

Report

	final.contigs
# contigs (≥ 0 bp)	275
# contigs (≥ 1000 bp)	95
Total length (≥ 0 bp)	696964
Total length (≥ 1000 bp)	630349
# contigs	117
Largest contig	23250
Total length	644329
Reference length	1283598
GC (%)	26.31
Reference GC (%)	26.30
N50	9177
NG50	532
N75	5658
L50	25
LG50	113
L75	48
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	49.906
Duplication ratio	1.006
# N's per 100 kbp	0.00
# mismatches per 100 kbp	404.78
# indels per 100 kbp	0.62
Largest alignment	23250
NA50	9177
NGA50	532
NA75	5658
LA50	25
LGA50	113
LA75	48

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	2593
# indels	4
# short indels	3
# long indels	1
Indels length	84

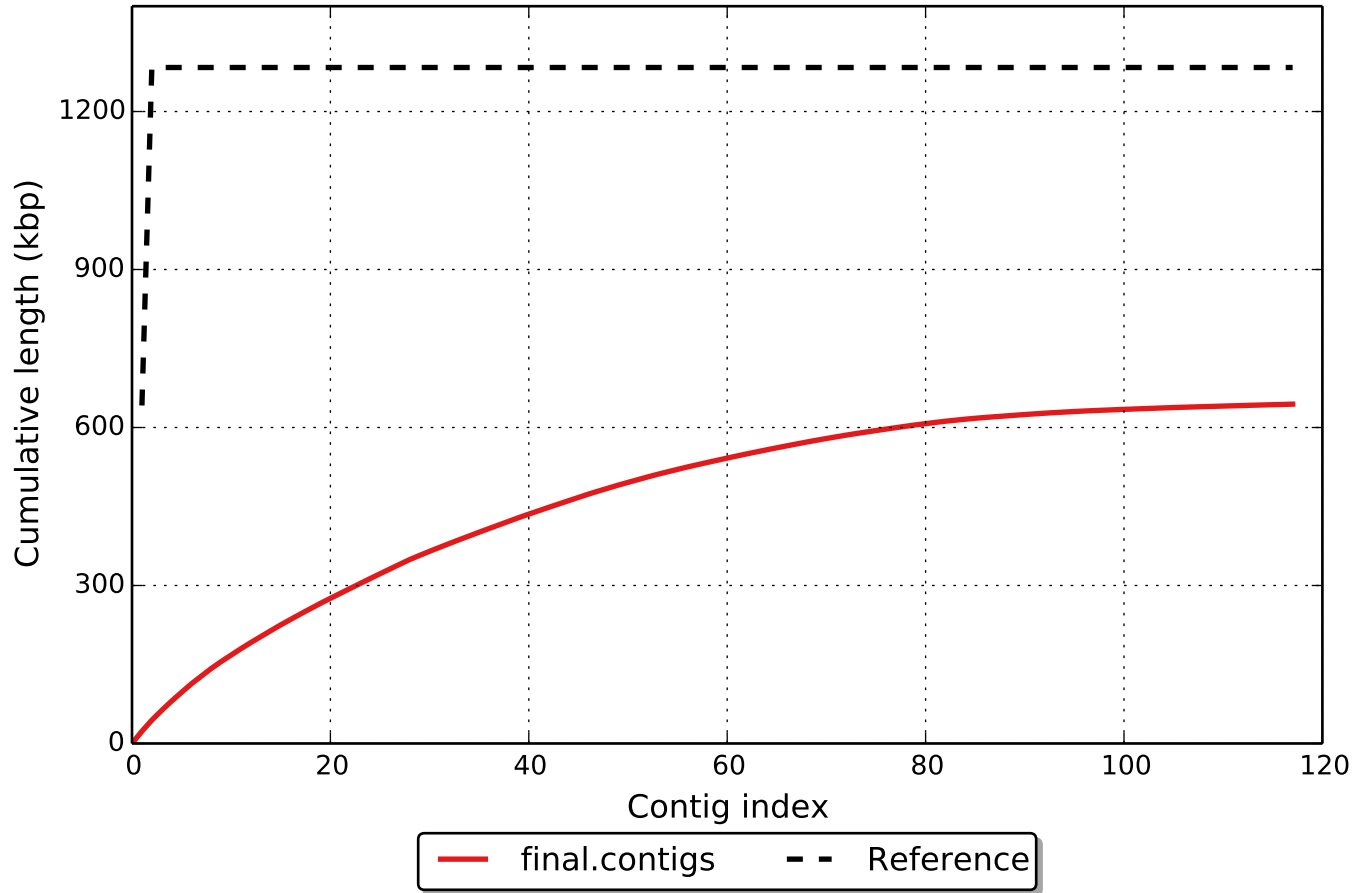
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

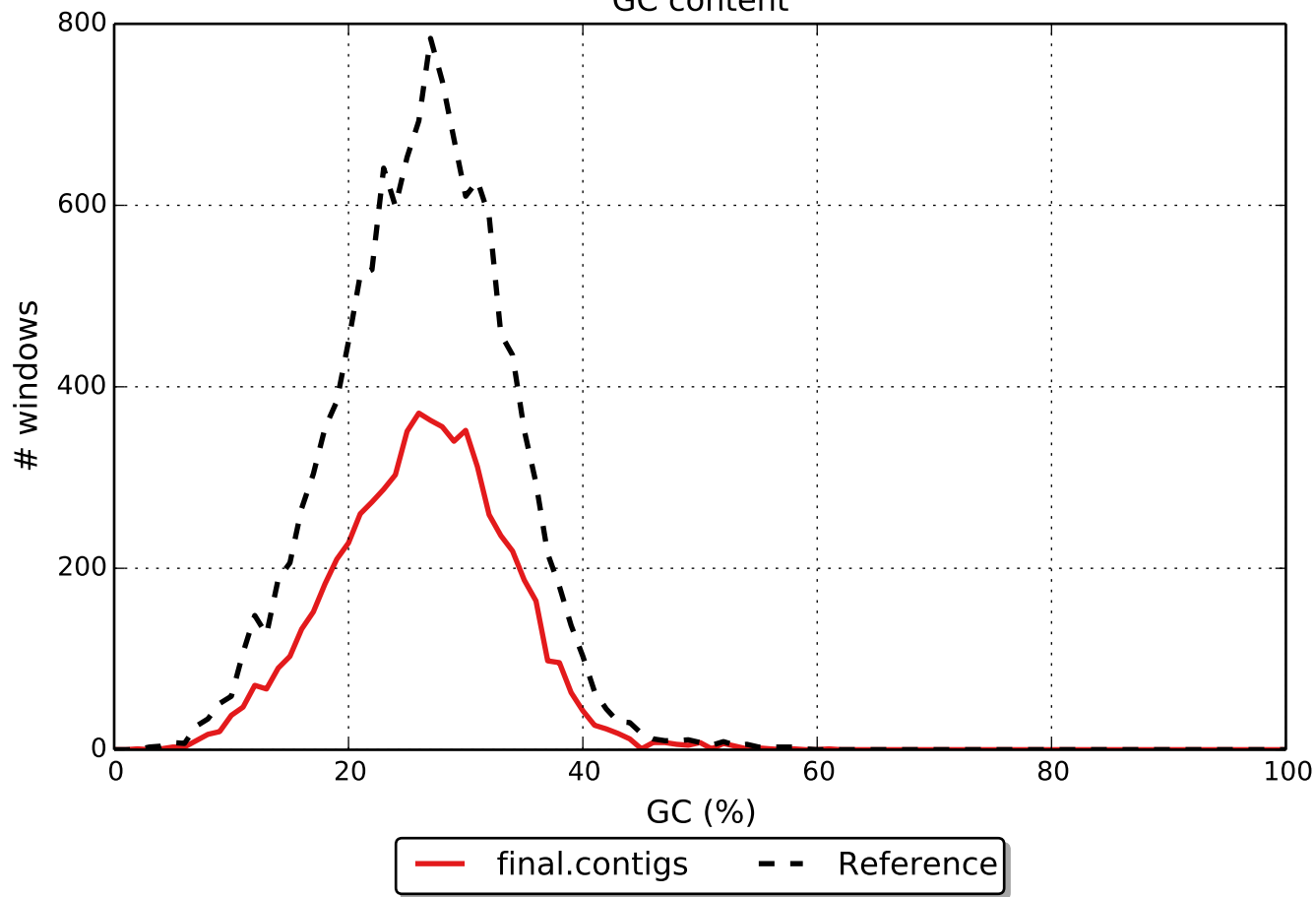
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

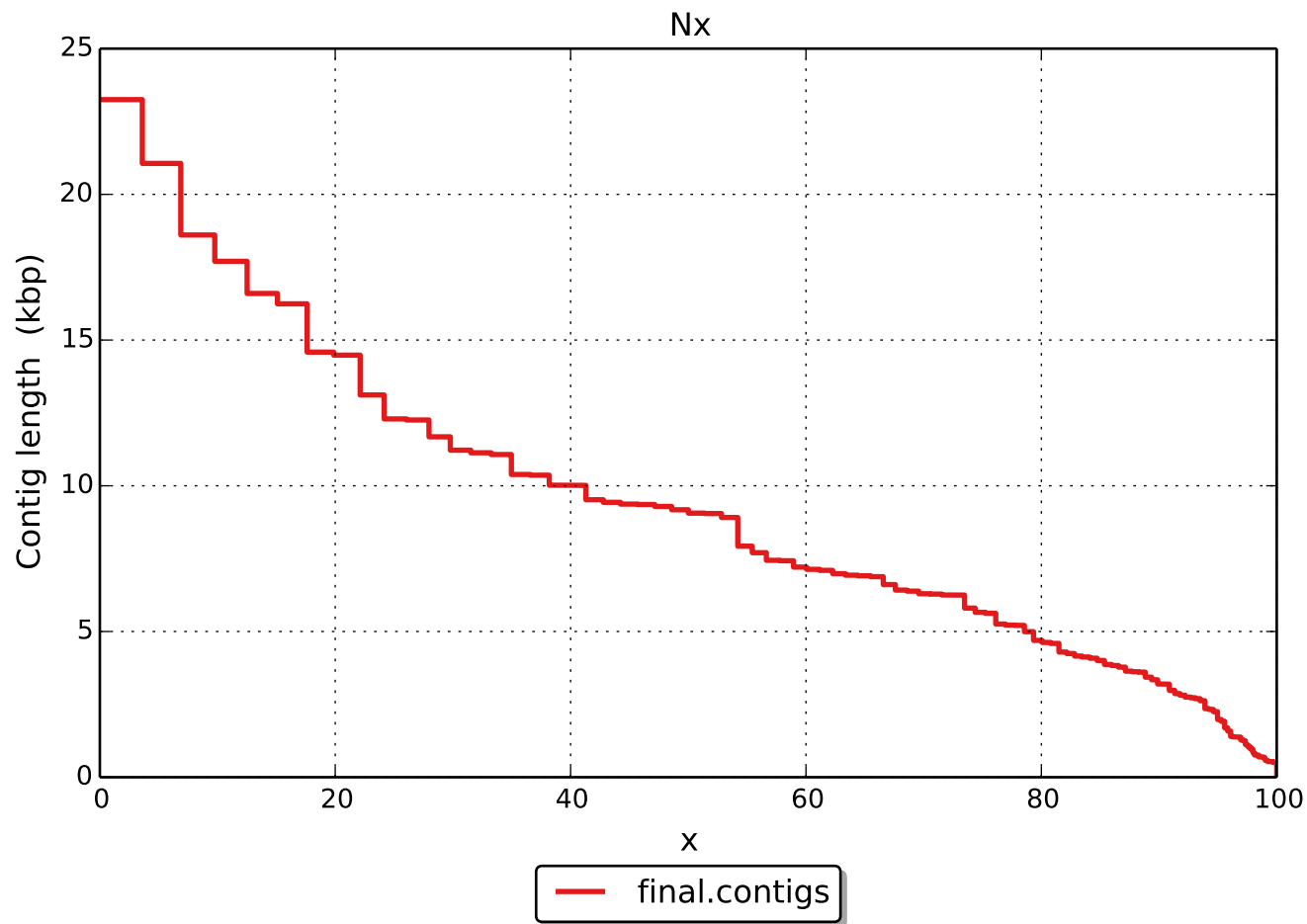
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

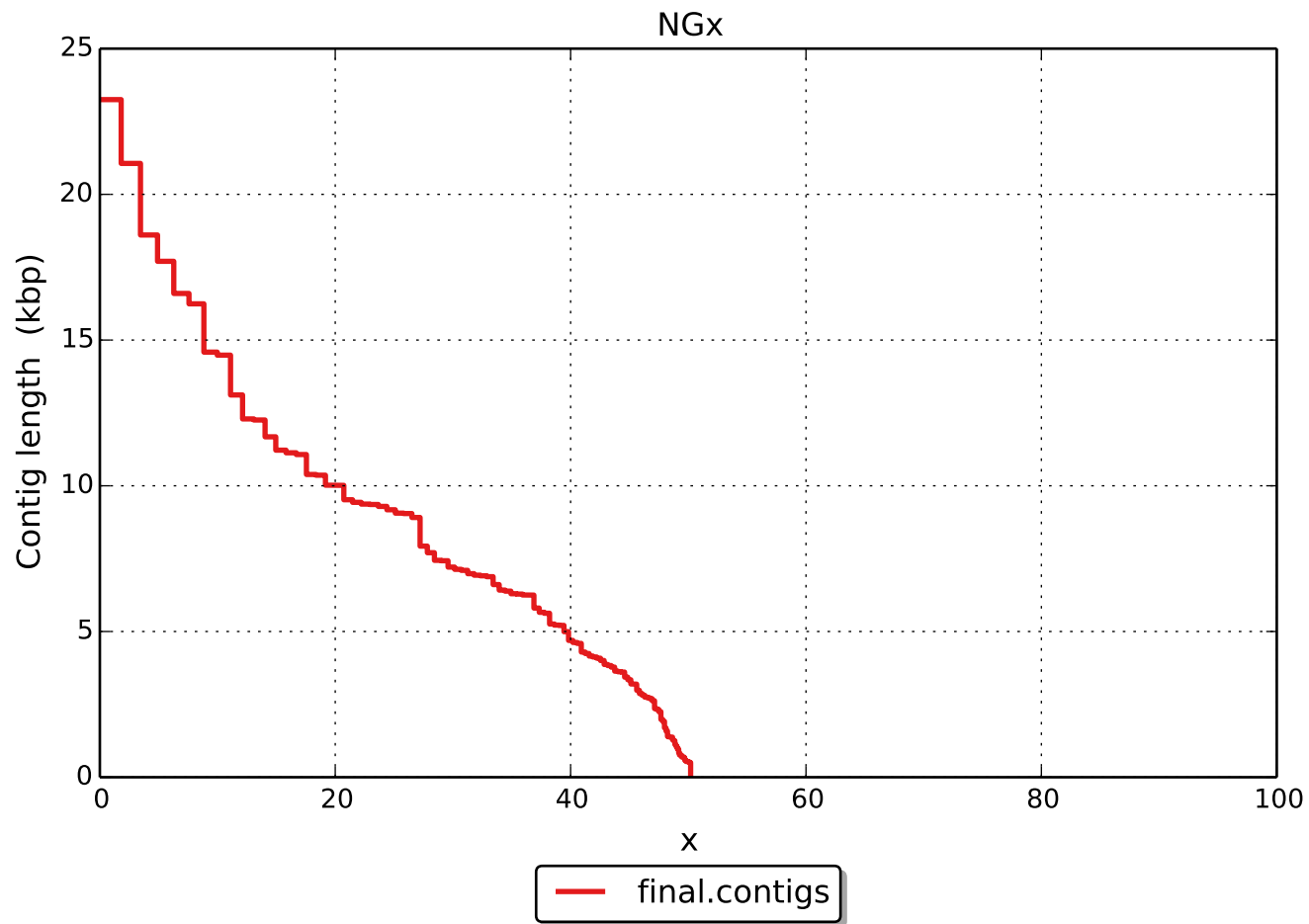
Cumulative length



GC content



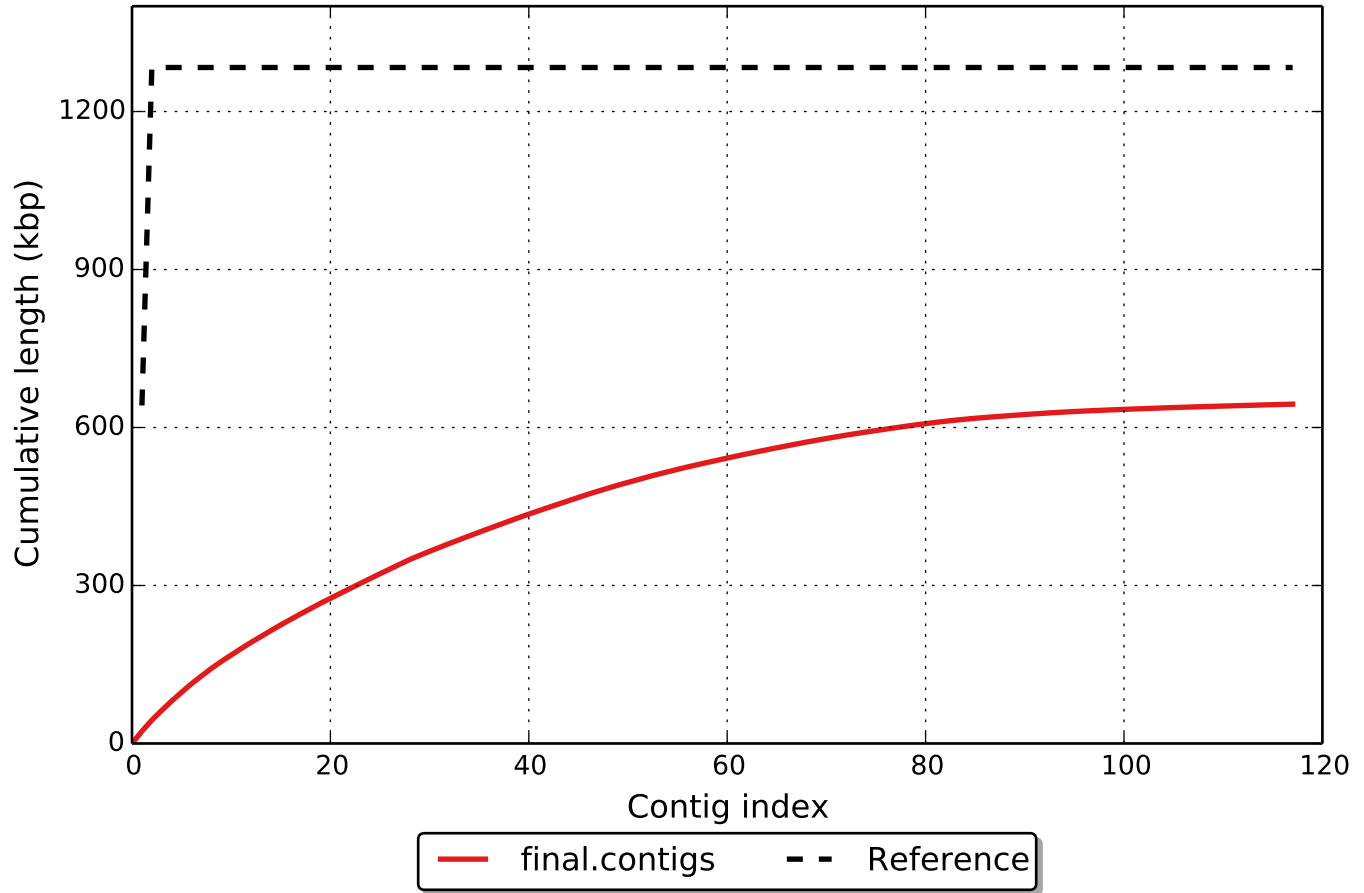


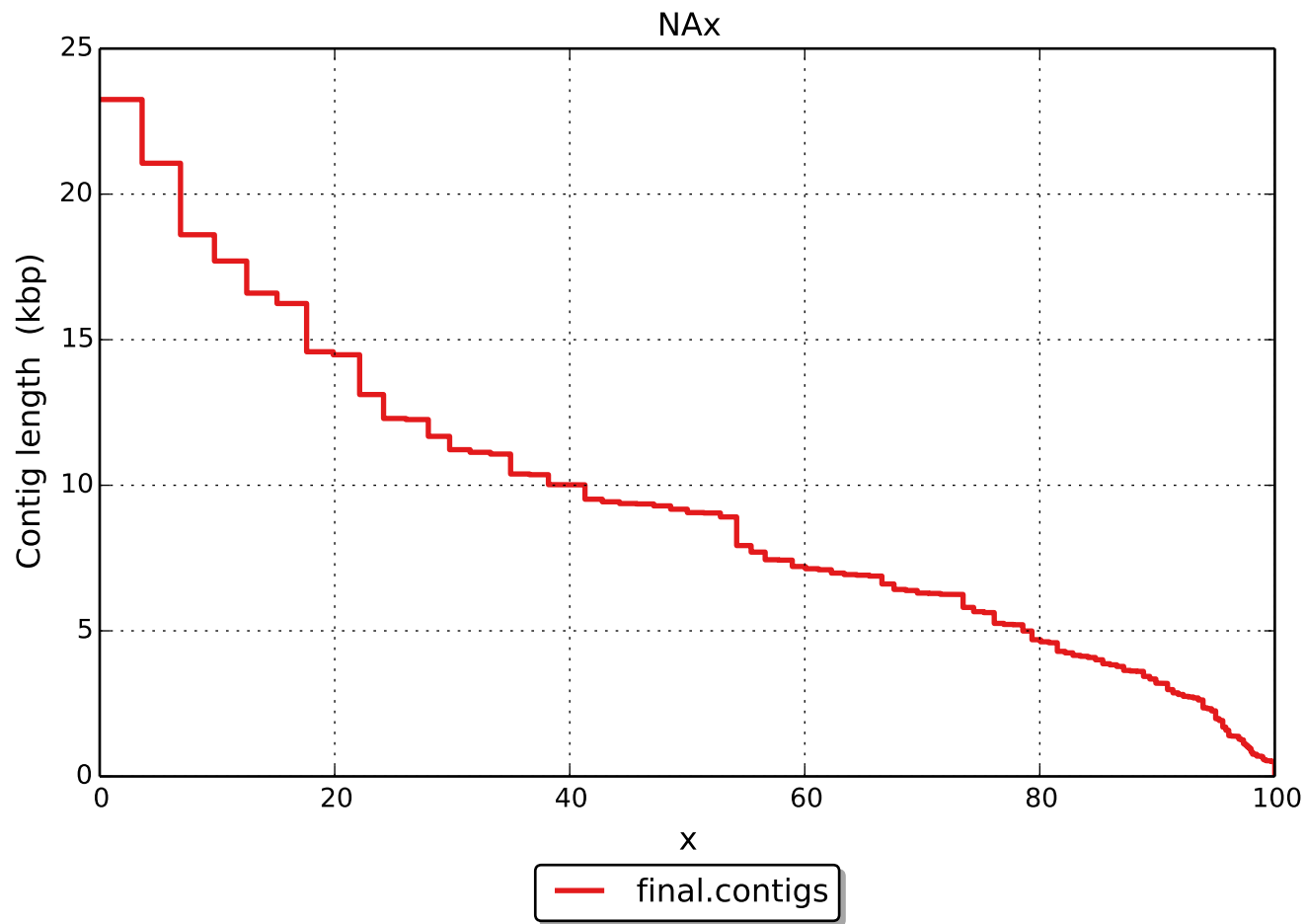


Misassemblies



Cumulative length (aligned contigs)





NGAx

