Report

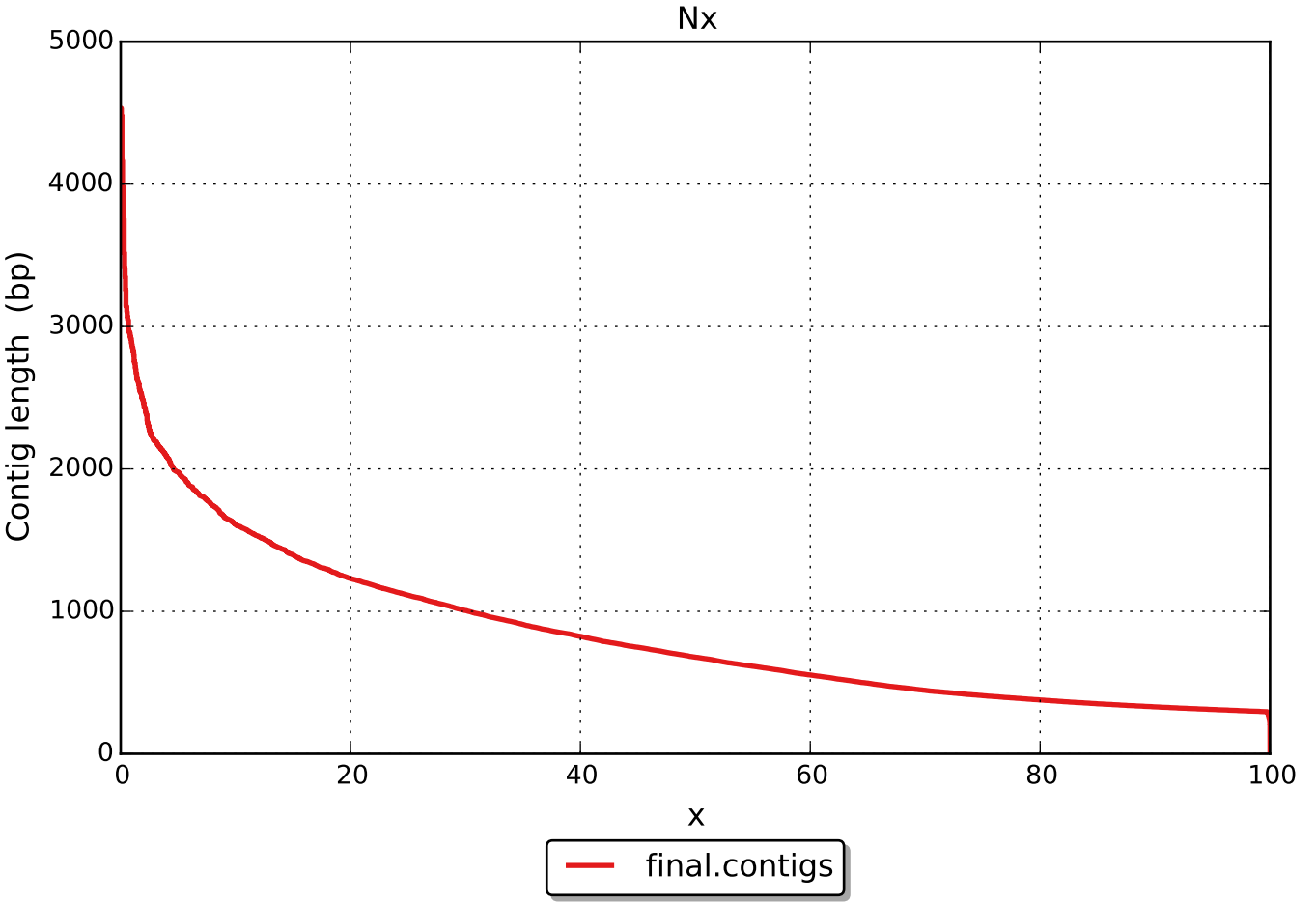
	final.contigs
# contigs (>= 0 bp)	13973
# contigs (>= 1000 bp)	1785
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	8354300
Total length (>= 1000 bp)	2532780
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	13973
Largest contig	4533
Total length	8354300
Reference length	4641652
GC (%)	50.70
Reference GC (%)	50.79
N50	678
NG50	1054
N75	408
NG75	795
L50	3800
LG50	1579
L75	7834
LG75	2852
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	12729 + 31 part
Unaligned length	6848791
Genome fraction (%)	31.716
Duplication ratio	1.023
# N's per 100 kbp	0.00
# mismatches per 100 kbp	671.46
# indels per 100 kbp	0.48
Largest alignment	4533
NGA50	-

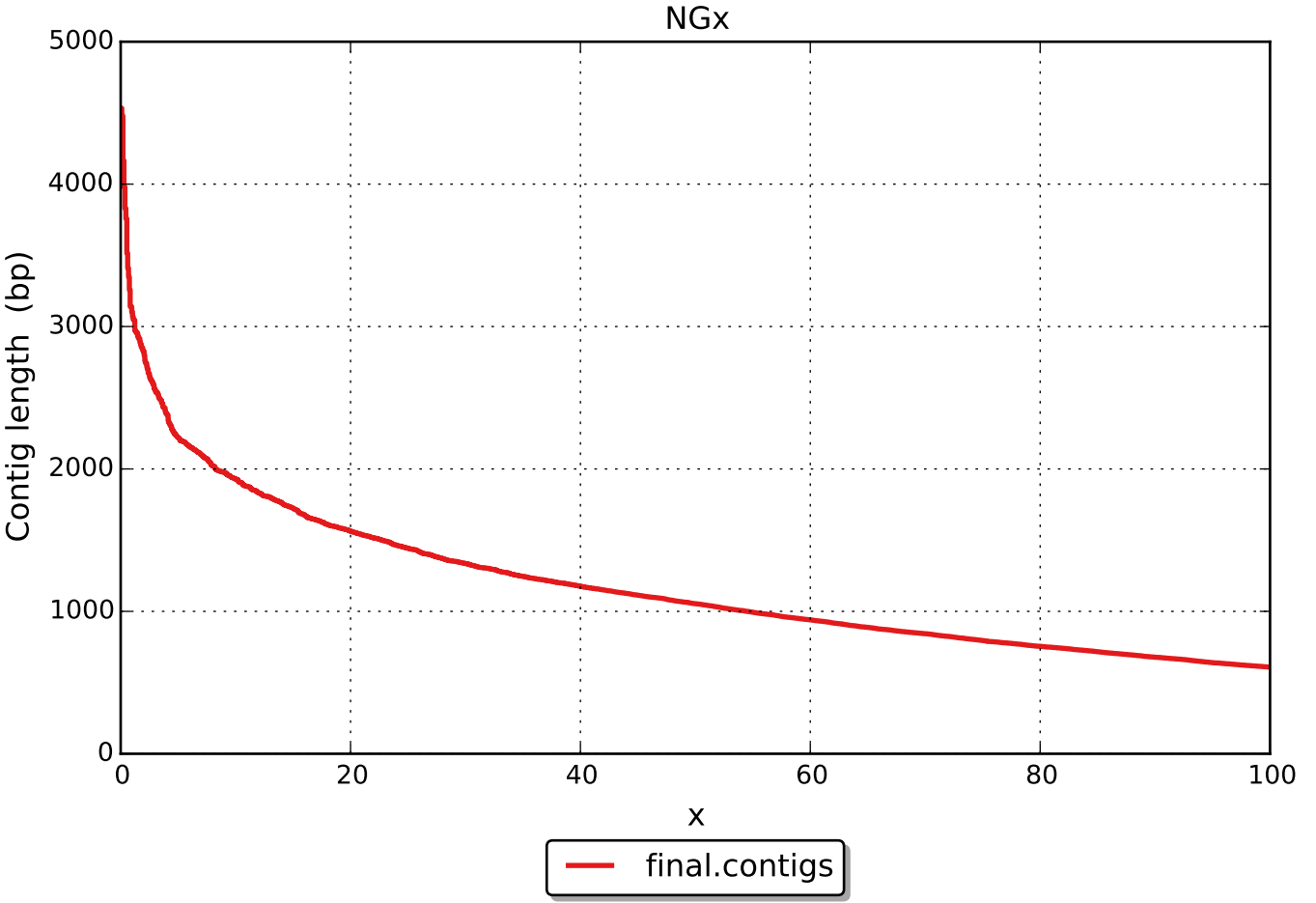
Misassemblies report

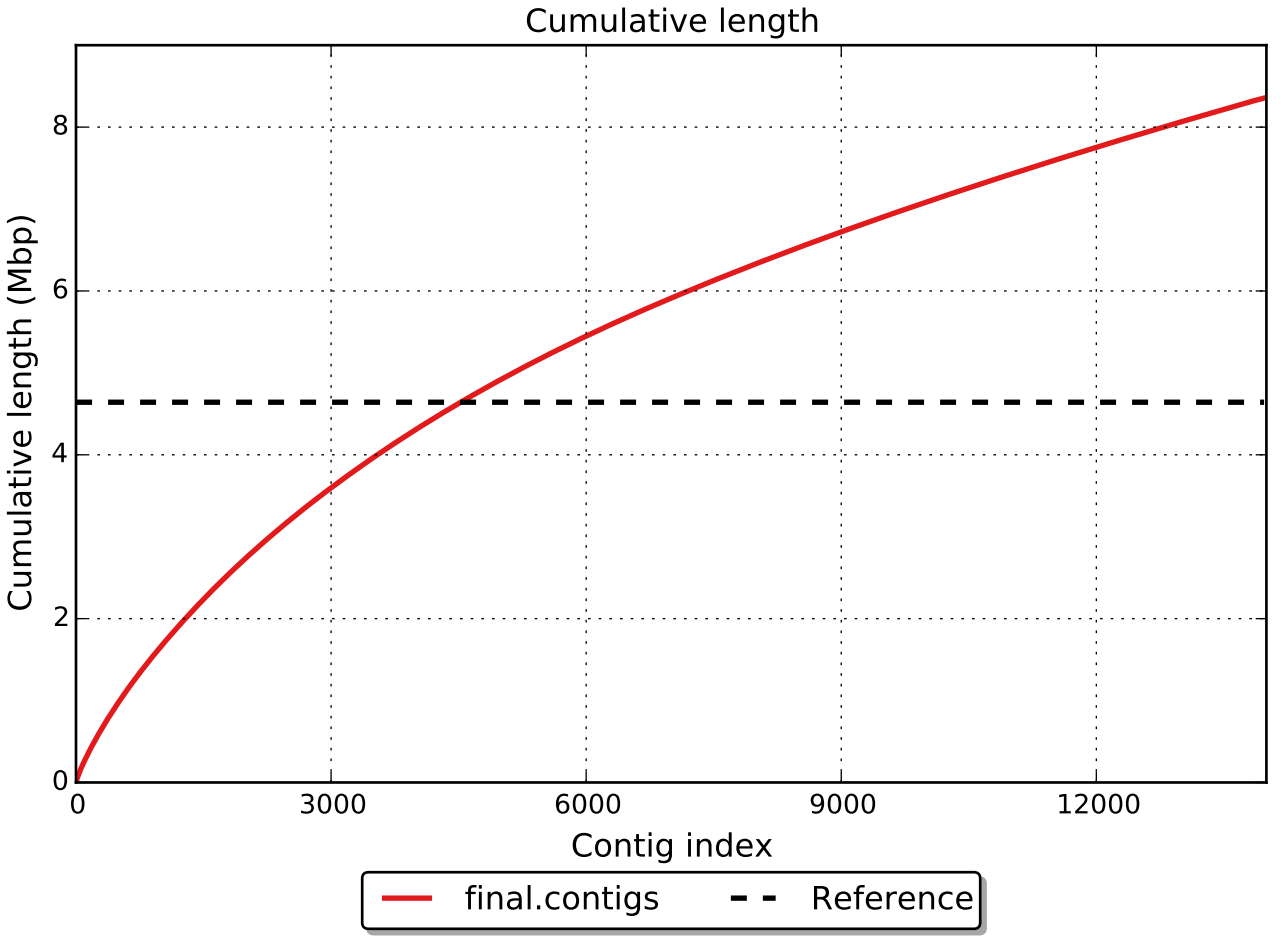
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	9885
# indels	7
# short indels	7
# long indels	0
Indels length	7

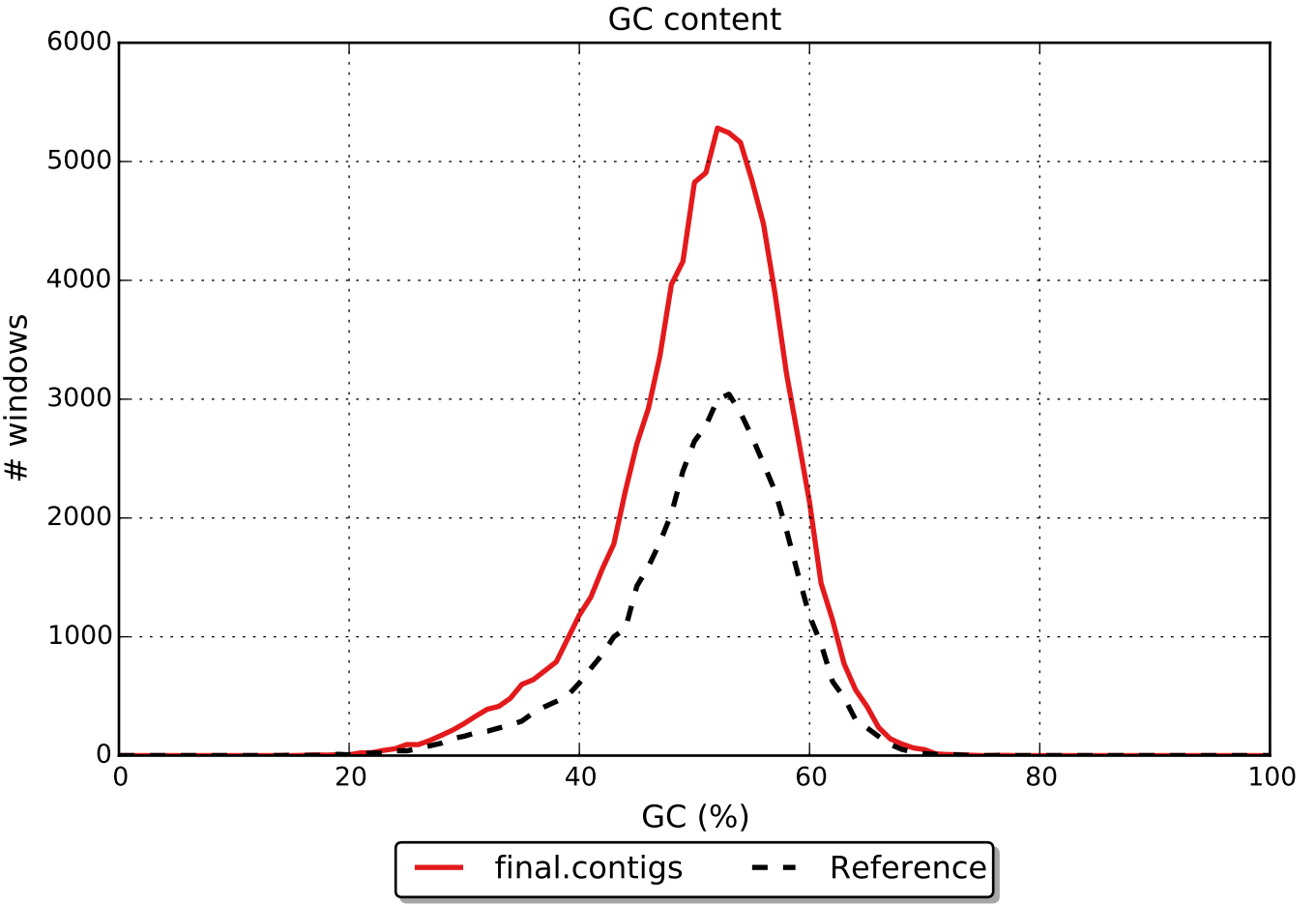
Unaligned report

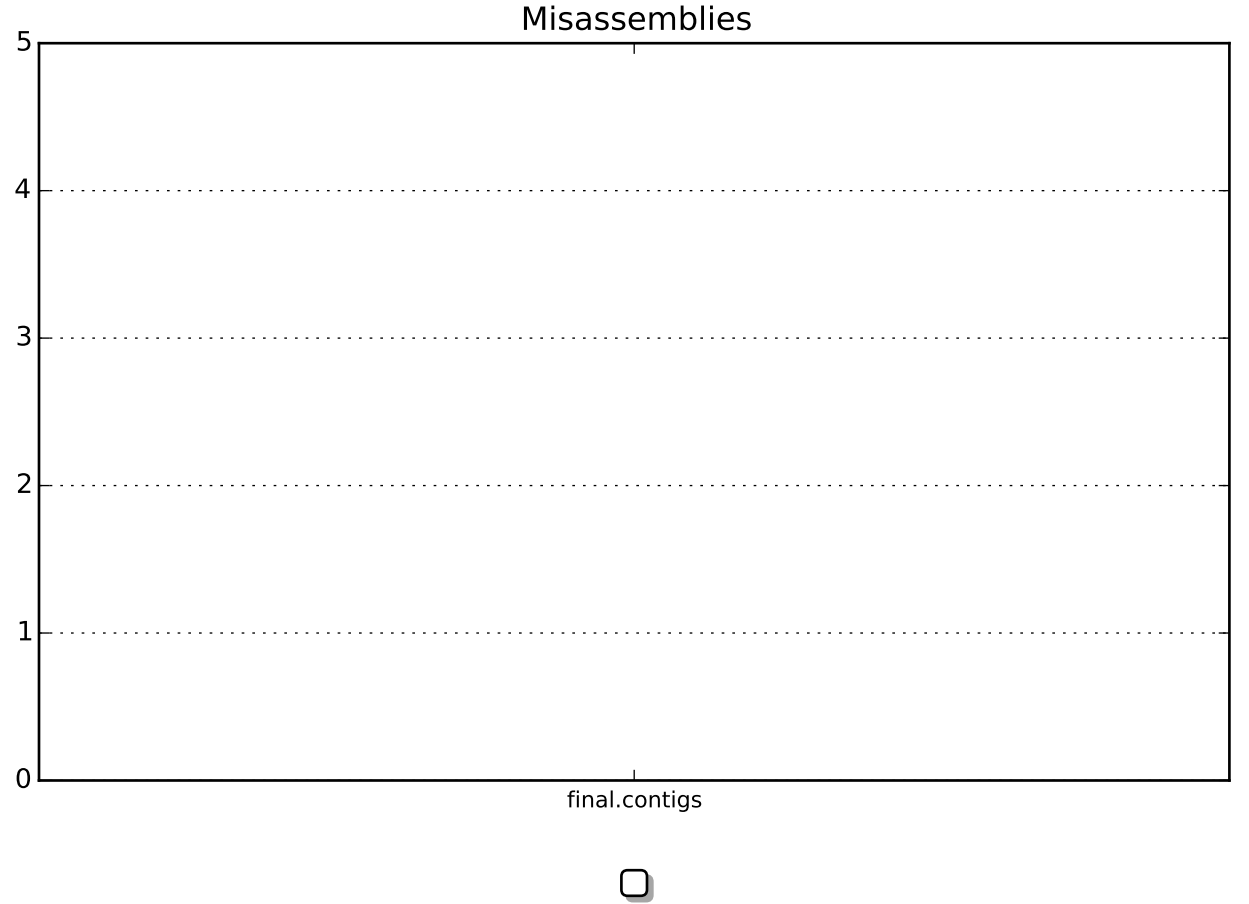
	final.contigs
# fully unaligned contigs	12729
Fully unaligned length	6839328
# partially unaligned contigs	31
# with misassembly	1
# both parts are significant	31
Partially unaligned length	9463
# N's	0

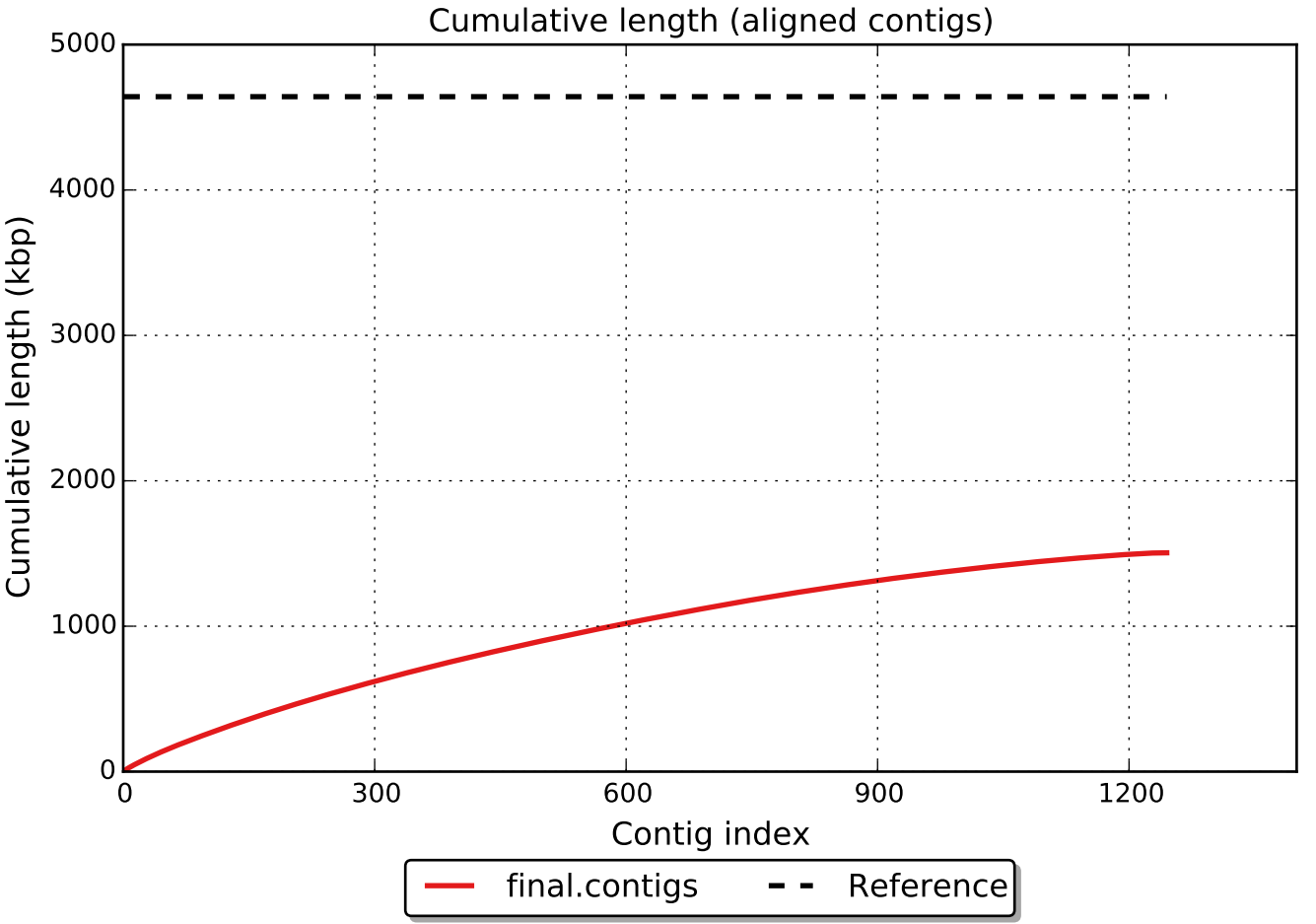

Nx
5000
4000
3000
2000
1000
0
Contig length (bp)
0
20
40
60
80
100
x
final.contigs

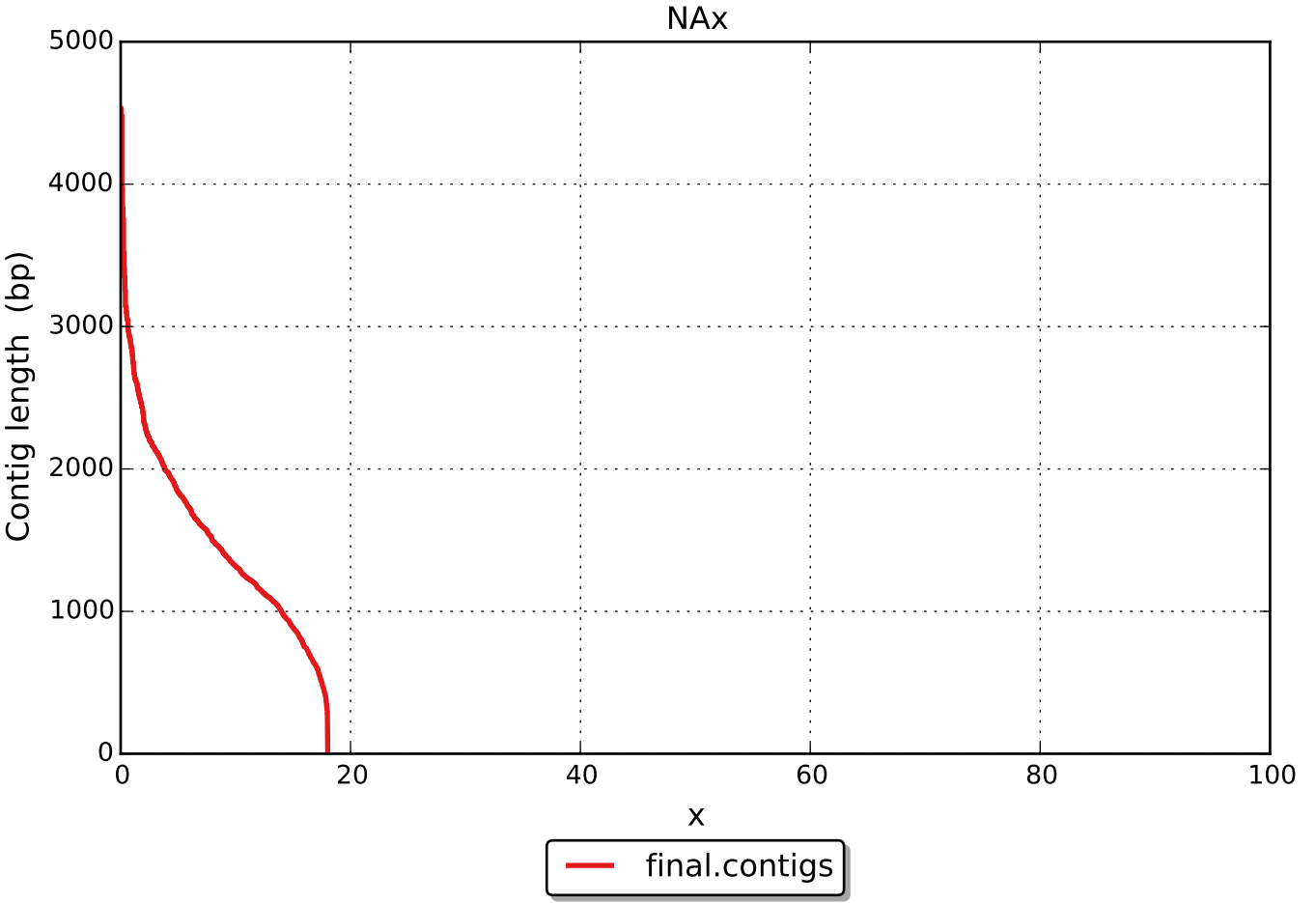

NGx
5000
4000
3000
2000
1000
0
Contig length (bp)
0
20
40
60
80
100
x
final.contigs

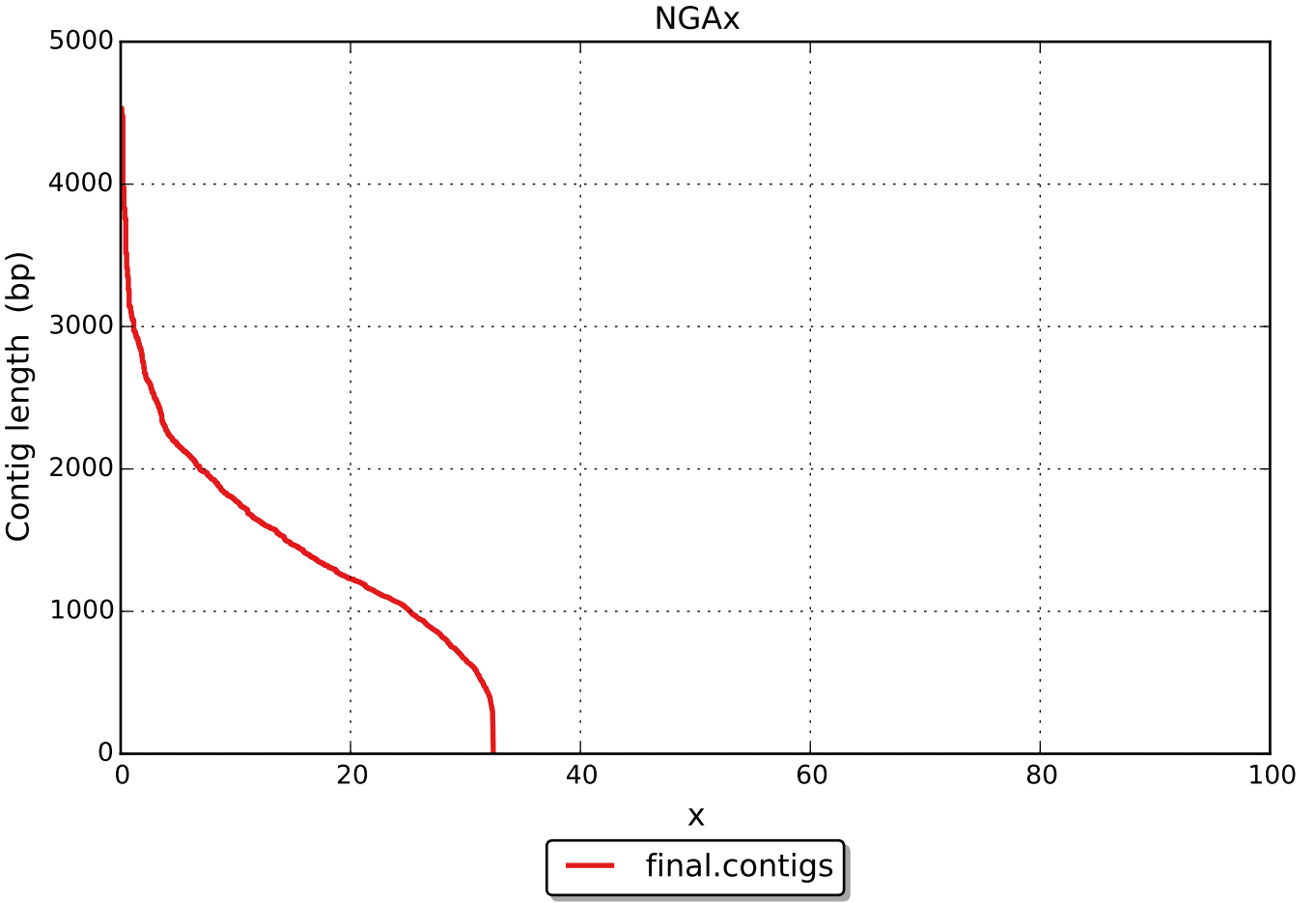

Cumulative length
Cumulative length (Mbp)
0
2
4
6
8
0
3000
6000
9000
12000
Contig index
final.contigs
Reference


GC content
6000
5000
4000
3000
2000
1000
0
windows
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
300
600
900
1200
Contig index
final.contigs
Reference


NAx
5000
4000
3000
2000
1000
0
Contig length (bp)
0
20
40
60
80
100
x
final.contigs


NGAx
5000
4000
3000
2000
1000
0
Contig length (bp)
0
20
40
60
80
100
x
final.contigs