Report

	final.contigs
# contigs (>= 0 bp)	2718
# contigs (>= 1000 bp)	1979
Total length (>= 0 bp)	5586606
Total length (>= 1000 bp)	5041323
# contigs	2718
Largest contig	12599
Total length	5586606
Reference length	5547323
GC (%)	50.49
Reference GC (%)	50.49
N50	2712
NG50	2728
N75	1634
NG75	1652
L50	653
LG50	645
L75	1319
LG75	1301
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.093
Duplication ratio	1.037
# N's per 100 kbp	0.00
# mismatches per 100 kbp	32.81
# indels per 100 kbp	0.00
Largest alignment	12599
NA50	2712
NGA50	2727
NA75	1634
NGA75	1652
LA50	653
LGA50	645
LA75	1319
LGA75	1301

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

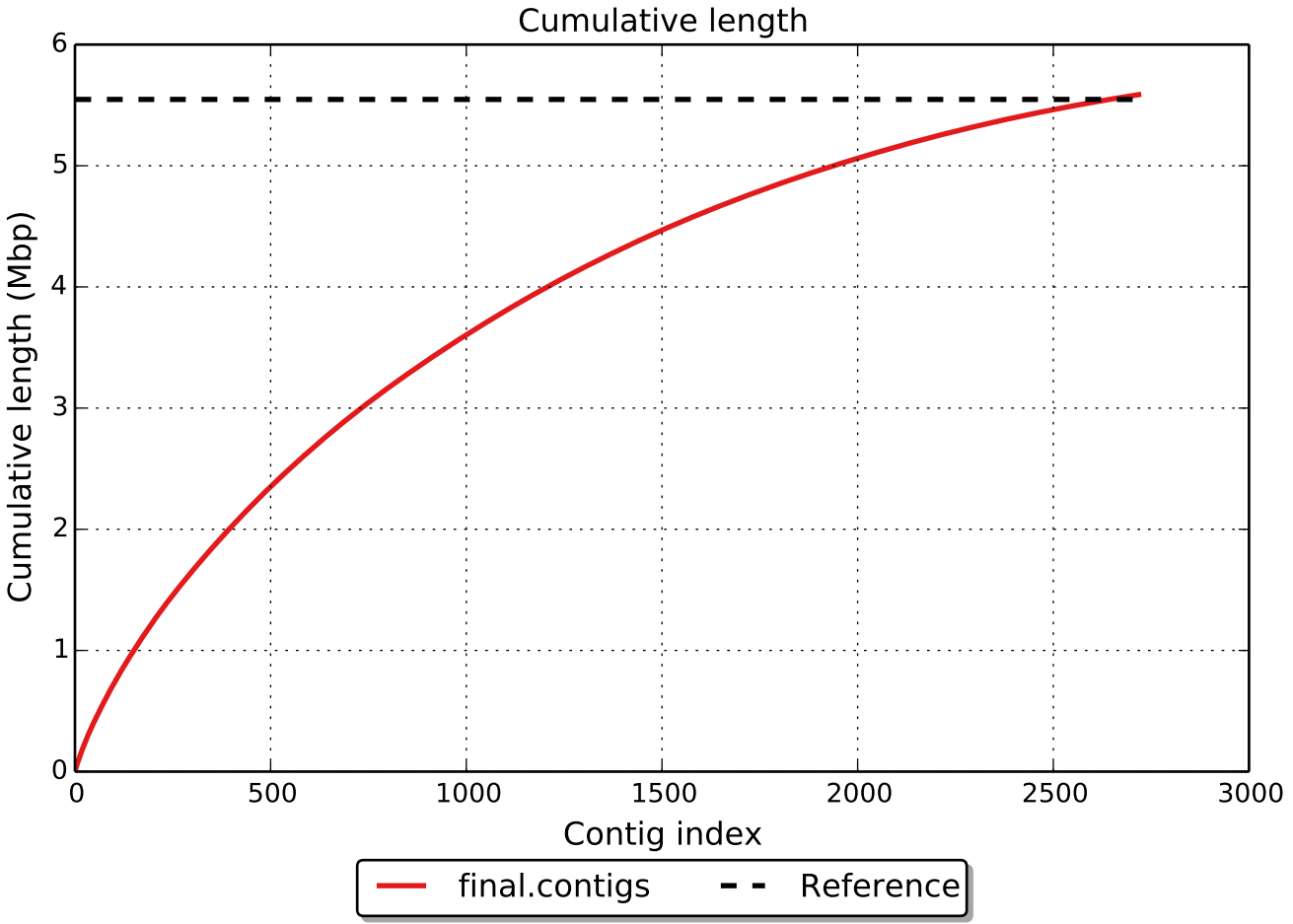
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	1767
# indels	0
# short indels	0
# long indels	0
Indels length	0

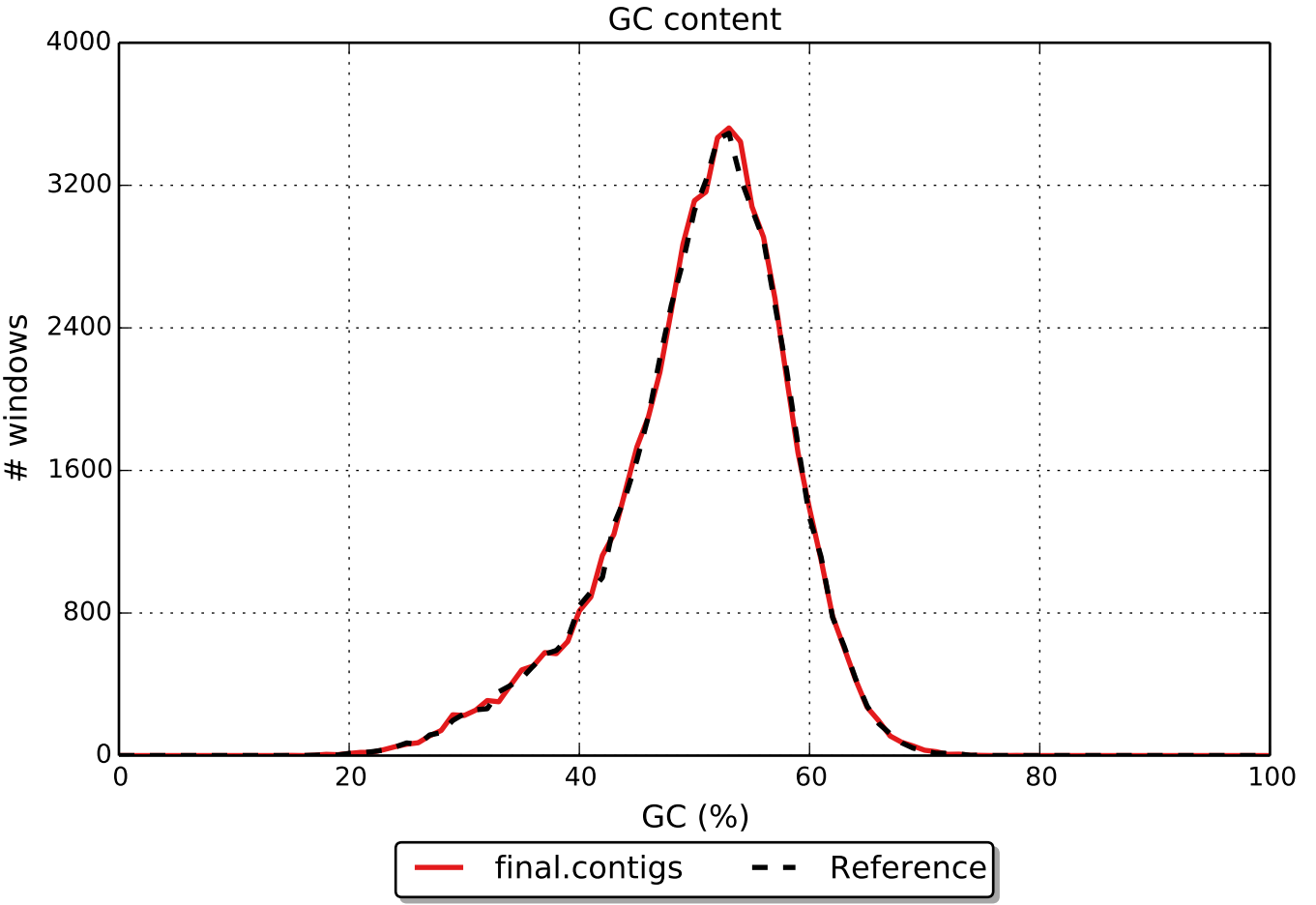
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

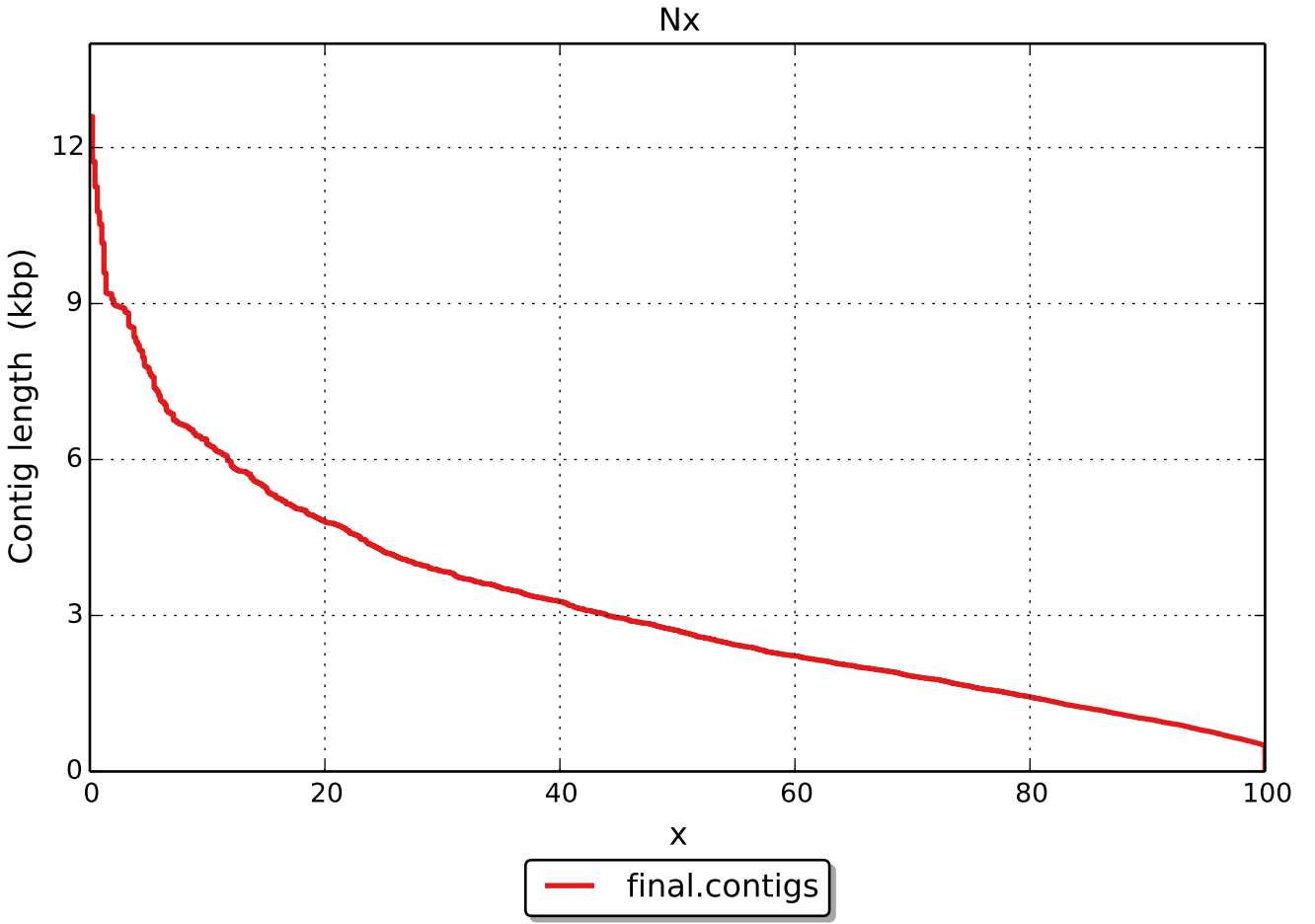
Unaligned report

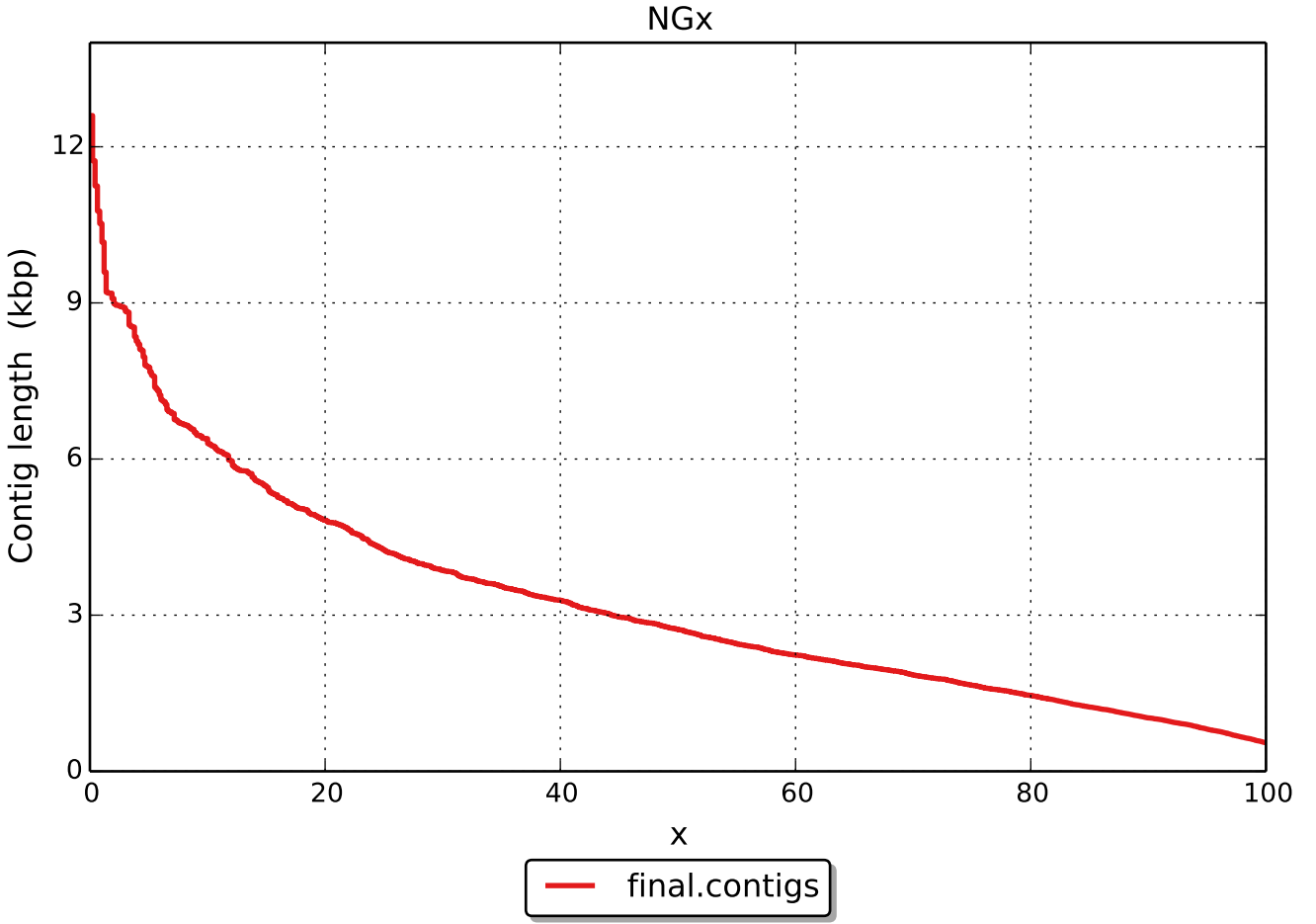
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

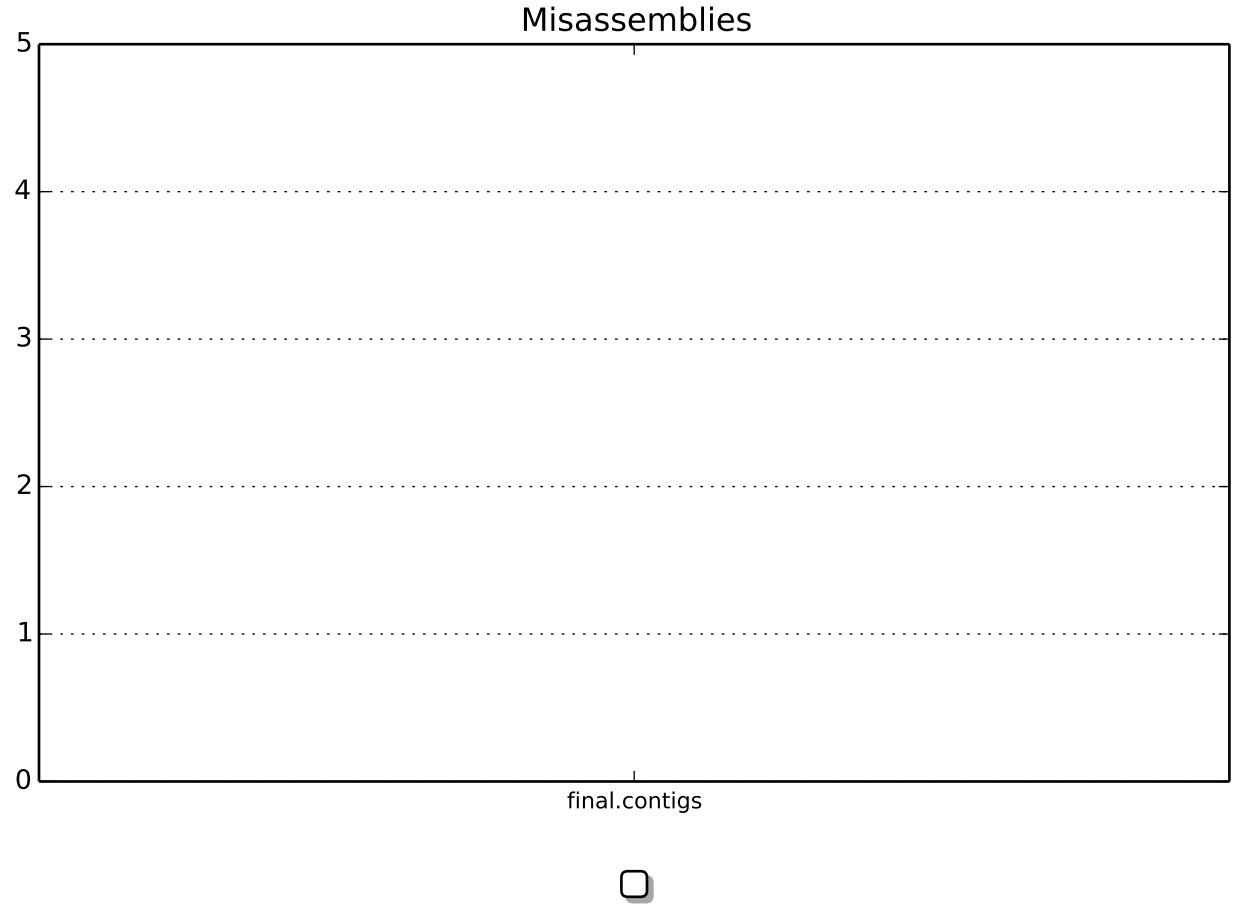
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

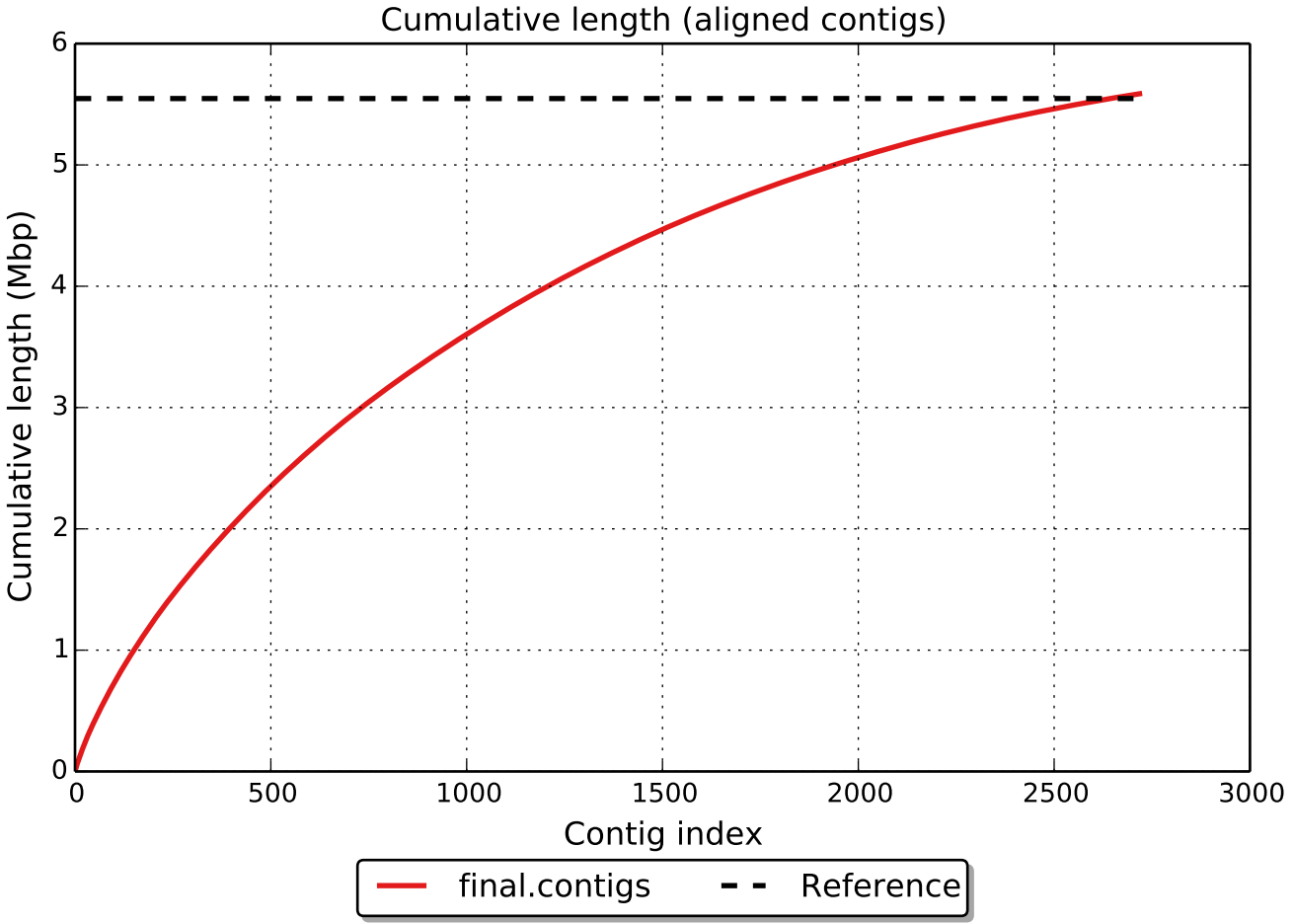

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
500
1000
1500
2000
2500
3000
Contig index
final.contigs
Reference

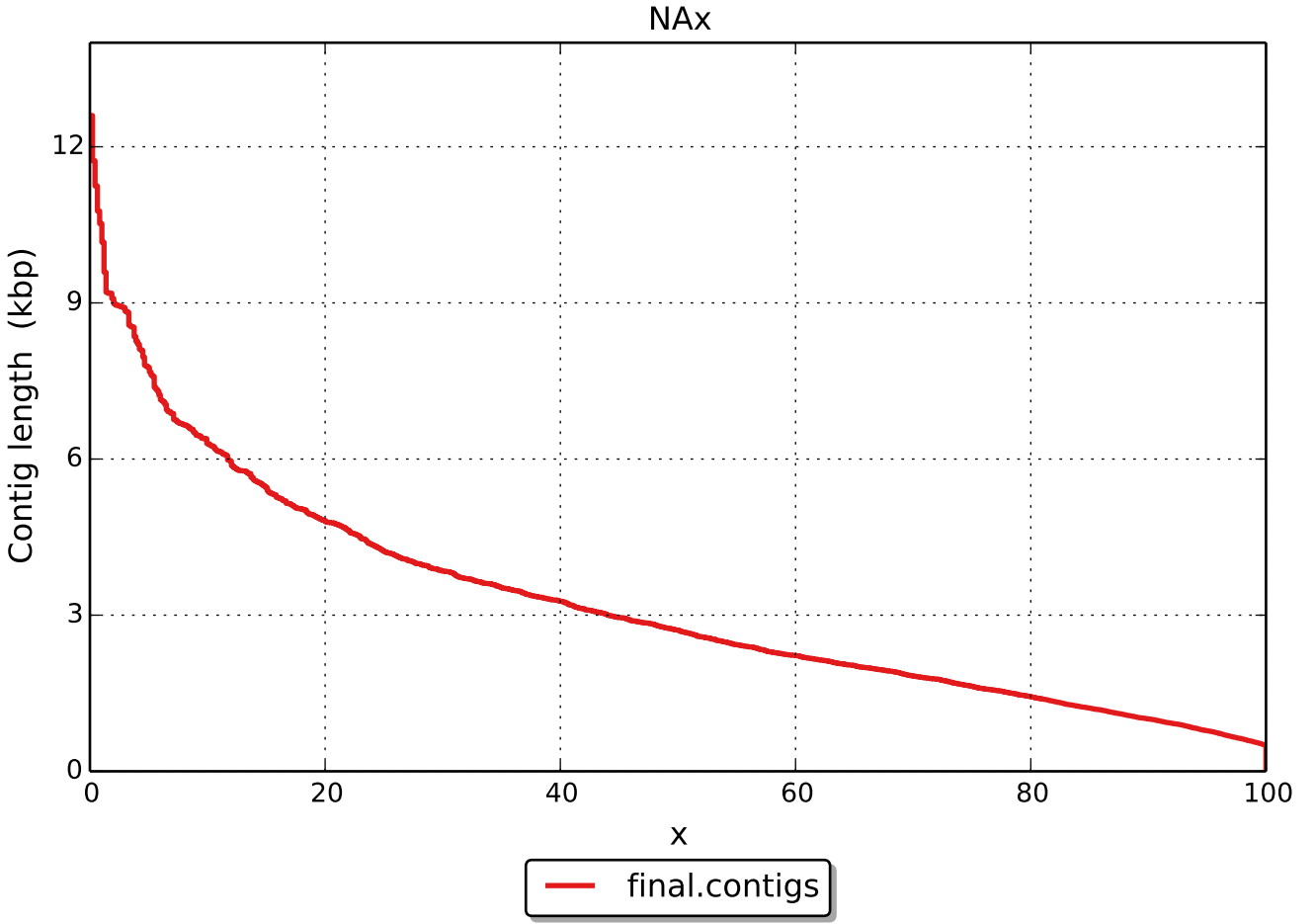

GC content
4000
3200
2400
1600
800
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

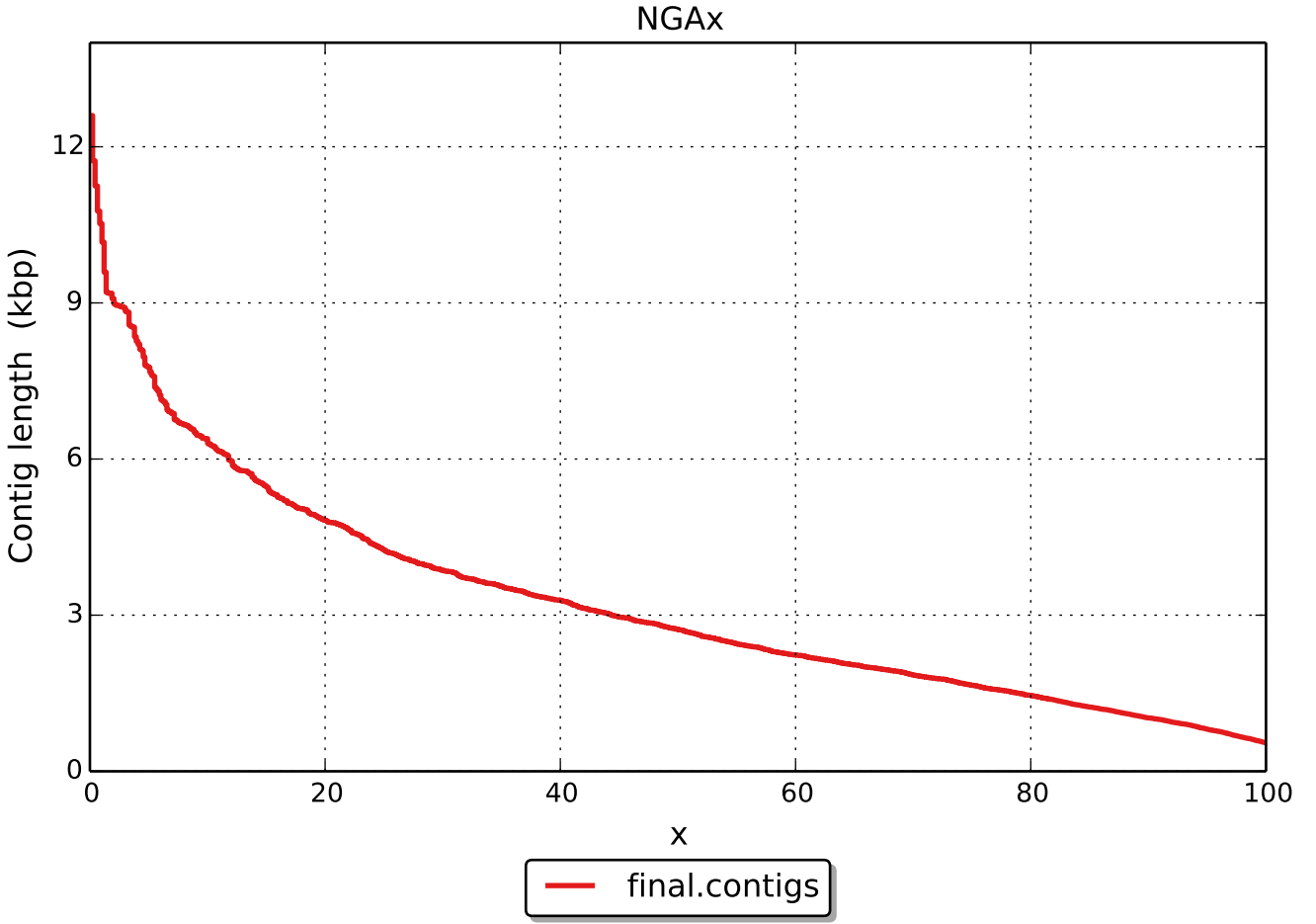

Nx
Contig length (kbp)
0
3
6
9
12
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs


Misassemblies
5
4
3
2
1
0
final.contigs


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
500
1000
1500
2000
2500
3000
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
0
3
6
9
12
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs