

## Report

	AJ292.SoDe2H
# contigs (>= 0 bp)	38824
# contigs (>= 1000 bp)	339
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	7777649
Total length (>= 1000 bp)	450773
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2267
Largest contig	4141
Total length	1744167
Reference length	5445112
GC (%)	55.50
Reference GC (%)	57.62
N50	757
N75	606
L50	830
L75	1475
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	859
# unaligned mis. contigs	3
# unaligned contigs	19 + 7 part
Unaligned length	19226
Genome fraction (%)	31.150
Duplication ratio	1.017
# N's per 100 kbp	890.28
# mismatches per 100 kbp	3.48
# indels per 100 kbp	2.77
Largest alignment	4141
Total aligned length	1700272
NA50	735
NGA50	-
NA75	595
LA50	848
LA75	1511

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

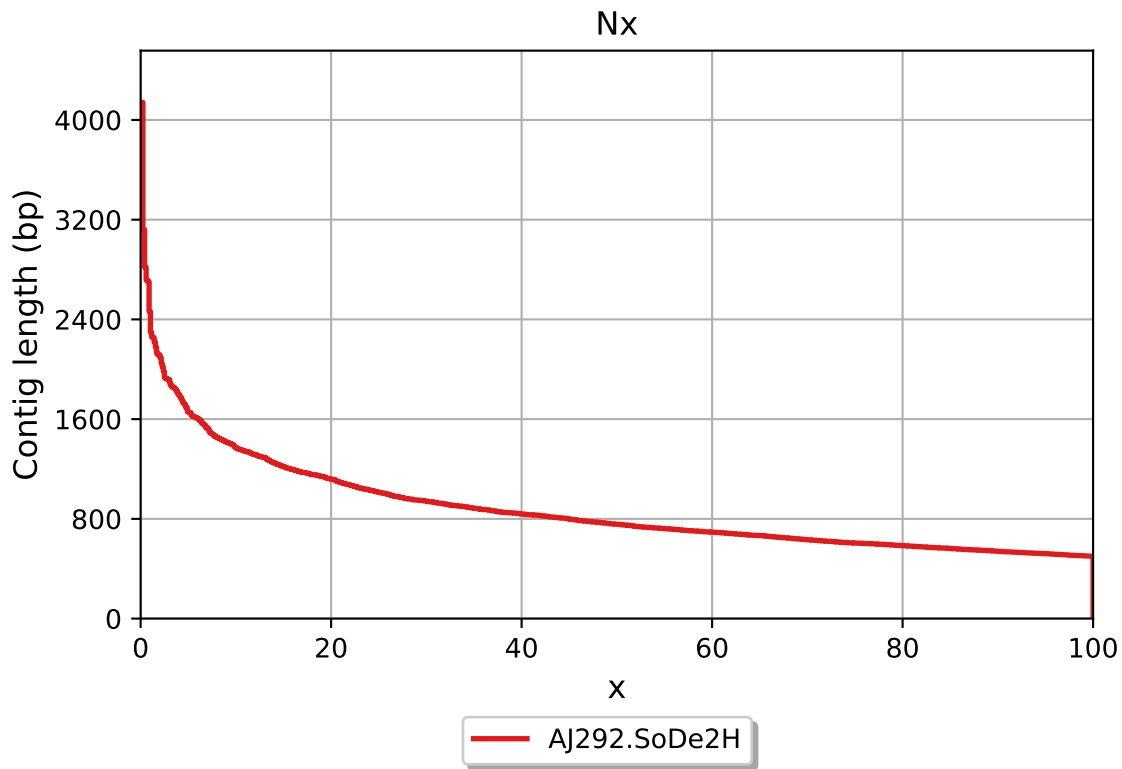
	AJ292.SoDe2H
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	859
# unaligned mis. contigs	3
# mismatches	59
# indels	47
# indels ( $\leq 5$ bp)	29
# indels ( $> 5$ bp)	18
Indels length	824

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).

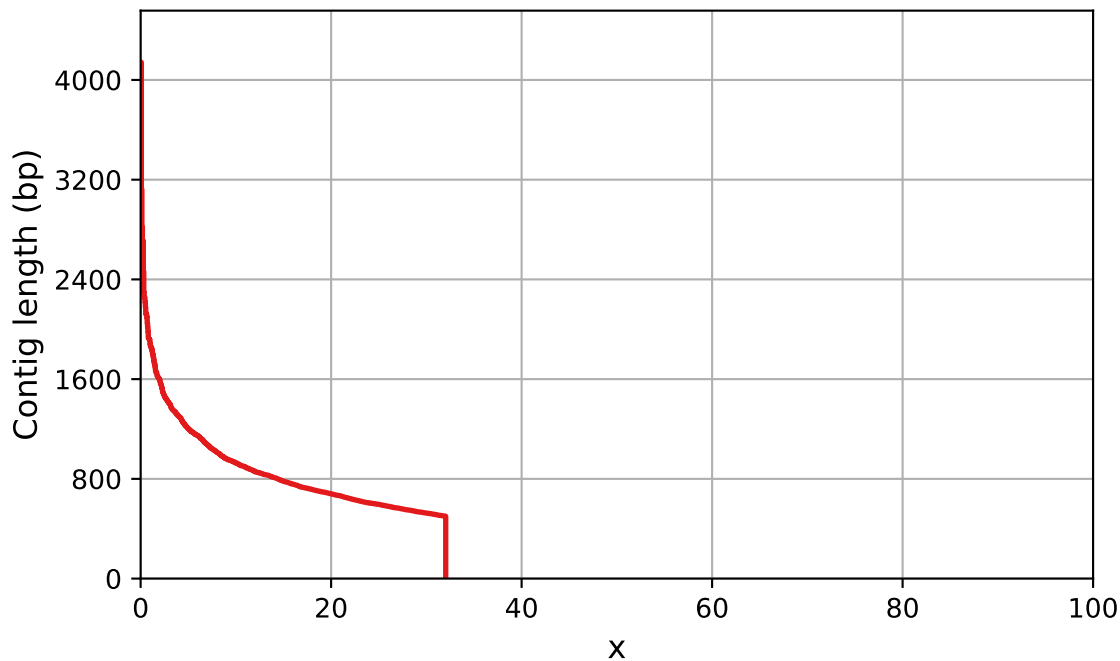
## Unaligned report

	AJ292.SoDe2H
# fully unaligned contigs	19
Fully unaligned length	14367
# partially unaligned contigs	7
Partially unaligned length	4859
# N's	15528

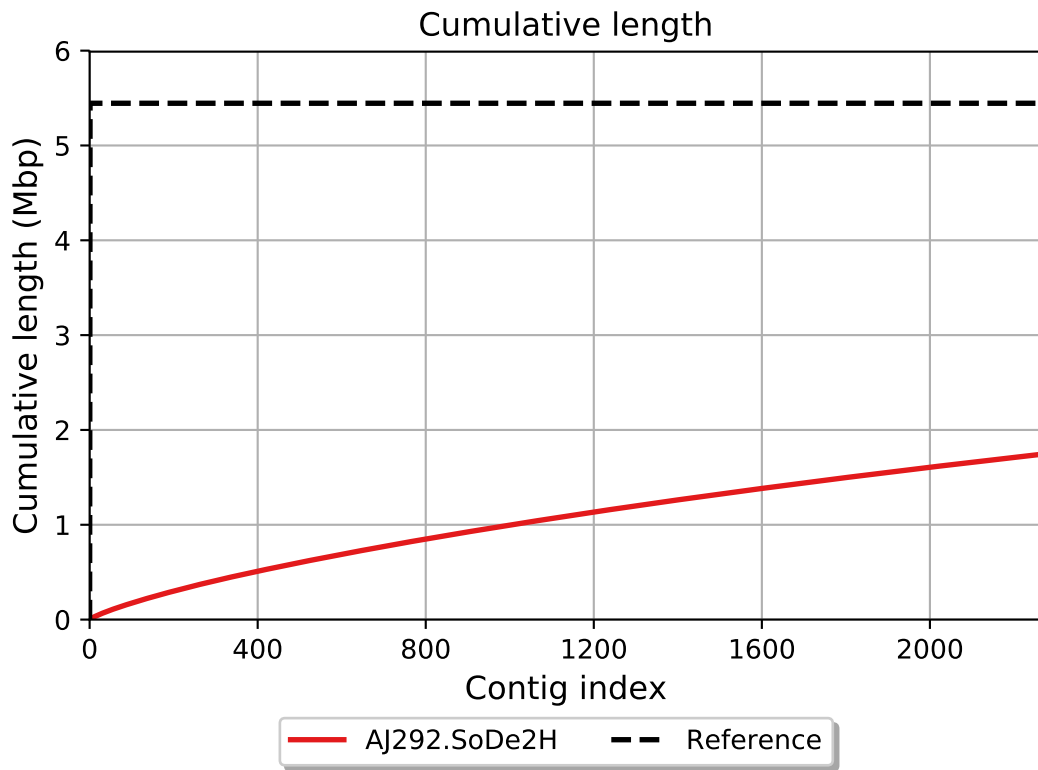
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



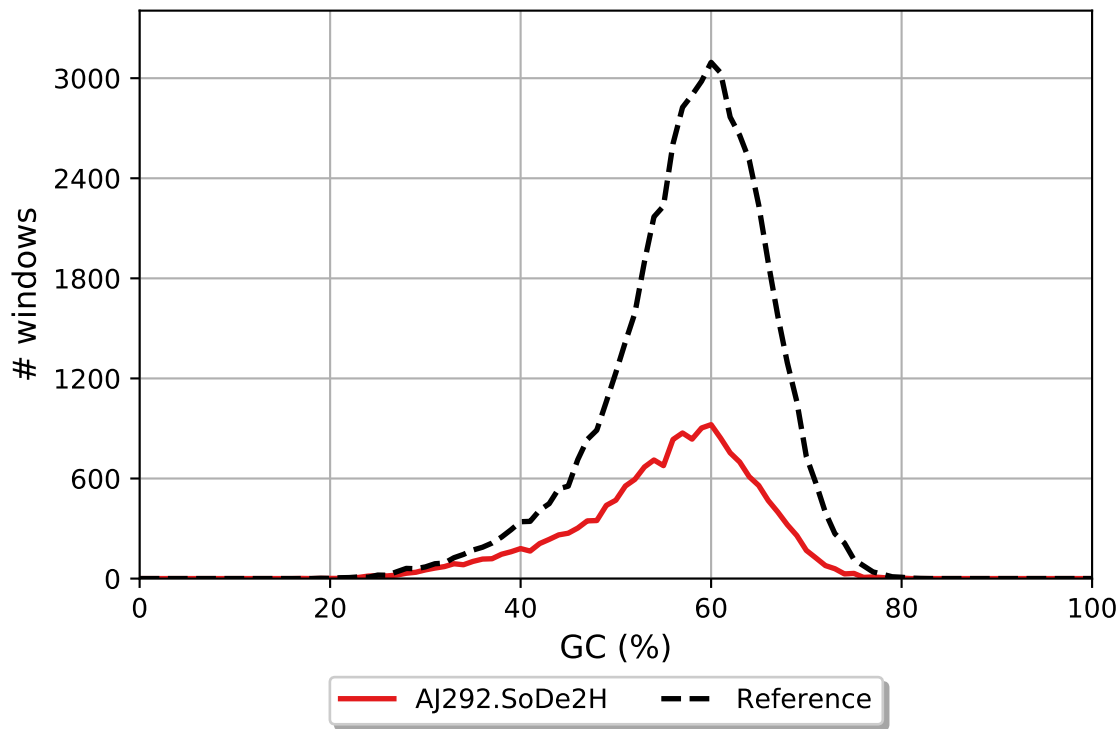
NGx



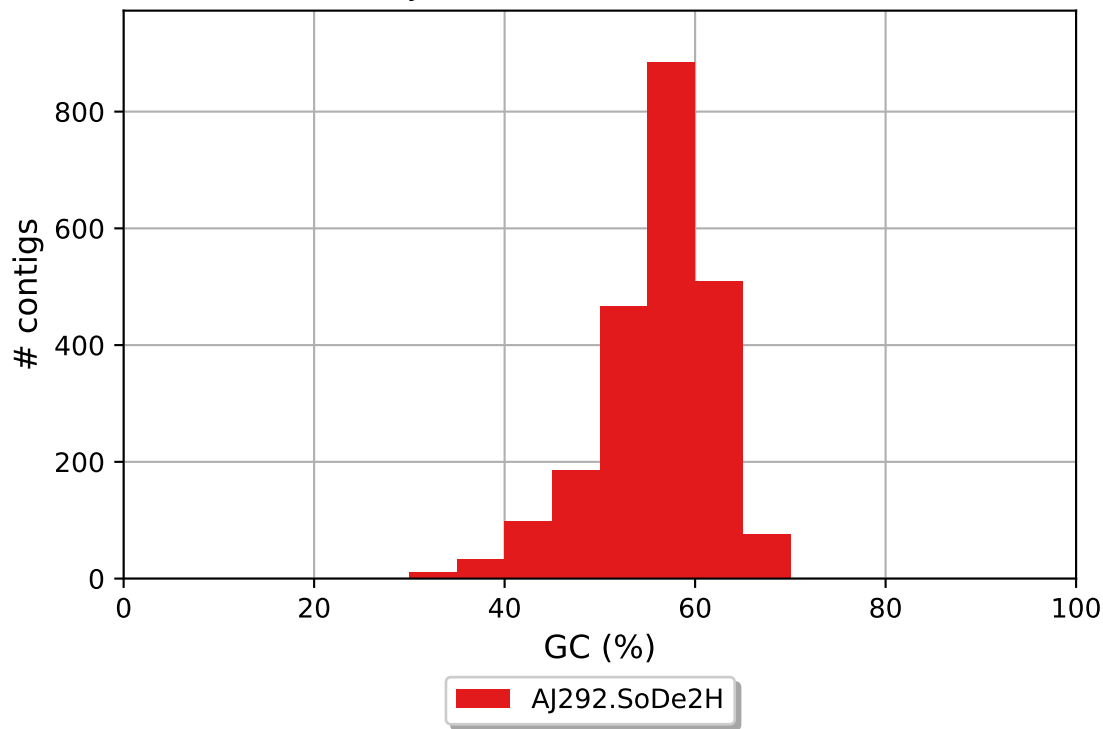
AJ292.SoDe2H



# GC content



AJ292.SoDe2H GC content

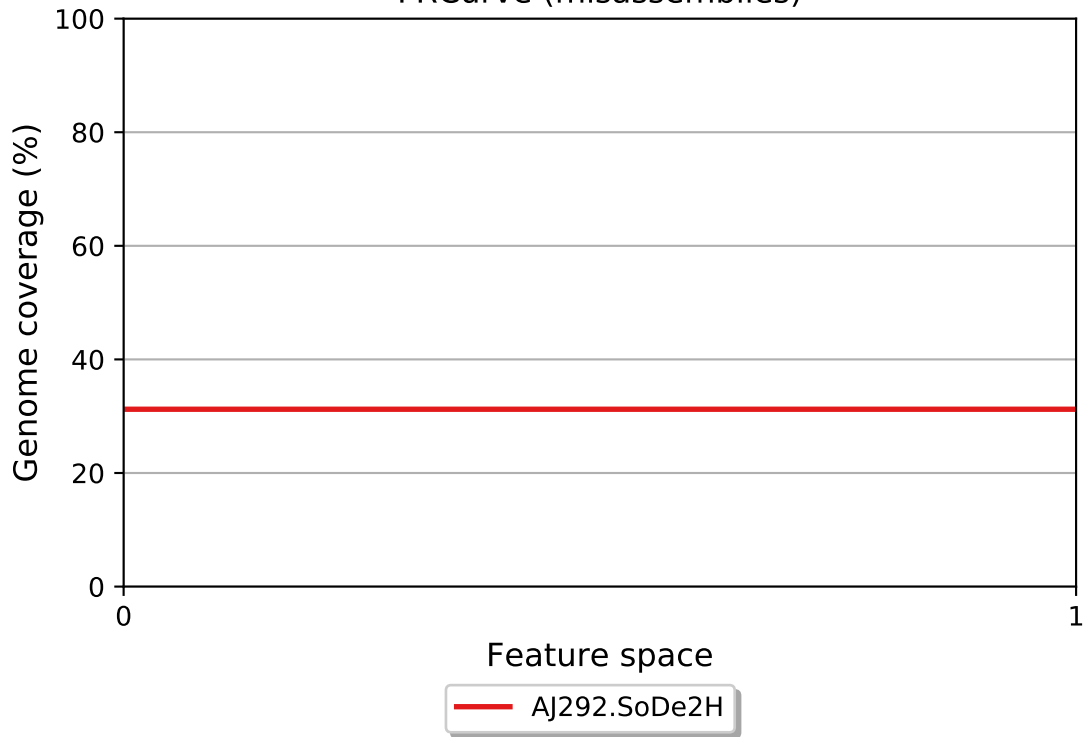


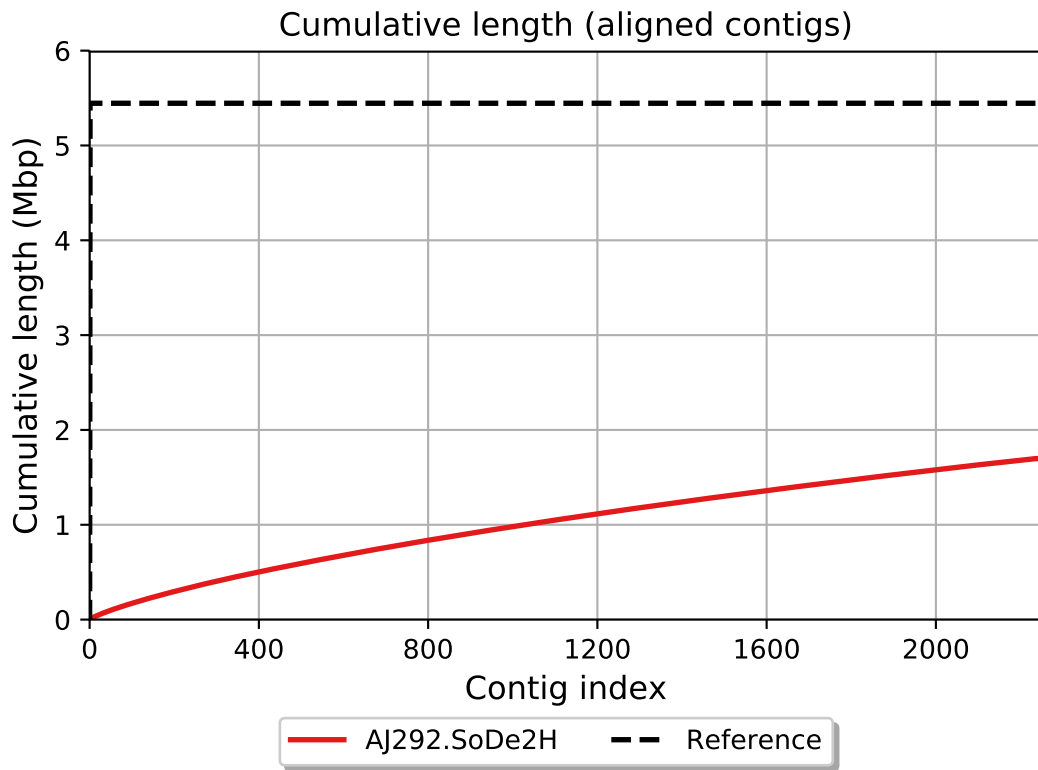


## Misassemblies

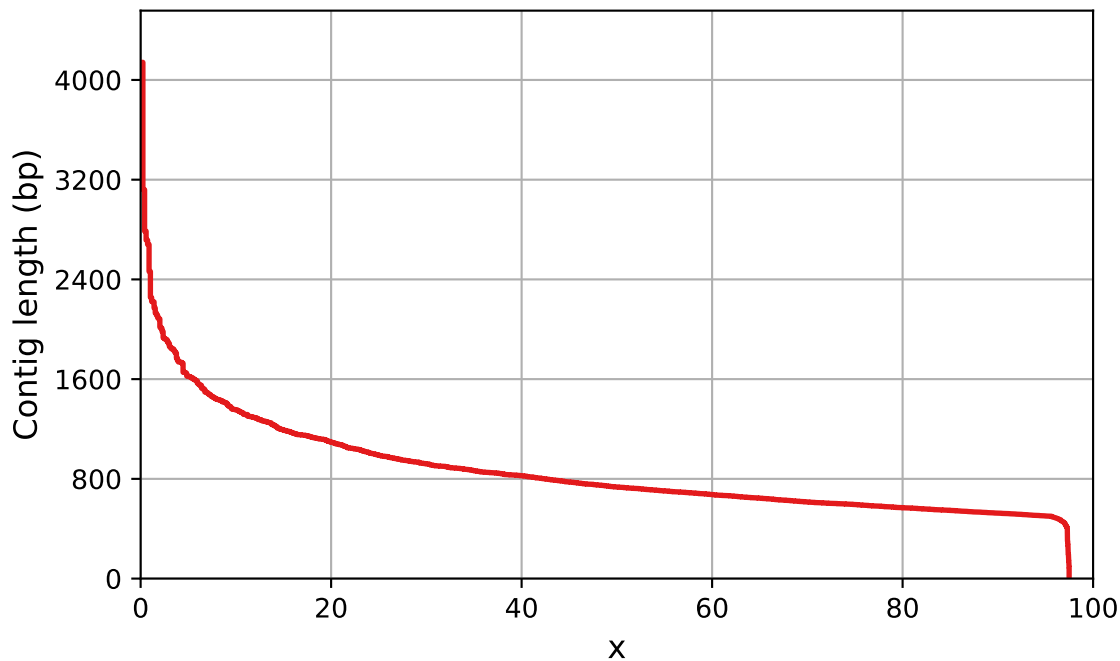


FRCurve (misassemblies)



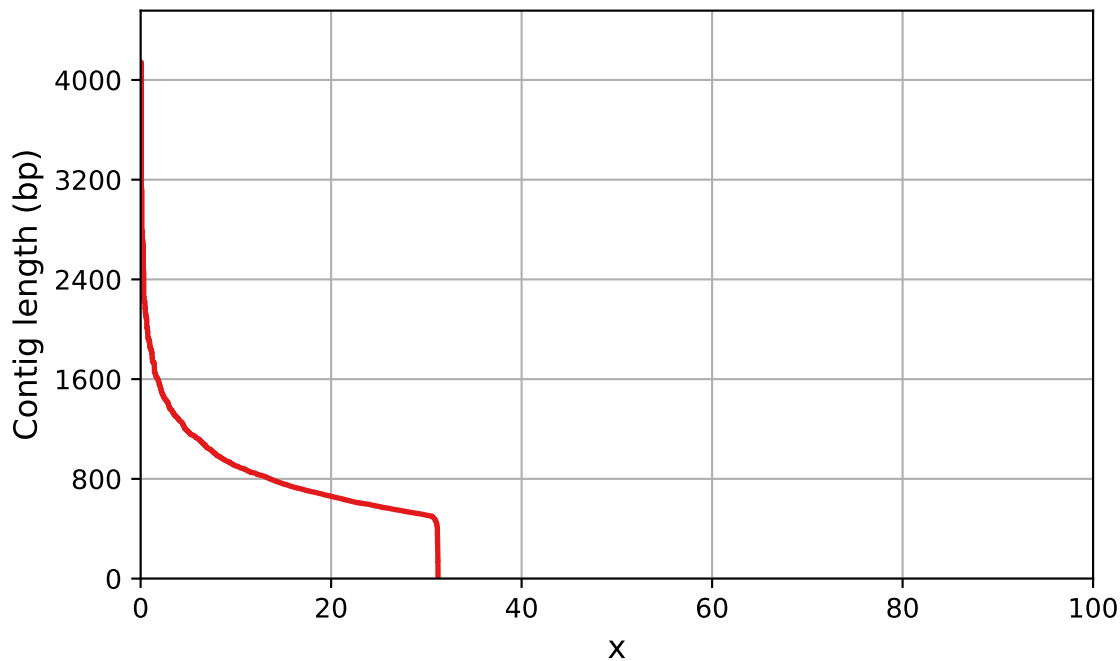


NAx



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# NGAx



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