

Report

	final.contigs
# contigs (≥ 0 bp)	3594
# contigs (≥ 1000 bp)	576
# contigs (≥ 5000 bp)	0
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 0 bp)	2463603
Total length (≥ 1000 bp)	810277
Total length (≥ 5000 bp)	0
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	2143
Largest contig	3631
Total length	1898792
Reference length	4641652
GC (%)	50.87
Reference GC (%)	50.79
N50	910
N75	683
L50	722
L75	1327
# misassemblies	8
# misassembled contigs	8
Misassembled contigs length	11178
# local misassemblies	2
# unaligned contigs	1 + 4 part
Unaligned length	1005
Genome fraction (%)	40.879
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	14.34
# indels per 100 kbp	0.90
Largest alignment	3631
NA50	909
NGA50	-
NA75	682
LA50	724
LA75	1330

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	8
# relocations	8
# translocations	0
# inversions	0
# misassembled contigs	8
Misassembled contigs length	11178
# local misassemblies	2
# mismatches	272
# indels	17
# short indels	17
# long indels	0
Indels length	24

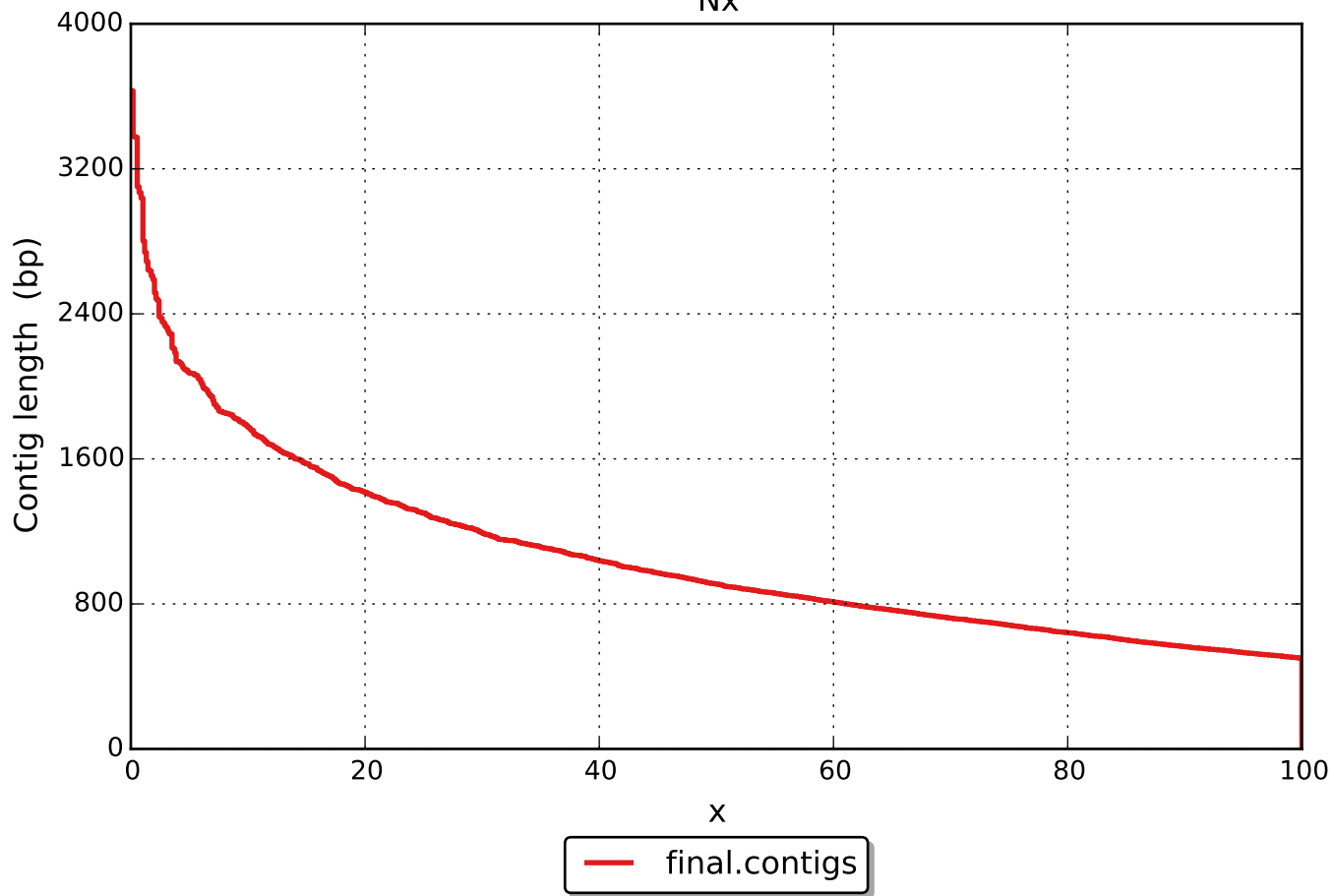
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

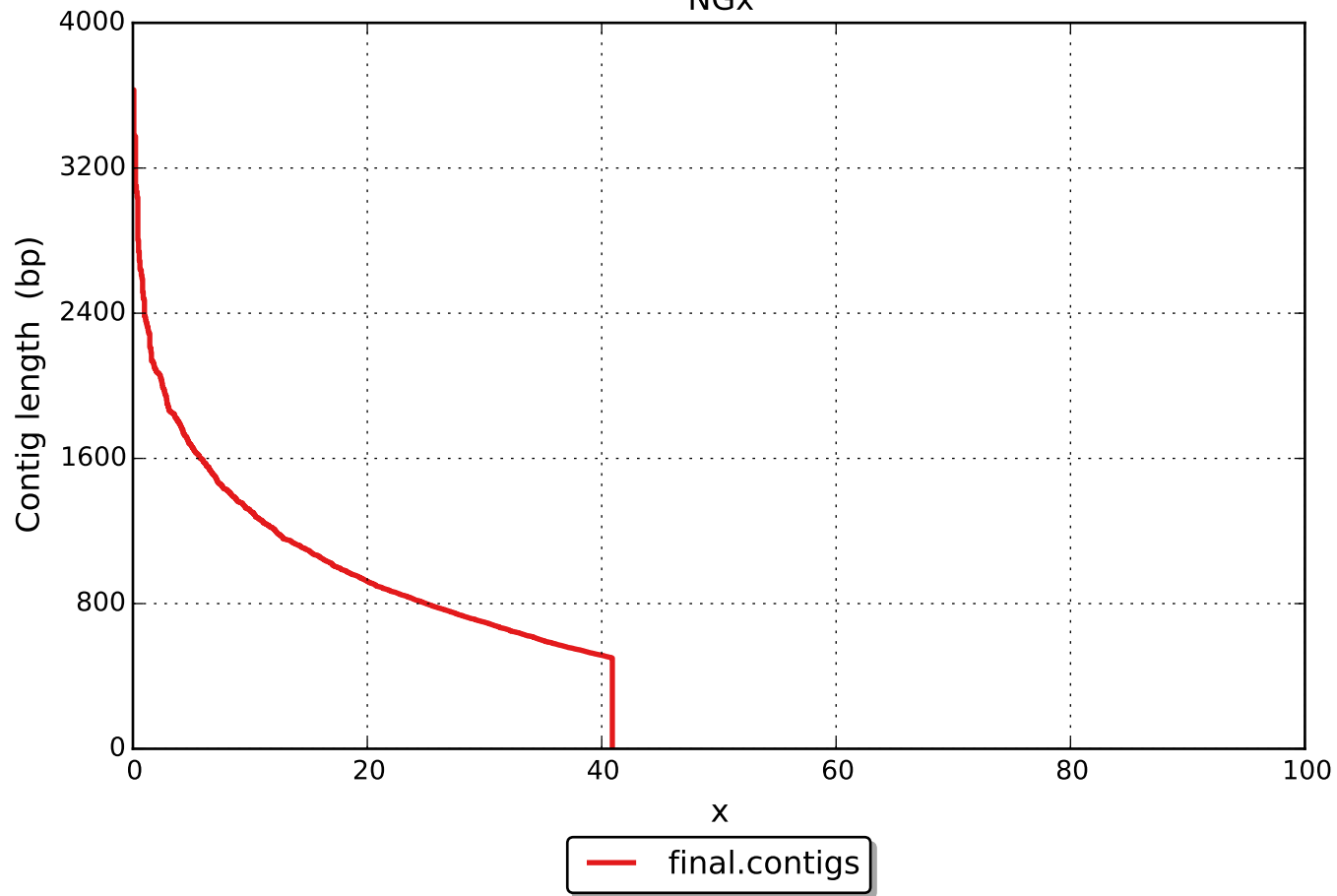
	final.contigs
# fully unaligned contigs	1
Fully unaligned length	708
# partially unaligned contigs	4
# with misassembly	0
# both parts are significant	0
Partially unaligned length	297
# N's	0

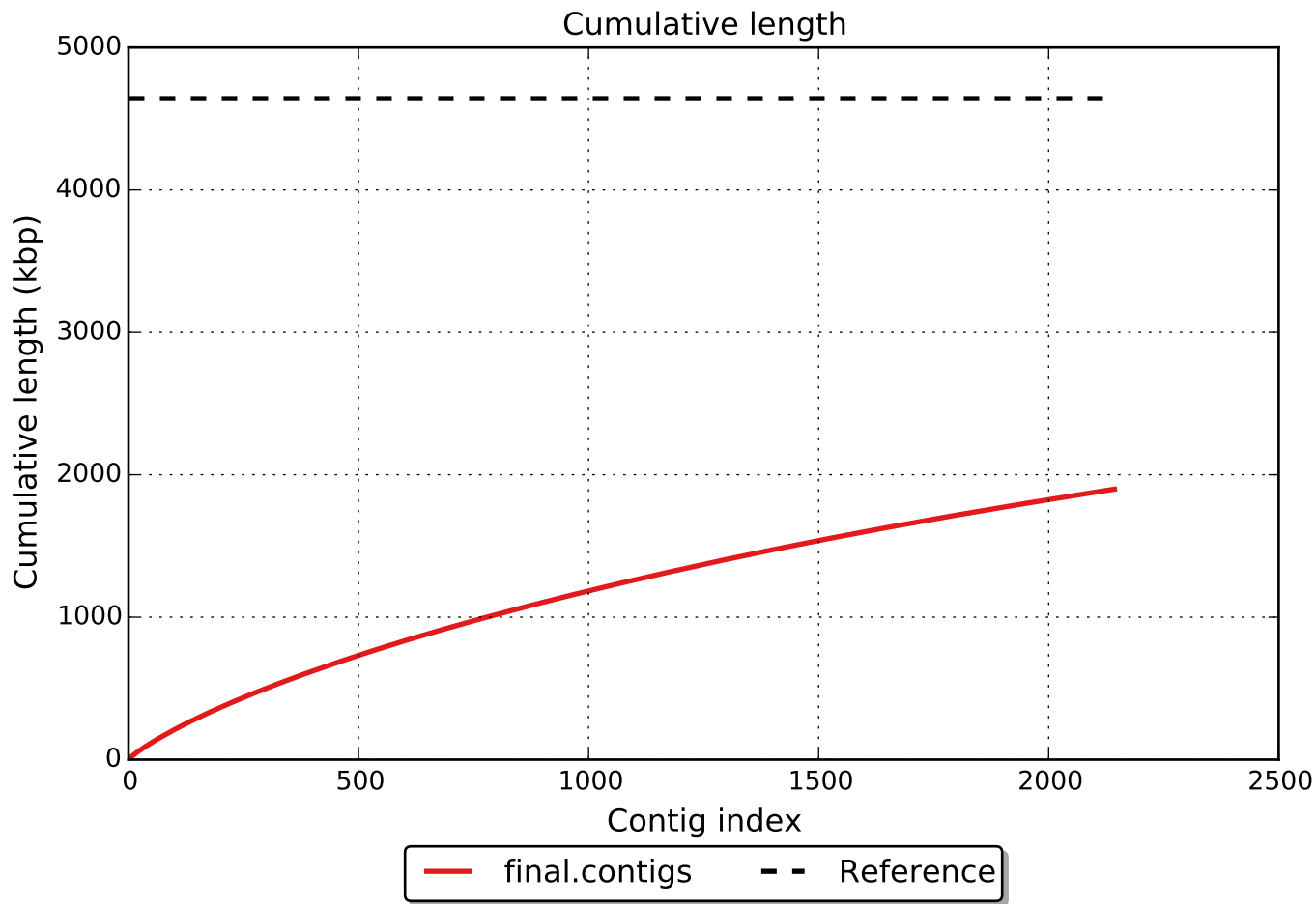
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

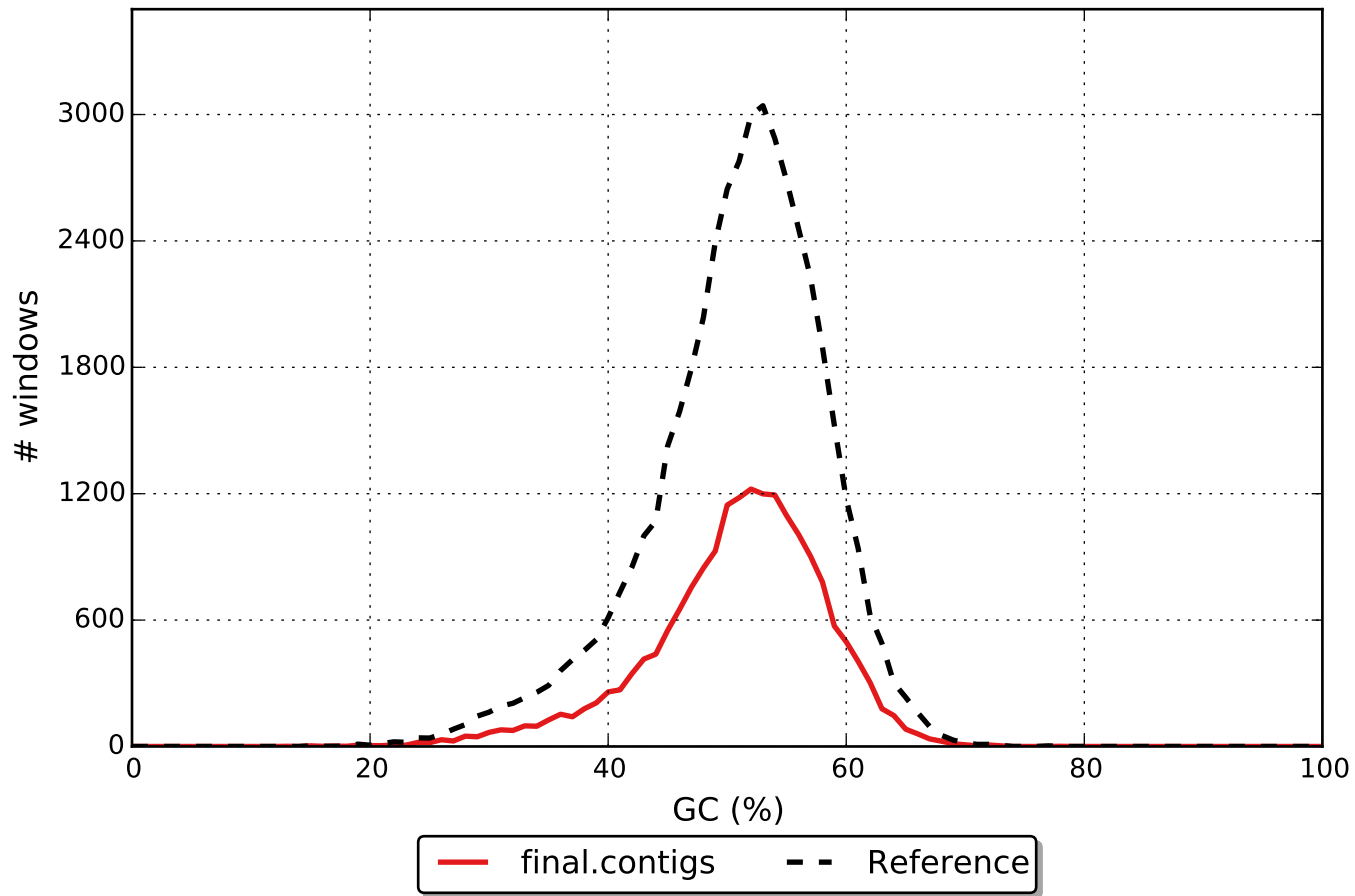


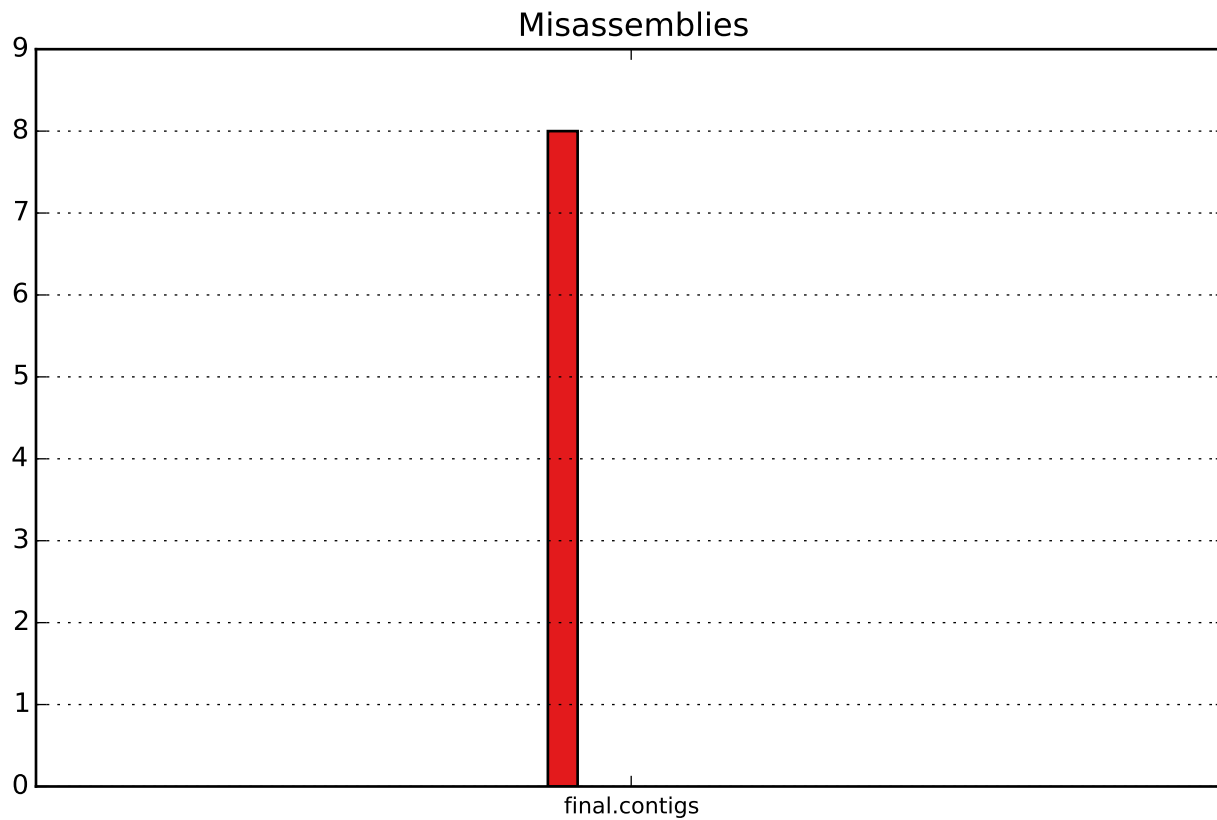
NGx



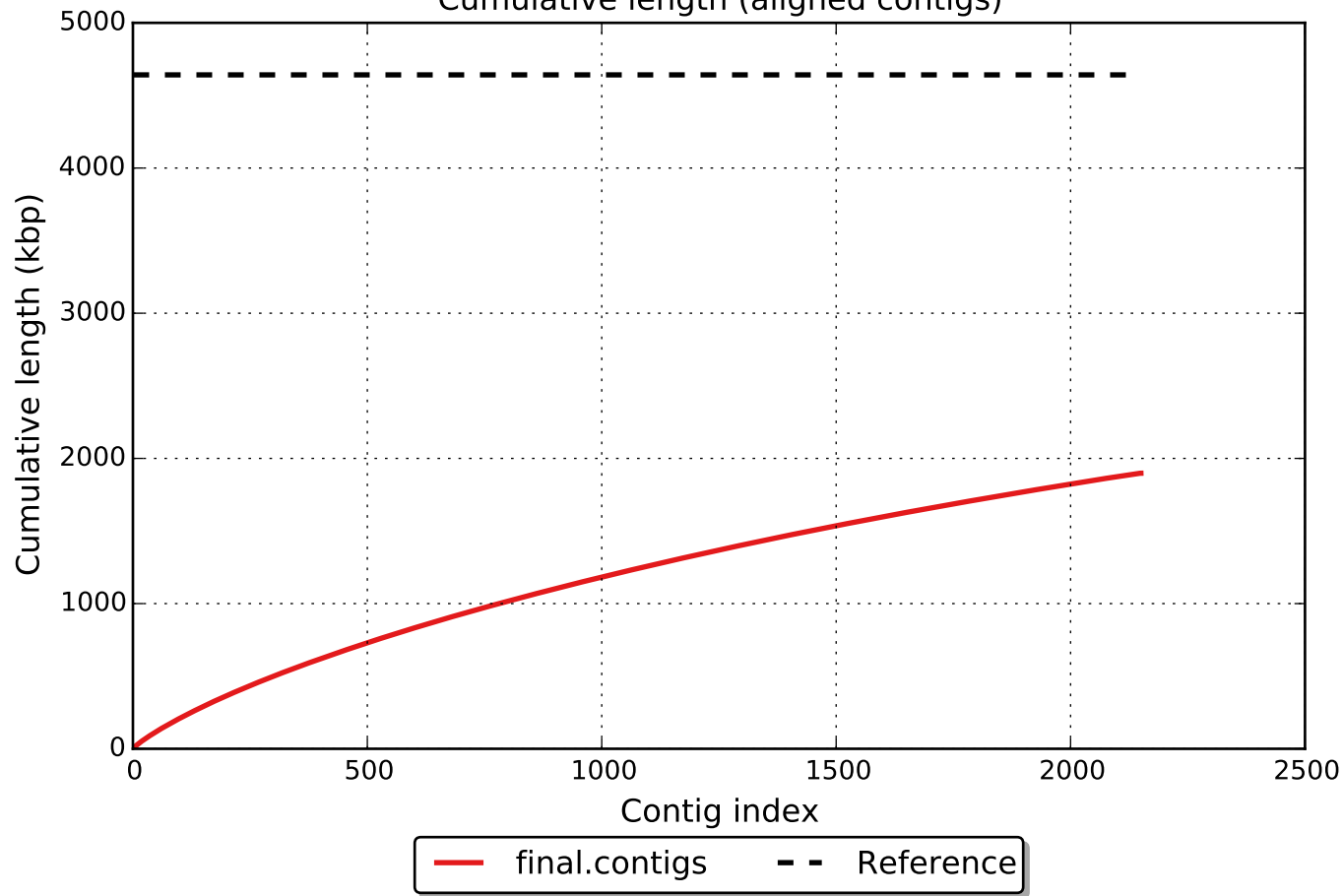


GC content

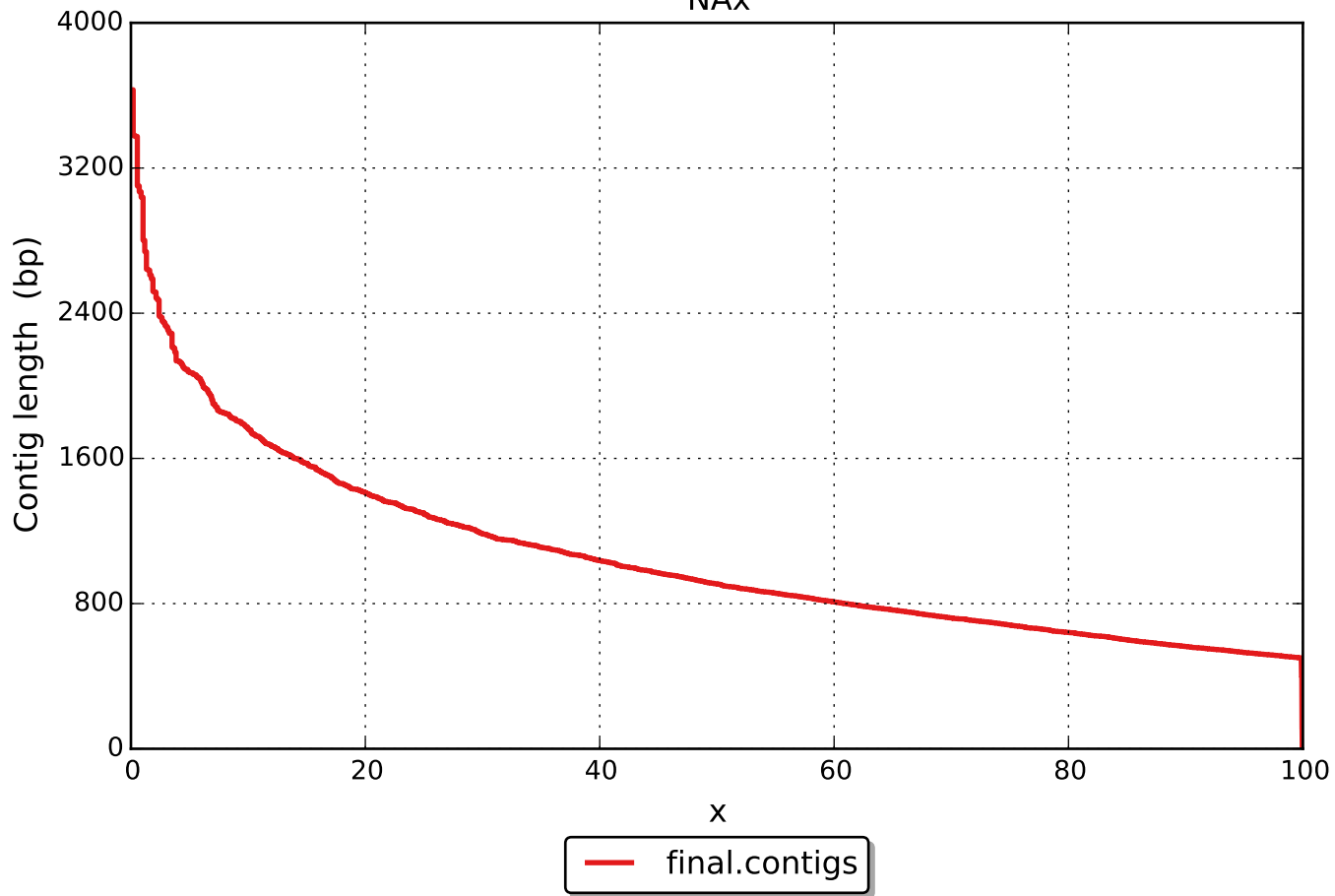




Cumulative length (aligned contigs)



NAx



NGAx

