

Report

	AJ055.SoDe2H
# contigs (>= 0 bp)	44254
# contigs (>= 1000 bp)	295
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	8525344
Total length (>= 1000 bp)	398452
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	2124
Largest contig	3463
Total length	1618182
Reference length	5504133
GC (%)	54.53
Reference GC (%)	57.38
N50	751
N75	603
L50	779
L75	1384
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	548
# unaligned mis. contigs	1
# unaligned contigs	94 + 6 part
Unaligned length	83989
Genome fraction (%)	27.577
Duplication ratio	1.011
# N's per 100 kbp	578.49
# mismatches per 100 kbp	1.71
# indels per 100 kbp	1.91
Largest alignment	3463
Total aligned length	1521547
NA50	714
NGA50	-
NA75	575
LA50	813
LA75	1447

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

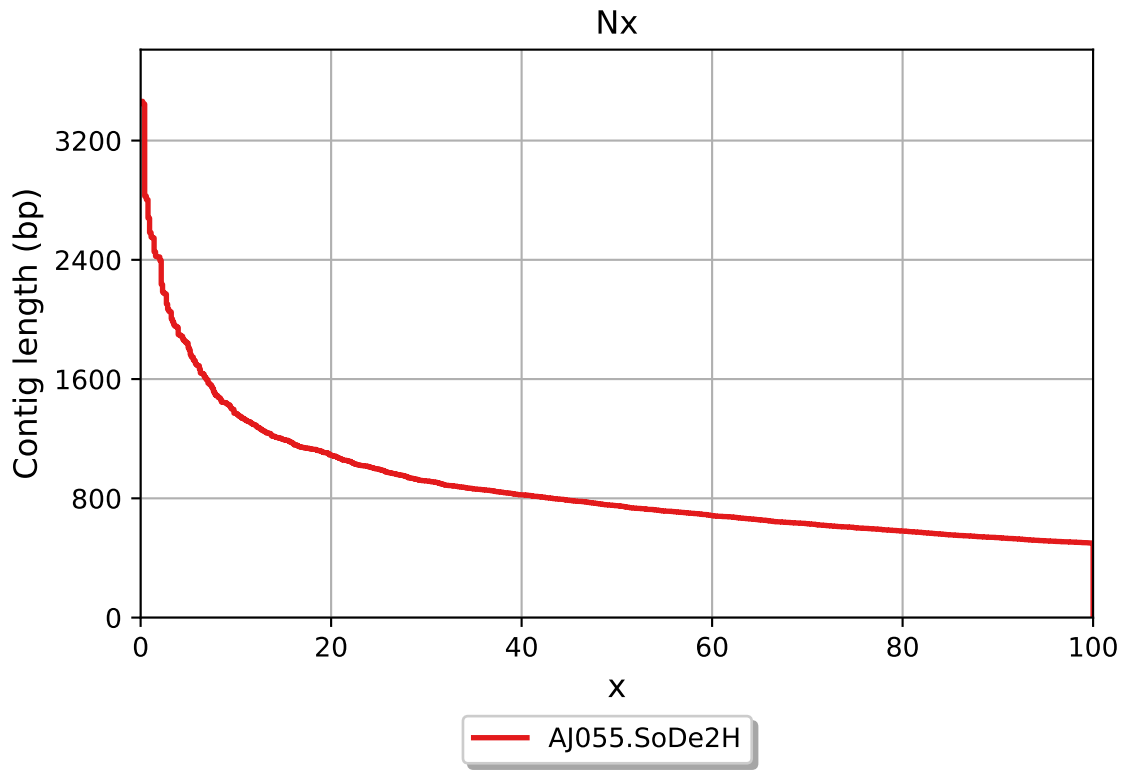
	AJ055.SoDe2H
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	548
# unaligned mis. contigs	1
# mismatches	26
# indels	29
# indels (≤ 5 bp)	24
# indels (> 5 bp)	5
Indels length	282

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).

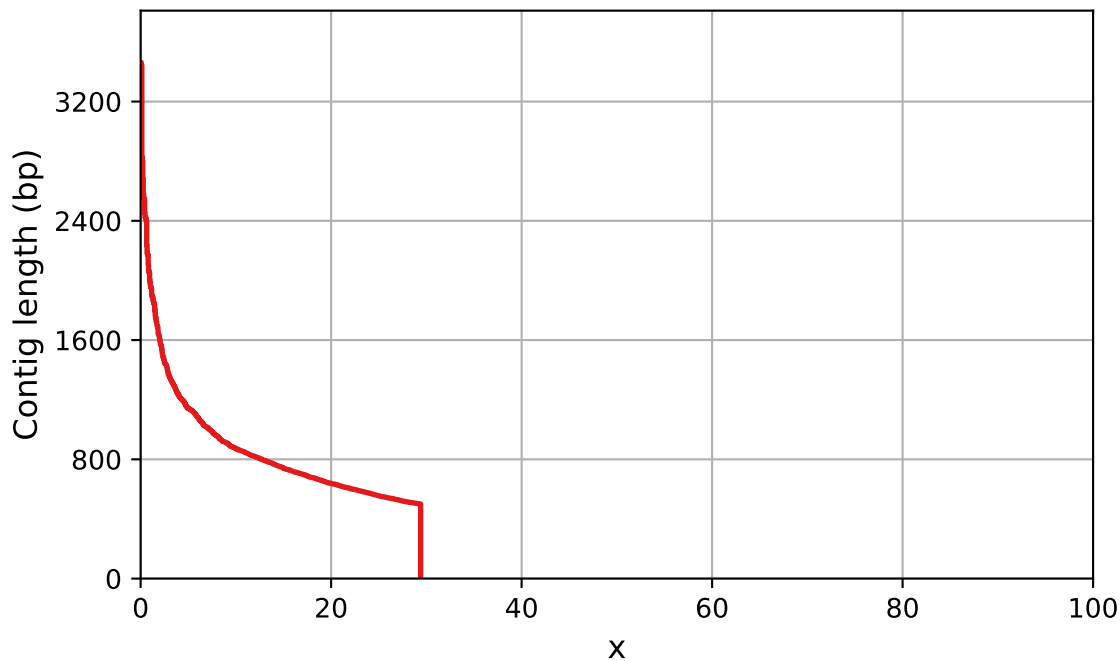
Unaligned report

	AJ055.SoDe2H
# fully unaligned contigs	94
Fully unaligned length	80230
# partially unaligned contigs	6
Partially unaligned length	3759
# N's	9361

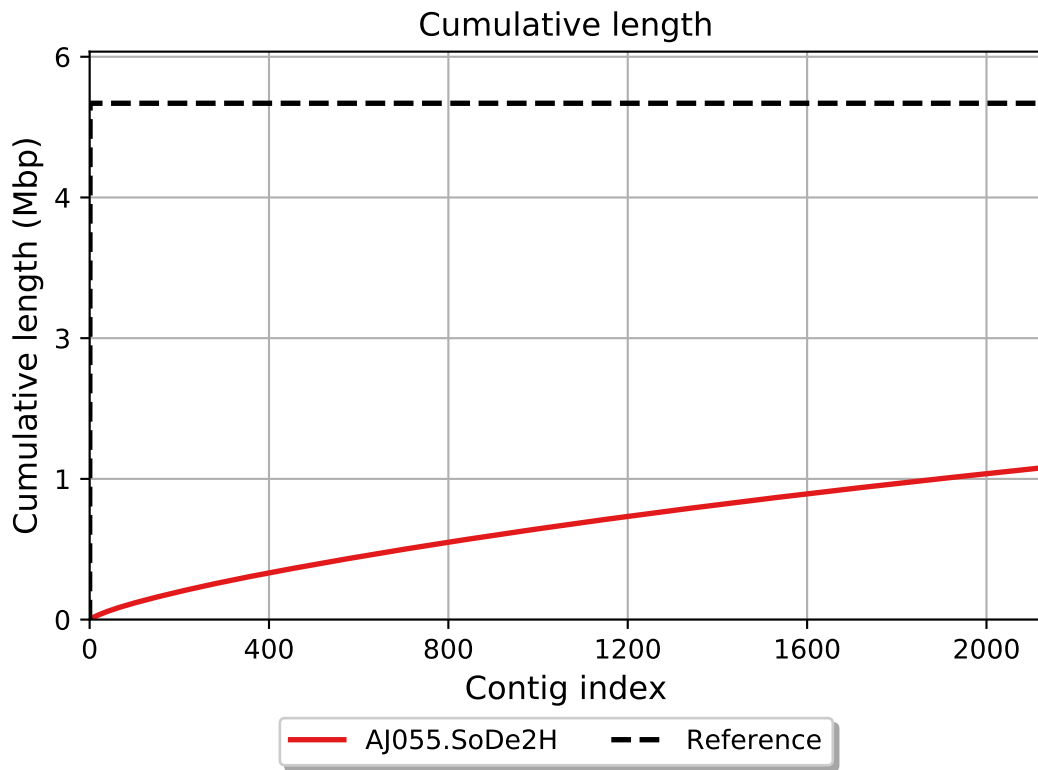
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



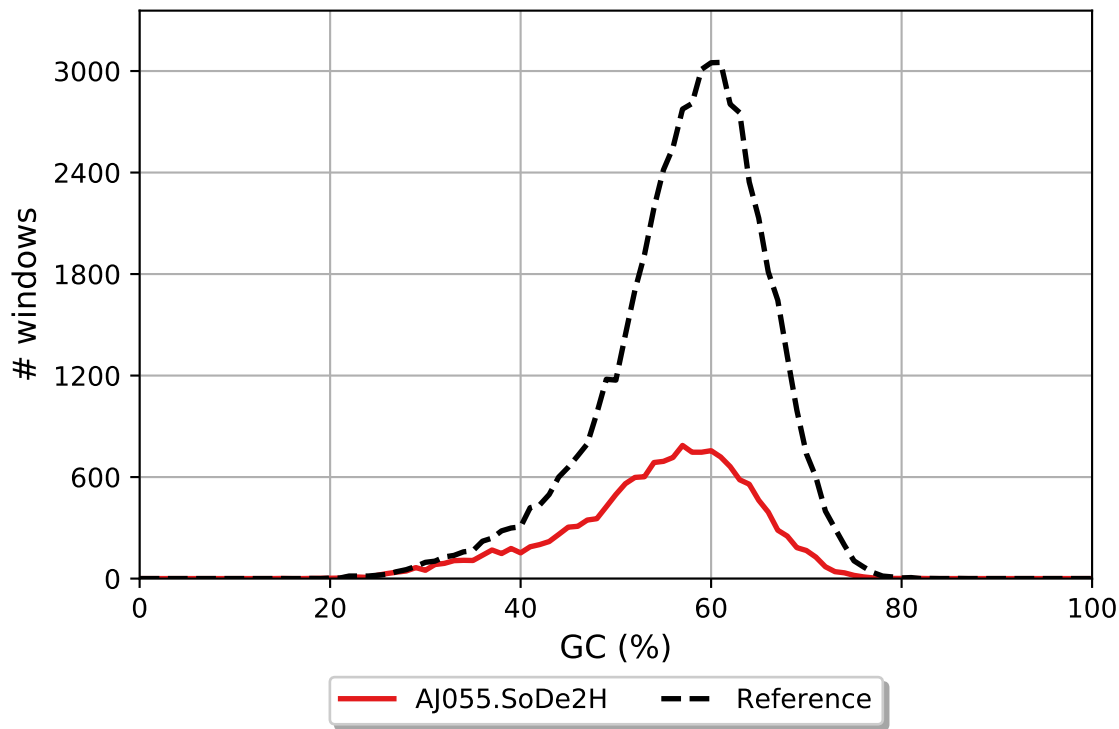
NGx



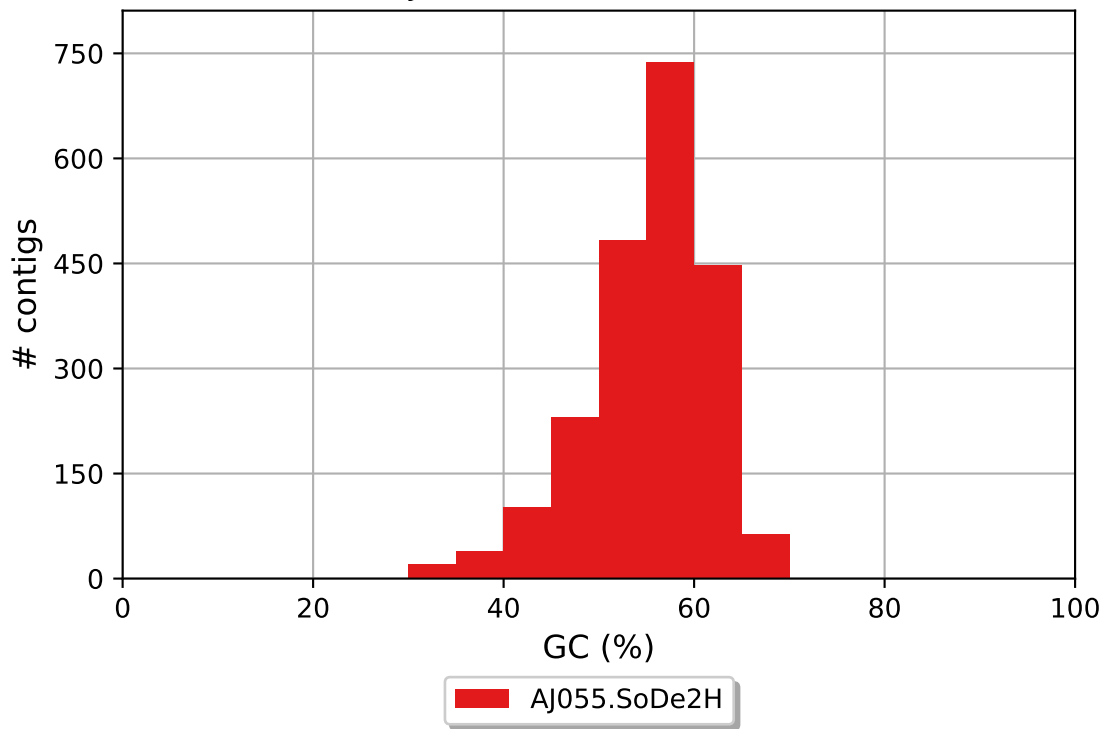
AJ055.SoDe2H



GC content



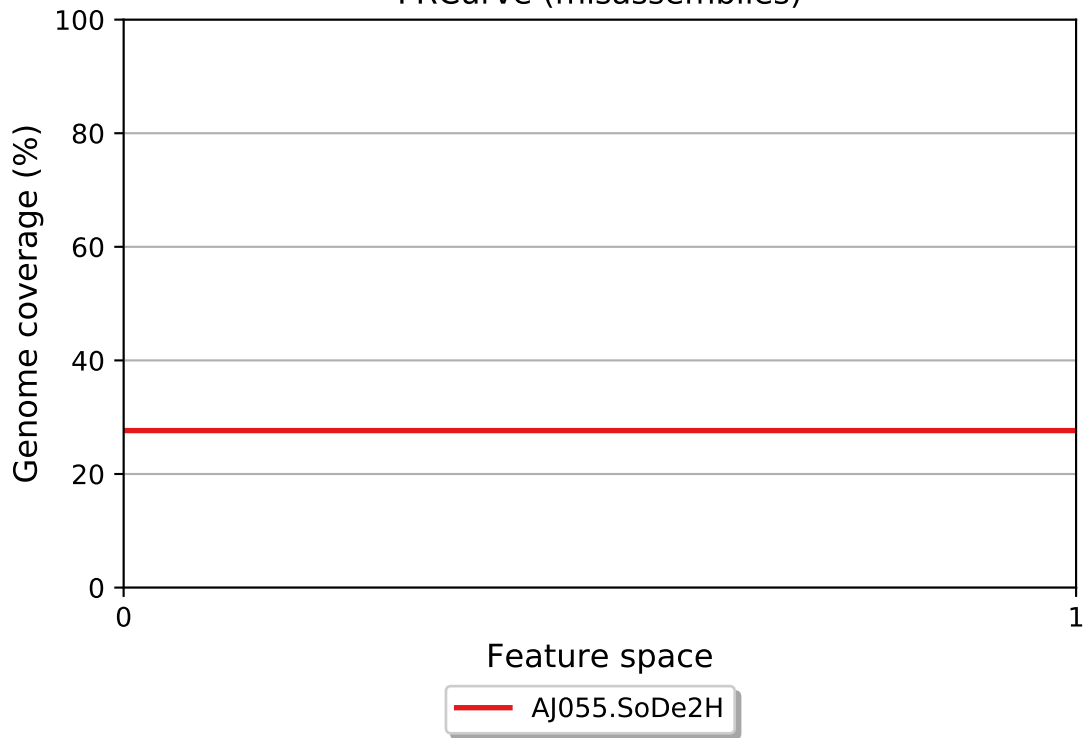
AJ055.SoDe2H GC content



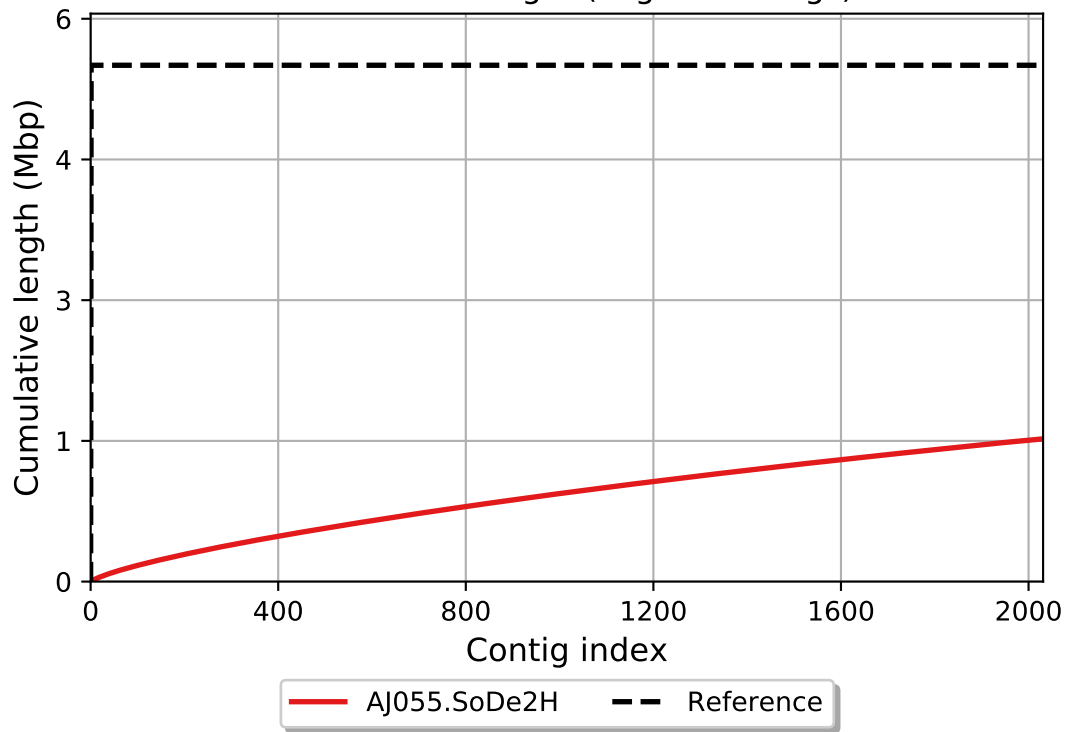
Misassemblies



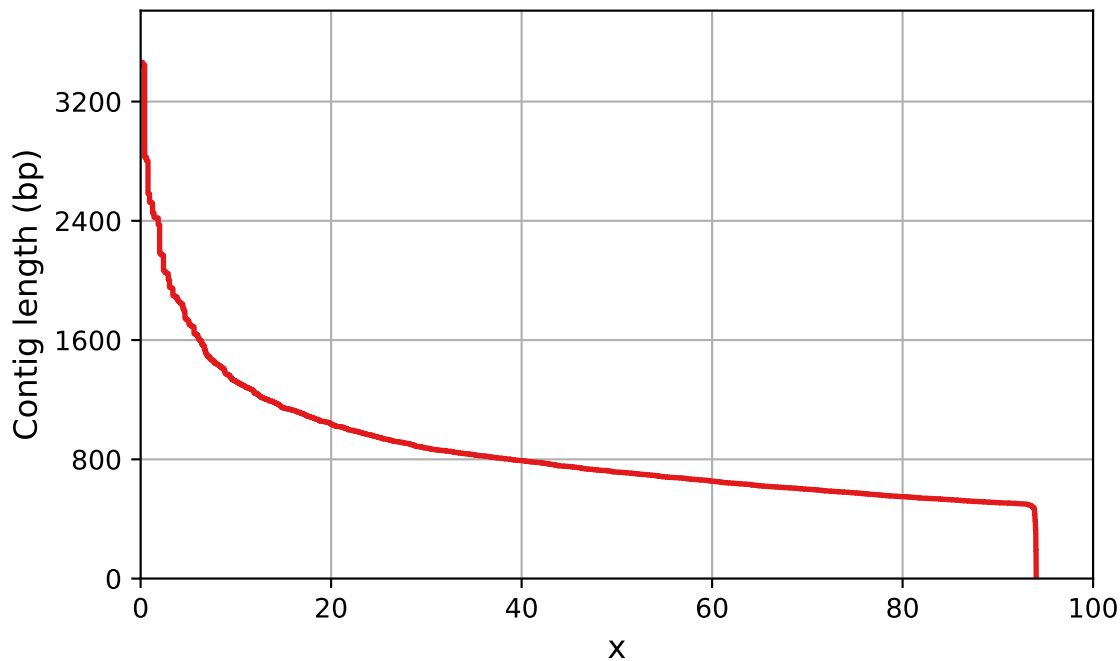
FRCurve (misassemblies)



Cumulative length (aligned contigs)

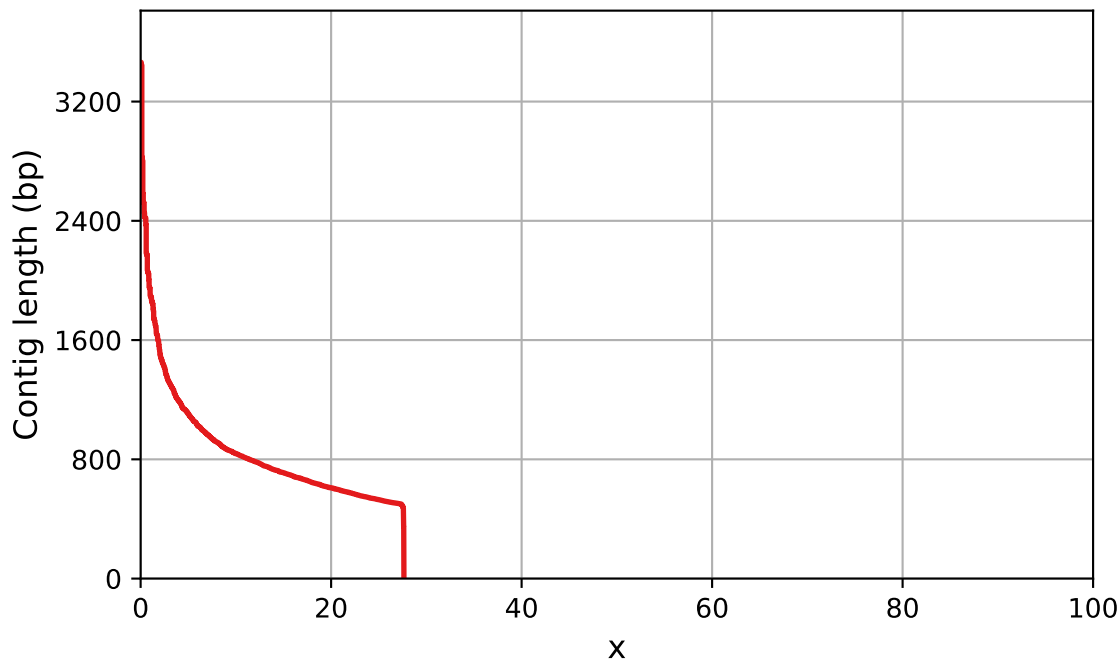


NAx



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NGAx



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