

Report

	final.contigs
# contigs (>= 0 bp)	102
# contigs (>= 1000 bp)	82
Total length (>= 0 bp)	619642
Total length (>= 1000 bp)	607382
# contigs	102
Largest contig	36312
Total length	619642
Reference length	615980
GC (%)	25.34
Reference GC (%)	25.35
N50	11348
NG50	11348
N75	6713
NG75	7210
L50	20
LG50	20
L75	37
LG75	36
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	1131
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.828
Duplication ratio	1.018
# N's per 100 kbp	0.00
# mismatches per 100 kbp	500.36
# indels per 100 kbp	0.00
Largest alignment	36312
NA50	11348
NGA50	11348
NA75	6713
NGA75	7210
LA50	20
LGA50	20
LA75	37
LGA75	36

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

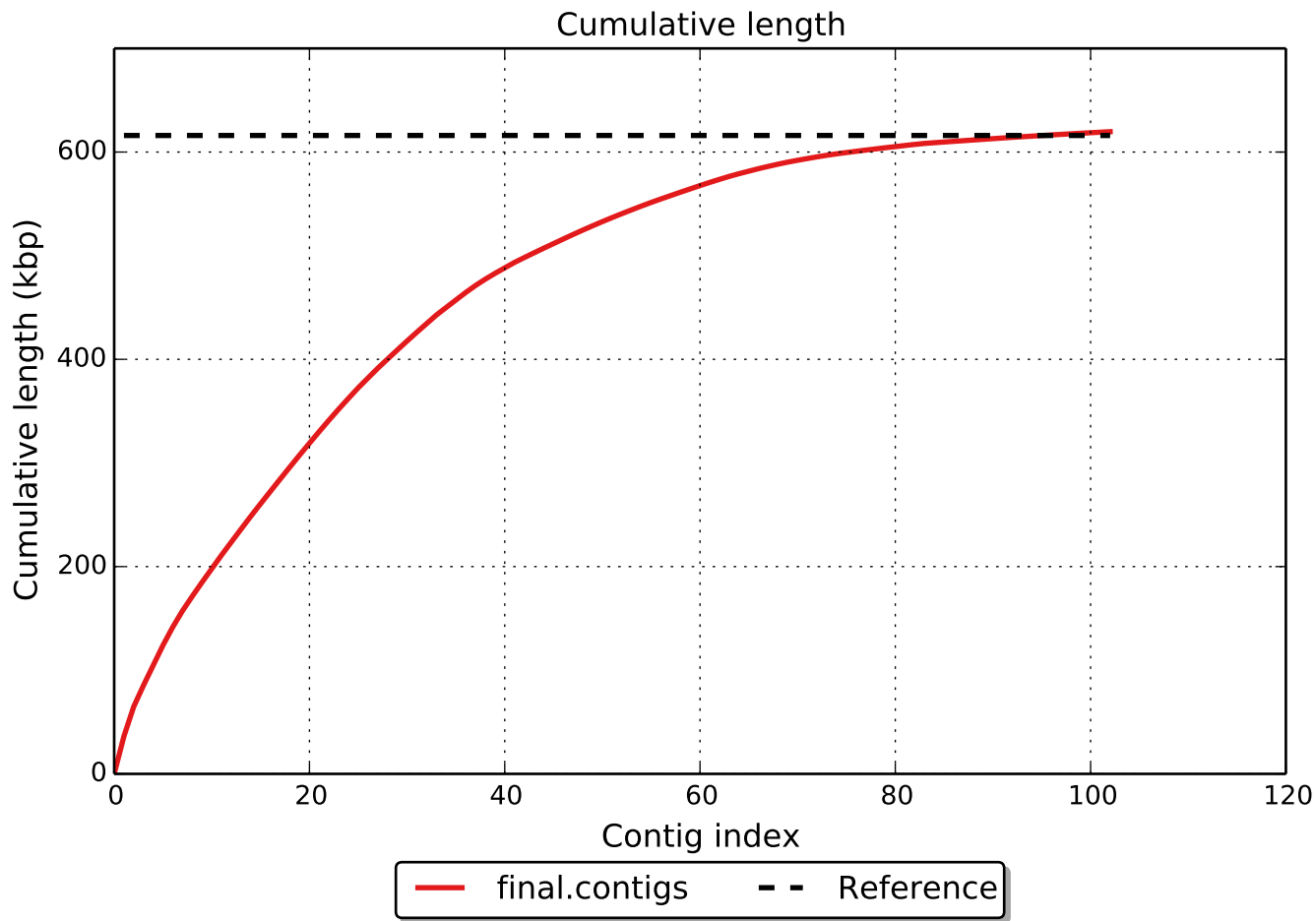
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	1131
# local misassemblies	0
# mismatches	3046
# indels	0
# short indels	0
# long indels	0
Indels length	0

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).

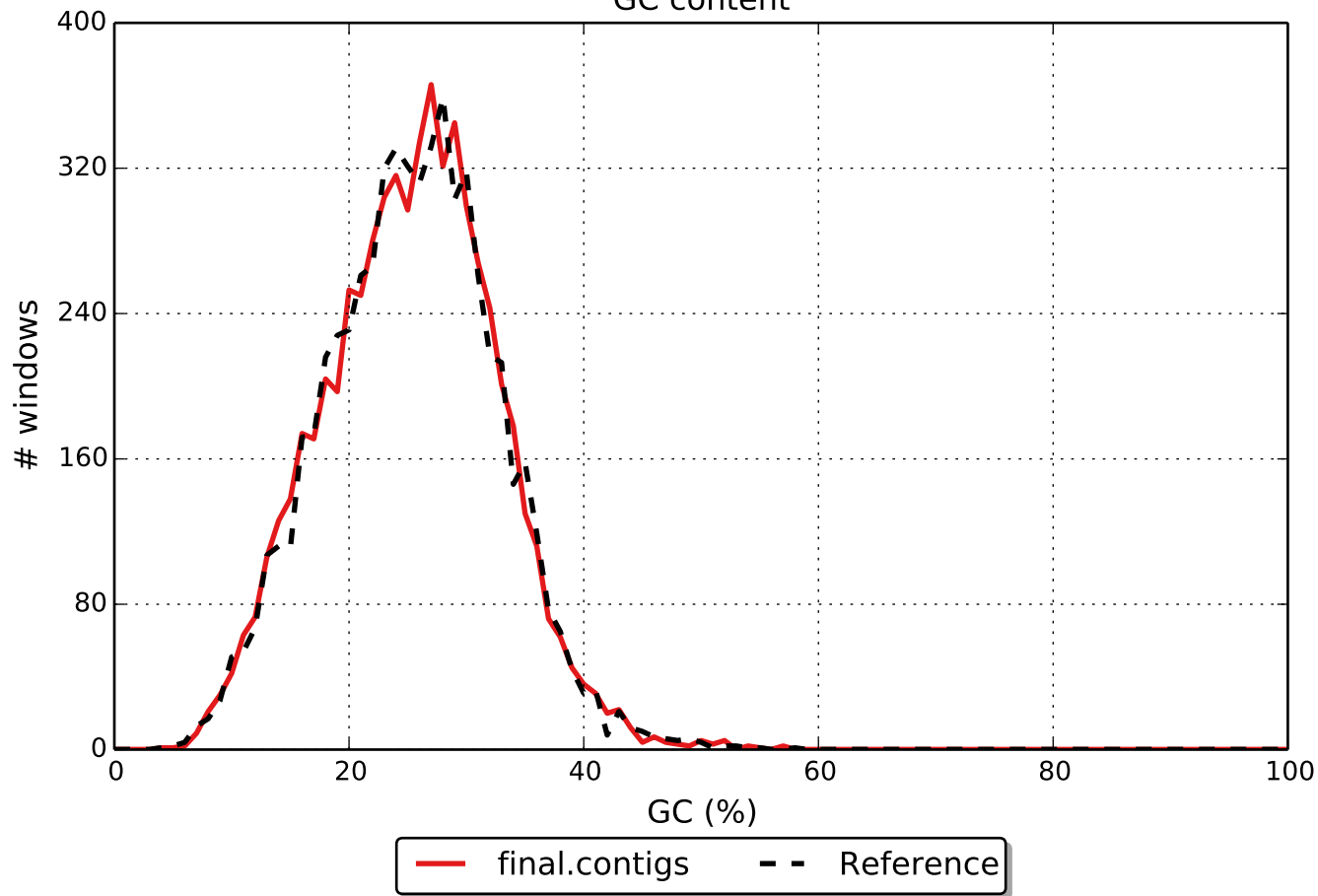
Unaligned report

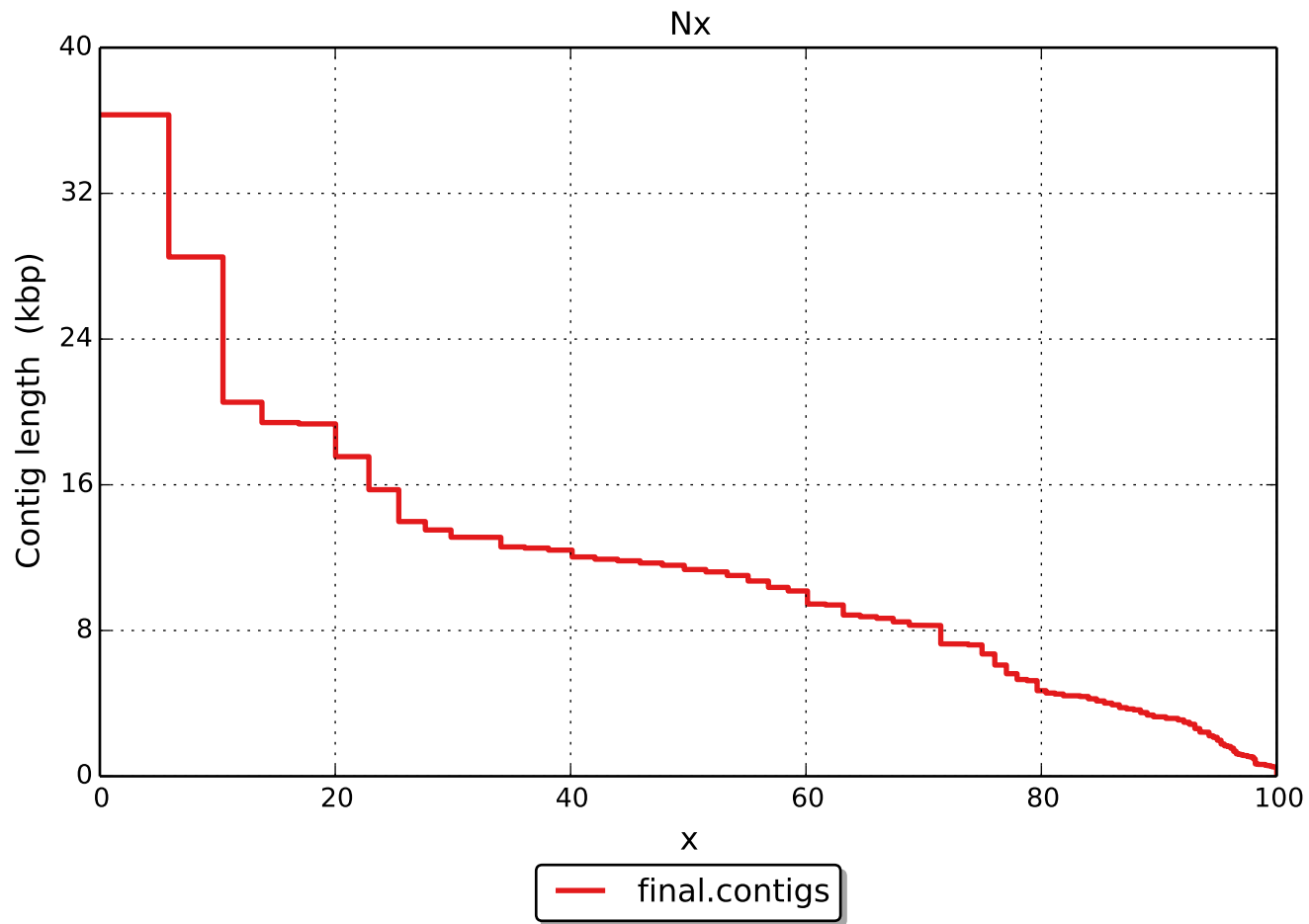
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

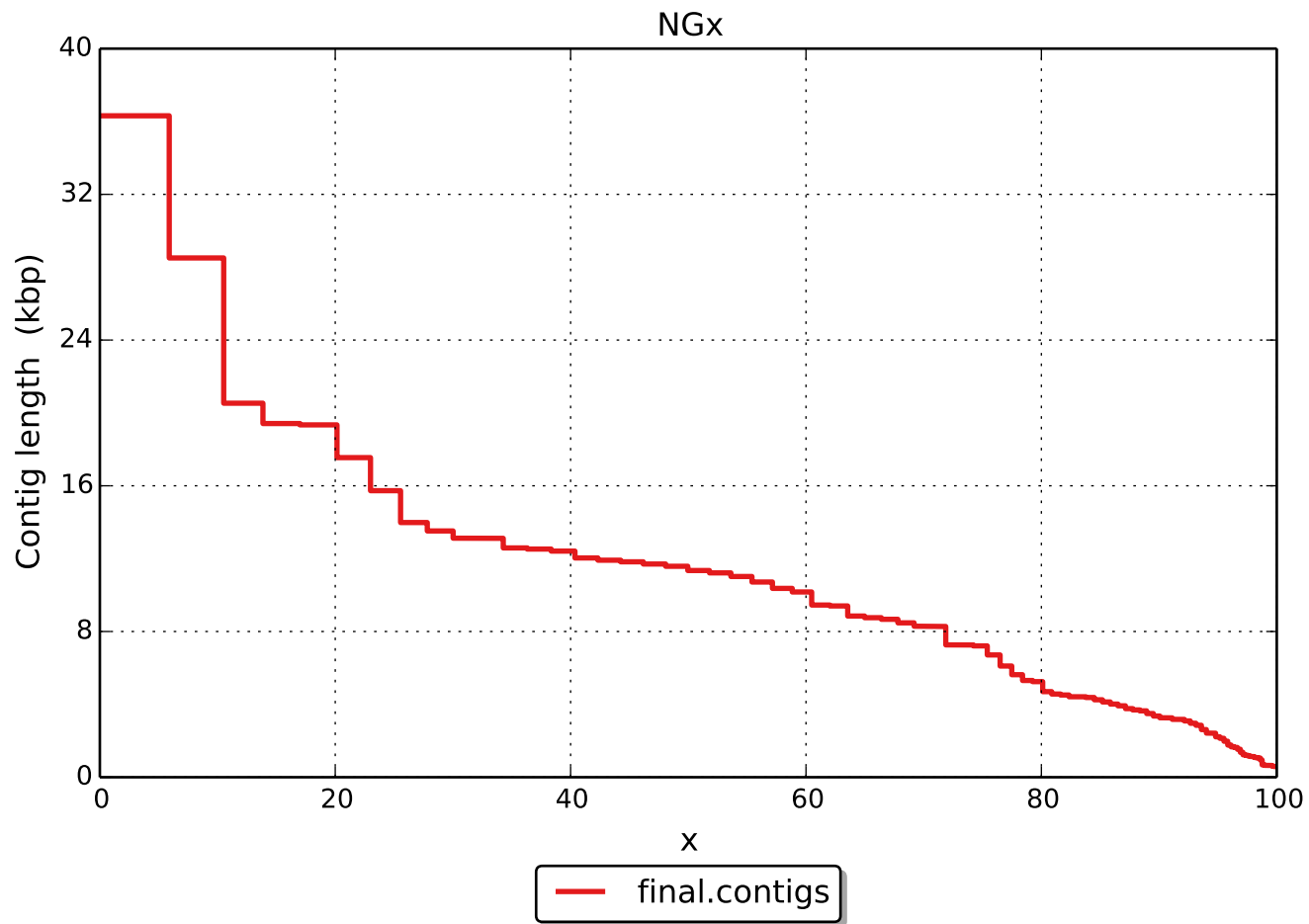
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



GC content

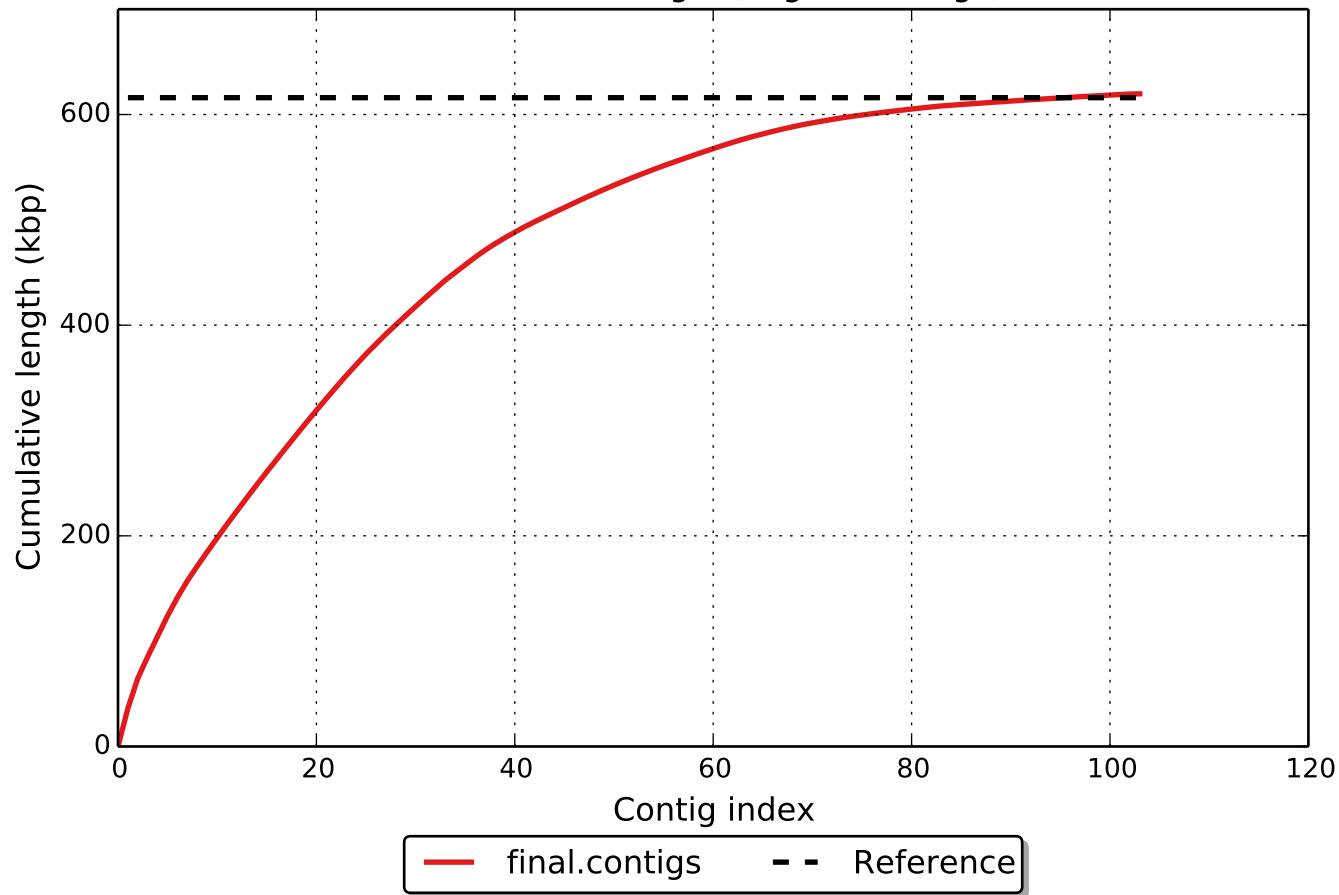


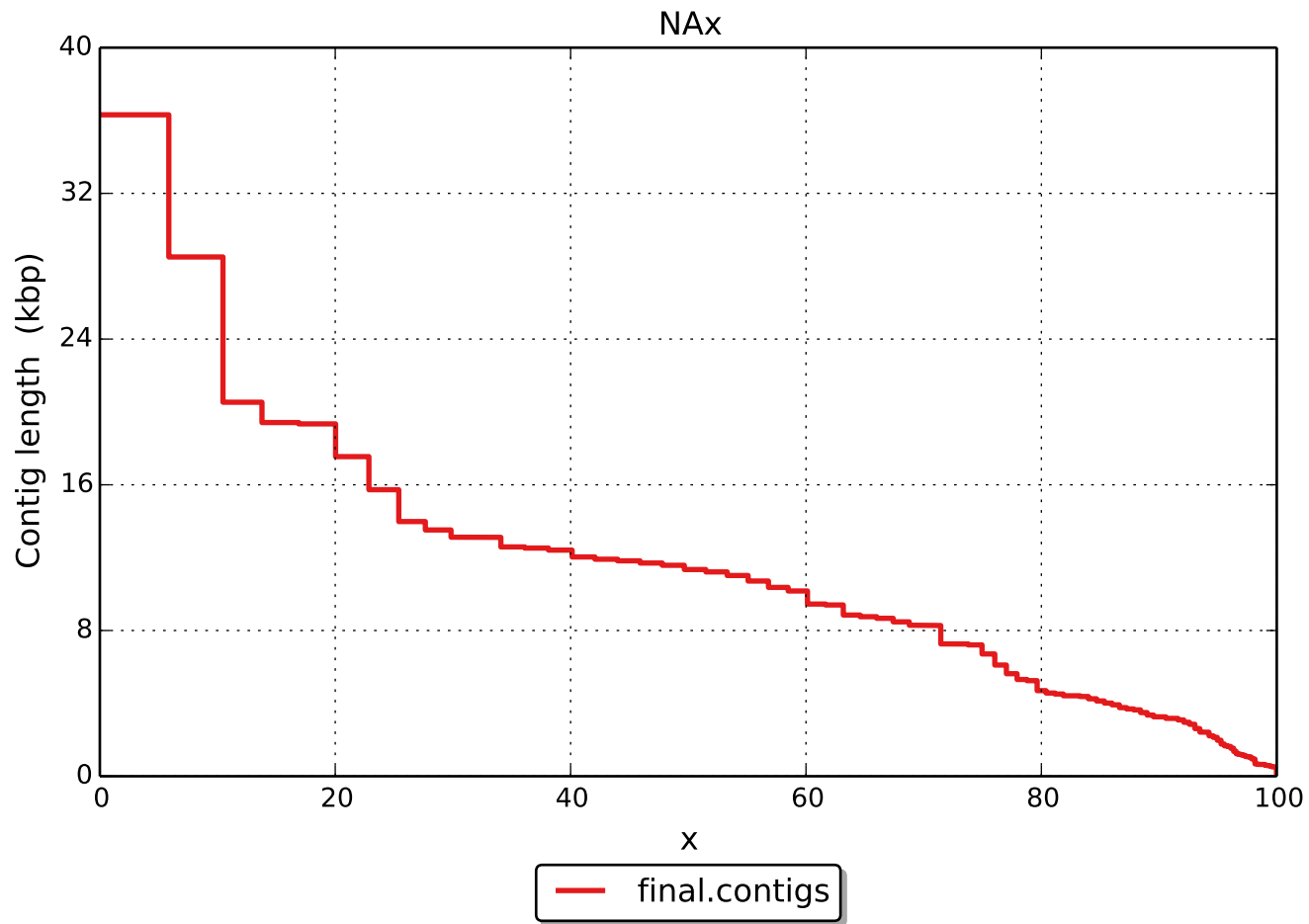






Cumulative length (aligned contigs)





NGAx

