

Report

	final.contigs
# contigs (≥ 1000 bp)	688
# contigs (≥ 5000 bp)	125
# contigs (≥ 10000 bp)	16
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 1000 bp)	2216435
Total length (≥ 5000 bp)	900779
Total length (≥ 10000 bp)	185067
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	1348
Largest contig	15363
Total length	2658148
Reference length	4857432
GC (%)	52.13
Reference GC (%)	52.22
N50	3386
NG50	677
N75	1580
L50	230
LG50	951
L75	512
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	53.263
Duplication ratio	1.027
# N's per 100 kbp	0.00
# mismatches per 100 kbp	430.23
# indels per 100 kbp	0.08
Largest alignment	15363
NA50	3386
NGA50	677
NA75	1580
LA50	230
LGA50	951
LA75	512

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

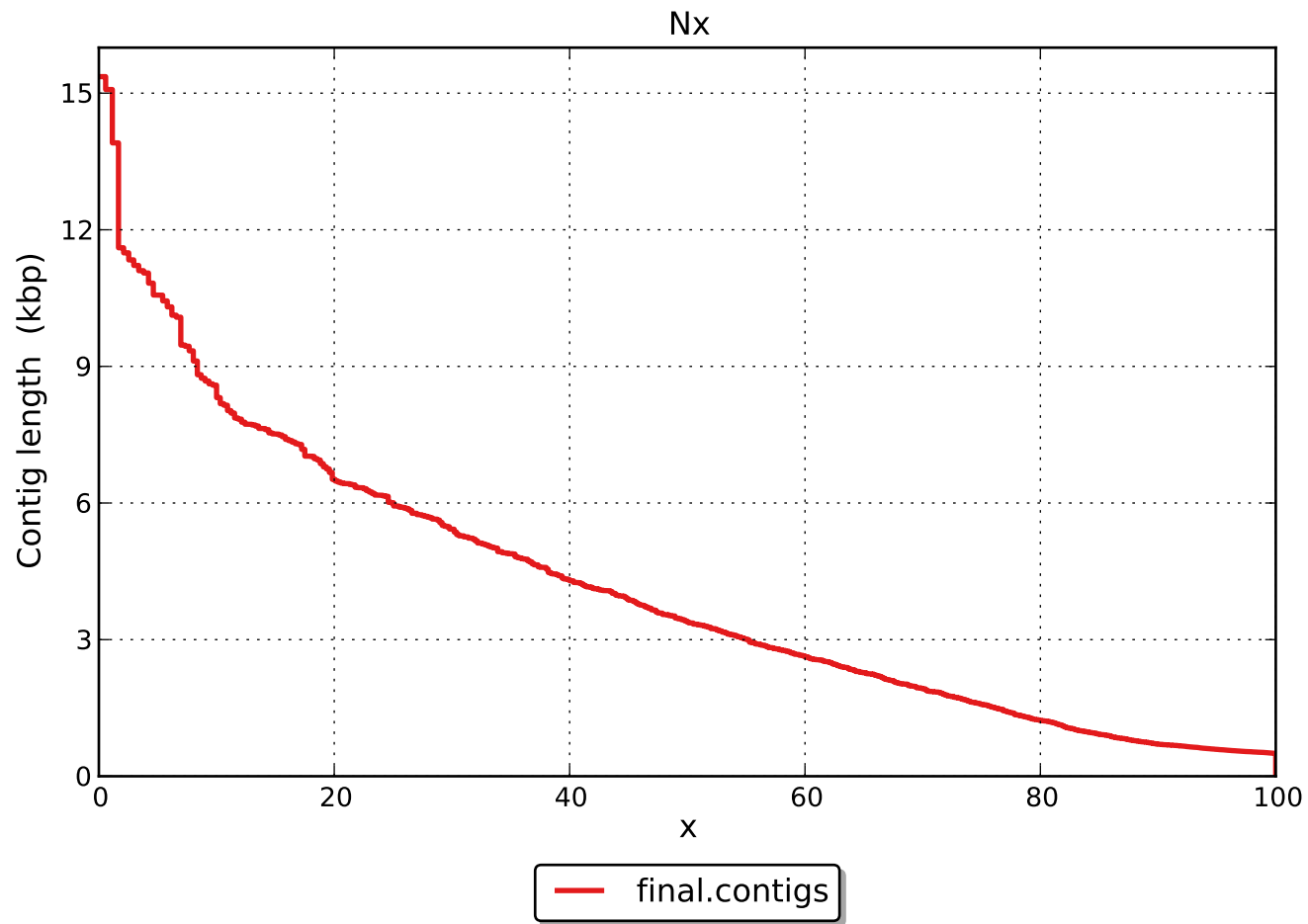
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	11131
# indels	2
# short indels	2
# long indels	0
Indels length	2

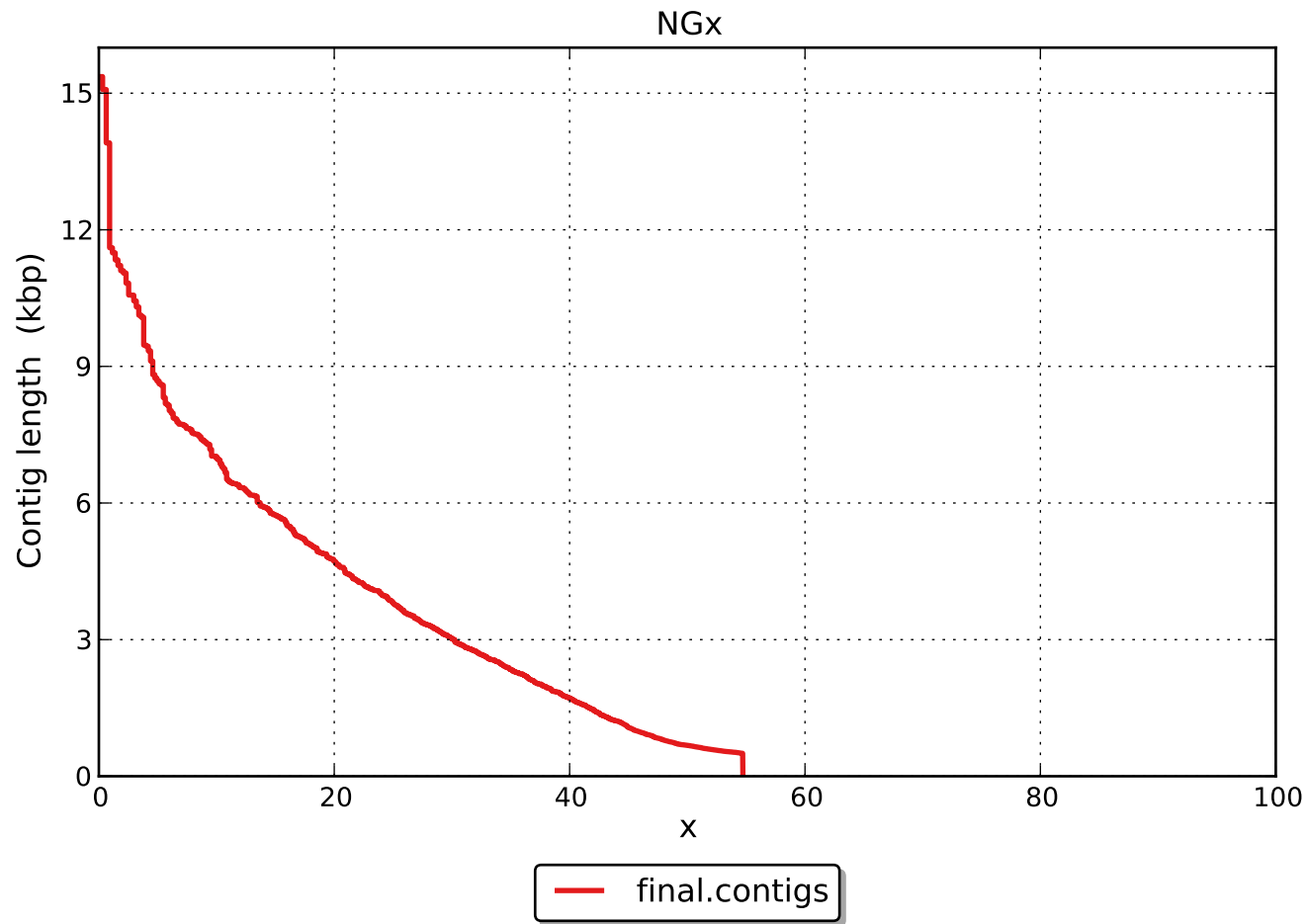
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

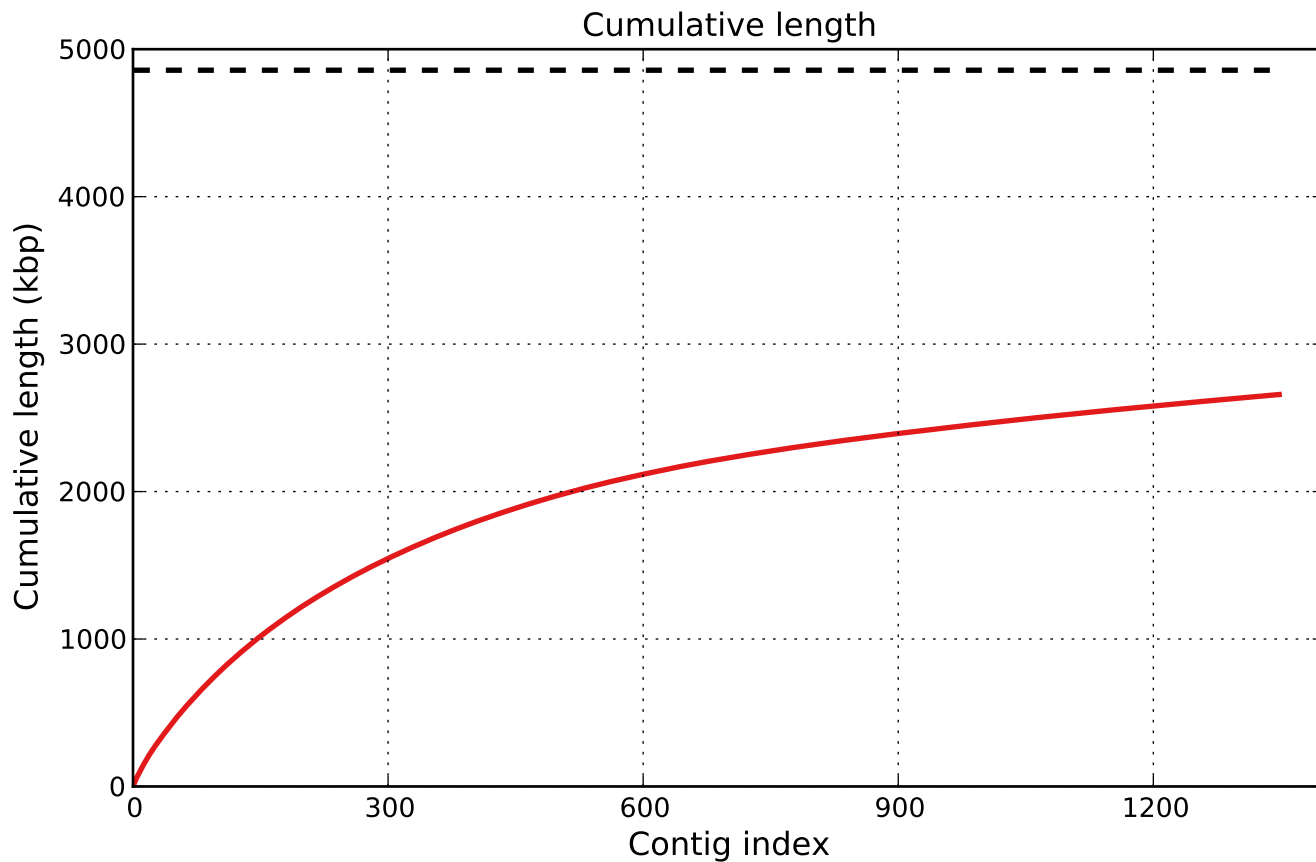
Unaligned report

	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

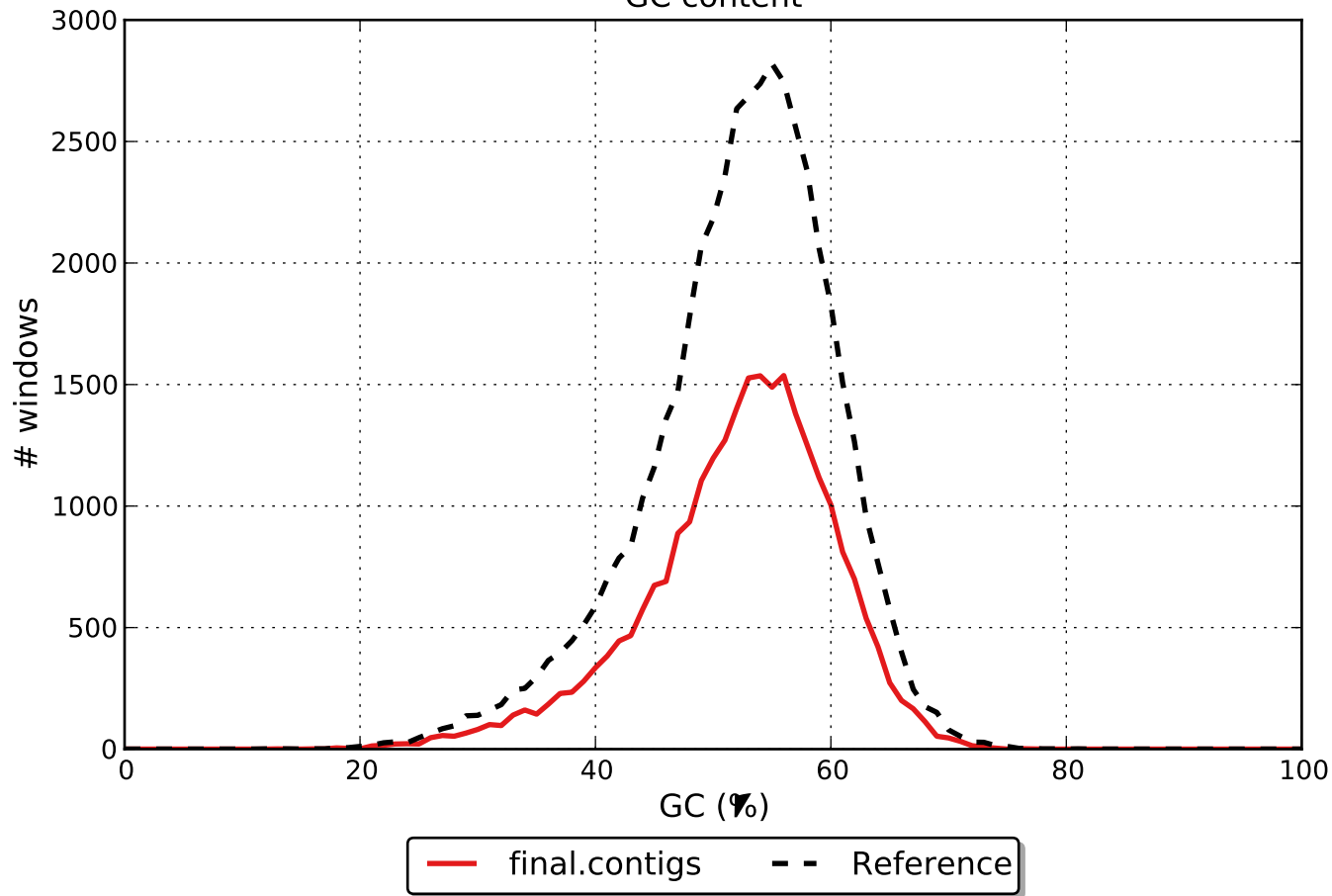
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).







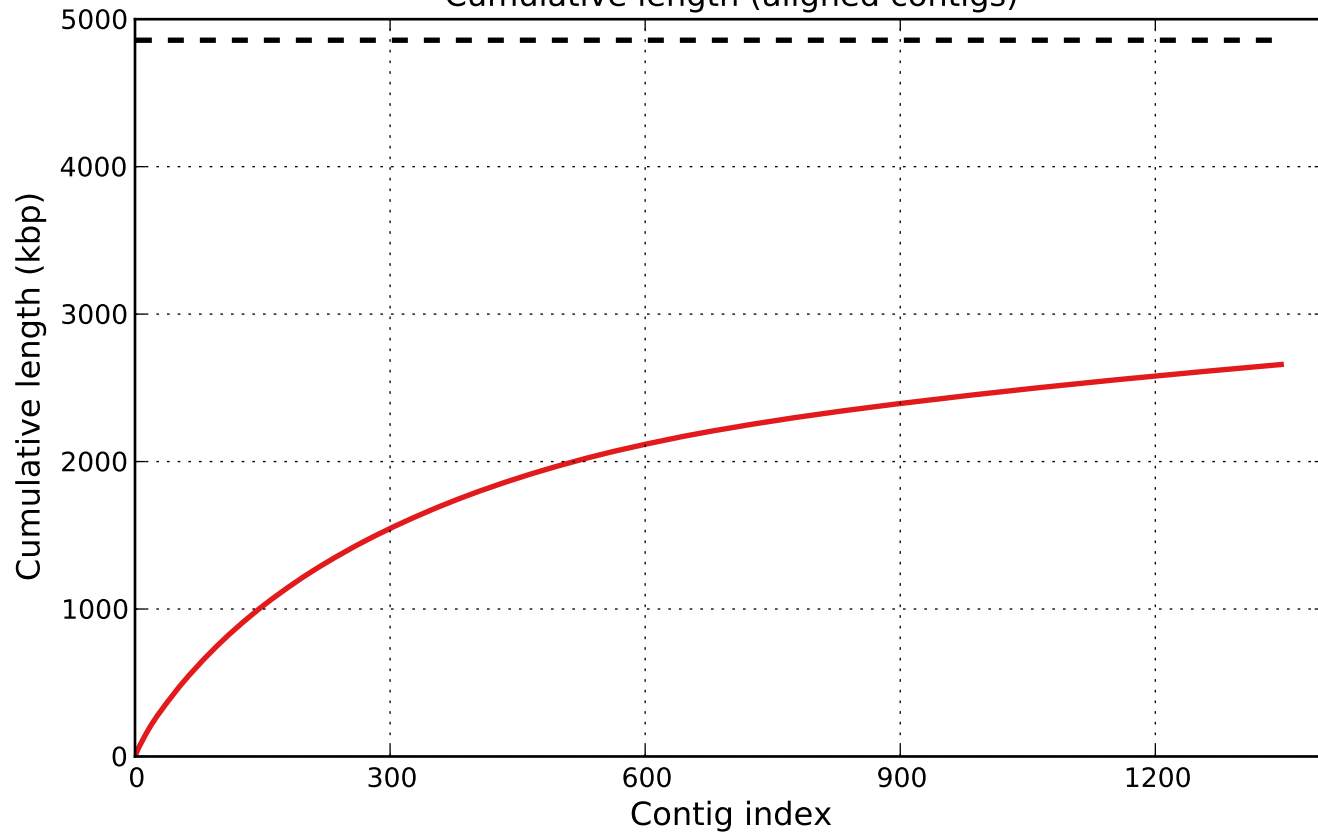
GC content



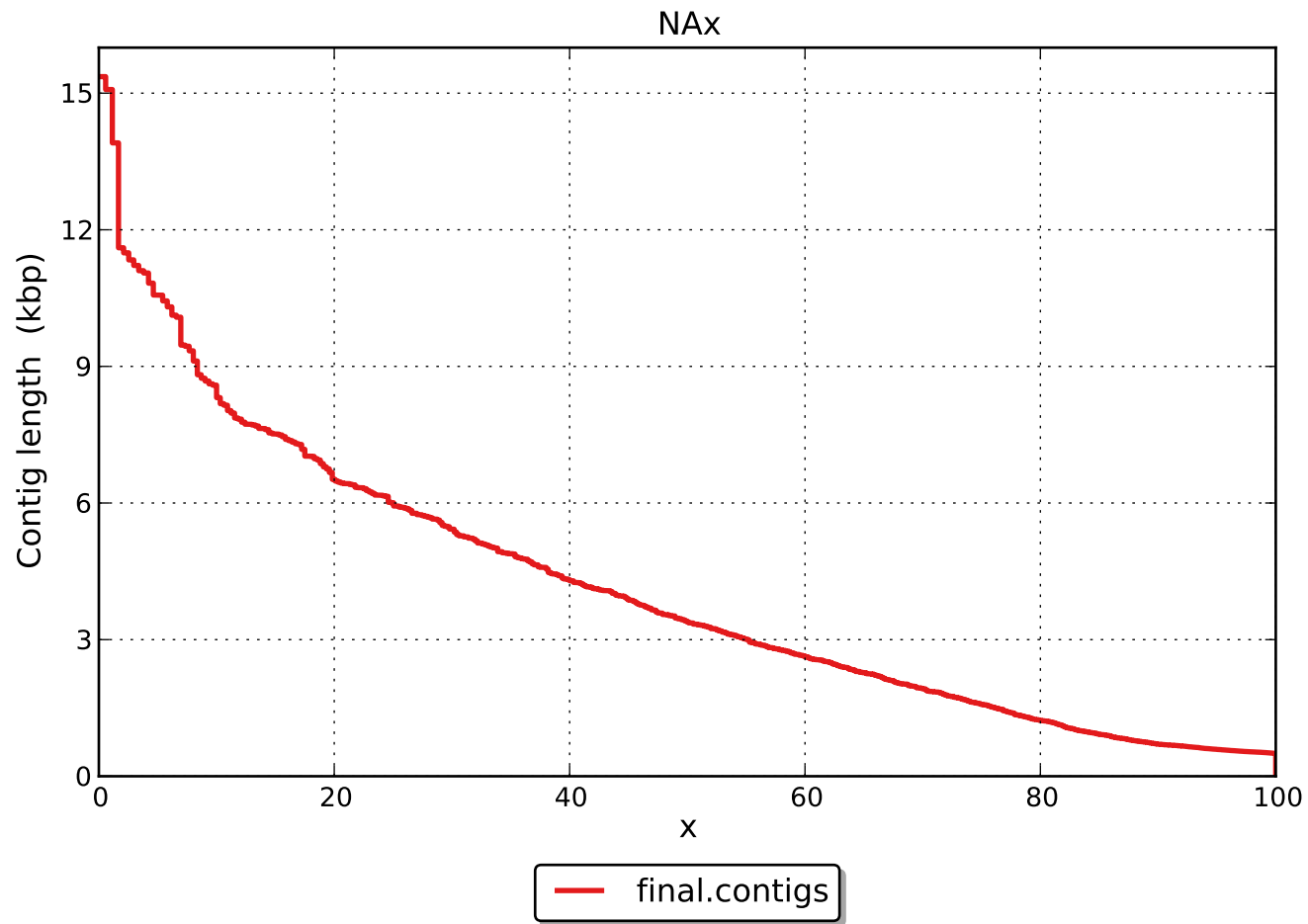
Misassemblies



Cumulative length (aligned contigs)



— final.contigs - - Reference



NGAx

