

Report

	final.contigs
# contigs (≥ 1000 bp)	1052
# contigs (≥ 5000 bp)	2
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 1000 bp)	1593592
Total length (≥ 5000 bp)	10865
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	3617
Largest contig	5668
Total length	3383312
Reference length	4857432
GC (%)	52.20
Reference GC (%)	52.22
N50	964
NG50	731
N75	700
L50	1152
LG50	2037
L75	2189
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	66.325
Duplication ratio	1.050
# N's per 100 kbp	0.00
# mismatches per 100 kbp	180.25
# indels per 100 kbp	0.06
Largest alignment	5668
NA50	964
NGA50	731
NA75	700
LA50	1152
LGA50	2037
LA75	2189

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

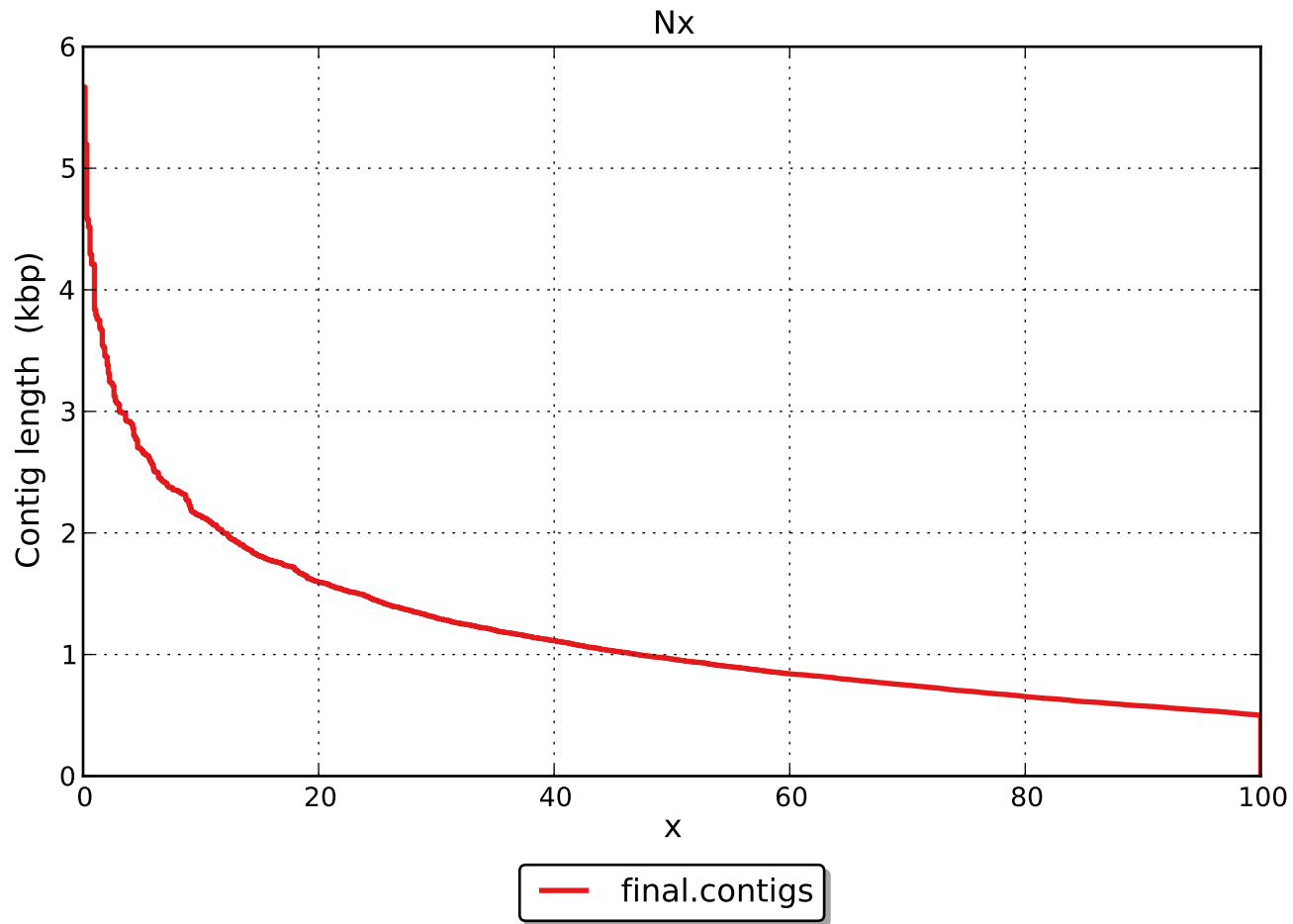
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	5807
# indels	2
# short indels	2
# long indels	0
Indels length	2

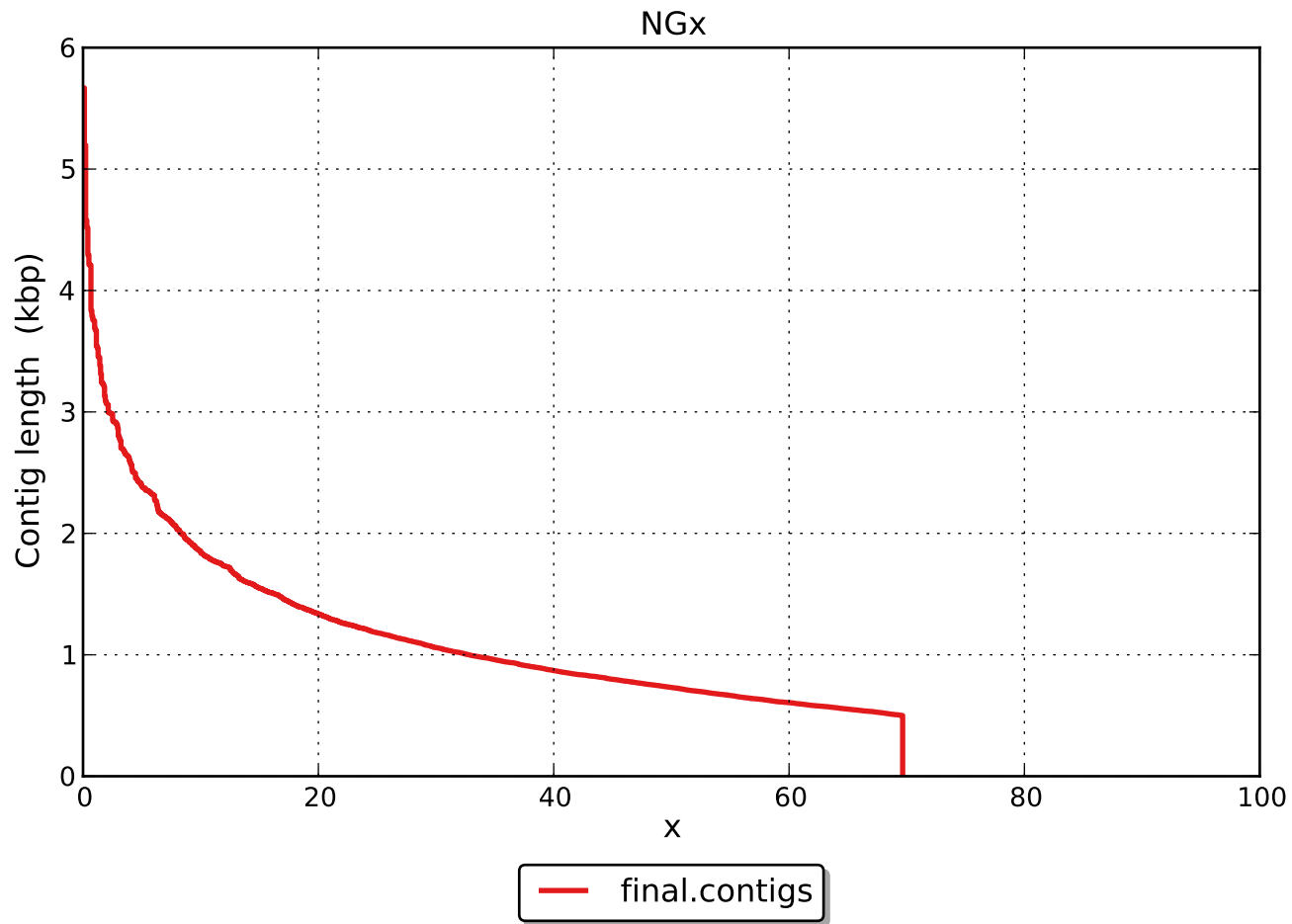
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

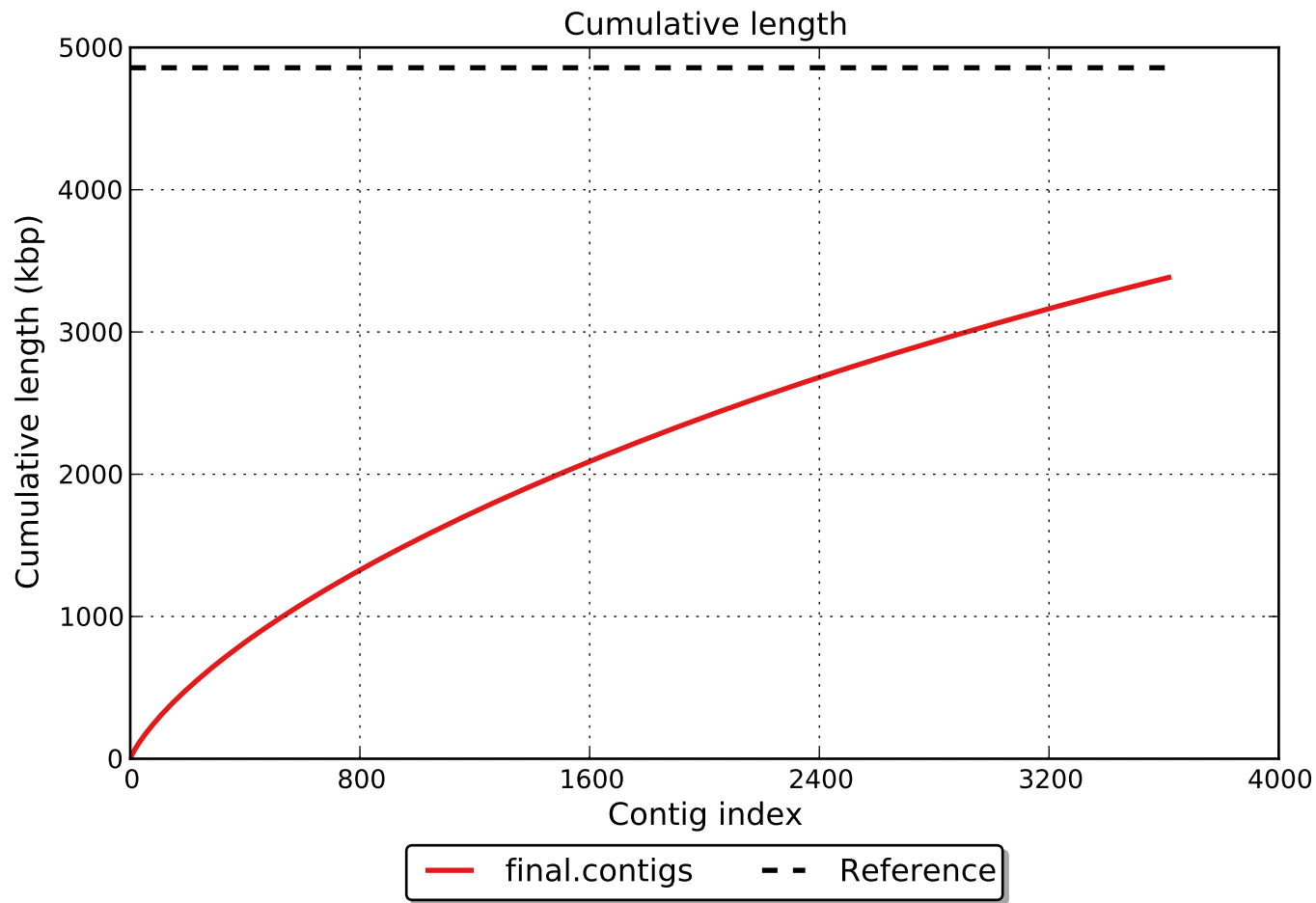
Unaligned report

	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

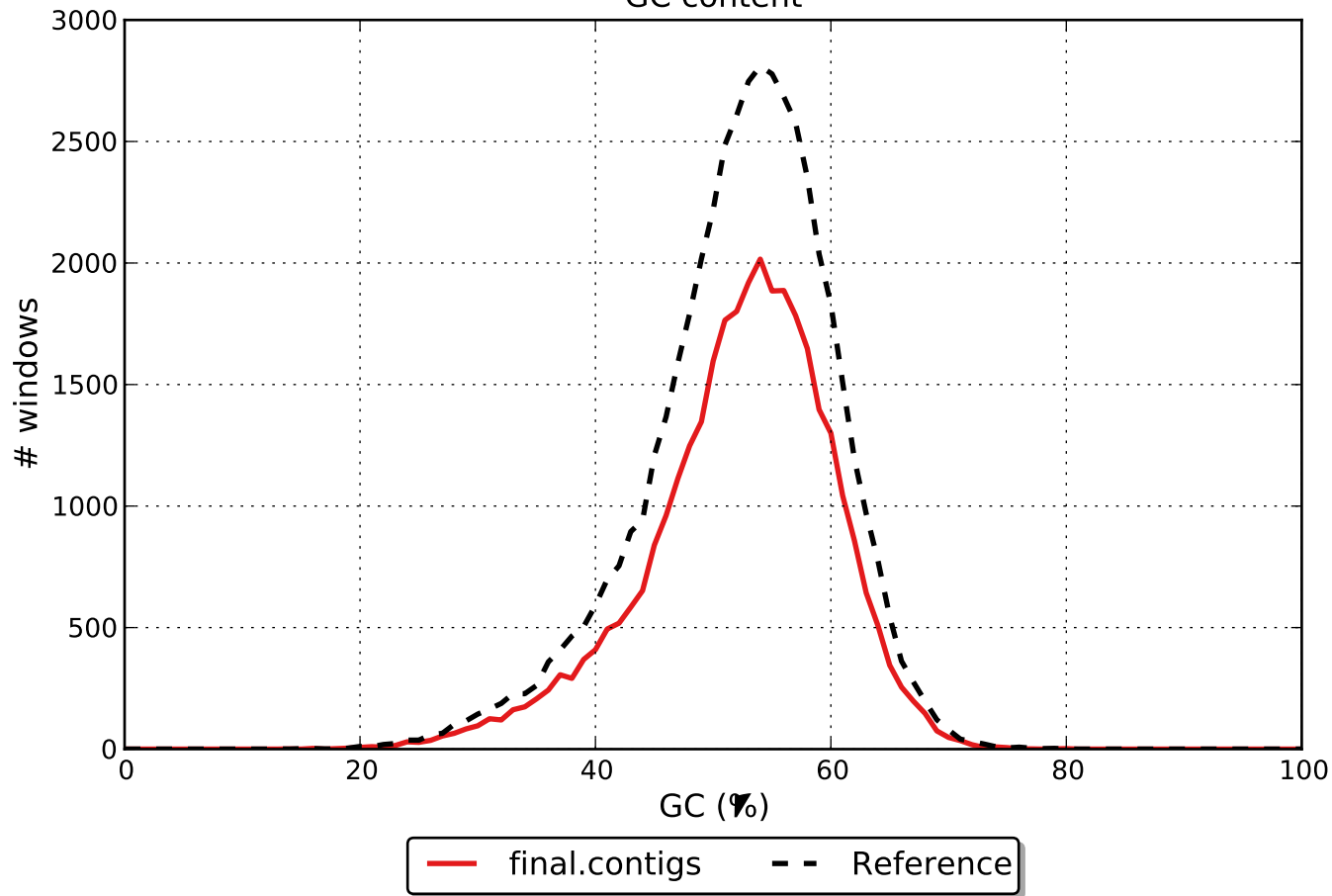
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).







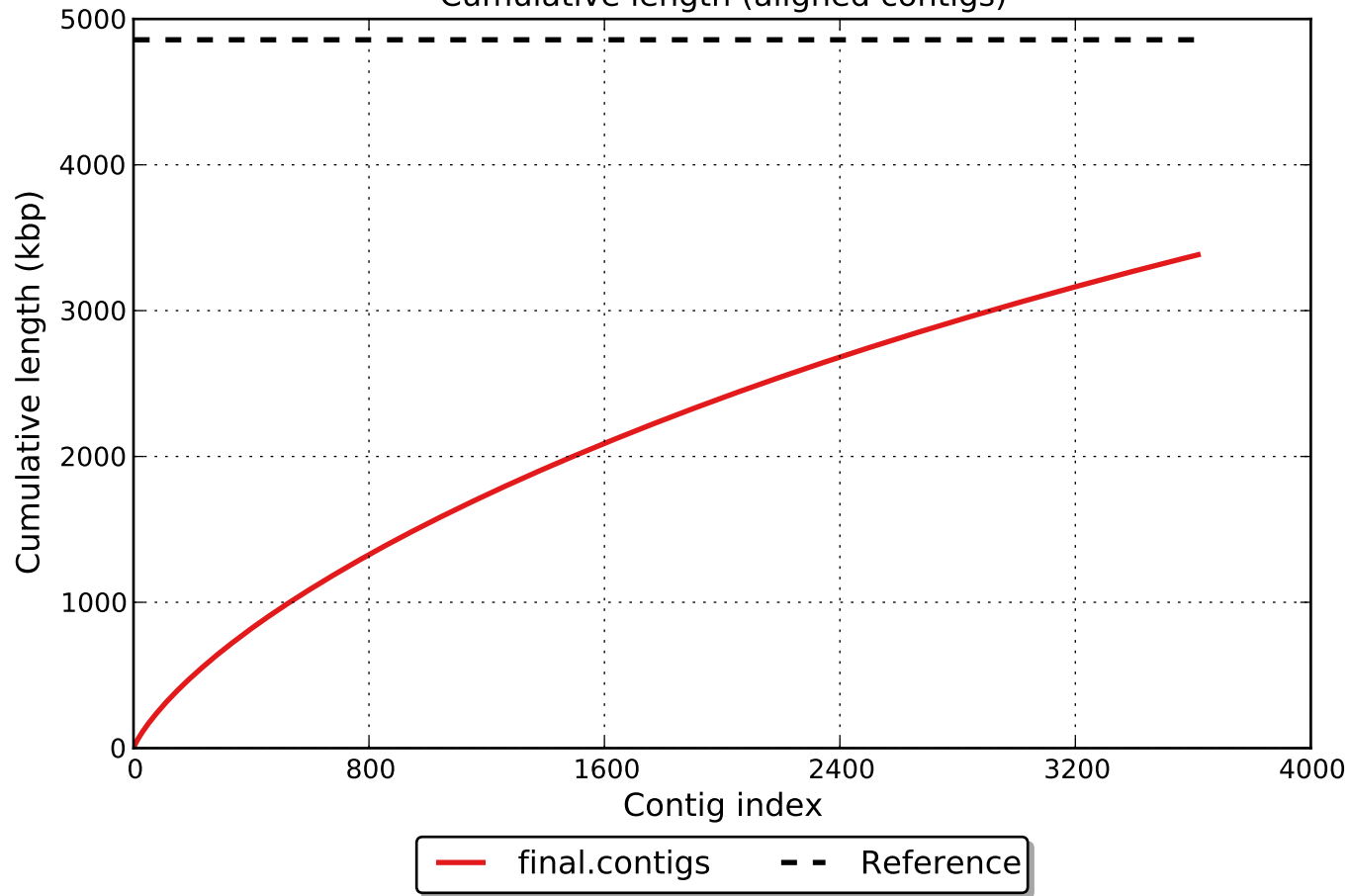
GC content

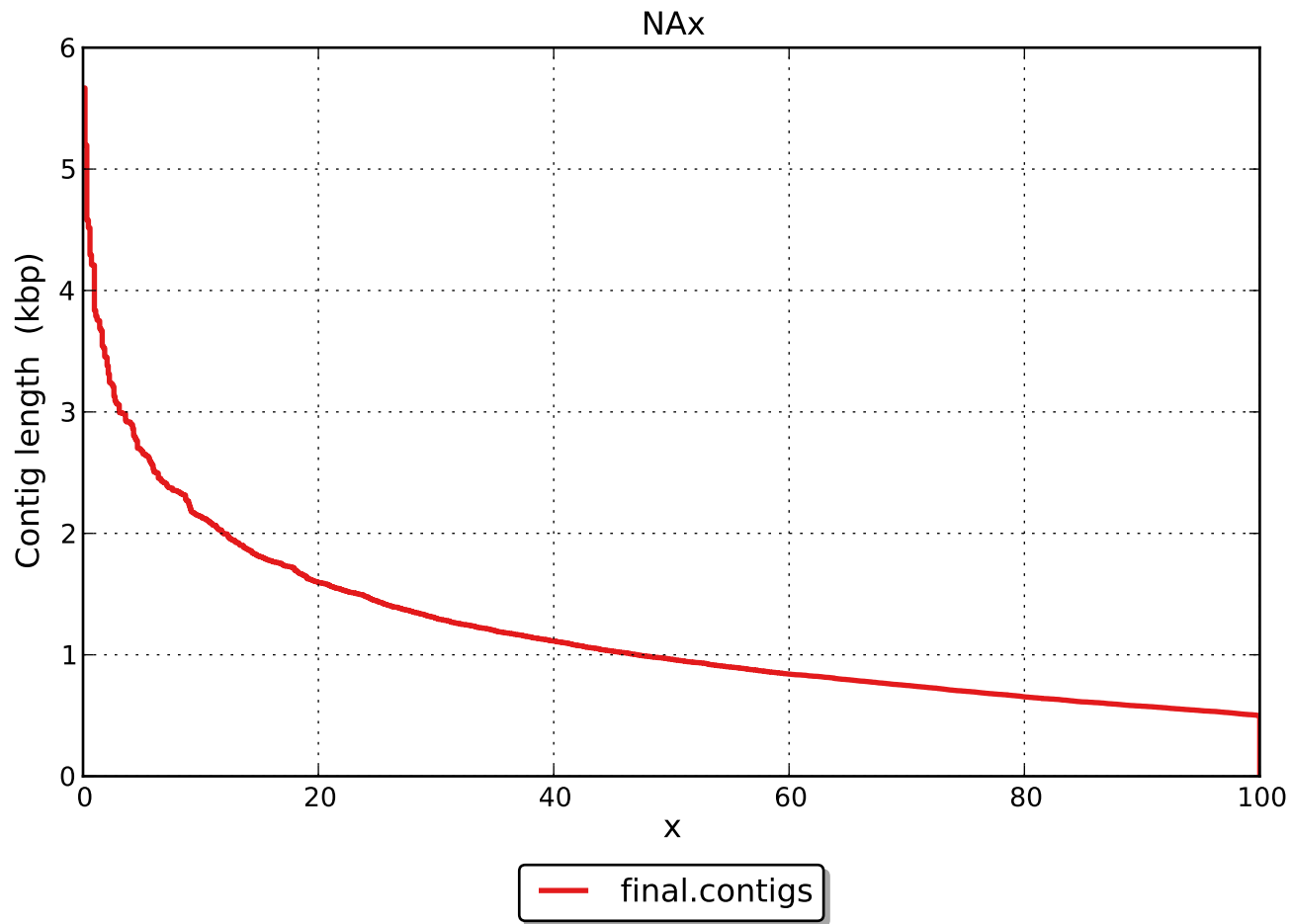


Misassemblies

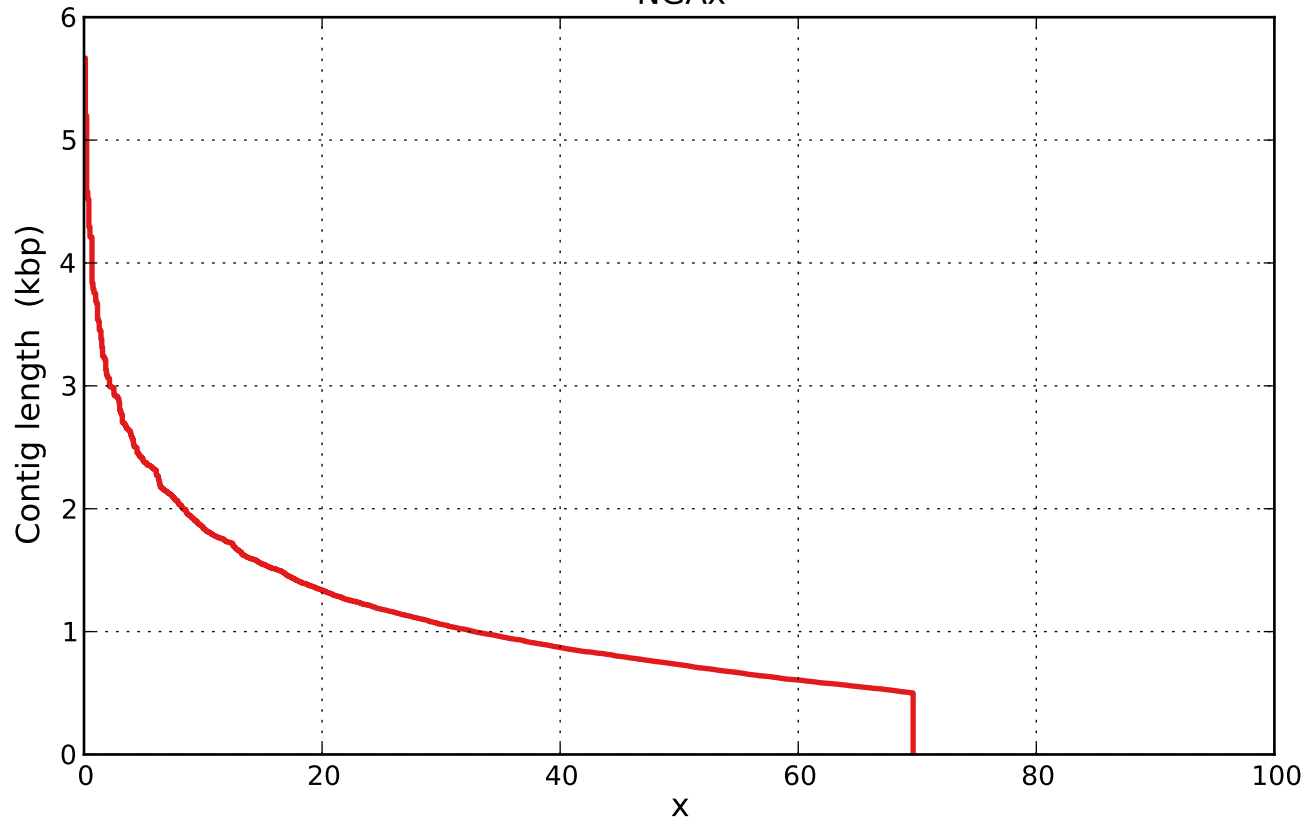


Cumulative length (aligned contigs)





NGAx



— final.contigs