Report

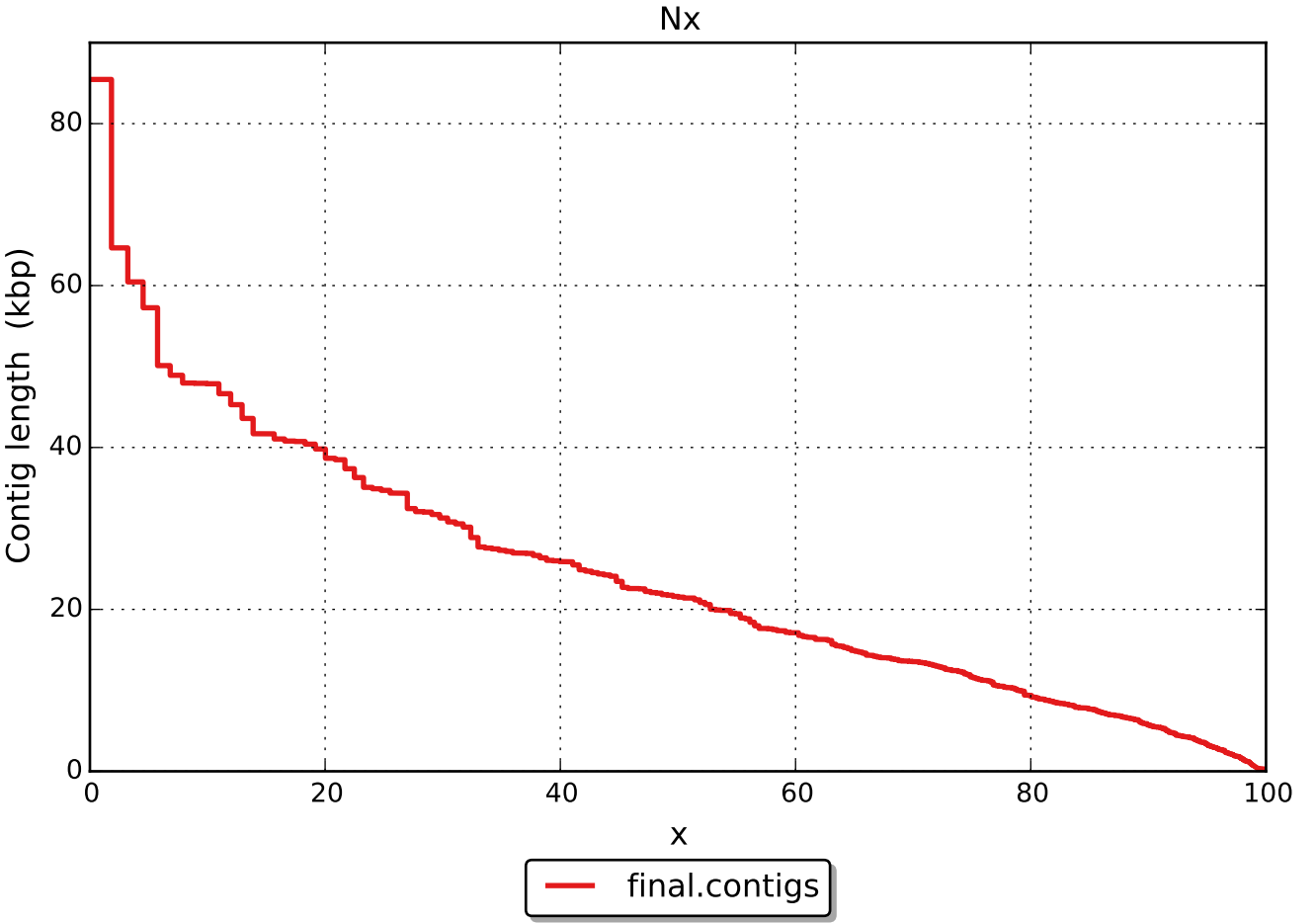
	final.contigs
# contigs (>= 0 bp)	520
# contigs (>= 1000 bp)	364
# contigs (>= 5000 bp)	241
# contigs (>= 10000 bp)	160
# contigs (>= 25000 bp)	52
# contigs (>= 50000 bp)	5
Total length (>= 0 bp)	4655654
Total length (>= 1000 bp)	4594340
Total length (>= 5000 bp)	4266773
Total length (>= 10000 bp)	3679268
Total length (>= 25000 bp)	1936808
Total length (>= 50000 bp)	317938
# contigs	520
Largest contig	85460
Total length	4655654
Reference length	4641652
GC (%)	50.76
Reference GC (%)	50.79
N50	21600
NG50	21600
N75	11661
NG75	11932
L50	69
LG50	69
L75	143
LG75	142
# misassemblies	3
# misassembled contigs	3
Misassembled contigs length	111486
# local misassemblies	2
# unaligned contigs	90 + 9 part
Unaligned length	41521
Genome fraction (%)	98.193
Duplication ratio	1.012
# N's per 100 kbp	0.00
# mismatches per 100 kbp	57.44
# indels per 100 kbp	0.24
Largest alignment	85460
NA50	21513
NGA50	21513
NA75	11427
NGA75	11546
LA50	70
LGA50	70
LA75	145
LGA75	144

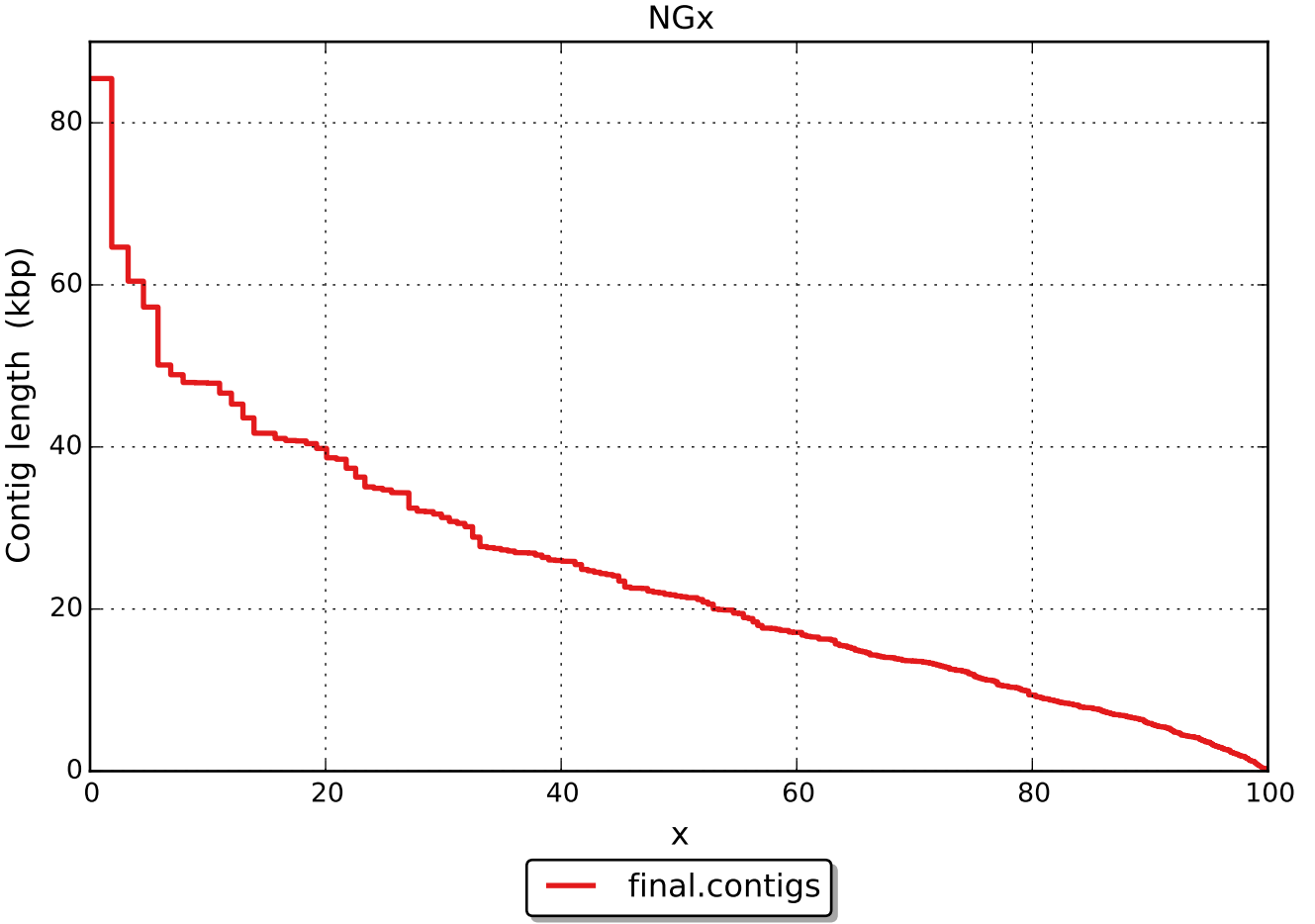
Misassemblies report

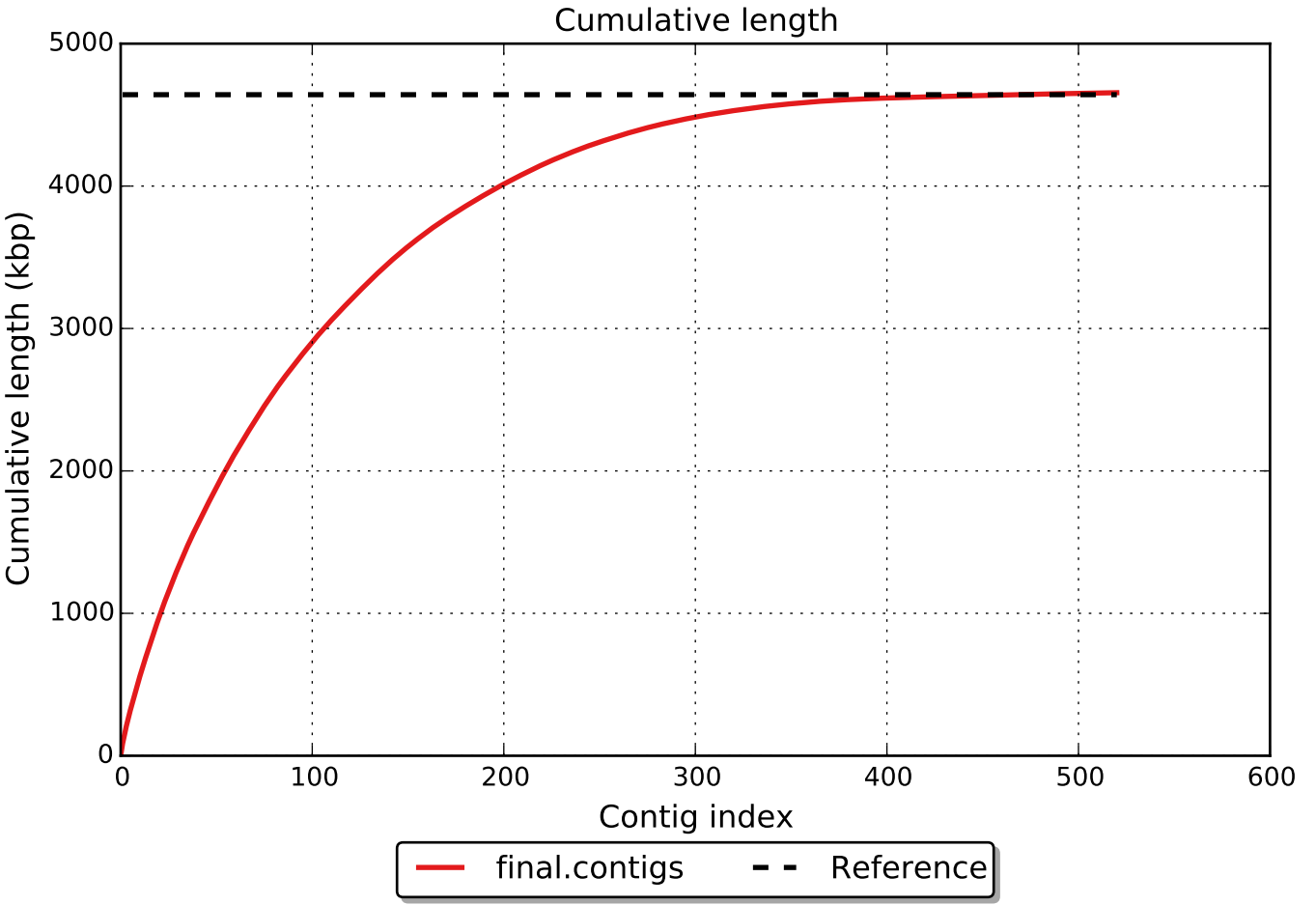
	final.contigs
# misassemblies	3
# relocations	3
# translocations	0
# inversions	0
# misassembled contigs	3
Misassembled contigs length	111486
# local misassemblies	2
# mismatches	2618
# indels	11
# short indels	10
# long indels	1
Indels length	92

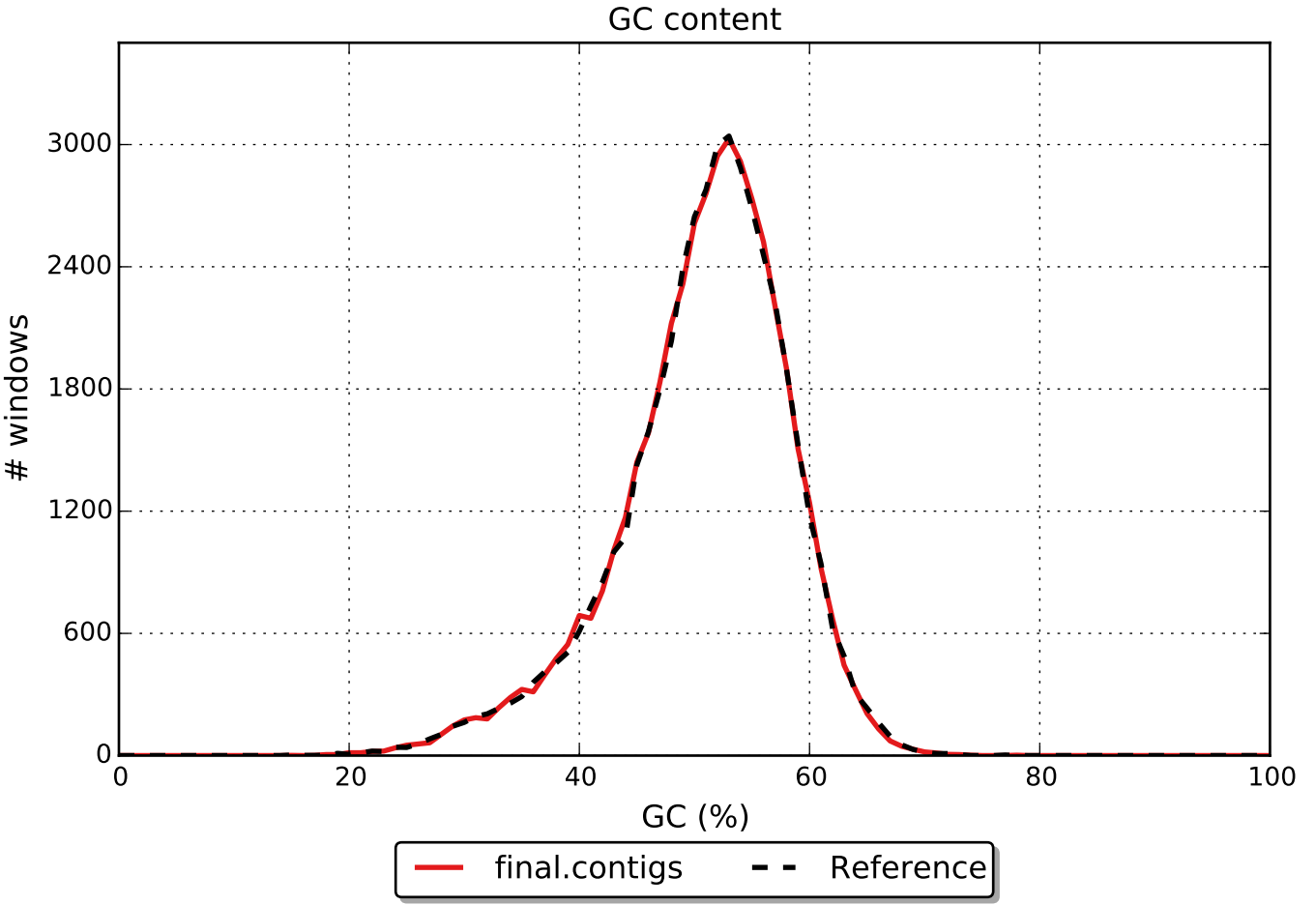
Unaligned report

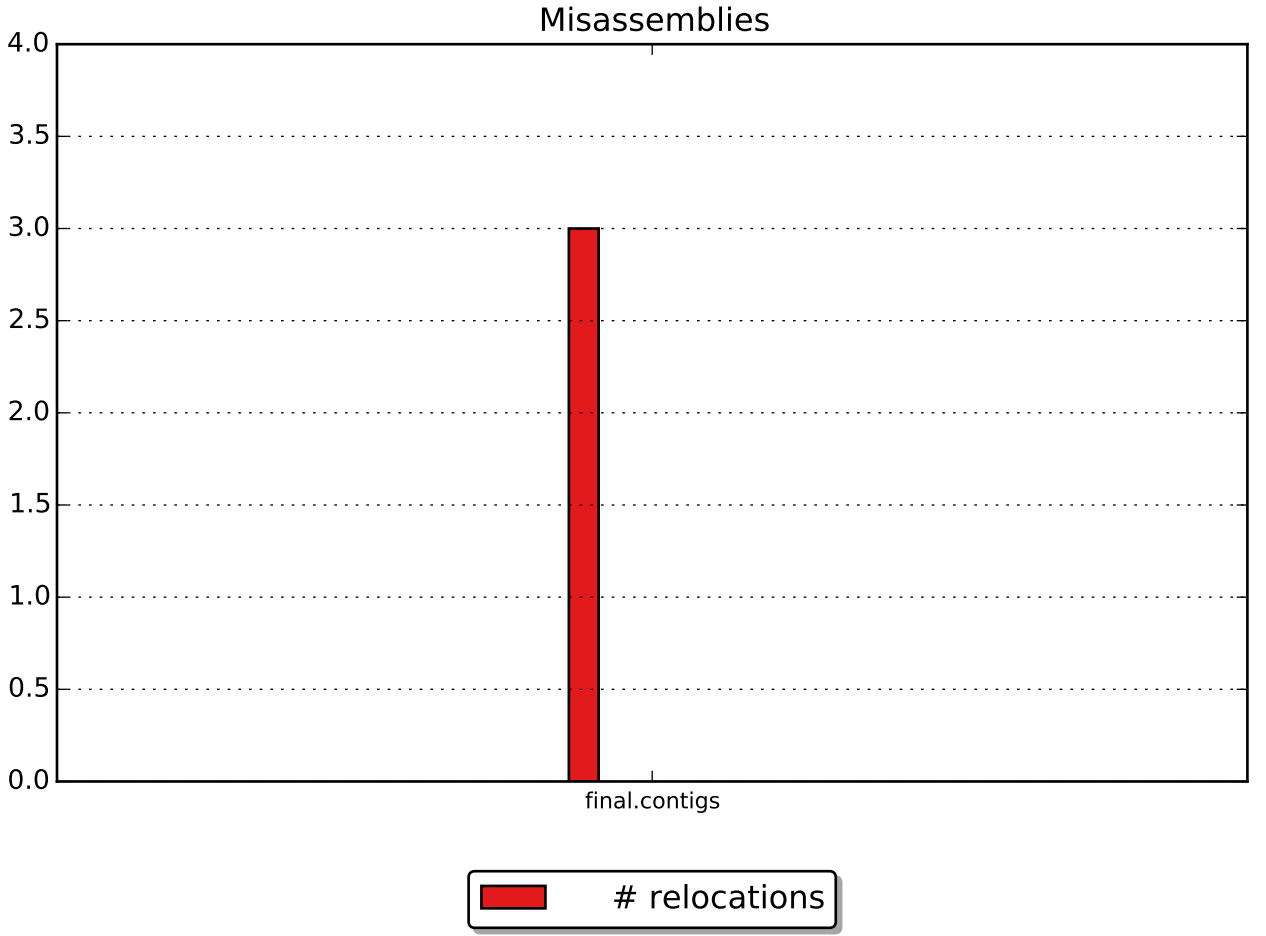
	final.contigs
# fully unaligned contigs	90
Fully unaligned length	32942
# partially unaligned contigs	9
# with misassembly	0
# both parts are significant	9
Partially unaligned length	8579
# N's	0

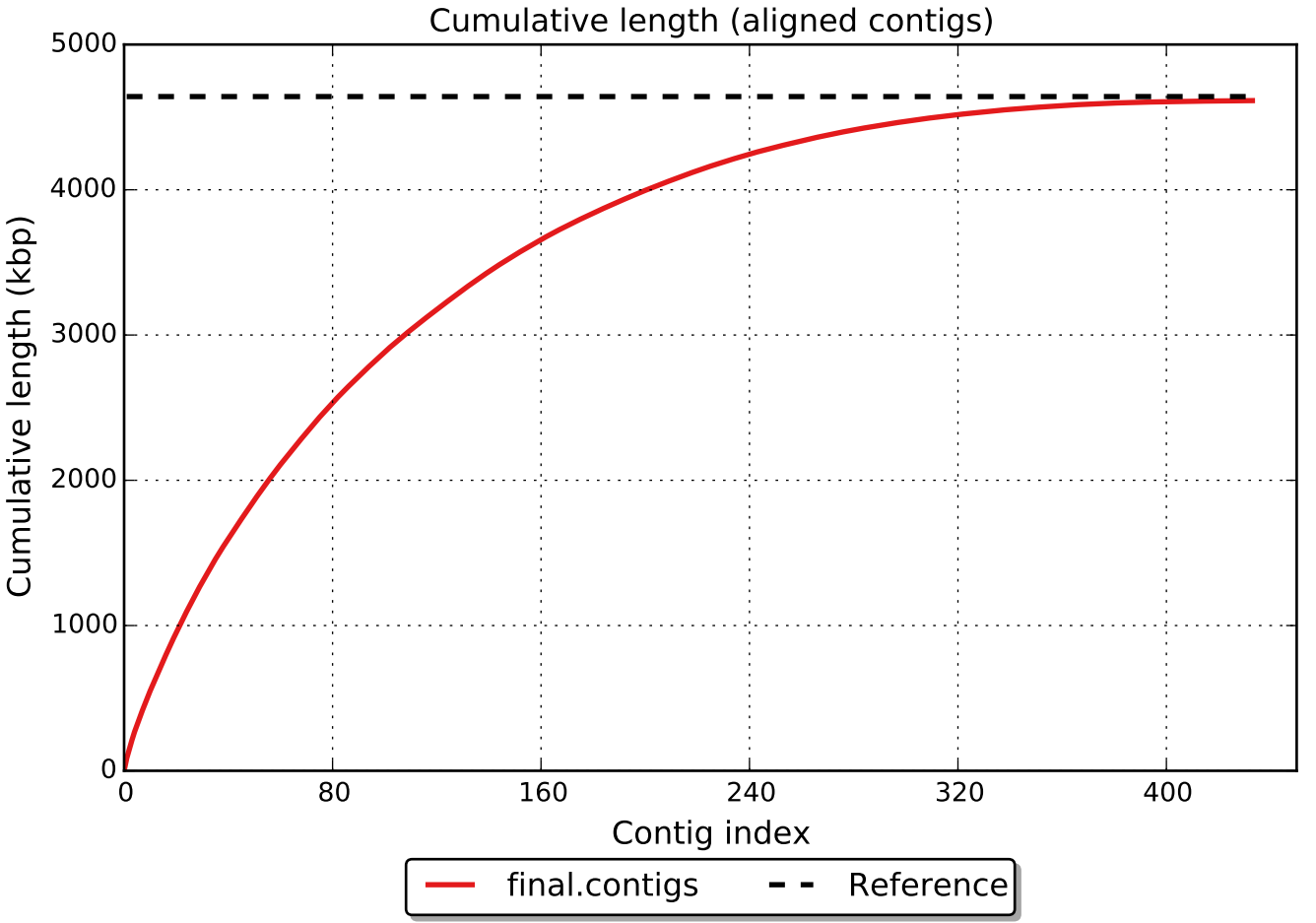

Nx
Contig length (kbp)
0
20
40
60
80
0
20
40
60
80
100
x
final.contigs

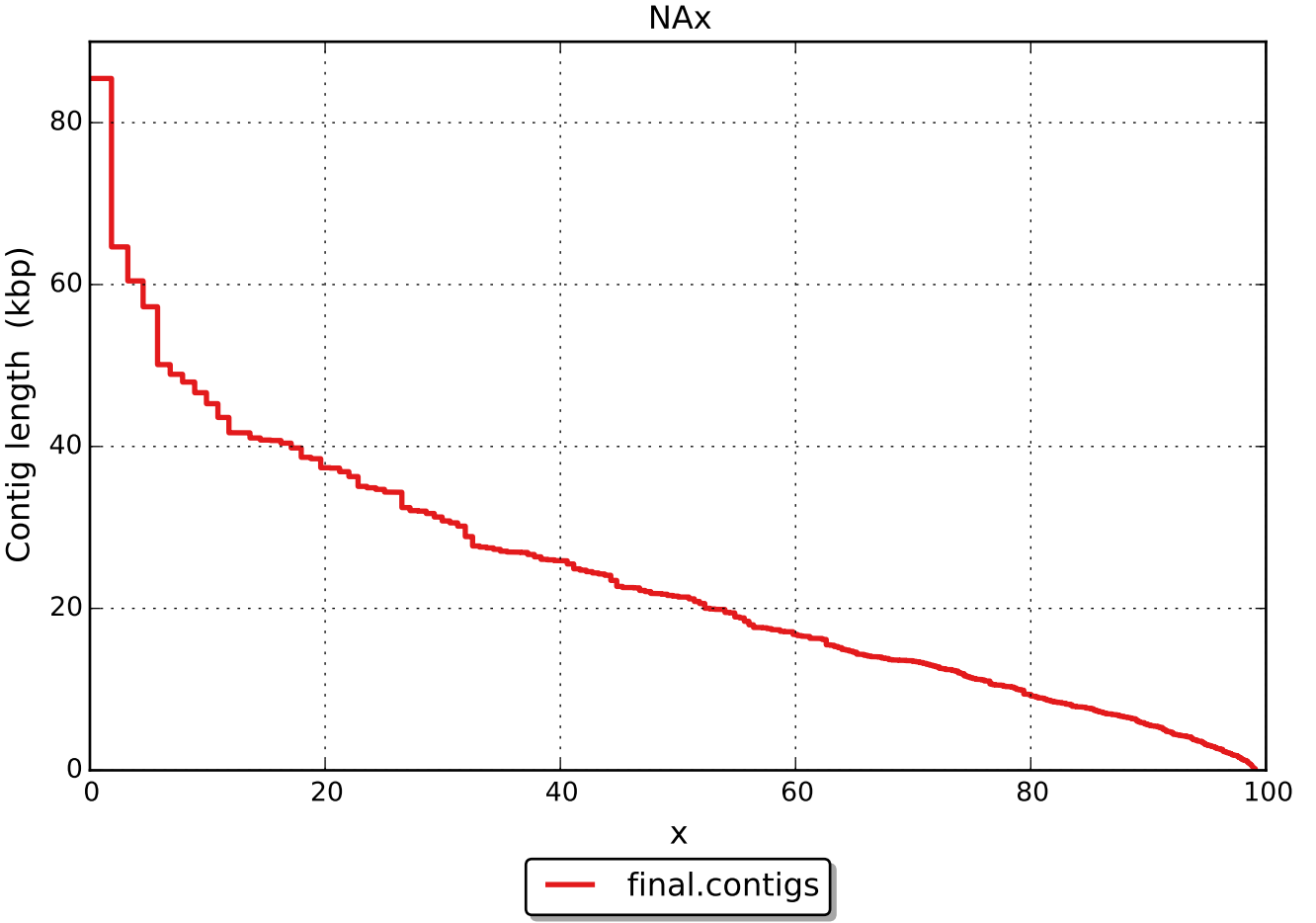

NGx
Contig length (kbp)
0
20
40
60
80
0
20
40
60
80
100
x
final.contigs

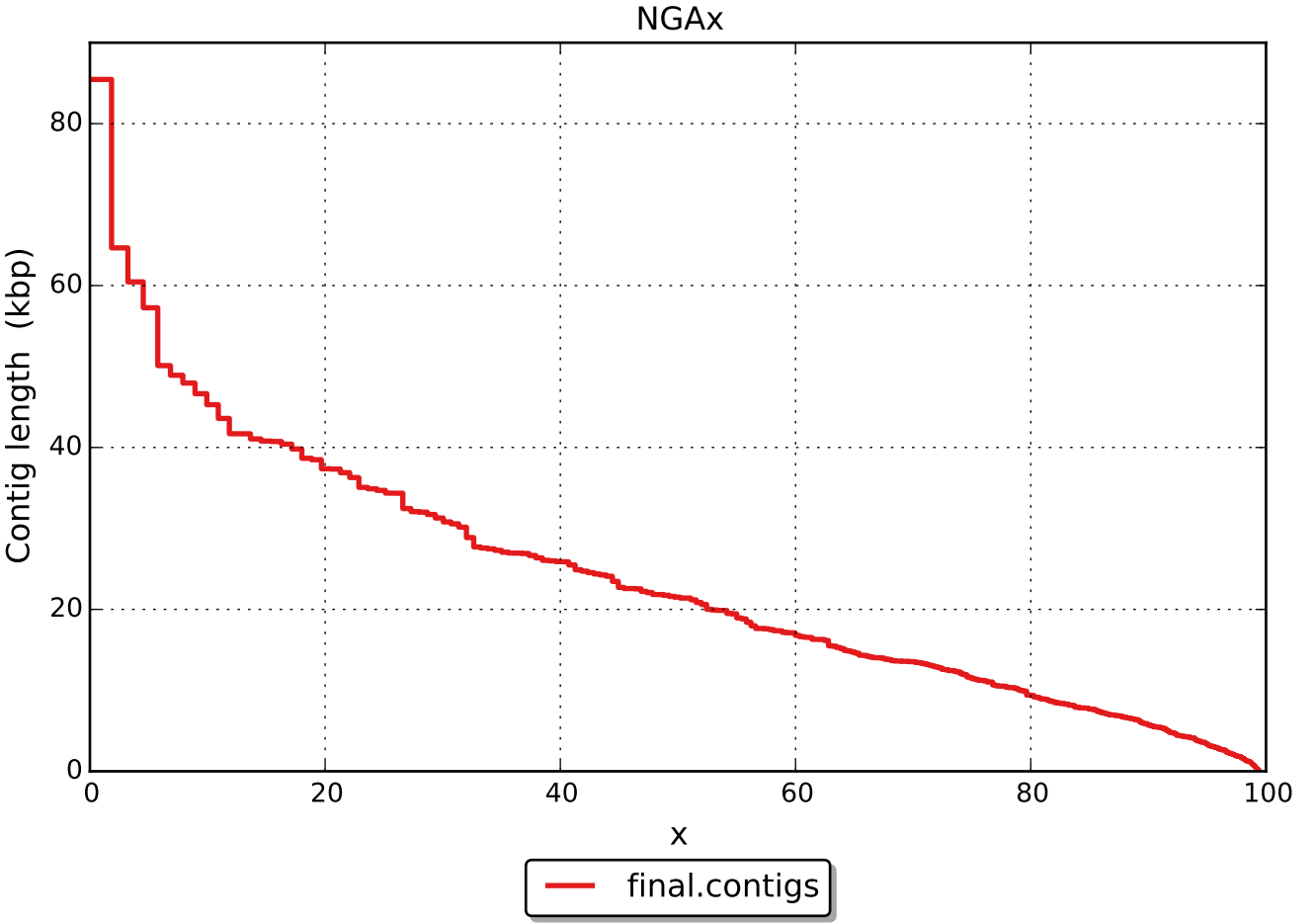

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
100
200
300
400
500
600
Contig index
final.contigs
Reference


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


Misassemblies
4.0
3.5
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
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