

Report

	final.contigs
# contigs (≥ 1000 bp)	5
# contigs (≥ 5000 bp)	0
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 1000 bp)	8643
Total length (≥ 5000 bp)	0
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	49
Largest contig	2127
Total length	36029
Reference length	4641652
GC (%)	51.65
Reference GC (%)	50.79
N50	683
N75	547
L50	17
L75	32
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	1650
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	279
Genome fraction (%)	0.770
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	604.36
# indels per 100 kbp	8.39
Largest alignment	2127
NA50	643
NGA50	-
NA75	545
LA50	18
LA75	33

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	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	1650
# local misassemblies	0
# mismatches	216
# indels	3
# short indels	3
# long indels	0
Indels length	6

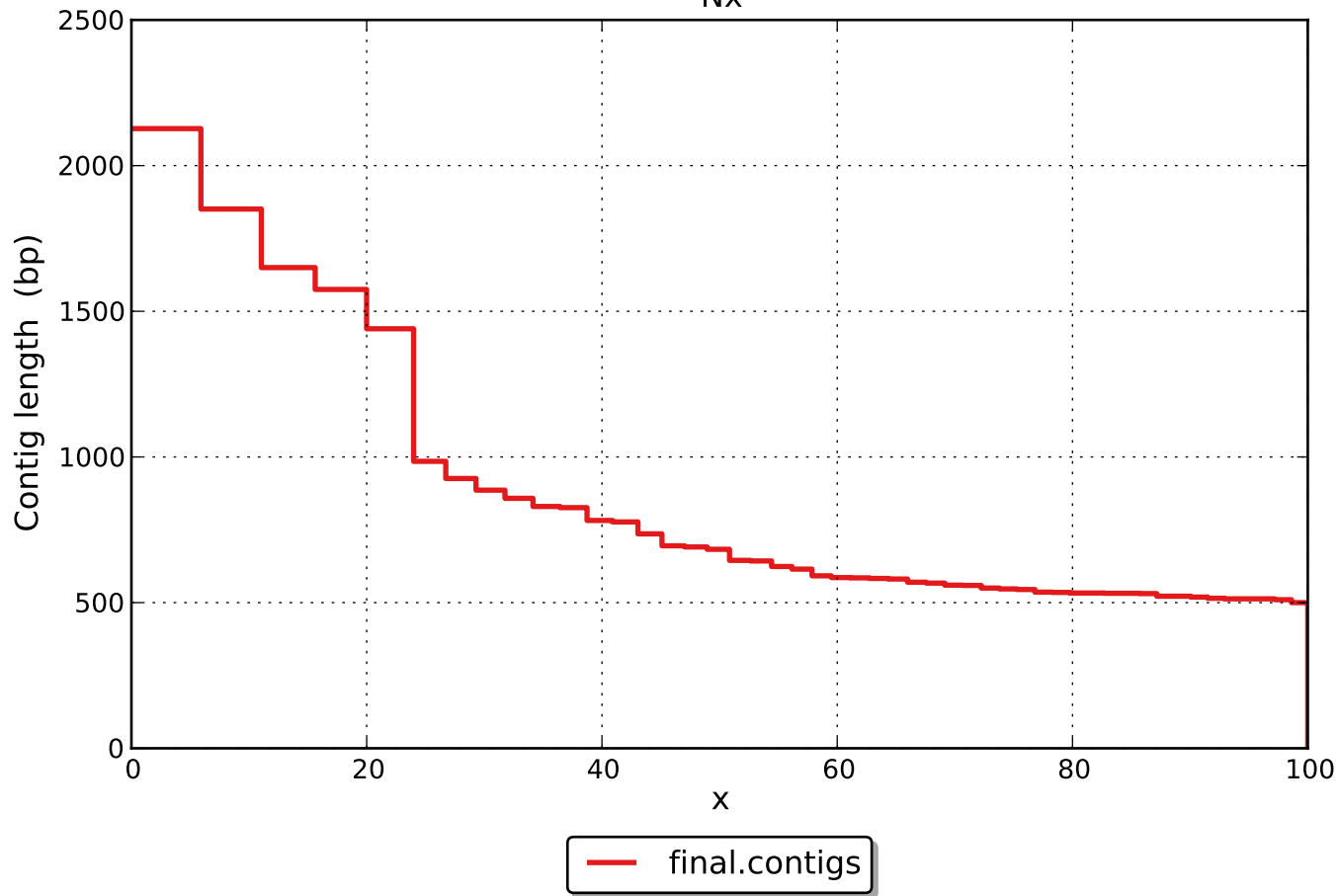
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

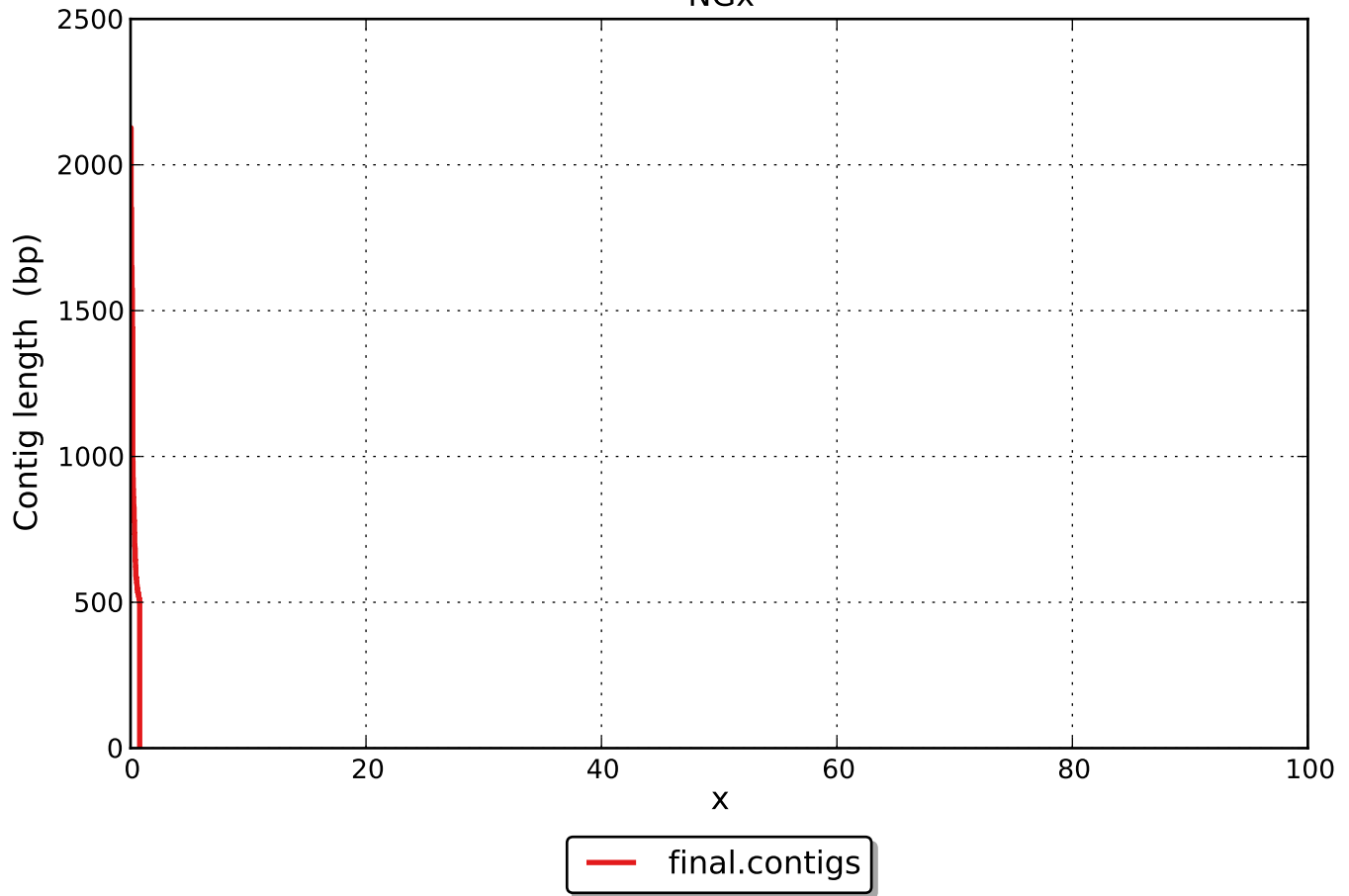
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	279
# N's	0

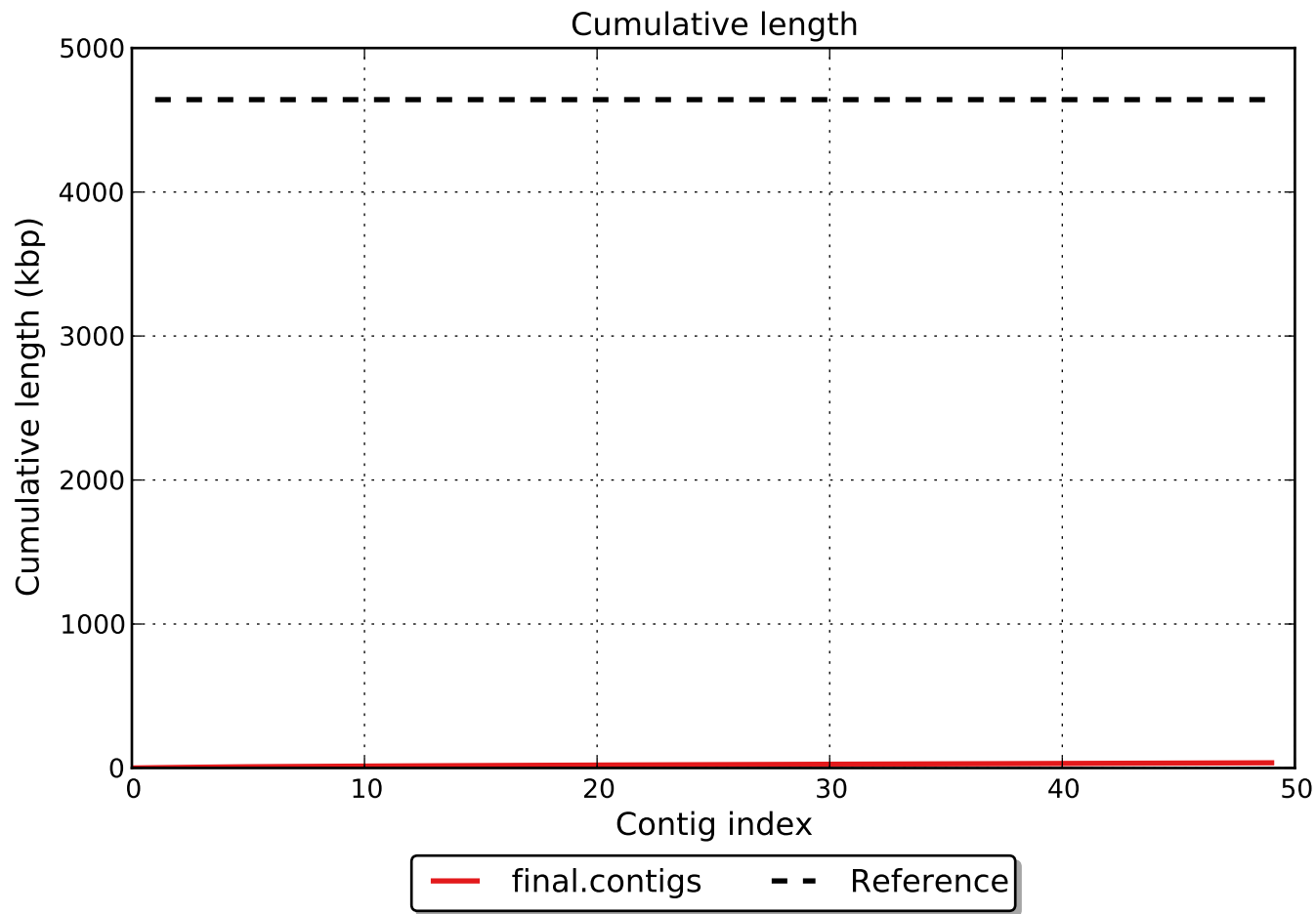
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

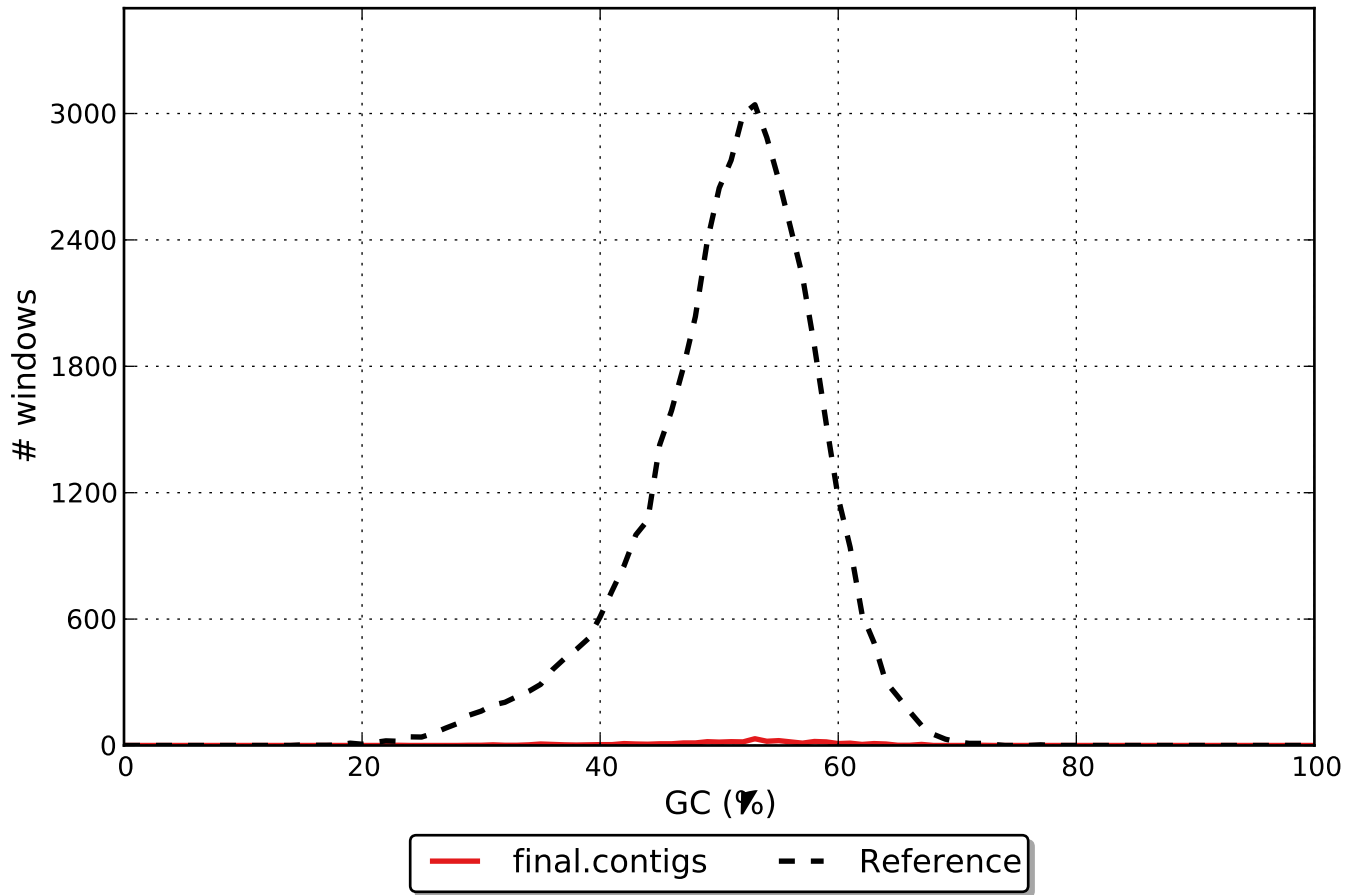


NGx



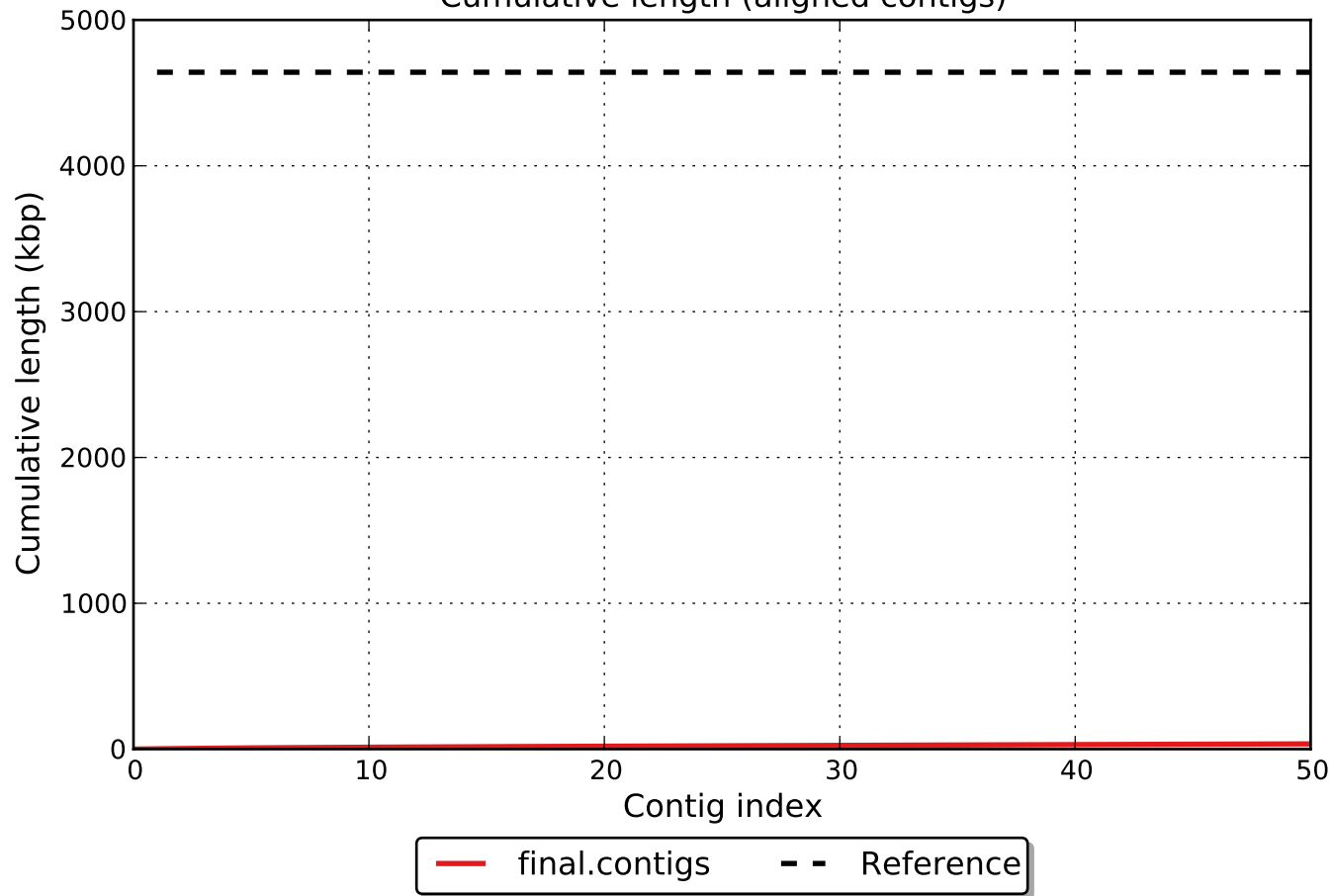


GC content

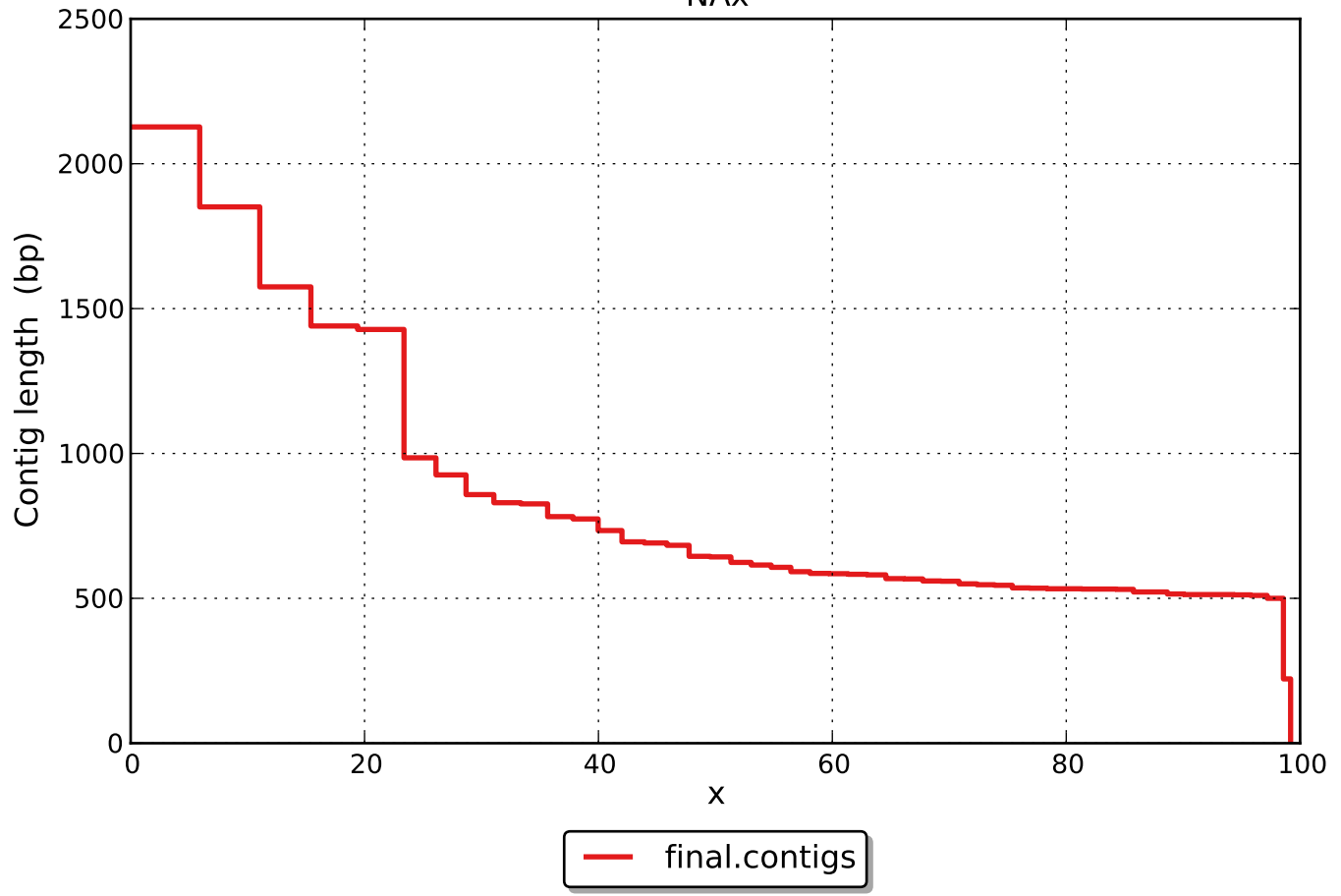




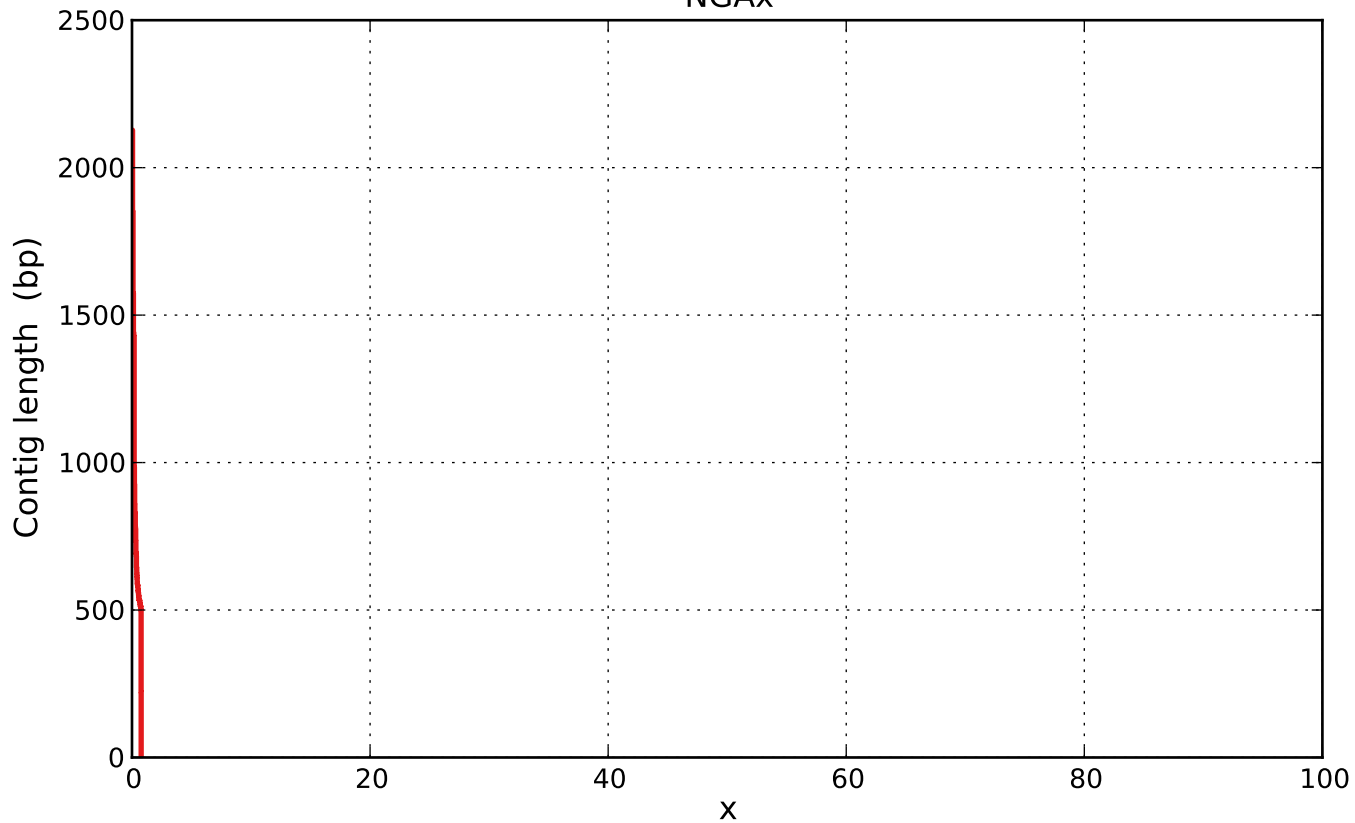
Cumulative length (aligned contigs)



NAx



NGAx



— final.contigs