Report

	final.contigs
# contigs (>= 0 bp)	9788
# contigs (>= 1000 bp)	1316
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	6323622
Total length (>= 1000 bp)	1750397
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	5556
Largest contig	3484
Total length	4695991
Reference length	4641652
GC (%)	50.72
Reference GC (%)	50.79
N50	865
NG50	870
N75	664
NG75	670
L50	1960
LG50	1929
L75	3516
LG75	3455
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	5096 + 7 part
Unaligned length	4166734
Genome fraction (%)	11.320
Duplication ratio	1.007
# N's per 100 kbp	0.00
# mismatches per 100 kbp	760.31
# indels per 100 kbp	0.57
Largest alignment	3481
NGA50	-

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

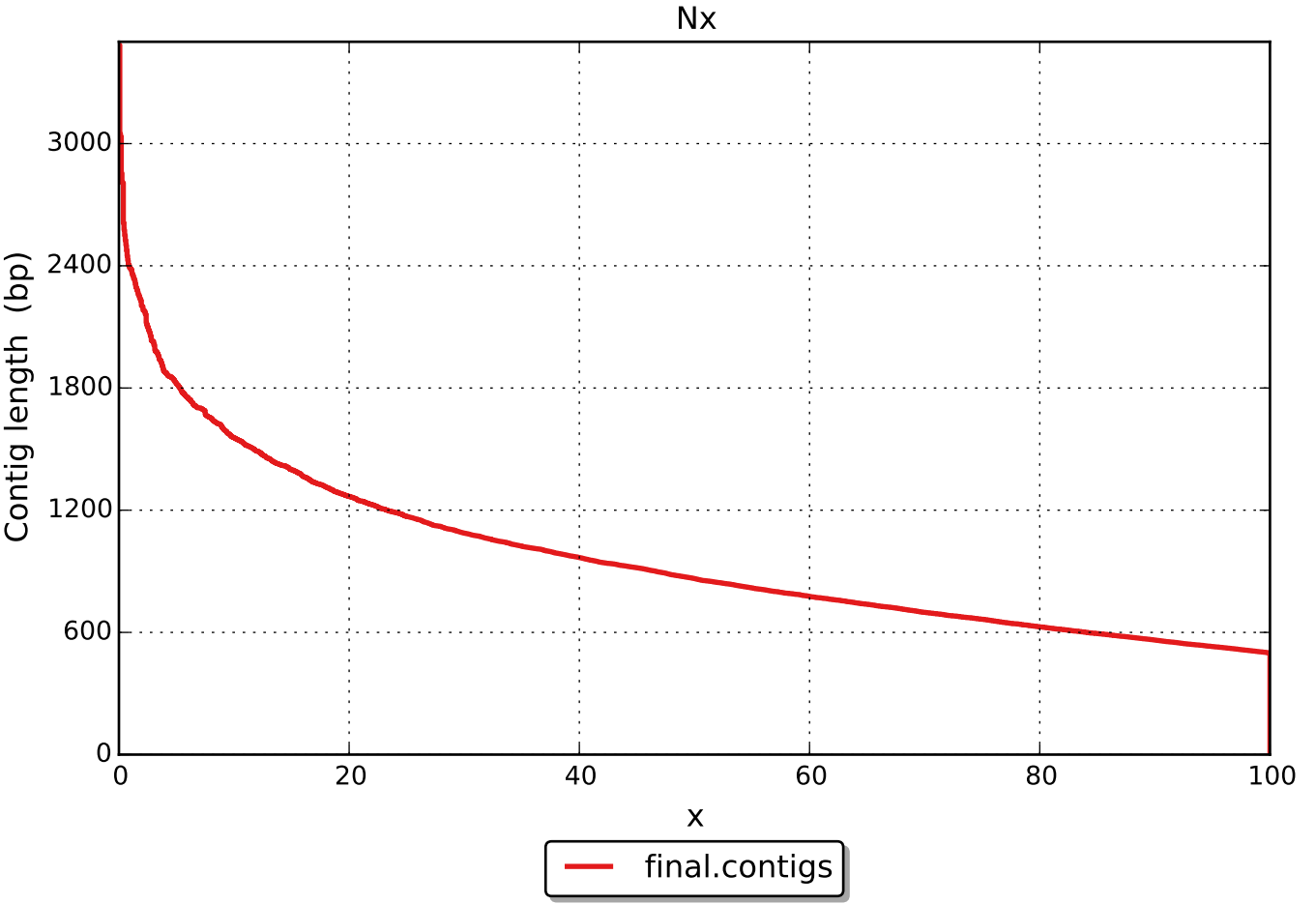
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	3995
# indels	3
# short indels	3
# long indels	0
Indels length	3

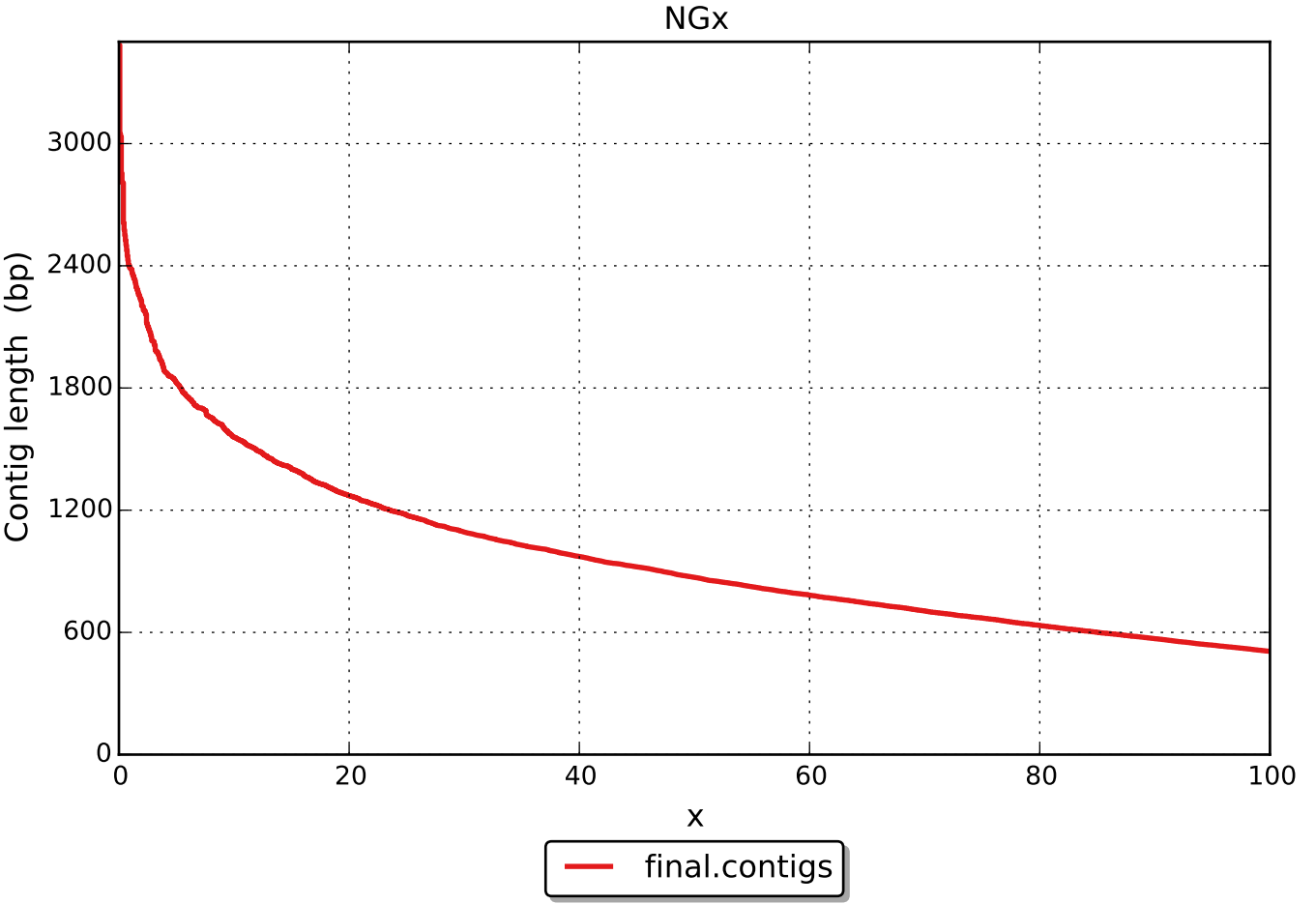
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

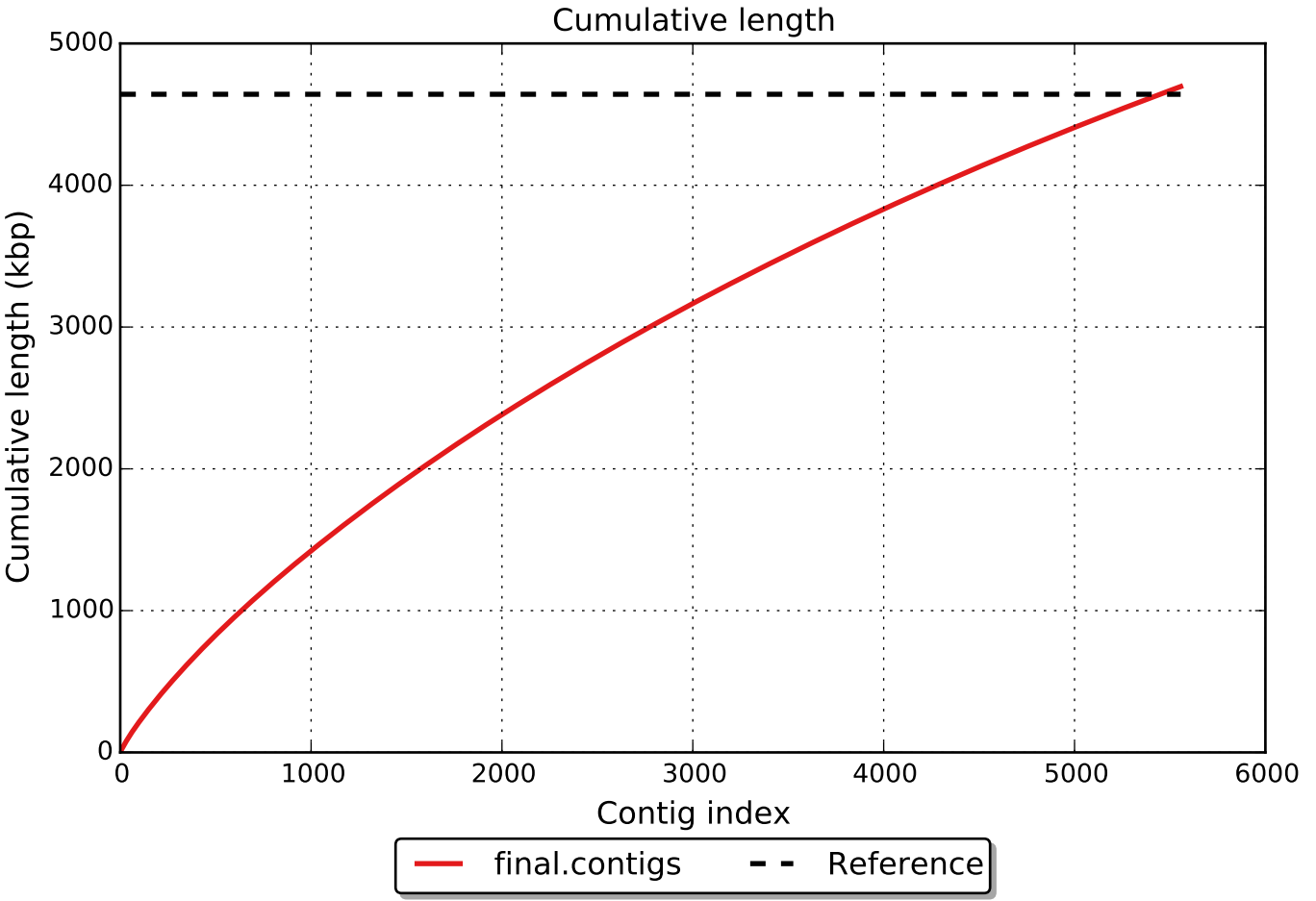
Unaligned report

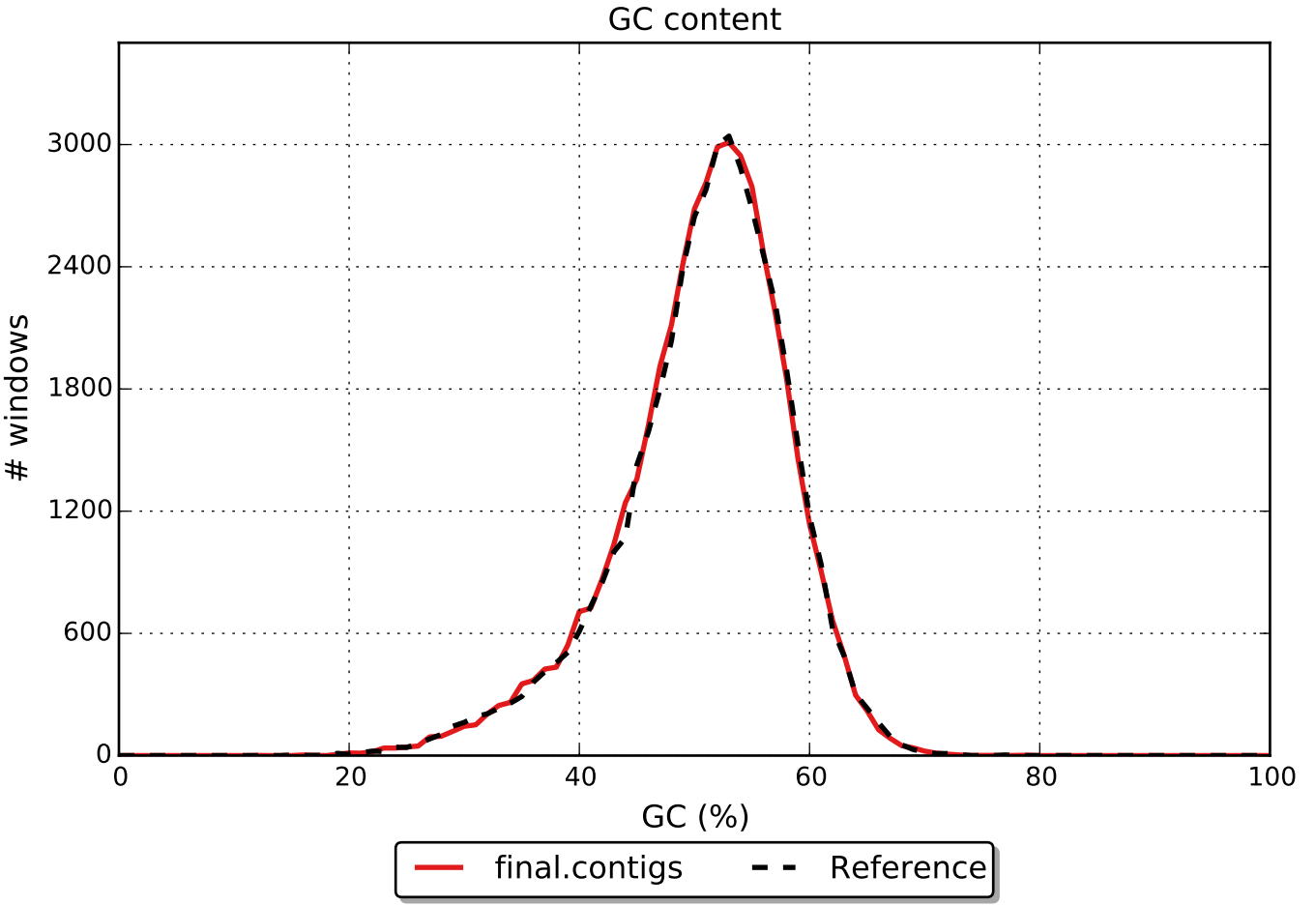
	final.contigs
# fully unaligned contigs	5096
Fully unaligned length	4163664
# partially unaligned contigs	7
# with misassembly	0
# both parts are significant	1
Partially unaligned length	3070
# N's	0

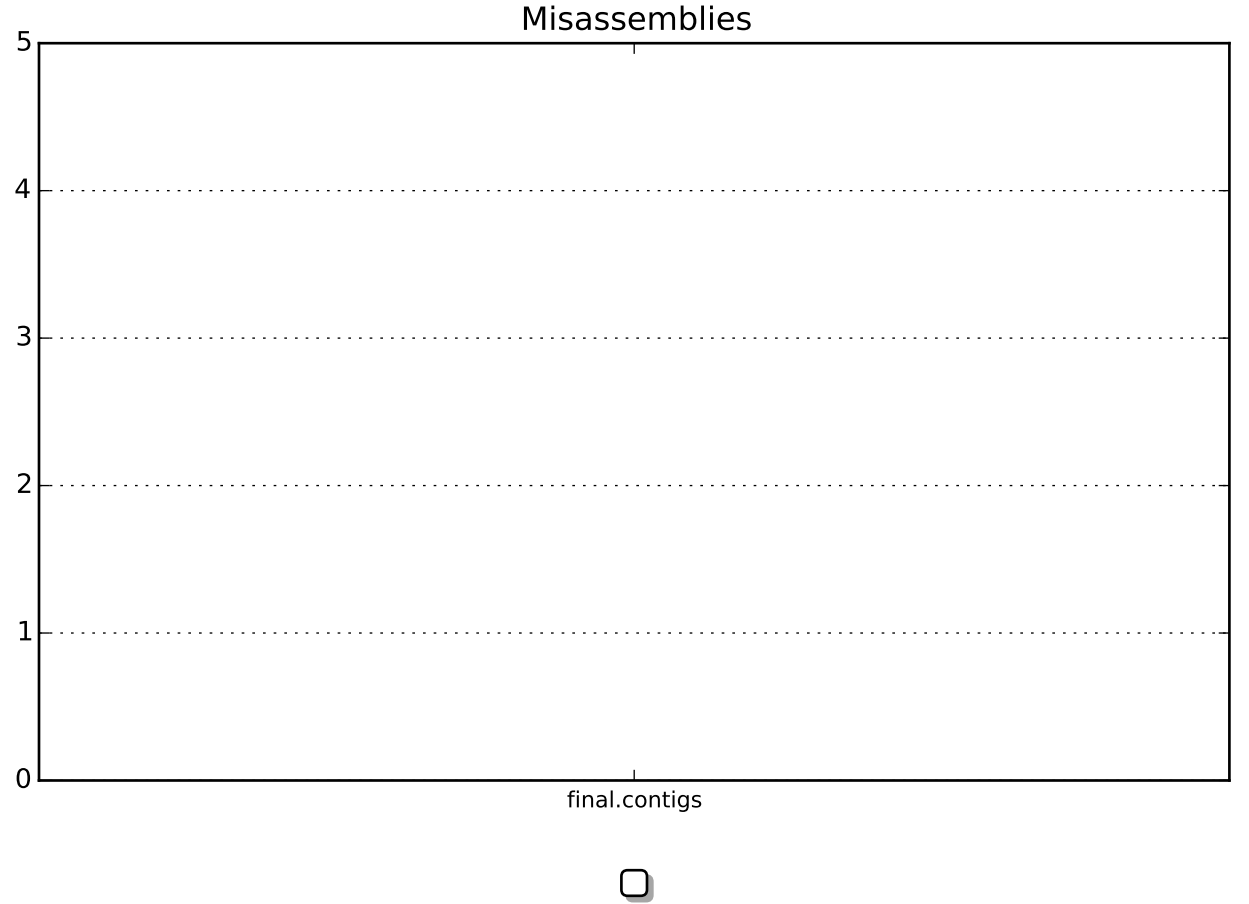
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

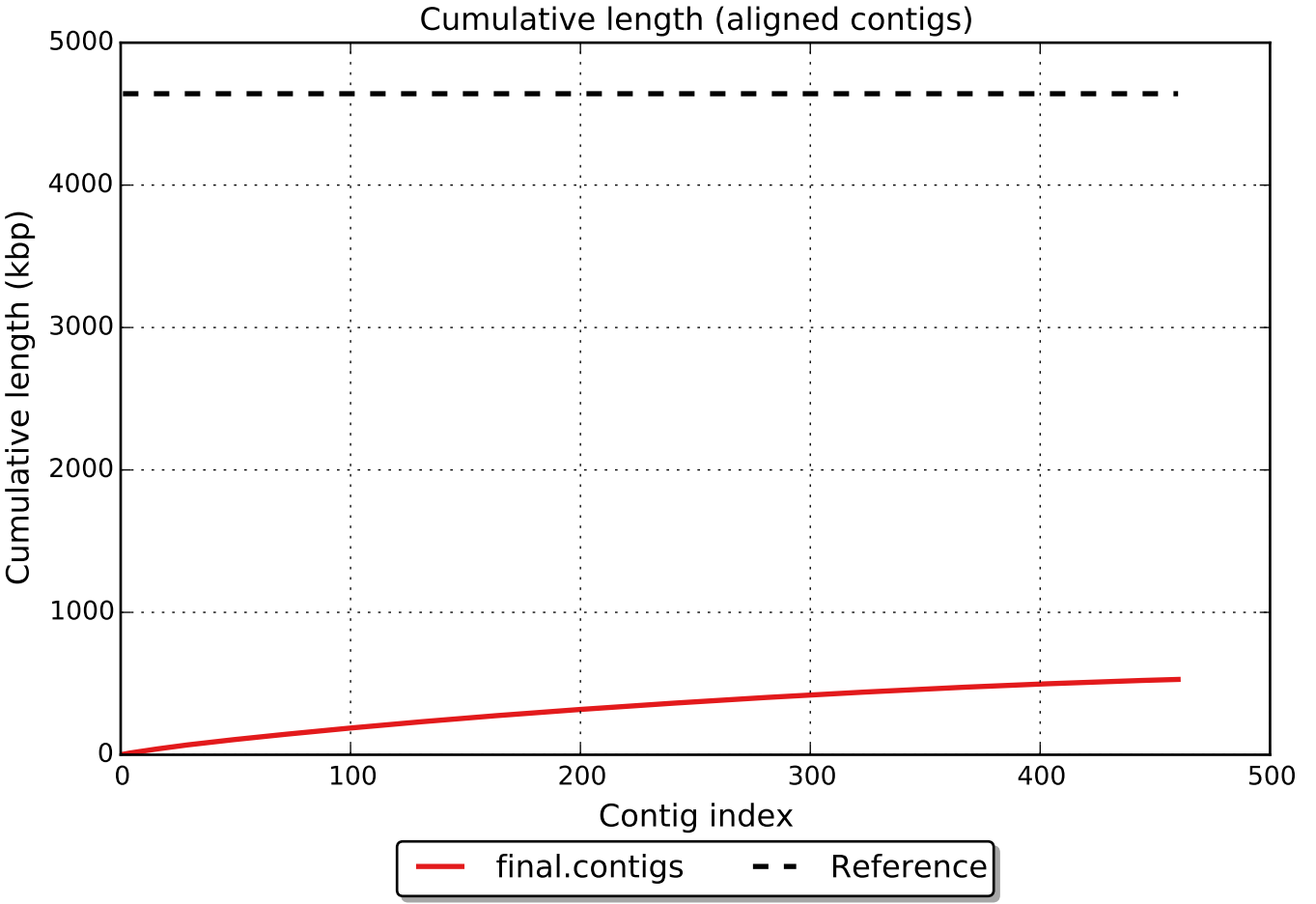

Nx
Contig length (bp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
final.contigs

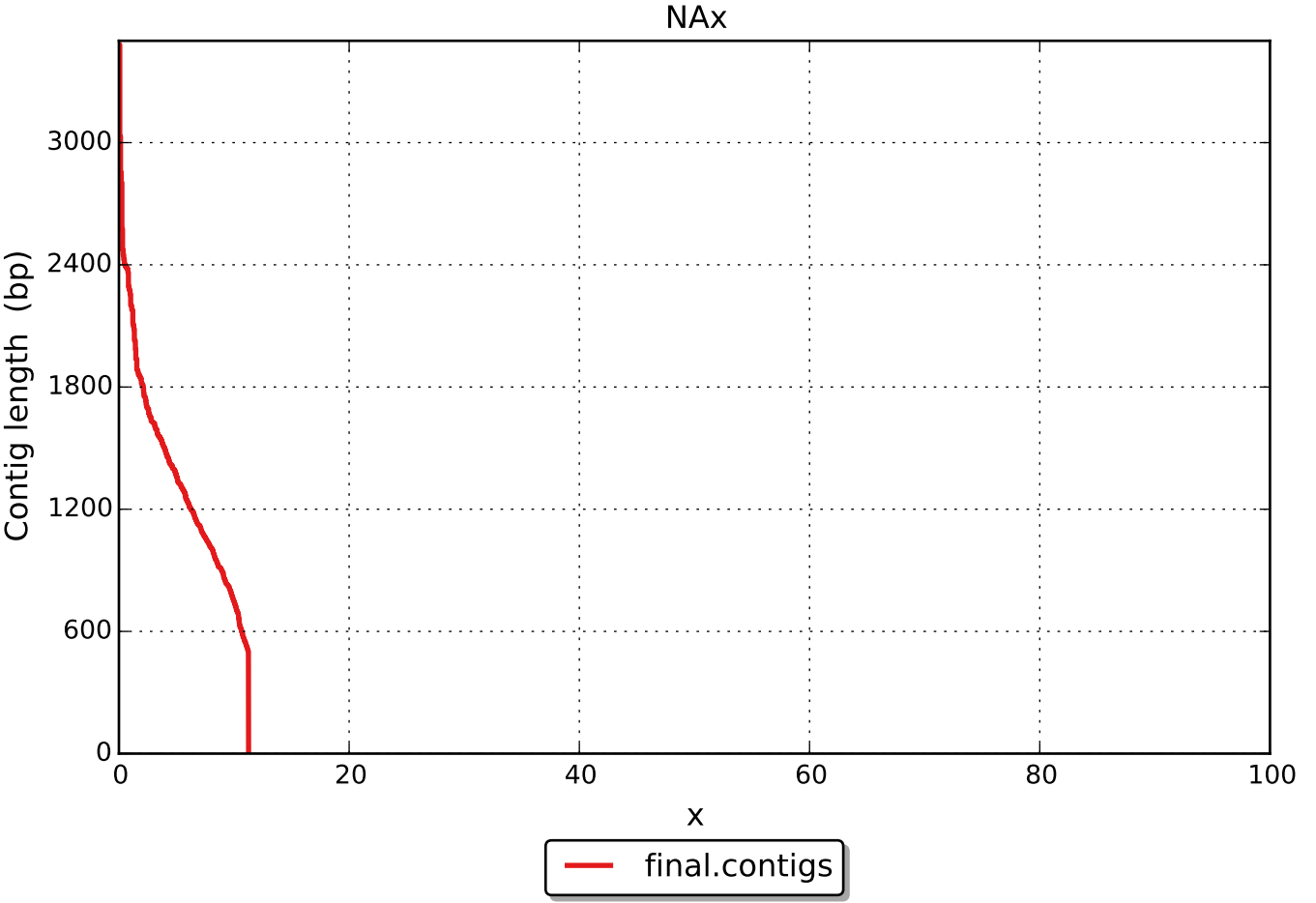

NGx
Contig length (bp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
final.contigs

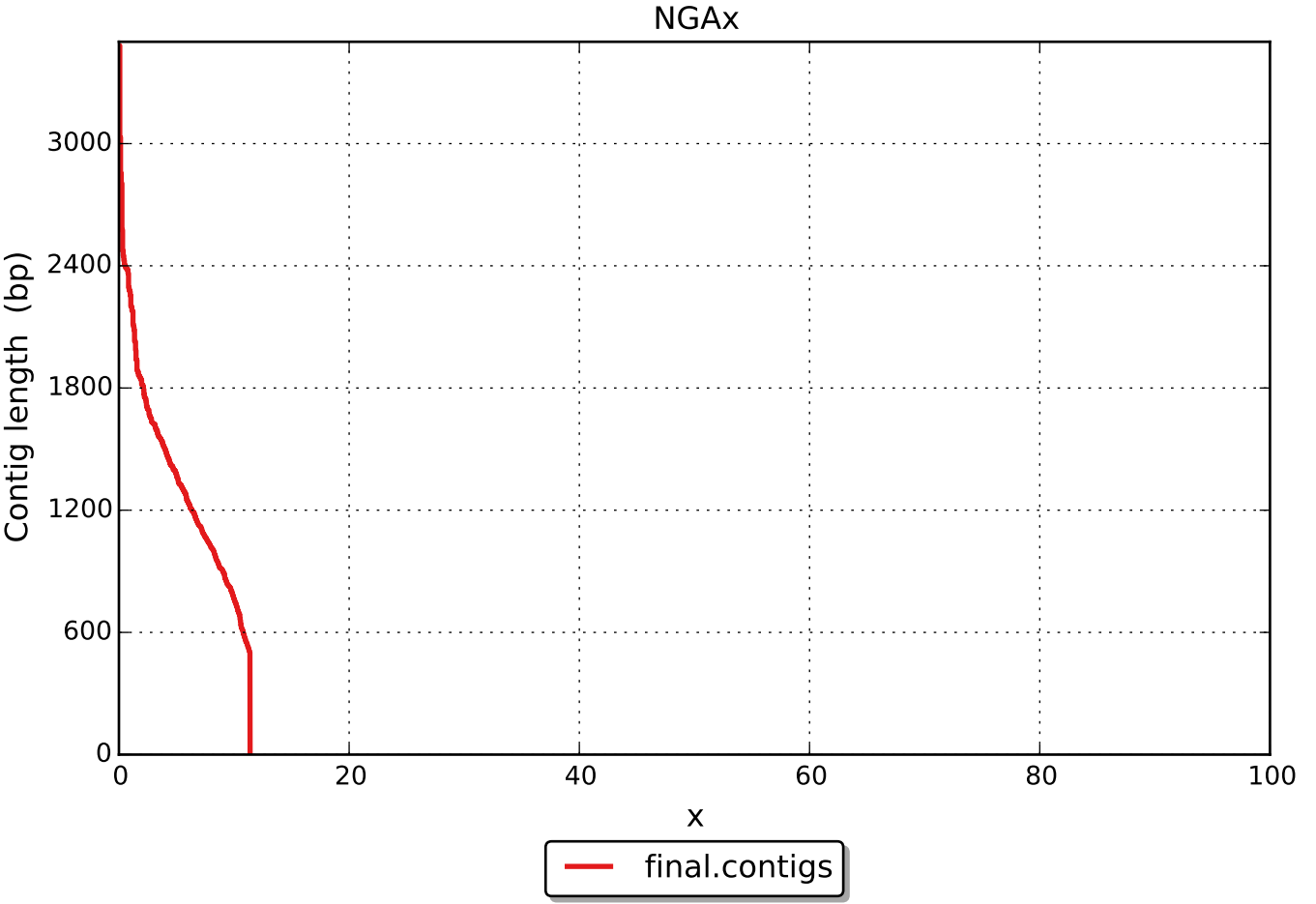

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
1000
2000
3000
4000
5000
6000
Contig index
final.contigs
Reference


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
100
200
300
400
500
Contig index
final.contigs
Reference


NAx
Contig length (bp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (bp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
final.contigs