

Report

	TARA_PON_RAW
# contigs (>= 1000 bp)	34
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	77047
Total length (>= 5000 bp)	6504
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	34
Largest contig	6504
Total length	77047
Reference length	3561038
GC (%)	49.48
Reference GC (%)	41.87
N50	3015
N75	1533
L50	10
L75	20
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	6 + 28 part
Unaligned length	74630
Genome fraction (%)	0.020
Duplication ratio	3.468
# N's per 100 kbp	0.00
# mismatches per 100 kbp	8751.79
# indels per 100 kbp	0.00
Largest alignment	136
Total aligned length	2417
NGA50	-

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

	TARA_PON_RAW
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	33
# possible misassemblies	35
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	61
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

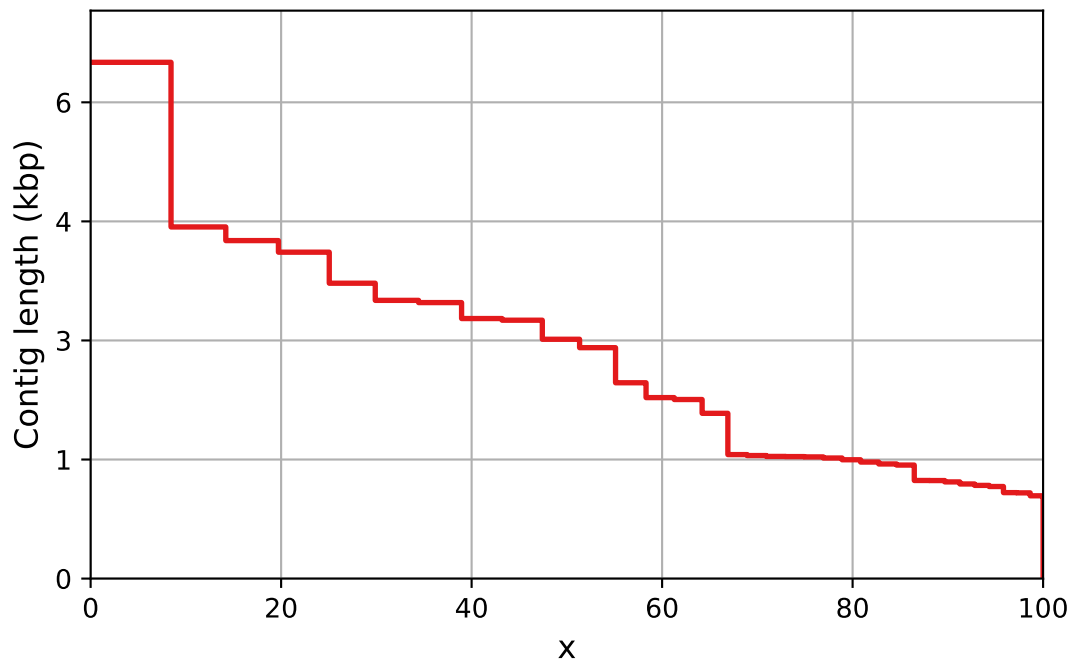
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	TARA_PON_RAW
# fully unaligned contigs	6
Fully unaligned length	11219
# partially unaligned contigs	28
Partially unaligned length	63411
# N's	0

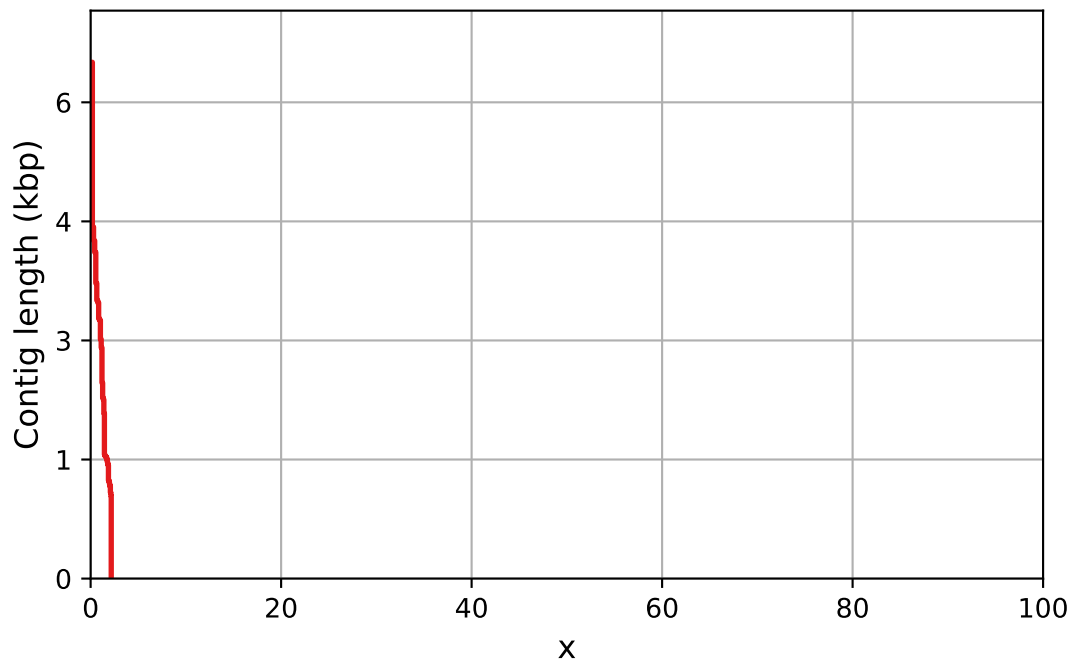
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

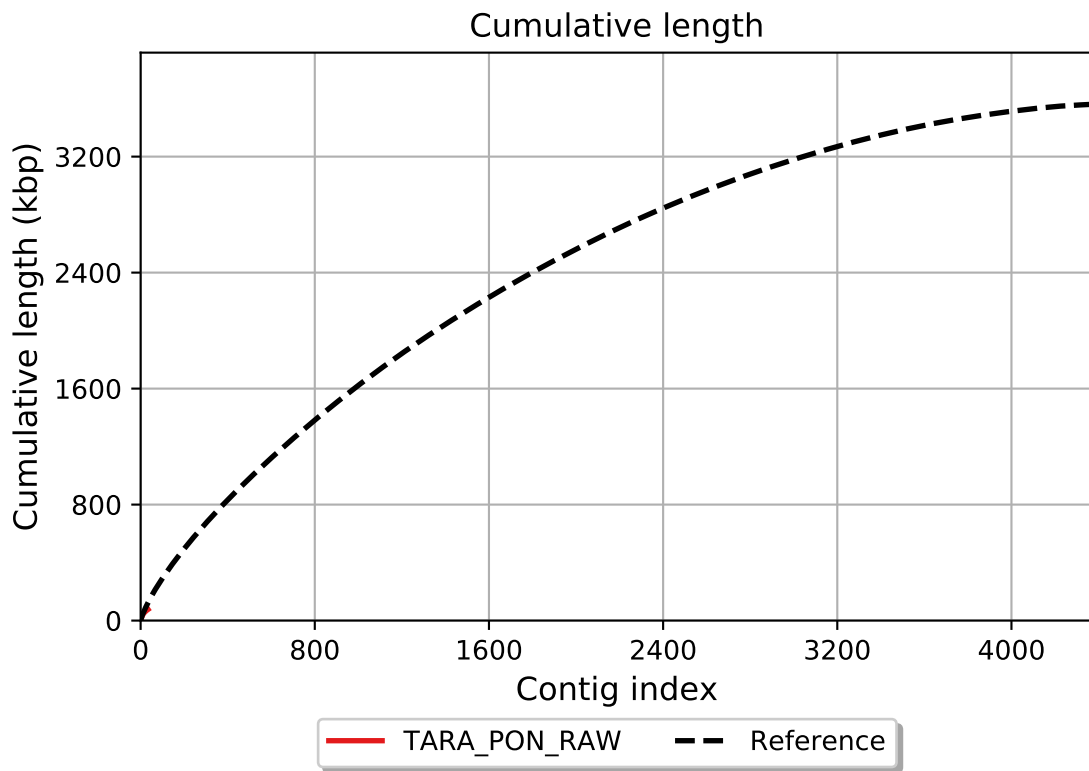


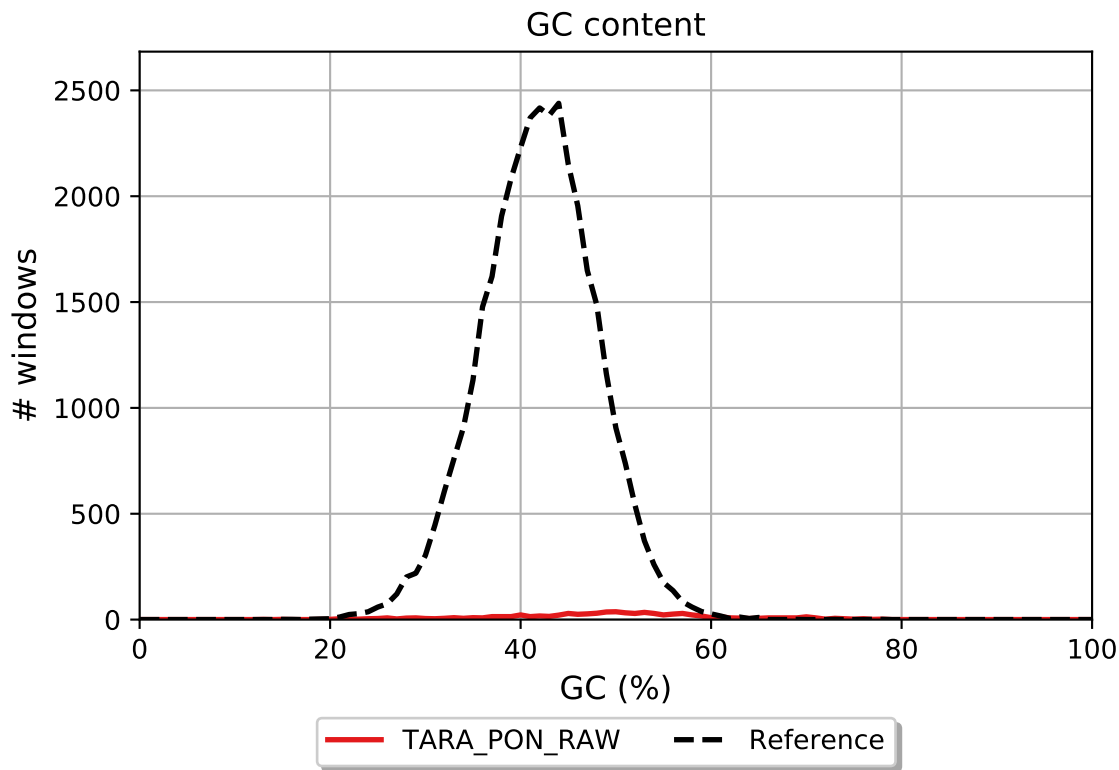
TARA_PON_RAW

NGx

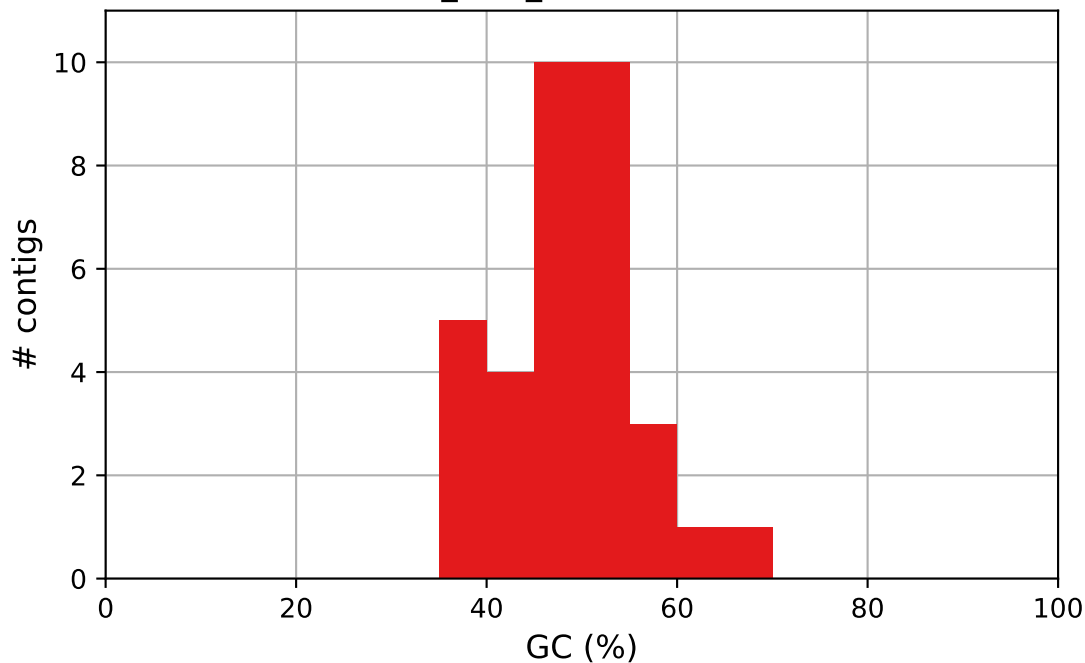


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TARA_PON_RAW GC content

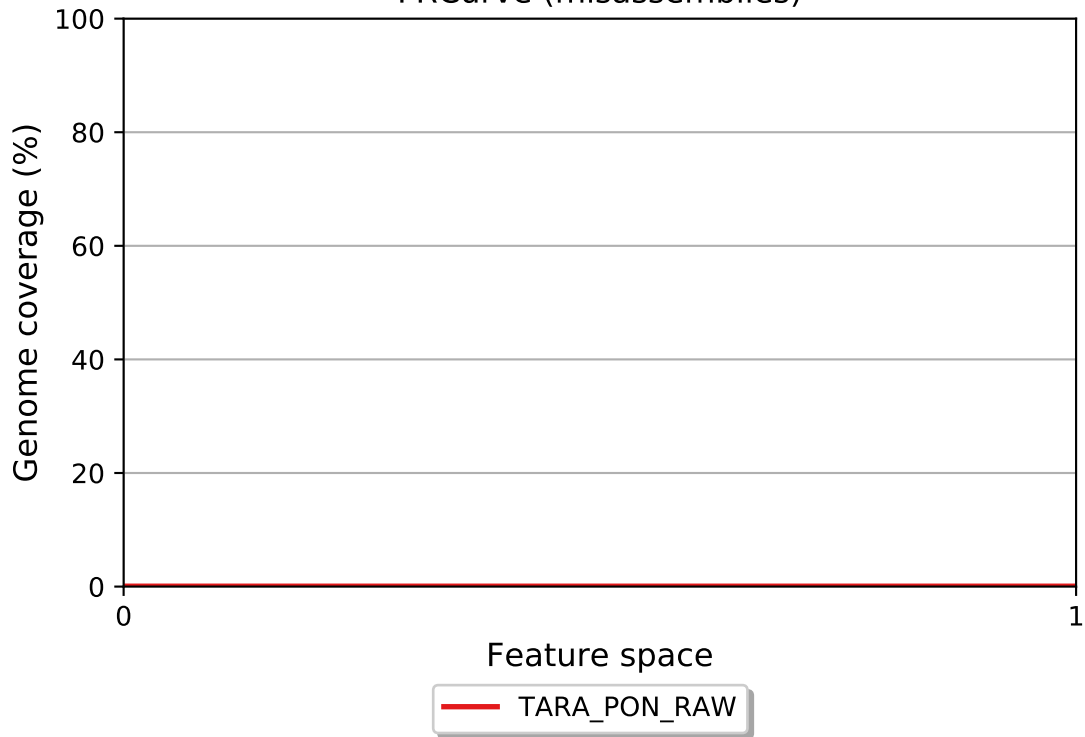


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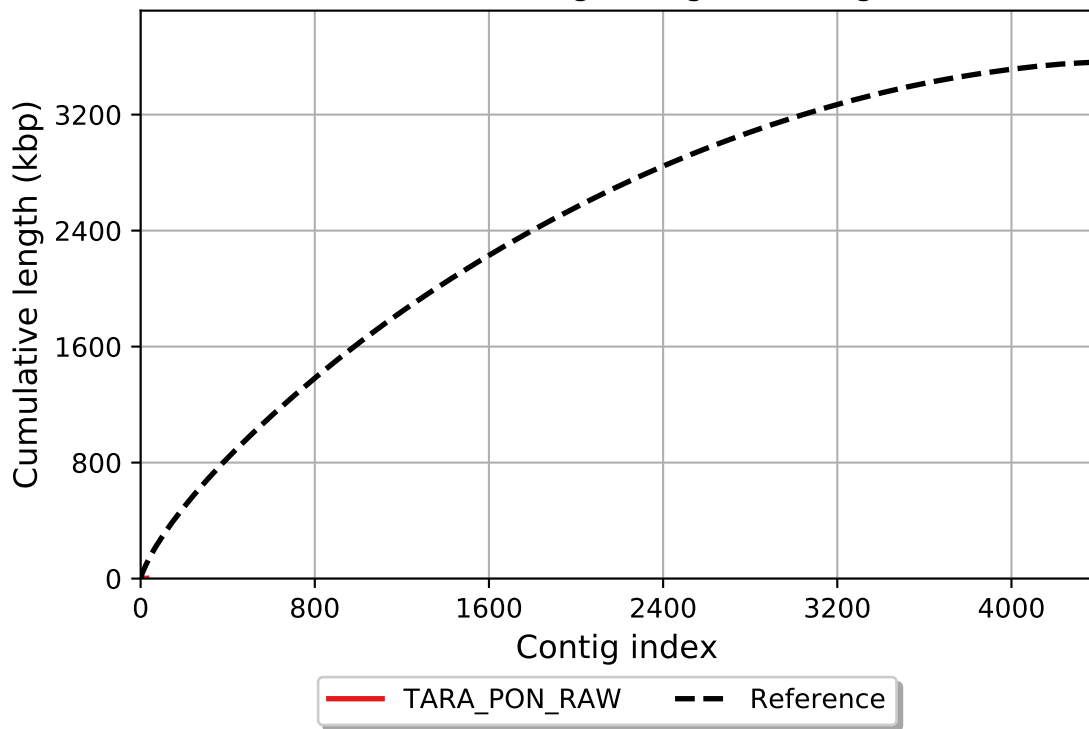
Misassemblies

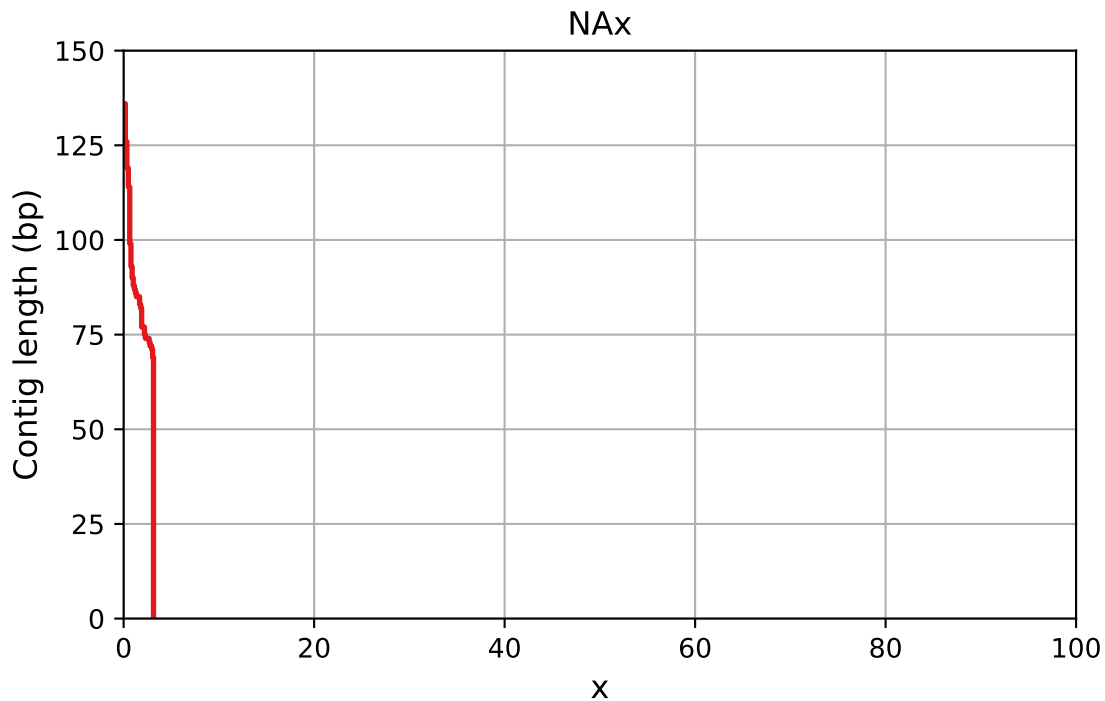


FRCurve (misassemblies)



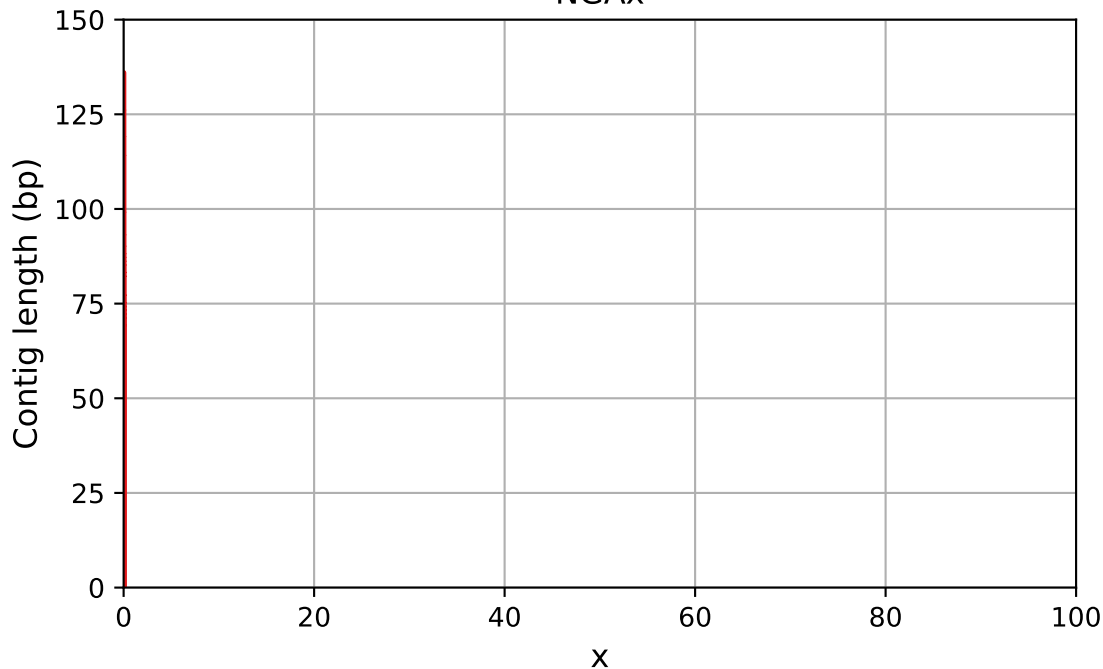
Cumulative length (aligned contigs)





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NGAx



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