Report

	final.contigs
# contigs (>= 1000 bp)	1347
# contigs (>= 5000 bp)	281
# contigs (>= 10000 bp)	32
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4716201
Total length (>= 5000 bp)	2073987
Total length (>= 10000 bp)	414611
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1661
Largest contig	21956
Total length	4945042
Reference length	4857432
GC (%)	52.23
Reference GC (%)	52.23
N50	4211
NG50	4276
N75	2529
NG75	2622
L50	369
LG50	359
L75	746
LG75	720
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	3170
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.957
Duplication ratio	1.029
# N's per 100 kbp	0.00
# mismatches per 100 kbp	28.29
# indels per 100 kbp	0.00
Largest alignment	21956
NA50	4211
NGA50	4276
NA75	2529
NGA75	2622
LA50	369
LGA50	359
LA75	746
LGA75	720

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

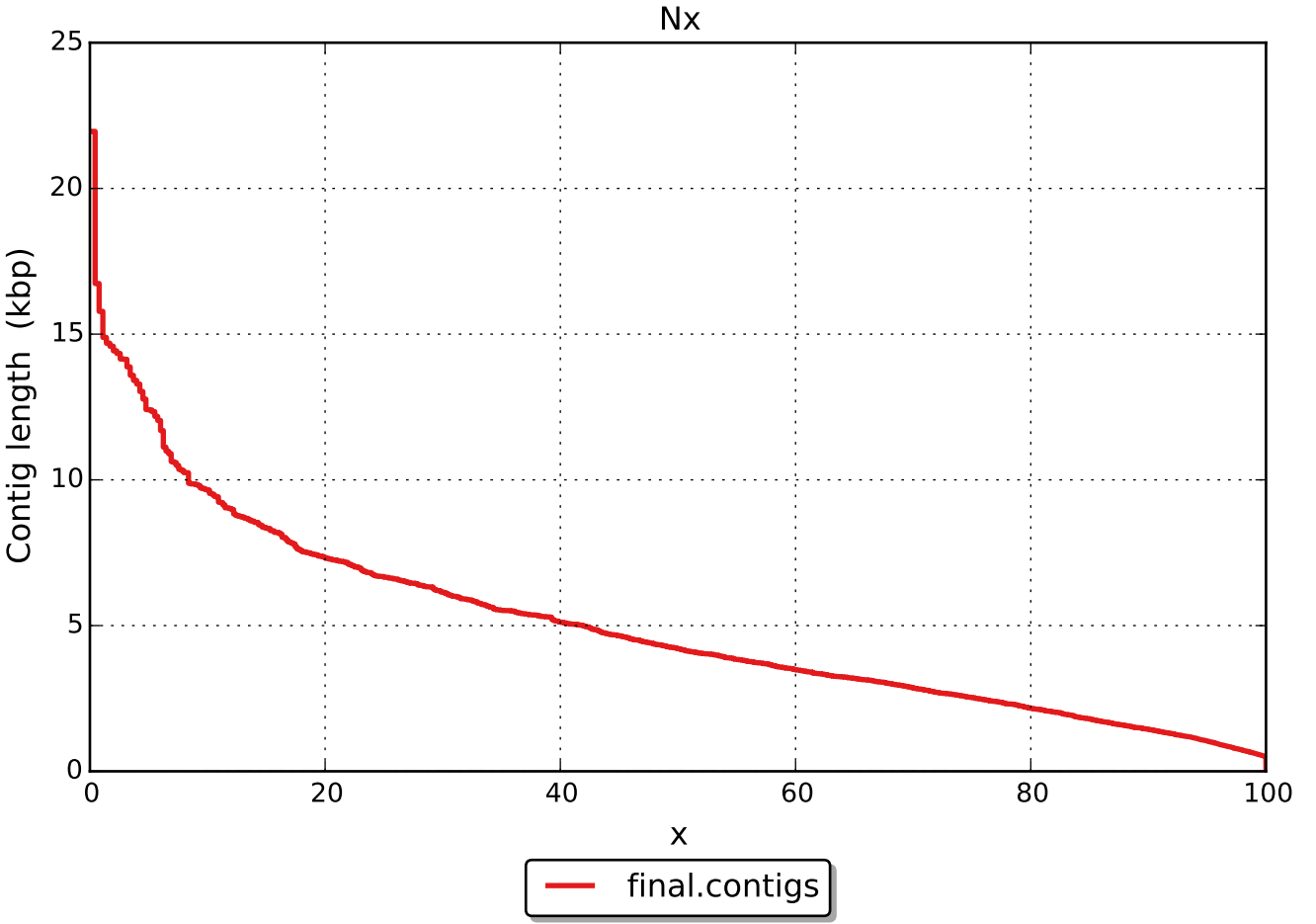
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	3170
# local misassemblies	0
# mismatches	1360
# indels	0
# short indels	0
# long indels	0
Indels length	0

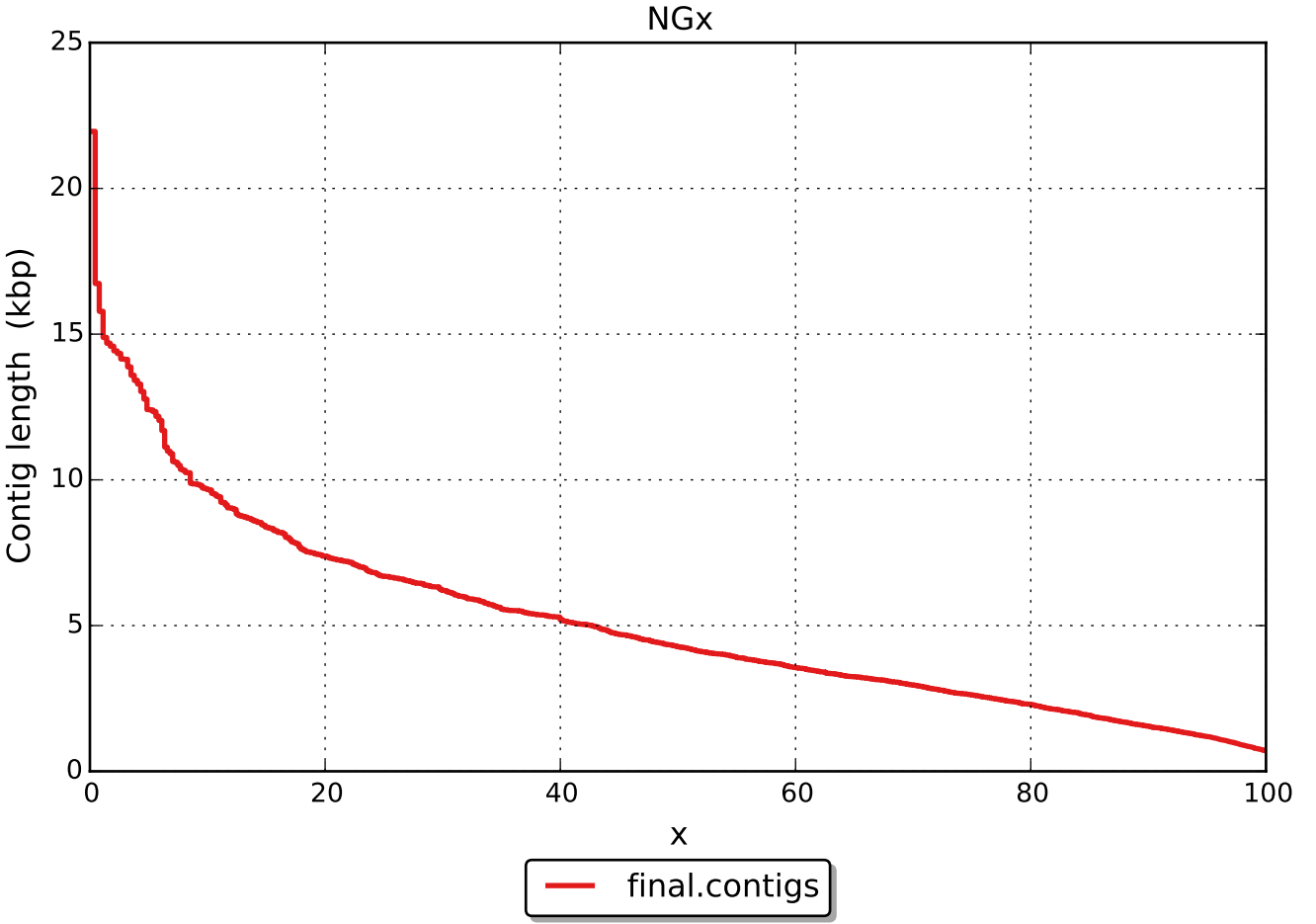
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

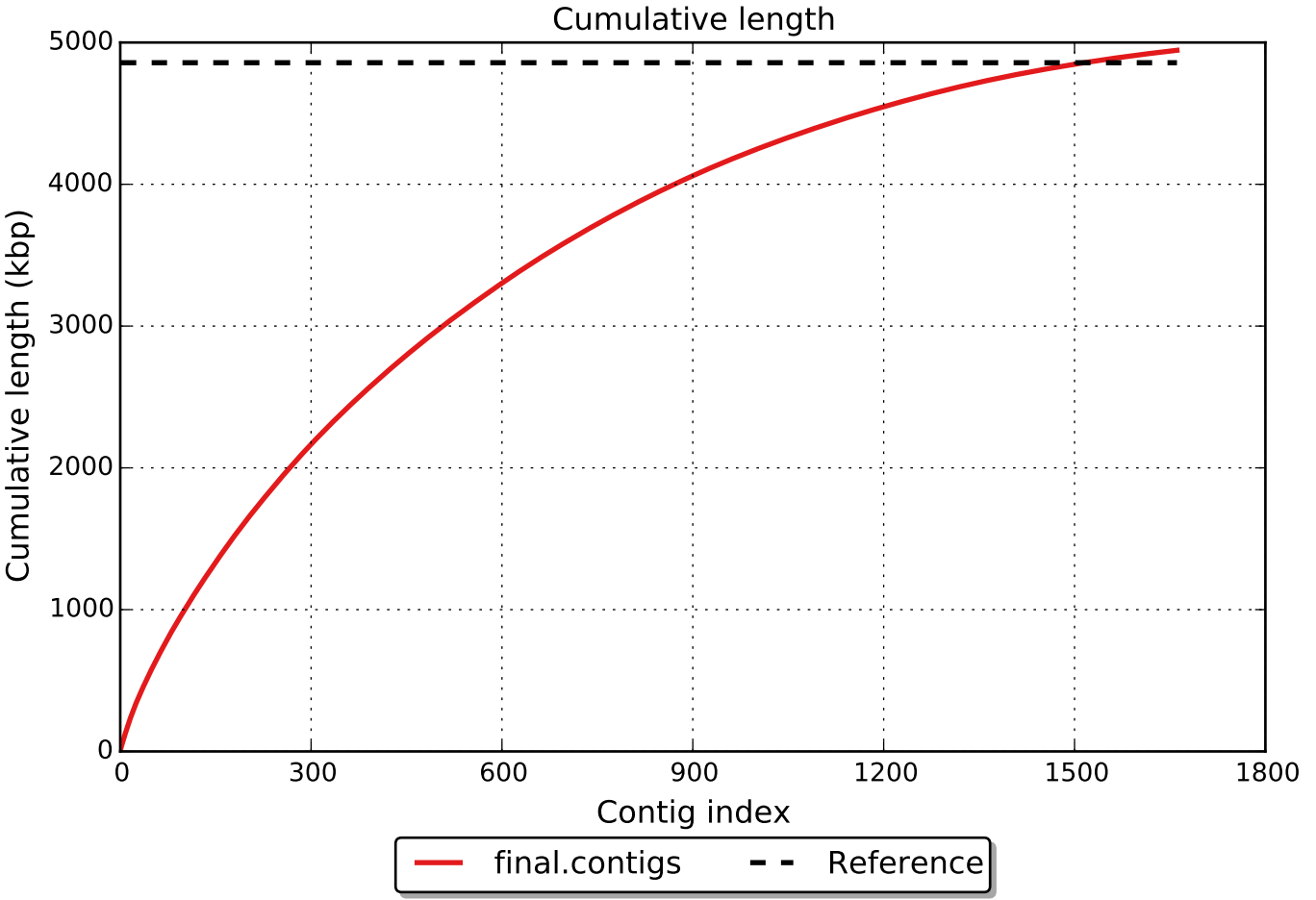
Unaligned report

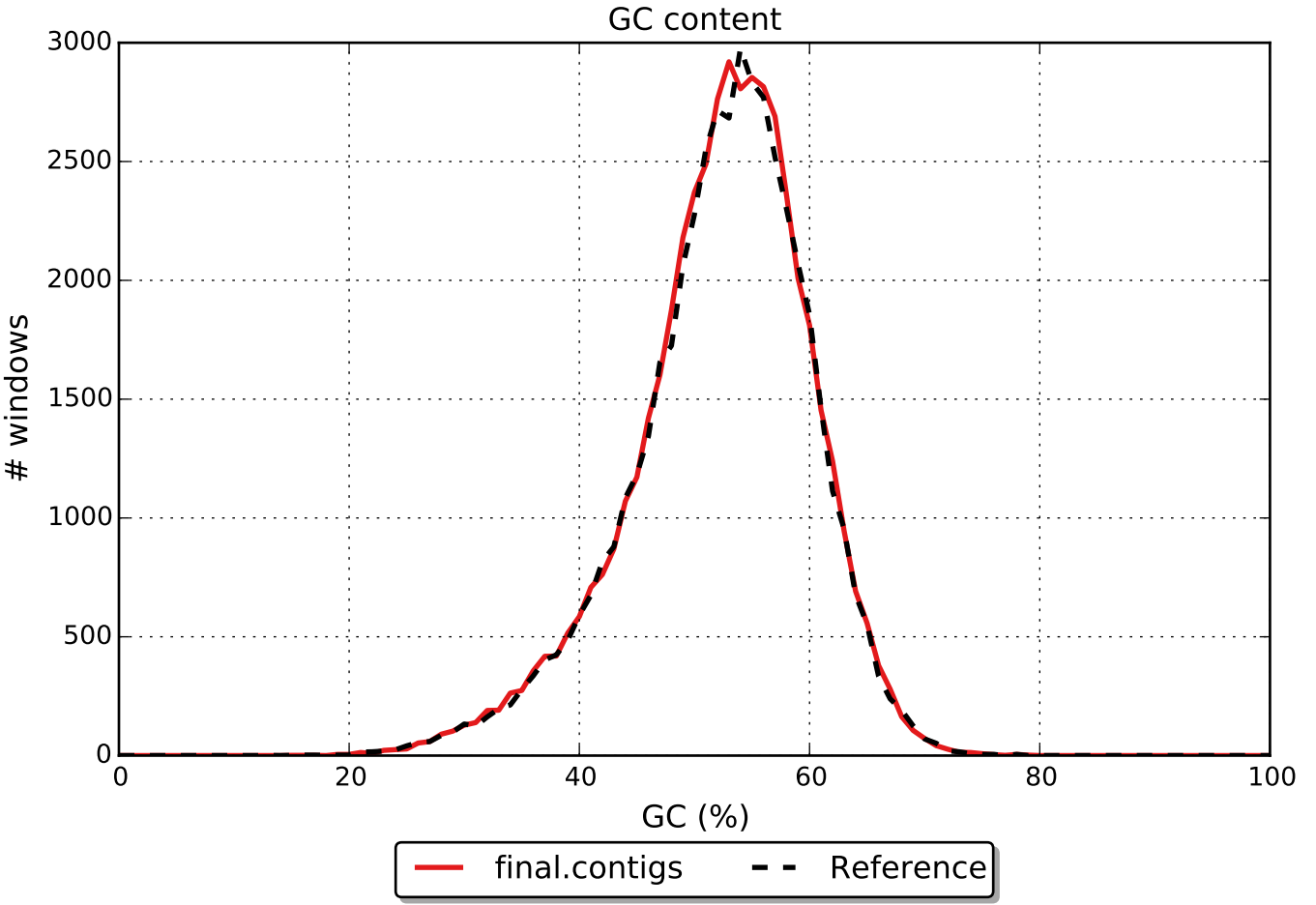
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

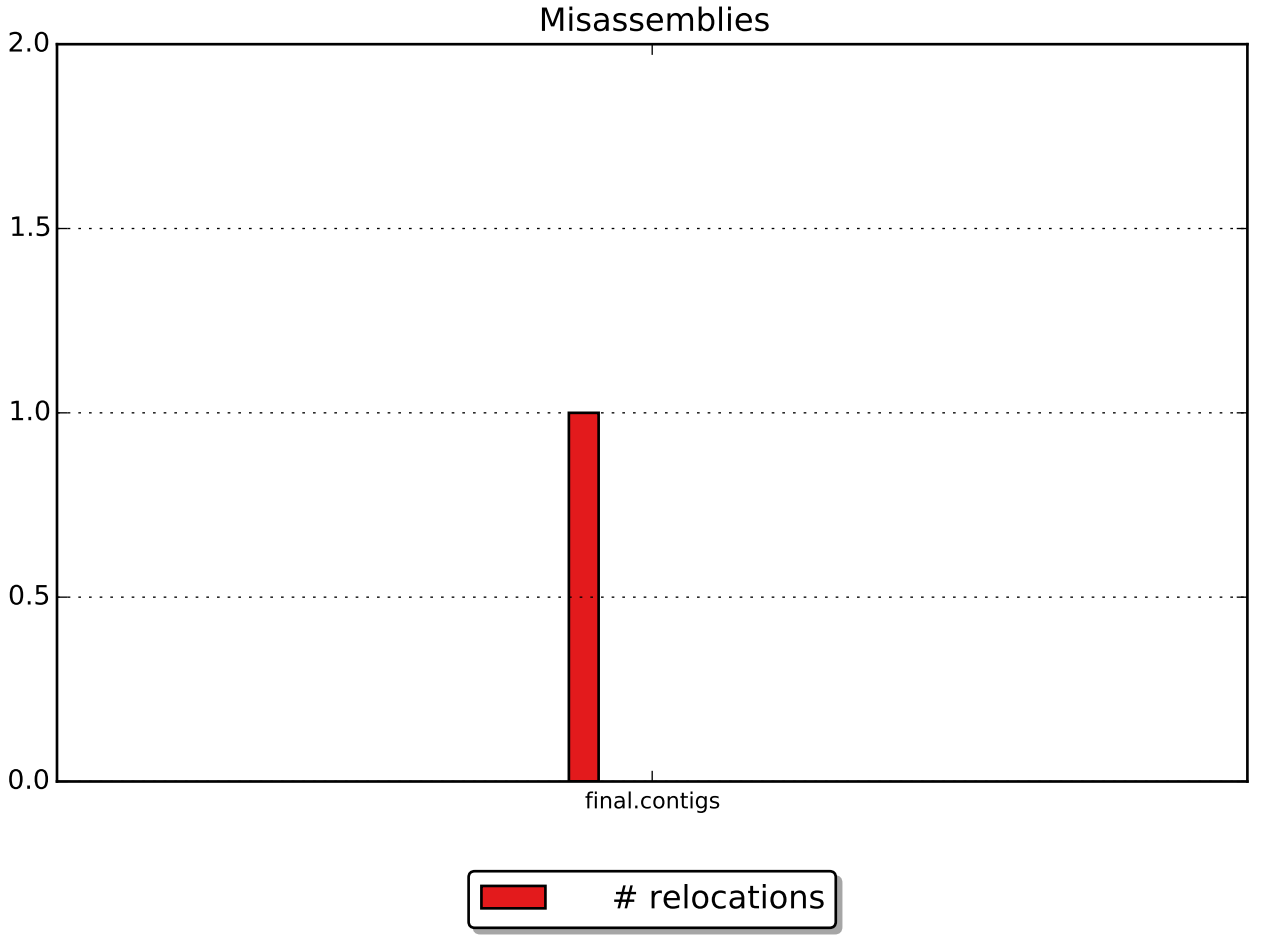
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

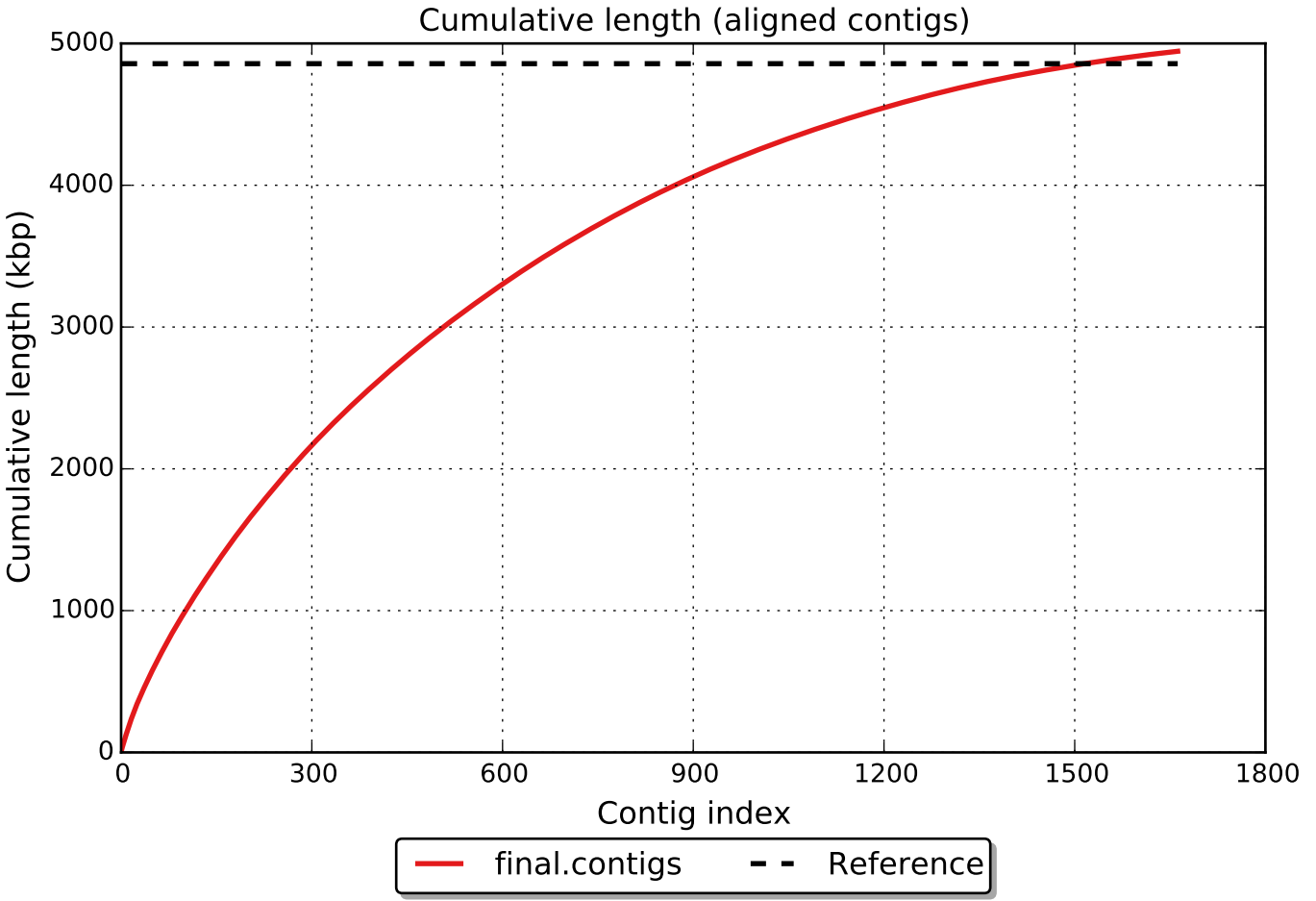

Nx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
final.contigs

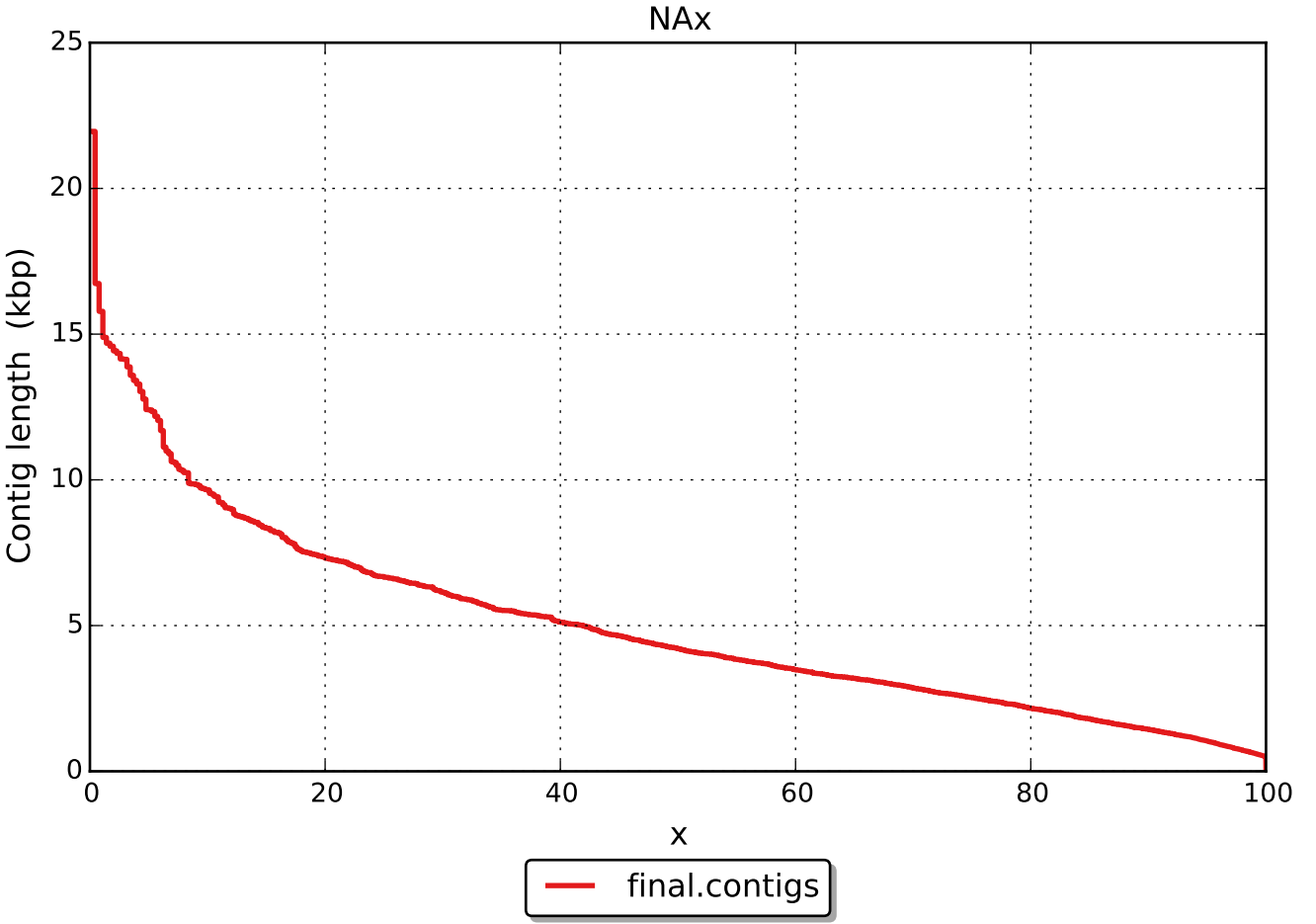

NGx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
final.contigs

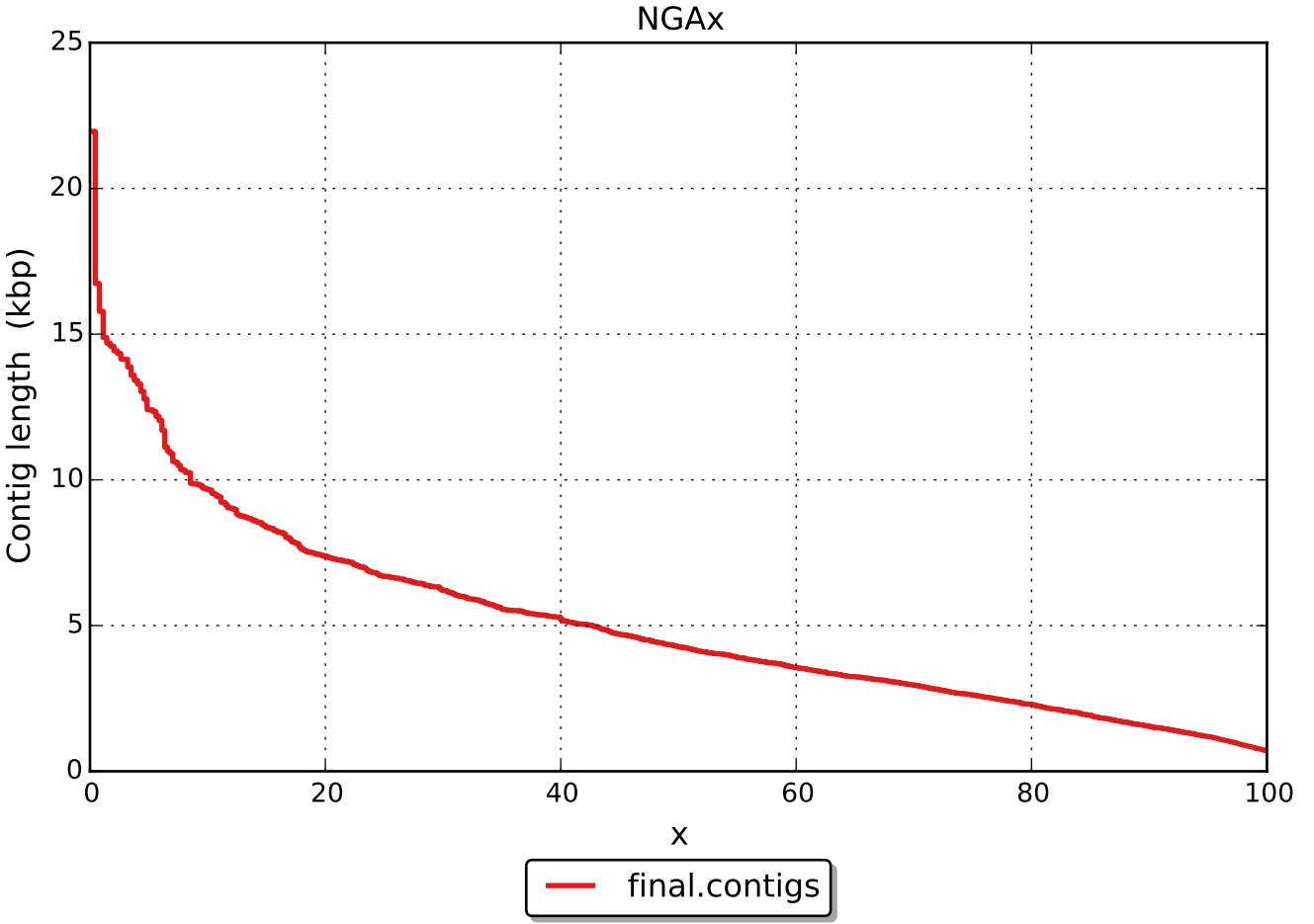

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
300
600
900
1200
1500
1800
Contig index
final.contigs
Reference


GC content
windows
GC (%)
0
500
1000
1500
2000
2500
3000
0
20
40
60
80
100
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
300
600
900
1200
1500
1800
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
final.contigs