

Report

	combined.final.contigs
# contigs (≥ 1000 bp)	6
# contigs (≥ 5000 bp)	3
# contigs (≥ 10000 bp)	2
# contigs (≥ 25000 bp)	1
# contigs (≥ 50000 bp)	1
Total length (≥ 1000 bp)	130792
Total length (≥ 5000 bp)	126947
Total length (≥ 10000 bp)	121128
Total length (≥ 25000 bp)	109683
Total length (≥ 50000 bp)	109683
# contigs	7
Largest contig	109683
Total length	131501
Reference length	2995049
GC (%)	56.15
Reference GC (%)	44.84
N50	109683
N75	109683
L50	1
L75	1
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 7 part
Unaligned length	130863
Genome fraction (%)	0.013
Duplication ratio	1.636
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1282.05
# indels per 100 kbp	0.00
Largest alignment	144
Total aligned length	638
NGA50	-

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

	combined.final.contigs
# 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	5
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

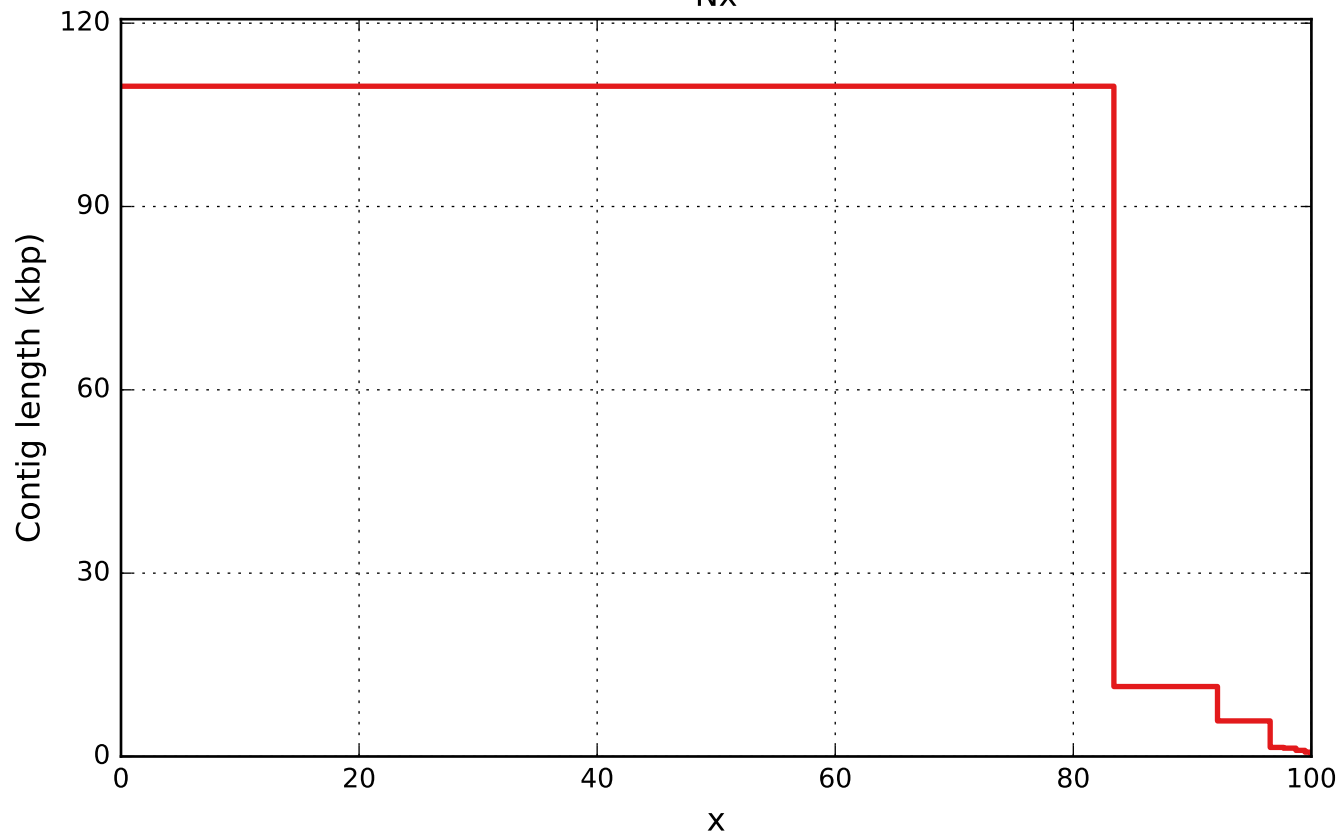
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	combined.final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	7
Partially unaligned length	130863
# N's	0

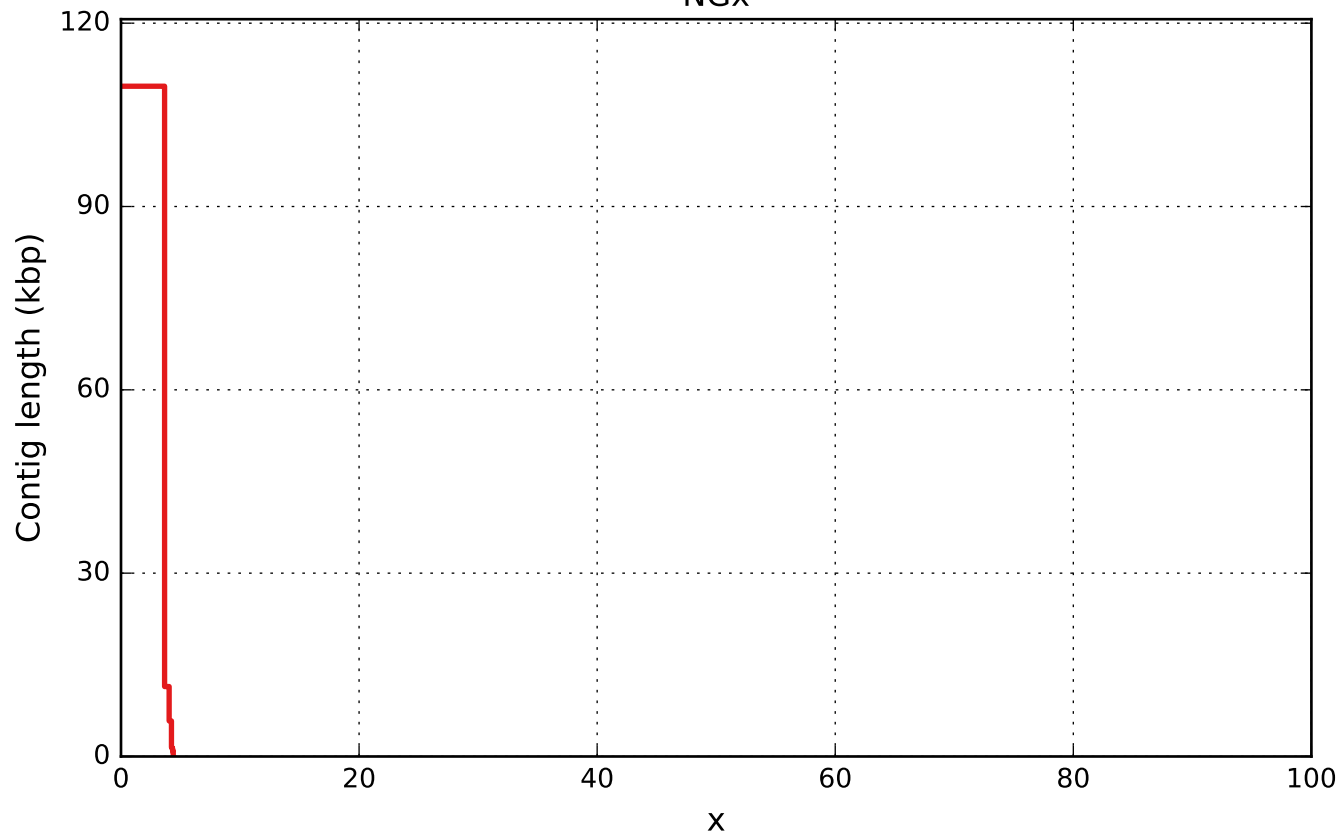
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

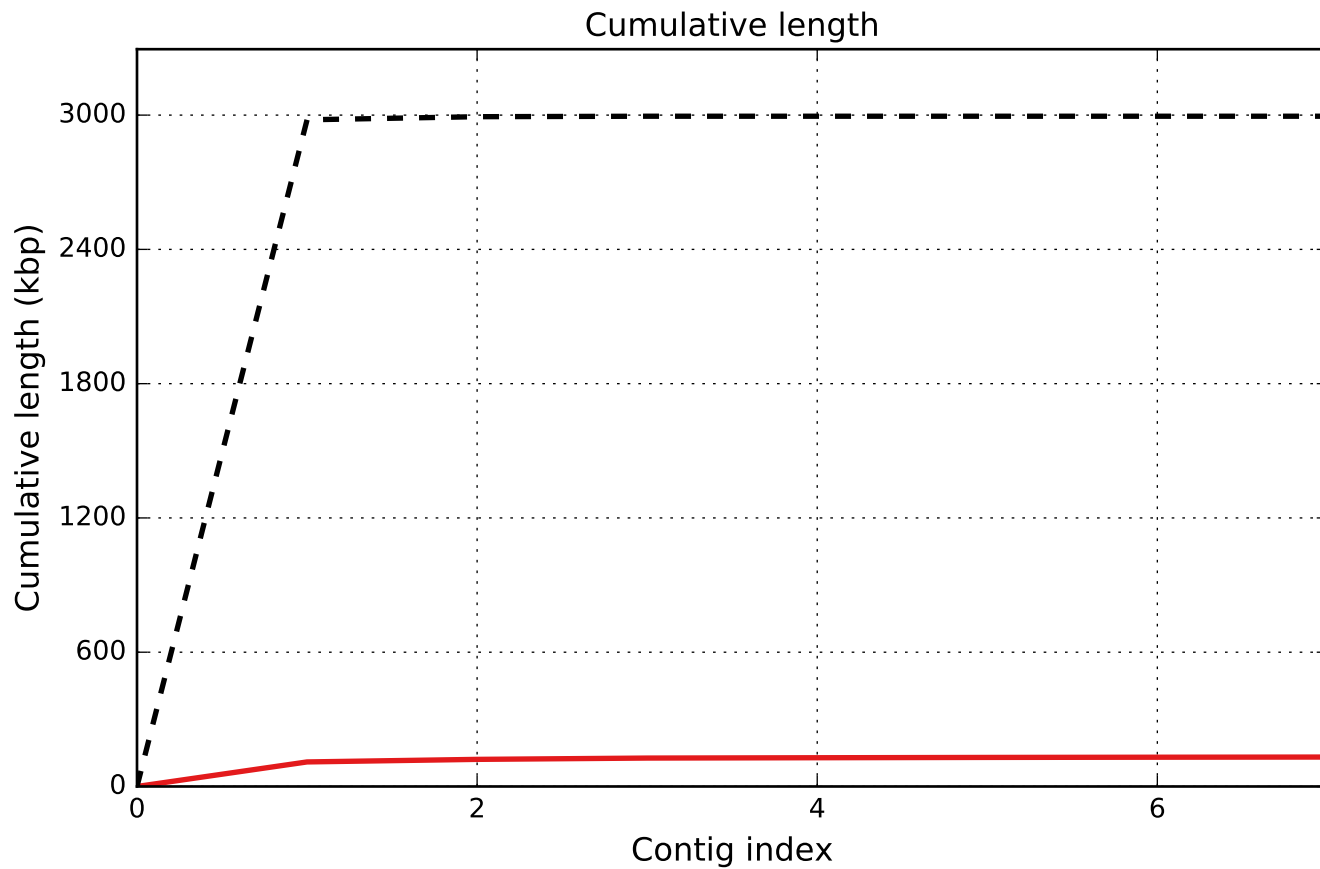


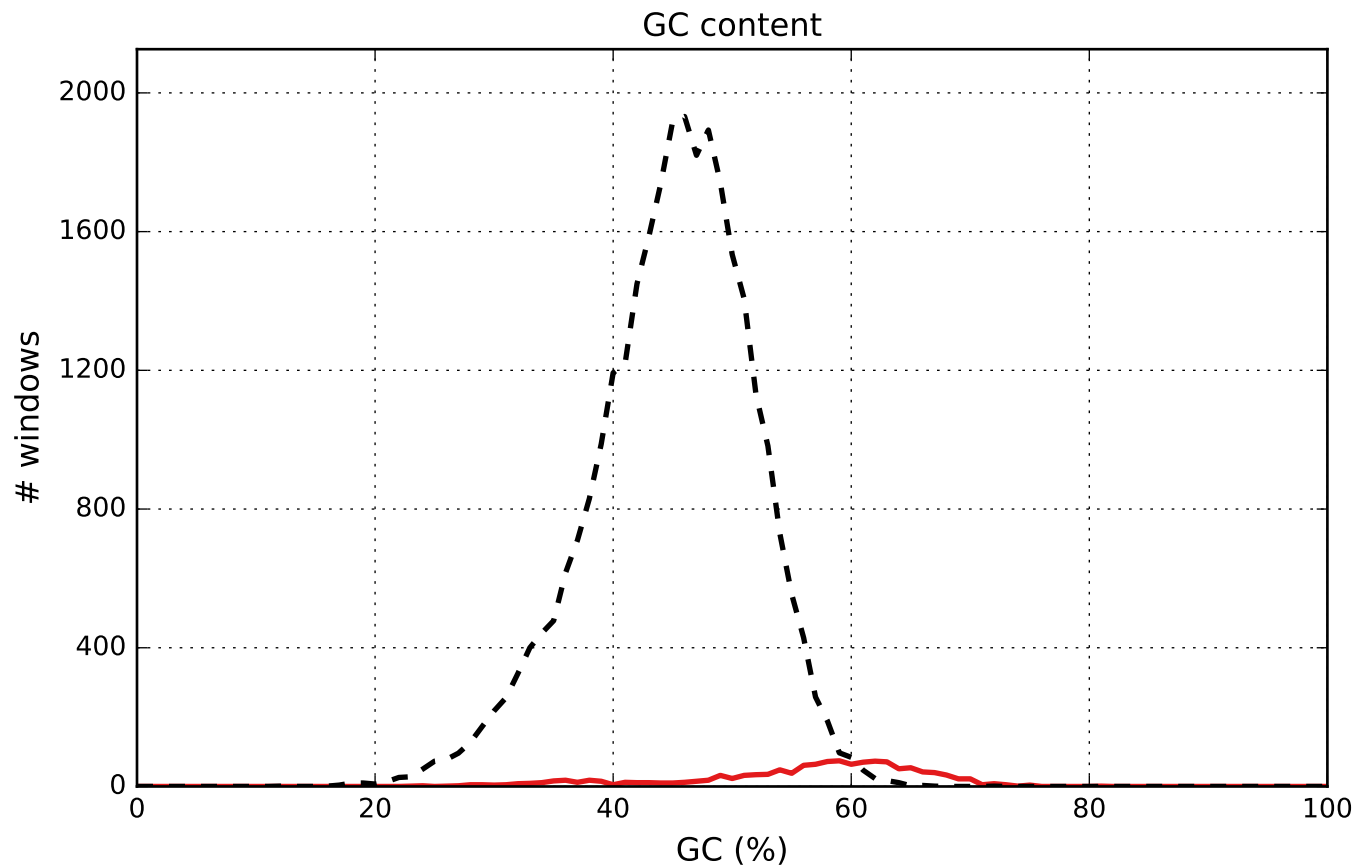
— combined.final.contigs

NGx

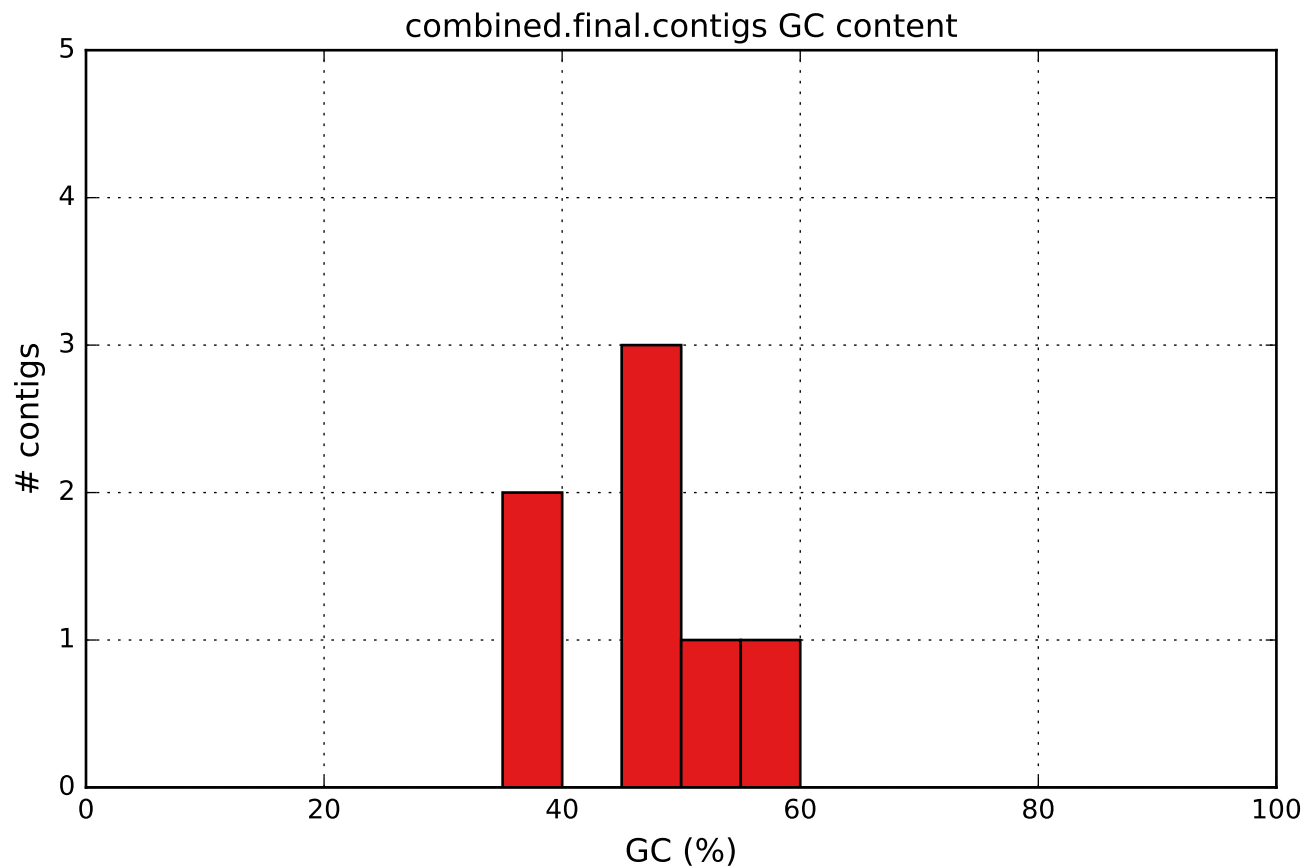


— combined.final.contigs

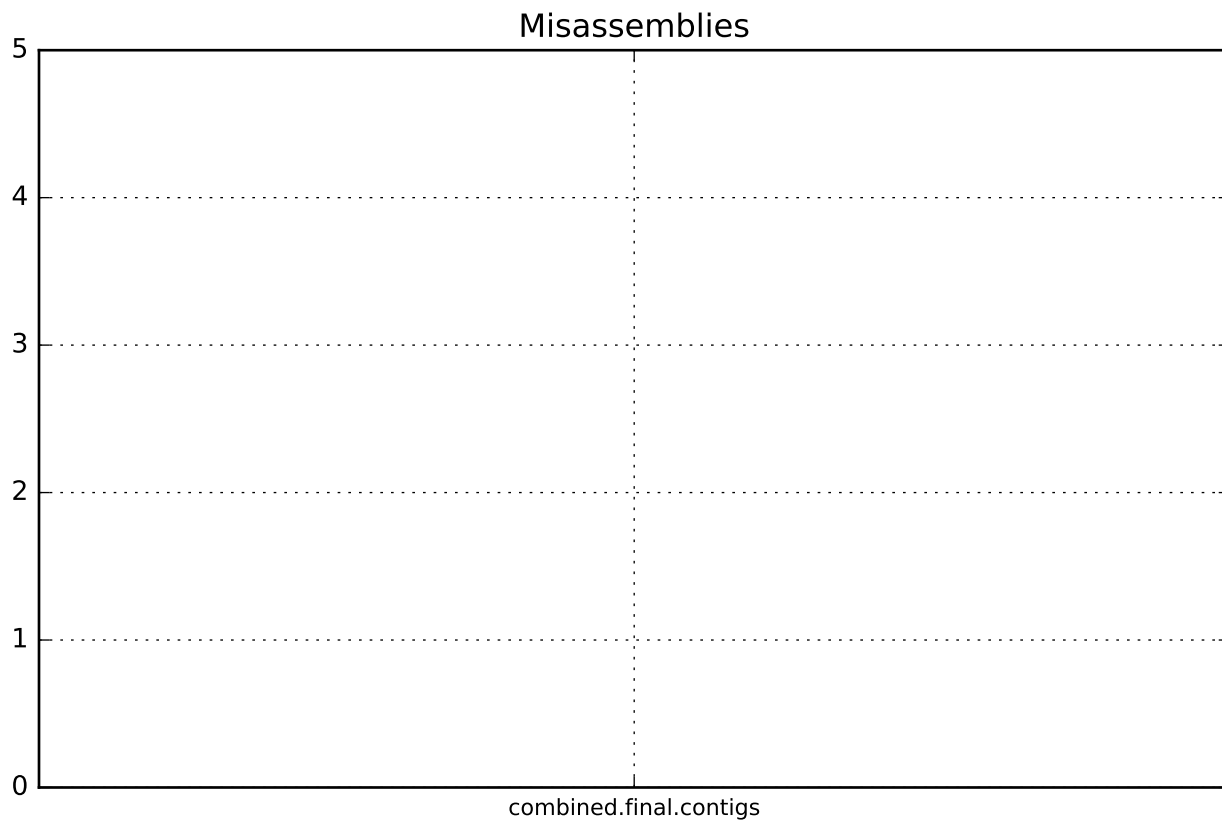




— combined.final.contigs - - Reference



combined.final.contigs

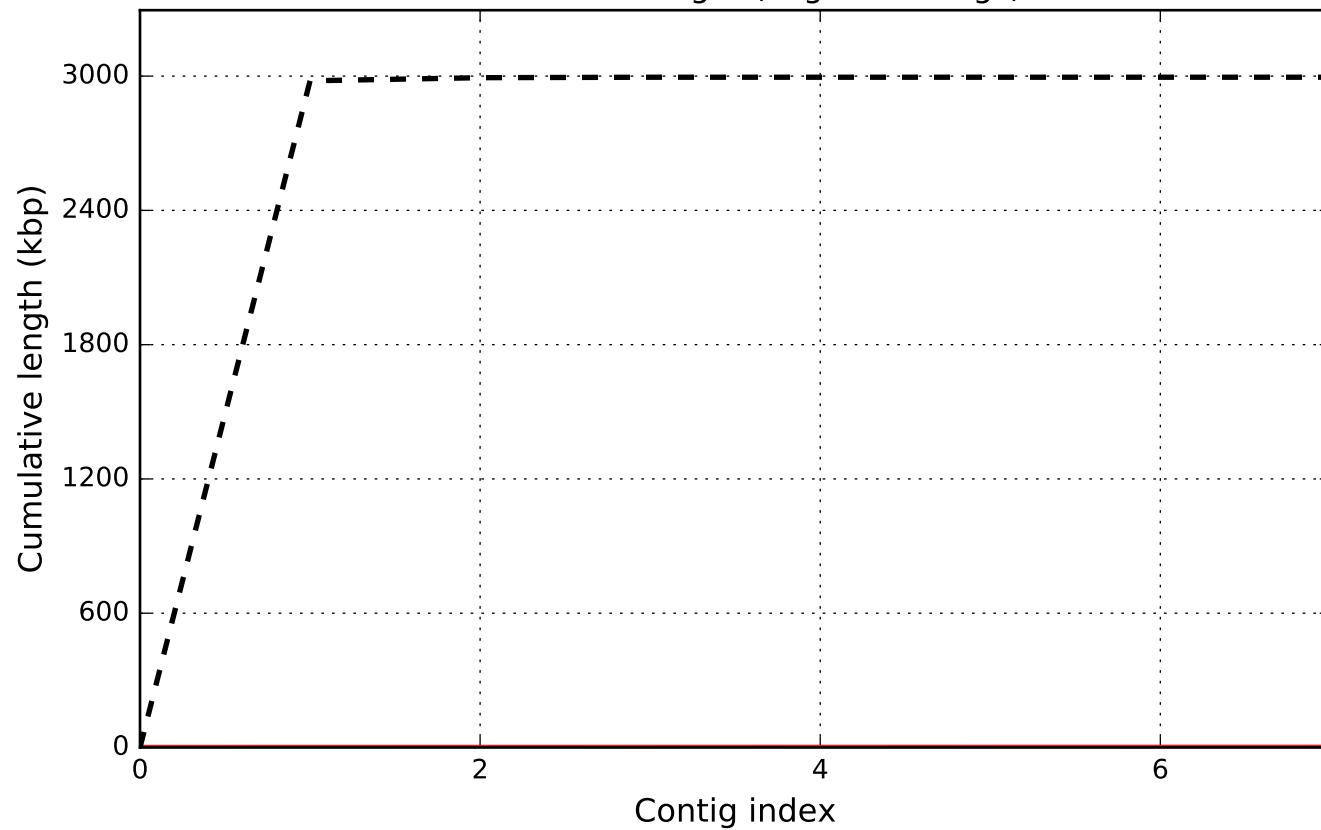


FRCurve (misassemblies)



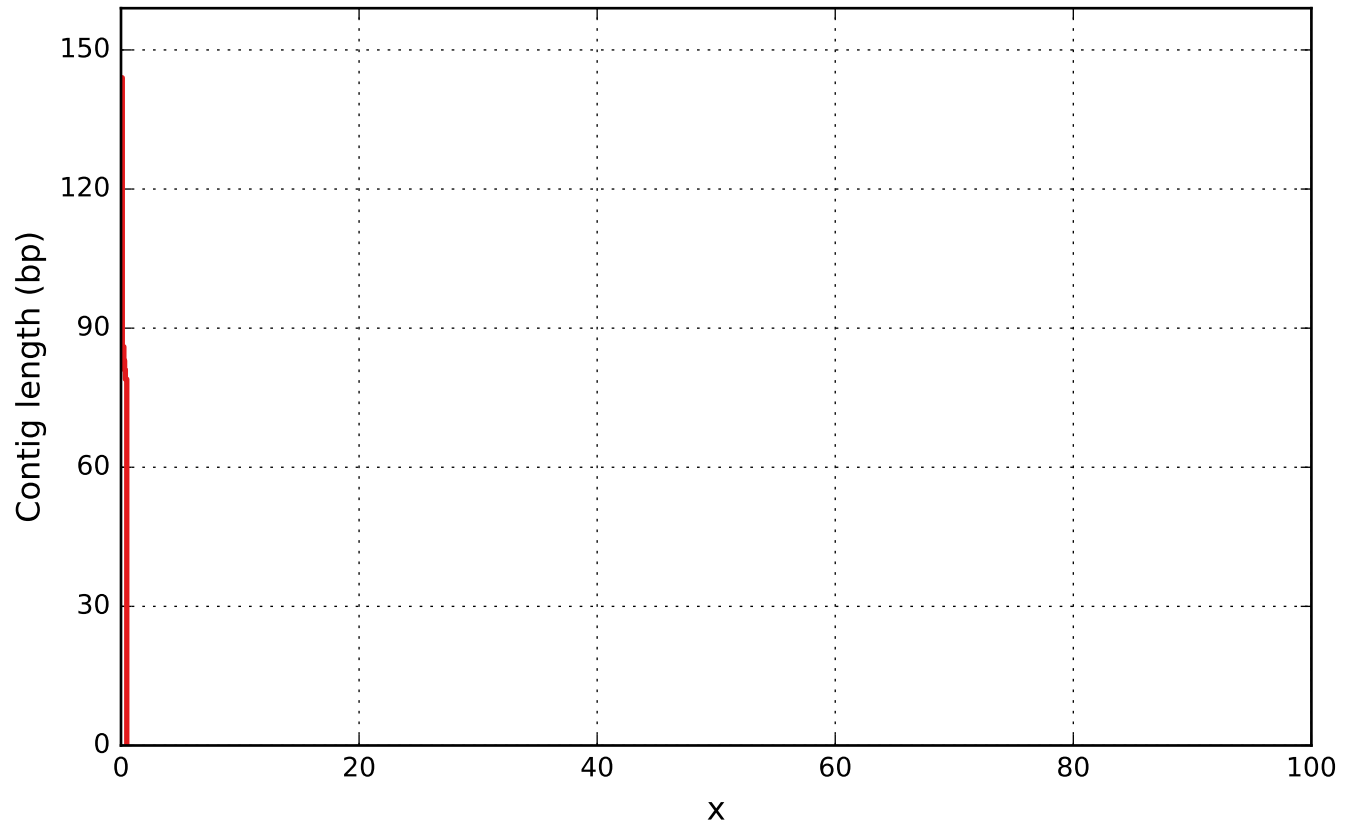
— combined.final.contigs

Cumulative length (aligned contigs)



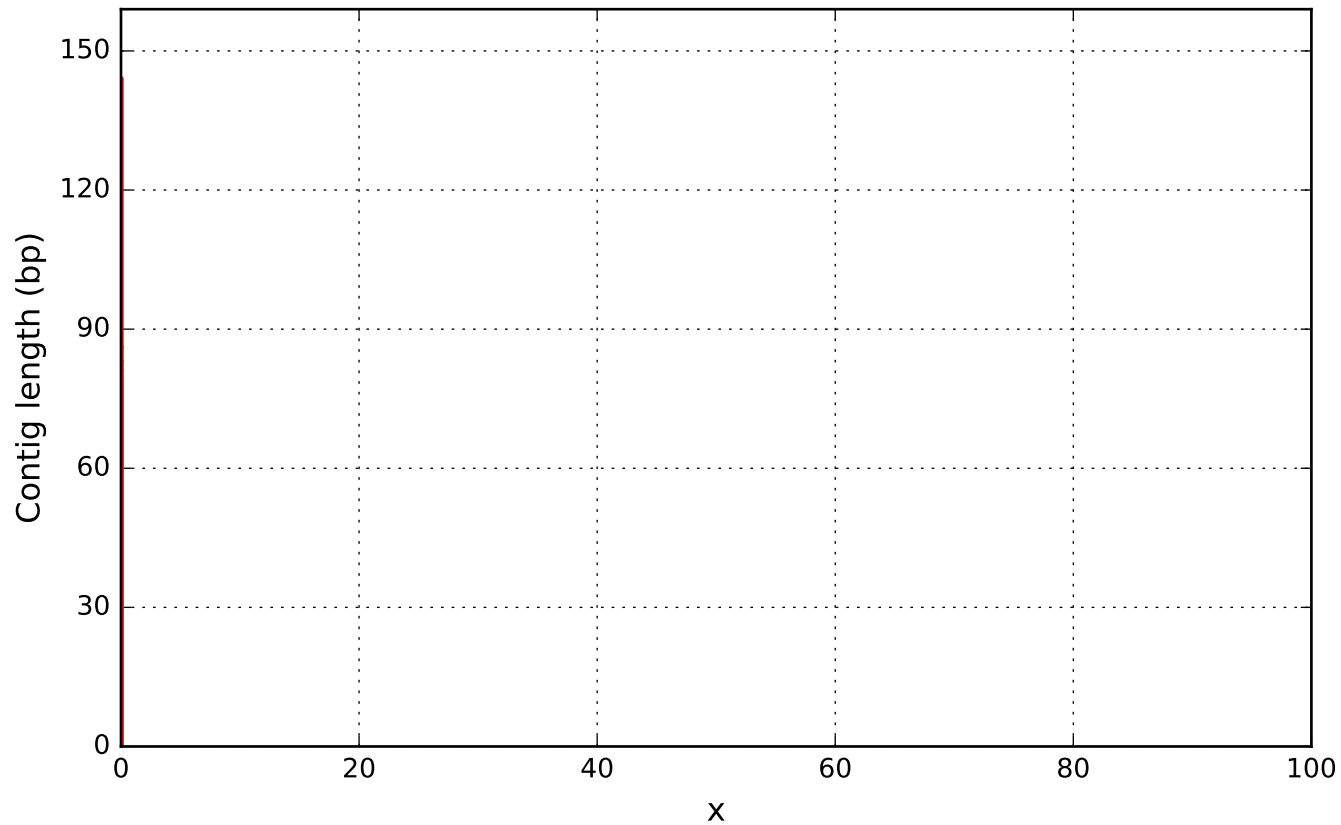
— combined.final.contigs - - Reference

NAx



— combined.final.contigs

NGAx



— combined.final.contigs