Report

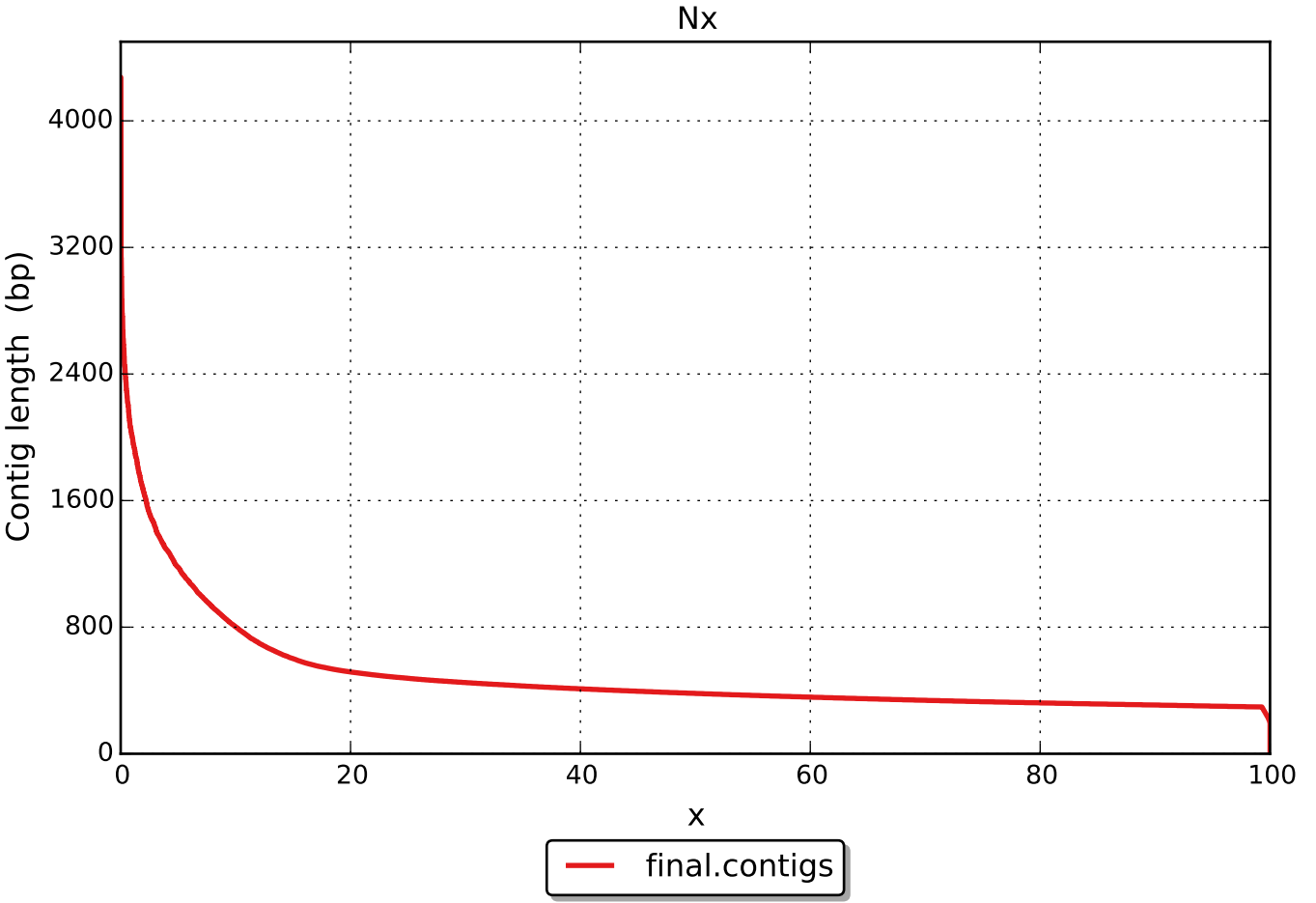
	final.contigs
# contigs (>= 0 bp)	71838
# contigs (>= 1000 bp)	1462
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	29195863
Total length (>= 1000 bp)	2036512
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	71838
Largest contig	4275
Total length	29195863
Reference length	4641652
GC (%)	50.72
Reference GC (%)	50.79
N50	381
NG50	929
N75	329
NG75	705
L50	27544
LG50	1757
L75	48239
LG75	3201
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	786
# local misassemblies	1
# unaligned contigs	68044 + 87 part
Unaligned length	26343468
Genome fraction (%)	57.197
Duplication ratio	1.074
# N's per 100 kbp	0.00
# mismatches per 100 kbp	420.51
# indels per 100 kbp	0.30
Largest alignment	4275
NGA50	517
LGA50	2244

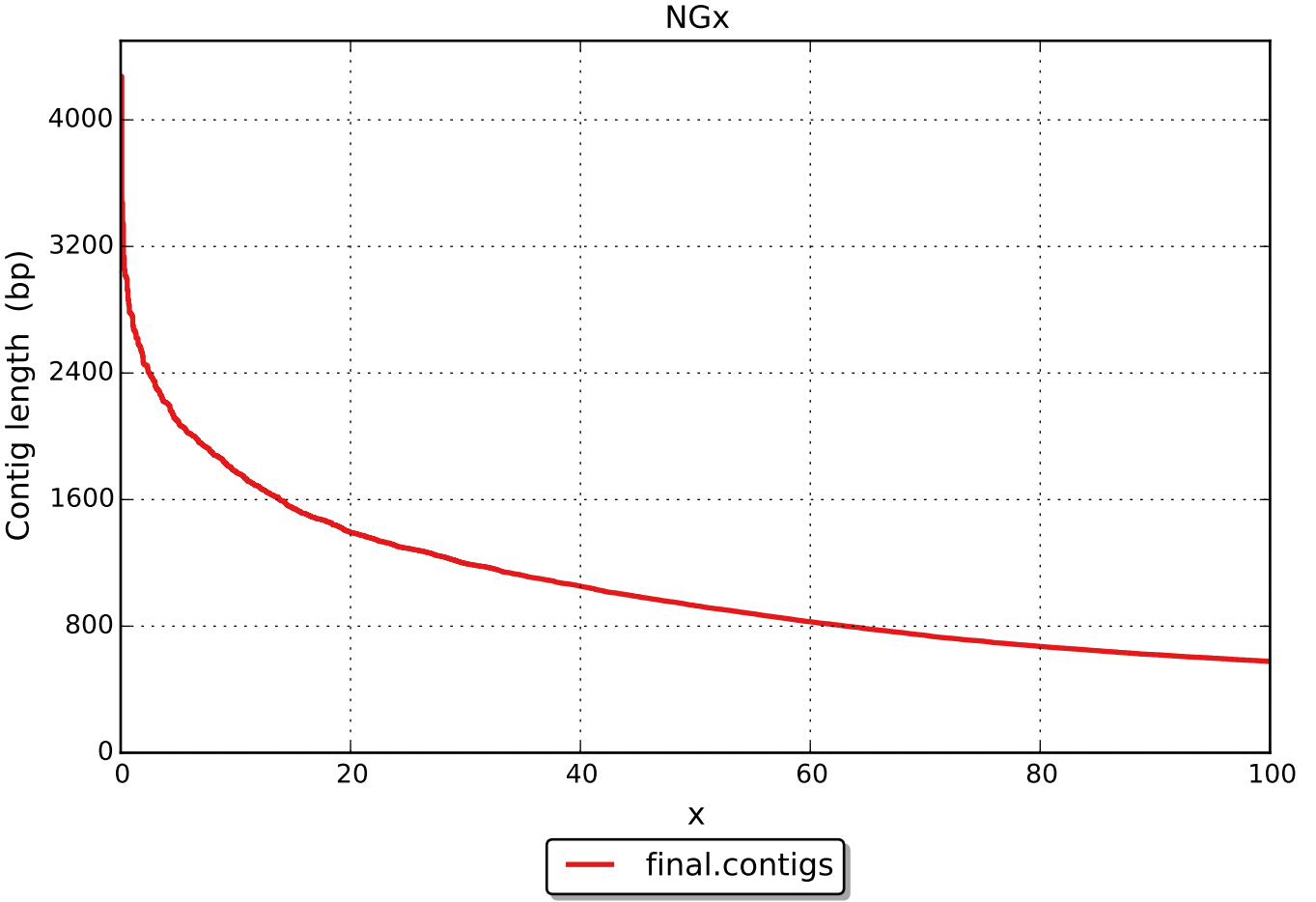
Misassemblies report

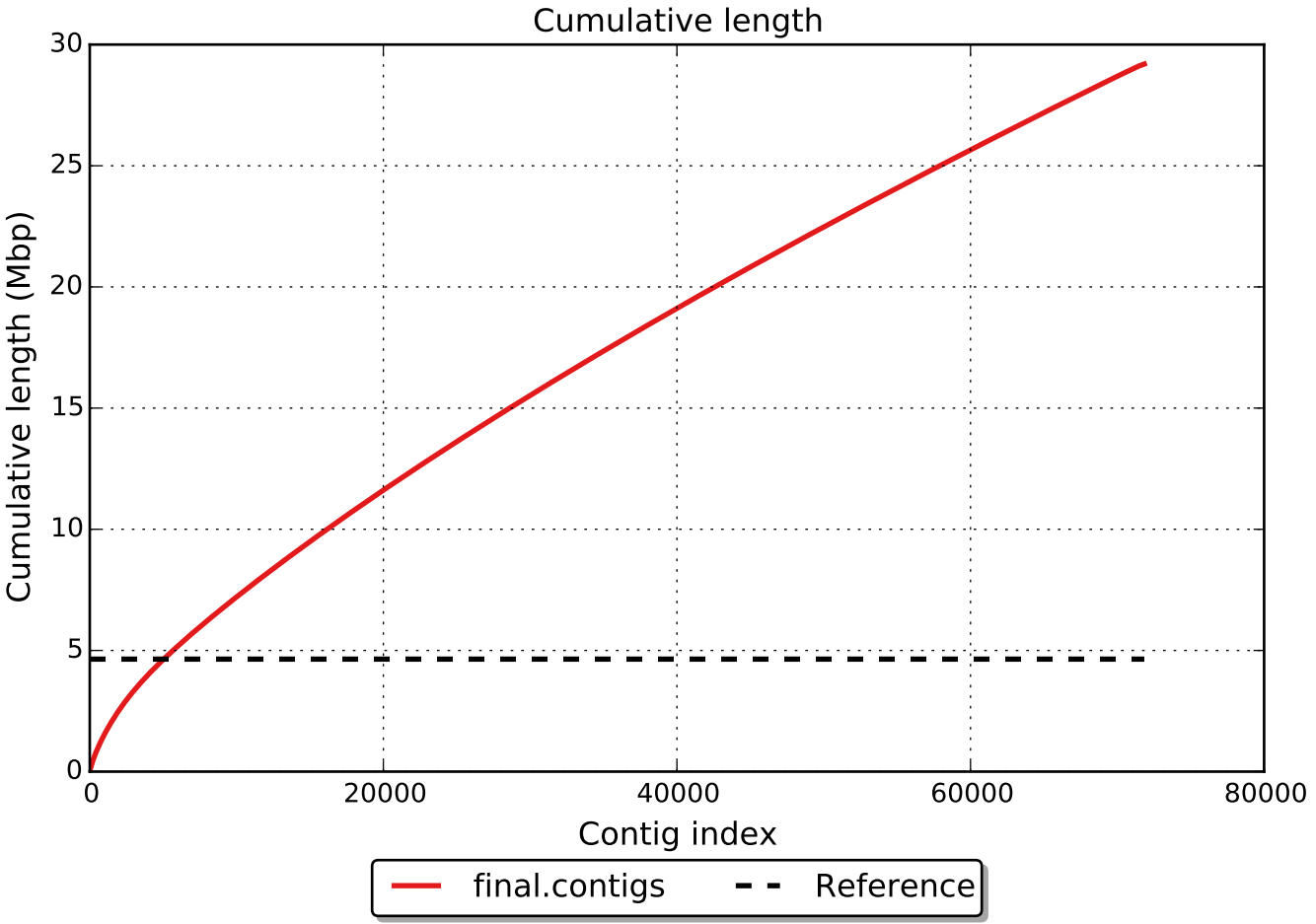
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# misassembled contigs	1
Misassembled contigs length	786
# local misassemblies	1
# mismatches	11164
# indels	8
# short indels	8
# long indels	0
Indels length	9

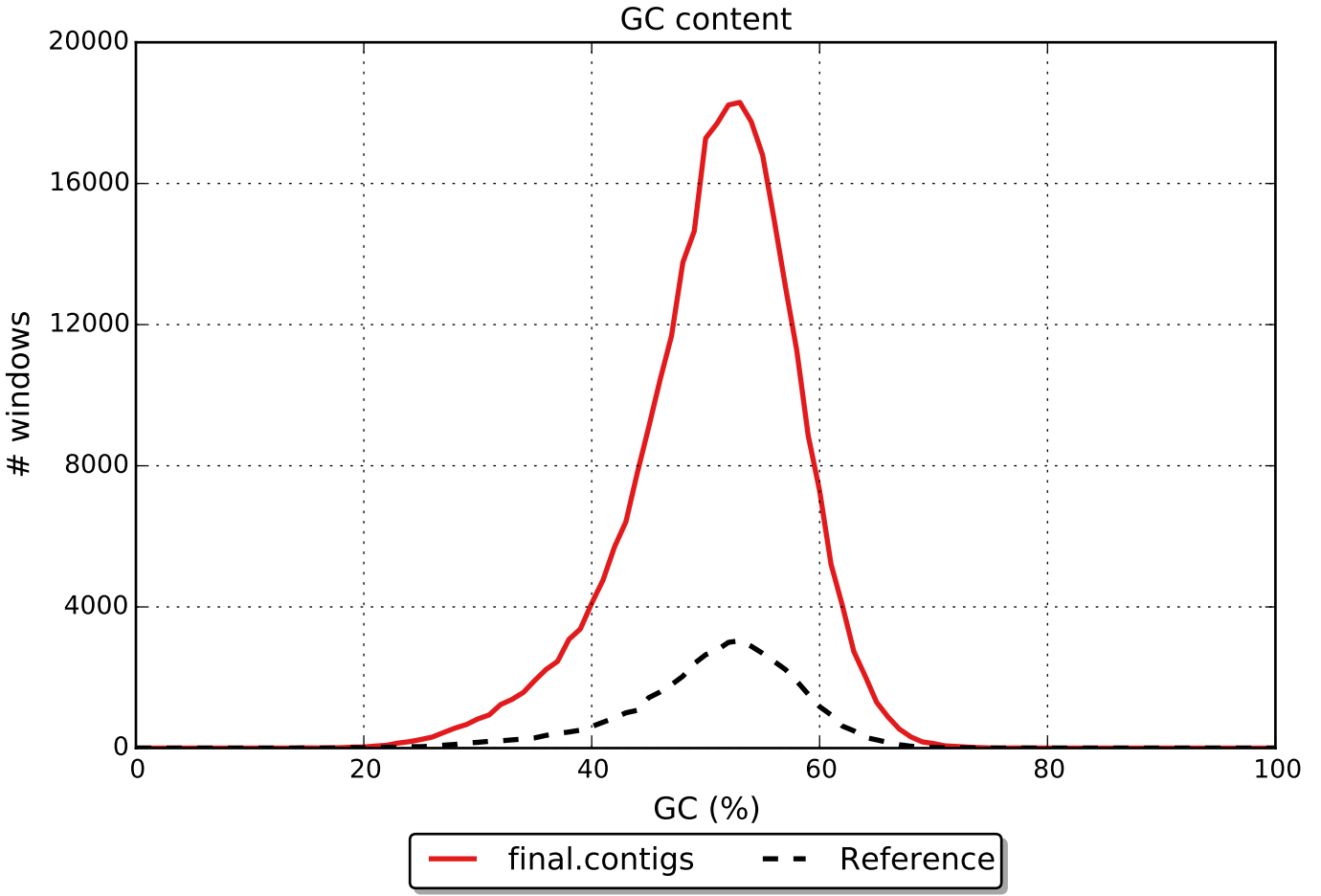
Unaligned report

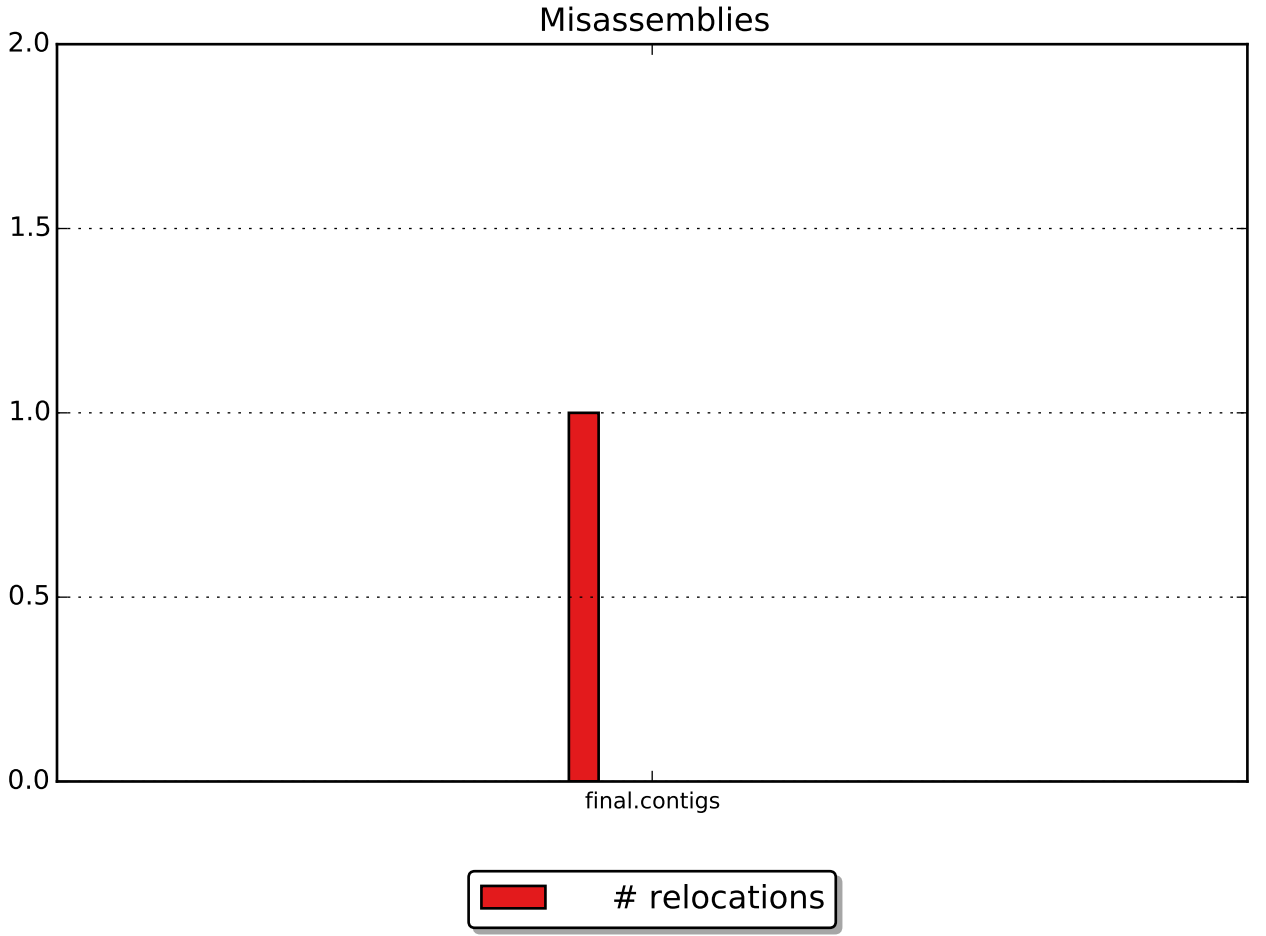
	final.contigs
# fully unaligned contigs	68044
Fully unaligned length	26321186
# partially unaligned contigs	87
# with misassembly	0
# both parts are significant	87
Partially unaligned length	22282
# N's	0

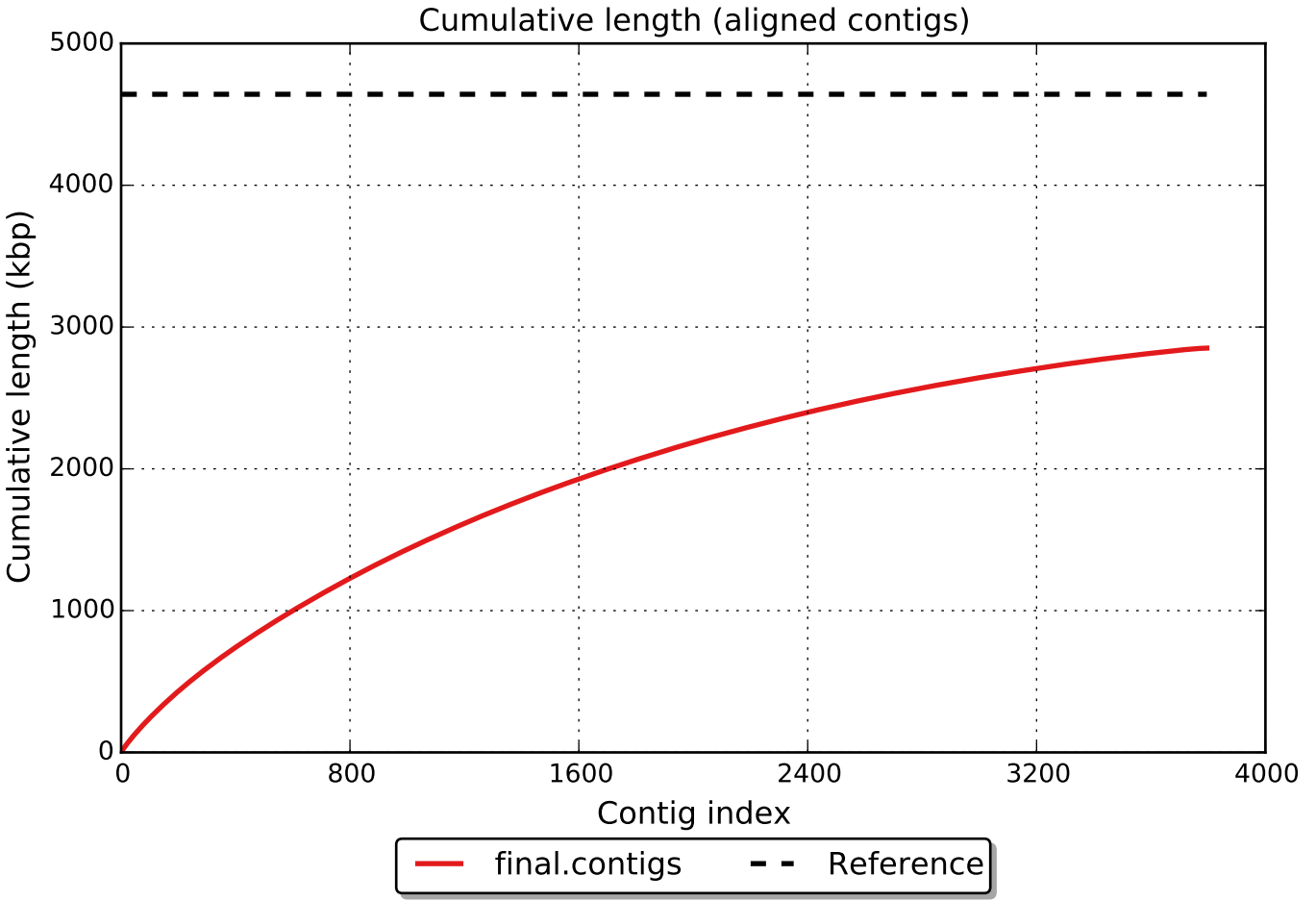

Nx
Contig length (bp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
final.contigs

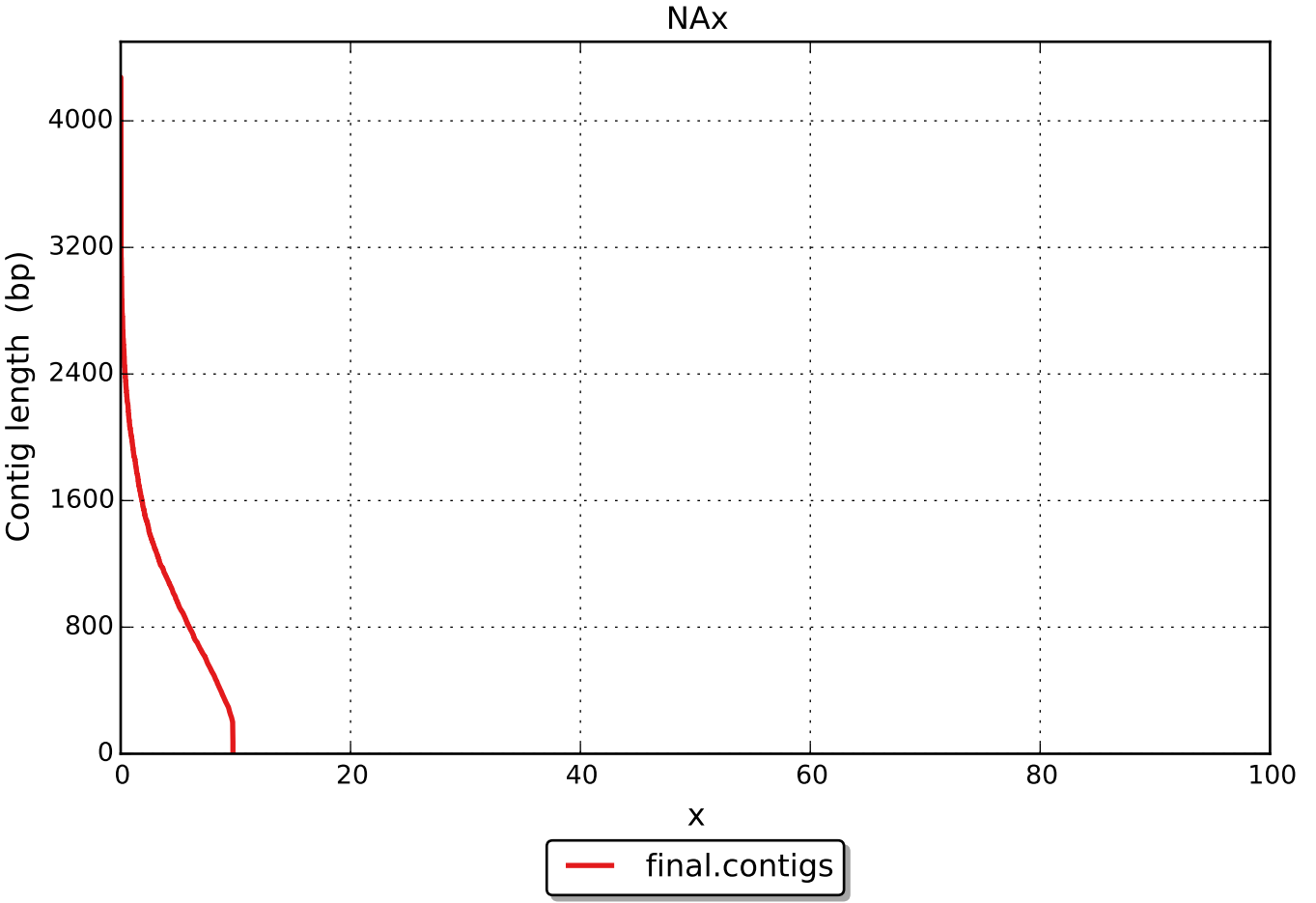

NGx
Contig length (bp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
final.contigs

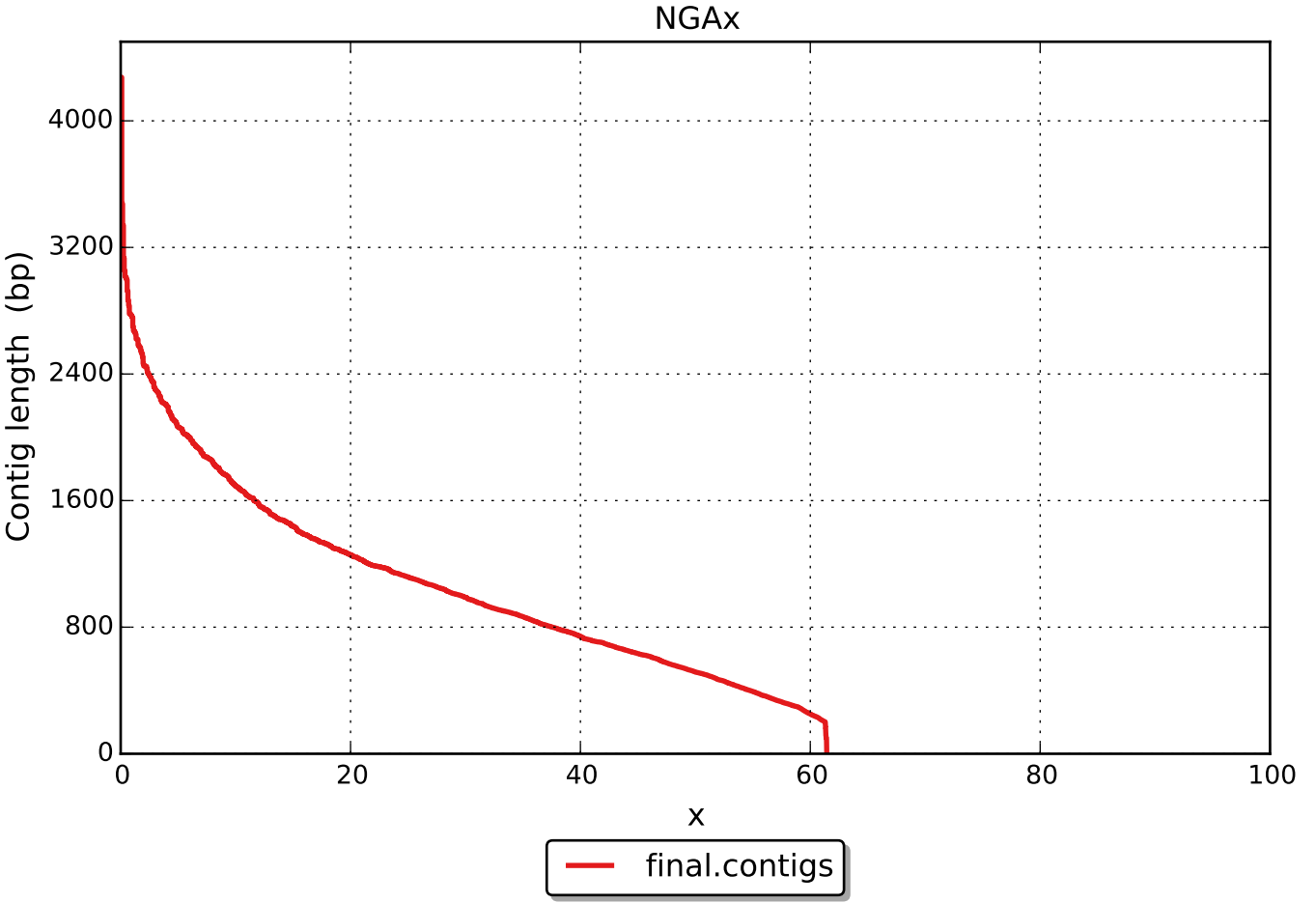

Cumulative length
Cumulative length (Mbp)
30
25
20
15
10
5
0
0
20000
40000
60000
80000
Contig index
final.contigs
Reference


GC content
20000
16000
12000
8000
4000
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference


Misassemblies
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
800
1600
2400
3200
4000
Contig index
final.contigs
Reference


NAx
Contig length (bp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (bp)
4000
3200
2400
1600
800
0
0
20
40
60
80
100
x
final.contigs