Report

	final.contigs
# contigs (>= 1000 bp)	1448
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	2261311
Total length (>= 5000 bp)	16039
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	4259
Largest contig	5668
Total length	4231276
Reference length	4857432
GC (%)	52.22
Reference GC (%)	52.22
N50	1054
NG50	944
N75	738
NG75	623
L50	1306
LG50	1621
L75	2517
LG75	3210
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	81.031
Duplication ratio	1.075
# N's per 100 kbp	0.00
# mismatches per 100 kbp	354.88
# indels per 100 kbp	0.10
Largest alignment	5668
NA50	1054
NGA50	944
NA75	738
NGA75	623
LA50	1306
LGA50	1621
LA75	2517
LGA75	3210

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

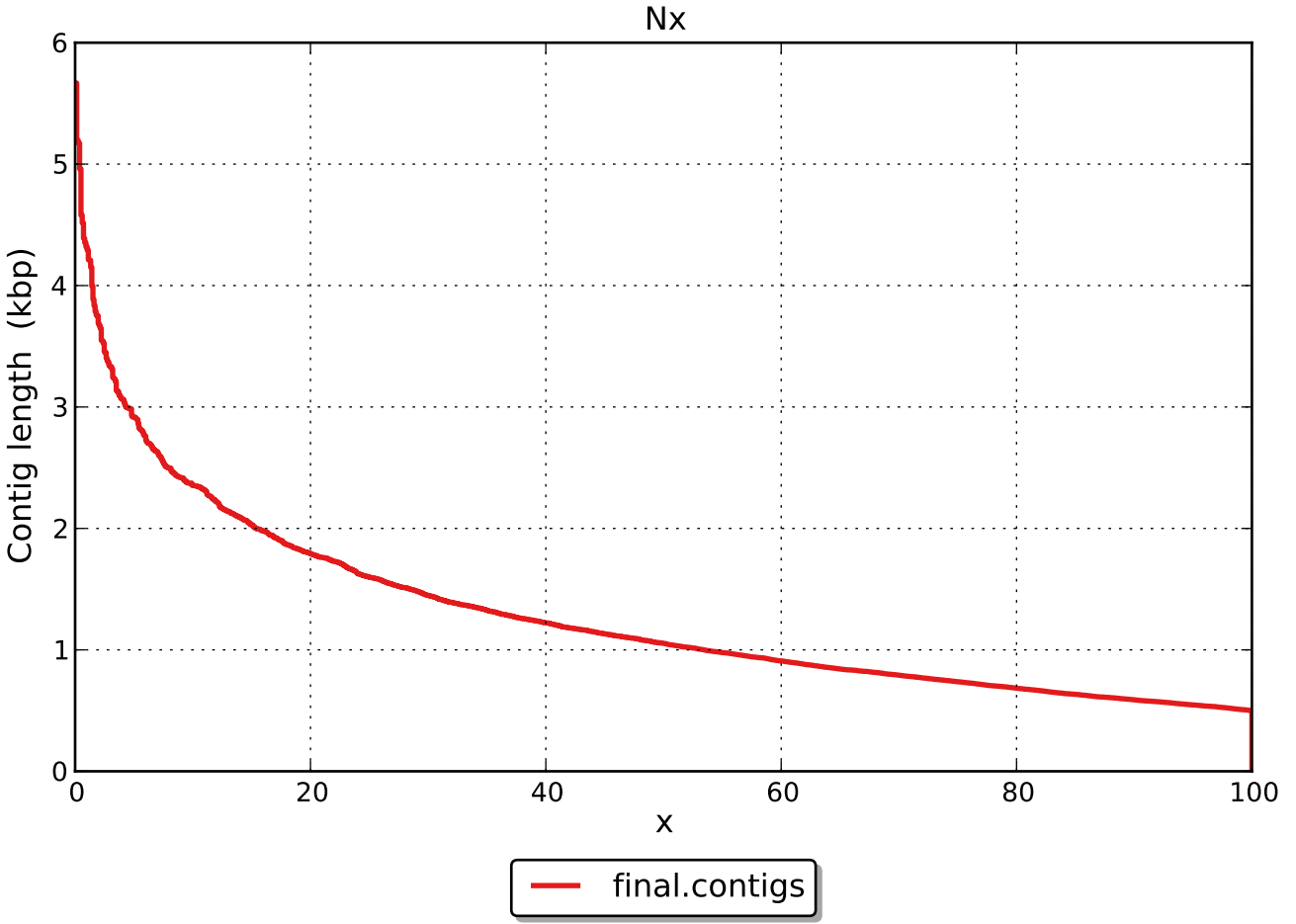
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	13968
# indels	4
# short indels	4
# long indels	0
Indels length	4

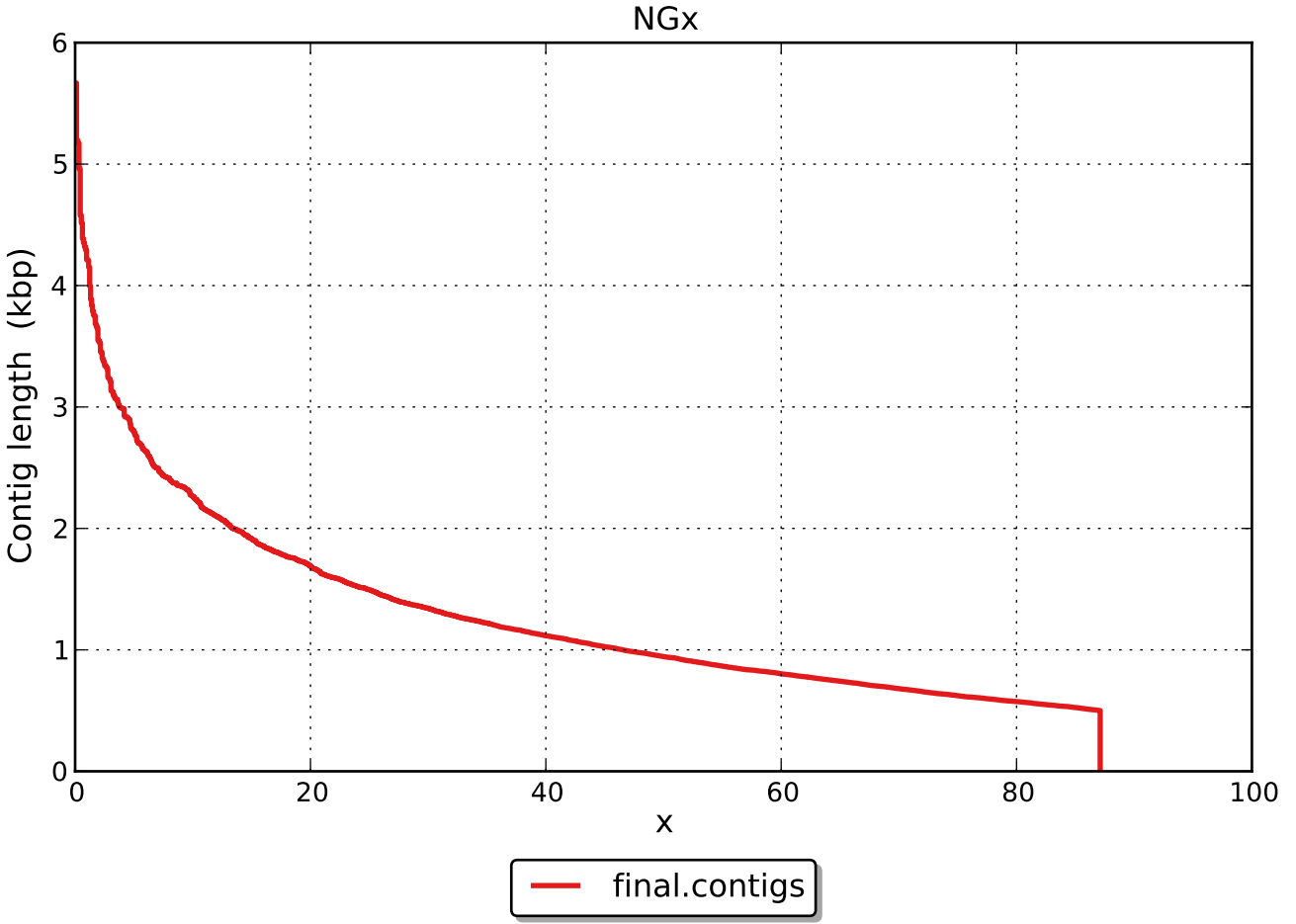
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

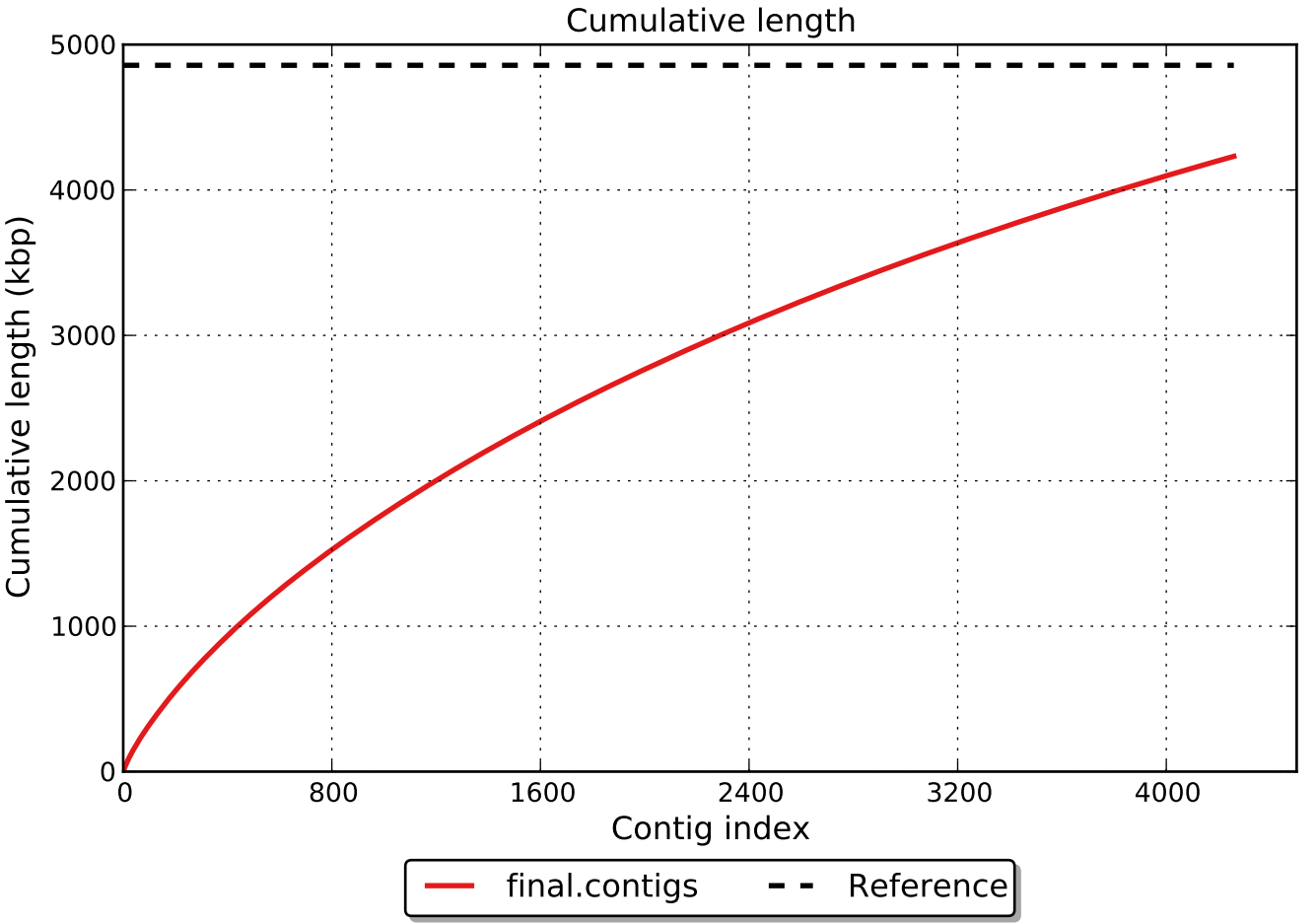
Unaligned report

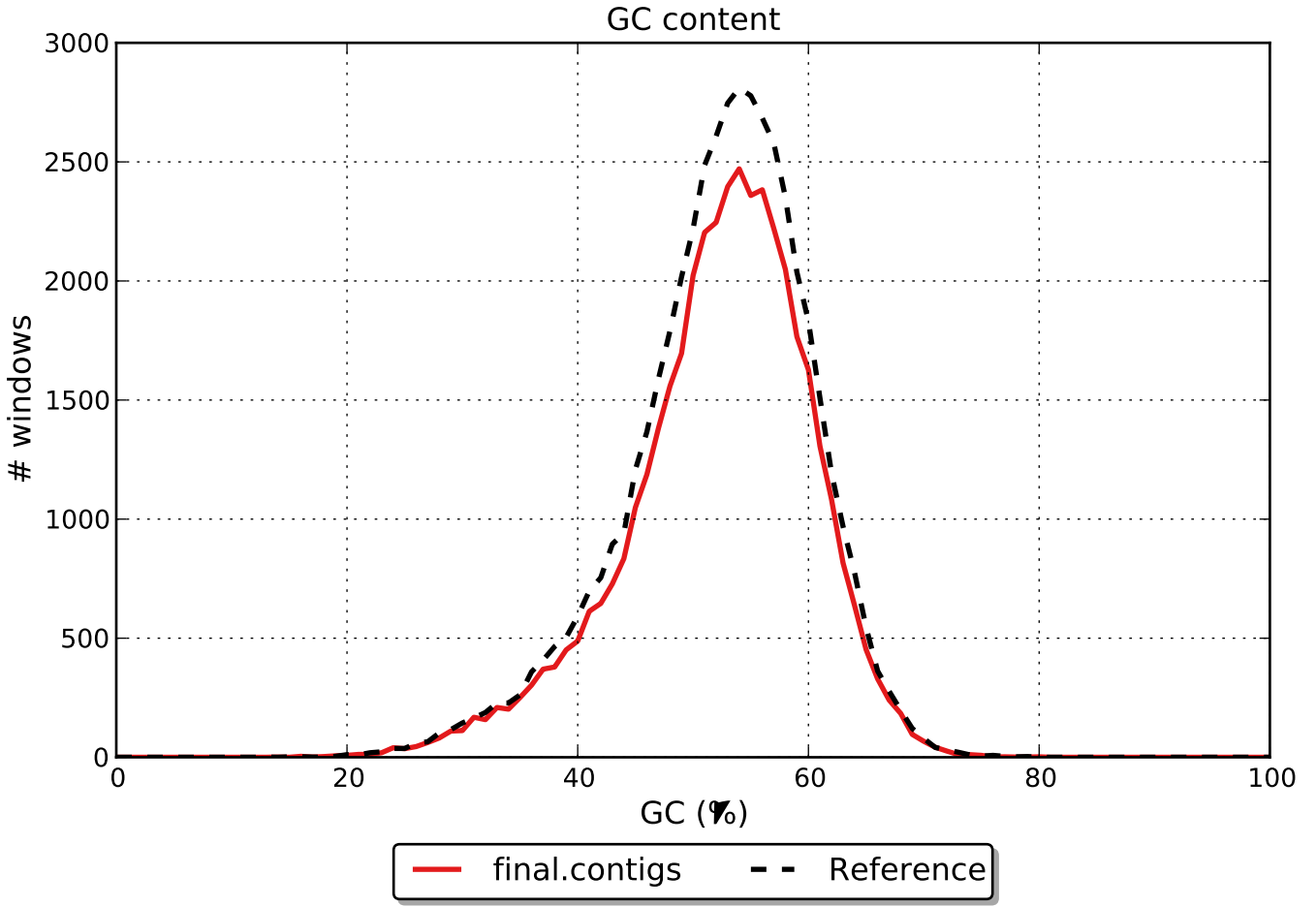
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

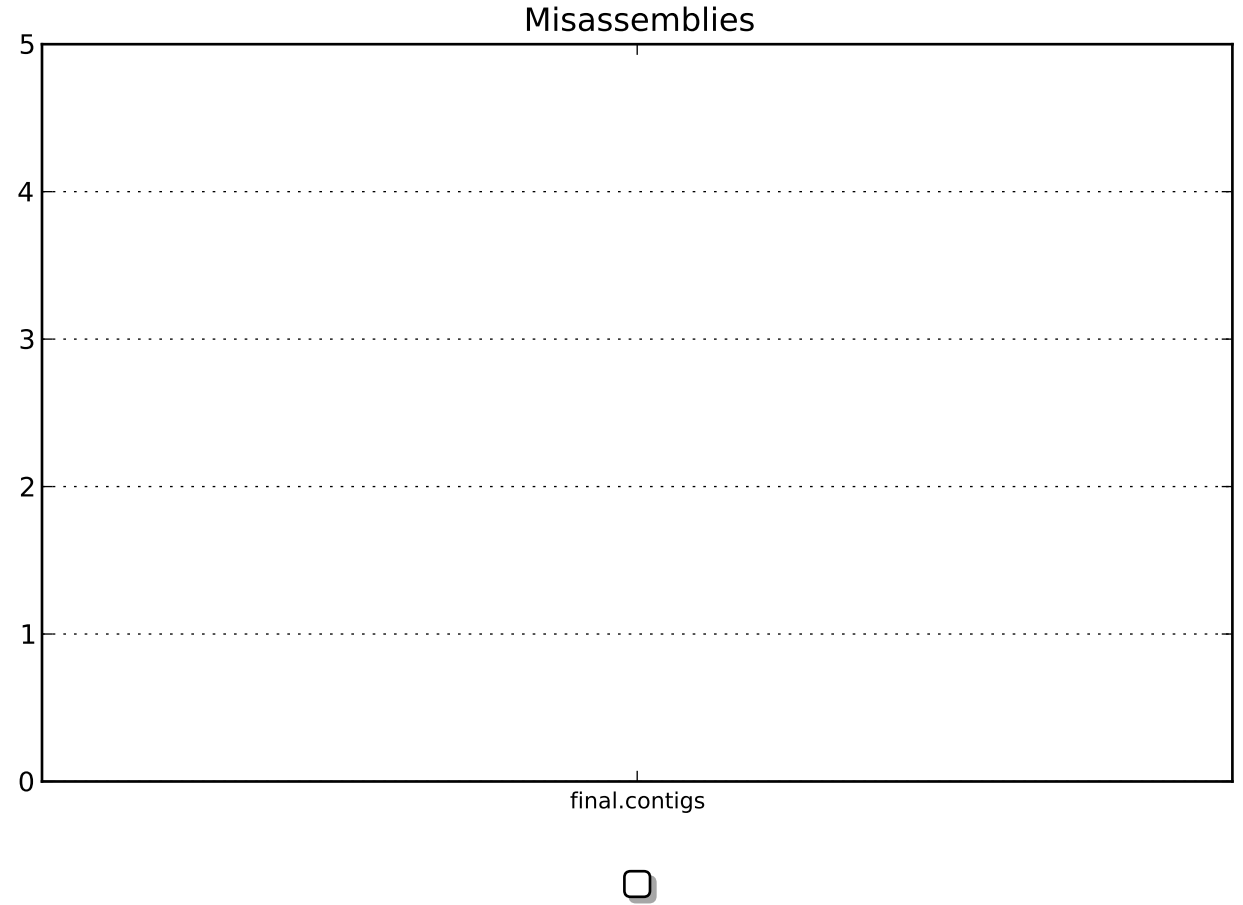
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

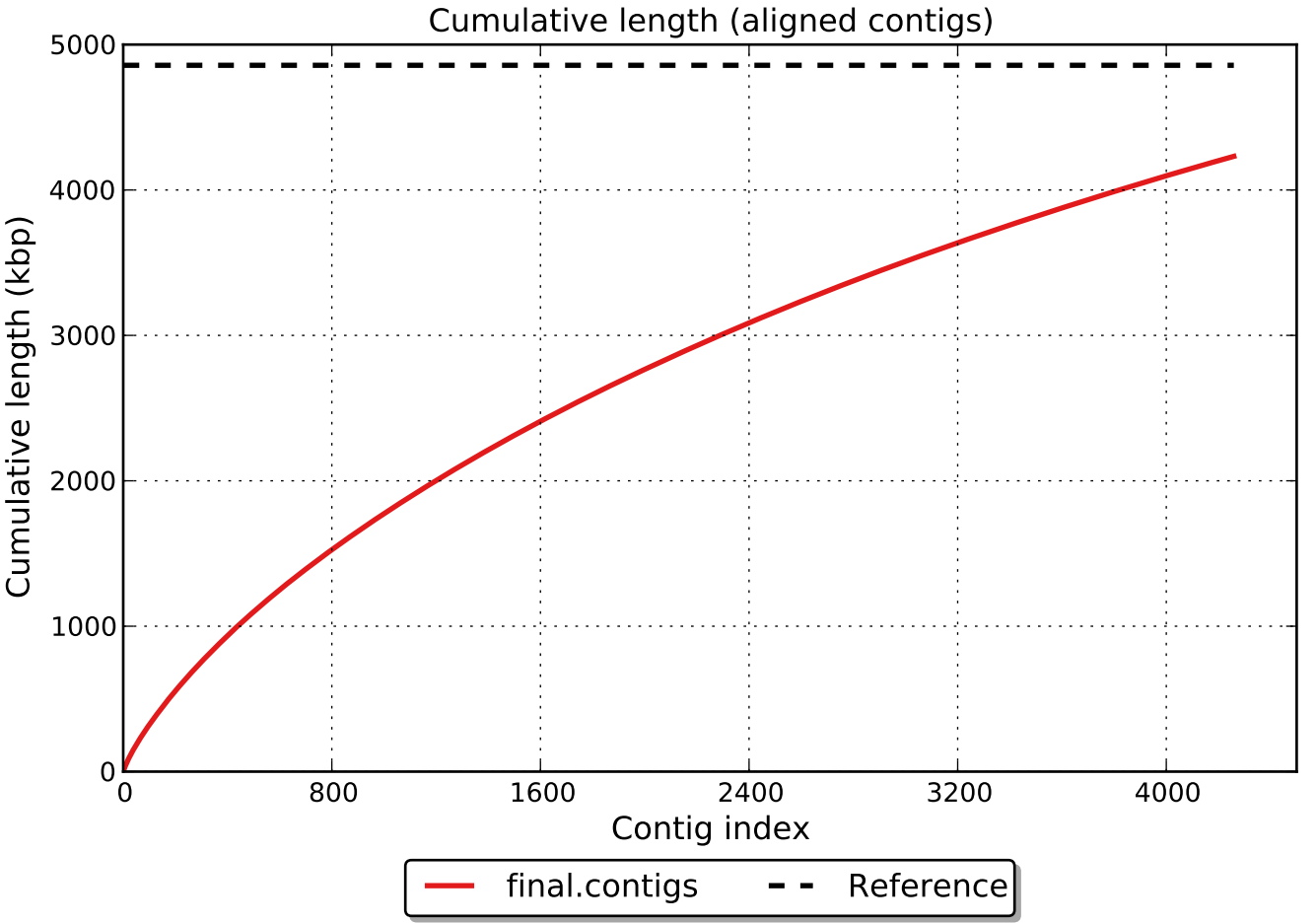

Nx
Contig length (kbp)
0
1
2
3
4
5
6
0
20
40
60
80
100
x
final.contigs

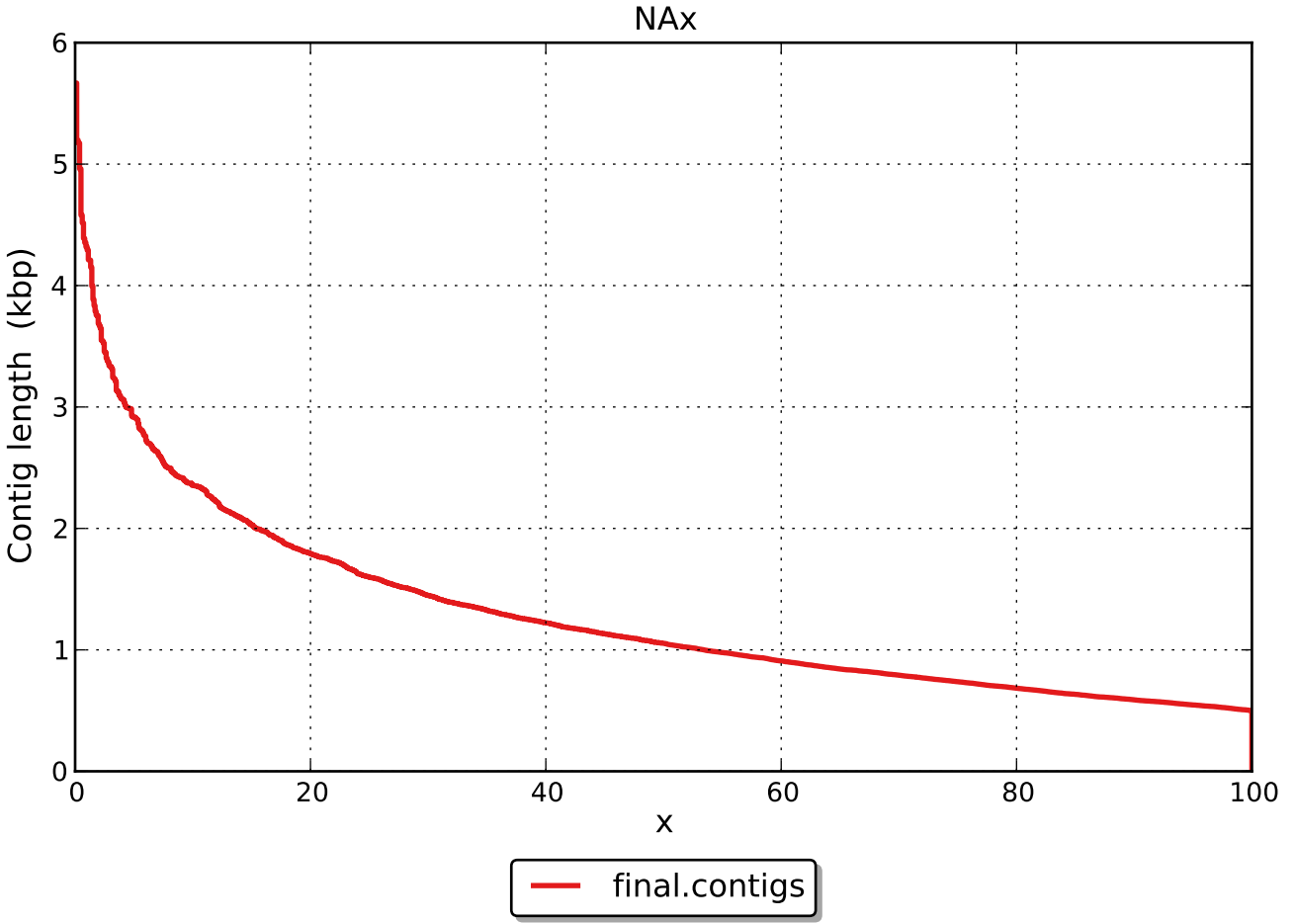

NGx
Contig length (kbp)
0
1
2
3
4
5
6
0
20
40
60
80
100
x
final.contigs

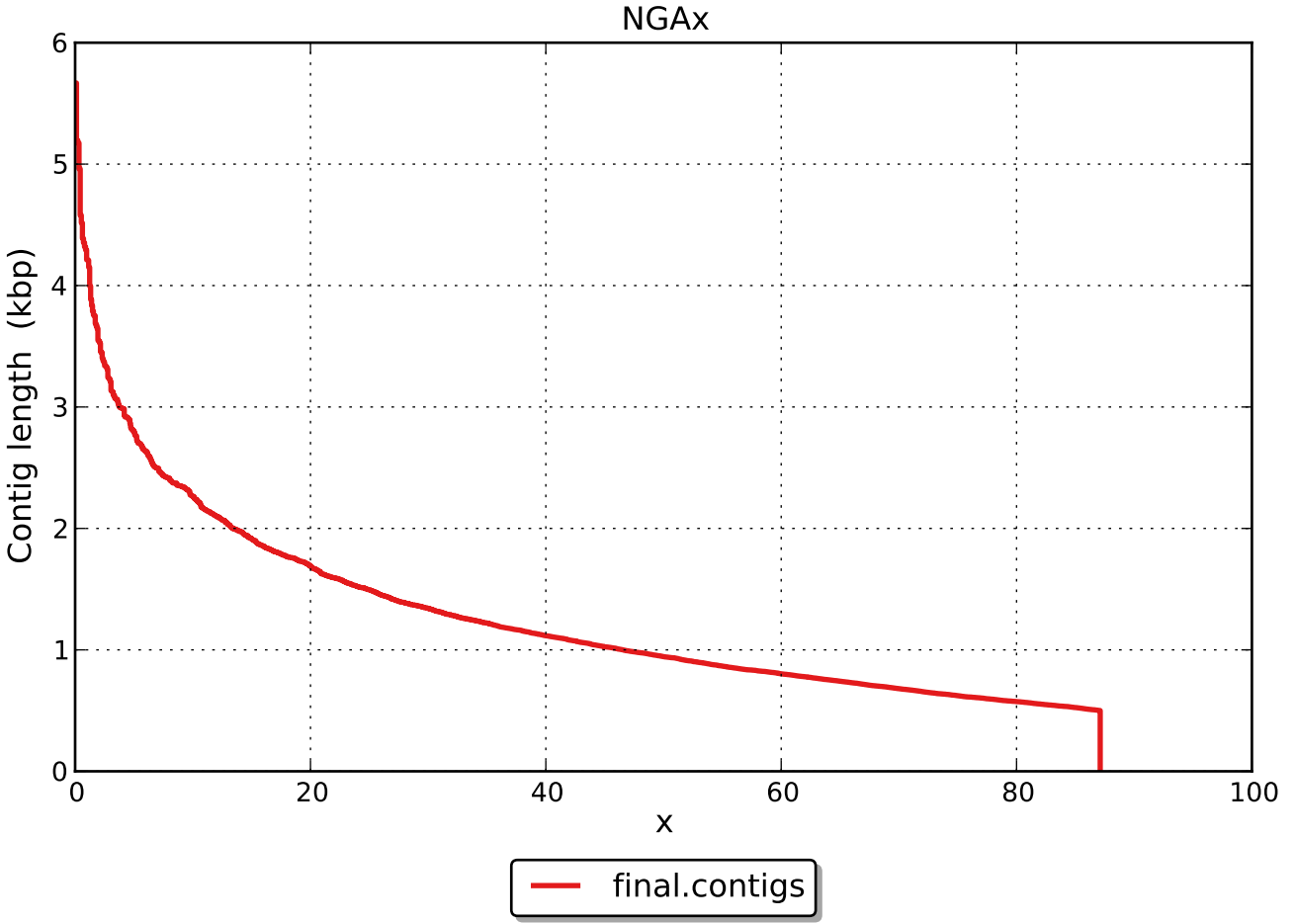

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
800
1600
2400
3200
4000
Contig index
final.contigs
Reference


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)
x
0
1
2
3
4
5
6
0
20
40
60
80
100
final.contigs


NGAx
Contig length (kbp)
x
0
1
2
3
4
5
6
0
20
40
60
80
100
final.contigs