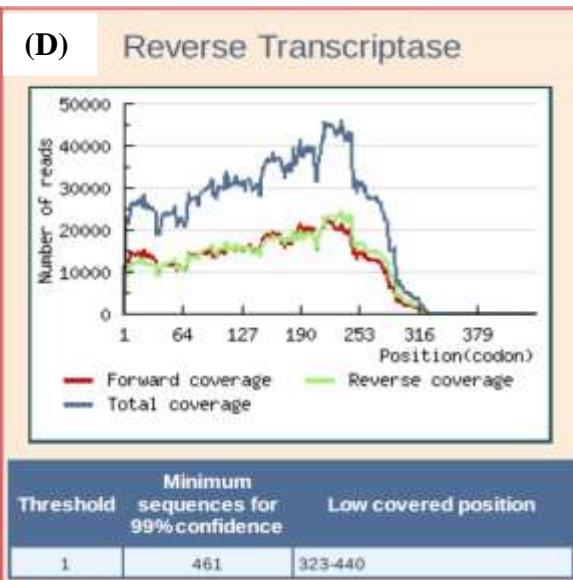
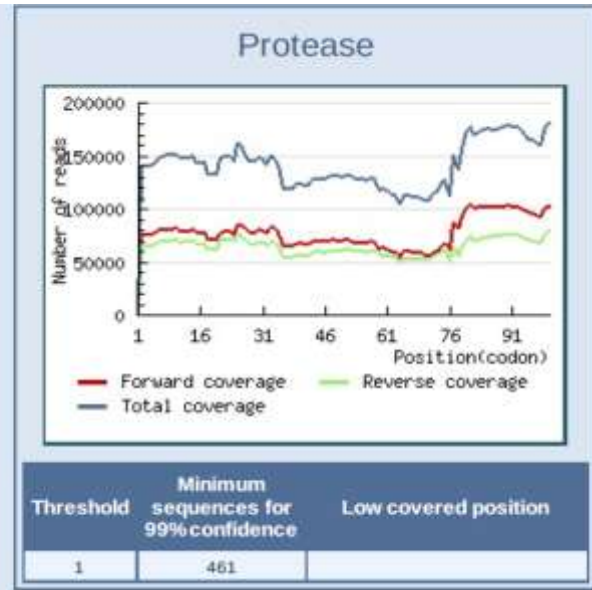
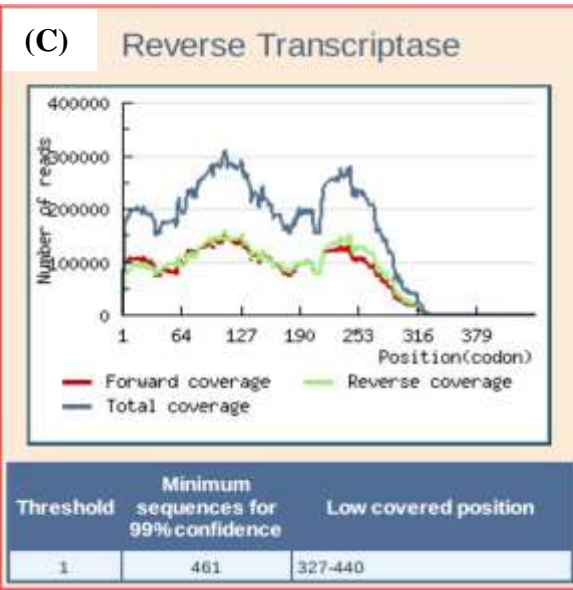
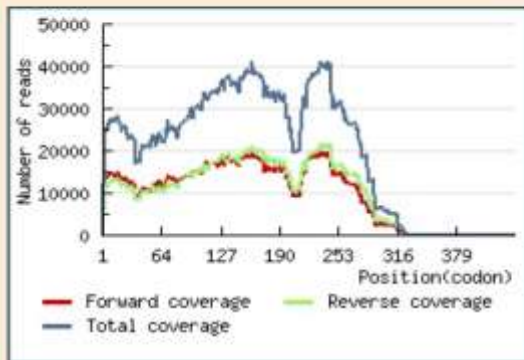


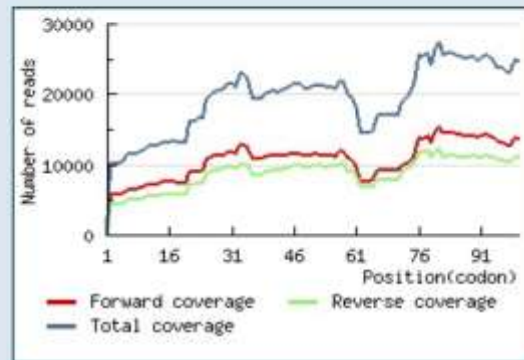
Additional file 1: Figure S1. Deep sequencing coverage. C – E shows sequencing coverage for samples with virological failure (L031, L054 and L064 respectively), F shows coverage for a sample with detectable viremia (L009) and G and H show coverage for virally suppressed samples (L074 and L075 respectively). Mutations were excluded from analysis for any of the following: noisy mutations filtering, coverage filtering, forward/reverse unbalanced frequency and forward/reverse unbalanced coverage.



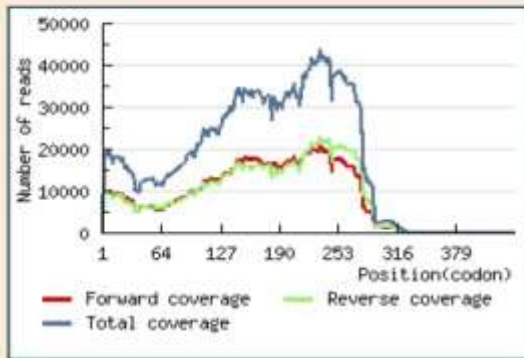
(F) Reverse Transcriptase

Threshold	Minimum sequences for 99% confidence	Low covered position
1	461	323-440

Protease

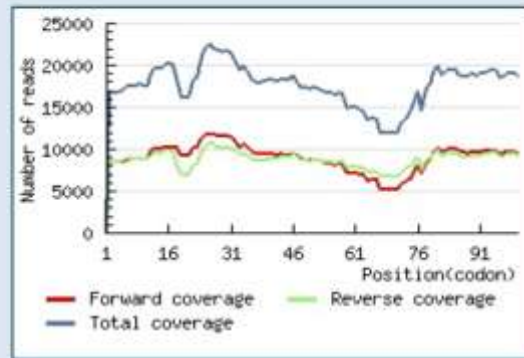


Threshold	Minimum sequences for 99% confidence	Low covered position
1	461	

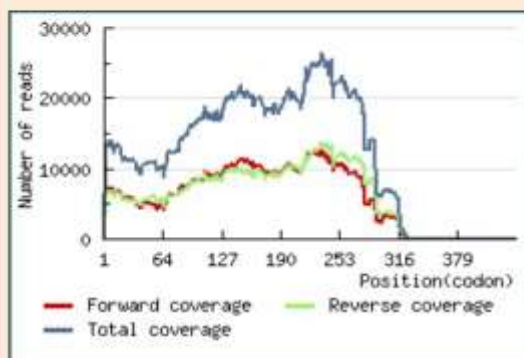
(G) Reverse Transcriptase

Threshold	Minimum sequences for 99% confidence	Low covered position
1	461	323-440

Protease

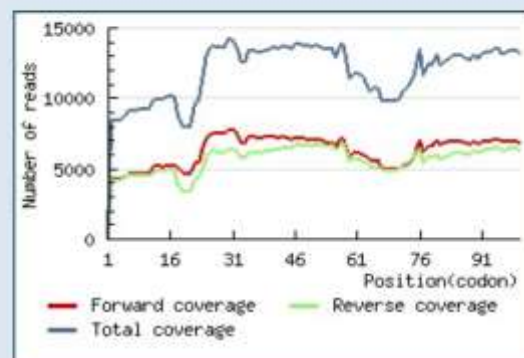


Threshold	Minimum sequences for 99% confidence	Low covered position
1	461	

(H) Reverse Transcriptase

Threshold	Minimum sequences for 99% confidence	Low covered position
1	461	323-440

Protease



Threshold	Minimum sequences for 99% confidence	Low covered position
1	461	