Report

	AJ218.CanuL
# contigs (>= 0 bp)	9
# contigs (>= 1000 bp)	9
# contigs (>= 5000 bp)	9
# contigs (>= 10000 bp)	9
# contigs (>= 25000 bp)	7
# contigs (>= 50000 bp)	7
Total length (>= 0 bp)	5696719
Total length (>= 1000 bp)	5696719
Total length (>= 5000 bp)	5696719
Total length (>= 10000 bp)	5696719
Total length (>= 25000 bp)	5664655
Total length (>= 50000 bp)	5664655
# contigs	9
Largest contig	1804543
Total length	5696719
Reference length	5465981
GC (%)	57.08
Reference GC (%)	57.29
N50	1353042
NG50	1353042
N75	533216
NG75	533216
L50	2
LG50	2
L75	4
LG75	4
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	1
# unaligned contigs	0 + 3 part
Unaligned length	231873
Genome fraction (%)	99.759
Duplication ratio	1.002
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4.62
# indels per 100 kbp	86.34
Largest alignment	1804543
Total aligned length	5464844
NA50	1353042
NGA50	1353042
NA75	533216
NGA75	533216
LA50	2
LGA50	2
LA75	4
LGA75	4

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

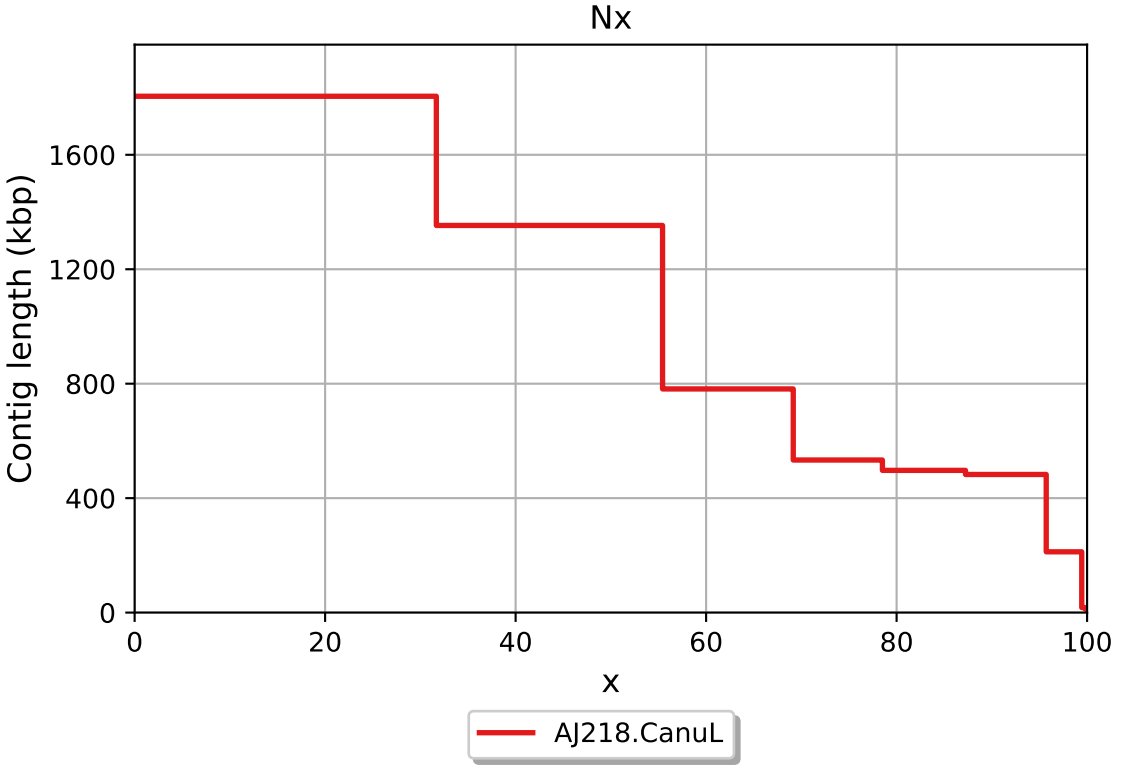
	AJ218.CanuL
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	1
# mismatches	252
# indels	4708
# indels (<= 5 bp)	4706
# indels (> 5 bp)	2
Indels length	4869

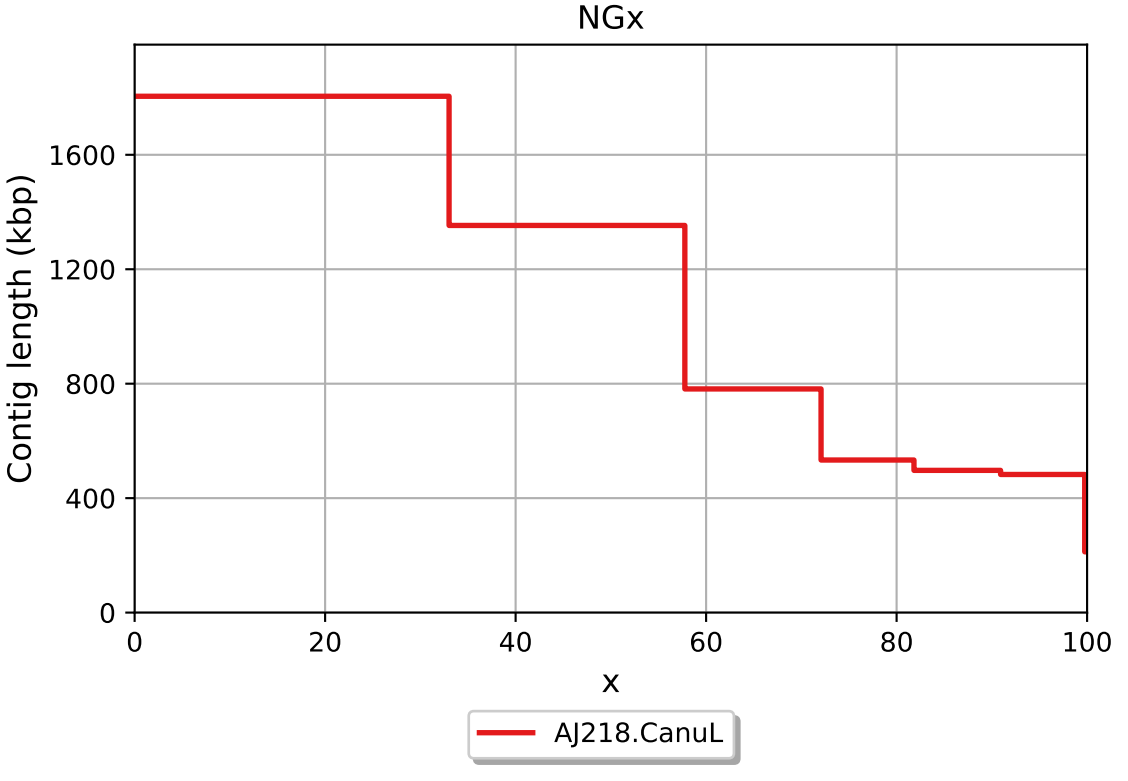
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

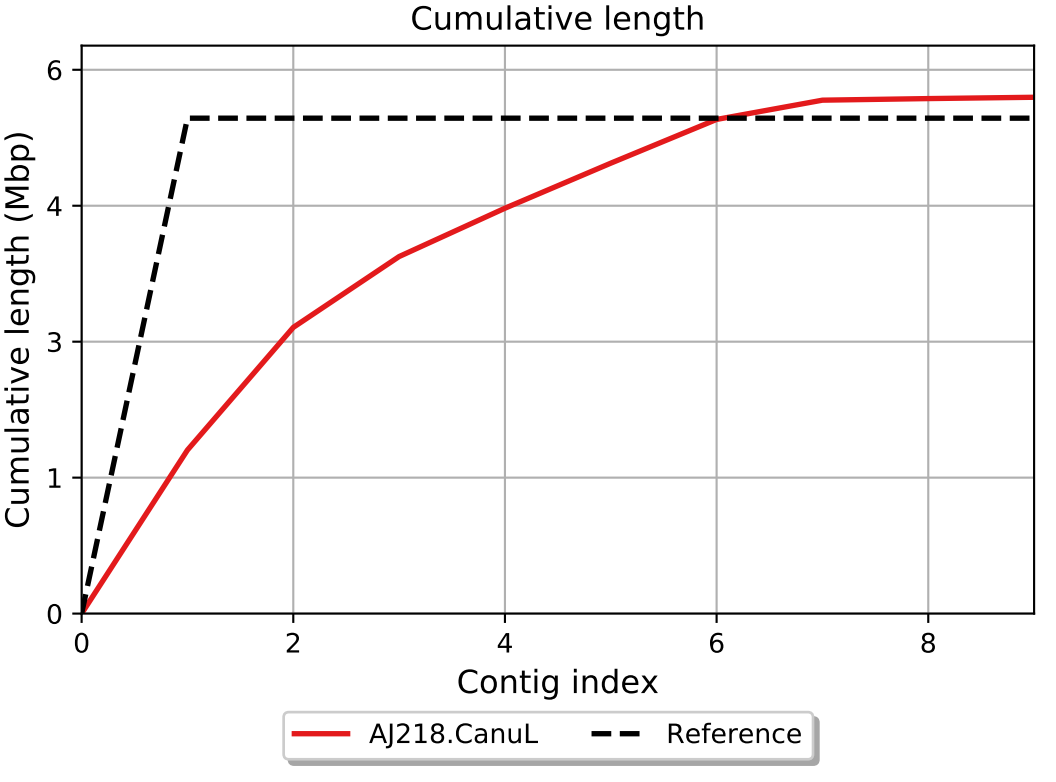
Unaligned report

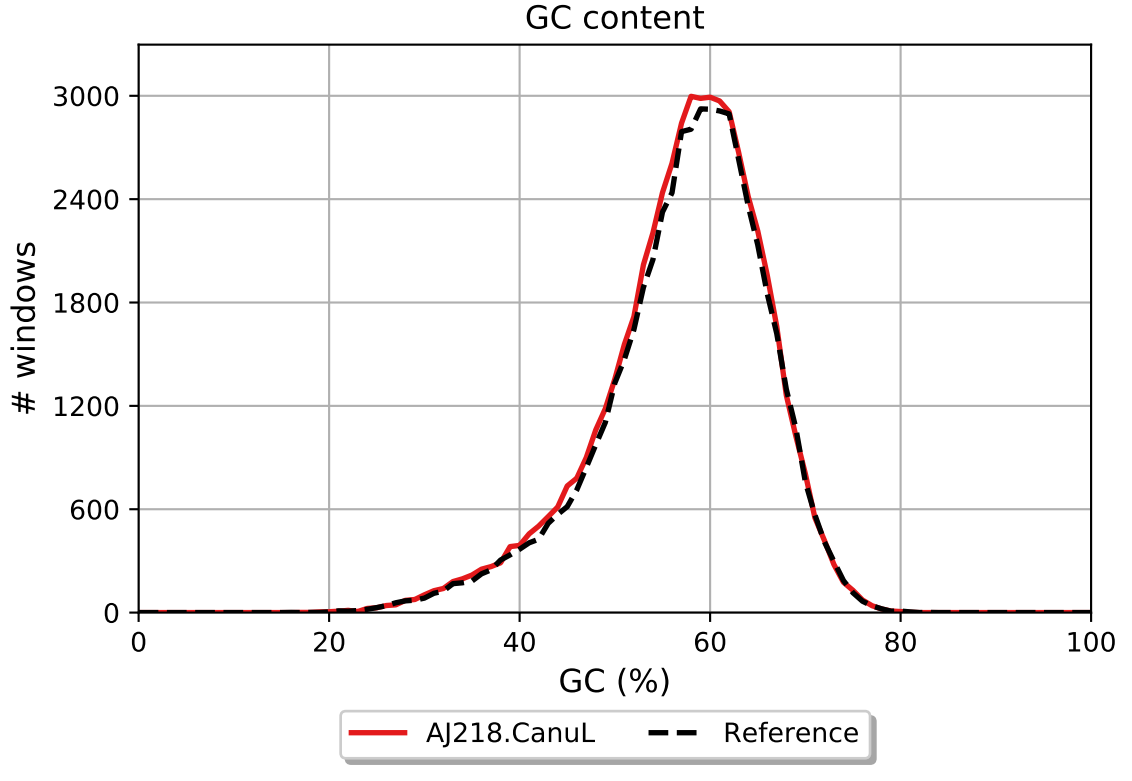
	AJ218.CanuL
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
Partially unaligned length	231873
# N's	0

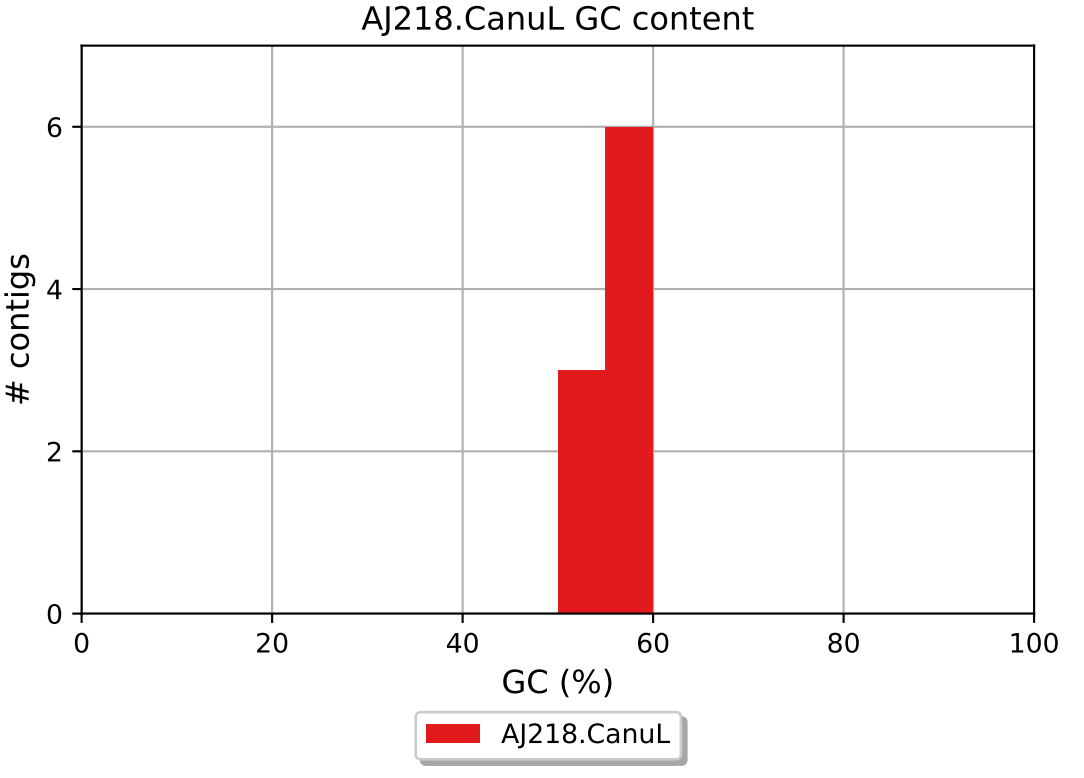
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

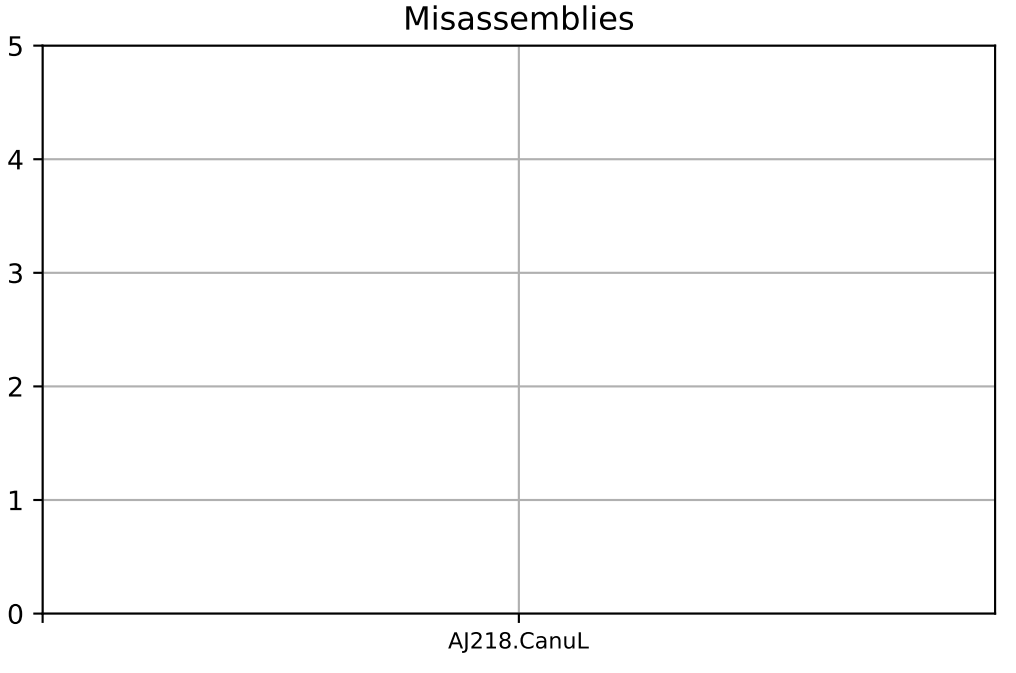

Nx
Contig length (kbp)
1600
1200
800
400
0
0
20
40
60
80
100
x
AJ218.CanuL

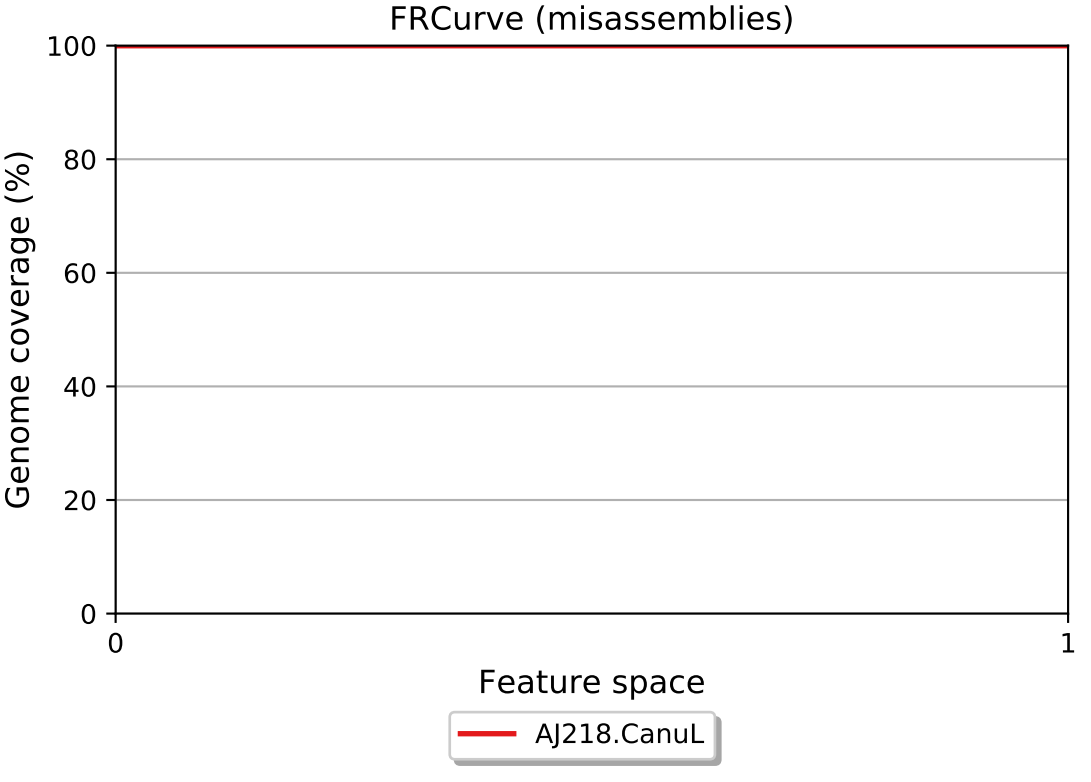

NGx
Contig length (kbp)
1600
1200
800
400
0
0
20
40
60
80
100
x
AJ218.CanuL

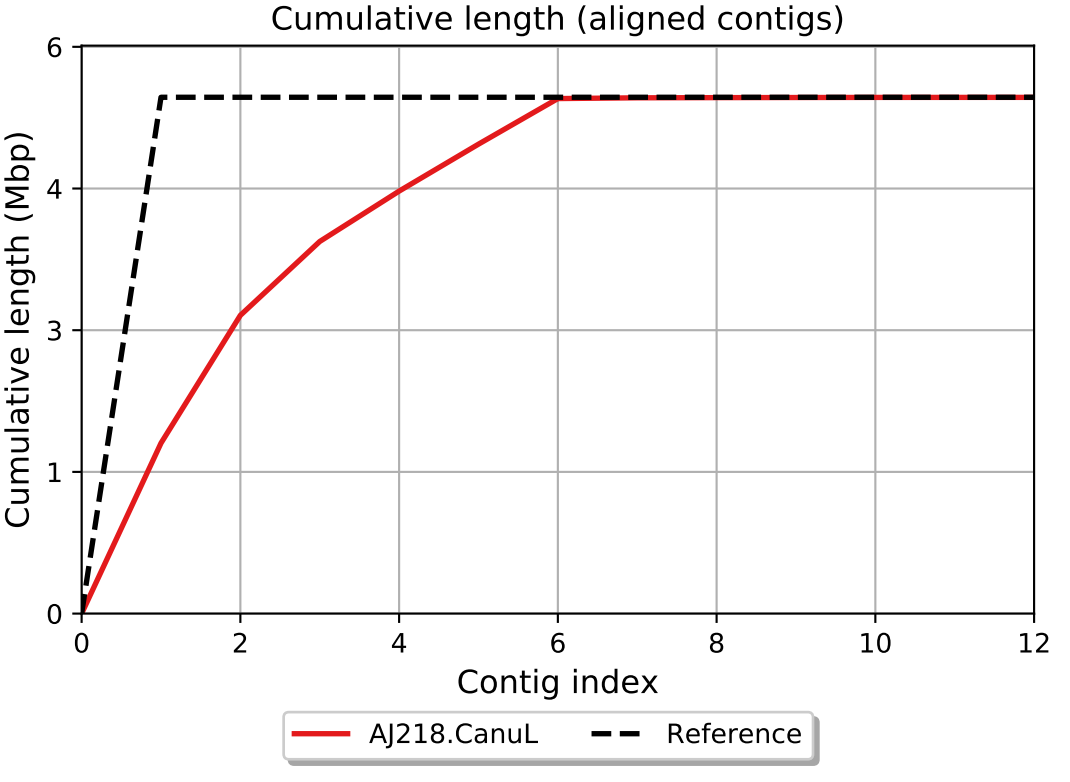

Cumulative length
Cumulative length (Mbp)
0
1
3
4
6
0
2
4
6
8
Contig index
AJ218.CanuL
Reference

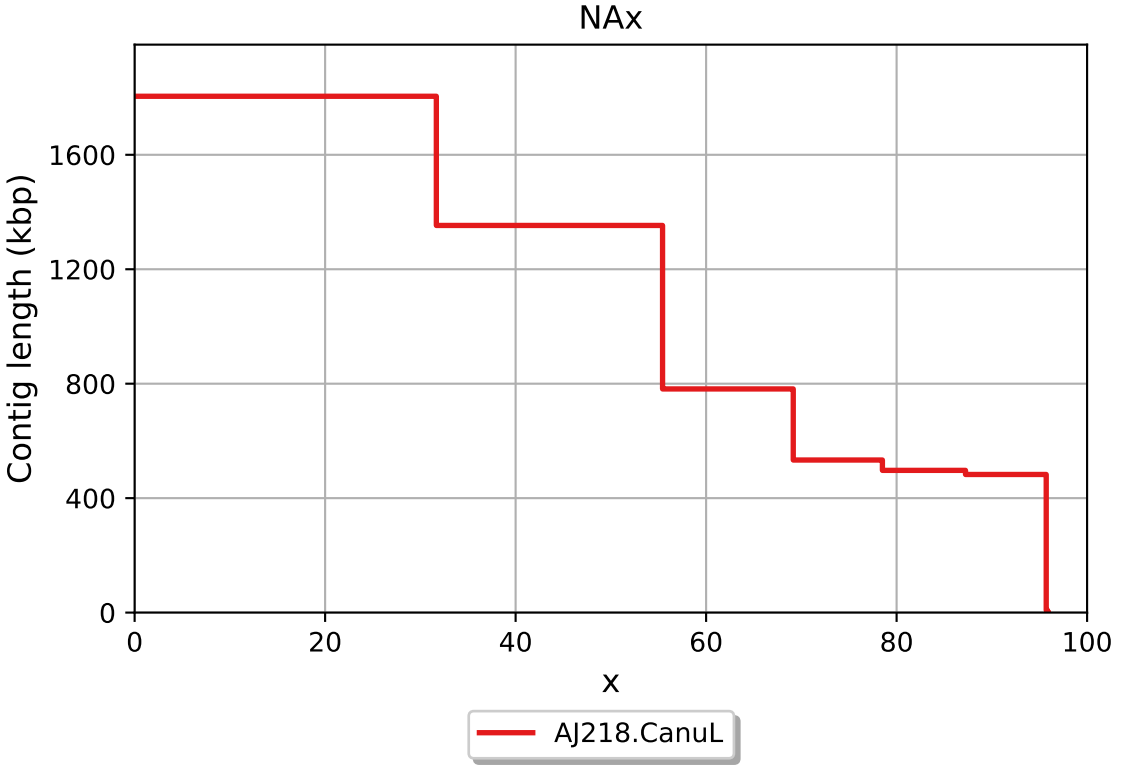

GC content
3000
2400
1800
1200
600
0
windows
0
20
40
60
80
100
GC (%)
AJ218.CanuL
Reference

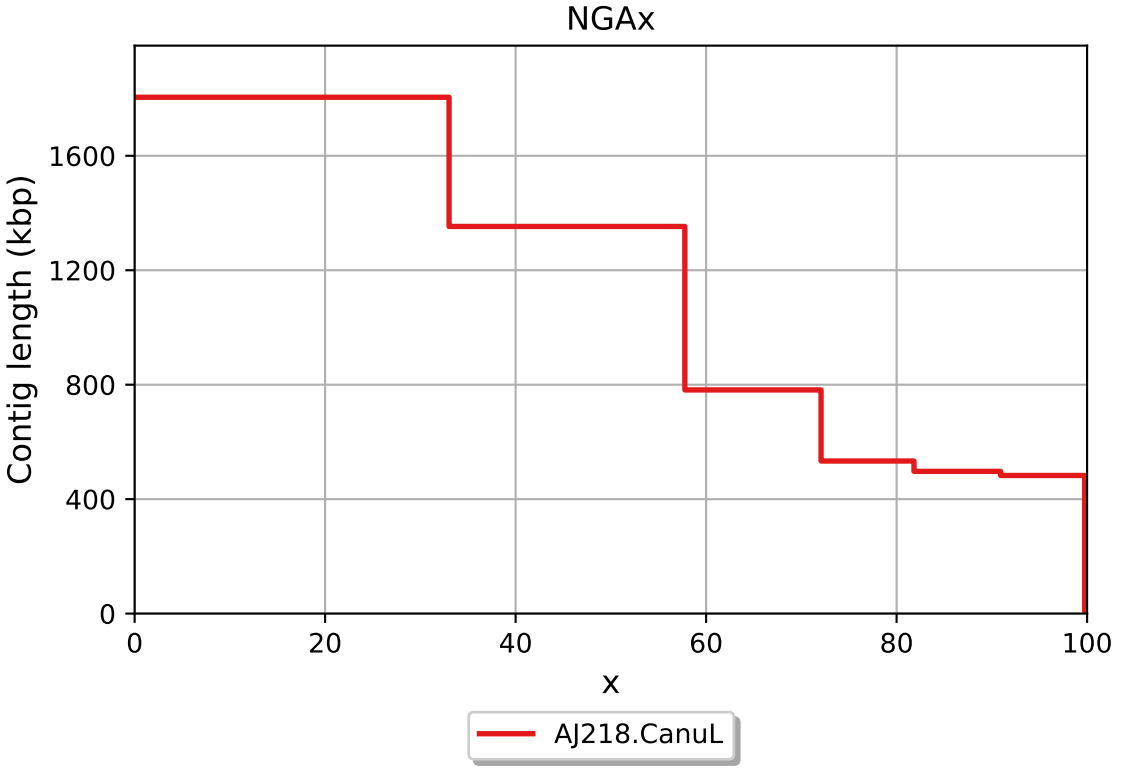

AJ218.CanuL GC content
contigs
0
2
4
6
0
20
40
60
80
100
GC (%)
AJ218.CanuL


Misassemblies
5
4
3
2
1
0
AJ218.CanuL


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


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
3
4
6
0
2
4
6
8
10
12
Contig index
AJ218.CanuL
Reference


NAx
Contig length (kbp)
1600
1200
800
400
0
0
20
40
60
80
100
x
AJ218.CanuL


NGAx
Contig length (kbp)
1600
1200
800
400
0
0
20
40
60
80
100
x
AJ218.CanuL