Report

	AJ218.SoDe2H
# contigs (>= 0 bp)	39733
# contigs (>= 1000 bp)	377
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	8145888
Total length (>= 1000 bp)	495623
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2476
Largest contig	3250
Total length	1913384
Reference length	5465981
GC (%)	55.04
Reference GC (%)	57.29
N50	761
N75	611
L50	910
L75	1612
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	733
# unaligned mis. contigs	3
# unaligned contigs	83 + 5 part
Unaligned length	65961
Genome fraction (%)	33.369
Duplication ratio	1.013
# N's per 100 kbp	686.69
# mismatches per 100 kbp	1.64
# indels per 100 kbp	2.14
Largest alignment	3250
Total aligned length	1828053
NA50	738
NGA50	-
NA75	590
LA50	935
LA75	1661

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

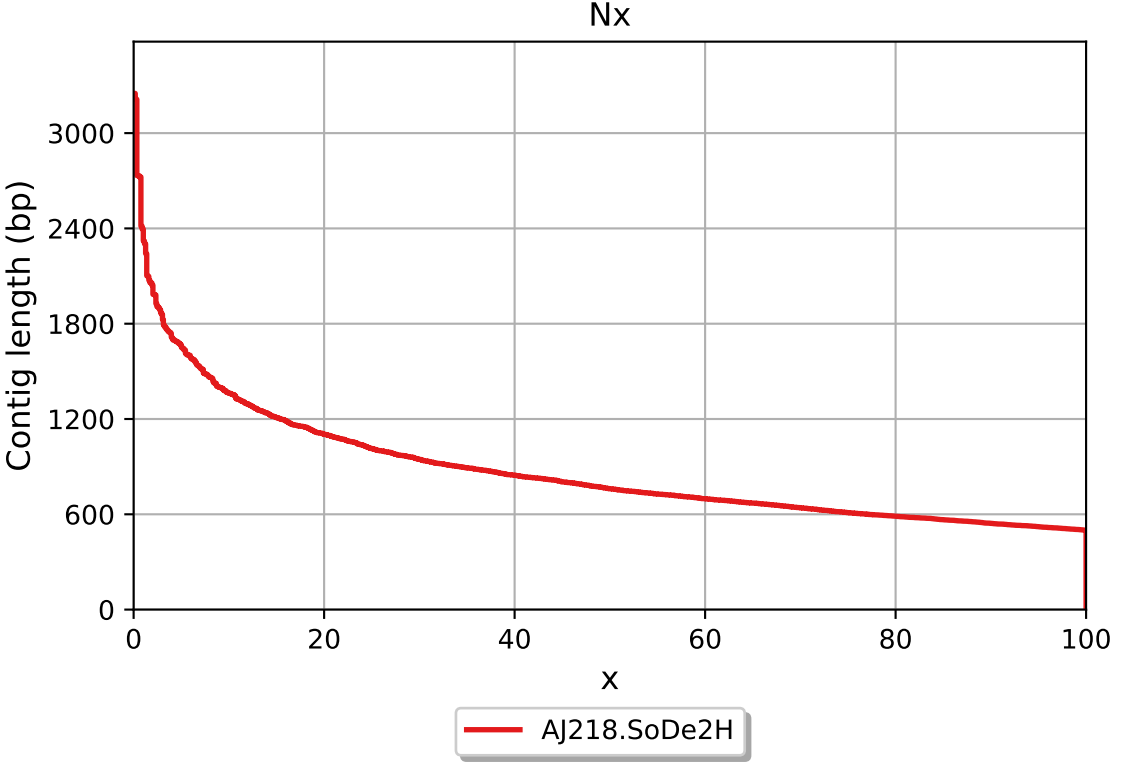
	AJ218.SoDe2H
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	733
# unaligned mis. contigs	3
# mismatches	30
# indels	39
# indels (<= 5 bp)	22
# indels (> 5 bp)	17
Indels length	635

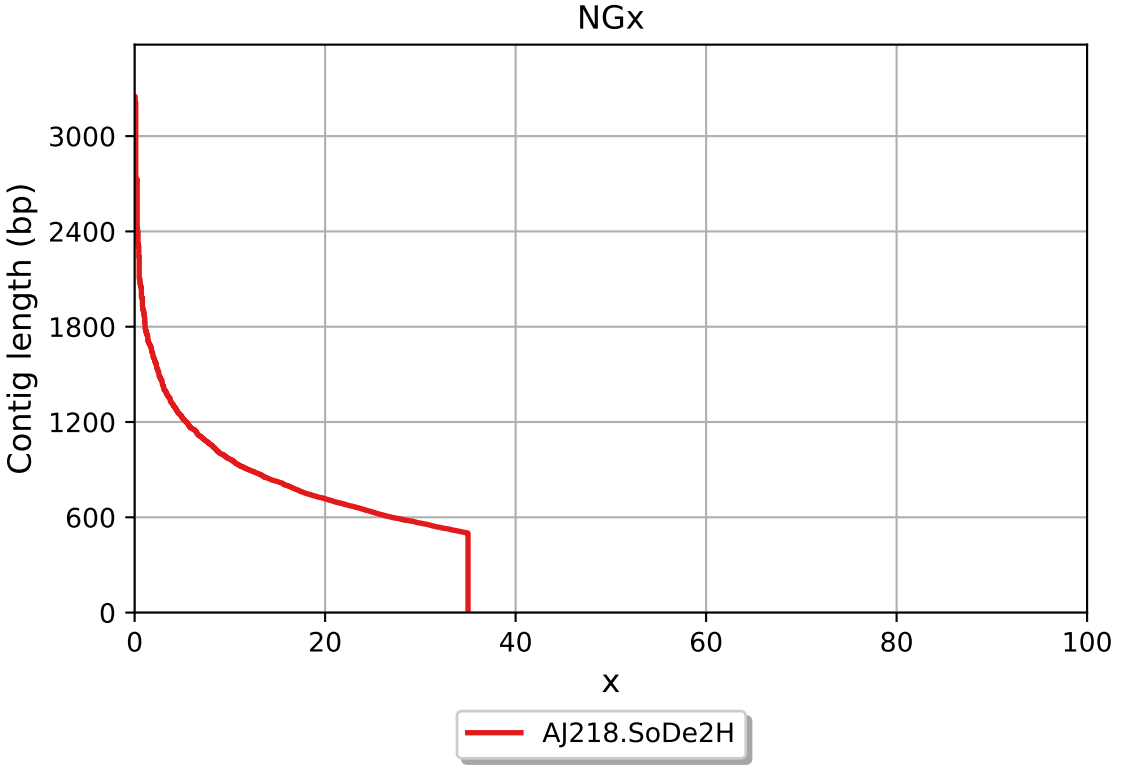
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

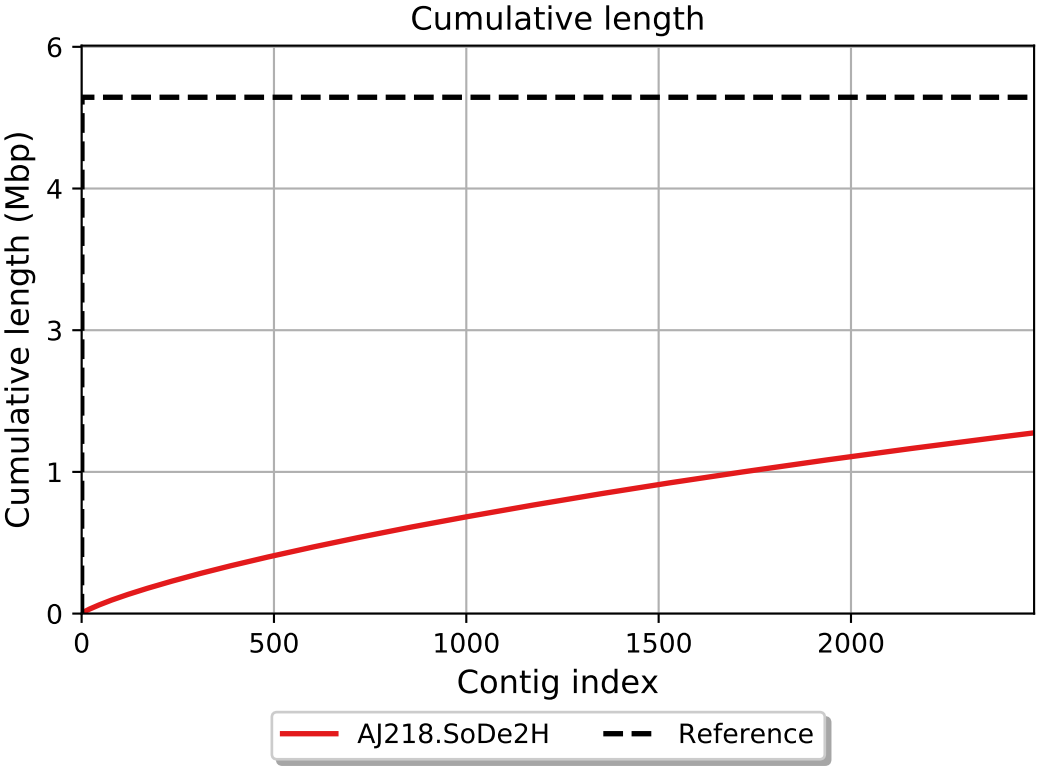
Unaligned report

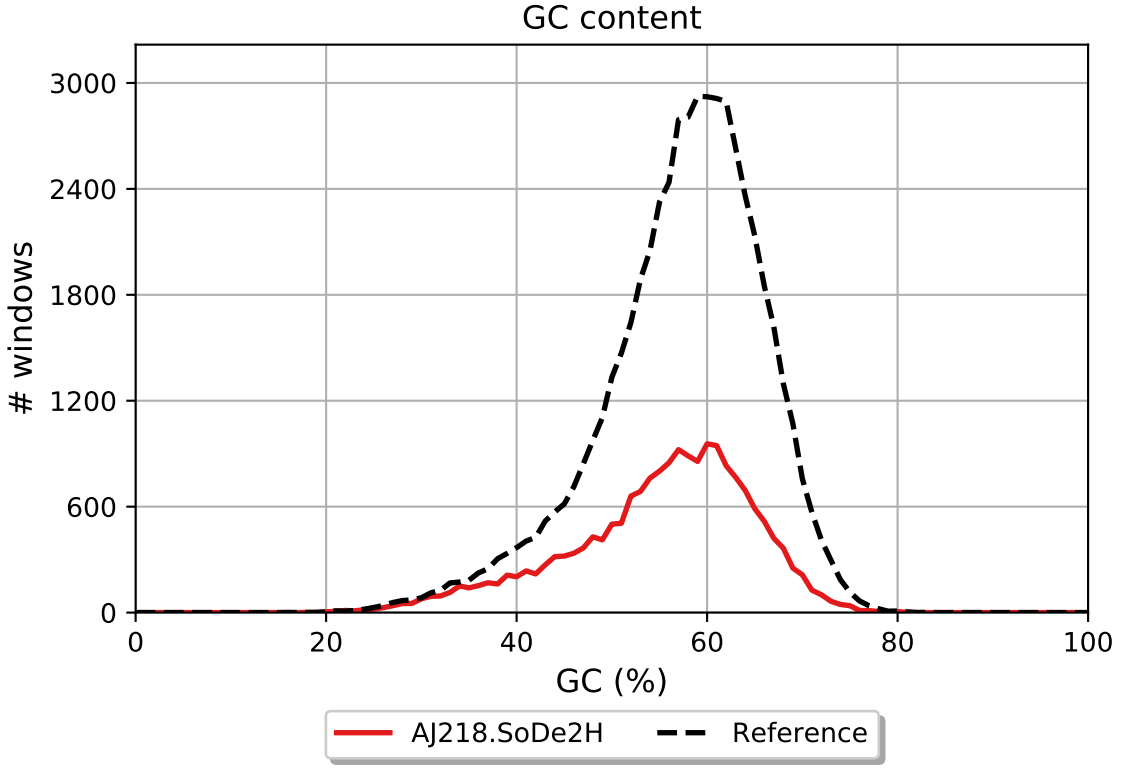
	AJ218.SoDe2H
# fully unaligned contigs	83
Fully unaligned length	61920
# partially unaligned contigs	5
Partially unaligned length	4041
# N's	13139

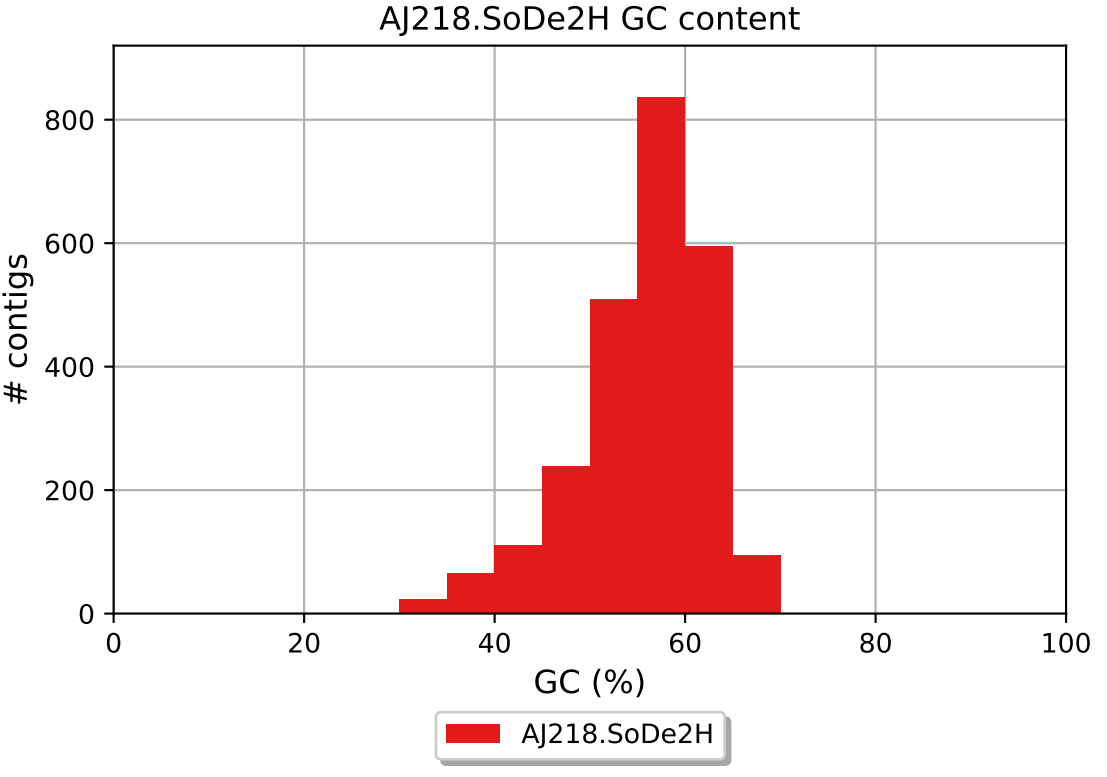
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

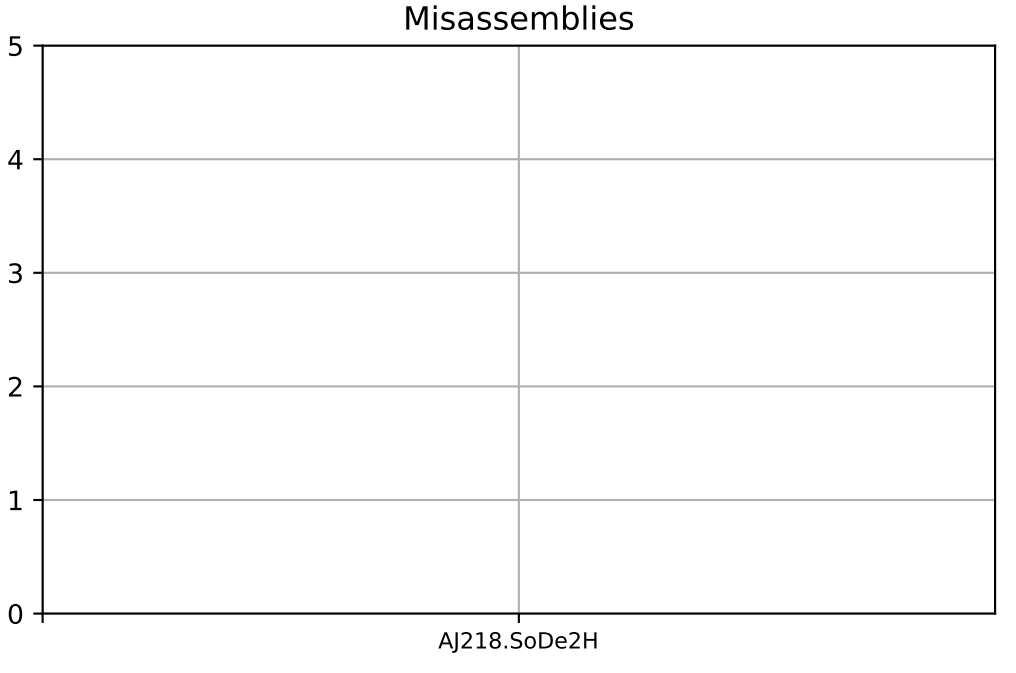

Nx
Contig length (bp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
AJ218.SoDe2H

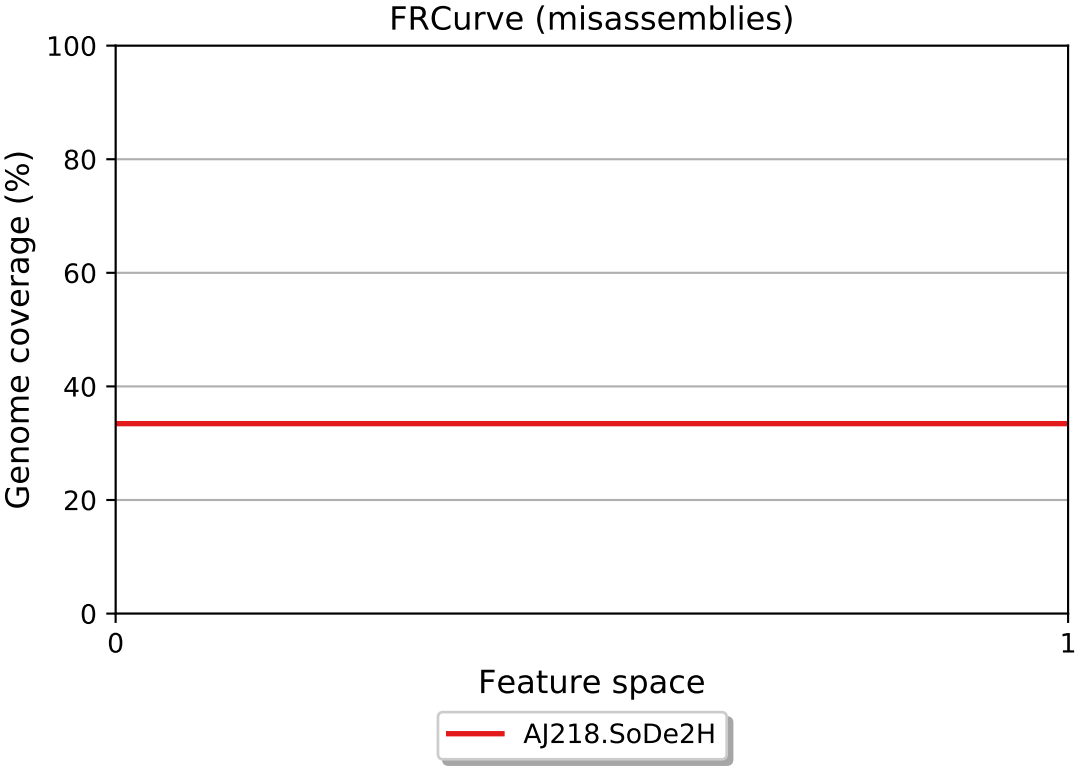

NGx
Contig length (bp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
AJ218.SoDe2H

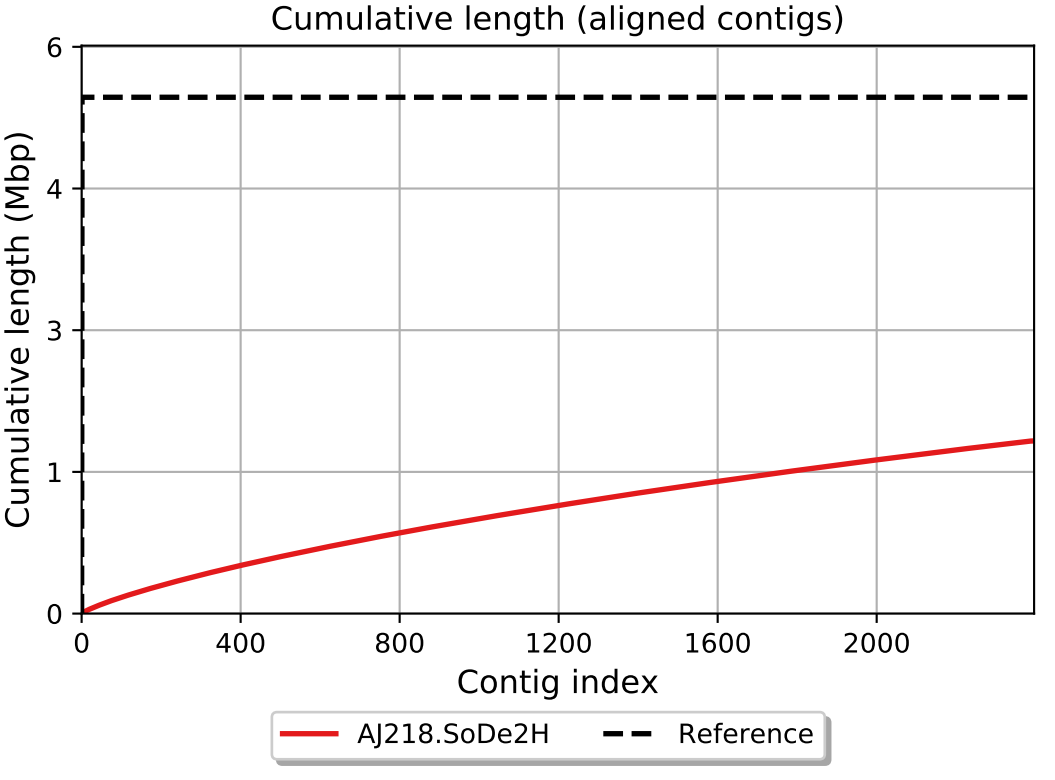

Cumulative length
Cumulative length (Mbp)
6
4
3
1
0
0
500
1000
1500
2000
Contig index
AJ218.SoDe2H
Reference

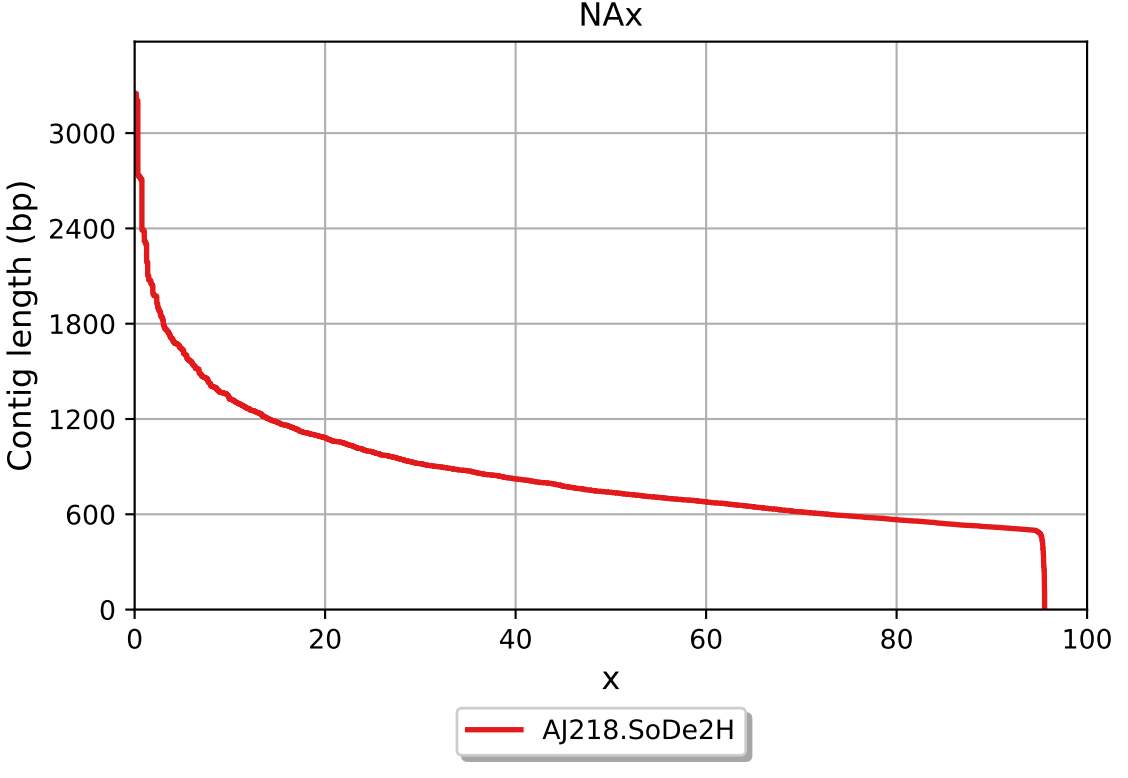

GC content
3000
2400
1800
1200
600
0
windows
0
20
40
60
80
100
GC (%)
AJ218.SoDe2H
Reference

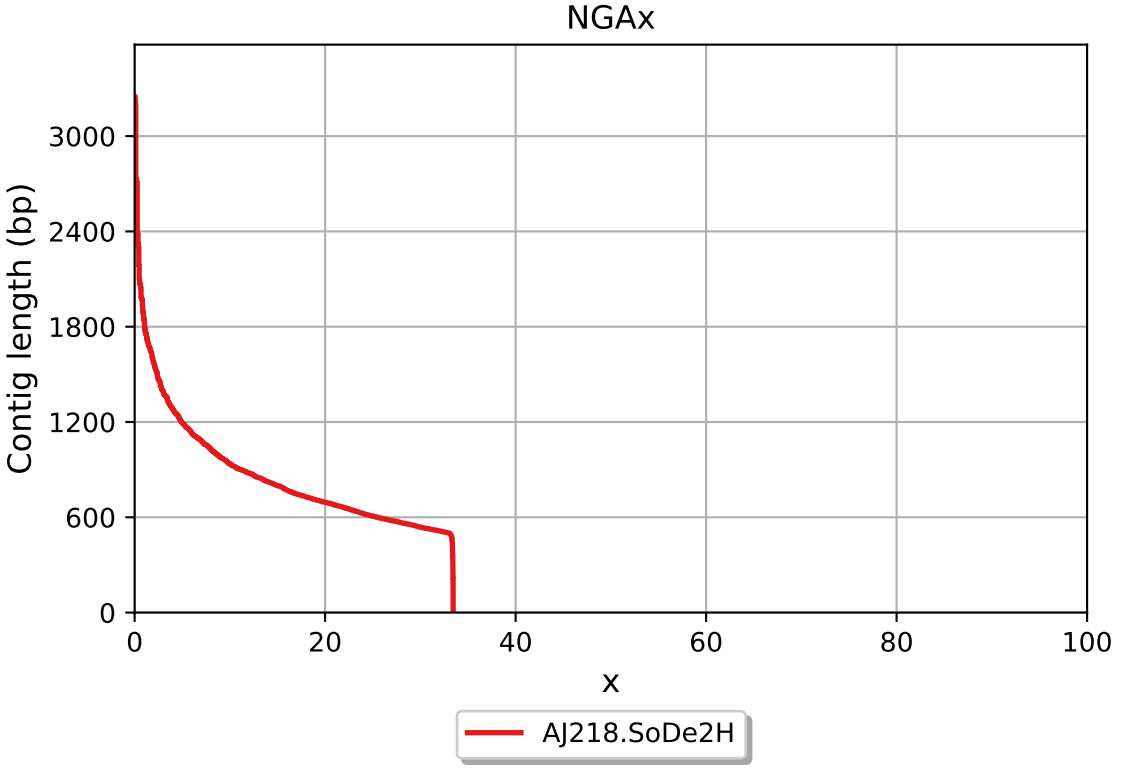

AJ218.SoDe2H GC content
contigs
0
200
400
600
800
0
20
40
60
80
100
GC (%)
AJ218.SoDe2H


Misassemblies
5
4
3
2
1
0
AJ218.SoDe2H


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
Feature space
AJ218.SoDe2H


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
3
4
6
0
400
800
1200
1600
2000
Contig index
AJ218.SoDe2H
Reference


NAx
Contig length (bp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
AJ218.SoDe2H


NGAx
Contig length (bp)
3000
2400
1800
1200
600
0
0
20
40
60
80
100
x
AJ218.SoDe2H