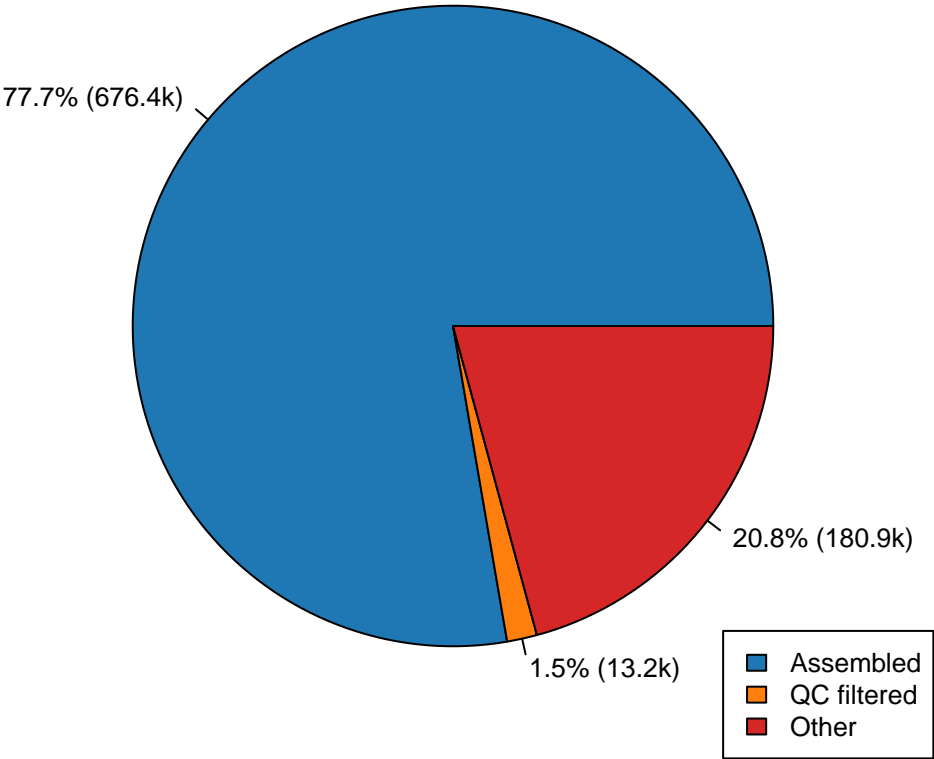
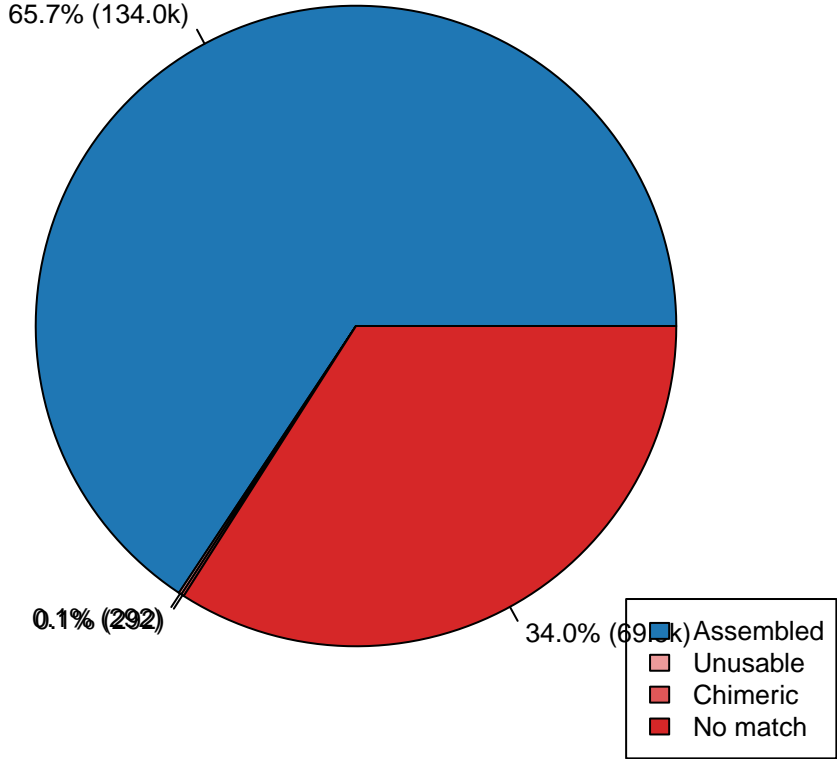


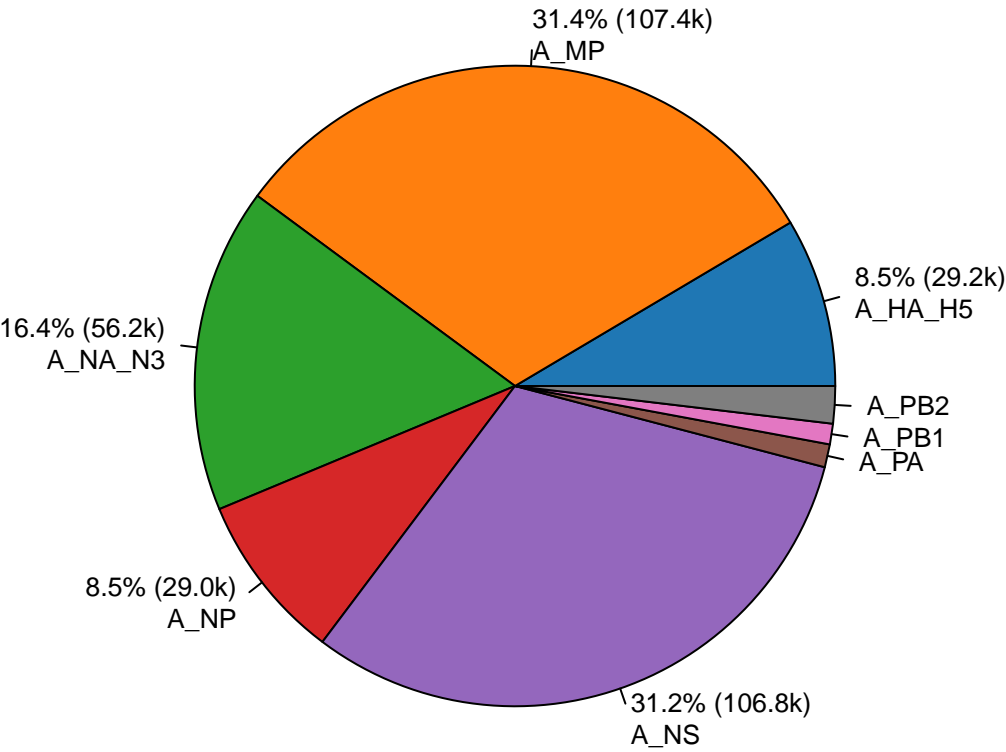
1. Percentages of total reads (R1 + R2)



2. Percentages of all read patterns passing QC



3. Percentages of assembled, merged-pair reads



SAMPLE "irma_output"

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.