

Report

	final.contigs
# contigs (>= 0 bp)	2394
# contigs (>= 1000 bp)	1462
# contigs (>= 5000 bp)	101
# contigs (>= 10000 bp)	5
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	4169554
Total length (>= 1000 bp)	3608376
Total length (>= 5000 bp)	655840
Total length (>= 10000 bp)	53689
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2054
Largest contig	11619
Total length	4039067
Reference length	4641652
GC (%)	50.77
Reference GC (%)	50.79
N50	2568
NG50	2243
N75	1526
NG75	1132
L50	496
LG50	622
L75	1002
LG75	1344
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	11265
# local misassemblies	3
# unaligned contigs	0 + 2 part
Unaligned length	94
Genome fraction (%)	86.954
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2.11
# indels per 100 kbp	0.07
Largest alignment	11619
NA50	2563
NGA50	2235
NA75	1524
NGA75	1127
LA50	497
LGA50	623
LA75	1004
LGA75	1347

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

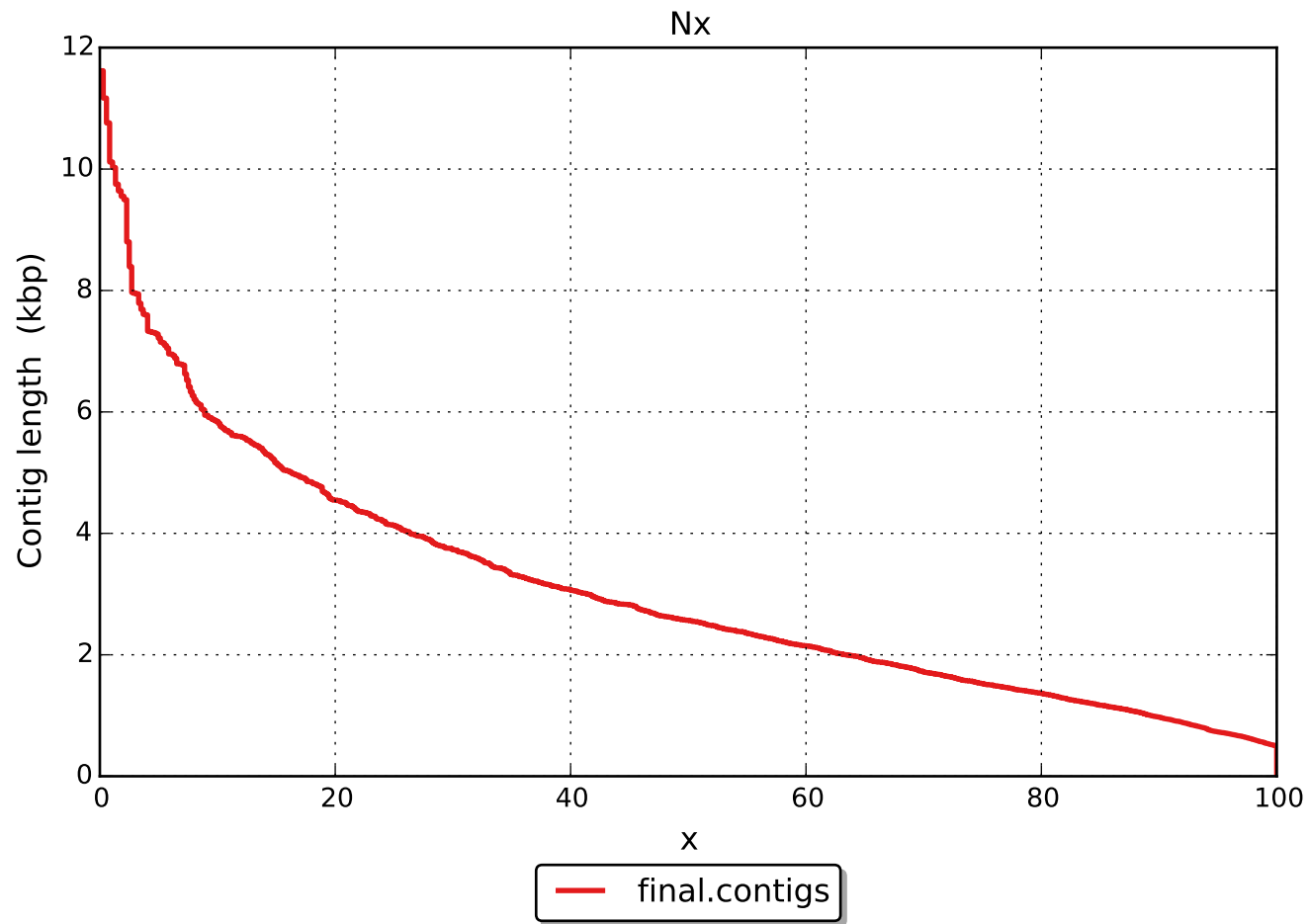
	final.contigs
# misassemblies	3
# relocations	3
# translocations	0
# inversions	0
# misassembled contigs	3
Misassembled contigs length	11265
# local misassemblies	3
# mismatches	85
# indels	3
# short indels	2
# long indels	1
Indels length	87

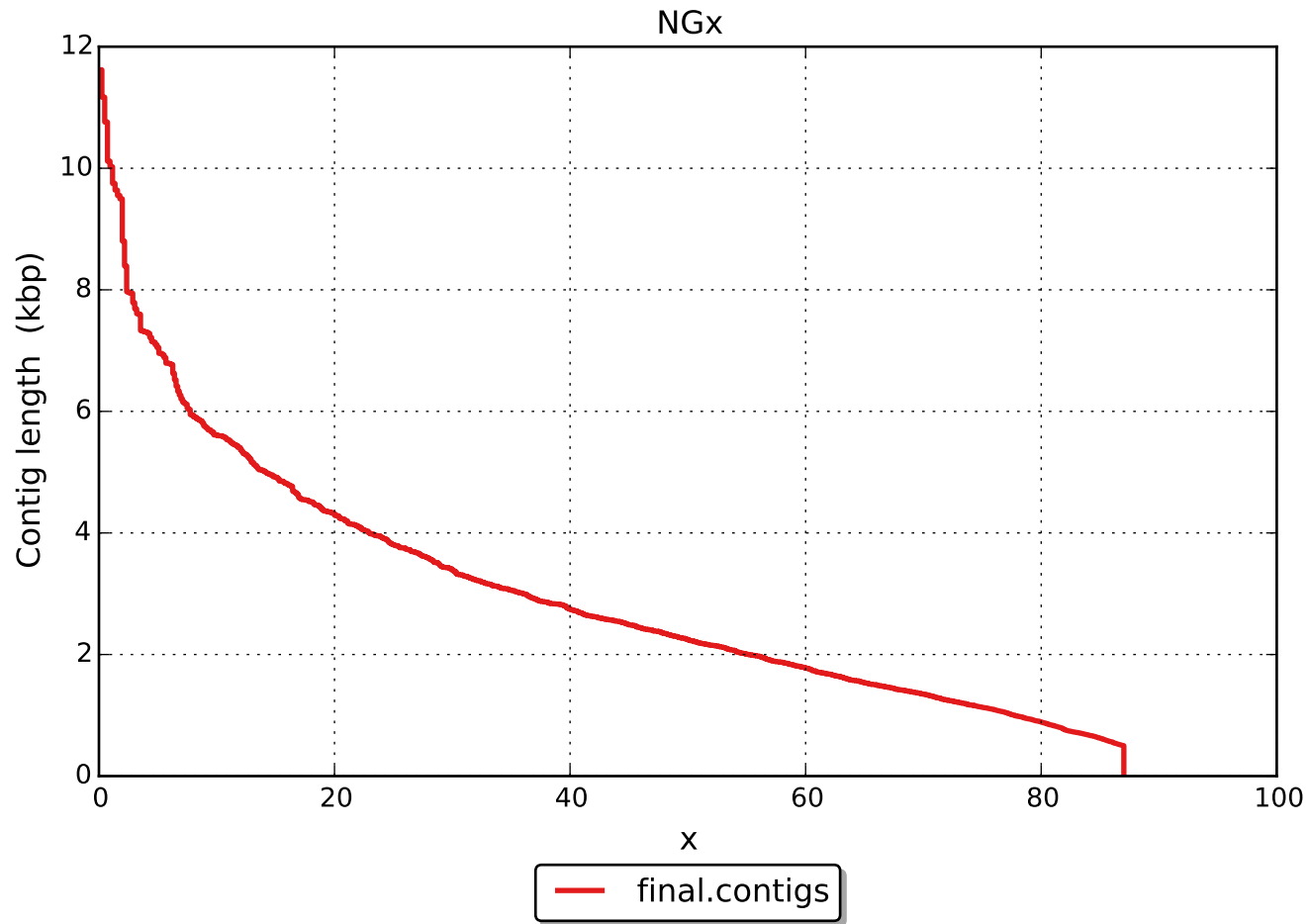
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

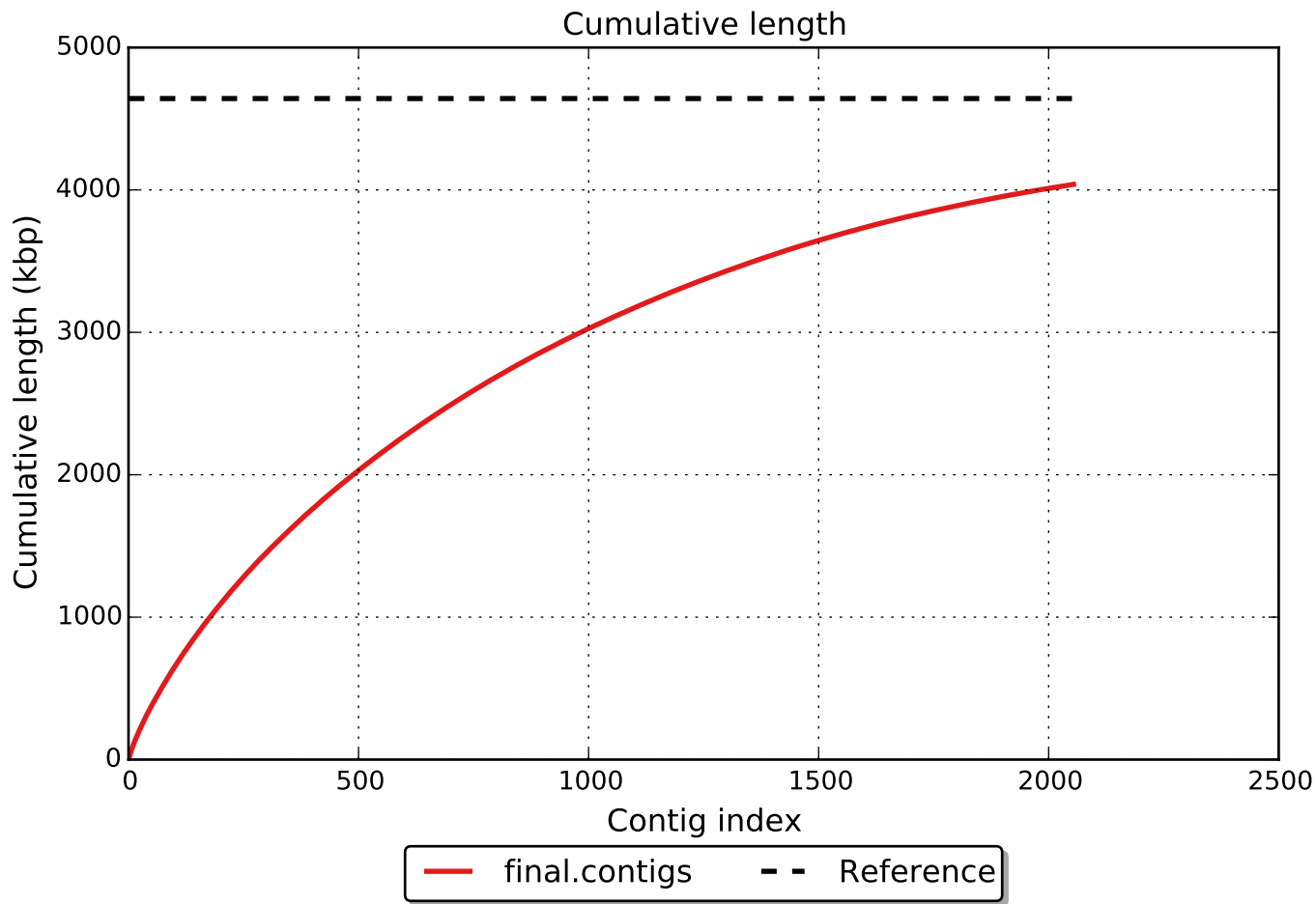
Unaligned report

	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	94
# N's	0

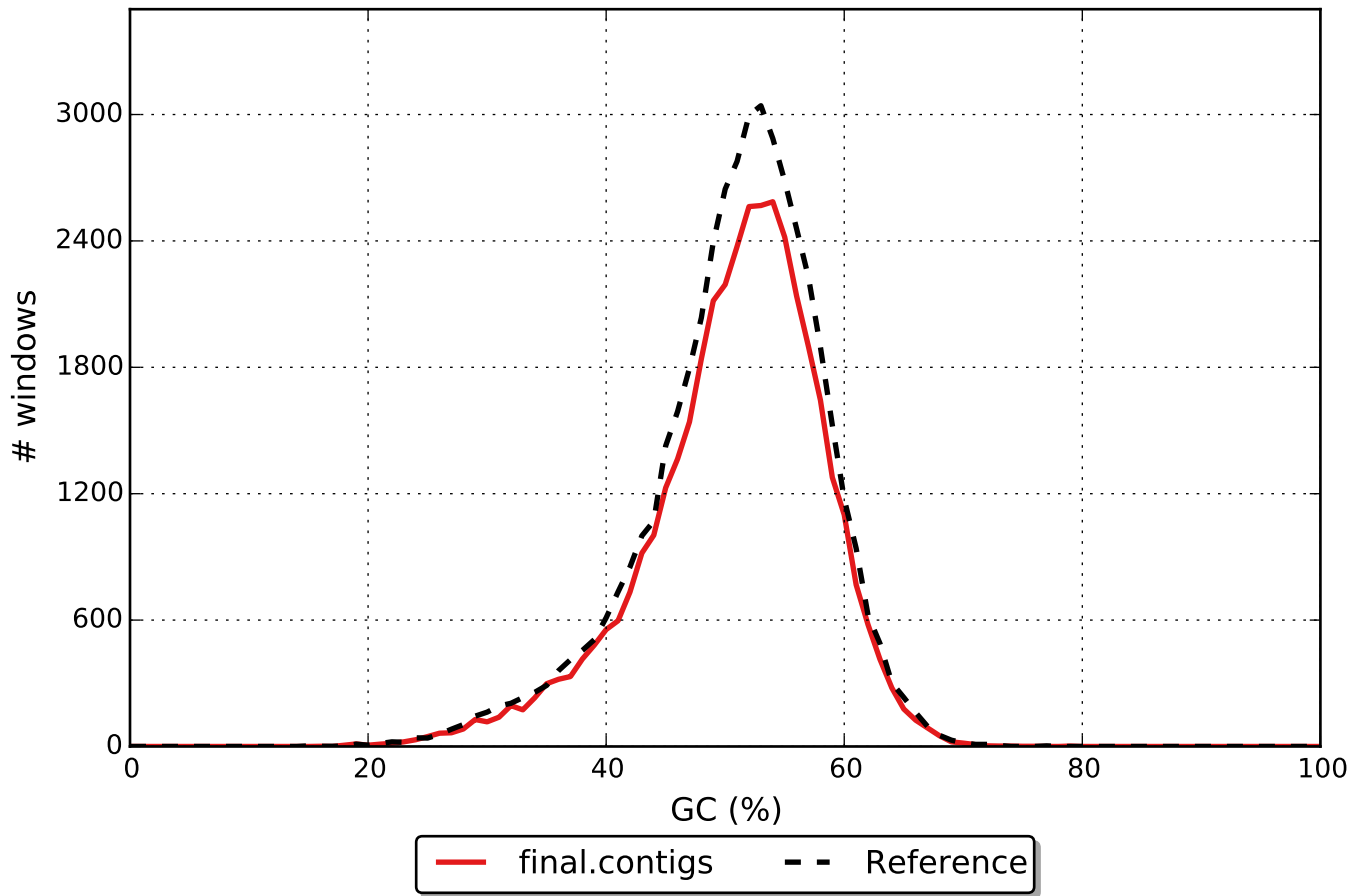
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

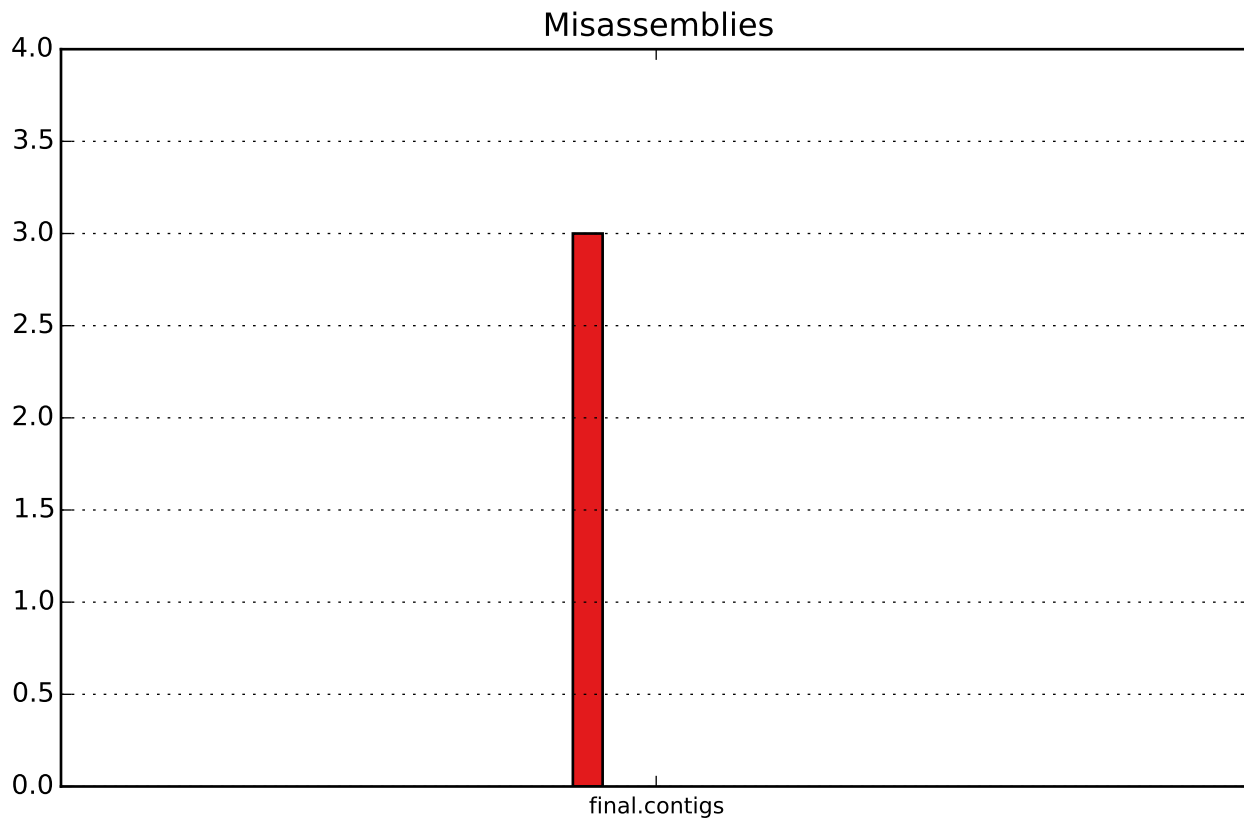




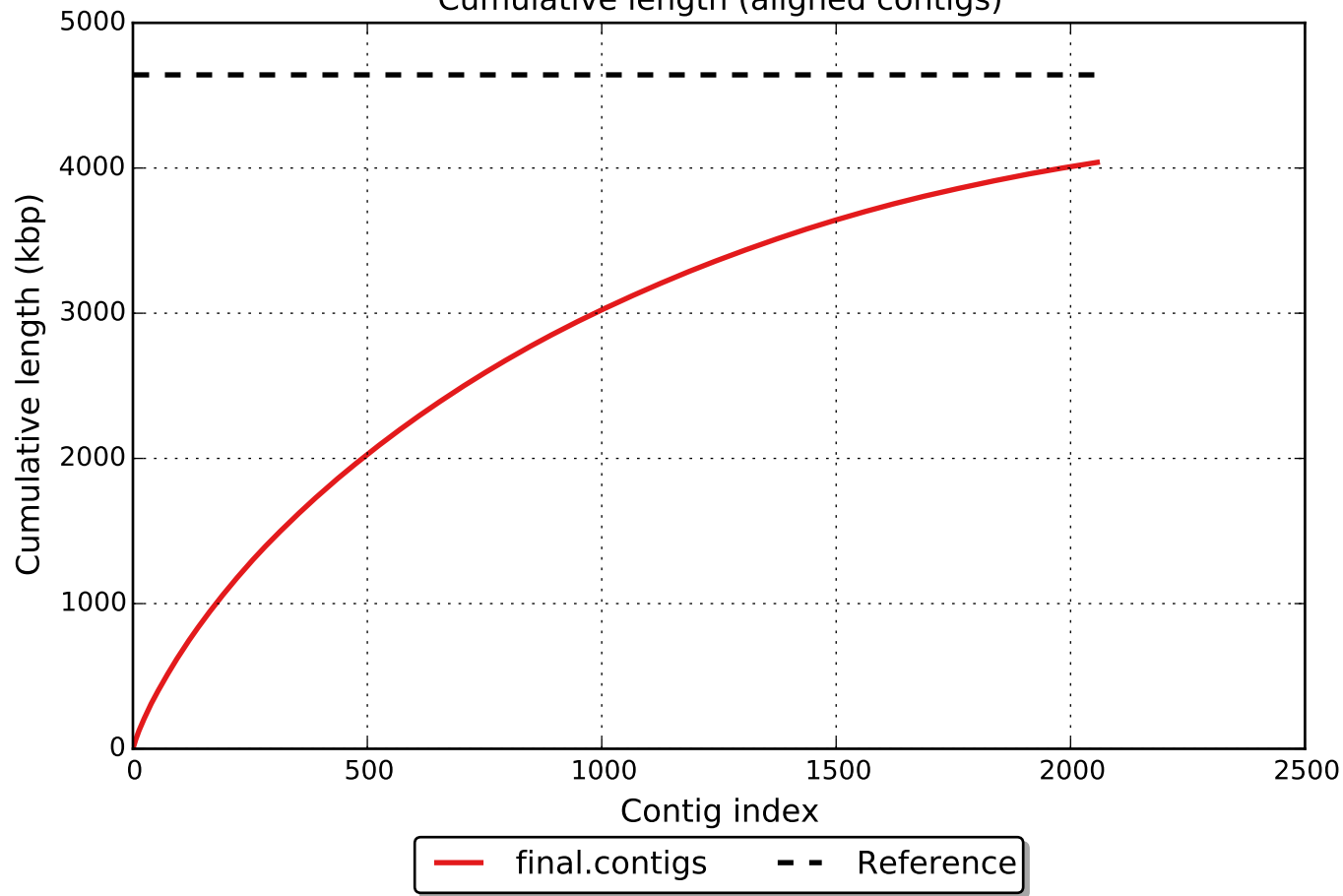


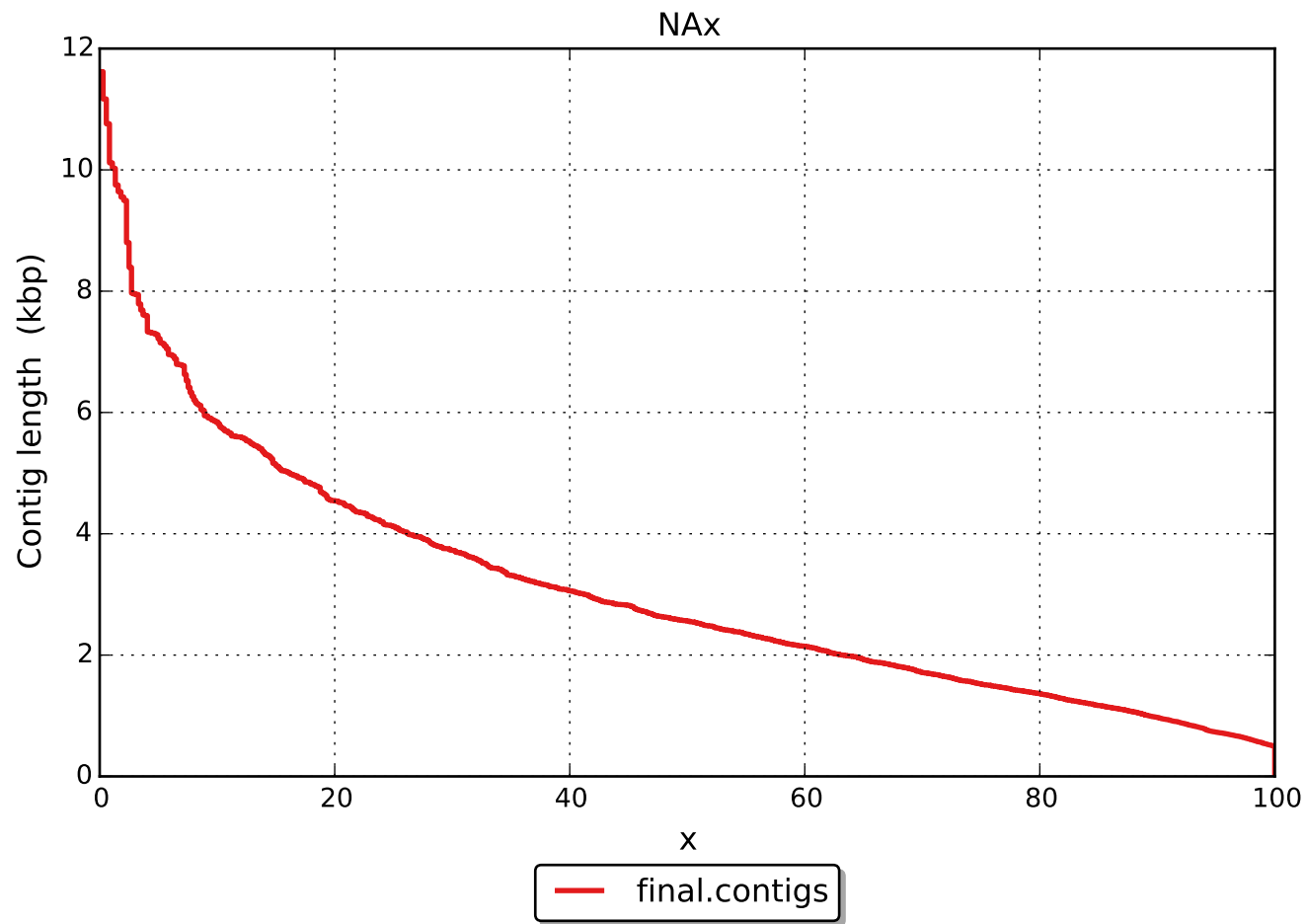
GC content





Cumulative length (aligned contigs)





NGAx

