Report

	final.contigs
# contigs (>= 0 bp)	10411
# contigs (>= 1000 bp)	1839
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	7076166
Total length (>= 1000 bp)	2660324
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	5524
Largest contig	4077
Total length	5261284
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	1007
NG50	1091
N75	725
NG75	819
L50	1810
LG50	1515
L75	3350
LG75	2746
# misassemblies	7
# misassembled contigs	7
Misassembled contigs length	7305
# local misassemblies	4
# unaligned contigs	48 + 49 part
Unaligned length	30496
Genome fraction (%)	93.747
Duplication ratio	1.202
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1263.59
# indels per 100 kbp	1.61
Largest alignment	4077
NA50	1005
NGA50	1087
NA75	721
NGA75	816
LA50	1813
LGA50	1517
LA75	3358
LGA75	2752

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

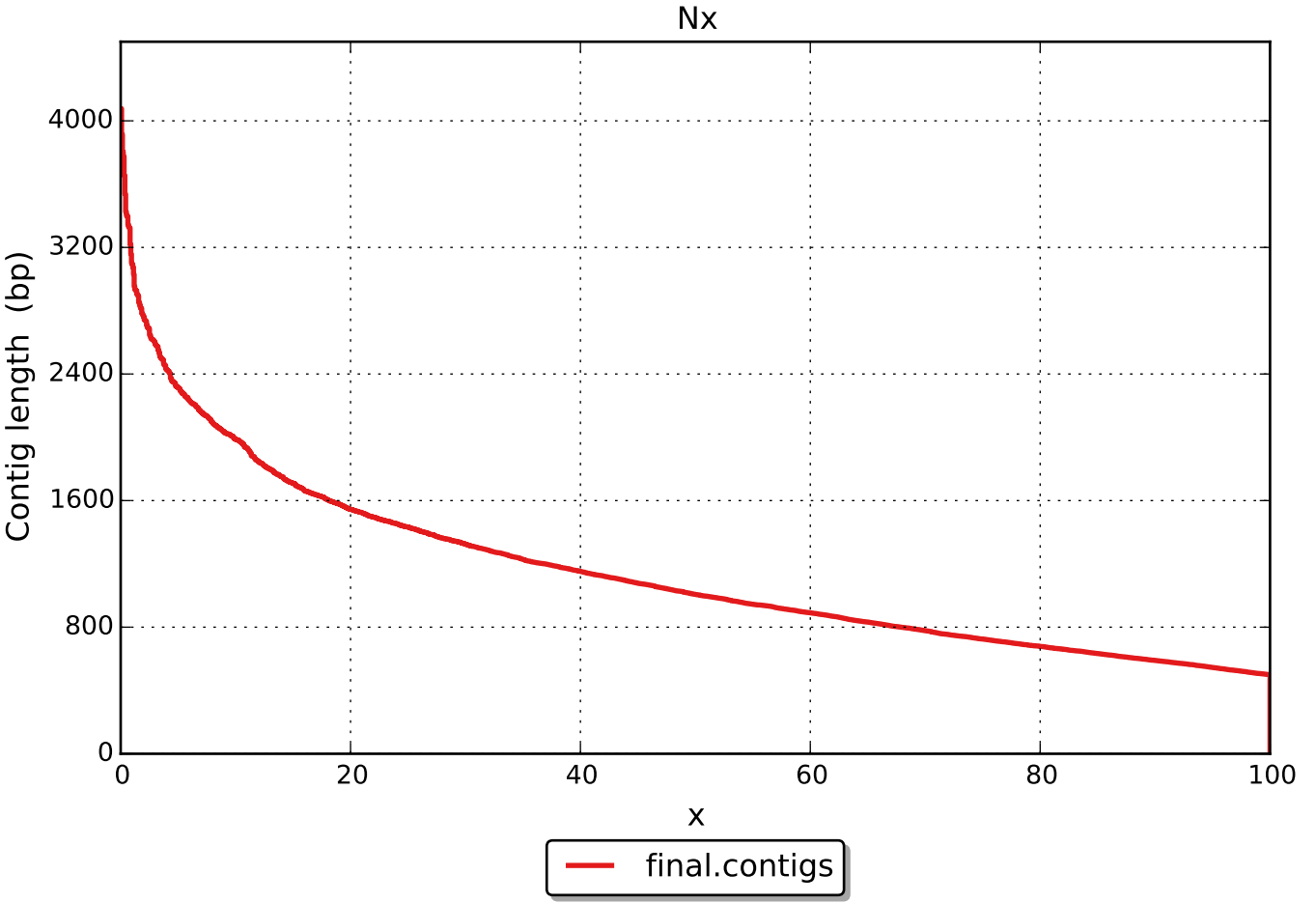
	final.contigs
# misassemblies	7
# relocations	6
# translocations	0
# inversions	1
# misassembled contigs	7
Misassembled contigs length	7305
# local misassemblies	4
# mismatches	54984
# indels	70
# short indels	69
# long indels	1
Indels length	155

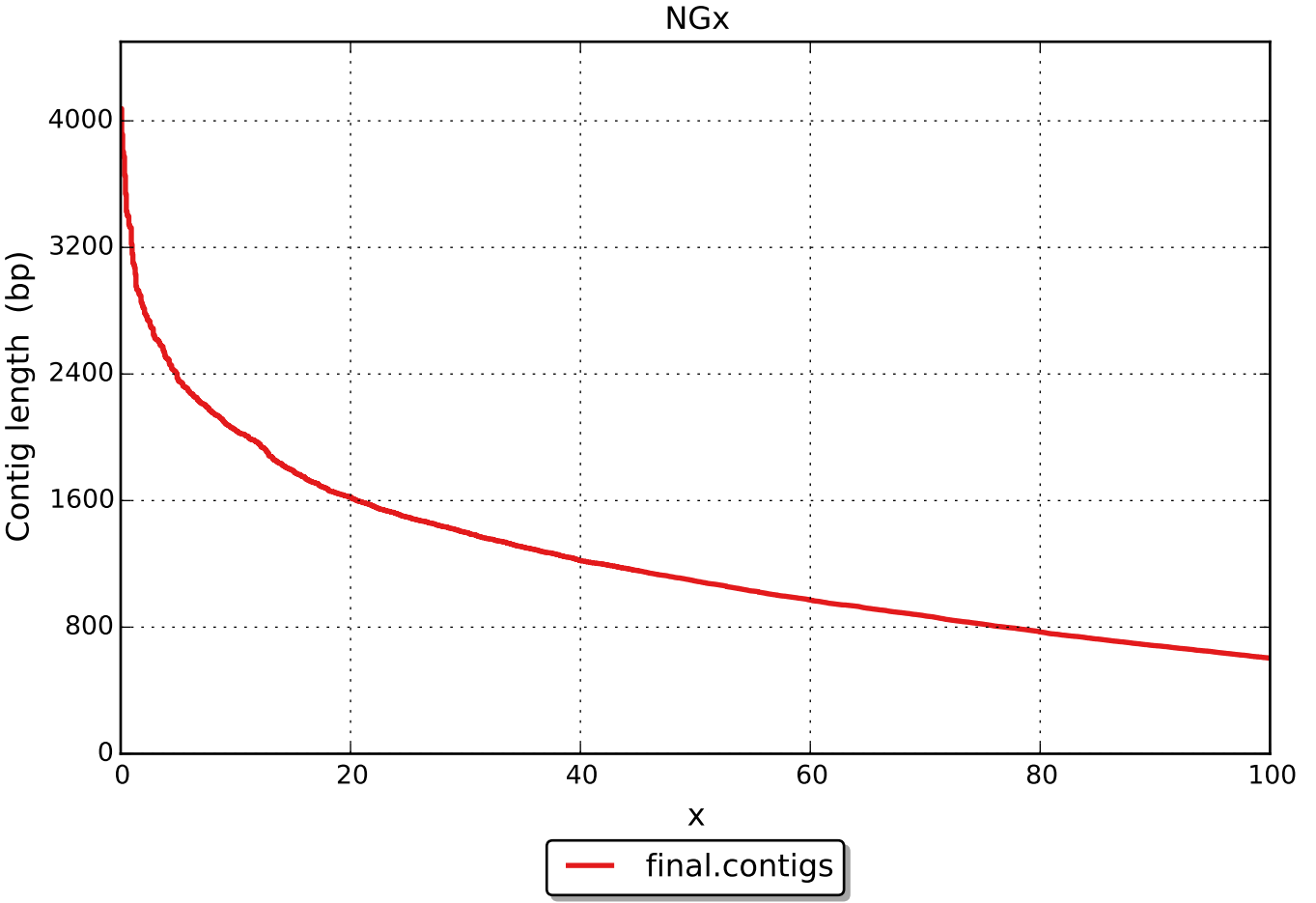
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

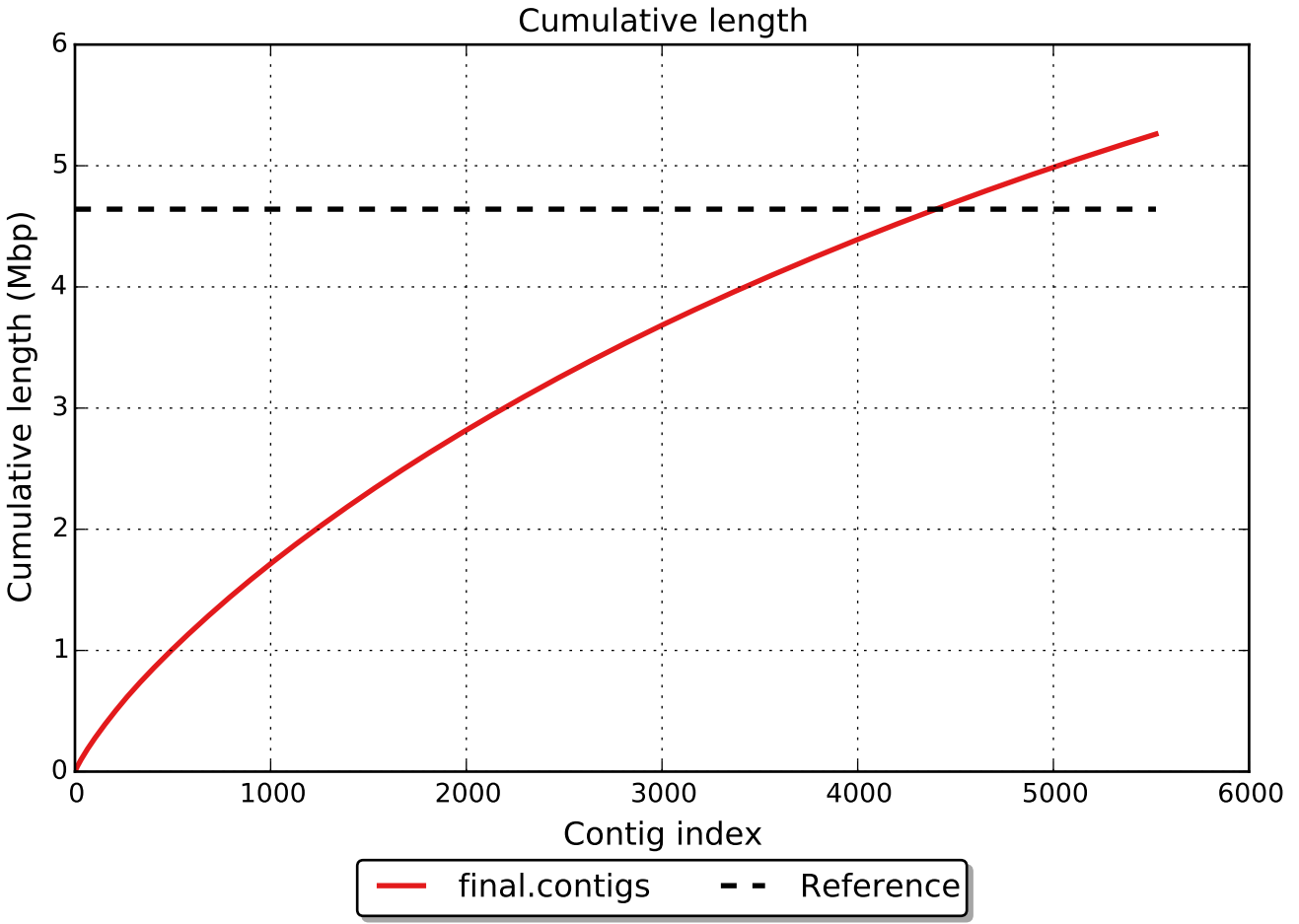
Unaligned report

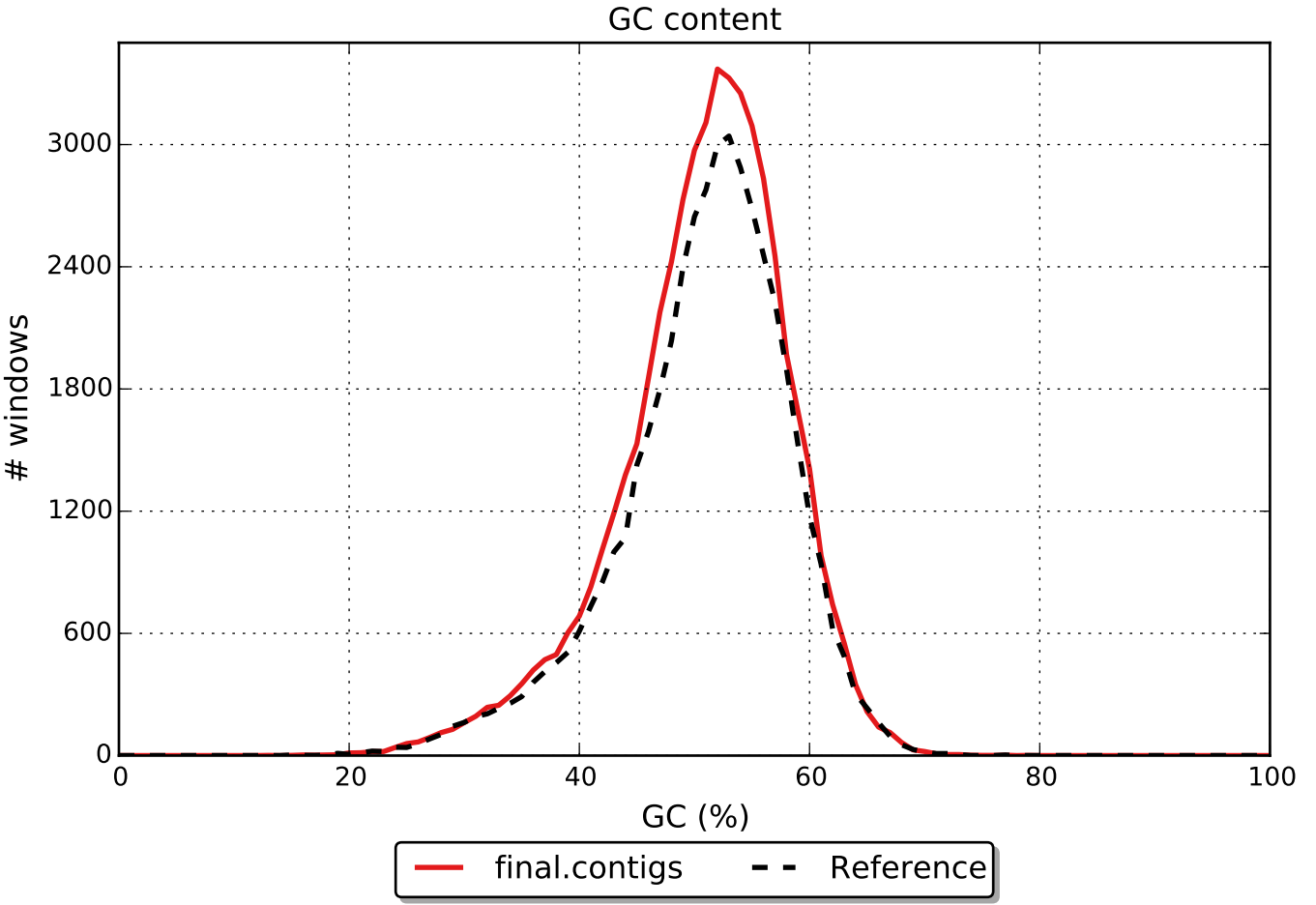
	final.contigs
# fully unaligned contigs	48
Fully unaligned length	26944
# partially unaligned contigs	49
# with misassembly	0
# both parts are significant	0
Partially unaligned length	3552
# N's	0

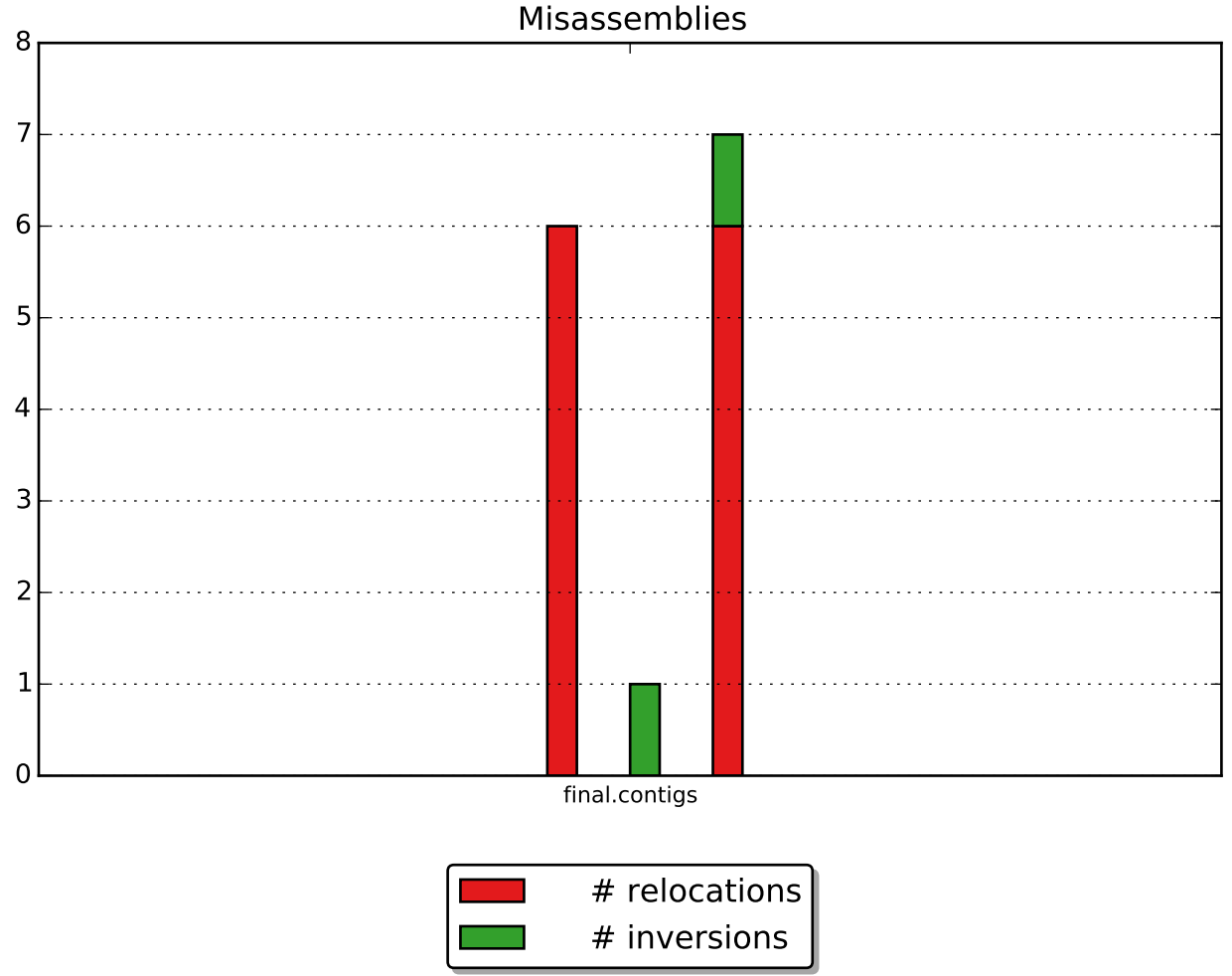
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

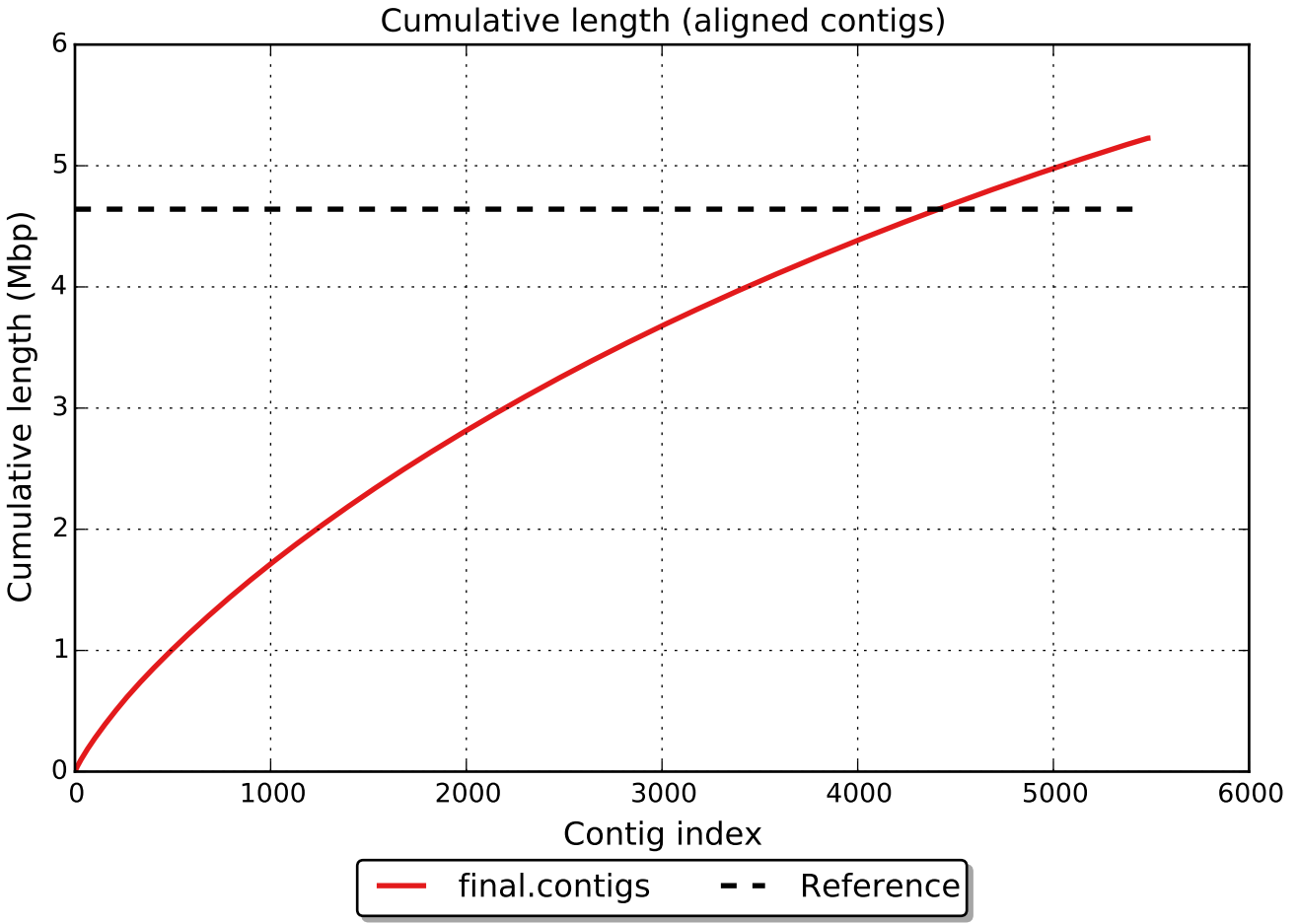

Nx
Contig length (bp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
final.contigs

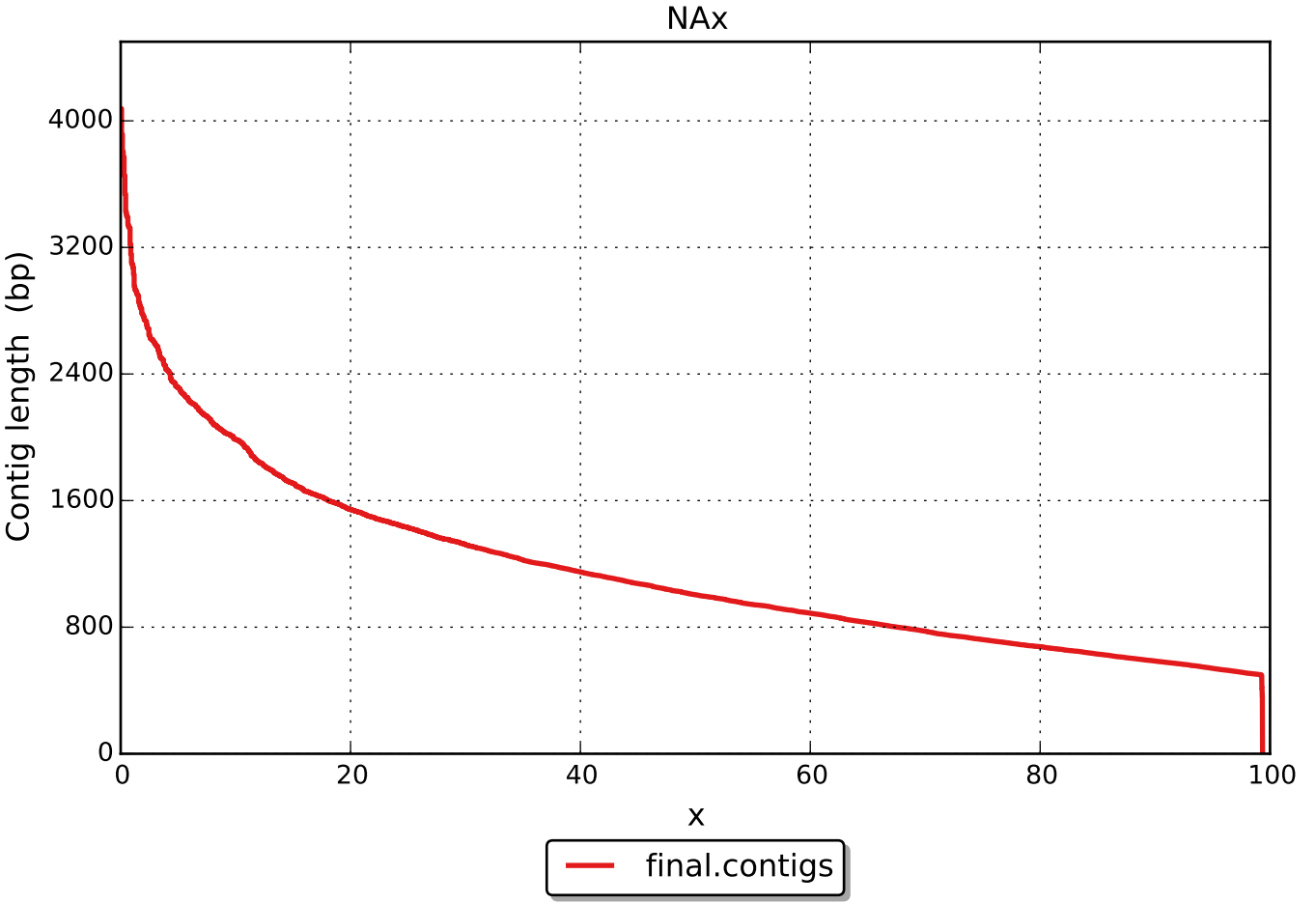

NGx
Contig length (bp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
final.contigs

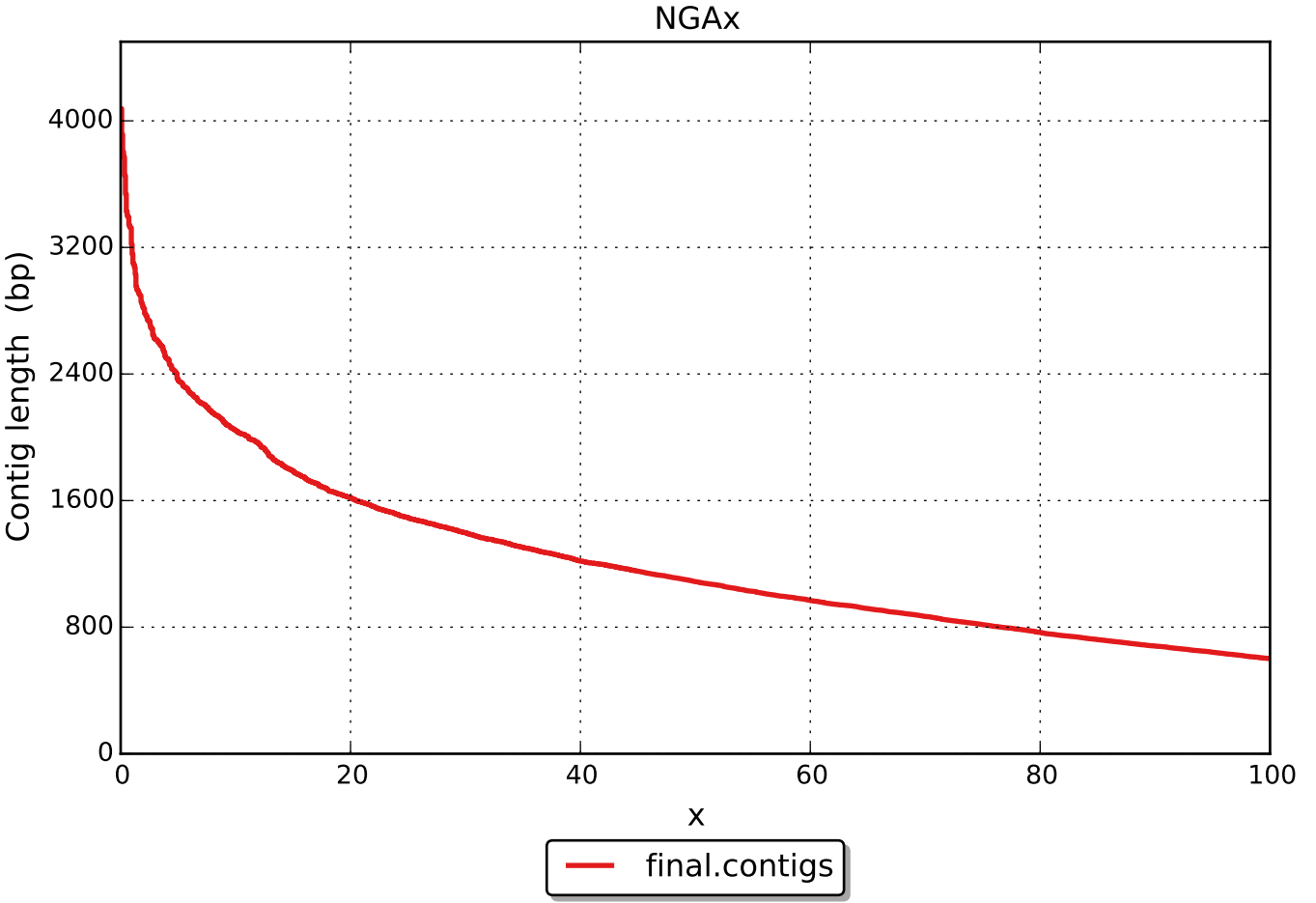

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
1000
2000
3000
4000
5000
6000
Contig index
final.contigs
Reference


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


Misassemblies
8
7
6
5
4
3
2
1
0
final.contigs
relocations
inversions


Cumulative length (aligned contigs)
Cumulative length (Mbp)
Contig index
0
1
2
3
4
5
6
0
1000
2000
3000
4000
5000
6000
final.contigs
Reference


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


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