

## Report

	site_D3_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)	2087
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	1
Largest contig	2087
Total length	2087
Reference length	4633577
GC (%)	45.62
Reference GC (%)	36.49
N50	2087
N75	2087
L50	1
L75	1
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 1 part
Unaligned length	1999
Genome fraction (%)	0.002
Duplication ratio	1.011
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1149.43
# indels per 100 kbp	1149.43
Largest alignment	88
Total aligned length	88
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

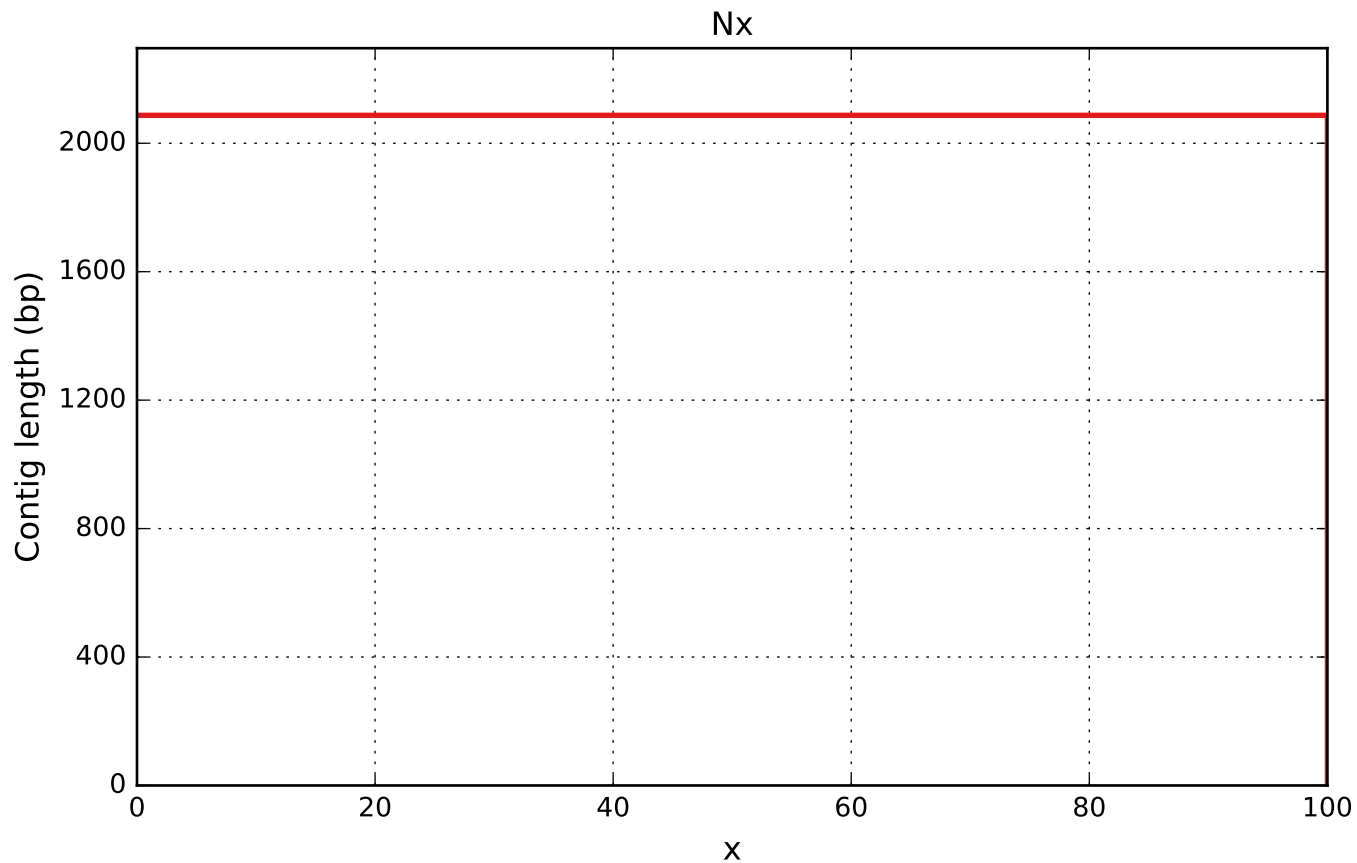
	site_D3_DNA.final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	1
# indels	1
# indels (<= 5 bp)	1
# indels (> 5 bp)	0
Indels length	1

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).

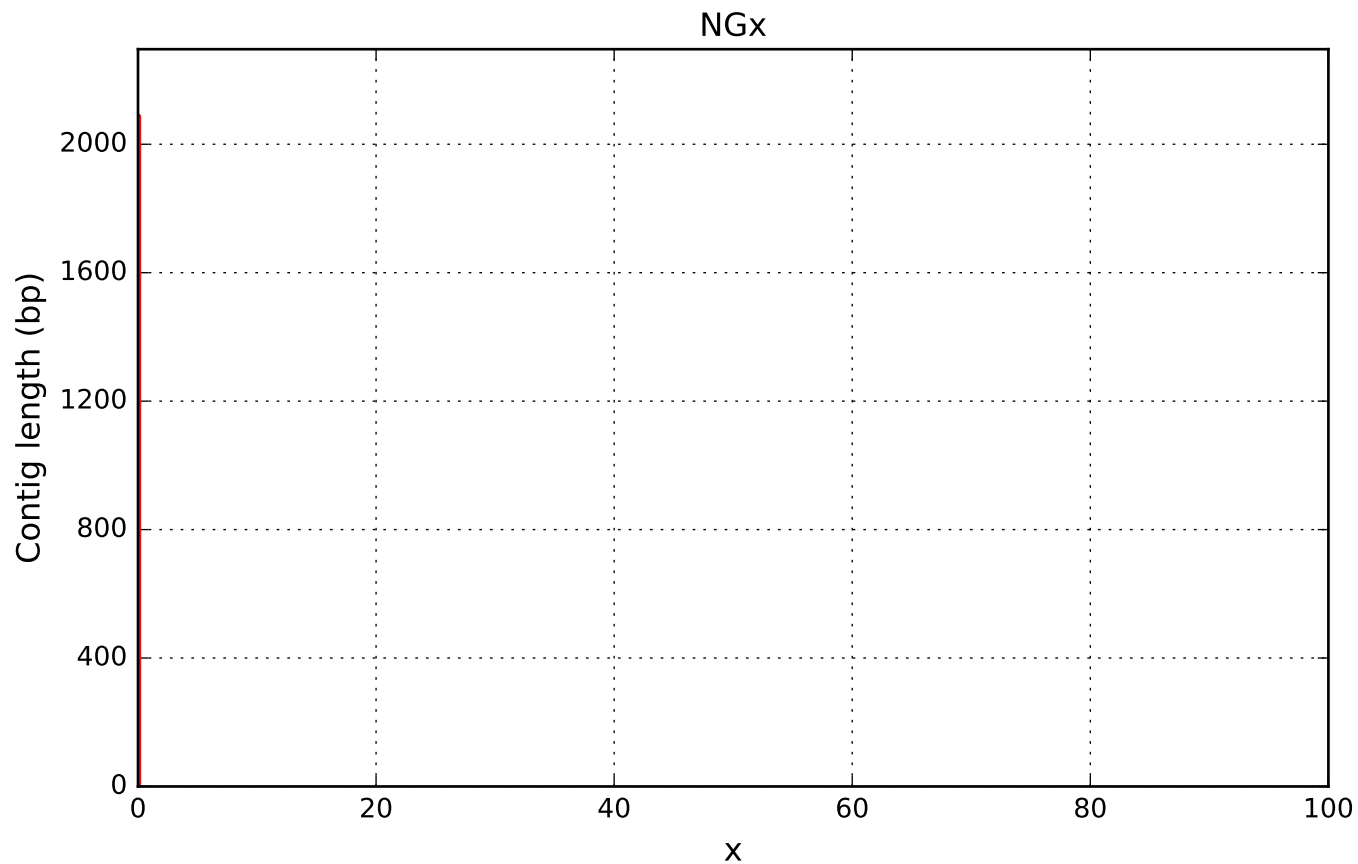
## Unaligned report

	site_D3_DNA.final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	1
Partially unaligned length	1999
# N's	0

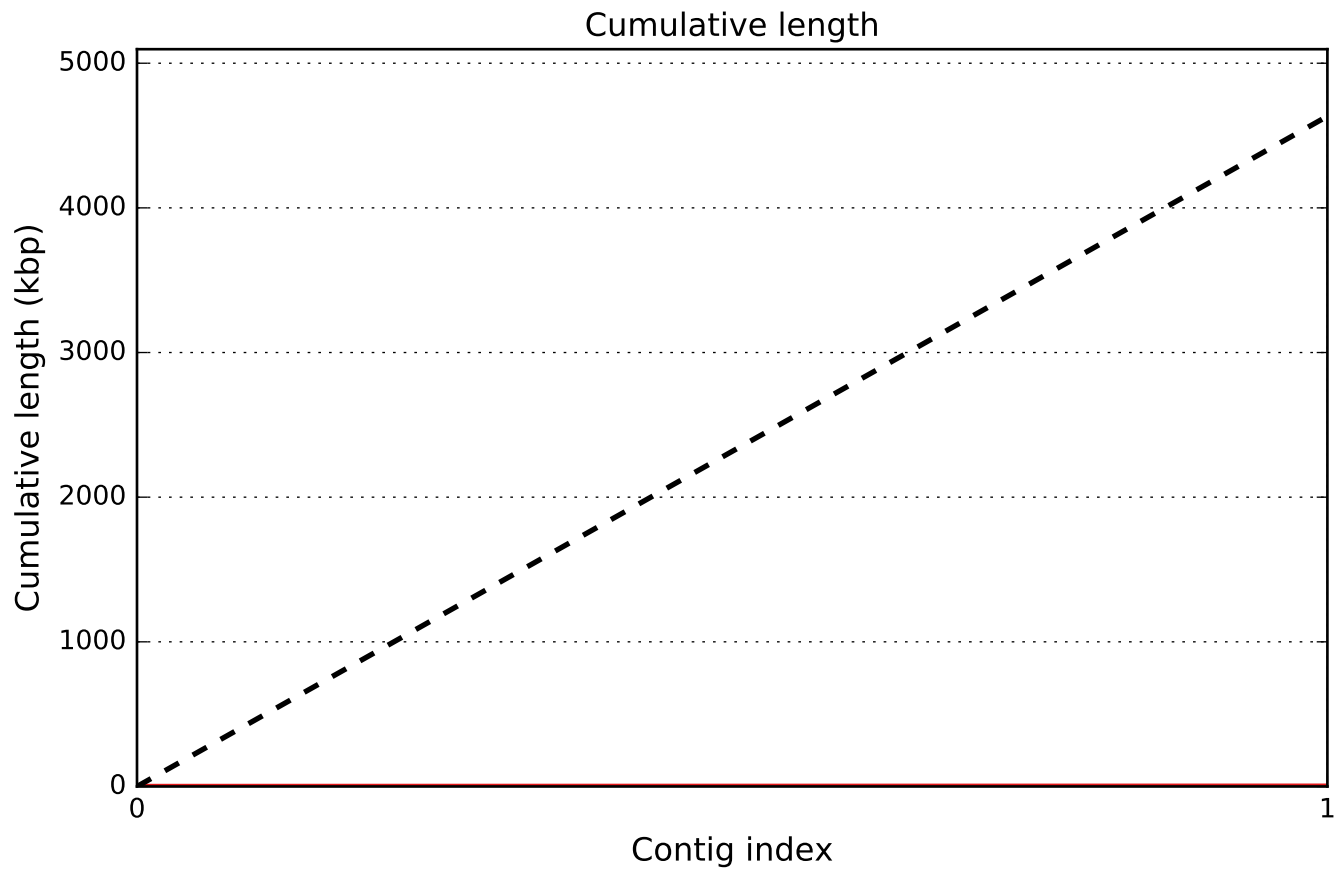
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

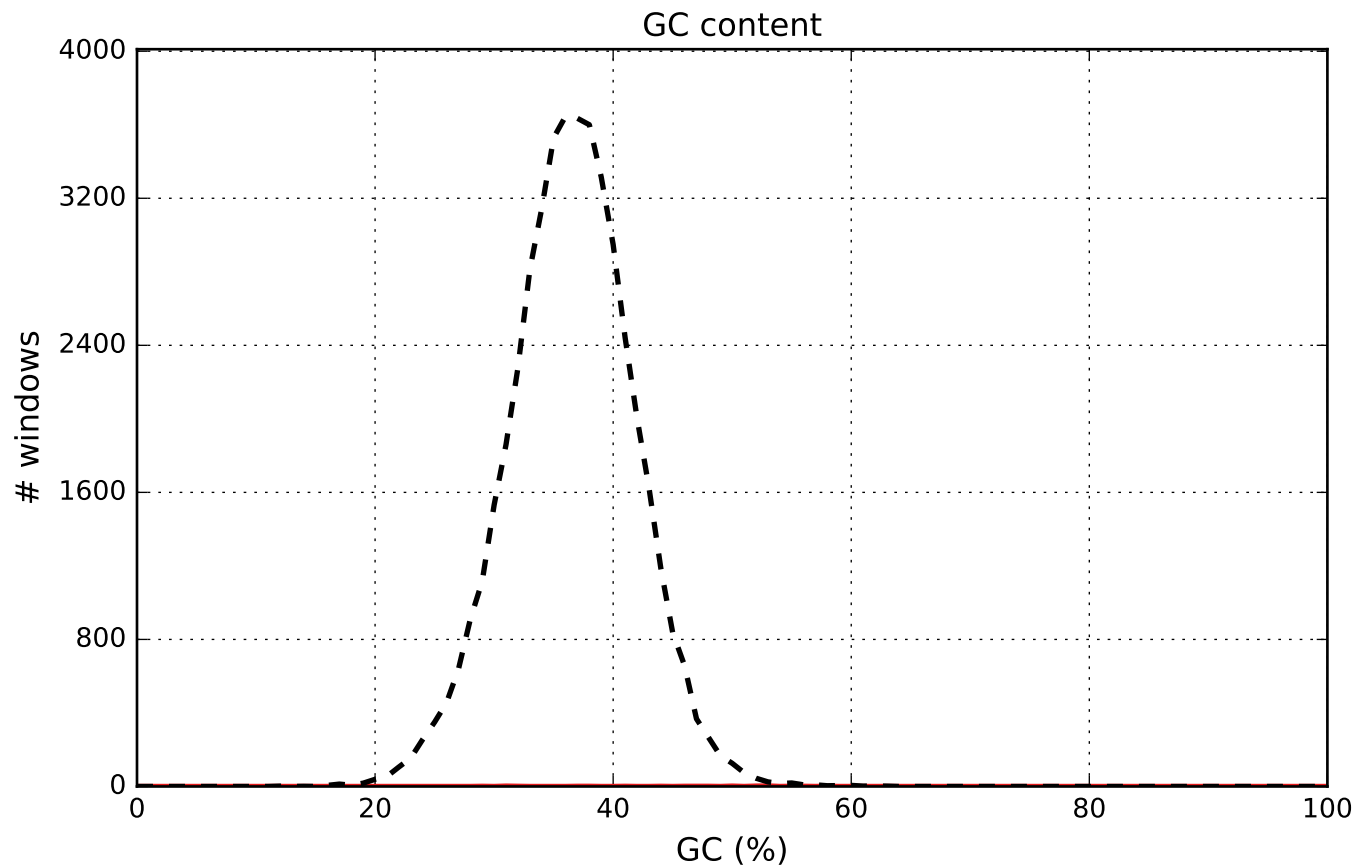


— site\_D3\_DNA.final.contigs

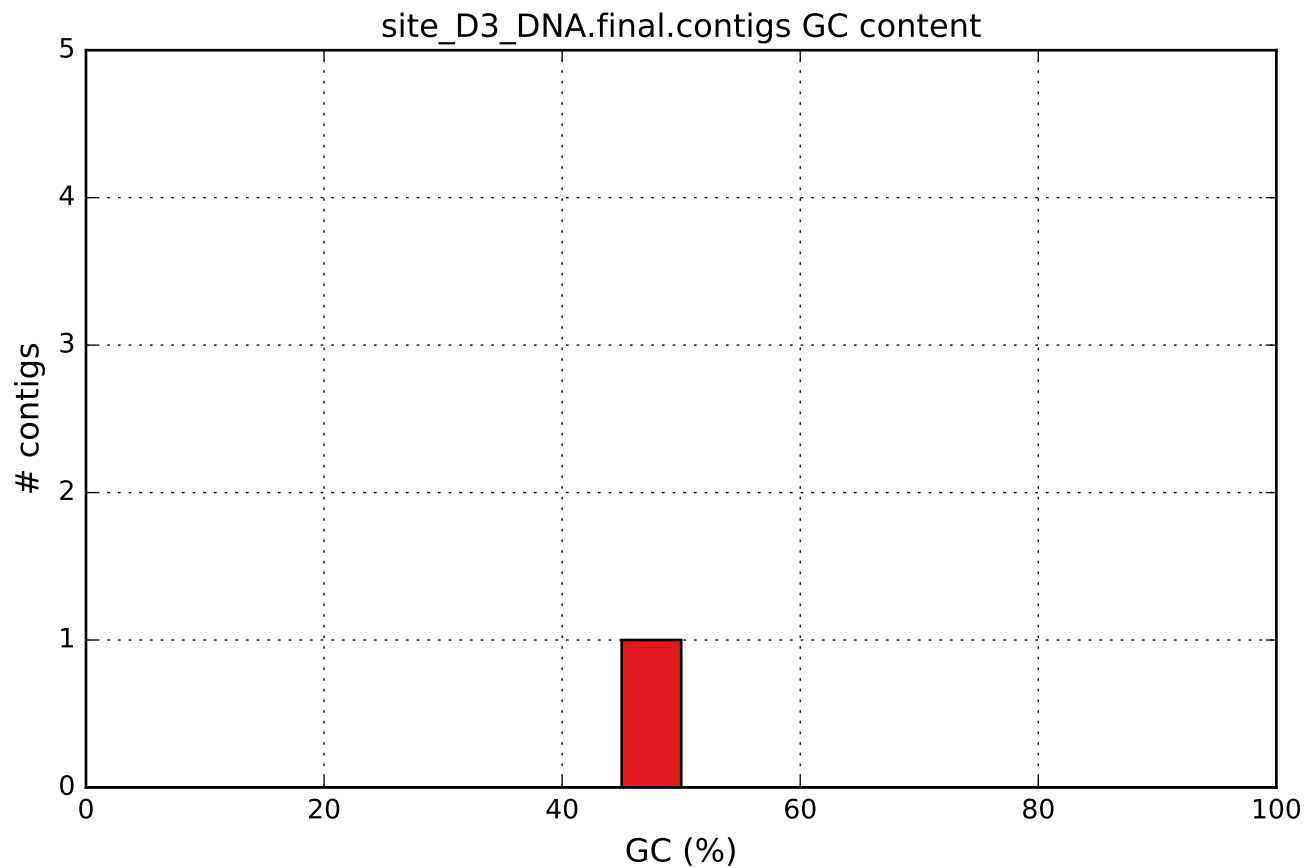


— site\_D3\_DNA.final.contigs



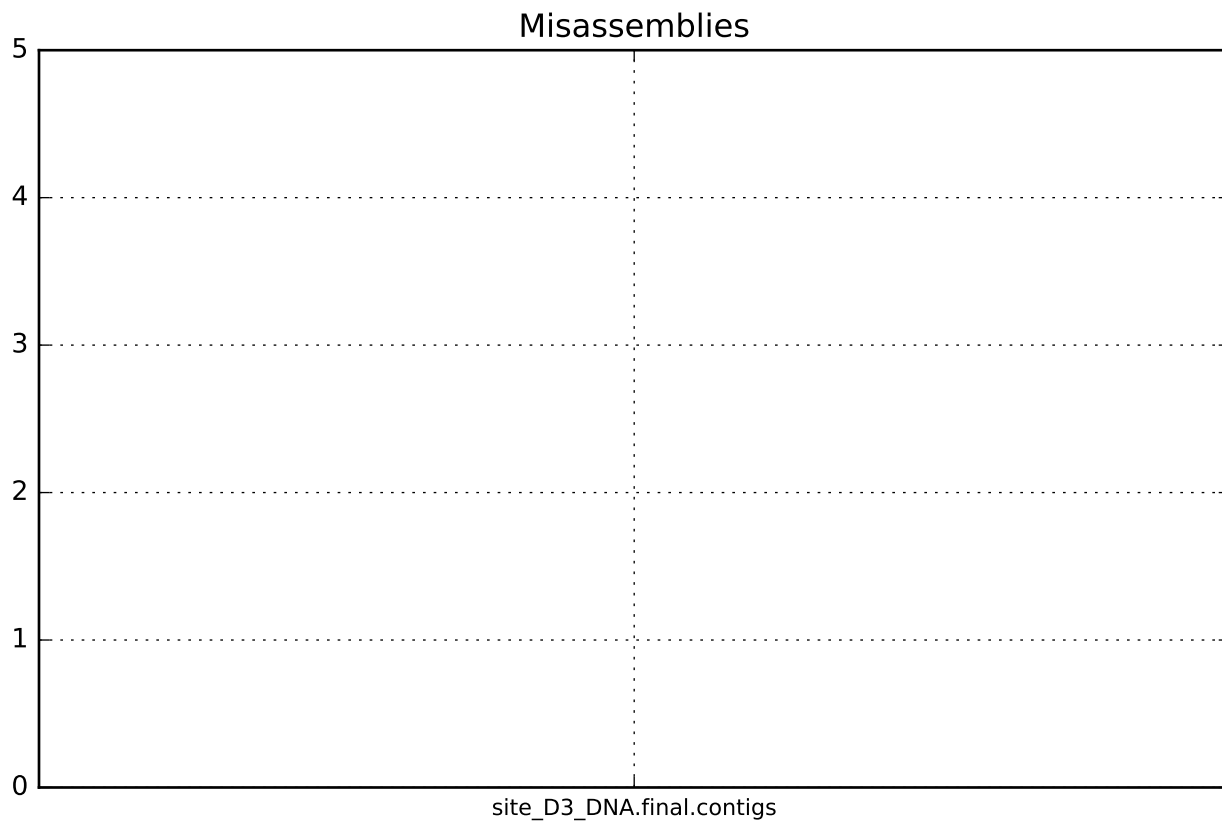


— site\_D3\_DNA.final.contigs    - - Reference

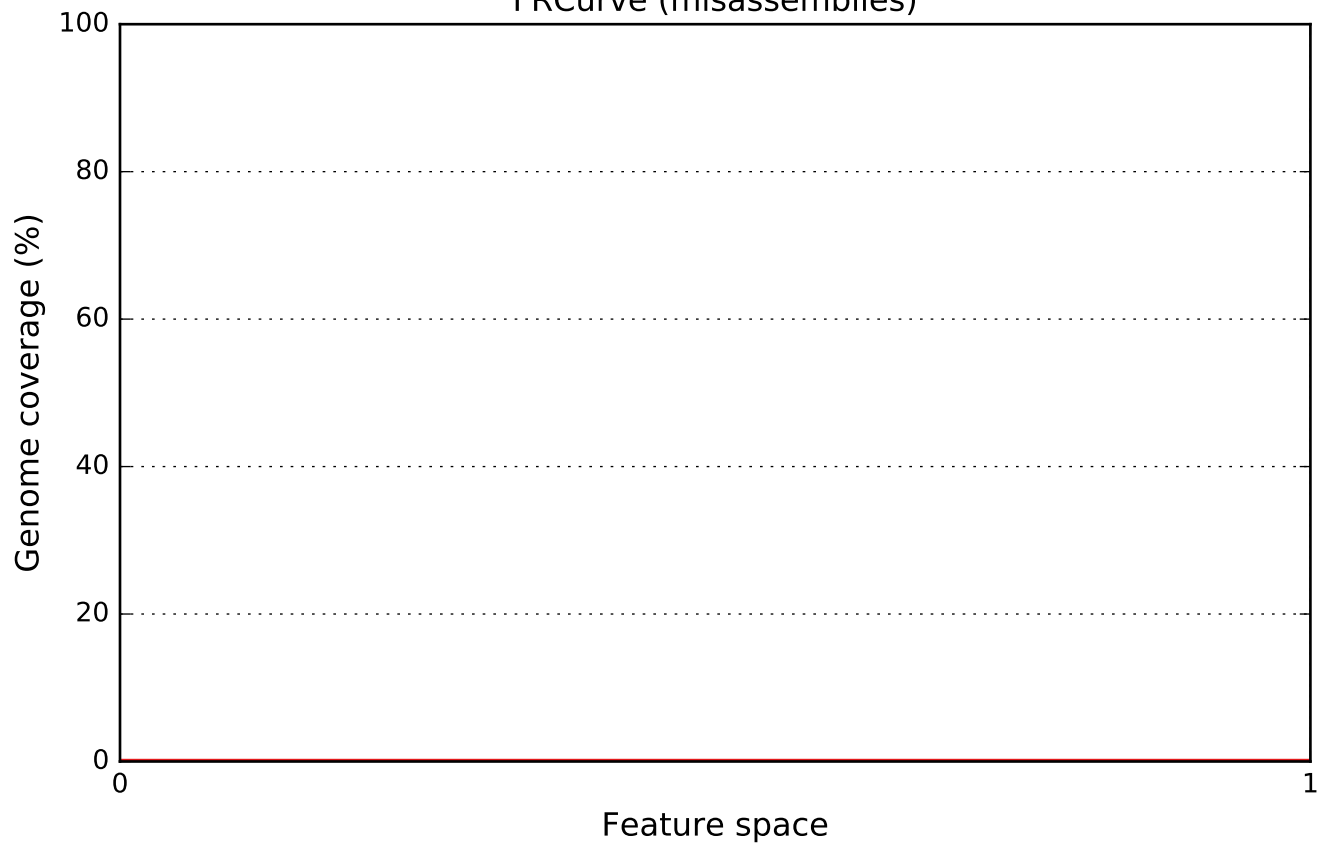


site\_D3\_DNA.final.contigs



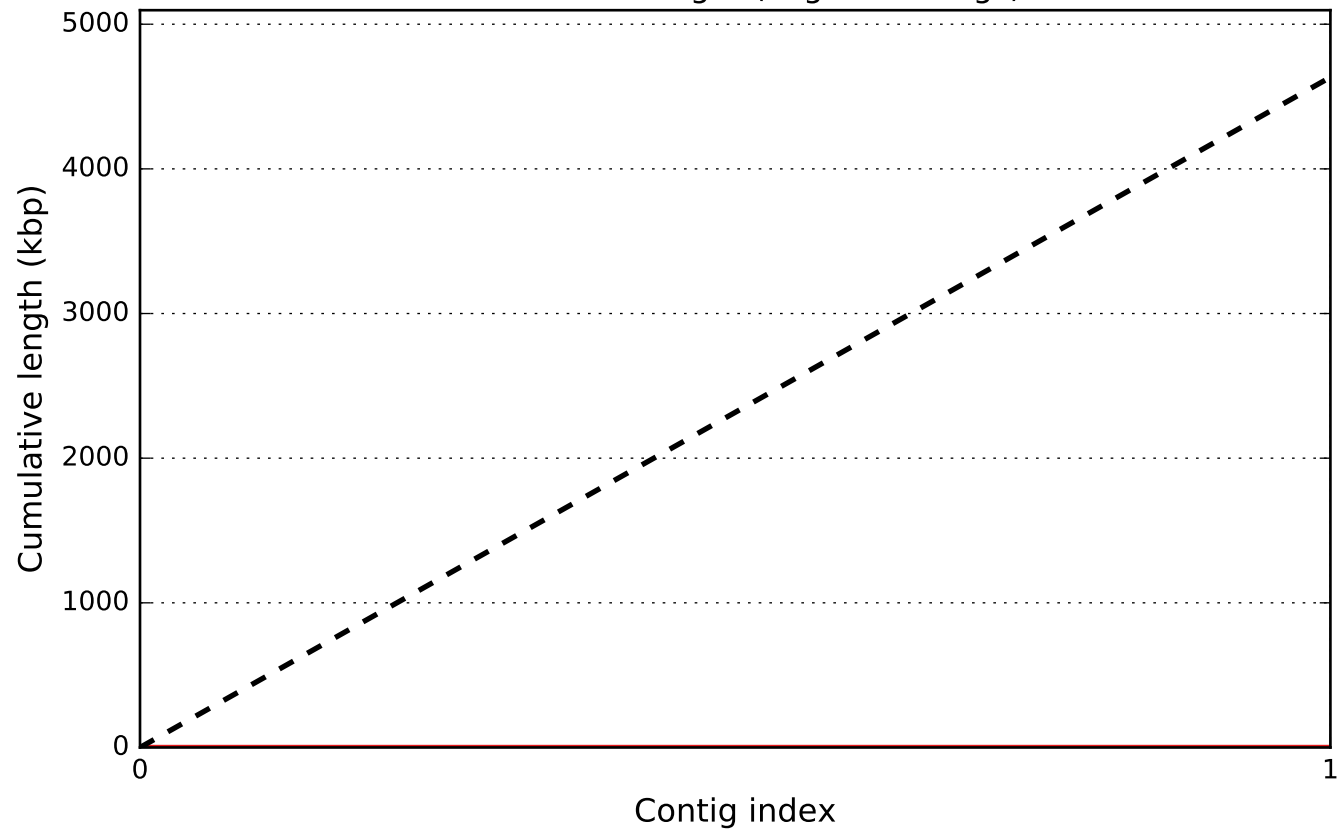


FRCurve (misassemblies)



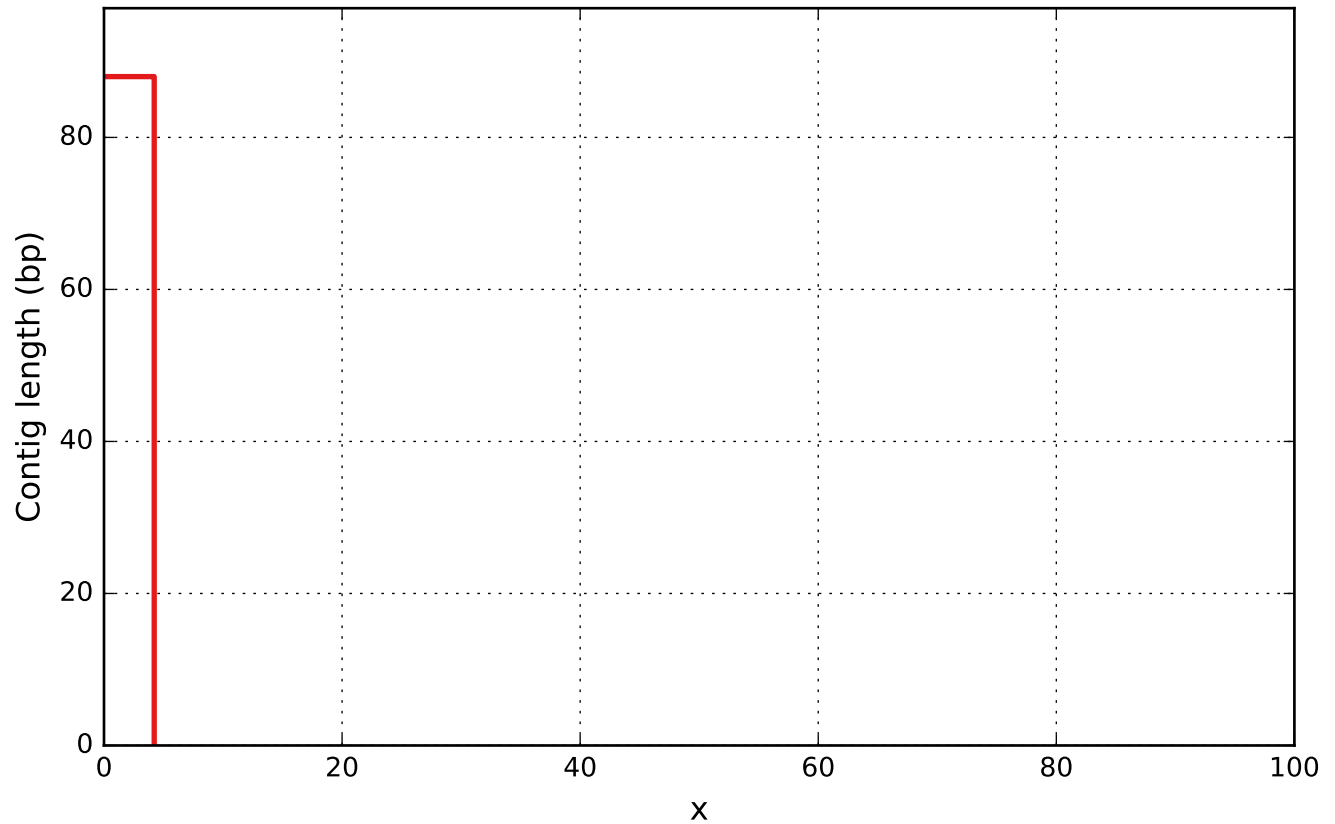
— site\_D3\_DNA.final.contigs

Cumulative length (aligned contigs)



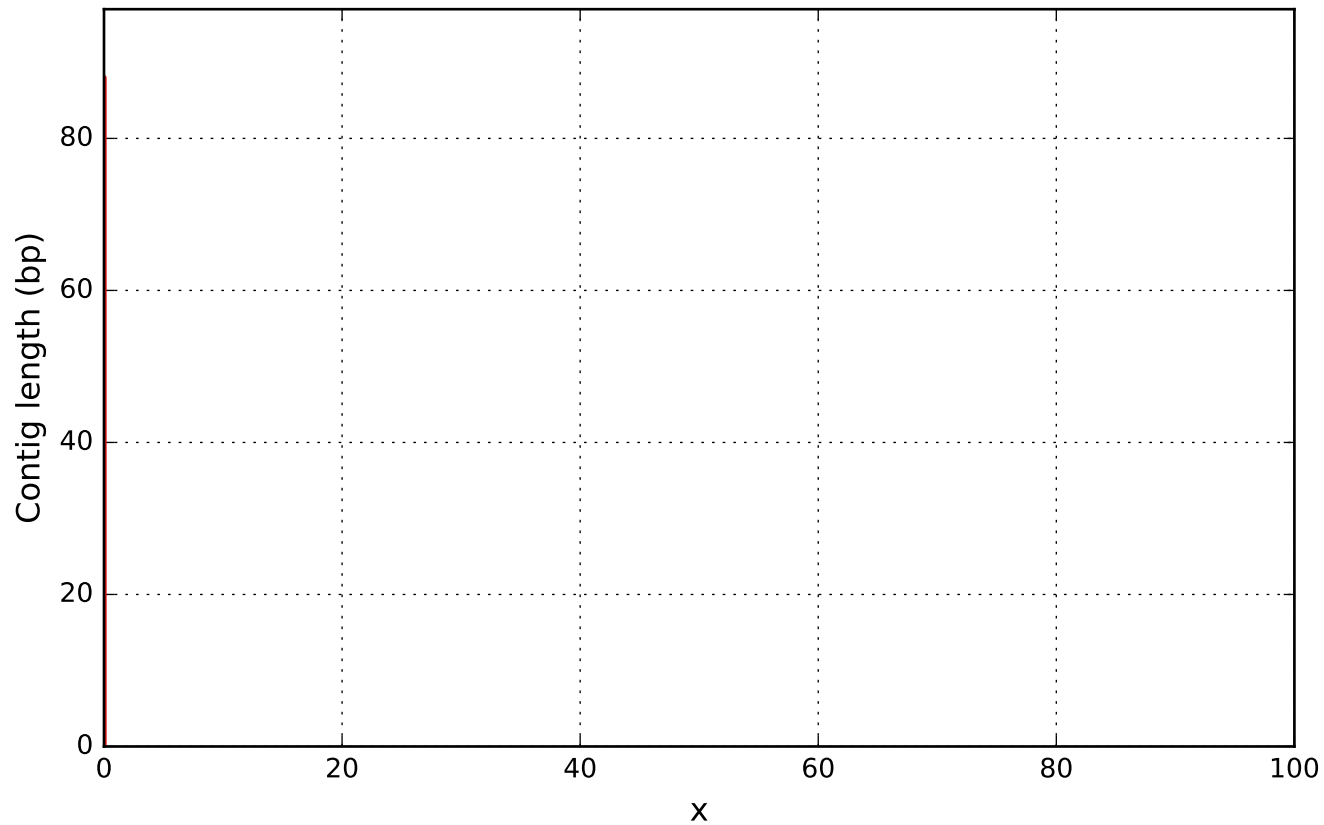
— site\_D3\_DNA.final.contigs    - - Reference

NAx



— site\_D3\_DNA.final.contigs

NGAx



— site\_D3\_DNA.final.contigs