

Report

	final.contigs
# contigs (>= 1000 bp)	115
# contigs (>= 5000 bp)	91
# contigs (>= 10000 bp)	82
# contigs (>= 25000 bp)	56
# contigs (>= 50000 bp)	32
Total length (>= 1000 bp)	4553543
Total length (>= 5000 bp)	4498722
Total length (>= 10000 bp)	4431525
Total length (>= 25000 bp)	4014870
Total length (>= 50000 bp)	3229822
# contigs	133
Largest contig	193070
Total length	4565076
Reference length	4641652
GC (℥)	50.75
Reference GC (℥)	50.79
N50	78692
NG50	78692
N75	37774
NG75	35144
L50	18
LG50	18
L75	37
LG75	39
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	98.214
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	7.19
# indels per 100 kbp	0.31
Largest alignment	193070
NA50	78692
NGA50	78692
NA75	37774
NGA75	35144
LA50	18
LGA50	18
LA75	37
LGA75	39

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
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# mismatches	328
# indels	14
# short indels	8
# long indels	6
Indels length	93

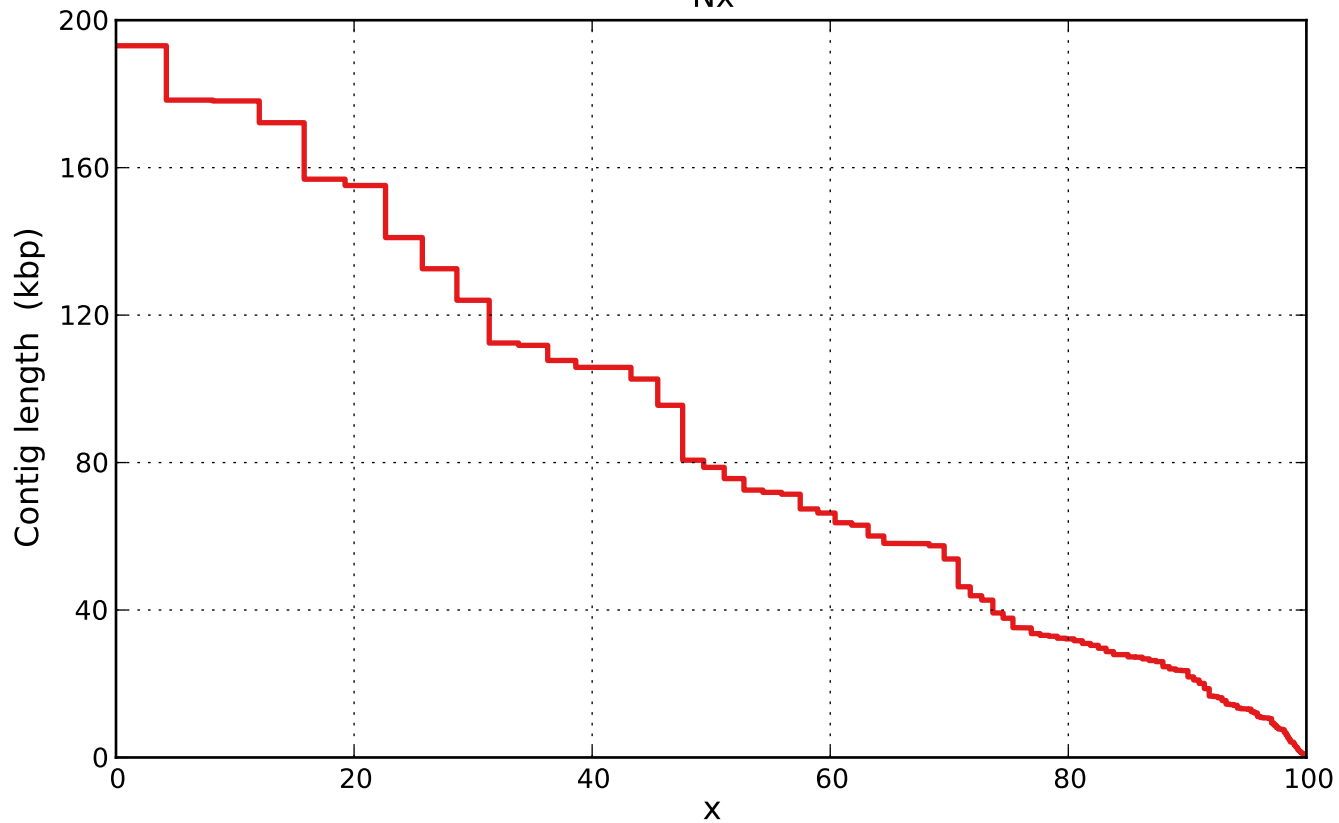
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

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

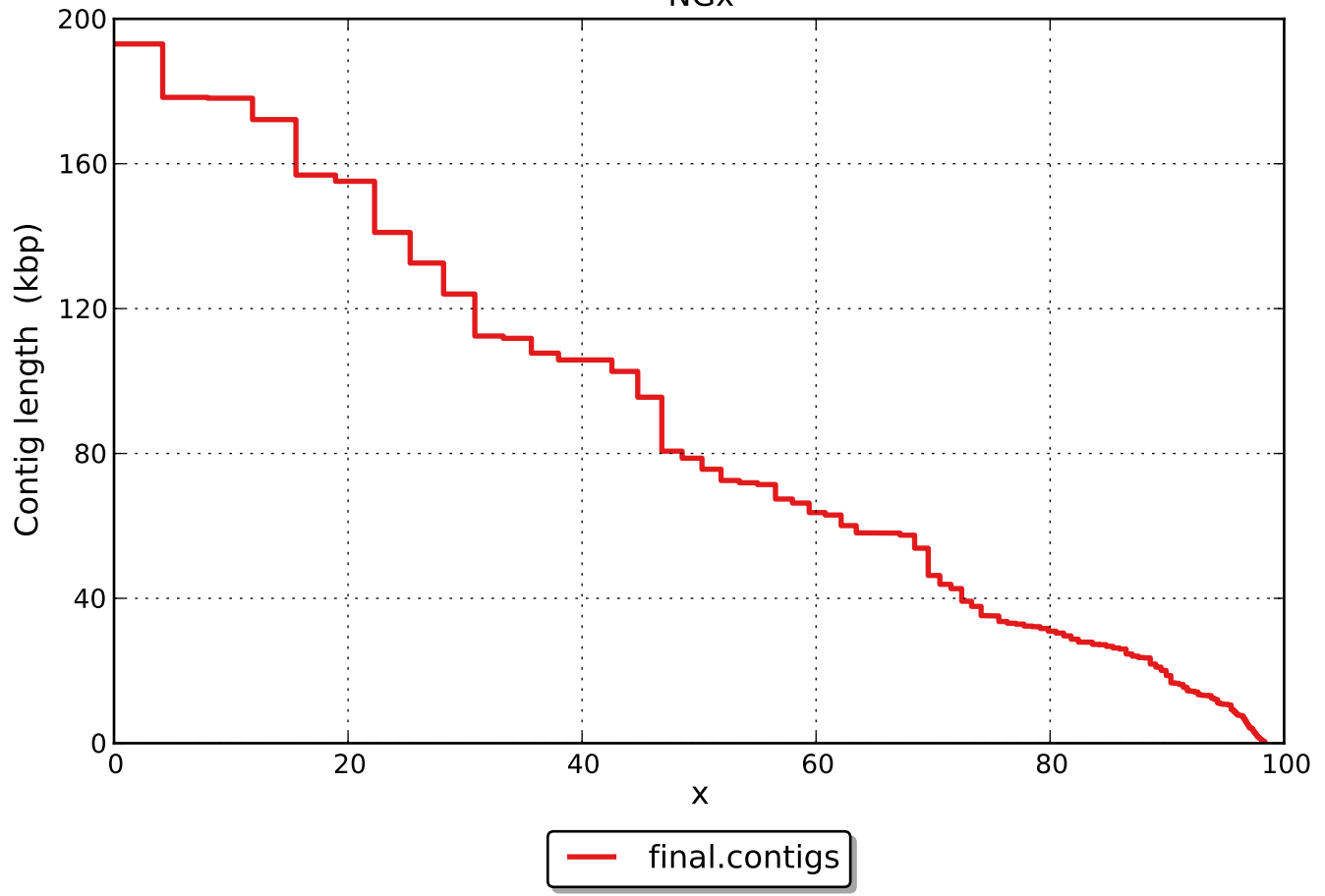
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

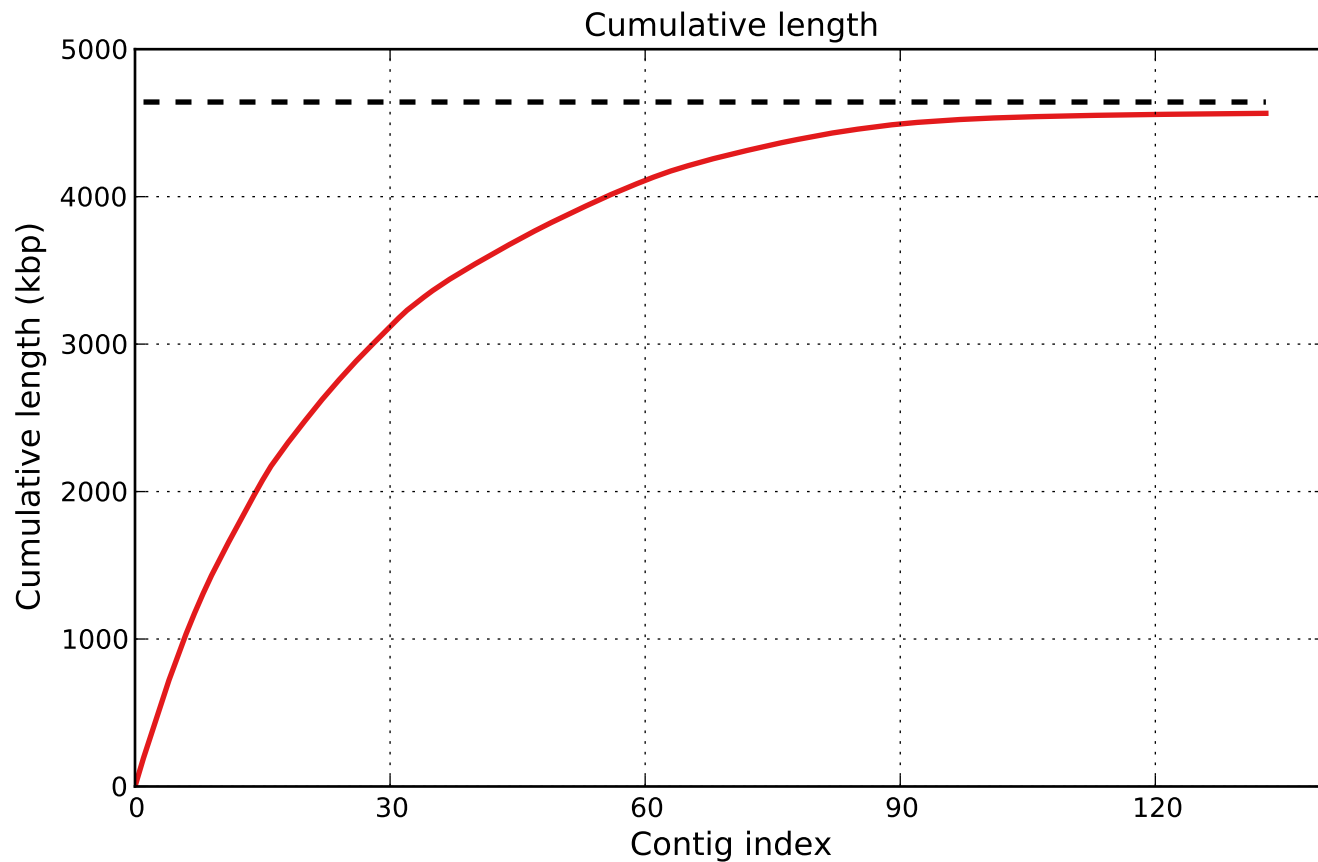
Nx



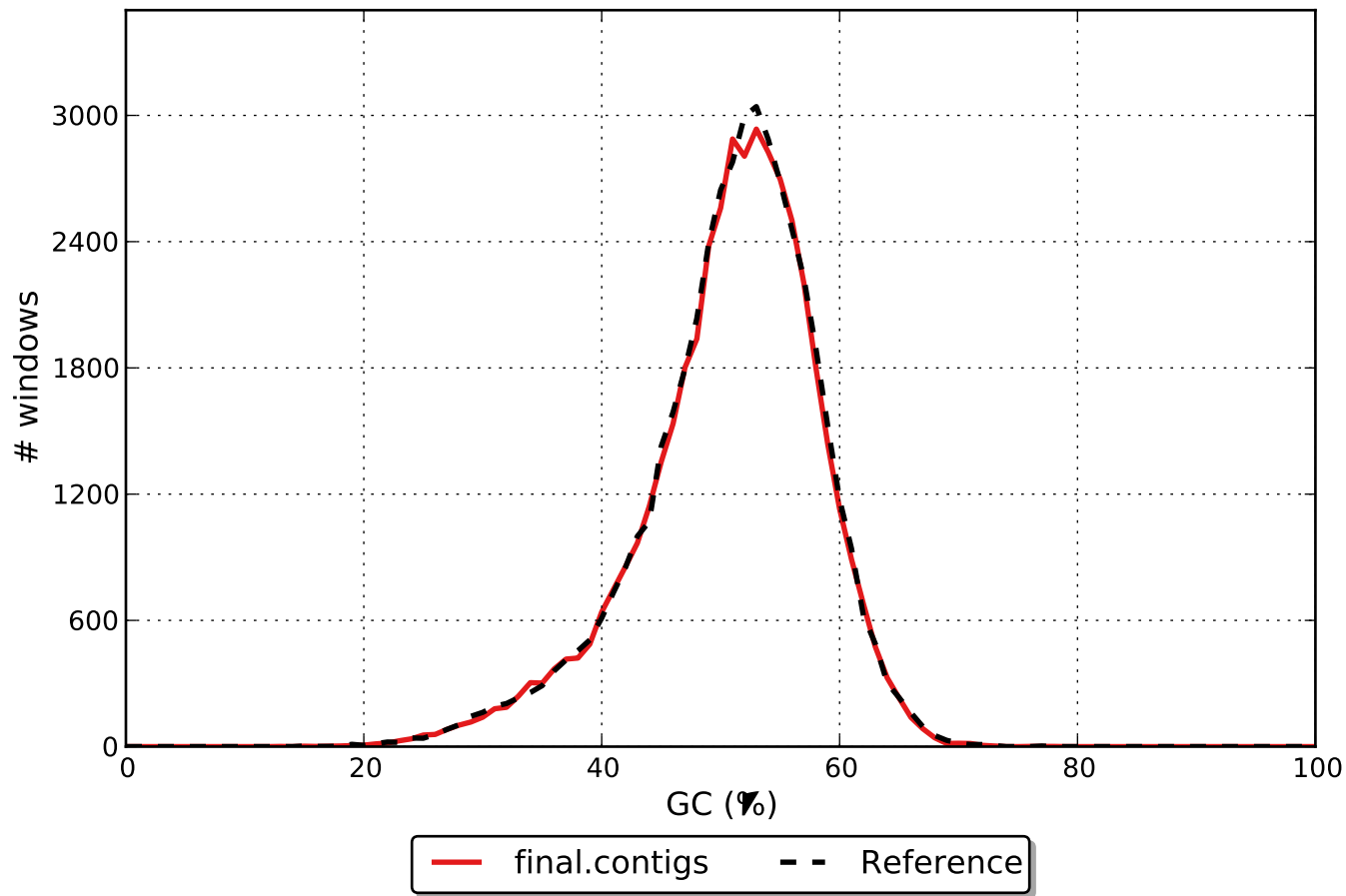
— final.contigs

NGx





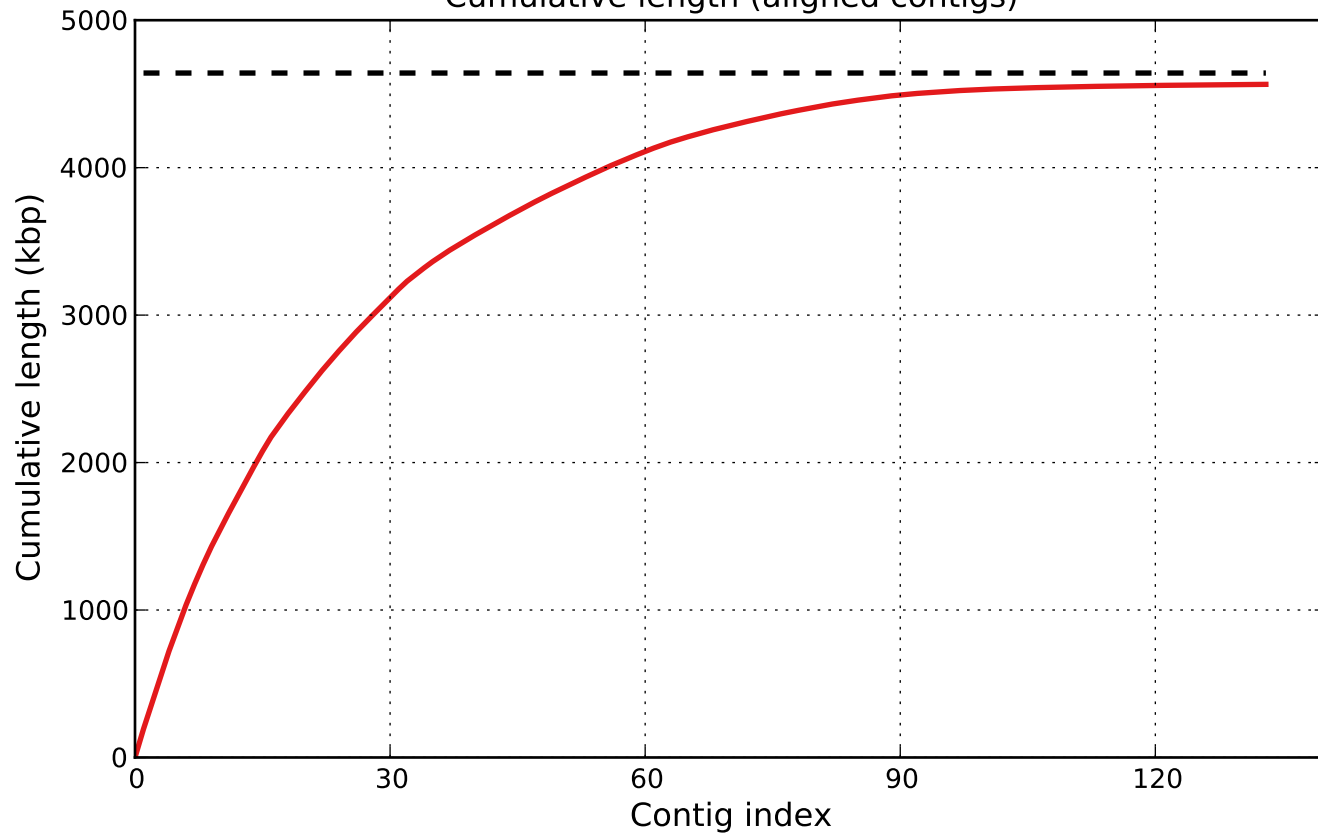
GC content



Misassemblies

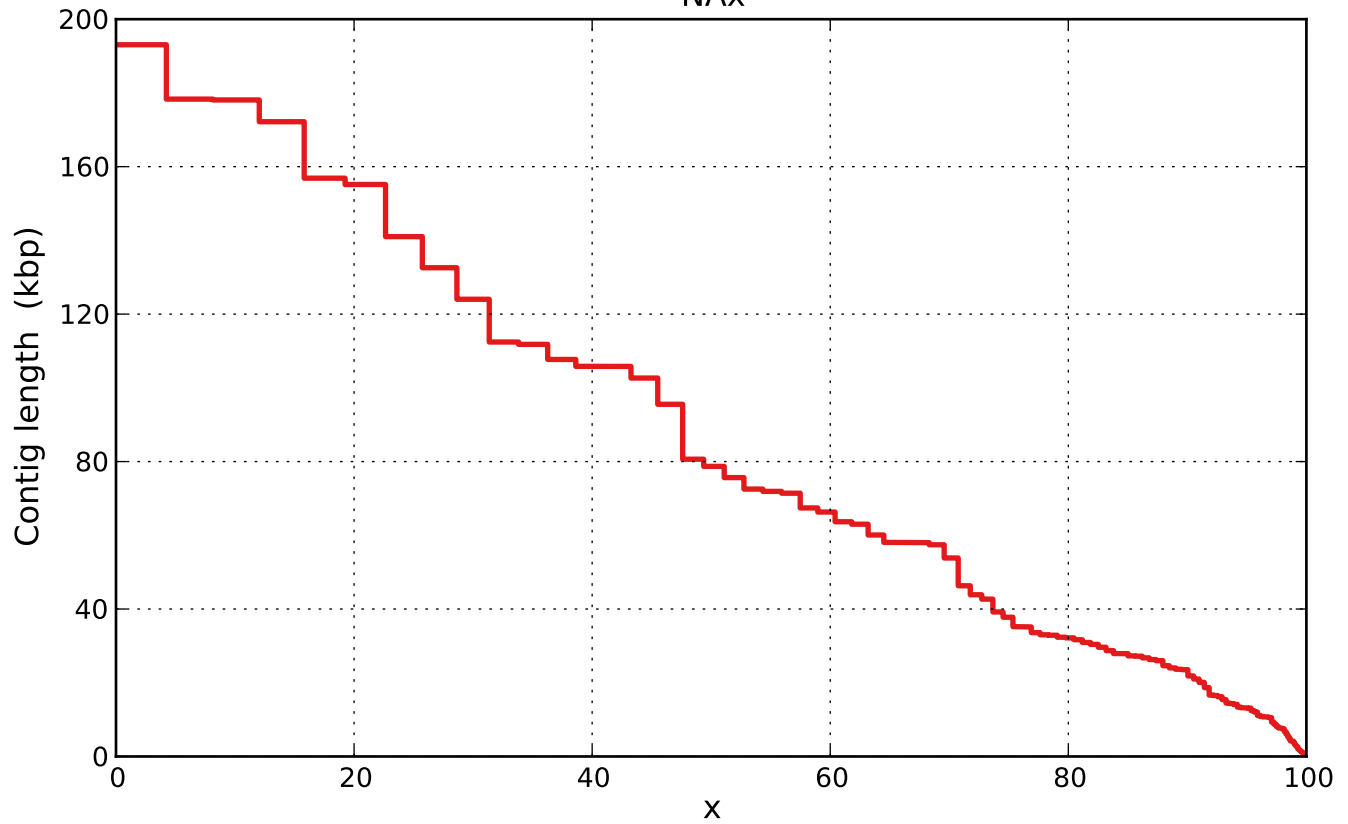


Cumulative length (aligned contigs)



— final.contigs - - Reference

NAx



— final.contigs

NGAx

