Report

	final.contigs
# contigs (>= 1000 bp)	1738
# contigs (>= 5000 bp)	3
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	2978122
Total length (>= 5000 bp)	16001
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3613
Largest contig	5370
Total length	4320768
Reference length	4641652
GC (%)	50.77
Reference GC (%)	50.79
N50	1383
NG50	1292
N75	902
NG75	805
L50	1041
LG50	1161
L75	2015
LG75	2297
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	89.073
Duplication ratio	1.045
# N's per 100 kbp	0.00
# mismatches per 100 kbp	33.16
# indels per 100 kbp	0.05
Largest alignment	5370
NA50	1383
NGA50	1292
NA75	902
NGA75	805
LA50	1041
LGA50	1161
LA75	2015
LGA75	2297

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

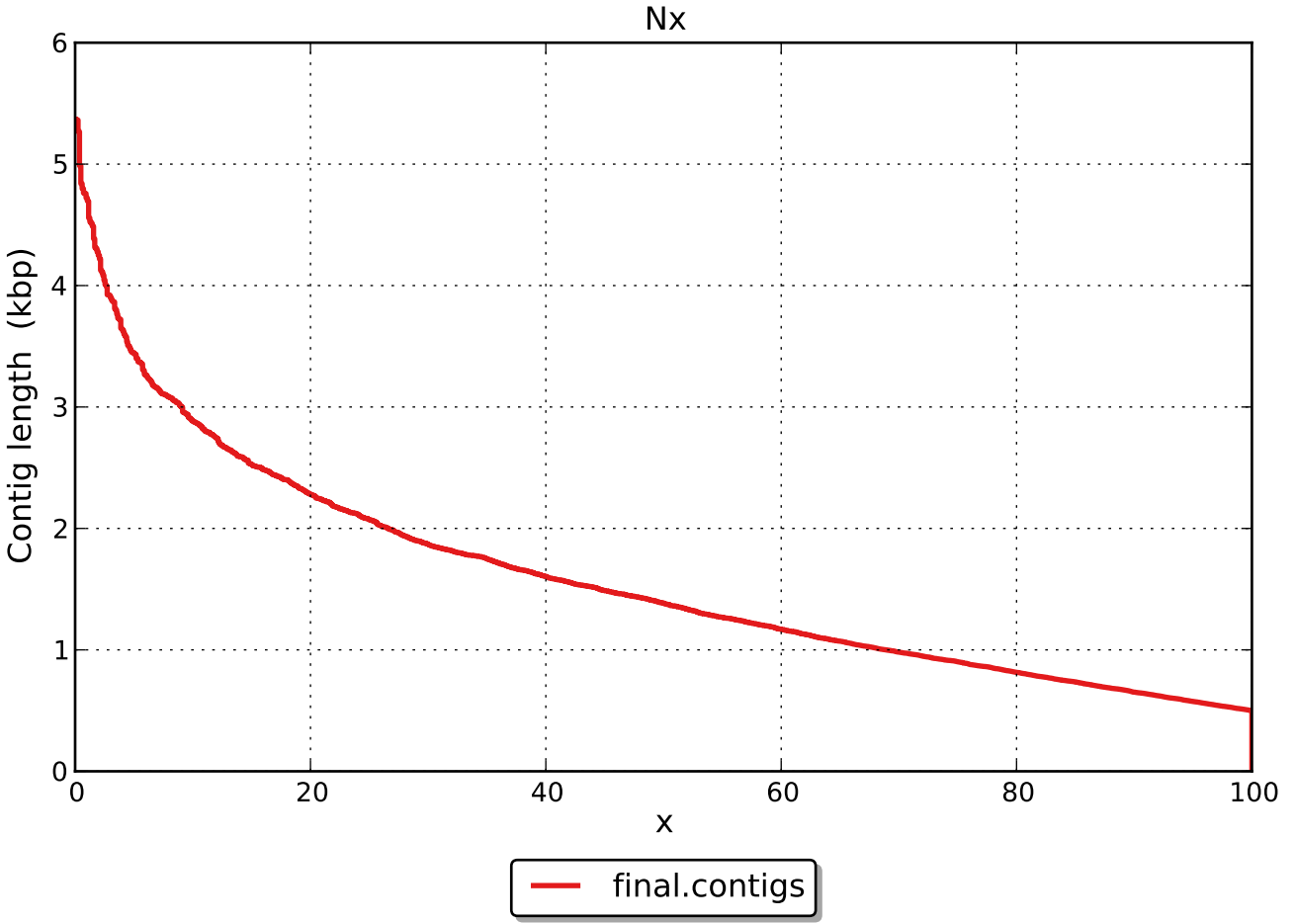
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	1371
# indels	2
# short indels	2
# long indels	0
Indels length	2

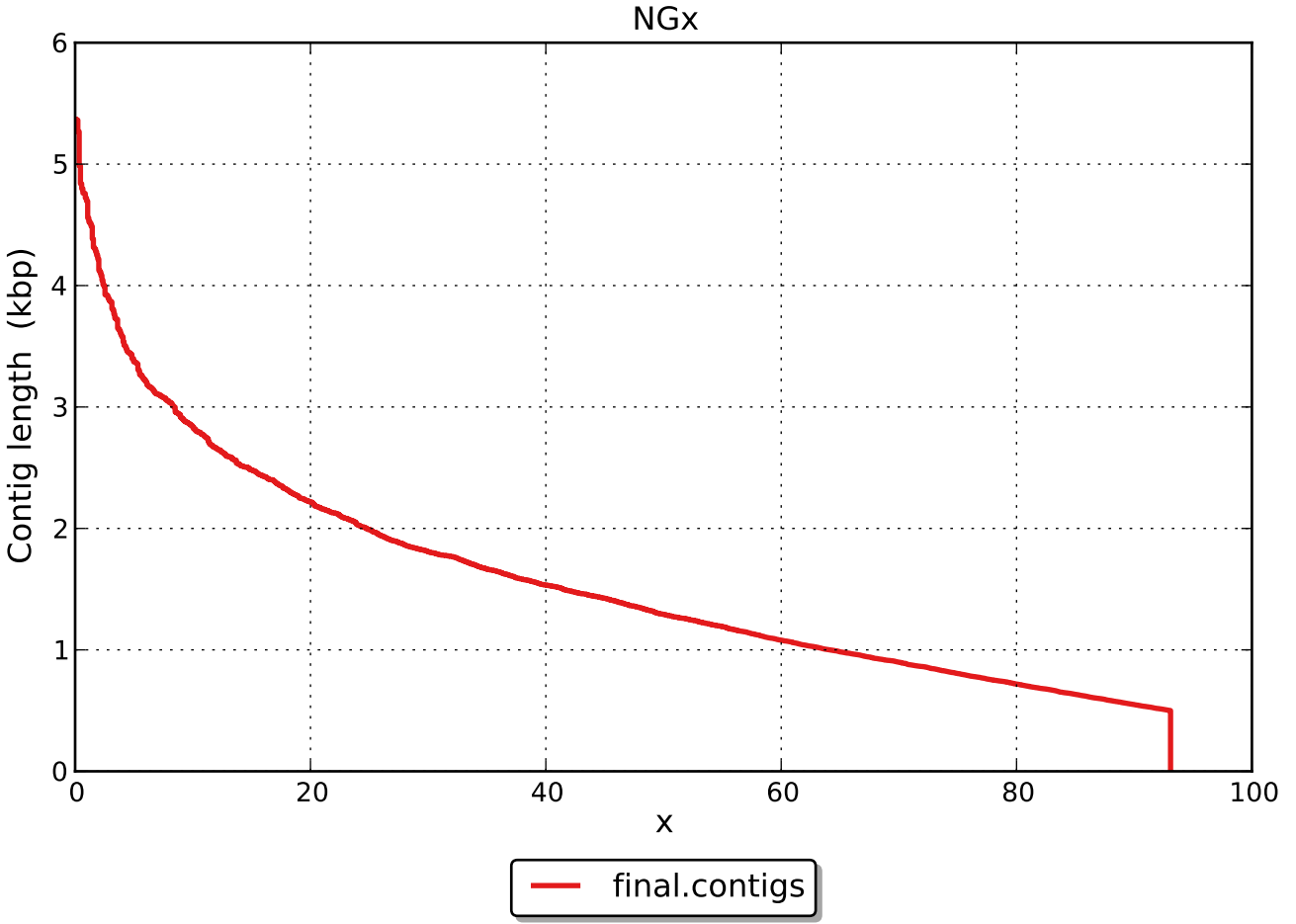
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

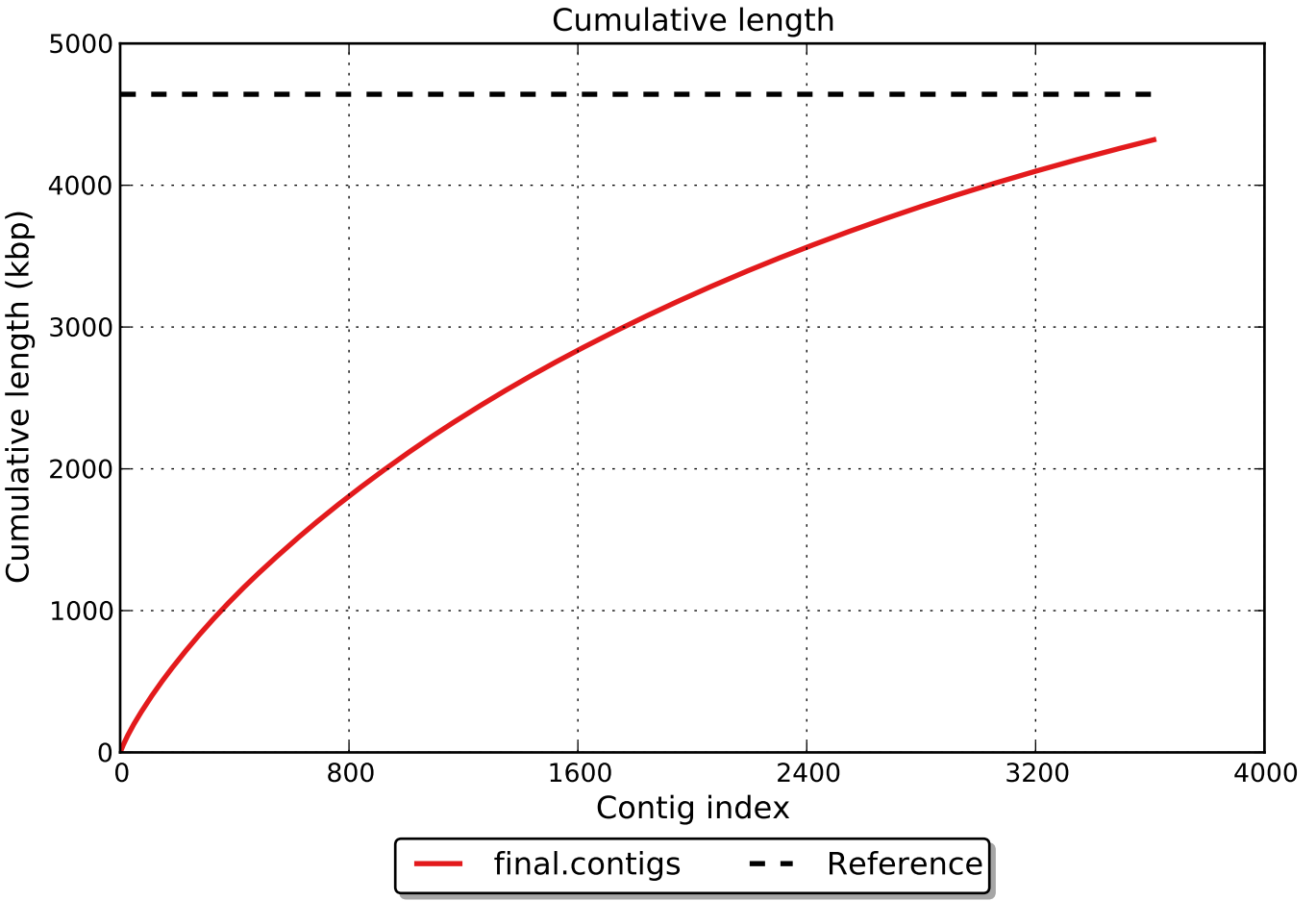
Unaligned report

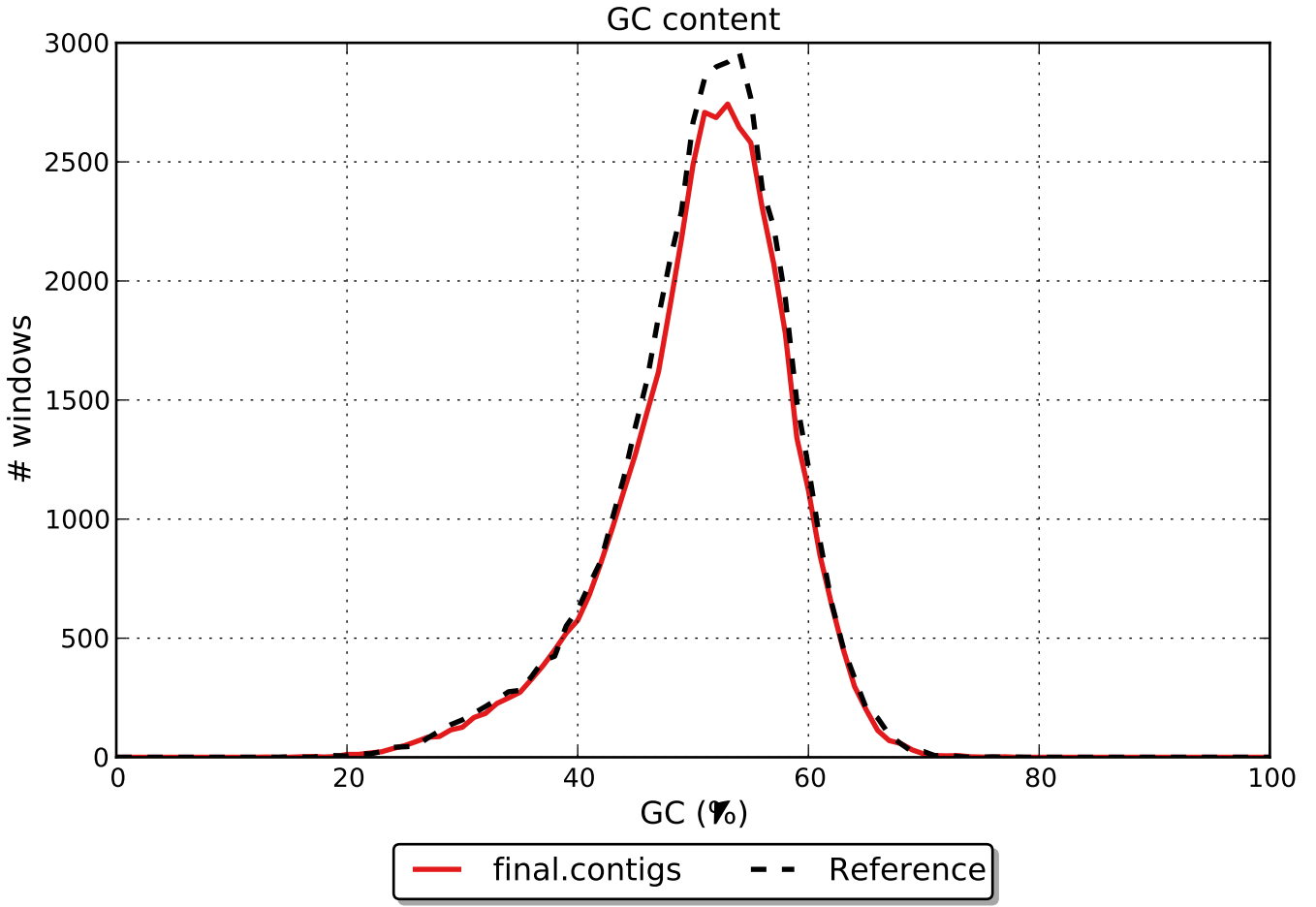
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

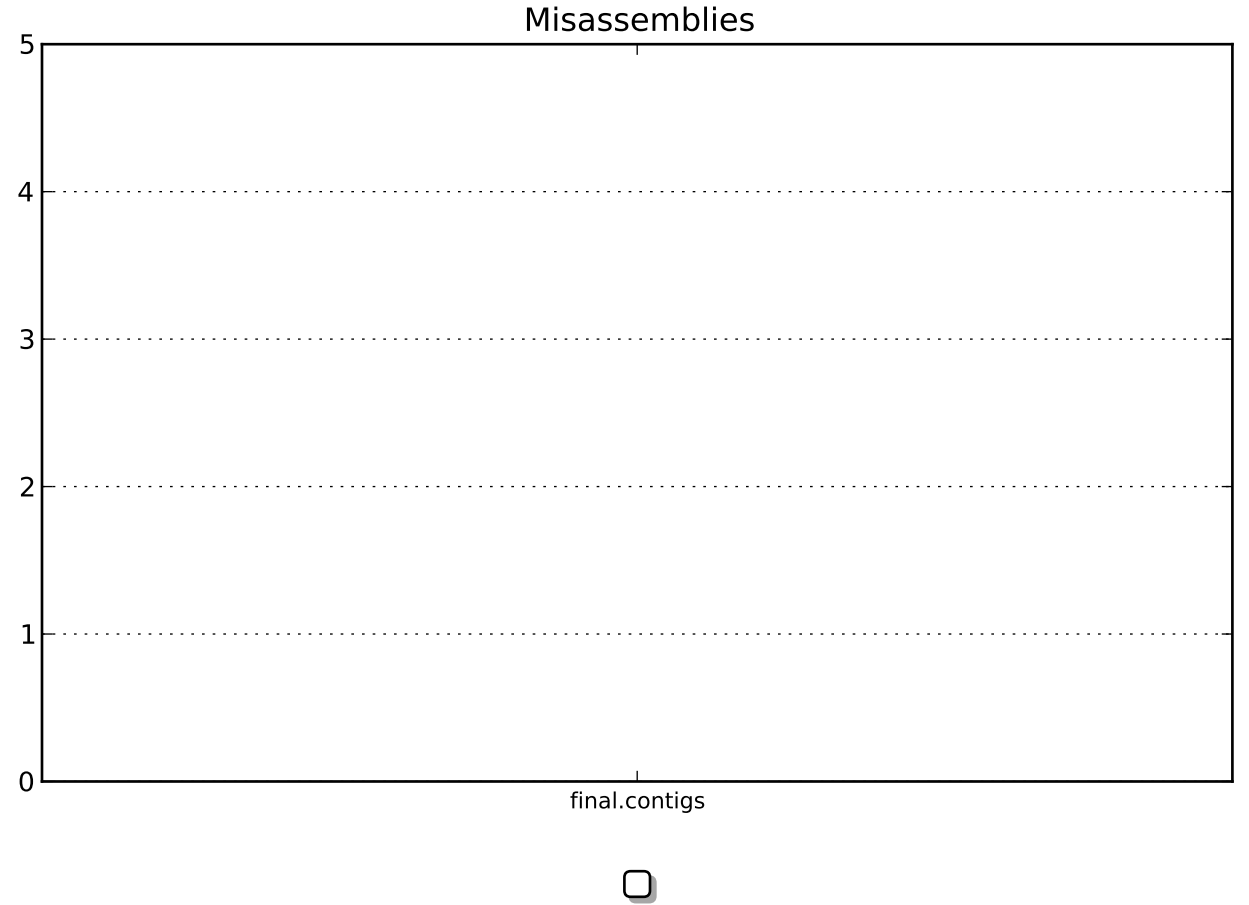
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

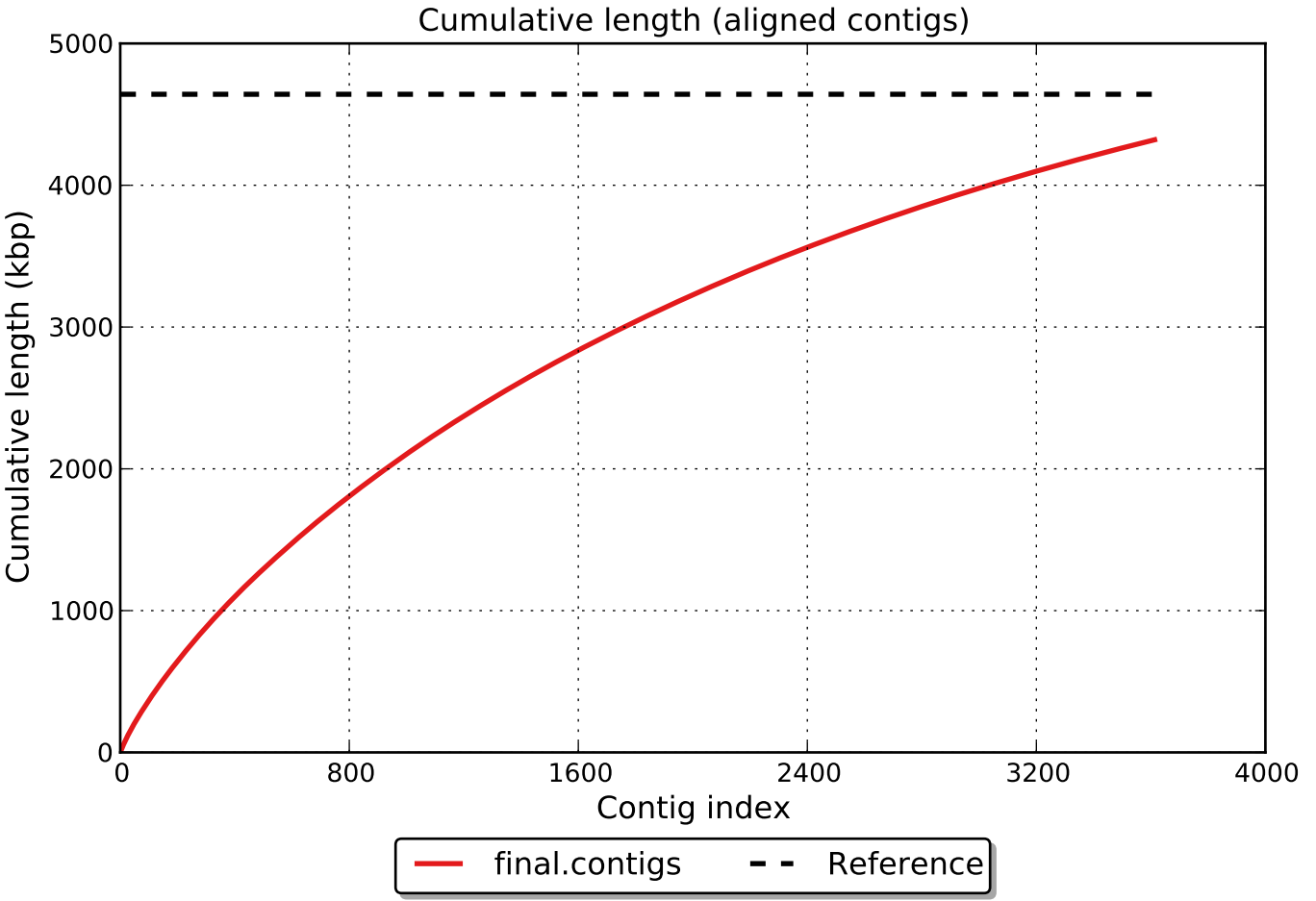

Nx
Contig length (kbp)
x
0
1
2
3
4
5
6
0
20
40
60
80
100
final.contigs

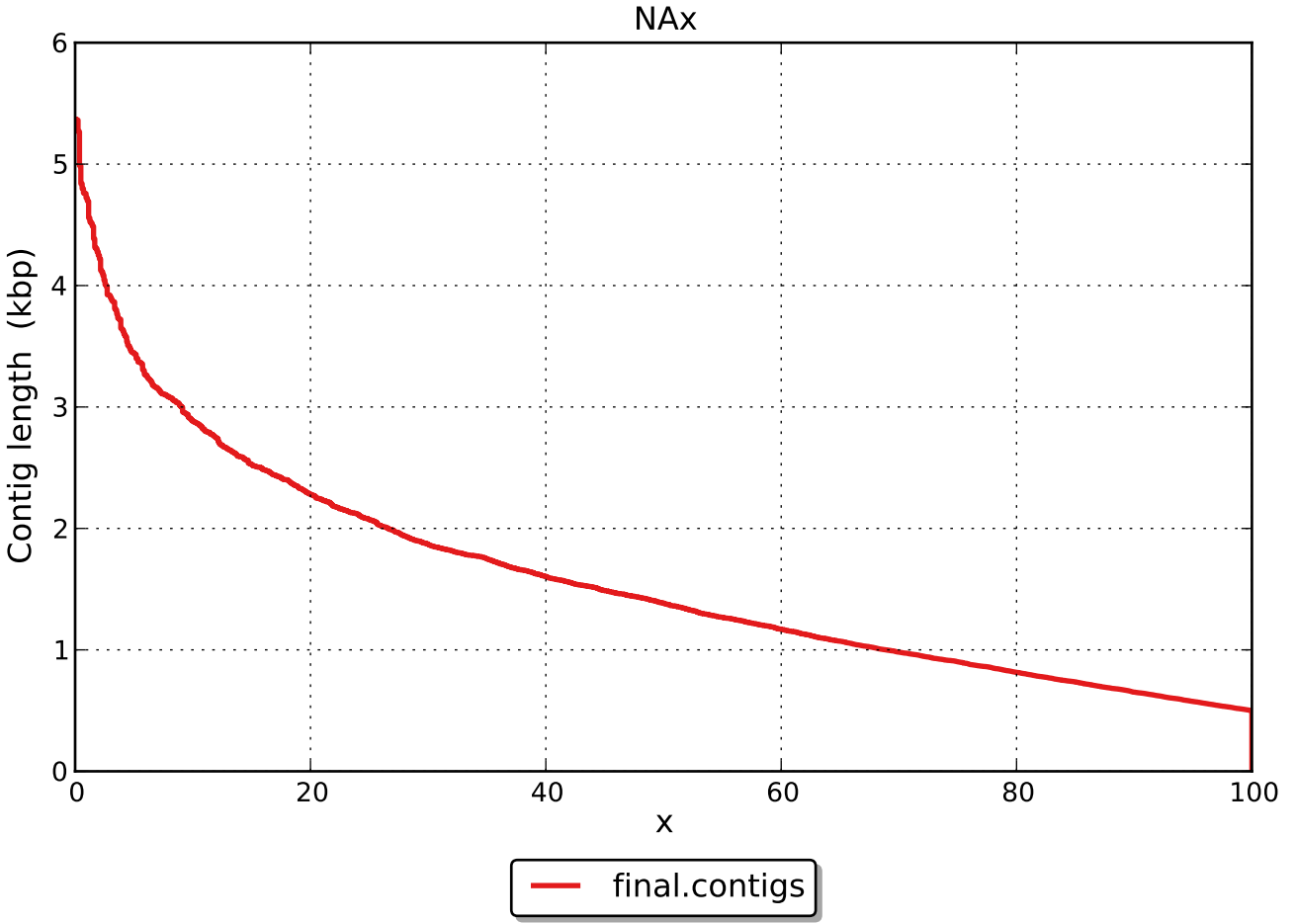

NGx
Contig length (kbp)
0
1
2
3
4
5
6
0
20
40
60
80
100
x
final.contigs

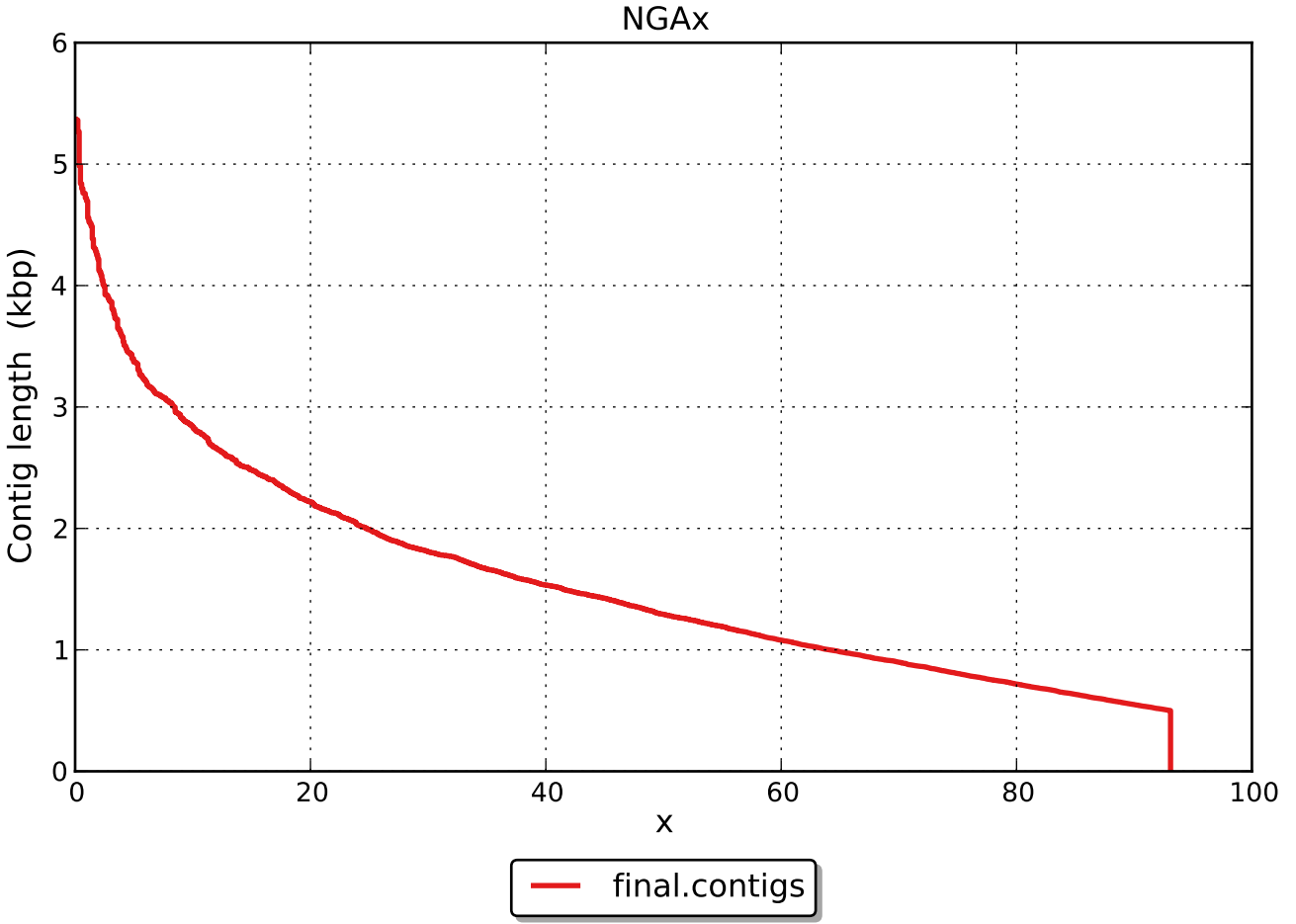

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
800
1600
2400
3200
4000
Contig index
final.contigs
Reference


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


Misassemblies
5
4
3
2
1
0
final.contigs


Cumulative length (aligned contigs)
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
800
1600
2400
3200
4000
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
x
0
1
2
3
4
5
6
0
20
40
60
80
100
final.contigs


NGAx
Contig length (kbp)
0
1
2
3
4
5
6
0
20
40
60
80
100
x
final.contigs