

Report

	final.contigs
# contigs (≥ 0 bp)	871
# contigs (≥ 1000 bp)	719
Total length (≥ 0 bp)	5252790
Total length (≥ 1000 bp)	5147207
# contigs	871
Largest contig	44173
Total length	5252790
Reference length	5547323
GC (%)	50.27
Reference GC (%)	50.48
N50	11277
NG50	10648
N75	5768
NG75	4960
L50	143
LG50	157
L75	303
LG75	344
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# unaligned contigs	0 + 4 part
Unaligned length	39605
Genome fraction (%)	92.479
Duplication ratio	1.016
# N's per 100 kbp	0.00
# mismatches per 100 kbp	40.56
# indels per 100 kbp	0.25
Largest alignment	44173
NA50	10958
NGA50	10462
NA75	5652
NGA75	4790
LA50	147
LGA50	160
LA75	310
LGA75	352

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

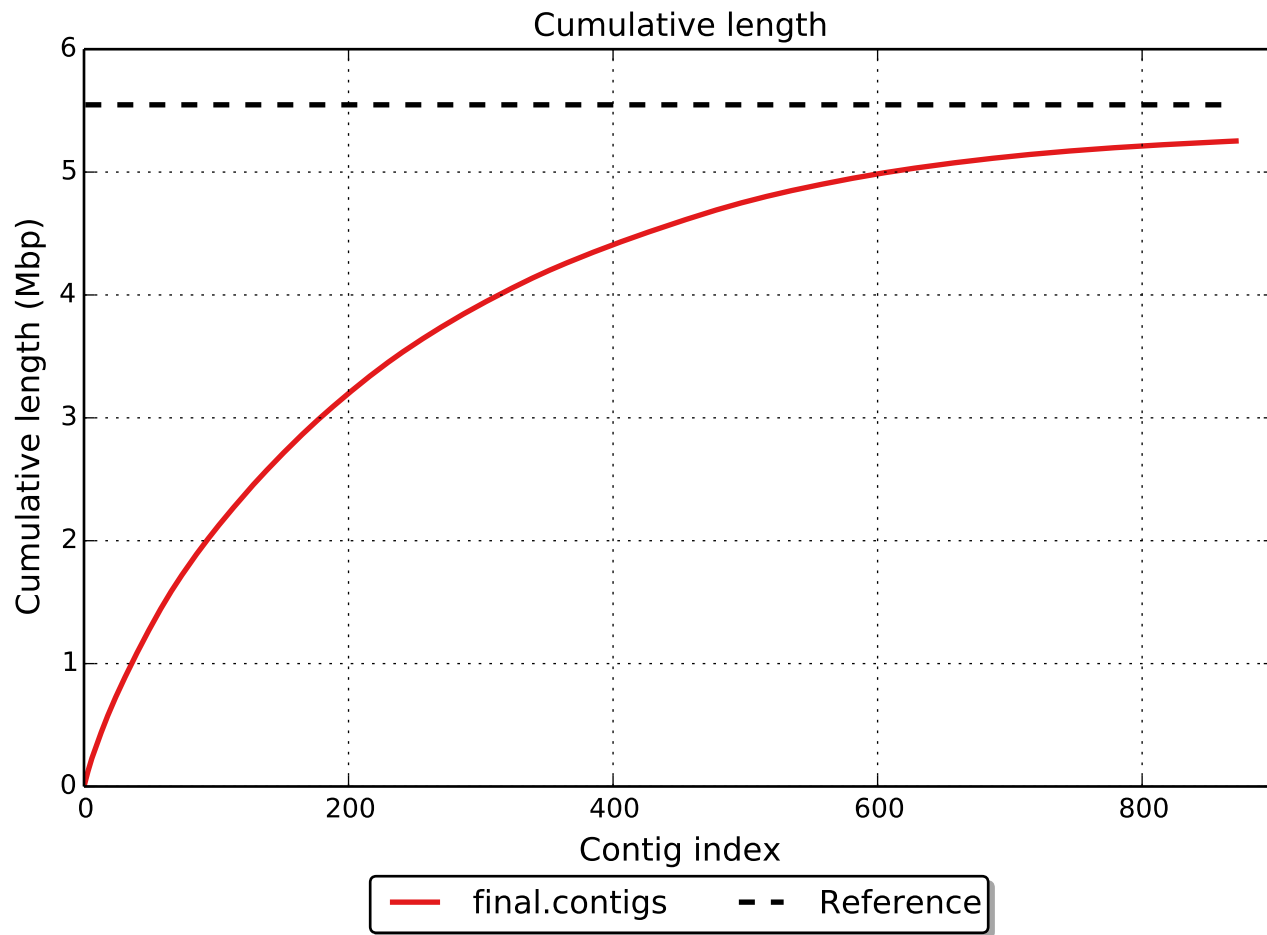
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	4
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	3
# mismatches	2081
# indels	13
# short indels	12
# long indels	1
Indels length	18

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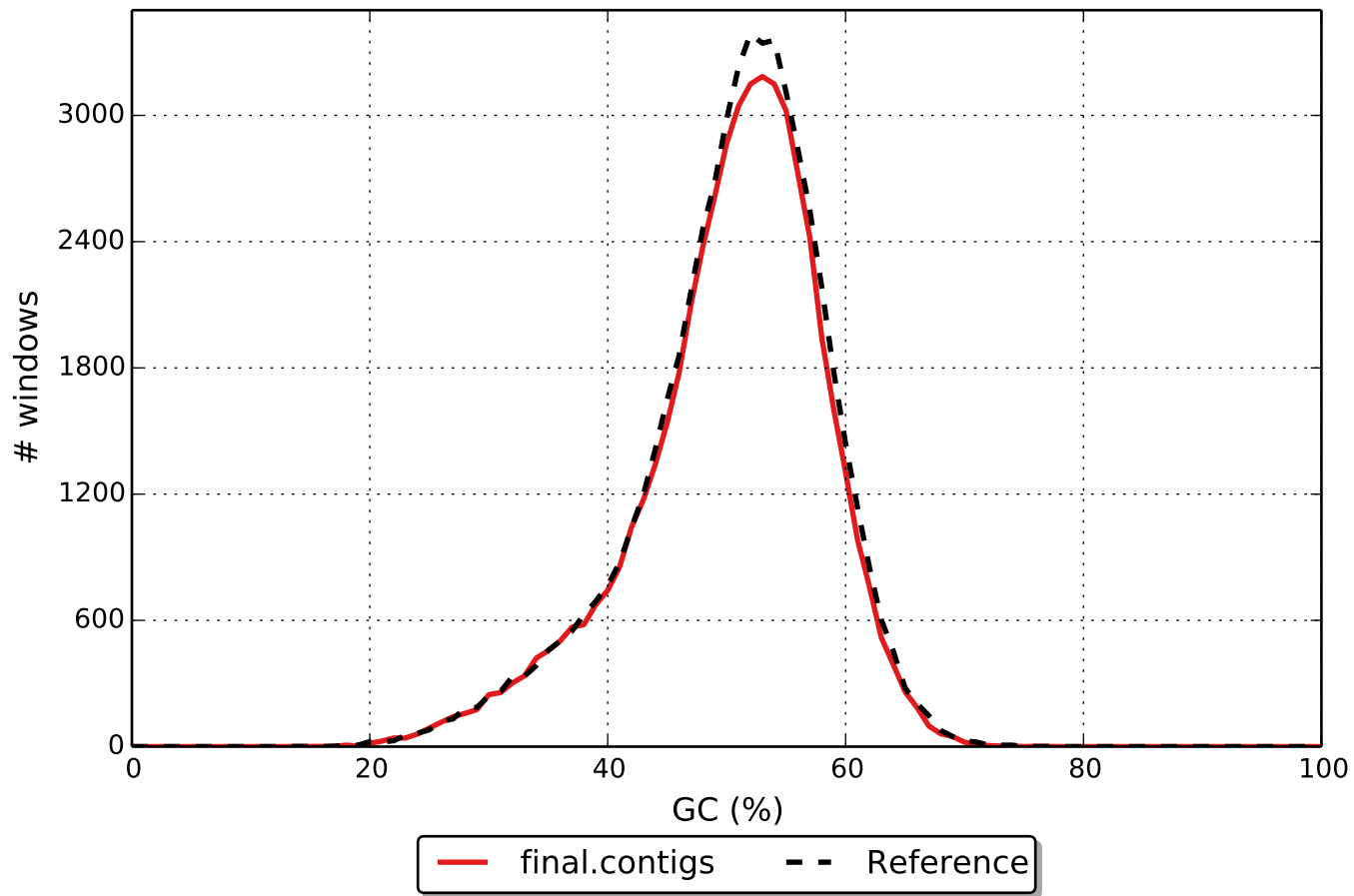
Unaligned report

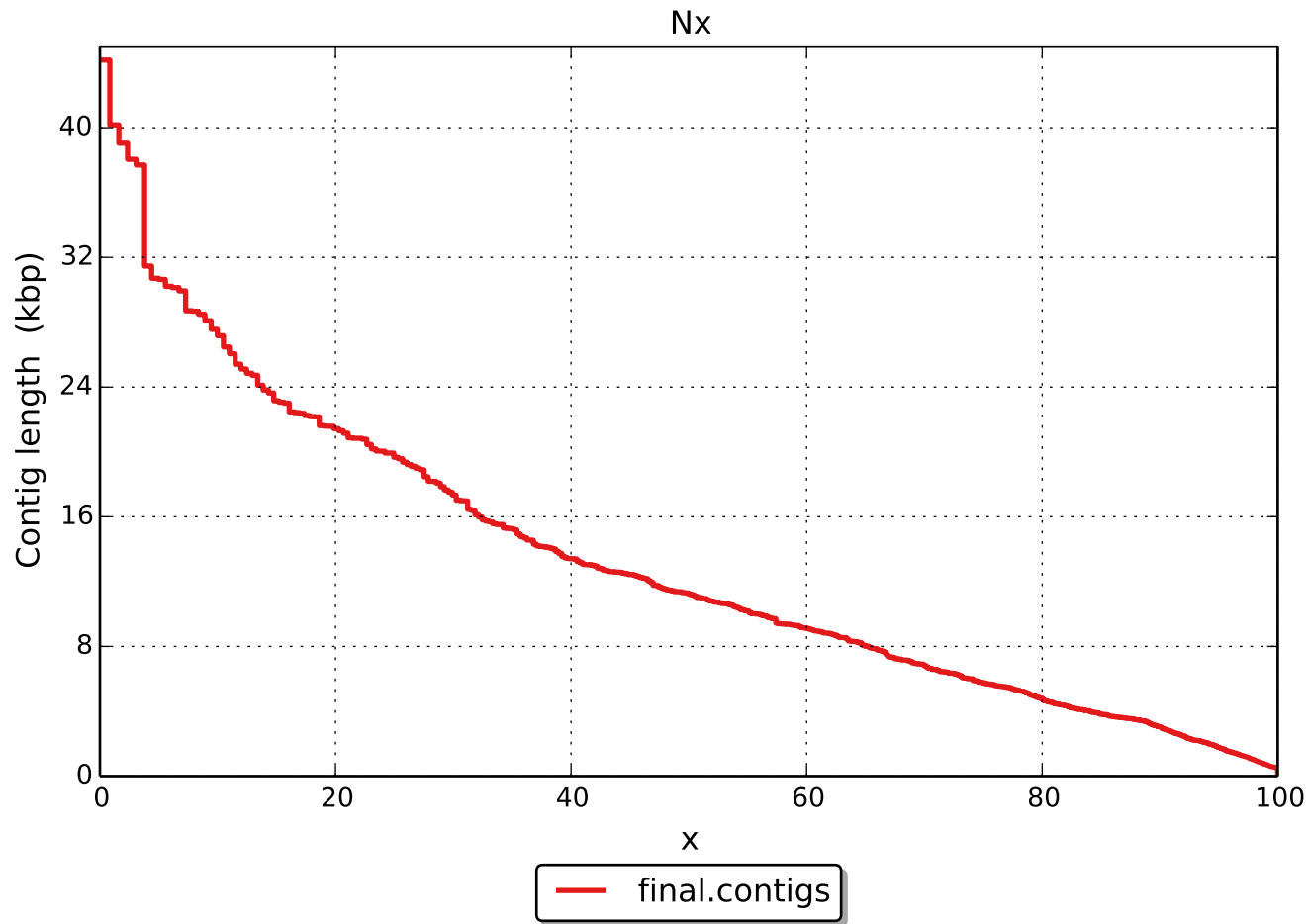
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	4
# with misassembly	0
# both parts are significant	4
Partially unaligned length	39605
# N's	0

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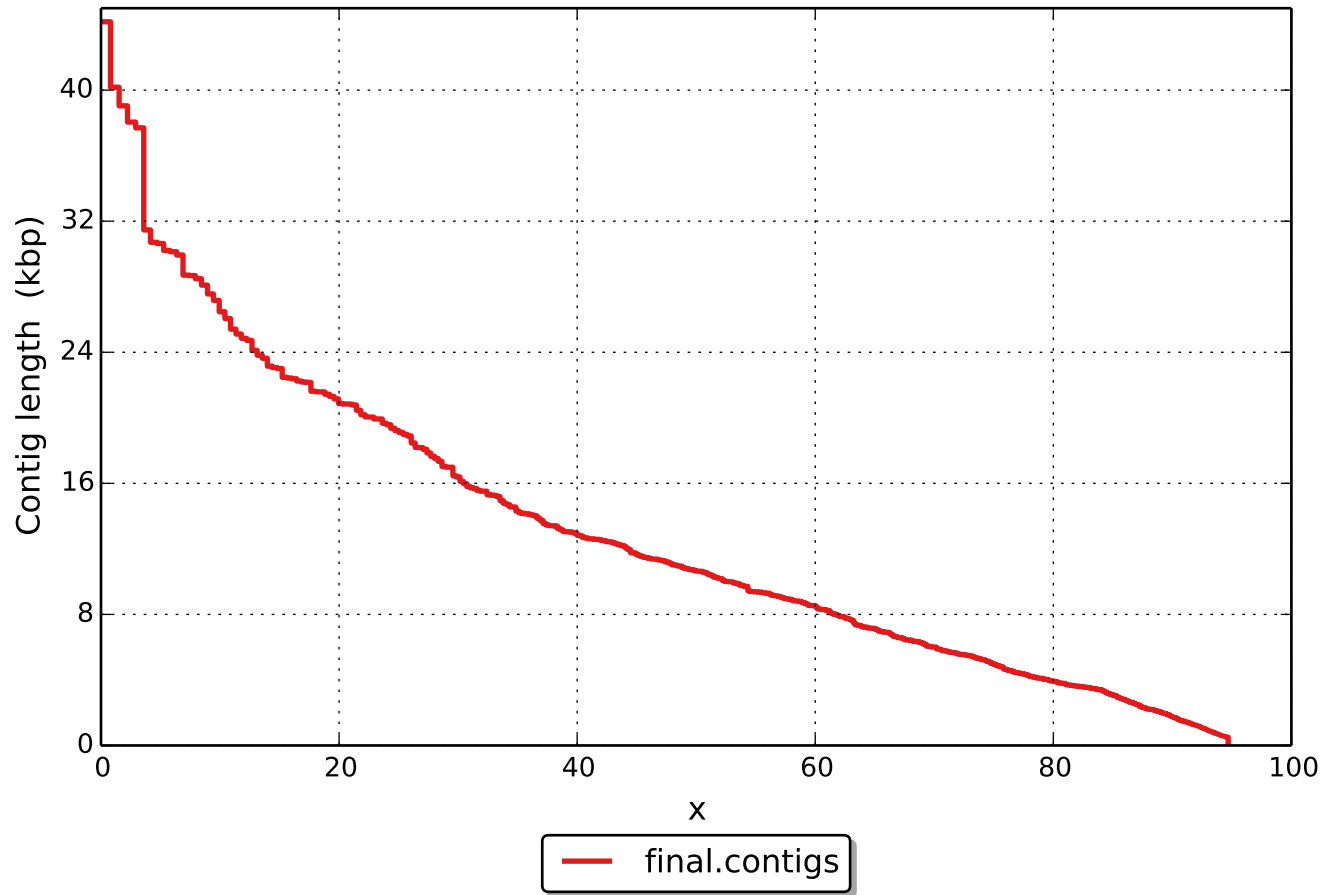


GC content



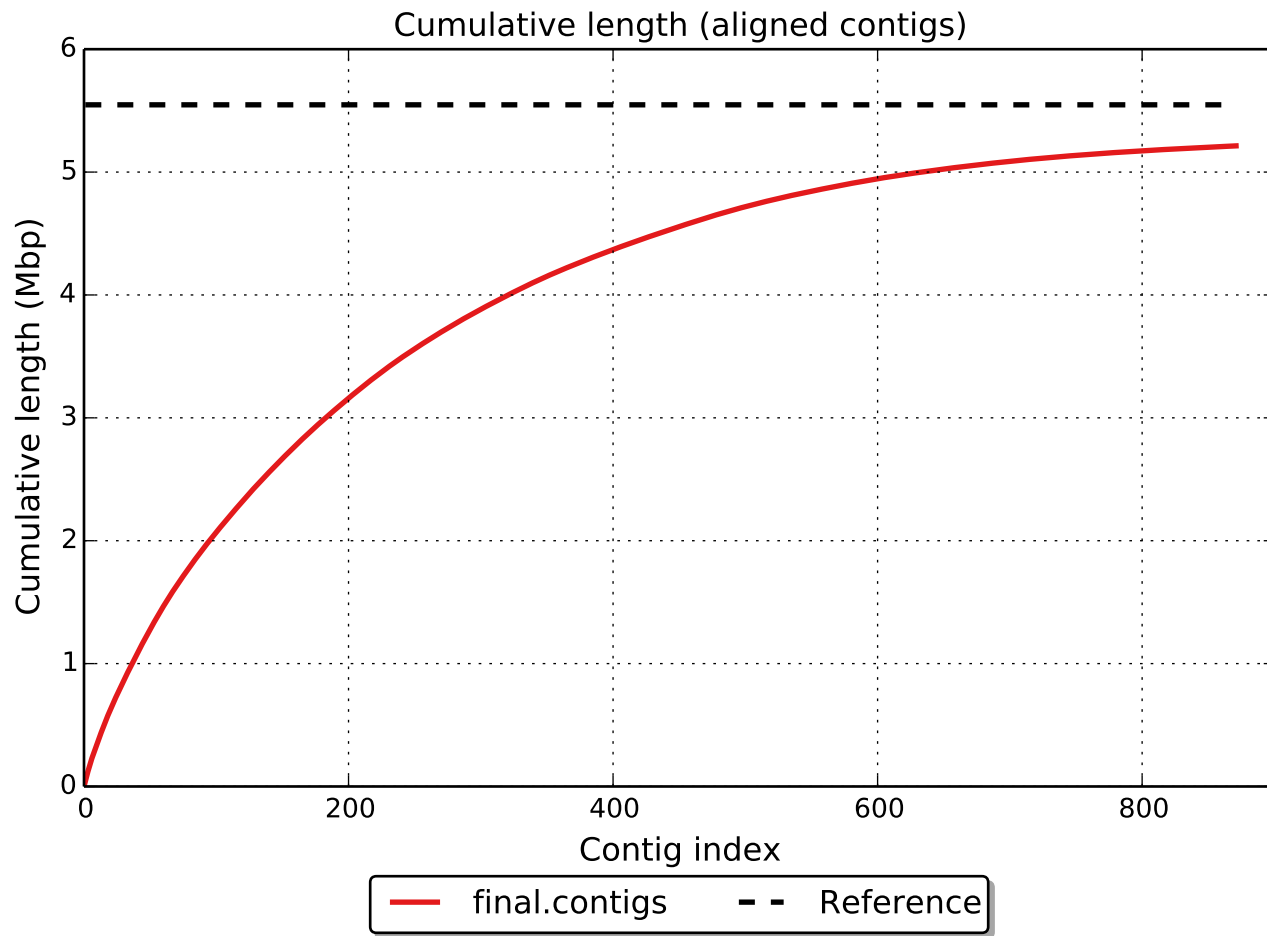


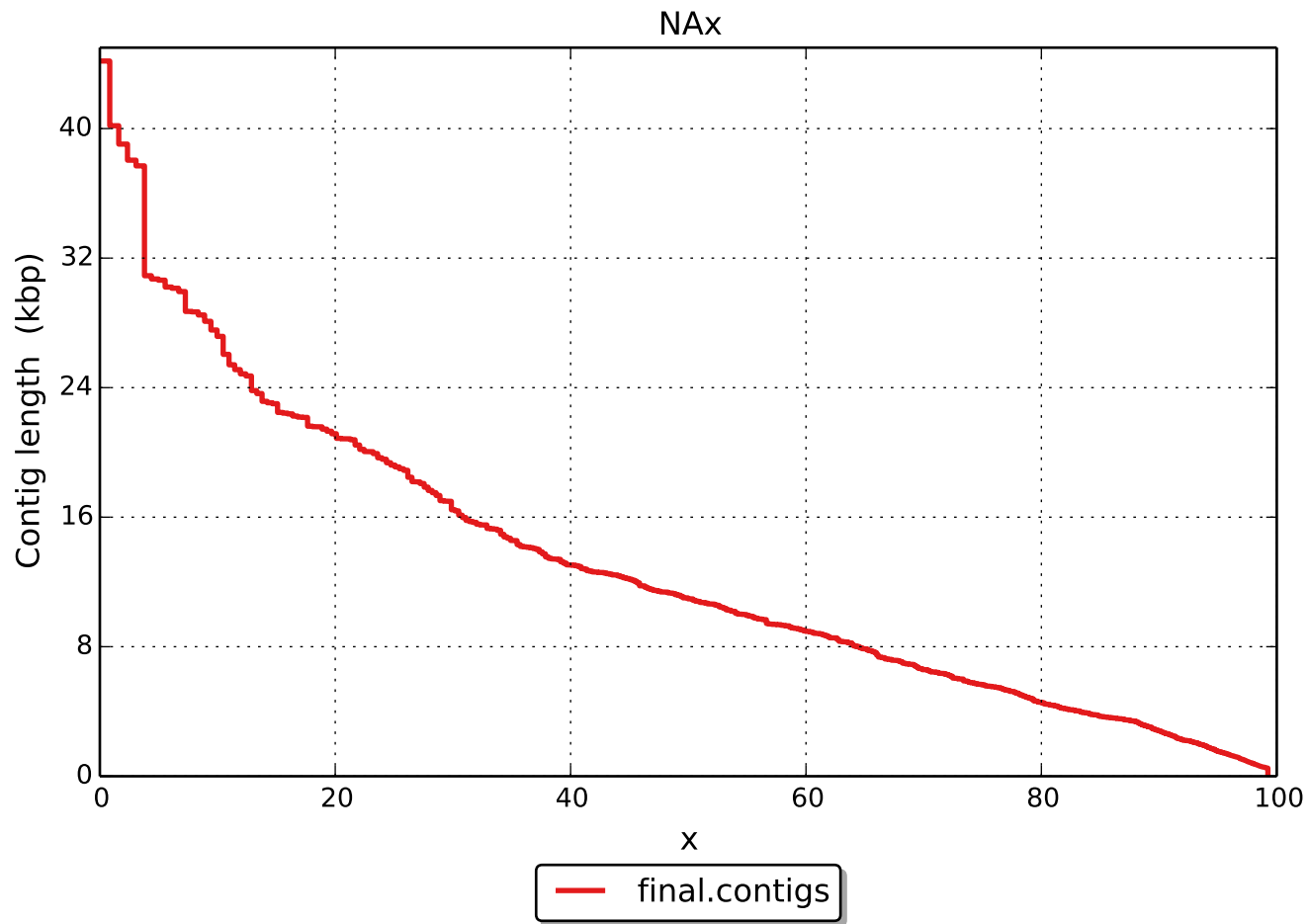
NGx



Misassemblies







NGAx

