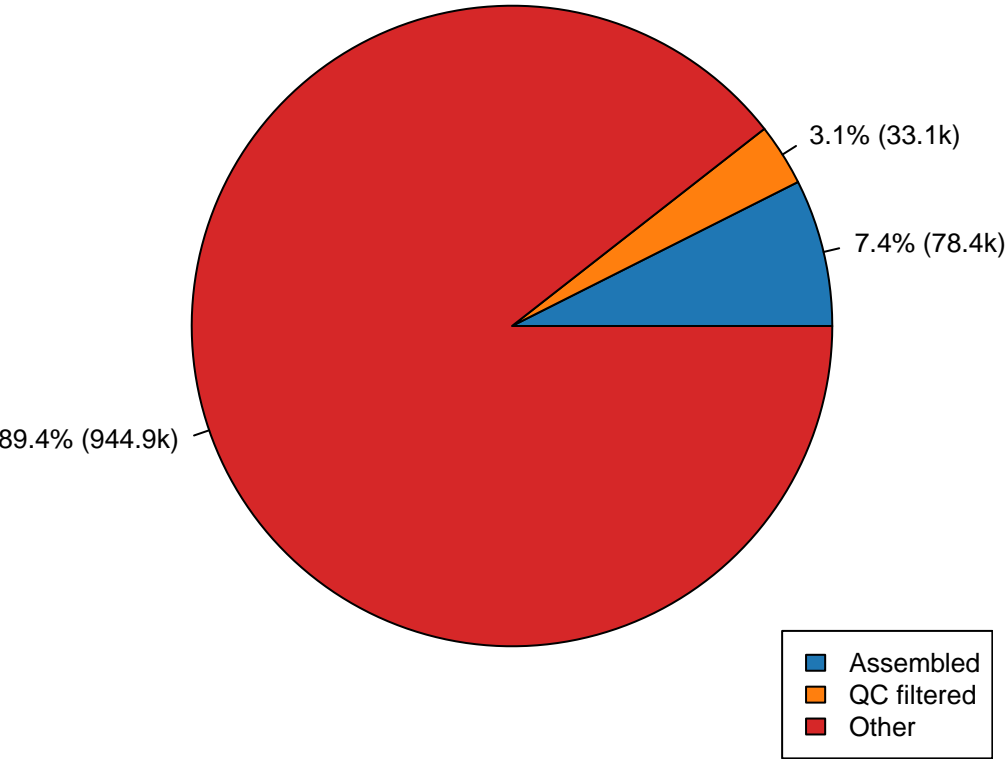
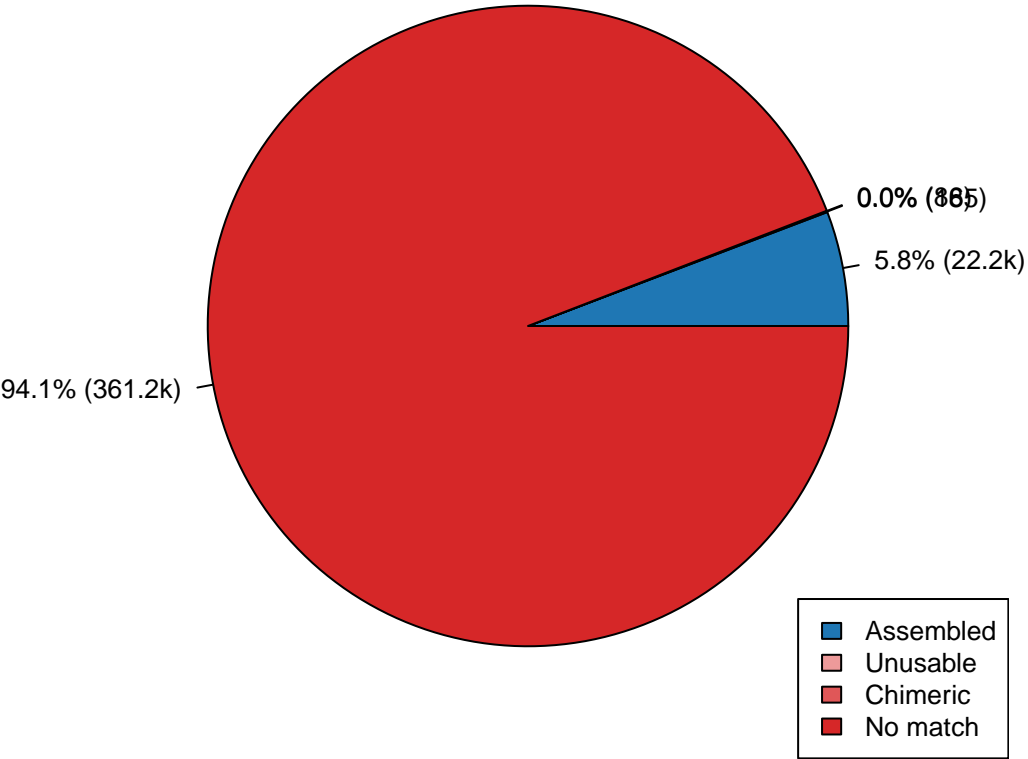


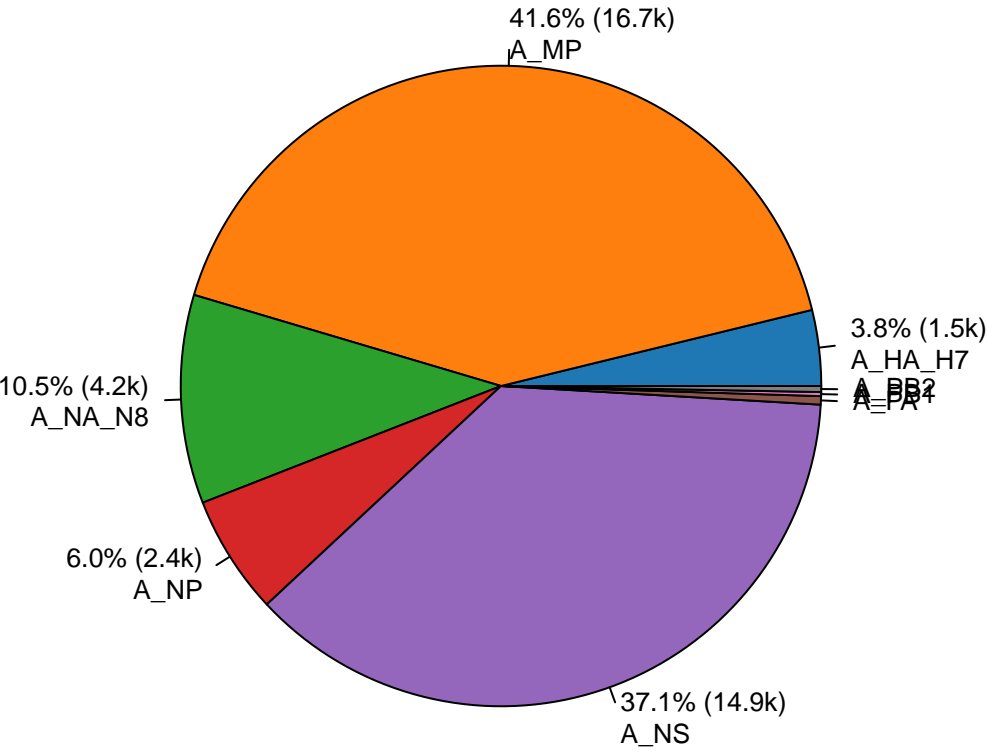
1. Percentages of total reads (R1 + R2)



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.