Report

	final.contigs
# contigs (>= 1000 bp)	7
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	31799
Total length (>= 5000 bp)	23126
Total length (>= 10000 bp)	16005
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	19
Largest contig	16005
Total length	39881
Reference length	5846582
GC (%)	51.41
Reference GC (%)	46.79
N50	7121
N75	1214
L50	2
L75	6
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# unaligned contigs	4 + 8 part
Unaligned length	33562
Genome fraction (%)	0.042
Duplication ratio	2.558
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4574.90
# indels per 100 kbp	0.00
Largest alignment	608
Total aligned length	2969
NGA50	-

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

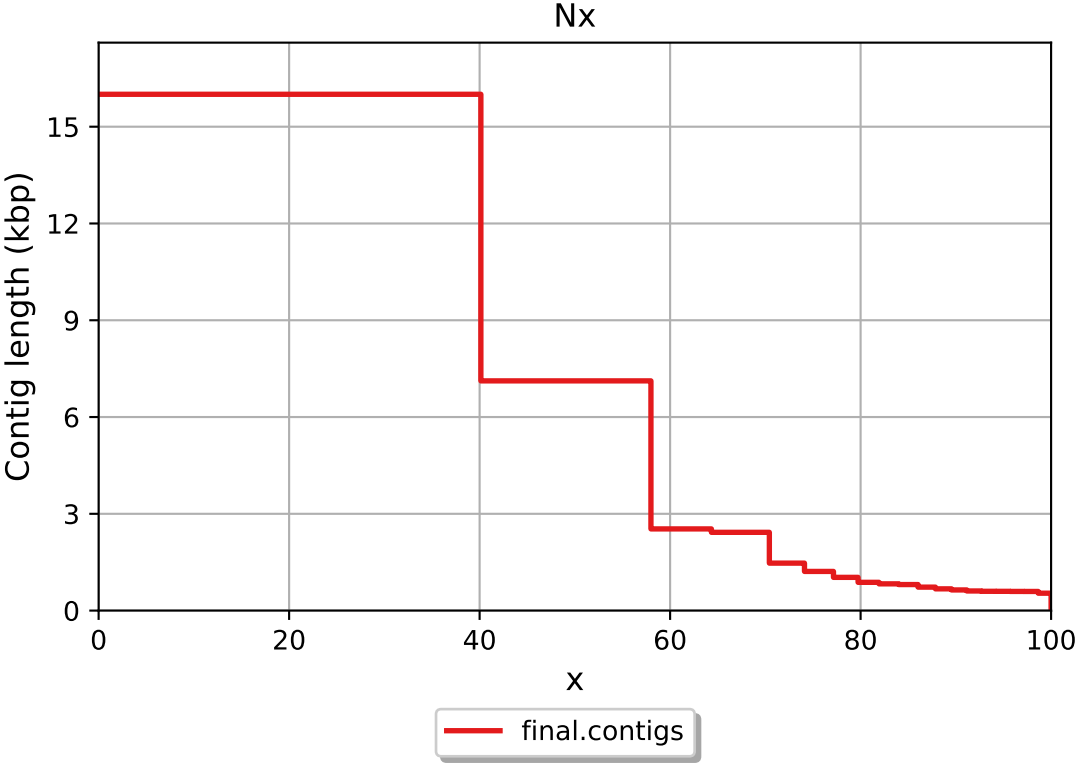
	final.contigs
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	6
# possible misassemblies	6
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	113
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

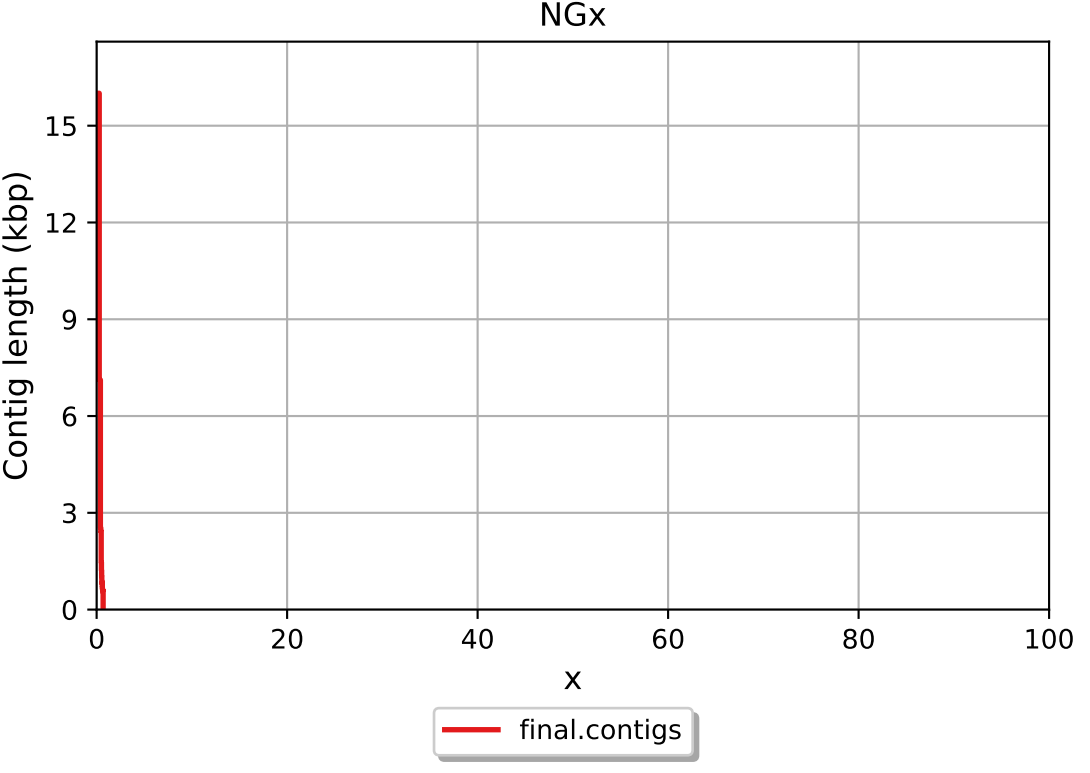
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

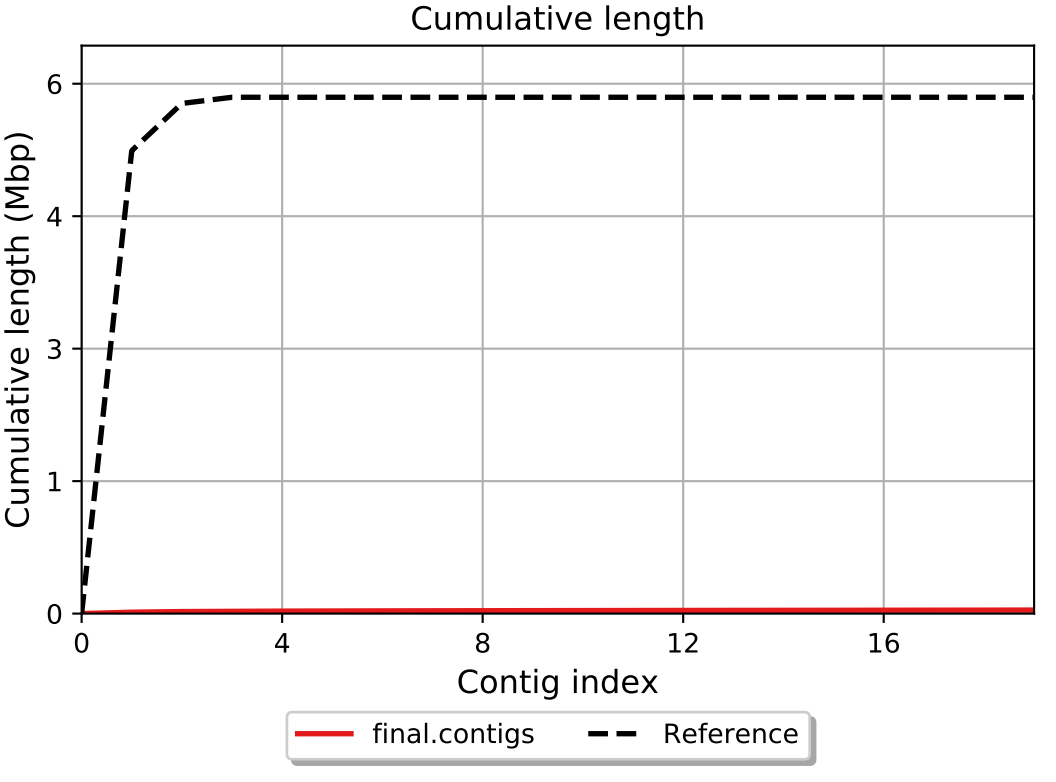
Unaligned report

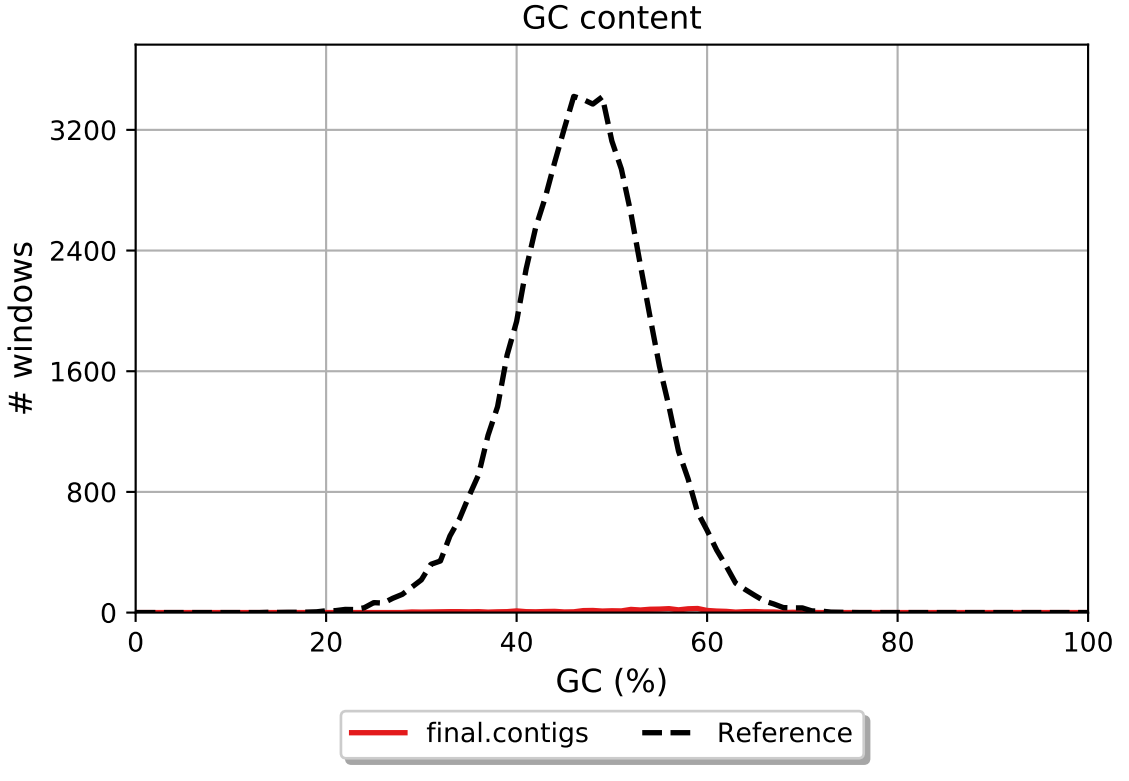
	final.contigs
# fully unaligned contigs	4
Fully unaligned length	2671
# partially unaligned contigs	8
Partially unaligned length	30891
# N's	0

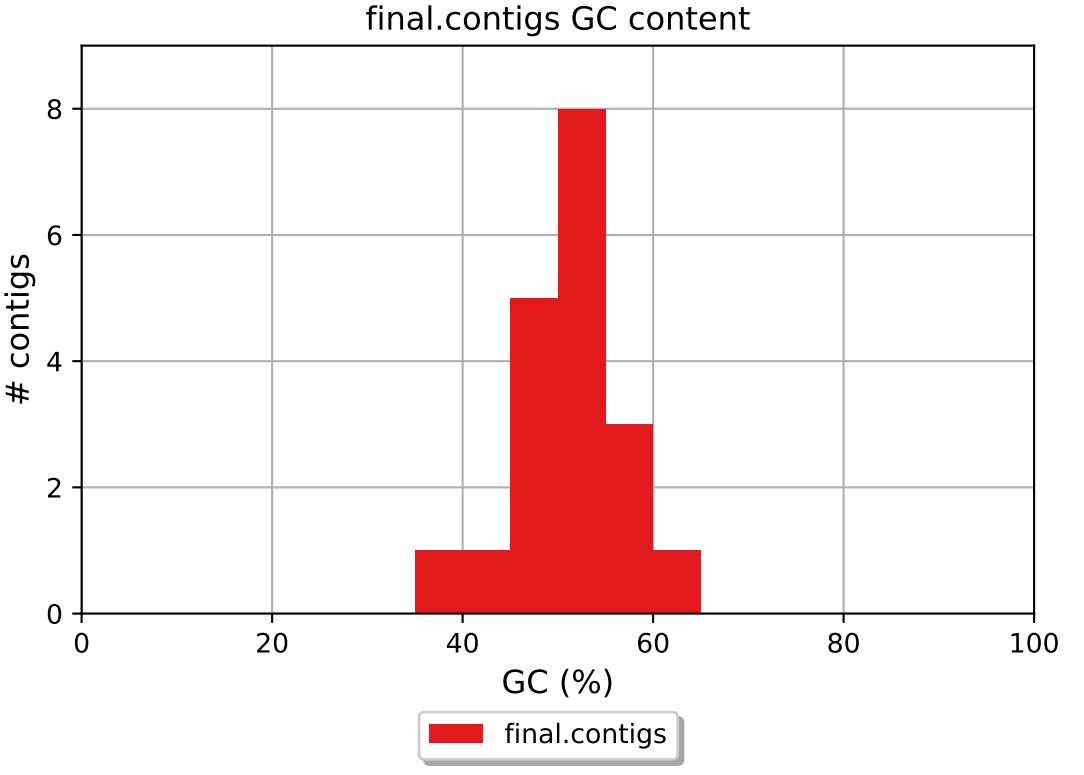
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

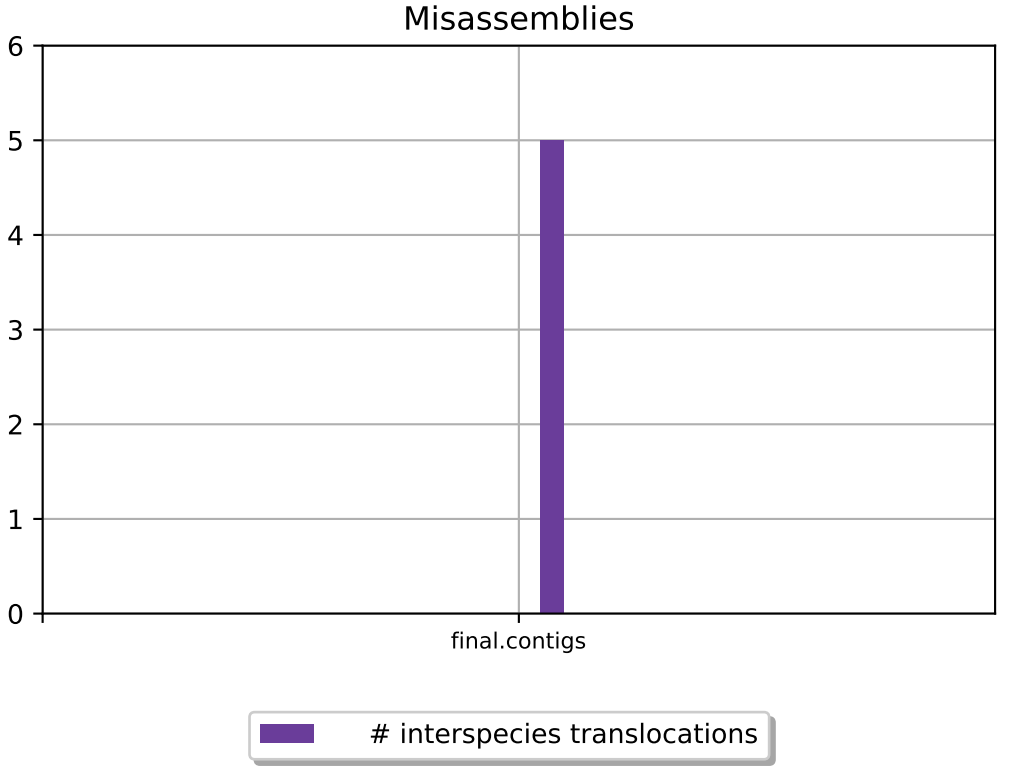

Nx
Contig length (kbp)
15
12
9
6
3
0
0
20
40
60
80
100
x
final.contigs

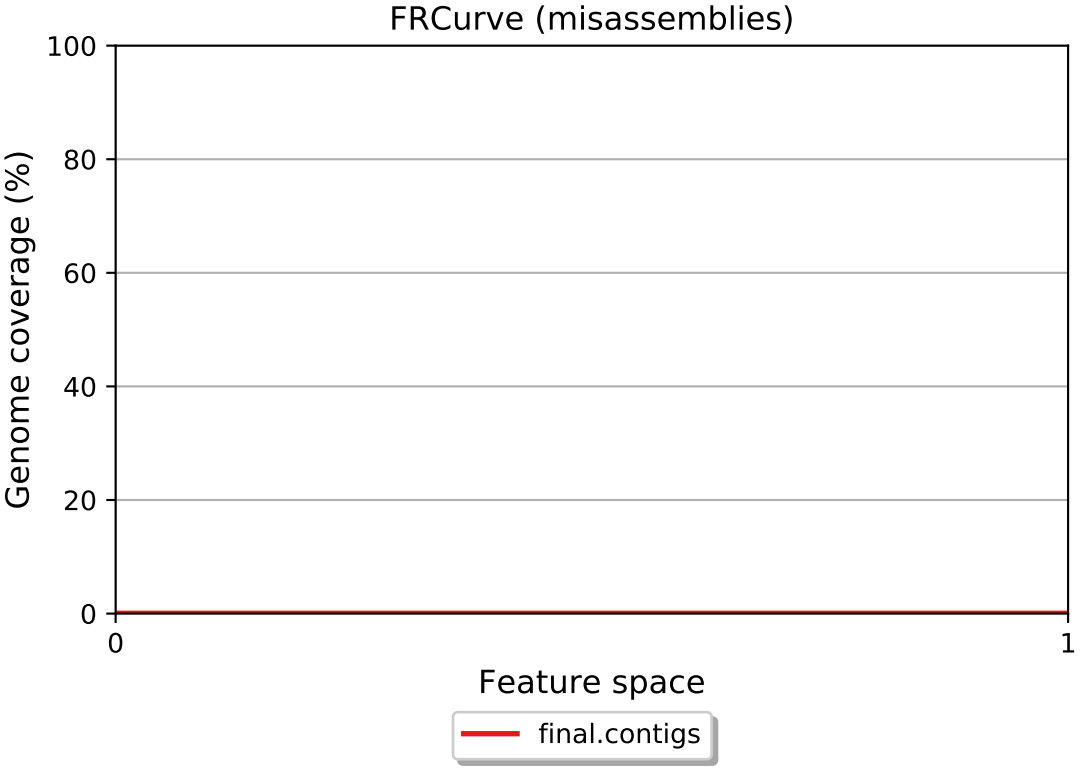

NGx
Contig length (kbp)
0
3
6
9
12
15
0
20
40
60
80
100
x
final.contigs

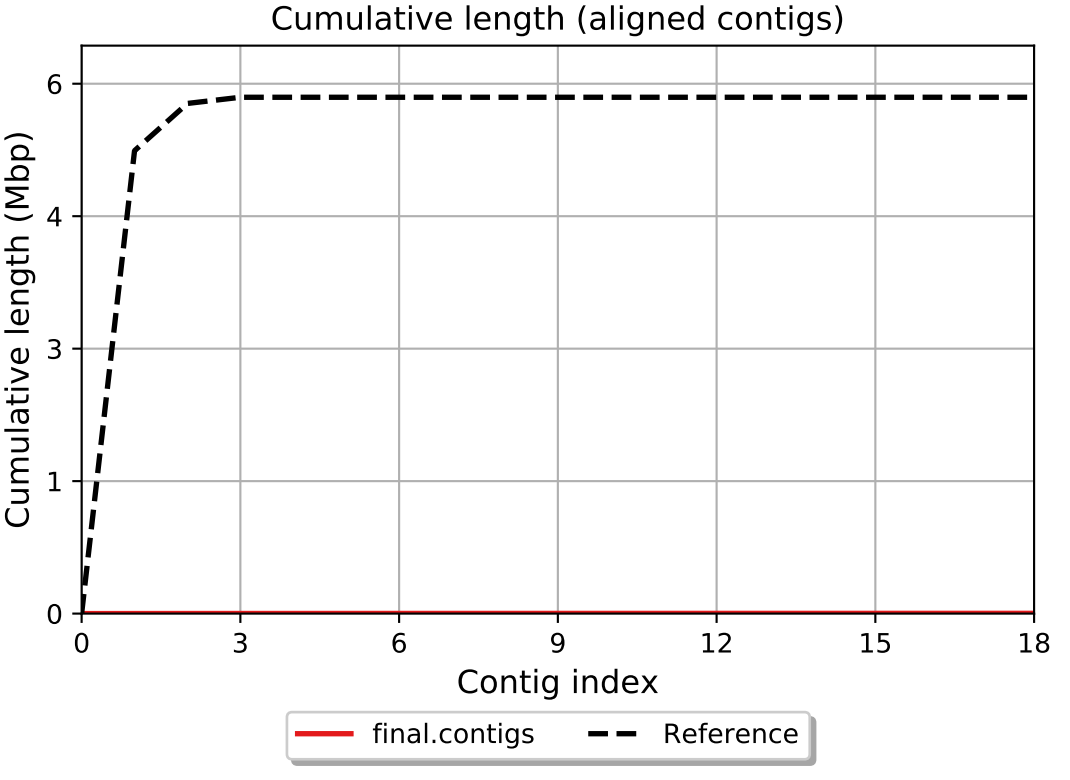

Cumulative length
Cumulative length (Mbp)
6
4
3
1
0
0
4
8
12
16
Contig index
final.contigs
Reference

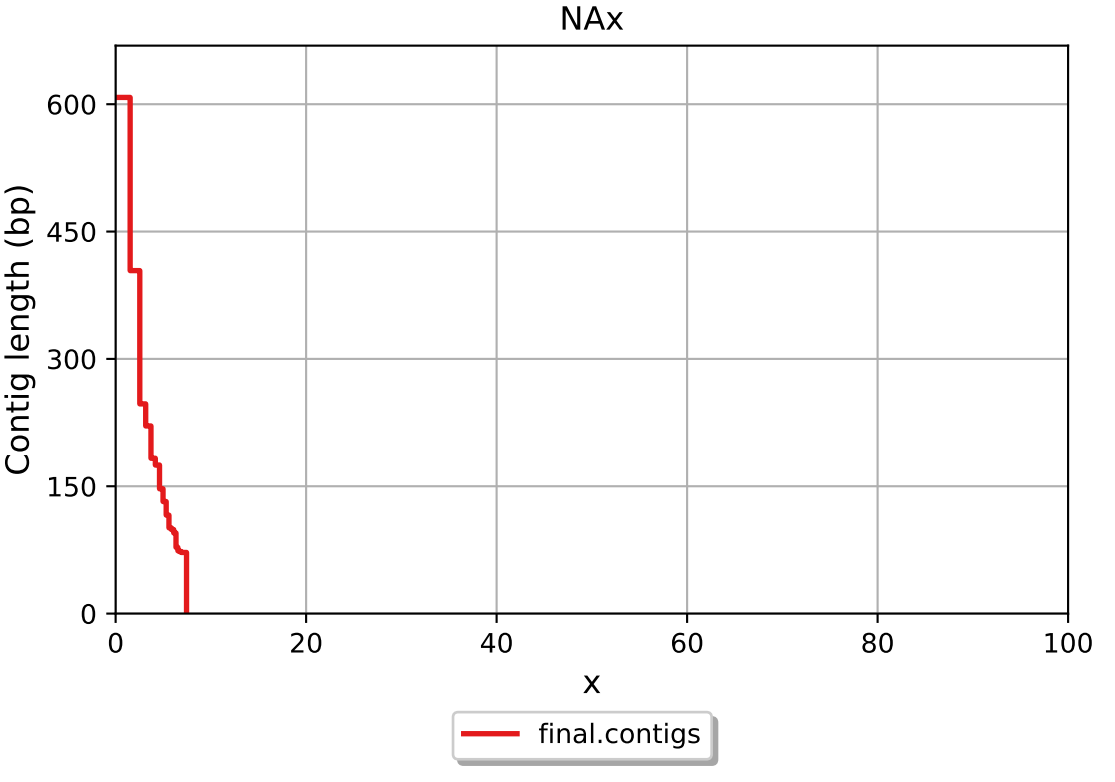

GC content
windows
3200
2400
1600
800
0
0
20
40
60
80
100
GC (%)
final.contigs
Reference

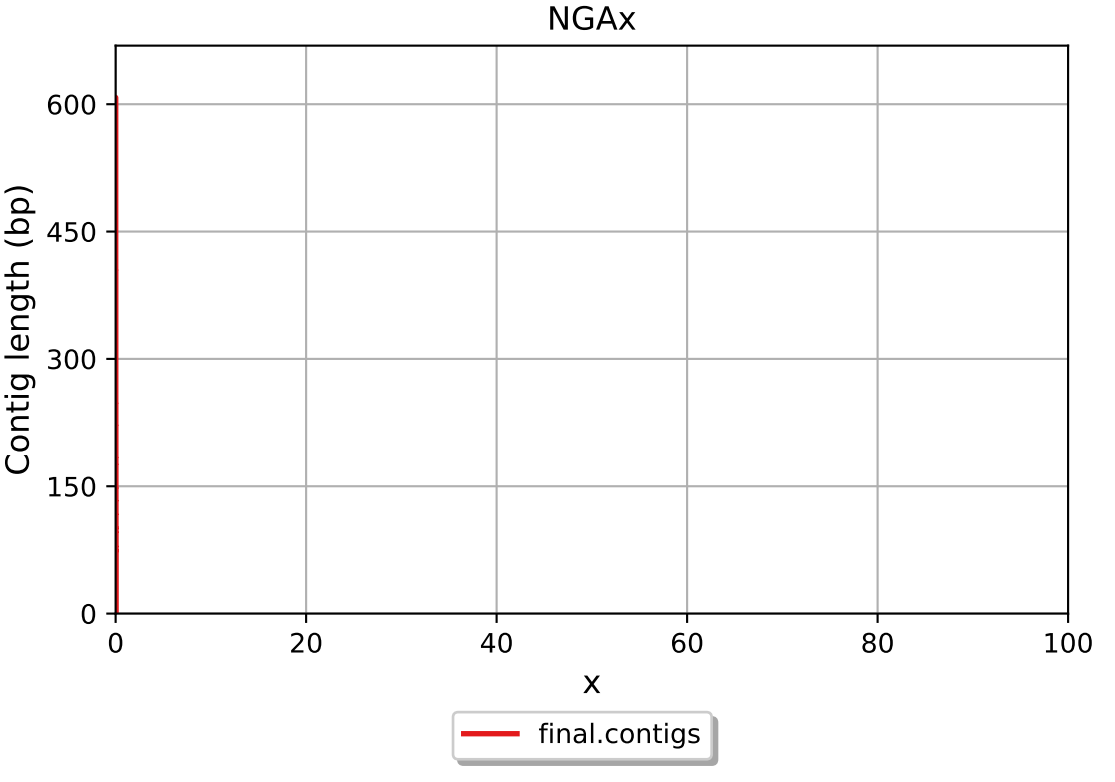

final.contigs GC content
contigs
0
2
4
6
8
0
20
40
60
80
100
GC (%)
final.contigs


Misassemblies
6
5
4
3
2
1
0
final.contigs
interspecies translocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
Feature space
final.contigs


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
3
4
6
0
3
6
9
12
15
18
Contig index
final.contigs
Reference


NAx
Contig length (bp)
600
450
300
150
0
0
20
40
60
80
100
x
final.contigs


NGAx
600
450
300
150
0
Contig length (bp)
0
20
40
60
80
100
x
final.contigs