

Report

	final.contigs
# contigs (>= 0 bp)	4468
# contigs (>= 1000 bp)	1538
Total length (>= 0 bp)	4350776
Total length (>= 1000 bp)	2270042
# contigs	4468
Largest contig	4132
Total length	4350776
Reference length	5478683
GC (%)	50.33
Reference GC (%)	50.49
N50	1030
NG50	876
N75	740
NG75	554
L50	1445
LG50	2041
L75	2694
LG75	4009
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	75.853
Duplication ratio	1.047
# N's per 100 kbp	0.00
# mismatches per 100 kbp	83.38
# indels per 100 kbp	0.10
Largest alignment	4132
NA50	1030
NGA50	876
NA75	740
NGA75	554
LA50	1445
LGA50	2041
LA75	2694
LGA75	4010

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

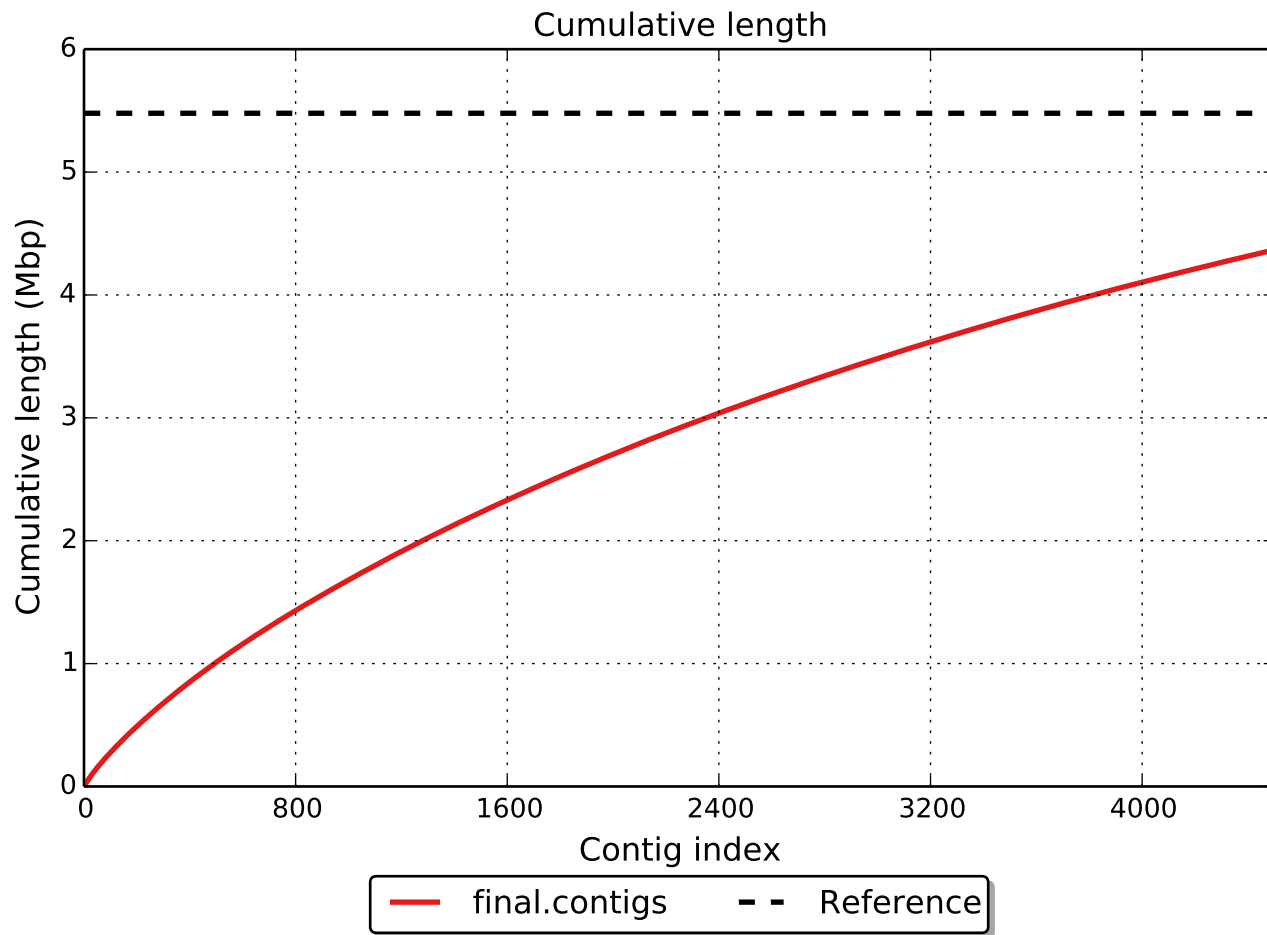
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	3465
# indels	4
# short indels	3
# long indels	1
Indels length	9

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).

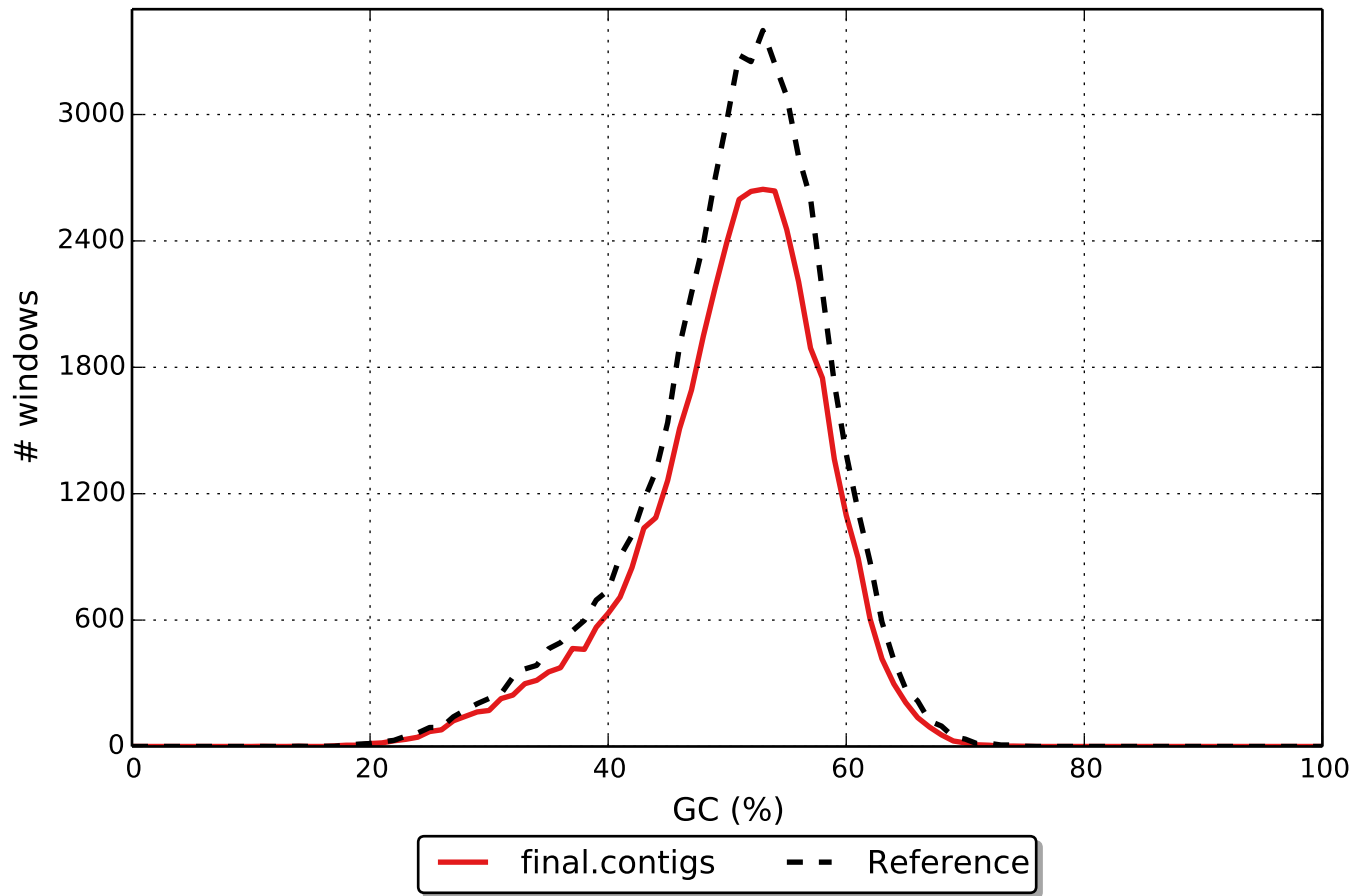
Unaligned report

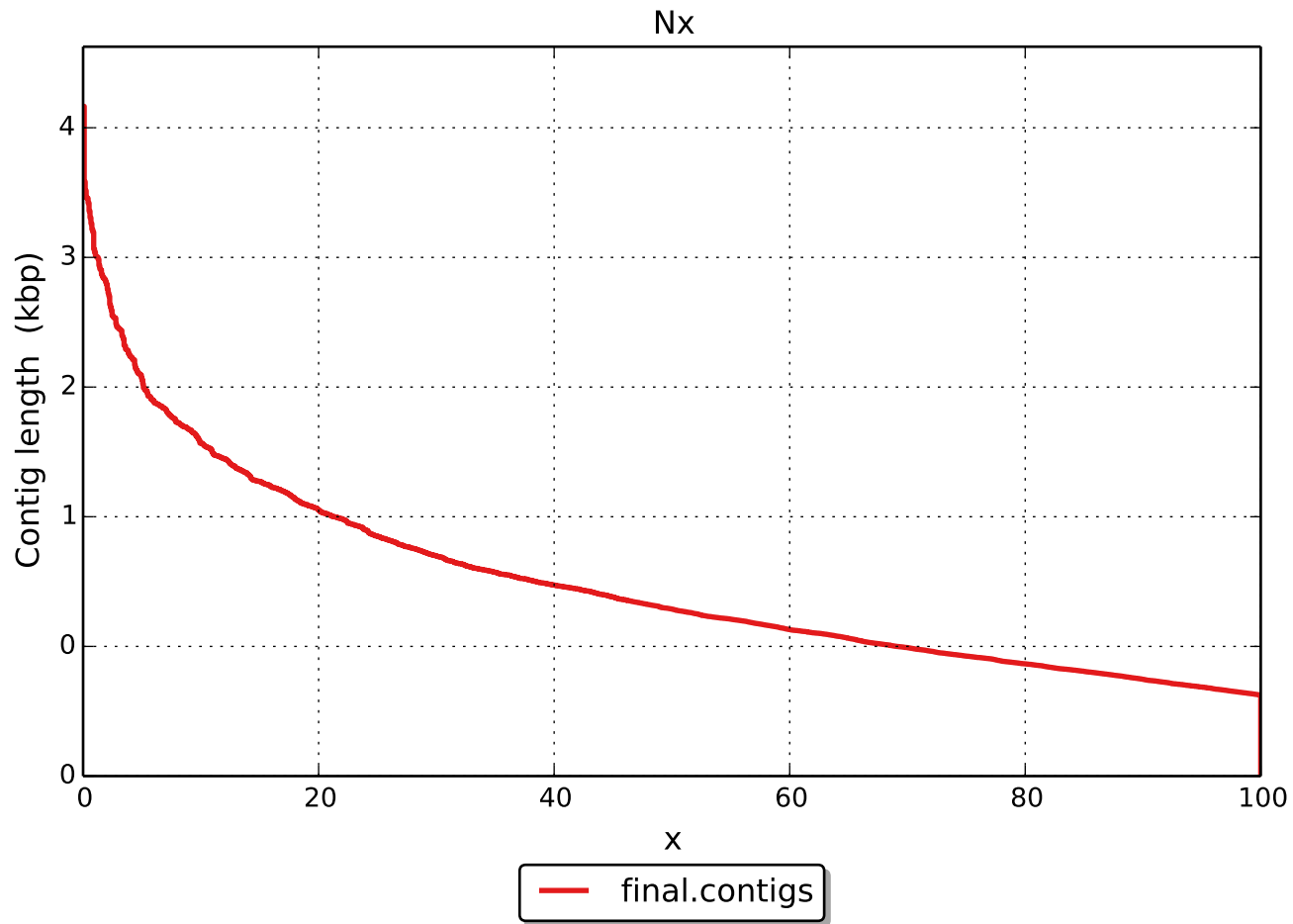
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

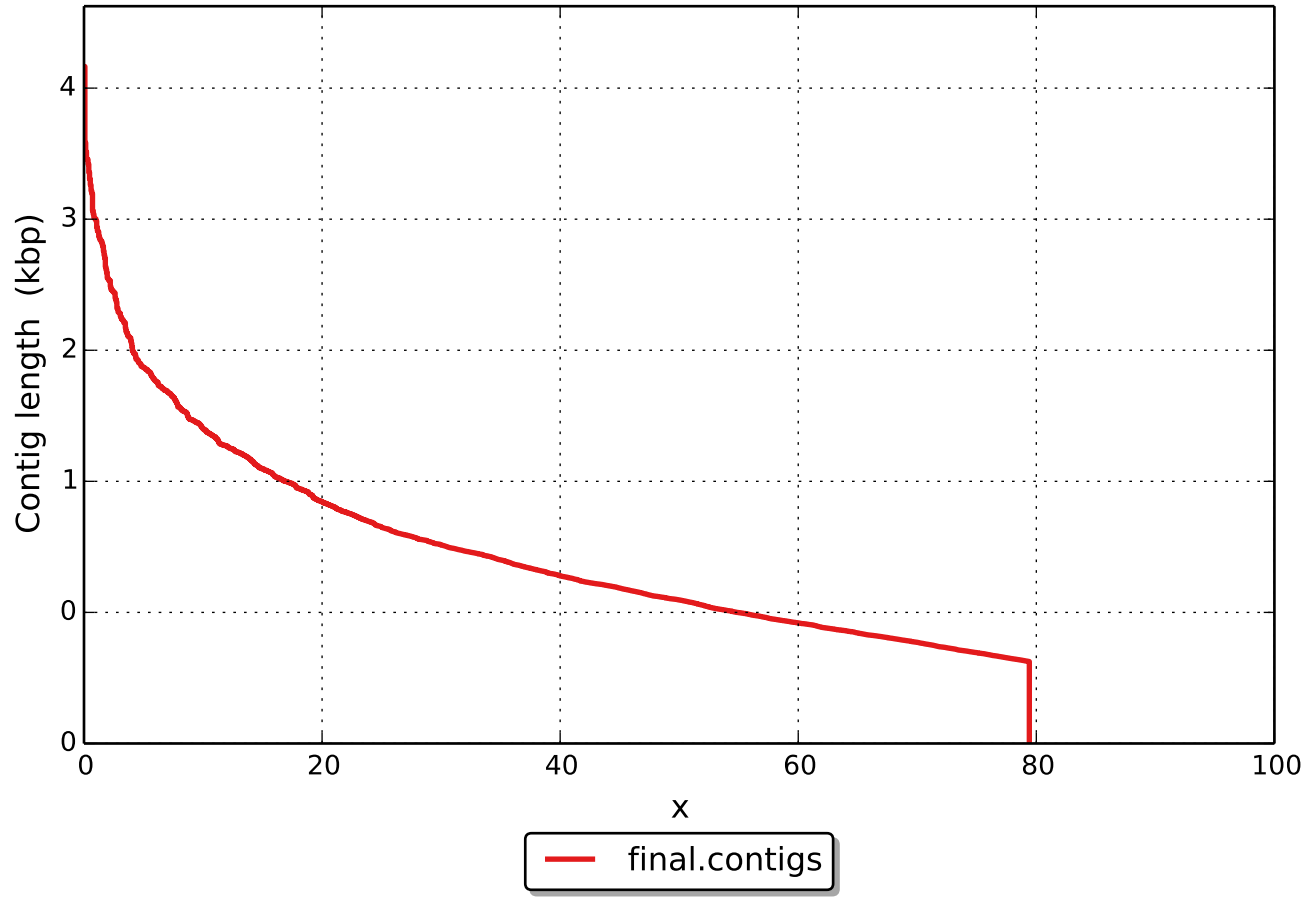


GC content



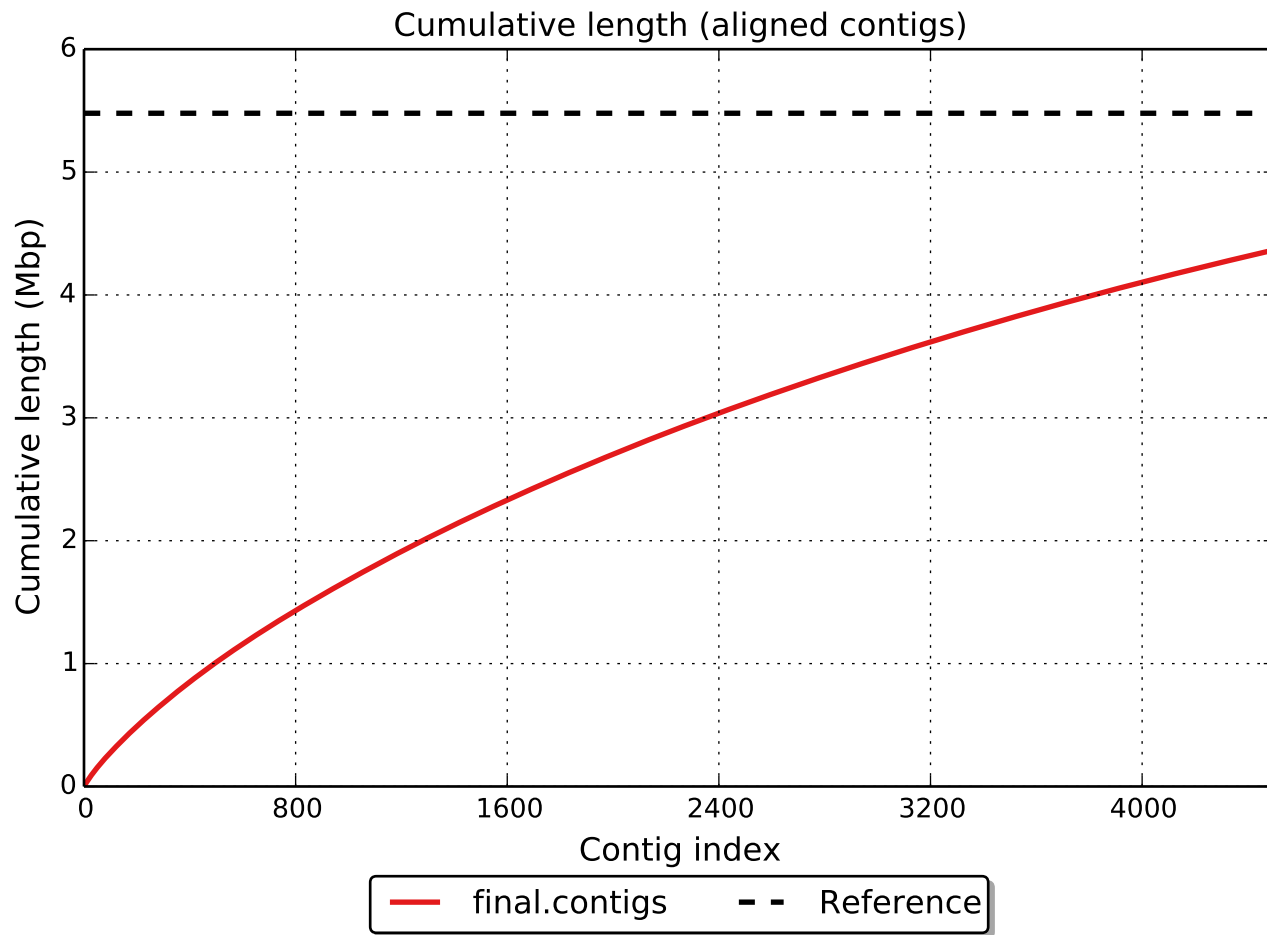


NGx

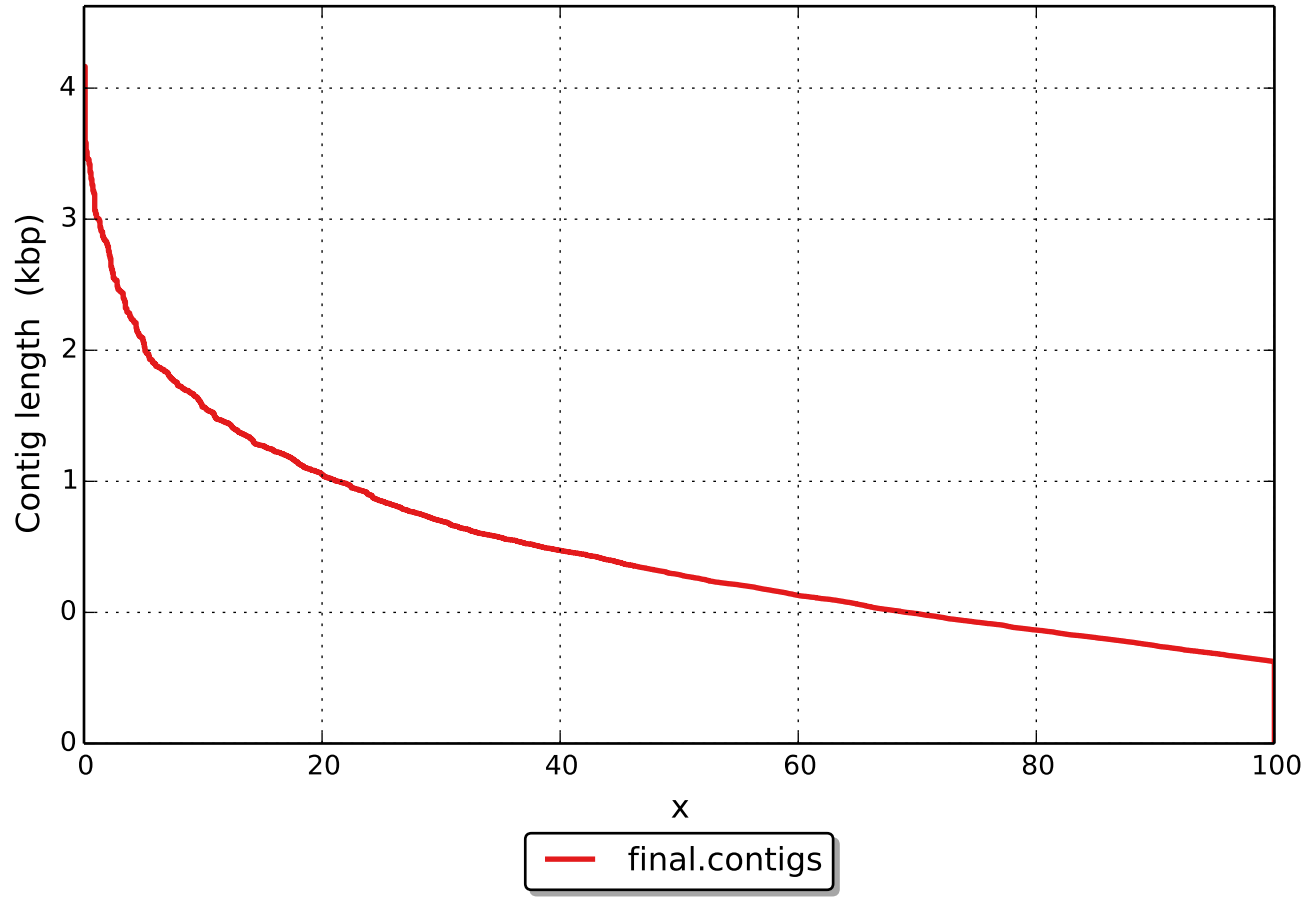


Misassemblies





NAx



NGAx

