

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)	7345
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	4
Largest contig	4433
Total length	8313
Reference length	3947342
GC (%)	40.94
Reference GC (%)	57.28
N50	4433
N75	1867
L50	1
L75	2
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 4 part
Unaligned length	8010
Genome fraction (%)	0.008
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	330.03
# indels per 100 kbp	0.00
Largest alignment	80
Total aligned length	303
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

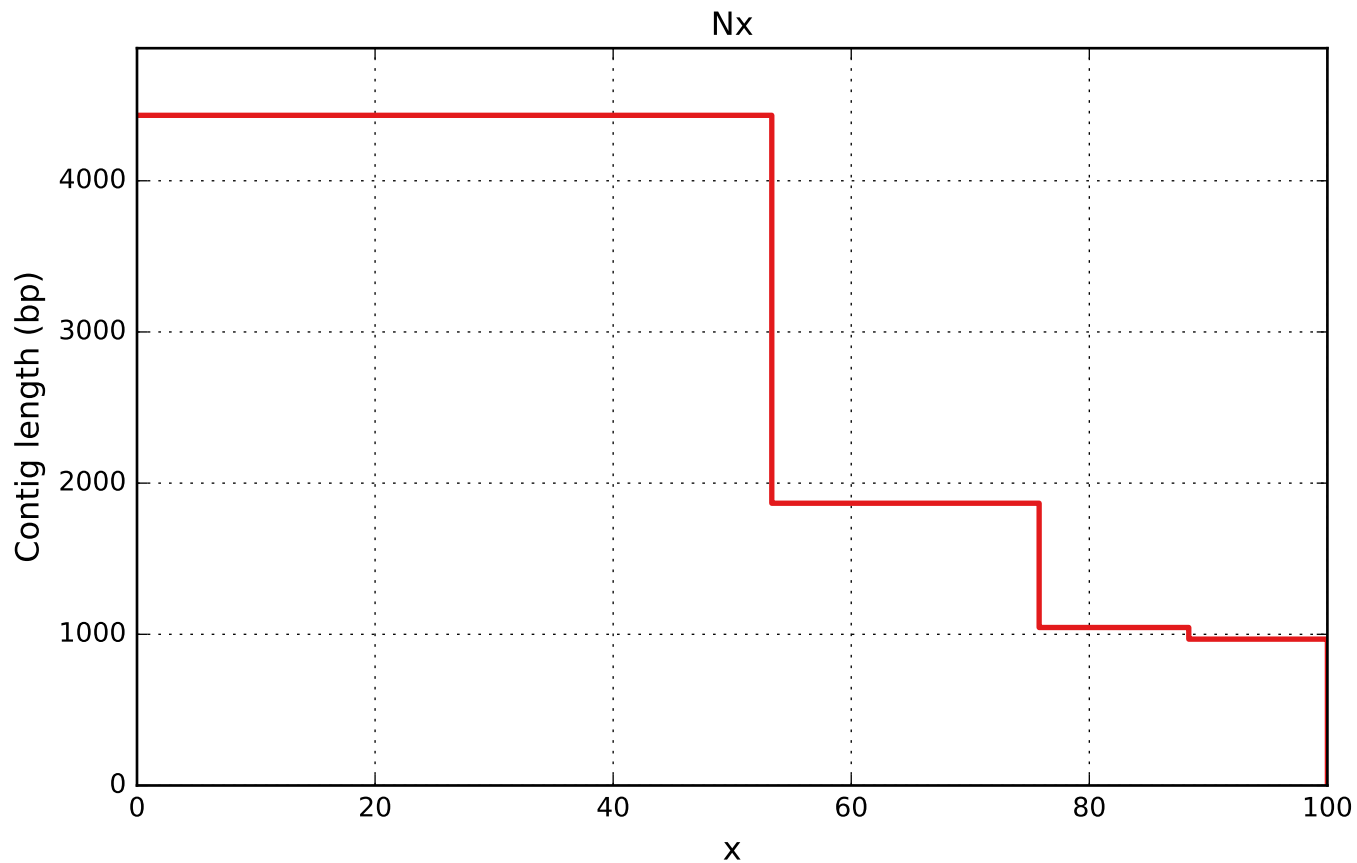
	site_D3_DNA.final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches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

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).

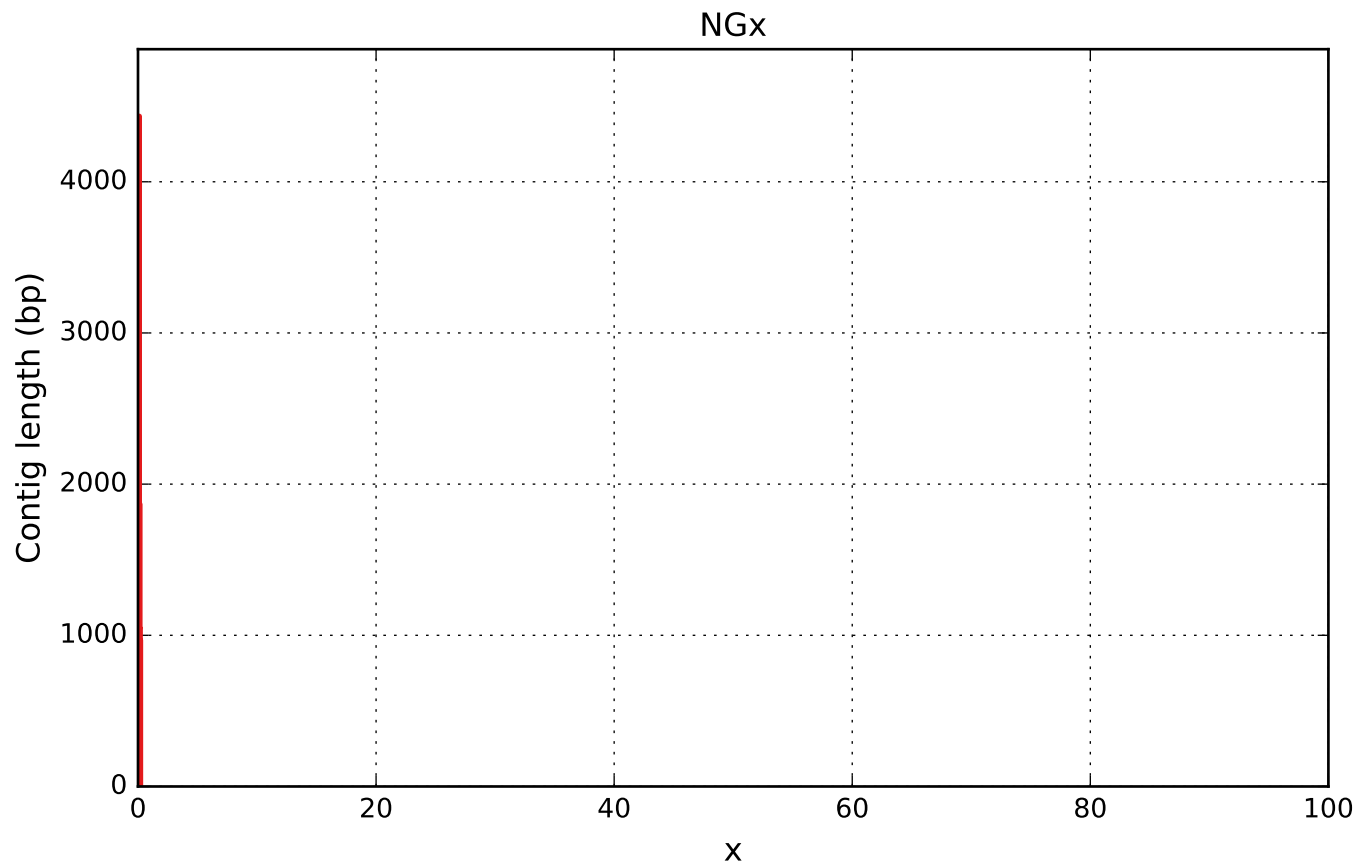
Unaligned report

	site_D3_DNA.final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	4
Partially unaligned length	8010
# N's	0

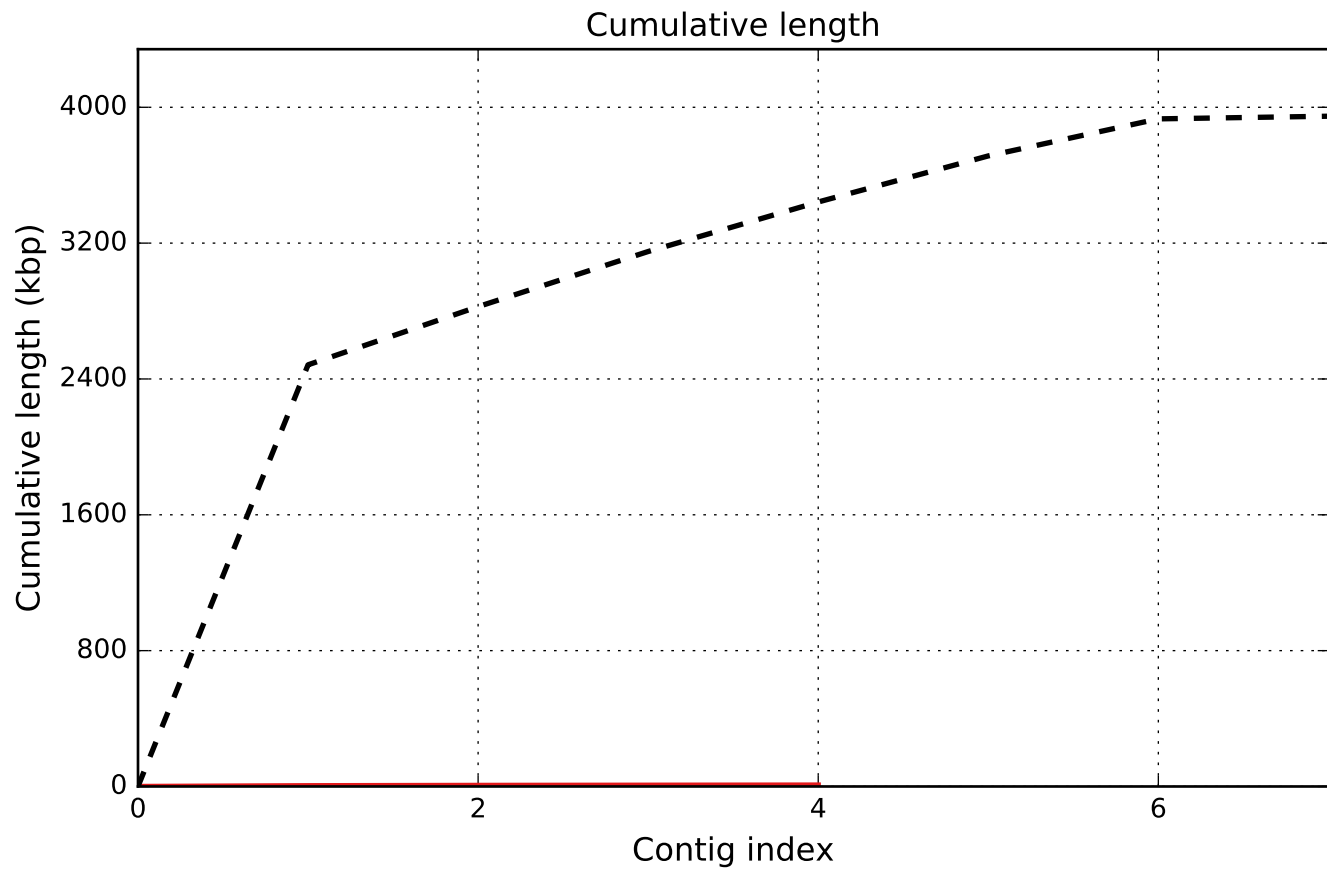
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

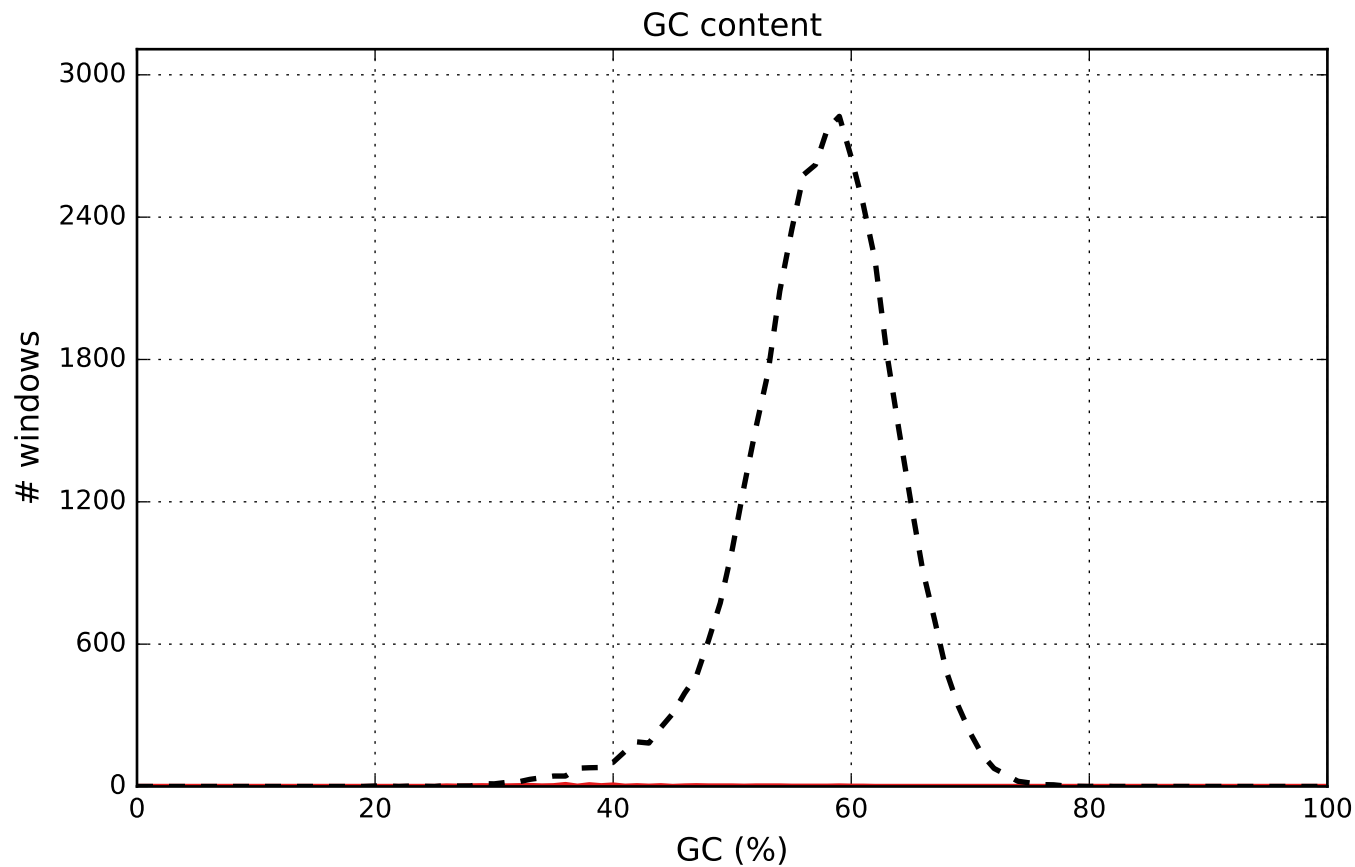


— site_D3_DNA.final.contigs

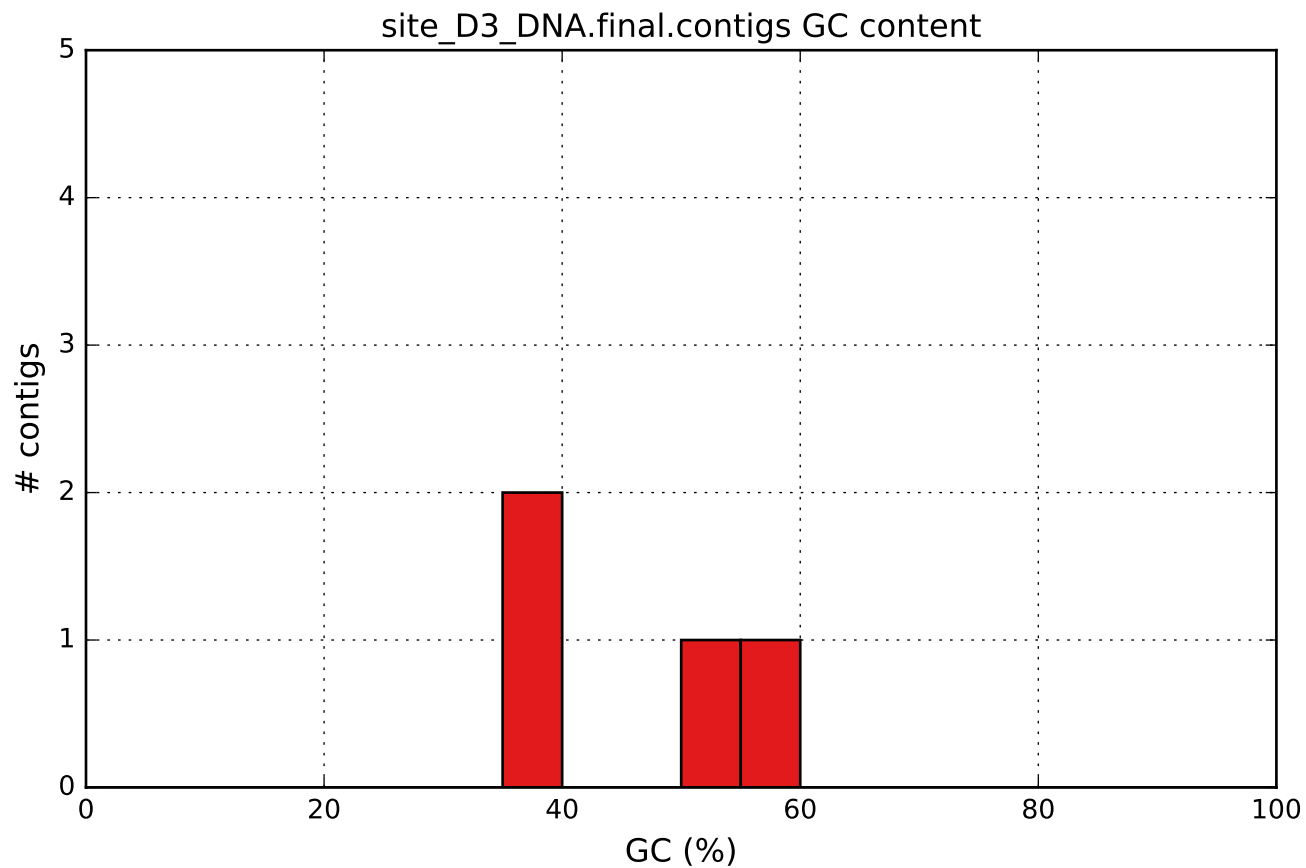


— site_D3_DNA.final.contigs

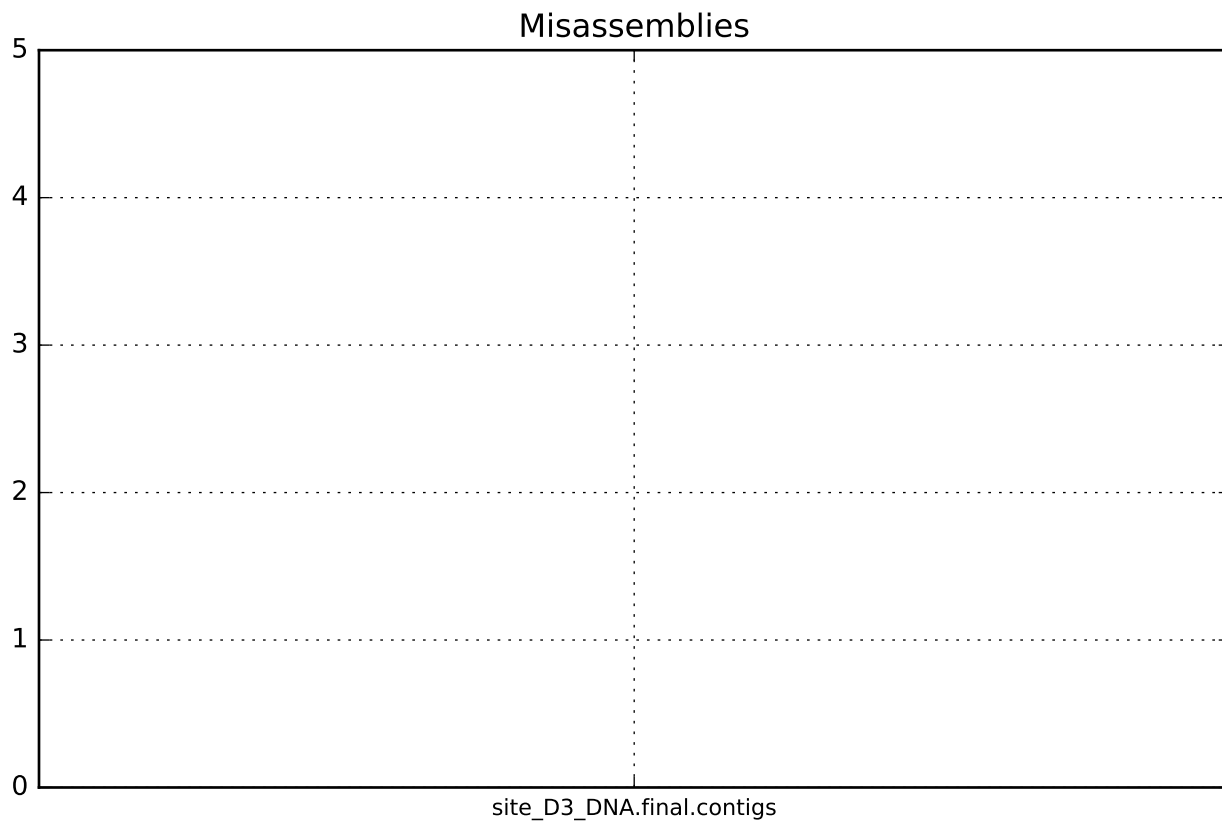




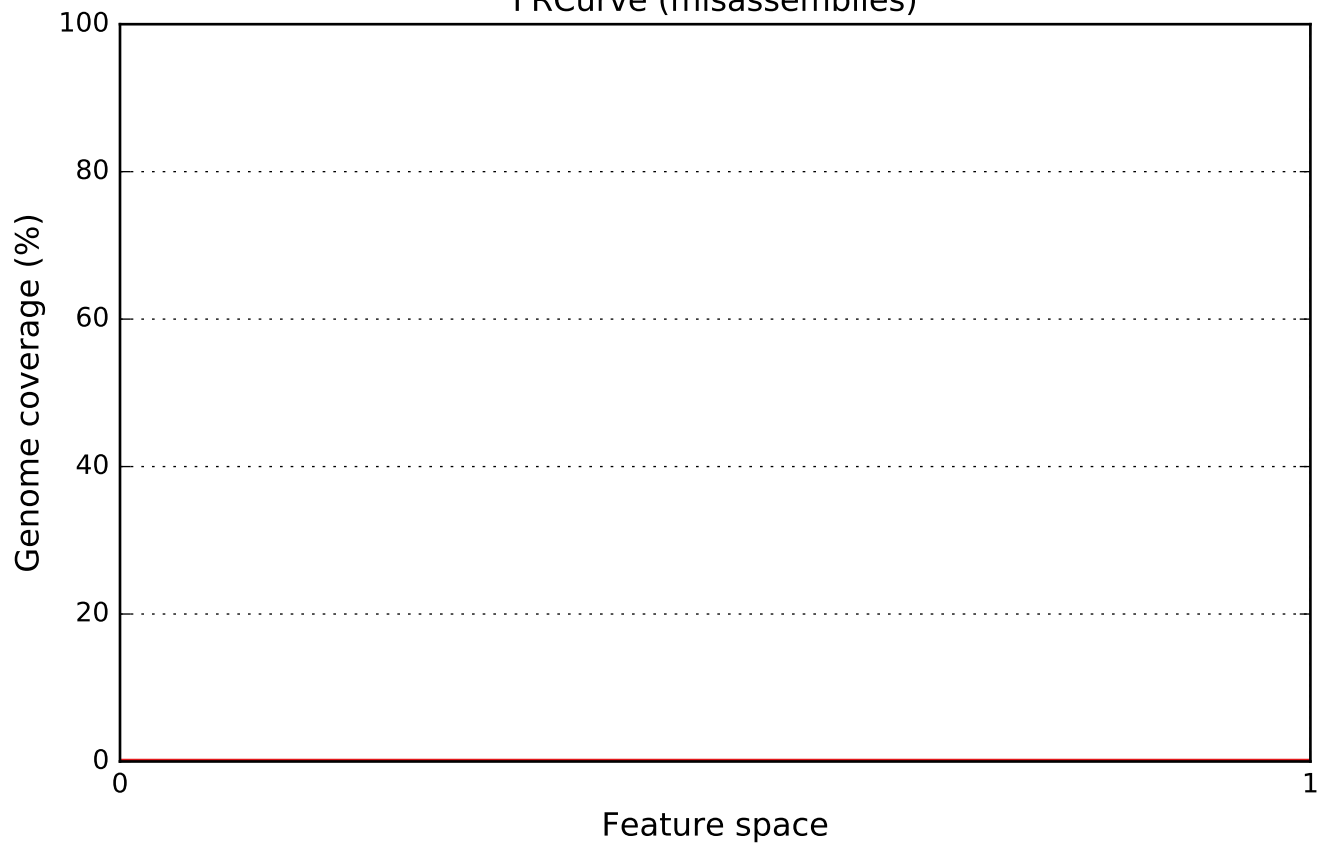
— site_D3_DNA.final.contigs - - Reference



site_D3_DNA.final.contigs

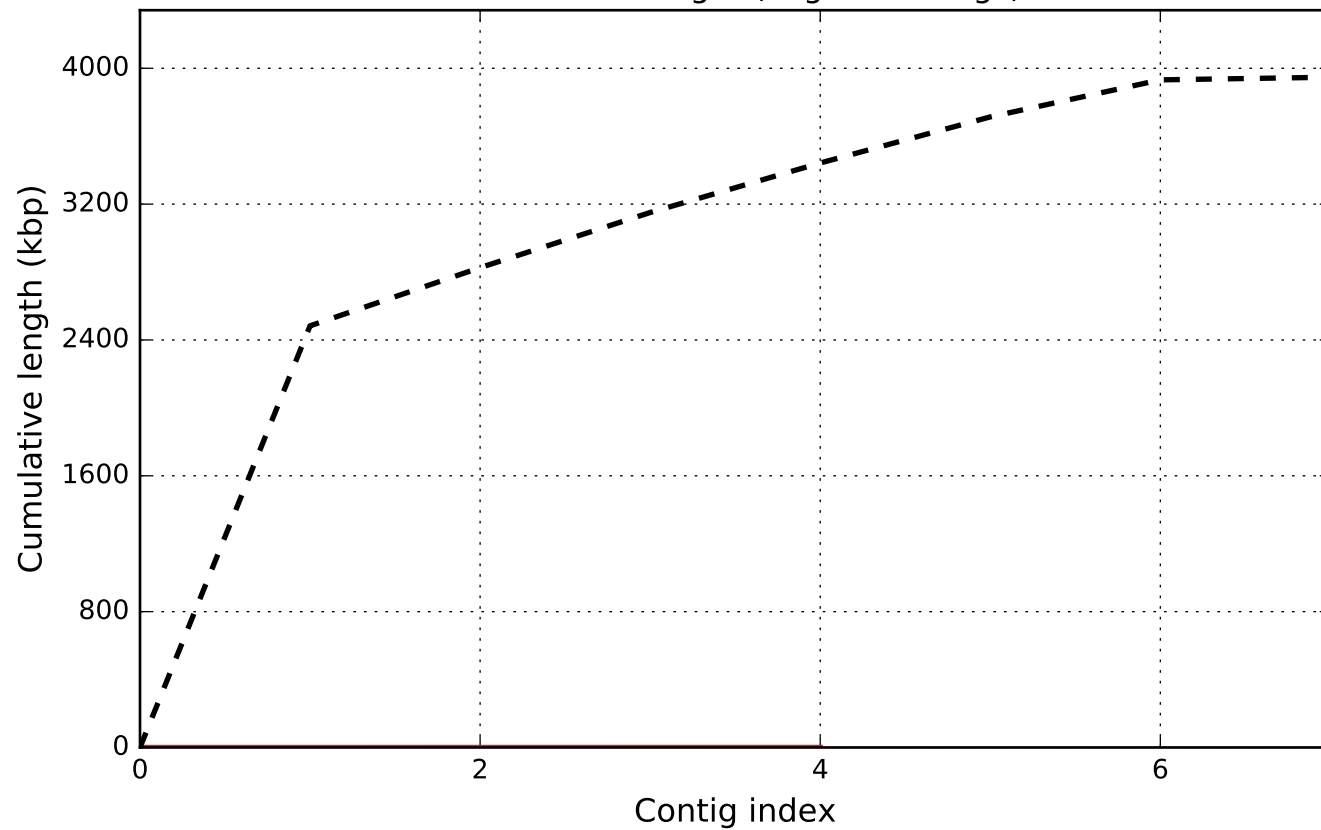


FRCurve (misassemblies)



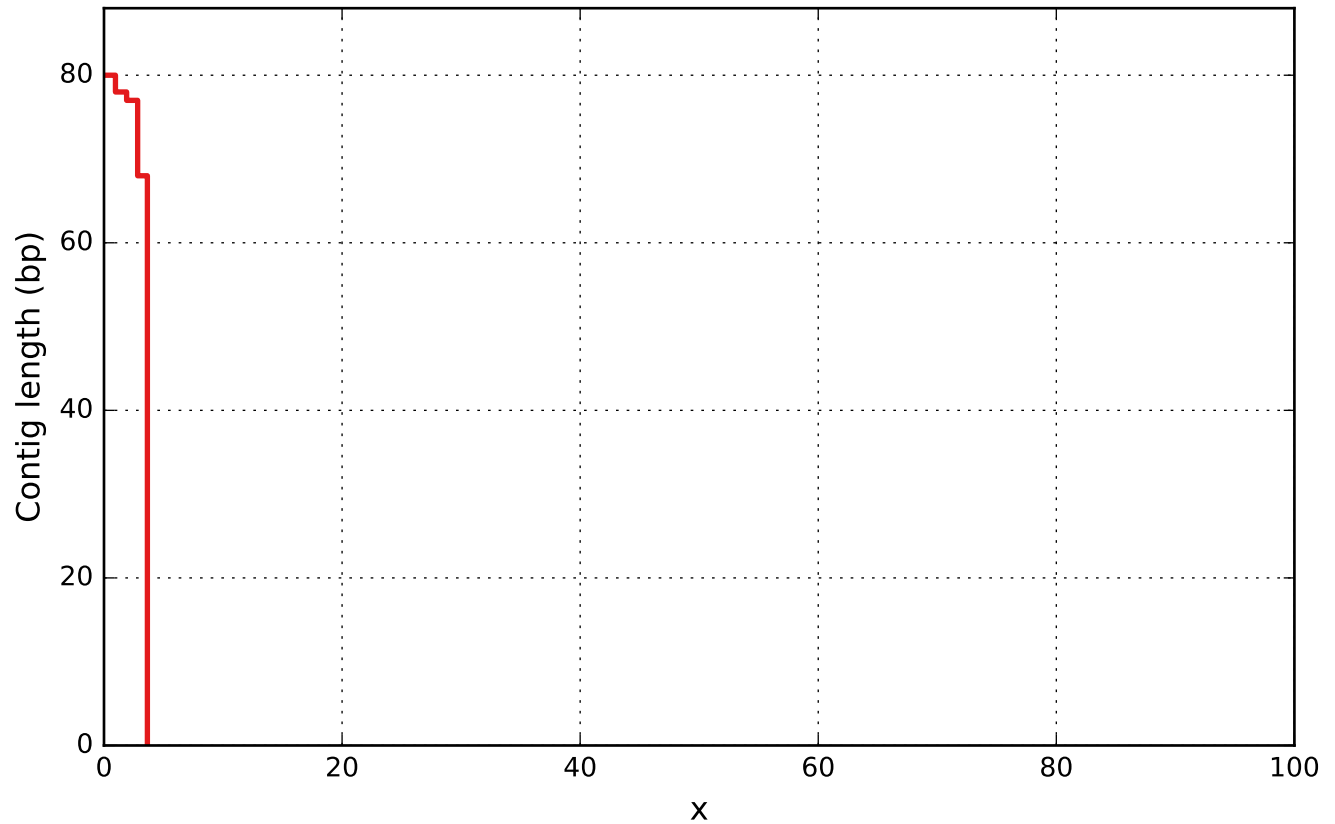
— site_D3_DNA.final.contigs

Cumulative length (aligned contigs)



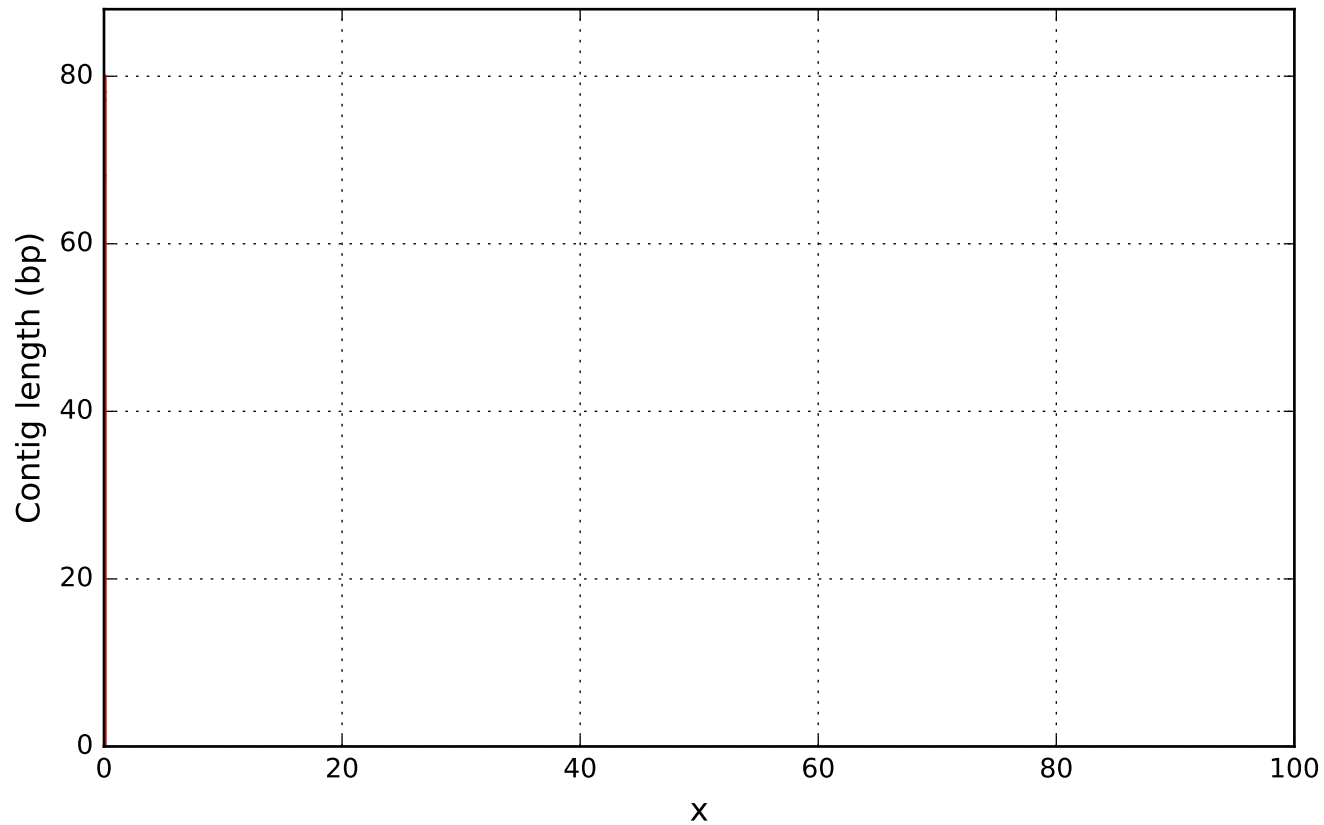
— site_D3_DNA.final.contigs - - Reference

NAx



— site_D3_DNA.final.contigs

NGAx



— site_D3_DNA.final.contigs