Report

	final.contigs
# contigs (>= 1000 bp)	1853
# contigs (>= 5000 bp)	15
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	3366426
Total length (>= 5000 bp)	90452
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3446
Largest contig	8764
Total length	4525590
Reference length	4641652
GC (%)	50.78
Reference GC (%)	50.78
N50	1531
NG50	1494
N75	986
NG75	949
L50	965
LG50	1004
L75	1881
LG75	1971
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	3248
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	92.658
Duplication ratio	1.052
# N's per 100 kbp	0.00
# mismatches per 100 kbp	84.45
# indels per 100 kbp	0.07
Largest alignment	8764
NA50	1527
NGA50	1494
NA75	985
NGA75	948
LA50	966
LGA50	1004
LA75	1883
LGA75	1973

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

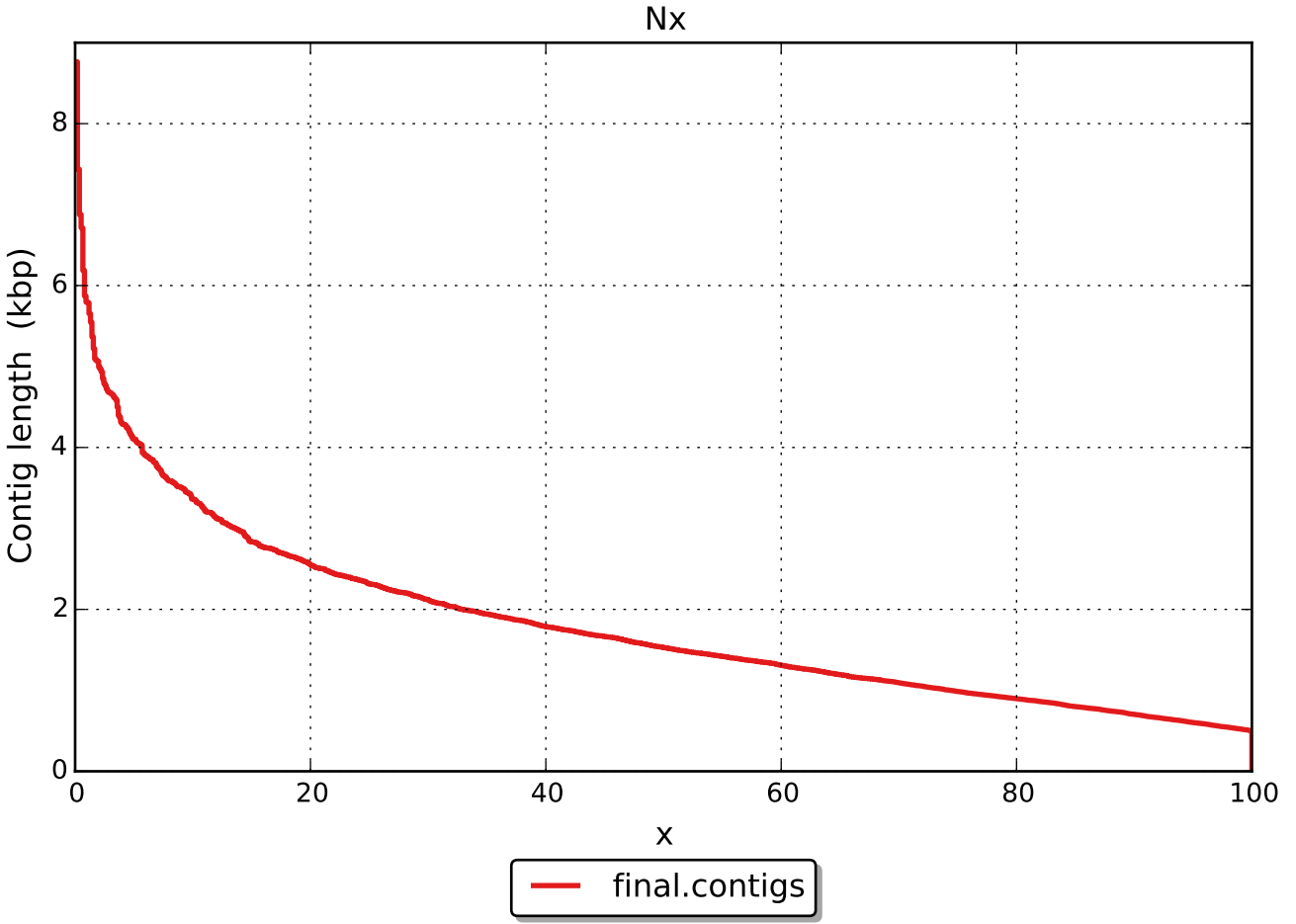
	final.contigs
# misassemblies	2
# relocations	2
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	3248
# local misassemblies	0
# mismatches	3632
# indels	3
# short indels	3
# long indels	0
Indels length	3

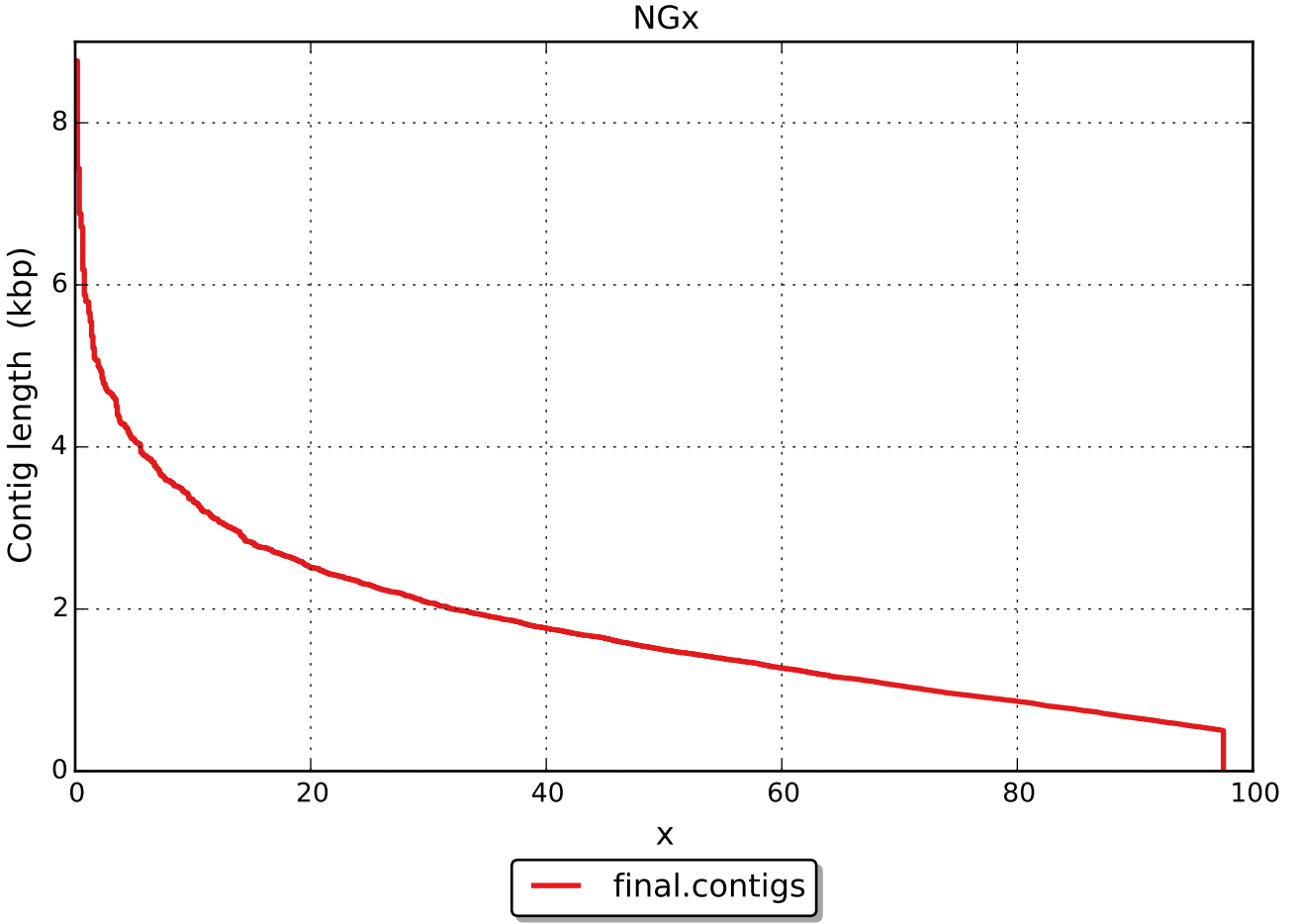
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

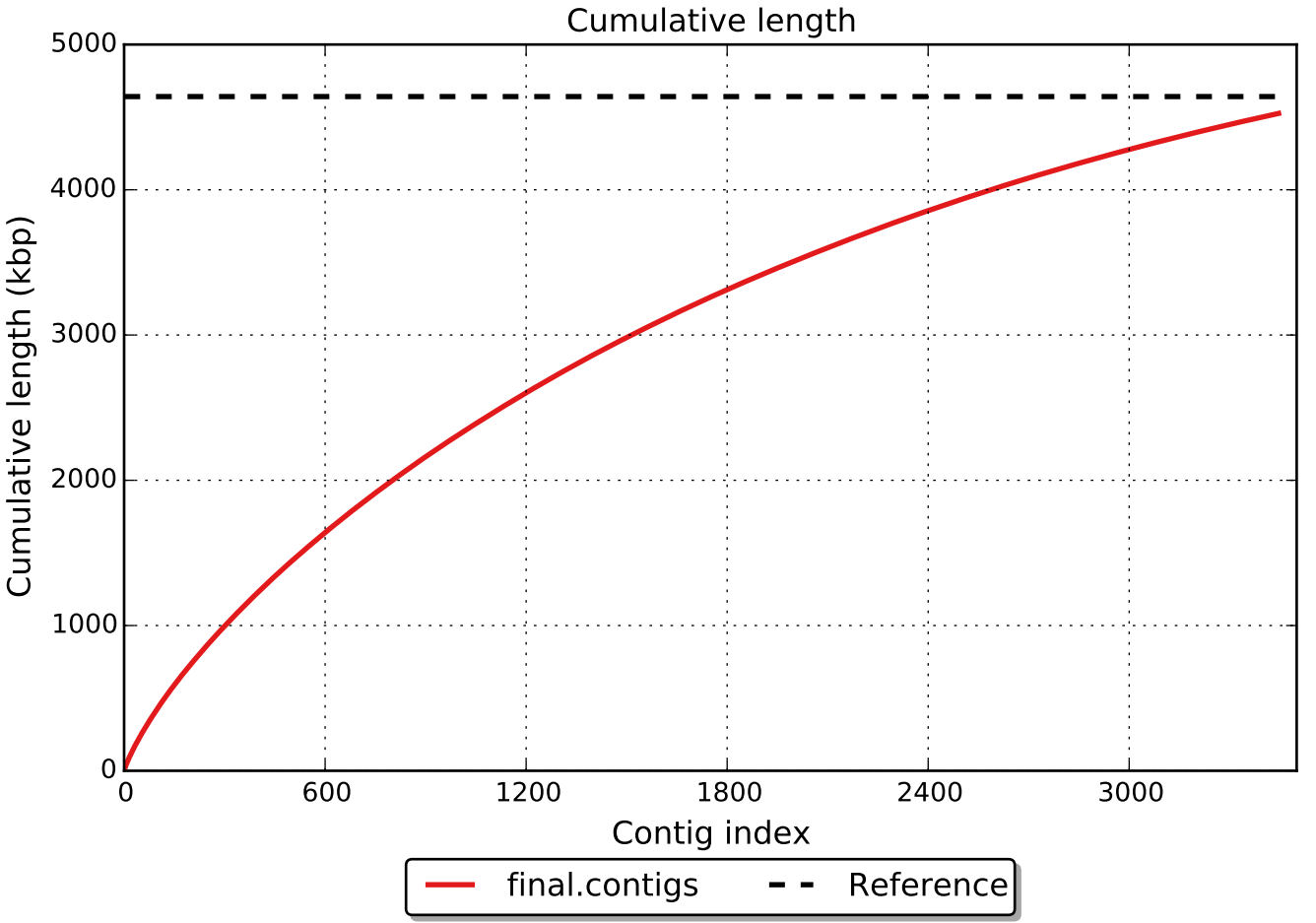
Unaligned report

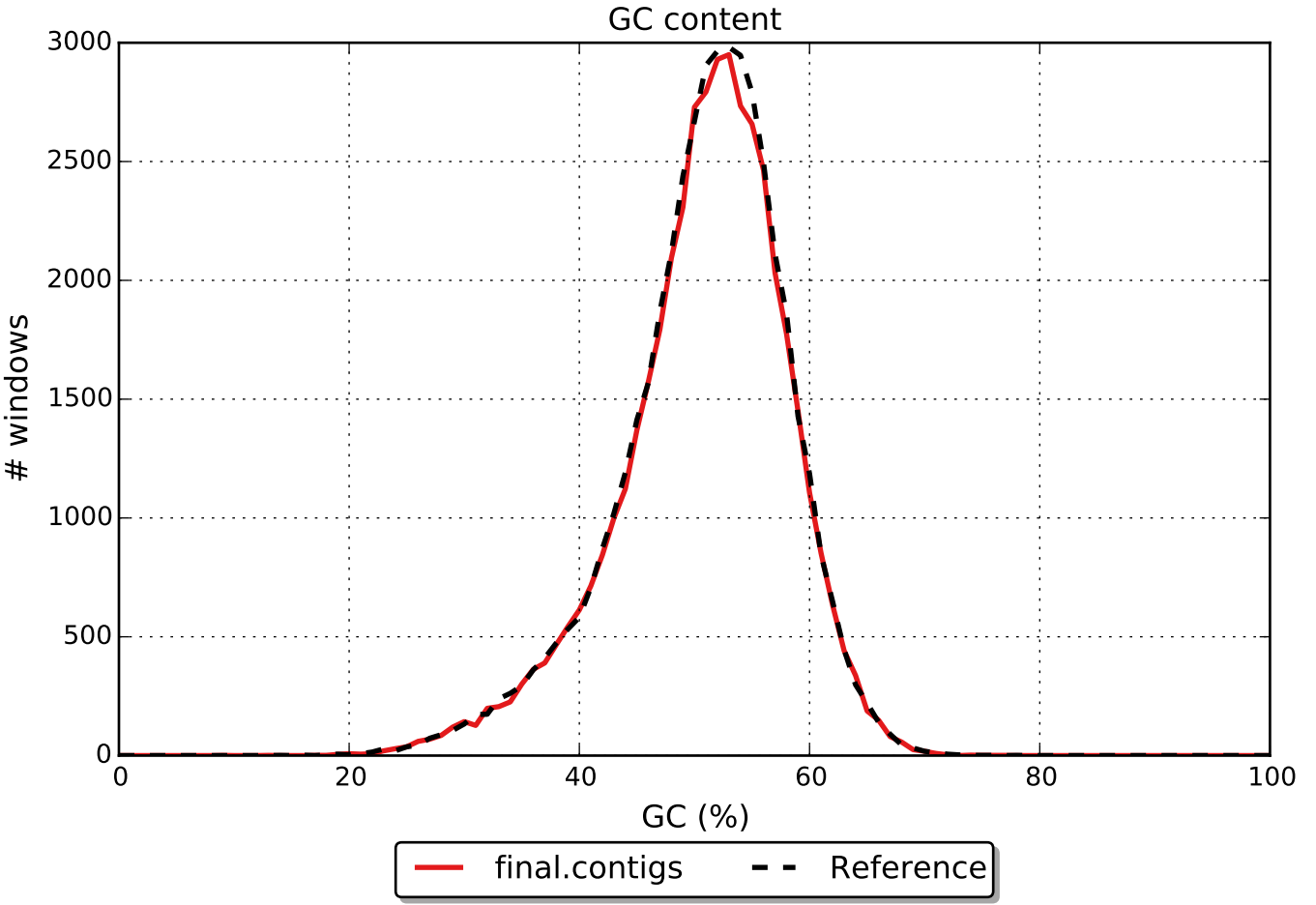
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

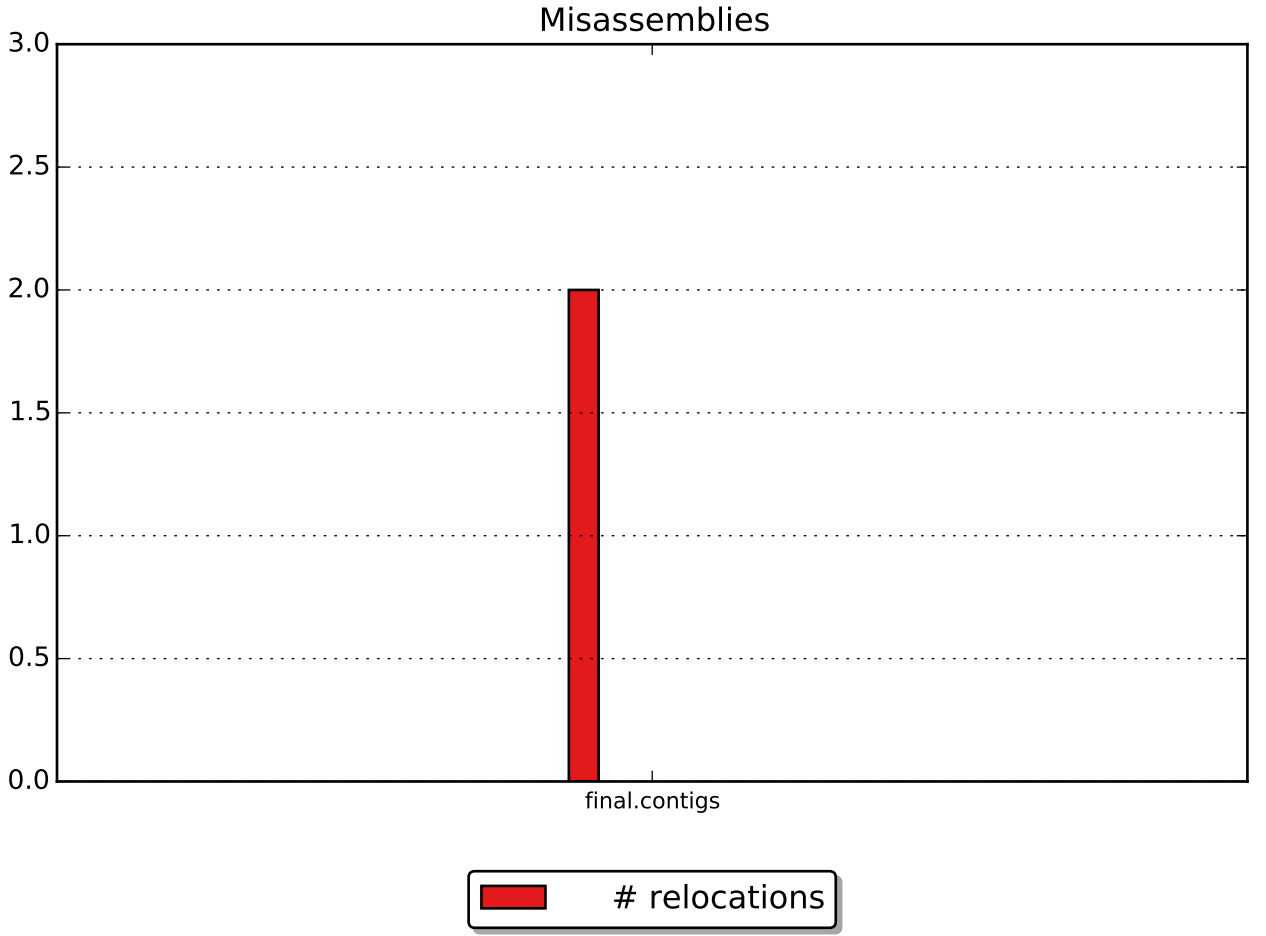
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

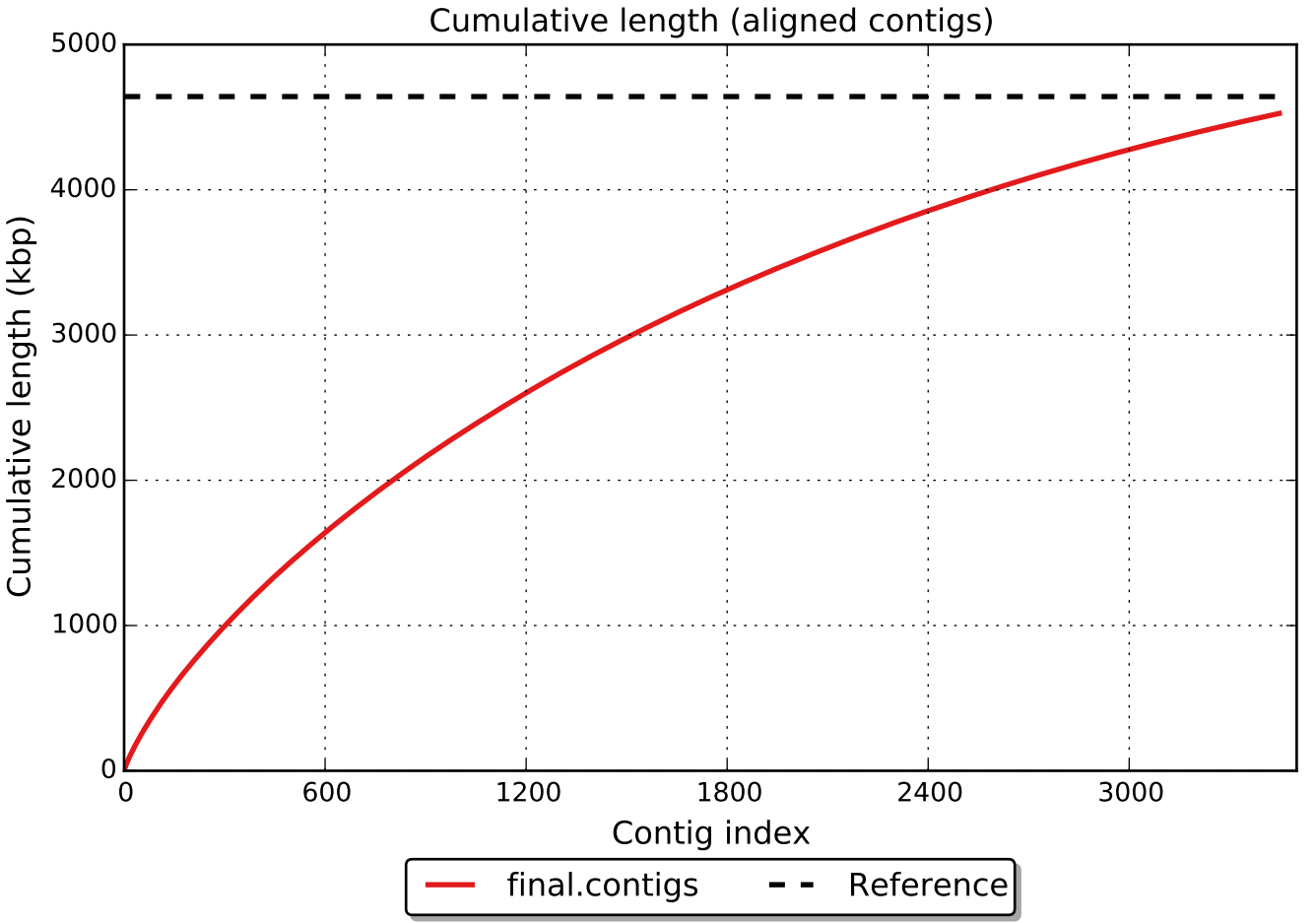

Nx
Contig length (kbp)
0
2
4
6
8
0
20
40
60
80
100
x
final.contigs

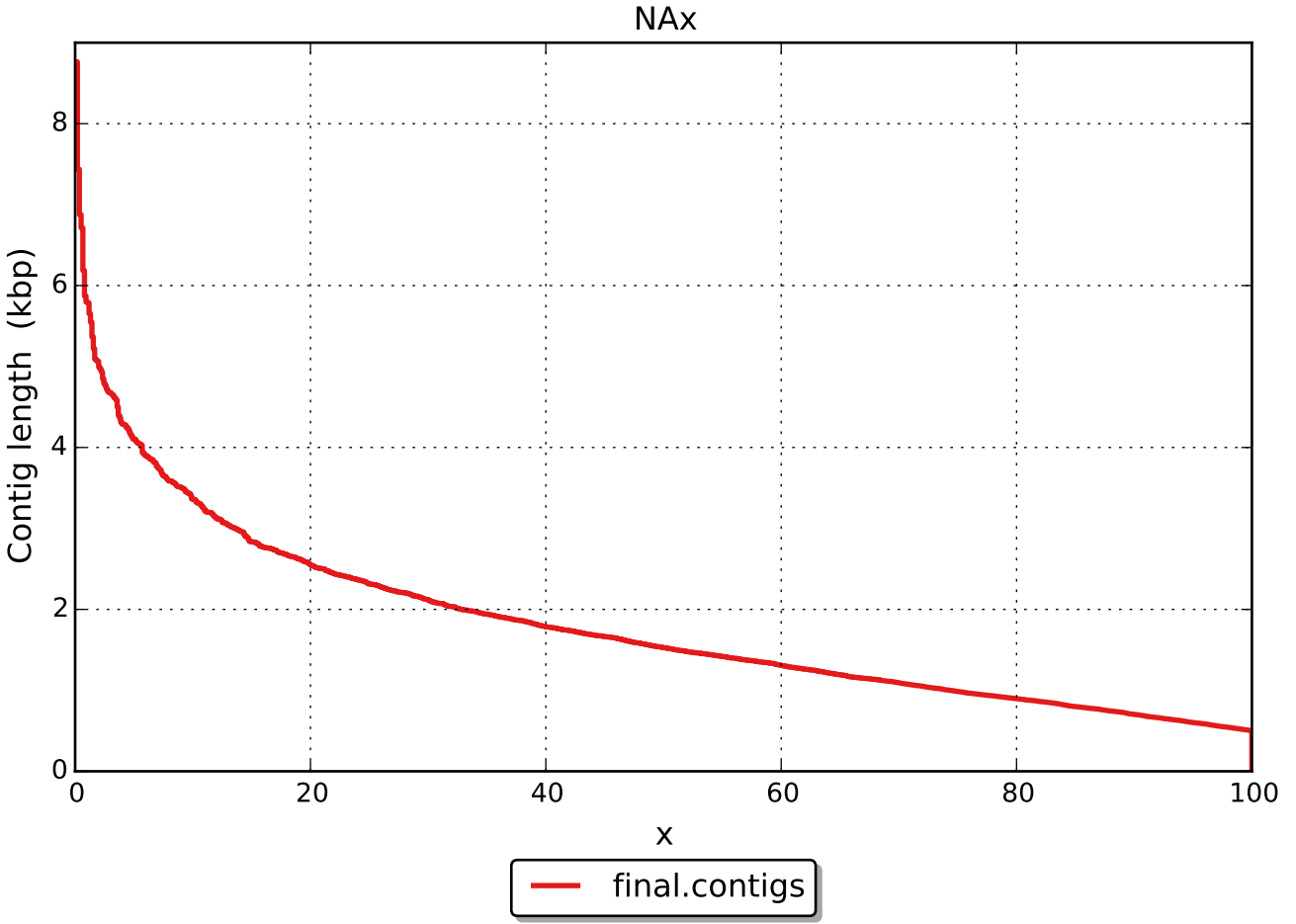

NGx
Contig length (kbp)
0
2
4
6
8
0
20
40
60
80
100
x
final.contigs

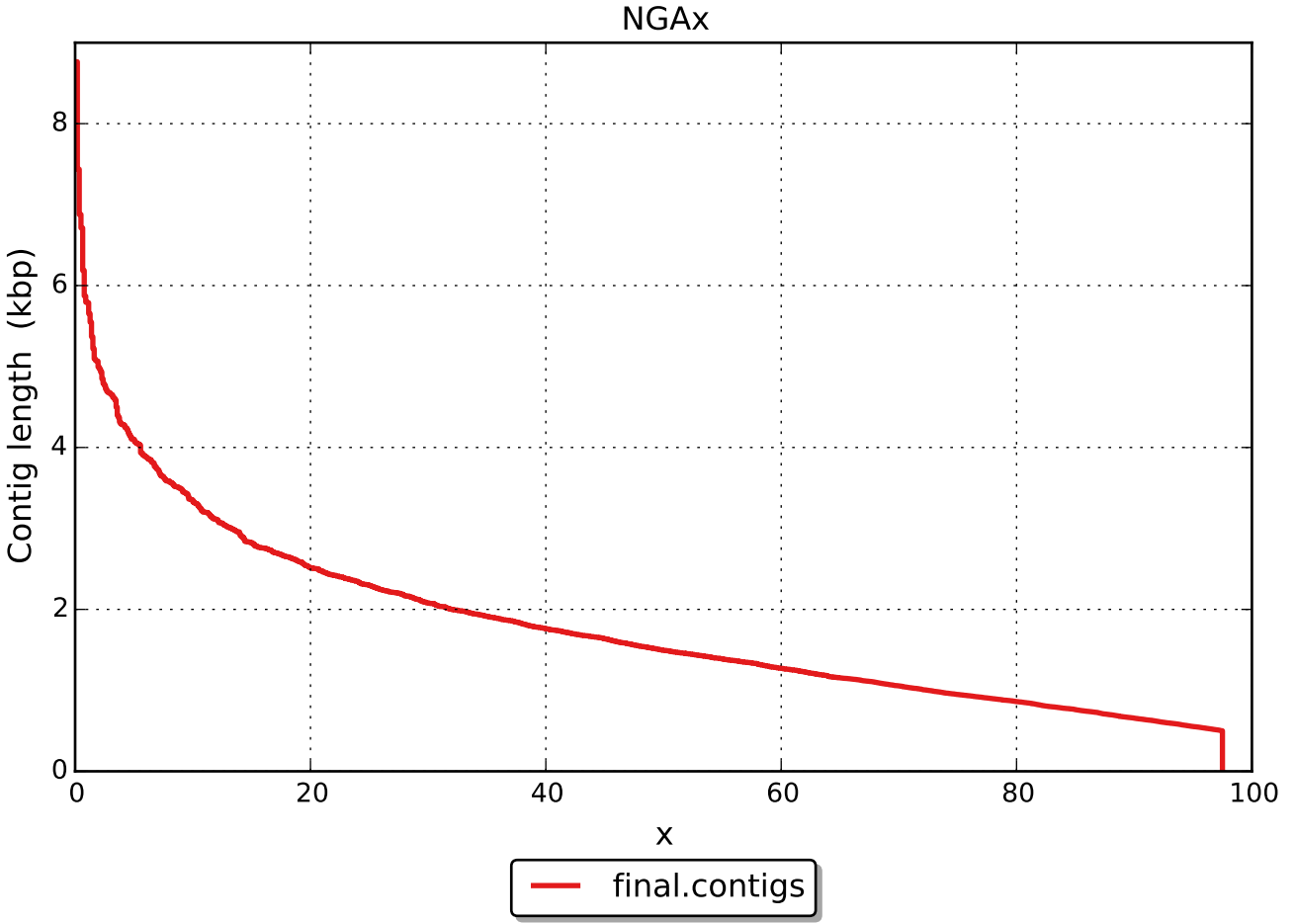

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
600
1200
1800
2400
3000
Contig index
final.contigs
Reference


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


Misassemblies
3.0
2.5
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
600
1200
1800
2400
3000
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
0
2
4
6
8
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
0
2
4
6
8
0
20
40
60
80
100
x
final.contigs