Report

	pacbio.contigs
# contigs (>= 0 bp)	9
# contigs (>= 1000 bp)	9
# contigs (>= 5000 bp)	9
# contigs (>= 10000 bp)	9
# contigs (>= 25000 bp)	4
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	3135573
Total length (>= 1000 bp)	3135573
Total length (>= 5000 bp)	3135573
Total length (>= 10000 bp)	3135573
Total length (>= 25000 bp)	3048456
Total length (>= 50000 bp)	2979568
# contigs	9
Largest contig	2763567
Total length	3135573
Reference length	2919198
GC (%)	37.79
Reference GC (%)	37.88
N50	2763567
NG50	2763567
N75	2763567
NG75	2763567
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	188
# misassembled contigs	1
Misassembled contigs length	2763567
# local misassemblies	37
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# unaligned contigs	3 + 6 part
Unaligned length	551396
Genome fraction (%)	85.210
Duplication ratio	1.039
# N's per 100 kbp	0.00
# mismatches per 100 kbp	391.89
# indels per 100 kbp	18.77
Largest alignment	137654
Total aligned length	2582278
NA50	24552
NGA50	29113
NA75	5023
NGA75	10307
LA50	31
LGA50	27
LA75	86
LGA75	66

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

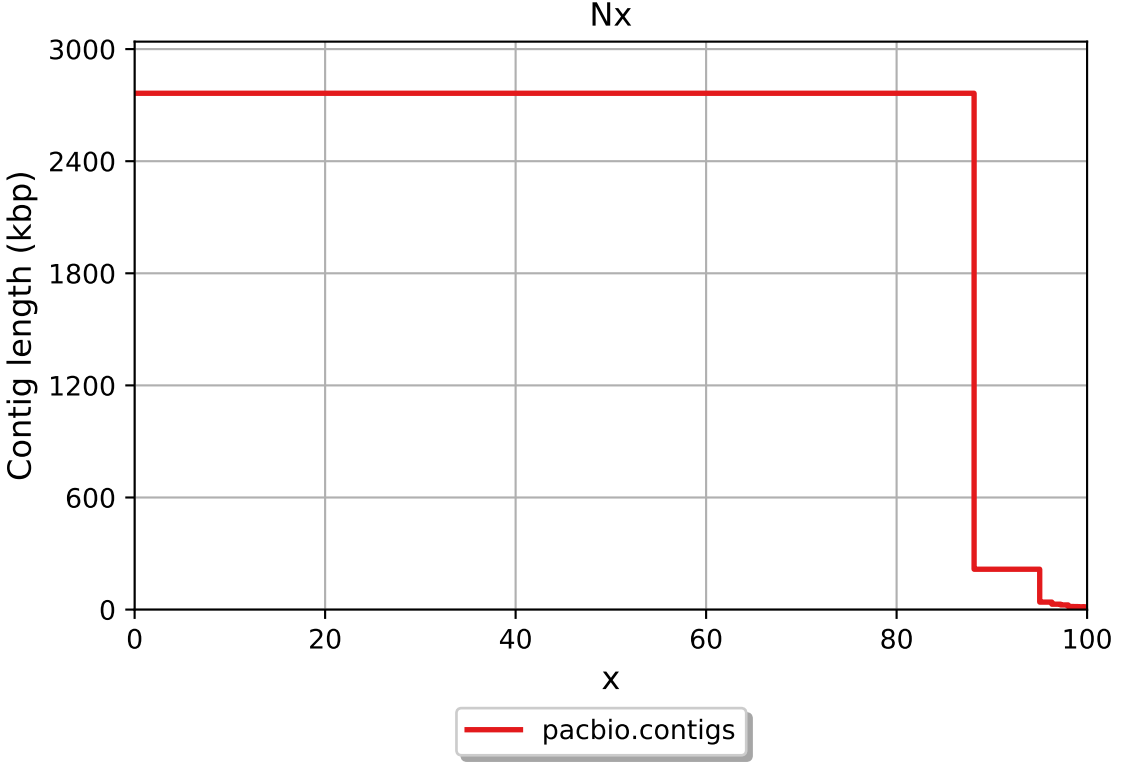
	pacbio.contigs
# misassemblies	188
# contig misassemblies	188
# c. relocations	176
# c. translocations	10
# c. inversions	2
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	2763567
# local misassemblies	37
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	4
# mismatches	9748
# indels	467
# indels (<= 5 bp)	431
# indels (> 5 bp)	36
Indels length	1499

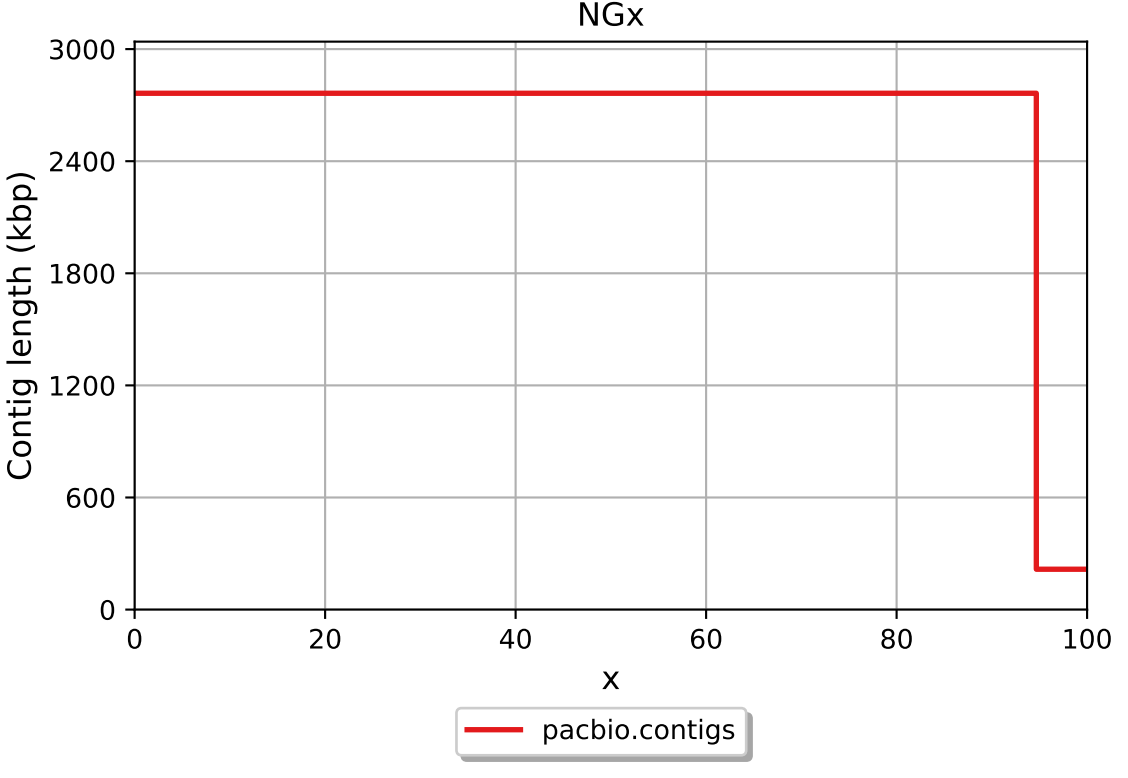
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

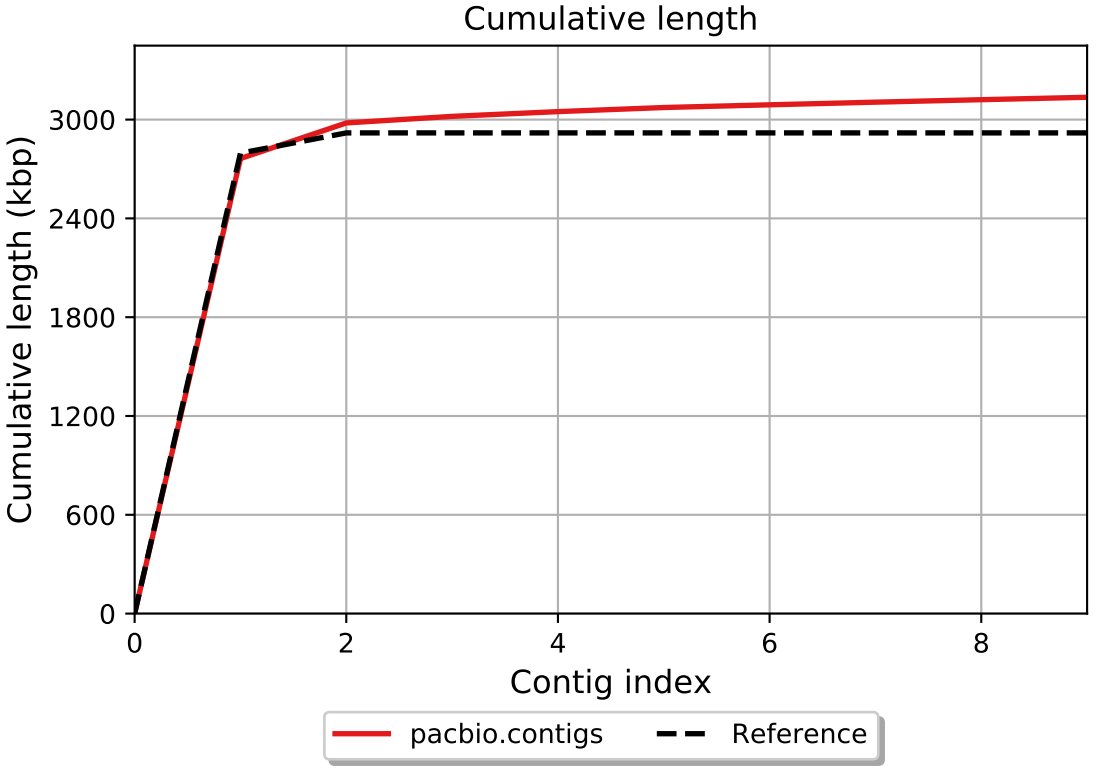
Unaligned report

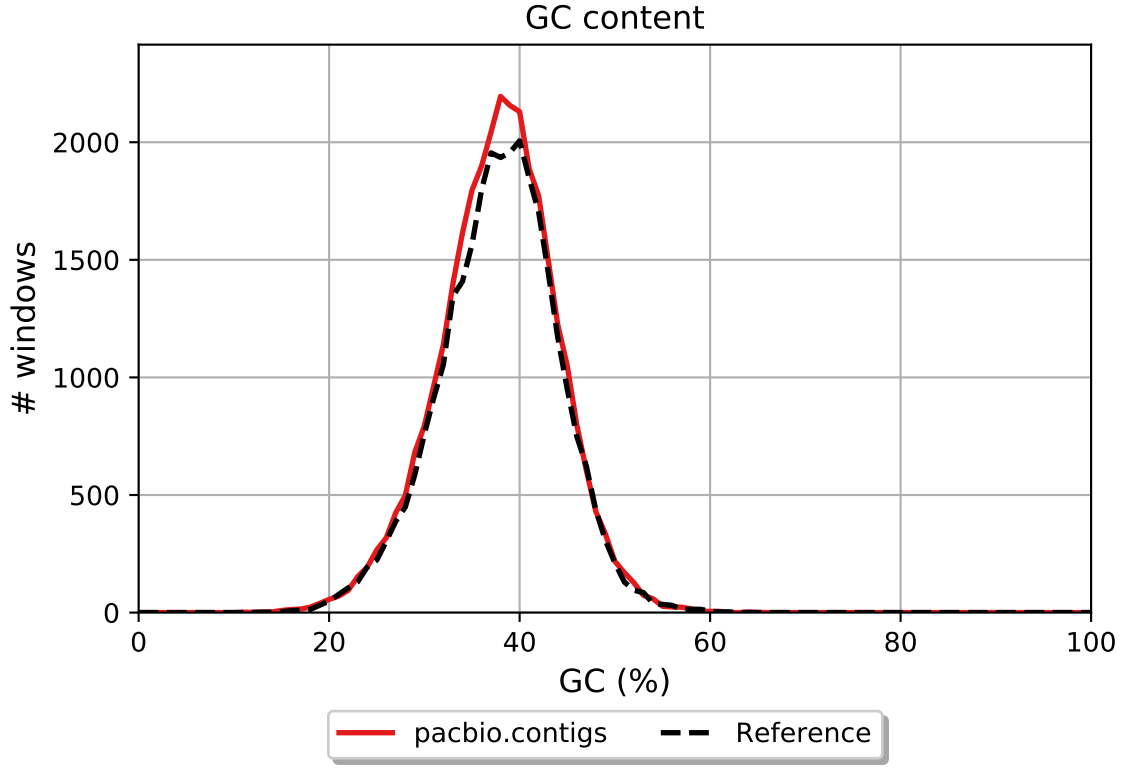
	pacbio.contigs
# fully unaligned contigs	3
Fully unaligned length	56337
# partially unaligned contigs	6
Partially unaligned length	495059
# N's	0

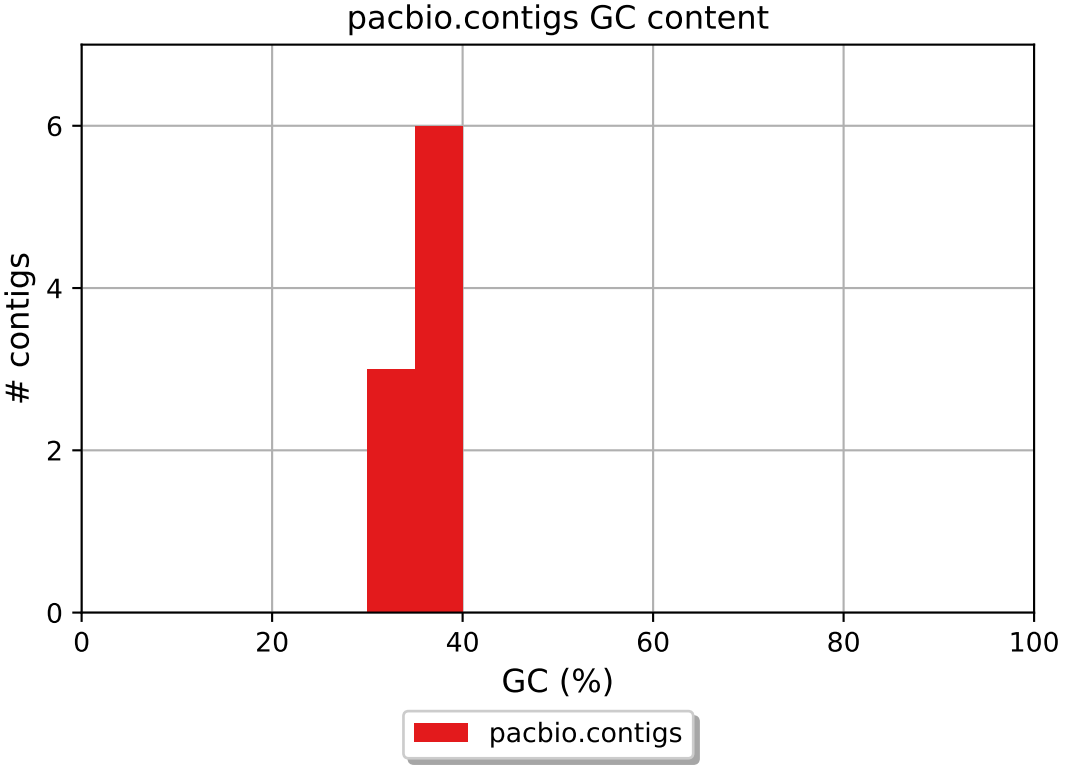
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).


Nx
3000
2400
1800
1200
600
0
Contig length (kbp)
0
20
40
60
80
100
x
pacbio.contigs

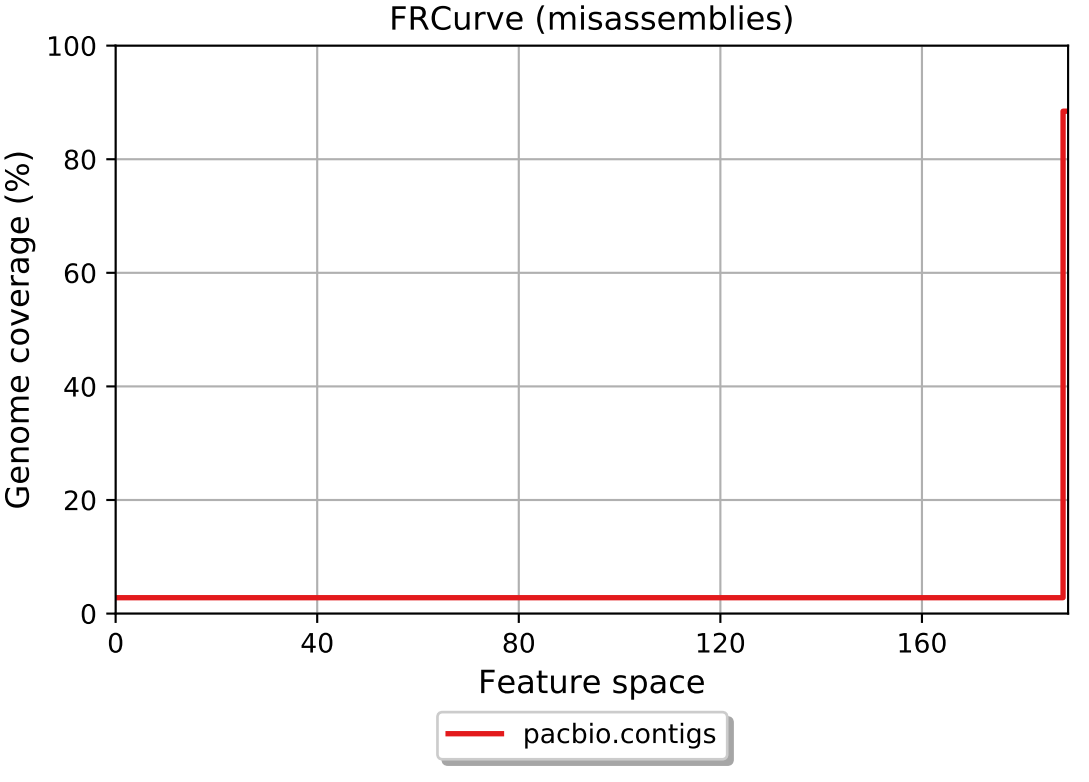

NGx
3000
2400
1800
1200
600
0
Contig length (kbp)
0
20
40
60
80
100
x
pacbio.contigs

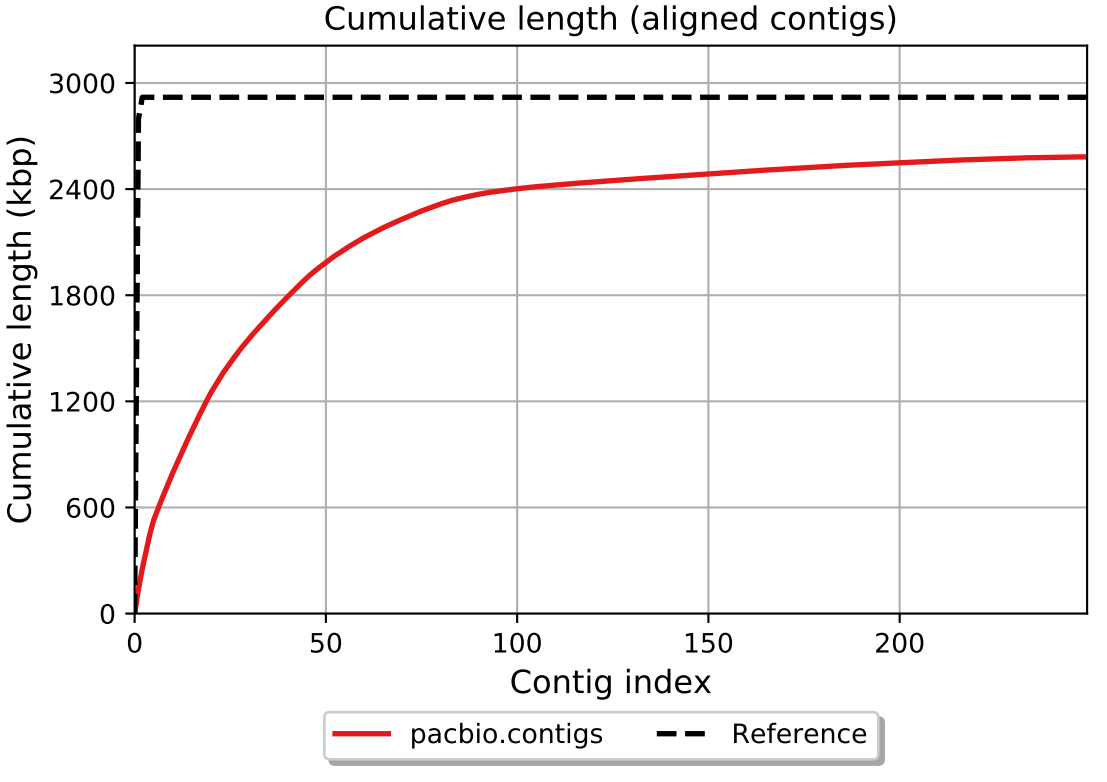

Cumulative length
Cumulative length (kbp)
3000
2400
1800
1200
600
0
0
2
4
6
8
Contig index
pacbio.contigs
Reference

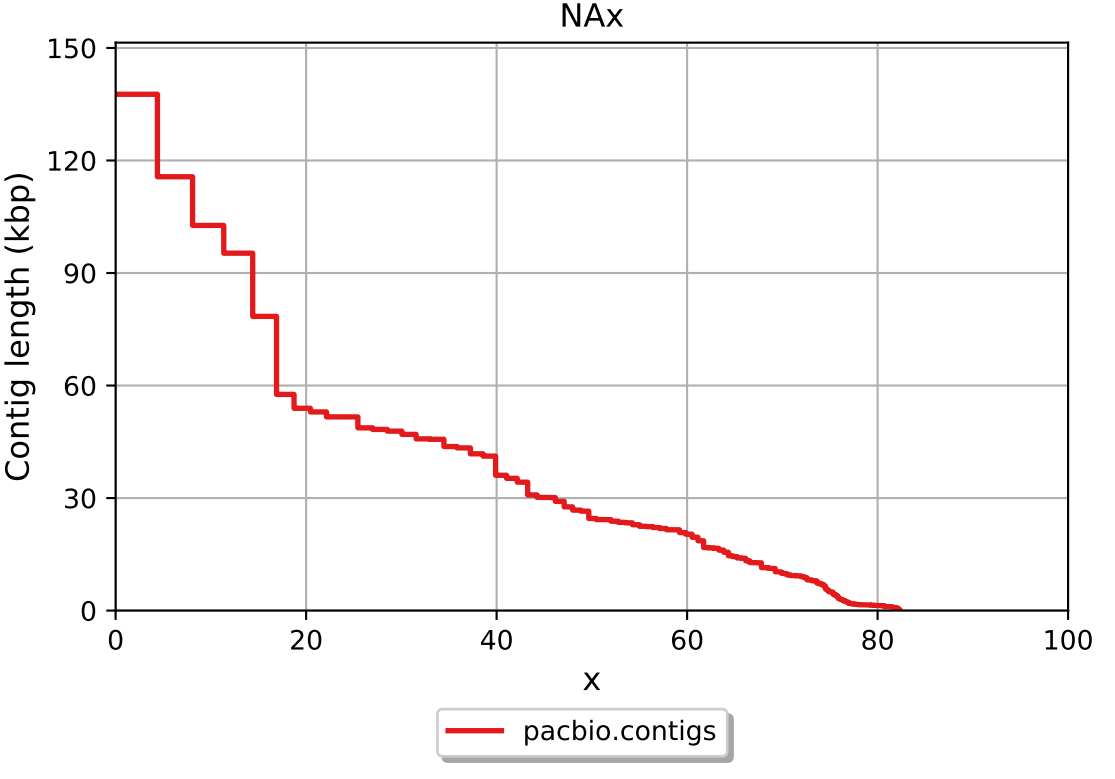

GC content
windows
2000
1500
1000
500
0
0
20
40
60
80
100
GC (%)
pacbio.contigs
Reference

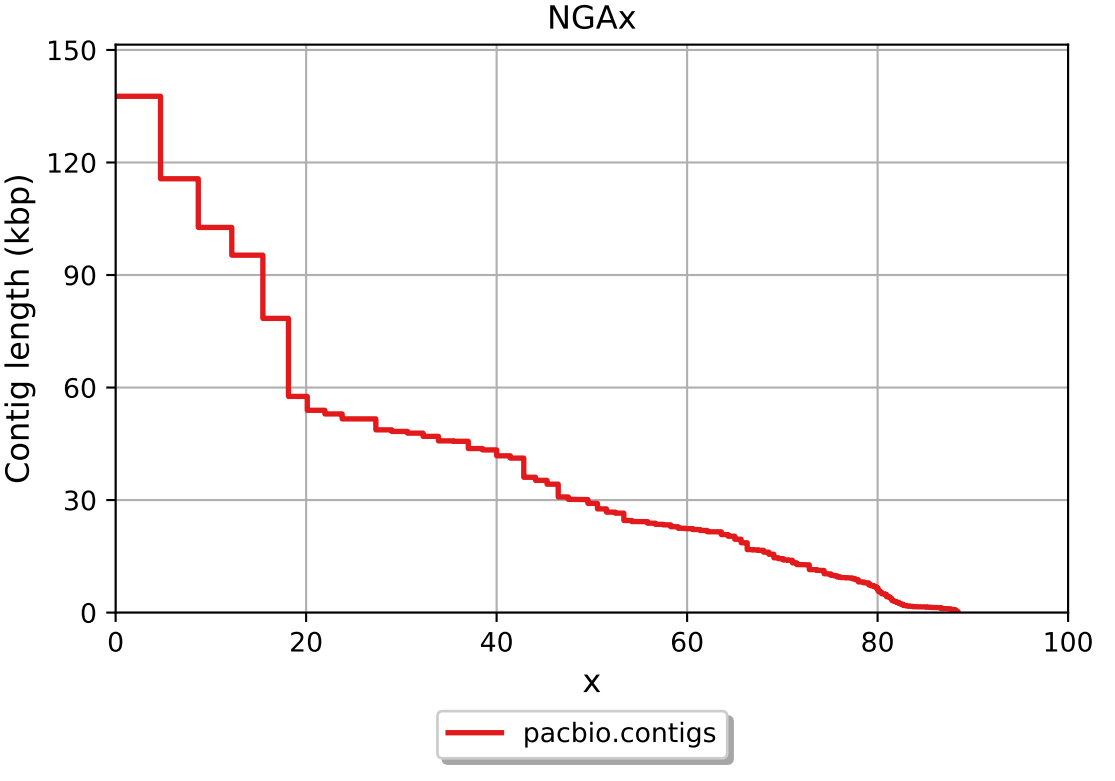

pacbio.contigs GC content
contigs
0
2
4
6
0
20
40
60
80
100
GC (%)
pacbio.contigs

Misassemblies
200
160
120
80
40
0
pacbio.contigs
relocations
translocations
inversions


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
40
80
120
160
Feature space
pacbio.contigs


Cumulative length (aligned contigs)
Cumulative length (kbp)
3000
2400
1800
1200
600
0
0
50
100
150
200
Contig index
pacbio.contigs
Reference


NAx
150
120
90
60
30
0
Contig length (kbp)
0
20
40
60
80
100
x
pacbio.contigs


NGAx
150
120
90
60
30
0
Contig length (kbp)
0
20
40
60
80
100
x
pacbio.contigs