

Report

	final.contigs
# contigs (>= 0 bp)	1044
# contigs (>= 1000 bp)	291
Total length (>= 0 bp)	2006897
Total length (>= 1000 bp)	1733229
# contigs	399
Largest contig	25589
Total length	1803953
Reference length	3785550
GC (%)	32.29
Reference GC (%)	32.26
N50	8216
N75	4398
L50	65
L75	138
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	47.324
Duplication ratio	1.007
# N's per 100 kbp	0.00
# mismatches per 100 kbp	415.47
# indels per 100 kbp	0.00
Largest alignment	25589
NA50	8216
NA75	4398
LA50	65
LA75	138

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

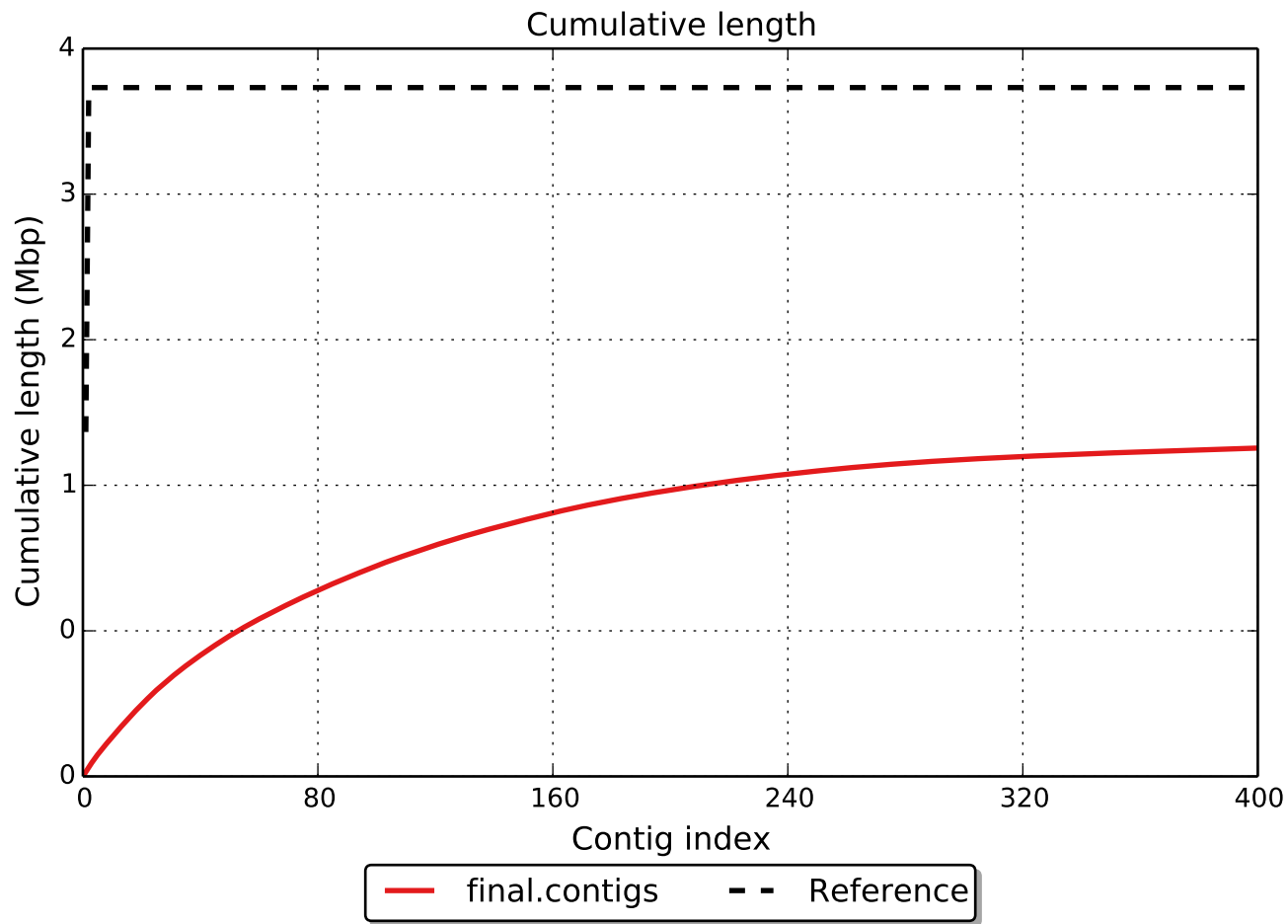
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	7443
# indels	0
# short indels	0
# long indels	0
Indels length	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).

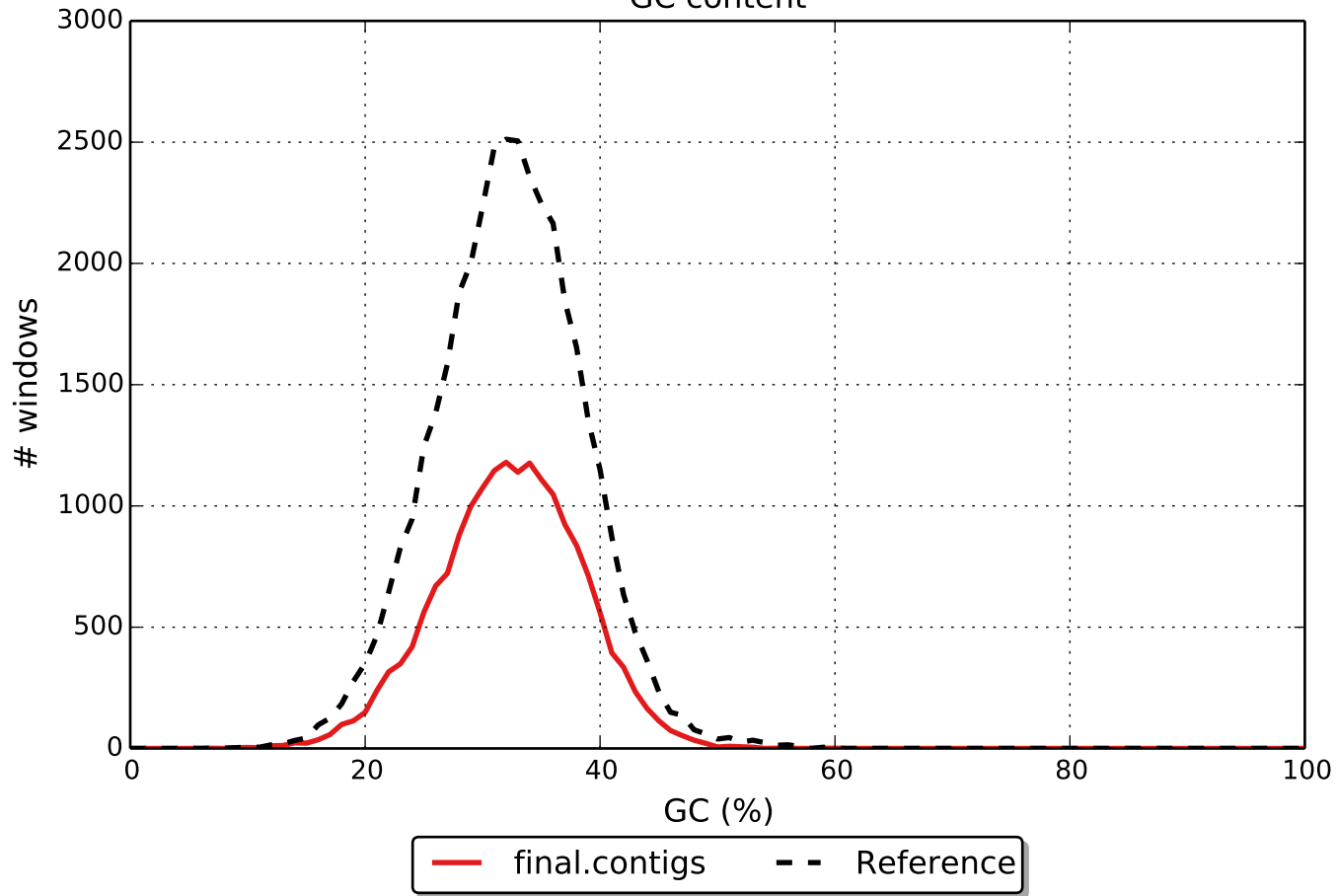
Unaligned report

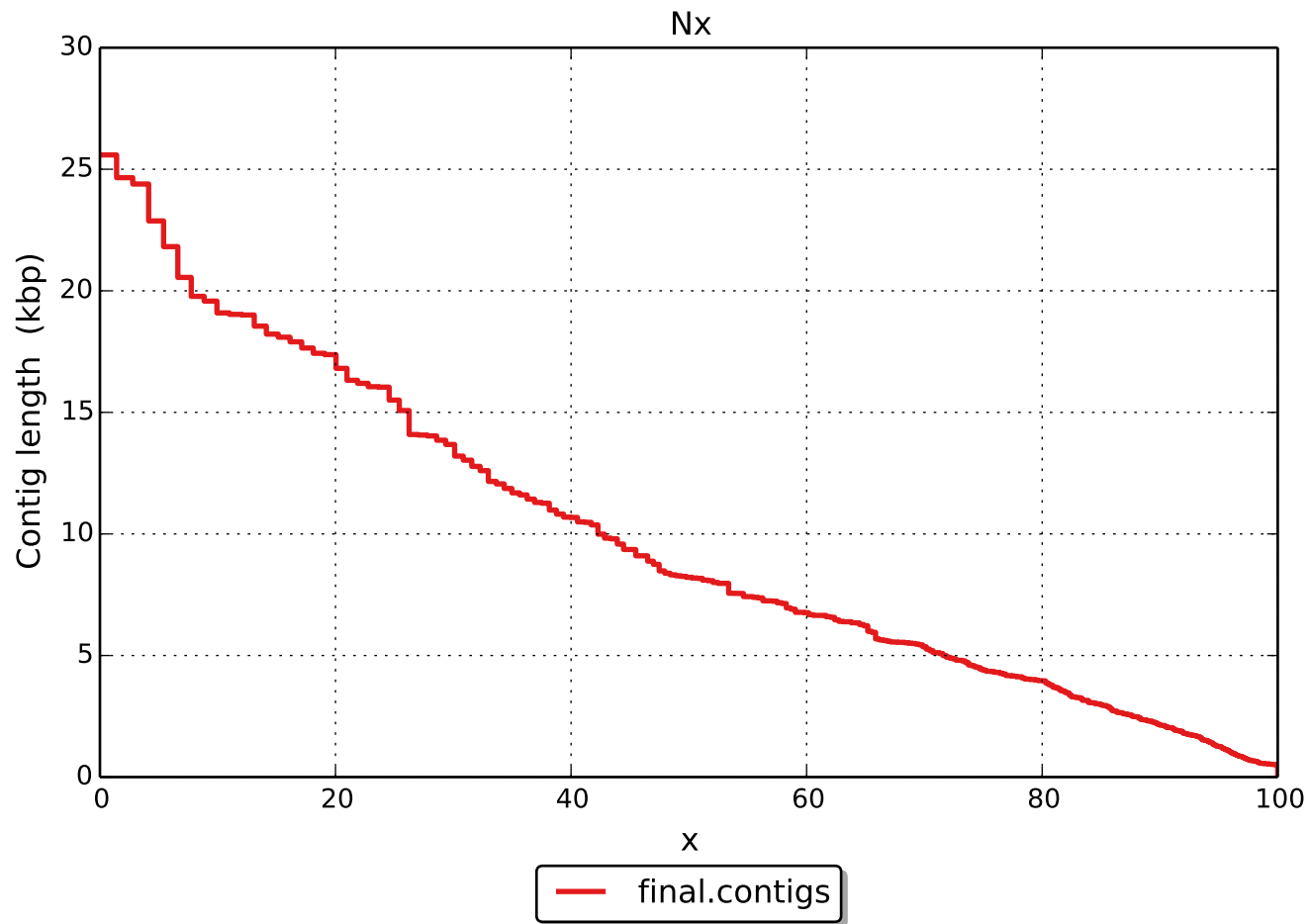
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

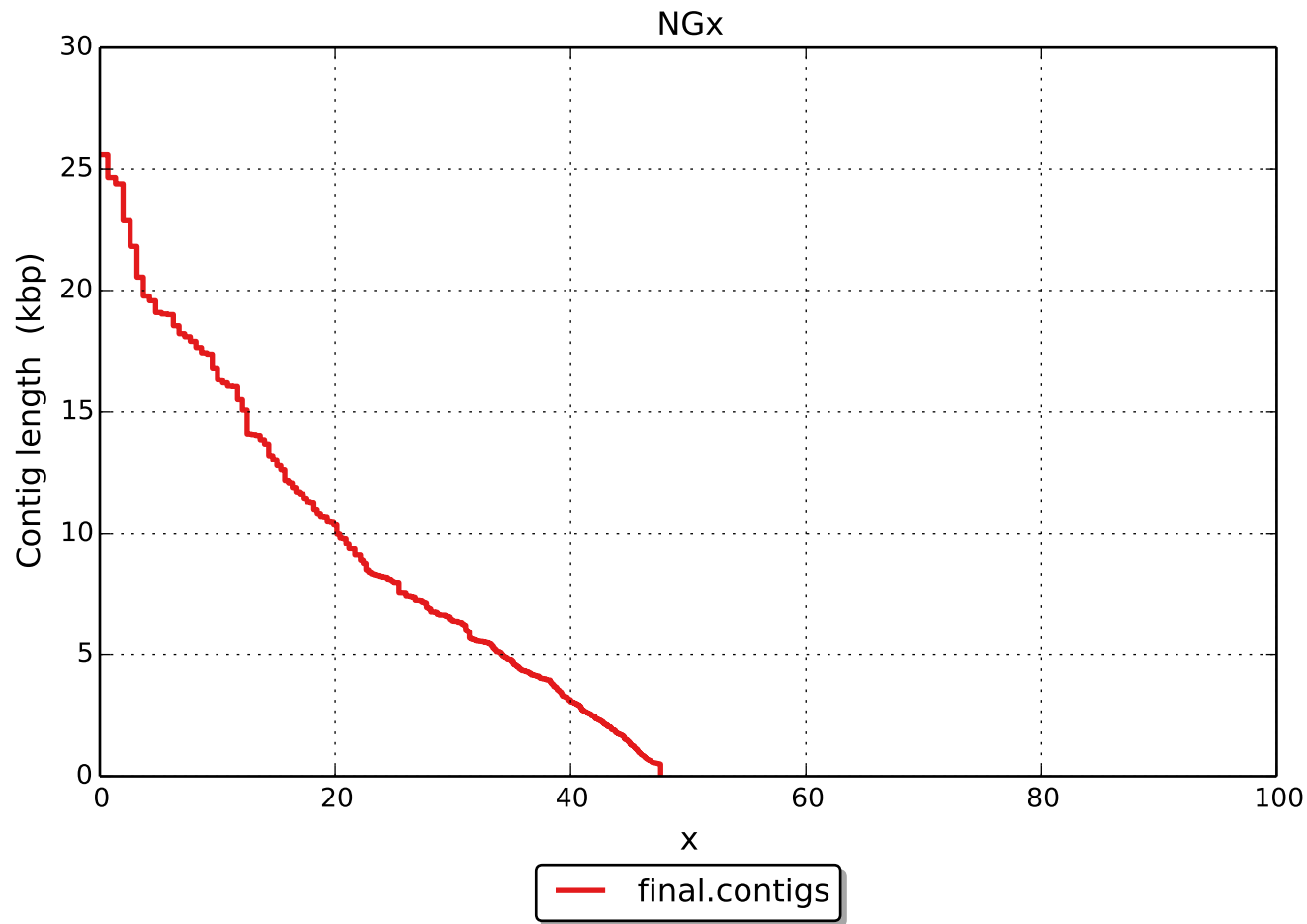
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



GC content

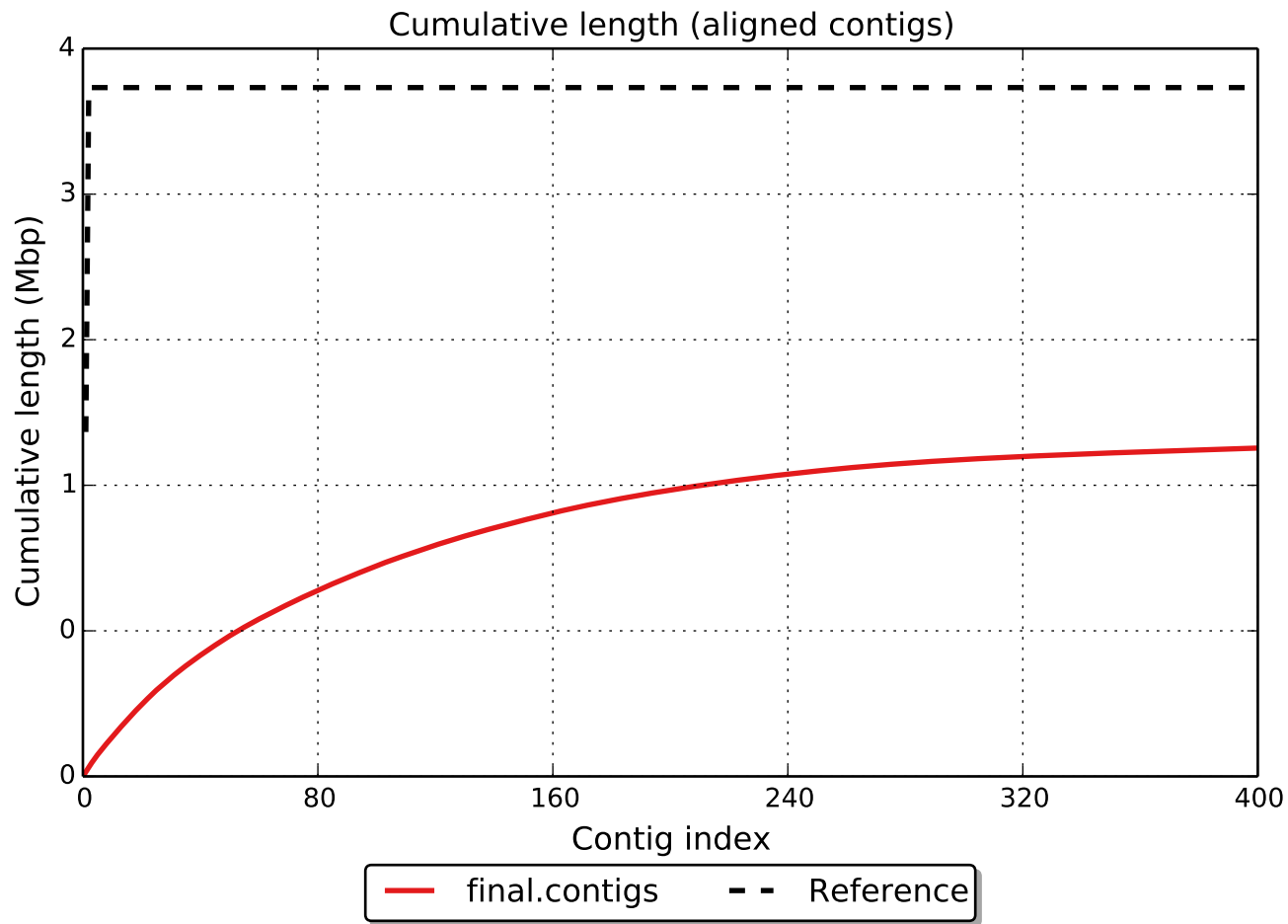


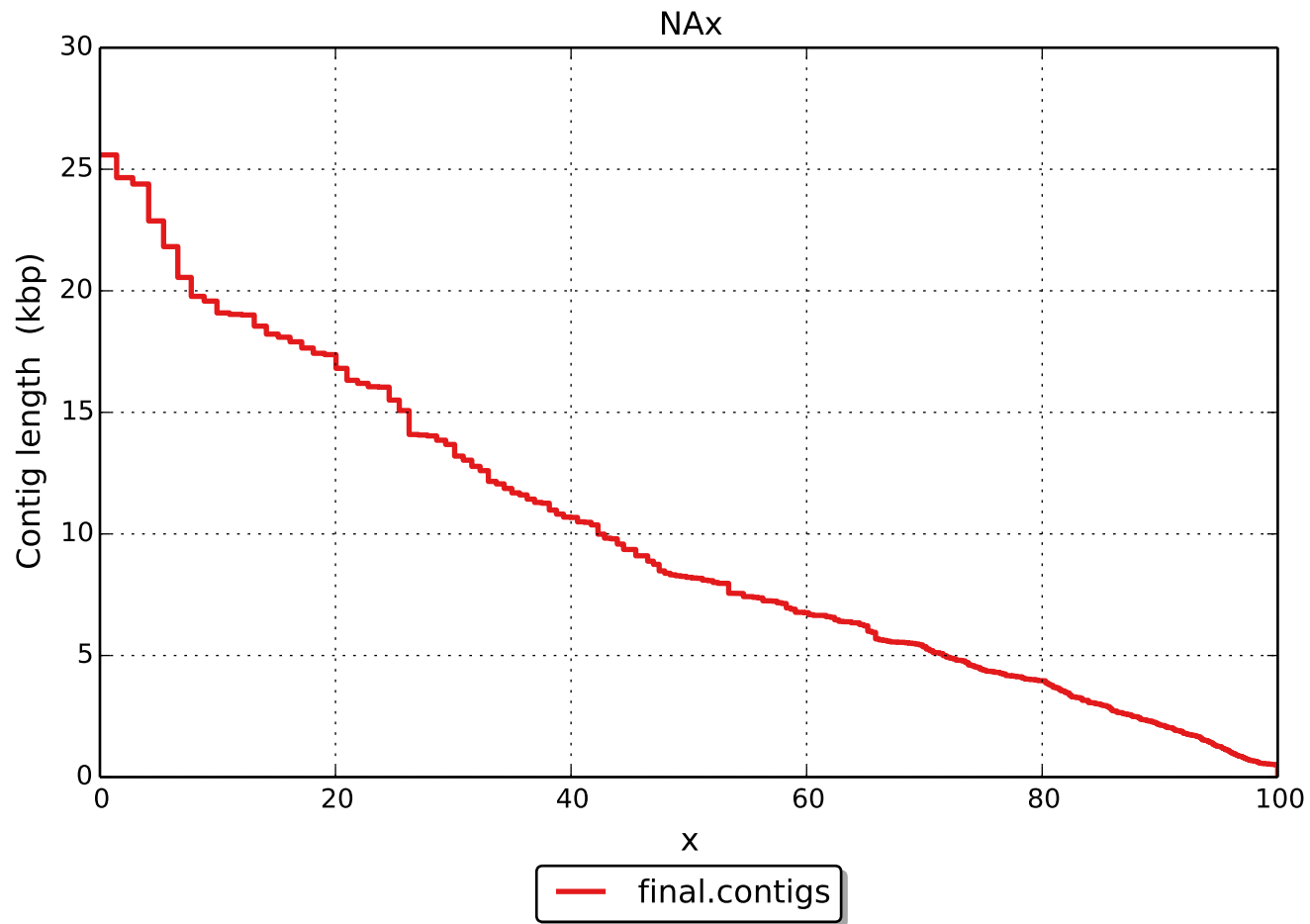




Misassemblies







NGAx

