Report

	final.contigs
# contigs (>= 1000 bp)	1419
# contigs (>= 5000 bp)	255
# contigs (>= 10000 bp)	27
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4705967
Total length (>= 5000 bp)	1856419
Total length (>= 10000 bp)	344528
Total length (>= 25000 bp)	31965
Total length (>= 50000 bp)	0
# contigs	1732
Largest contig	31965
Total length	4938167
Reference length	4857432
GC (%)	52.23
Reference GC (%)	52.23
N50	3970
NG50	4024
N75	2327
NG75	2414
L50	393
LG50	383
L75	794
LG75	768
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	9233
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.923
Duplication ratio	1.028
# N's per 100 kbp	0.00
# mismatches per 100 kbp	8.89
# indels per 100 kbp	0.04
Largest alignment	31965
NA50	3964
NGA50	4024
NA75	2326
NGA75	2411
LA50	394
LGA50	383
LA75	795
LGA75	769

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

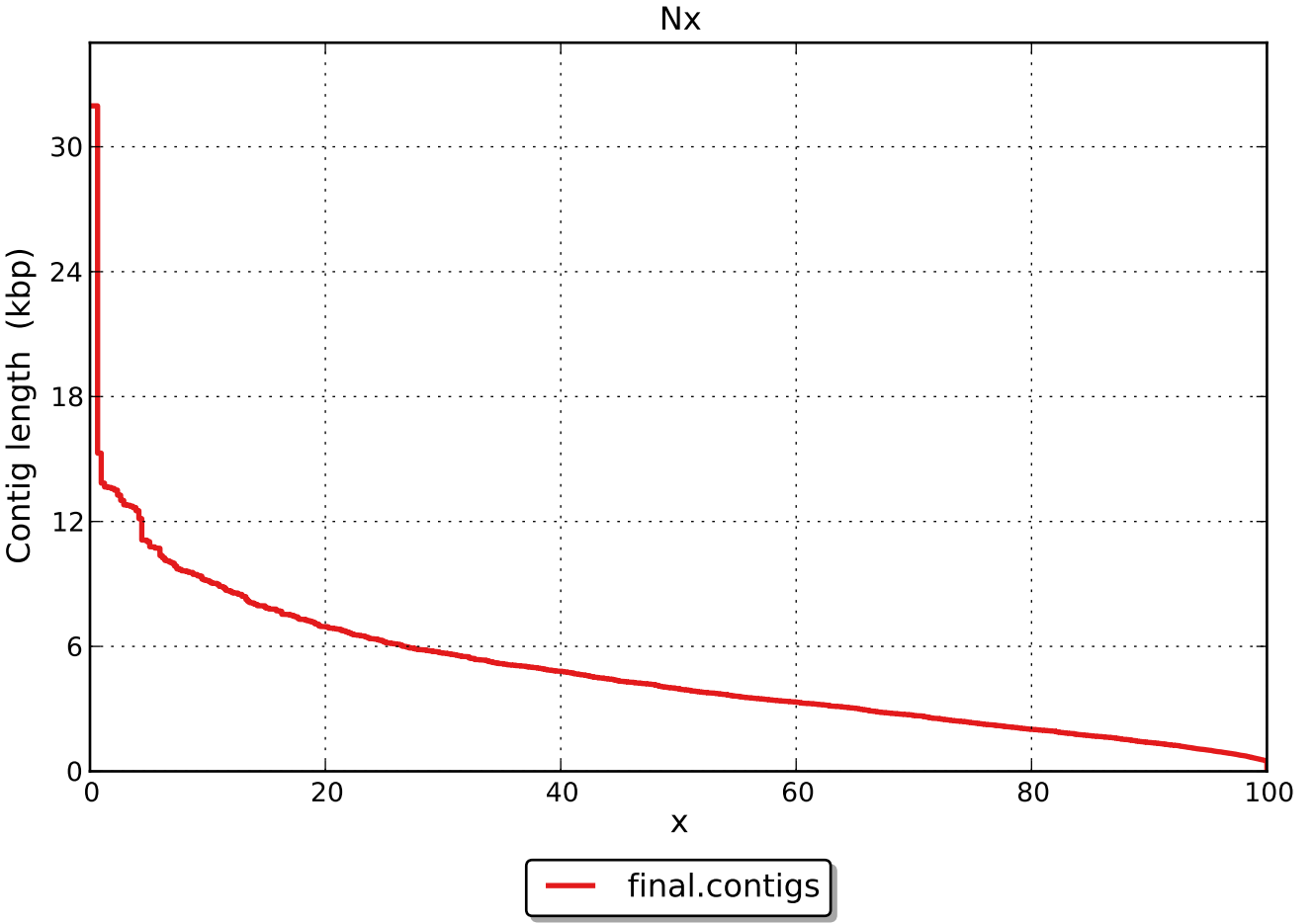
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	9233
# local misassemblies	0
# mismatches	427
# indels	2
# short indels	2
# long indels	0
Indels length	2

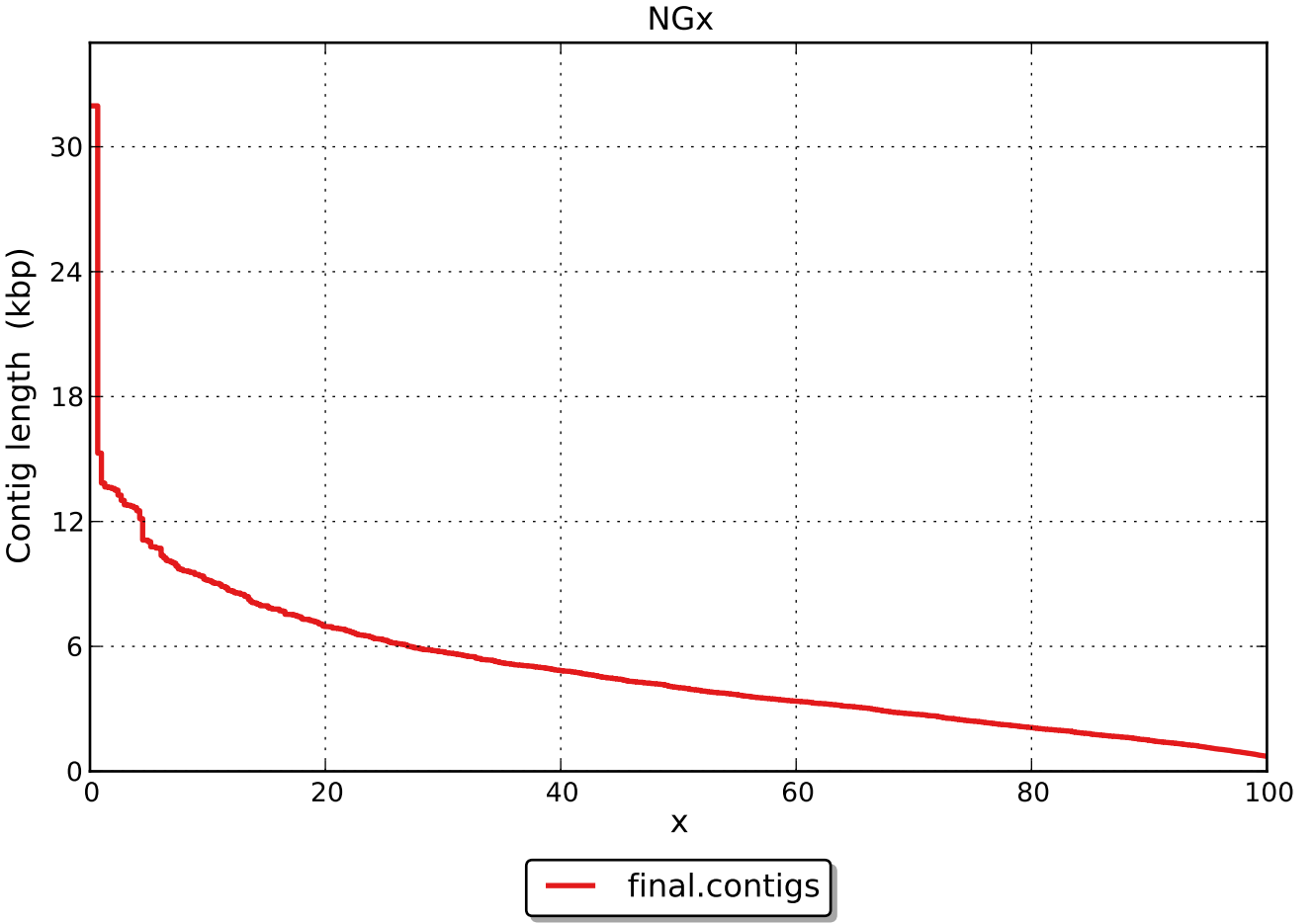
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

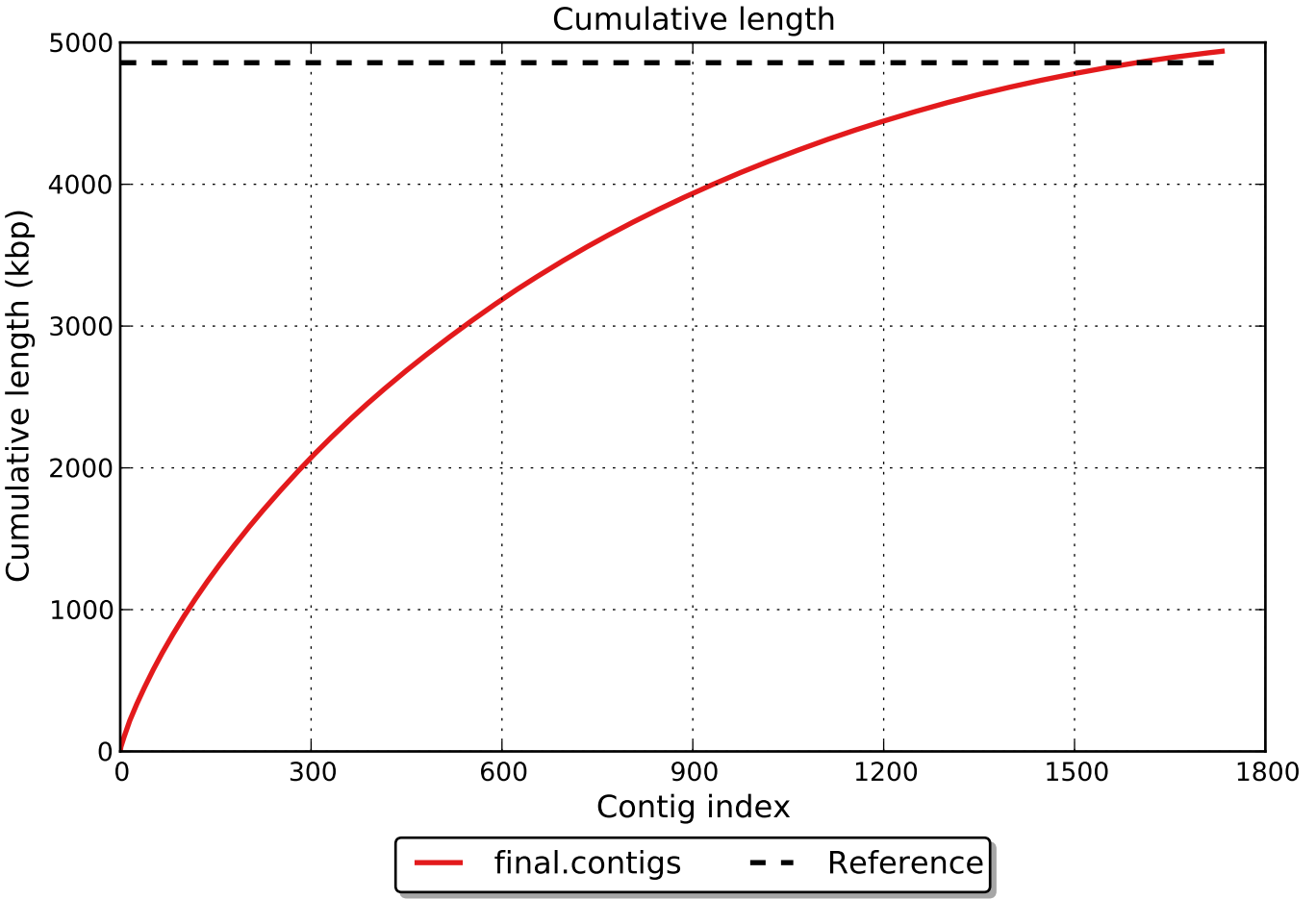
Unaligned report

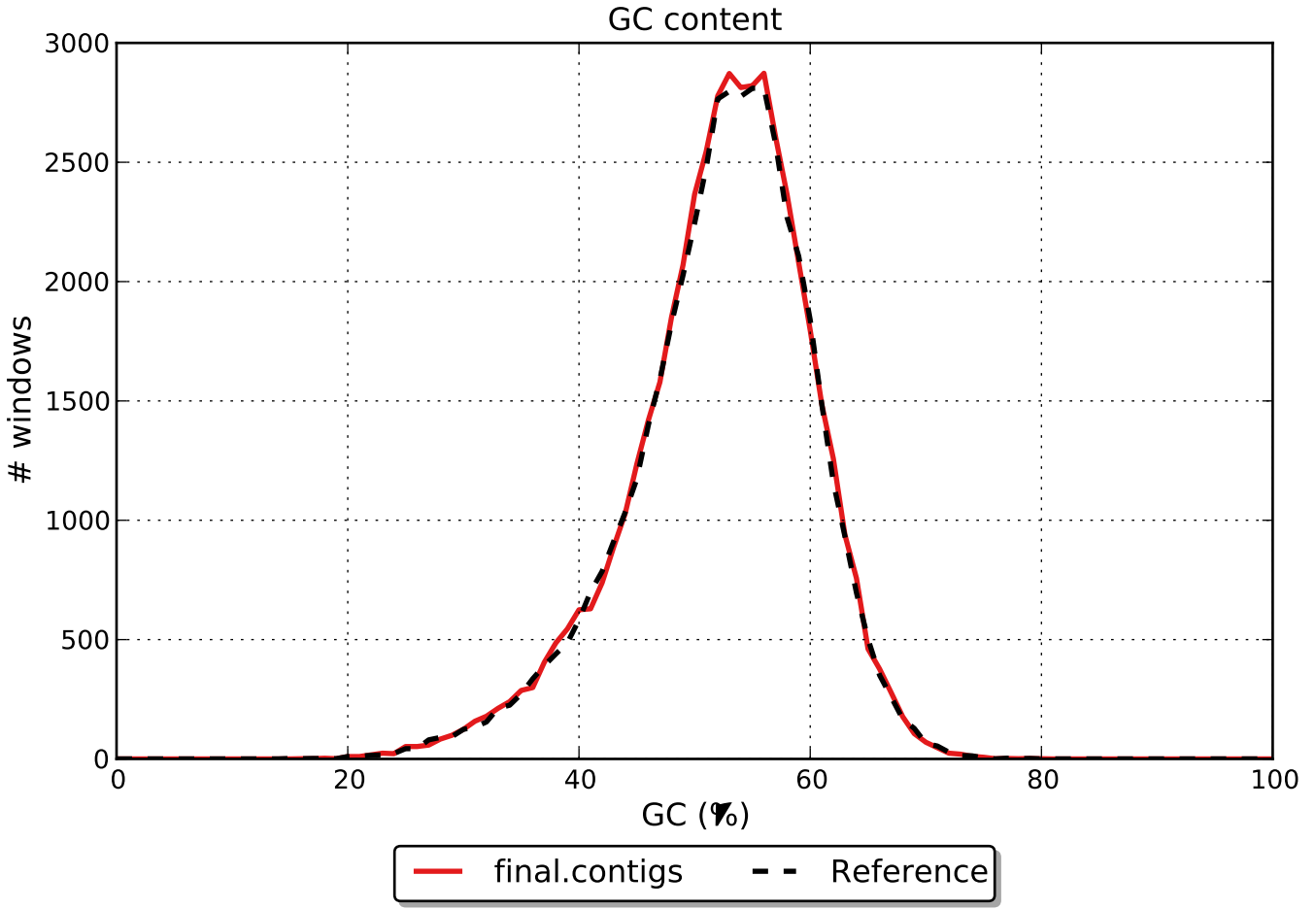
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

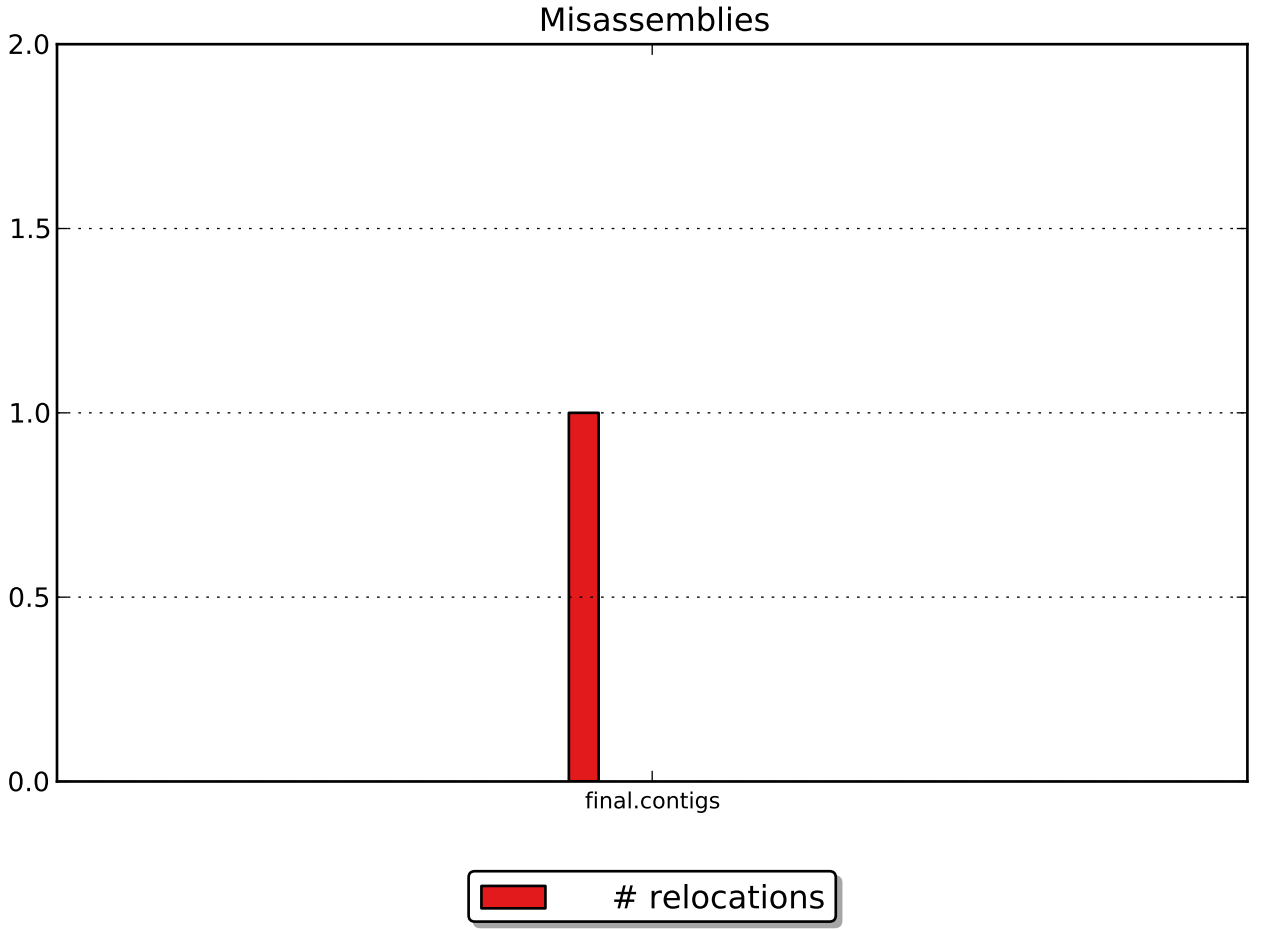
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

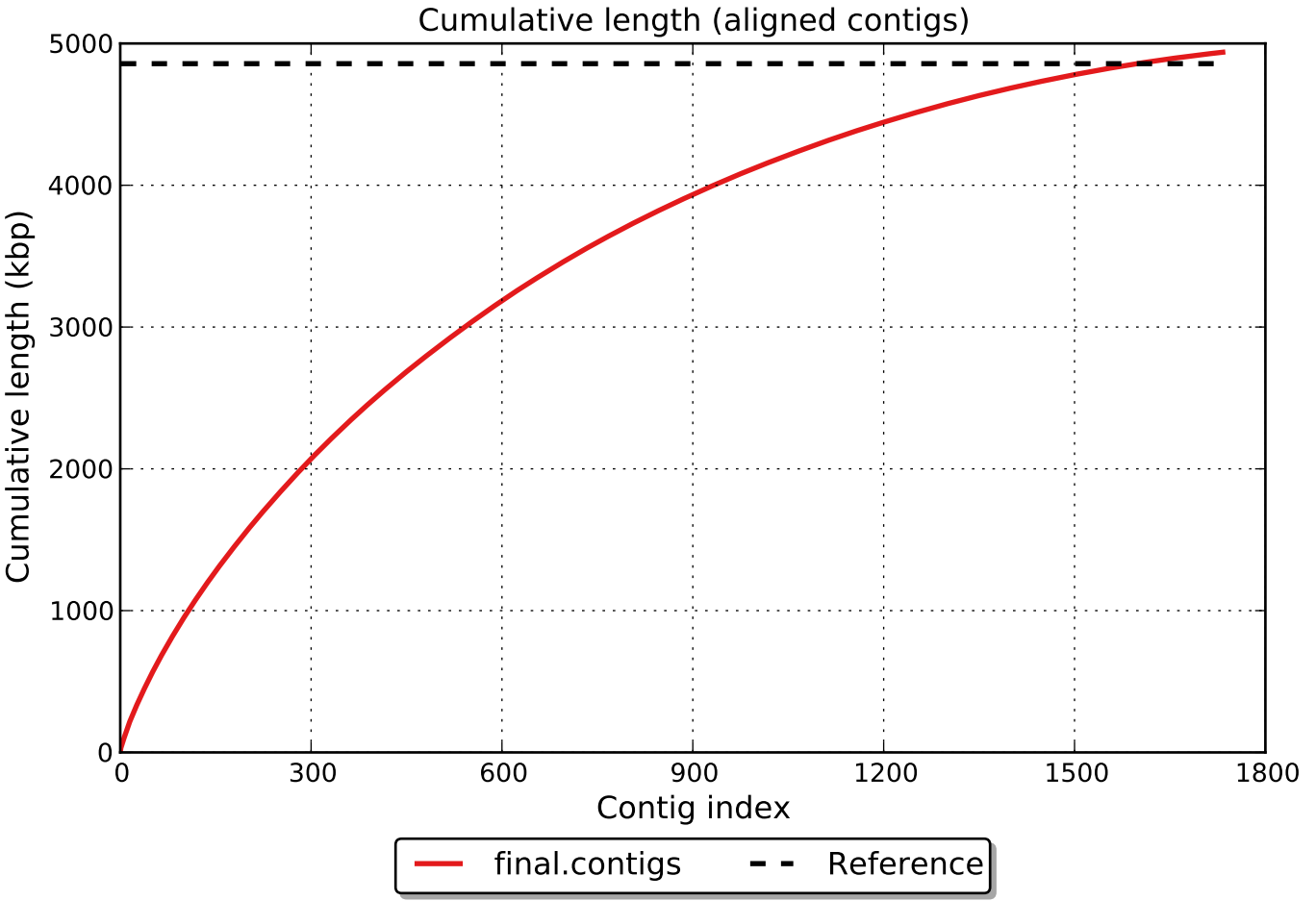

Nx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
final.contigs

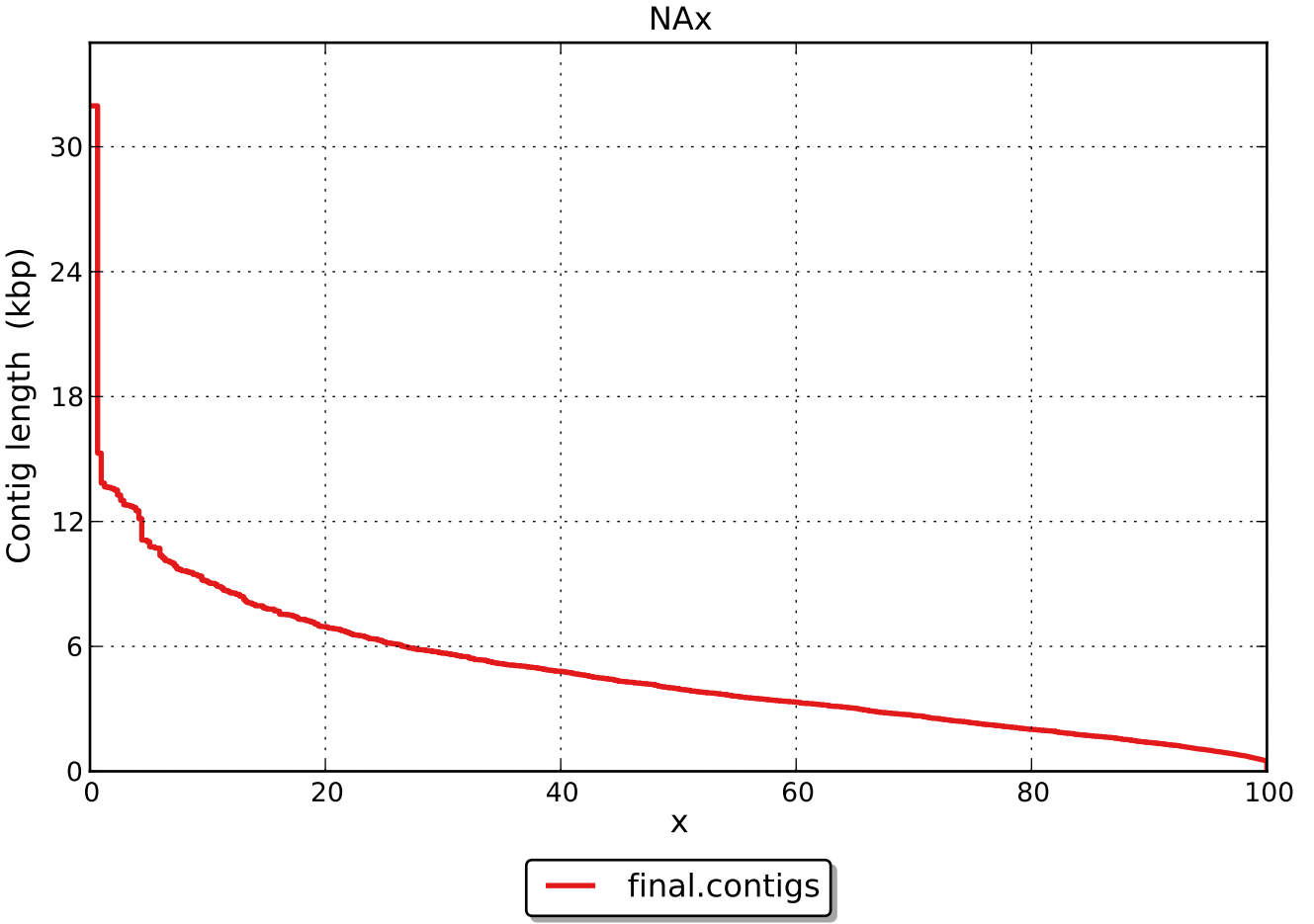

NGx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
final.contigs

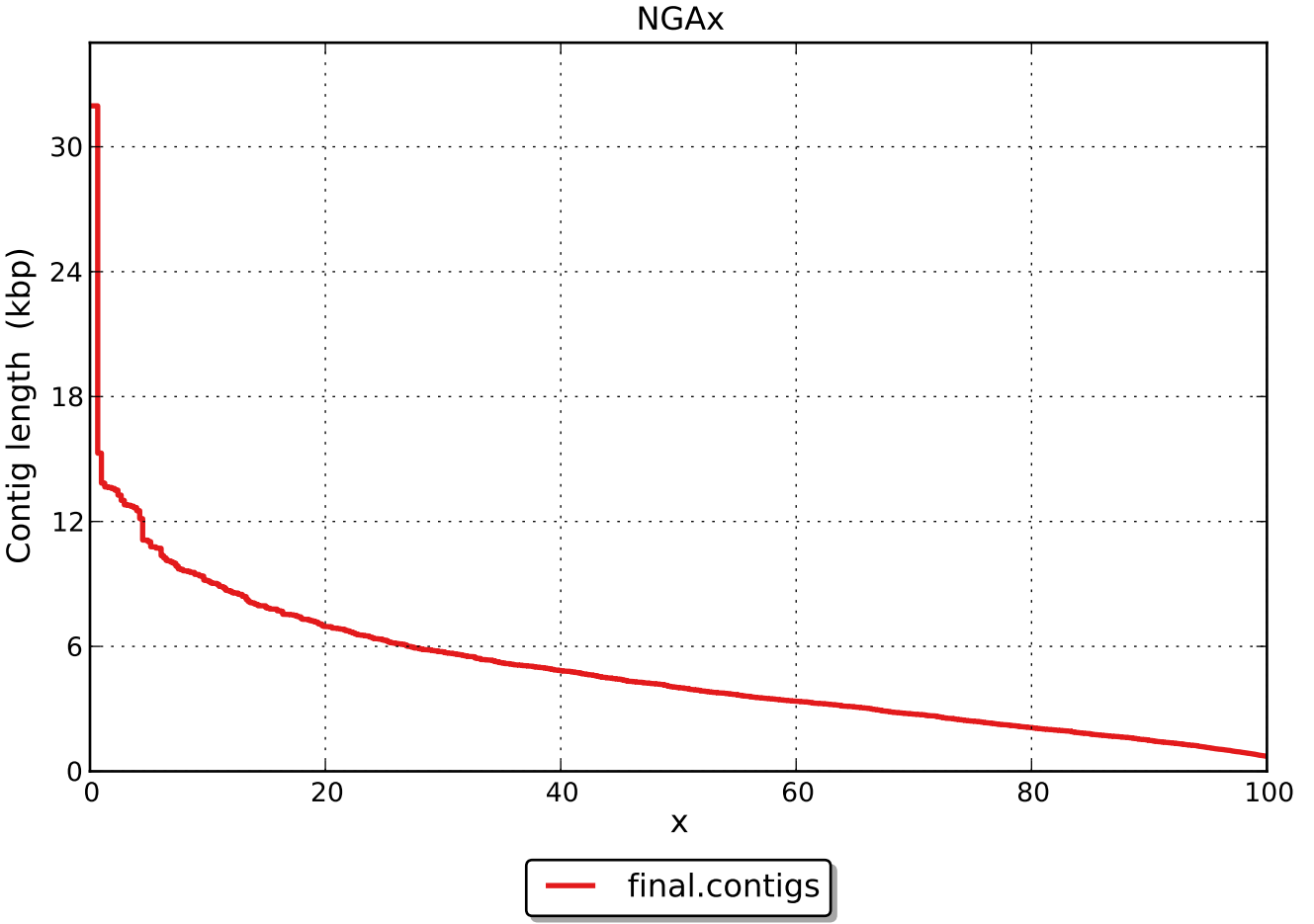

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
300
600
900
1200
1500
1800
Contig index
final.contigs
Reference


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


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
300
600
900
1200
1500
1800
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
30
24
18
12
6
0
0
20
40
60
80
100
x
final.contigs