Report

	final.contigs
# contigs (>= 0 bp)	37328
# contigs (>= 1000 bp)	1913
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	16928197
Total length (>= 1000 bp)	2916630
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	6182
Largest contig	4310
Total length	5772054
Reference length	4641652
GC (%)	50.73
Reference GC (%)	50.79
N50	1007
NG50	1175
N75	675
NG75	863
L50	1883
LG50	1363
L75	3632
LG75	2522
# misassemblies	7
# misassembled contigs	7
Misassembled contigs length	8546
# local misassemblies	11
# unaligned contigs	555 + 91 part
Unaligned length	314431
Genome fraction (%)	93.451
Duplication ratio	1.258
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1031.50
# indels per 100 kbp	0.85
Largest alignment	4310
NA50	1003
NGA50	1169
NA75	669
NGA75	860
LA50	1887
LGA50	1365
LA75	3643
LGA75	2527

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

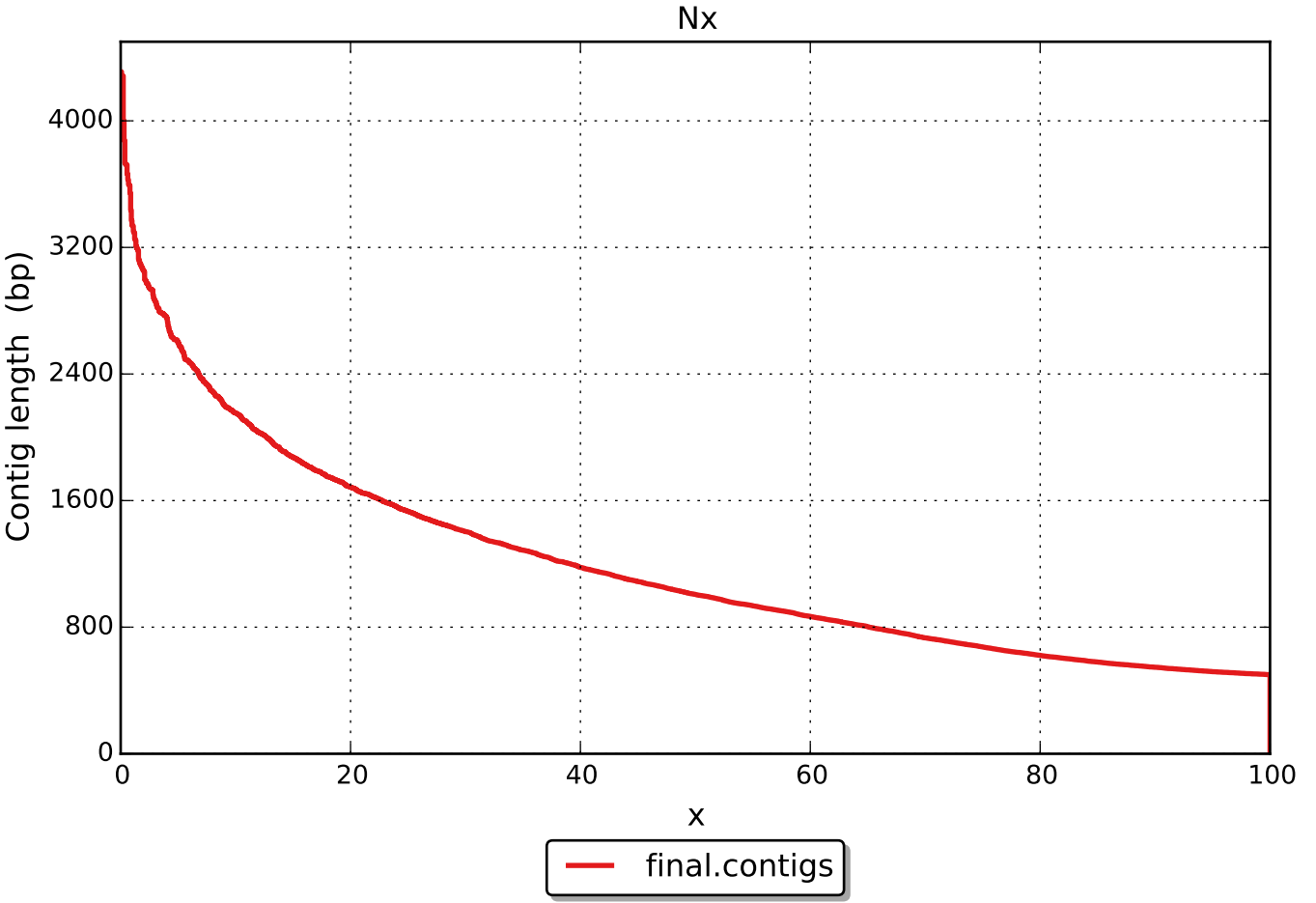
	final.contigs
# misassemblies	7
# relocations	3
# translocations	0
# inversions	4
# misassembled contigs	7
Misassembled contigs length	8546
# local misassemblies	11
# mismatches	44743
# indels	37
# short indels	37
# long indels	0
Indels length	37

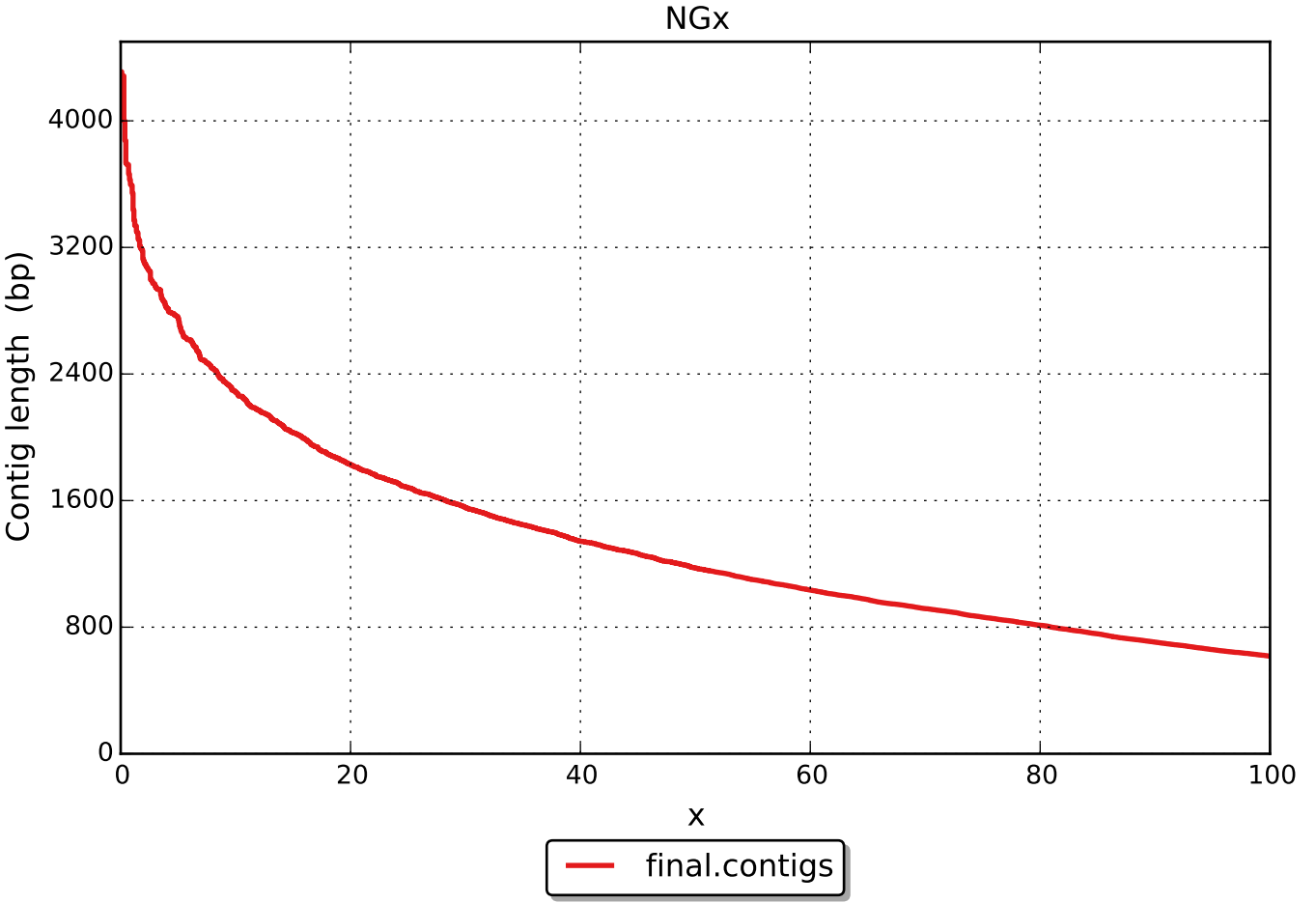
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

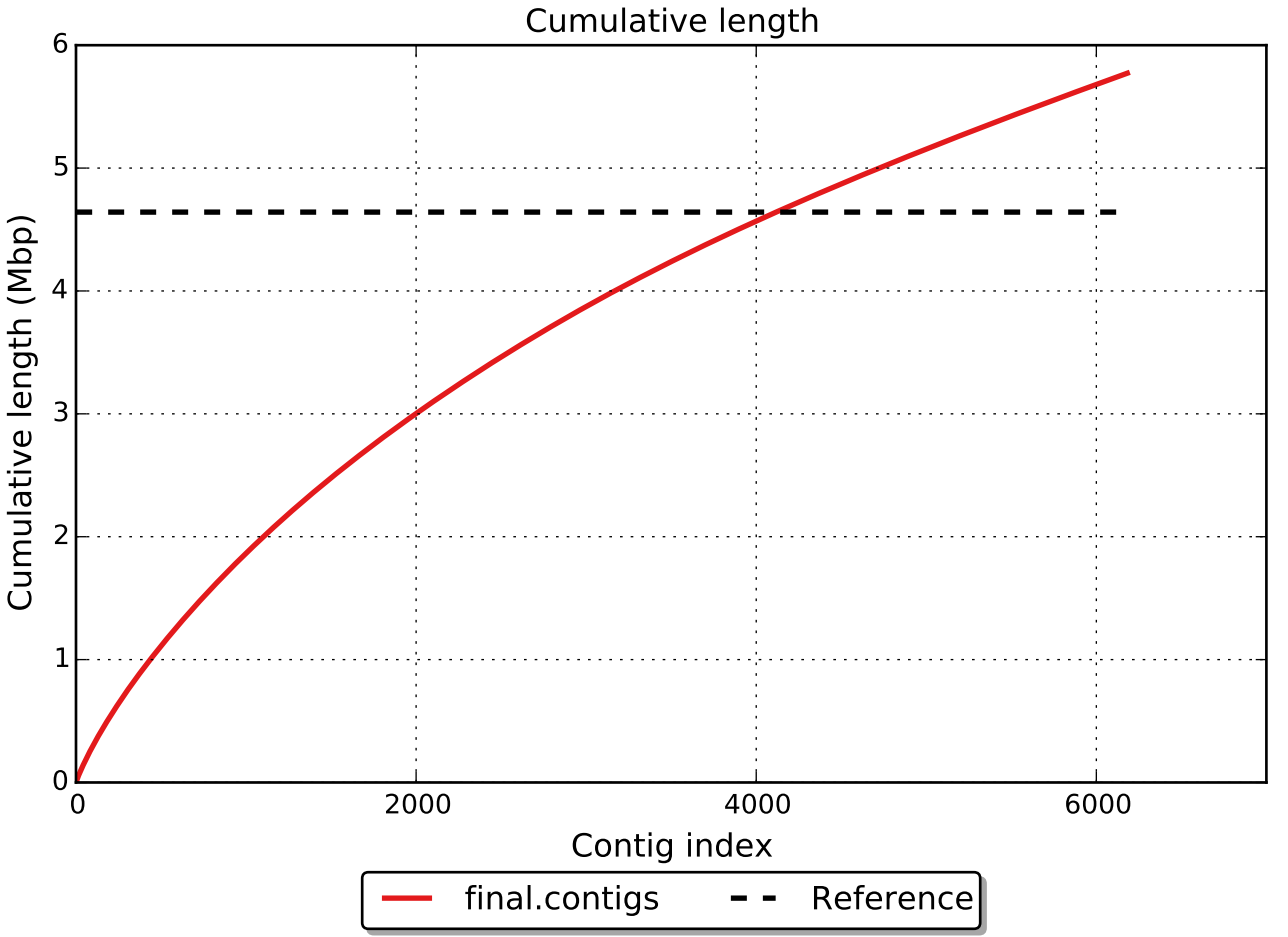
Unaligned report

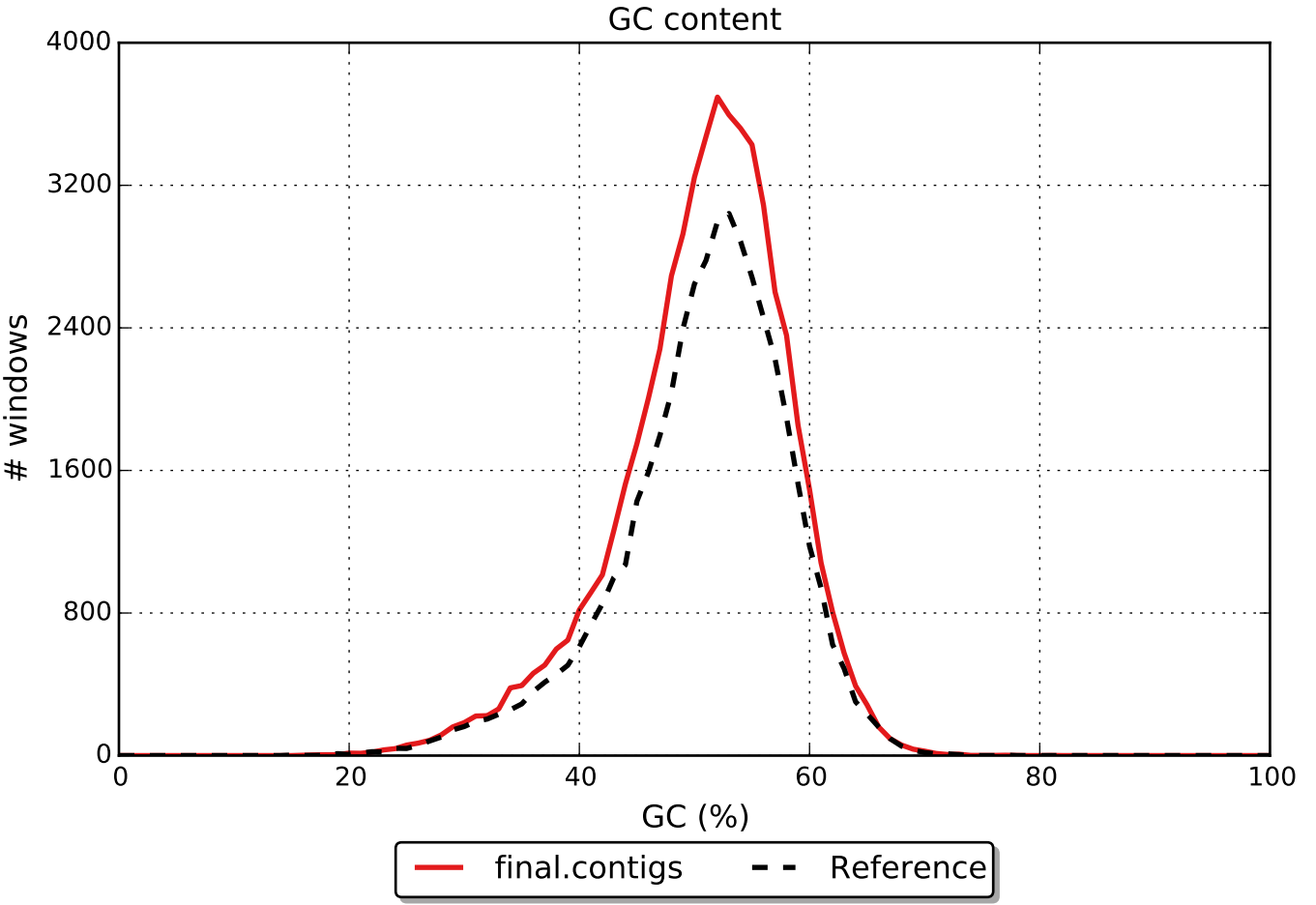
	final.contigs
# fully unaligned contigs	555
Fully unaligned length	301737
# partially unaligned contigs	91
# with misassembly	0
# both parts are significant	0
Partially unaligned length	12694
# N's	0

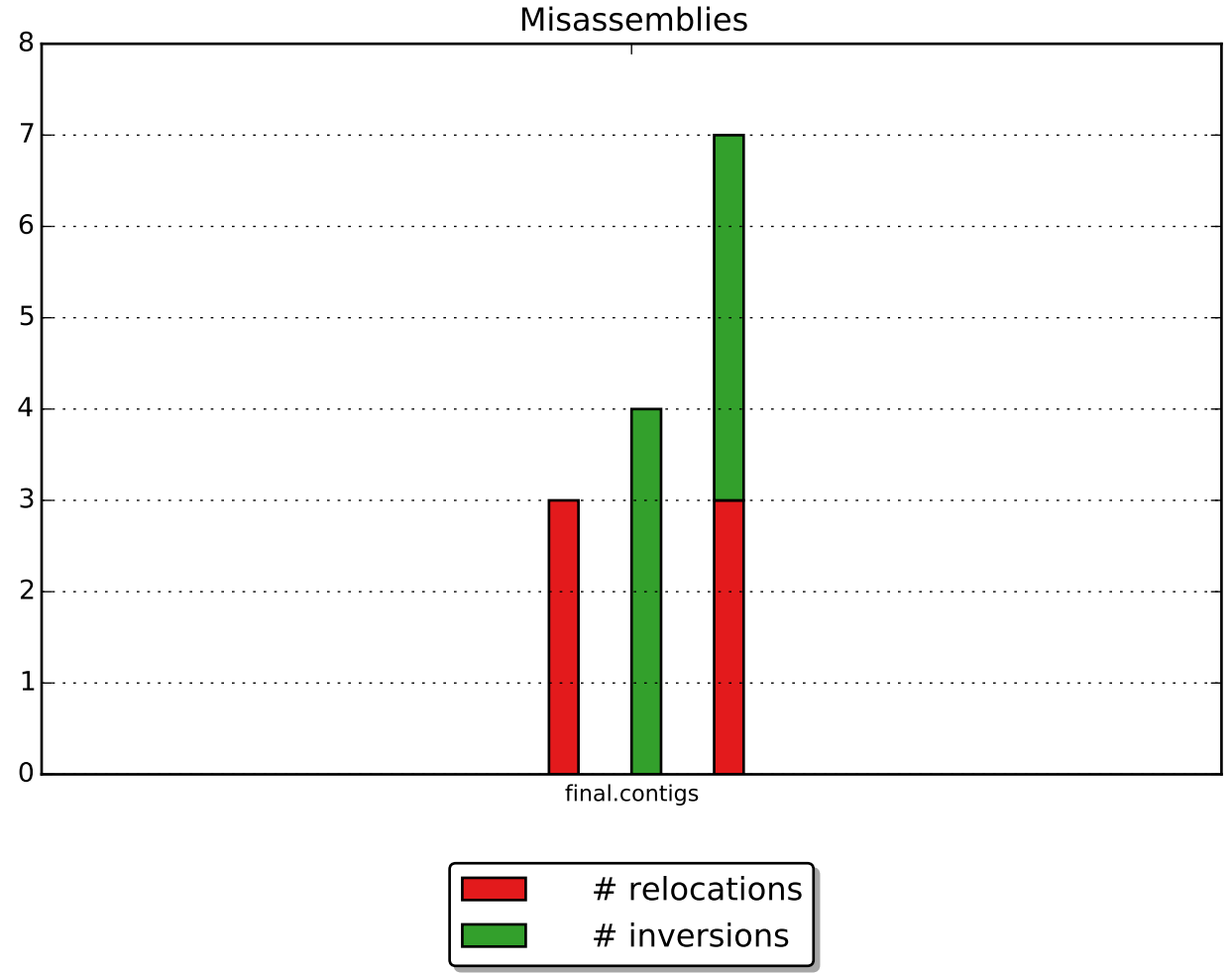
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

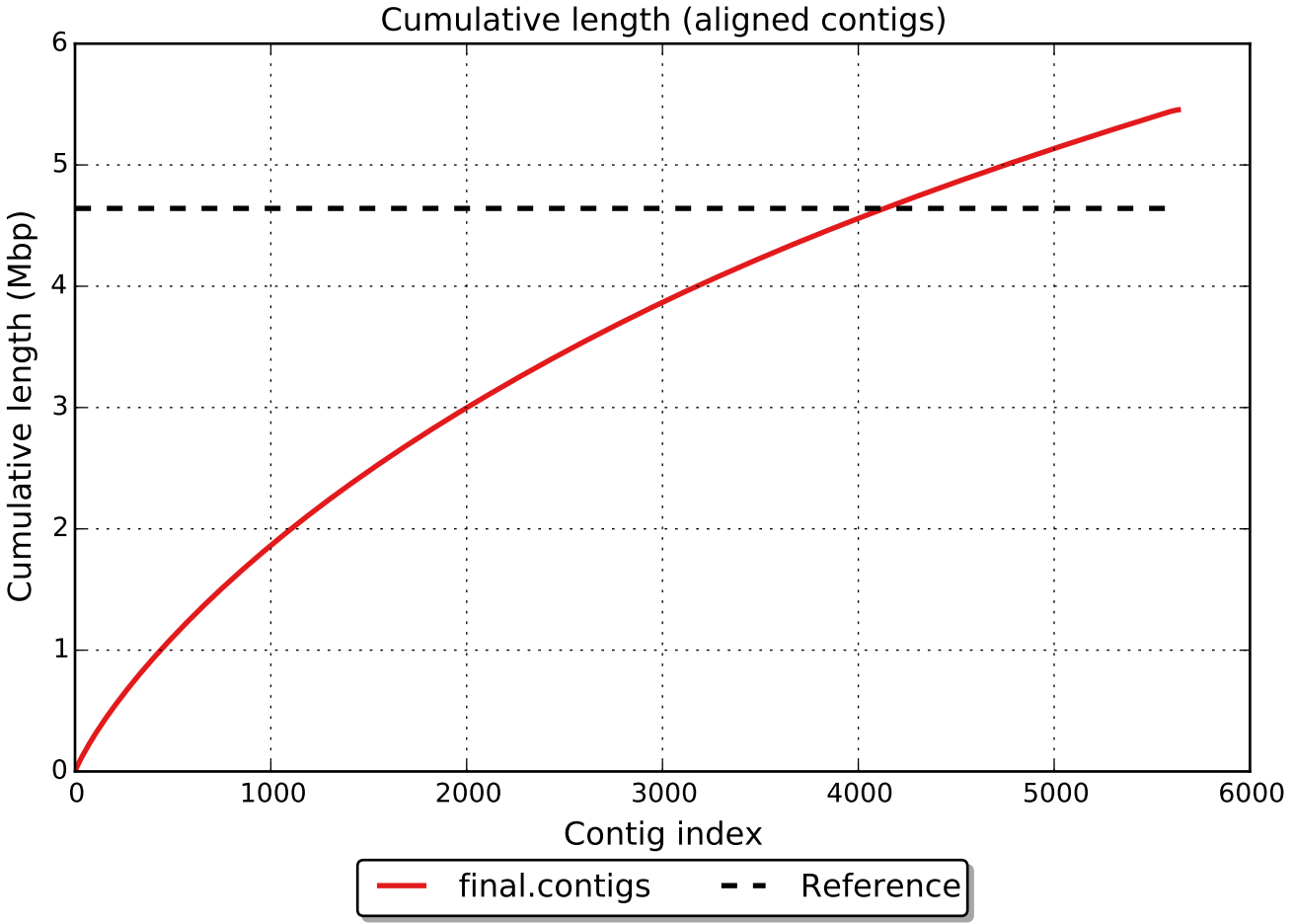

Nx
Contig length (bp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
final.contigs

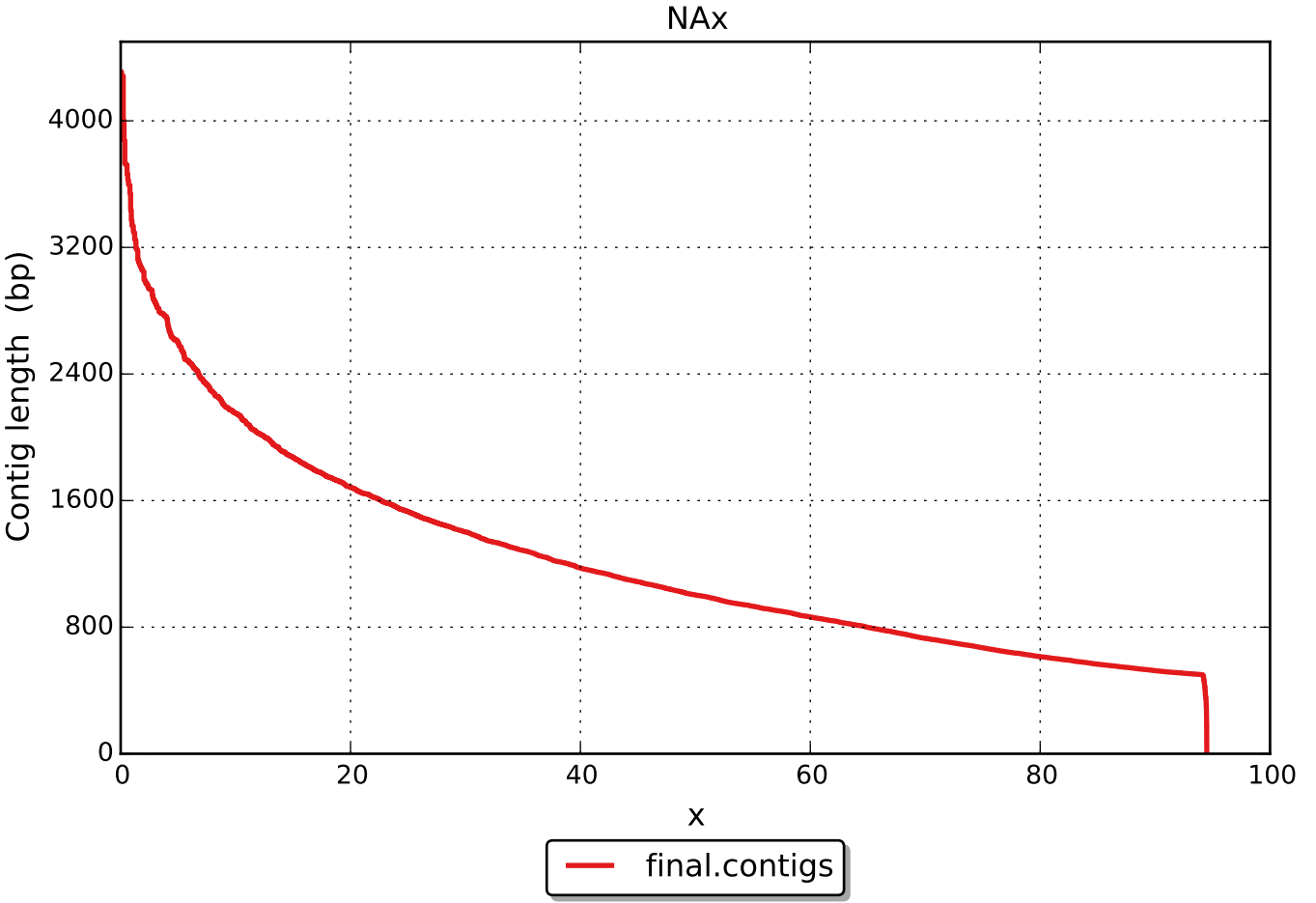

NGx
Contig length (bp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
final.contigs

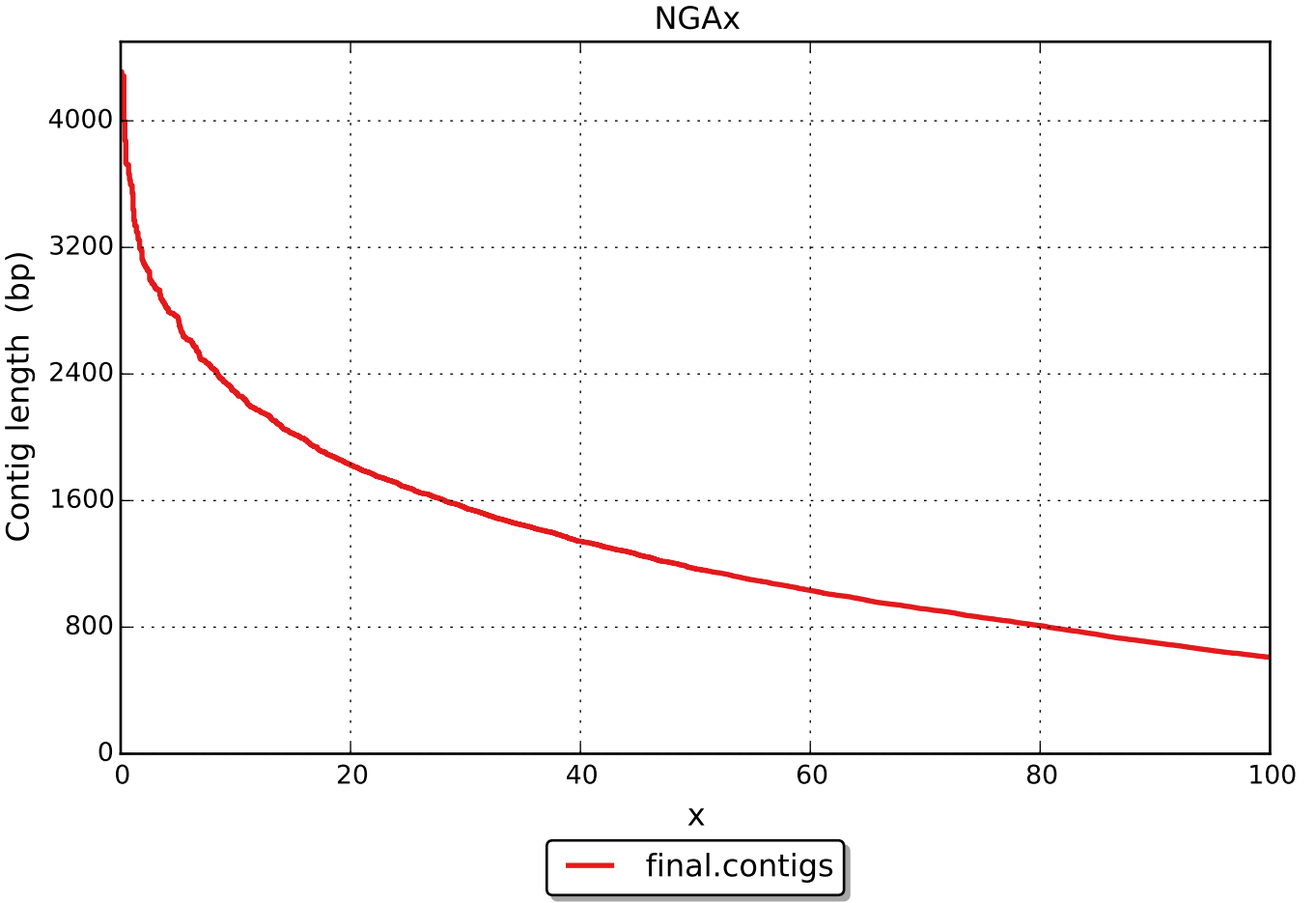

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
2000
4000
6000
Contig index
final.contigs
Reference


GC content
4000
3200
2400
1600
800
0
windows
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)
0
1
2
3
4
5
6
0
1000
2000
3000
4000
5000
6000
Contig index
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