Report

	final.contigs
# contigs (>= 0 bp)	3558
# contigs (>= 1000 bp)	1692
# contigs (>= 5000 bp)	162
# contigs (>= 10000 bp)	12
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	5505255
Total length (>= 1000 bp)	4579850
Total length (>= 5000 bp)	1096625
Total length (>= 10000 bp)	135969
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2356
Largest contig	15834
Total length	5055979
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	2998
NG50	3183
N75	1716
NG75	2027
L50	542
LG50	475
L75	1100
LG75	933
# misassemblies	12
# misassembled contigs	12
Misassembled contigs length	36417
# local misassemblies	1
# unaligned contigs	30 + 29 part
Unaligned length	19674
Genome fraction (%)	98.064
Duplication ratio	1.106
# N's per 100 kbp	0.00
# mismatches per 100 kbp	502.55
# indels per 100 kbp	1.23
Largest alignment	15834
NA50	2970
NGA50	3179
NA75	1708
NGA75	2013
LA50	543
LGA50	475
LA75	1103
LGA75	936

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

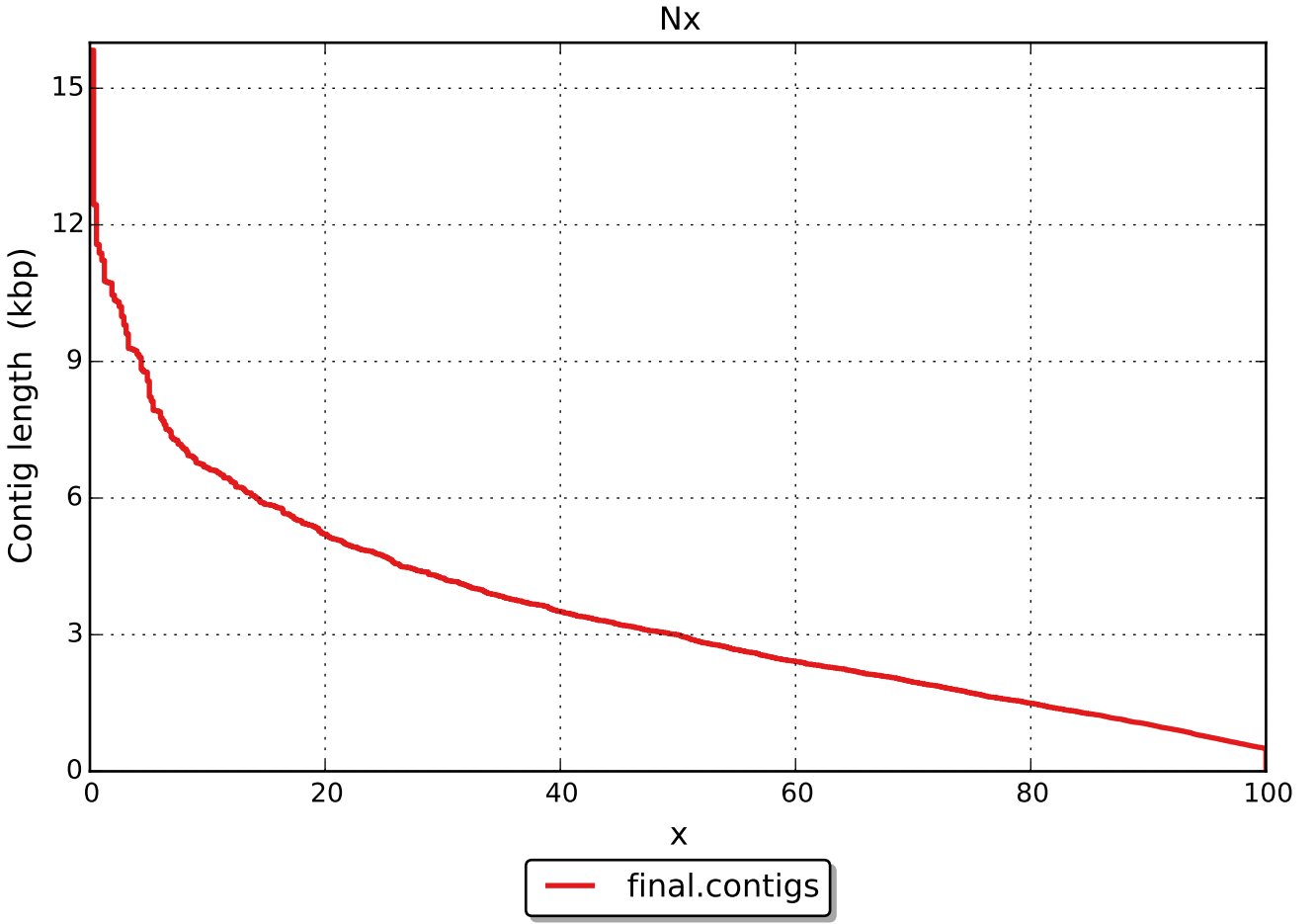
	final.contigs
# misassemblies	12
# relocations	12
# translocations	0
# inversions	0
# misassembled contigs	12
Misassembled contigs length	36417
# local misassemblies	1
# mismatches	22875
# indels	56
# short indels	55
# long indels	1
Indels length	78

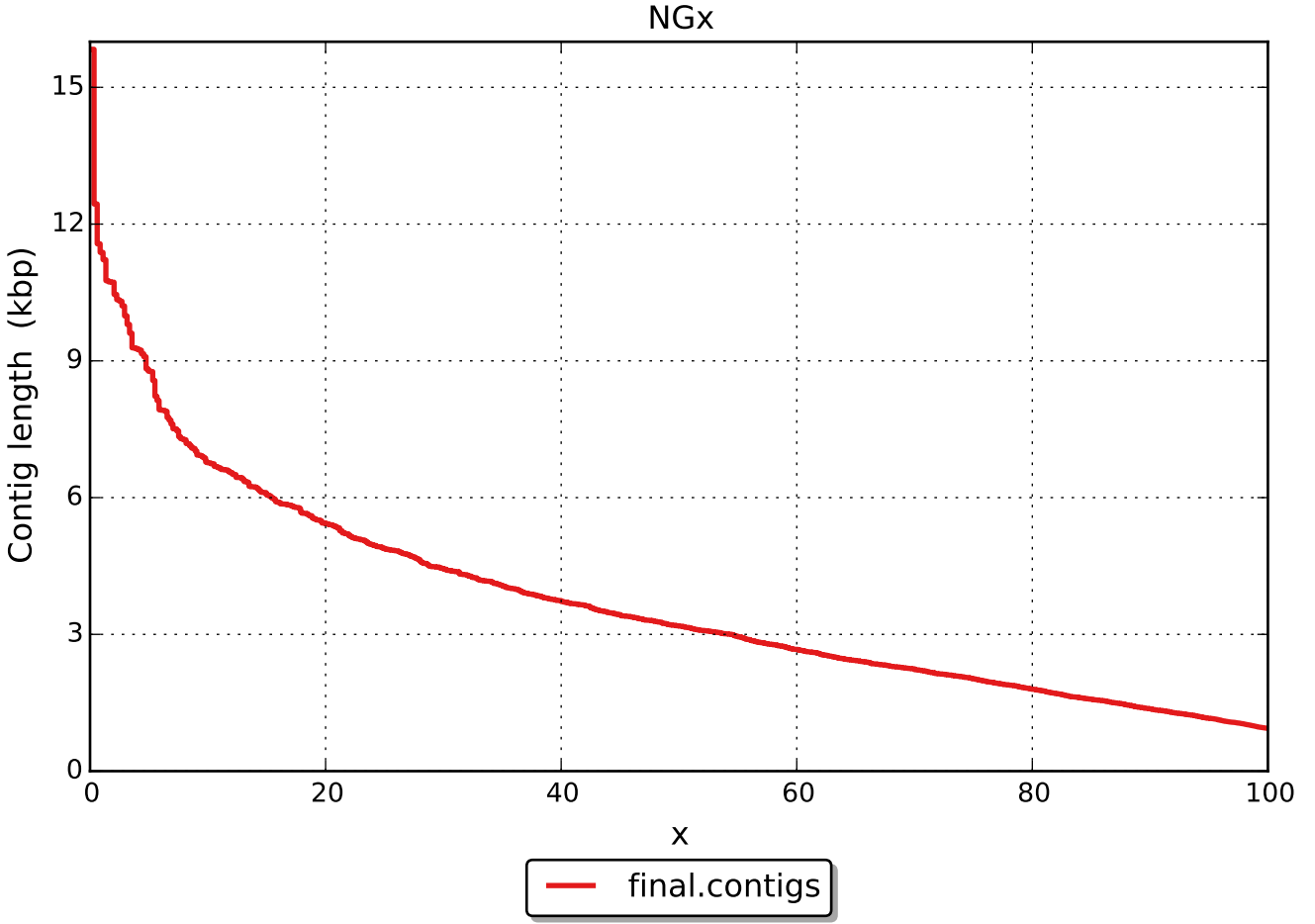
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

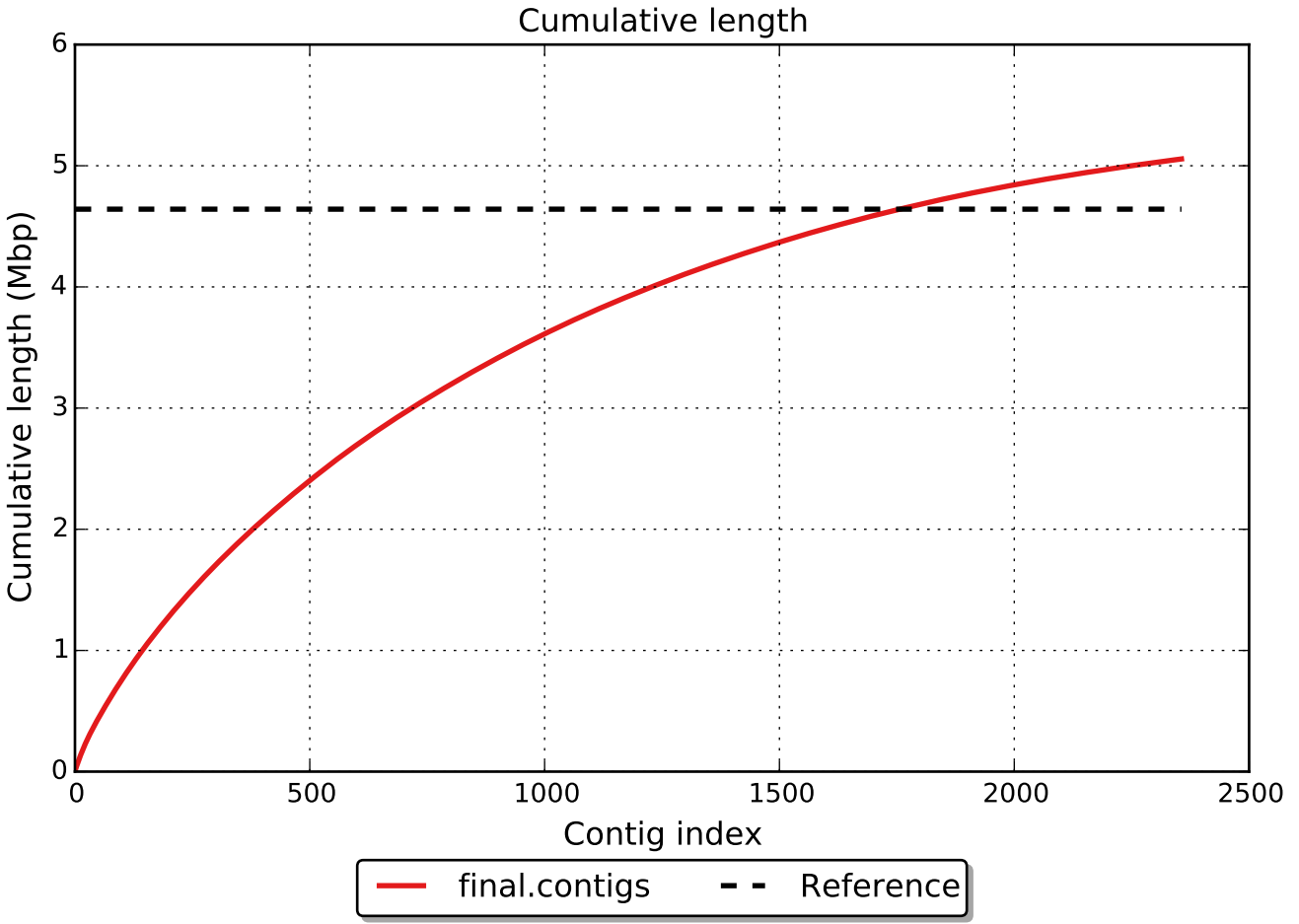
Unaligned report

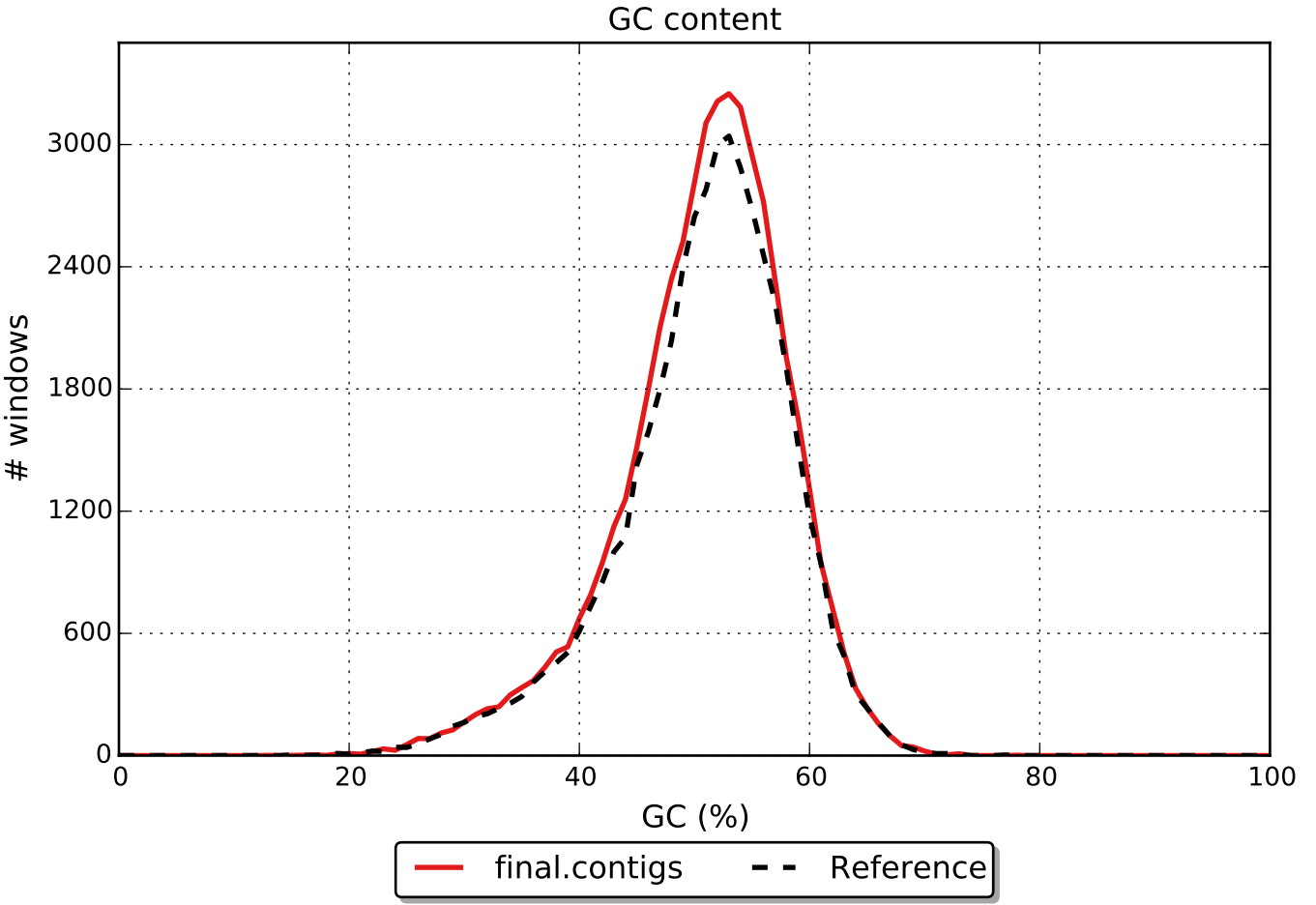
	final.contigs
# fully unaligned contigs	30
Fully unaligned length	16702
# partially unaligned contigs	29
# with misassembly	0
# both parts are significant	0
Partially unaligned length	2972
# N's	0

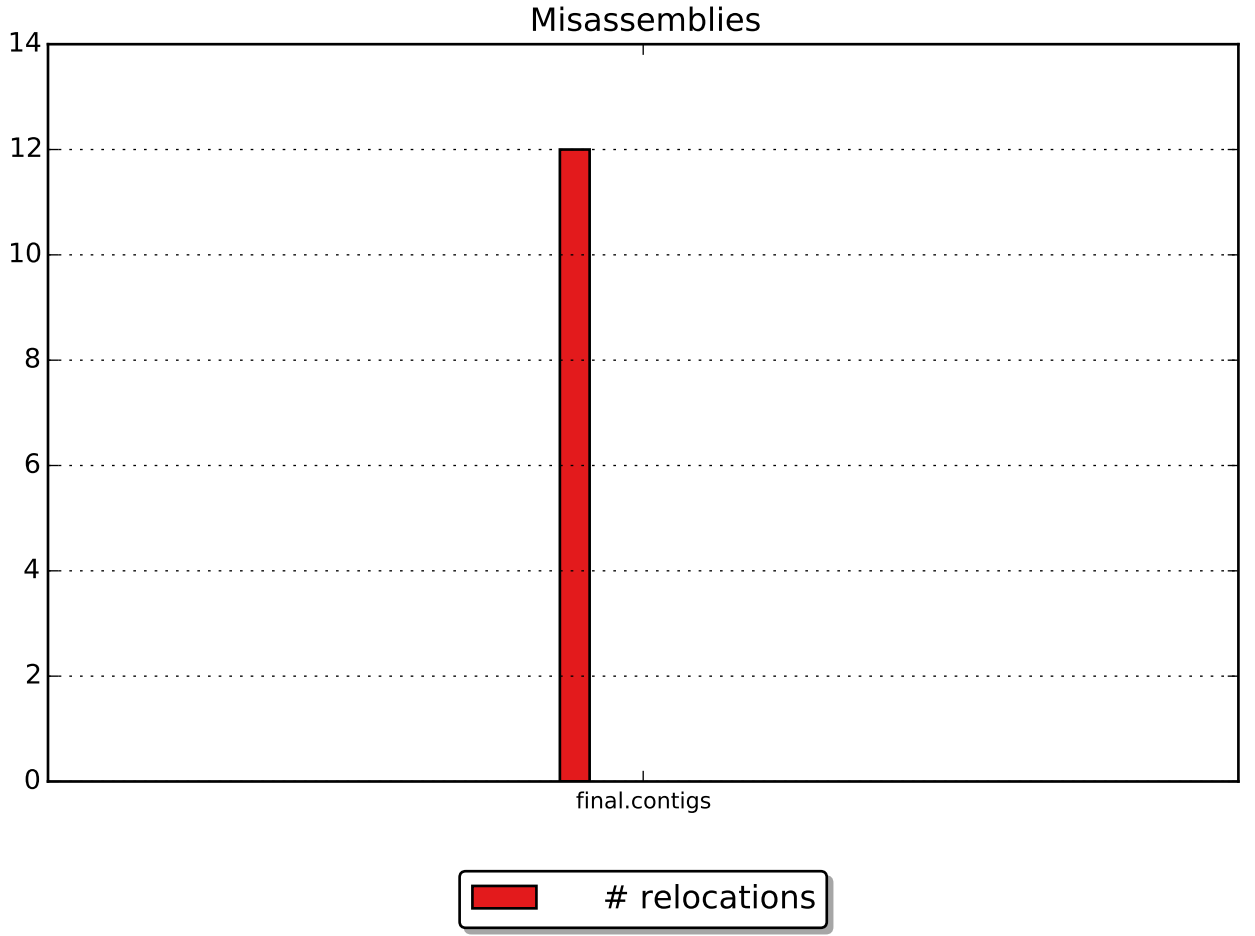
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

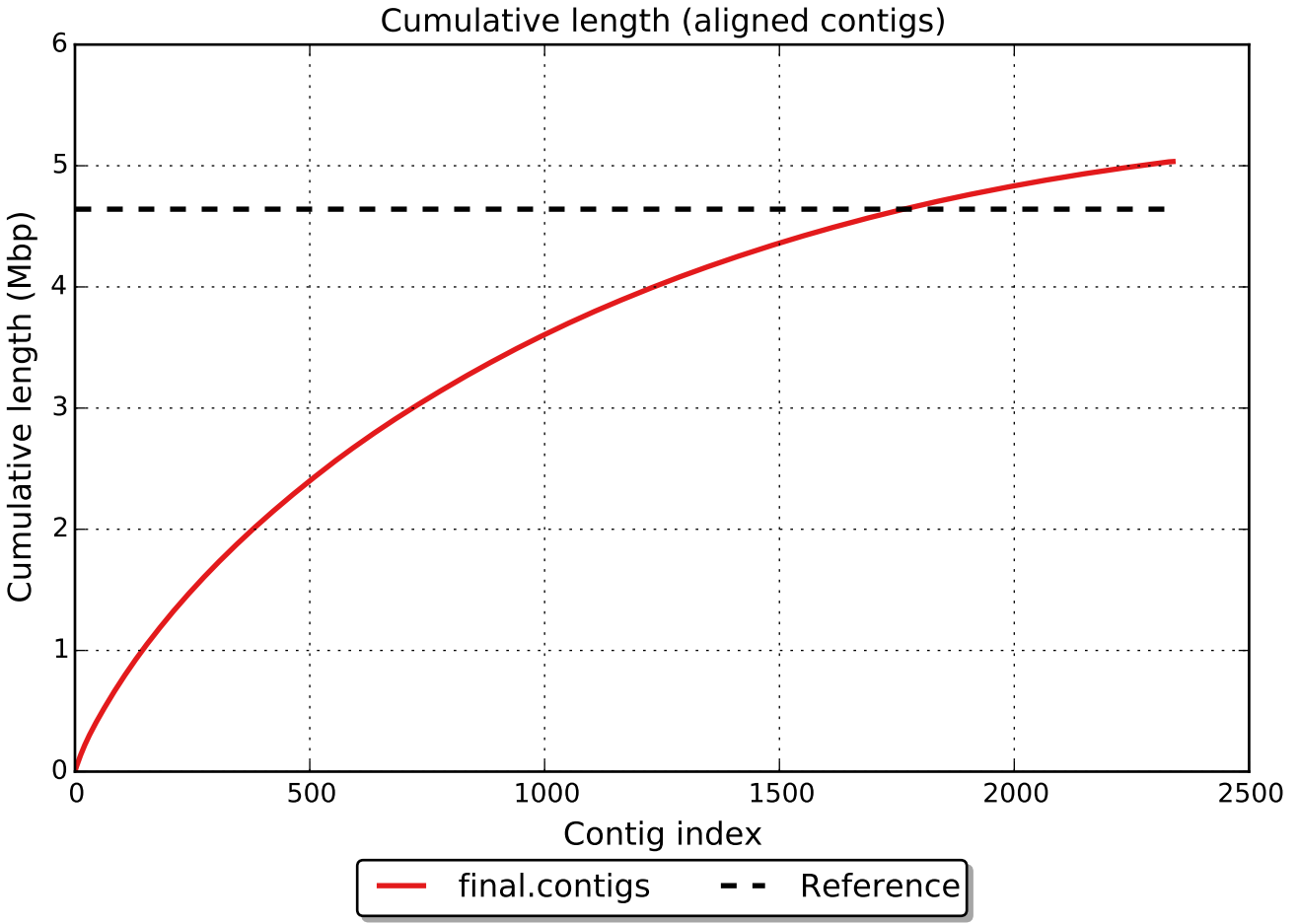

Nx
Contig length (kbp)
15
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs

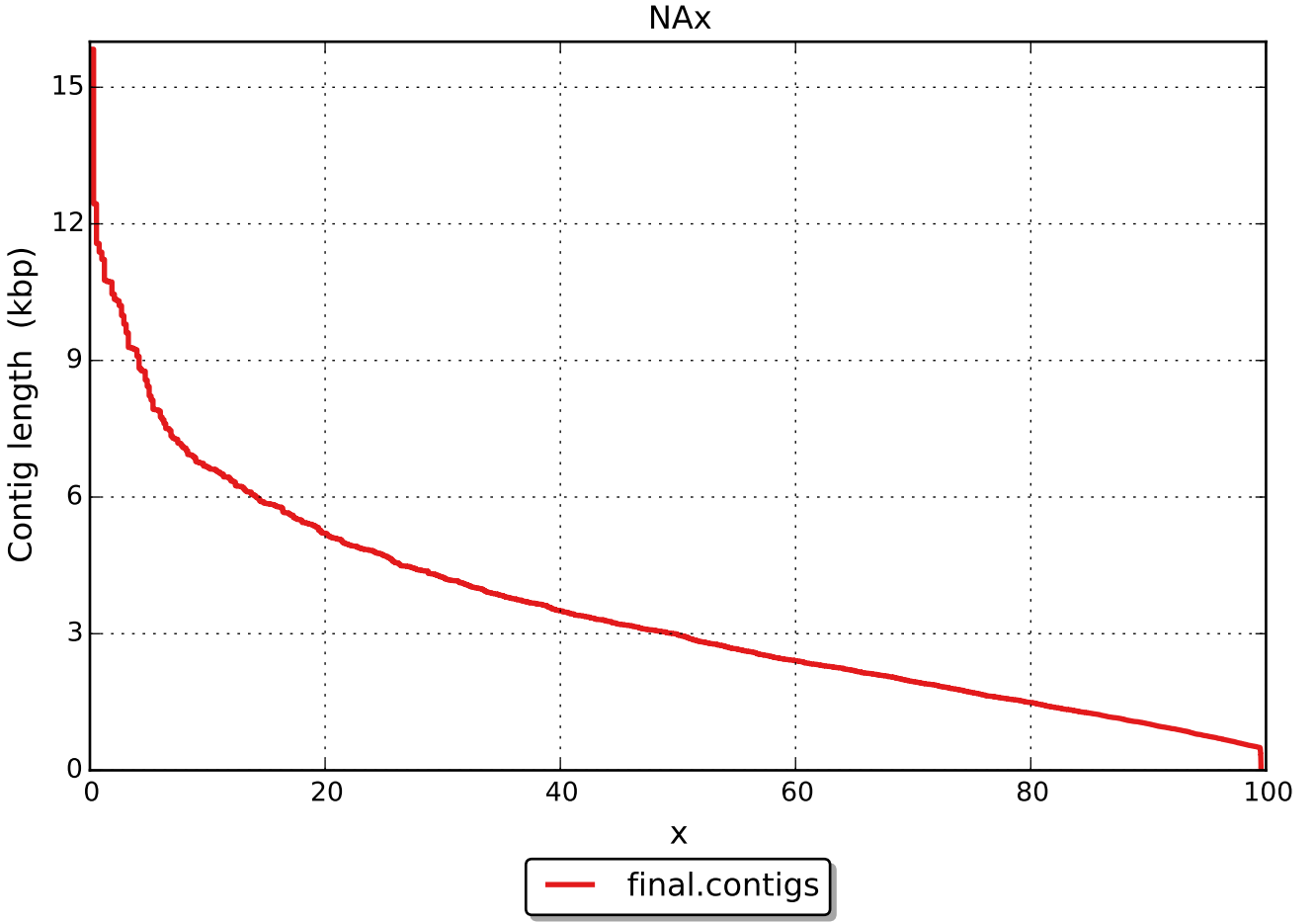

NGx
Contig length (kbp)
15
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs

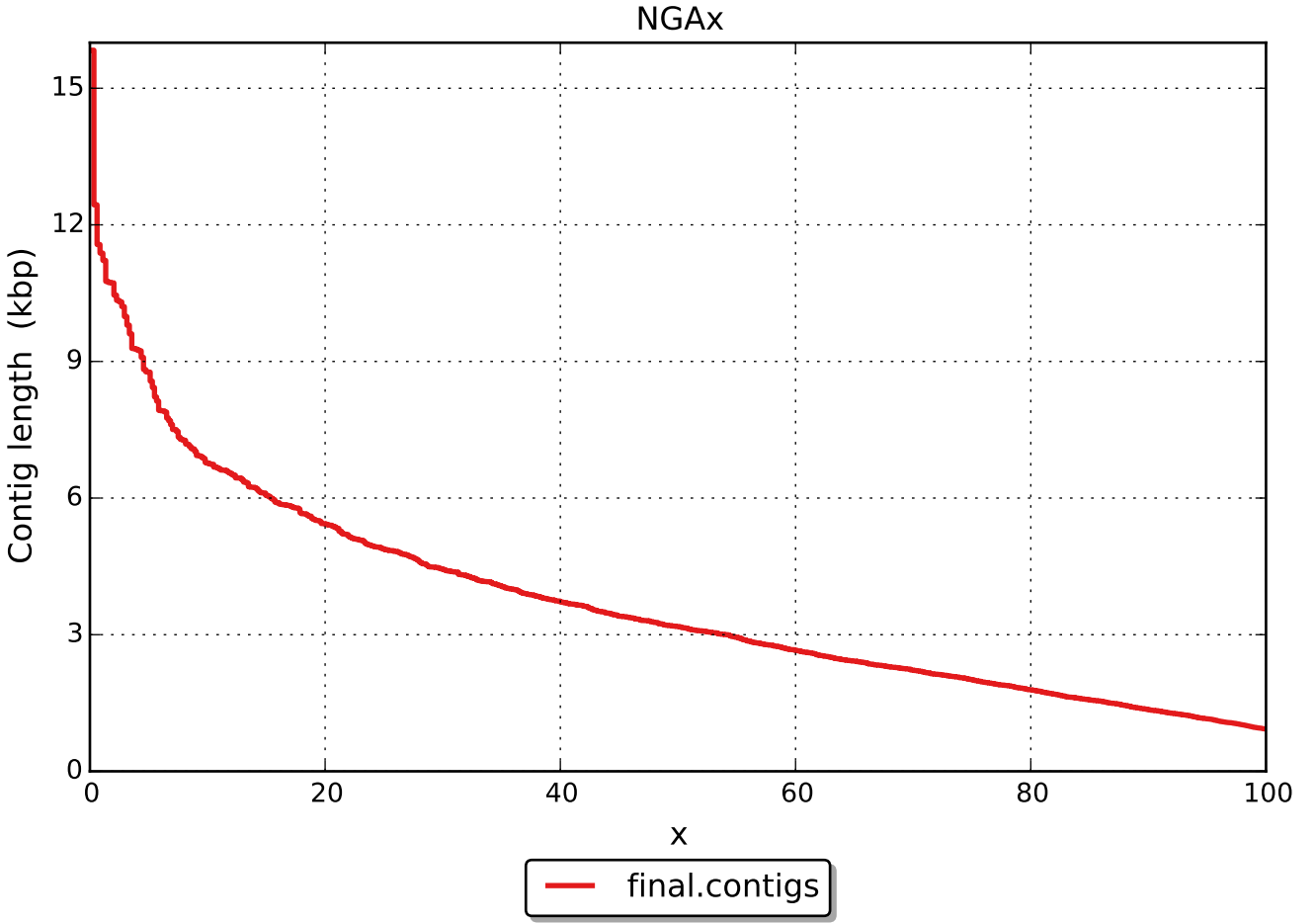

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
500
1000
1500
2000
2500
Contig index
final.contigs
Reference


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


Misassemblies
14
12
10
8
6
4
2
0
final.contigs
relocations


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
500
1000
1500
2000
2500
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