

Report

	final.contigs
# contigs (≥ 0 bp)	4725
# contigs (≥ 1000 bp)	1618
Total length (≥ 0 bp)	4596383
Total length (≥ 1000 bp)	2388686
# contigs	4725
Largest contig	4140
Total length	4596383
Reference length	5478683
GC (%)	50.29
Reference GC (%)	50.49
N50	1026
NG50	909
N75	739
NG75	603
L50	1529
LG50	1986
L75	2849
LG75	3838
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	79.200
Duplication ratio	1.059
# N's per 100 kbp	0.00
# mismatches per 100 kbp	143.35
# indels per 100 kbp	0.14
Largest alignment	4140
NA50	1026
NGA50	909
NA75	739
NGA75	603
LA50	1529
LGA50	1986
LA75	2849
LGA75	3838

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

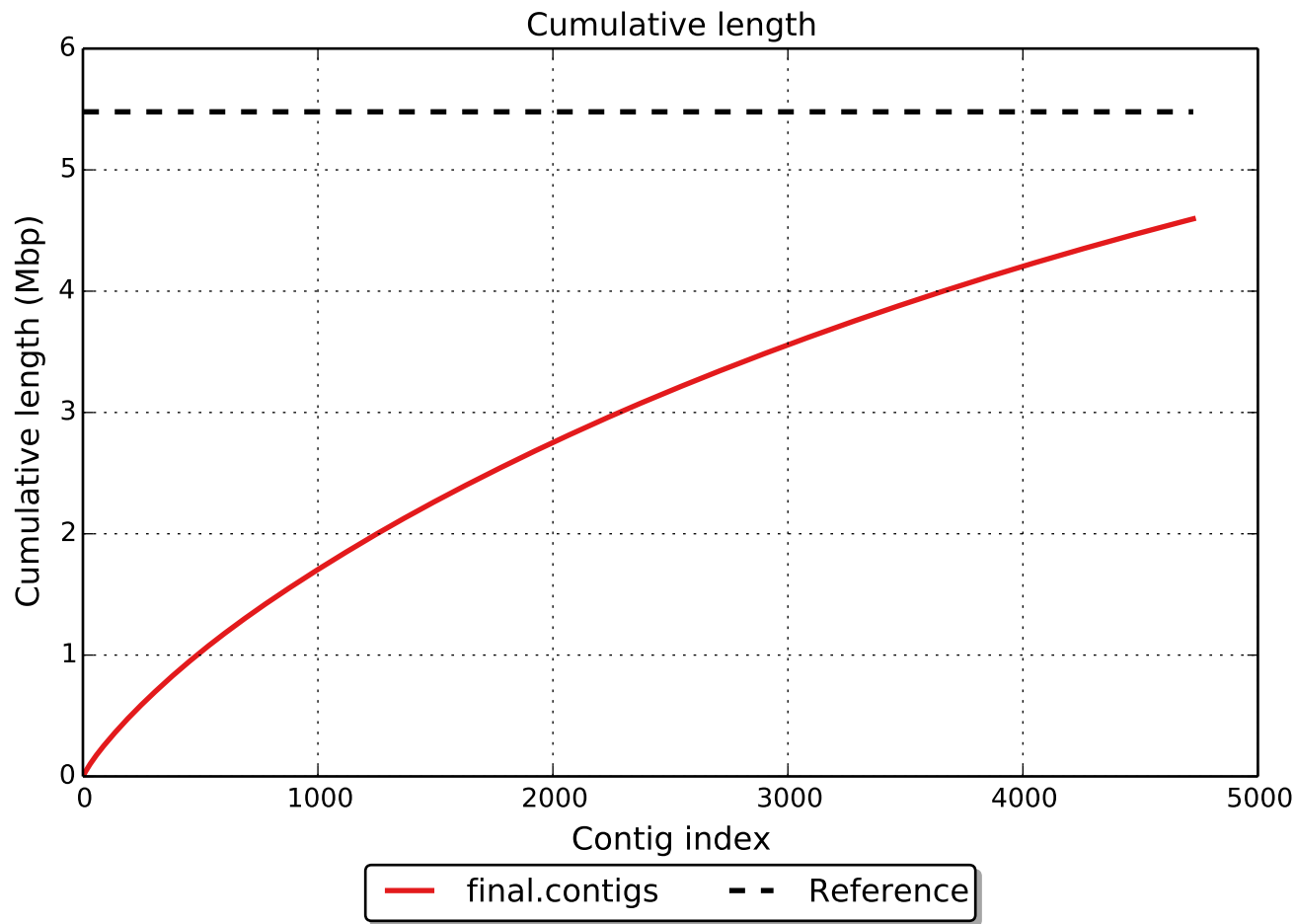
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	6220
# indels	6
# short indels	5
# long indels	1
Indels length	11

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).

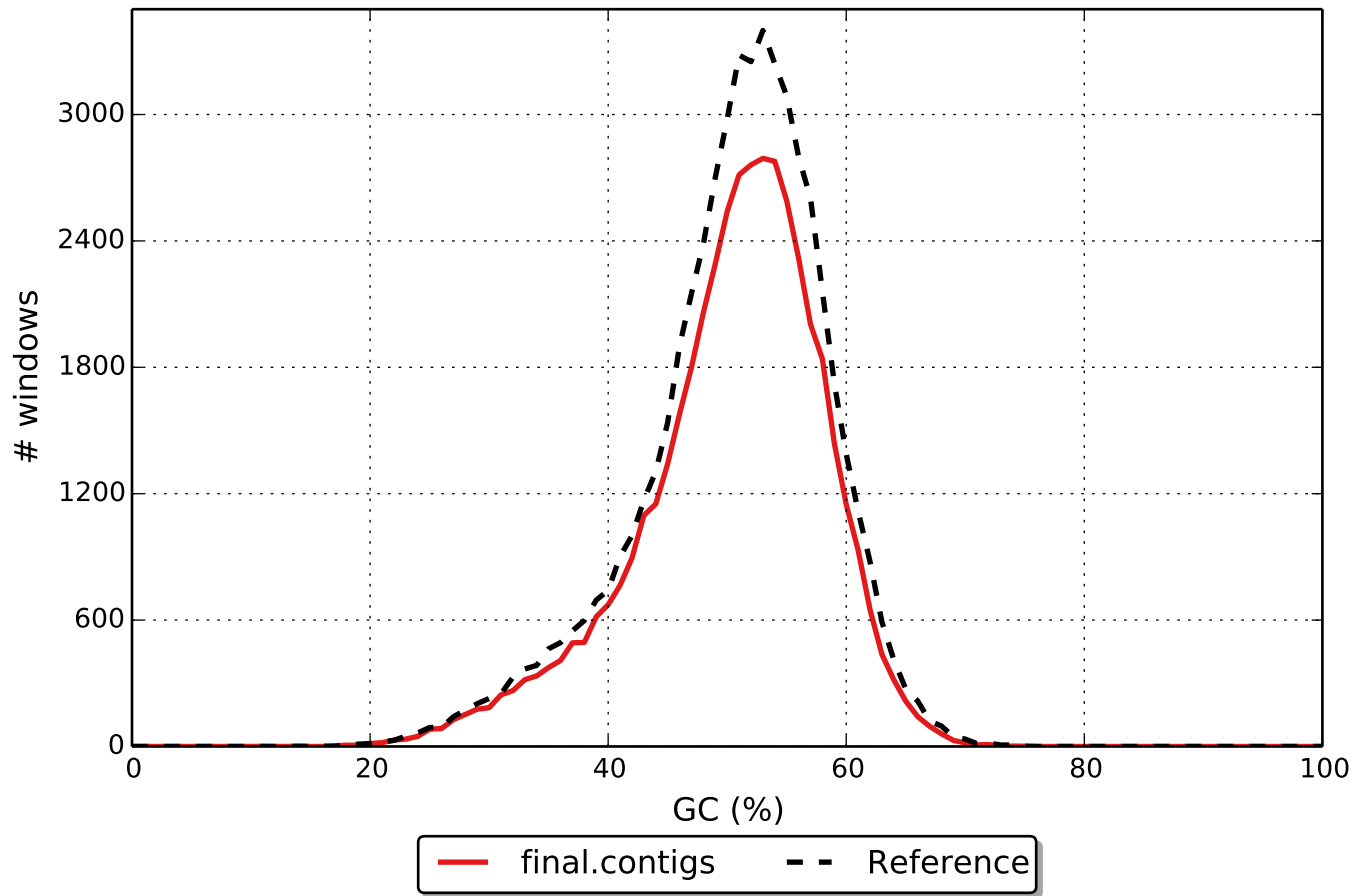
Unaligned report

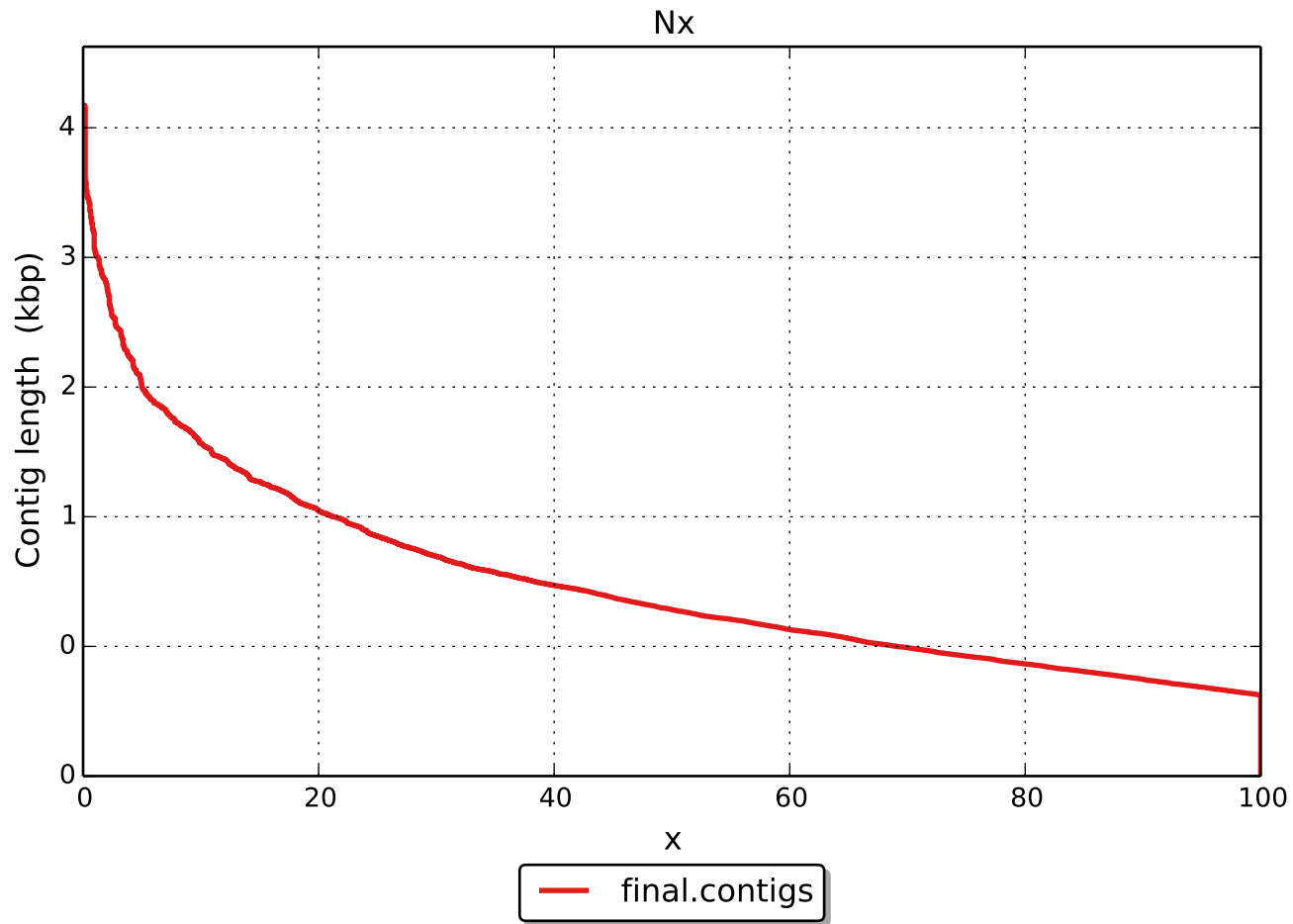
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

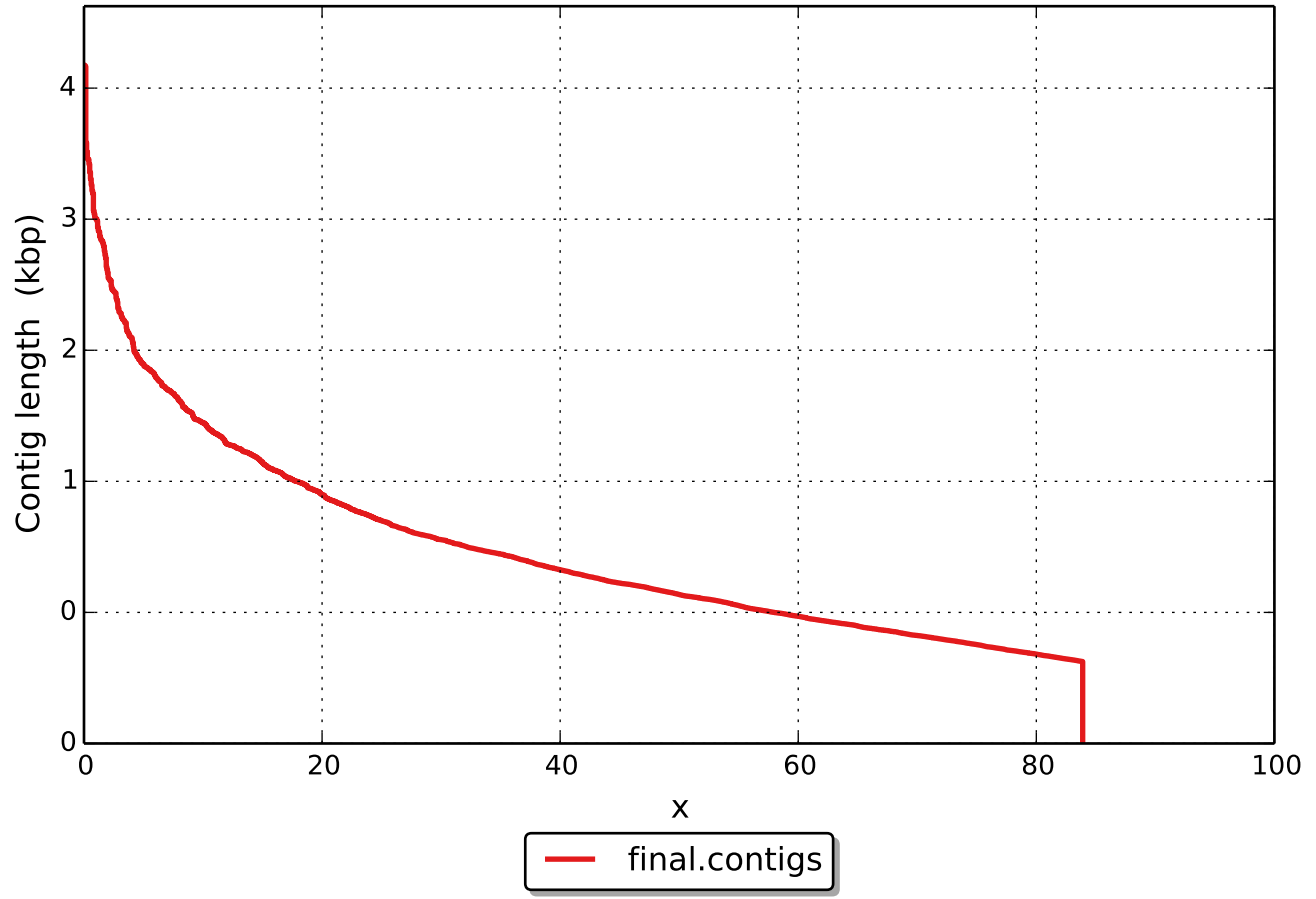


GC content



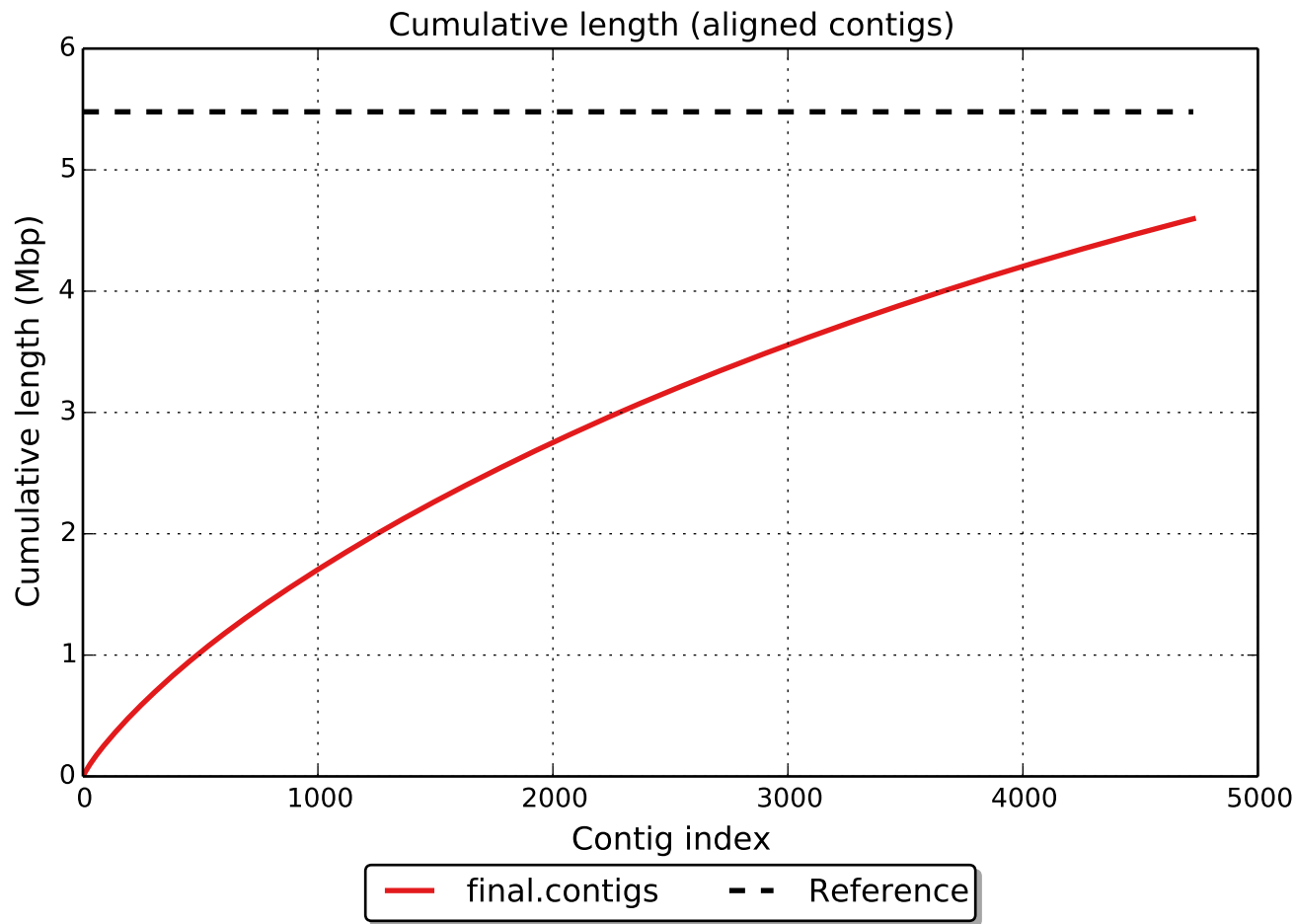


NGx

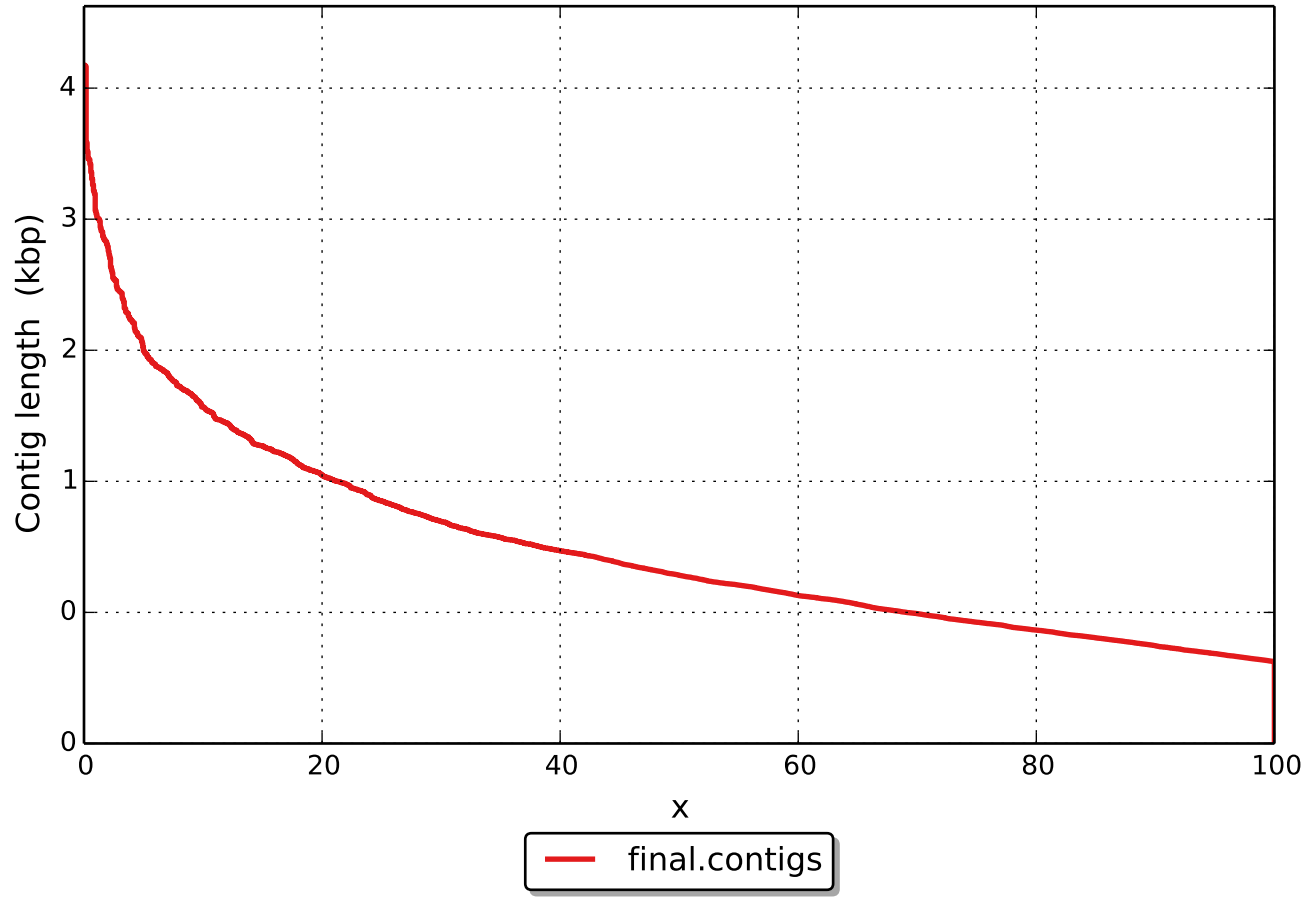


Misassemblies





NAx



NGAx

