Report

	tig00000001_pilon
# contigs (>= 0 bp)	1
# contigs (>= 1000 bp)	1
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	2773702
Total length (>= 1000 bp)	2773702
Total length (>= 5000 bp)	2773702
Total length (>= 10000 bp)	2773702
Total length (>= 25000 bp)	2773702
Total length (>= 50000 bp)	2773702
# contigs	1
Largest contig	2773702
Total length	2773702
Reference length	2765010
GC (%)	38.11
Reference GC (%)	38.11
N50	2773702
NG50	2773702
N75	2773702
NG75	2773702
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	2773702
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	100.000
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.36
Largest alignment	2195416
Total aligned length	2773702
NA50	2195416
NGA50	2195416
NA75	2195416
NGA75	2195416
LA50	1
LGA50	1
LA75	1
LGA75	1

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

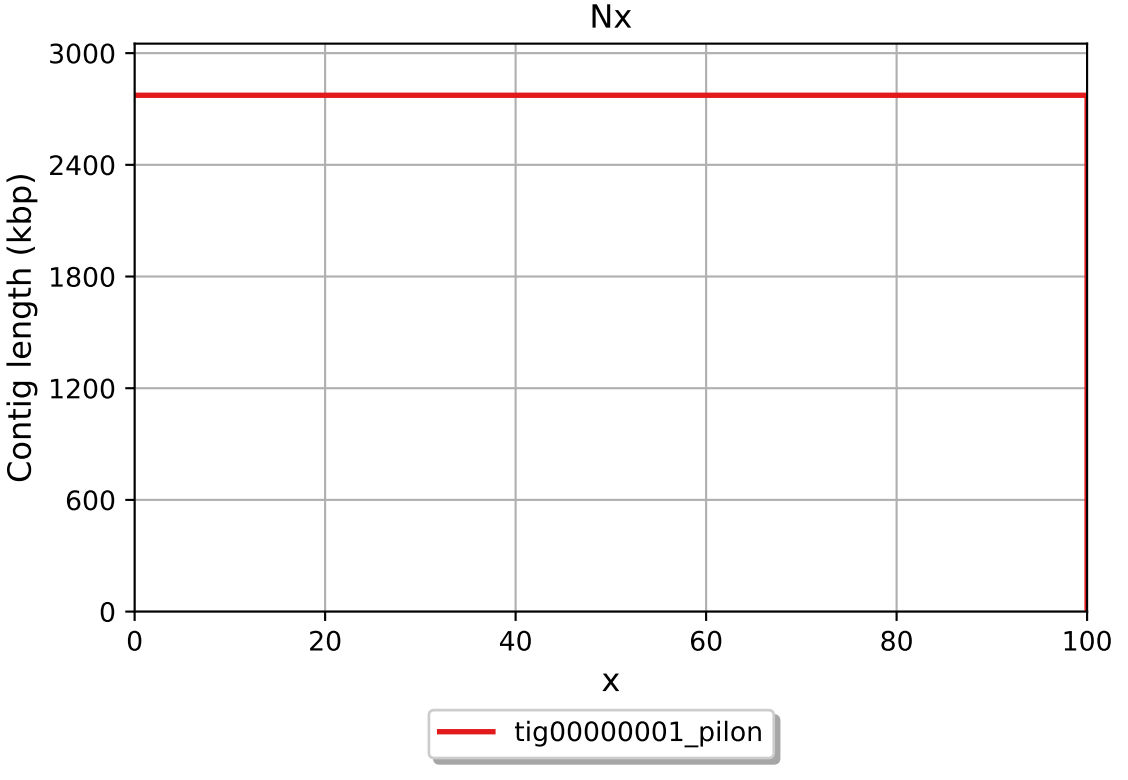
	tig00000001_pilon
# misassemblies	1
# contig misassemblies	1
# c. relocations	1
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	2773702
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	0
# indels	10
# indels (<= 5 bp)	10
# indels (> 5 bp)	0
Indels length	11

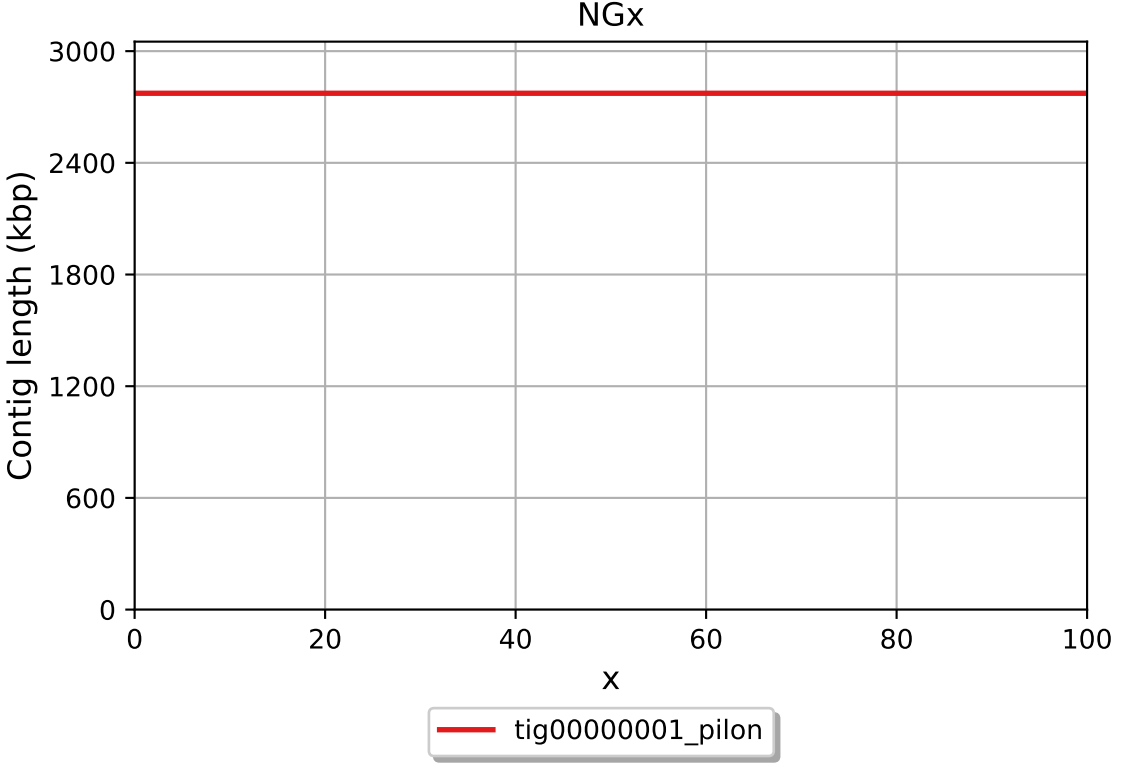
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

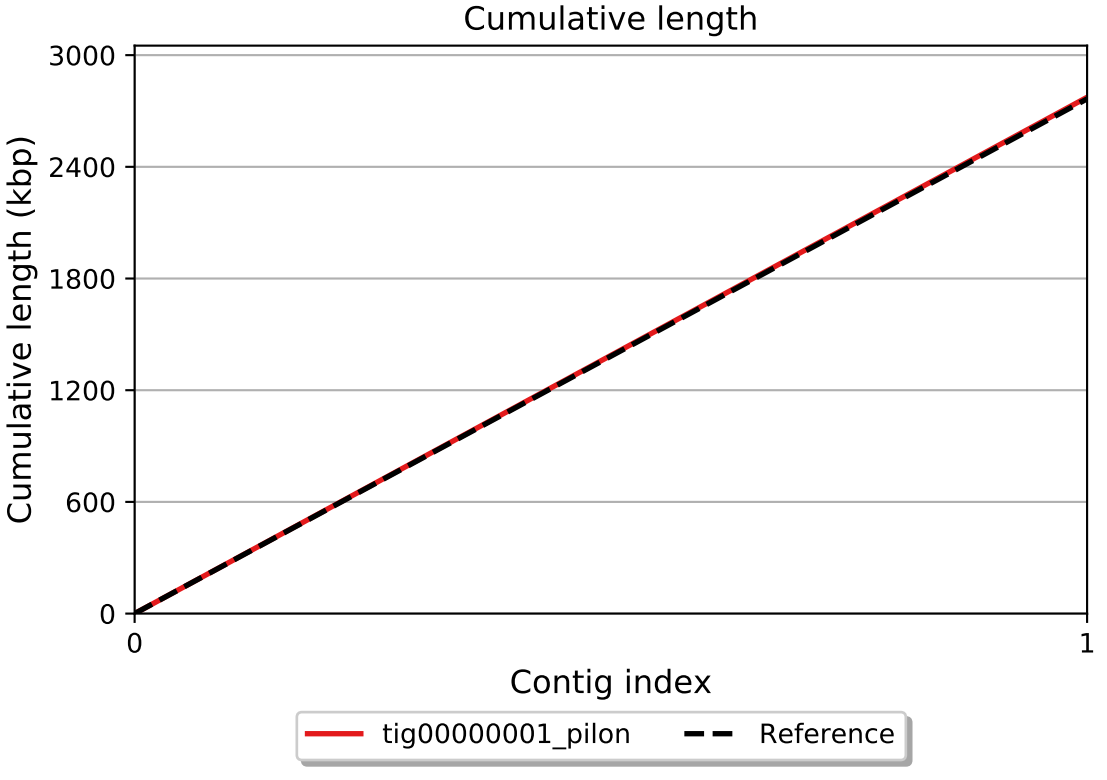
Unaligned report

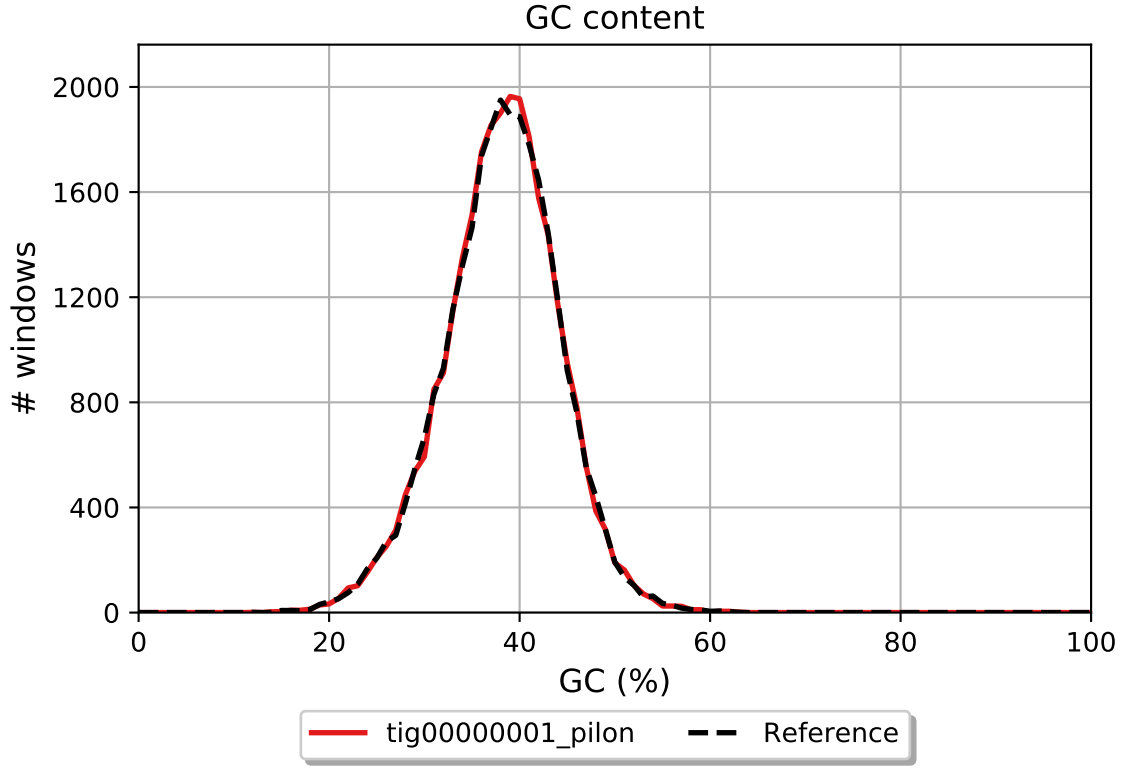
	tig00000001_pilon
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

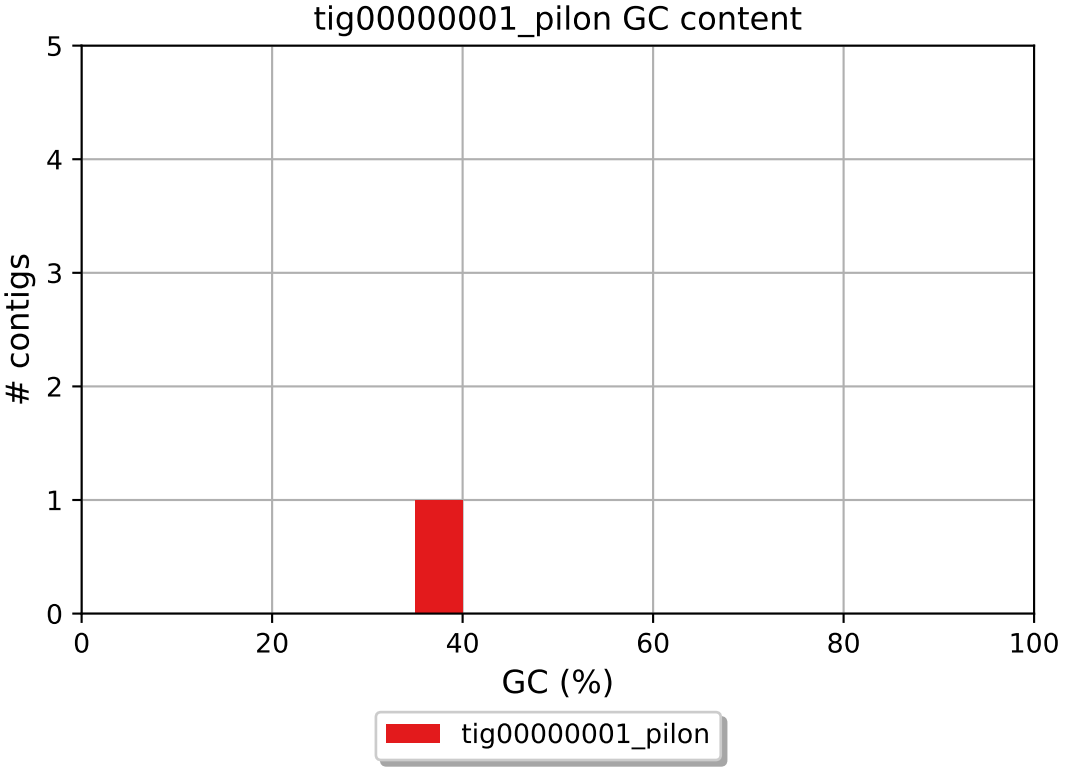
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

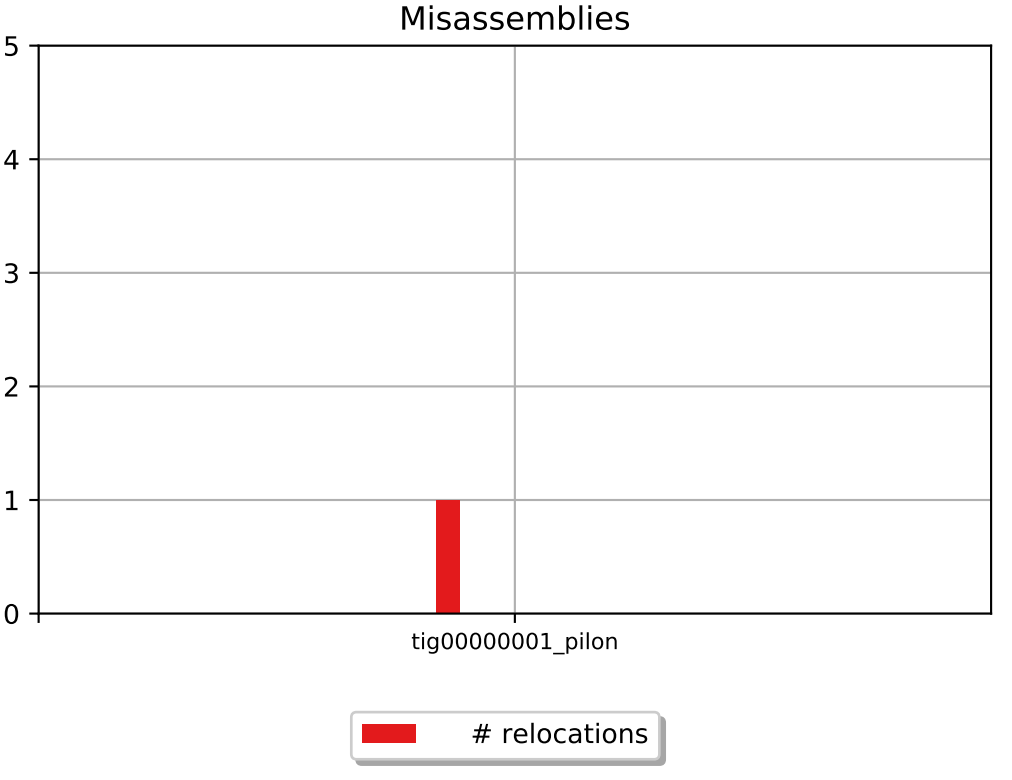

Nx
3000
2400
1800
1200
600
0
Contig length (kbp)
0
20
40
60
80
100
x
tig00000001_pilon

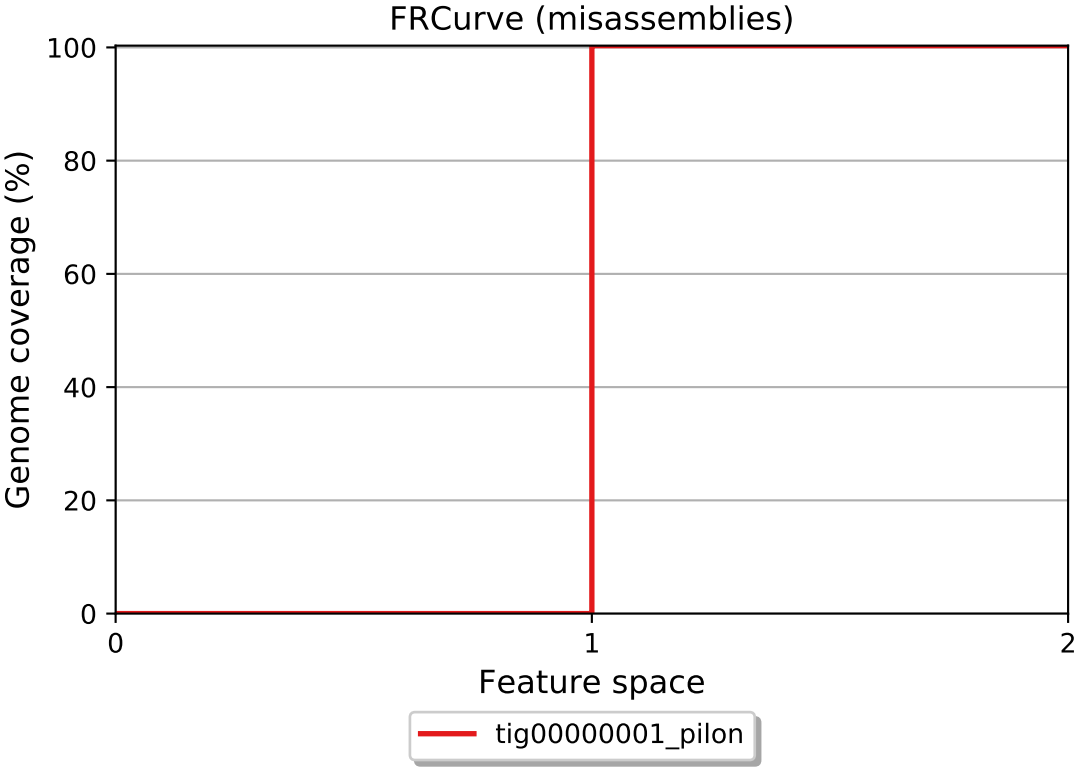

NGx
Contig length (kbp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
tig00000001_pilon

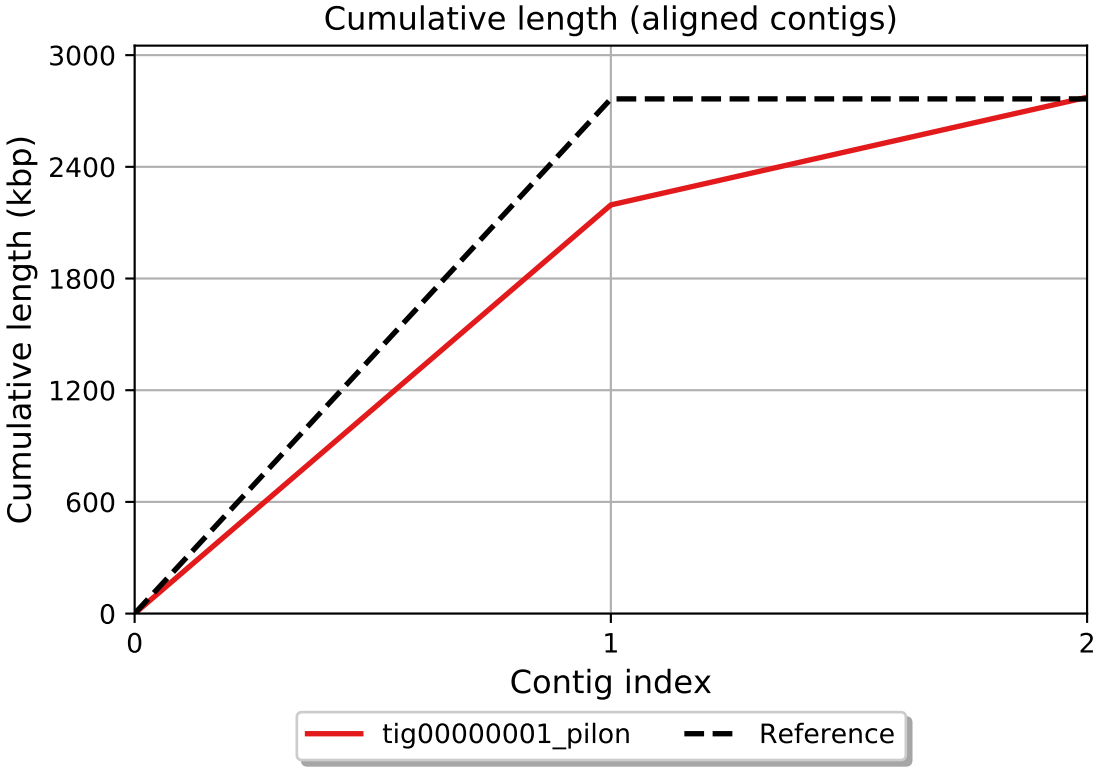

Cumulative length
3000
2400
1800
1200
600
0
Cumulative length (kbp)
0
1
Contig index
tig00000001_pilon
Reference

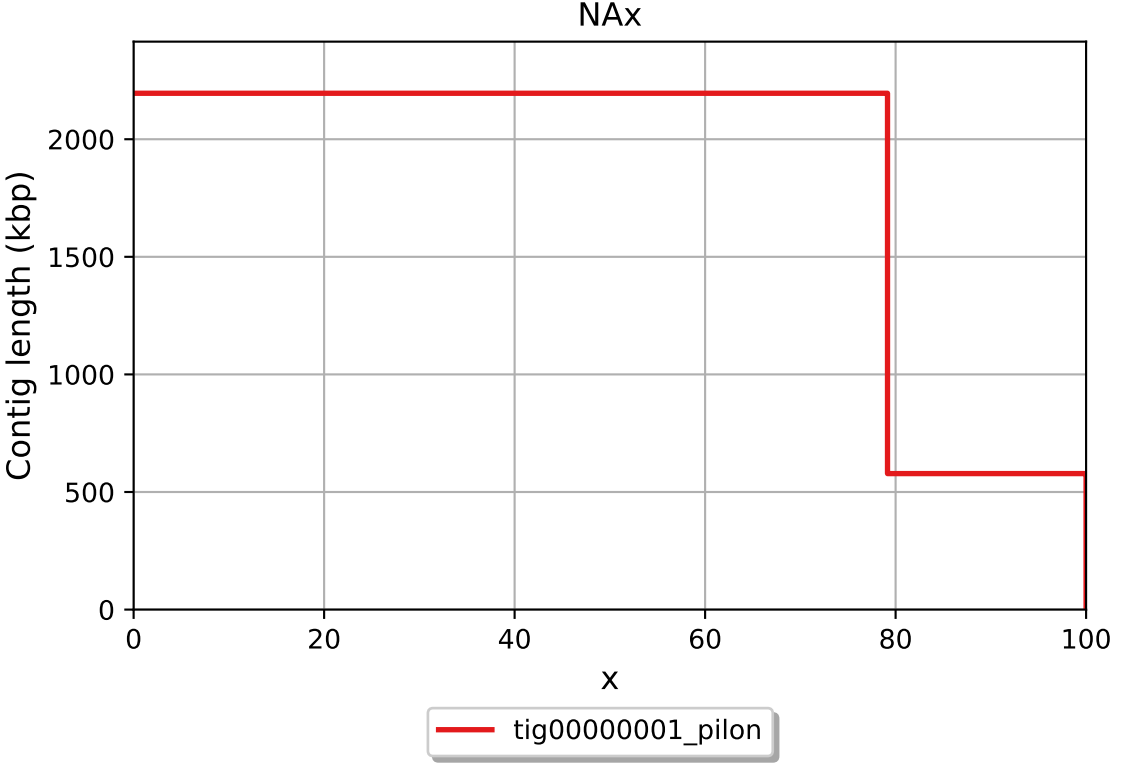

GC content
windows
2000
1600
1200
800
400
0
0
20
40
60
80
100
GC (%)
tig00000001_pilon
Reference

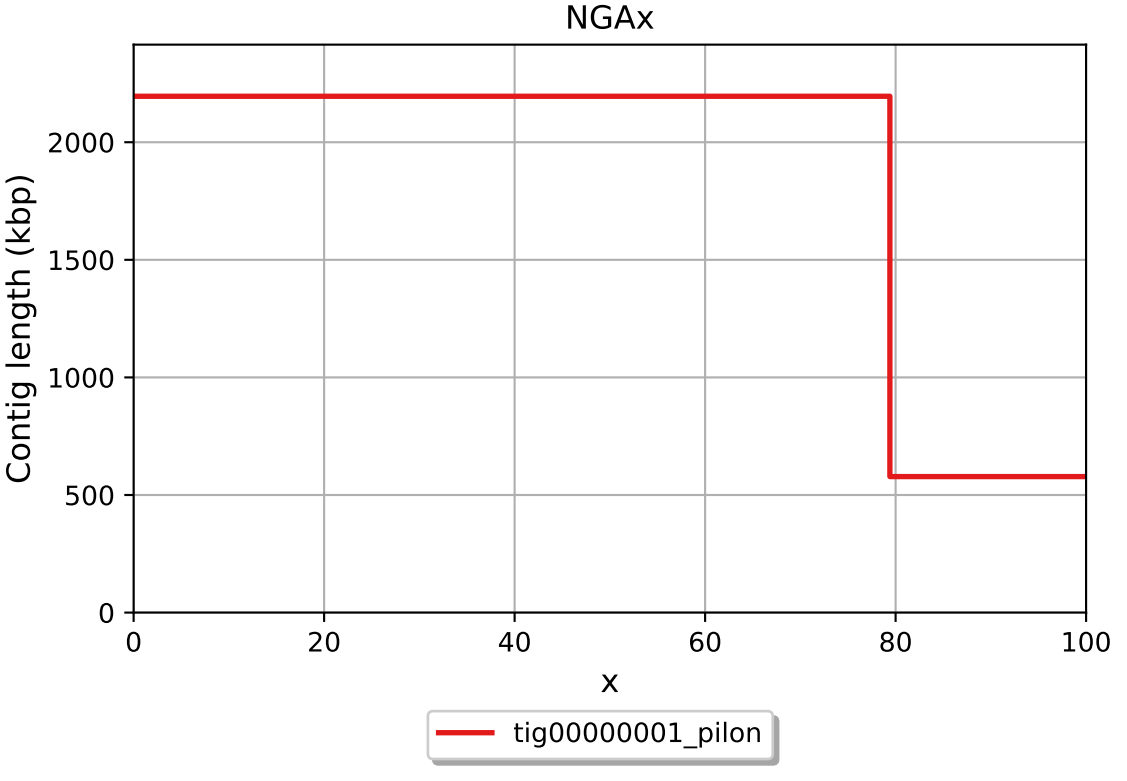

tig00000001_pilon GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
tig00000001_pilon


Misassemblies
5
4
3
2
1
0
tig00000001_pilon
relocations


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
2
Feature space
tig00000001_pilon


Cumulative length (aligned contigs)
Cumulative length (kbp)
3000
2400
1800
1200
600
0
0
1
2
Contig index
tig00000001_pilon
Reference


NAx
Contig length (kbp)
2000
1500
1000
500
0
0
20
40
60
80
100
x
tig00000001_pilon


NGAx
Contig length (kbp)
2000
1500
1000
500
0
0
20
40
60
80
100
x
tig00000001_pilon