

QUAST

Quality Assessment Tool for Genome Assemblies

10 December 2025, Wednesday, 05:57:17

[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).

Worst Median Best Show heatmap

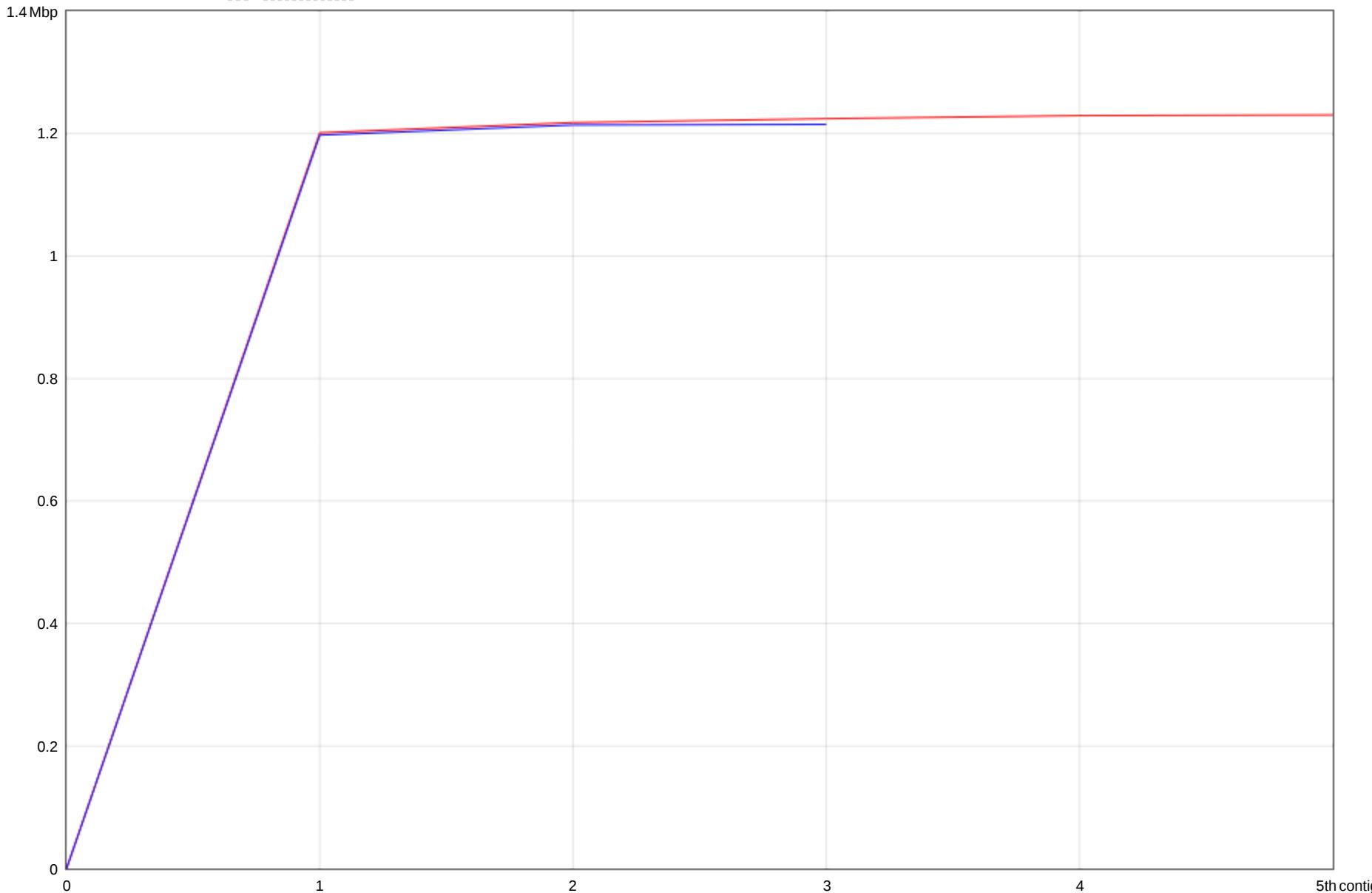
Statistics without reference SPADES Flye

# contigs	5	3
# contigs (≥ 0 bp)	76	3
# contigs (≥ 1000 bp)	5	2
# contigs (≥ 5000 bp)	4	2
# contigs (≥ 10000 bp)	2	2
# contigs (≥ 25000 bp)	1	1
# contigs (≥ 50000 bp)	1	1
Largest contig	1 201 420	1 197 568
Total length	1 230 427	1 214 984
Total length (≥ 0 bp)	1 238 572	1 214 984
Total length (≥ 1000 bp)	1 230 427	1 213 988
Total length (≥ 5000 bp)	1 229 353	1 213 988
Total length (≥ 10000 bp)	1 217 938	1 213 988
Total length (≥ 25000 bp)	1 201 420	1 197 568
Total length (≥ 50000 bp)	1 201 420	1 197 568
N50	1 201 420	1 197 568
N90	1 201 420	1 197 568
auN	1 173 373	1 180 624
L50	1	1
L90	1	1
GC (%)	40.42	40.44

Per base quality

# N's per 100 kbp	0	0
# N's	0	0

Plots: Cumulative length Nx GC content



SPADES
 Flye

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