

Report

	final.contigs
# contigs (≥ 1000 bp)	453
# contigs (≥ 5000 bp)	0
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 1000 bp)	604859
Total length (≥ 5000 bp)	0
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	2386
Largest contig	4215
Total length	1924254
Reference length	4641652
GC (%)	50.81
Reference GC (%)	50.79
N50	812
N75	631
L50	854
L75	1525
# misassemblies	7
# misassembled contigs	7
Misassembled contigs length	10957
# local misassemblies	5
# unaligned contigs	0 + 6 part
Unaligned length	974
Genome fraction (%)	41.403
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	15.56
# indels per 100 kbp	0.83
Largest alignment	4215
NA50	811
NGA50	-
NA75	631
LA50	856
LA75	1529

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	7
# relocations	6
# translocations	0
# inversions	1
# possibly misassembled contigs	1
# misassembled contigs	7
Misassembled contigs length	10957
# local misassemblies	5
# mismatches	299
# indels	16
# short indels	15
# long indels	1
Indels length	67

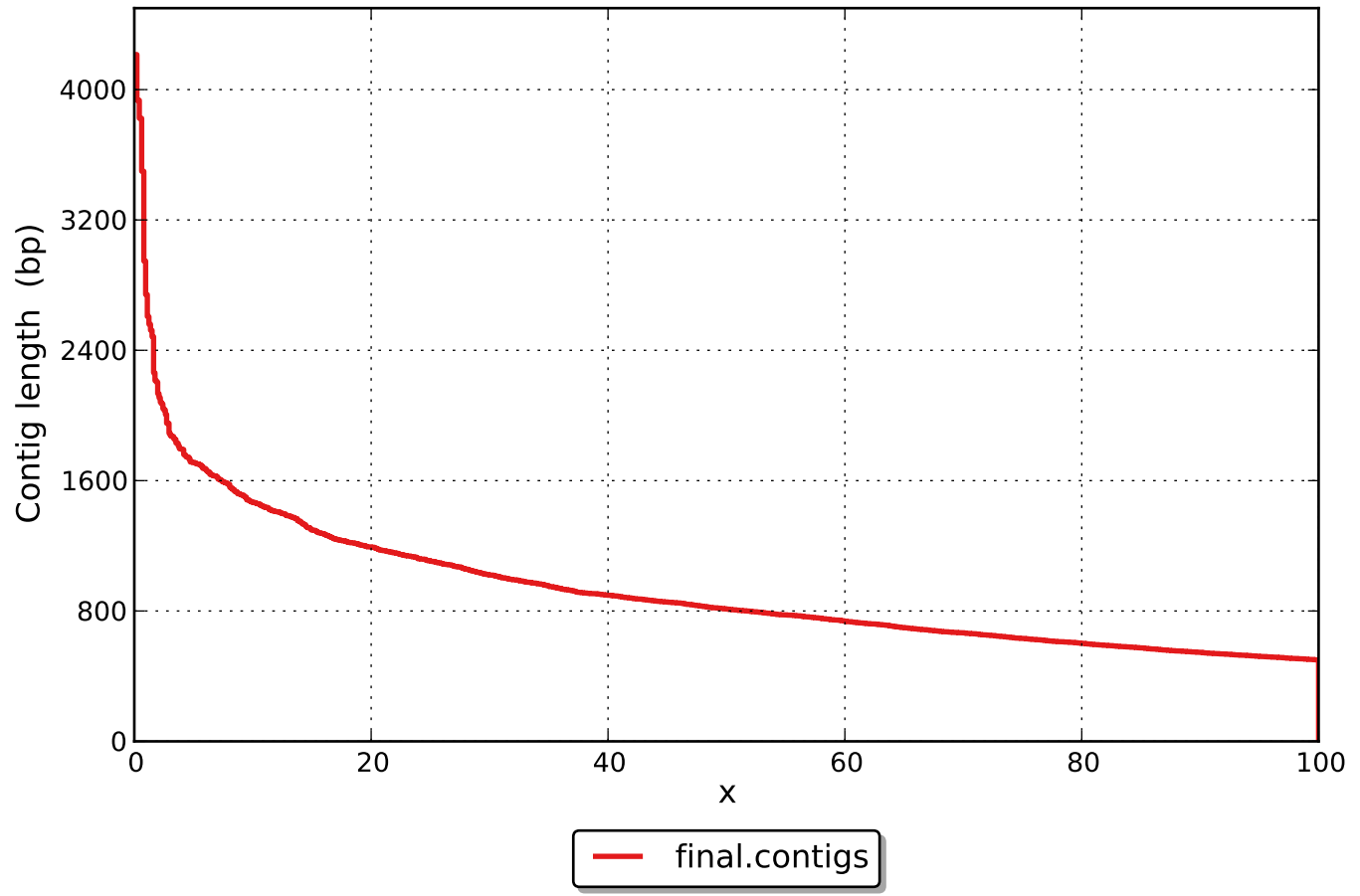
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

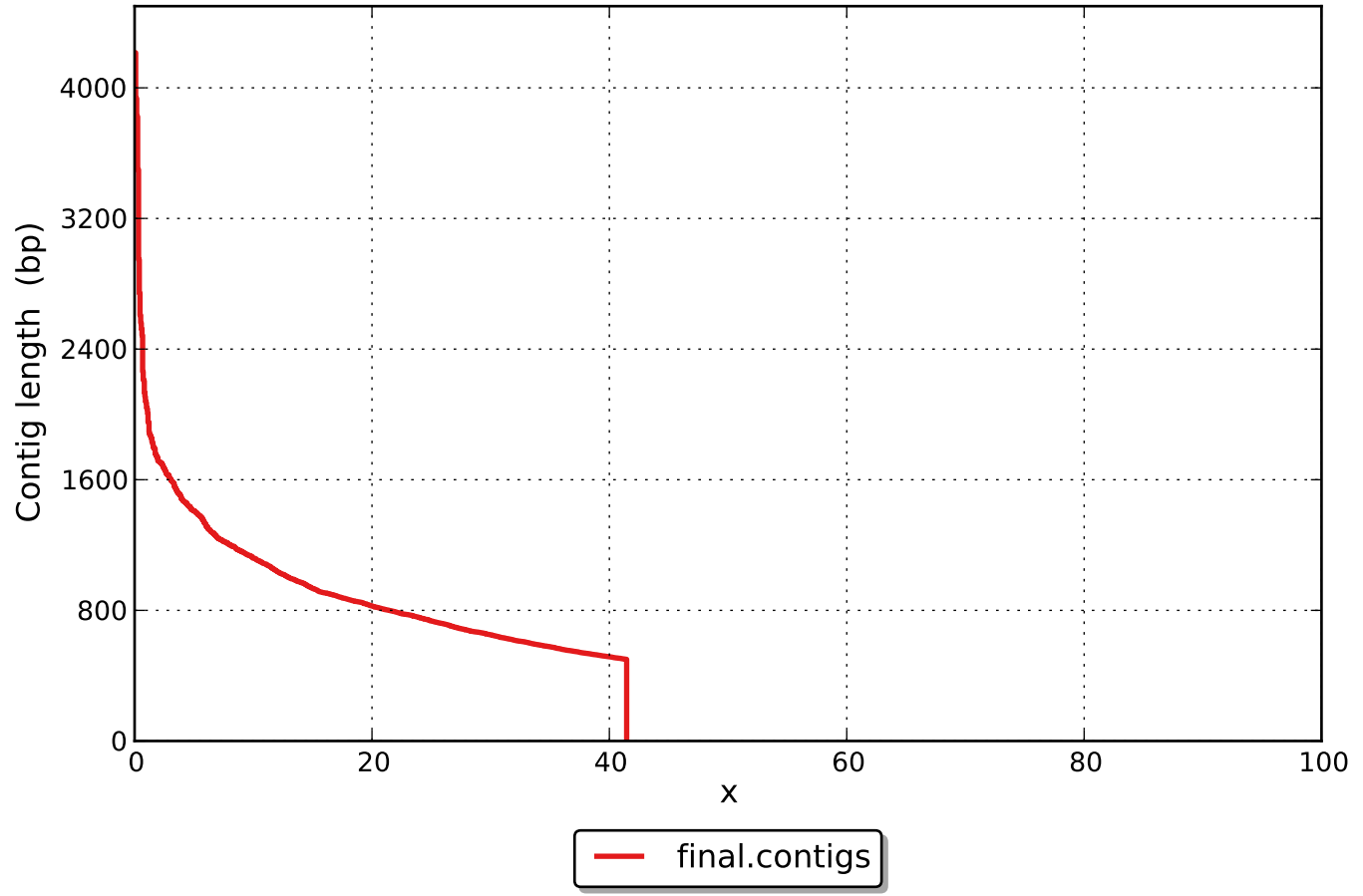
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	6
# with misassembly	0
# both parts are significant	1
Partially unaligned length	974
# N's	0

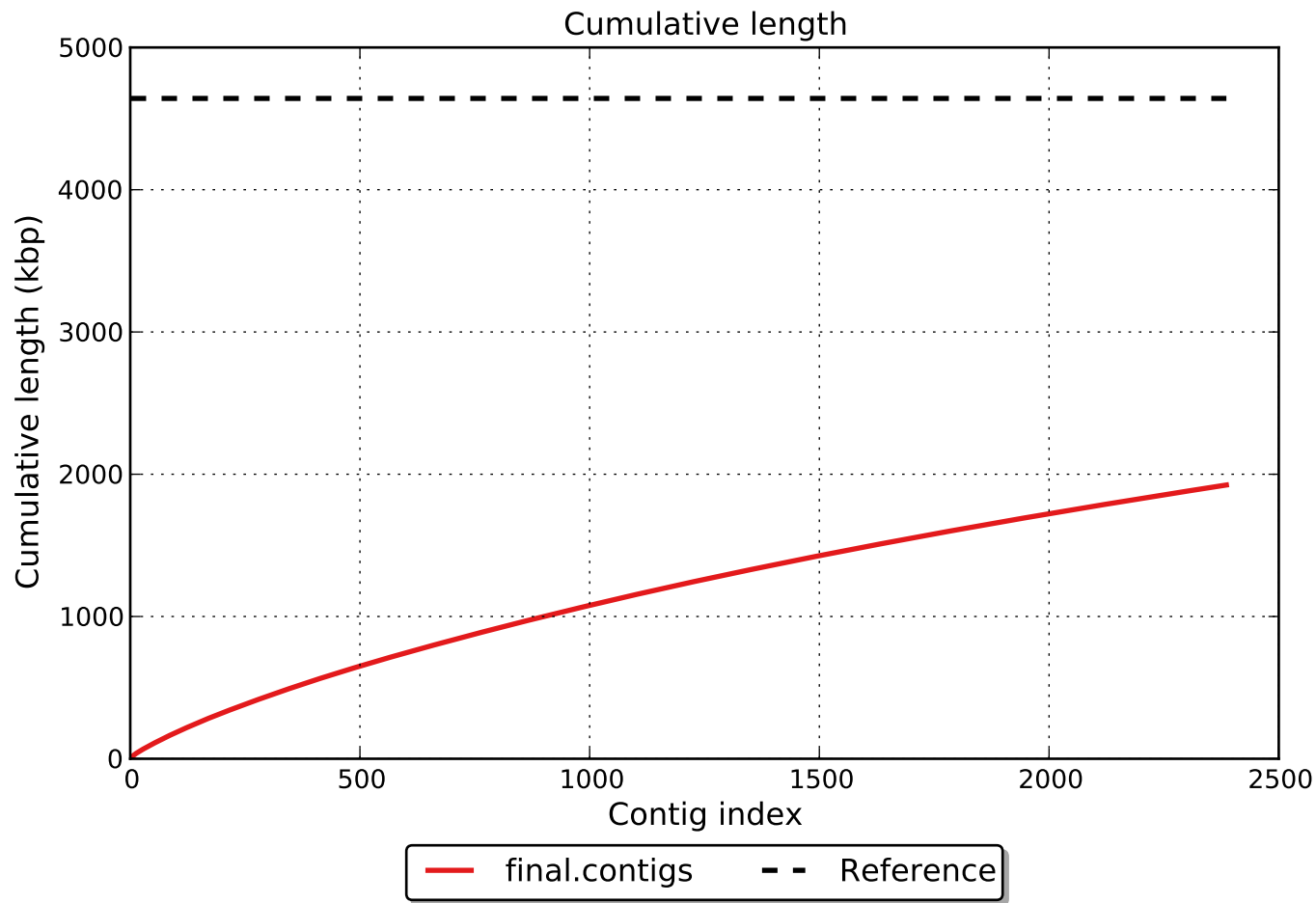
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

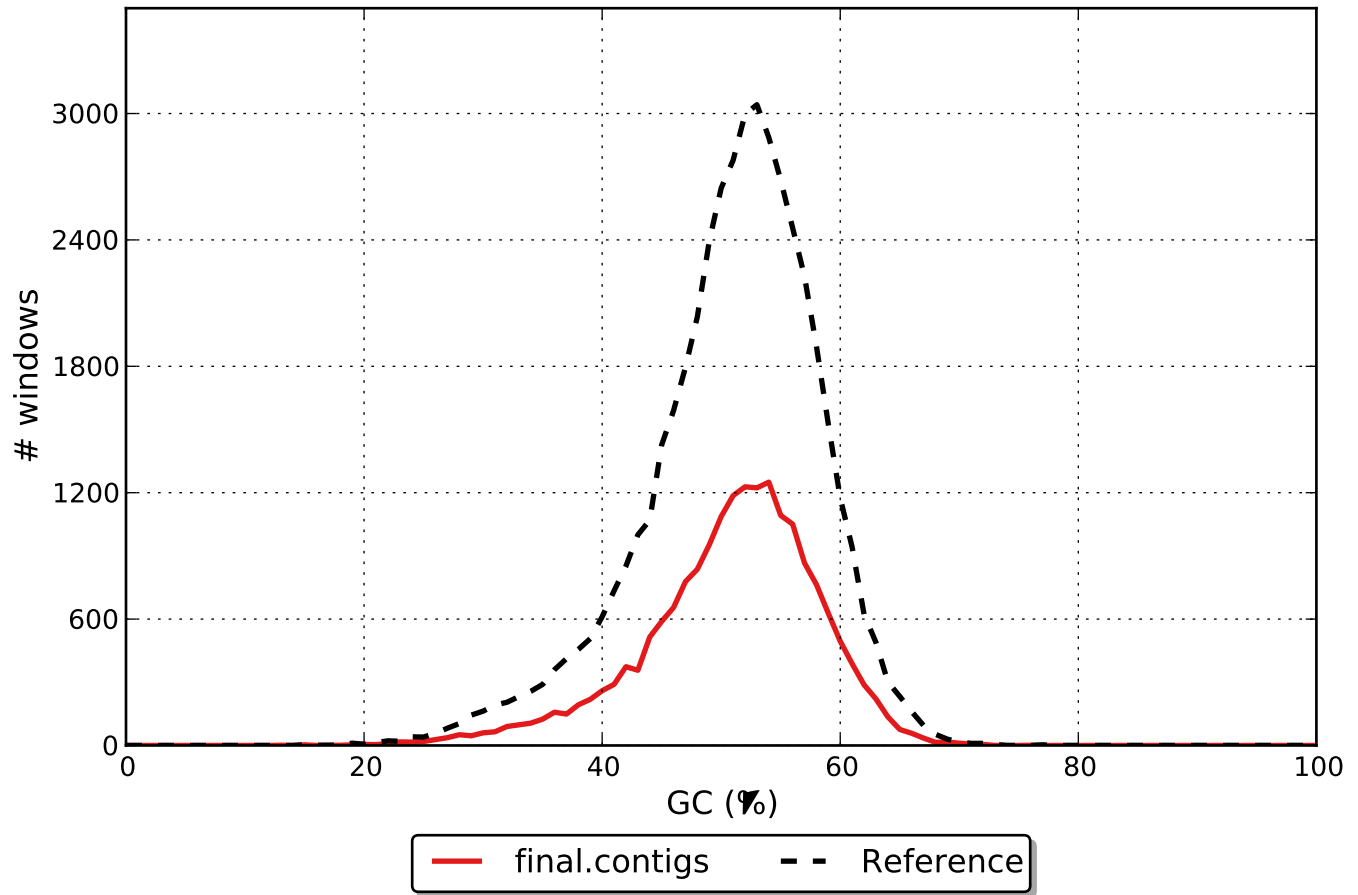


NGx

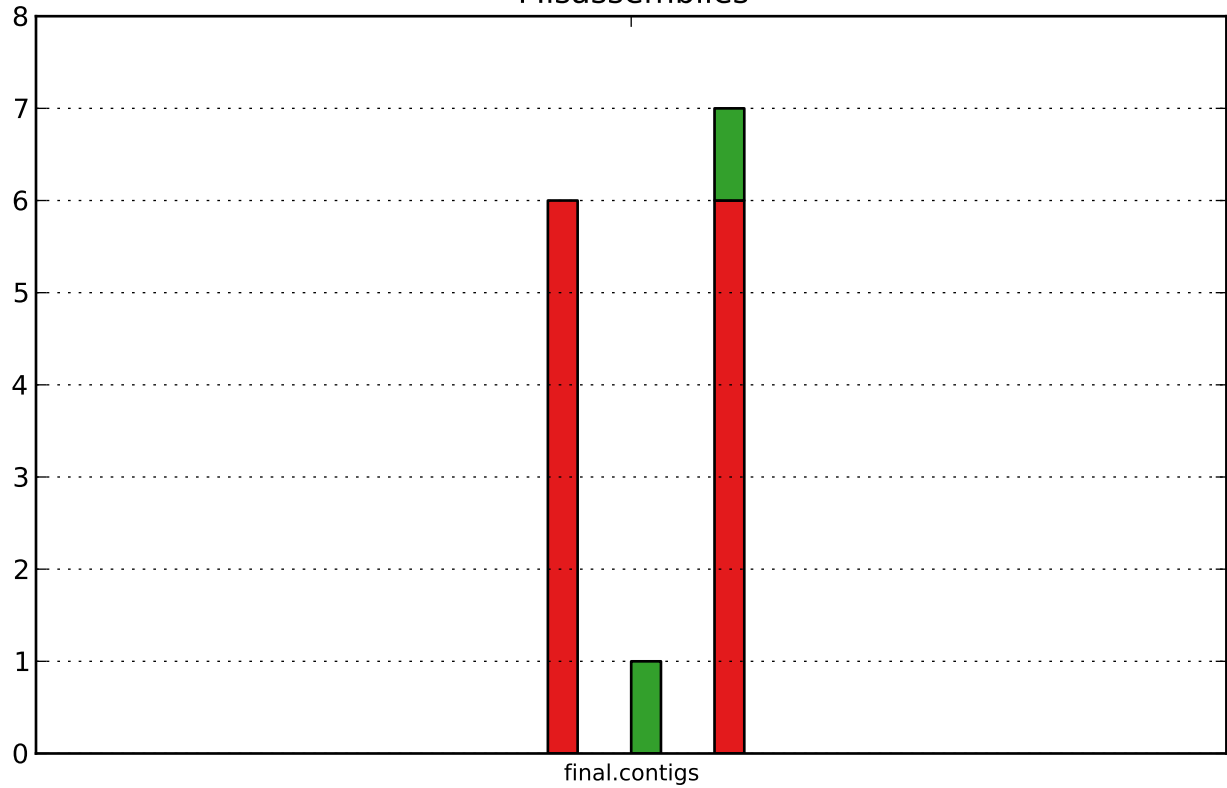




GC content



Misassemblies

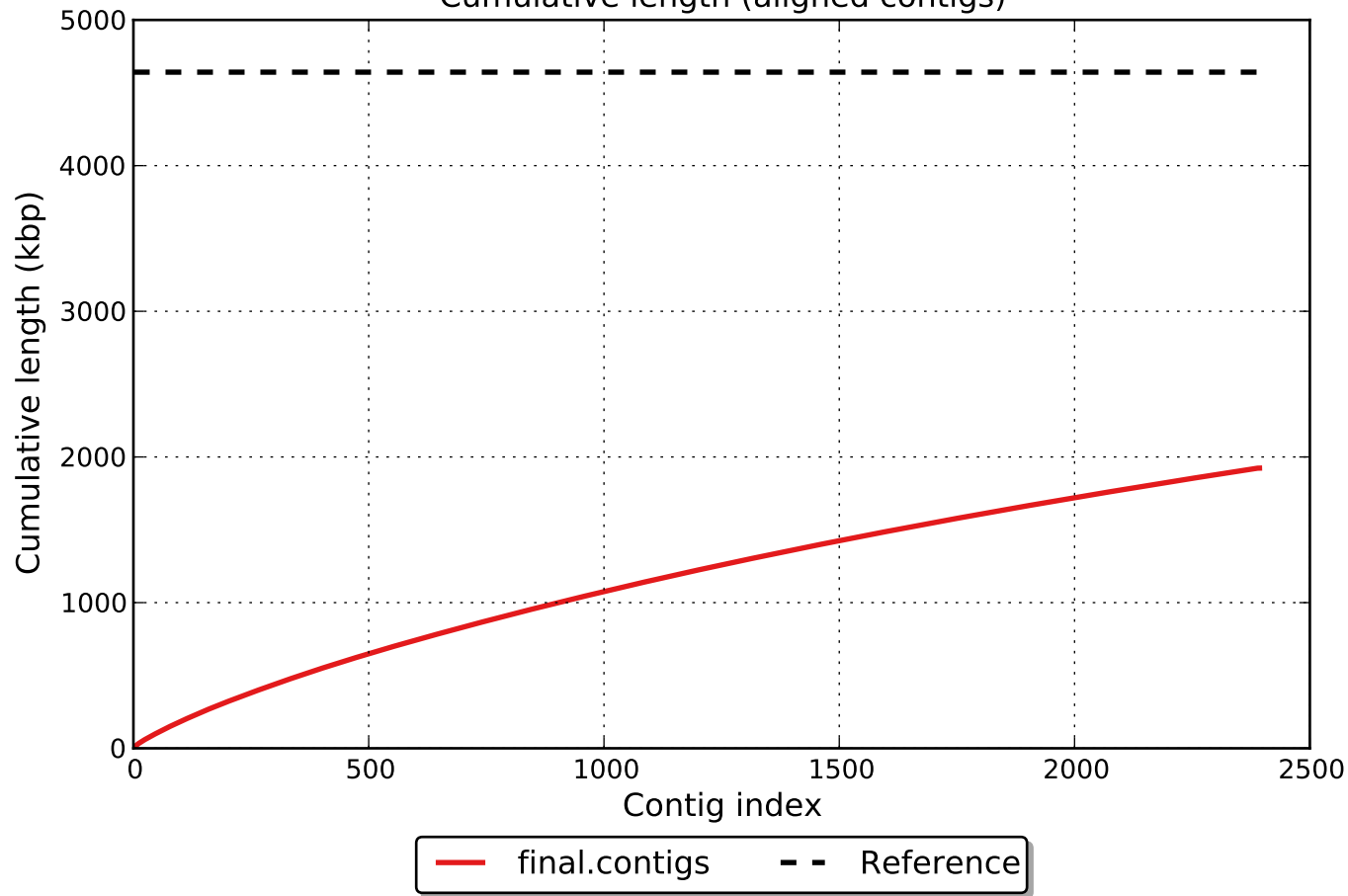


relocations

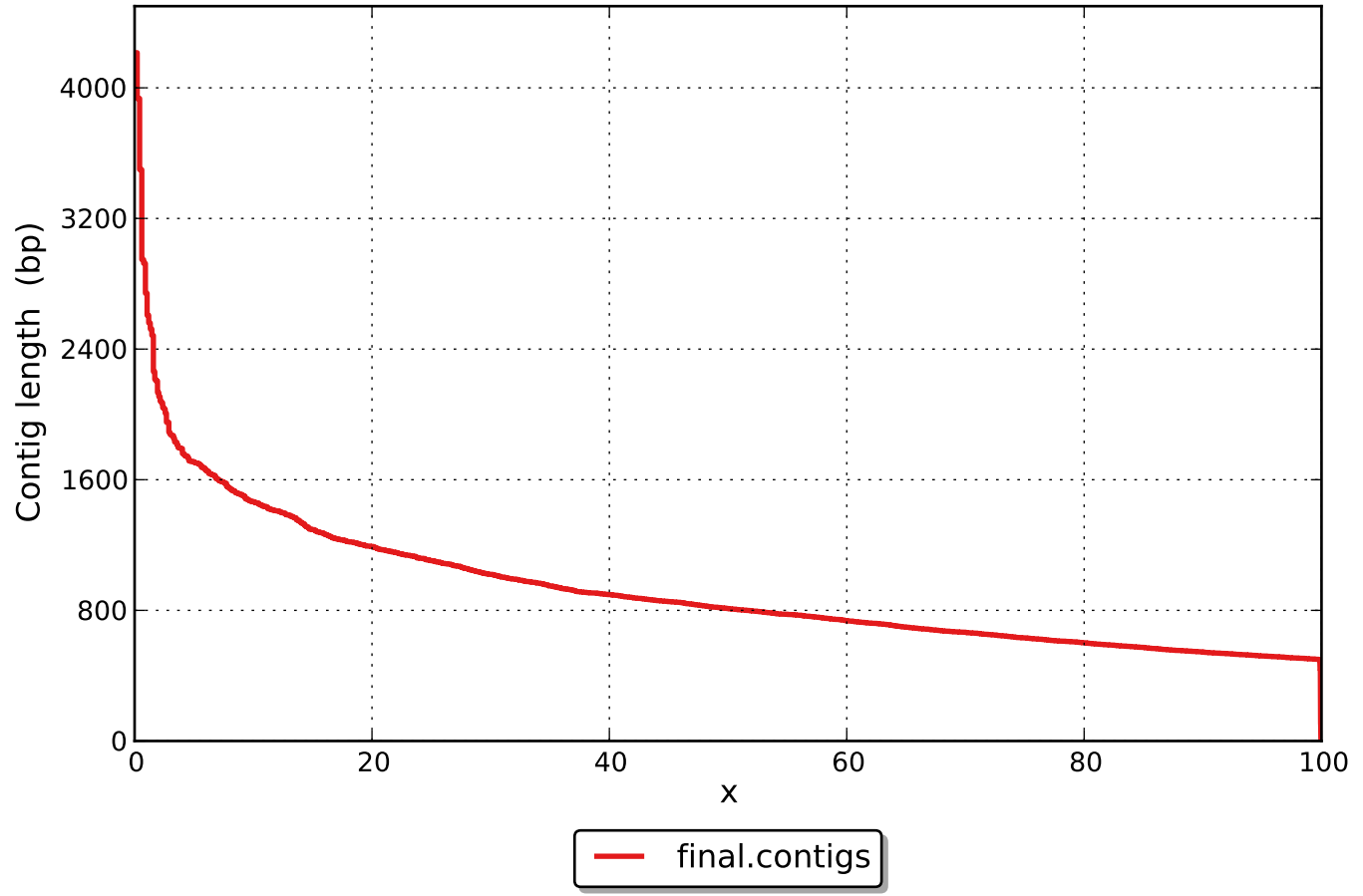


inversions

Cumulative length (aligned contigs)



NAx



NGAx

