Report

	final.contigs
# contigs (>= 0 bp)	3133
# contigs (>= 1000 bp)	1033
Total length (>= 0 bp)	3006464
Total length (>= 1000 bp)	1517038
# contigs	3133
Largest contig	4208
Total length	3006464
Reference length	1892775
GC (%)	32.32
Reference GC (%)	32.26
N50	1007
NG50	1301
N75	732
NG75	1048
L50	1020
LG50	534
L75	1895
LG75	938
# misassemblies	53
# misassembled contigs	52
Misassembled contigs length	61830
# local misassemblies	0
# unaligned contigs	2 + 1 part
Unaligned length	3088
Genome fraction (%)	88.152
Duplication ratio	1.800
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1331.54
# indels per 100 kbp	0.48
Largest alignment	4208
NA50	993
NGA50	1291
NA75	726
NGA75	1032
LA50	1031
LGA50	539
LA75	1914
LGA75	948

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

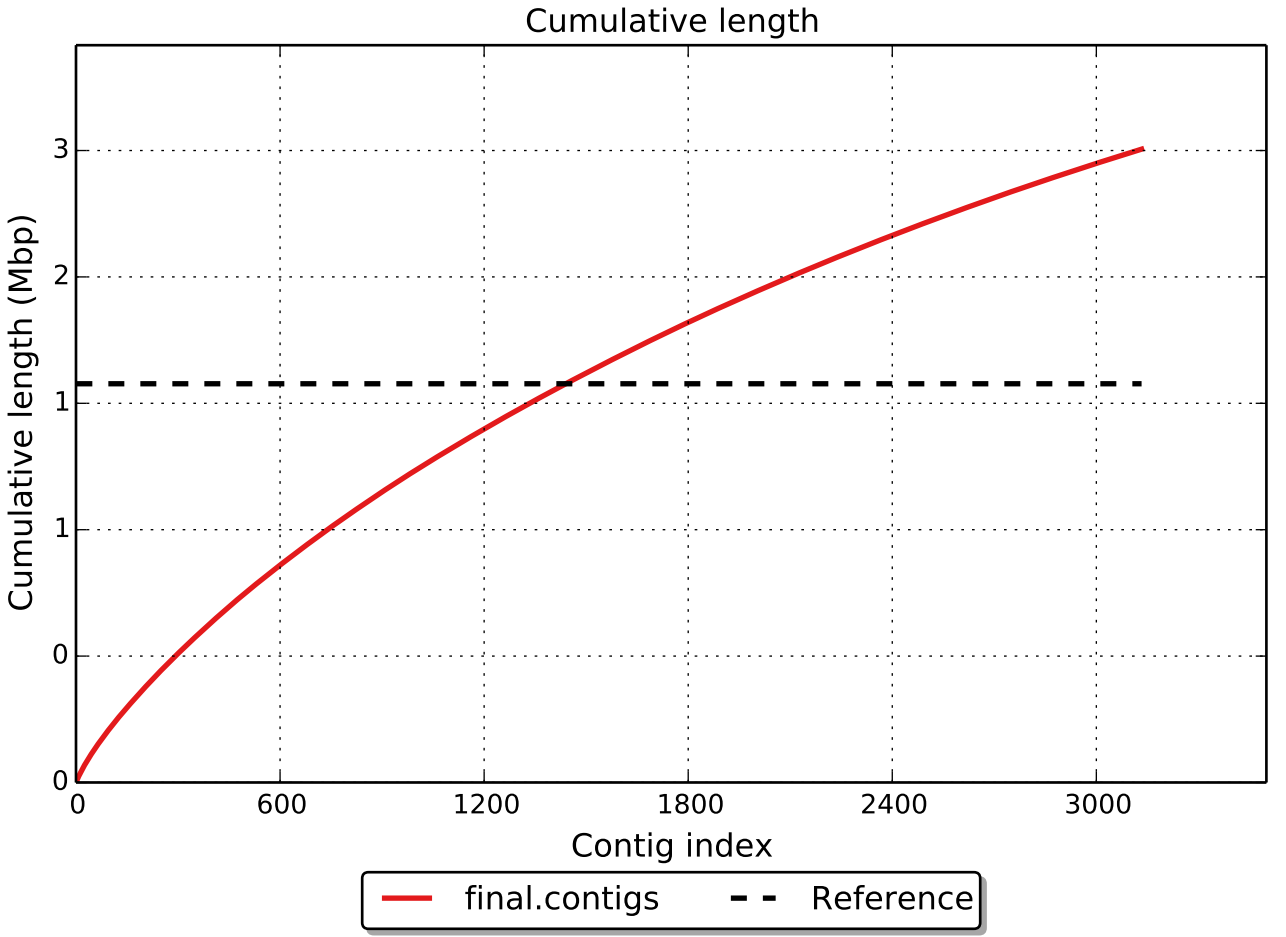
	final.contigs
# misassemblies	53
# relocations	53
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	52
Misassembled contigs length	61830
# local misassemblies	0
# mismatches	22217
# indels	8
# short indels	8
# long indels	0
Indels length	8

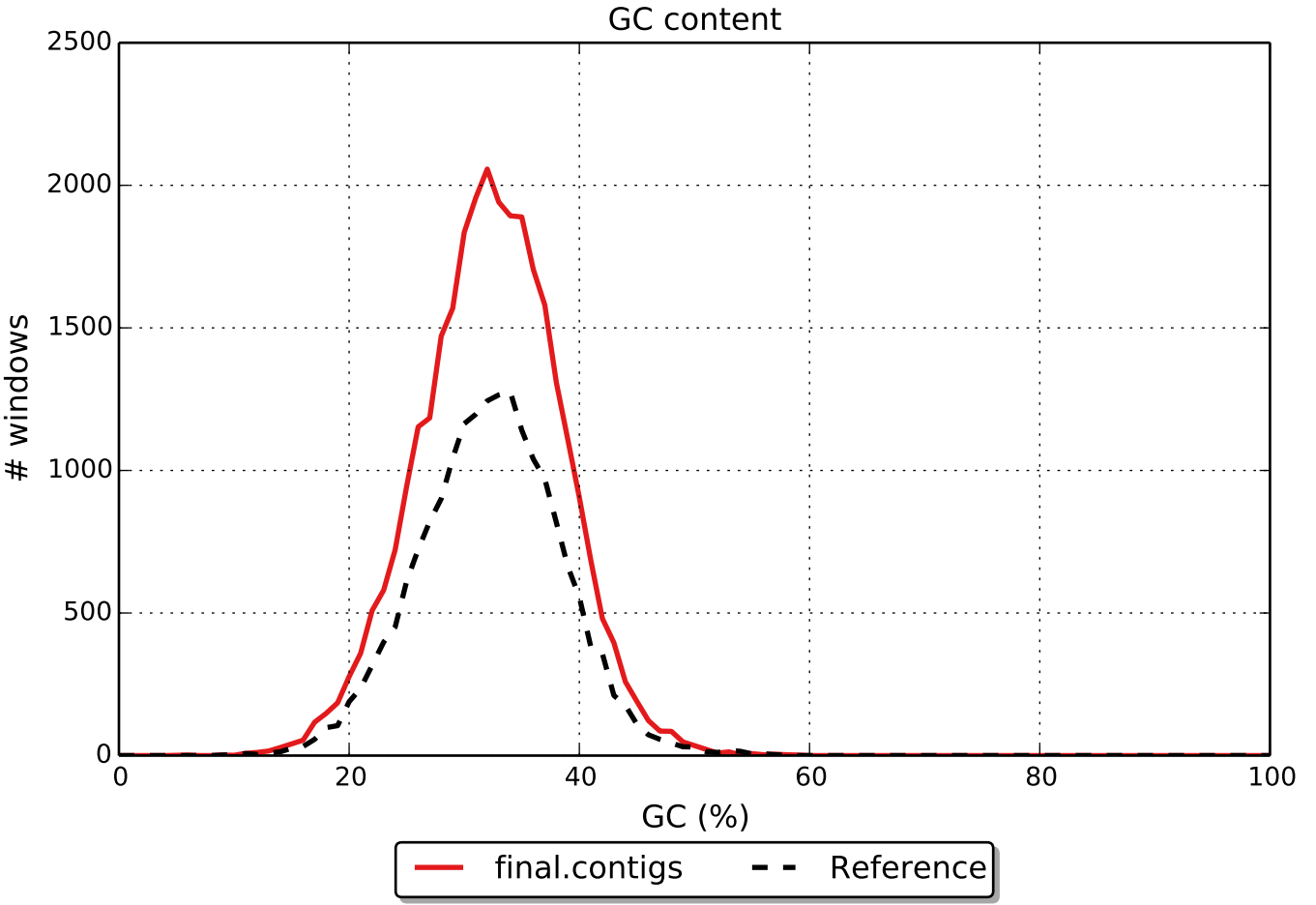
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

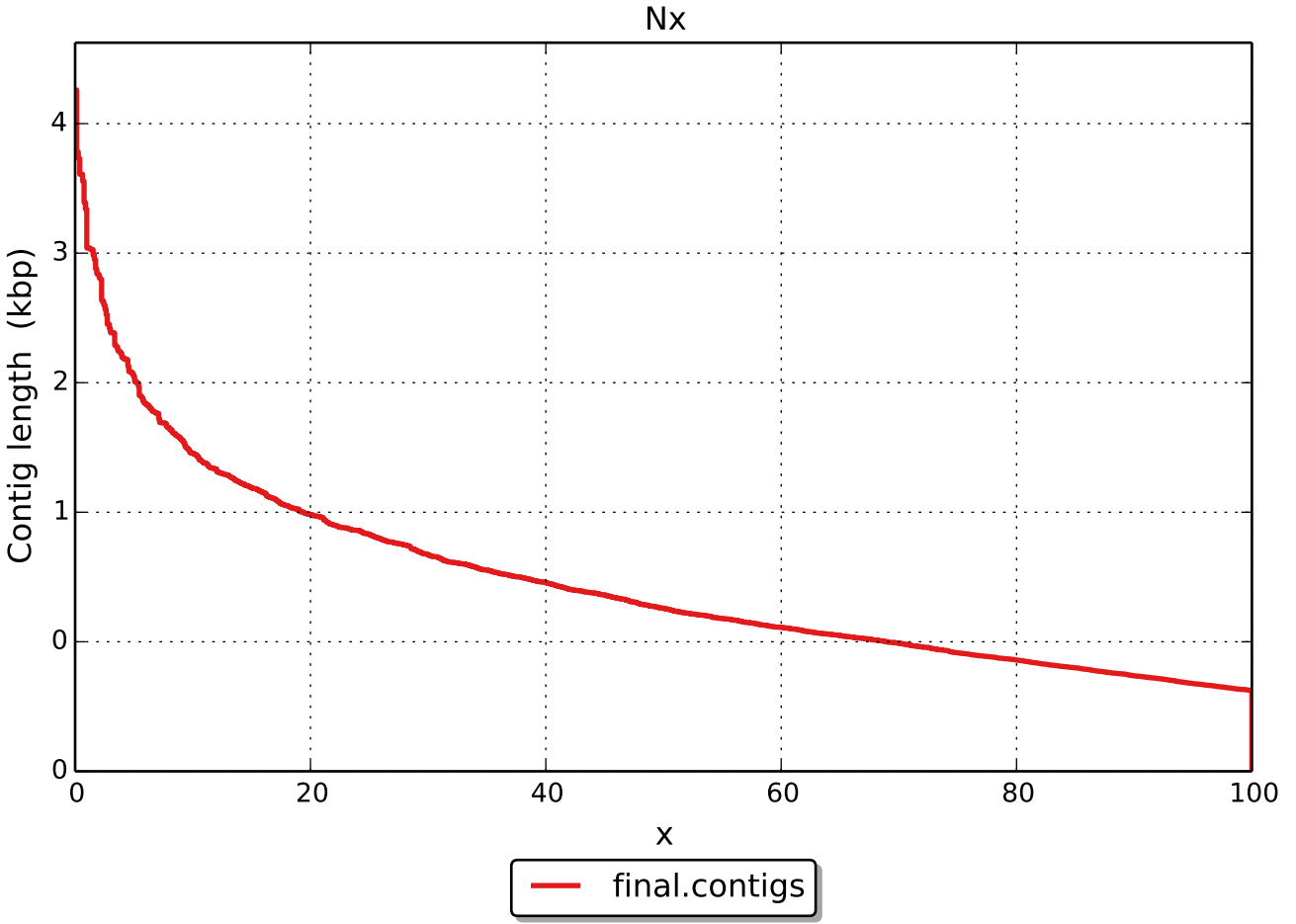
Unaligned report

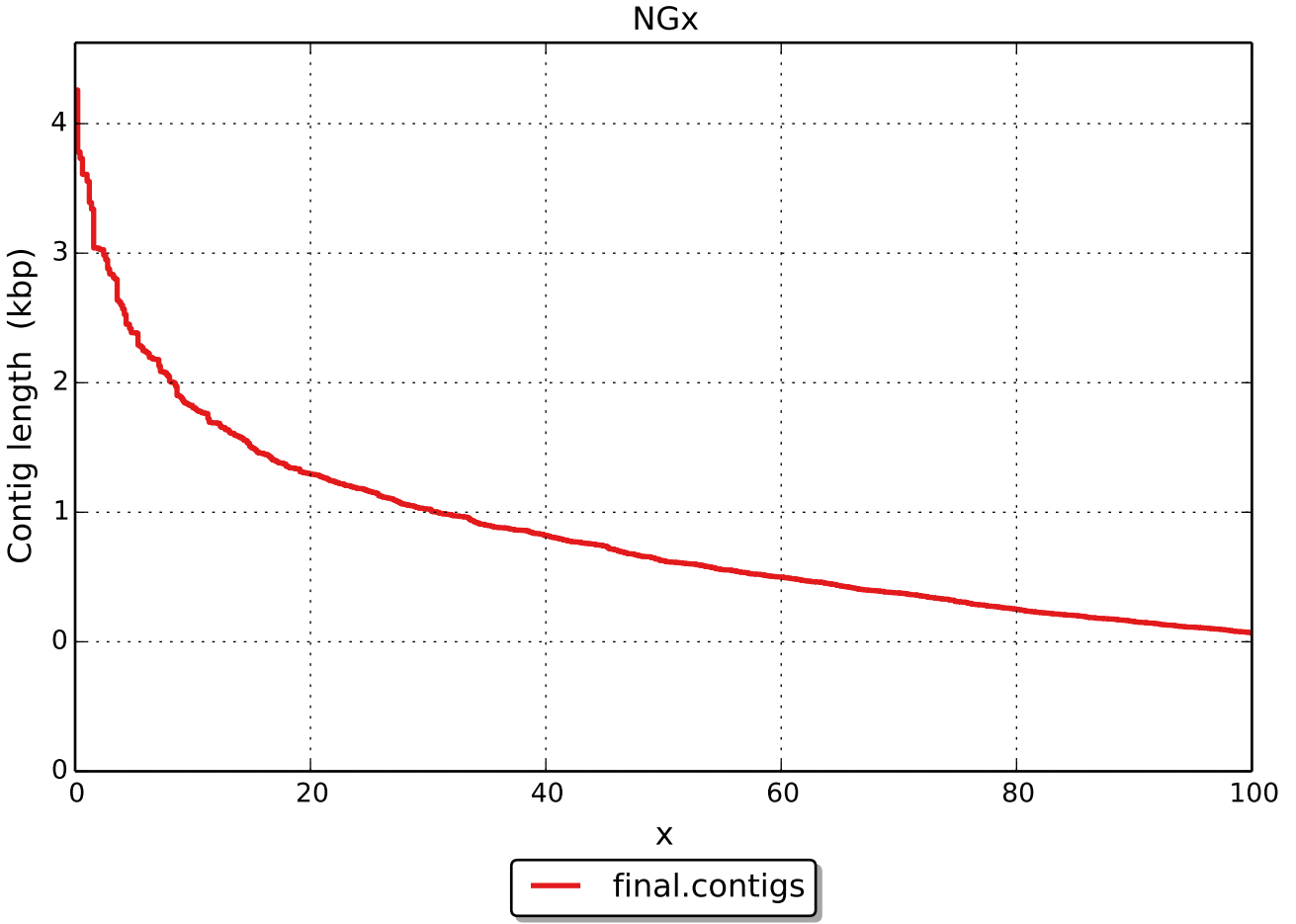
	final.contigs
# fully unaligned contigs	2
Fully unaligned length	1784
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	1304
# N's	0

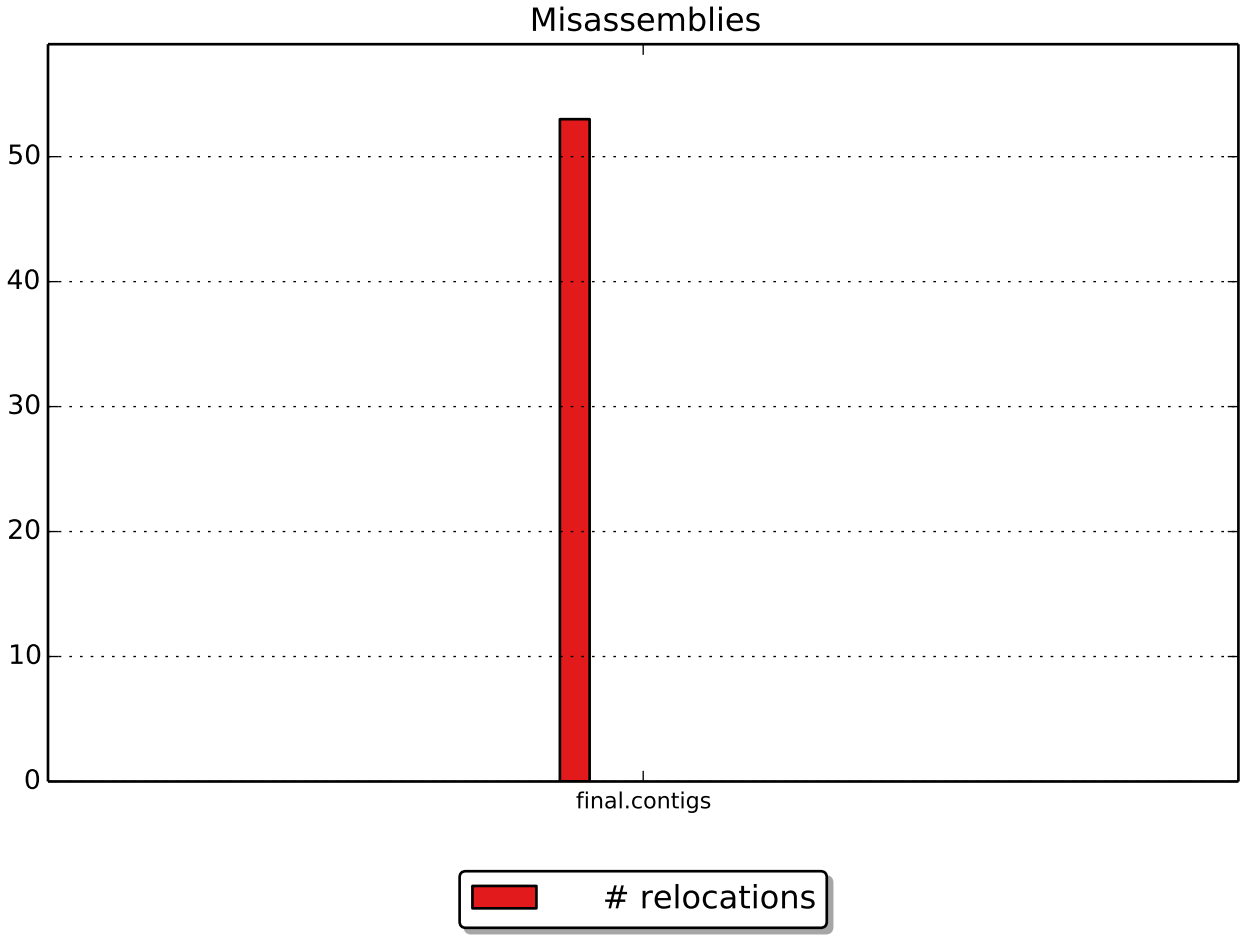
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

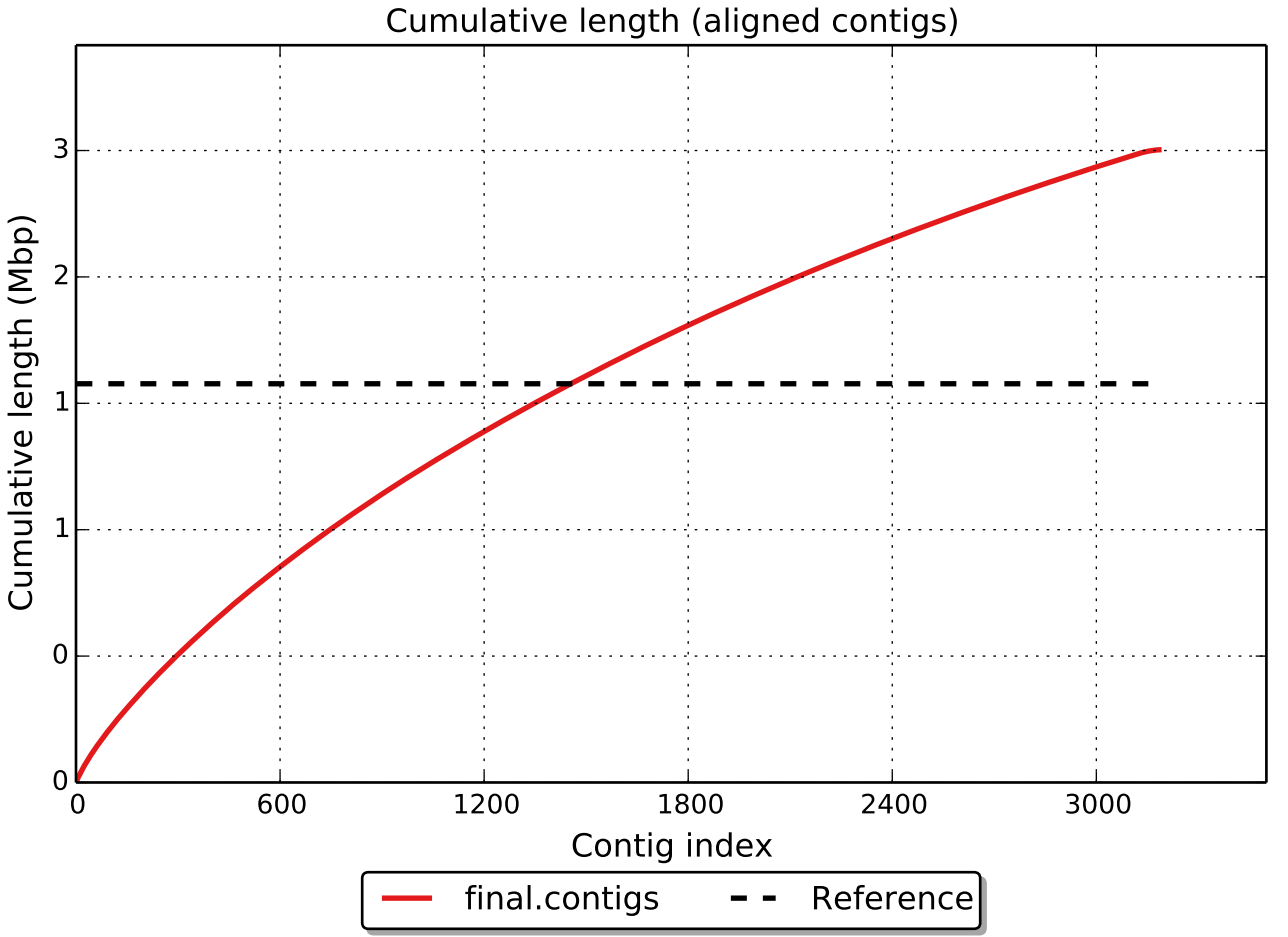

Cumulative length
Cumulative length (Mbp)
3
2
1
1
0
0
0
600
1200
1800
2400
3000
Contig index
final.contigs
Reference

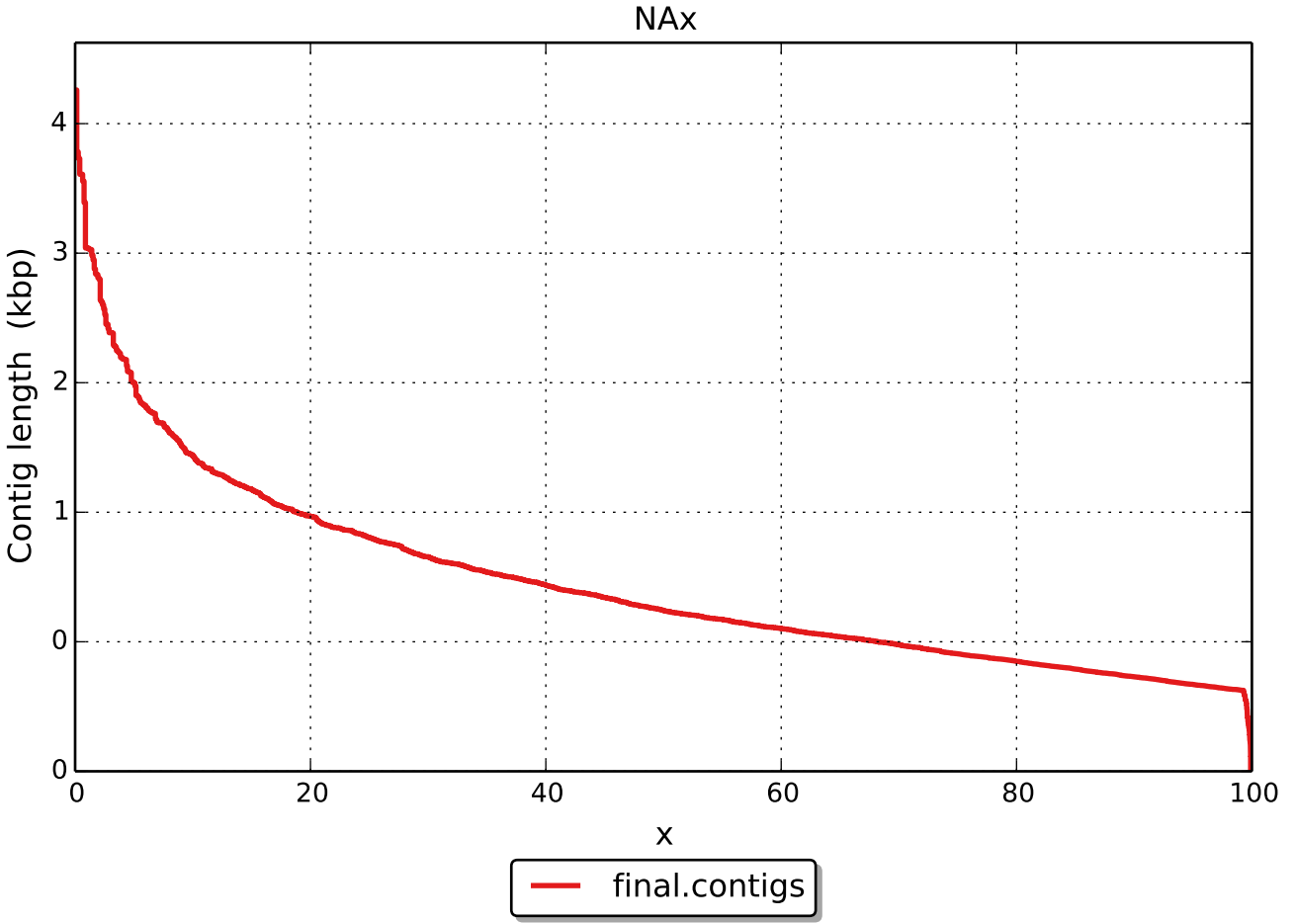

GC content
2500
2000
1500
1000
500
0
windows
0
20
40
60
80
100
GC (%)
final.contigs
Reference

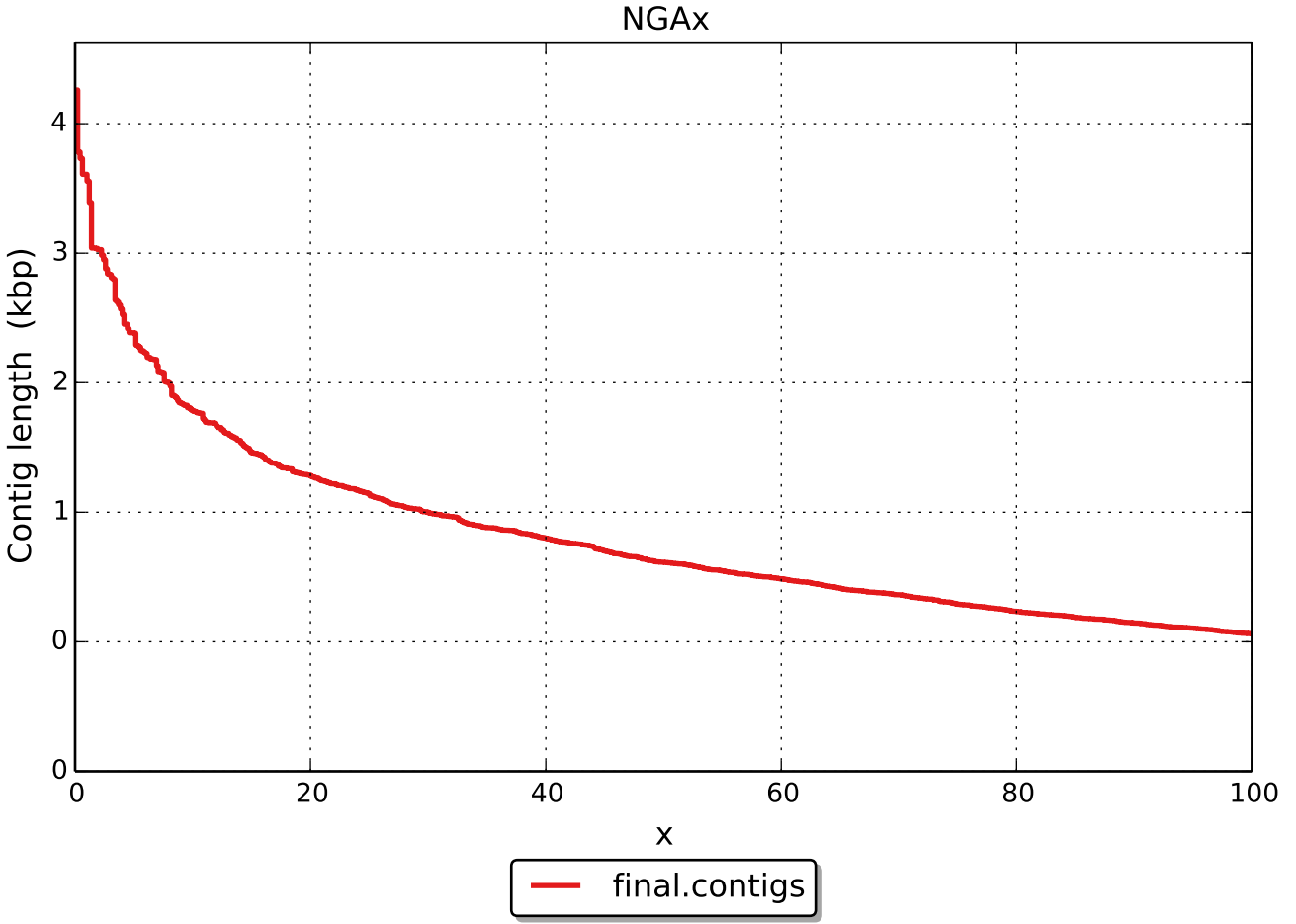

Nx
Contig length (kbp)
0
1
2
3
4
0
20
40
60
80
100
x
final.contigs


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


Misassemblies
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
0
20
40
60
80
100
x
final.contigs


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