

Report

	final.contigs
# contigs (>= 0 bp)	269
# contigs (>= 1000 bp)	258
Total length (>= 0 bp)	3709443
Total length (>= 1000 bp)	3701411
# contigs	269
Largest contig	58143
Total length	3709443
Reference length	1892775
GC (%)	32.26
Reference GC (%)	32.27
N50	21298
NG50	32823
N75	12857
NG75	26145
L50	59
LG50	24
L75	113
LG75	40
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	115 + 50 part
Unaligned length	1804479
Genome fraction (%)	99.761
Duplication ratio	1.009
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.69
# indels per 100 kbp	0.00
Largest alignment	50661
NA50	4795
NGA50	28639
NGA75	18071
LA50	88
LGA50	26
LGA75	47

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

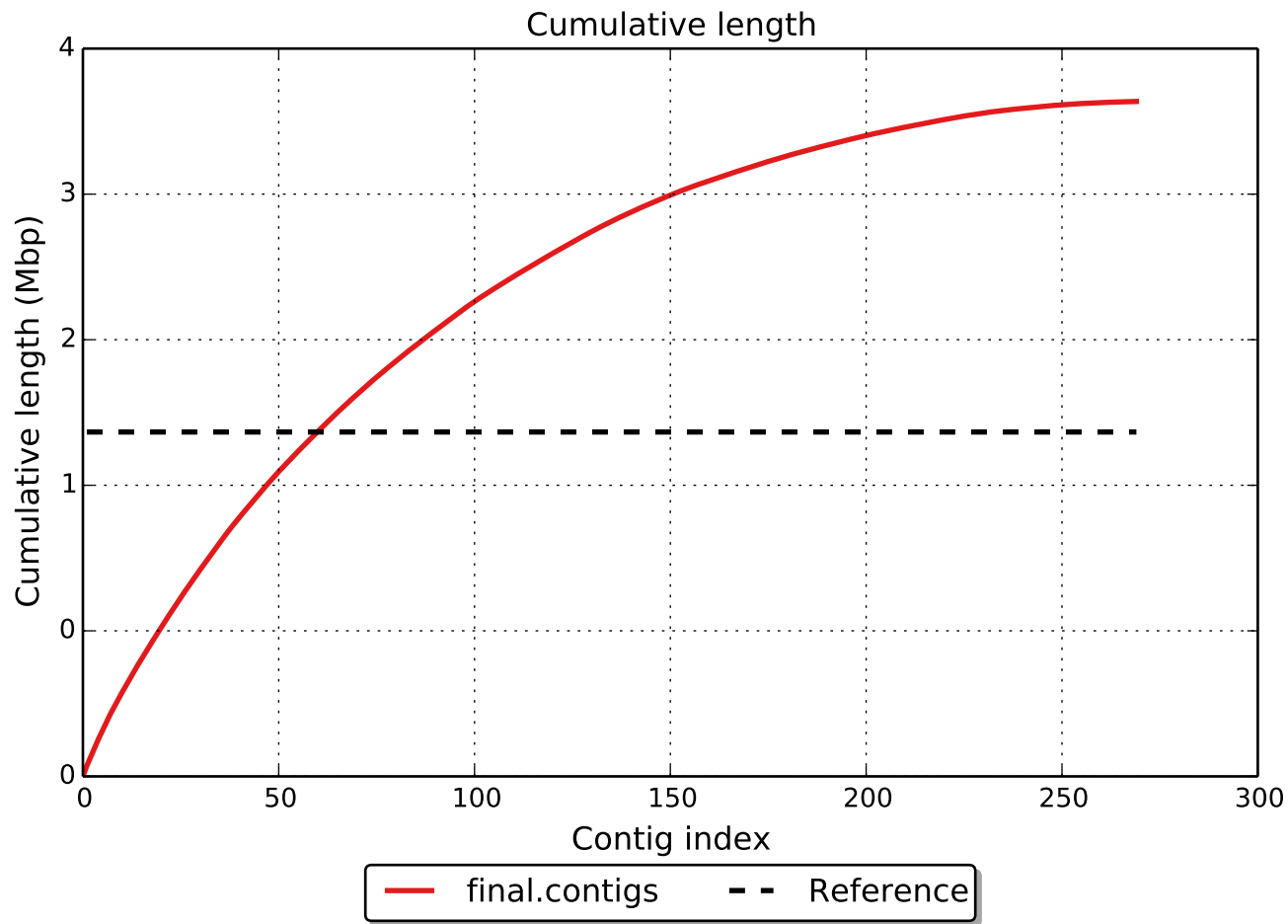
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	13
# indels	0
# short indels	0
# long indels	0
Indels length	0

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).

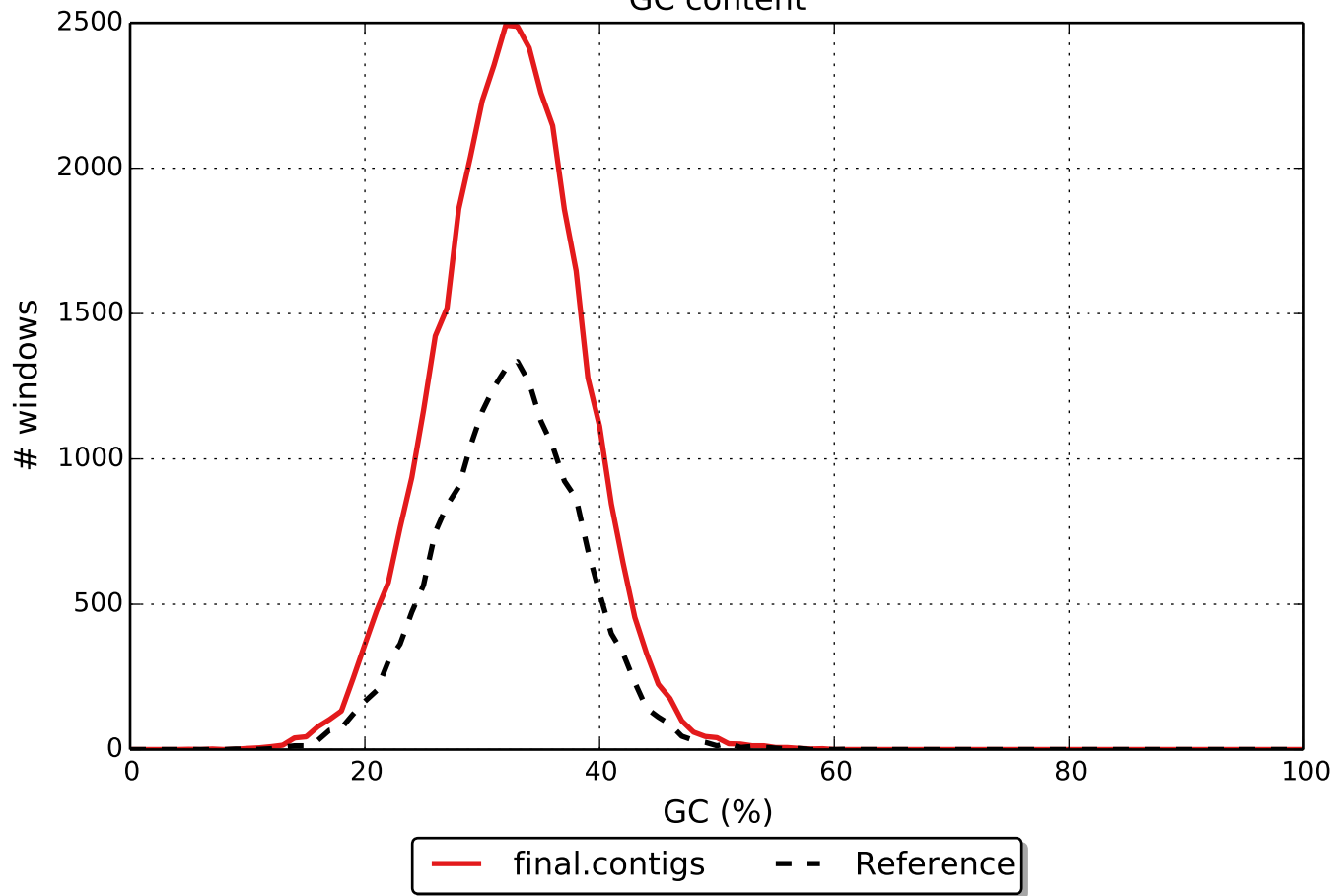
Unaligned report

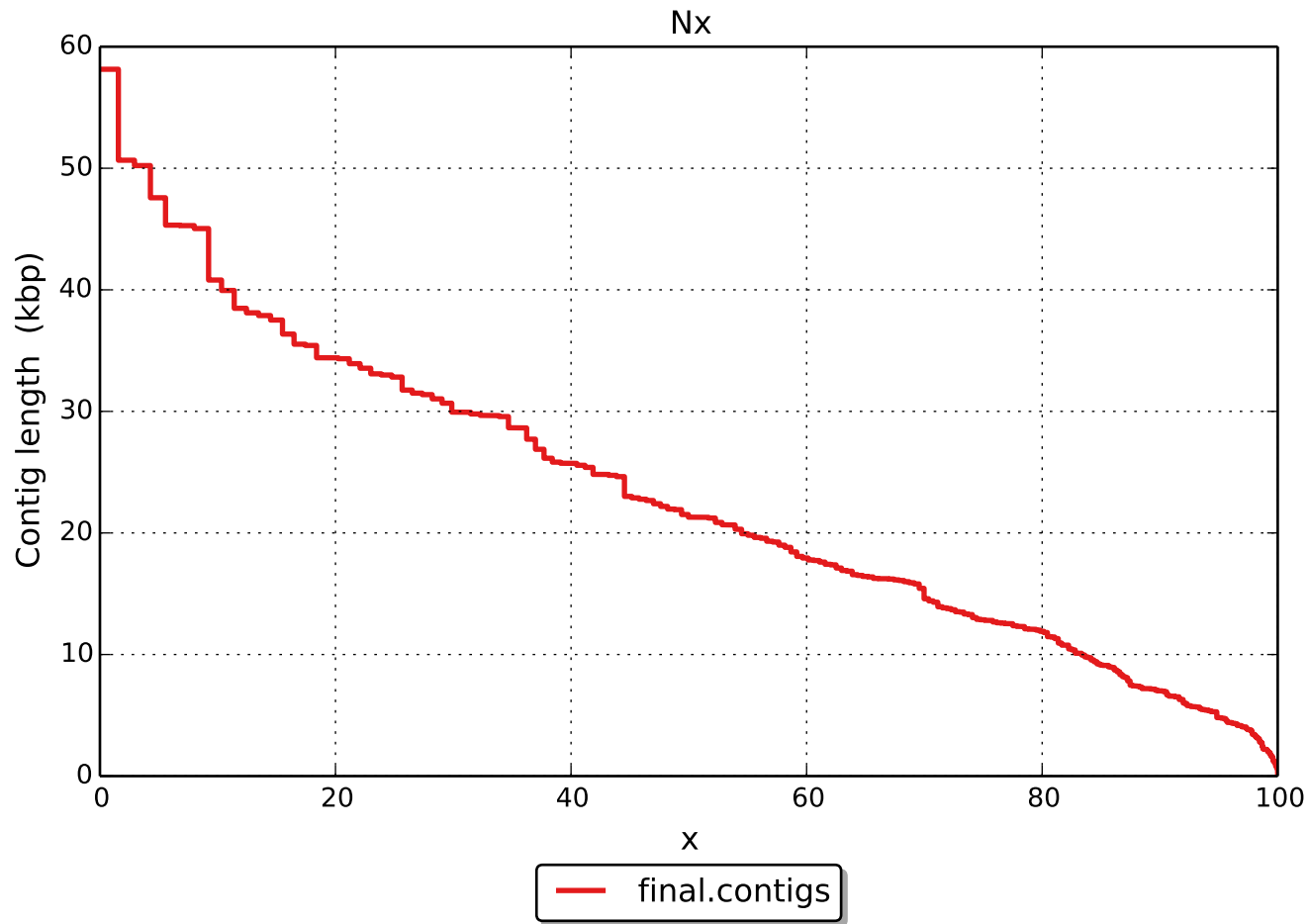
	final.contigs
# fully unaligned contigs	115
Fully unaligned length	1221760
# partially unaligned contigs	50
# with misassembly	7
# both parts are significant	0
Partially unaligned length	582719
# N's	0

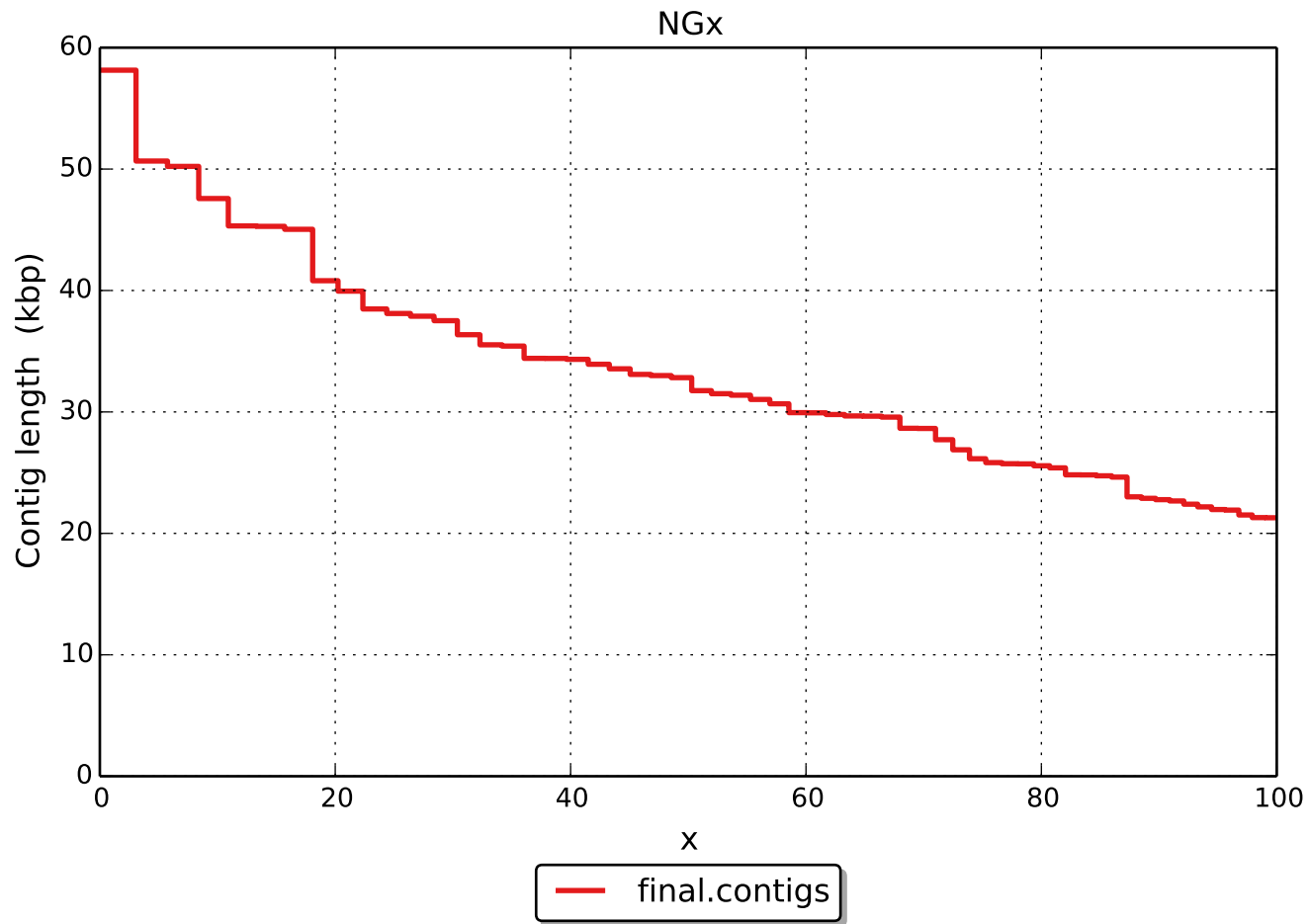
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



GC content



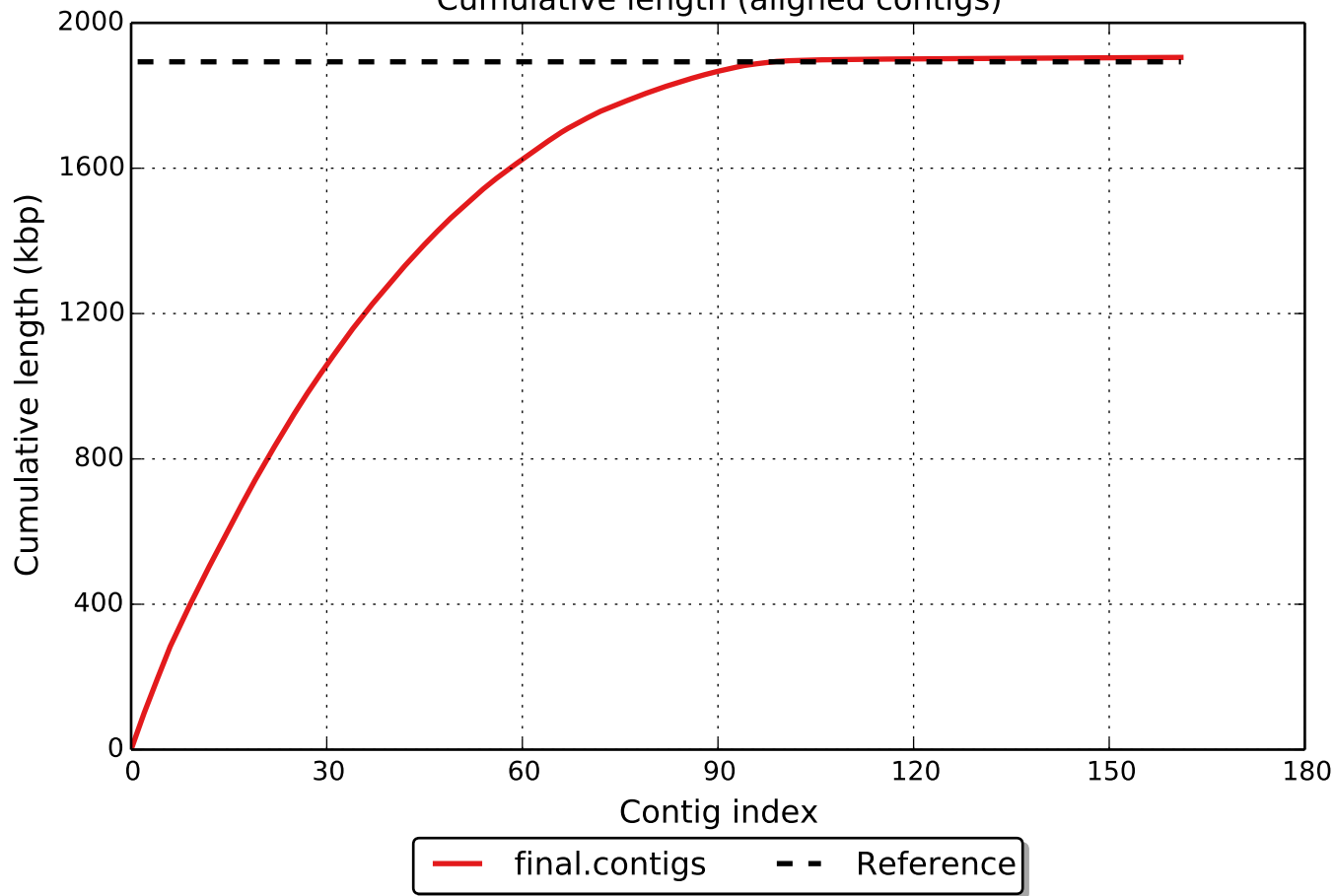


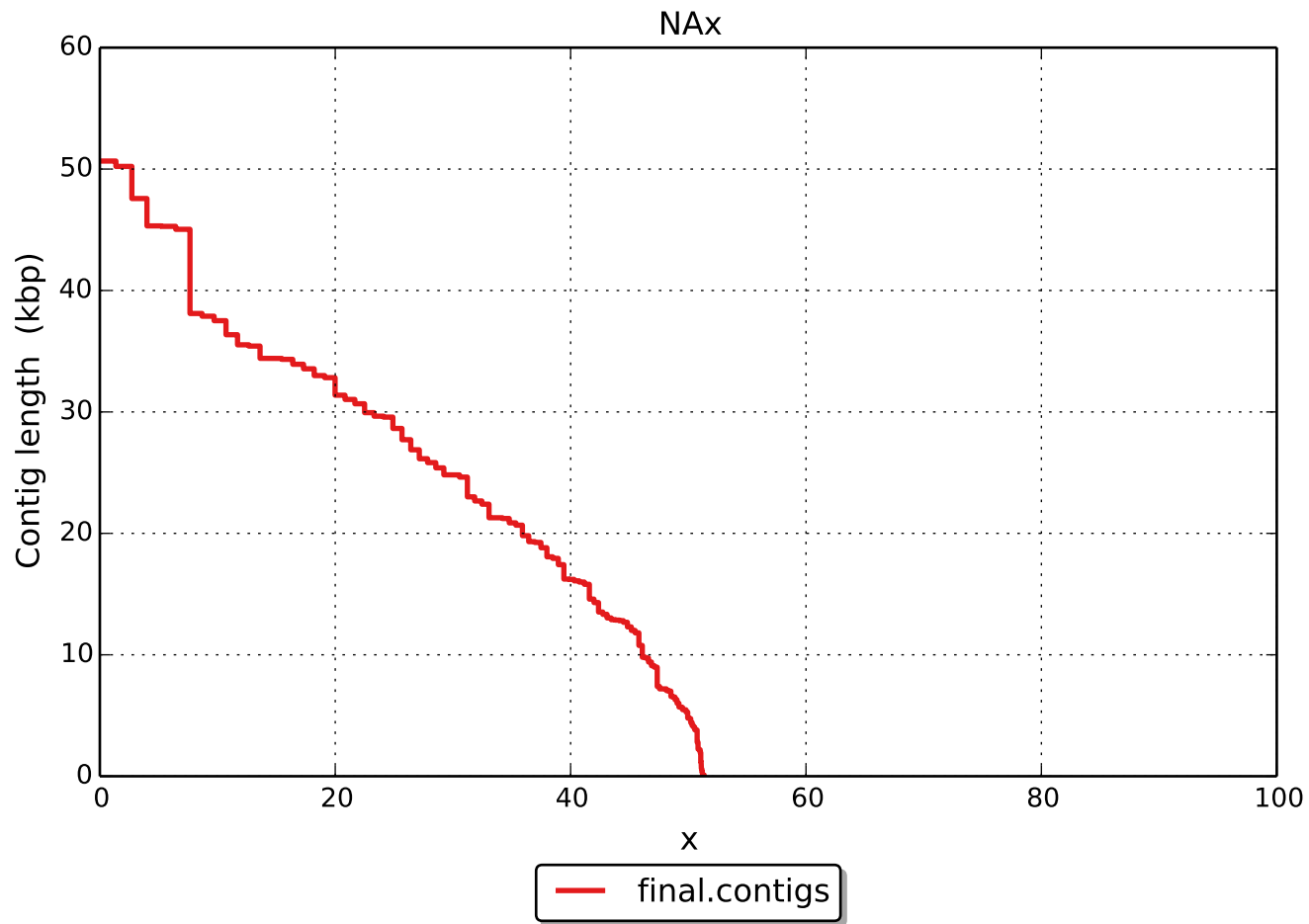


Misassemblies



Cumulative length (aligned contigs)





NGAx

