Report

	final.contigs
# contigs (>= 1000 bp)	341
# contigs (>= 5000 bp)	233
# contigs (>= 10000 bp)	161
# contigs (>= 25000 bp)	45
# contigs (>= 50000 bp)	7
Total length (>= 1000 bp)	4571300
Total length (>= 5000 bp)	4254695
Total length (>= 10000 bp)	3719732
Total length (>= 25000 bp)	1788684
Total length (>= 50000 bp)	474477
# contigs	362
Largest contig	80531
Total length	4587372
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	20536
NG50	20363
N75	12887
NG75	12392
L50	68
LG50	69
L75	137
LG75	140
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	5
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.173
Duplication ratio	1.007
# N's per 100 kbp	0.00
# mismatches per 100 kbp	10.56
# indels per 100 kbp	0.07
Largest alignment	80531
NA50	20536
NGA50	20363
NA75	12887
NGA75	12392
LA50	68
LGA50	69
LA75	137
LGA75	140

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

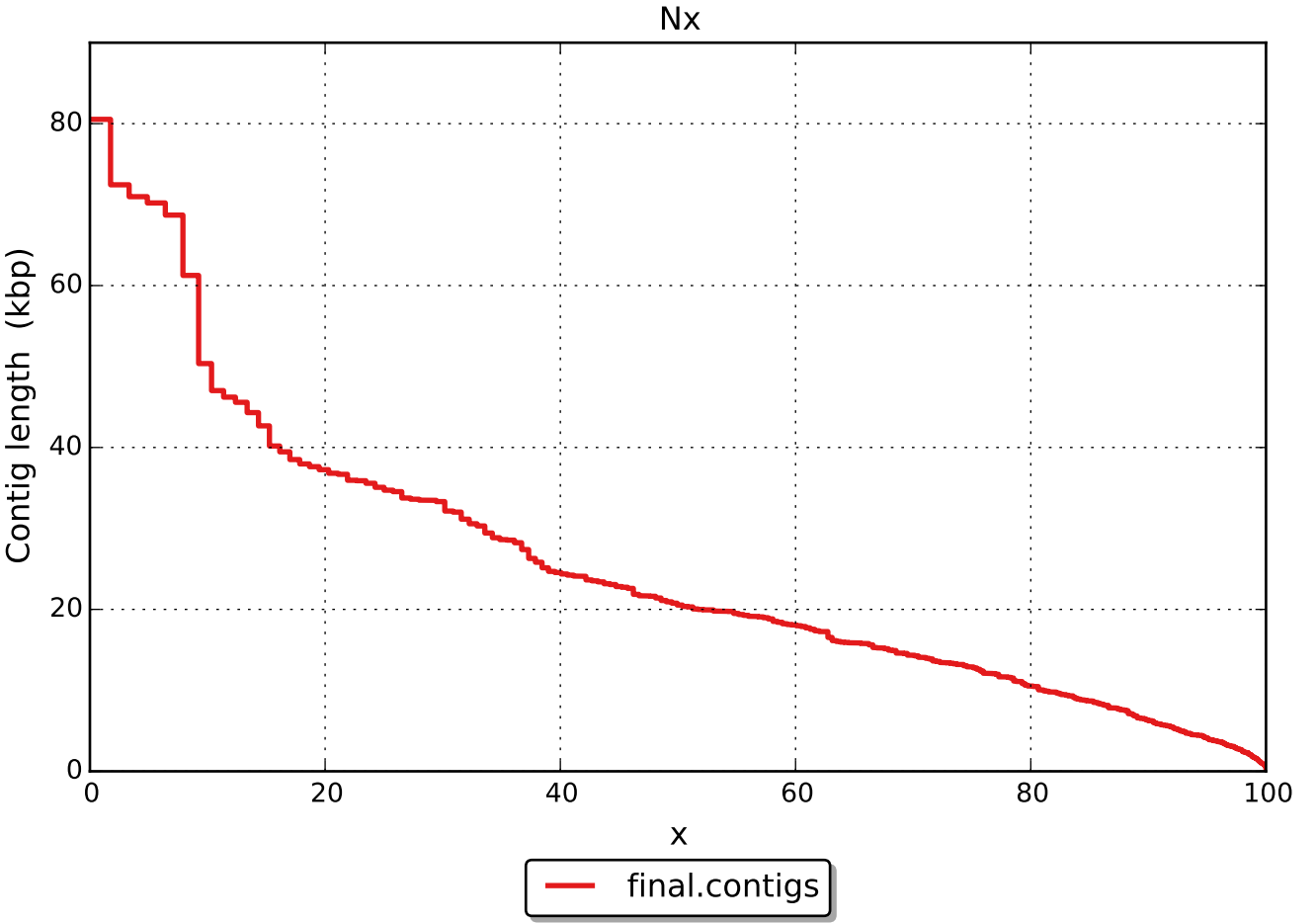
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	5
# mismatches	481
# indels	3
# short indels	3
# long indels	0
Indels length	3

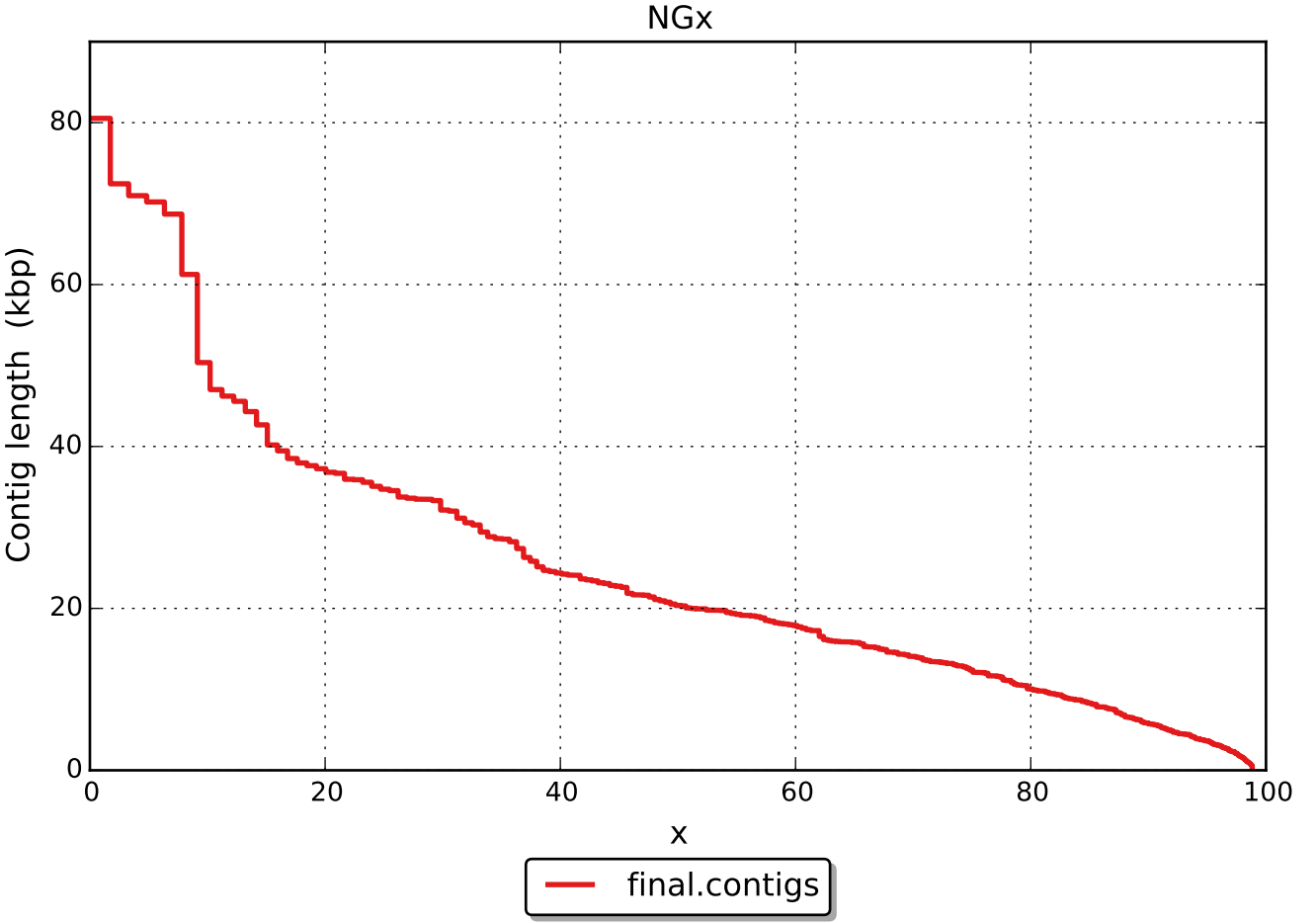
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

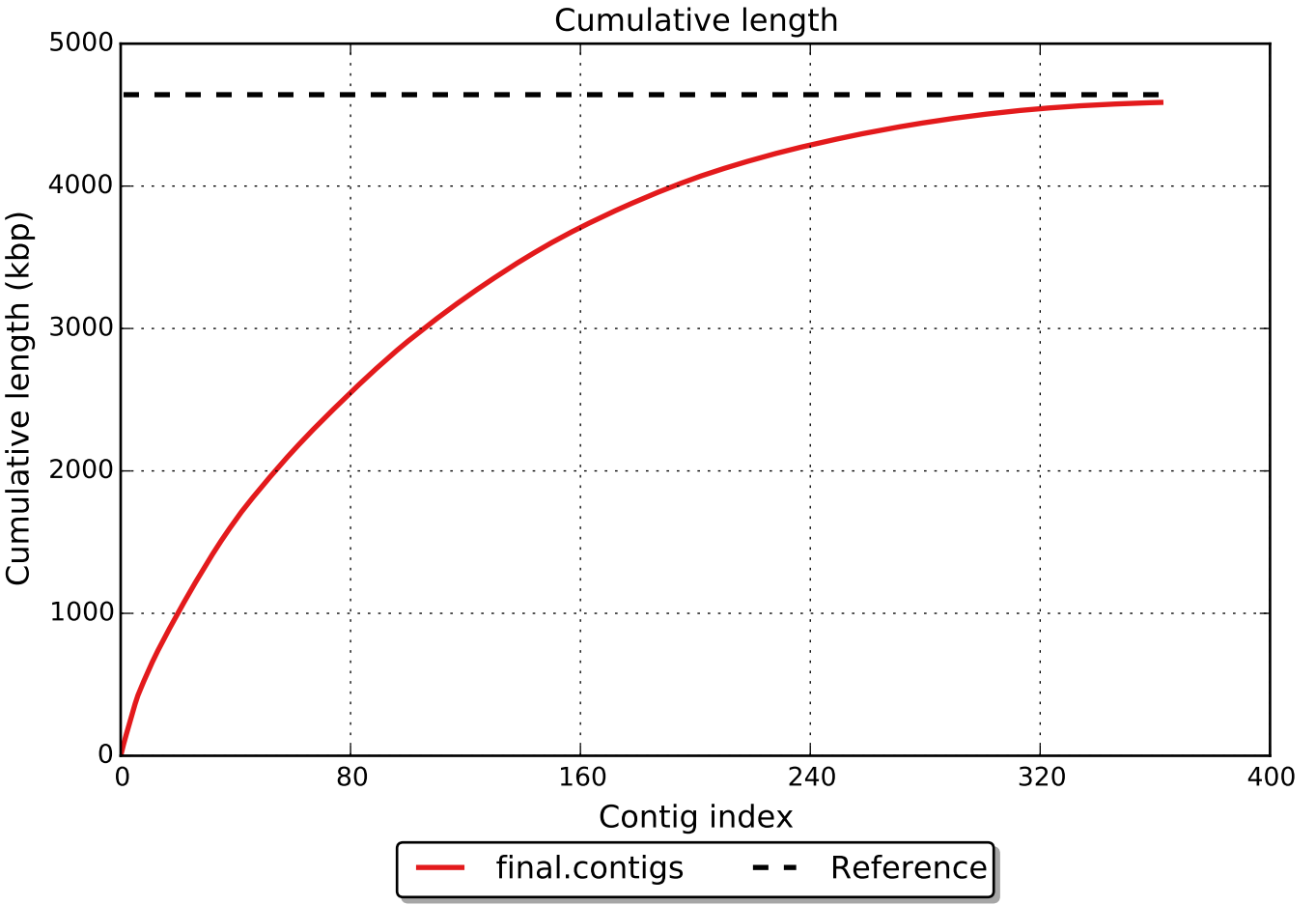
Unaligned report

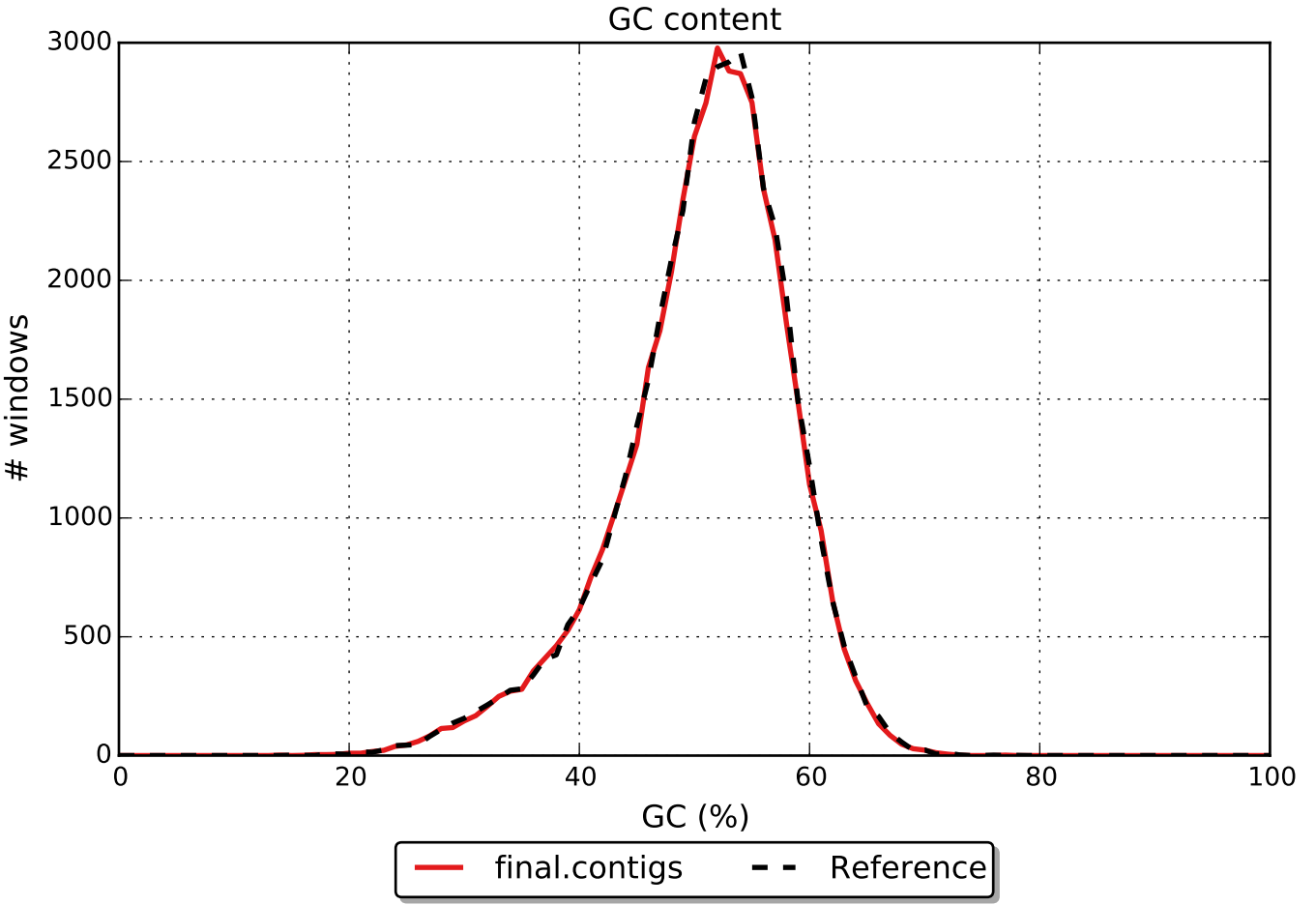
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

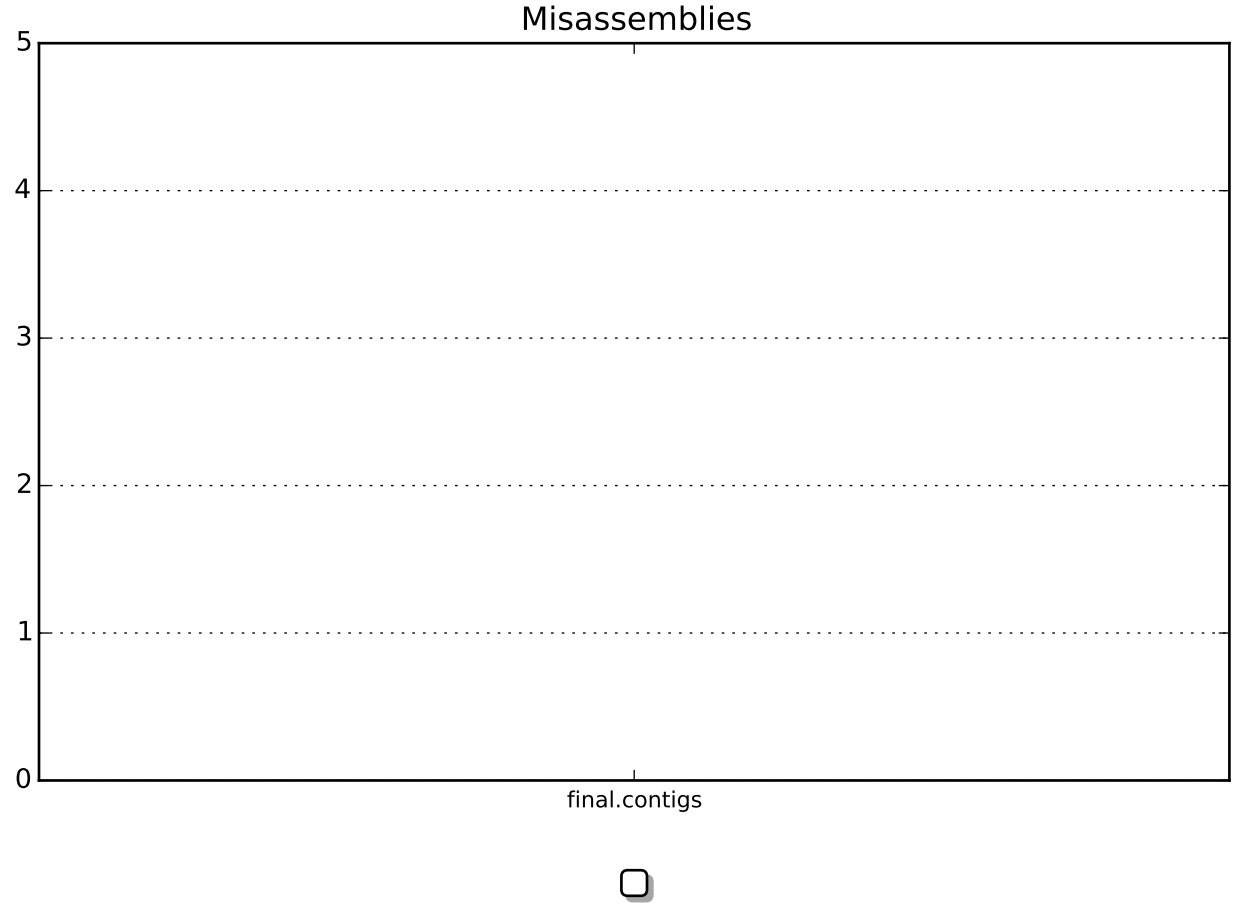
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

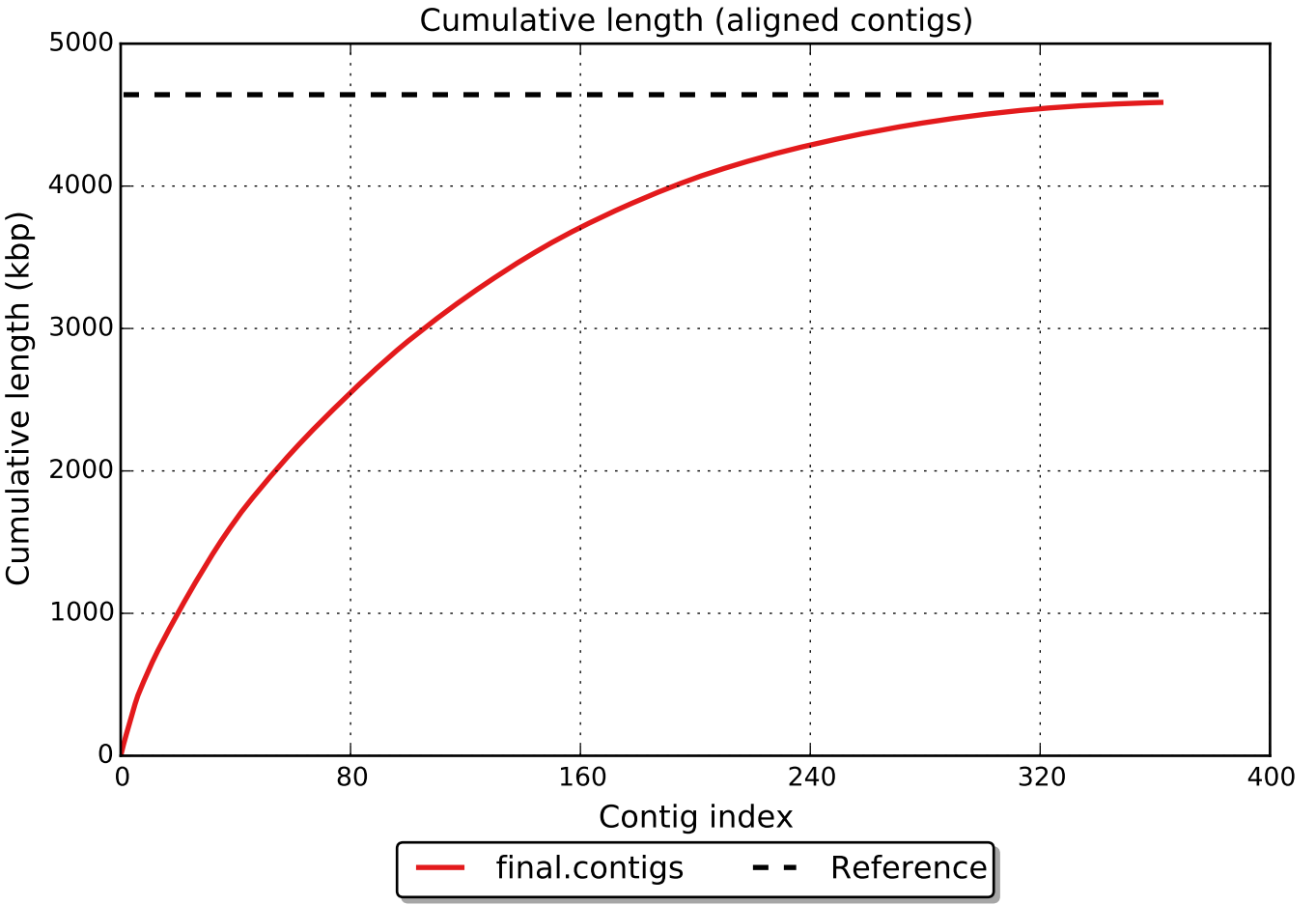

Nx
Contig length (kbp)
0
20
40
60
80
0
20
40
60
80
100
x
final.contigs

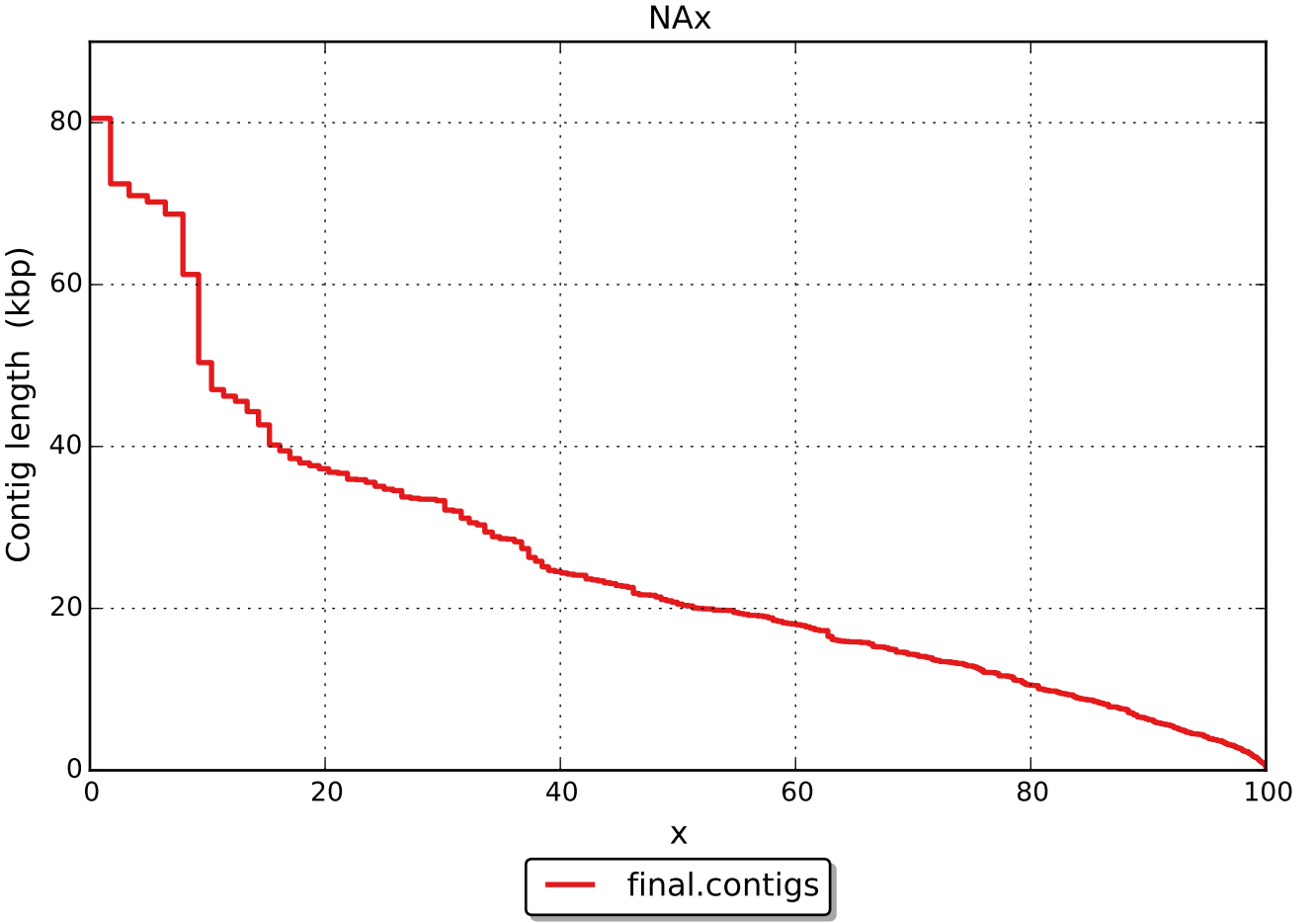

NGx
Contig length (kbp)
0
20
40
60
80
0
20
40
60
80
100
x
final.contigs

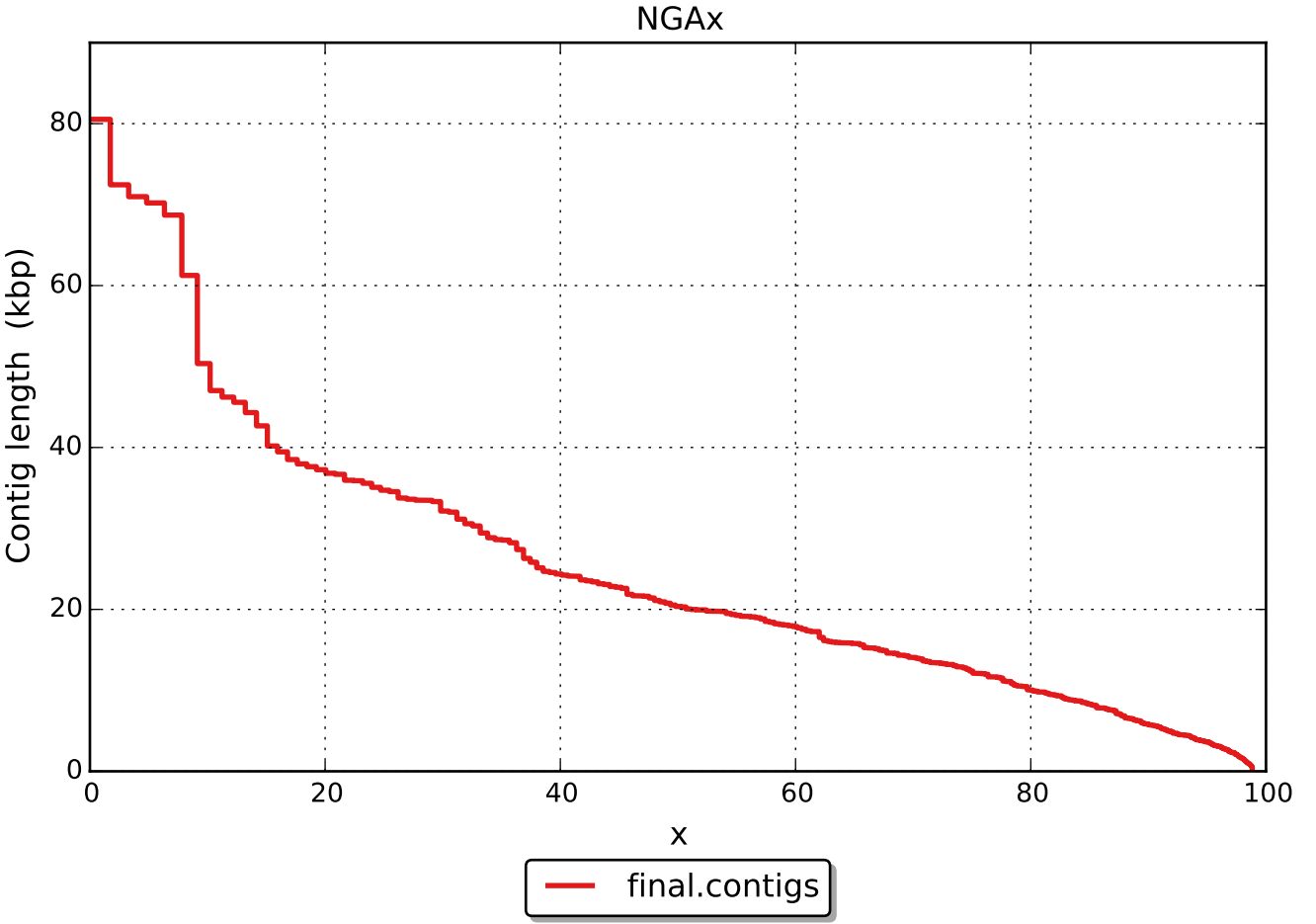

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
80
160
240
320
400
Contig index
final.contigs
Reference


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


Misassemblies
5
4
3
2
1
0
final.contigs


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
80
160
240
320
400
Contig index
final.contigs
Reference


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


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