

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)	4612
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	9
Largest contig	2250
Total length	8896
Reference length	4610381
GC (%)	53.07
Reference GC (%)	59.05
N50	1123
N75	731
L50	3
L75	6
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	1
# unaligned contigs	0 + 6 part
Unaligned length	5039
Genome fraction (%)	0.064
Duplication ratio	1.304
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2670.72
# indels per 100 kbp	304.26
Largest alignment	1387
Total aligned length	2961
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

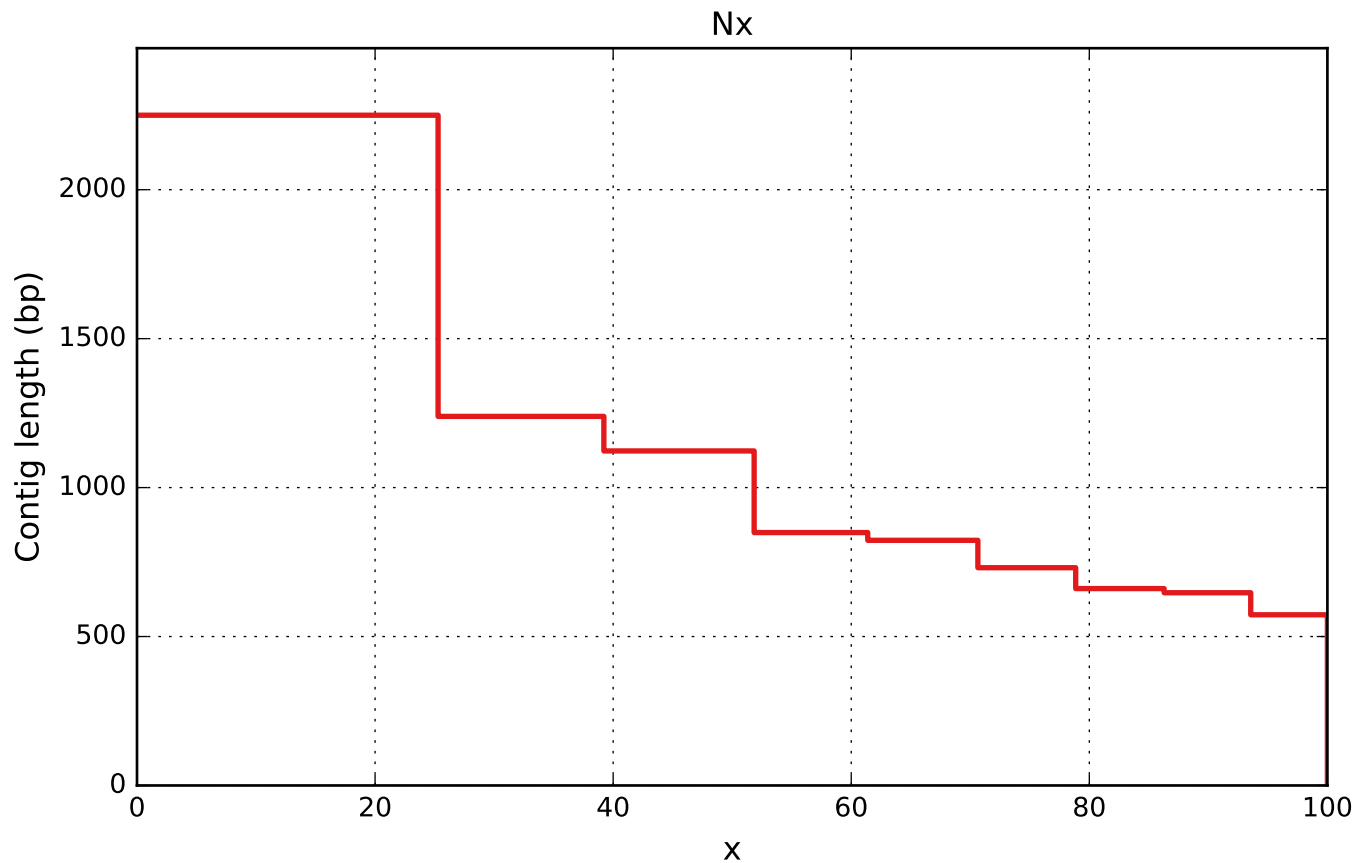
	site_D3_DNA.final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	1
# possible misassemblies	1
# local misassemblies	0
# unaligned mis. contigs	1
# mismatches	79
# indels	9
# indels (<= 5 bp)	9
# indels (> 5 bp)	0
Indels length	9

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).

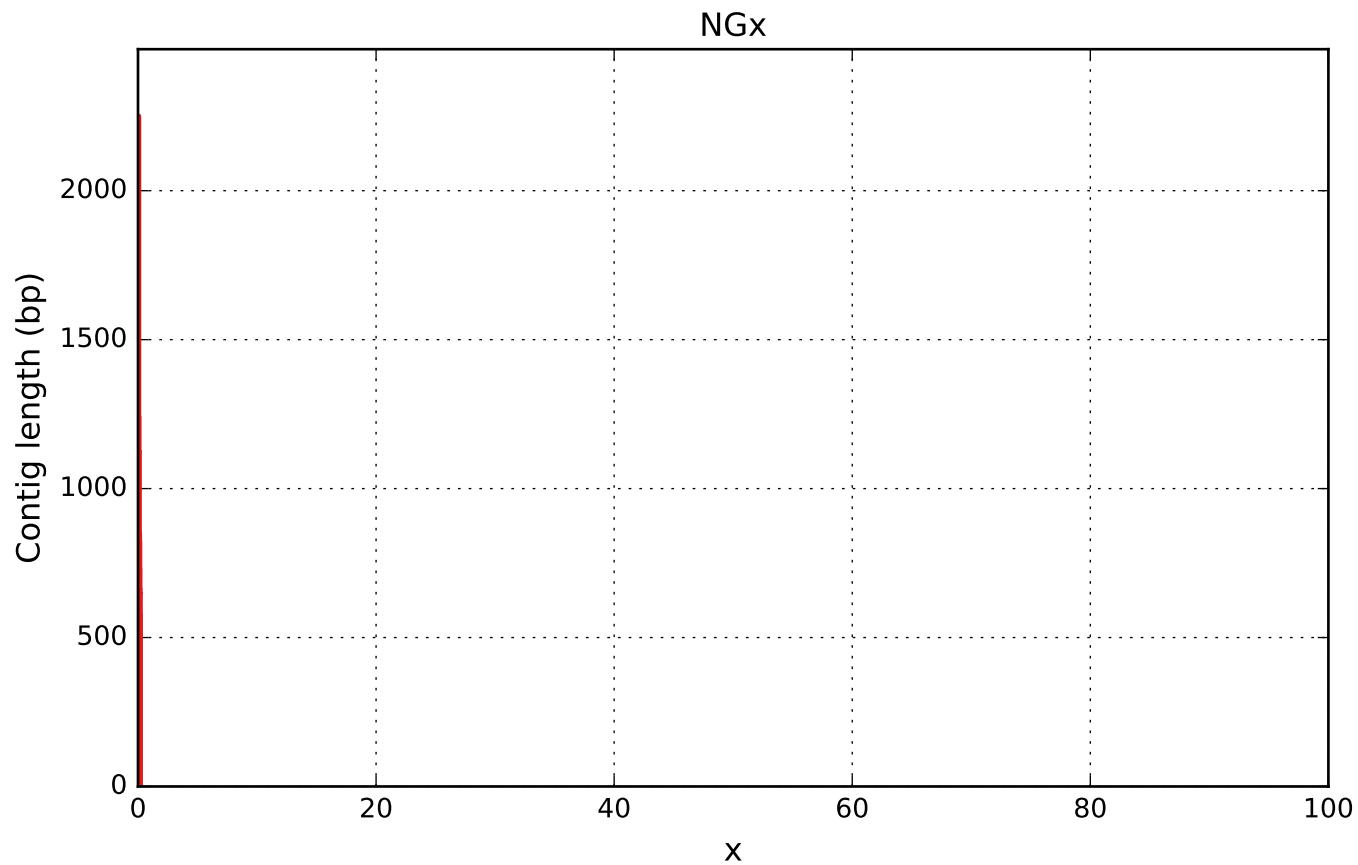
Unaligned report

	site_D3_DNA.final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	6
Partially unaligned length	5039
# N's	0

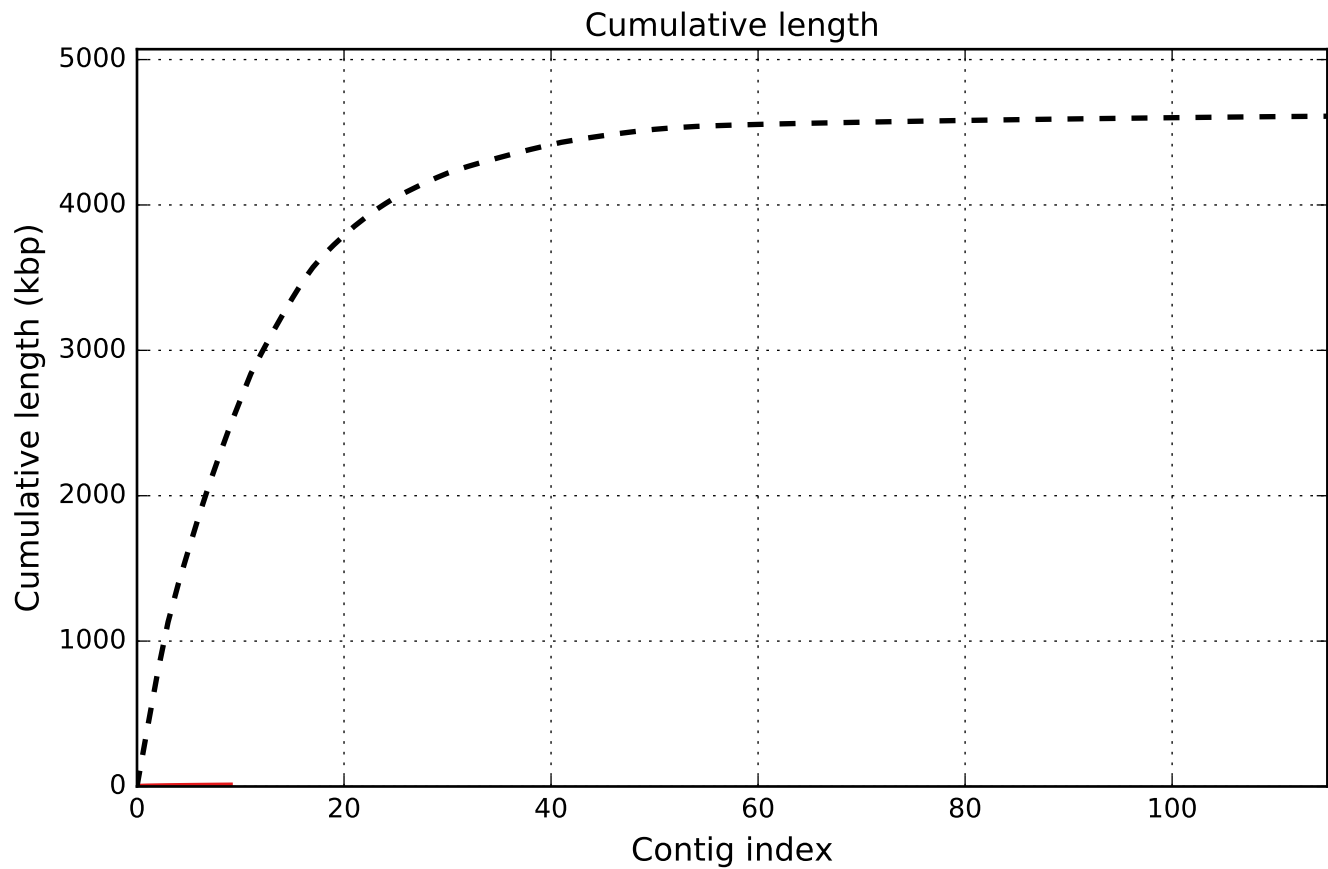
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

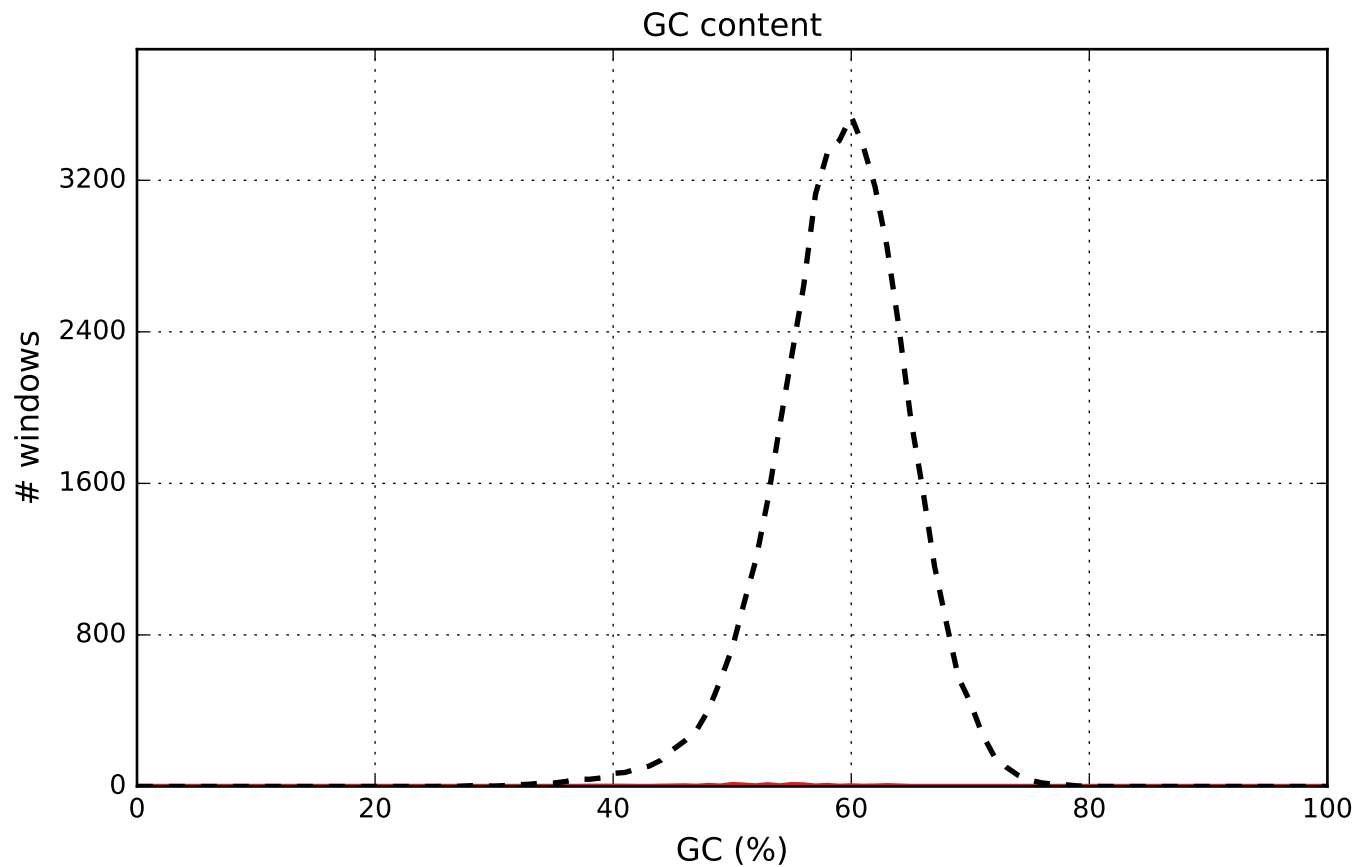


— site_D3_DNA.final.contigs

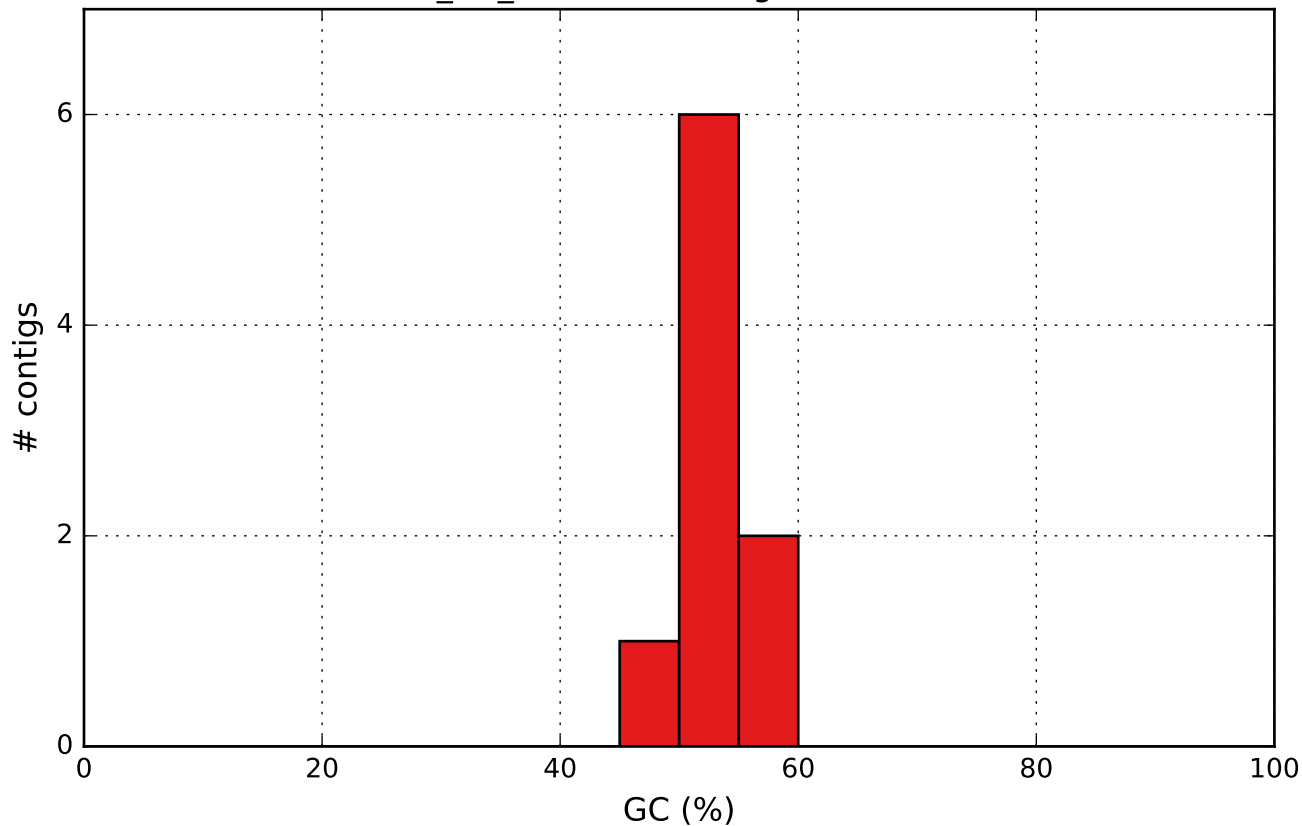


— site_D3_DNA.final.contigs

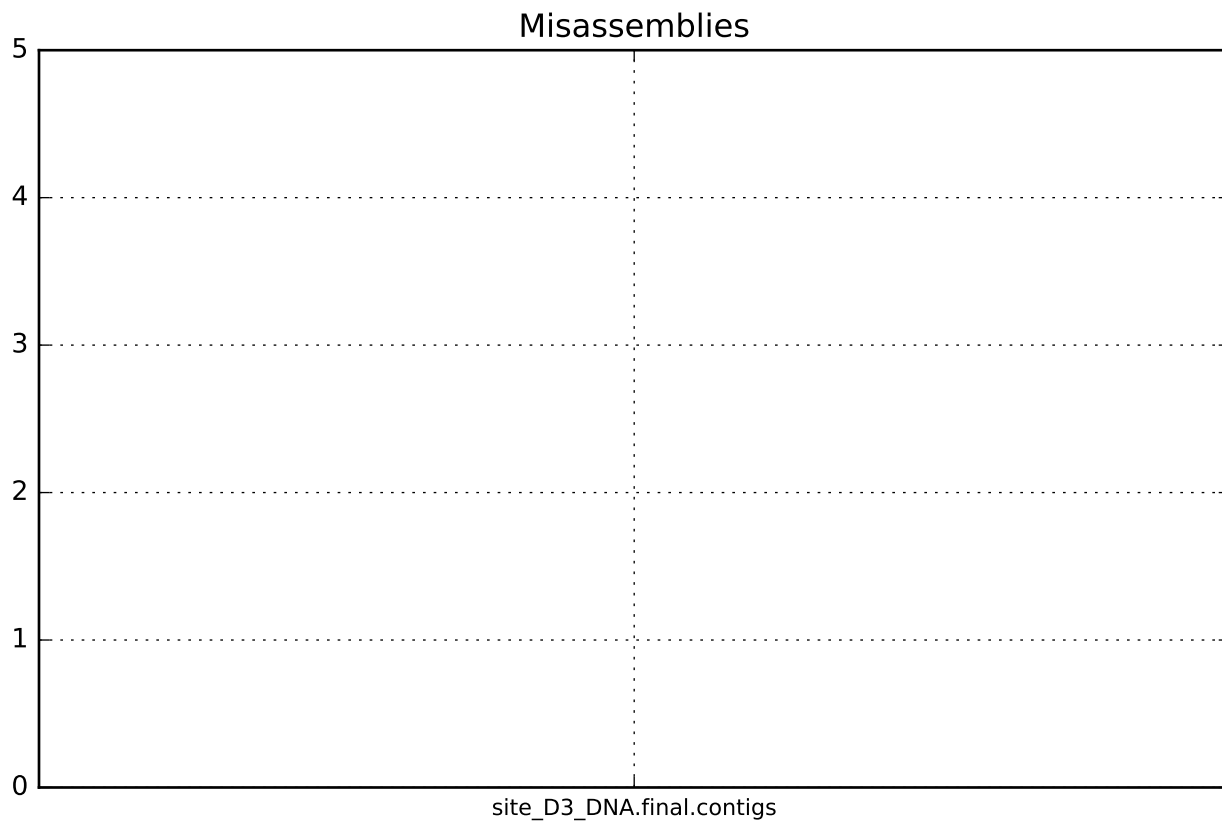




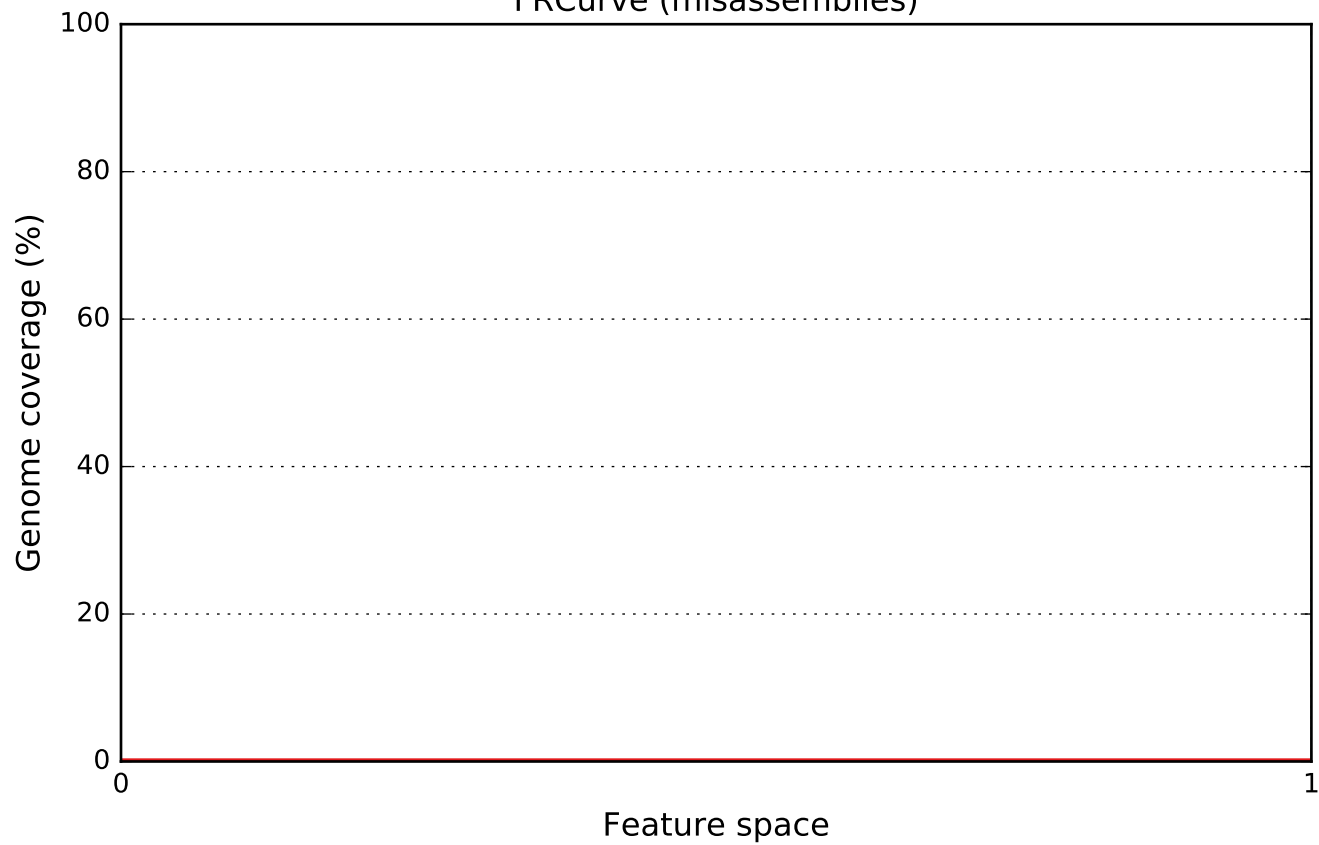
site_D3_DNA.final.contigs GC content



site_D3_DNA.final.contigs

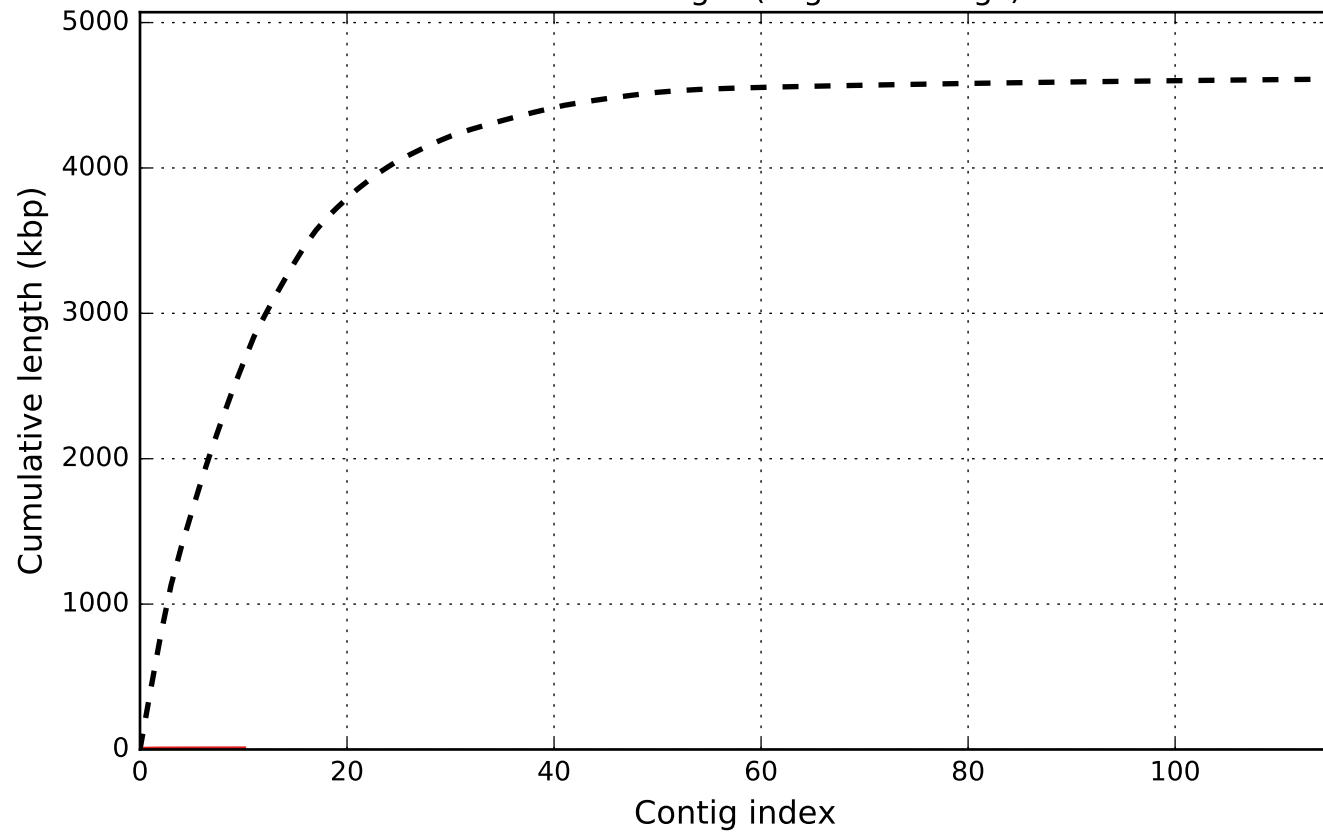


FRCurve (misassemblies)

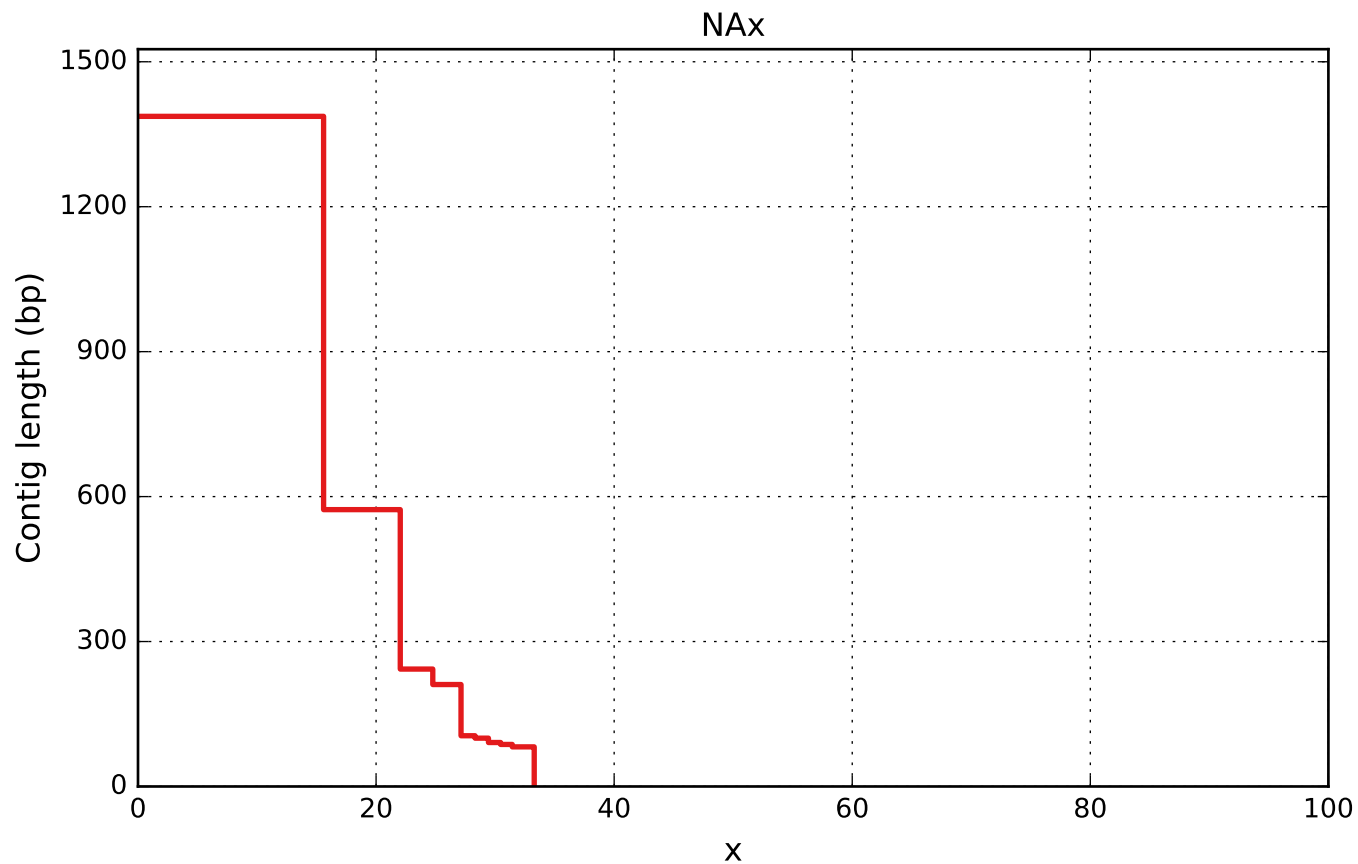


— site_D3_DNA.final.contigs

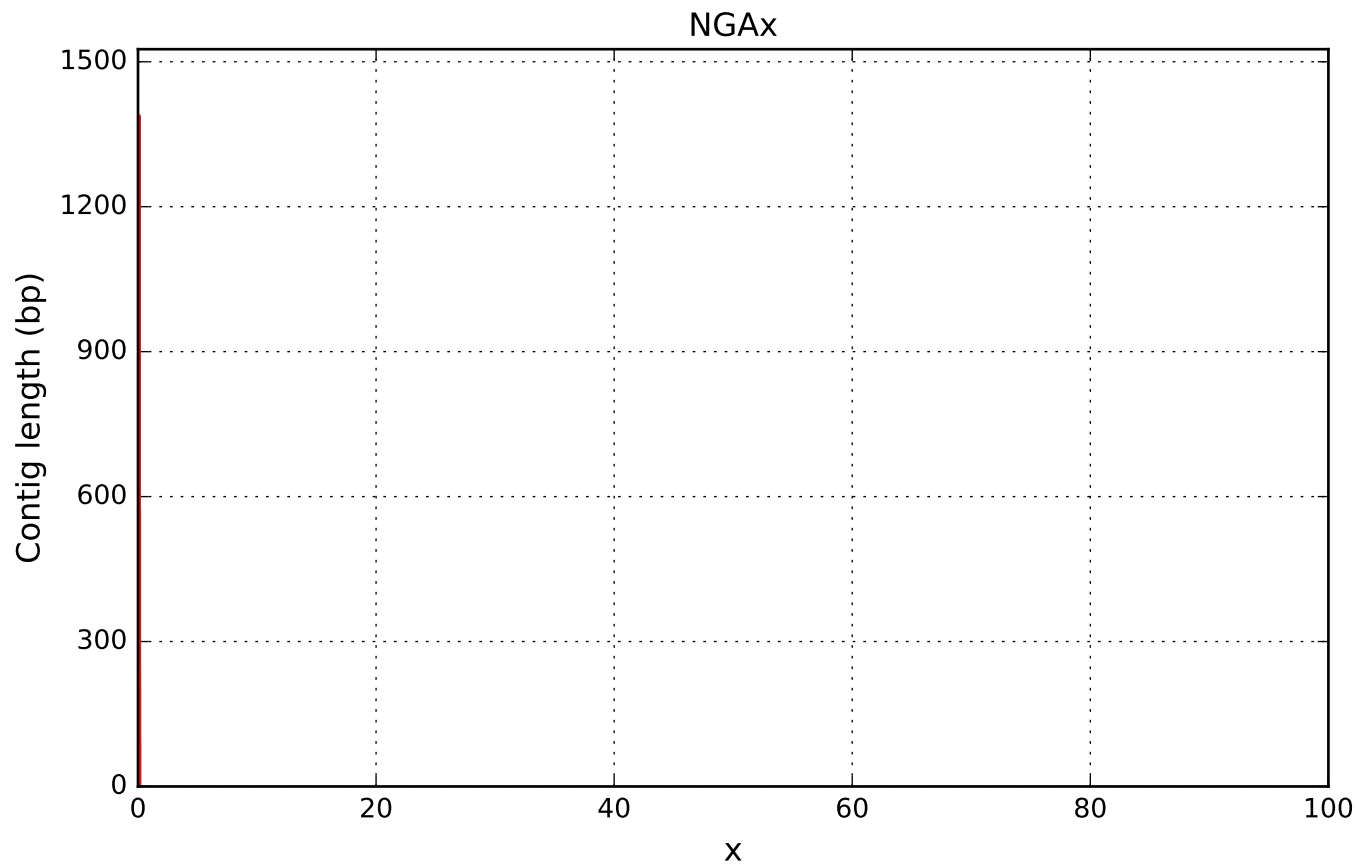
Cumulative length (aligned contigs)



— site_D3_DNA.final.contigs - - Reference



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