

## Report

	final.contigs
# contigs (>= 0 bp)	117
# contigs (>= 1000 bp)	95
Total length (>= 0 bp)	644329
Total length (>= 1000 bp)	630349
# contigs	117
Largest contig	23250
Total length	644329
Reference length	641799
GC (%)	26.31
Reference GC (%)	26.30
N50	9177
NG50	9177
N75	5658
NG75	5658
L50	25
LG50	25
L75	48
LG75	48
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.503
Duplication ratio	1.019
# N's per 100 kbp	0.00
# mismatches per 100 kbp	522.31
# indels per 100 kbp	0.63
Largest alignment	23250
NA50	9177
NGA50	9177
NA75	5658
NGA75	5658
LA50	25
LGA50	25
LA75	48
LGA75	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

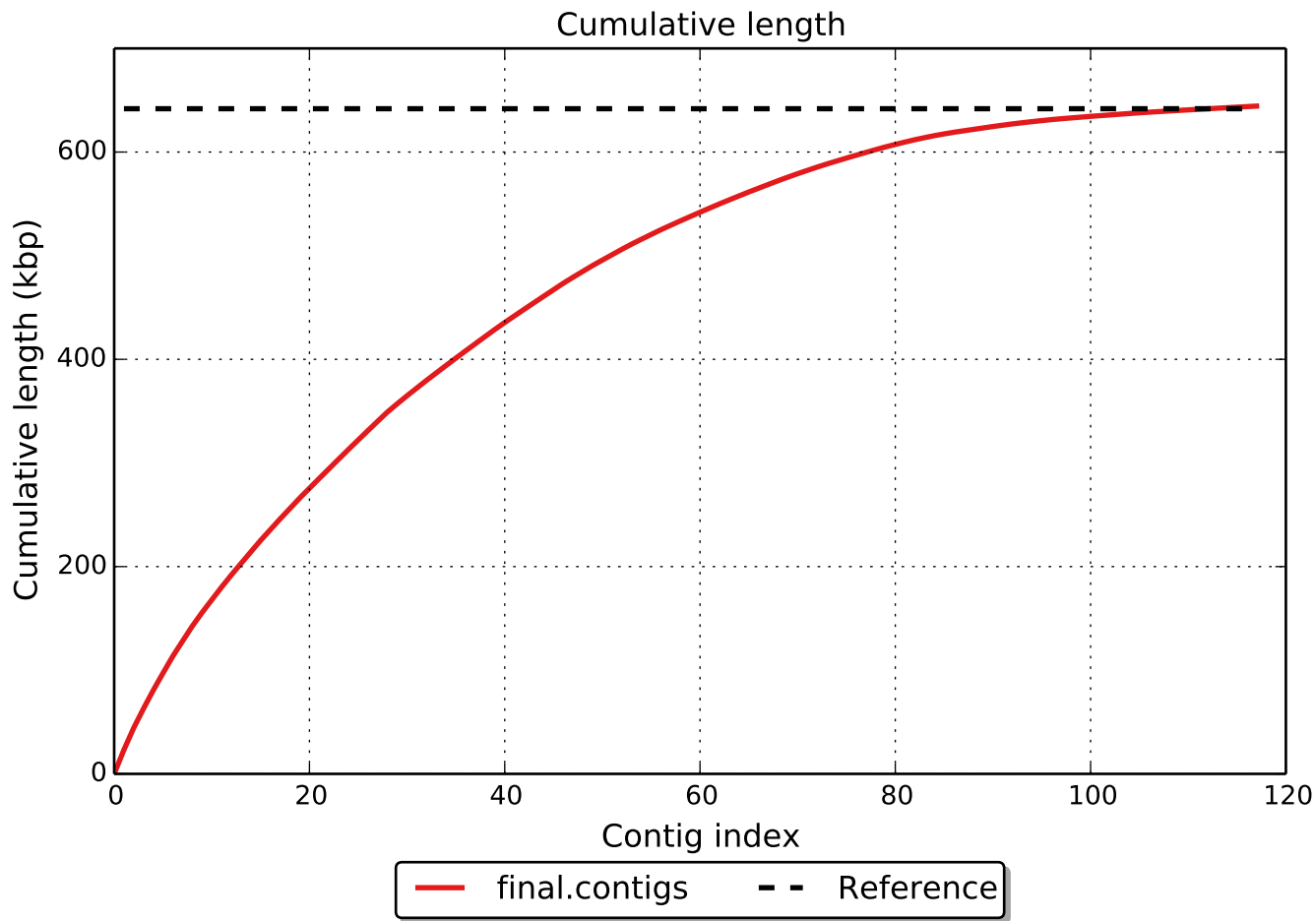
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	3302
# indels	4
# short indels	3
# long indels	1
Indels length	84

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

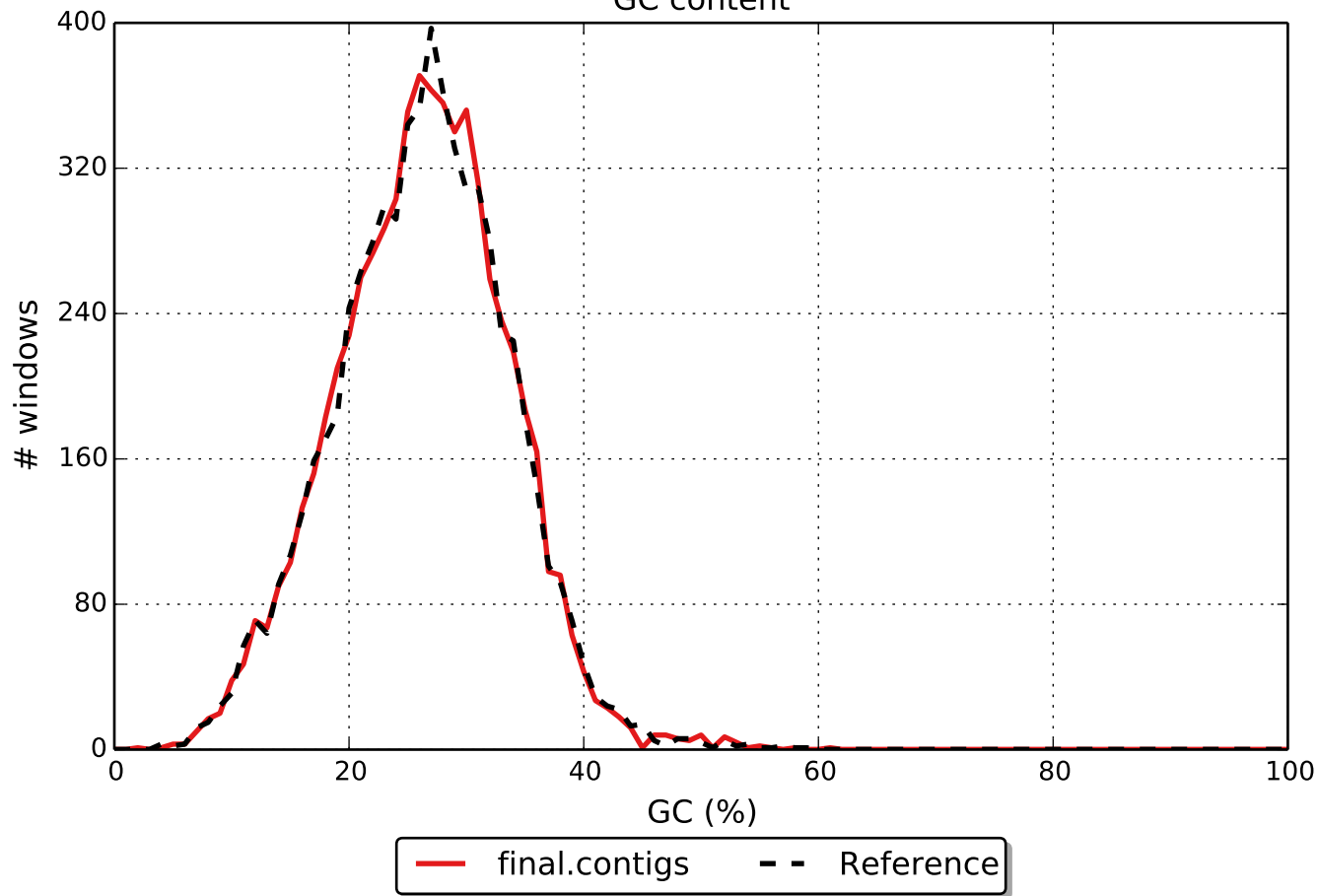
## Unaligned report

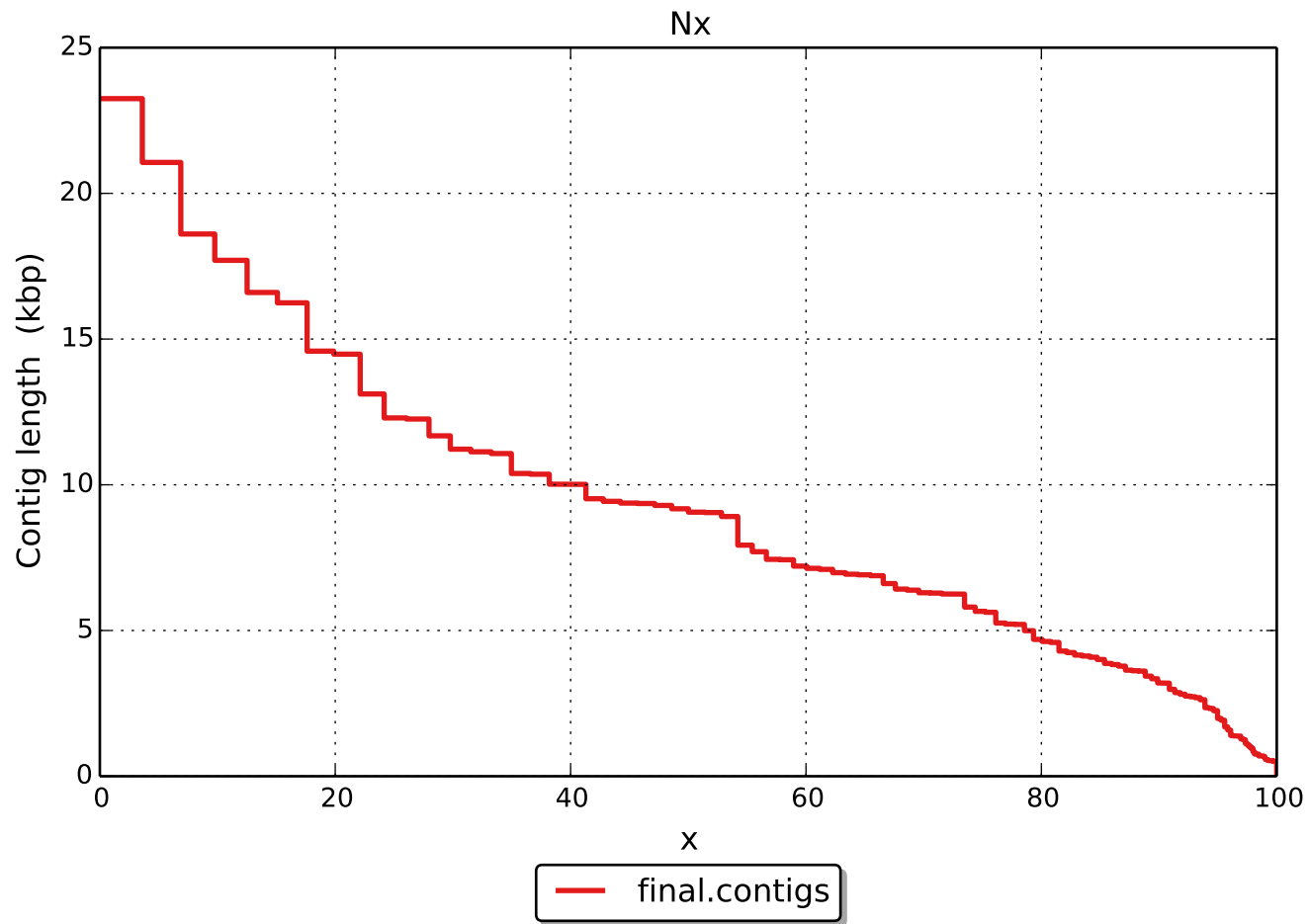
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

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

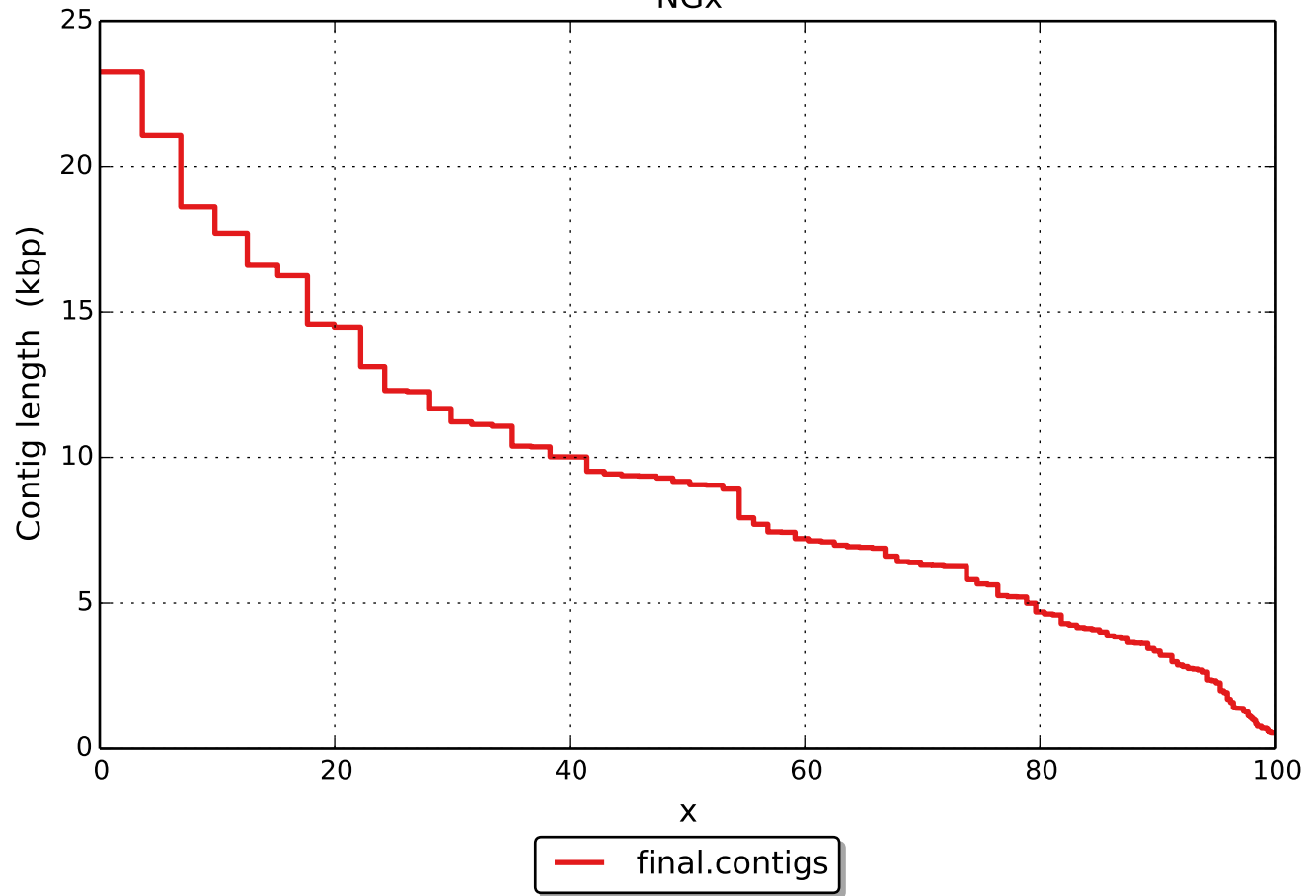


GC content





NGx

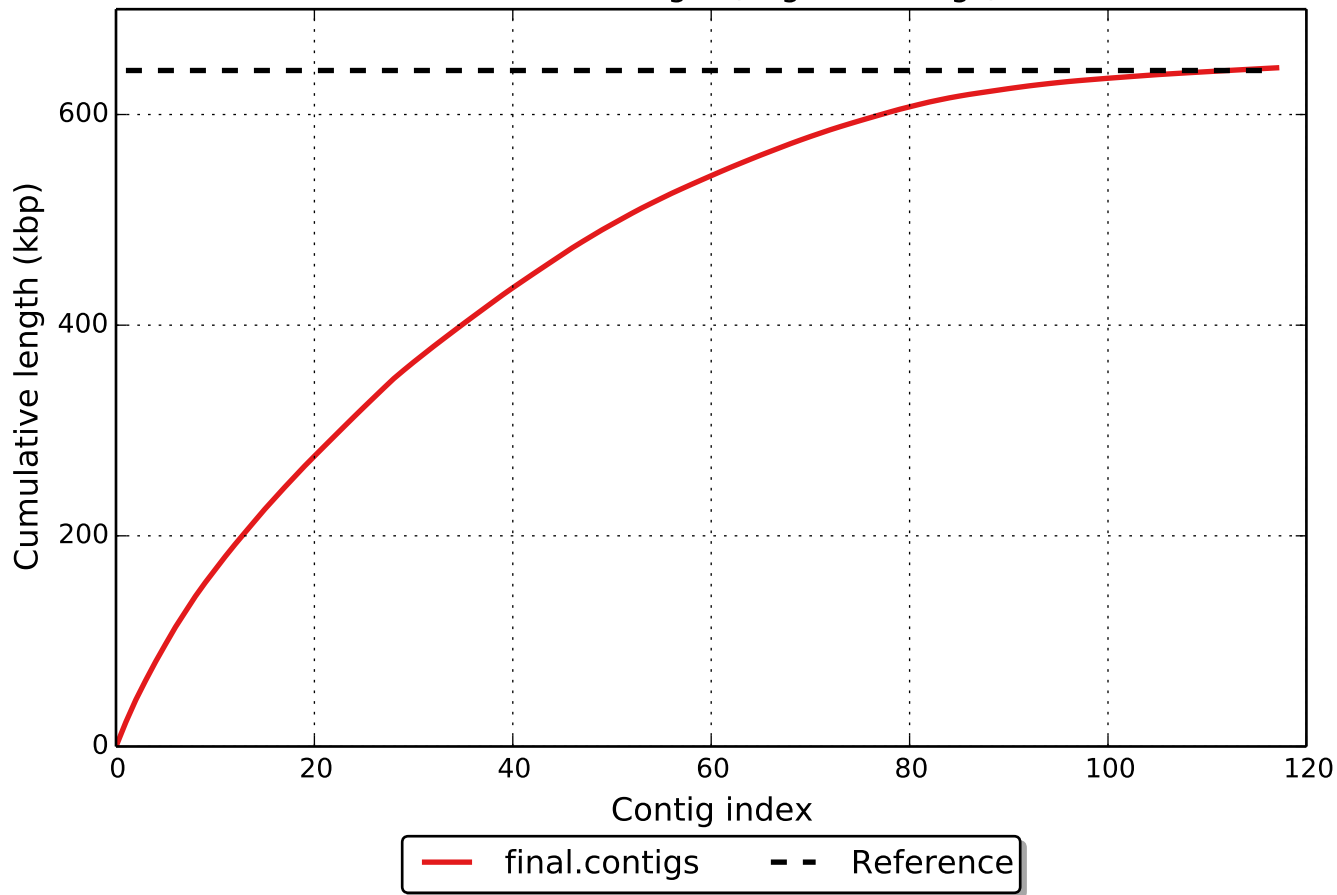


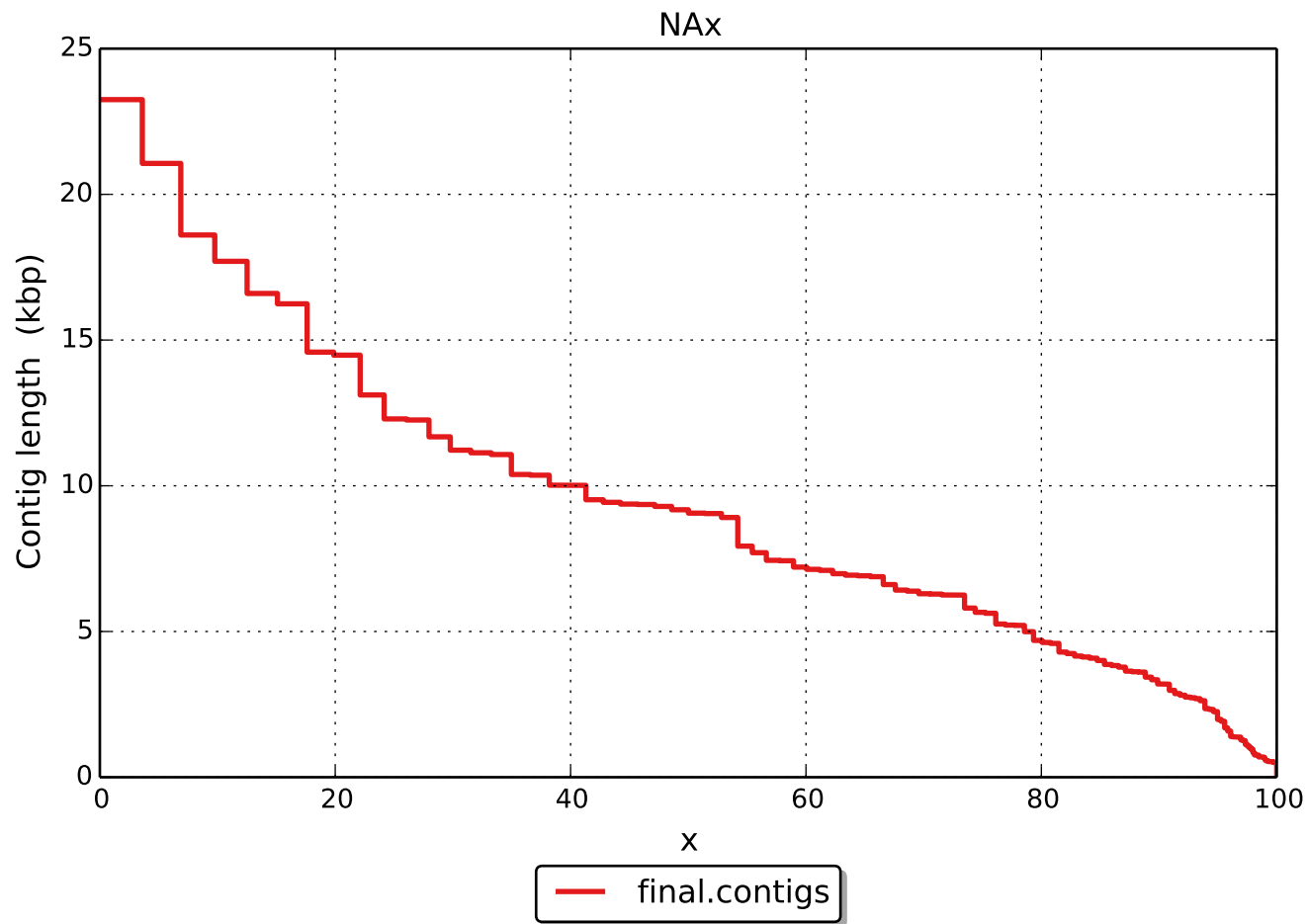
# Misassemblies





Cumulative length (aligned contigs)





NGAx

