

Report

	site_D3_DNA.final.contigs
# contigs (>= 1000 bp)	5
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	14441
Total length (>= 5000 bp)	5267
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	6
Largest contig	5267
Total length	15119
Reference length	2077614
GC (%)	47.03
Reference GC (%)	39.47
N50	4124
N75	3047
L50	2
L75	3
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 5 part
Unaligned length	14025
Genome fraction (%)	0.053
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2833.64
# indels per 100 kbp	182.82
Largest alignment	678
Total aligned length	1094
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

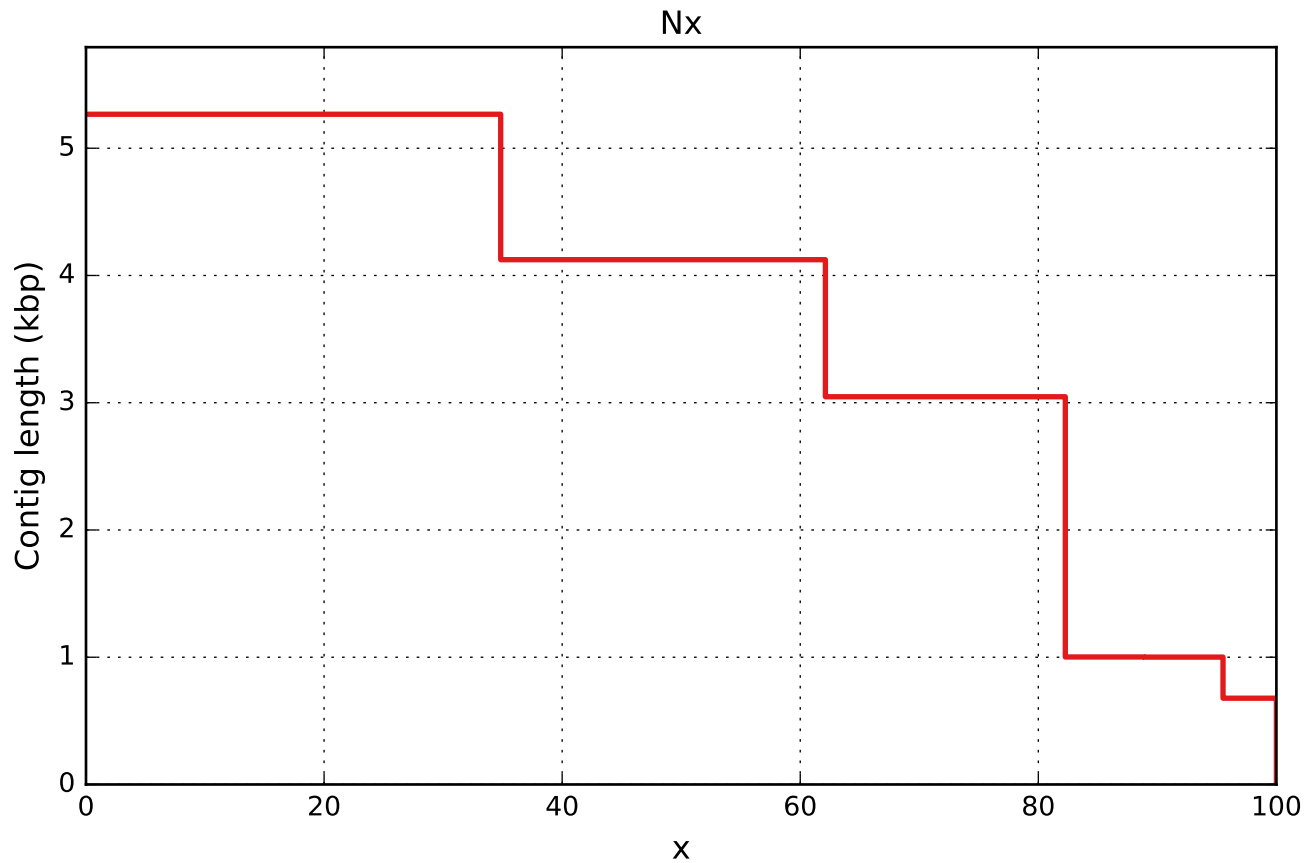
	site_D3_DNA.final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	31
# indels	2
# indels (<= 5 bp)	2
# indels (> 5 bp)	0
Indels length	2

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

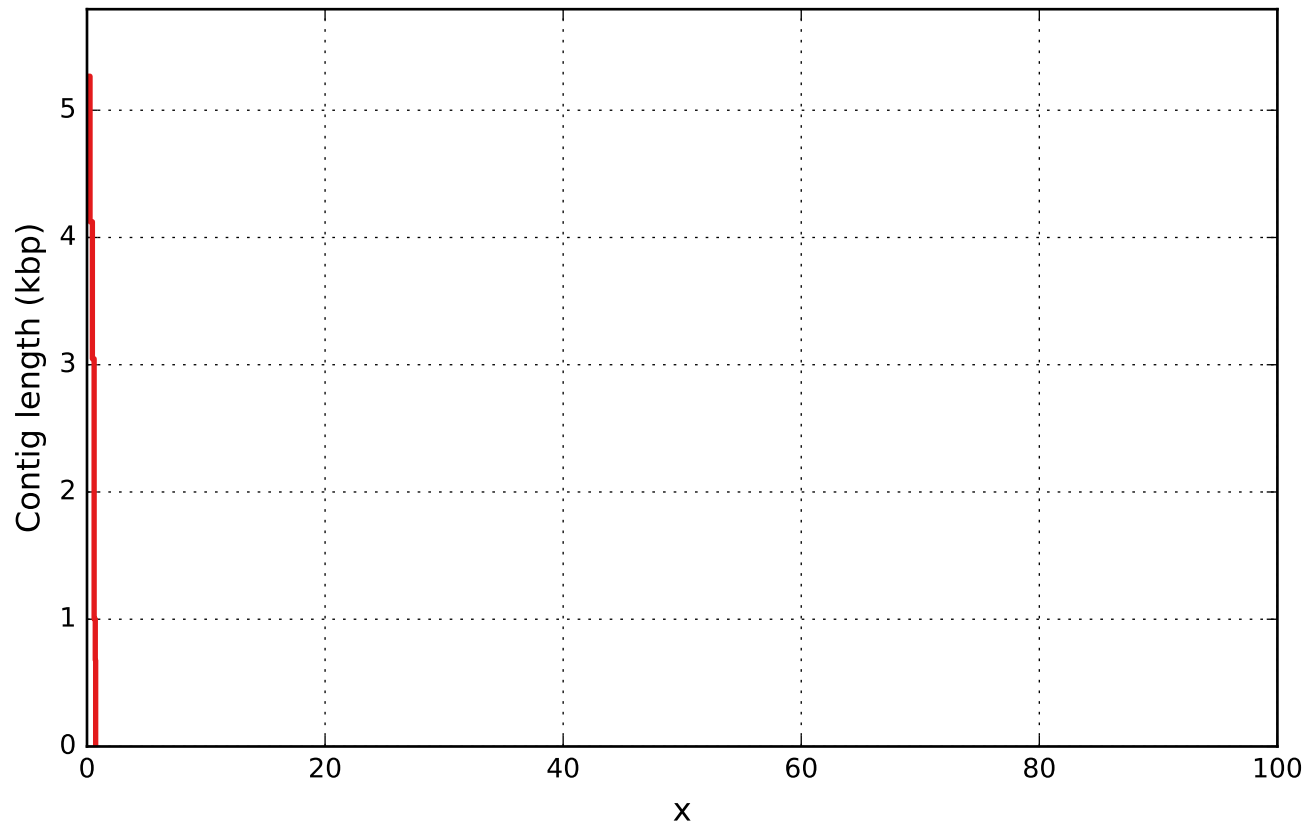
	site_D3_DNA.final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	5
Partially unaligned length	14025
# N's	0

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).

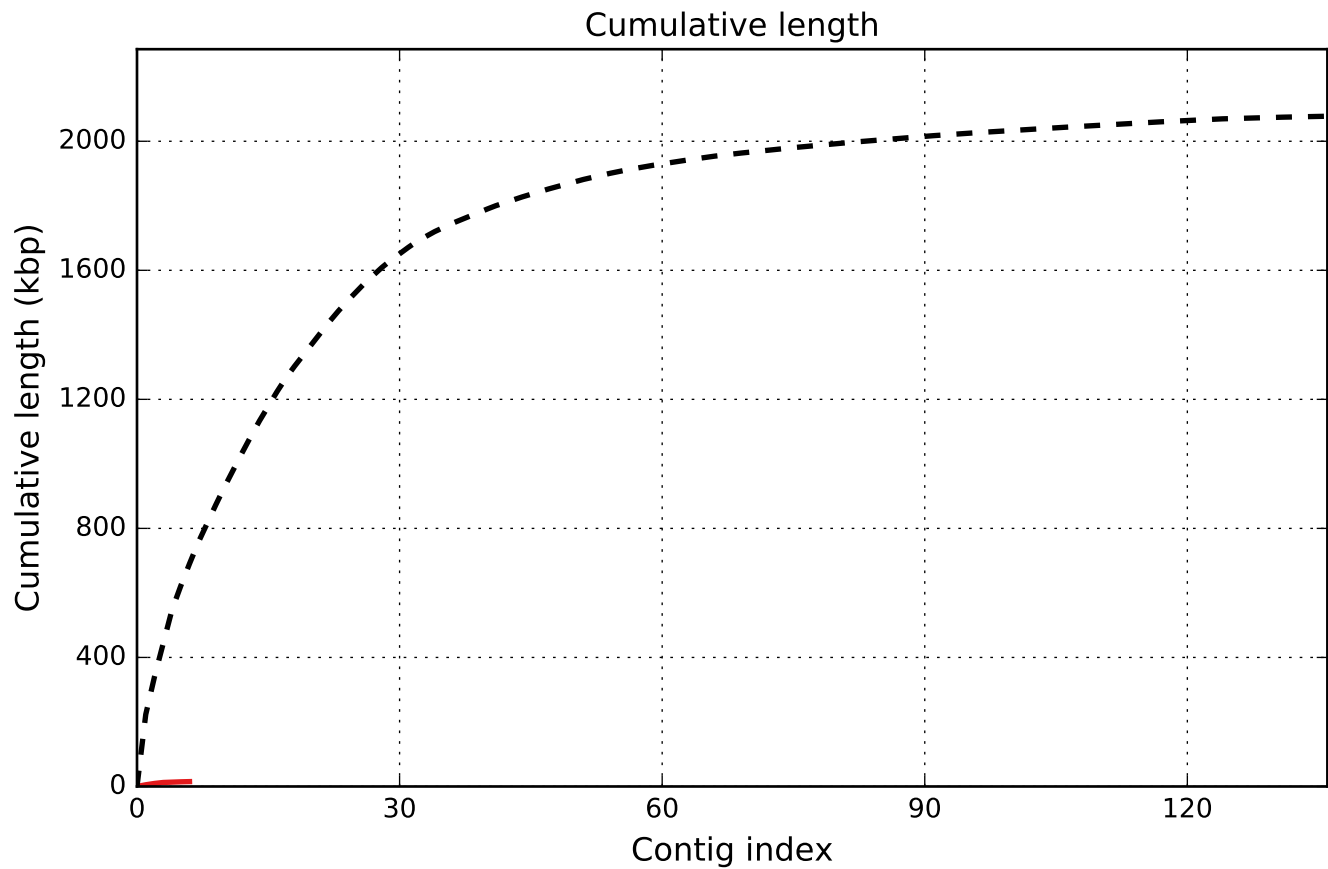


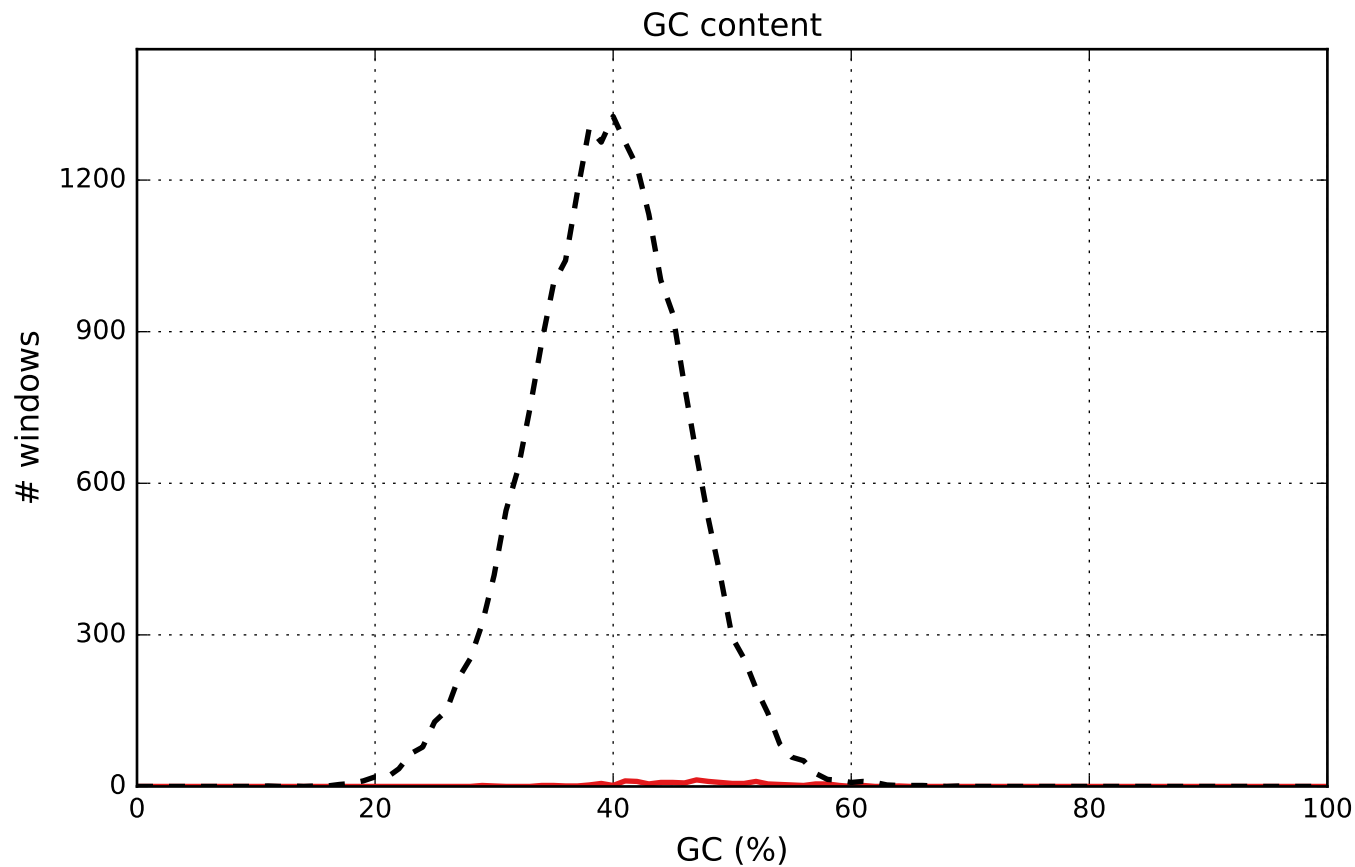
— site_D3_DNA.final.contigs

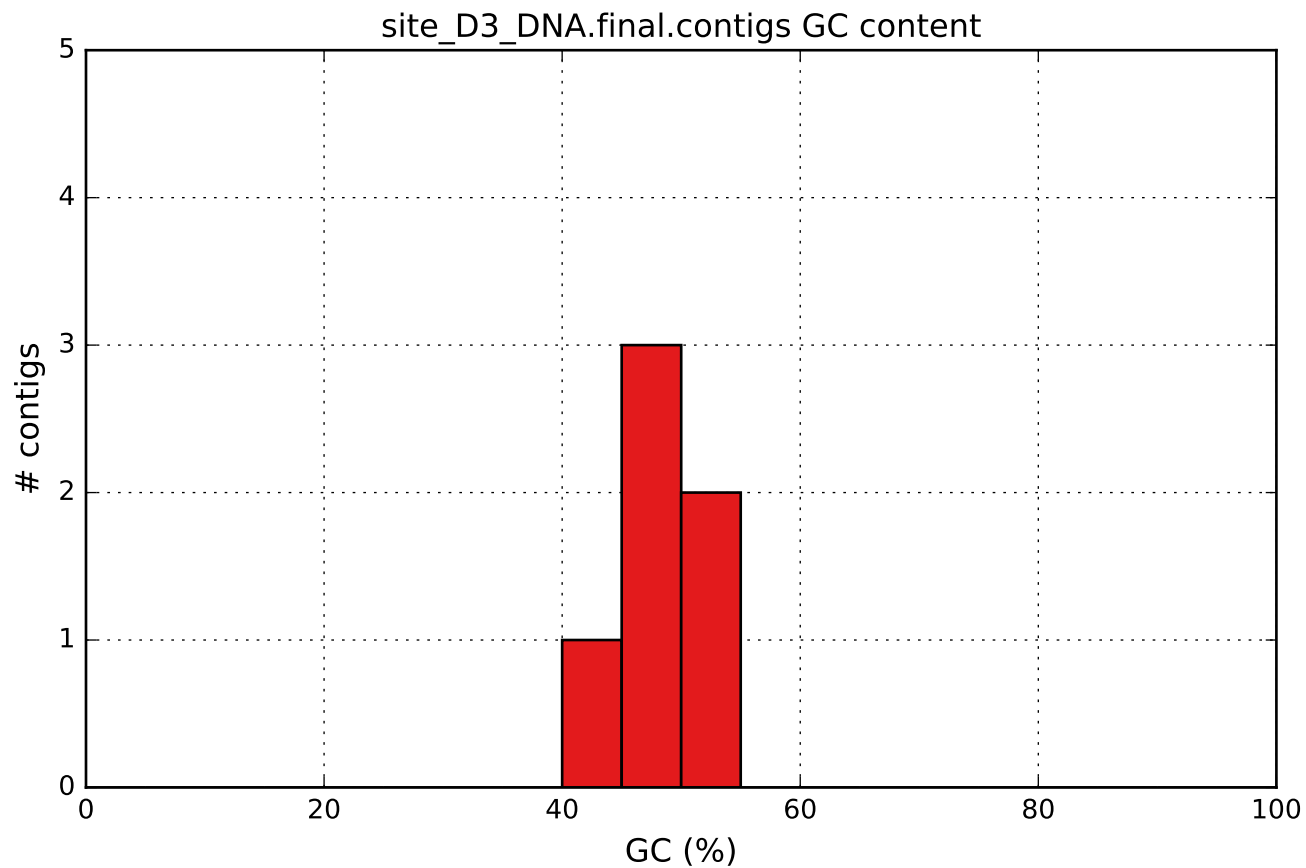
NGx



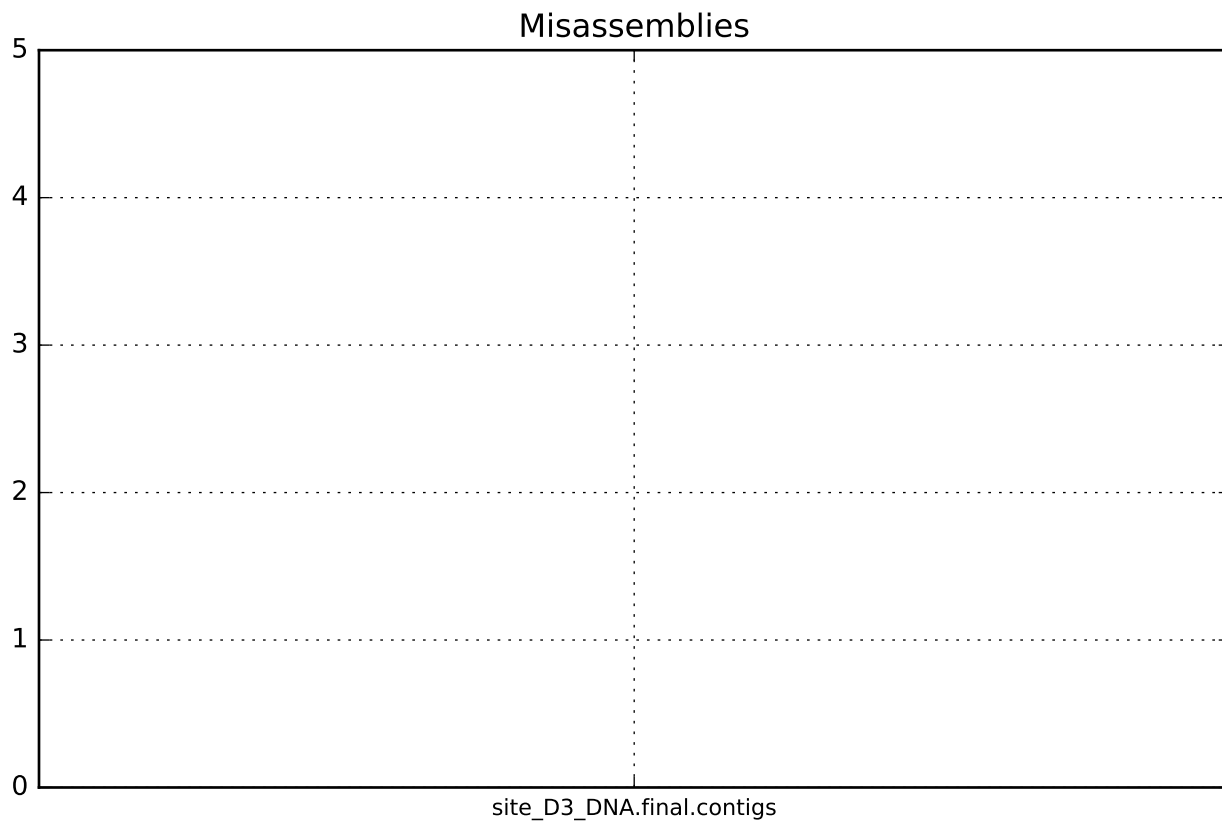
— site_D3_DNA.final.contigs



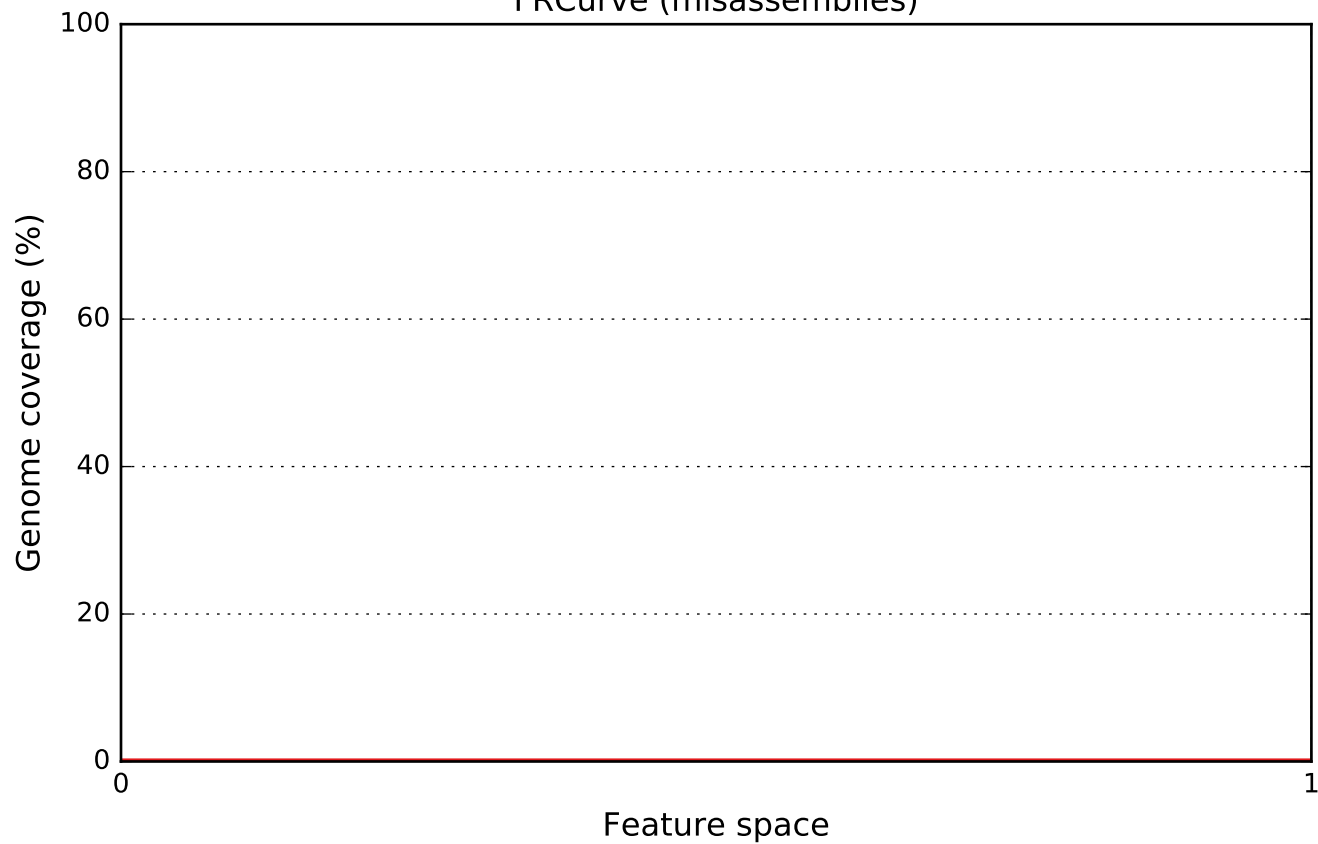




site_D3_DNA.final.contigs

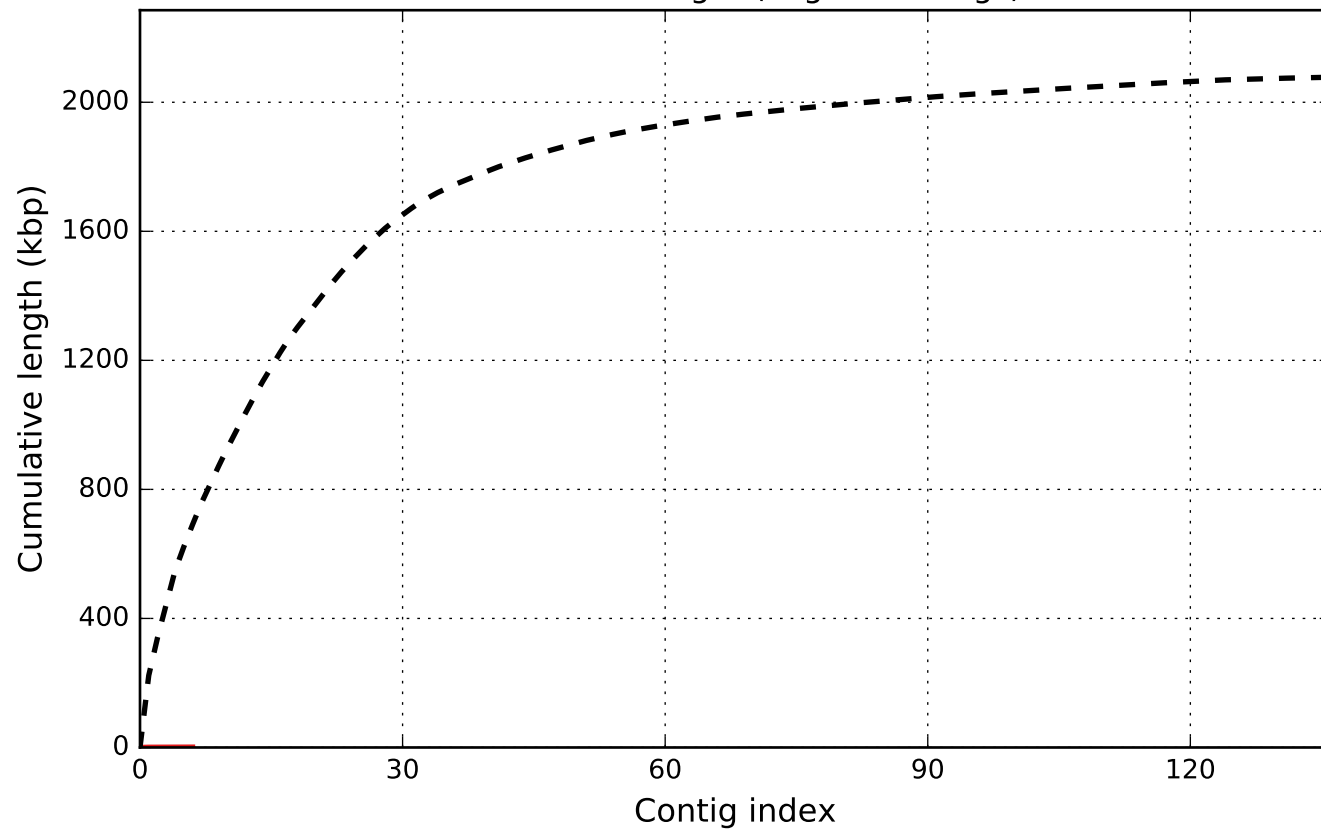


FRCurve (misassemblies)



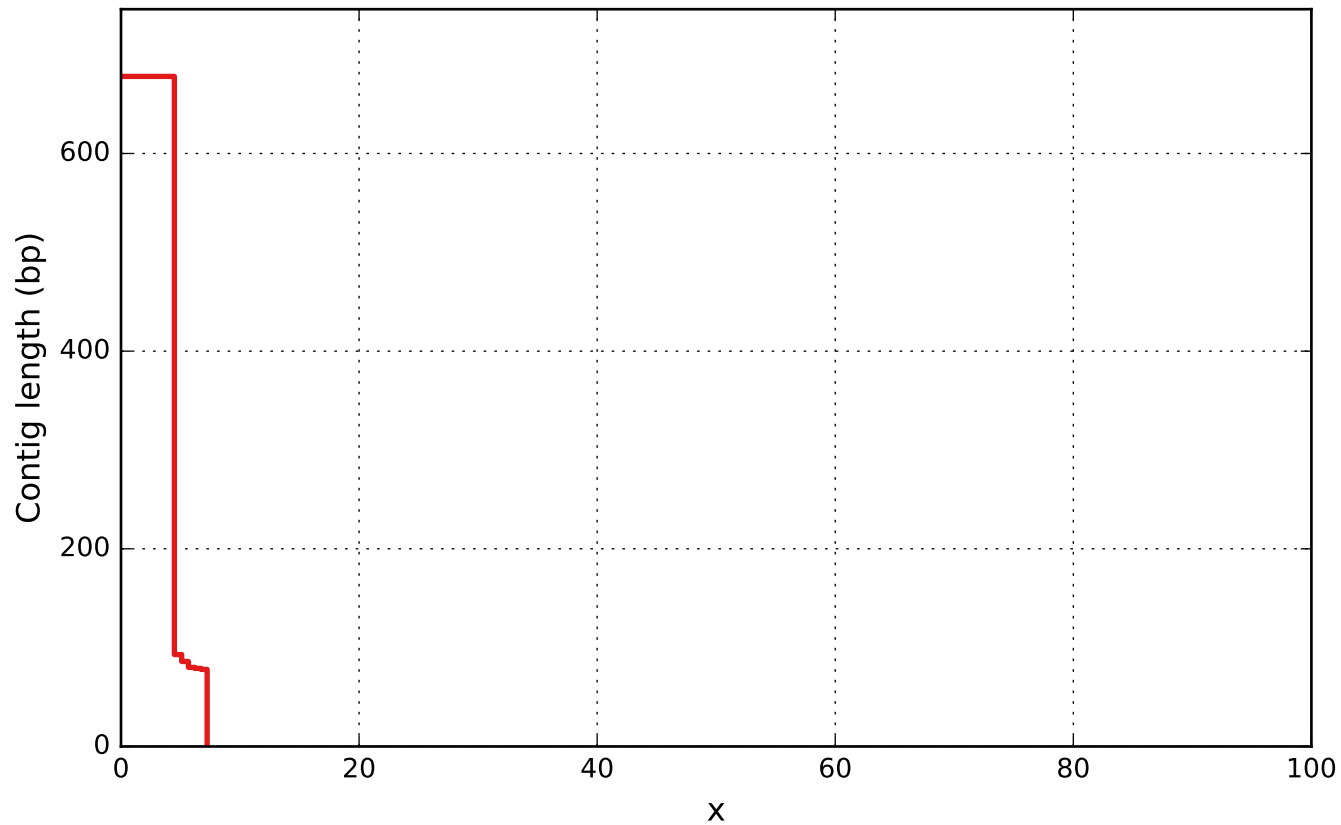
— site_D3_DNA.final.contigs

Cumulative length (aligned contigs)



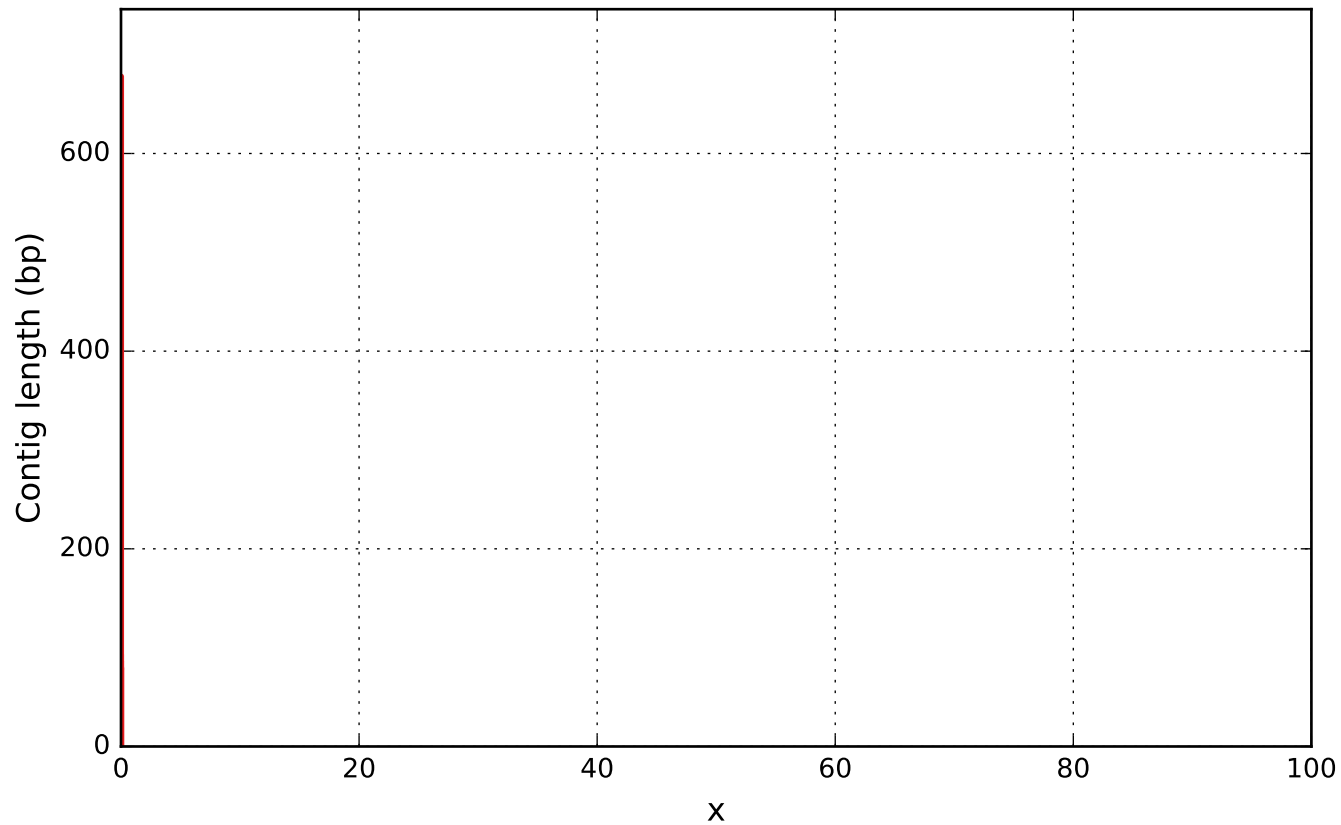
— site_D3_DNA.final.contigs - - Reference

NAx



— site_D3_DNA.final.contigs

NGAx



— site_D3_DNA.final.contigs