

Report

	final.contigs
# contigs (>= 1000 bp)	1880
# contigs (>= 5000 bp)	5
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	3163032
Total length (>= 5000 bp)	26688
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3927
Largest contig	5692
Total length	4635539
Reference length	4857432
GC (℥)	52.23
Reference GC (℥)	52.23
N50	1329
NG50	1278
N75	883
NG75	832
L50	1143
LG50	1228
L75	2215
LG75	2408
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (℥)	91.119
Duplication ratio	1.047
# N's per 100 kbp	0.00
# mismatches per 100 kbp	39.79
# indels per 100 kbp	0.02
Largest alignment	5692
NA50	1329
NGA50	1278
NA75	883
NGA75	832
LA50	1143
LGA50	1228
LA75	2215
LGA75	2408

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

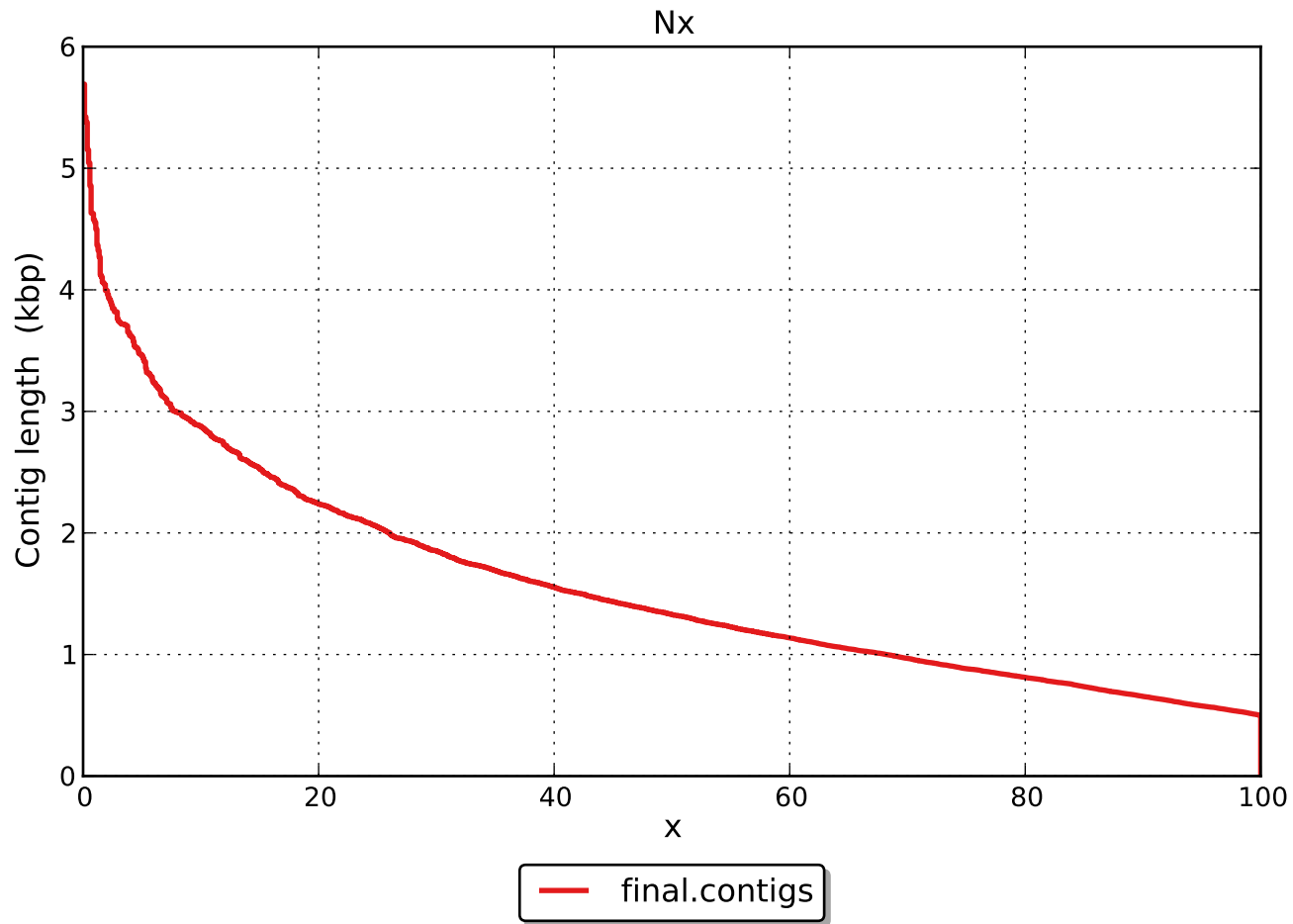
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	1761
# indels	1
# short indels	1
# long indels	0
Indels length	1

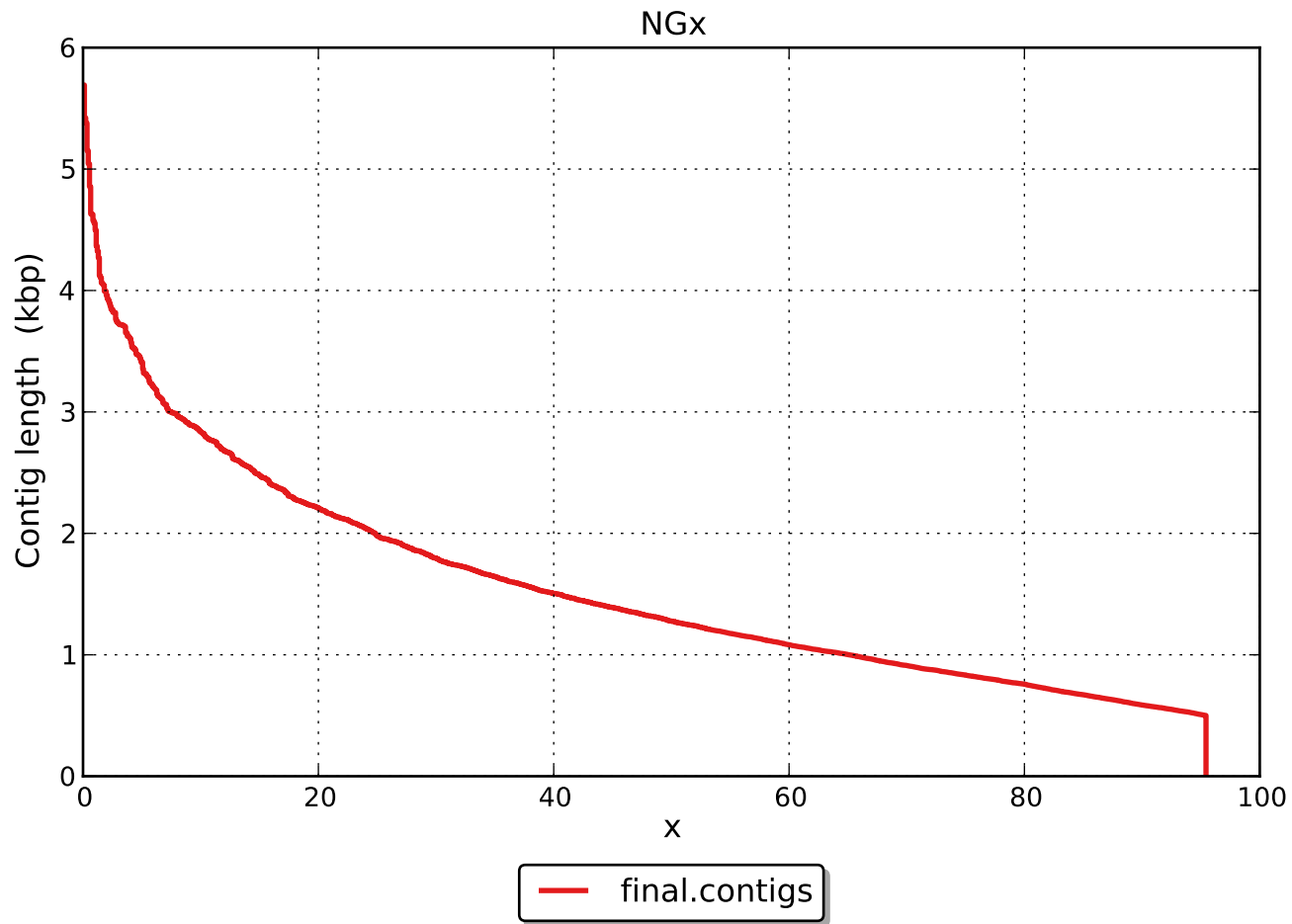
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

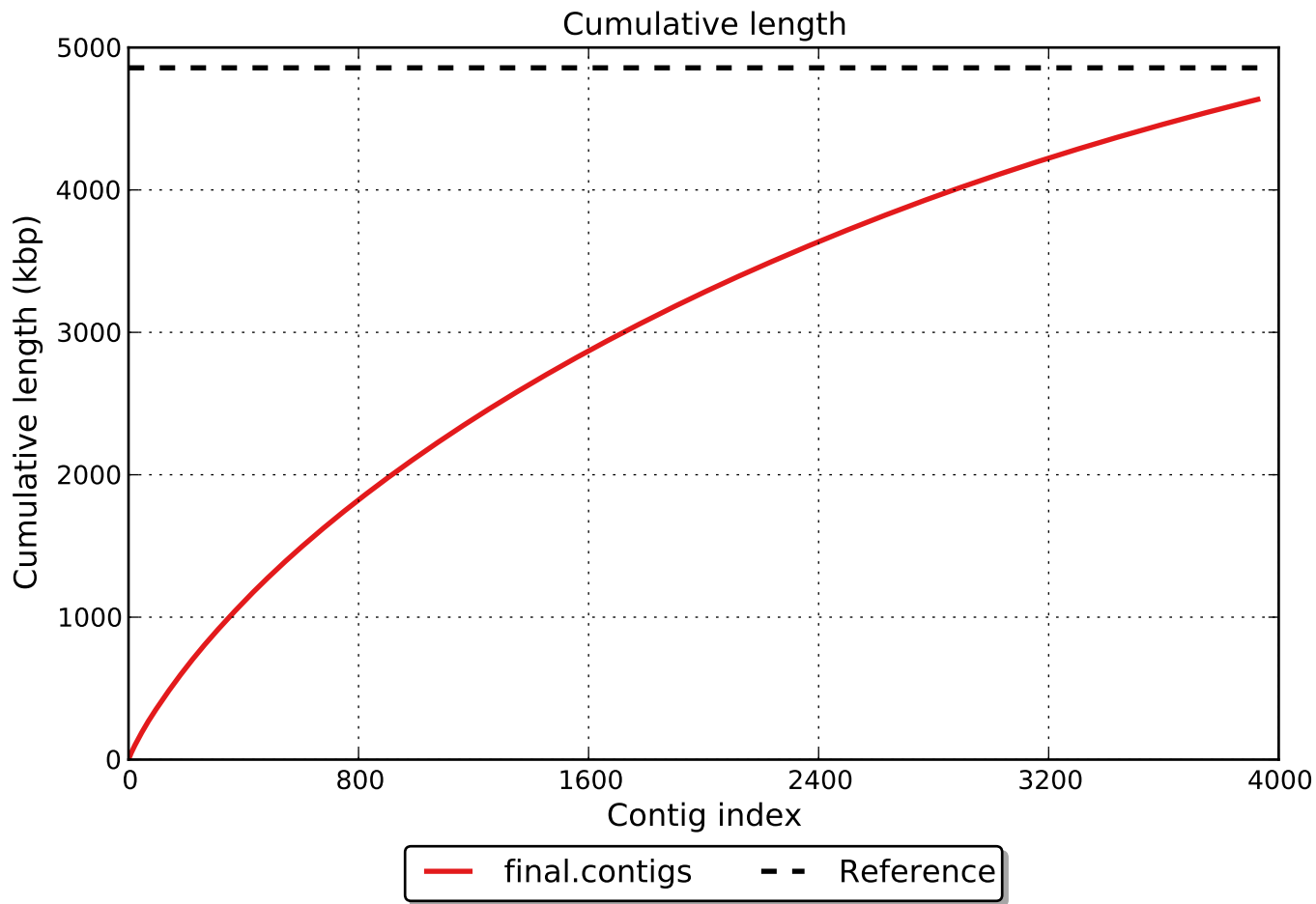
Unaligned report

	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

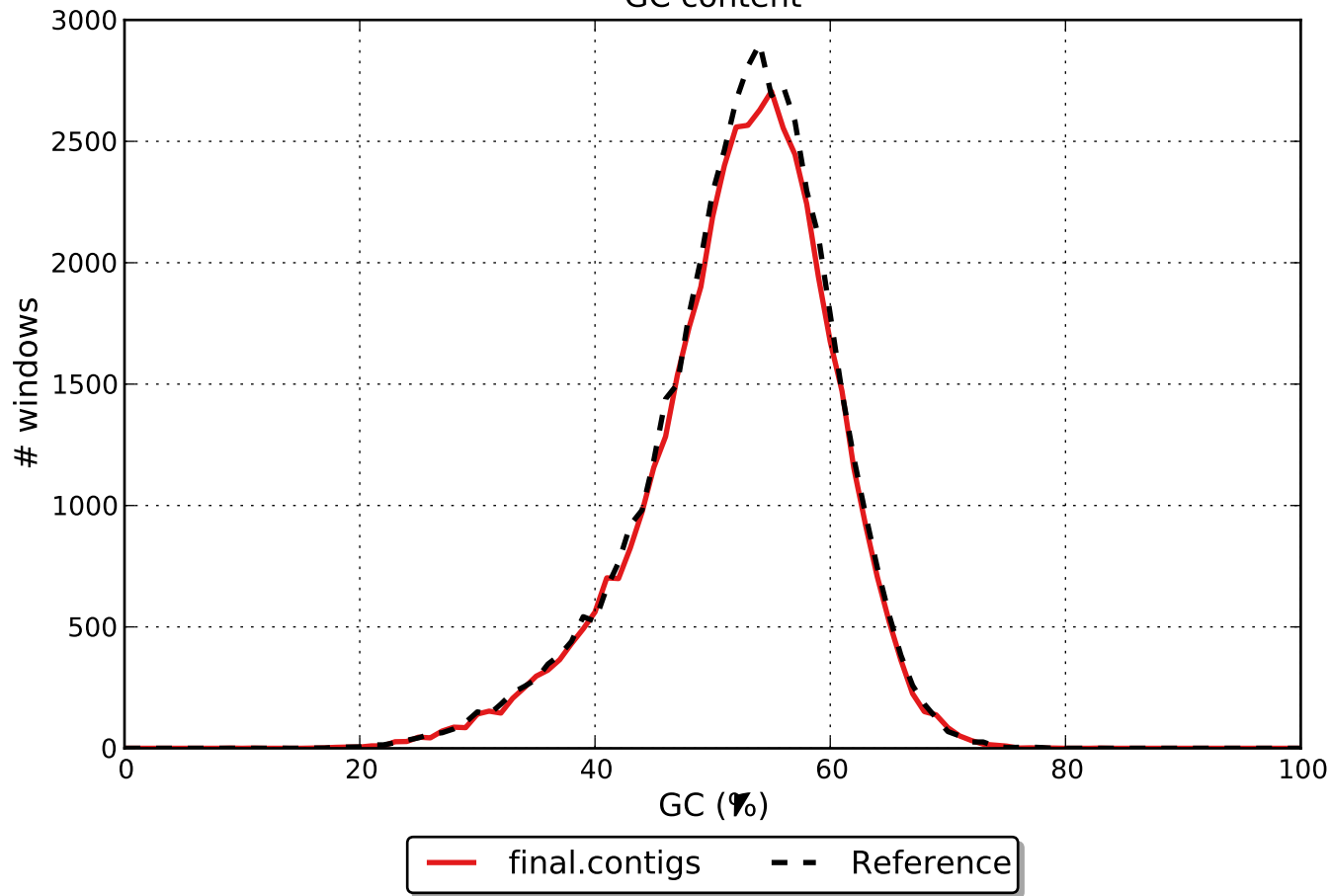
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



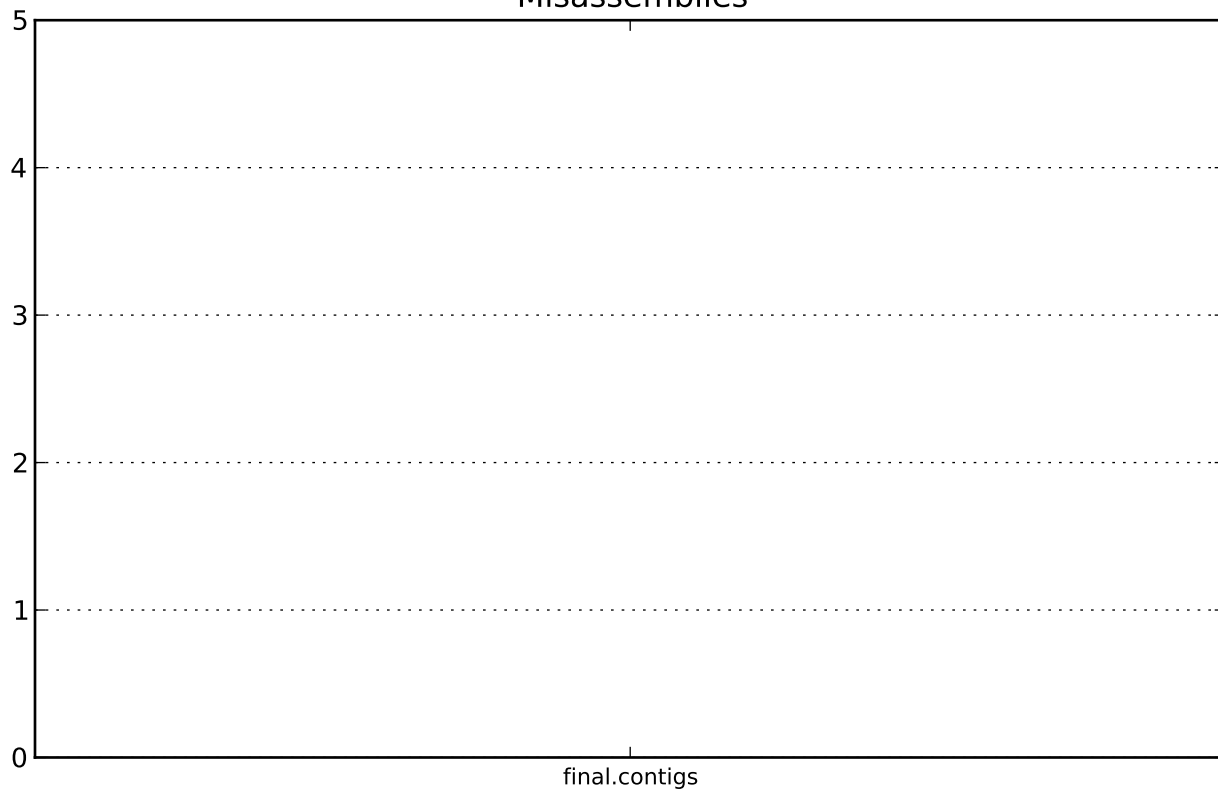




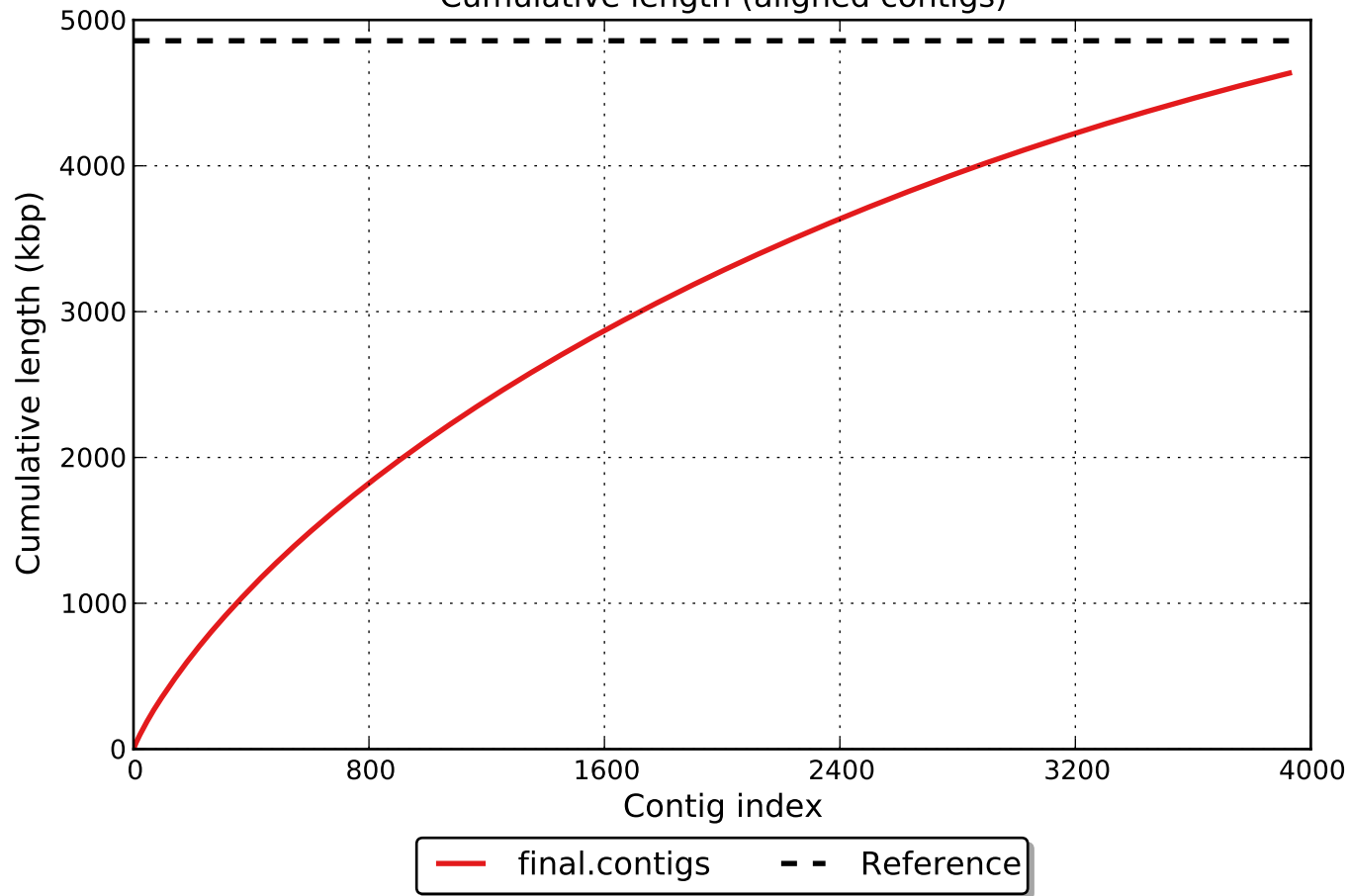
GC content

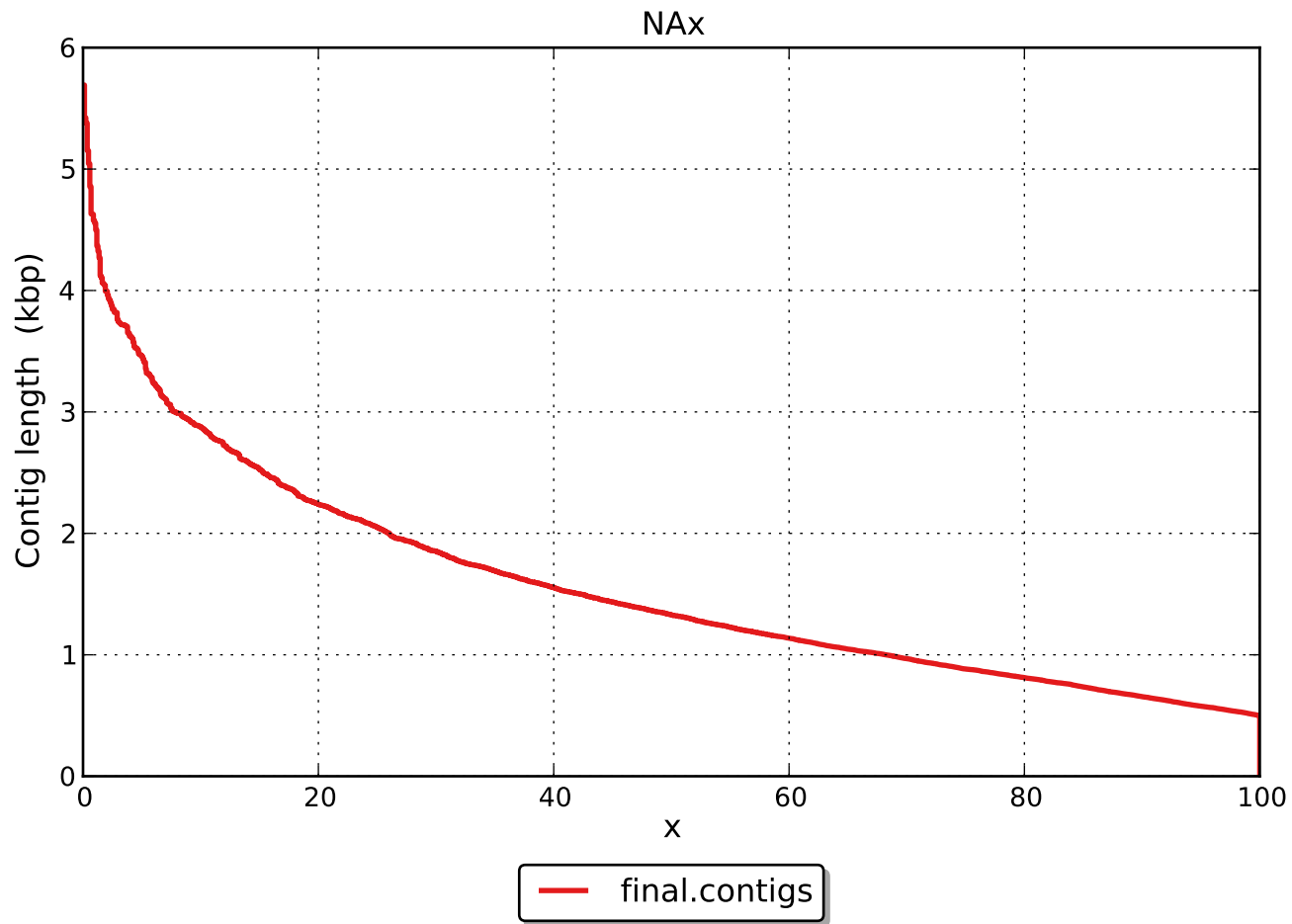


Misassemblies

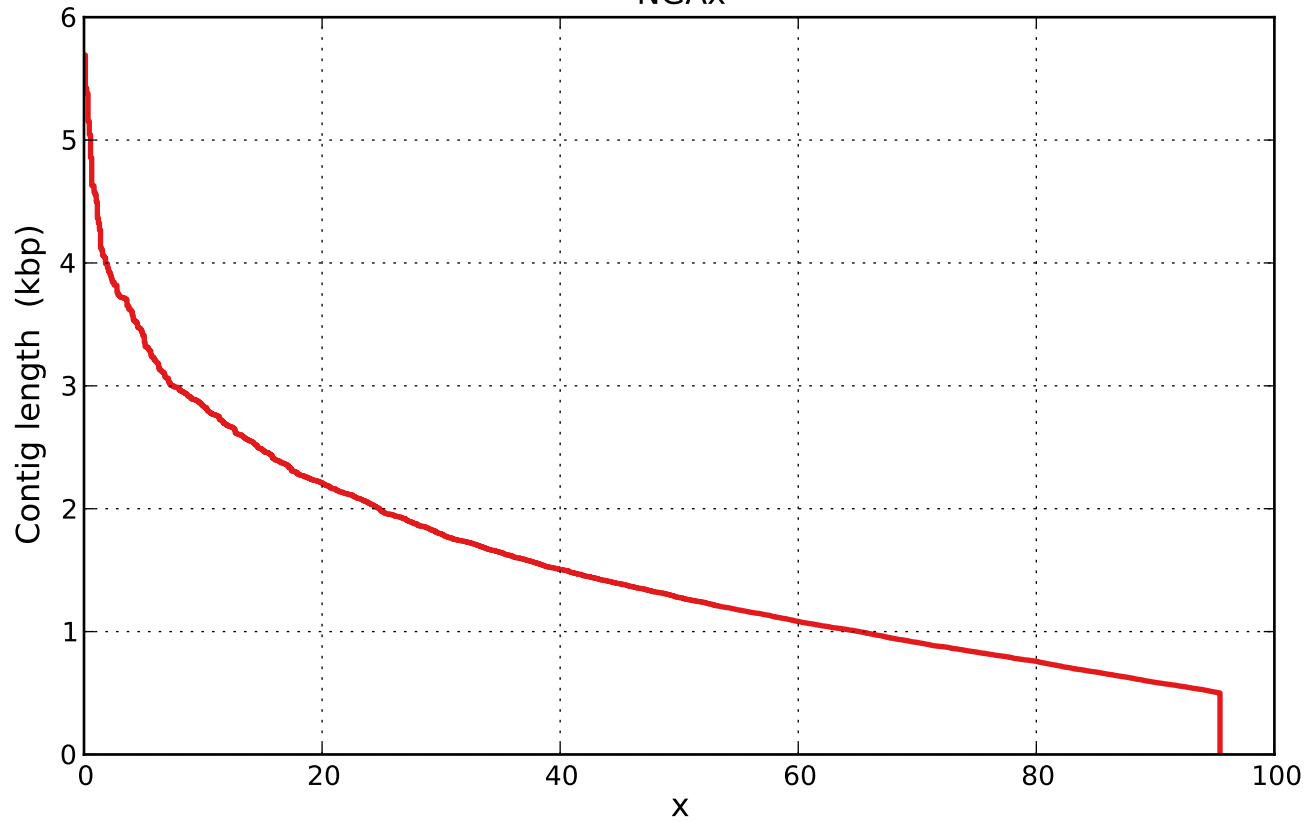


Cumulative length (aligned contigs)





NGAx



— final.contigs