Report

	final.contigs
# contigs (>= 0 bp)	3792
# contigs (>= 1000 bp)	227
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	2049768
Total length (>= 1000 bp)	291397
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1566
Largest contig	3782
Total length	1180398
Reference length	4641652
GC (%)	50.79
Reference GC (%)	50.79
N50	737
N75	601
L50	582
L75	1026
# misassemblies	9
# misassembled contigs	9
Misassembled contigs length	10664
# local misassemblies	1
# unaligned contigs	3 + 3 part
Unaligned length	2001
Genome fraction (%)	25.284
Duplication ratio	1.004
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1069.45
# indels per 100 kbp	1.28
Largest alignment	3782
NA50	736
NGA50	-
NA75	600
LA50	584
LA75	1030

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

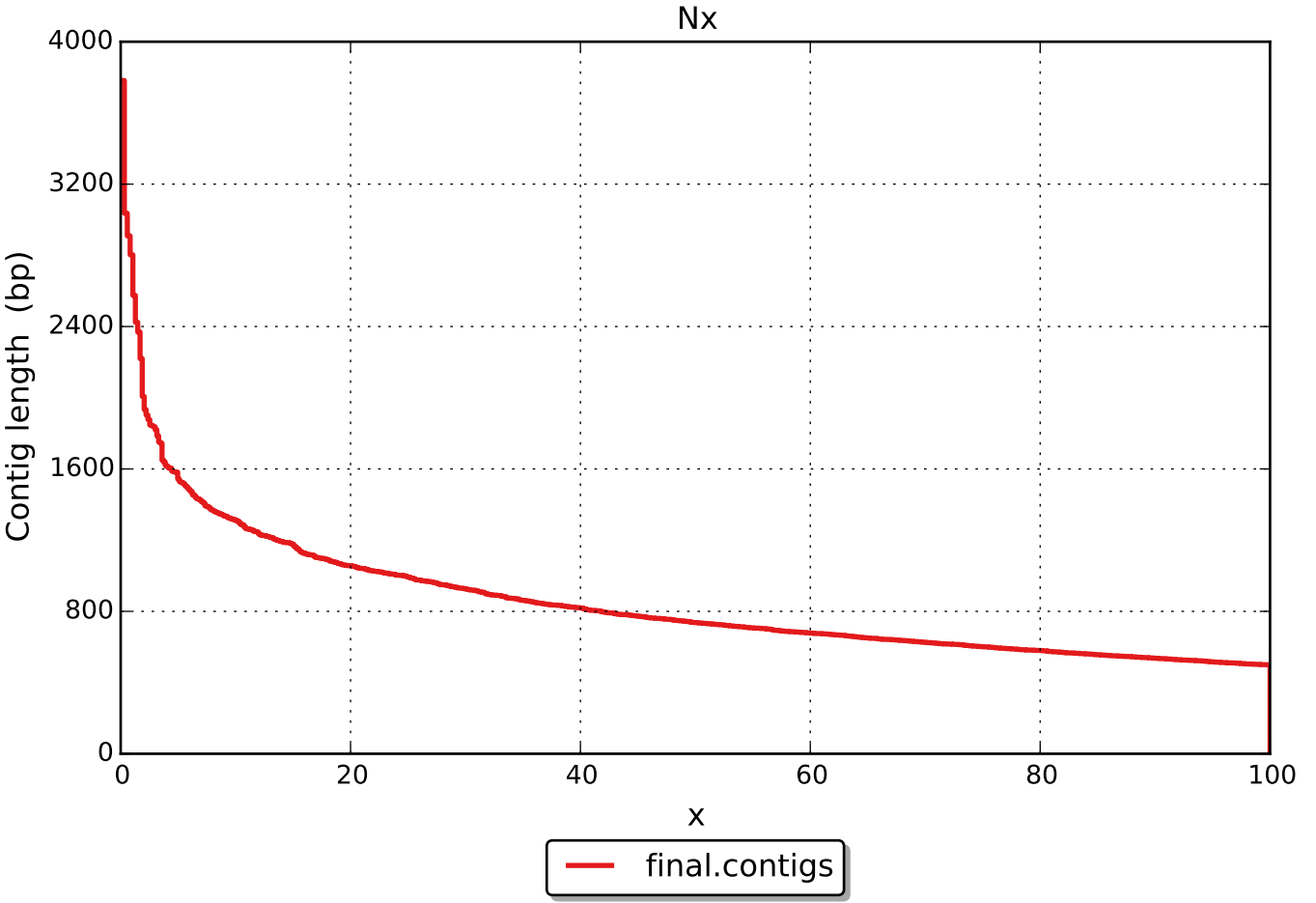
	final.contigs
# misassemblies	9
# relocations	8
# translocations	0
# inversions	1
# misassembled contigs	9
Misassembled contigs length	10664
# local misassemblies	1
# mismatches	12551
# indels	15
# short indels	14
# long indels	1
Indels length	31

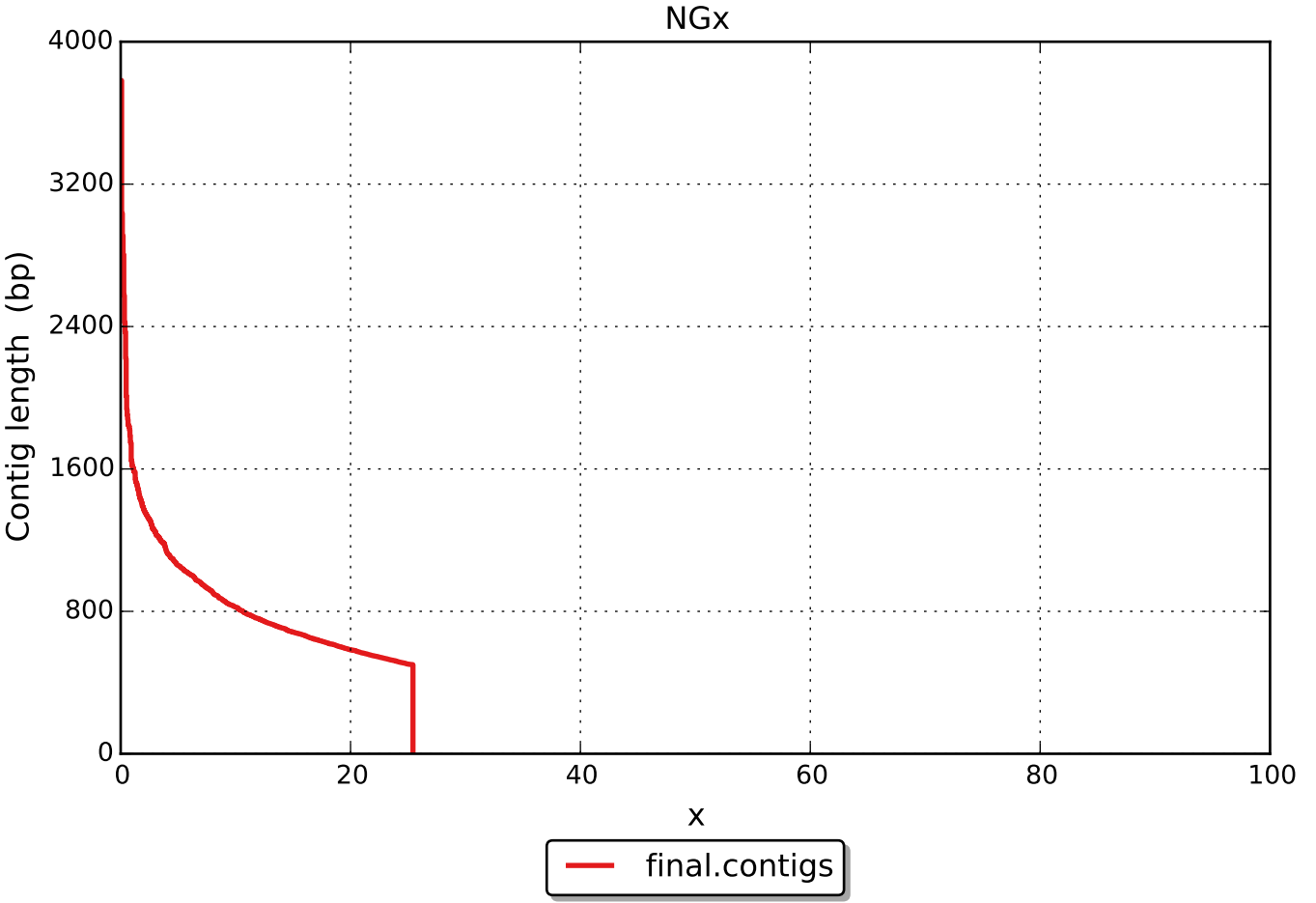
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

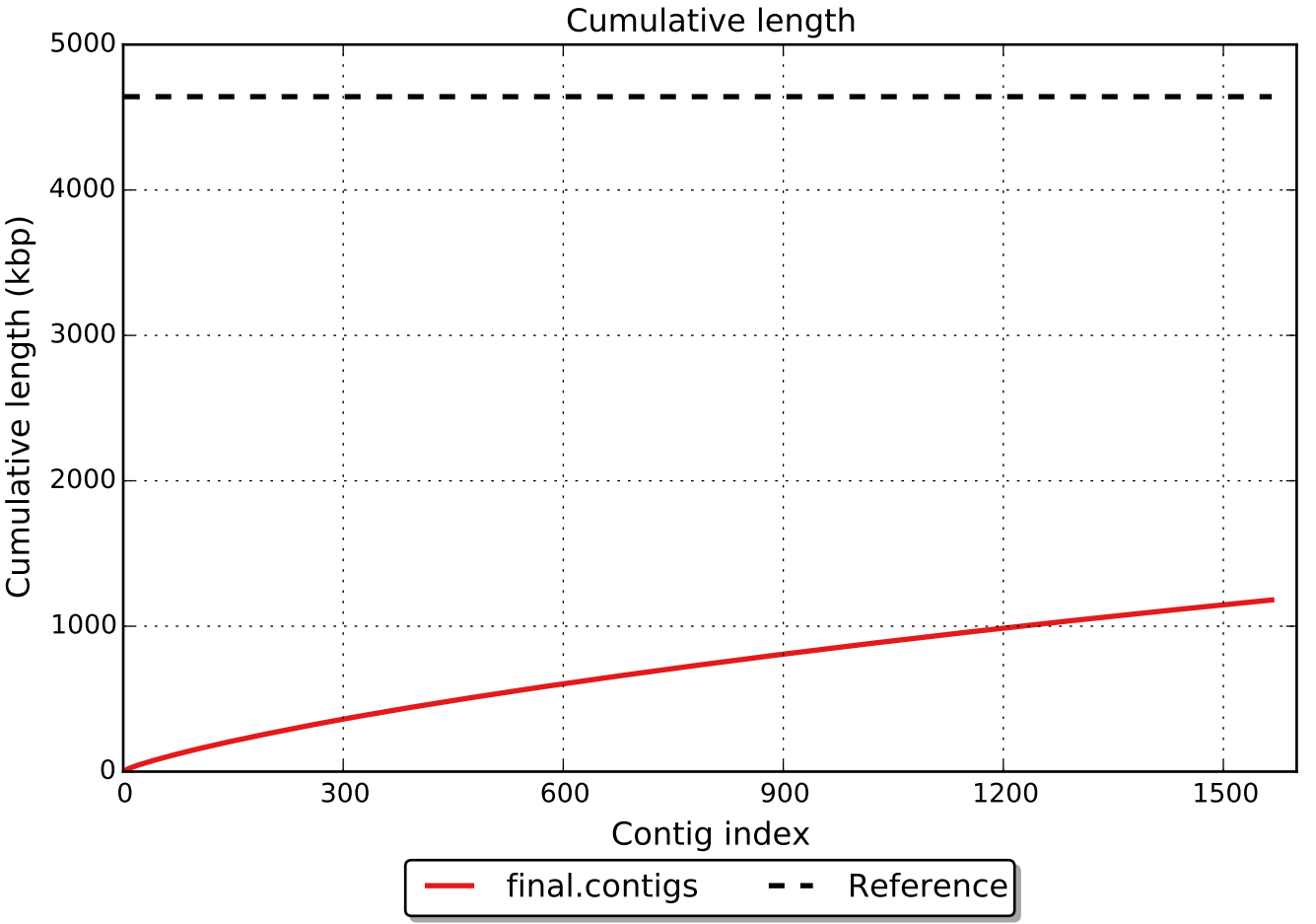
Unaligned report

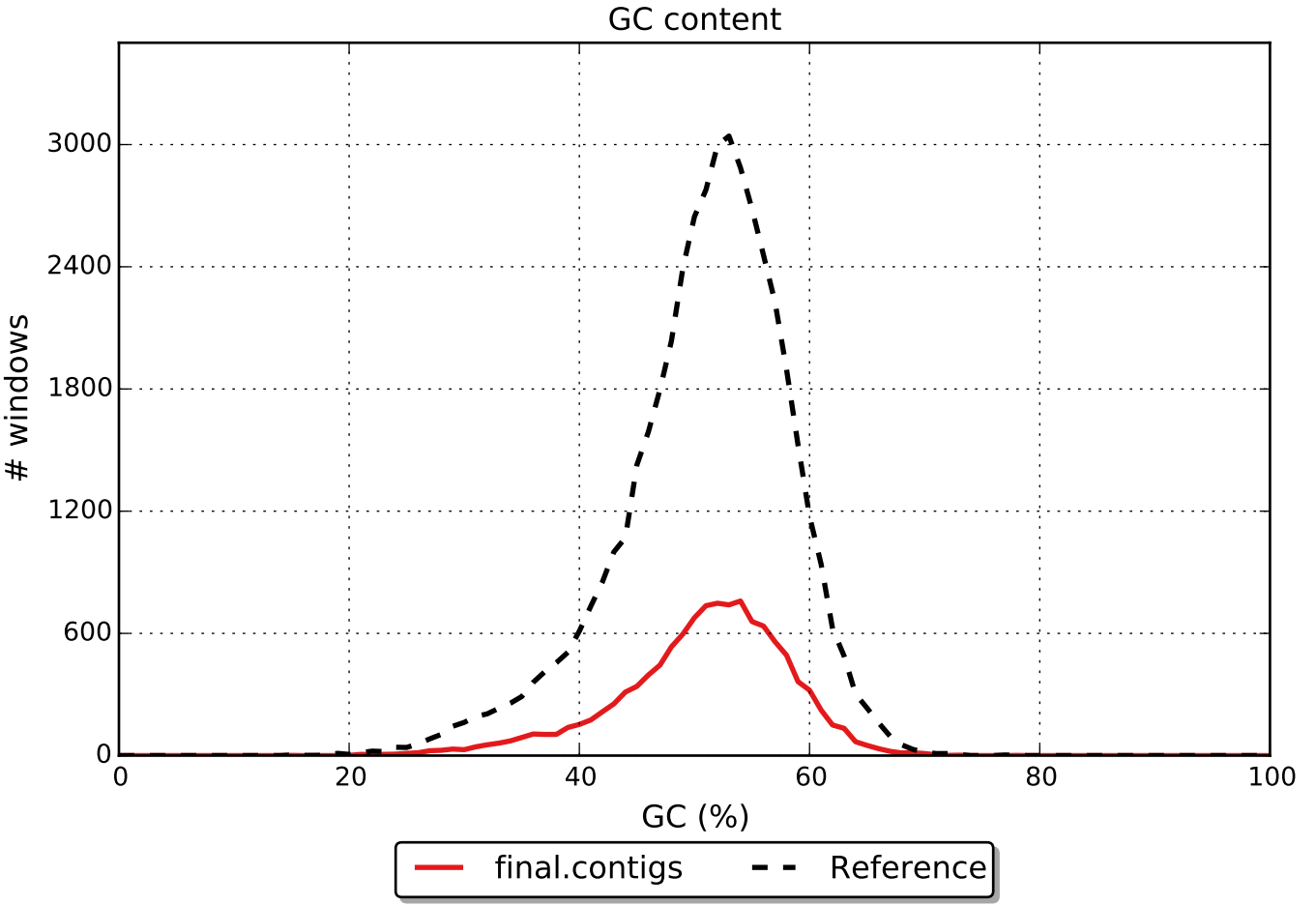
	final.contigs
# fully unaligned contigs	3
Fully unaligned length	1943
# partially unaligned contigs	3
# with misassembly	0
# both parts are significant	0
Partially unaligned length	58
# N's	0

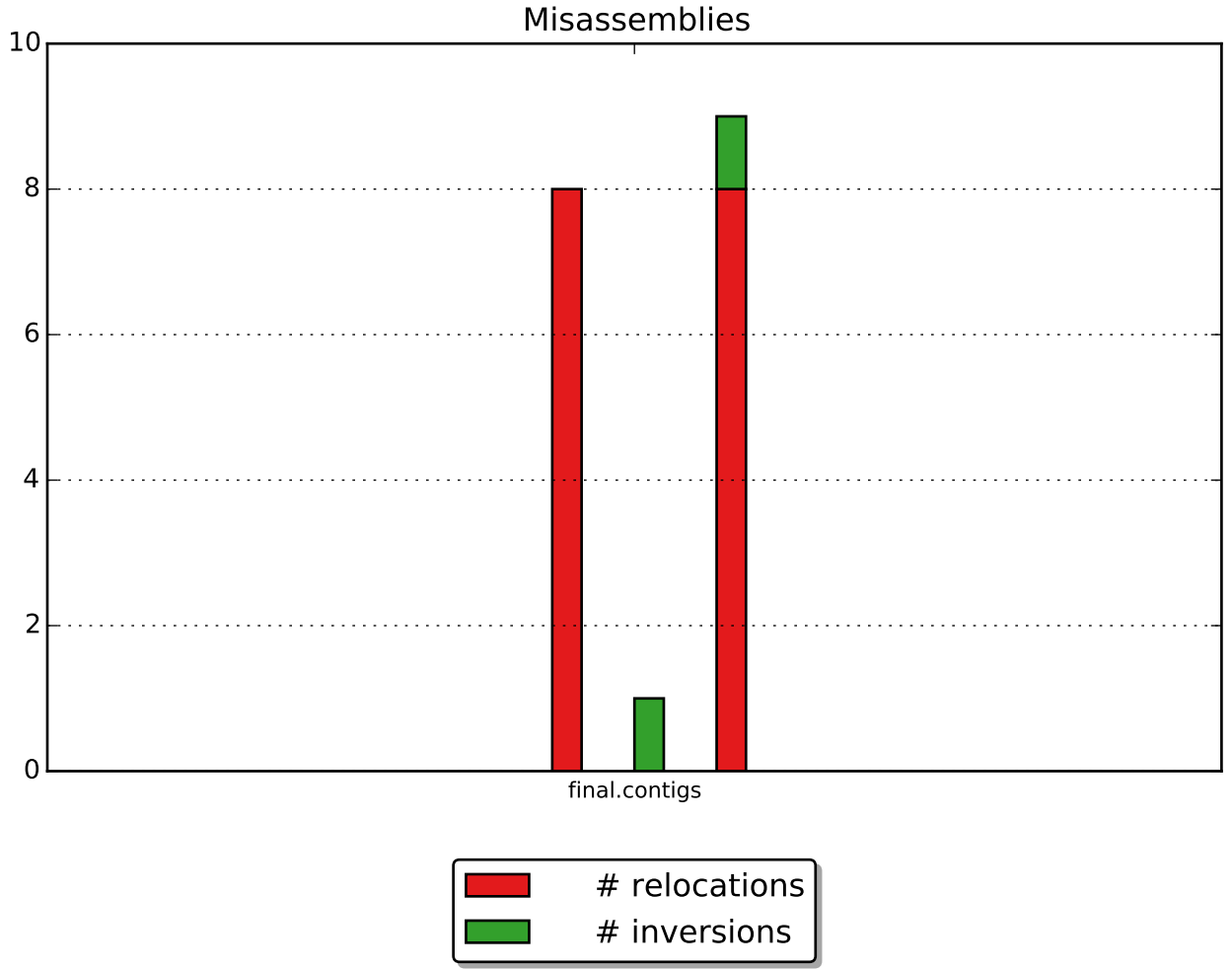
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

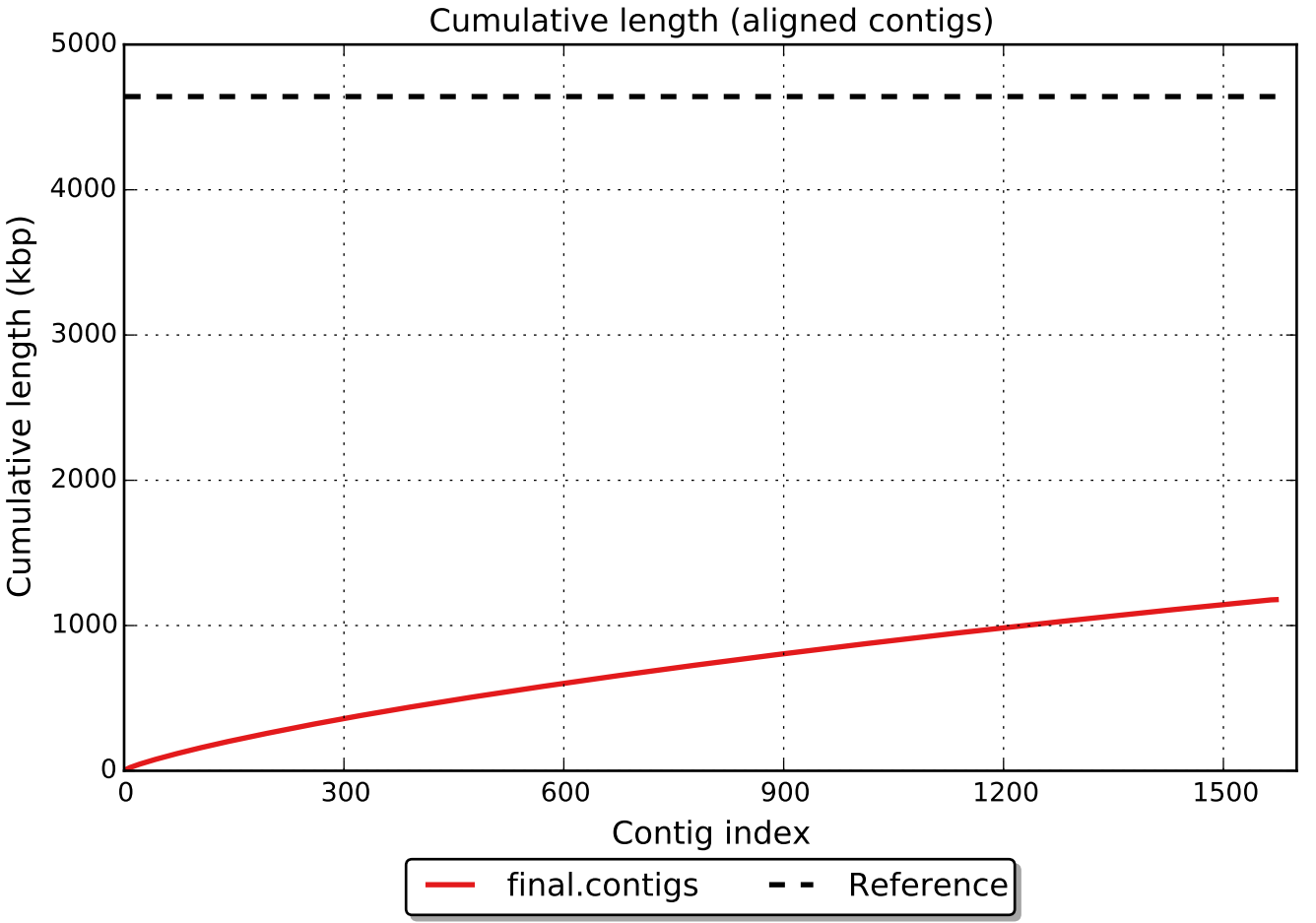

Nx
4000
3200
2400
1600
800
0
Contig length (bp)
0
20
40
60
80
100
x
final.contigs

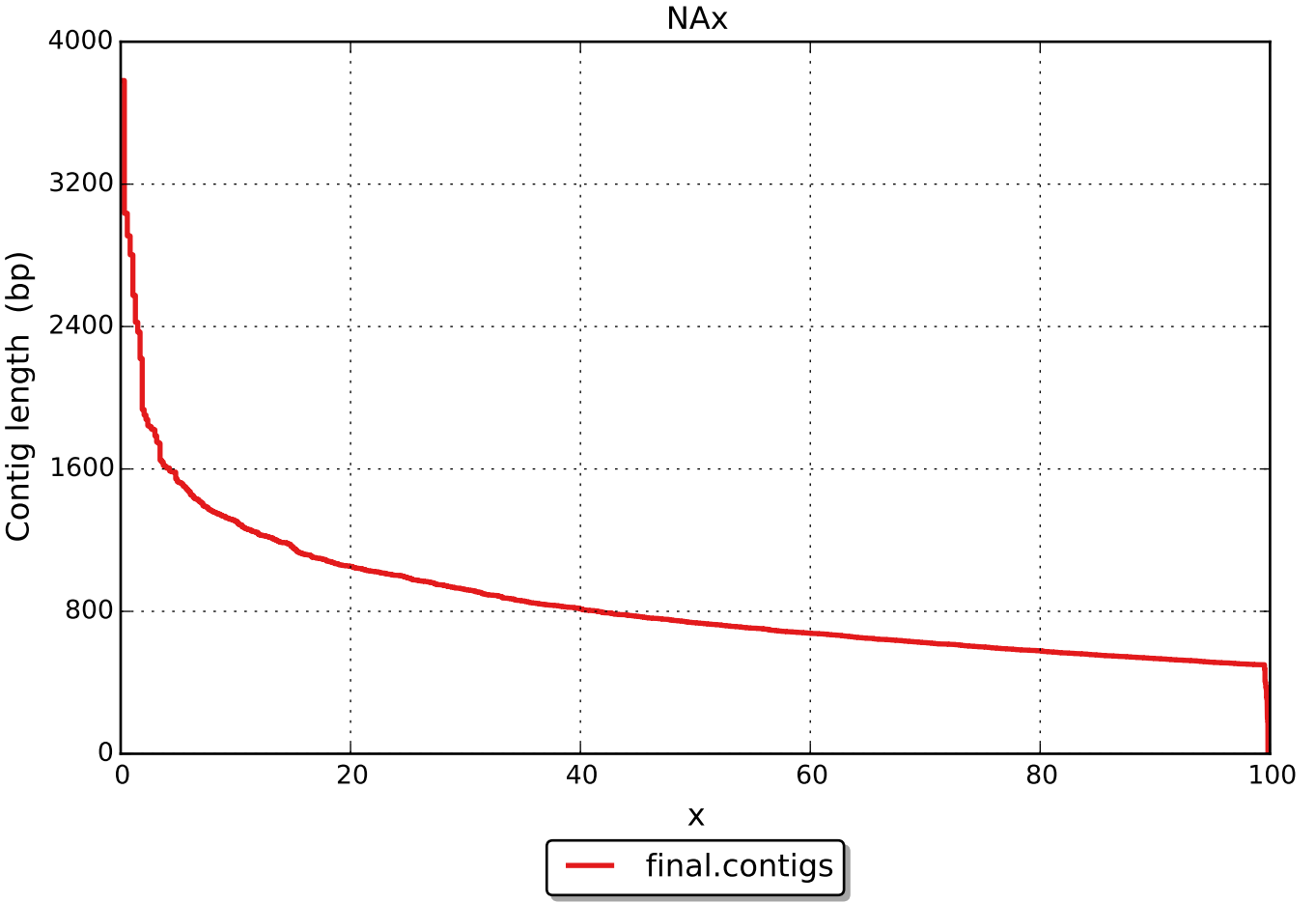

NGx
Contig length (bp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
final.contigs

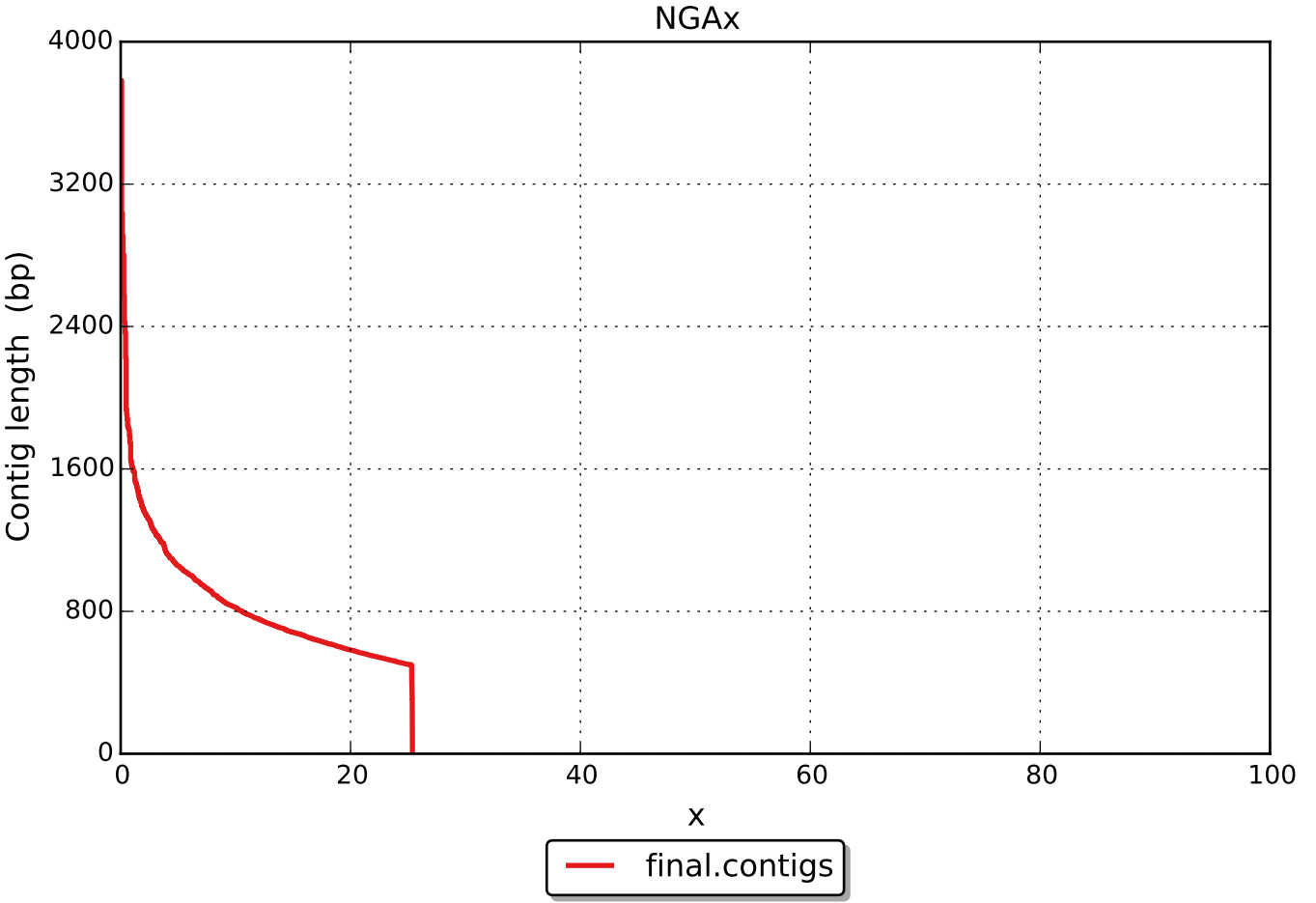

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
300
600
900
1200
1500
Contig index
final.contigs
Reference


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
inversions


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
4000
3200
2400
1600
800
0
Contig length (bp)
0
20
40
60
80
100
x
final.contigs


NGAx
4000
3200
2400
1600
800
0
Contig length (bp)
0
20
40
60
80
100
x
final.contigs