Report

	final.contigs
# contigs (>= 0 bp)	1720
# contigs (>= 1000 bp)	1089
Total length (>= 0 bp)	10896284
Total length (>= 1000 bp)	10635632
# contigs	1259
Largest contig	67238
Total length	10754558
Reference length	10957366
GC (%)	50.39
Reference GC (%)	50.49
N50	17117
NG50	16605
N75	8418
NG75	8032
L50	197
LG50	203
L75	427
LG75	445
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 1 part
Unaligned length	50
Genome fraction (%)	97.307
Duplication ratio	1.009
# N's per 100 kbp	0.00
# mismatches per 100 kbp	5.82
# indels per 100 kbp	0.02
Largest alignment	67238
NA50	17117
NGA50	16605
NA75	8418
NGA75	8032
LA50	197
LGA50	203
LA75	427
LGA75	445

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

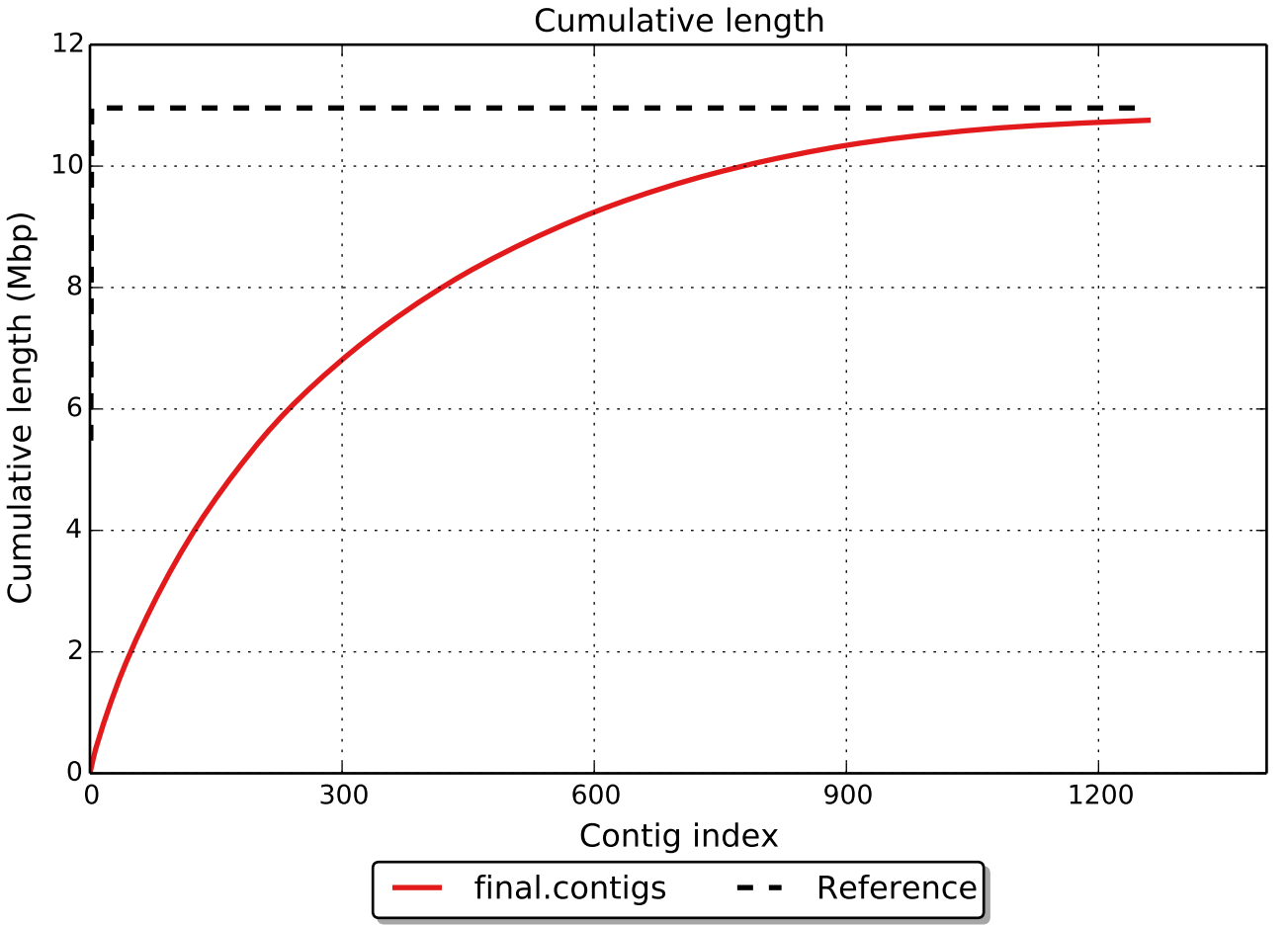
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	621
# indels	2
# short indels	0
# long indels	2
Indels length	24

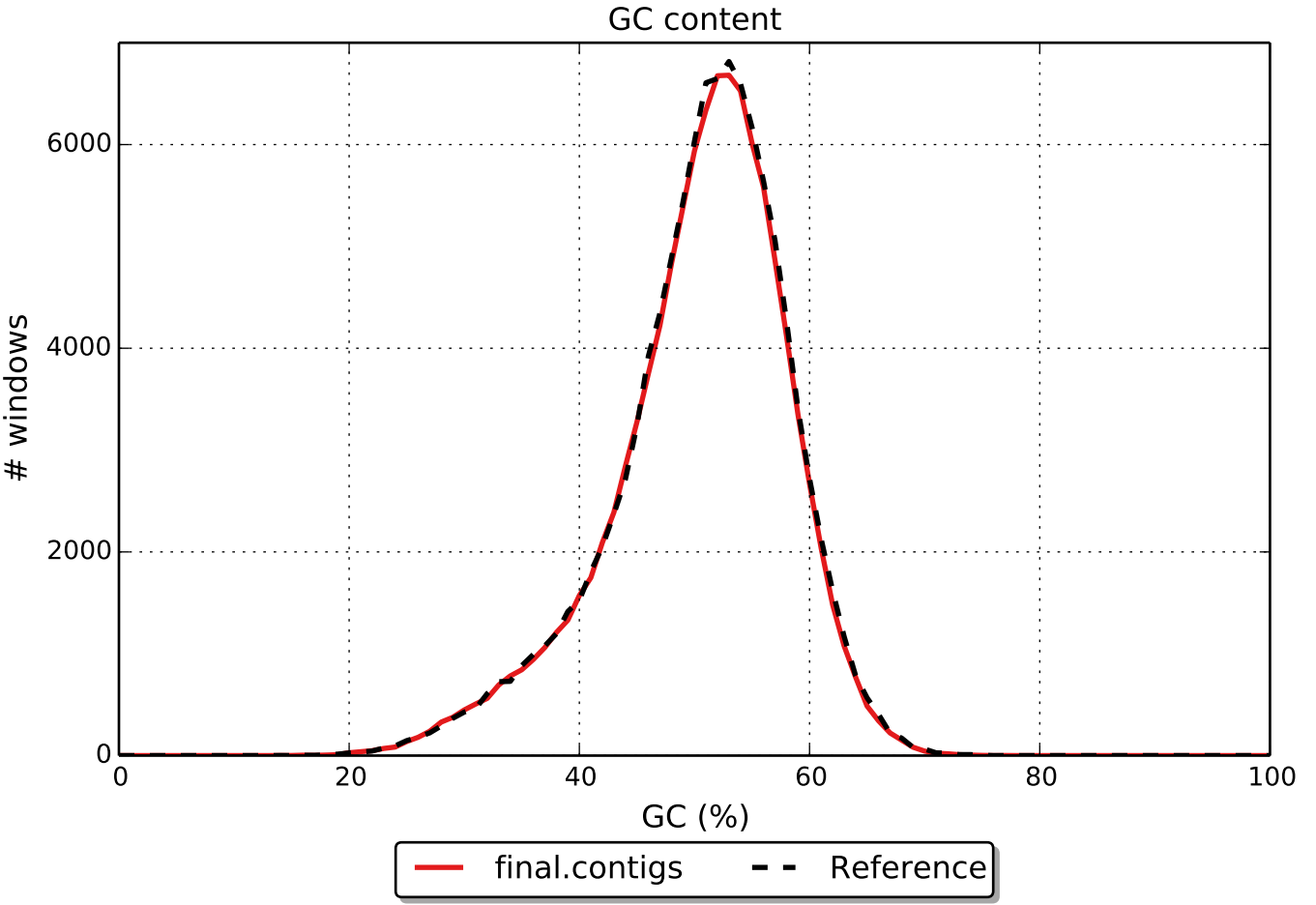
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

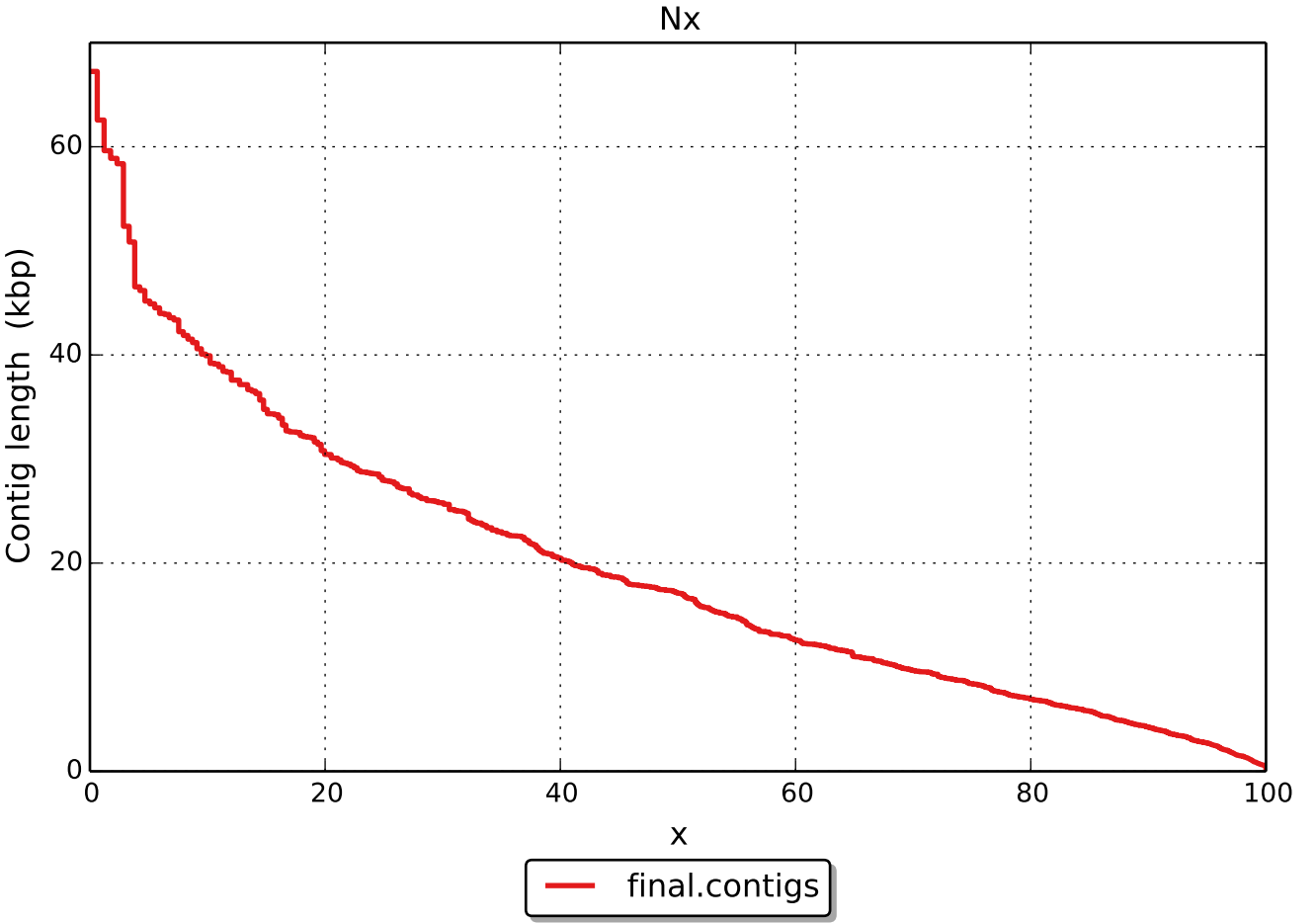
Unaligned report

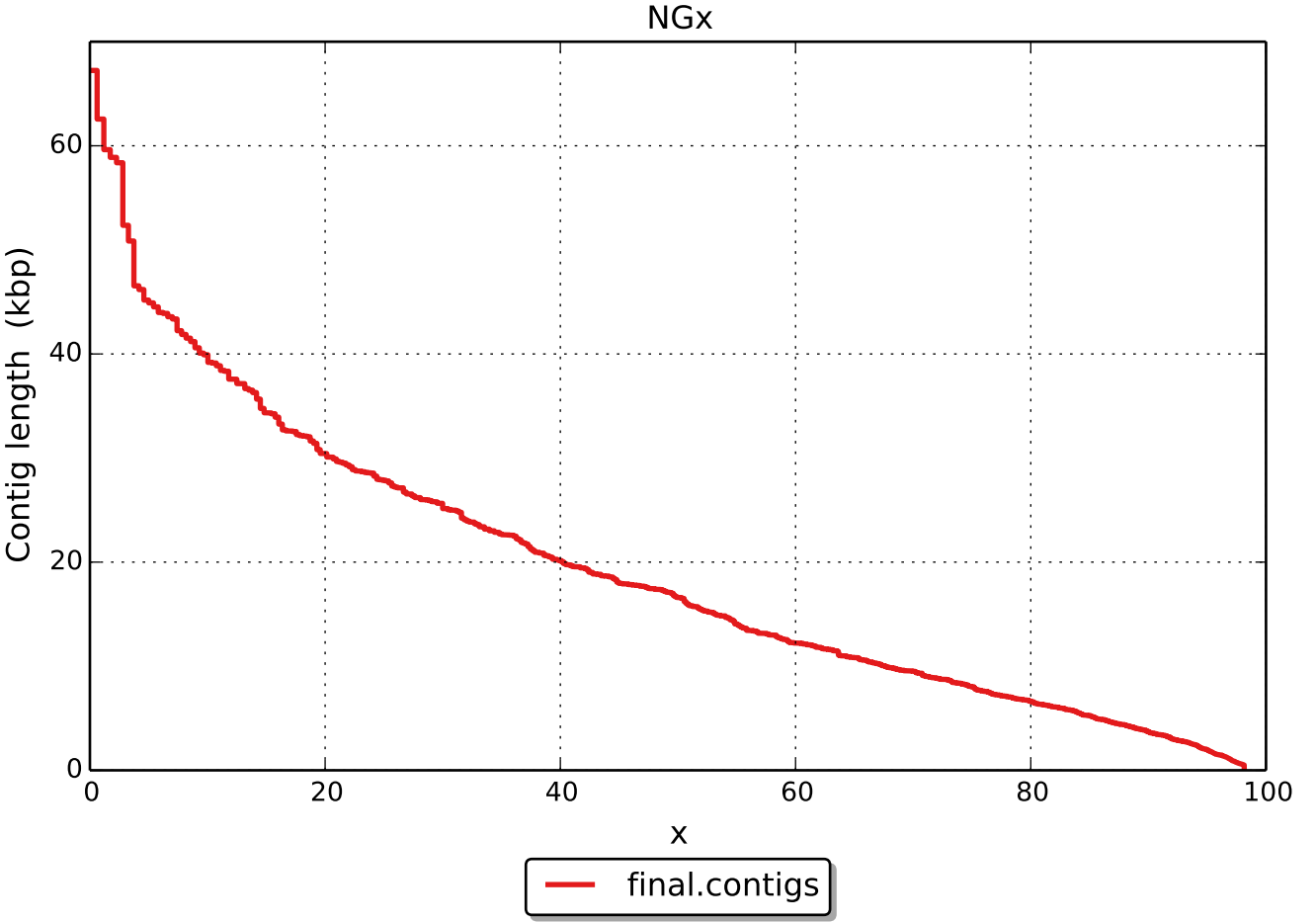
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	50
# N's	0

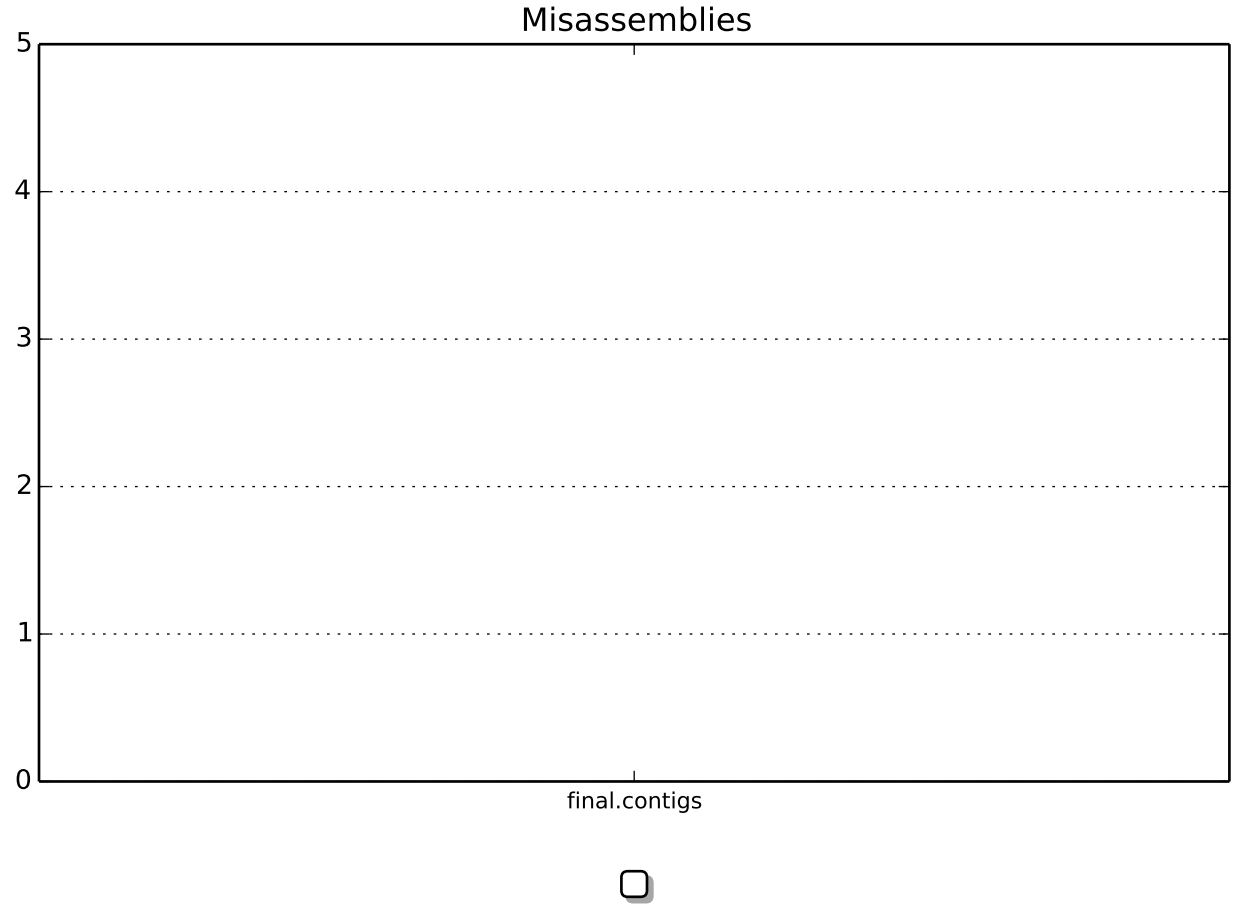
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

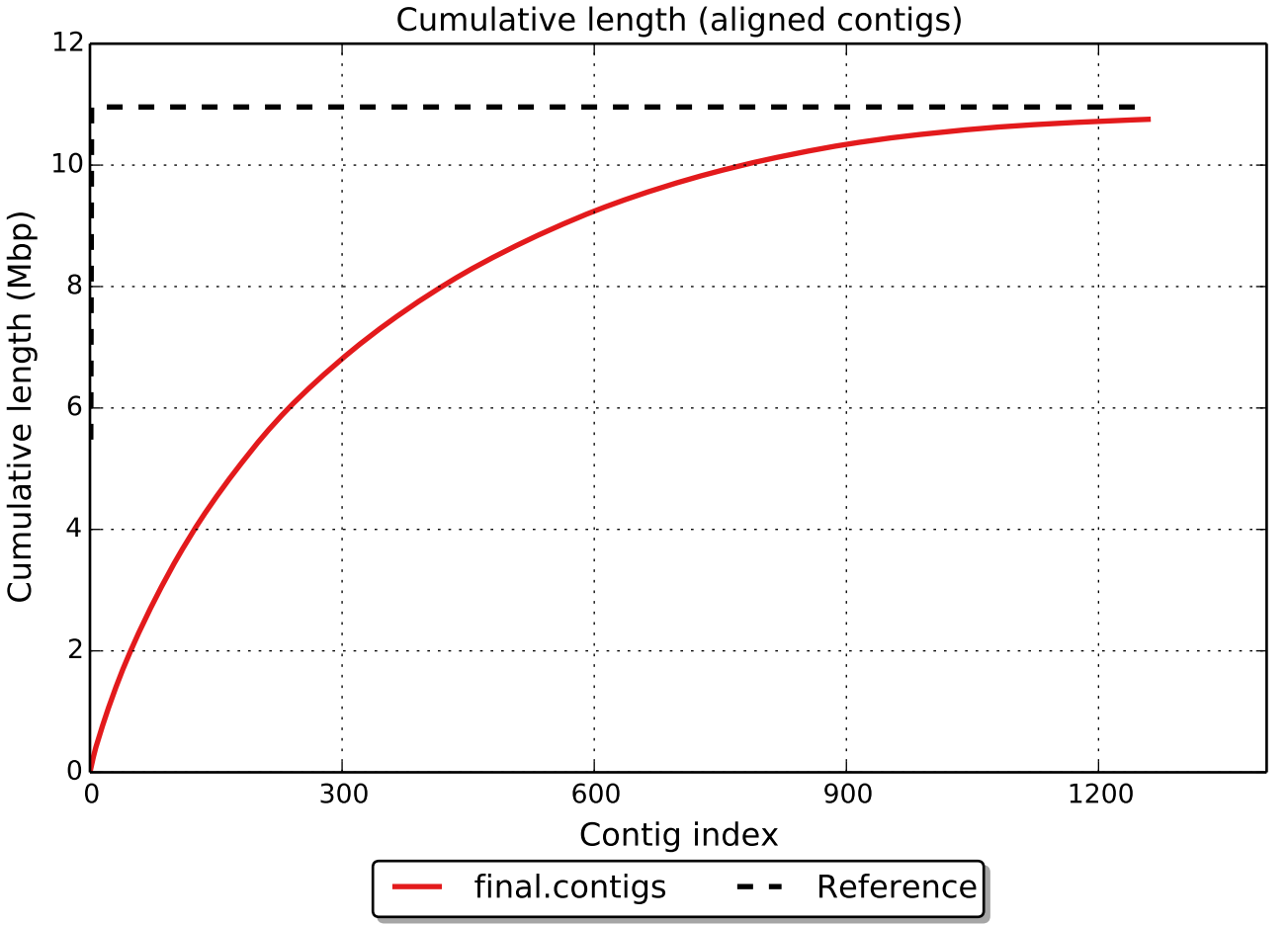

Cumulative length
Cumulative length (Mbp)
0
2
4
6
8
10
12
0
300
600
900
1200
Contig index
final.contigs
Reference

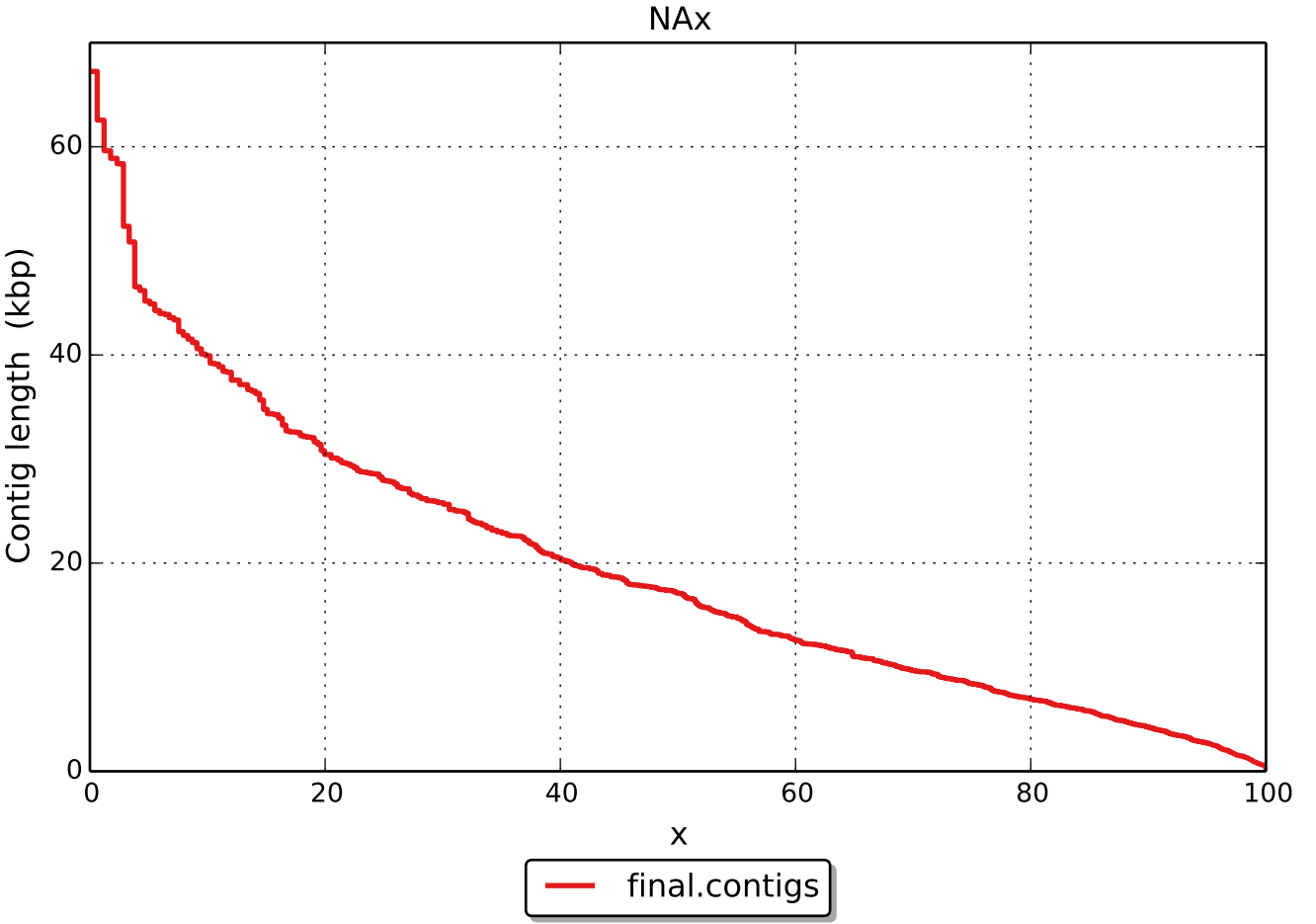

GC content
windows
GC (%)
0
2000
4000
6000
0
20
40
60
80
100
final.contigs
Reference

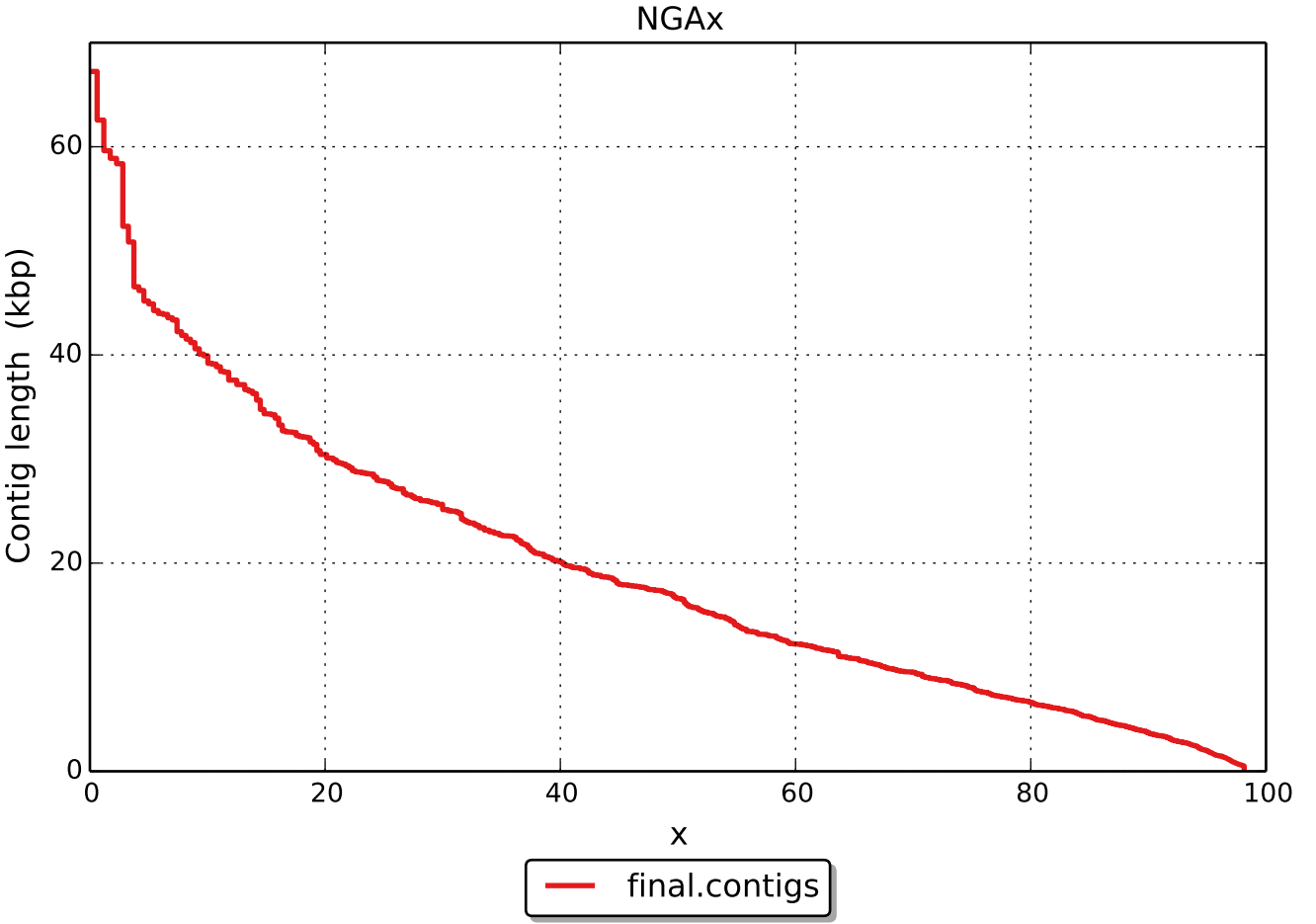

Nx
Contig length (kbp)
0
20
40
60
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
0
20
40
60
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
300
600
900
1200
Contig index
final.contigs
Reference


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


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