

## Report

	site_D3_DNA.final.contigs
# contigs (>= 1000 bp)	3
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	6328
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	4
Largest contig	3777
Total length	6898
Reference length	1424092
GC (%)	49.71
Reference GC (%)	38.87
N50	3777
N75	1548
L50	1
L75	2
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 3 part
Unaligned length	6040
Genome fraction (%)	0.048
Duplication ratio	1.267
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2954.21
# indels per 100 kbp	295.42
Largest alignment	570
Total aligned length	858
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

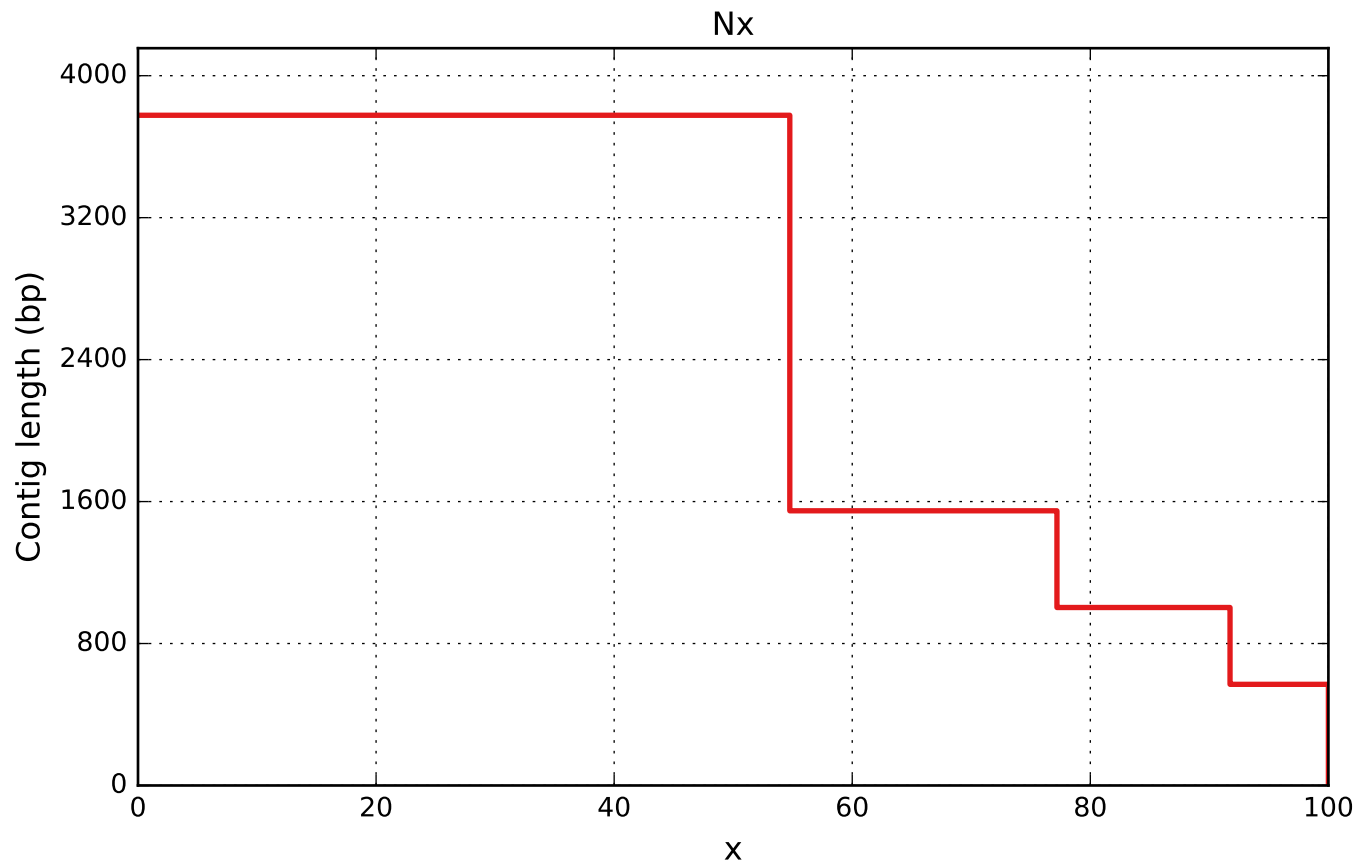
	site_D3_DNA.final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	20
# indels	2
# indels (<= 5 bp)	2
# indels (> 5 bp)	0
Indels length	2

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).

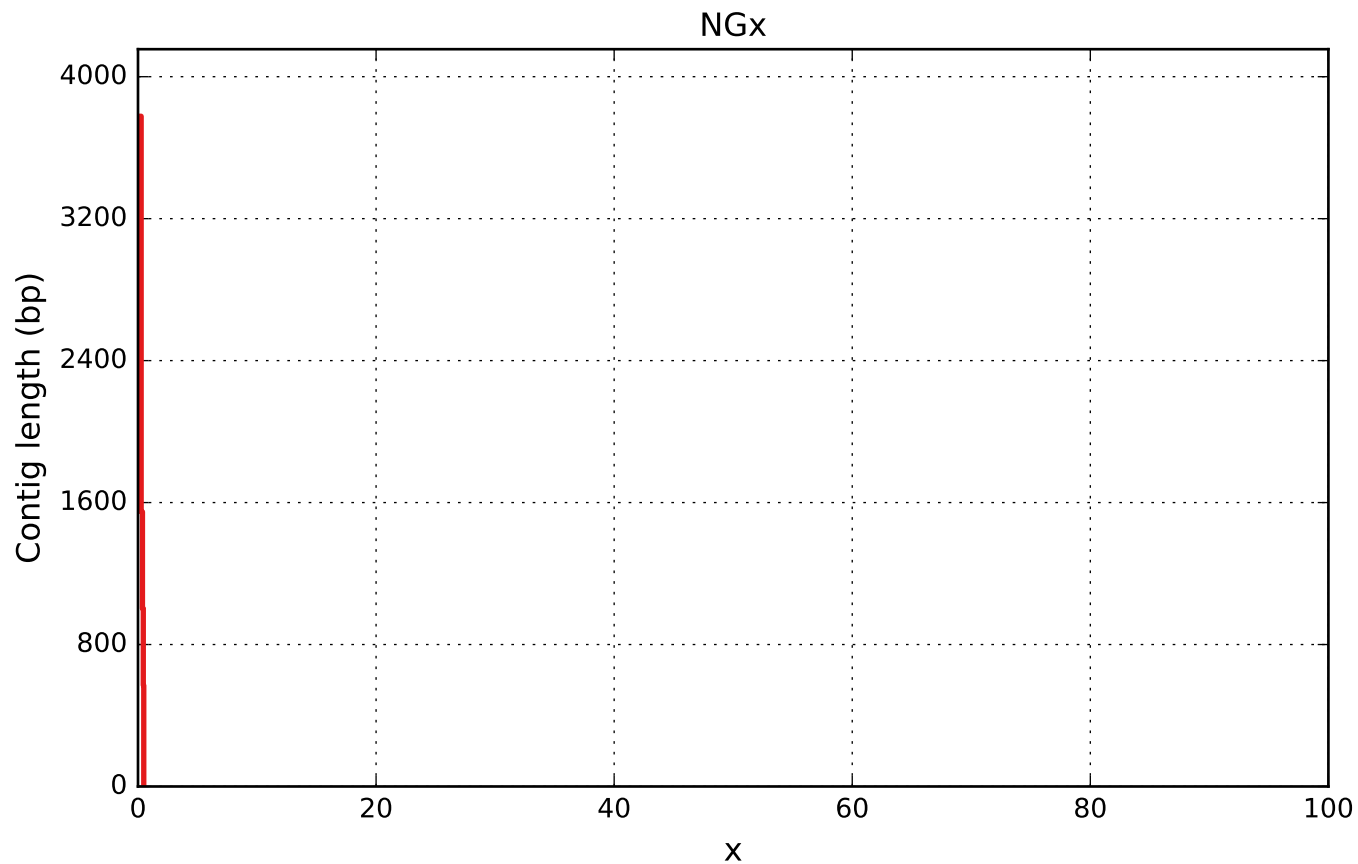
## Unaligned report

	site_D3_DNA.final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	3
Partially unaligned length	6040
# N's	0

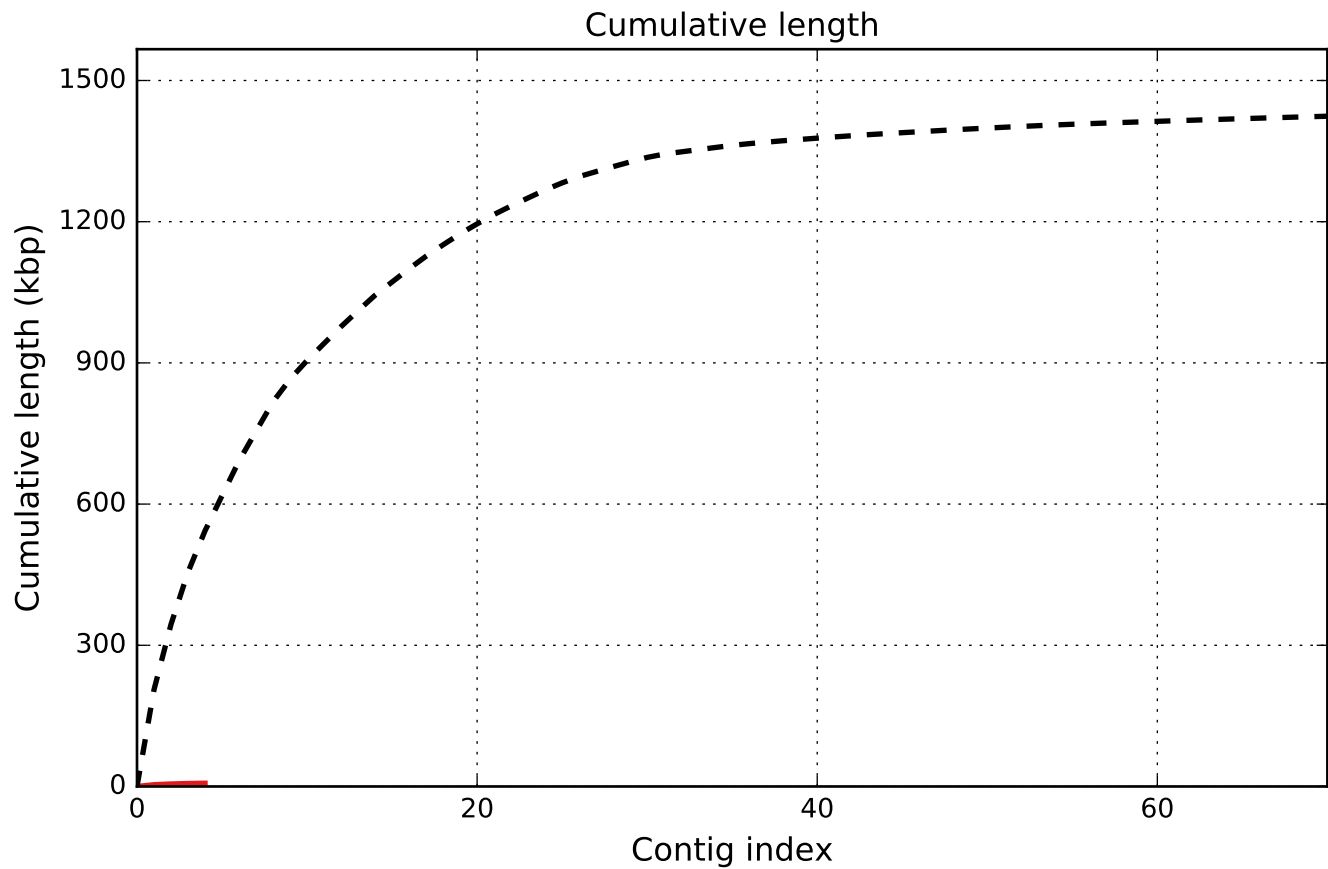
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



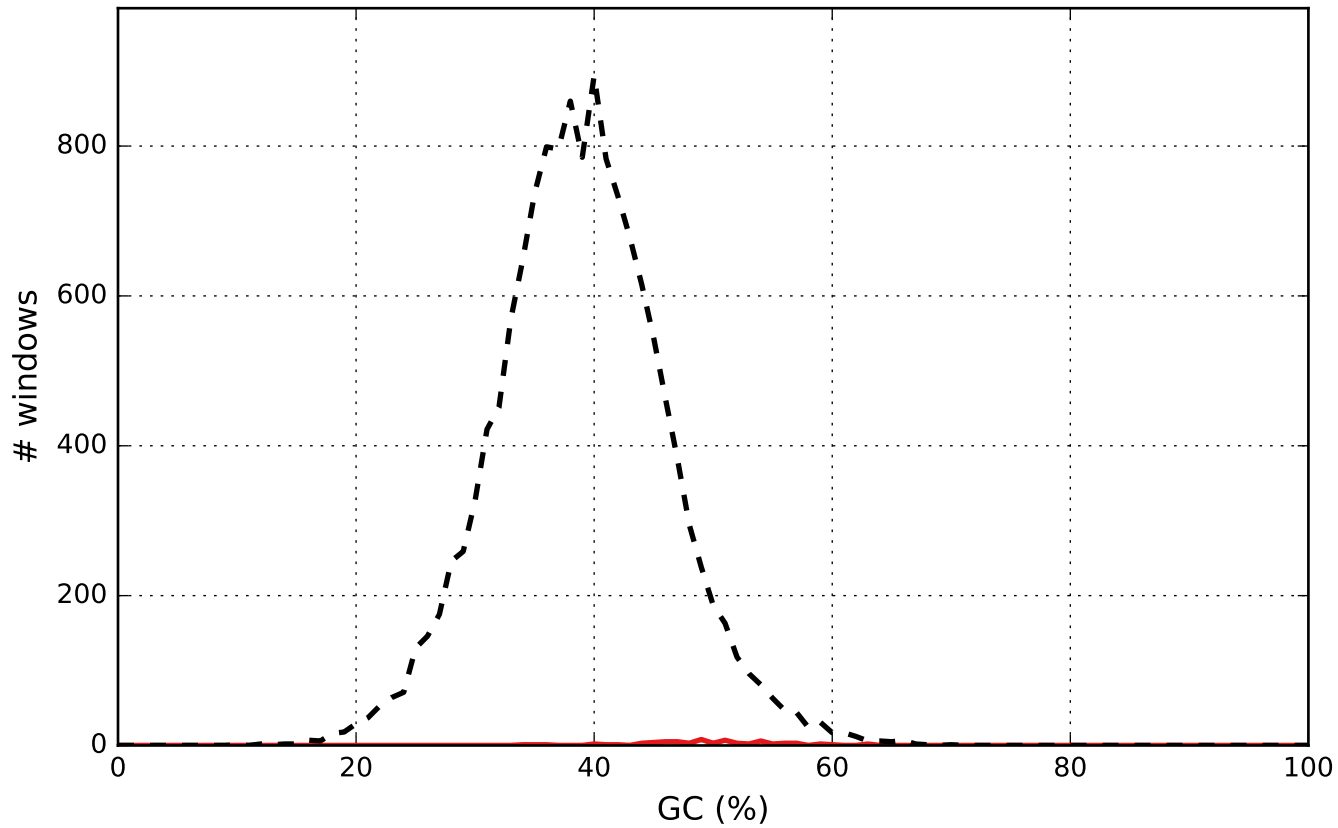
— site\_D3\_DNA.final.contigs



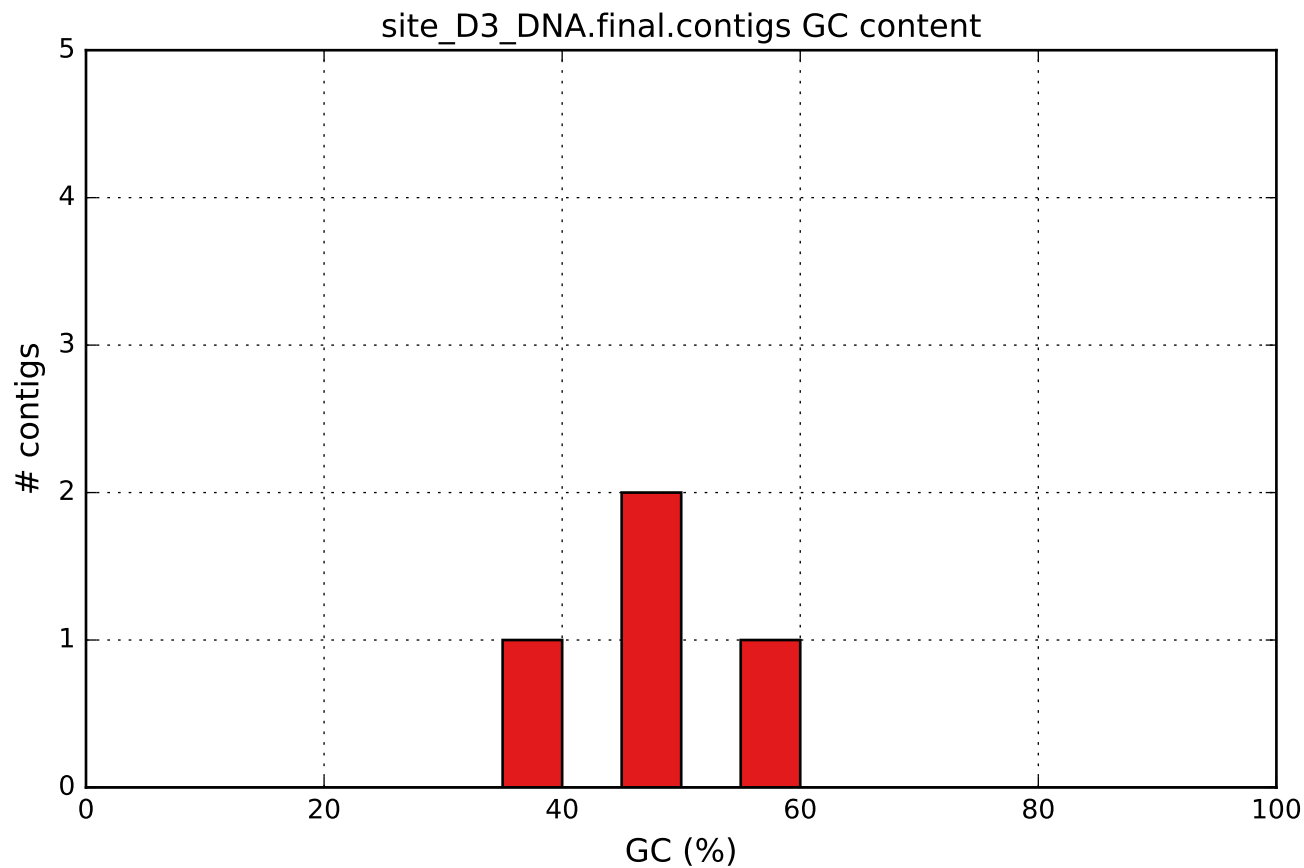
— site\_D3\_DNA.final.contigs



# GC content

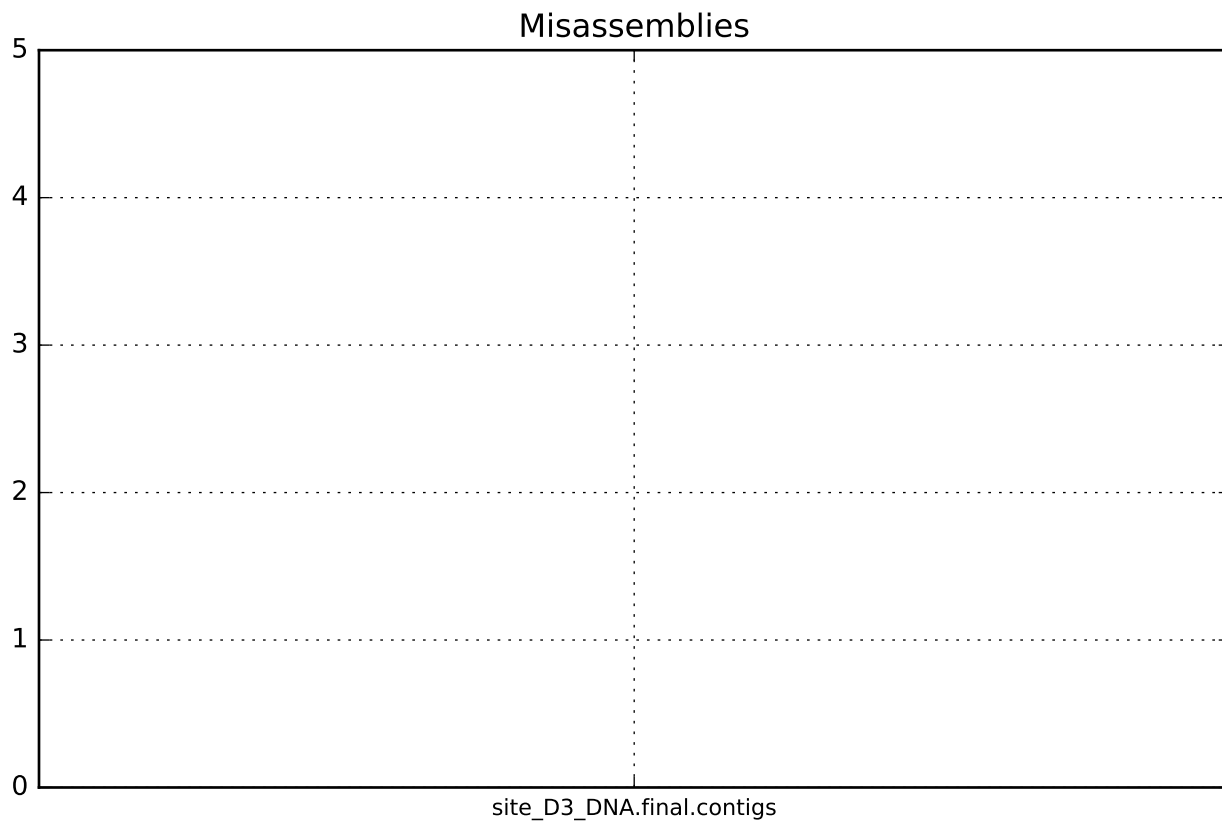


— site\_D3\_DNA.final.contigs    - - Reference

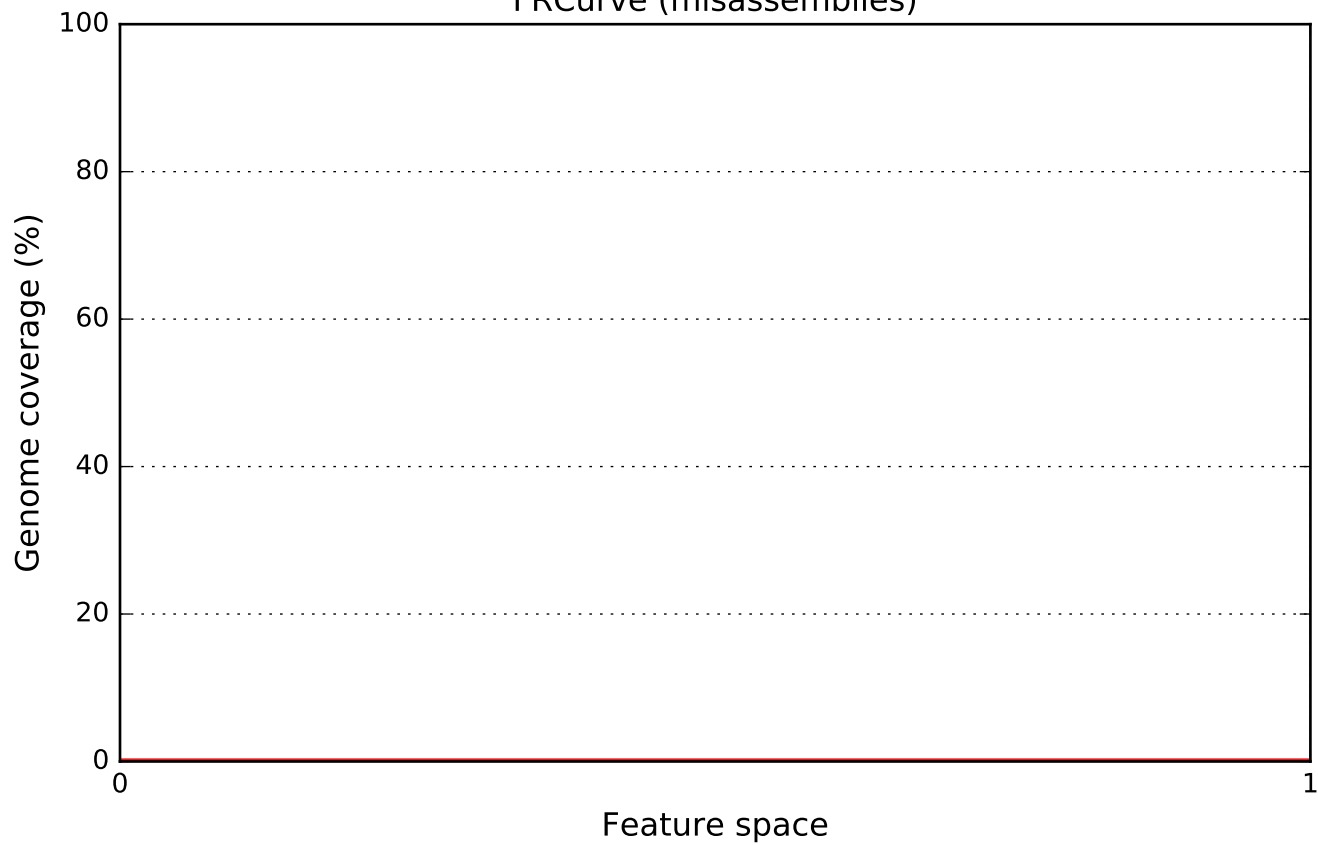


site\_D3\_DNA.final.contigs



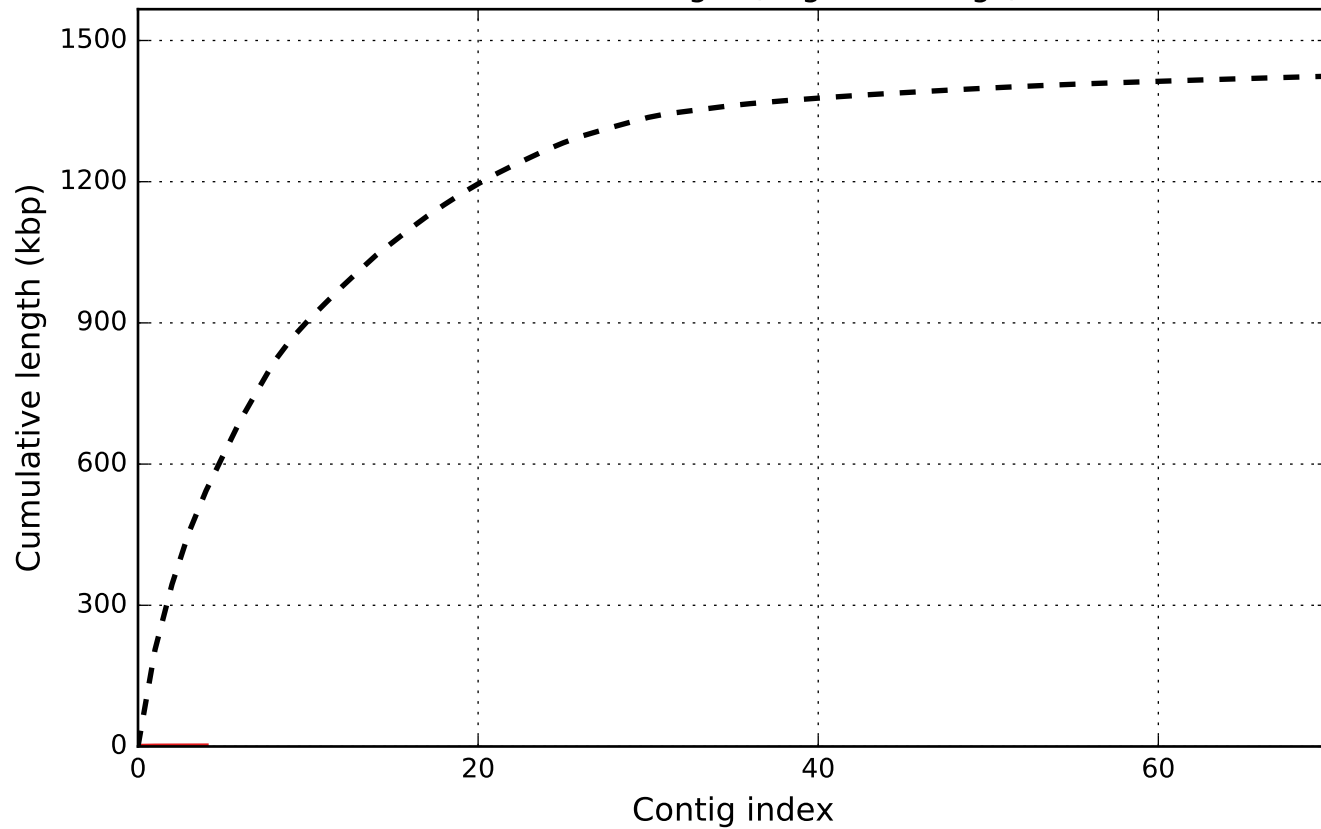


FRCurve (misassemblies)



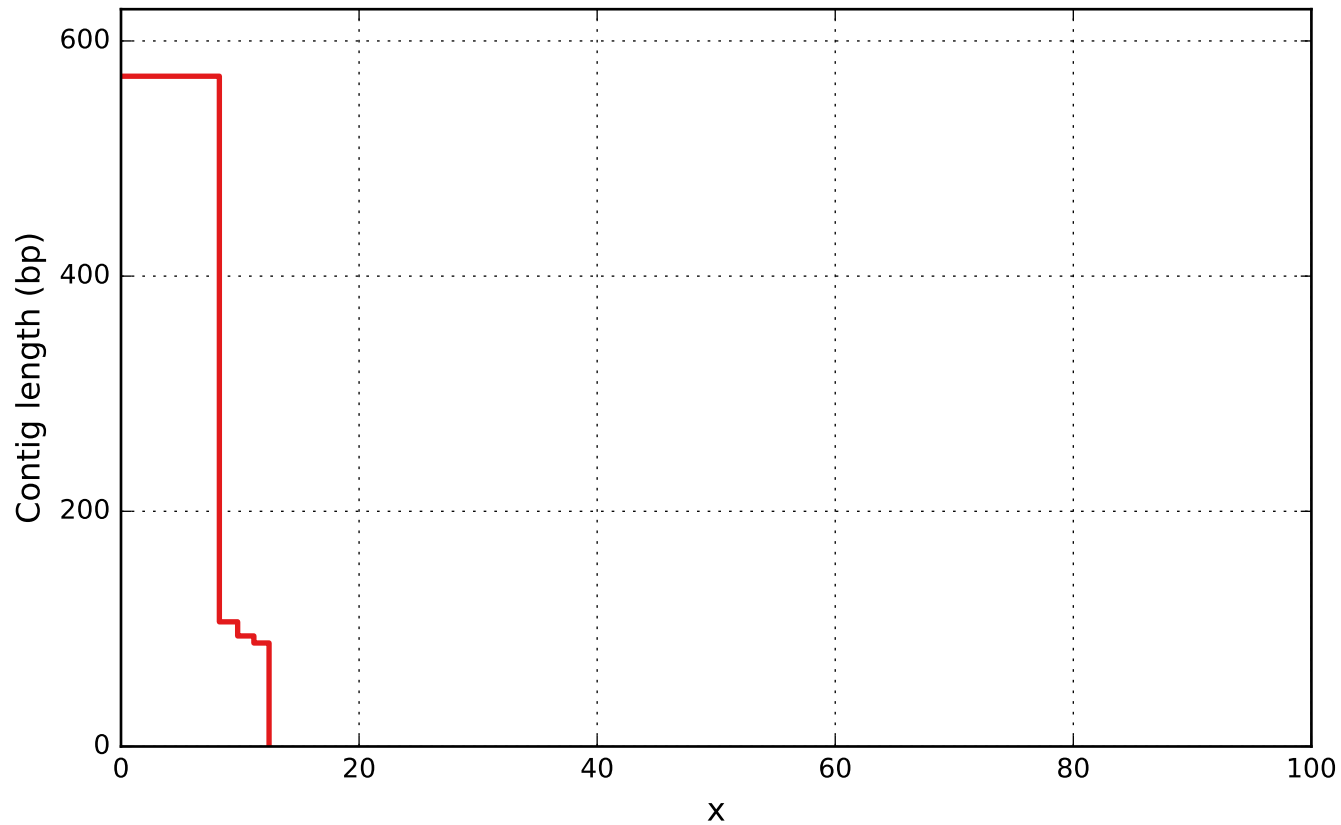
— site\_D3\_DNA.final.contigs

Cumulative length (aligned contigs)



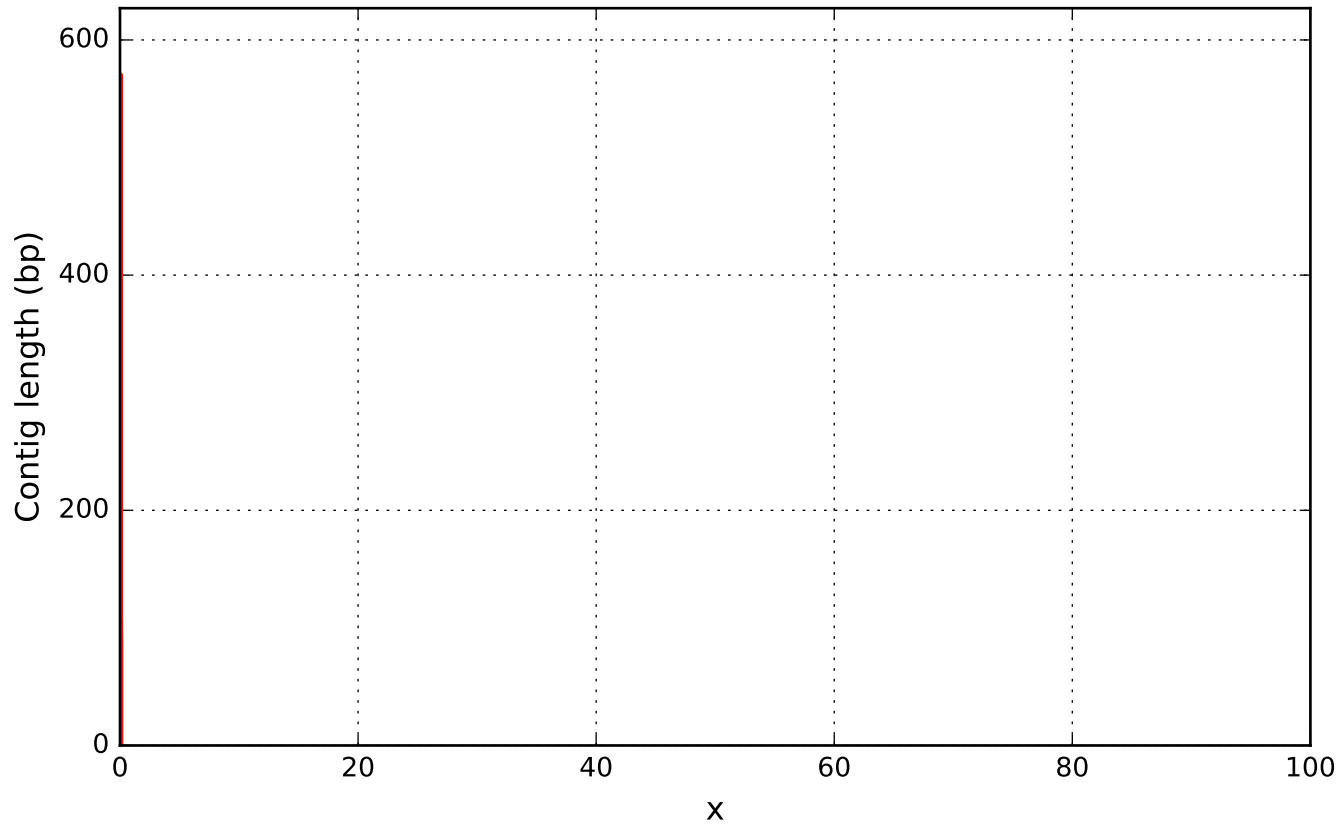
— site\_D3\_DNA.final.contigs    - - Reference

NAx



— site\_D3\_DNA.final.contigs

NGAx



— site\_D3\_DNA.final.contigs