

Report

	final.contigs
# contigs (≥ 0 bp)	1126
# contigs (≥ 1000 bp)	480
Total length (≥ 0 bp)	1329051
Total length (≥ 1000 bp)	958247
# contigs	851
Largest contig	8613
Total length	1228283
Reference length	1283598
GC (%)	26.32
Reference GC (%)	26.31
N50	1743
NG50	1651
N75	1060
NG75	990
L50	215
LG50	231
L75	444
LG75	485
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	92.529
Duplication ratio	1.049
# N's per 100 kbp	0.00
# mismatches per 100 kbp	65.34
# indels per 100 kbp	0.17
Largest alignment	8613
NA50	1743
NGA50	1651
NA75	1060
NGA75	990
LA50	215
LGA50	231
LA75	444
LGA75	485

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	776
# indels	2
# short indels	2
# long indels	0
Indels length	2

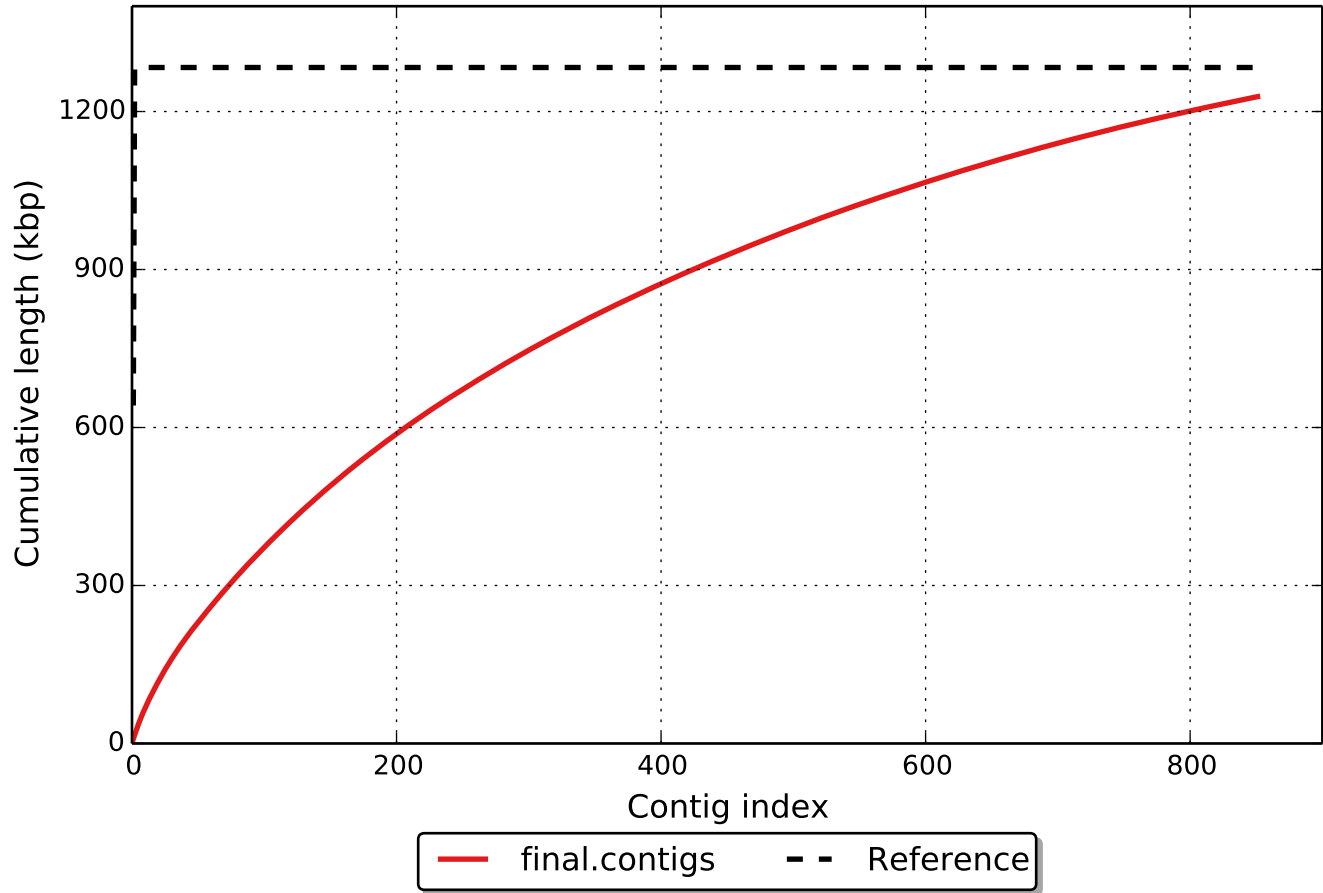
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

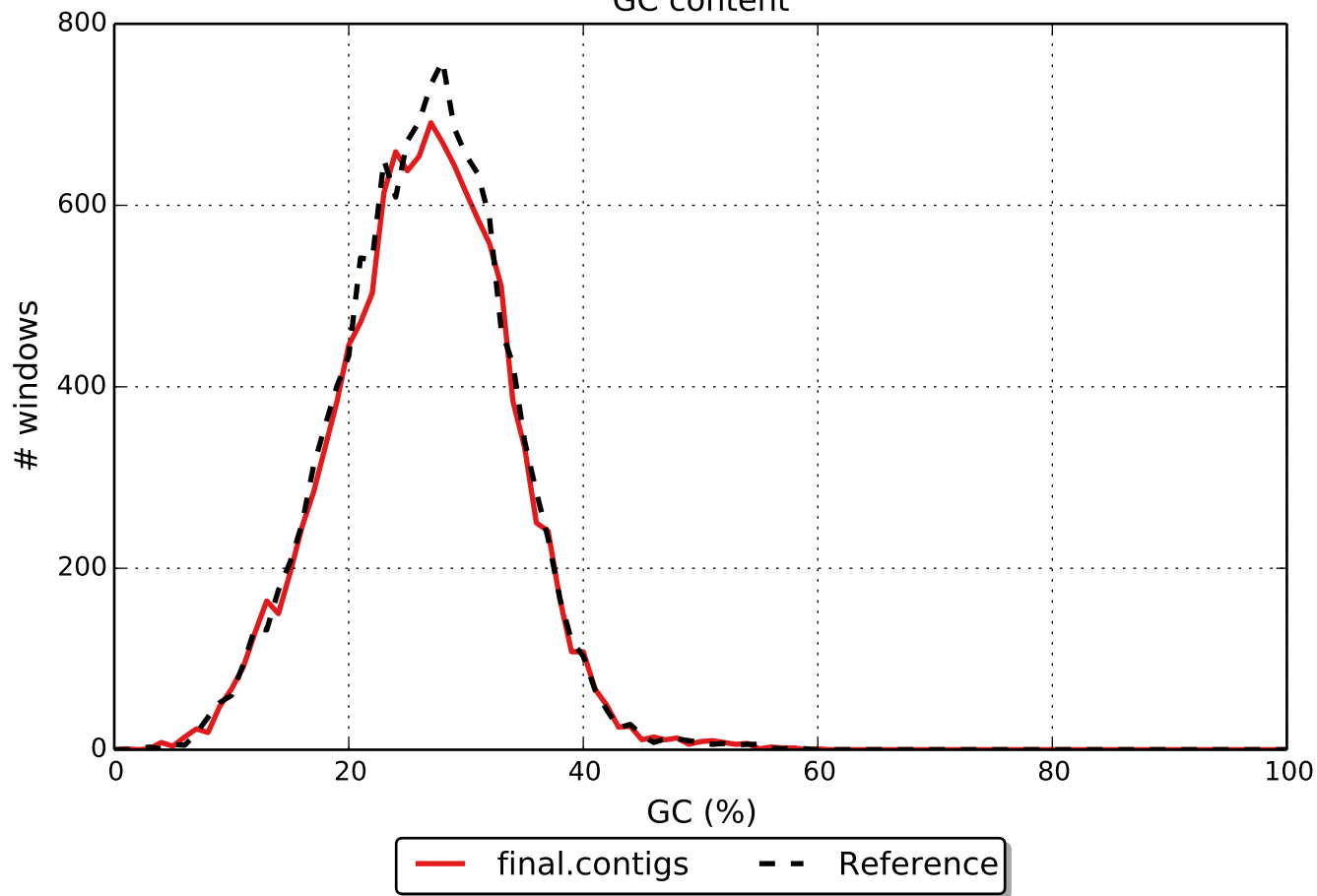
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

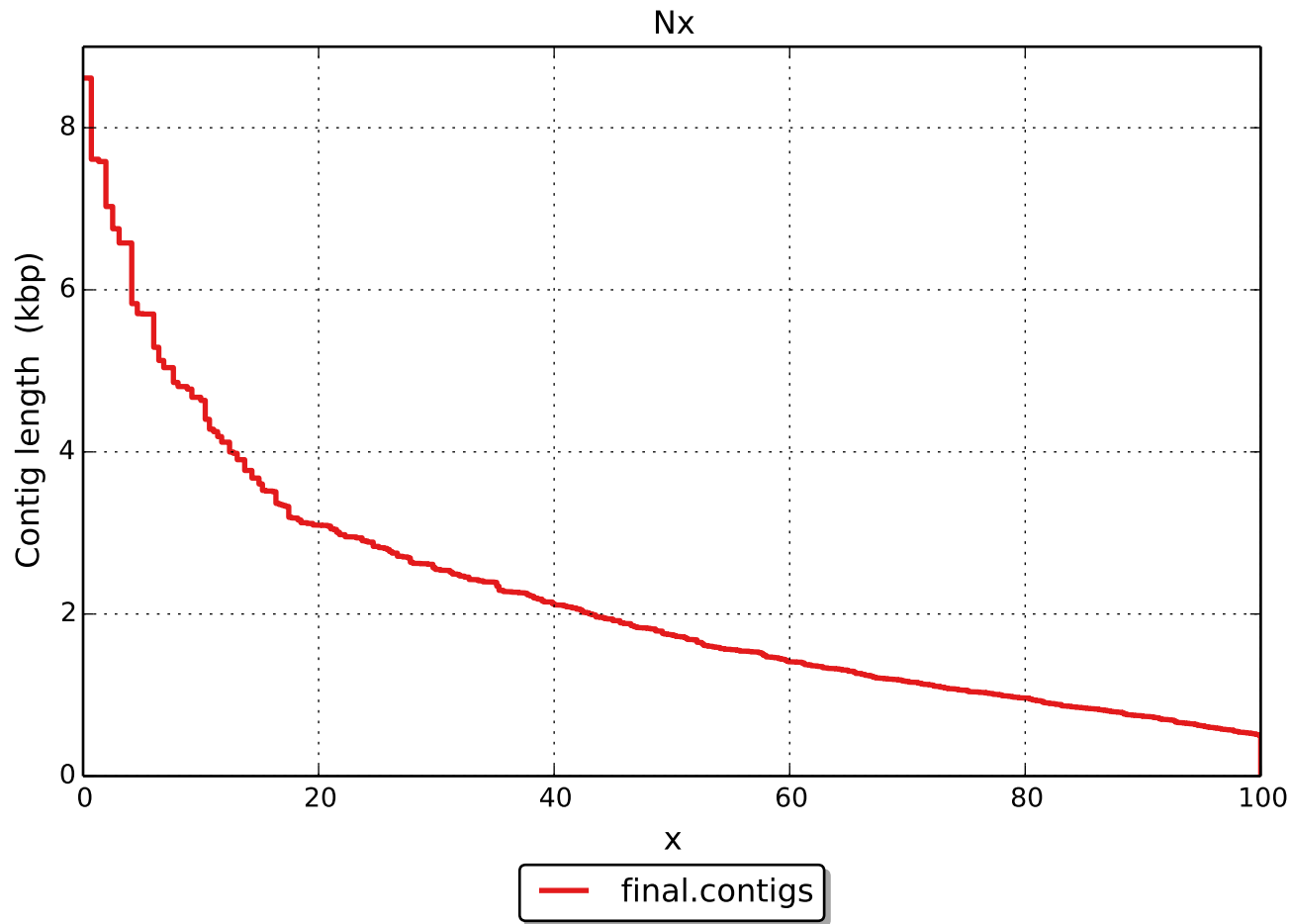
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Cumulative length

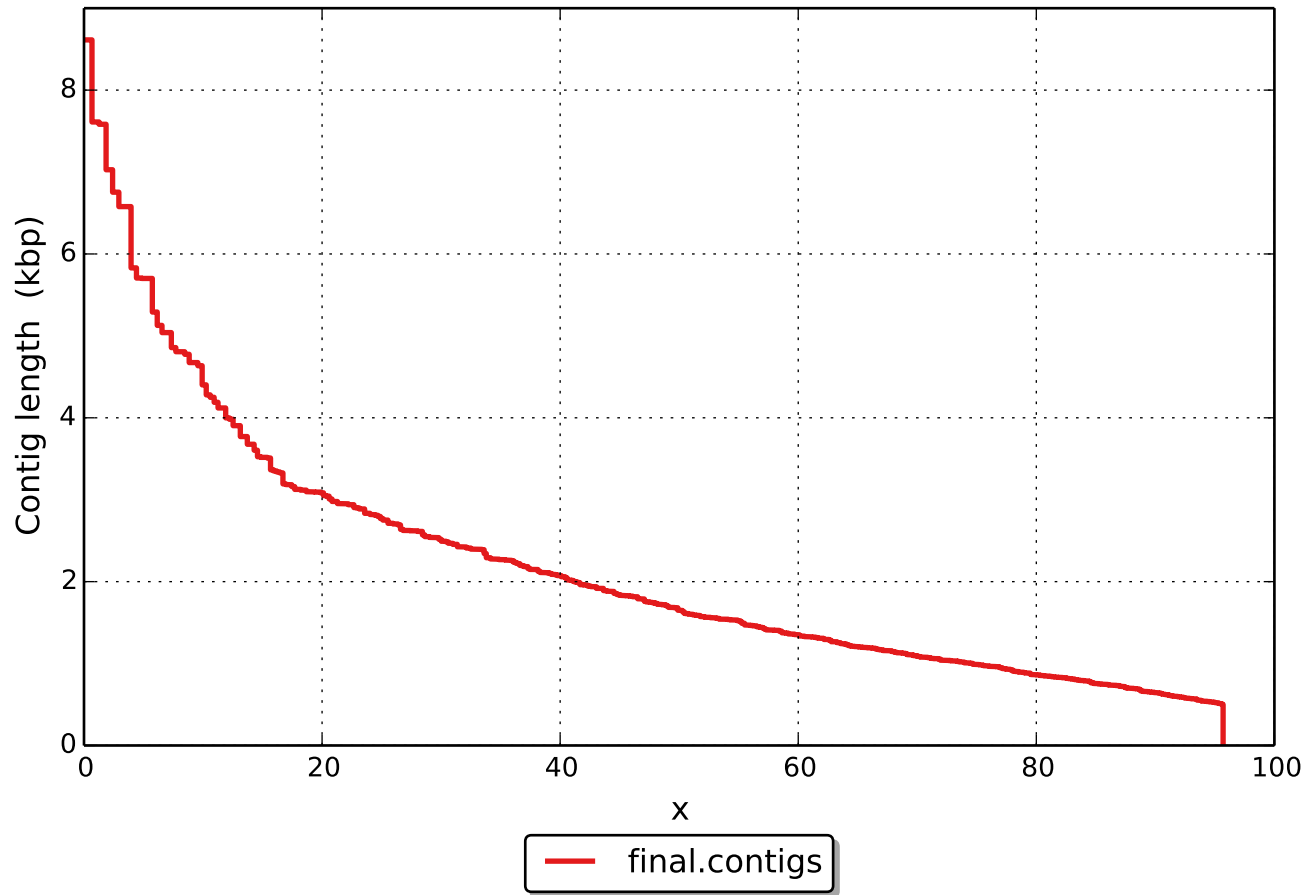


GC content





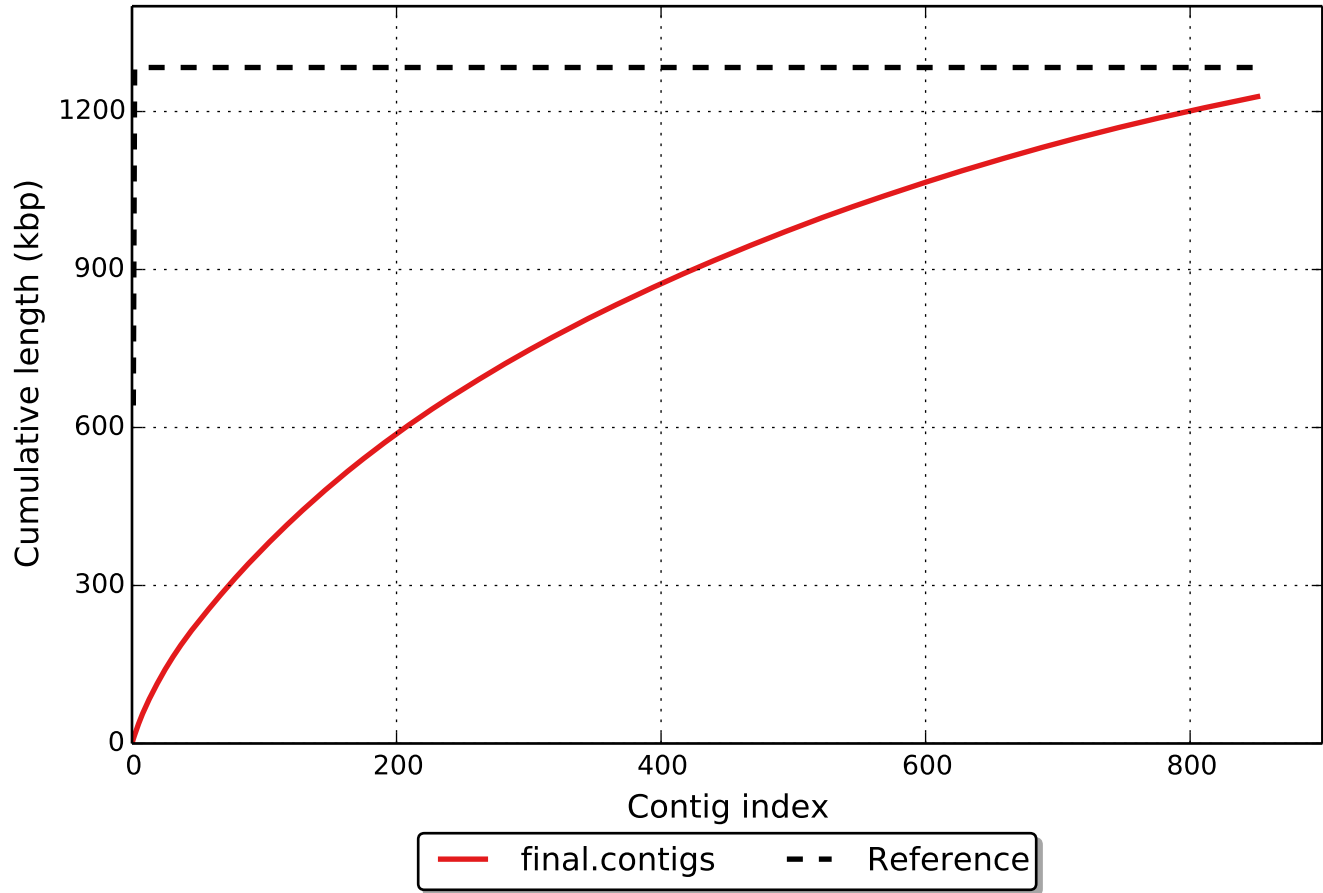
NGx



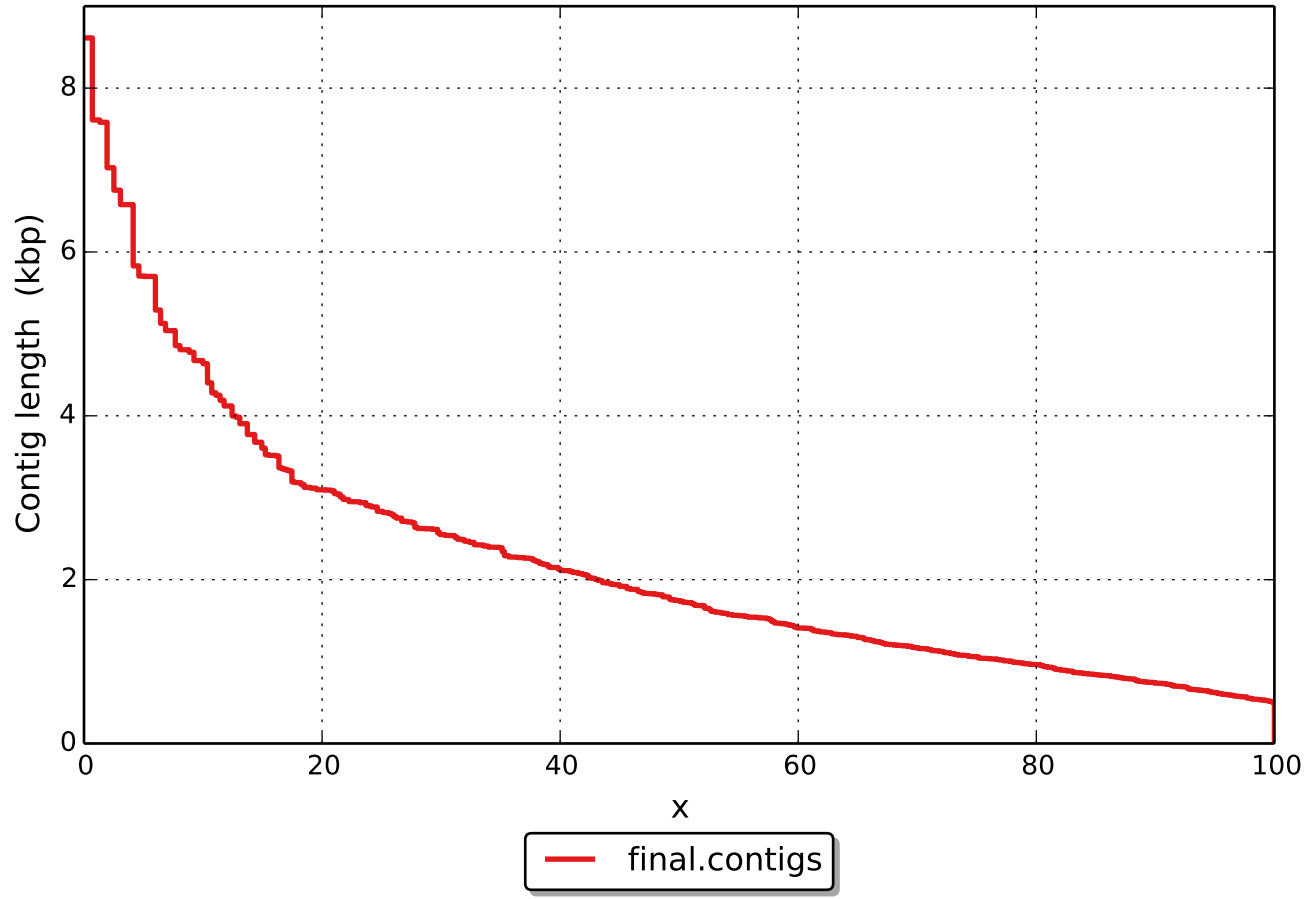
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

