Report

	final.contigs
# contigs (>= 0 bp)	2374
# contigs (>= 1000 bp)	1160
Total length (>= 0 bp)	3327266
Total length (>= 1000 bp)	2493604
# contigs	2374
Largest contig	8768
Total length	3327266
Reference length	1892775
GC (%)	32.25
Reference GC (%)	32.26
N50	1860
NG50	2952
N75	999
NG75	2184
L50	540
LG50	231
L75	1162
LG75	419
# misassemblies	16
# misassembled contigs	16
Misassembled contigs length	13747
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	316
Genome fraction (%)	89.317
Duplication ratio	1.968
# N's per 100 kbp	0.00
# mismatches per 100 kbp	836.64
# indels per 100 kbp	0.12
Largest alignment	8768
NA50	714
NGA50	1725
NGA75	938
LA50	1012
LGA50	328
LGA75	713

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

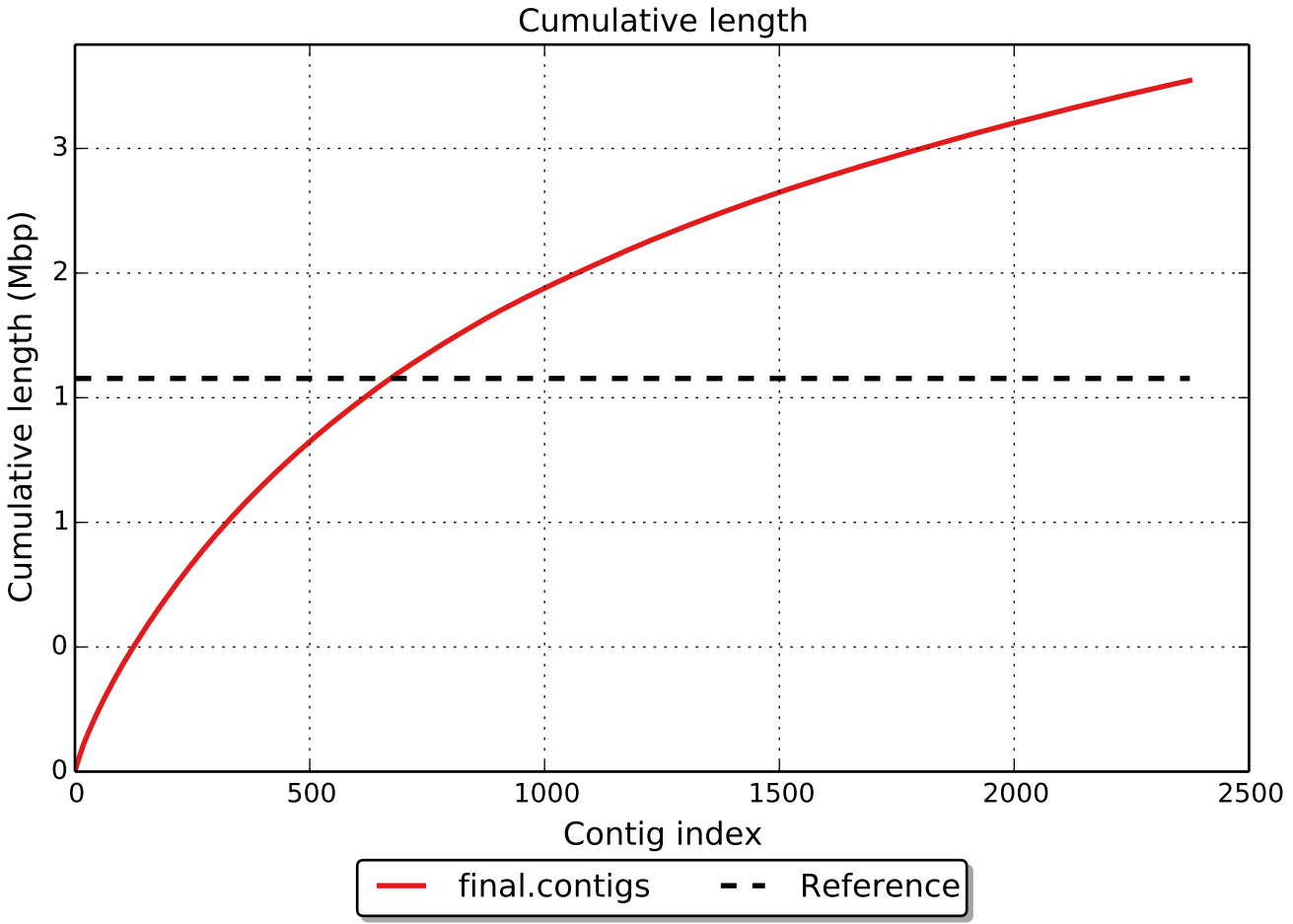
	final.contigs
# misassemblies	16
# relocations	16
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	16
Misassembled contigs length	13747
# local misassemblies	0
# mismatches	14144
# indels	2
# short indels	2
# long indels	0
Indels length	2

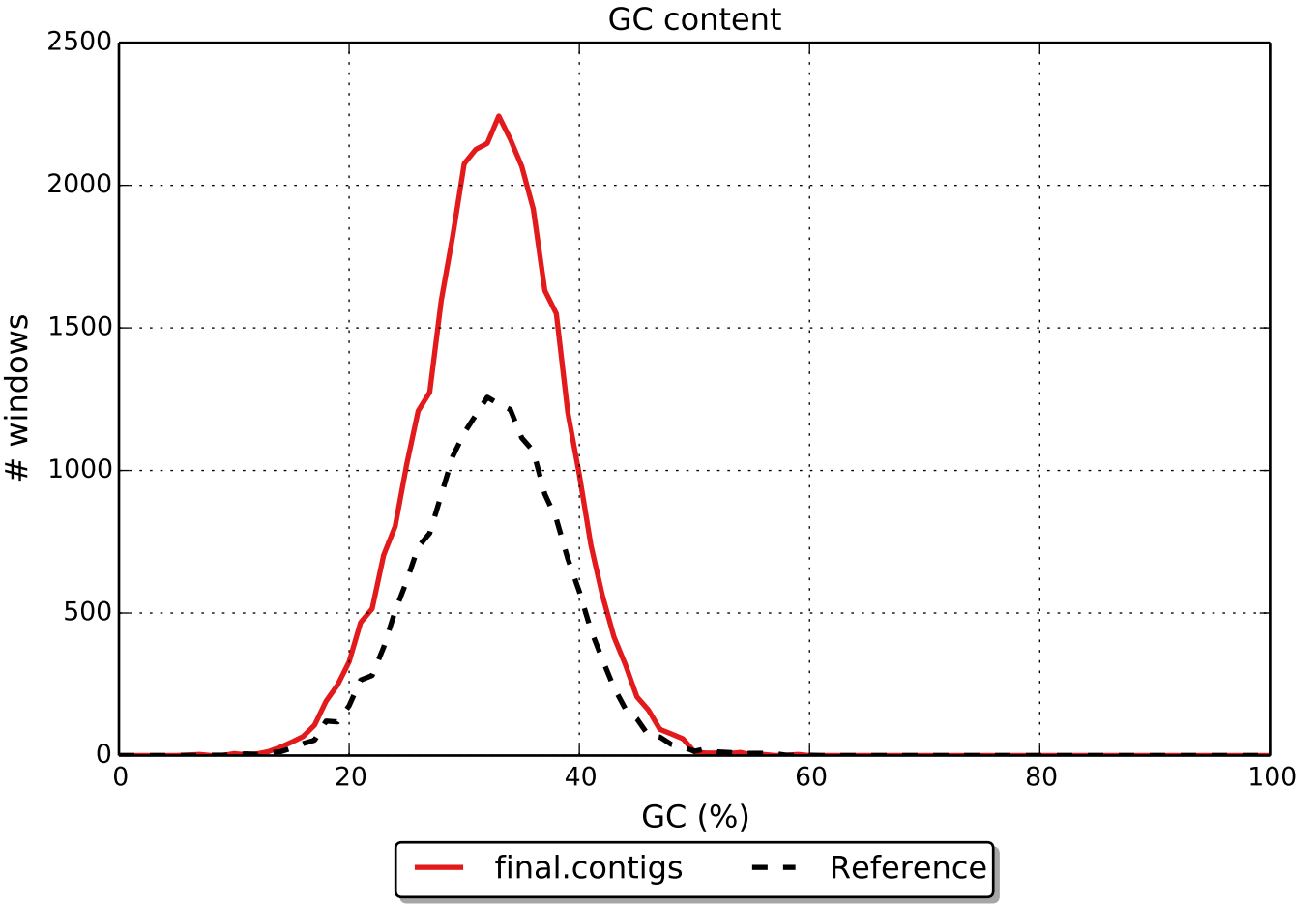
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

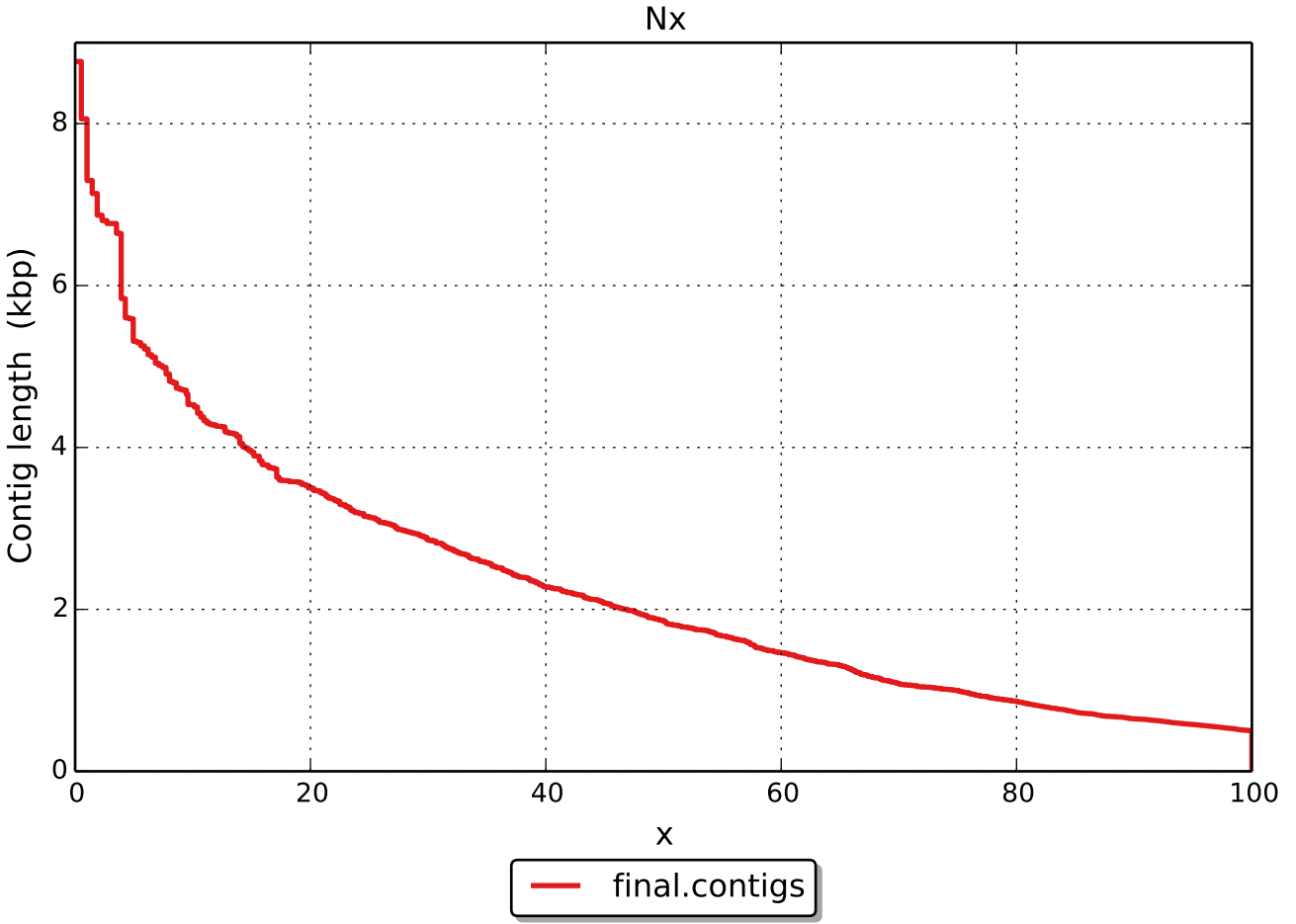
Unaligned report

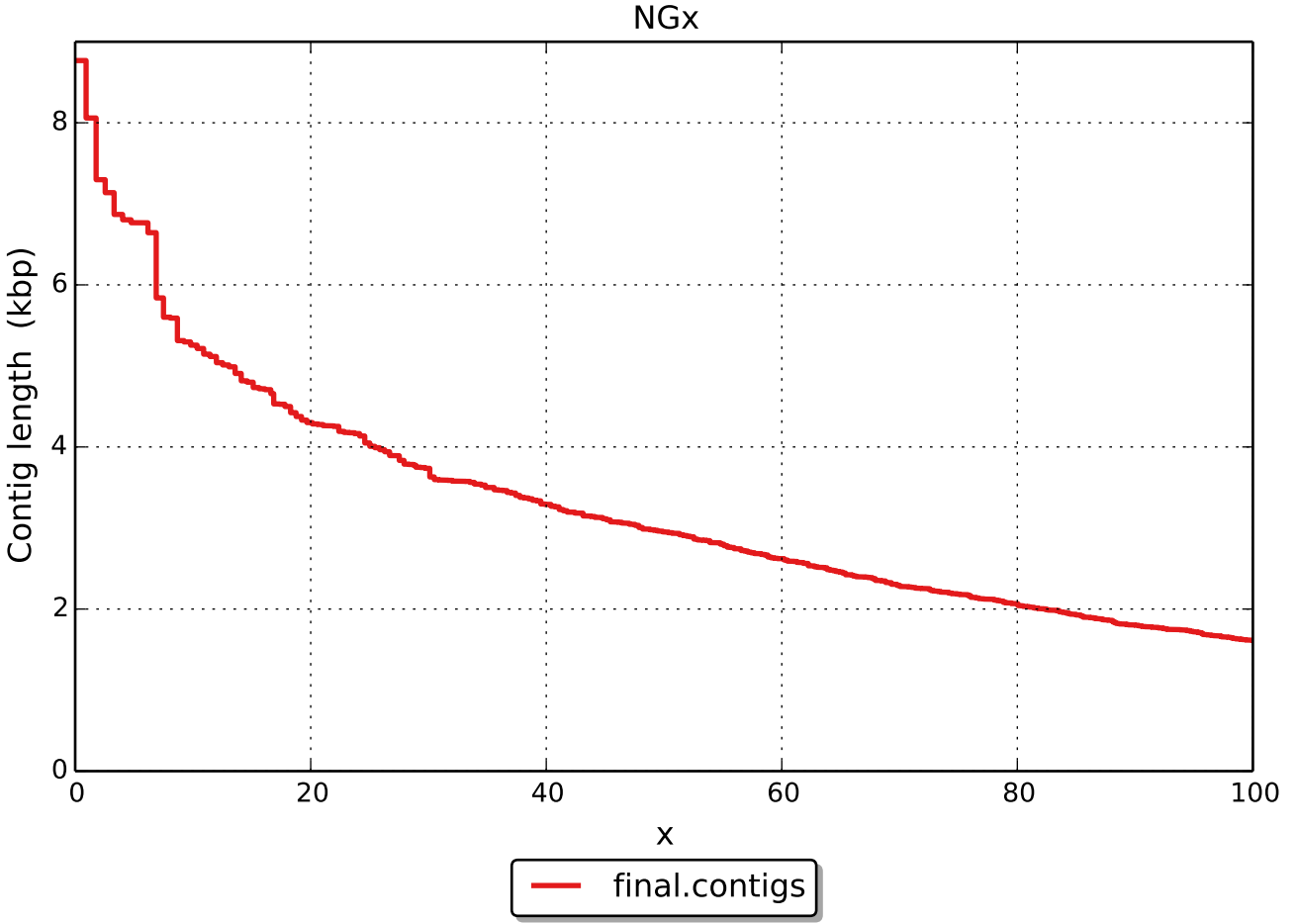
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	316
# N's	0

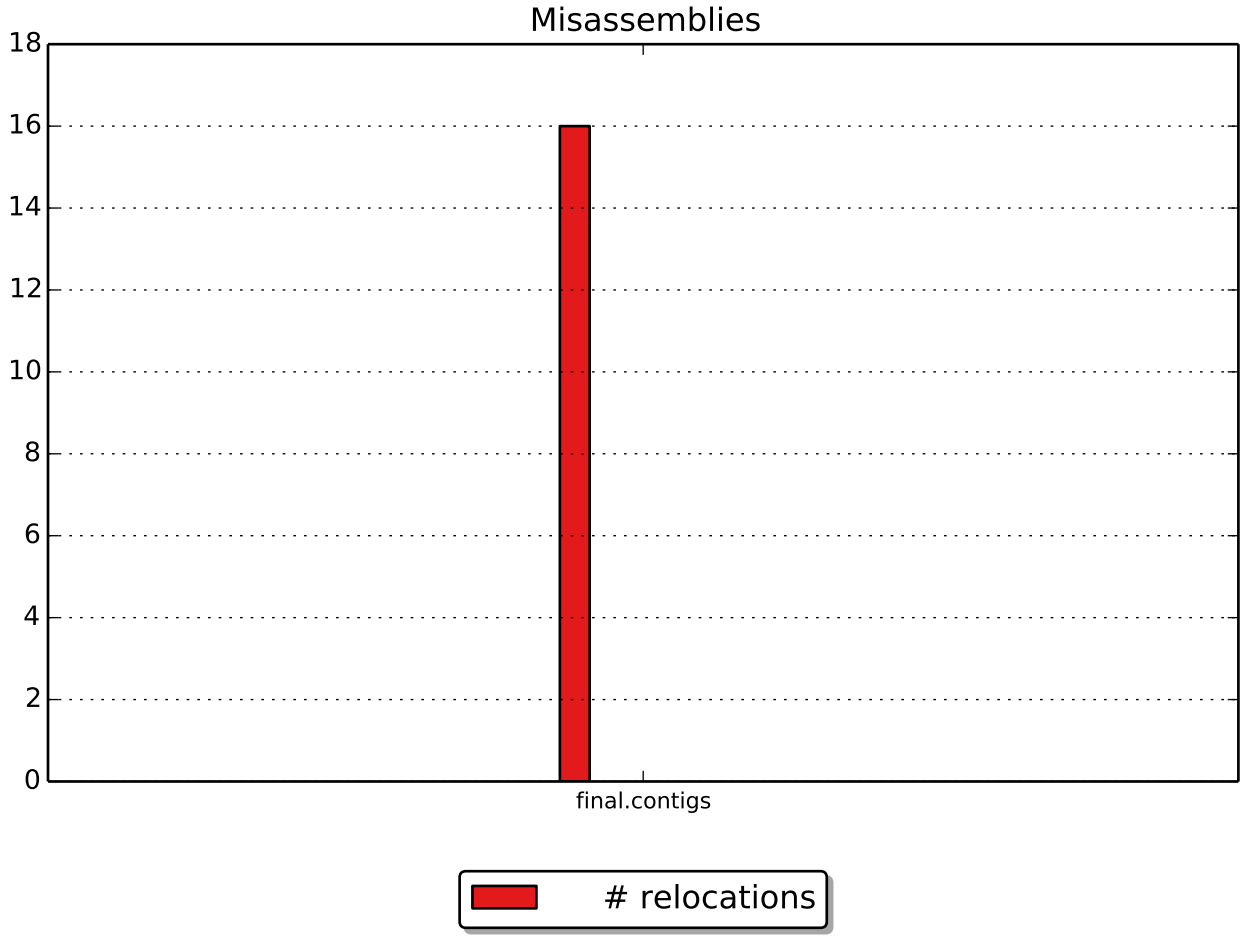
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

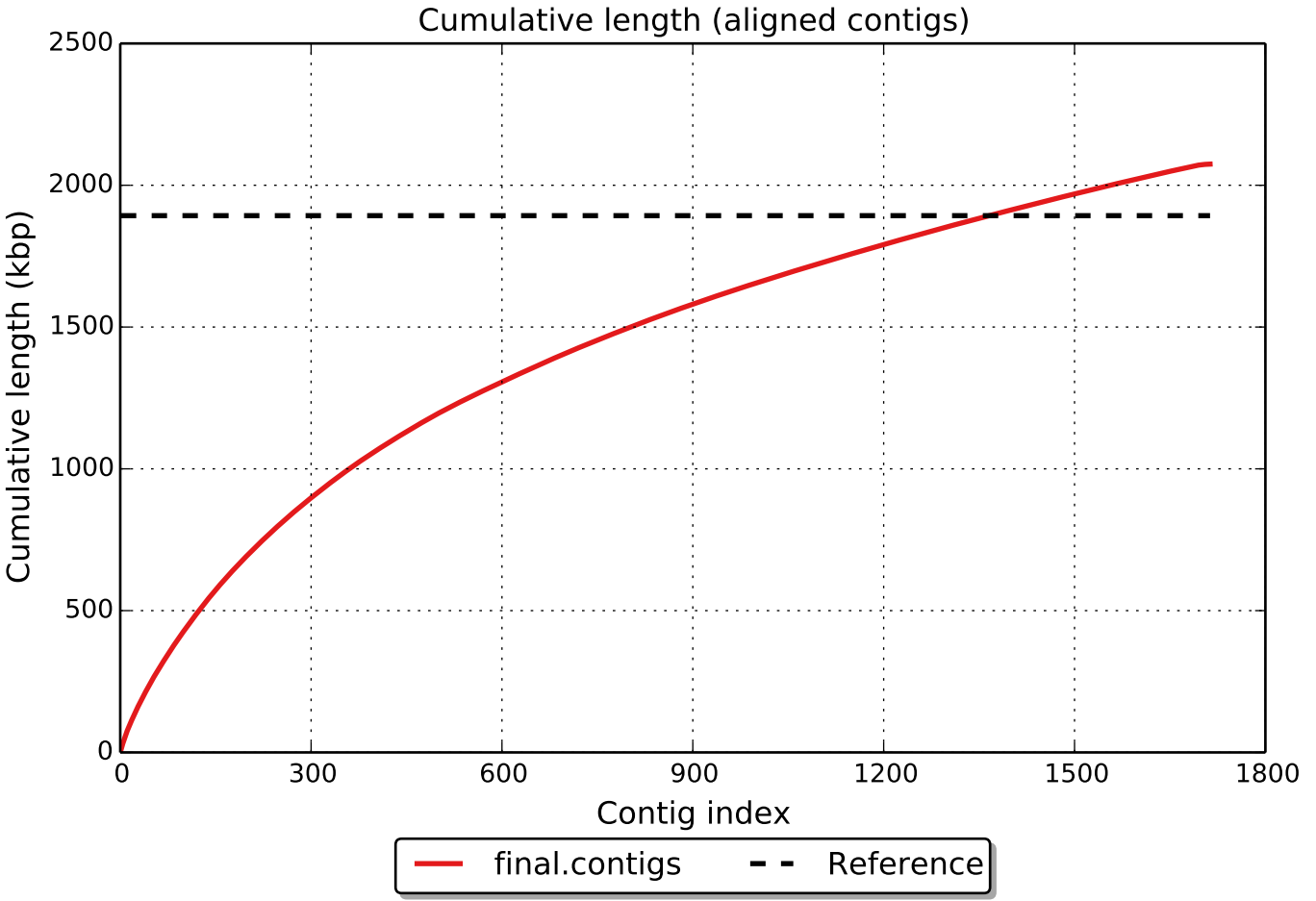

Cumulative length
Cumulative length (Mbp)
3
2
1
1
0
0
0
500
1000
1500
2000
2500
Contig index
final.contigs
Reference

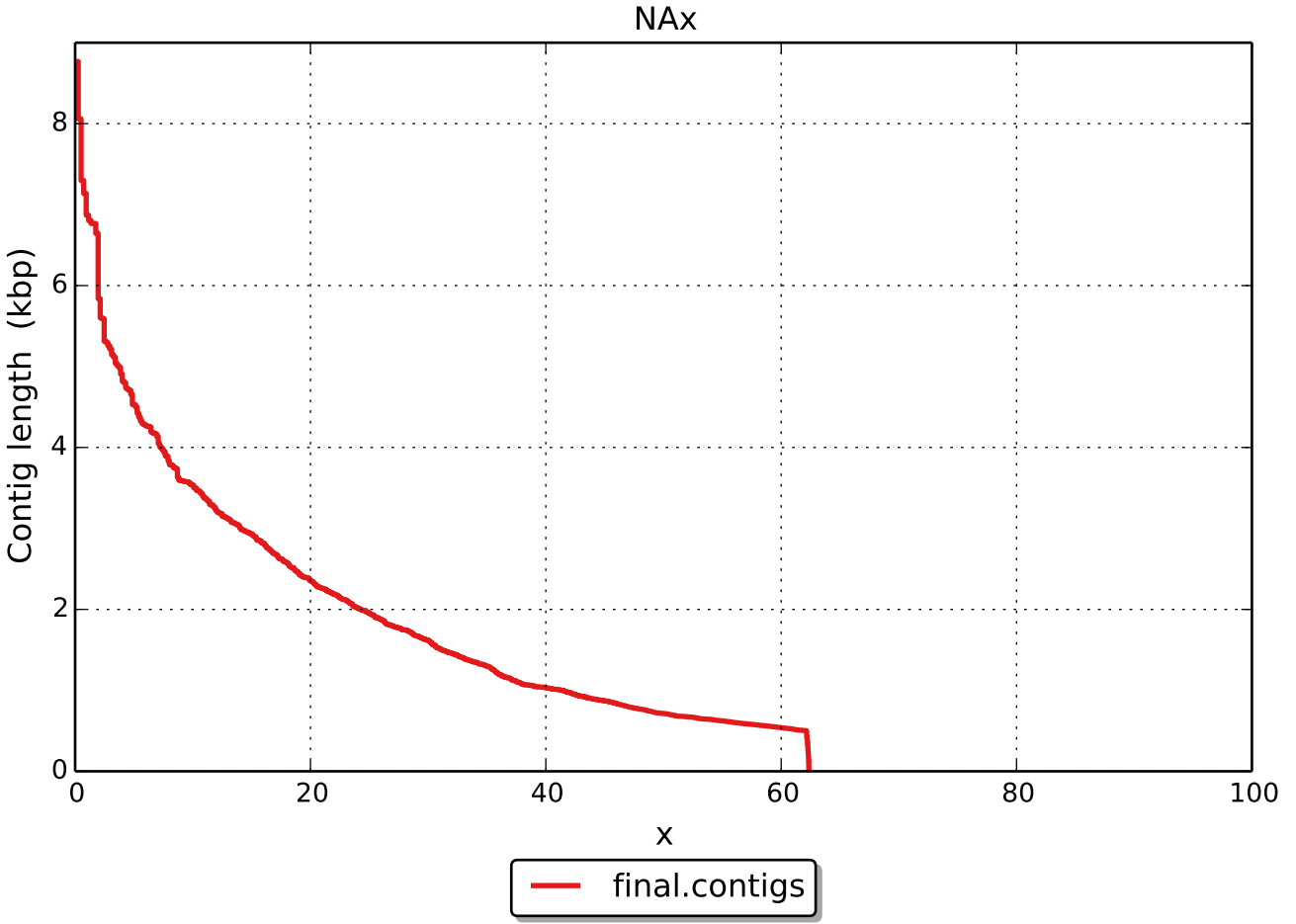

GC content
2500
2000
1500
1000
500
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

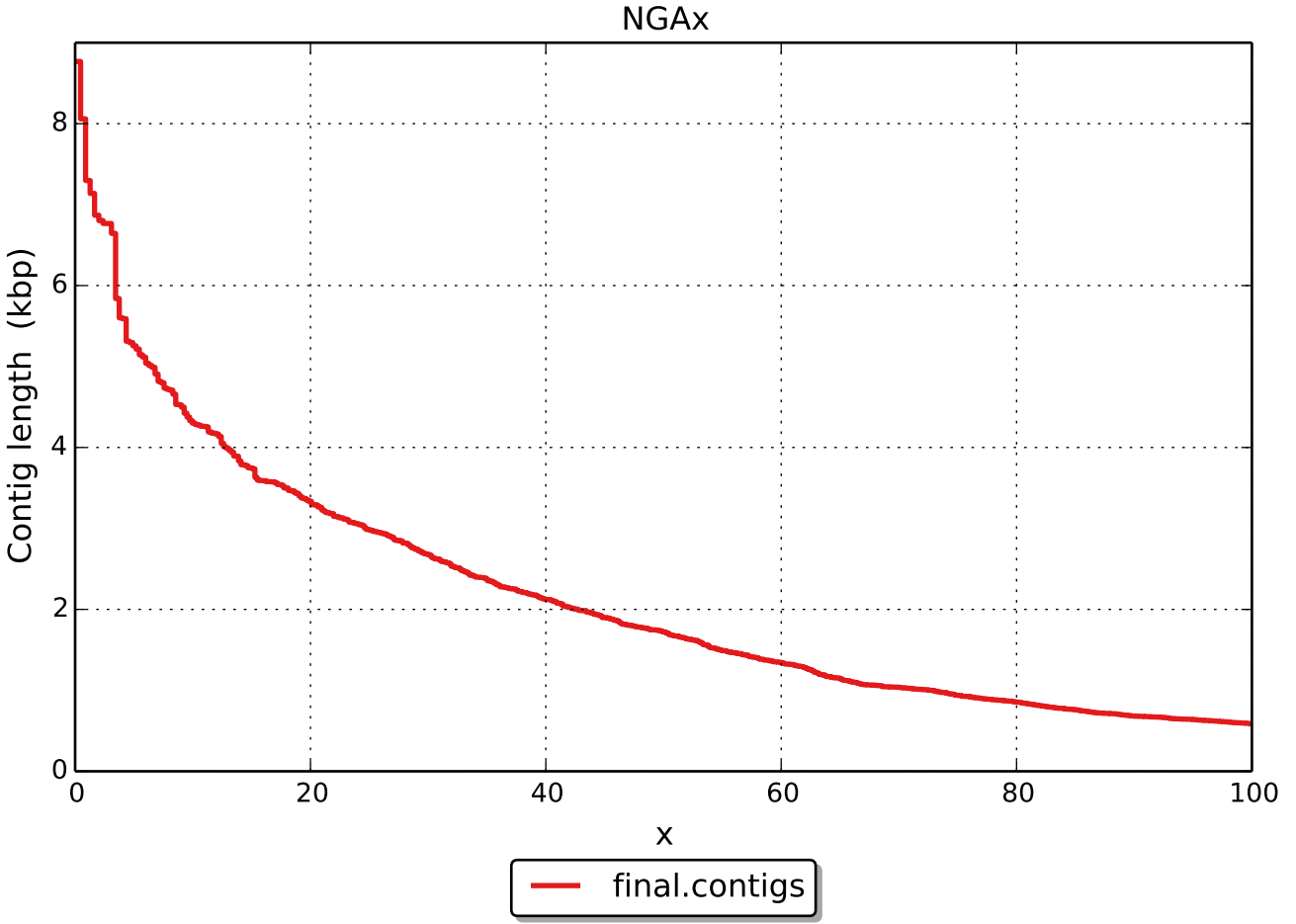

Nx
Contig length (kbp)
0
2
4
6
8
0
20
40
60
80
100
x
final.contigs


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


Misassemblies
18
16
14
12
10
8
6
4
2
0
final.contigs
relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
2500
2000
1500
1000
500
0
0
300
600
900
1200
1500
1800
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