

Report

	AJ218.SoDe2L
# contigs (>= 0 bp)	23708
# contigs (>= 1000 bp)	1029
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	6932710
Total length (>= 1000 bp)	1468156
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3727
Largest contig	4511
Total length	3343474
Reference length	5465981
GC (%)	56.37
Reference GC (%)	57.29
N50	926
NG50	631
N75	689
L50	1241
LG50	2637
L75	2296
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	137
# unaligned mis. contigs	0
# unaligned contigs	121 + 0 part
Unaligned length	111719
Genome fraction (%)	58.833
Duplication ratio	1.005
# N's per 100 kbp	63.89
# mismatches per 100 kbp	1.55
# indels per 100 kbp	0.44
Largest alignment	4511
Total aligned length	3229100
NA50	908
NGA50	604
NA75	666
LA50	1263
LGA50	2703
LA75	2348

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

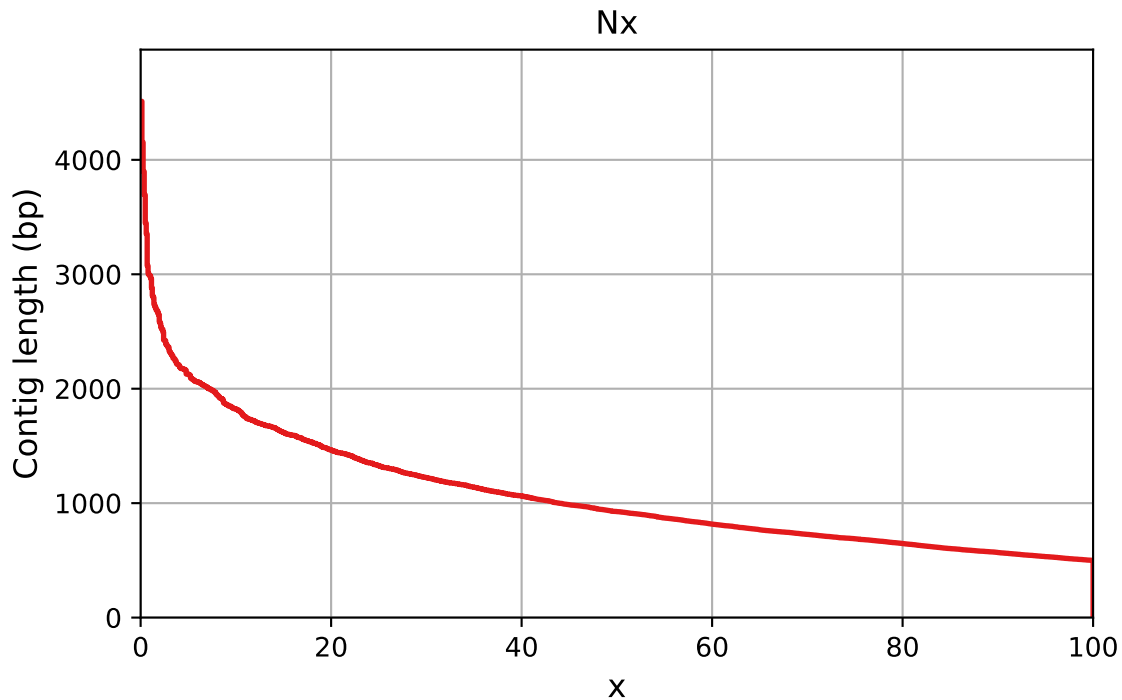
	AJ218.SoDe2L
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	137
# unaligned mis. contigs	0
# mismatches	50
# indels	14
# indels (≤ 5 bp)	13
# indels (> 5 bp)	1
Indels length	24

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

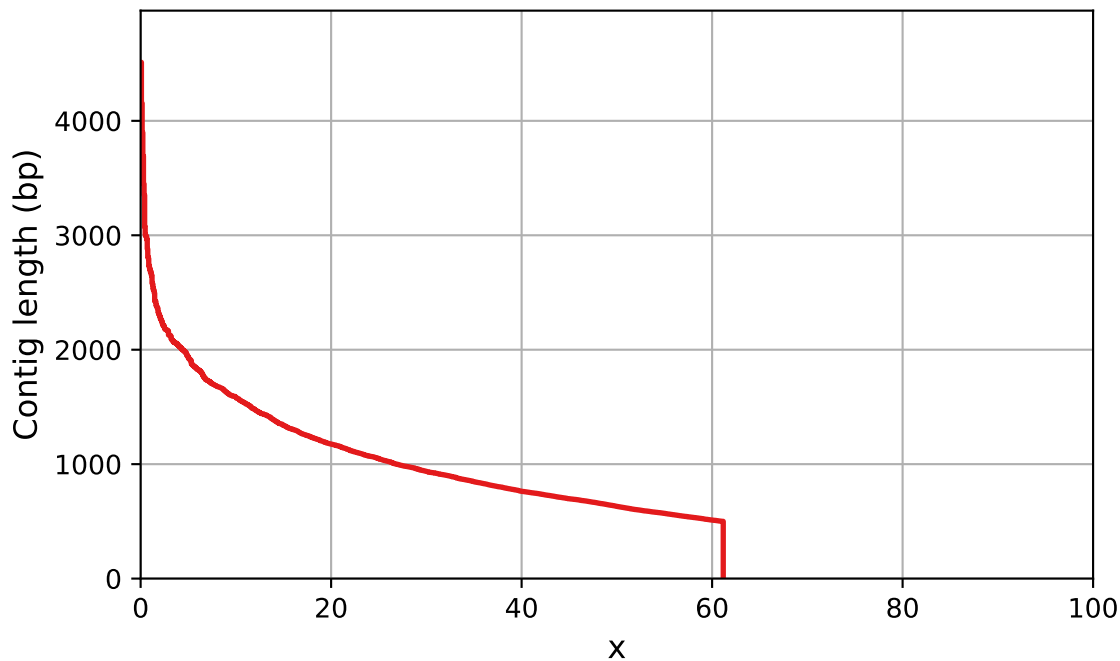
	AJ218.SoDe2L
# fully unaligned contigs	121
Fully unaligned length	111719
# partially unaligned contigs	0
Partially unaligned length	0
# N's	2136

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).

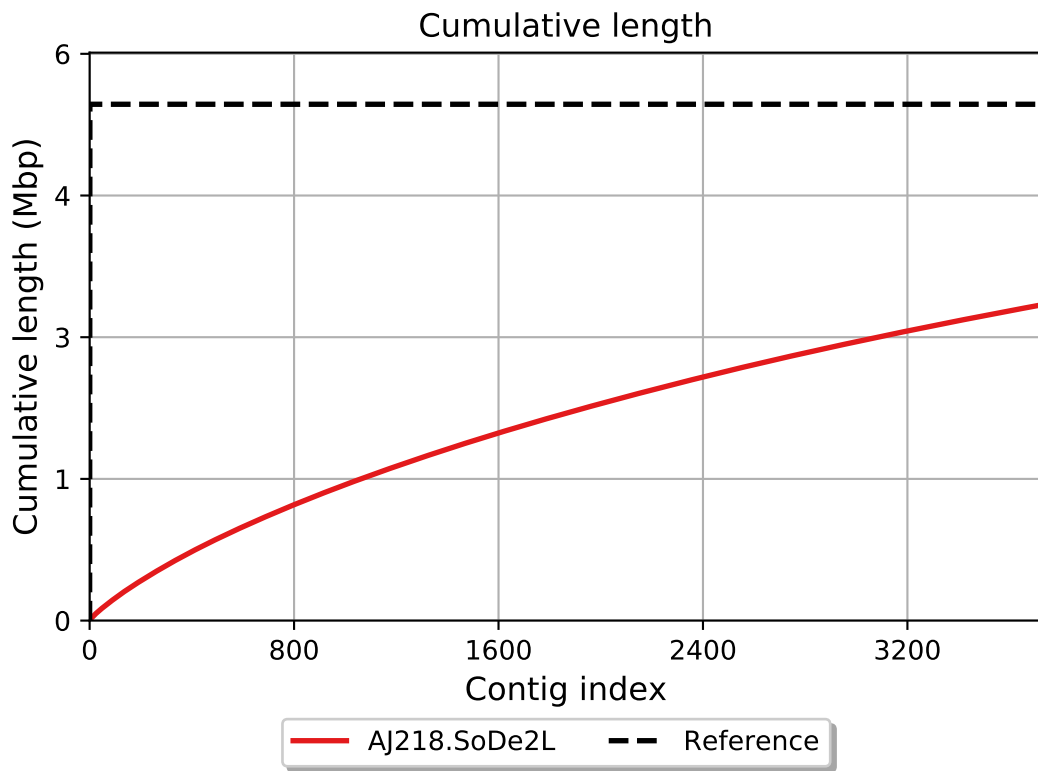


Aj218.SoDe2L

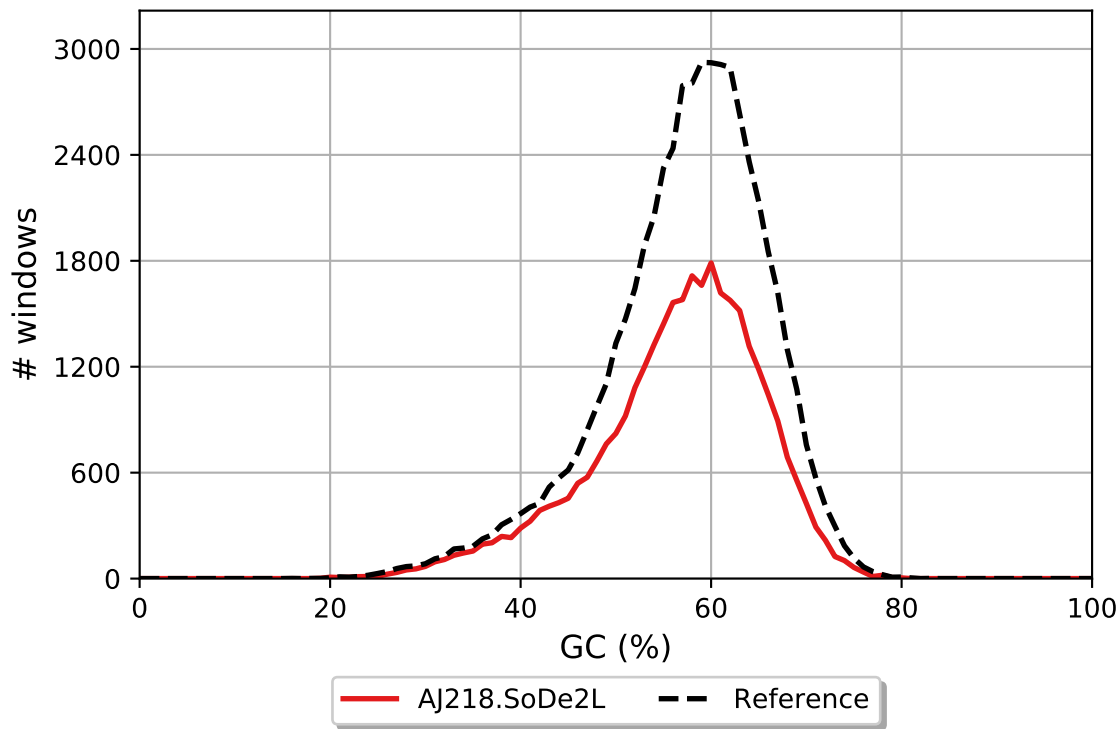
NGx



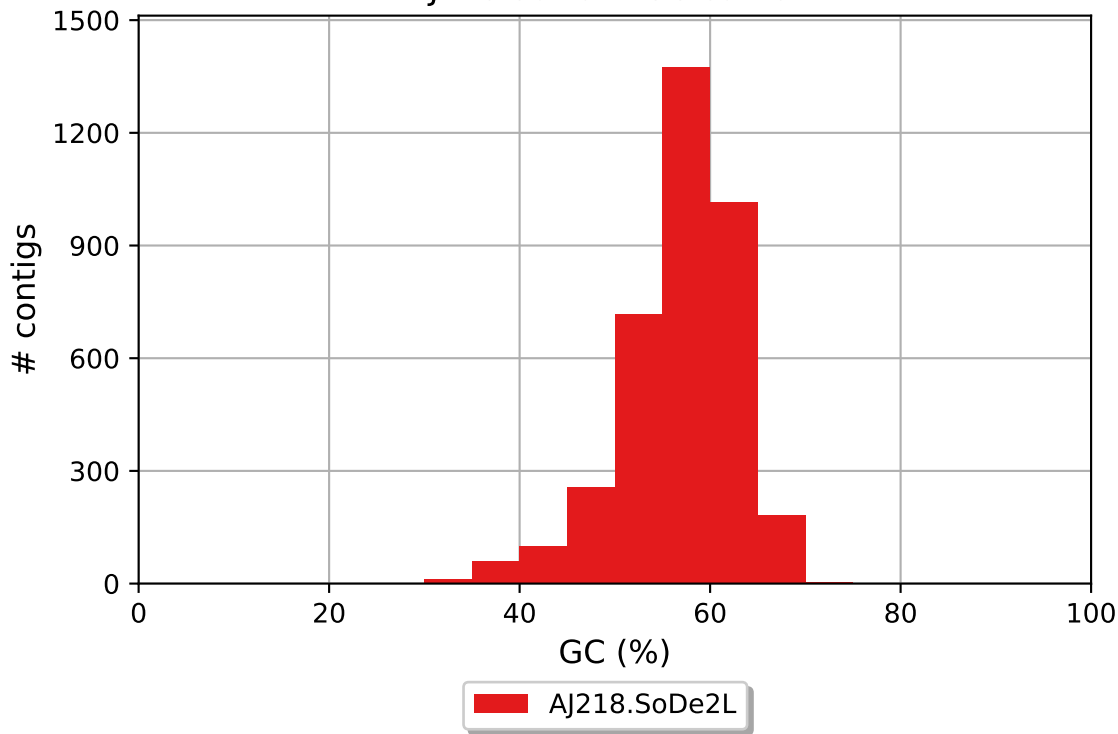
Aj218.SoDe2L



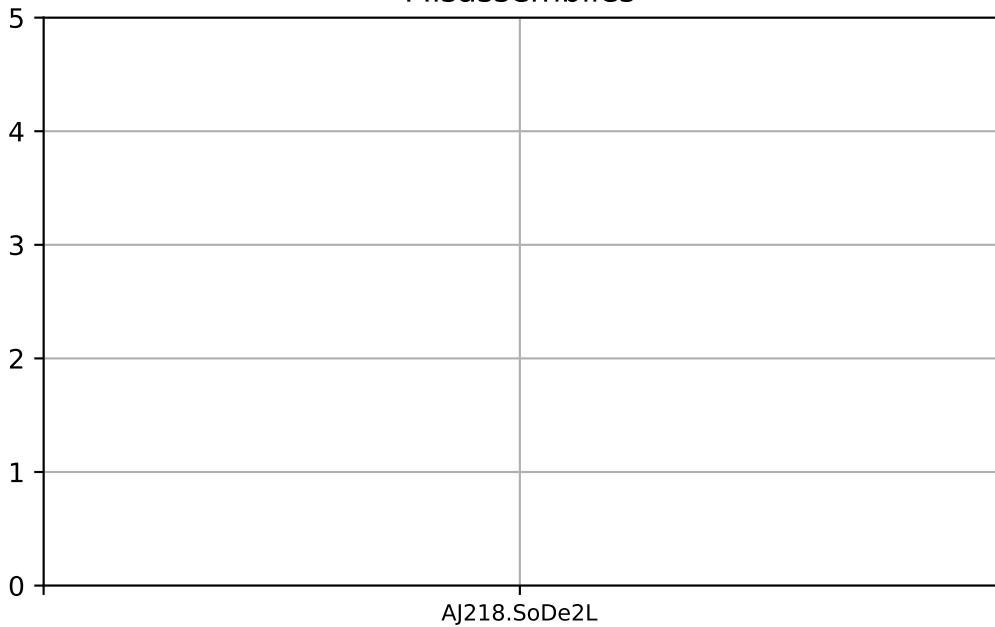
GC content



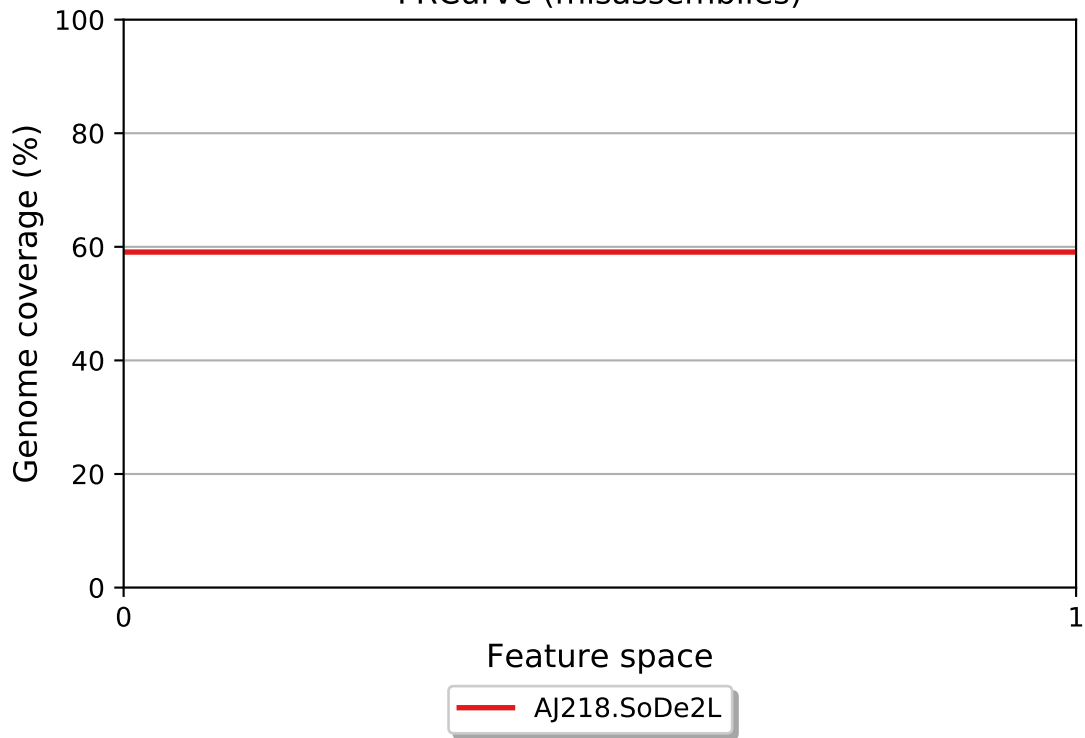
AJ218.SoDe2L GC content



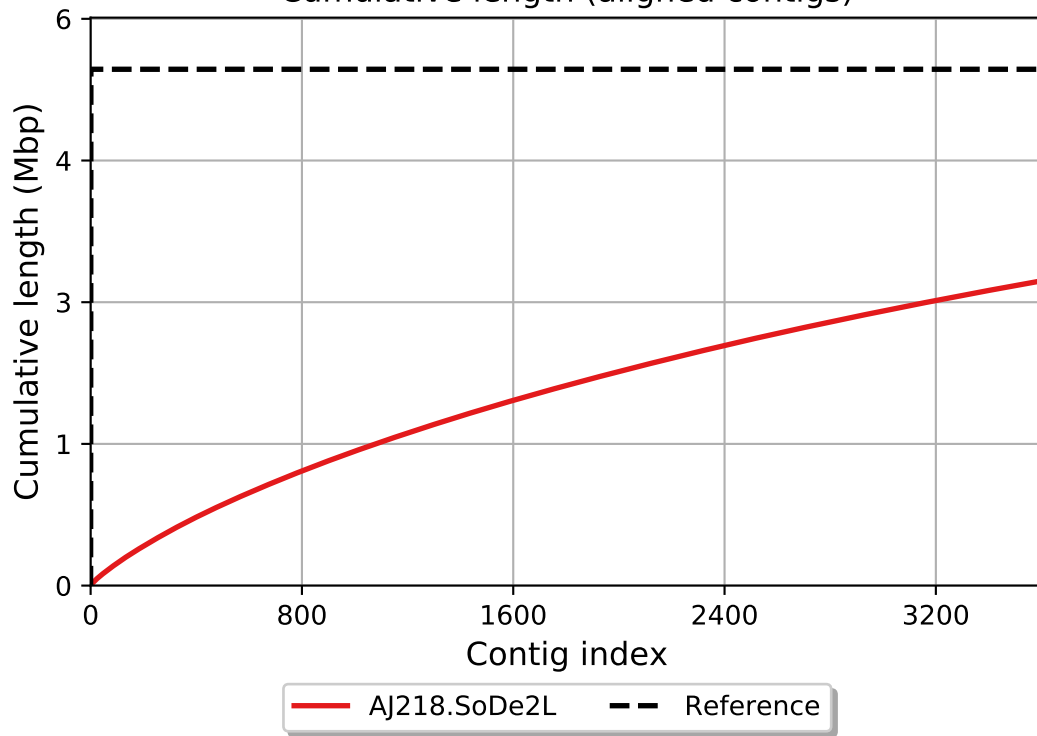
Misassemblies



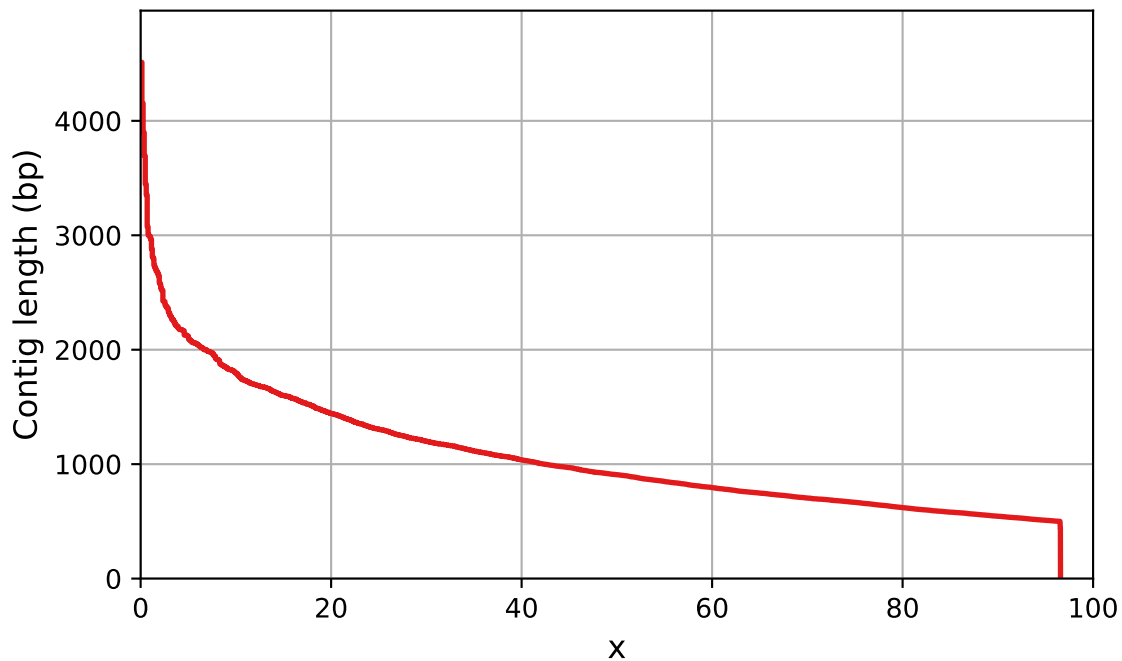
FRCurve (misassemblies)



Cumulative length (aligned contigs)

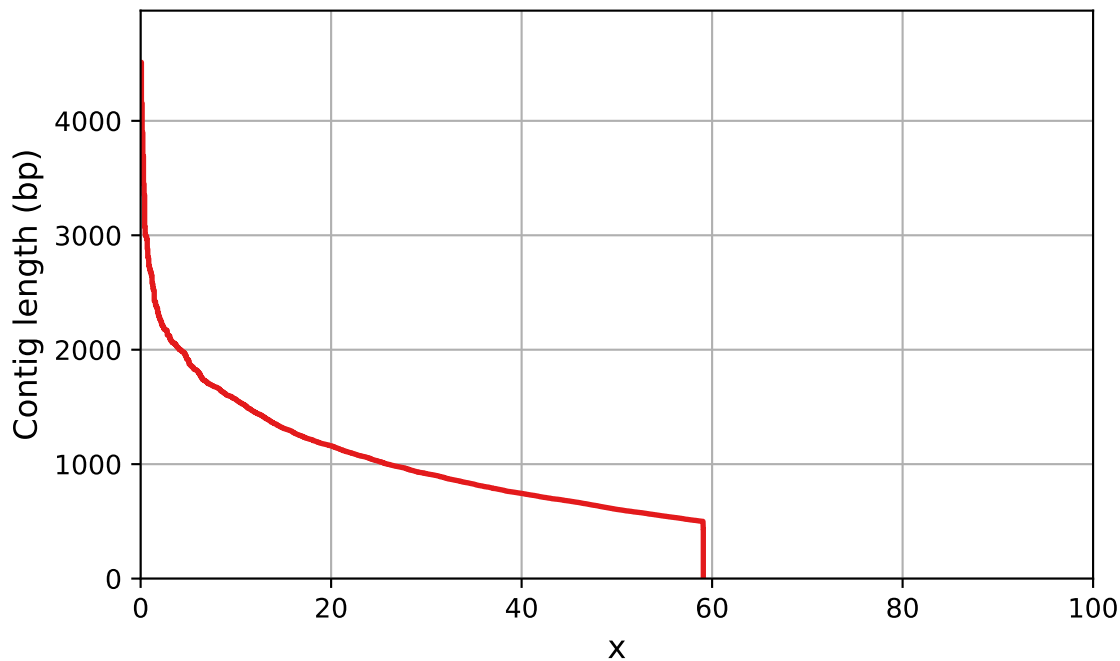


NAx



AJ218.SoDe2L

NGAx



AJ218.SoDe2L