Report

	final.contigs
# contigs (>= 0 bp)	1060
# contigs (>= 1000 bp)	879
Total length (>= 0 bp)	3729979
Total length (>= 1000 bp)	3595334
# contigs	1060
Largest contig	21305
Total length	3729979
Reference length	1892775
GC (%)	32.25
Reference GC (%)	32.25
N50	5431
NG50	8985
N75	3048
NG75	7136
L50	213
LG50	81
L75	442
LG75	142
# misassemblies	20
# misassembled contigs	20
Misassembled contigs length	65990
# local misassemblies	0
# unaligned contigs	186 + 88 part
Unaligned length	1188354
Genome fraction (%)	99.499
Duplication ratio	1.350
# N's per 100 kbp	0.00
# mismatches per 100 kbp	663.04
# indels per 100 kbp	0.42
Largest alignment	21305
NA50	2443
NGA50	6402
NGA75	4003
LA50	330
LGA50	101
LGA75	194

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

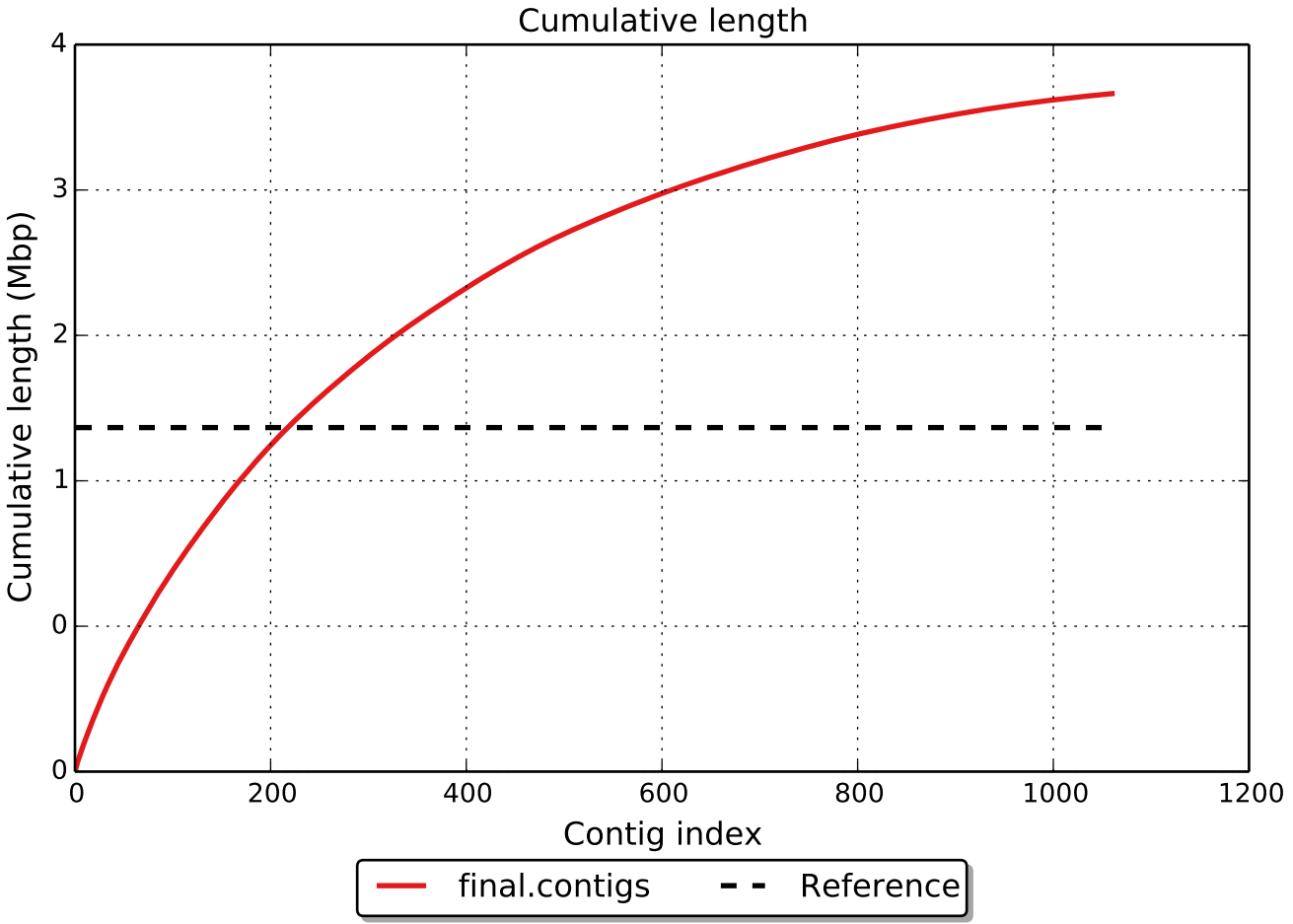
	final.contigs
# misassemblies	20
# relocations	18
# translocations	0
# inversions	2
# possibly misassembled contigs	45
# misassembled contigs	20
Misassembled contigs length	65990
# local misassemblies	0
# mismatches	12487
# indels	8
# short indels	7
# long indels	1
Indels length	31

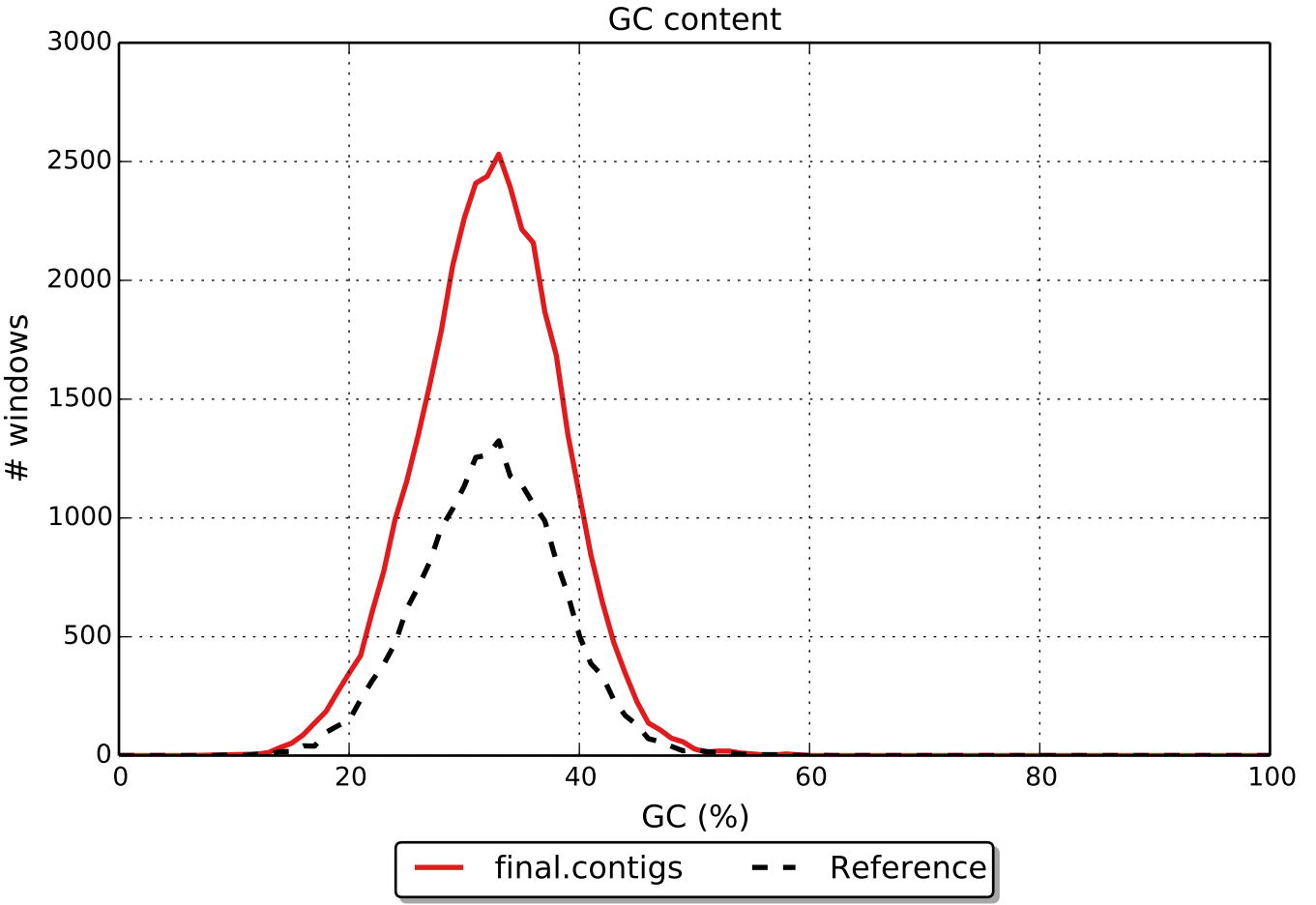
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

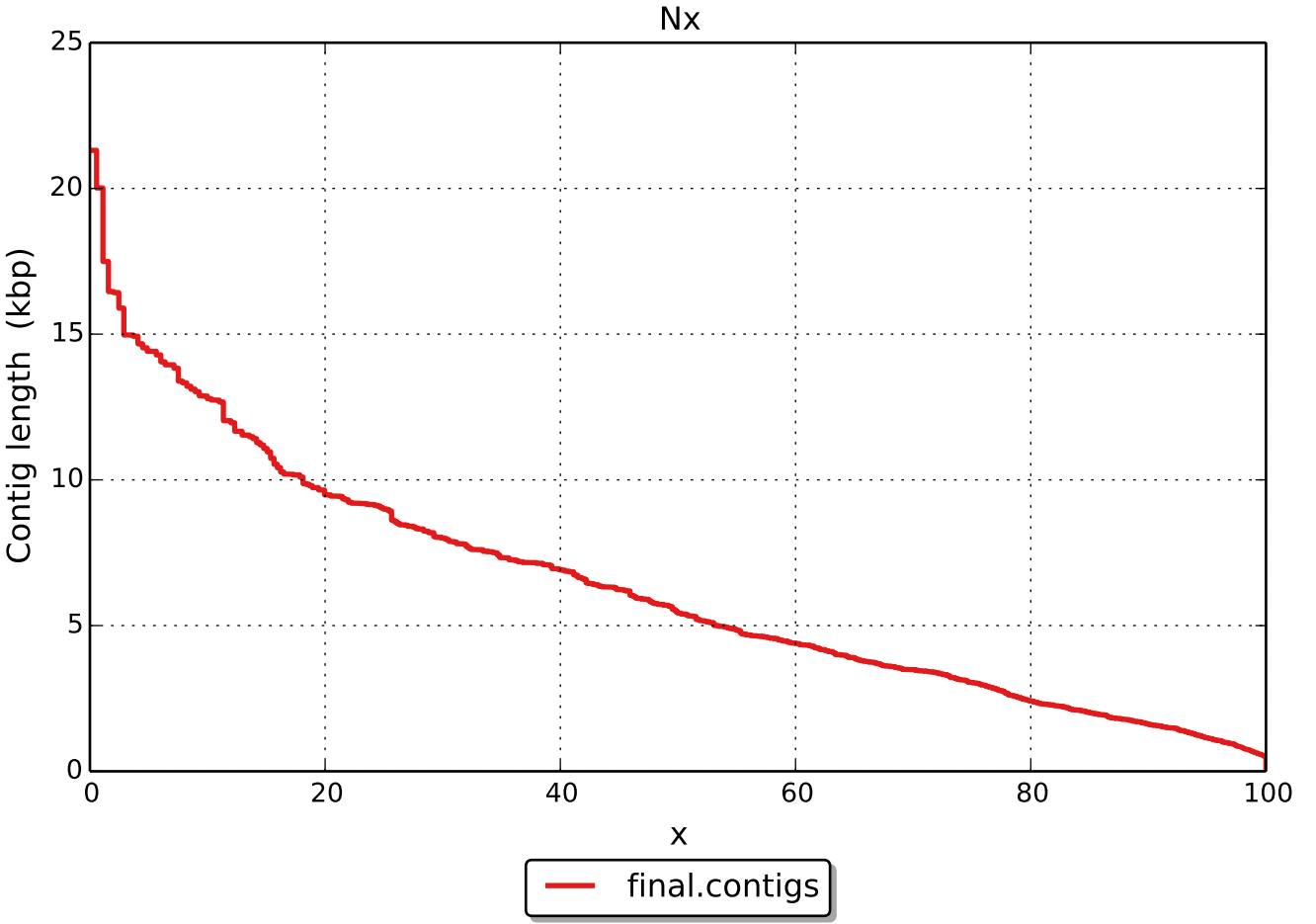
Unaligned report

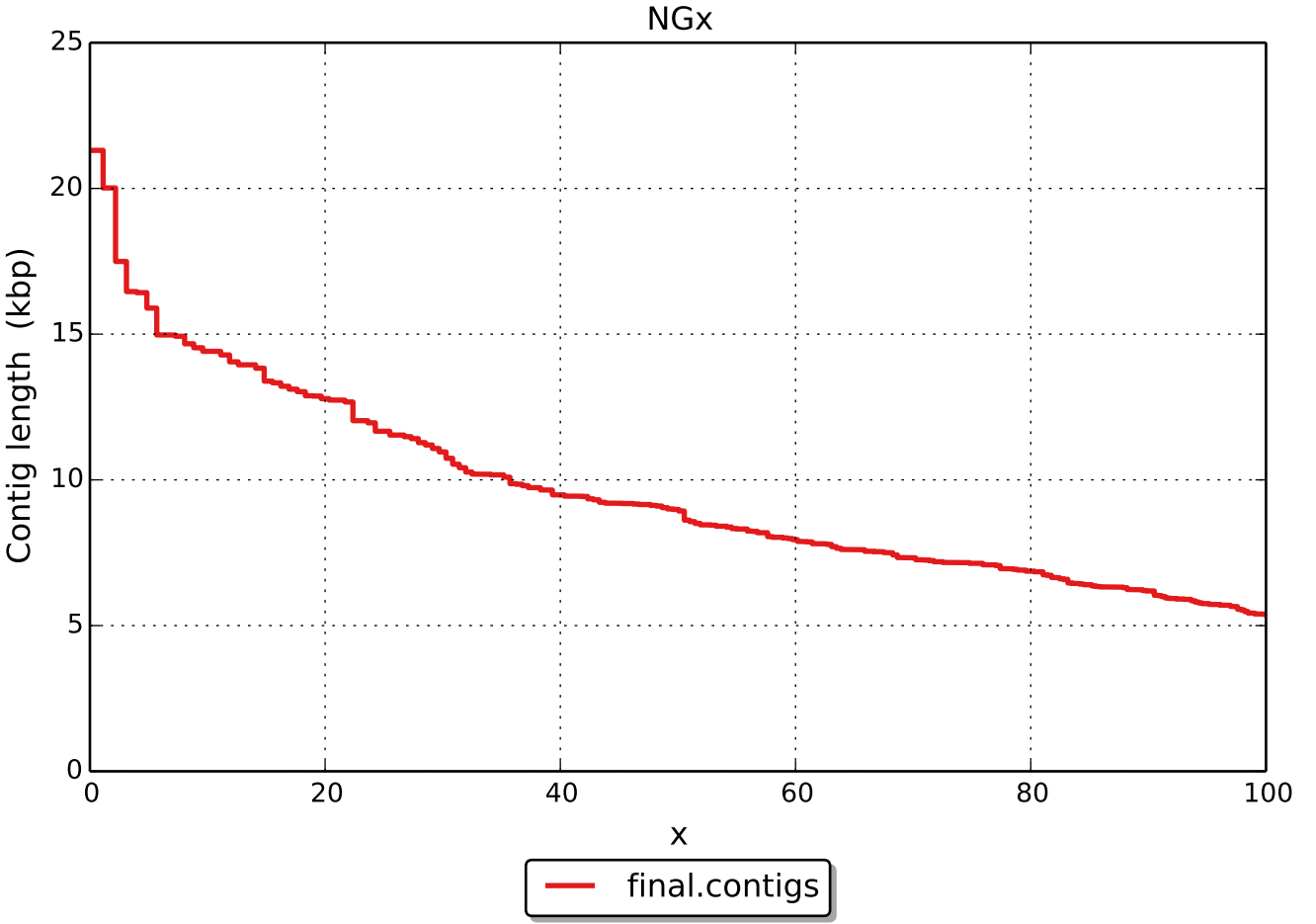
	final.contigs
# fully unaligned contigs	186
Fully unaligned length	853997
# partially unaligned contigs	88
# with misassembly	6
# both parts are significant	41
Partially unaligned length	334357
# N's	0

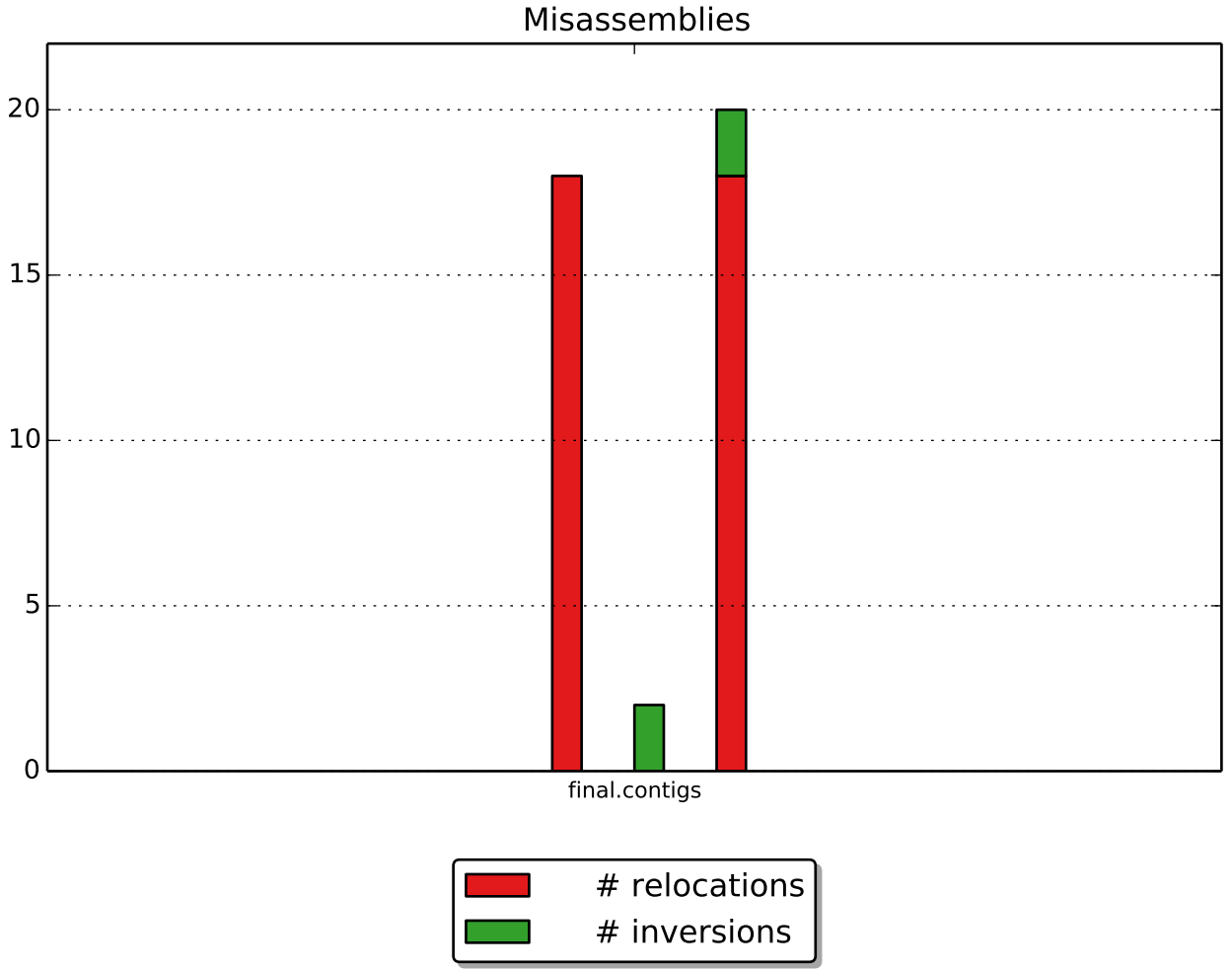
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

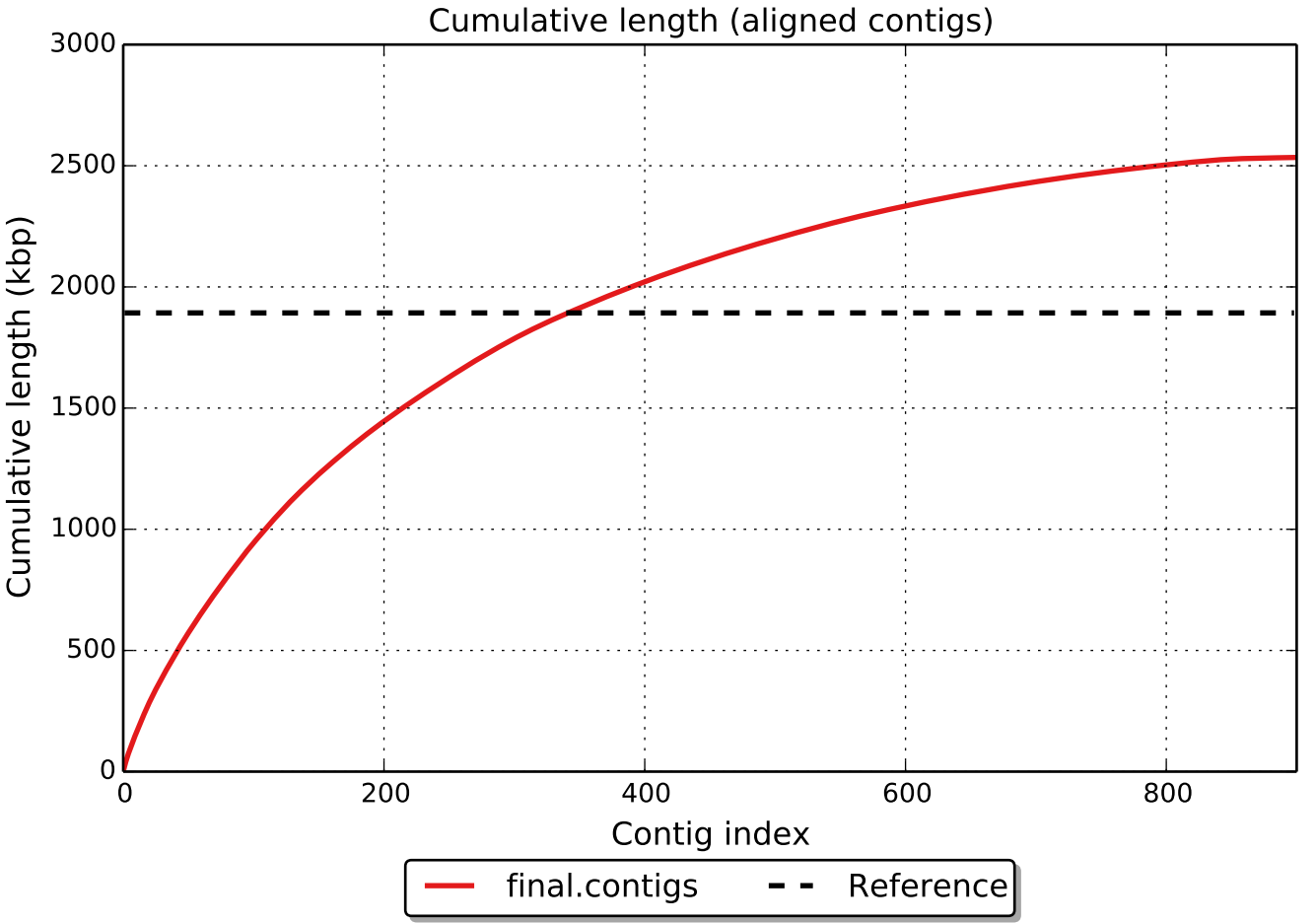

Cumulative length
Cumulative length (Mbp)
4
3
2
1
0
0
0
200
400
600
800
1000
1200
Contig index
final.contigs
Reference

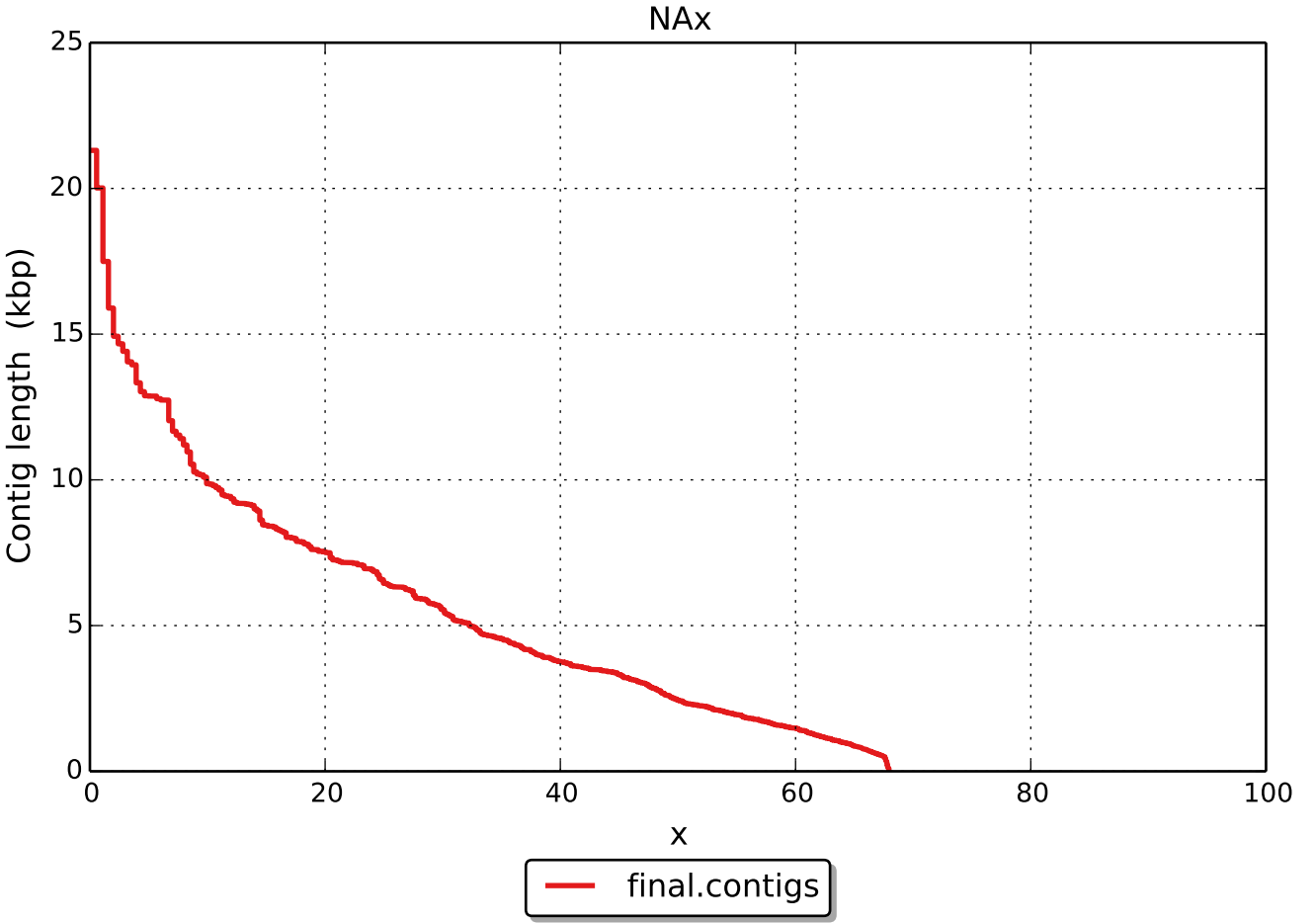

GC content
3000
2500
2000
1500
1000
500
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

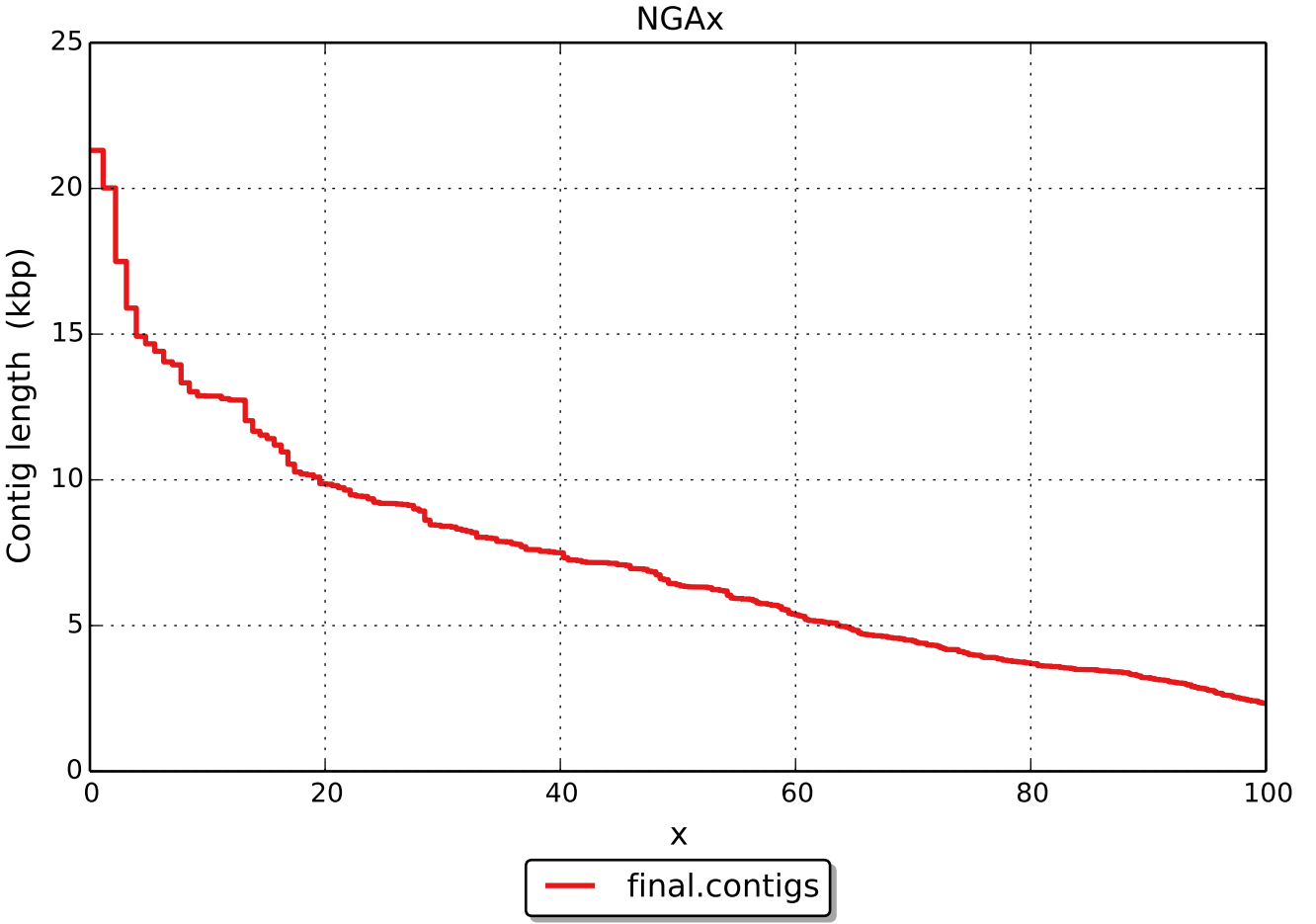

Nx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
final.contigs


Misassemblies
20
15
10
5
0
final.contigs
relocations
inversions


Cumulative length (aligned contigs)
Cumulative length (kbp)
3000
2500
2000
1500
1000
500
0
0
200
400
600
800
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
25
20
15
10
5
0
0
20
40
60
80
100
x
final.contigs