Report

	final.contigs
# contigs (>= 1000 bp)	161
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	204397
Total length (>= 5000 bp)	6476
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1455
Largest contig	6476
Total length	1052787
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	708
N75	584
L50	554
L75	966
# misassemblies	10
# misassembled contigs	10
Misassembled contigs length	17018
# local misassemblies	2
# unaligned contigs	0 + 7 part
Unaligned length	286
Genome fraction (%)	22.634
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	397.78
# indels per 100 kbp	10.66
Largest alignment	6082
NA50	706
NGA50	-
NA75	582
LA50	557
LA75	970

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

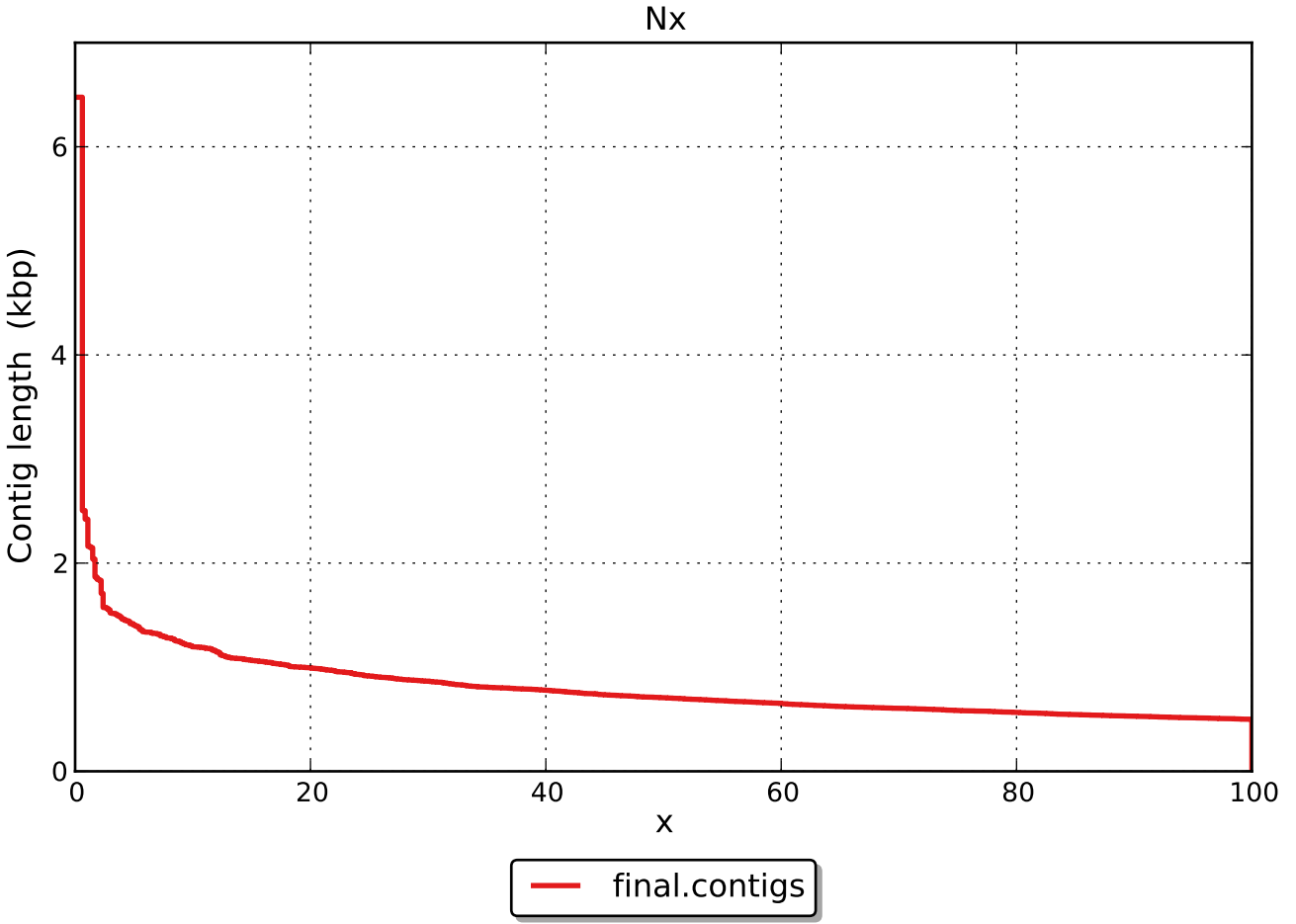
	final.contigs
# misassemblies	10
# relocations	10
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	10
Misassembled contigs length	17018
# local misassemblies	2
# mismatches	4179
# indels	112
# short indels	110
# long indels	2
Indels length	194

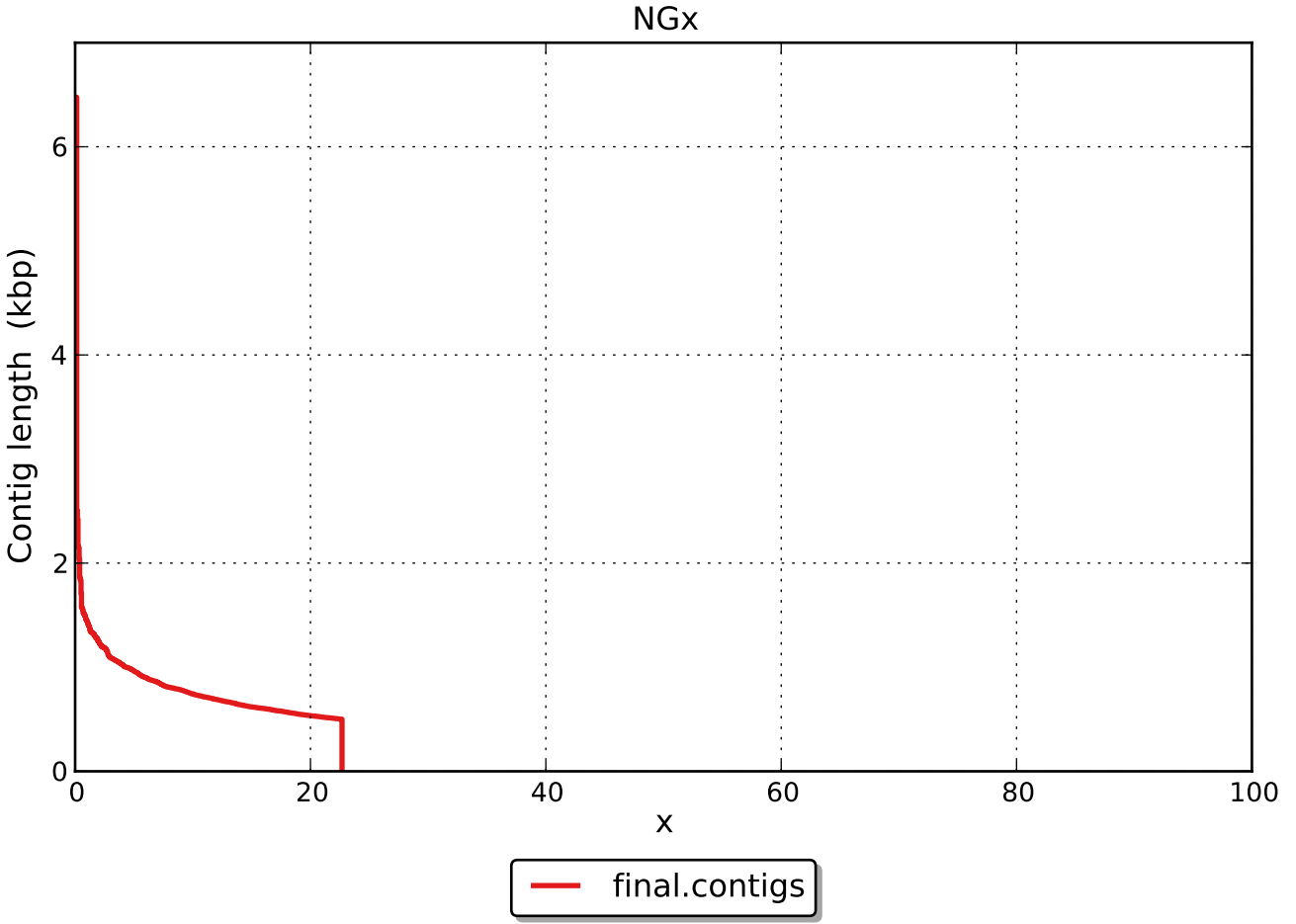
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

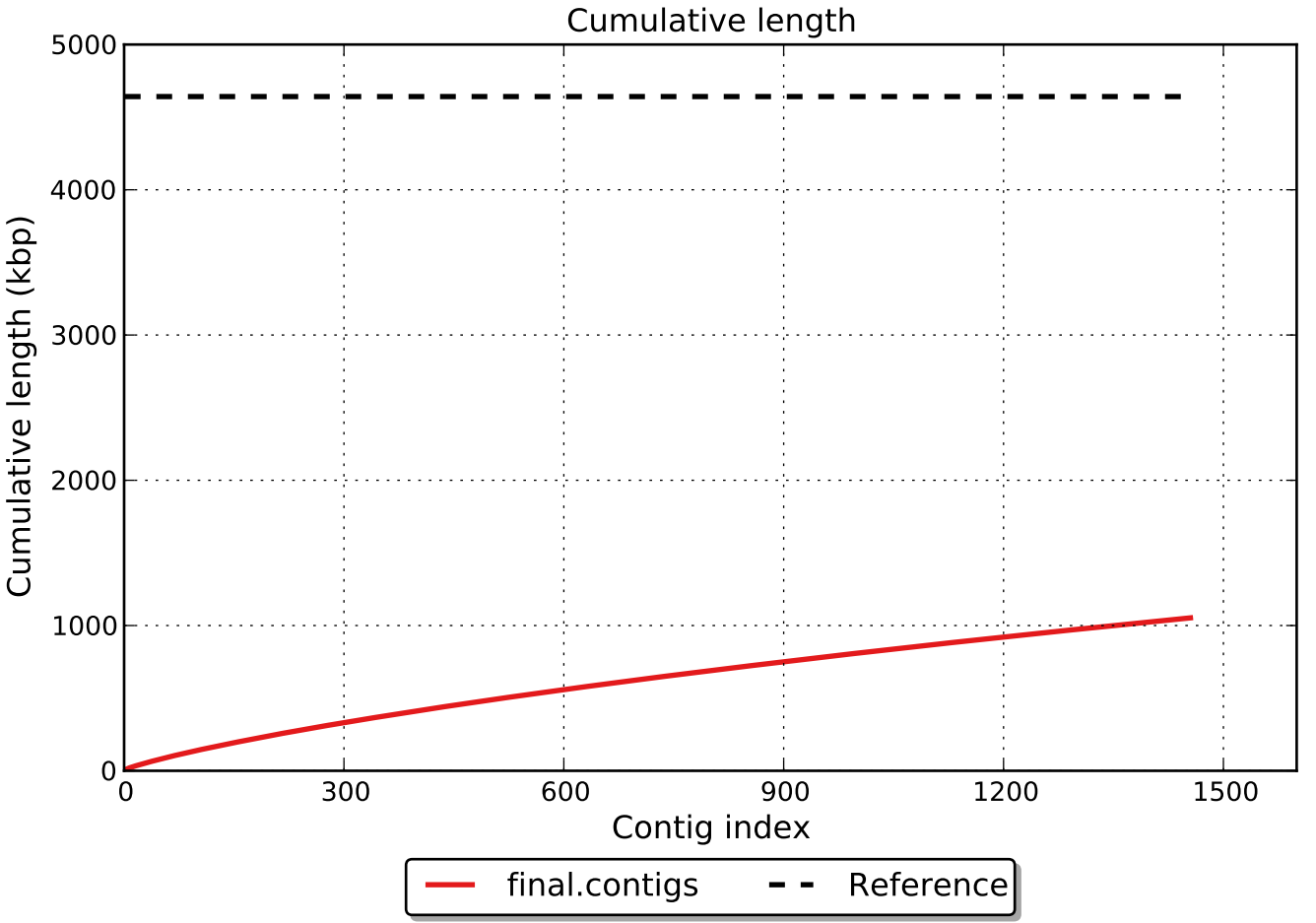
Unaligned report

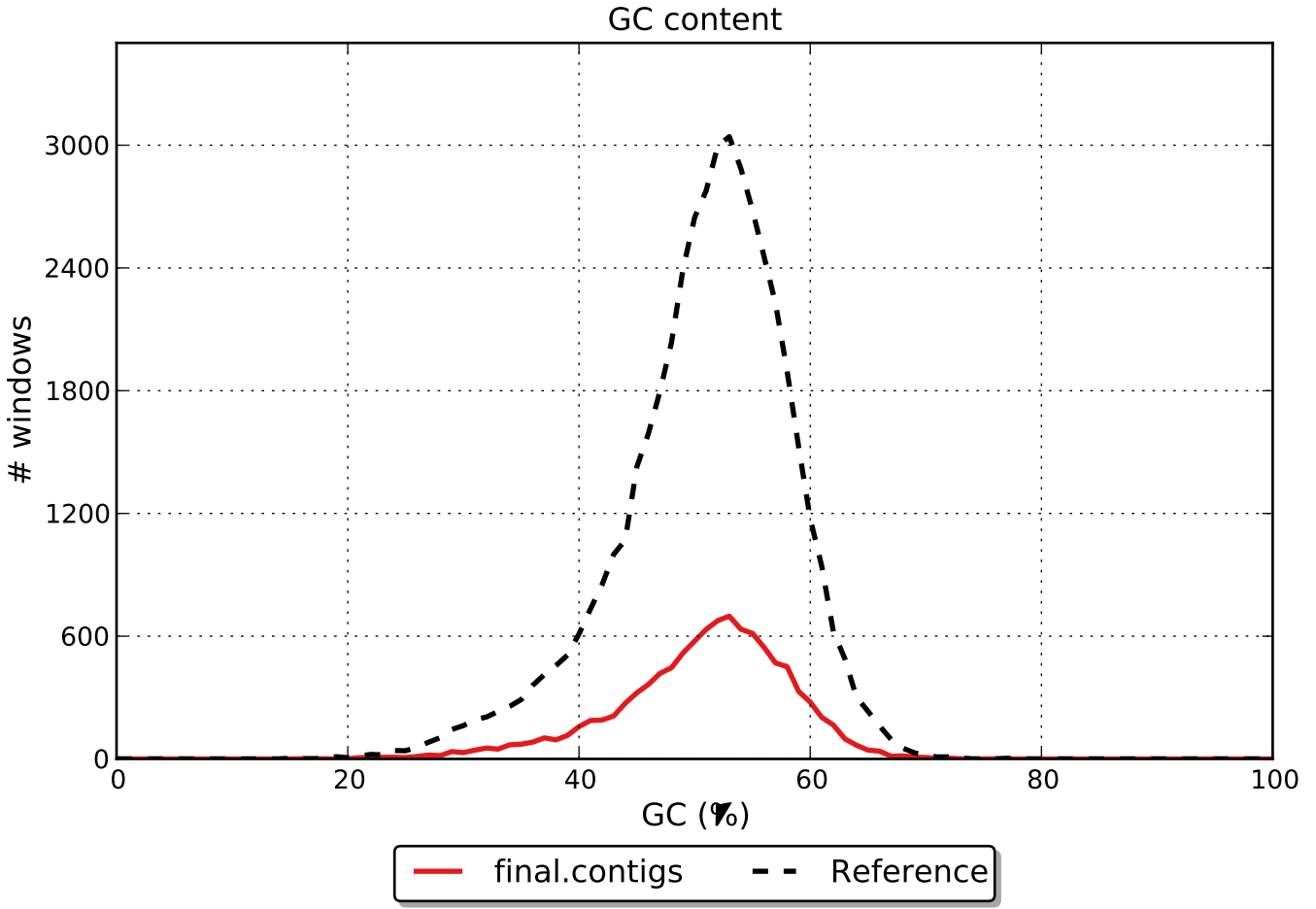
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	7
# with misassembly	0
# both parts are significant	0
Partially unaligned length	286
# N's	0

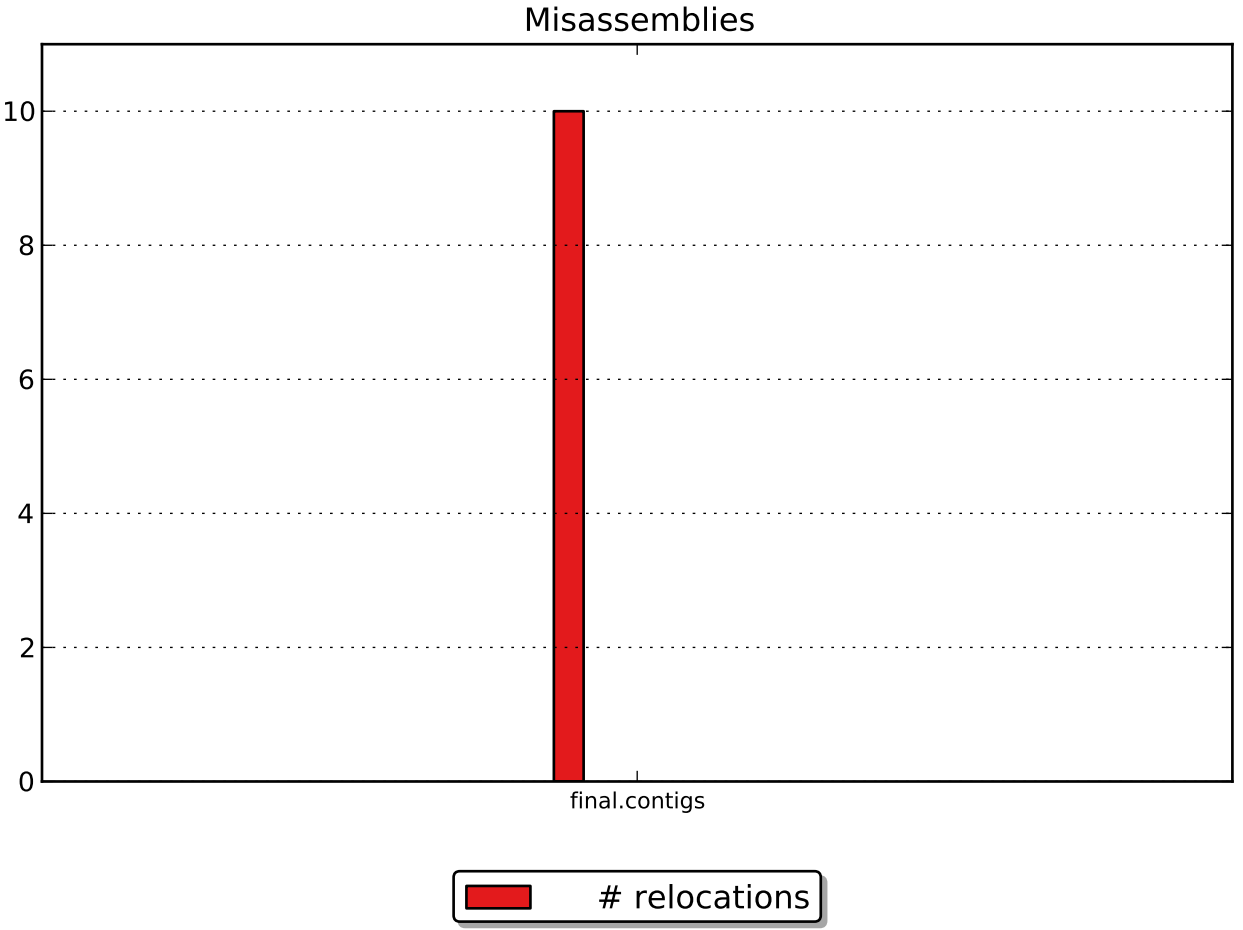
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

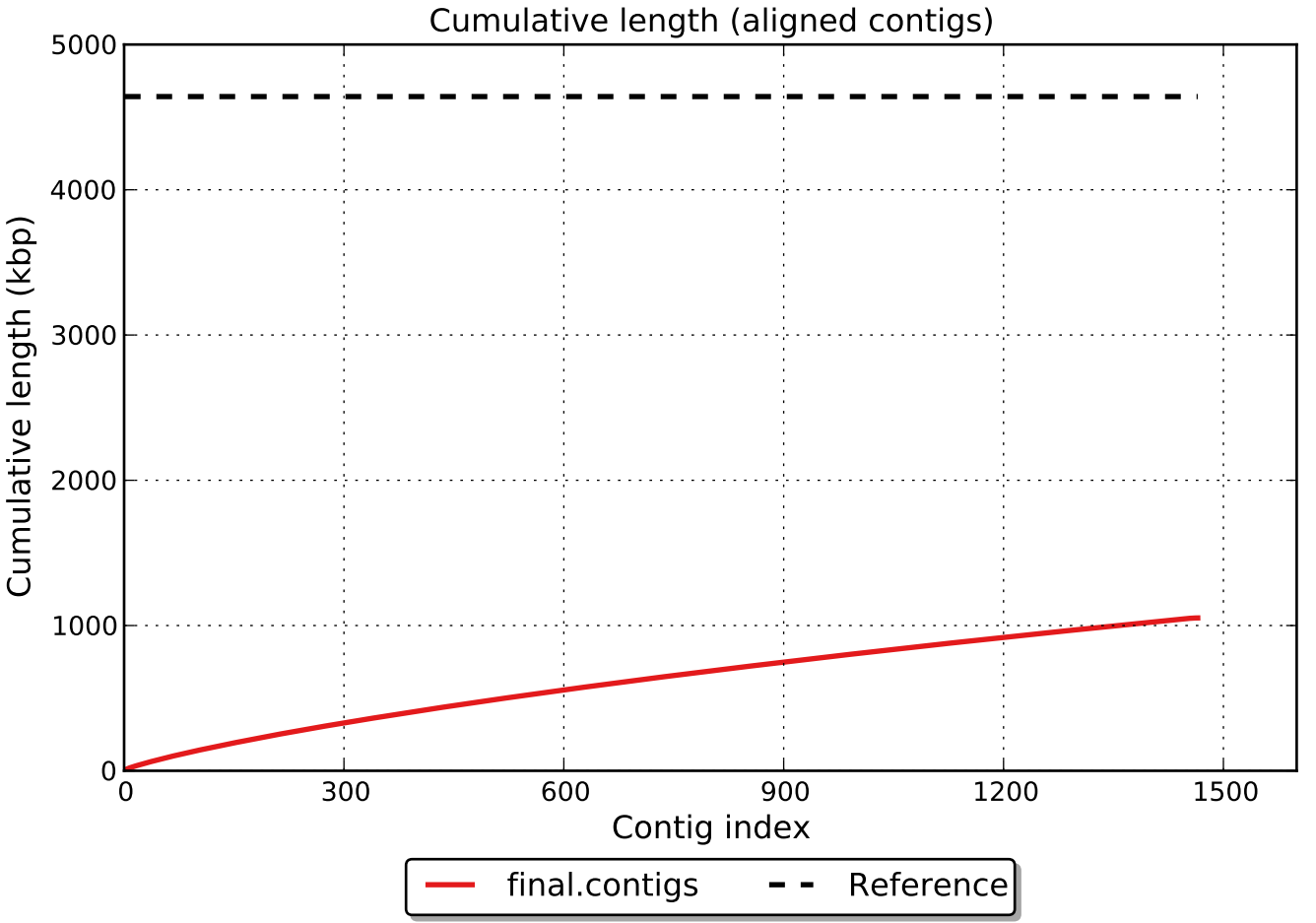

Nx
Contig length (kbp)
0
2
4
6
0
20
40
60
80
100
x
final.contigs

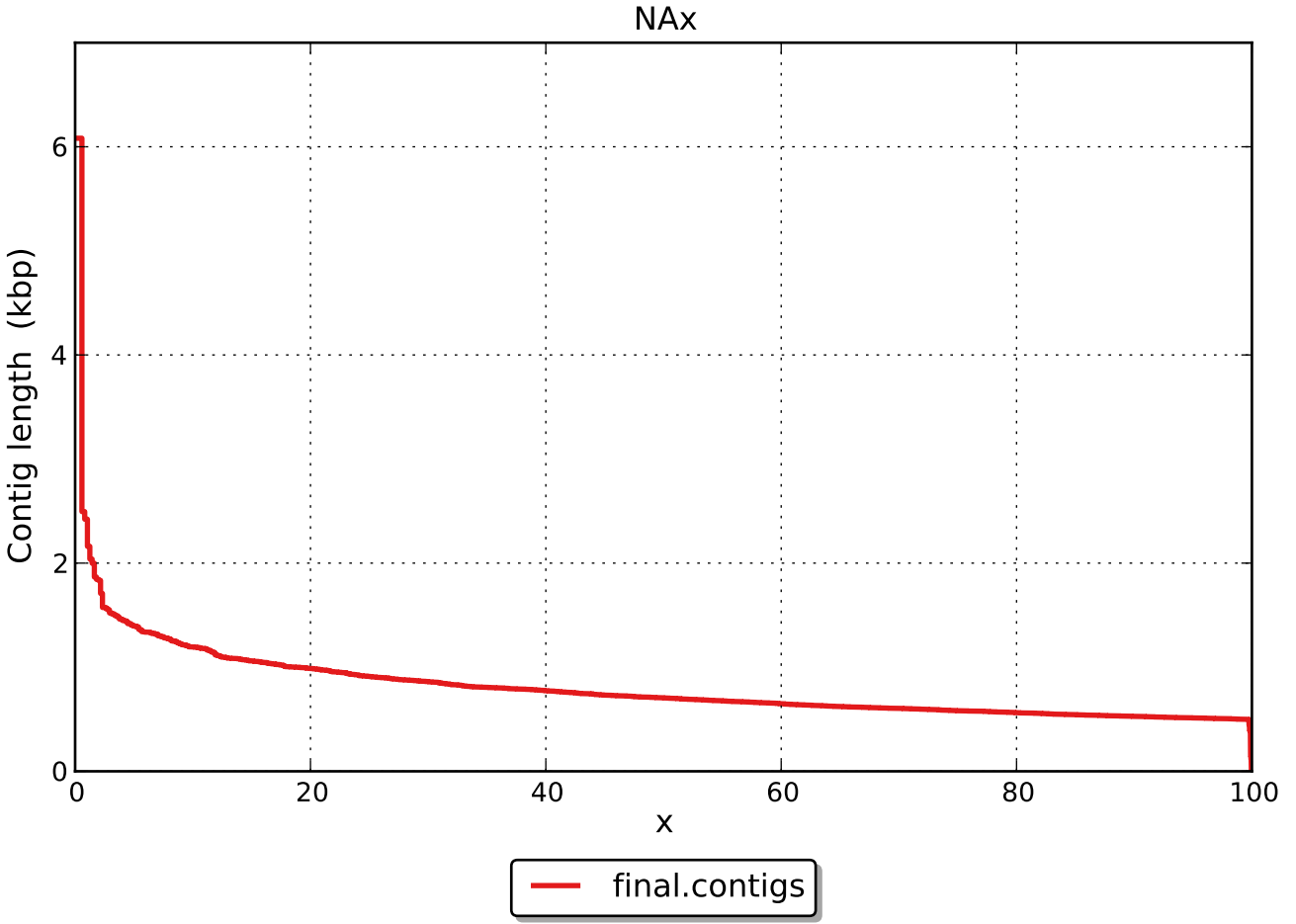

NGx
Contig length (kbp)
0
2
4
6
0
20
40
60
80
100
x
final.contigs

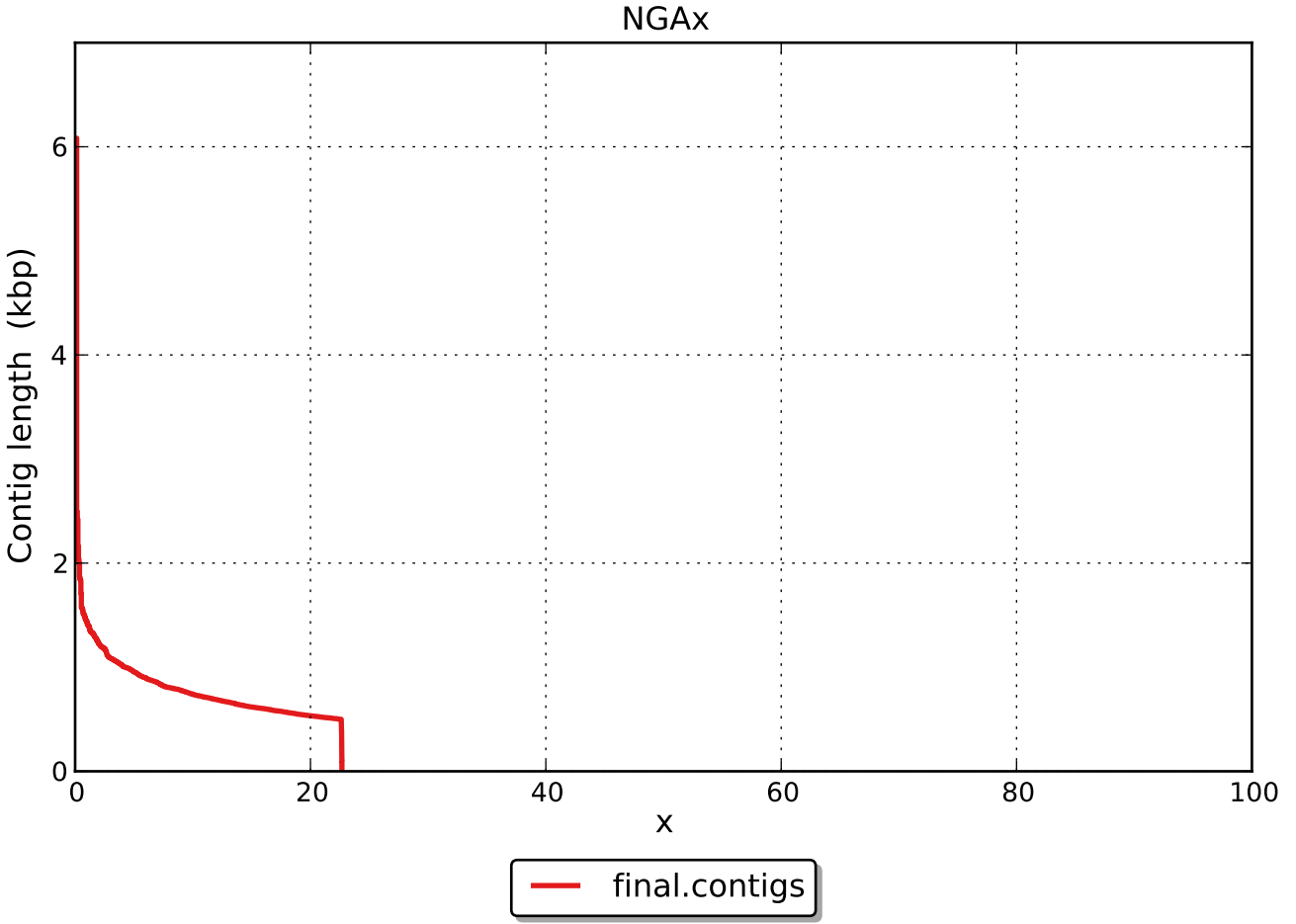

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
300
600
900
1200
1500
Contig index
final.contigs
Reference


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
300
600
900
1200
1500
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
0
2
4
6
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
0
2
4
6
0
20
40
60
80
100
x
final.contigs