Report

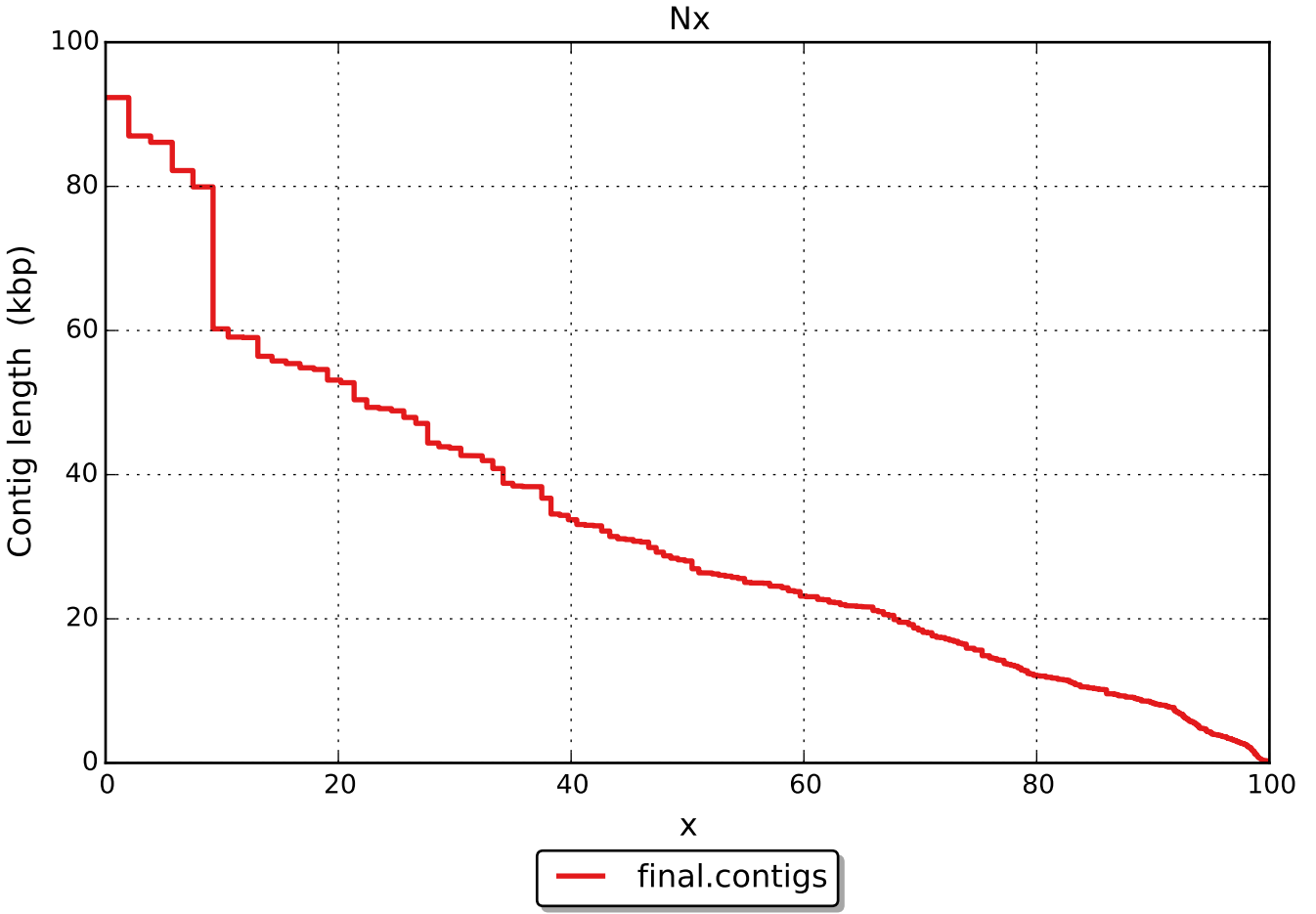
	final.contigs
# contigs (>= 0 bp)	394
# contigs (>= 1000 bp)	272
# contigs (>= 5000 bp)	193
# contigs (>= 10000 bp)	146
# contigs (>= 25000 bp)	60
# contigs (>= 50000 bp)	16
Total length (>= 0 bp)	4630903
Total length (>= 1000 bp)	4582994
Total length (>= 5000 bp)	4350294
Total length (>= 10000 bp)	3982556
Total length (>= 25000 bp)	2567638
Total length (>= 50000 bp)	1039192
# contigs	394
Largest contig	92325
Total length	4630903
Reference length	4641652
GC (%)	50.74
Reference GC (%)	50.79
N50	28023
NG50	28023
N75	15650
NG75	15650
L50	51
LG50	51
L75	105
LG75	105
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	44151
# local misassemblies	4
# unaligned contigs	65 + 4 part
Unaligned length	27165
Genome fraction (%)	98.315
Duplication ratio	1.009
# N's per 100 kbp	0.00
# mismatches per 100 kbp	32.63
# indels per 100 kbp	0.07
Largest alignment	92325
NA50	28023
NGA50	28023
NA75	15650
NGA75	15650
LA50	51
LGA50	51
LA75	105
LGA75	105

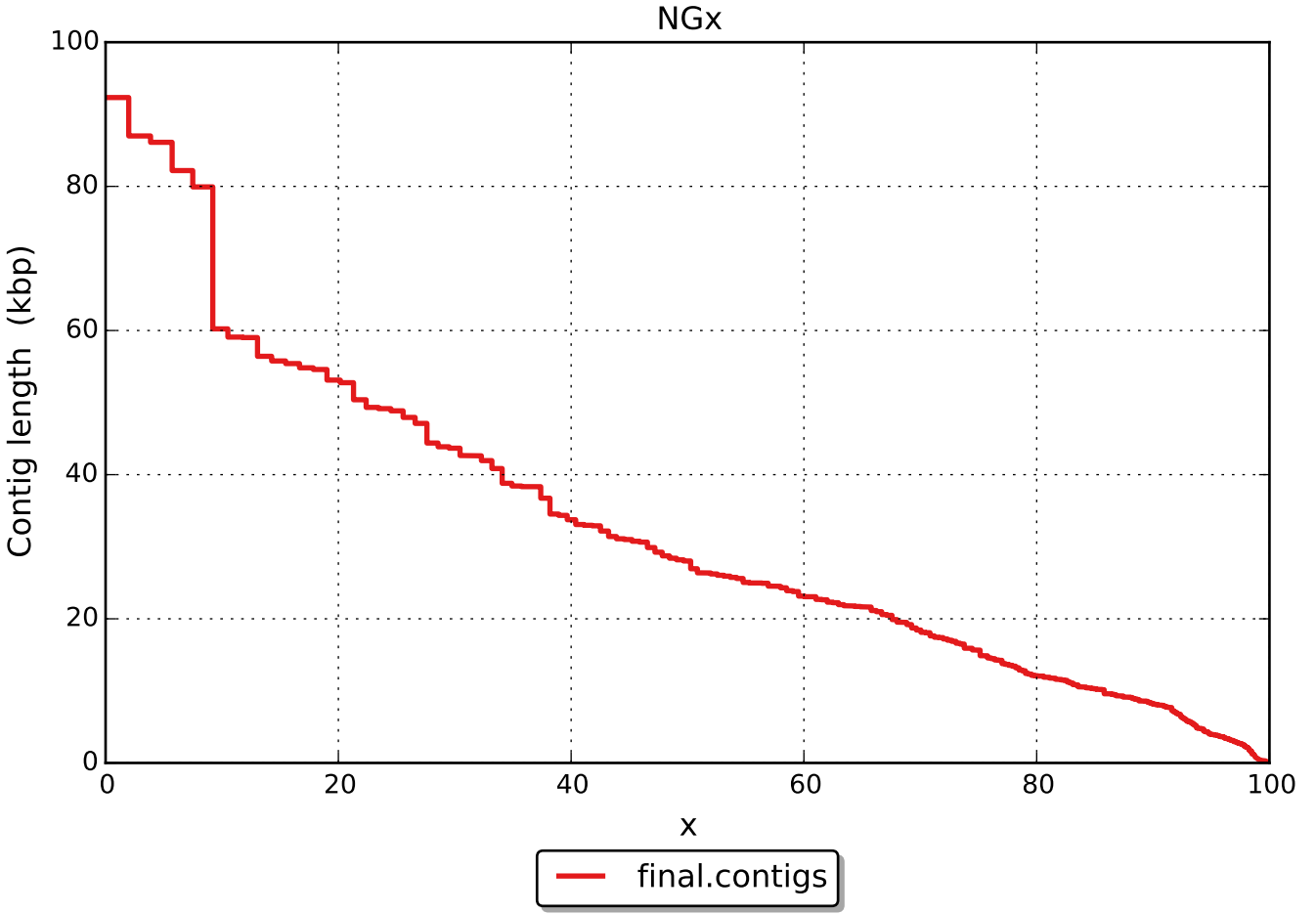
Misassemblies report

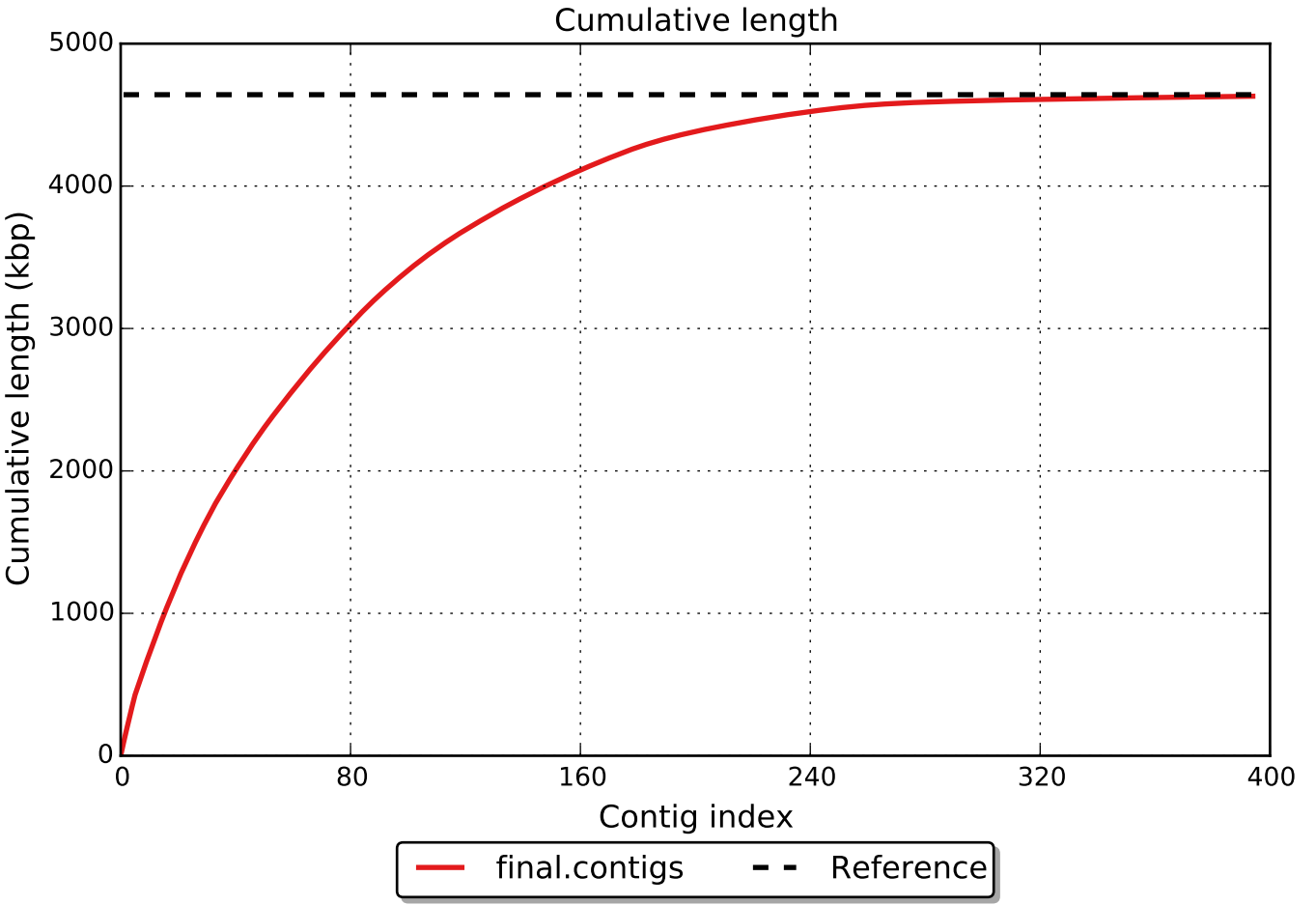
	final.contigs
# misassemblies	2
# relocations	2
# translocations	0
# inversions	0
# misassembled contigs	2
Misassembled contigs length	44151
# local misassemblies	4
# mismatches	1489
# indels	3
# short indels	3
# long indels	0
Indels length	3

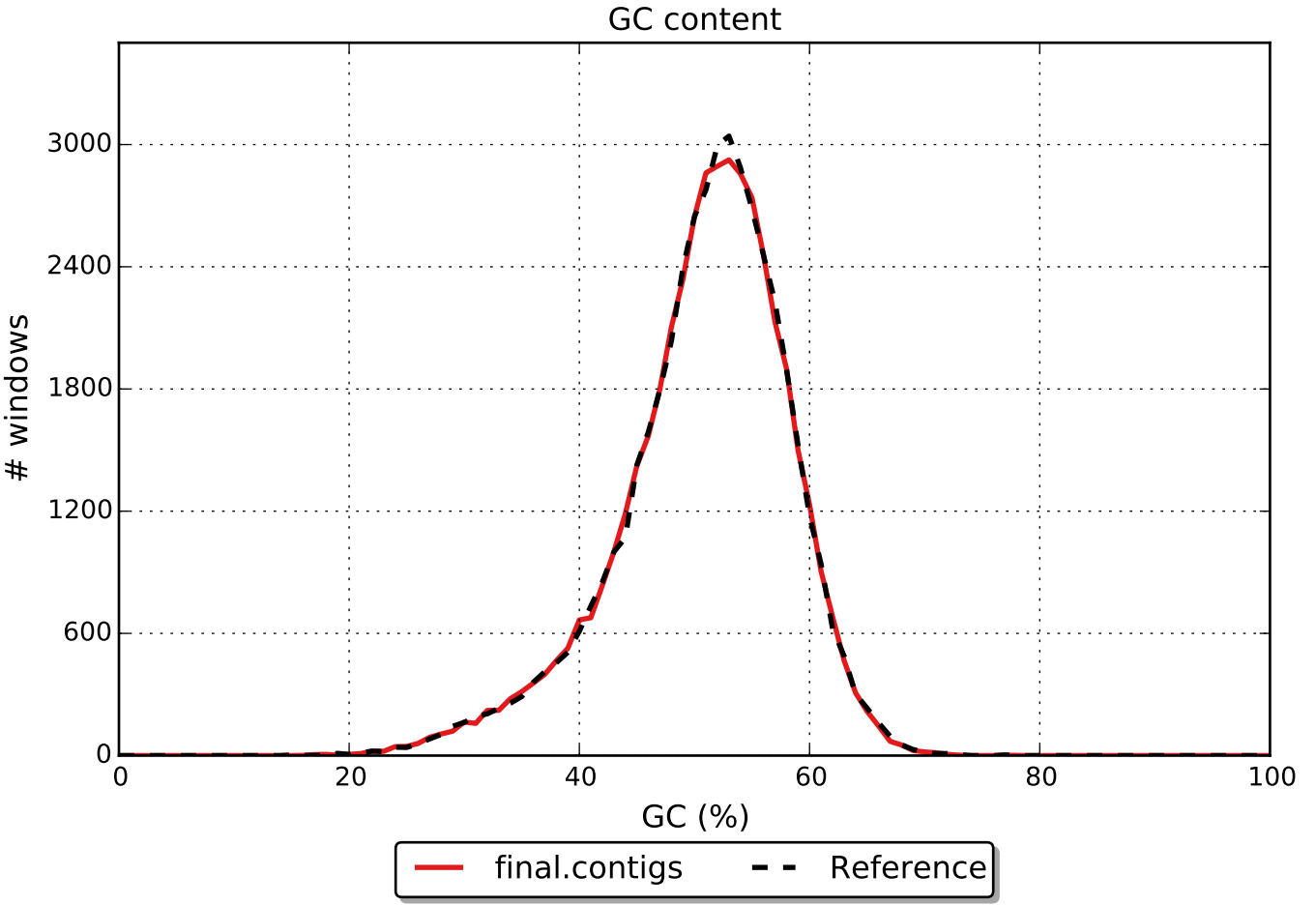
Unaligned report

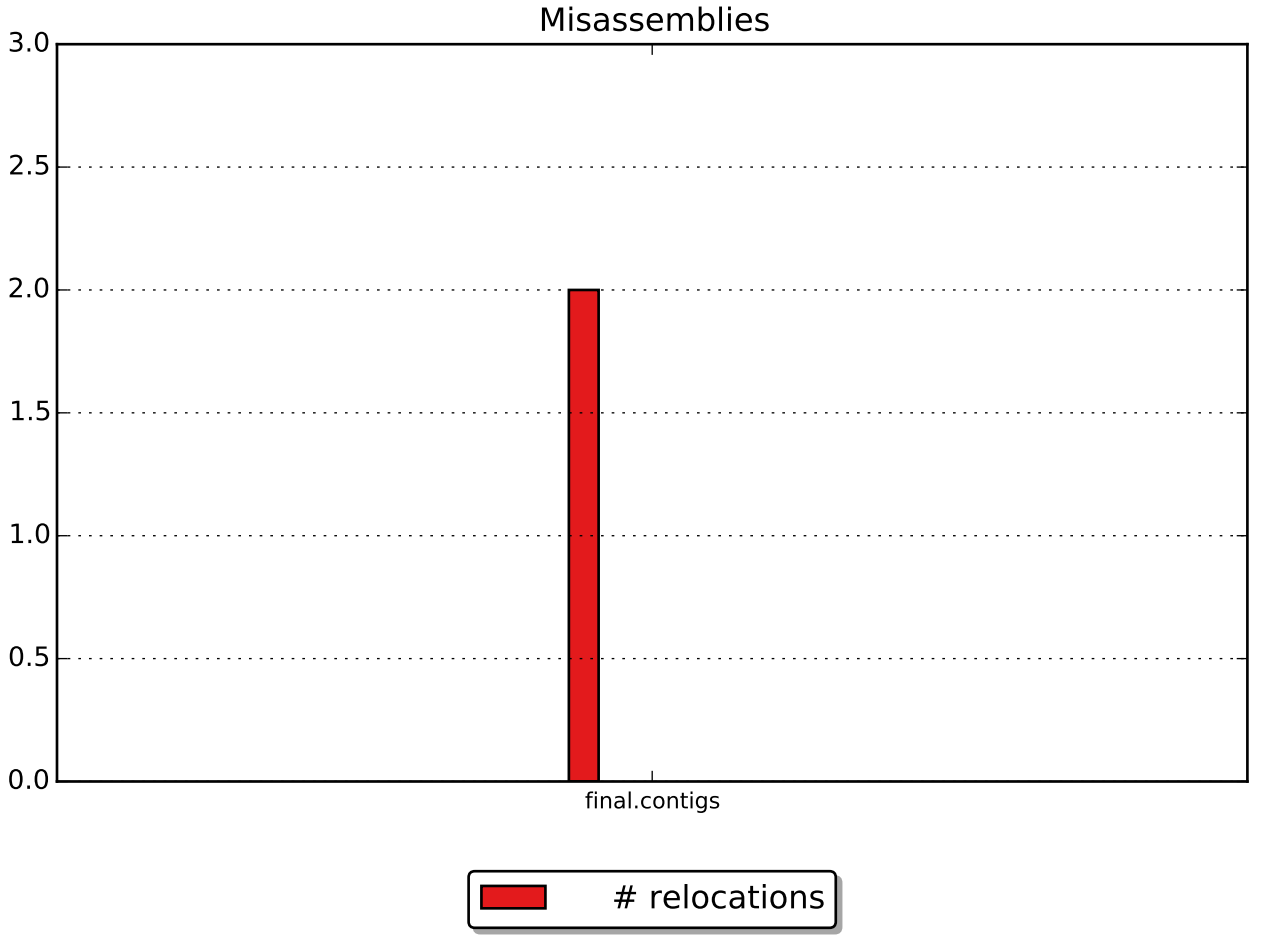
	final.contigs
# fully unaligned contigs	65
Fully unaligned length	25499
# partially unaligned contigs	4
# with misassembly	0
# both parts are significant	4
Partially unaligned length	1666
# N's	0

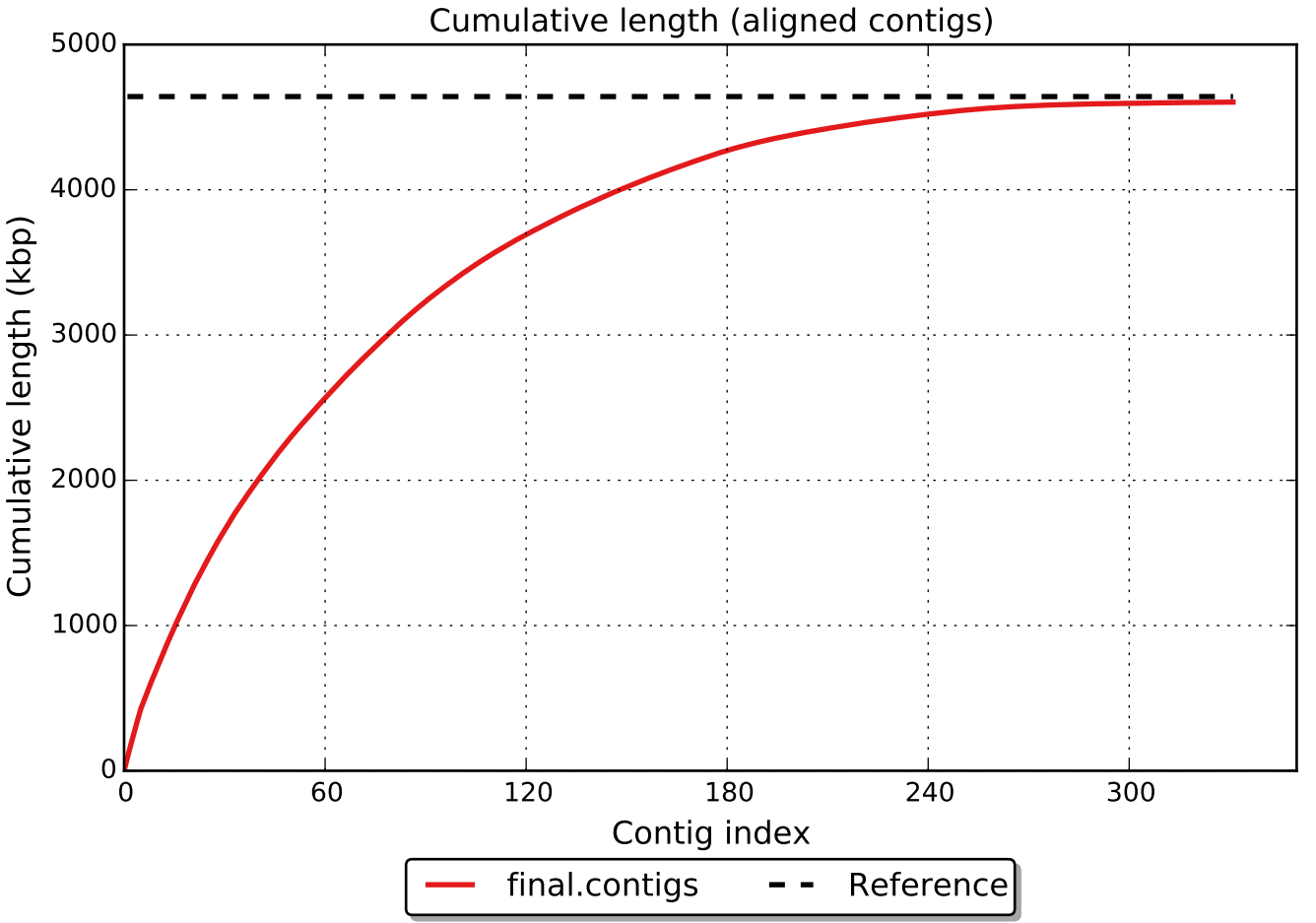

Nx
Contig length (kbp)
100
80
60
40
20
0
0
20
40
60
80
100
x
final.contigs

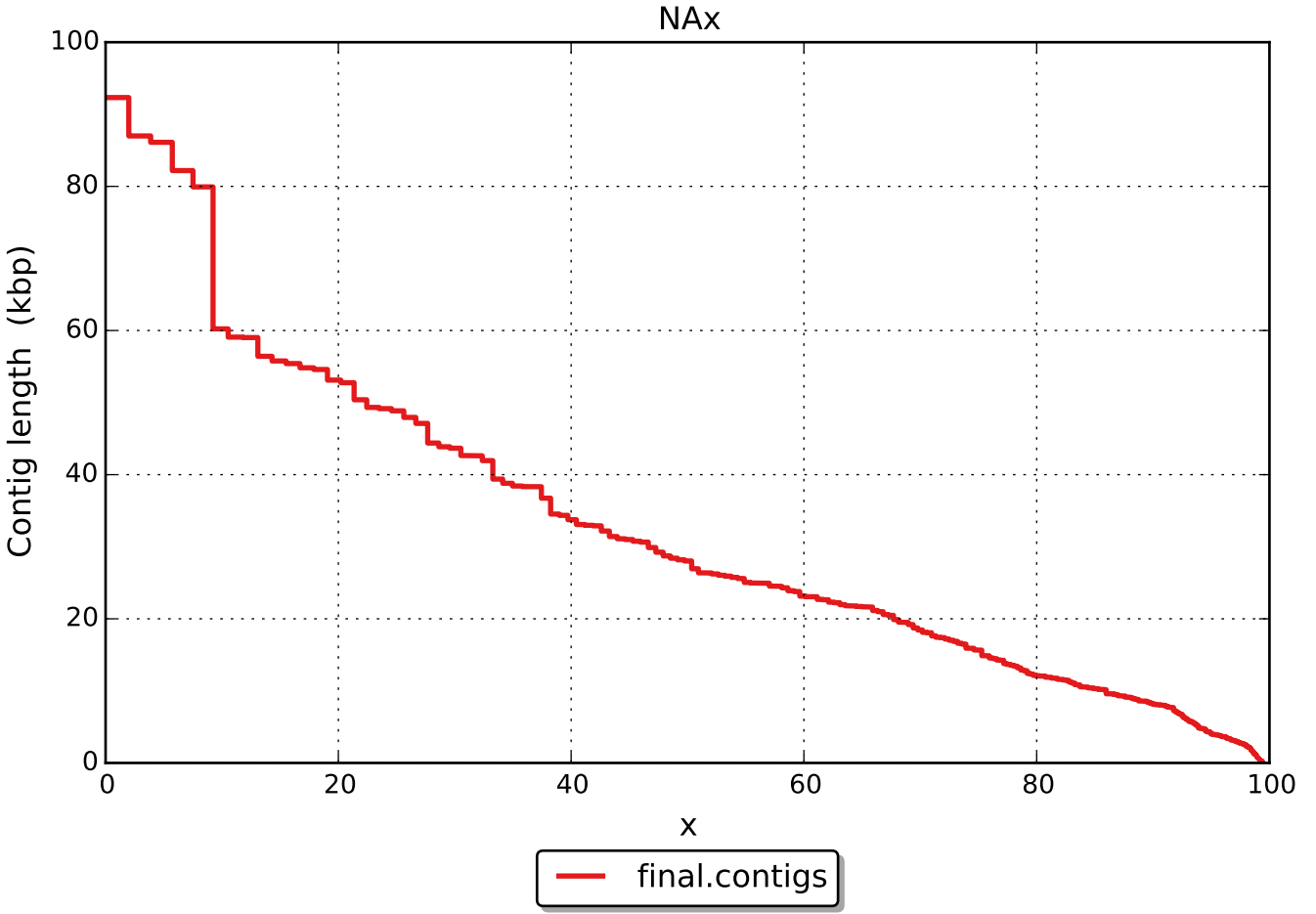

NGx
Contig length (kbp)
100
80
60
40
20
0
0
20
40
60
80
100
x
final.contigs

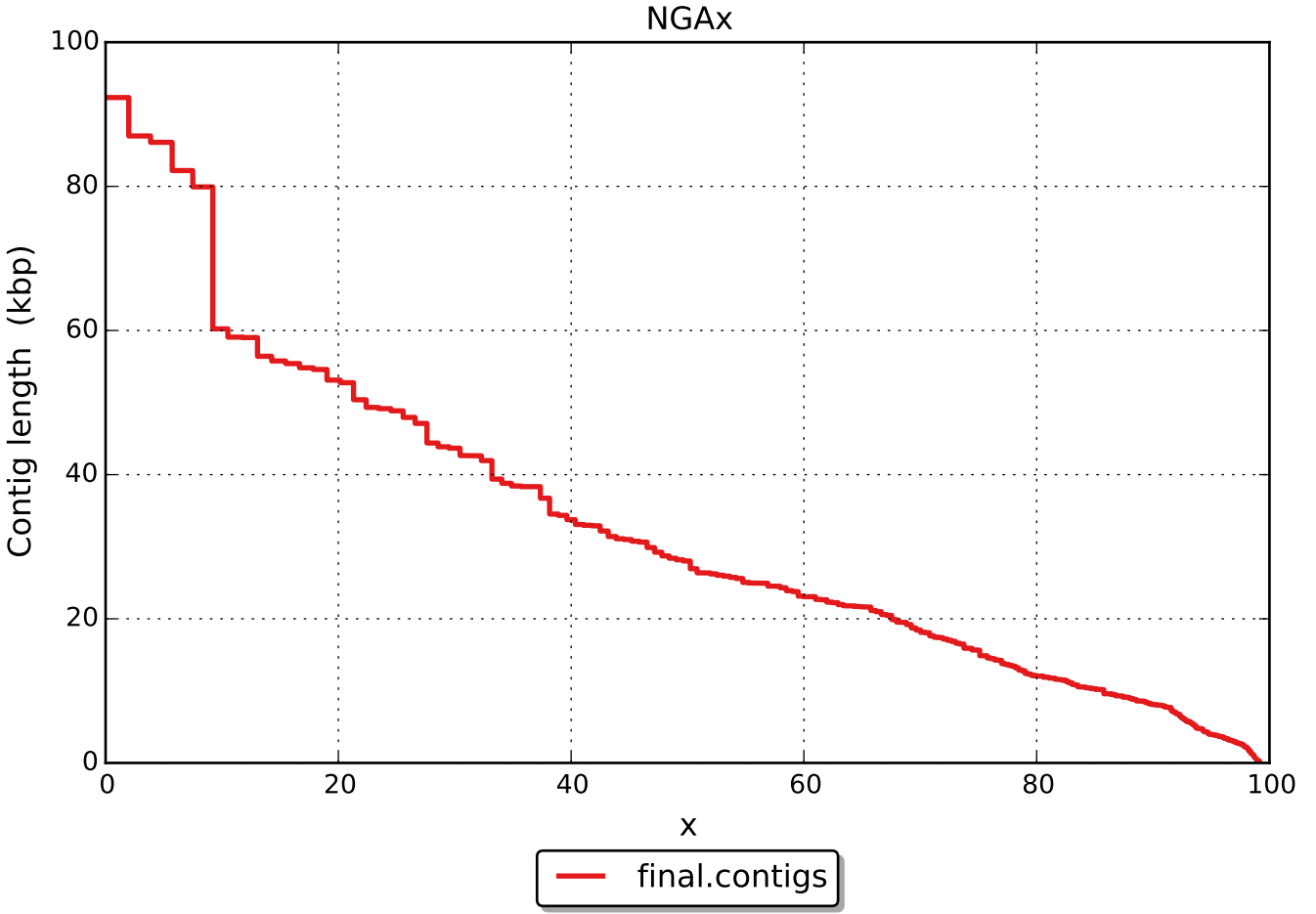

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
80
160
240
320
400
Contig index
final.contigs
Reference


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


Misassemblies
3.0
2.5
2.0
1.5
1.0
0.5
0.0
final.contigs
relocations


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
60
120
180
240
300
Contig index
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