

Report

	final.contigs
# contigs (≥ 0 bp)	127
# contigs (≥ 1000 bp)	123
Total length (≥ 0 bp)	1292592
Total length (≥ 1000 bp)	1289336
# contigs	127
Largest contig	52933
Total length	1292592
Reference length	641799
GC (%)	26.30
Reference GC (%)	26.31
N50	16928
NG50	26394
N75	9299
NG75	19500
L50	25
LG50	9
L75	51
LG75	16
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	53 + 6 part
Unaligned length	636265
Genome fraction (%)	99.968
Duplication ratio	1.023
# N's per 100 kbp	0.00
# mismatches per 100 kbp	57.51
# indels per 100 kbp	0.00
Largest alignment	40683
NA50	1360
NGA50	16403
NGA75	9299
LA50	61
LGA50	13
LGA75	26

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	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	369
# indels	0
# short indels	0
# long indels	0
Indels length	0

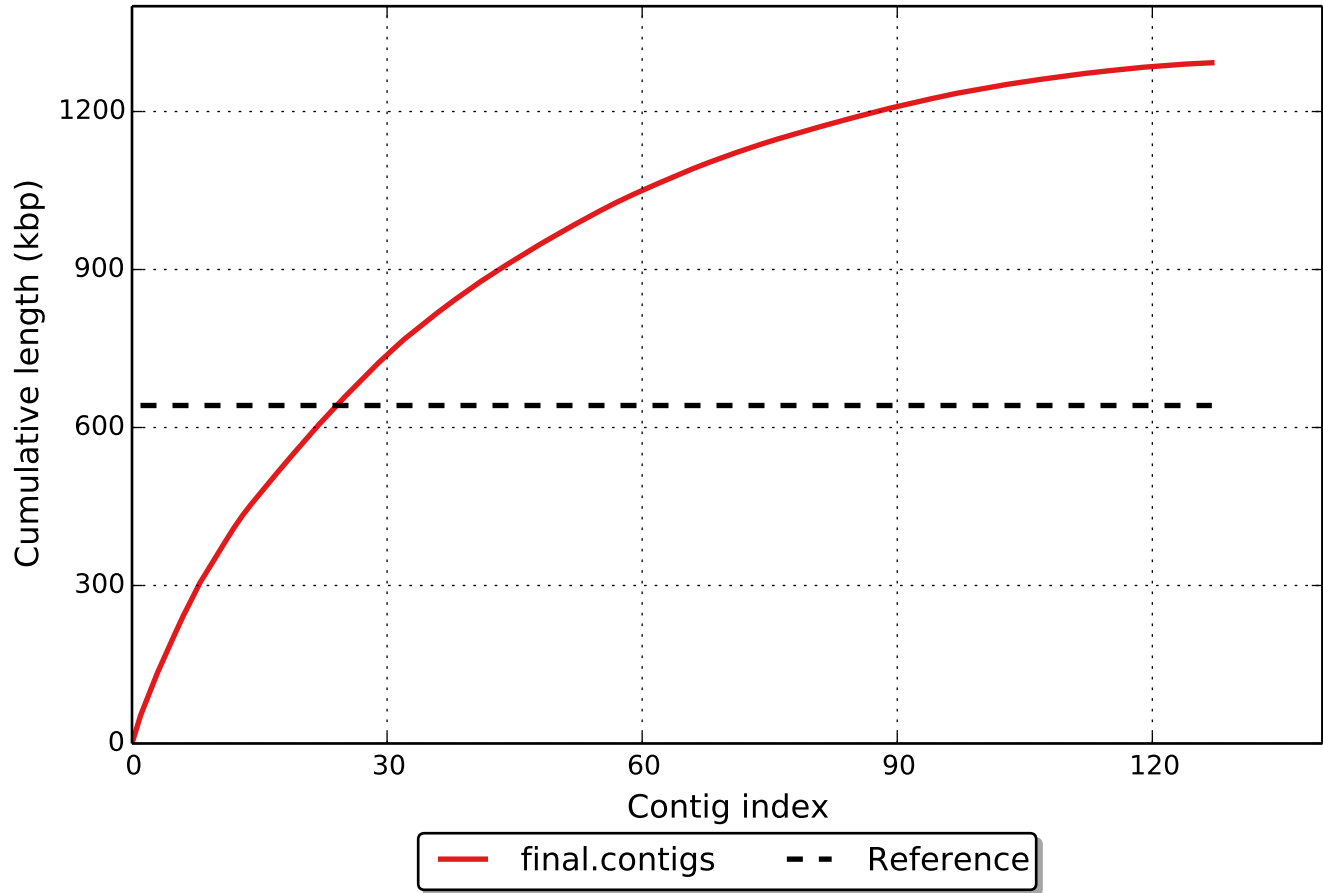
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

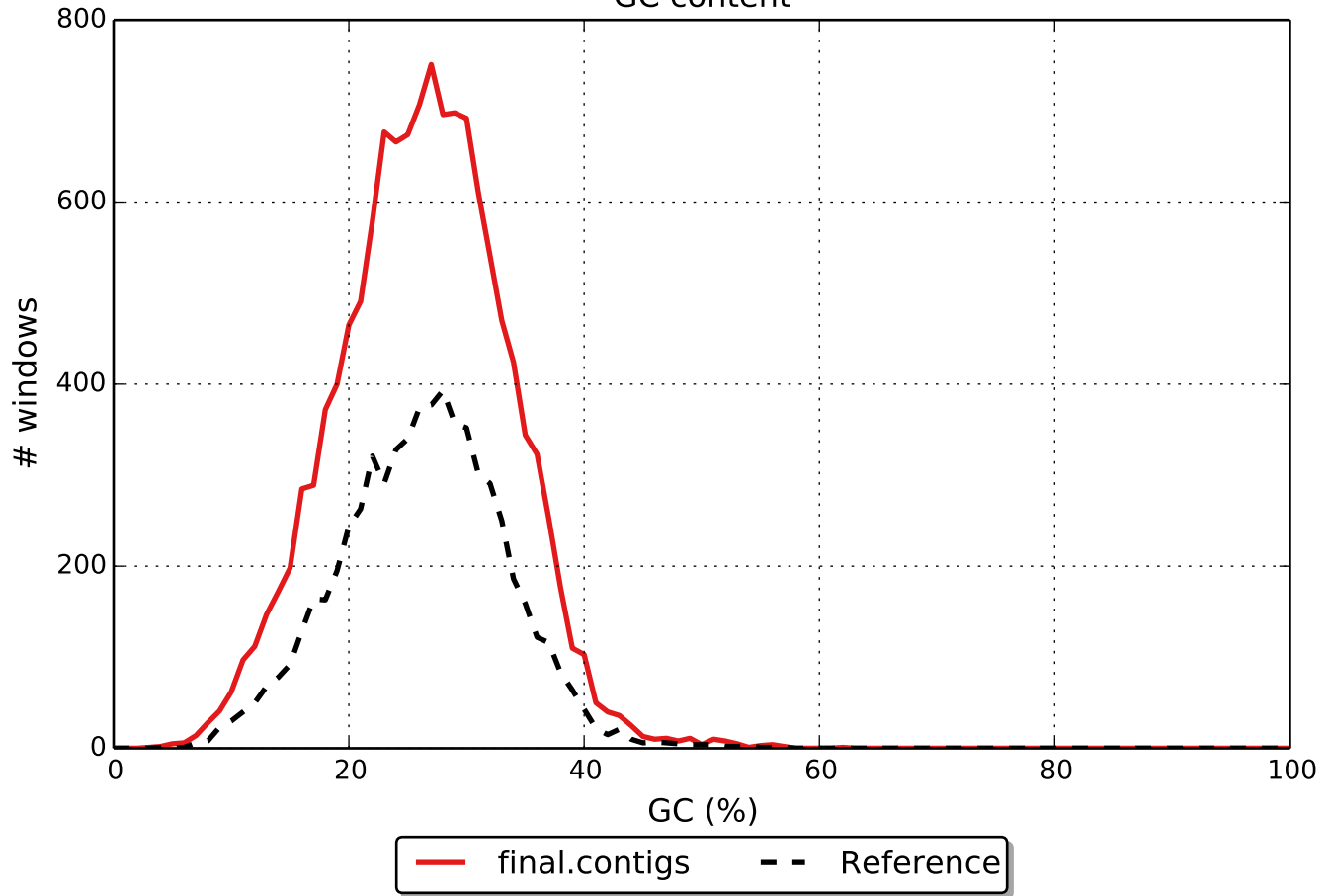
	final.contigs
# fully unaligned contigs	53
Fully unaligned length	581604
# partially unaligned contigs	6
# with misassembly	0
# both parts are significant	0
Partially unaligned length	54661
# N's	0

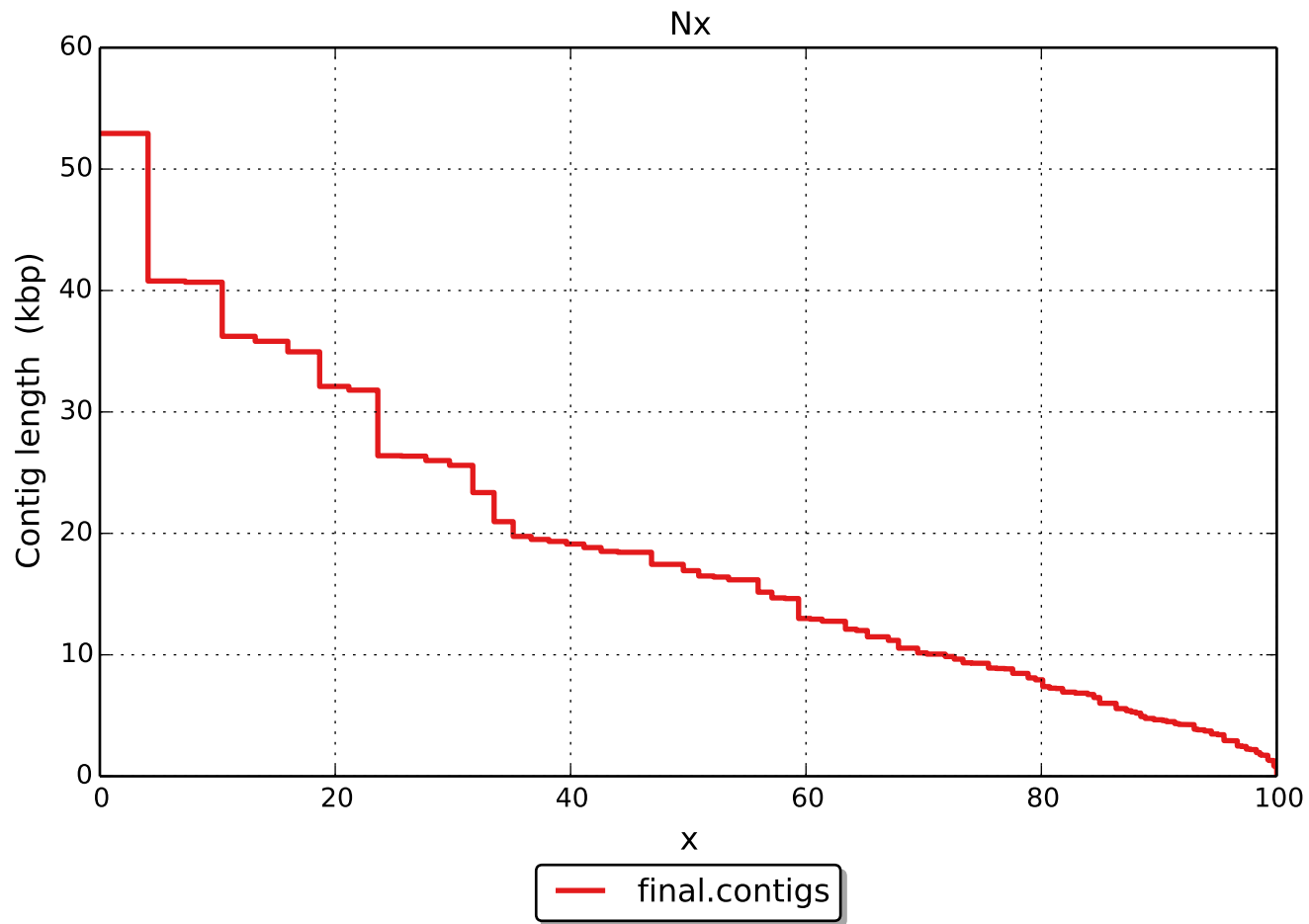
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

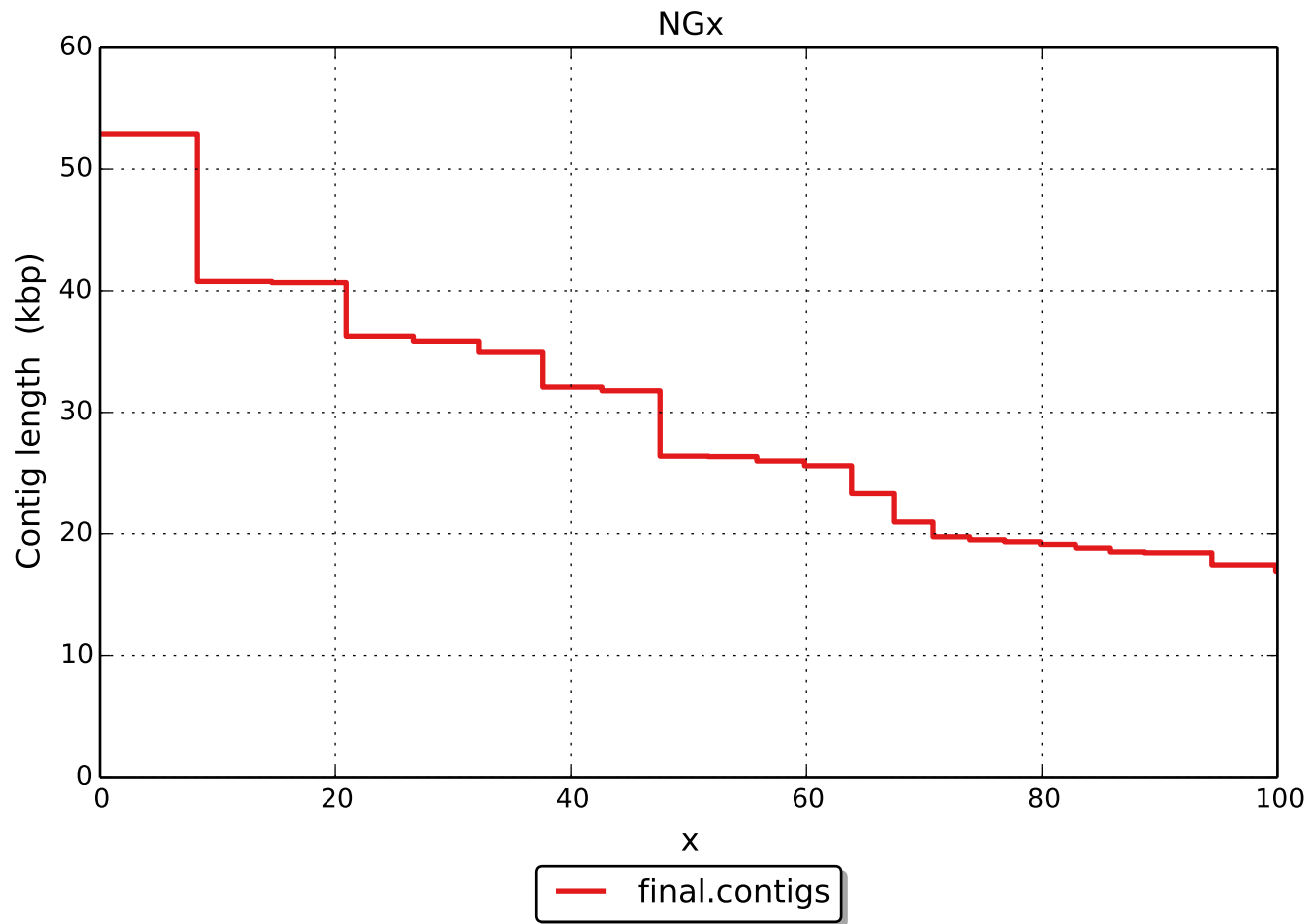
Cumulative length



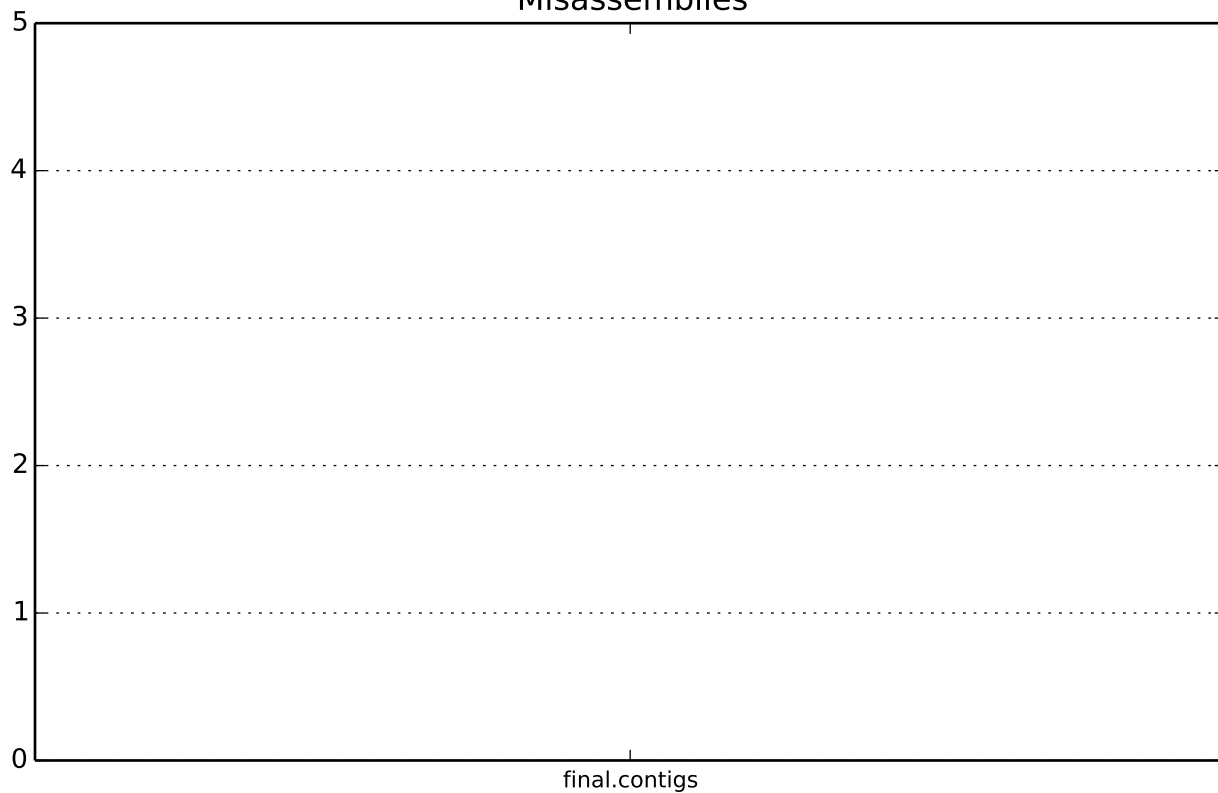
GC content

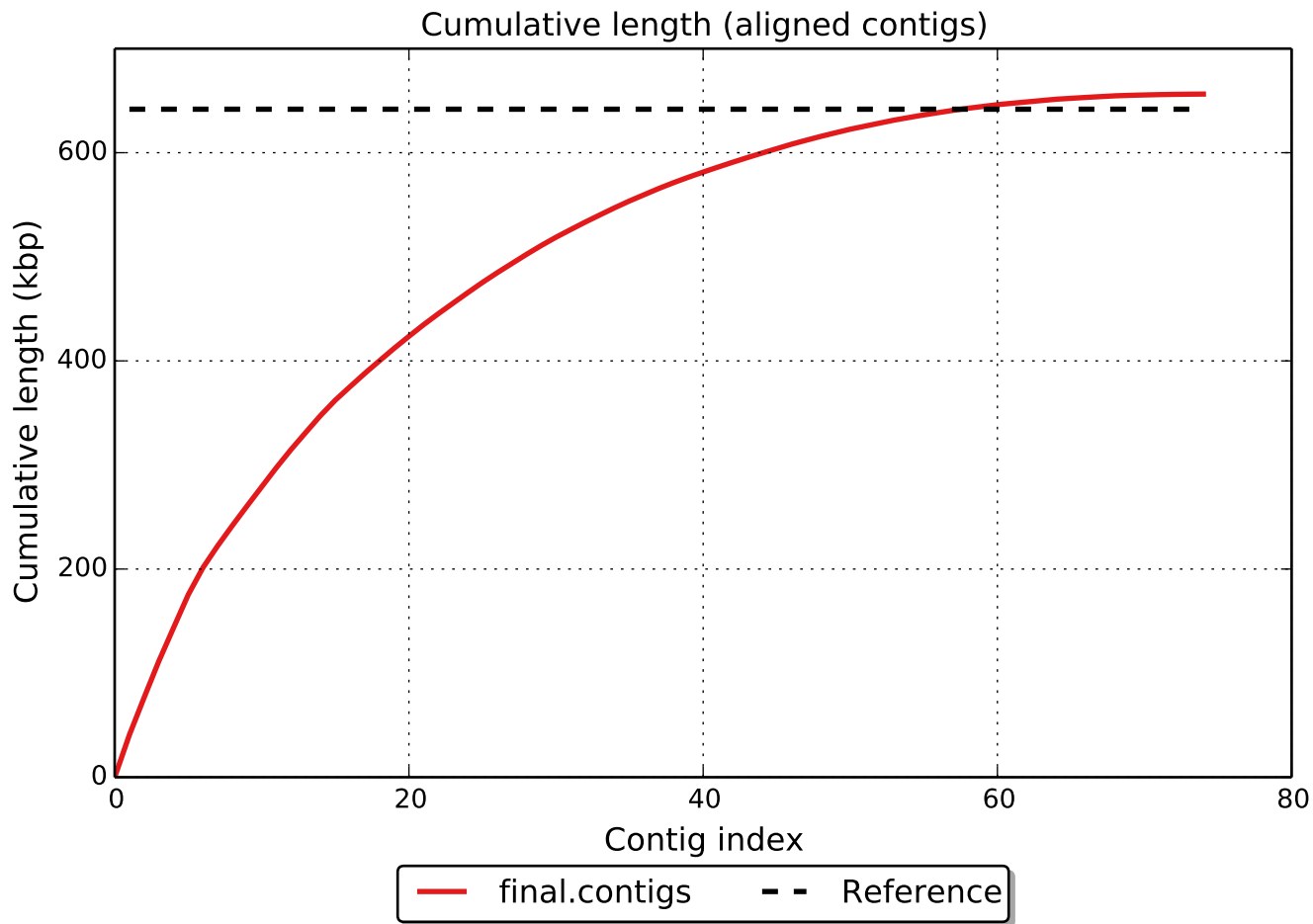




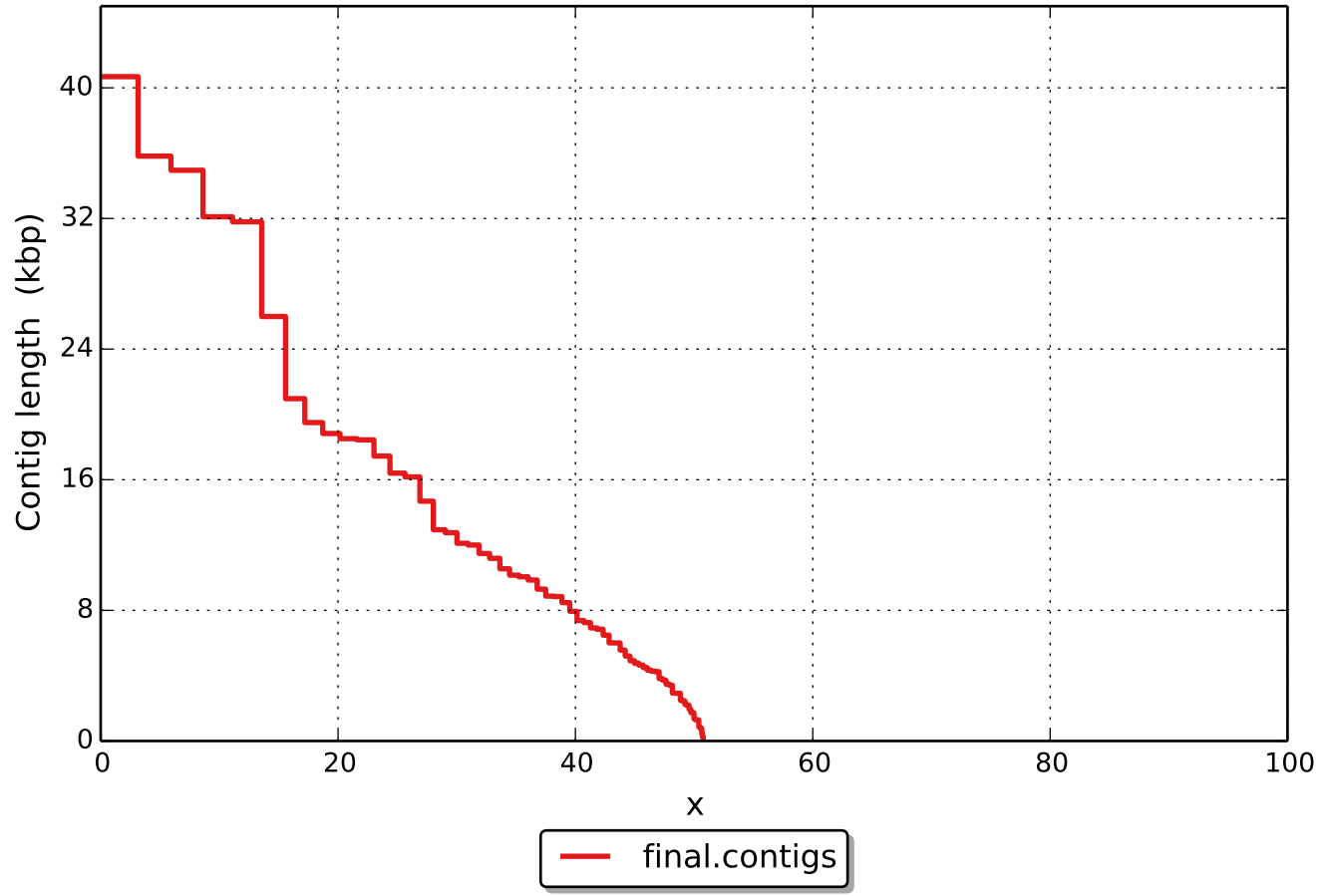


Misassemblies





NAx



NGAx

