Report

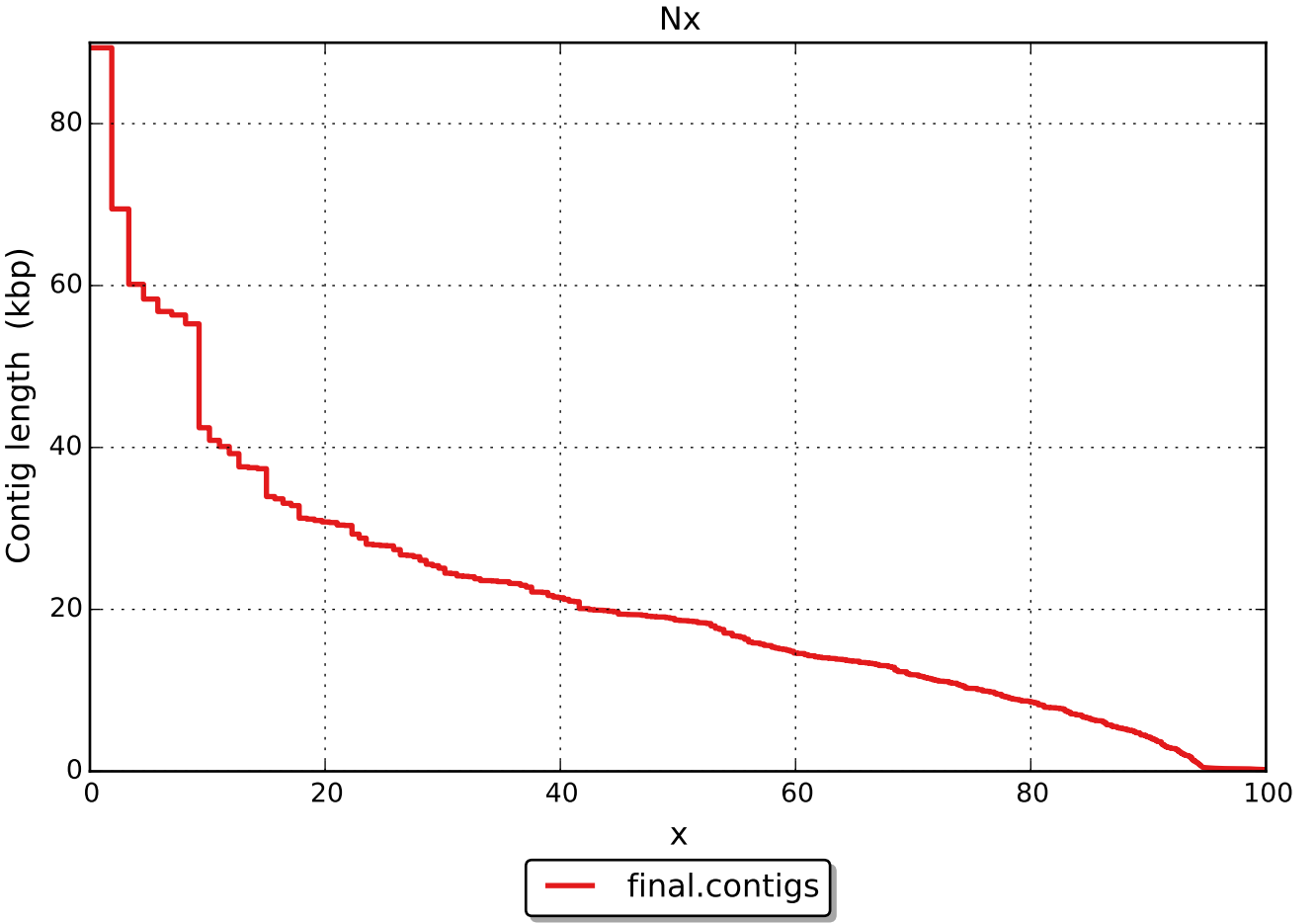
	final.contigs
# contigs (>= 0 bp)	1211
# contigs (>= 1000 bp)	357
# contigs (>= 5000 bp)	258
# contigs (>= 10000 bp)	174
# contigs (>= 25000 bp)	39
# contigs (>= 50000 bp)	7
Total length (>= 0 bp)	4802171
Total length (>= 1000 bp)	4524747
Total length (>= 5000 bp)	4256780
Total length (>= 10000 bp)	3644157
Total length (>= 25000 bp)	1449341
Total length (>= 50000 bp)	445743
# contigs	1211
Largest contig	89368
Total length	4802171
Reference length	4641652
GC (%)	50.76
Reference GC (%)	50.79
N50	18678
NG50	19068
N75	10236
NG75	11124
L50	84
LG50	80
L75	170
LG75	159
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	581 + 5 part
Unaligned length	194473
Genome fraction (%)	98.386
Duplication ratio	1.009
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4.23
# indels per 100 kbp	0.00
Largest alignment	89368
NA50	18678
NGA50	19068
NA75	10236
NGA75	11124
LA50	84
LGA50	80
LA75	170
LGA75	159

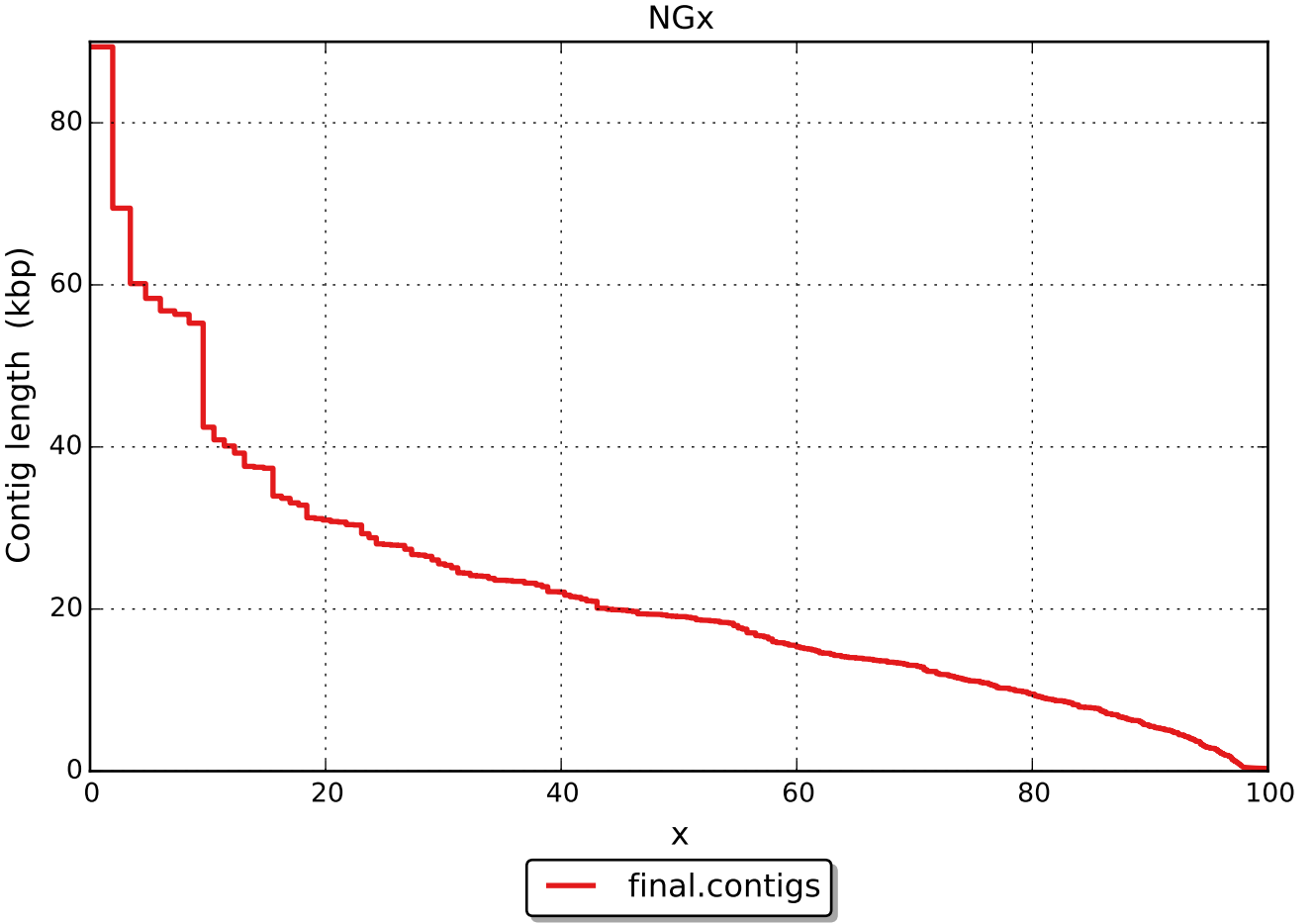
Misassemblies report

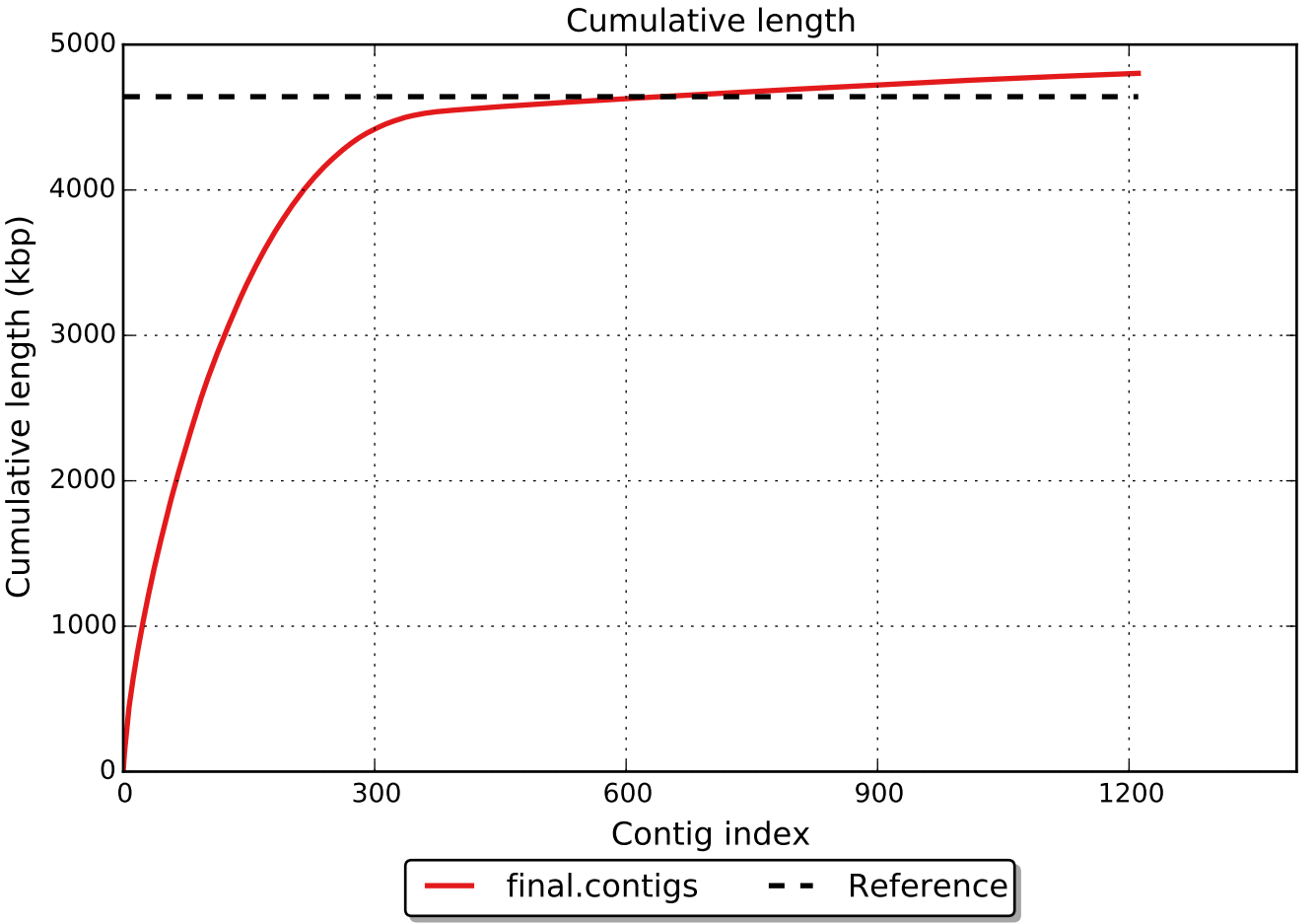
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	193
# indels	0
# short indels	0
# long indels	0
Indels length	0

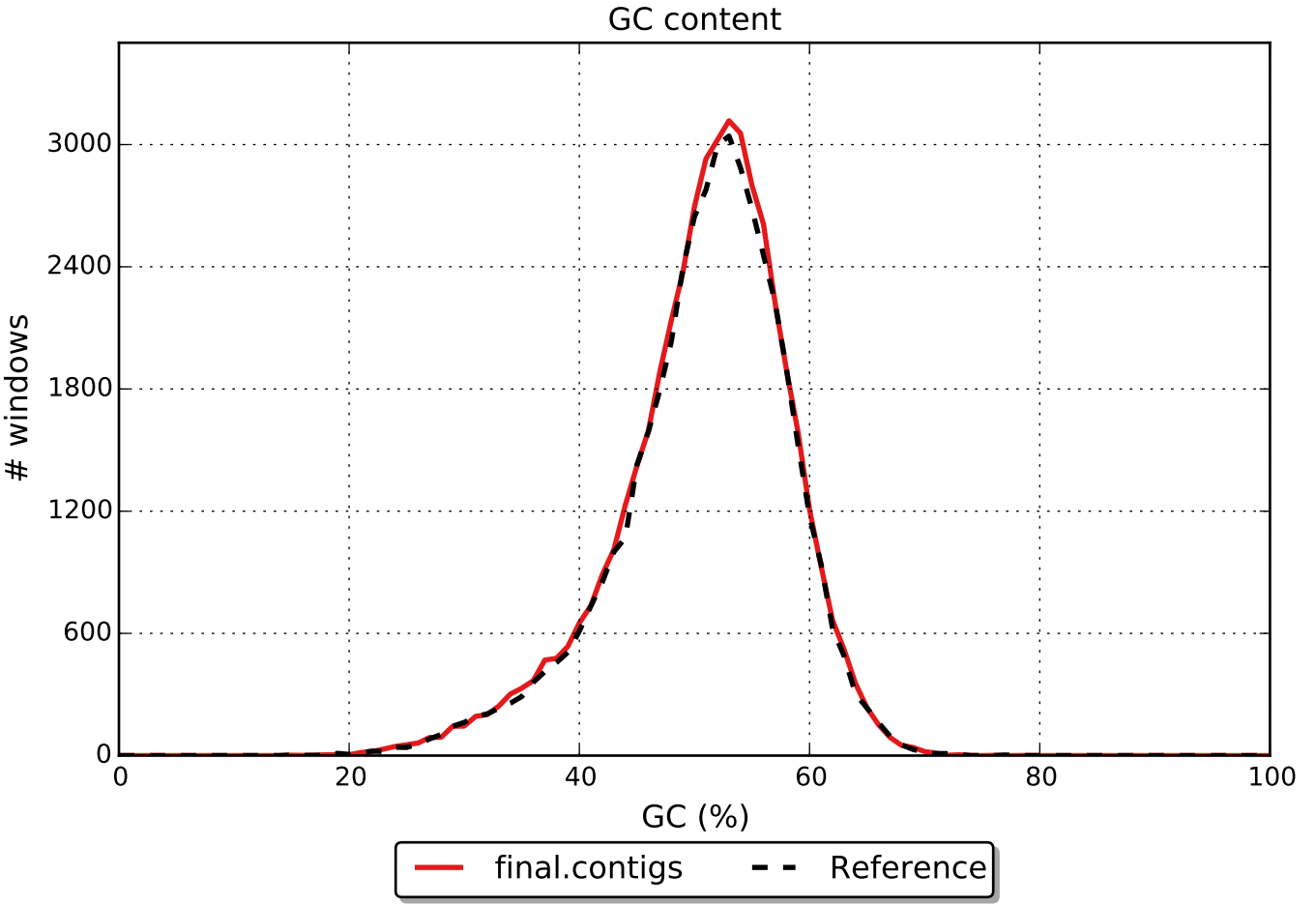
Unaligned report

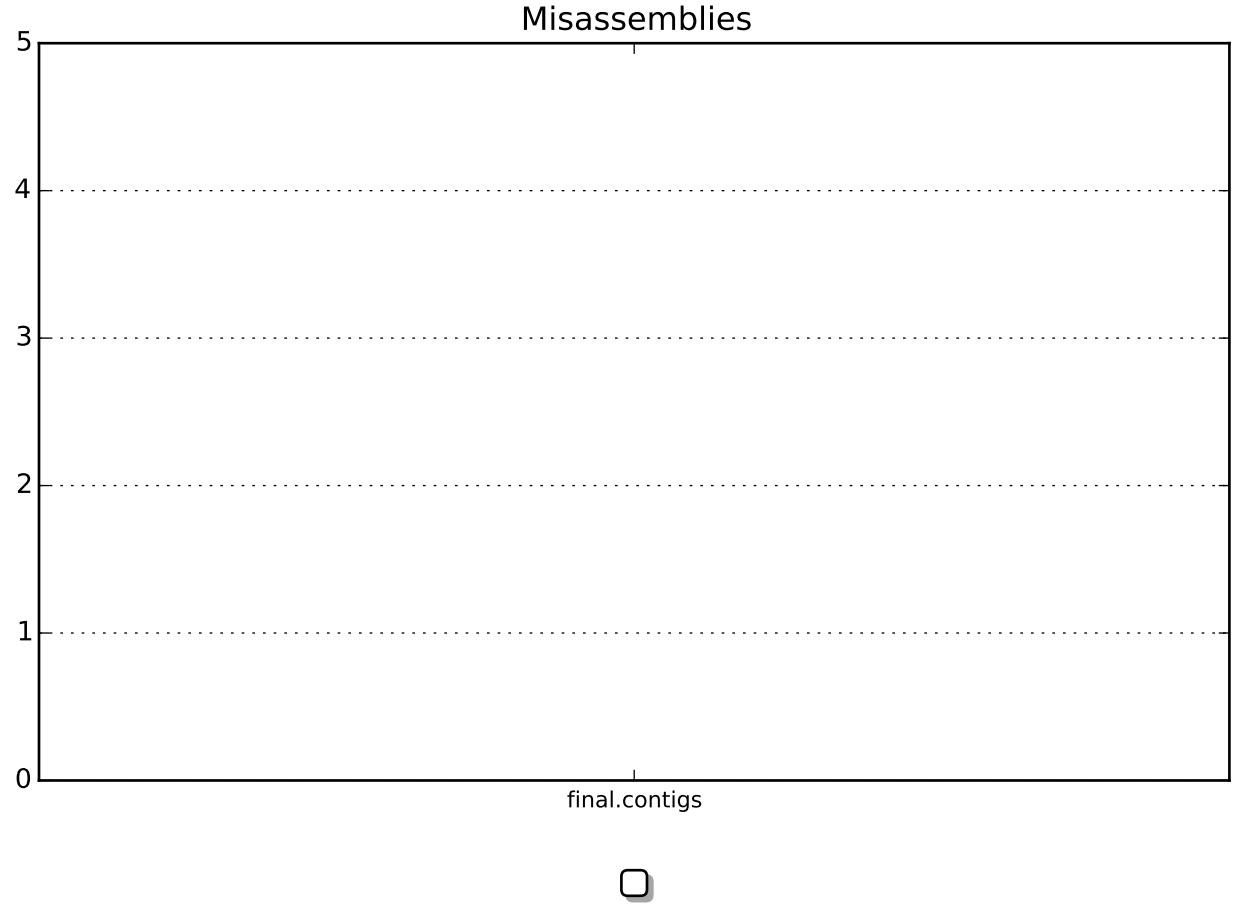
	final.contigs
# fully unaligned contigs	581
Fully unaligned length	193414
# partially unaligned contigs	5
# with misassembly	0
# both parts are significant	5
Partially unaligned length	1059
# N's	0

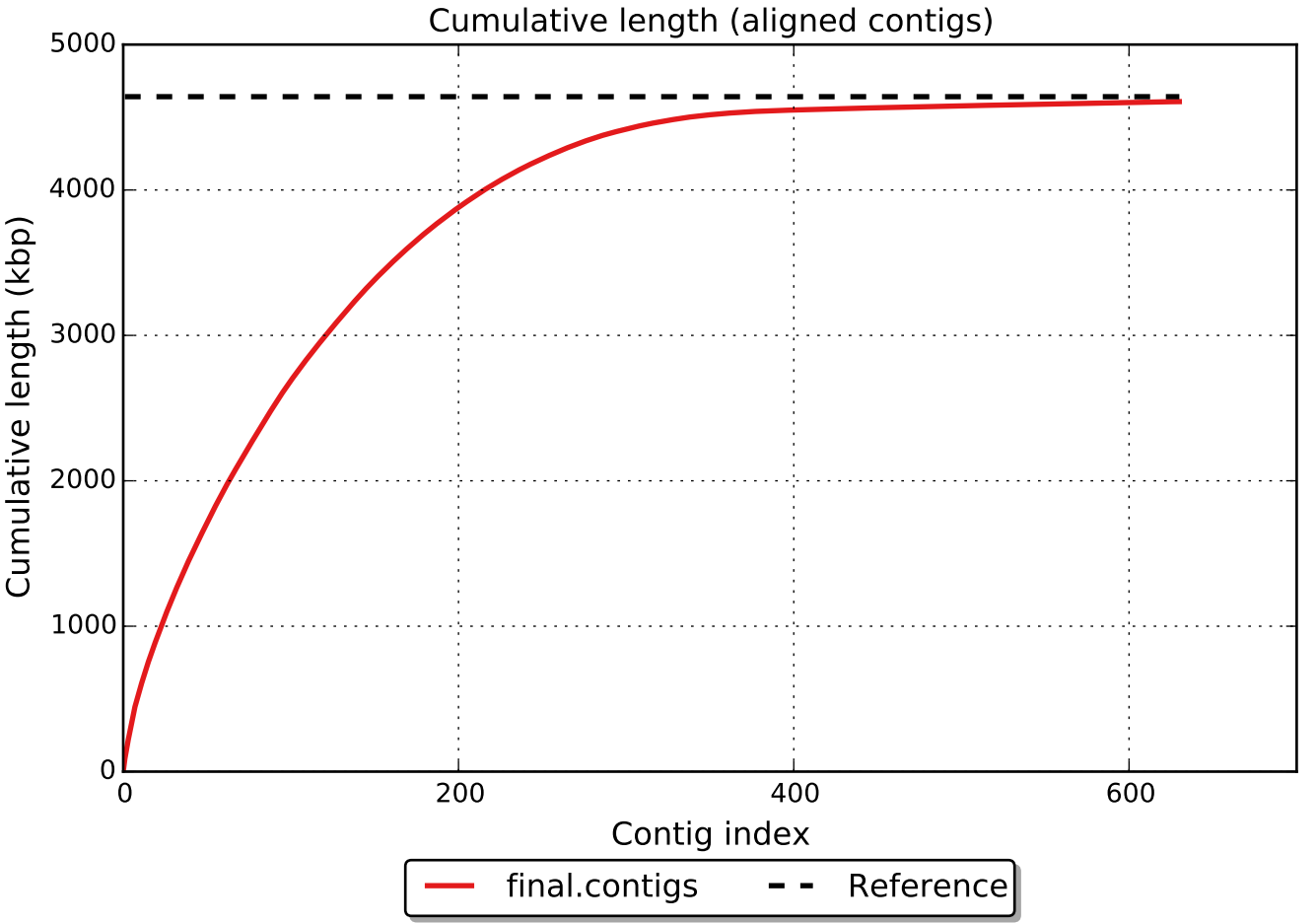

Nx
Contig length (kbp)
0
20
40
60
80
0
20
40
60
80
100
x
final.contigs

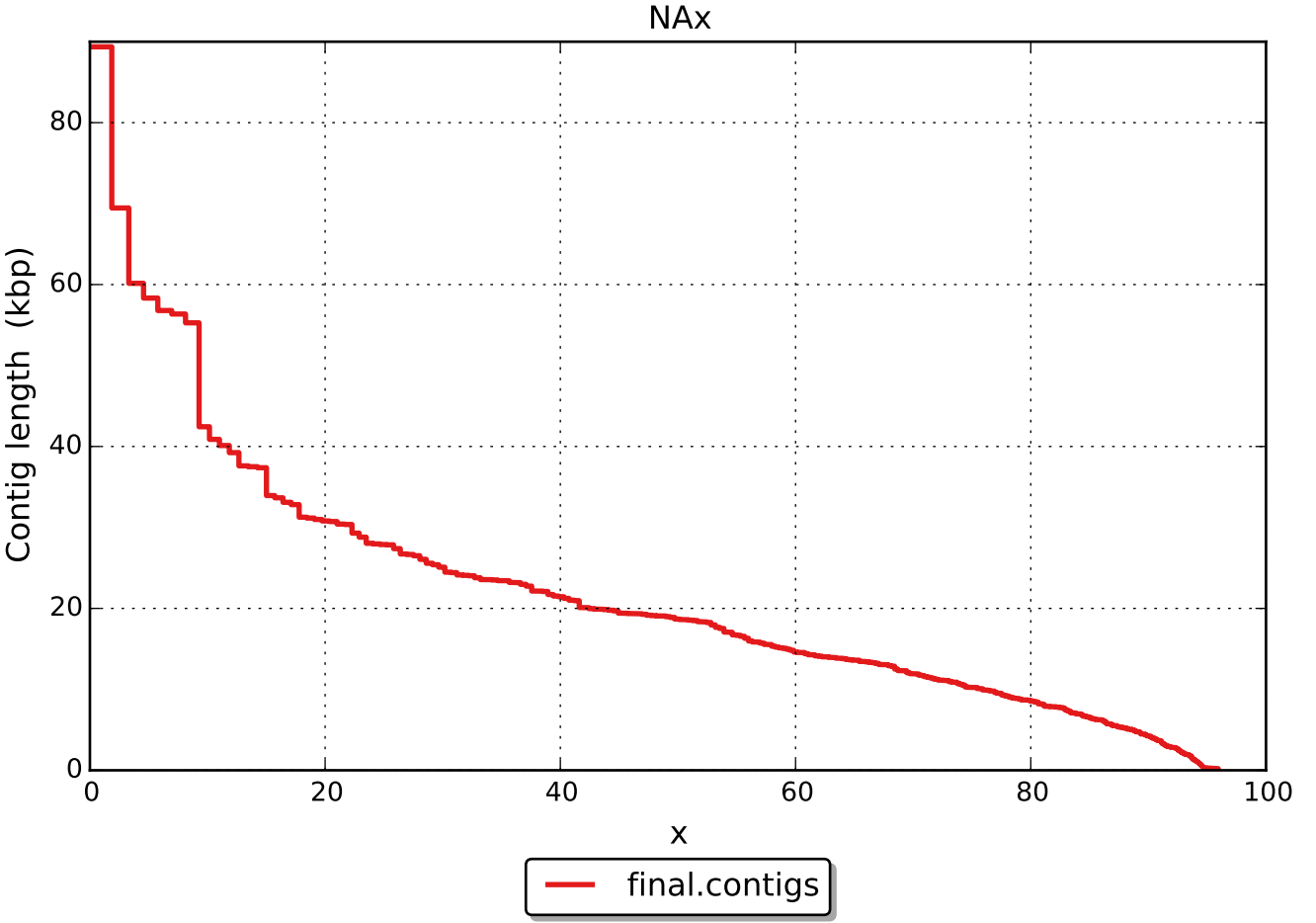

NGx
Contig length (kbp)
0
20
40
60
80
0
20
40
60
80
100
x
final.contigs

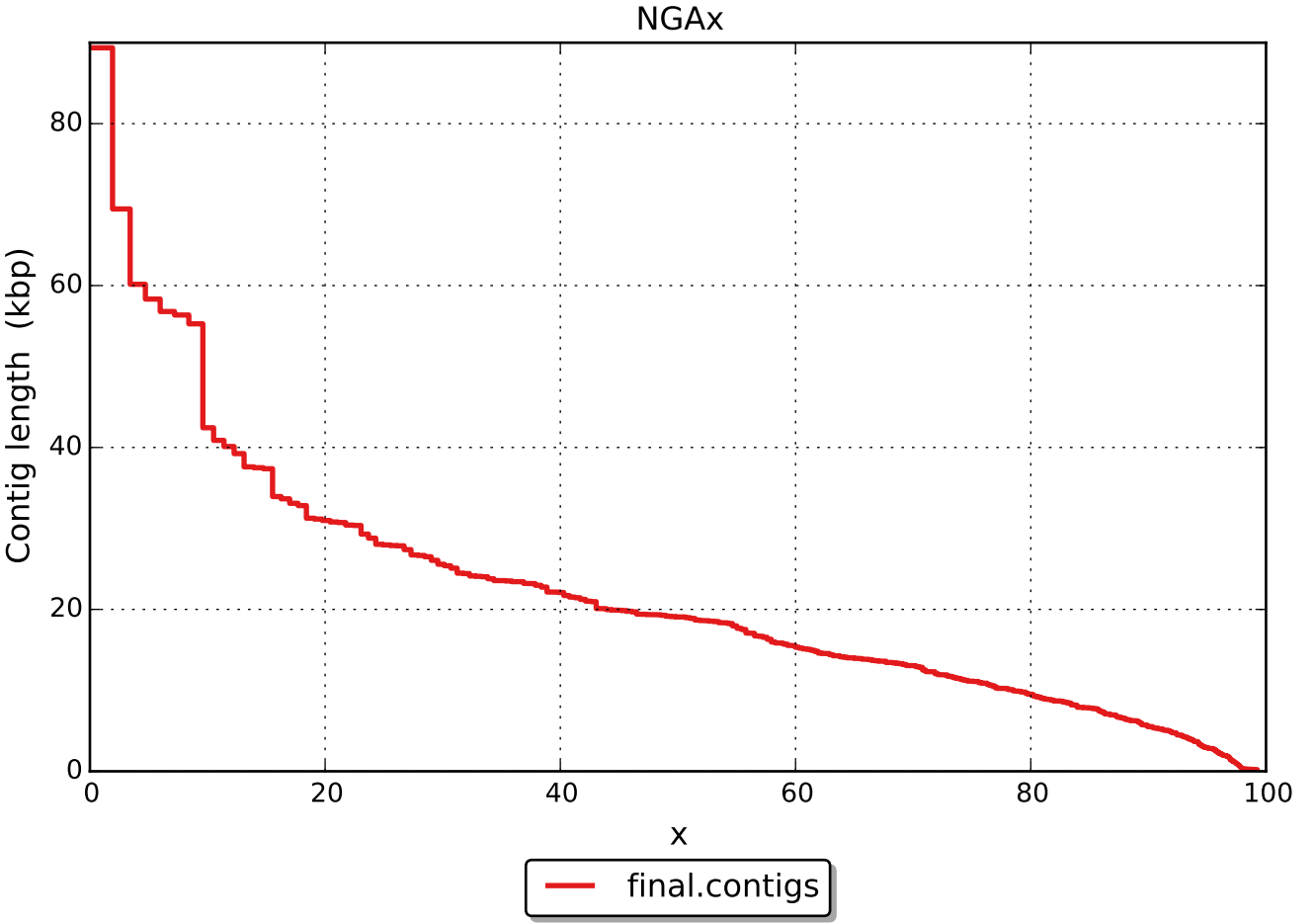

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
300
600
900
1200
Contig index
final.contigs
Reference


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
200
400
600
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