

Report

	final.contigs
# contigs (≥ 0 bp)	48356
# contigs (≥ 1000 bp)	0
# contigs (≥ 5000 bp)	0
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	14889940
Total length (≥ 1000 bp)	0
Total length (≥ 5000 bp)	0
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	729
Largest contig	977
Total length	412461
Reference length	4641652
GC (%)	50.81
Reference GC (%)	50.79
N50	546
N75	517
L50	332
L75	526
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	474 + 0 part
Unaligned length	256626
Genome fraction (%)	3.357
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	44.28
# indels per 100 kbp	0.00
Largest alignment	977
NGA50	-

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
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	69
# indels	0
# short indels	0
# long indels	0
Indels length	0

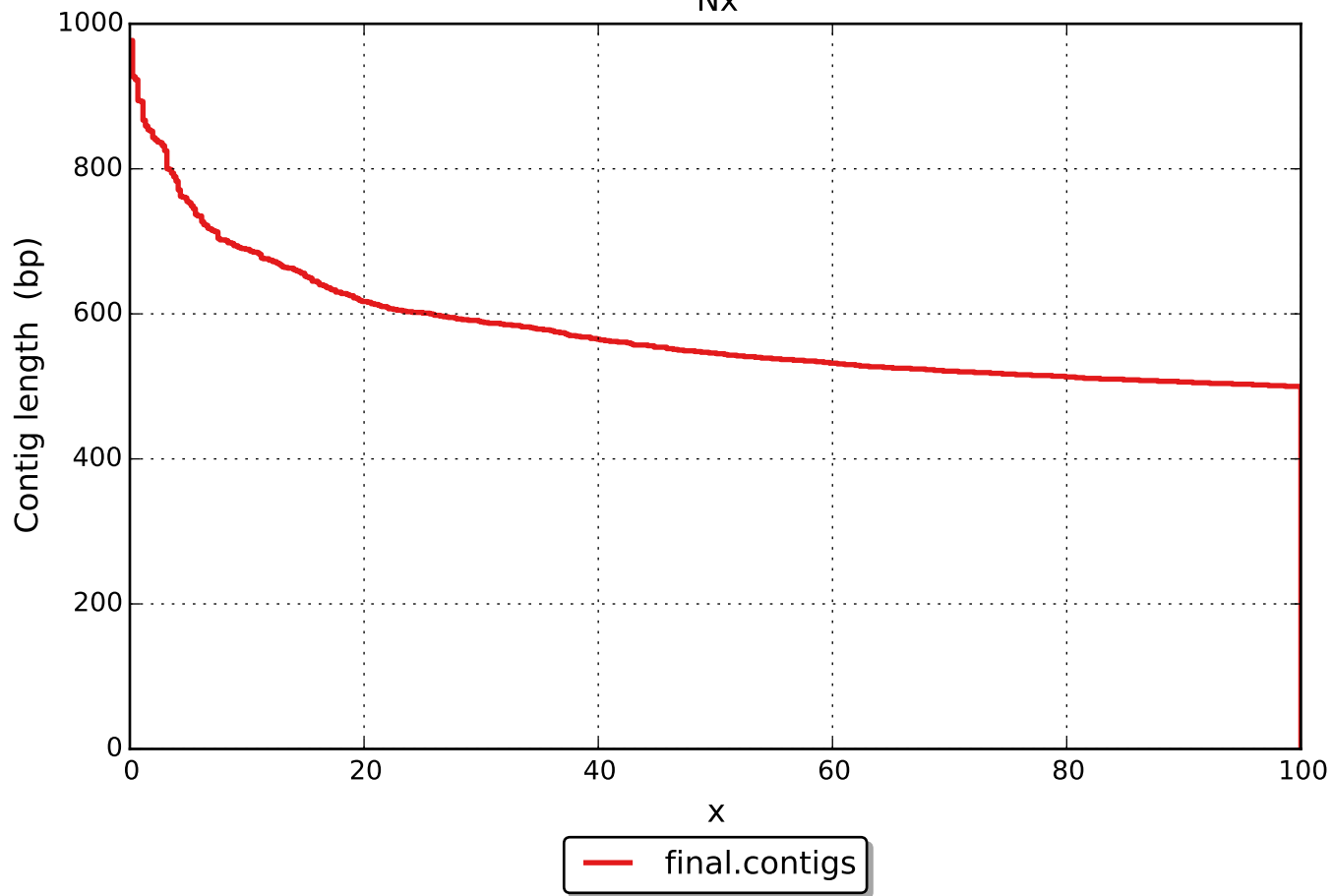
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

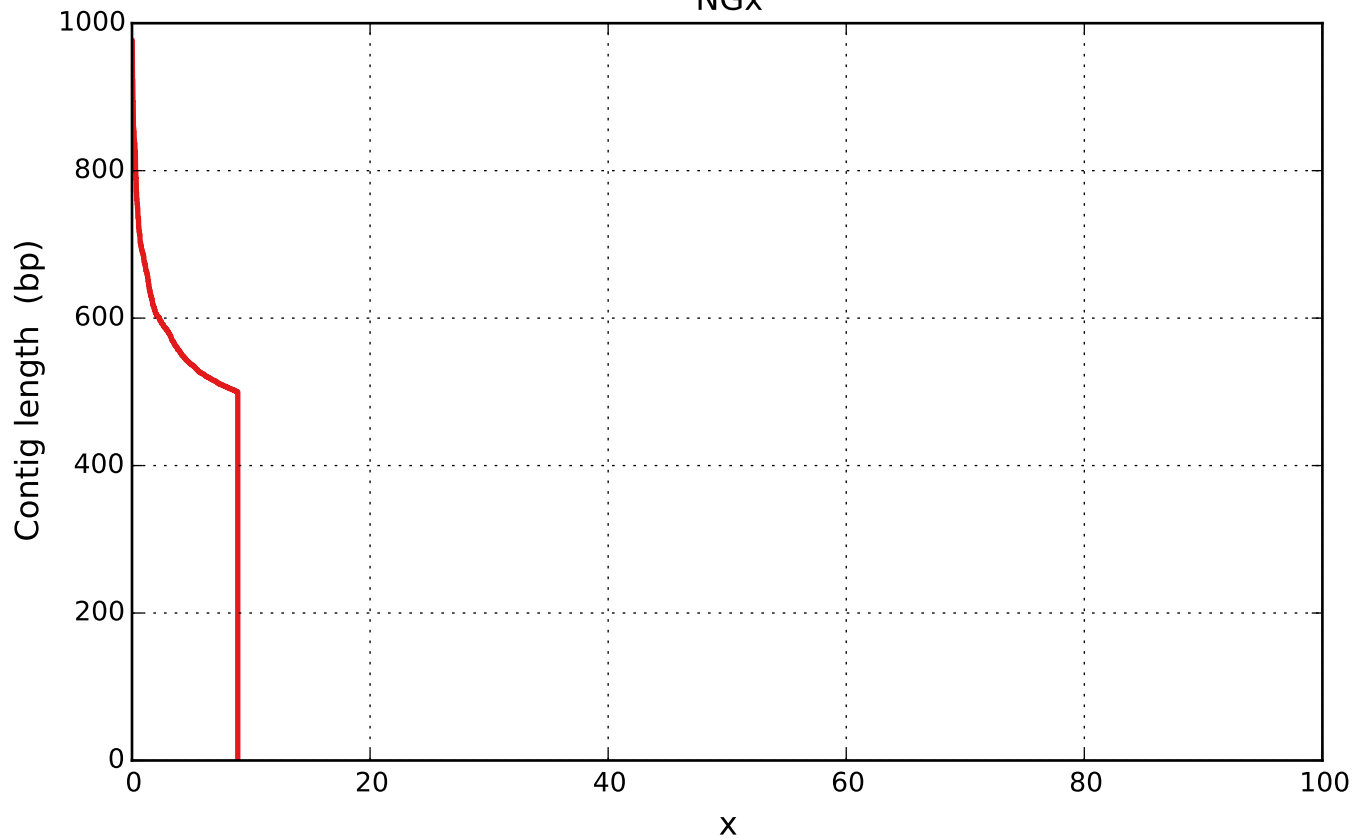
	final.contigs
# fully unaligned contigs	474
Fully unaligned length	256626
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

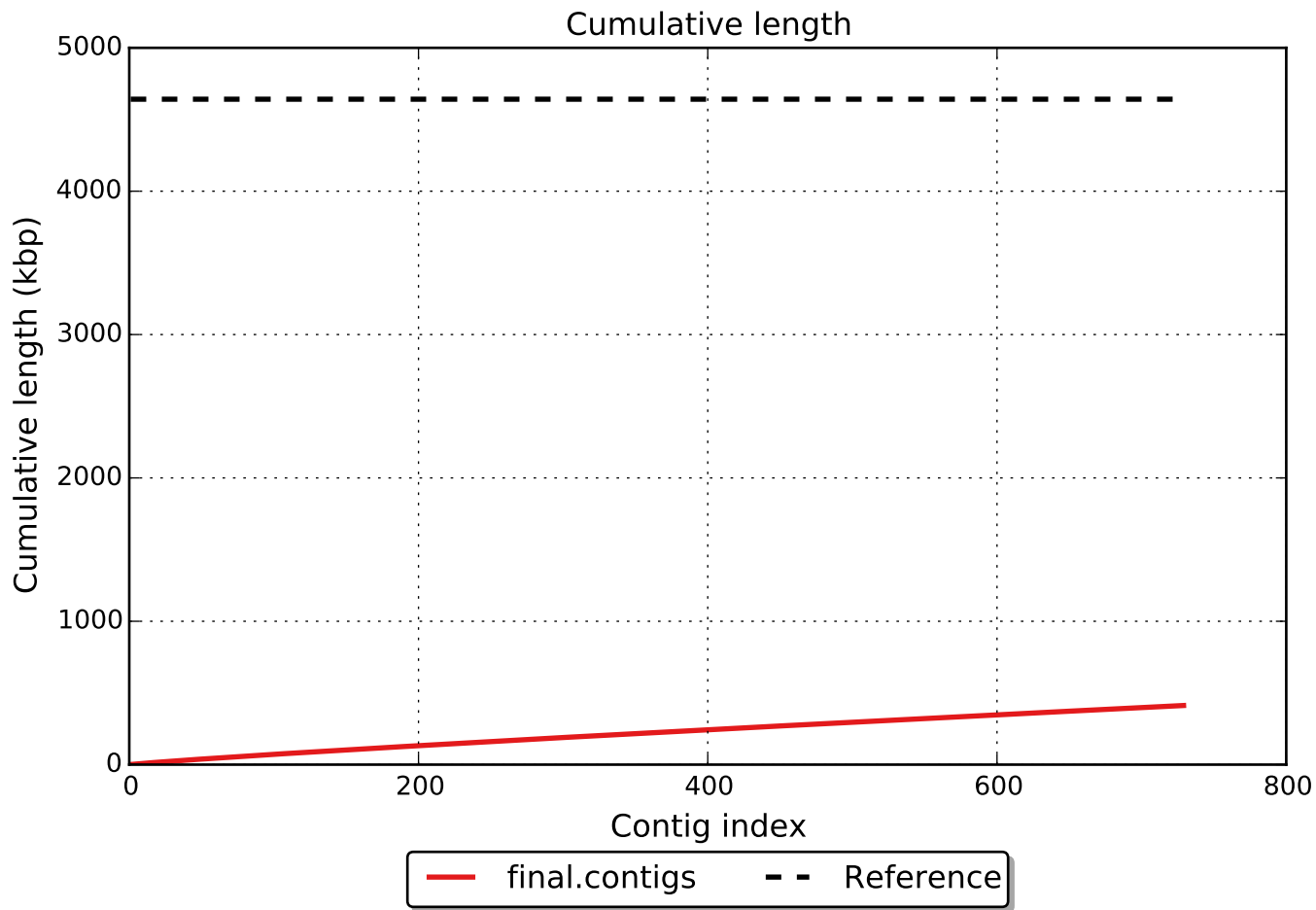
Nx



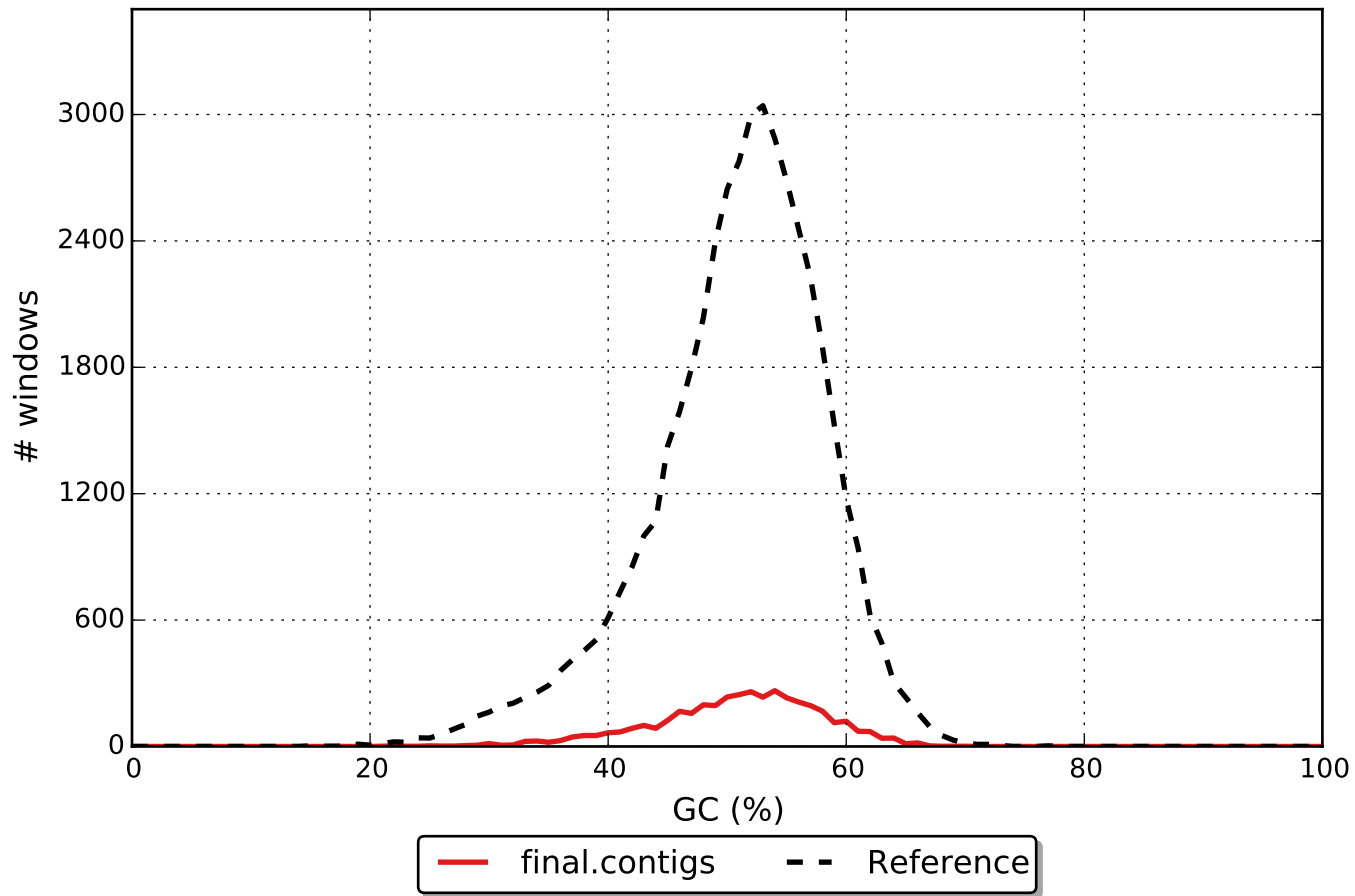
NGx



— final.contigs



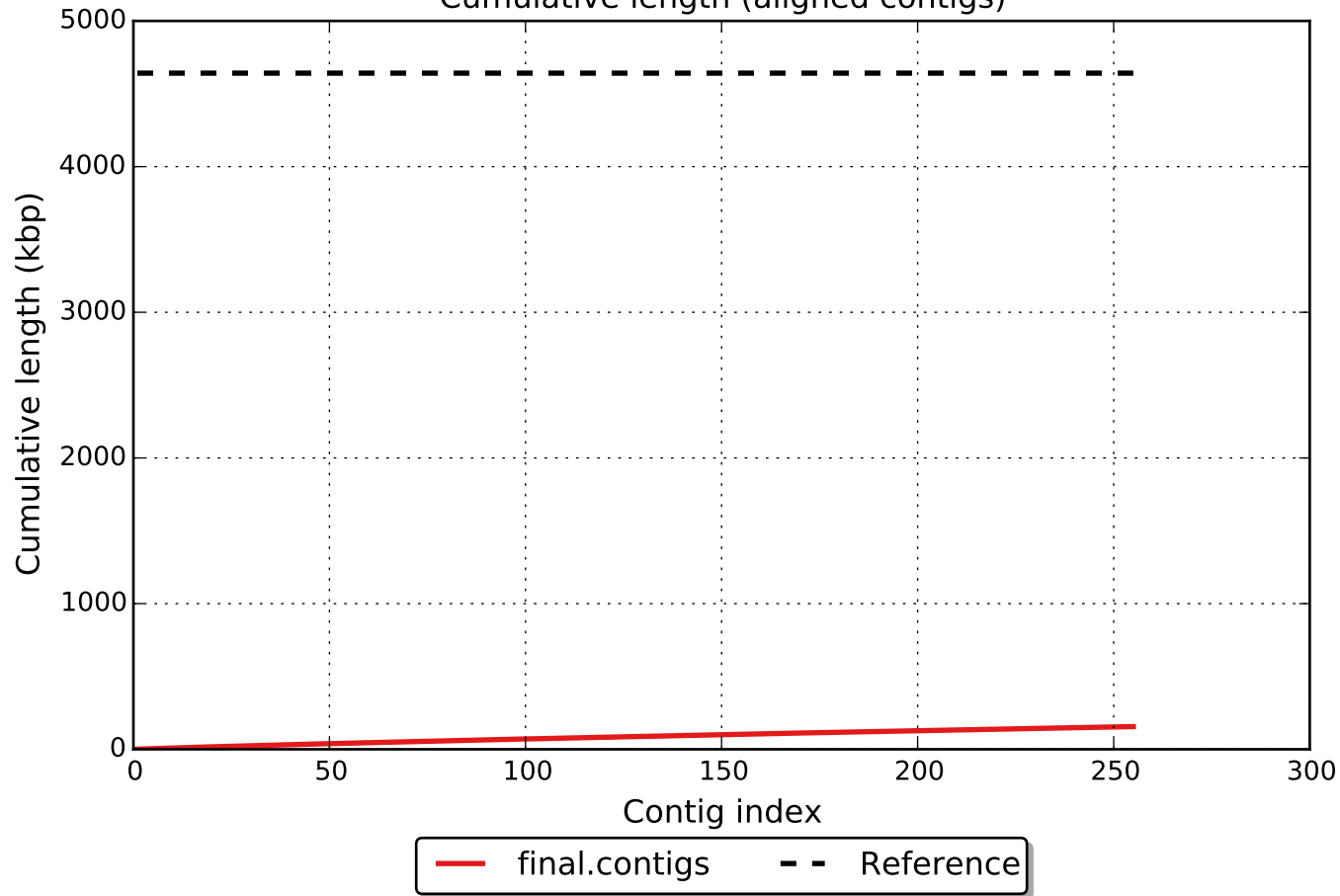
GC content



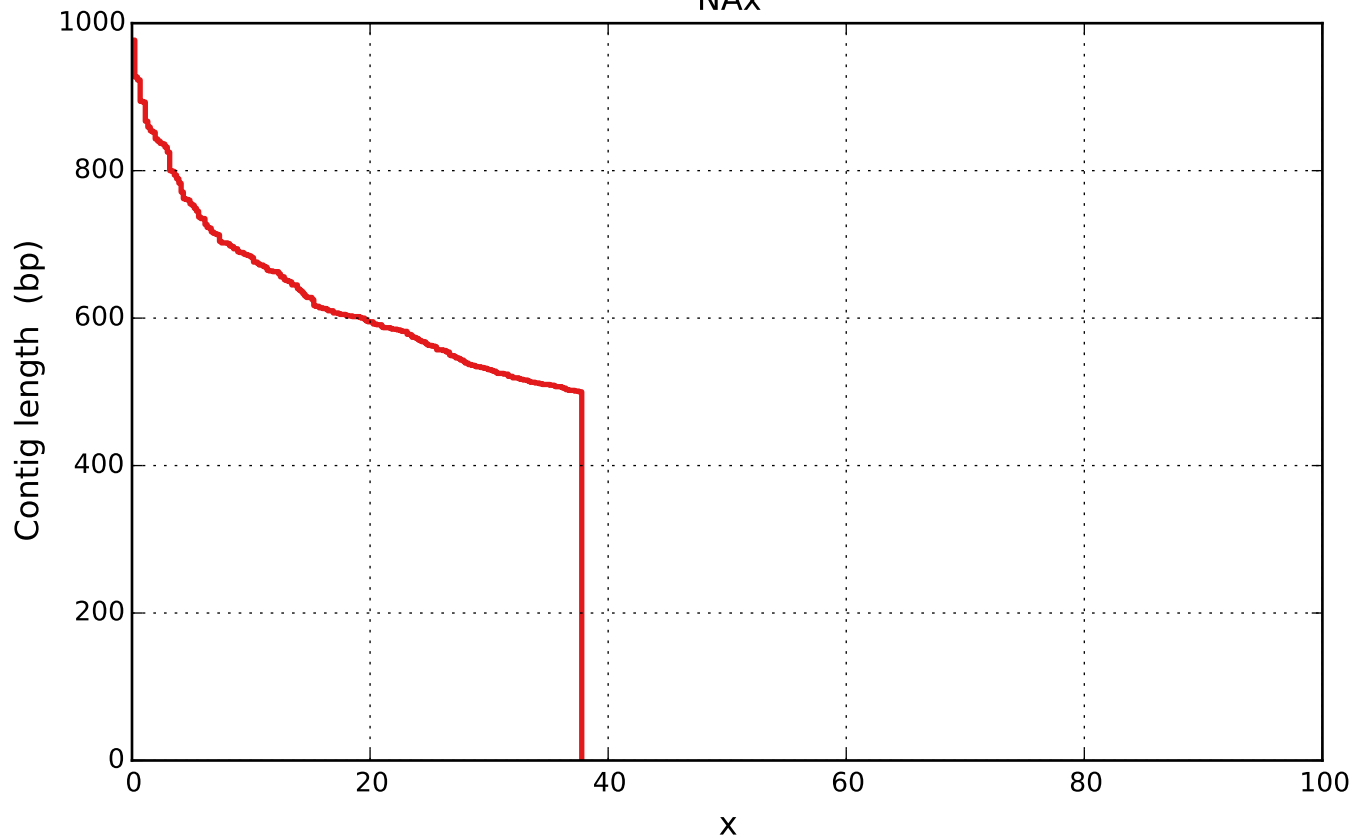
Misassemblies



Cumulative length (aligned contigs)



NAx



— final.contigs

NGAx

