Report

	final.contigs
# contigs (>= 0 bp)	1102
# contigs (>= 1000 bp)	907
# contigs (>= 5000 bp)	326
# contigs (>= 10000 bp)	91
# contigs (>= 25000 bp)	4
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	4602703
Total length (>= 1000 bp)	4479604
Total length (>= 5000 bp)	2949468
Total length (>= 10000 bp)	1304949
Total length (>= 25000 bp)	110743
Total length (>= 50000 bp)	0
# contigs	1041
Largest contig	31232
Total length	4578485
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	6693
NG50	6681
N75	3941
NG75	3794
L50	214
LG50	219
L75	436
LG75	448
# misassemblies	8
# misassembled contigs	8
Misassembled contigs length	66802
# local misassemblies	7
# unaligned contigs	0 + 2 part
Unaligned length	147
Genome fraction (%)	97.379
Duplication ratio	1.013
# N's per 100 kbp	0.00
# mismatches per 100 kbp	183.45
# indels per 100 kbp	0.31
Largest alignment	31232
NA50	6689
NGA50	6673
NA75	3866
NGA75	3707
LA50	216
LGA50	221
LA75	440
LGA75	452

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

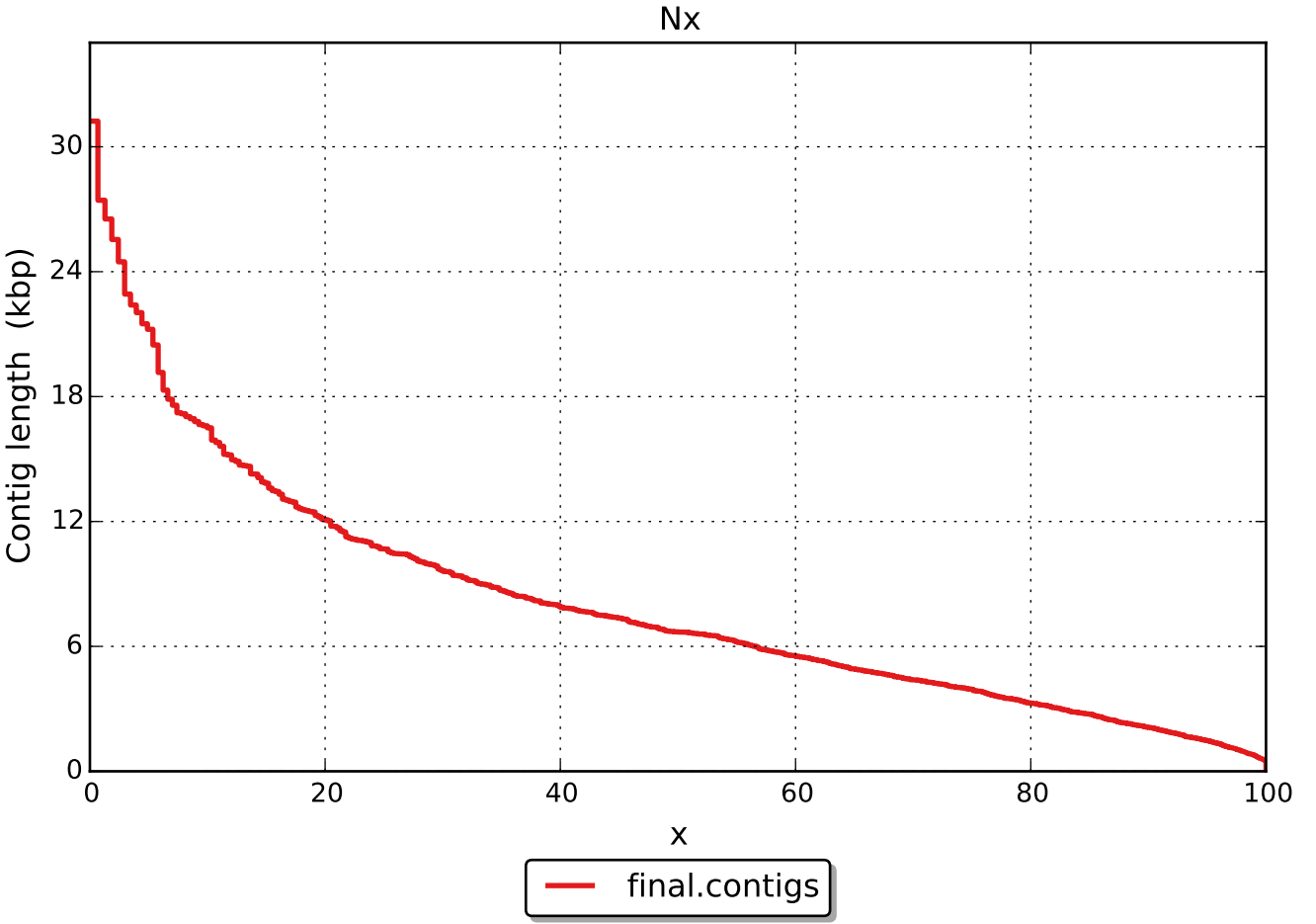
	final.contigs
# misassemblies	8
# relocations	8
# translocations	0
# inversions	0
# misassembled contigs	8
Misassembled contigs length	66802
# local misassemblies	7
# mismatches	8292
# indels	14
# short indels	14
# long indels	0
Indels length	27

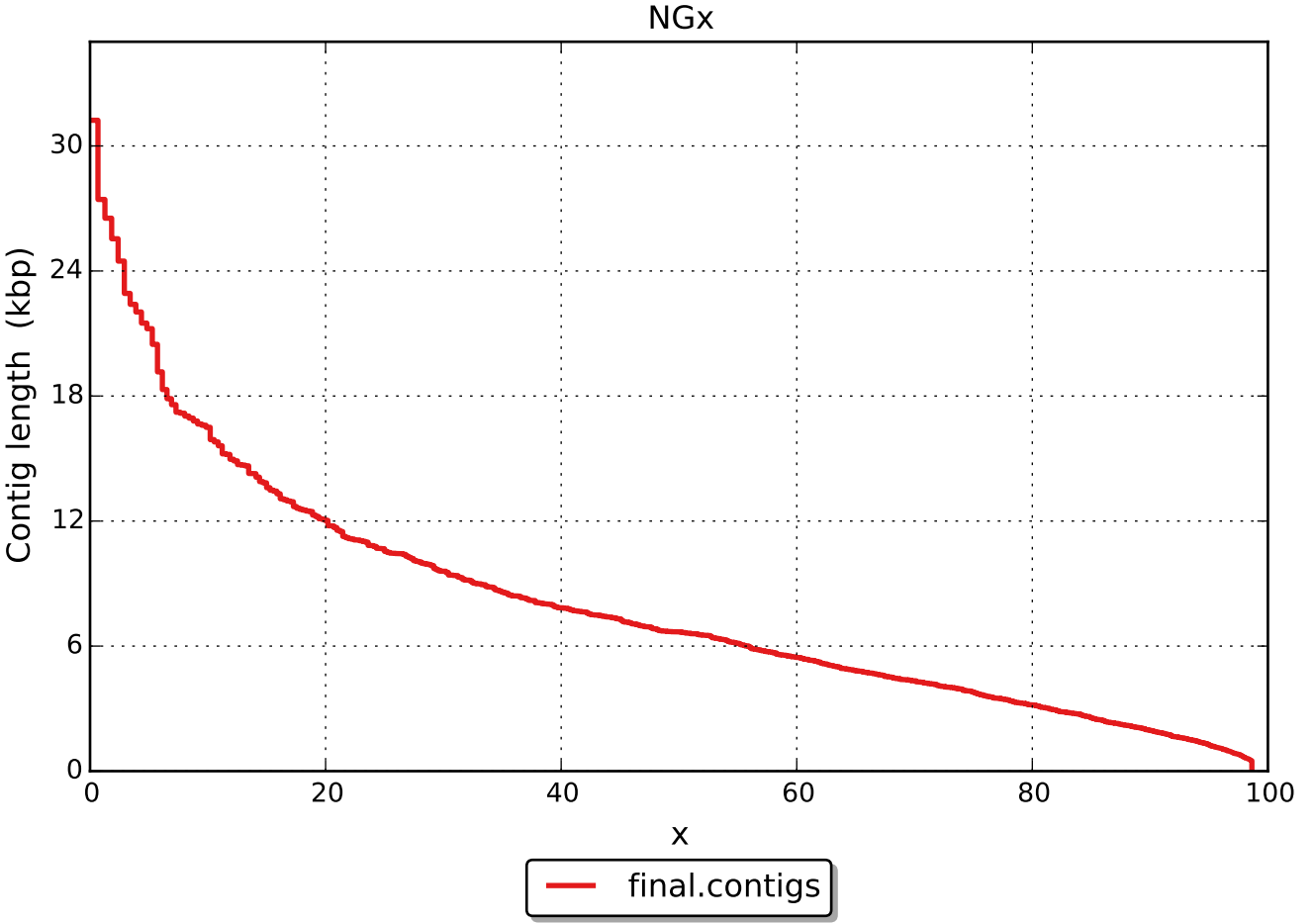
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

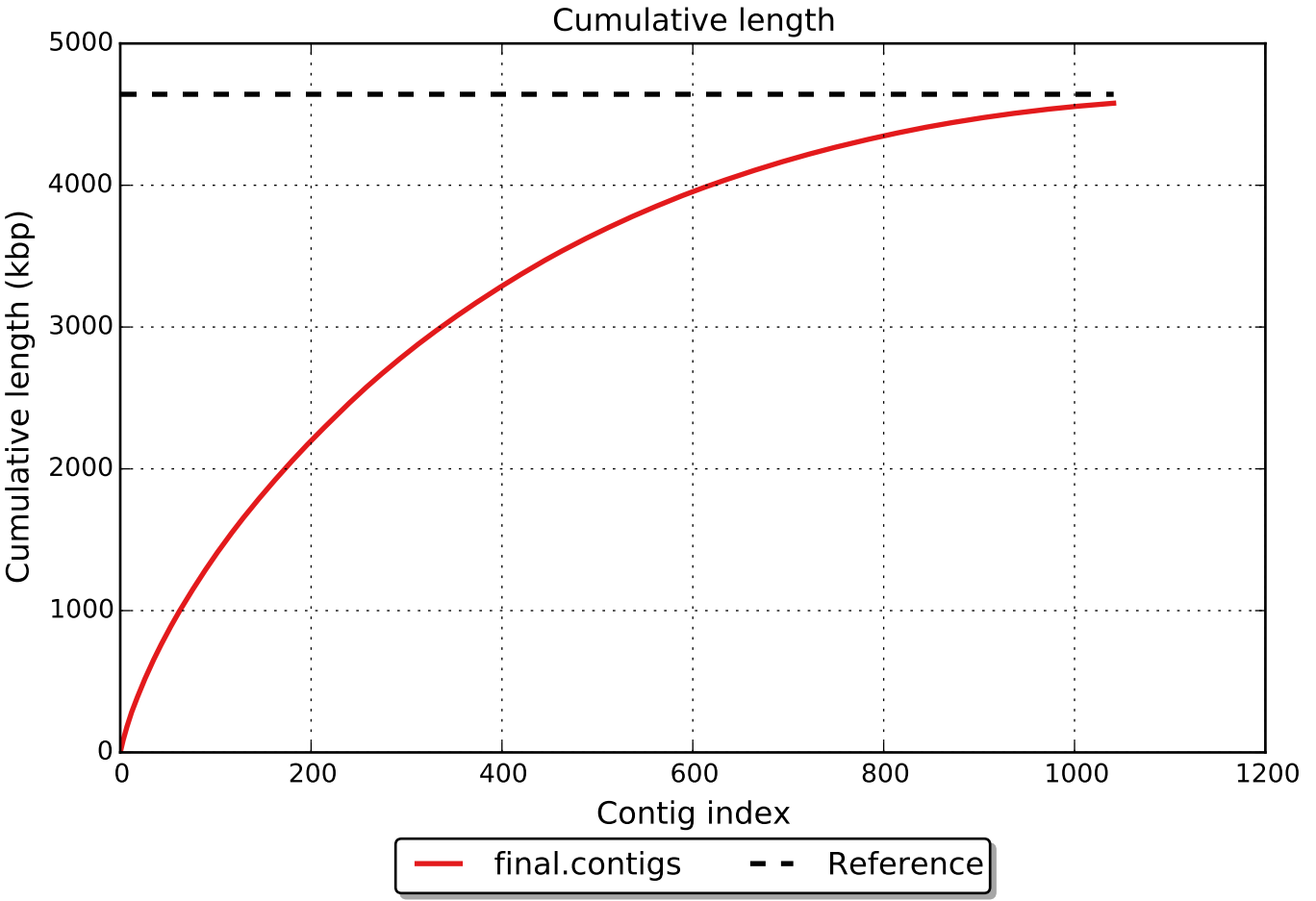
Unaligned report

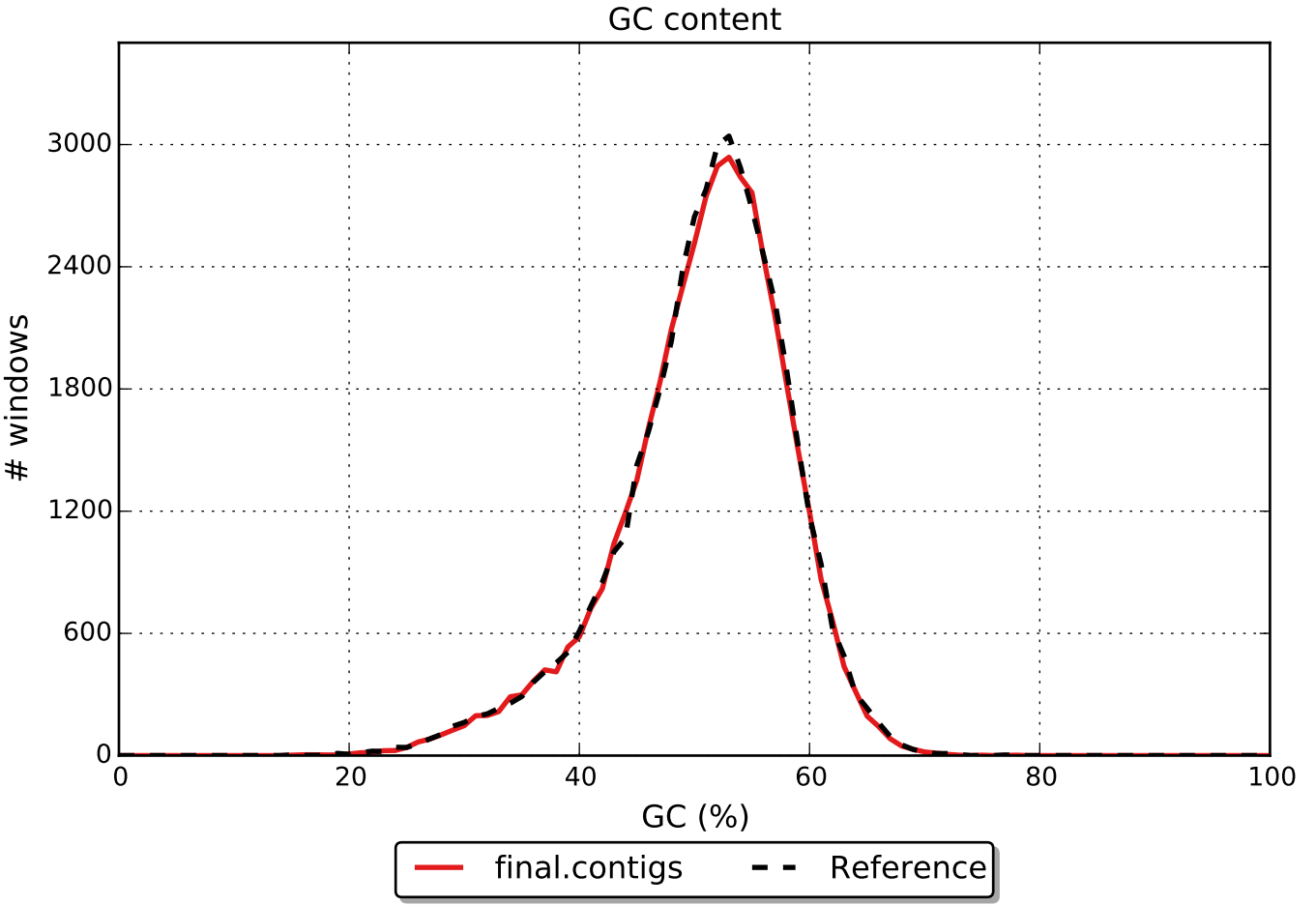
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	147
# N's	0

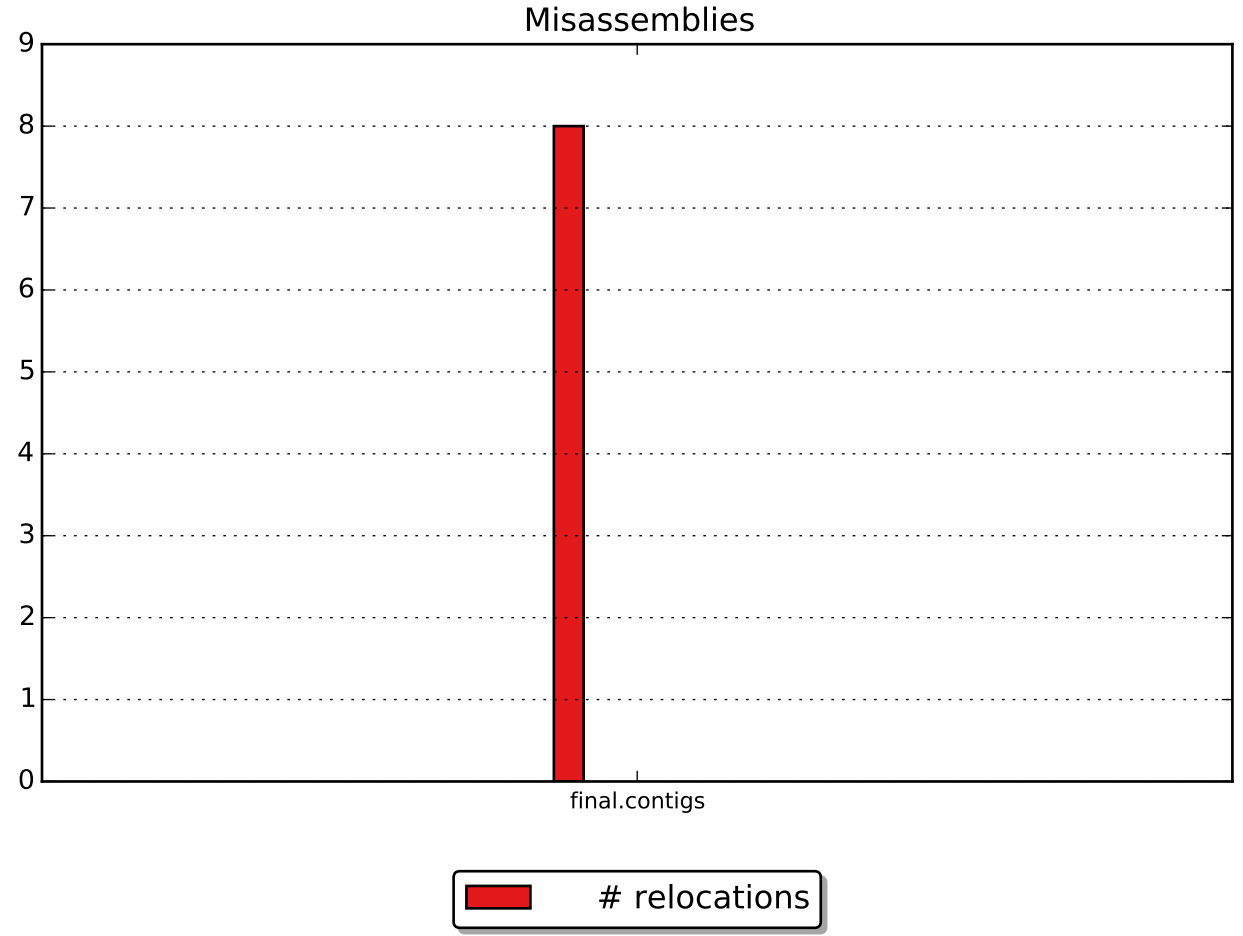
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

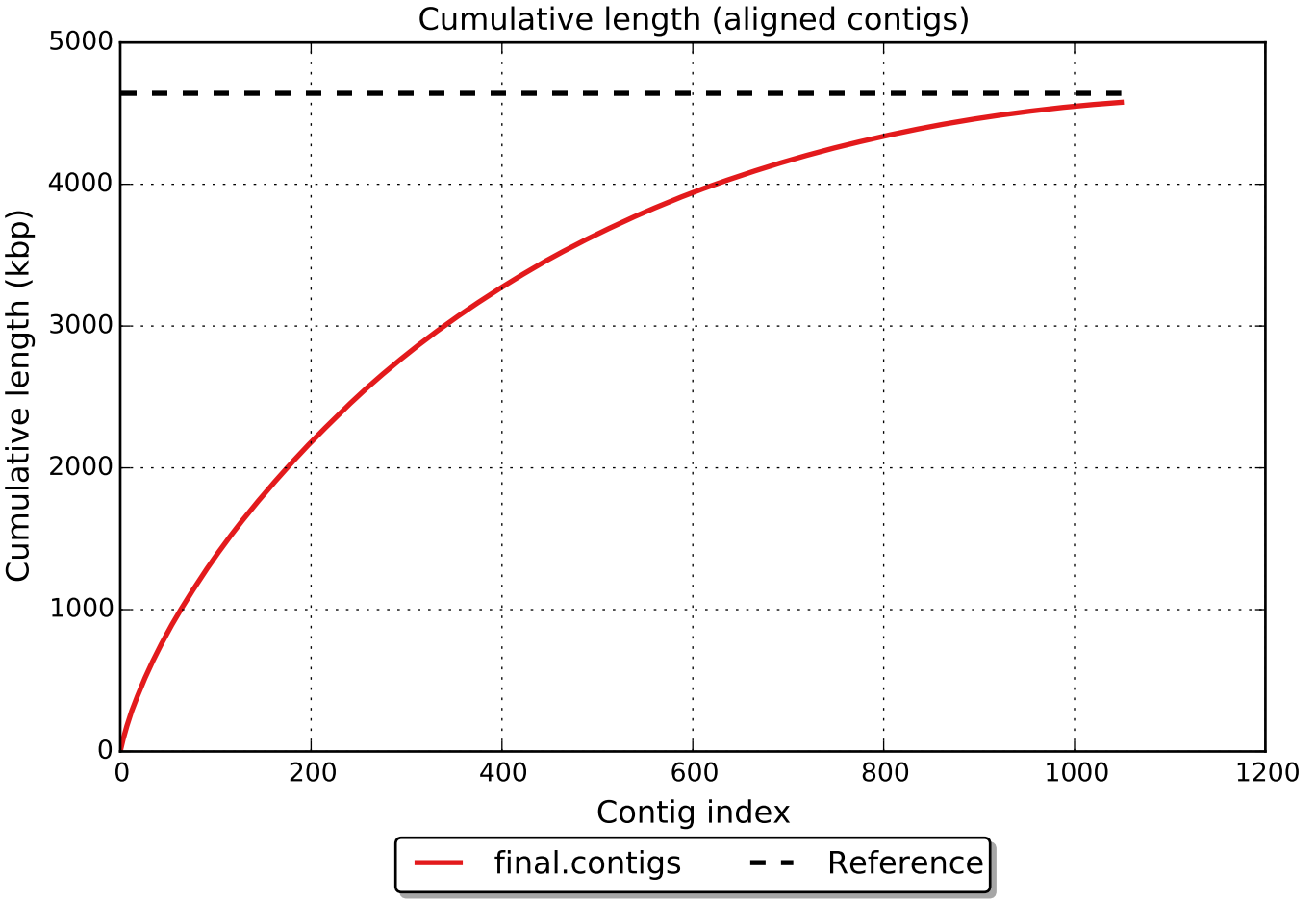

Nx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
final.contigs

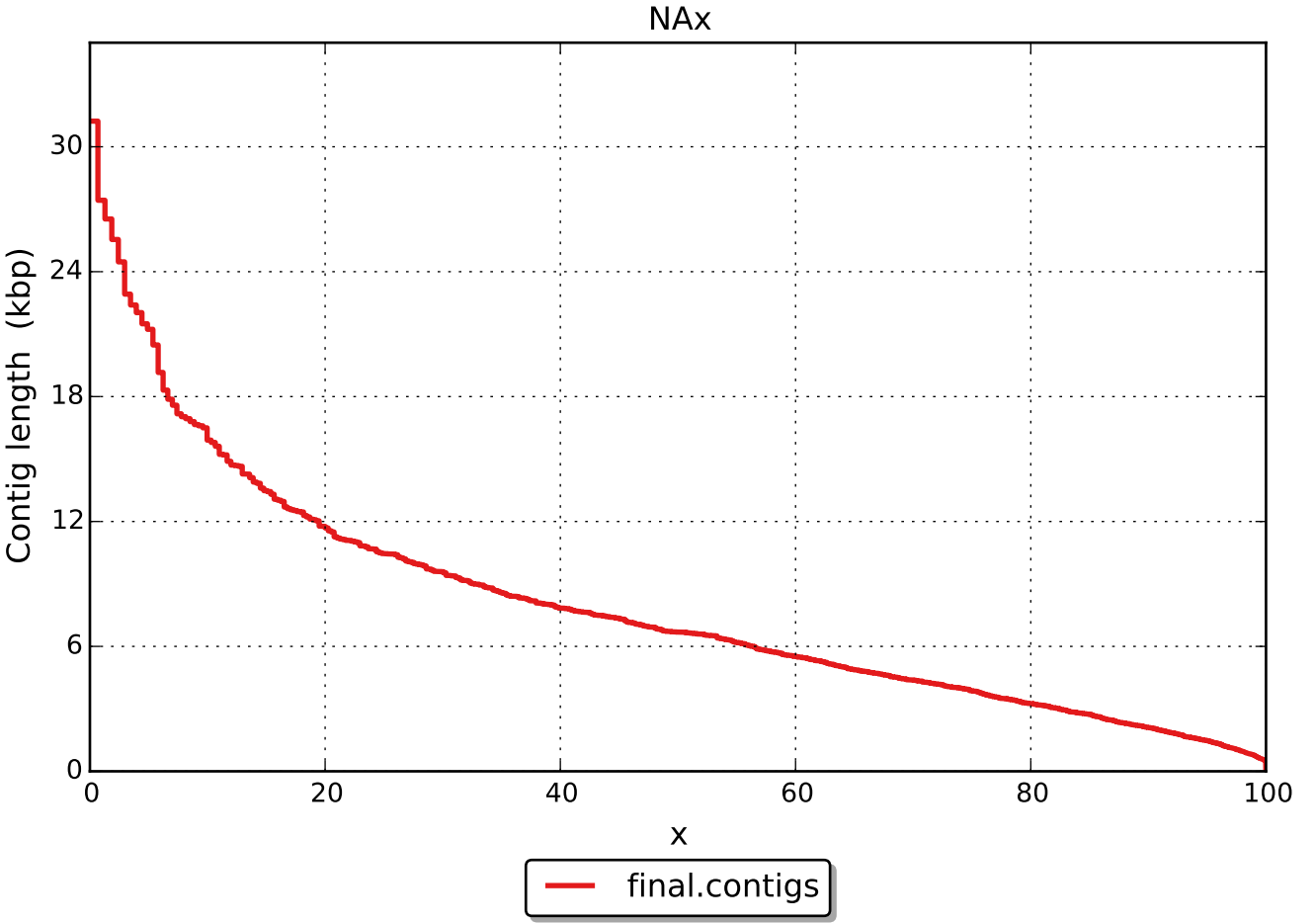

NGx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
final.contigs

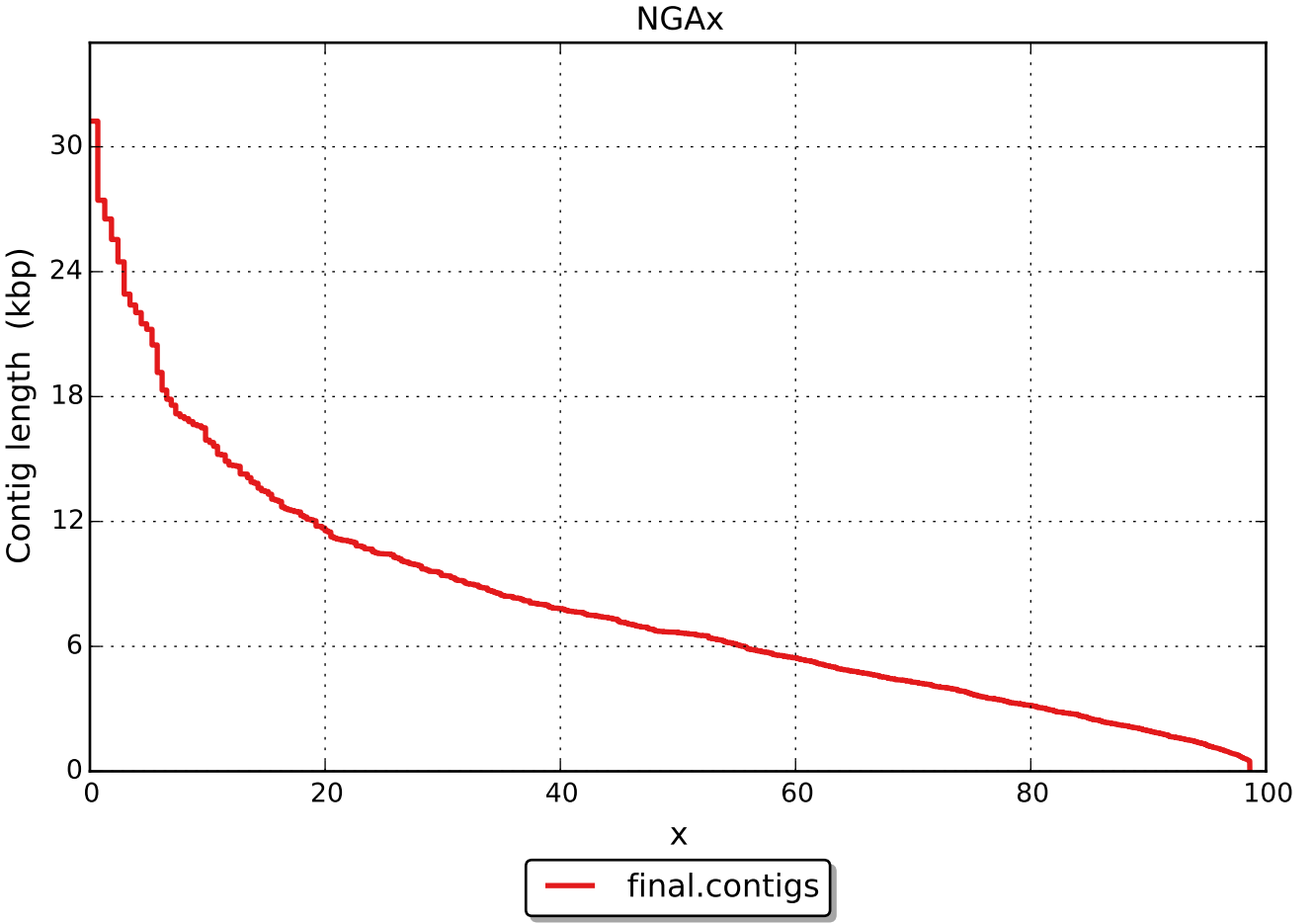

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
200
400
600
800
1000
1200
Contig index
final.contigs
Reference


GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference


Misassemblies
9
8
7
6
5
4
3
2
1
0
final.contigs
relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
200
400
600
800
1000
1200
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
final.contigs