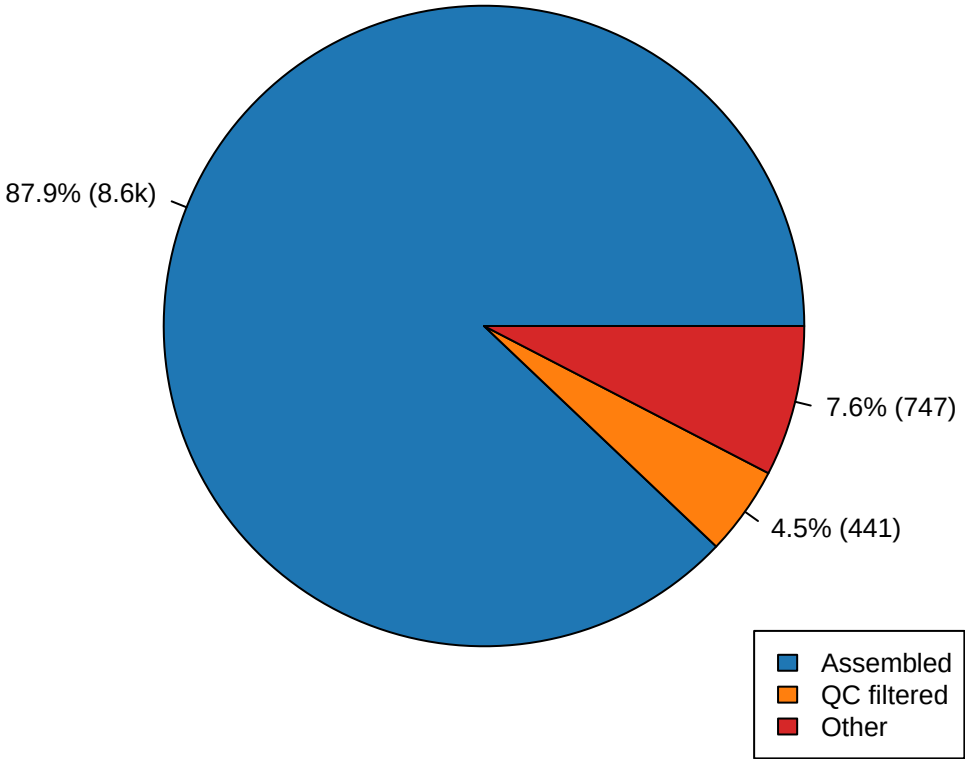
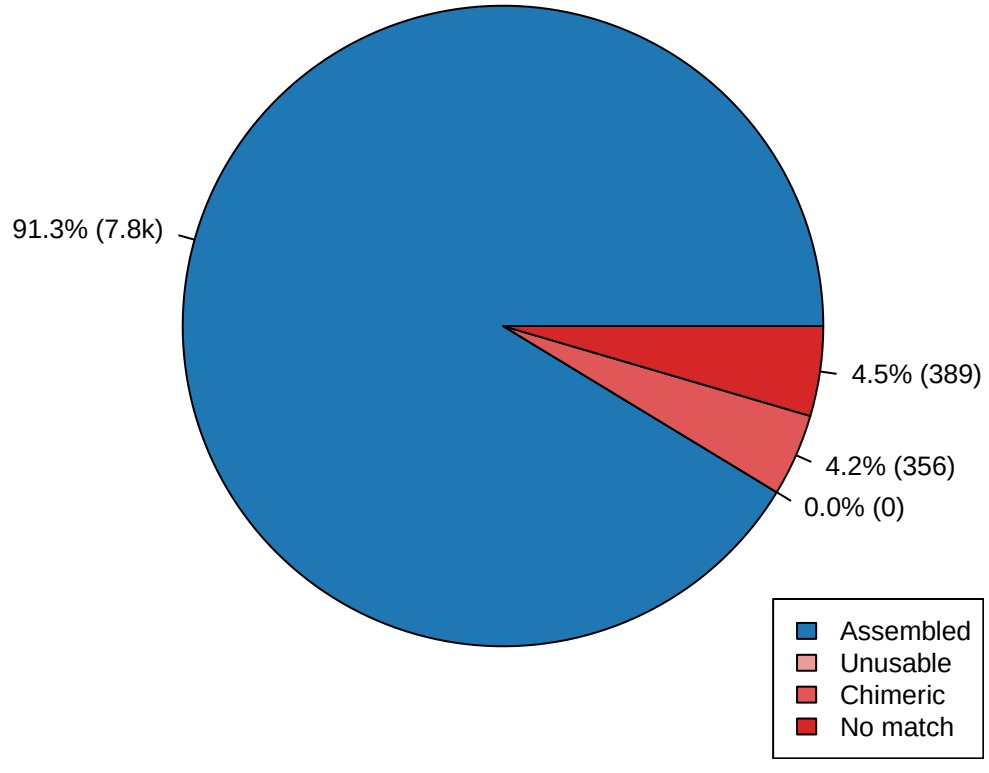
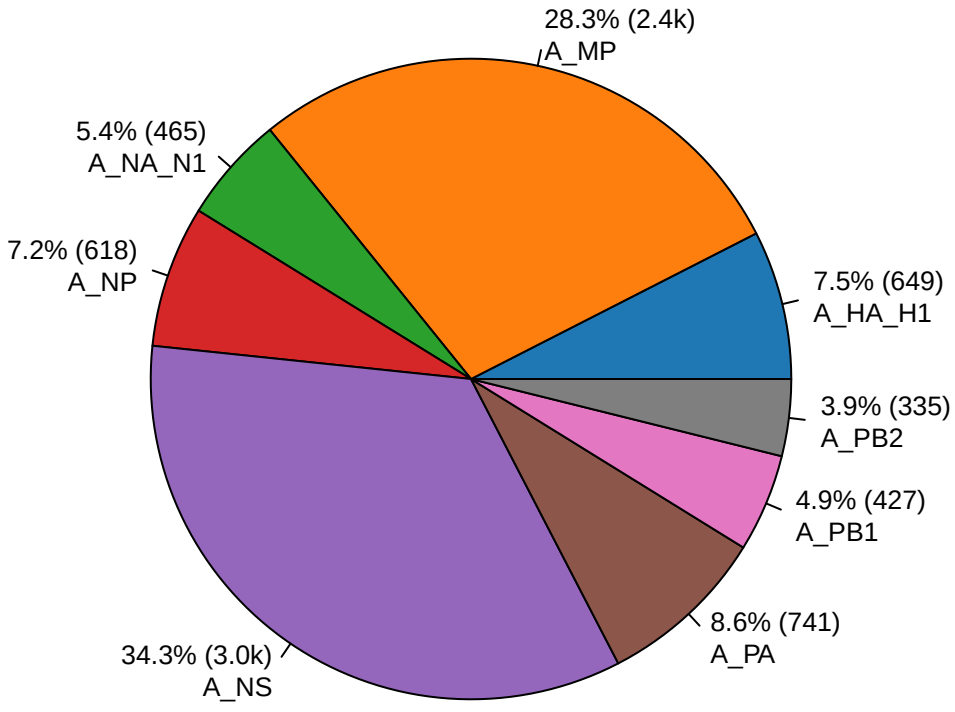
1. Percentages of total reads



2. Percentages of all read patterns passing QC



3. Percentages of assembled reads



SAMPLE "CHOI−041_N0_PJ6FV5"

READ PROPORTIONS.

1. Percentages of total read counts
   − 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 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.