Report

	final.contigs
# contigs (>= 0 bp)	2114
# contigs (>= 1000 bp)	726
# contigs (>= 5000 bp)	356
# contigs (>= 10000 bp)	138
# contigs (>= 25000 bp)	9
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	5251951
Total length (>= 1000 bp)	4688033
Total length (>= 5000 bp)	3677081
Total length (>= 10000 bp)	2127605
Total length (>= 25000 bp)	251349
Total length (>= 50000 bp)	0
# contigs	911
Largest contig	33629
Total length	4808591
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	9179
NG50	9477
N75	5142
NG75	5487
L50	167
LG50	158
L75	343
LG75	319
# misassemblies	9
# misassembled contigs	8
Misassembled contigs length	30694
# local misassemblies	8
# unaligned contigs	48 + 15 part
Unaligned length	29382
Genome fraction (%)	98.515
Duplication ratio	1.045
# N's per 100 kbp	0.00
# mismatches per 100 kbp	180.57
# indels per 100 kbp	0.44
Largest alignment	33627
NA50	9179
NGA50	9474
NA75	5136
NGA75	5433
LA50	167
LGA50	158
LA75	343
LGA75	320

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

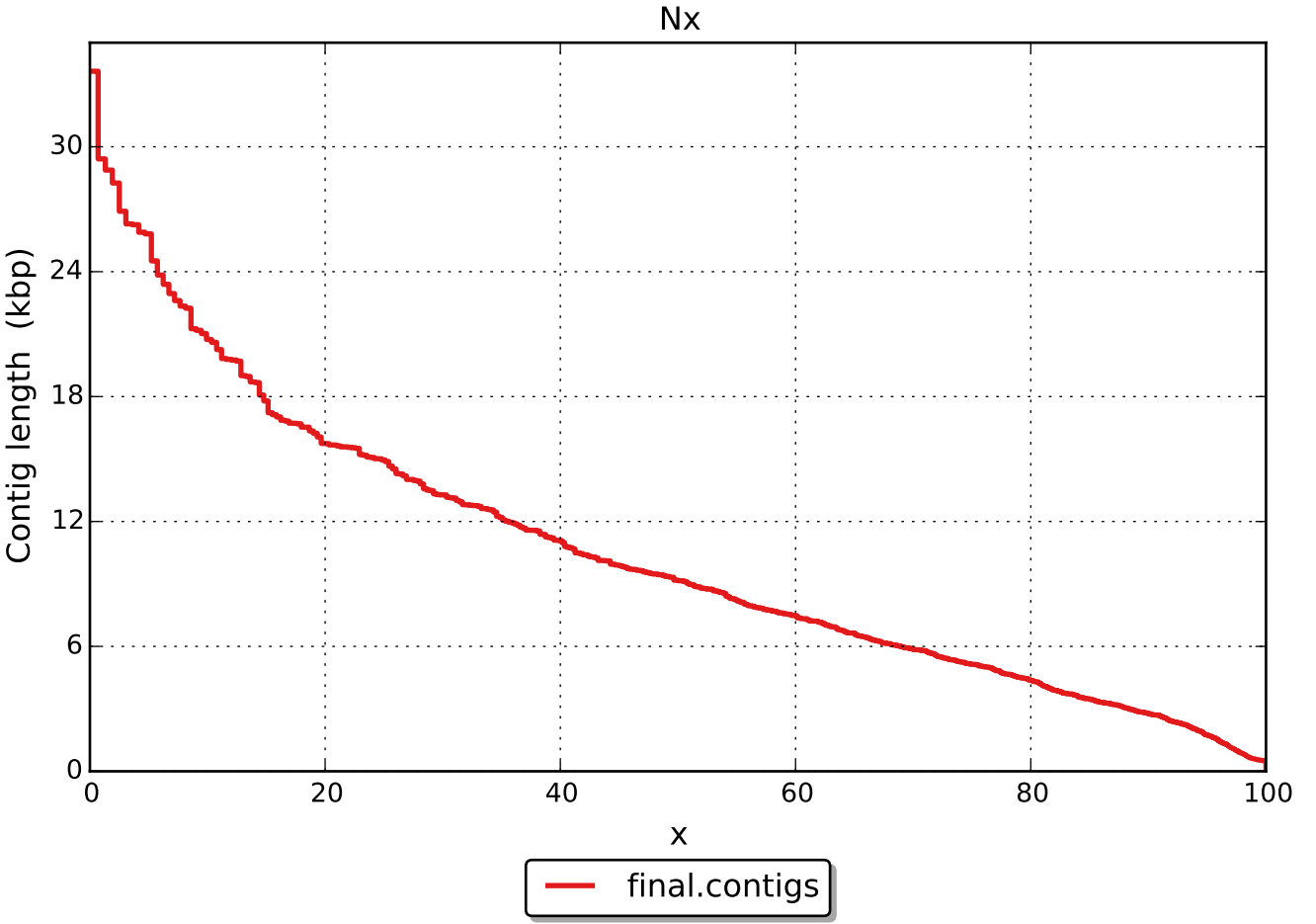
	final.contigs
# misassemblies	9
# relocations	9
# translocations	0
# inversions	0
# misassembled contigs	8
Misassembled contigs length	30694
# local misassemblies	8
# mismatches	8257
# indels	20
# short indels	20
# long indels	0
Indels length	20

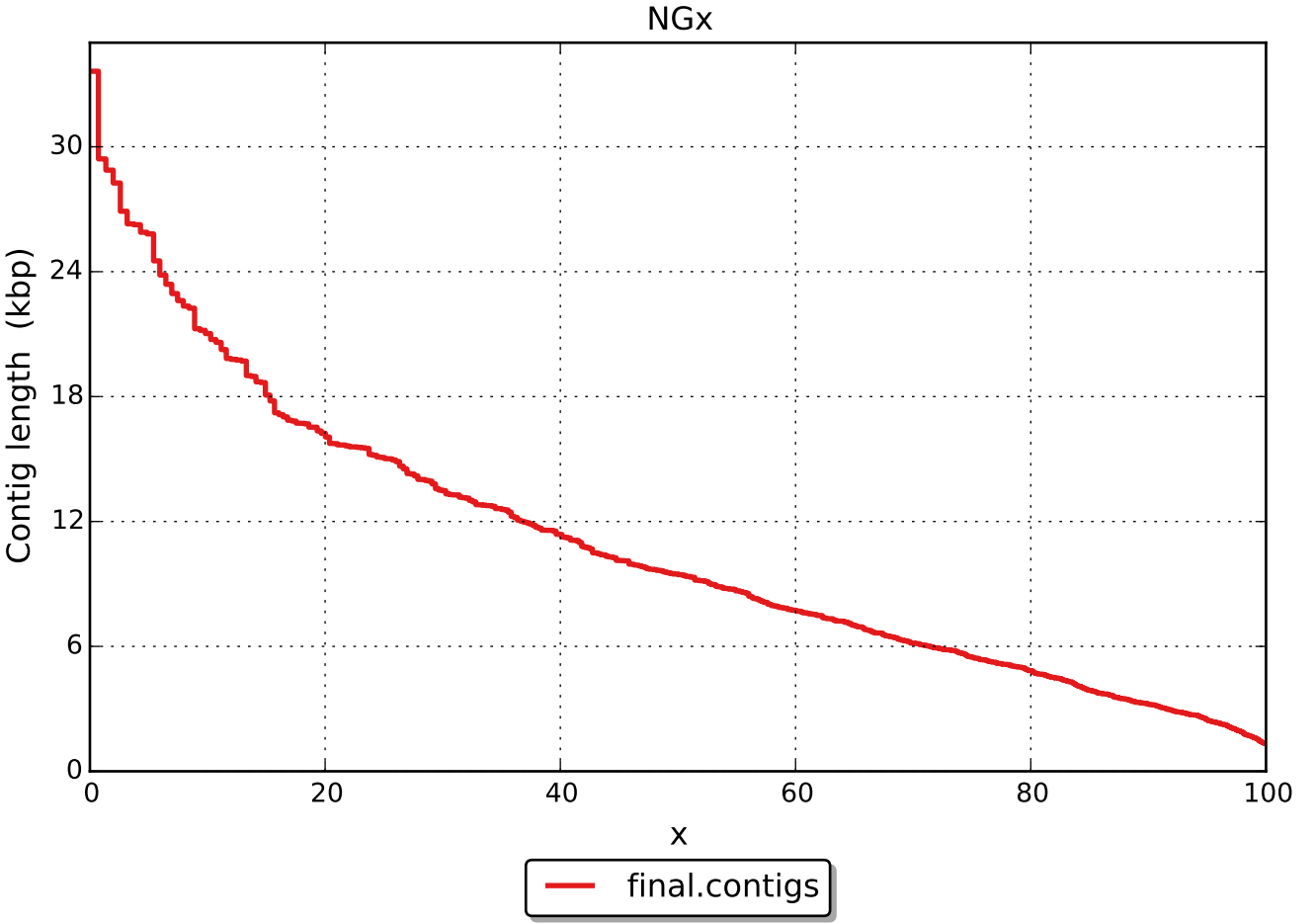
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

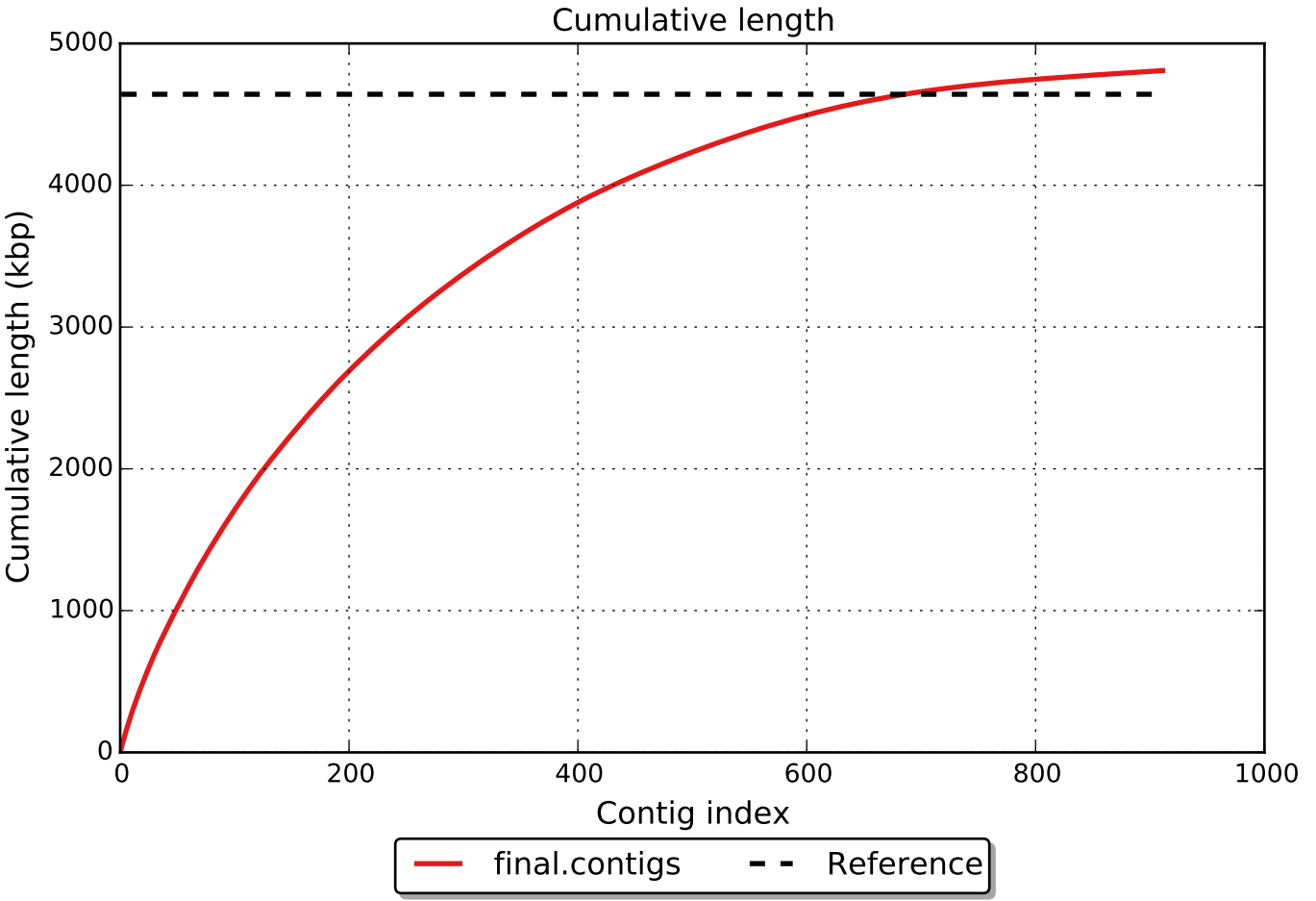
Unaligned report

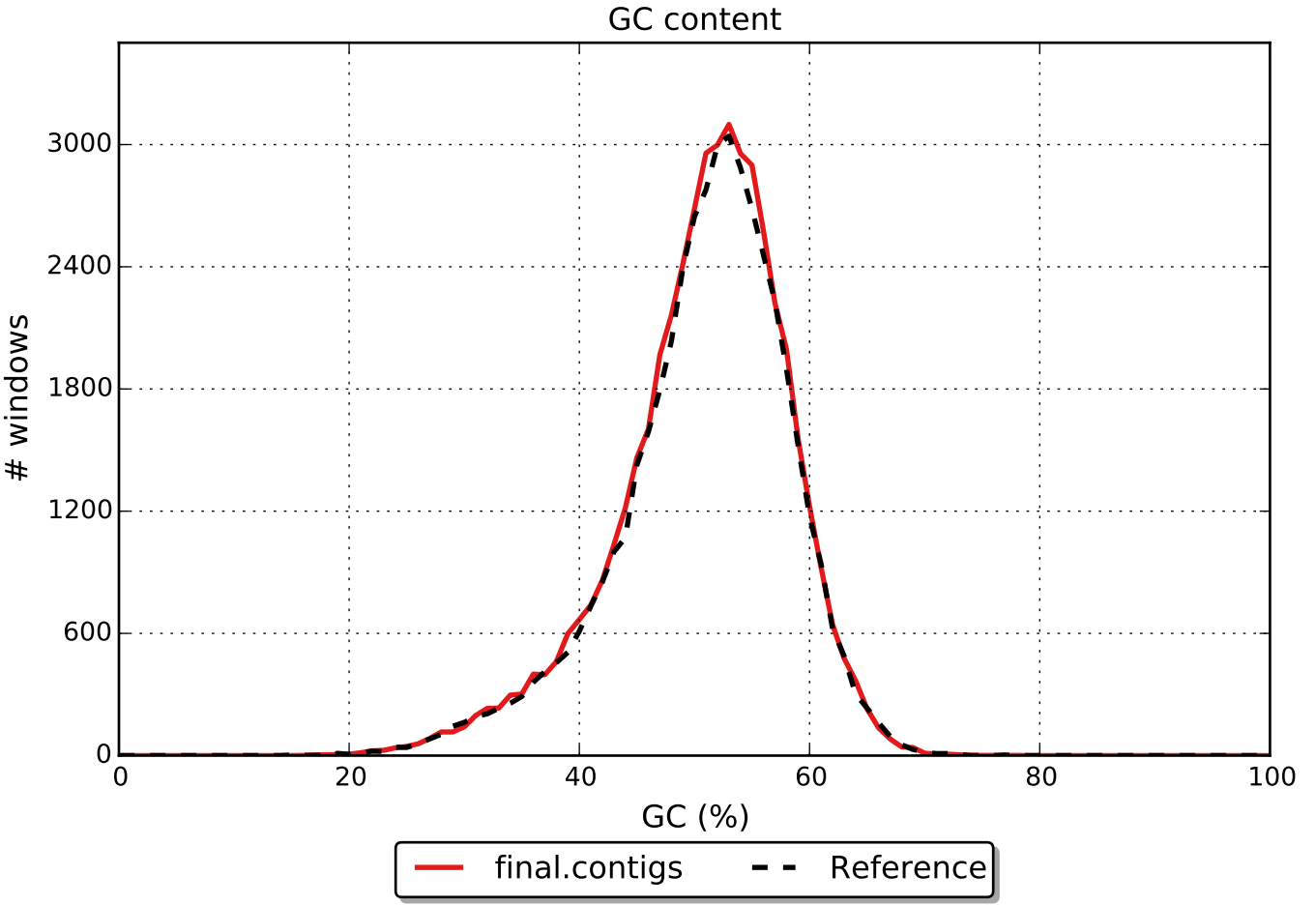
	final.contigs
# fully unaligned contigs	48
Fully unaligned length	27619
# partially unaligned contigs	15
# with misassembly	0
# both parts are significant	0
Partially unaligned length	1763
# N's	0

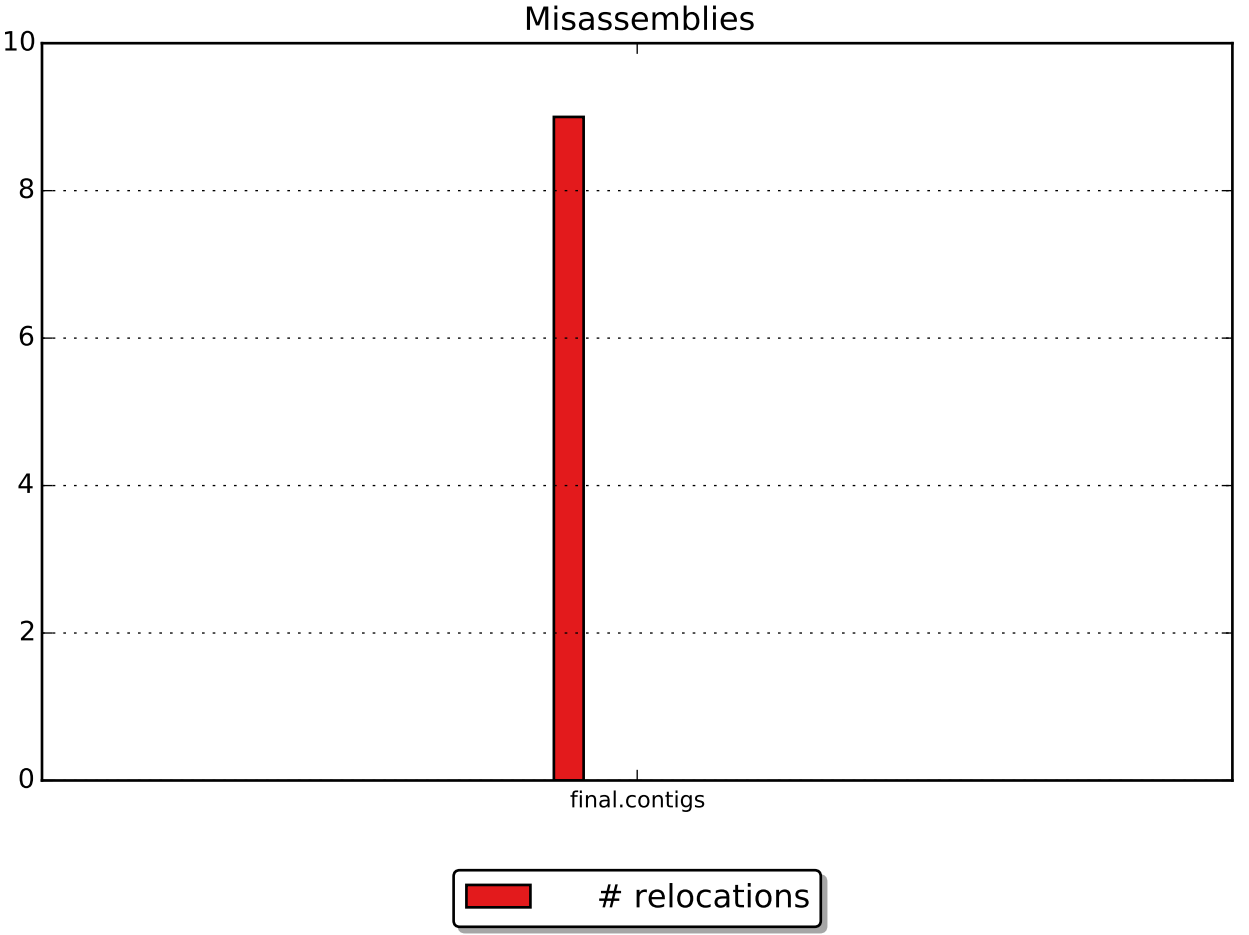
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

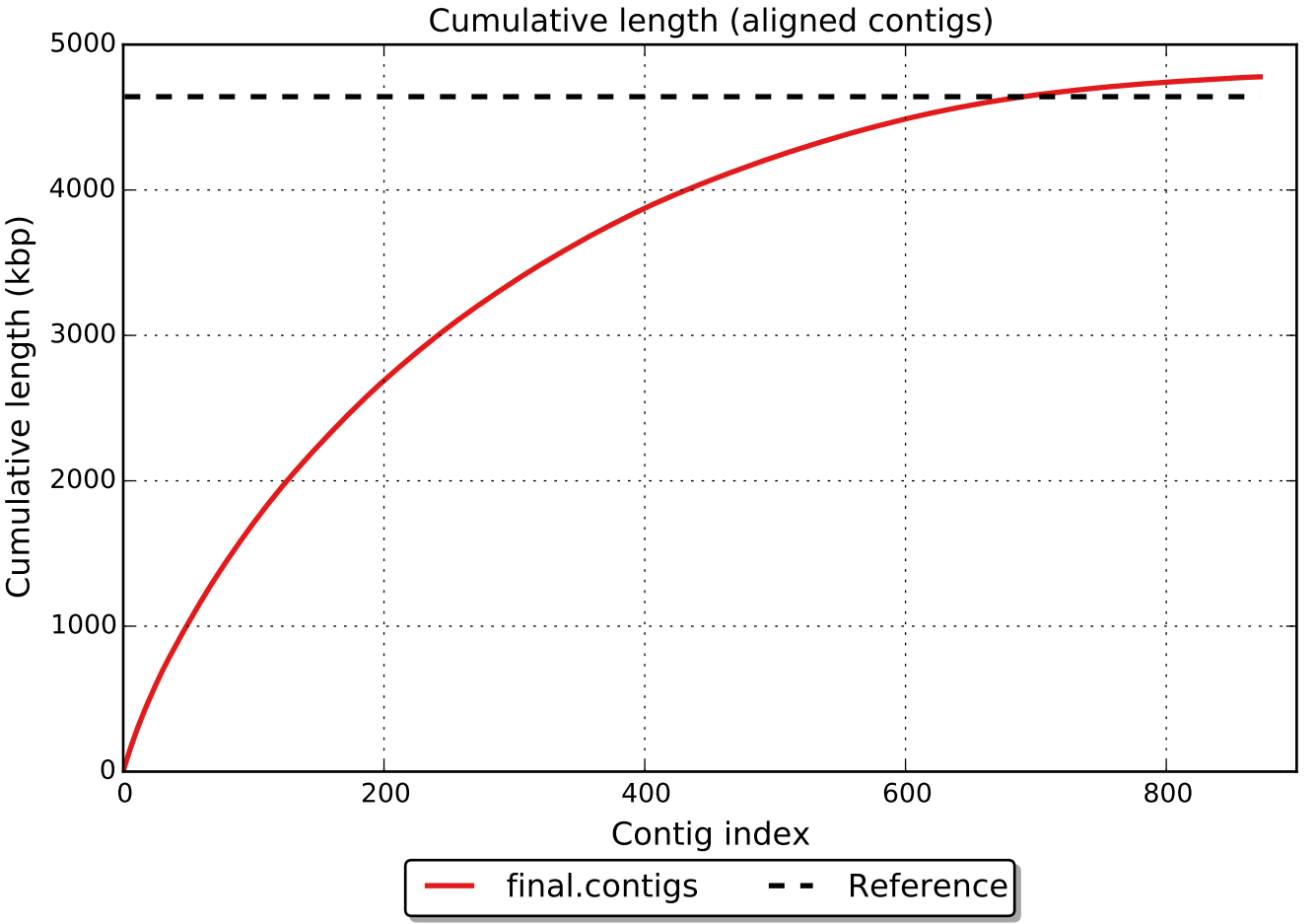

Nx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
final.contigs

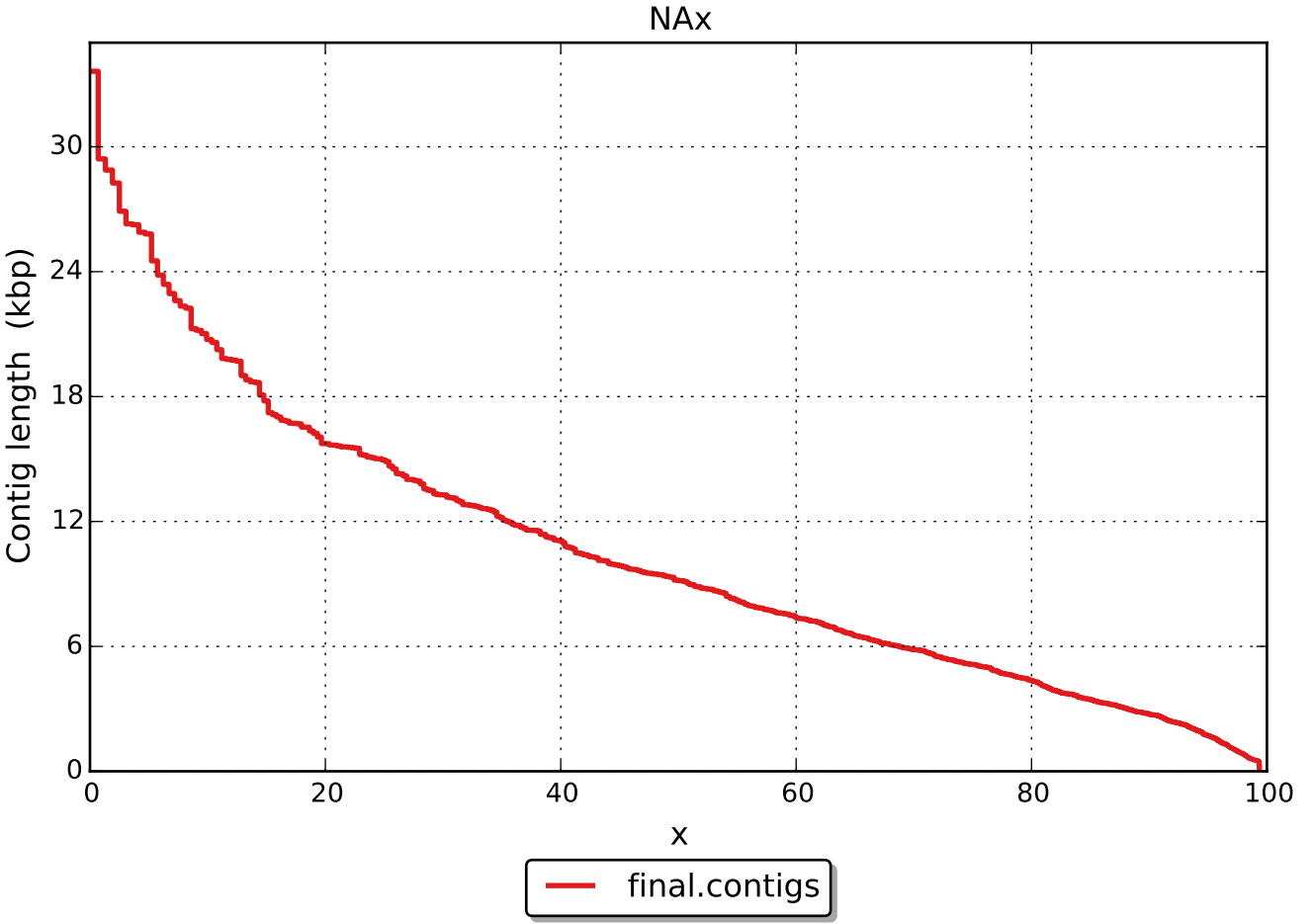

NGx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
final.contigs

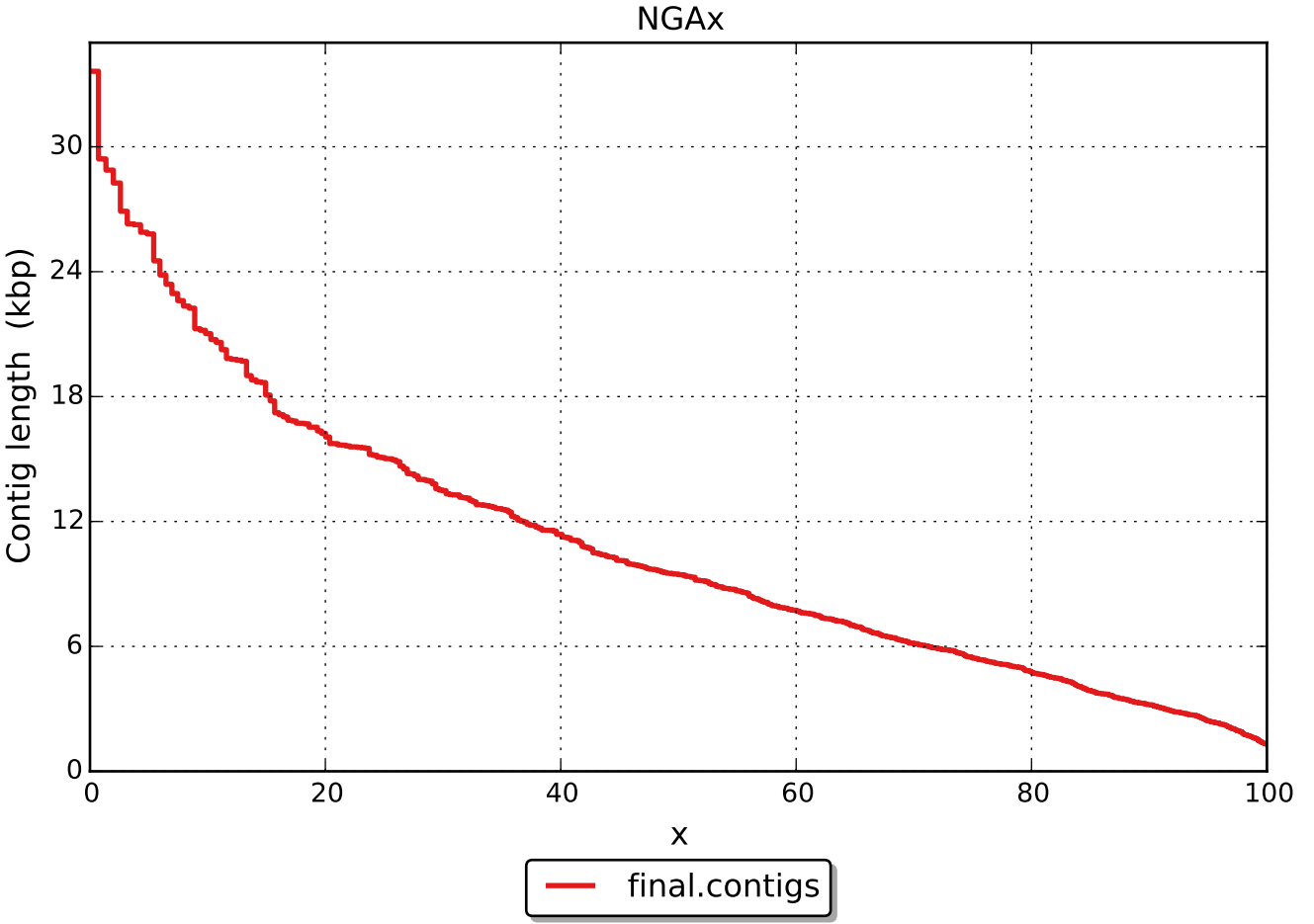

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
200
400
600
800
1000
Contig index
final.contigs
Reference


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


Misassemblies
10
8
6
4
2
0
final.contigs
relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
200
400
600
800
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