Report

	final.contigs
# contigs (>= 0 bp)	738
# contigs (>= 1000 bp)	593
Total length (>= 0 bp)	3756986
Total length (>= 1000 bp)	3689909
# contigs	638
Largest contig	37555
Total length	3726052
Reference length	3785550
GC (%)	32.25
Reference GC (%)	32.26
N50	9000
NG50	8978
N75	4921
NG75	4882
L50	127
LG50	130
L75	266
LG75	275
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	97.220
Duplication ratio	1.012
# N's per 100 kbp	0.00
# mismatches per 100 kbp	6.39
# indels per 100 kbp	0.00
Largest alignment	37555
NA50	9000
NGA50	8978
NA75	4921
NGA75	4882
LA50	127
LGA50	130
LA75	266
LGA75	275

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

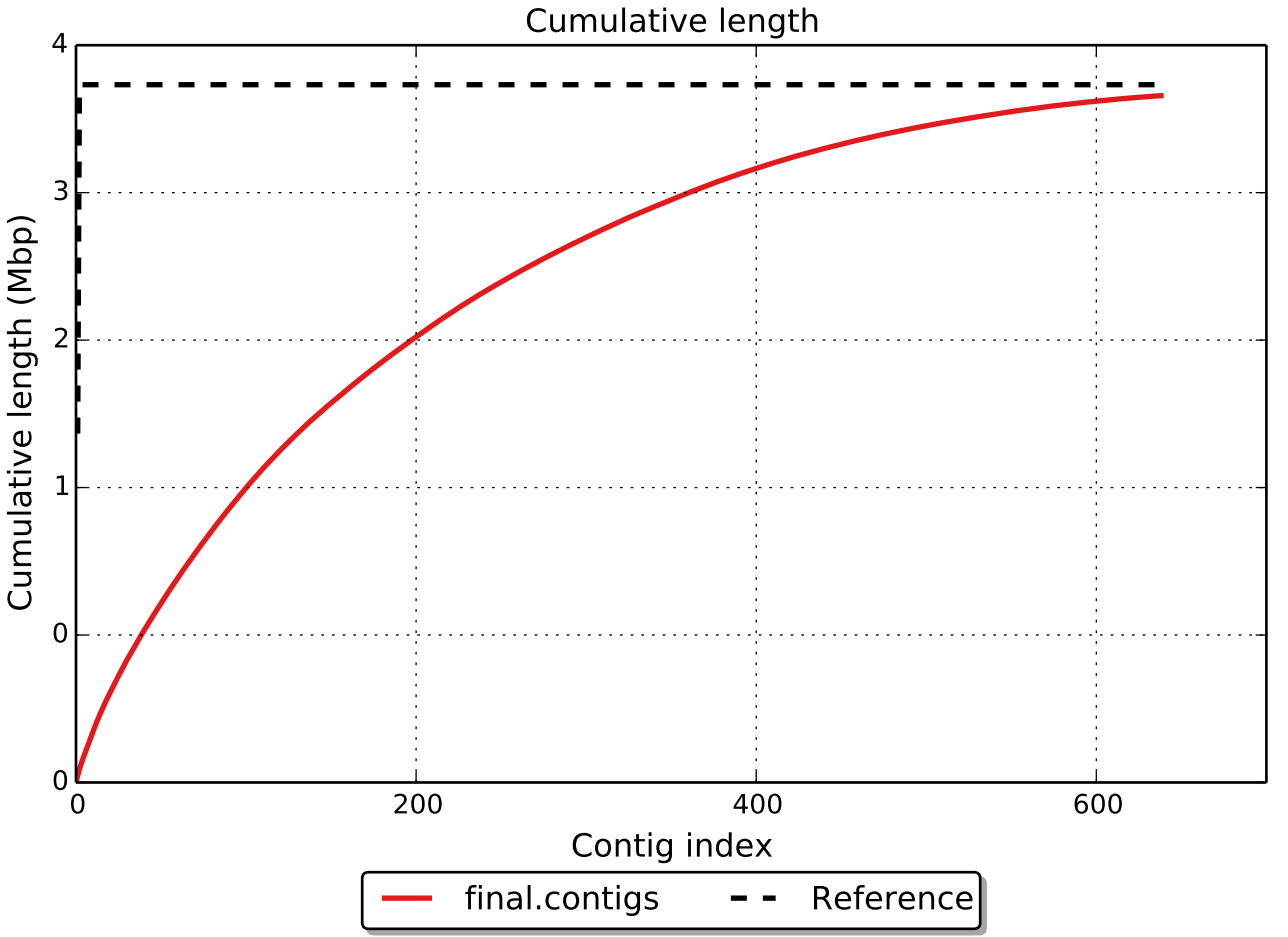
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	235
# indels	0
# short indels	0
# long indels	0
Indels length	0

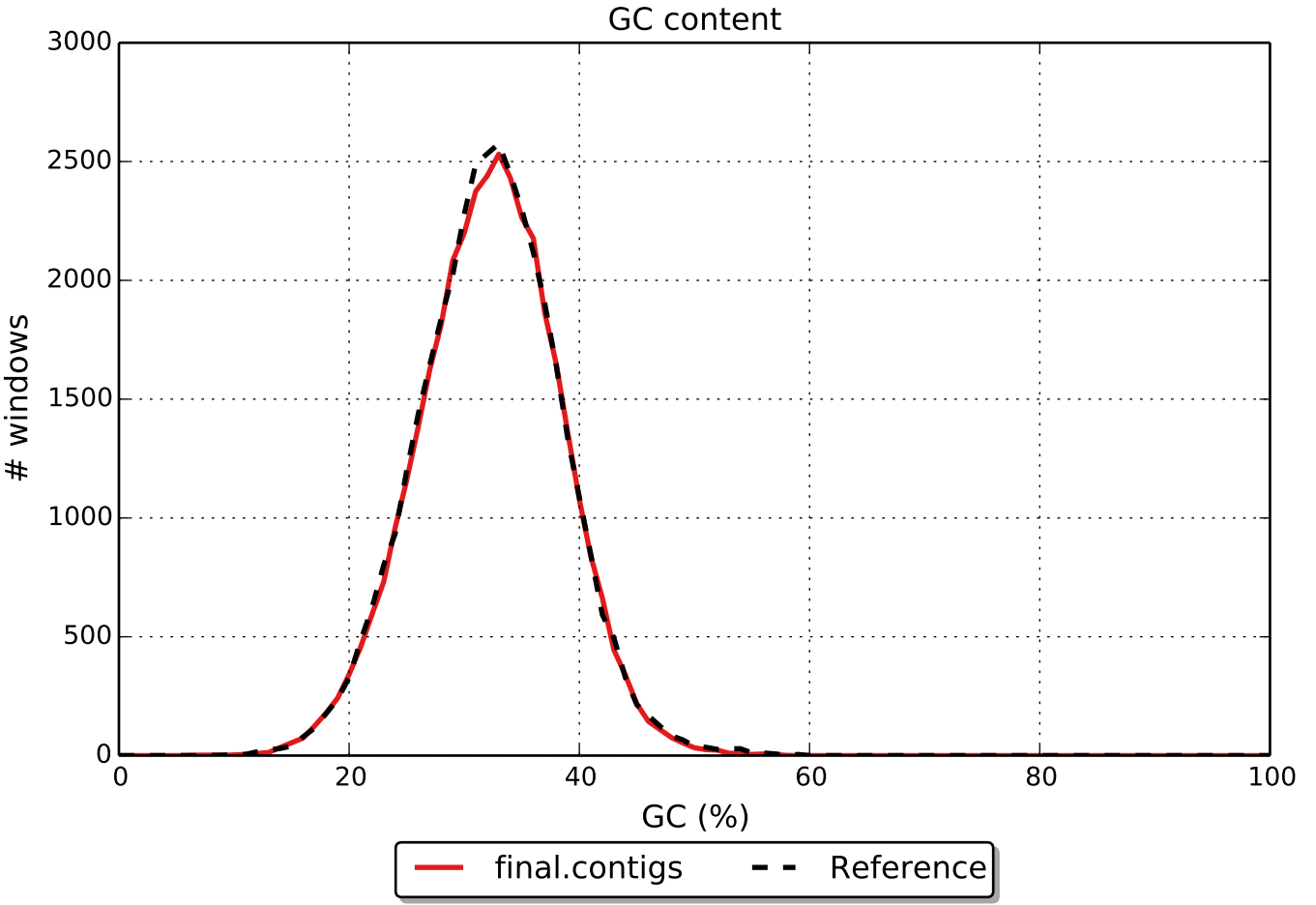
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

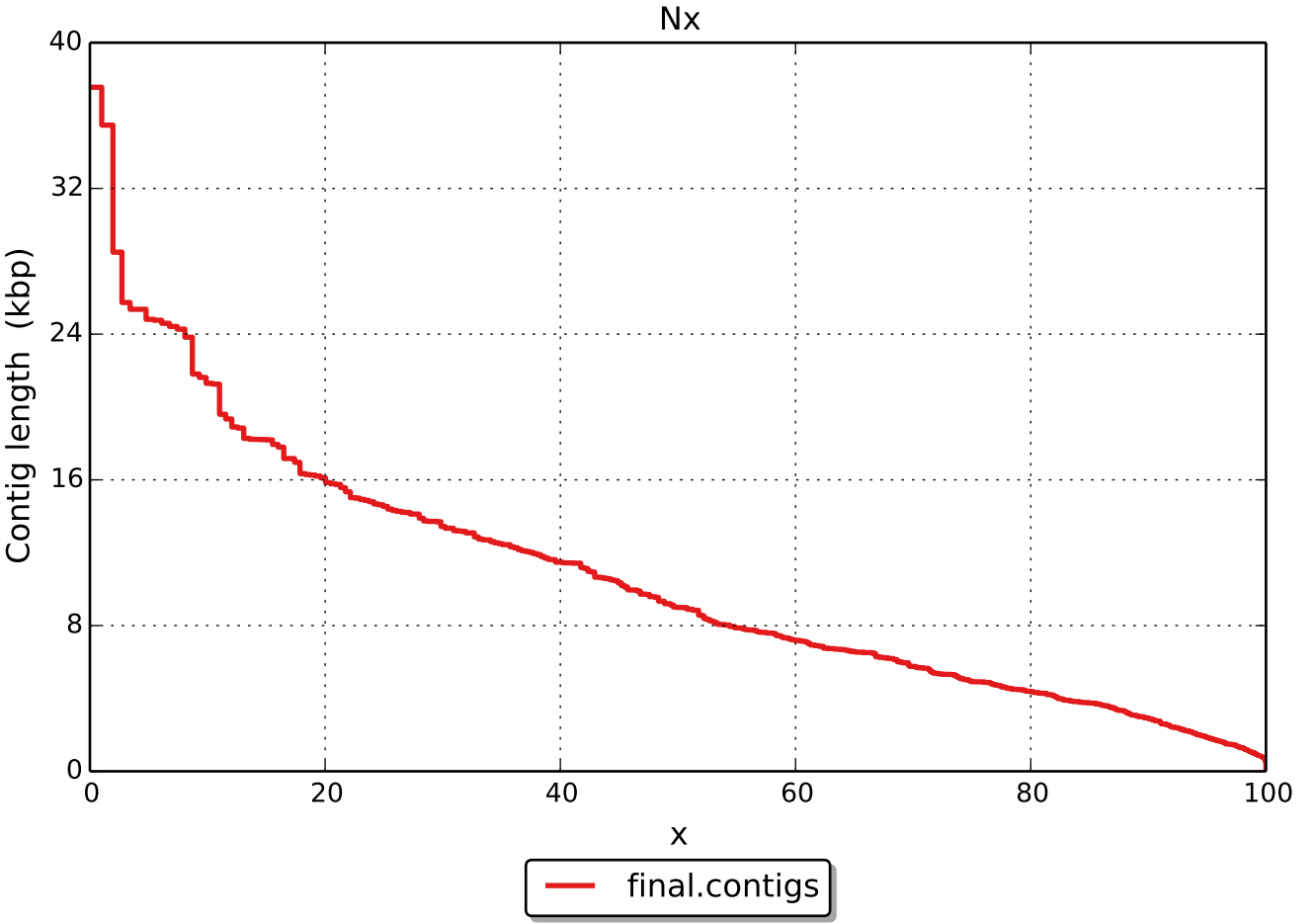
Unaligned report

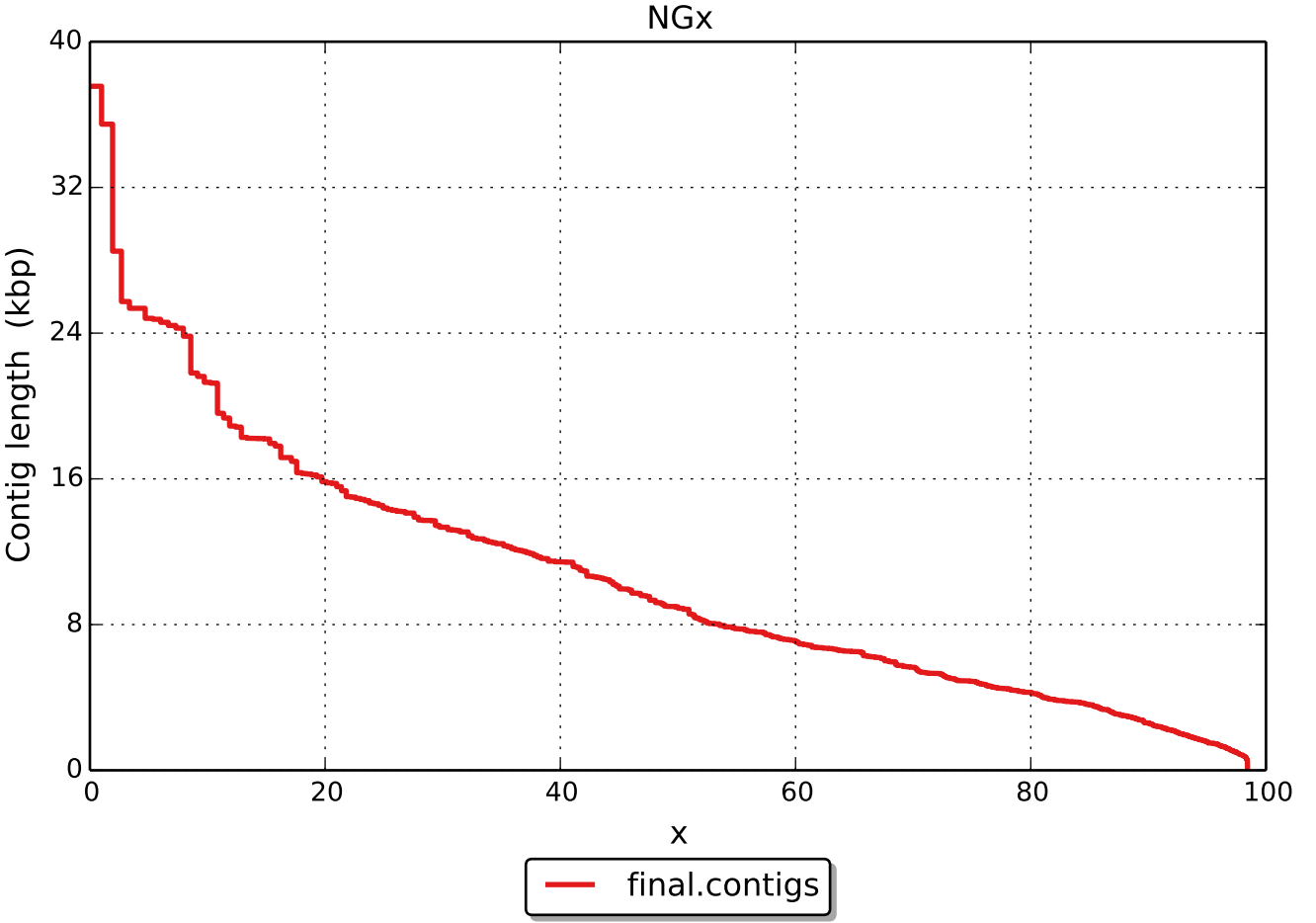
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

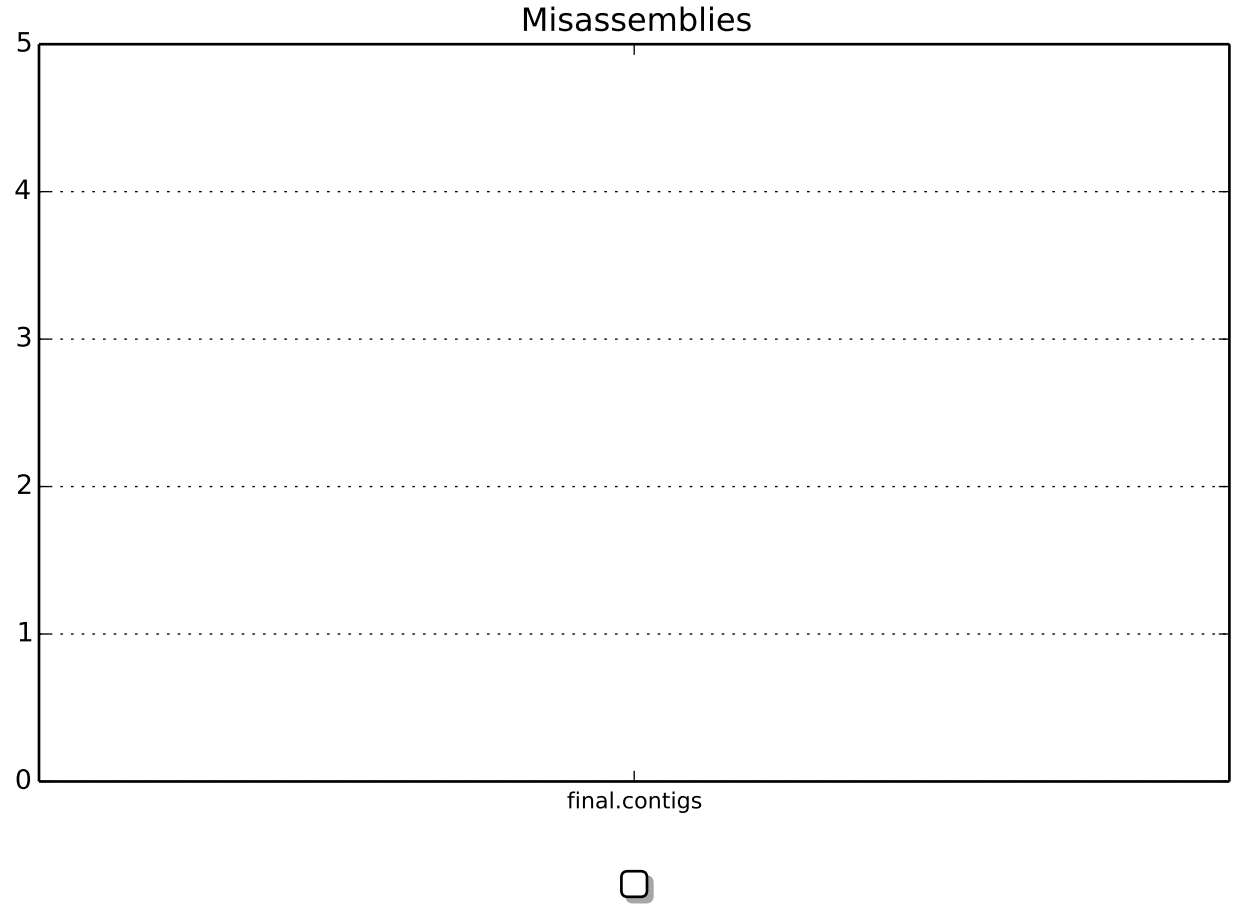
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

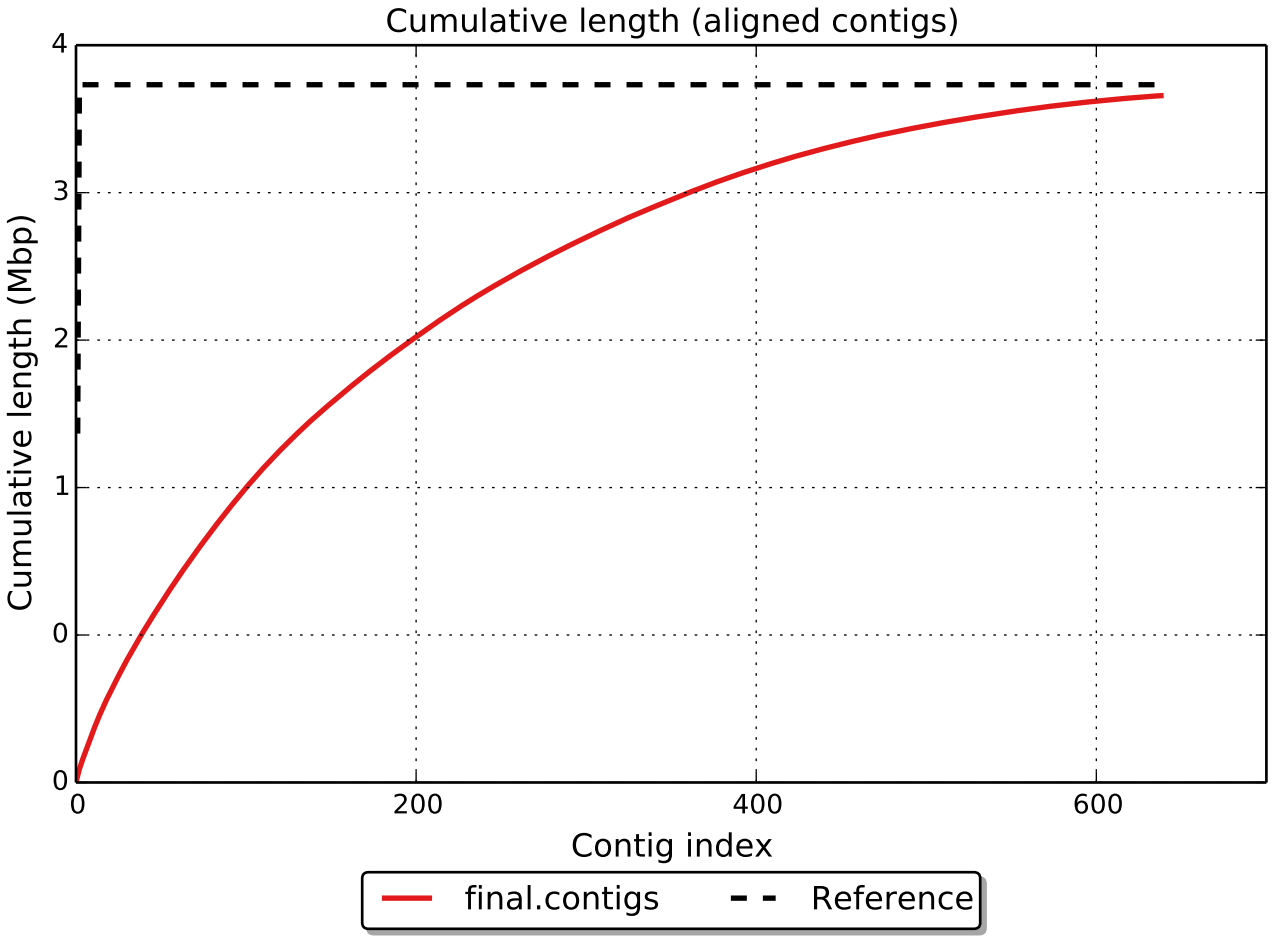

Cumulative length
Cumulative length (Mbp)
4
3
2
1
0
0
200
400
600
Contig index
final.contigs
Reference

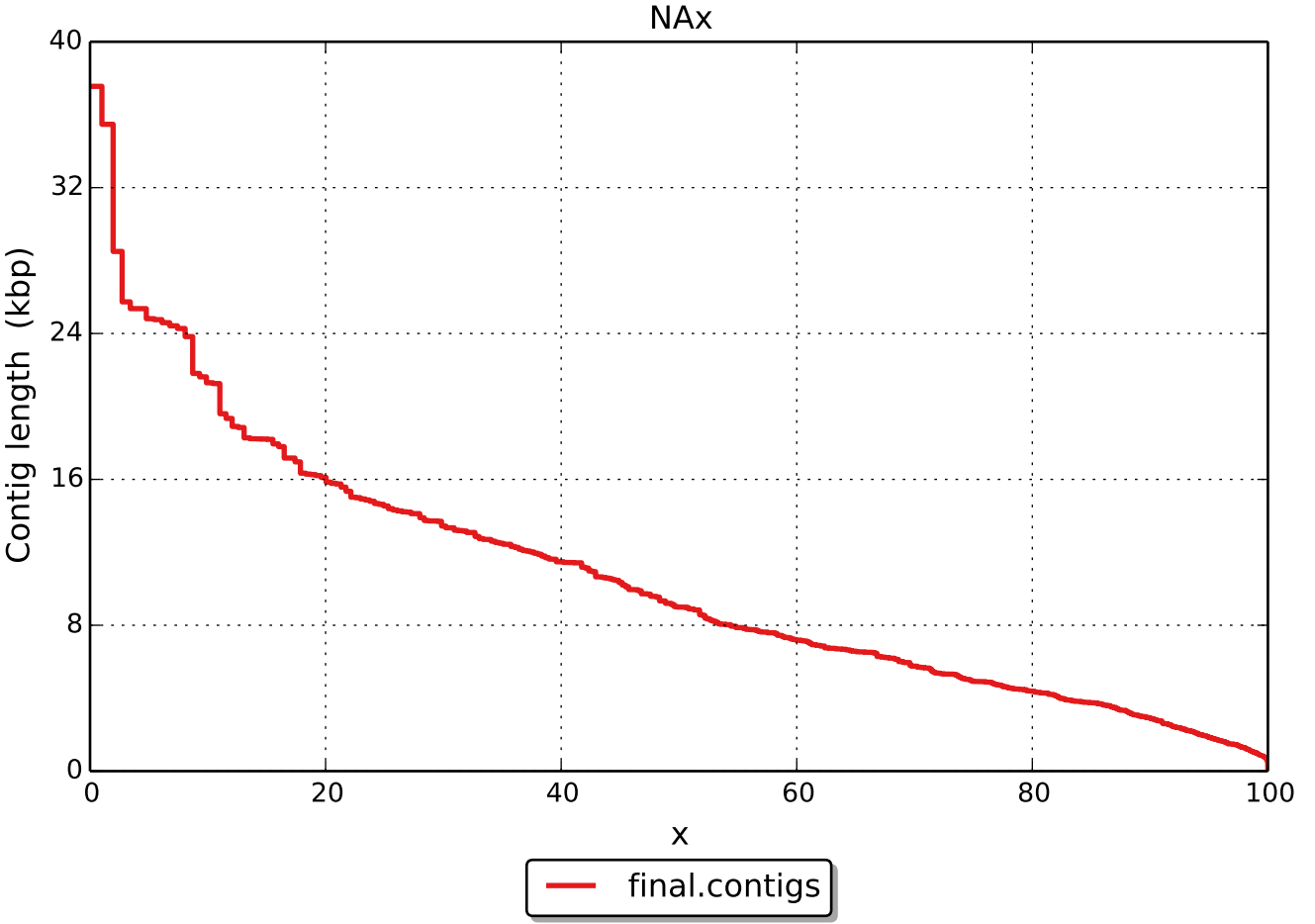

GC content
3000
2500
2000
1500
1000
500
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

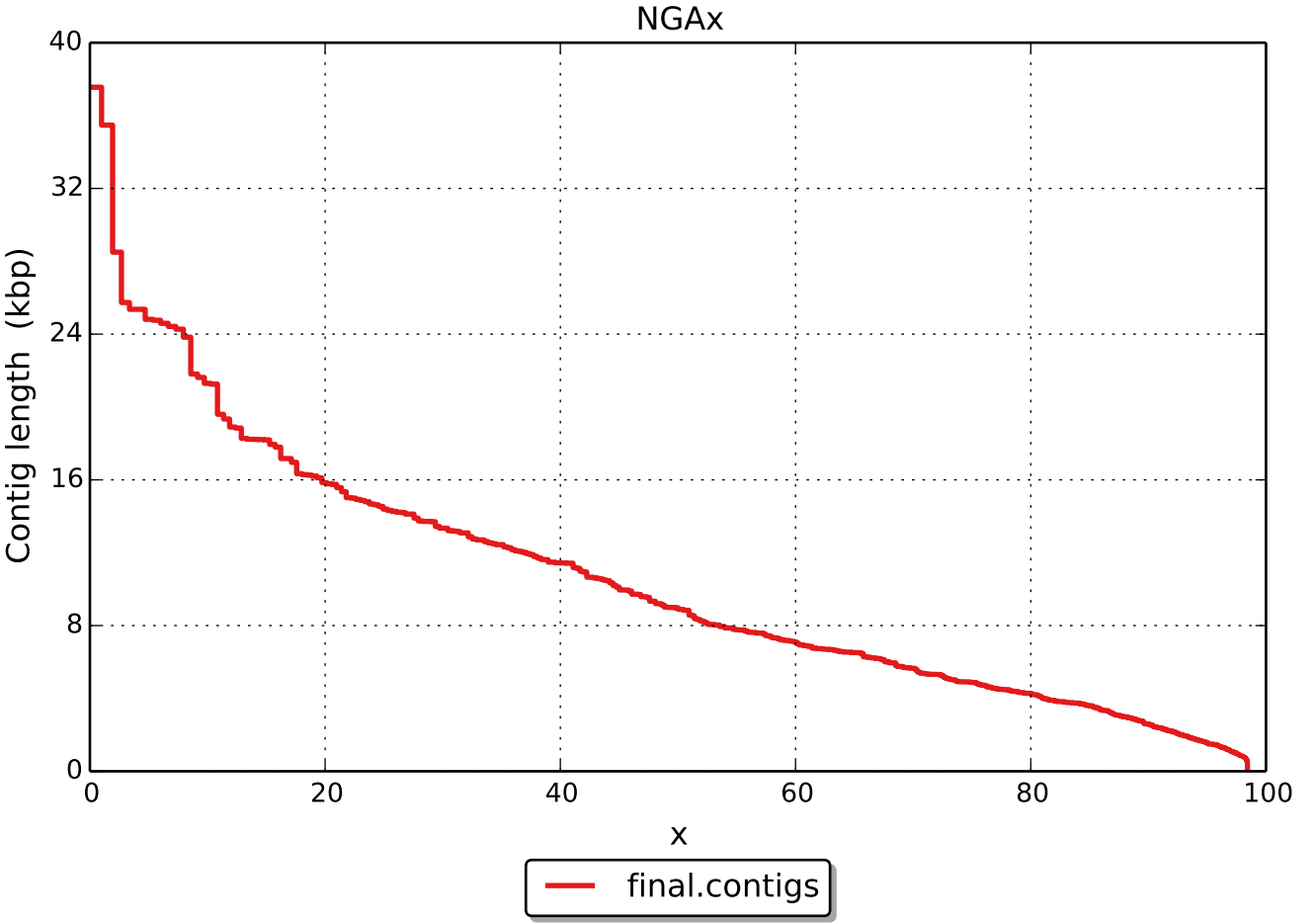

Nx
Contig length (kbp)
40
32
24
16
8
0
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
40
32
24
16
8
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)
Contig index
0
1
2
3
4
0
200
400
600
final.contigs
Reference


NAx
Contig length (kbp)
40
32
24
16
8
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
40
32
24
16
8
0
0
20
40
60
80
100
x
final.contigs