

Report

	final.contigs
# contigs (>= 0 bp)	340
# contigs (>= 1000 bp)	258
Total length (>= 0 bp)	3729744
Total length (>= 1000 bp)	3701411
# contigs	269
Largest contig	58143
Total length	3709443
Reference length	3785550
GC (%)	32.26
Reference GC (%)	32.26
N50	21298
NG50	21287
N75	12857
NG75	12583
L50	59
LG50	60
L75	113
LG75	118
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.439
Duplication ratio	1.006
# N's per 100 kbp	0.00
# mismatches per 100 kbp	10.57
# indels per 100 kbp	0.00
Largest alignment	58143
NA50	21298
NGA50	21287
NA75	12857
NGA75	12583
LA50	59
LGA50	60
LA75	113
LGA75	118

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

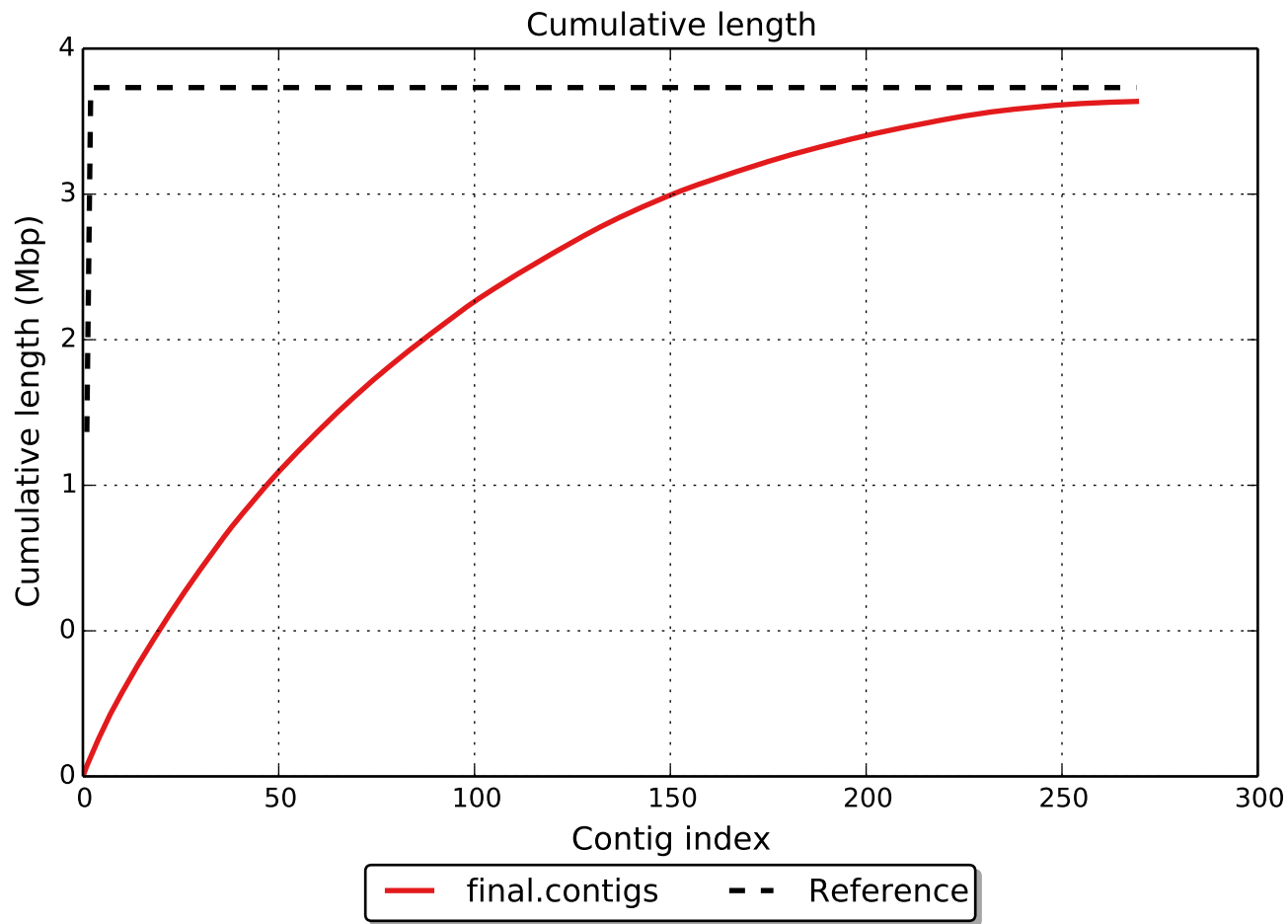
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	390
# indels	0
# short indels	0
# long indels	0
Indels length	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).

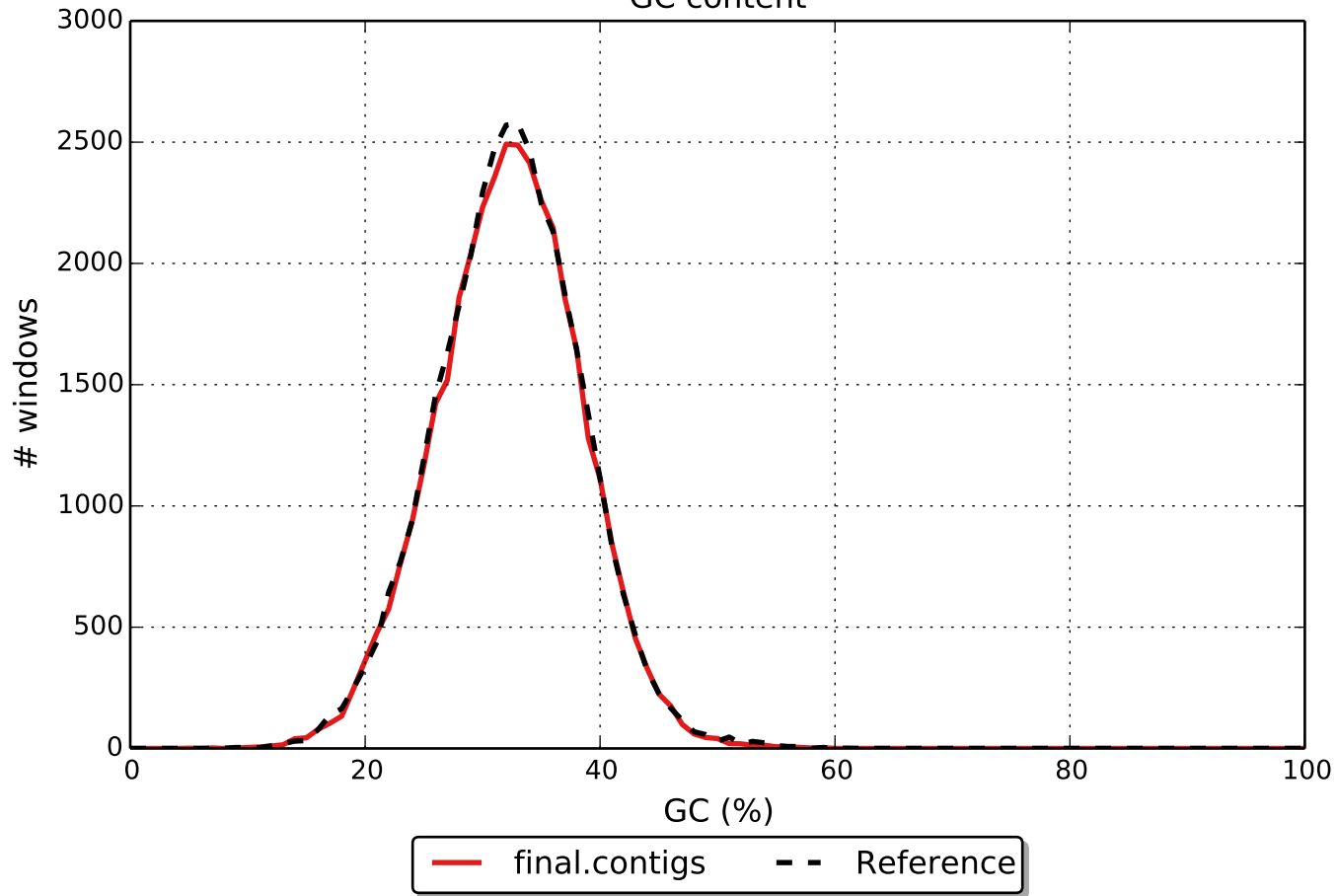
Unaligned report

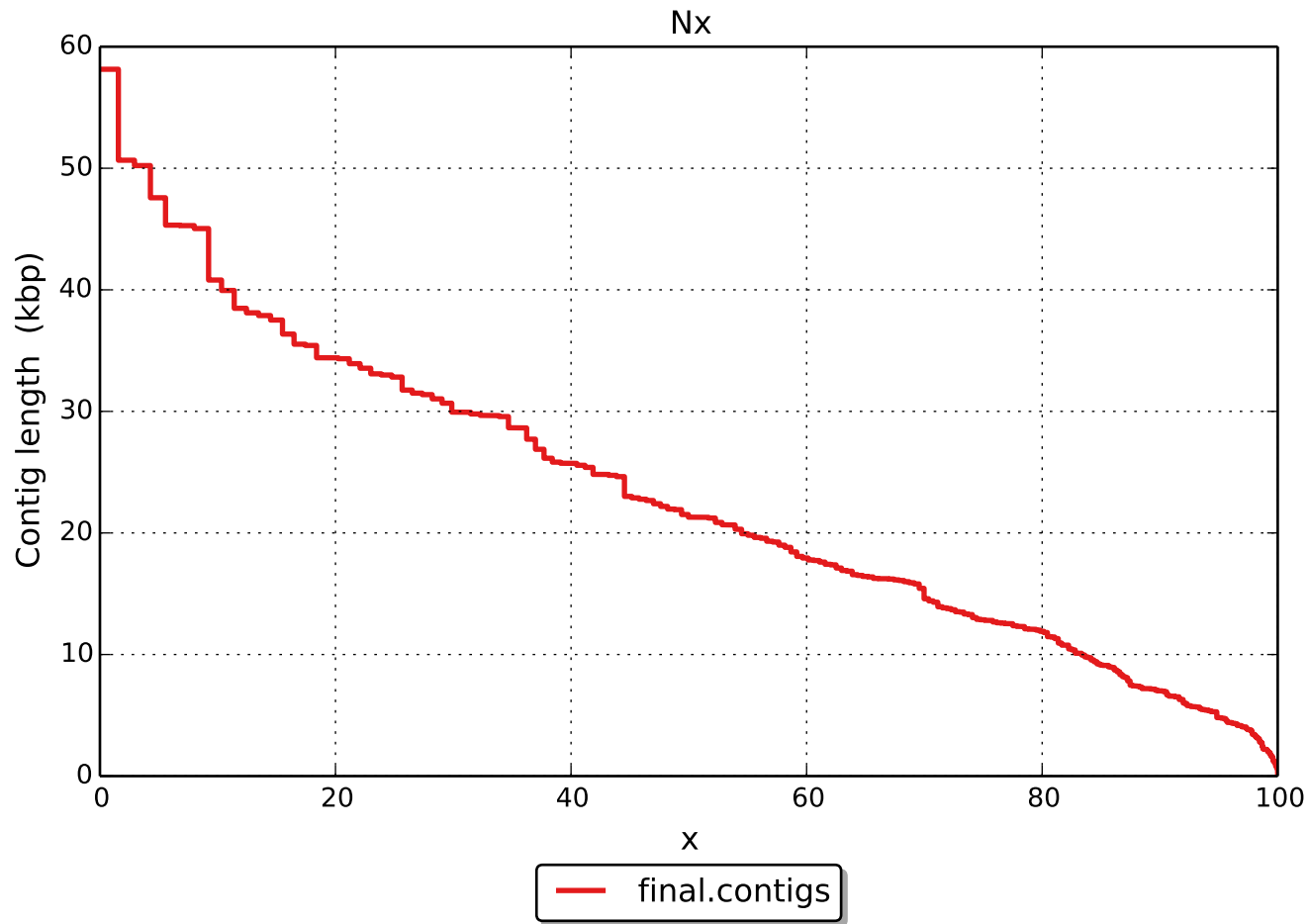
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

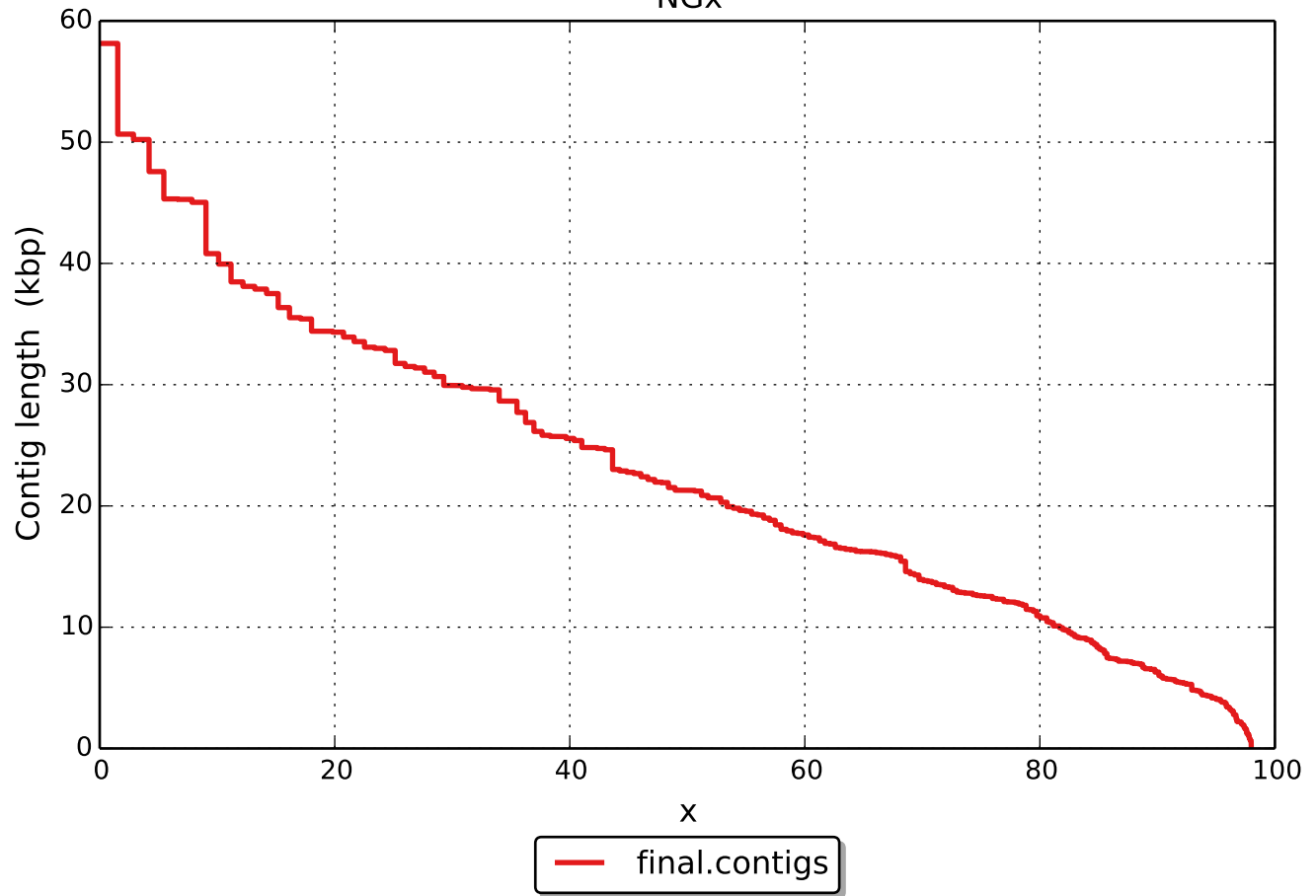


GC content



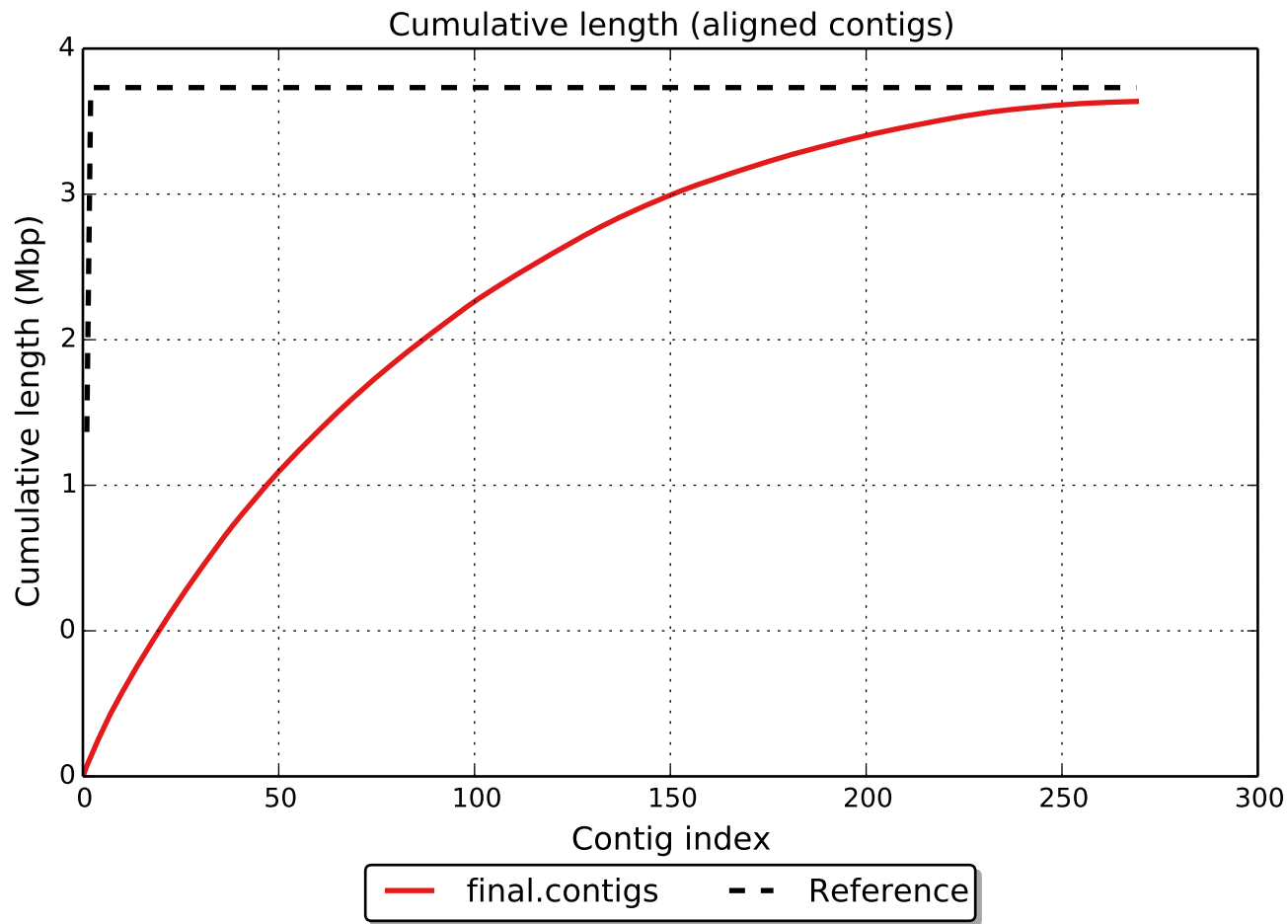


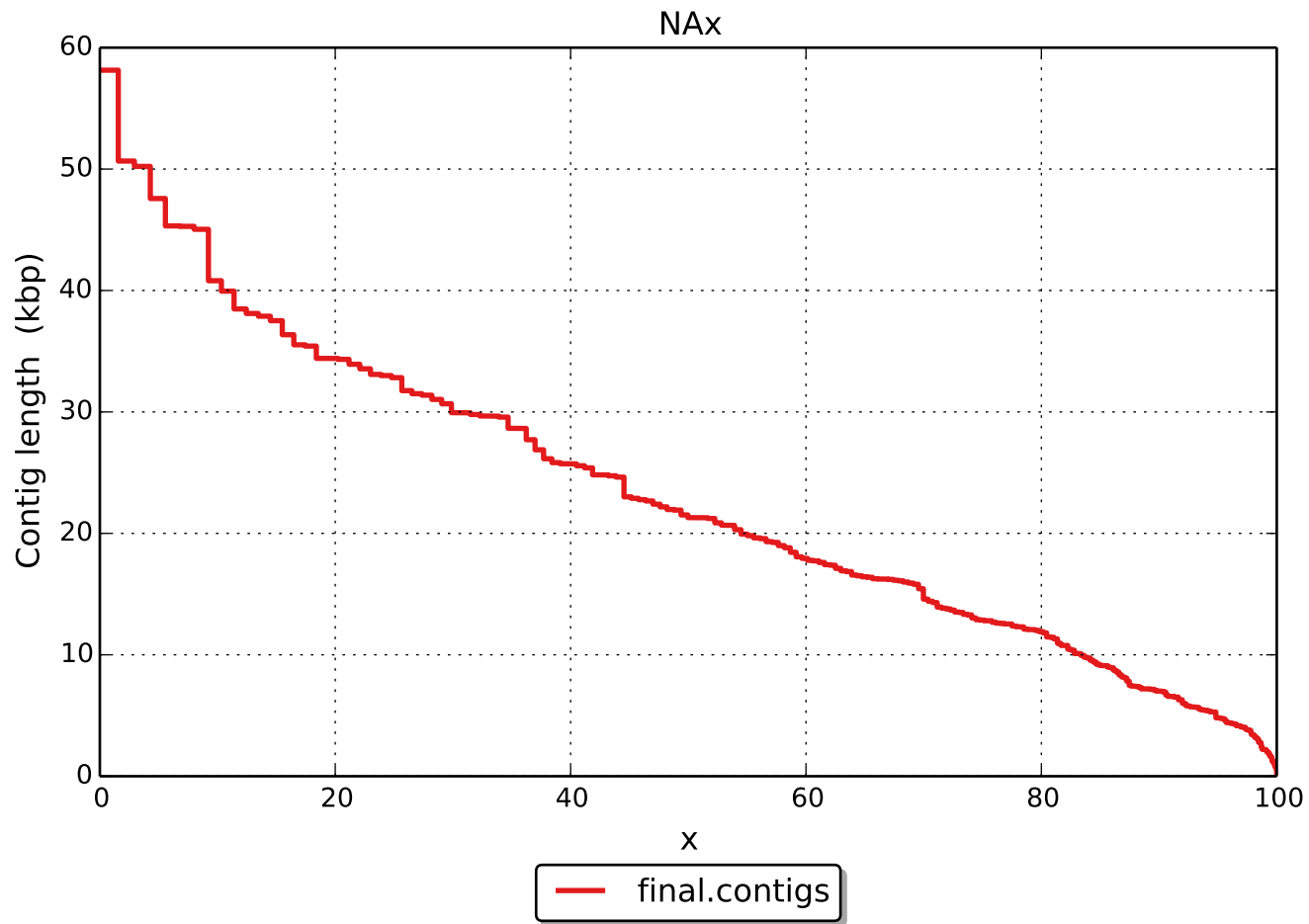
NGx



Misassemblies







NGAx

