Report

	final.contigs
# contigs (>= 0 bp)	13973
# contigs (>= 1000 bp)	1785
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	8354300
Total length (>= 1000 bp)	2532780
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	5903
Largest contig	4533
Total length	5401180
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	957
NG50	1054
N75	699
NG75	795
L50	1957
LG50	1579
L75	3617
LG75	2852
# misassemblies	5
# misassembled contigs	5
Misassembled contigs length	6136
# local misassemblies	5
# unaligned contigs	92 + 65 part
Unaligned length	57165
Genome fraction (%)	93.383
Duplication ratio	1.233
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1262.86
# indels per 100 kbp	1.41
Largest alignment	4533
NA50	956
NGA50	1051
NA75	695
NGA75	792
LA50	1961
LGA50	1582
LA75	3626
LGA75	2858

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

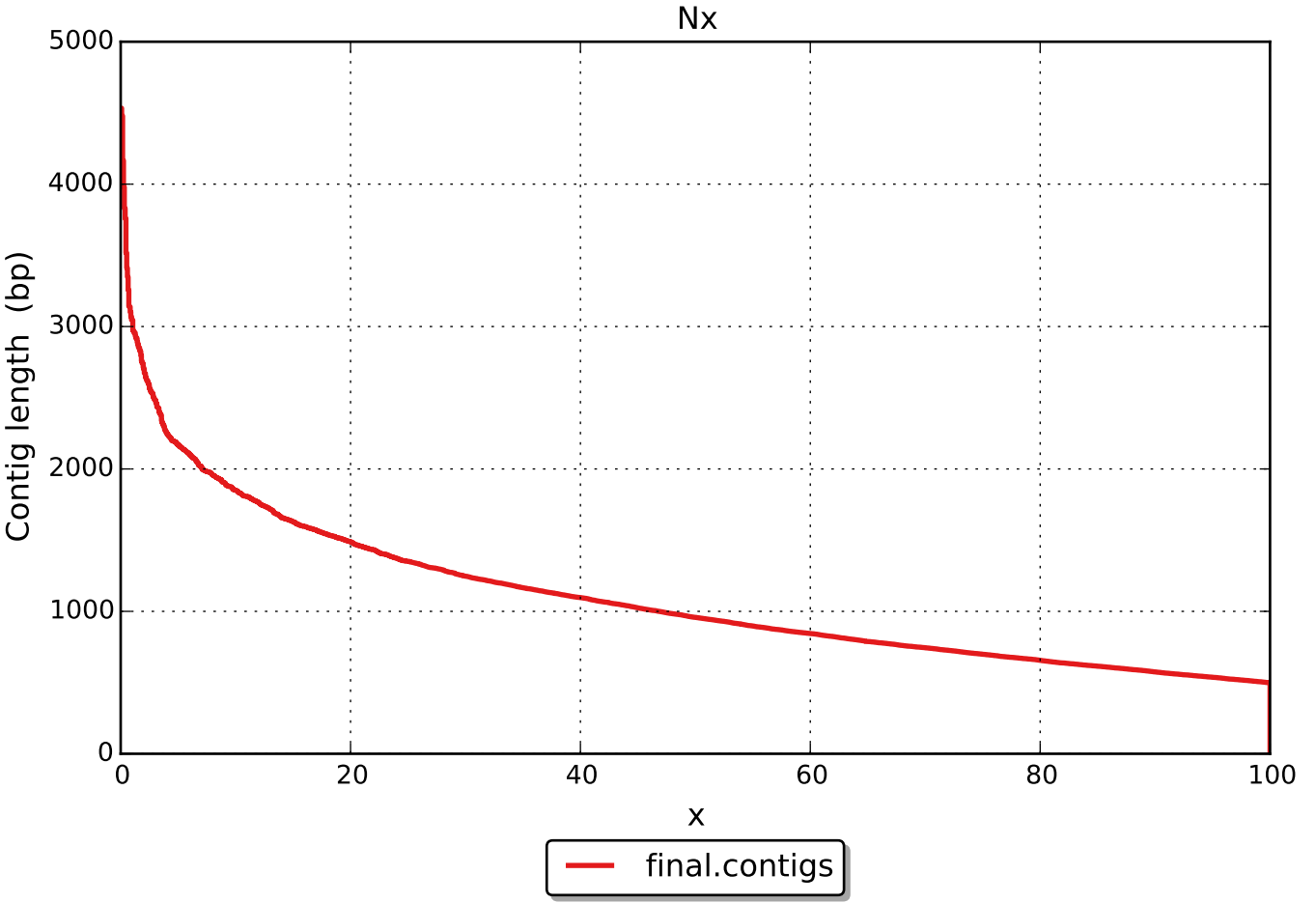
	final.contigs
# misassemblies	5
# relocations	4
# translocations	0
# inversions	1
# misassembled contigs	5
Misassembled contigs length	6136
# local misassemblies	5
# mismatches	54739
# indels	61
# short indels	60
# long indels	1
Indels length	146

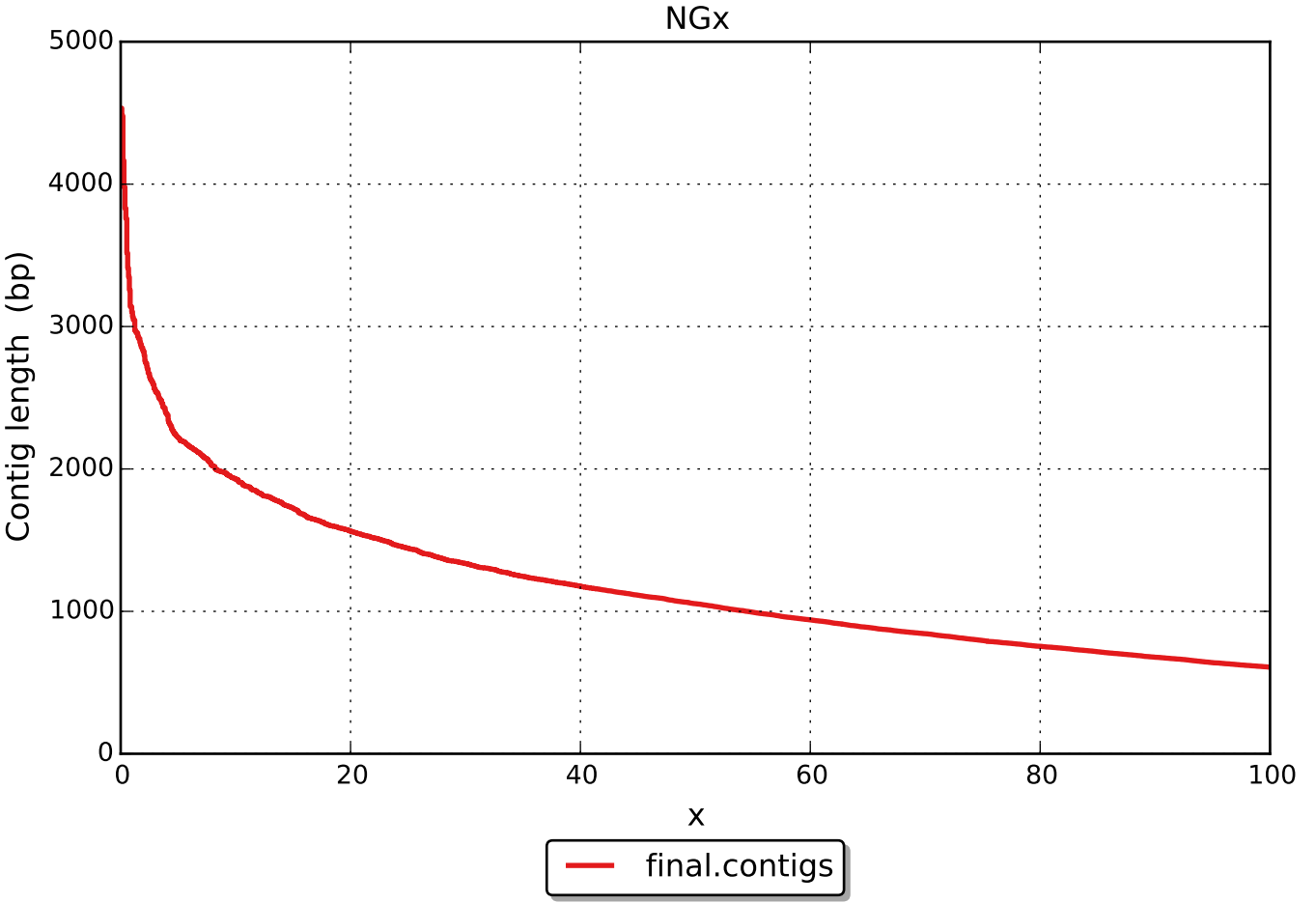
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

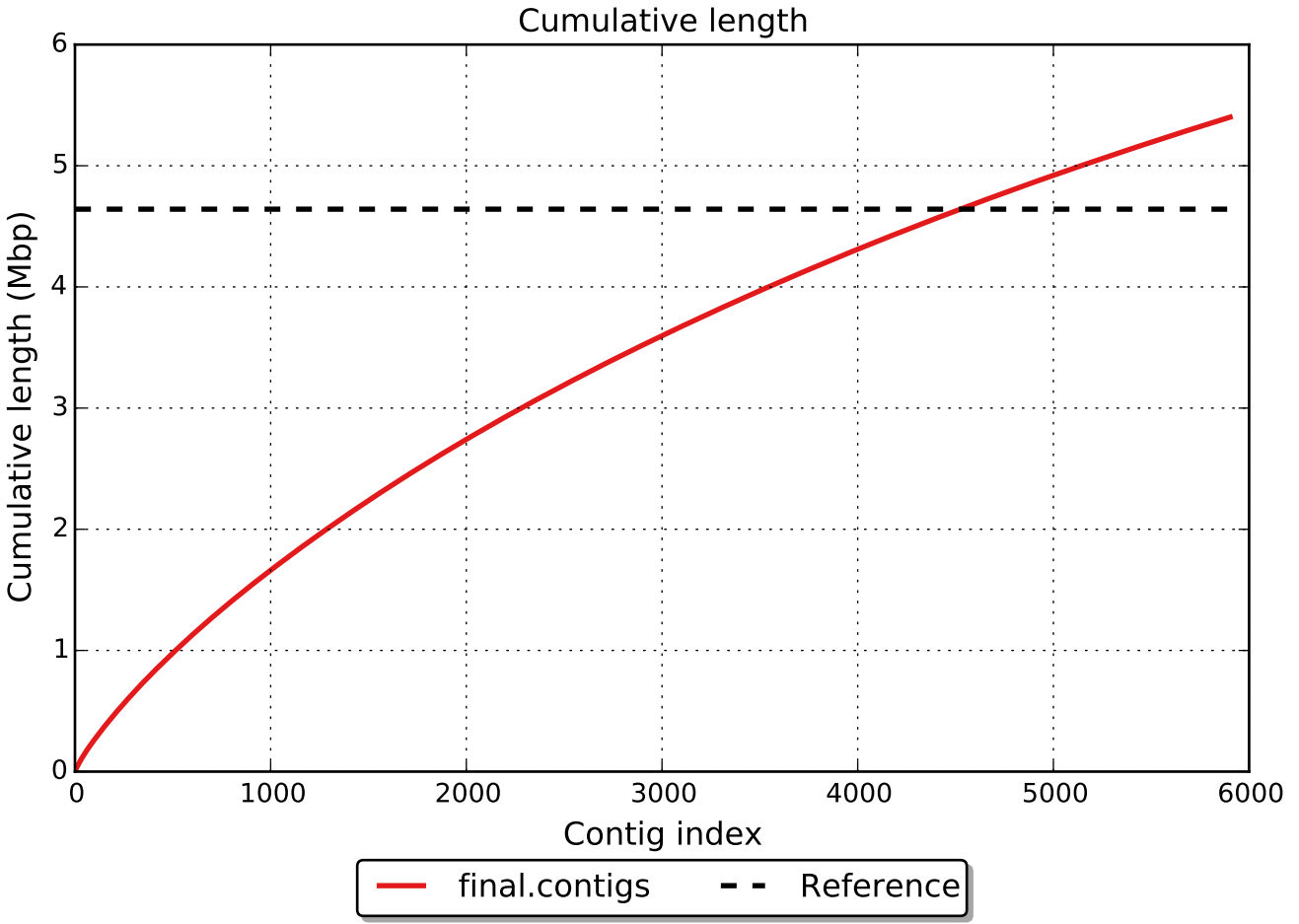
Unaligned report

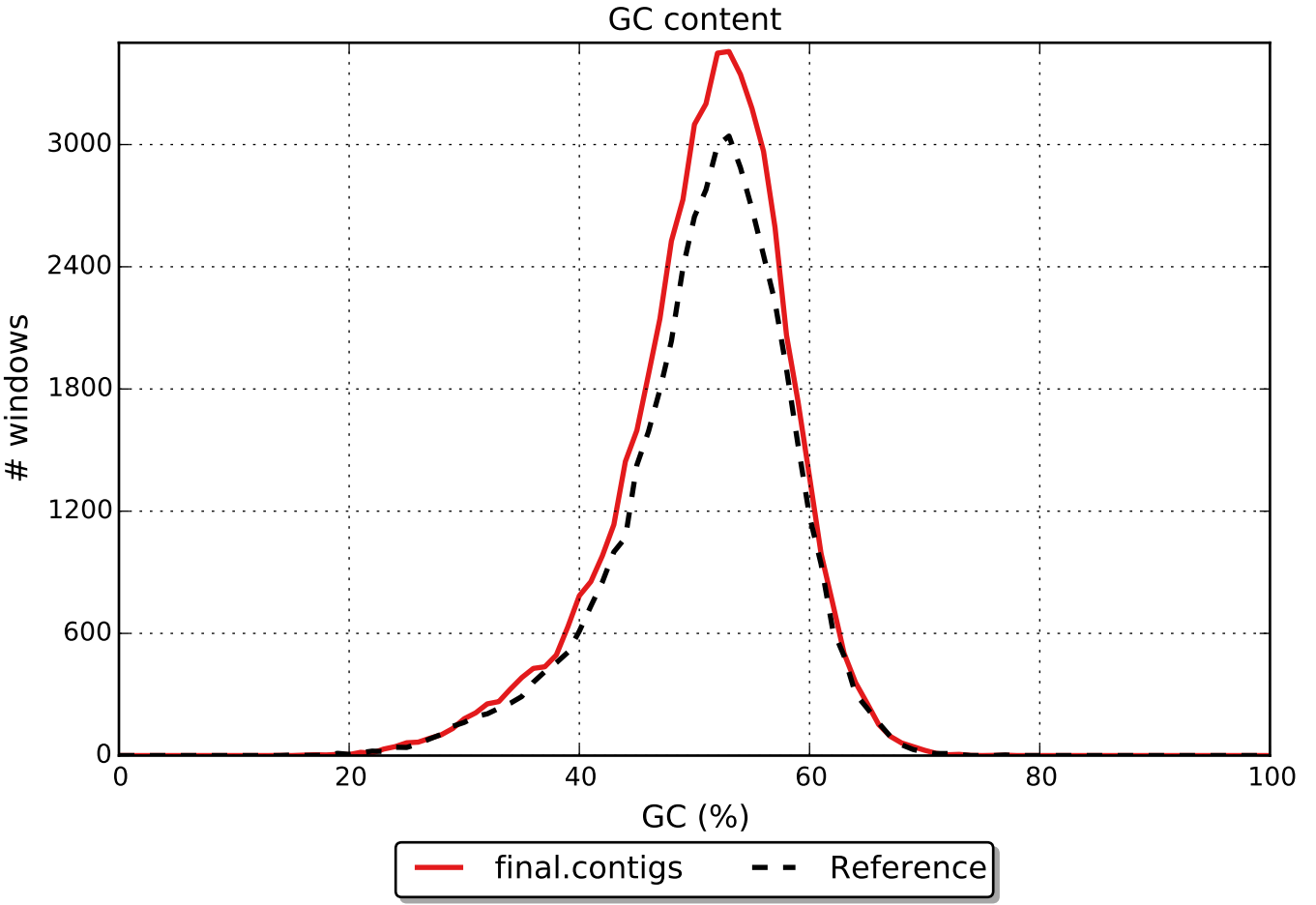
	final.contigs
# fully unaligned contigs	92
Fully unaligned length	50217
# partially unaligned contigs	65
# with misassembly	0
# both parts are significant	0
Partially unaligned length	6948
# N's	0

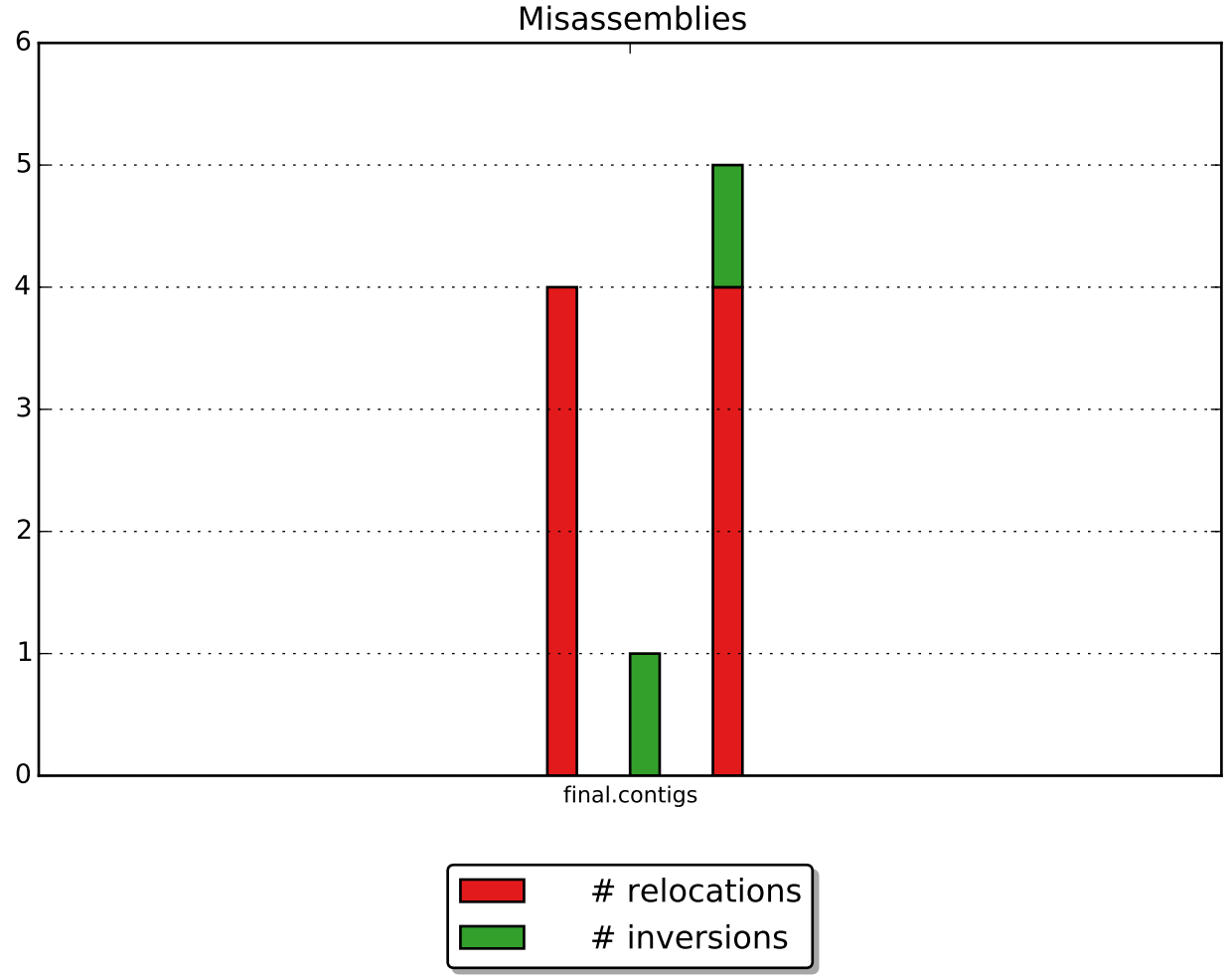
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

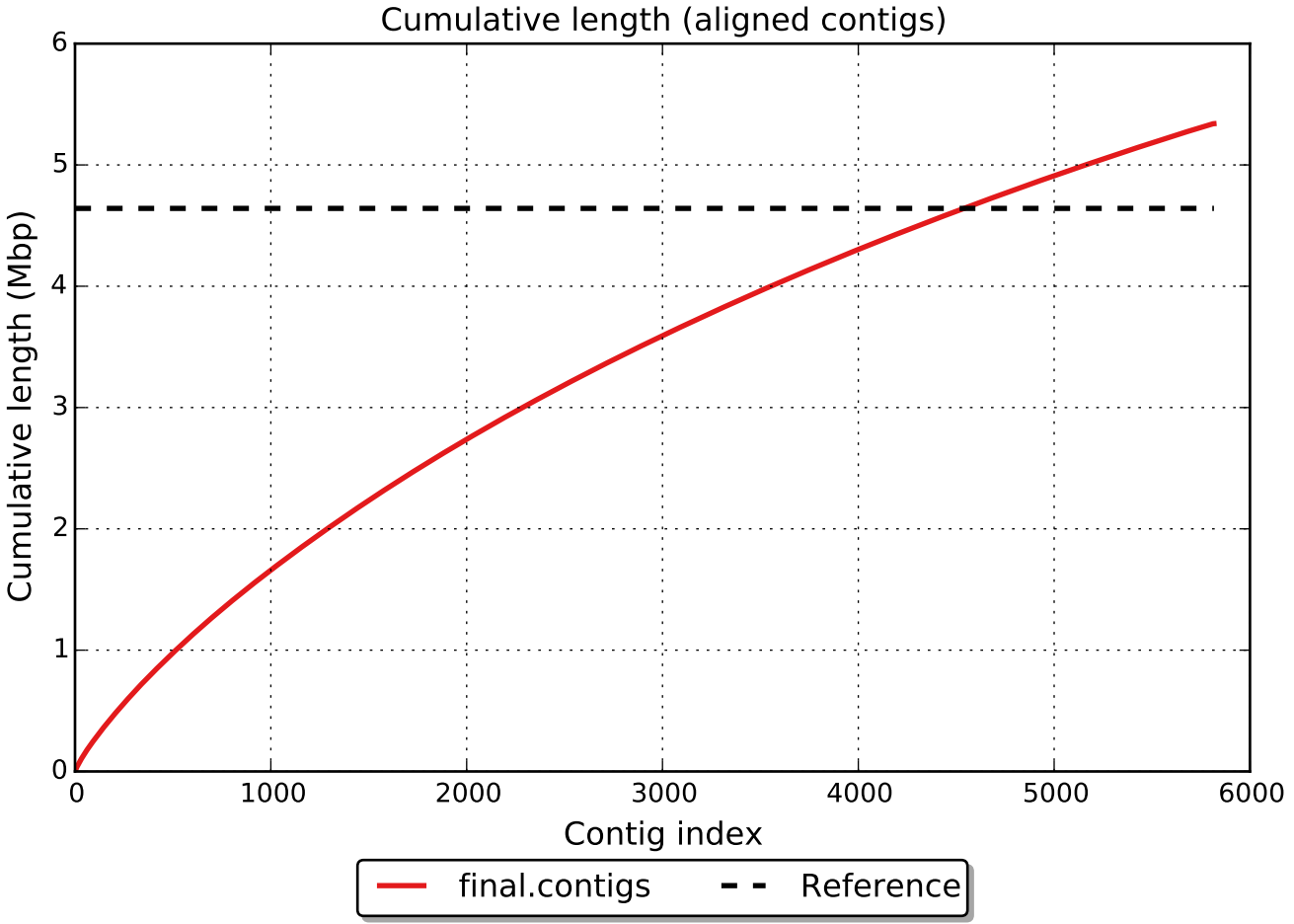

Nx
5000
4000
3000
2000
1000
0
Contig length (bp)
0
20
40
60
80
100
x
final.contigs

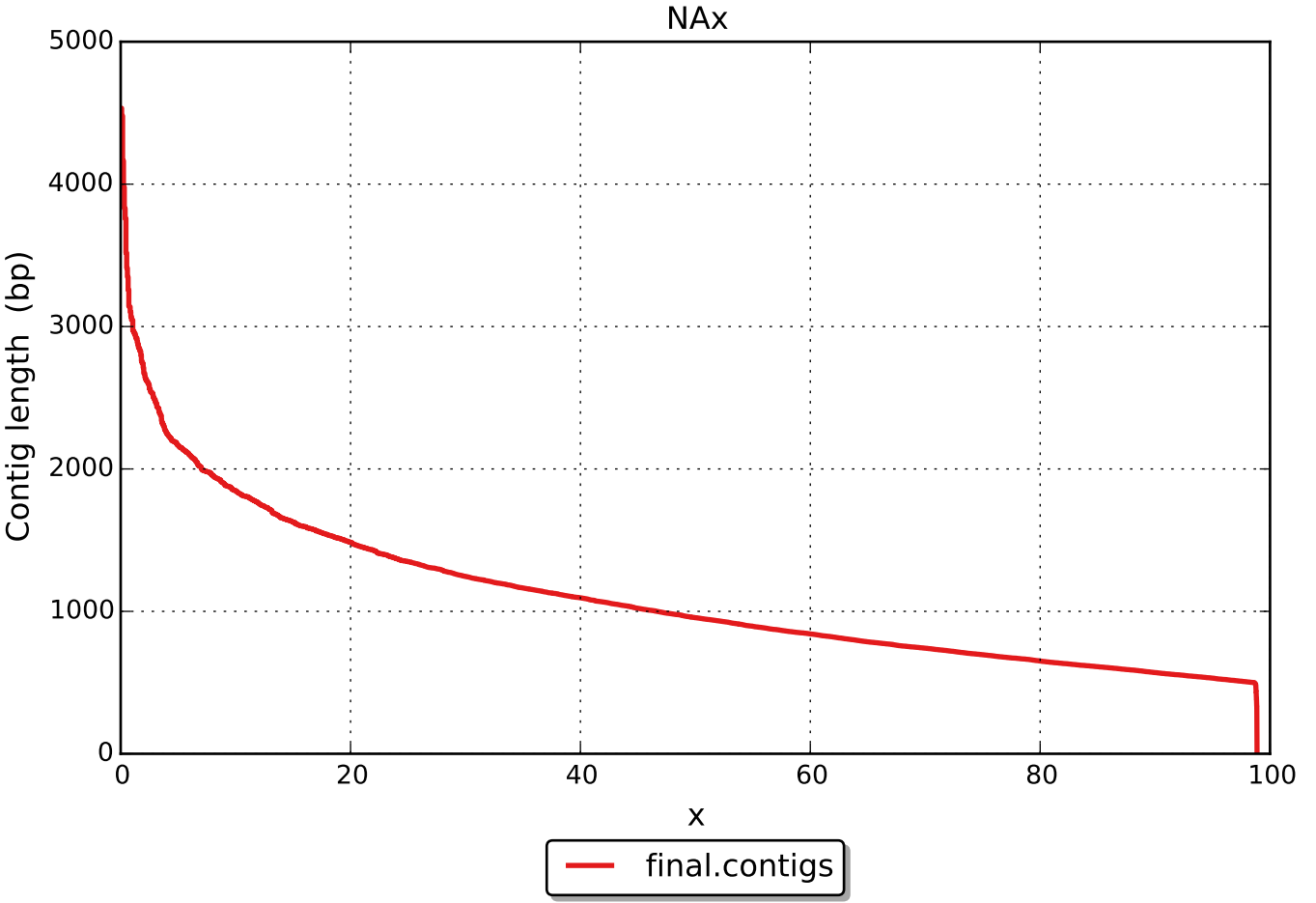

NGx
5000
4000
3000
2000
1000
0
Contig length (bp)
0
20
40
60
80
100
x
final.contigs

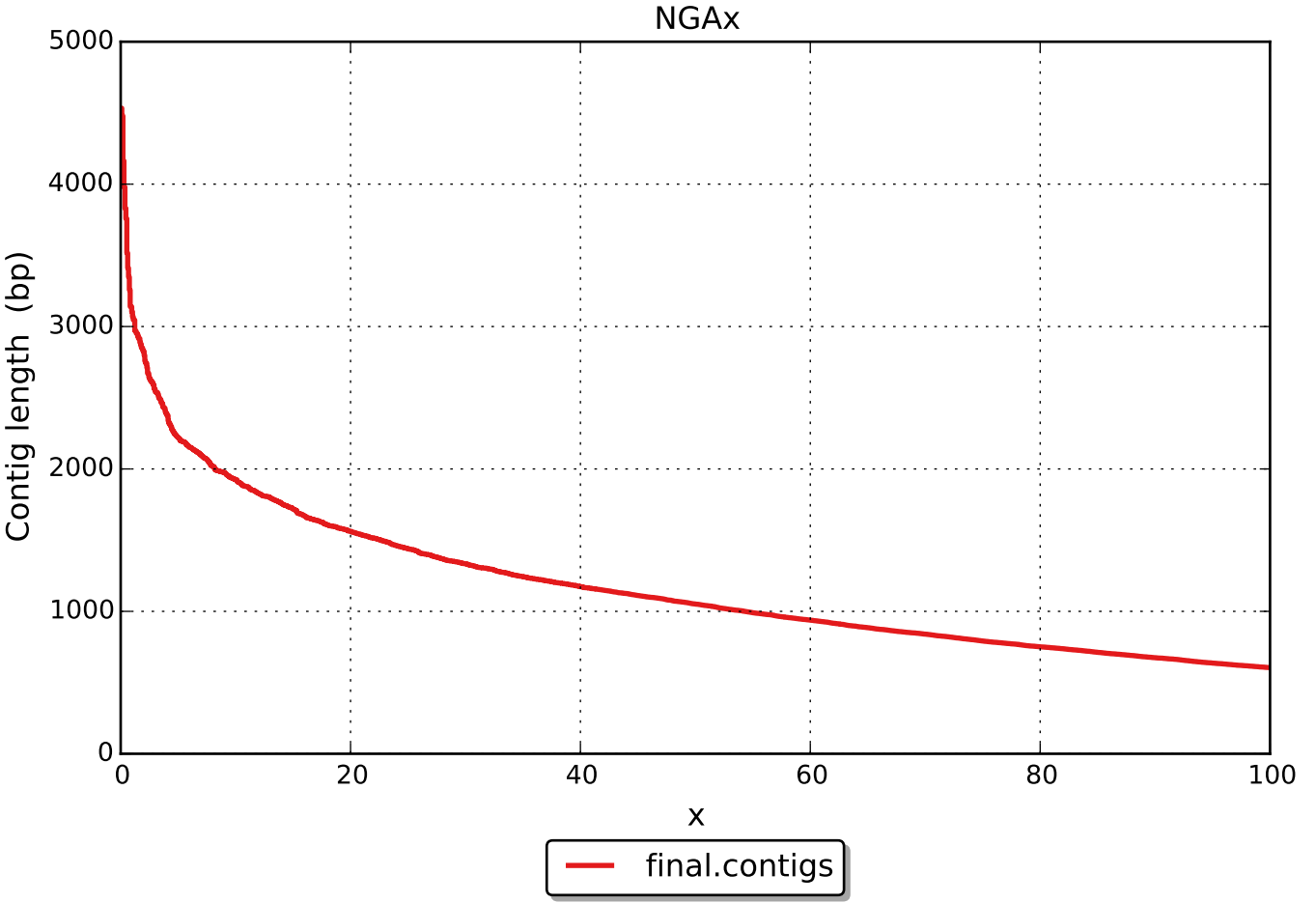

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
1000
2000
3000
4000
5000
6000
Contig index
final.contigs
Reference


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


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


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


NAx
5000
4000
3000
2000
1000
0
Contig length (bp)
0
20
40
60
80
100
x
final.contigs


NGAx
5000
4000
3000
2000
1000
0
Contig length (bp)
0
20
40
60
80
100
x
final.contigs