Report

	final.contigs
# contigs (>= 1000 bp)	1385
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	2180703
Total length (>= 5000 bp)	6977
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3975
Largest contig	6977
Total length	4004161
Reference length	4641652
GC (%)	50.71
Reference GC (%)	50.79
N50	1067
NG50	950
N75	746
NG75	627
L50	1213
LG50	1529
L75	2343
LG75	3042
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	80.355
Duplication ratio	1.074
# N's per 100 kbp	0.00
# mismatches per 100 kbp	367.23
# indels per 100 kbp	0.16
Largest alignment	6977
NA50	1067
NGA50	950
NA75	746
NGA75	627
LA50	1213
LGA50	1529
LA75	2343
LGA75	3042

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

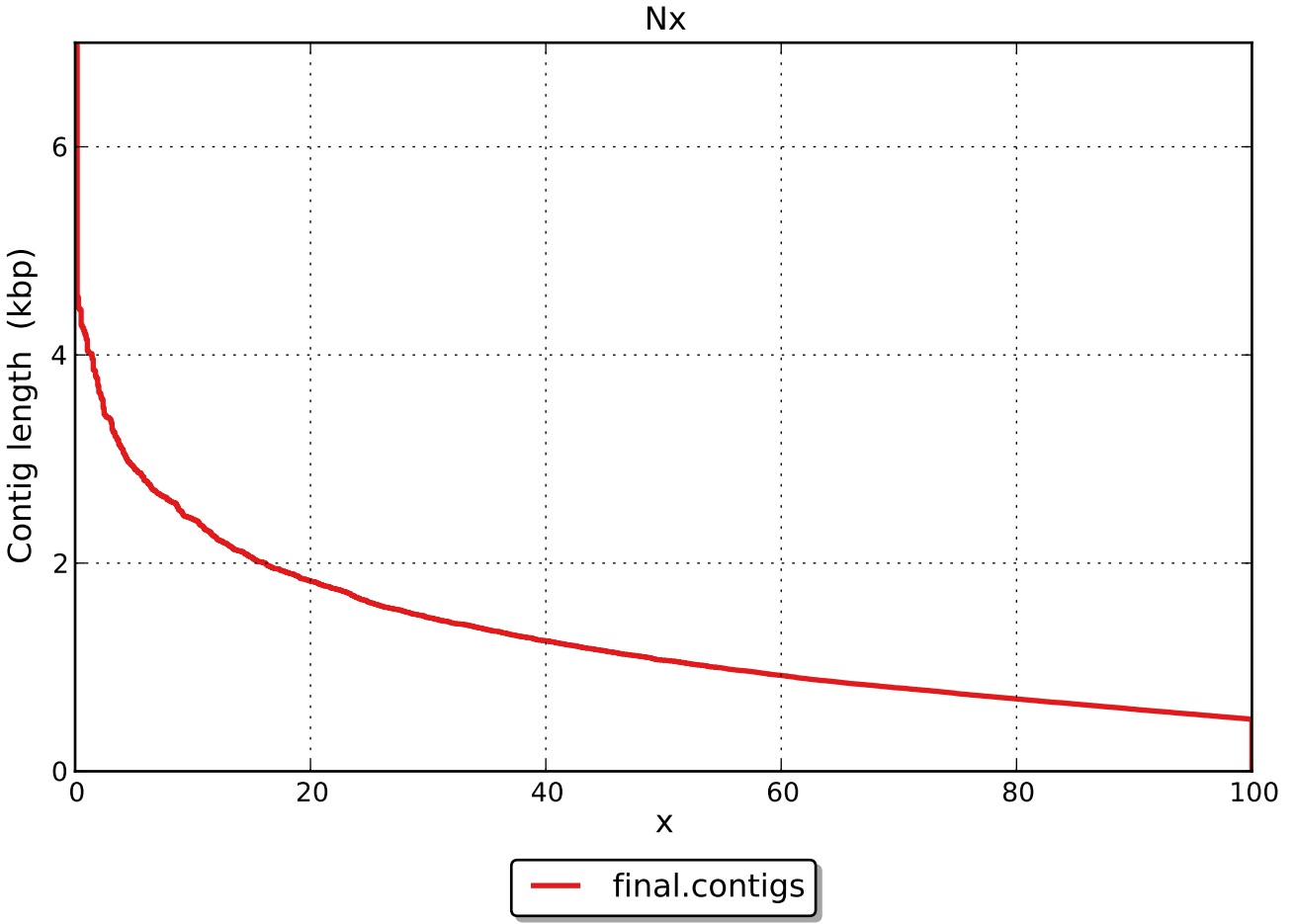
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	13697
# indels	6
# short indels	6
# long indels	0
Indels length	6

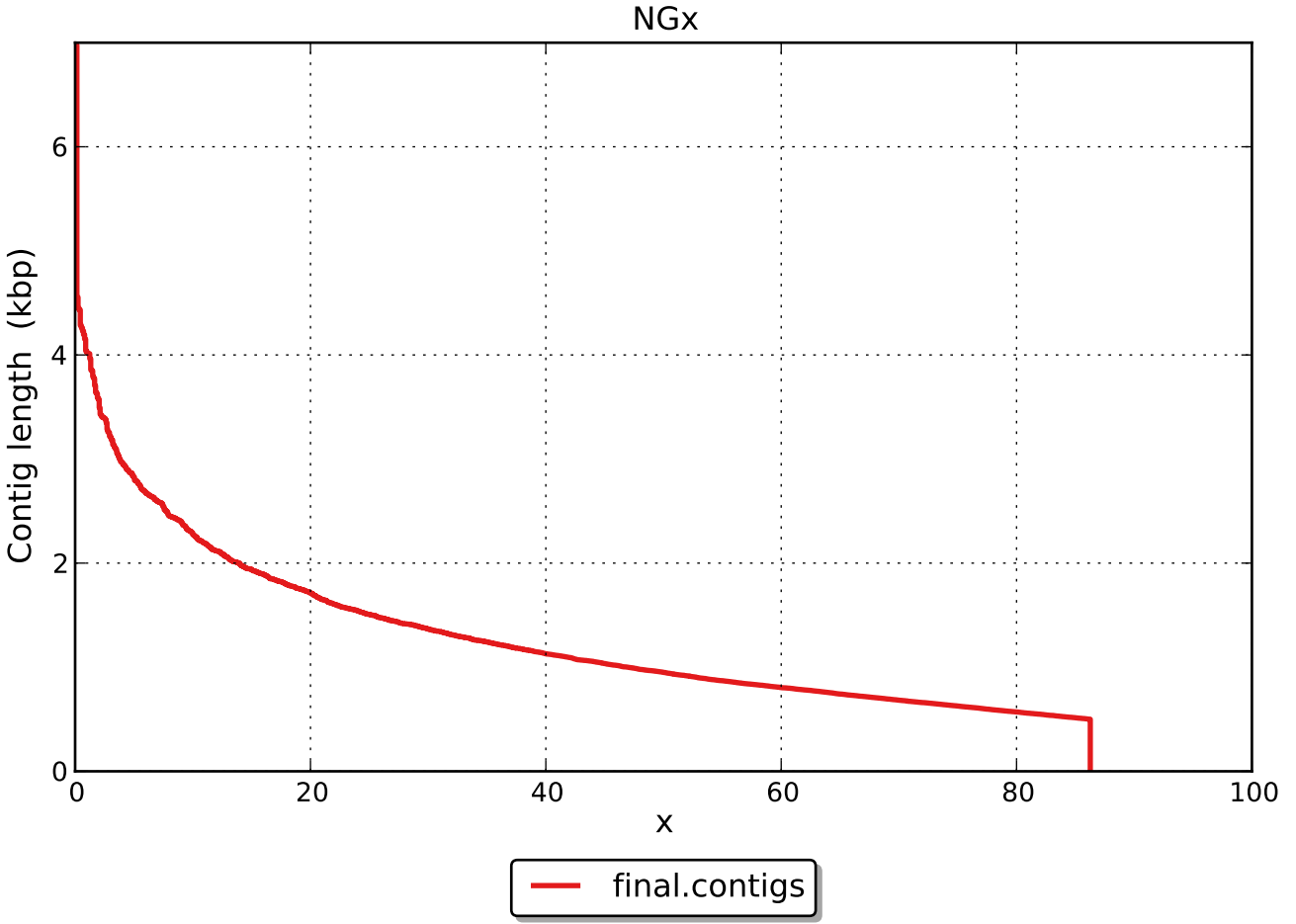
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

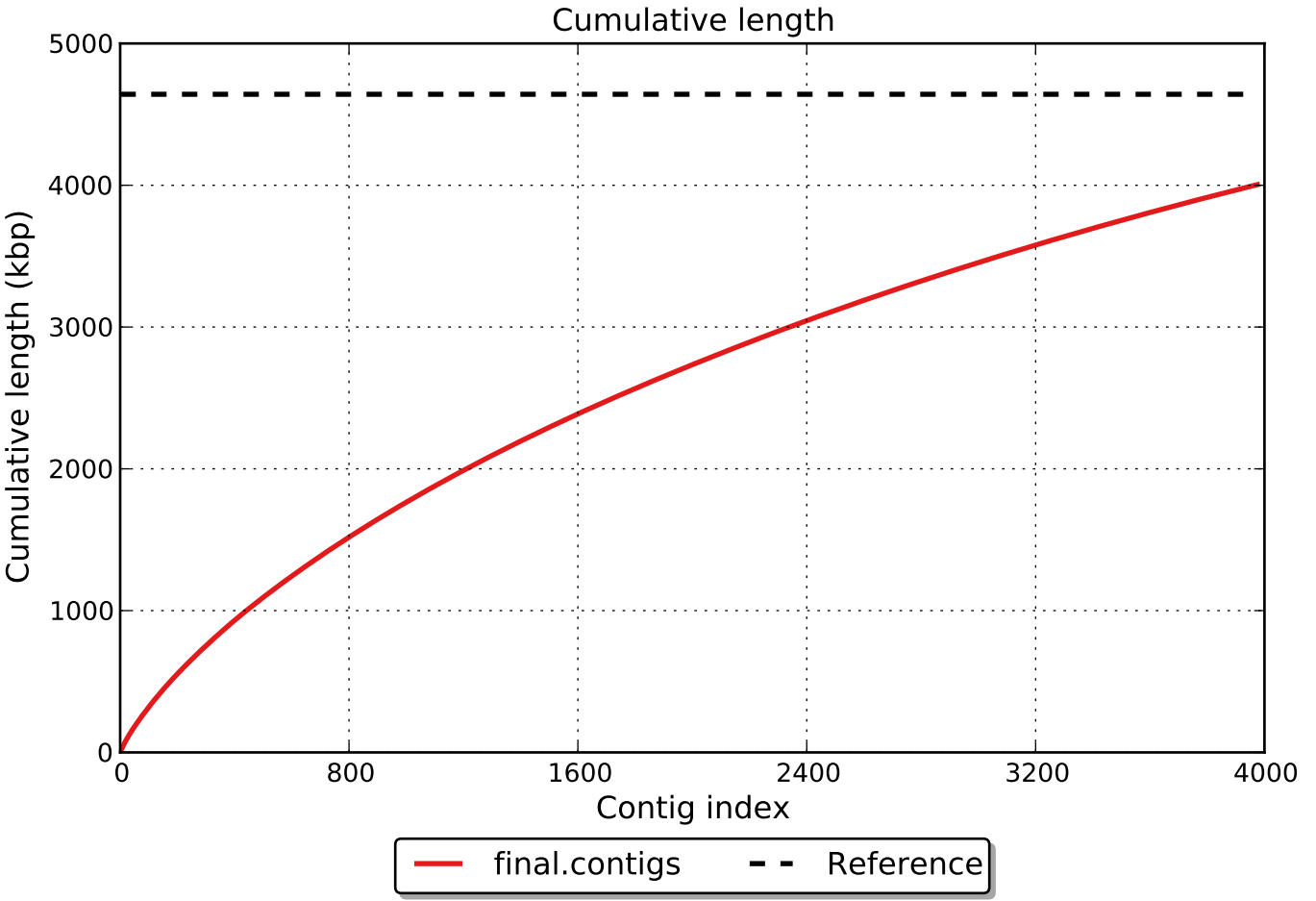
Unaligned report

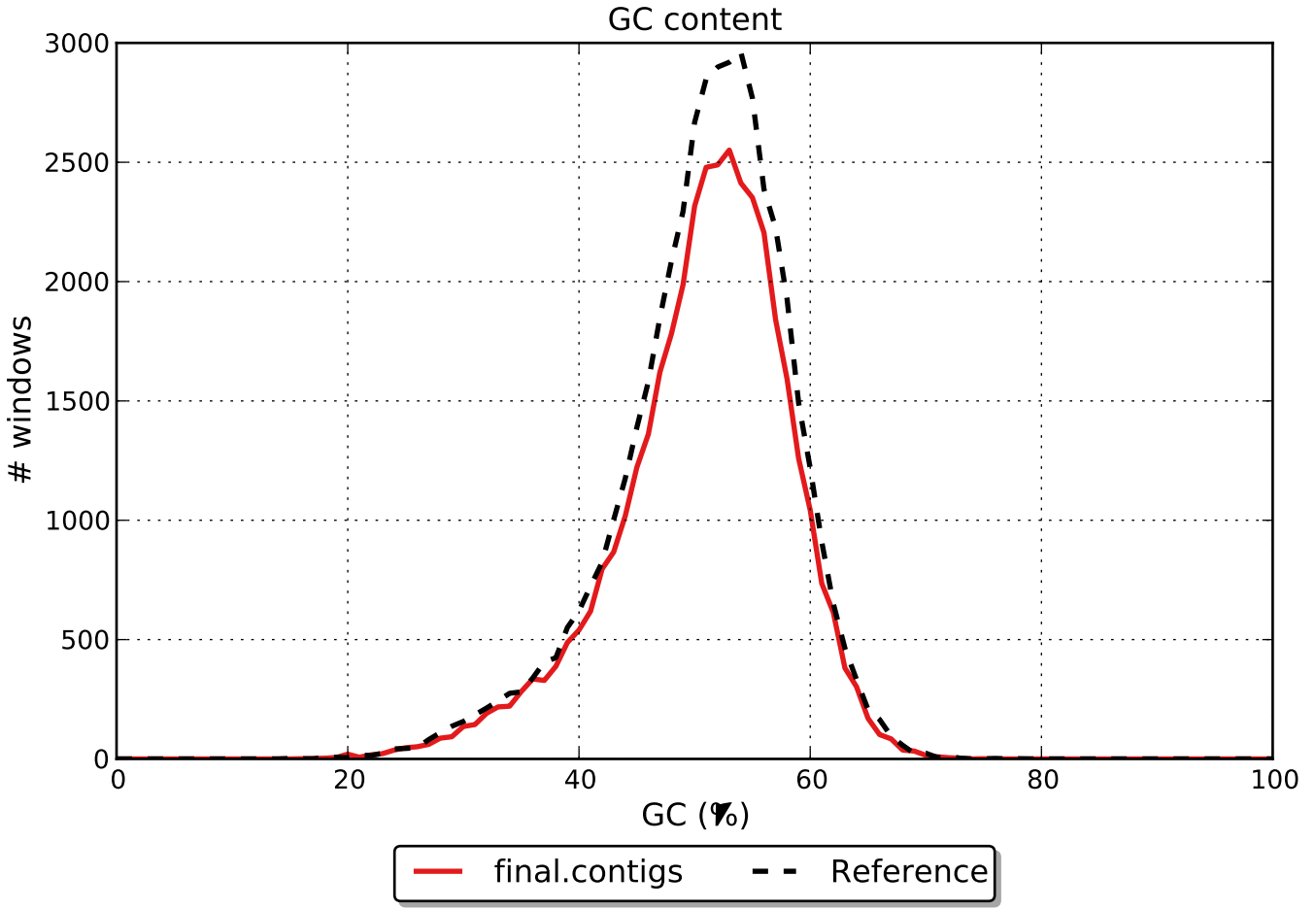
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

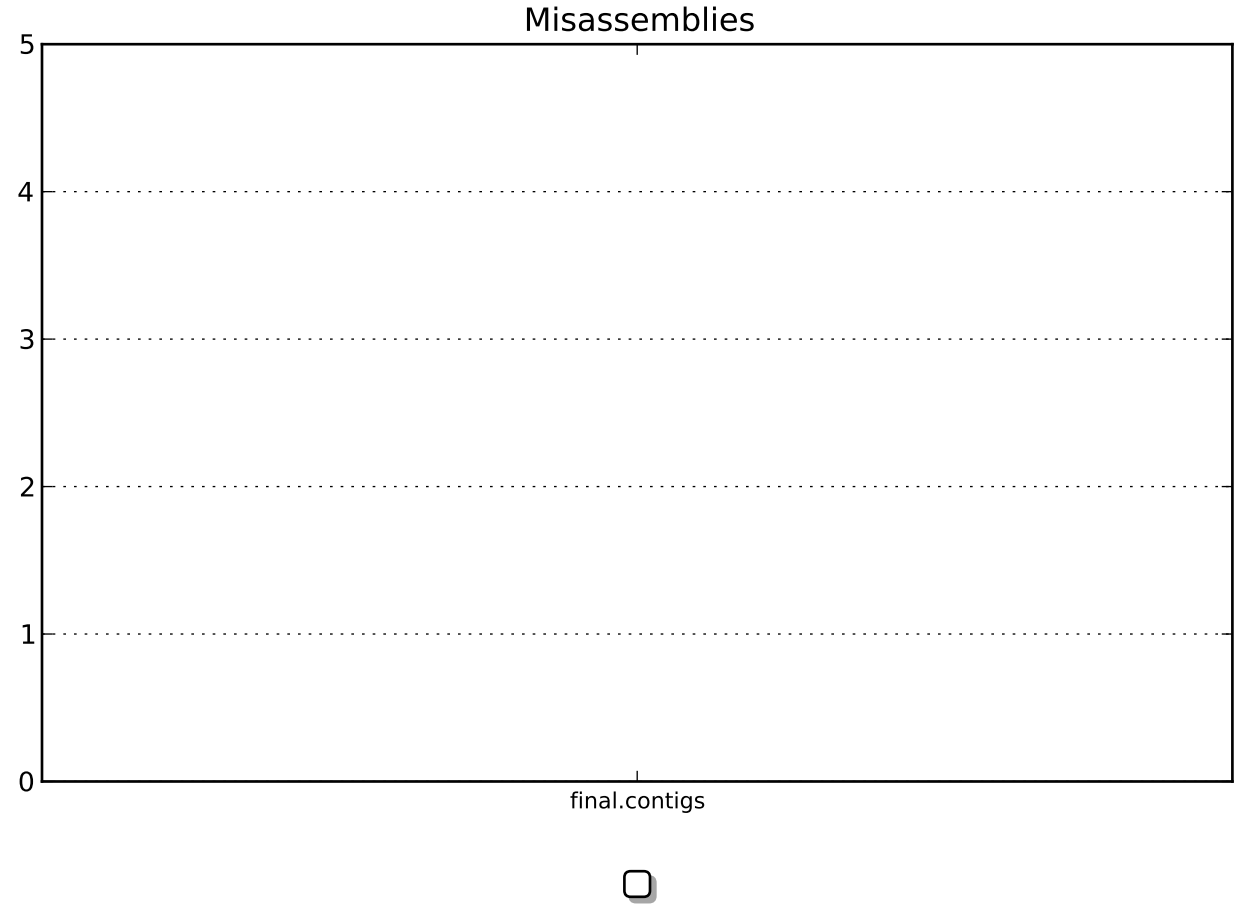
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

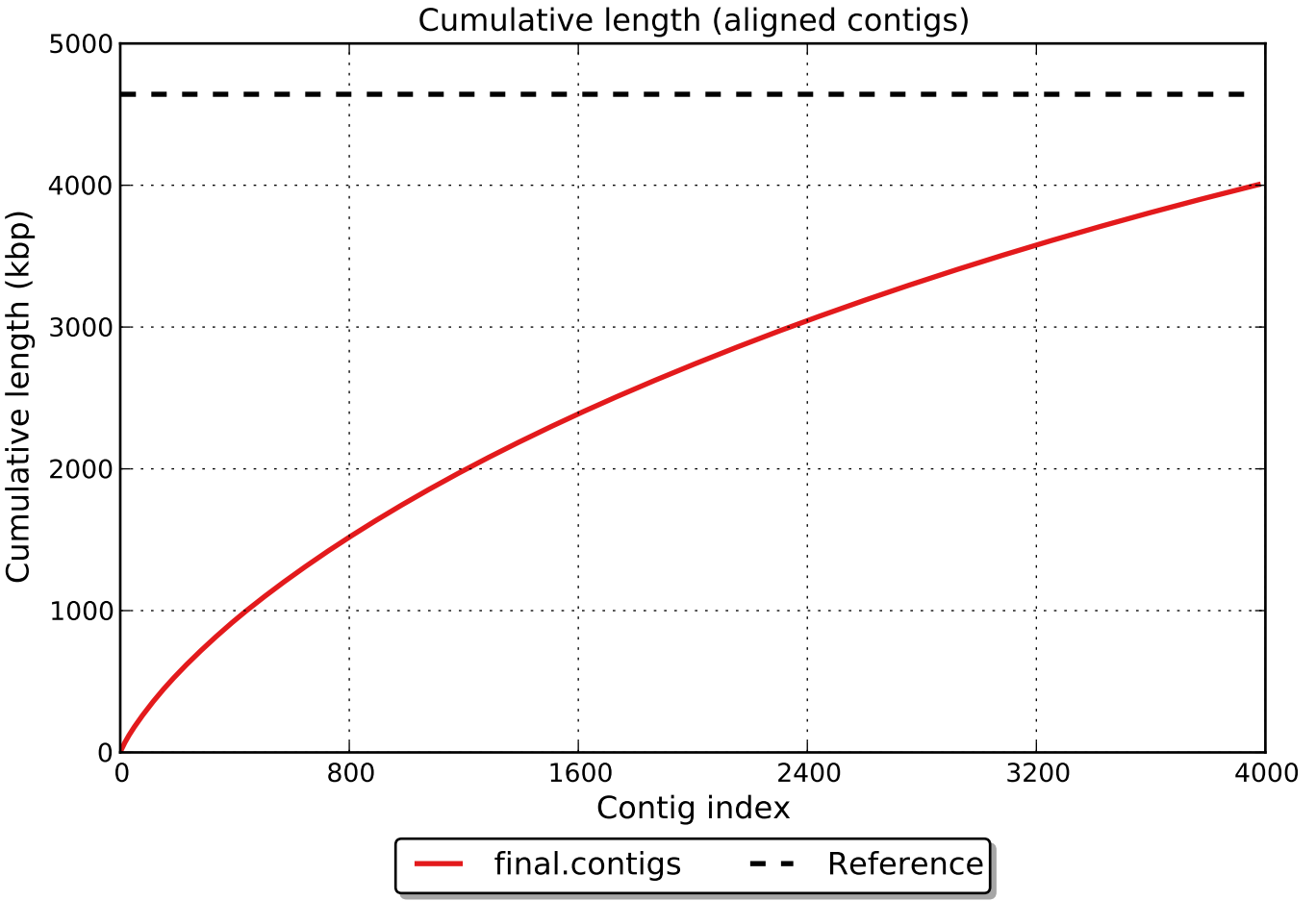

Nx
Contig length (kbp)
0
2
4
6
0
20
40
60
80
100
x
final.contigs

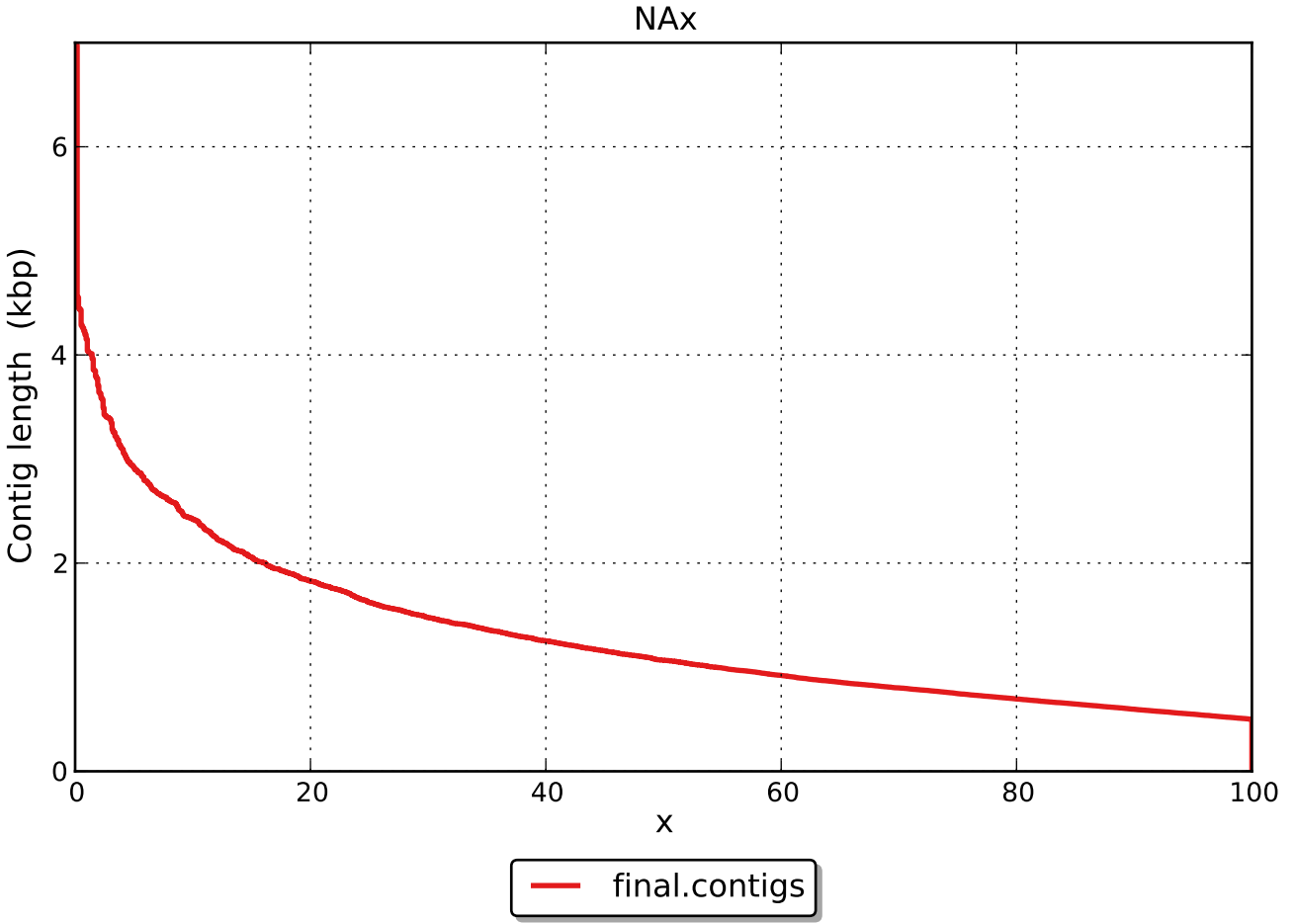

NGx
Contig length (kbp)
0
2
4
6
0
20
40
60
80
100
x
final.contigs

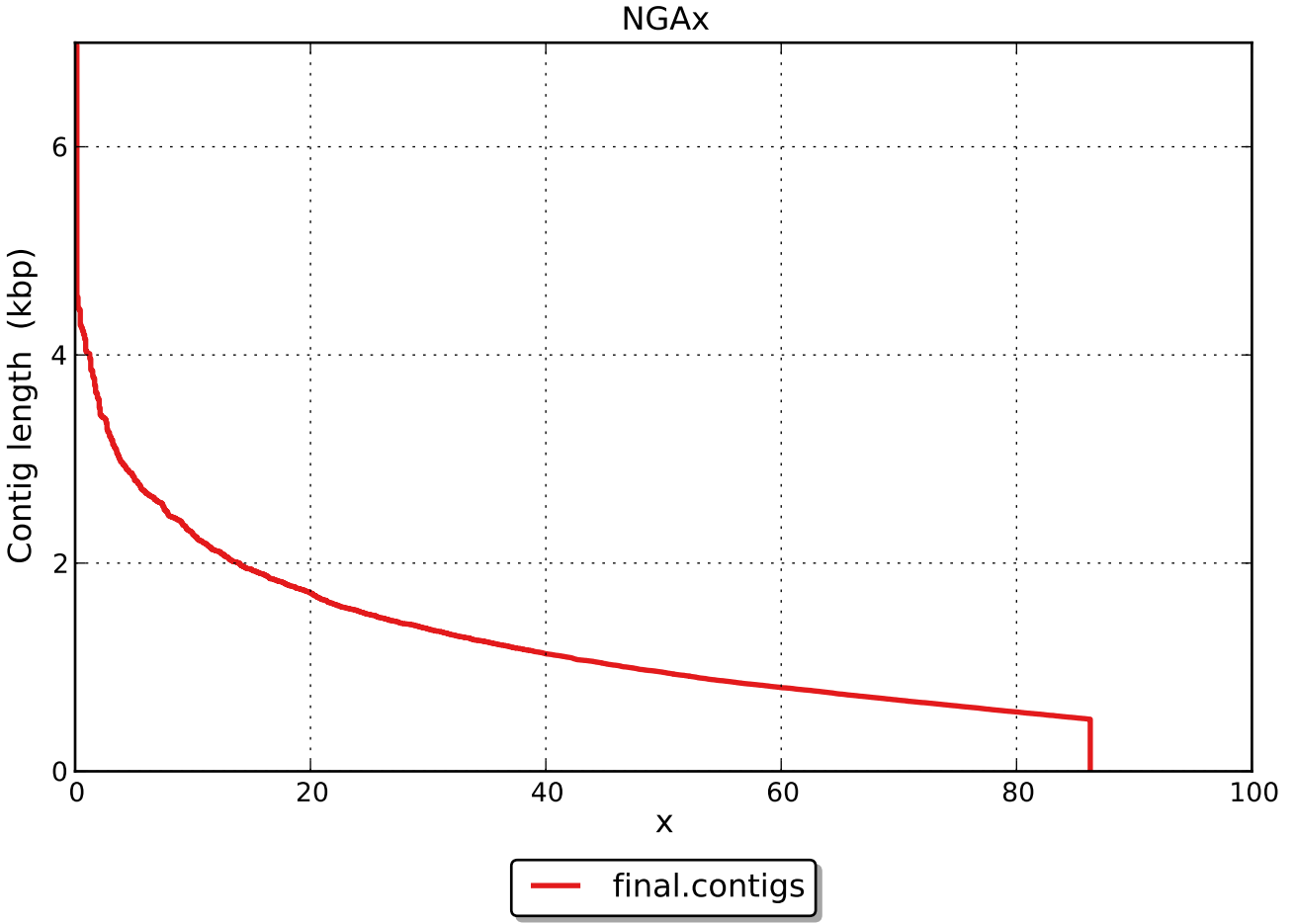

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
800
1600
2400
3200
4000
Contig index
final.contigs
Reference


GC content
3000
2500
2000
1500
1000
500
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference


Misassemblies
5
4
3
2
1
0
final.contigs


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
800
1600
2400
3200
4000
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
0
2
4
6
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
0
2
4
6
0
20
40
60
80
100
x
final.contigs