

Report

	final.contigs
# contigs (≥ 0 bp)	2009
# contigs (≥ 1000 bp)	1342
Total length (≥ 0 bp)	10917684
Total length (≥ 1000 bp)	10644343
# contigs	1517
Largest contig	62726
Total length	10765681
Reference length	10957366
GC (%)	50.39
Reference GC (%)	50.50
N50	12427
NG50	12148
N75	6576
NG75	6335
L50	265
LG50	273
L75	563
LG75	585
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	36757
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.580
Duplication ratio	1.013
# N's per 100 kbp	0.00
# mismatches per 100 kbp	16.44
# indels per 100 kbp	0.10
Largest alignment	62726
NA50	12324
NGA50	12140
NA75	6576
NGA75	6327
LA50	266
LGA50	274
LA75	564
LGA75	586

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

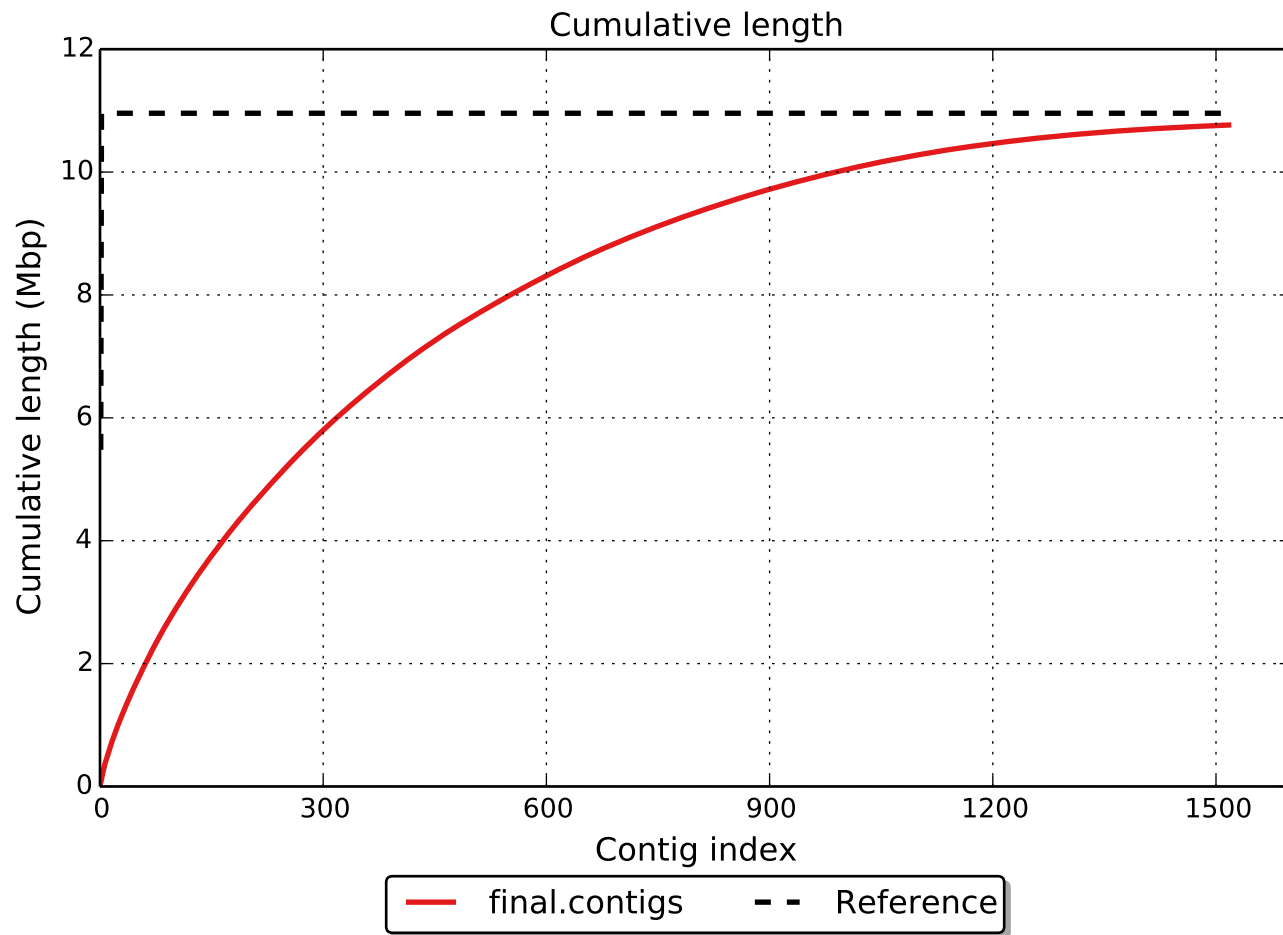
	final.contigs
# misassemblies	3
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	2
# possibly misassembled contigs	0
# misassembled contigs	3
Misassembled contigs length	36757
# local misassemblies	0
# mismatches	1758
# indels	11
# short indels	8
# long indels	3
Indels length	42

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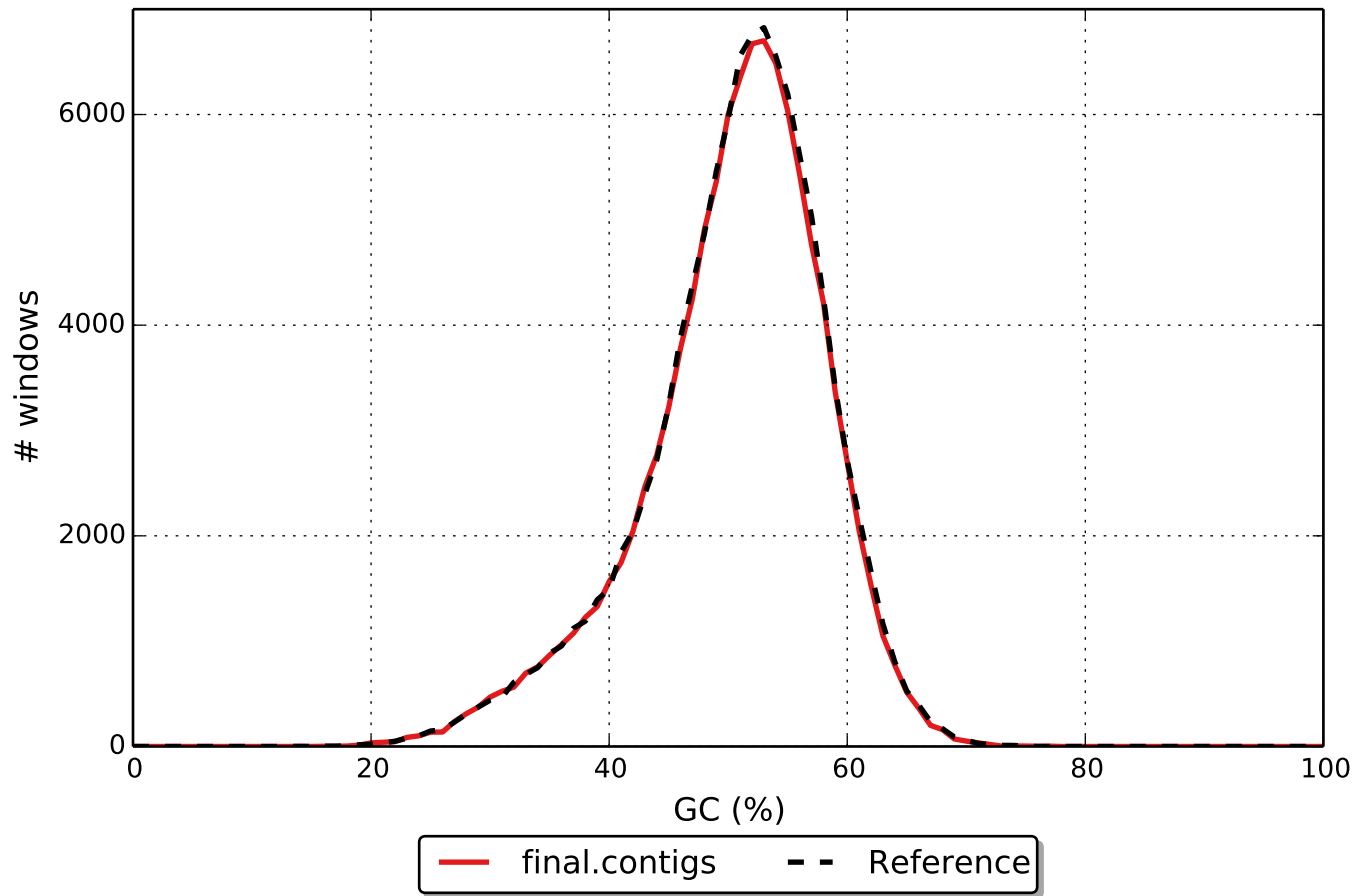
Unaligned report

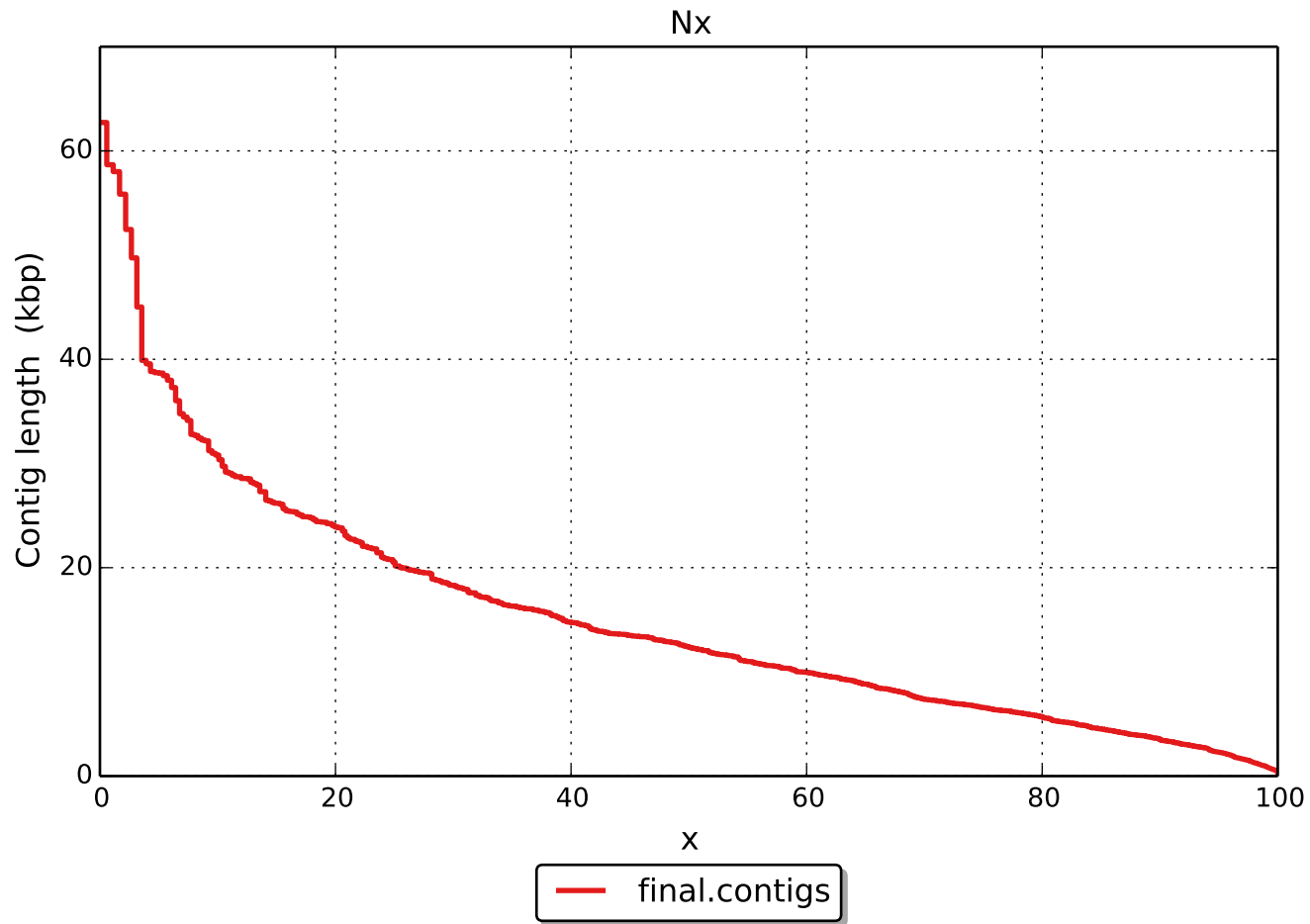
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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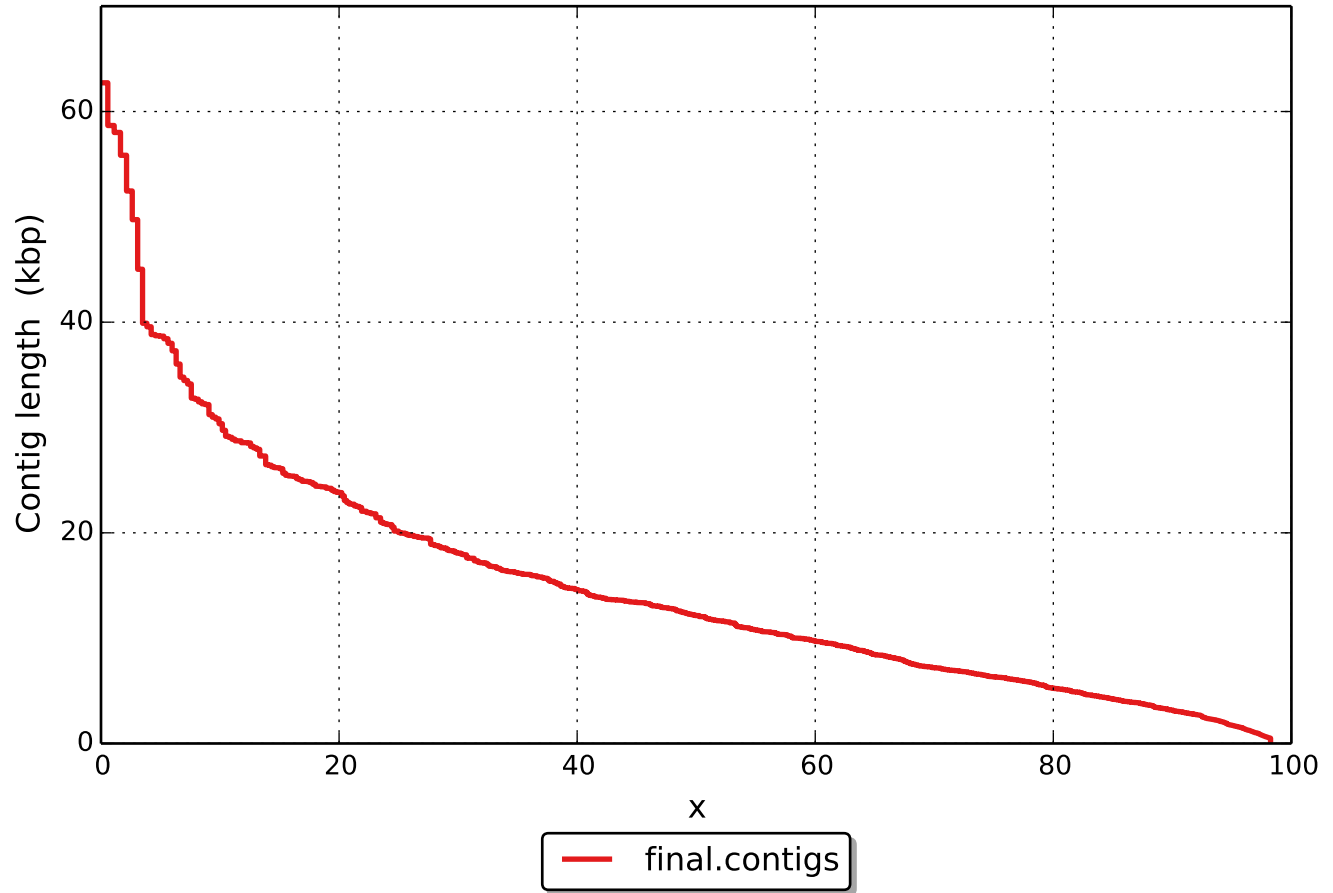


GC content

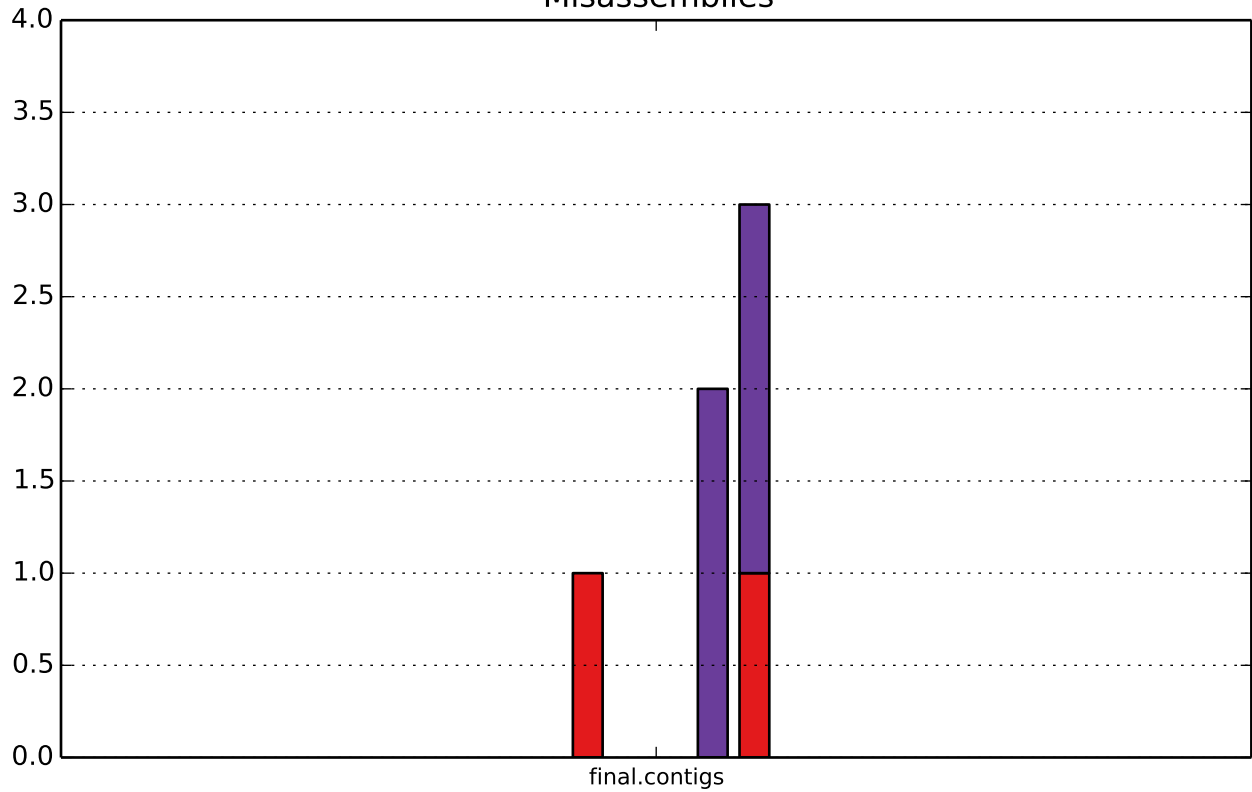


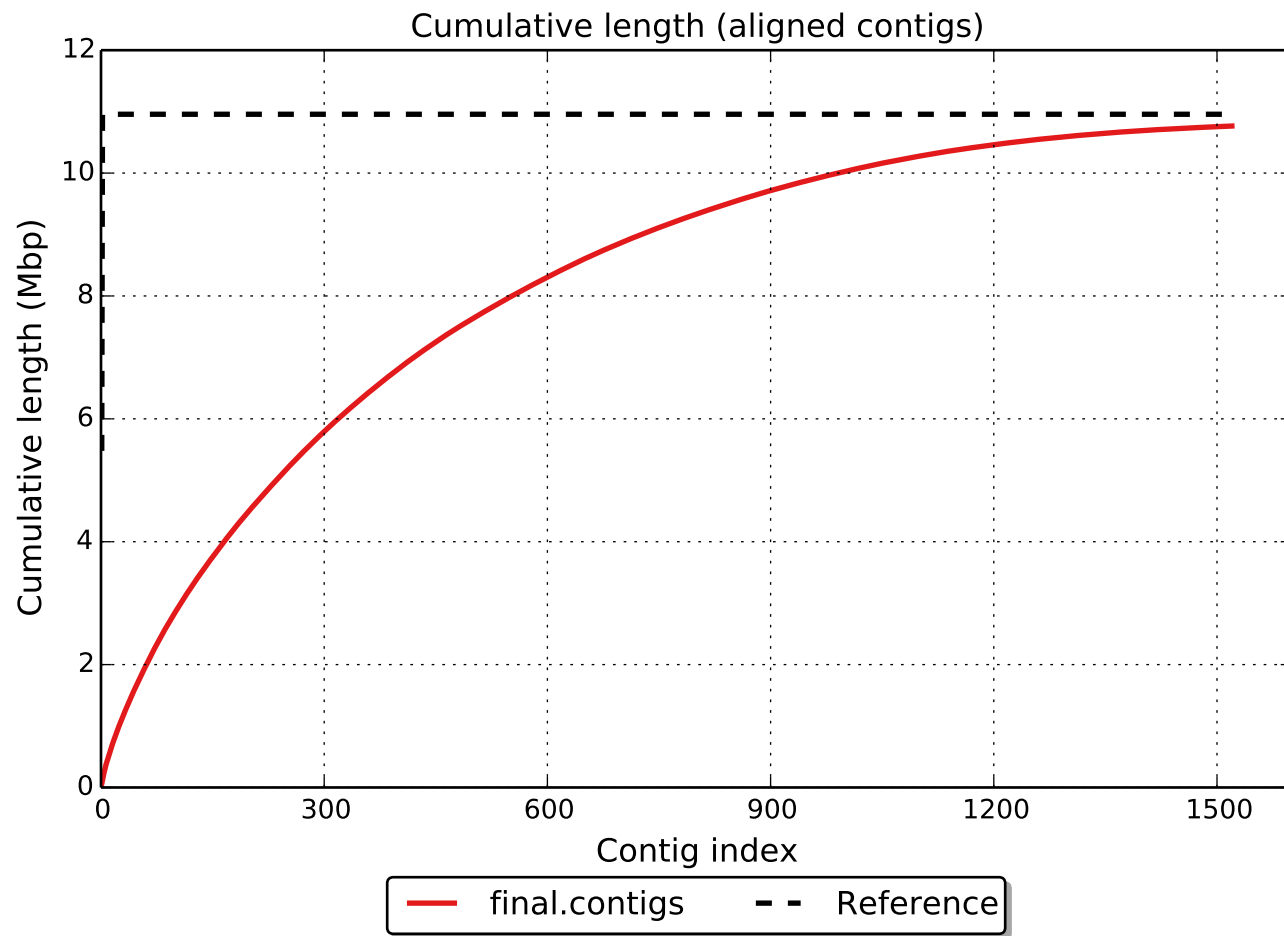


NGx

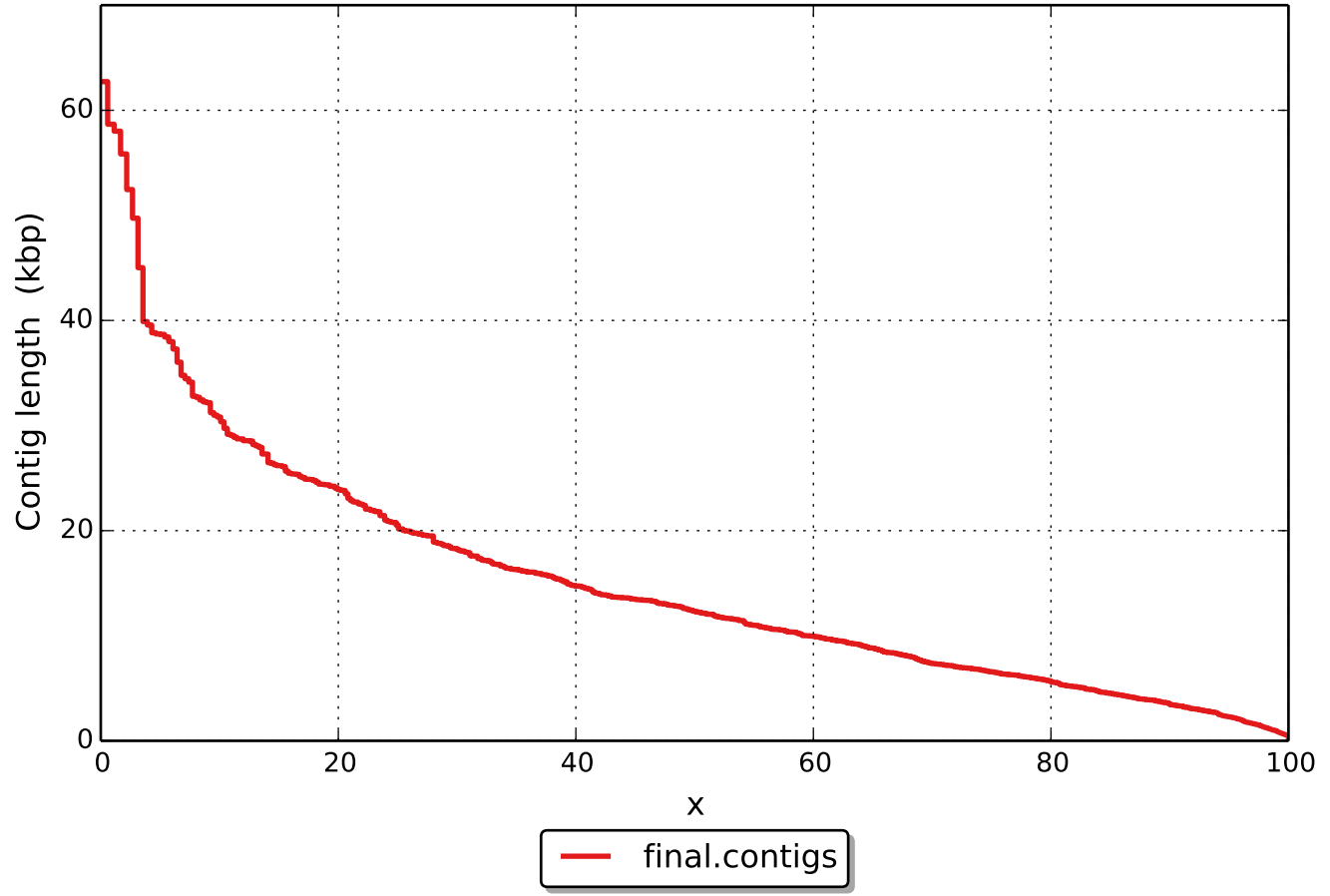


Misassemblies





NAx



NGAx

