

## Report

	site_D3_DNA.final.contigs
# contigs (>= 0 bp)	159996
# contigs (>= 1000 bp)	29014
# contigs (>= 5000 bp)	2518
# contigs (>= 10000 bp)	793
# contigs (>= 25000 bp)	147
# contigs (>= 50000 bp)	45
Total length (>= 0 bp)	143195816
Total length (>= 1000 bp)	77191869
Total length (>= 5000 bp)	28417181
Total length (>= 10000 bp)	16770281
Total length (>= 25000 bp)	7225360
Total length (>= 50000 bp)	3705511
# contigs	82264
Largest contig	173476
Total length	113373814
Reference length	93795223
N50	1730
N75	839
L50	13027
L75	37595
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	2179
# local misassemblies	1
# unaligned mis. contigs	8
# unaligned contigs	82144 + 75 part
Unaligned length	113332574
Genome fraction (%)	0.041
Duplication ratio	1.582
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2893.10
# indels per 100 kbp	239.38
Largest alignment	1387
Total aligned length	24476

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

	site_D3_DNA.final.contigs
# misassemblies	1
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	1
# misassembled contigs	1
Misassembled contigs length	2179
# possibly misassembled contigs	2
# possible misassemblies	3
# local misassemblies	1
# unaligned mis. contigs	8
# mismatches	1124
# indels	93
# indels (<= 5 bp)	93
# indels (> 5 bp)	0
Indels length	118

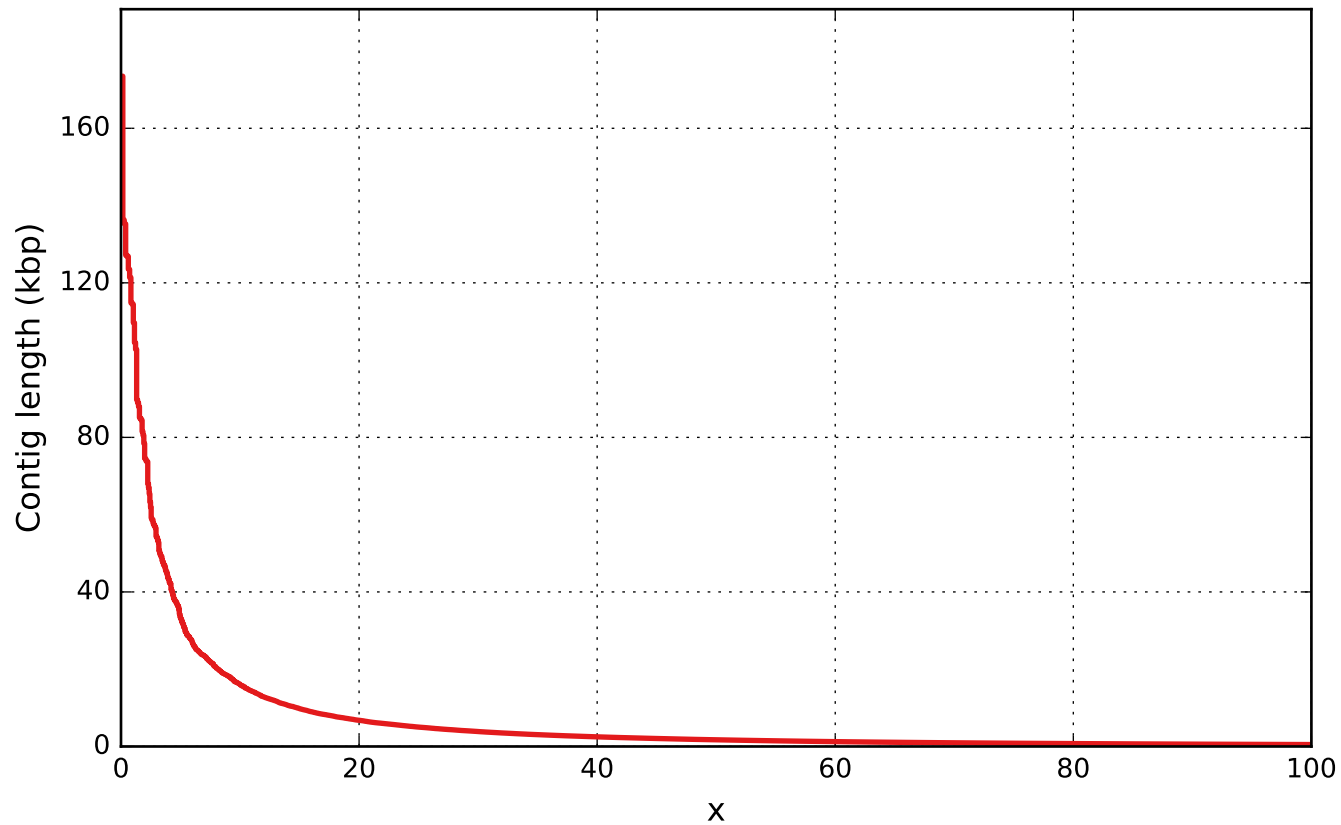
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	site_D3_DNA.final.contigs
# fully unaligned contigs	82144
Fully unaligned length	113128466
# partially unaligned contigs	75
Partially unaligned length	204108
# N's	0

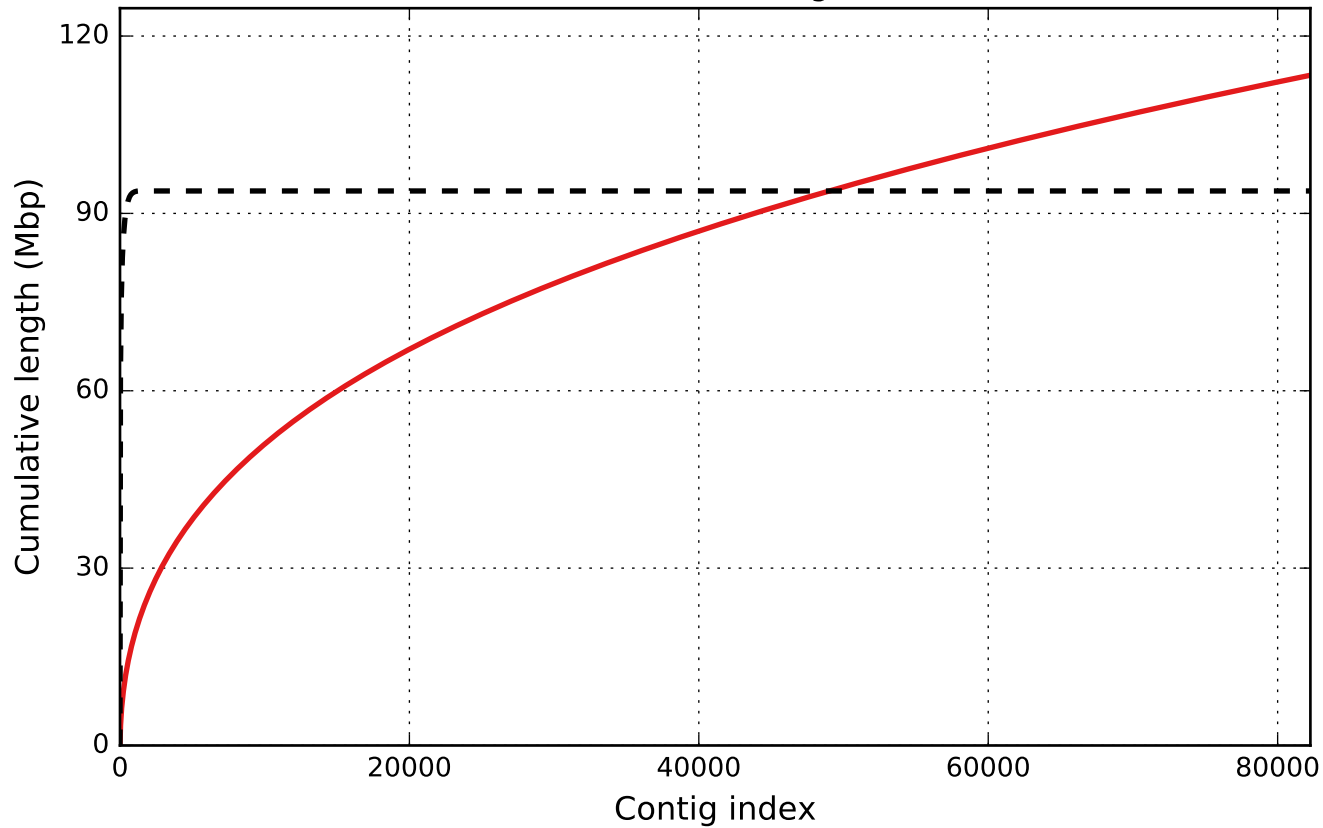
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

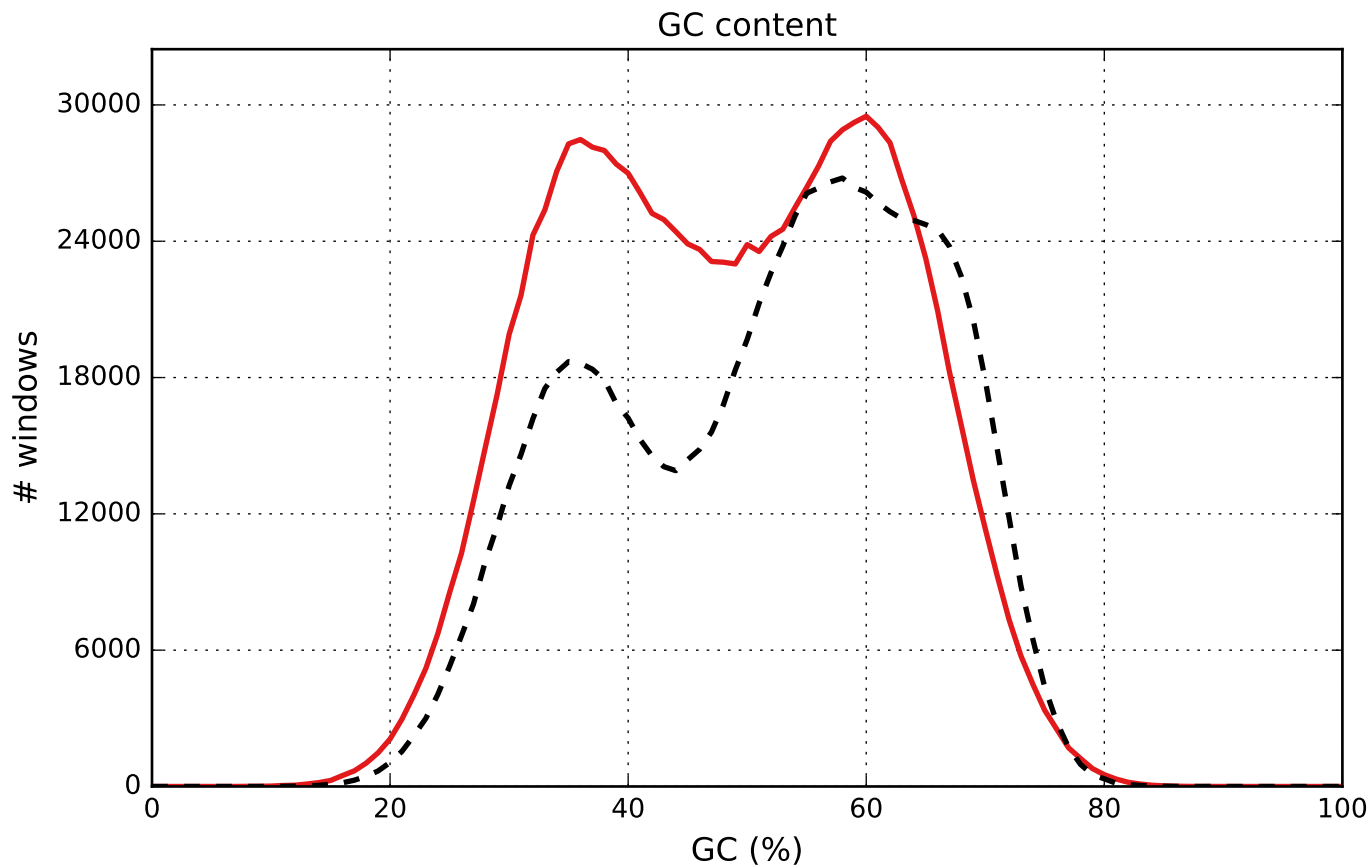


— site\_D3\_DNA.final.contigs

Cumulative length

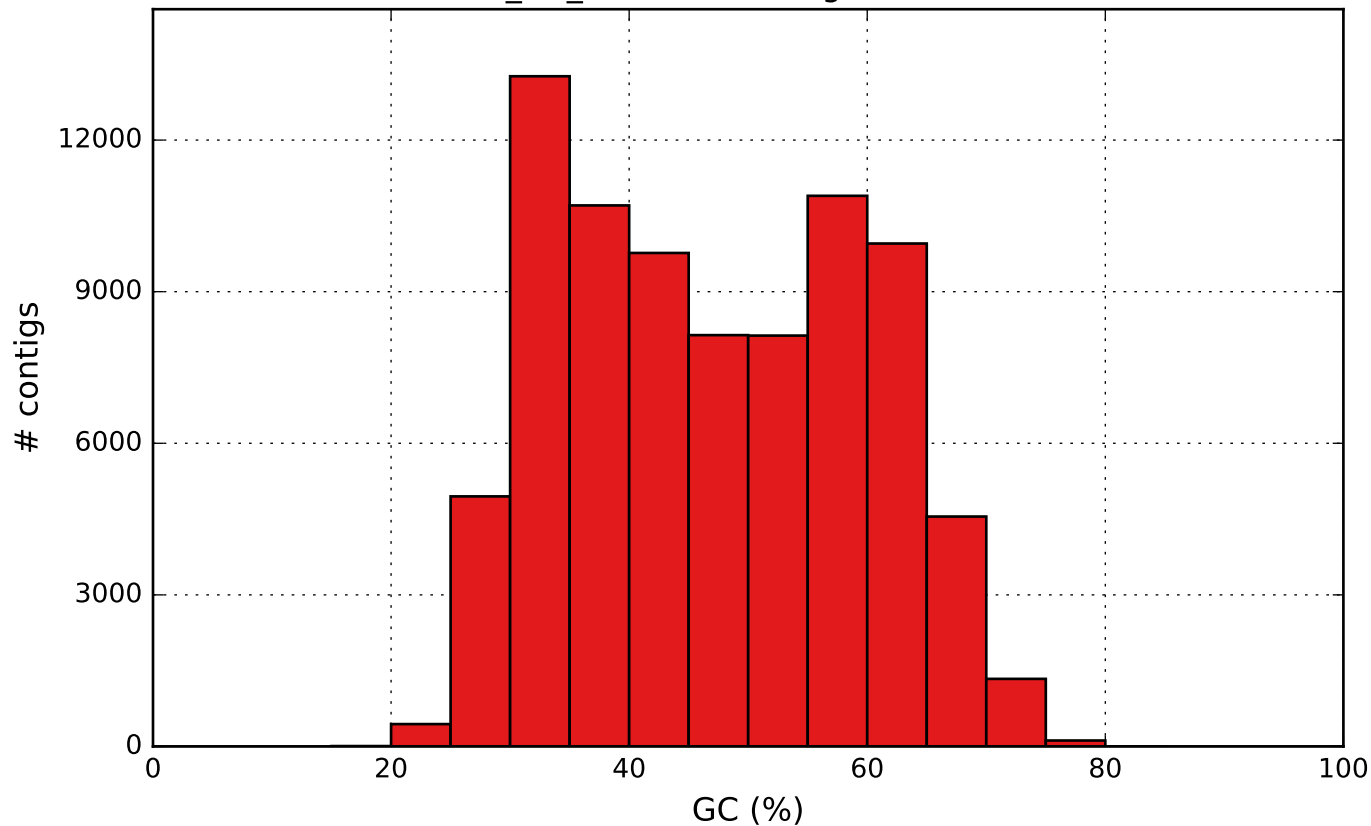


— site\_D3\_DNA.final.contigs    - - Reference

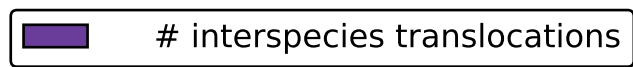
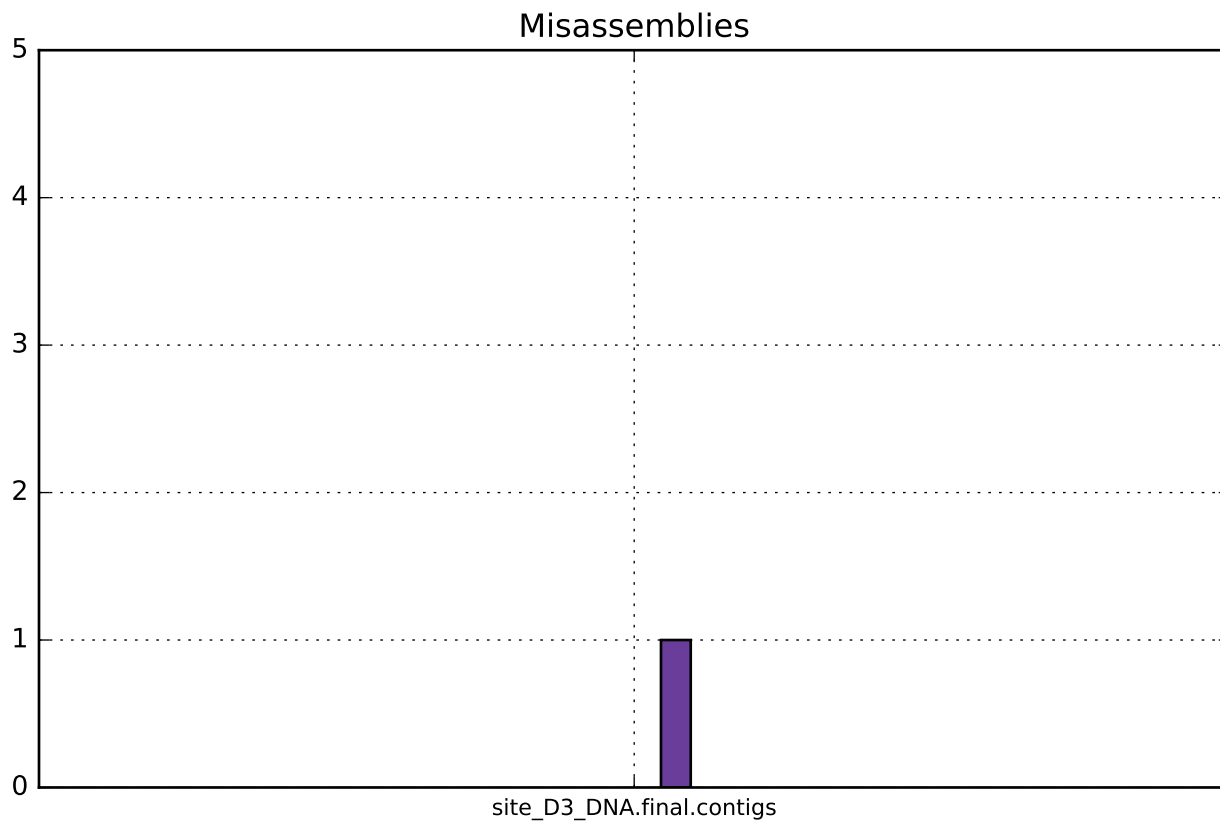


— site\_D3\_DNA.final.contigs    - - Reference

site\_D3\_DNA.final.contigs GC content

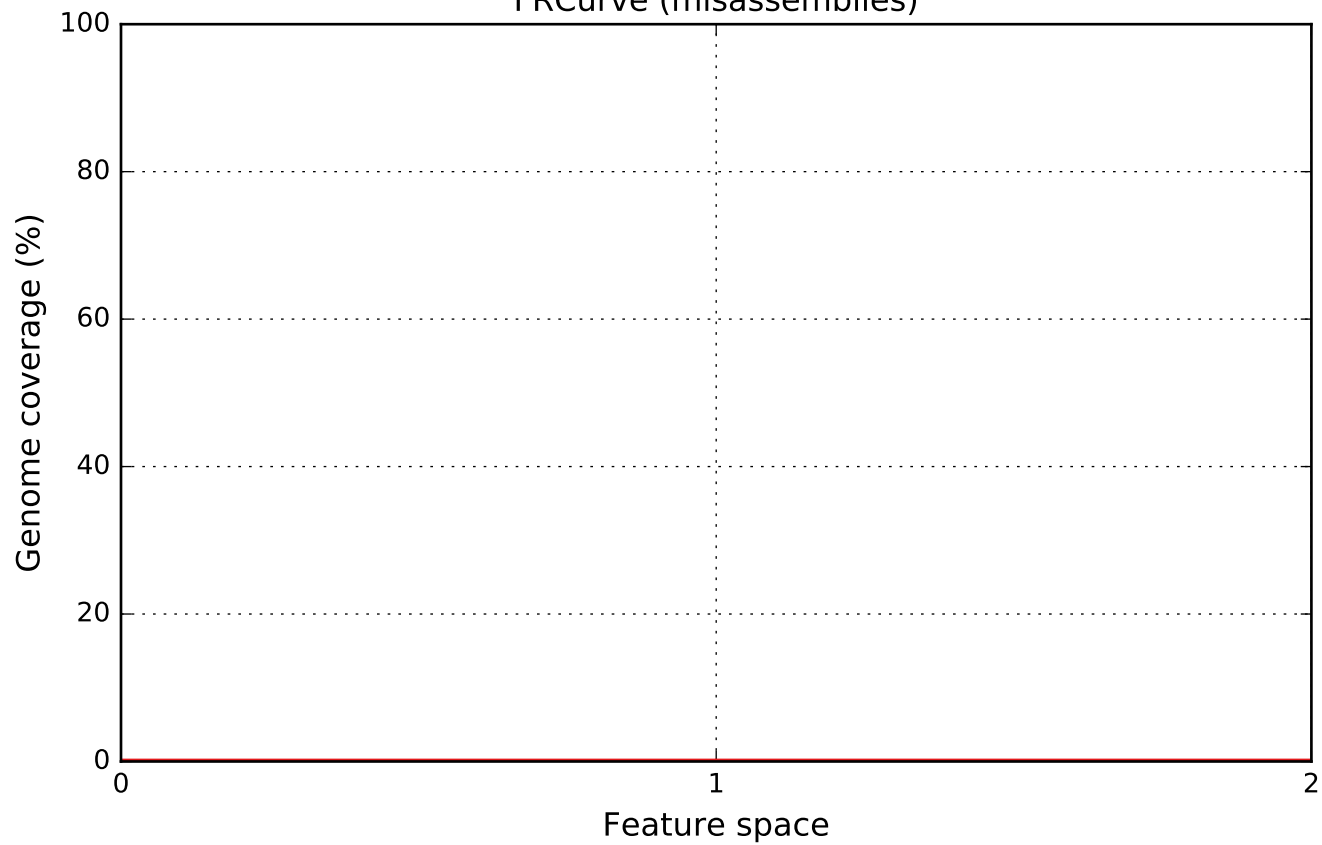


site\_D3\_DNA.final.contigs

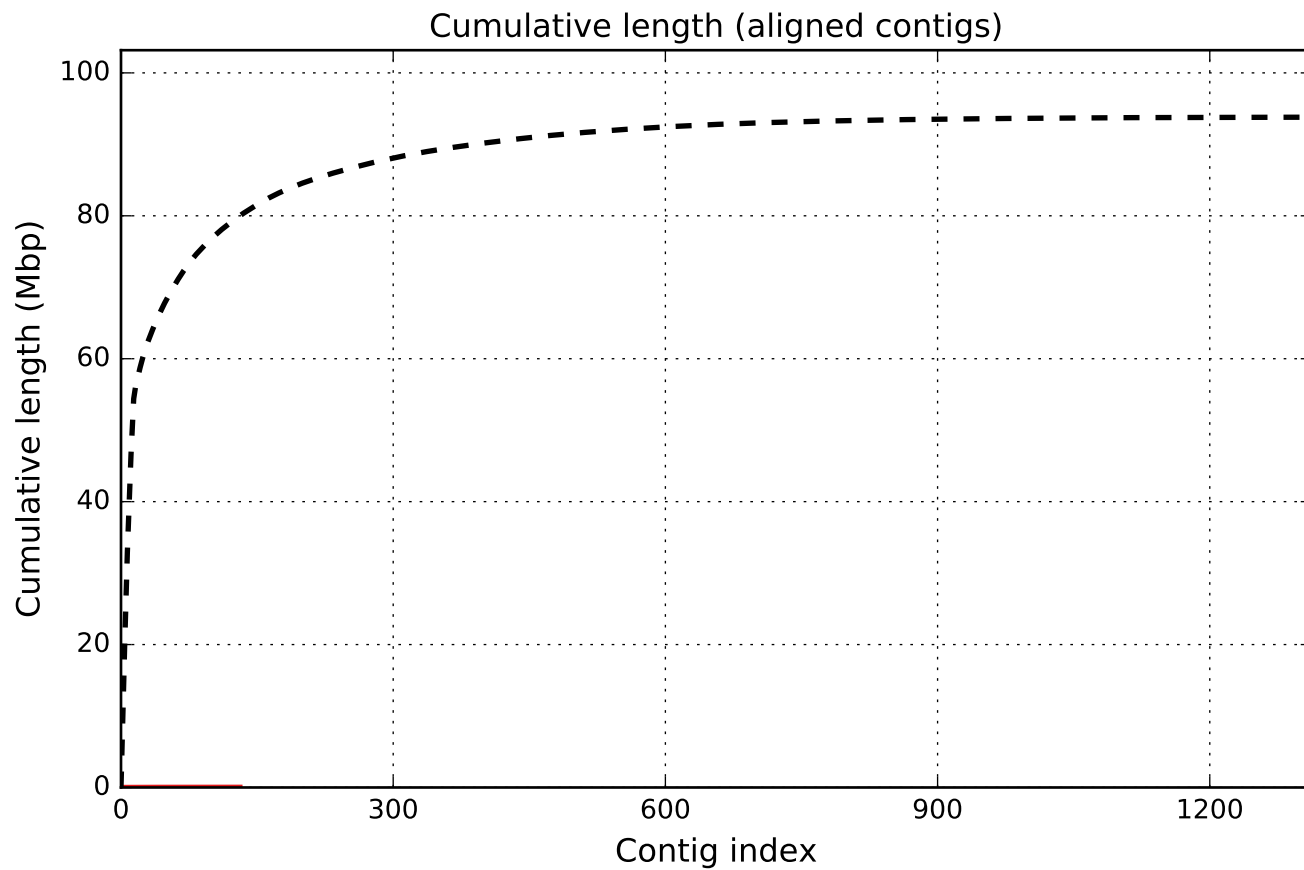




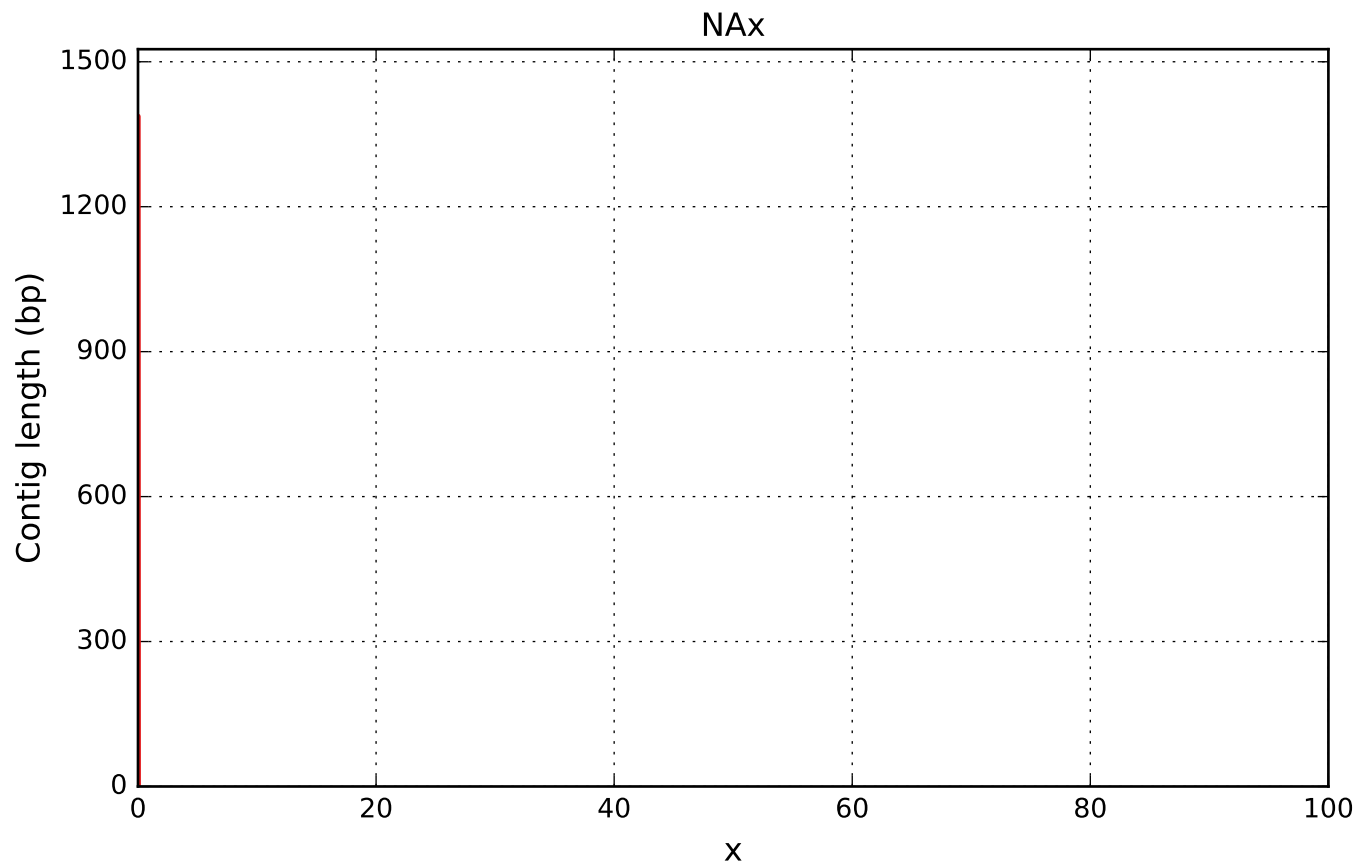
FRCurve (misassemblies)



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