Description of figures output by IRMA

ADDITIONAL FILE 6
Read percentages

1) Assembled reads versus QC filtered and additionally filtered reads
2) Percentages of read patterns passing QC versus unusable and chimeric reads
3) Percentages of merged-pair reads for each assembled gene segment
Coverage diagram

(A) Read depth per site [y-axis] is depicted for the length of the gene segment [x-axis]. Called single nucleotide variants [SNV] are colored by minor allele.

(B) Observed normalized frequency is given for each SNV ordered by position and colored by minor allele. The paired-end read overlap disagreement rate is given in black. The consensus allele is given on the x-axis with the minor allele.
Phasing heat map

Every called single nucleotide variant [SNV] is pairwise compared to each other SNV. If the SNVs are linked, they color in dark red while unlinked SNVs are colored in bright yellow. Called SNVs are compared using four distance measures: Jaccard distance, mutual association distance, scaled and transformed joint frequency, and an experimental enrichment distance. Clustered SNVs are considered to be in phase or linked to the same viral sub-population segment, qualitatively speaking.