

Report

	contigs
# contigs (≥ 0 bp)	571
# contigs (≥ 1000 bp)	6
# contigs (≥ 5000 bp)	0
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	151099
Total length (≥ 1000 bp)	10617
Total length (≥ 5000 bp)	0
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	10
Largest contig	3609
Total length	13241
Reference length	4641652
GC (%)	51.94
Reference GC (%)	50.79
N50	1470
N75	1007
L50	3
L75	6
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	3921
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	0.281
Duplication ratio	1.015
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1448.72
# indels per 100 kbp	7.67
Largest alignment	3609
NA50	1367
NGA50	-
NA75	914
LA50	3
LA75	6

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

	contigs
# misassemblies	3
# relocations	3
# translocations	0
# inversions	0
# misassembled contigs	3
Misassembled contigs length	3921
# local misassemblies	0
# mismatches	189
# indels	1
# short indels	1
# long indels	0
Indels length	1

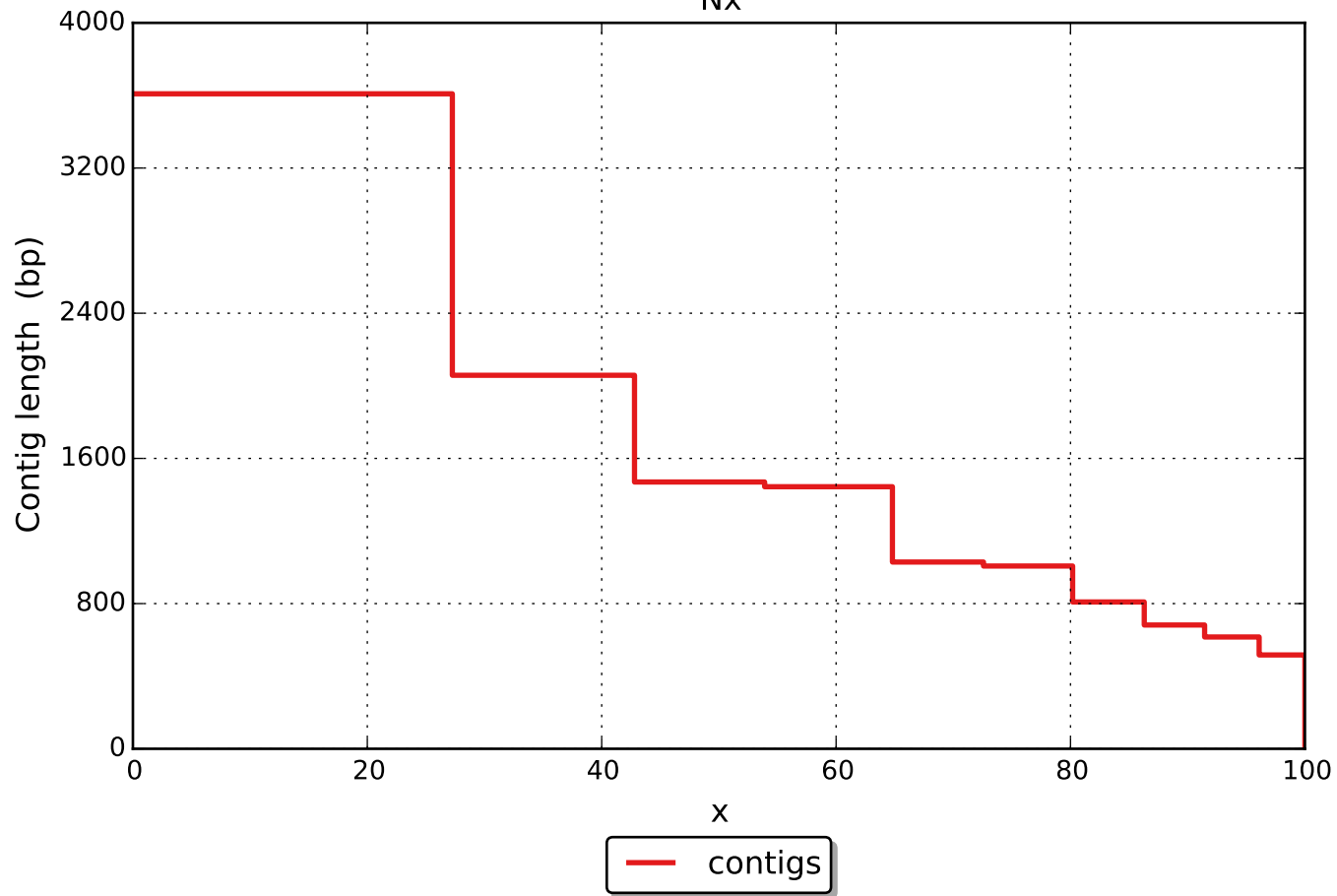
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

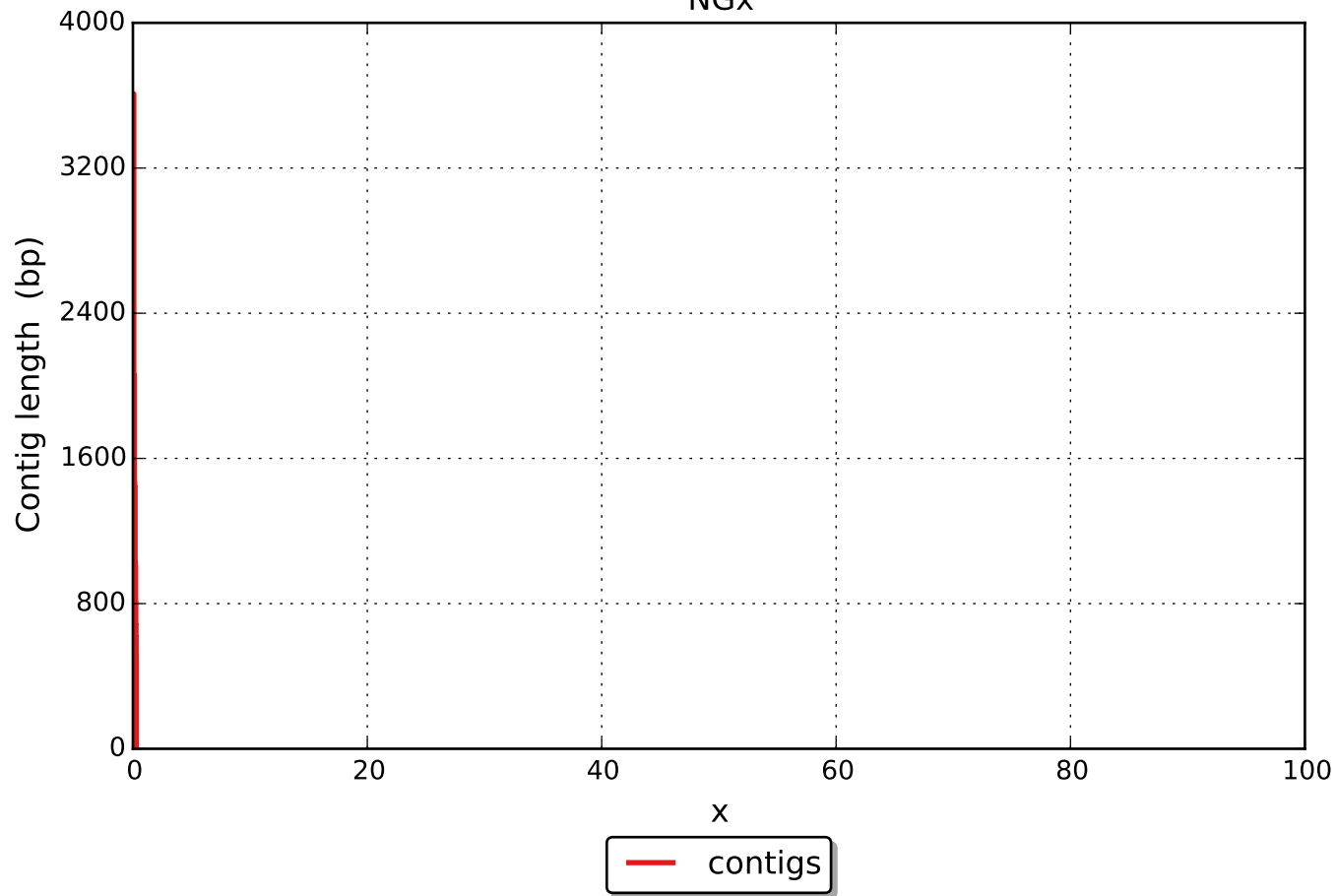
	contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

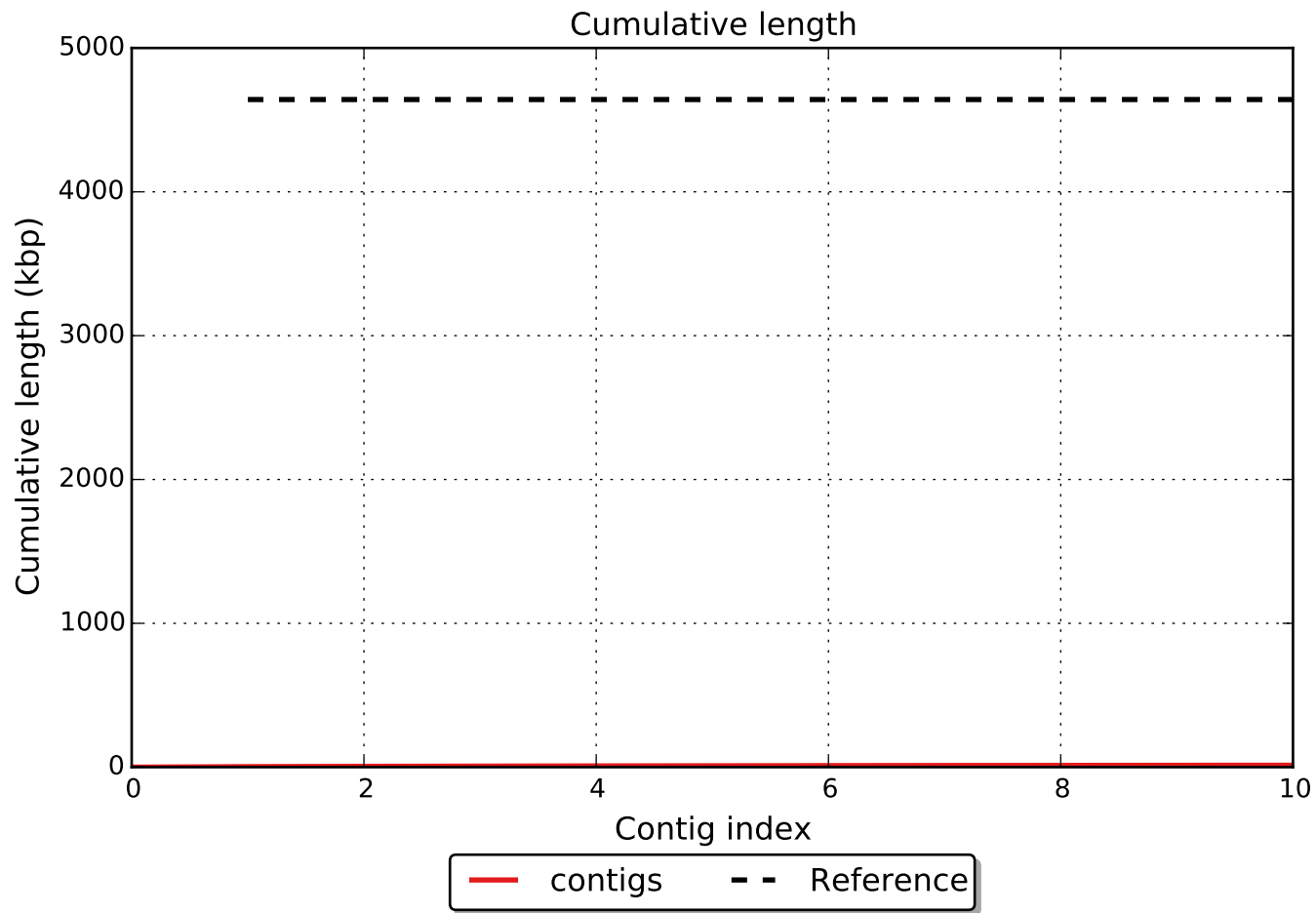
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

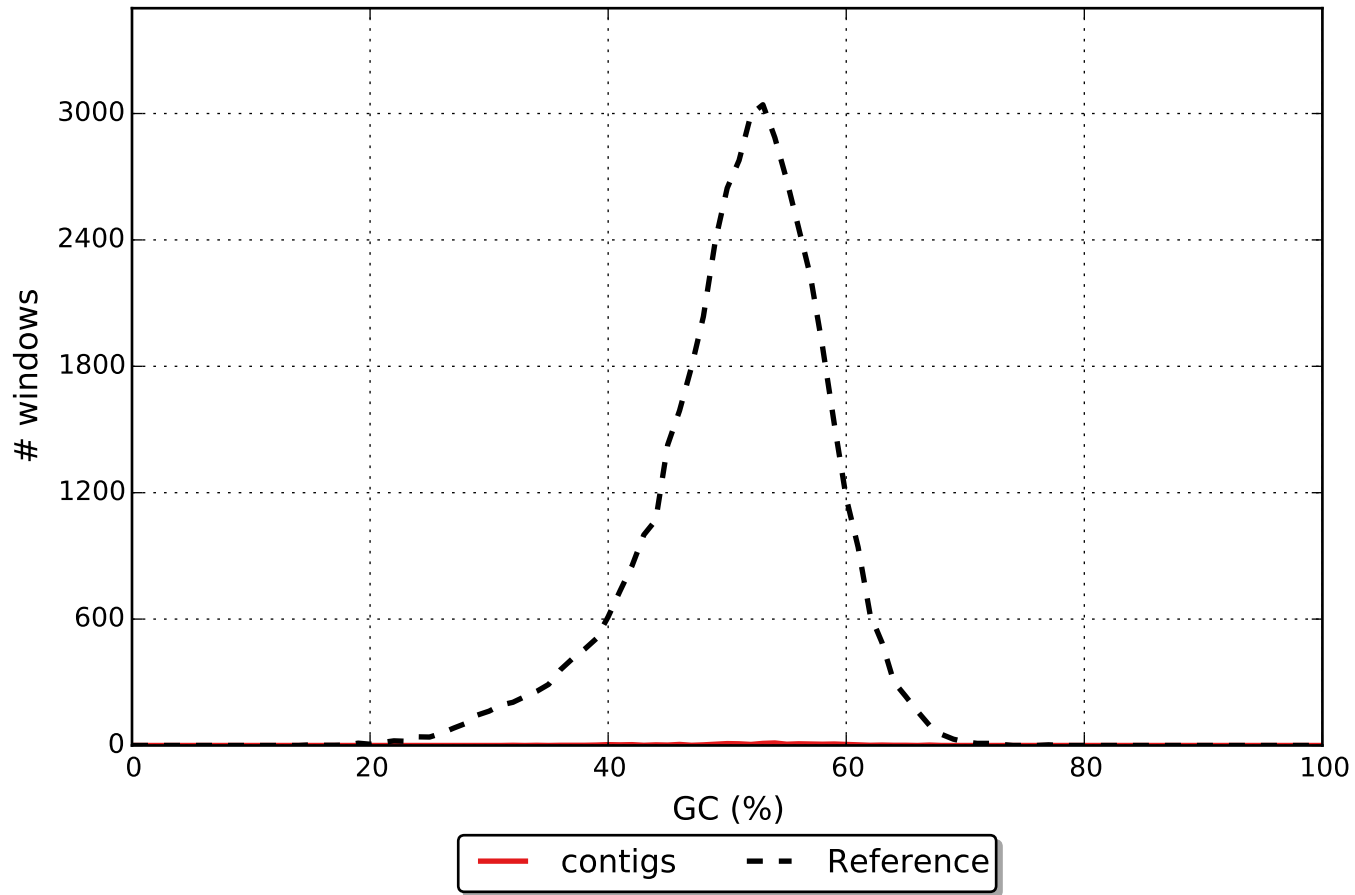


NGx

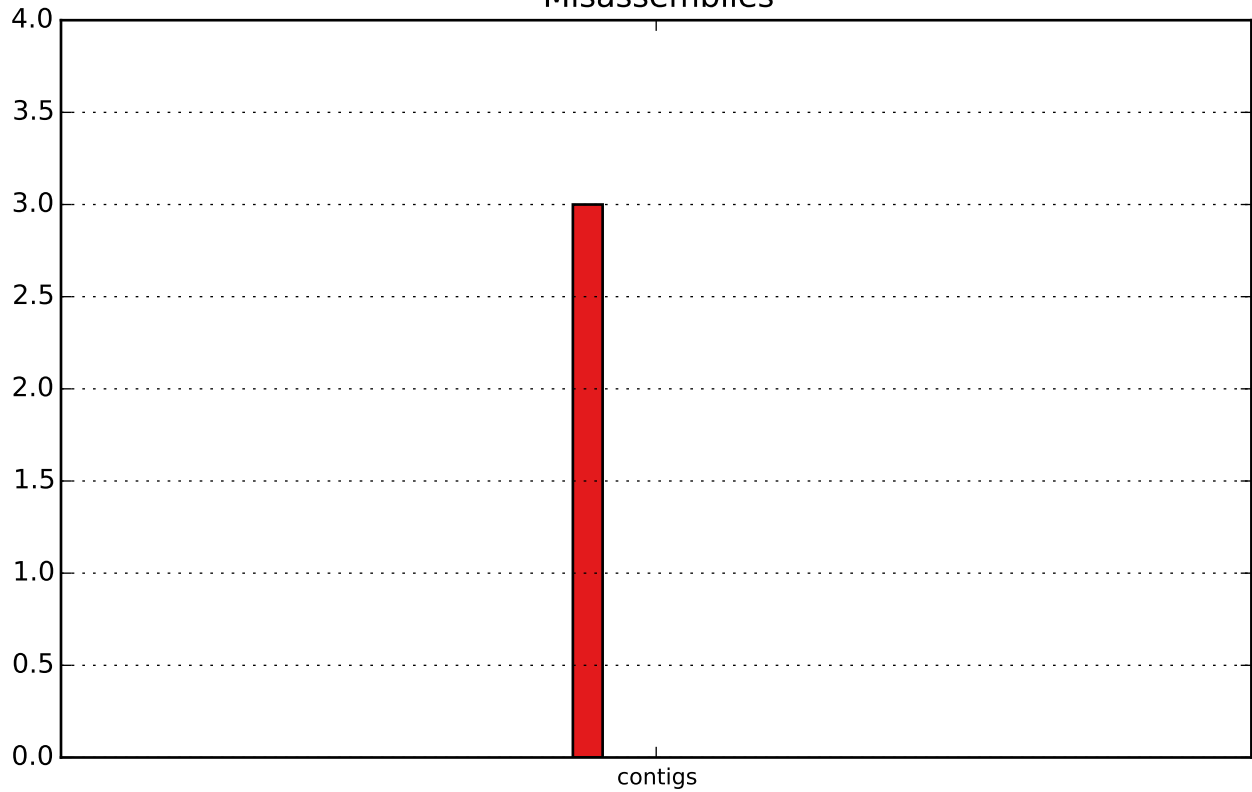




GC content

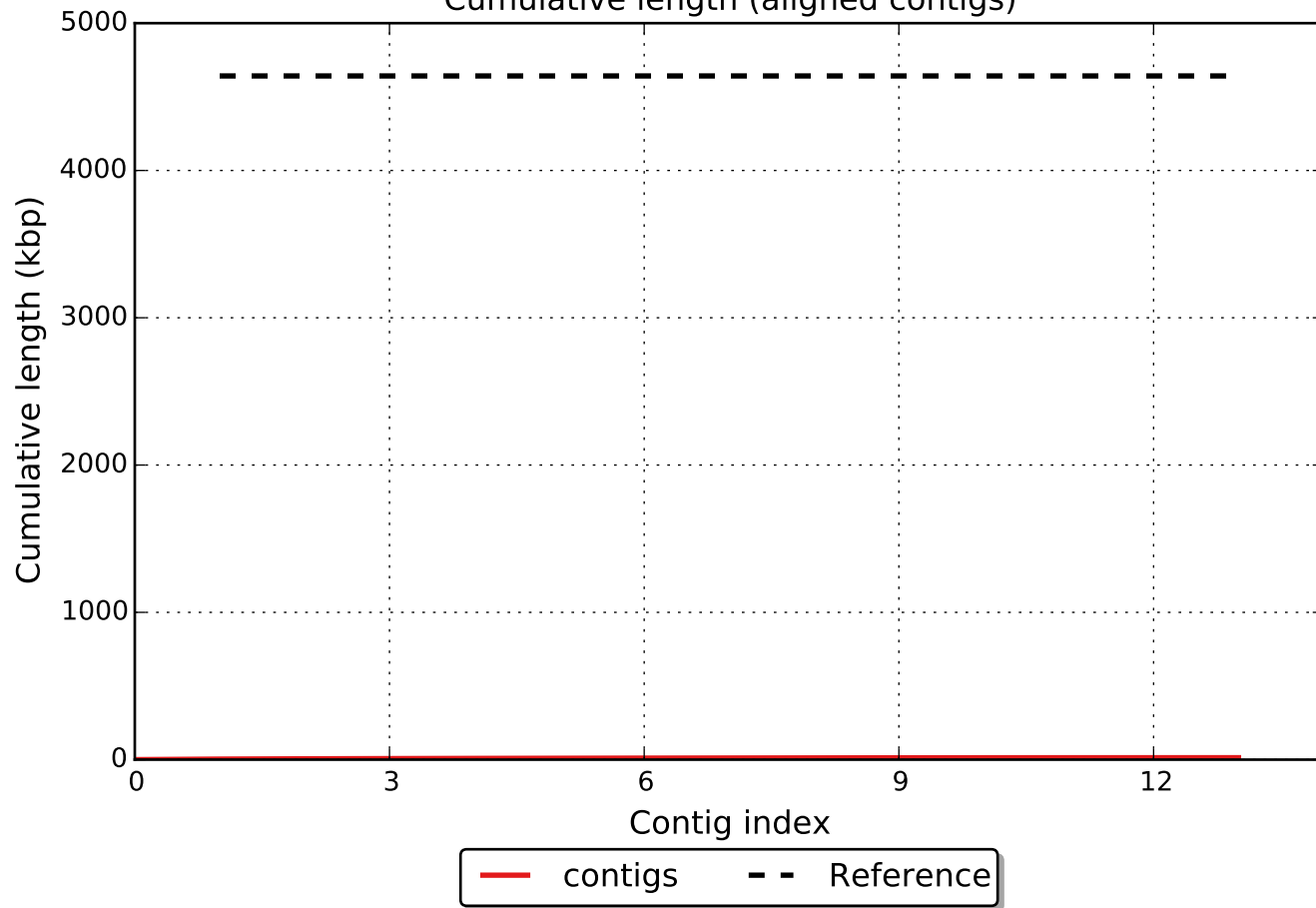


Misassemblies

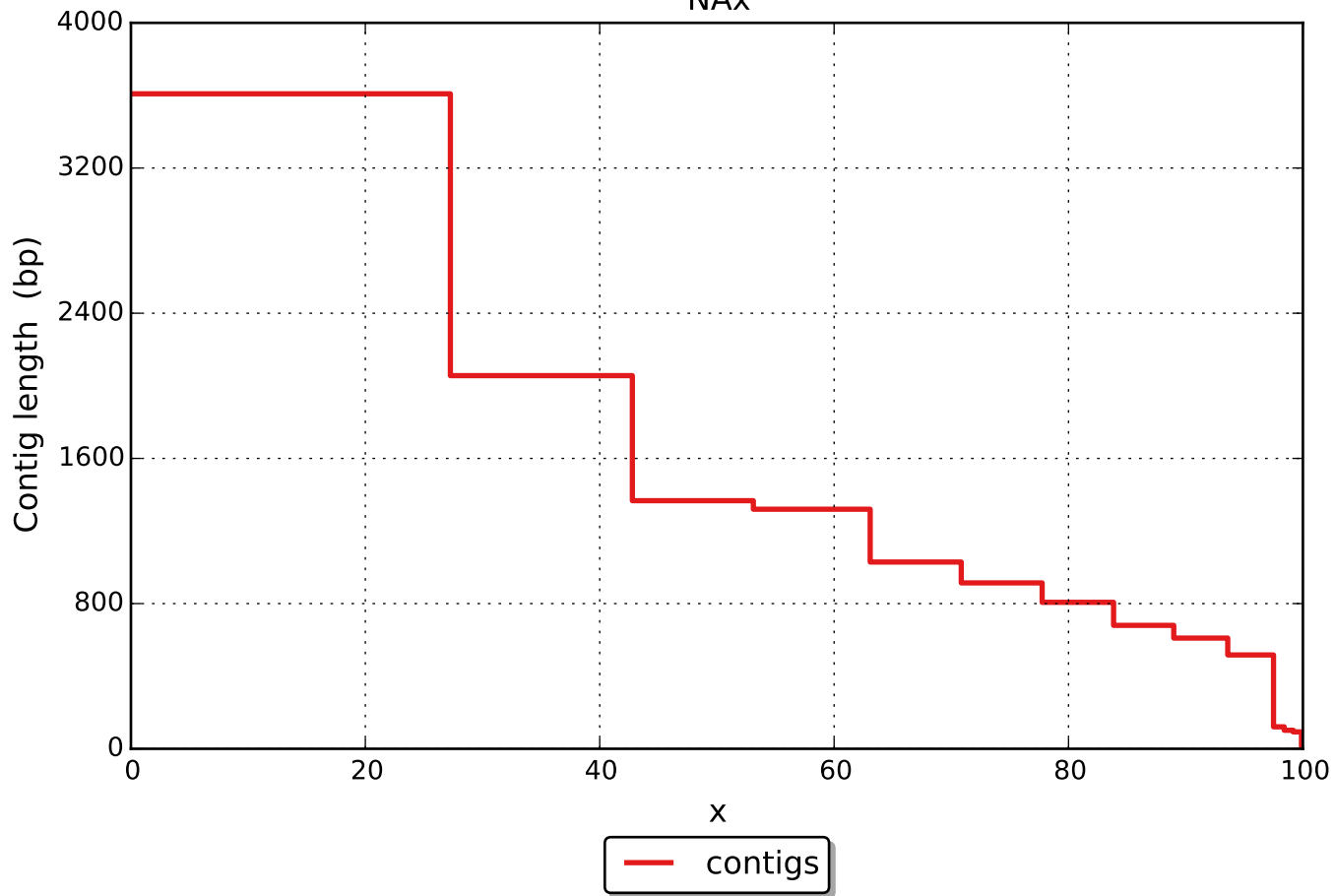


 # relocations

Cumulative length (aligned contigs)



NAx



NGAx

