

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	3
# misassembled contigs	3
Misassembled contigs length	1599
# local misassemblies	1
# unaligned contigs	11 + 2 part
Unaligned length	6376
Genome fraction (%)	8.479
Duplication ratio	1.032
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1414.29
# indels per 100 kbp	0.51
Largest alignment	977
NA50	544
NGA50	-
NA75	516
LA50	332
LA75	528

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	3
# relocations	2
# translocations	0
# inversions	1
# misassembled contigs	3
Misassembled contigs length	1599
# local misassemblies	1
# mismatches	5566
# indels	2
# short indels	2
# long indels	0
Indels length	2

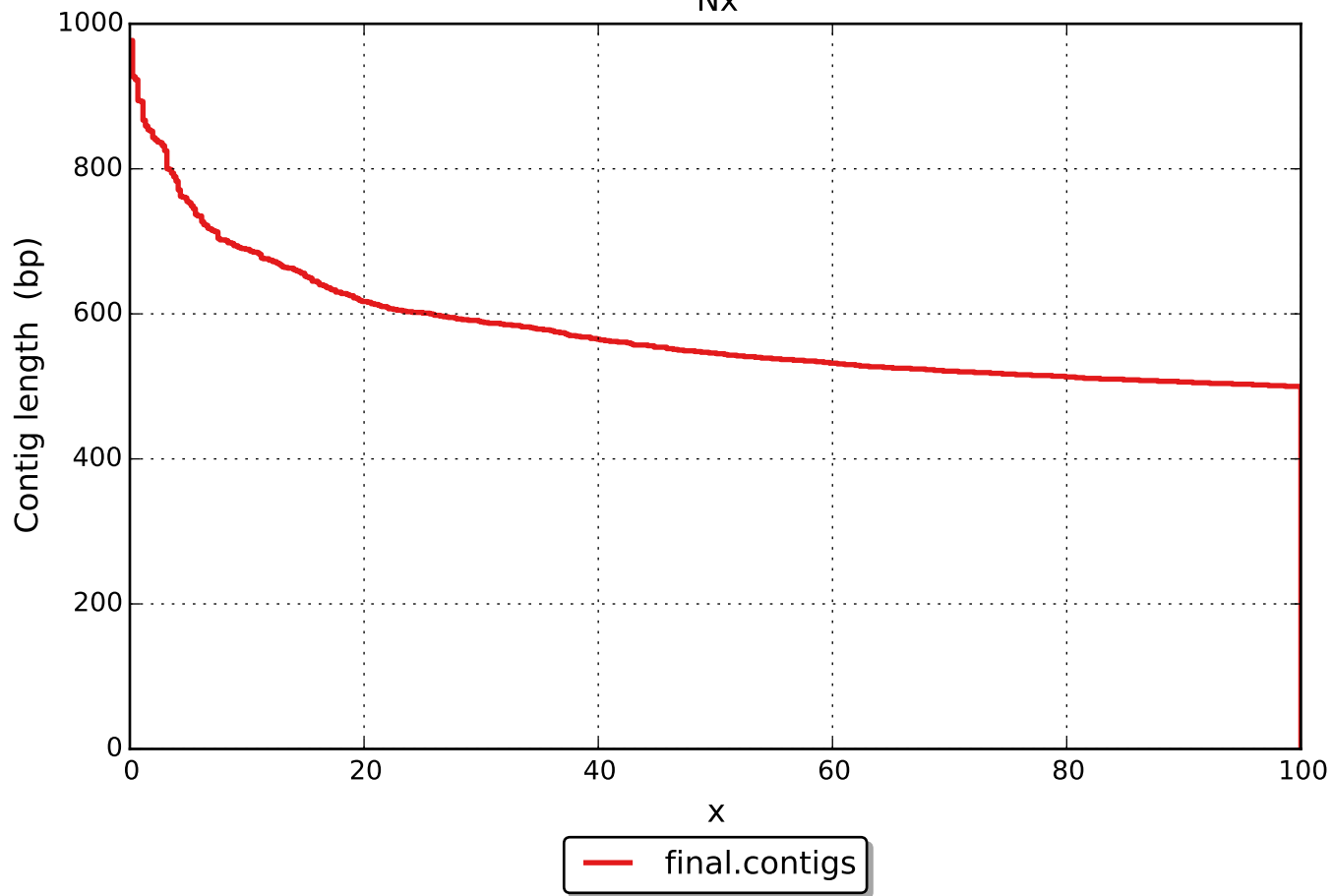
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

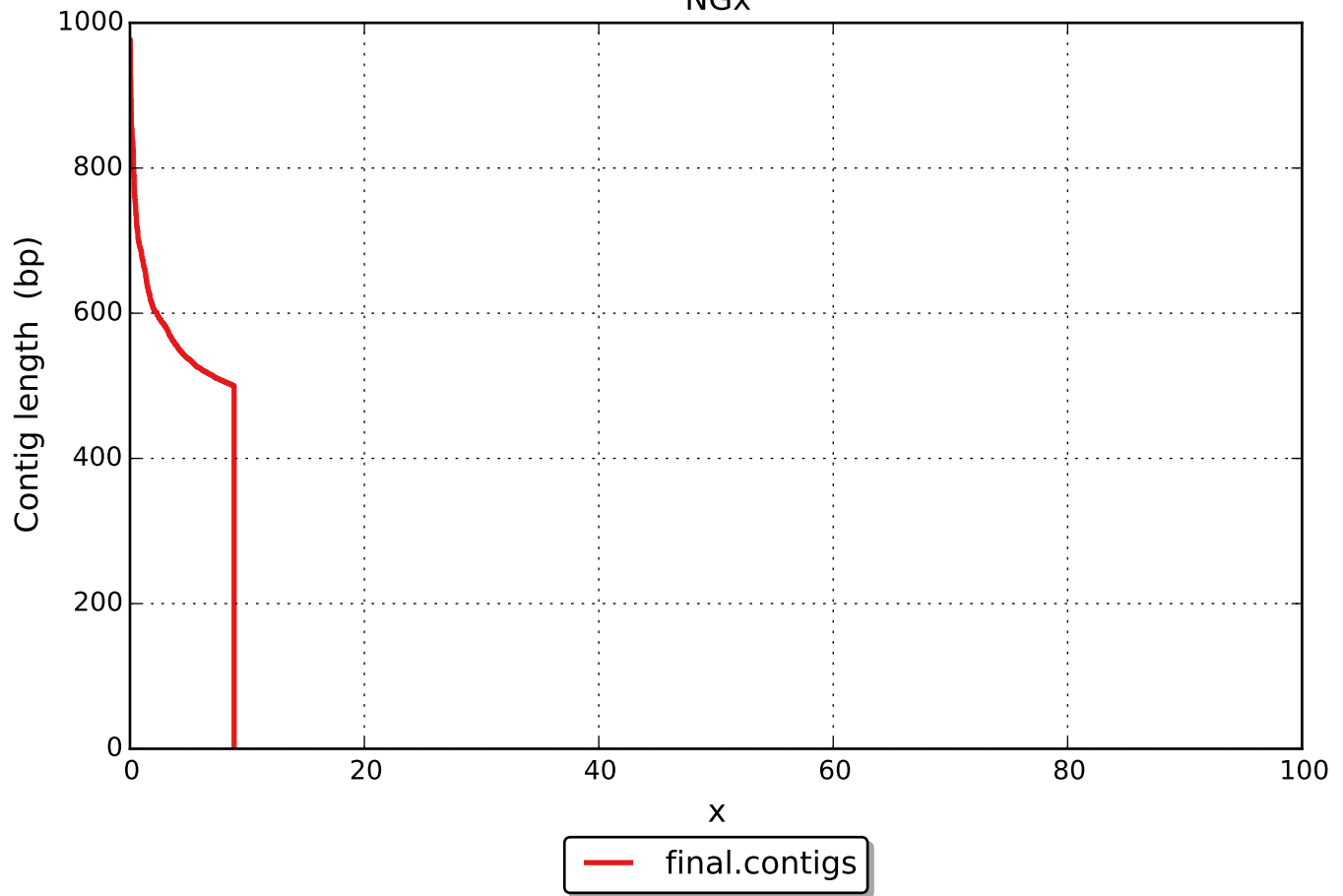
	final.contigs
# fully unaligned contigs	11
Fully unaligned length	6110
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	266
# N's	0

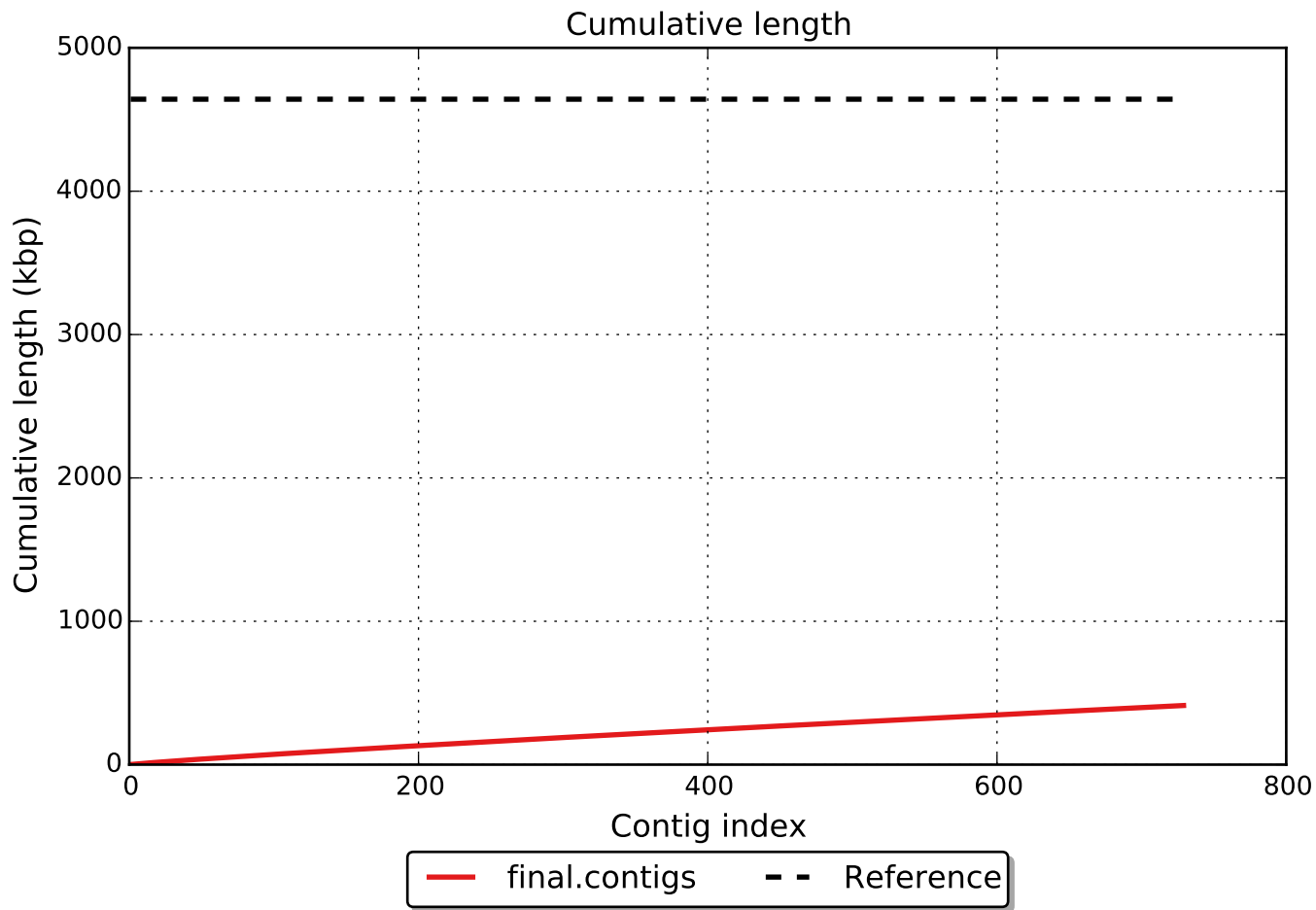
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

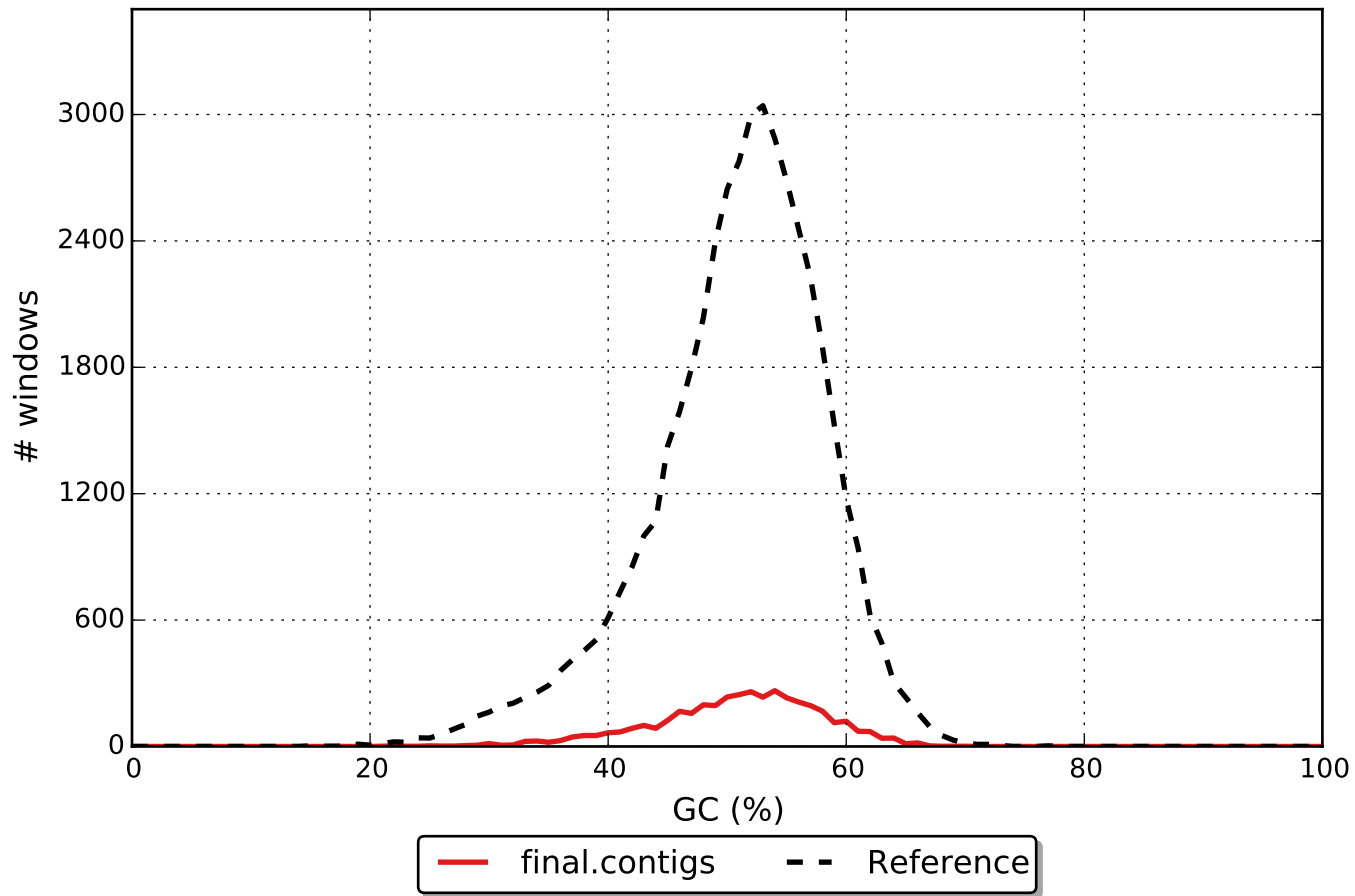


NGx

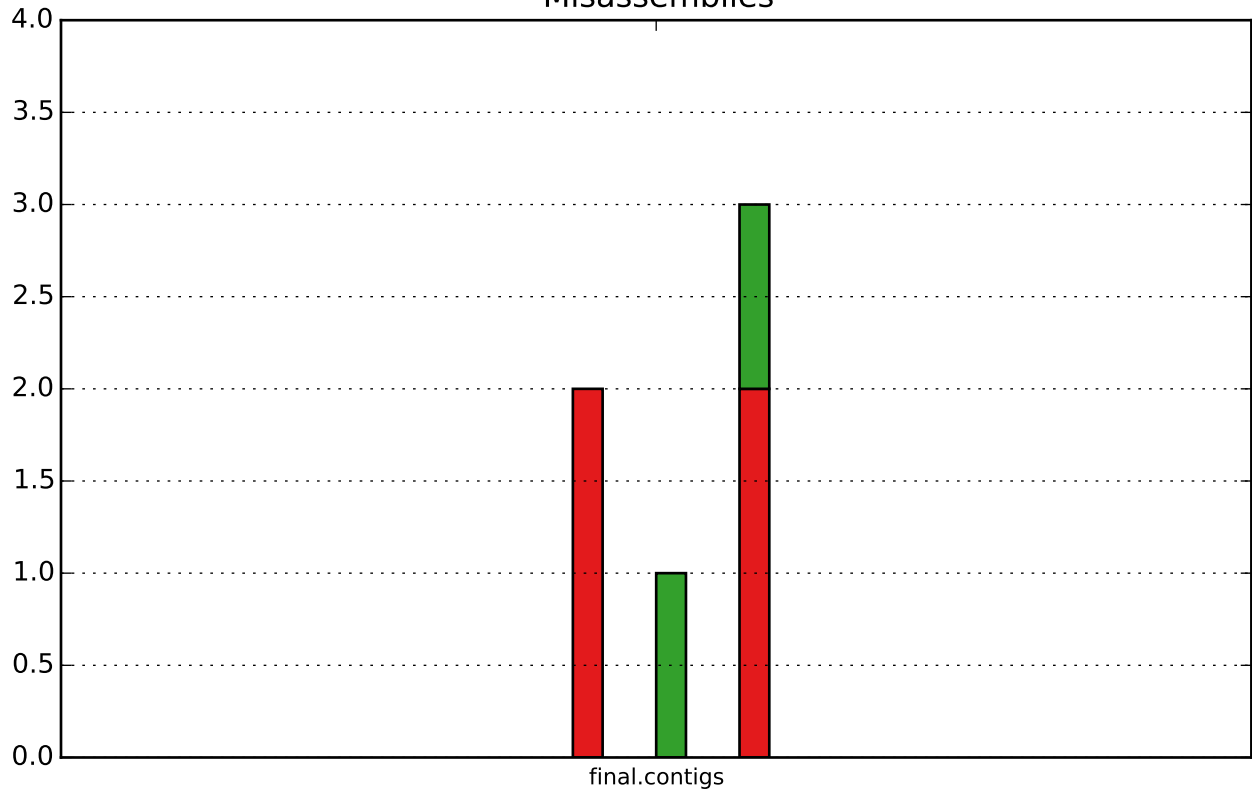




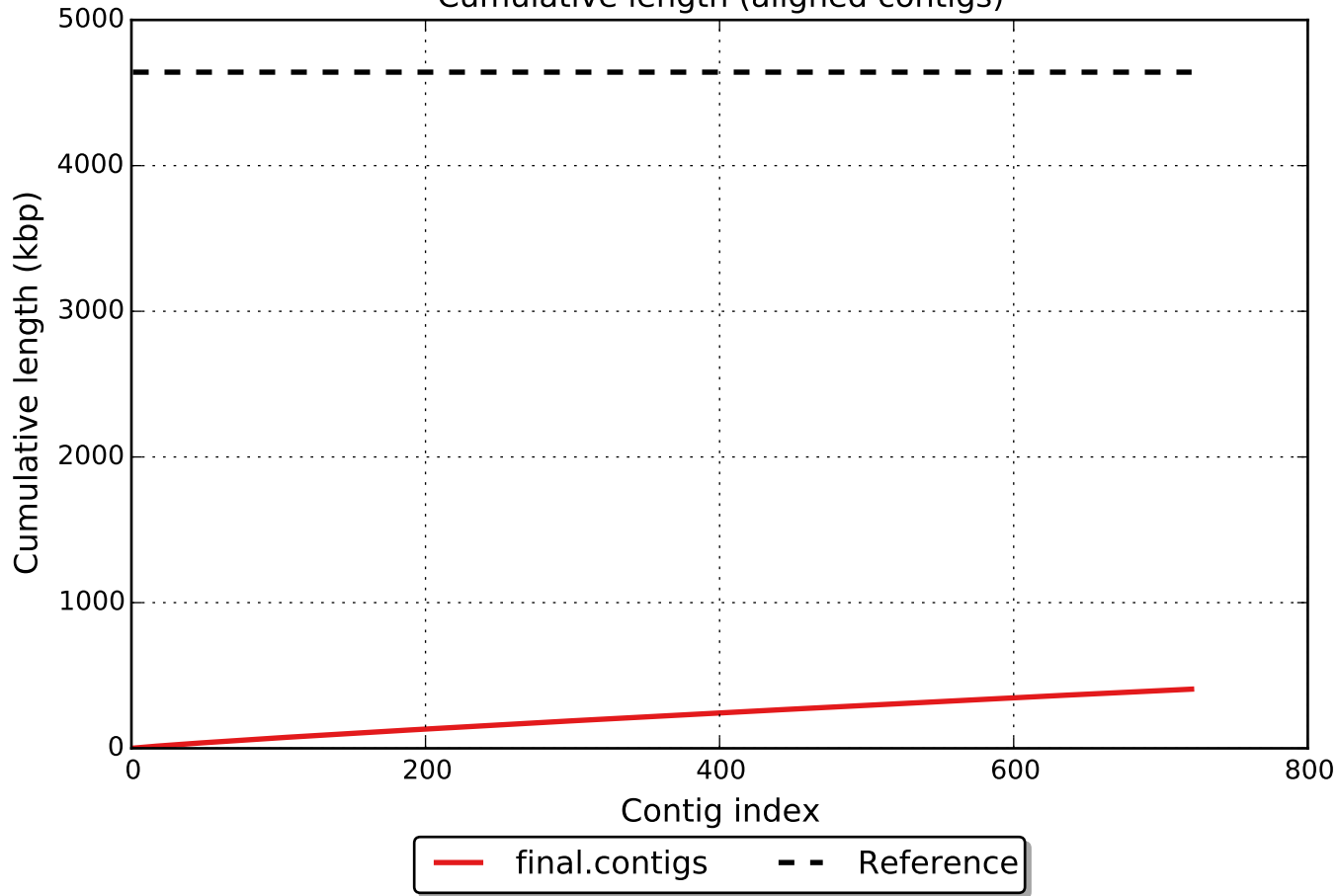
GC content



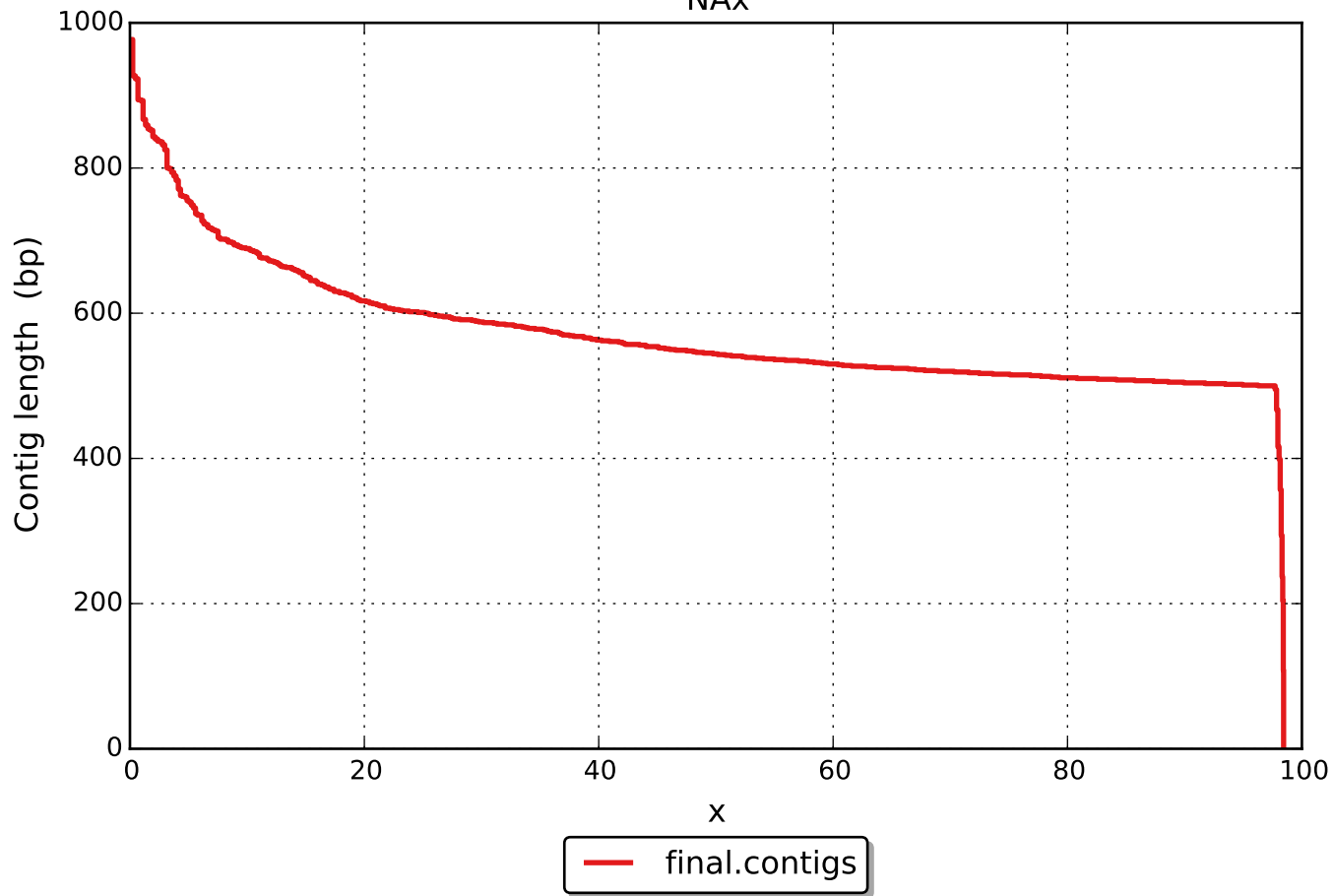
Misassemblies



Cumulative length (aligned contigs)



NAx



NGAx

