

Report

	final.contigs
# contigs (>= 0 bp)	312
# contigs (>= 1000 bp)	244
Total length (>= 0 bp)	1252602
Total length (>= 1000 bp)	1210316
# contigs	288
Largest contig	18968
Total length	1244192
Reference length	1231960
GC (%)	25.36
Reference GC (%)	25.34
N50	7100
NG50	7373
N75	3778
NG75	3790
L50	59
LG50	58
L75	118
LG75	116
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.884
Duplication ratio	1.021
# N's per 100 kbp	0.00
# mismatches per 100 kbp	30.13
# indels per 100 kbp	0.00
Largest alignment	18968
NA50	7100
NGA50	7373
NA75	3778
NGA75	3790
LA50	59
LGA50	58
LA75	118
LGA75	116

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	367
# indels	0
# short indels	0
# long indels	0
Indels length	0

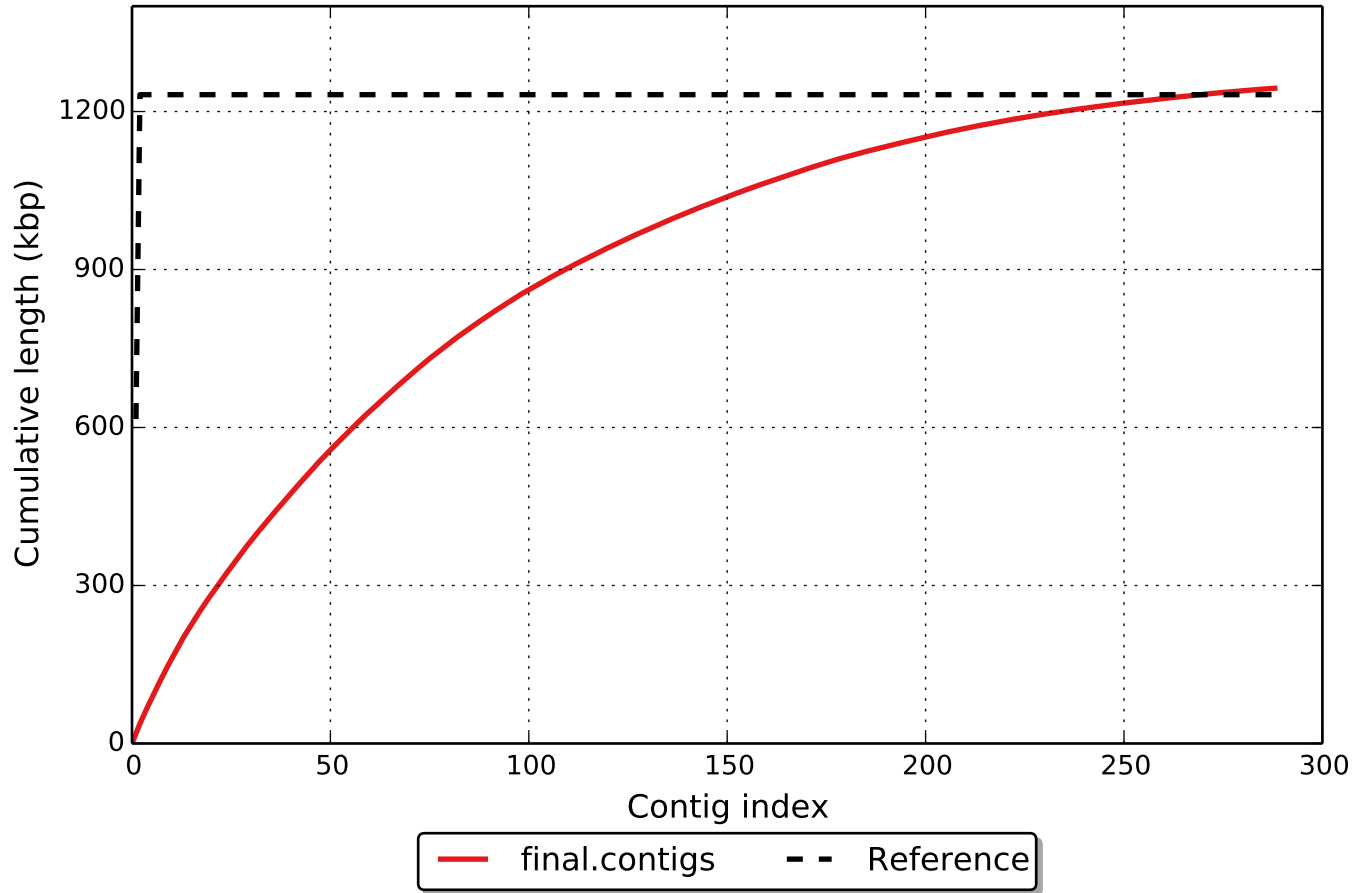
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

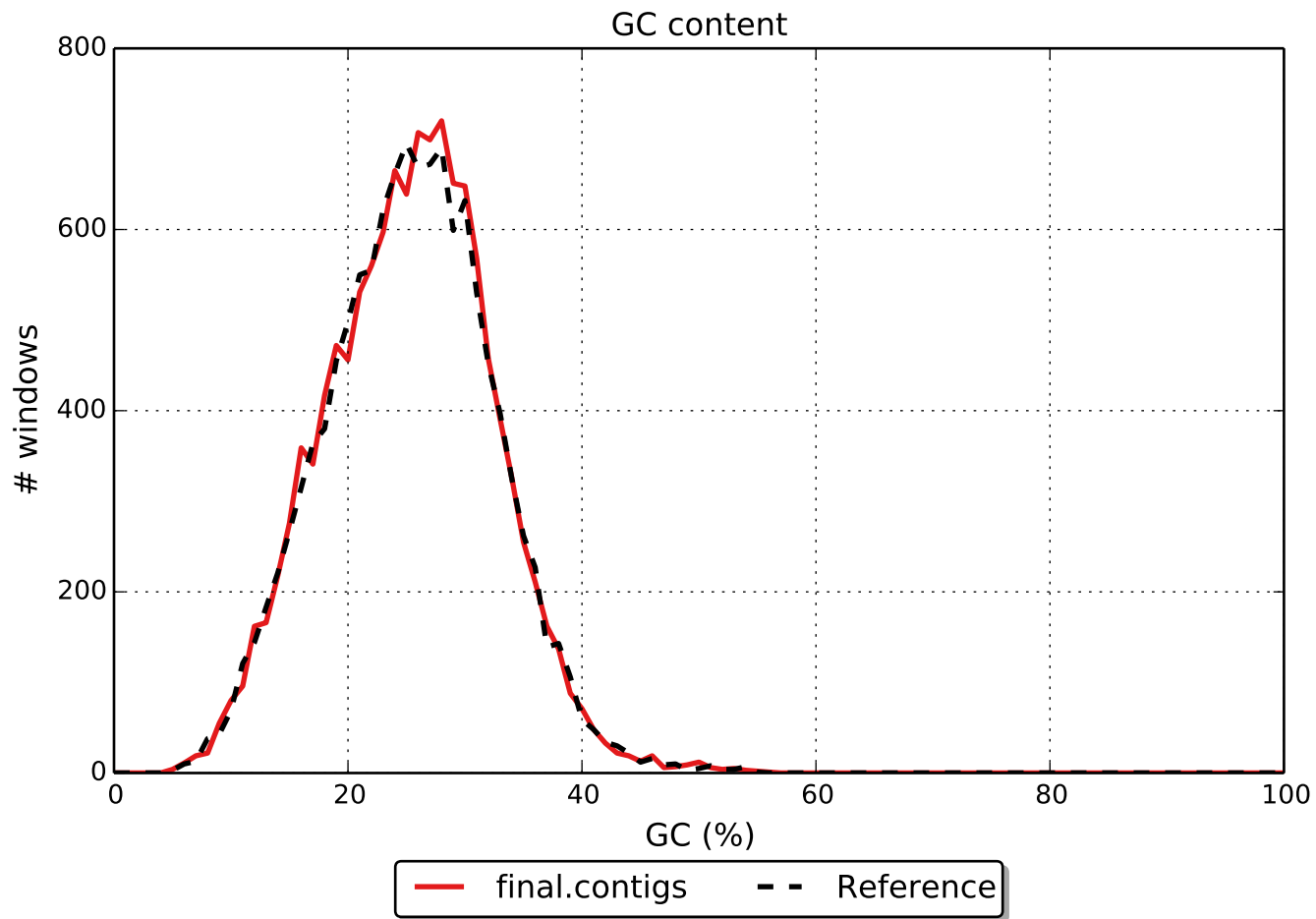
Unaligned report

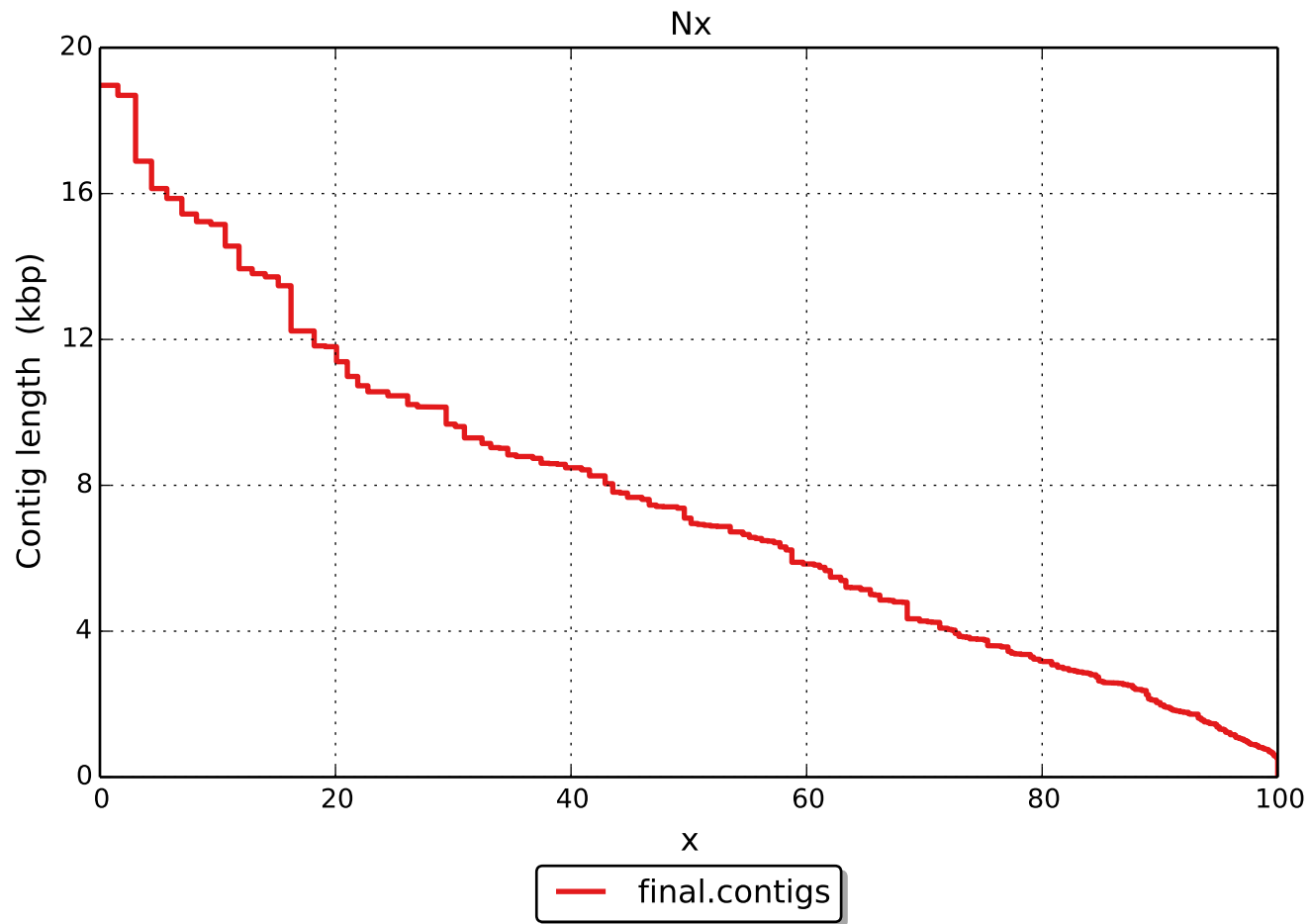
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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).

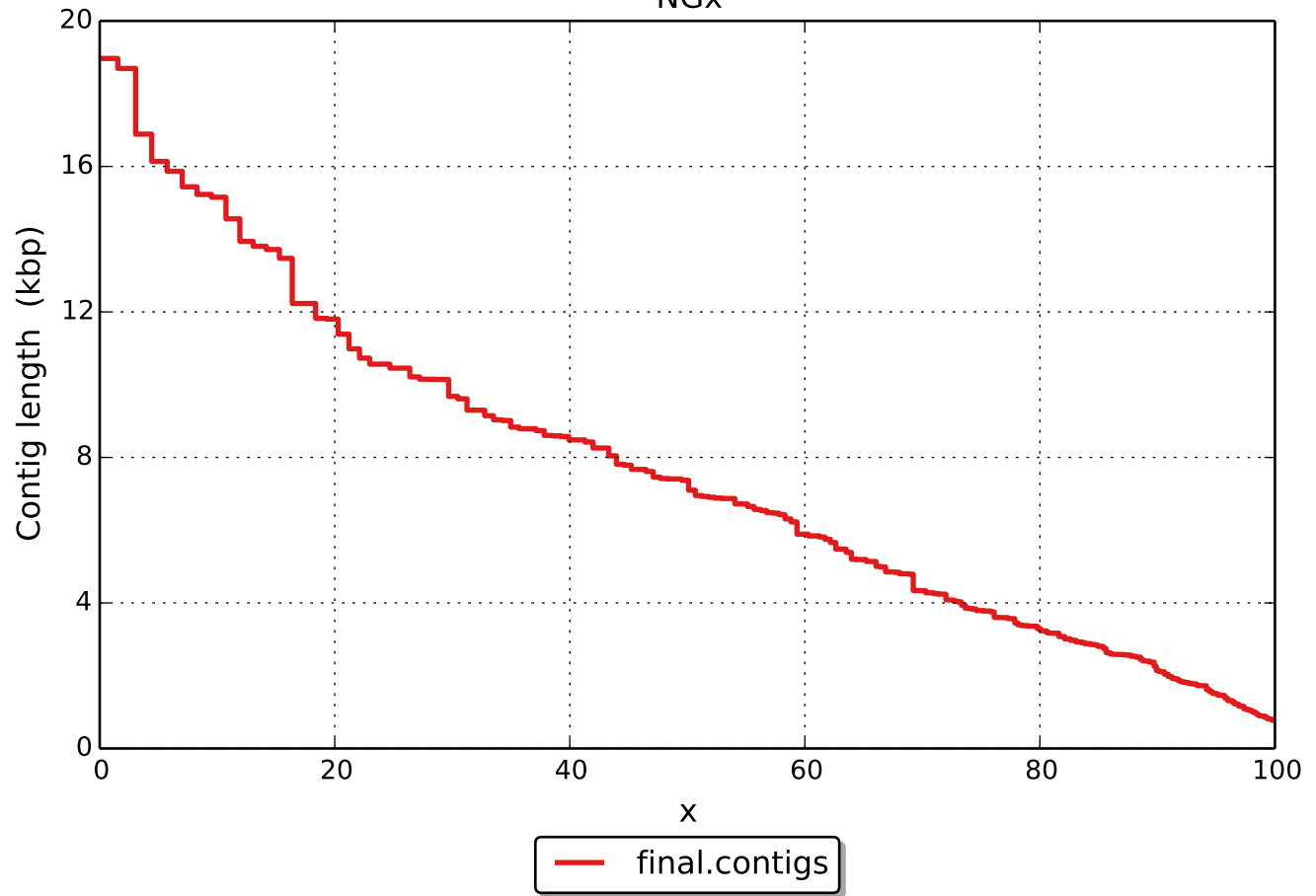
Cumulative length







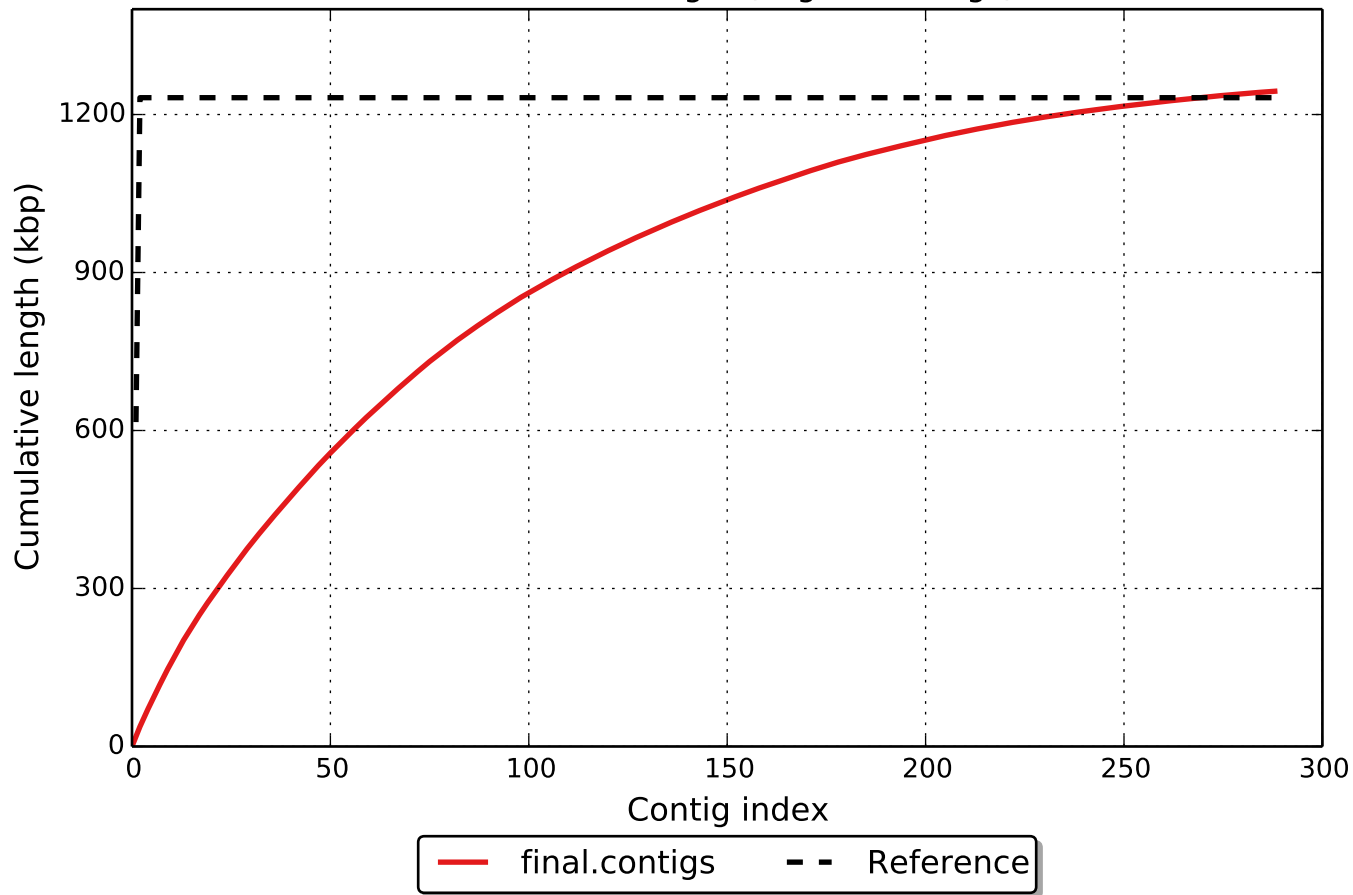
NGx

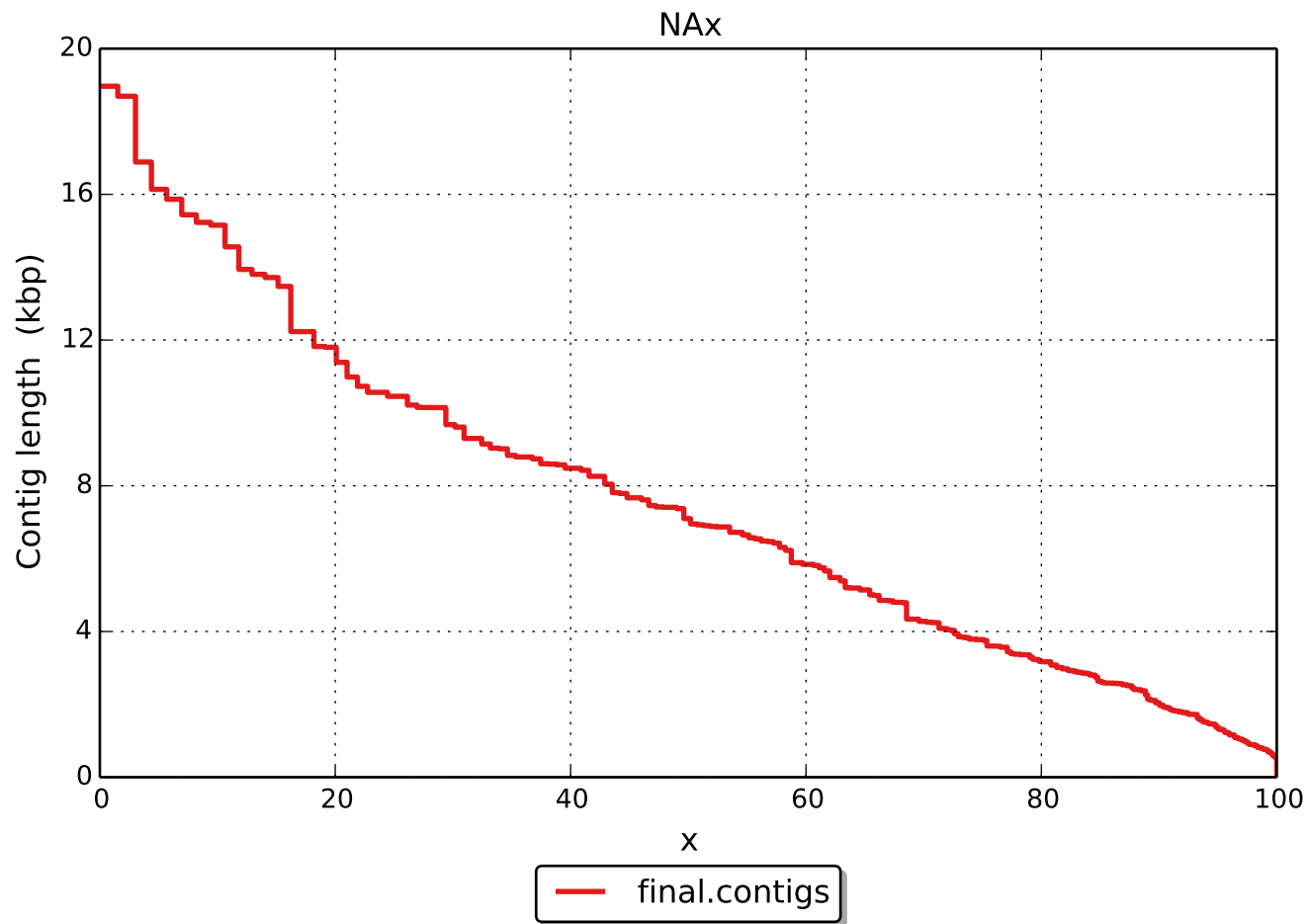


Misassemblies



Cumulative length (aligned contigs)





NGAx

