

Report

	site_D3_DNA.final.contigs
# contigs (>= 1000 bp)	4
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	6579
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	13
Largest contig	2250
Total length	12651
Reference length	5344419
GC (%)	50.99
Reference GC (%)	63.27
N50	1123
N75	714
L50	4
L75	8
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# unaligned mis. contigs	1
# unaligned contigs	0 + 6 part
Unaligned length	6025
Genome fraction (%)	0.058
Duplication ratio	2.136
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3030.30
# indels per 100 kbp	257.90
Largest alignment	1387
Total aligned length	3647
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

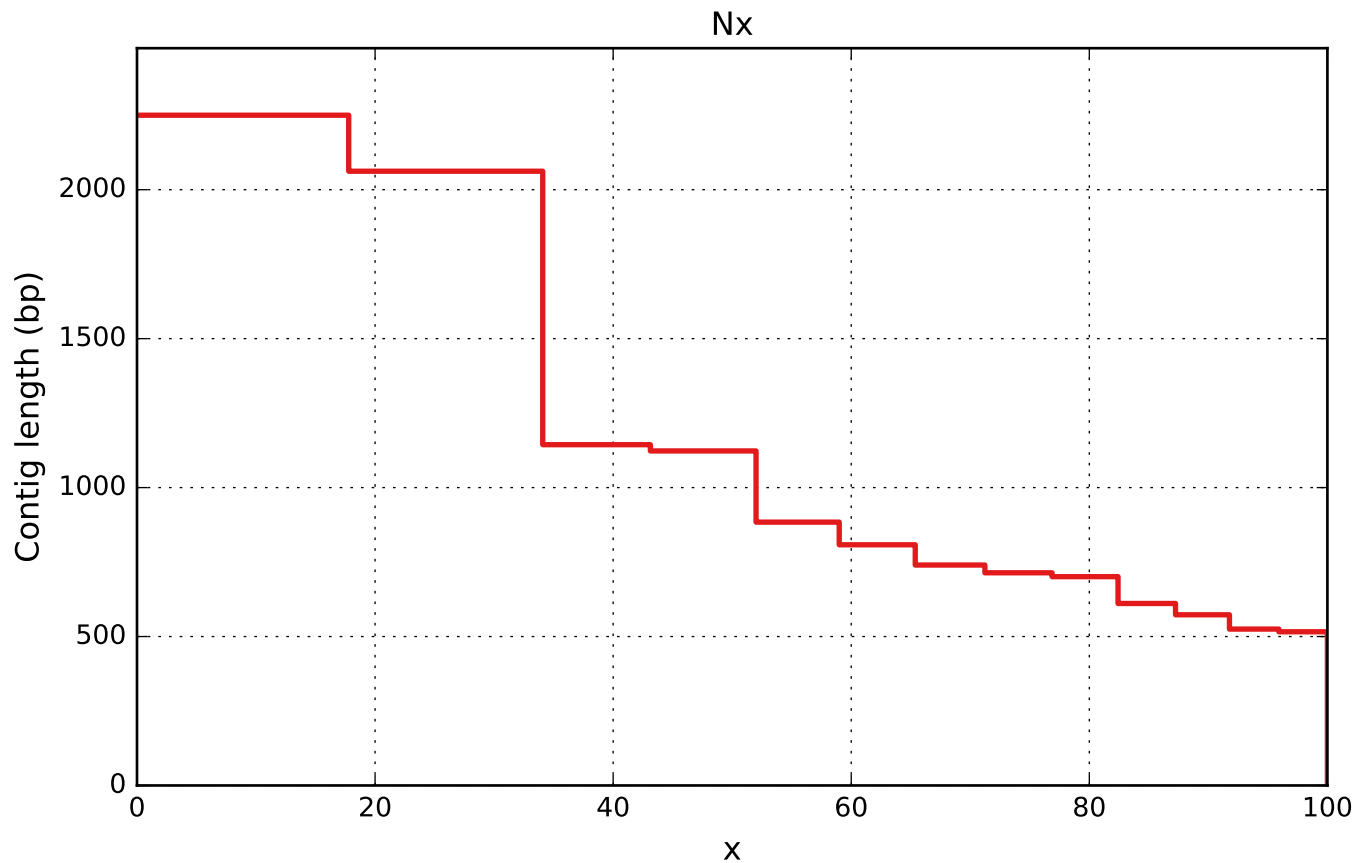
	site_D3_DNA.final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	1
# unaligned mis. contigs	1
# mismatches	94
# indels	8
# indels (<= 5 bp)	8
# indels (> 5 bp)	0
Indels length	8

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).

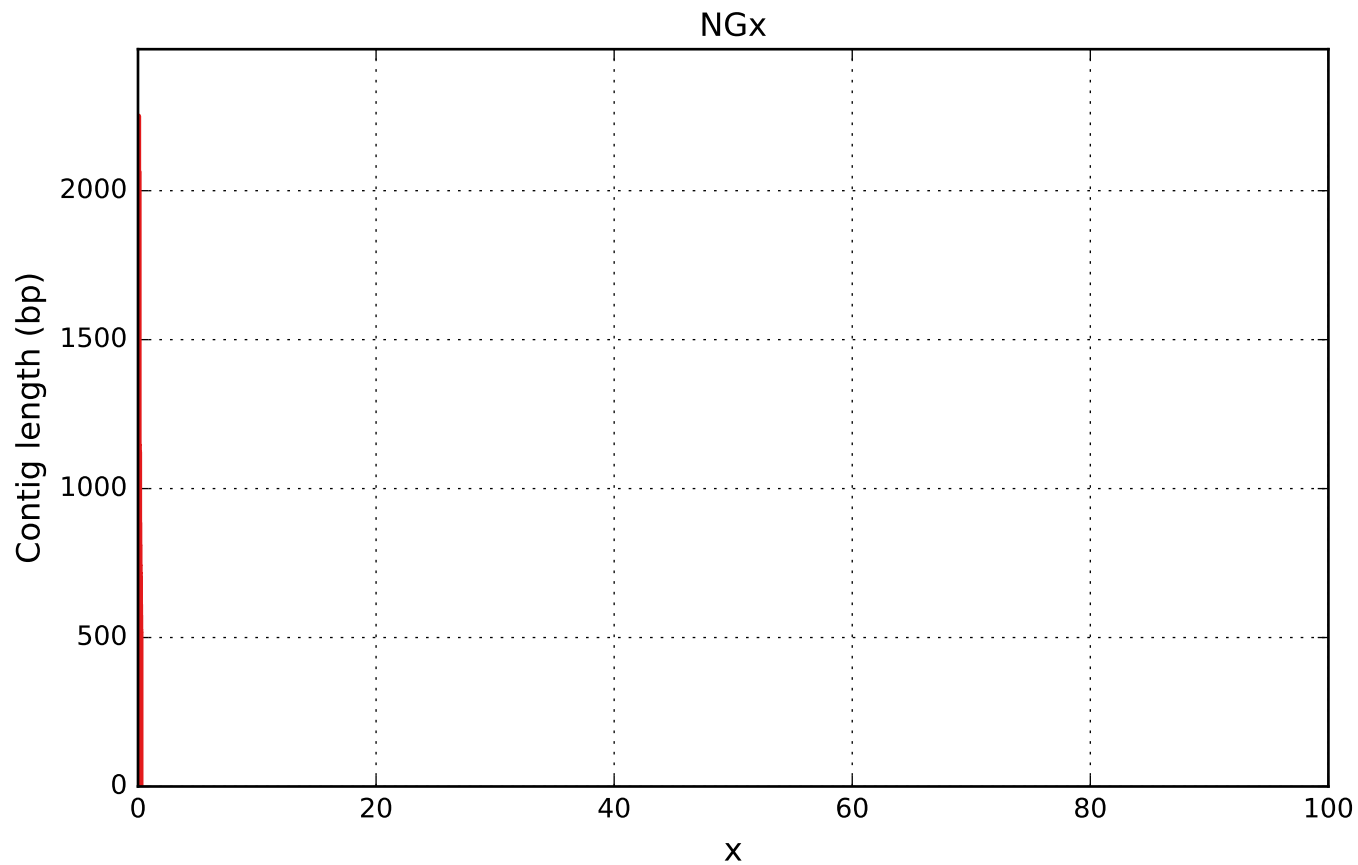
Unaligned report

	site_D3_DNA.final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	6
Partially unaligned length	6025
# N's	0

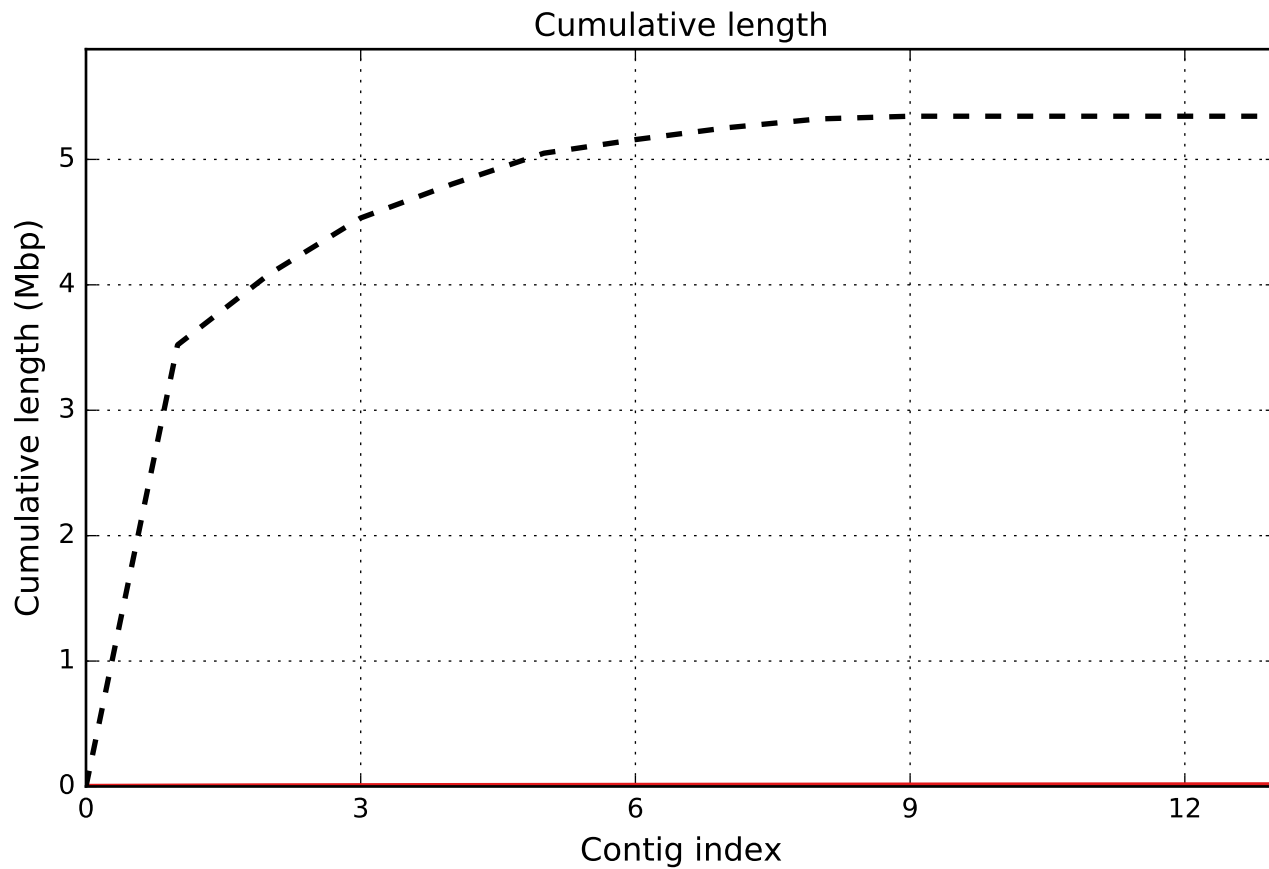
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

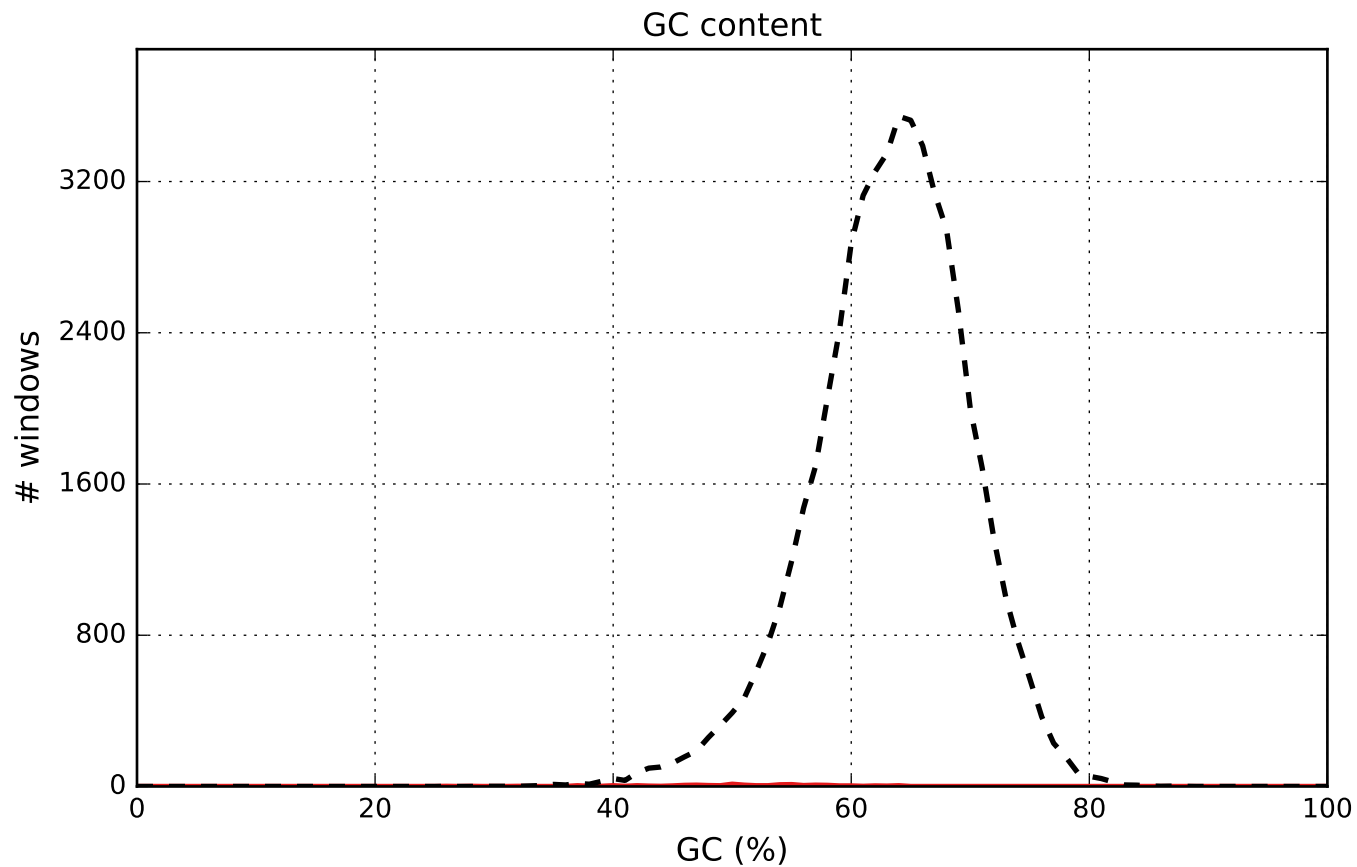


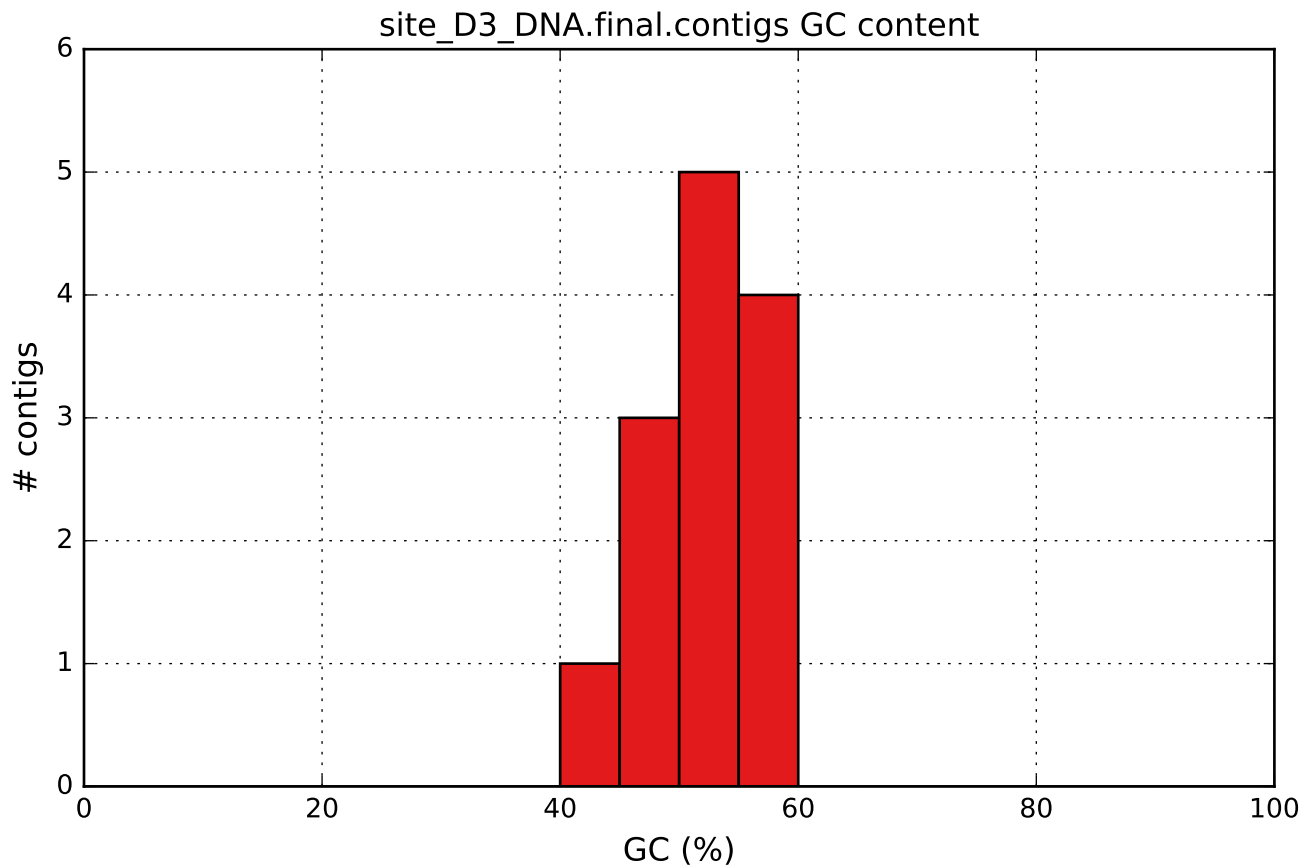
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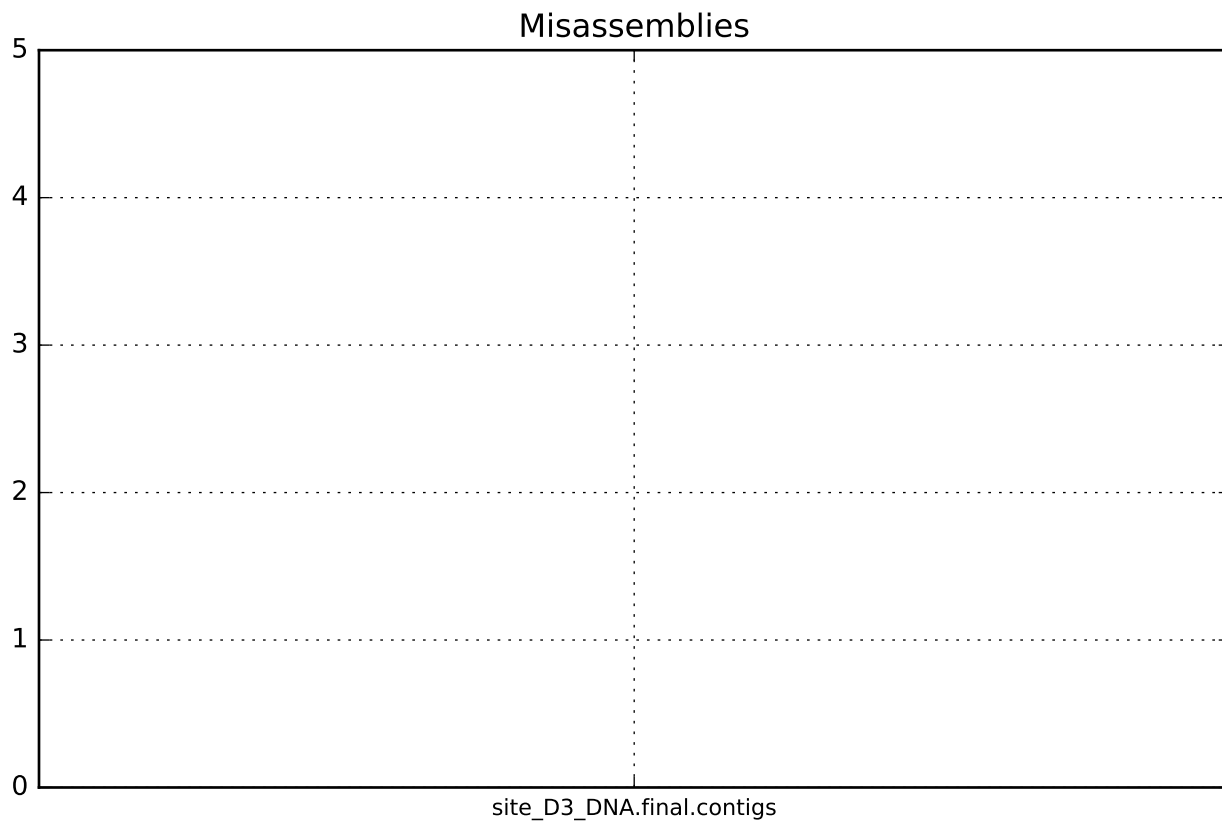
— site_D3_DNA.final.contigs



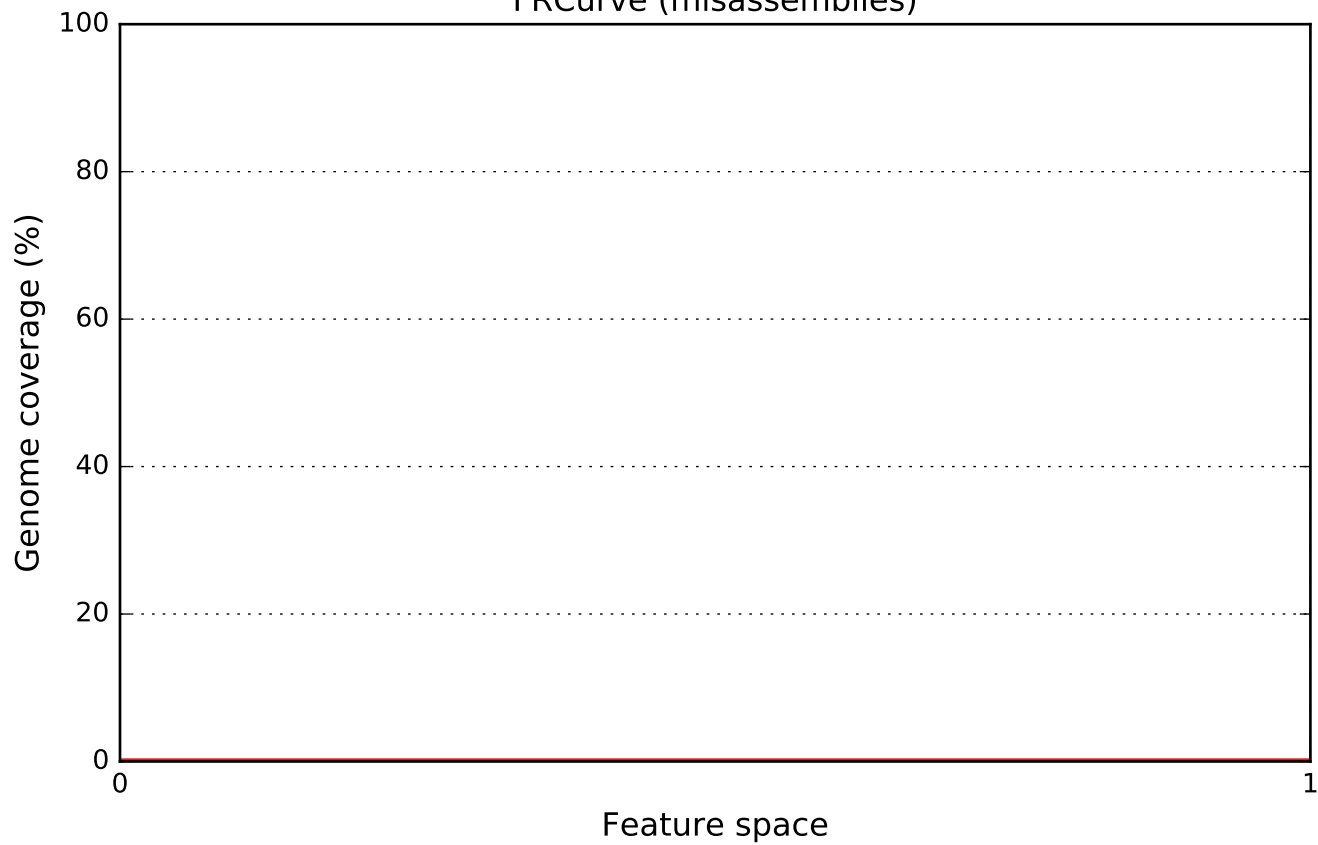




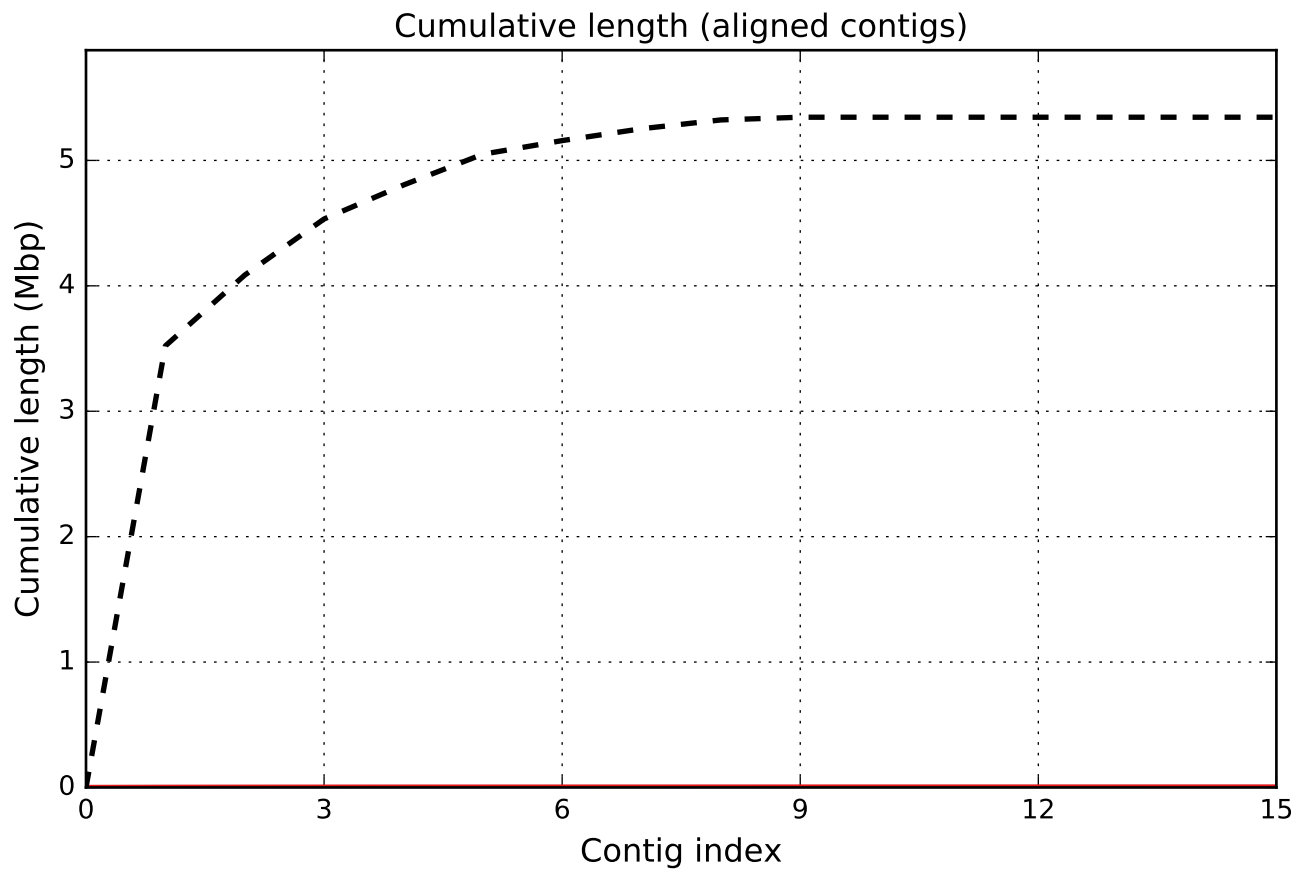
site_D3_DNA.final.contigs

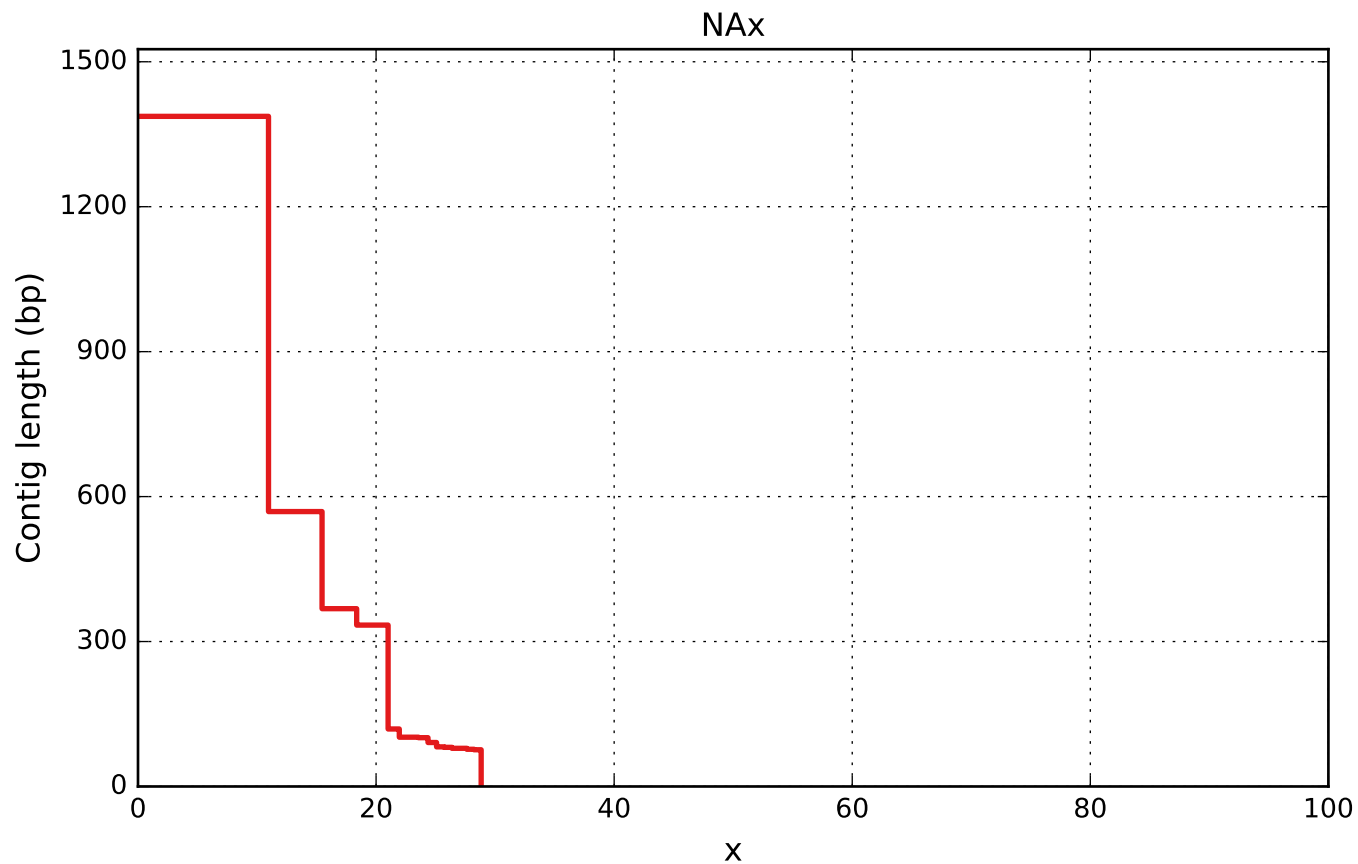


FRCurve (misassemblies)

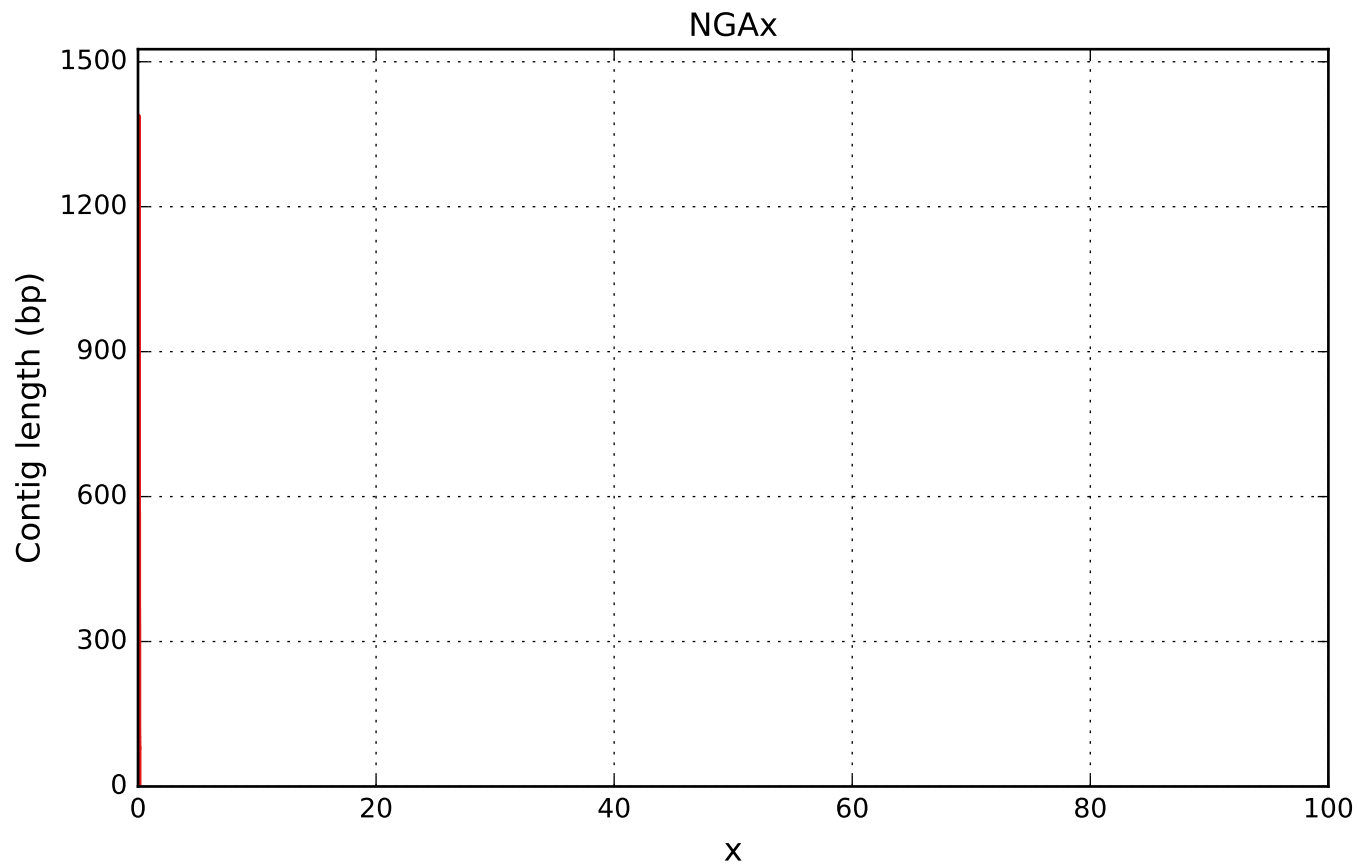


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