

Report

	final.contigs
# contigs (≥ 0 bp)	113
# contigs (≥ 1000 bp)	105
Total length (≥ 0 bp)	1240742
Total length (≥ 1000 bp)	1235606
# contigs	111
Largest contig	48138
Total length	1240062
Reference length	1231960
GC (%)	25.34
Reference GC (%)	25.35
N50	17367
NG50	17367
N75	10805
NG75	11002
L50	23
LG50	23
L75	46
LG75	45
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.947
Duplication ratio	1.007
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.24
# indels per 100 kbp	0.00
Largest alignment	48138
NA50	17367
NGA50	17367
NA75	10805
NGA75	11002
LA50	23
LGA50	23
LA75	46
LGA75	45

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	3
# indels	0
# short indels	0
# long indels	0
Indels length	0

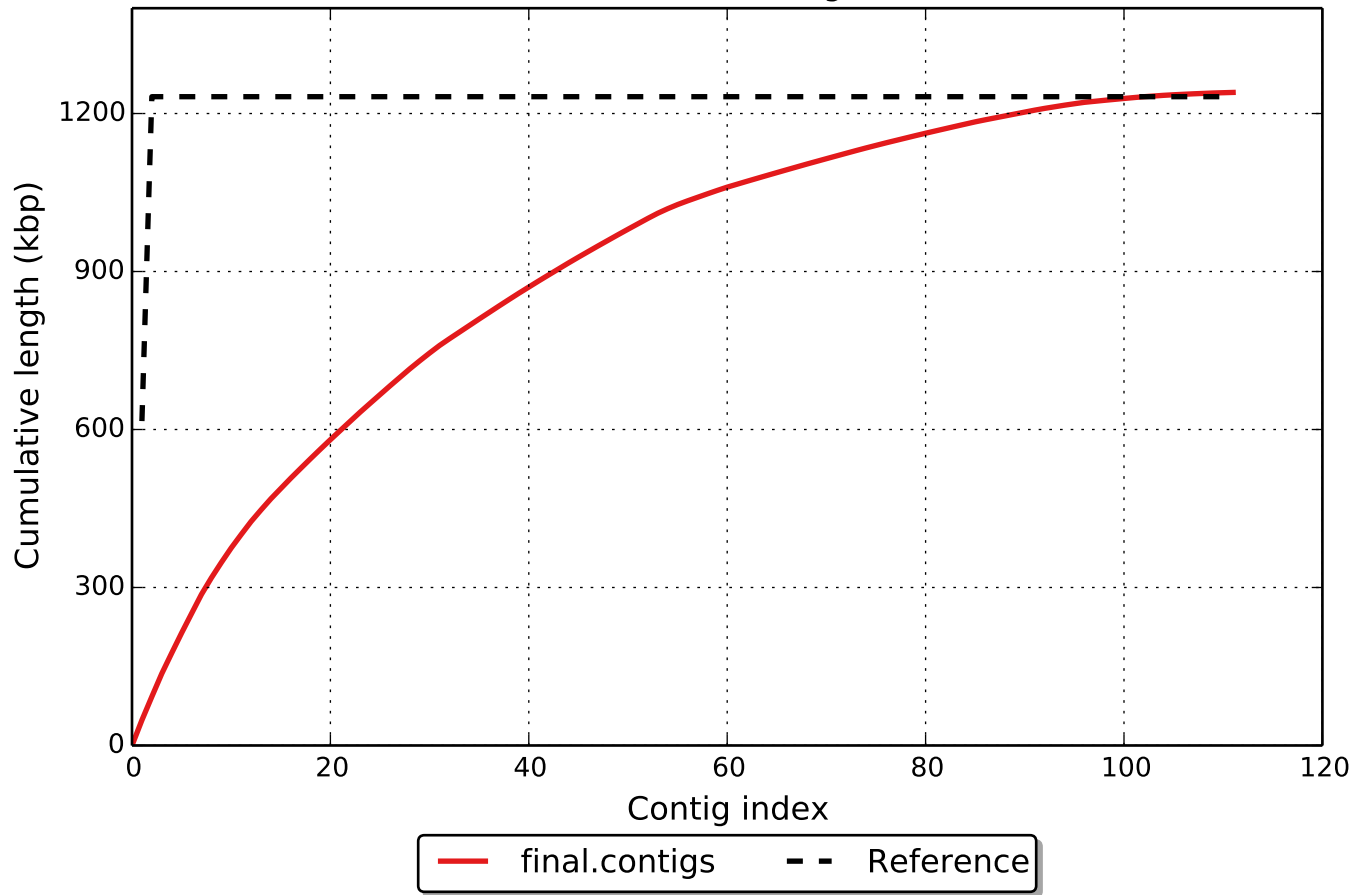
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

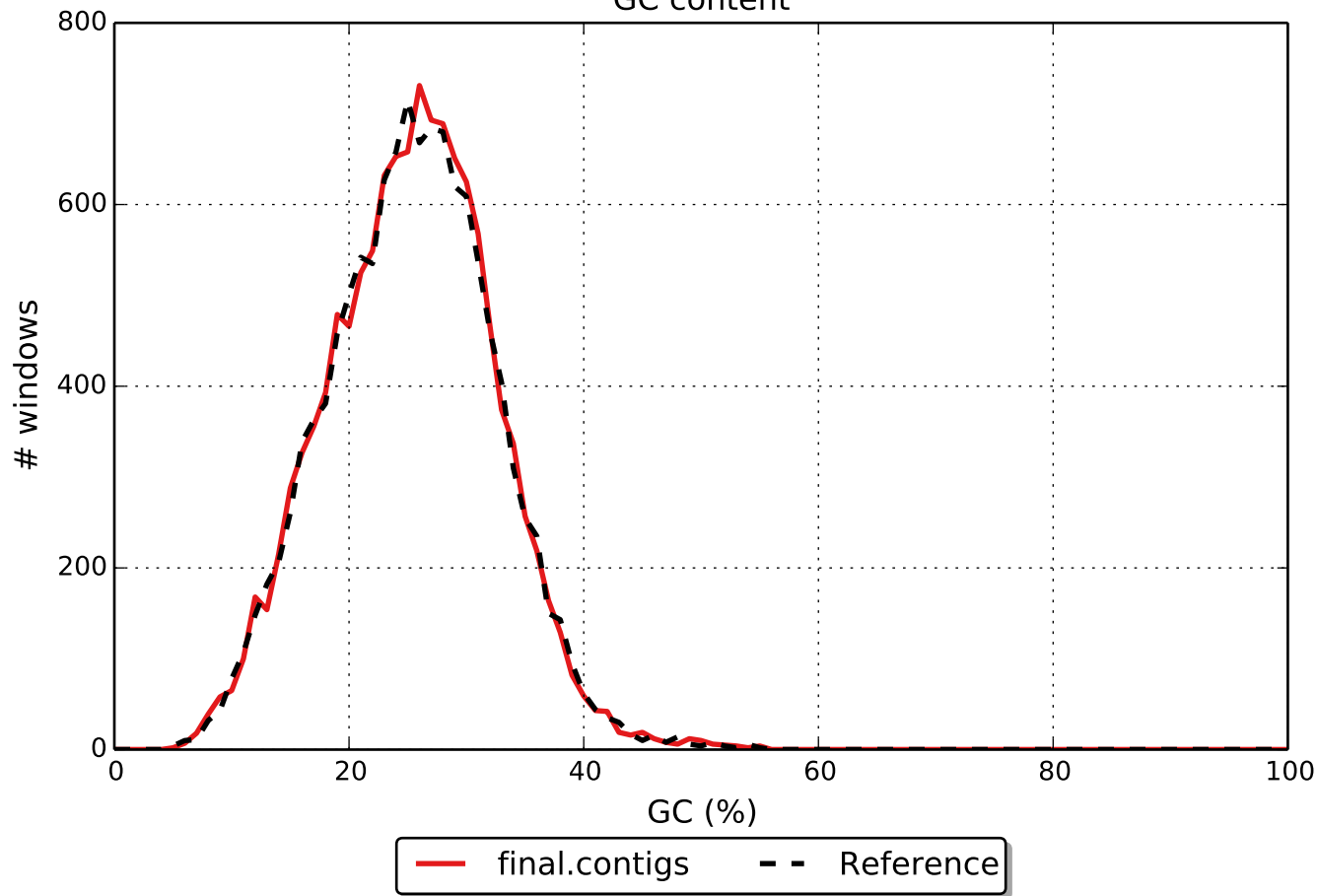
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

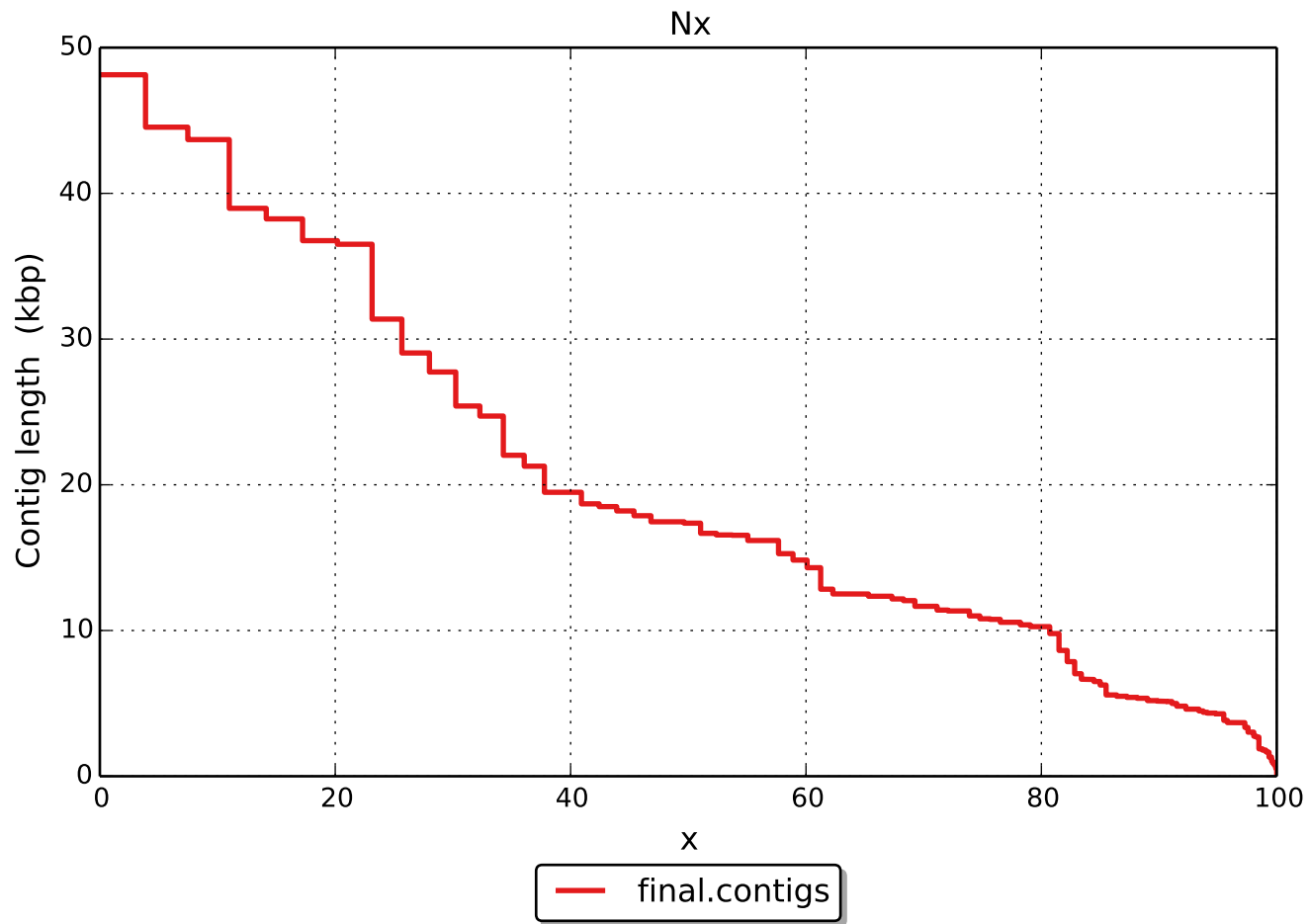
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Cumulative length

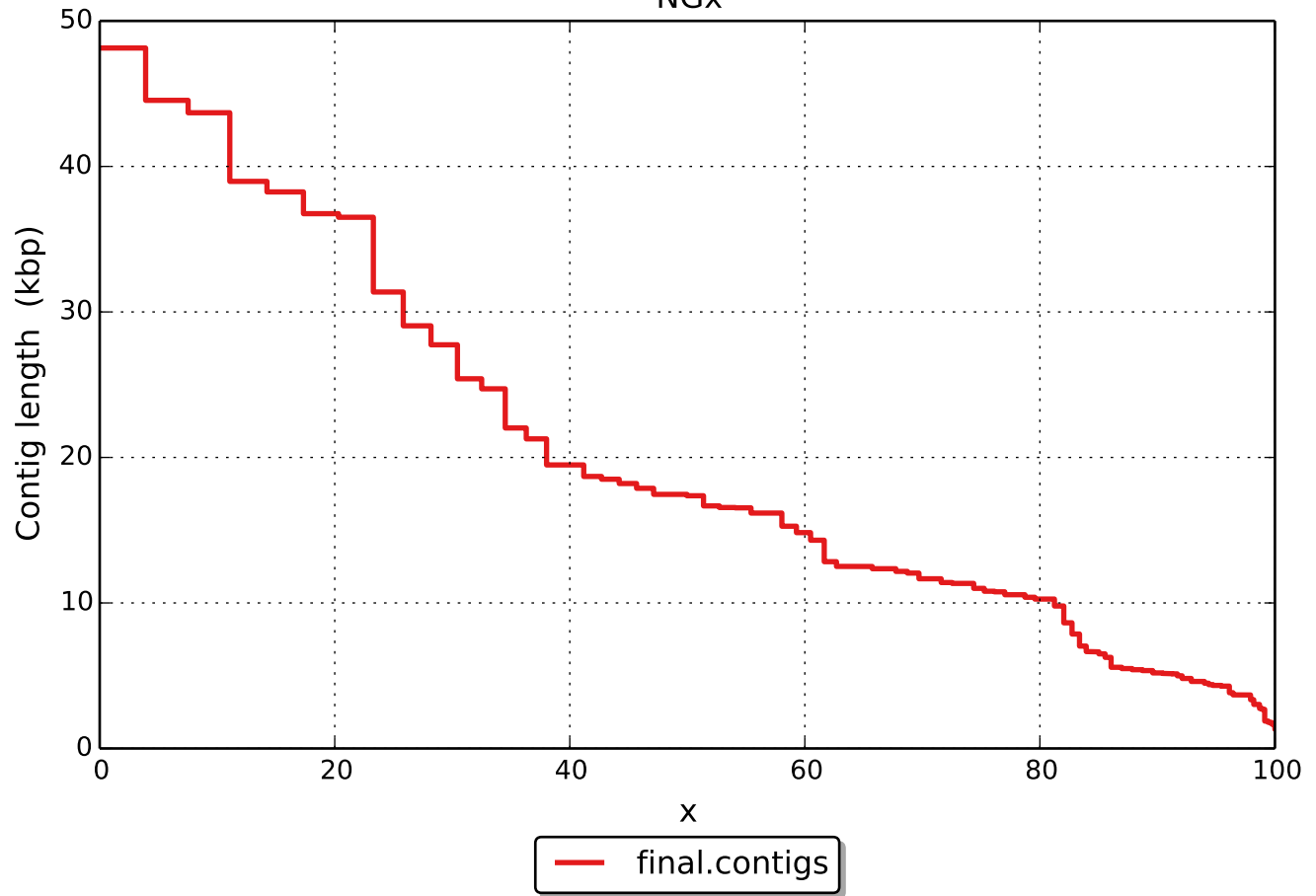


GC content





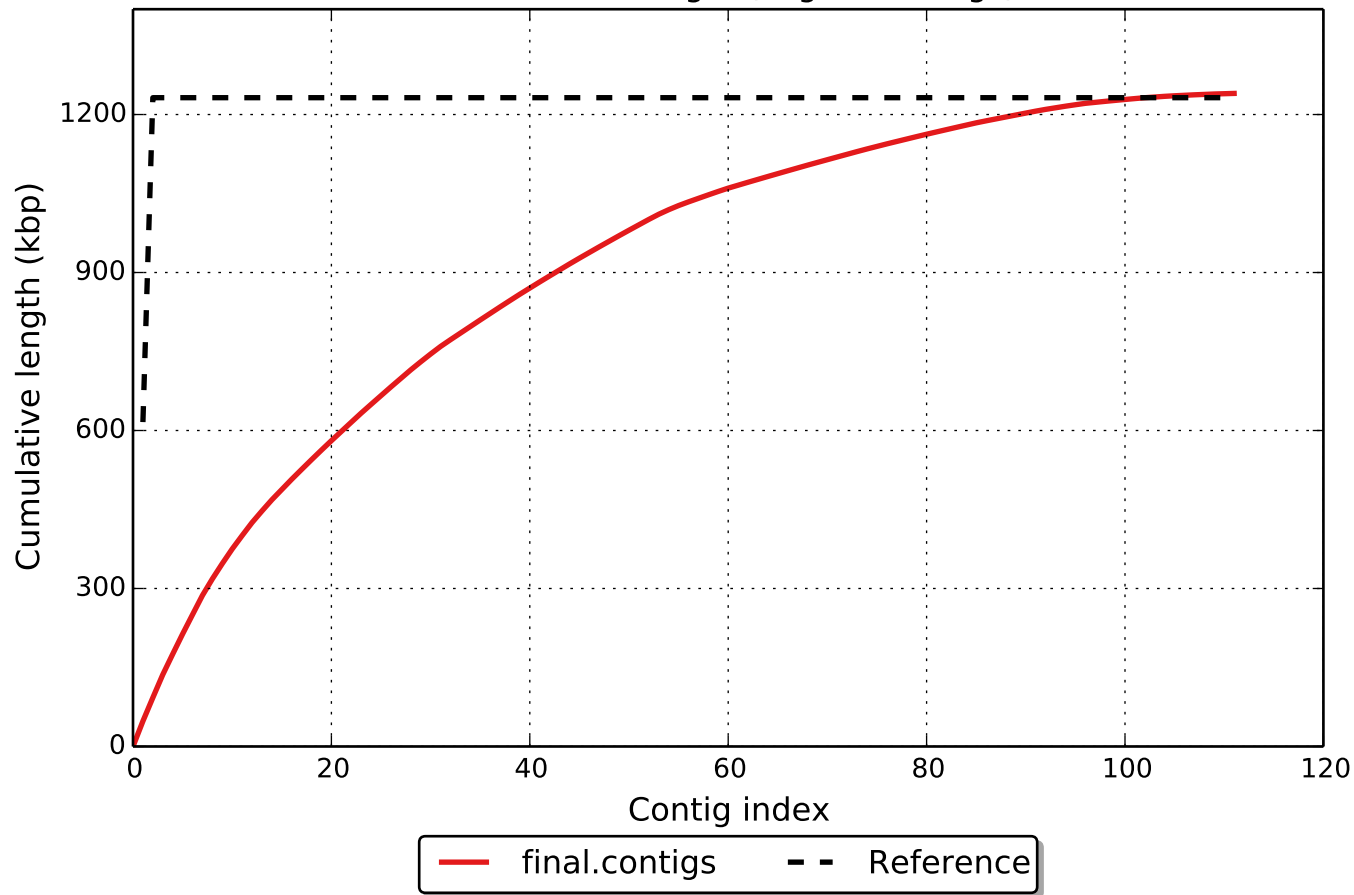
NGx

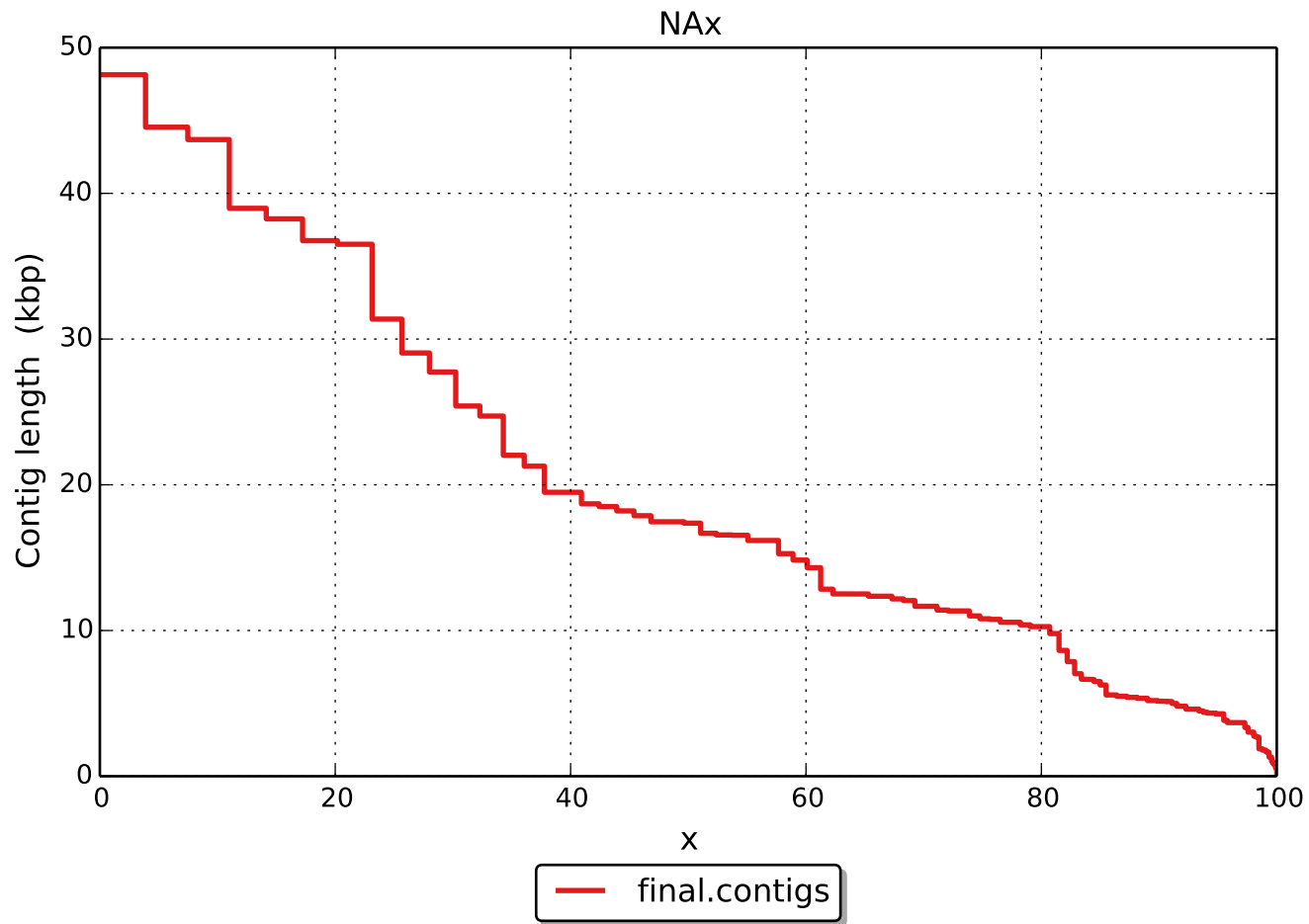


Misassemblies



Cumulative length (aligned contigs)





NGAx

