

Report

	final.contigs
# contigs (≥ 0 bp)	975
# contigs (≥ 1000 bp)	286
Total length (≥ 0 bp)	898866
Total length (≥ 1000 bp)	416895
# contigs	975
Largest contig	4410
Total length	898866
Reference length	615980
GC (%)	25.49
Reference GC (%)	25.35
N50	956
NG50	1221
N75	693
NG75	937
L50	320
LG50	186
L75	597
LG75	333
# misassemblies	15
# misassembled contigs	15
Misassembled contigs length	12970
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	451
Genome fraction (%)	90.044
Duplication ratio	1.620
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1149.37
# indels per 100 kbp	0.36
Largest alignment	4410
NA50	949
NGA50	1200
NA75	690
NGA75	929
LA50	321
LGA50	187
LA75	600
LGA75	334

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

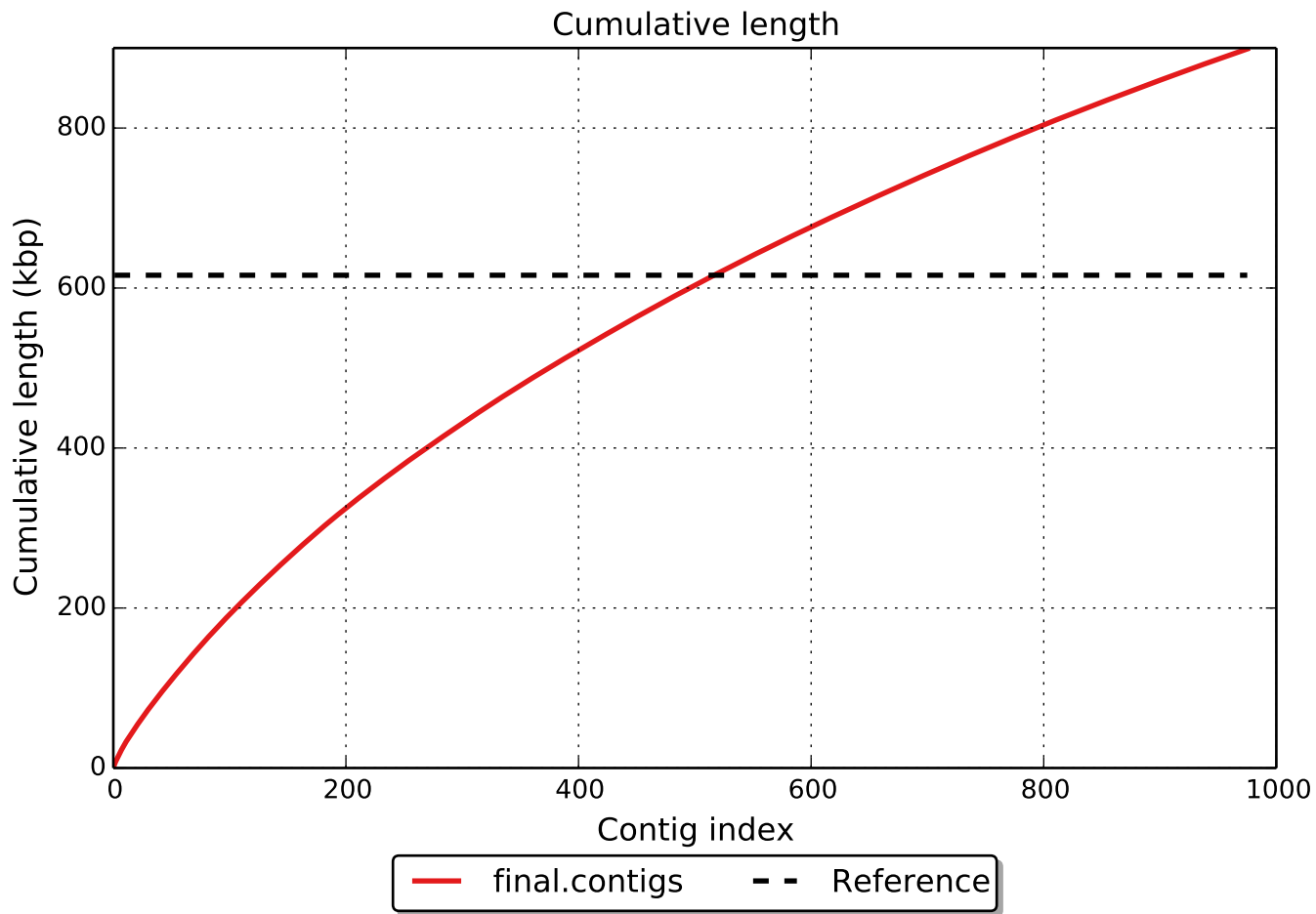
	final.contigs
# misassemblies	15
# relocations	15
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	15
Misassembled contigs length	12970
# local misassemblies	0
# mismatches	6375
# indels	2
# short indels	2
# long indels	0
Indels length	2

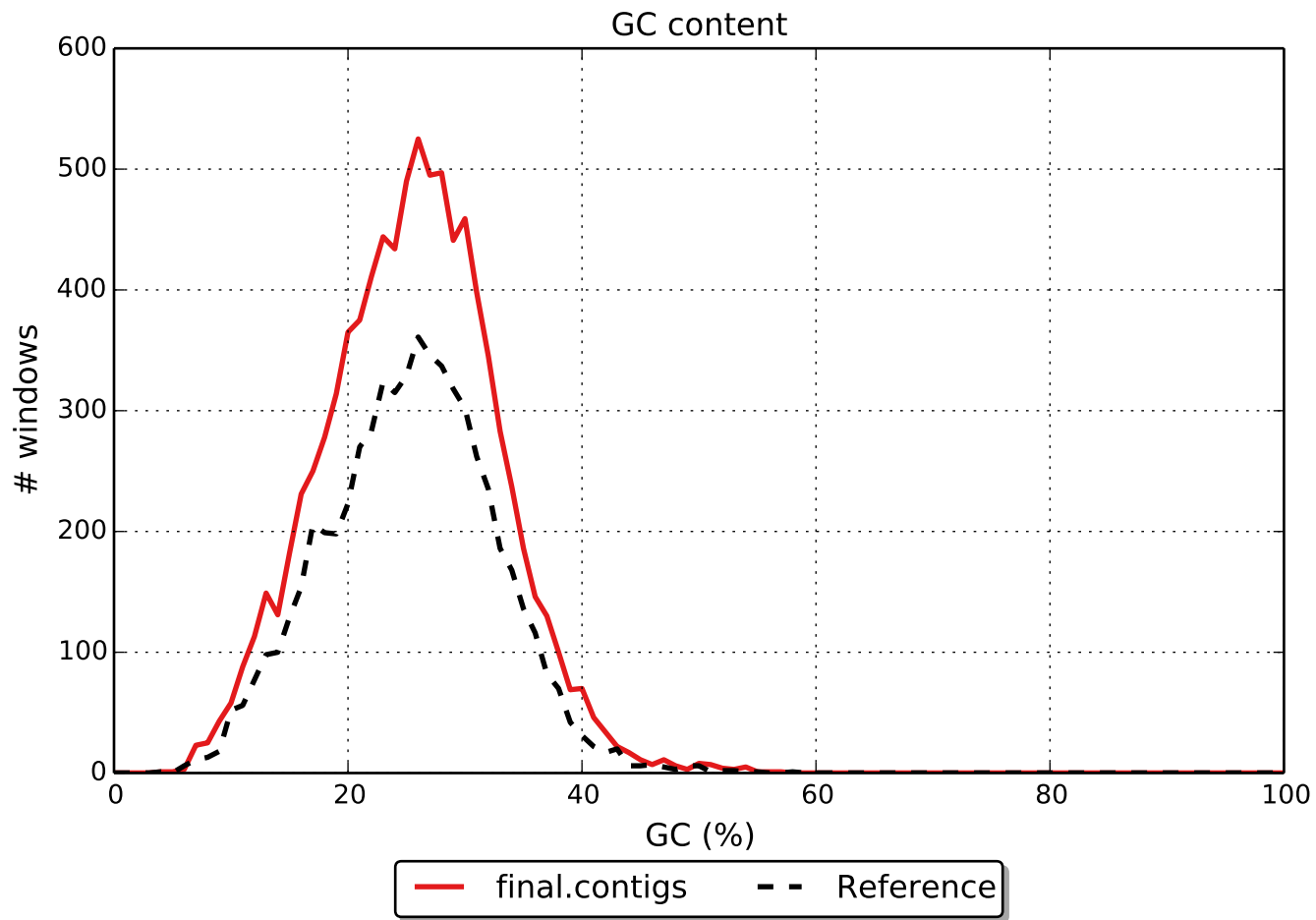
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

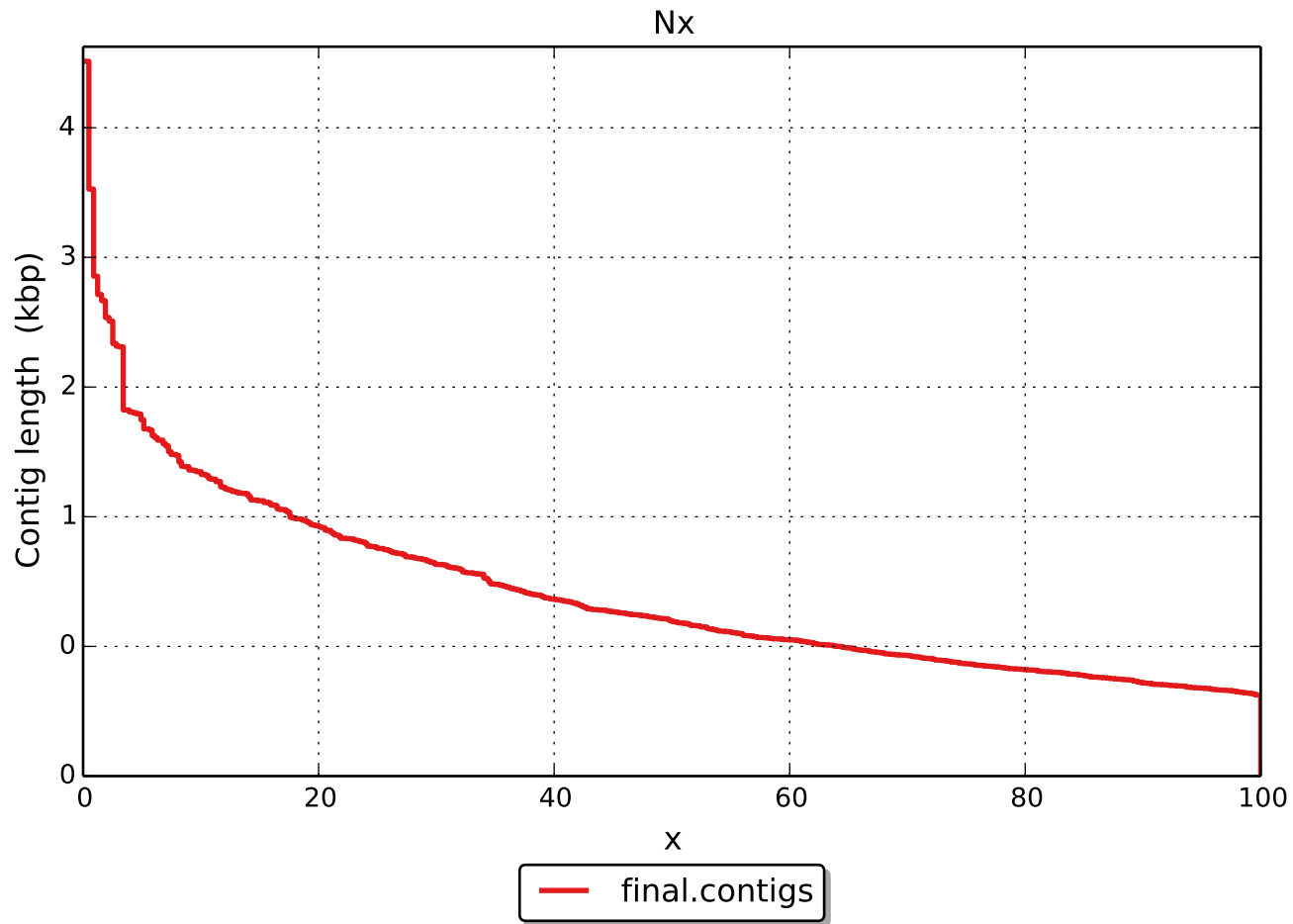
Unaligned report

	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	451
# N's	0

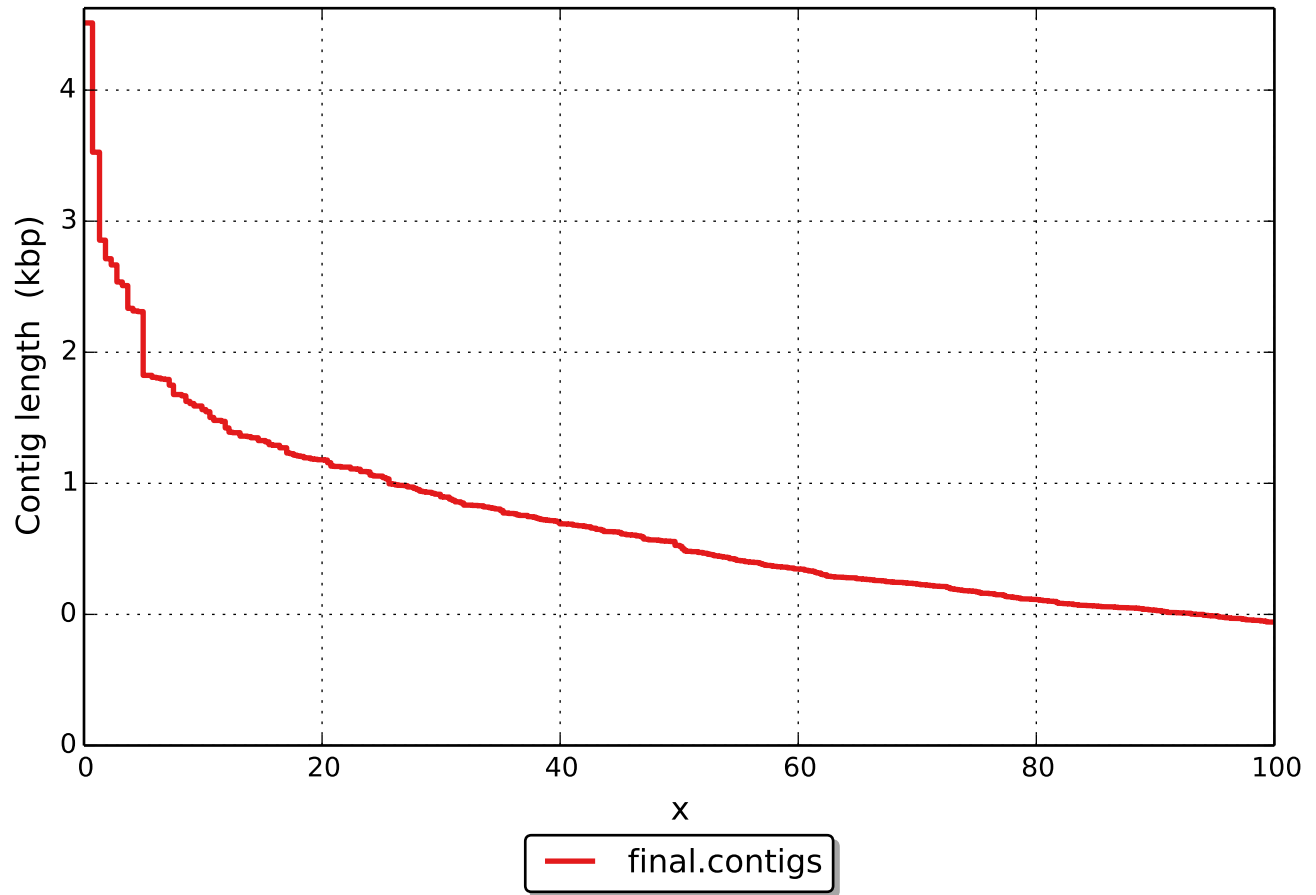
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



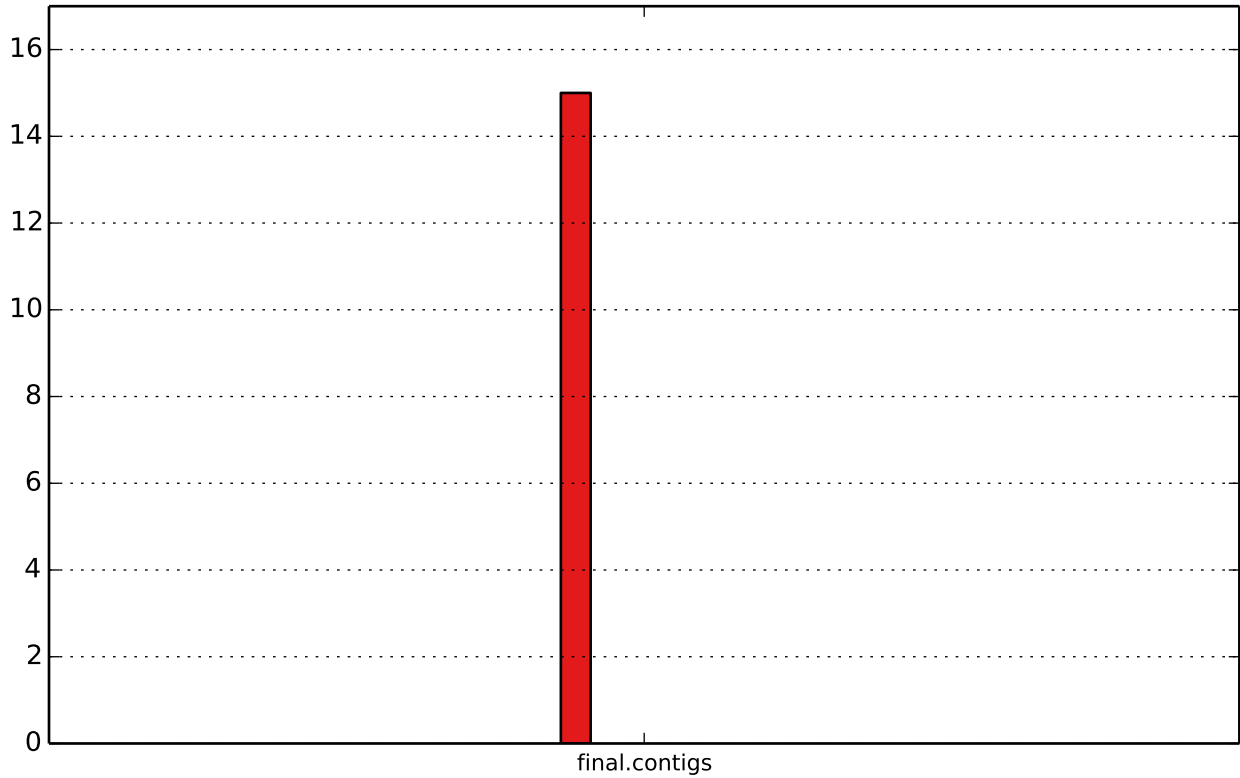


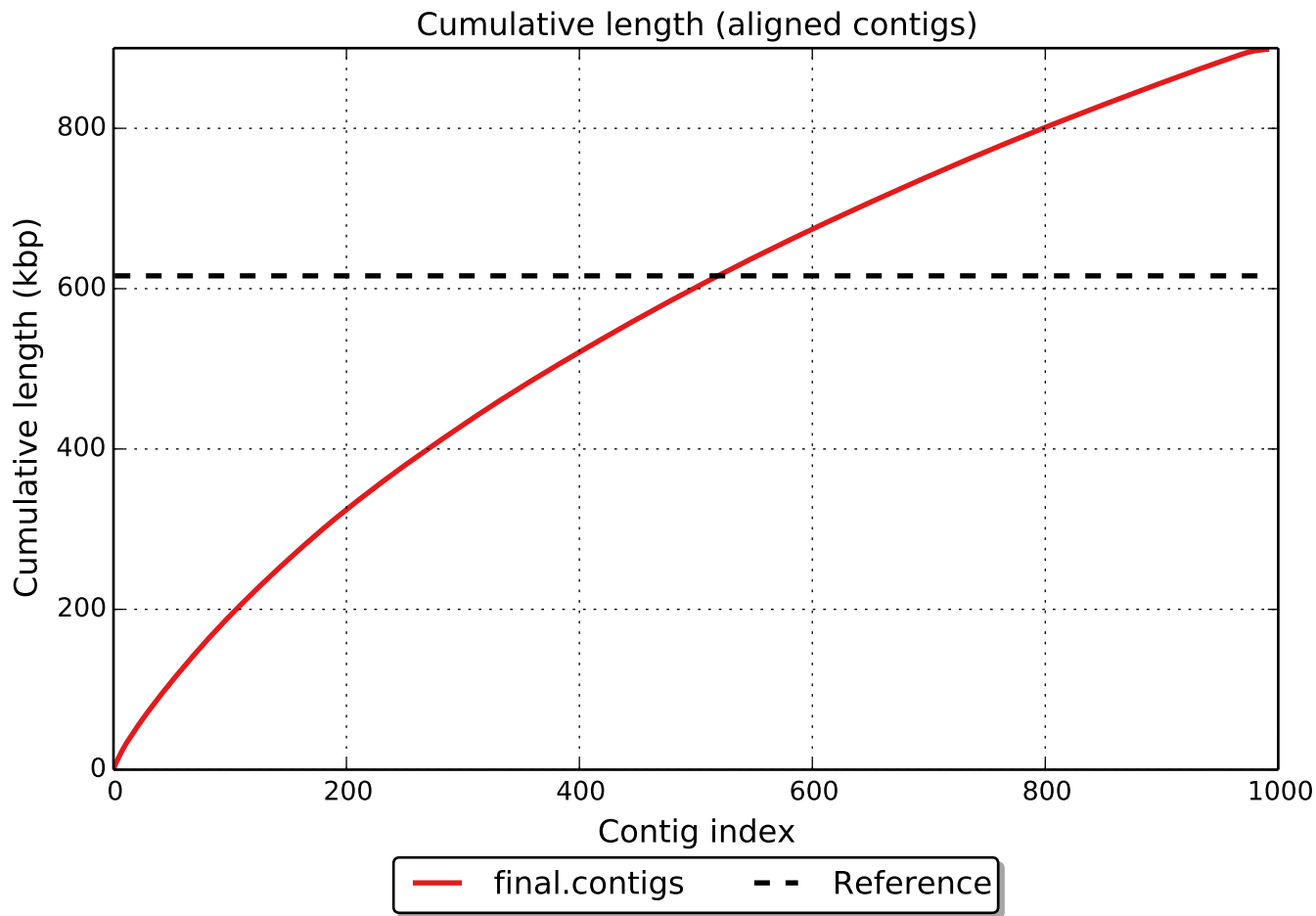


NGx

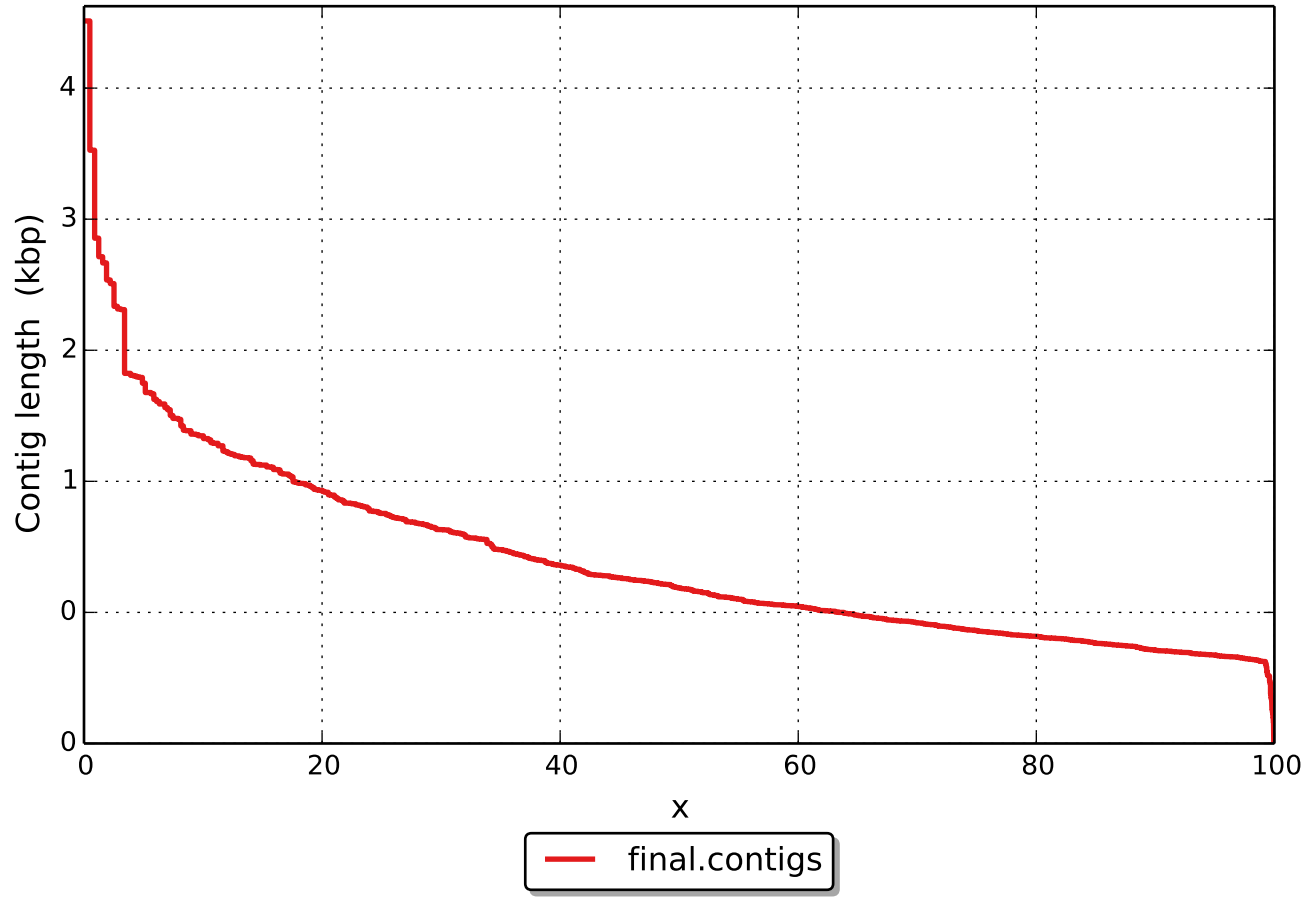


Misassemblies





NAx



NGAx

