Report

	final.contigs
# contigs (>= 1000 bp)	1475
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	2208444
Total length (>= 5000 bp)	5476
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	4092
Largest contig	5476
Total length	4066188
Reference length	4641652
GC (%)	50.78
Reference GC (%)	50.79
N50	1060
NG50	965
N75	758
NG75	644
L50	1305
LG50	1590
L75	2445
LG75	3062
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# unaligned contigs	0 + 2 part
Unaligned length	77
Genome fraction (%)	82.424
Duplication ratio	1.063
# N's per 100 kbp	0.00
# mismatches per 100 kbp	172.67
# indels per 100 kbp	0.24
Largest alignment	5476
NA50	1060
NGA50	965
NA75	758
NGA75	643
LA50	1305
LGA50	1590
LA75	2445
LGA75	3063

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

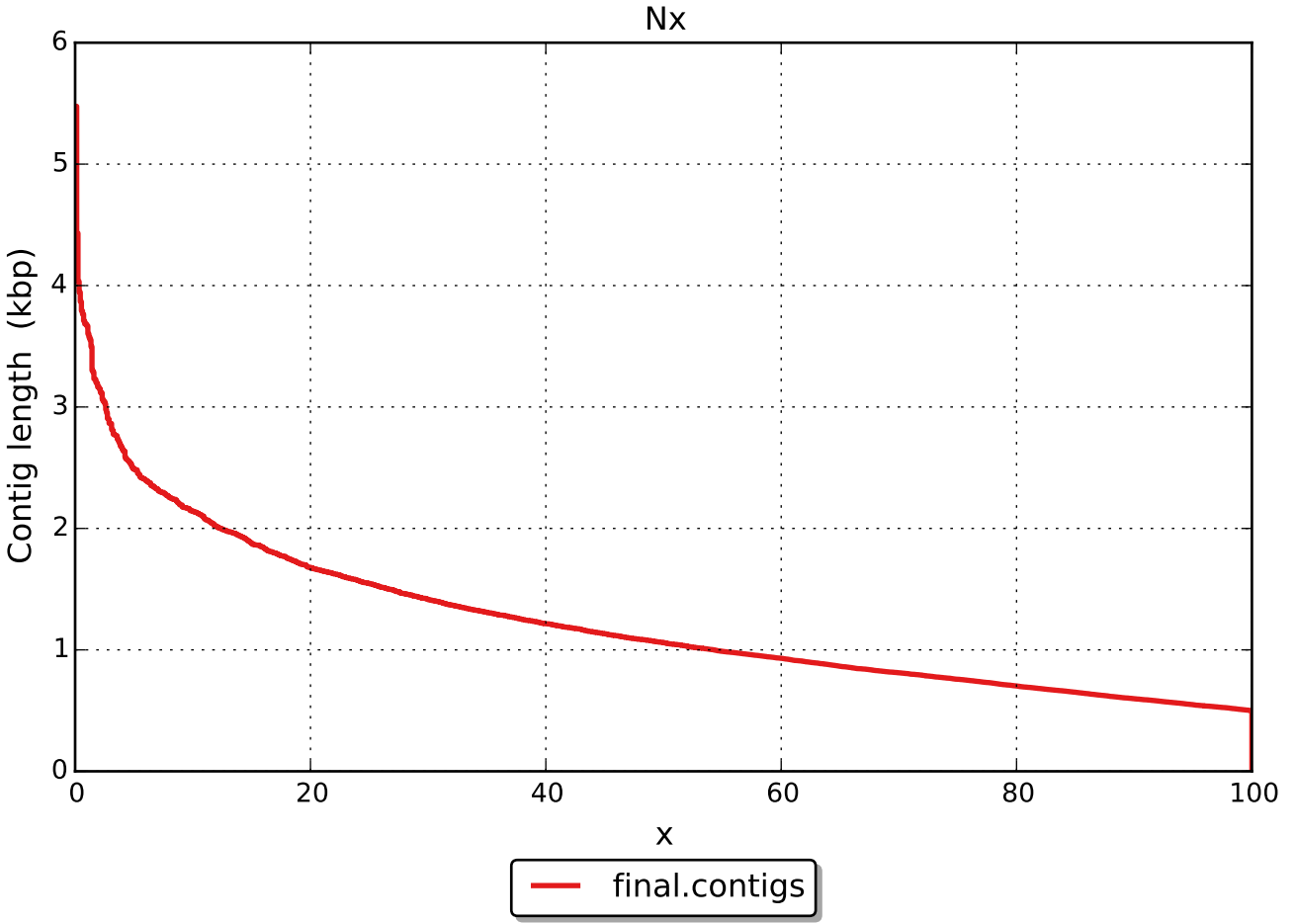
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	2
# mismatches	6606
# indels	9
# short indels	9
# long indels	0
Indels length	10

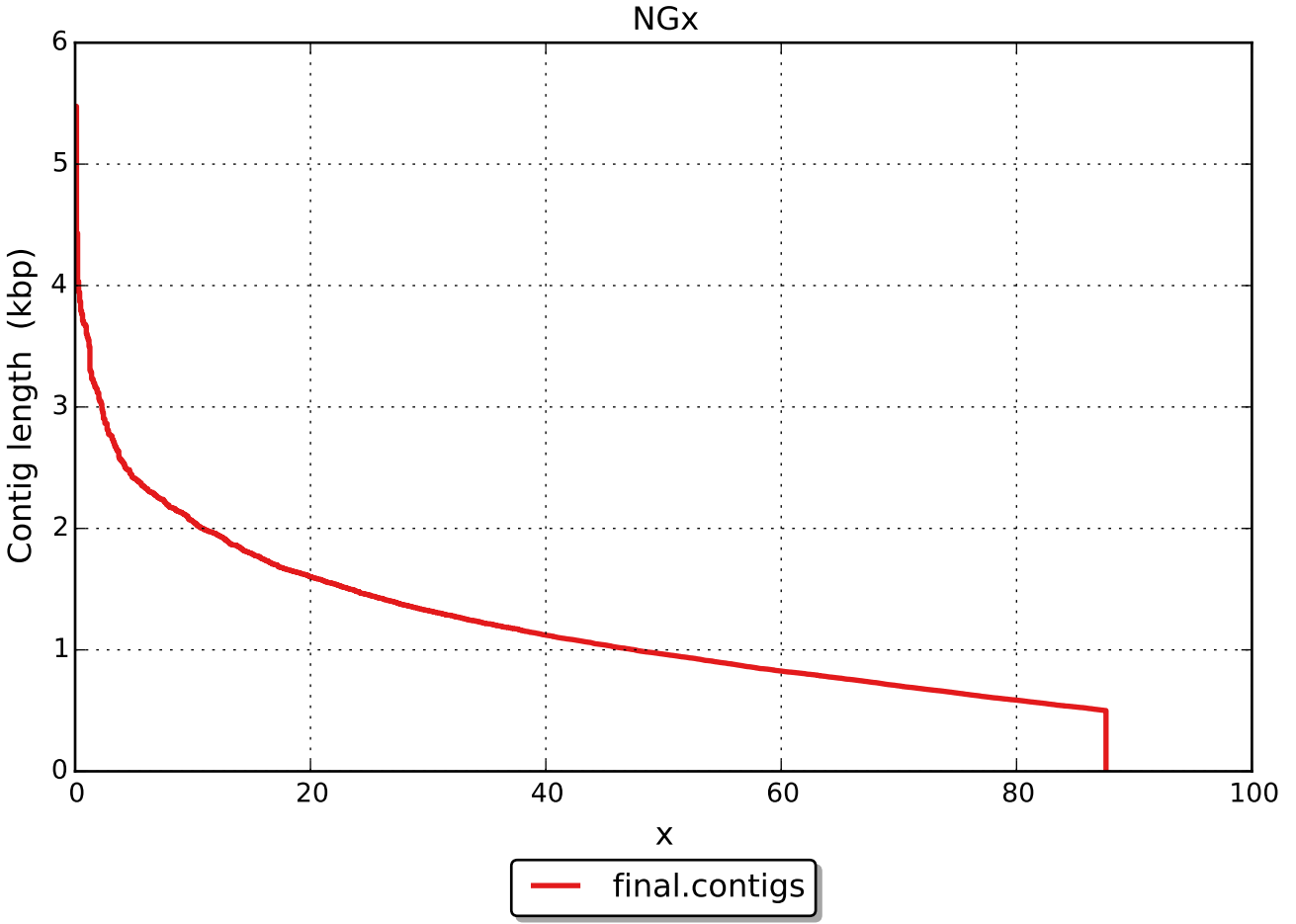
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

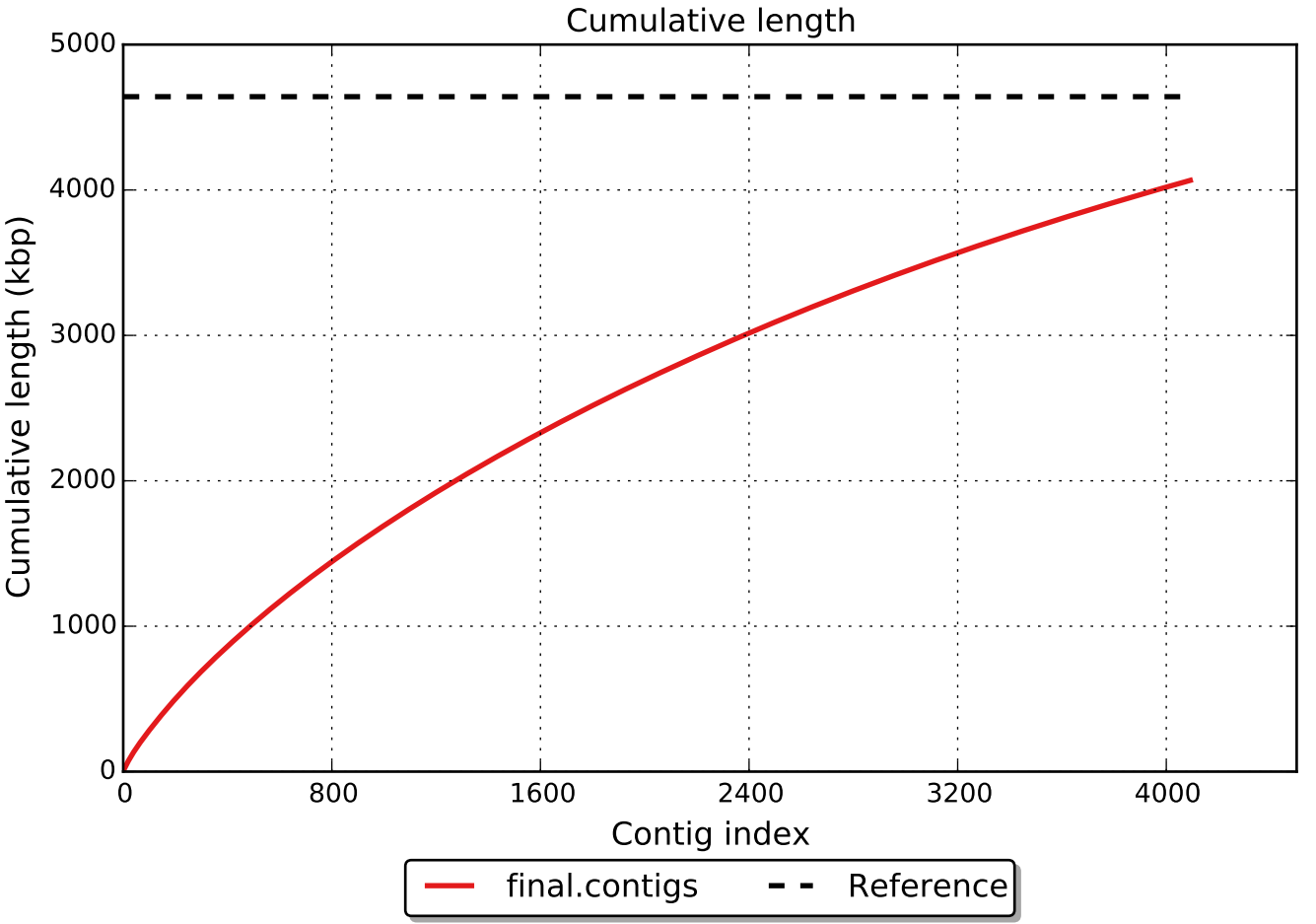
Unaligned report

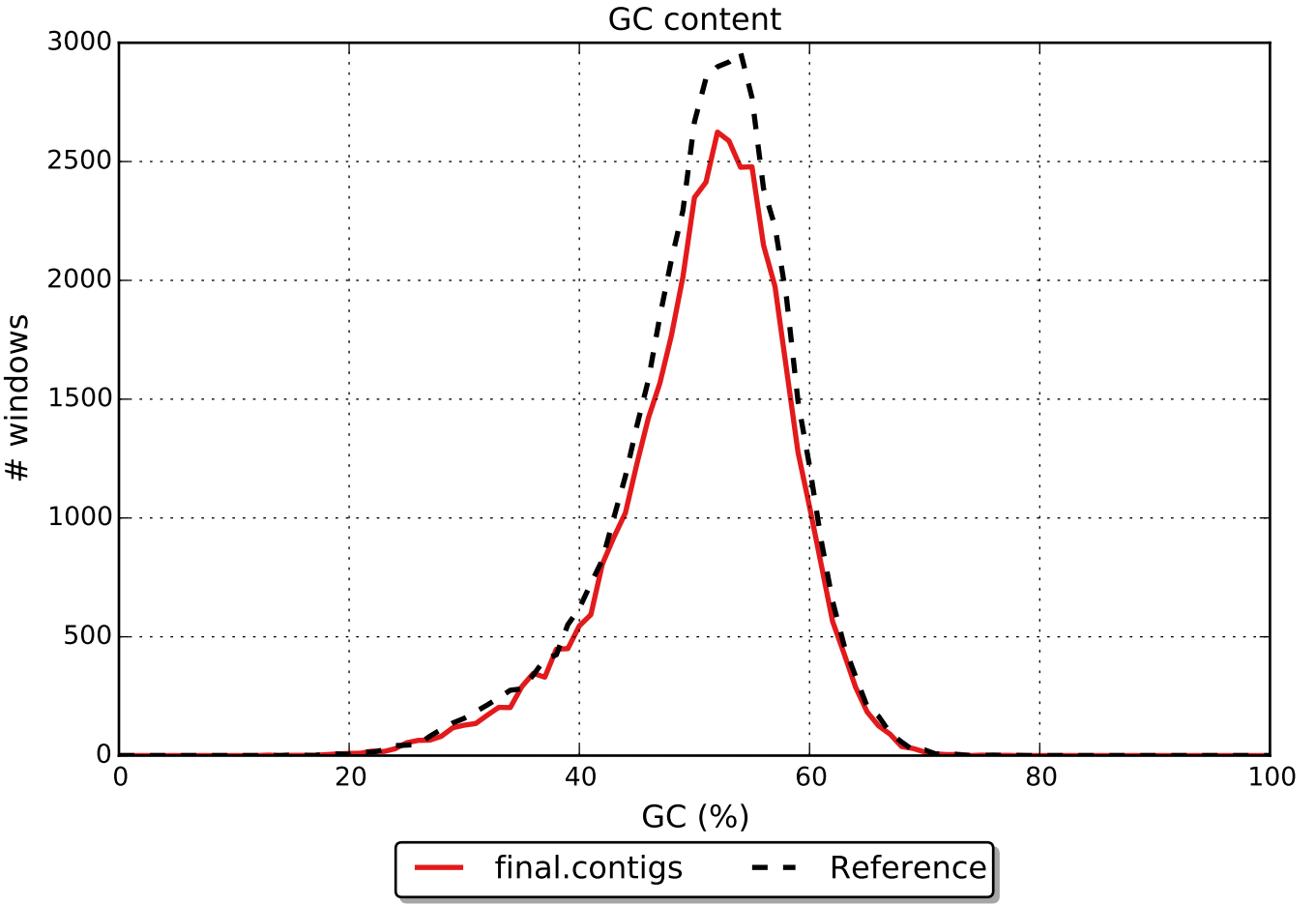
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
# with misassembly	0
# both parts are significant	0
Partially unaligned length	77
# N's	0

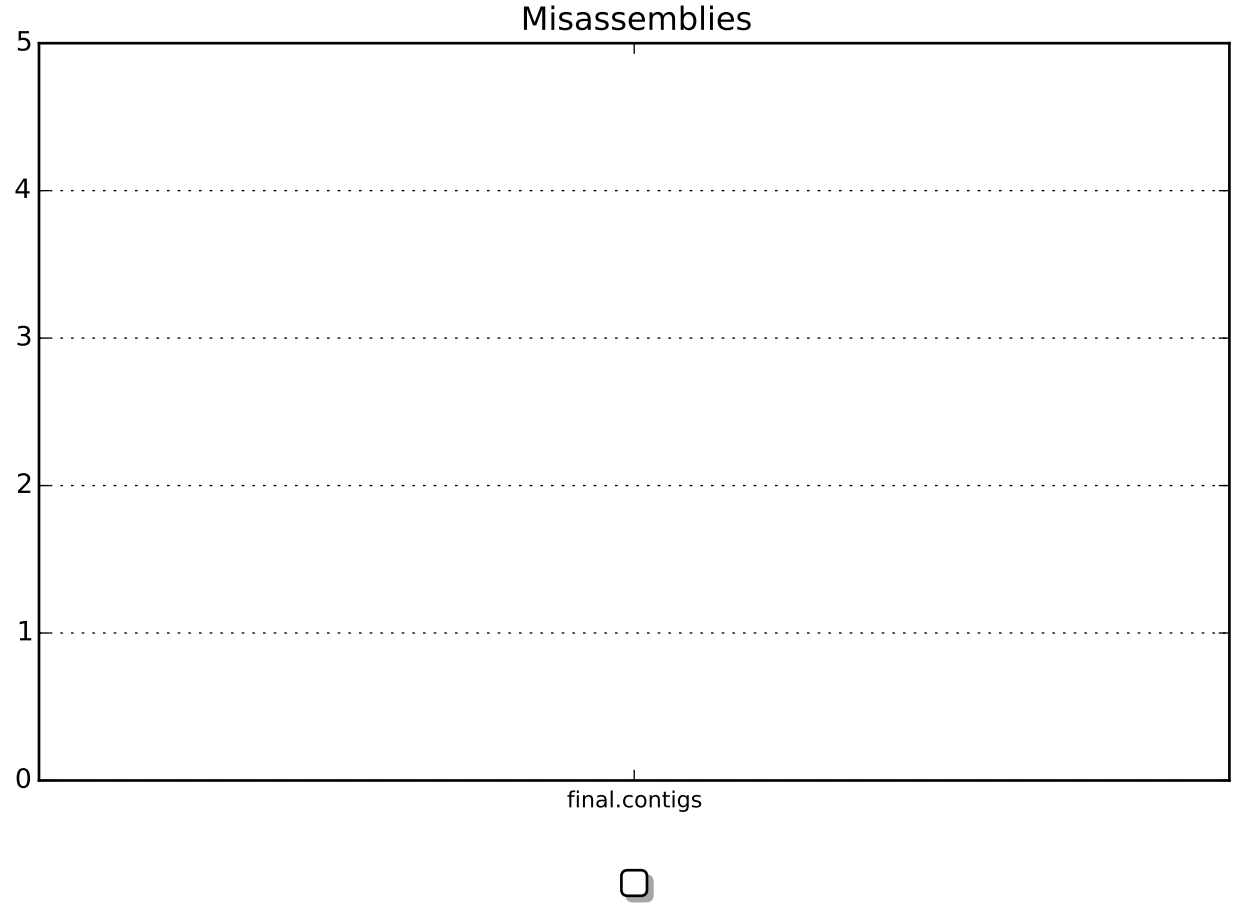
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

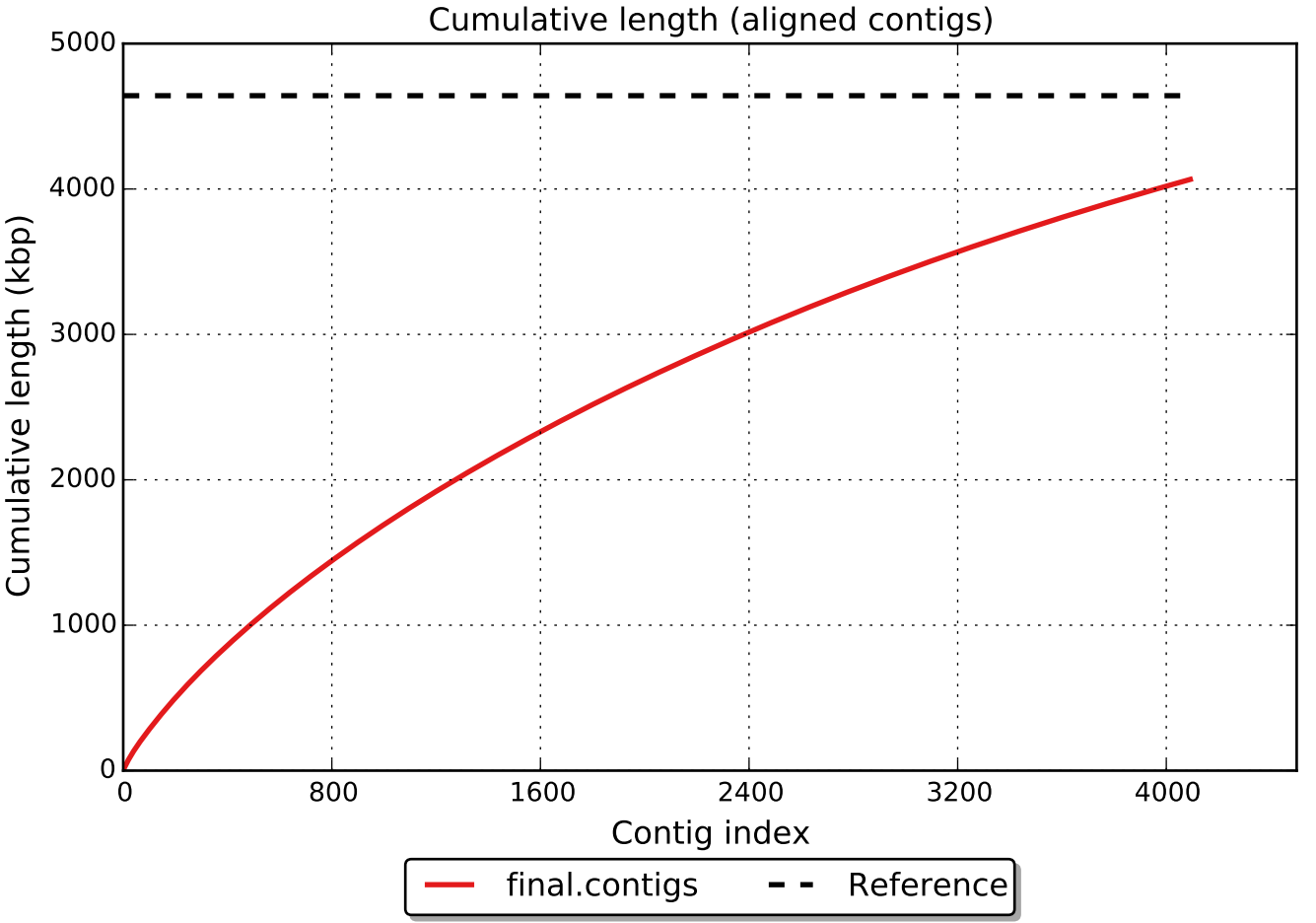

Nx
Contig length (kbp)
0
1
2
3
4
5
6
0
20
40
60
80
100
x
final.contigs

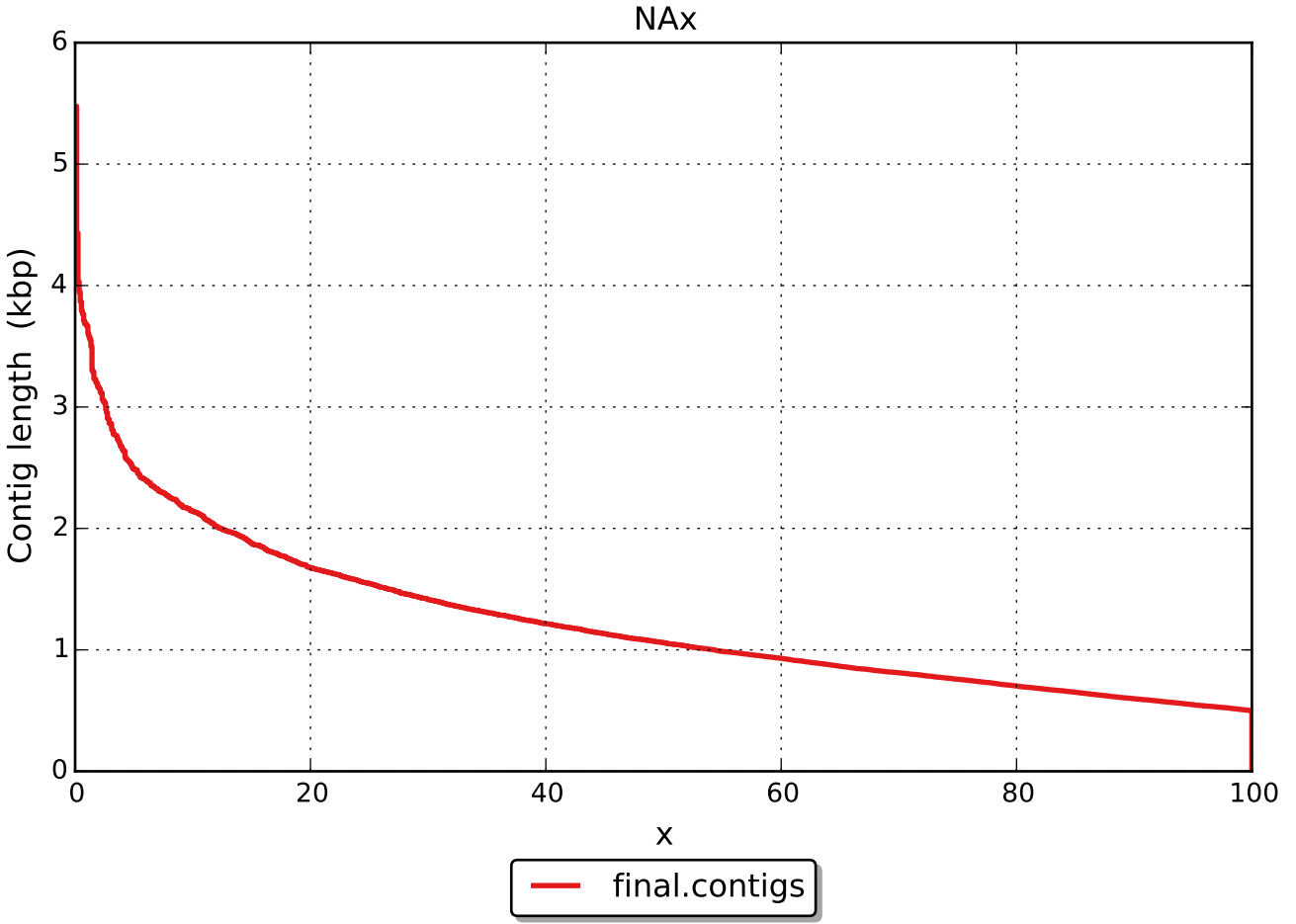

NGx
Contig length (kbp)
0
1
2
3
4
5
6
0
20
40
60
80
100
x
final.contigs

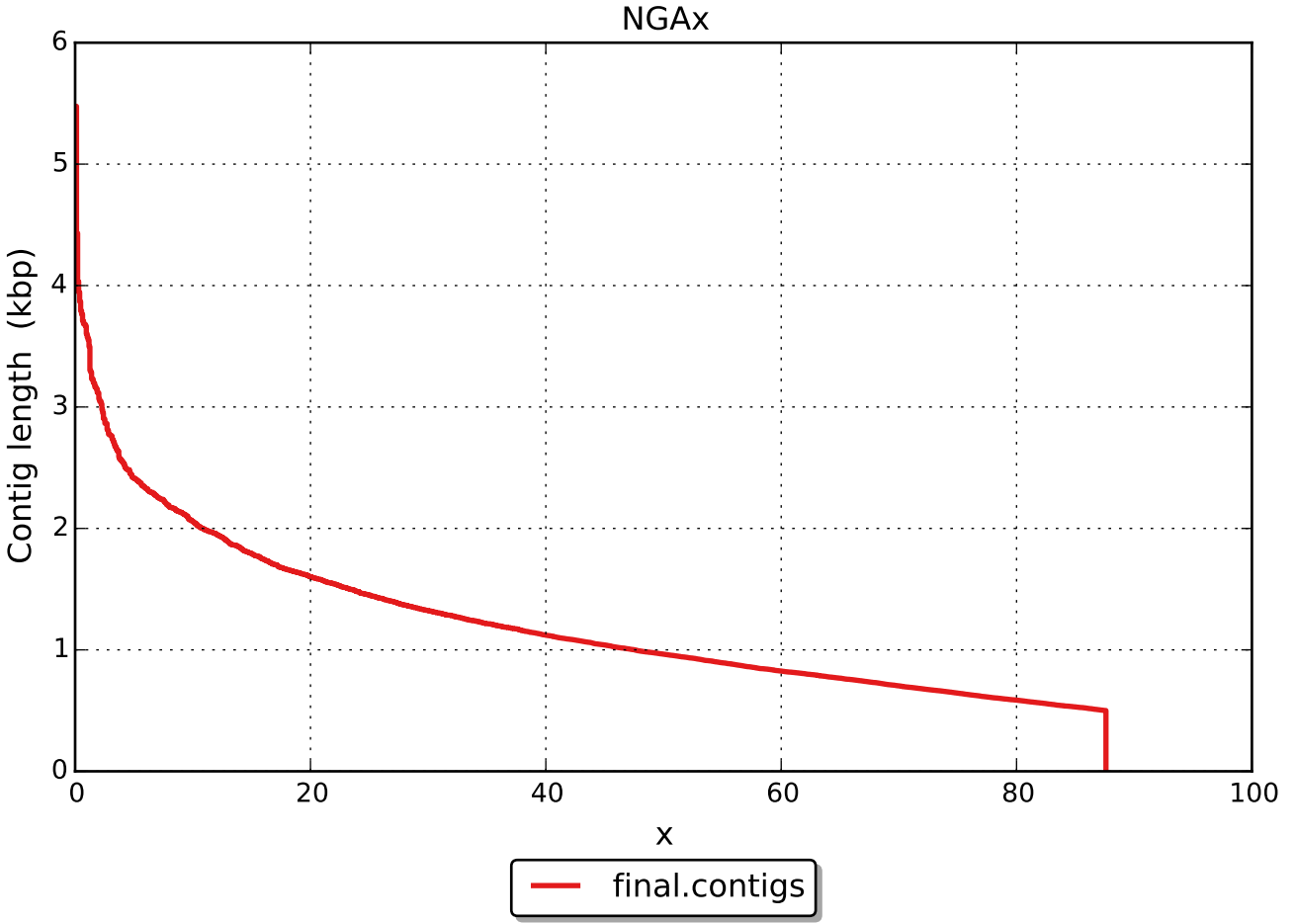

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
800
1600
2400
3200
4000
Contig index
final.contigs
Reference


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)
0
1
2
3
4
5
6
0
20
40
60
80
100
x
final.contigs


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