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

READ PROPORTIONS.
1. Percentages of total read counts (R1 & R2)
   - ASSEMBLED: influenza reads in final assemblies.
   - QC FILTERED: didn’t pass length/median quality thresholds.
   - OTHER: non-flu and contaminant/poor flu signal.
2. Percentages of all read patterns passing QC process
   - Patterns are clustered or non-redundant reads.
   - ASSEMBLED: excellent influenza read patterns.
   - UNUSABLE: poor or contaminant flu patterns.
   - CHIMERIC: flu patterns matching both strands.
   - NO MATCH: non-flu read patterns.
3. Percentages of assembled, merged-pair read counts
   - Shows the proportion of gene segments to the genome.
   - Paired-end reads have been merged into a single count unless not applicable: single-end reads have been used.
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.