

Report

	final.contigs
# contigs (>= 0 bp)	160003
# contigs (>= 1000 bp)	29015
# contigs (>= 5000 bp)	2518
# contigs (>= 10000 bp)	793
# contigs (>= 25000 bp)	147
# contigs (>= 50000 bp)	45
Total length (>= 0 bp)	143197478
Total length (>= 1000 bp)	77190945
Total length (>= 5000 bp)	28416388
Total length (>= 10000 bp)	16770281
Total length (>= 25000 bp)	7225360
Total length (>= 50000 bp)	3705511
# contigs	82269
Largest contig	173476
Total length	113374975
Reference length	93795223
N50	1730
N75	839
L50	13029
L75	37598
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	2179
# local misassemblies	1
# structural variations	0
# unaligned mis. contigs	8
# unaligned contigs	82149 + 75 part
Unaligned length	113333735
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

	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
# structural variations	0
# unaligned mis. contigs	8
# mismatches	1124
# indels	93
# indels (≤ 5 bp)	93
# indels (> 5 bp)	0
Indels length	118

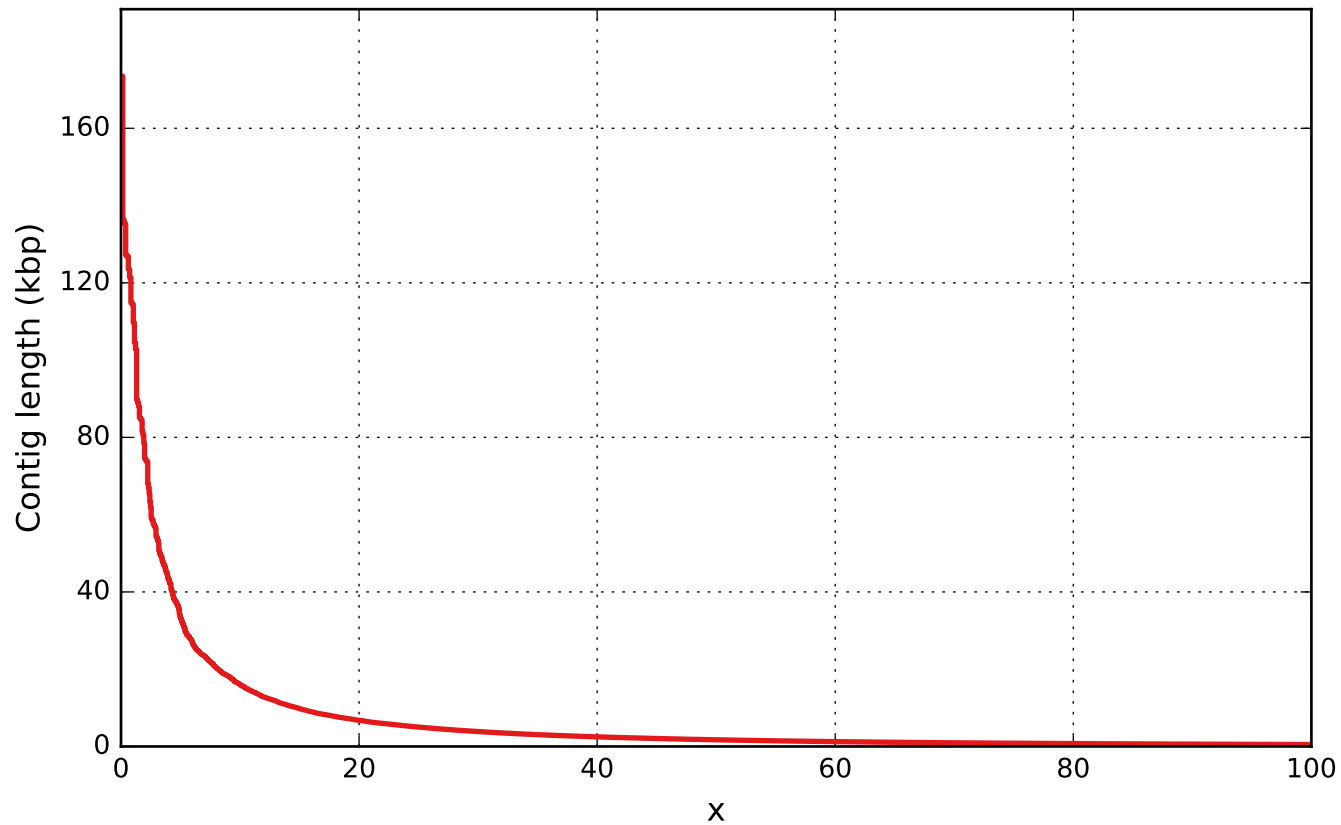
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	final.contigs
# fully unaligned contigs	82149
Fully unaligned length	113129627
# partially unaligned contigs	75
Partially unaligned length	204108
# N's	0

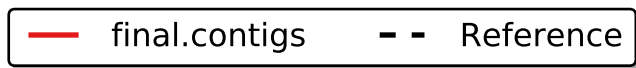
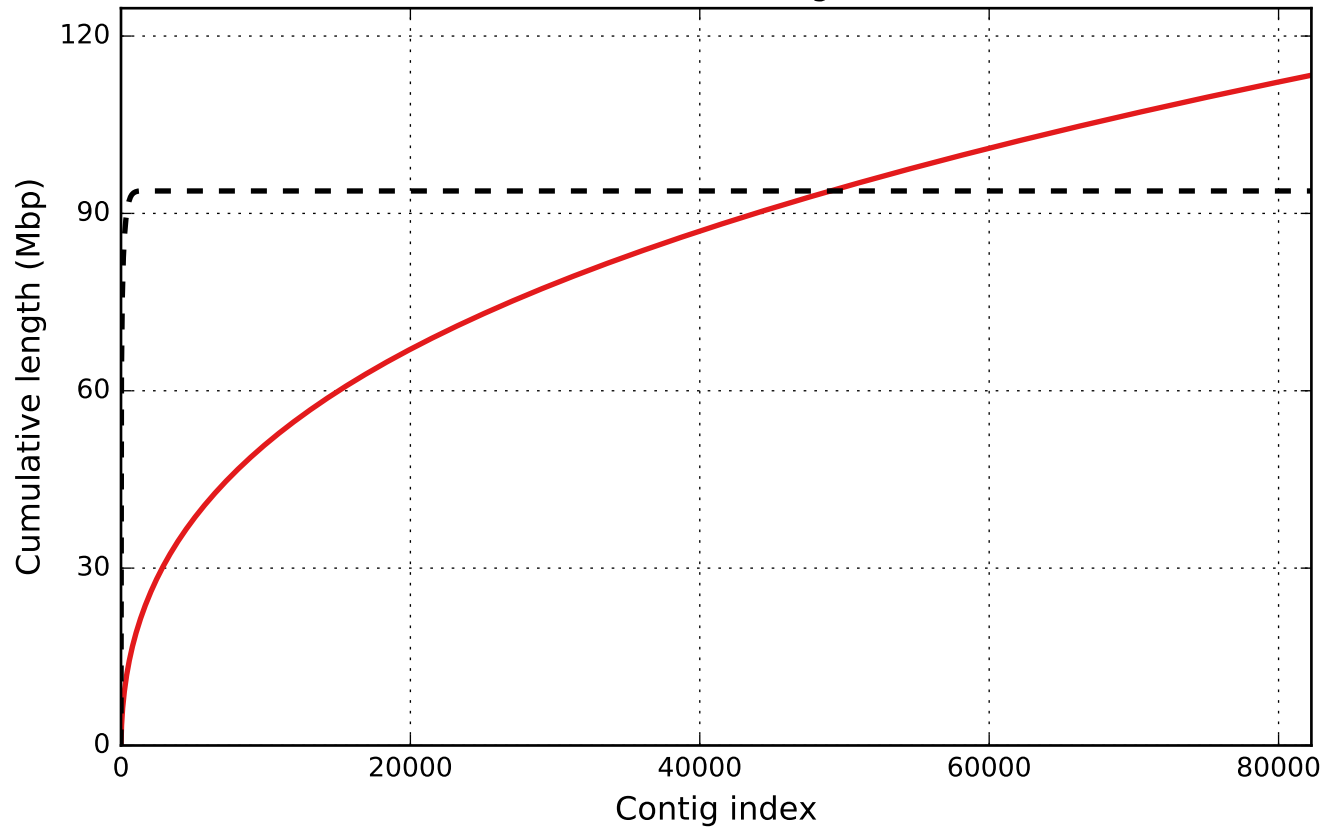
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

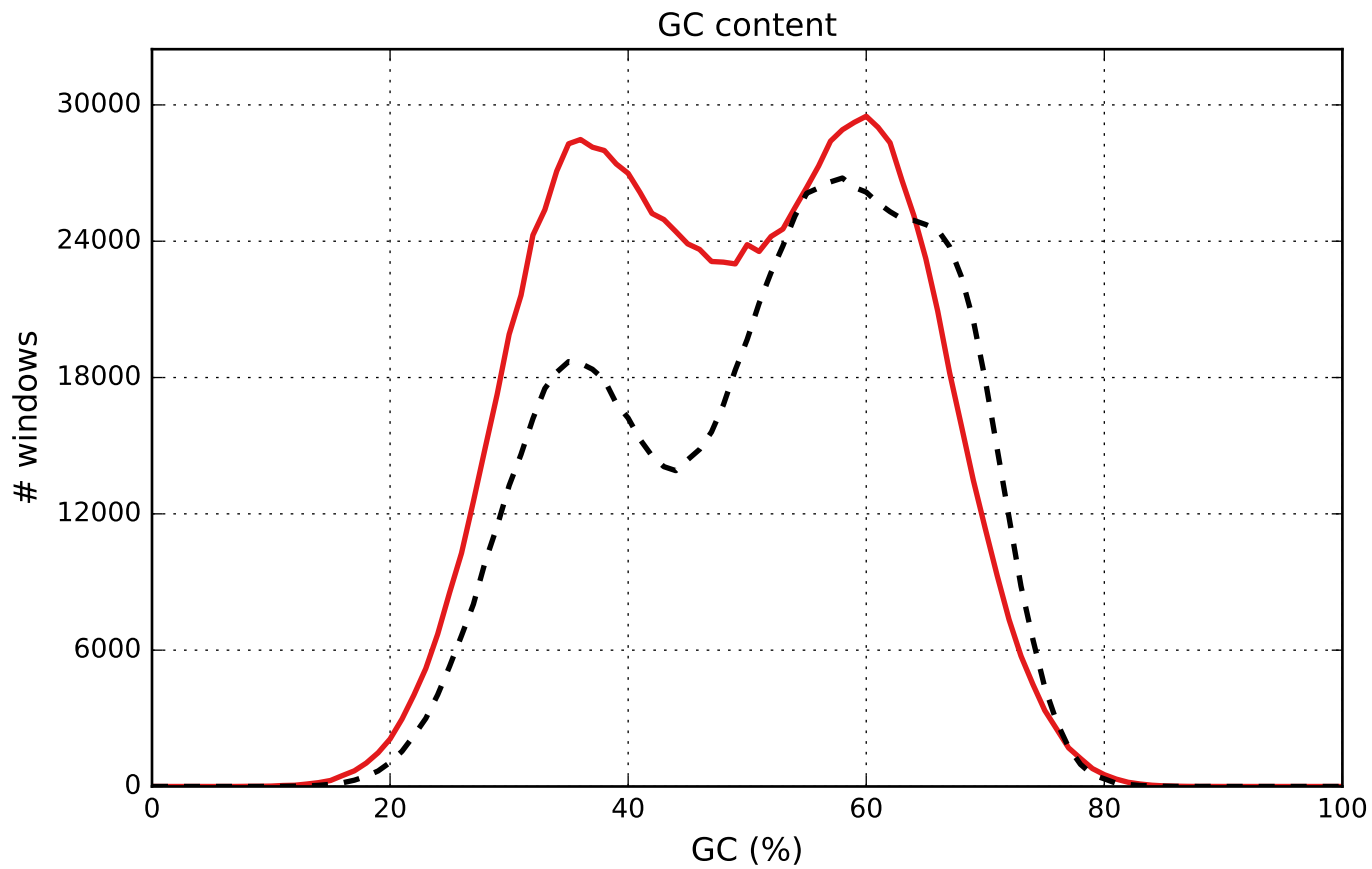
Nx



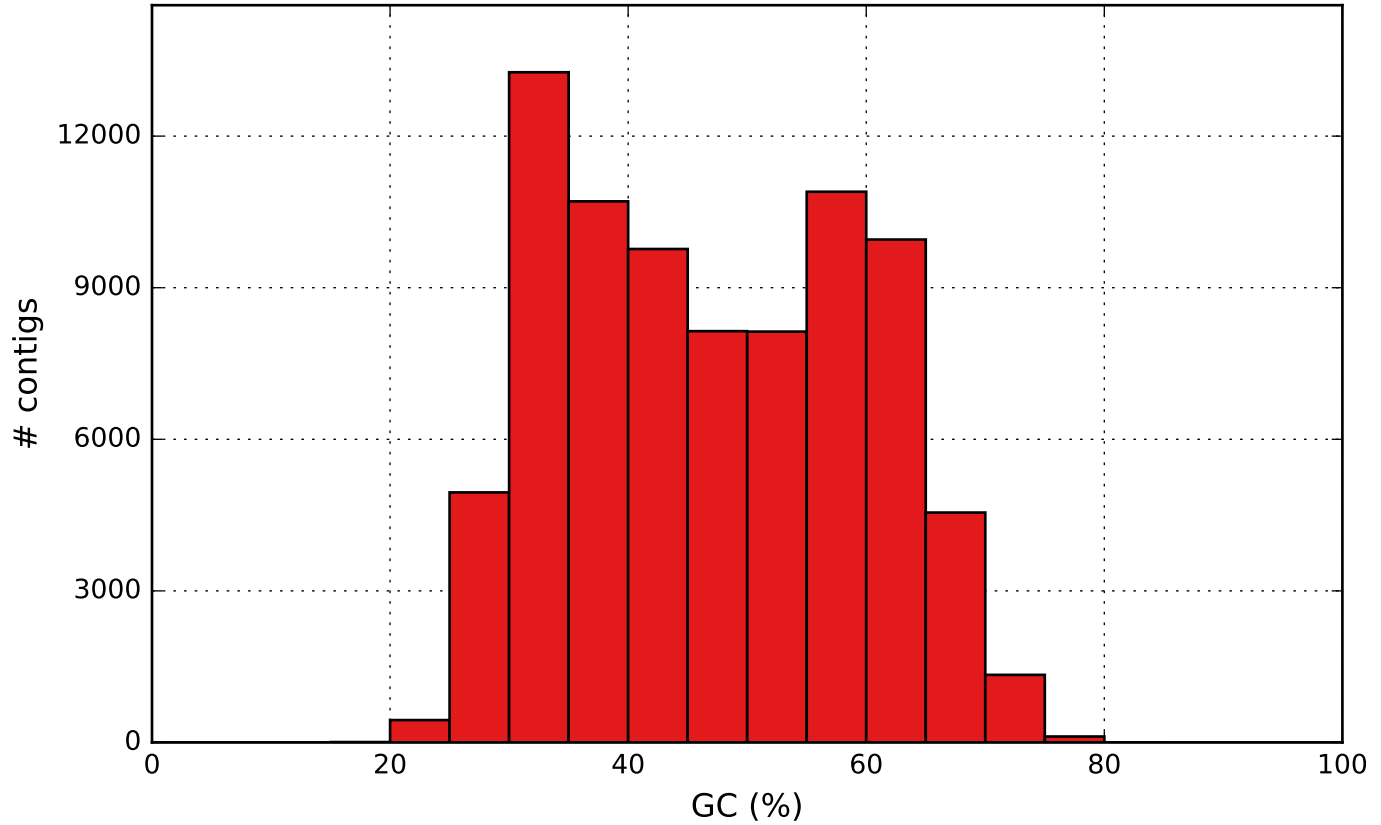
— final.contigs

Cumulative length

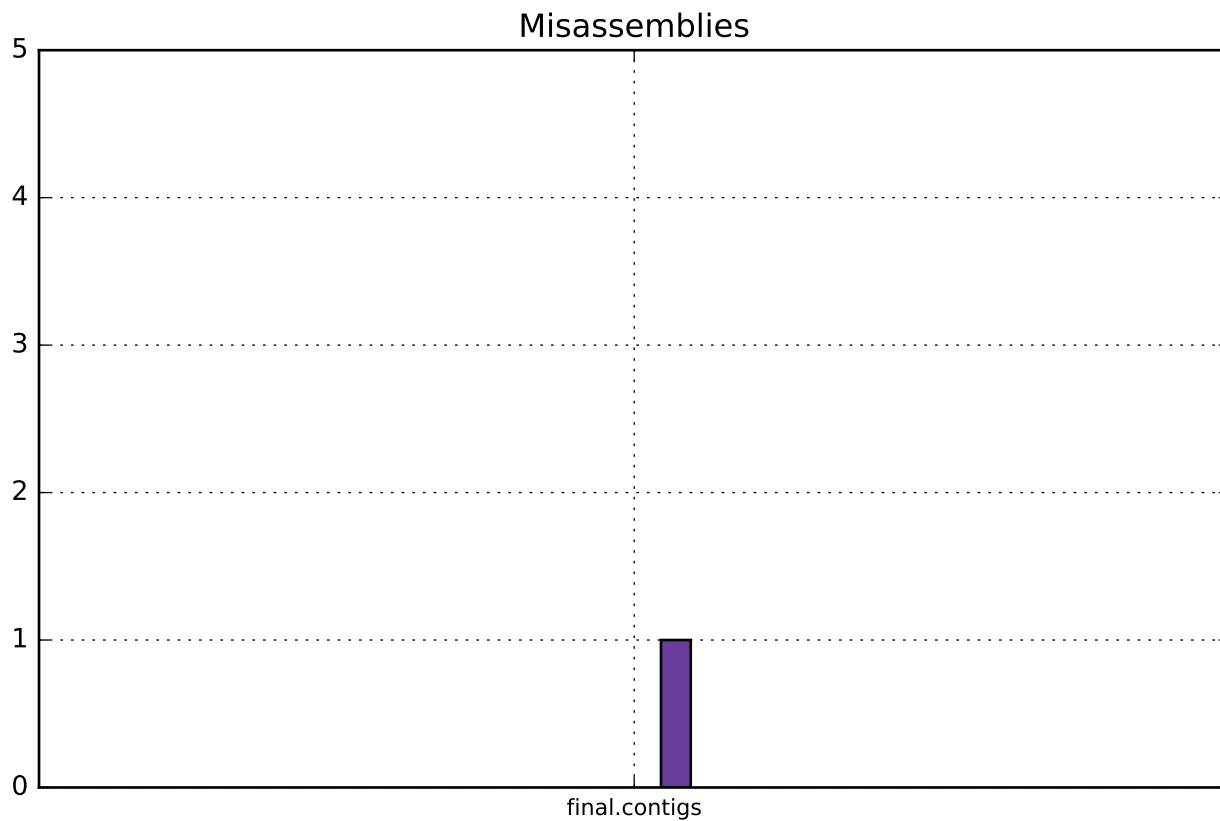





final.contigs GC content

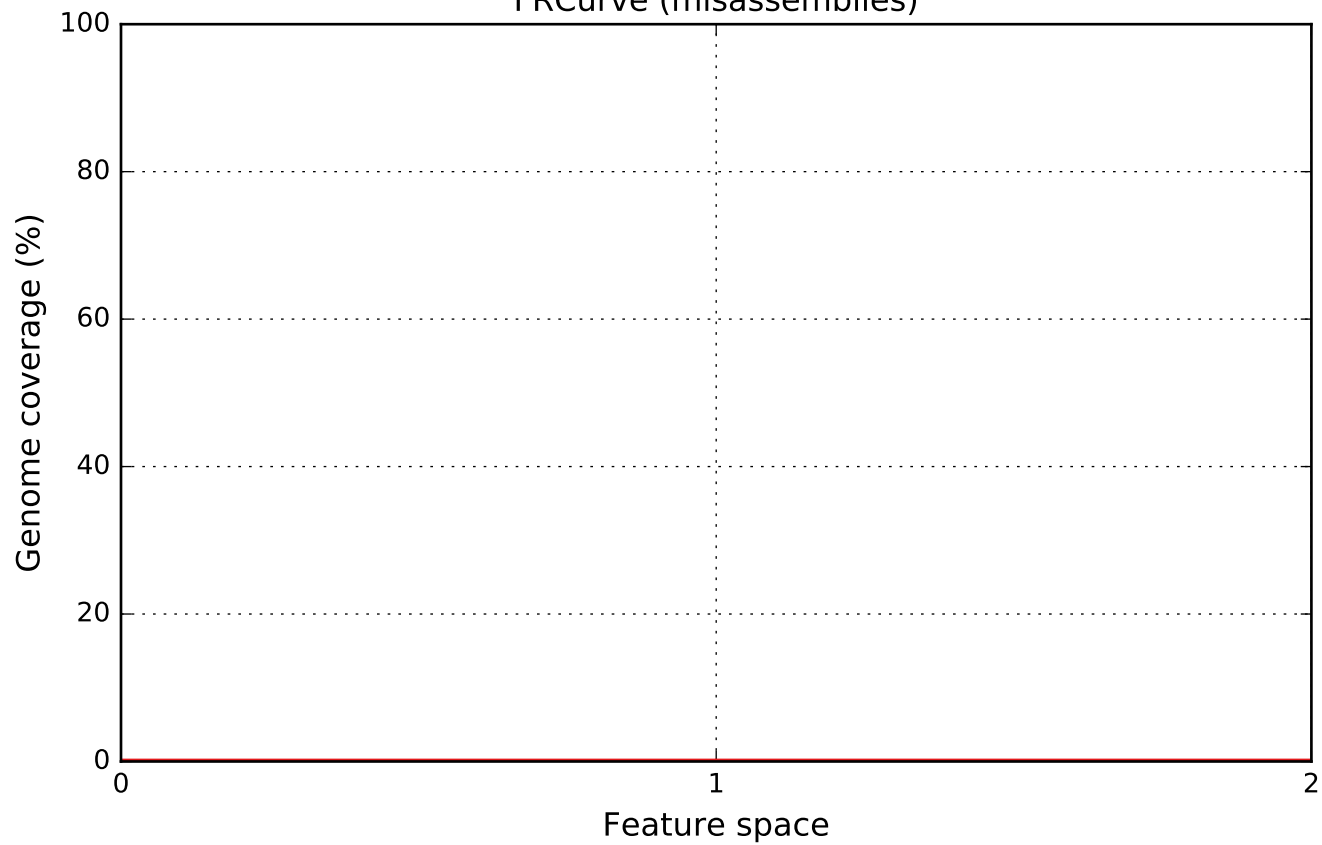


final.contigs

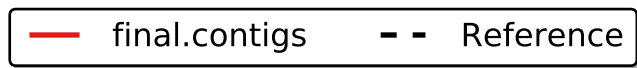
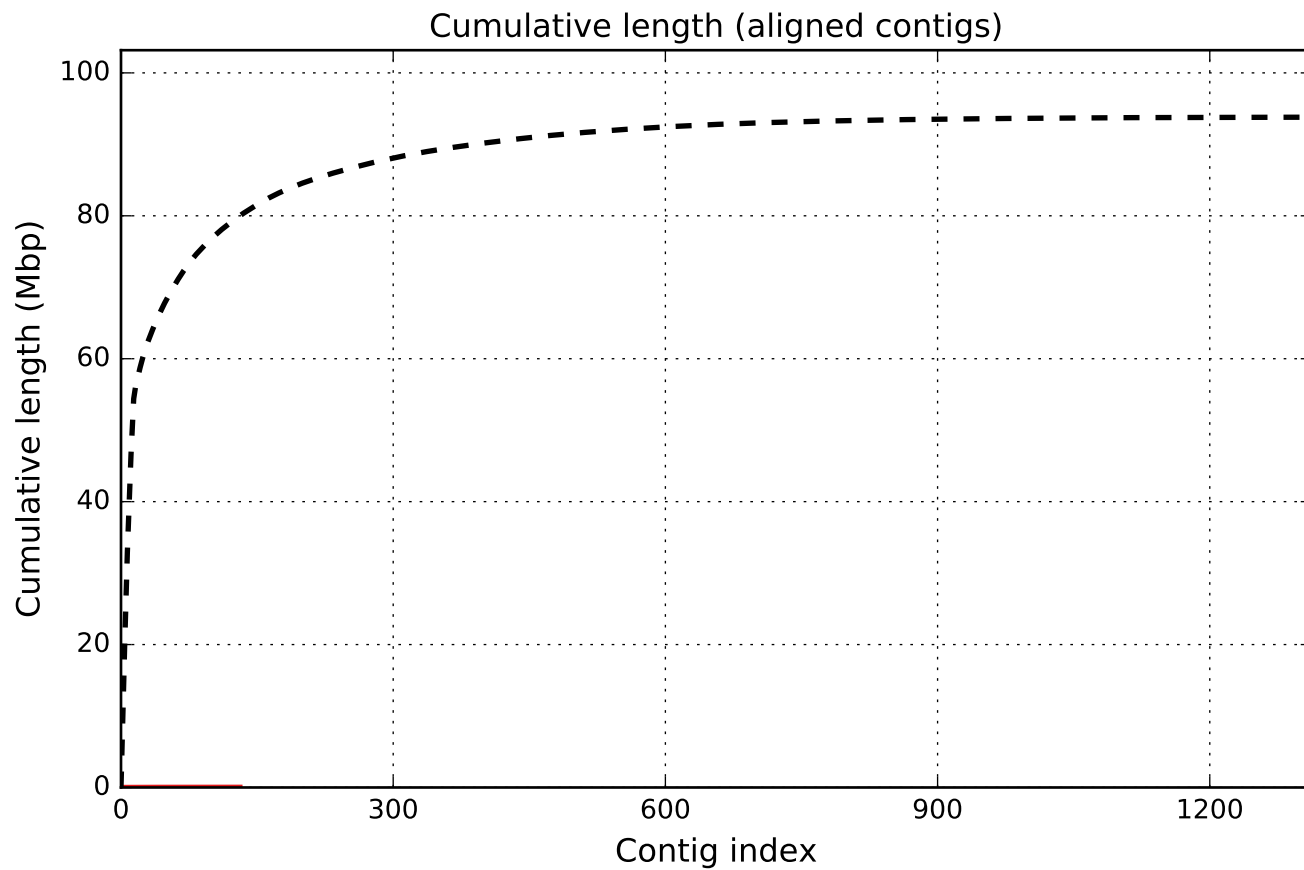


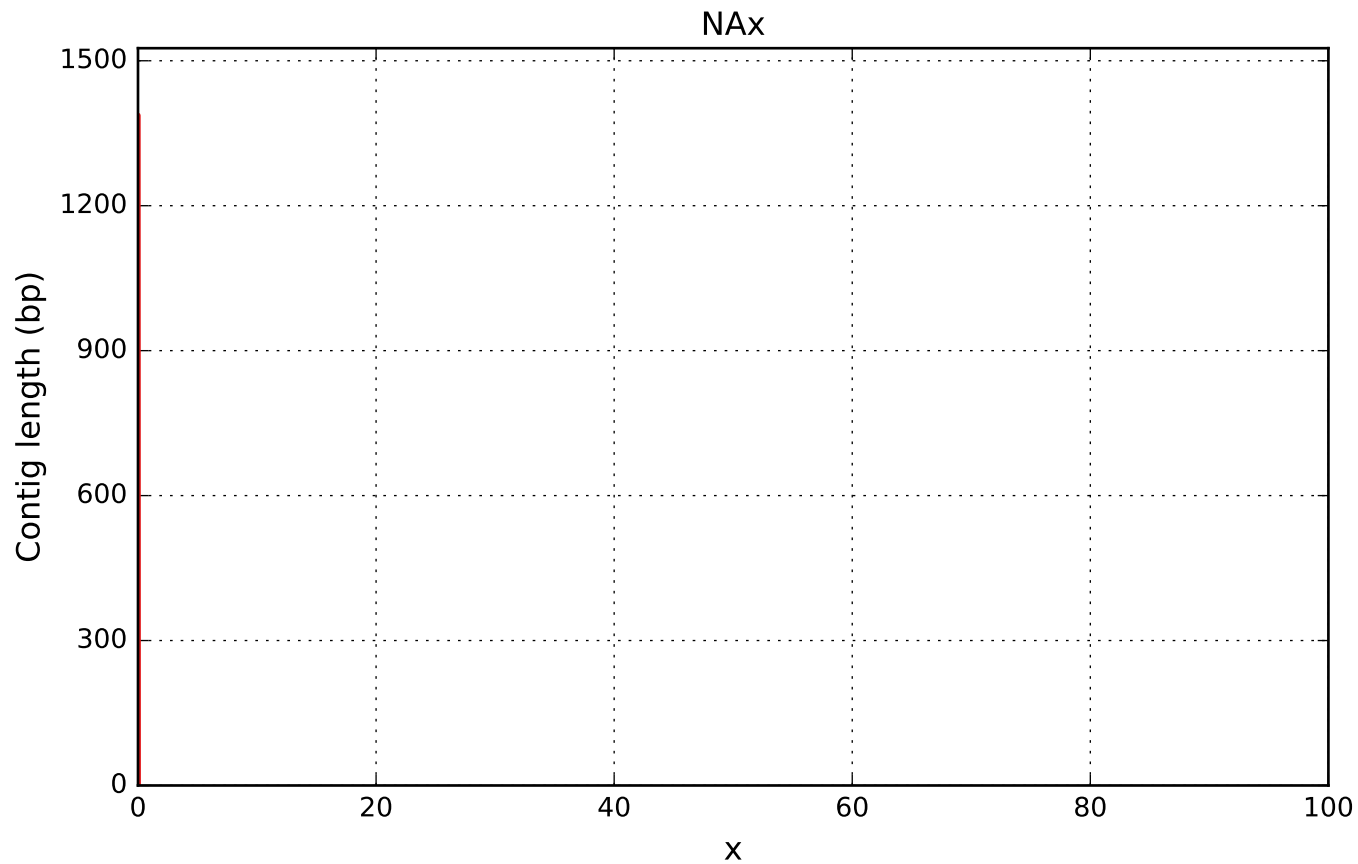
 # interspecies translocations

FRCurve (misassemblies)



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