

Report

	final.contigs
# contigs (>= 1000 bp)	838
# contigs (>= 5000 bp)	29
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	1844133
Total length (>= 5000 bp)	183972
Total length (>= 10000 bp)	12848
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1724
Largest contig	12848
Total length	2444665
Reference length	4641652
GC (%)	50.73
Reference GC (%)	50.79
N50	1920
NG50	566
N75	1010
L50	390
LG50	1491
L75	828
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	51.090
Duplication ratio	1.031
# N's per 100 kbp	0.00
# mismatches per 100 kbp	394.62
# indels per 100 kbp	0.08
Largest alignment	12845
NA50	1920
NGA50	566
NA75	1010
LA50	390
LGA50	1491
LA75	828

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

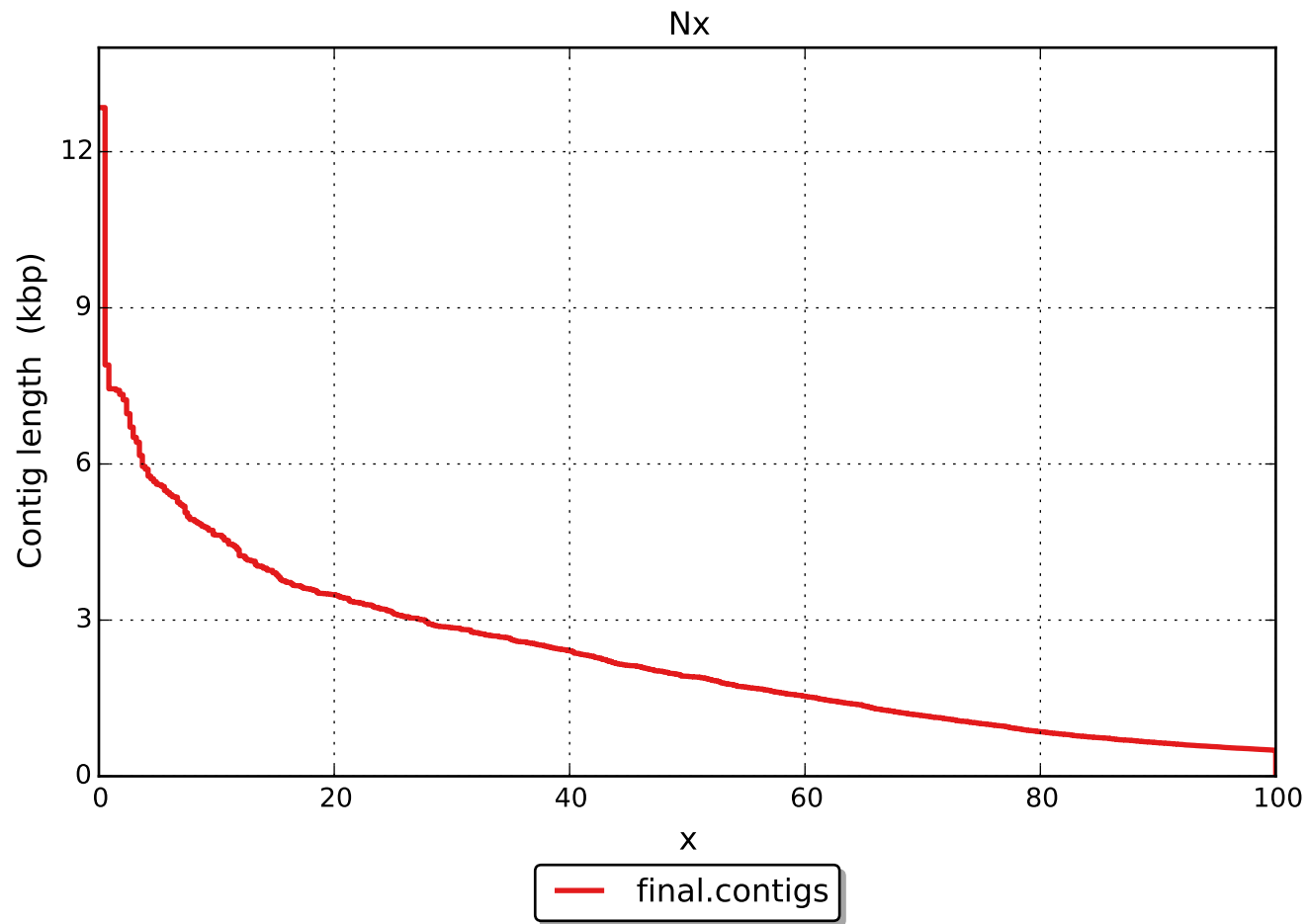
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	9358
# indels	2
# short indels	2
# long indels	0
Indels length	2

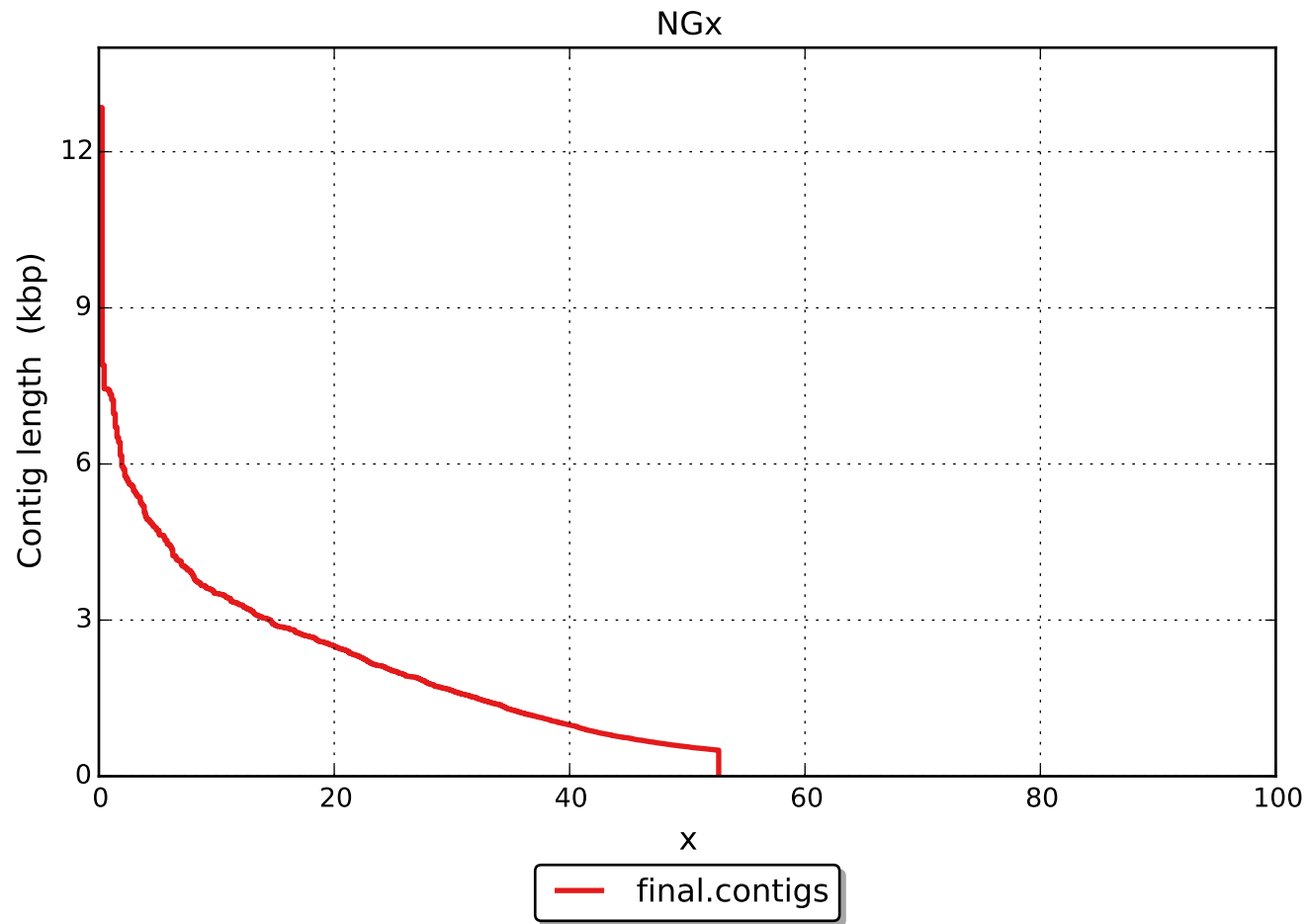
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

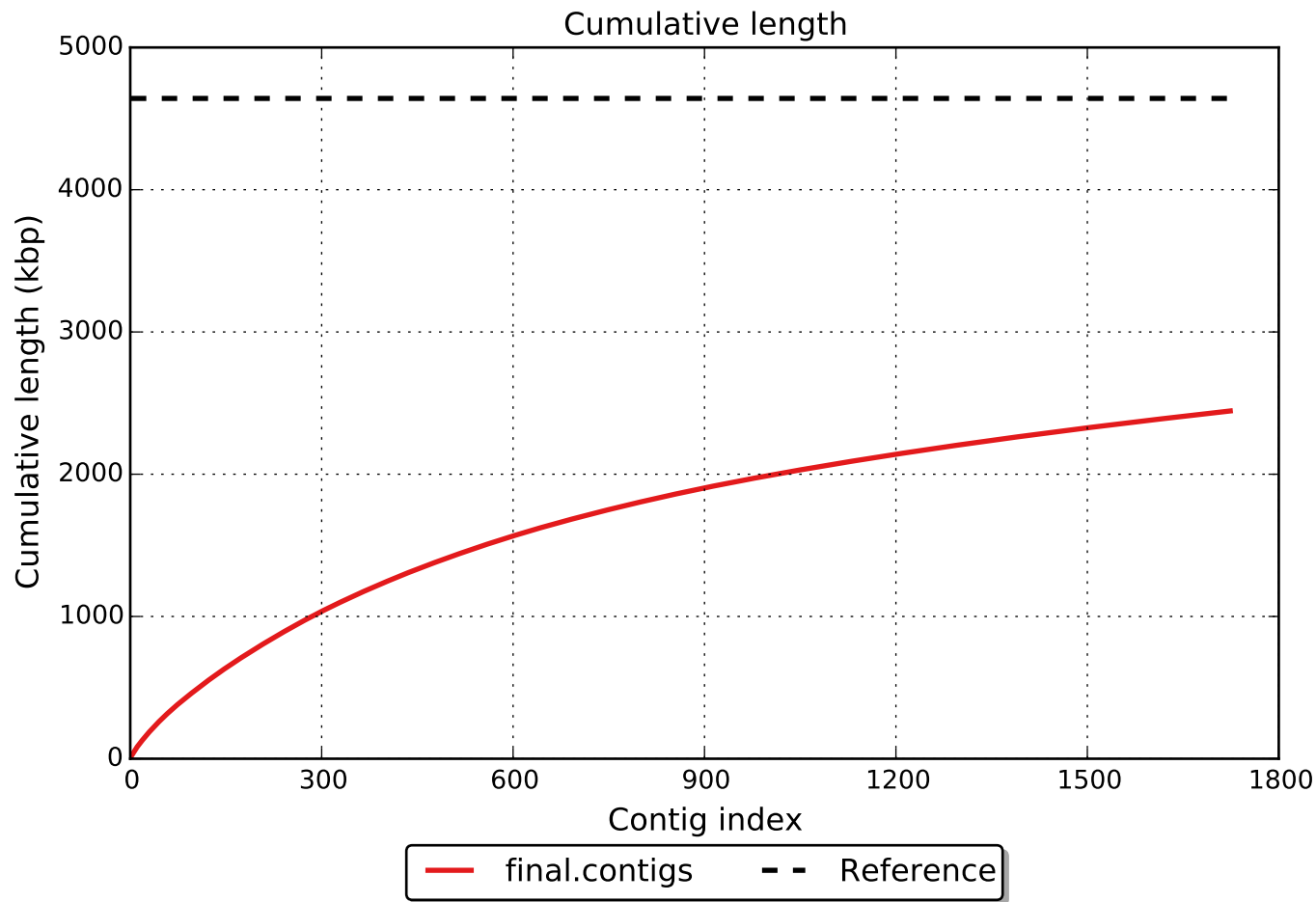
Unaligned report

	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

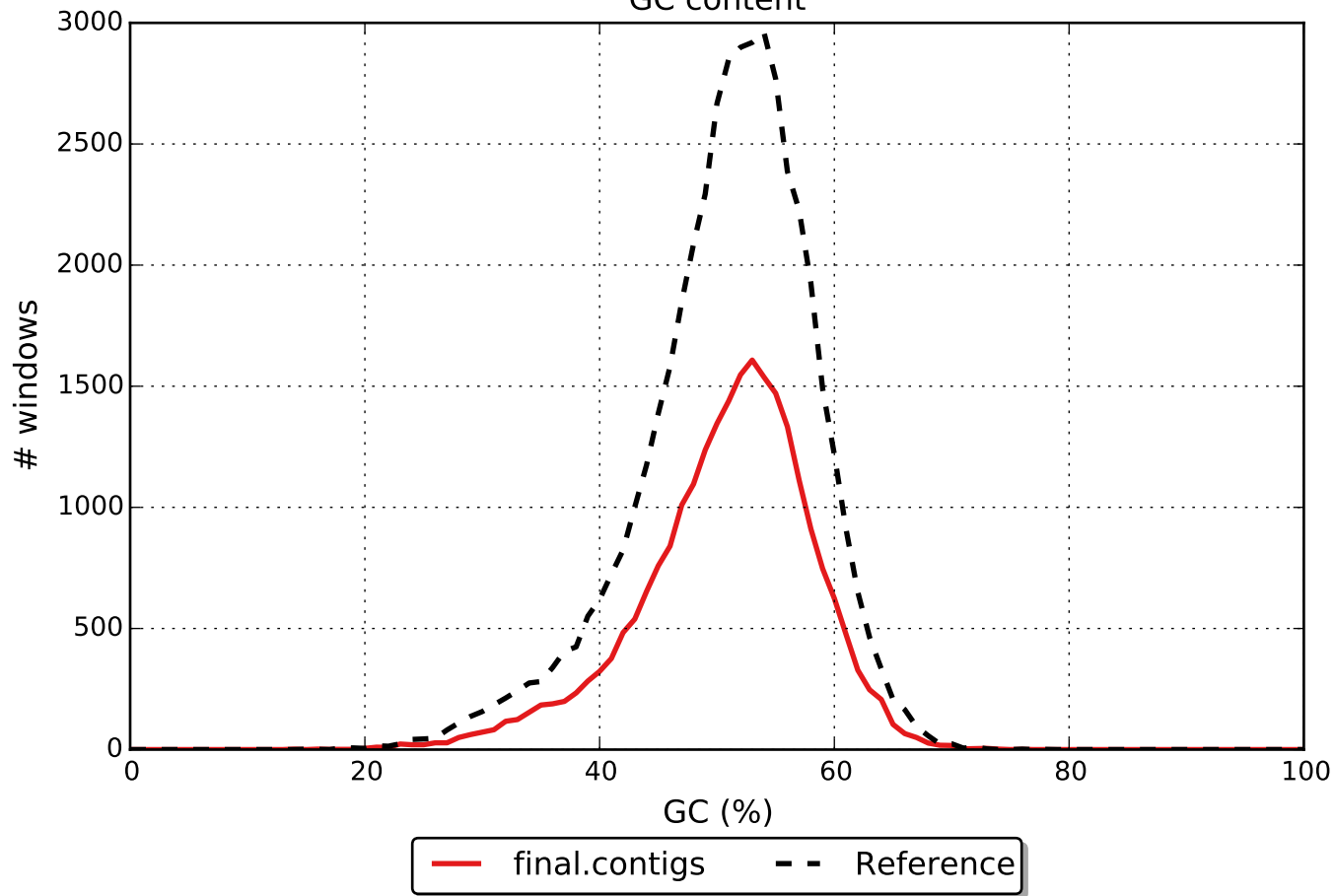
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).







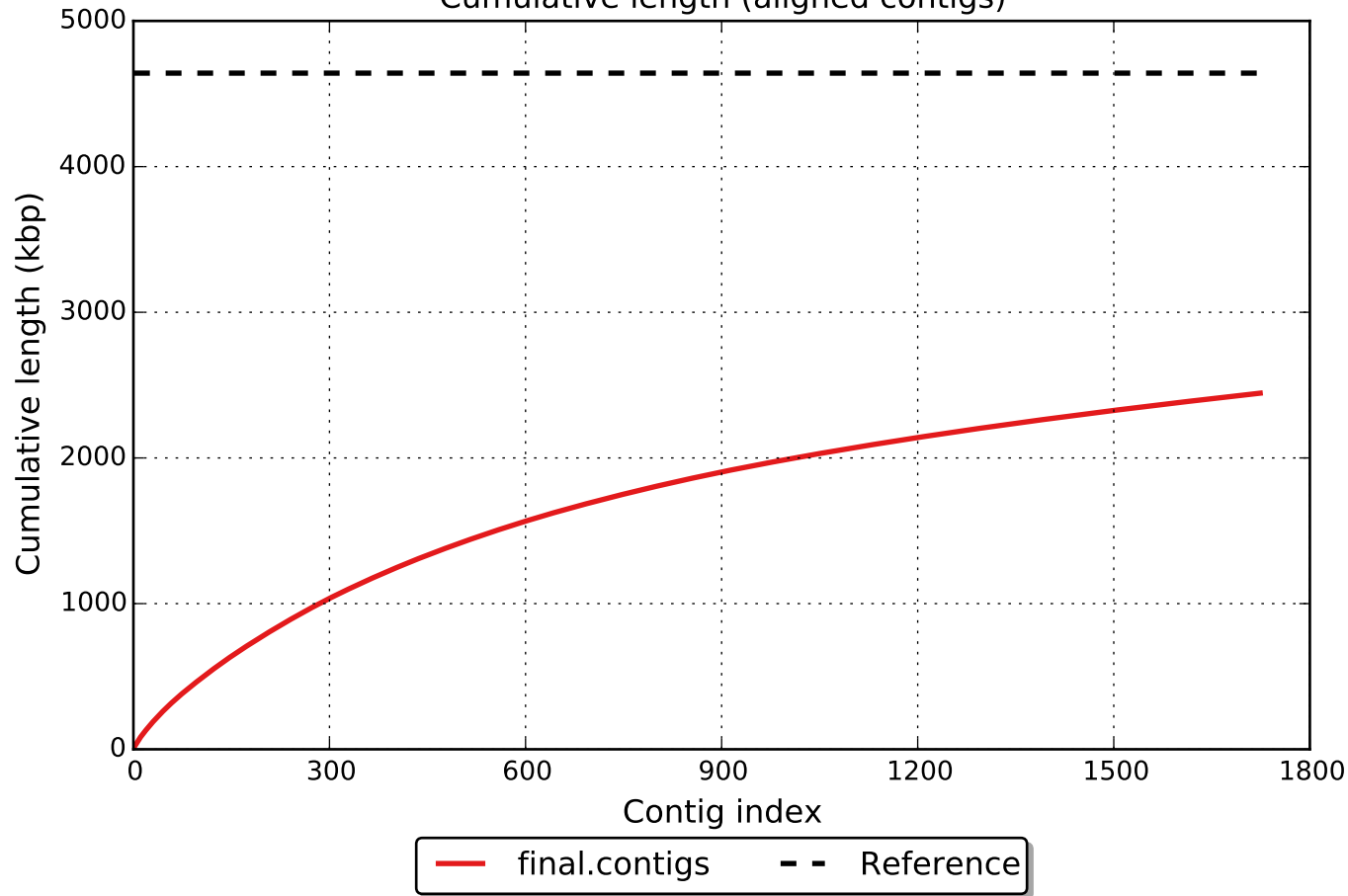
GC content

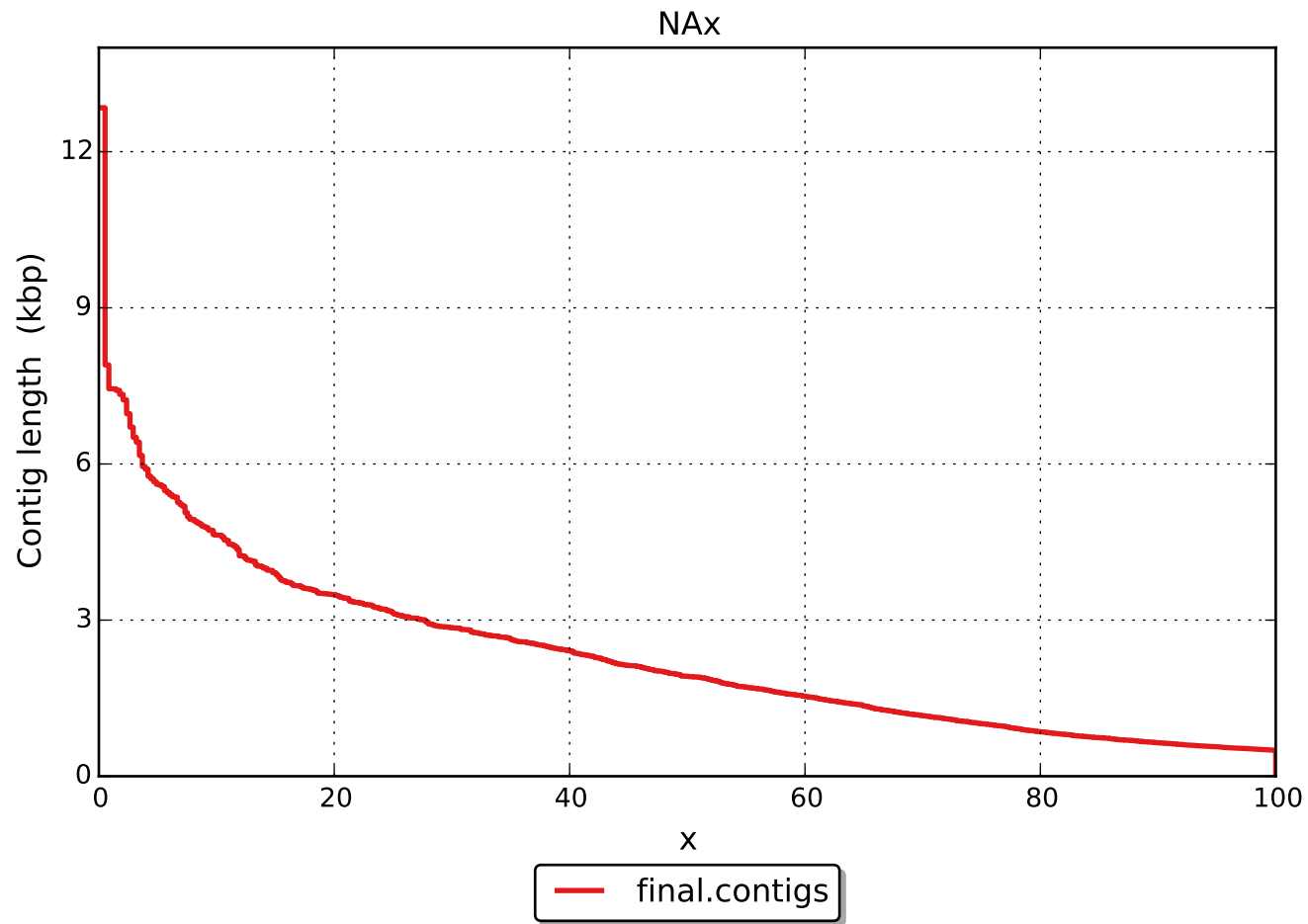


Misassemblies



Cumulative length (aligned contigs)





NGAx

