

Report

	final.contigs
# contigs (≥ 1000 bp)	939
# contigs (≥ 5000 bp)	19
# contigs (≥ 10000 bp)	2
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 1000 bp)	1908317
Total length (≥ 5000 bp)	126257
Total length (≥ 10000 bp)	21159
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	2557
Largest contig	11097
Total length	3010217
Reference length	4857432
GC (%)	52.14
Reference GC (%)	52.22
N50	1404
NG50	698
N75	776
L50	597
LG50	1571
L75	1339
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	59.612
Duplication ratio	1.040
# N's per 100 kbp	0.00
# mismatches per 100 kbp	318.31
# indels per 100 kbp	0.00
Largest alignment	11097
NA50	1404
NGA50	698
NA75	776
LA50	597
LGA50	1571
LA75	1339

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

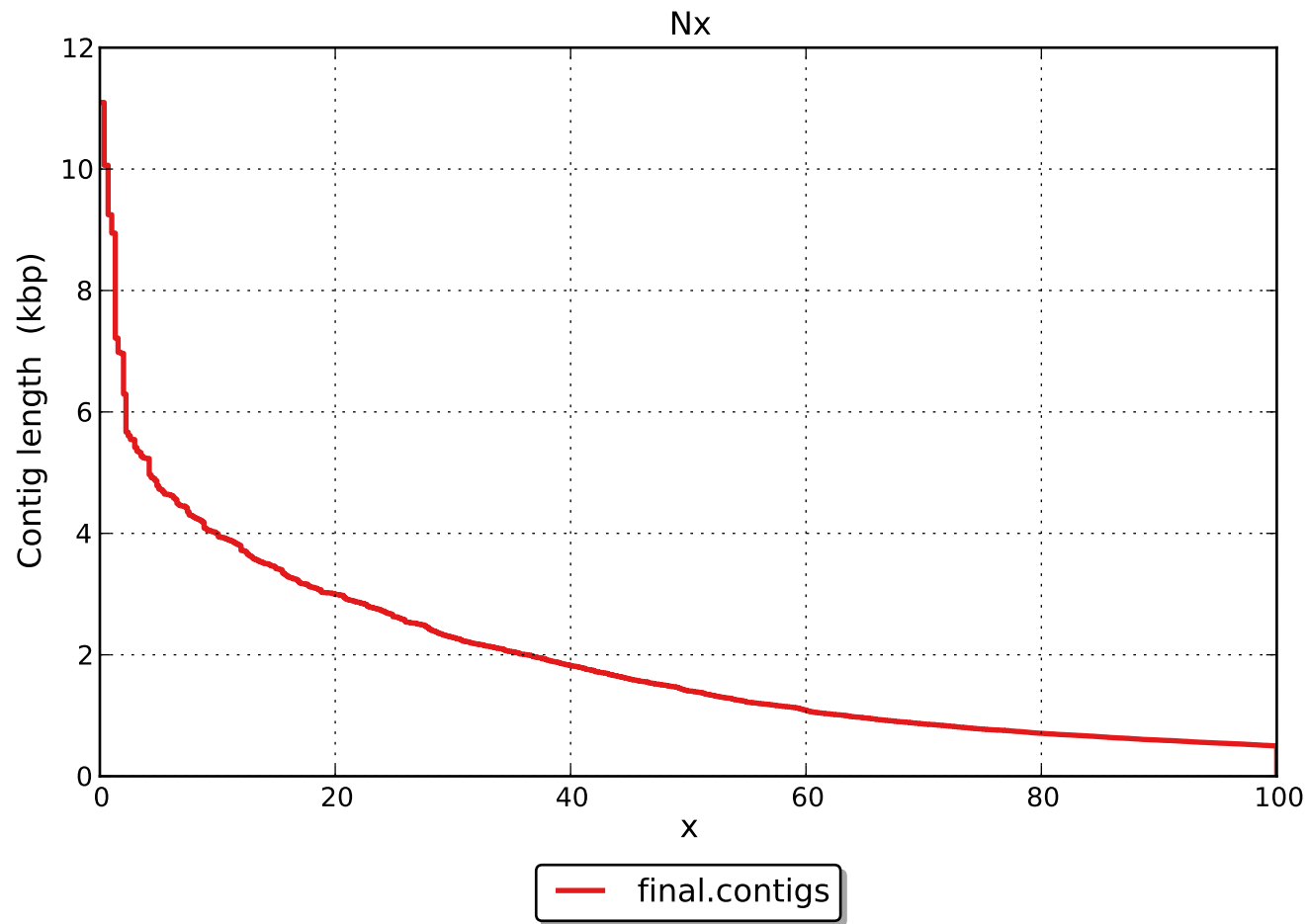
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	9217
# indels	0
# short indels	0
# long indels	0
Indels length	0

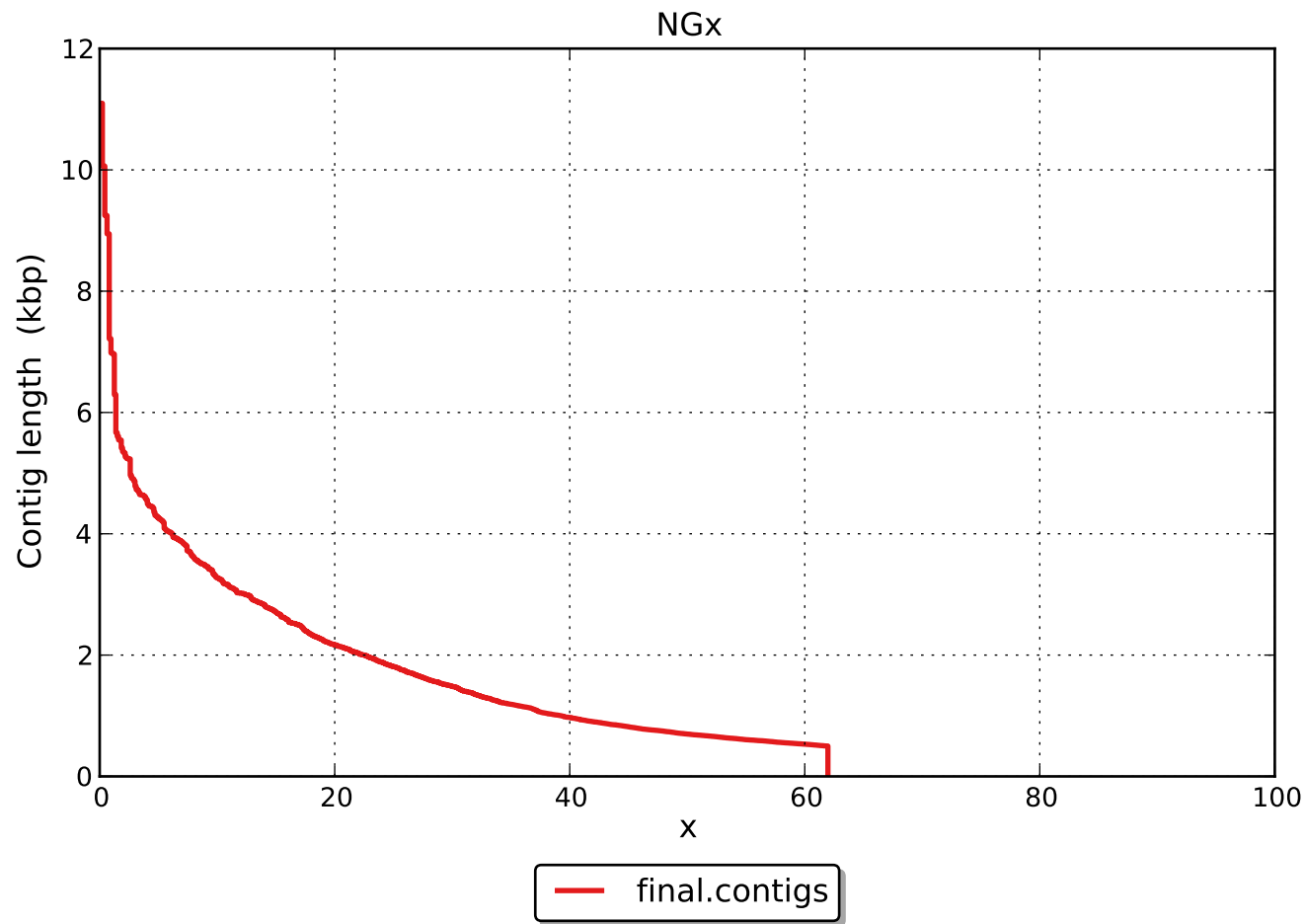
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

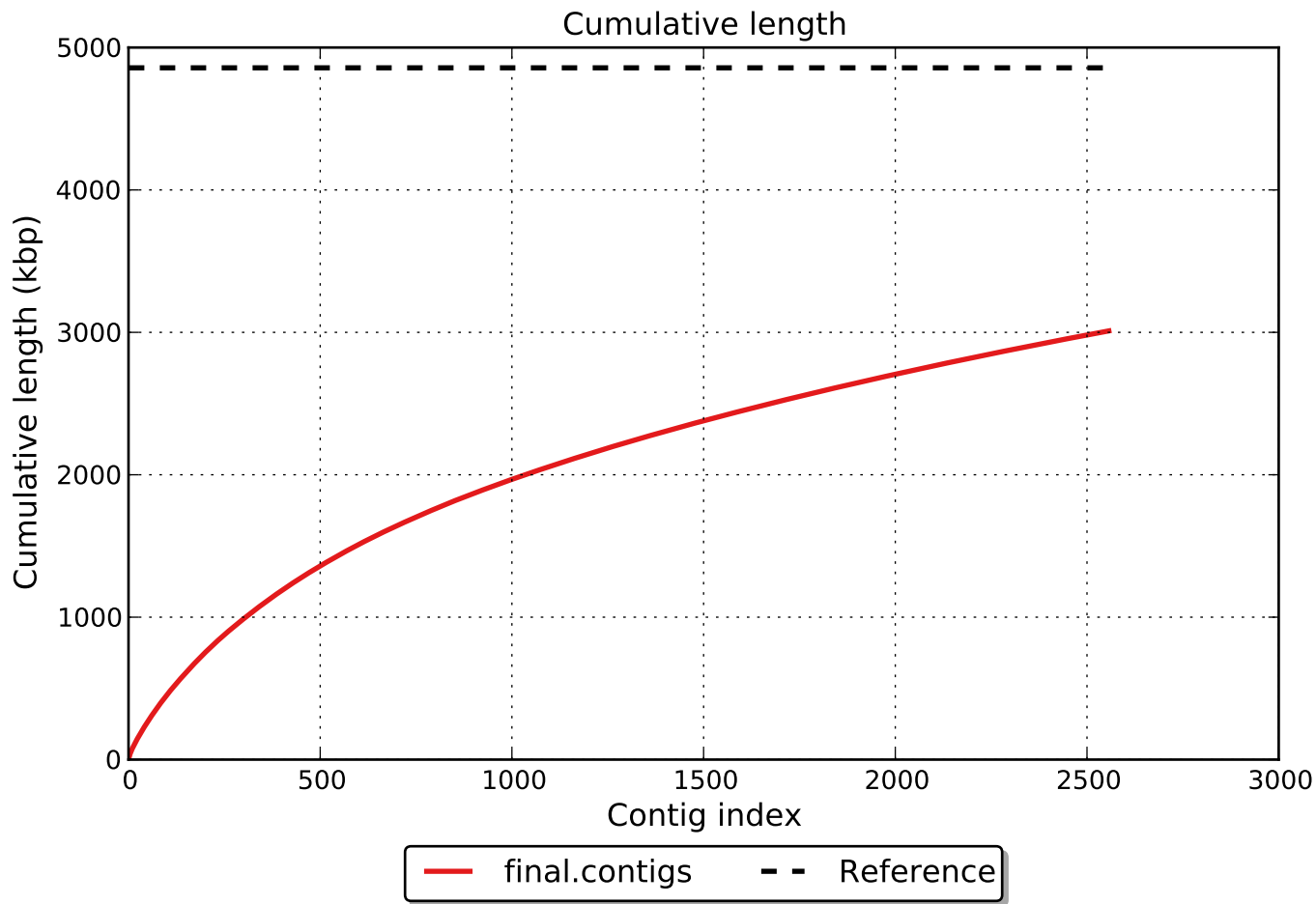
Unaligned report

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

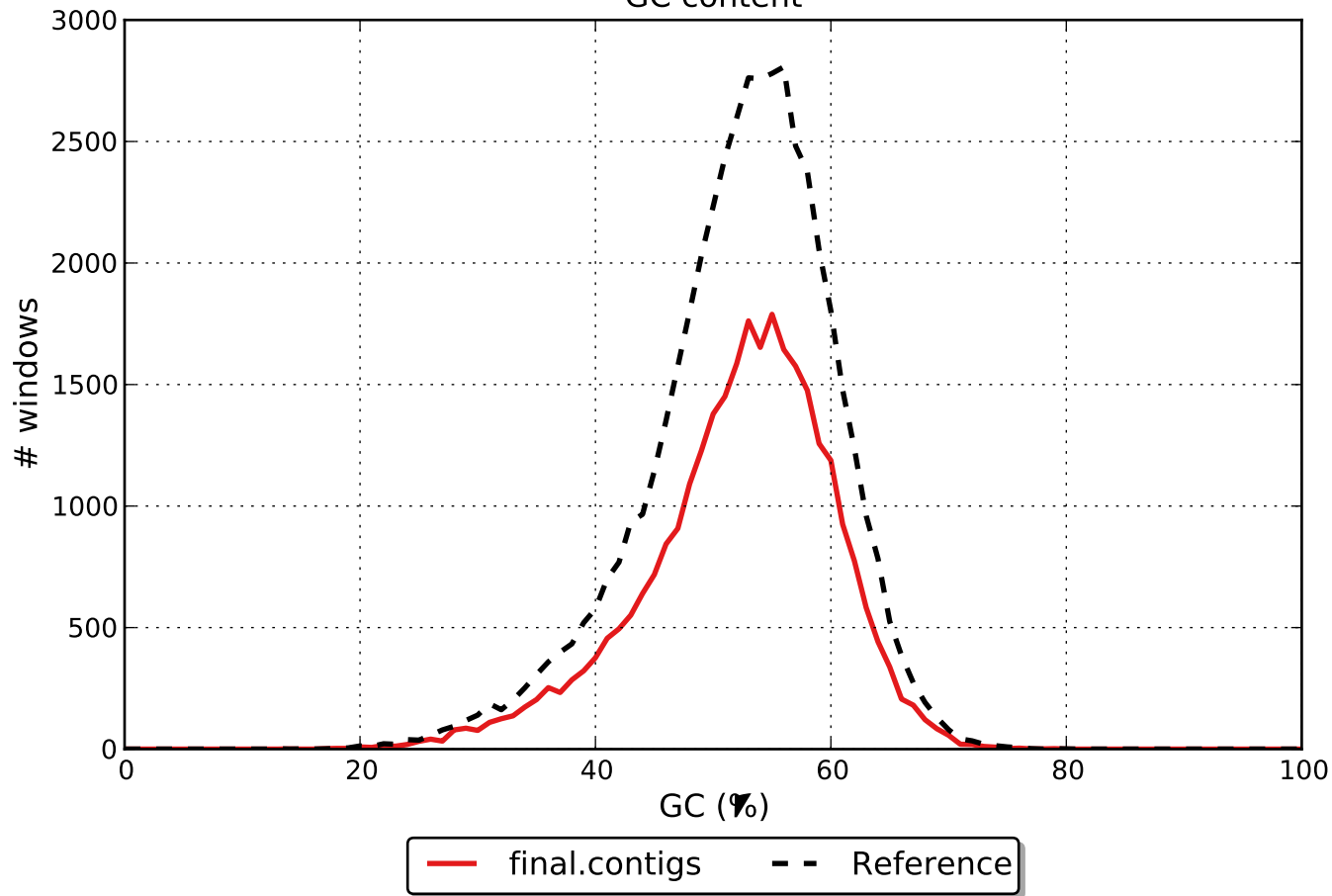
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).







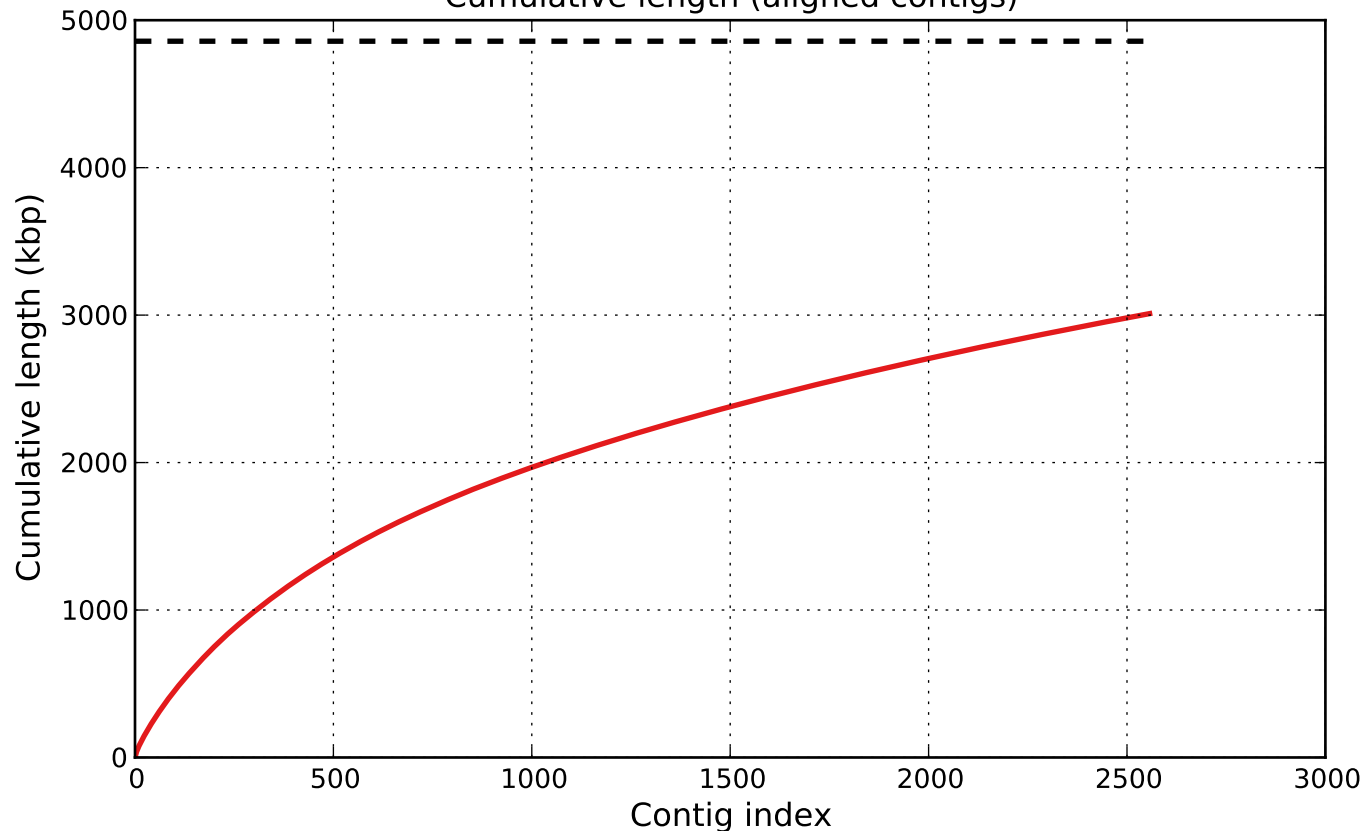
GC content



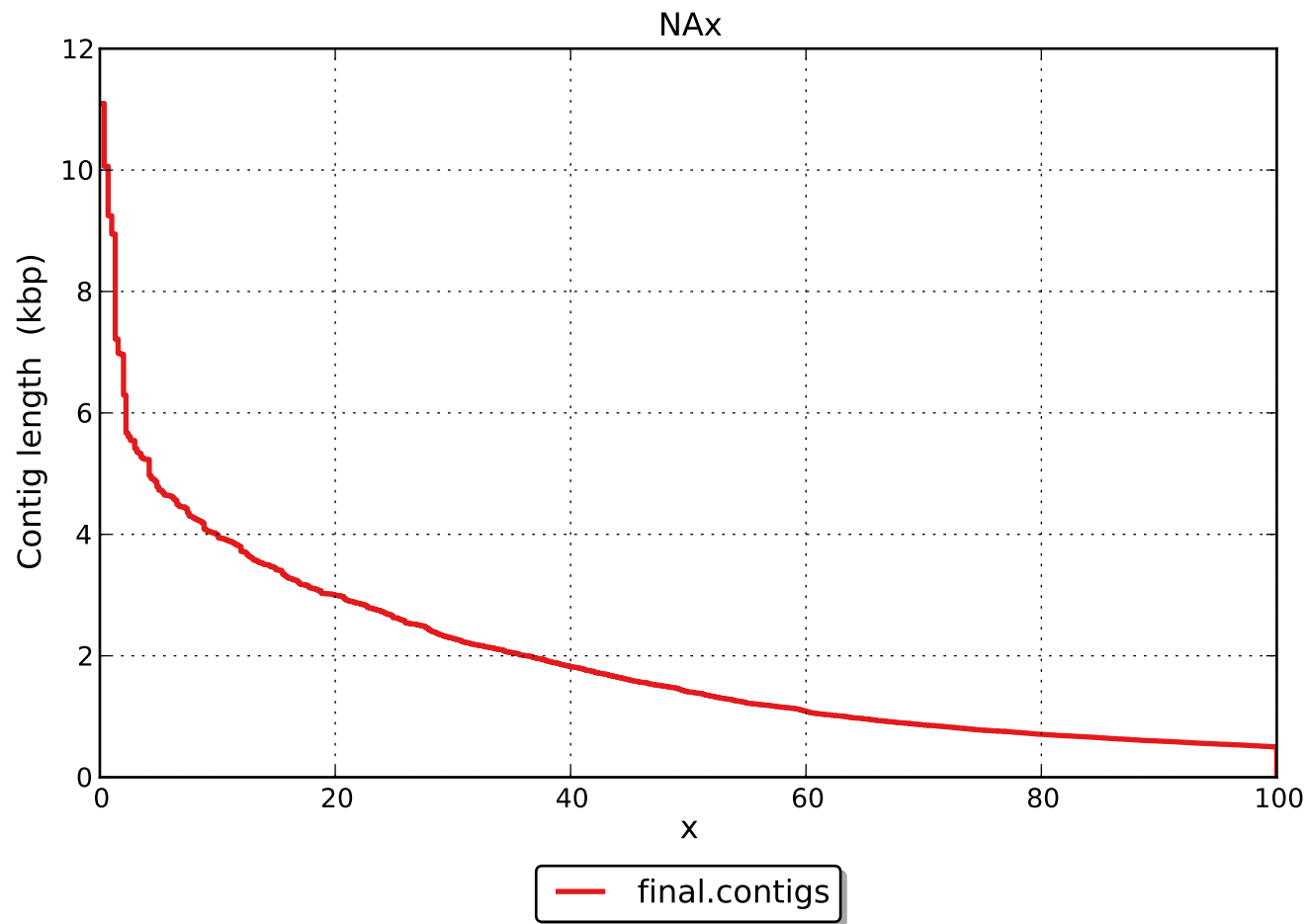
Misassemblies



Cumulative length (aligned contigs)



— final.contigs - - Reference



NGAx

