

Report

	site_D1_DNA.final.contigs
# contigs (≥ 1000 bp)	6
# contigs (≥ 5000 bp)	0
# contigs (≥ 10000 bp)	0
# contigs (≥ 25000 bp)	0
# contigs (≥ 50000 bp)	0
Total length (≥ 1000 bp)	11580
Total length (≥ 5000 bp)	0
Total length (≥ 10000 bp)	0
Total length (≥ 25000 bp)	0
Total length (≥ 50000 bp)	0
# contigs	15
Largest contig	2893
Total length	17763
Reference length	3576081
GC (%)	52.41
Reference GC (%)	51.82
N50	1785
N75	854
L50	4
L75	8
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 7 part
Unaligned length	11142
Genome fraction (%)	0.100
Duplication ratio	1.856
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2494.39
# indels per 100 kbp	140.13
Largest alignment	1015
Total aligned length	4171
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

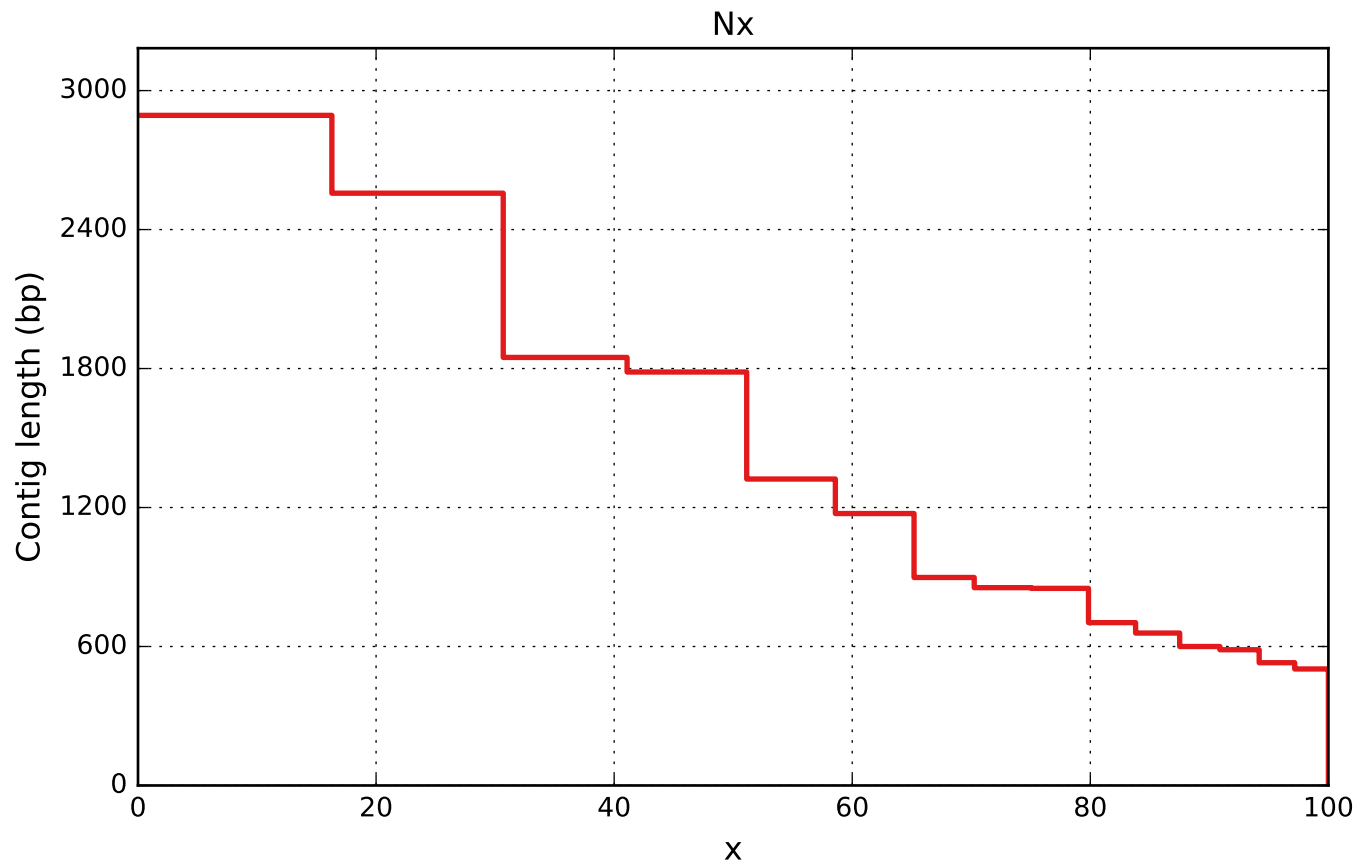
	site_D1_DNA.final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs	0
# mismatches	89
# indels	5
# indels (<= 5 bp)	5
# indels (> 5 bp)	0
Indels length	5

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).

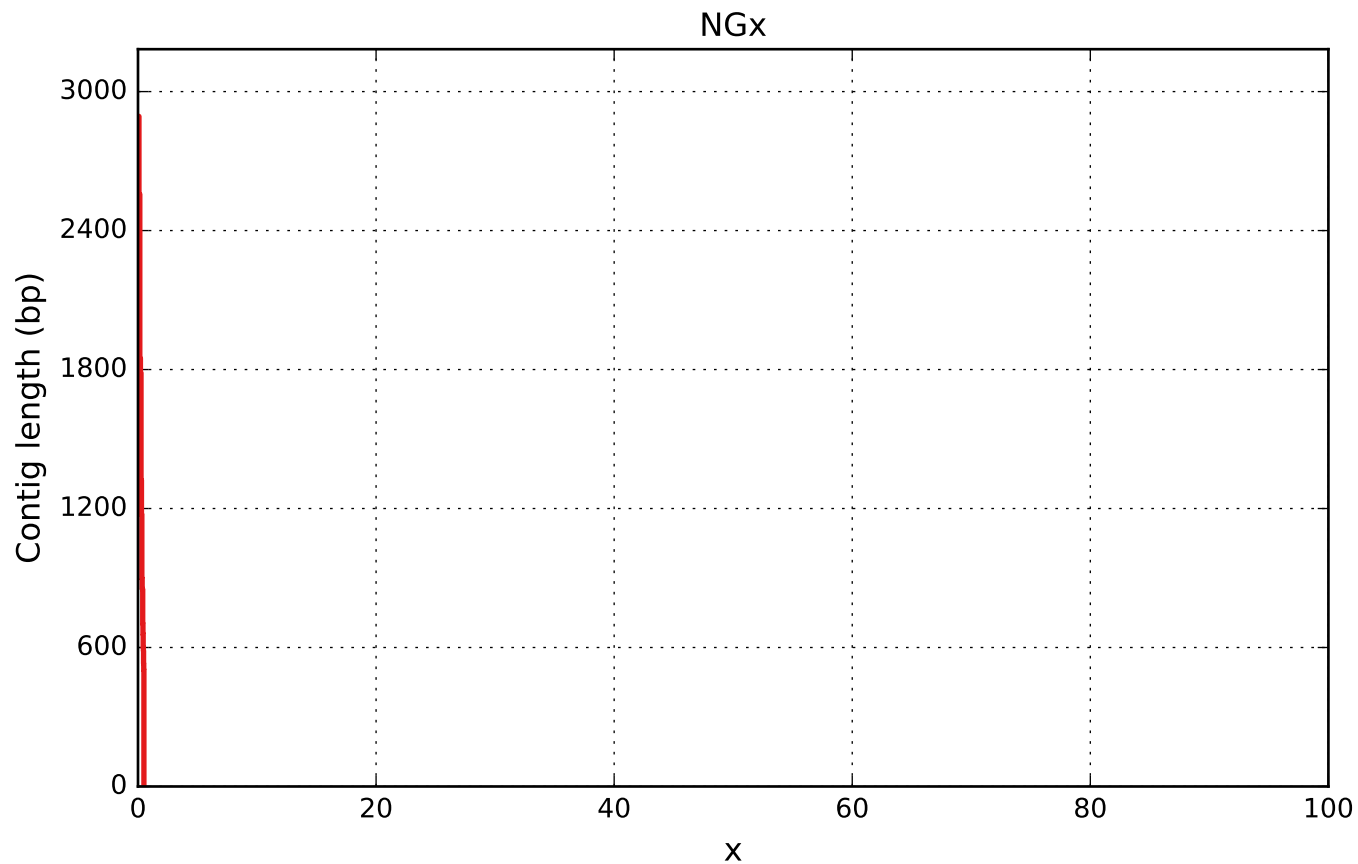
Unaligned report

	site_D1_DNA.final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	7
Partially unaligned length	11142
# N's	0

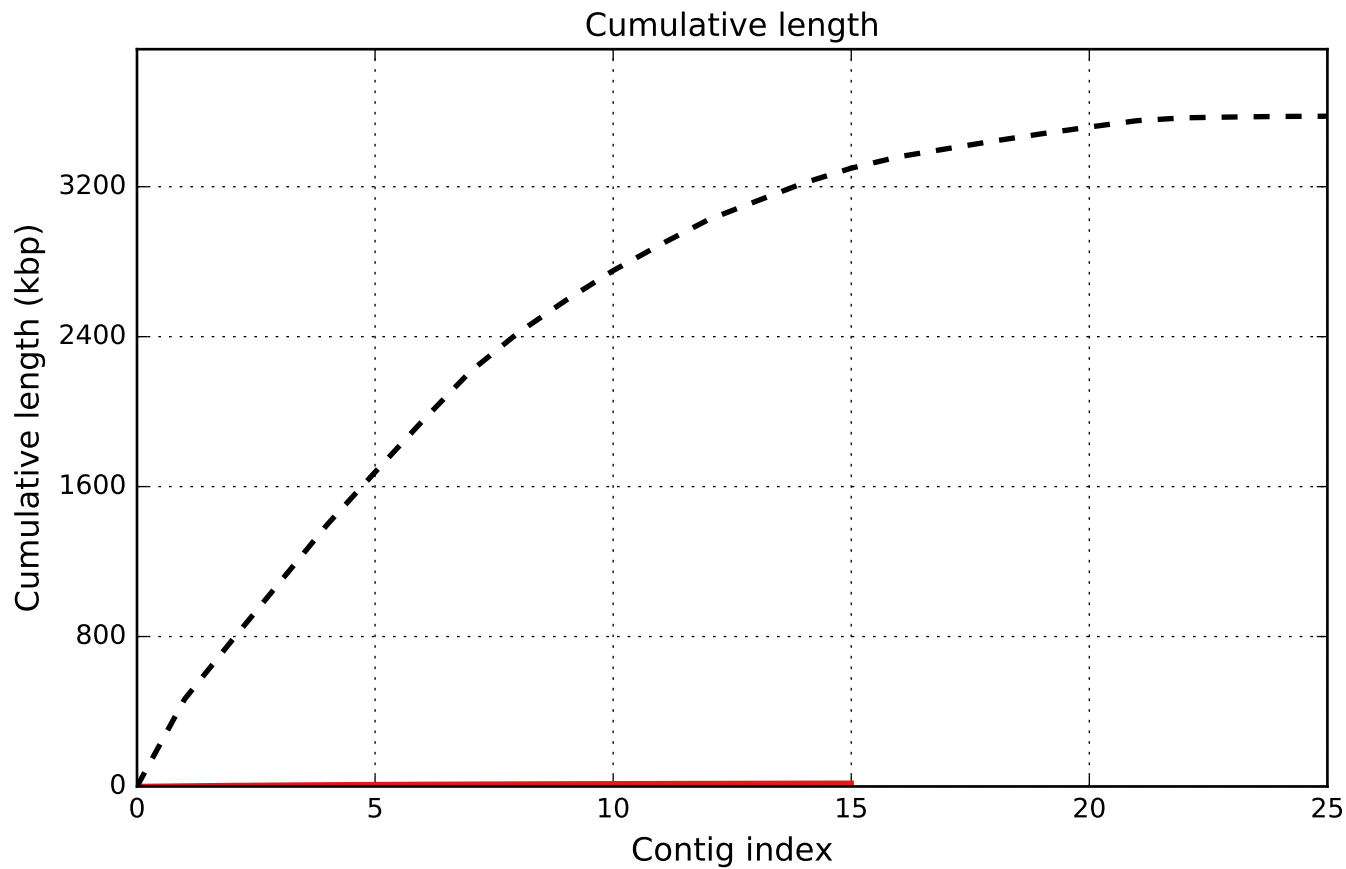
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

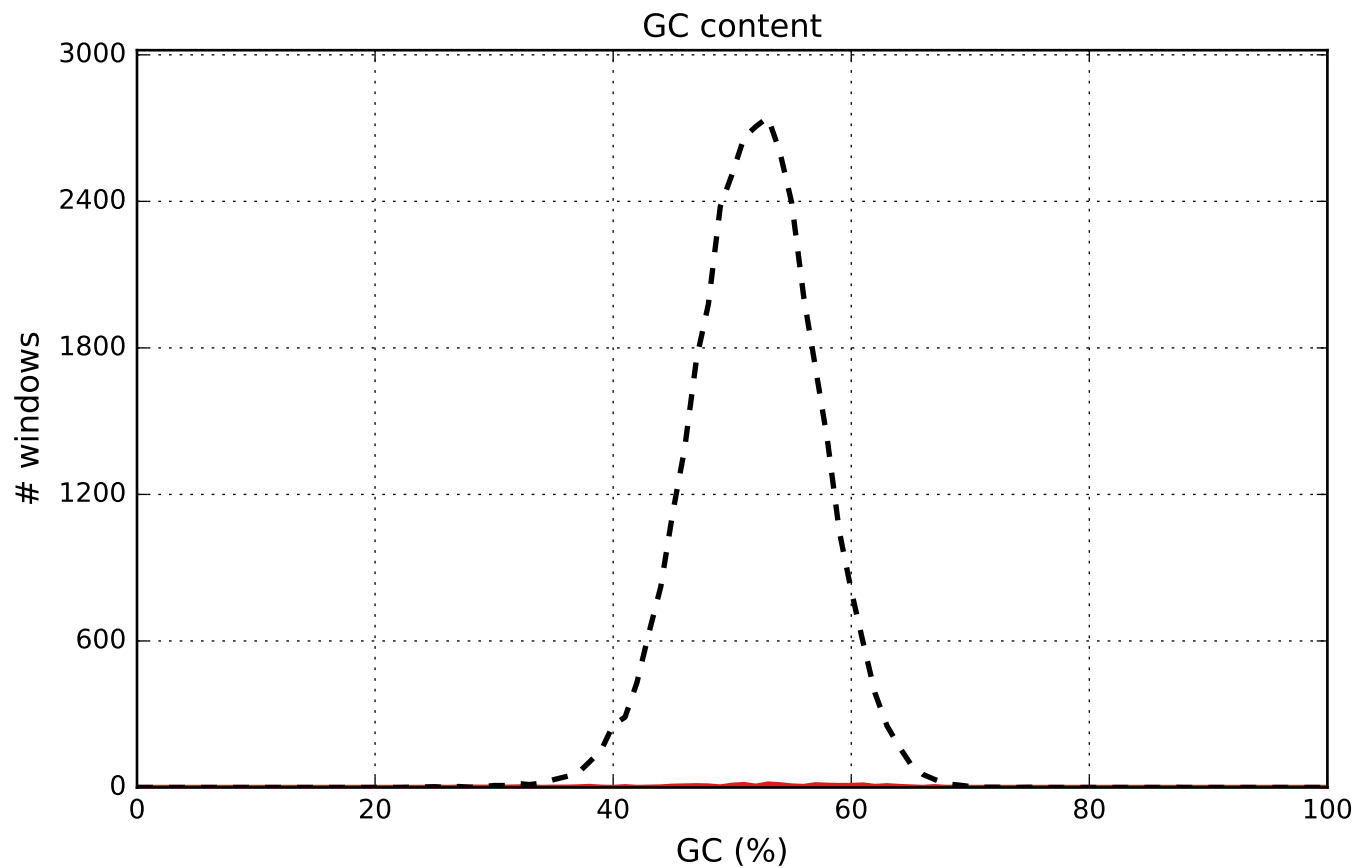


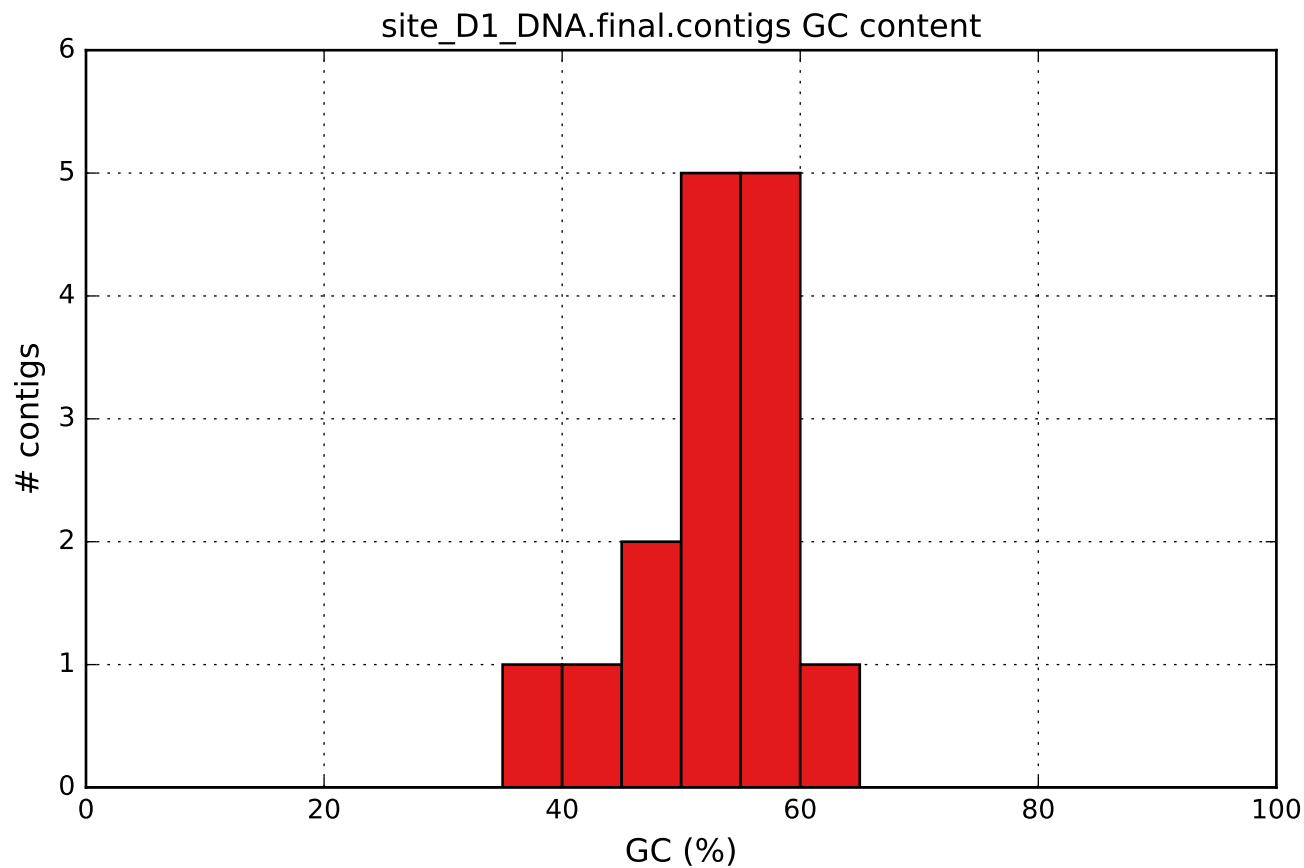
— site_D1_DNA.final.contigs



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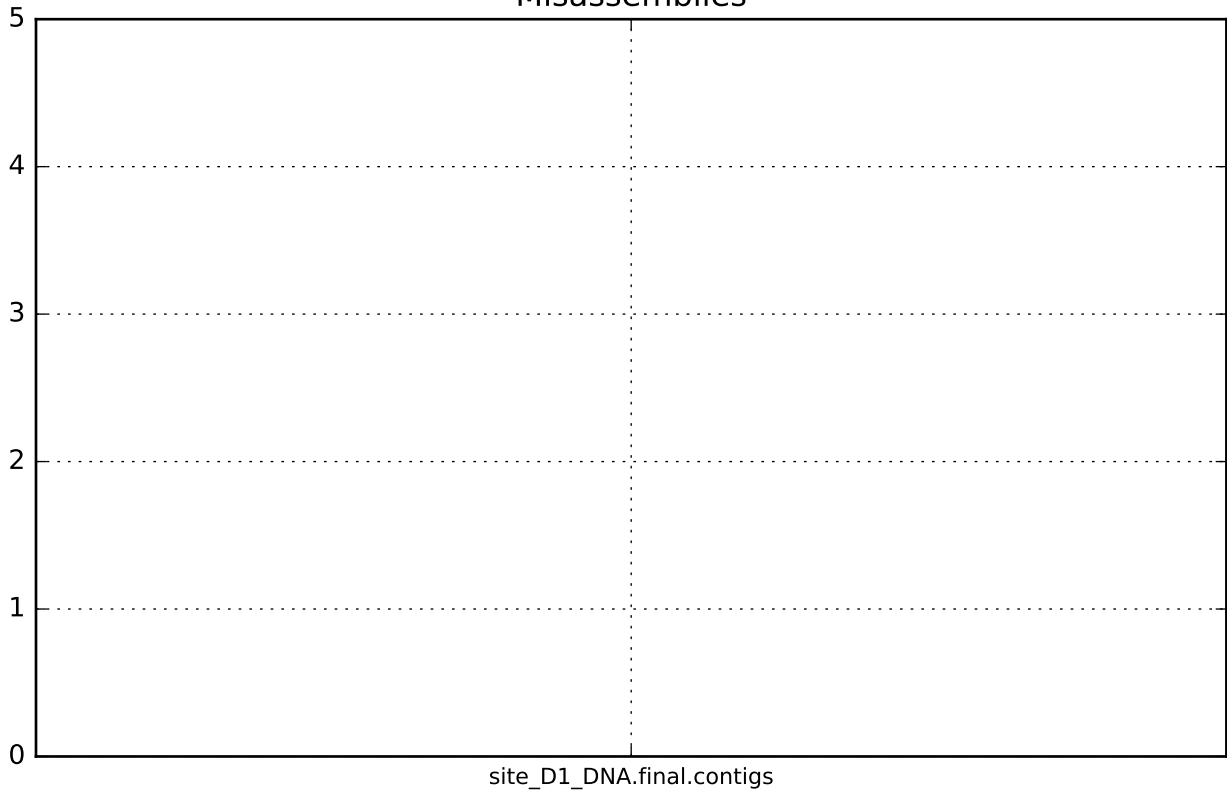




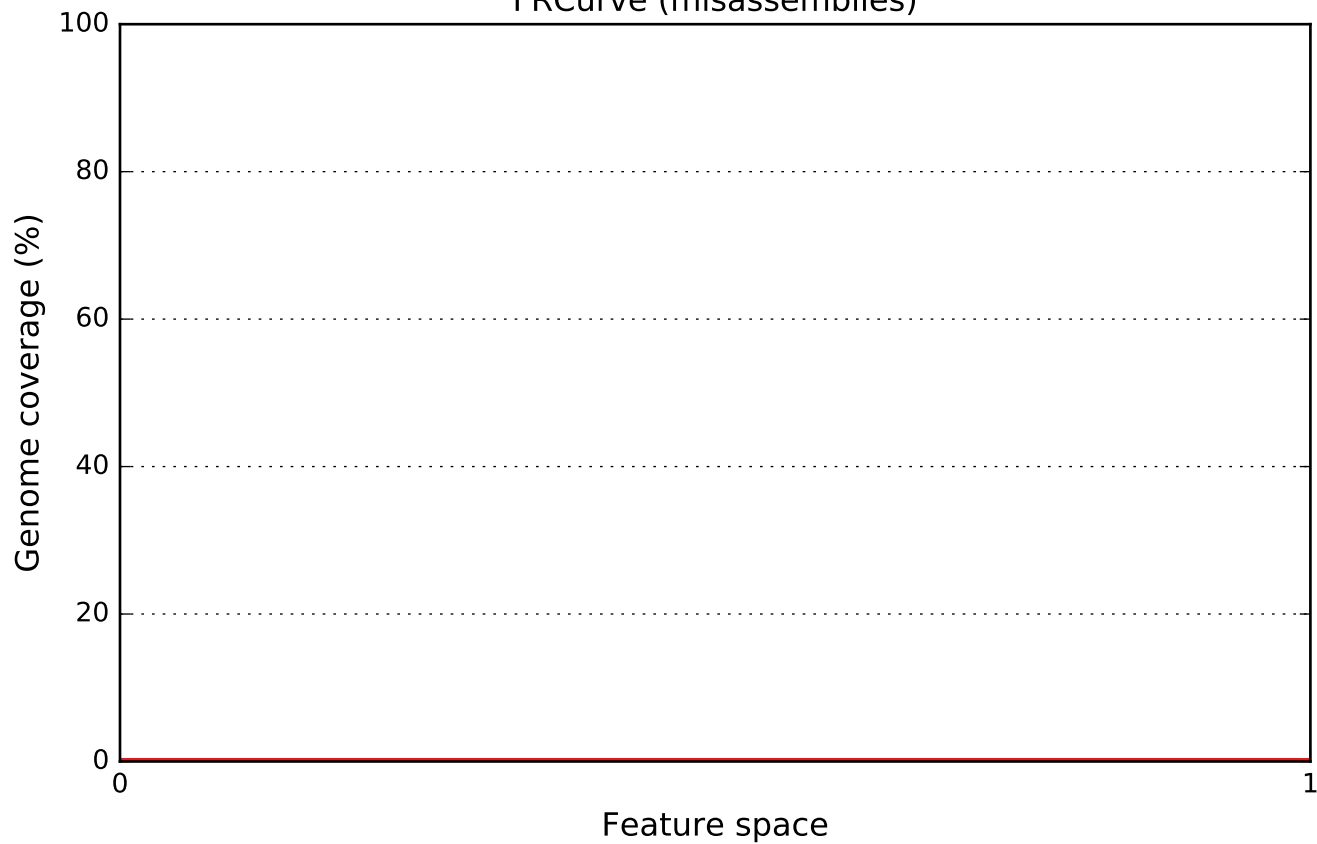


site_D1_DNA.final.contigs

Misassemblies

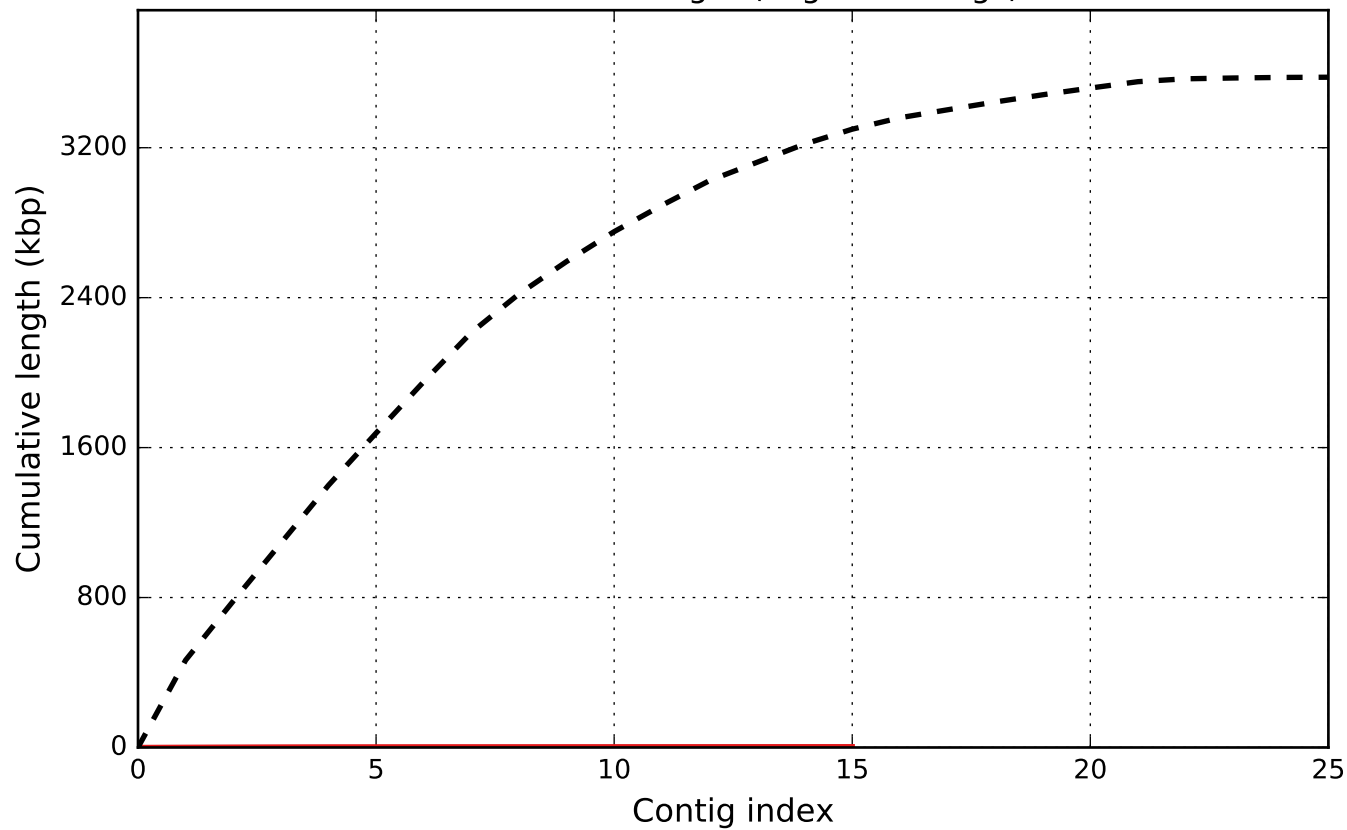


FRCurve (misassemblies)

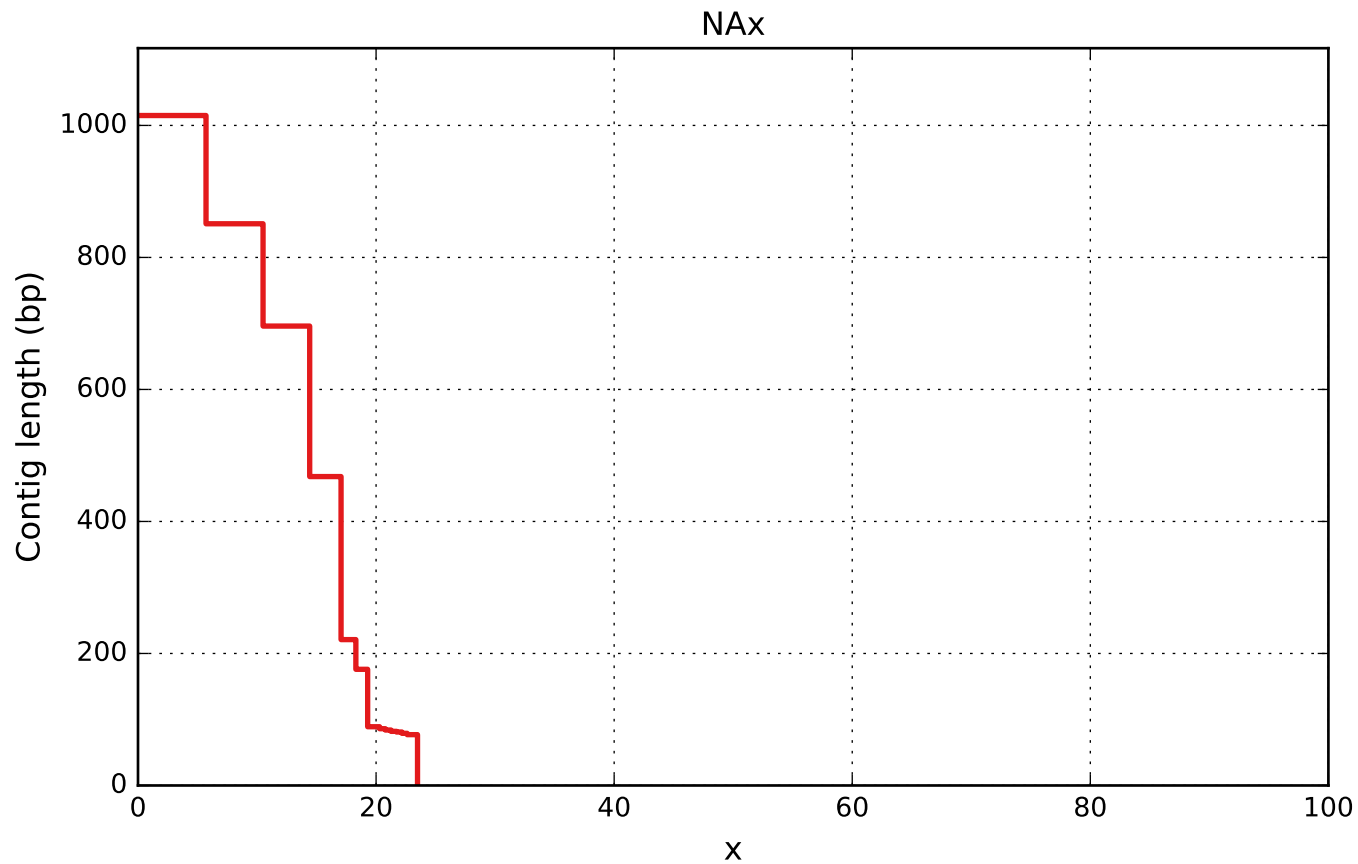


— site_D1_DNA.final.contigs

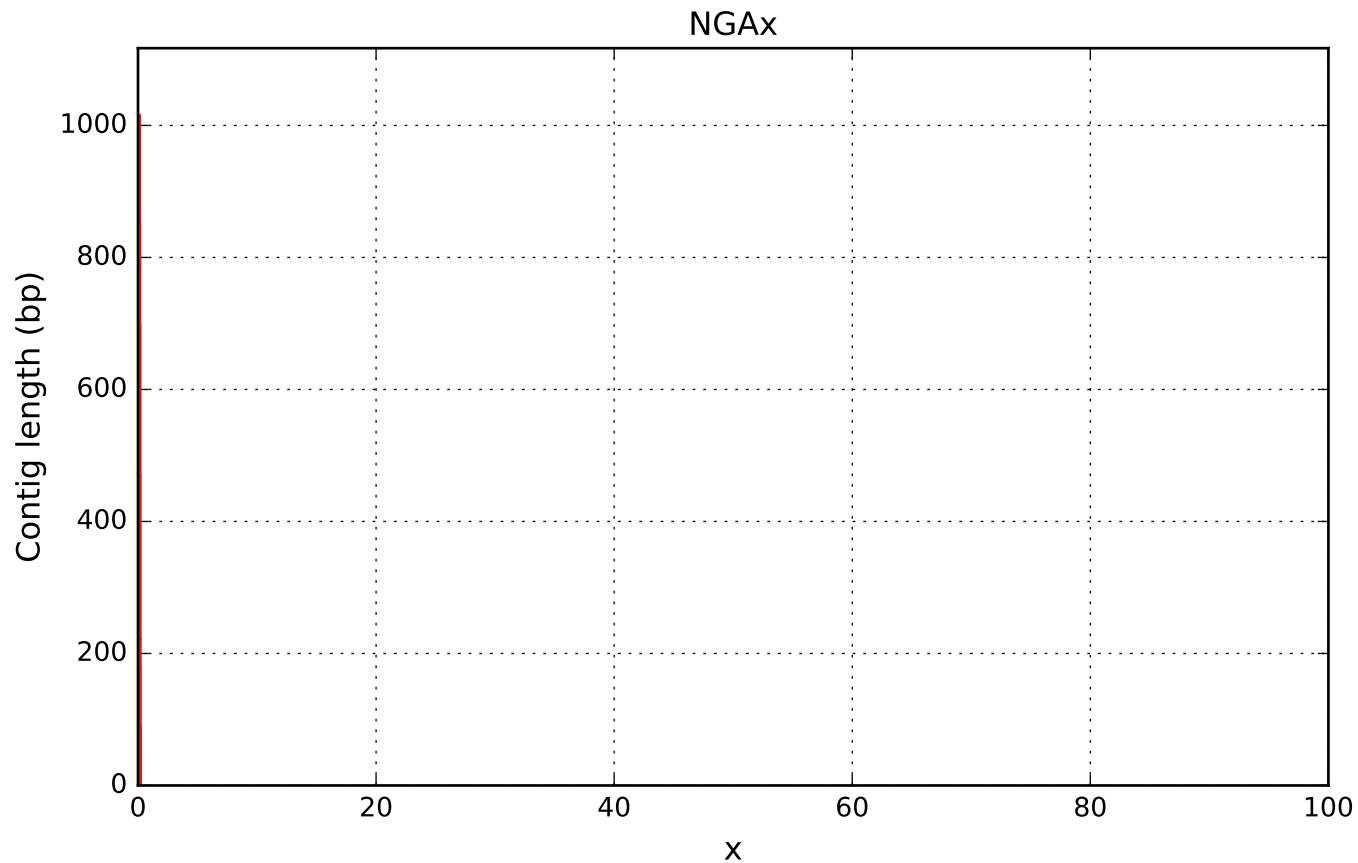
Cumulative length (aligned contigs)



— site_D1_DNA.final.contigs - - Reference



— site_D1_DNA.final.contigs



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