

Report

	bin_7
# contigs (>= 0 bp)	3464
# contigs (>= 1000 bp)	3464
# contigs (>= 5000 bp)	925
# contigs (>= 10000 bp)	196
# contigs (>= 25000 bp)	15
# contigs (>= 50000 bp)	0
Total length (>= 0 bp)	16261463
Total length (>= 1000 bp)	16261463
Total length (>= 5000 bp)	7720439
Total length (>= 10000 bp)	2881987
Total length (>= 25000 bp)	452829
Total length (>= 50000 bp)	0
# contigs	3464
Largest contig	42507
Total length	16261463
Reference length	3633537
N50	4806
N75	3325
L50	1009
L75	2040
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	3462 + 2 part
Unaligned length	16261312
Genome fraction (%)	0.004
Duplication ratio	1.493
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	76
Total aligned length	151

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

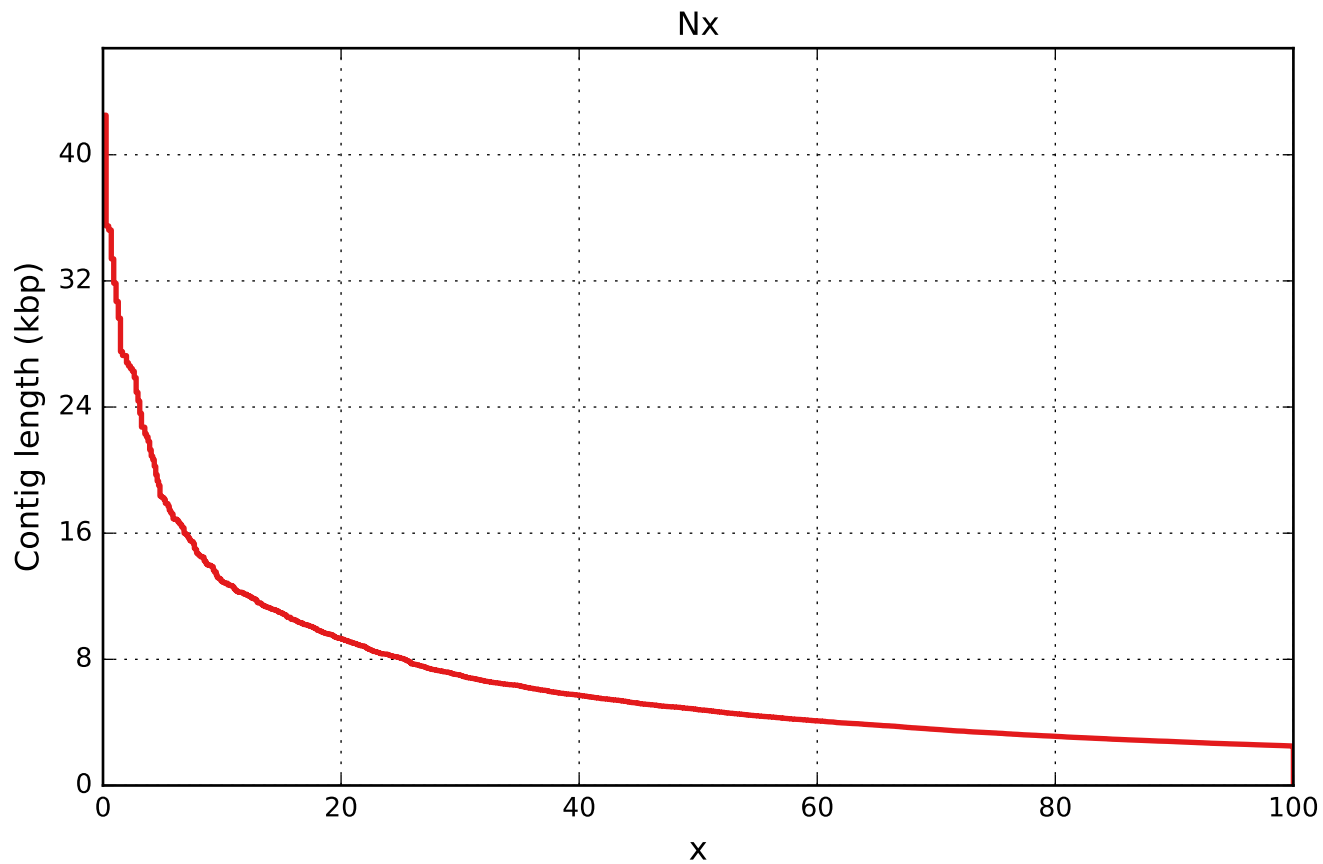
	bin_7
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	0
# indels	0
# 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).

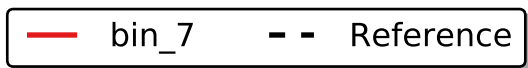
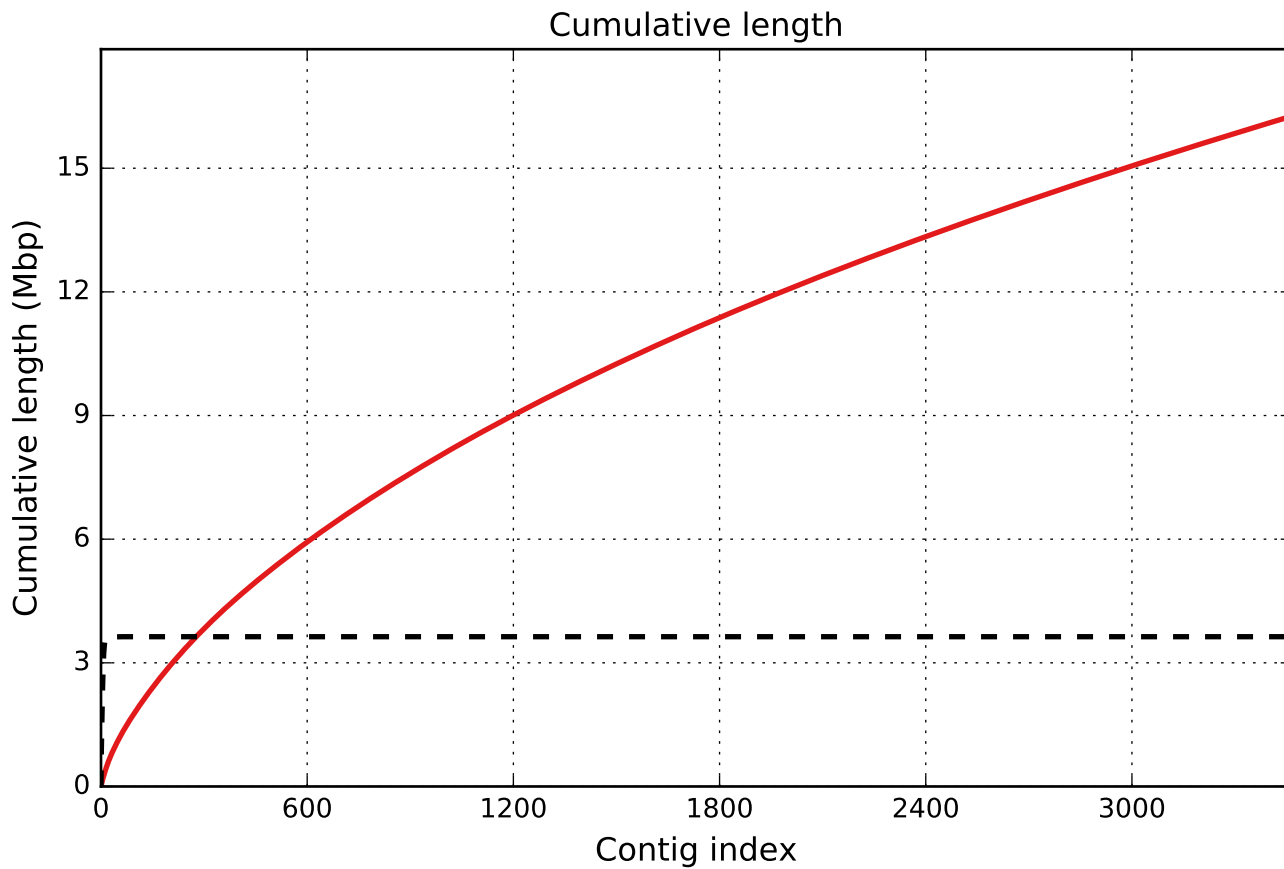
Unaligned report

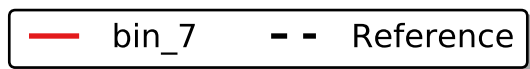
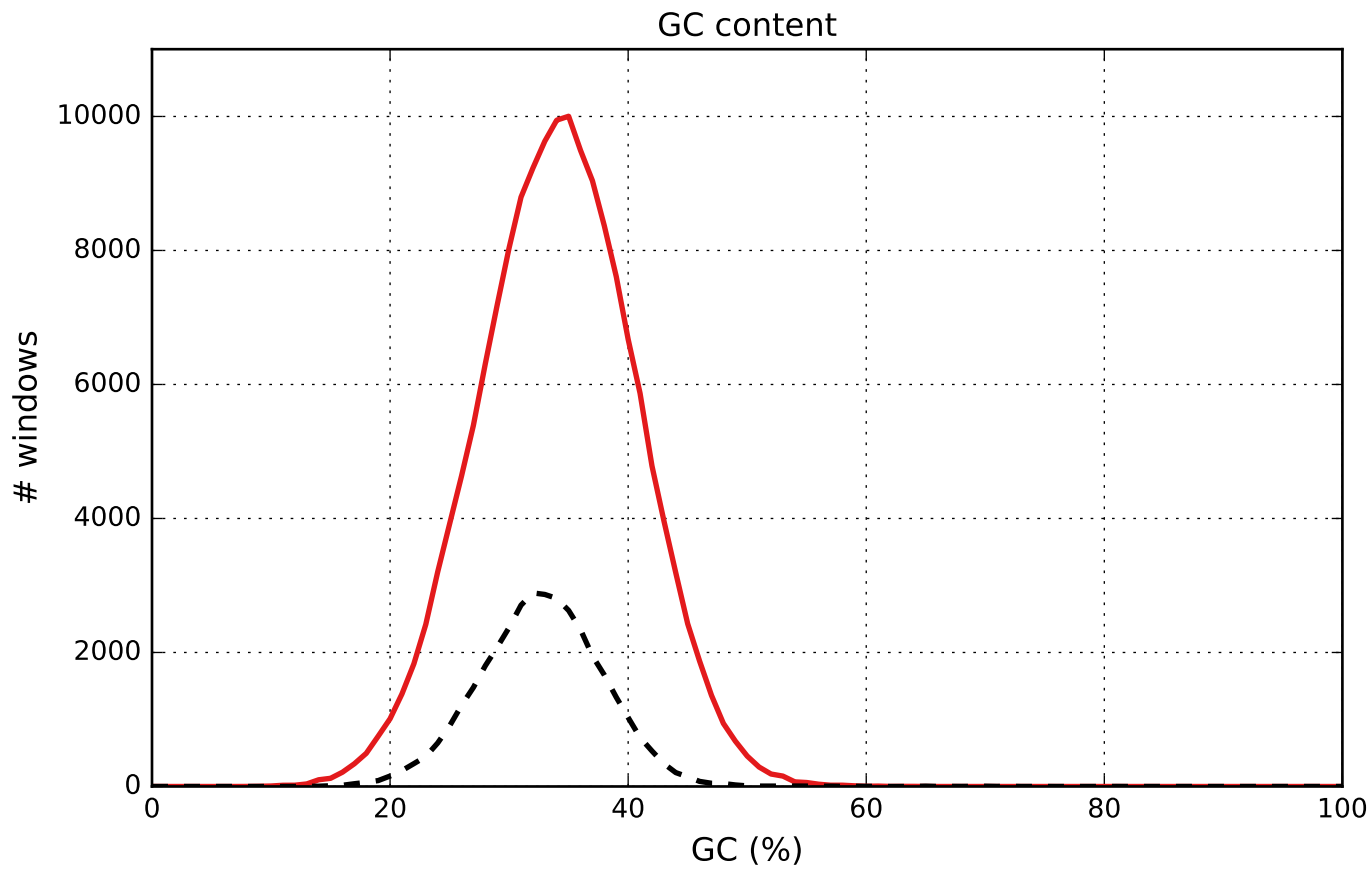
	bin_7
# fully unaligned contigs	3462
Fully unaligned length	16232002
# partially unaligned contigs	2
Partially unaligned length	29310
# N's	0

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).

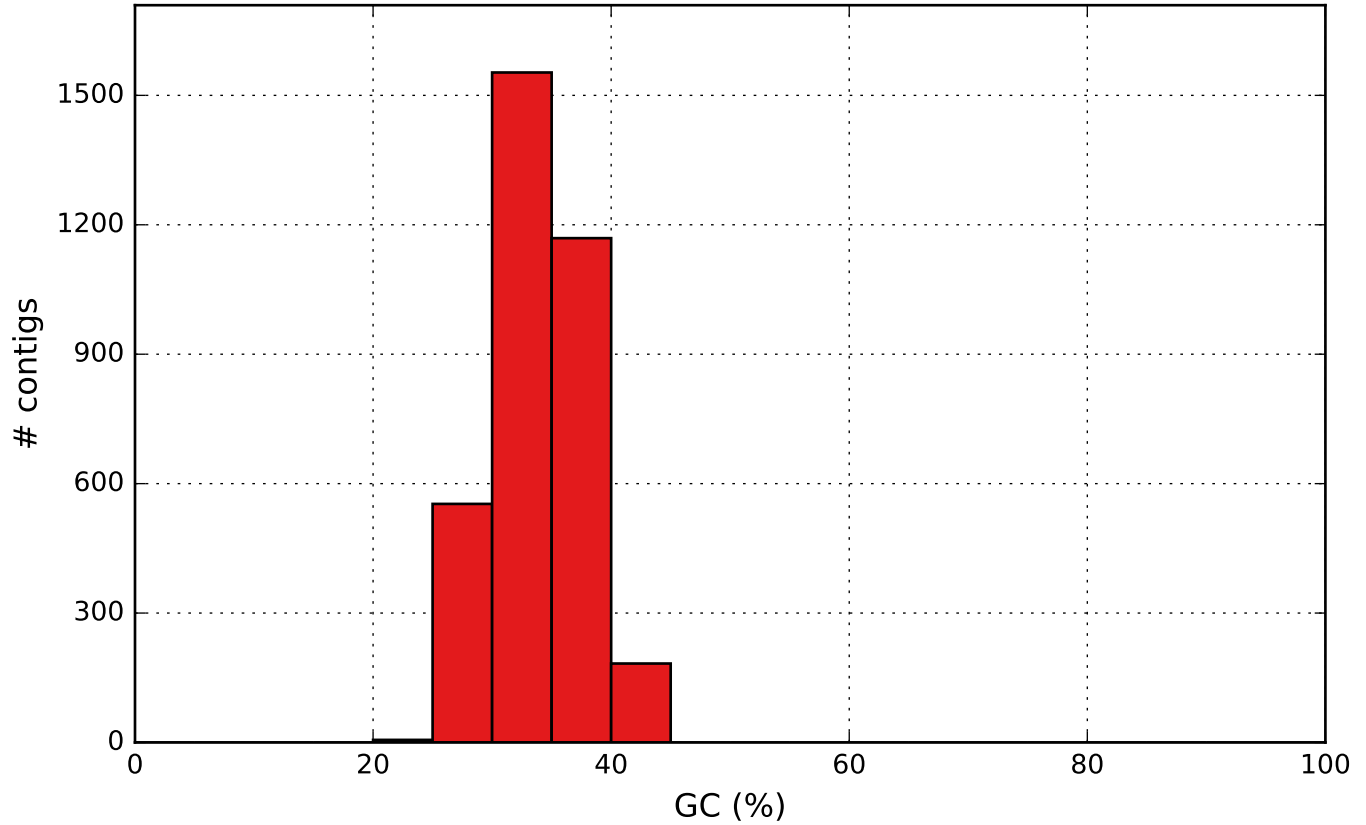


bin_7



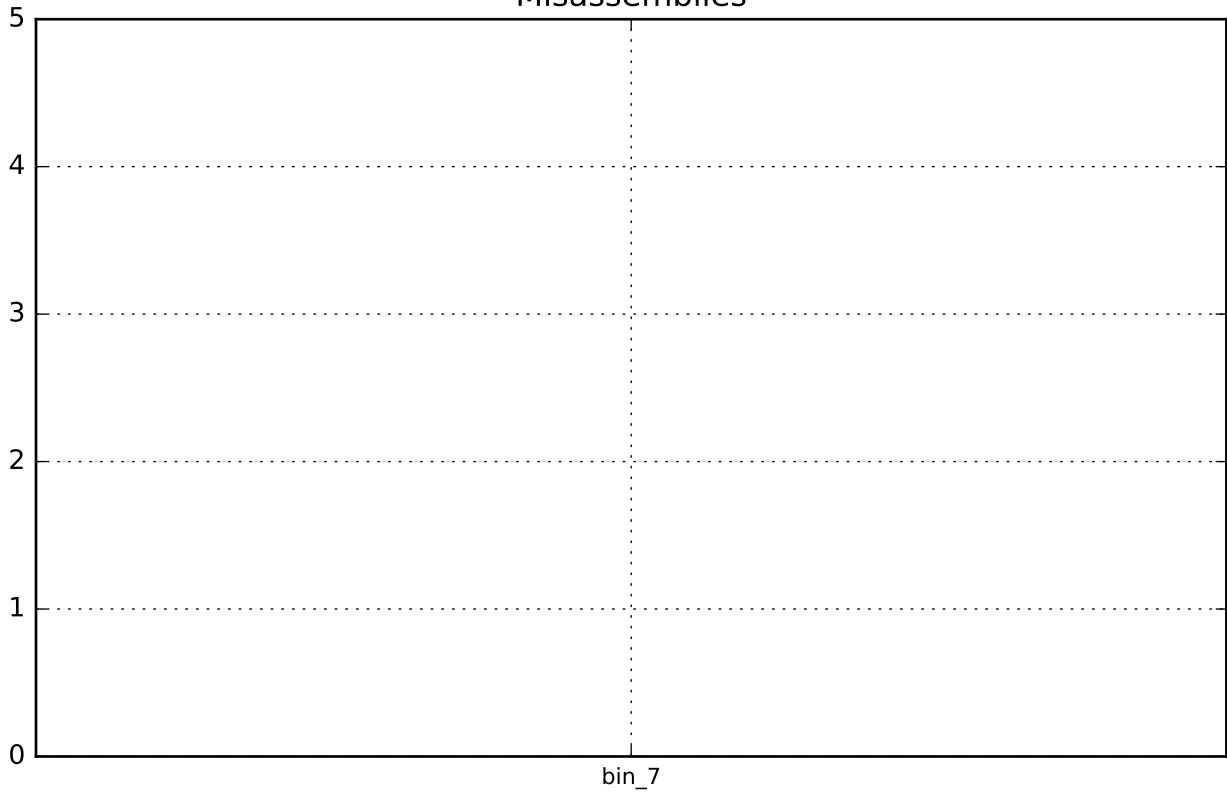


bin_7 GC content

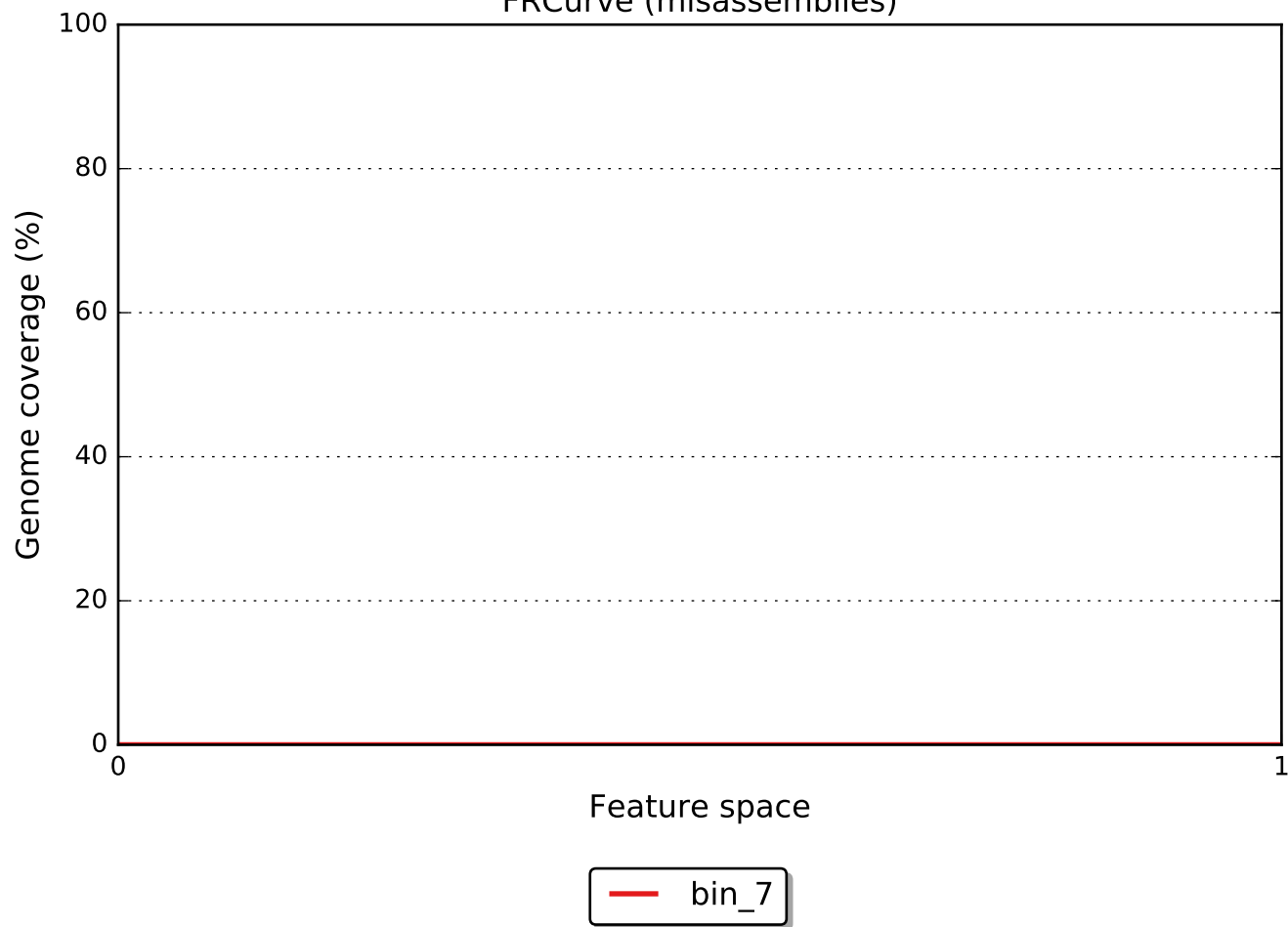


bin_7

Misassemblies



FRCurve (misassemblies)



Cumulative length (aligned contigs)

