

Report

	site_D1_DNA.final.contigs
# contigs (≥ 1000 bp)	2
# contigs (≥ 5000 bp)	0
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 1000 bp)	6490
Total length (≥ 5000 bp)	0
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	5
Largest contig	3933
Total length	8879
Reference length	3910325
GC (%)	43.02
Reference GC (%)	62.16
N50	2557
N75	945
L50	2
L75	3
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 4 part
Unaligned length	7746
Genome fraction (%)	0.012
Duplication ratio	2.442
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2370.69
# indels per 100 kbp	0.00
Largest alignment	219
Total aligned length	533
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

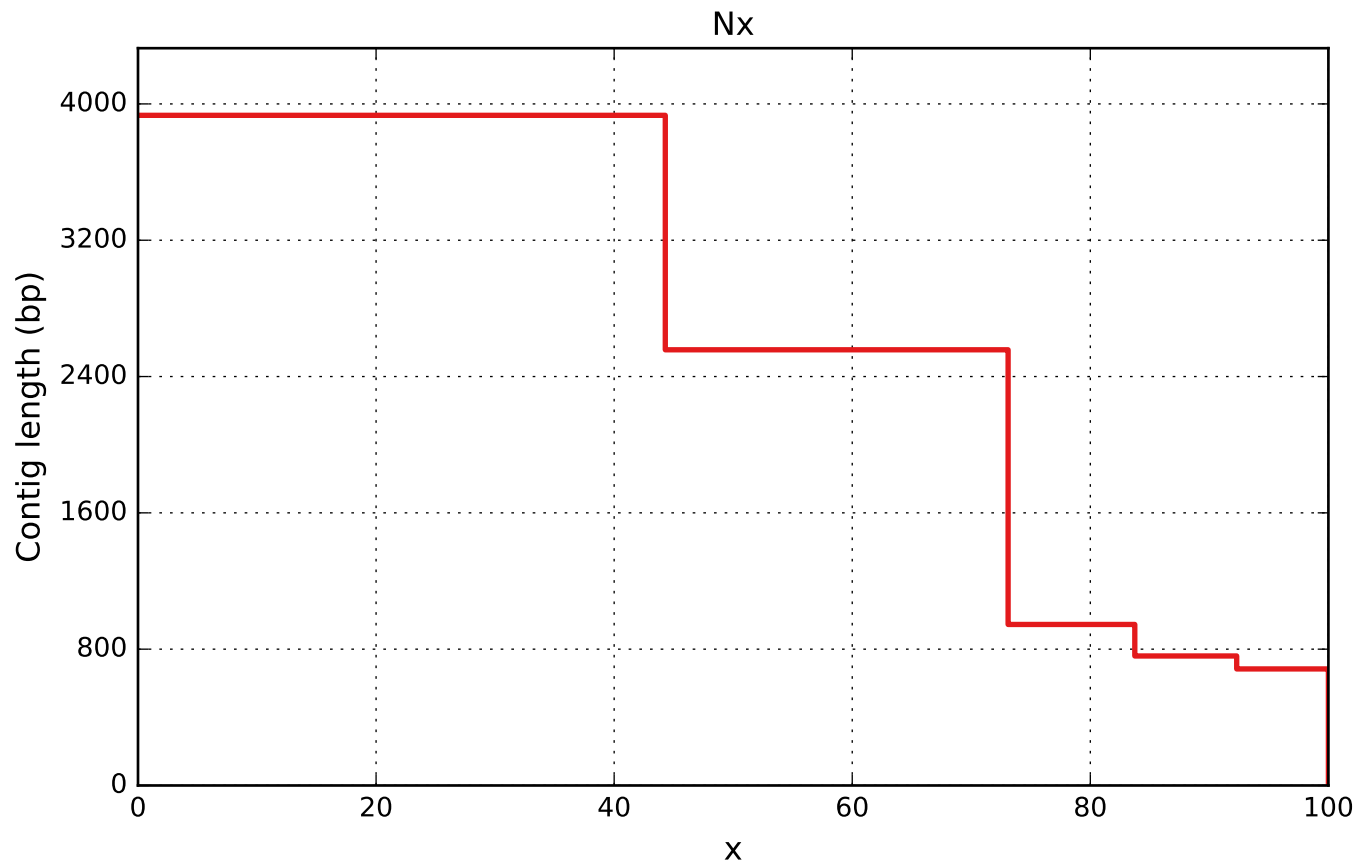
	site_D1_DNA.final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs	0
# mismatches	11
# 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).

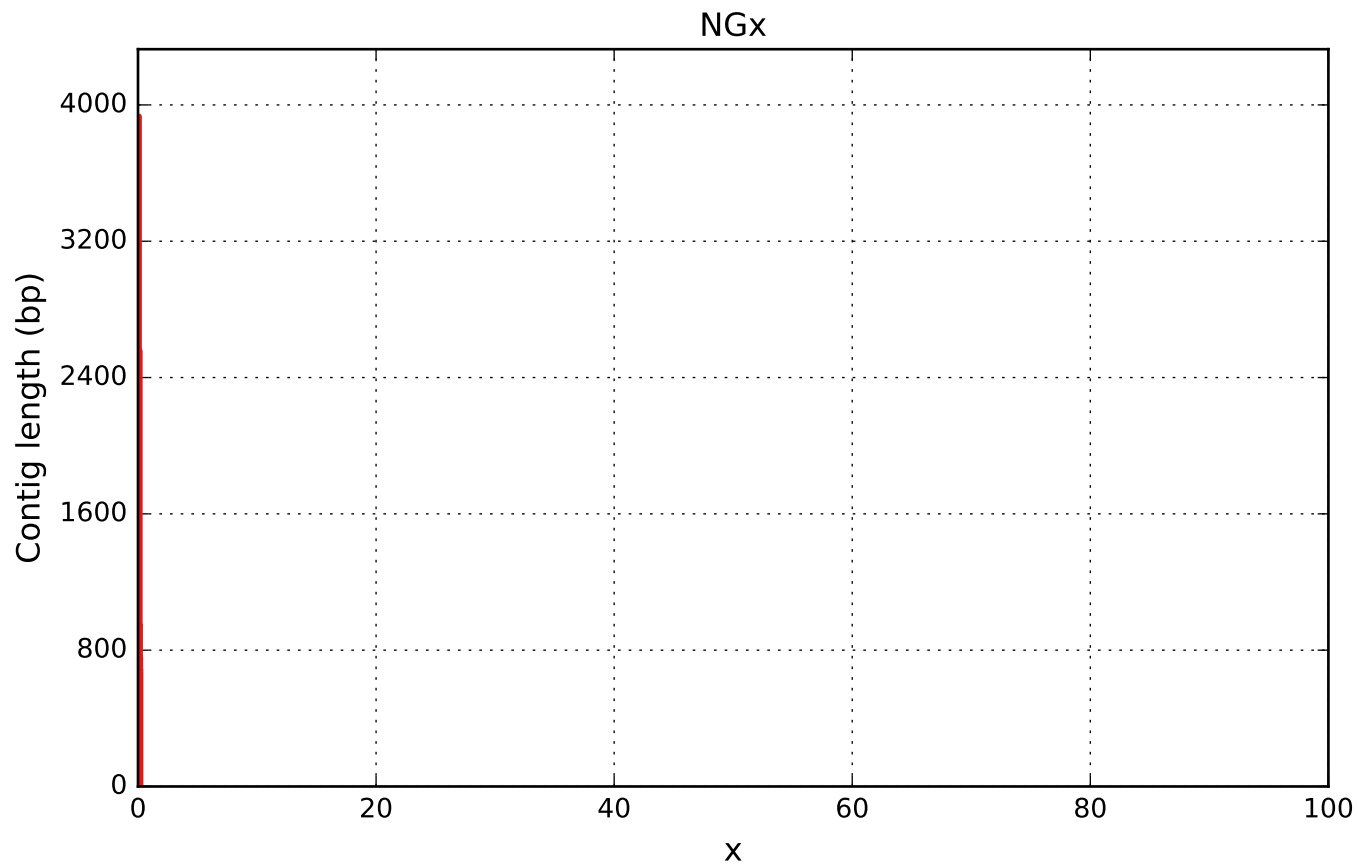
Unaligned report

	site_D1_DNA.final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	4
Partially unaligned length	7746
# N's	0

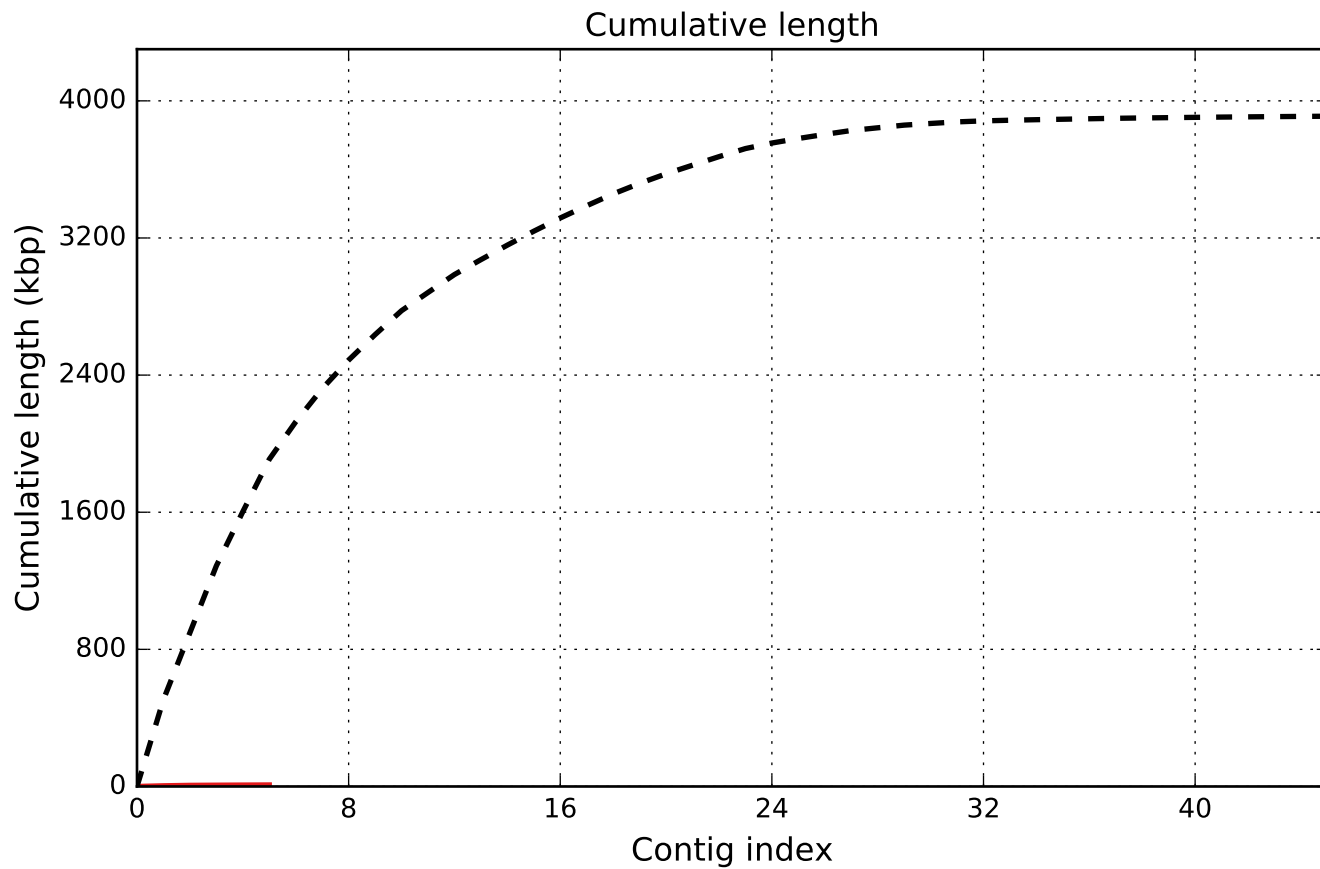
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



— site_D1_DNA.final.contigs

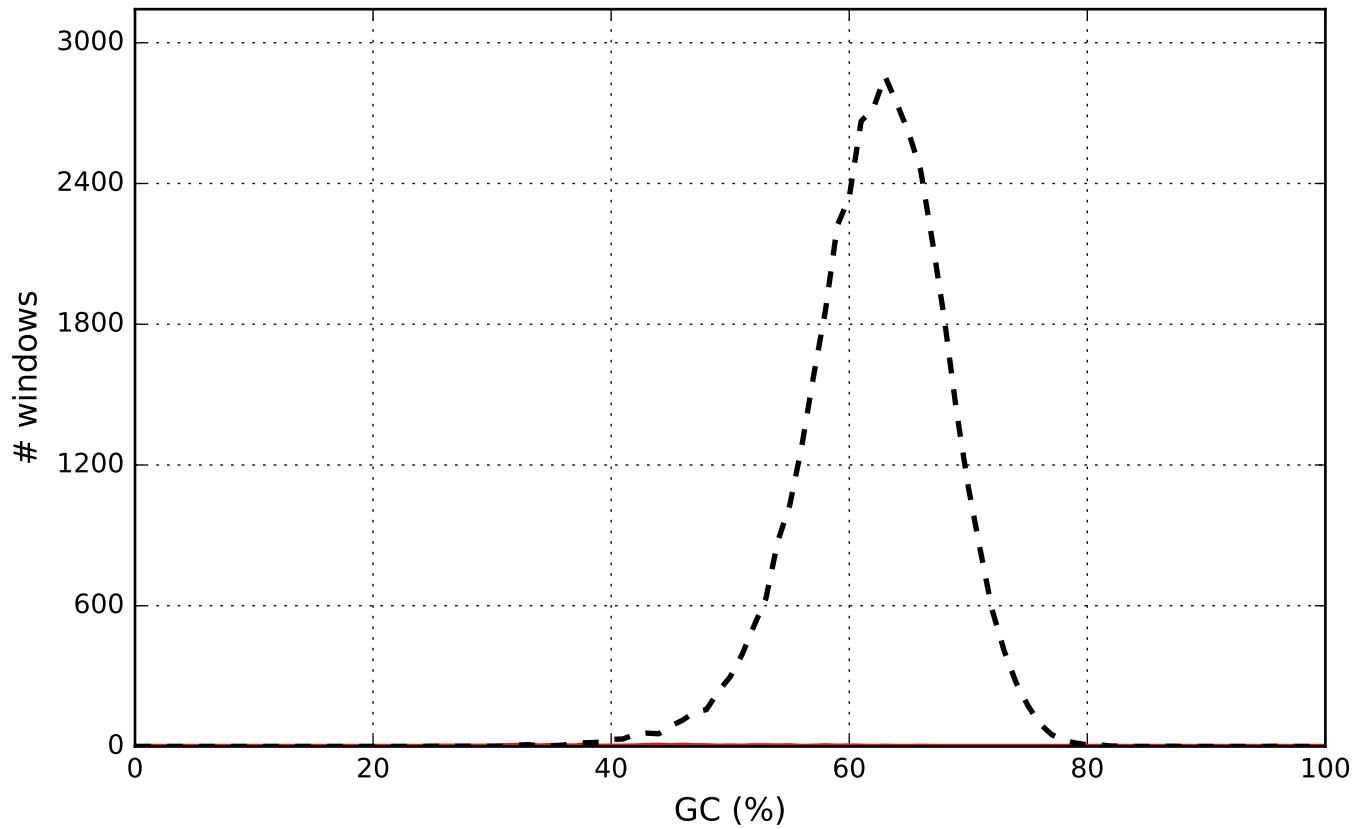


— site_D1_DNA.final.contigs

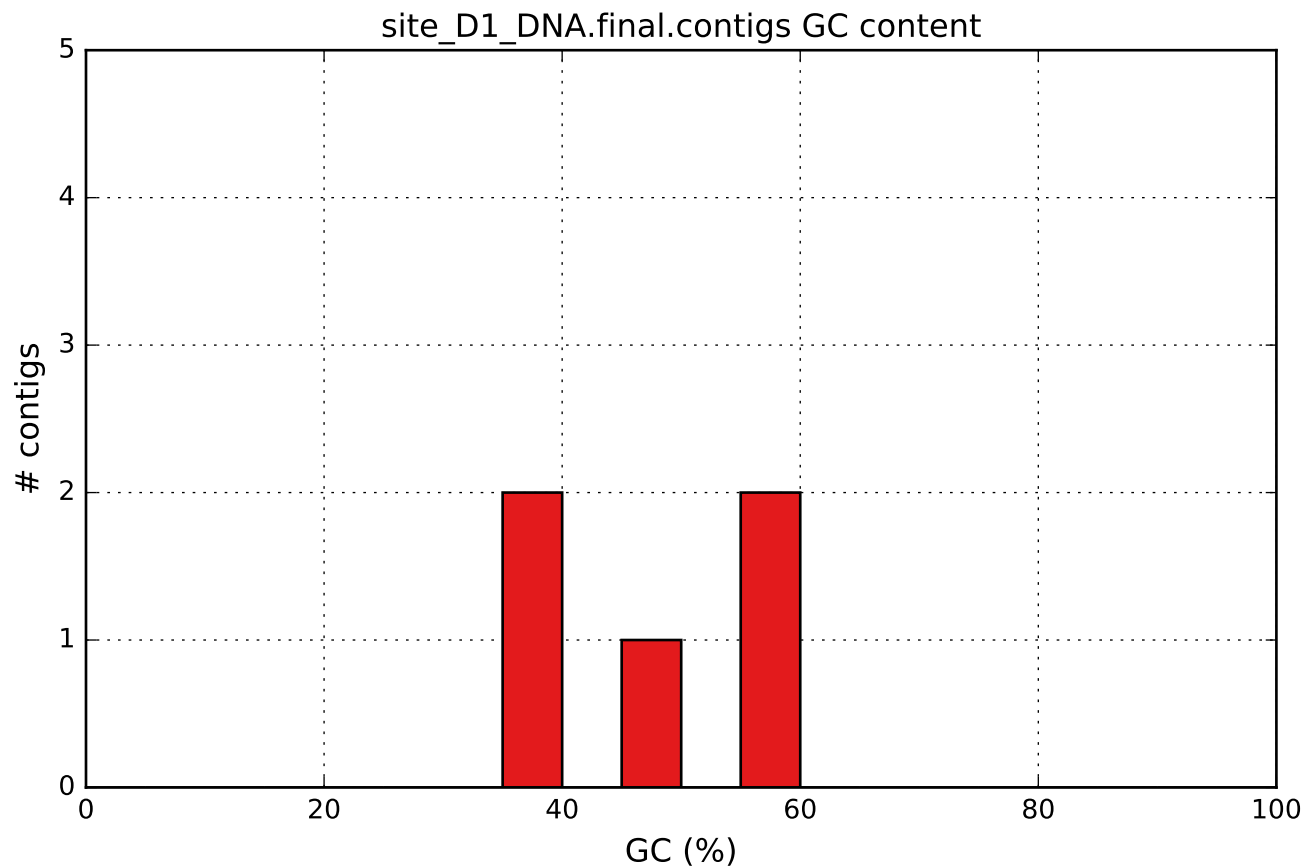


— site_D1_DNA.final.contigs - - Reference

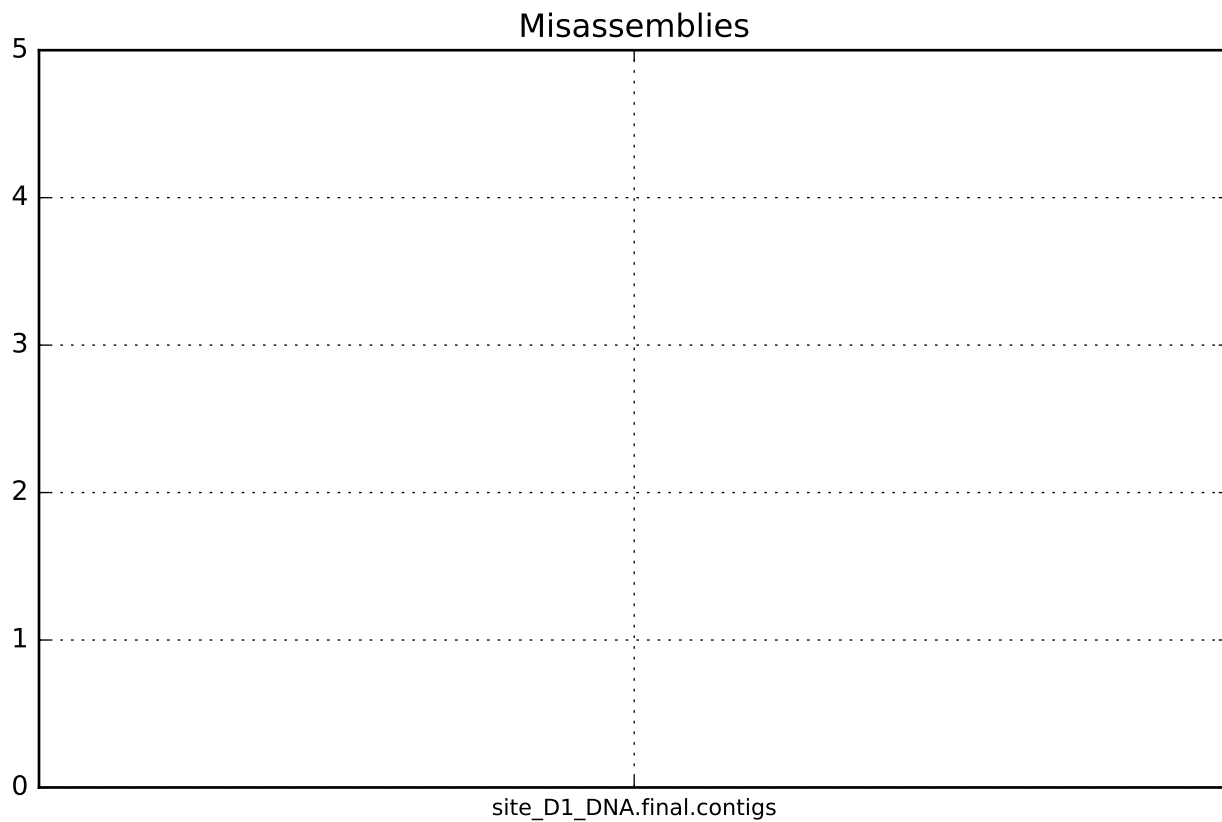
GC content



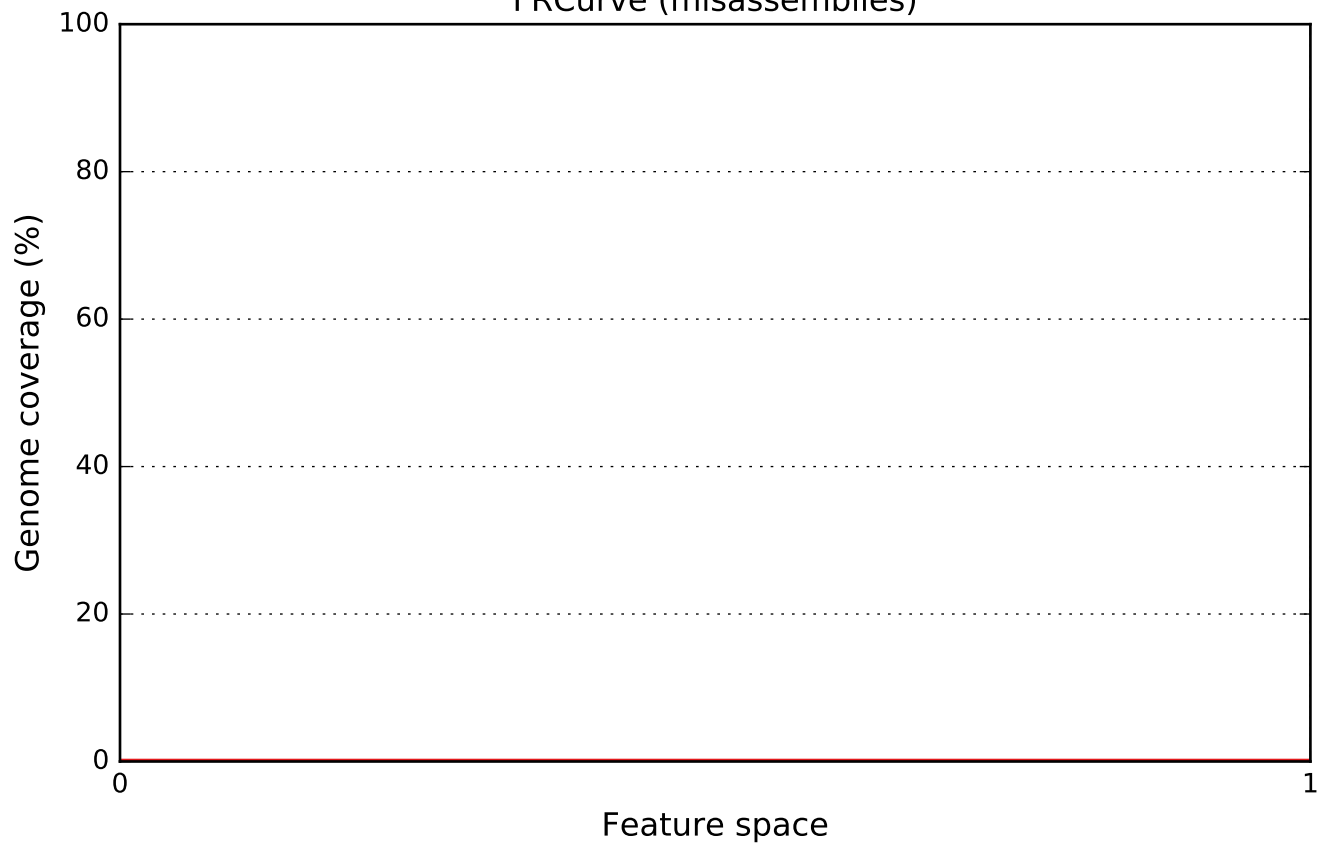
— site_D1_DNA.final.contigs - - Reference



site_D1_DNA.final.contigs

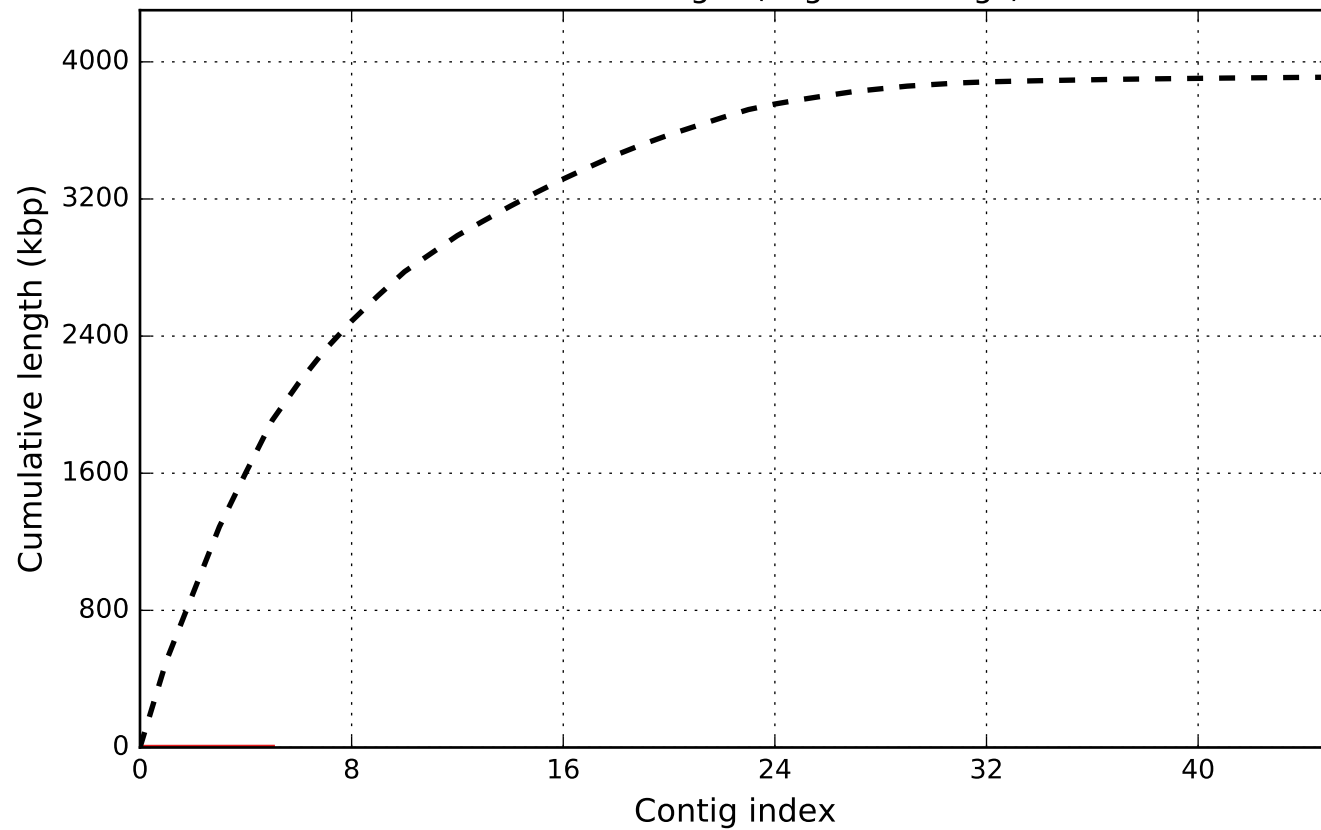


FRCurve (misassemblies)



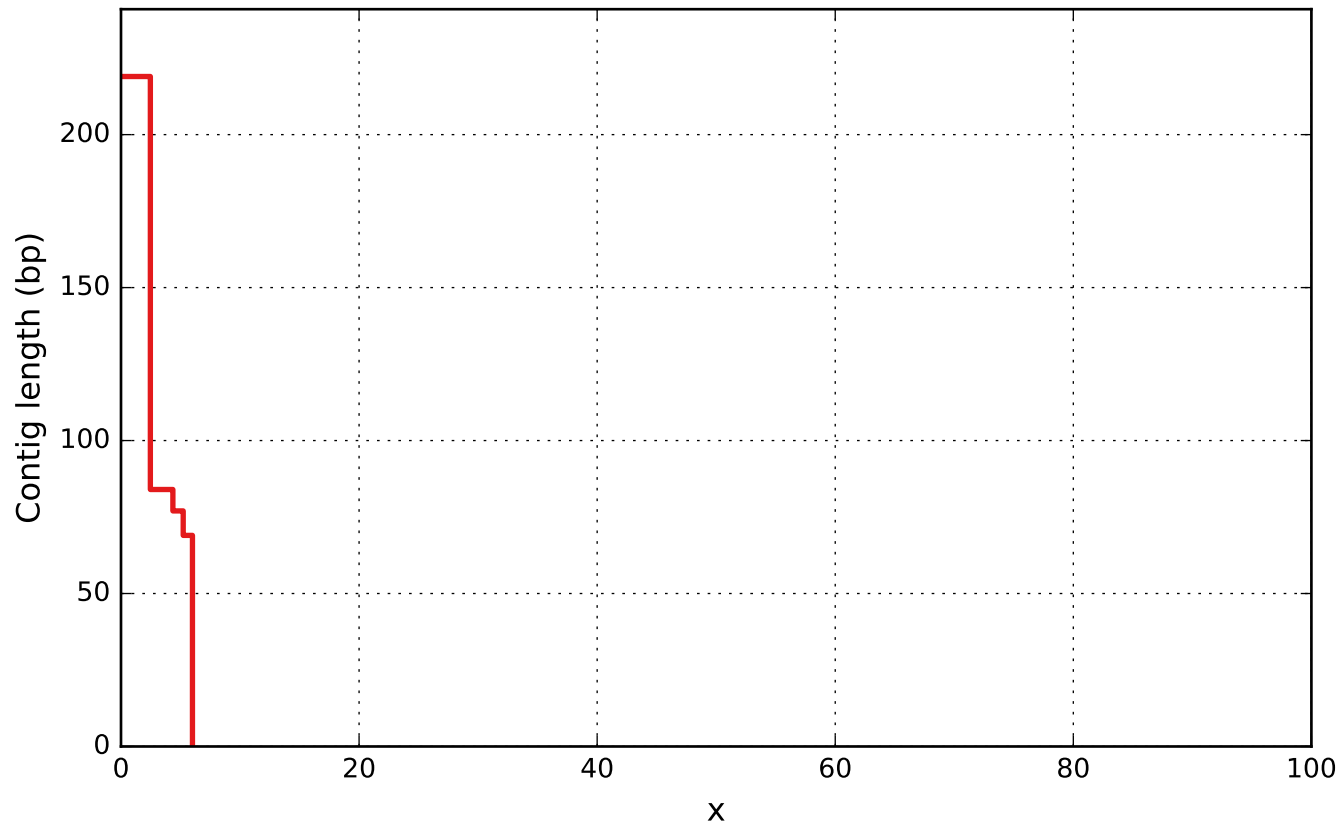
— site_D1_DNA.final.contigs

Cumulative length (aligned contigs)



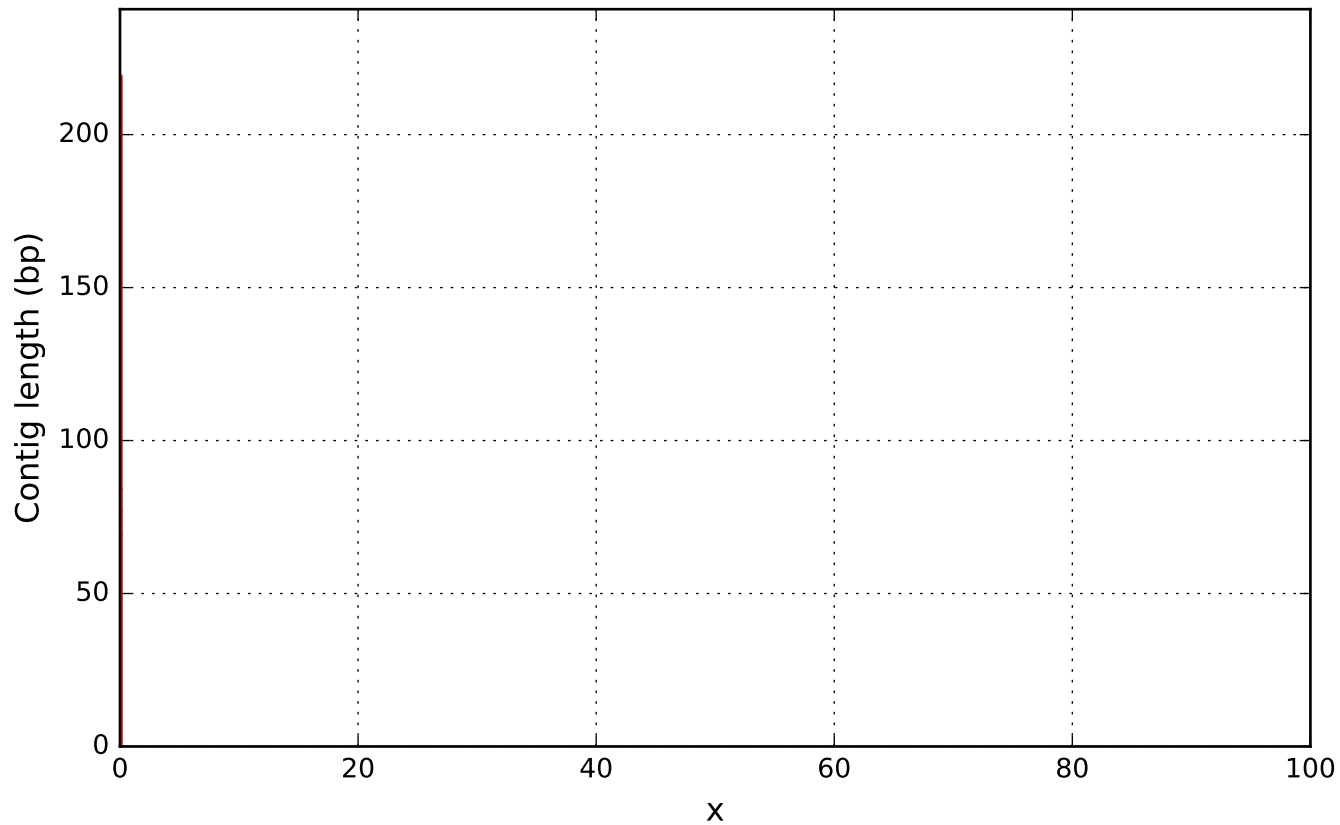
— site_D1_DNA.final.contigs - - Reference

NAx



— site_D1_DNA.final.contigs

NGAx



— site_D1_DNA.final.contigs