

Report

	contigs
# contigs (>= 0 bp)	538
# contigs (>= 1000 bp)	538
# contigs (>= 5000 bp)	527
# contigs (>= 10000 bp)	439
# contigs (>= 25000 bp)	119
# contigs (>= 50000 bp)	58
Total length (>= 0 bp)	27925069
Total length (>= 1000 bp)	27925069
Total length (>= 5000 bp)	27887318
Total length (>= 10000 bp)	27179176
Total length (>= 25000 bp)	22179986
Total length (>= 50000 bp)	20246631
# contigs	538
Largest contig	2787429
Total length	27925069
Reference length	24162007
GC (%)	31.63
Reference GC (%)	33.51
N50	350884
NG50	568844
N75	33804
NG75	148468
L50	16
LG50	11
L75	76
LG75	34
# misassemblies	161
# misassembled contigs	85
Misassembled contigs length	17805527
# local misassemblies	212
# unaligned mis. contigs	11
# unaligned contigs	171 + 178 part
Unaligned length	3771654
Genome fraction (%)	85.638
Duplication ratio	1.167
# N's per 100 kbp	0.00
# mismatches per 100 kbp	323.24
# indels per 100 kbp	186.89
Largest alignment	2719392
Total aligned length	24138674
NA50	187789
NGA50	234087
NA75	20008
NGA75	63420
LA50	31
LGA50	22
LA75	156
LGA75	70

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

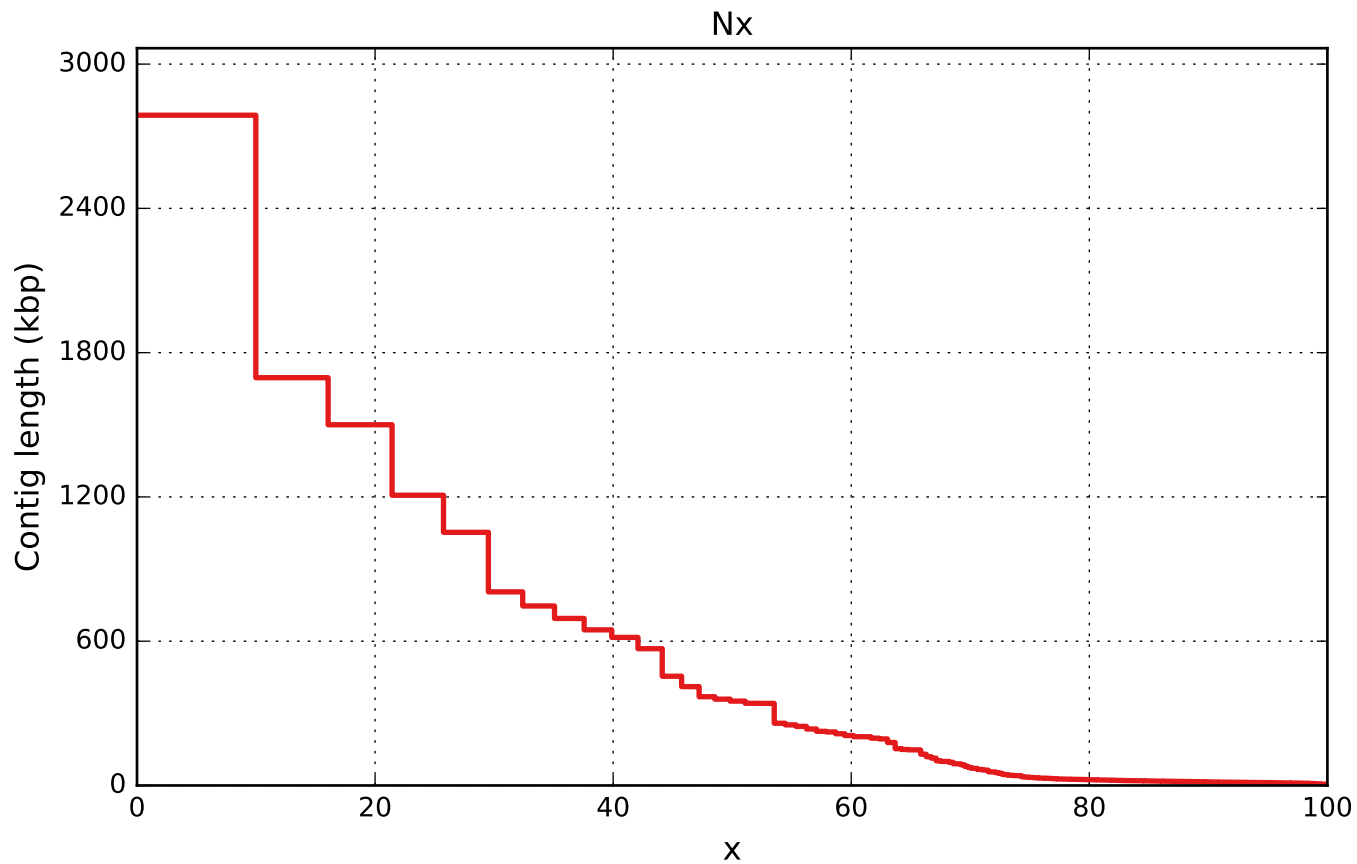
	contigs
# misassemblies	161
# relocations	157
# translocations	0
# inversions	4
# misassembled contigs	85
Misassembled contigs length	17805527
# local misassemblies	212
# unaligned mis. contigs	11
# mismatches	66885
# indels	38671
# indels (<= 5 bp)	37117
# indels (> 5 bp)	1554
Indels length	67114

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

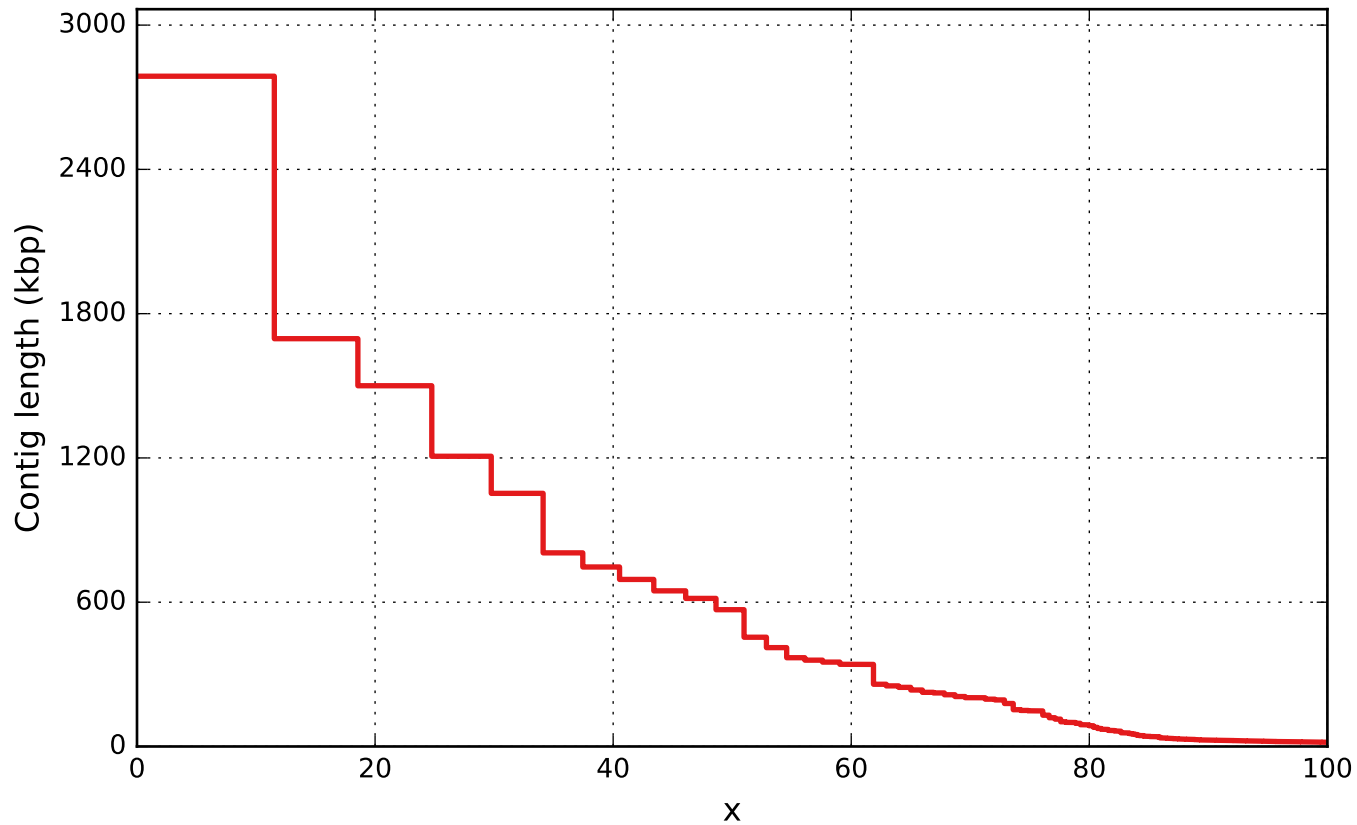
	contigs
# fully unaligned contigs	171
Fully unaligned length	2116938
# partially unaligned contigs	178
Partially unaligned length	1654716
# N's	0

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).

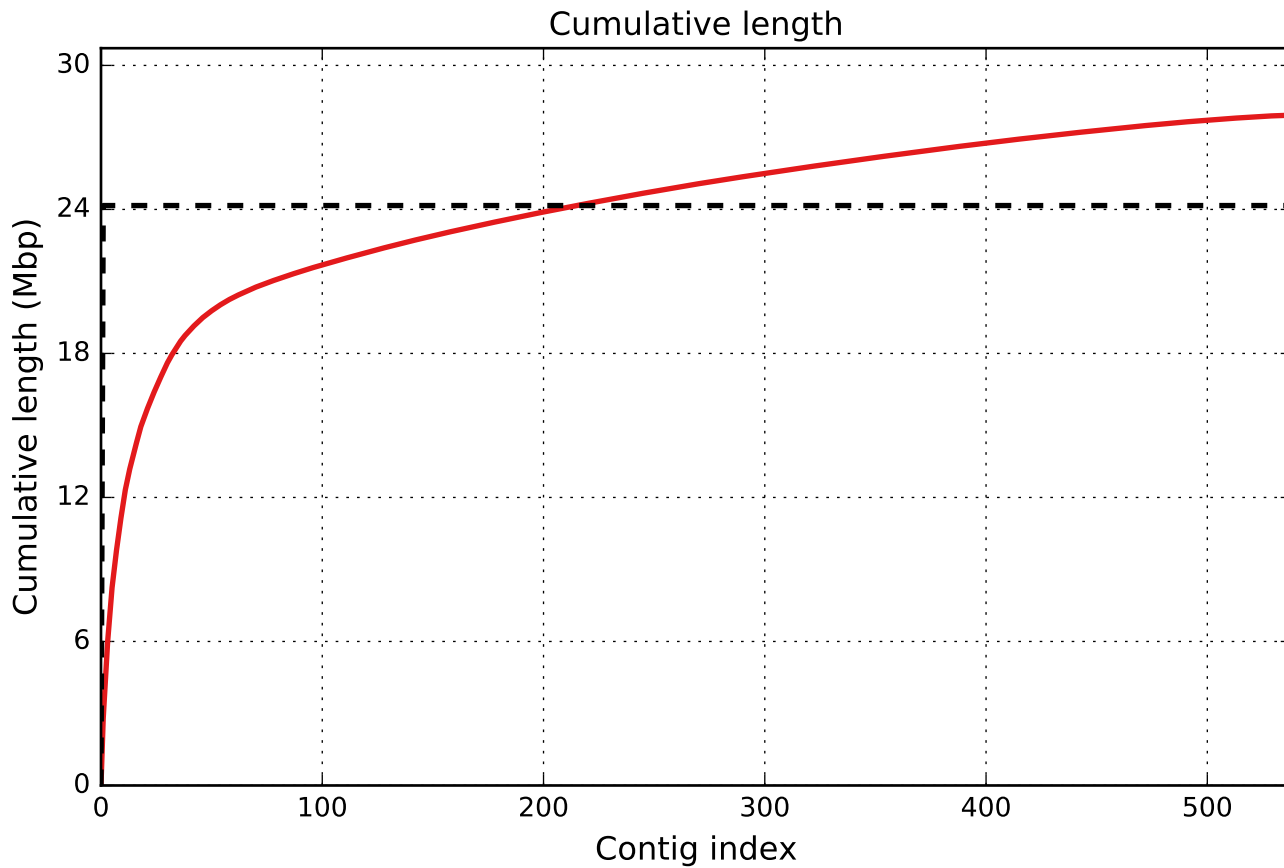


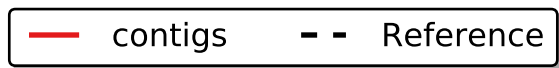
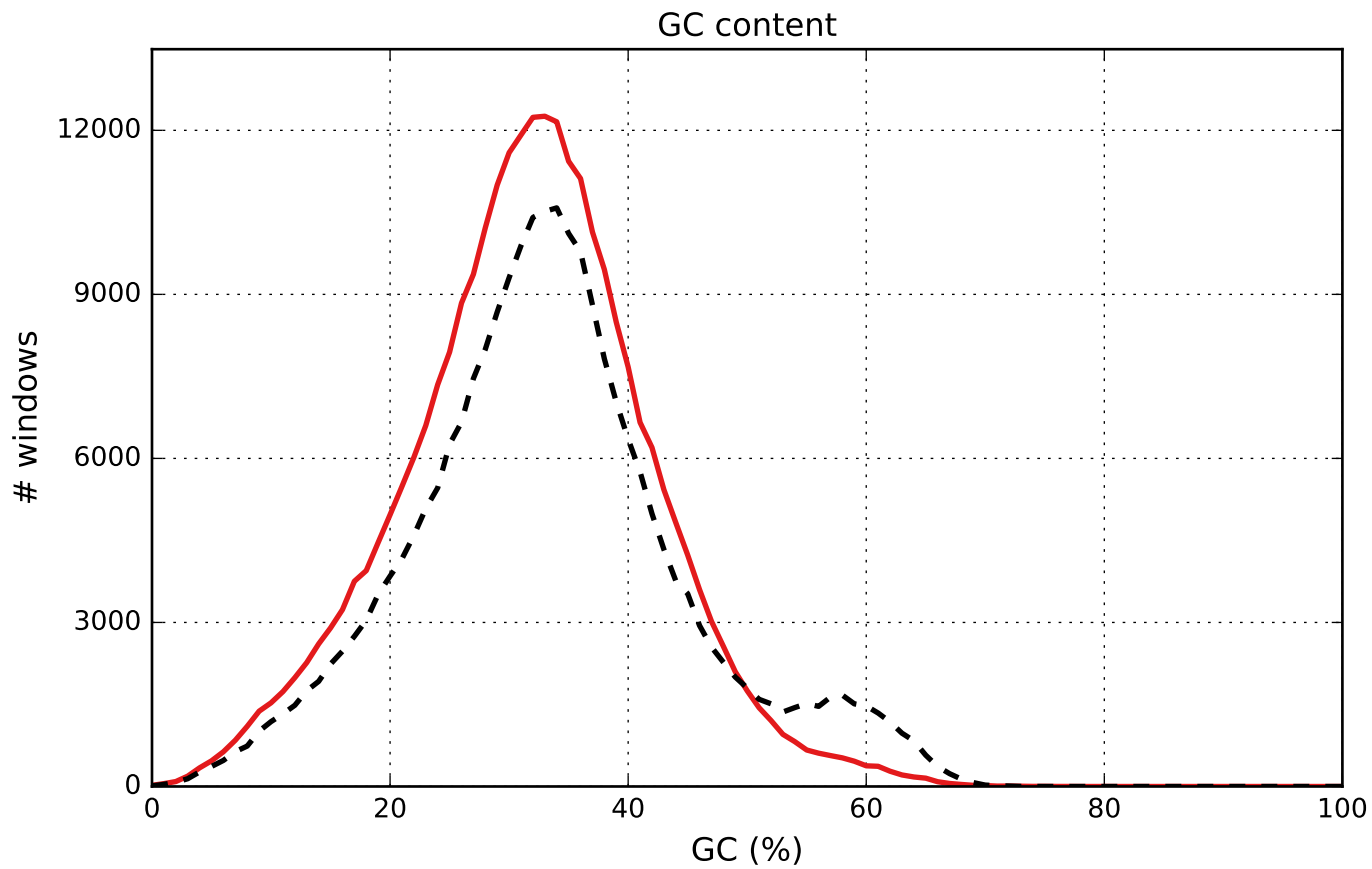
— contigs

NGx

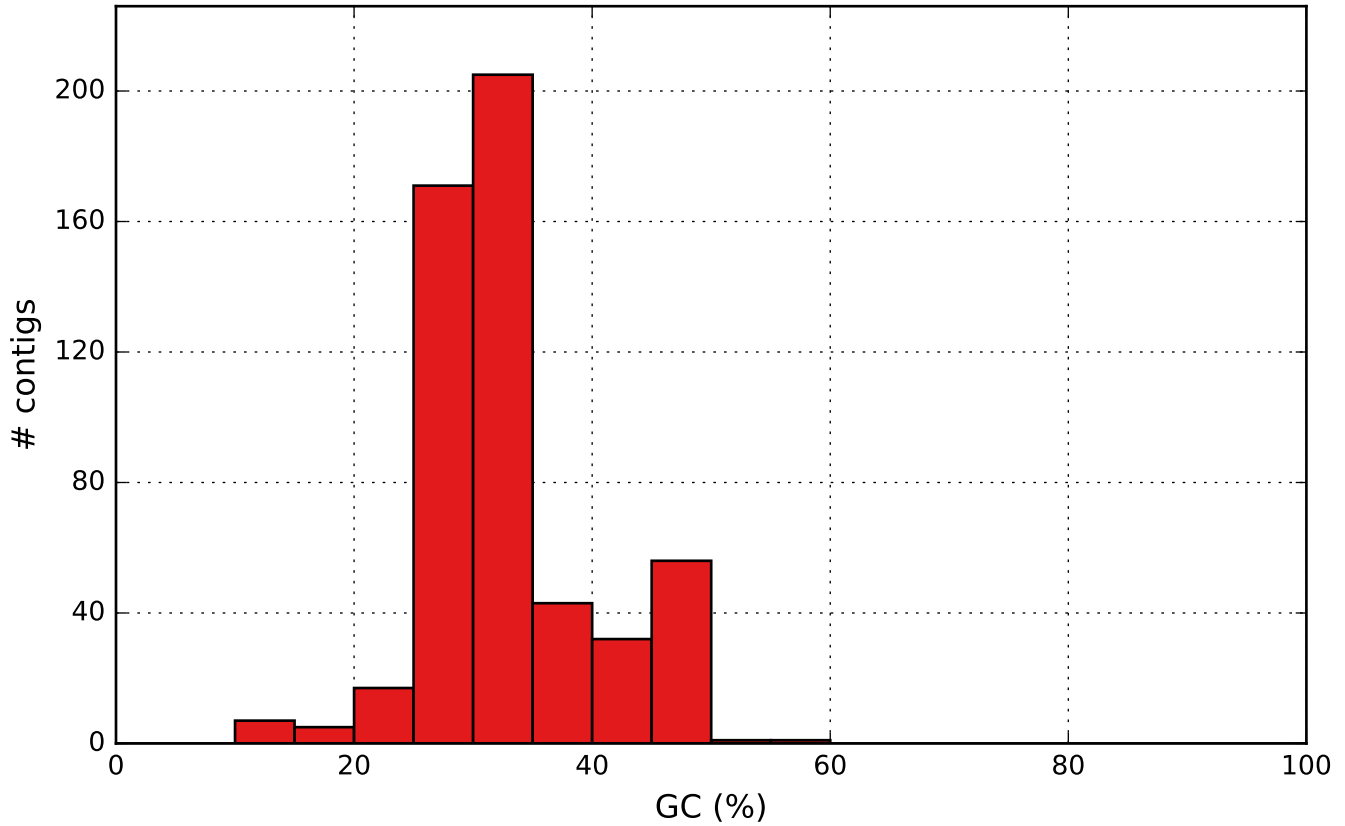


— contigs



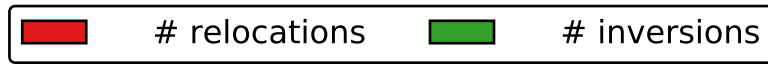
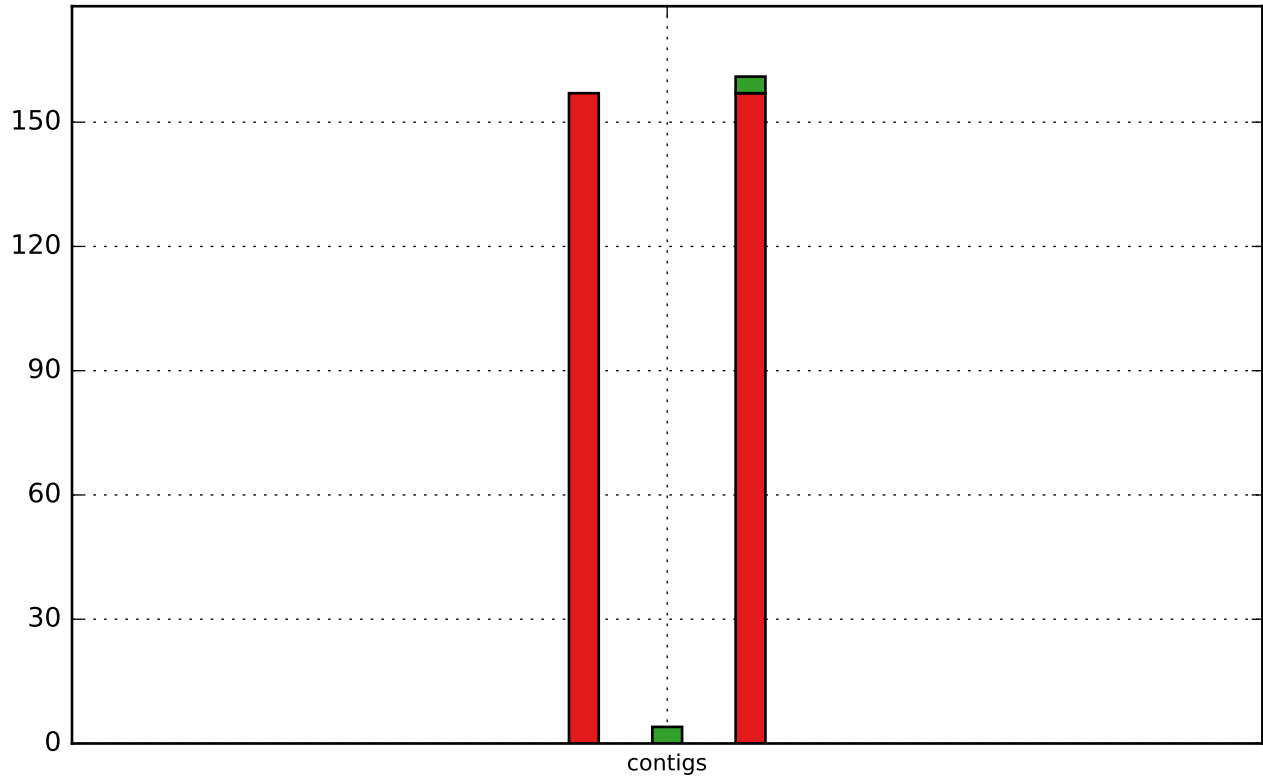


contigs GC content

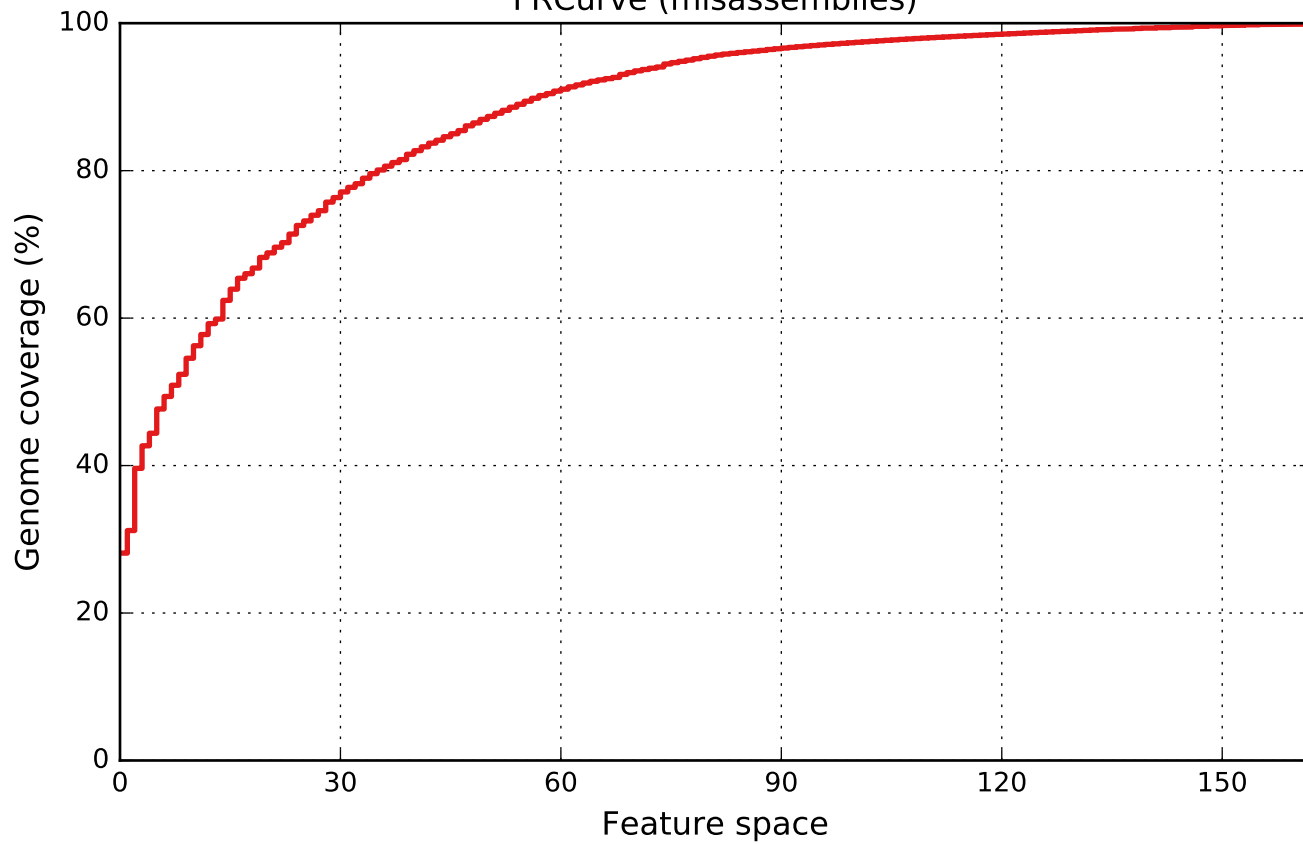


contigs

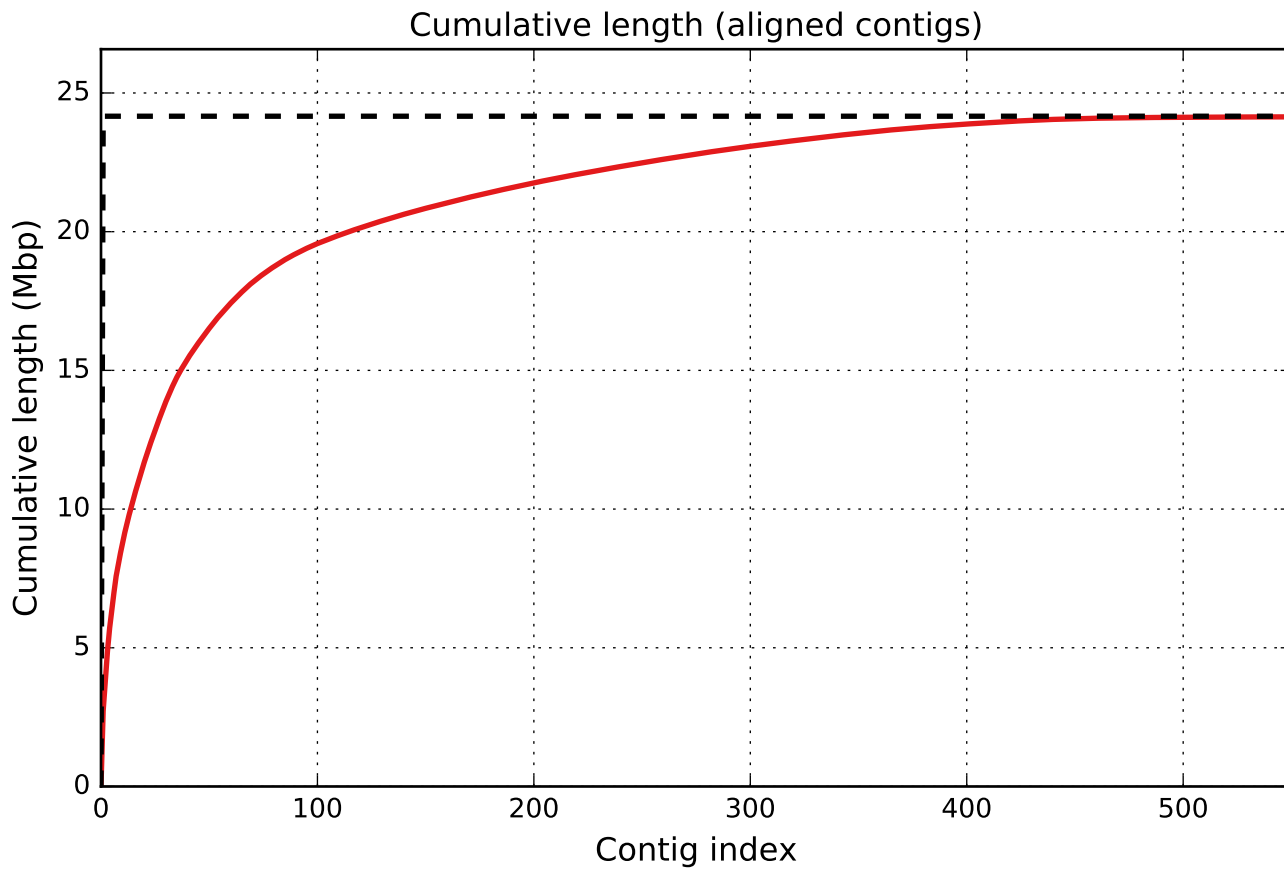
Misassemblies



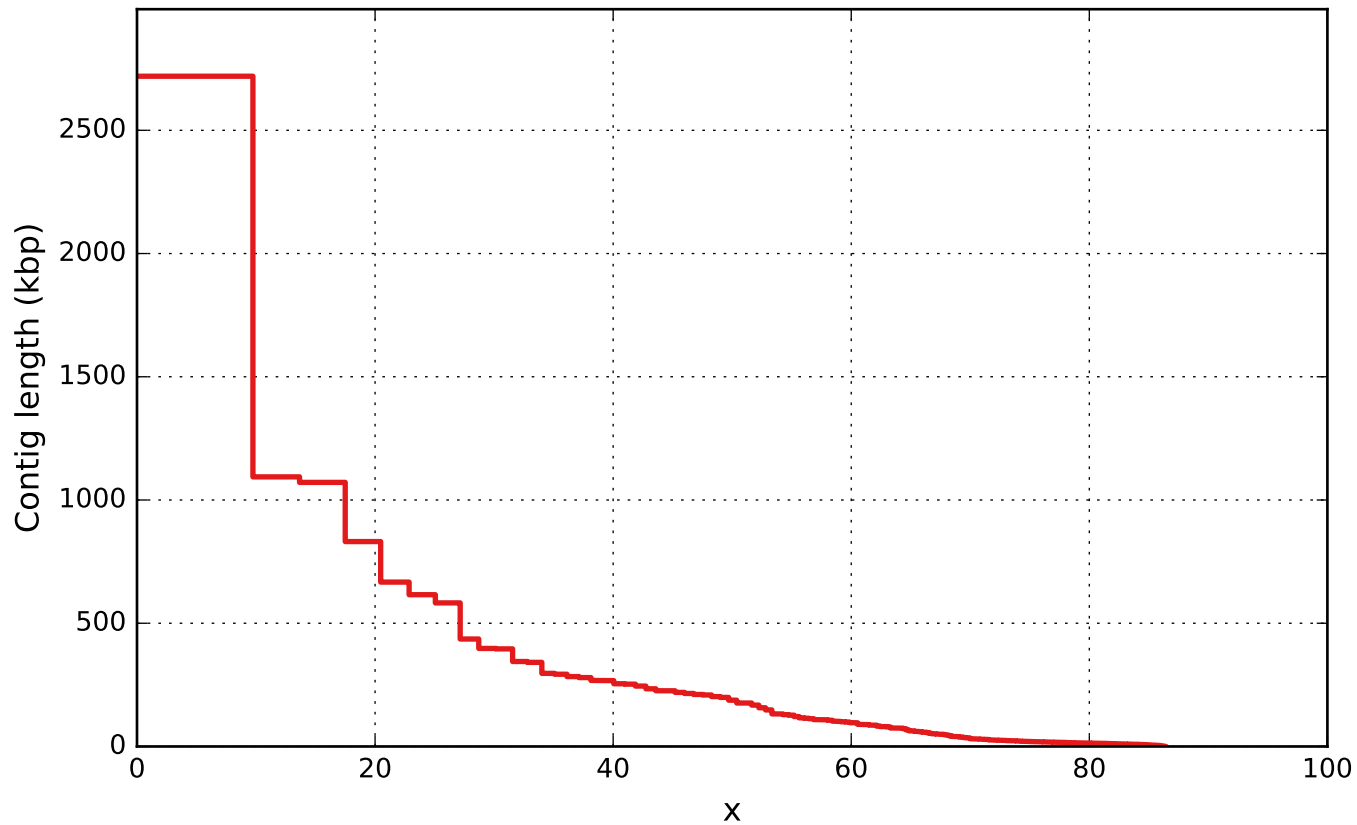
FRCurve (misassemblies)



— contigs

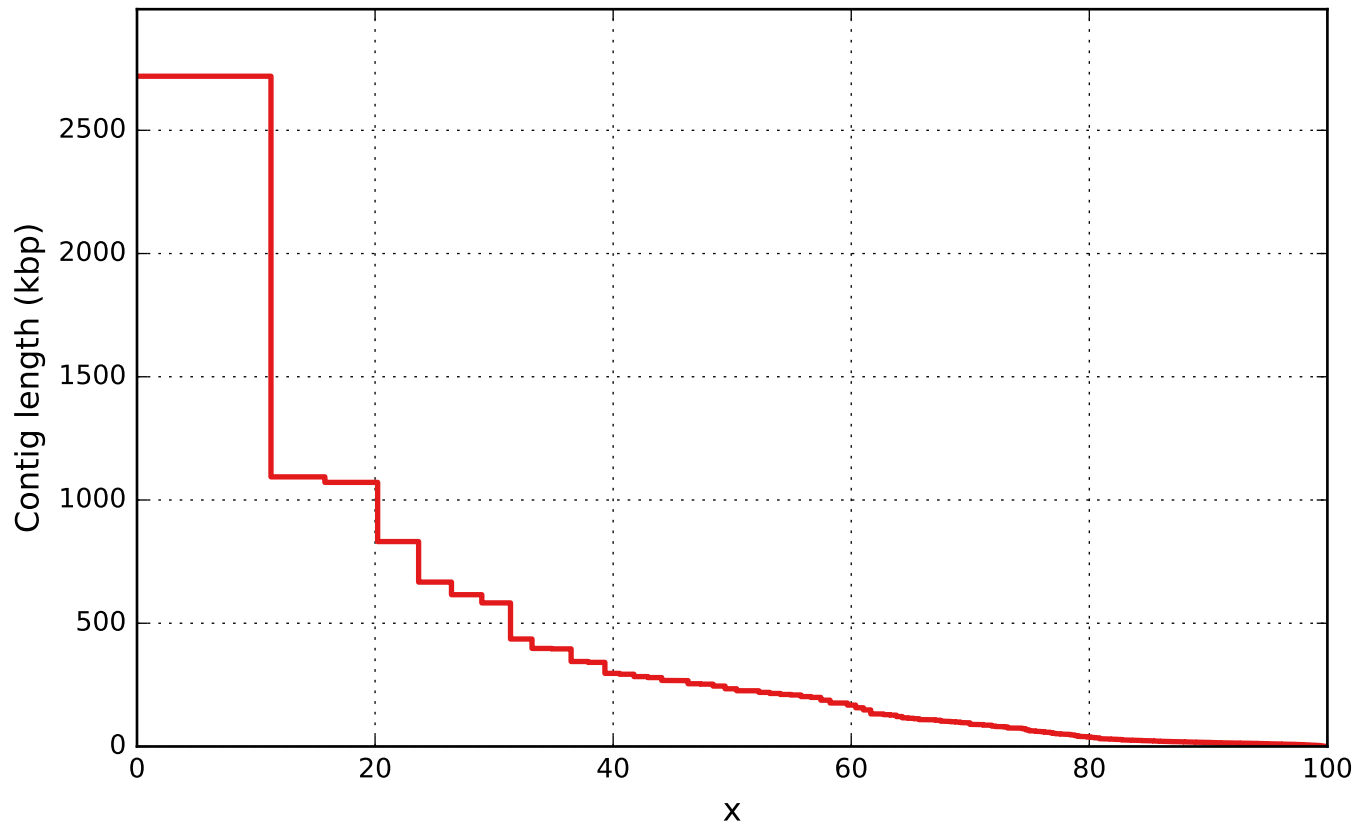


NAx



— contigs

NGAx



— contigs