

Report

	scaffolds
# contigs (≥ 1000 bp)	1
# contigs (≥ 5000 bp)	1
# contigs (≥ 10000 bp)	1
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 1000 bp)	15628
Total length (≥ 5000 bp)	15628
Total length (≥ 10000 bp)	15628
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	2
Largest contig	15628
Total length	16470
Reference length	4641652
GC (%)	53.76
Reference GC (%)	50.78
N50	15628
N75	15628
L50	1
L75	1
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 2 part
Unaligned length	14922
Genome fraction (%)	0.031
Duplication ratio	1.076
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4172.46
# indels per 100 kbp	69.54
Largest alignment	785
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

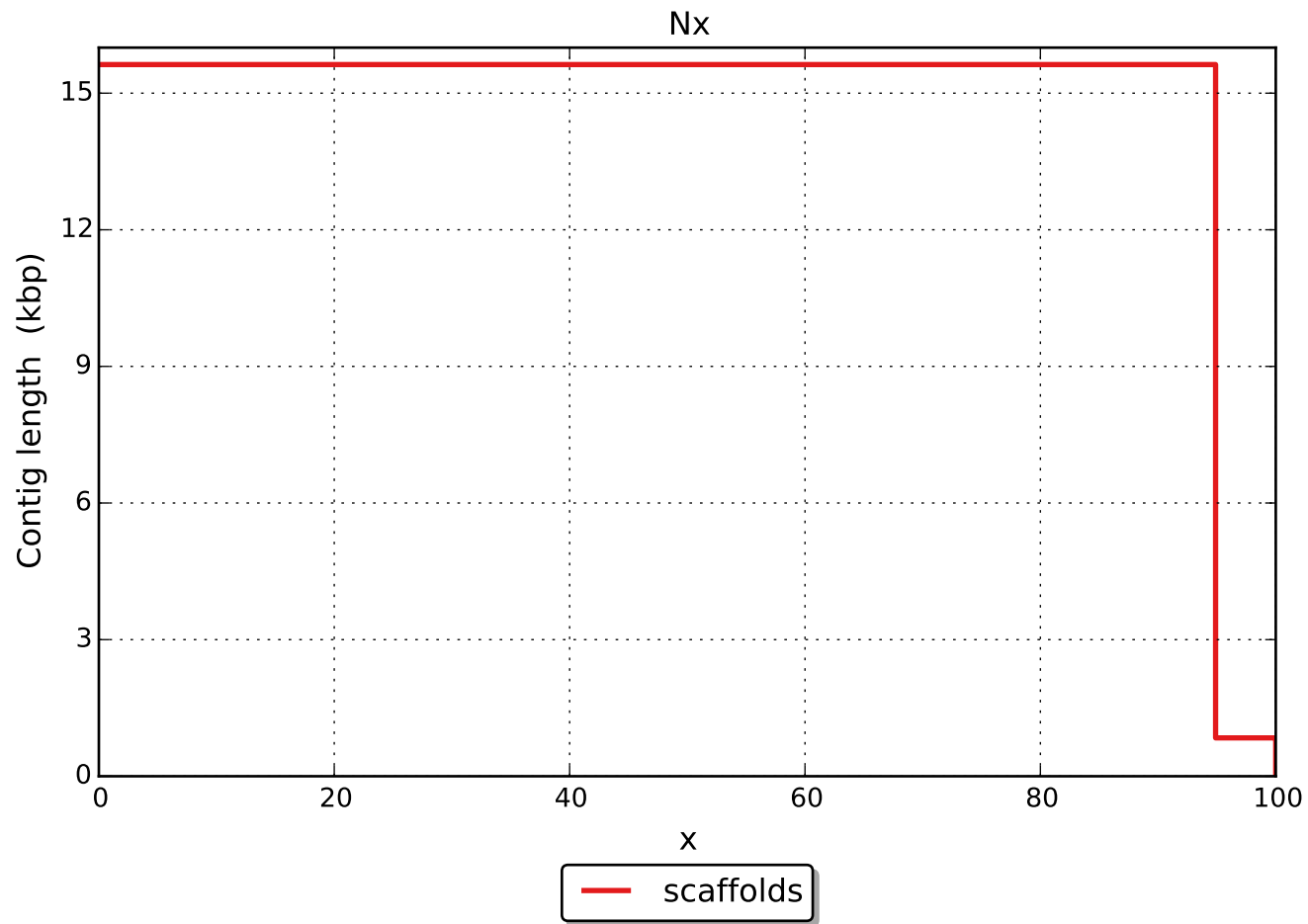
	scaffolds
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	1
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	60
# indels	1
# short indels	1
# long indels	0
Indels length	1

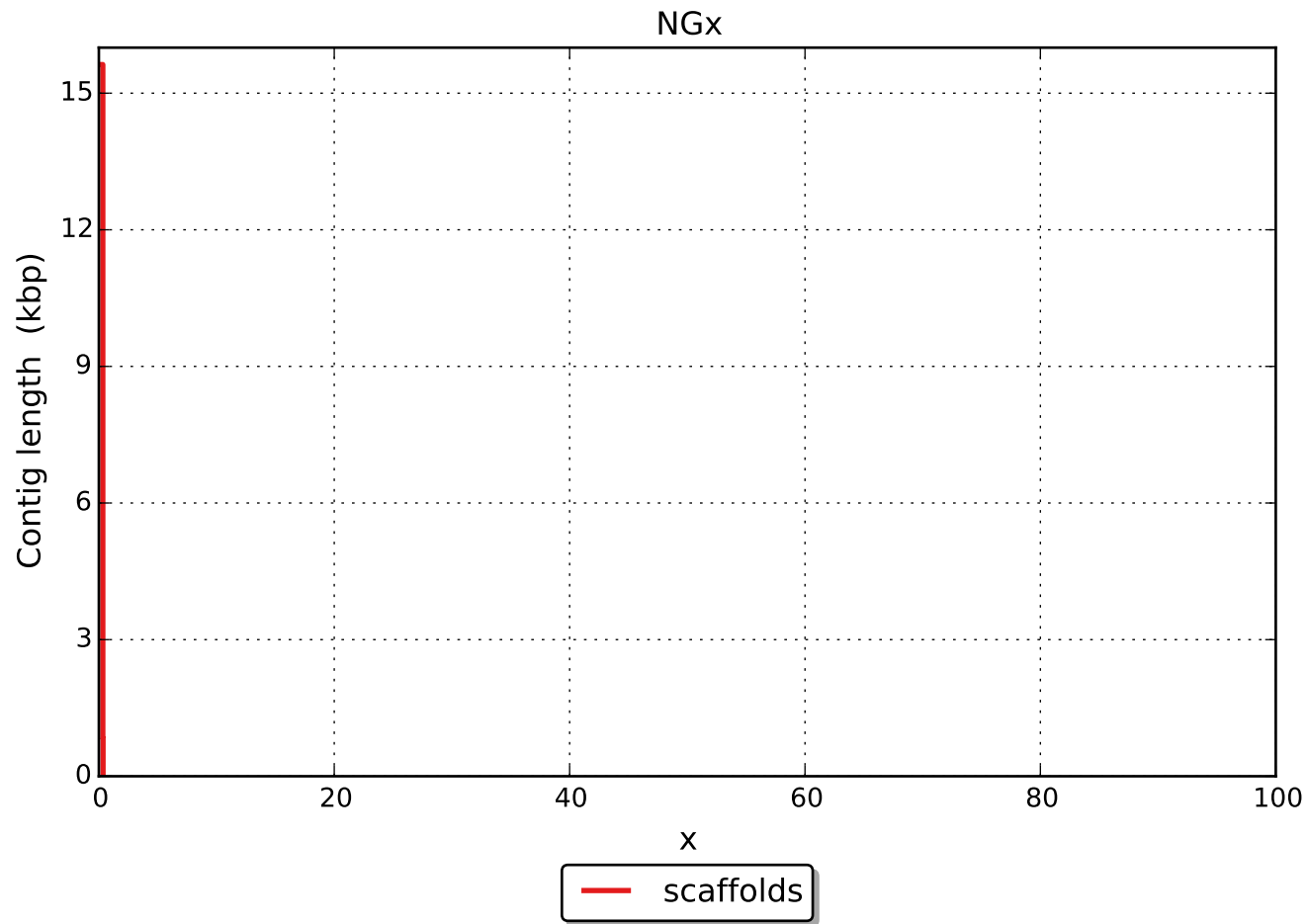
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

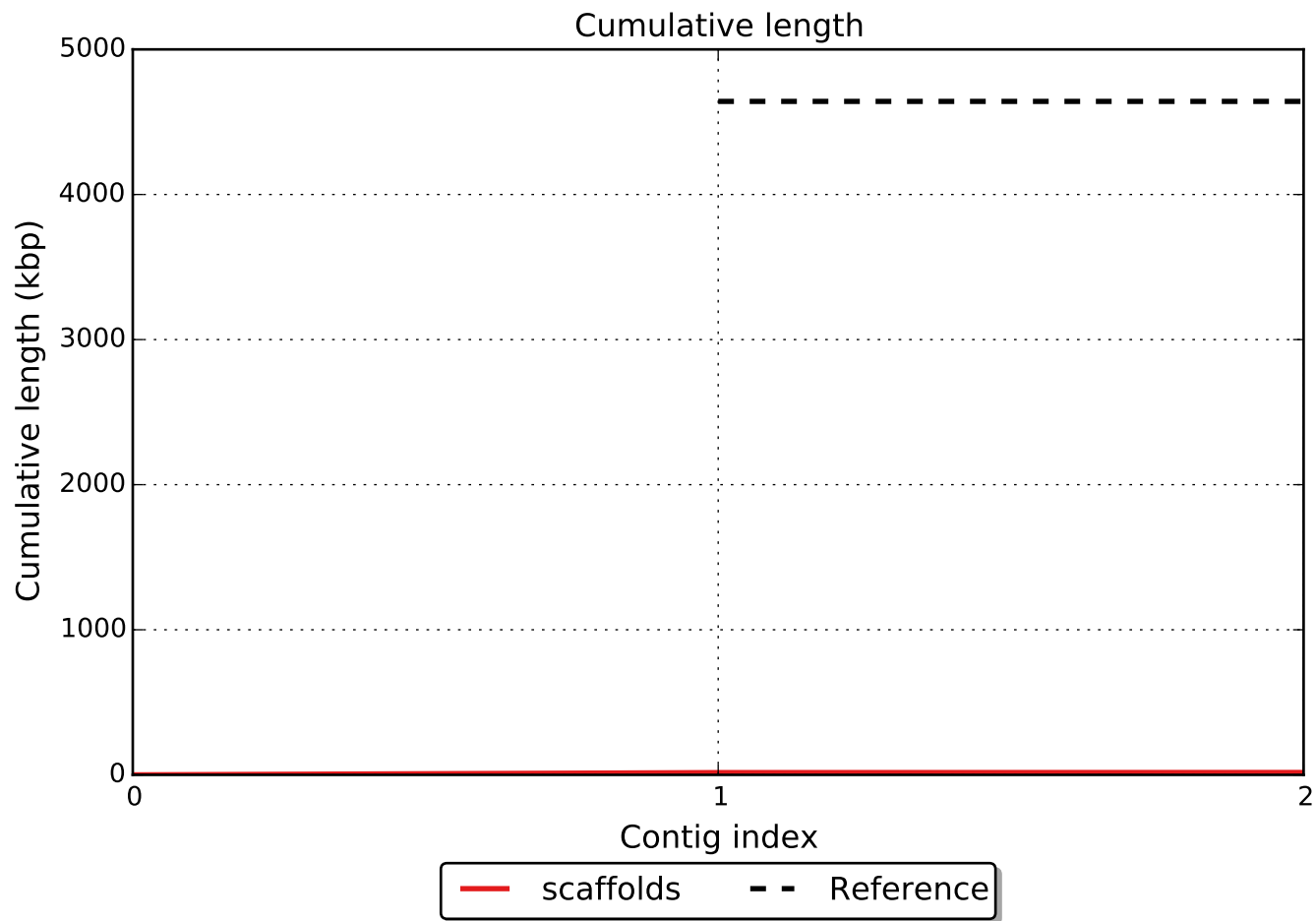
Unaligned report

	scaffolds
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	1
# both parts are significant	1
Partially unaligned length	14922
# N's	0

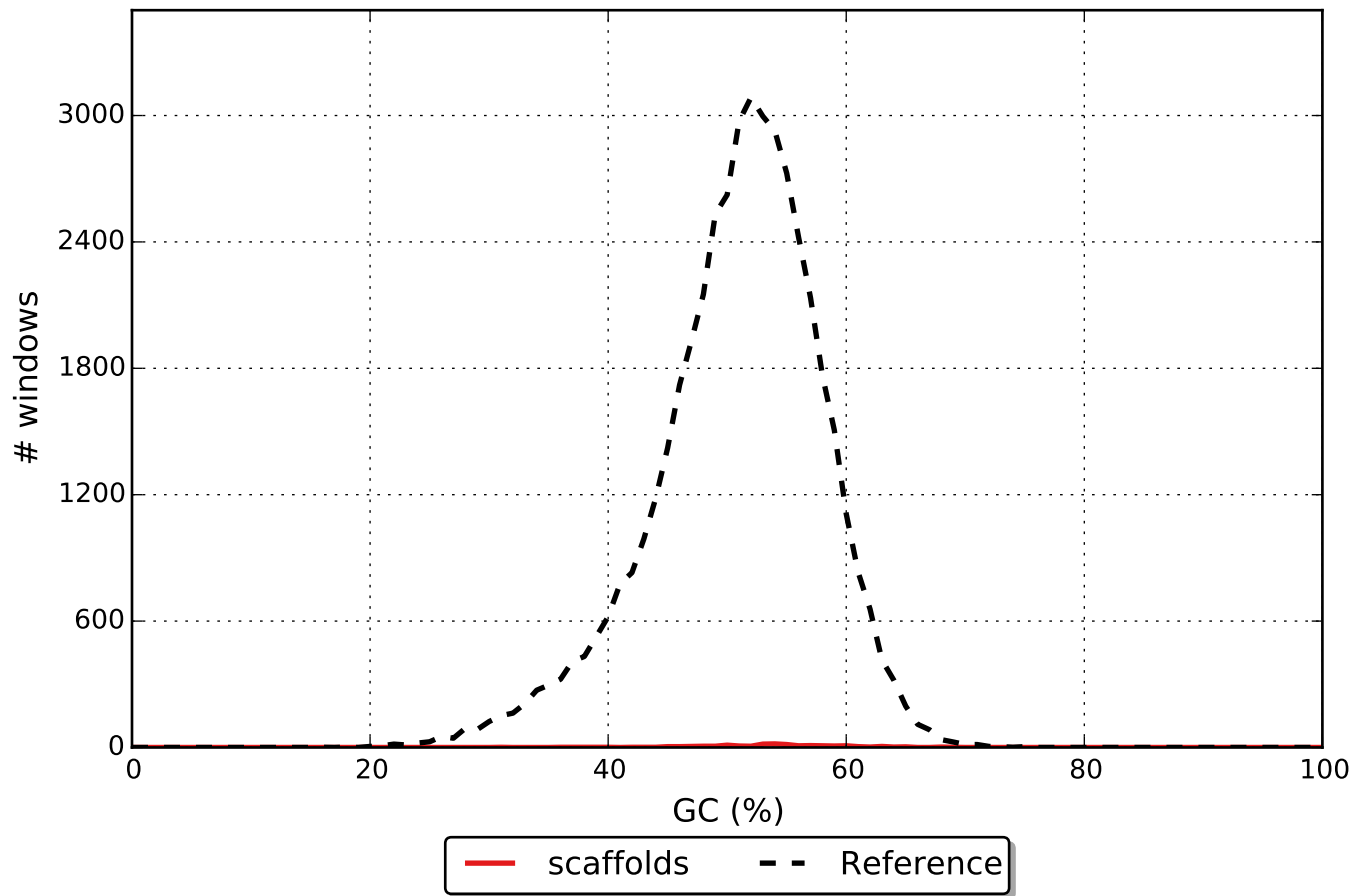
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



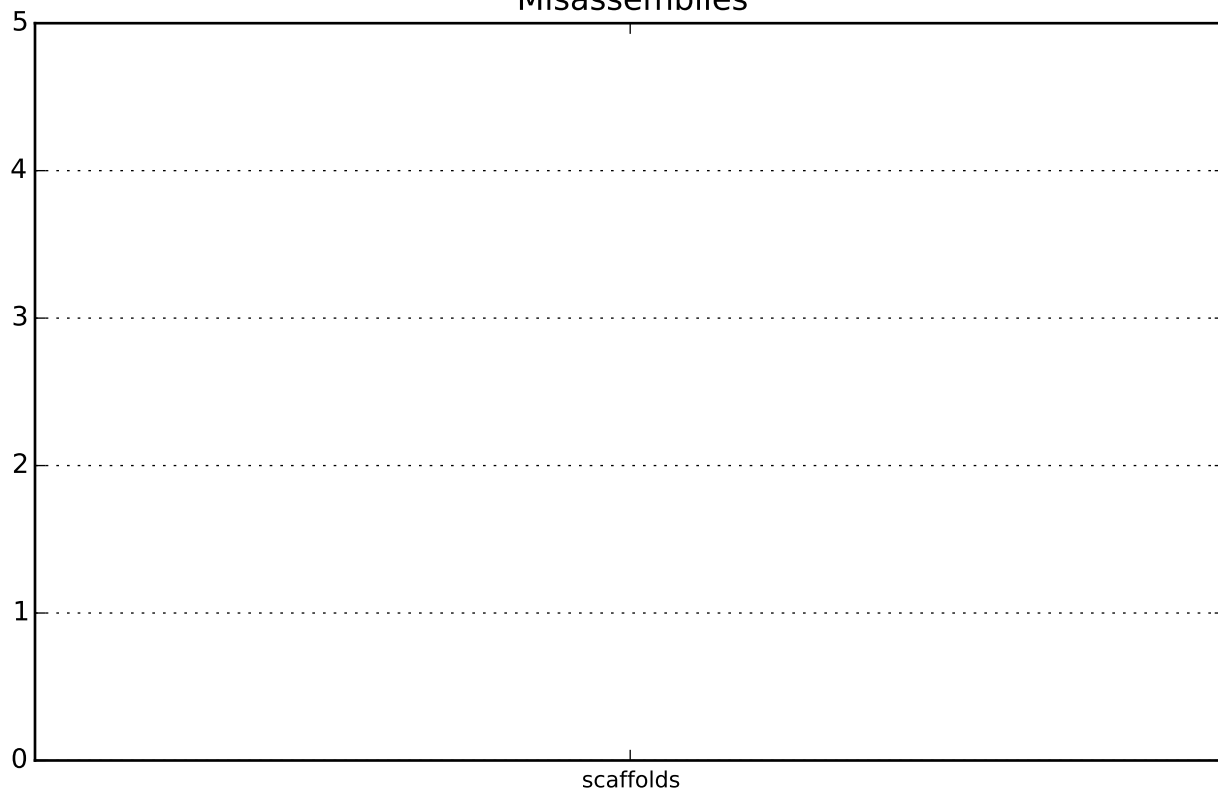




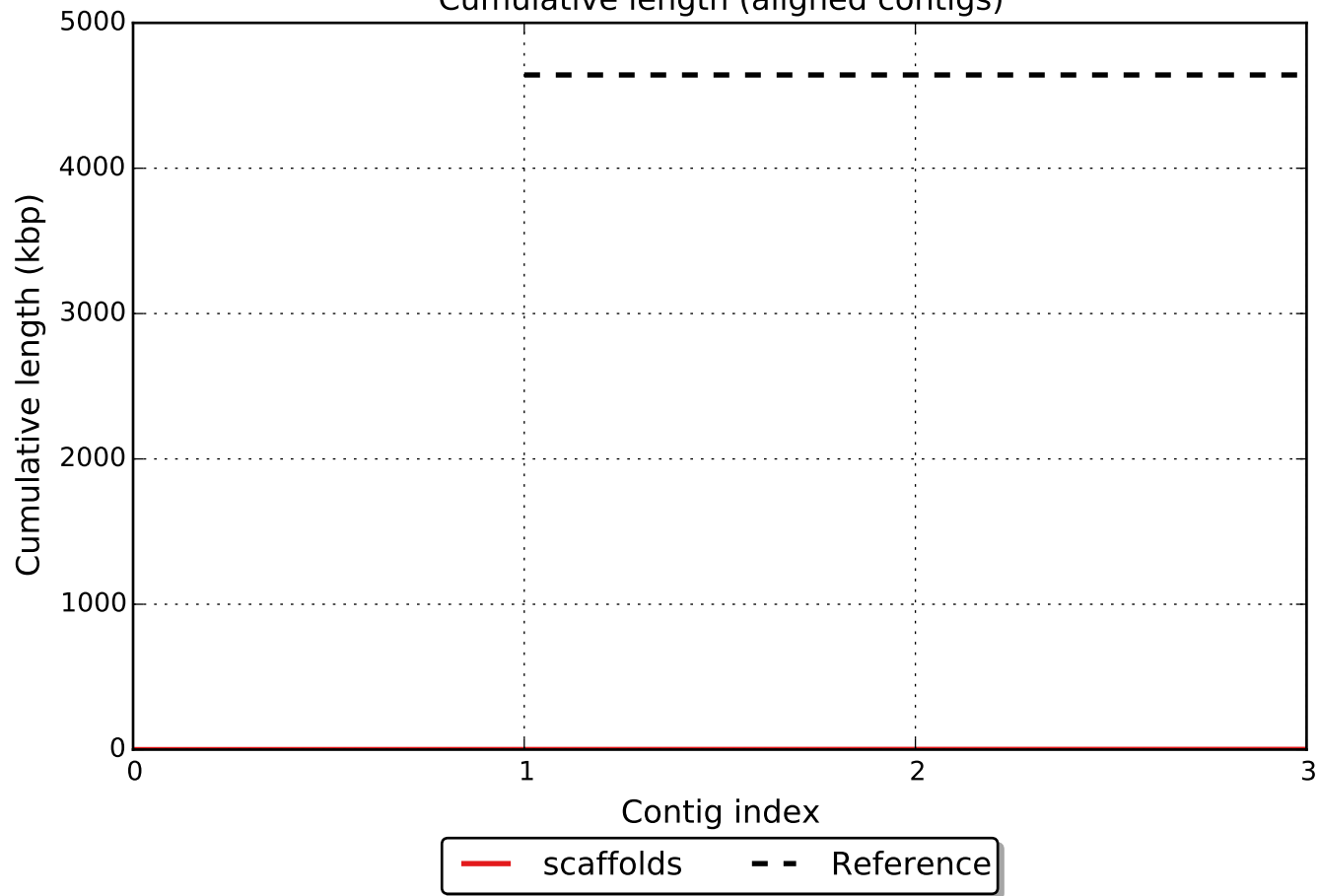
GC content



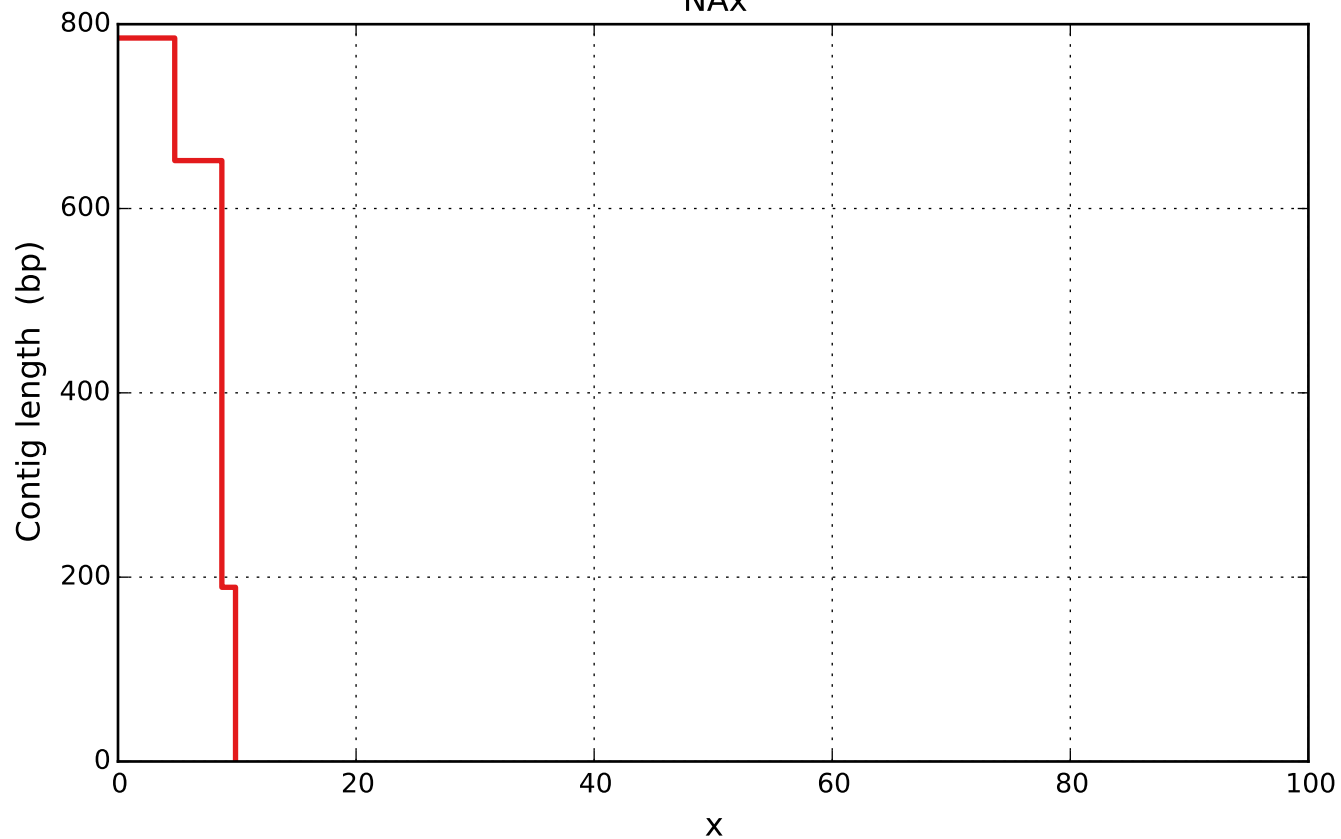
Misassemblies



Cumulative length (aligned contigs)



NAx



— scaffolds

NGAx

