Report

	final.contigs
# contigs (>= 1000 bp)	1570
# contigs (>= 5000 bp)	190
# contigs (>= 10000 bp)	14
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4488041
Total length (>= 5000 bp)	1309968
Total length (>= 10000 bp)	168998
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2078
Largest contig	16780
Total length	4858231
Reference length	4857432
GC (%)	52.20
Reference GC (%)	52.22
N50	3197
NG50	3198
N75	1890
NG75	1890
L50	477
LG50	476
L75	965
LG75	965
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	2589
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	96.639
Duplication ratio	1.035
# N's per 100 kbp	0.00
# mismatches per 100 kbp	43.33
# indels per 100 kbp	0.02
Largest alignment	16780
NA50	3197
NGA50	3198
NA75	1890
NGA75	1890
LA50	477
LGA50	476
LA75	965
LGA75	965

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

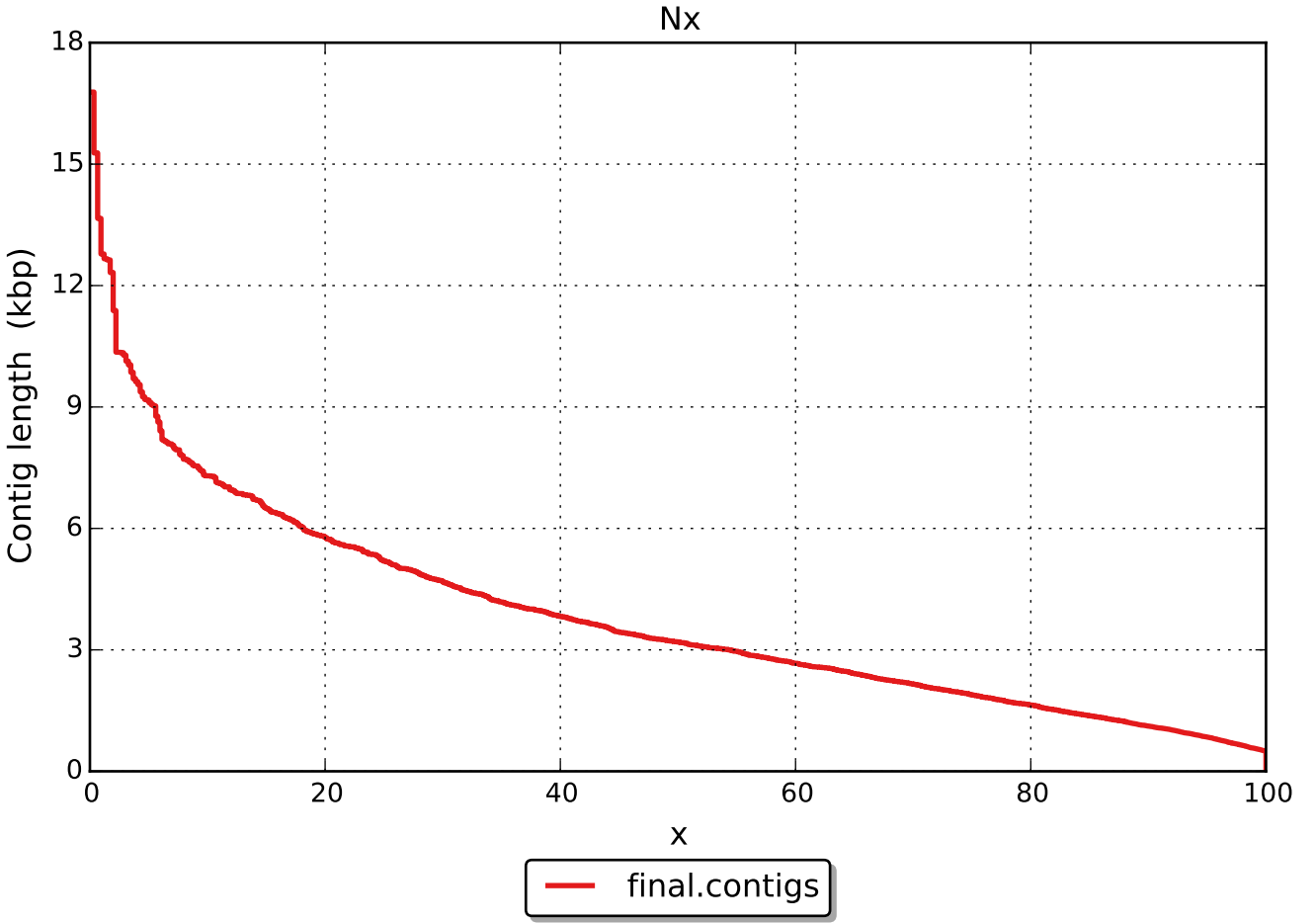
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	2589
# local misassemblies	0
# mismatches	2034
# indels	1
# short indels	1
# long indels	0
Indels length	1

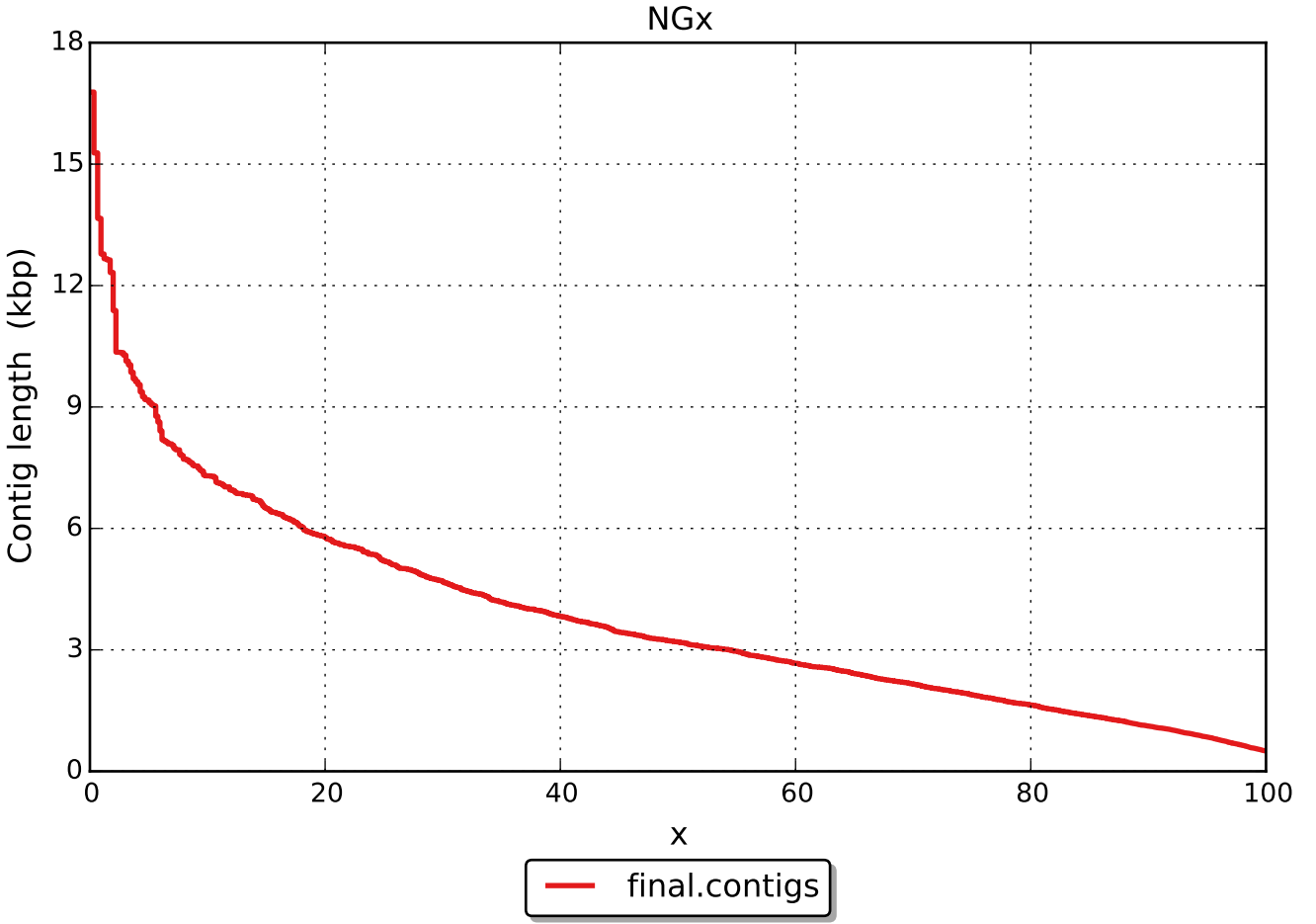
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

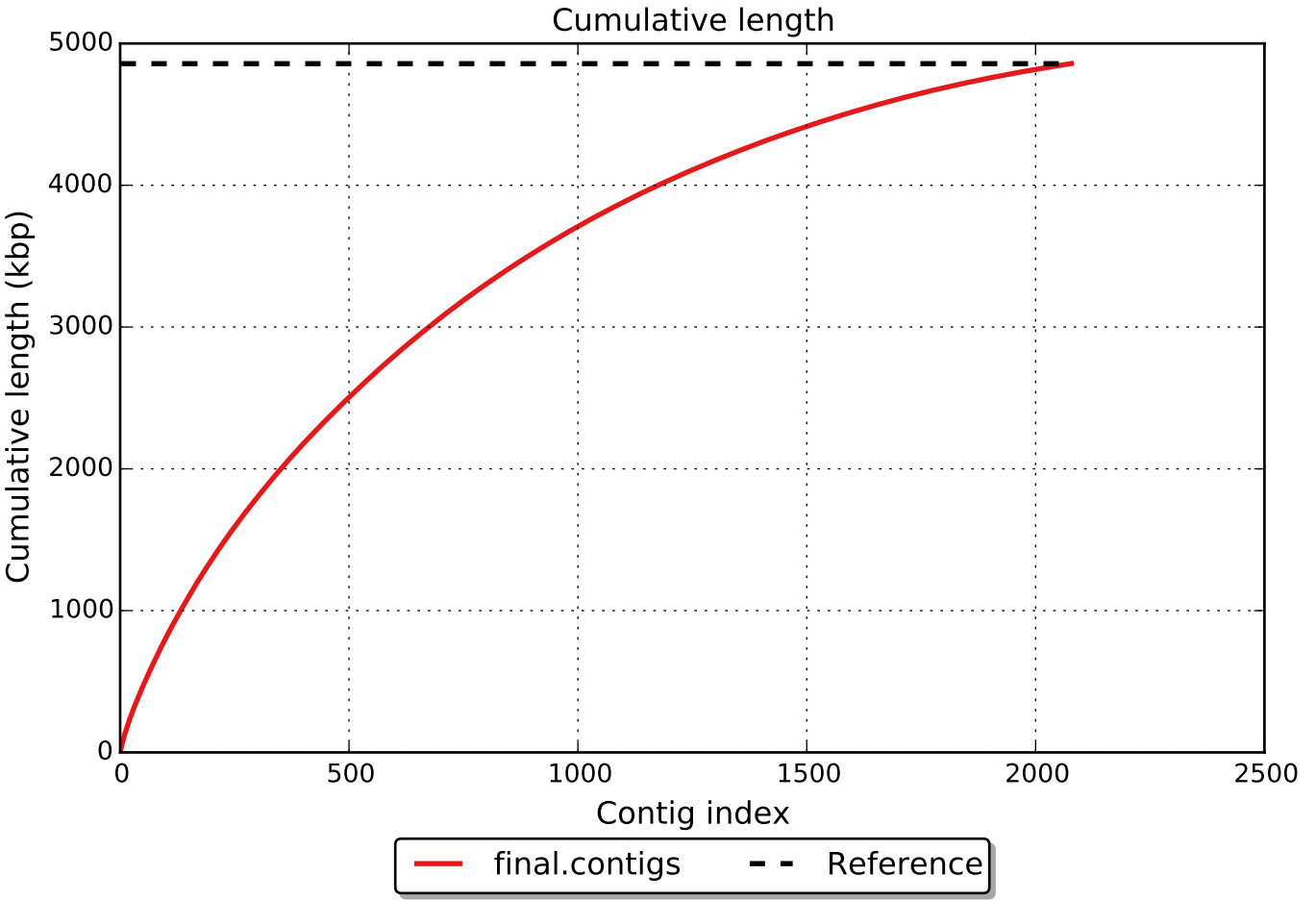
Unaligned report

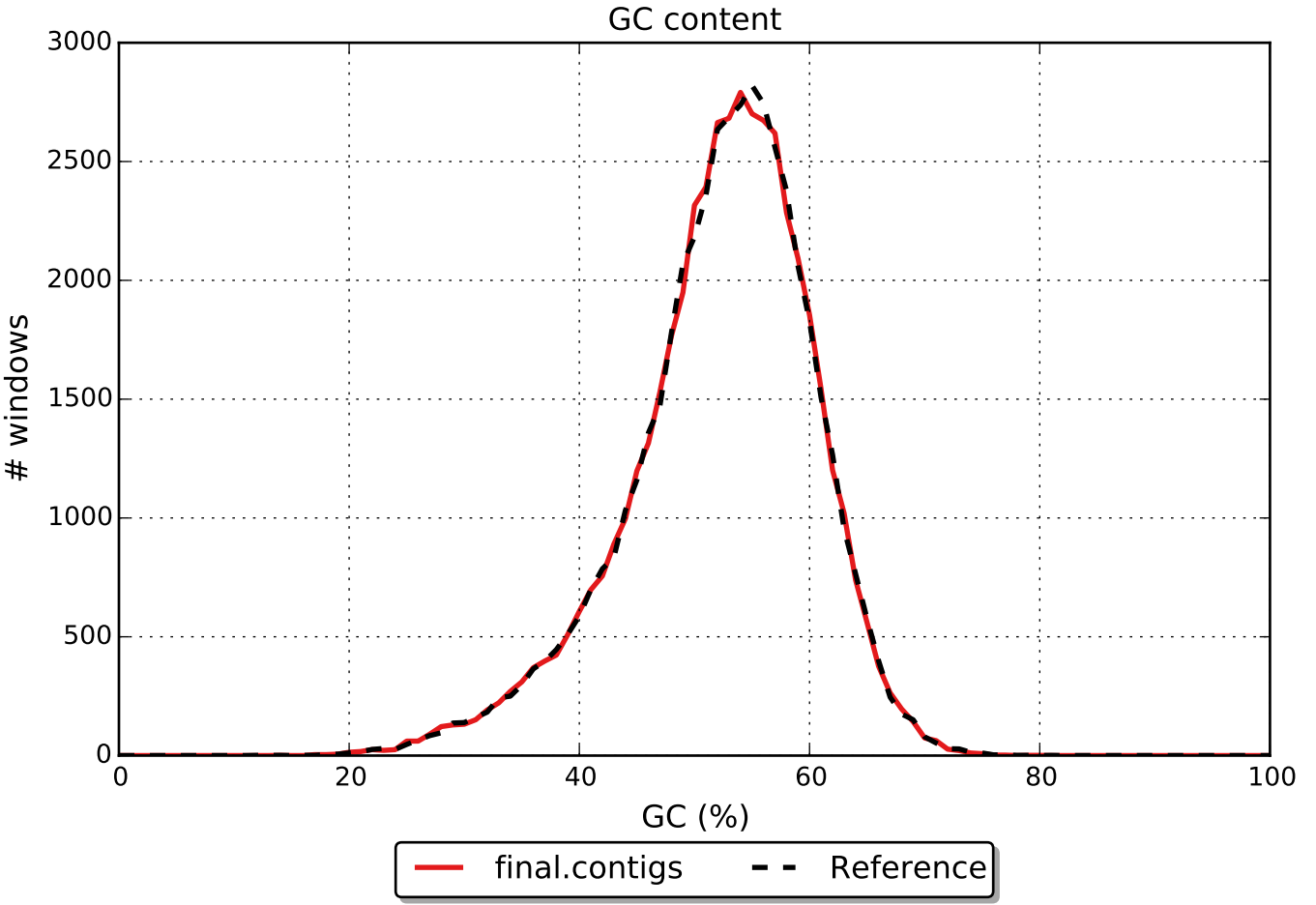
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

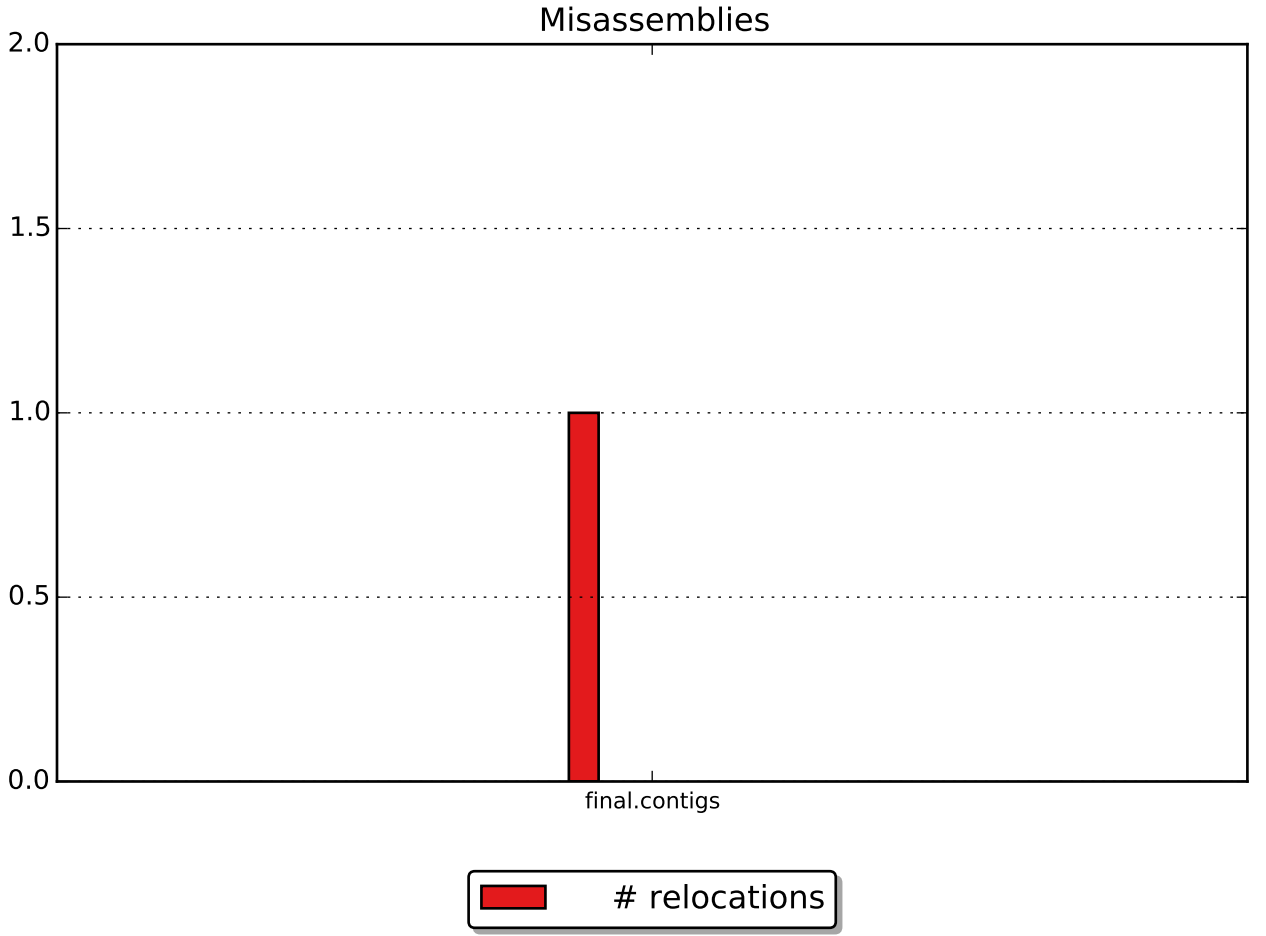
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

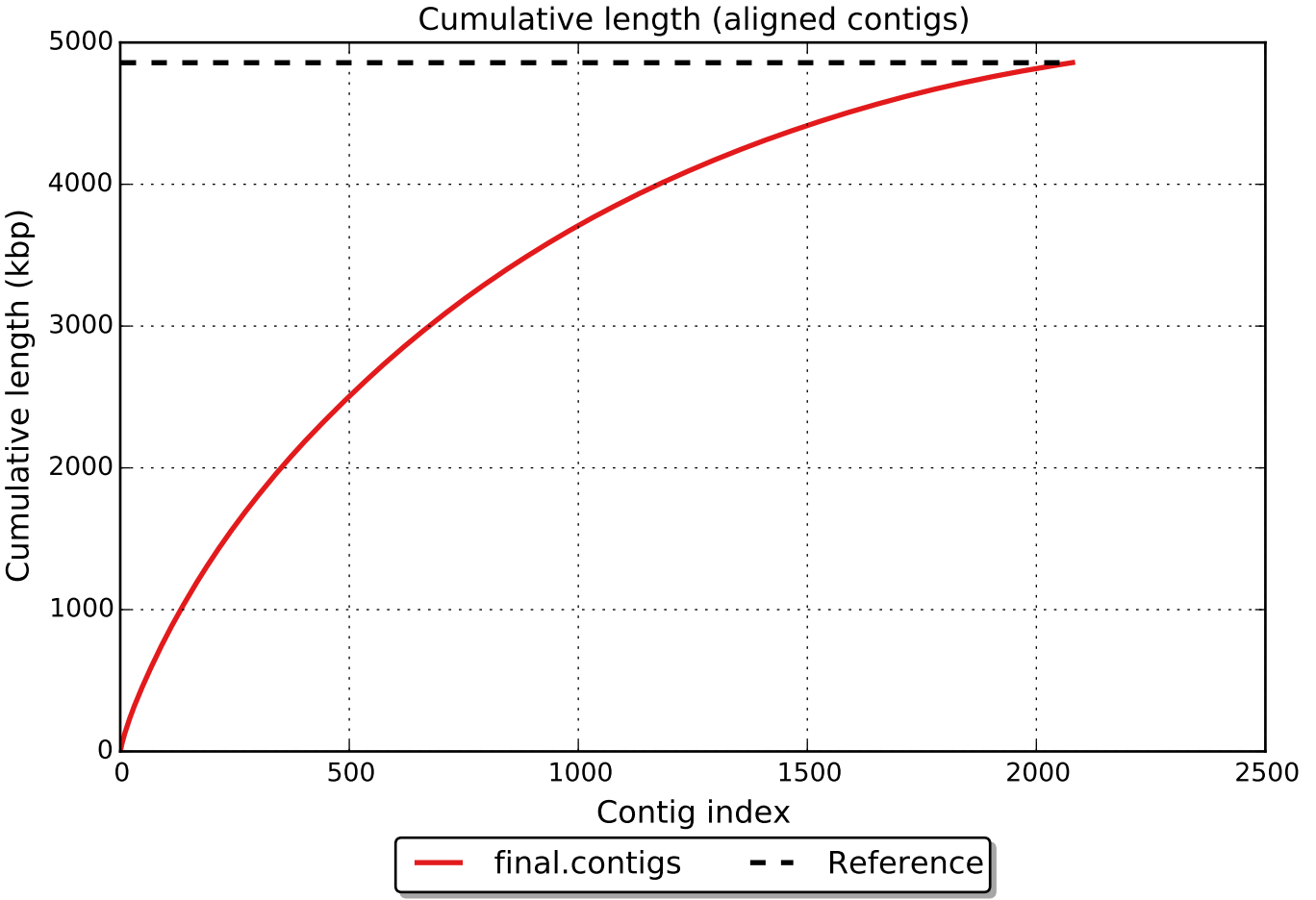

Nx
Contig length (kbp)
18
15
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs

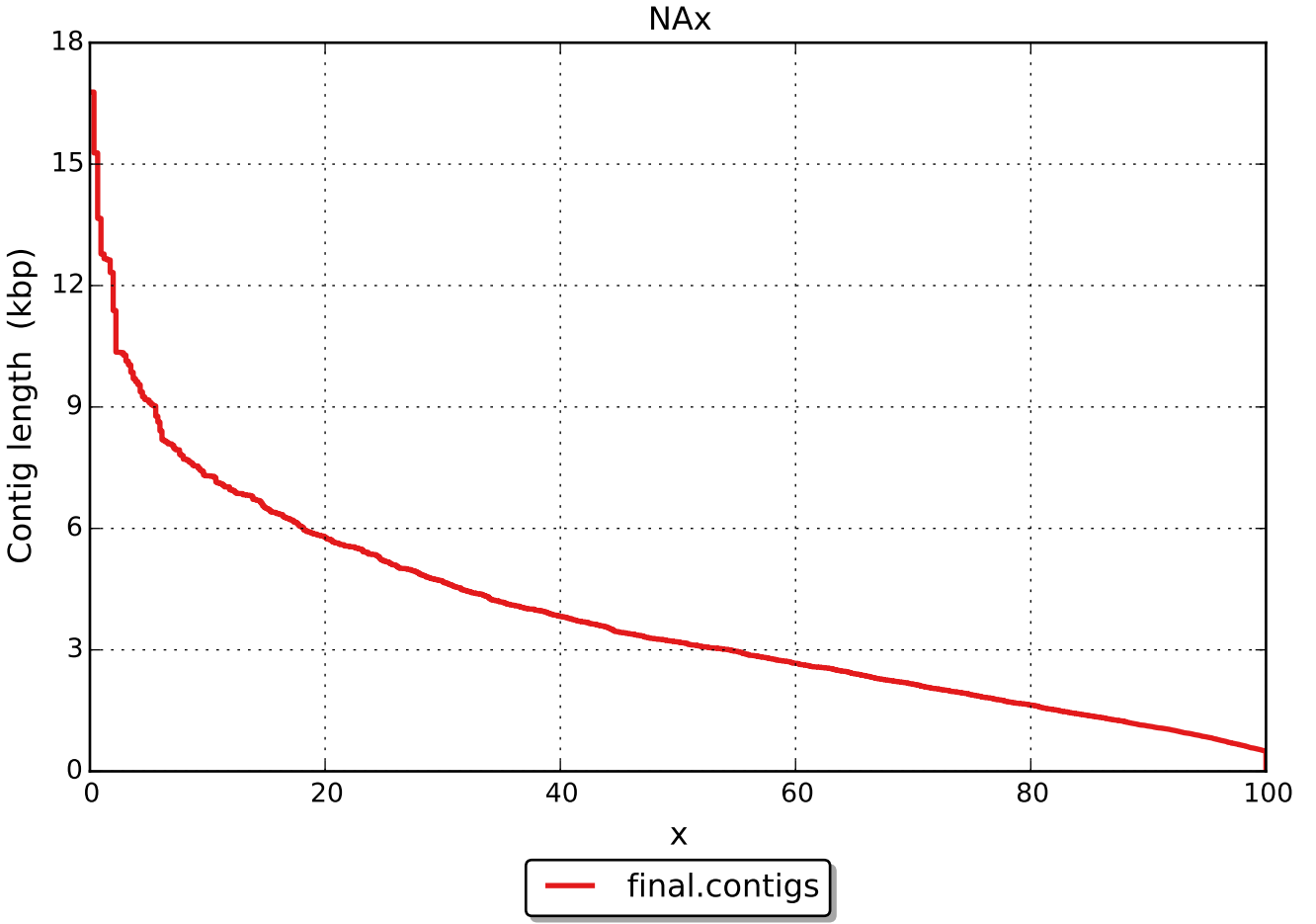

NGx
Contig length (kbp)
18
15
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs

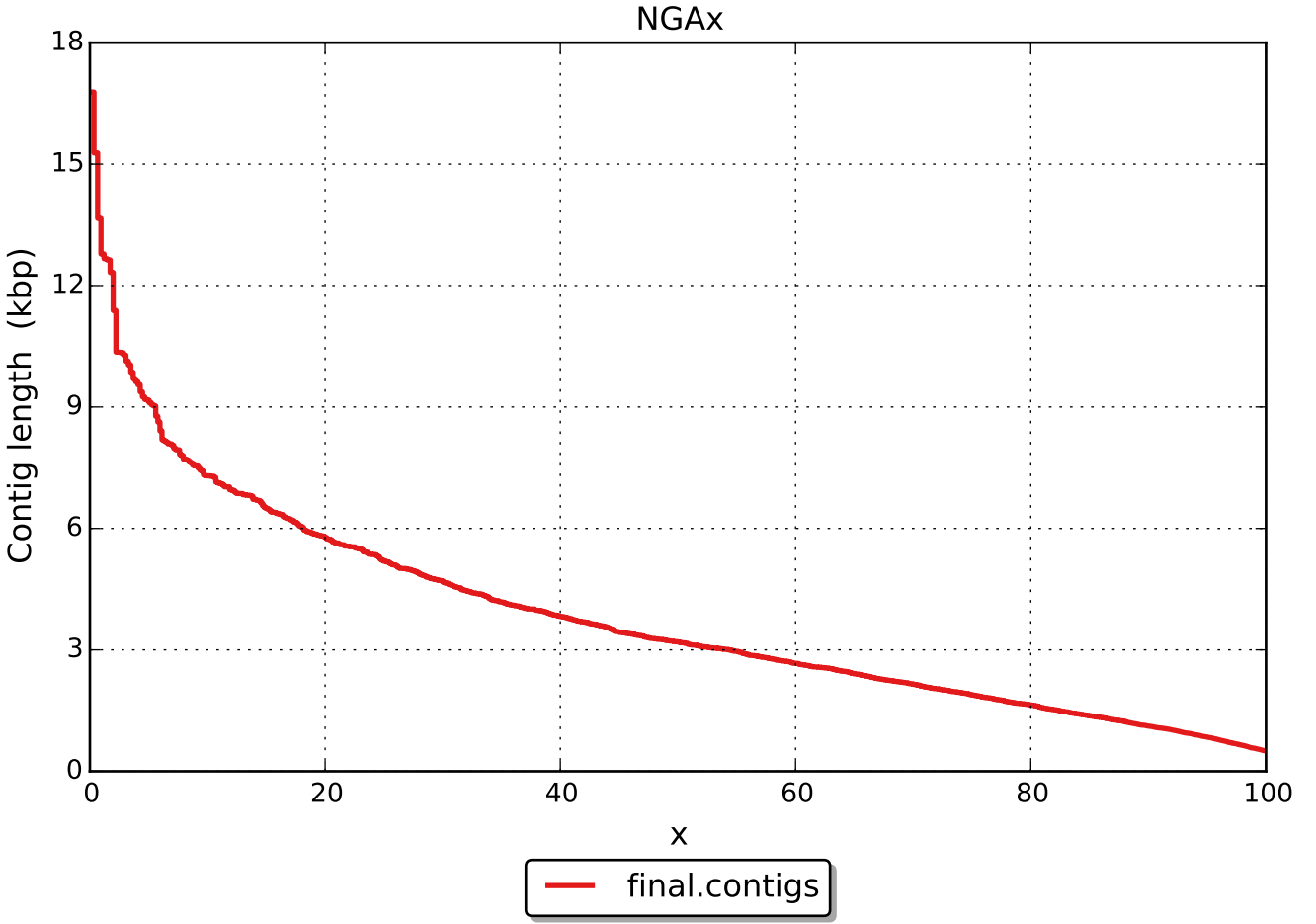

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
500
1000
1500
2000
2500
Contig index
final.contigs
Reference


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
500
1000
1500
2000
2500
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
18
15
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
18
15
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs