Report

	final.contigs
# contigs (>= 1000 bp)	1948
# contigs (>= 5000 bp)	45
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	4050014
Total length (>= 5000 bp)	266818
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3064
Largest contig	8333
Total length	4870718
Reference length	4857432
GC (%)	52.22
Reference GC (%)	52.23
N50	1960
NG50	1962
N75	1222
NG75	1225
L50	807
LG50	804
L75	1589
LG75	1581
# misassemblies	2
# misassembled contigs	2
Misassembled contigs length	1545
# local misassemblies	0
# unaligned contigs	0 + 3 part
Unaligned length	377
Genome fraction (%)	95.743
Duplication ratio	1.047
# N's per 100 kbp	0.00
# mismatches per 100 kbp	60.85
# indels per 100 kbp	0.04
Largest alignment	8333
NA50	1960
NGA50	1962
NA75	1221
NGA75	1225
LA50	807
LGA50	804
LA75	1590
LGA75	1581

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

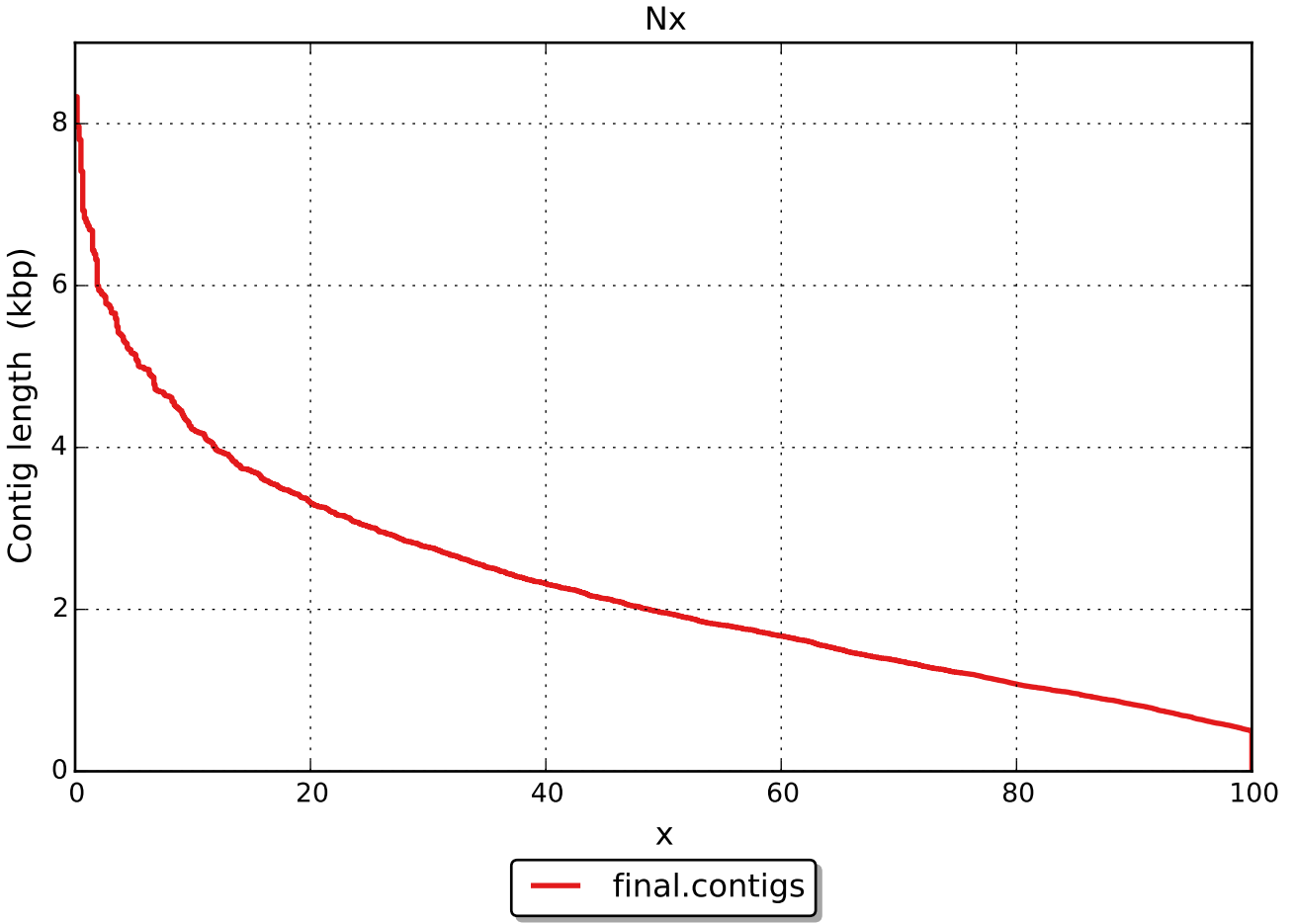
	final.contigs
# misassemblies	2
# relocations	0
# translocations	0
# inversions	2
# possibly misassembled contigs	0
# misassembled contigs	2
Misassembled contigs length	1545
# local misassemblies	0
# mismatches	2830
# indels	2
# short indels	2
# long indels	0
Indels length	2

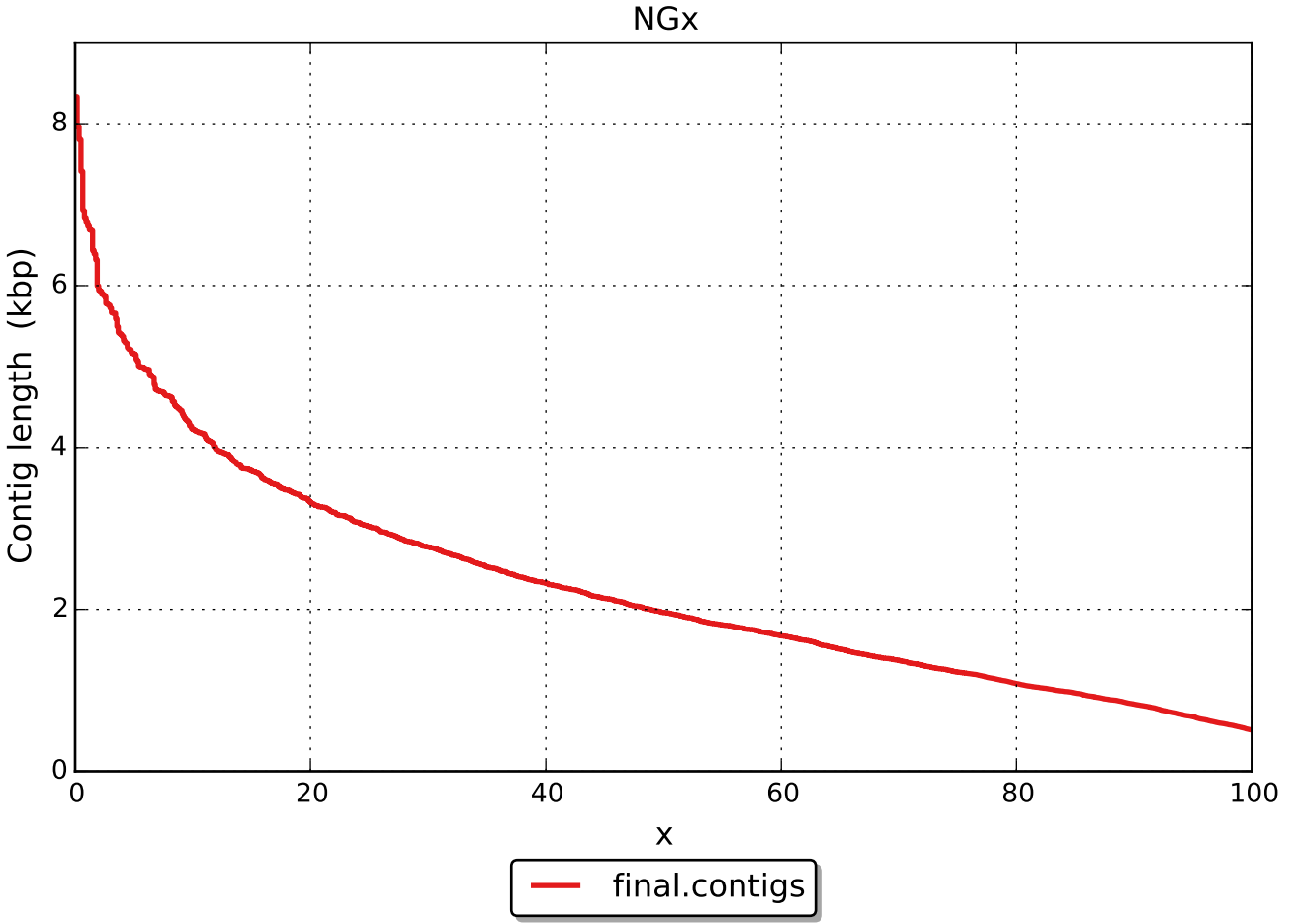
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

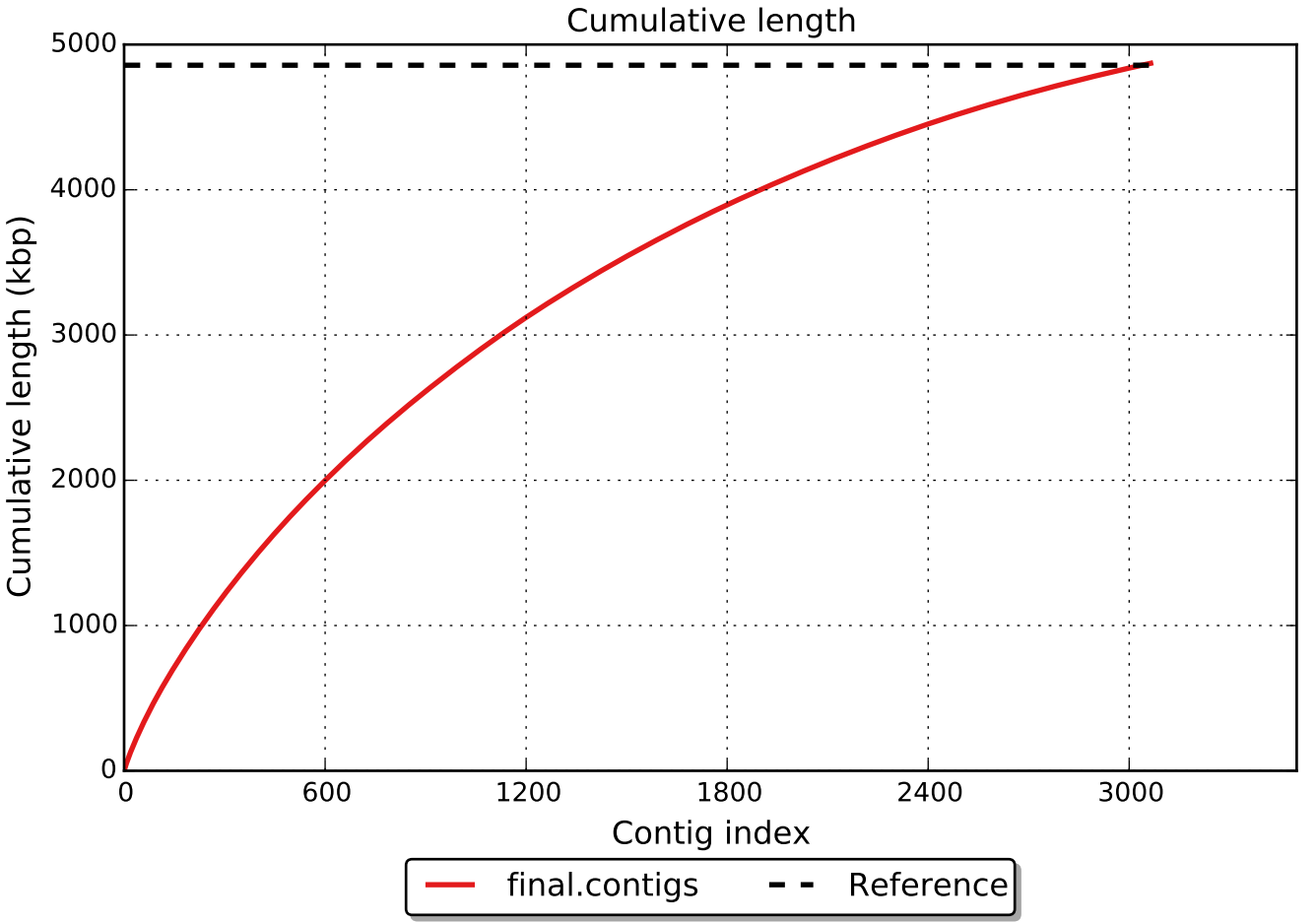
Unaligned report

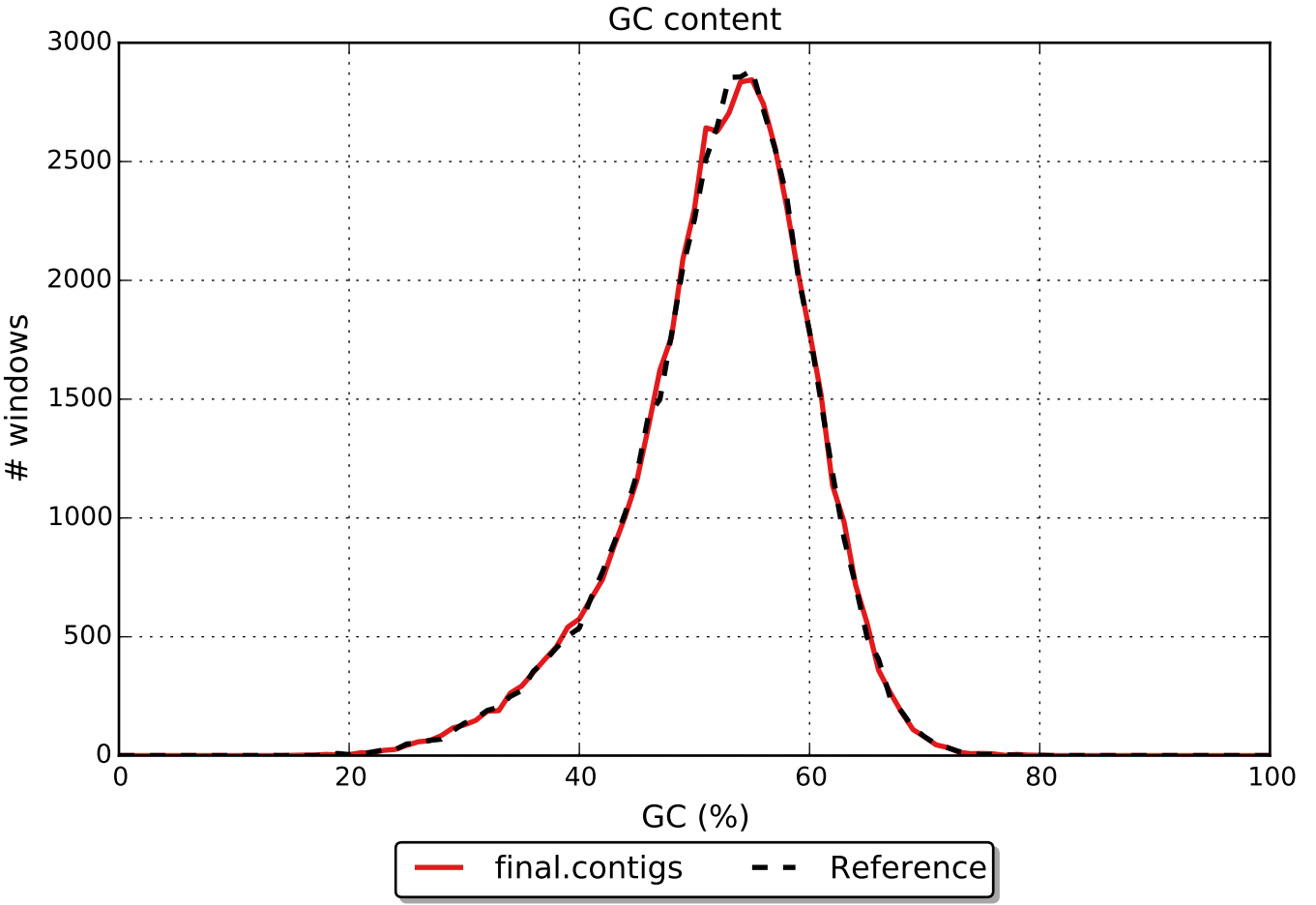
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
# with misassembly	0
# both parts are significant	0
Partially unaligned length	377
# N's	0

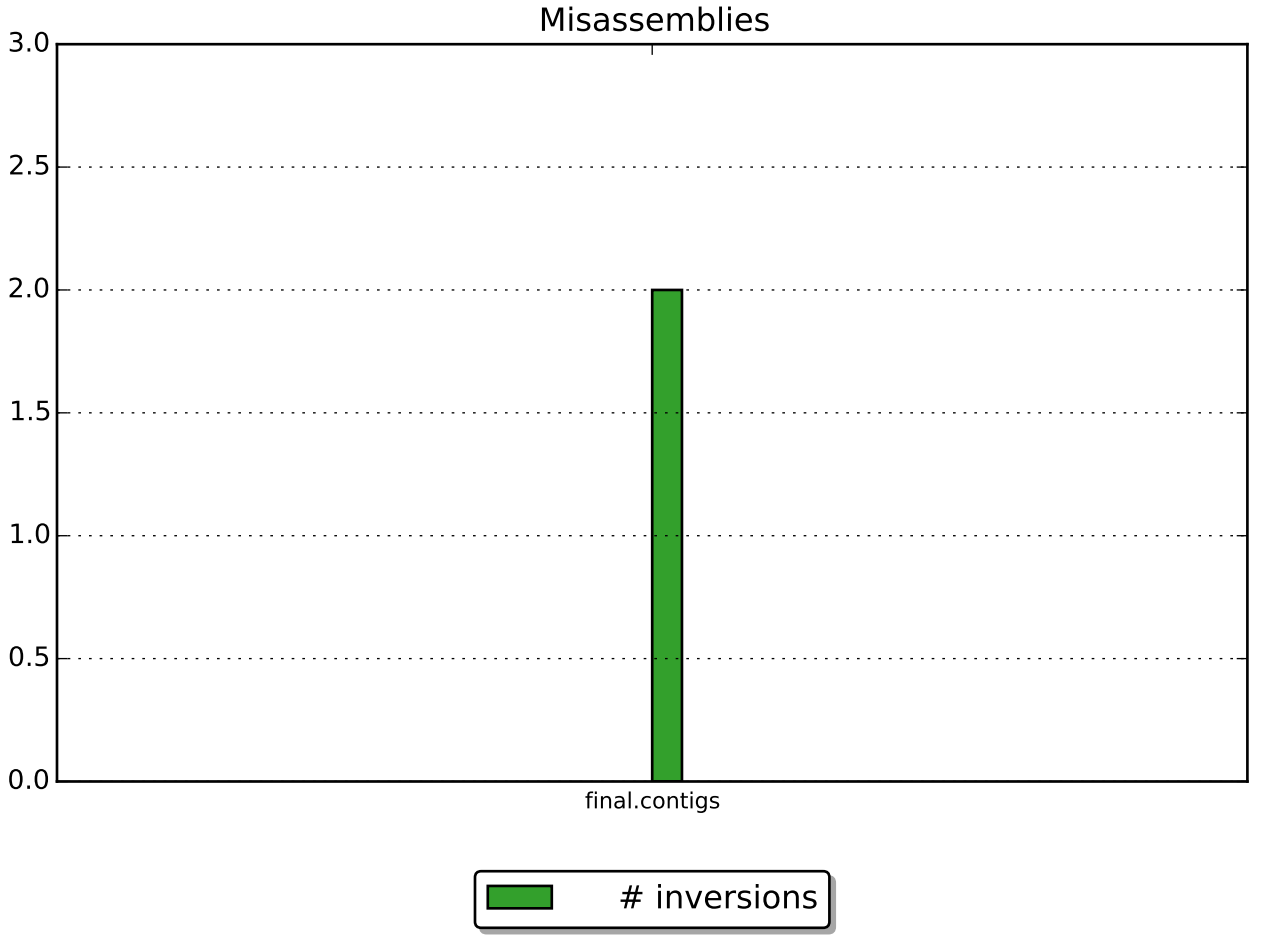
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

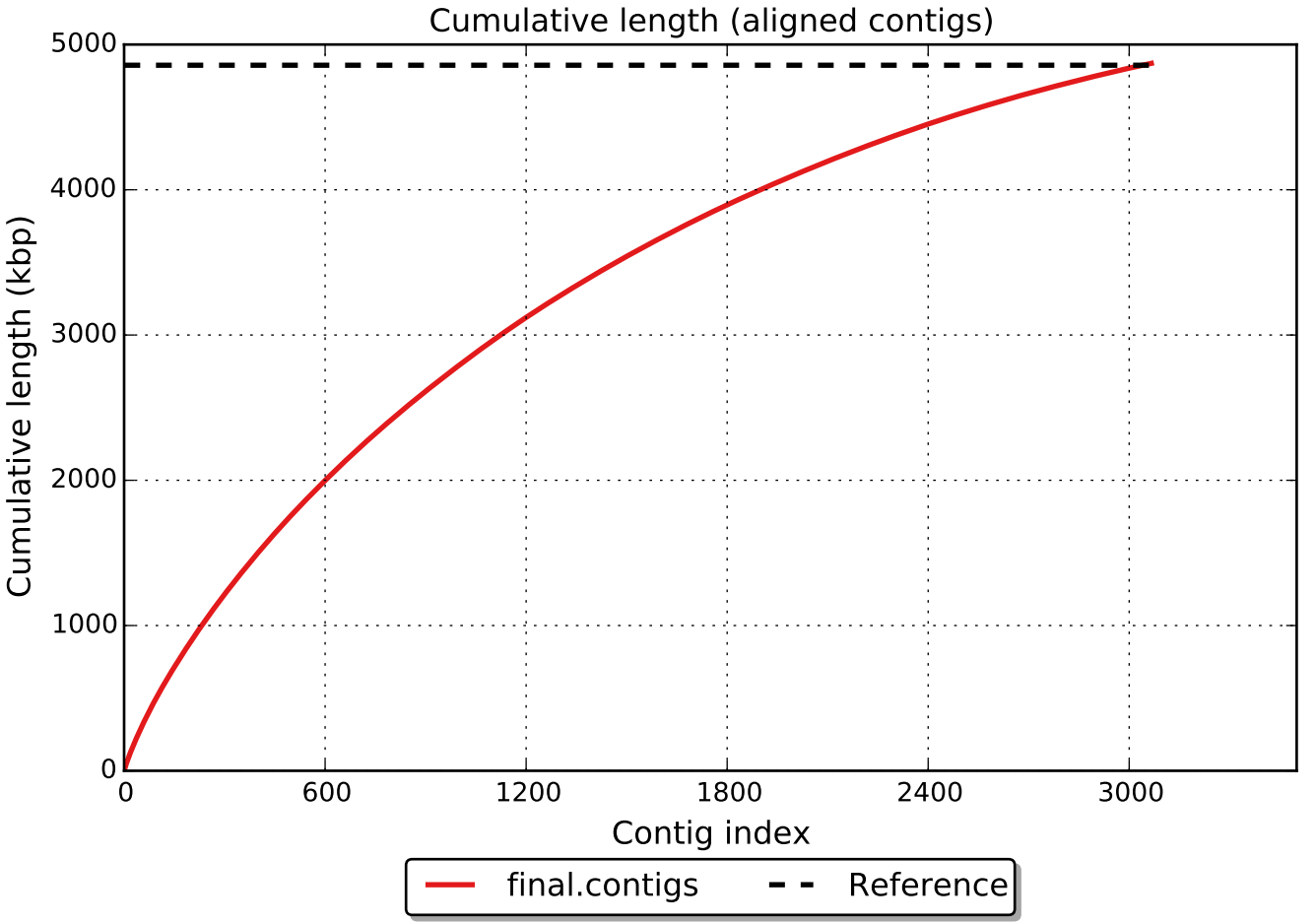

Nx
Contig length (kbp)
0
2
4
6
8
0
20
40
60
80
100
x
final.contigs

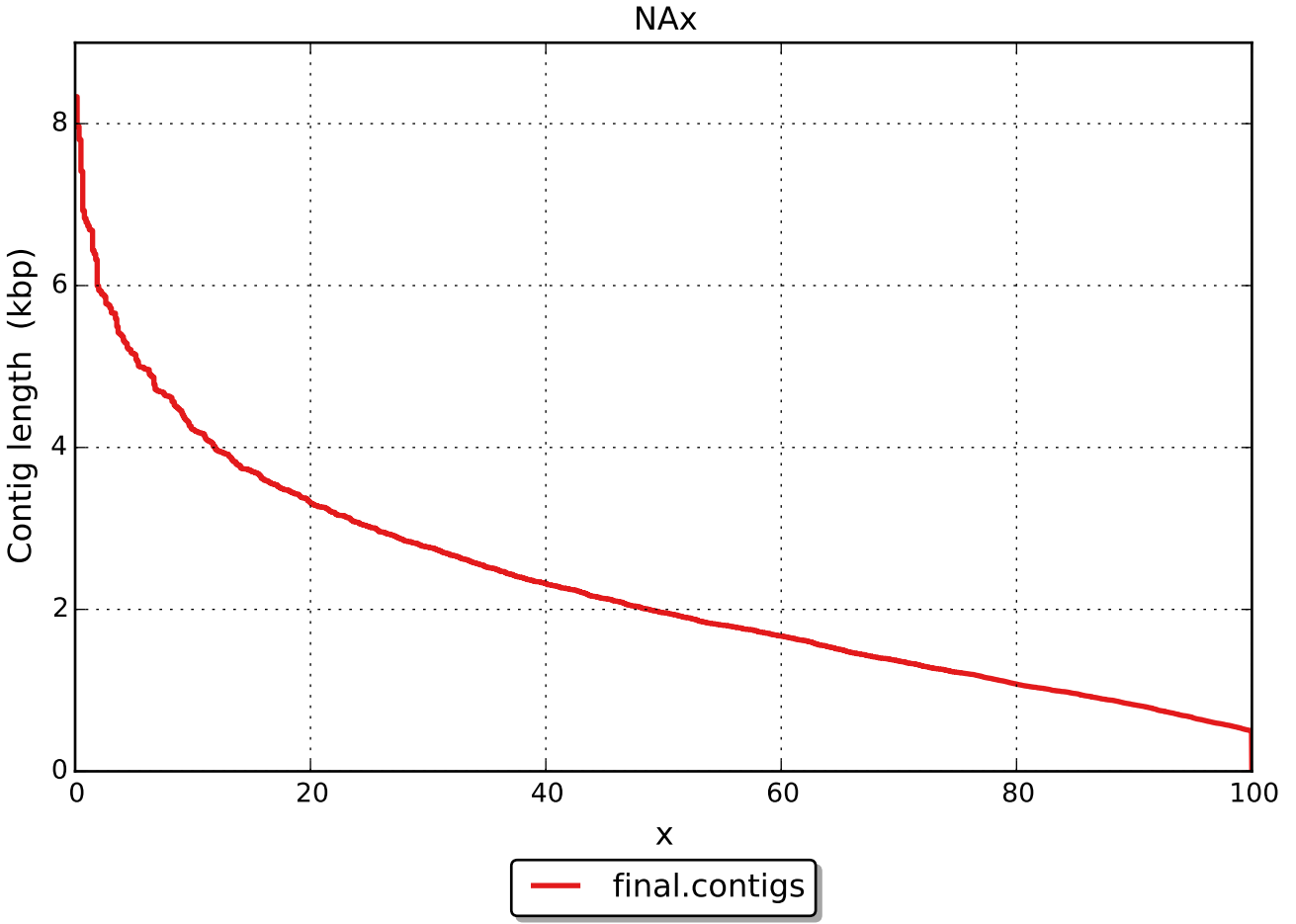

NGx
Contig length (kbp)
0
2
4
6
8
0
20
40
60
80
100
x
final.contigs

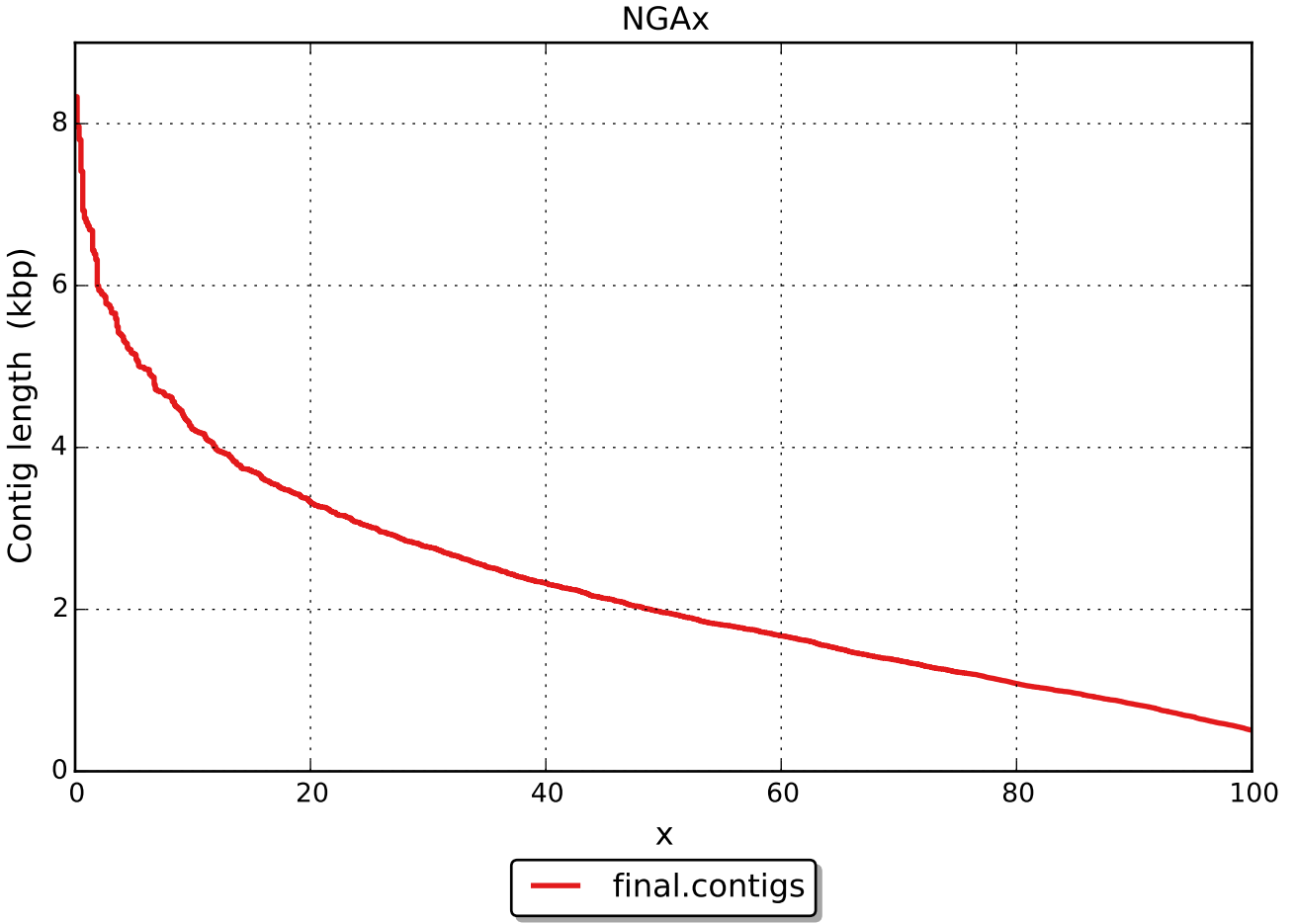

Cumulative length
Cumulative length (kbp)
5000
4000
3000
2000
1000
0
0
600
1200
1800
2400
3000
Contig index
final.contigs
Reference


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


Misassemblies
3.0
2.5
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
600
1200
1800
2400
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