Report

	final.contigs
# contigs (>= 1000 bp)	1456
# contigs (>= 5000 bp)	198
# contigs (>= 10000 bp)	16
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4356951
Total length (>= 5000 bp)	1368068
Total length (>= 10000 bp)	186164
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1868
Largest contig	16655
Total length	4661944
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	3417
NG50	3429
N75	2053
NG75	2067
L50	432
LG50	429
L75	876
LG75	868
# misassemblies	8
# misassembled contigs	8
Misassembled contigs length	50881
# local misassemblies	5
# unaligned contigs	0 + 2 part
Unaligned length	516
Genome fraction (%)	96.583
Duplication ratio	1.040
# N's per 100 kbp	0.00
# mismatches per 100 kbp	361.81
# indels per 100 kbp	0.42
Largest alignment	14941
NA50	3391
NGA50	3411
NA75	2048
NGA75	2066
LA50	436
LGA50	433
LA75	880
LGA75	872

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

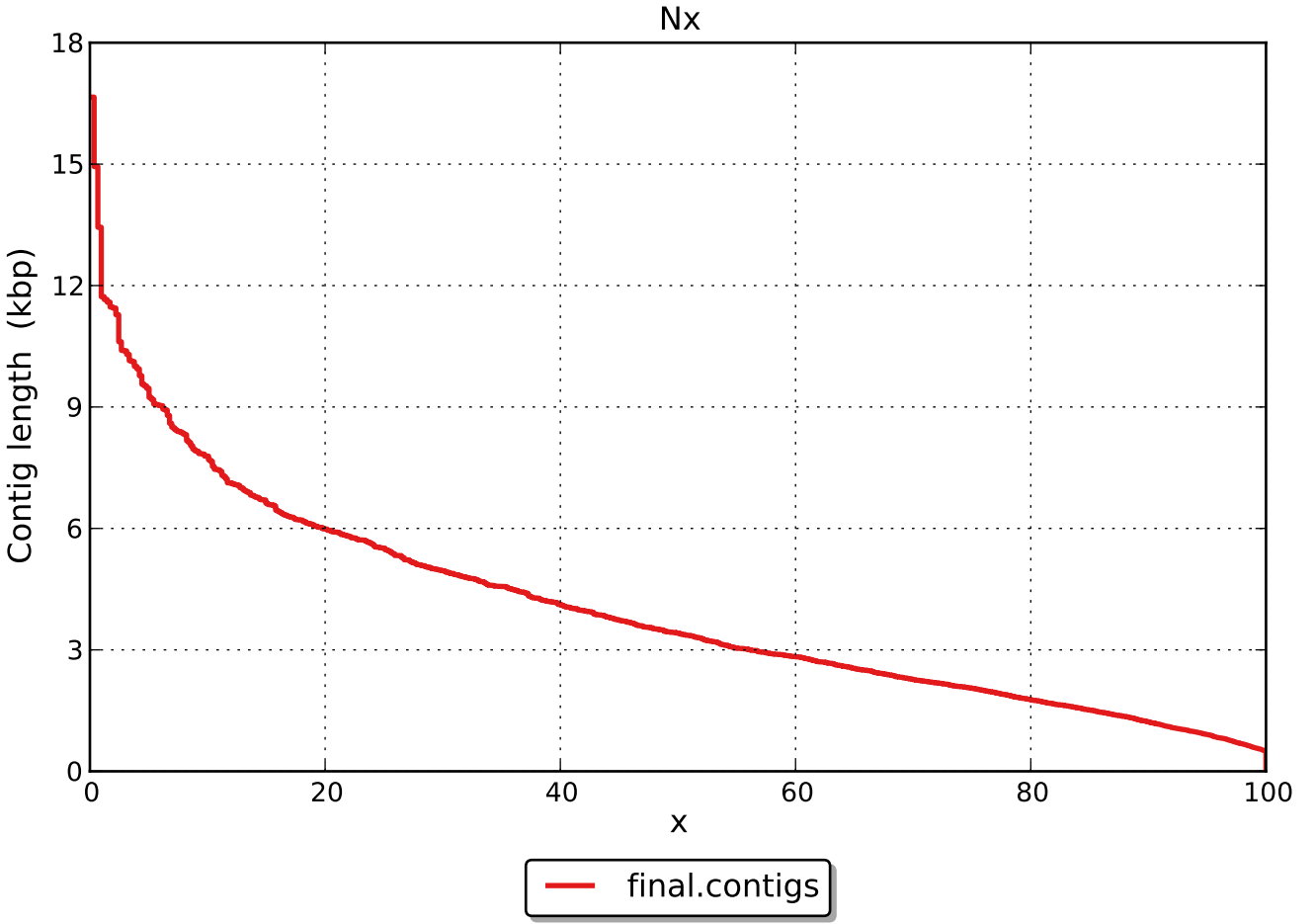
	final.contigs
# misassemblies	8
# relocations	8
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	8
Misassembled contigs length	50881
# local misassemblies	5
# mismatches	16220
# indels	19
# short indels	19
# long indels	0
Indels length	19

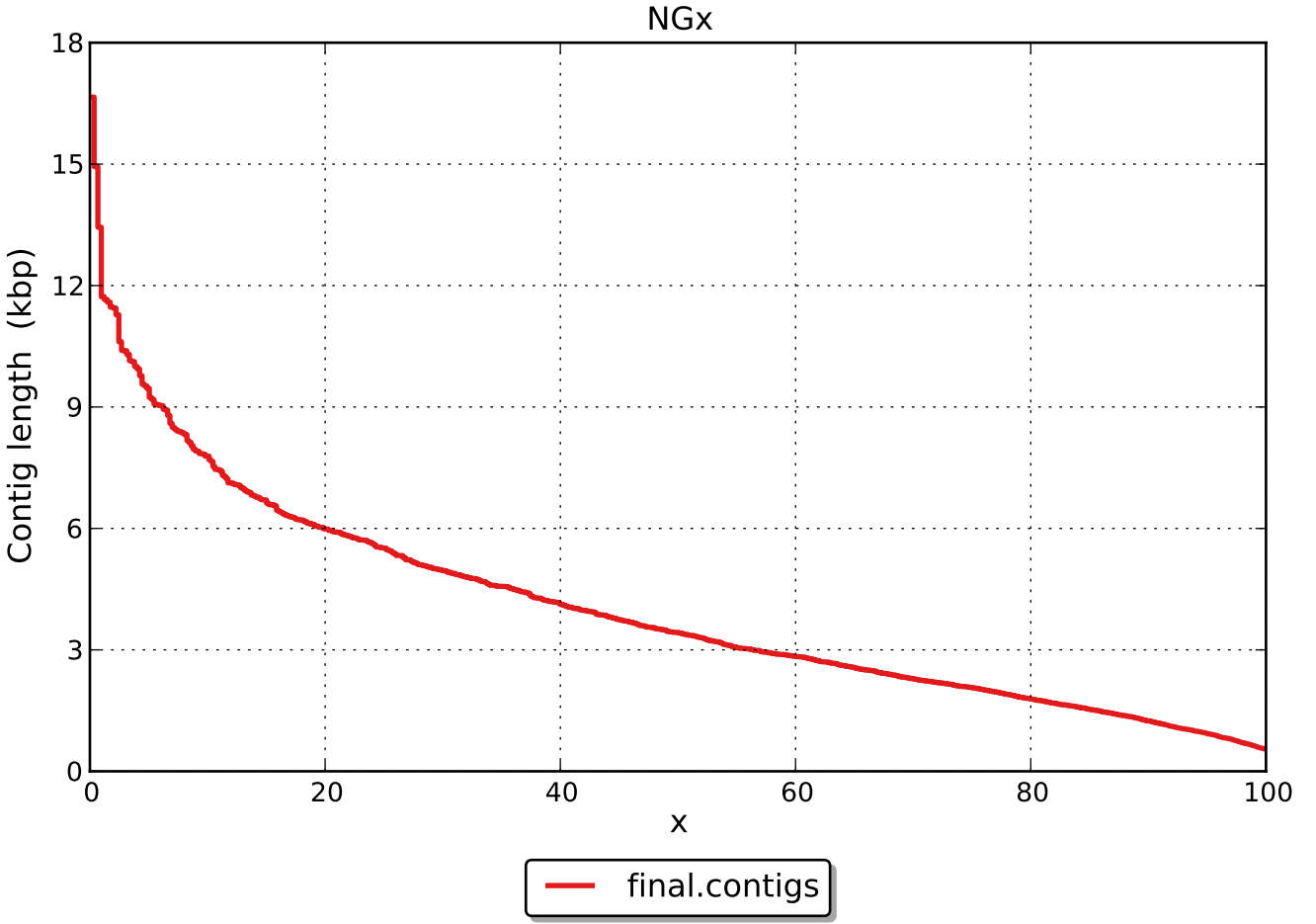
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

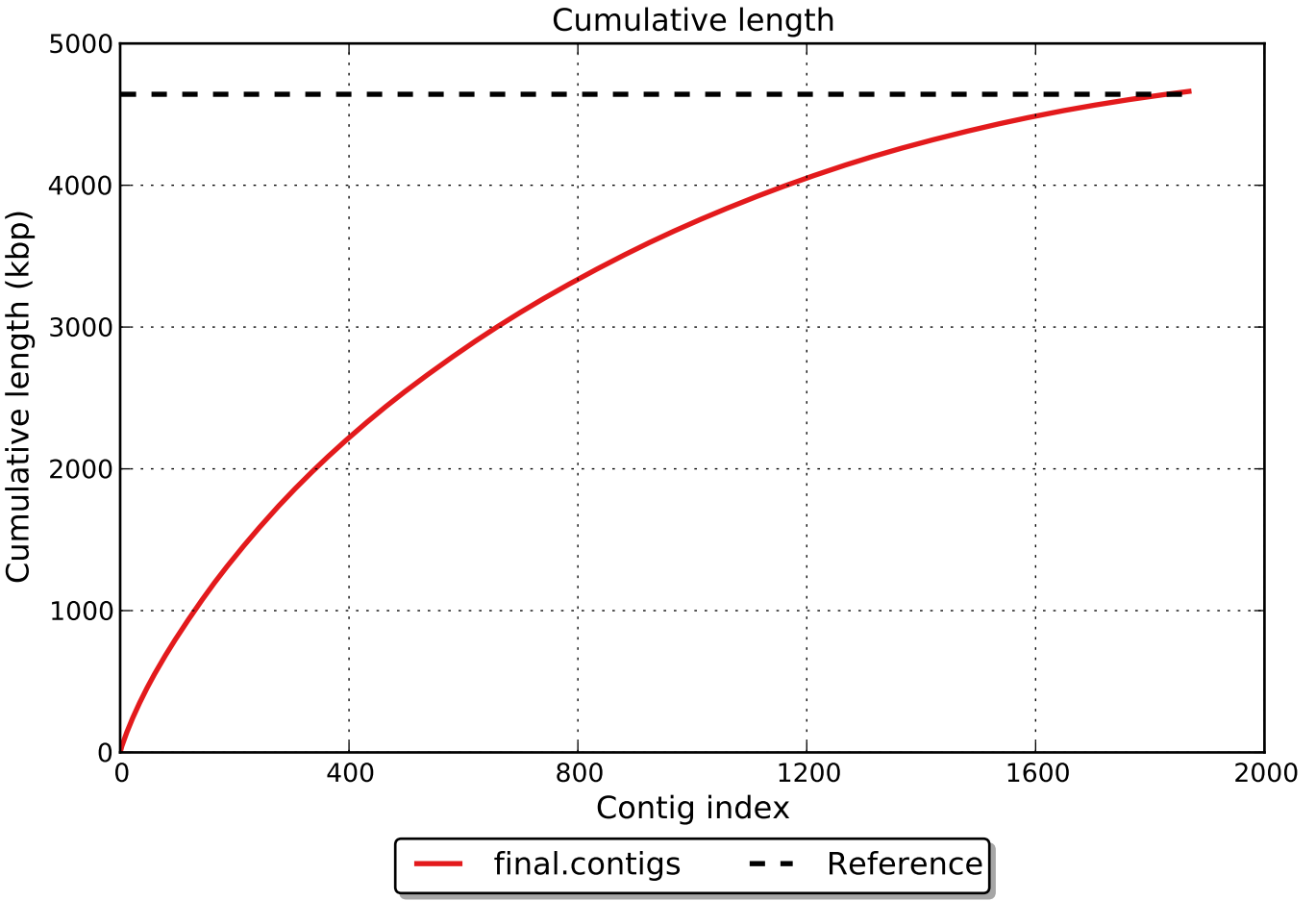
Unaligned report

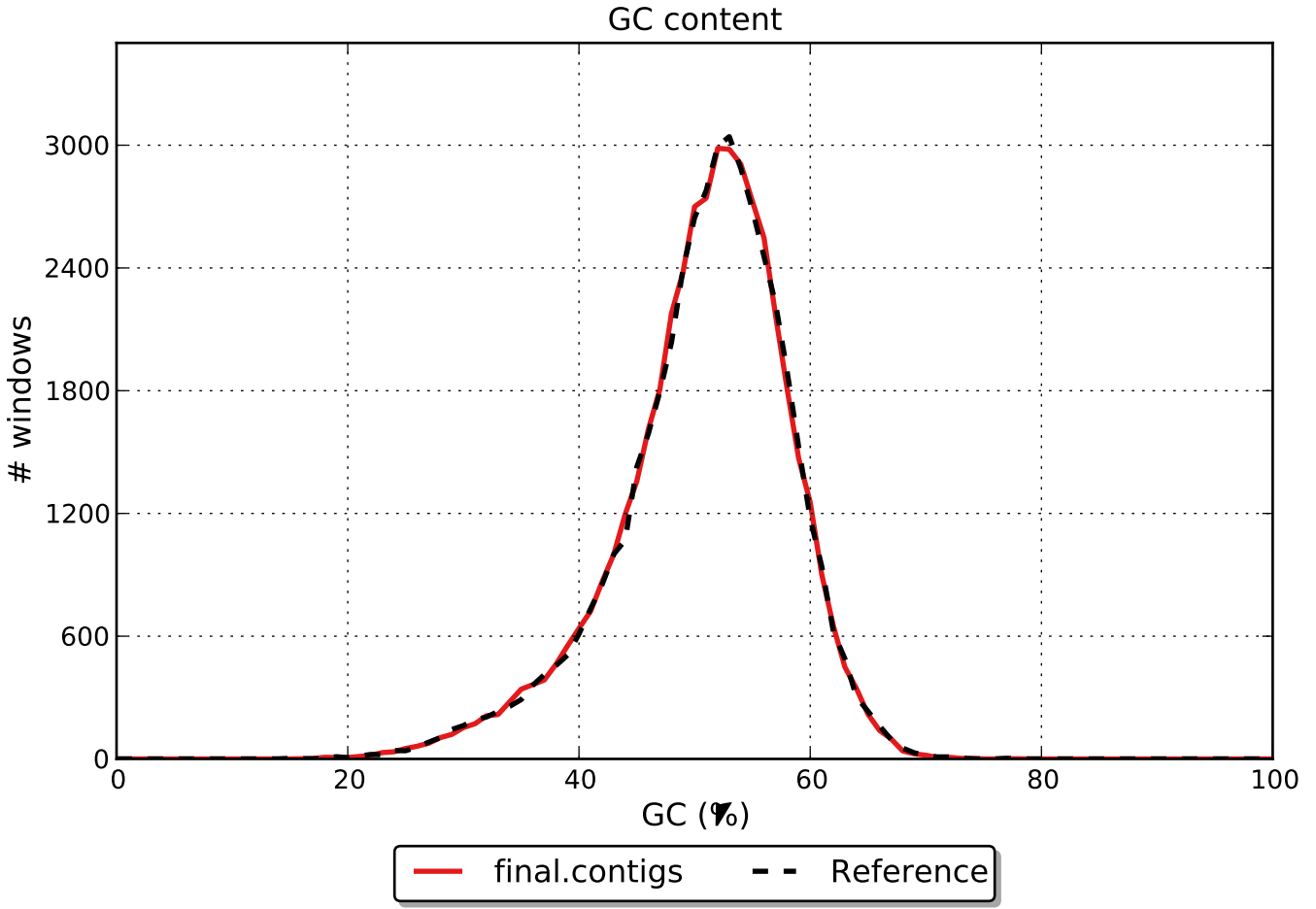
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	516
# N's	0

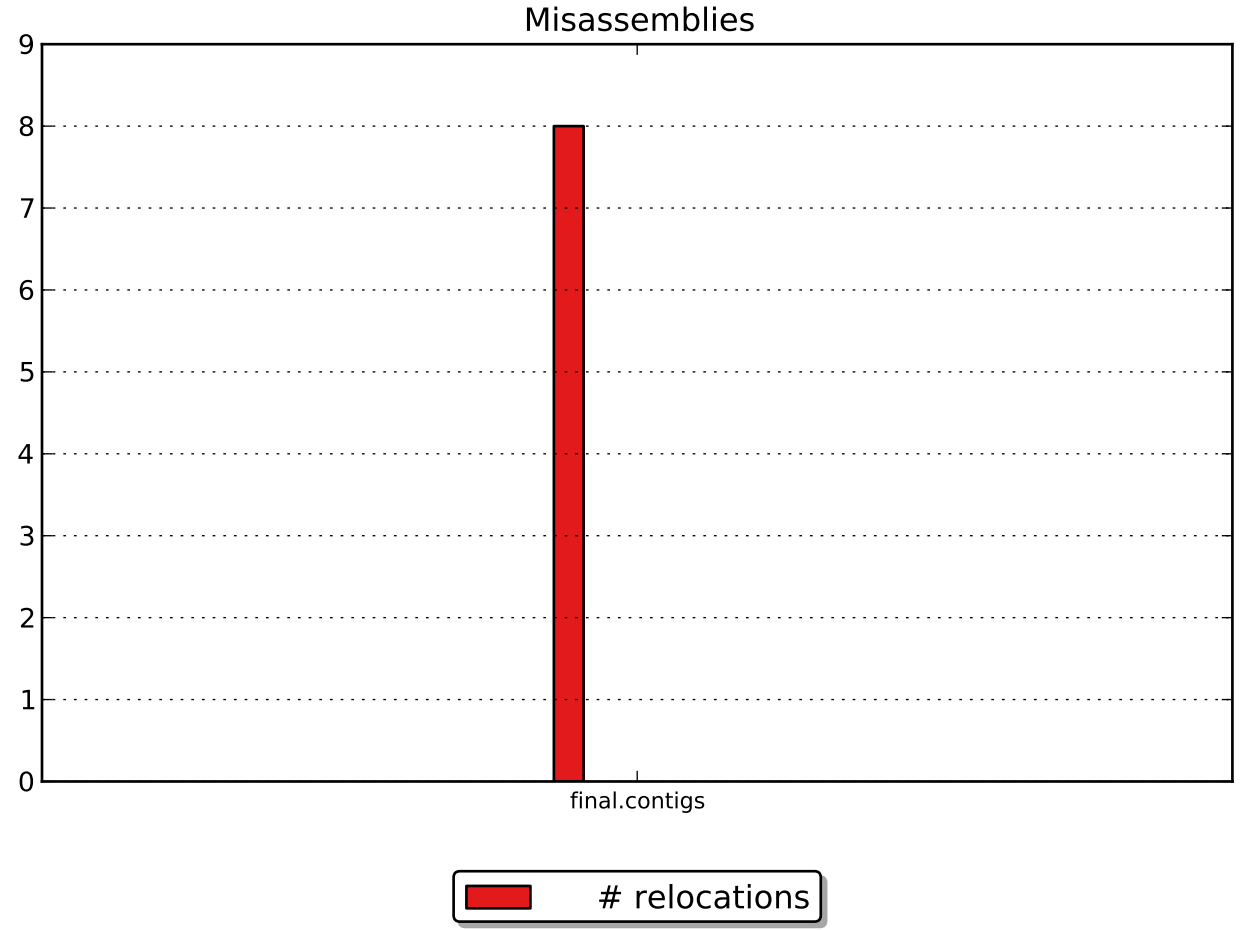
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

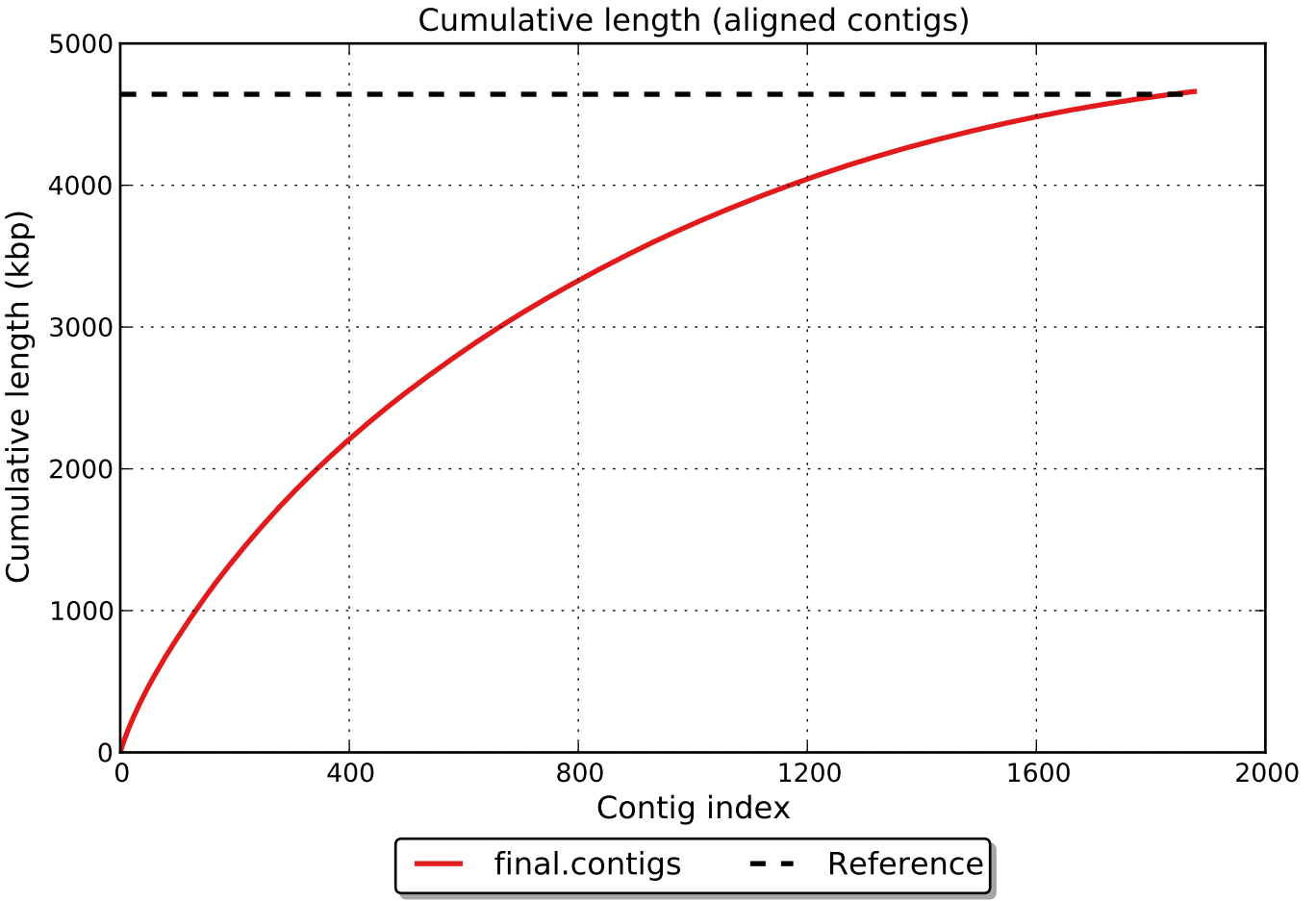

Nx
Contig length (kbp)
18
15
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs

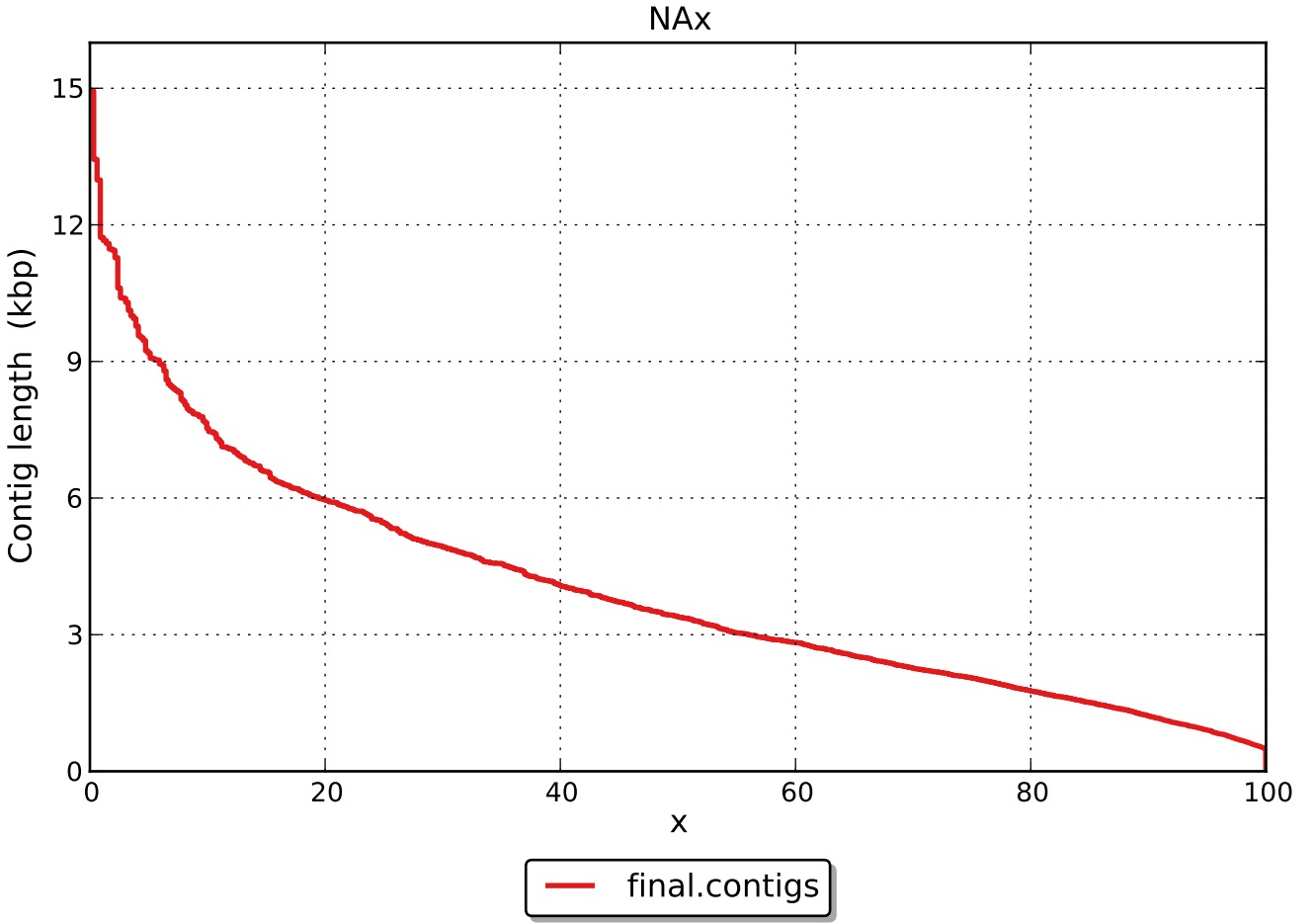

NGx
Contig length (kbp)
18
15
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs

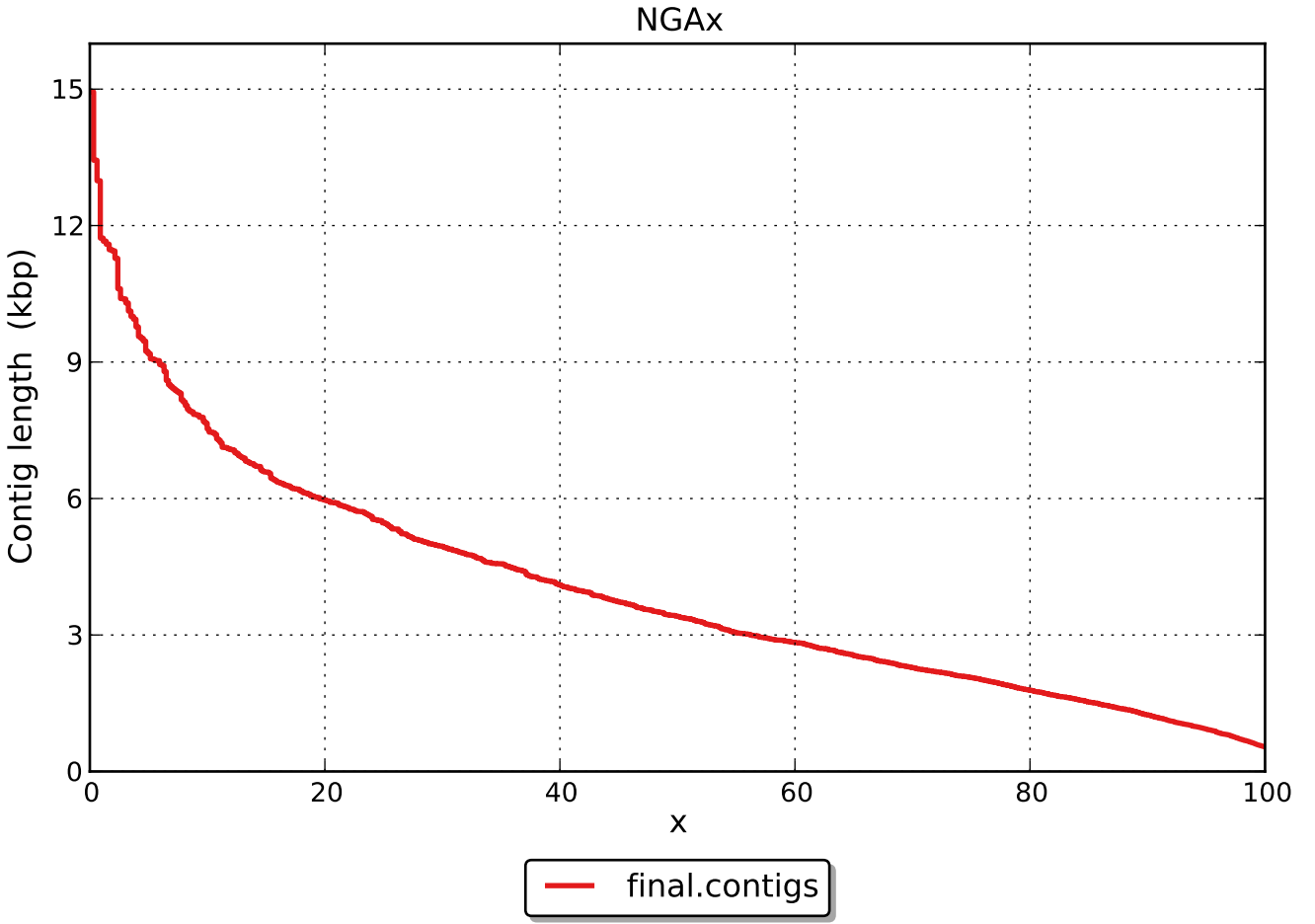

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
400
800
1200
1600
2000
Contig index
final.contigs
Reference


GC content
windows
GC (%)
0
600
1200
1800
2400
3000
0
20
40
60
80
100
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
400
800
1200
1600
2000
Contig index
final.contigs
Reference


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


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