

Report

	site_D3_DNA.final.contigs
# contigs (≥ 1000 bp)	3
# contigs (≥ 5000 bp)	1
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 1000 bp)	8219
Total length (≥ 5000 bp)	5303
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	5
Largest contig	5303
Total length	9469
Reference length	4305801
GC (%)	34.55
Reference GC (%)	34.36
N50	5303
N75	1444
L50	1
L75	3
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	1
# unaligned contigs	0 + 3 part
Unaligned length	7819
Genome fraction (%)	0.019
Duplication ratio	1.990
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2774.43
# indels per 100 kbp	120.63
Largest alignment	353
Total aligned length	830
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

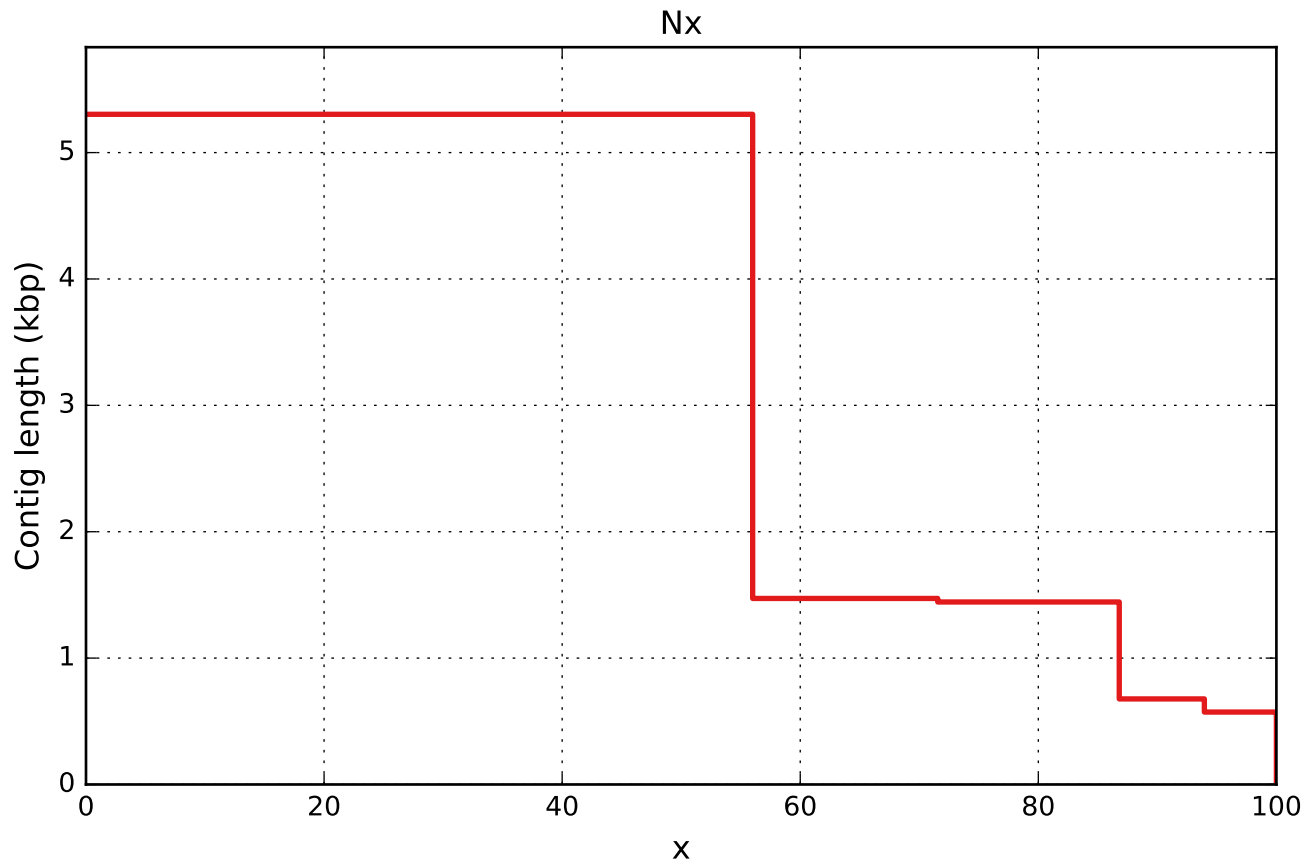
	site_D3_DNA.final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# unaligned mis. contigs	1
# mismatches	23
# indels	1
# indels (<= 5 bp)	1
# indels (> 5 bp)	0
Indels length	1

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

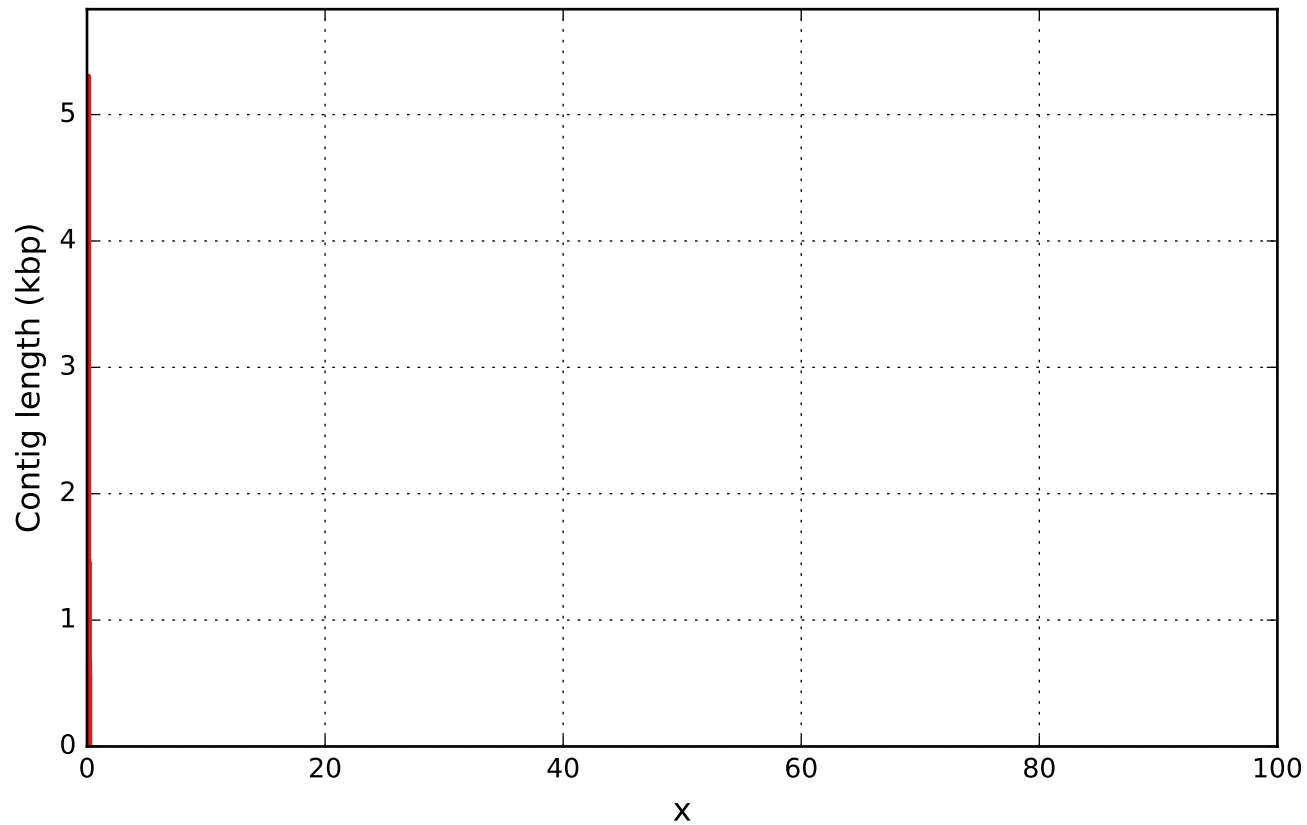
	site_D3_DNA.final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
Partially unaligned length	7819
# N's	0

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).

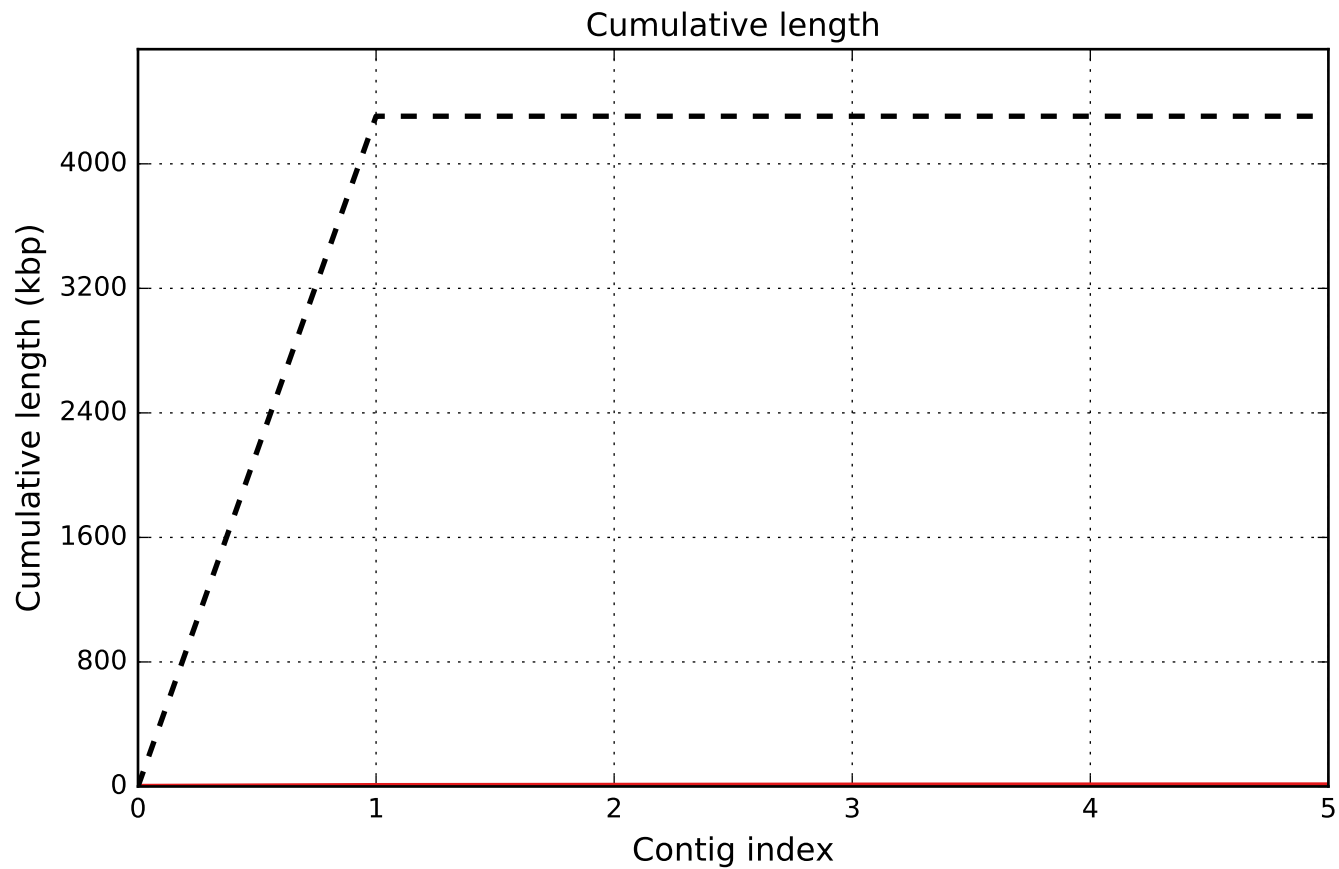


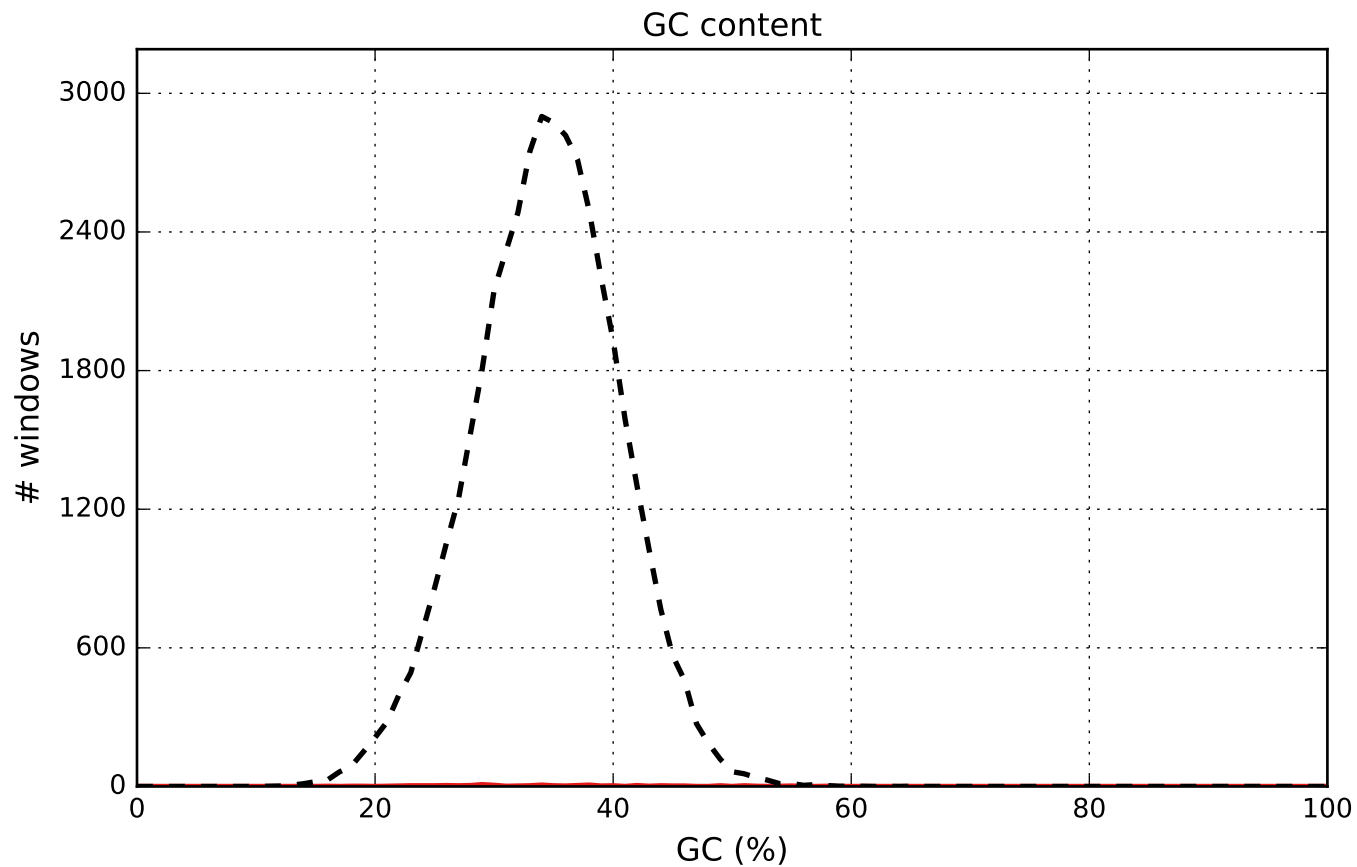
— site_D3_DNA.final.contigs

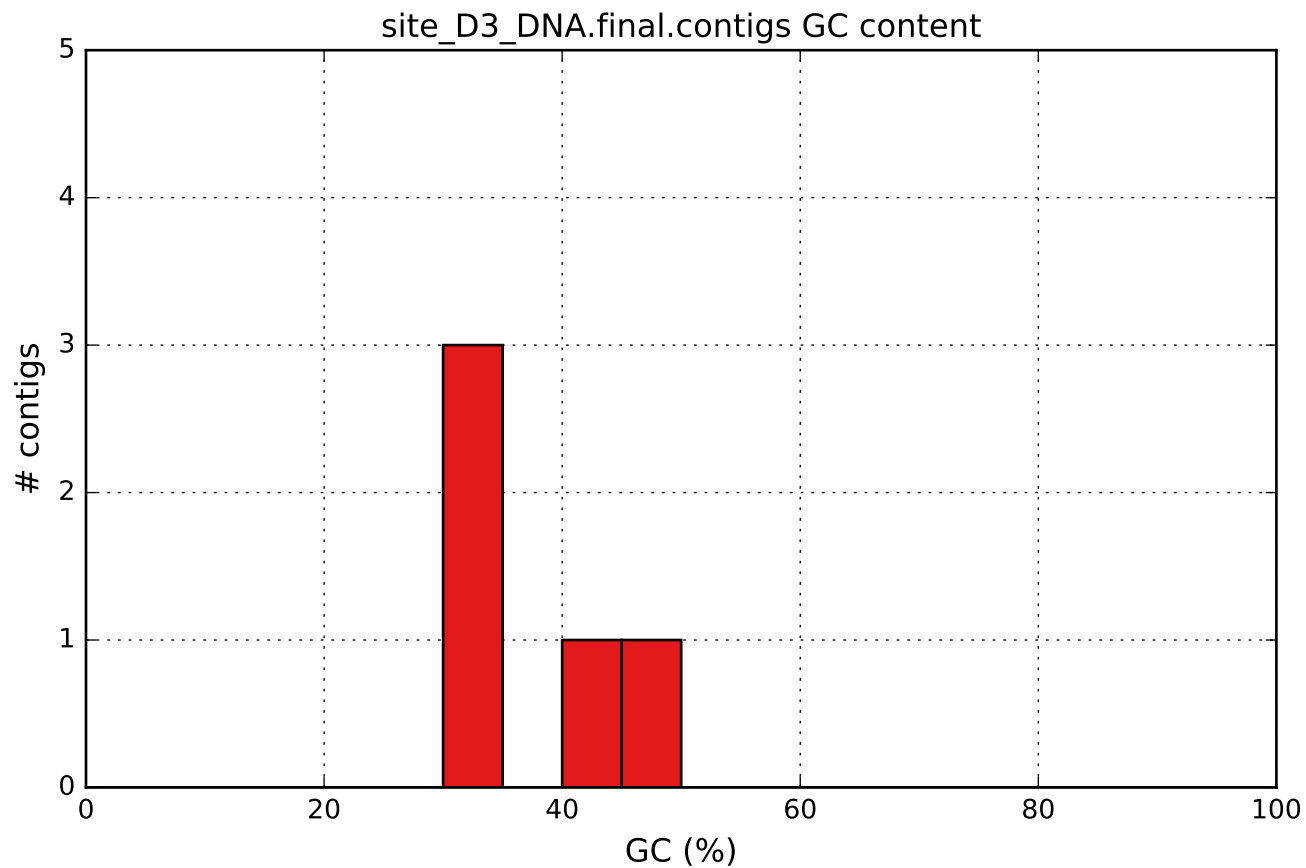
NGx



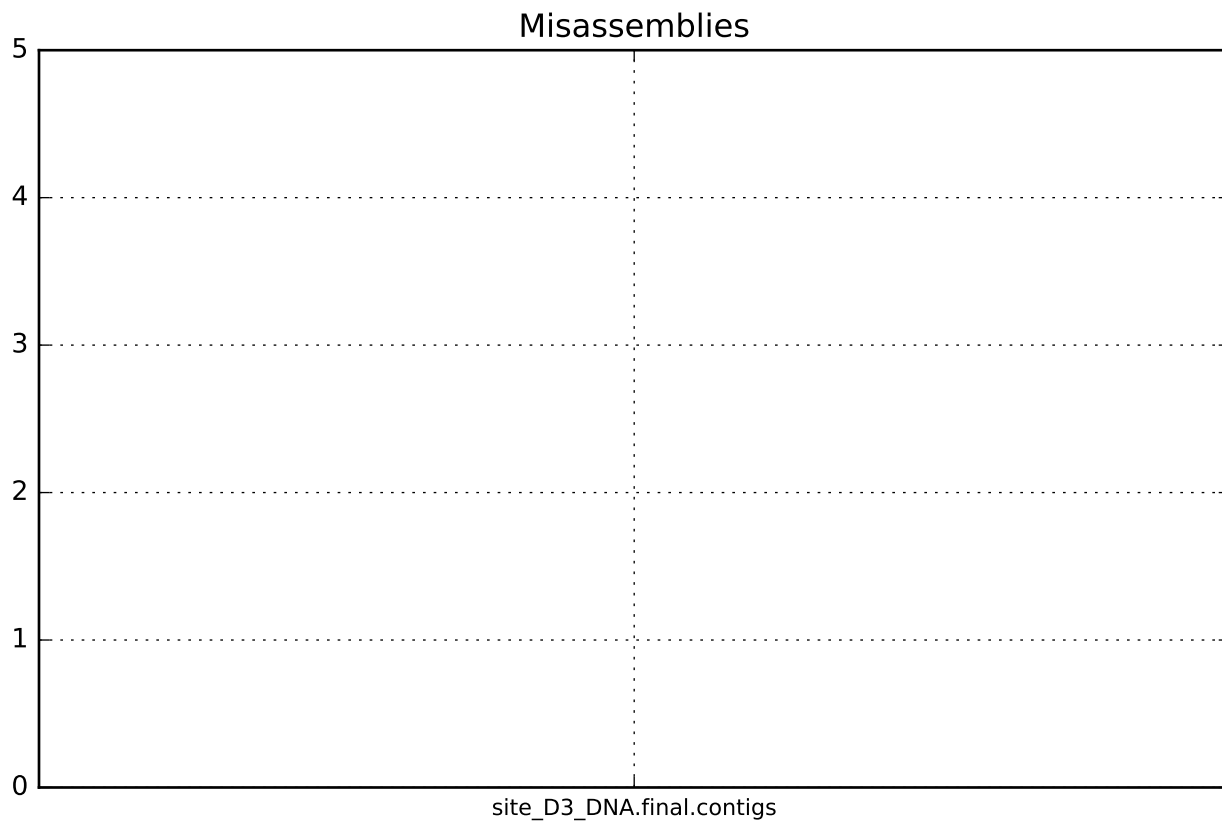
— site_D3_DNA.final.contigs



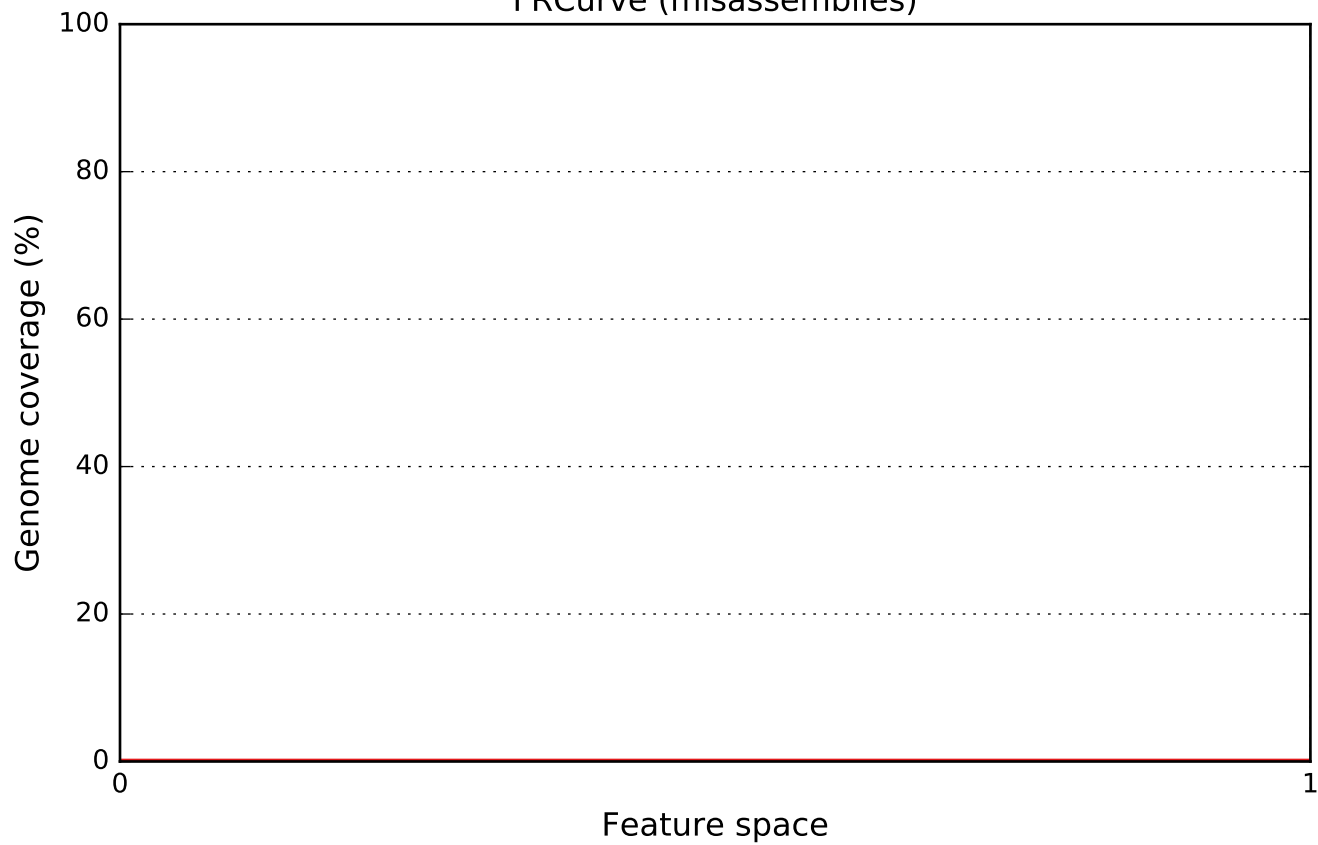




site_D3_DNA.final.contigs

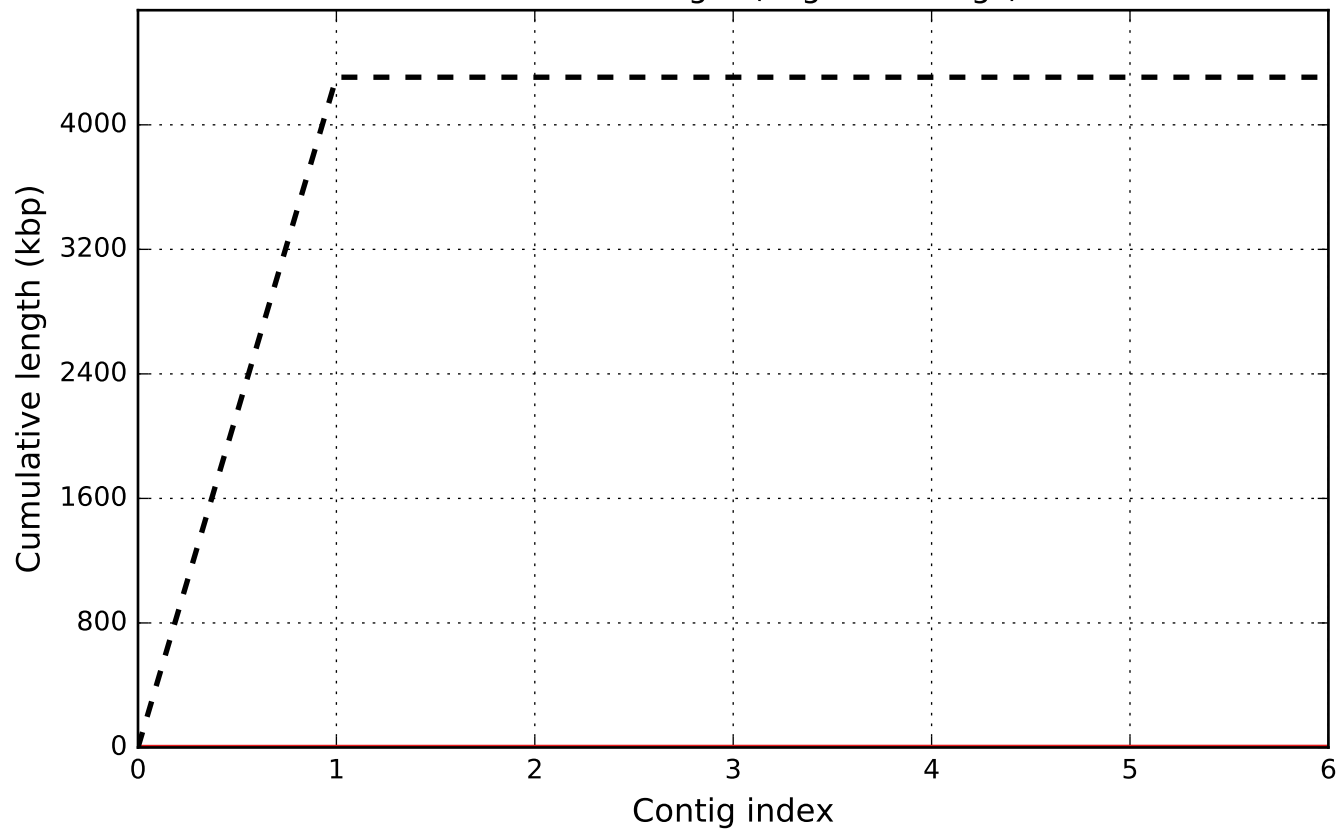


FRCurve (misassemblies)



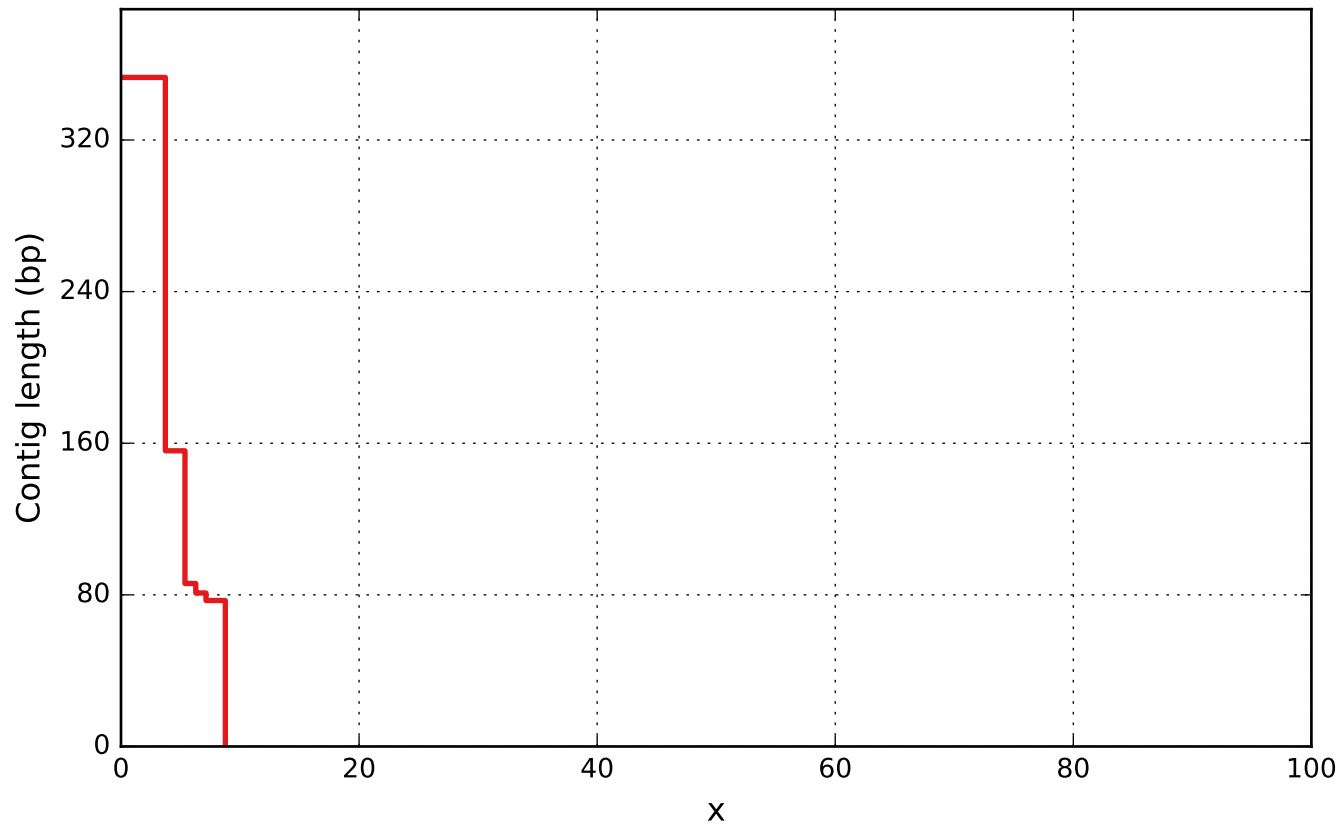
— site_D3_DNA.final.contigs

Cumulative length (aligned contigs)



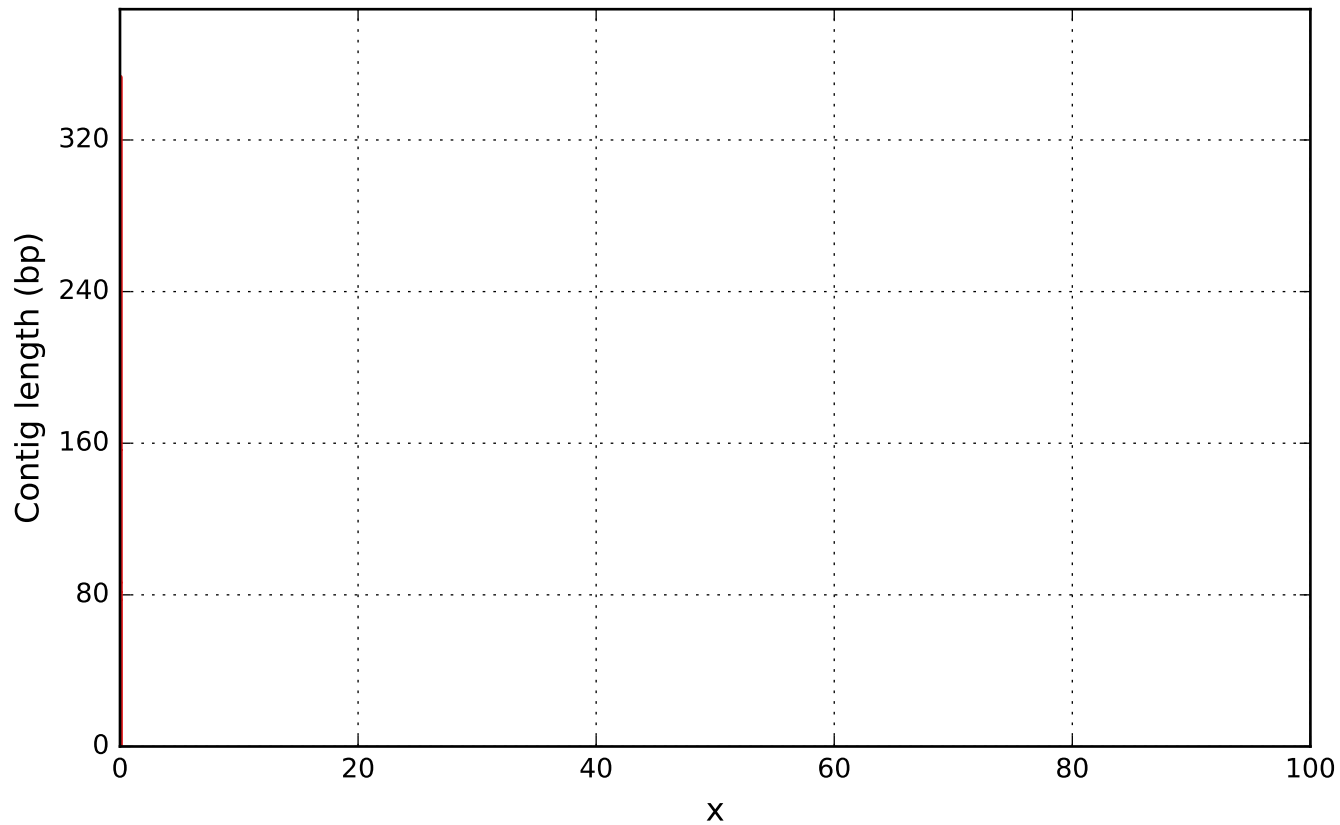
— site_D3_DNA.final.contigs - - Reference

NAx



— site_D3_DNA.final.contigs

NGAx



— site_D3_DNA.final.contigs