Report

	final.contigs
# contigs (>= 1000 bp)	1383
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	2195389
Total length (>= 5000 bp)	6977
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	4018
Largest contig	6977
Total length	4049564
Reference length	4641652
GC (%)	50.76
Reference GC (%)	50.79
N50	1063
NG50	949
N75	747
NG75	635
L50	1218
LG50	1512
L75	2367
LG75	3013
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	81.178
Duplication ratio	1.075
# N's per 100 kbp	0.00
# mismatches per 100 kbp	362.63
# indels per 100 kbp	0.27
Largest alignment	6977
NA50	1063
NGA50	949
NA75	747
NGA75	635
LA50	1218
LGA50	1512
LA75	2368
LGA75	3013

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

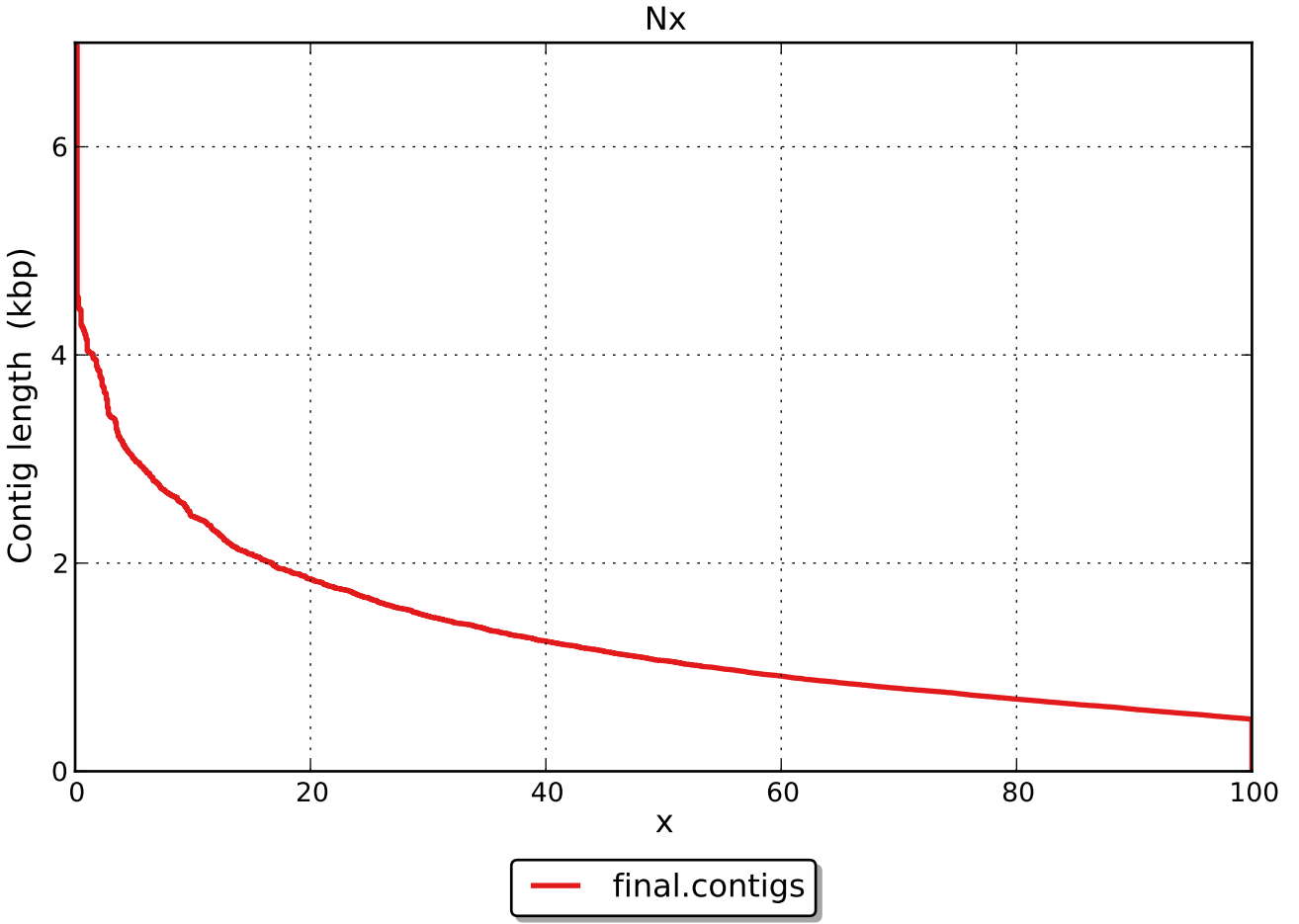
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	13664
# indels	10
# short indels	10
# long indels	0
Indels length	10

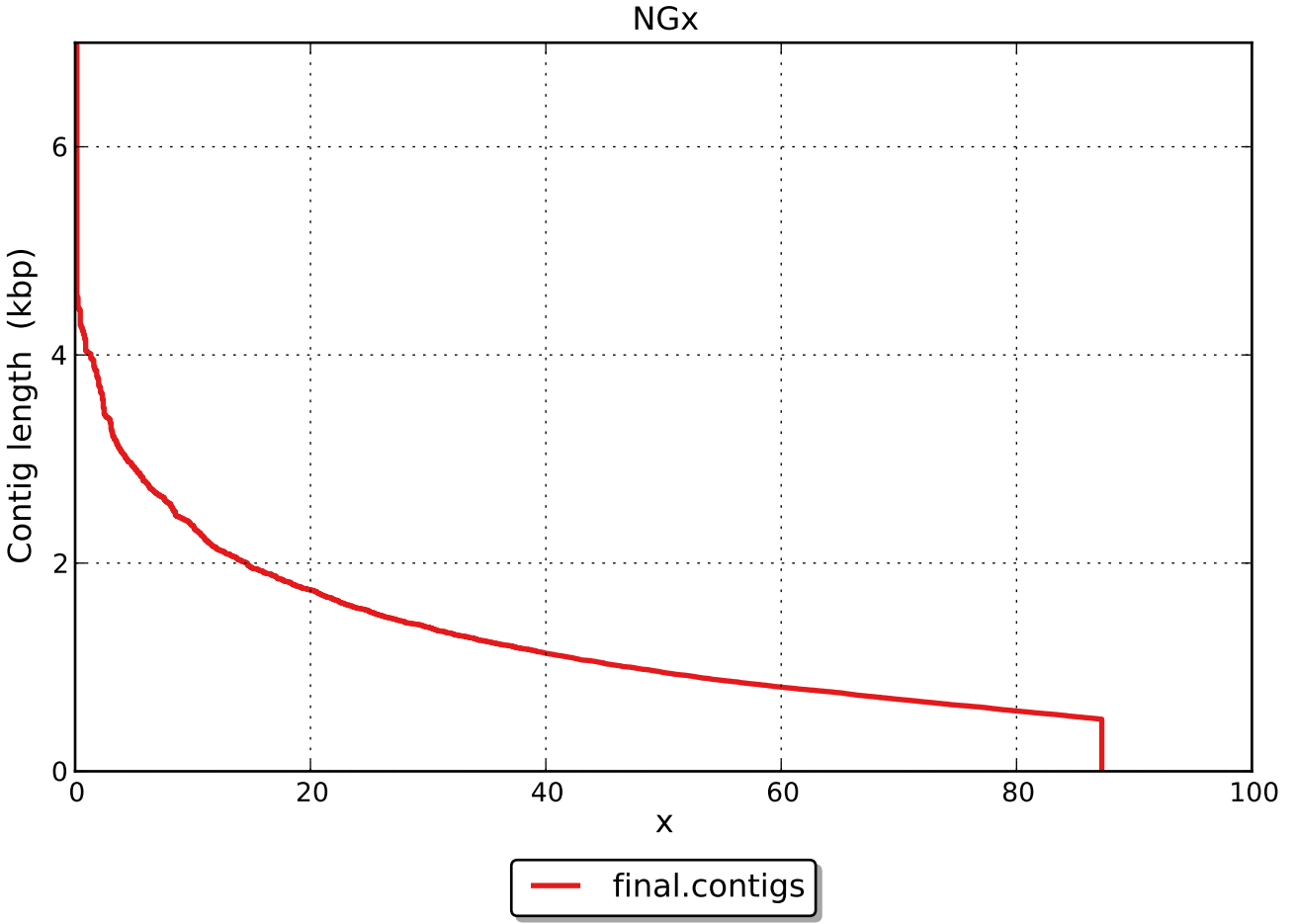
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

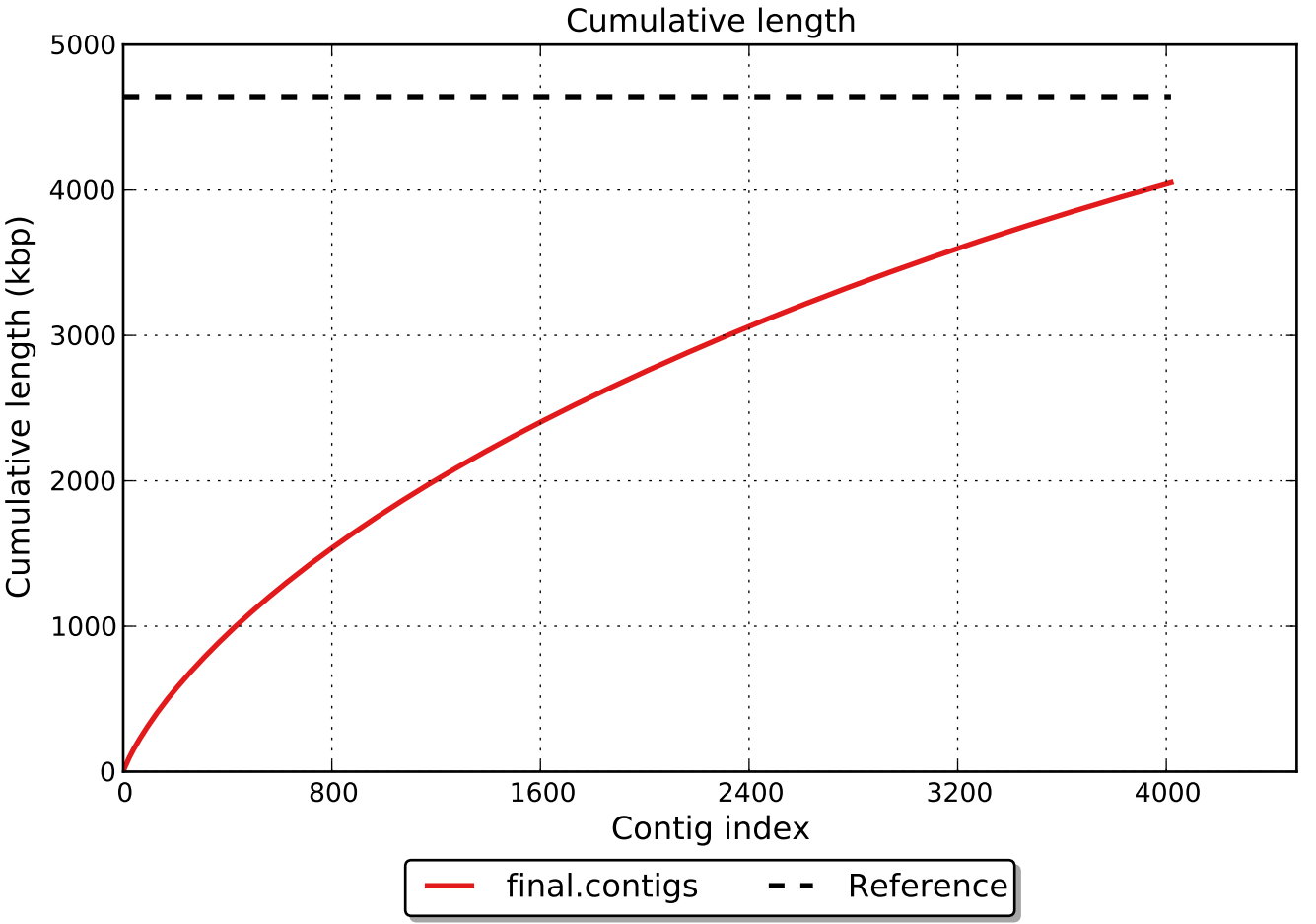
Unaligned report

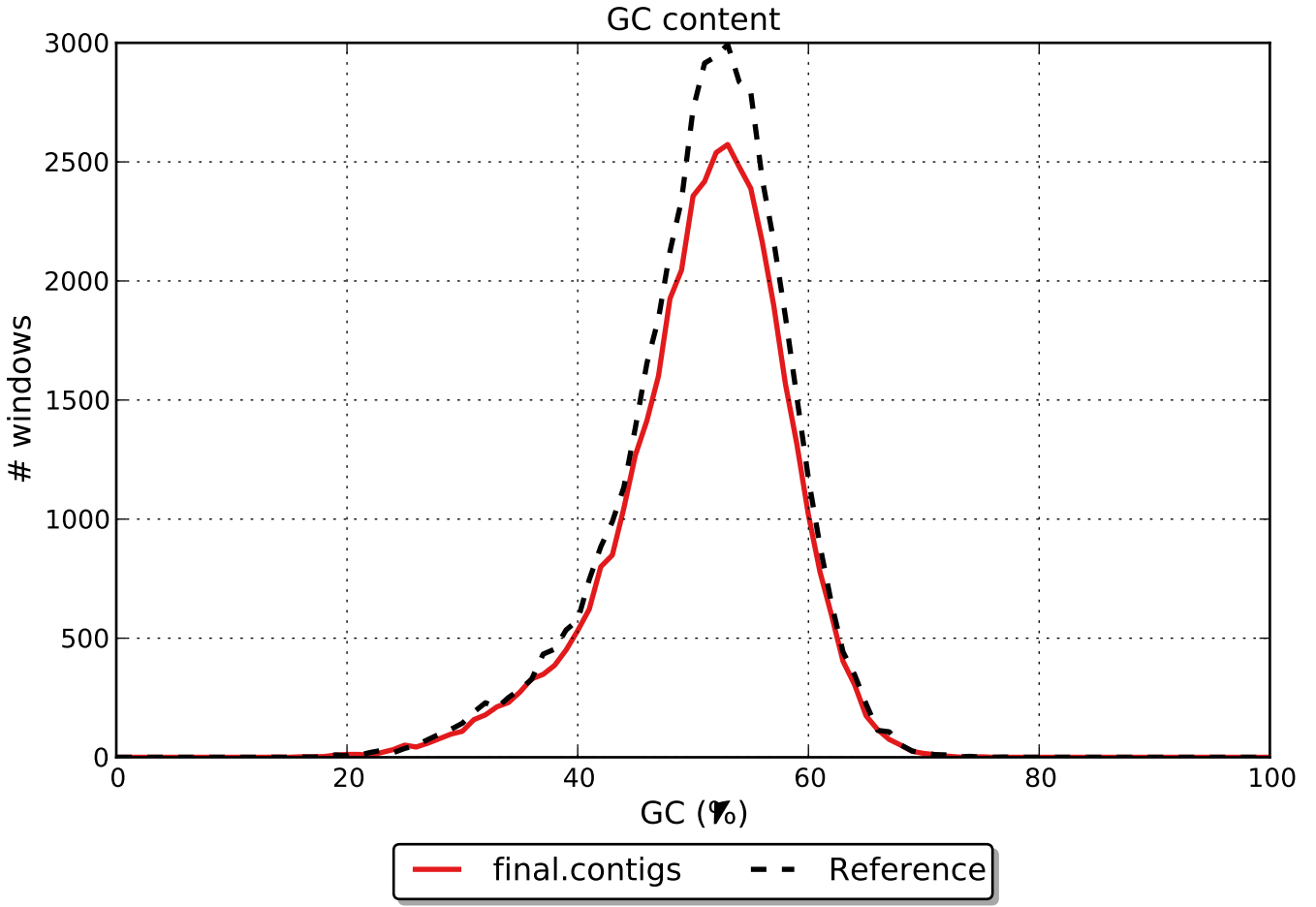
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

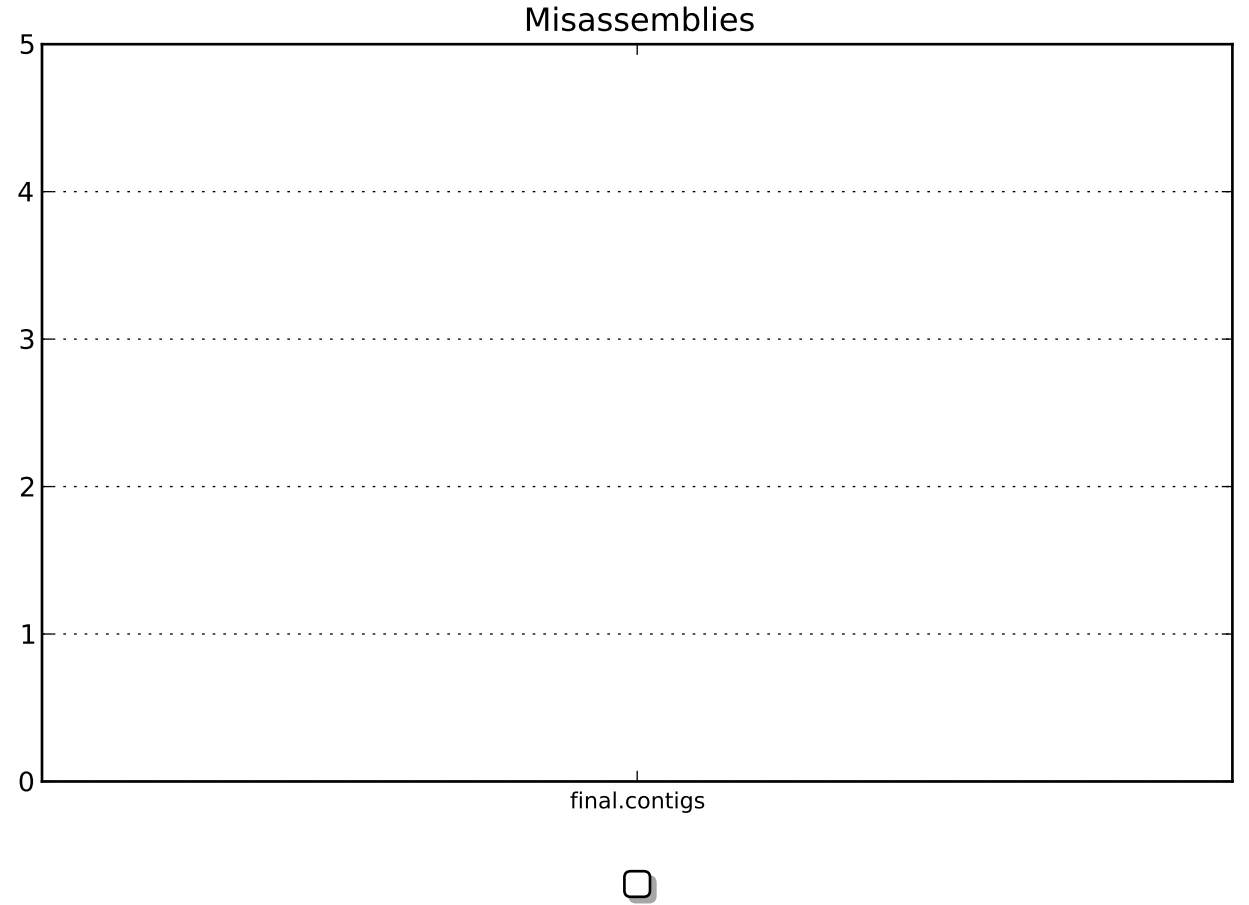
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

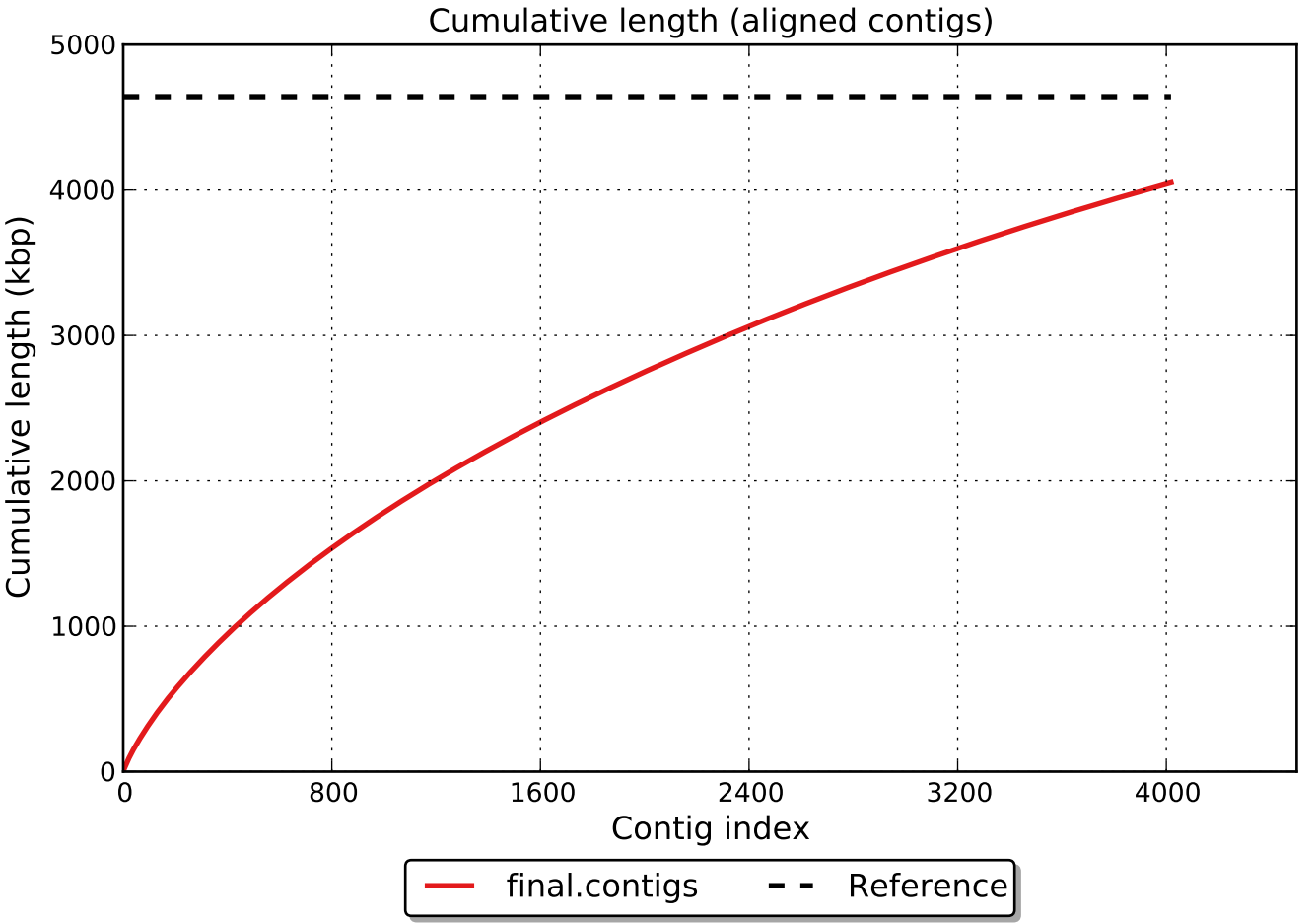

Nx
Contig length (kbp)
0
2
4
6
0
20
40
60
80
100
x
final.contigs

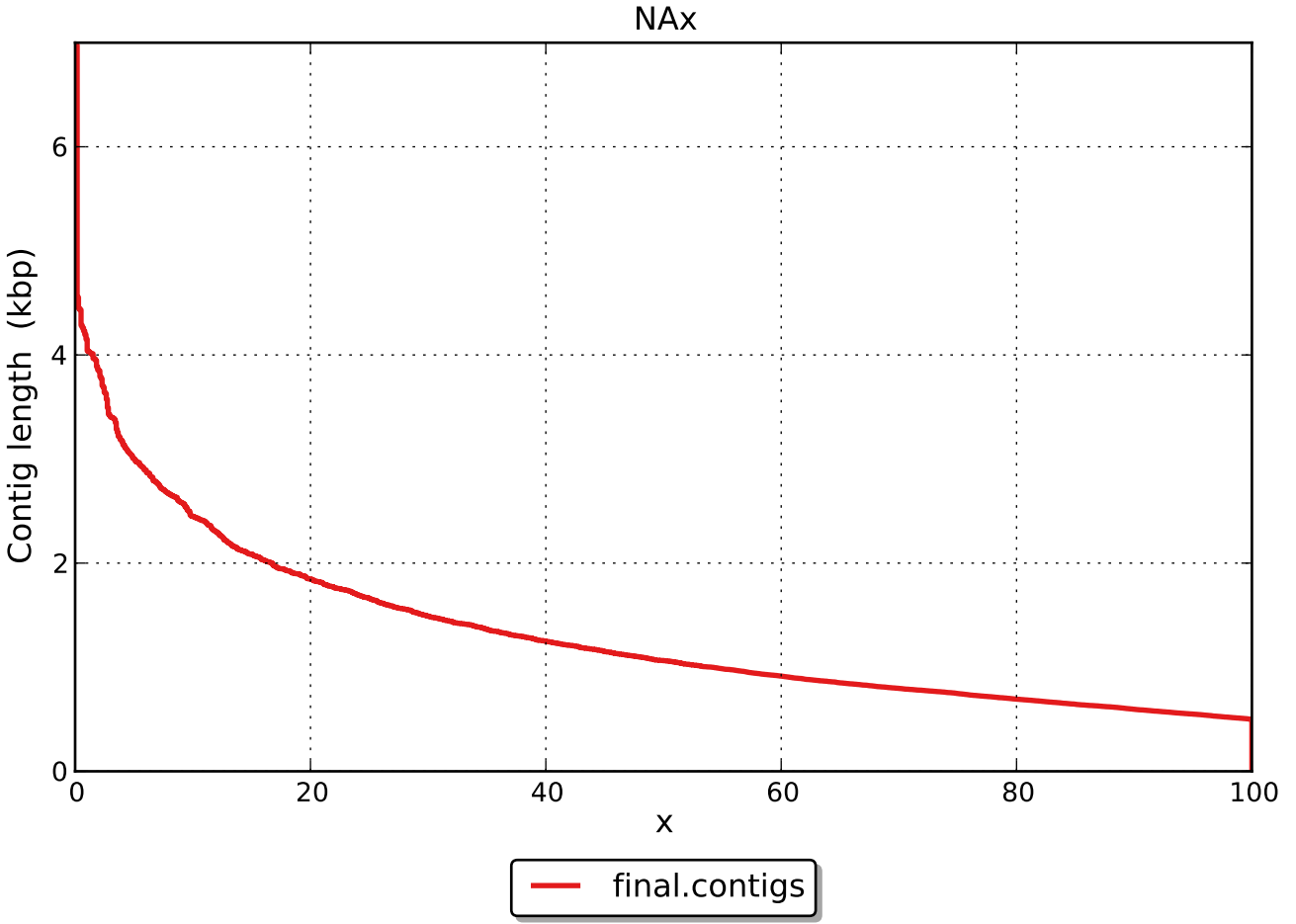

NGx
Contig length (kbp)
0
2
4
6
0
20
40
60
80
100
x
final.contigs

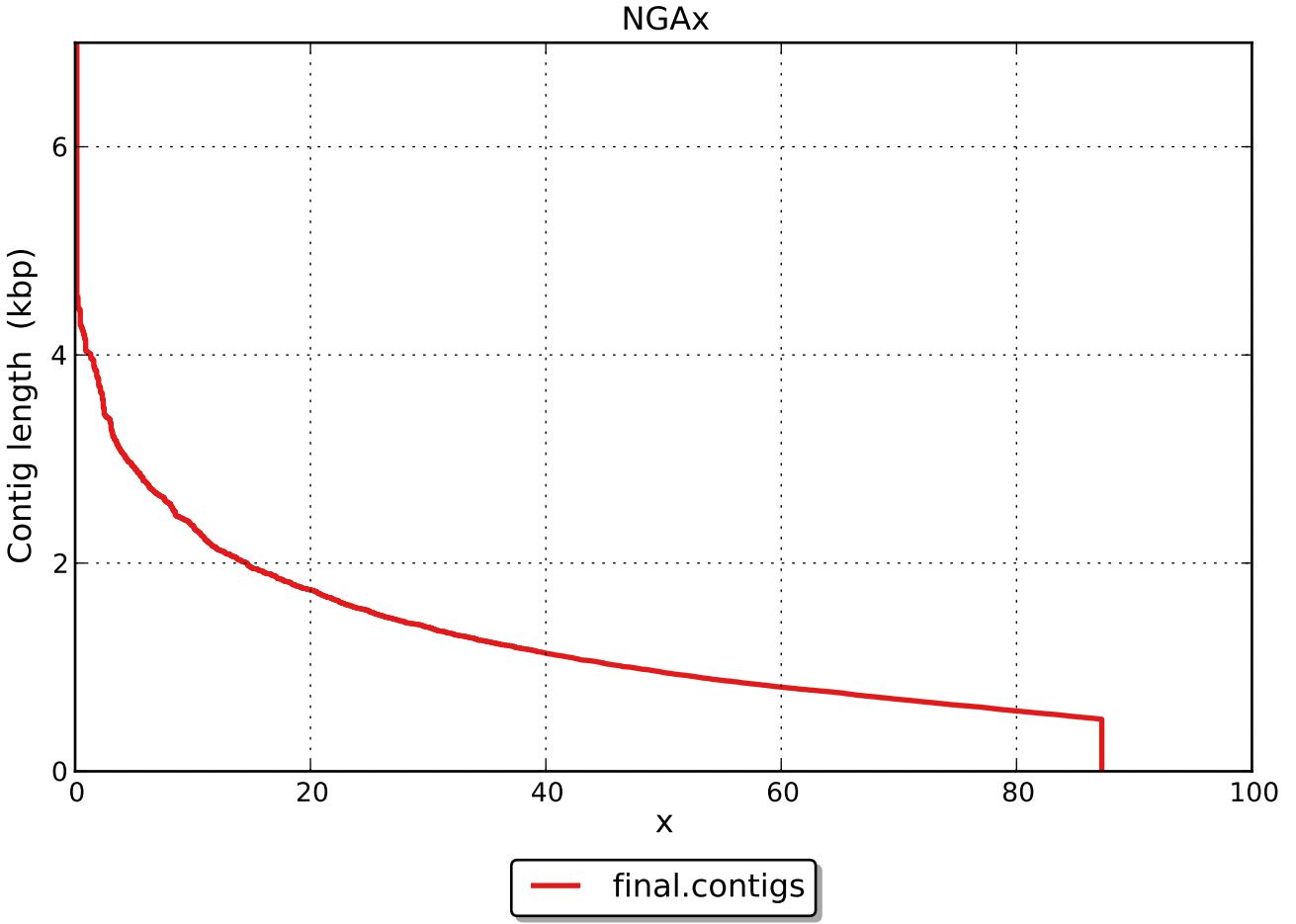

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
800
1600
2400
3200
4000
Contig index
final.contigs
Reference


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