Report

	final.contigs
# contigs (>= 0 bp)	12752
# contigs (>= 1000 bp)	3860
Total length (>= 0 bp)	11170344
Total length (>= 1000 bp)	6267536
# contigs	8711
Largest contig	5549
Total length	9747978
Reference length	11094646
GC (%)	50.37
Reference GC (%)	50.48
N50	1239
NG50	1119
N75	843
NG75	697
L50	2606
LG50	3179
L75	4997
LG75	6317
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned contigs	0 + 1 part
Unaligned length	135
Genome fraction (%)	85.914
Duplication ratio	1.053
# N's per 100 kbp	0.00
# mismatches per 100 kbp	89.61
# indels per 100 kbp	0.08
Largest alignment	5549
NA50	1239
NGA50	1119
NA75	843
NGA75	697
LA50	2606
LGA50	3179
LA75	4998
LGA75	6317

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

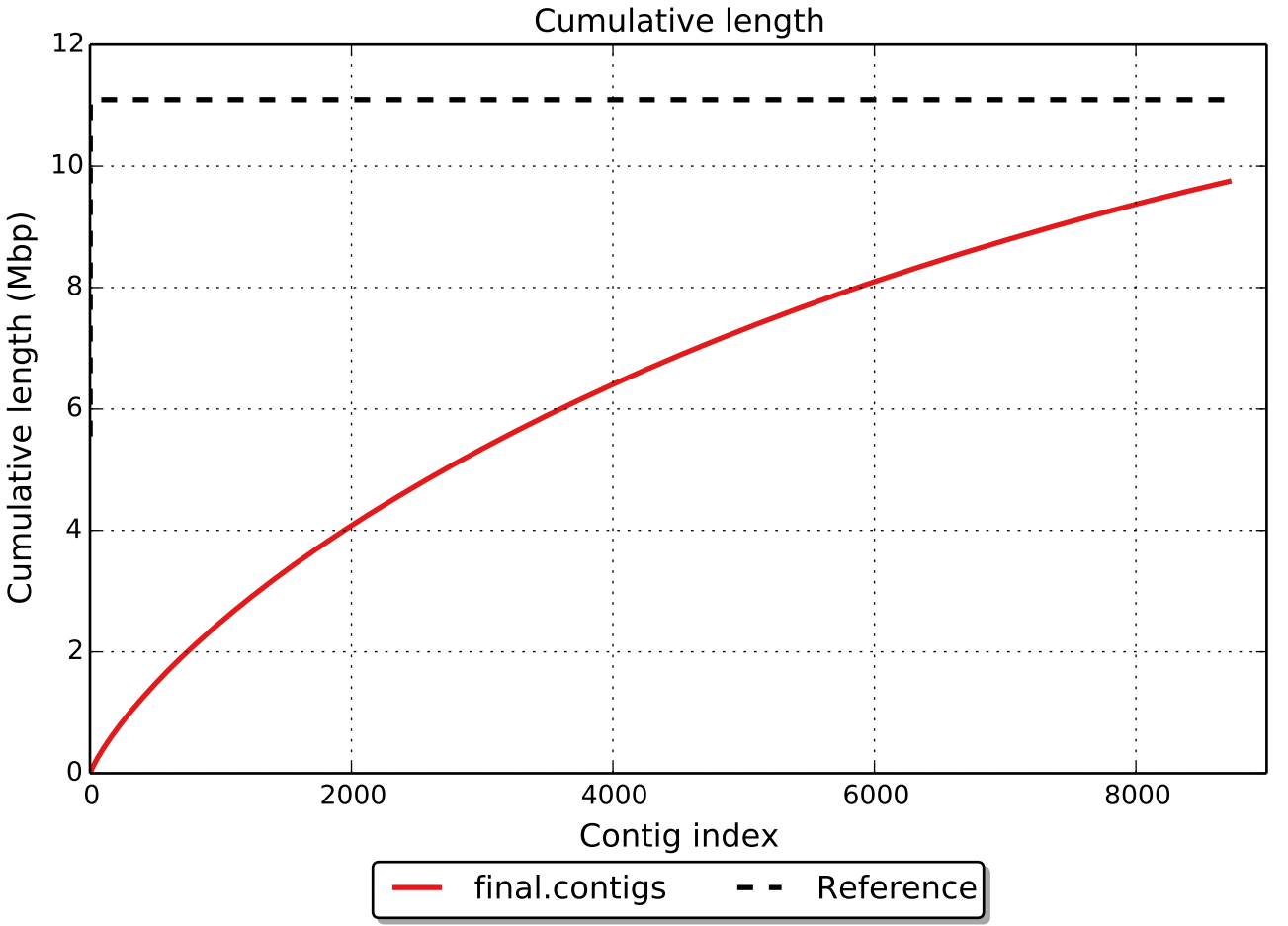
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# possibly misassembled contigs	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# mismatches	8541
# indels	8
# short indels	7
# long indels	1
Indels length	13

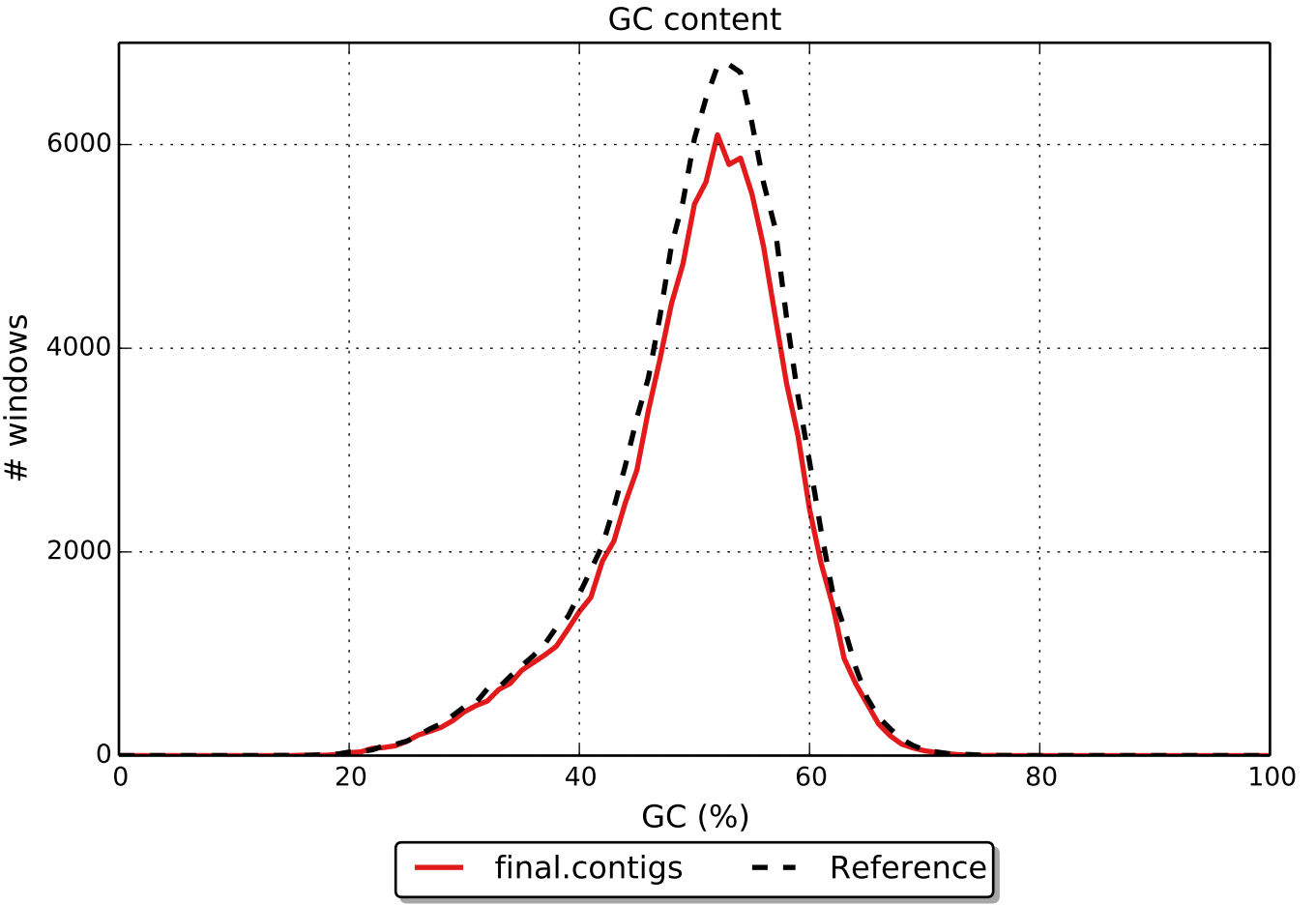
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

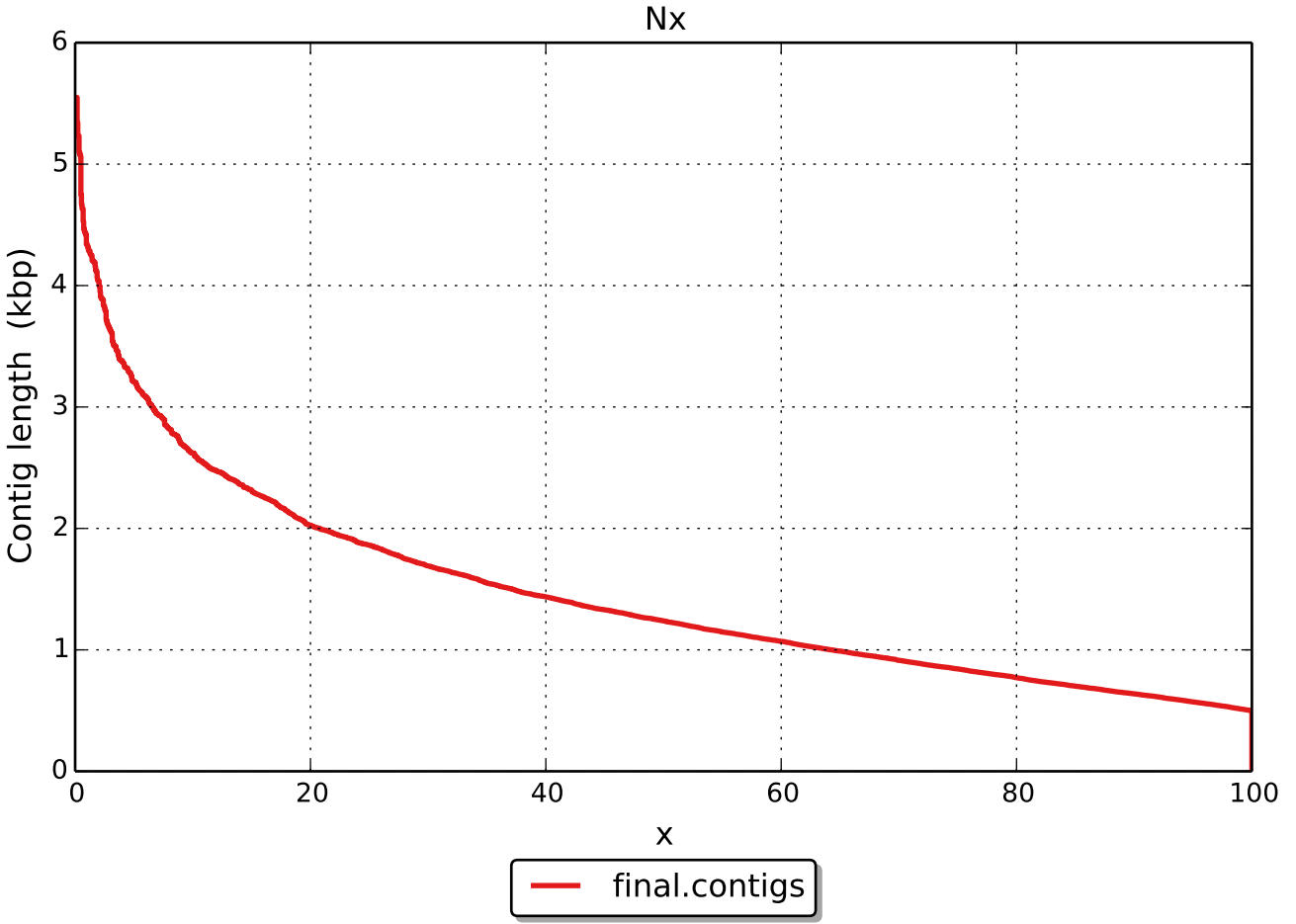
Unaligned report

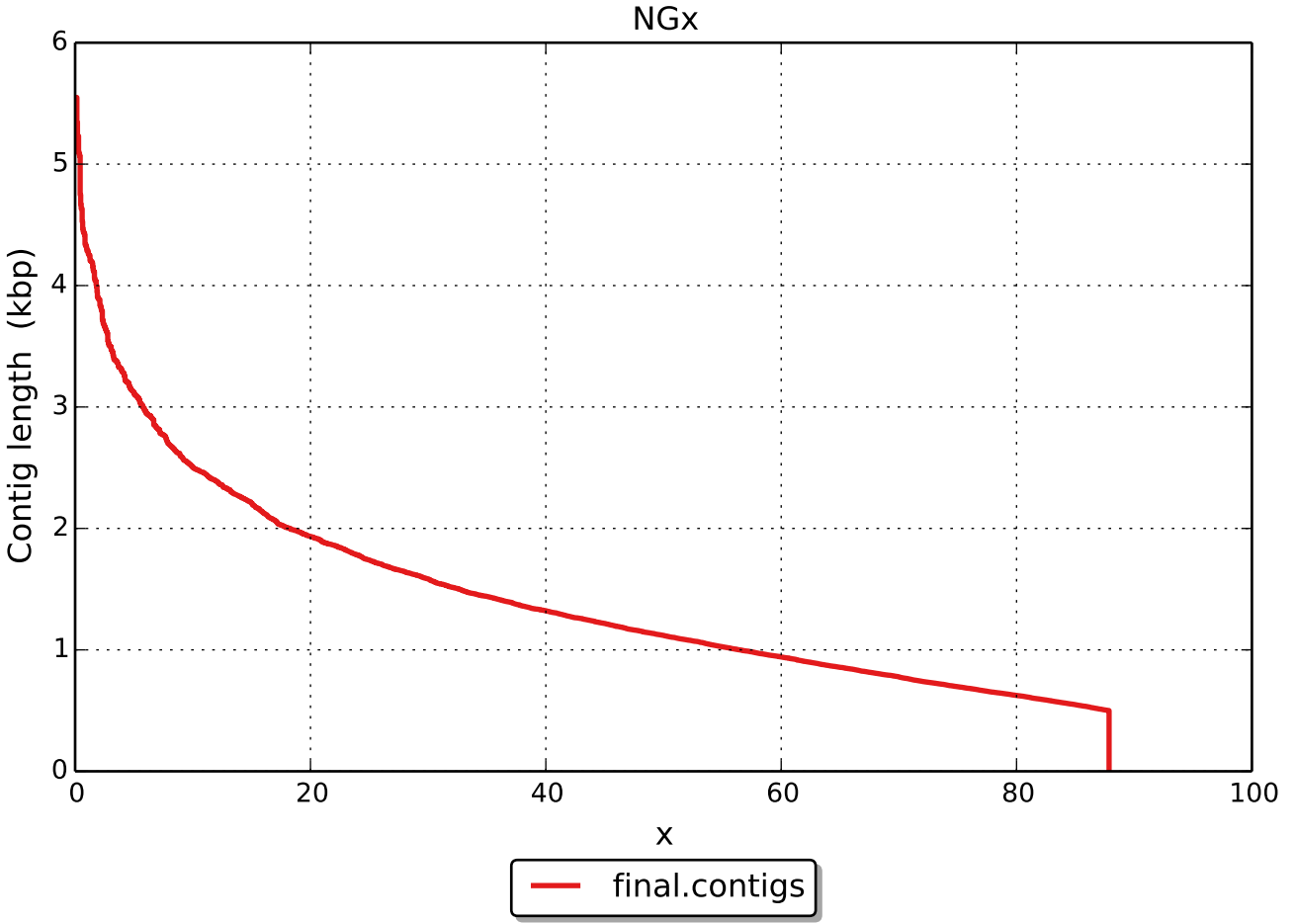
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
# with misassembly	0
# both parts are significant	0
Partially unaligned length	135
# N's	0

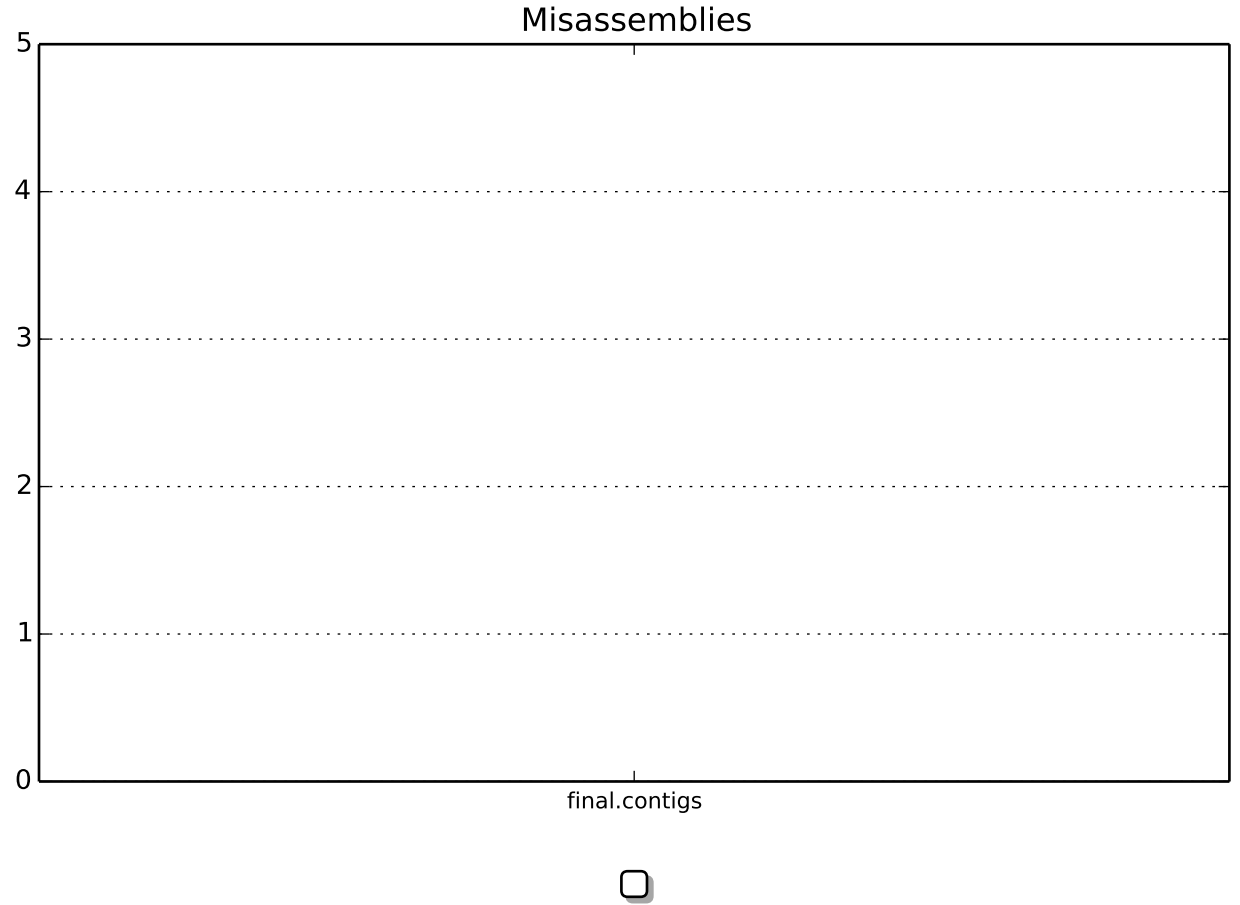
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

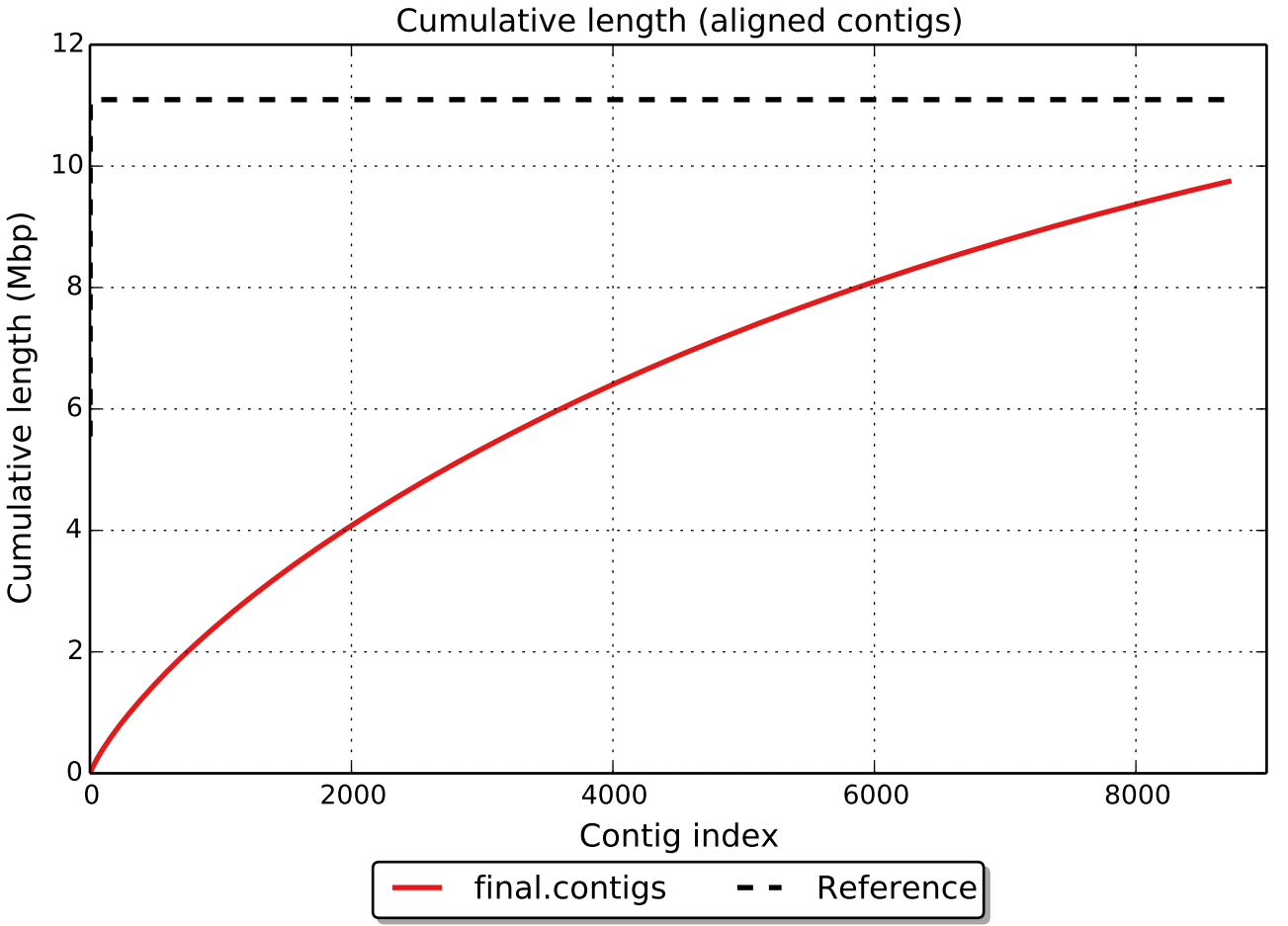

Cumulative length
Cumulative length (Mbp)
0
2
4
6
8
10
12
0
2000
4000
6000
8000
Contig index
final.contigs
Reference

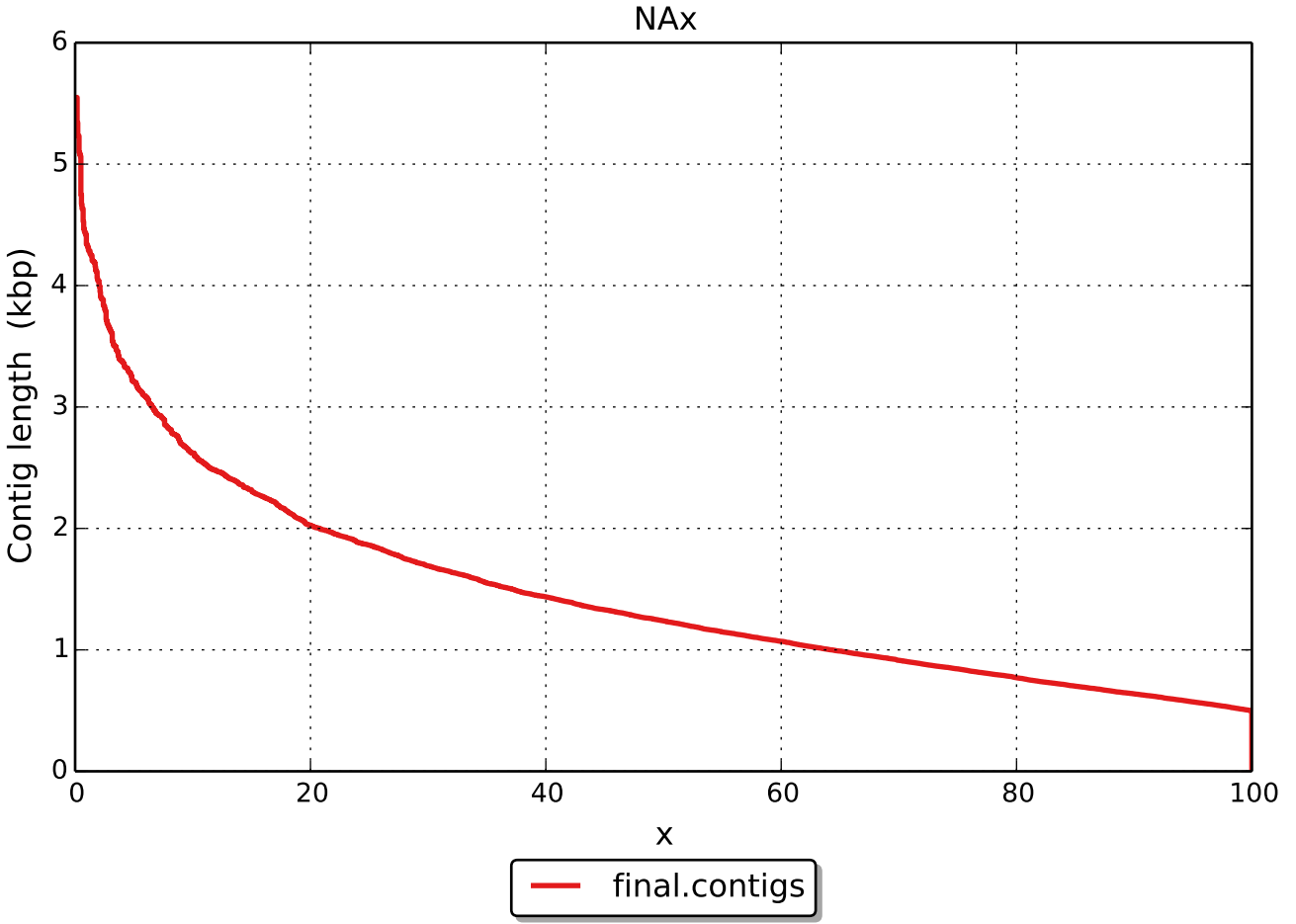

GC content
windows
6000
4000
2000
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

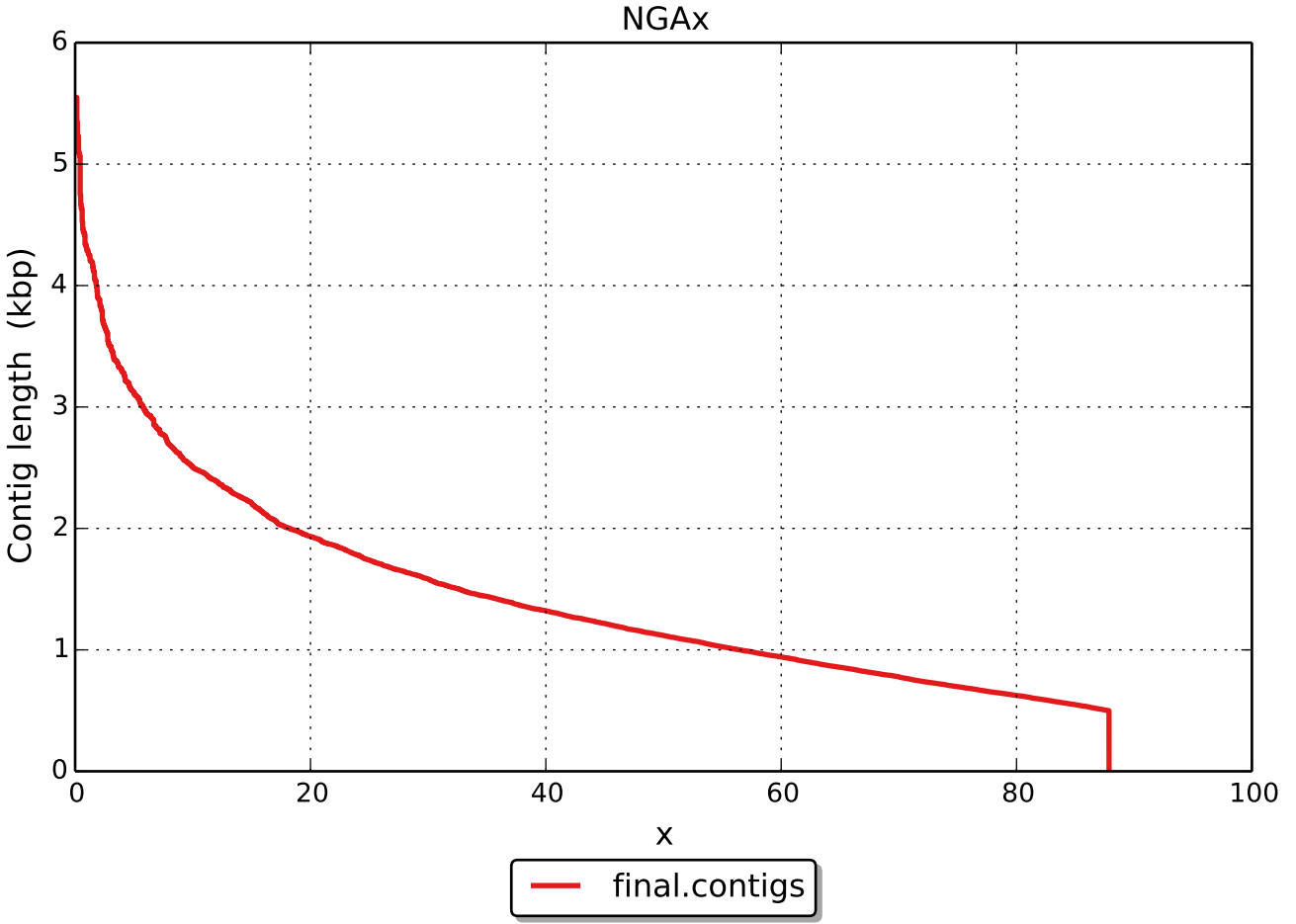

Nx
Contig length (kbp)
0
1
2
3
4
5
6
0
20
40
60
80
100
x
final.contigs


NGx
Contig length (kbp)
0
1
2
3
4
5
6
0
20
40
60
80
100
x
final.contigs


Misassemblies
5
4
3
2
1
0
final.contigs


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


NAx
Contig length (kbp)
0
1
2
3
4
5
6
0
20
40
60
80
100
x
final.contigs


NGAx
Contig length (kbp)
0
1
2
3
4
5
6
0
20
40
60
80
100
x
final.contigs