Report

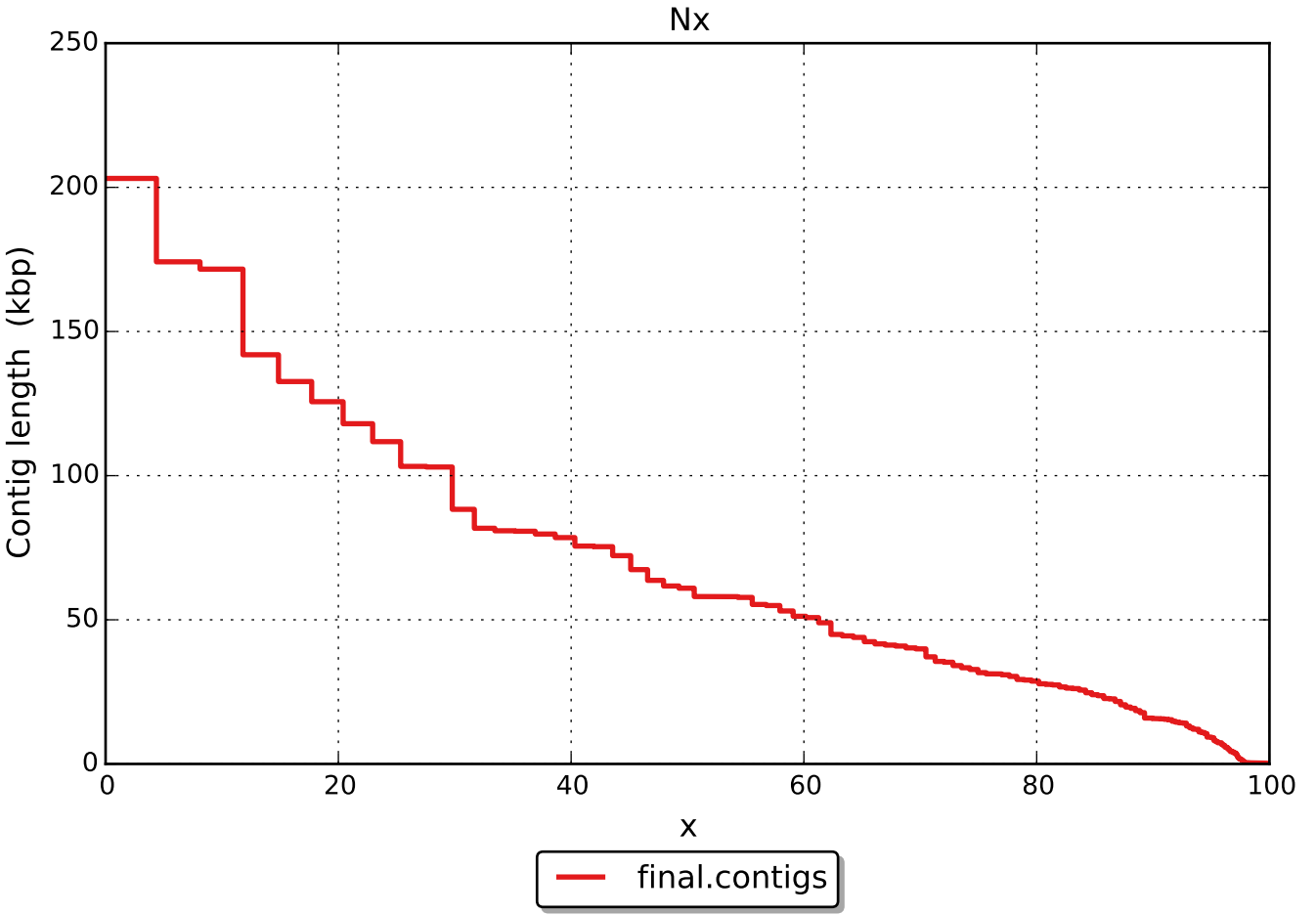
	final.contigs
# contigs (>= 0 bp)	437
# contigs (>= 1000 bp)	129
# contigs (>= 5000 bp)	104
# contigs (>= 10000 bp)	92
# contigs (>= 25000 bp)	63
# contigs (>= 50000 bp)	32
Total length (>= 0 bp)	4650409
Total length (>= 1000 bp)	4548228
Total length (>= 5000 bp)	4489034
Total length (>= 10000 bp)	4400897
Total length (>= 25000 bp)	3916029
Total length (>= 50000 bp)	2849208
# contigs	437
Largest contig	203098
Total length	4650409
Reference length	4641652
GC (%)	50.76
Reference GC (%)	50.79
N50	60955
NG50	60955
N75	31671
NG75	32765
L50	23
LG50	23
L75	49
LG75	48
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned contigs	183 + 0 part
Unaligned length	62986
Genome fraction (%)	98.543
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3.59
# indels per 100 kbp	0.07
Largest alignment	203098
NA50	60955
NGA50	60955
NA75	31671
NGA75	32765
LA50	23
LGA50	23
LA75	49
LGA75	48

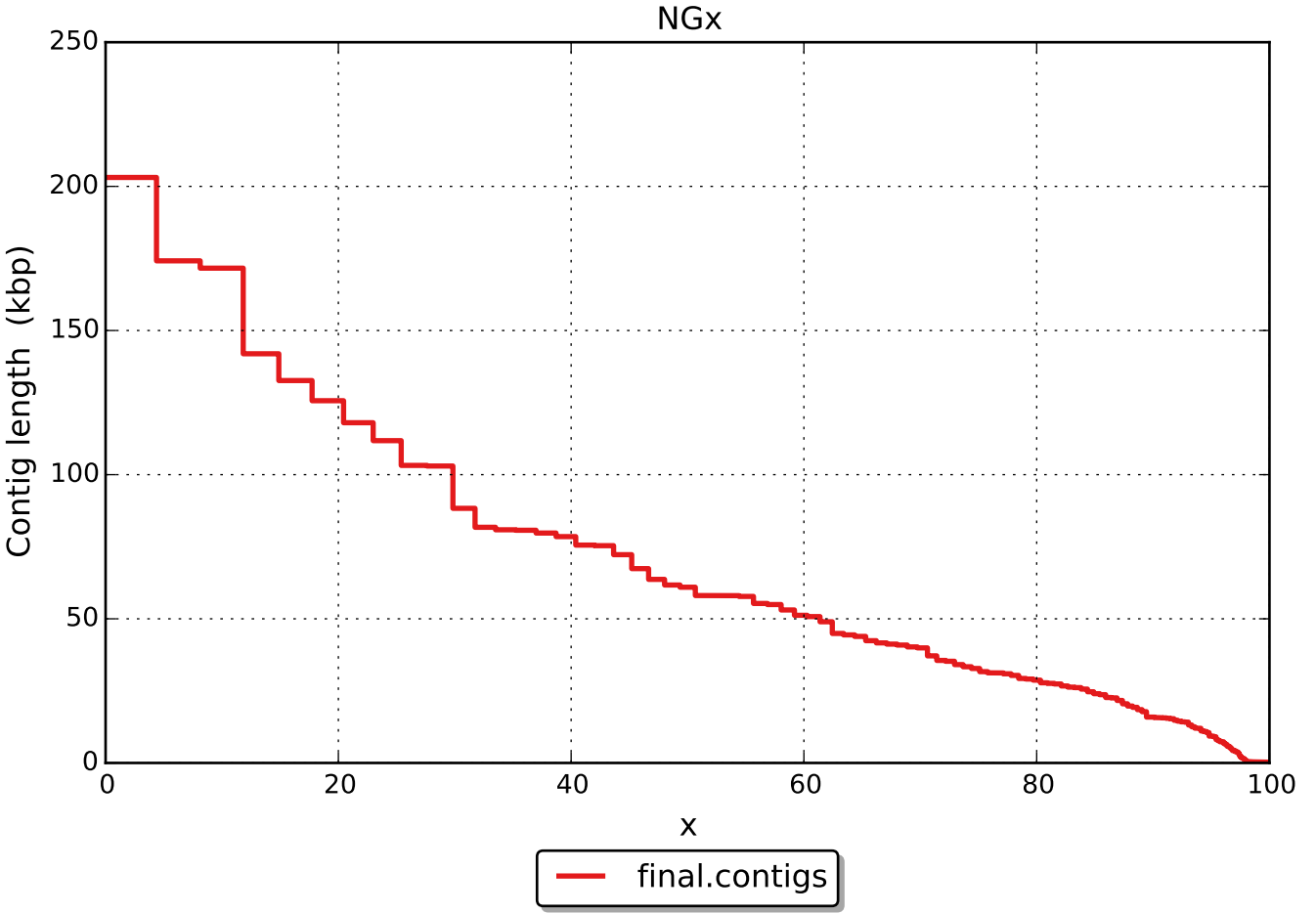
Misassemblies report

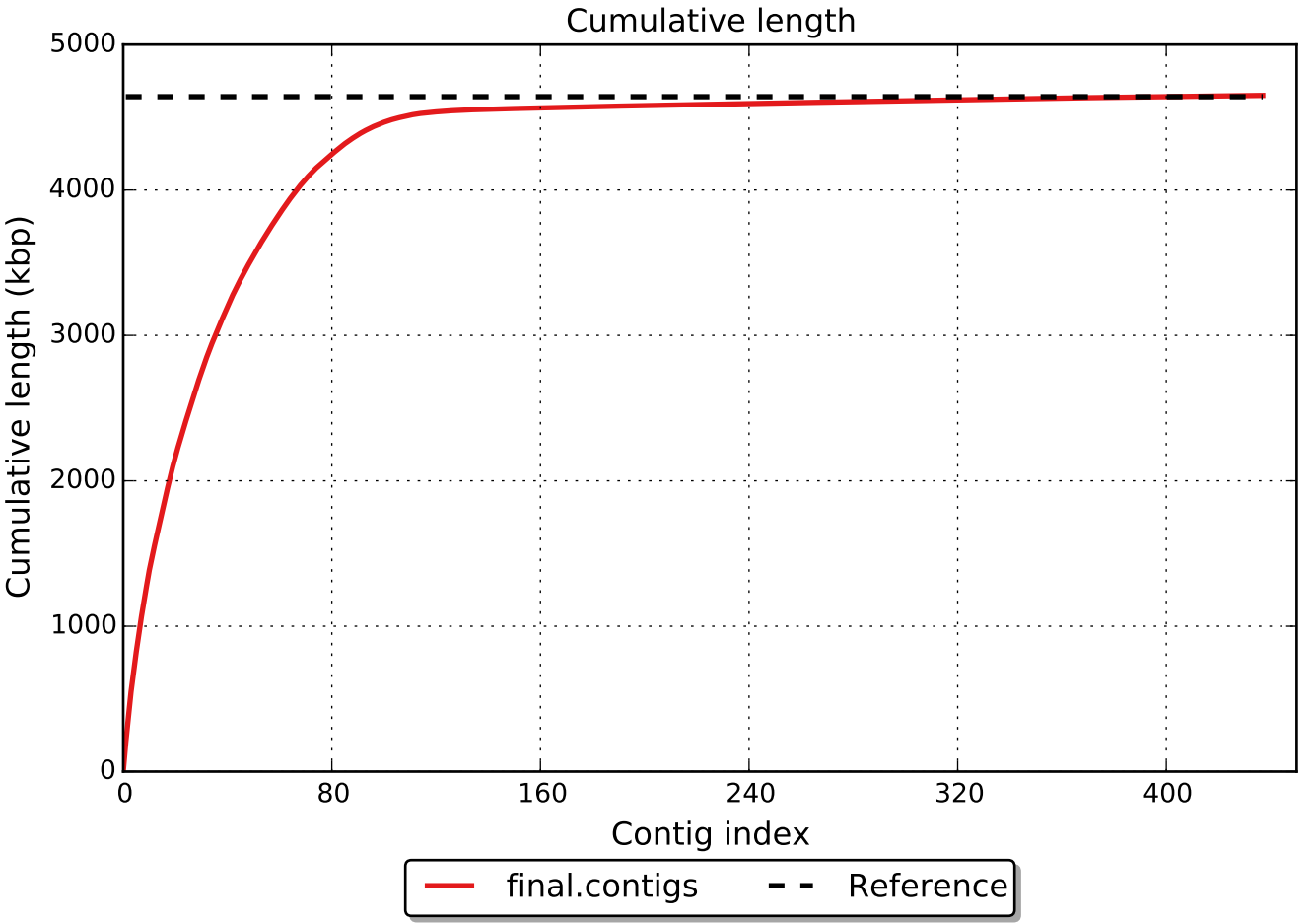
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# mismatches	164
# indels	3
# short indels	3
# long indels	0
Indels length	3

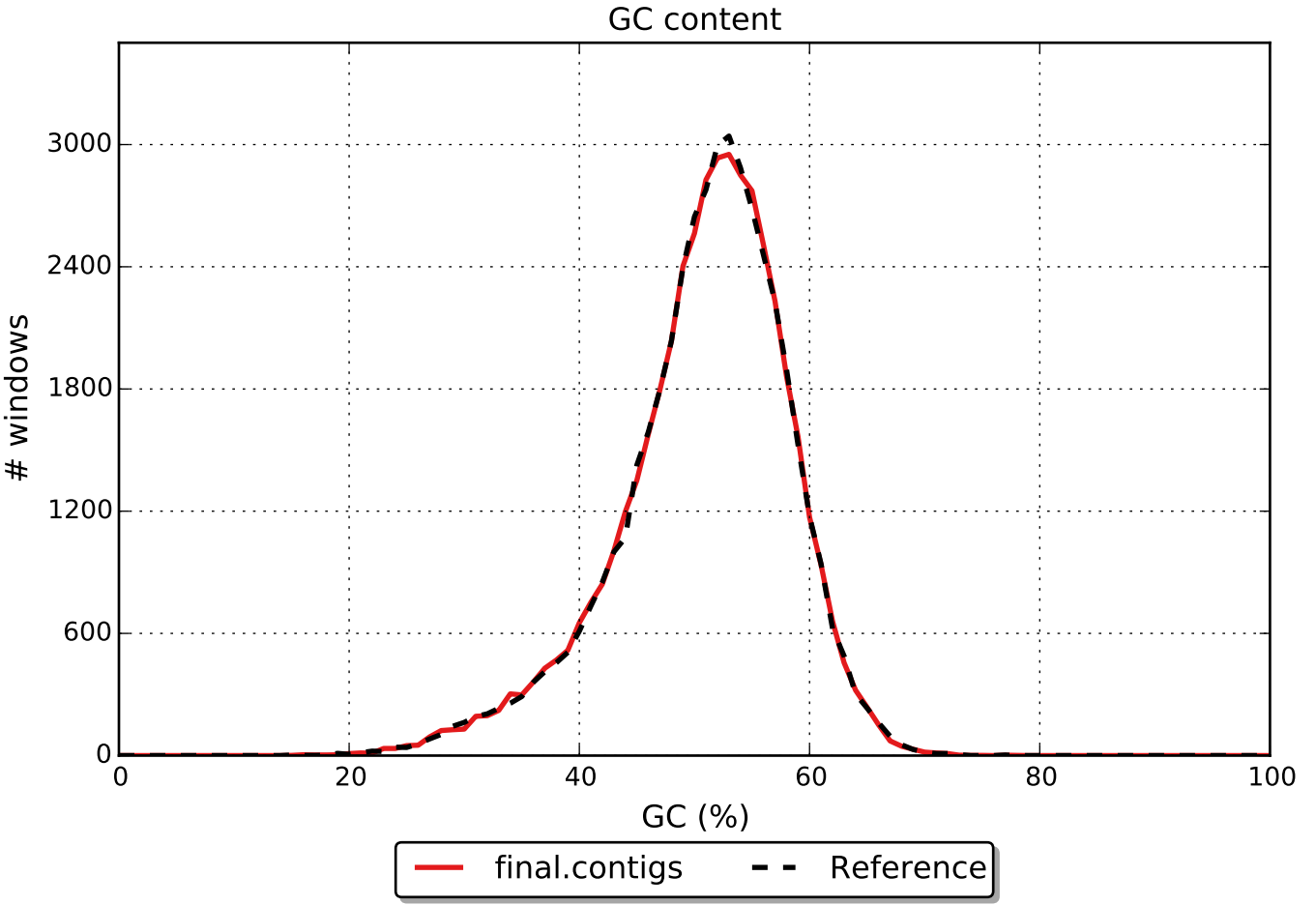
Unaligned report

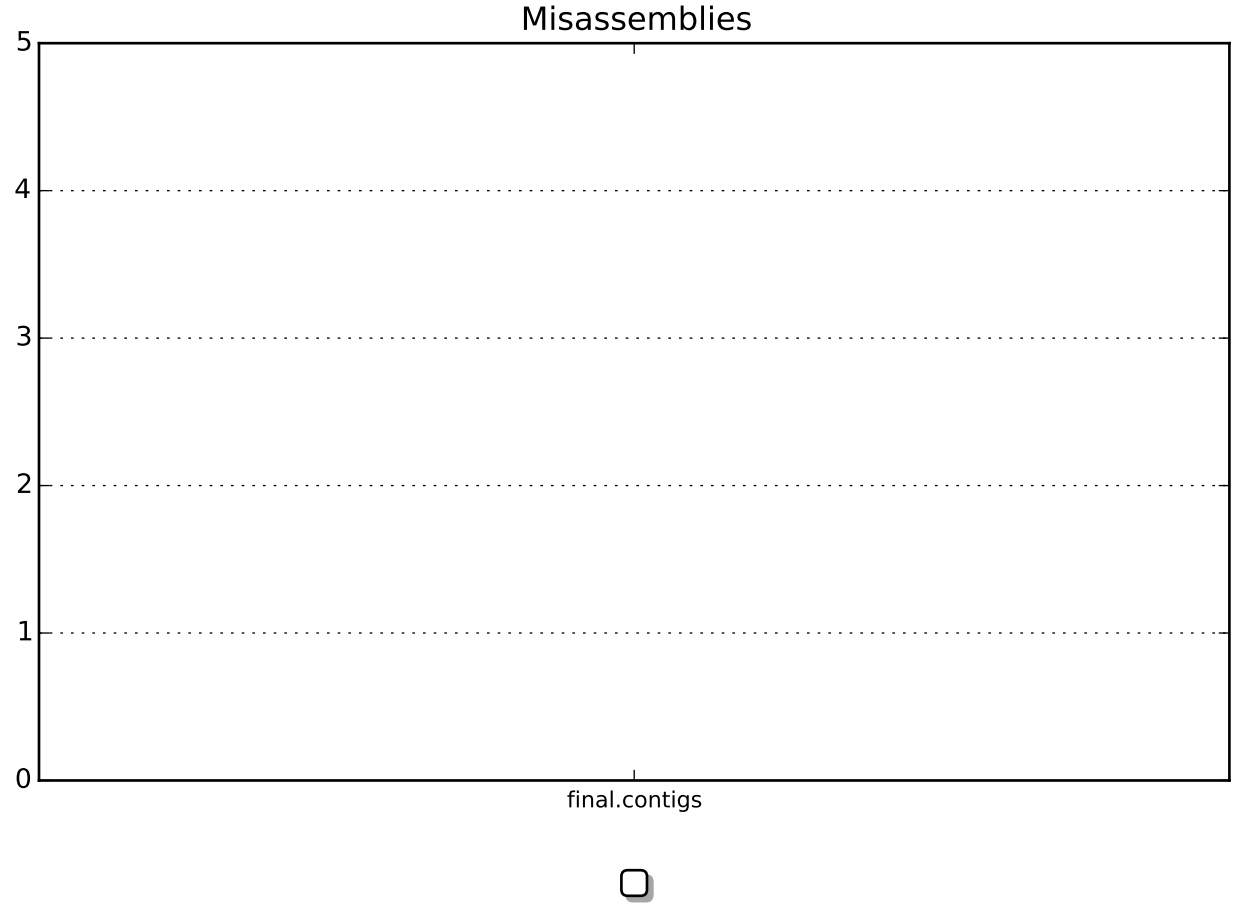
	final.contigs
# fully unaligned contigs	183
Fully unaligned length	62986
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

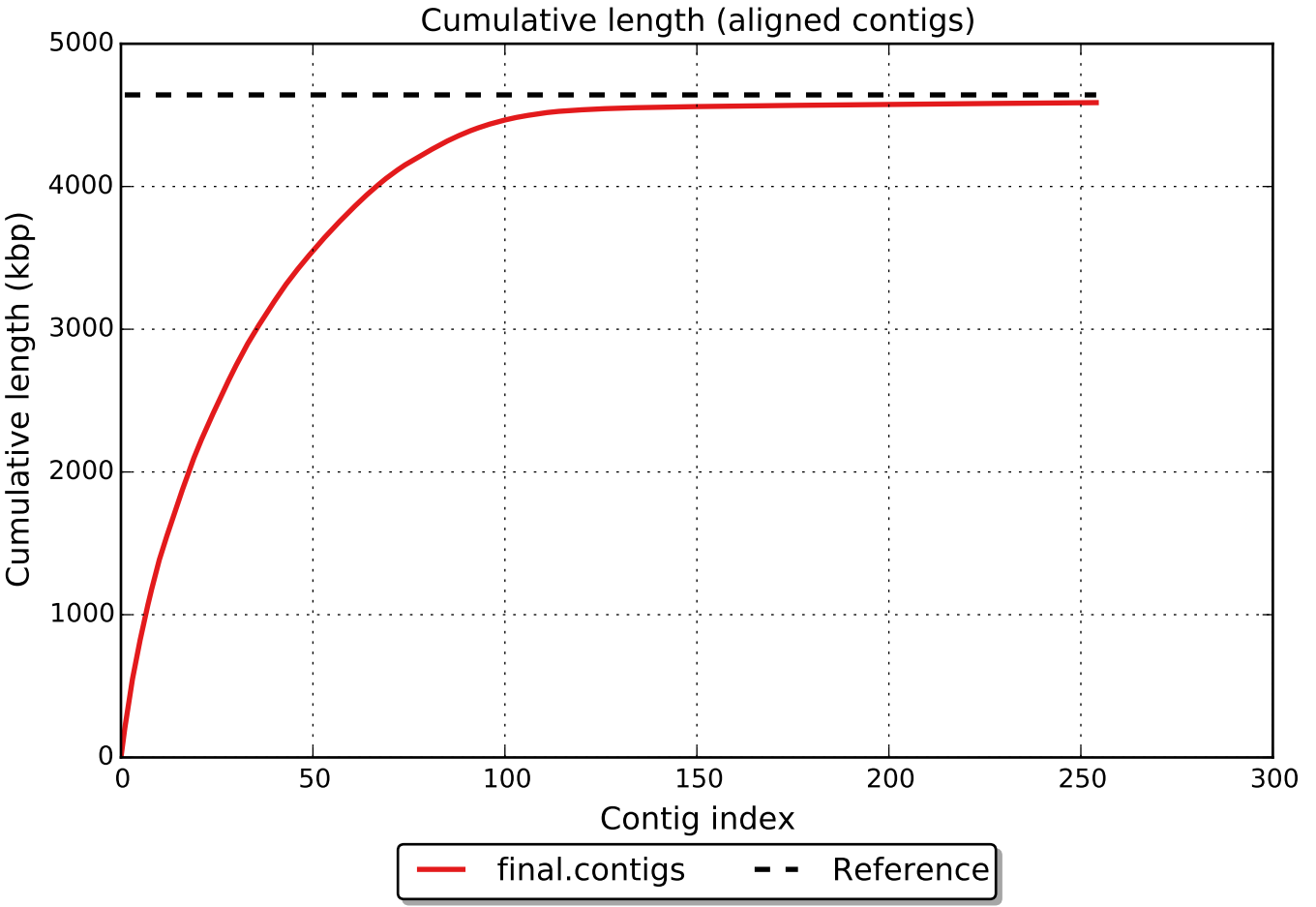

Nx
250
200
150
100
50
0
Contig length (kbp)
0
20
40
60
80
100
x
final.contigs

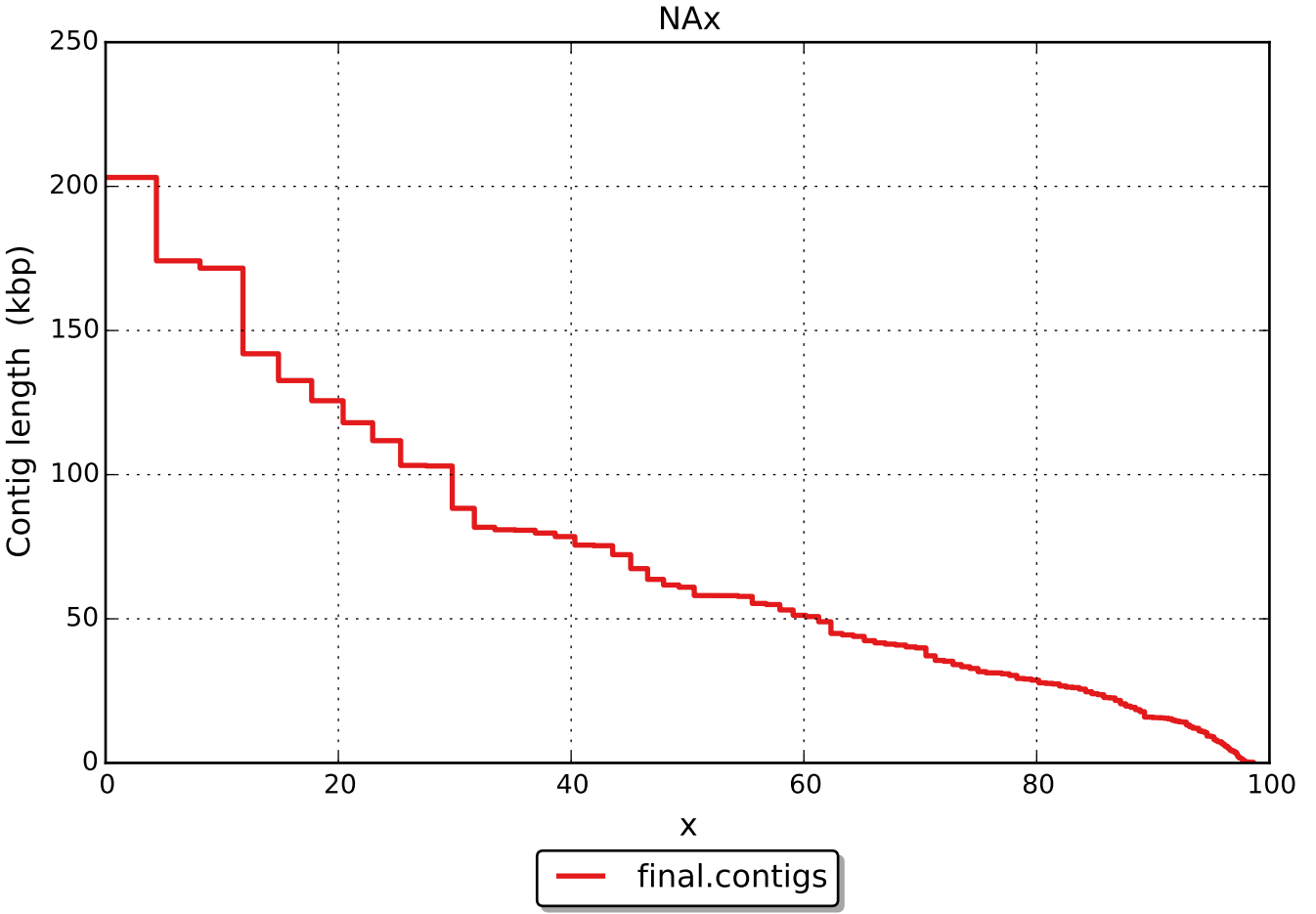

NGx
250
200
150
100
50
0
Contig length (kbp)
0
20
40
60
80
100
x
final.contigs

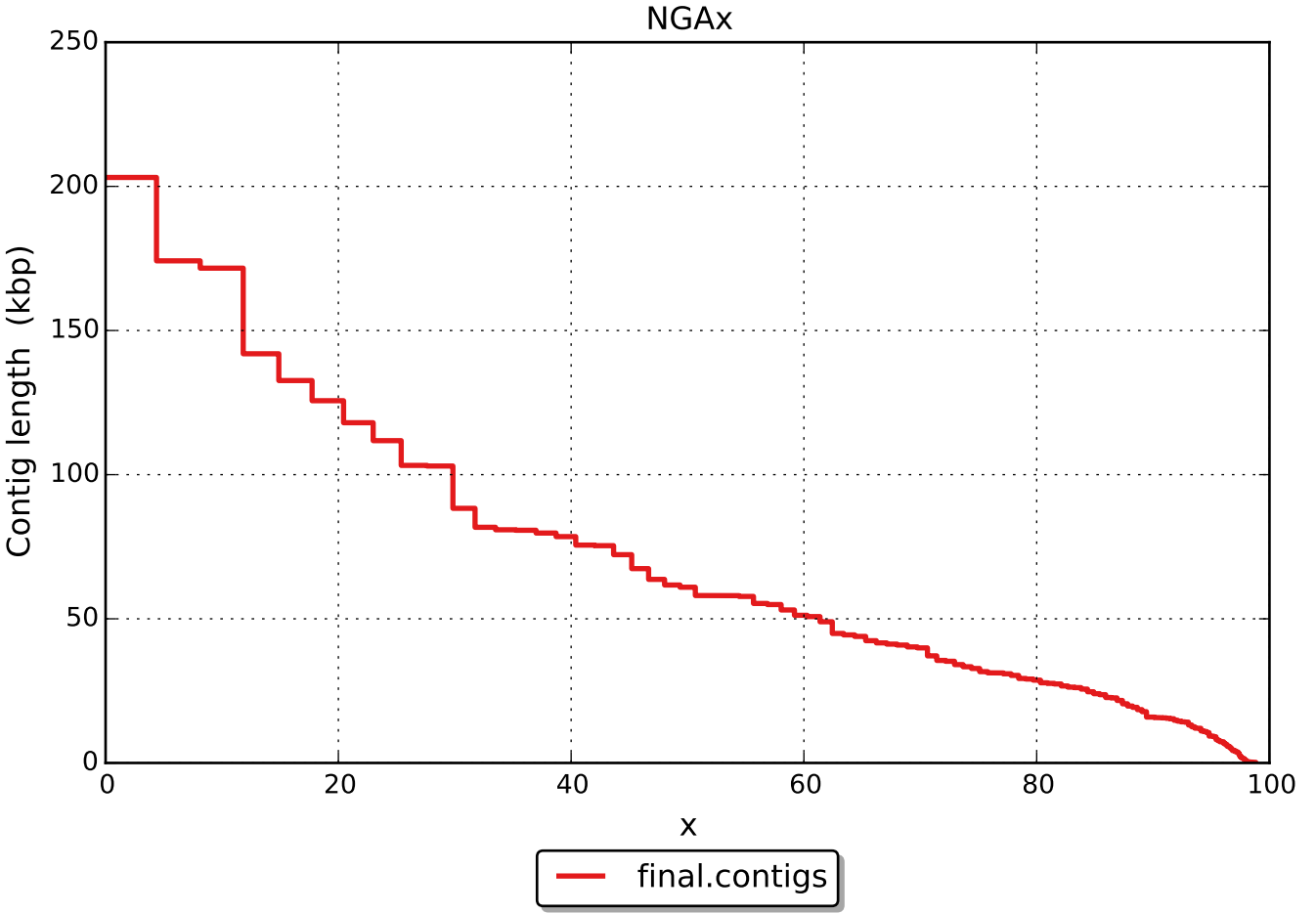

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
80
160
240
320
400
Contig index
final.contigs
Reference


GC content
windows
3000
2400
1800
1200
600
0
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
50
100
150
200
250
300
Contig index
final.contigs
Reference


NAx
250
200
150
100
50
0
Contig length (kbp)
0
20
40
60
80
100
x
final.contigs


NGAx
250
200
150
100
50
0
Contig length (kbp)
0
20
40
60
80
100
x
final.contigs