

Report

	final.contigs
# contigs (≥ 0 bp)	508
# contigs (≥ 1000 bp)	395
Total length (≥ 0 bp)	5264893
Total length (≥ 1000 bp)	5187603
# contigs	508
Largest contig	95259
Total length	5264893
Reference length	5478683
GC (%)	50.29
Reference GC (%)	50.49
N50	26971
NG50	25902
N75	14646
NG75	12632
L50	61
LG50	65
L75	126
LG75	138
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	3111
# local misassemblies	0
# unaligned contigs	0 + 2 part
Unaligned length	29827
Genome fraction (%)	94.813
Duplication ratio	1.008
# N's per 100 kbp	0.00
# mismatches per 100 kbp	11.49
# indels per 100 kbp	0.12
Largest alignment	95259
NA50	26664
NGA50	25580
NA75	14010
NGA75	12341
LA50	62
LGA50	66
LA75	128
LGA75	141

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

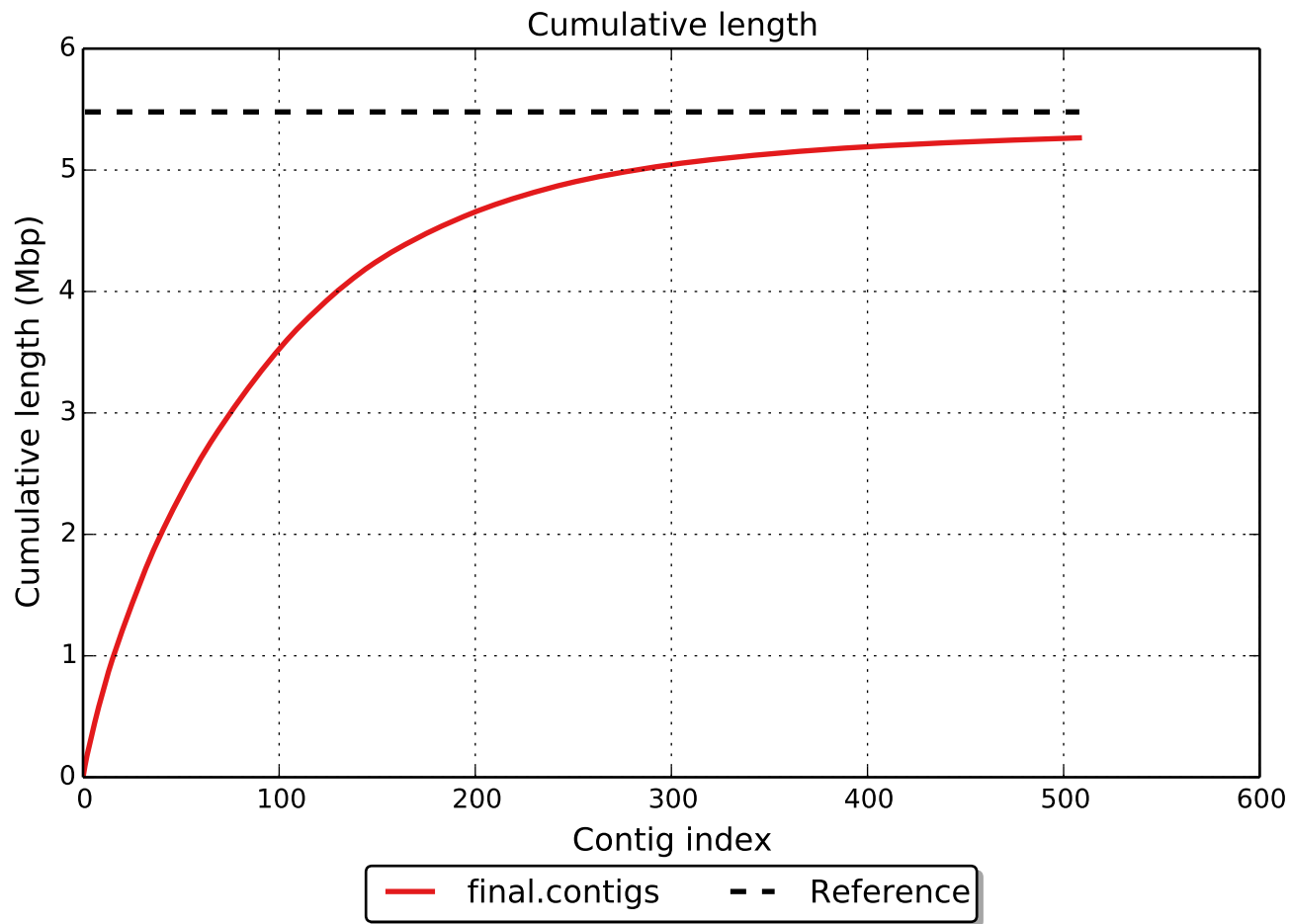
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	2
# misassembled contigs	1
Misassembled contigs length	3111
# local misassemblies	0
# mismatches	597
# indels	6
# short indels	3
# long indels	3
Indels length	65

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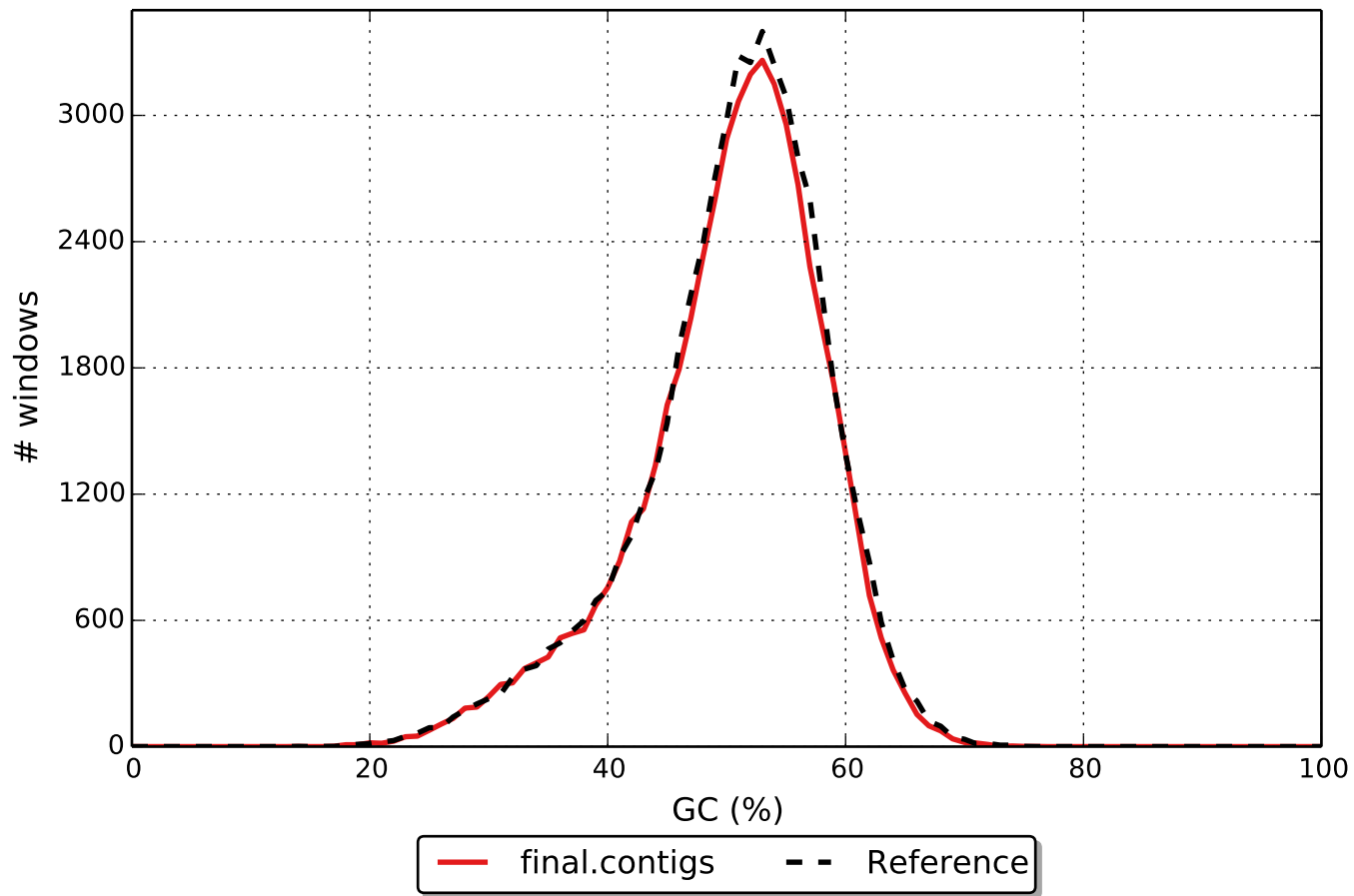
Unaligned report

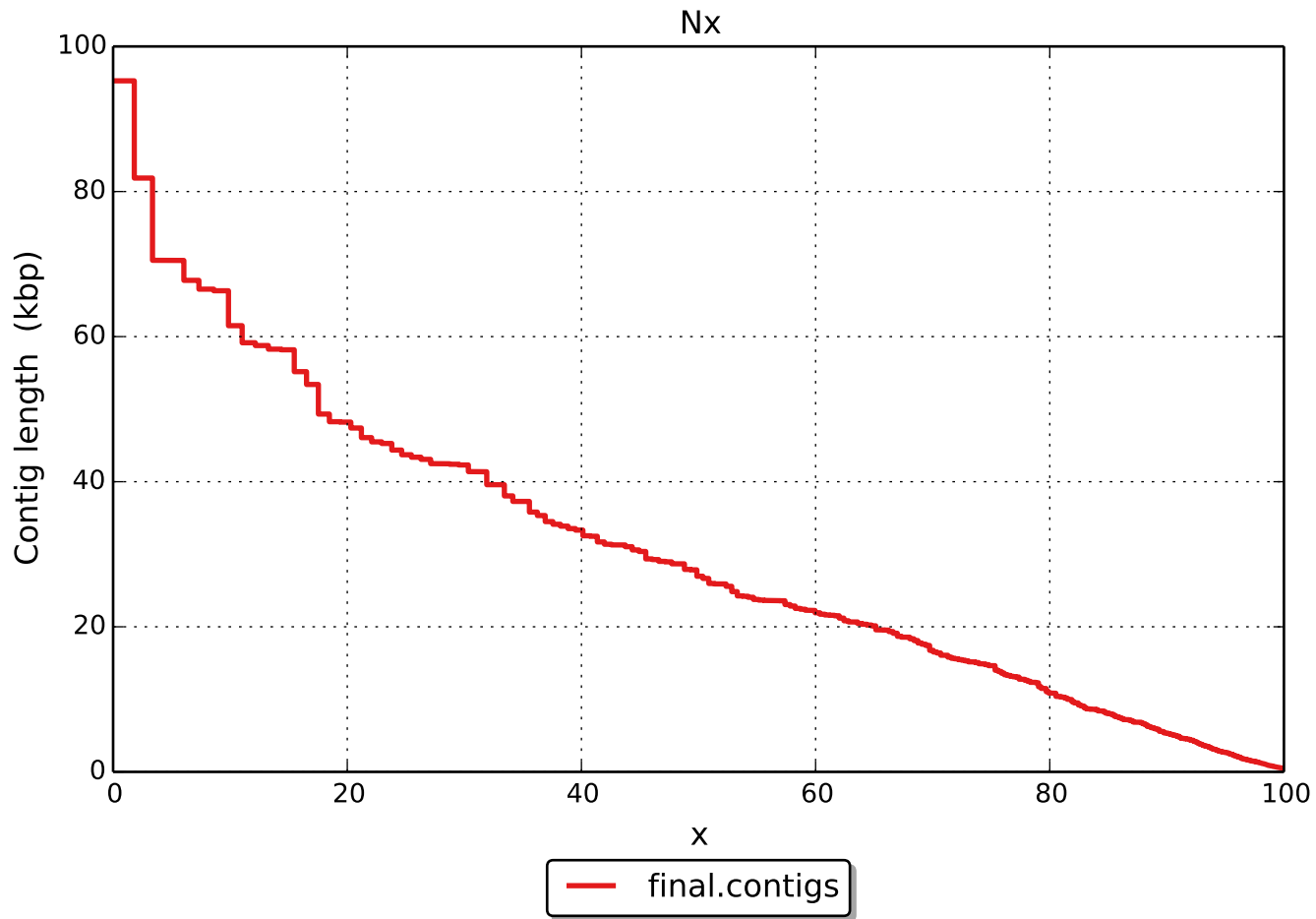
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	2
Partially unaligned length	29827
# N's	0

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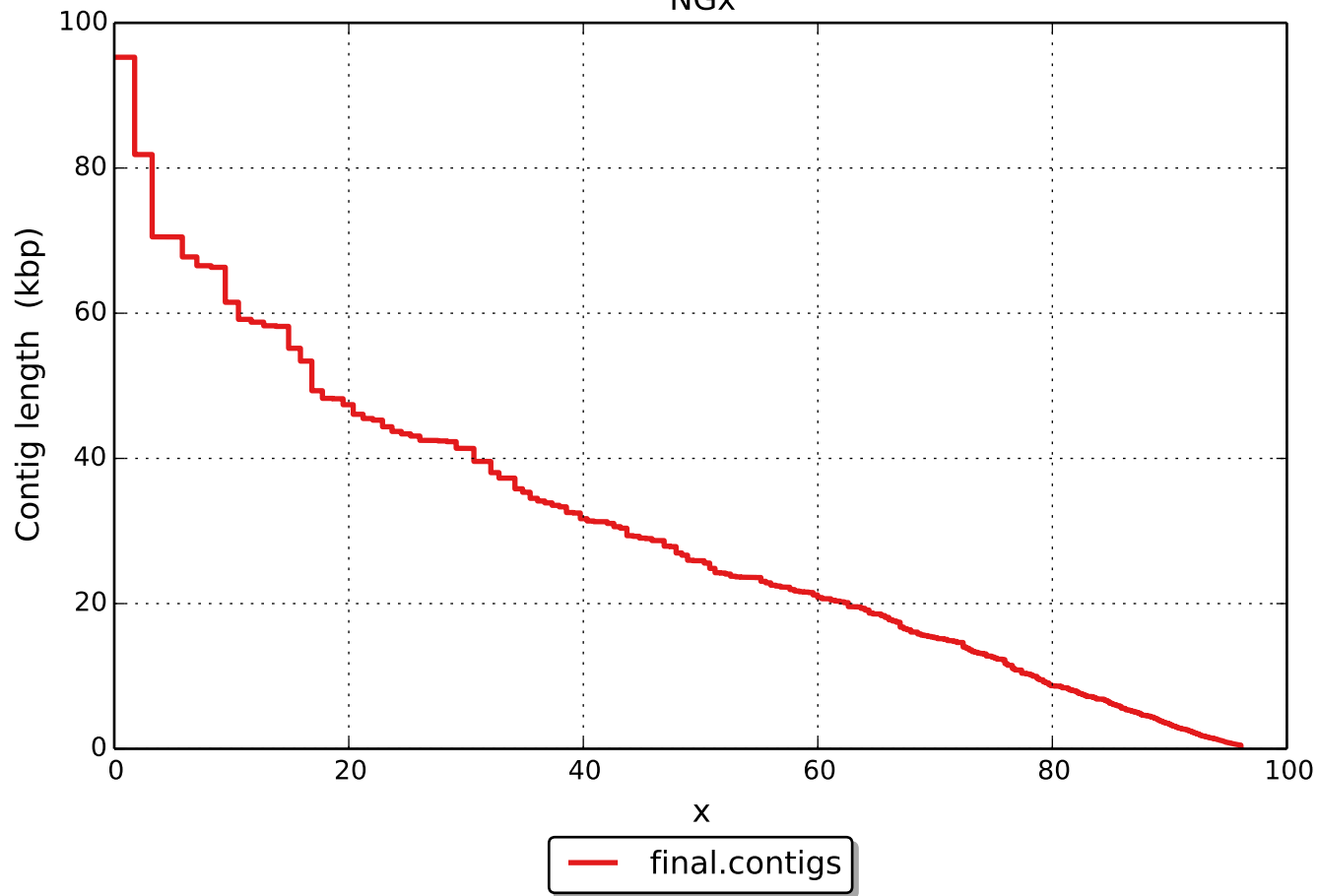


GC content





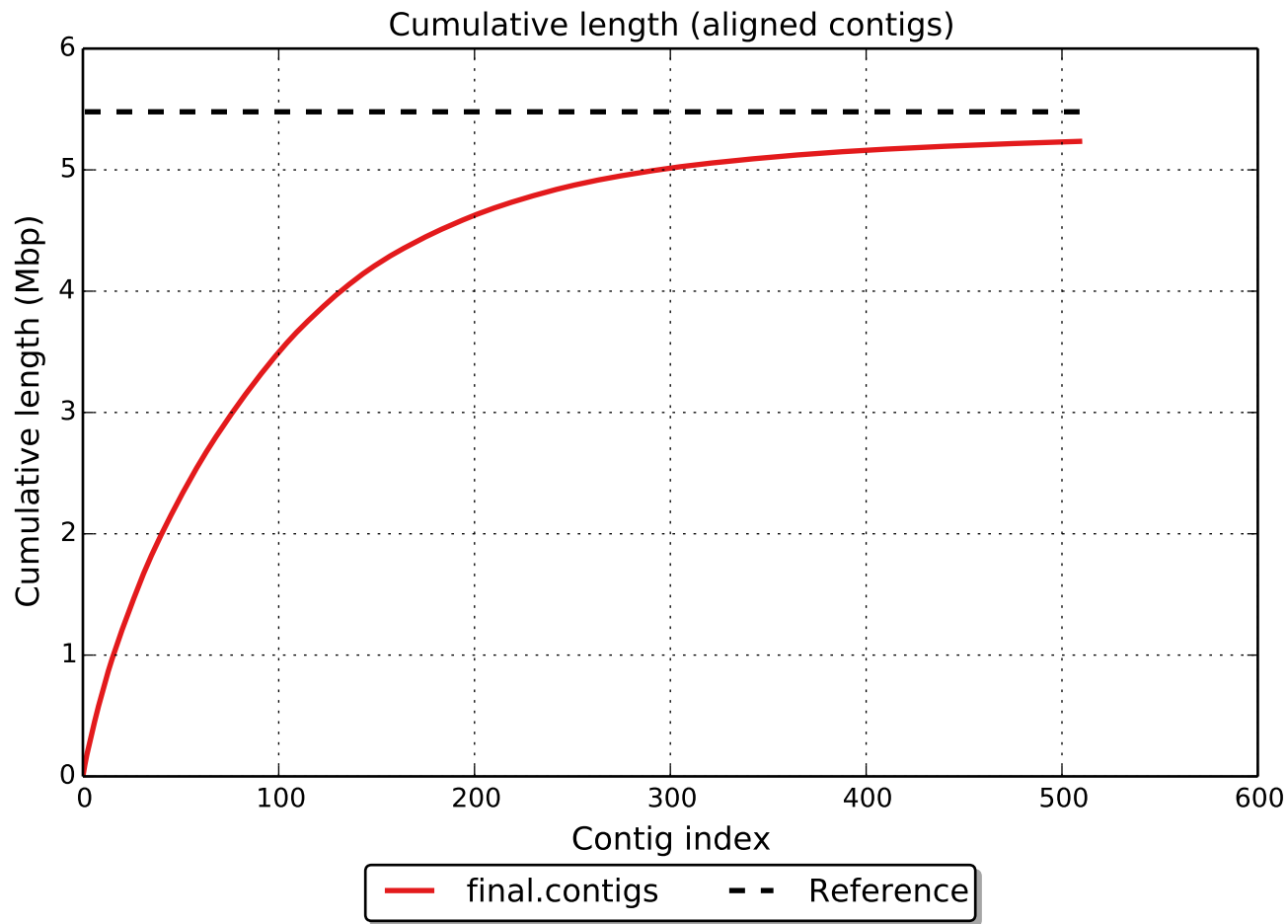
NGx



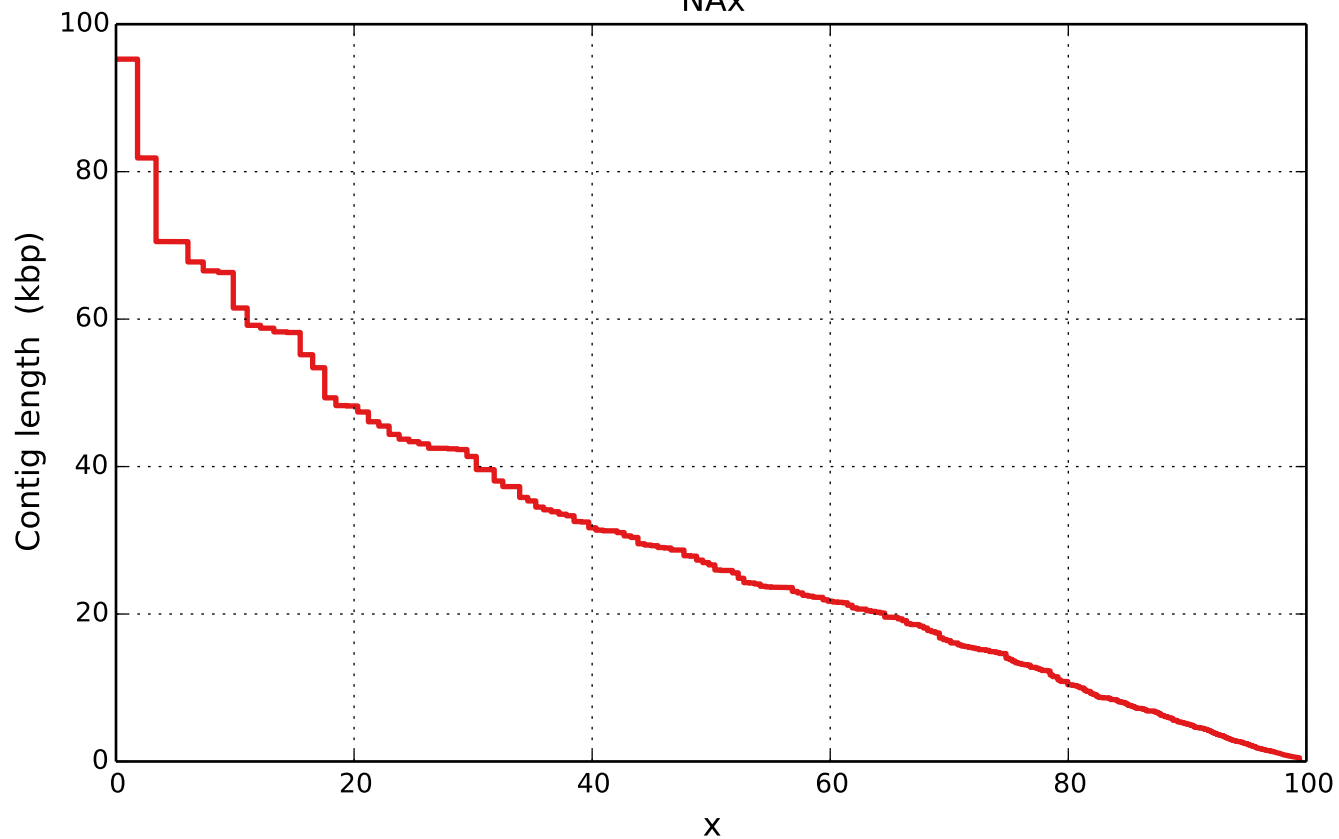
Misassemblies



 # relocations



NAx



— final.contigs

NGAx

