Report

	final.contigs
# contigs (>= 0 bp)	14318
# contigs (>= 1000 bp)	3227
Total length (>= 0 bp)	10818148
Total length (>= 1000 bp)	4752888
# contigs	9221
Largest contig	4277
Total length	8997543
Reference length	10957366
GC (%)	50.42
Reference GC (%)	50.49
N50	1036
NG50	899
N75	741
NG75	583
L50	2978
LG50	3993
L75	5551
LG75	7779
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	1784
# local misassemblies	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	81.982
Duplication ratio	1.059
# N's per 100 kbp	0.00
# mismatches per 100 kbp	137.63
# indels per 100 kbp	0.10
Largest alignment	4277
NA50	1036
NGA50	899
NA75	741
NGA75	583
LA50	2978
LGA50	3993
LA75	5551
LGA75	7779

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

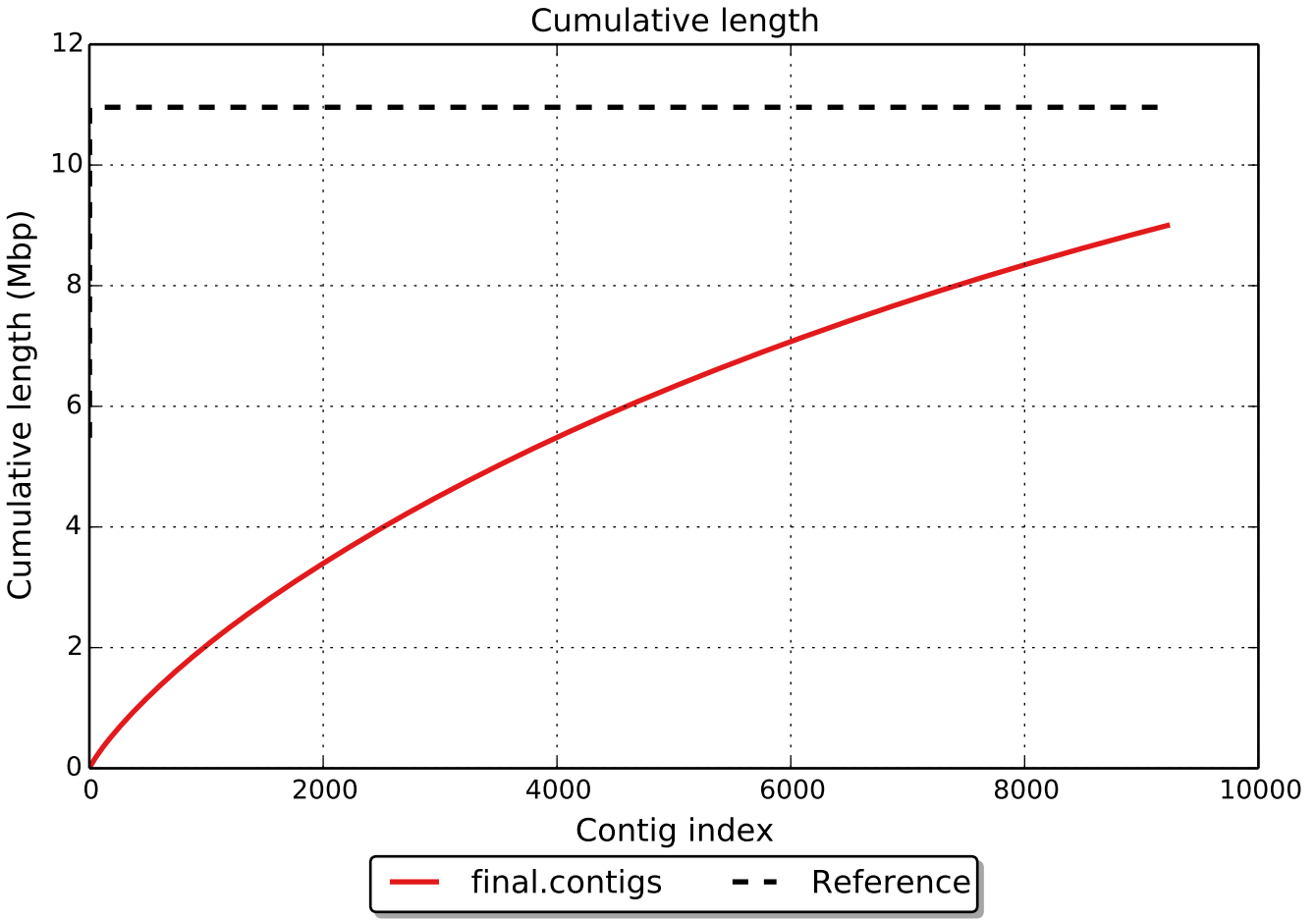
	final.contigs
# misassemblies	1
# relocations	1
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	1
Misassembled contigs length	1784
# local misassemblies	0
# mismatches	12363
# indels	9
# short indels	5
# long indels	4
Indels length	56

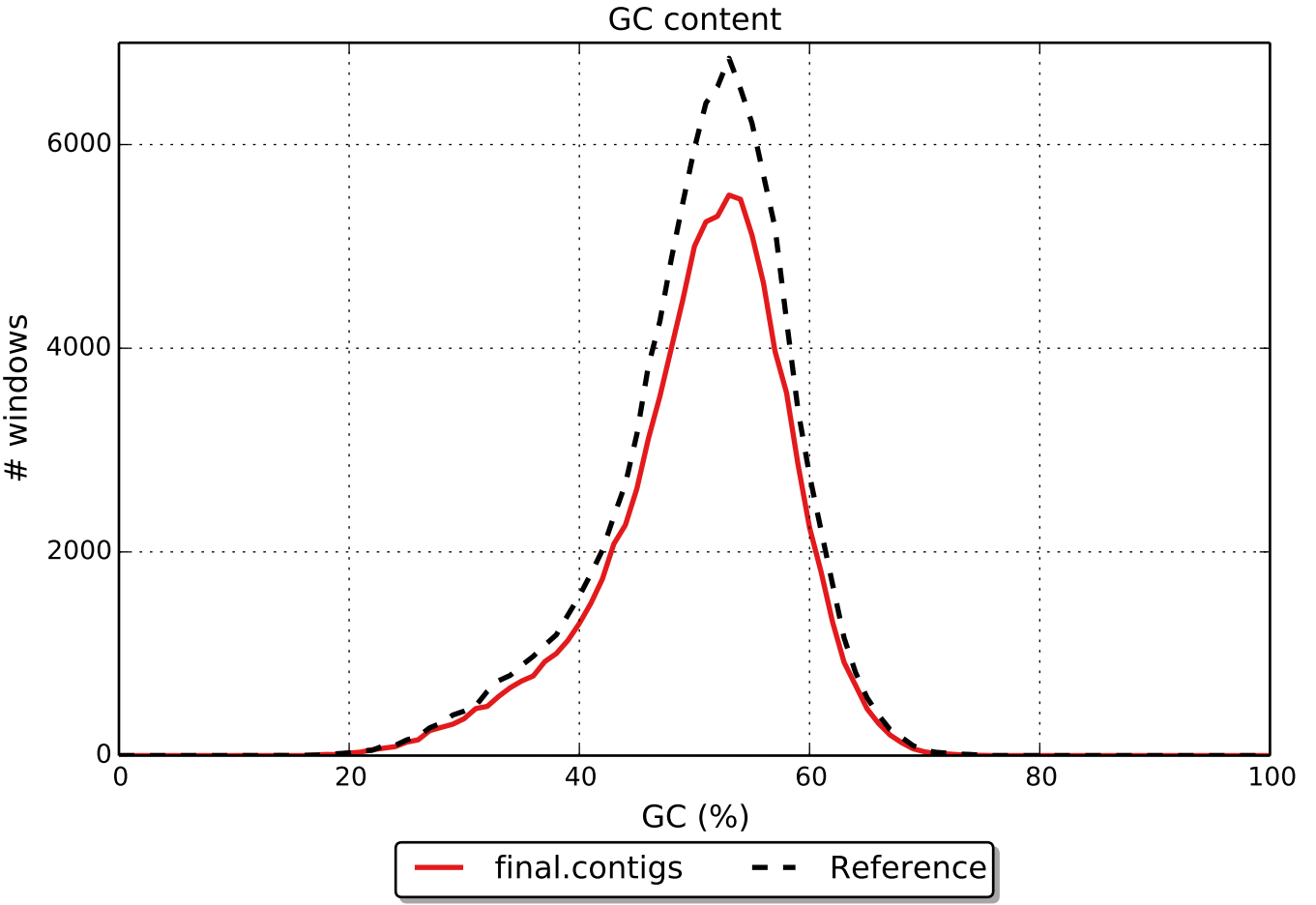
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

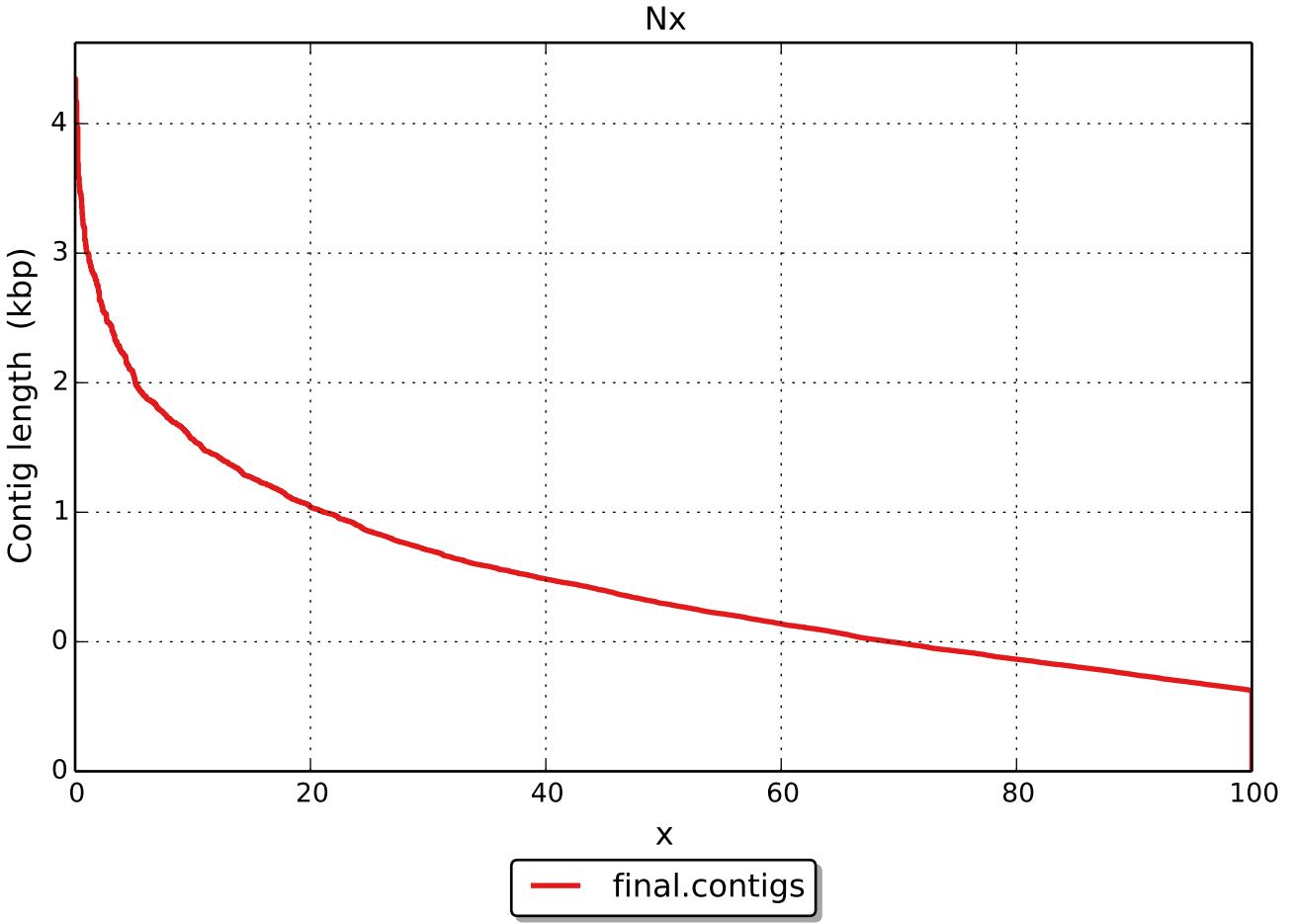
Unaligned report

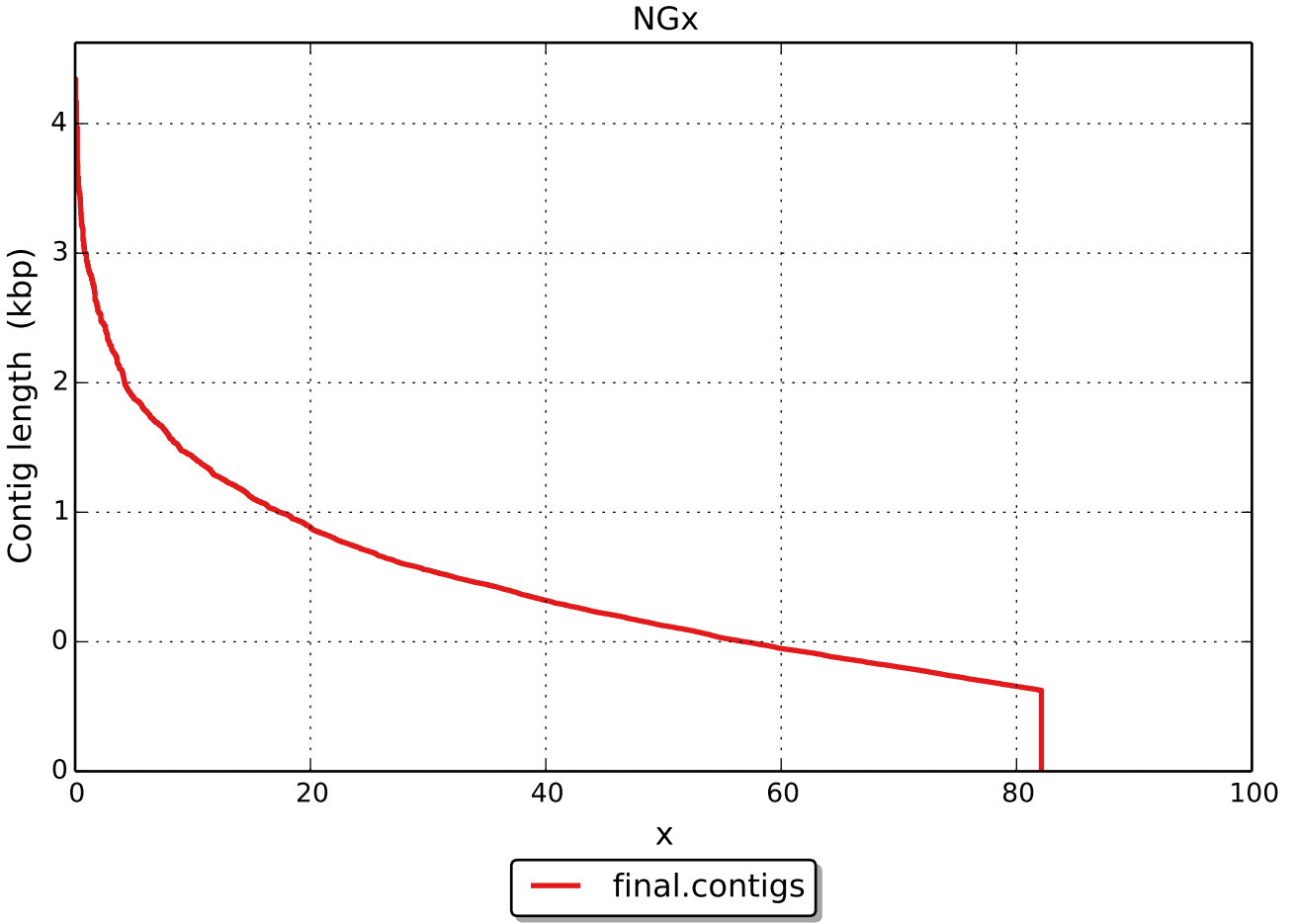
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
# with misassembly	0
# both parts are significant	0
Partially unaligned length	0
# N's	0

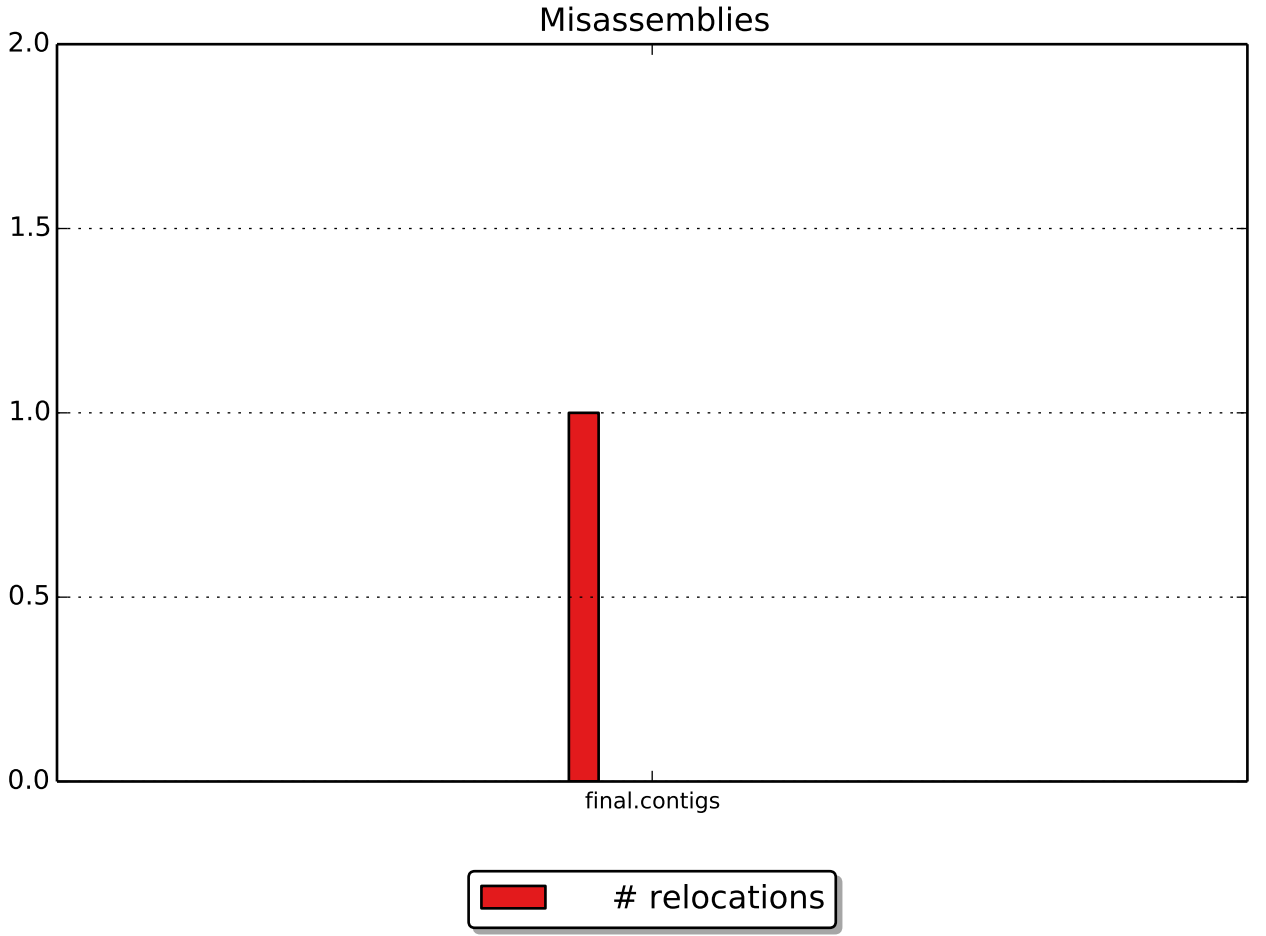
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

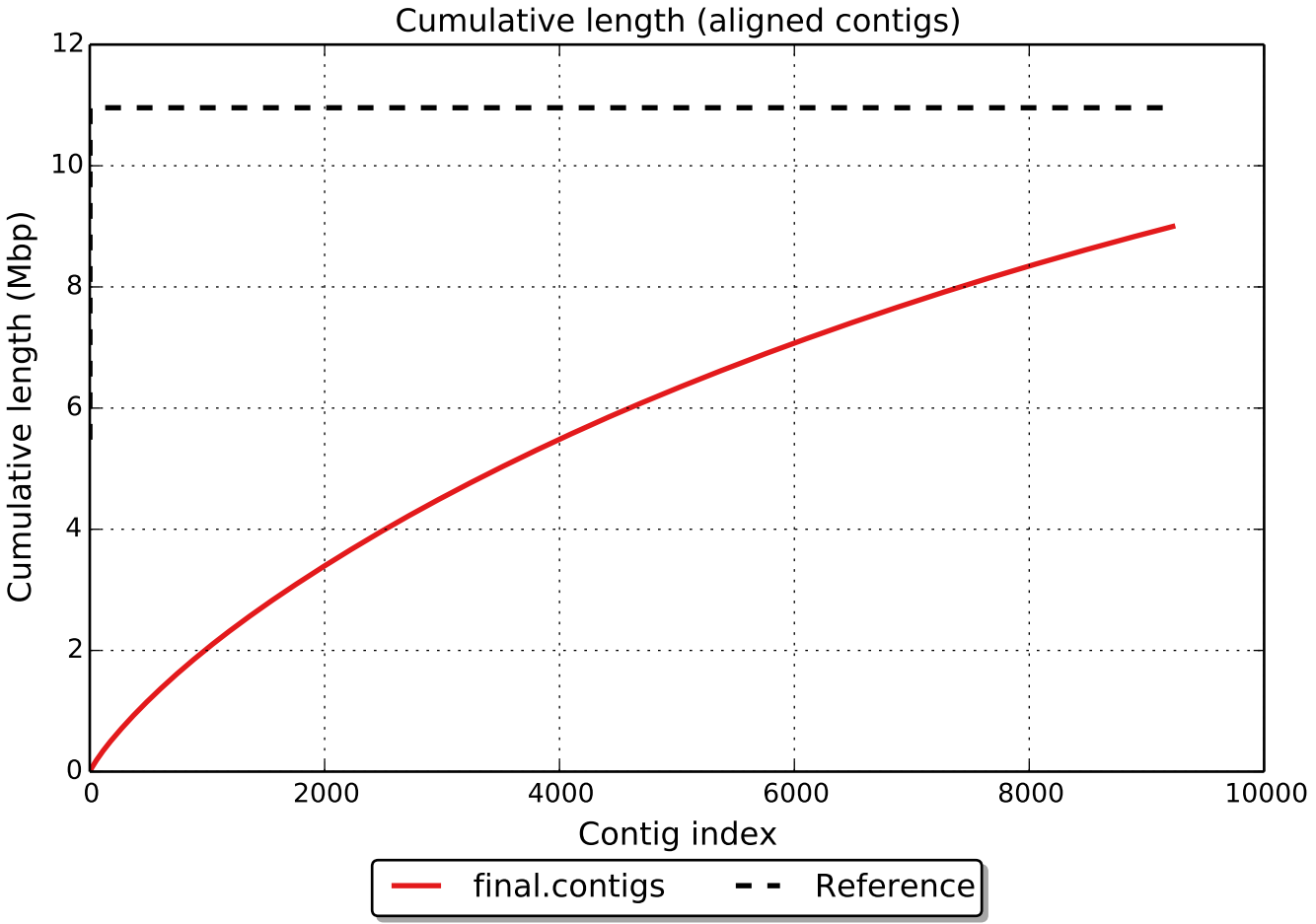

Cumulative length
Cumulative length (Mbp)
Contig index
0
2
4
6
8
10
12
0
2000
4000
6000
8000
10000
final.contigs
Reference

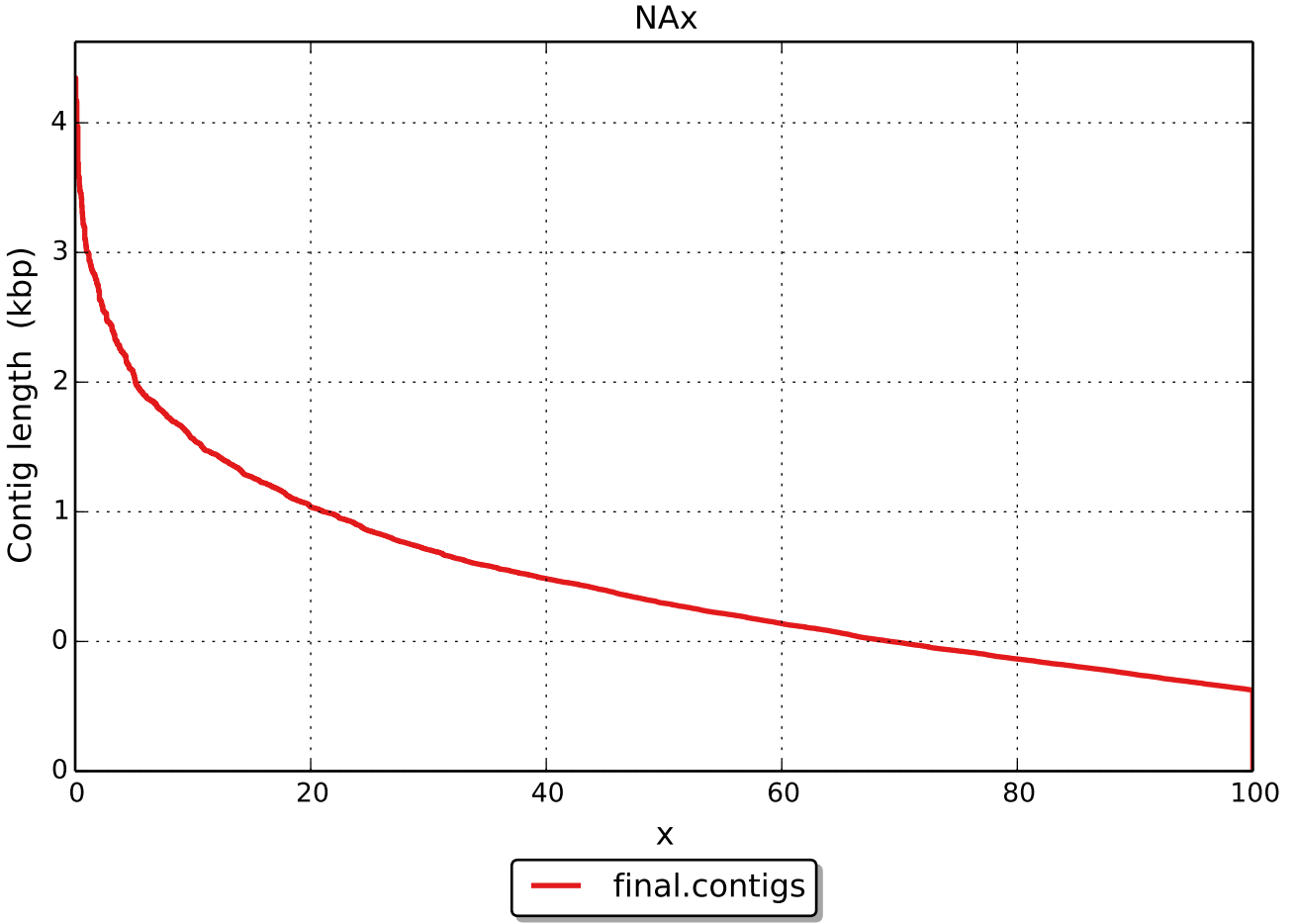

GC content
windows
6000
4000
2000
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

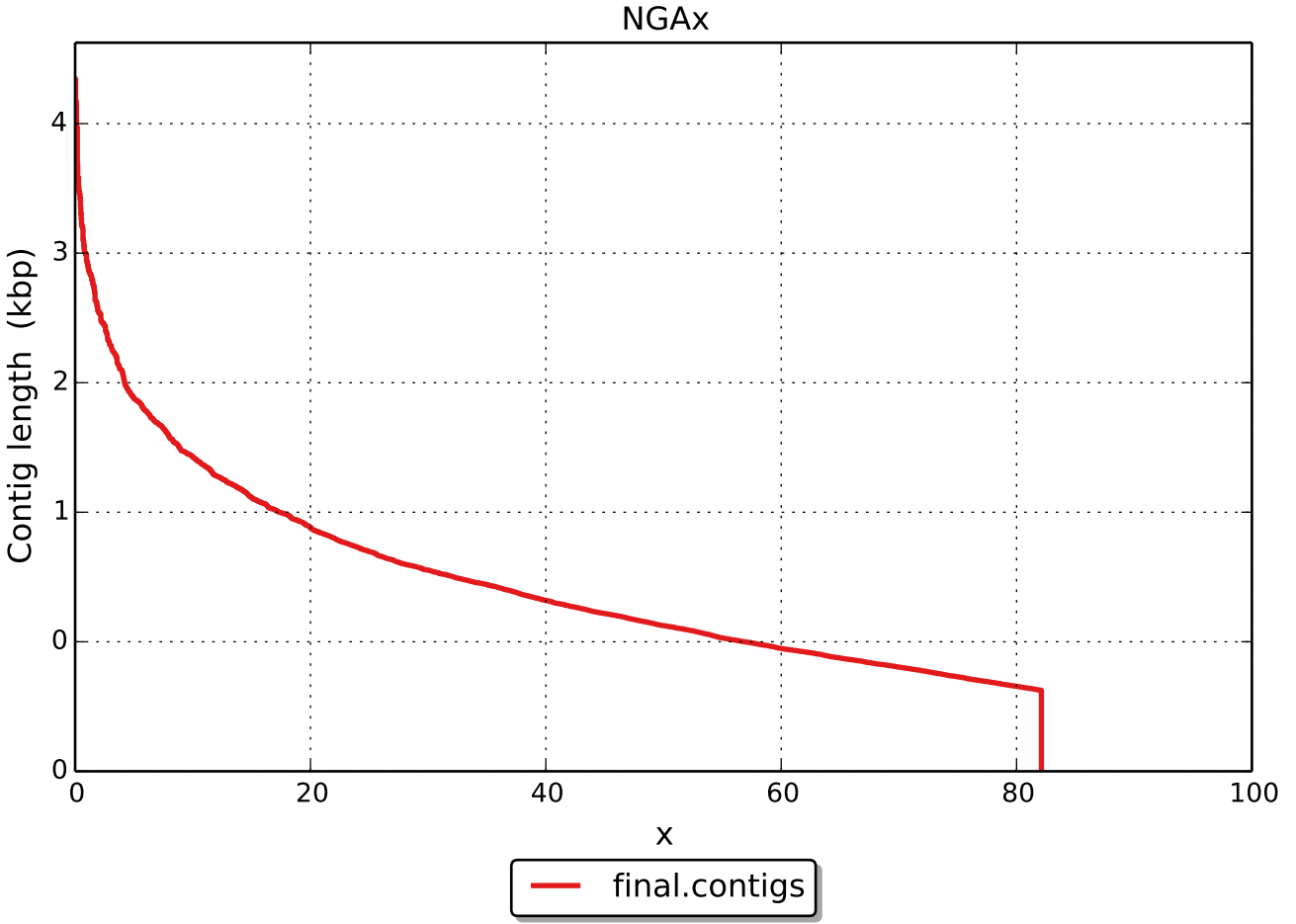

Nx
Contig length (kbp)
0
1
2
3
4
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
4
3
2
1
0
0
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
2
4
6
8
10
12
0
2000
4000
6000
8000
10000
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