

# Report

	AJ292.SoDe2L
# contigs (>= 0 bp)	23366
# contigs (>= 1000 bp)	916
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	6685279
Total length (>= 1000 bp)	1312226
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	3521
Largest contig	4259
Total length	3106641
Reference length	5445112
GC (%)	56.68
Reference GC (%)	57.62
N50	894
NG50	579
N75	673
L50	1173
LG50	2806
L75	2175
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	205
# unaligned mis. contigs	0
# unaligned contigs	5 + 0 part
Unaligned length	3440
Genome fraction (%)	56.646
Duplication ratio	1.006
# N's per 100 kbp	116.62
# mismatches per 100 kbp	1.78
# indels per 100 kbp	0.65
Largest alignment	4233
Total aligned length	3098285
NA50	891
NGA50	577
NA75	670
LA50	1175
LGA50	2813
LA75	2180

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

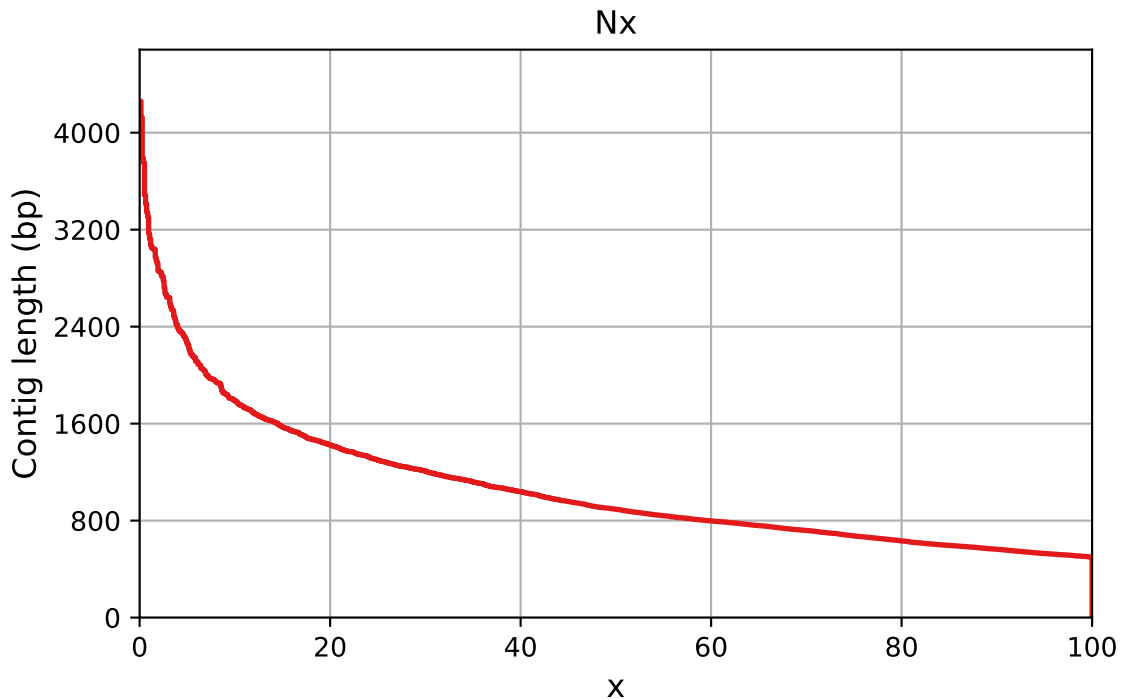
	AJ292.SoDe2L
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	205
# unaligned mis. contigs	0
# mismatches	55
# indels	20
# indels ( $\leq 5$ bp)	17
# indels ( $> 5$ bp)	3
Indels length	220

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

## Unaligned report

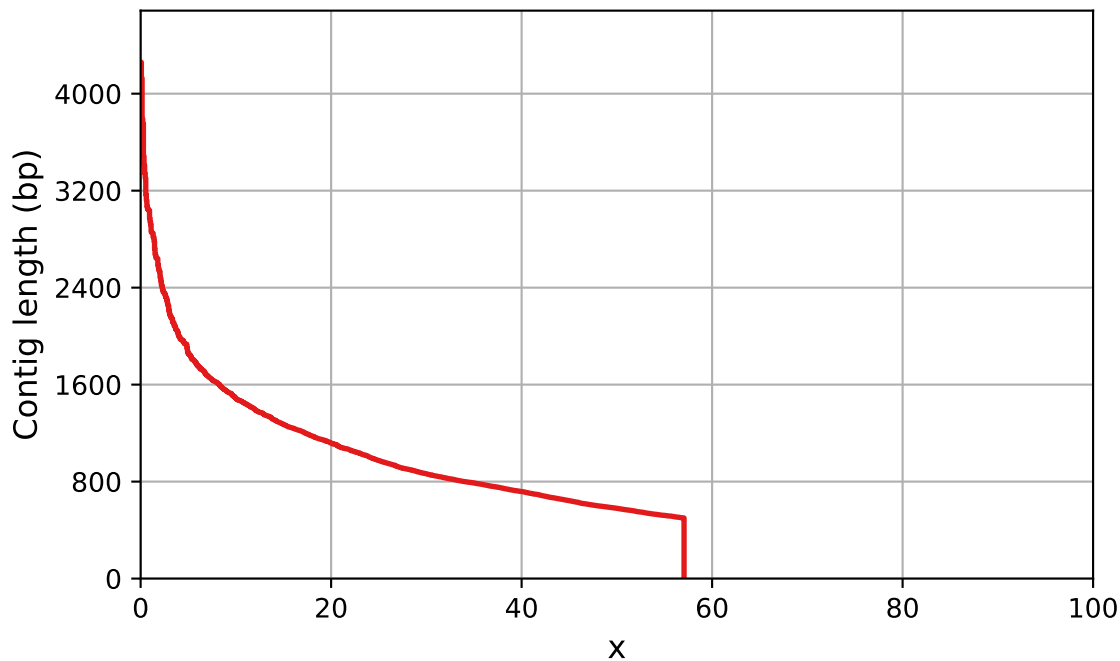
	AJ292.SoDe2L
# fully unaligned contigs	5
Fully unaligned length	3440
# partially unaligned contigs	0
Partially unaligned length	0
# N's	3623

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

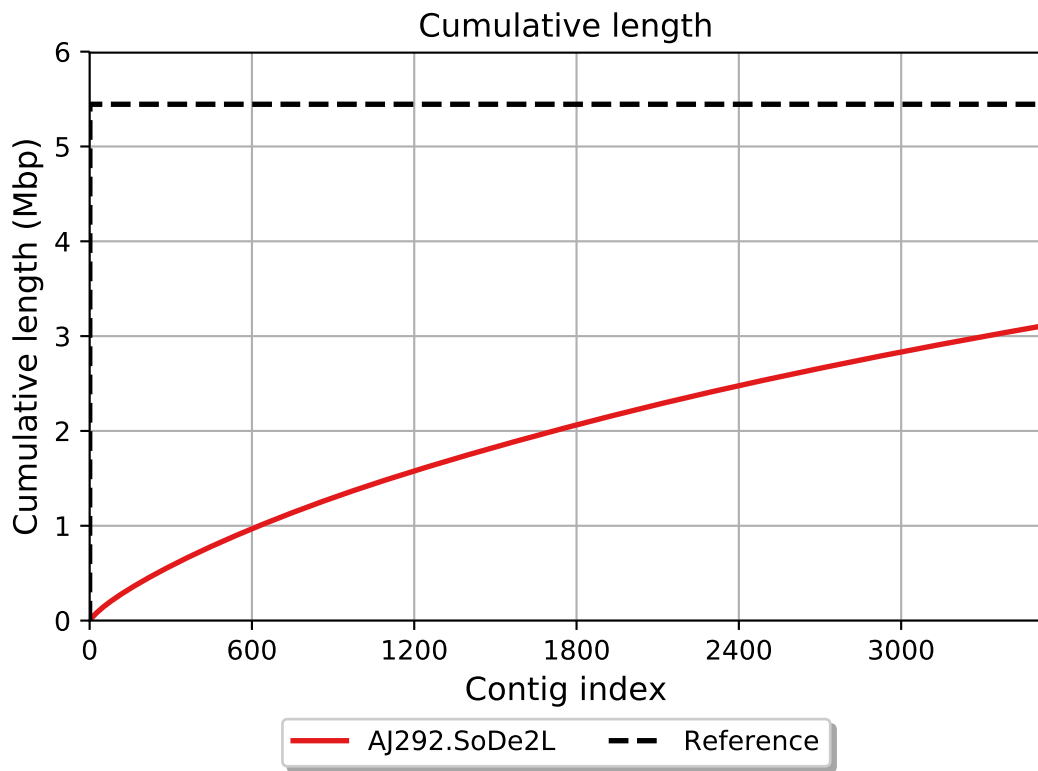


Aj292.SoDe2L

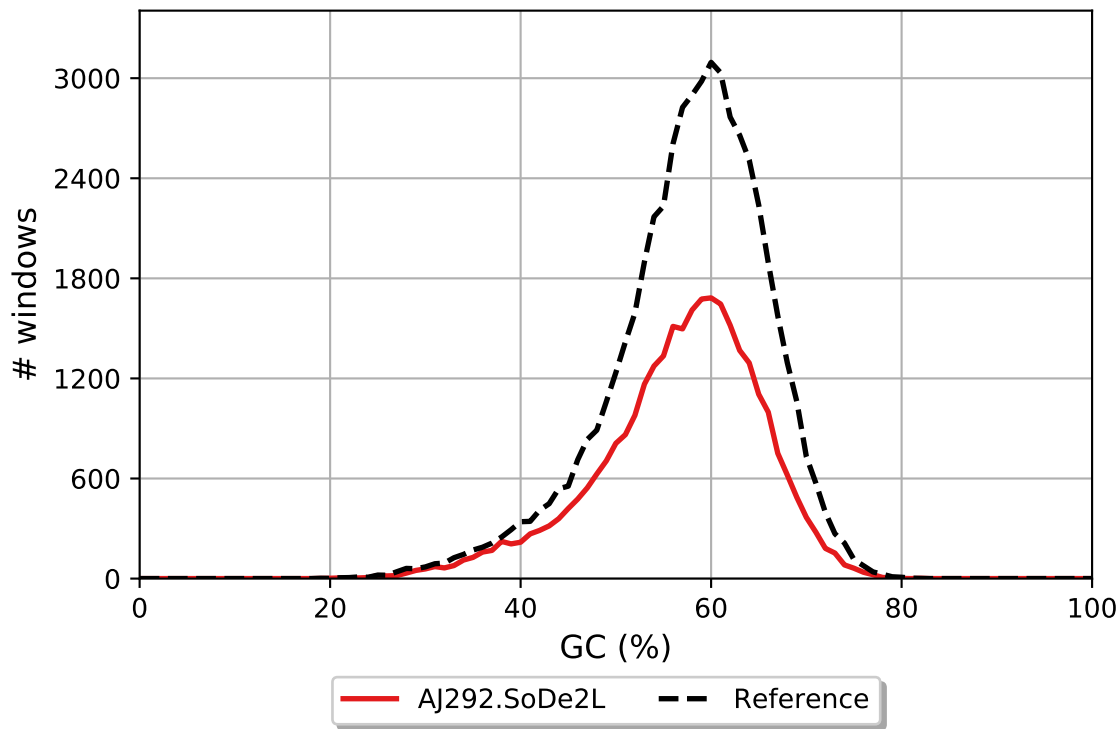
NGx



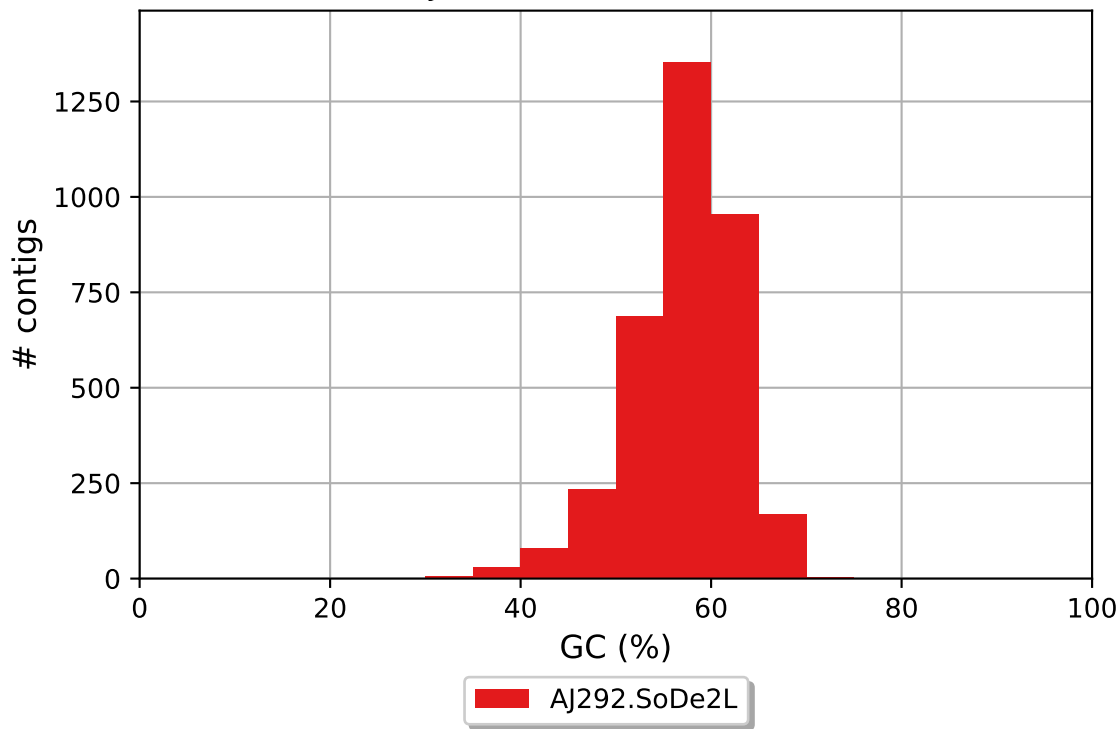
AJ292.SoDe2L



## GC content

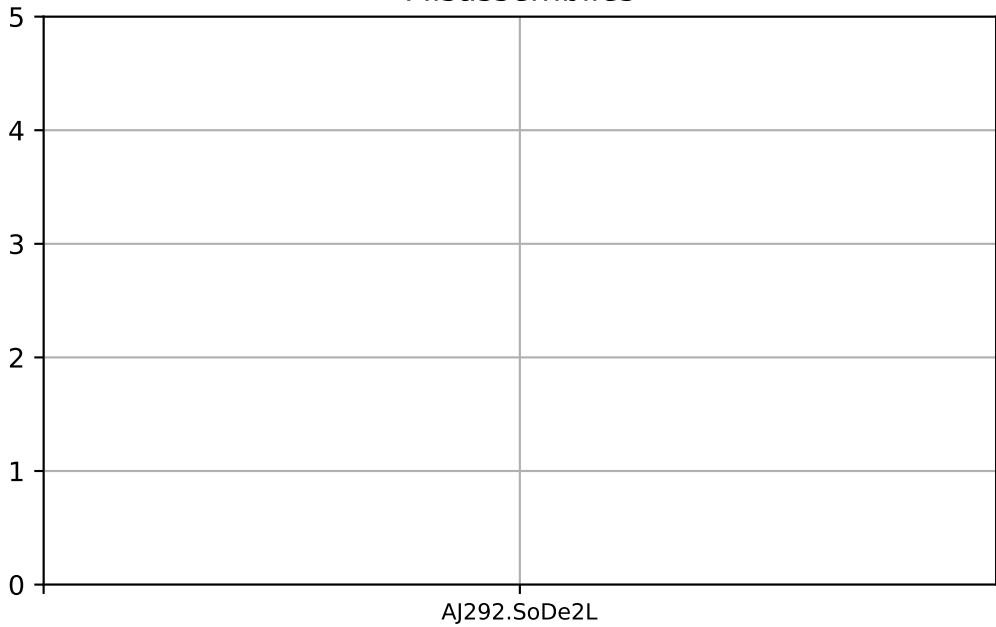


AJ292.SoDe2L GC content

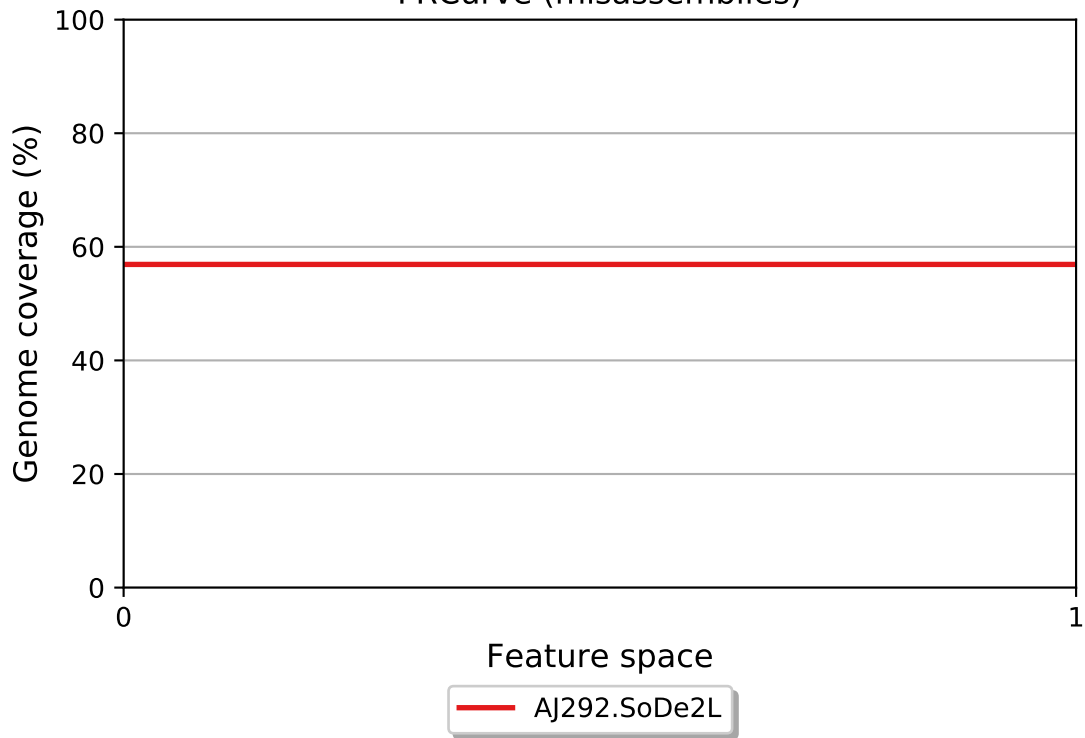




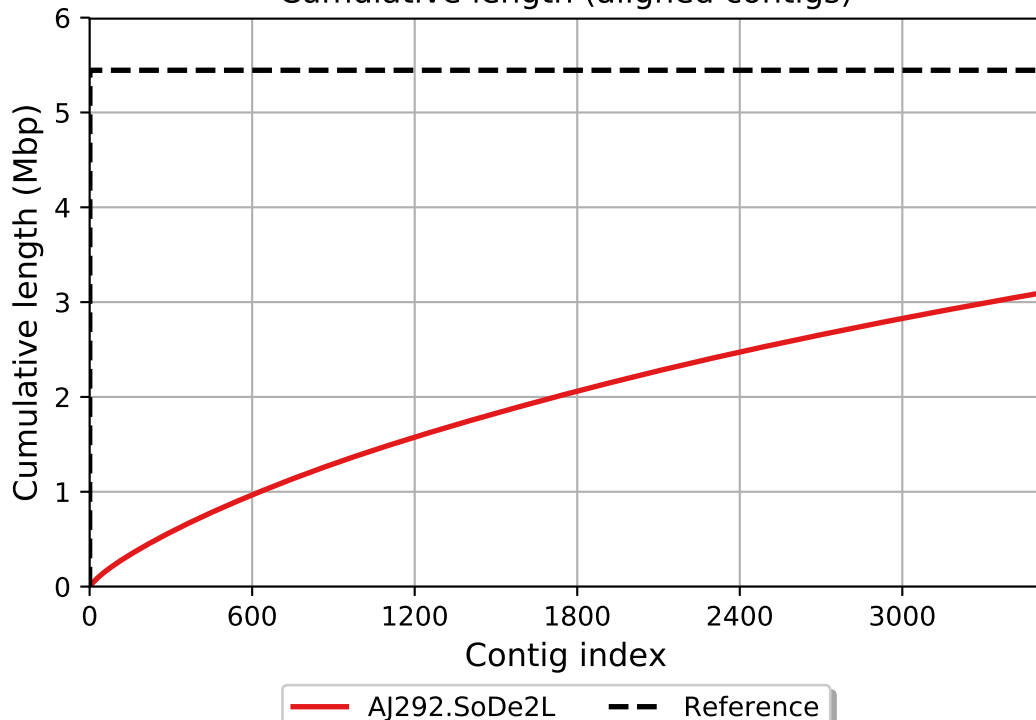
## Misassemblies



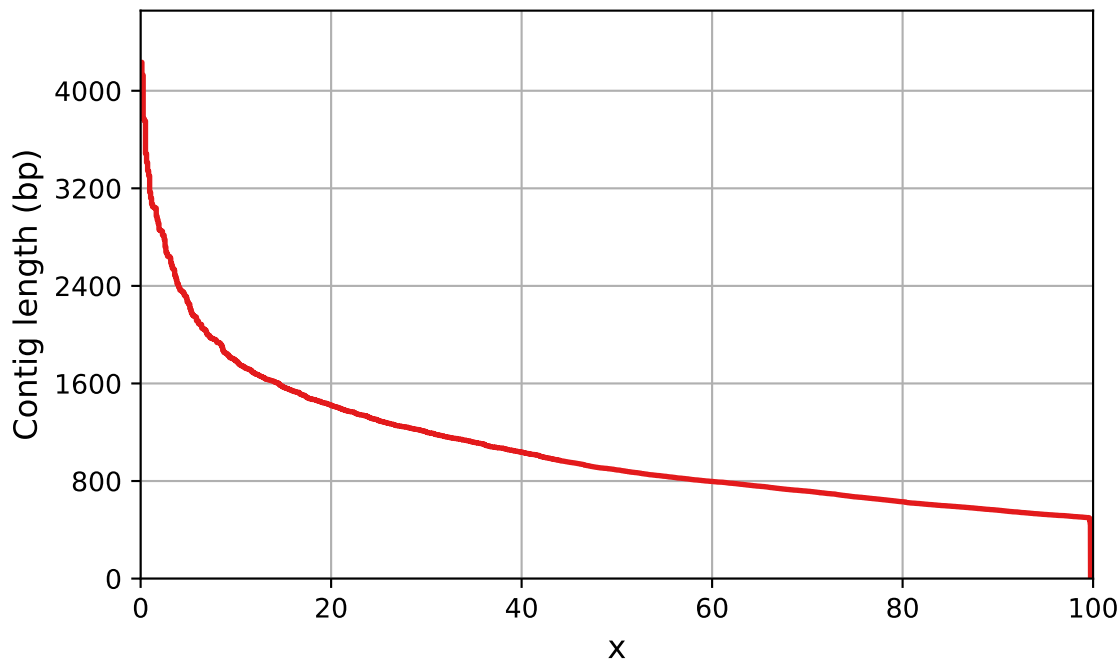
FRCurve (misassemblies)



Cumulative length (aligned contigs)

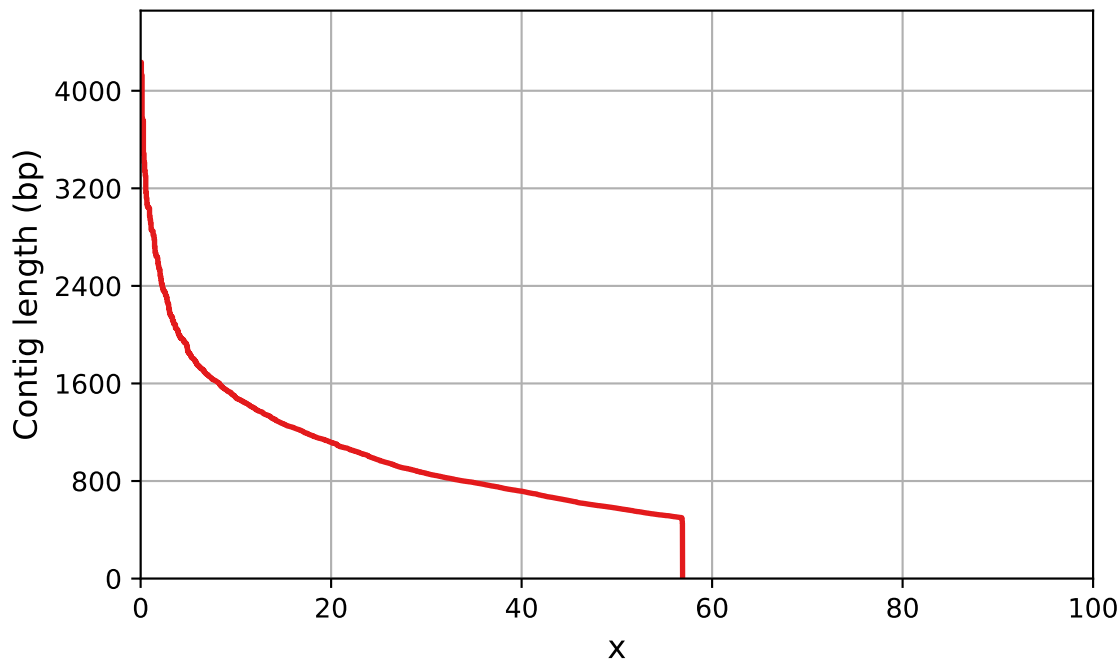


NAx



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# NGAx



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