

Report

	final.contigs
# contigs (≥ 0 bp)	359
# contigs (≥ 1000 bp)	290
Total length (≥ 0 bp)	1247089
Total length (≥ 1000 bp)	1197042
# contigs	359
Largest contig	17058
Total length	1247089
Reference length	615980
GC (%)	25.36
Reference GC (%)	25.35
N50	5168
NG50	8237
N75	2997
NG75	7051
L50	76
LG50	29
L75	153
LG75	49
# misassemblies	21
# misassembled contigs	19
Misassembled contigs length	98513
# local misassemblies	0
# unaligned contigs	41 + 16 part
Unaligned length	233295
Genome fraction (%)	99.442
Duplication ratio	1.655
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1724.61
# indels per 100 kbp	2.94
Largest alignment	17058
NA50	3558
NGA50	7051
NA75	1252
NGA75	4948
LA50	98
LGA50	34
LA75	238
LGA75	61

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	21
# relocations	21
# translocations	0
# inversions	0
# possibly misassembled contigs	15
# misassembled contigs	19
Misassembled contigs length	98513
# local misassemblies	0
# mismatches	10564
# indels	18
# short indels	18
# long indels	0
Indels length	18

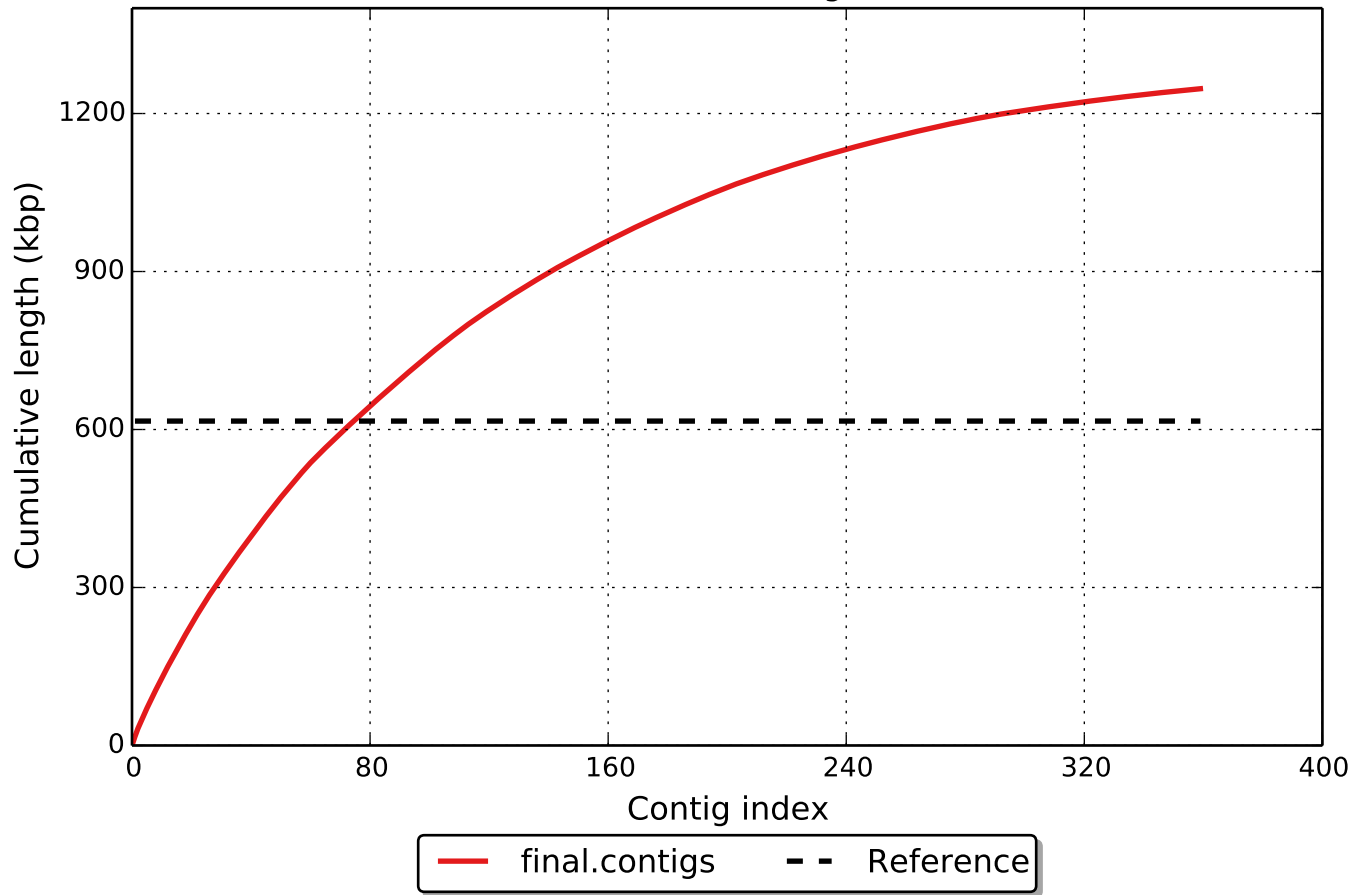
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

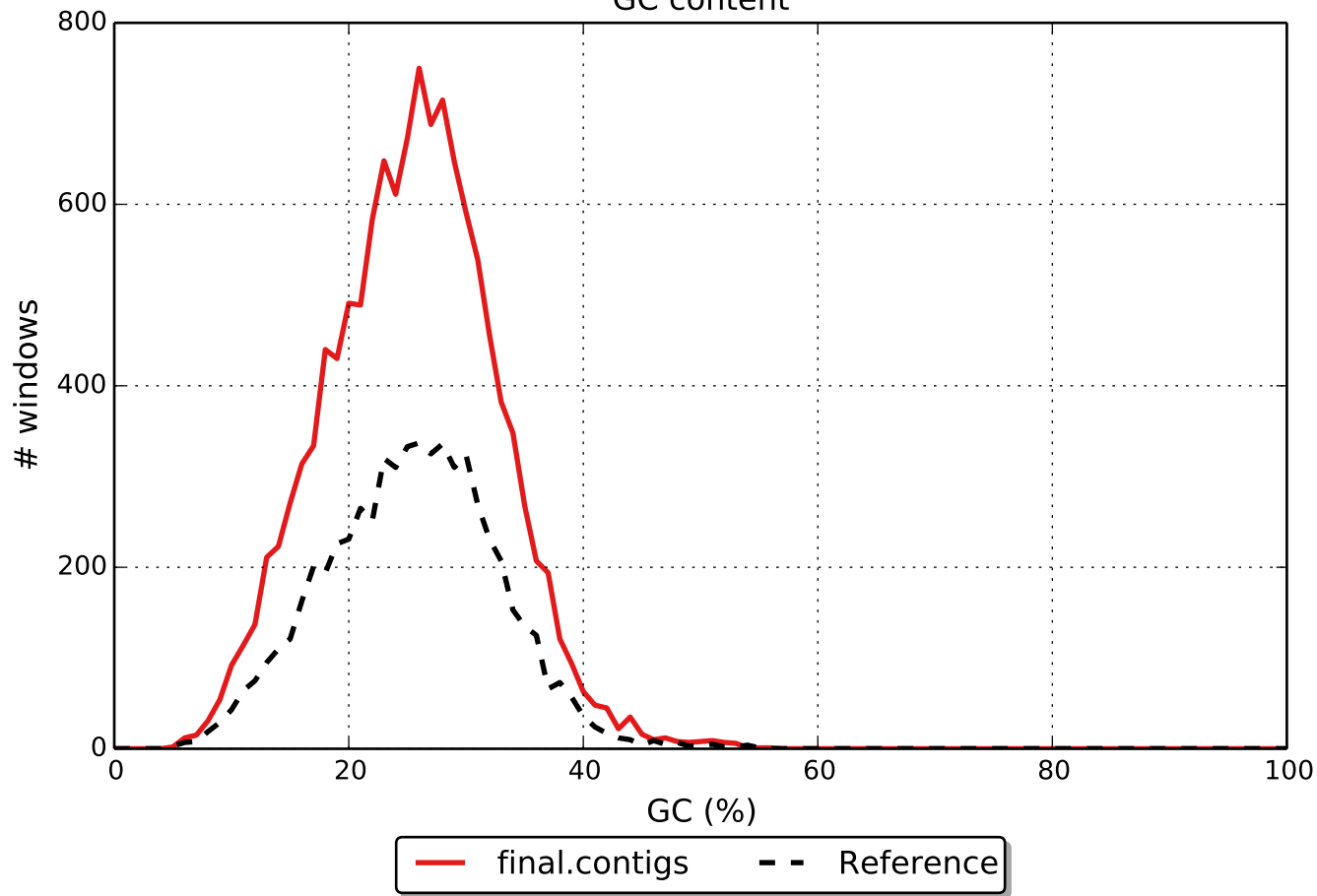
	final.contigs
# fully unaligned contigs	41
Fully unaligned length	163572
# partially unaligned contigs	16
# with misassembly	0
# both parts are significant	14
Partially unaligned length	69723
# N's	0

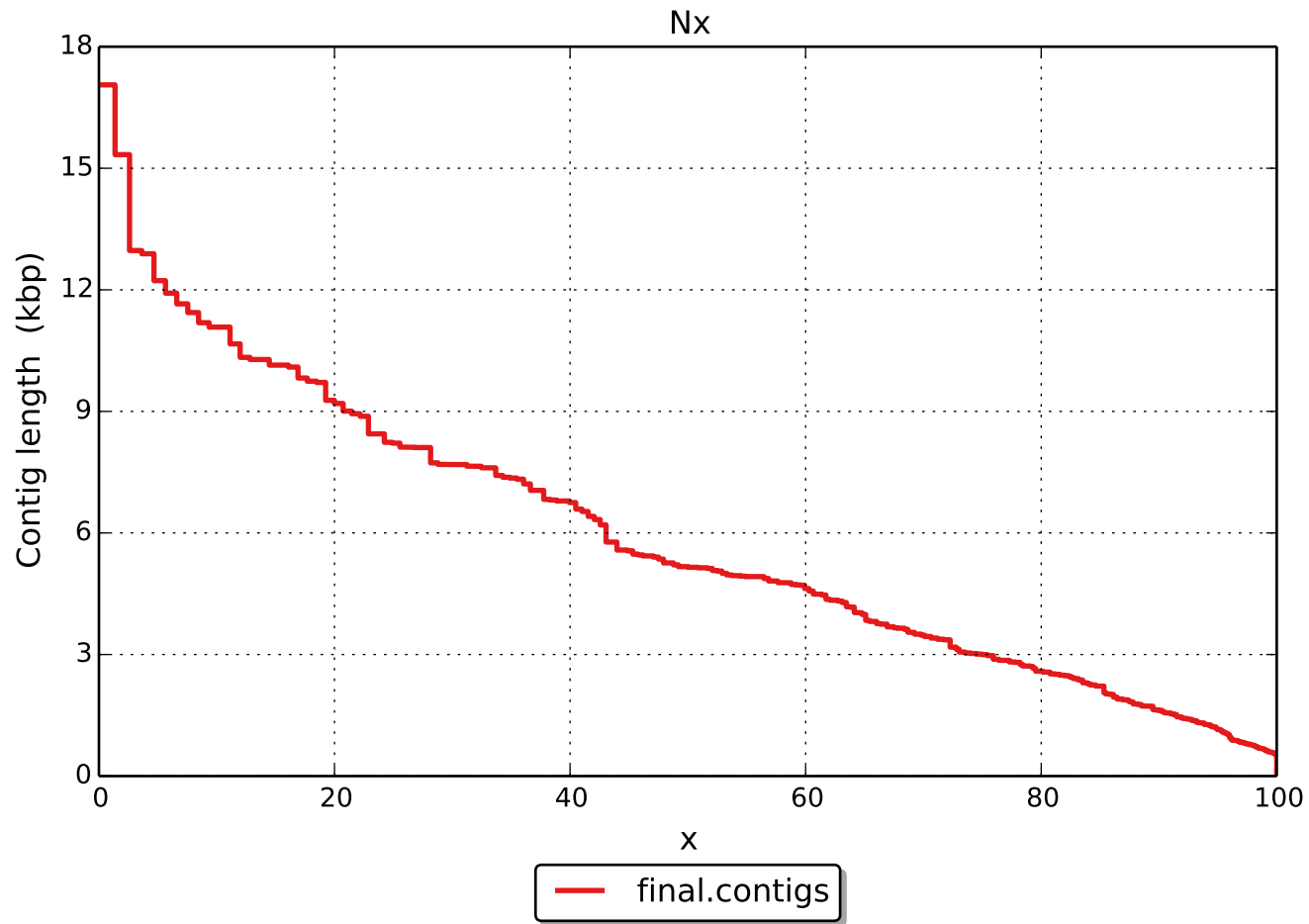
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

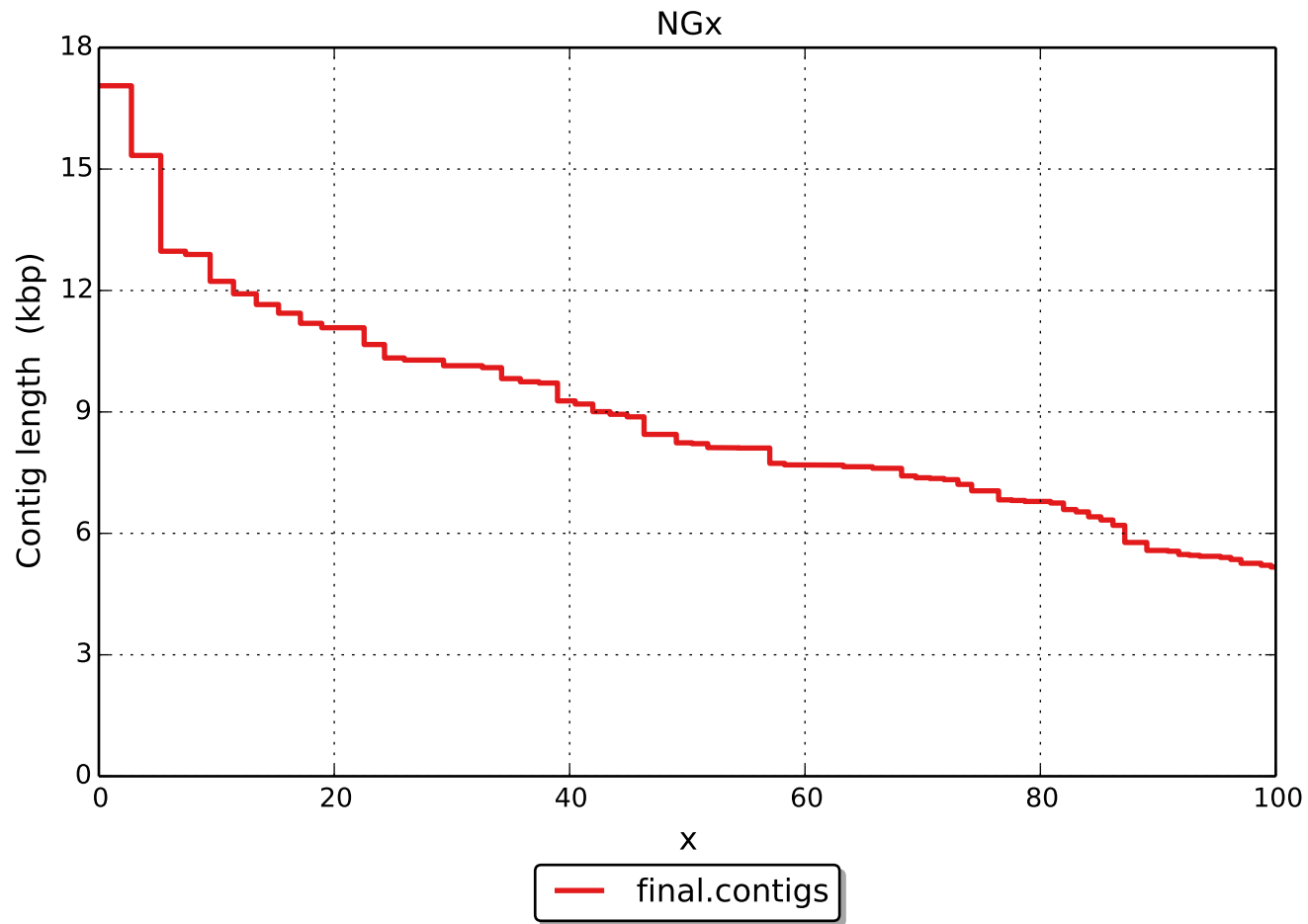
Cumulative length



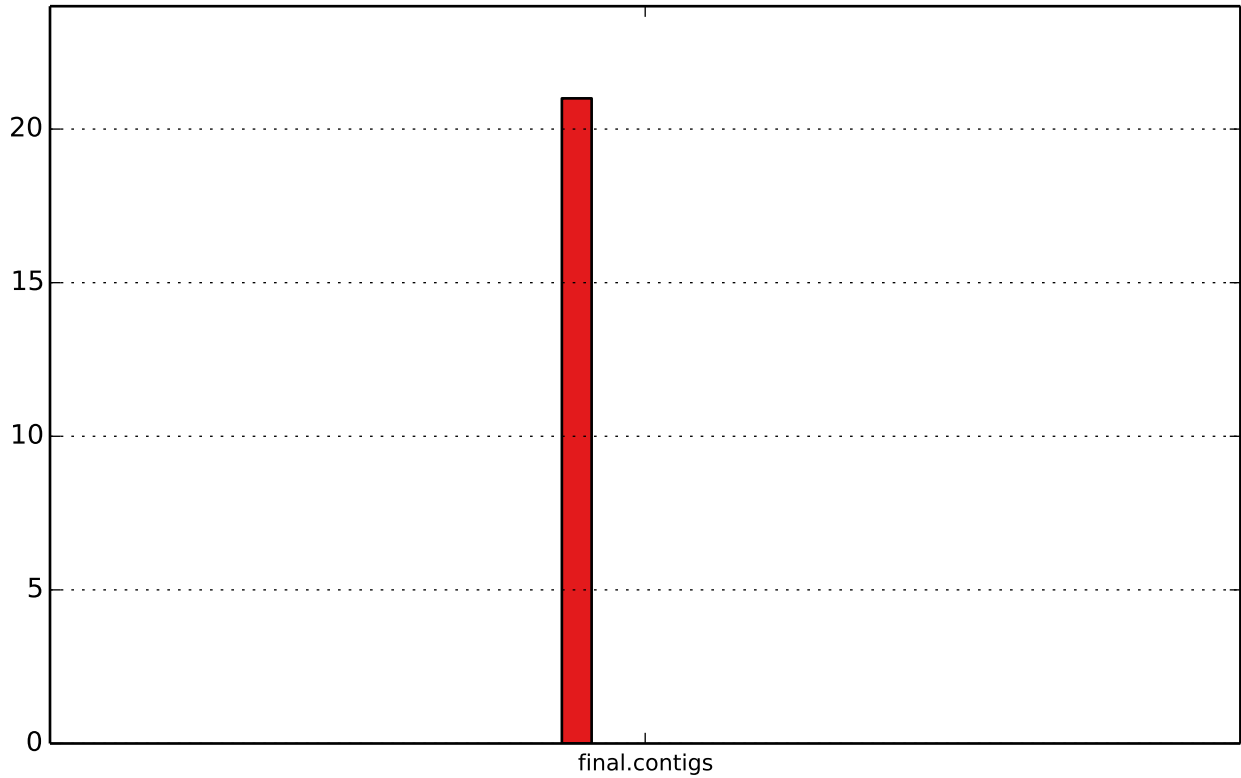
GC content





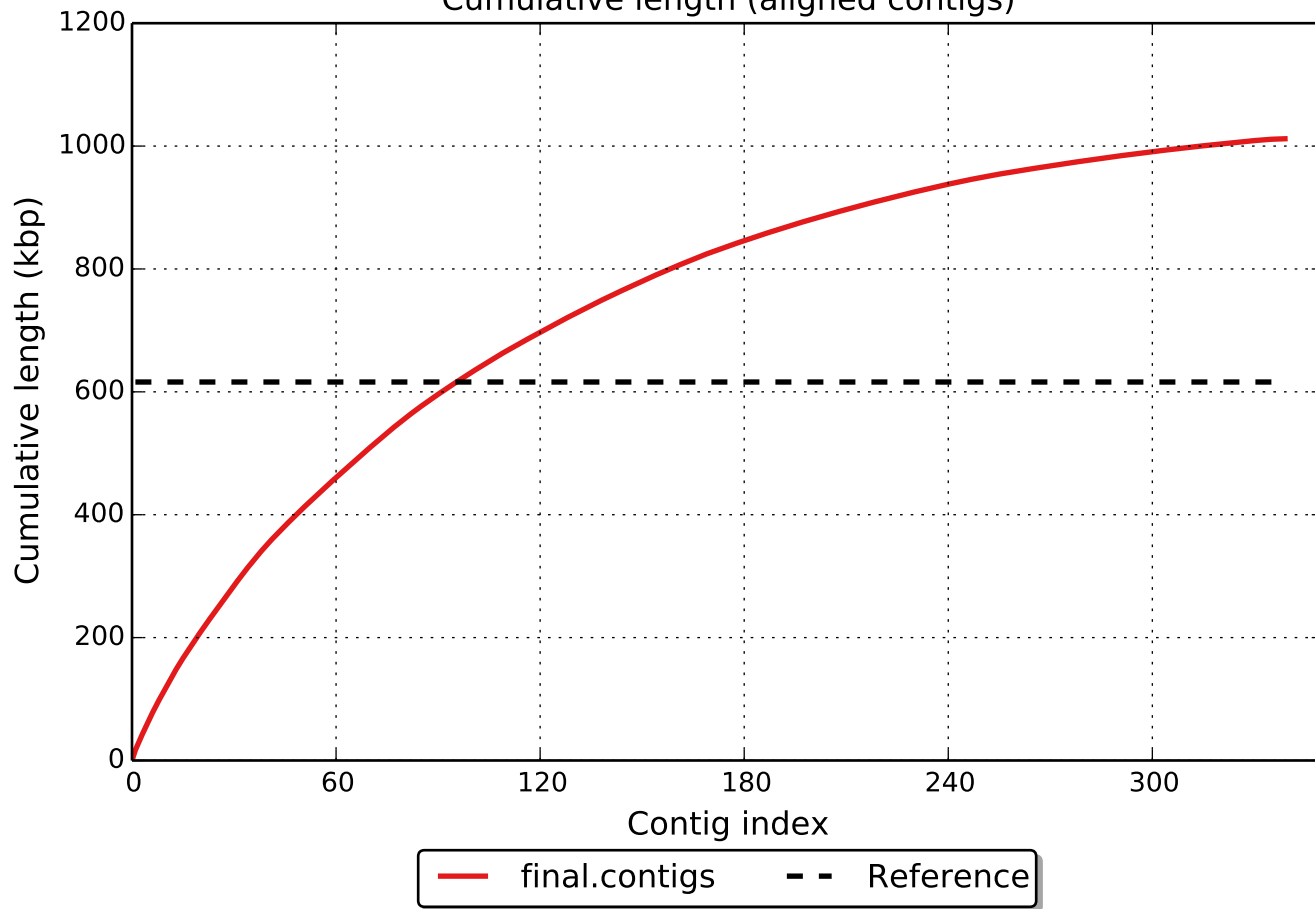


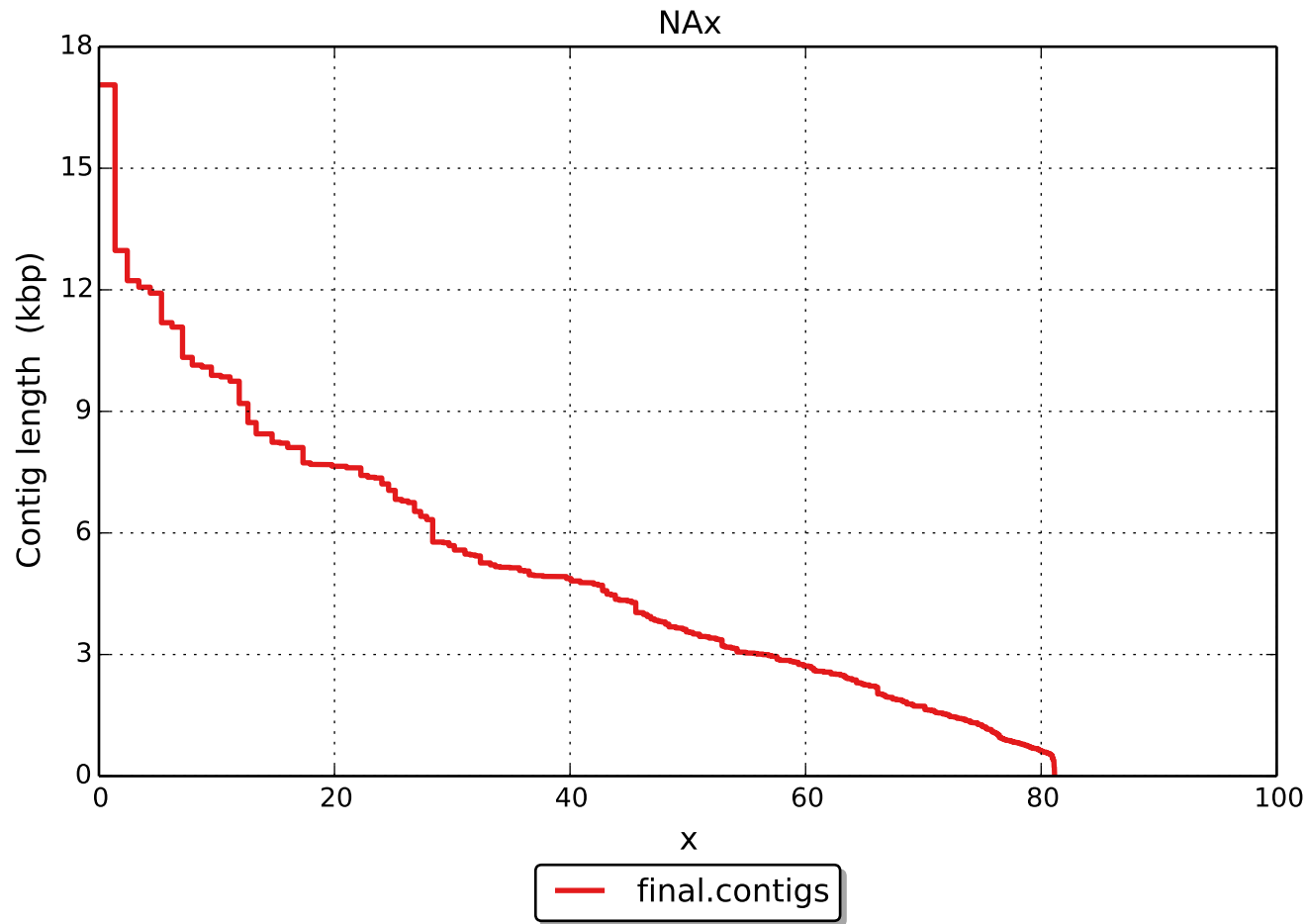
Misassemblies



 # relocations

Cumulative length (aligned contigs)





NGAx

