Report

	final.contigs
# contigs (>= 0 bp)	380
# contigs (>= 1000 bp)	360
Total length (>= 0 bp)	3719689
Total length (>= 1000 bp)	3703658
# contigs	380
Largest contig	61161
Total length	3719689
Reference length	1892775
GC (%)	32.25
Reference GC (%)	32.27
N50	15222
NG50	24446
N75	8940
NG75	19164
L50	78
LG50	31
L75	155
LG75	52
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	147 + 70 part
Unaligned length	1787456
Genome fraction (%)	99.953
Duplication ratio	1.021
# N's per 100 kbp	0.00
# mismatches per 100 kbp	15.59
# indels per 100 kbp	0.00
Largest alignment	61161
NA50	3612
NGA50	18798
NGA75	11795
LA50	132
LGA50	35
LGA75	69

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

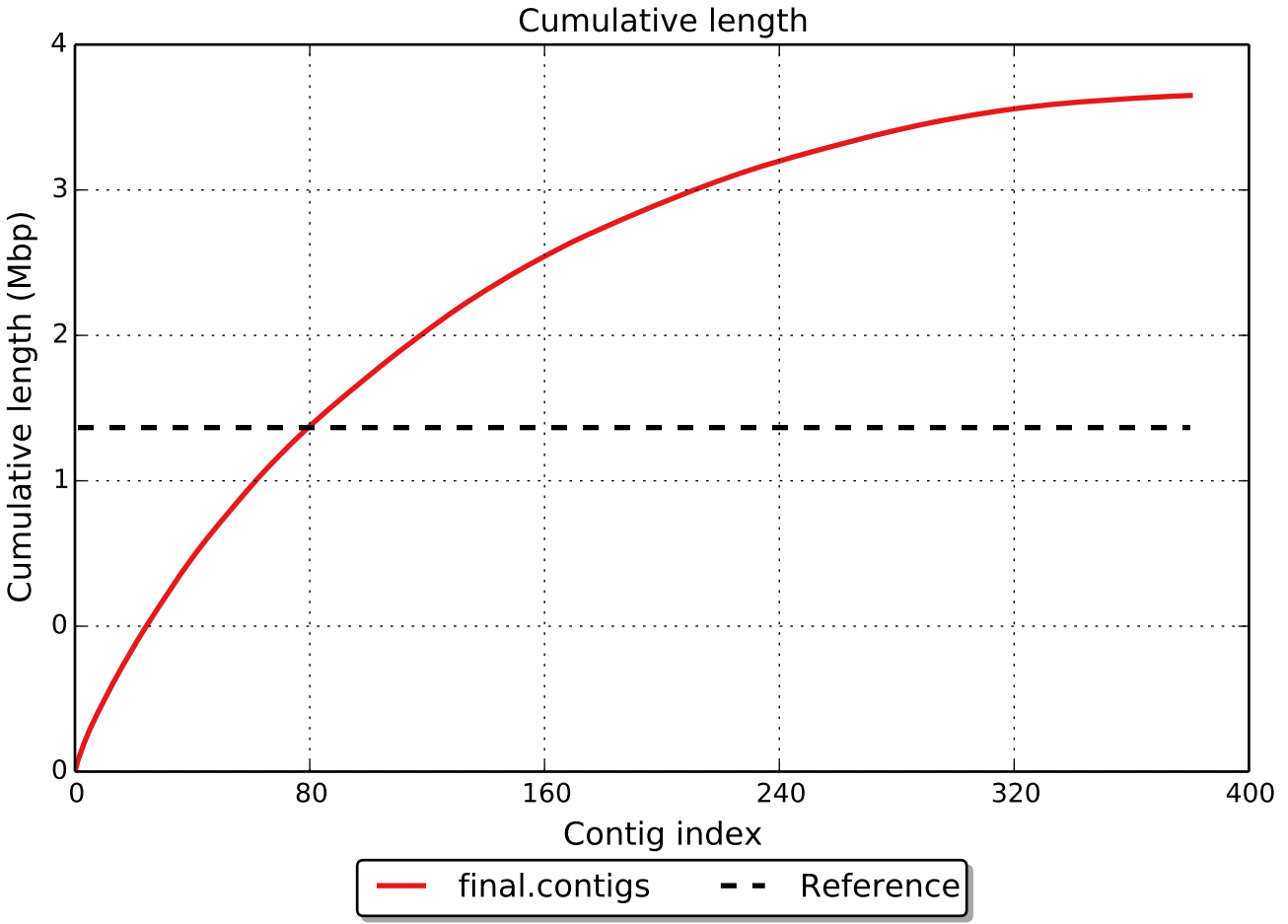
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	3
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	295
# indels	0
# short indels	0
# long indels	0
Indels length	0

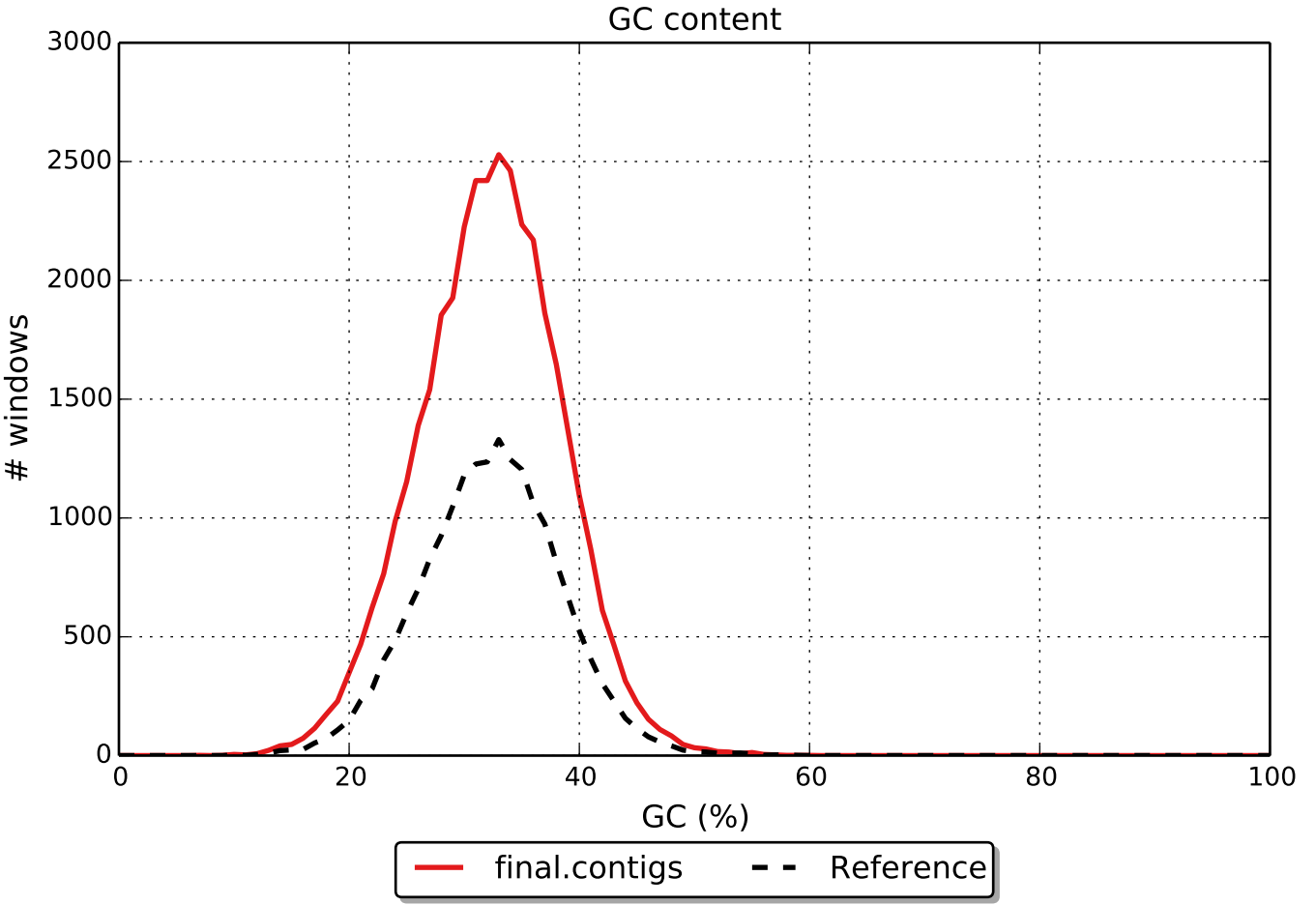
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

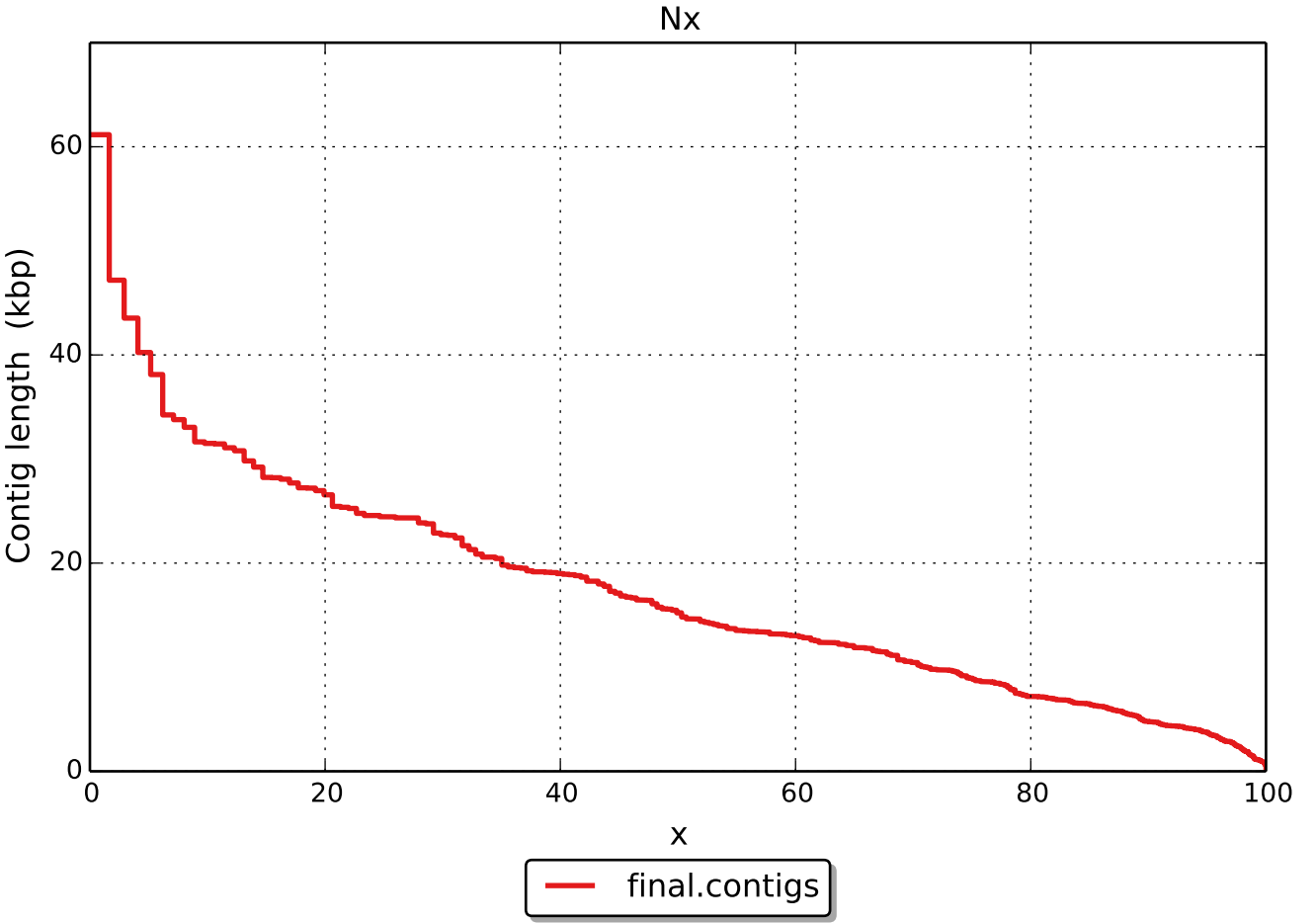
Unaligned report

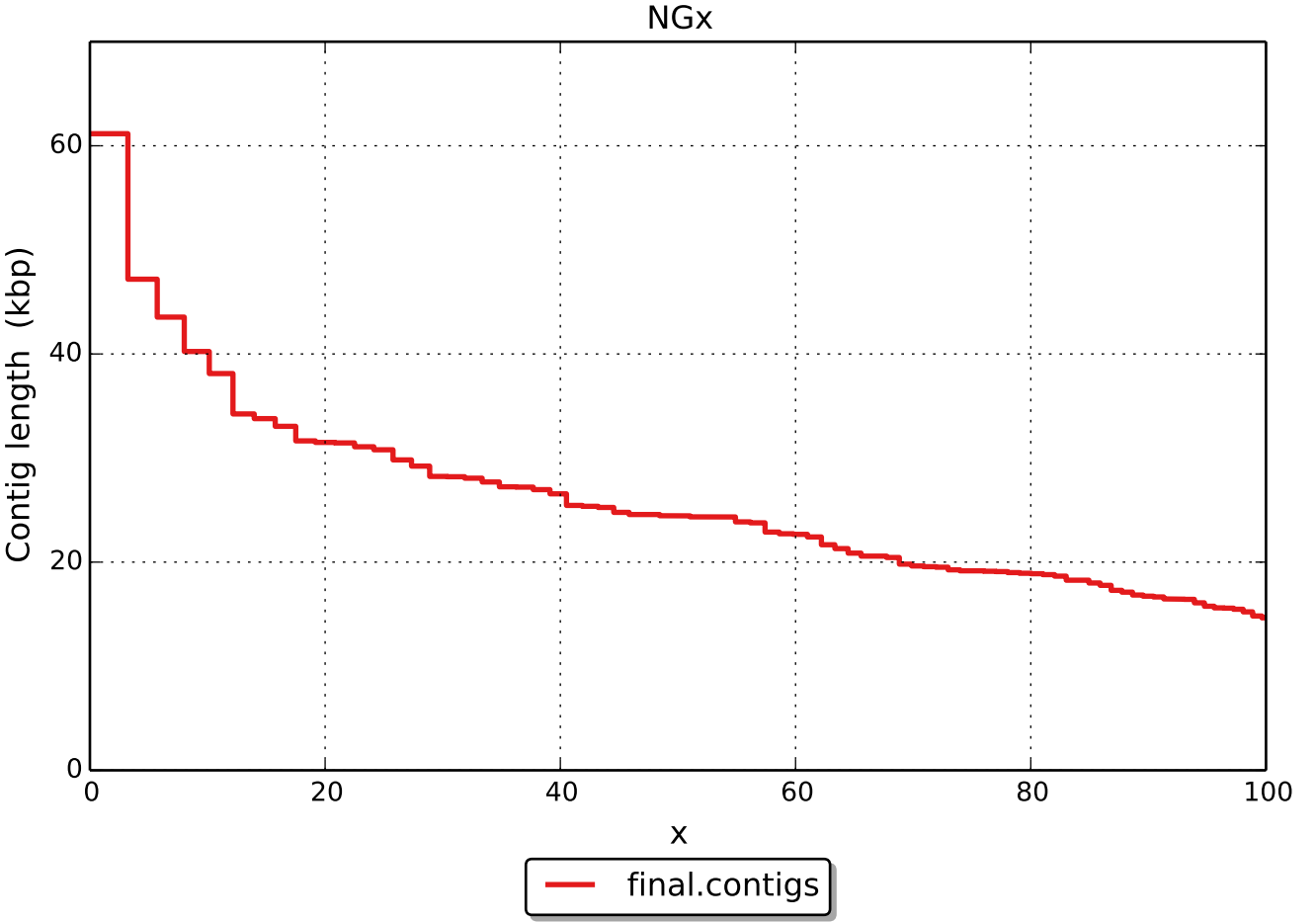
	final.contigs
# fully unaligned contigs	147
Fully unaligned length	1120755
# partially unaligned contigs	70
# with misassembly	6
# both parts are significant	3
Partially unaligned length	666701
# N's	0

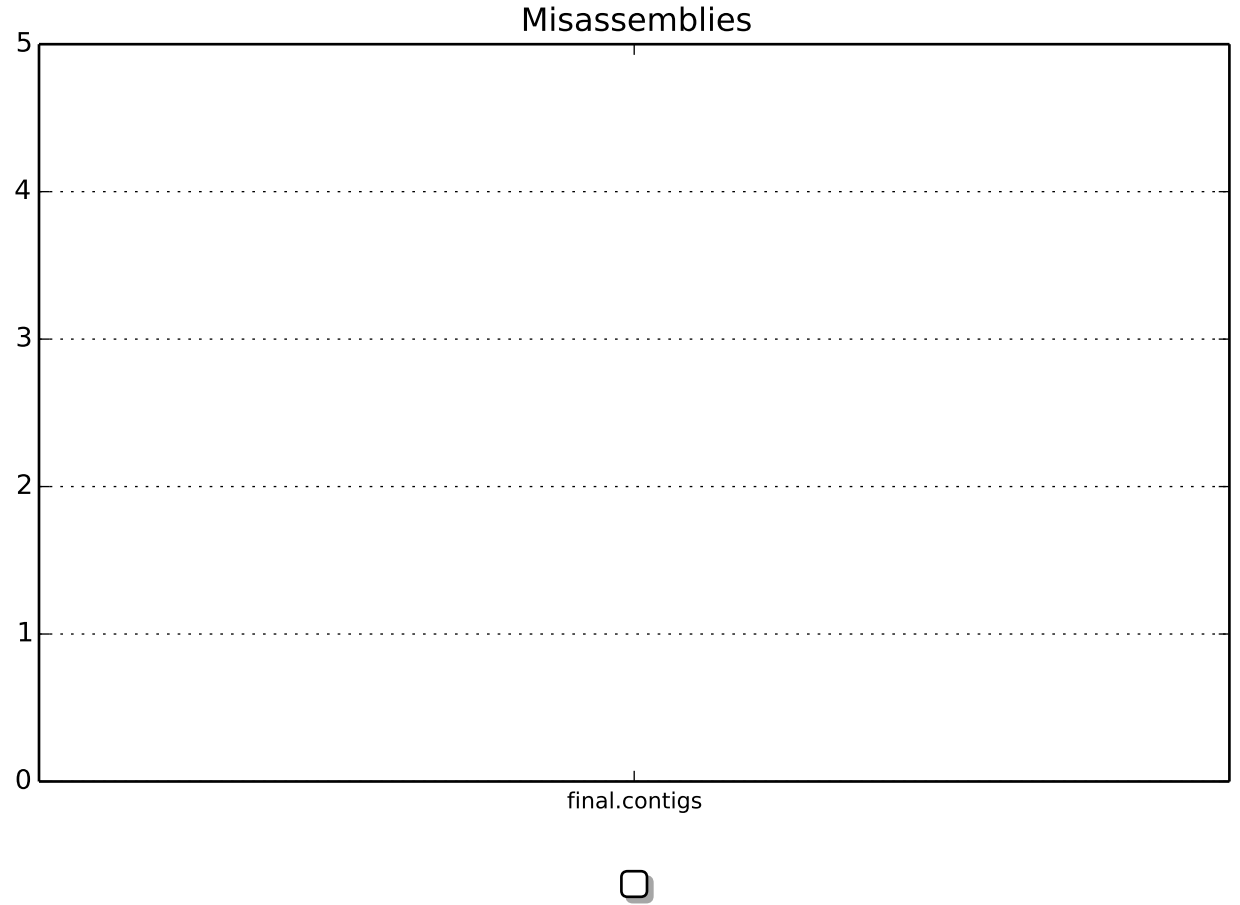
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

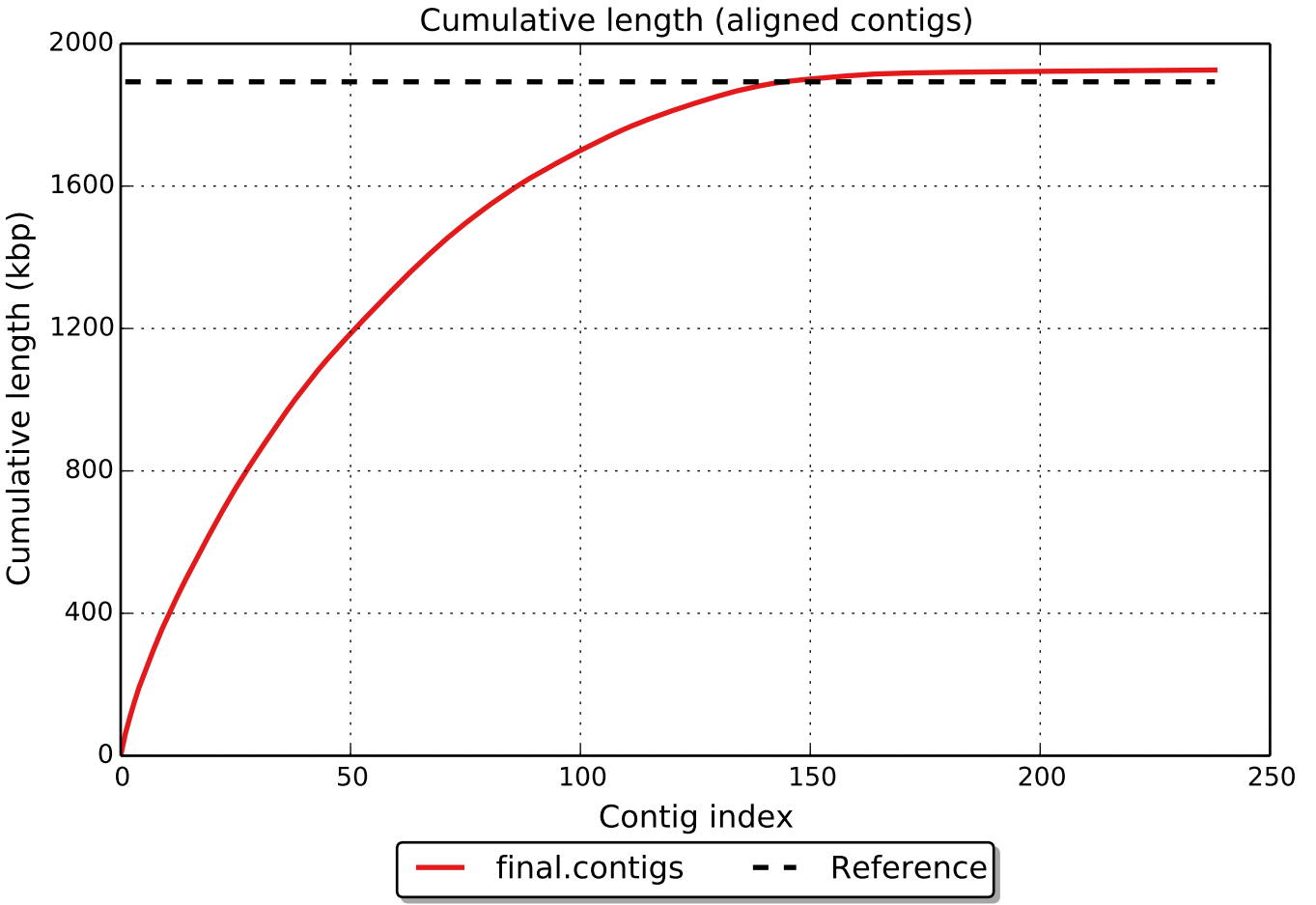

Cumulative length
Cumulative length (Mbp)
4
3
2
1
0
0
80
160
240
320
400
Contig index
final.contigs
Reference

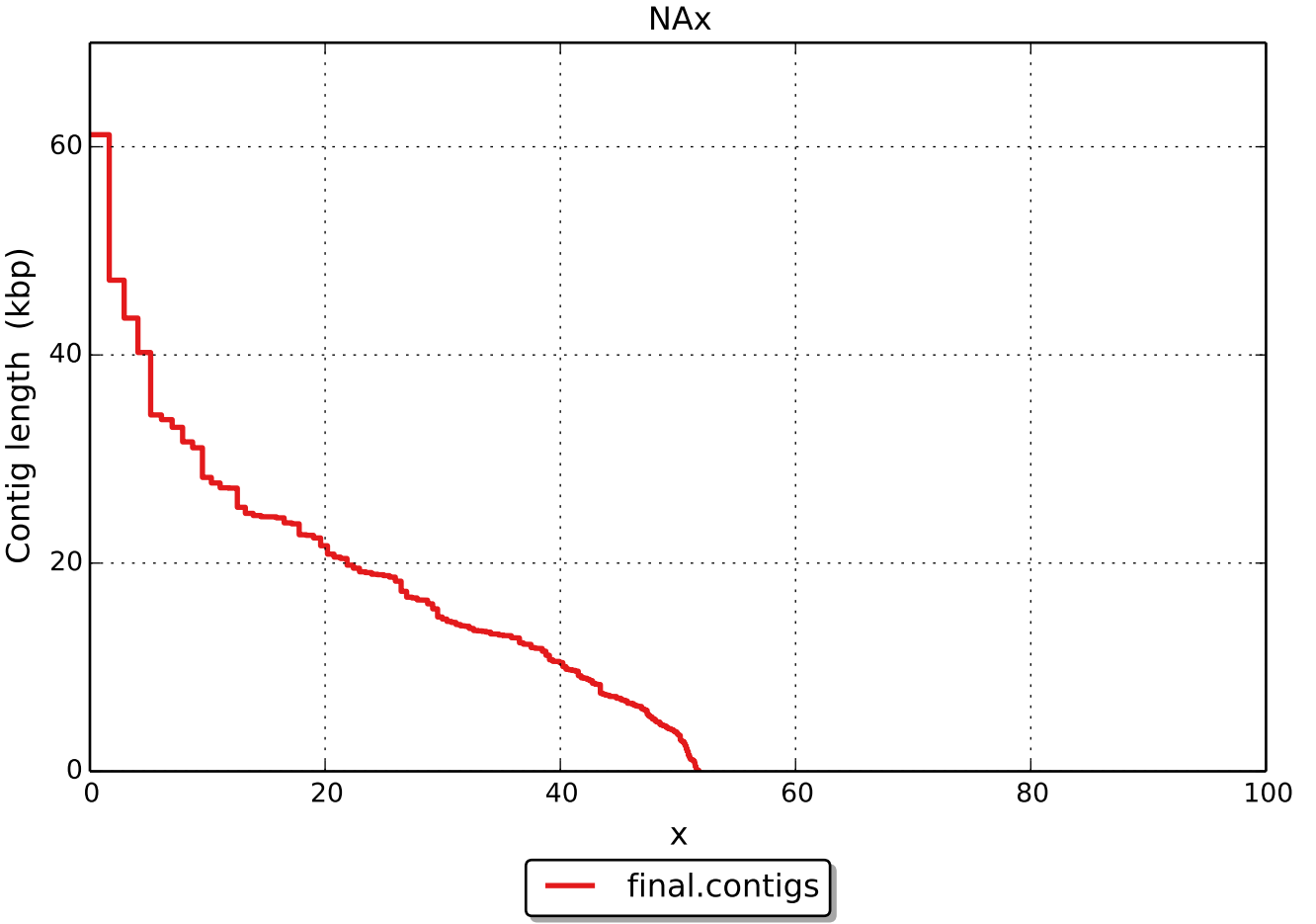

GC content
3000
2500
2000
1500
1000
500
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

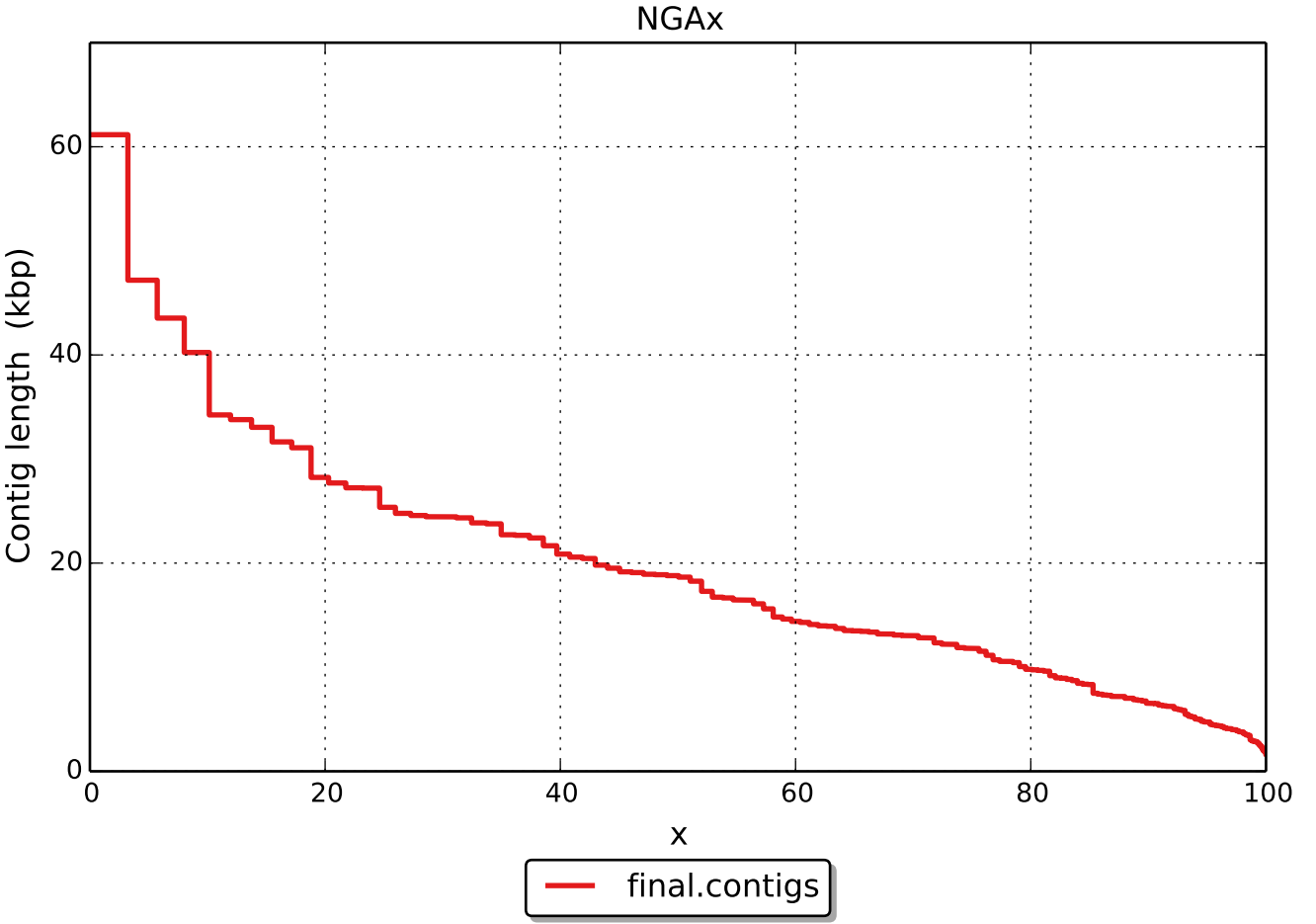

Nx
Contig length (kbp)
0
20
40
60
0
20
40
60
80
100
x
final.contigs


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 (kbp)
2000
1600
1200
800
400
0
0
50
100
150
200
250
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