Report

	AJ218.MiniCL
# contigs (>= 0 bp)	14
# contigs (>= 1000 bp)	14
# contigs (>= 5000 bp)	14
# contigs (>= 10000 bp)	14
# contigs (>= 25000 bp)	14
# contigs (>= 50000 bp)	14
Total length (>= 0 bp)	5675913
Total length (>= 1000 bp)	5675913
Total length (>= 5000 bp)	5675913
Total length (>= 10000 bp)	5675913
Total length (>= 25000 bp)	5675913
Total length (>= 50000 bp)	5675913
# contigs	14
Largest contig	1168567
Total length	5675913
Reference length	5465981
GC (%)	57.08
Reference GC (%)	57.29
N50	615749
NG50	615749
N75	459808
NG75	459808
L50	3
LG50	3
L75	6
LG75	6
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	10
# unaligned mis. contigs	1
# unaligned contigs	0 + 3 part
Unaligned length	202098
Genome fraction (%)	99.273
Duplication ratio	1.009
# N's per 100 kbp	0.00
# mismatches per 100 kbp	20.60
# indels per 100 kbp	455.20
Largest alignment	1163455
Total aligned length	5472727
NA50	610591
NGA50	610591
NA75	459808
NGA75	459808
LA50	3
LGA50	3
LA75	6
LGA75	6

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

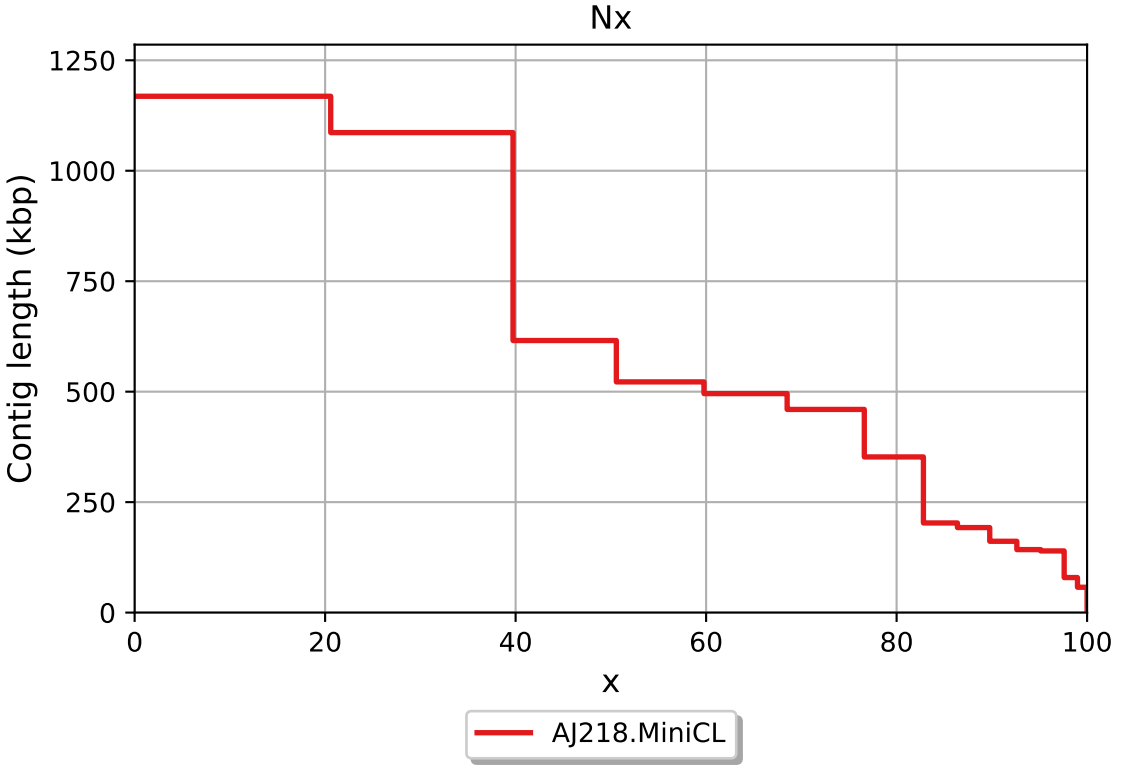
	AJ218.MiniCL
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	10
# unaligned mis. contigs	1
# mismatches	1118
# indels	24700
# indels (<= 5 bp)	24617
# indels (> 5 bp)	83
Indels length	32959

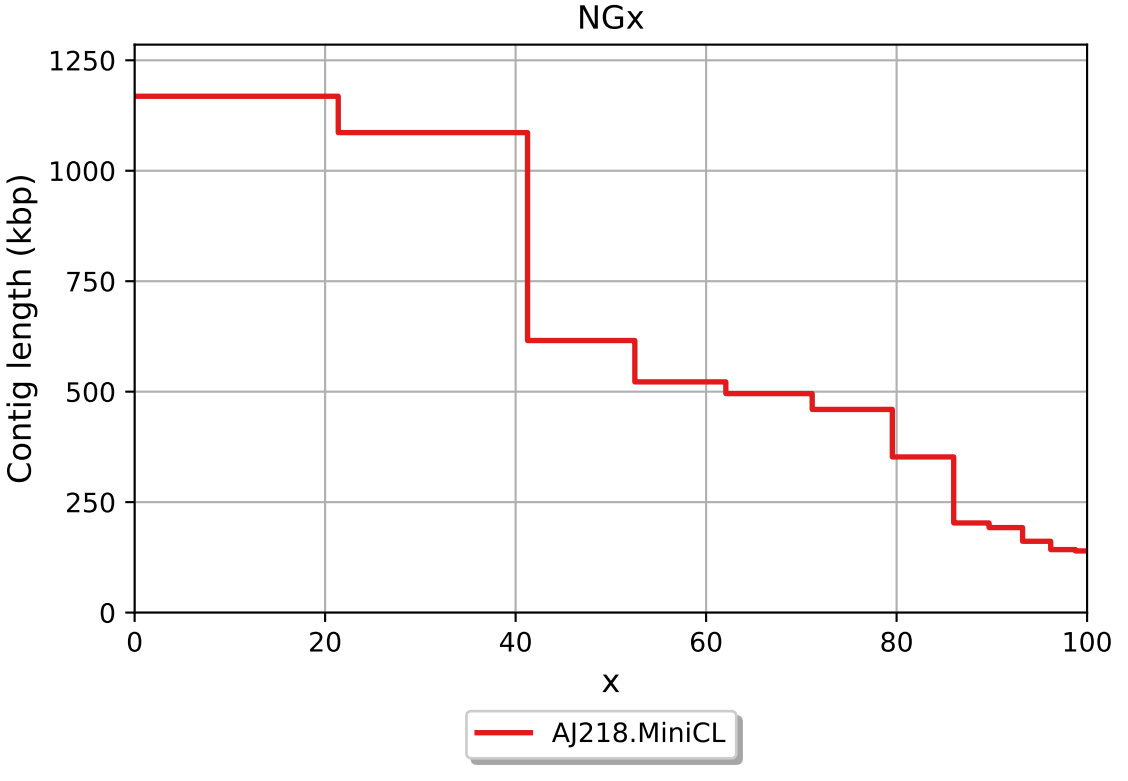
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

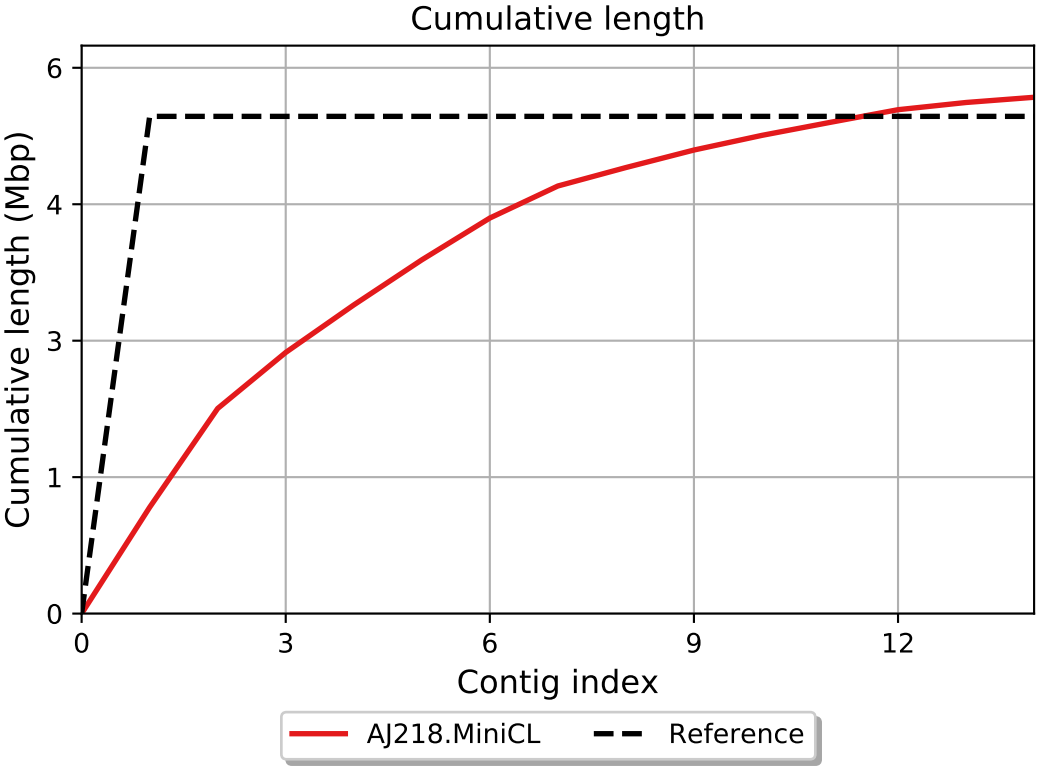
Unaligned report

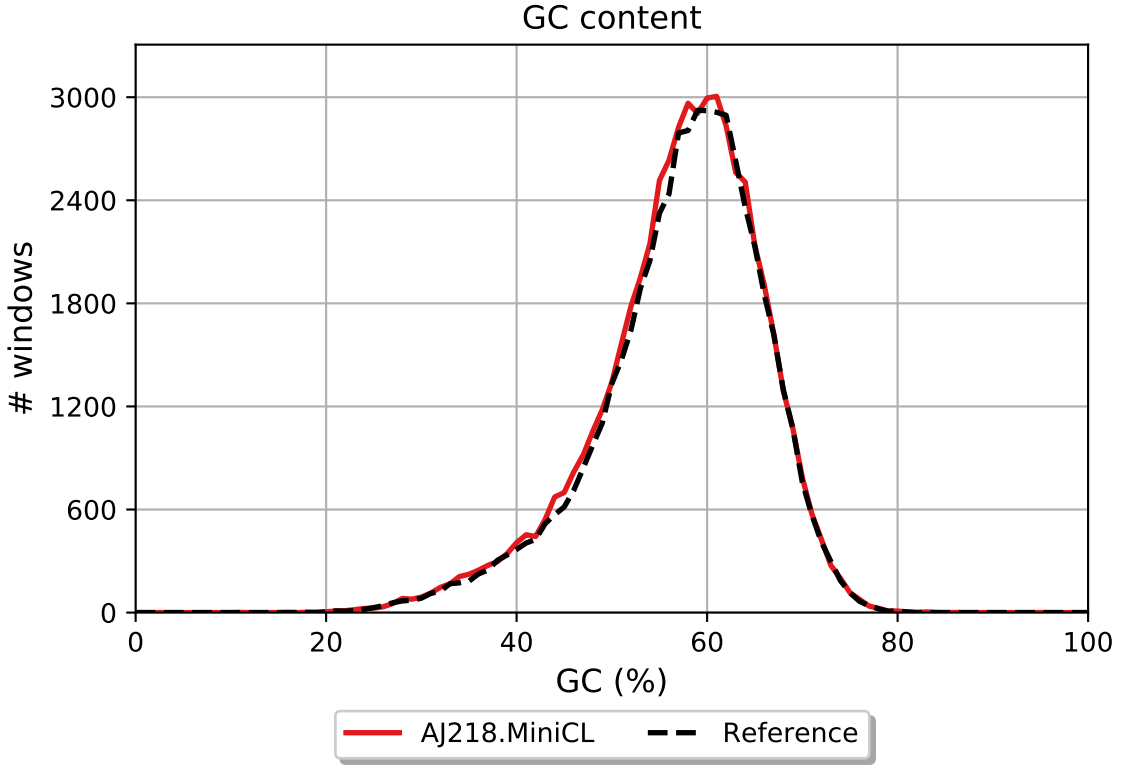
	AJ218.MiniCL
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
Partially unaligned length	202098
# N's	0

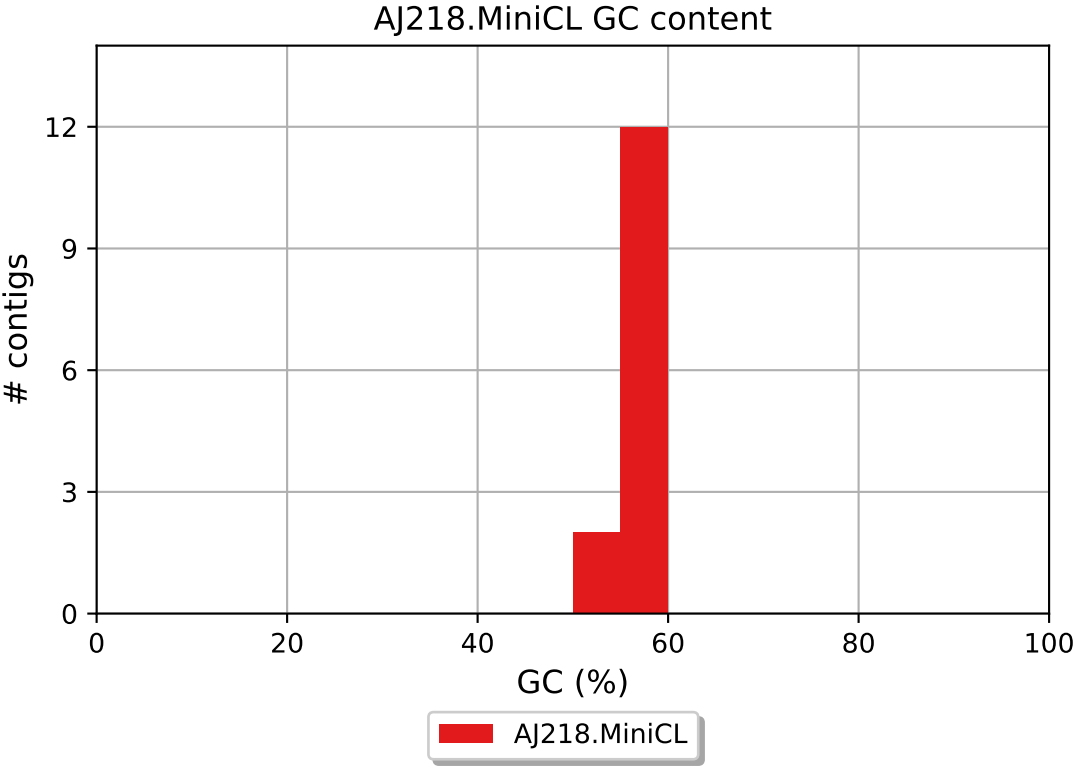
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).


Nx
Contig length (kbp)
1250
1000
750
500
250
0
0
20
40
60
80
100
x
AJ218.MiniCL

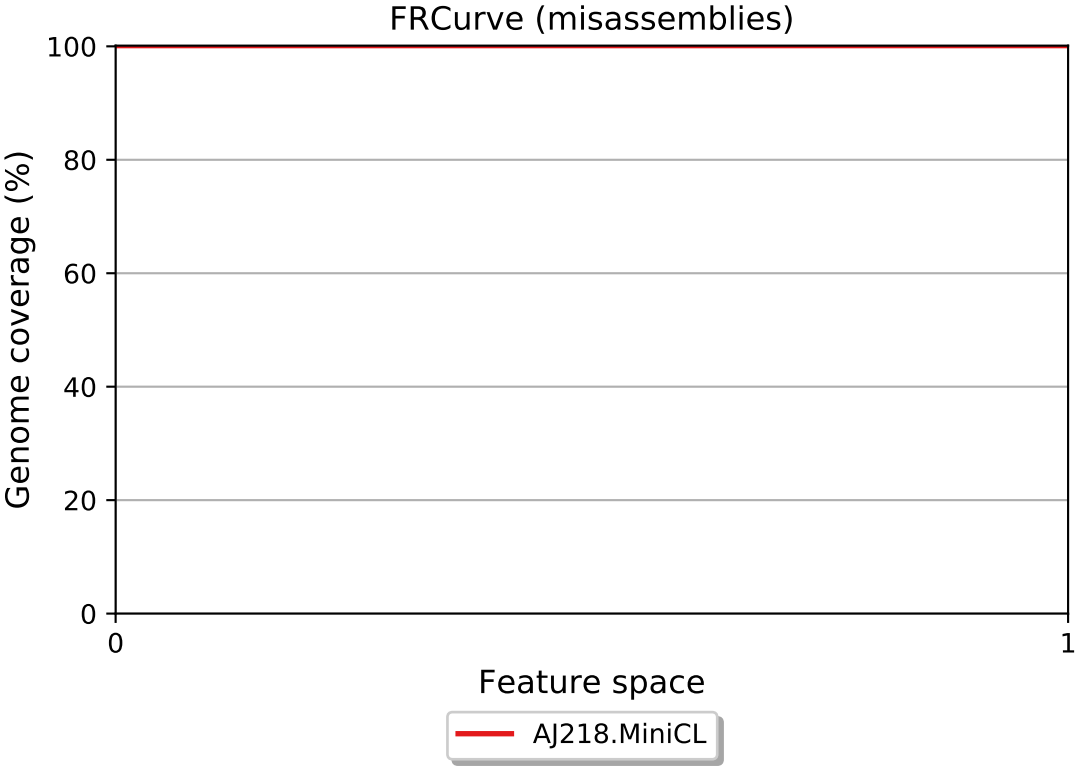

NGx
Contig length (kbp)
1250
1000
750
500
250
0
0
20
40
60
80
100
x
AJ218.MiniCL

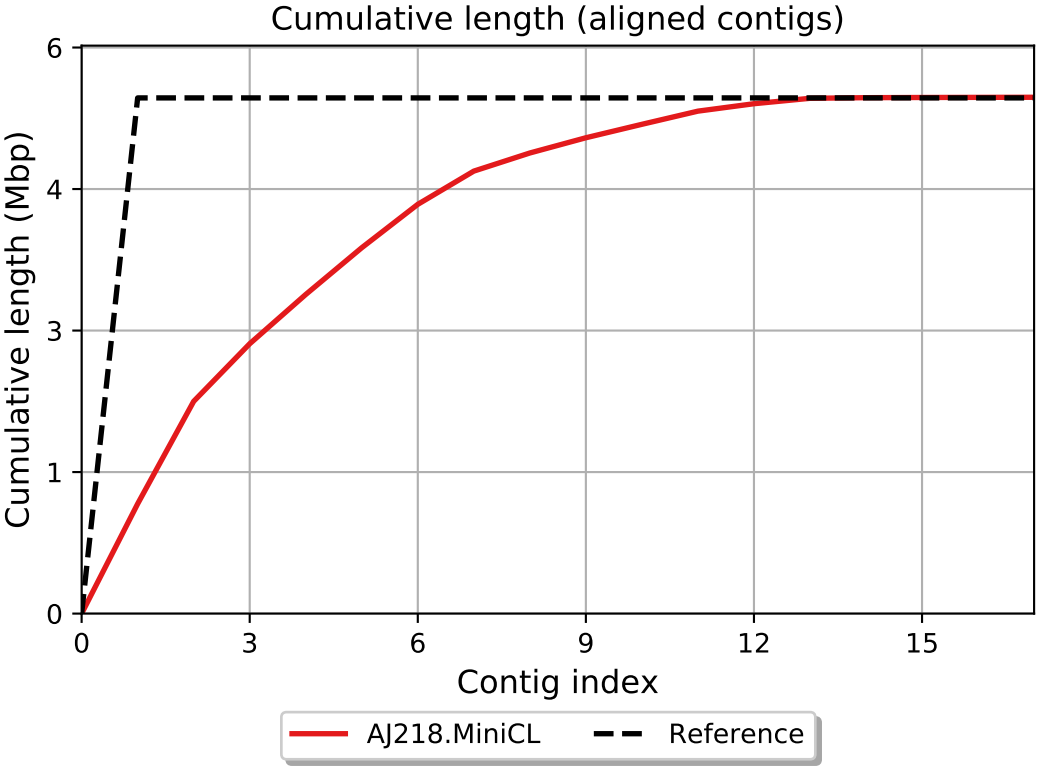

Cumulative length
Cumulative length (Mbp)
0
1
3
4
6
0
3
6
9
12
Contig index
AJ218.MiniCL
Reference

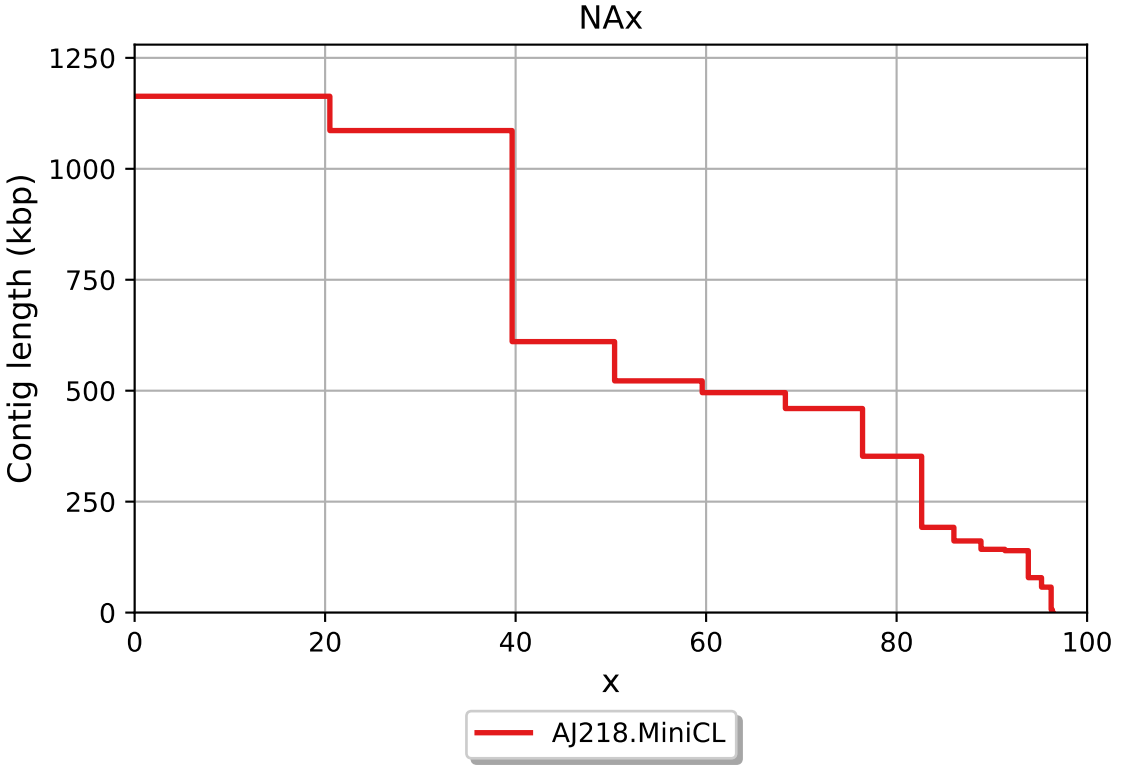

GC content
3000
2400
1800
1200
600
0
windows
0
20
40
60
80
100
GC (%)
AJ218.MiniCL
Reference

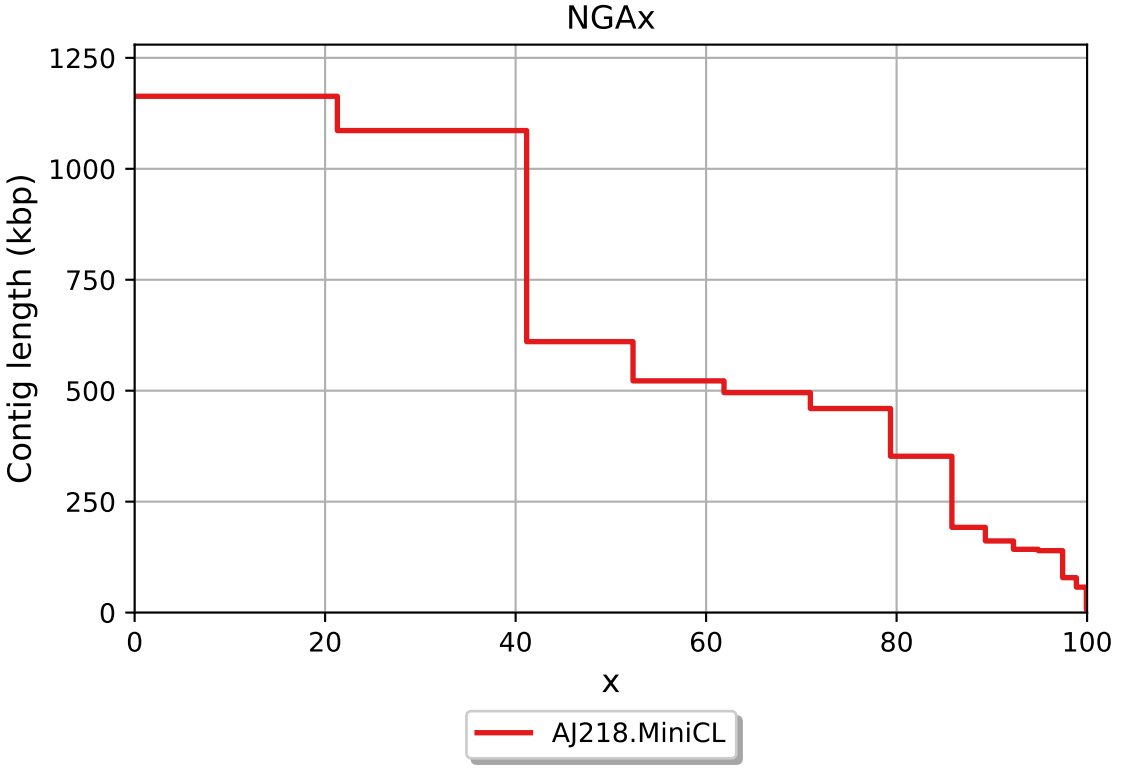

AJ218.MiniCL GC content
contigs
0
3
6
9
12
0
20
40
60
80
100
GC (%)
AJ218.MiniCL

Misassemblies
5
4
3
2
1
0
AJ218.MiniCL


FRCurve (misassemblies)
100
80
60
40
20
0
Genome coverage (%)
0
1
Feature space
AJ218.MiniCL


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
3
4
6
0
3
6
9
12
15
Contig index
AJ218.MiniCL
Reference


NAx
Contig length (kbp)
1250
1000
750
500
250
0
0
20
40
60
80
100
x
AJ218.MiniCL


NGAx
Contig length (kbp)
1250
1000
750
500
250
0
0
20
40
60
80
100
x
AJ218.MiniCL