Report

	final.contigs
# contigs (>= 1000 bp)	1565
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	2404034
Total length (>= 5000 bp)	5476
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	4013
Largest contig	5476
Total length	4151221
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	1112
NG50	1025
N75	782
NG75	681
L50	1253
LG50	1483
L75	2370
LG75	2873
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	3047
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	84.688
Duplication ratio	1.056
# N's per 100 kbp	0.00
# mismatches per 100 kbp	84.20
# indels per 100 kbp	0.10
Largest alignment	5476
NA50	1112
NGA50	1025
NA75	782
NGA75	681
LA50	1253
LGA50	1484
LA75	2370
LGA75	2873

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

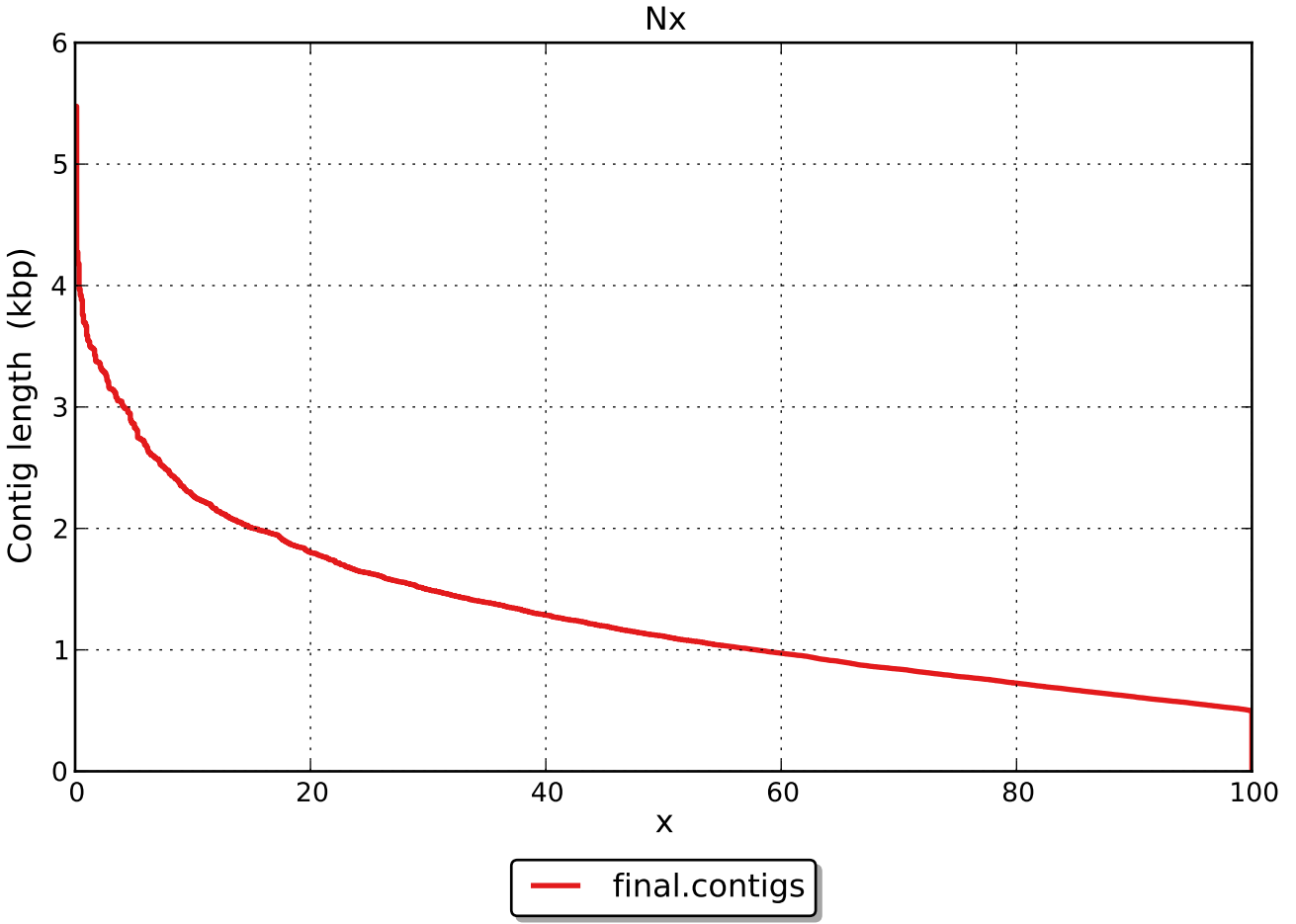
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	3047
# local misassemblies	0
# mismatches	3310
# indels	4
# short indels	4
# long indels	0
Indels length	4

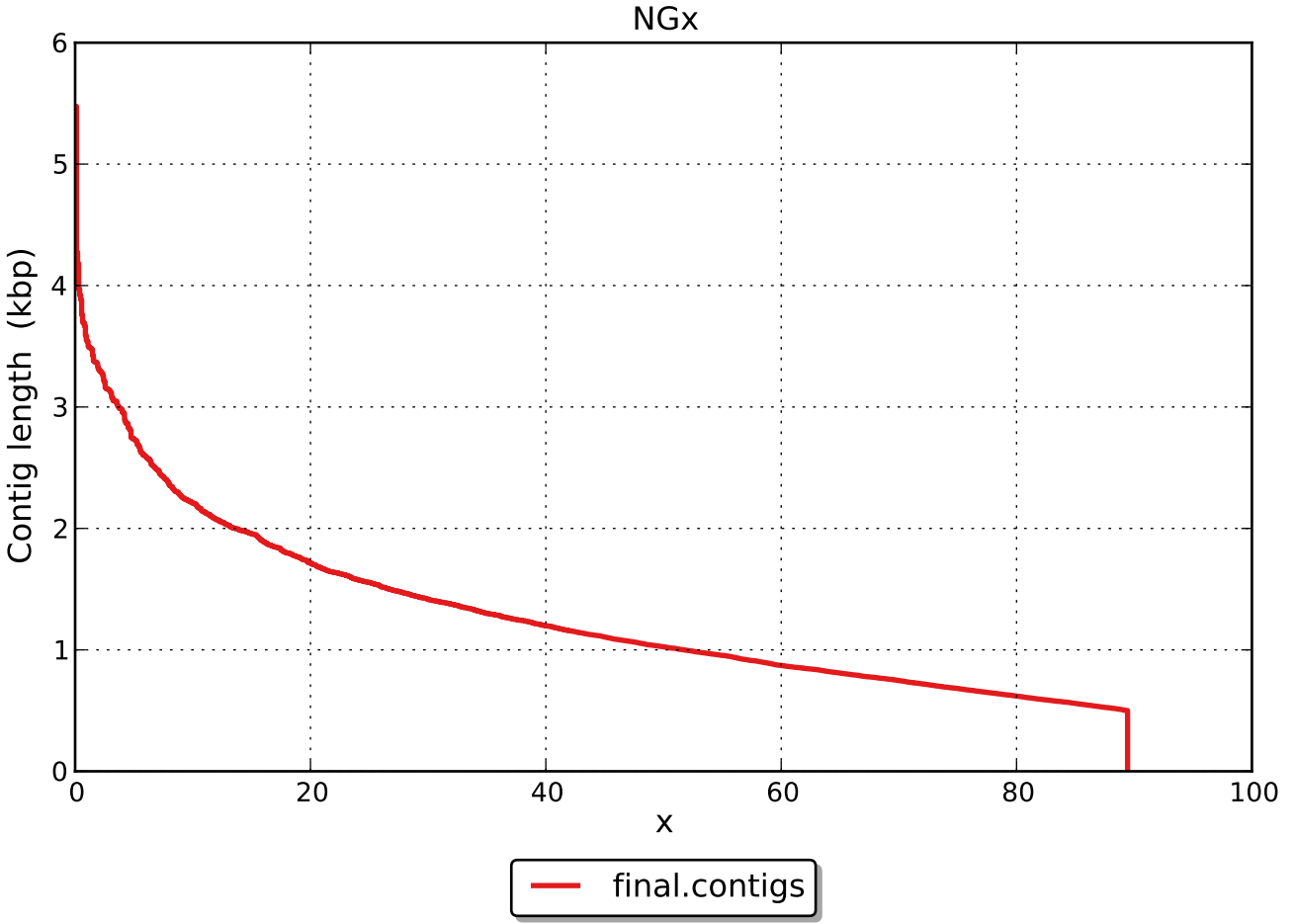
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

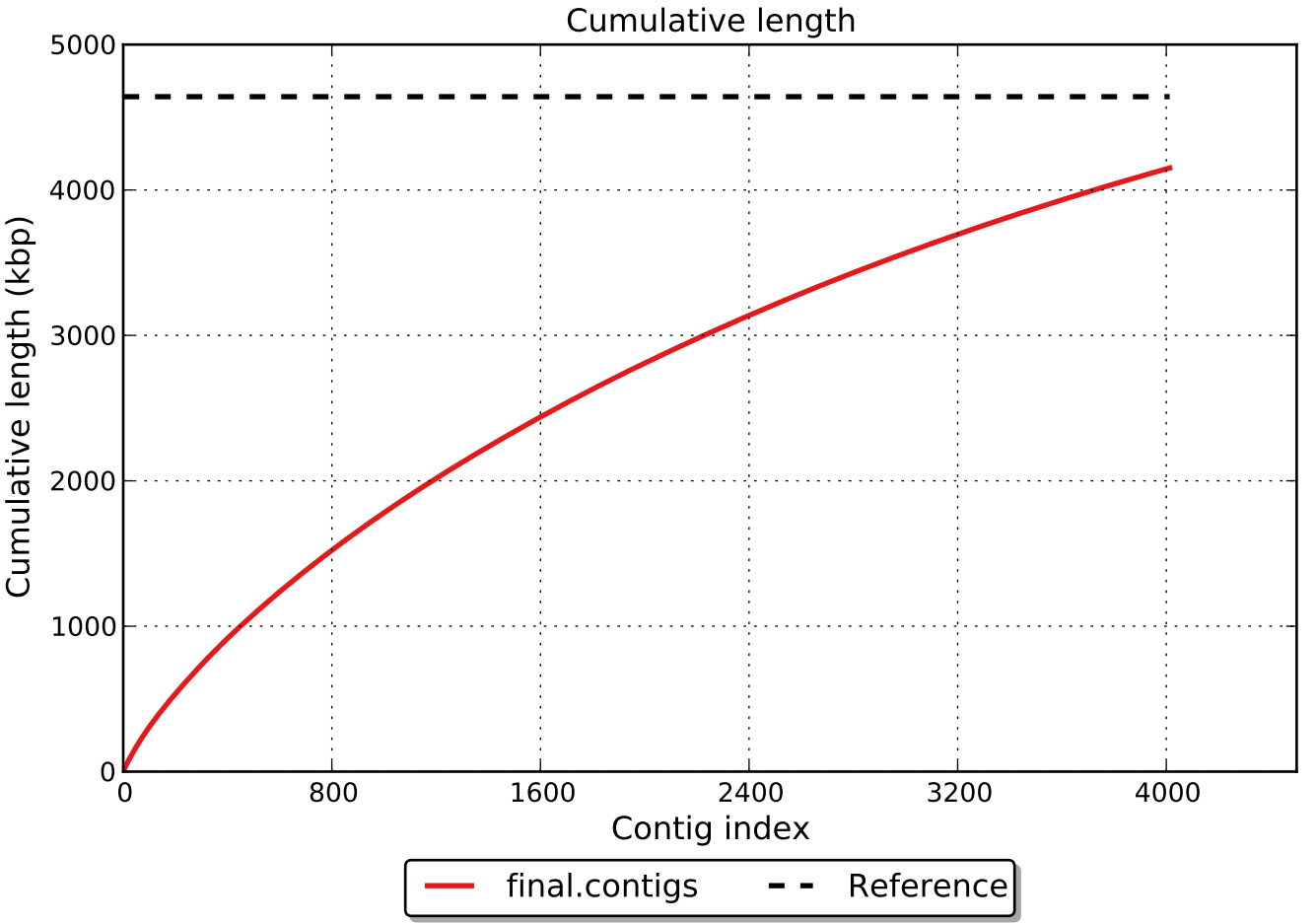
Unaligned report

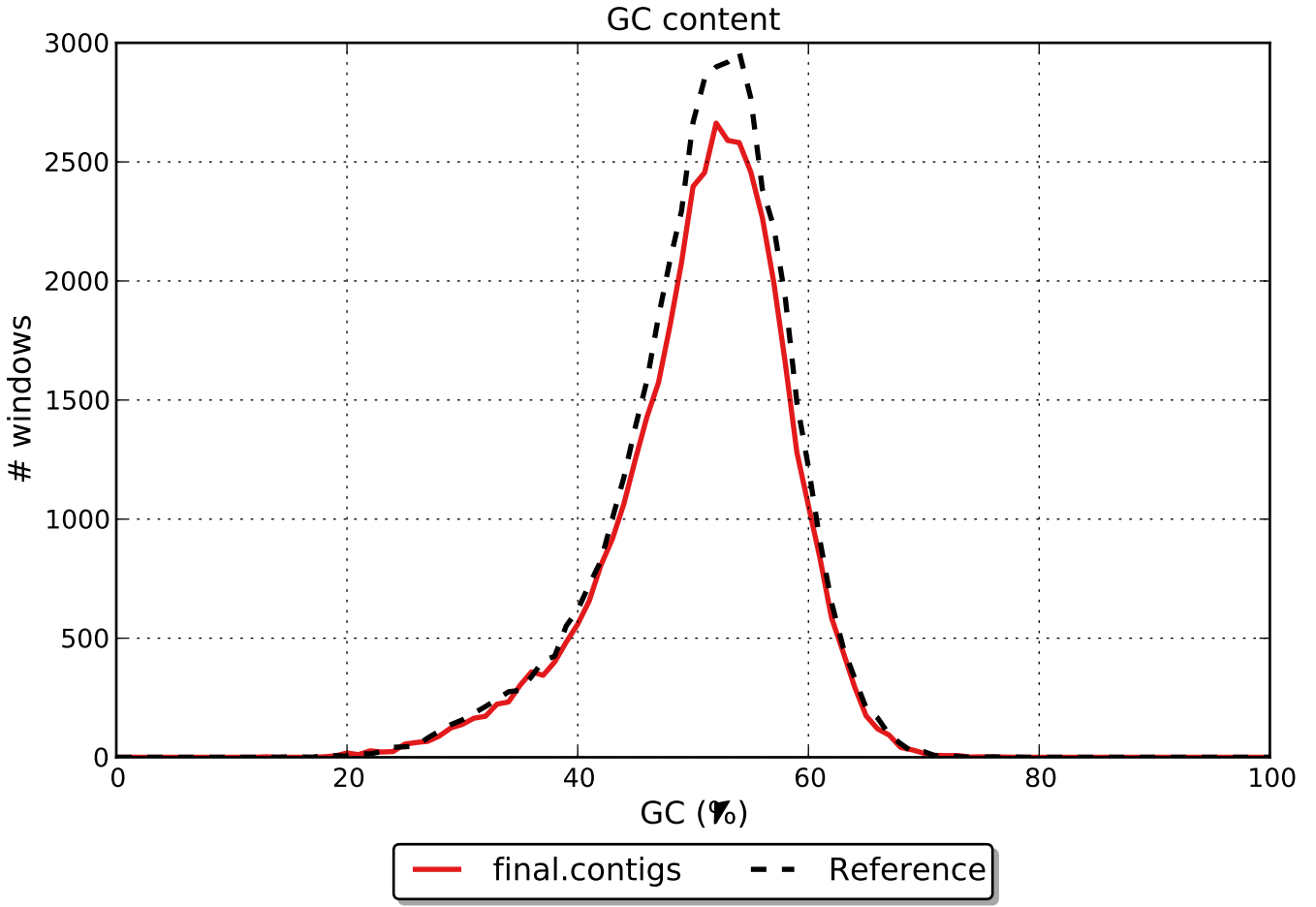
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

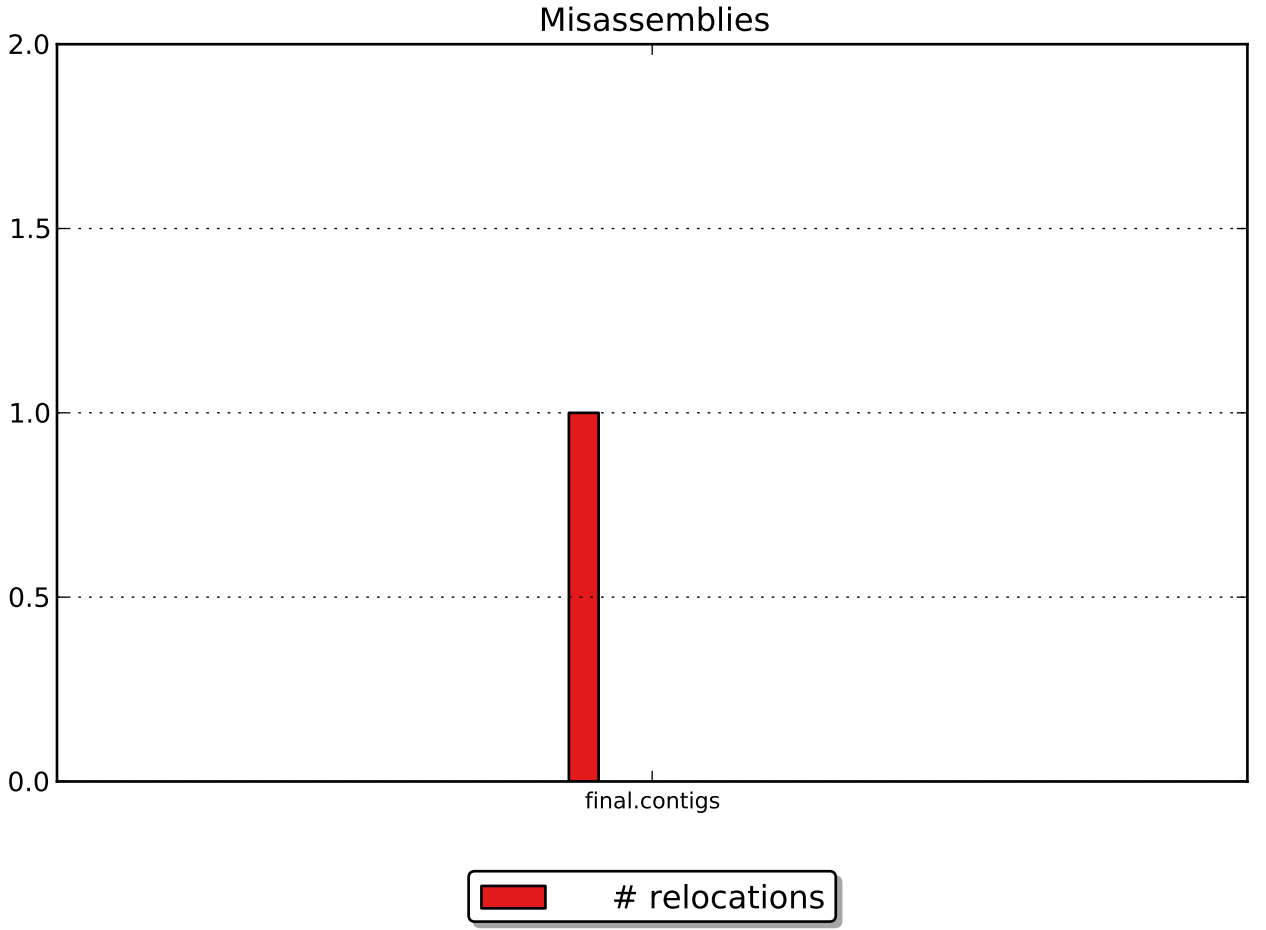
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

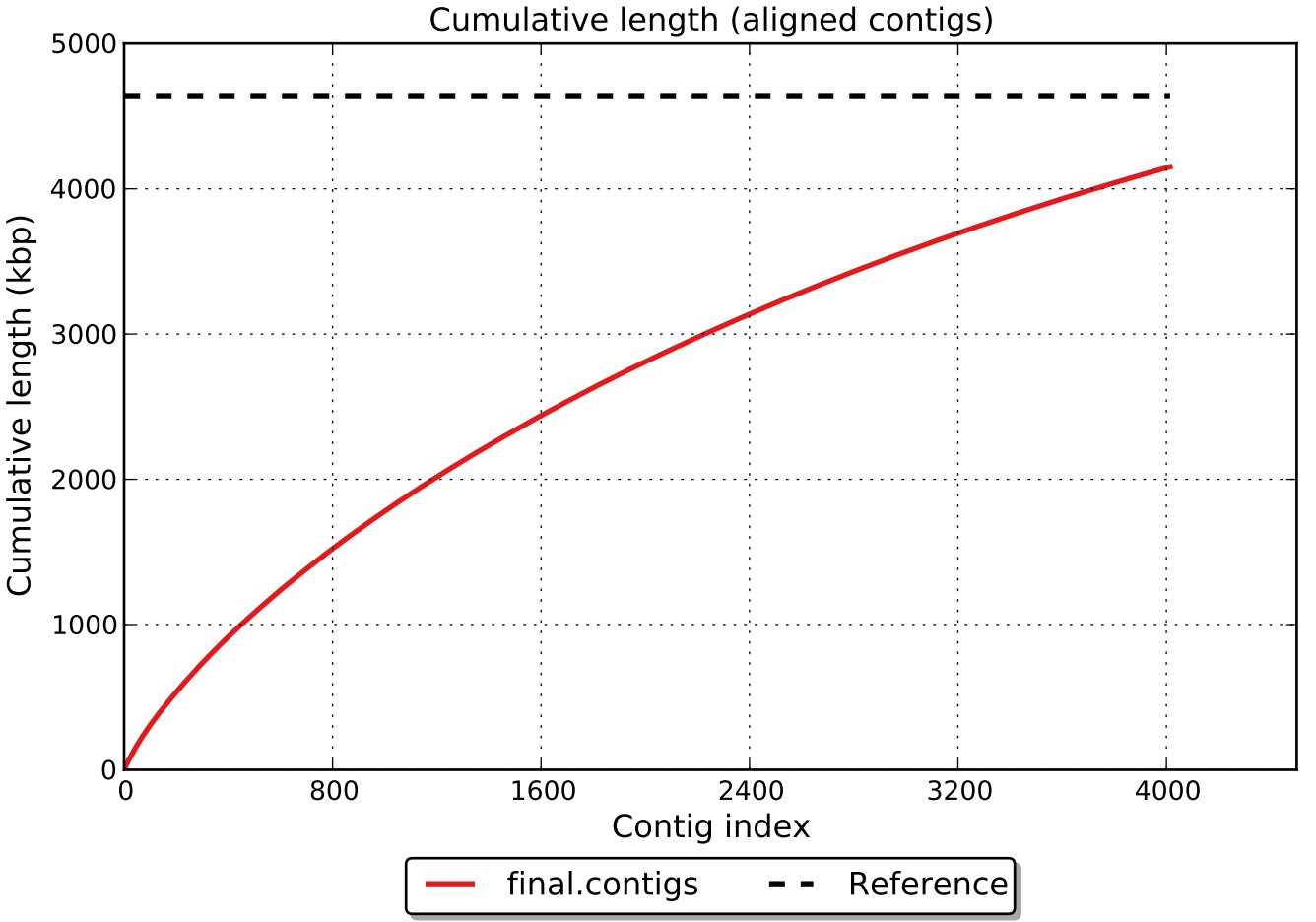

Nx
Contig length (kbp)
x
0
1
2
3
4
5
6
0
20
40
60
80
100
final.contigs

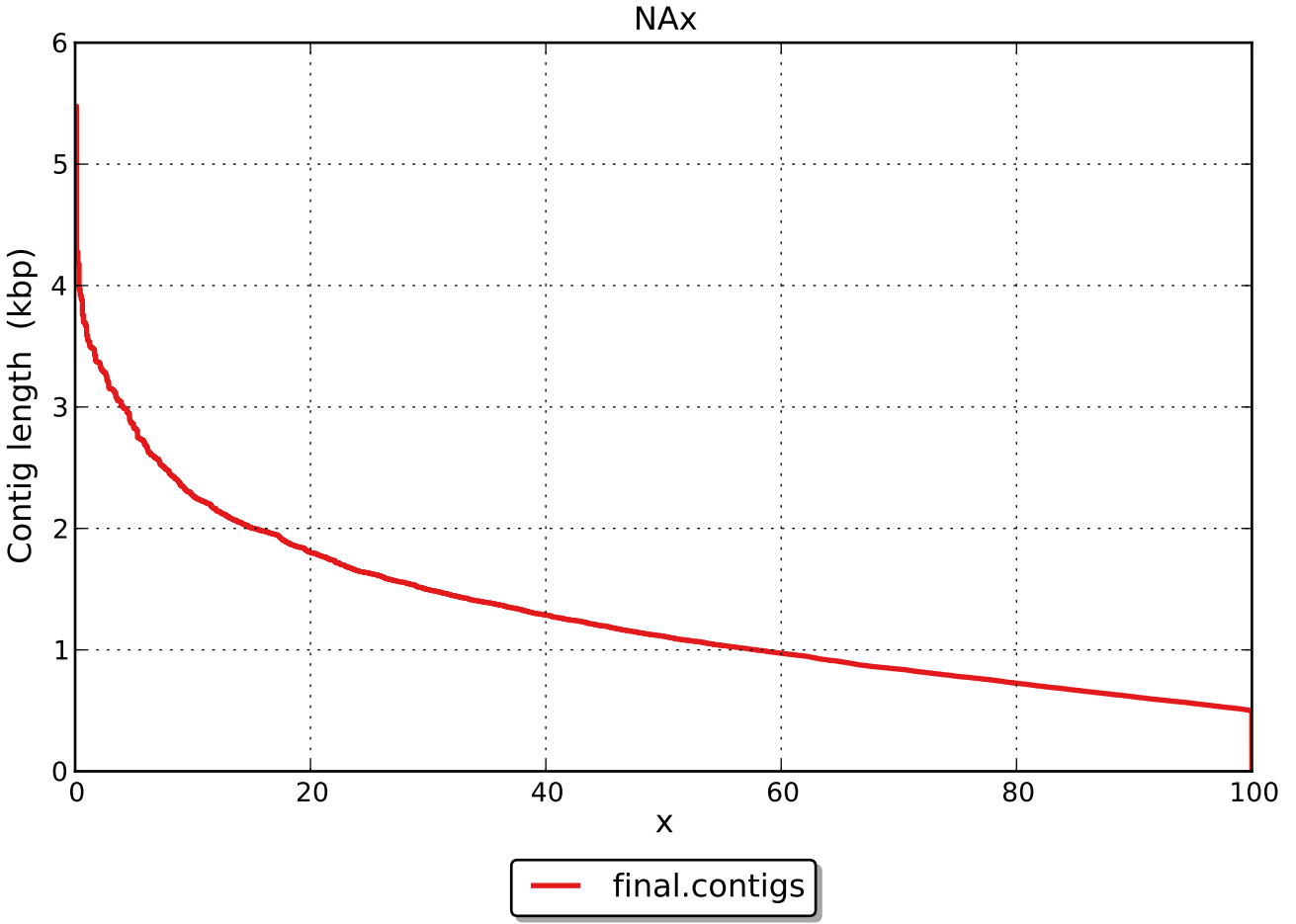

NGx
Contig length (kbp)
0
1
2
3
4
5
6
0
20
40
60
80
100
x
final.contigs

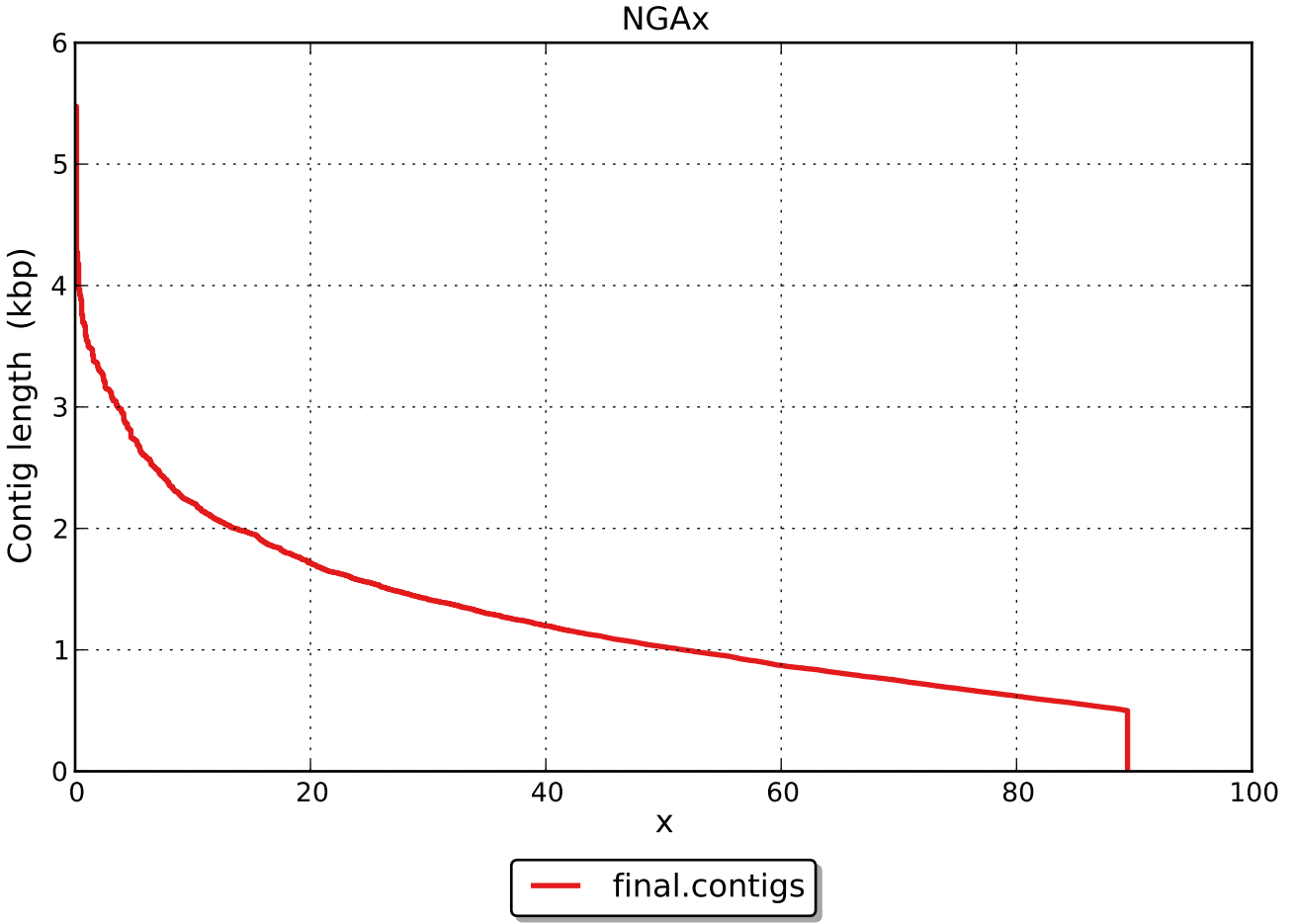

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
800
1600
2400
3200
4000
Contig index
final.contigs
Reference


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


Misassemblies
2.0
1.5
1.0
0.5
0.0
final.contigs
relocations


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