Report

	final.contigs
# contigs (>= 0 bp)	1529
# contigs (>= 1000 bp)	97
# contigs (>= 5000 bp)	71
# contigs (>= 10000 bp)	64
# contigs (>= 25000 bp)	51
# contigs (>= 50000 bp)	30
Total length (>= 0 bp)	5138054
Total length (>= 1000 bp)	4570962
Total length (>= 5000 bp)	4505576
Total length (>= 10000 bp)	4451214
Total length (>= 25000 bp)	4246891
Total length (>= 50000 bp)	3494929
# contigs	280
Largest contig	327154
Total length	4681104
Reference length	4641652
GC (%)	50.76
Reference GC (%)	50.79
N50	97989
NG50	97989
N75	49077
NG75	55030
L50	15
LG50	15
L75	31
LG75	30
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	187197
# local misassemblies	2
# unaligned contigs	7 + 11 part
Unaligned length	5191
Genome fraction (%)	98.767
Duplication ratio	1.020
# N's per 100 kbp	0.00
# mismatches per 100 kbp	22.58
# indels per 100 kbp	0.13
Largest alignment	327154
NA50	95621
NGA50	97989
NA75	47140
NGA75	49077
LA50	16
LGA50	15
LA75	32
LGA75	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).

Misassemblies report

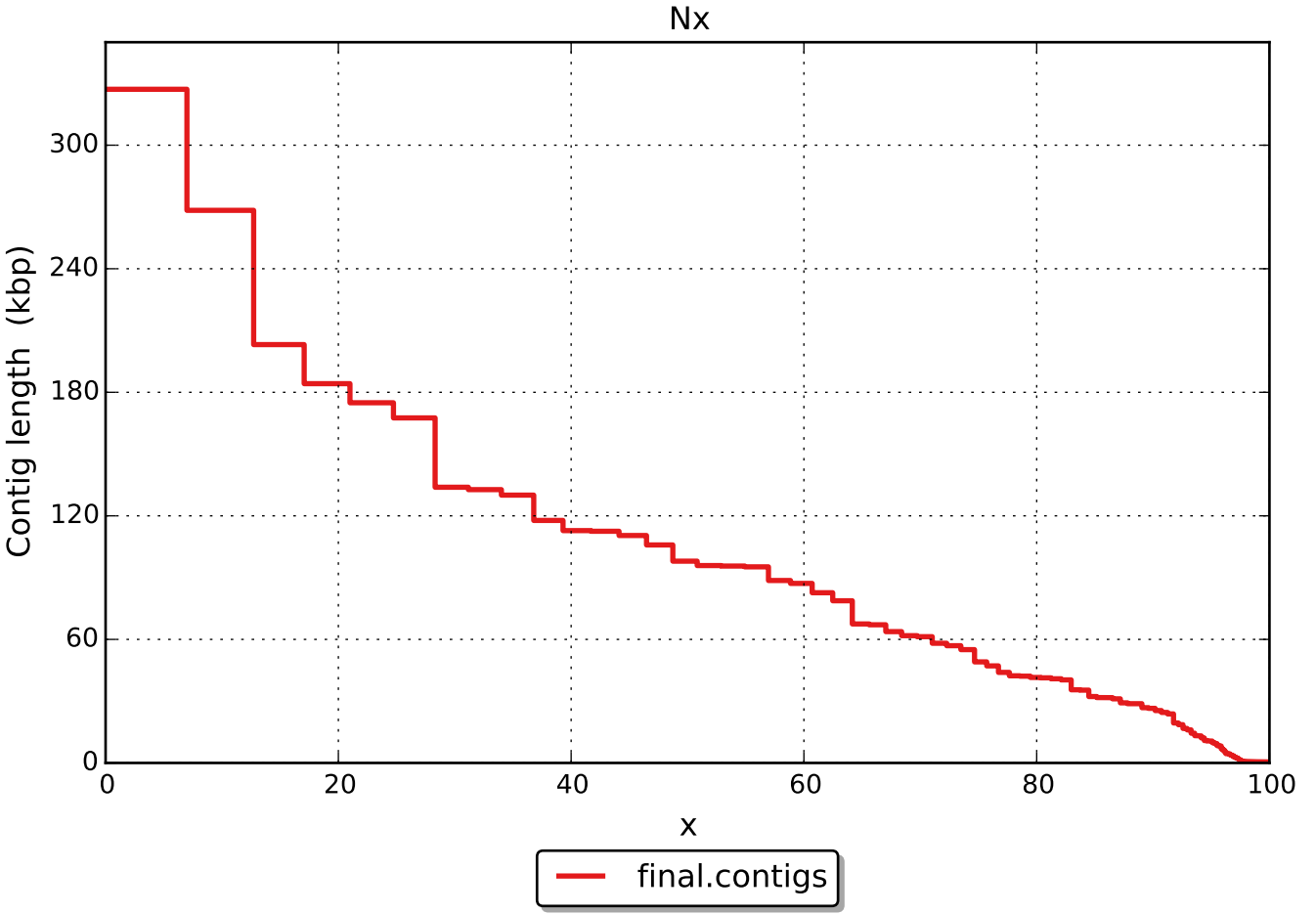
	final.contigs
# misassemblies	3
# relocations	2
# translocations	0
# inversions	1
# misassembled contigs	3
Misassembled contigs length	187197
# local misassemblies	2
# mismatches	1035
# indels	6
# short indels	5
# long indels	1
Indels length	86

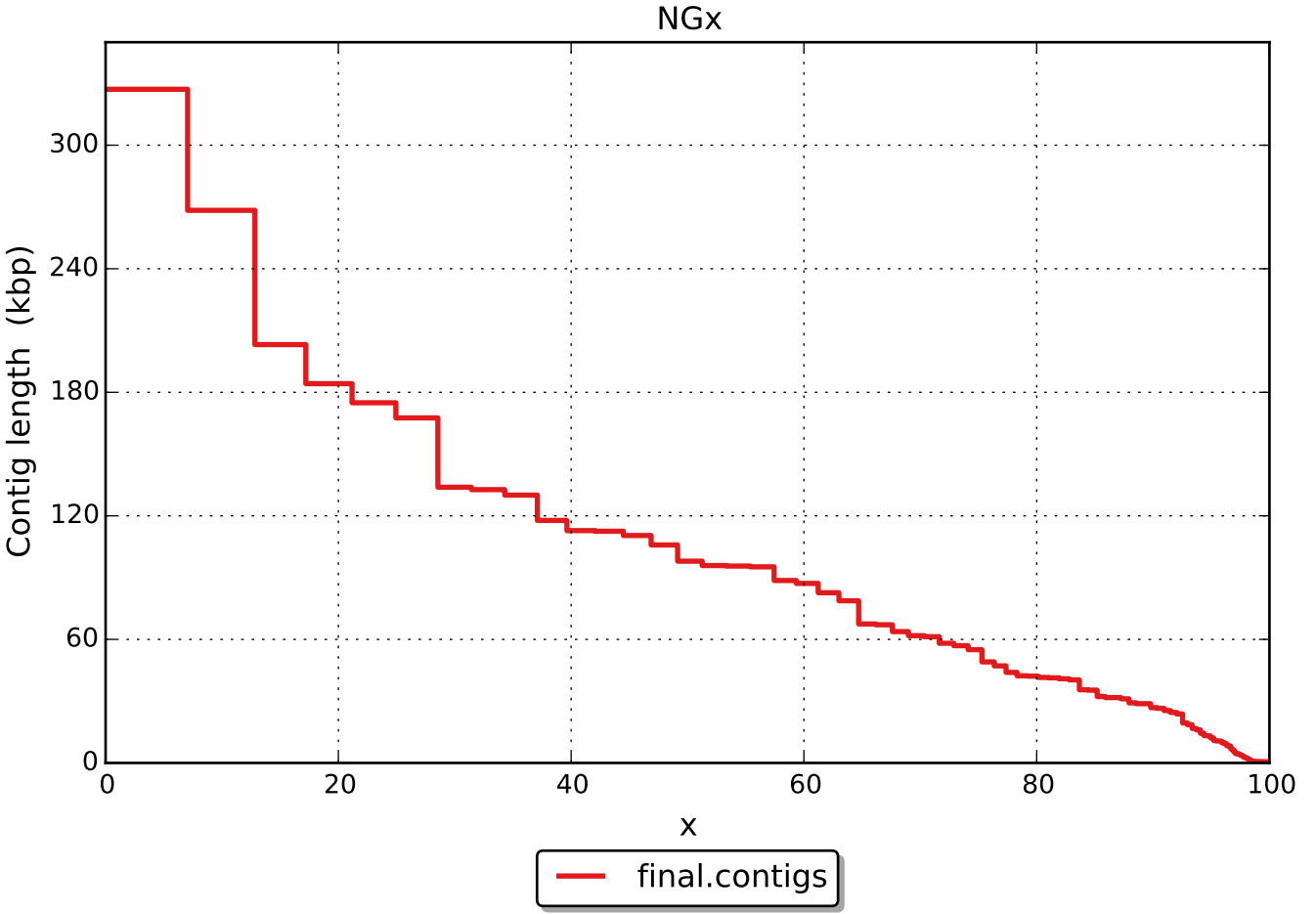
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

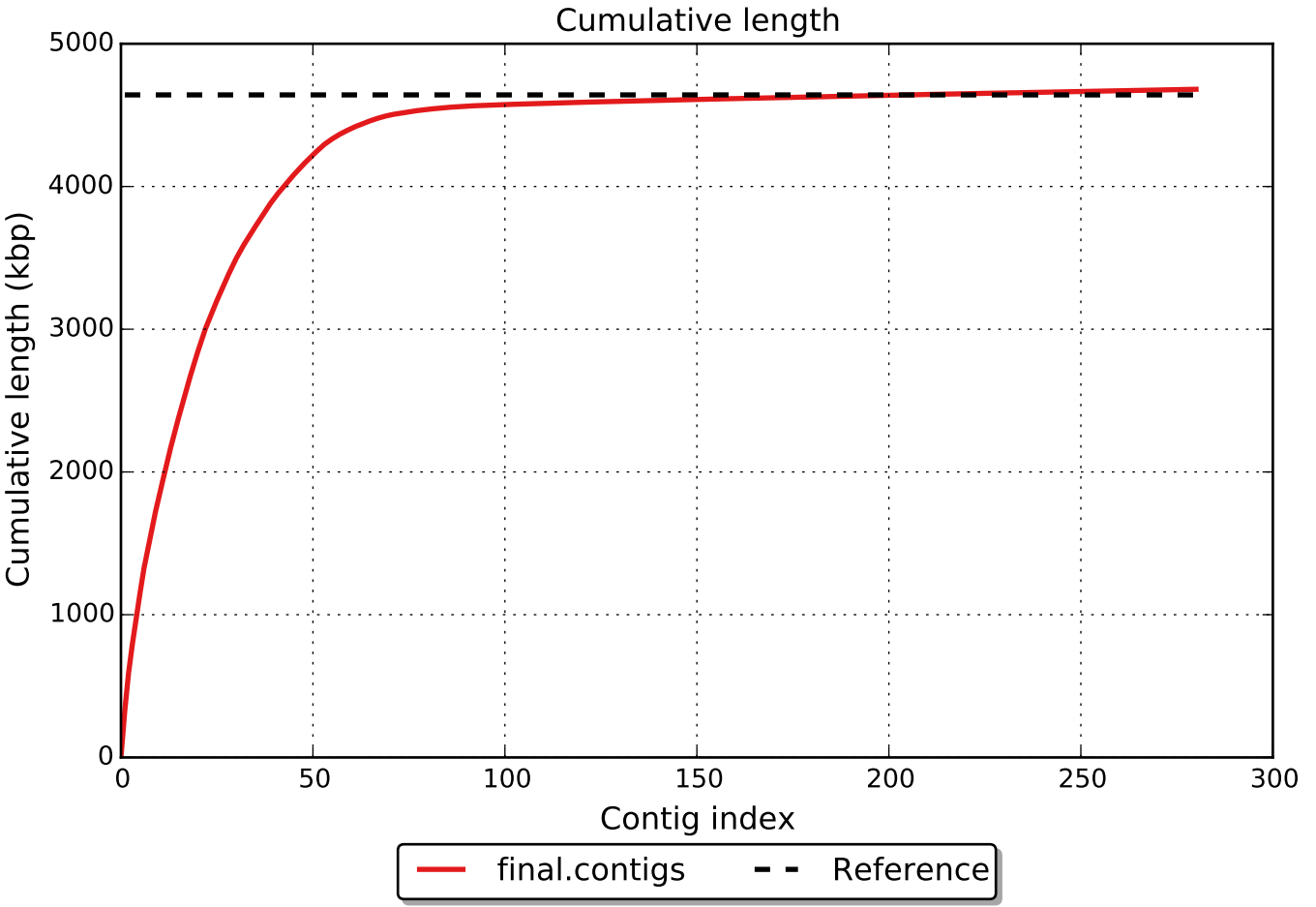
Unaligned report

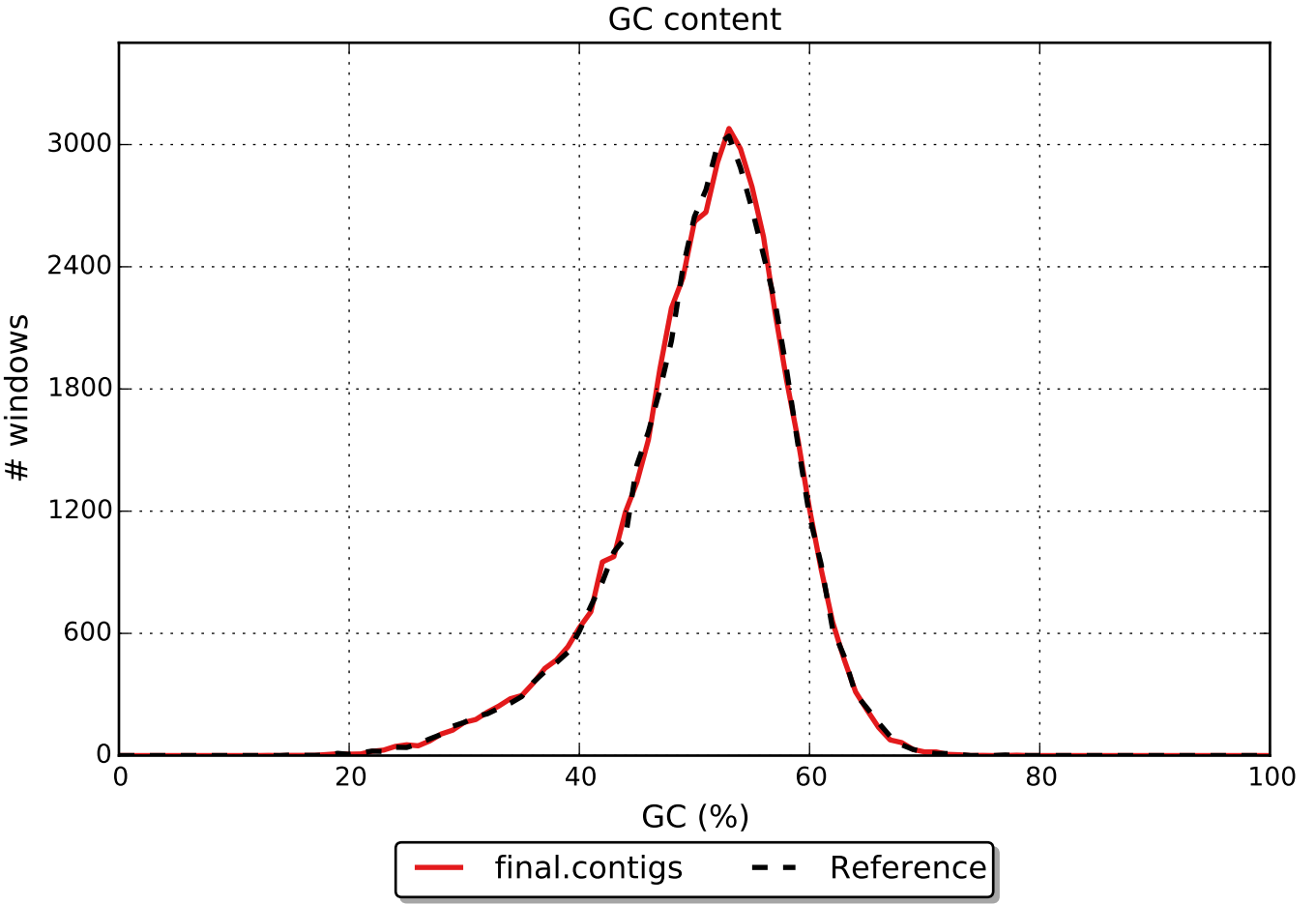
	final.contigs
# fully unaligned contigs	7
Fully unaligned length	3862
# partially unaligned contigs	11
# with misassembly	0
# both parts are significant	0
Partially unaligned length	1329
# N's	0

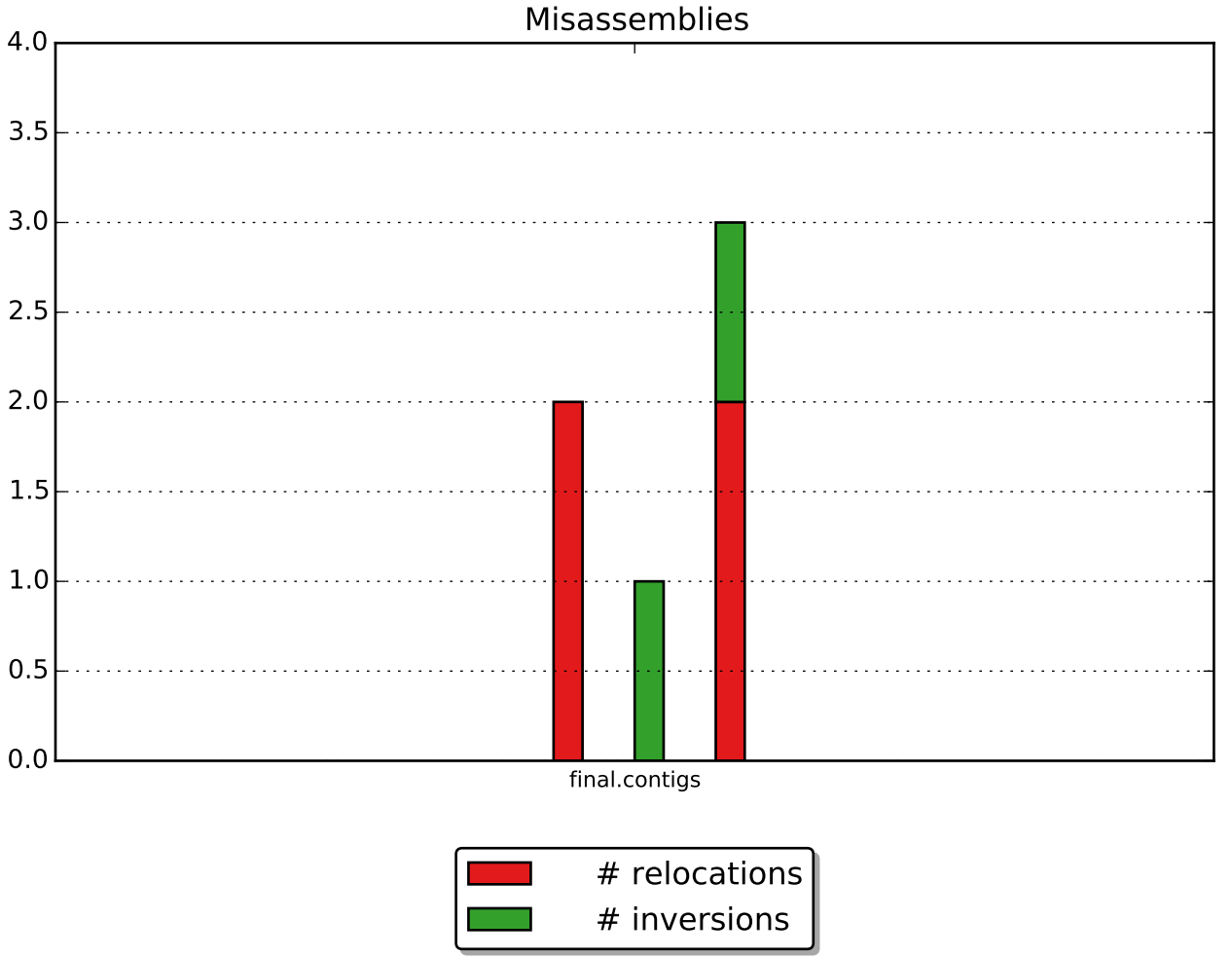
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

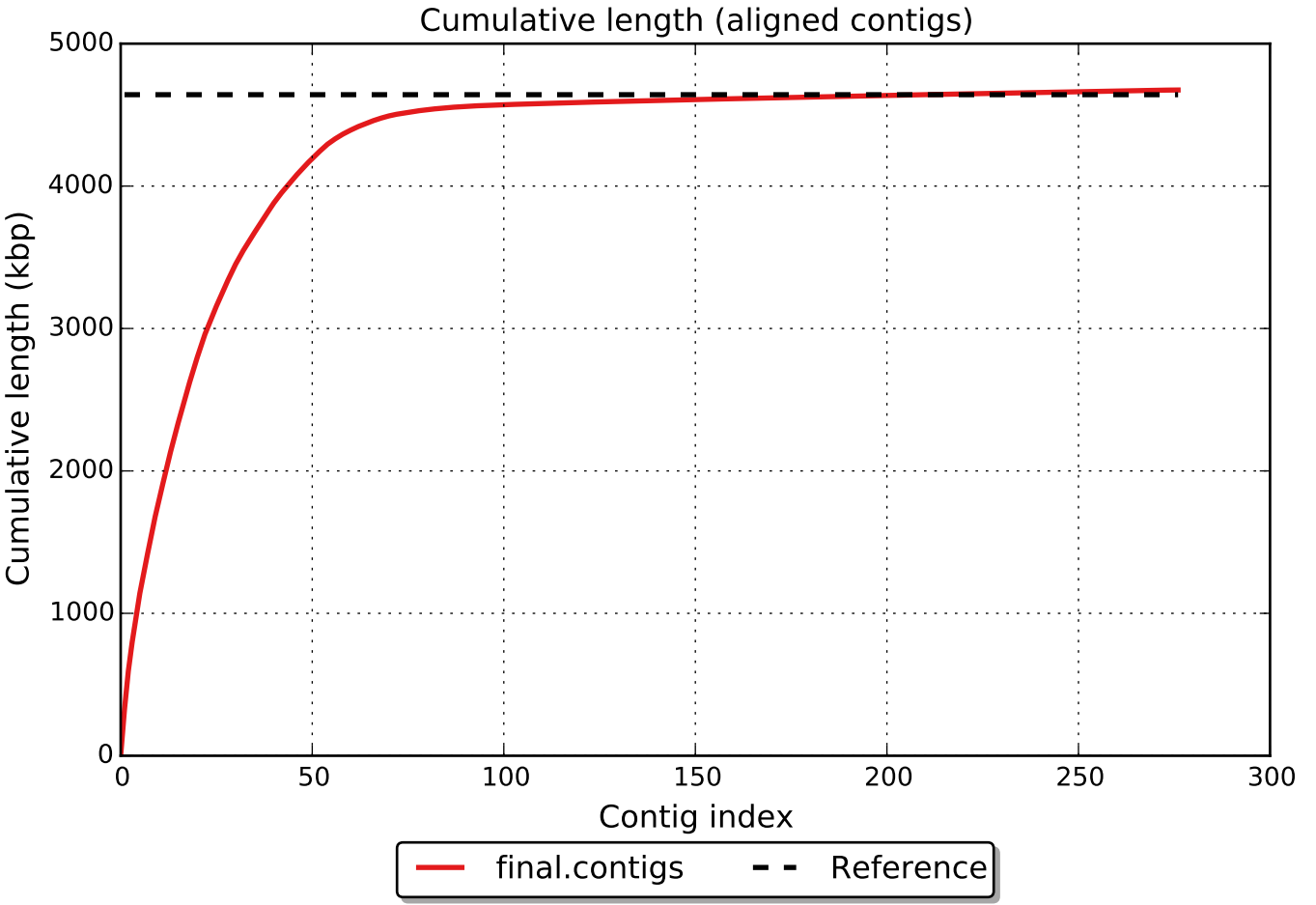

Nx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
final.contigs

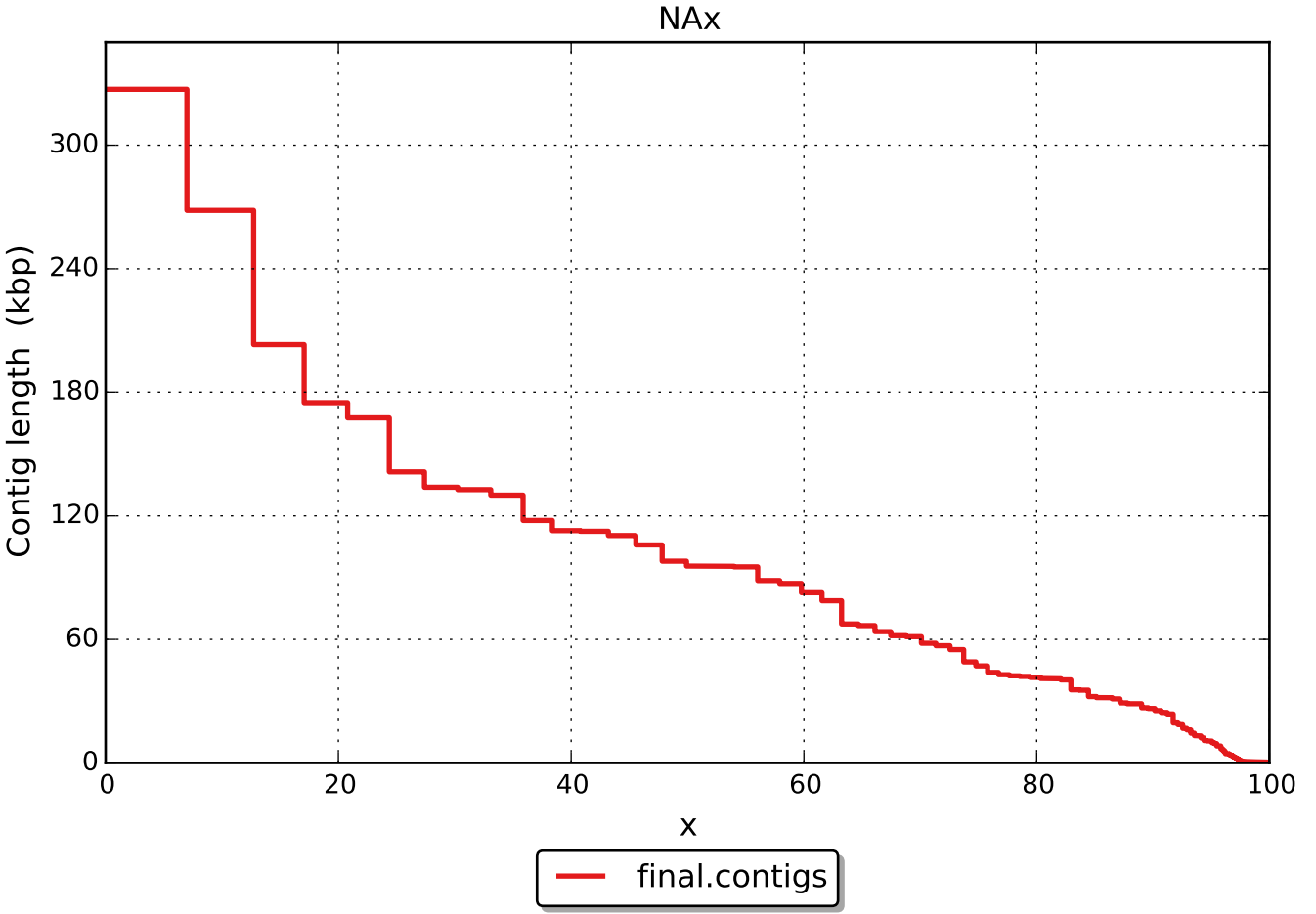

NGx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
final.contigs

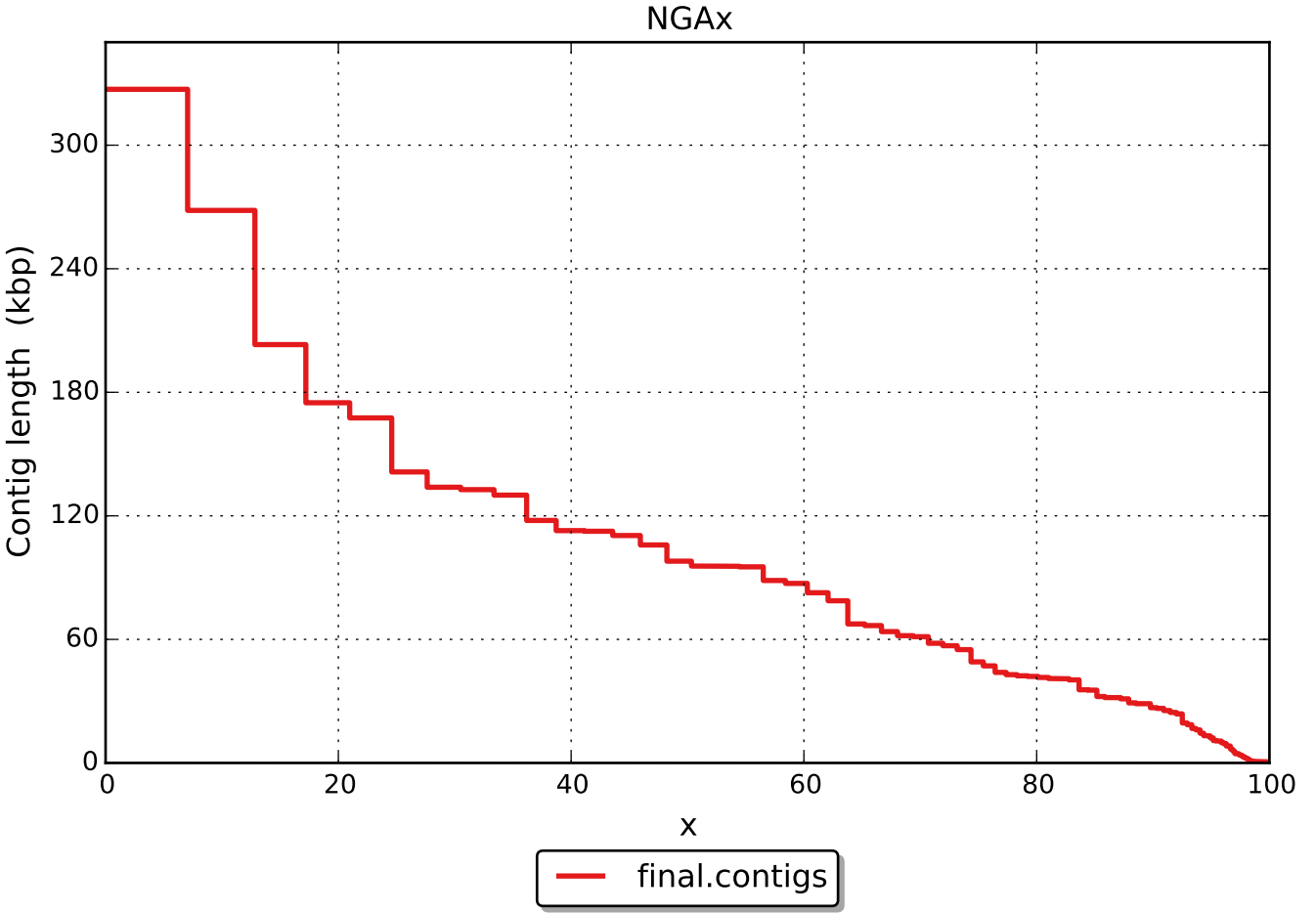

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
50
100
150
200
250
300
Contig index
final.contigs
Reference


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


Misassemblies
4.0
3.5
3.0
2.5
2.0
1.5
1.0
0.5
0.0
final.contigs
relocations
inversions


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
50
100
150
200
250
300
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
300
240
180
120
60
0
0
20
40
60
80
100
x
final.contigs