

## Report

	site_D1_DNA.final.contigs
# contigs ( $\geq 1000$ bp)	6
# 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)	13432
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	18
Largest contig	4881
Total length	21876
Reference length	4292461
GC (%)	35.30
Reference GC (%)	33.40
N50	1328
N75	752
L50	5
L75	10
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 12 part
Unaligned length	17122
Genome fraction (%)	0.031
Duplication ratio	3.545
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1789.71
# indels per 100 kbp	372.86
Largest alignment	689
Total aligned length	2031
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

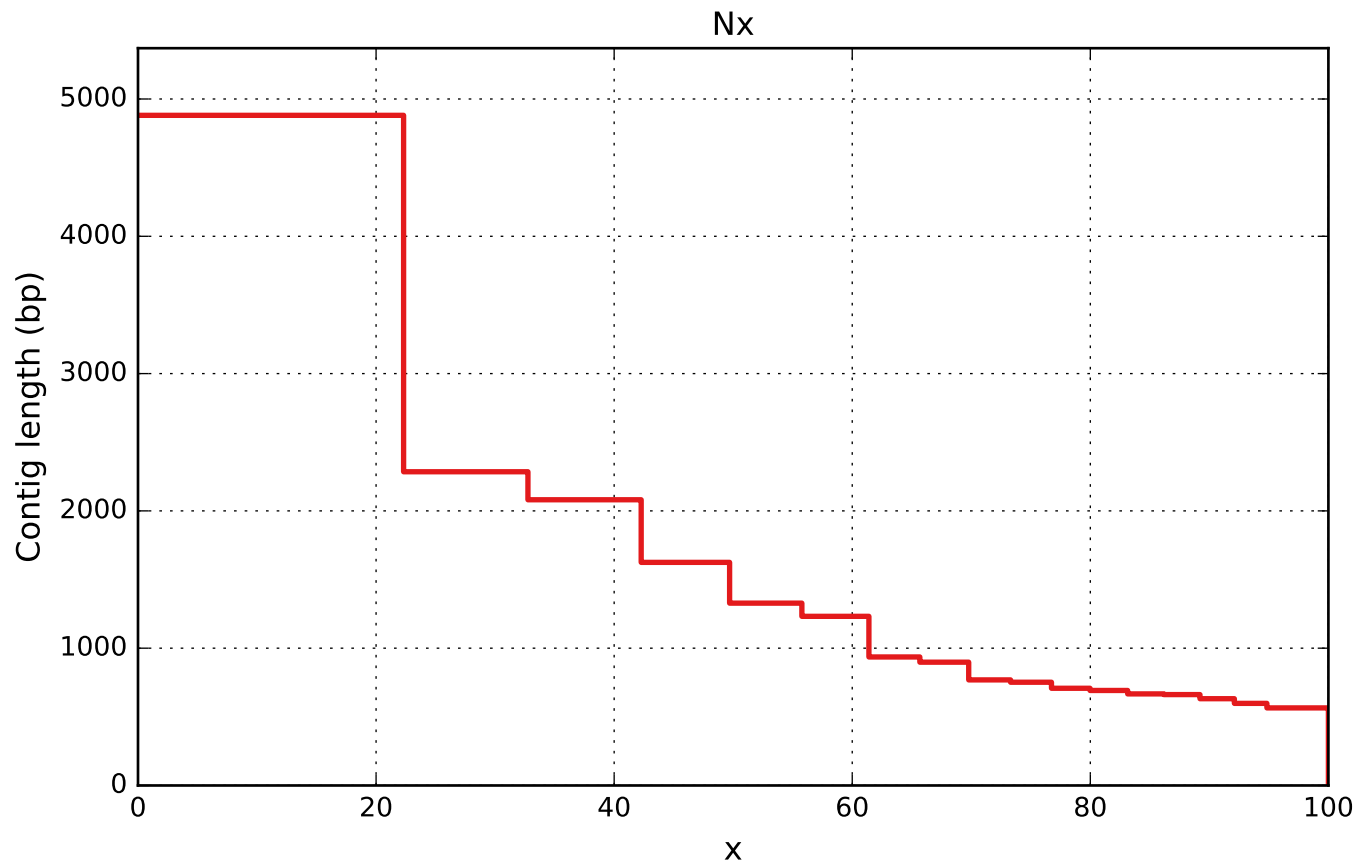
	site_D1_DNA.final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs	0
# mismatches	24
# indels	5
# indels (<= 5 bp)	5
# indels (> 5 bp)	0
Indels length	6

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).

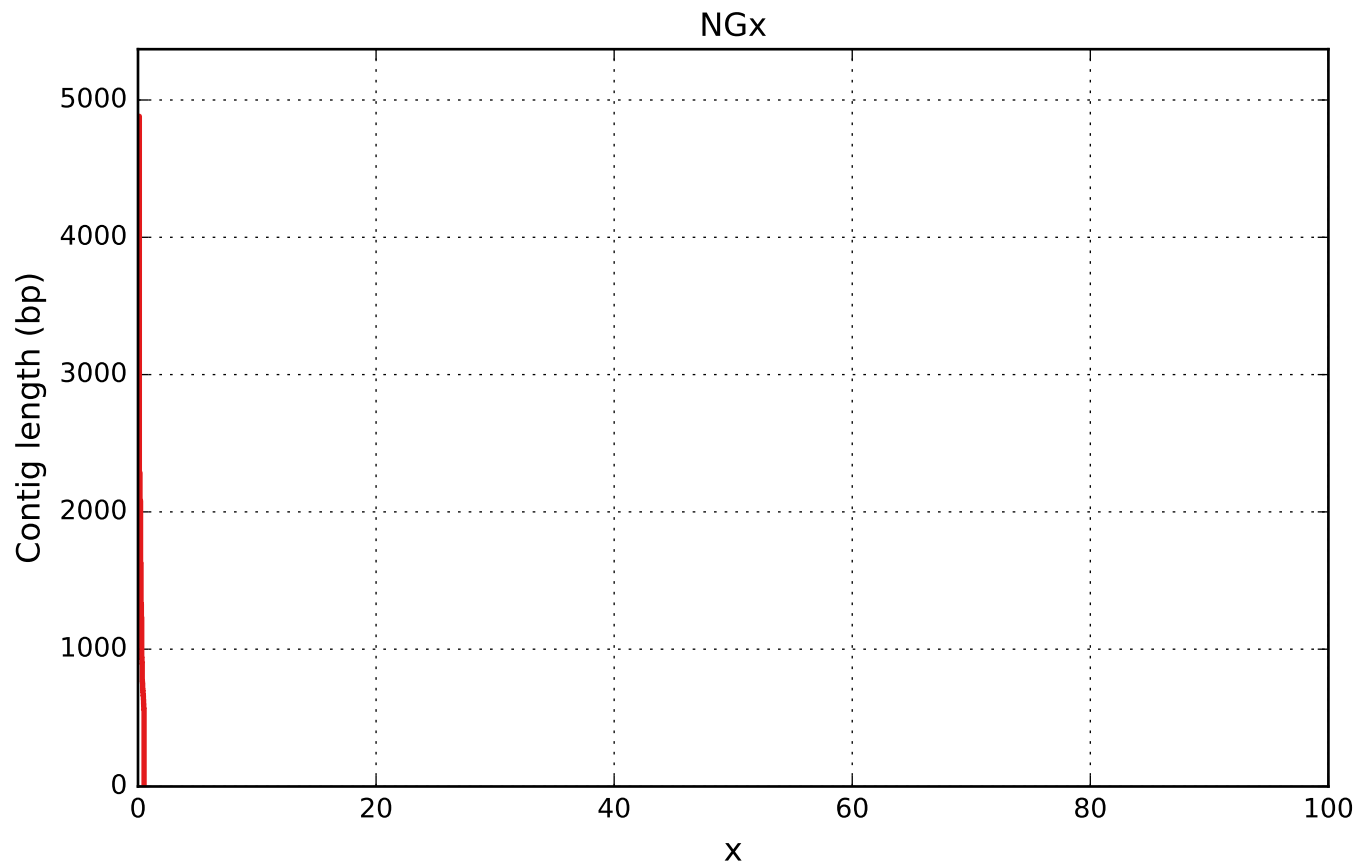
## Unaligned report

	site_D1_DNA.final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	12
Partially unaligned length	17122
# N's	0

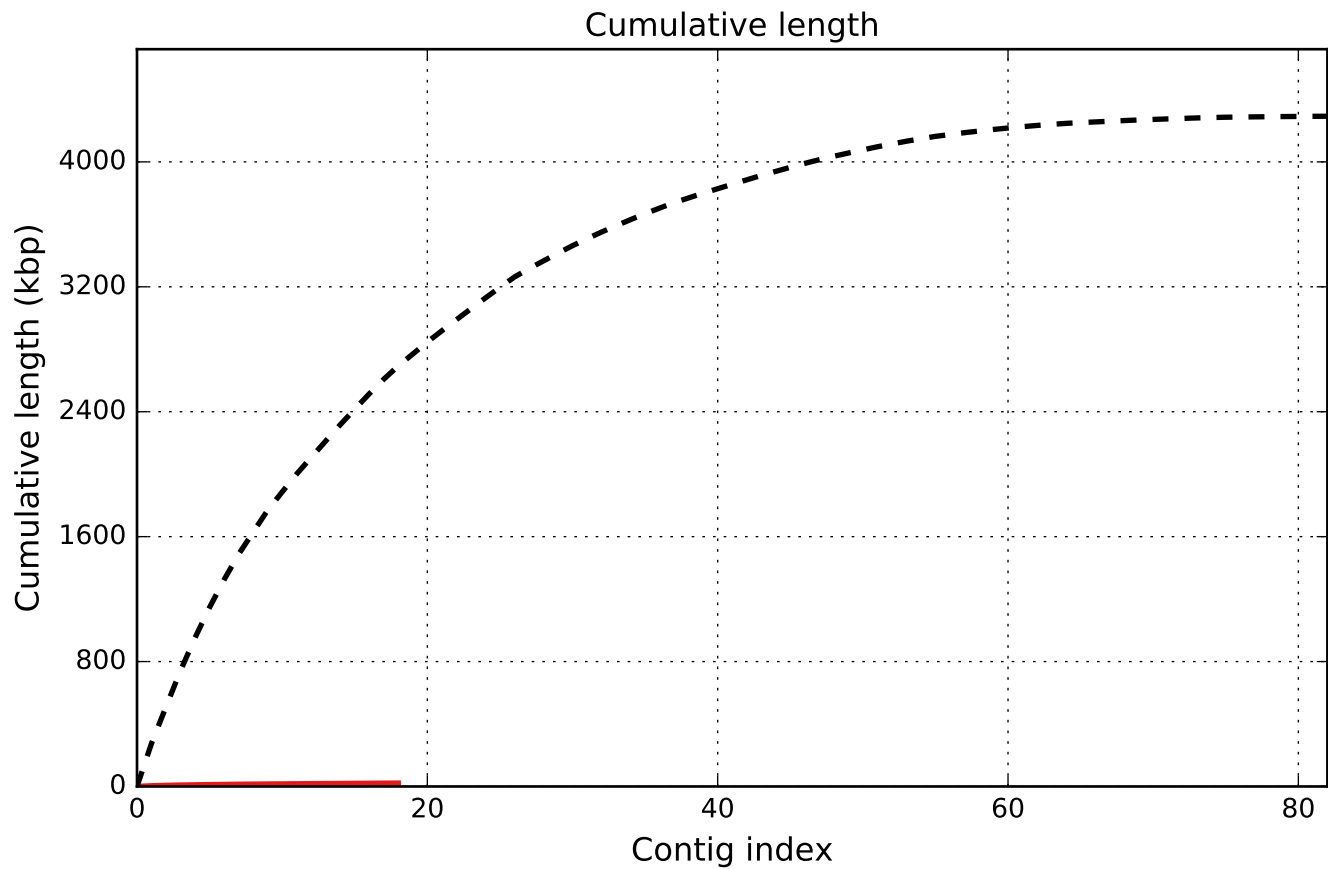
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

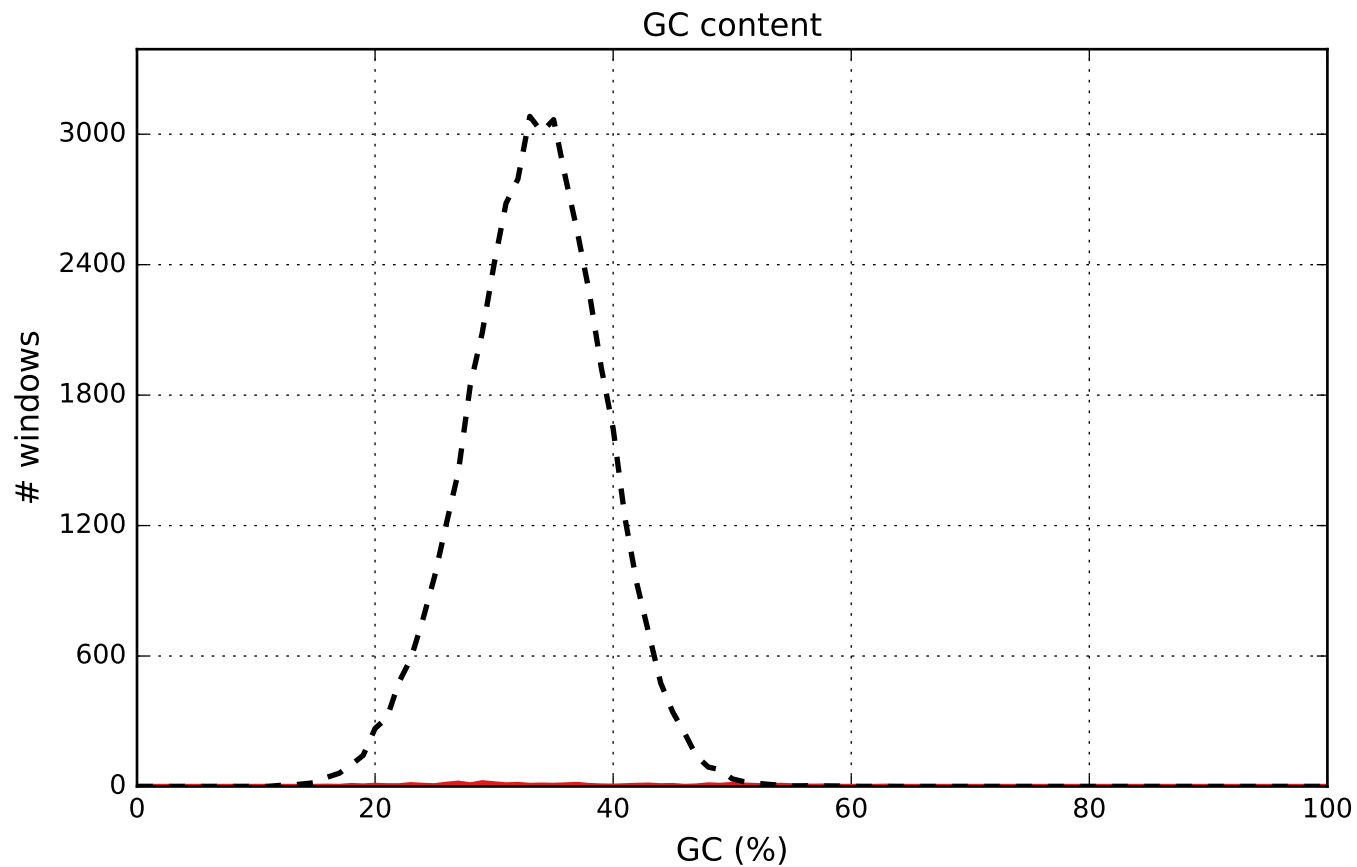


— site\_D1\_DNA.final.contigs



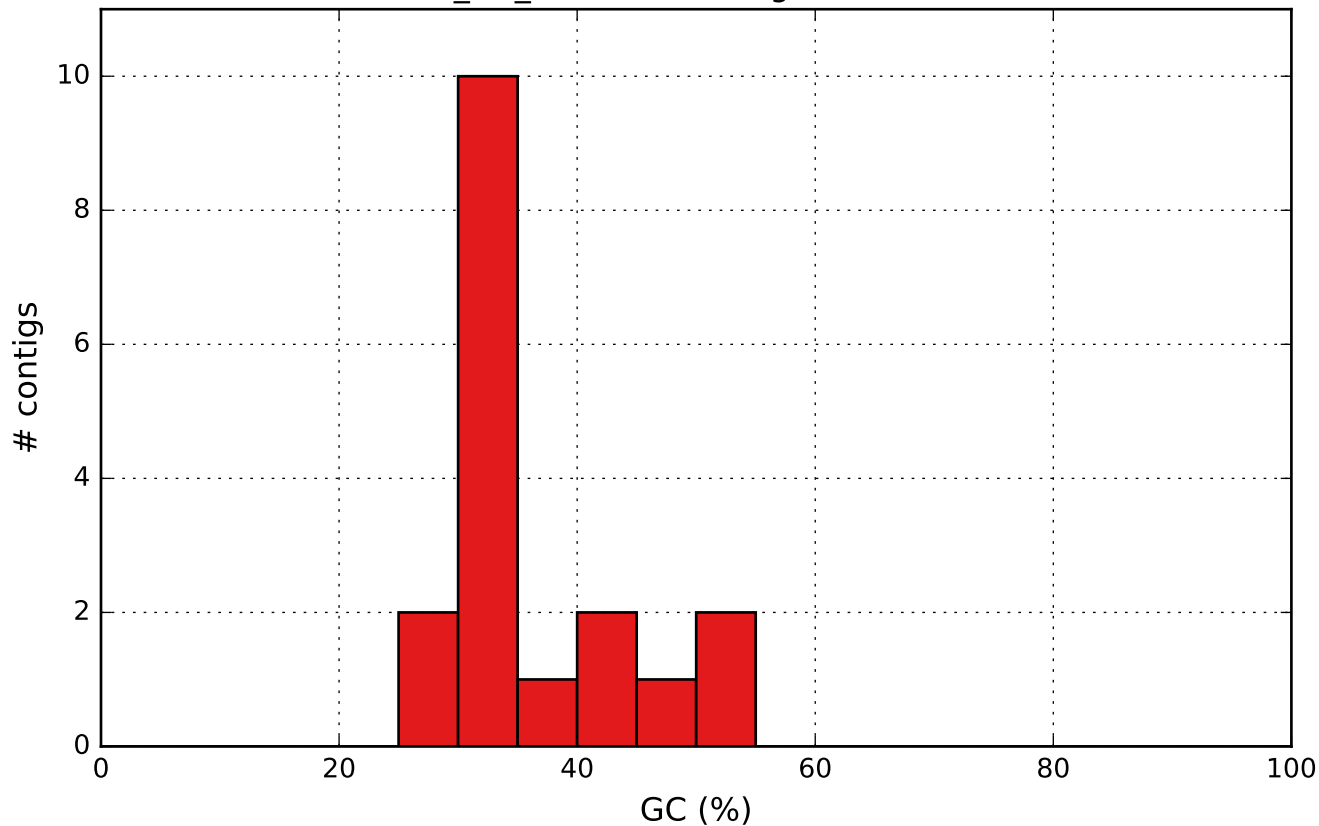
— site\_D1\_DNA.final.contigs





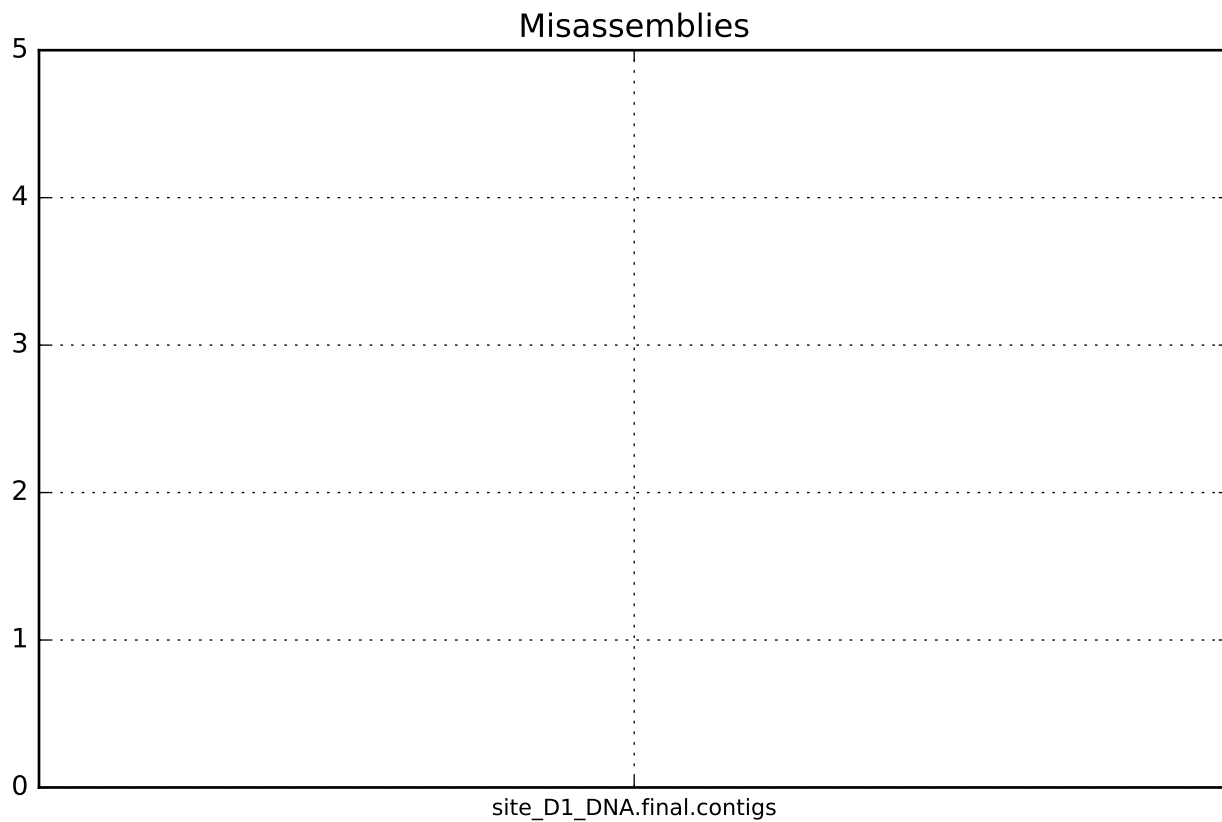
— site\_D1\_DNA.final.contigs    - - Reference

site\_D1\_DNA.final.contigs GC content

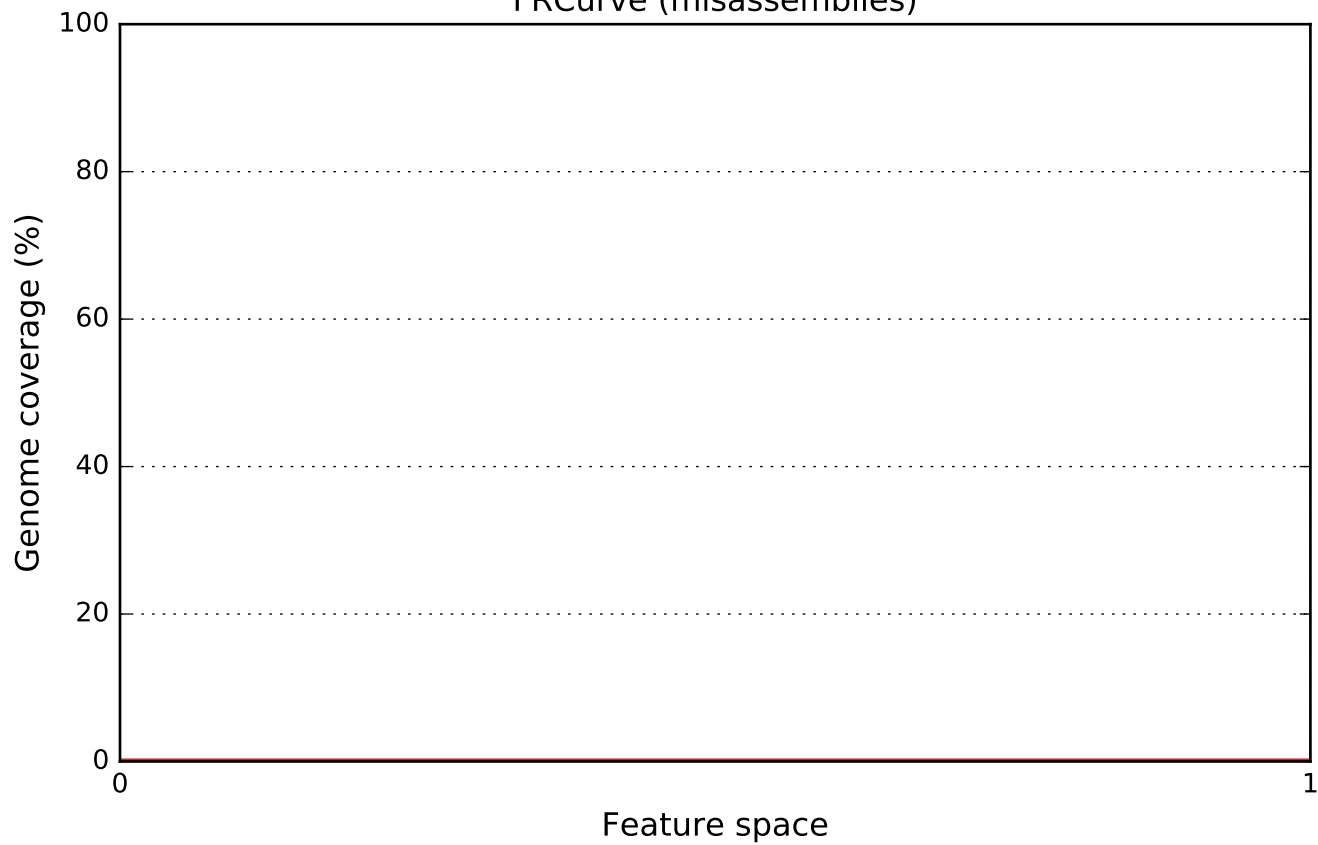


site\_D1\_DNA.final.contigs



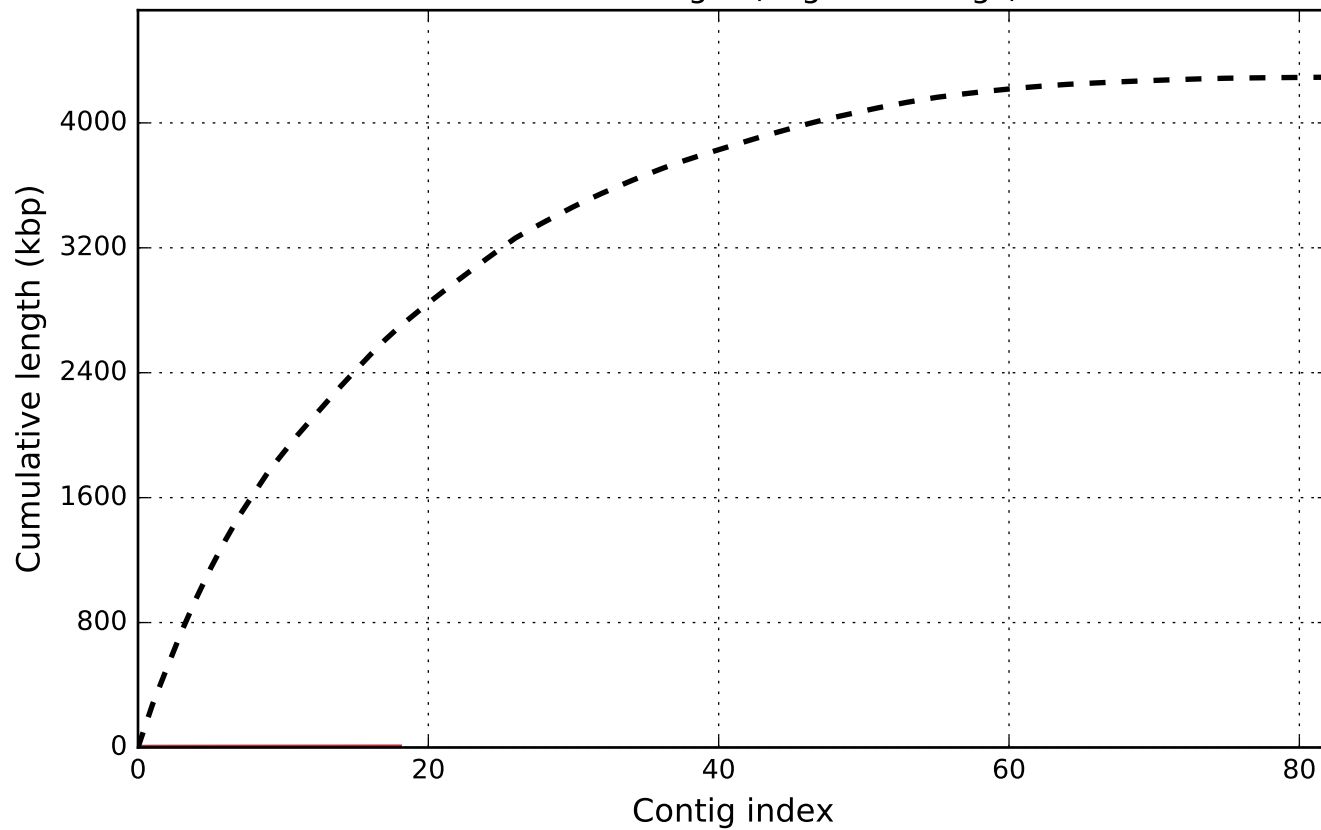


FRCurve (misassemblies)



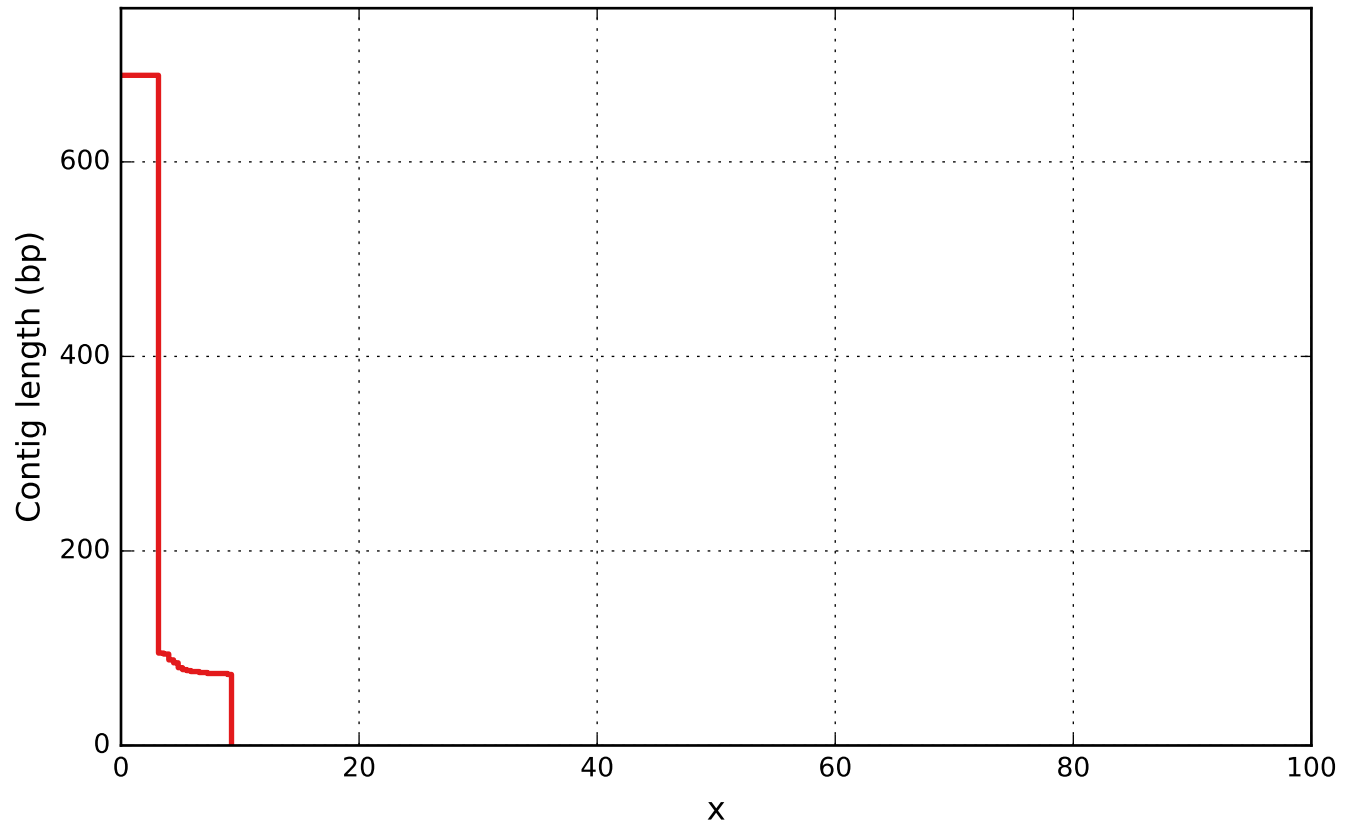
— site\_D1\_DNA.final.contigs

Cumulative length (aligned contigs)



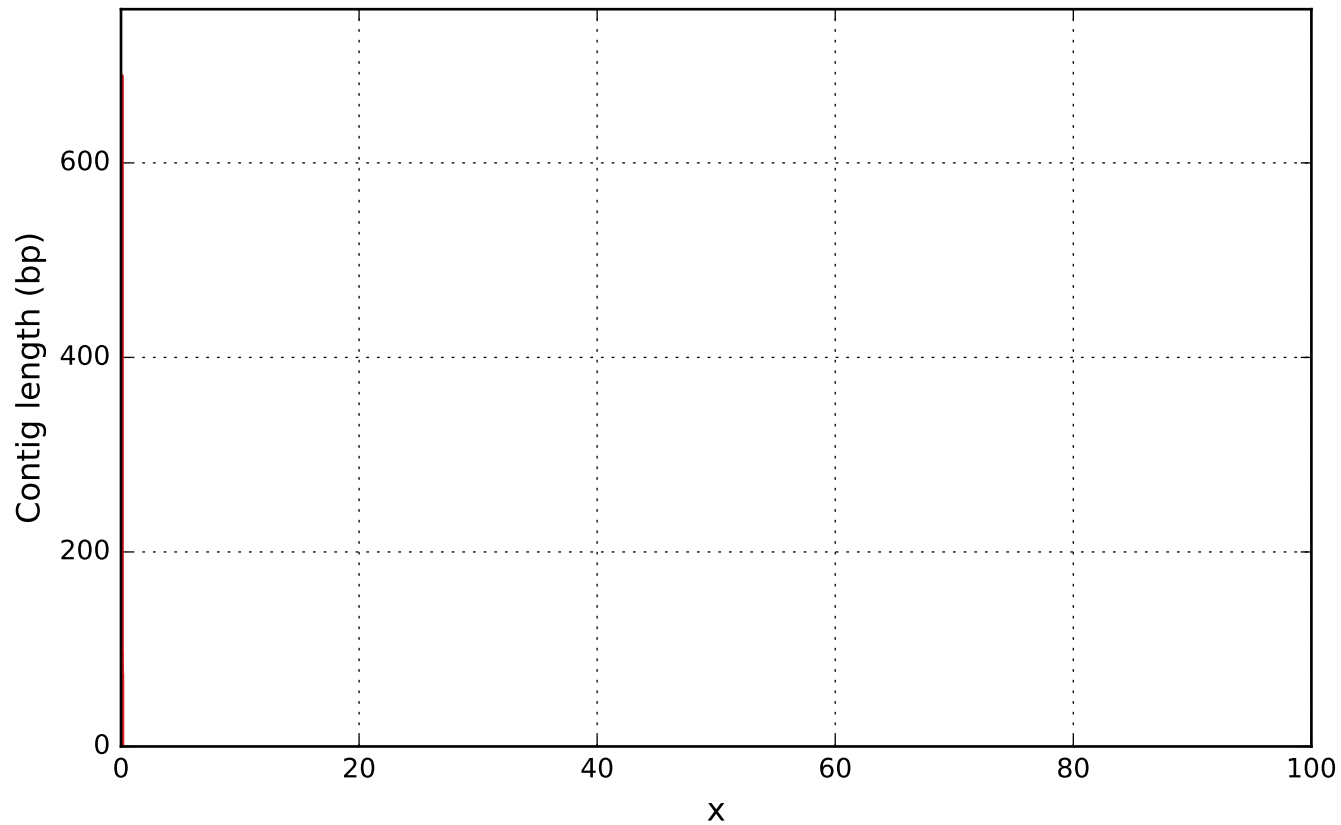
— site\_D1\_DNA.final.contigs    - - Reference

NAx



— site\_D1\_DNA.final.contigs

NGAx



— site\_D1\_DNA.final.contigs