

Report

	corrected_assembly
# contigs (>= 0 bp)	538
# contigs (>= 1000 bp)	538
# contigs (>= 5000 bp)	527
# contigs (>= 10000 bp)	439
# contigs (>= 25000 bp)	118
# contigs (>= 50000 bp)	58
Total length (>= 0 bp)	27925150
Total length (>= 1000 bp)	27925150
Total length (>= 5000 bp)	27887417
Total length (>= 10000 bp)	27178842
Total length (>= 25000 bp)	22153856
Total length (>= 50000 bp)	20244960
# contigs	538
Largest contig	2785036
Total length	27925150
Reference length	24162007
GC (%)	31.64
Reference GC (%)	33.51
N50	351076
NG50	569034
N75	33808
NG75	148438
L50	16
LG50	11
L75	76
LG75	34
# misassemblies	153
# misassembled contigs	84
Misassembled contigs length	17779969
# local misassemblies	222
# unaligned mis. contigs	16
# unaligned contigs	168 + 184 part
Unaligned length	3739095
Genome fraction (%)	85.742
Duplication ratio	1.167
# N's per 100 kbp	0.00
# mismatches per 100 kbp	325.38
# indels per 100 kbp	123.42
Largest alignment	2720194
Total aligned length	24171359
NA50	199171
NGA50	234128
NA75	20137
NGA75	72188
LA50	30
LGA50	22
LA75	151
LGA75	68

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

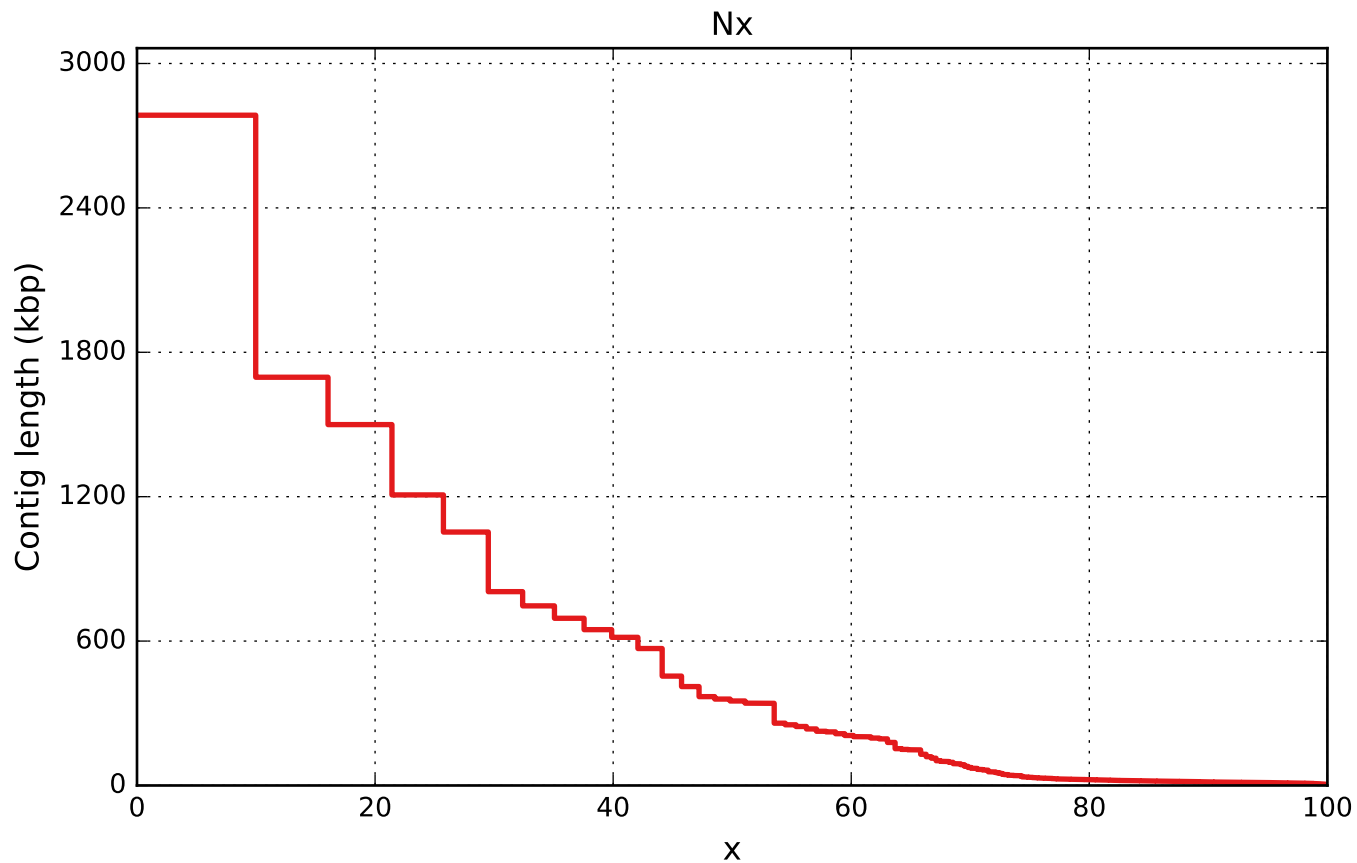
	corrected_assembly
# misassemblies	153
# relocations	149
# translocations	0
# inversions	4
# misassembled contigs	84
Misassembled contigs length	17779969
# local misassemblies	222
# unaligned mis. contigs	16
# mismatches	67410
# indels	25569
# indels (≤ 5 bp)	24067
# indels (> 5 bp)	1502
Indels length	51834

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

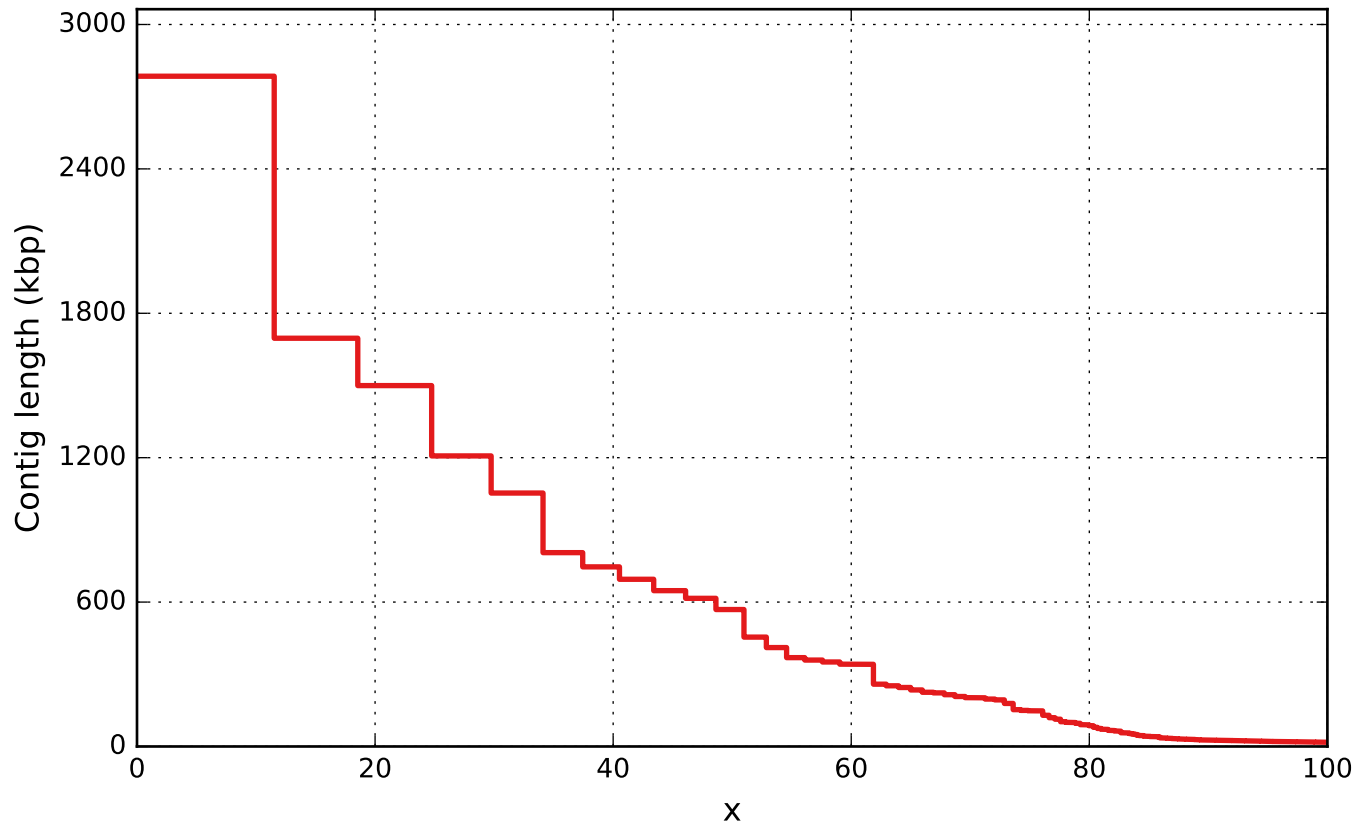
	corrected_assembly
# fully unaligned contigs	168
Fully unaligned length	2077941
# partially unaligned contigs	184
Partially unaligned length	1661154
# N's	0

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).

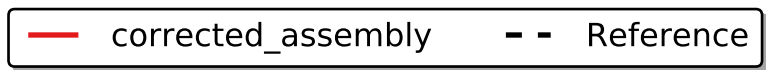
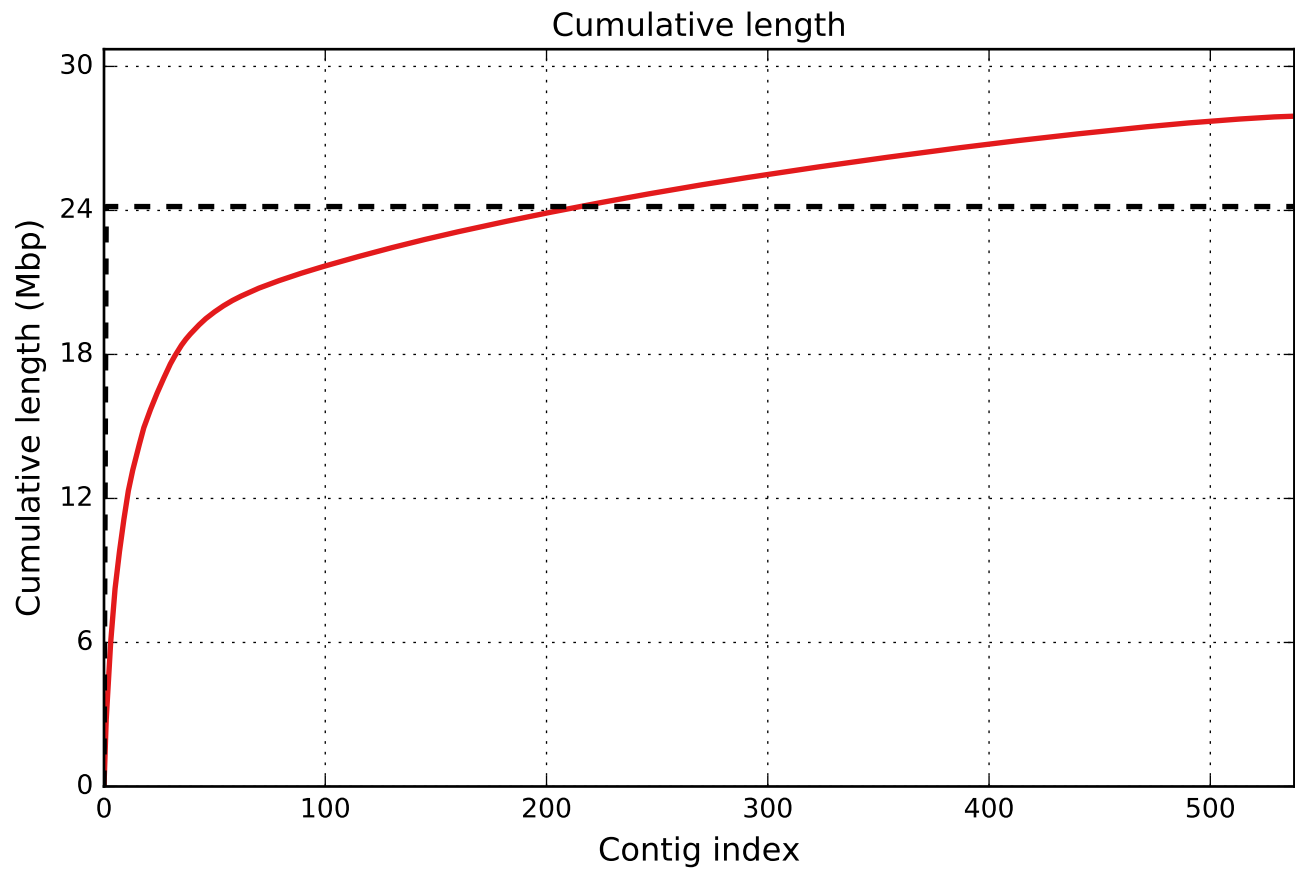


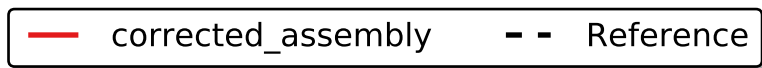
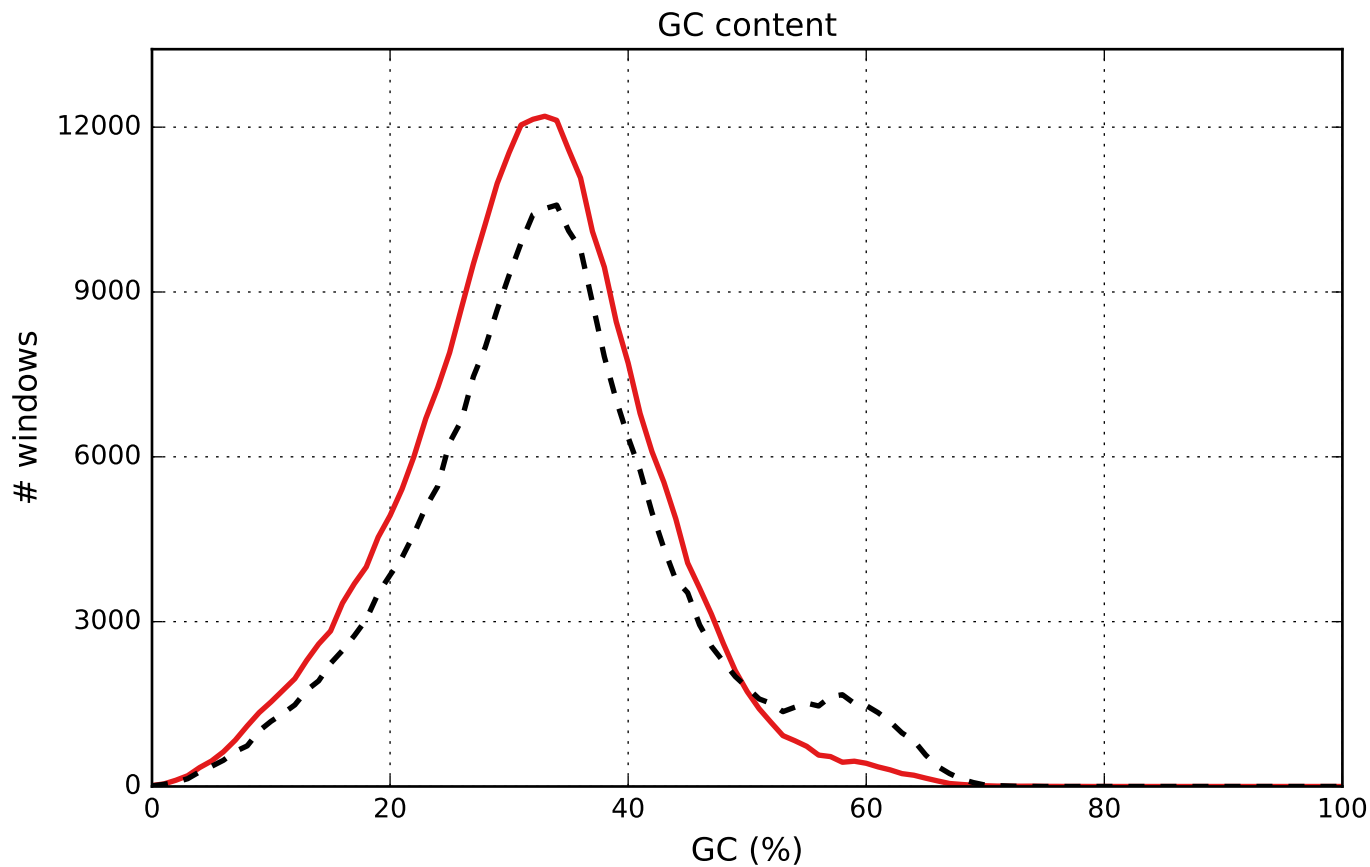
— corrected_assembly

NGx

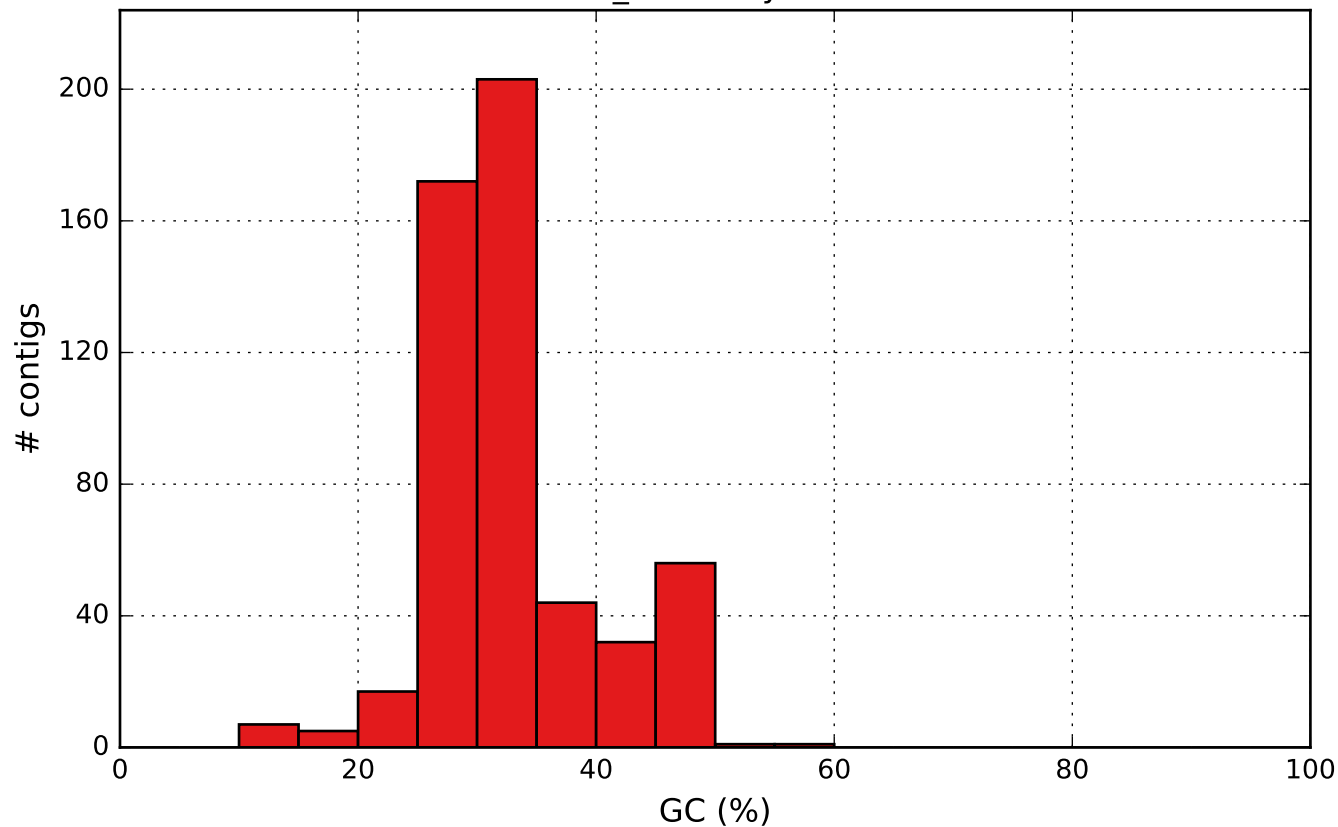


— corrected_assembly



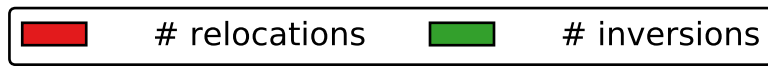
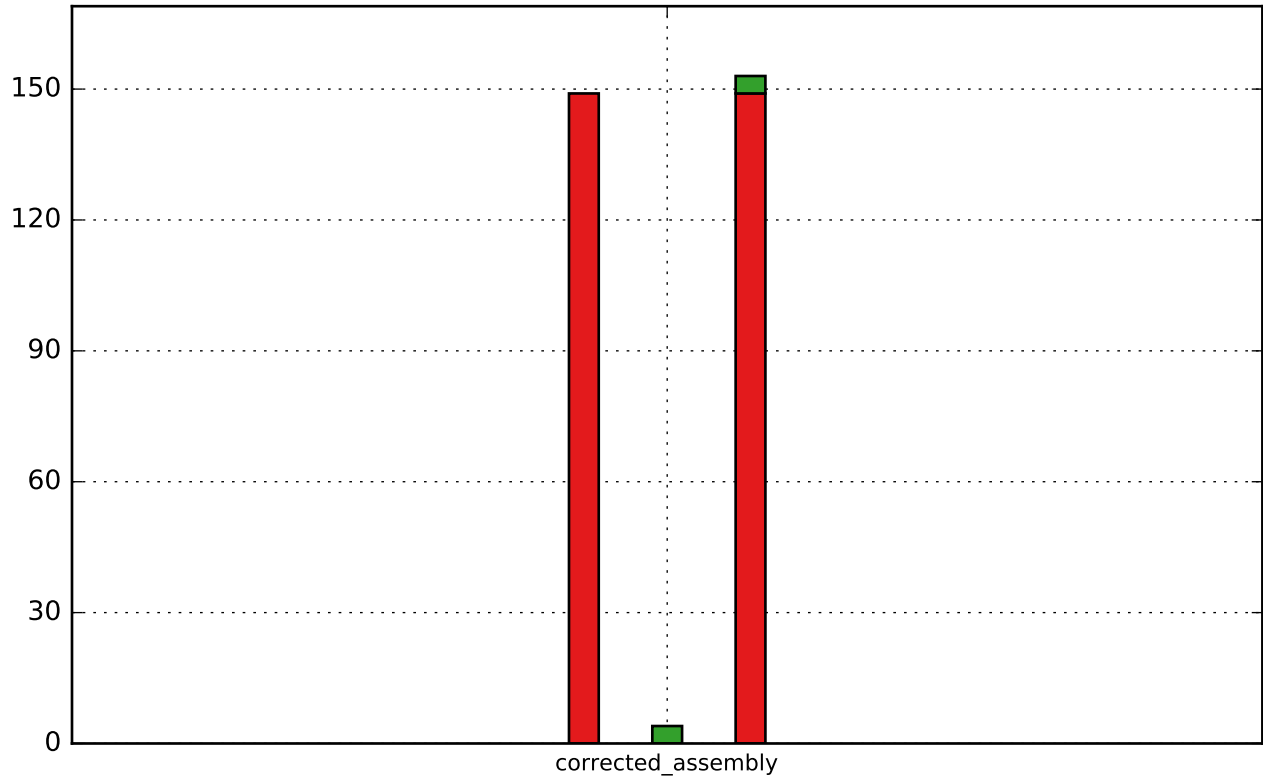


corrected_assembly GC content

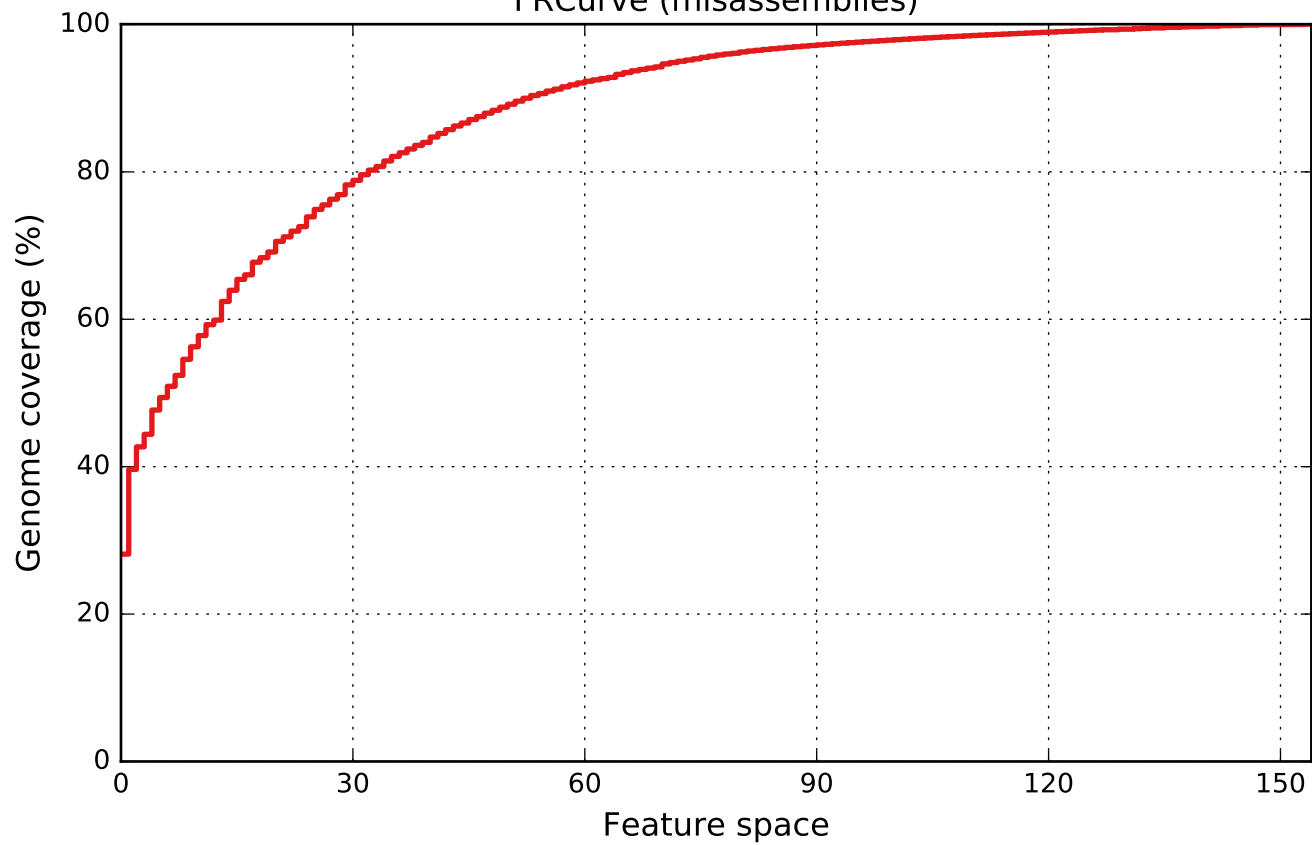


corrected_assembly

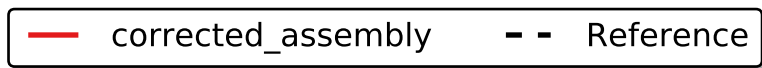
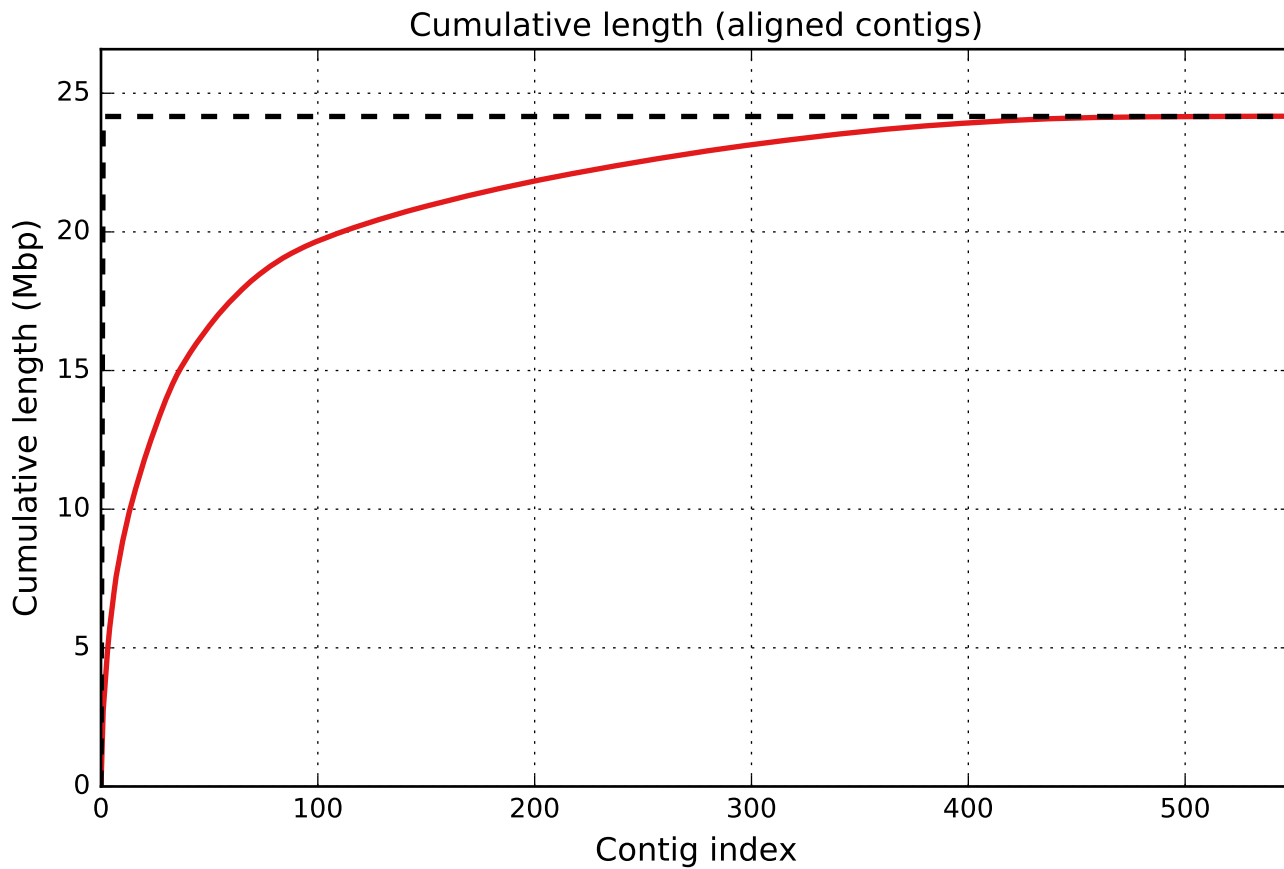
Misassemblies



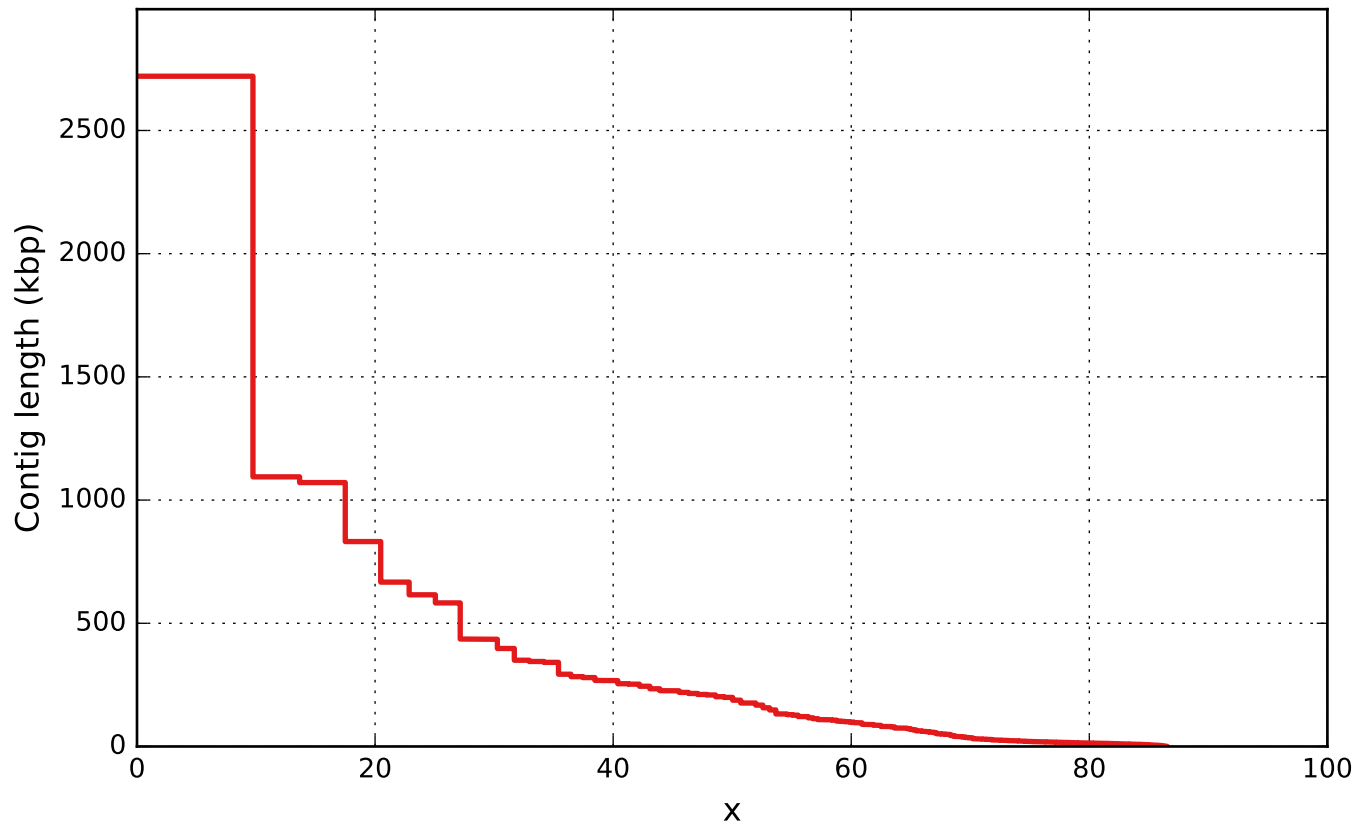
FRCurve (misassemblies)



— corrected_assembly

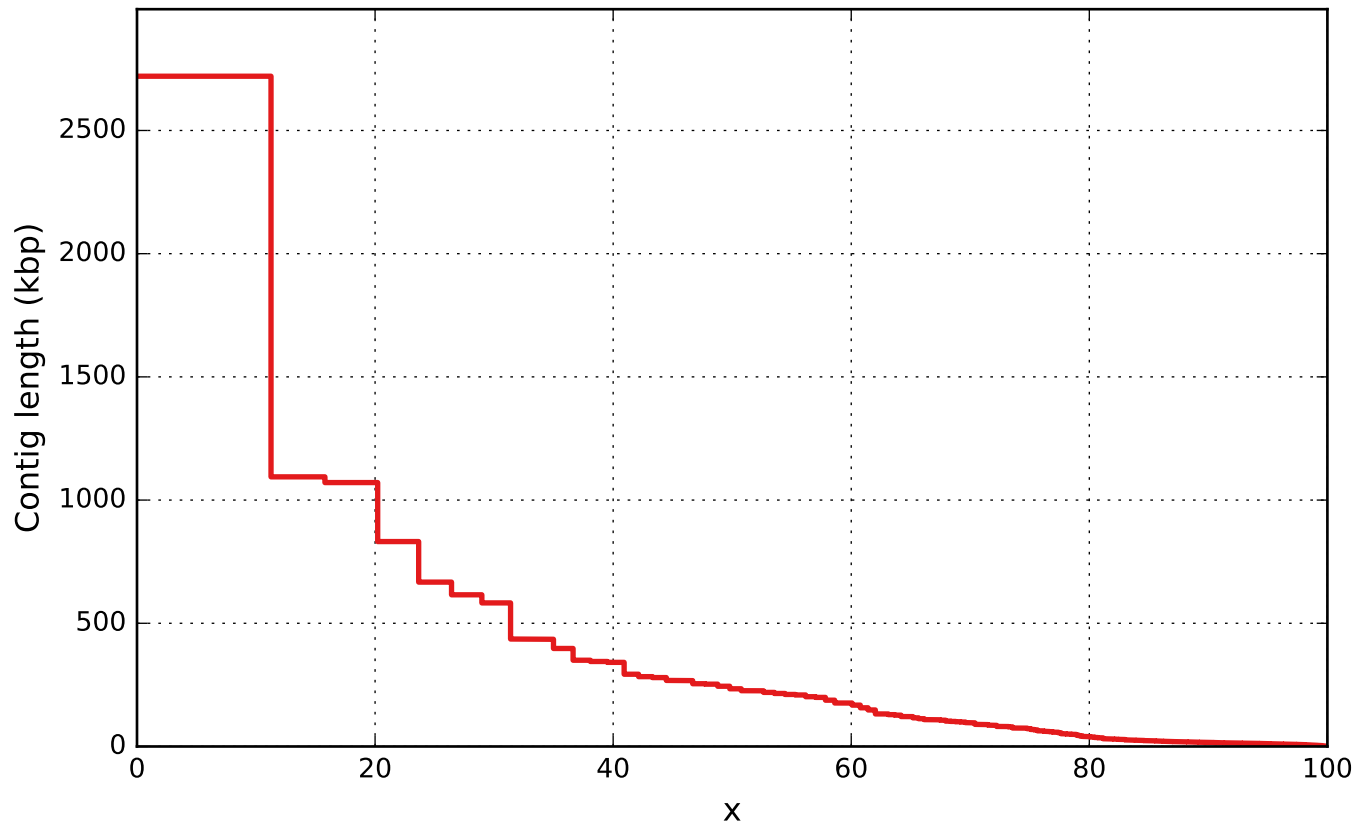


NAx



— corrected_assembly

NGAx



— corrected_assembly