Report

	final.contigs
# contigs (>= 1000 bp)	907
# contigs (>= 5000 bp)	5
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	1531865
Total length (>= 5000 bp)	30977
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2727
Largest contig	7423
Total length	2776877
Reference length	4641652
GC (%)	50.81
Reference GC (%)	50.79
N50	1112
NG50	635
N75	719
L50	772
LG50	1913
L75	1559
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	521
# local misassemblies	0
# unaligned contigs	0 + 3 part
Unaligned length	155
Genome fraction (%)	57.077
Duplication ratio	1.048
# N's per 100 kbp	0.00
# mismatches per 100 kbp	347.86
# indels per 100 kbp	0.30
Largest alignment	7423
NA50	1112
NGA50	634
NA75	719
LA50	772
LGA50	1914
LA75	1559

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

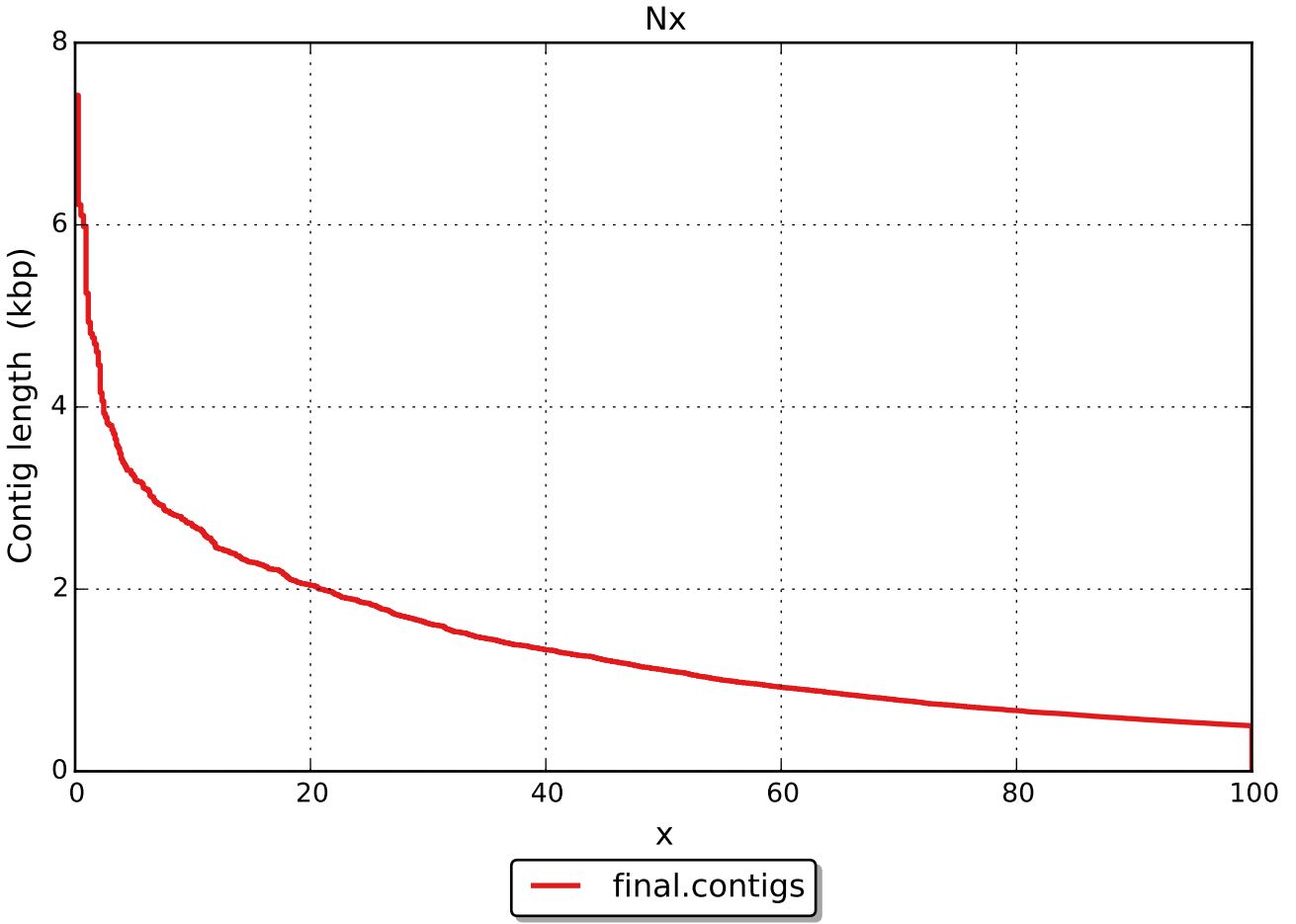
	final.contigs
# misassemblies	1
# relocations	0
# translocations	0
# inversions	1
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	521
# local misassemblies	0
# mismatches	9216
# indels	8
# short indels	8
# long indels	0
Indels length	8

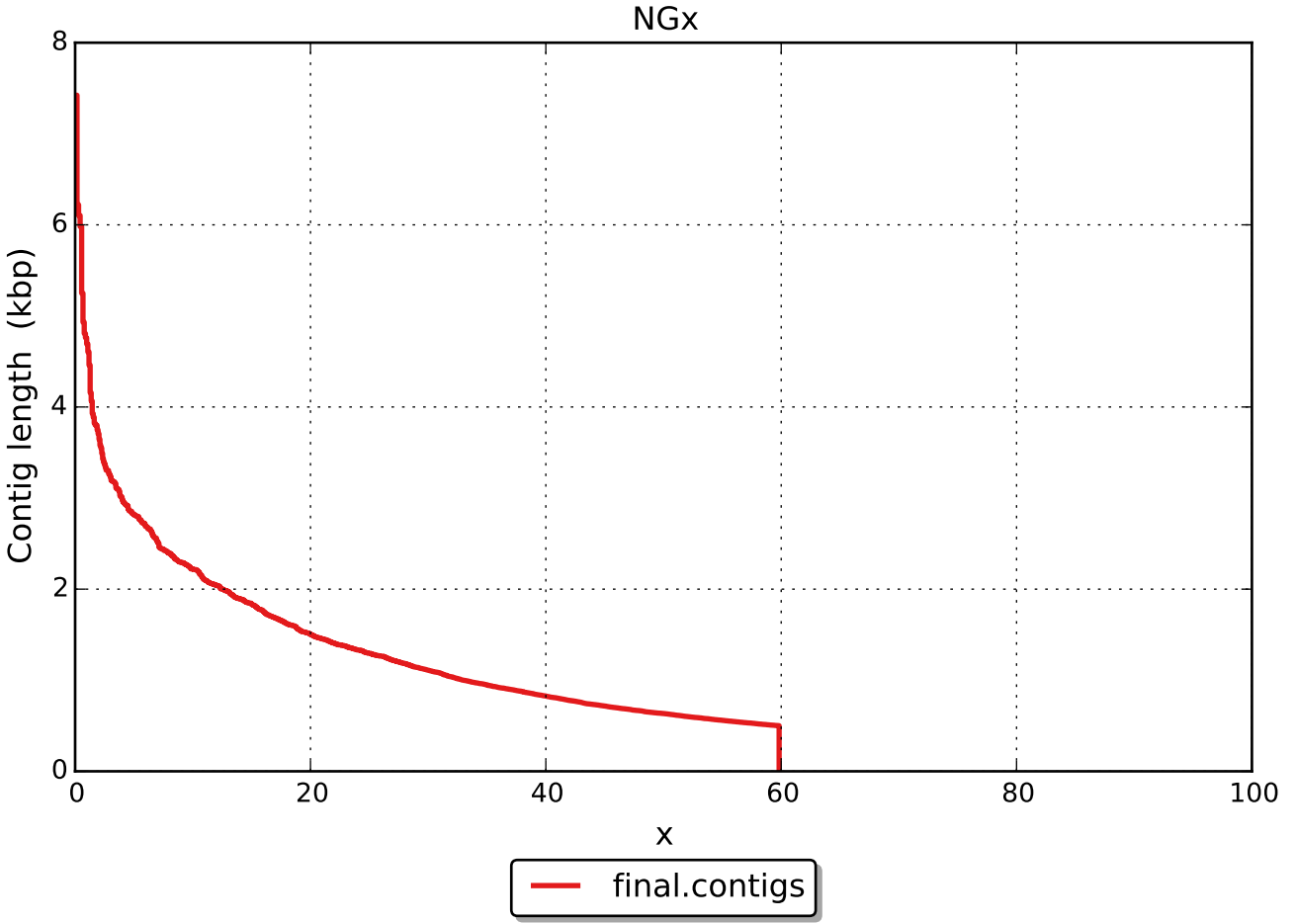
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

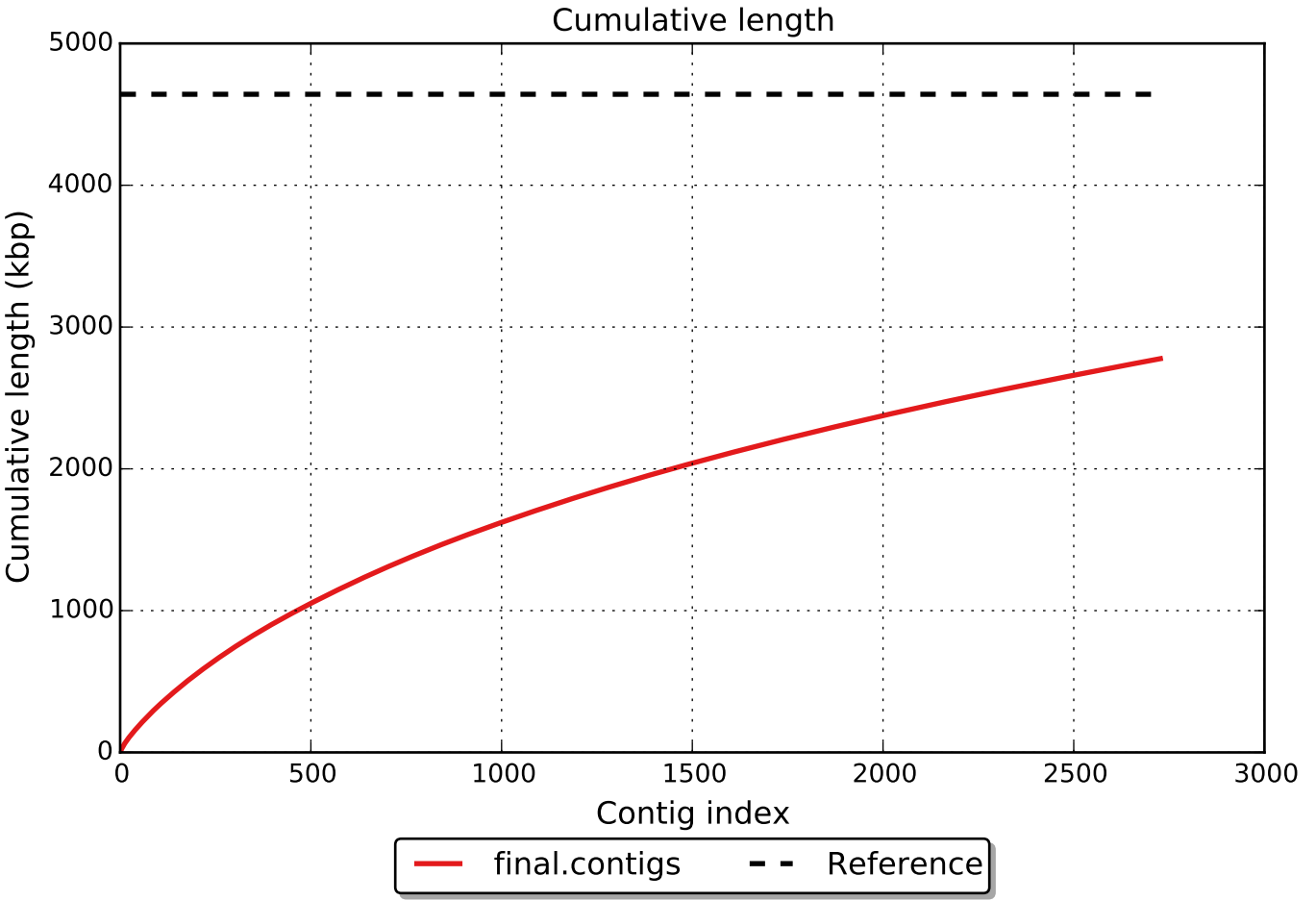
Unaligned report

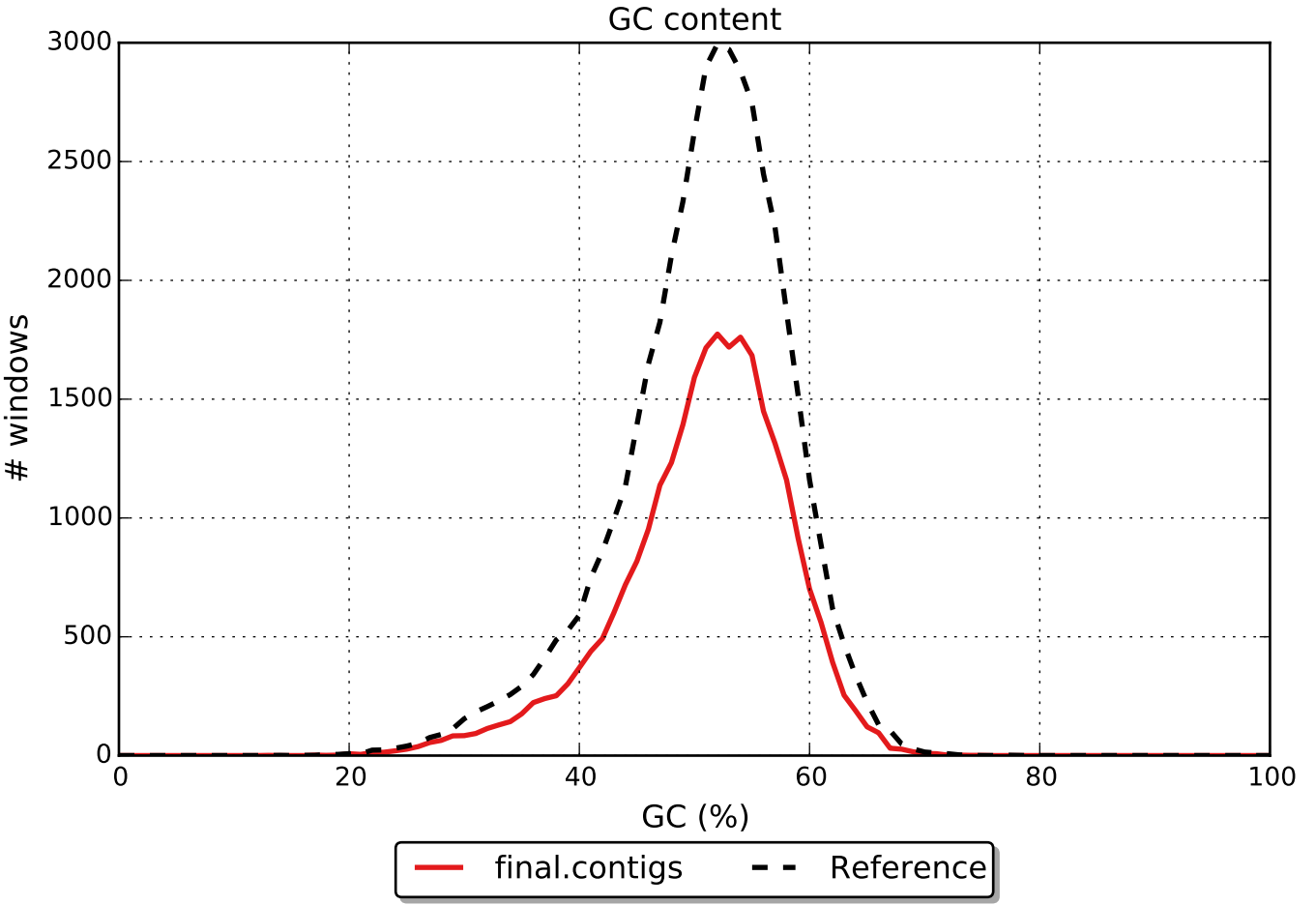
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
# with misassembly	0
# both parts are significant	0
Partially unaligned length	155
# N's	0

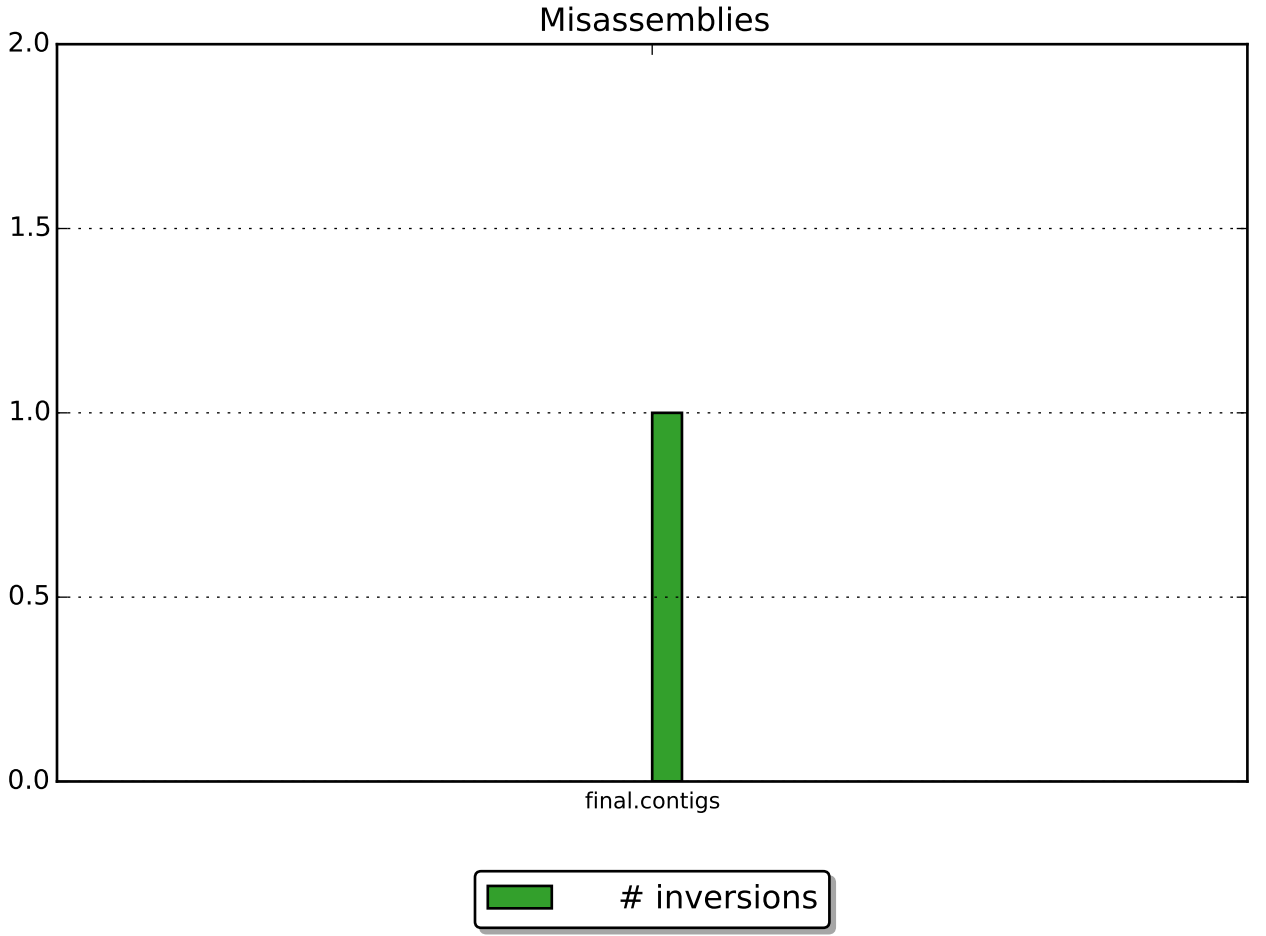
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

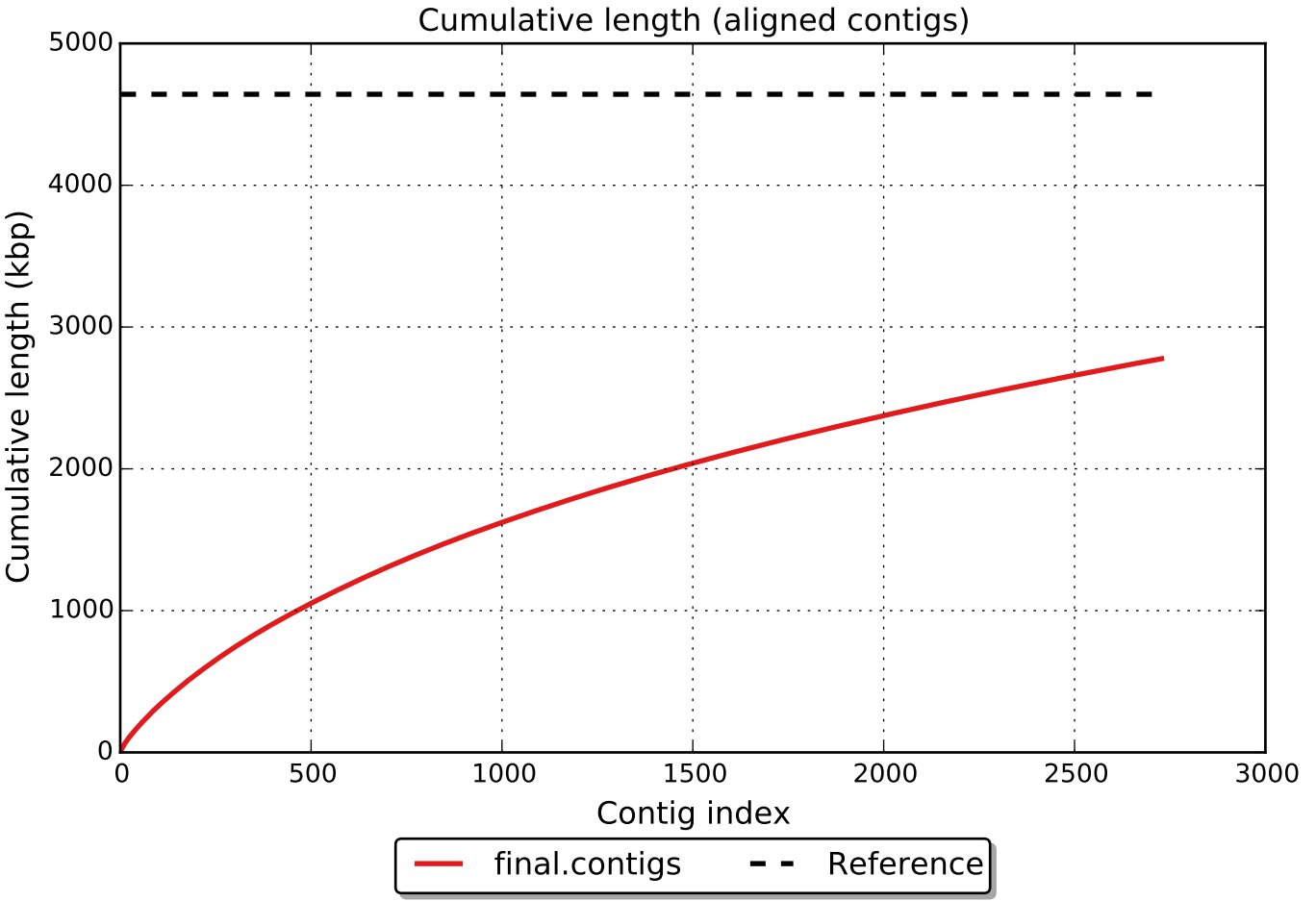

Nx
Contig length (kbp)
0
2
4
6
8
0
20
40
60
80
100
x
final.contigs

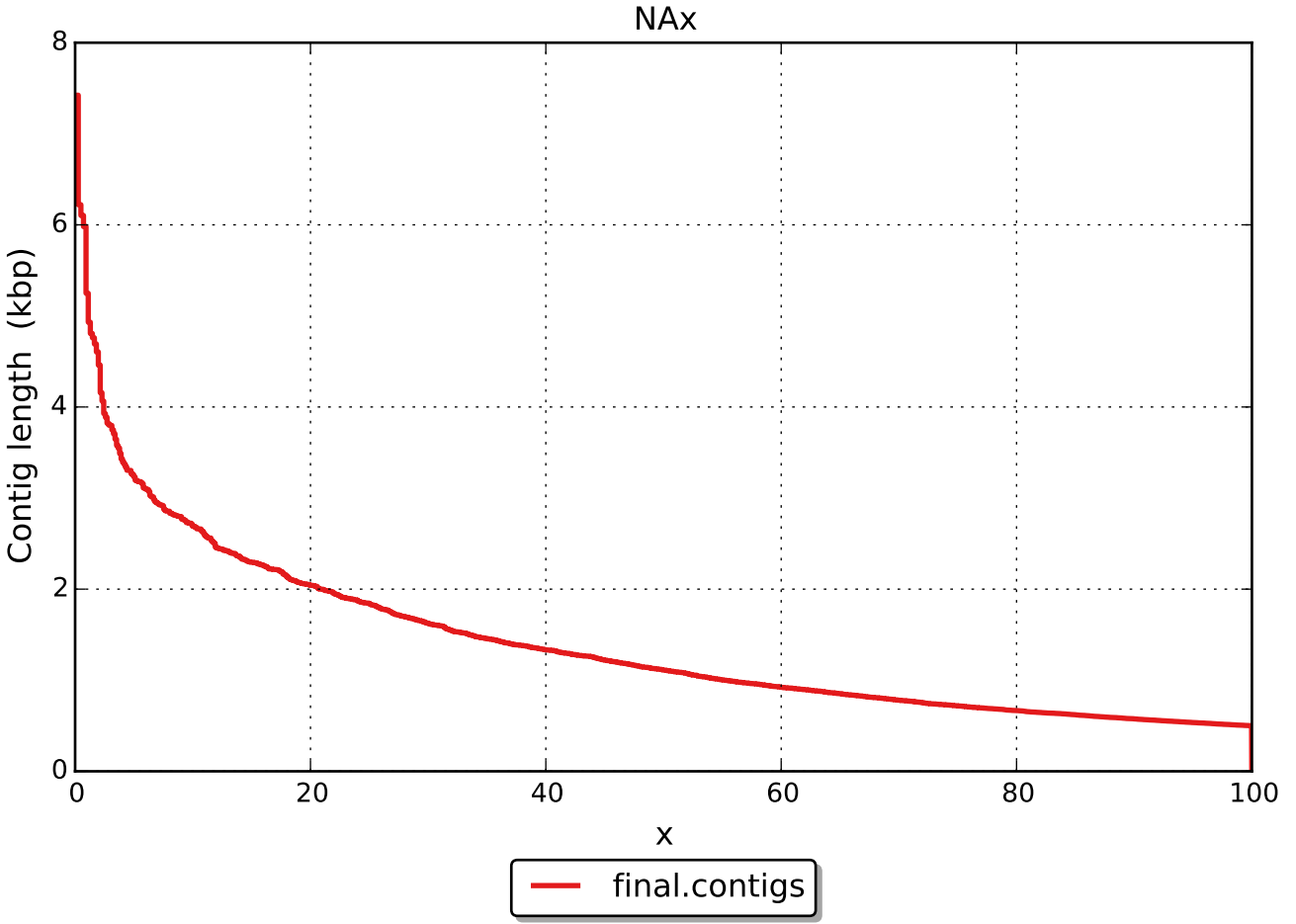

NGx
Contig length (kbp)
0
2
4
6
8
0
20
40
60
80
100
x
final.contigs

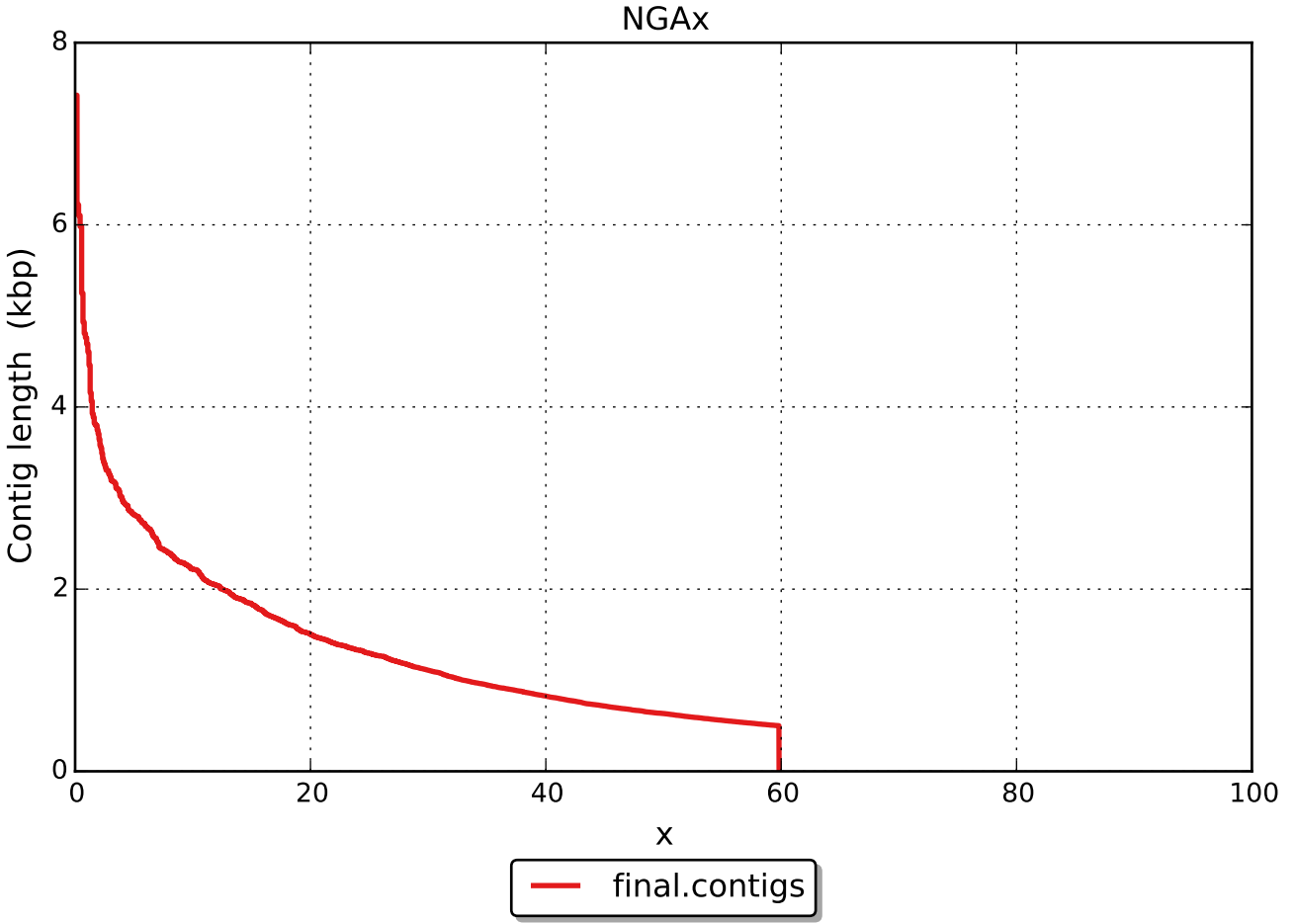

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
500
1000
1500
2000
2500
3000
Contig index
final.contigs
Reference


GC content
3000
2500
2000
1500
1000
500
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference


Misassemblies
2.0
1.5
1.0
0.5
0.0
final.contigs
inversions


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
500
1000
1500
2000
2500
3000
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
0
2
4
6
8
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
0
2
4
6
8
0
20
40
60
80
100
x
final.contigs