Report

	final.contigs
# contigs (>= 0 bp)	2674
# contigs (>= 1000 bp)	1849
Total length (>= 0 bp)	5173234
Total length (>= 1000 bp)	4569487
# contigs	2674
Largest contig	12599
Total length	5173234
Reference length	5547323
GC (%)	50.28
Reference GC (%)	50.48
N50	2541
NG50	2373
N75	1521
NG75	1303
L50	637
LG50	713
L75	1293
LG75	1492
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	1135
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	89.817
Duplication ratio	1.038
# N's per 100 kbp	0.00
# mismatches per 100 kbp	38.09
# indels per 100 kbp	0.20
Largest alignment	12599
NA50	2541
NGA50	2373
NA75	1521
NGA75	1303
LA50	637
LGA50	713
LA75	1293
LGA75	1492

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

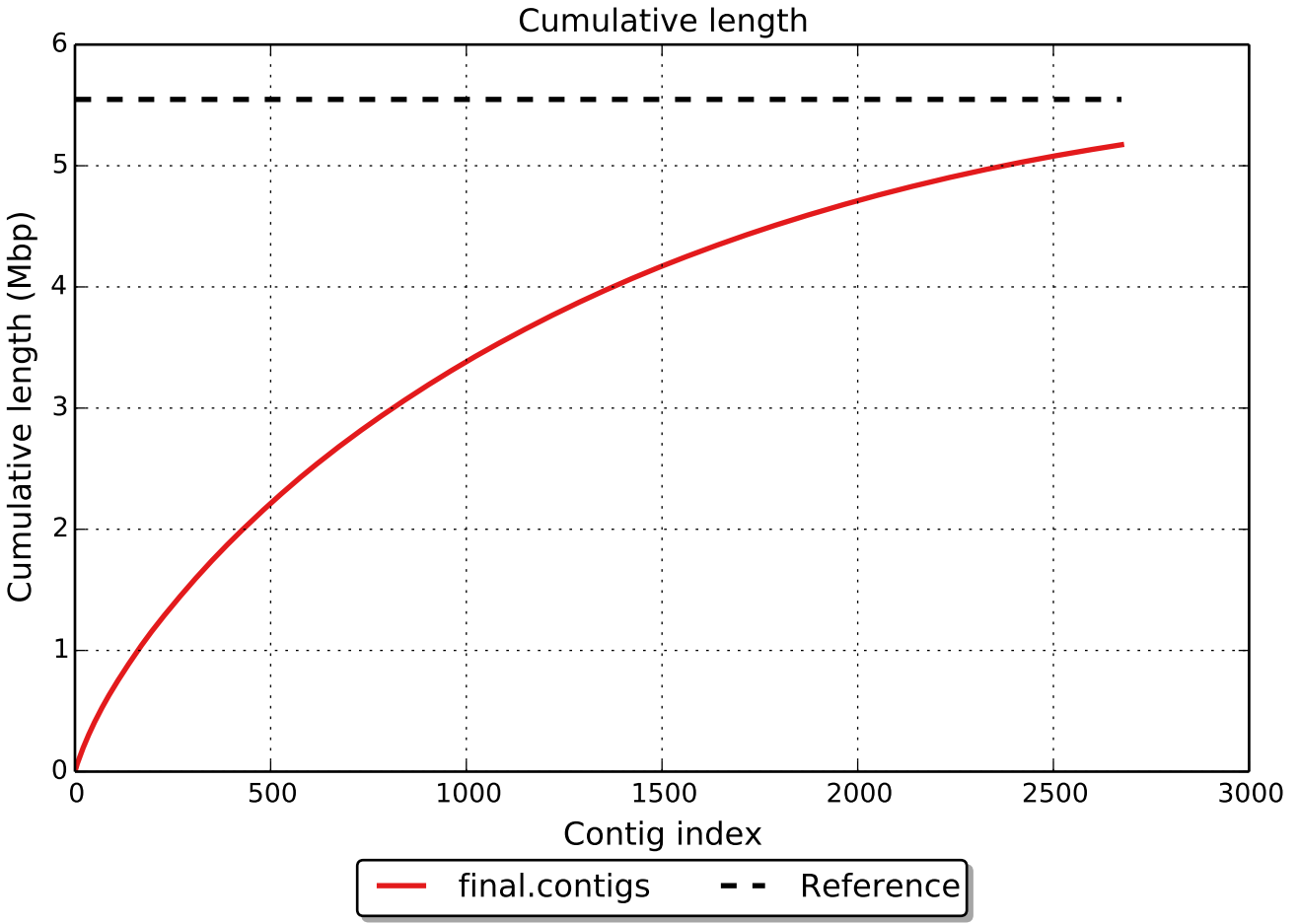
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	1135
# local misassemblies	0
# mismatches	1898
# indels	10
# short indels	8
# long indels	2
Indels length	35

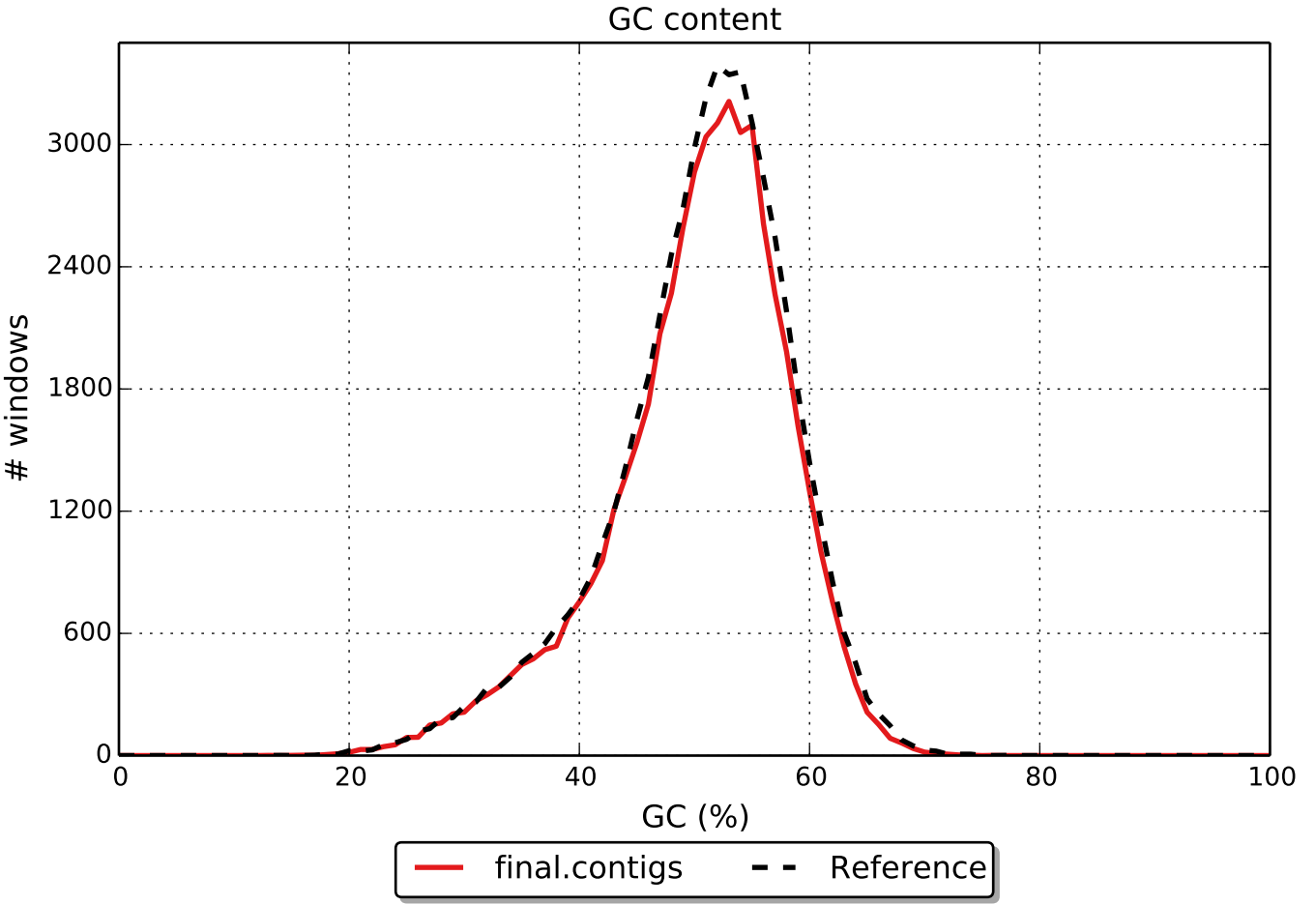
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

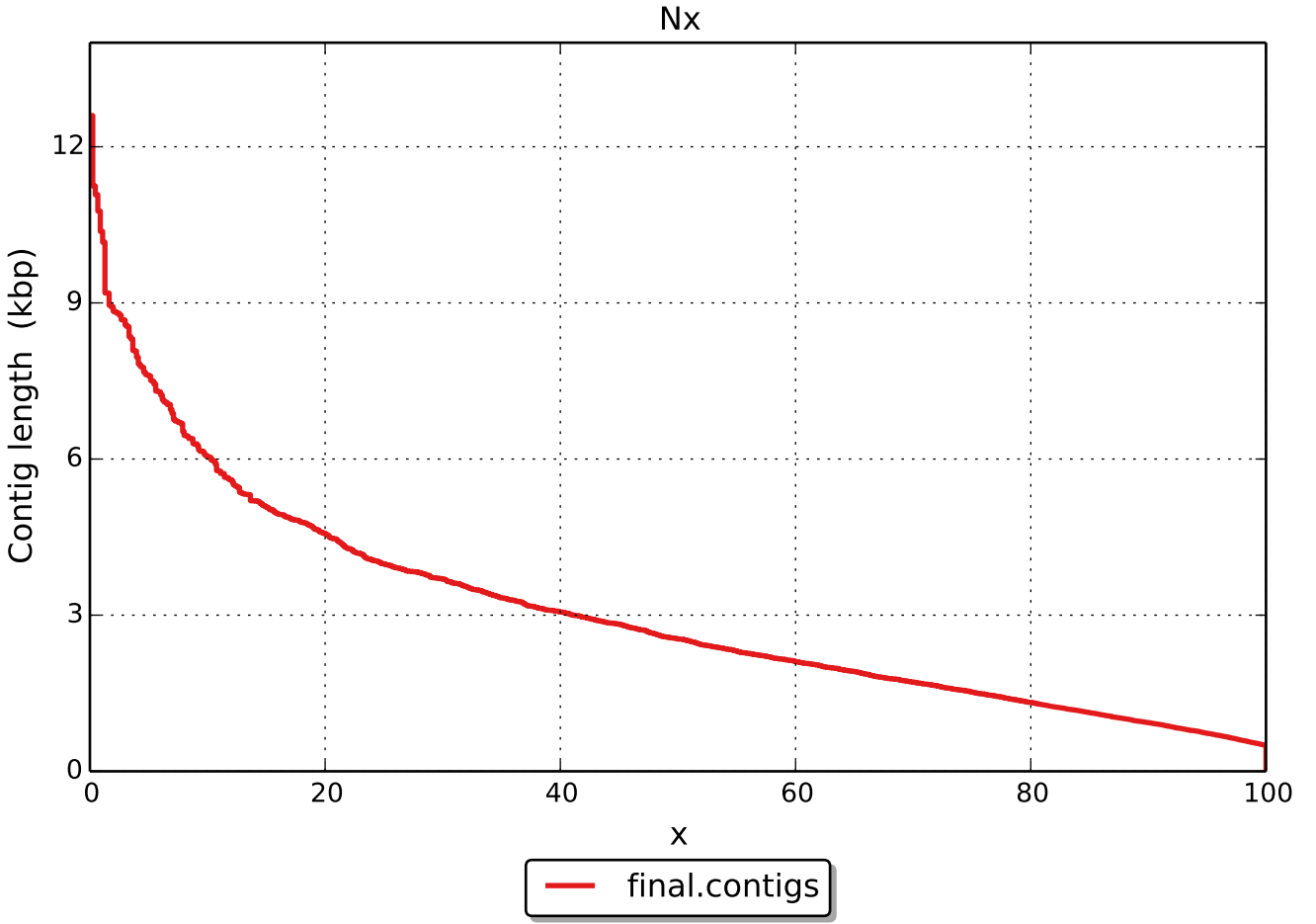
Unaligned report

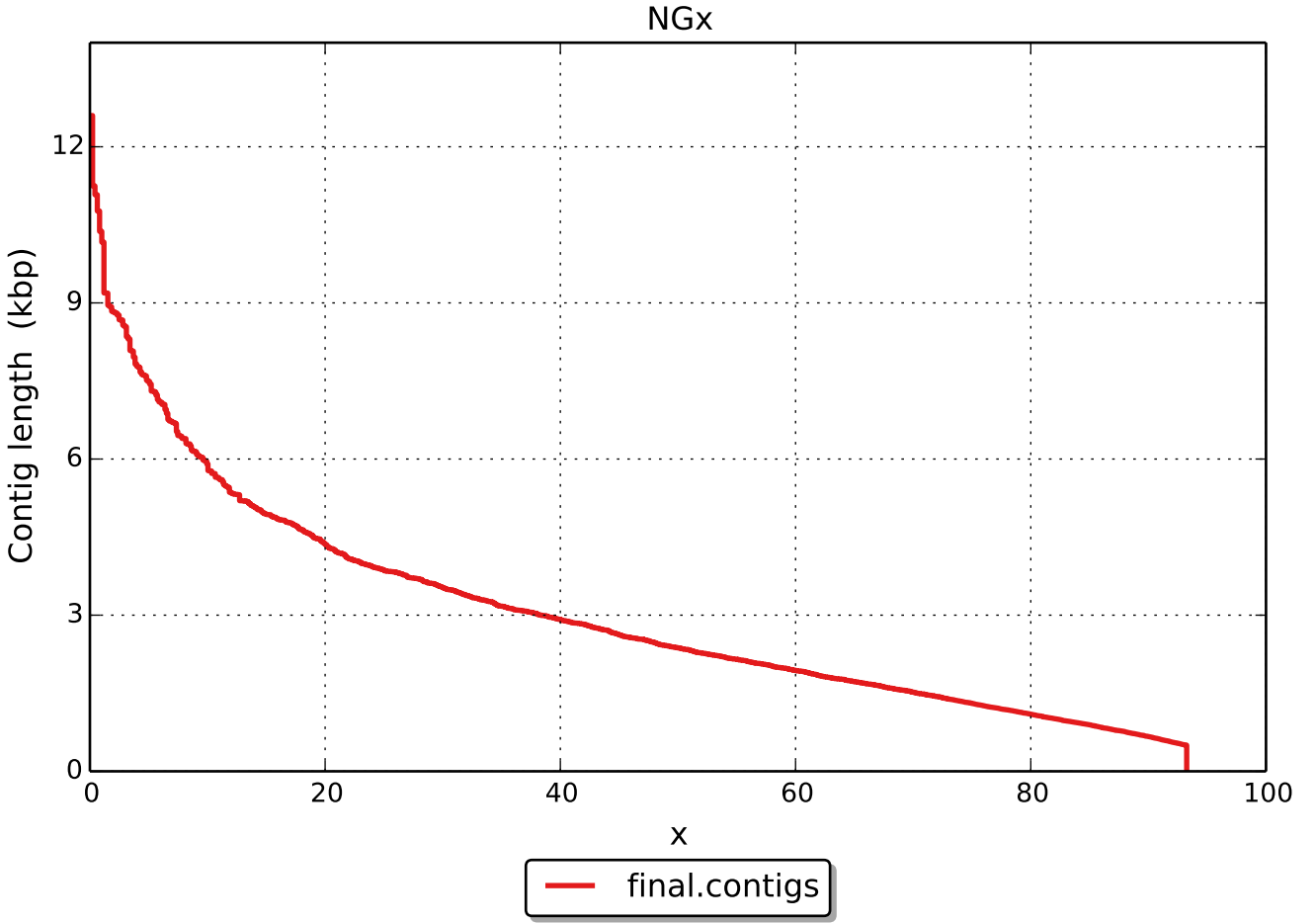
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

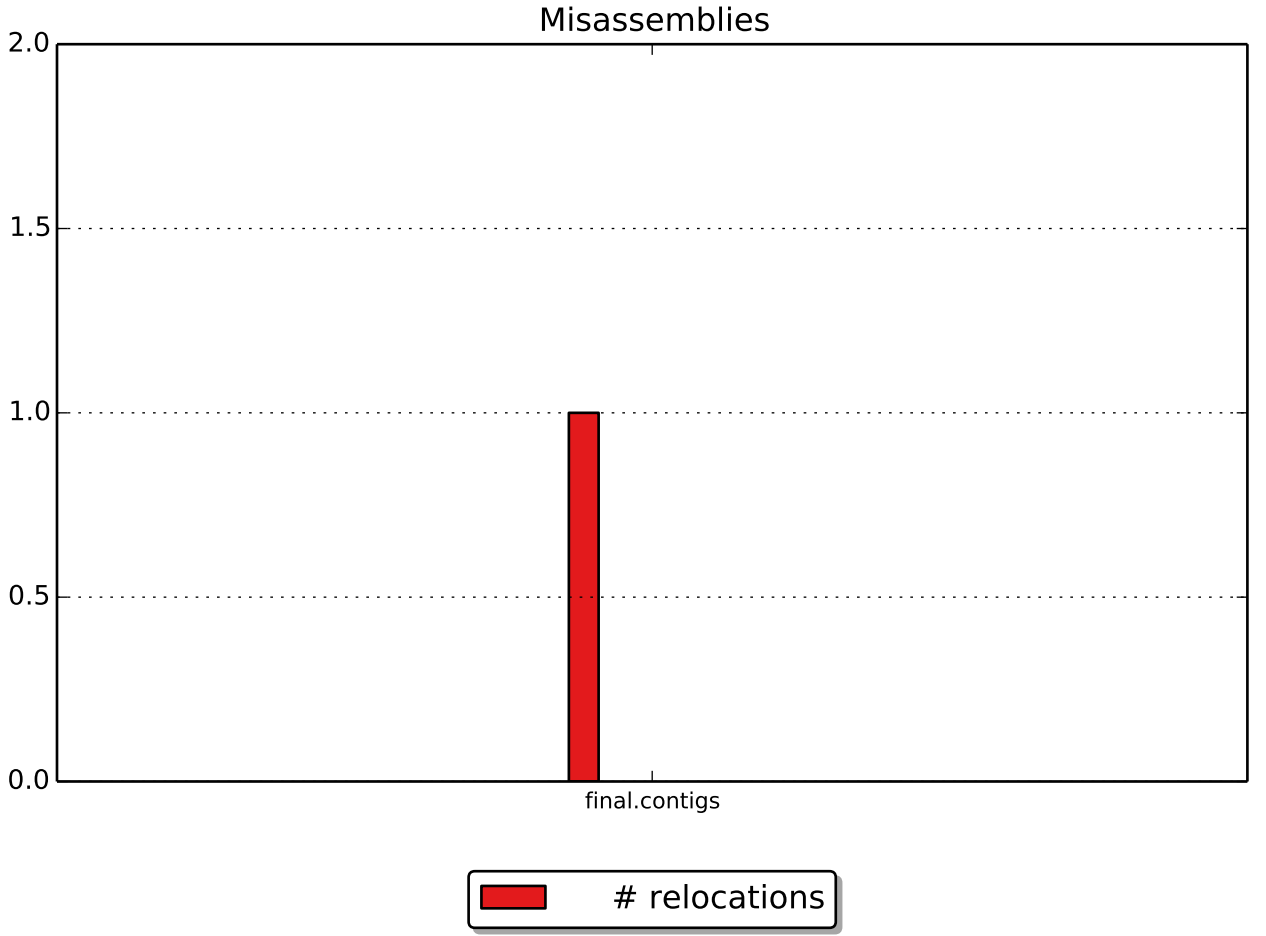
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

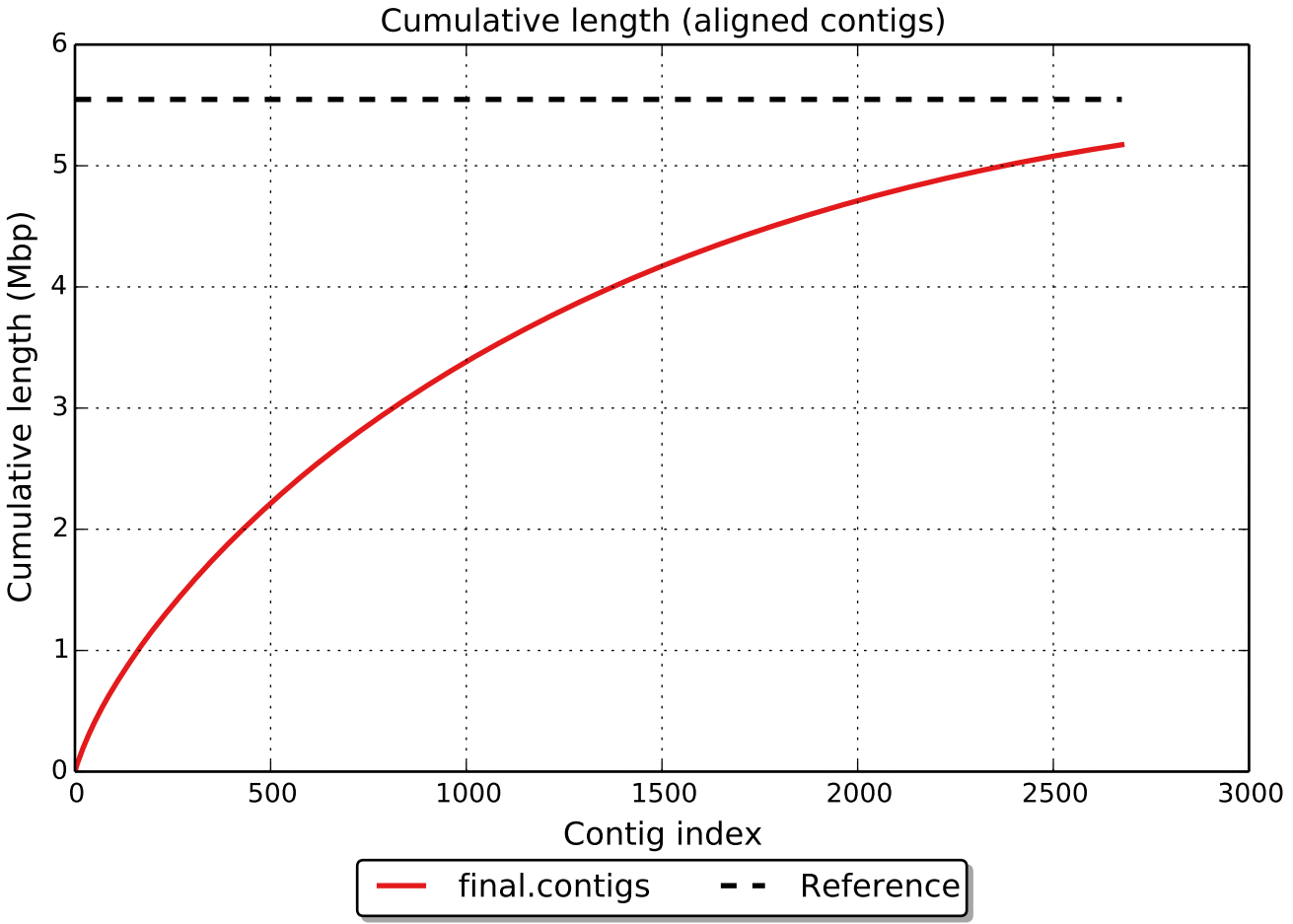

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
500
1000
1500
2000
2500
3000
Contig index
final.contigs
Reference

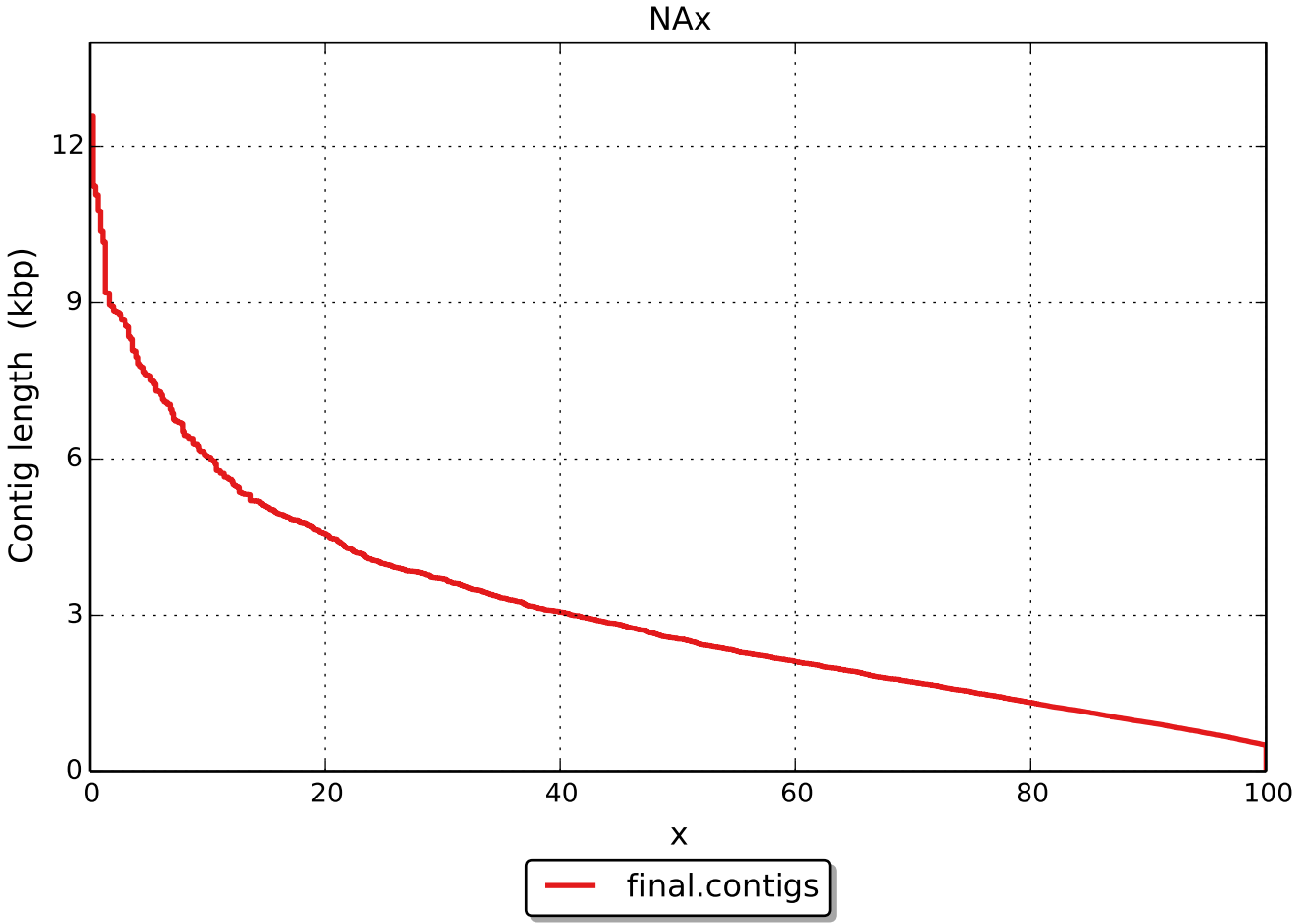

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

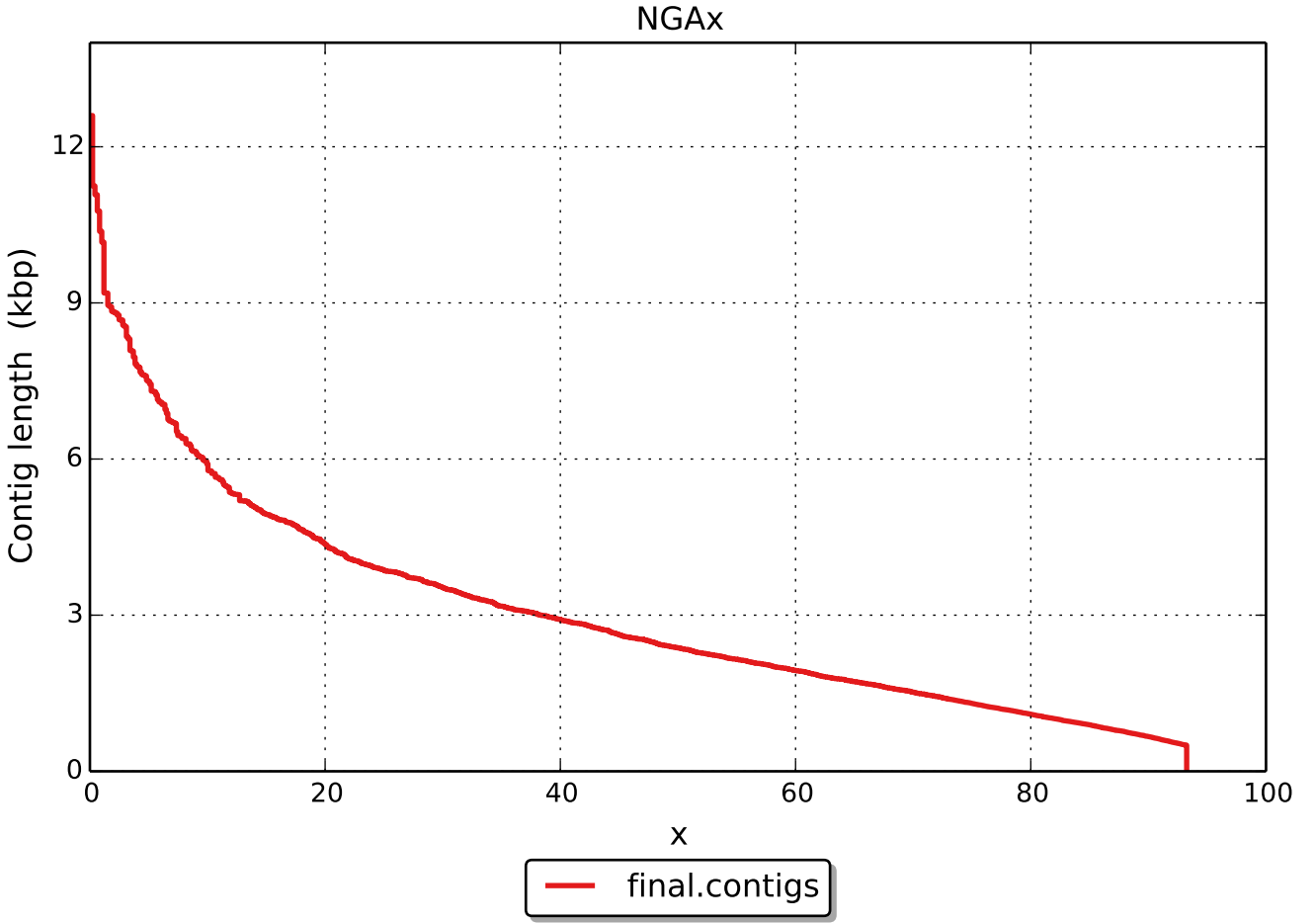

Nx
Contig length (kbp)
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs


Misassemblies
2.0
1.5
1.0
0.5
0.0
final.contigs
relocations


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
500
1000
1500
2000
2500
3000
Contig index
final.contigs
Reference


NAx
Contig length (kbp)
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs