Report

	final.contigs
# contigs (>= 0 bp)	4810
# contigs (>= 1000 bp)	1728
Total length (>= 0 bp)	4705662
Total length (>= 1000 bp)	2528707
# contigs	4810
Largest contig	4582
Total length	4705662
Reference length	5547323
GC (%)	50.51
Reference GC (%)	50.49
N50	1054
NG50	933
N75	746
NG75	611
L50	1557
LG50	1983
L75	2890
LG75	3826
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	2463
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	80.980
Duplication ratio	1.048
# N's per 100 kbp	0.00
# mismatches per 100 kbp	80.96
# indels per 100 kbp	0.20
Largest alignment	4582
NA50	1054
NGA50	933
NA75	746
NGA75	611
LA50	1557
LGA50	1983
LA75	2890
LGA75	3827

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

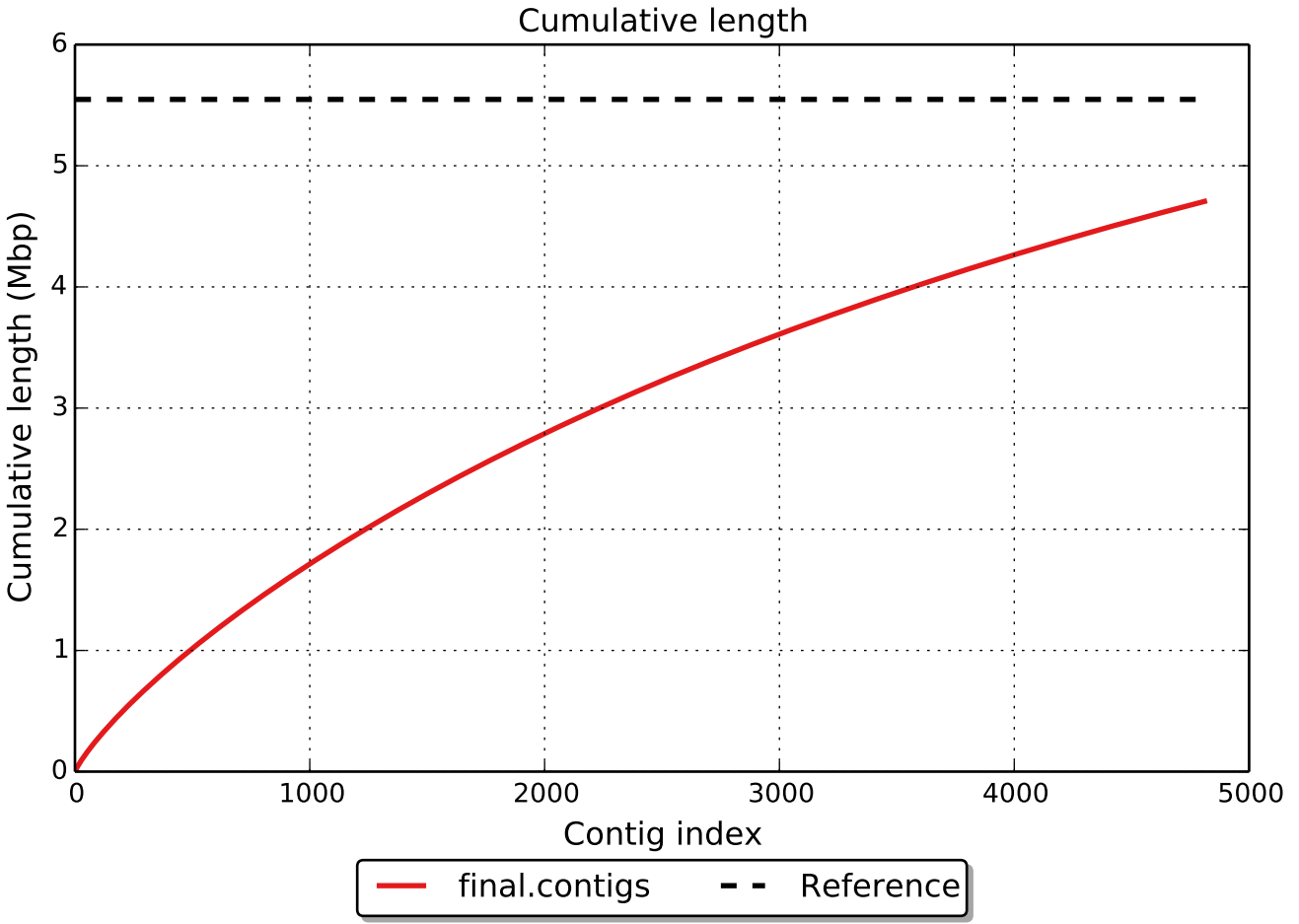
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	2463
# local misassemblies	0
# mismatches	3637
# indels	9
# short indels	9
# long indels	0
Indels length	9

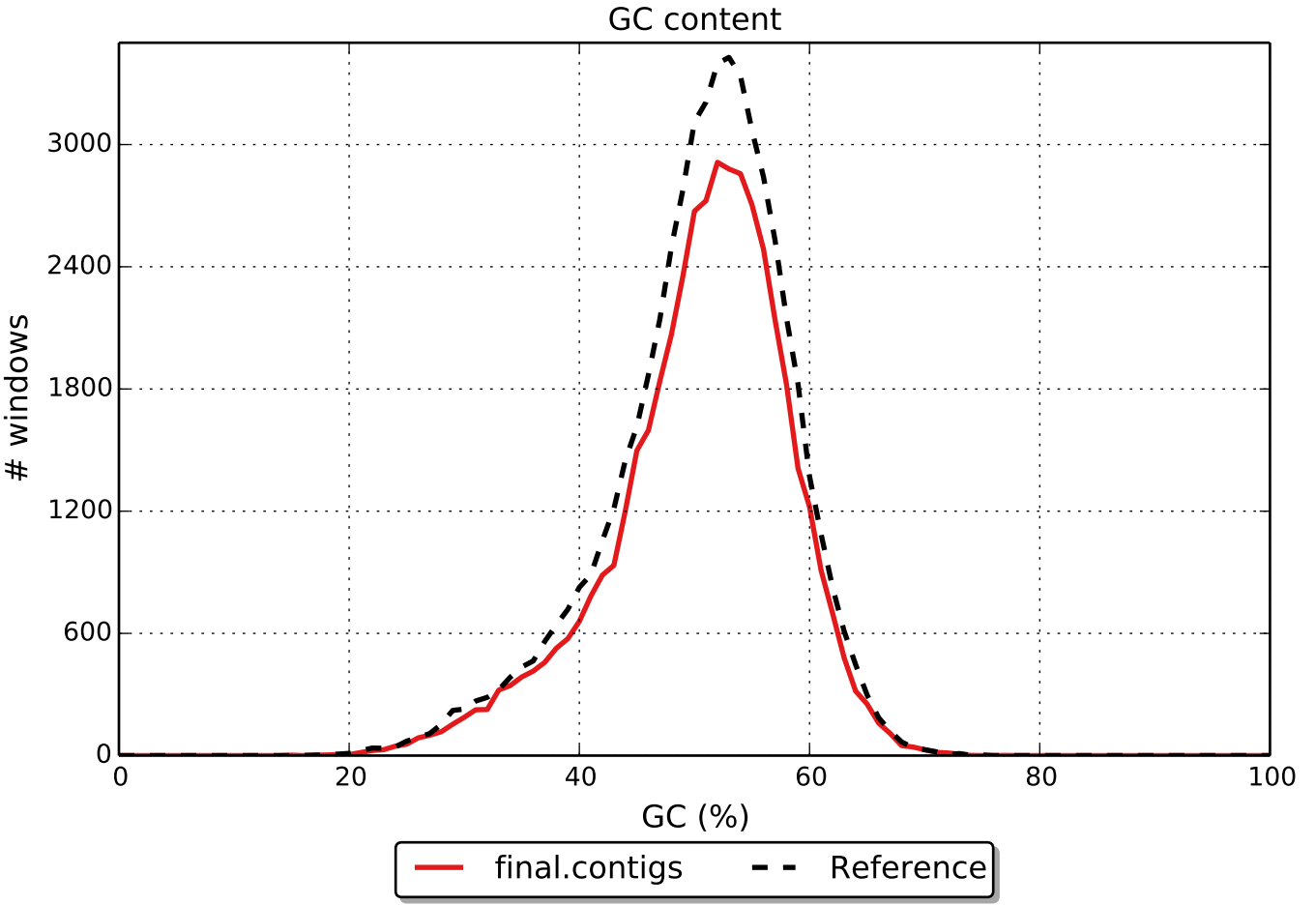
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

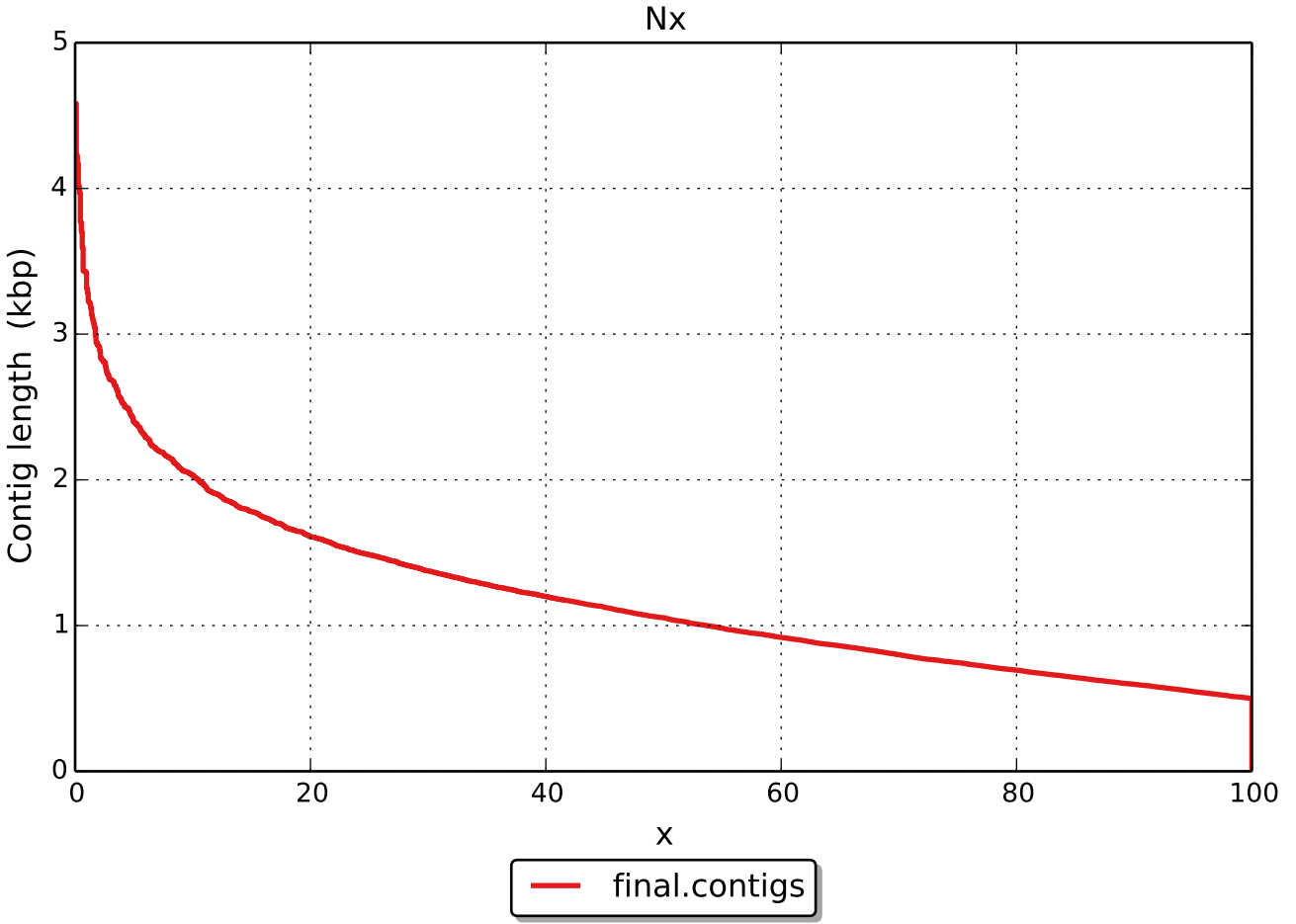
Unaligned report

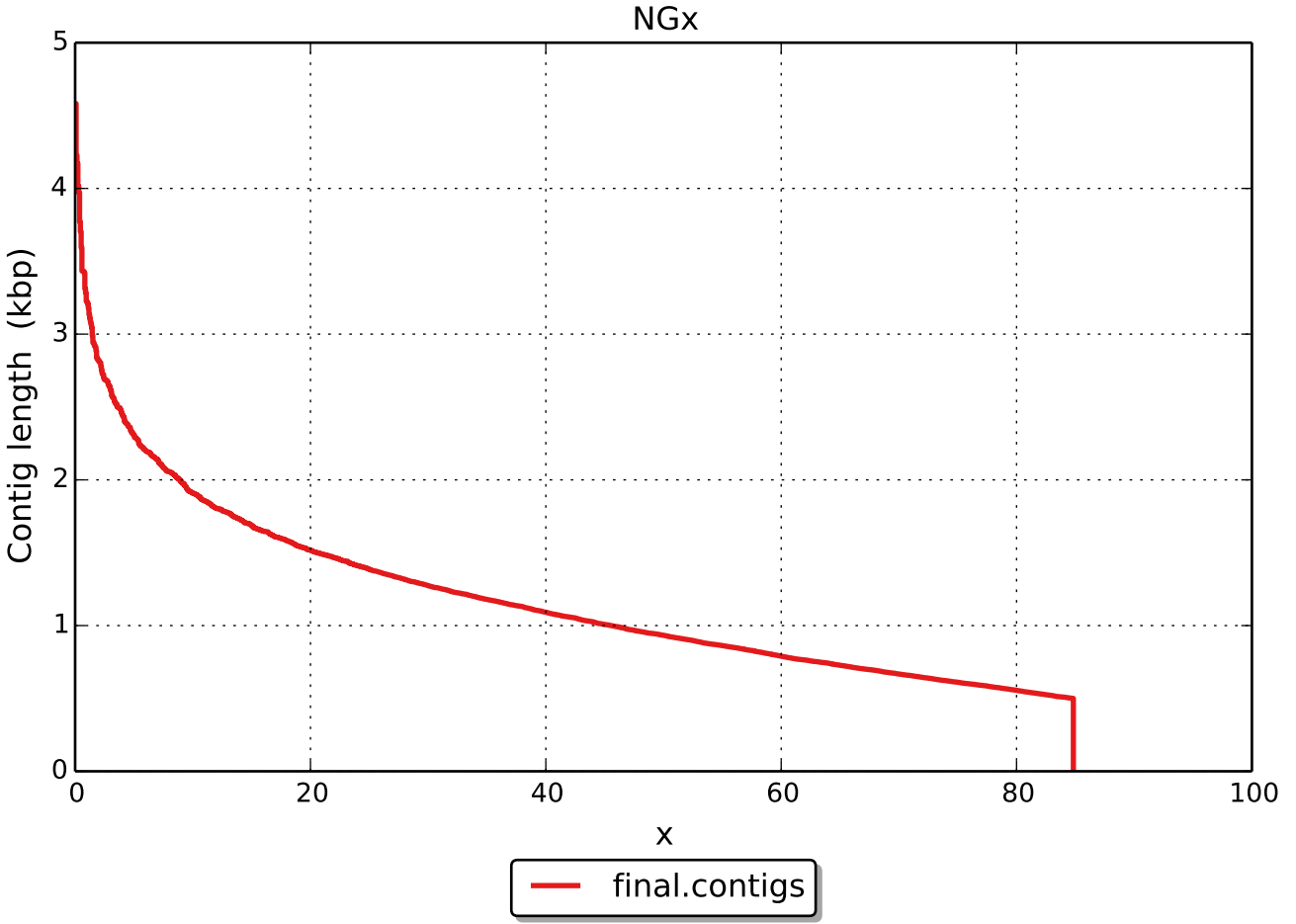
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

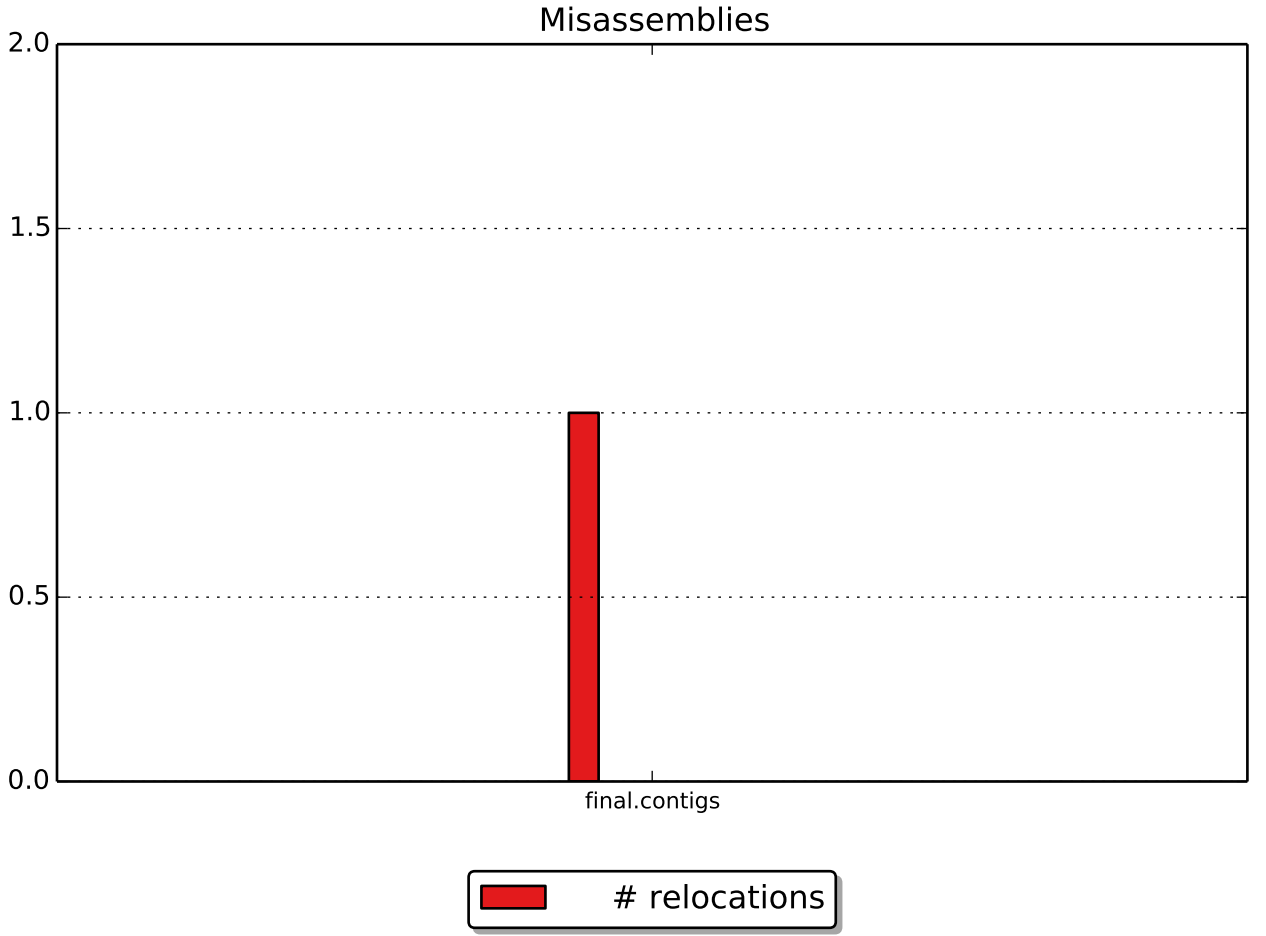
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

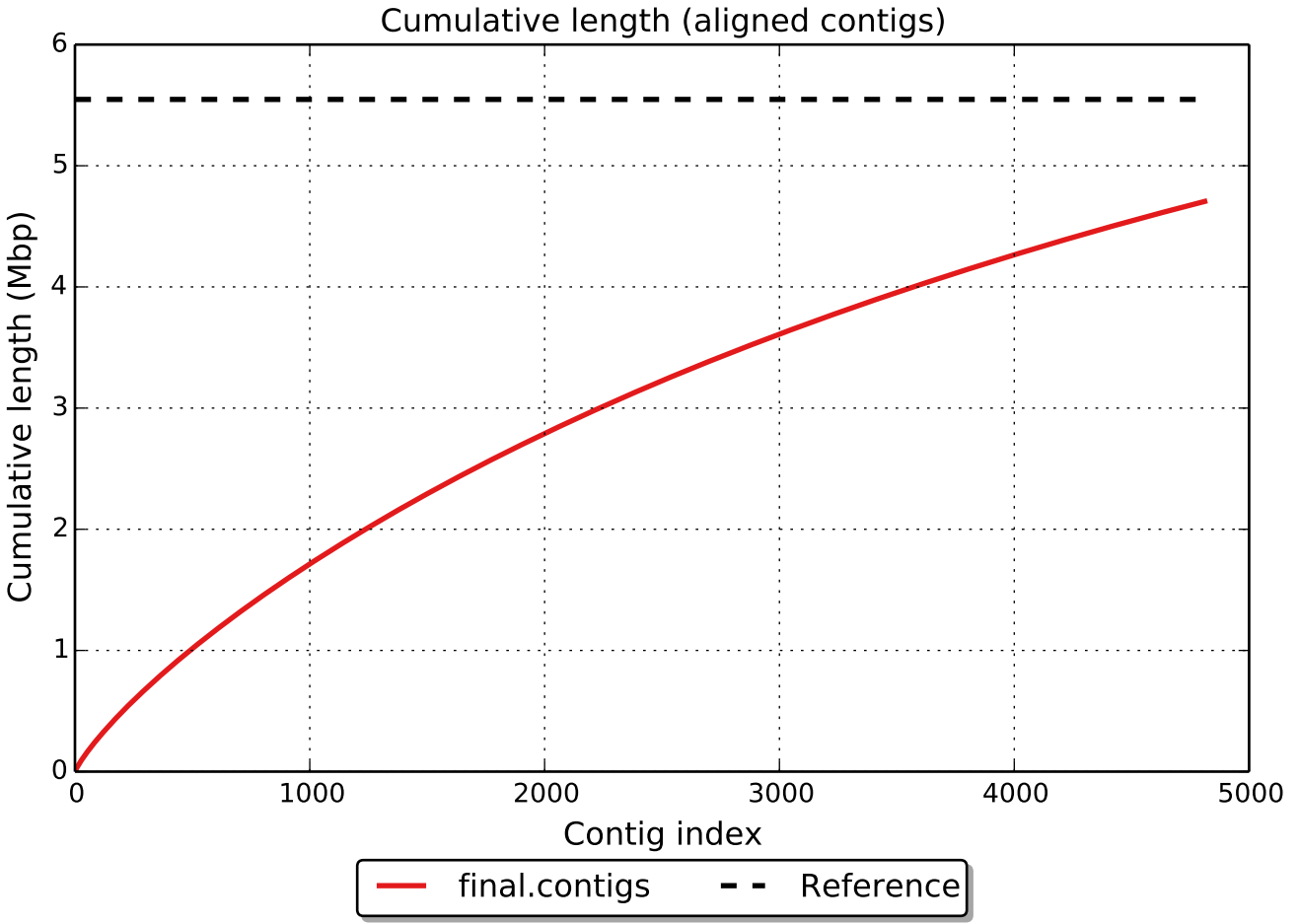

Cumulative length
Cumulative length (Mbp)
0
1
2
3
4
5
6
0
1000
2000
3000
4000
5000
Contig index
final.contigs
Reference

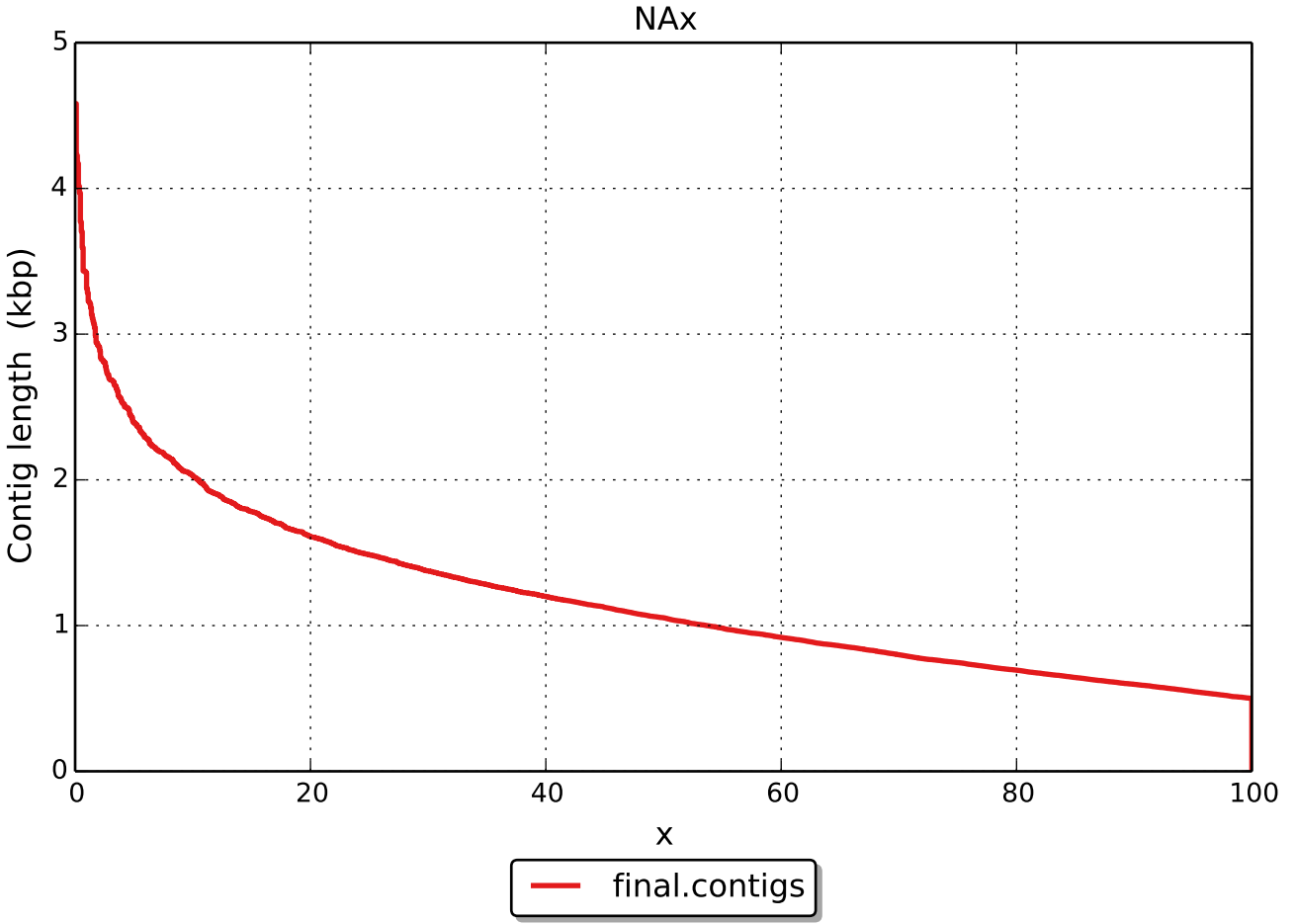

GC content
windows
3000
2400
1800
1200
600
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

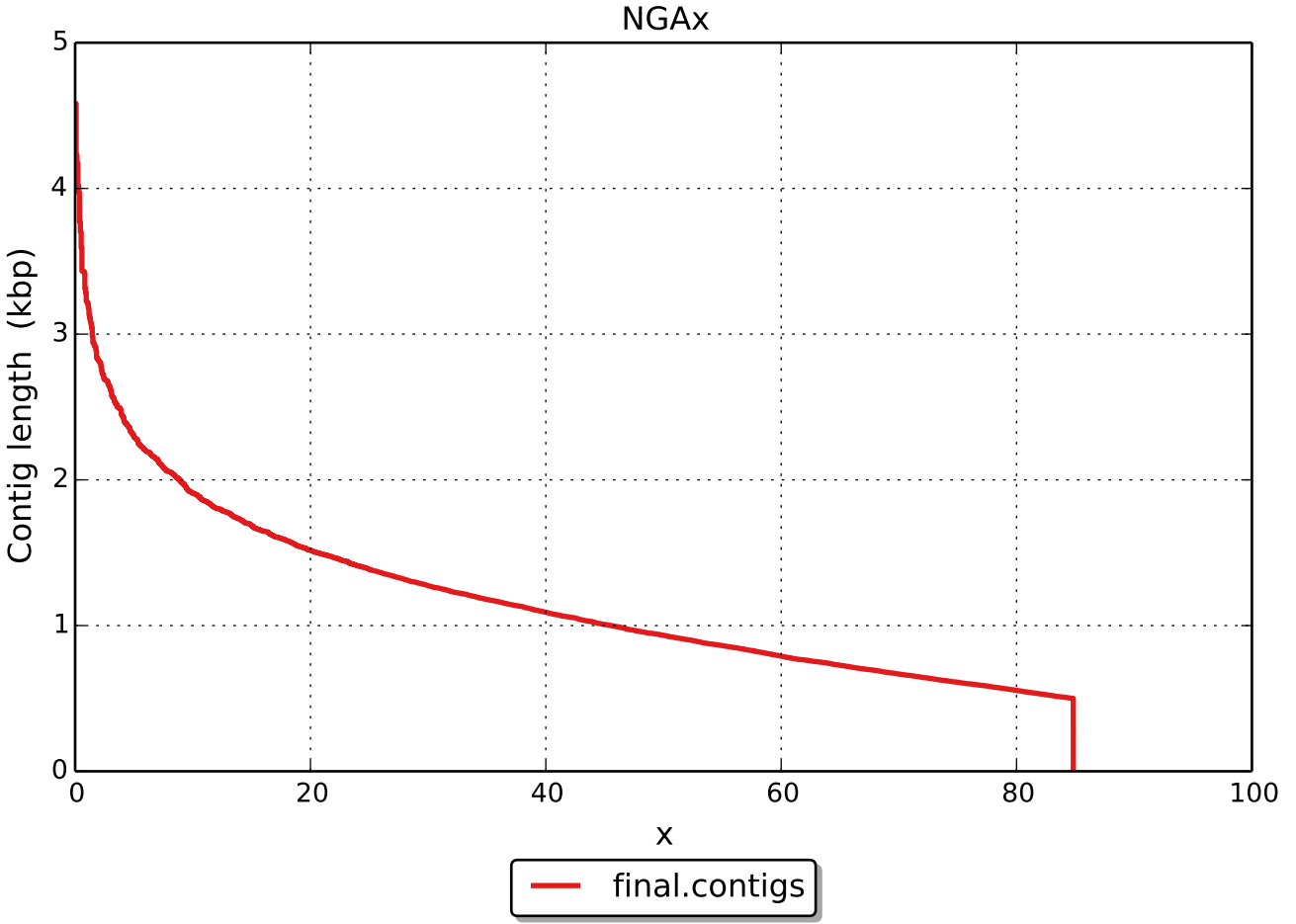

Nx
Contig length (kbp)
0
1
2
3
4
5
0
20
40
60
80
100
x
final.contigs


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
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