Report

	final.contigs
# contigs (>= 0 bp)	9788
# contigs (>= 1000 bp)	1316
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	6323622
Total length (>= 1000 bp)	1750397
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	5556
Largest contig	3484
Total length	4695991
Reference length	4641652
GC (%)	50.72
Reference GC (%)	50.79
N50	865
NG50	870
N75	664
NG75	670
L50	1960
LG50	1929
L75	3516
LG75	3455
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	2011
# local misassemblies	4
# unaligned contigs	56 + 39 part
Unaligned length	35510
Genome fraction (%)	86.590
Duplication ratio	1.160
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1708.20
# indels per 100 kbp	1.89
Largest alignment	3481
NA50	861
NGA50	867
NA75	663
NGA75	668
LA50	1965
LGA50	1933
LA75	3525
LGA75	3464

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

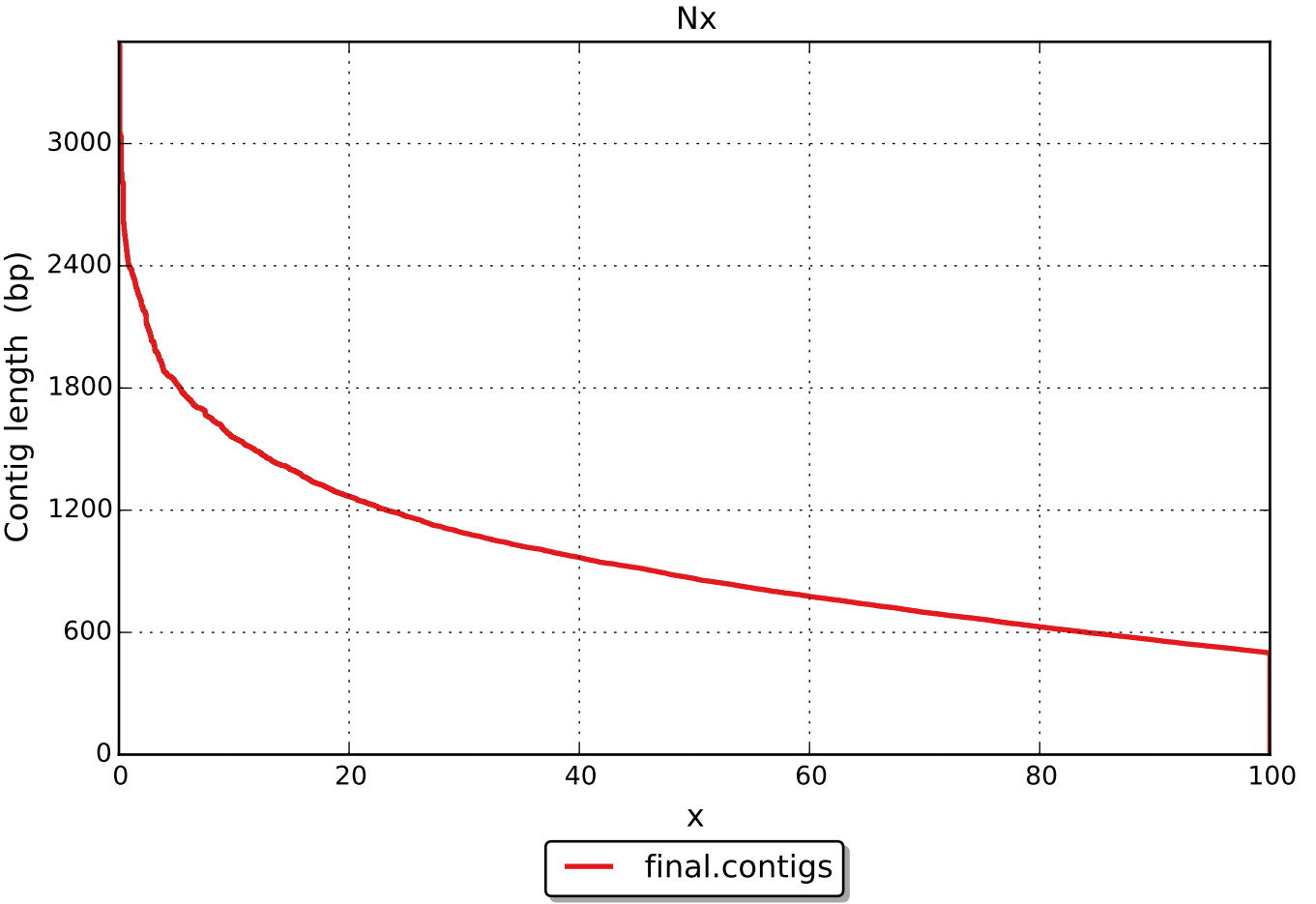
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# misassembled contigs	1
Misassembled contigs length	2011
# local misassemblies	4
# mismatches	68656
# indels	76
# short indels	75
# long indels	1
Indels length	98

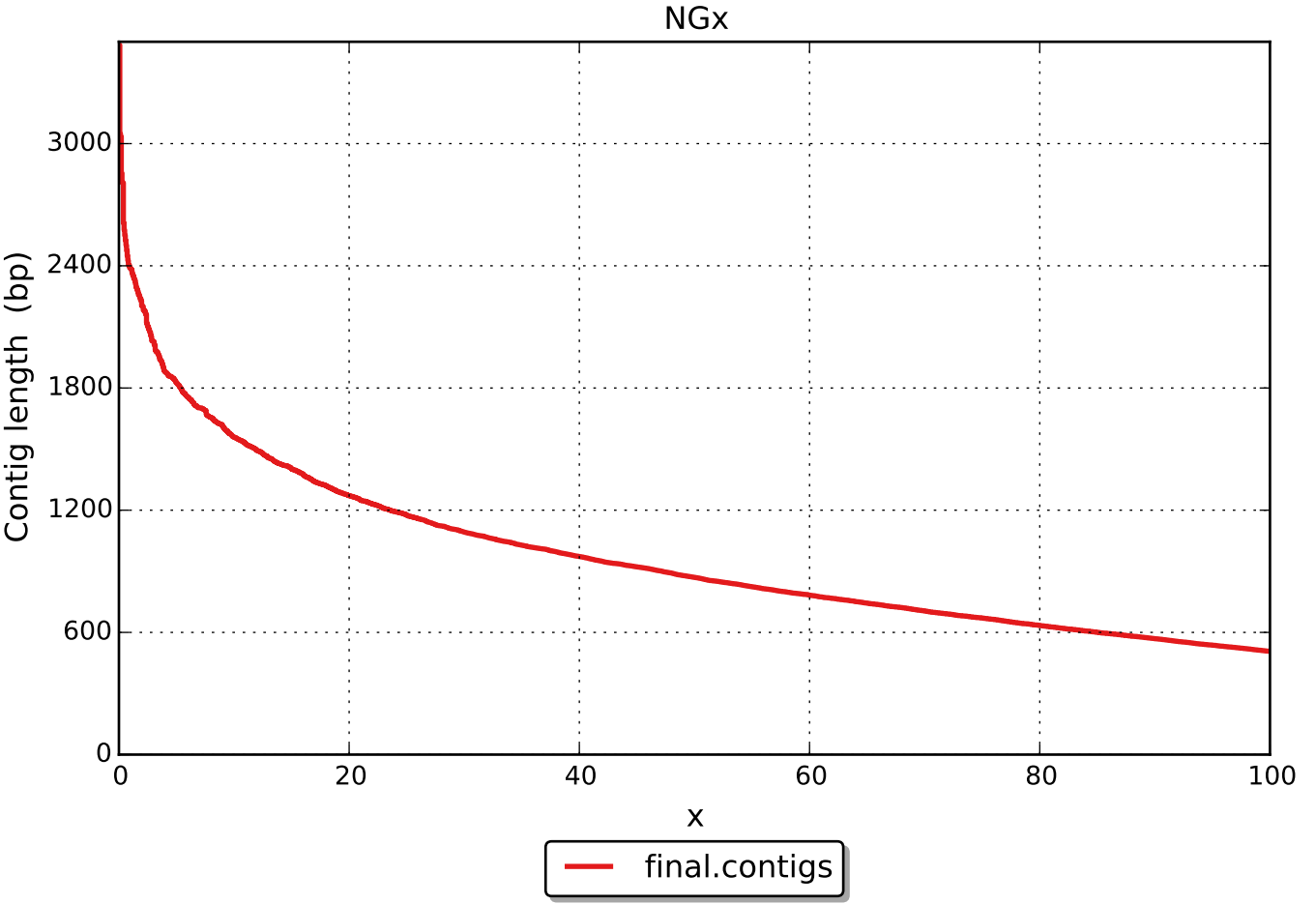
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

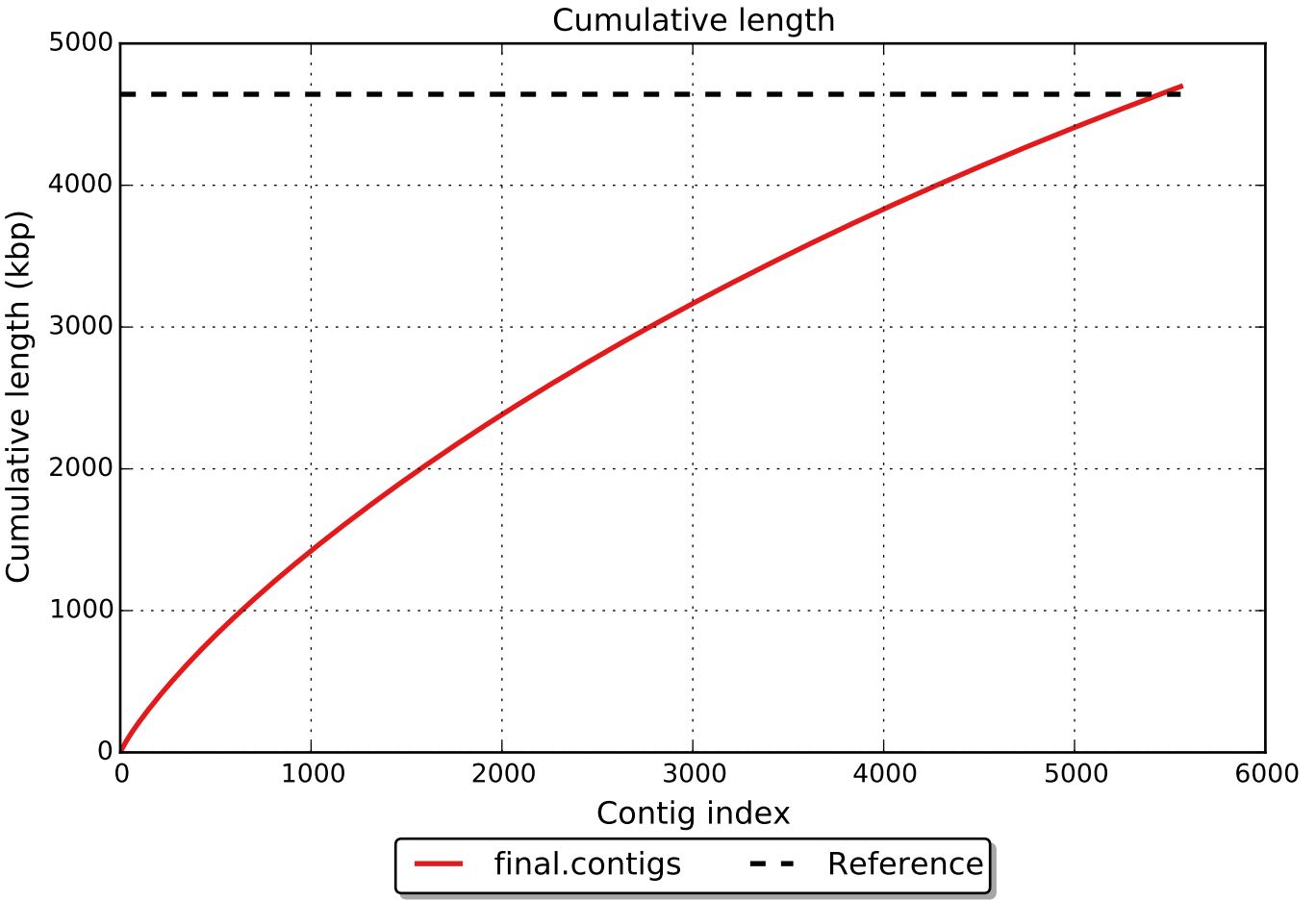
Unaligned report

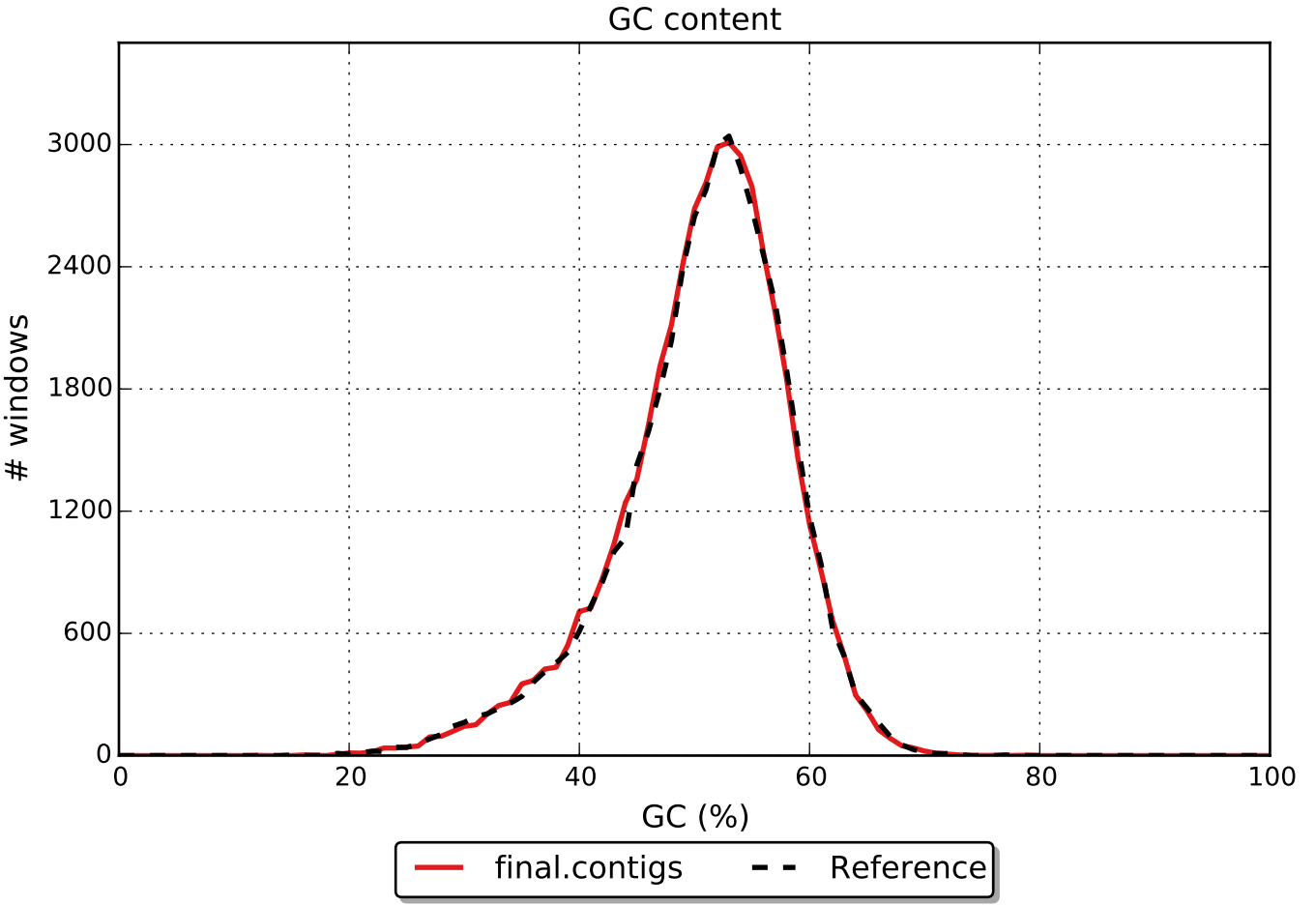
	final.contigs
# fully unaligned contigs	56
Fully unaligned length	32618
# partially unaligned contigs	39
# with misassembly	0
# both parts are significant	0
Partially unaligned length	2892
# N's	0

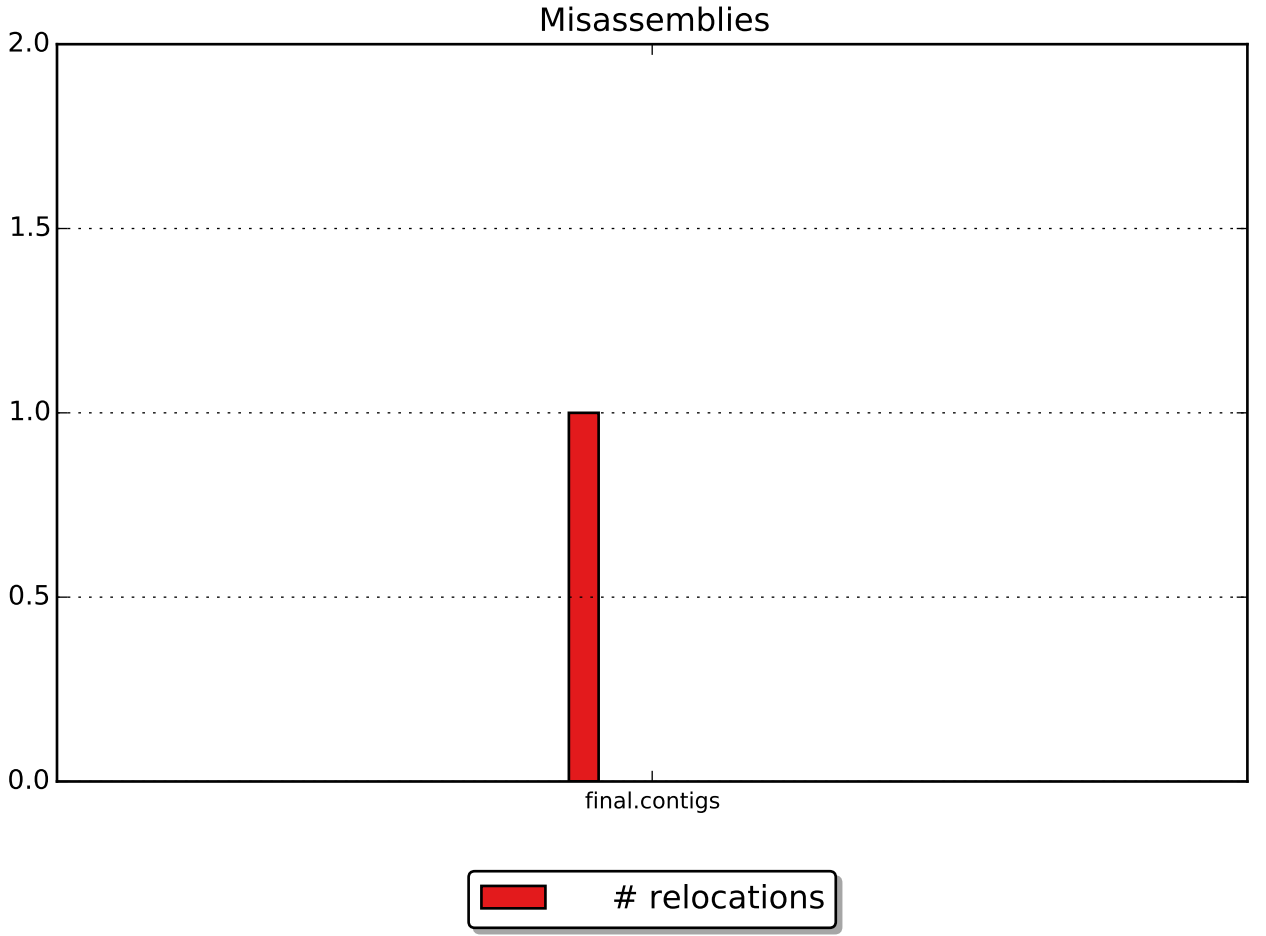
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

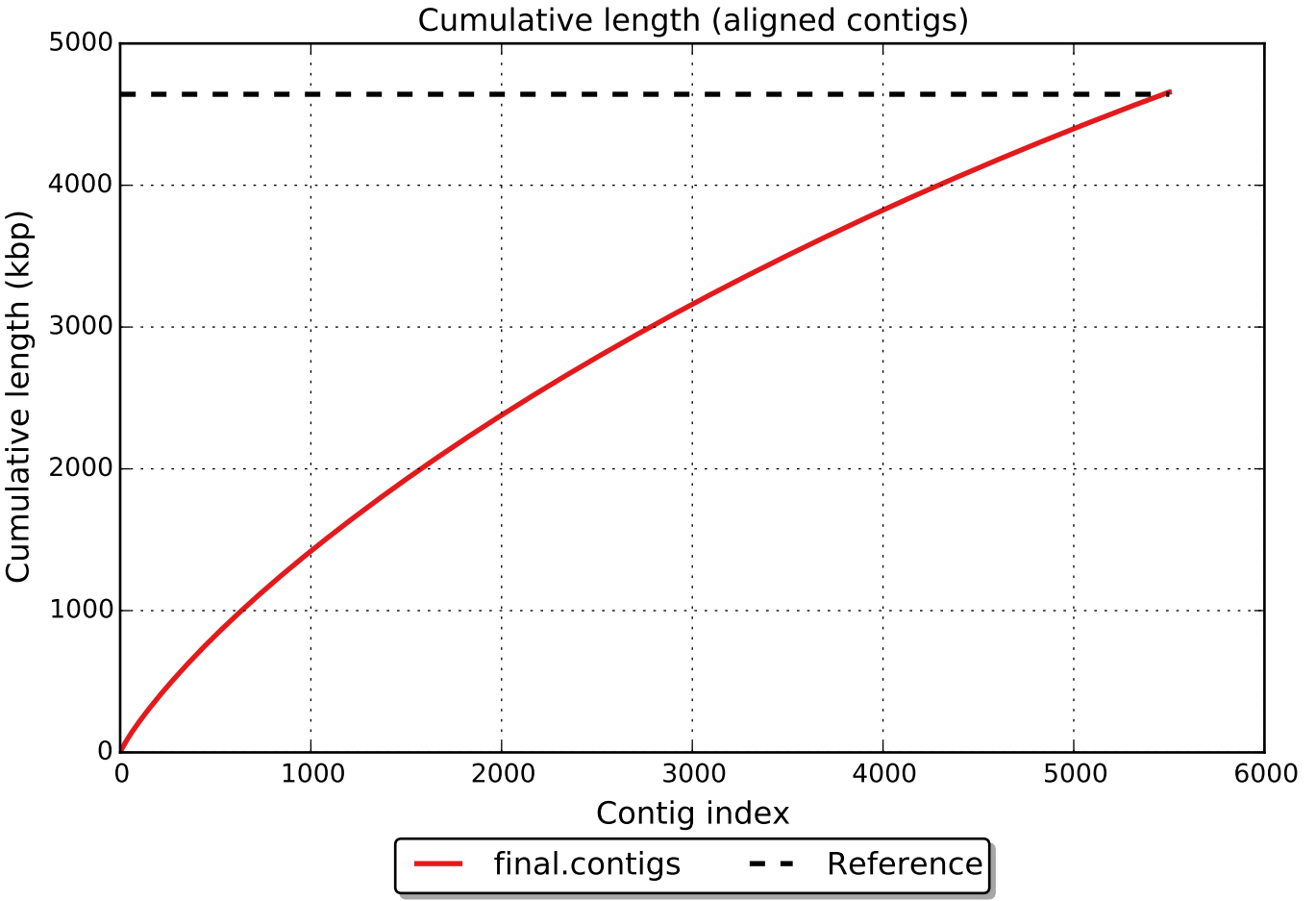

Nx
Contig length (bp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
final.contigs

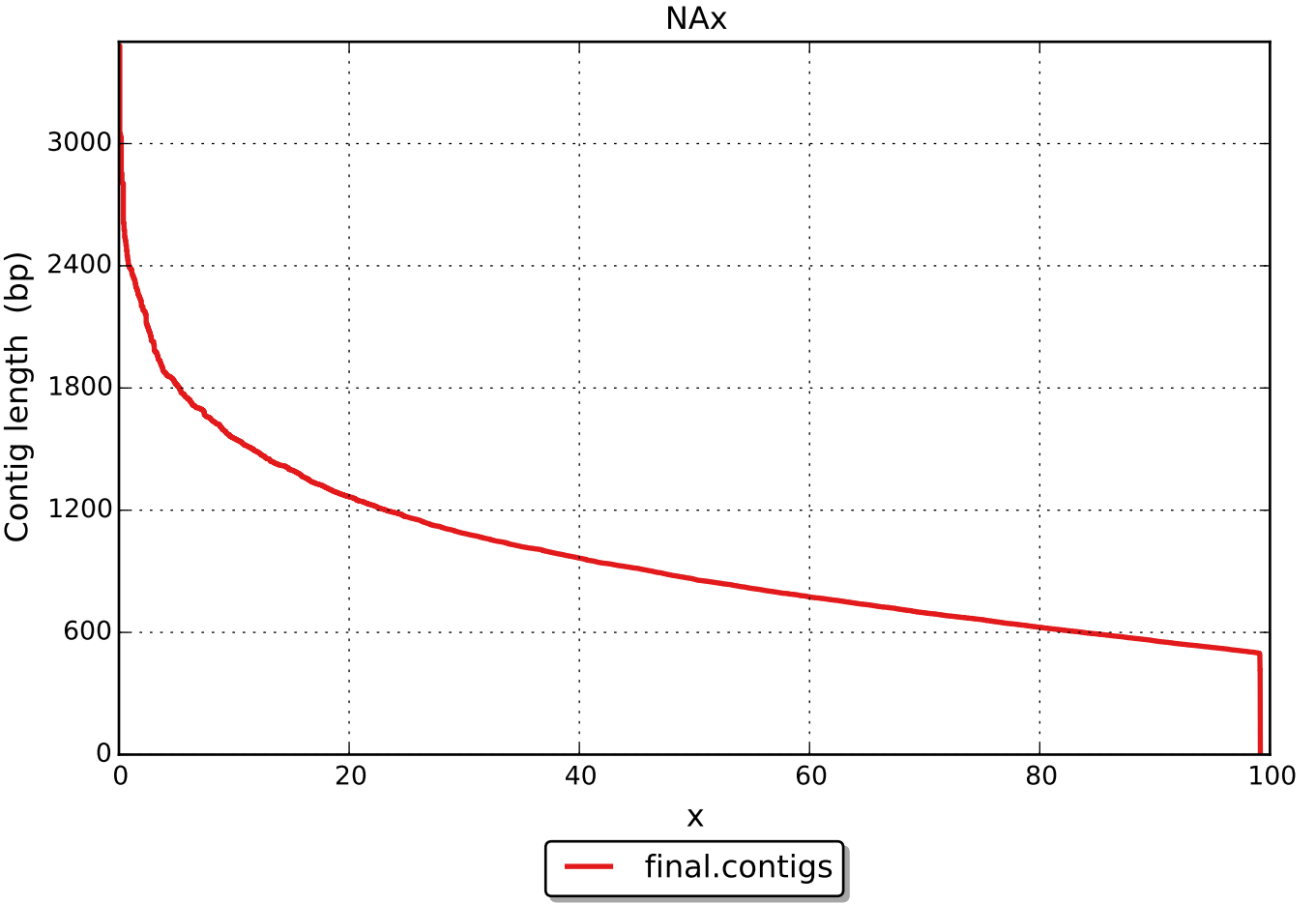

NGx
Contig length (bp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
final.contigs

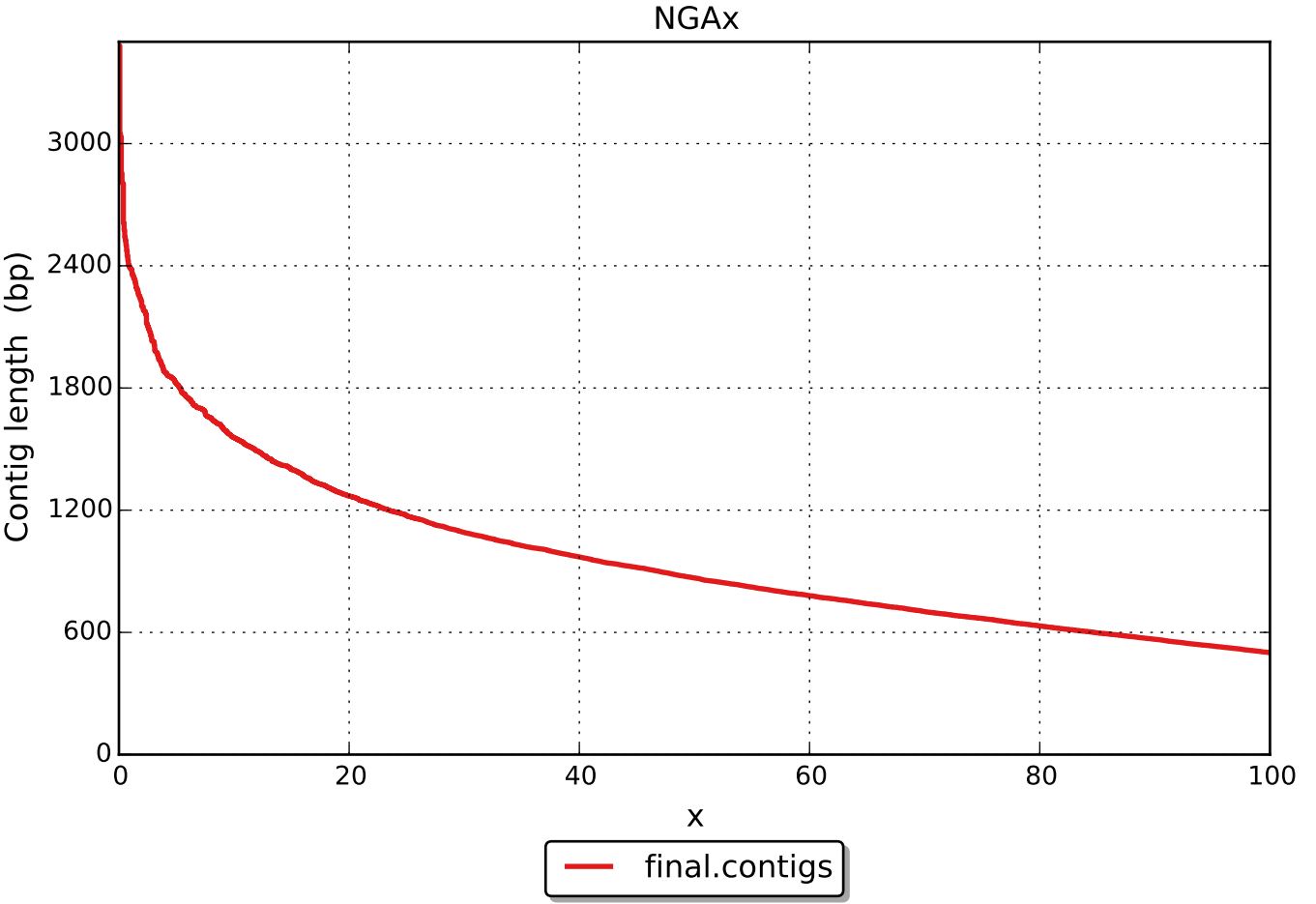

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
1000
2000
3000
4000
5000
6000
Contig index
final.contigs
Reference


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


Misassemblies
2.0
1.5
1.0
0.5
0.0
final.contigs
relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
1000
2000
3000
4000
5000
6000
Contig index
final.contigs
Reference


NAx
Contig length (bp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (bp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
final.contigs