

Report

	final.contigs
# contigs (≥ 0 bp)	1568
# contigs (≥ 1000 bp)	302
Total length (≥ 0 bp)	1148514
Total length (≥ 1000 bp)	432774
# contigs	1025
Largest contig	4169
Total length	945995
Reference length	1283598
GC (%)	26.40
Reference GC (%)	26.31
N50	935
NG50	774
N75	714
L50	344
LG50	542
L75	633
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	70.221
Duplication ratio	1.050
# N's per 100 kbp	0.00
# mismatches per 100 kbp	161.20
# indels per 100 kbp	0.22
Largest alignment	4169
NA50	935
NGA50	774
NA75	714
LA50	344
LGA50	542
LA75	633

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	1453
# indels	2
# short indels	2
# long indels	0
Indels length	2

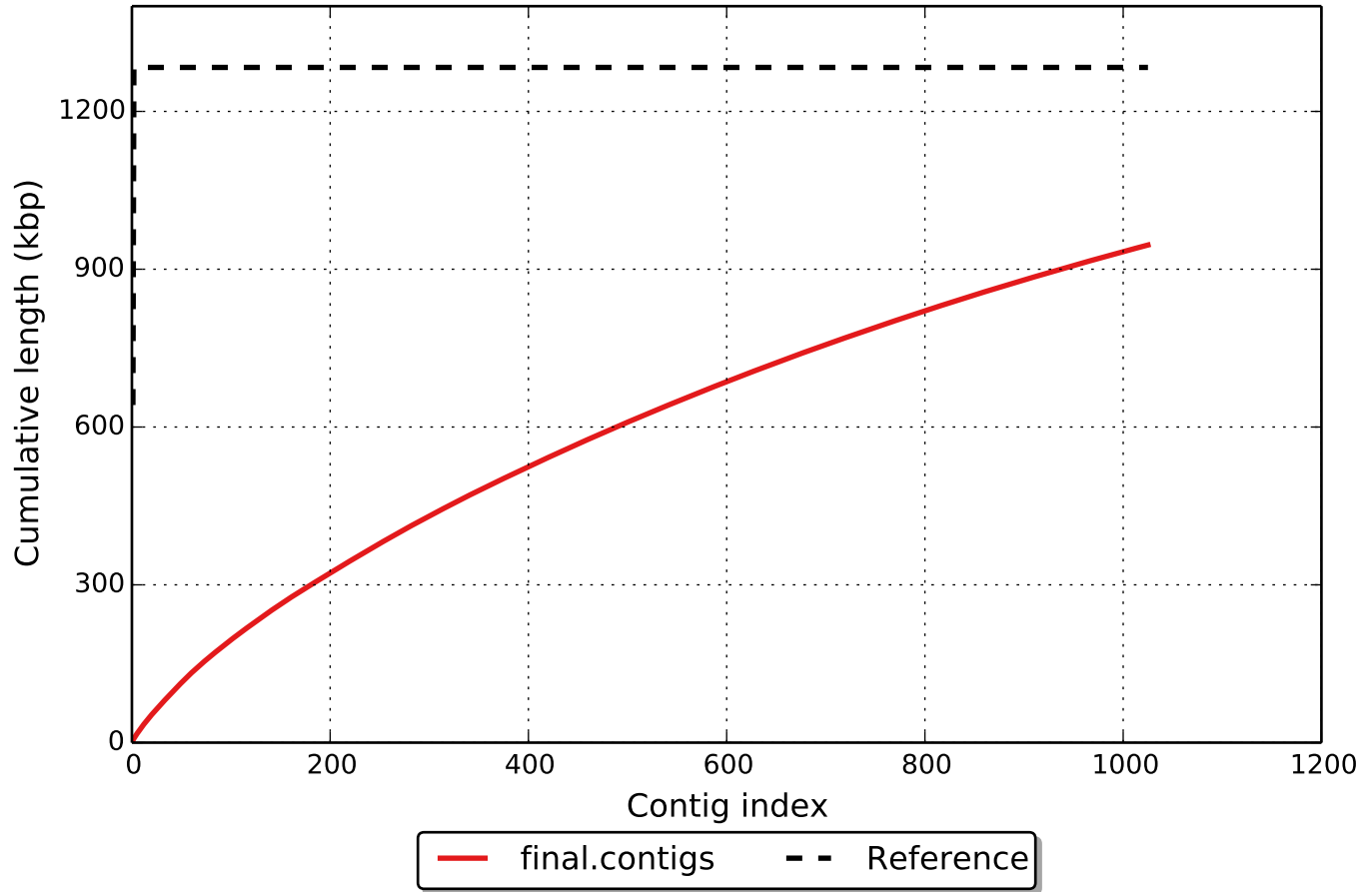
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

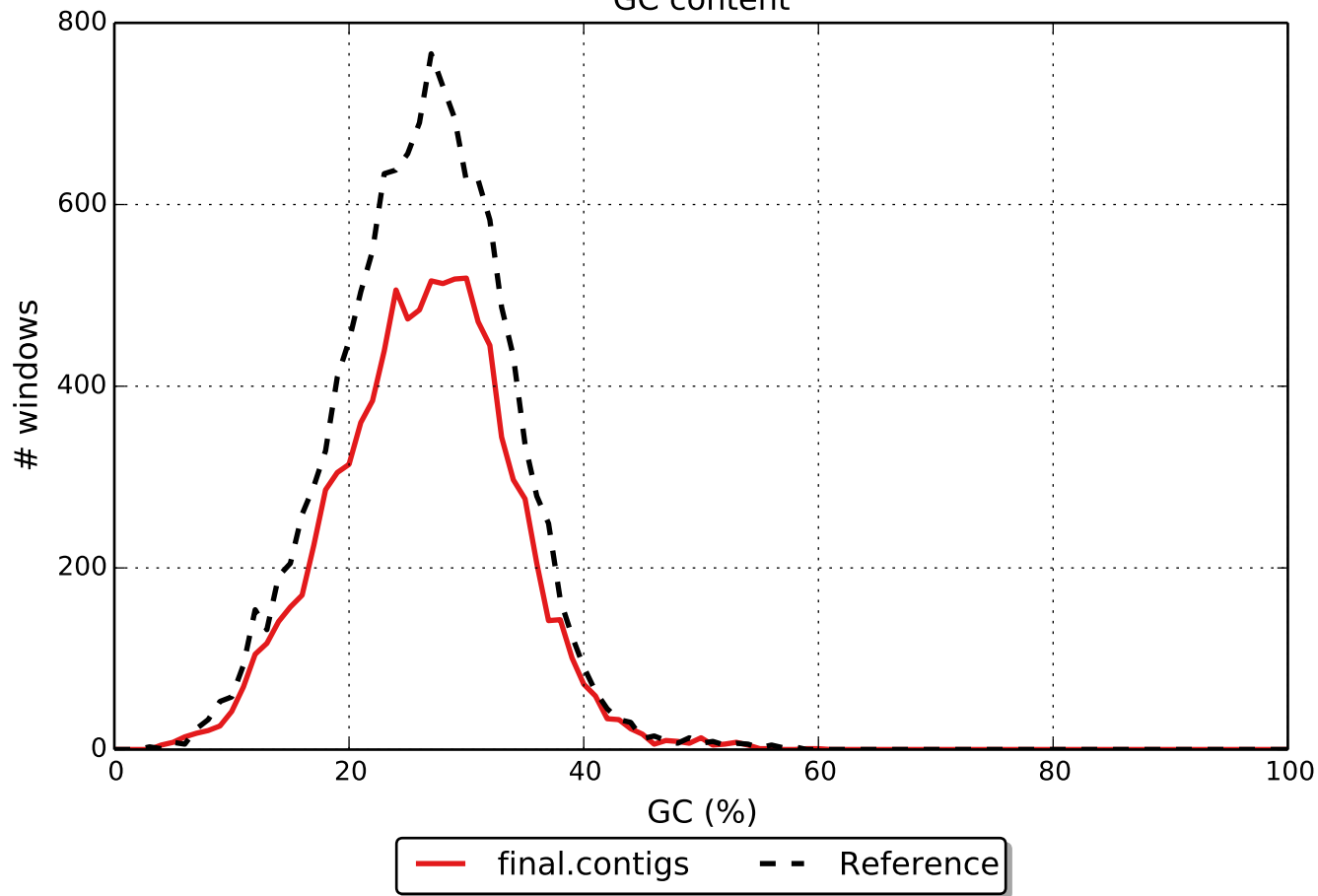
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

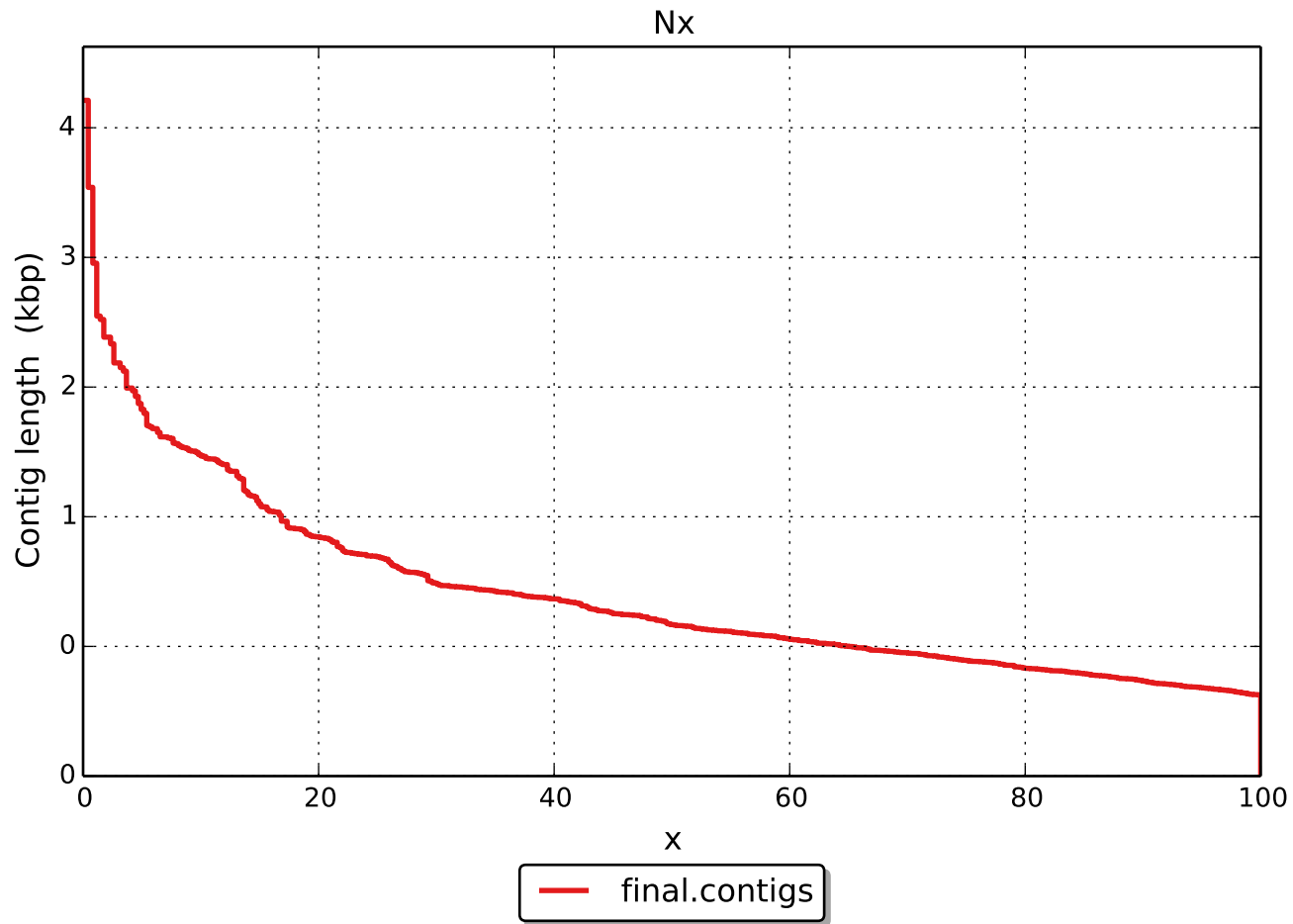
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Cumulative length

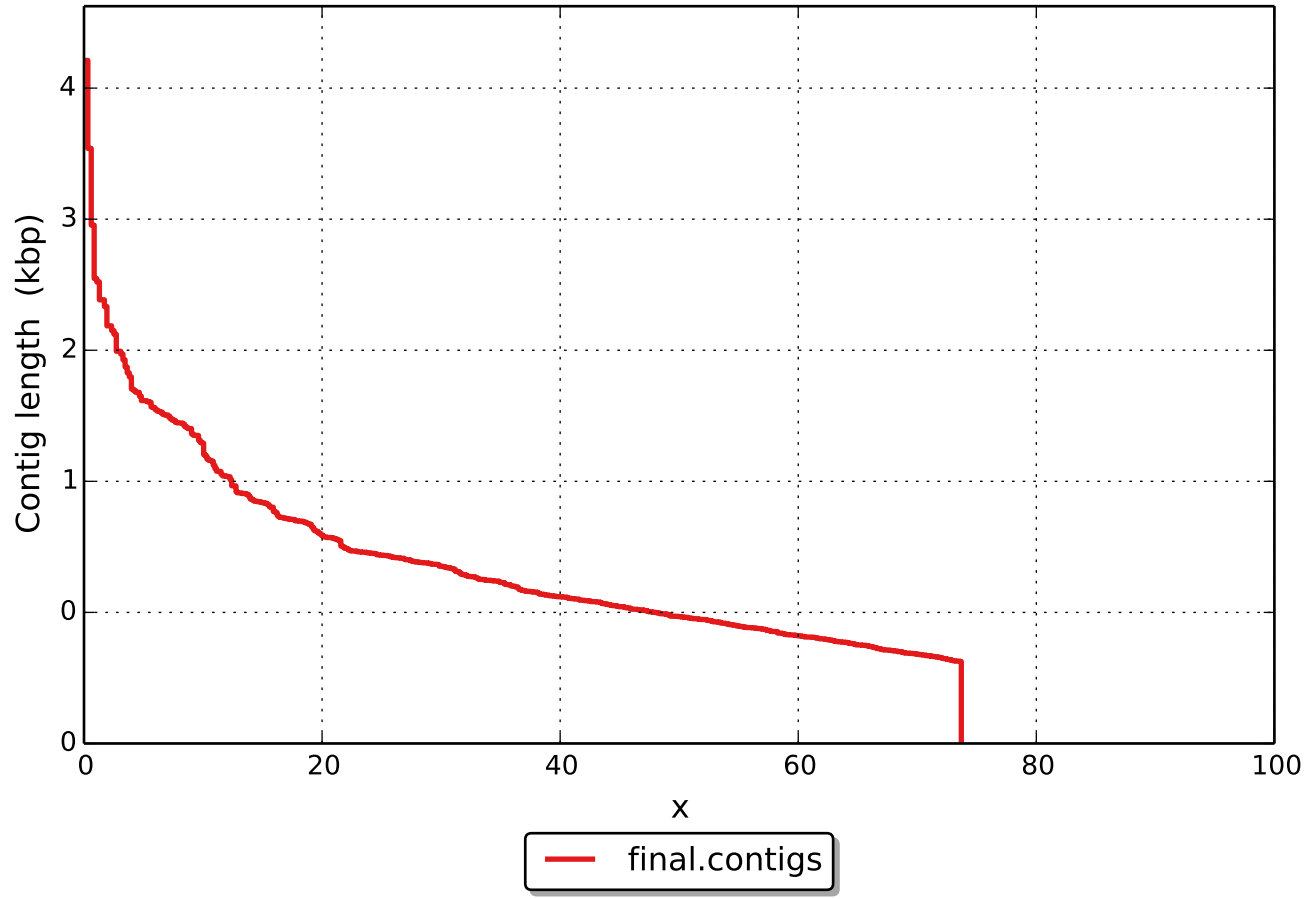


GC content





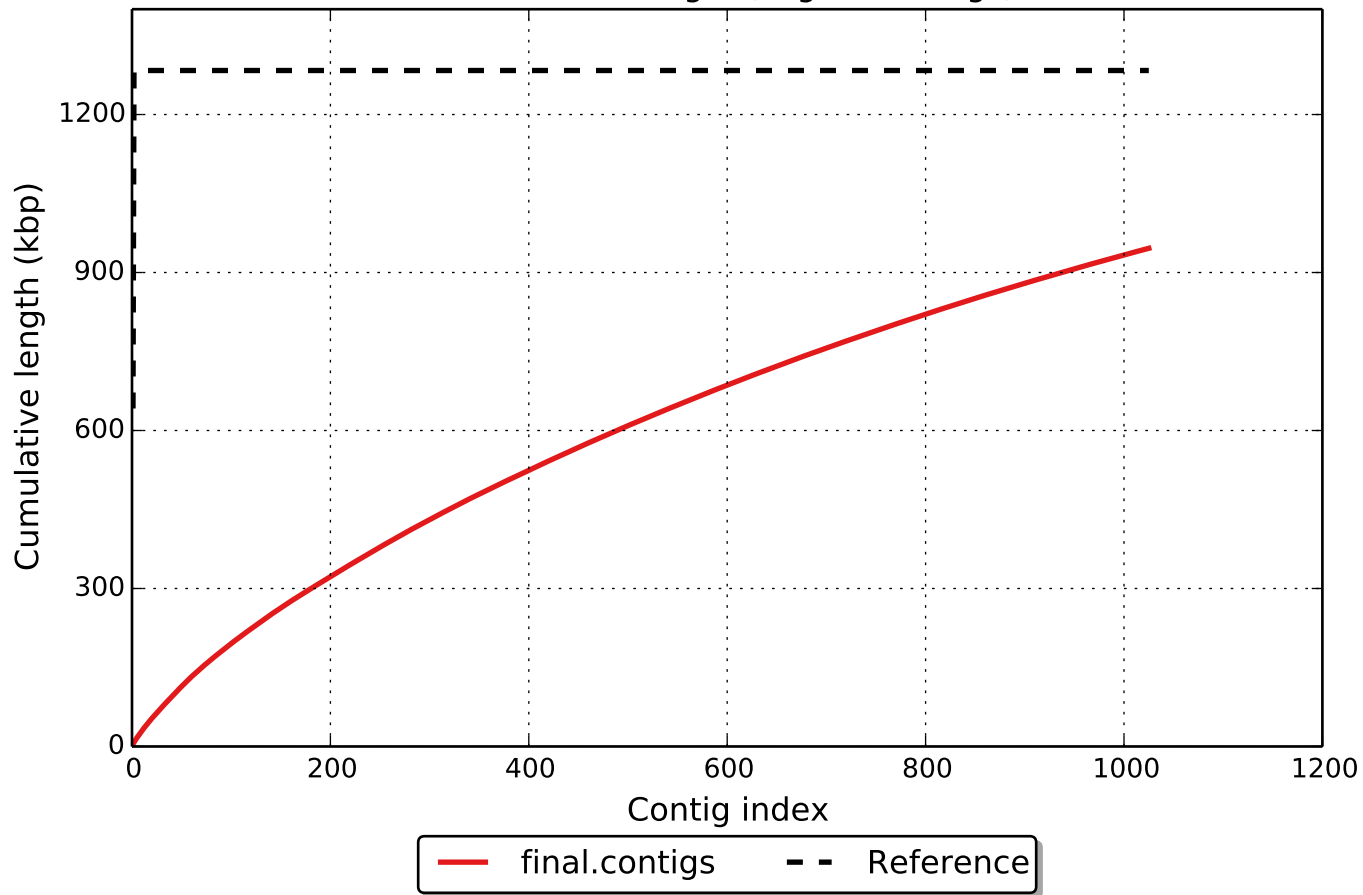
NGx



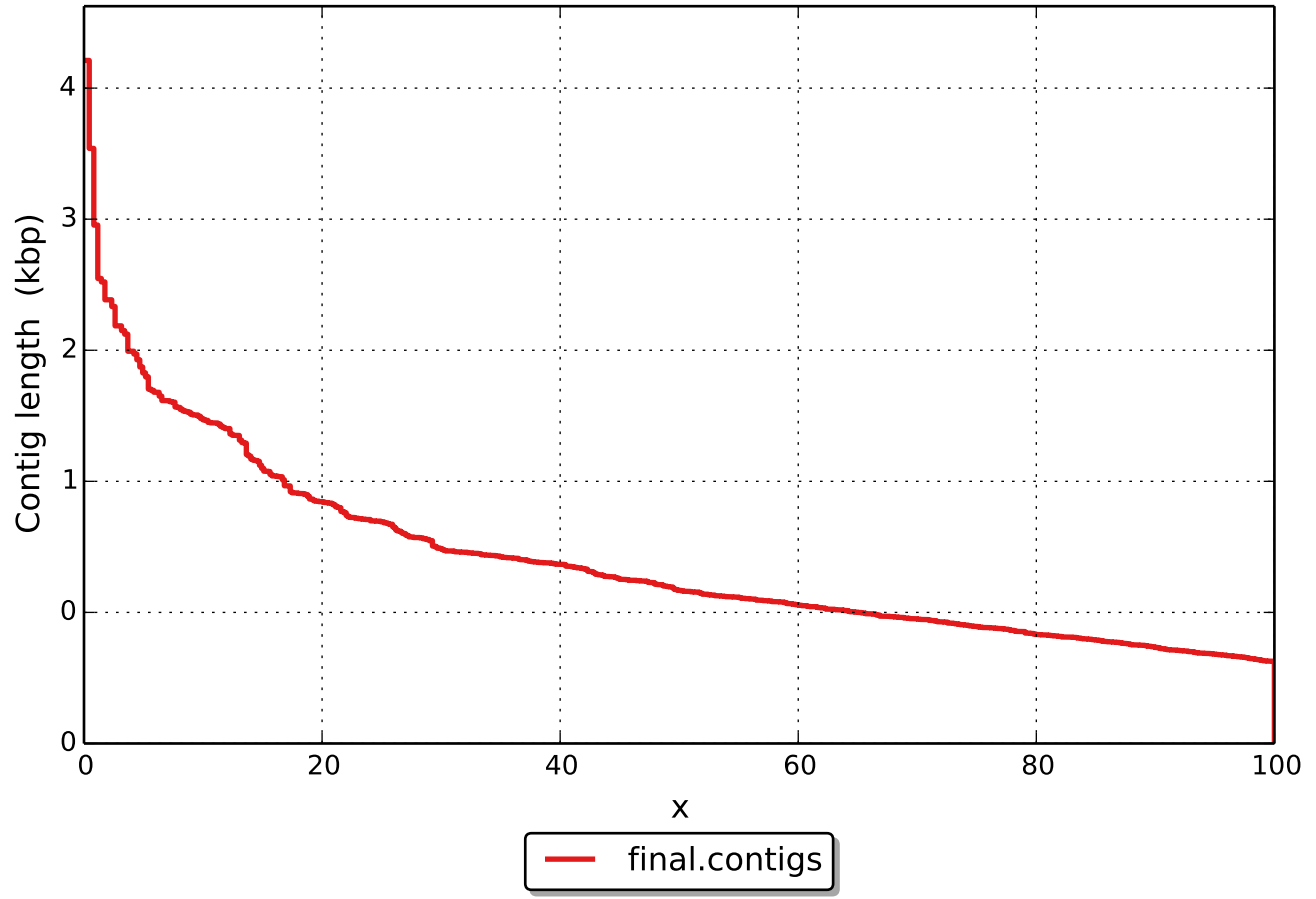
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

