Report

	final.contigs
# contigs (>= 0 bp)	1871
# contigs (>= 1000 bp)	5
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	789615
Total length (>= 1000 bp)	6174
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	341
Largest contig	1369
Total length	207946
Reference length	4641652
GC (%)	50.67
Reference GC (%)	50.79
N50	582
N75	537
L50	148
L75	241
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	1111
# local misassemblies	0
# unaligned contigs	42 + 9 part
Unaligned length	25055
Genome fraction (%)	3.927
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3442.18
# indels per 100 kbp	10.97
Largest alignment	1322
NA50	570
NGA50	-
NA75	519
LA50	150
LA75	246

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

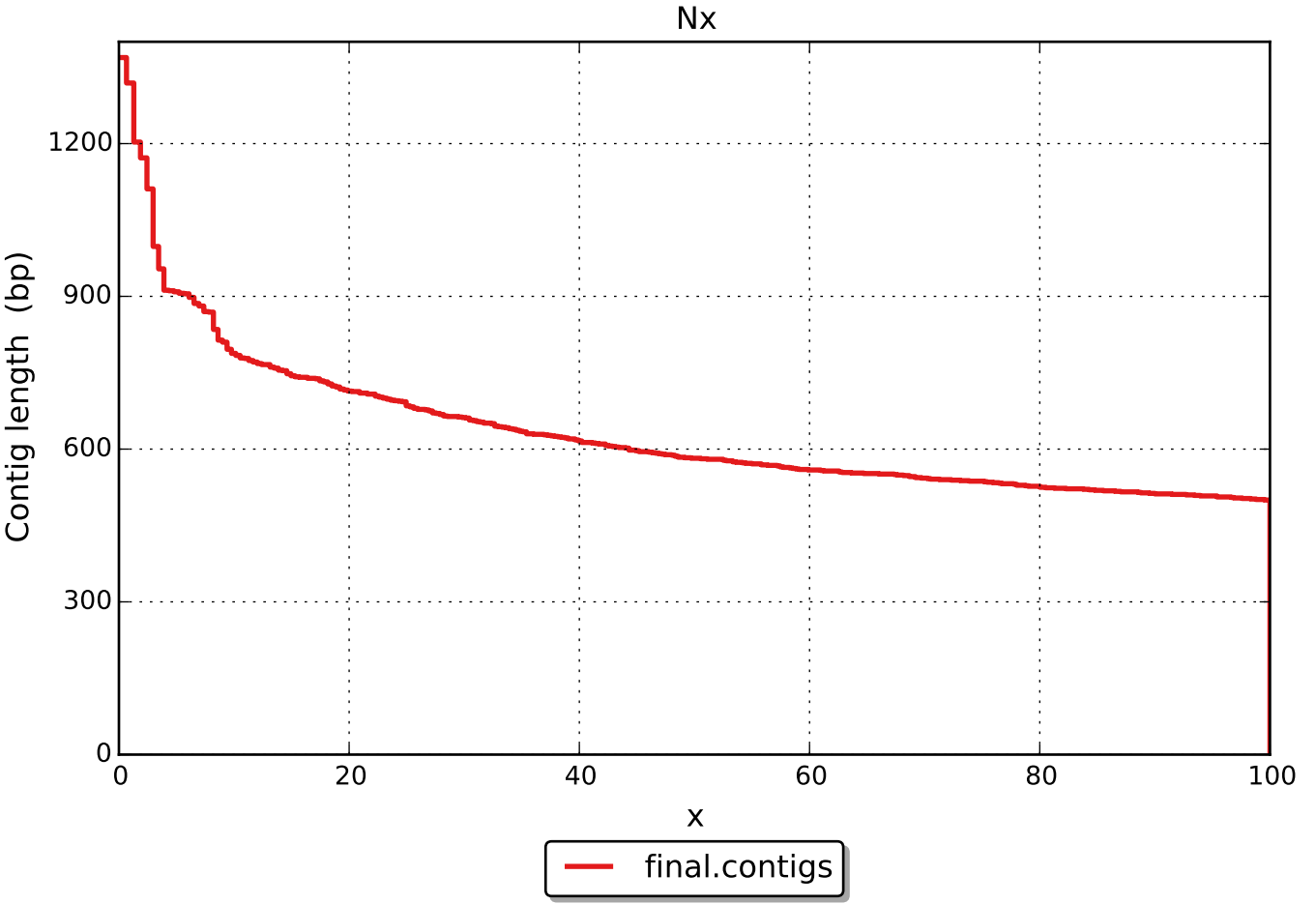
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# misassembled contigs	1
Misassembled contigs length	1111
# local misassemblies	0
# mismatches	6274
# indels	20
# short indels	20
# long indels	0
Indels length	20

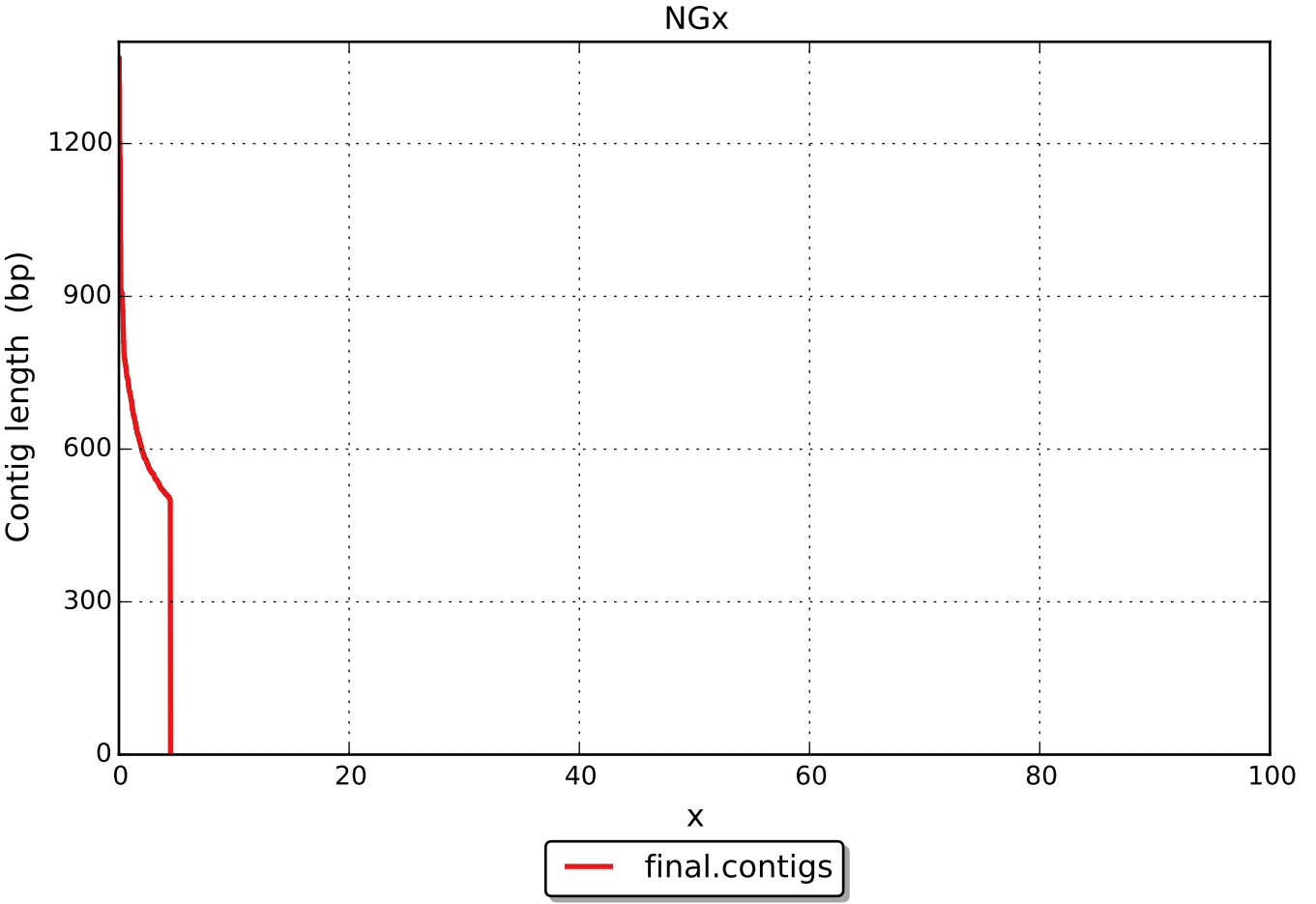
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

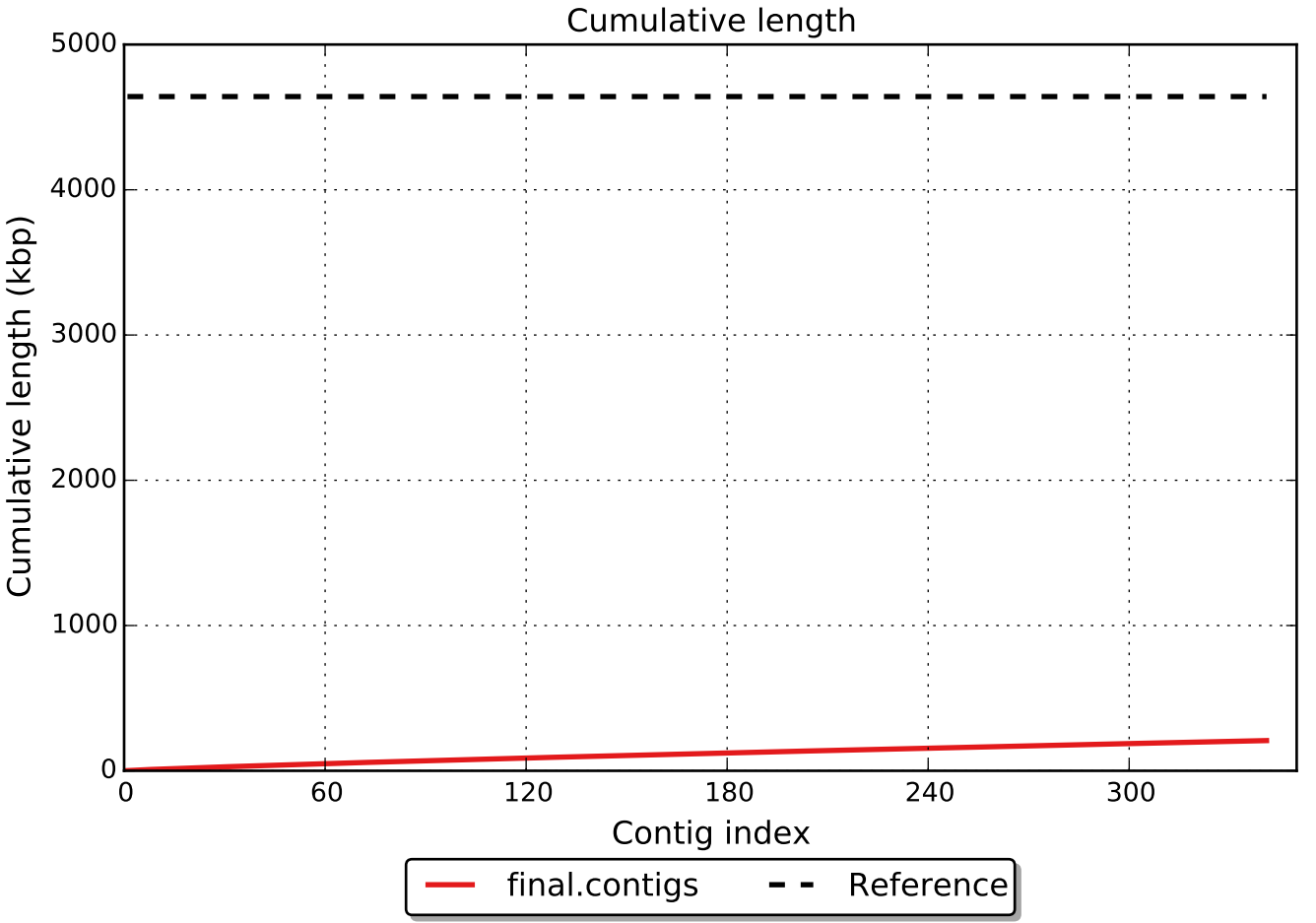
Unaligned report

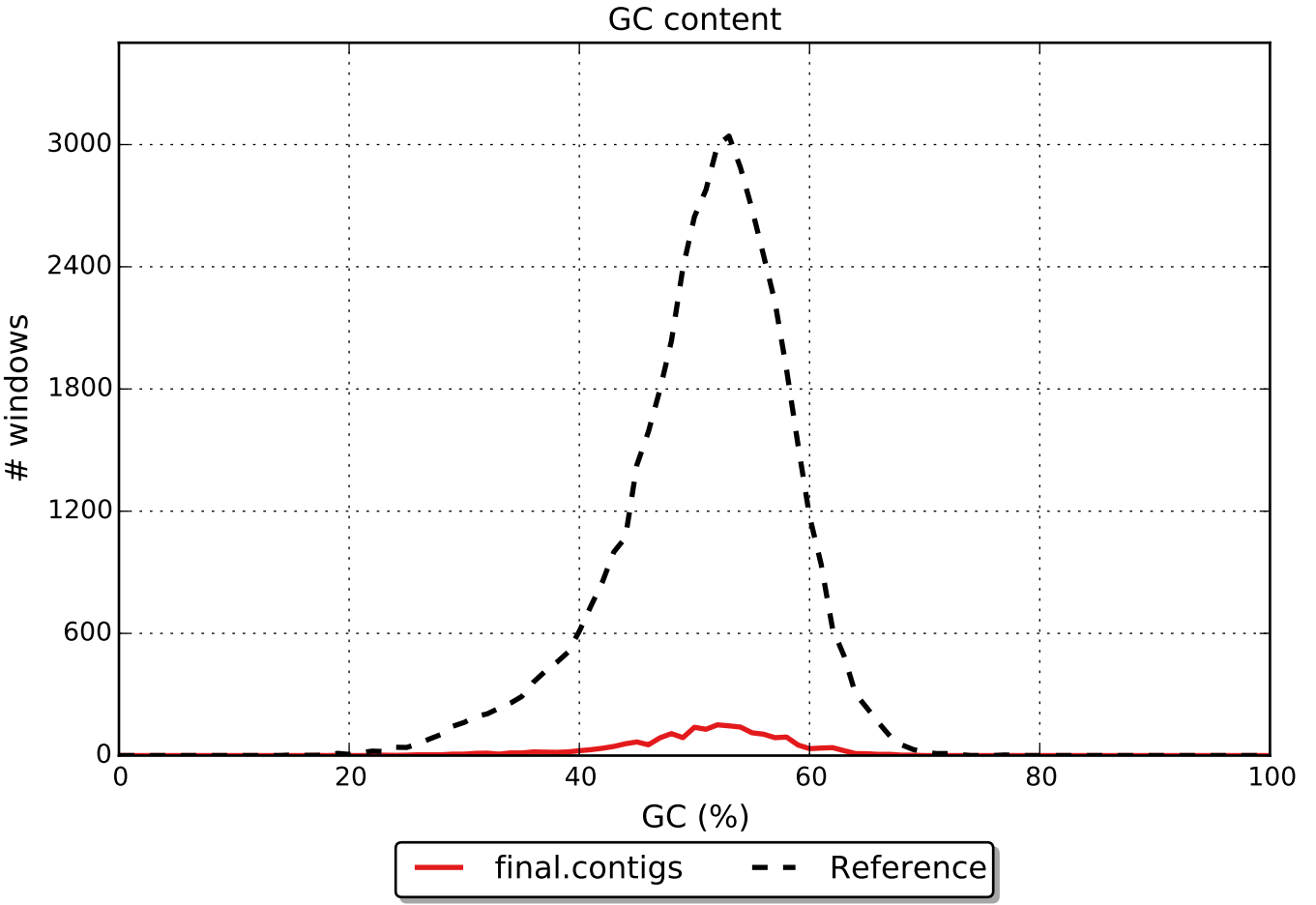
	final.contigs
# fully unaligned contigs	42
Fully unaligned length	23900
# partially unaligned contigs	9
# with misassembly	0
# both parts are significant	0
Partially unaligned length	1155
# N's	0

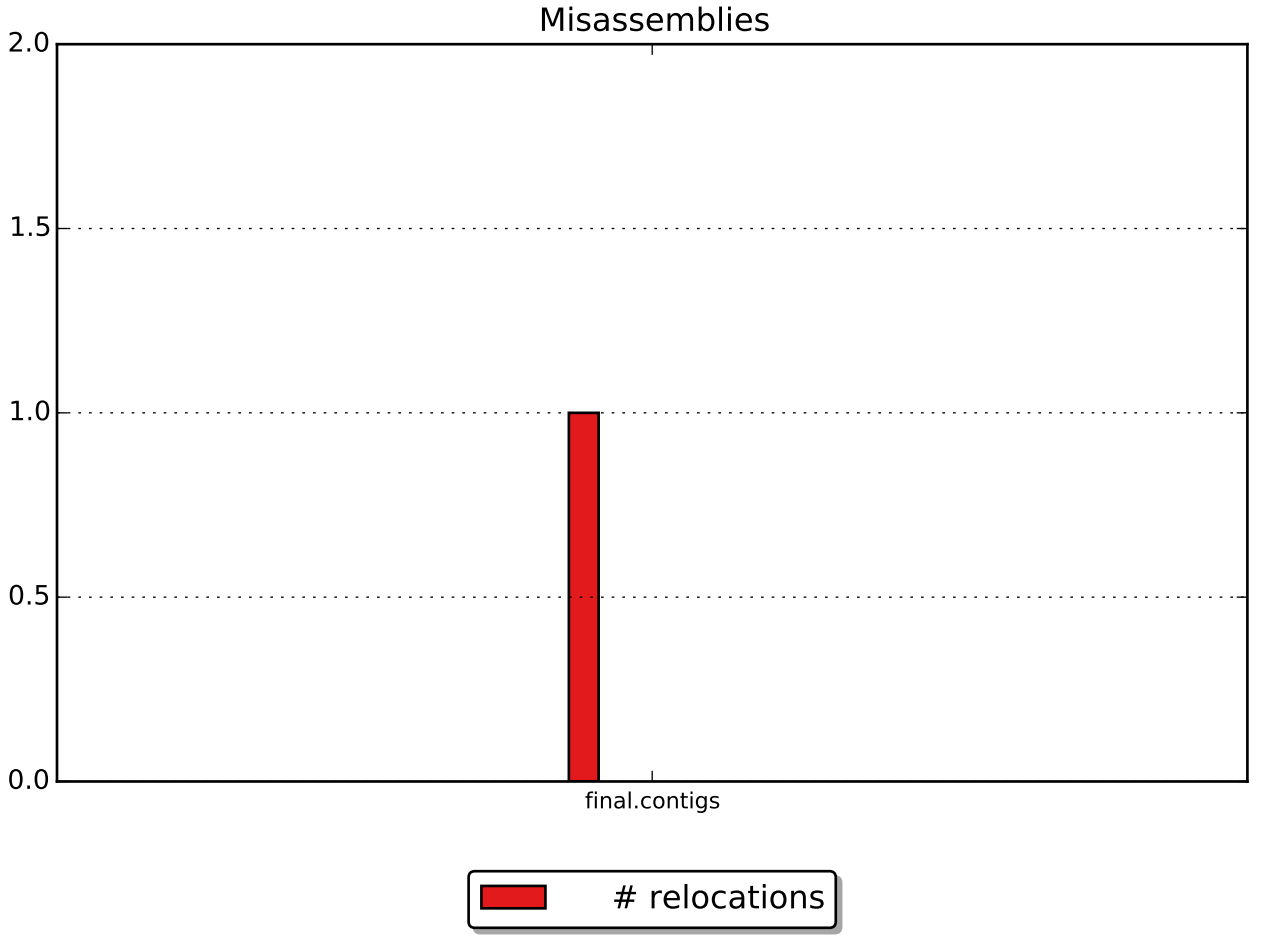
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

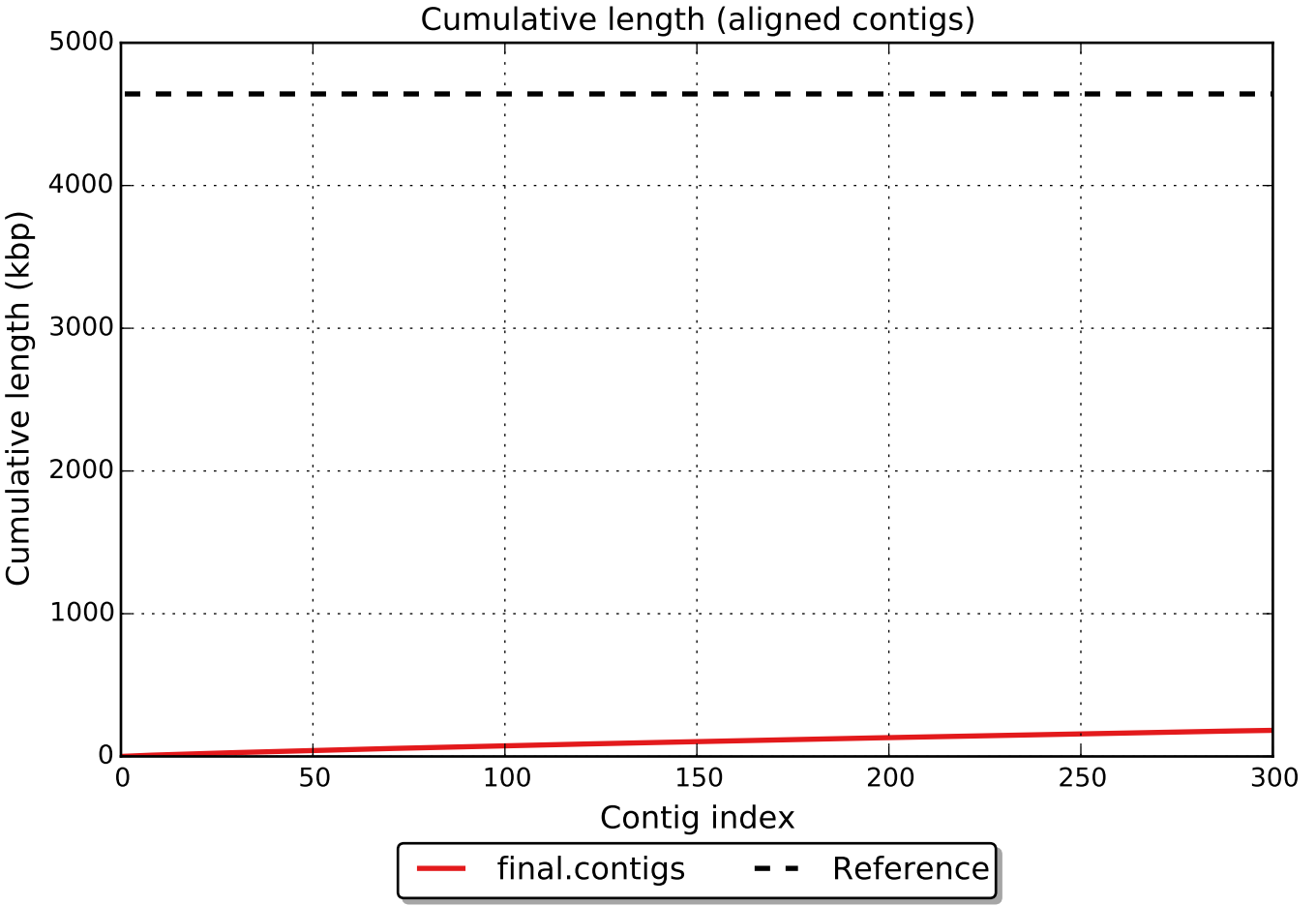

Nx
Contig length (bp)
1200
900
600
300
0
0
20
40
60
80
100
x
final.contigs

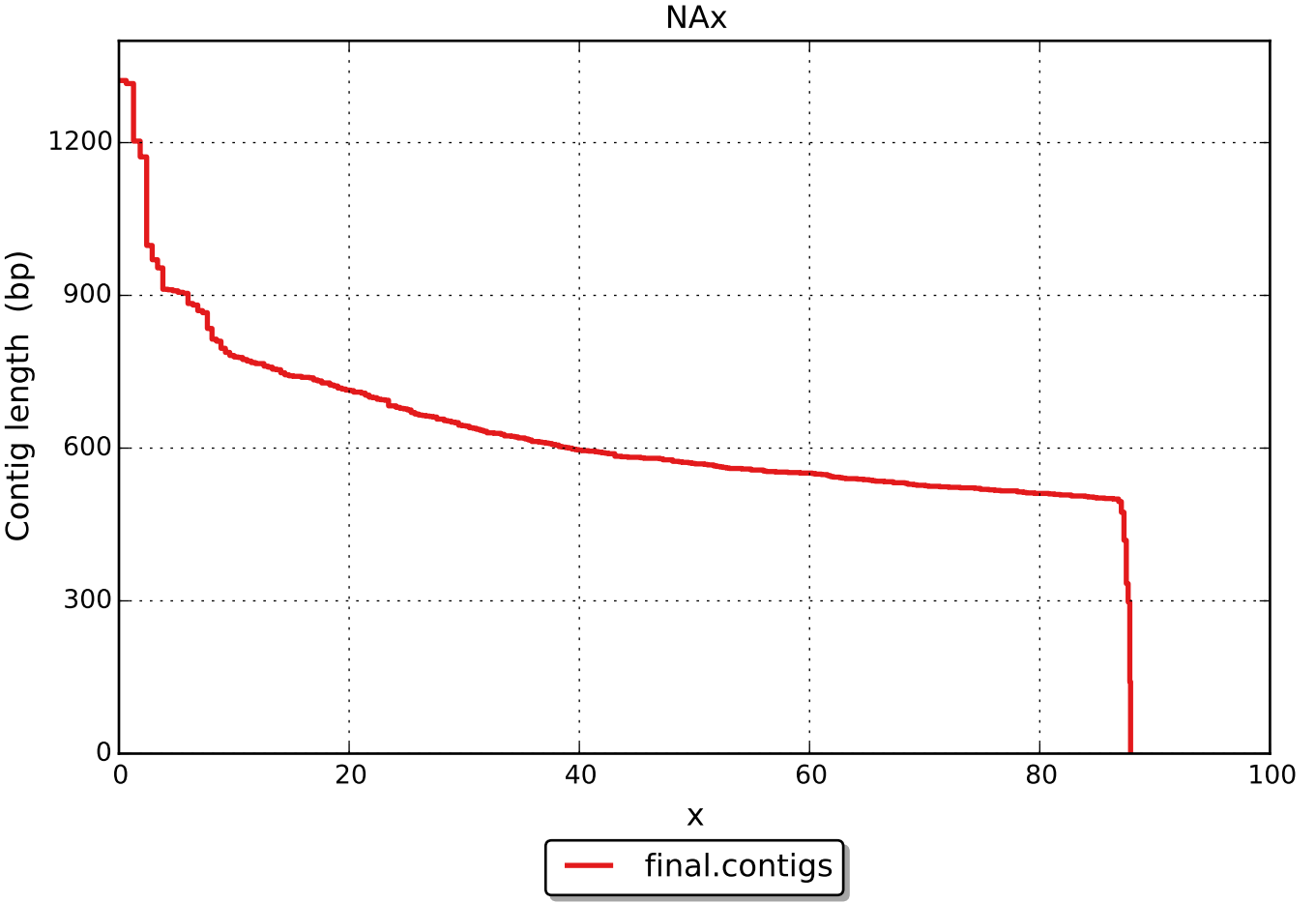

NGx
Contig length (bp)
1200
900
600
300
0
0
20
40
60
80
100
x
final.contigs

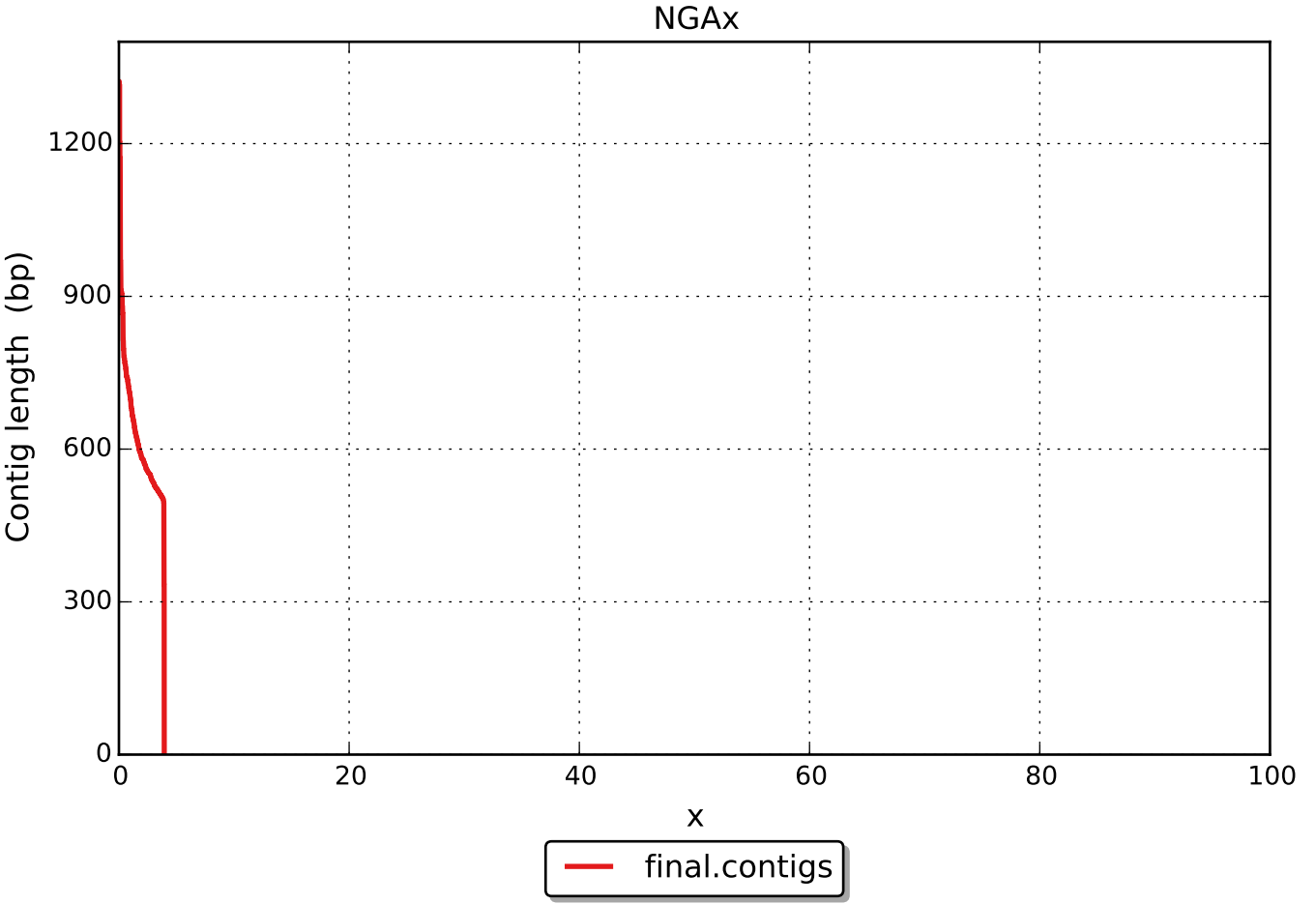

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
60
120
180
240
300
Contig index
final.contigs
Reference


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


Misassemblies
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
50
100
150
200
250
300
Contig index
final.contigs
Reference


NAx
Contig length (bp)
1200
900
600
300
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (bp)
1200
900
600
300
0
0
20
40
60
80
100
x
final.contigs