Report

	final.contigs
# contigs (>= 0 bp)	521
# contigs (>= 1000 bp)	406
Total length (>= 0 bp)	5310759
Total length (>= 1000 bp)	5233349
# contigs	521
Largest contig	91538
Total length	5310759
Reference length	5547323
GC (%)	50.29
Reference GC (%)	50.48
N50	25017
NG50	22969
N75	12269
NG75	10898
L50	65
LG50	70
L75	142
LG75	157
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	0 + 3 part
Unaligned length	86847
Genome fraction (%)	93.464
Duplication ratio	1.008
# N's per 100 kbp	0.00
# mismatches per 100 kbp	20.87
# indels per 100 kbp	0.25
Largest alignment	91538
NA50	22969
NGA50	21700
NA75	11607
NGA75	10098
LA50	68
LGA50	73
LA75	149
LGA75	166

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

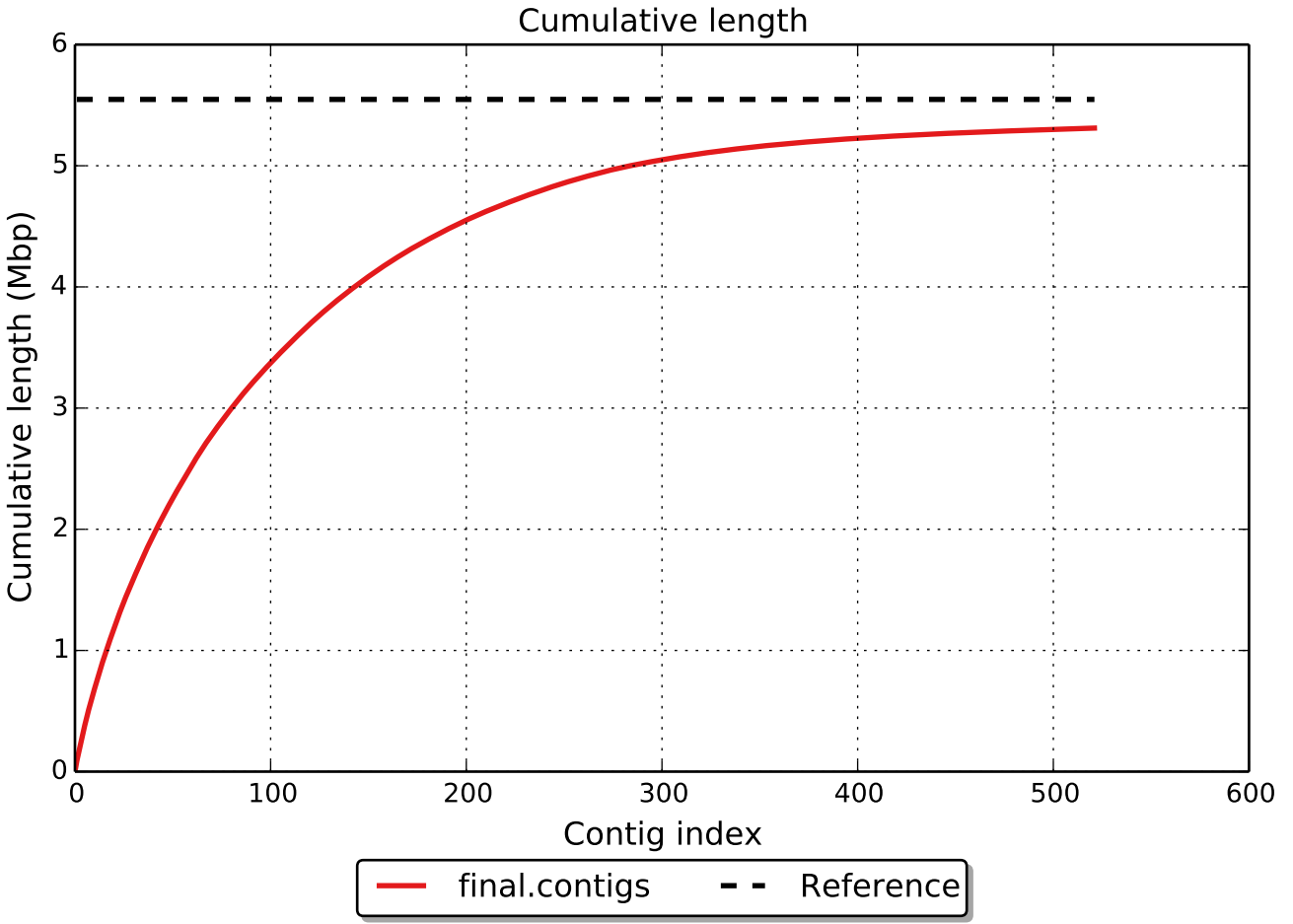
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	3
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	1082
# indels	13
# short indels	12
# long indels	1
Indels length	18

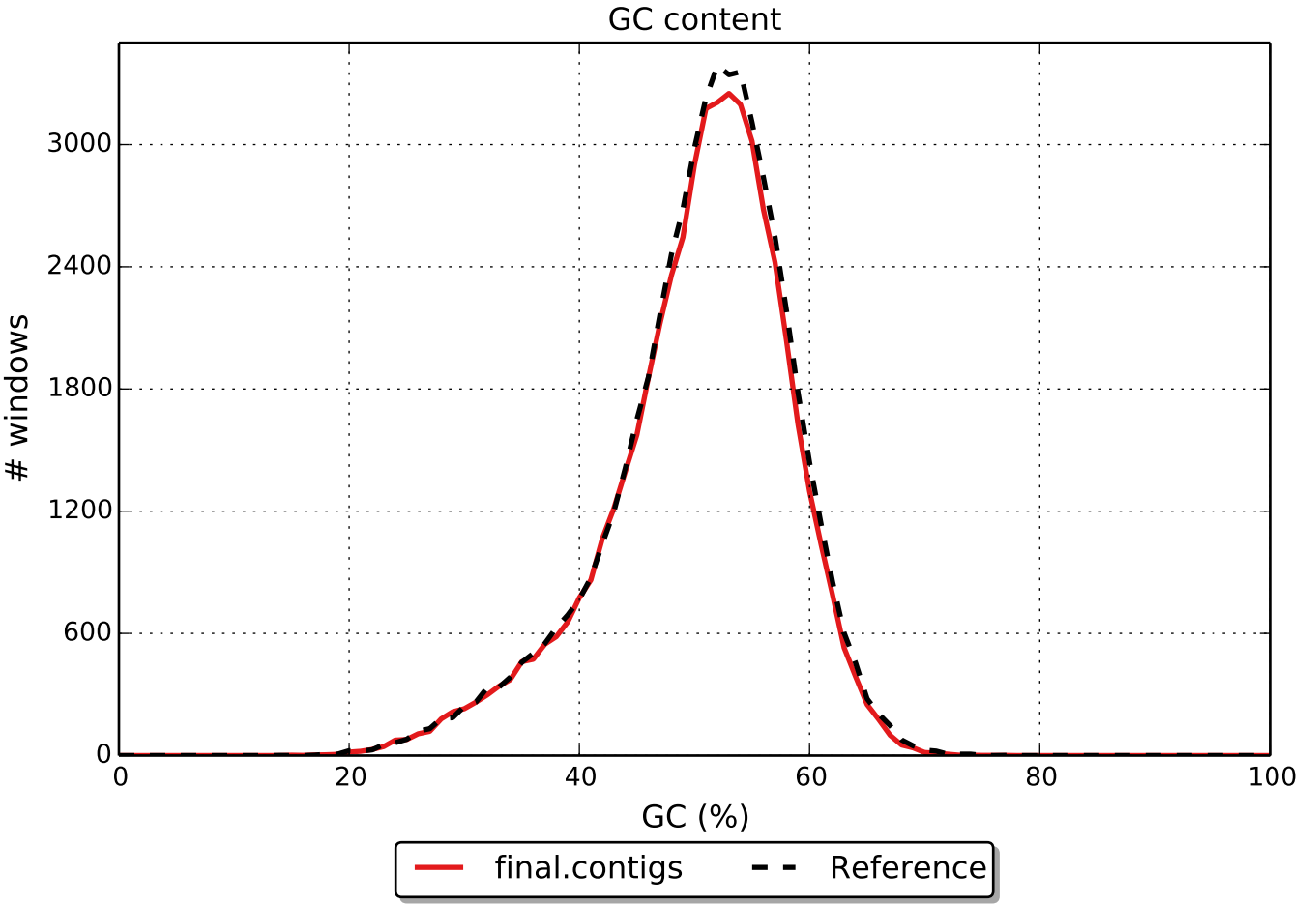
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

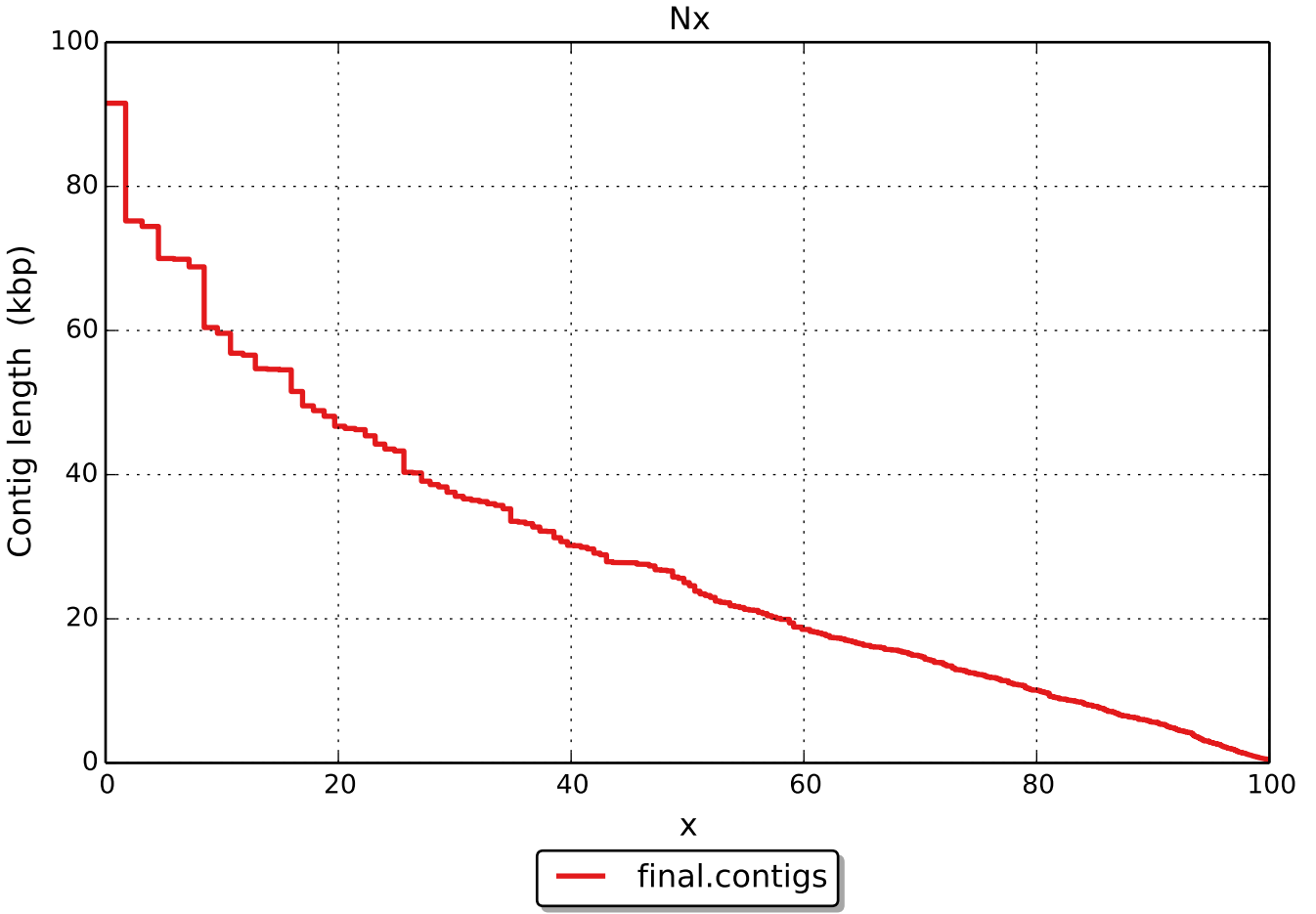
Unaligned report

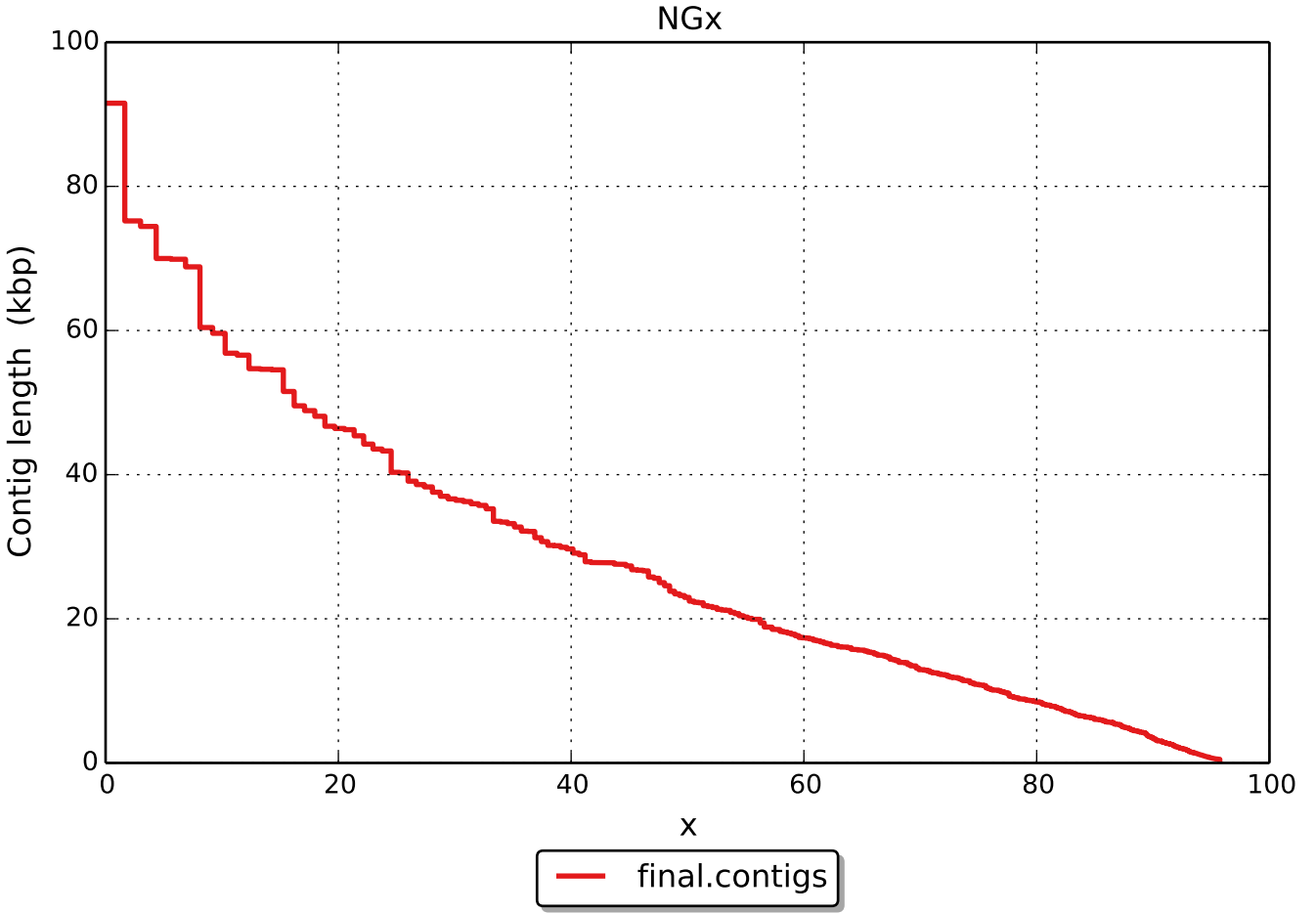
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
# with misassembly	0
# both parts are significant	3
Partially unaligned length	86847
# N's	0

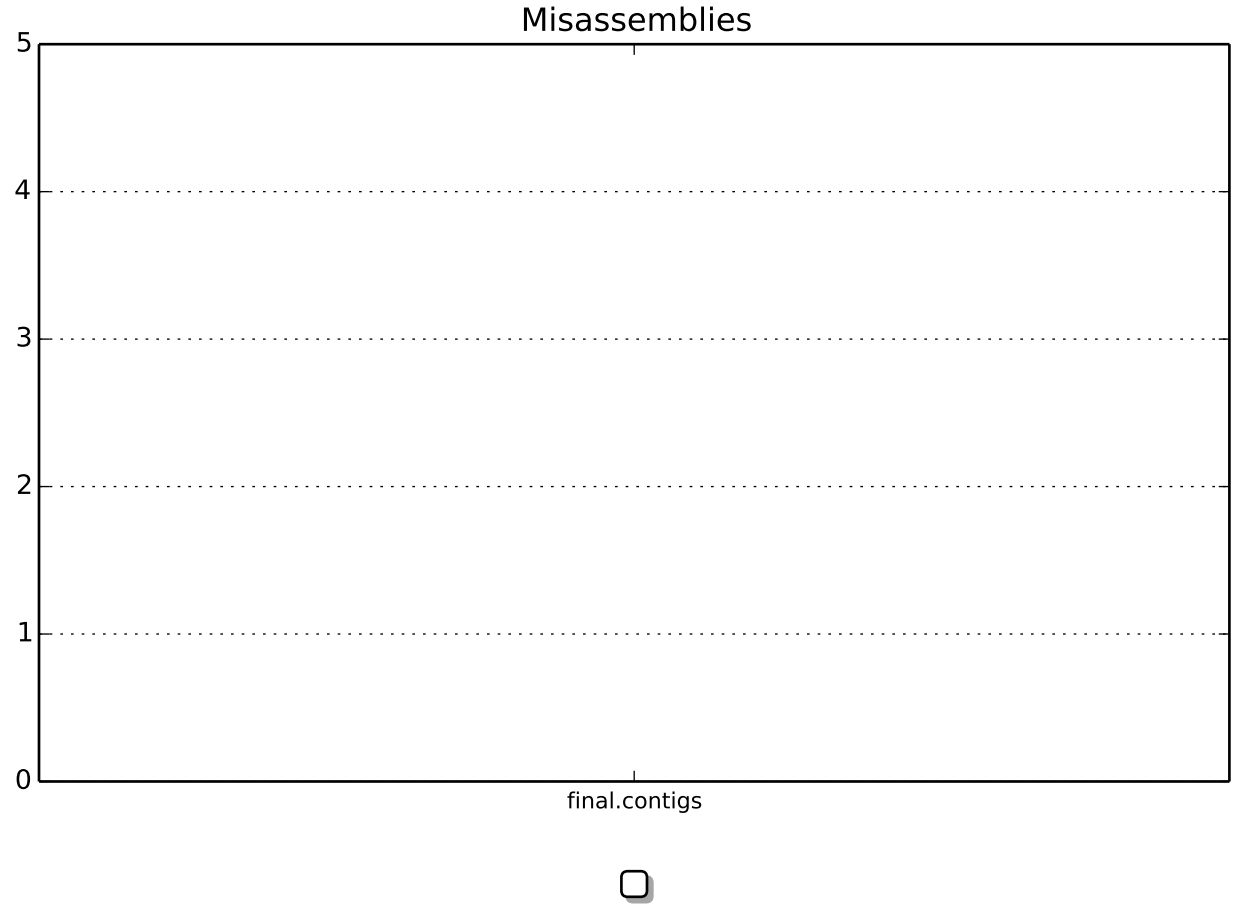
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

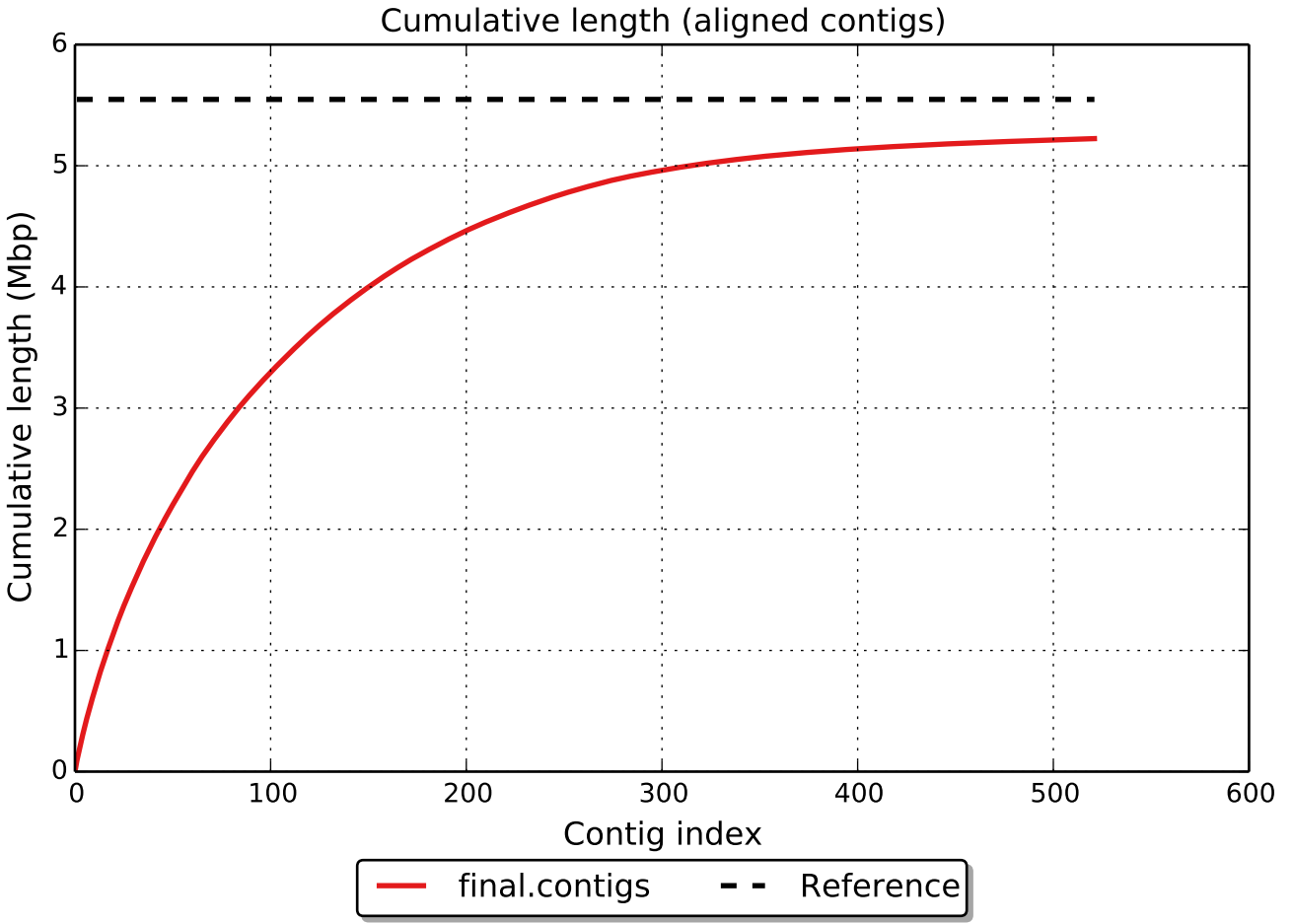

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
100
200
300
400
500
600
Contig index
final.contigs
Reference

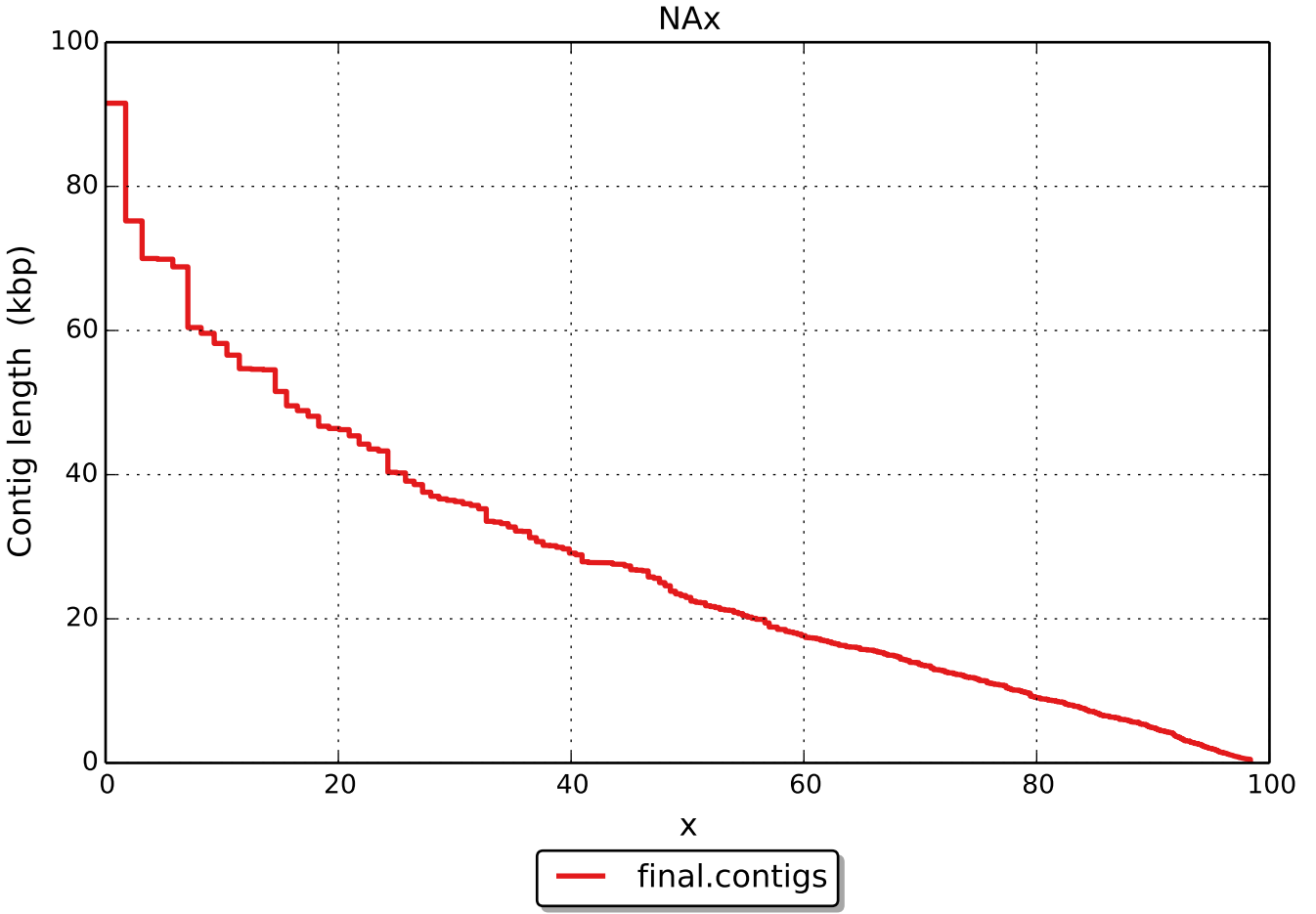

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

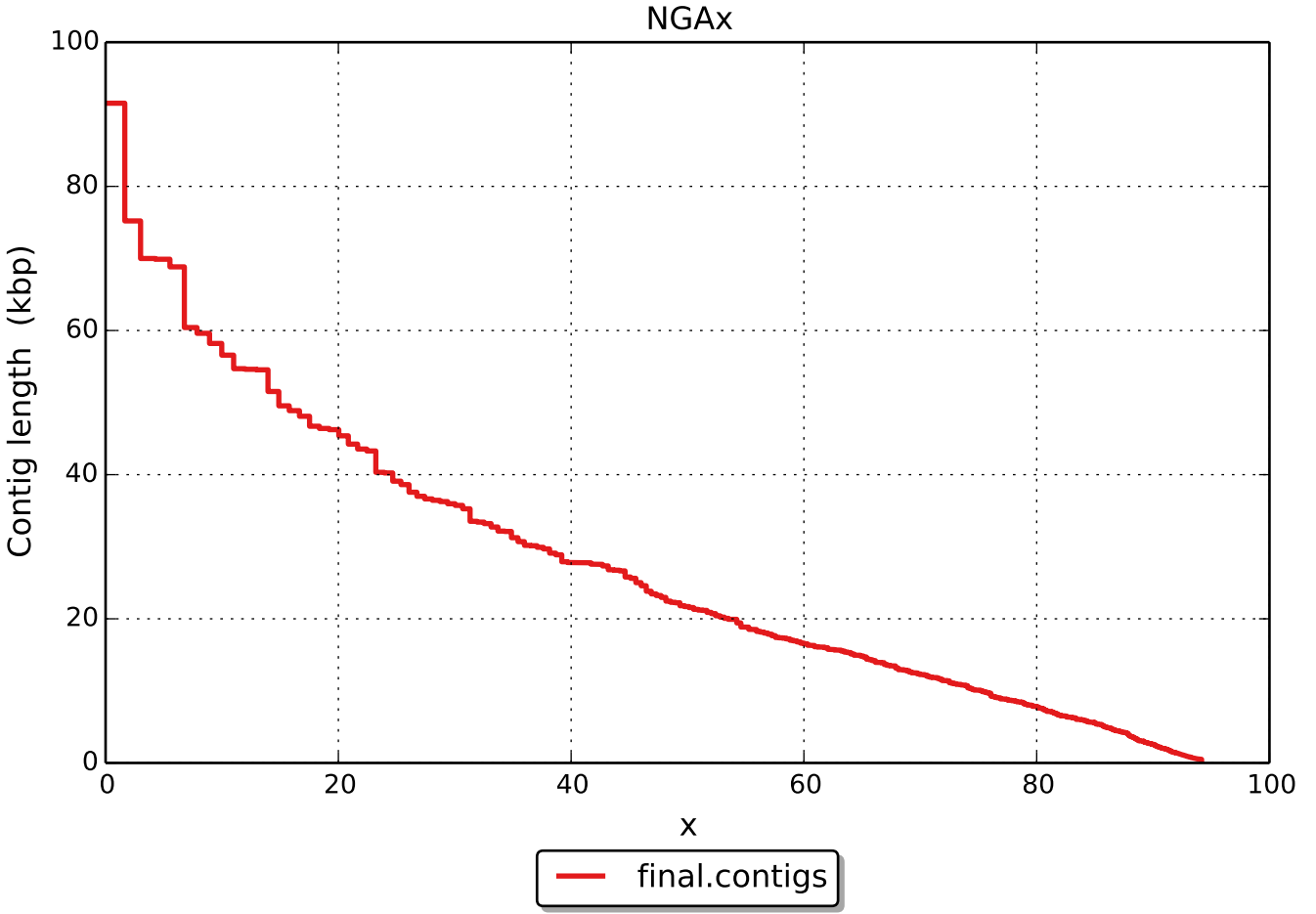

Nx
Contig length (kbp)
100
80
60
40
20
0
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
100
80
60
40
20
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
5
6
0
100
200
300
400
500
600
final.contigs
Reference


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


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