Report

	final.contigs
# contigs (>= 0 bp)	3045
# contigs (>= 1000 bp)	1269
Total length (>= 0 bp)	3249332
Total length (>= 1000 bp)	1974481
# contigs	3045
Largest contig	5155
Total length	3249332
Reference length	1892775
GC (%)	32.28
Reference GC (%)	32.26
N50	1173
NG50	1568
N75	816
NG75	1275
L50	948
LG50	444
L75	1780
LG75	781
# misassemblies	57
# misassembled contigs	55
Misassembled contigs length	85490
# local misassemblies	0
# unaligned contigs	1 + 3 part
Unaligned length	1890
Genome fraction (%)	90.601
Duplication ratio	1.894
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1419.12
# indels per 100 kbp	0.47
Largest alignment	5155
NA50	1157
NGA50	1523
NA75	808
NGA75	1259
LA50	965
LGA50	453
LA75	1806
LGA75	796

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

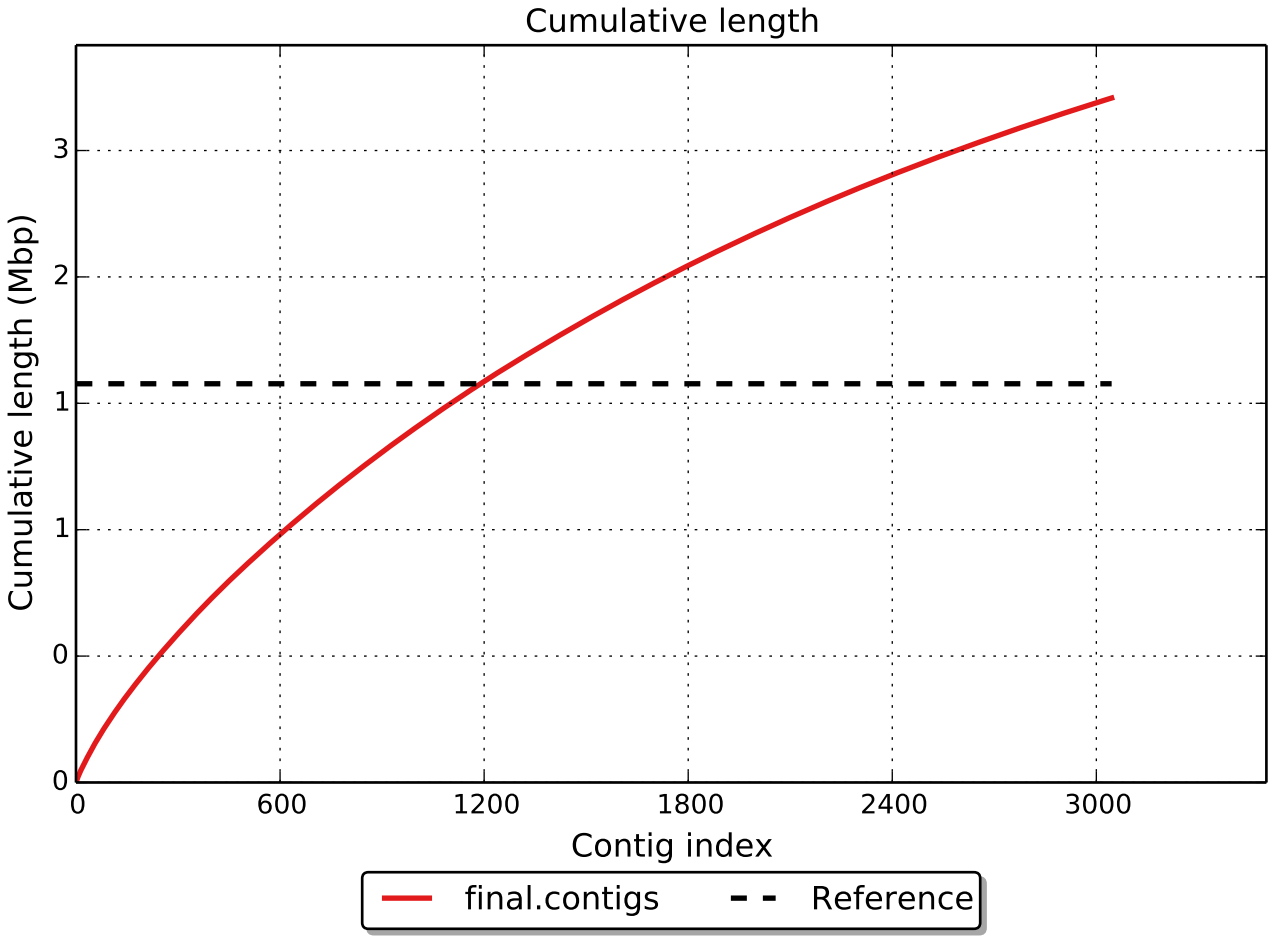
	final.contigs
# misassemblies	57
# relocations	57
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	55
Misassembled contigs length	85490
# local misassemblies	0
# mismatches	24336
# indels	8
# short indels	8
# long indels	0
Indels length	8

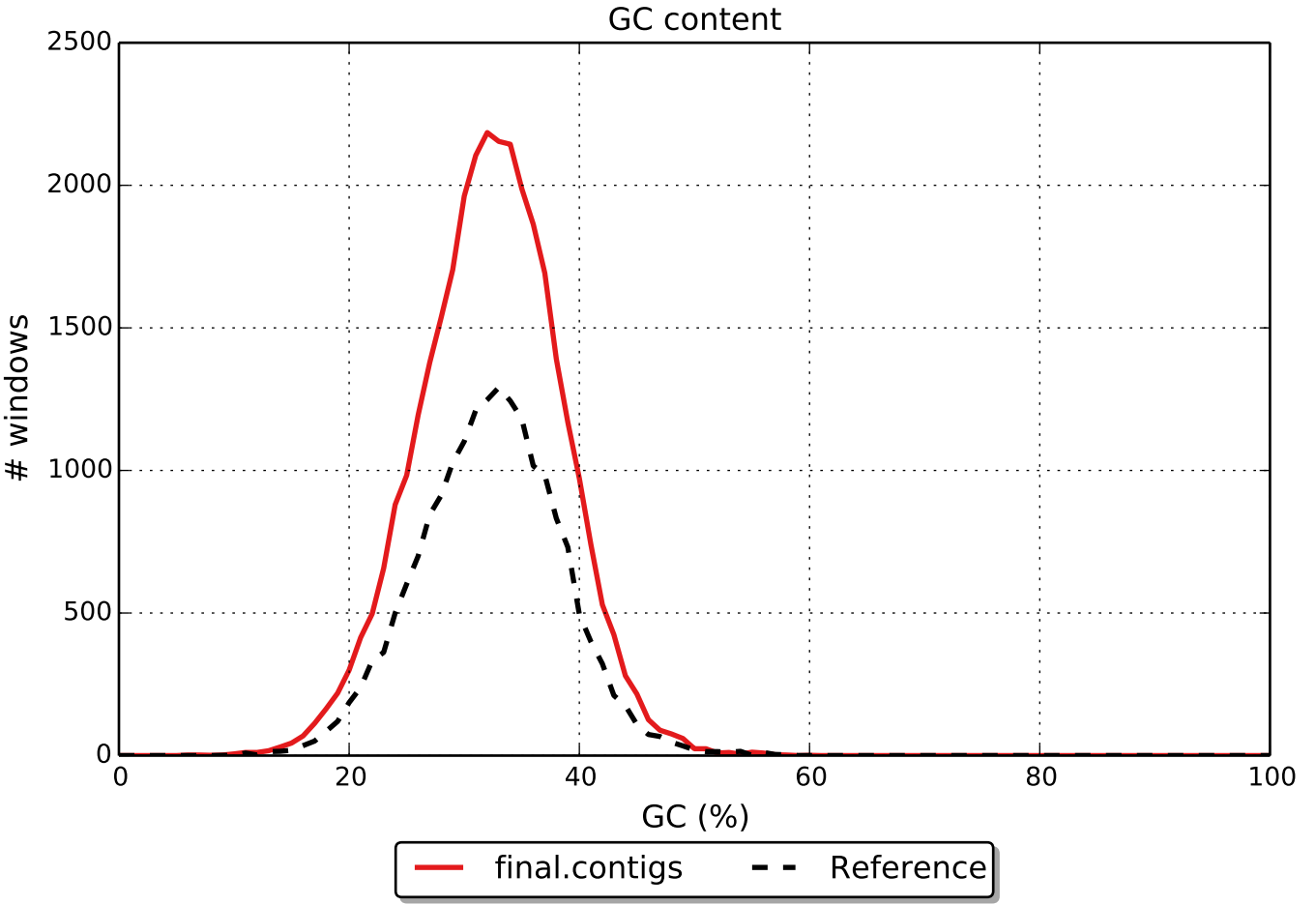
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

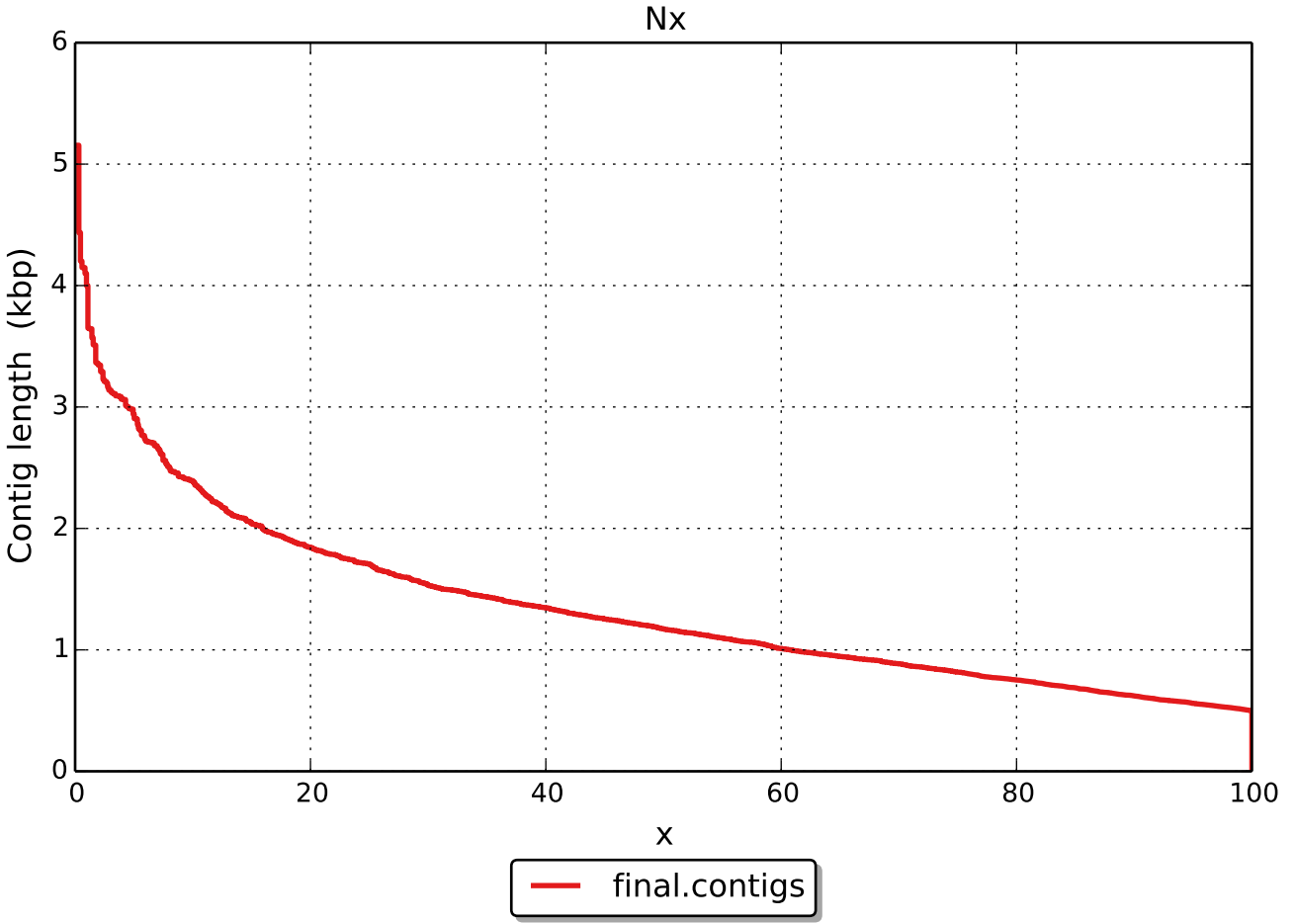
Unaligned report

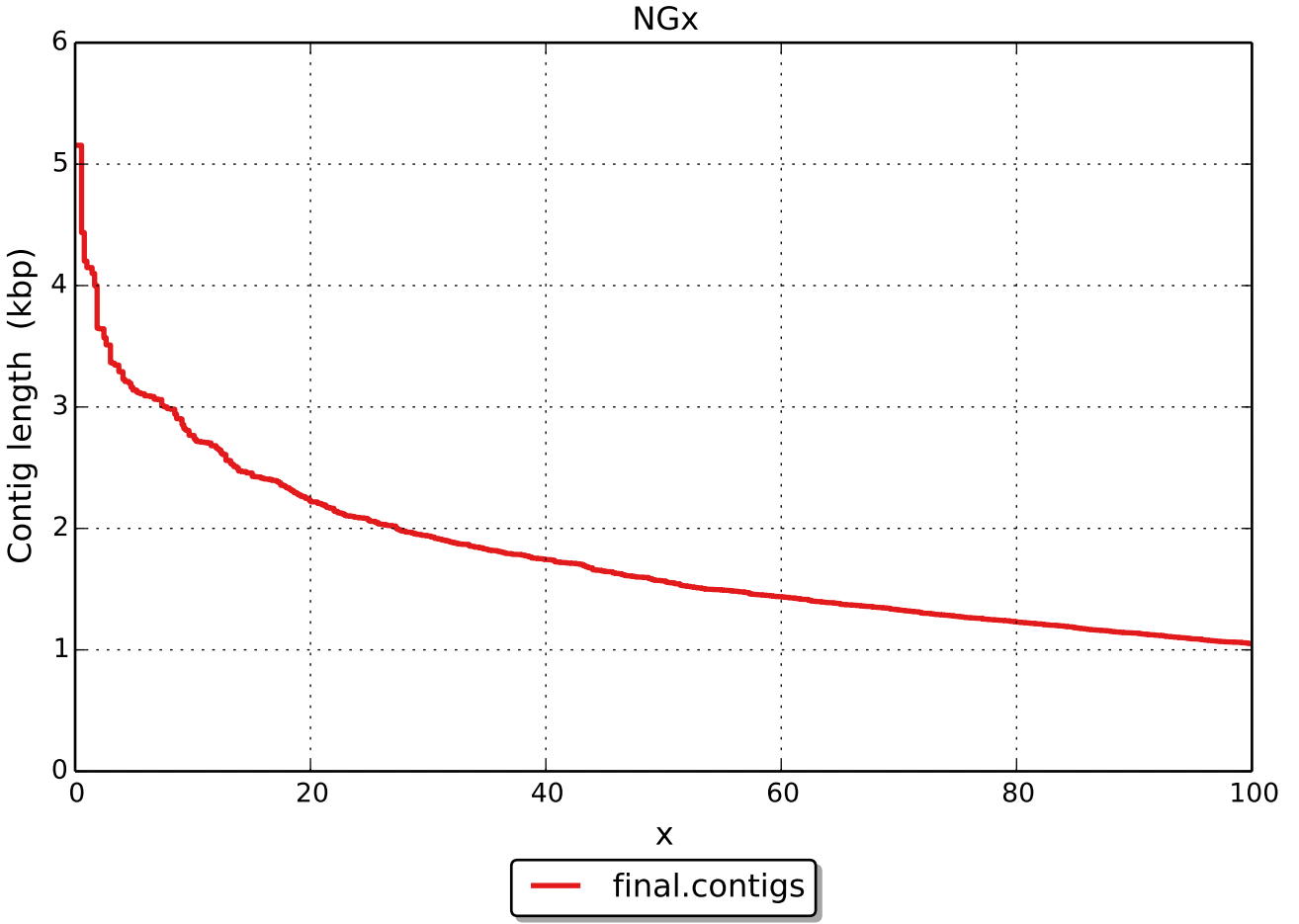
	final.contigs
# fully unaligned contigs	1
Fully unaligned length	924
# partially unaligned contigs	3
# with misassembly	0
# both parts are significant	0
Partially unaligned length	966
# N's	0

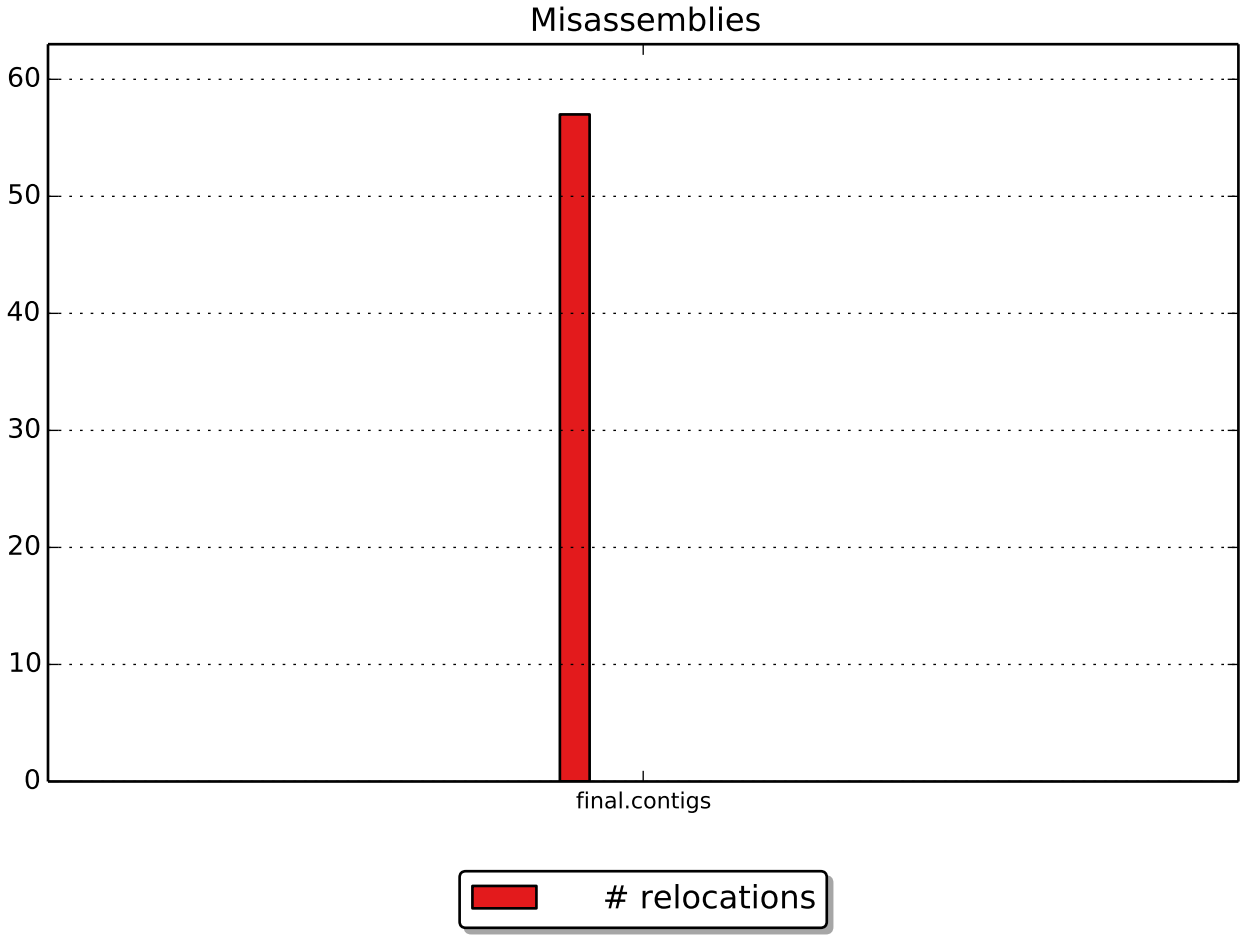
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

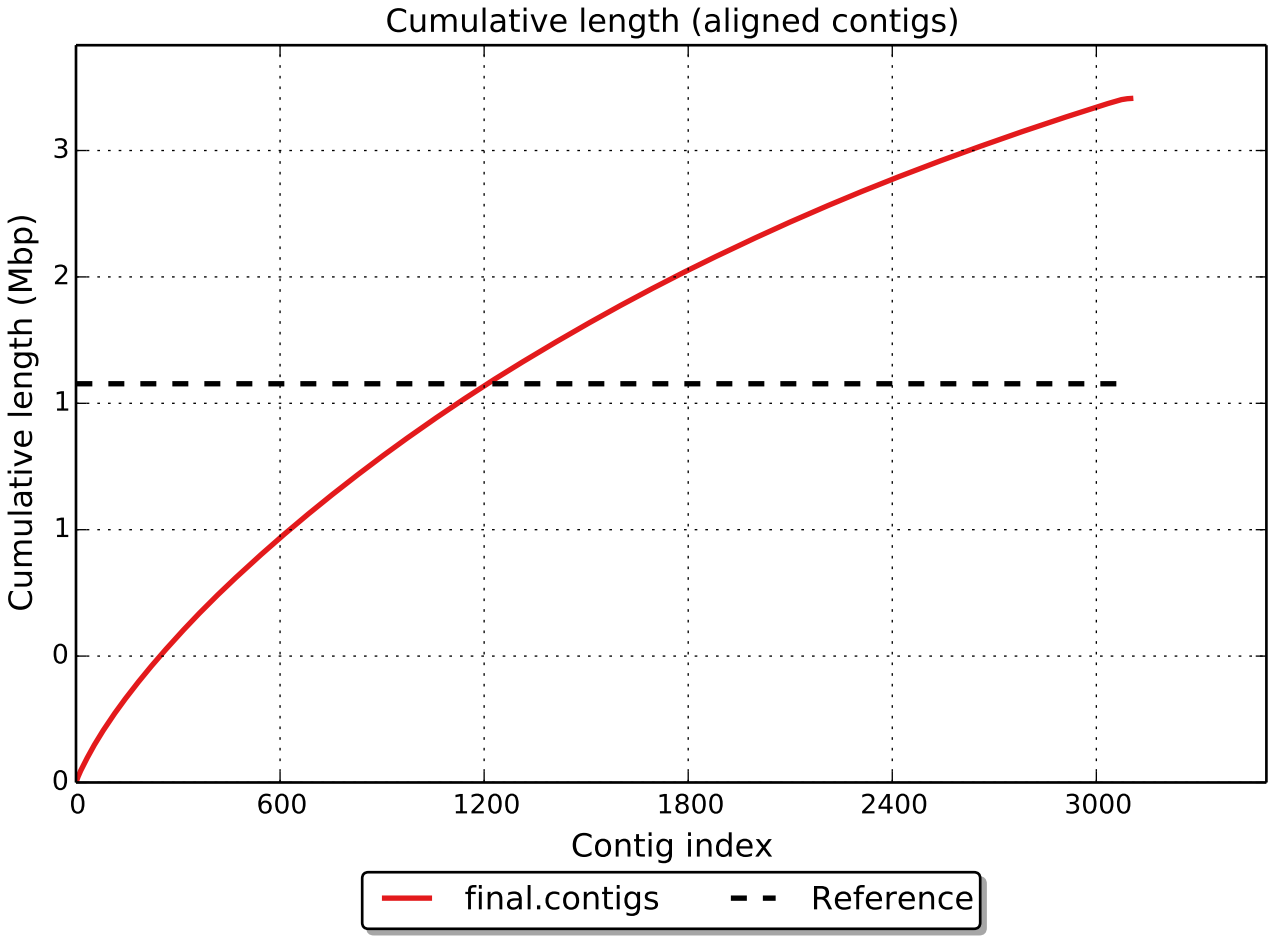

Cumulative length
Cumulative length (Mbp)
3
2
1
1
0
0
0
600
1200
1800
2400
3000
Contig index
final.contigs
Reference

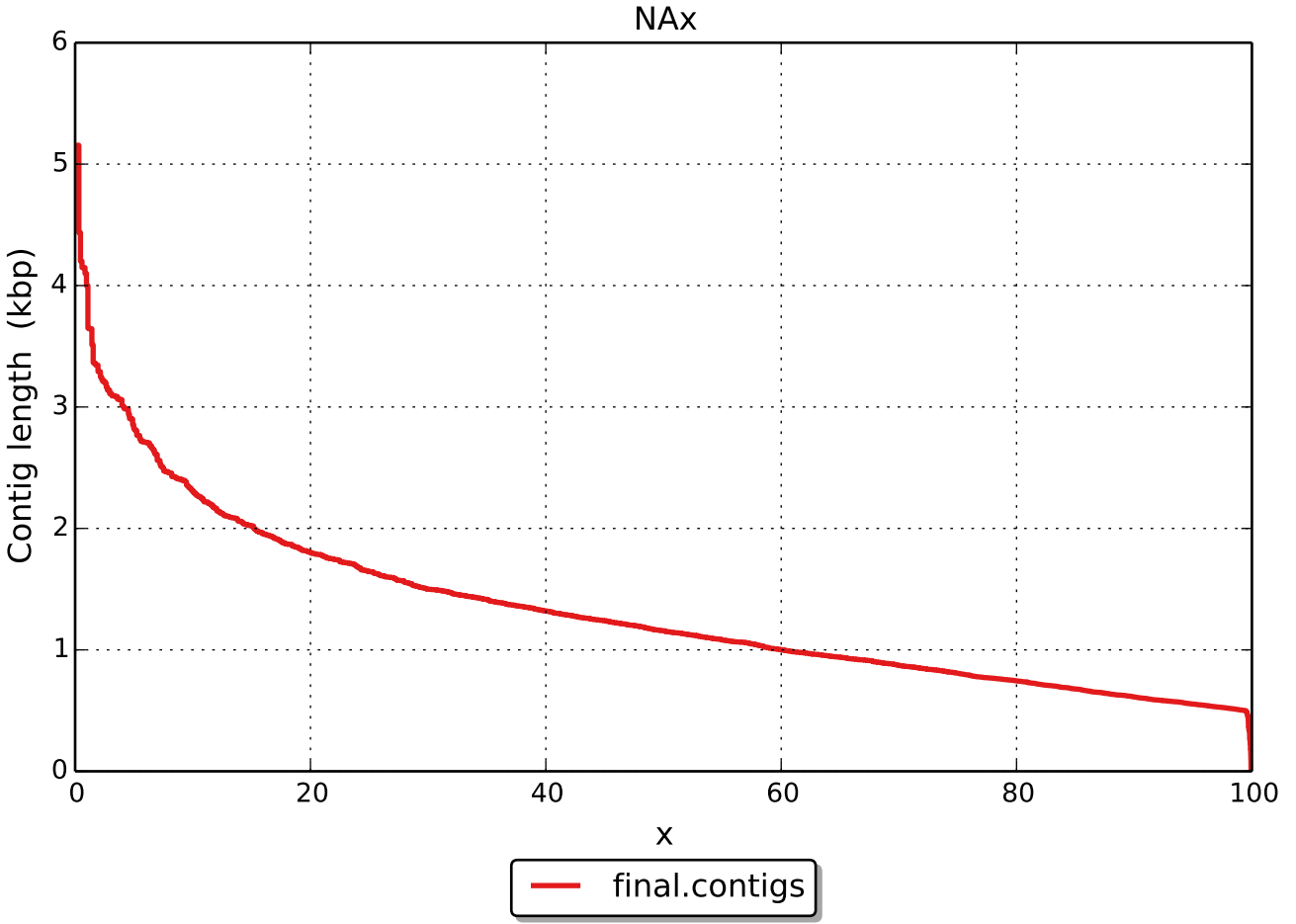

GC content
2500
2000
1500
1000
500
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

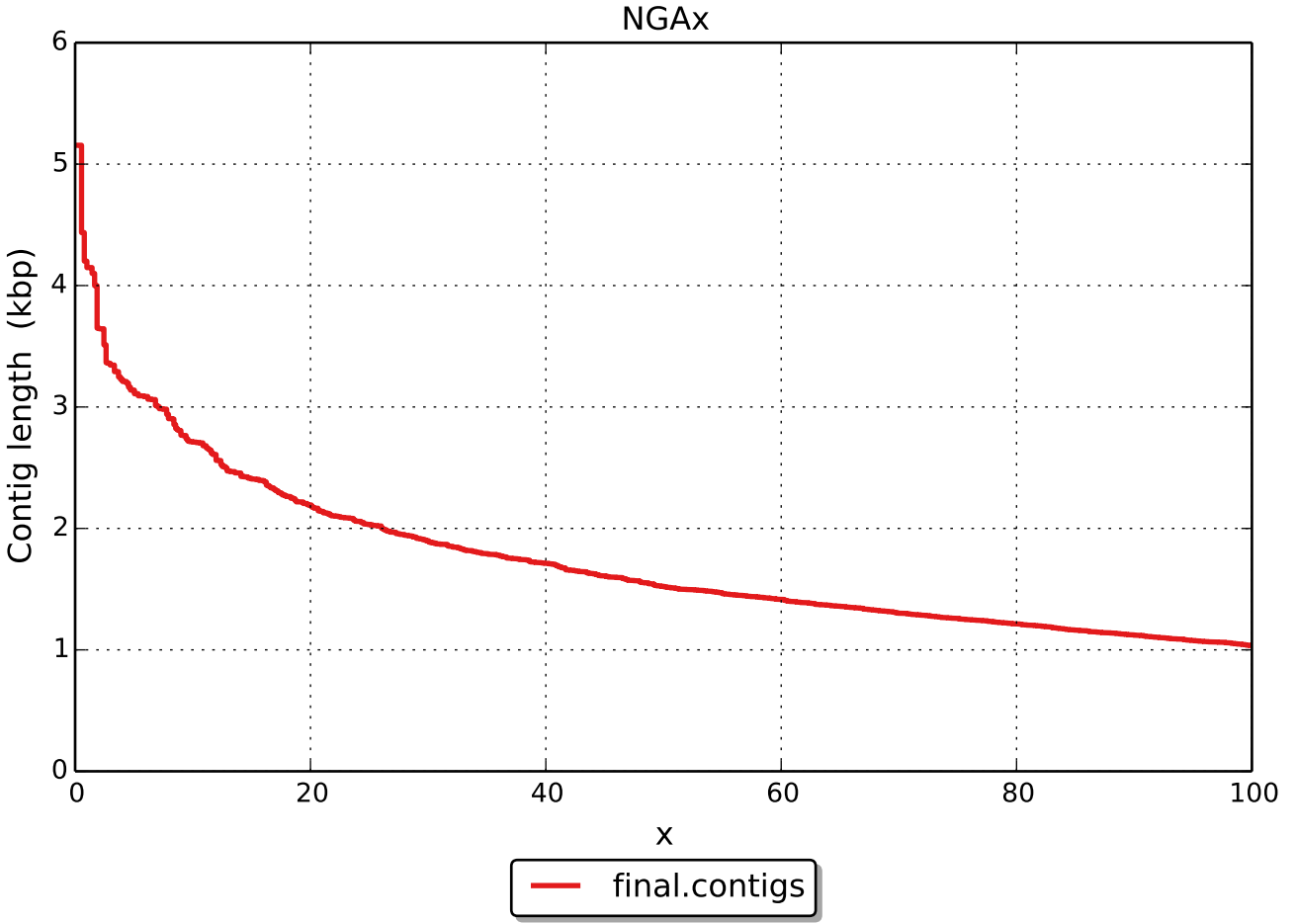

Nx
Contig length (kbp)
0
1
2
3
4
5
6
0
20
40
60
80
100
x
final.contigs


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


Misassemblies
60
50
40
30
20
10
0
final.contigs
relocations


Cumulative length (aligned contigs)
Cumulative length (Mbp)
3
2
1
1
0
0
0
600
1200
1800
2400
3000
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)
x
0
1
2
3
4
5
6
0
20
40
60
80
100
final.contigs