

# Report

	site_D1_DNA.final.contigs
# contigs ( $\geq 1000$ bp)	0
# contigs ( $\geq 5000$ bp)	0
# contigs ( $\geq 10000$ bp)	0
# contigs ( $\geq 25000$ bp)	0
# contigs ( $\geq 50000$ bp)	0
Total length ( $\geq 1000$ bp)	0
Total length ( $\geq 5000$ bp)	0
Total length ( $\geq 10000$ bp)	0
Total length ( $\geq 25000$ bp)	0
Total length ( $\geq 50000$ bp)	0
# contigs	3
Largest contig	669
Total length	1793
Reference length	3442017
GC (%)	52.26
Reference GC (%)	58.88
N50	622
N75	502
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 + 0 part
Unaligned length	0
Genome fraction (%)	0.009
Duplication ratio	5.803
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2589.00
# indels per 100 kbp	0.00
Largest alignment	215
Total aligned length	509
NGA50	-

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

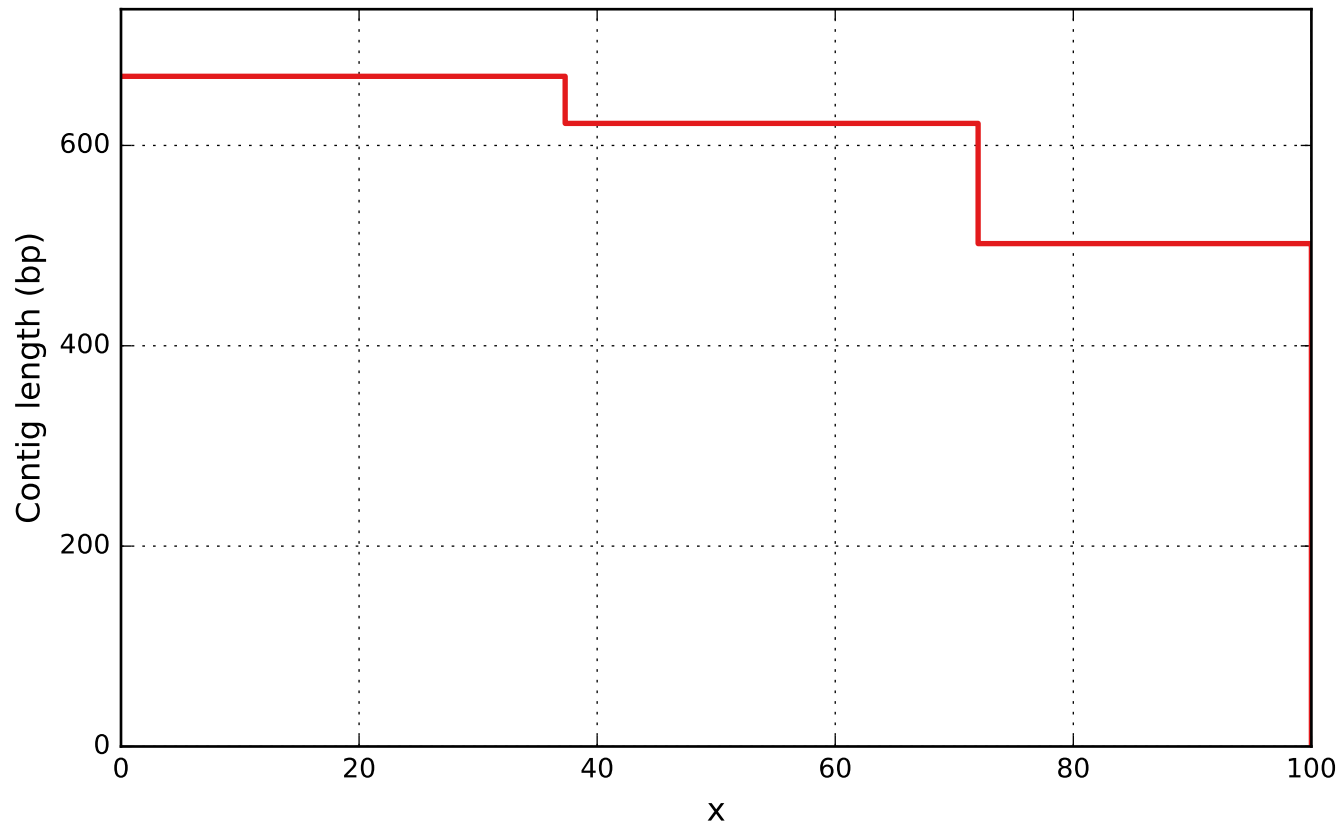
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

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

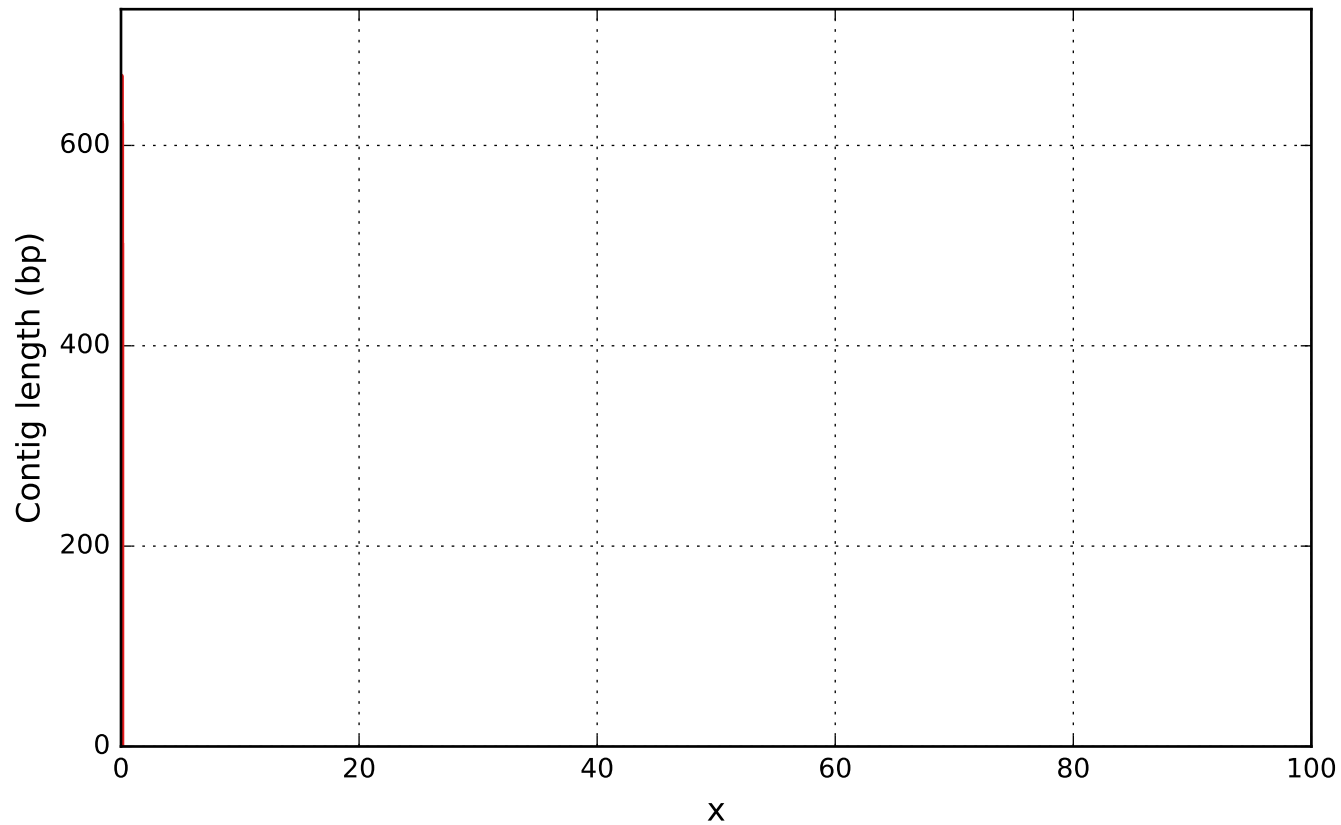
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

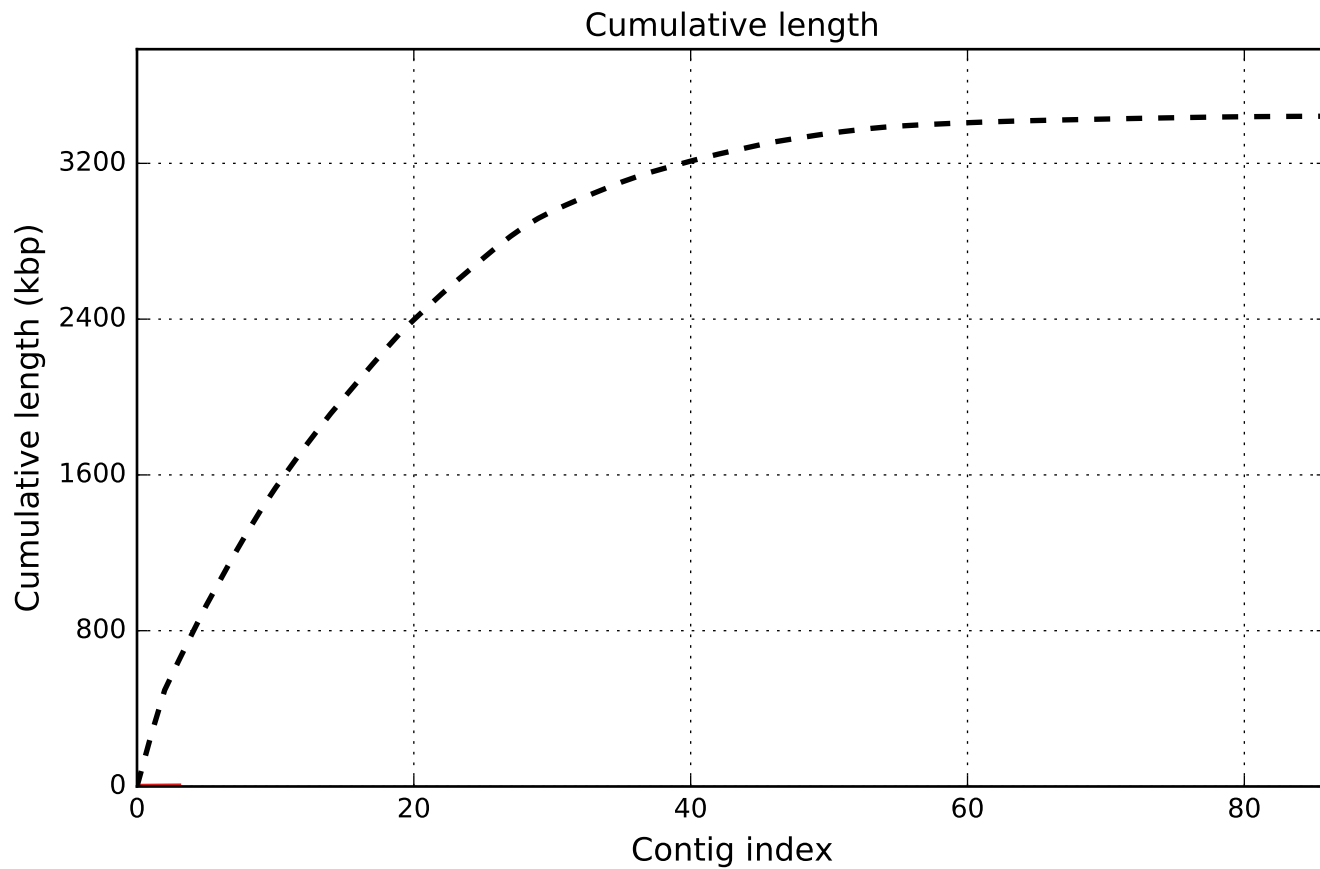


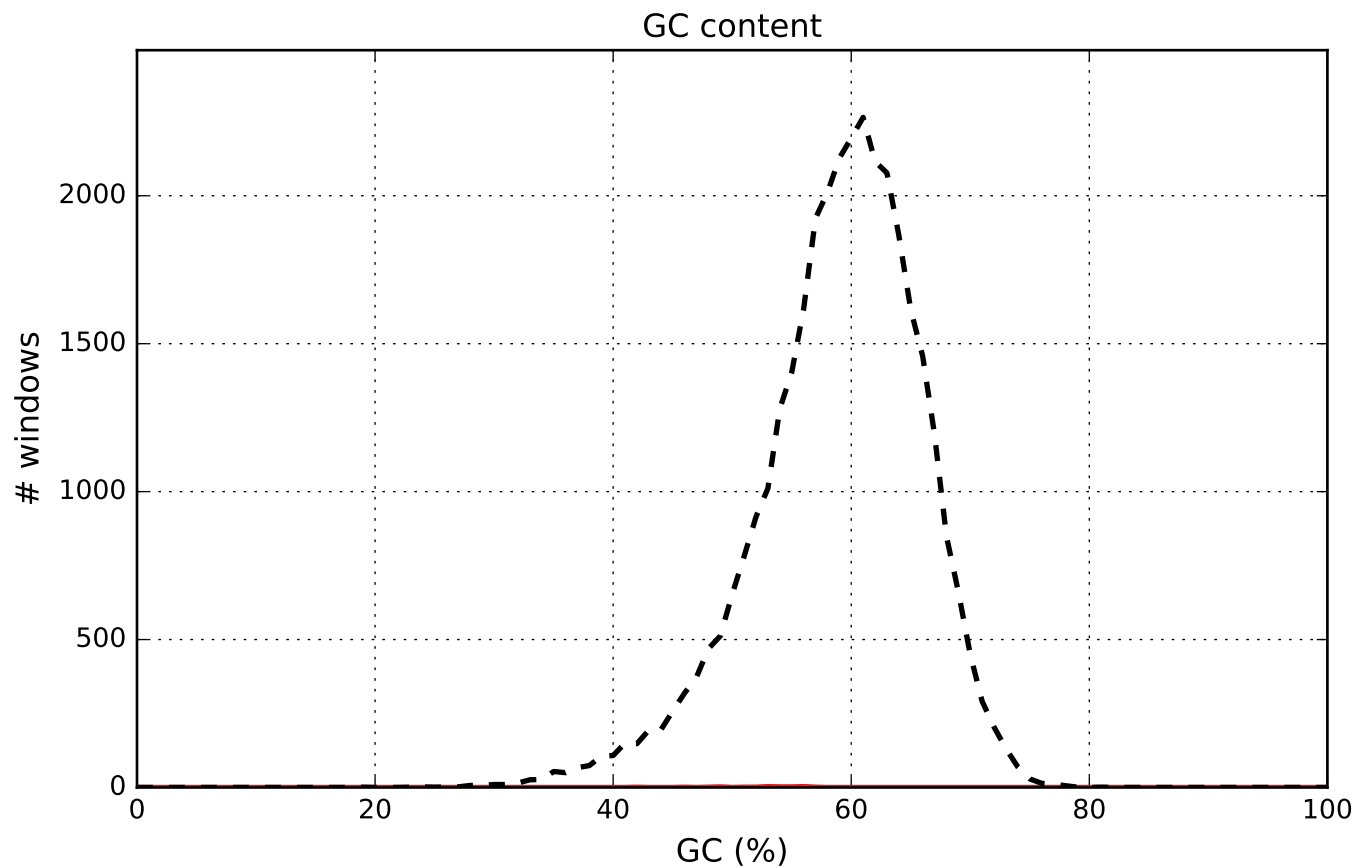
— site\_D1\_DNA.final.contigs

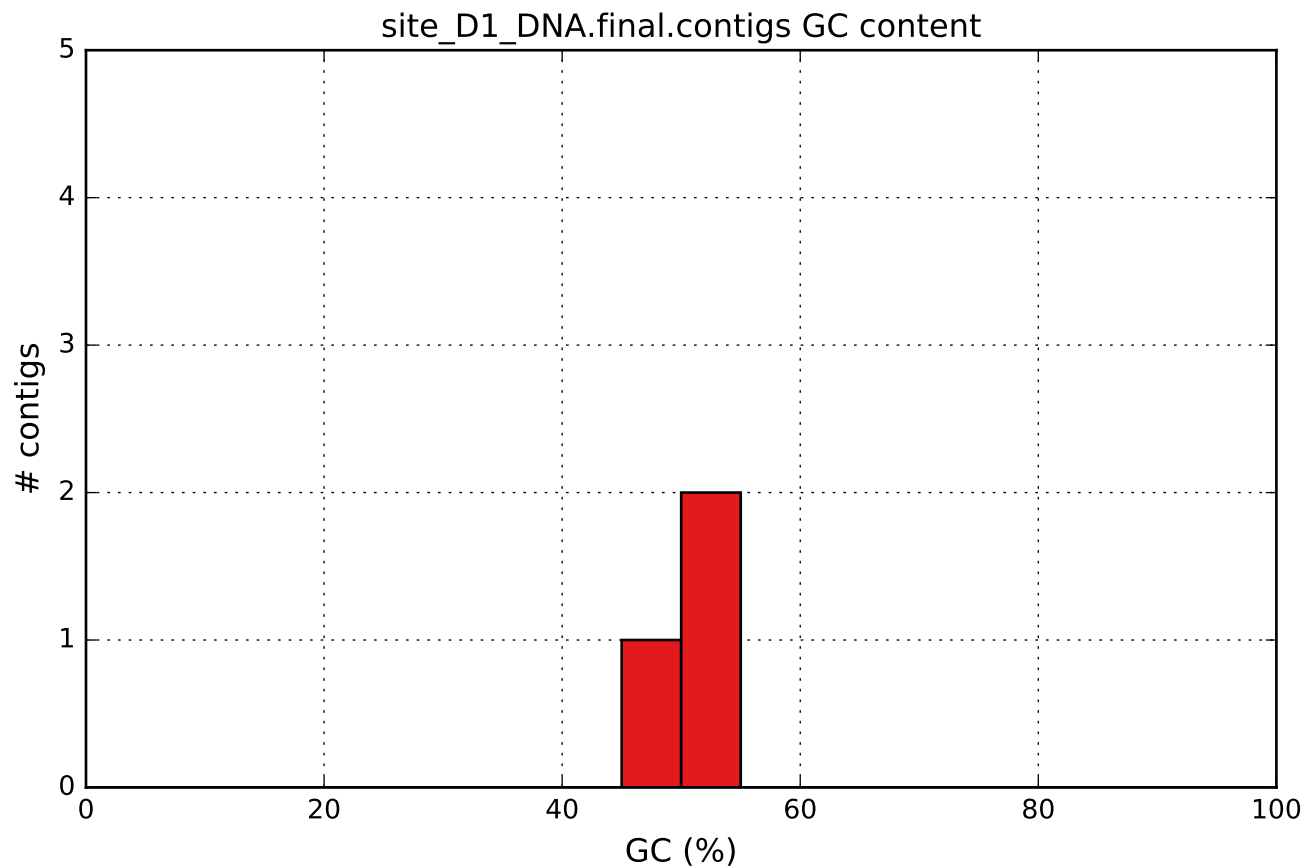
NGx



— site\_D1\_DNA.final.contigs



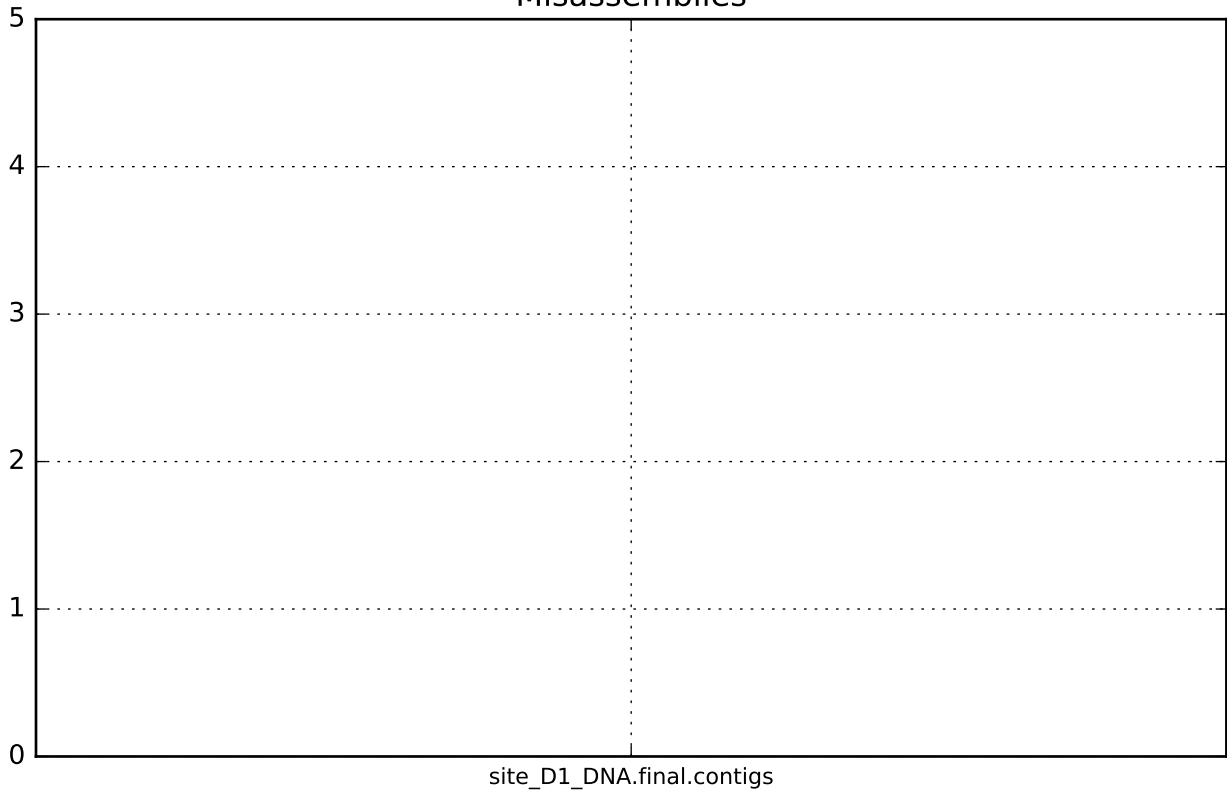




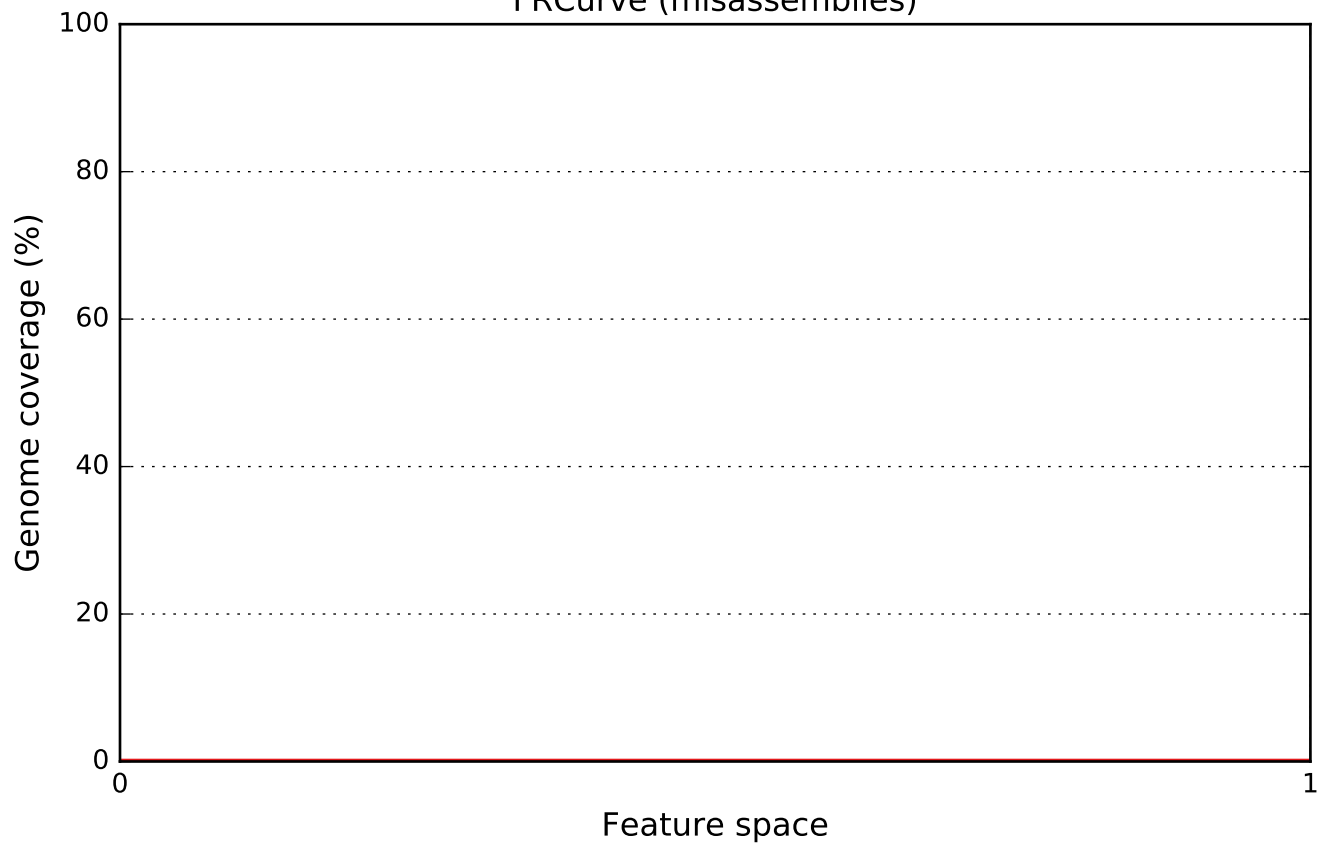
site\_D1\_DNA.final.contigs



# Misassemblies

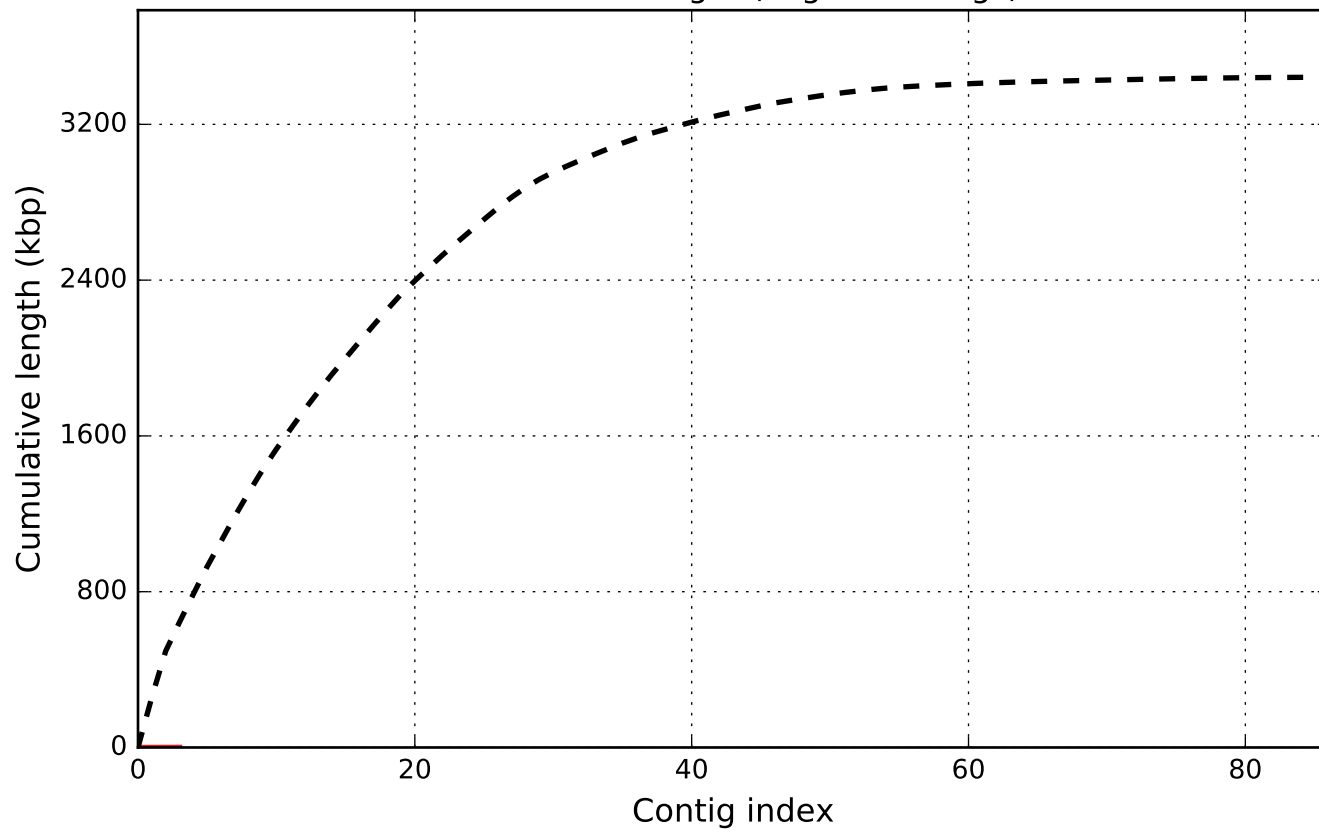


FRCurve (misassemblies)



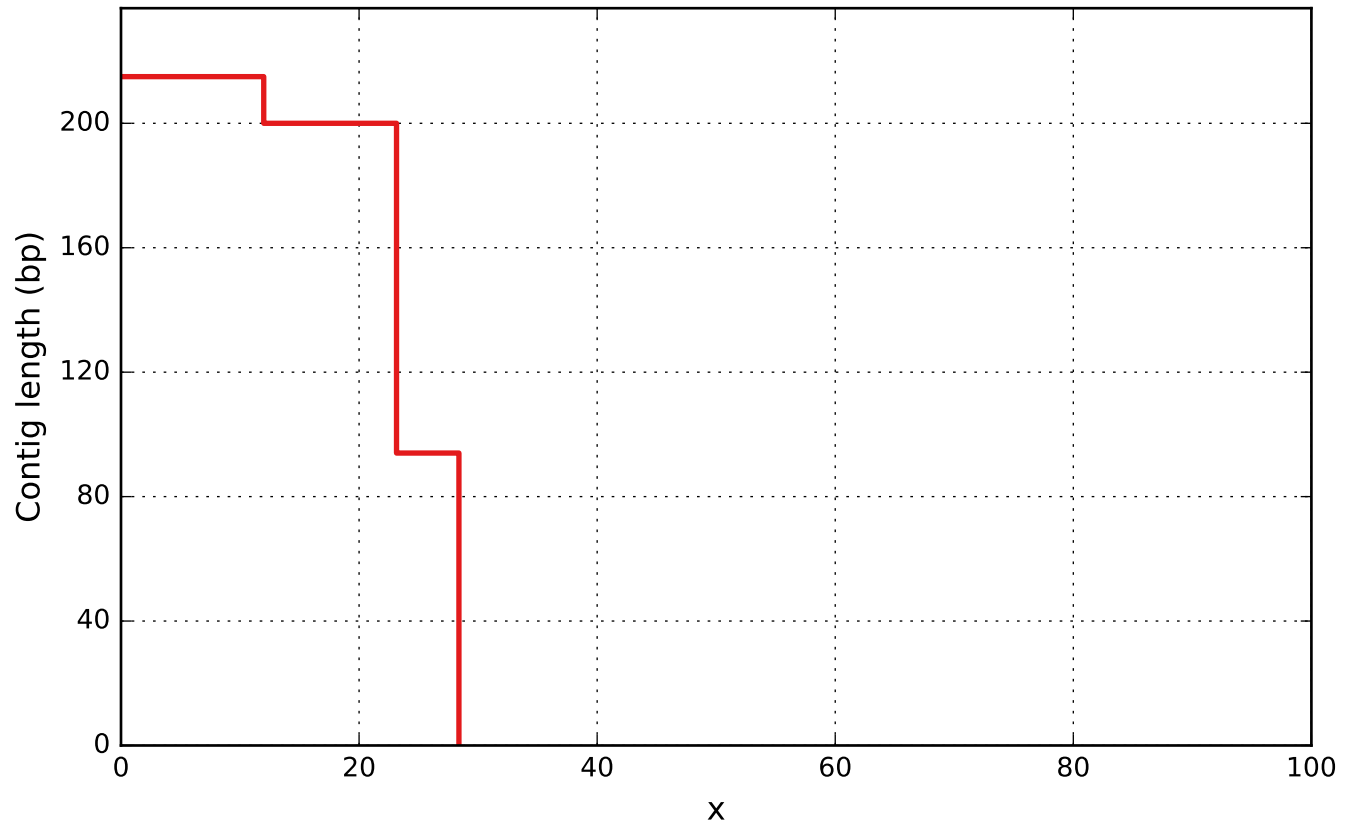
— site\_D1\_DNA.final.contigs

Cumulative length (aligned contigs)



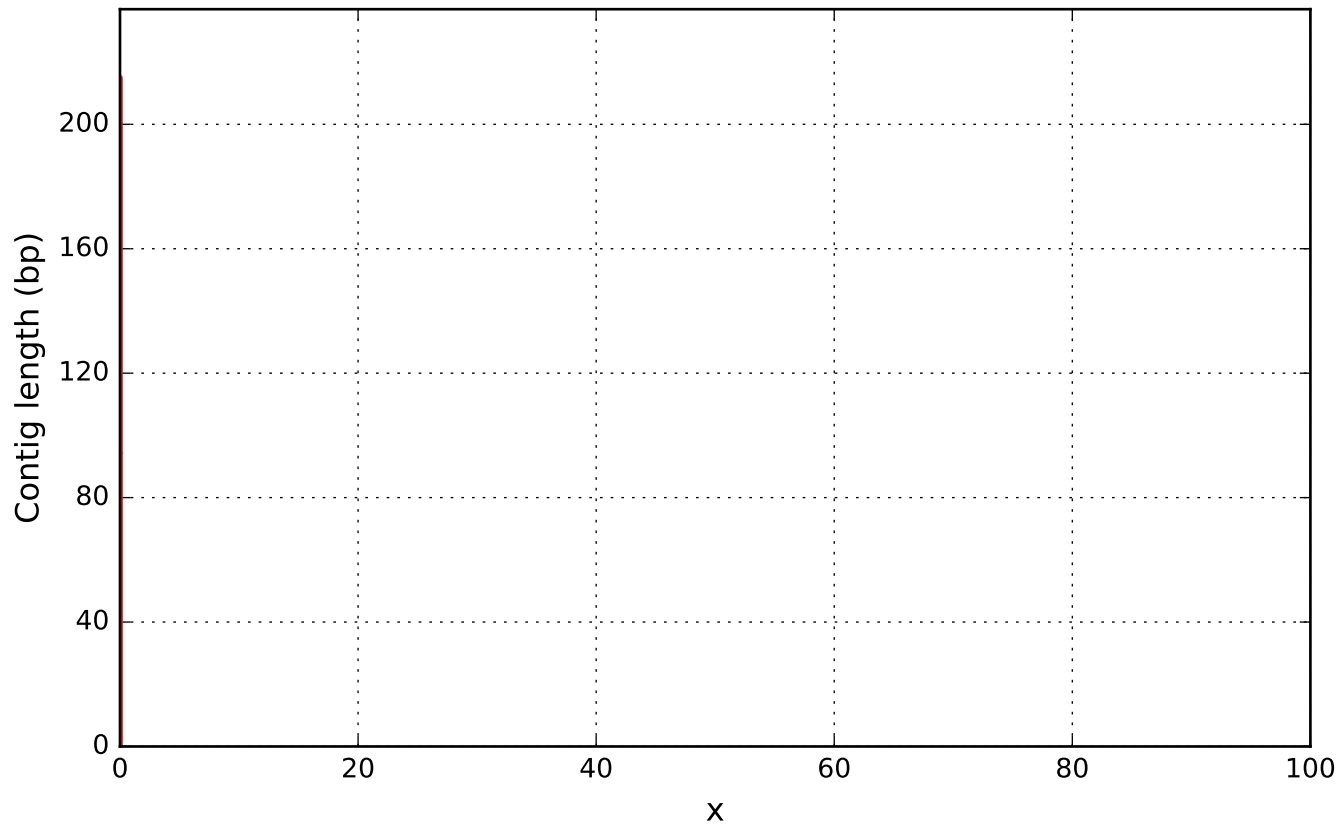
— site\_D1\_DNA.final.contigs      - - Reference

NAx



— site\_D1\_DNA.final.contigs

NGAx



— site\_D1\_DNA.final.contigs