

27 March 2025, Thursday, 12:56:23

[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 "reference_genome" | 1 641 481 bp | 1 fragment | 30.55 % G+C
7637 genomic features

Worst

Median

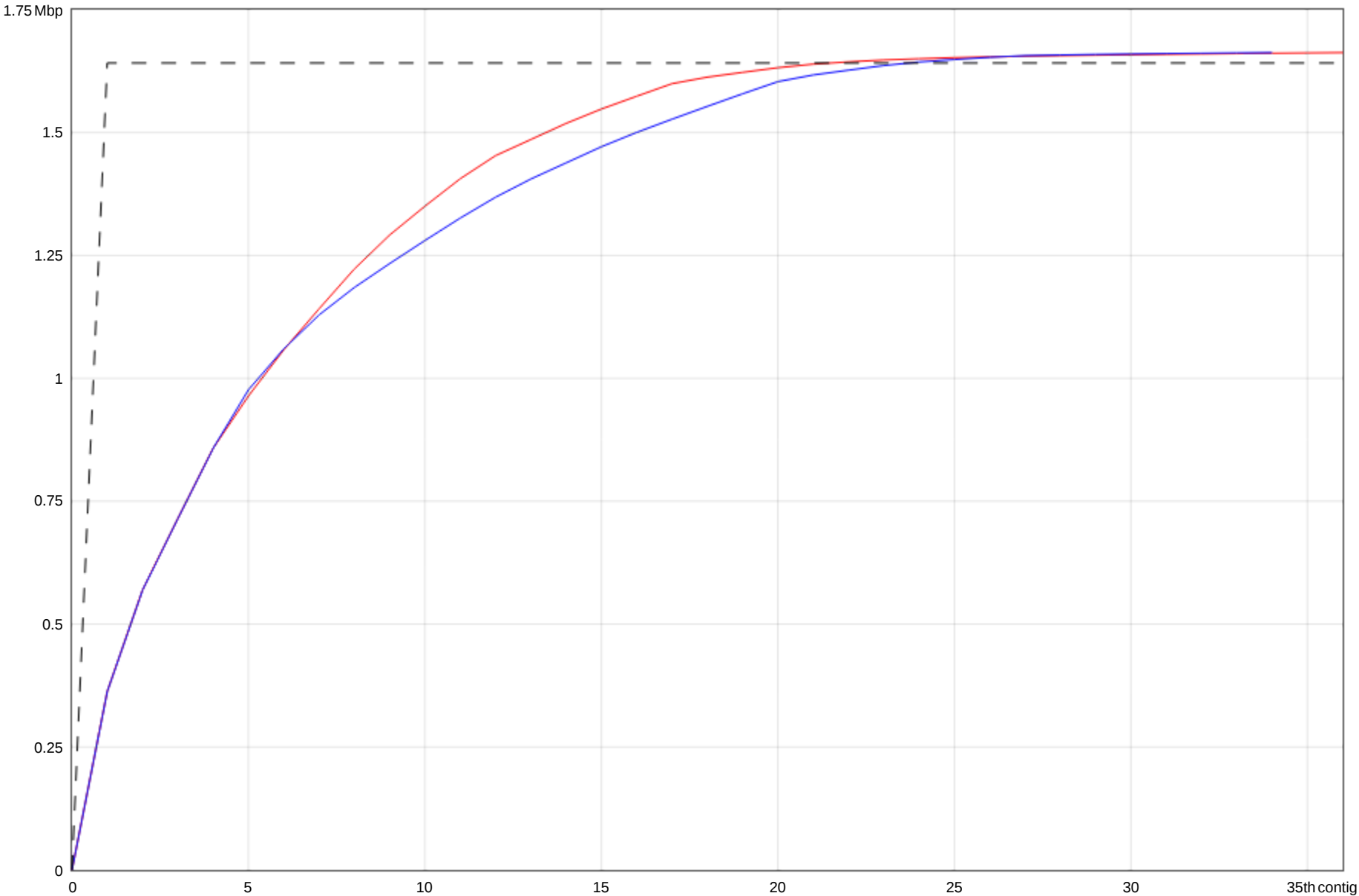
Best

☒ Show heatmap

Alignment-based statistics	Spades_Default	Spades_Careful
Genome fraction (%)	98.023	98.056
Duplication ratio	1.001	1.001
# genomic features	7462 + 99 part	7460 + 104 part
Largest alignment	258 383	258 383
Total aligned length	1 611 002	1 611 574
NGA50	83 240	73 736
LGA50	7	7
Misassemblies		
# misassemblies	8	8
Misassembled contigs length	842 810	902 886
Per base quality		
# mismatches per 100 kbp	376.1	374.85
# indels per 100 kbp	15.58	15.7
# N's per 100 kbp	0	0
Statistics without reference		
# contigs	36	34
Largest contig	363 181	362 857
Total length	1 662 539	1 662 469
Total length (>= 1000 bp)	1 656 470	1 658 832
Total length (>= 10000 bp)	1 612 709	1 617 137
Total length (>= 50000 bp)	1 406 073	1 184 881

[Extended report](#)

Plots: Cumulative length Nx NAx NGx NGAx Misassemblies Genomic features GC content



Contigs are ordered from largest (contig #1) to smallest.