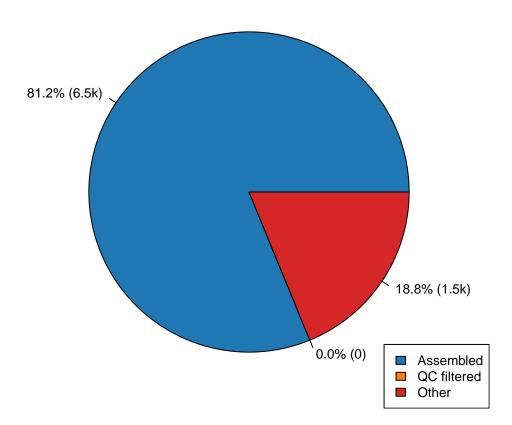
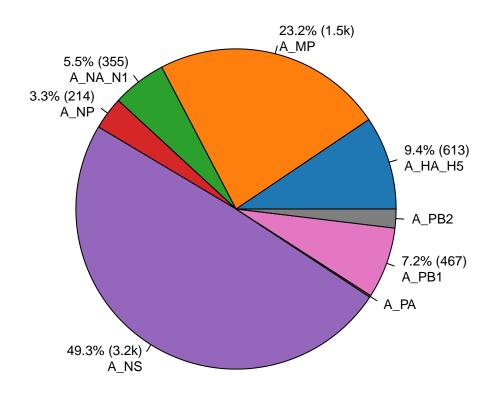
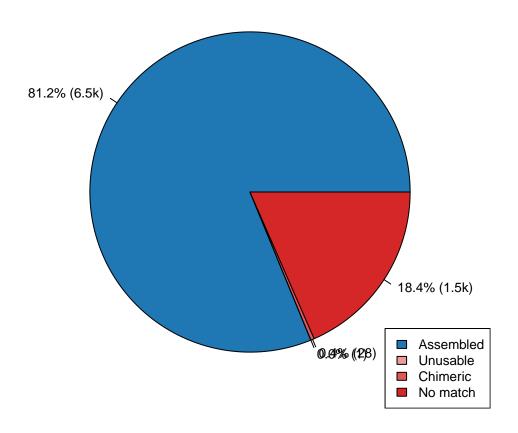
## 1. Percentages of total reads



## 3. Percentages of assembled reads



## 2. Percentages of all read patterns passing QC



SAMPLE "sample03"

## 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.