Report

	final.contigs
# contigs (>= 0 bp)	5064
# contigs (>= 1000 bp)	1812
Total length (>= 0 bp)	4940799
Total length (>= 1000 bp)	2645384
# contigs	5064
Largest contig	4582
Total length	4940799
Reference length	5547323
GC (%)	50.48
Reference GC (%)	50.49
N50	1048
NG50	963
N75	743
NG75	651
L50	1641
LG50	1943
L75	3045
LG75	3700
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	2463
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	84.160
Duplication ratio	1.058
# N's per 100 kbp	0.00
# mismatches per 100 kbp	133.01
# indels per 100 kbp	0.21
Largest alignment	4582
NA50	1048
NGA50	962
NA75	743
NGA75	650
LA50	1641
LGA50	1944
LA75	3046
LGA75	3701

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

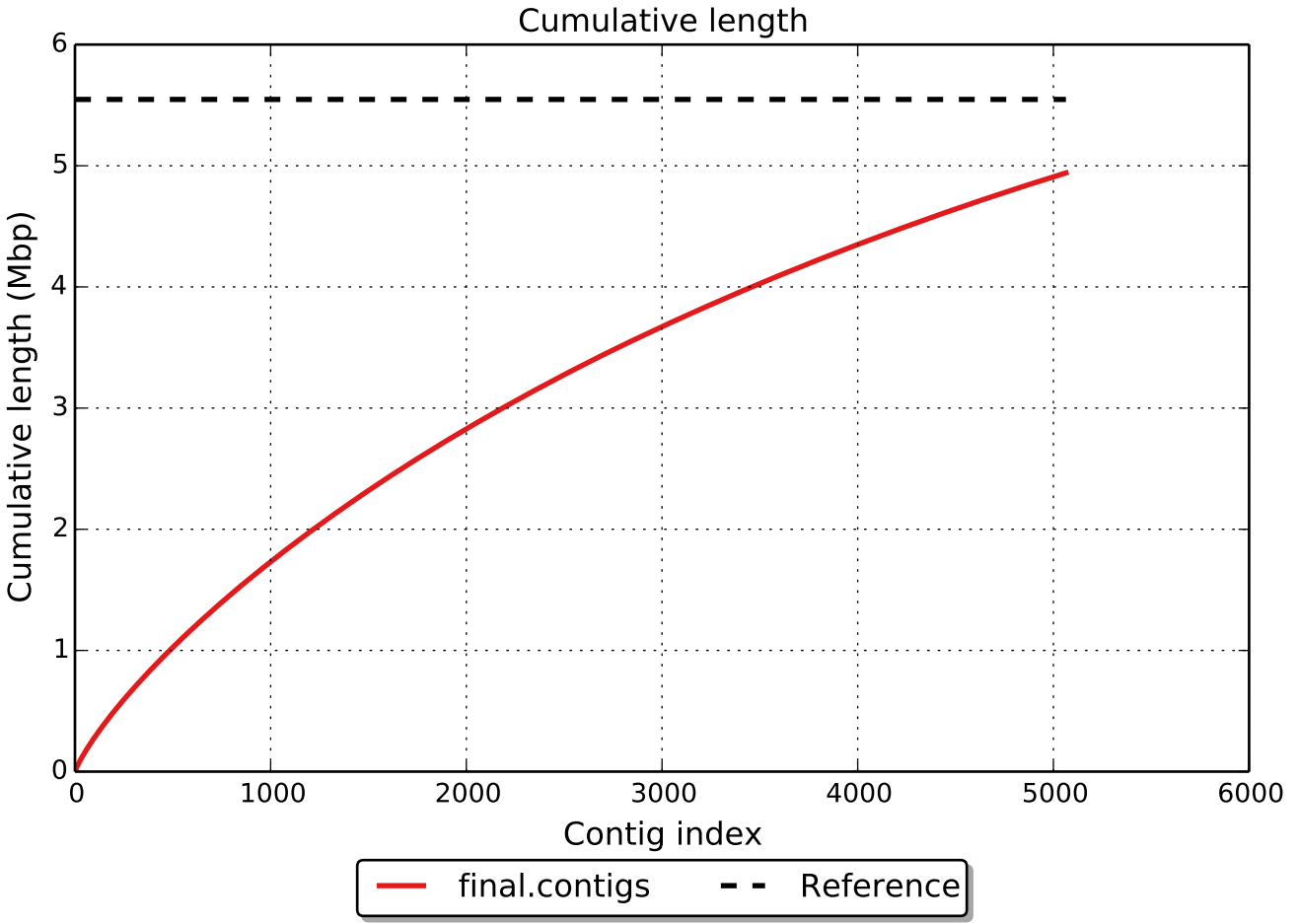
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	2463
# local misassemblies	0
# mismatches	6210
# indels	10
# short indels	10
# long indels	0
Indels length	10

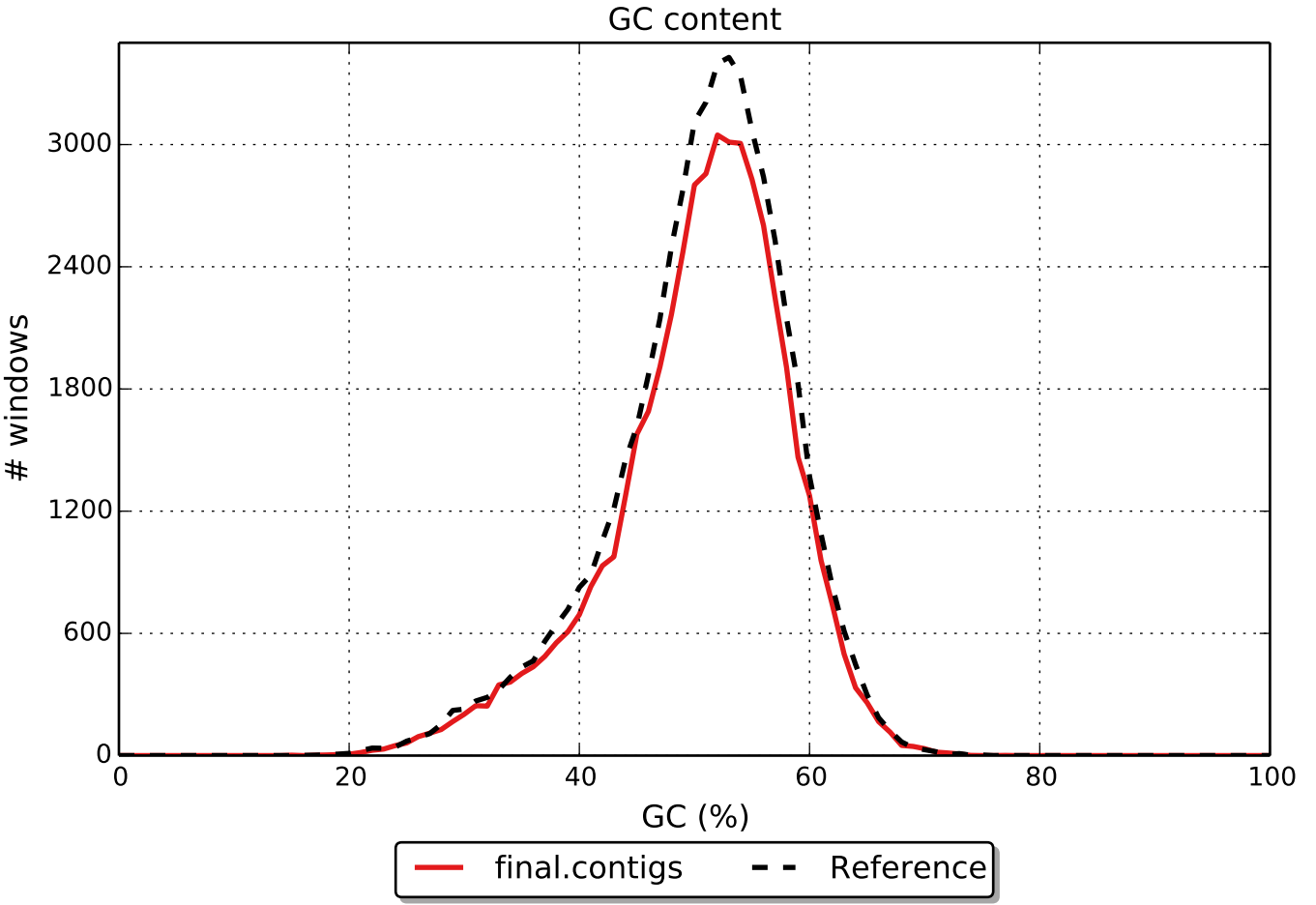
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

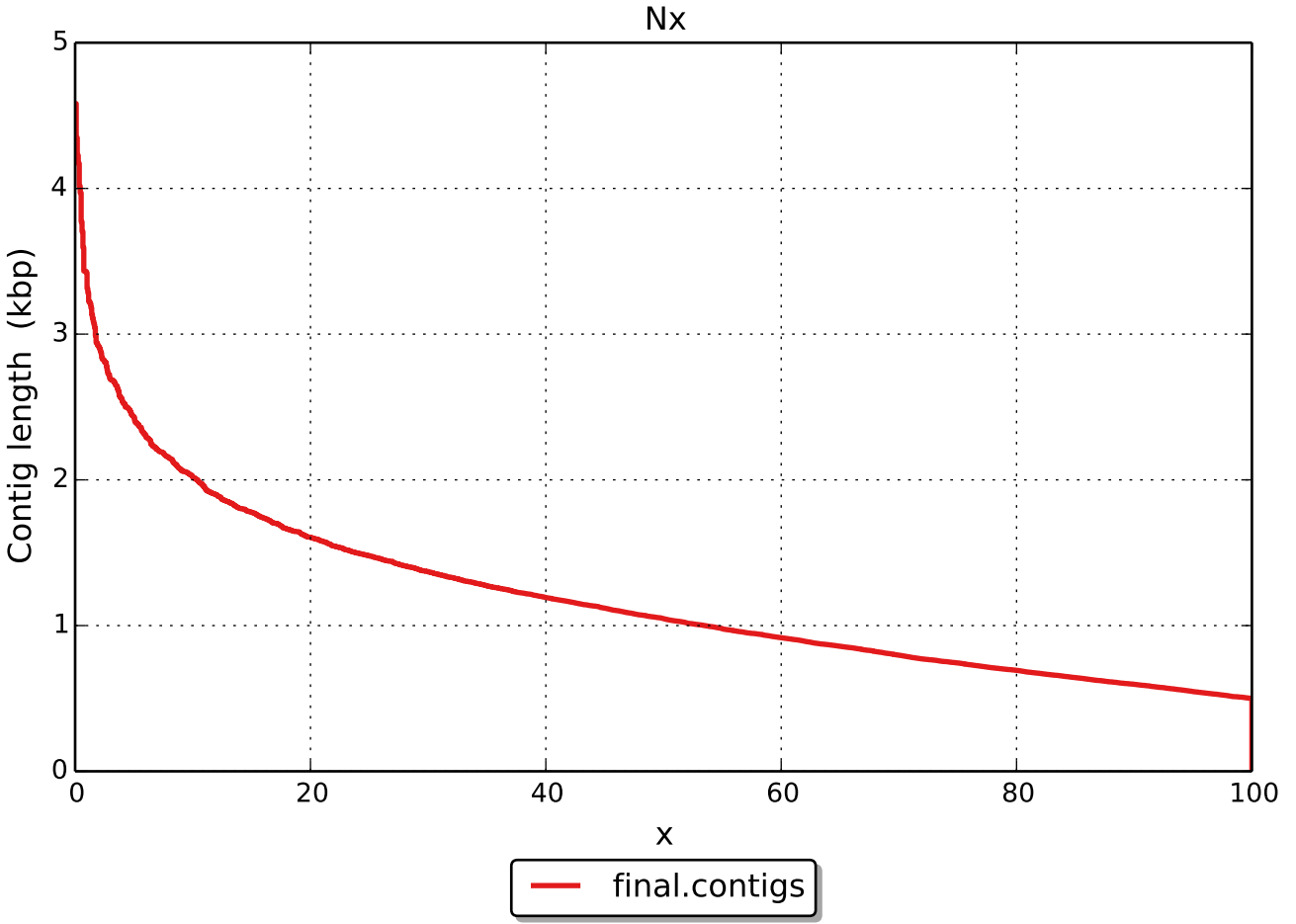
Unaligned report

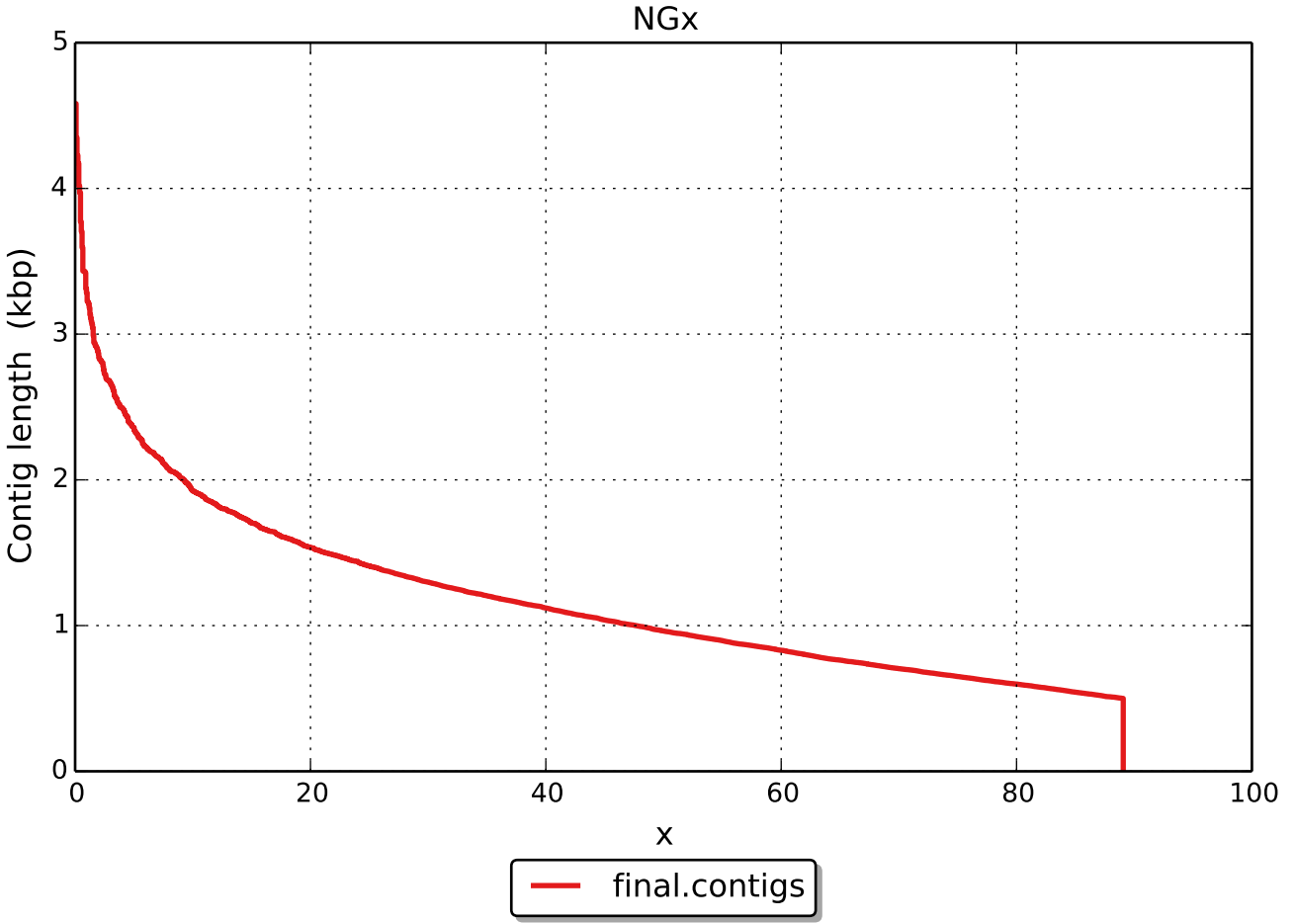
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

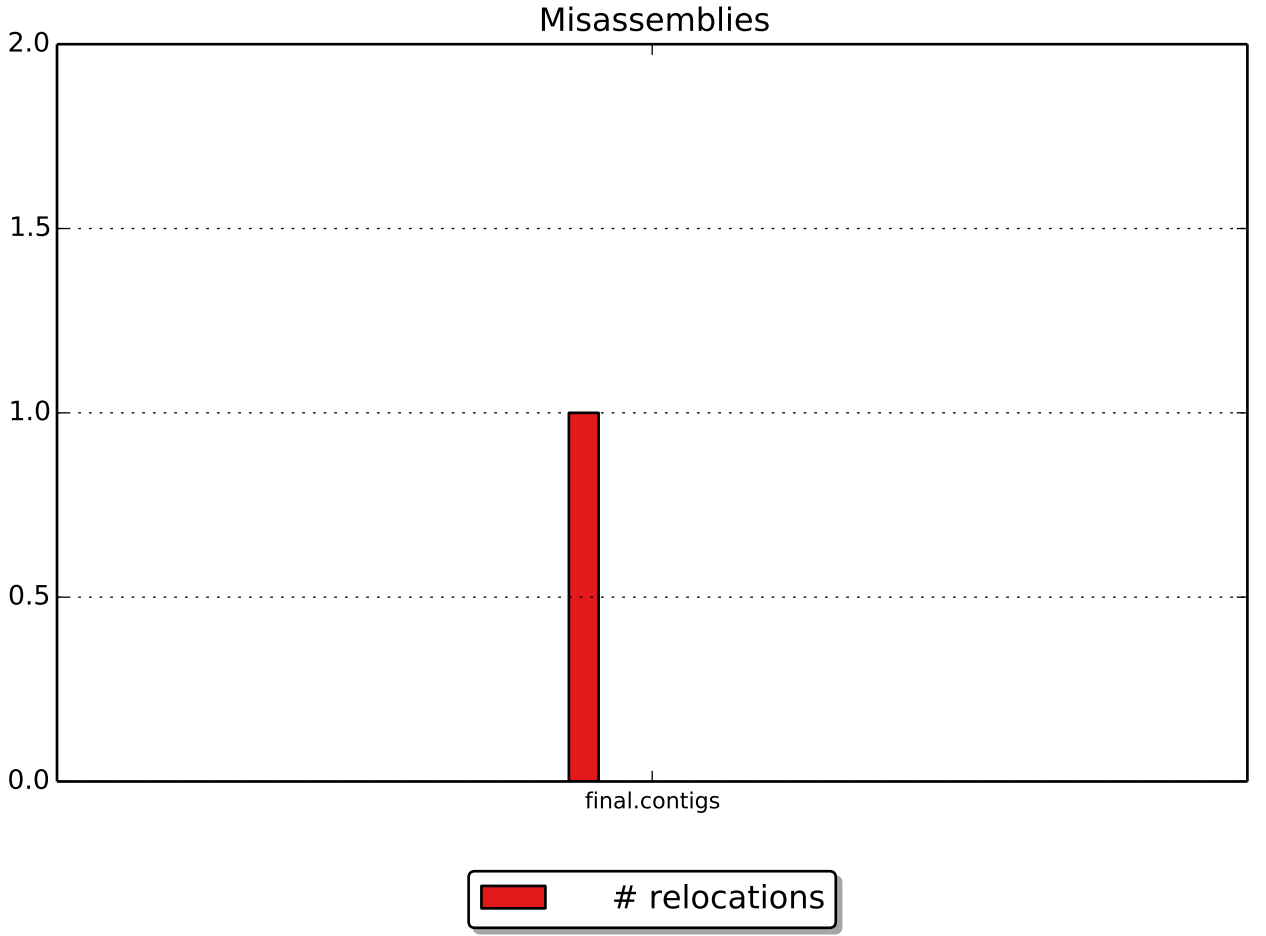
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

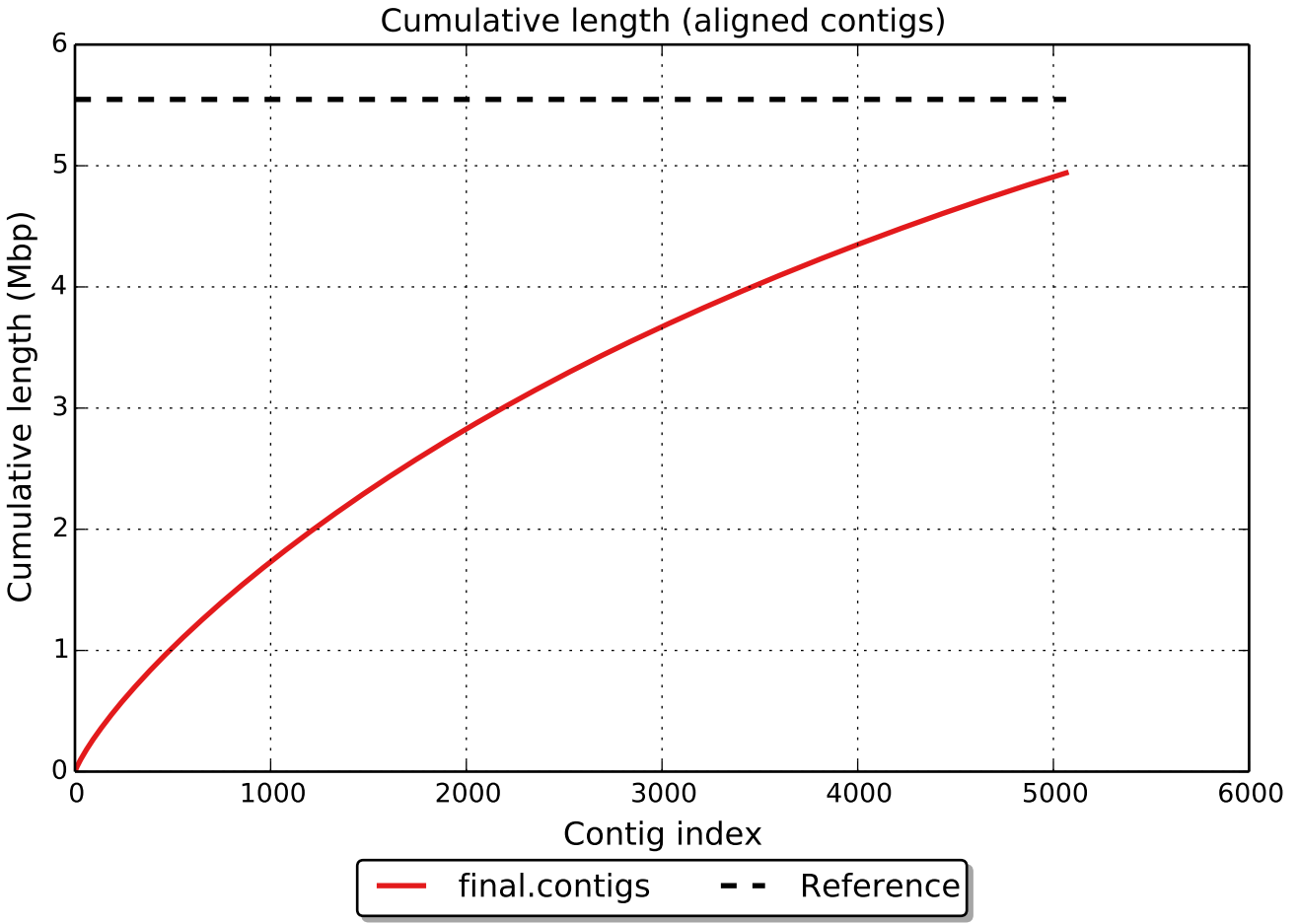

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
1000
2000
3000
4000
5000
6000
Contig index
final.contigs
Reference

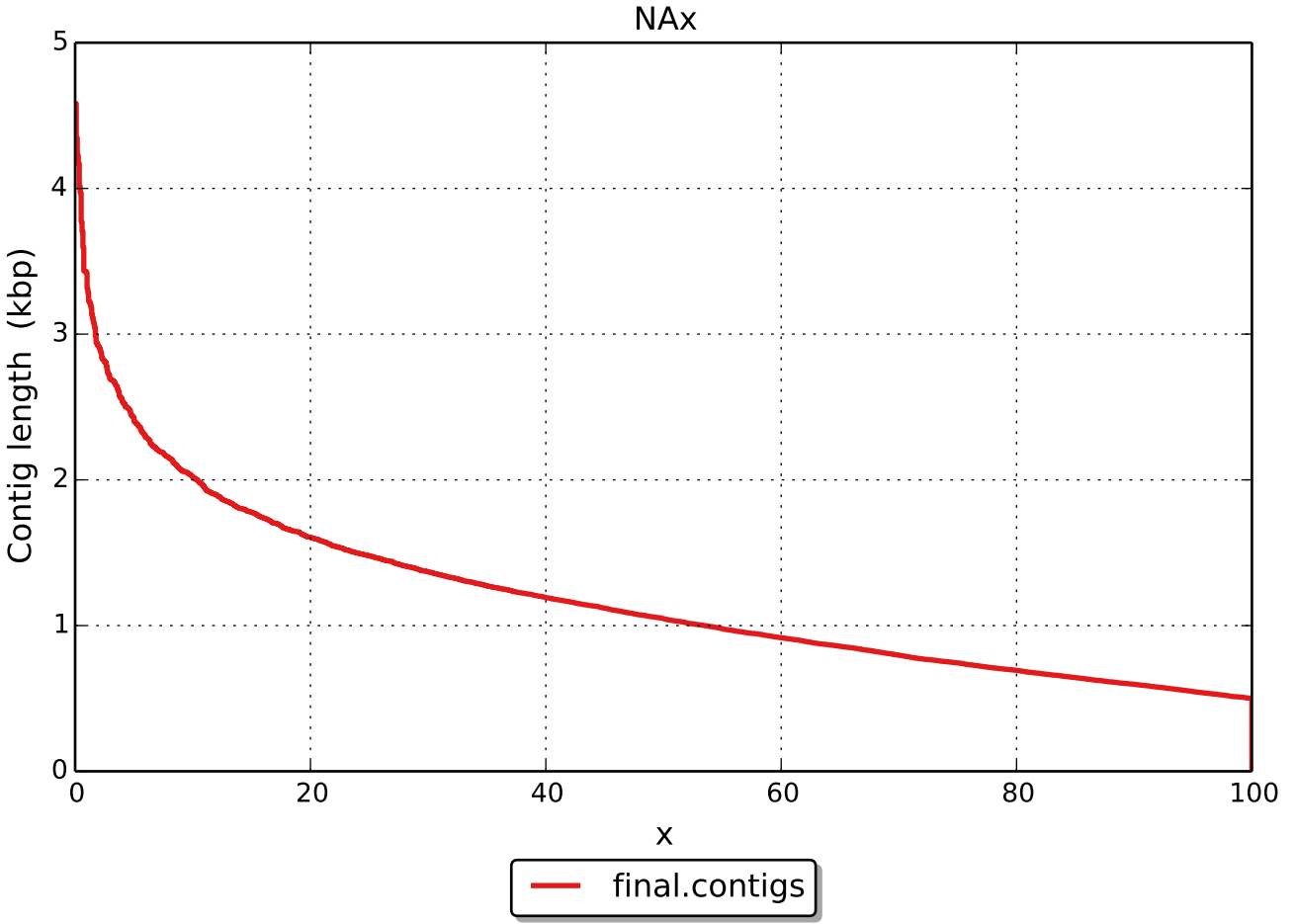

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

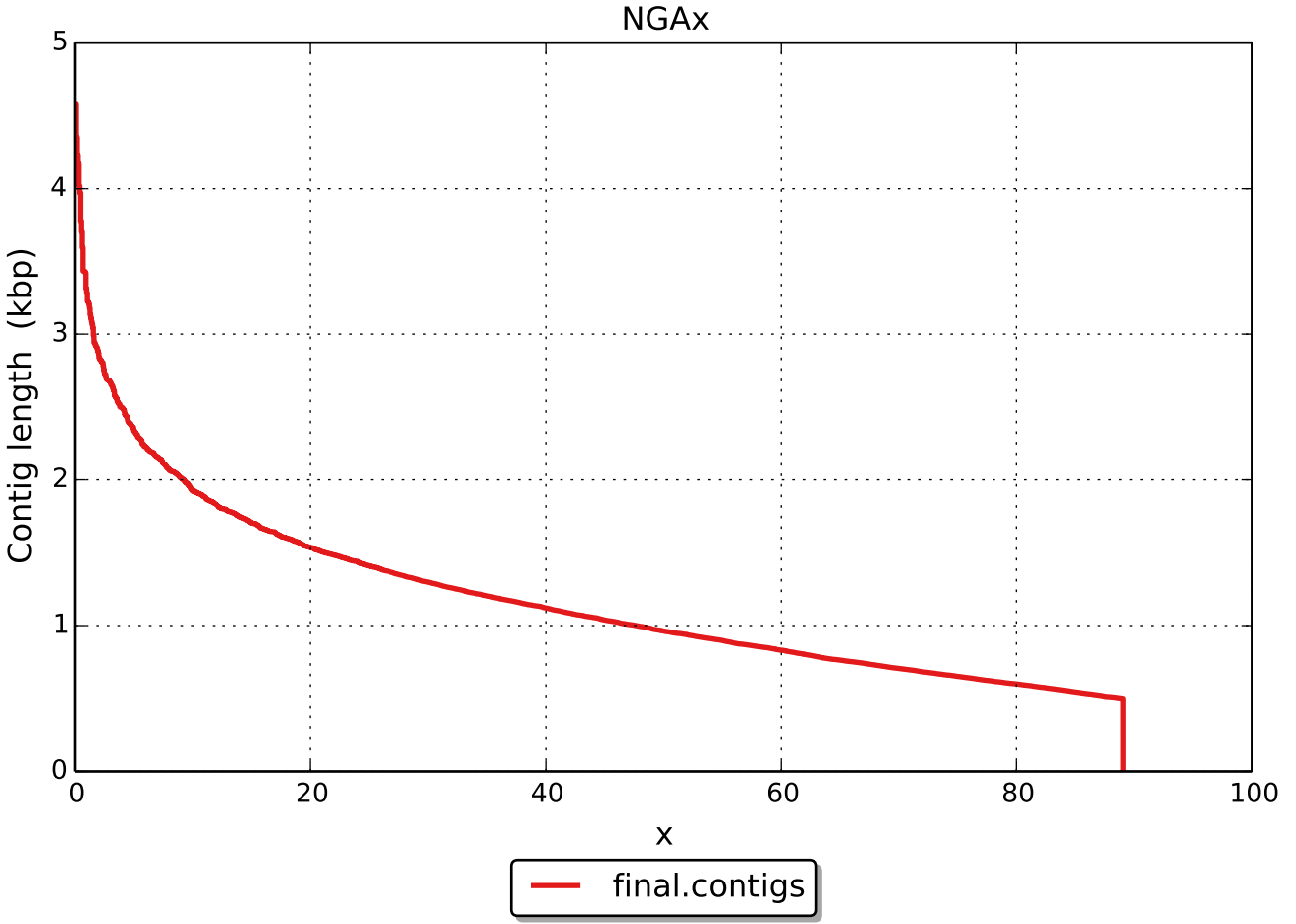

Nx
Contig length (kbp)
0
1
2
3
4
5
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
0
1
2
3
4
5
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
1000
2000
3000
4000
5000
6000
Contig index
final.contigs
Reference


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


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