

Report

	final.contigs
# contigs (≥ 0 bp)	97
# contigs (≥ 1000 bp)	97
Total length (≥ 0 bp)	1290438
Total length (≥ 1000 bp)	1290438
# contigs	97
Largest contig	45036
Total length	1290438
Reference length	641799
GC (%)	26.29
Reference GC (%)	26.30
N50	19749
NG50	29739
N75	12569
NG75	24192
L50	23
LG50	9
L75	44
LG75	15
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	44 + 4 part
Unaligned length	643659
Genome fraction (%)	99.950
Duplication ratio	1.008
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	45036
NA50	1495
NGA50	18548
NGA75	12992
LA50	49
LGA50	12
LGA75	22

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
# possibly misassembled contigs	1
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	0
# indels	0
# short indels	0
# long indels	0
Indels length	0

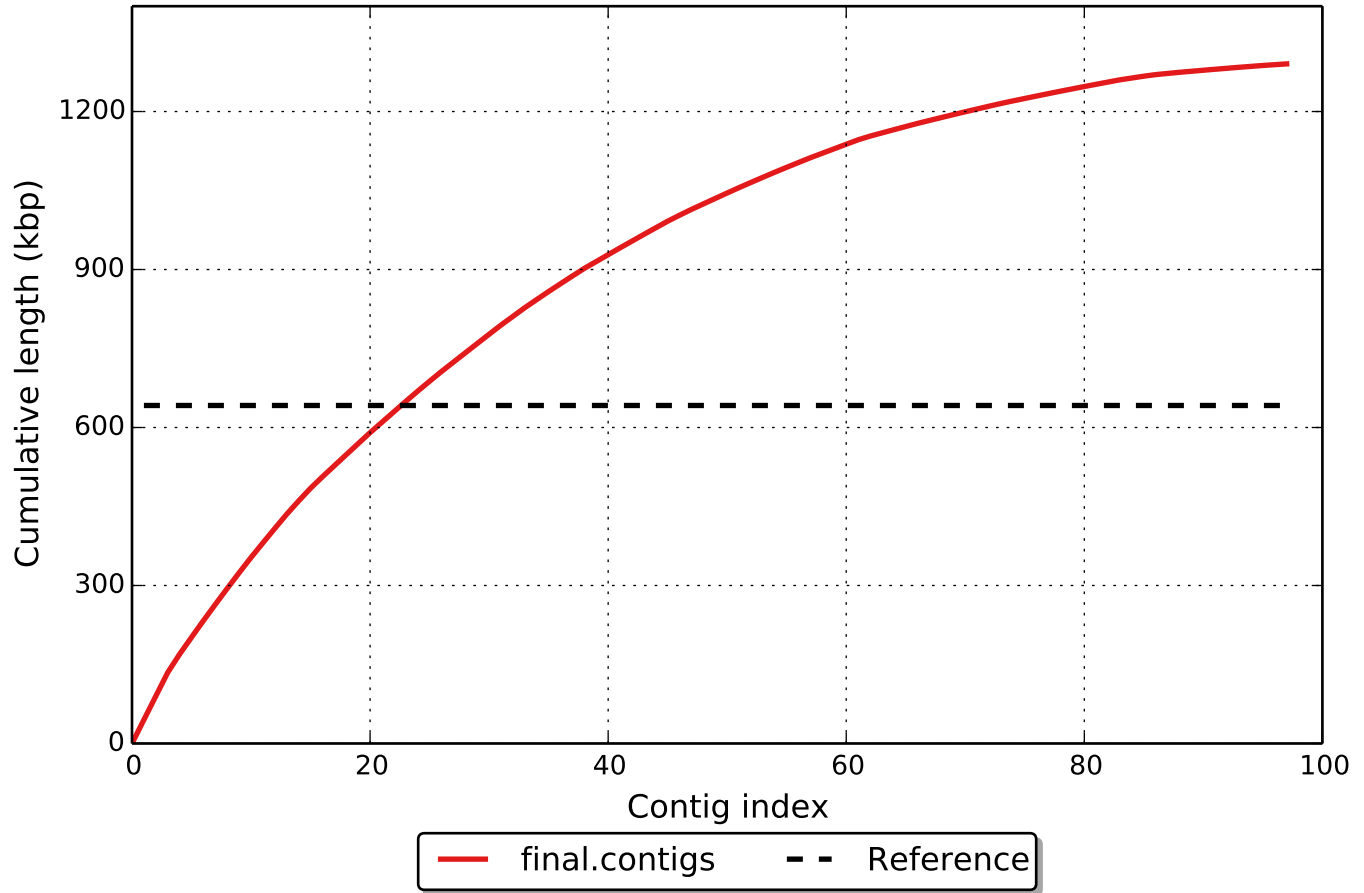
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

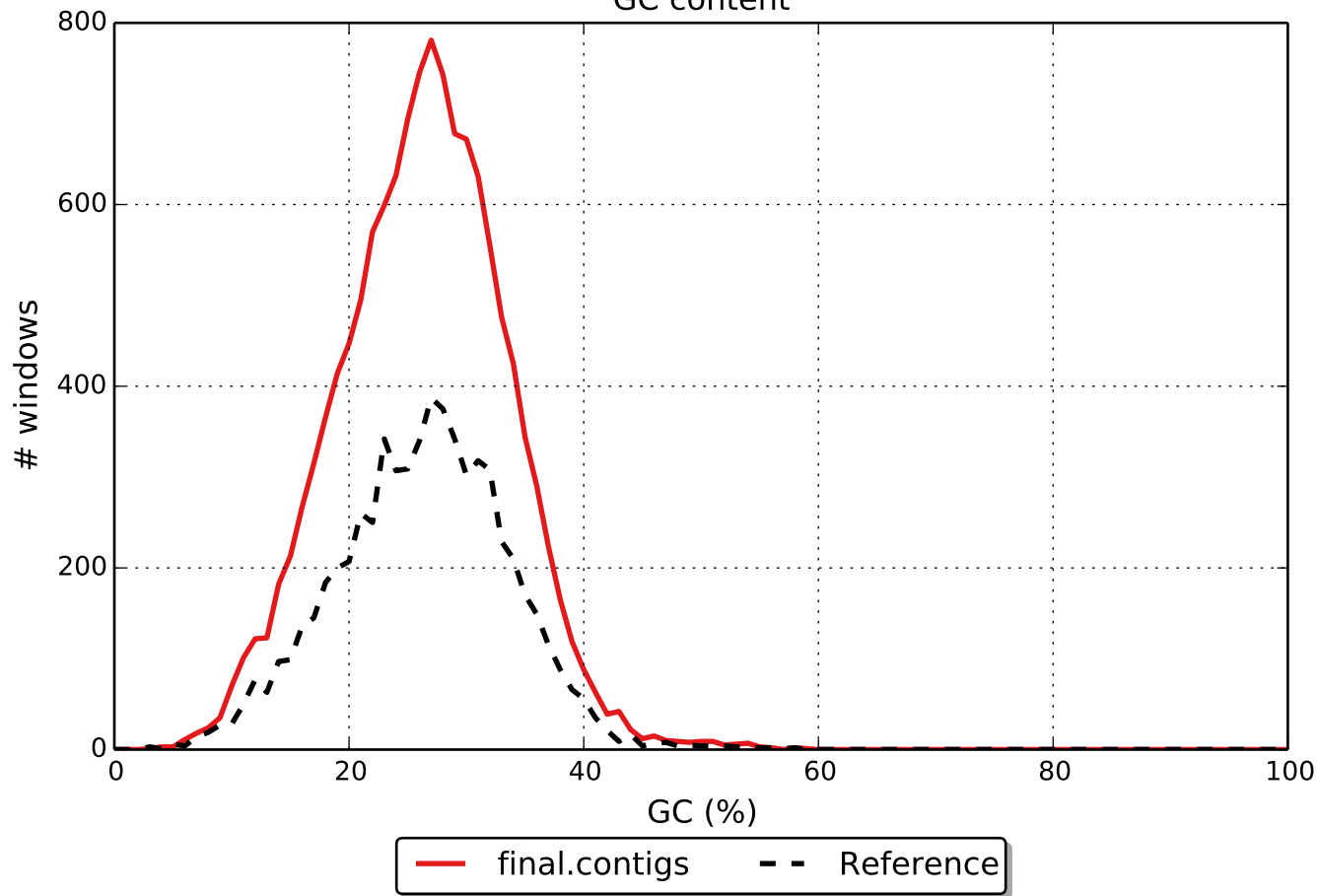
	final.contigs
# fully unaligned contigs	44
Fully unaligned length	566348
# partially unaligned contigs	4
# with misassembly	1
# both parts are significant	1
Partially unaligned length	77311
# N's	0

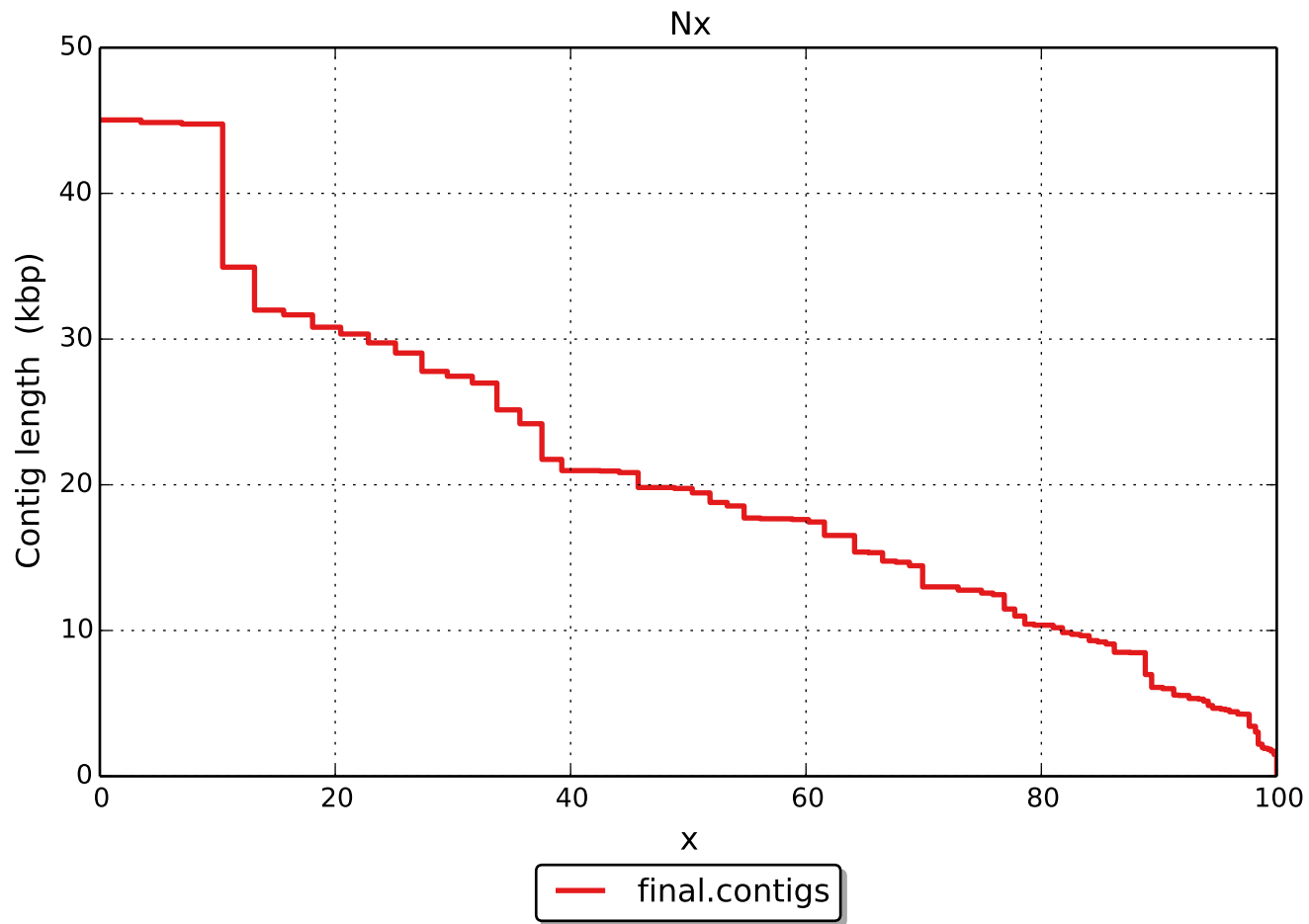
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

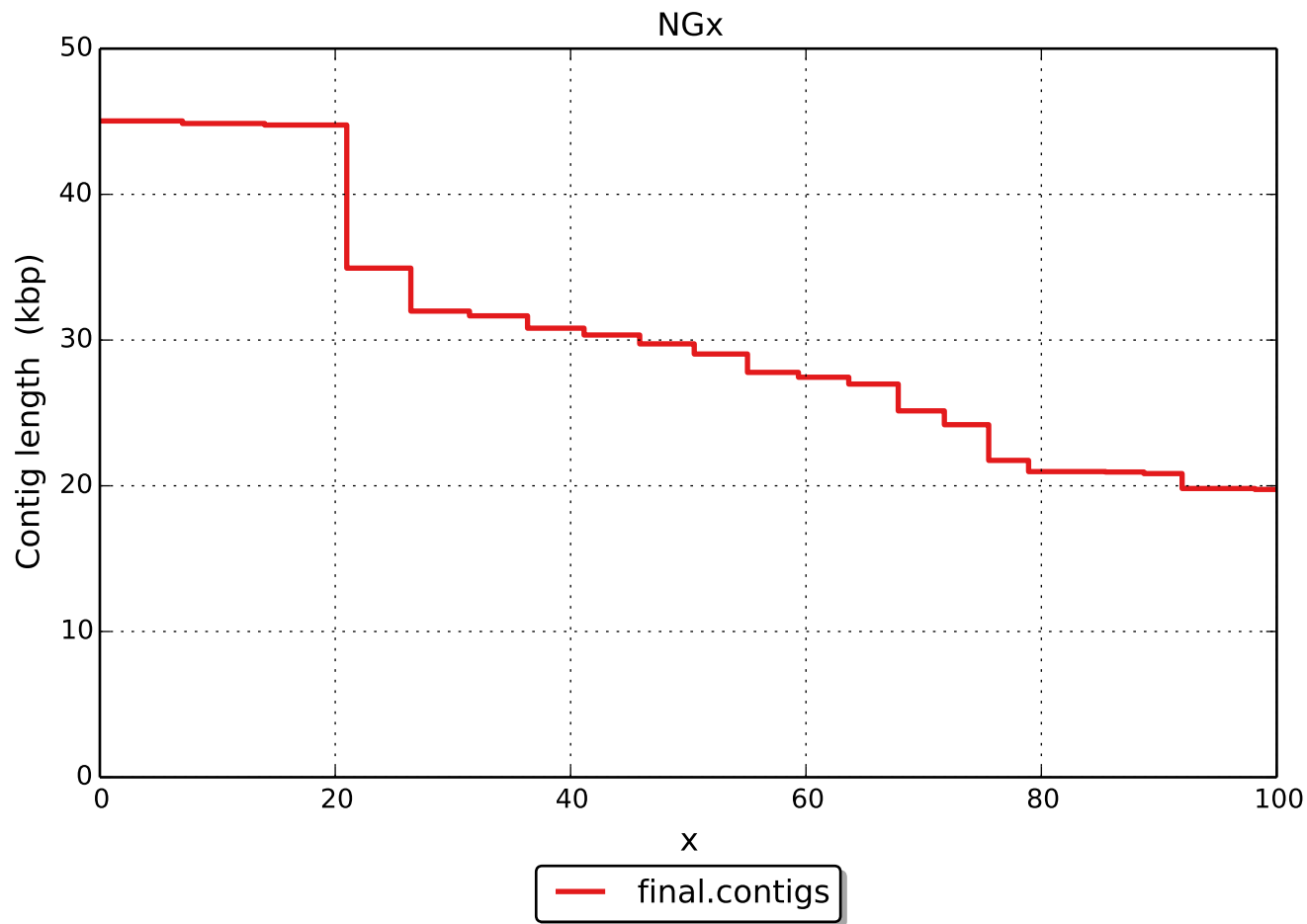
Cumulative length



GC content



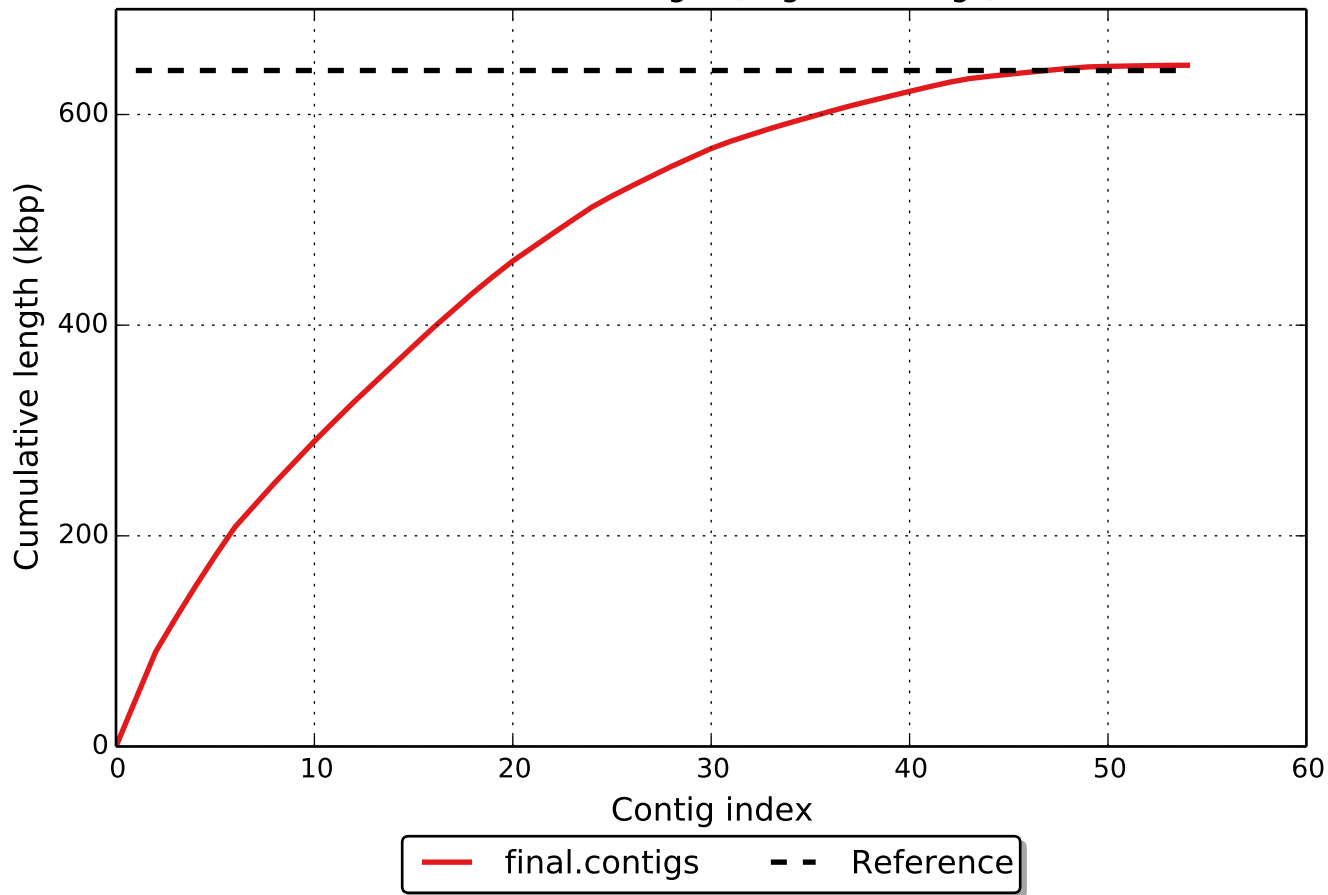


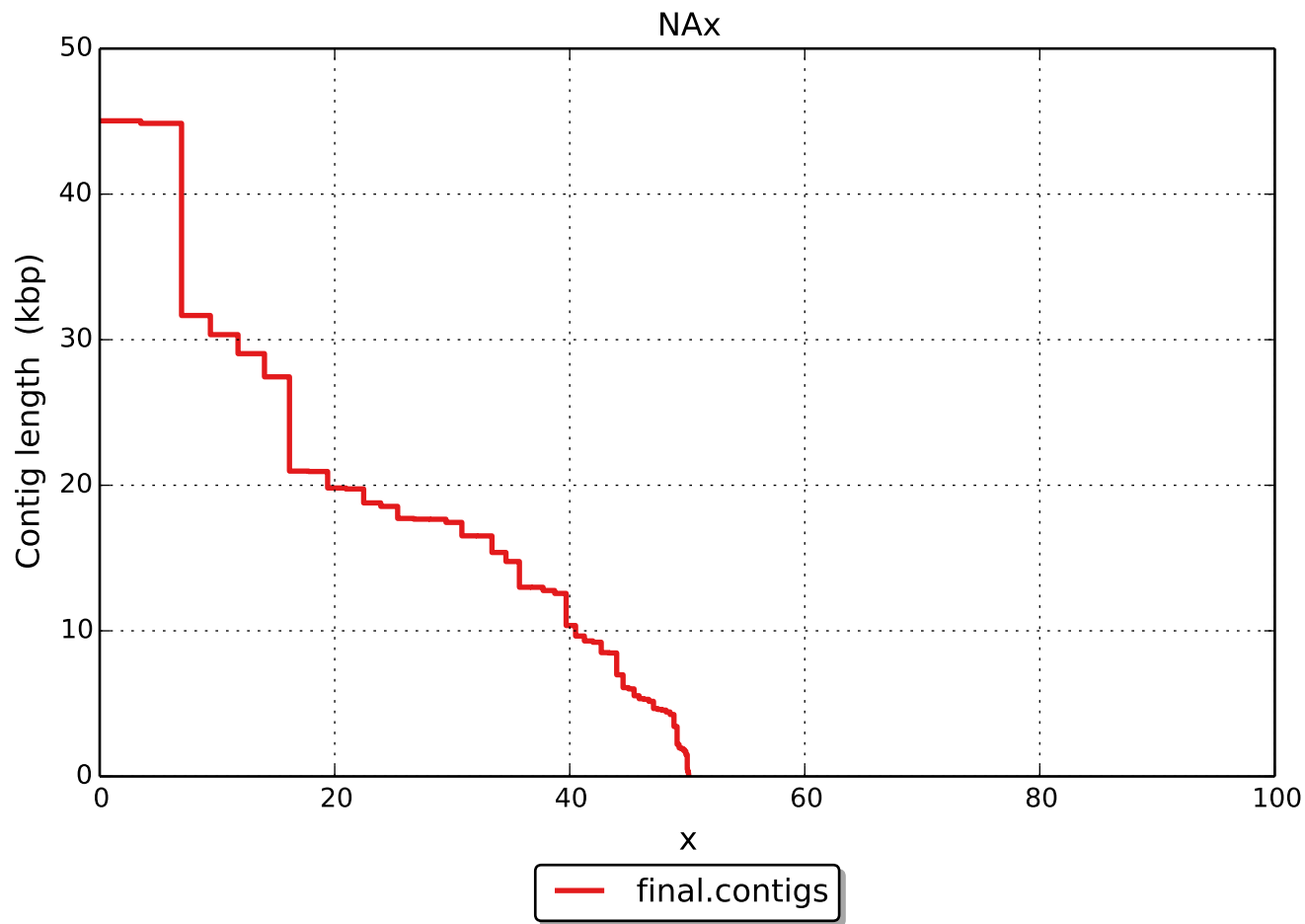


Misassemblies



Cumulative length (aligned contigs)





NGAx

