

Report

	corrected_DNA
# contigs (>= 0 bp)	522
# contigs (>= 1000 bp)	522
# contigs (>= 5000 bp)	518
# contigs (>= 10000 bp)	456
# contigs (>= 25000 bp)	125
# contigs (>= 50000 bp)	62
Total length (>= 0 bp)	33628515
Total length (>= 1000 bp)	33628515
Total length (>= 5000 bp)	33617261
Total length (>= 10000 bp)	33094350
Total length (>= 25000 bp)	27736641
Total length (>= 50000 bp)	25778906
# contigs	522
Largest contig	2322263
Total length	33628515
Reference length	33643051
GC (%)	31.15
Reference GC (%)	31.13
N50	446274
NG50	446274
N75	84359
NG75	84359
L50	19
LG50	19
L75	54
LG75	54
# misassemblies	7
# misassembled contigs	6
Misassembled contigs length	5953694
# local misassemblies	33
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.924
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	236.12
# indels per 100 kbp	102.66
Largest alignment	2322168
Total aligned length	33626778
NA50	407732
NGA50	407732
NA75	84359
NGA75	84359
LA50	23
LGA50	23
LA75	60
LGA75	60

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

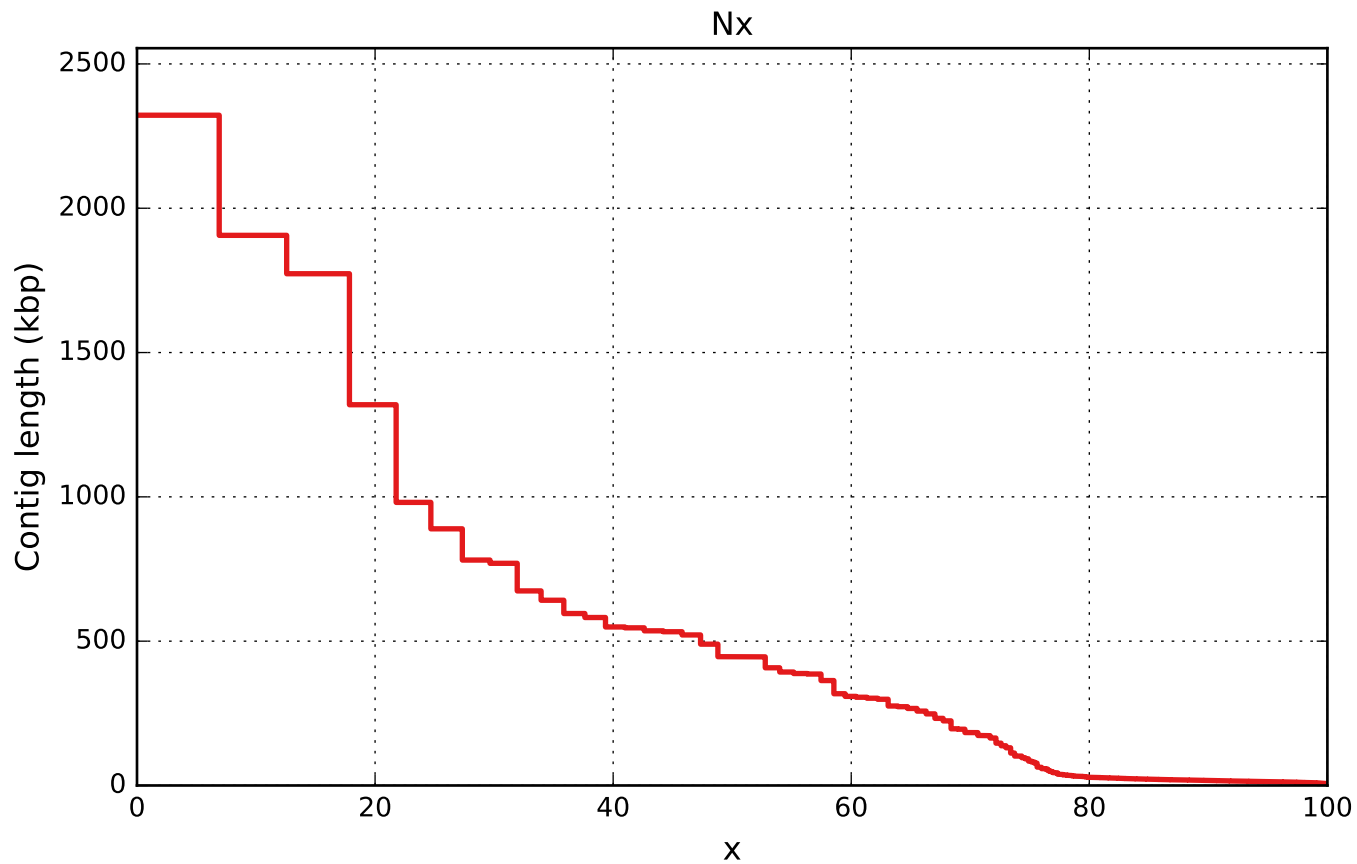
	corrected_DNA
# misassemblies	7
# relocations	7
# translocations	0
# inversions	0
# misassembled contigs	6
Misassembled contigs length	5953694
# local misassemblies	33
# unaligned mis. contigs	0
# mismatches	79377
# indels	34512
# indels (≤ 5 bp)	32449
# indels (> 5 bp)	2063
Indels length	69935

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

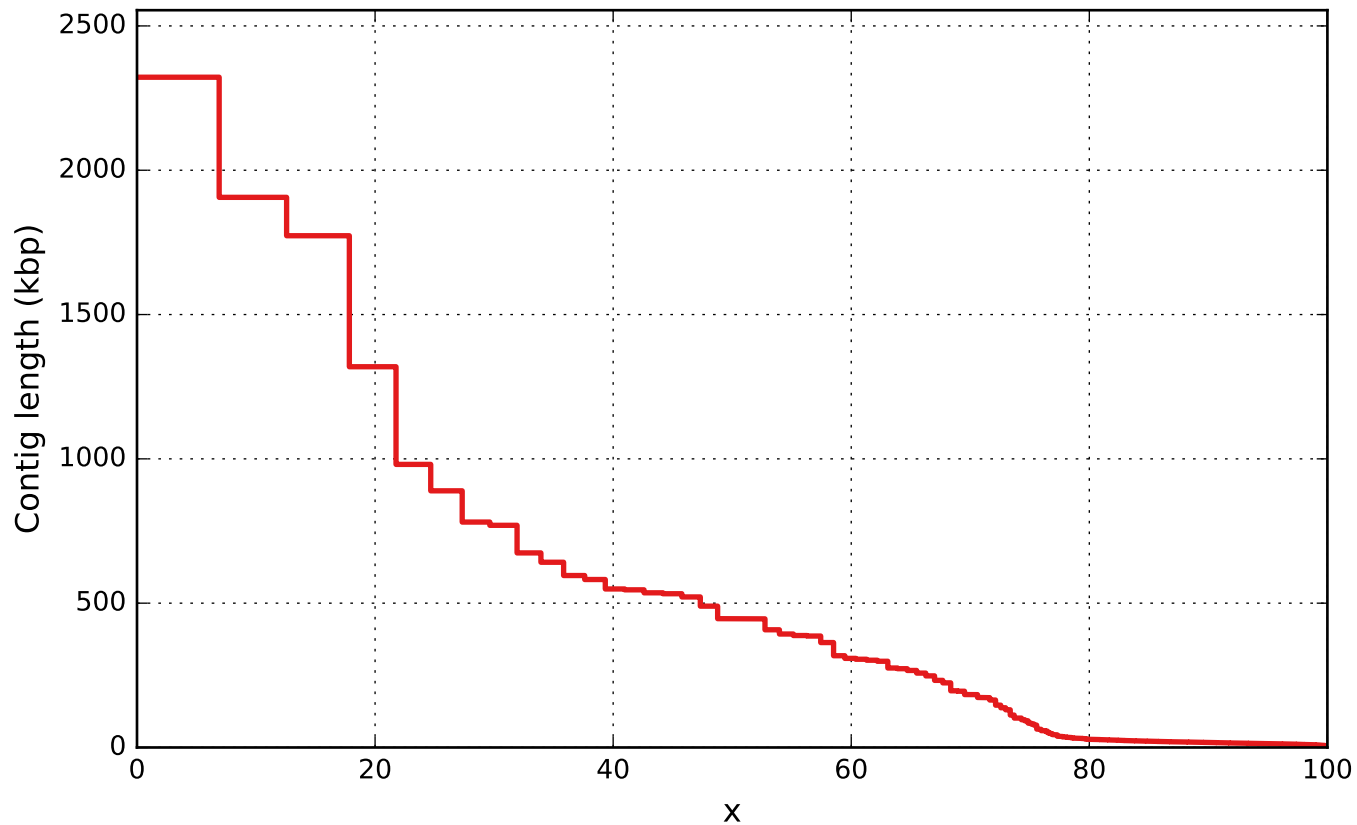
	corrected_DNA
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

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).

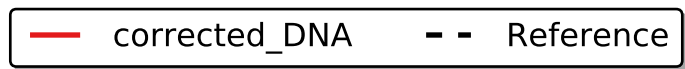
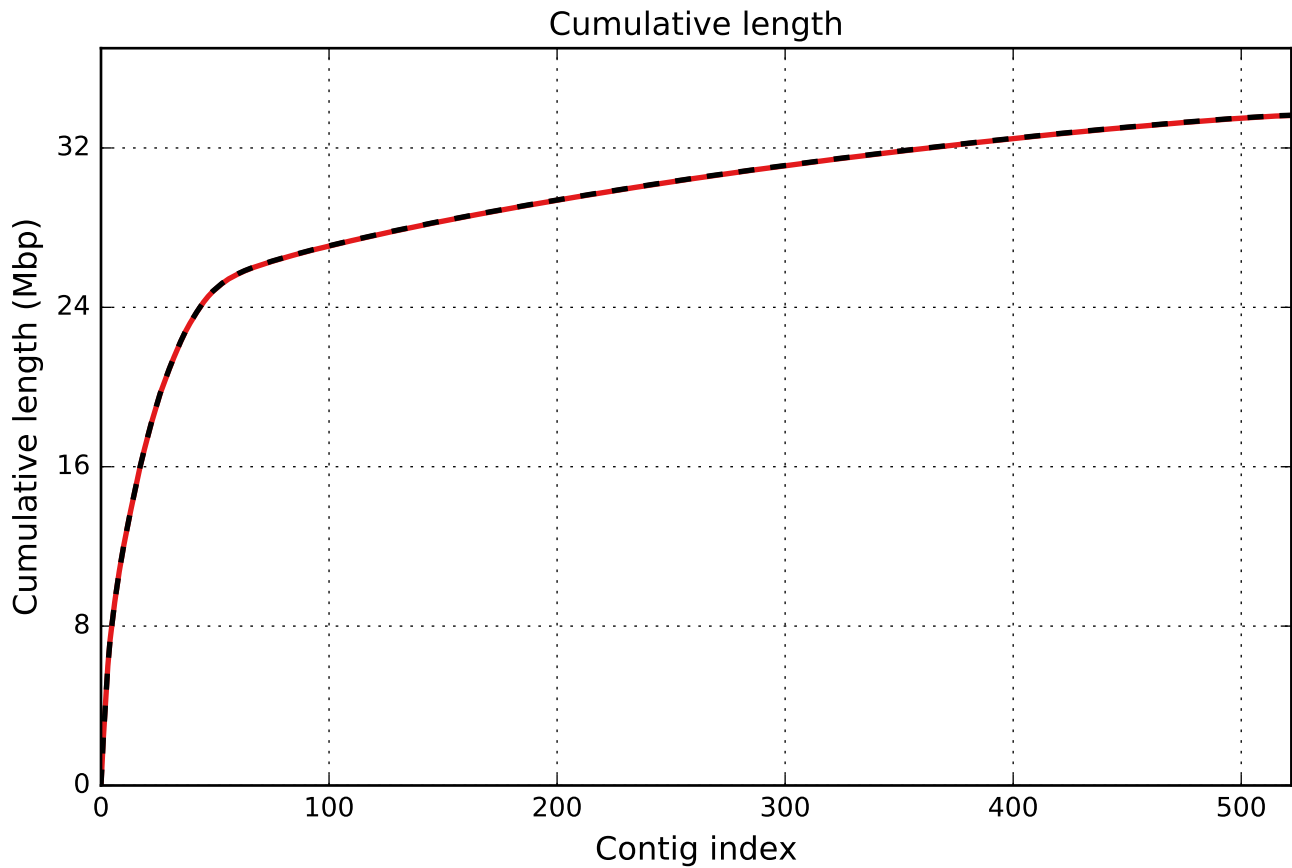


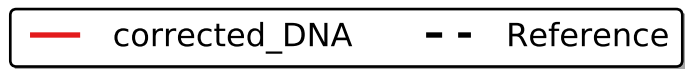
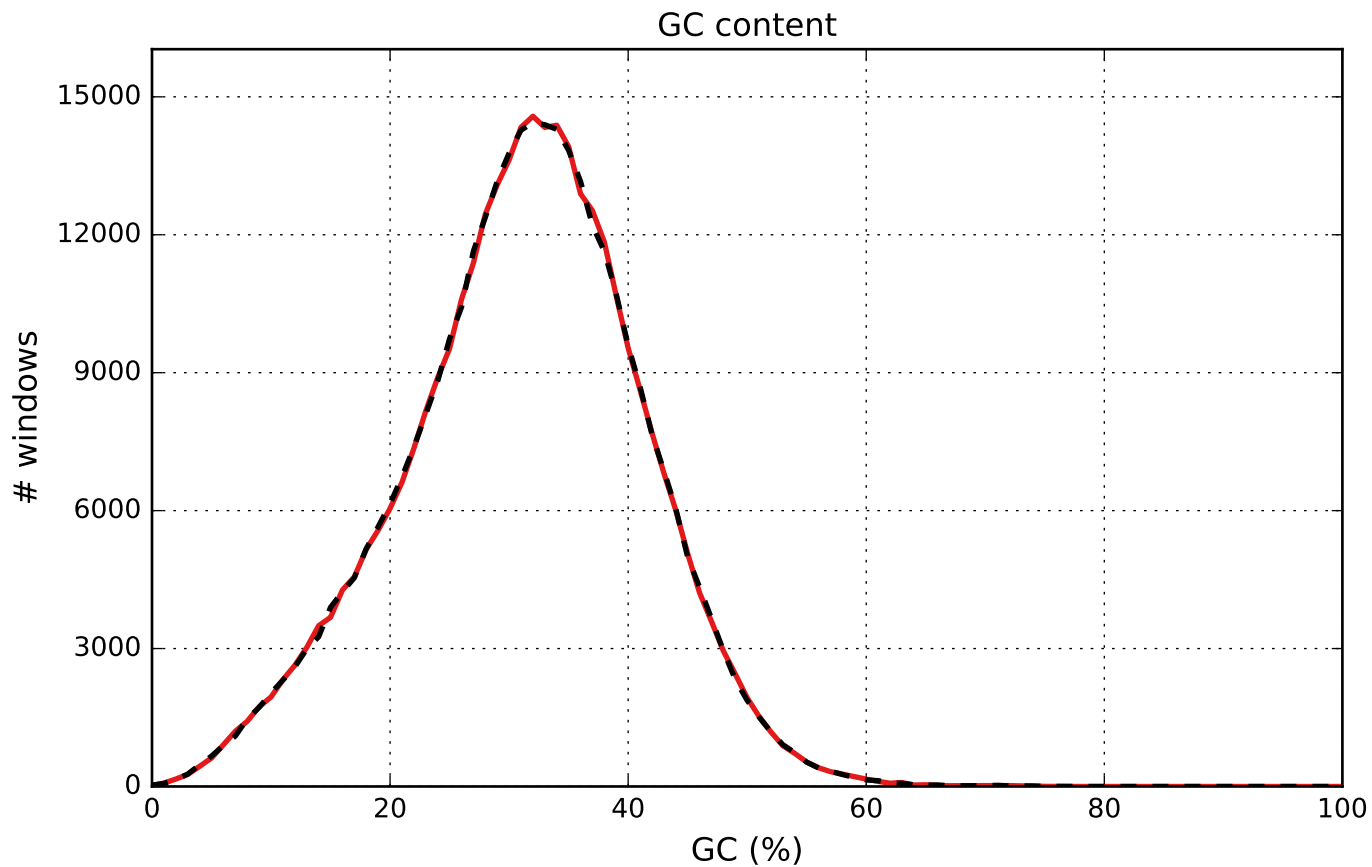
— corrected_DNA

NGx

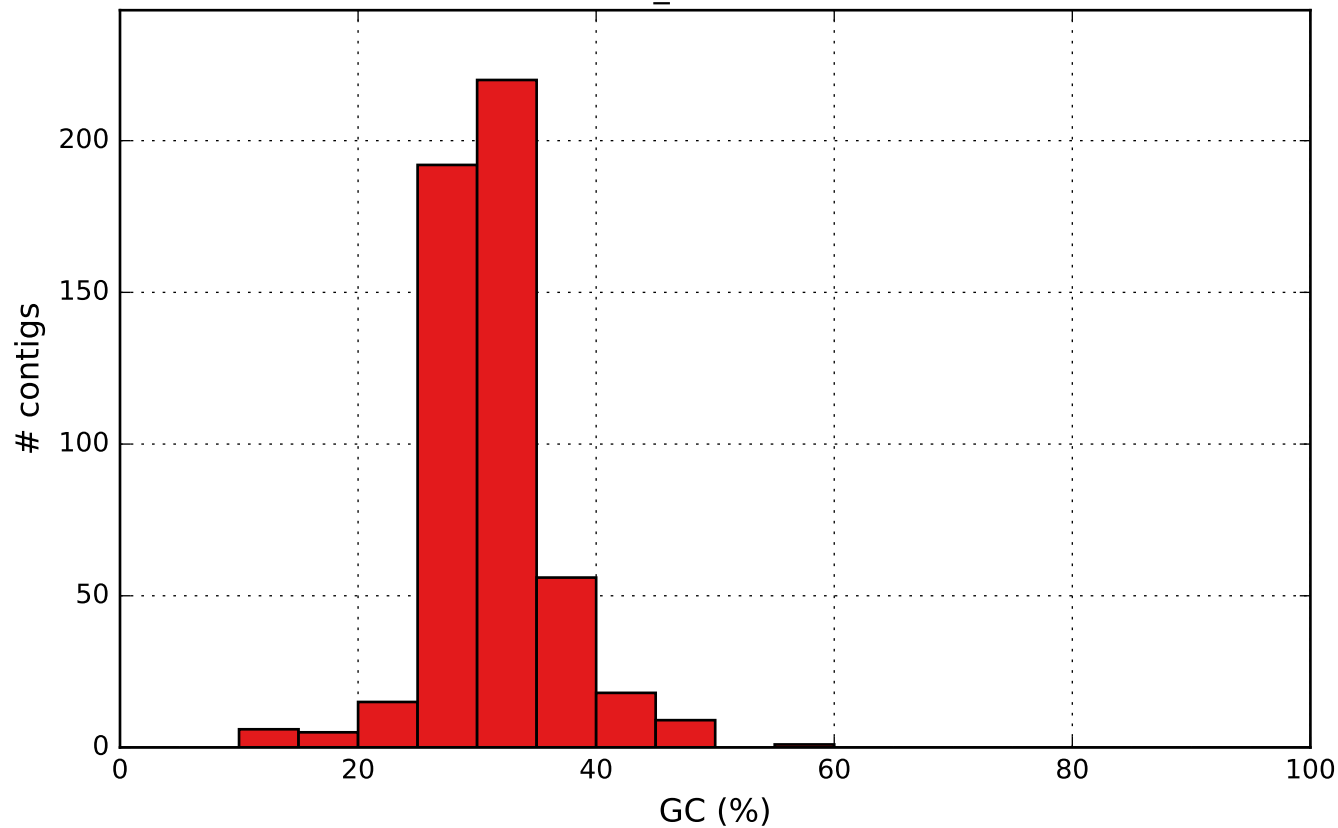


— corrected_DNA

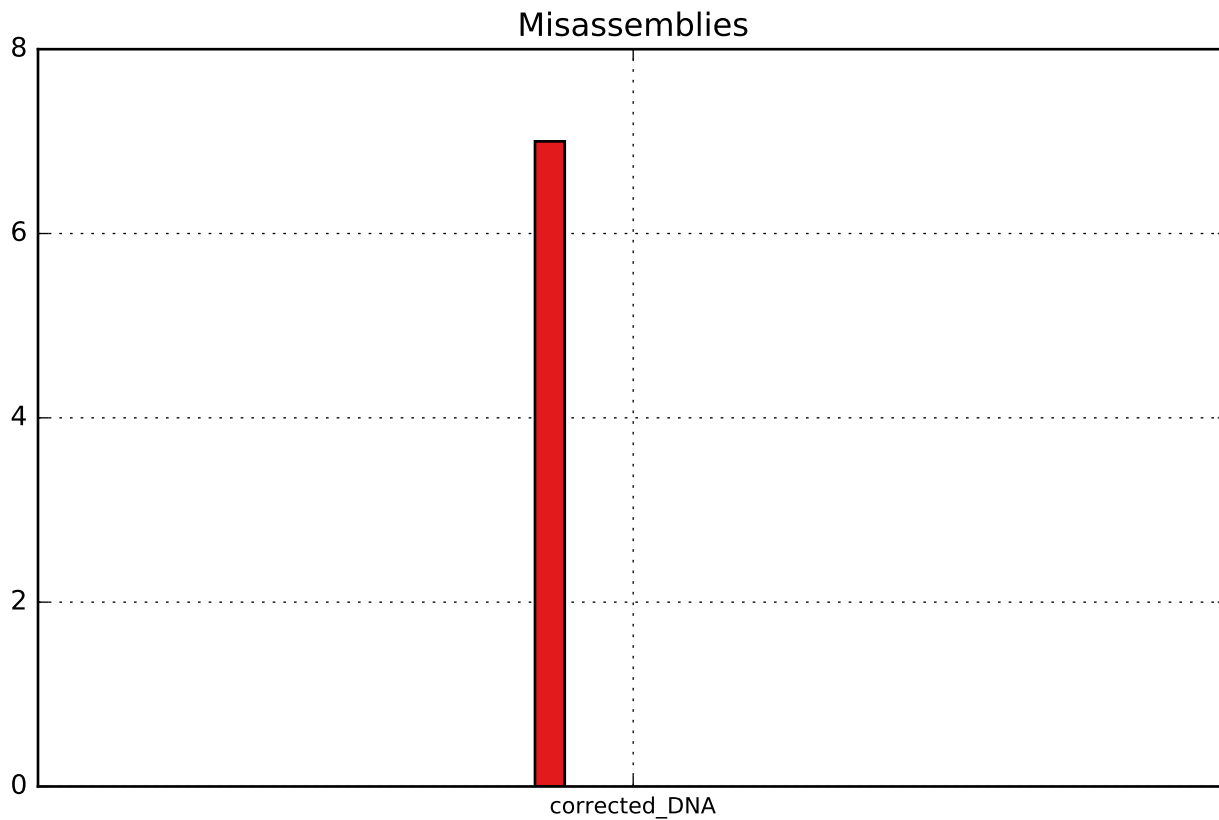




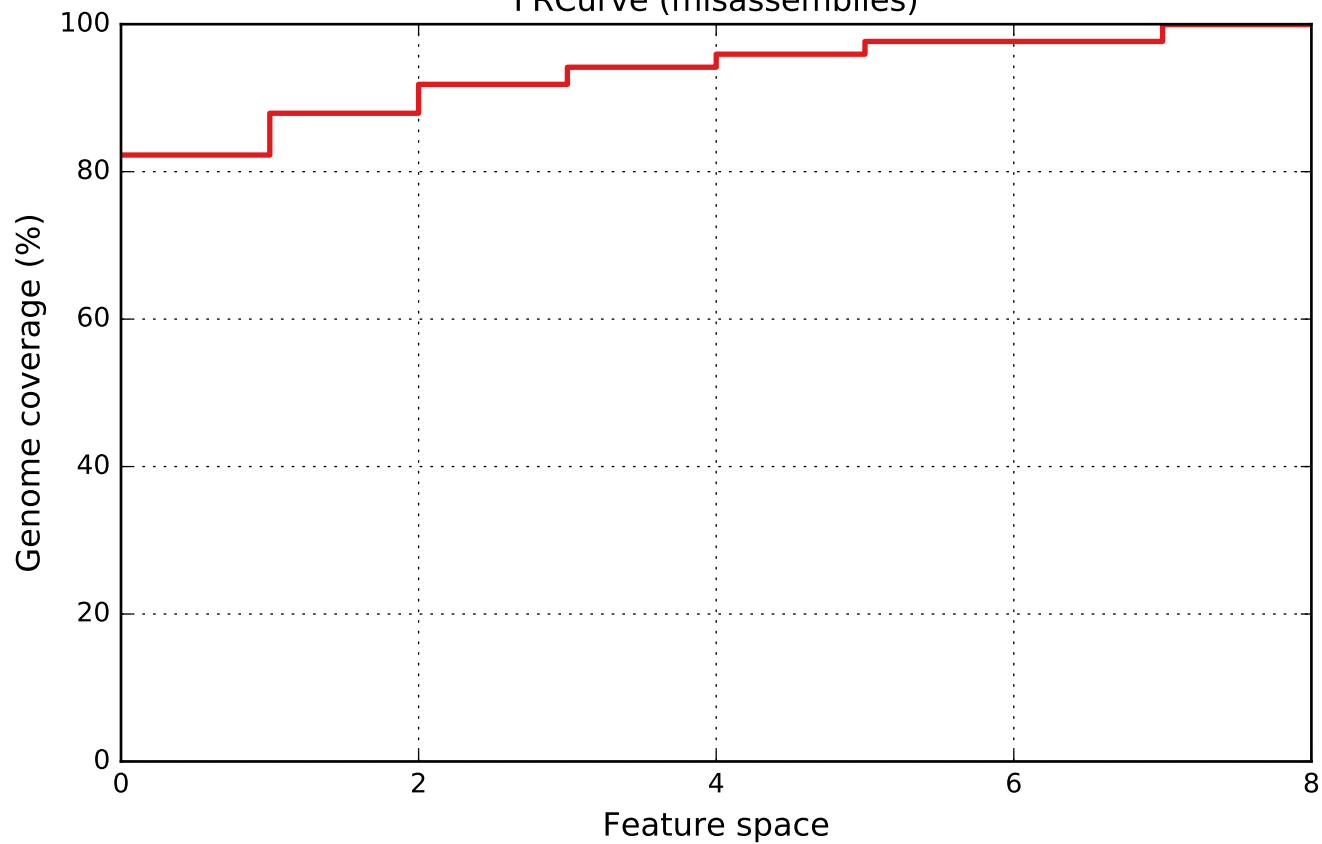
corrected_DNA GC content



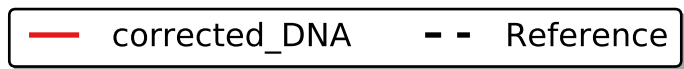
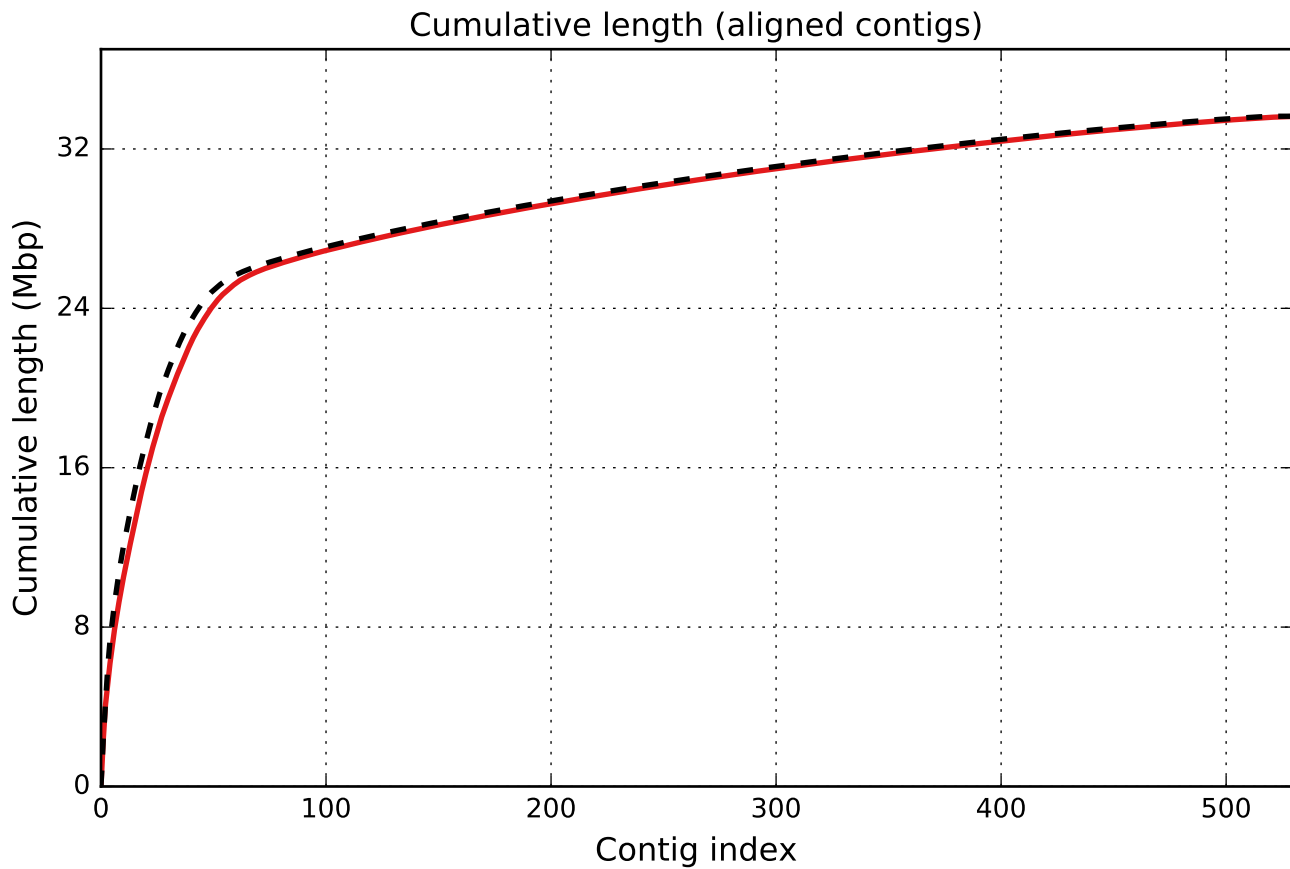
corrected_DNA

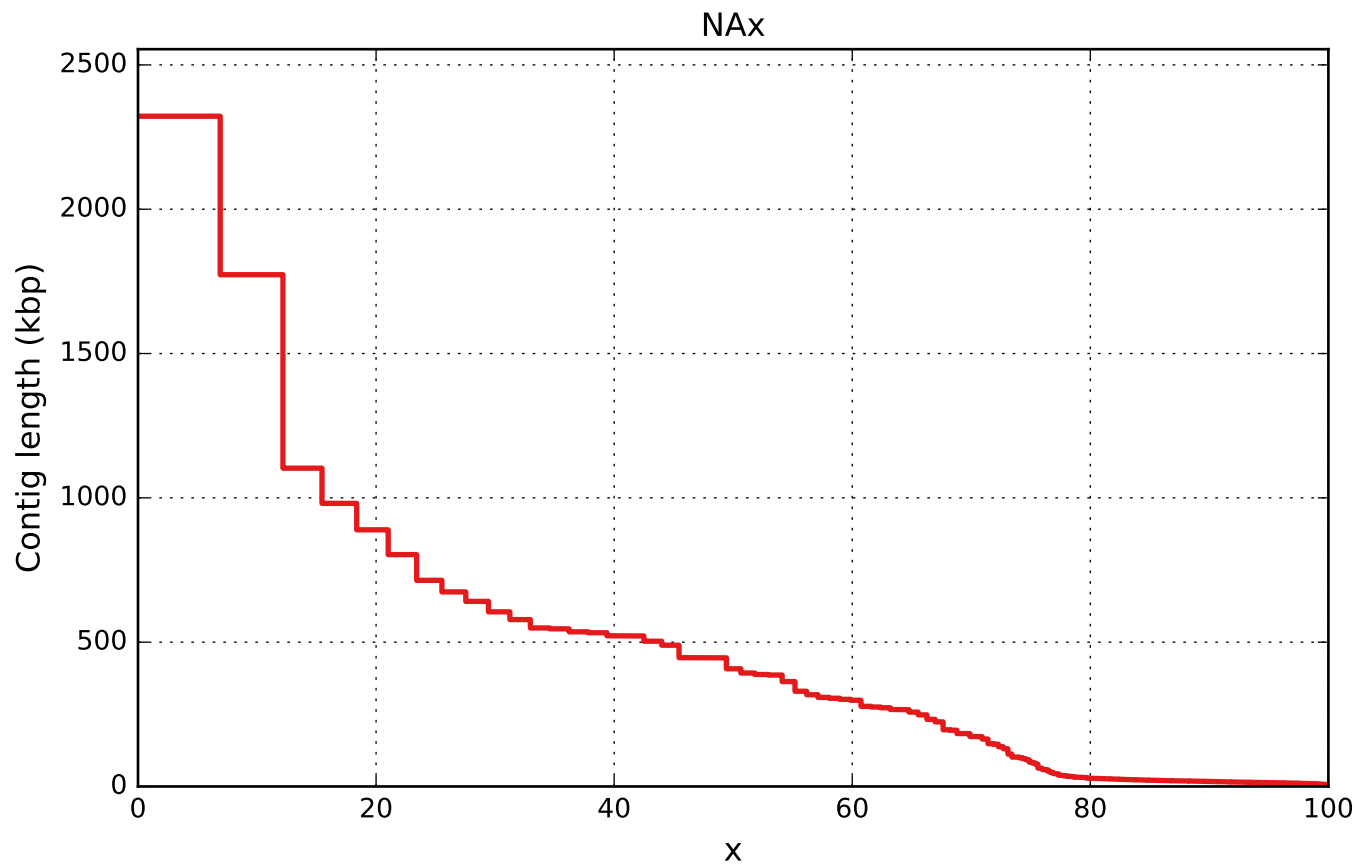


FRCurve (misassemblies)

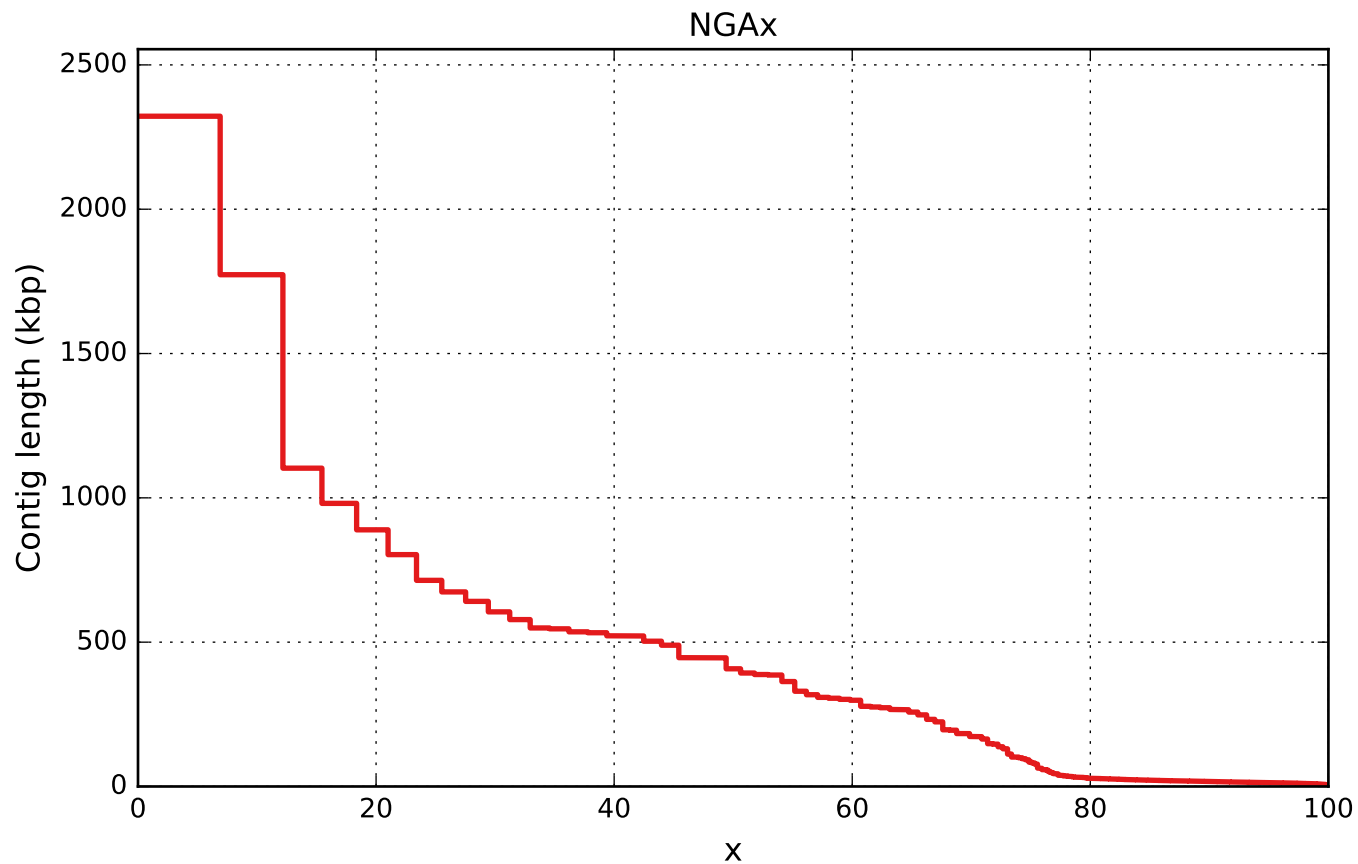


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