

QUAST

Quality Assessment Tool for Genome Assemblies

26 September 2025, Friday, 15:54:04

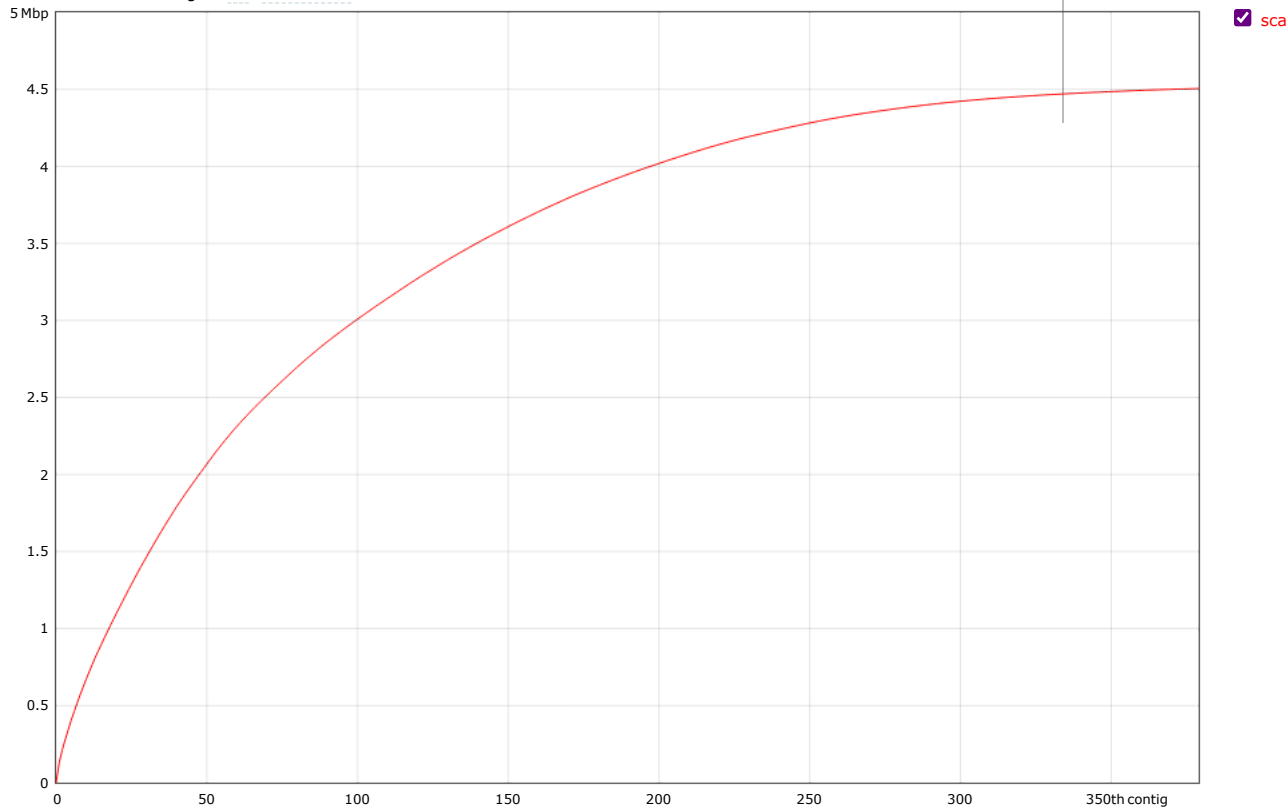
[View in Icarus contig browser](#)

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

Statistics without reference	scaffolds
# contigs	379
# contigs ( $\geq 0$ bp)	622
# contigs ( $\geq 1000$ bp)	336
# contigs ( $\geq 5000$ bp)	227
# contigs ( $\geq 10000$ bp)	150
# contigs ( $\geq 25000$ bp)	54
# contigs ( $\geq 50000$ bp)	10
Largest contig	128 095
Total length	4 505 107
Total length ( $\geq 0$ bp)	4 542 330
Total length ( $\geq 1000$ bp)	4 472 256
Total length ( $\geq 5000$ bp)	4 179 531
Total length ( $\geq 10000$ bp)	3 609 110
Total length ( $\geq 25000$ bp)	2 172 428
Total length ( $\geq 50000$ bp)	673 103
N50	23 694
N90	6386
auN	29 118
L50	58
L90	206
GC (%)	50.79
Per base quality	
# N's per 100 kbp	18.42
# N's	830

171st contig:  
**3 803 985, scaffolds**

Plots: Cumulative length [Nx](#) [GC content](#)



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