

Report

	site_D1_DNA.final.contigs
# contigs (≥ 1000 bp)	1
# contigs (≥ 5000 bp)	0
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 1000 bp)	1601
Total length (≥ 5000 bp)	0
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	2
Largest contig	1601
Total length	2485
Reference length	4282232
GC (%)	50.50
Reference GC (%)	66.99
N50	1601
N75	884
L50	1
L75	2
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 2 part
Unaligned length	2316
Genome fraction (%)	0.004
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4733.73
# indels per 100 kbp	0.00
Largest alignment	88
Total aligned length	169
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

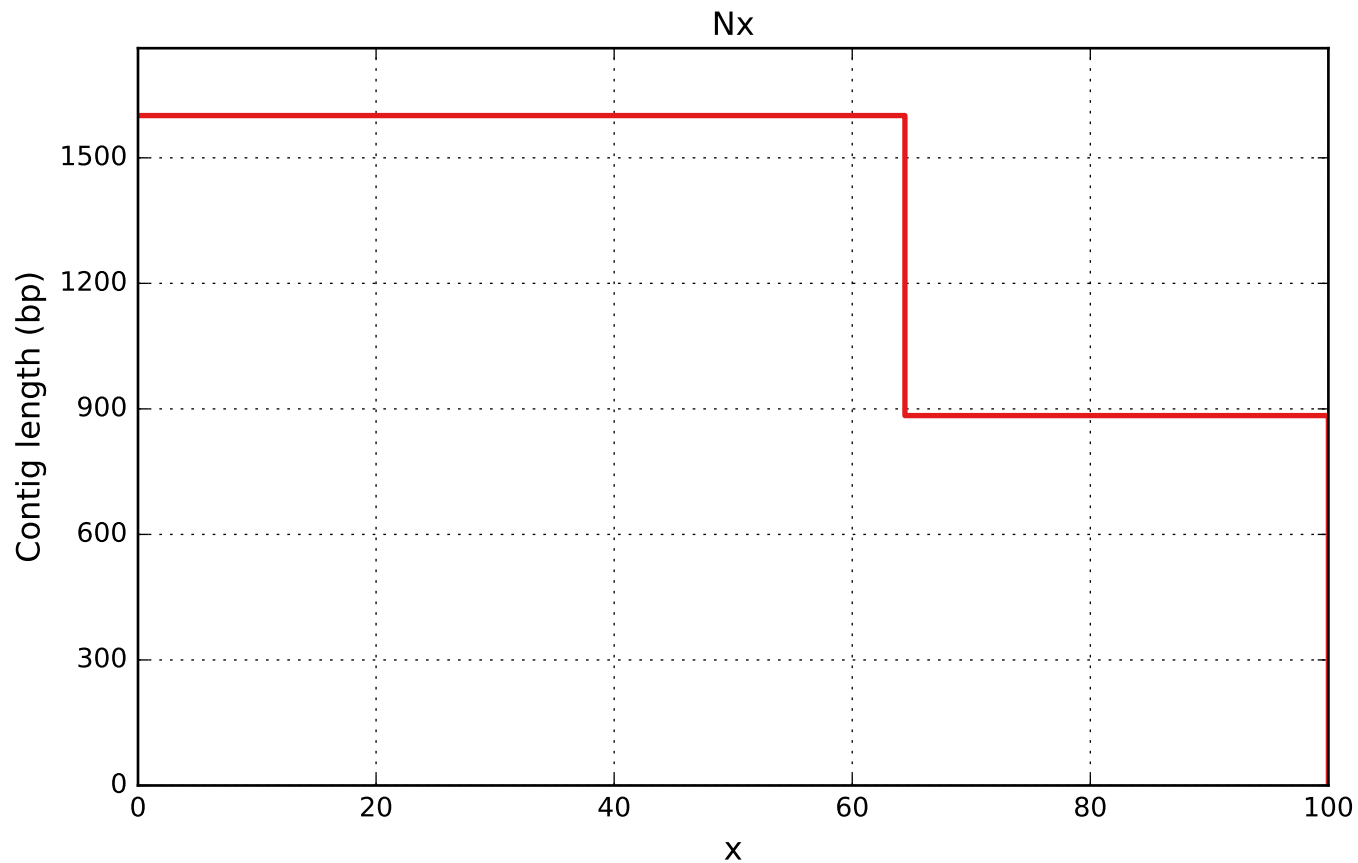
	site_D1_DNA.final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs	0
# mismatches	8
# 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).

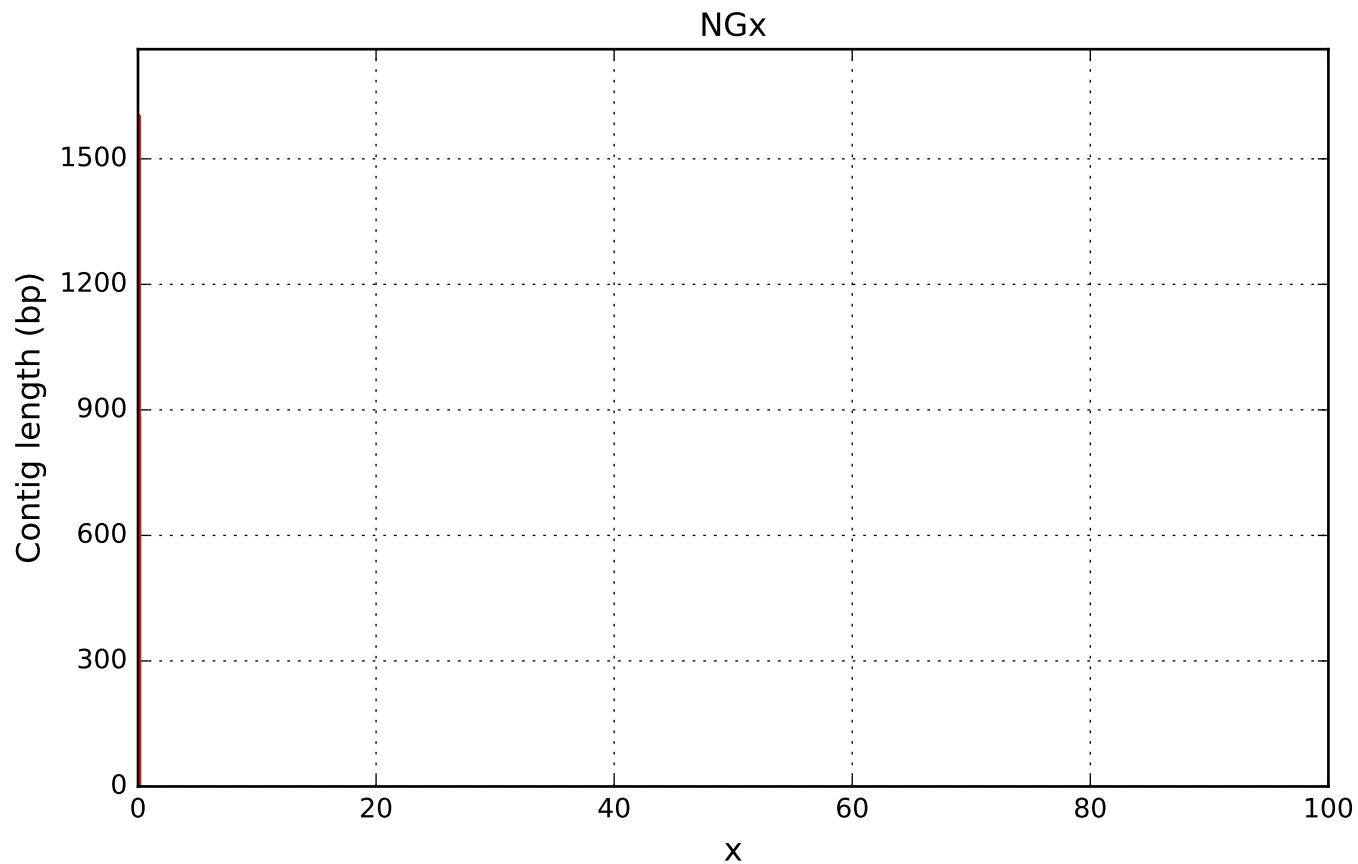
Unaligned report

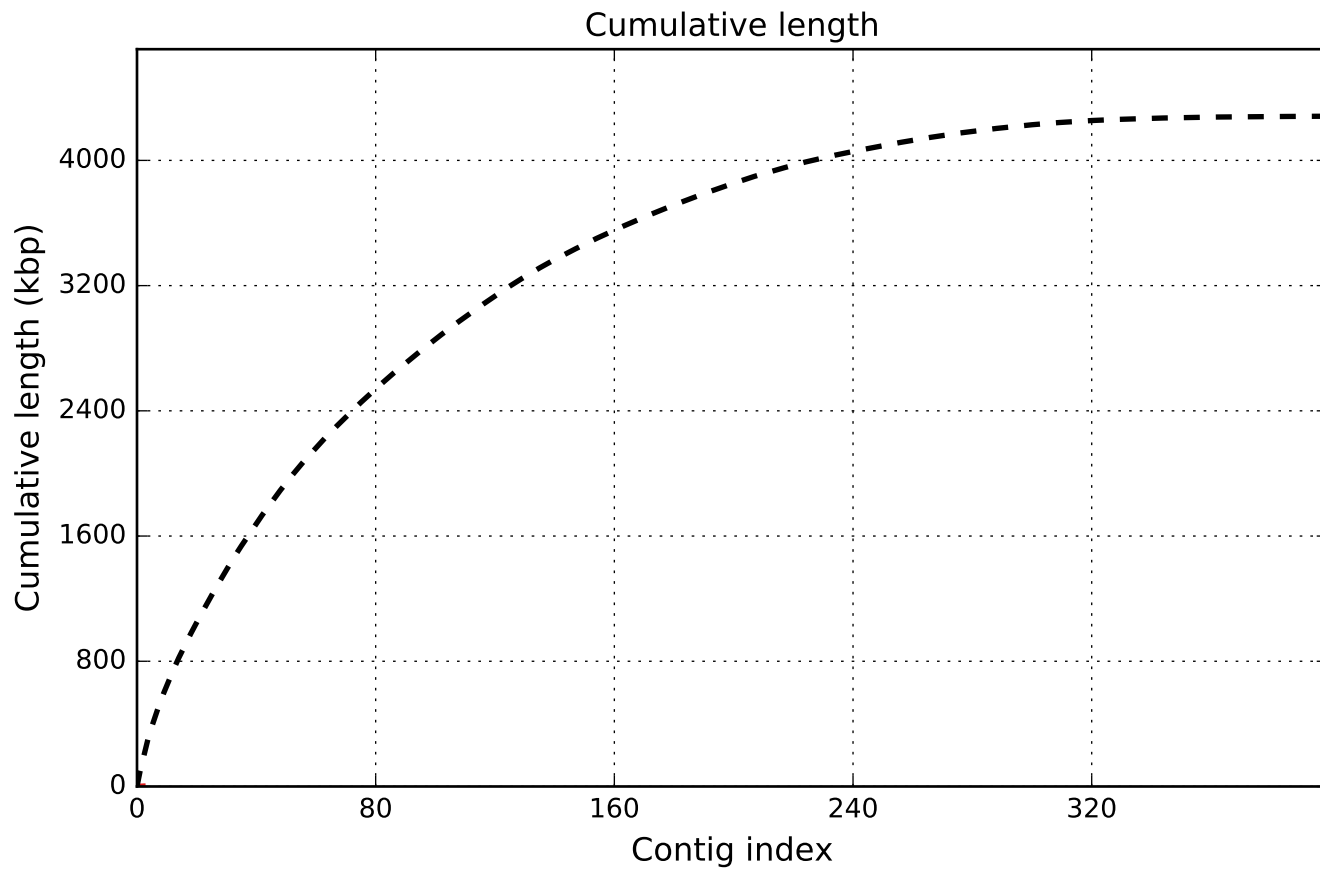
	site_D1_DNA.final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
Partially unaligned length	2316
# N's	0

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).



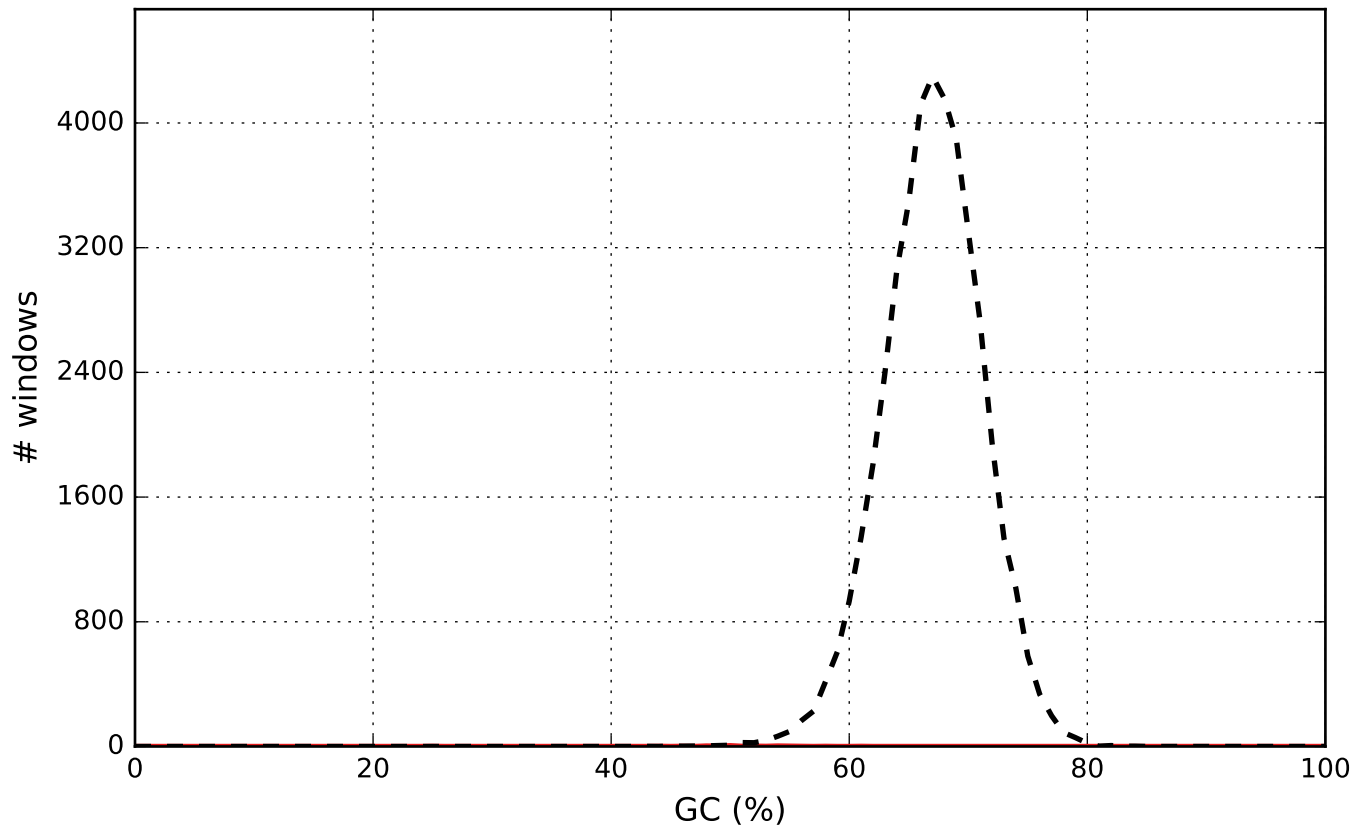
— site_D1_DNA.final.contigs

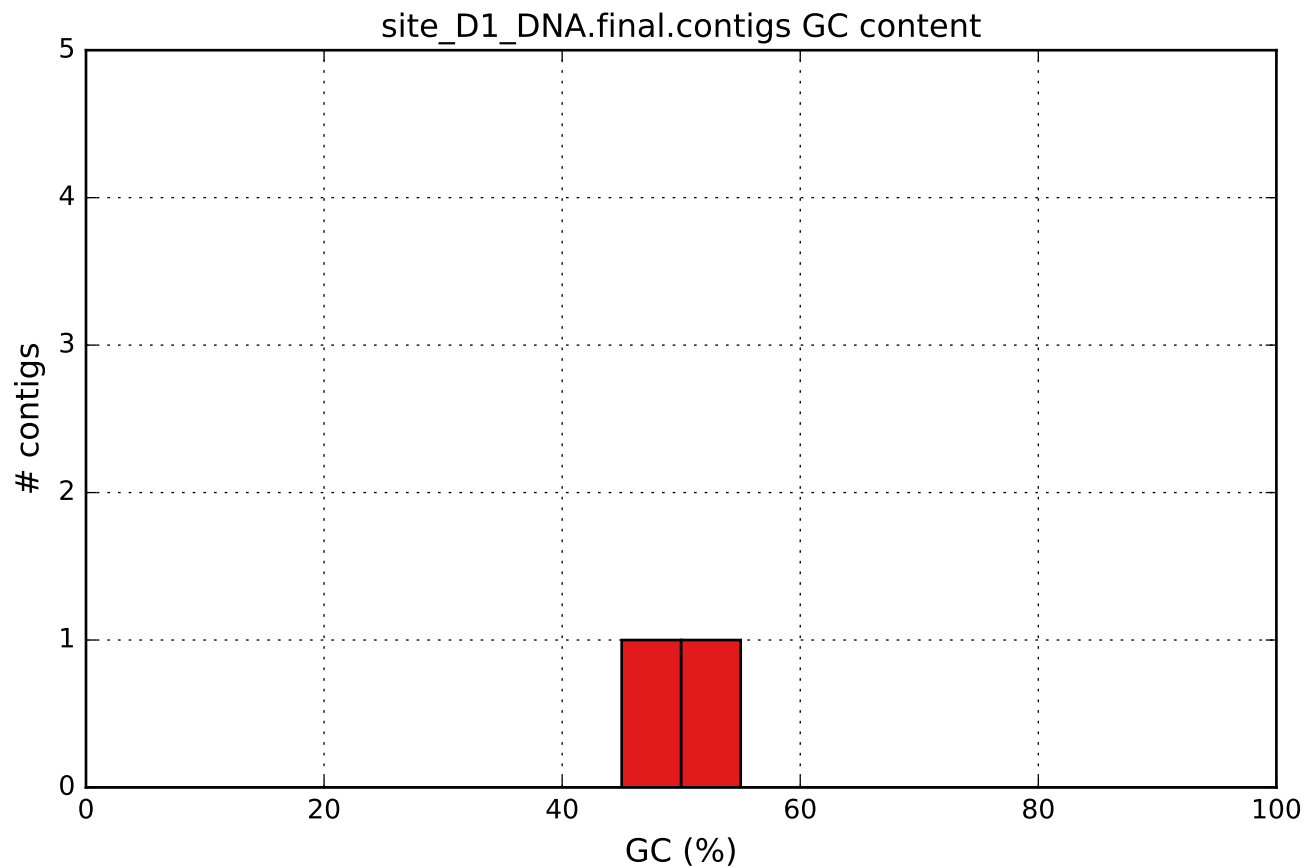




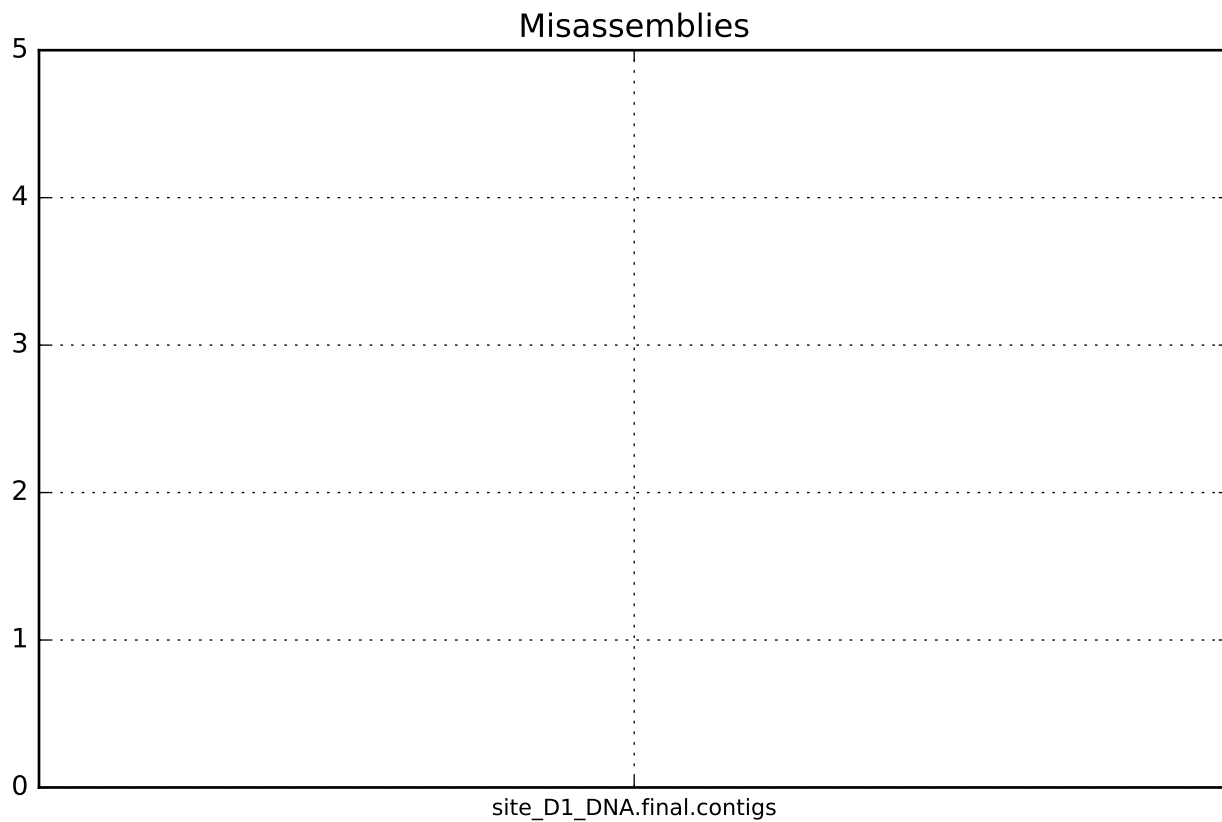
— site_D1_DNA.final.contigs - - Reference

GC content

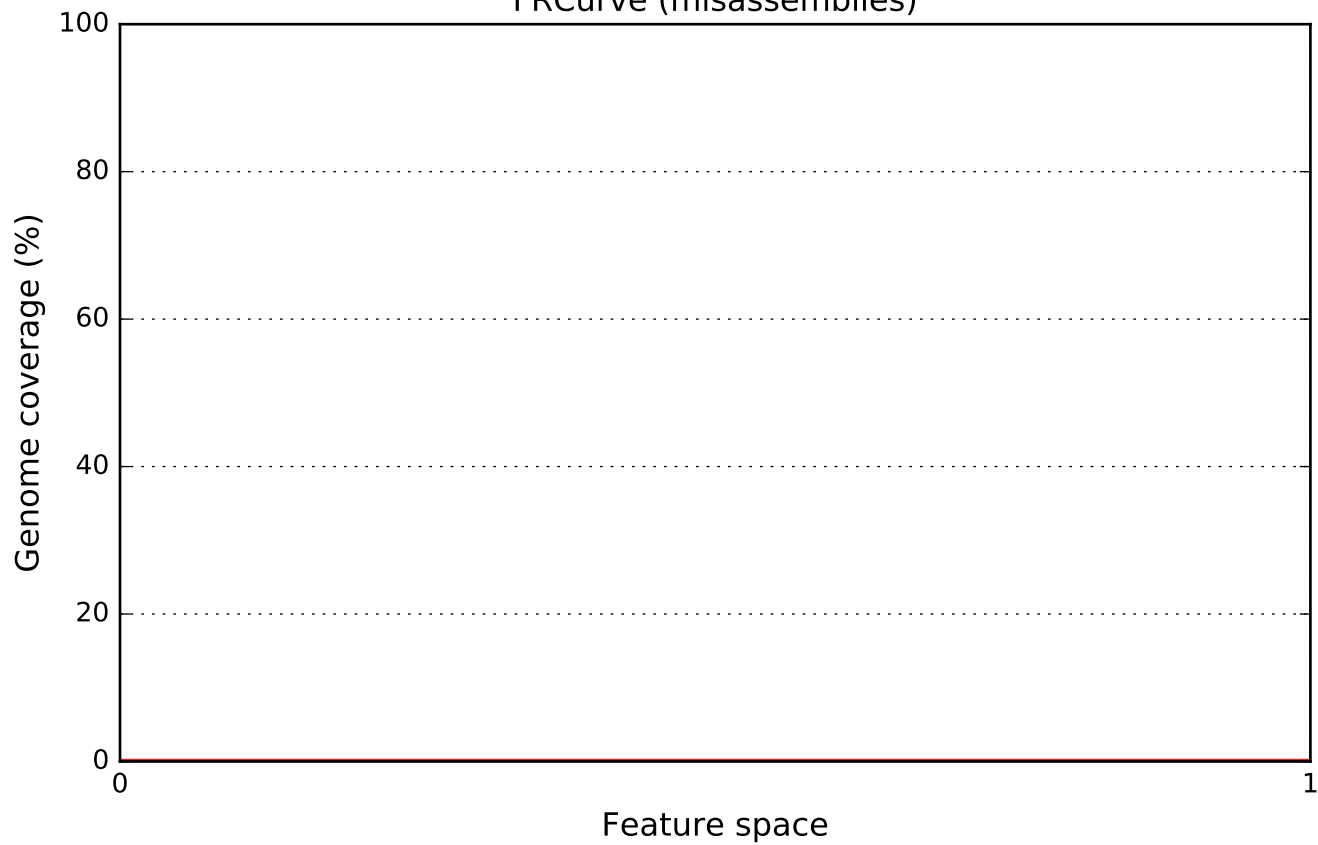




site_D1_DNA.final.contigs

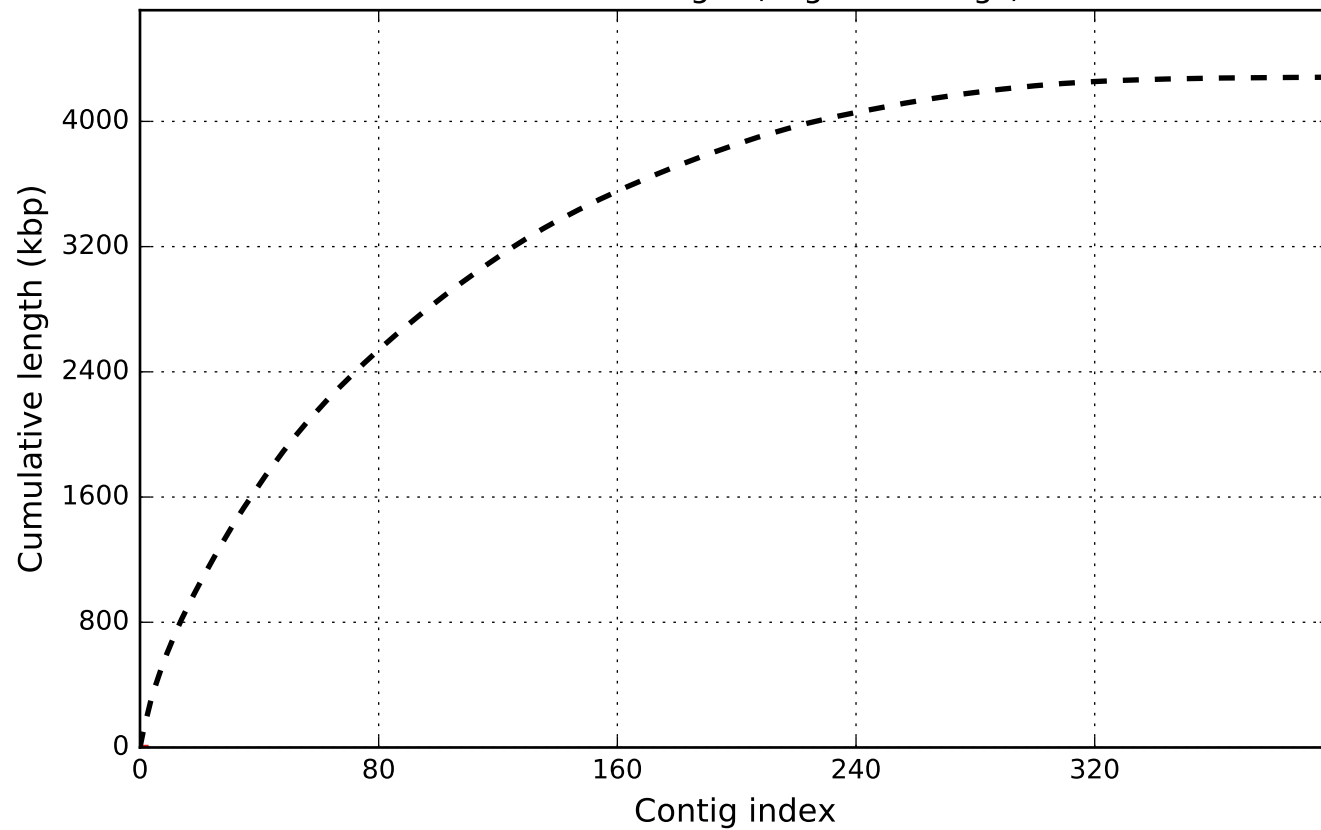


FRCurve (misassemblies)



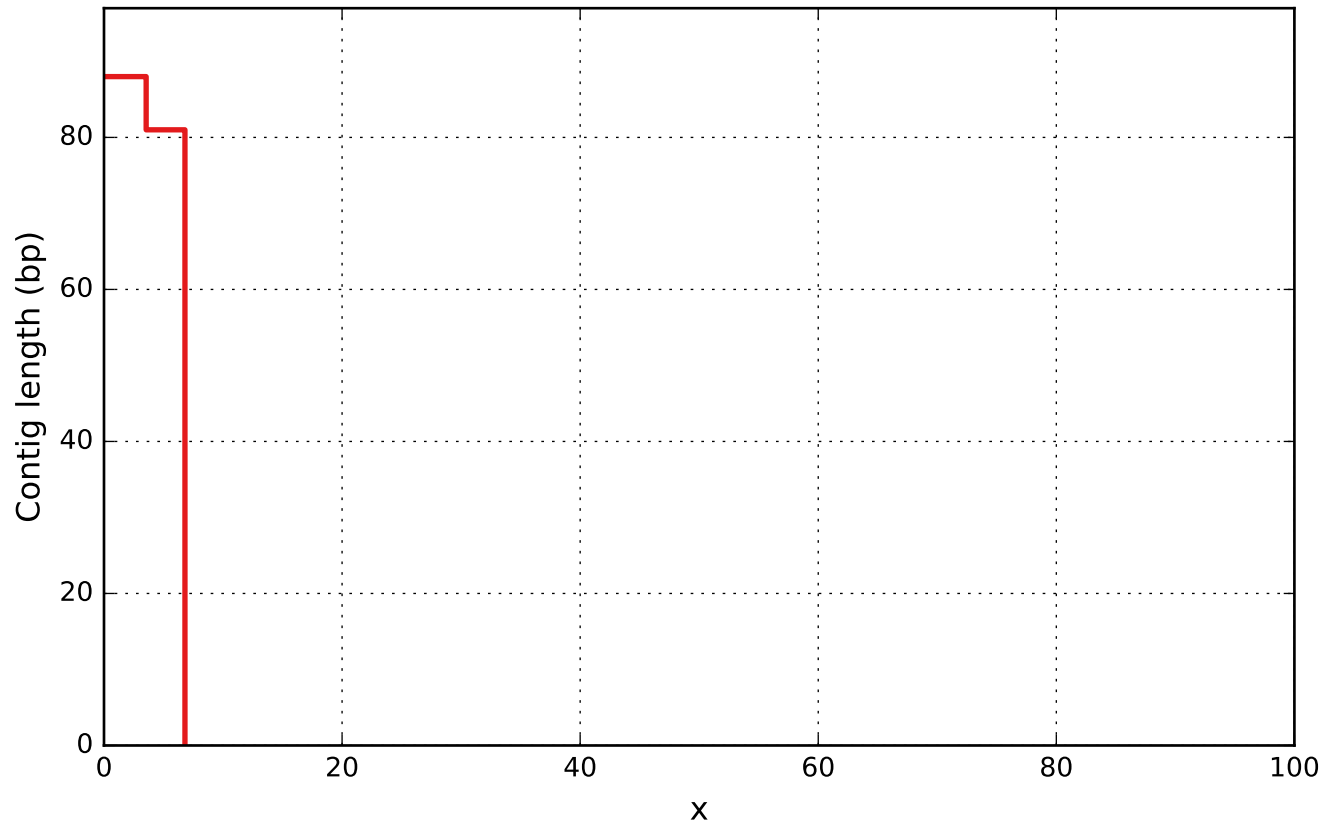
— site_D1_DNA.final.contigs

Cumulative length (aligned contigs)



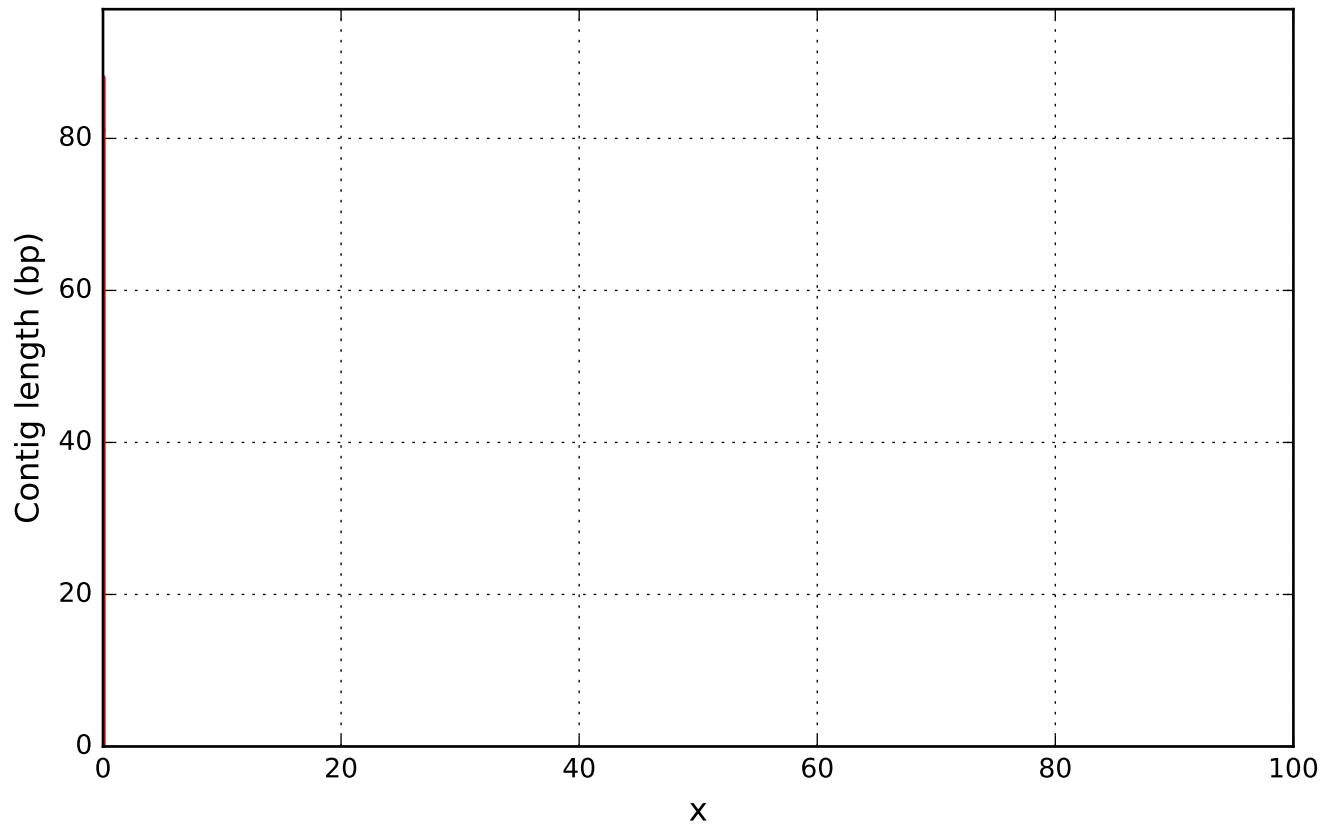
— site_D1_DNA.final.contigs - - Reference

NAx



— site_D1_DNA.final.contigs

NGAx



— site_D1_DNA.final.contigs