

Report

	final.contigs
# contigs (≥ 0 bp)	481
# contigs (≥ 1000 bp)	146
Total length (≥ 0 bp)	724691
Total length (≥ 1000 bp)	575096
# contigs	245
Largest contig	15816
Total length	641029
Reference length	1231960
GC (%)	25.36
Reference GC (%)	25.35
N50	4661
NG50	643
N75	2314
L50	42
LG50	200
L75	91
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	51.059
Duplication ratio	1.019
# N's per 100 kbp	0.00
# mismatches per 100 kbp	451.81
# indels per 100 kbp	0.00
Largest alignment	15816
NA50	4661
NGA50	643
NA75	2314
LA50	42
LGA50	200
LA75	91

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	2842
# indels	0
# short indels	0
# long indels	0
Indels length	0

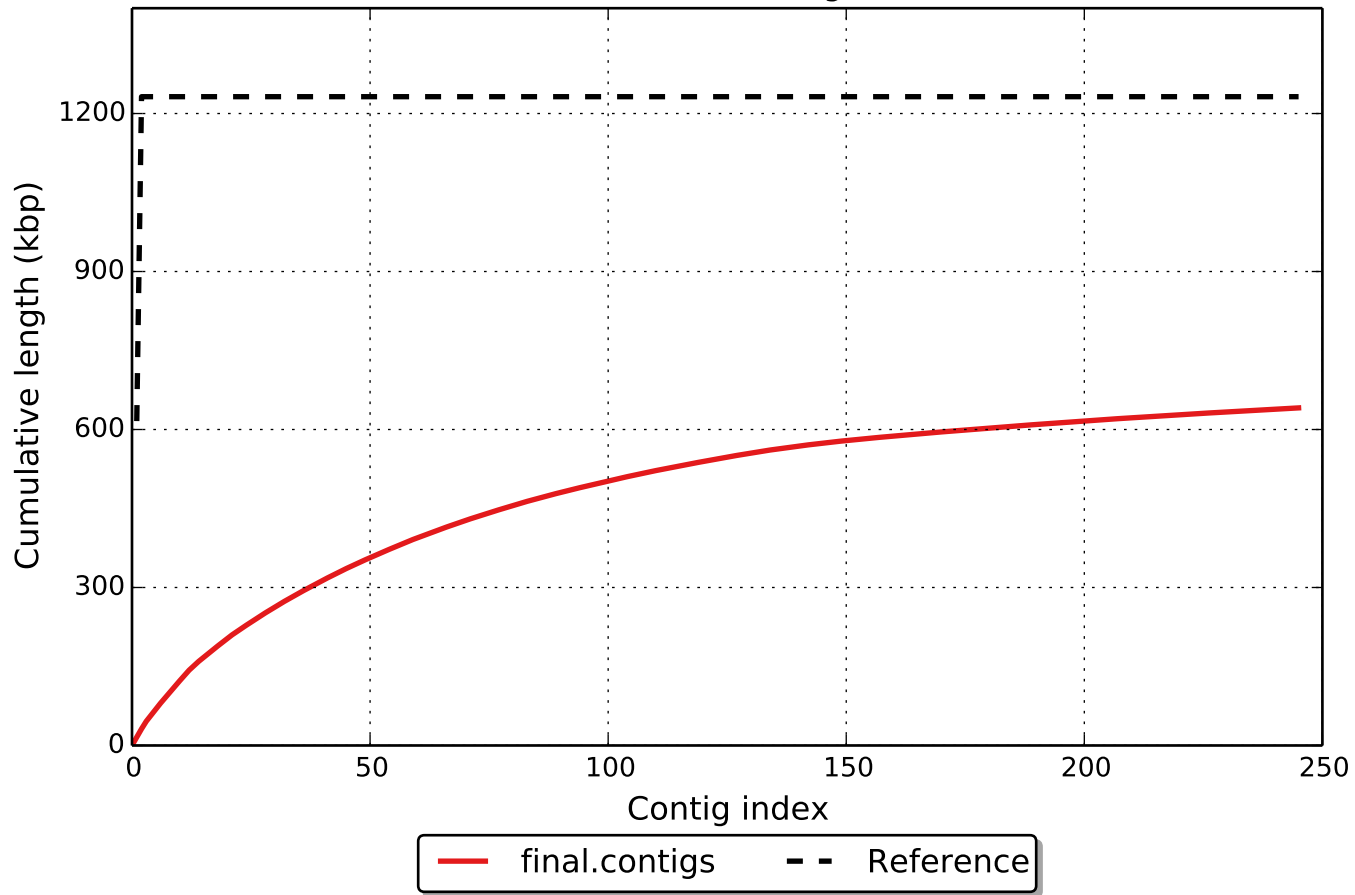
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

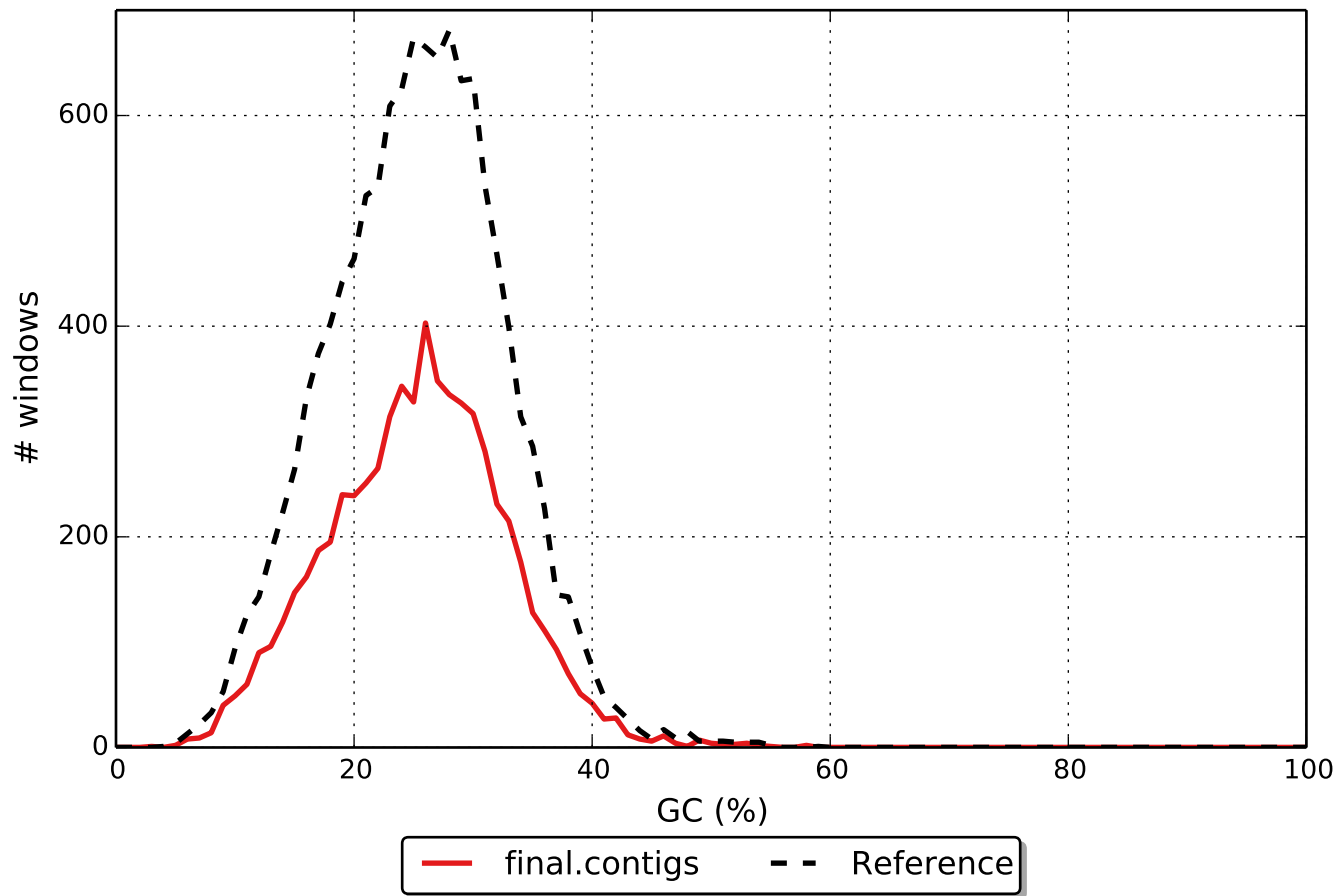
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

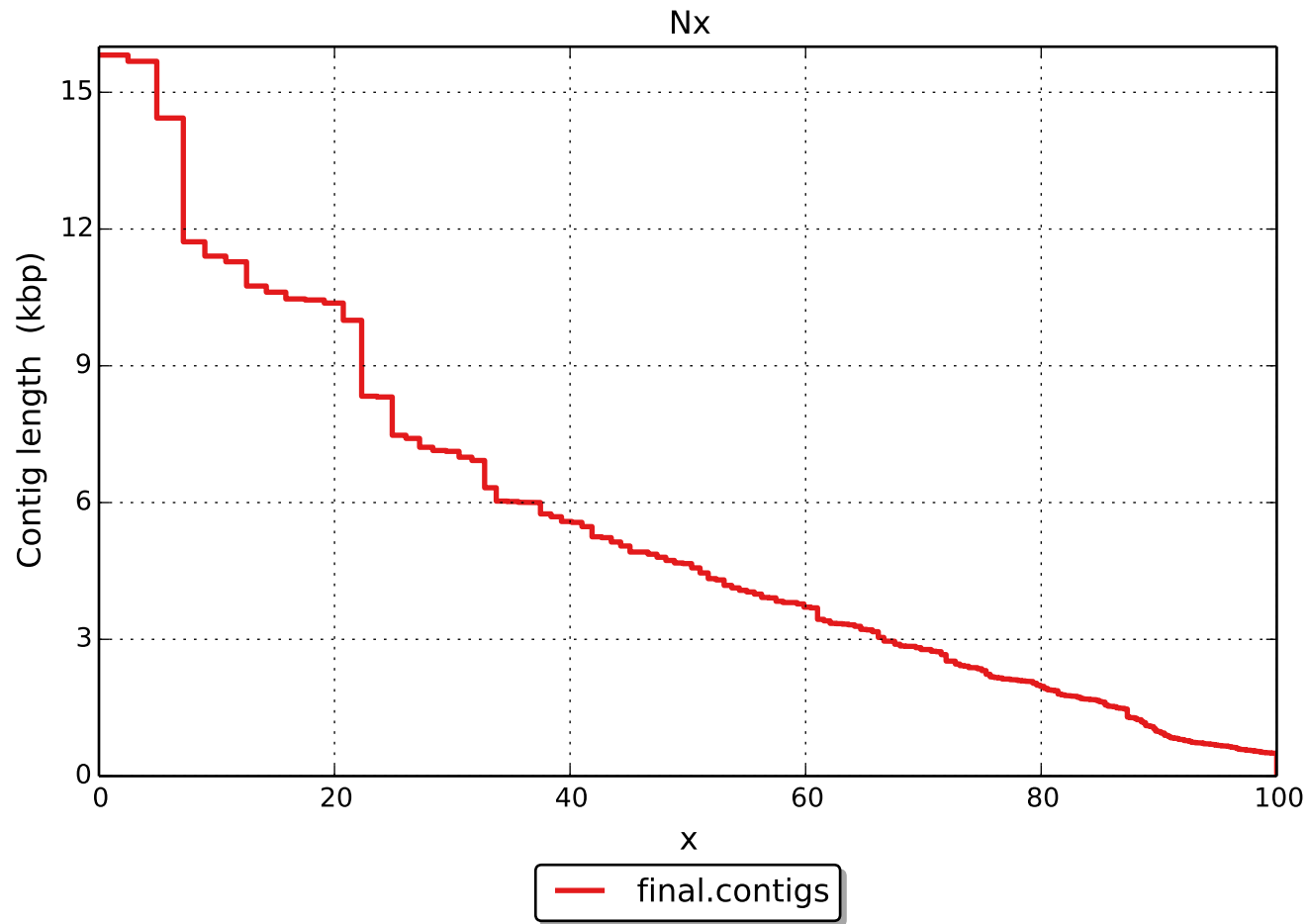
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

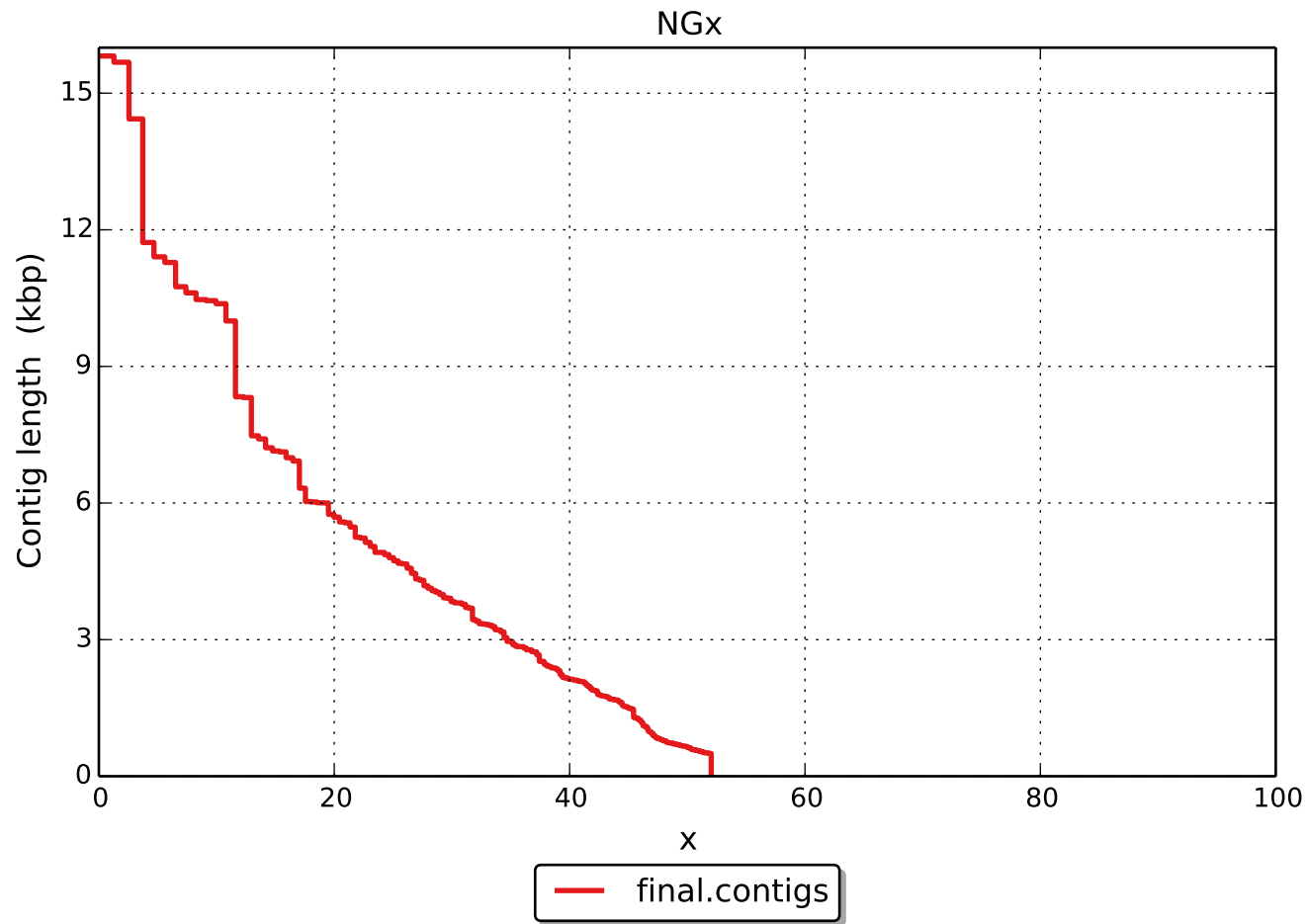
Cumulative length



GC content



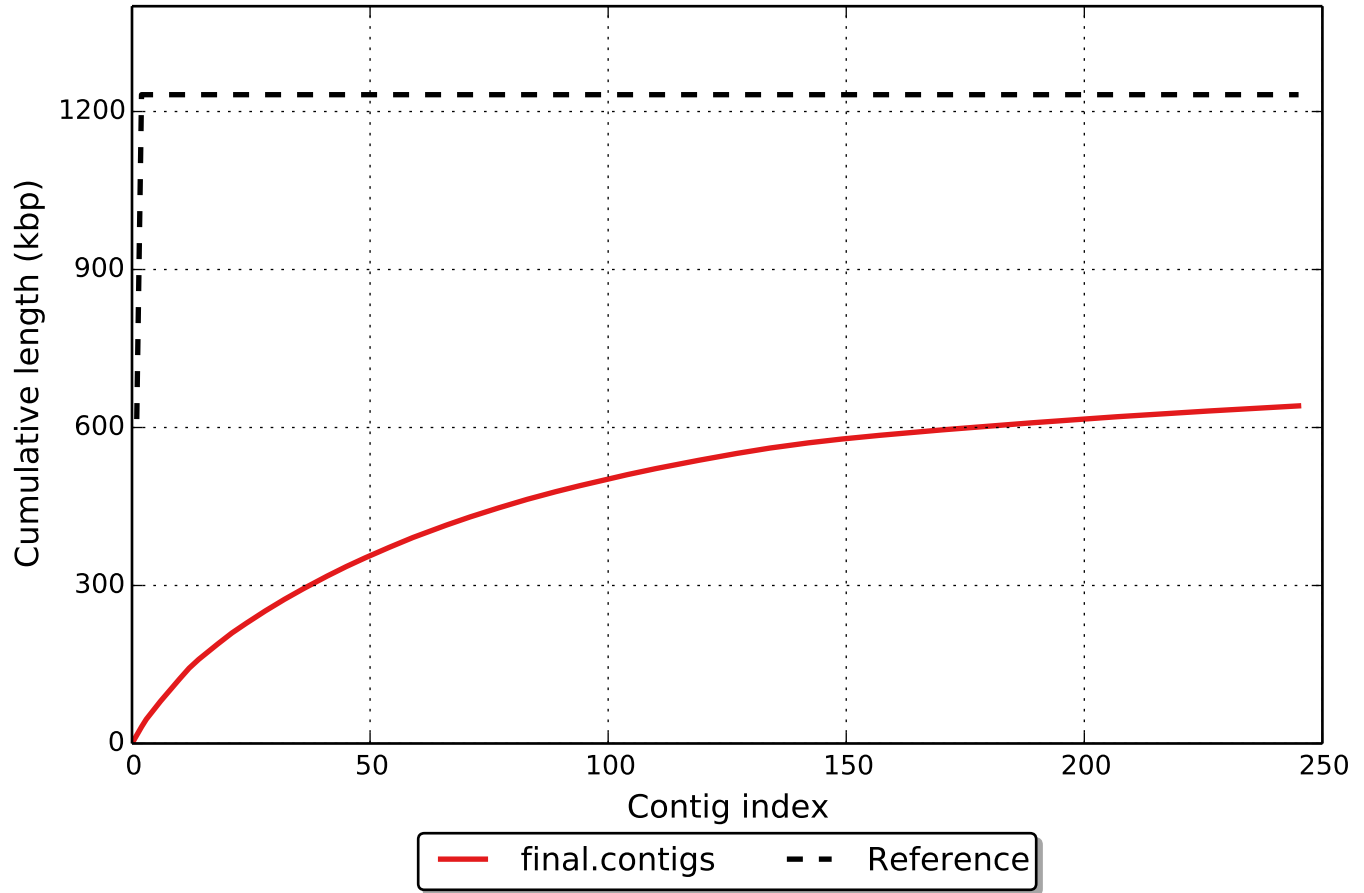


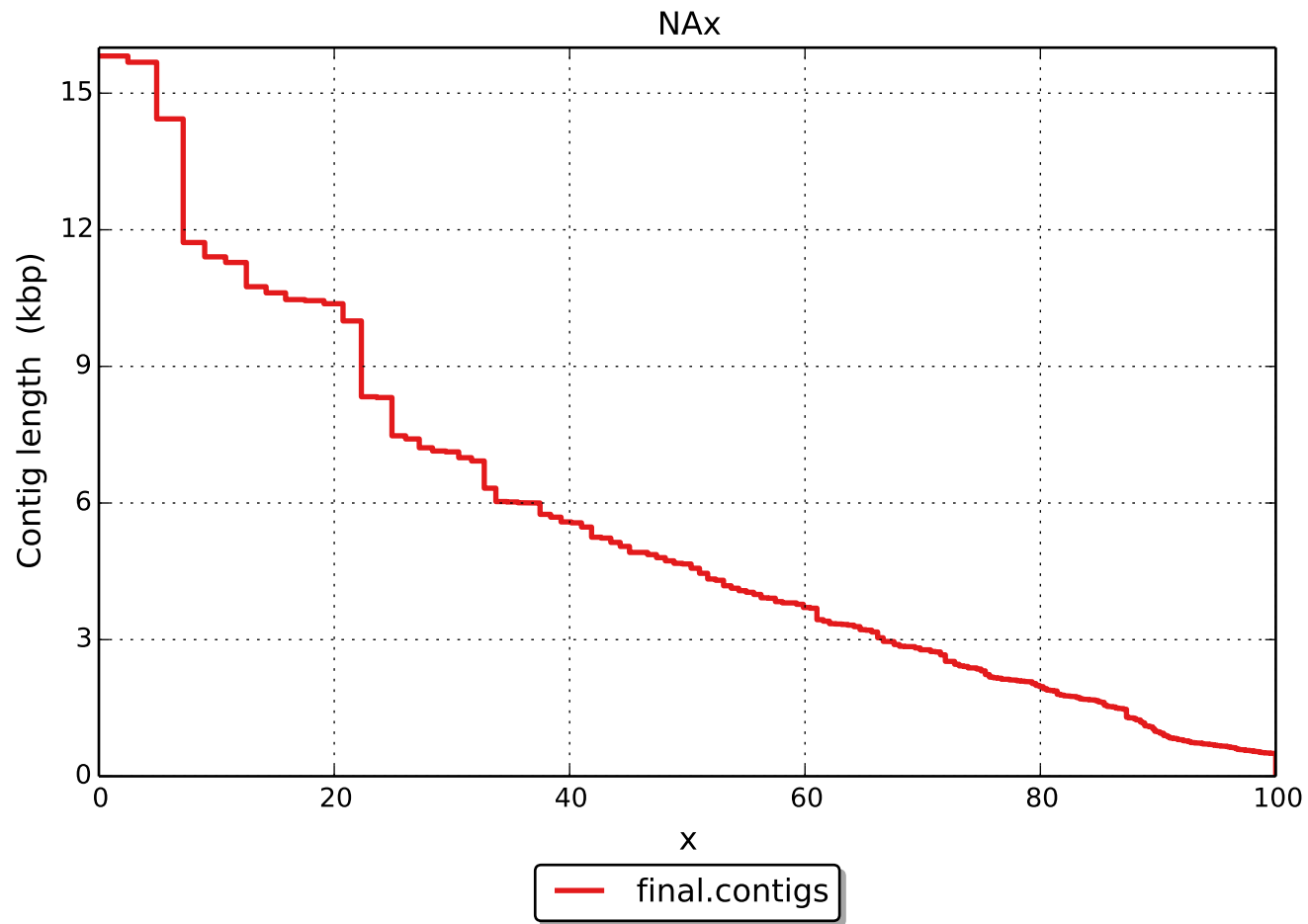


Misassemblies



Cumulative length (aligned contigs)





NGAx

