Report

	final.contigs
# contigs (>= 0 bp)	7003
# contigs (>= 1000 bp)	1400
Total length (>= 0 bp)	6817146
Total length (>= 1000 bp)	4405709
# contigs	3021
Largest contig	18257
Total length	5492492
Reference length	11094646
GC (%)	50.31
Reference GC (%)	50.48
N50	3100
N75	1336
L50	494
L75	1152
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 1 part
Unaligned length	11
Genome fraction (%)	88.057
Duplication ratio	1.032
# N's per 100 kbp	0.00
# mismatches per 100 kbp	611.61
# indels per 100 kbp	0.31
Largest alignment	18257
NA50	3100
NA75	1336
LA50	494
LA75	1152

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

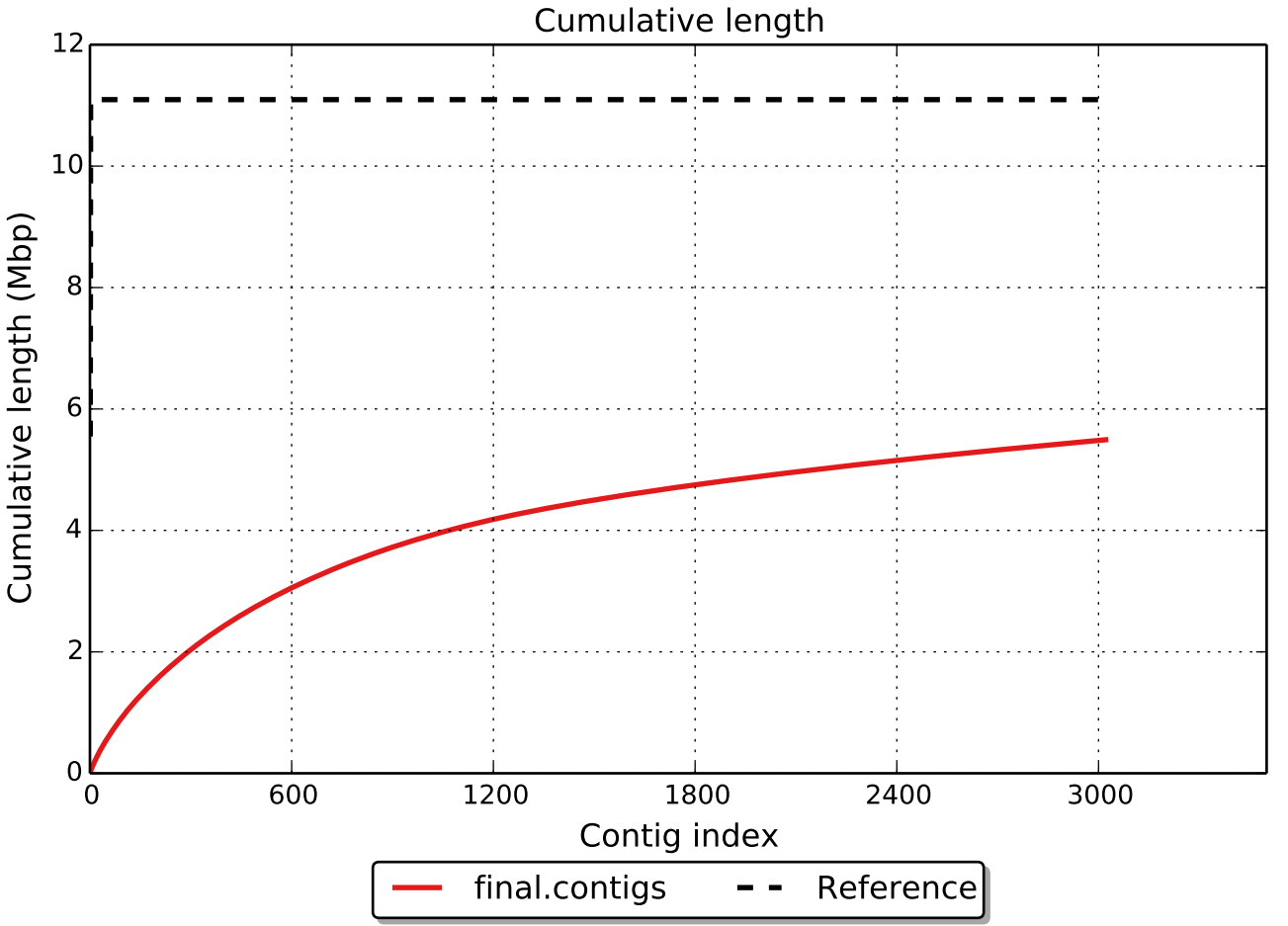
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	59752
# indels	30
# short indels	29
# long indels	1
Indels length	36

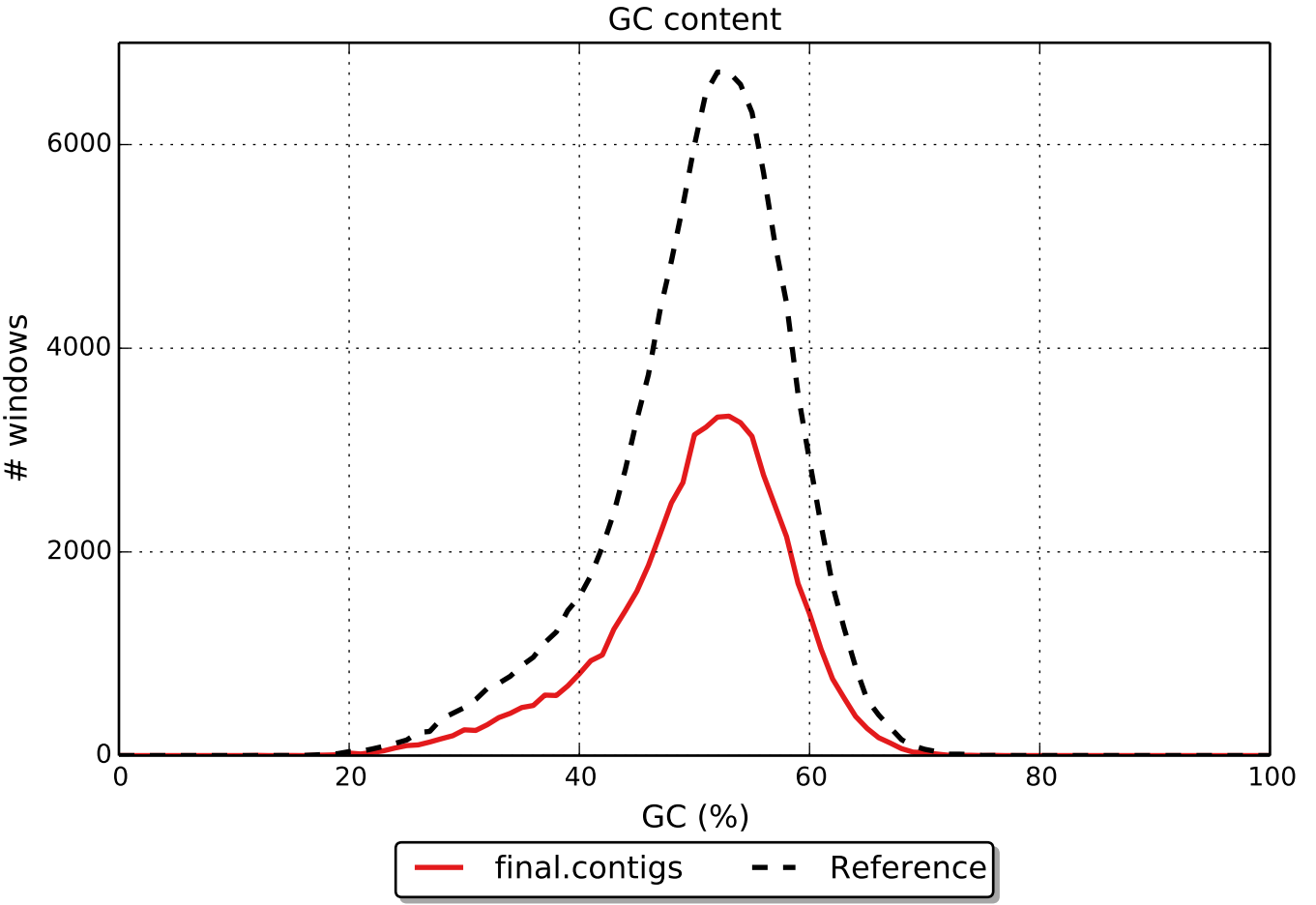
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

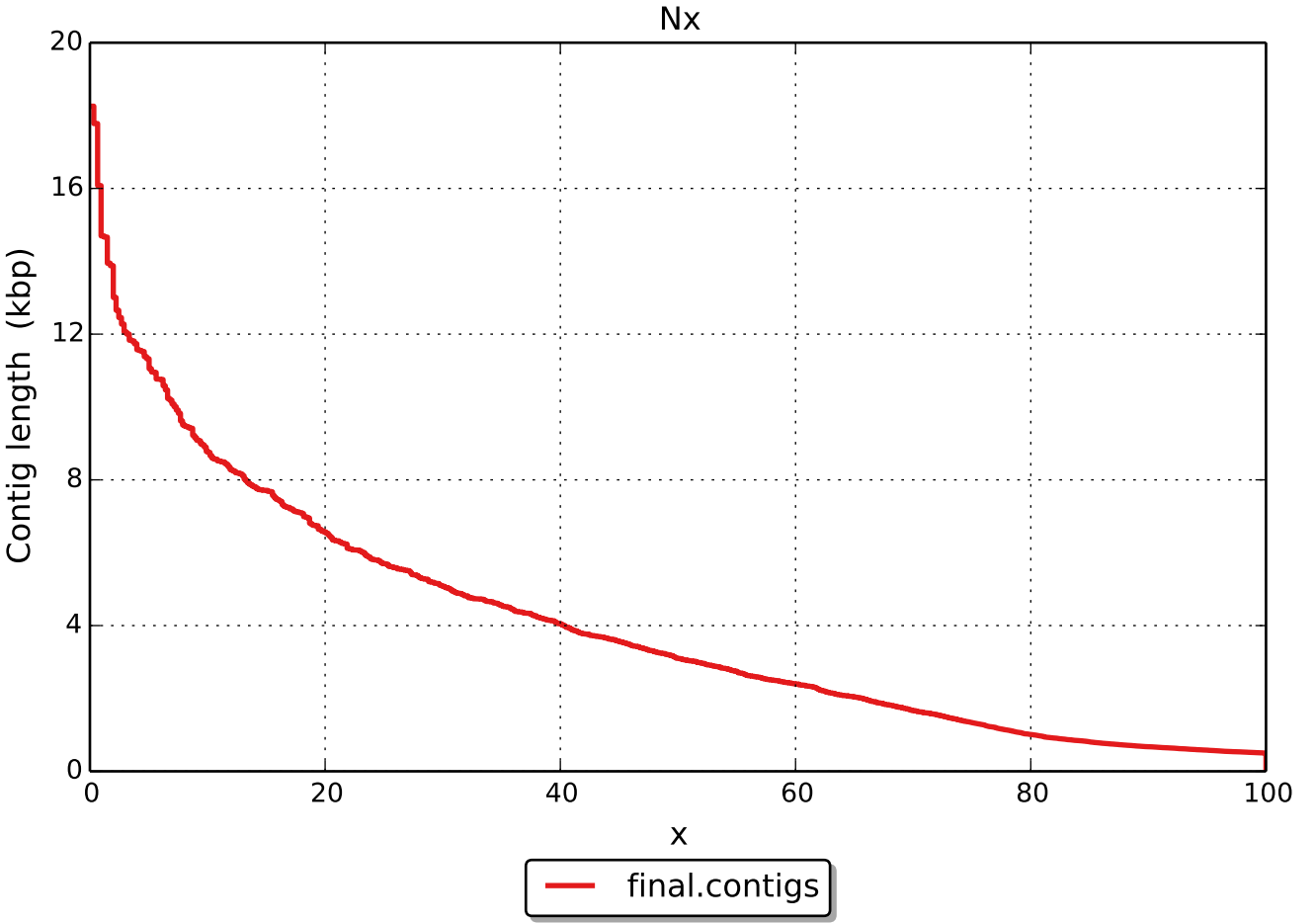
Unaligned report

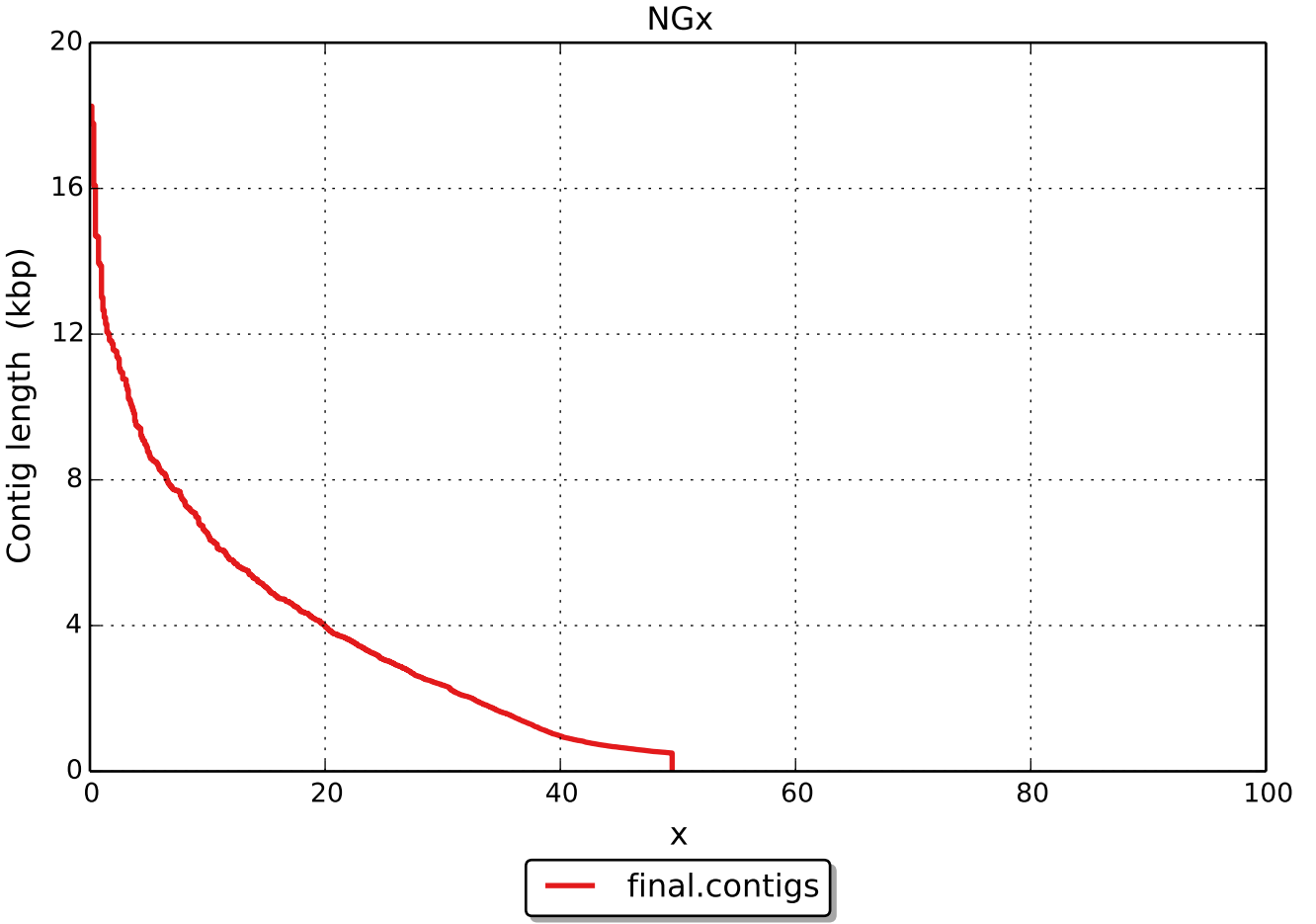
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	11
# N's	0

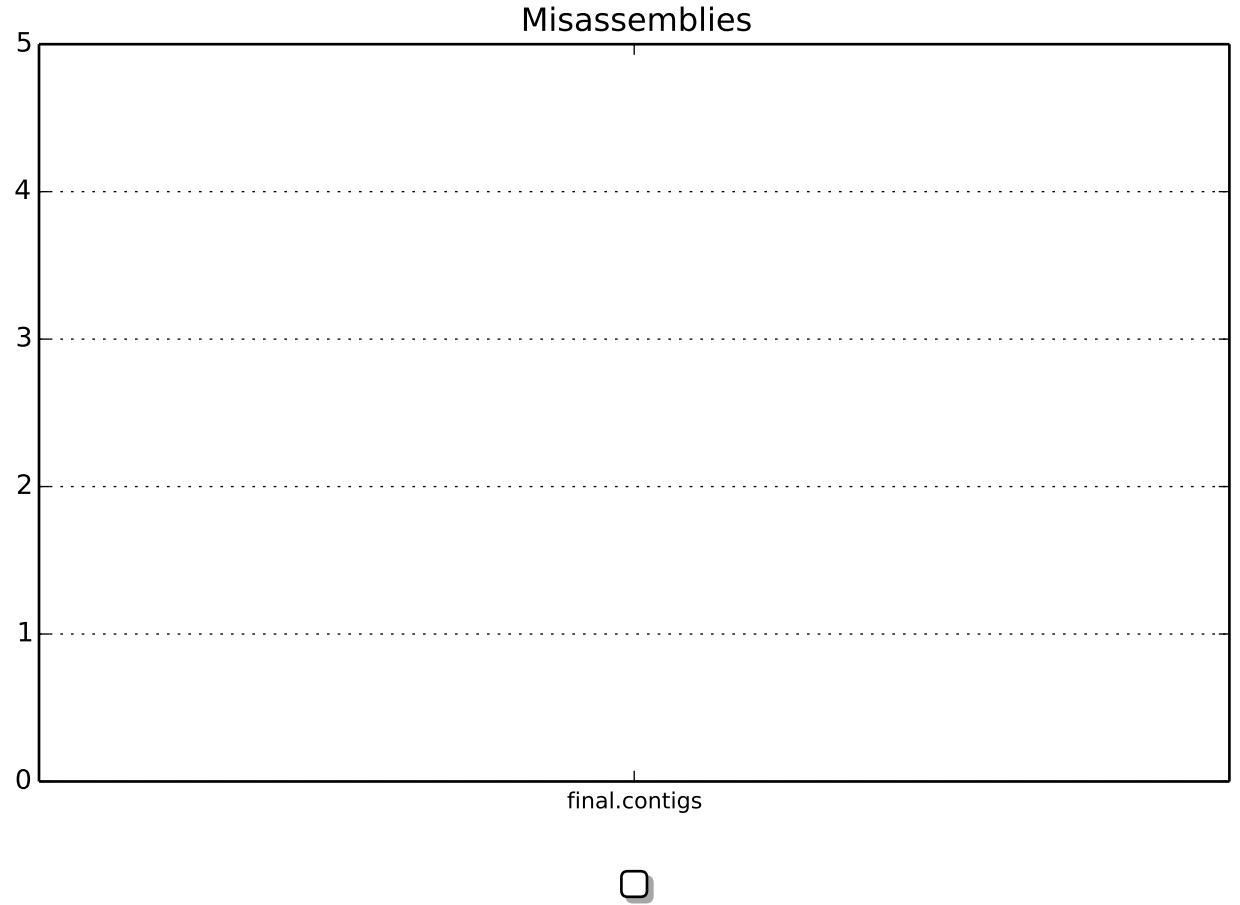
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

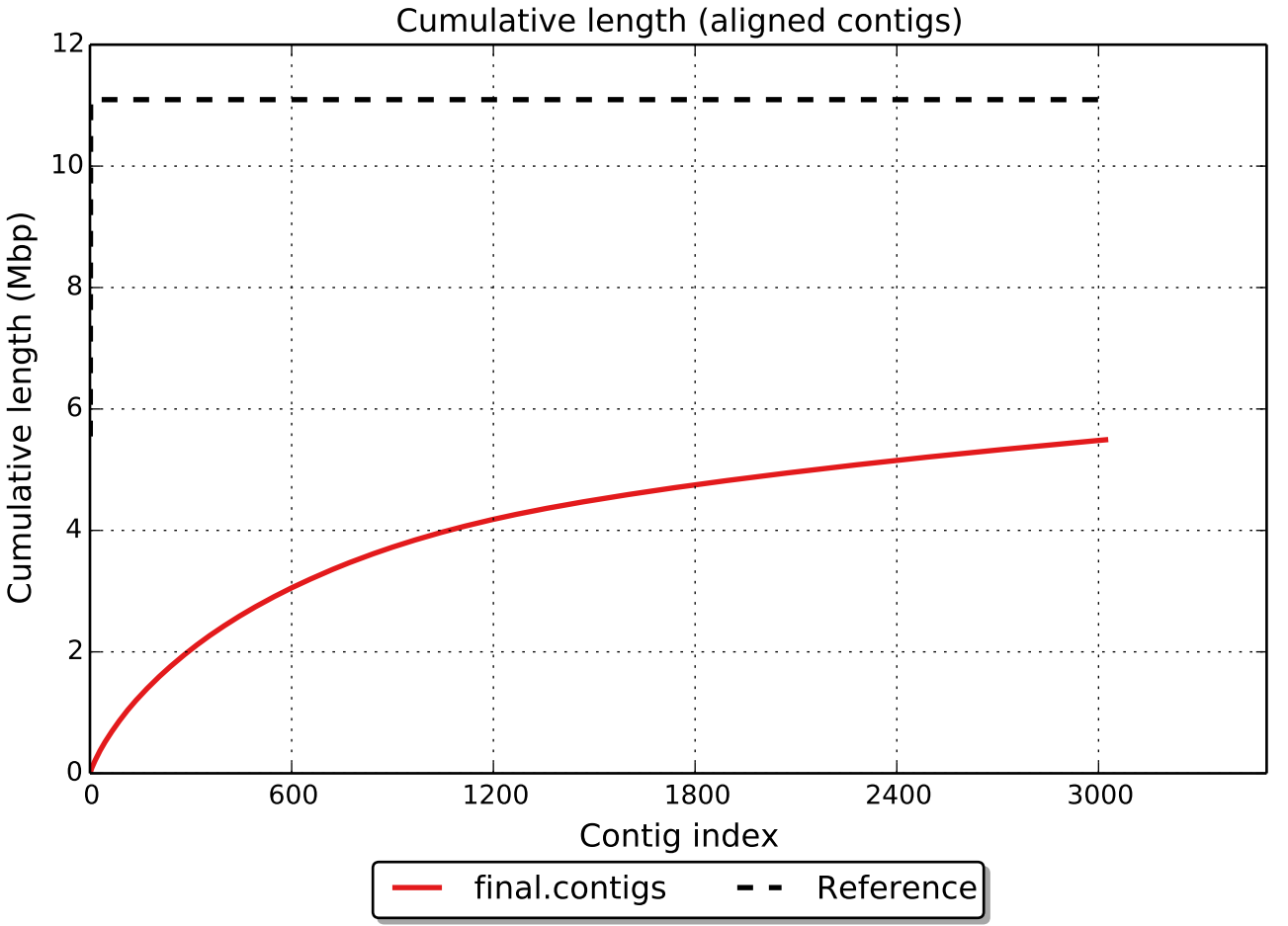

Cumulative length
Cumulative length (Mbp)
0
2
4
6
8
10
12
0
600
1200
1800
2400
3000
Contig index
final.contigs
Reference

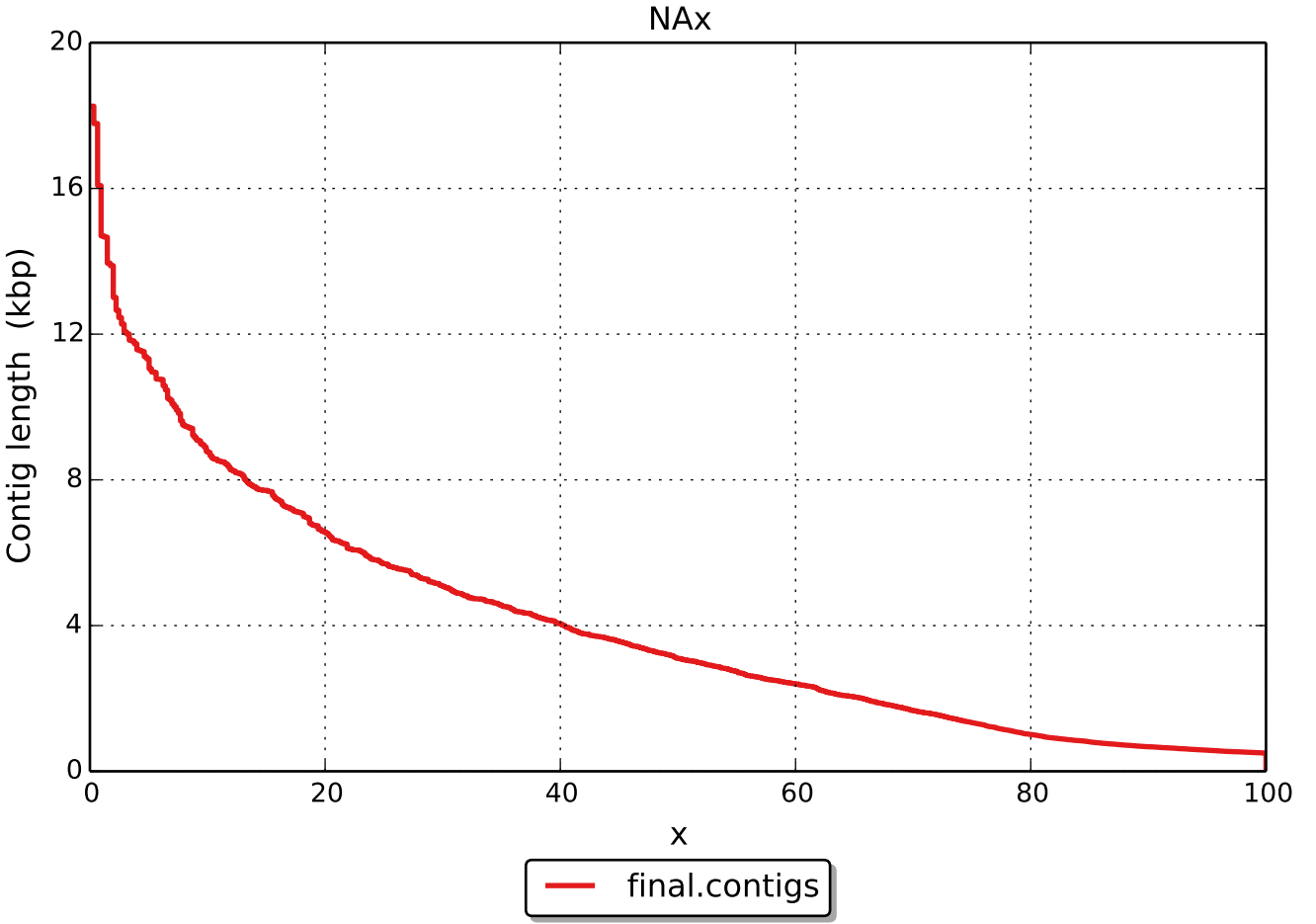

GC content
windows
6000
4000
2000
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

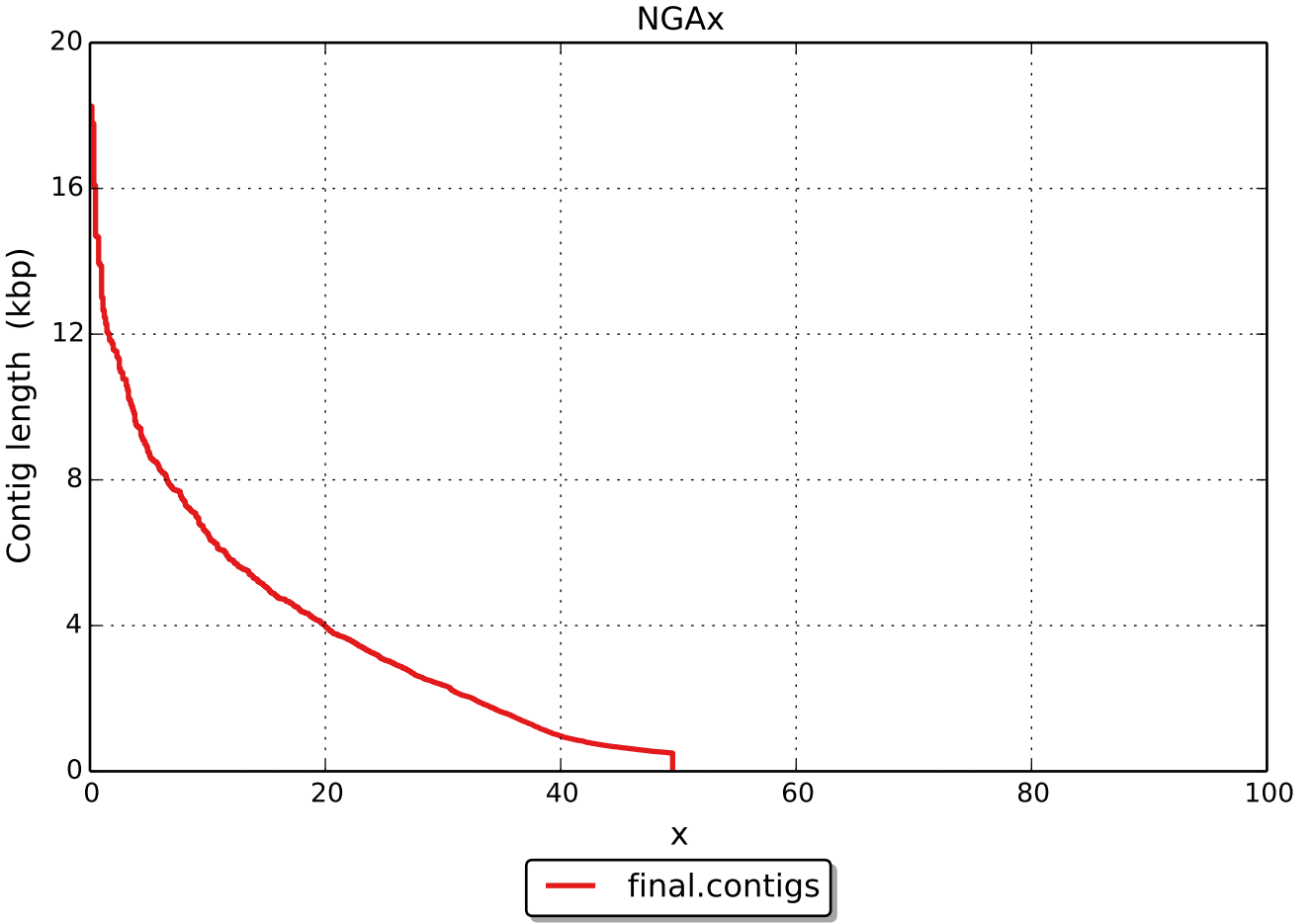

Nx
Contig length (kbp)
20
16
12
8
4
0
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
20
16
12
8
4
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
2
4
6
8
10
12
0
600
1200
1800
2400
3000
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
20
16
12
8
4
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
20
16
12
8
4
0
0
20
40
60
80
100
x
final.contigs