

Report

	final.contigs
# contigs (≥ 0 bp)	1530
# contigs (≥ 1000 bp)	286
Total length (≥ 0 bp)	1102952
Total length (≥ 1000 bp)	416895
# contigs	975
Largest contig	4410
Total length	898866
Reference length	1231960
GC (%)	25.49
Reference GC (%)	25.35
N50	956
NG50	753
N75	693
L50	320
LG50	517
L75	597
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	81.498
Duplication ratio	1.077
# N's per 100 kbp	0.00
# mismatches per 100 kbp	330.67
# indels per 100 kbp	0.20
Largest alignment	4410
NA50	956
NGA50	753
NA75	693
LA50	320
LGA50	517
LA75	597

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).

Misassemblies report

	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	3320
# indels	2
# short indels	2
# long indels	0
Indels length	2

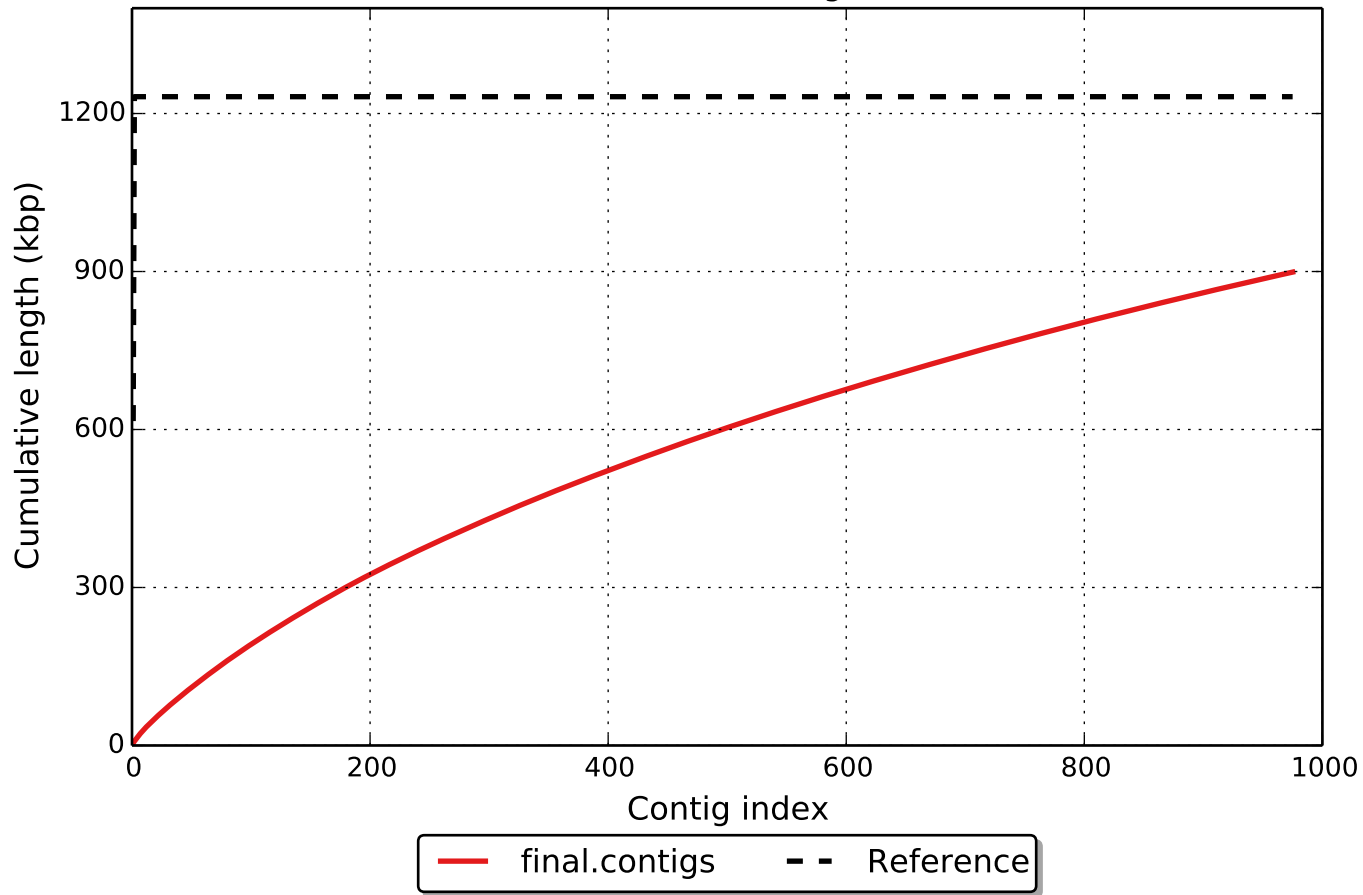
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

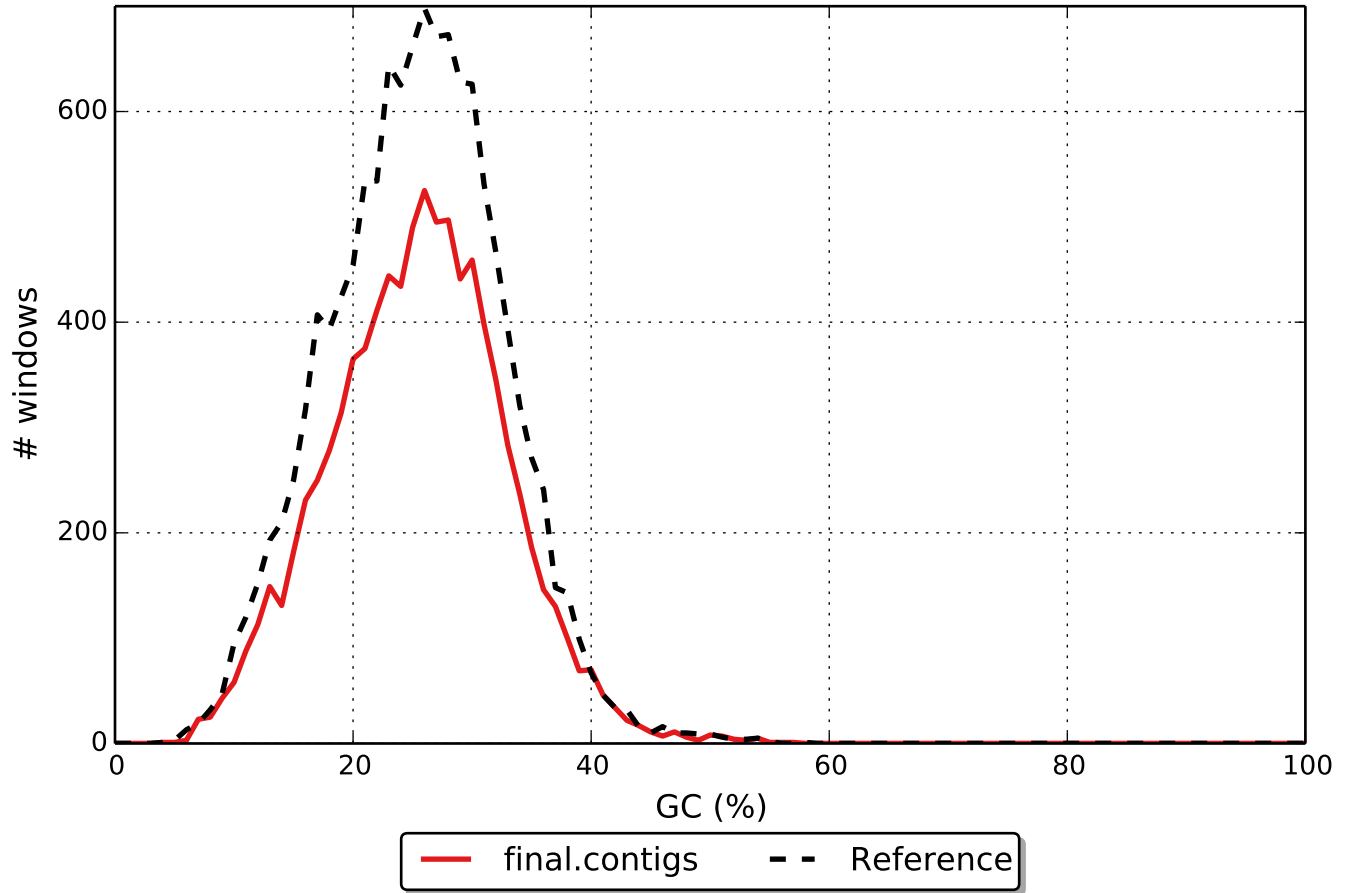
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

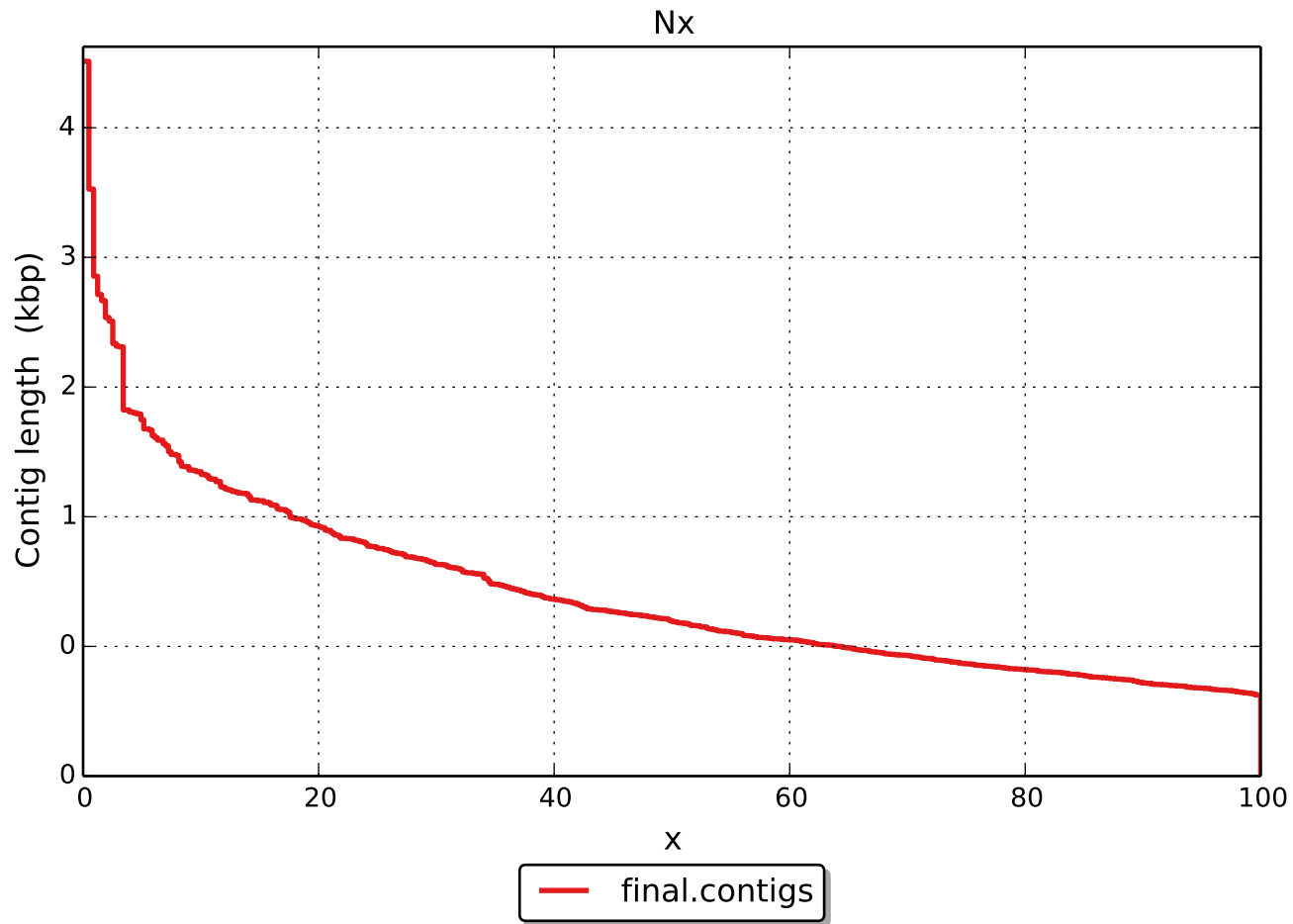
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Cumulative length

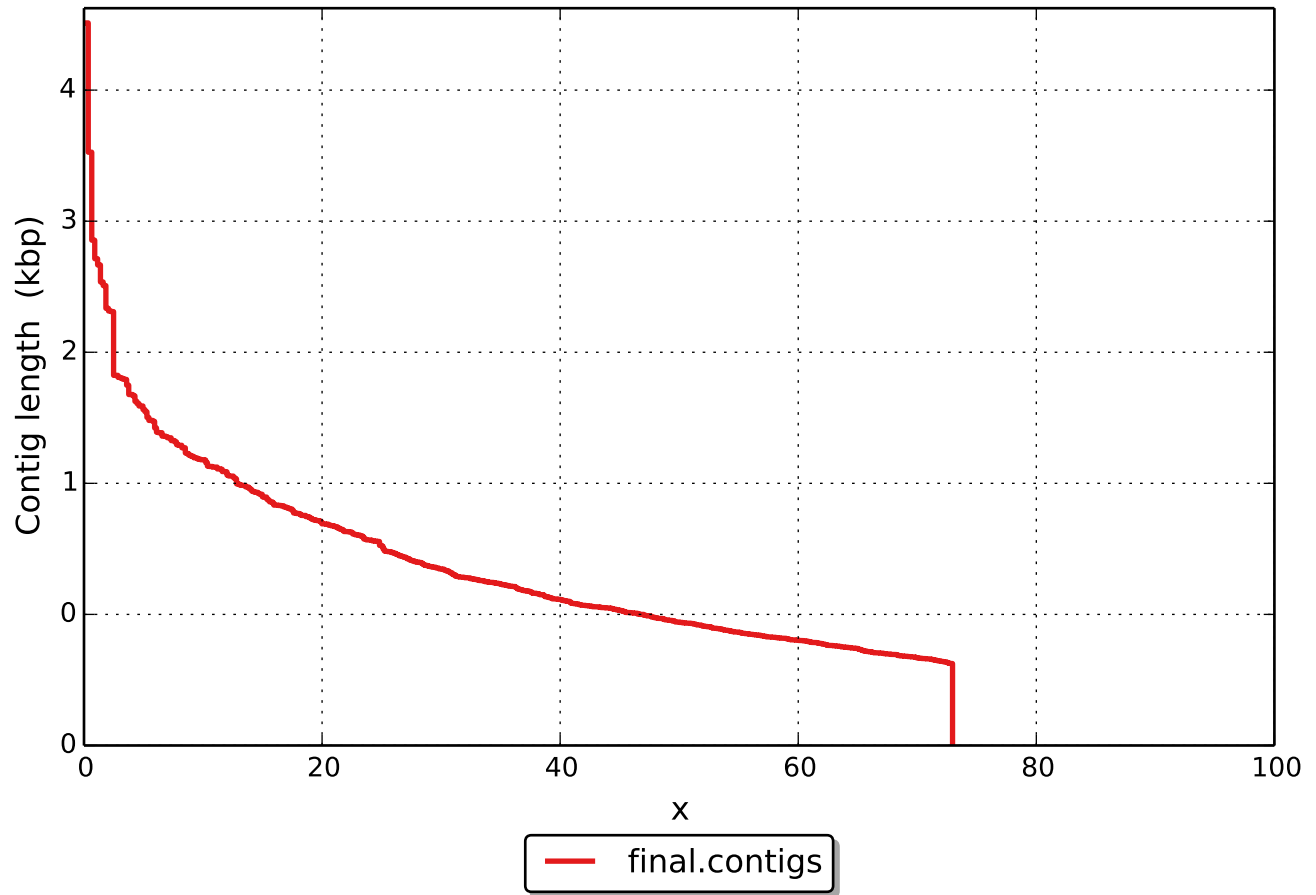


GC content





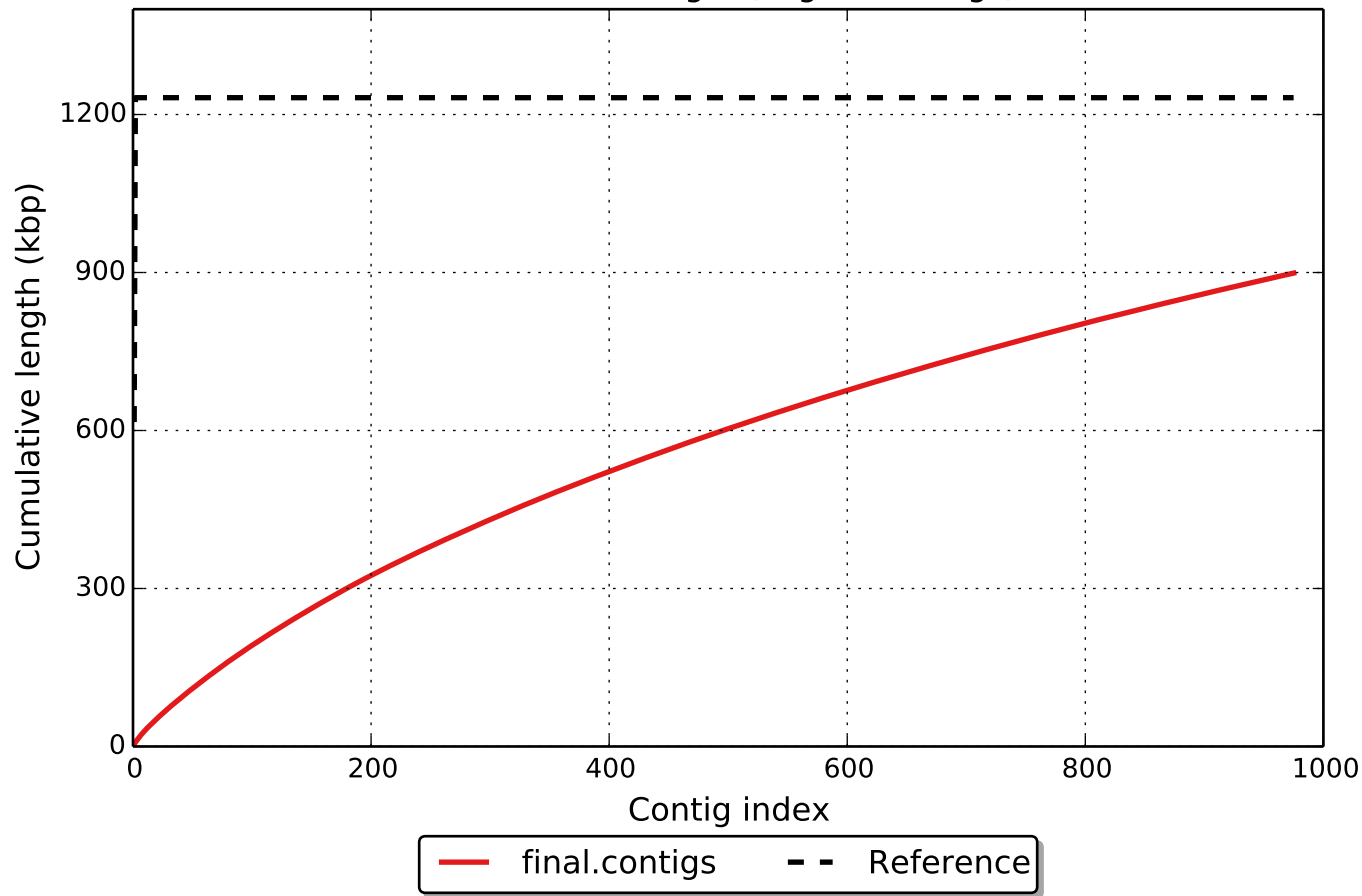
NGx



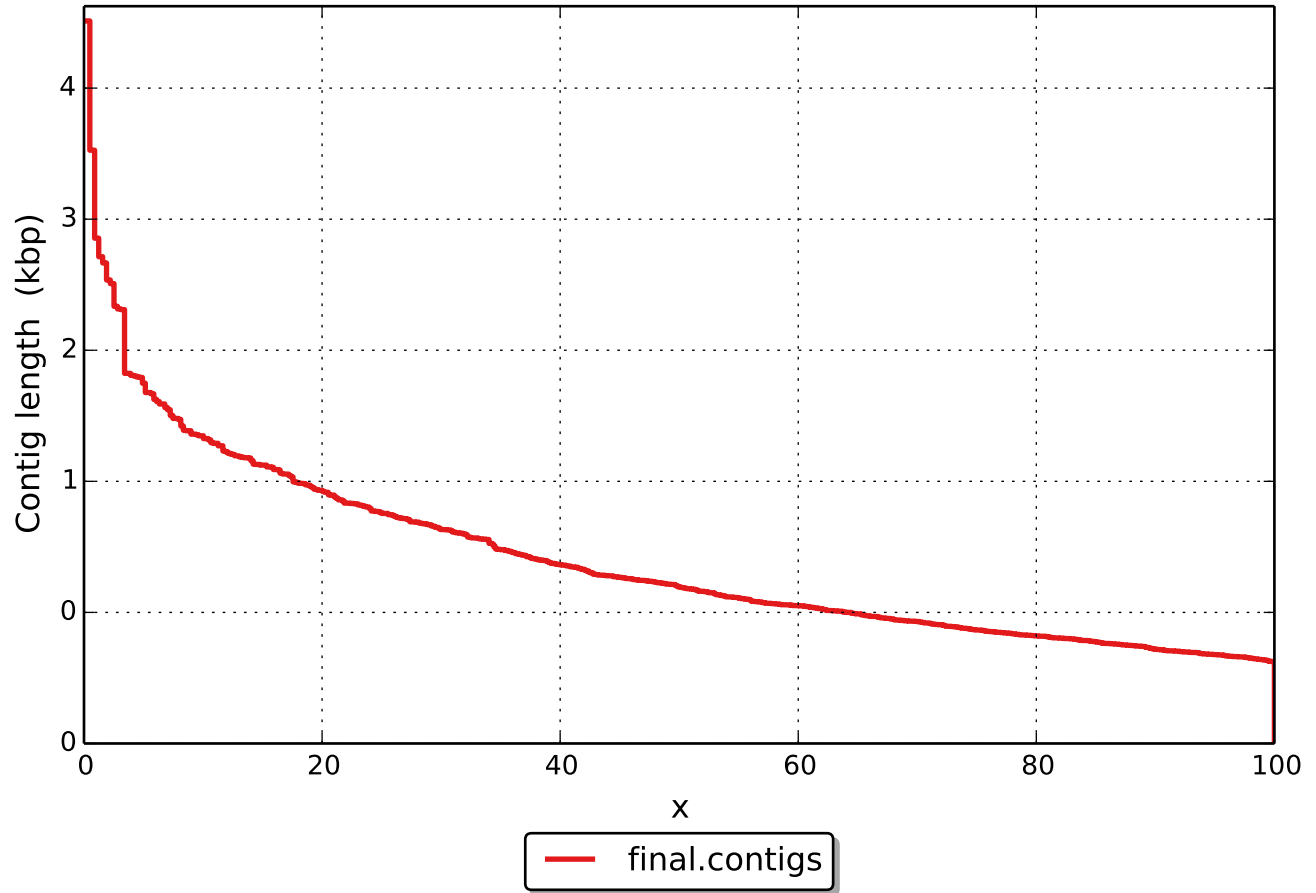
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

