Report

	ref
# contigs (>= 0 bp)	61
# contigs (>= 1000 bp)	61
# contigs (>= 5000 bp)	50
# contigs (>= 10000 bp)	46
# contigs (>= 25000 bp)	40
# contigs (>= 50000 bp)	36
Total length (>= 0 bp)	674918548
Total length (>= 1000 bp)	674918548
Total length (>= 5000 bp)	674891566
Total length (>= 10000 bp)	674858128
Total length (>= 25000 bp)	674758534
Total length (>= 50000 bp)	674623615
# contigs	338
Largest contig	152907495
Total length	2654621305
Reference length	2728222451
GC (%)	41.67
Reference GC (%)	41.67
N50	46334773
NG50	46334773
N75	21983050
NG75	21153448
L50	19
LG50	19
L75	39
LG75	41
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# possible TEs	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	100.000
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	152907495
Total aligned length	2654621305
NA50	46334773
NGA50	46334773
NA75	21983050
NGA75	21153448
LA50	19
LGA50	19
LA75	39
LGA75	41

All statistics are based on contigs of size >= 400 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

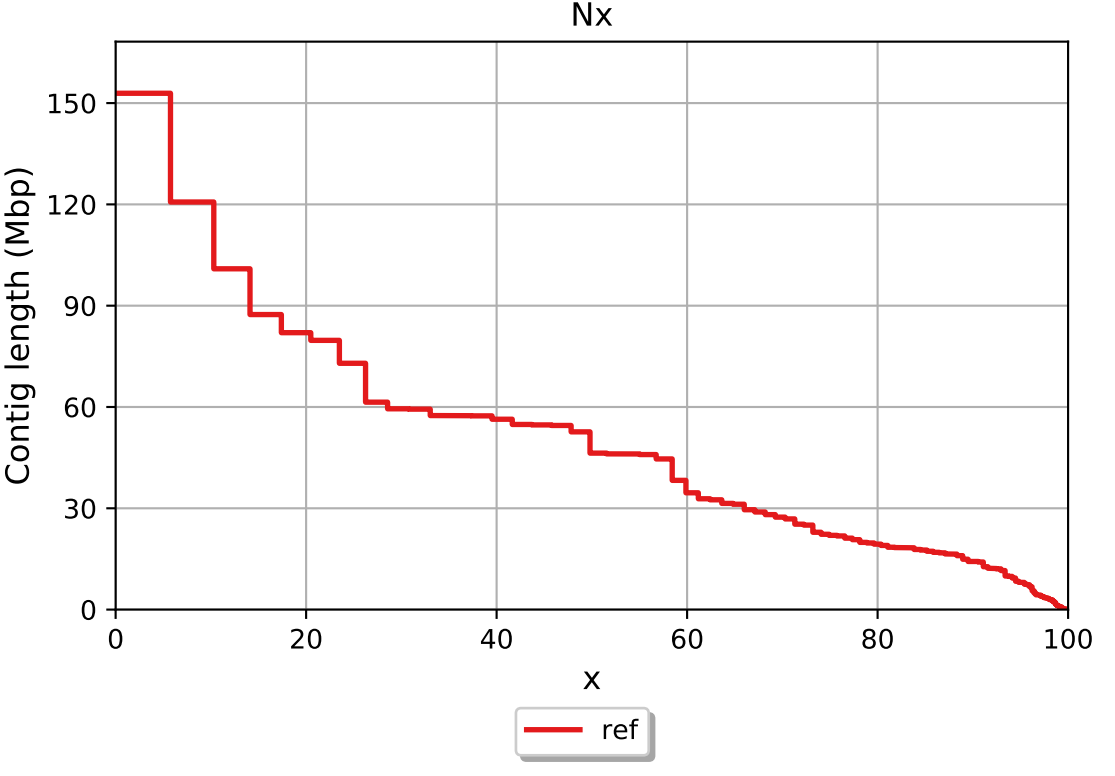
	ref
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# misassemblies caused by fragmented reference	0
# possible TEs	0
# unaligned mis. contigs	0
# mismatches	0
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

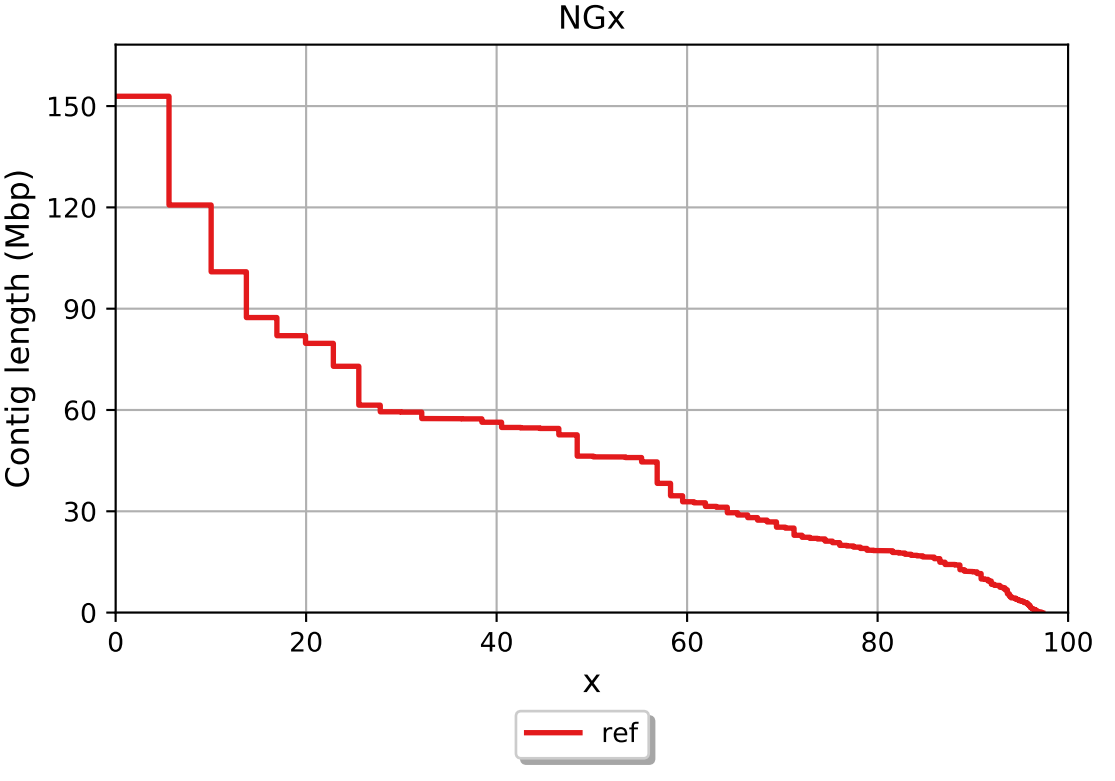
All statistics are based on contigs of size >= 400 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

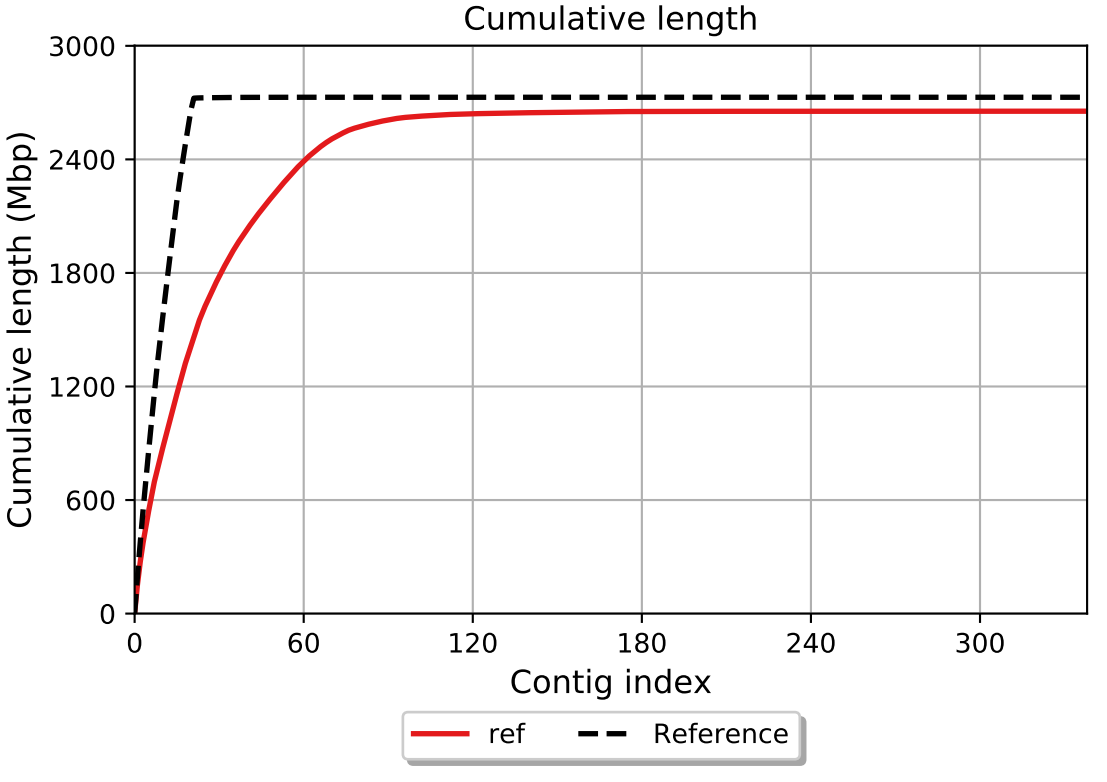
Unaligned report

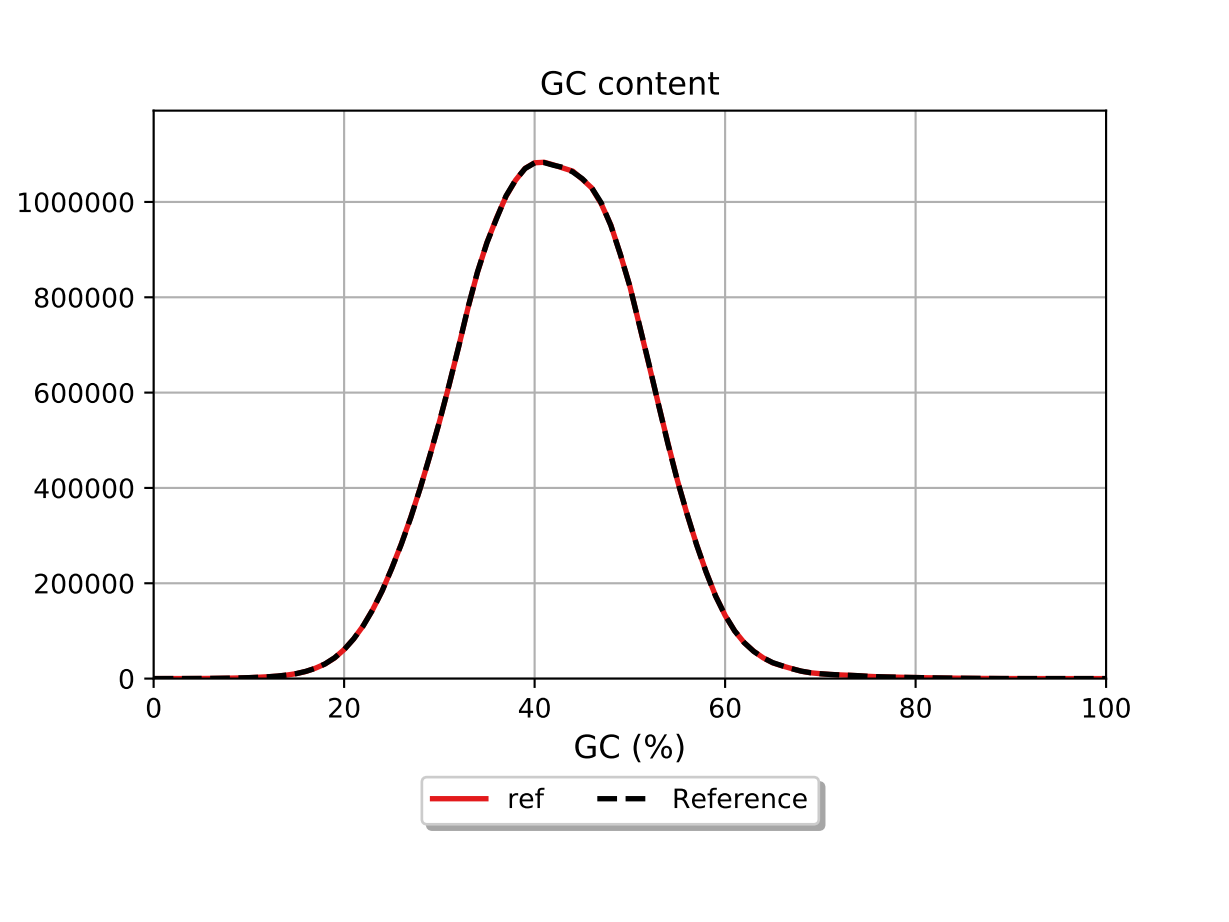
	ref
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

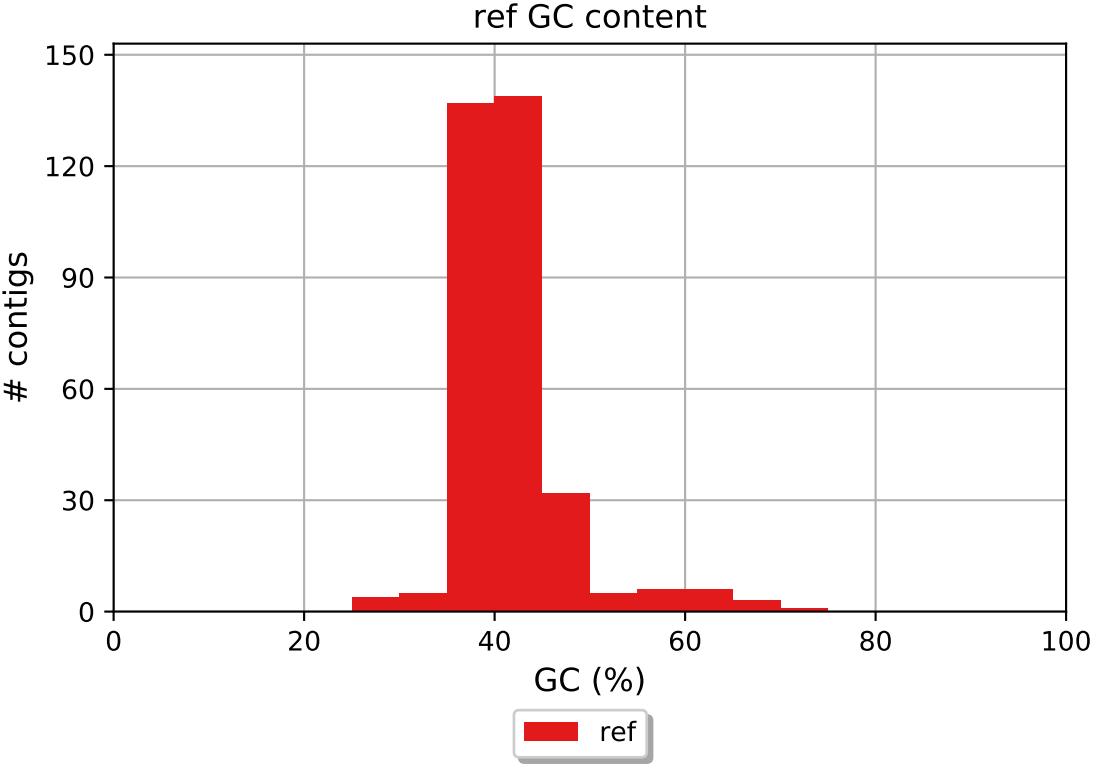
All statistics are based on contigs of size >= 400 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

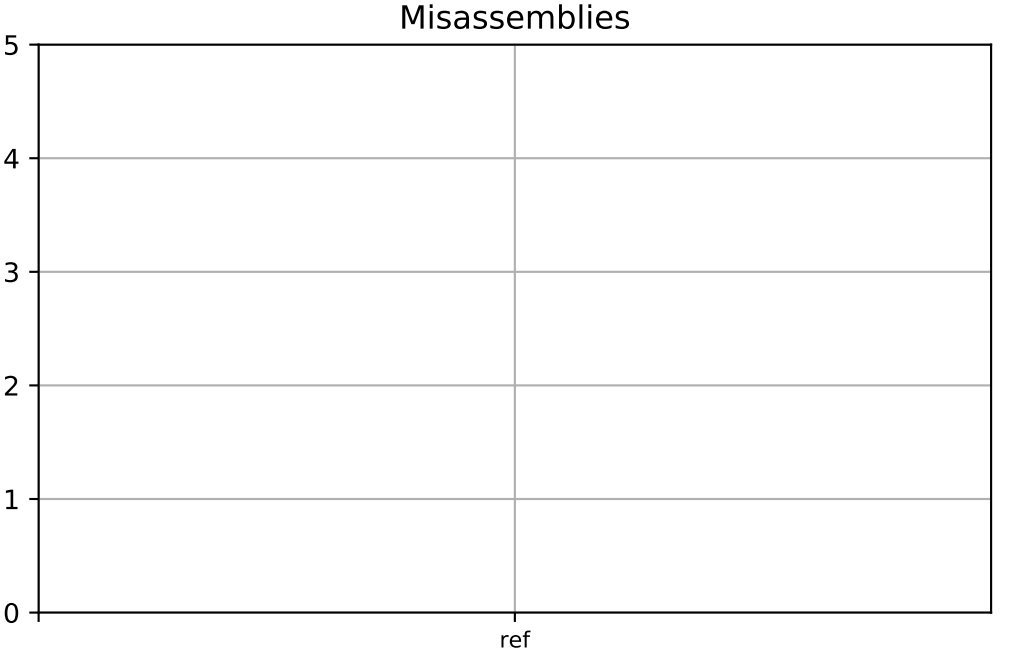

Nx
Contig length (Mbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
ref

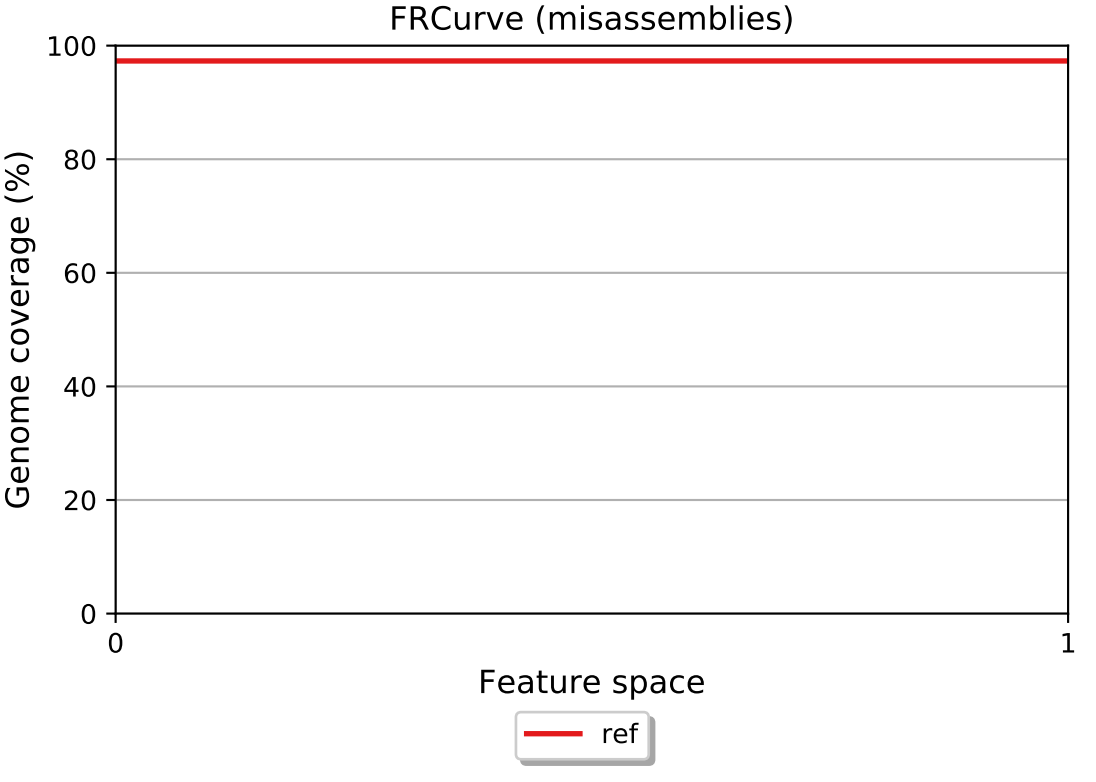

NGx
Contig length (Mbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
ref

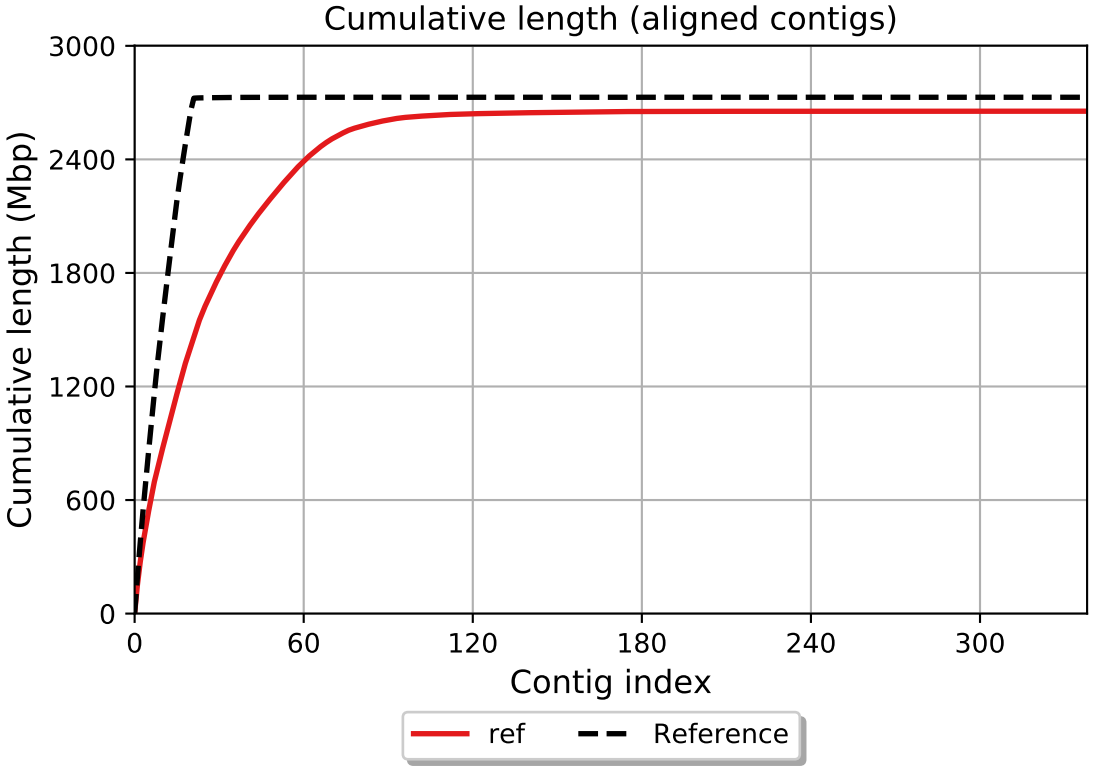

Cumulative length
Cumulative length (Mbp)
3000
2400
1800
1200
600
0
0
60
120
180
240
300
Contig index
ref
Reference

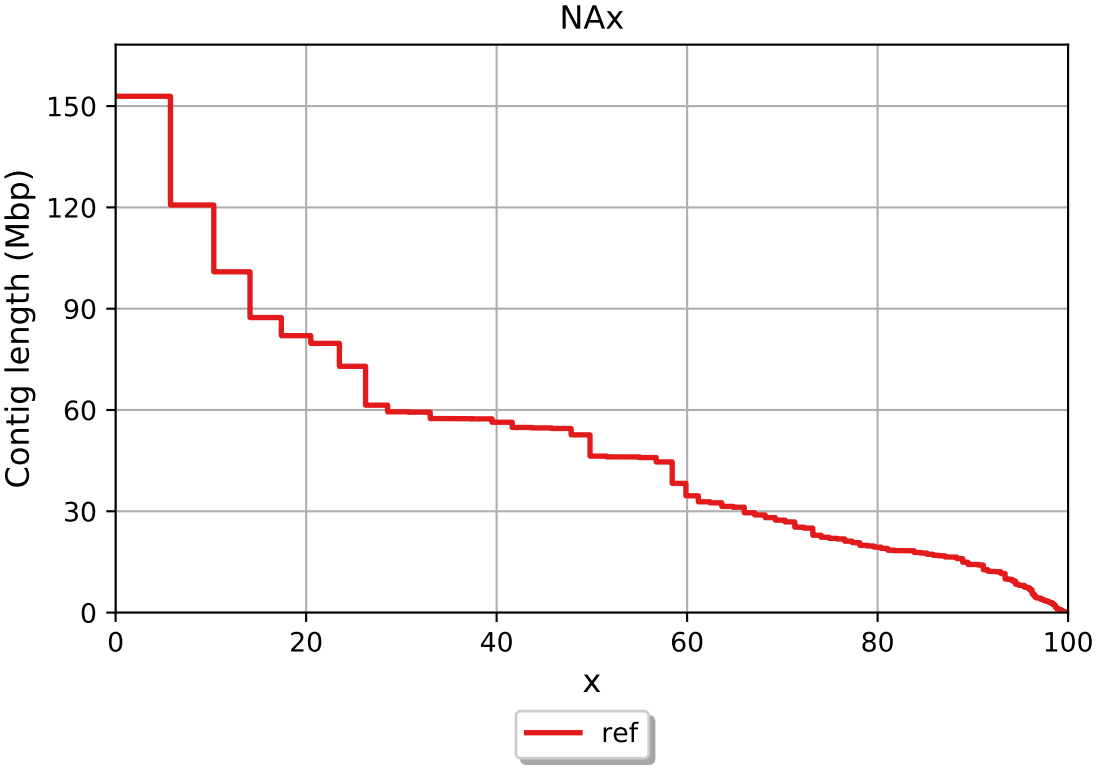

GC content
1000000
800000
600000
400000
200000
0
0
20
40
60
80
100
GC (%)
ref
Reference

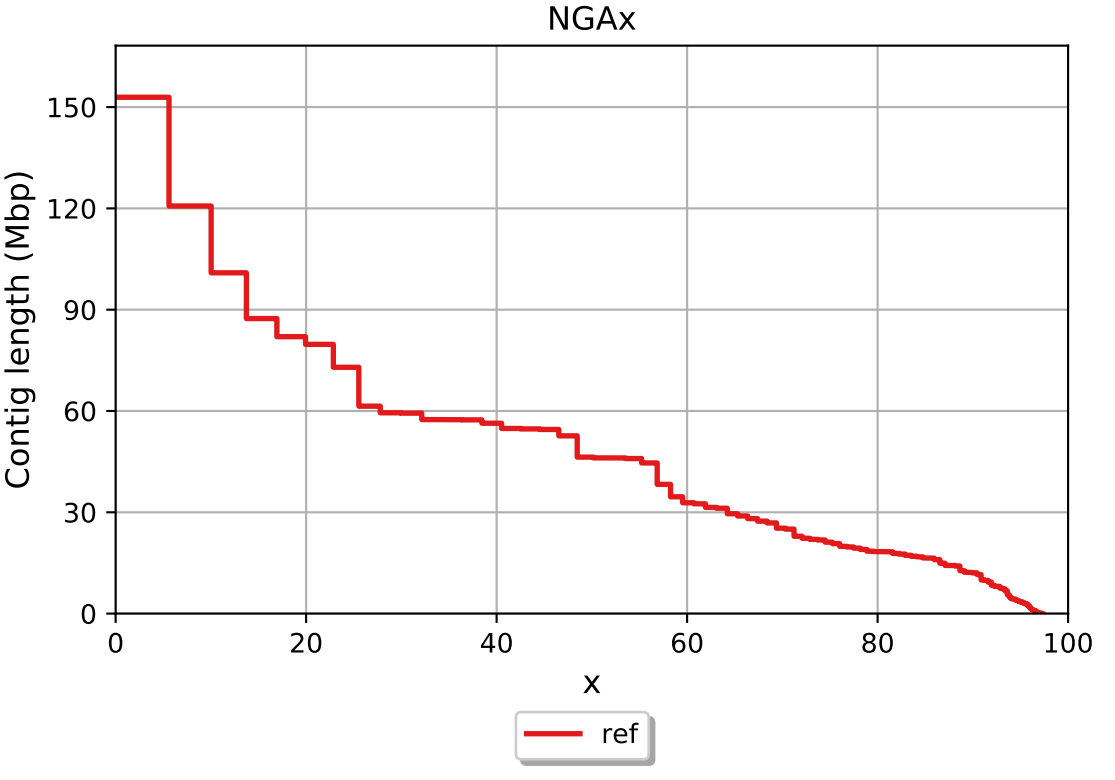

ref GC content
150
120
90
60
30
0
contigs
0
20
40
60
80
100
GC (%)
ref


Misassemblies
5
4
3
2
1
0
ref


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


Cumulative length (aligned contigs)
Cumulative length (Mbp)
3000
2400
1800
1200
600
0
0
60
120
180
240
300
Contig index
ref
Reference


NAx
Contig length (Mbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
ref


NGAx
Contig length (Mbp)
150
120
90
60
30
0
0
20
40
60
80
100
x
ref