

Report

	final.contigs
# contigs (>= 0 bp)	558
# contigs (>= 1000 bp)	423
Total length (>= 0 bp)	1232902
Total length (>= 1000 bp)	1134938
# contigs	558
Largest contig	11592
Total length	1232902
Reference length	615980
GC (%)	25.33
Reference GC (%)	25.35
N50	2927
NG50	4649
N75	1757
NG75	3663
L50	137
LG50	52
L75	268
LG75	89
# misassemblies	37
# misassembled contigs	36
Misassembled contigs length	136834
# local misassemblies	0
# unaligned contigs	3 + 3 part
Unaligned length	8122
Genome fraction (%)	98.151
Duplication ratio	2.026
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1814.62
# indels per 100 kbp	3.97
Largest alignment	11592
NA50	2814
NGA50	4289
NA75	1614
NGA75	3297
LA50	147
LGA50	55
LA75	288
LGA75	96

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	37
# relocations	37
# translocations	0
# inversions	0
# possibly misassembled contigs	5
# misassembled contigs	36
Misassembled contigs length	136834
# local misassemblies	0
# mismatches	10971
# indels	24
# short indels	24
# long indels	0
Indels length	24

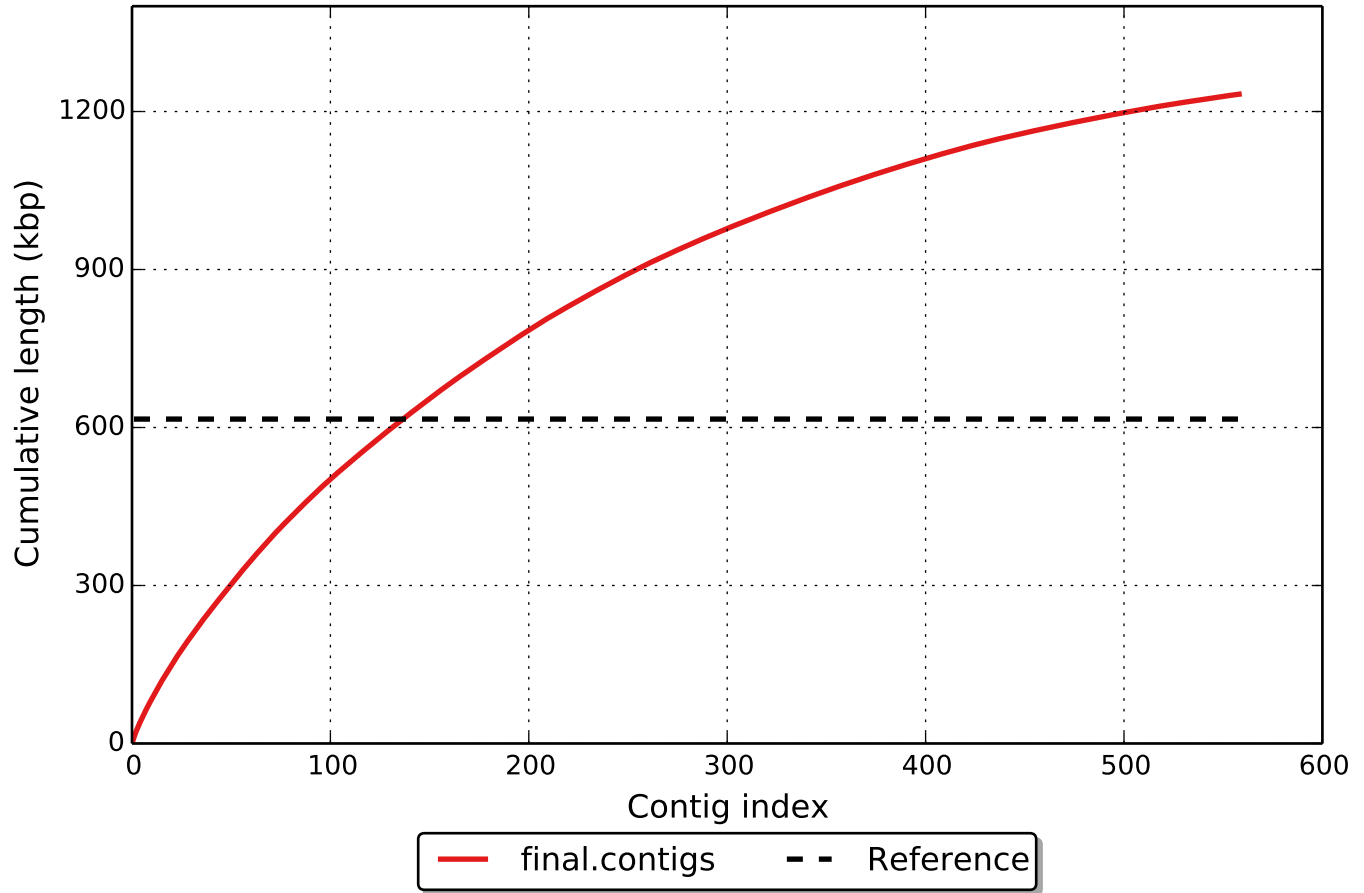
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

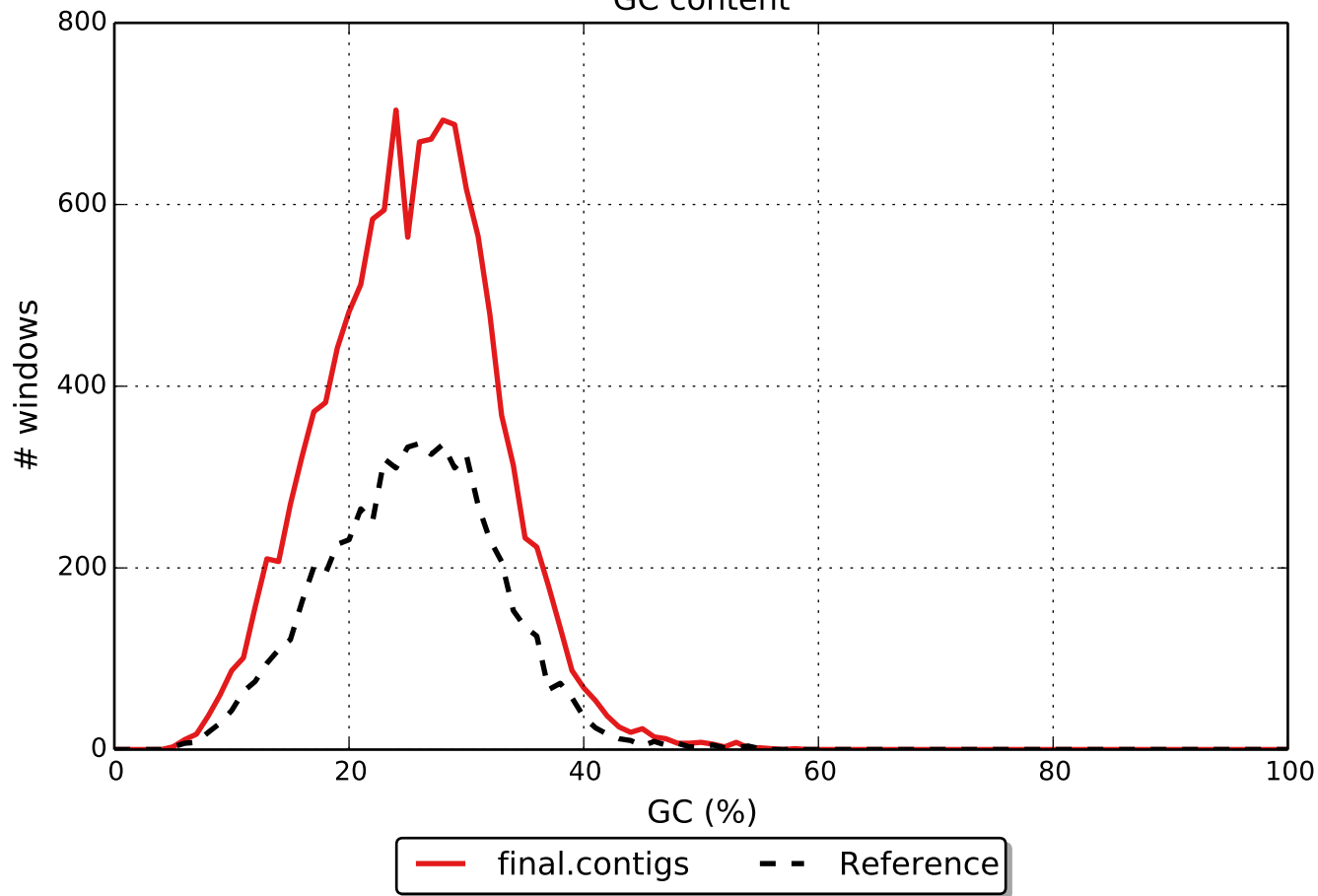
	final.contigs
# fully unaligned contigs	3
Fully unaligned length	5495
# partially unaligned contigs	3
# with misassembly	1
# both parts are significant	2
Partially unaligned length	2627
# N's	0

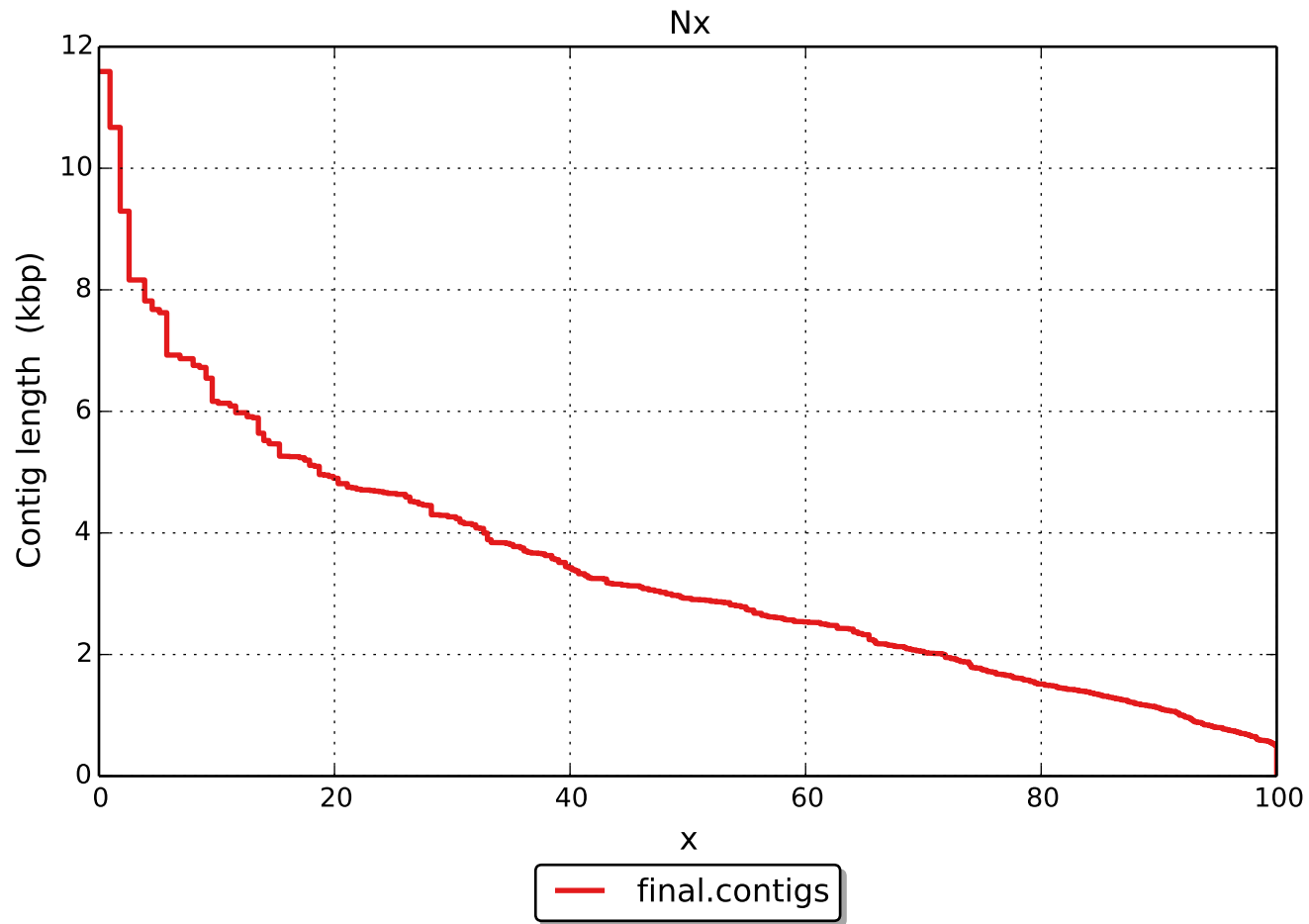
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

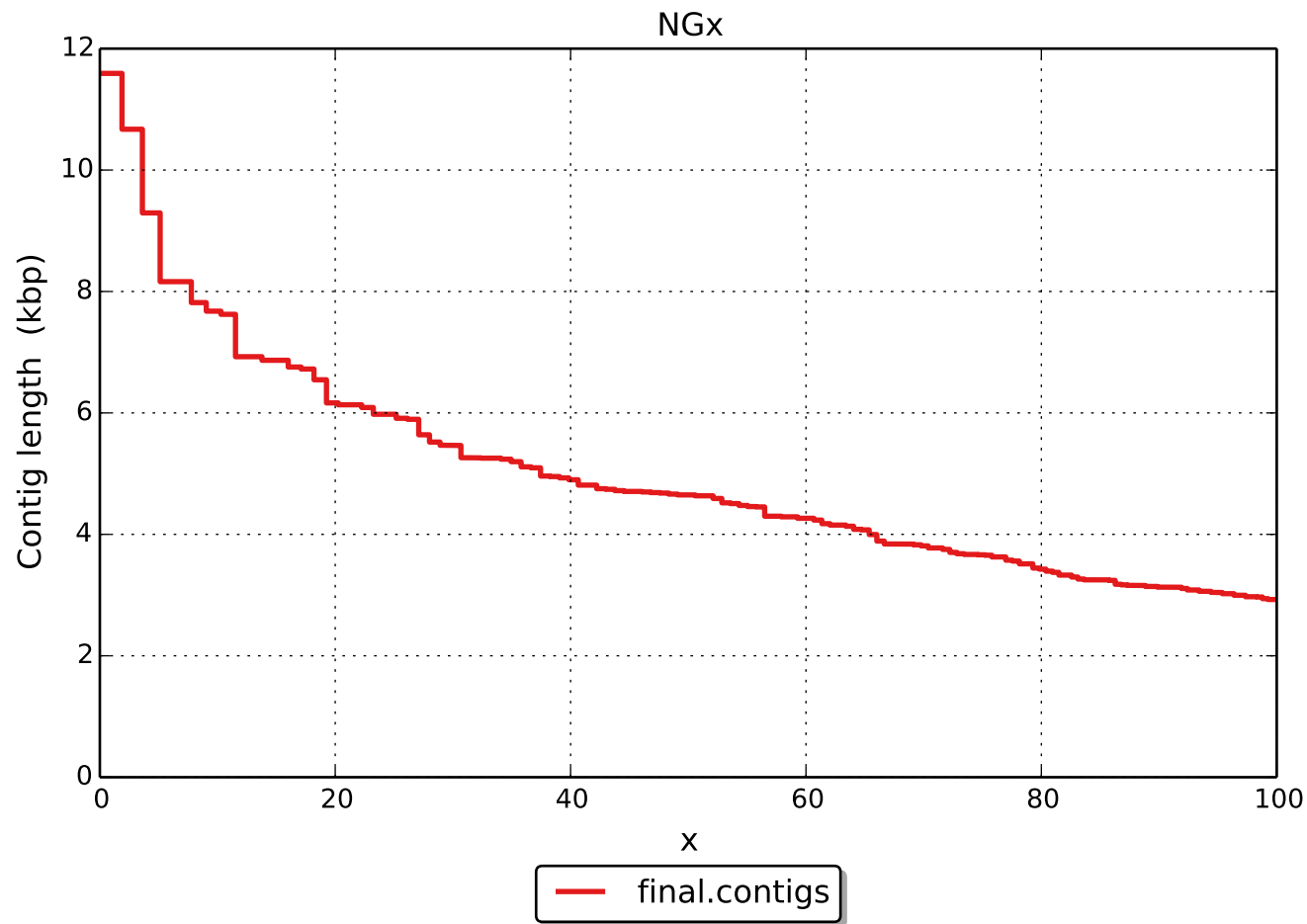
Cumulative length



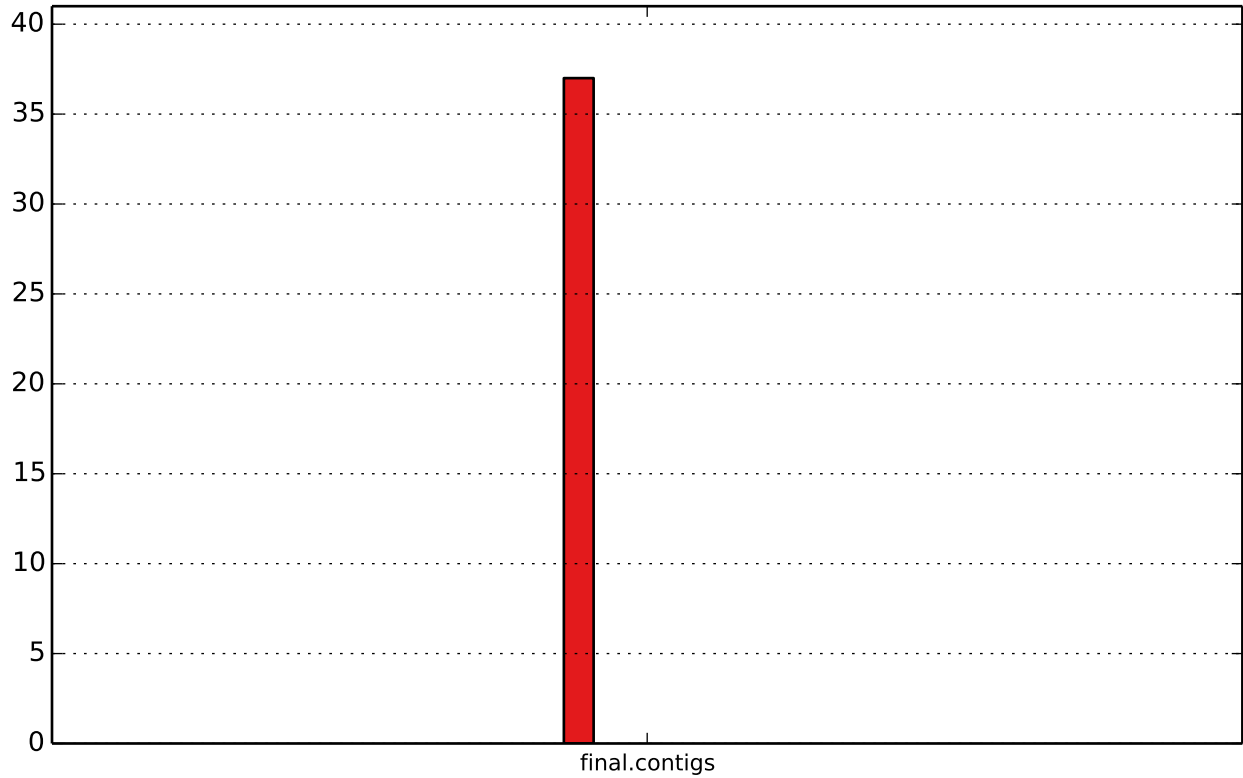
GC content





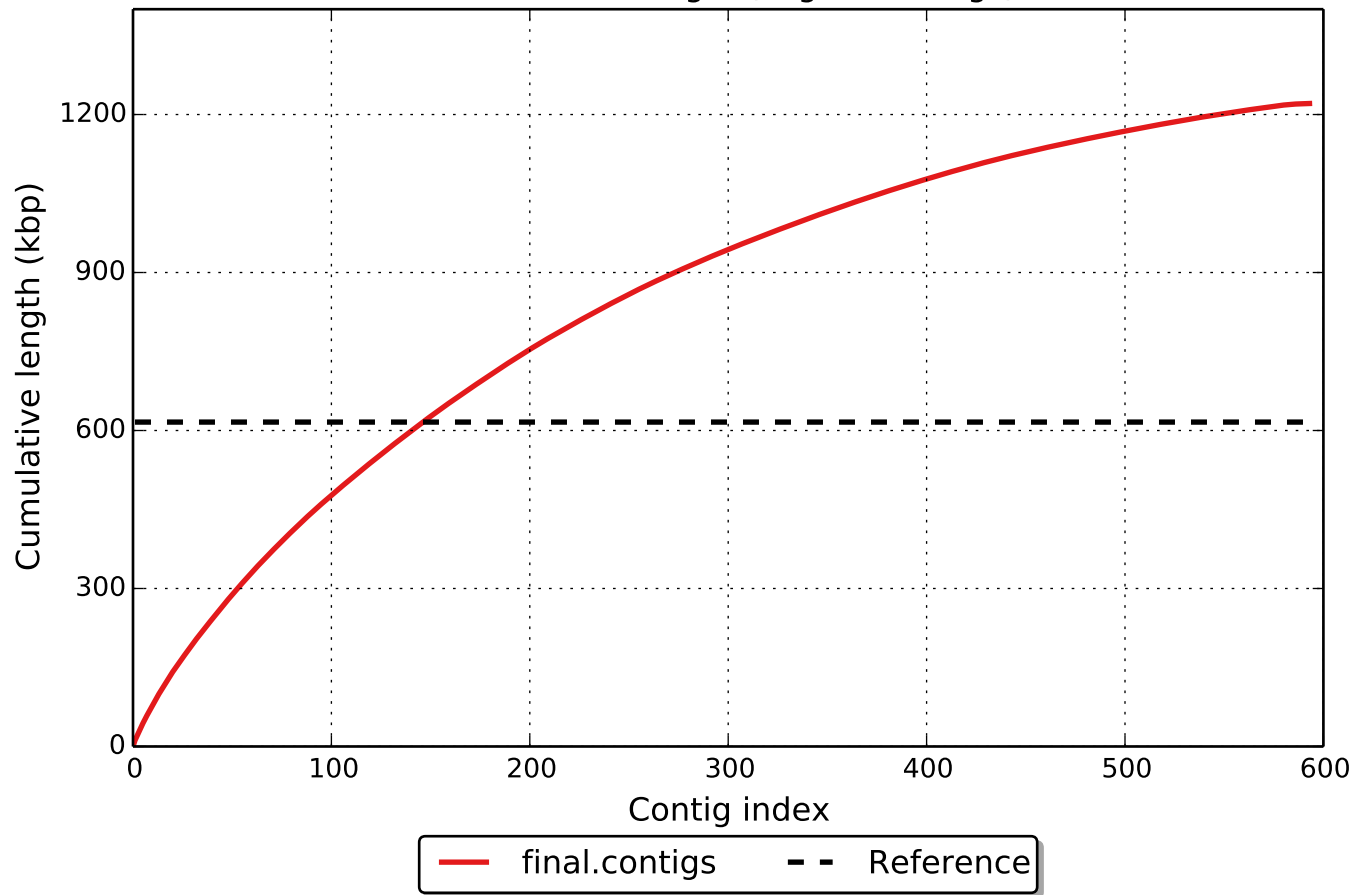


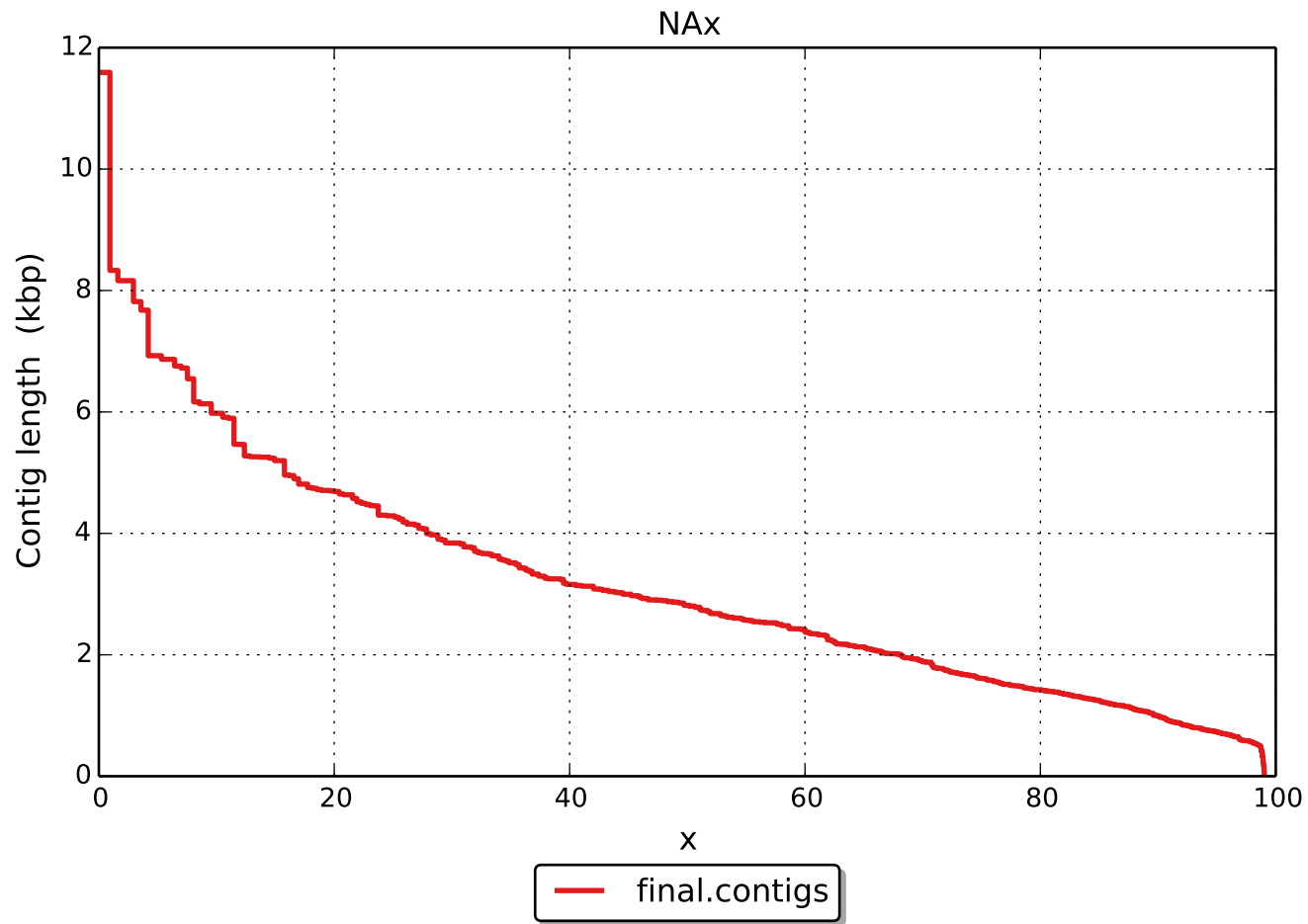
Misassemblies



 # relocations

Cumulative length (aligned contigs)





NGAx

