

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](#)

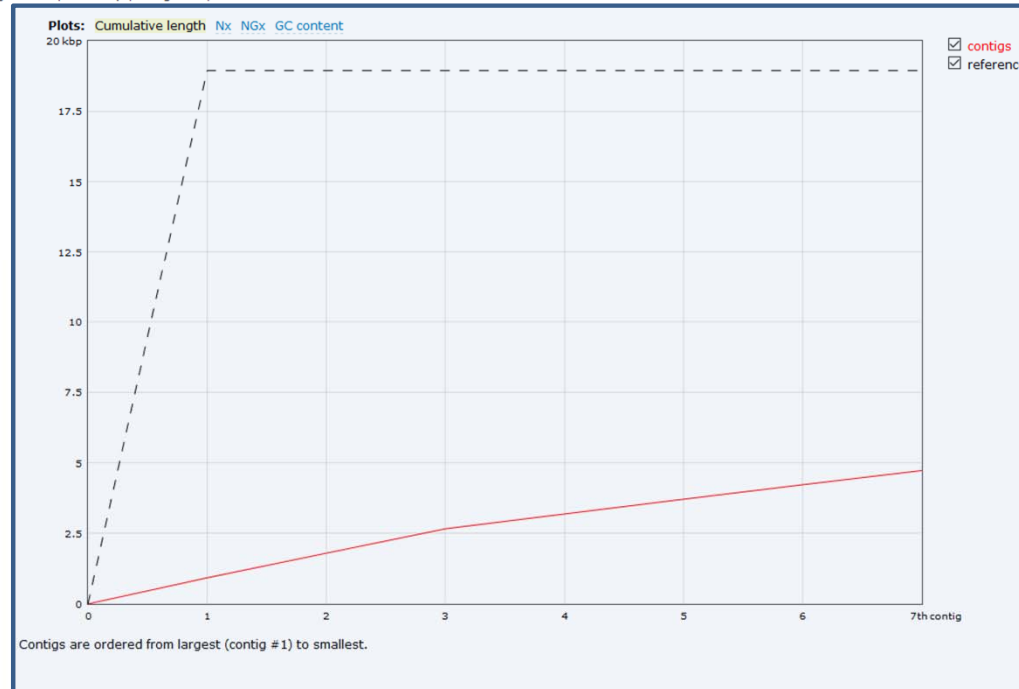
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Aligned to "GCF_000889155.1_ViralProj51245_genomic" | 18 940 bp | 1 fragment | 42.01 % G+C

Genome statistics	contigs
NGA50	-
Mismatches	
# N's per 100 kbp	0
Statistics without reference	
# contigs	7
Largest contig	925
Total length	4727
Total length (≥ 1000 bp)	0
Total length (≥ 10000 bp)	0
Total length (≥ 50000 bp)	0
Predicted genes	
# 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?

We now have a preliminary assembly!

Preliminary Assembly



Improve the quality of the assembly: Polishing



- **We can map the quality filtered reads to this preliminary assembly.**
- **This is similar to the initial read mapping to the reference genome done previously.**

Improve the quality of the assembly: Polishing



- The read sequences may disagree with the assembly sequence at certain positions.
- Identifying these differences will enable us to correct small-scale errors, yielding a more accurate final assembly.
- A final assembly will be generated with the corrected sequences.