

Report

	final.contigs
# contigs (>= 0 bp)	143
# contigs (>= 1000 bp)	90
# contigs (>= 5000 bp)	67
# contigs (>= 10000 bp)	61
# contigs (>= 25000 bp)	50
# contigs (>= 50000 bp)	32
Total length (>= 0 bp)	4595772
Total length (>= 1000 bp)	4573144
Total length (>= 5000 bp)	4517468
Total length (>= 10000 bp)	4472916
Total length (>= 25000 bp)	4305569
Total length (>= 50000 bp)	3657424
# contigs	103
Largest contig	327234
Total length	4581865
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	111999
NG50	111999
N75	57946
NG75	57946
L50	14
LG50	14
L75	29
LG75	29
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	30855
# local misassemblies	4
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.555
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	6.36
# indels per 100 kbp	0.11
Largest alignment	327234
NA50	111999
NGA50	111999
NA75	57943
NGA75	57943
LA50	14
LGA50	14
LA75	29
LGA75	29

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	2
# relocations	2
# translocations	0
# inversions	0
# misassembled contigs	2
Misassembled contigs length	30855
# local misassemblies	4
# mismatches	291
# indels	5
# short indels	5
# long indels	0
Indels length	5

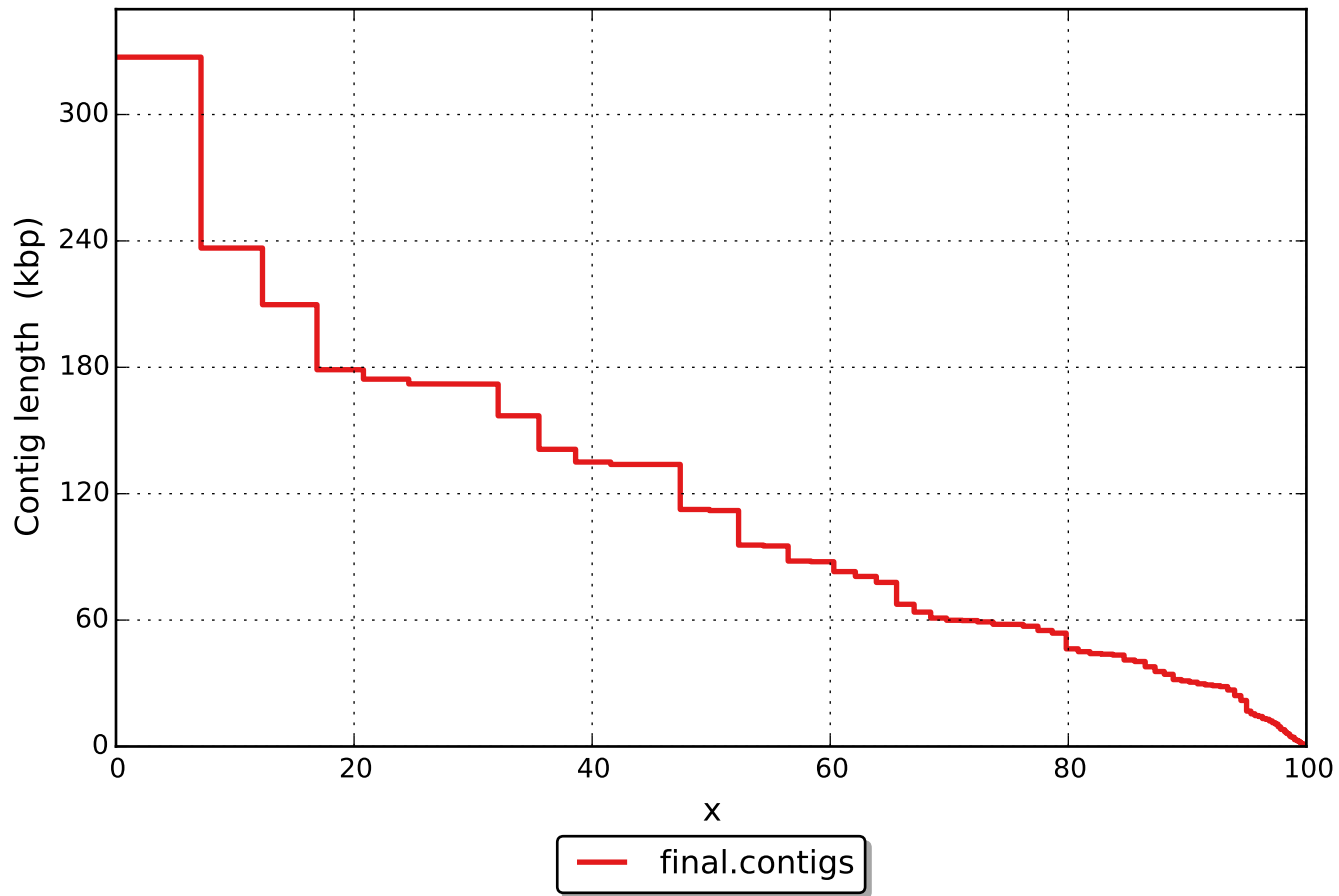
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

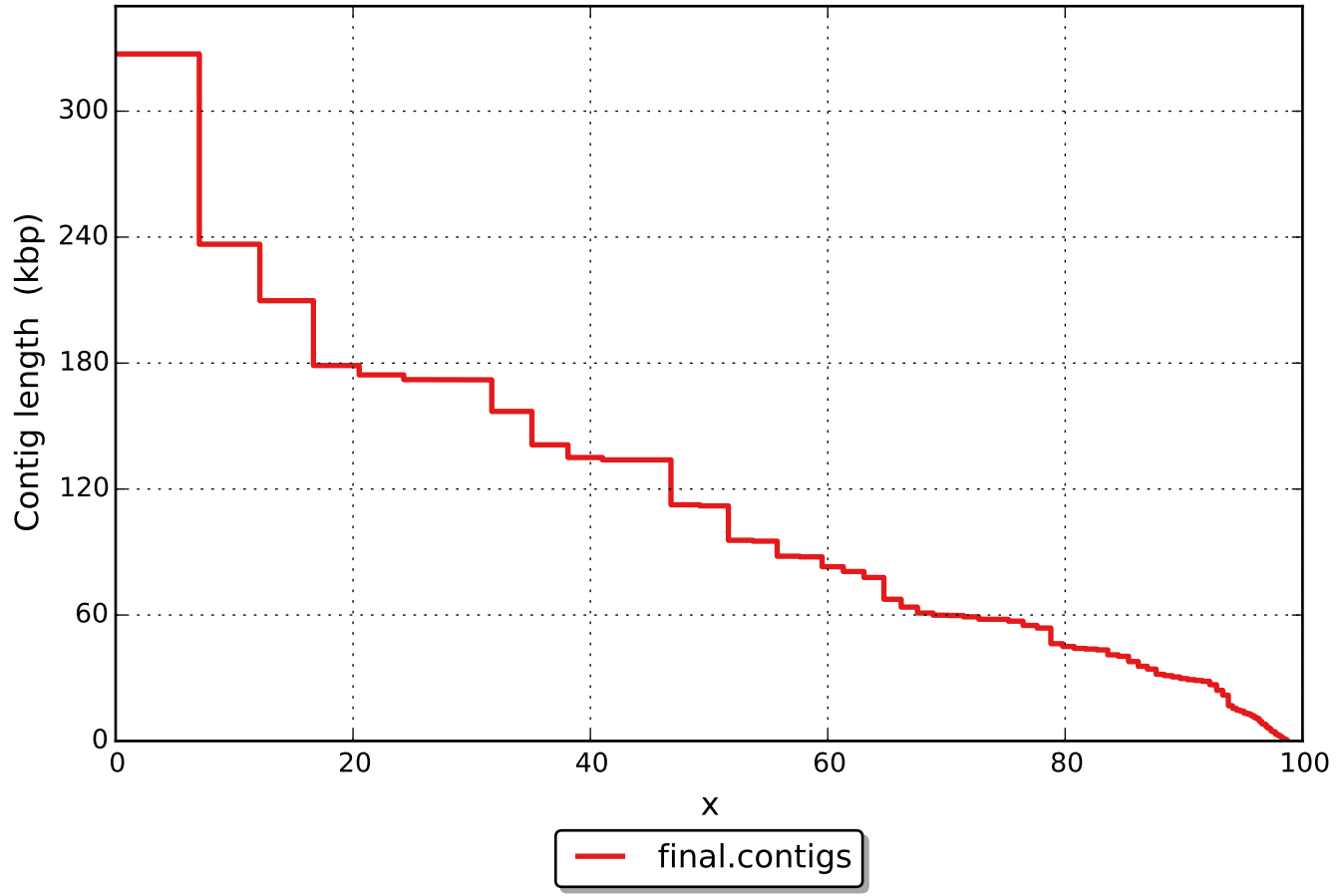
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

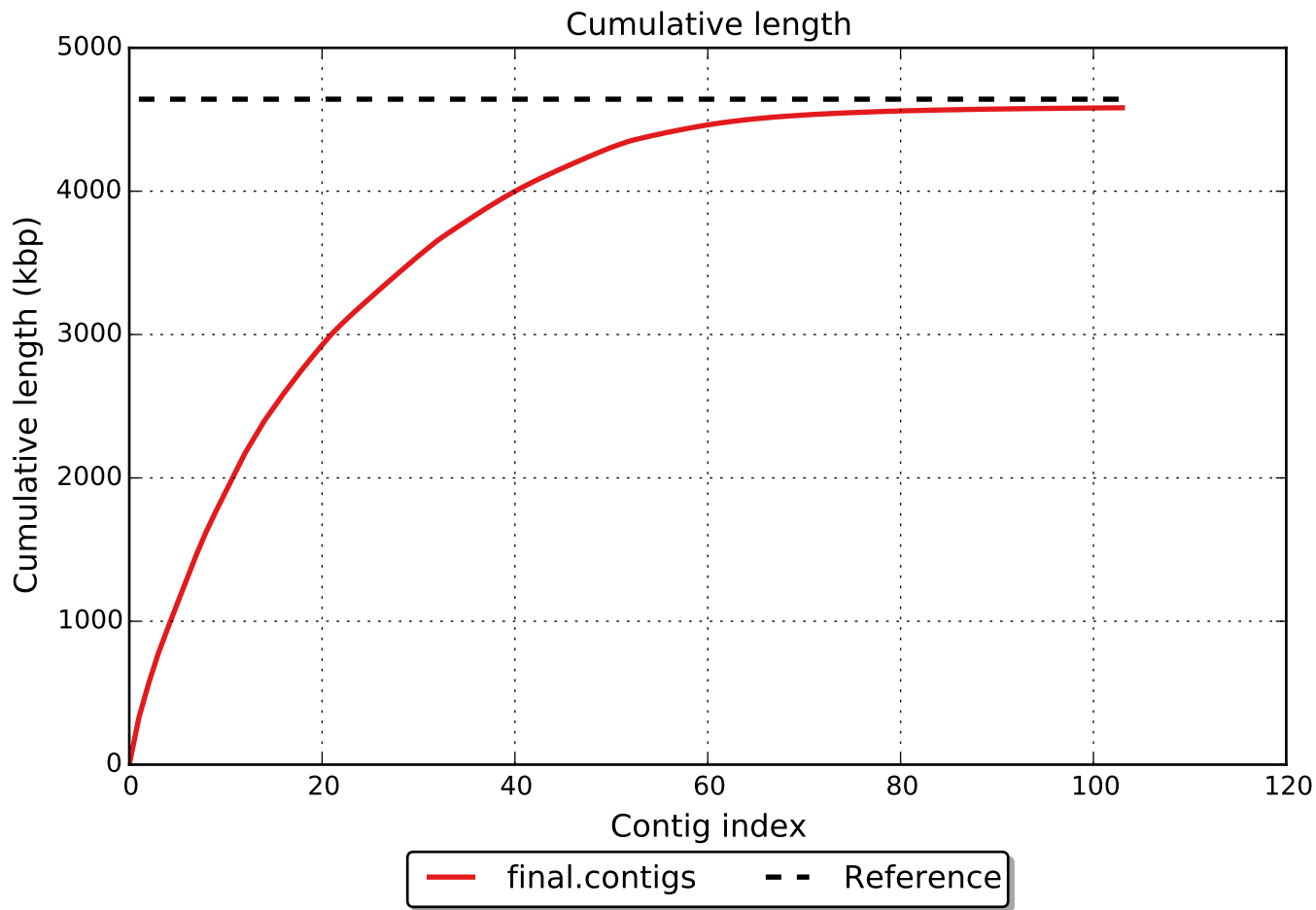
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

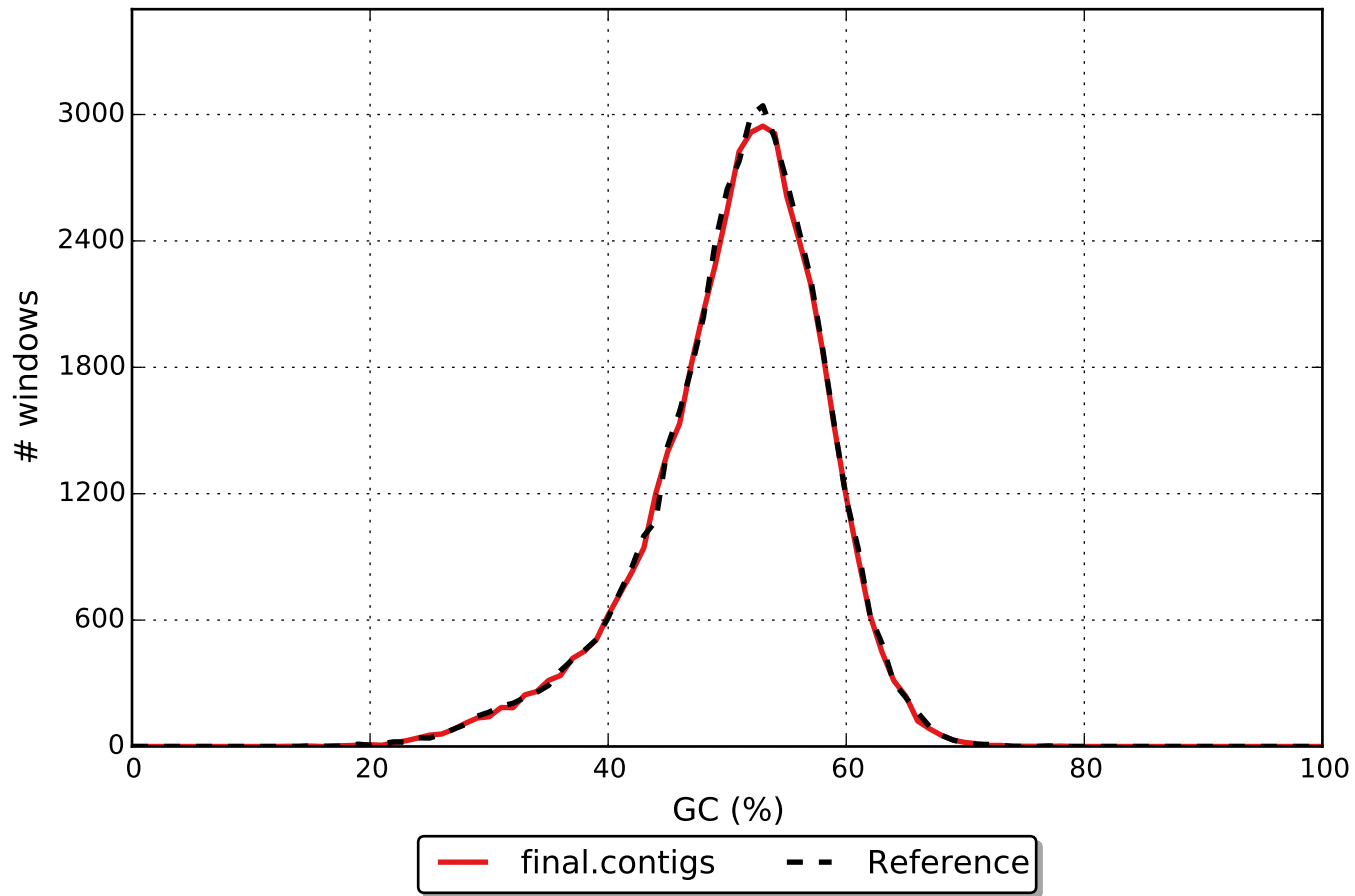


NGx

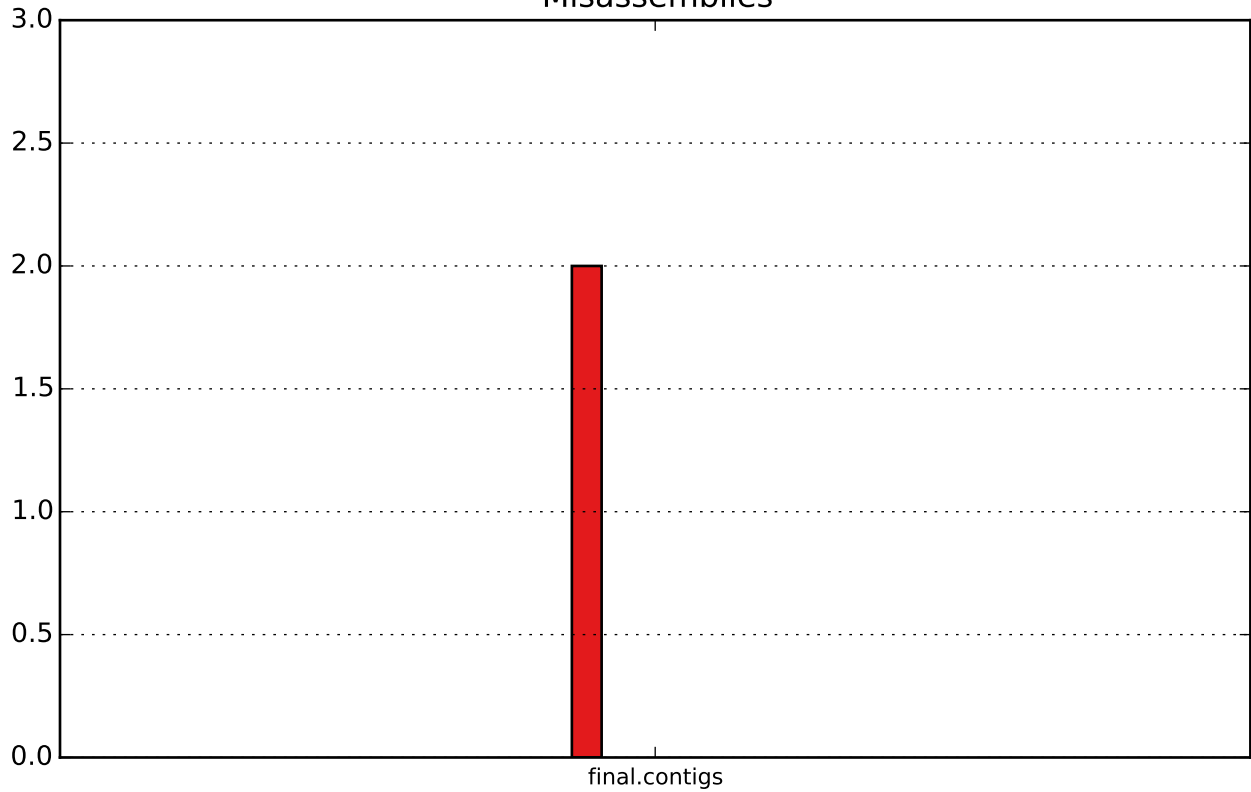




GC content

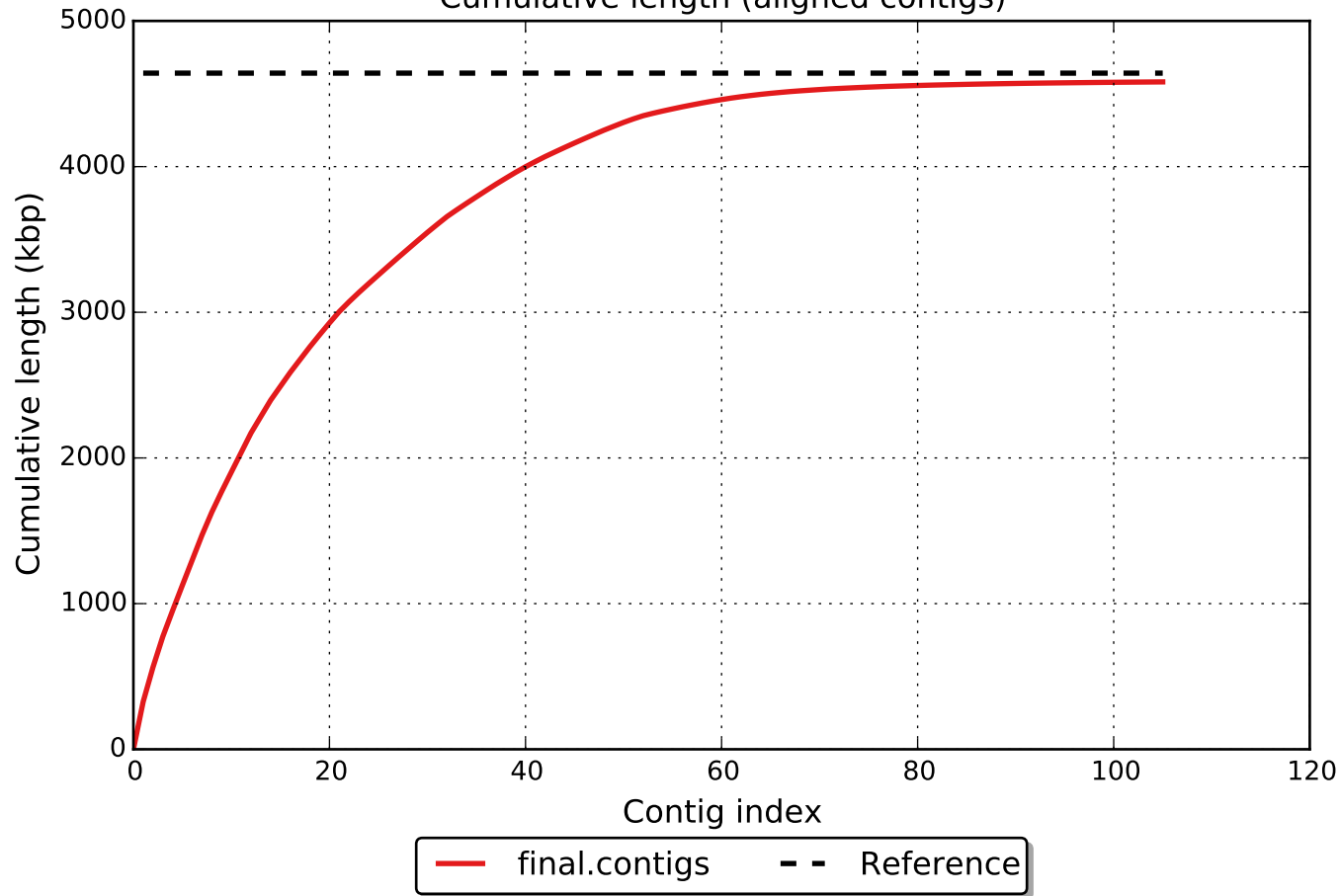


Misassemblies

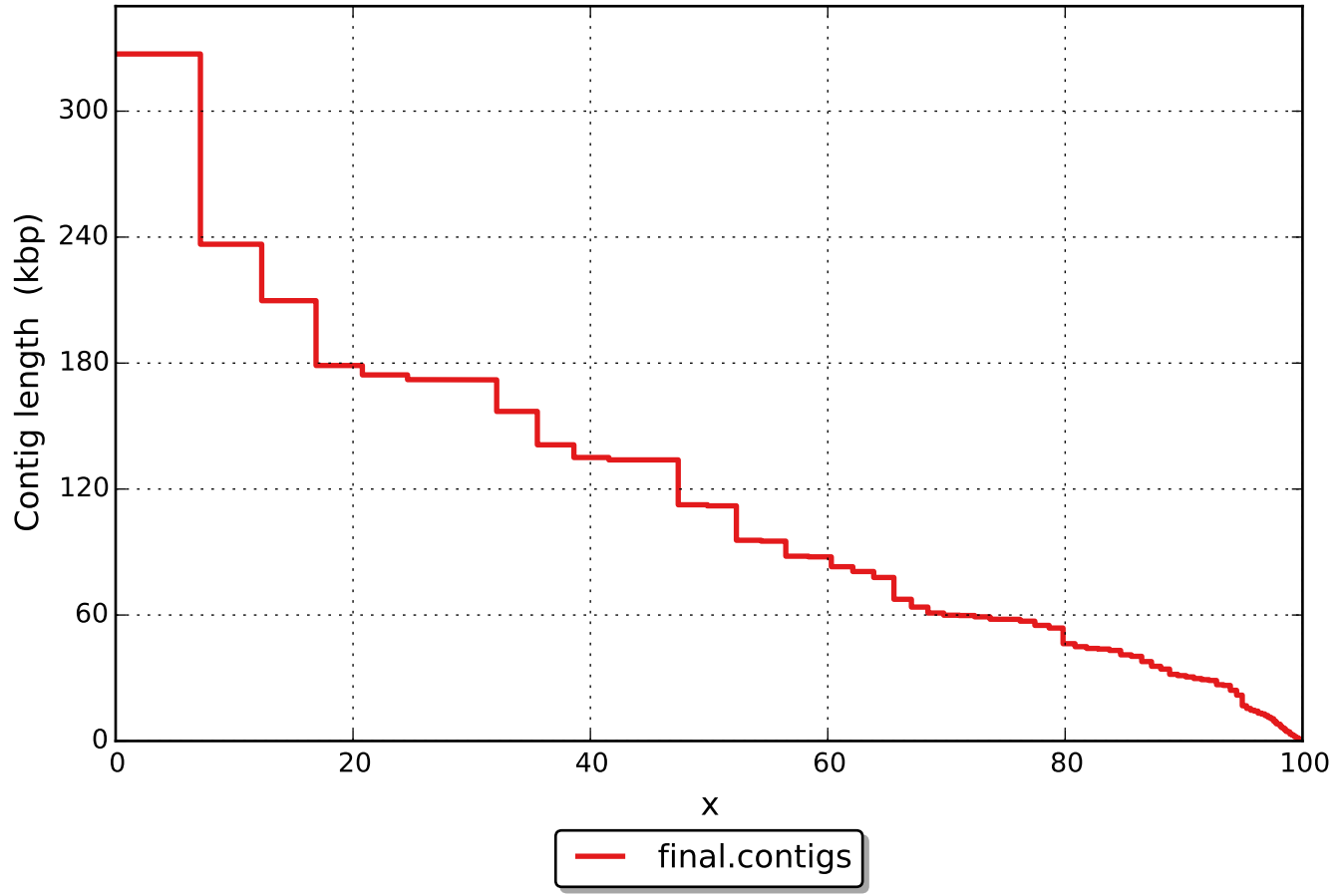


 # relocations

Cumulative length (aligned contigs)



NAx



NGAx

