

## Report

	site_D3_DNA.final.contigs
# contigs ( $\geq$ 1000 bp)	5
# 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)	7641
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	8
Largest contig	1841
Total length	9429
Reference length	5687995
GC (%)	38.83
Reference GC (%)	32.99
N50	1473
N75	1196
L50	3
L75	5
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	2
# unaligned contigs	0 + 5 part
Unaligned length	6905
Genome fraction (%)	0.017
Duplication ratio	2.610
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2688.73
# indels per 100 kbp	0.00
Largest alignment	353
Total aligned length	1324
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

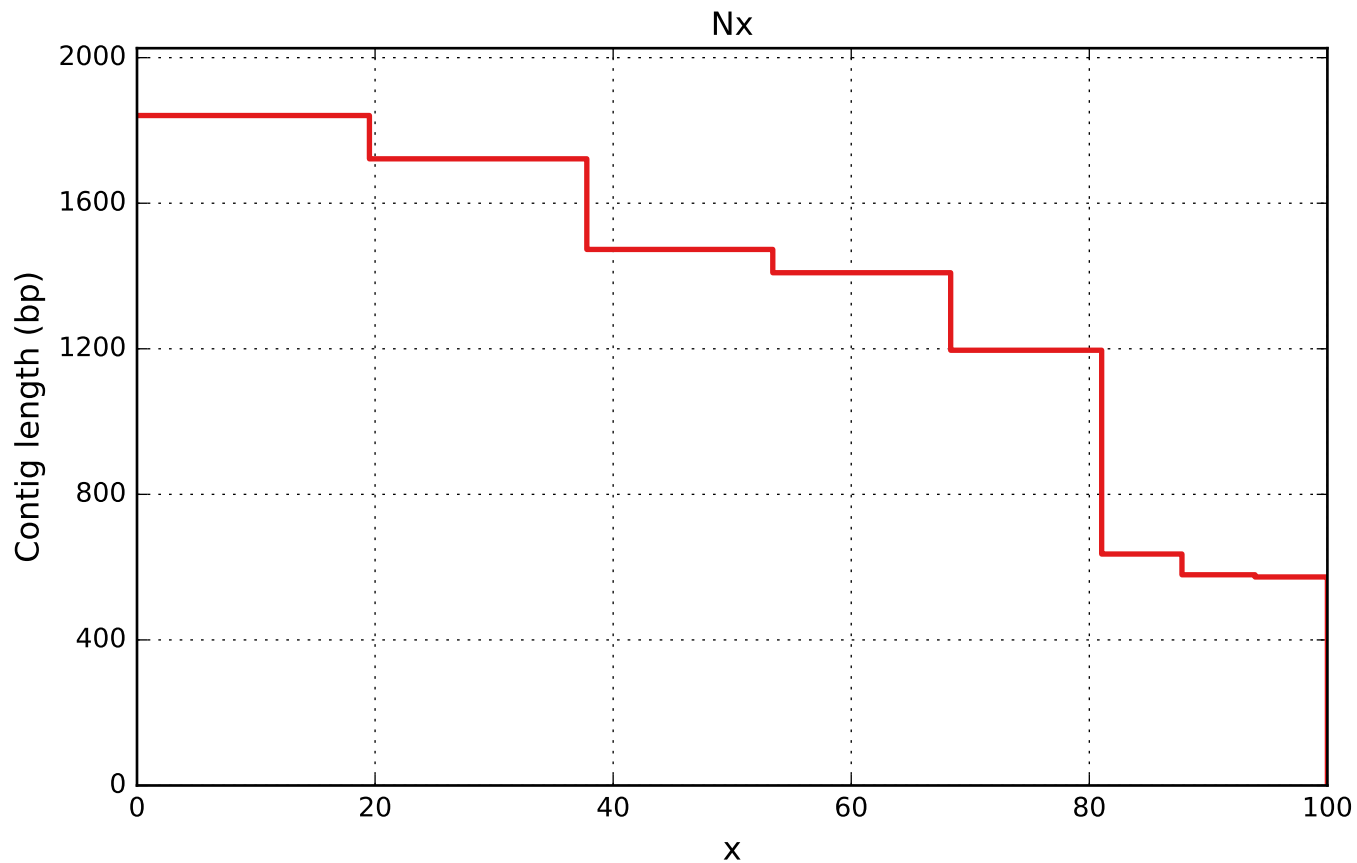
	site_D3_DNA.final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# unaligned mis. contigs	2
# mismatches	26
# 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).

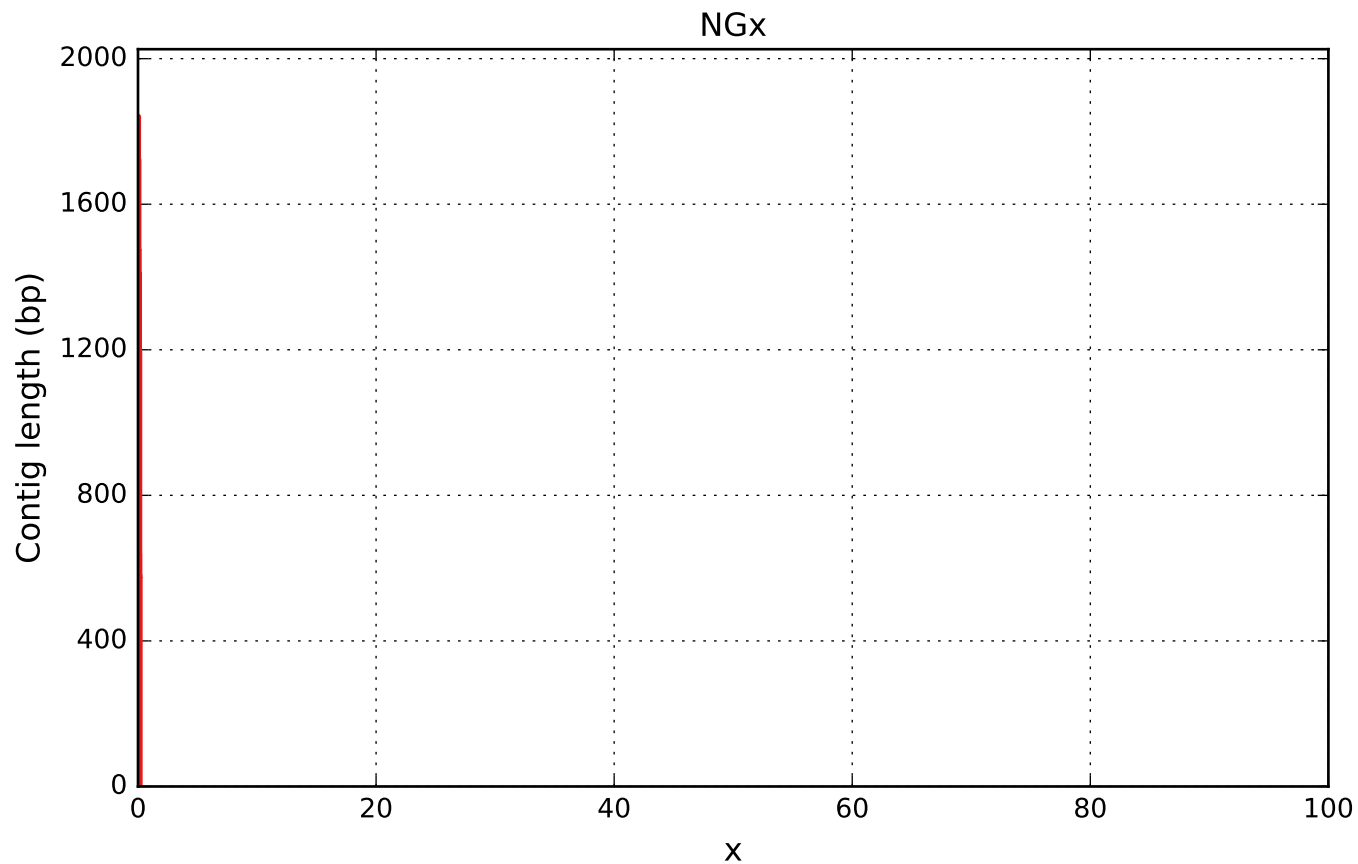
## Unaligned report

	site_D3_DNA.final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	5
Partially unaligned length	6905
# N's	0

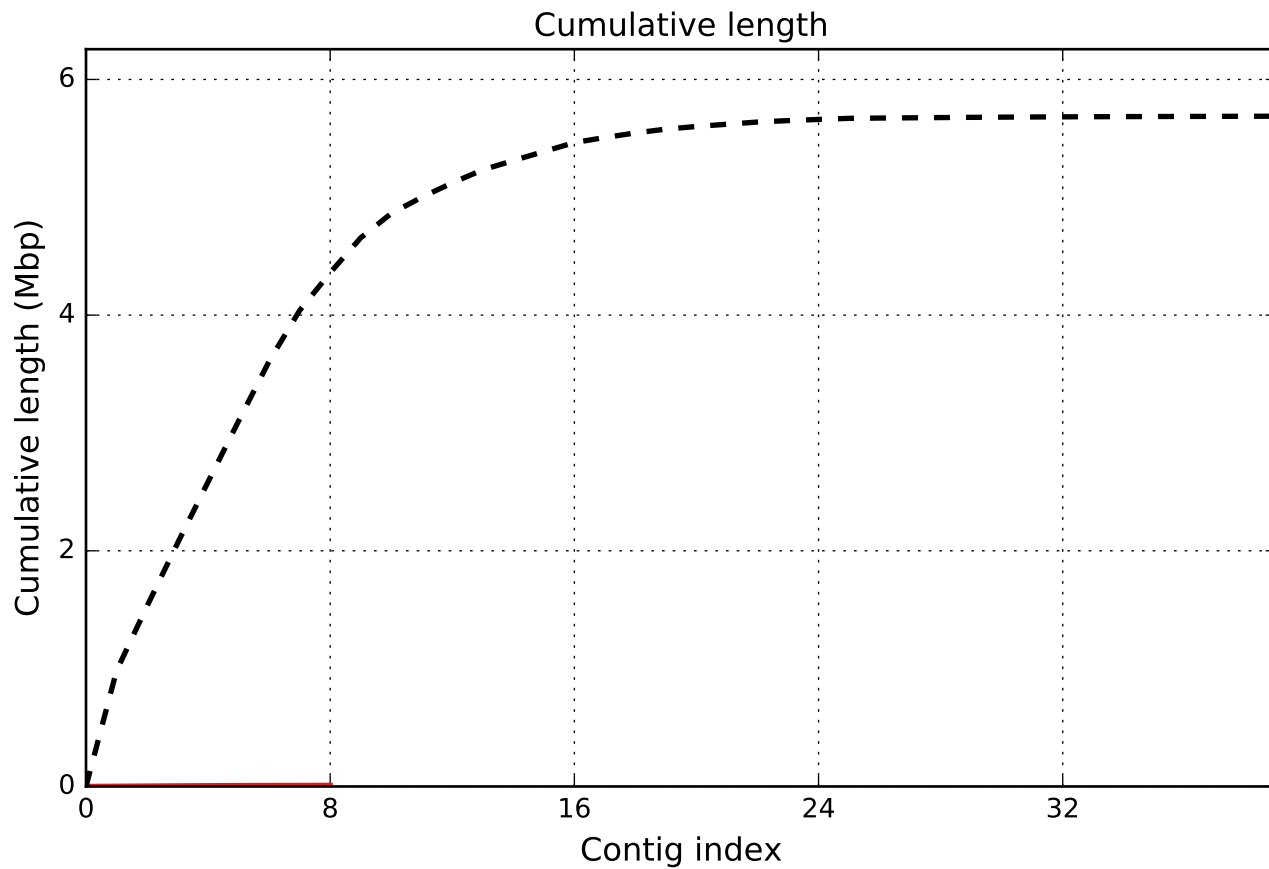
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



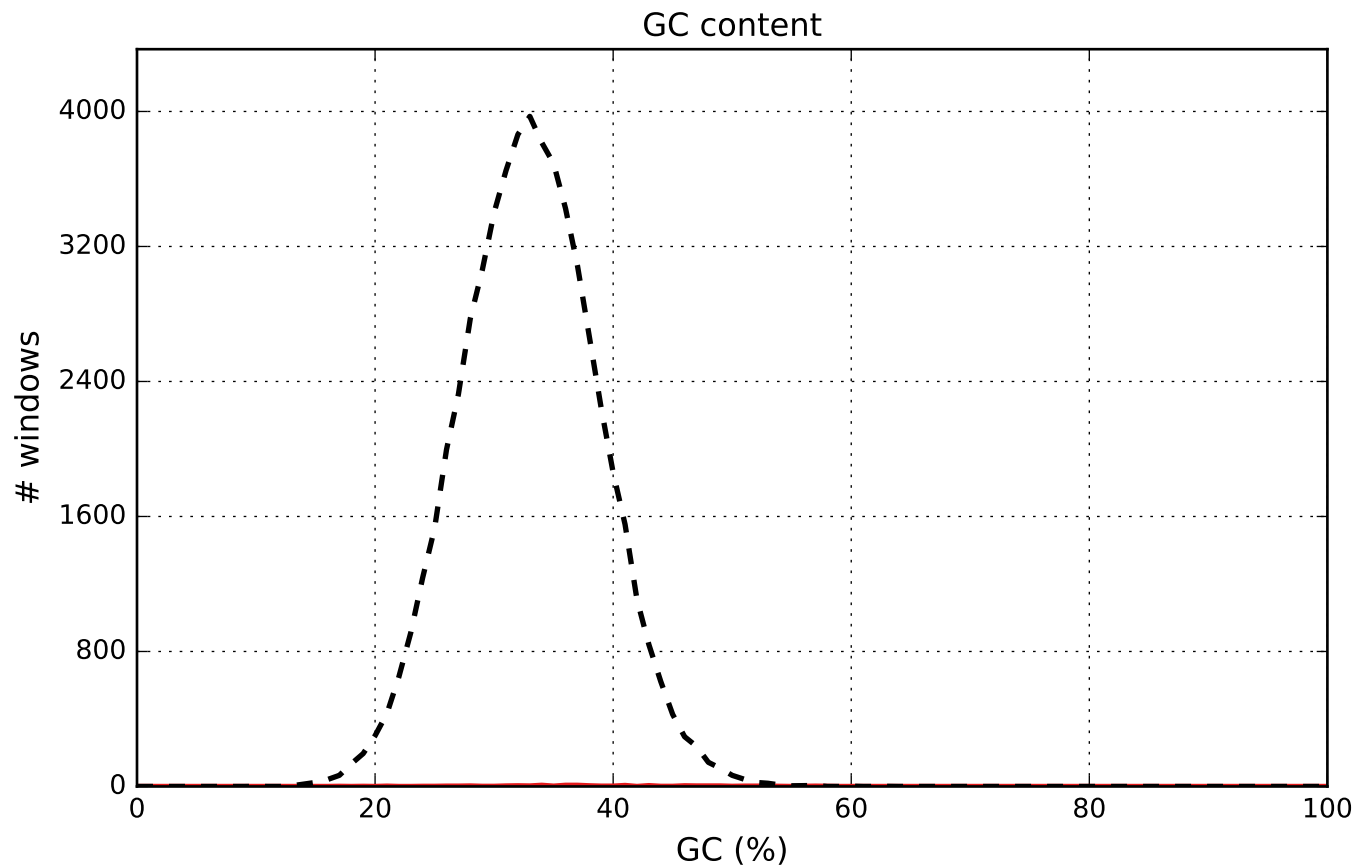
— site\_D3\_DNA.final.contigs



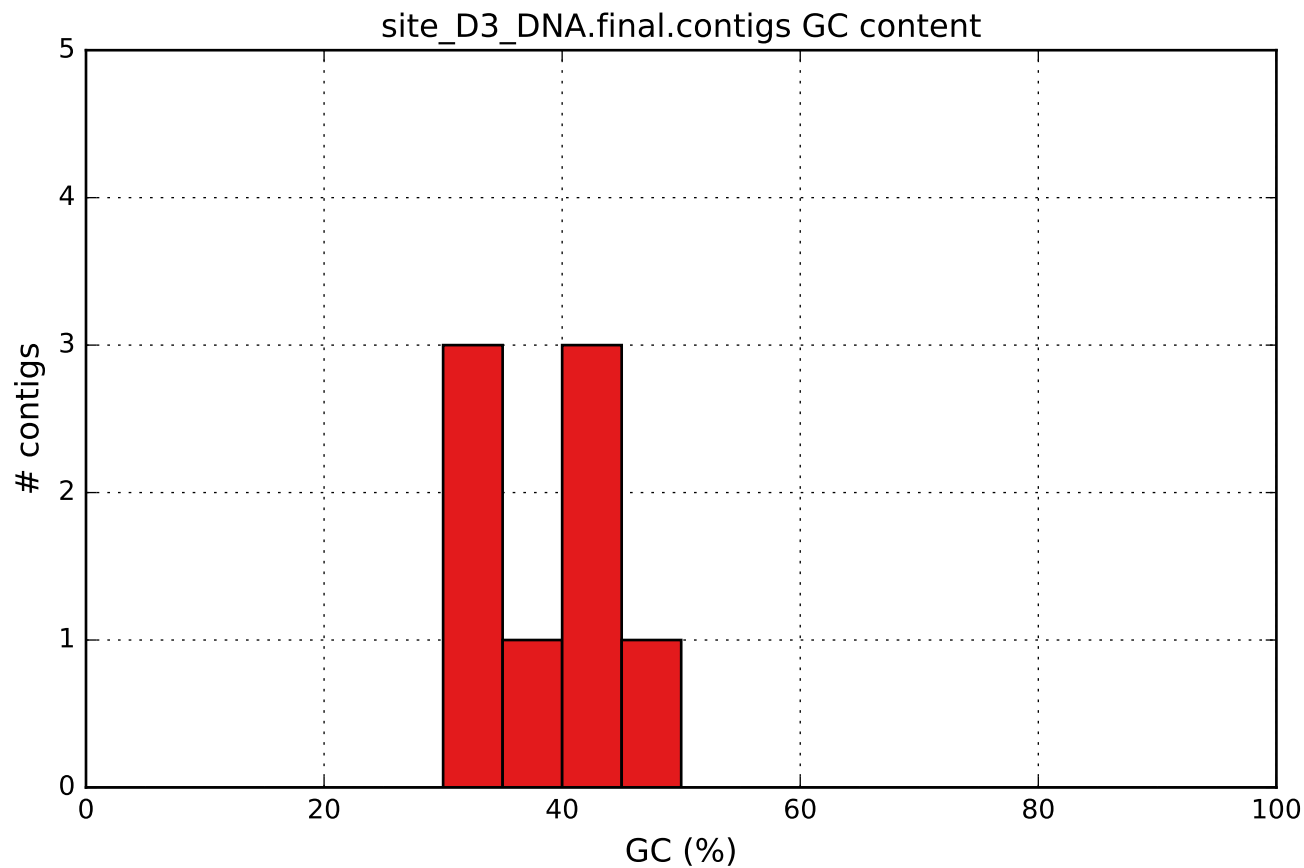
— site\_D3\_DNA.final.contigs



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

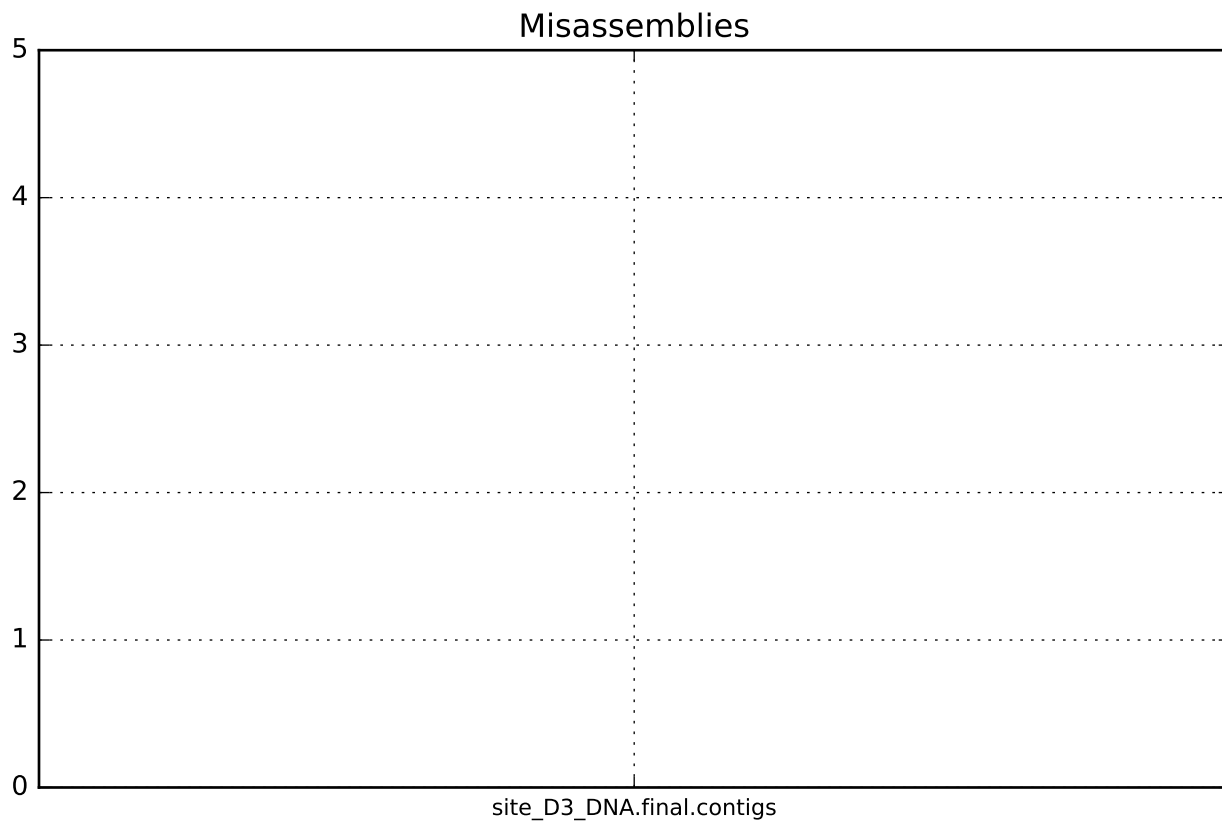


— site\_D3\_DNA.final.contigs      - - Reference

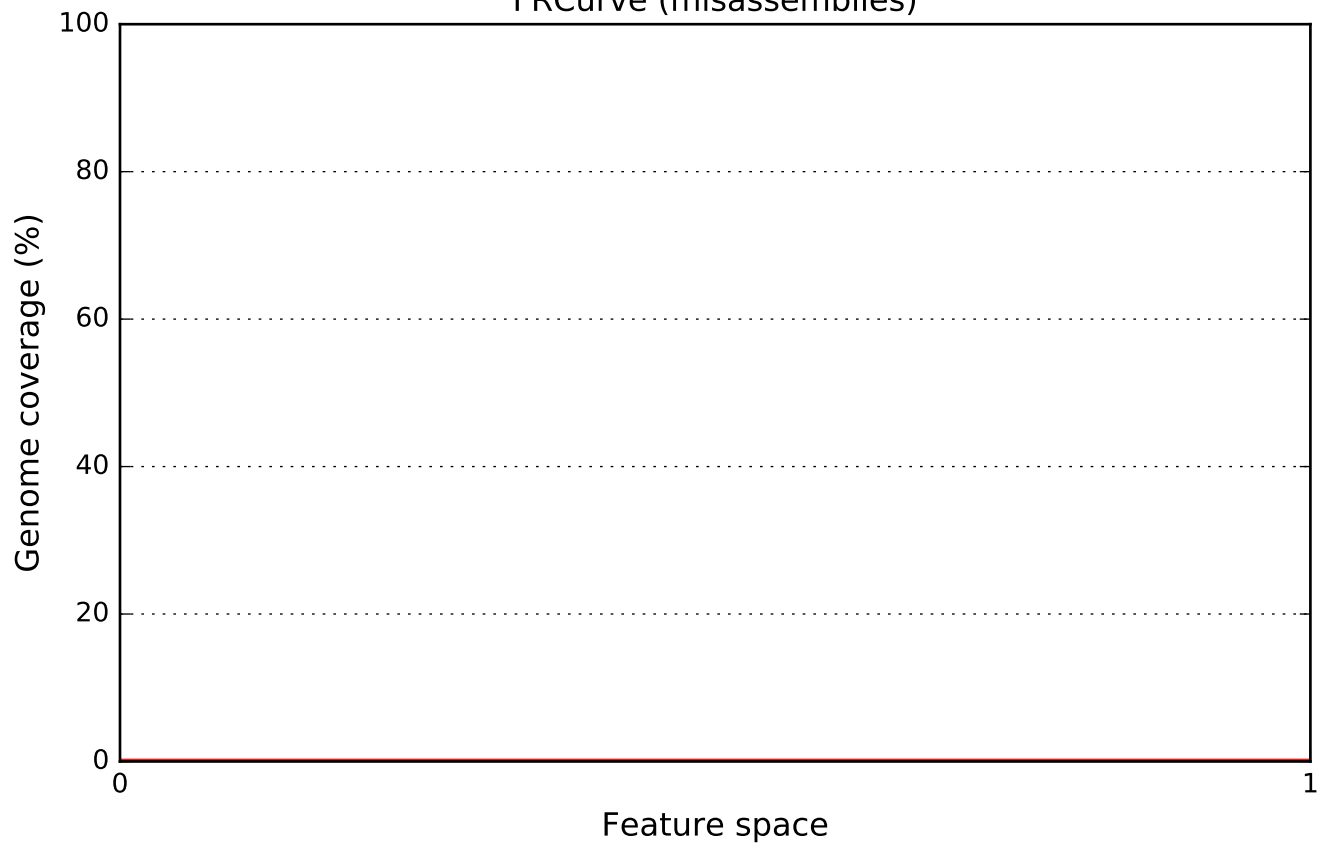


site\_D3\_DNA.final.contigs

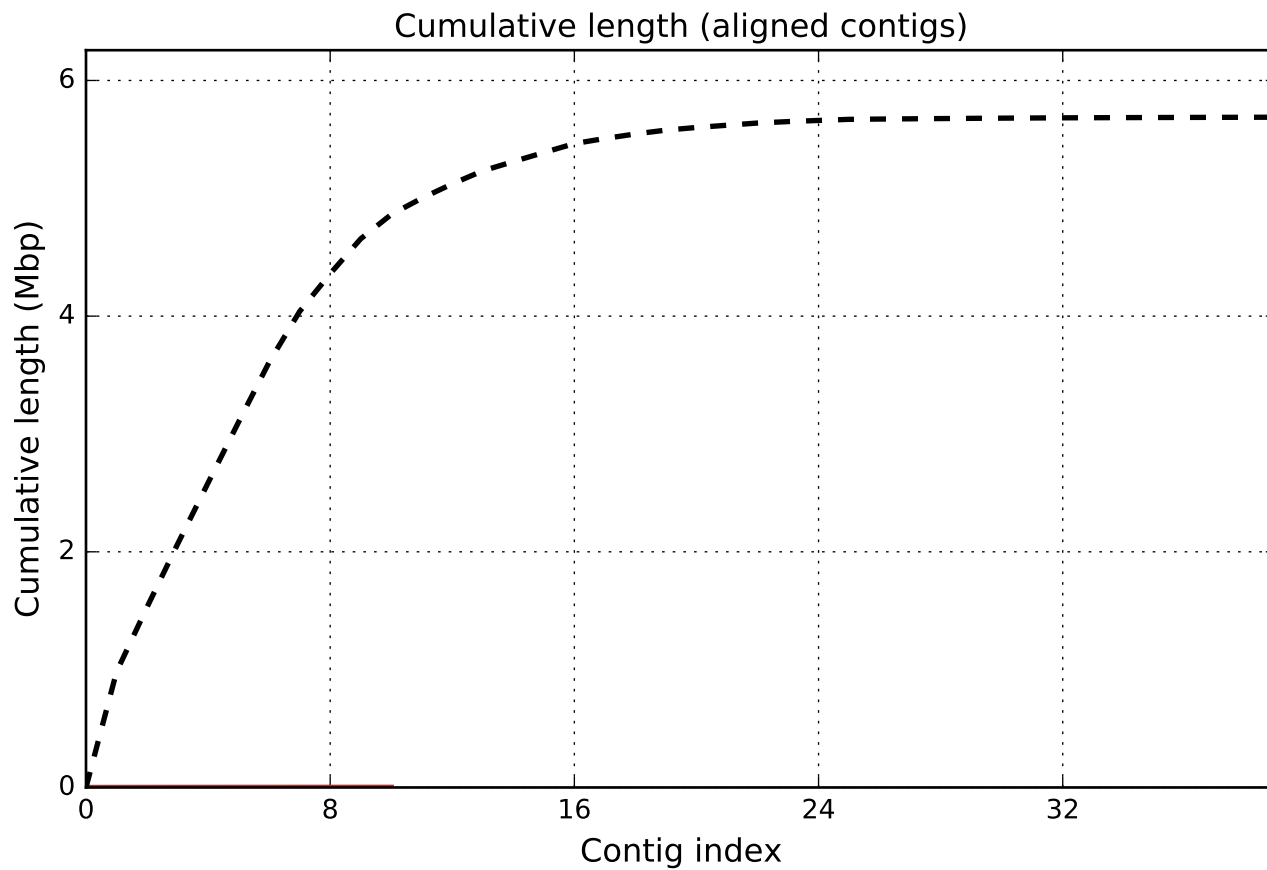




FRCurve (misassemblies)

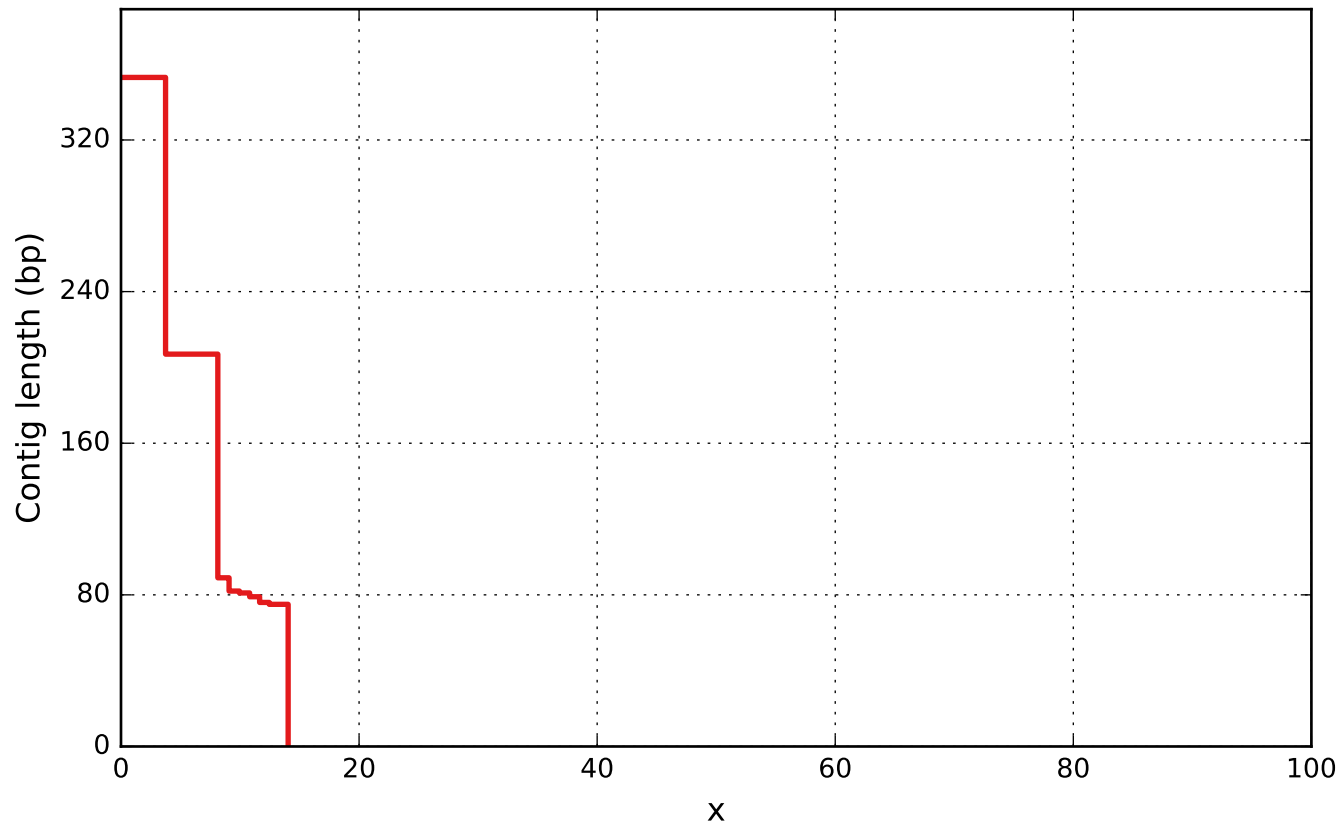


— site\_D3\_DNA.final.contigs



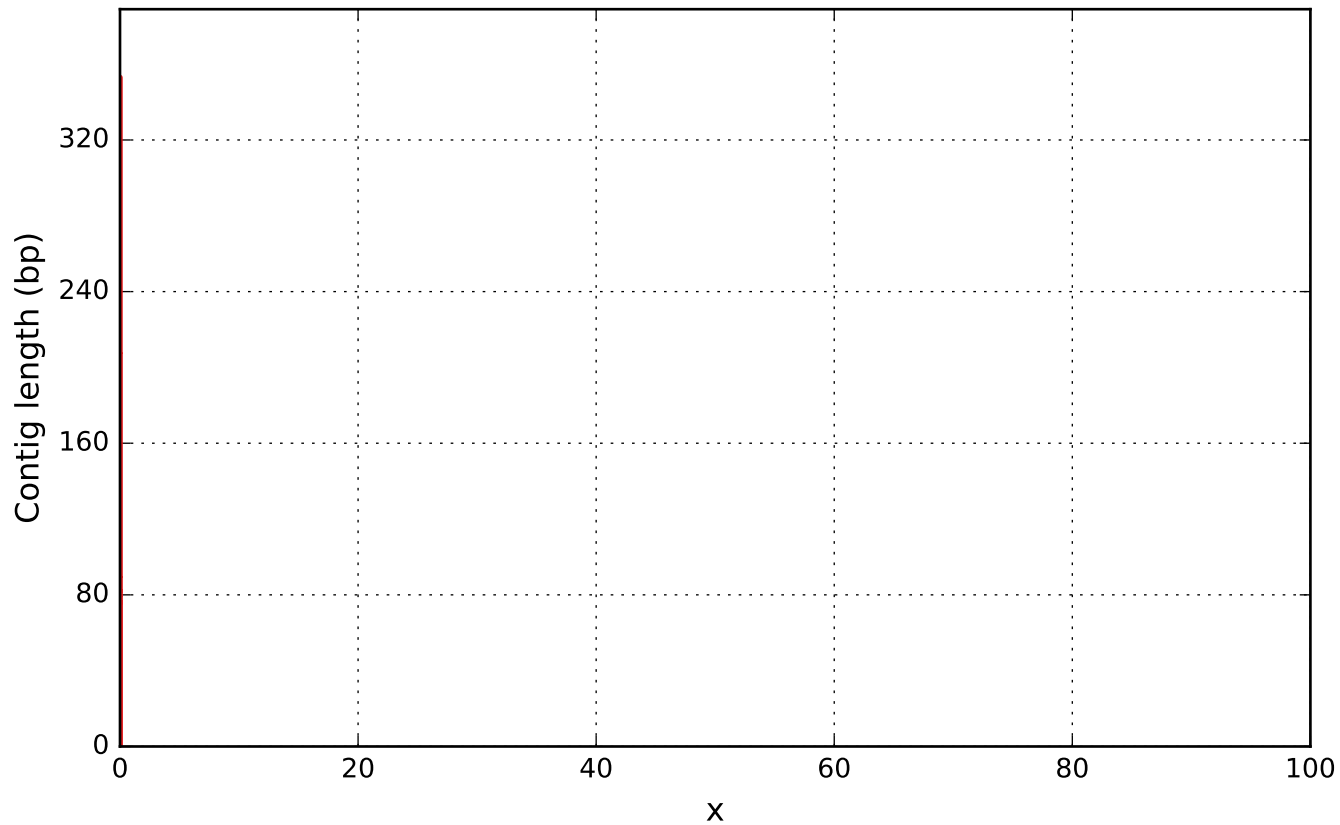
— site\_D3\_DNA.final.contigs    - - Reference

NAx



— site\_D3\_DNA.final.contigs

NGAx



— site\_D3\_DNA.final.contigs