

Report

	final.contigs
# contigs (≥ 0 bp)	2447
# contigs (≥ 1000 bp)	1412
Total length (≥ 0 bp)	3615864
Total length (≥ 1000 bp)	2864120
# contigs	2447
Largest contig	7824
Total length	3615864
Reference length	1892775
GC (%)	32.29
Reference GC (%)	32.26
N50	1847
NG50	2835
N75	1096
NG75	2249
L50	635
LG50	257
L75	1267
LG75	445
# misassemblies	77
# misassembled contigs	77
Misassembled contigs length	141726
# local misassemblies	0
# unaligned contigs	5 + 5 part
Unaligned length	8552
Genome fraction (%)	95.844
Duplication ratio	1.988
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1776.91
# indels per 100 kbp	1.38
Largest alignment	7824
NA50	1789
NGA50	2793
NA75	1053
NGA75	2187
LA50	651
LGA50	261
LA75	1308
LGA75	454

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

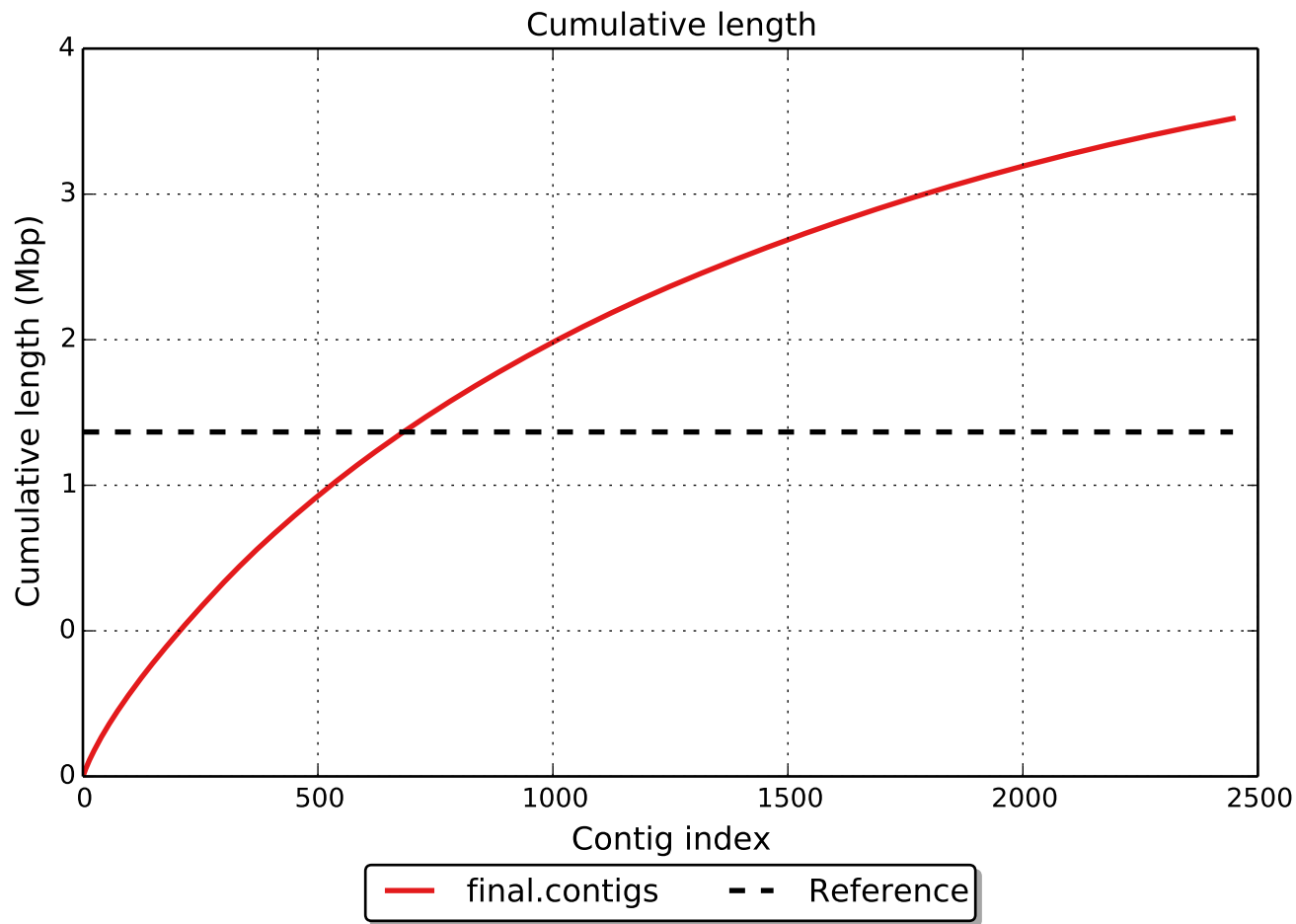
	final.contigs
# misassemblies	77
# relocations	76
# translocations	0
# inversions	1
# possibly misassembled contigs	2
# misassembled contigs	77
Misassembled contigs length	141726
# local misassemblies	0
# mismatches	32235
# indels	25
# short indels	25
# long indels	0
Indels length	25

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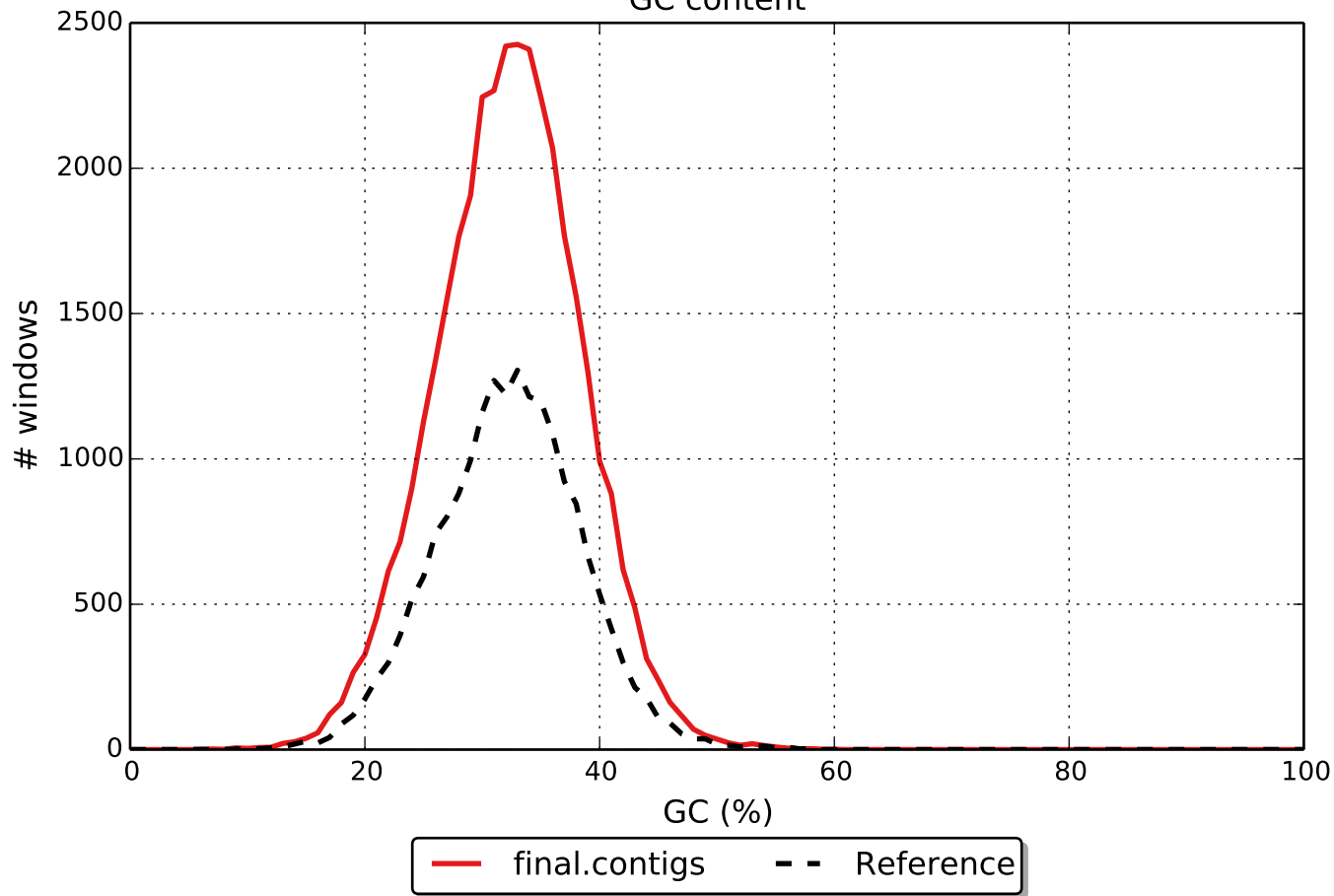
Unaligned report

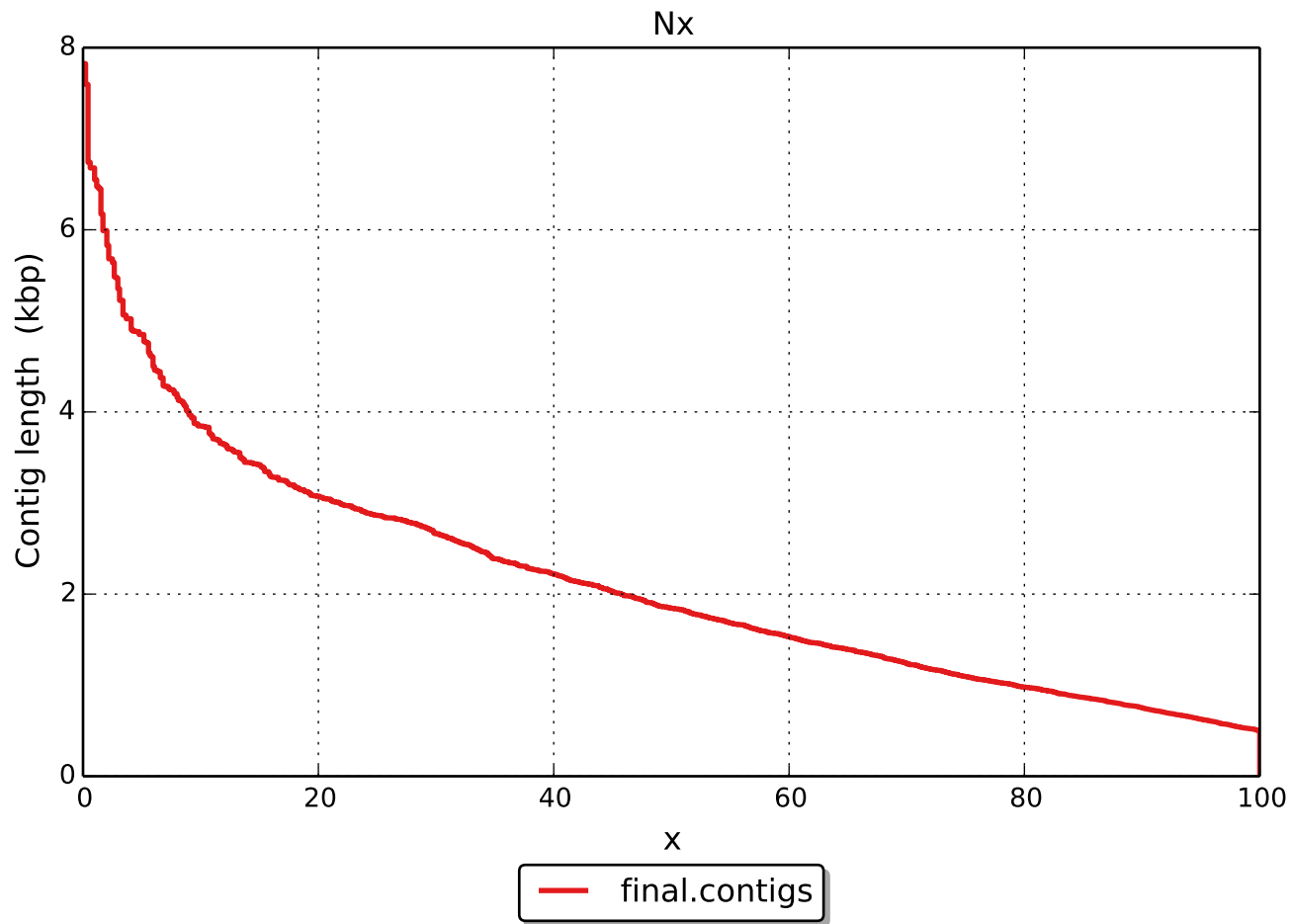
	final.contigs
# fully unaligned contigs	5
Fully unaligned length	6425
# partially unaligned contigs	5
# with misassembly	0
# both parts are significant	1
Partially unaligned length	2127
# N's	0

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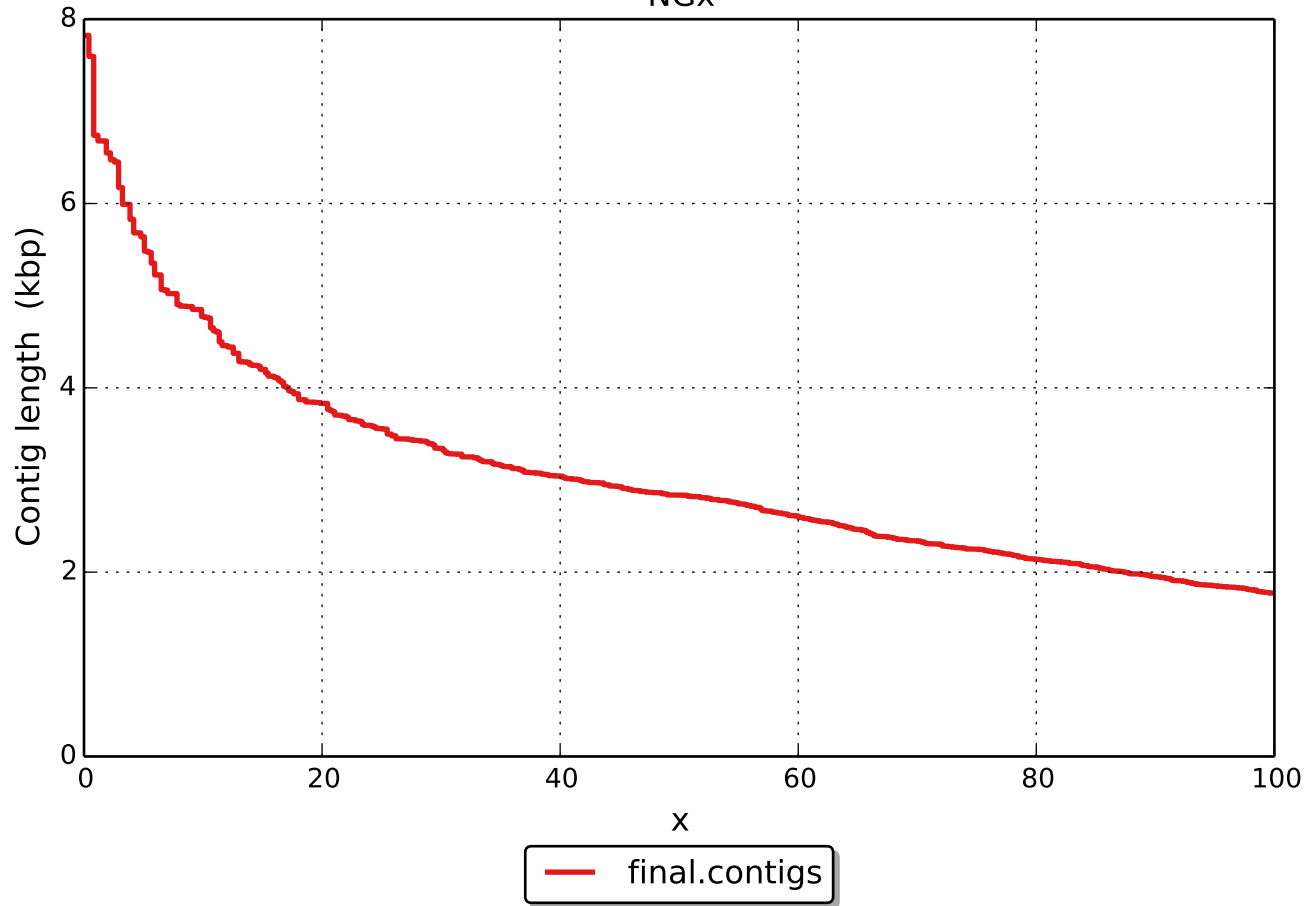


GC content

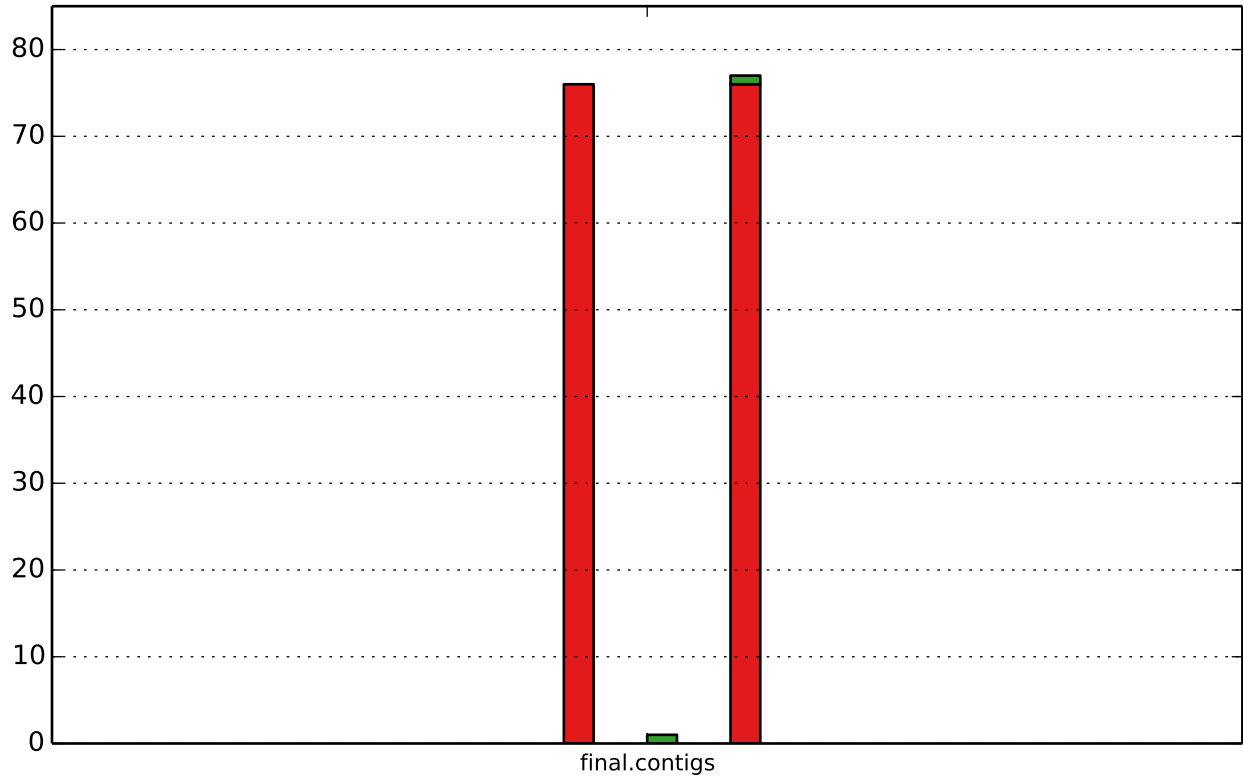


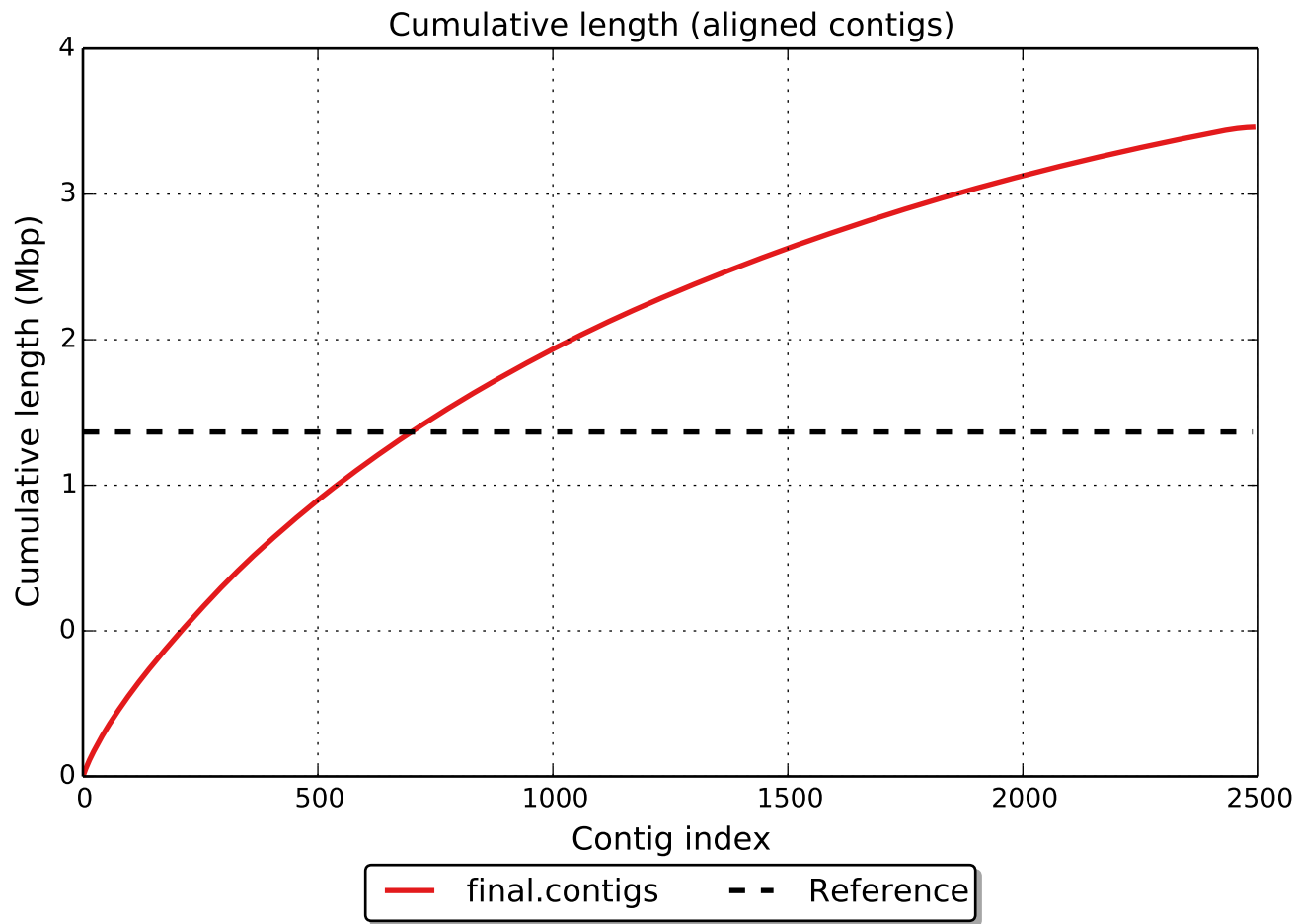


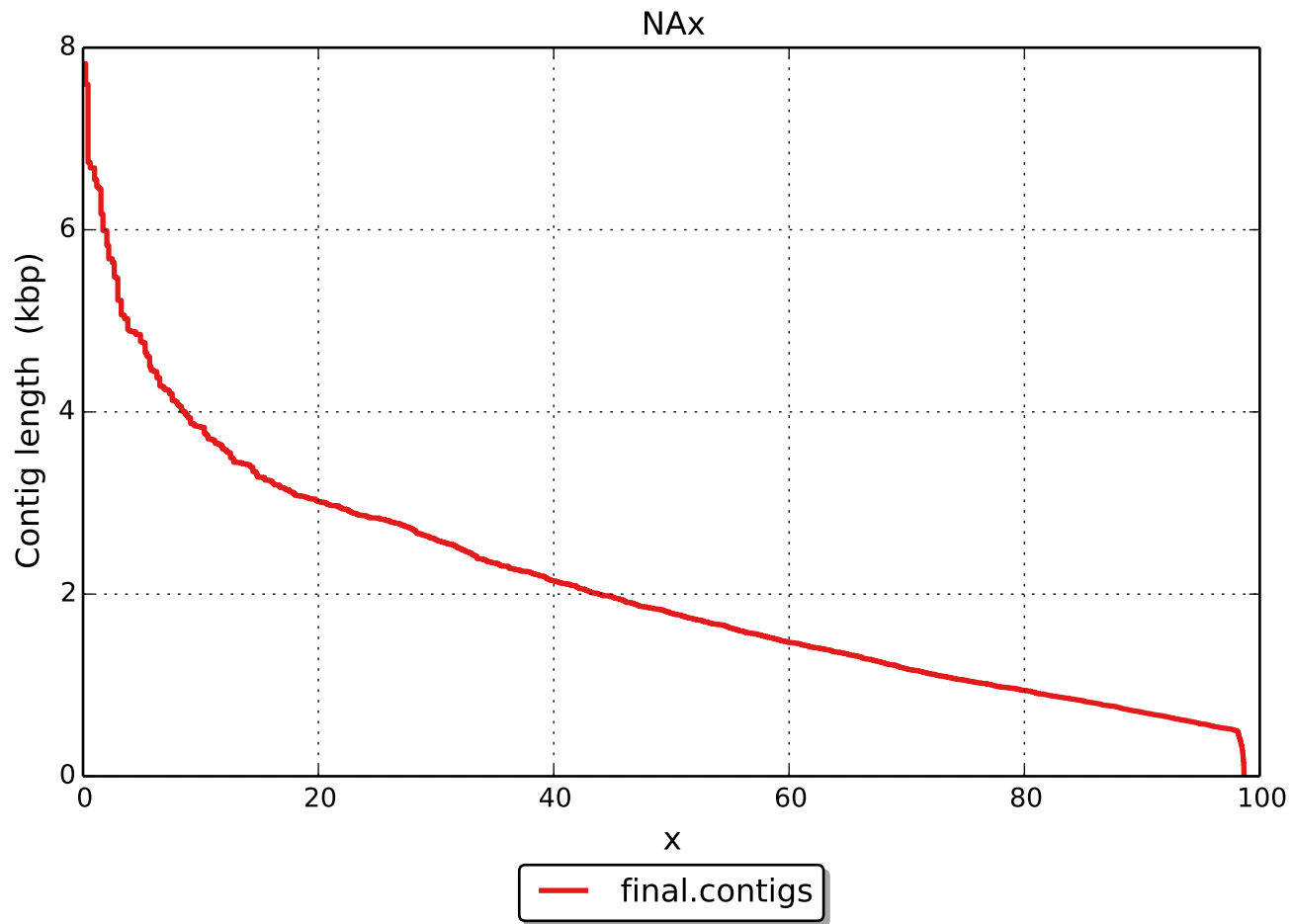
NGx



Misassemblies







NGAx

