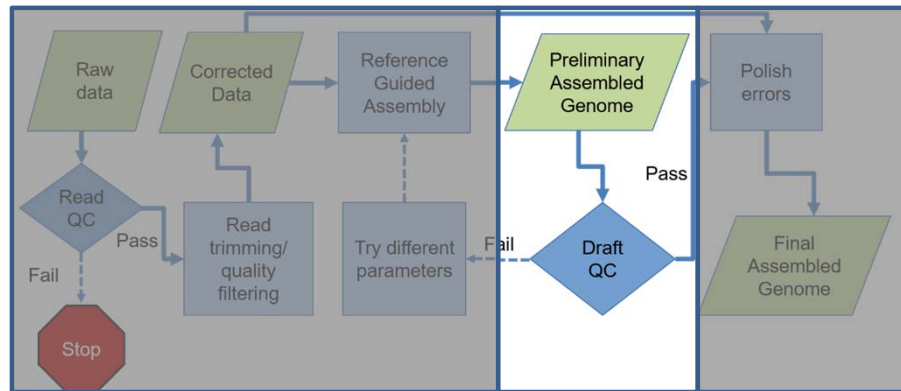
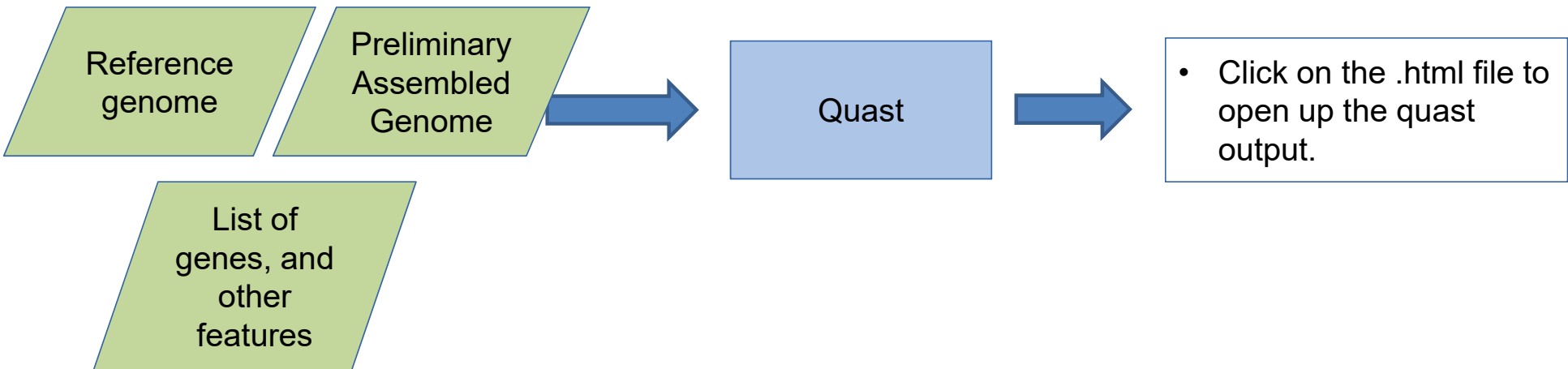


## Quality Control of the Preliminary Assembled Genome



- **Quast compares the preliminary assembly to a known genome from the same species.**
- **Also, identifies functional sequences, like genes and RNAs.**



# Assessing genome quality with QUAST.

## QUAST

Quality Assessment Tool for Genome Assemblies by [CAB](#)

10 January 2020, Friday, 08:30:06

[View in Icarus contig browser](#)

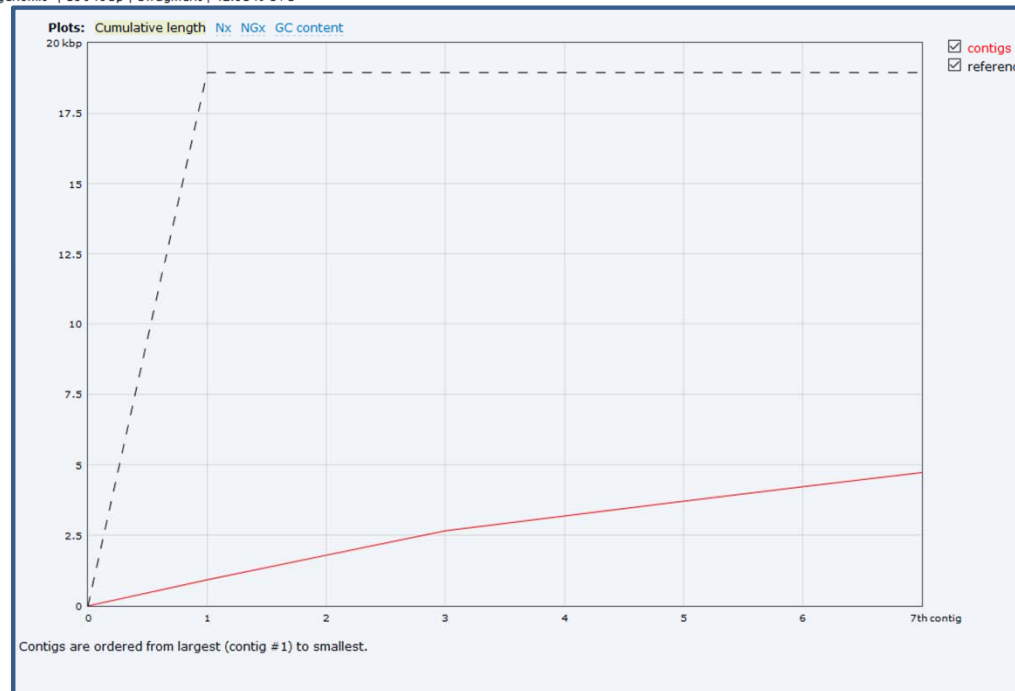
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $> 0$  bp)" and "Total length ( $> 0$  bp)" include all contigs).

Aligned to "GCF\_000889155.1\_ViralProj51245\_genomic" | 18 940 bp | 1 fragment | 42.01 % G+C

Genome statistics	contigs
NGA50	-
<b>Mismatches</b>	
# N's per 100 kbp	0
<b>Statistics without reference</b>	
# contigs	7
Largest contig	925
Total length	4727
Total length ( $\geq 1000$ bp)	0
Total length ( $\geq 10000$ bp)	0
Total length ( $\geq 50000$ bp)	0
<b>Predicted genes</b>	
# predicted genes (unique)	2

[Extended report](#)

- **Basic information about the assembly**



- Compare the length of the reference to the cumulative length of the contigs.
- Could the preliminary assembly contain a complete genome?