

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	26551601
GC (%)	31.15
Reference GC (%)	30.98
N50	446274
NG50	549201
N75	84359
NG75	317884
L50	19
LG50	13
L75	54
LG75	27
# misassemblies	238
# misassembled contigs	121
Misassembled contigs length	23992761
# local misassemblies	259
# unaligned mis. contigs	18
# unaligned contigs	152 + 207 part
Unaligned length	3983266
Genome fraction (%)	96.963
Duplication ratio	1.151
# N's per 100 kbp	0.00
# mismatches per 100 kbp	307.31
# indels per 100 kbp	129.36
Largest alignment	1260856
Total aligned length	29635215
NA50	211111
NGA50	283455
NA75	25480
NGA75	131861
LA50	39
LGA50	25
LA75	136
LGA75	58

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

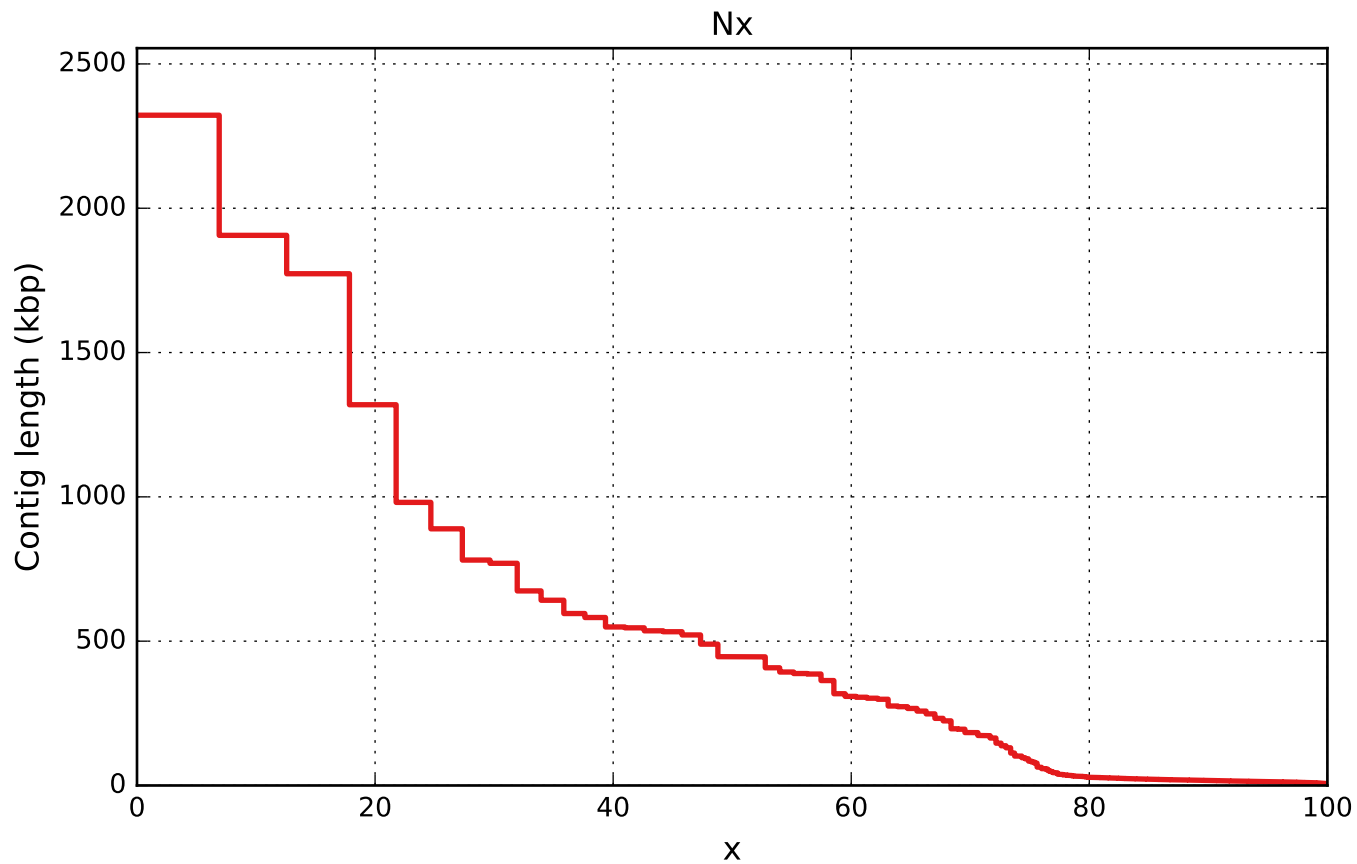
	corrected_DNA
# misassemblies	238
# relocations	237
# translocations	0
# inversions	1
# misassembled contigs	121
Misassembled contigs length	23992761
# local misassemblies	259
# unaligned mis. contigs	18
# mismatches	79117
# indels	33305
# indels (≤ 5 bp)	31098
# indels (> 5 bp)	2207
Indels length	71940

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

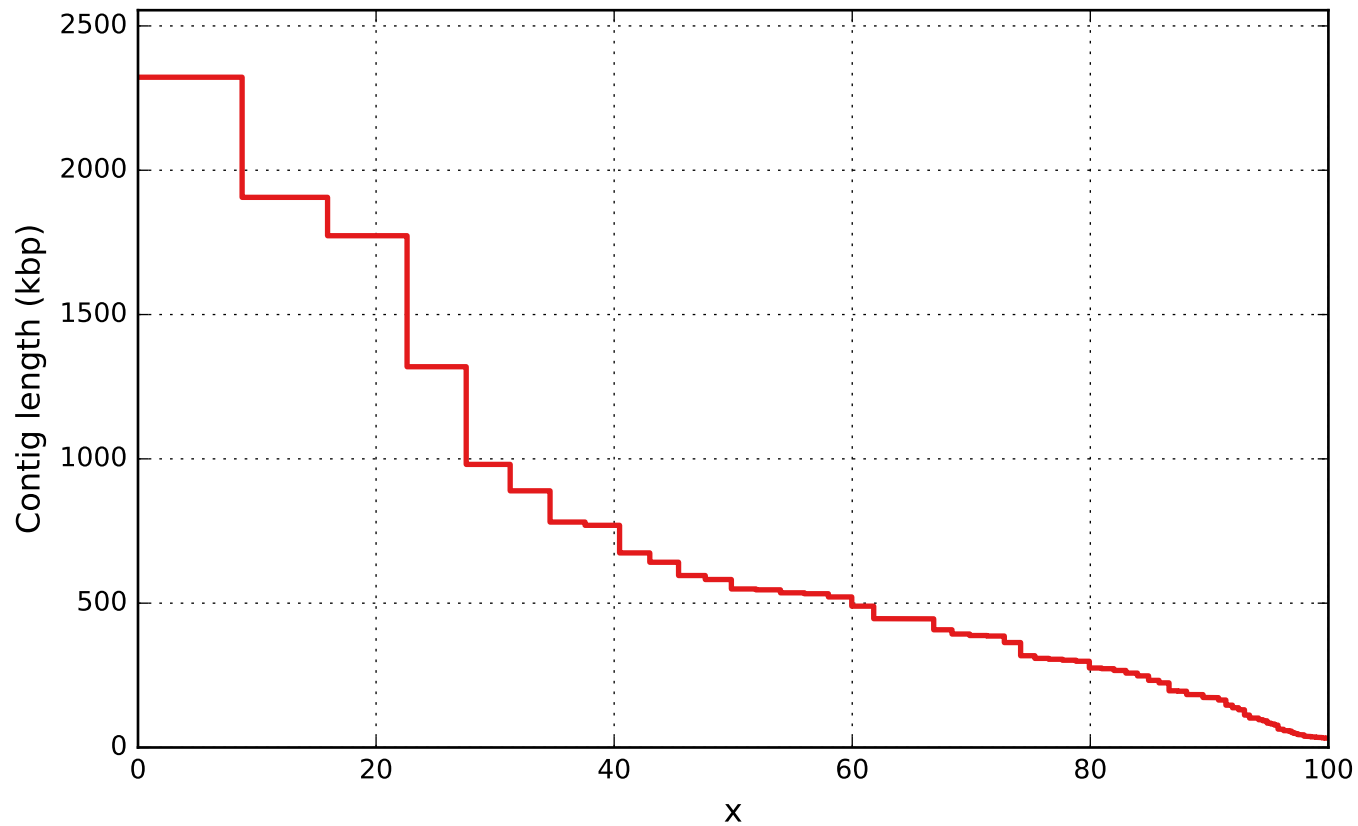
	corrected_DNA
# fully unaligned contigs	152
Fully unaligned length	2066526
# partially unaligned contigs	207
Partially unaligned length	1916740
# N's	0

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).

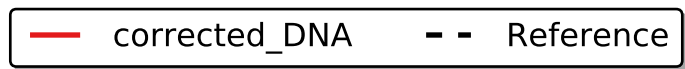
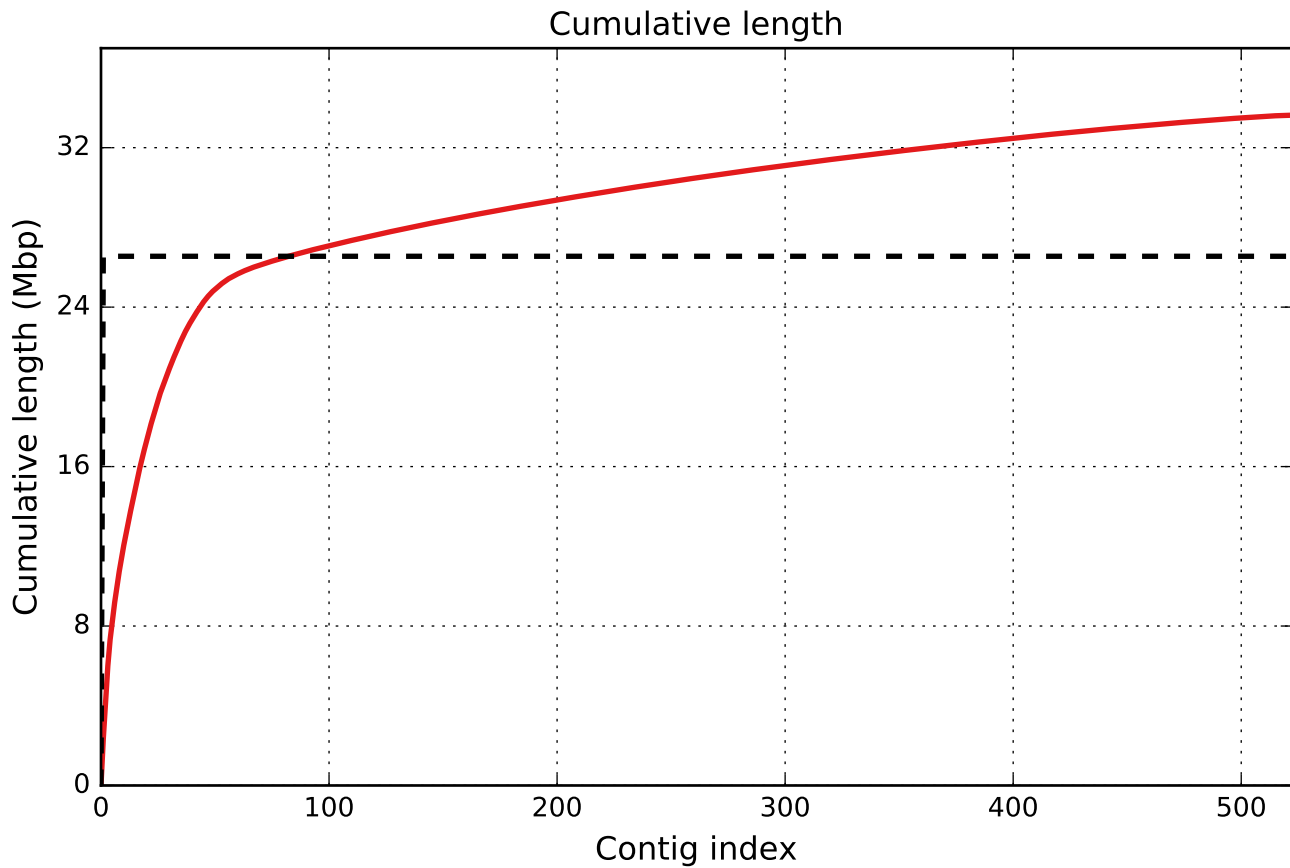


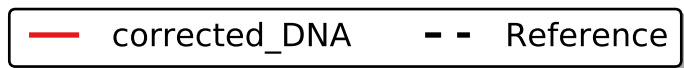
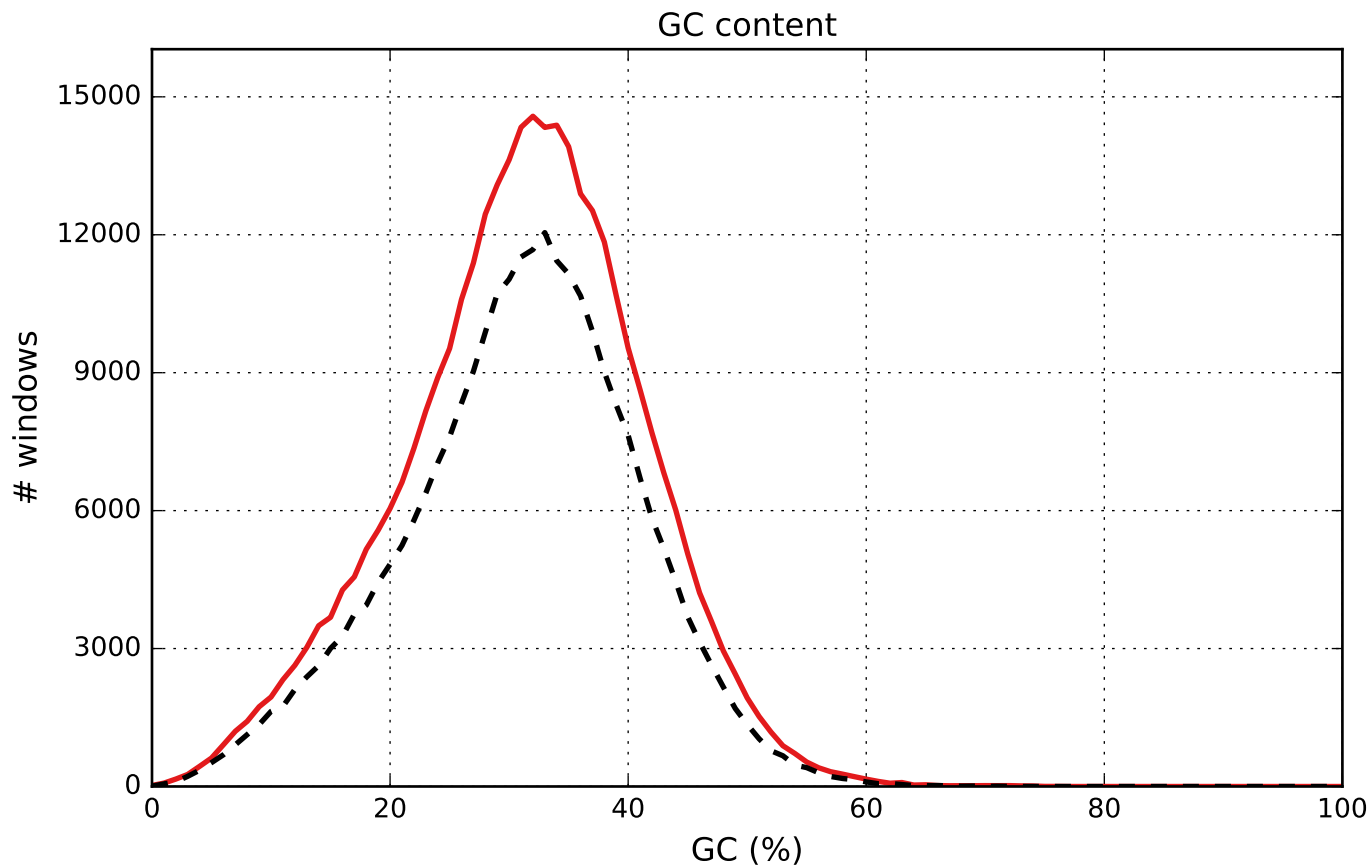
— corrected_DNA

NGx

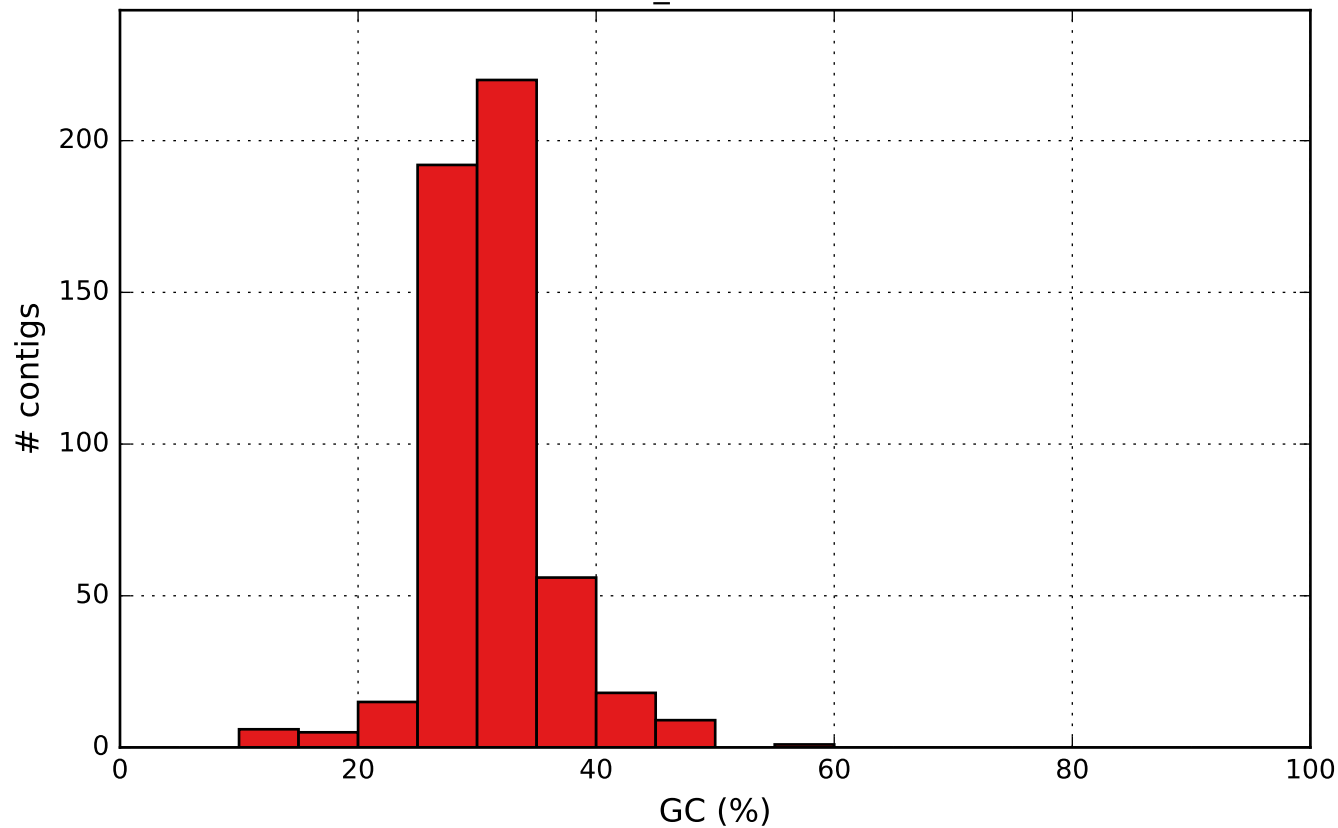


— corrected_DNA



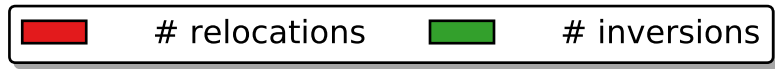
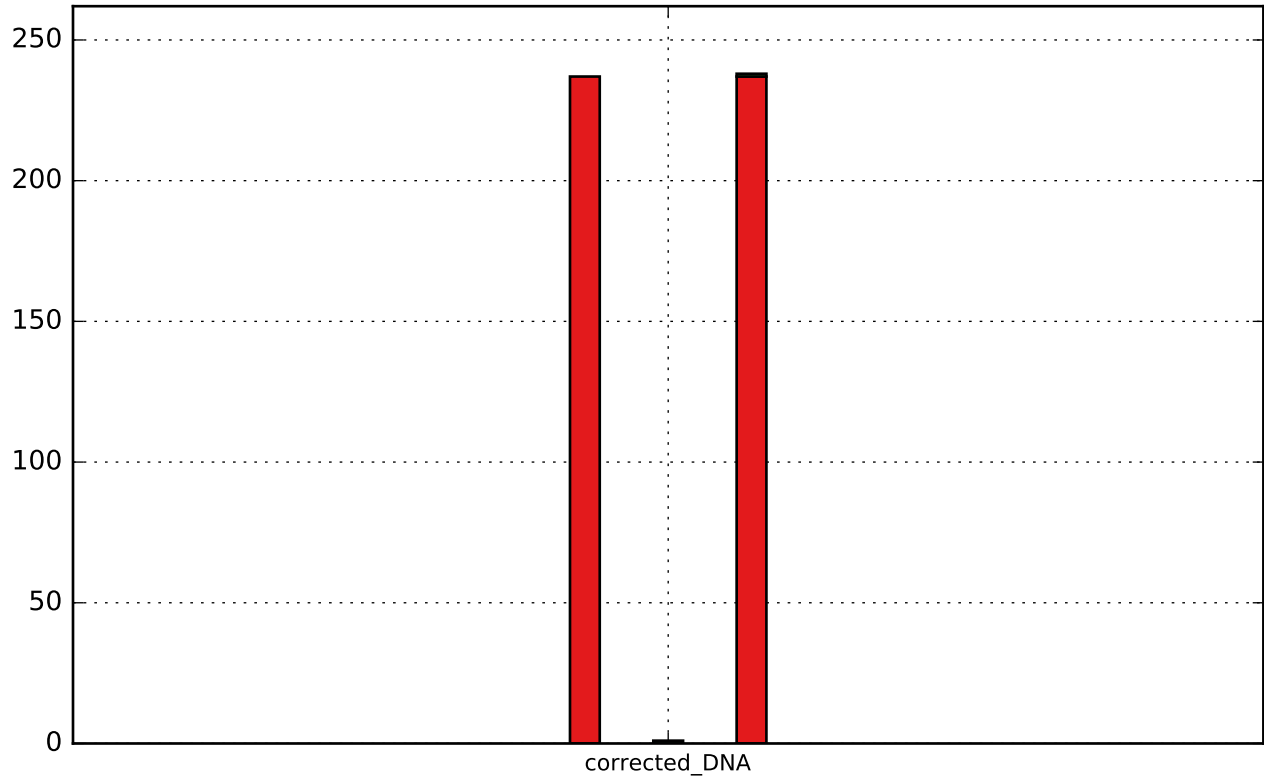


corrected_DNA GC content

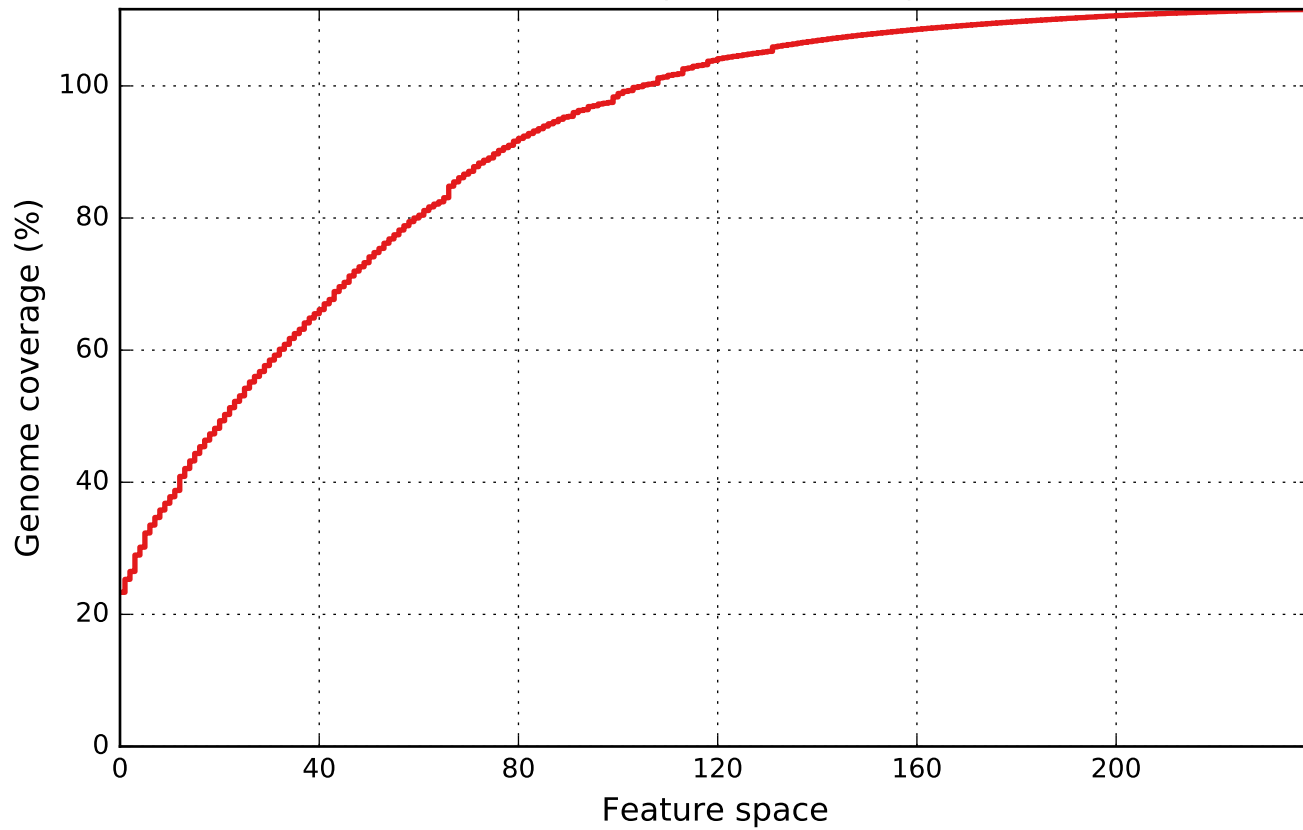


corrected_DNA

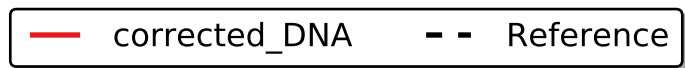
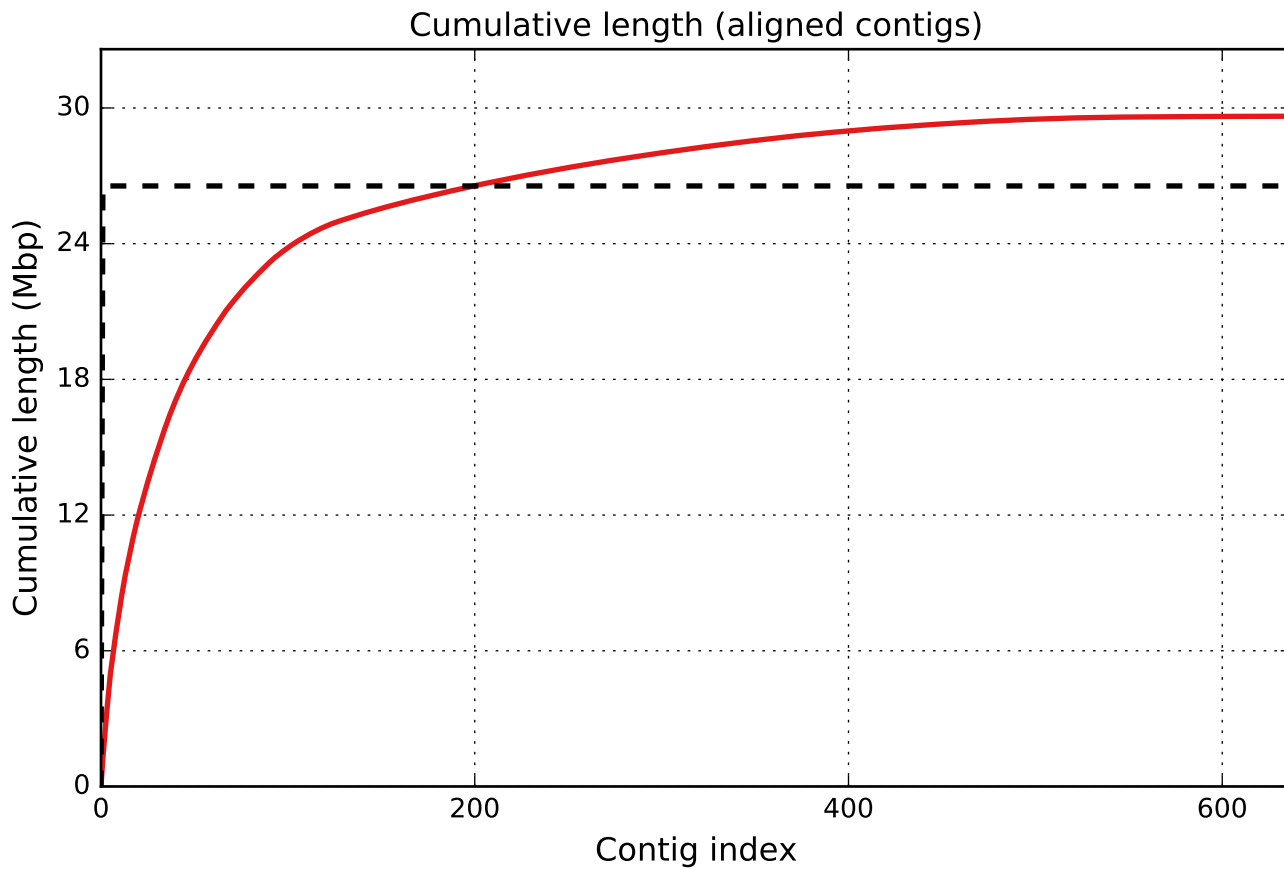
Misassemblies



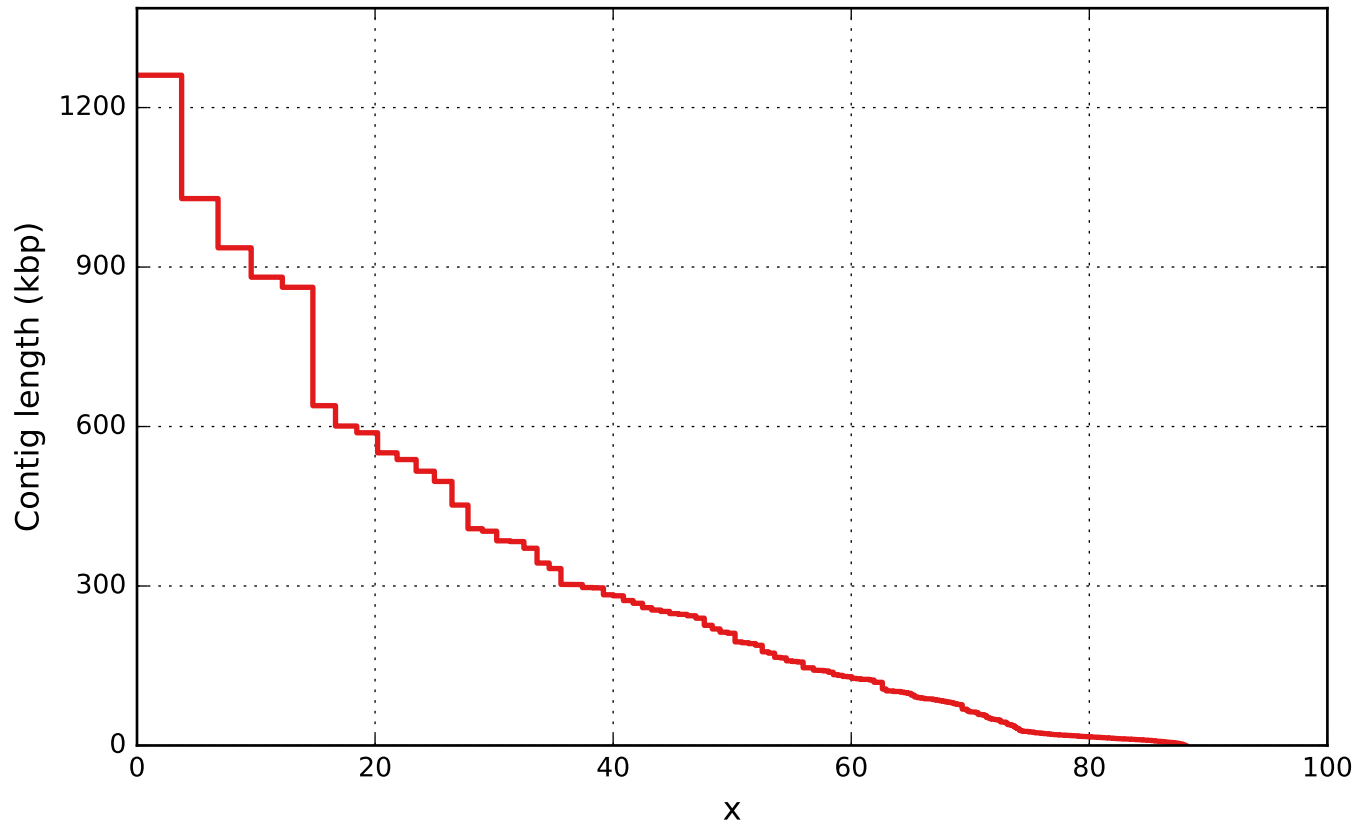
FRCurve (misassemblies)



— corrected_DNA

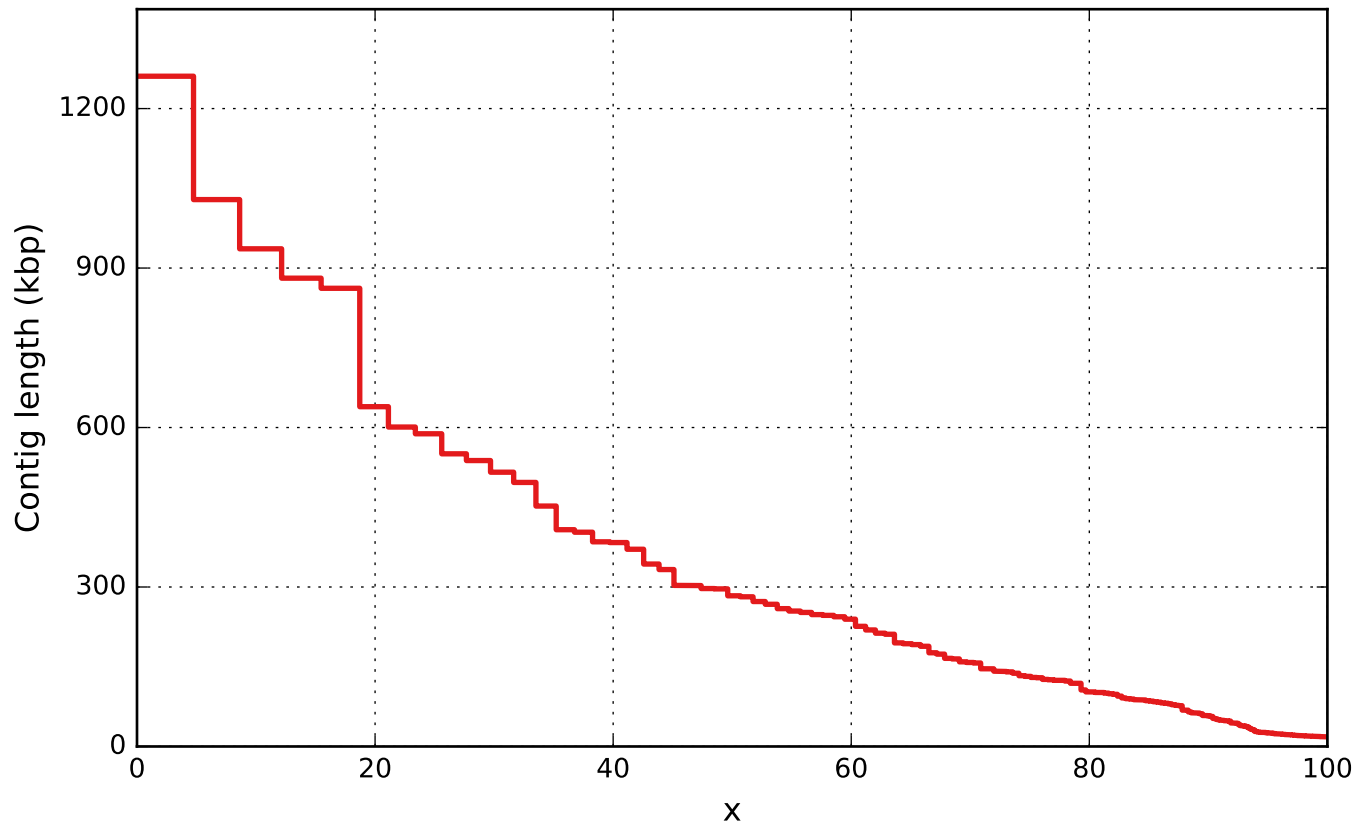


NAx



— corrected_DNA

NGAx



— corrected_DNA