Report

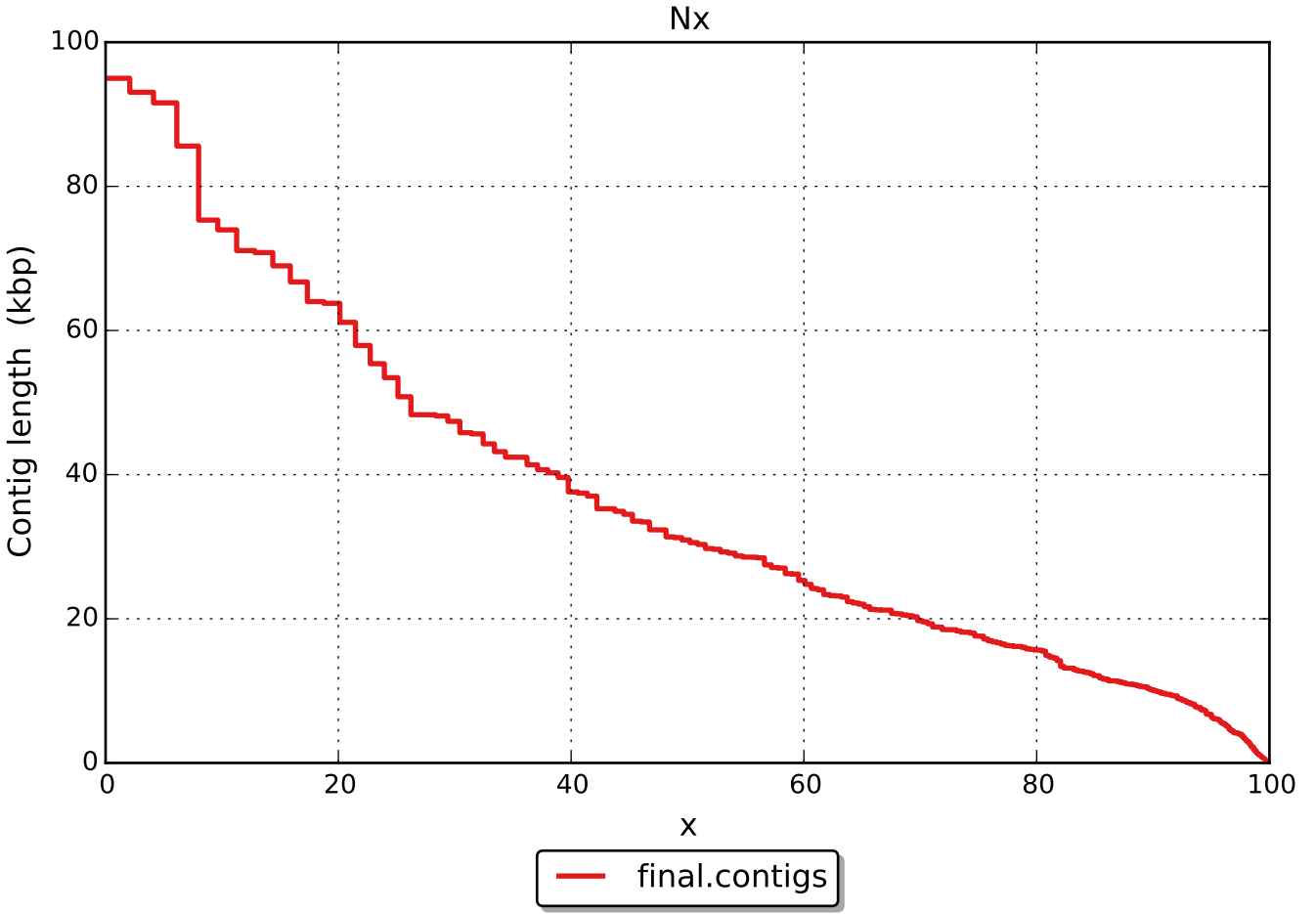
	final.contigs
# contigs (>= 0 bp)	318
# contigs (>= 1000 bp)	233
# contigs (>= 5000 bp)	184
# contigs (>= 10000 bp)	146
# contigs (>= 25000 bp)	61
# contigs (>= 50000 bp)	17
Total length (>= 0 bp)	4569350
Total length (>= 1000 bp)	4535541
Total length (>= 5000 bp)	4410087
Total length (>= 10000 bp)	4121602
Total length (>= 25000 bp)	2746097
Total length (>= 50000 bp)	1198644
# contigs	318
Largest contig	94996
Total length	4569350
Reference length	4641652
GC (%)	50.75
Reference GC (%)	50.79
N50	30931
NG50	30566
N75	17611
NG75	16956
L50	45
LG50	46
L75	94
LG75	97
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	98.300
Duplication ratio	1.001
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.72
# indels per 100 kbp	0.09
Largest alignment	94996
NA50	30931
NGA50	30566
NA75	17611
NGA75	16956
LA50	45
LGA50	46
LA75	94
LGA75	97

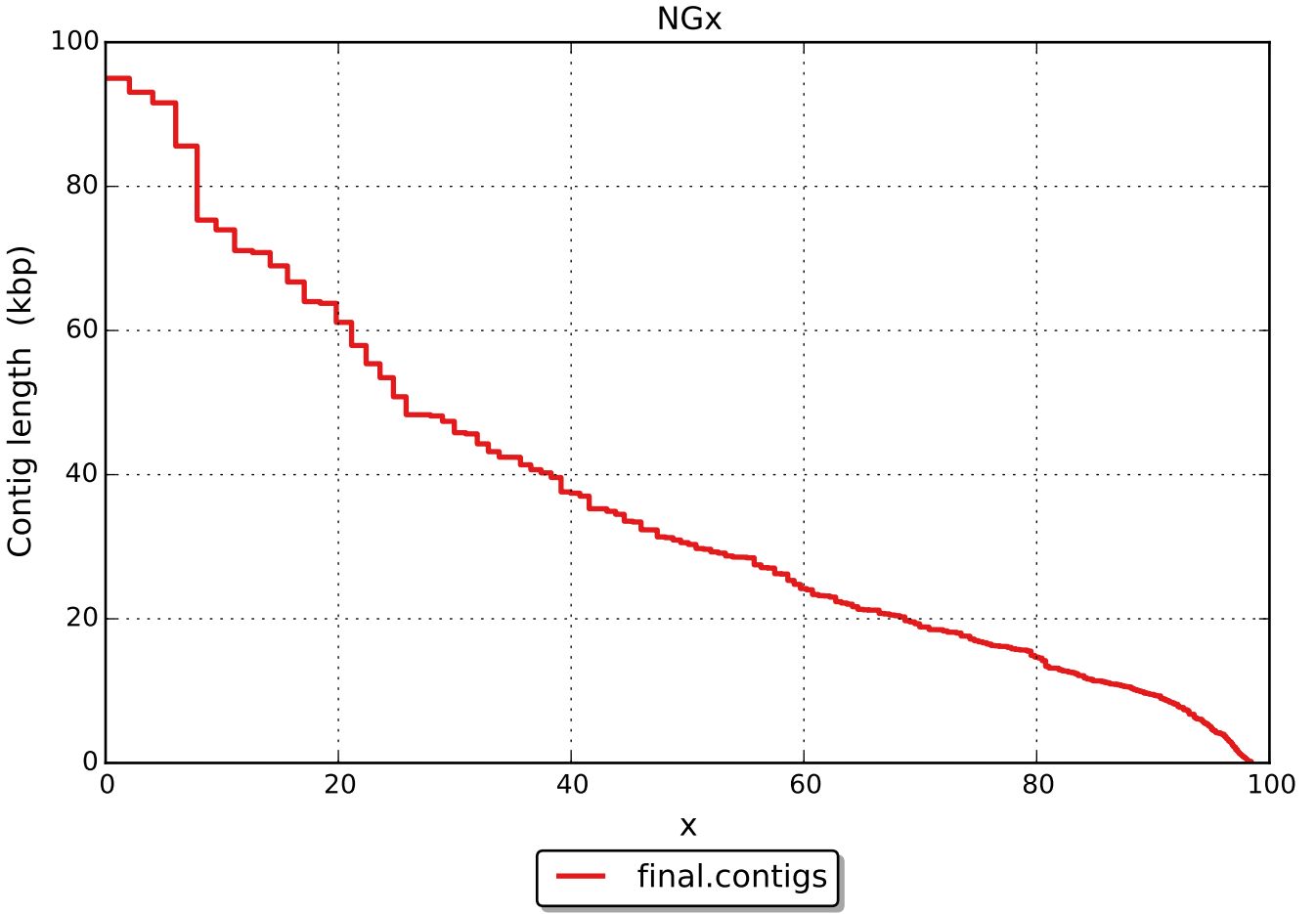
Misassemblies report

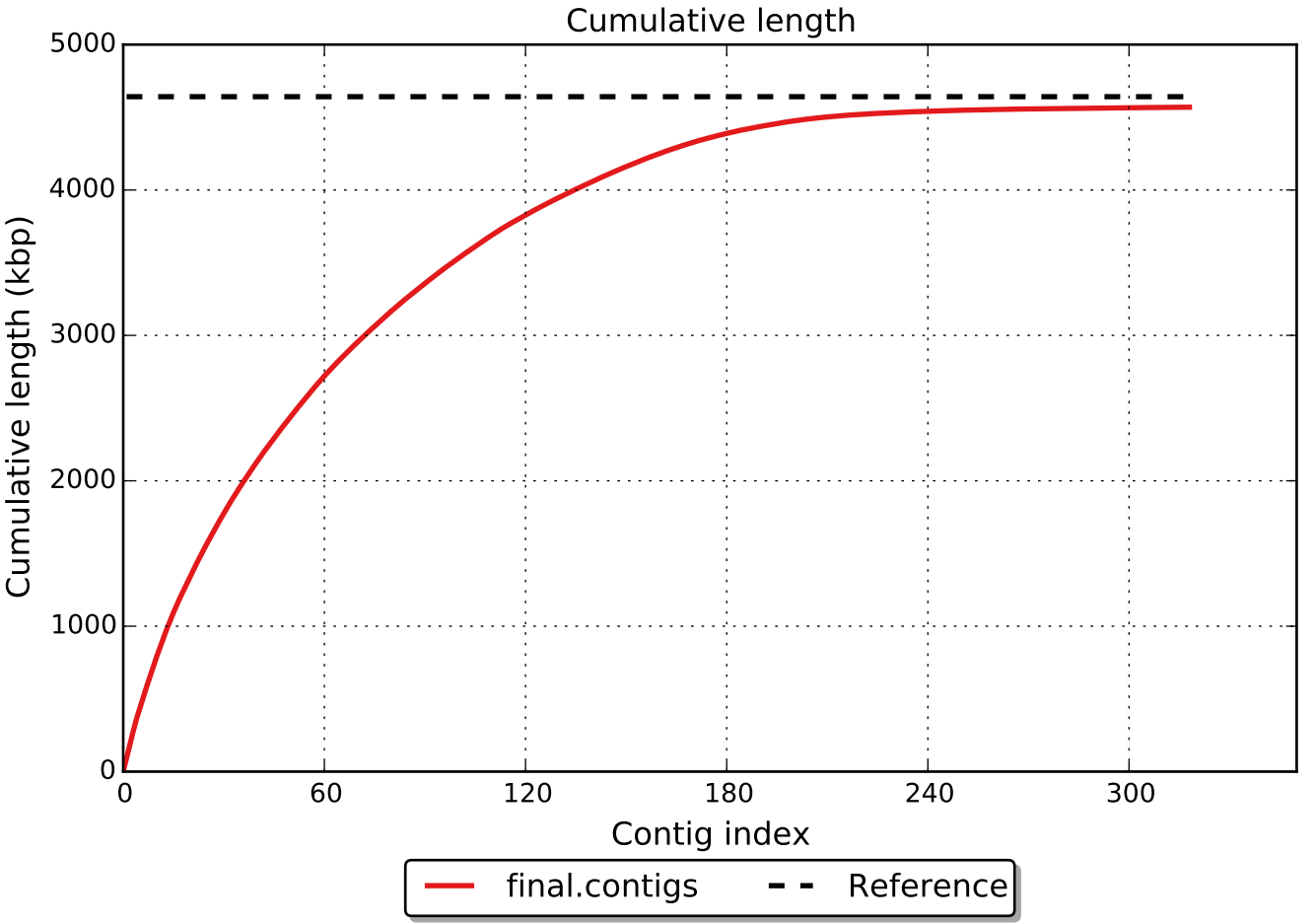
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# mismatches	33
# indels	4
# short indels	3
# long indels	1
Indels length	88

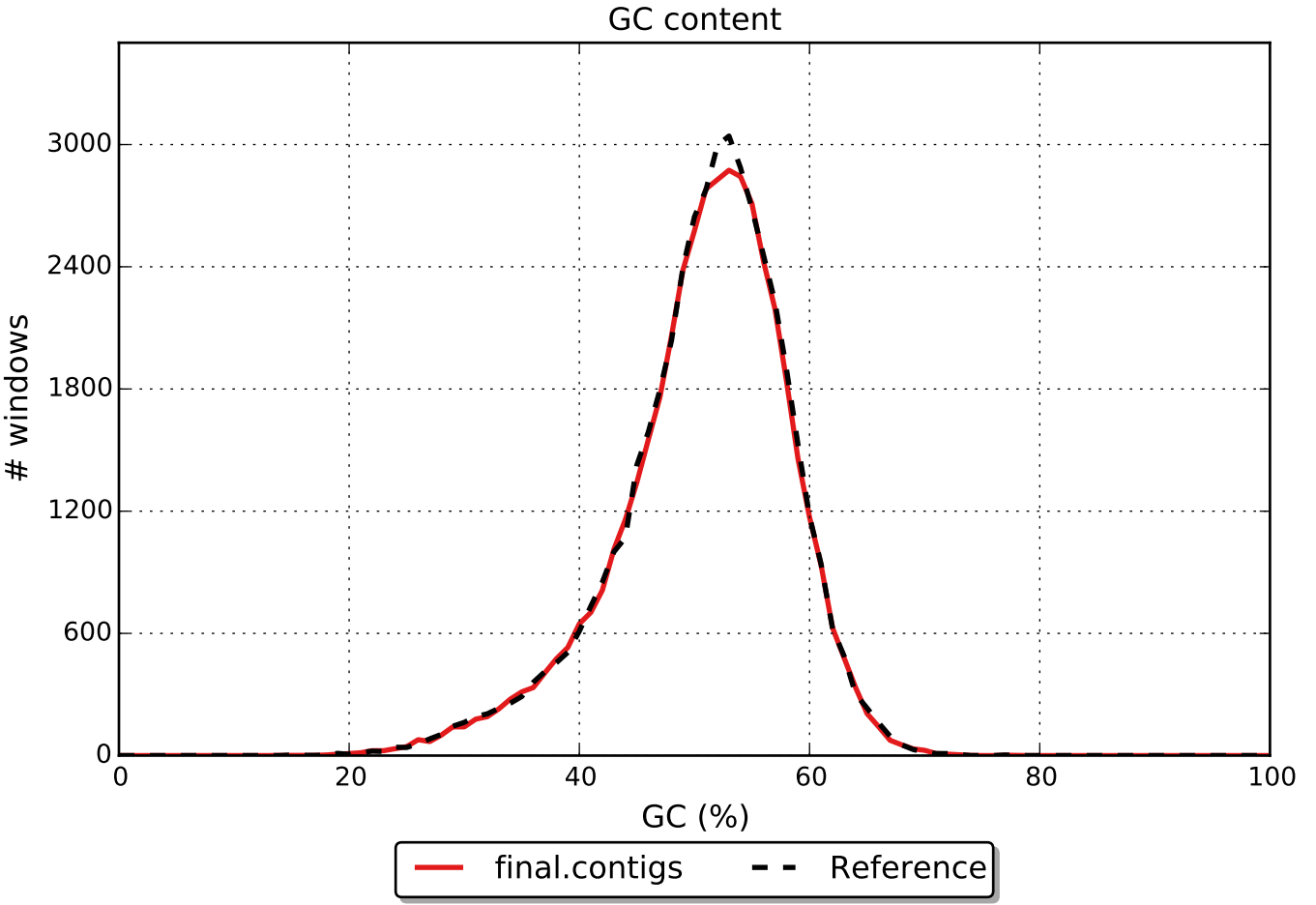
Unaligned report

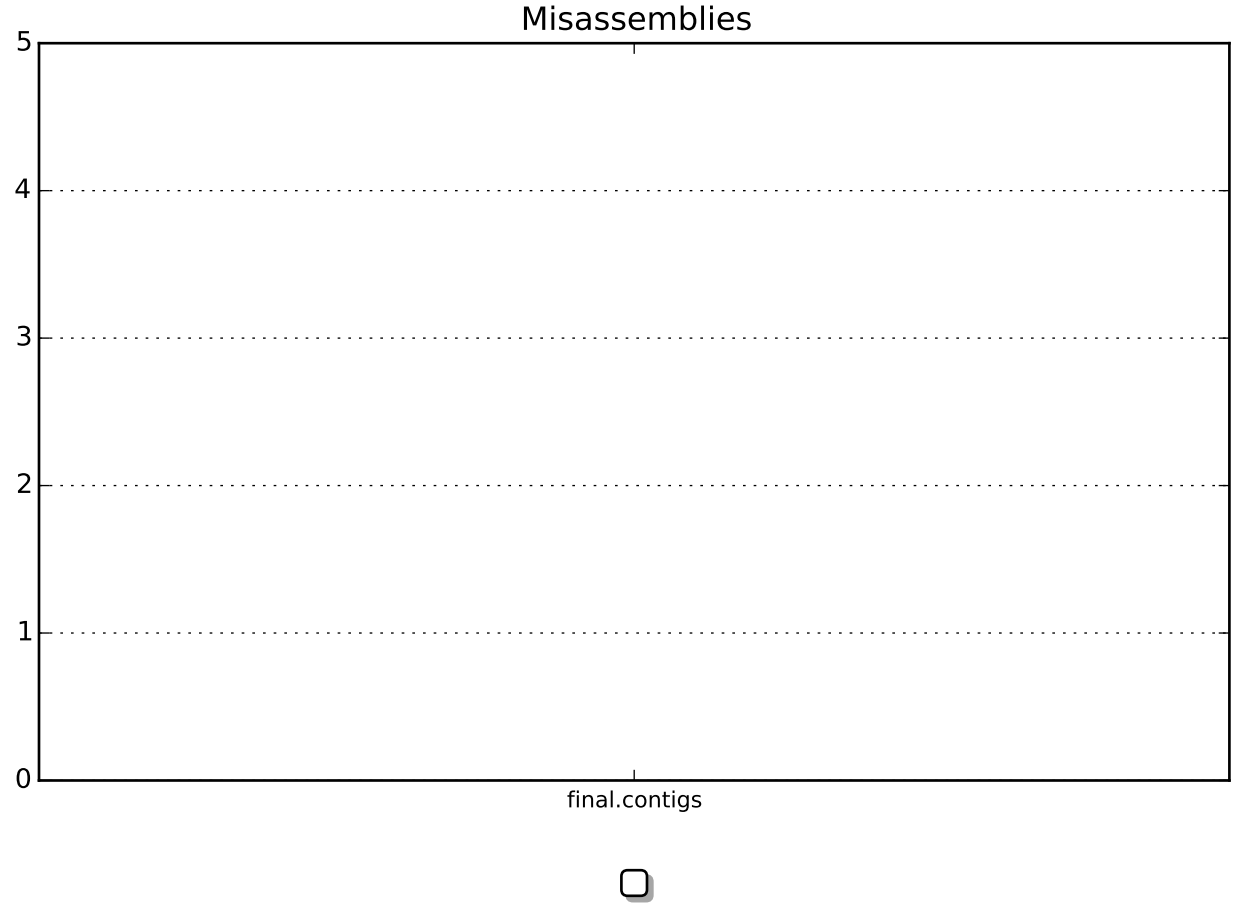
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

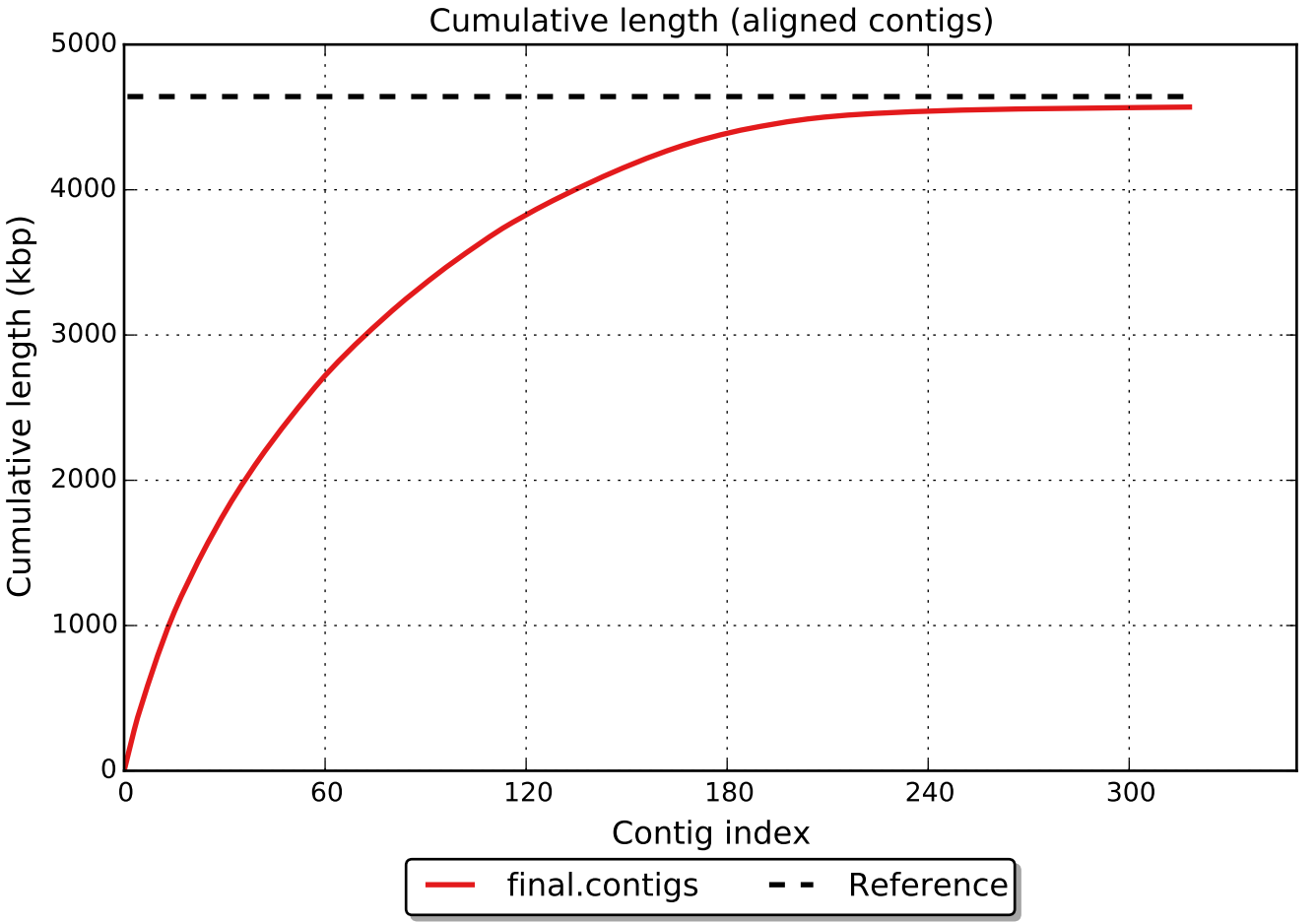

Nx
Contig length (kbp)
100
80
60
40
20
0
0
20
40
60
80
100
x
final.contigs

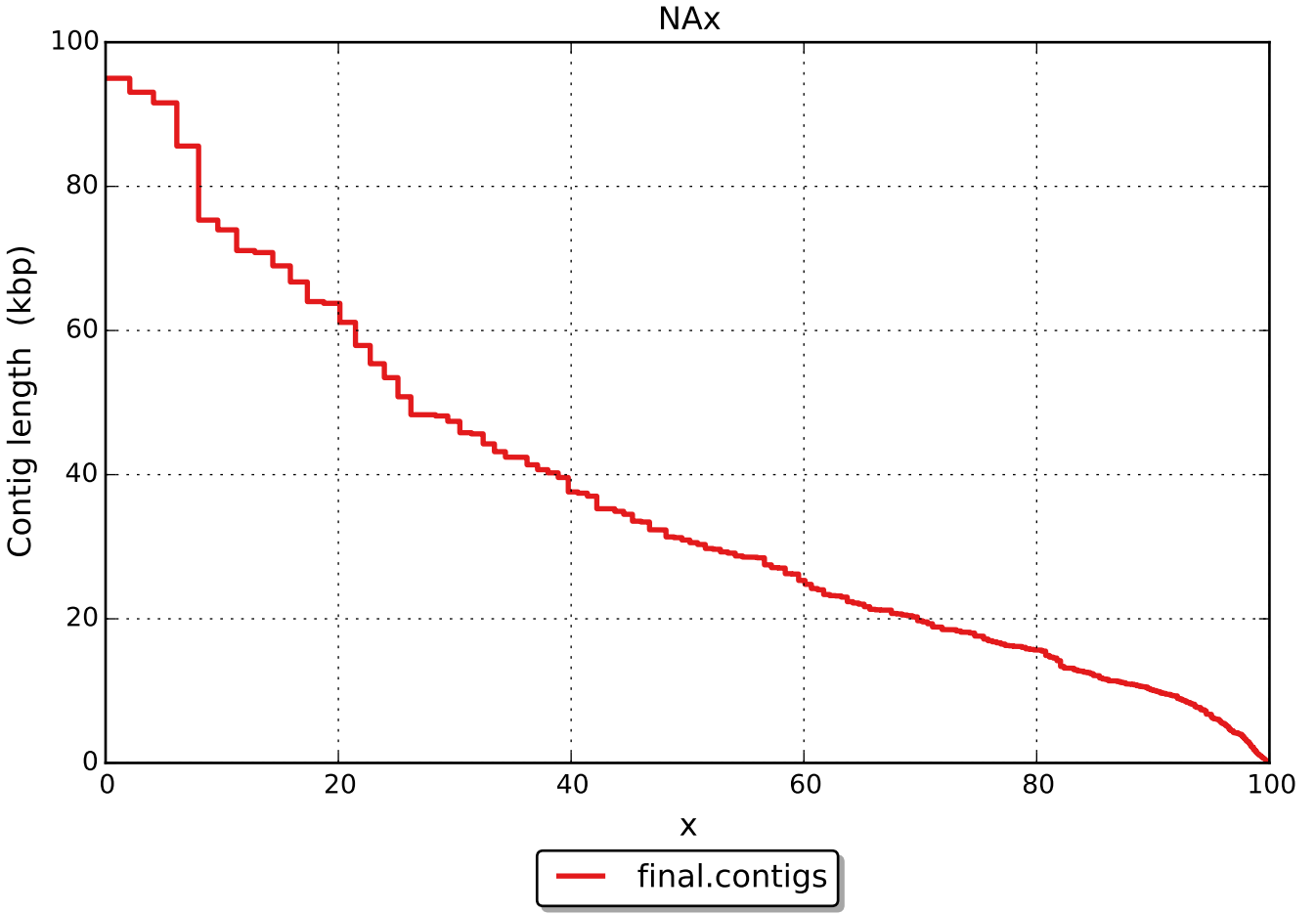

NGx
Contig length (kbp)
100
80
60
40
20
0
0
20
40
60
80
100
x
final.contigs

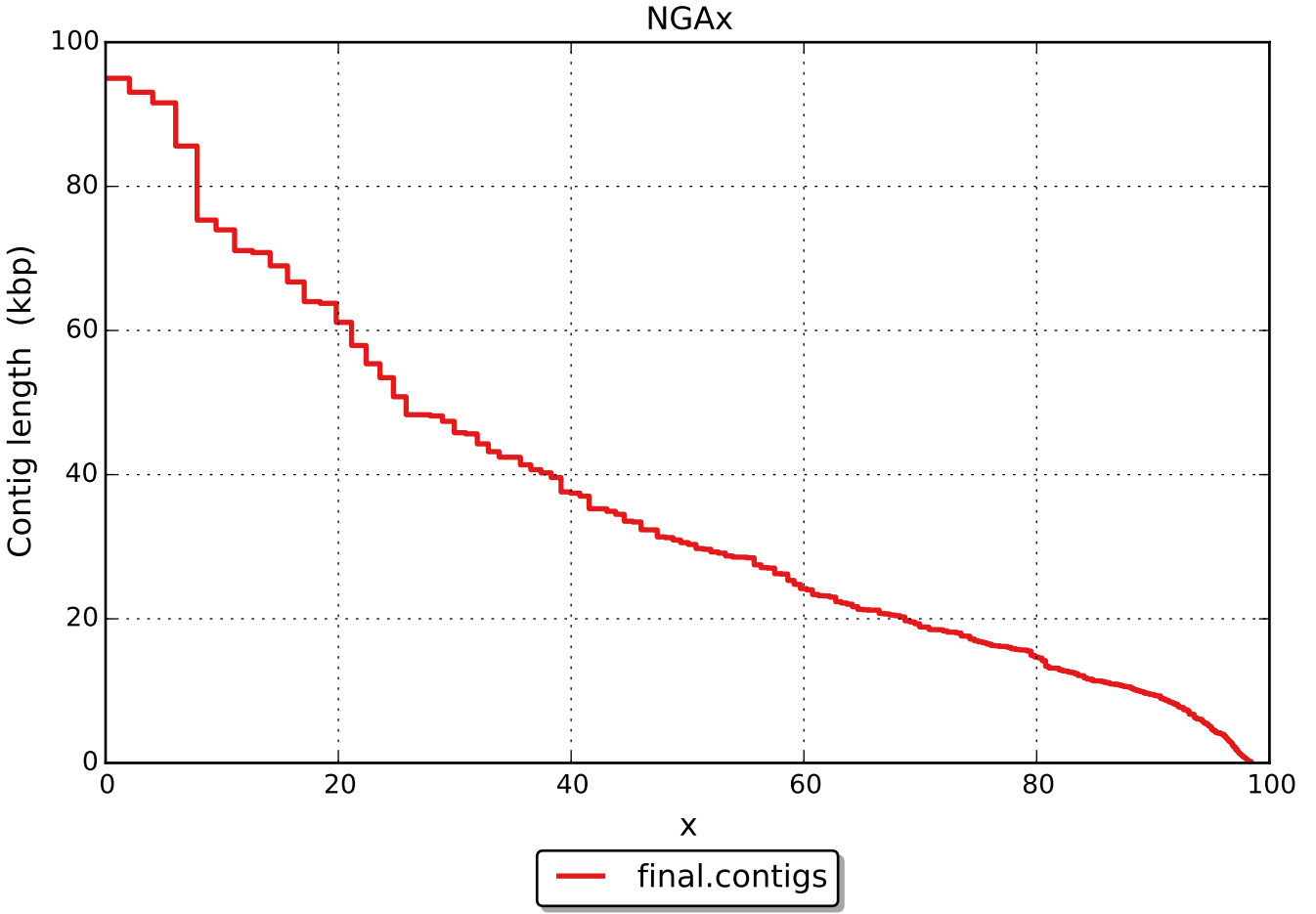

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
60
120
180
240
300
Contig index
final.contigs
Reference


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
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