

Report

	combined.final.contigs
# contigs (≥ 1000 bp)	7
# contigs (≥ 5000 bp)	2
# contigs (≥ 10000 bp)	2
# contigs (≥ 25000 bp)	1
# contigs (≥ 50000 bp)	0
Total length (≥ 1000 bp)	68695
Total length (≥ 5000 bp)	55576
Total length (≥ 10000 bp)	55576
Total length (≥ 25000 bp)	44784
Total length (≥ 50000 bp)	0
# contigs	12
Largest contig	44784
Total length	71579
Reference length	3910325
GC (%)	58.04
Reference GC (%)	62.16
N50	44784
N75	10792
L50	1
L75	2
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 9 part
Unaligned length	69099
Genome fraction (%)	0.029
Duplication ratio	2.199
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1595.74
# indels per 100 kbp	354.61
Largest alignment	219
Total aligned length	1269
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

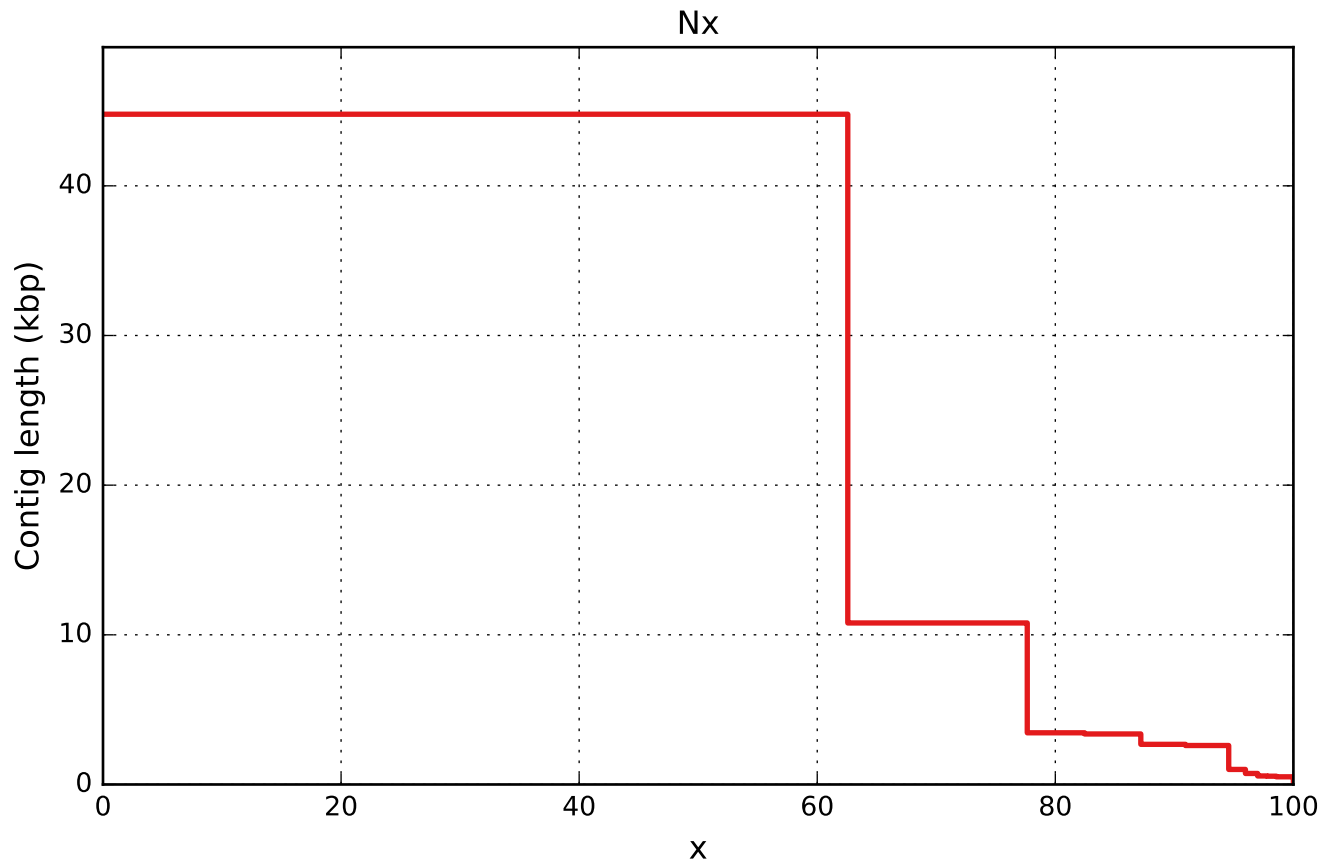
	combined.final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	1
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	18
# indels	4
# indels (<= 5 bp)	4
# indels (> 5 bp)	0
Indels length	4

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

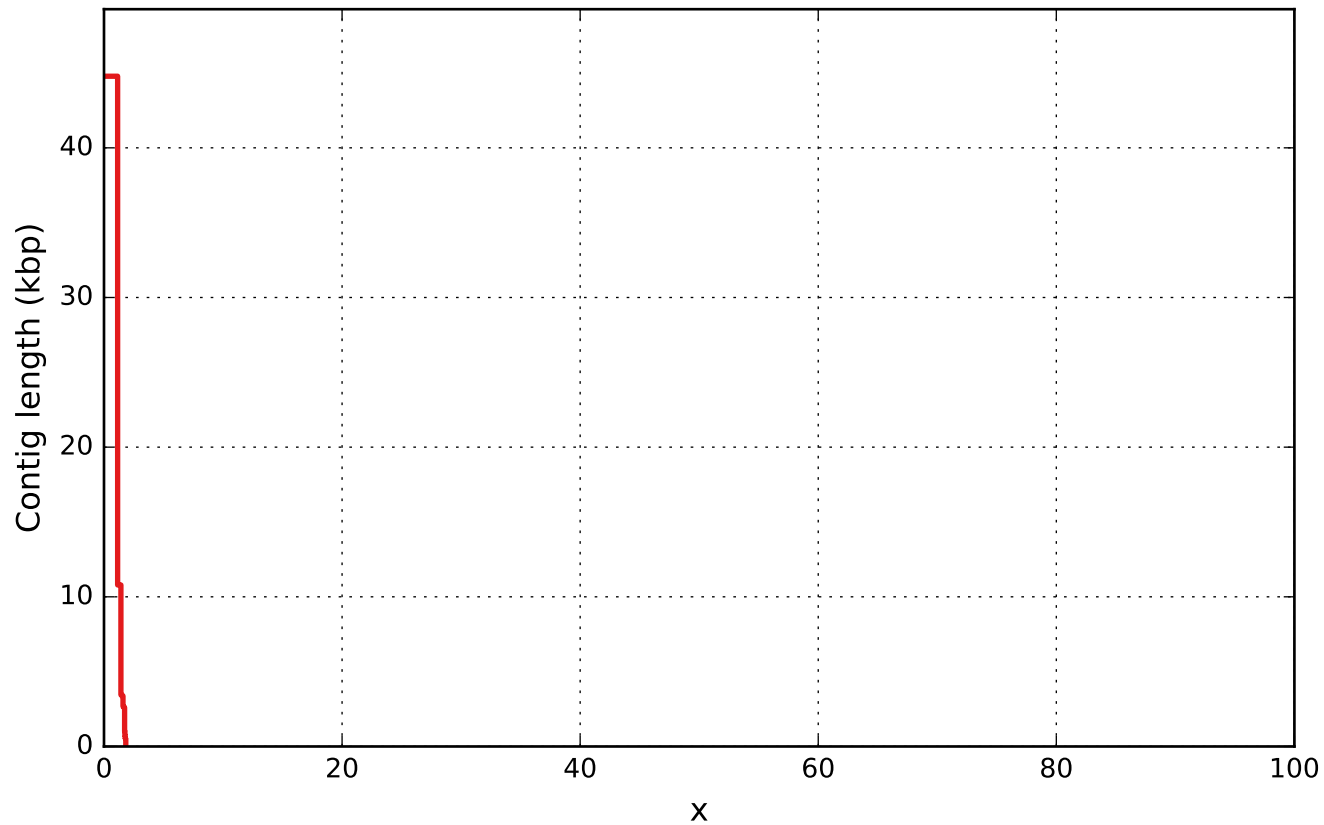
	combined.final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	9
Partially unaligned length	69099
# N's	0

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).

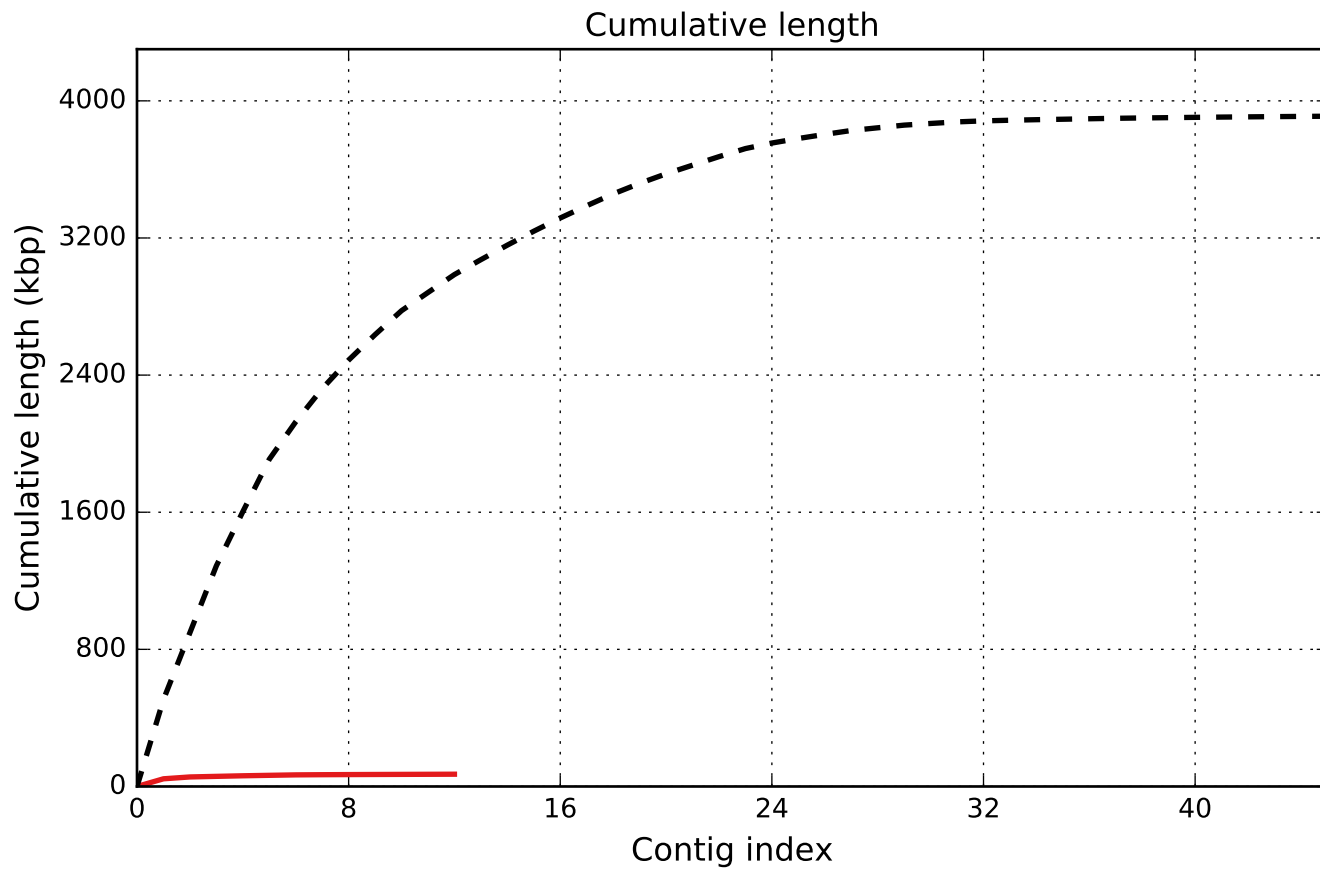


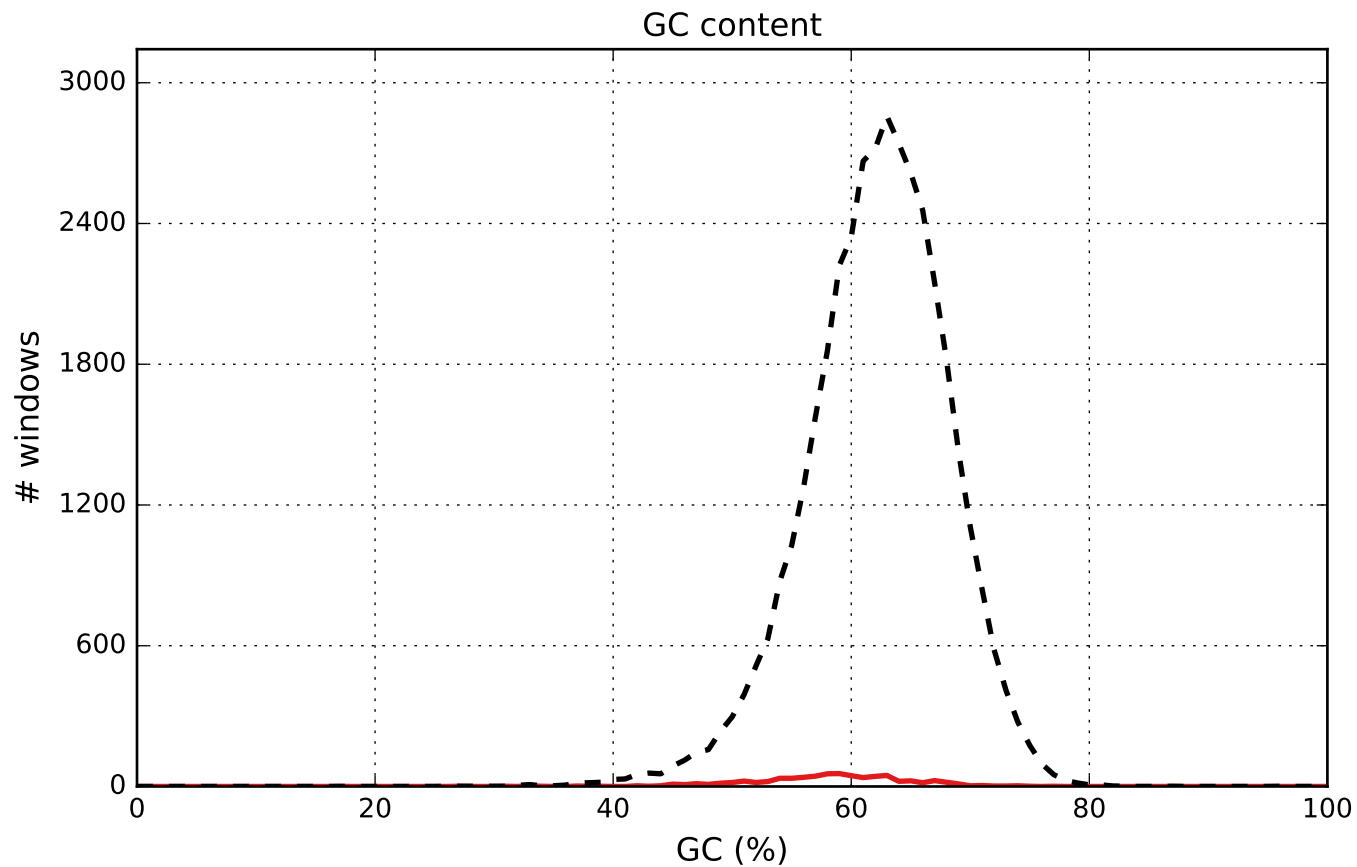
— combined.final.contigs

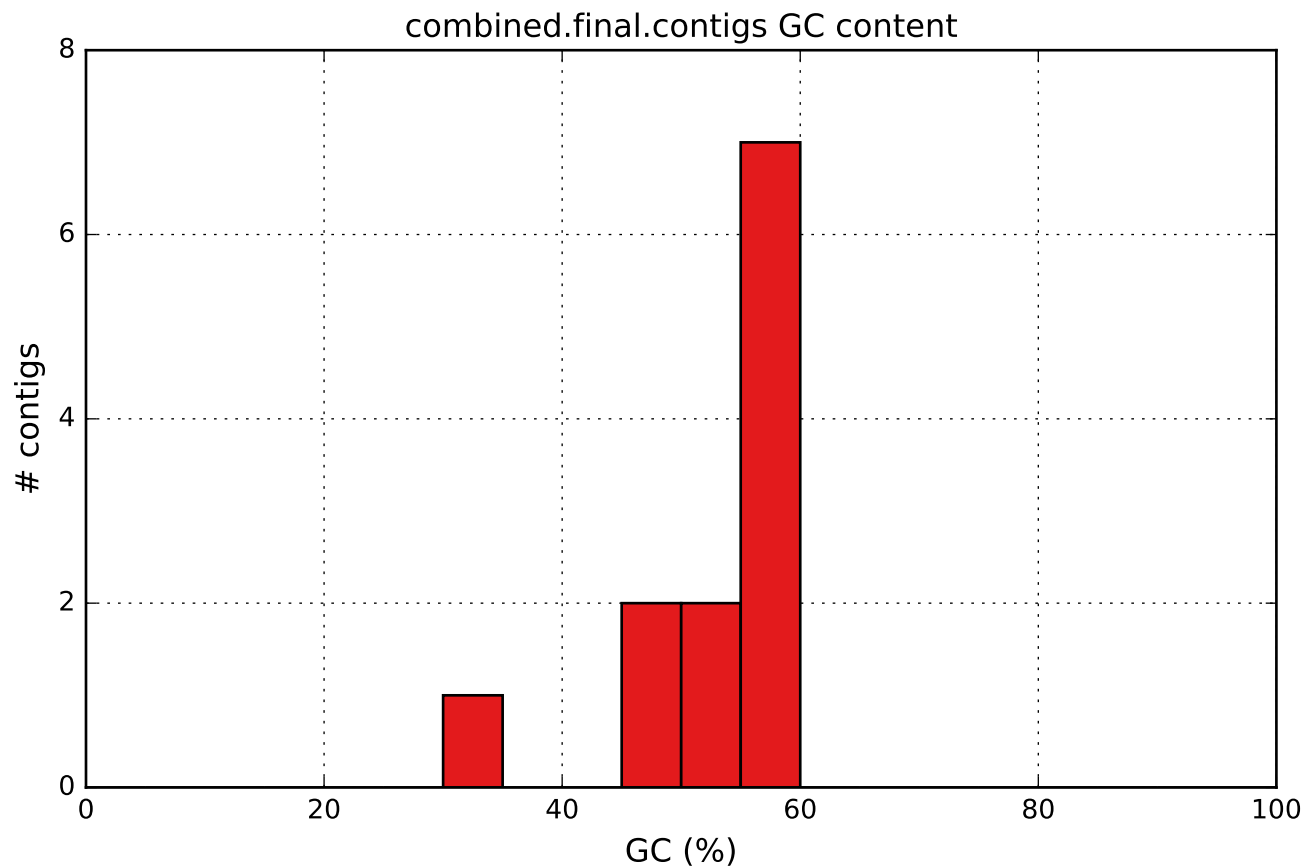
NGx



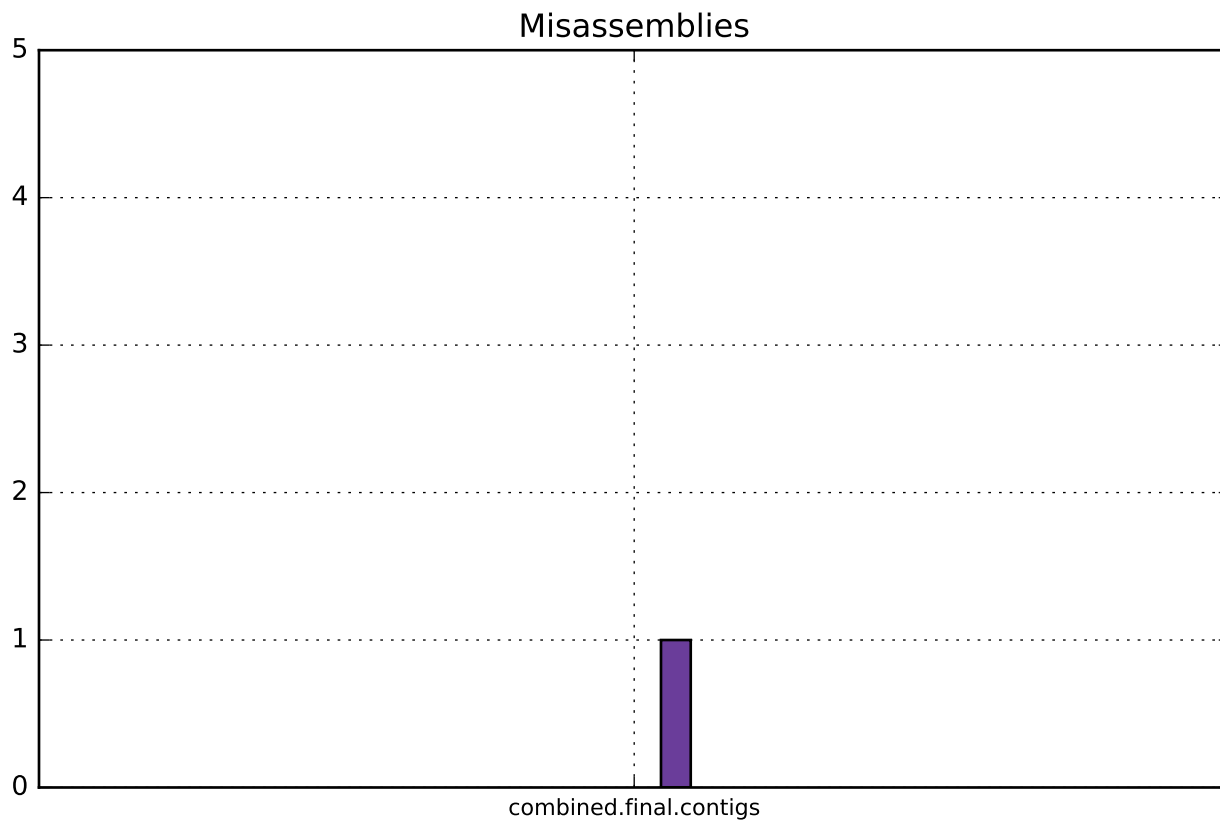
— combined.final.contigs






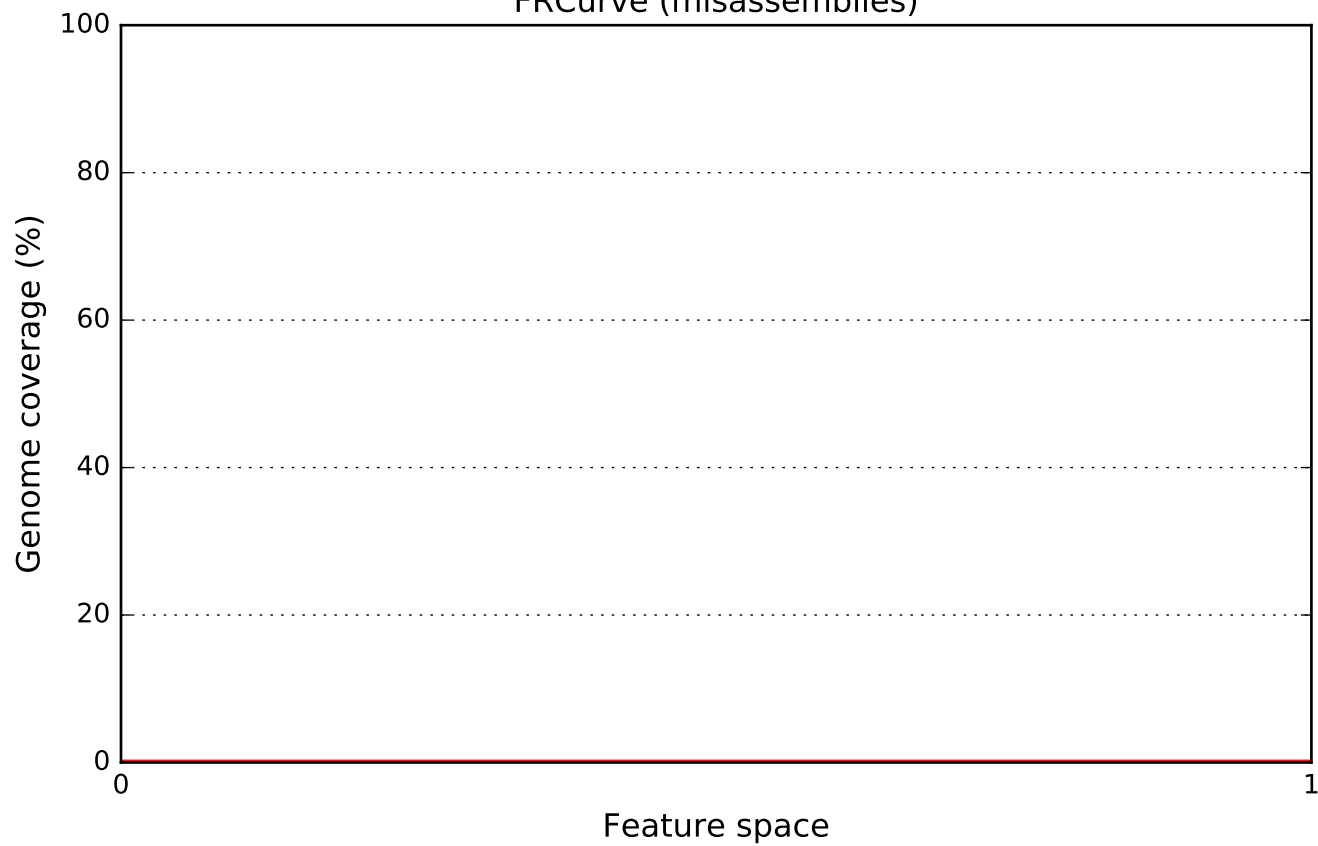


combined.final.contigs



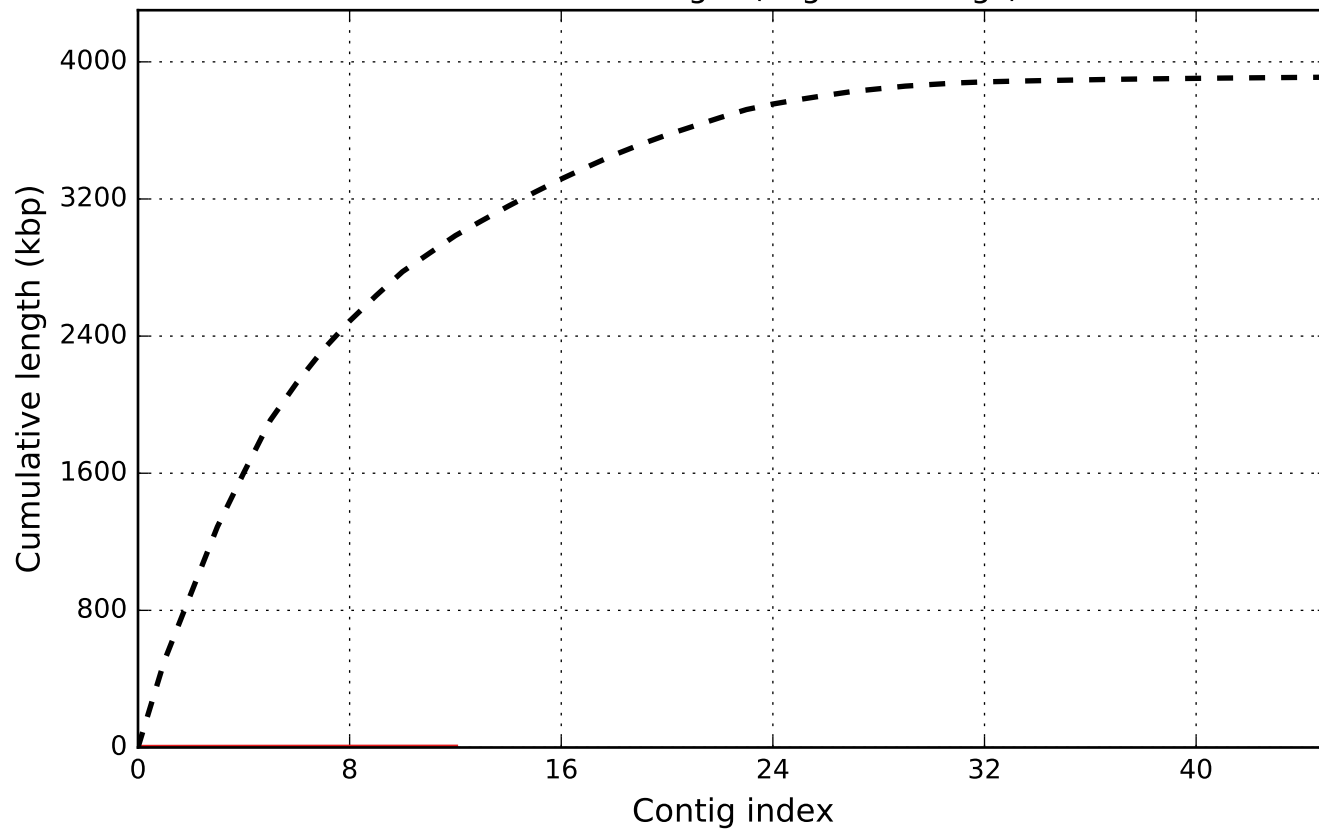
 # interspecies translocations

FRCurve (misassemblies)



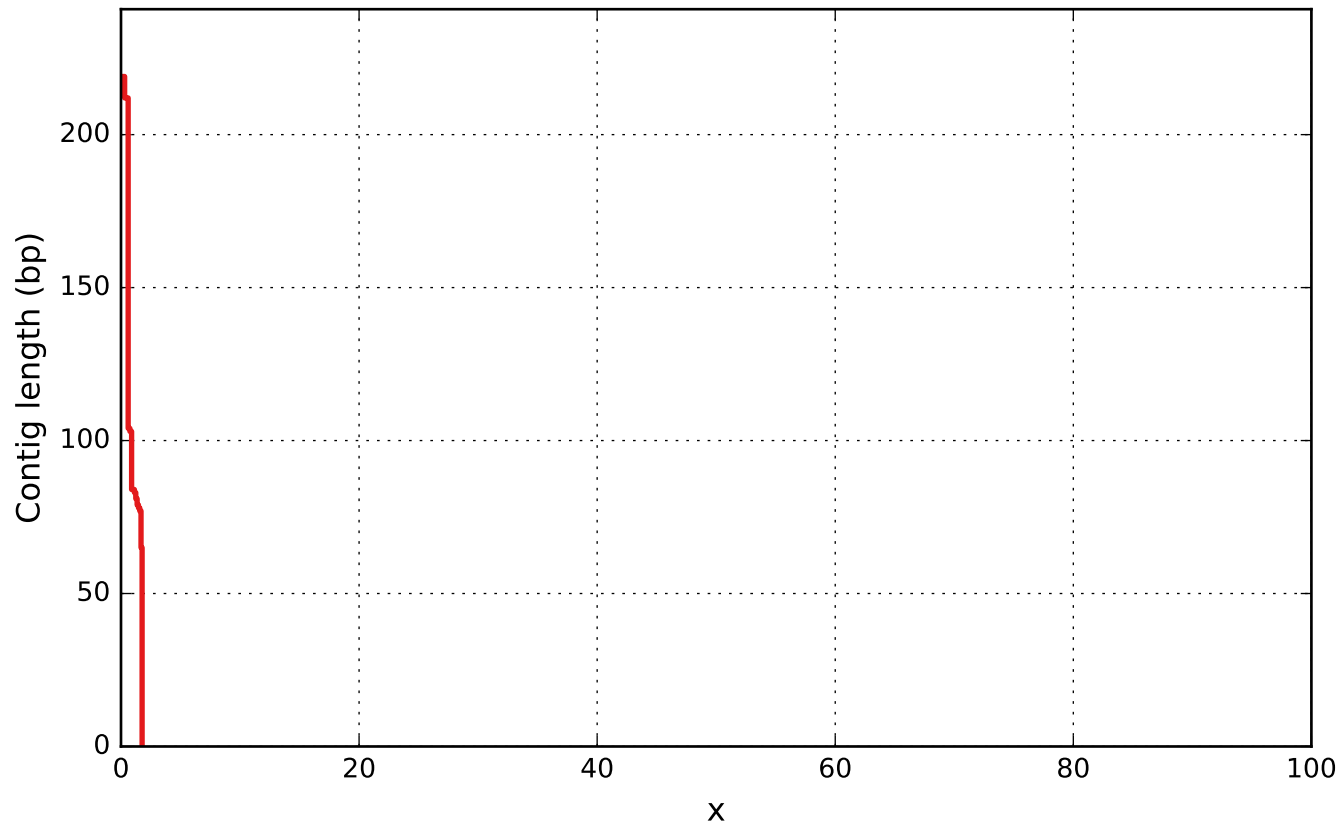
— combined.final.contigs

Cumulative length (aligned contigs)



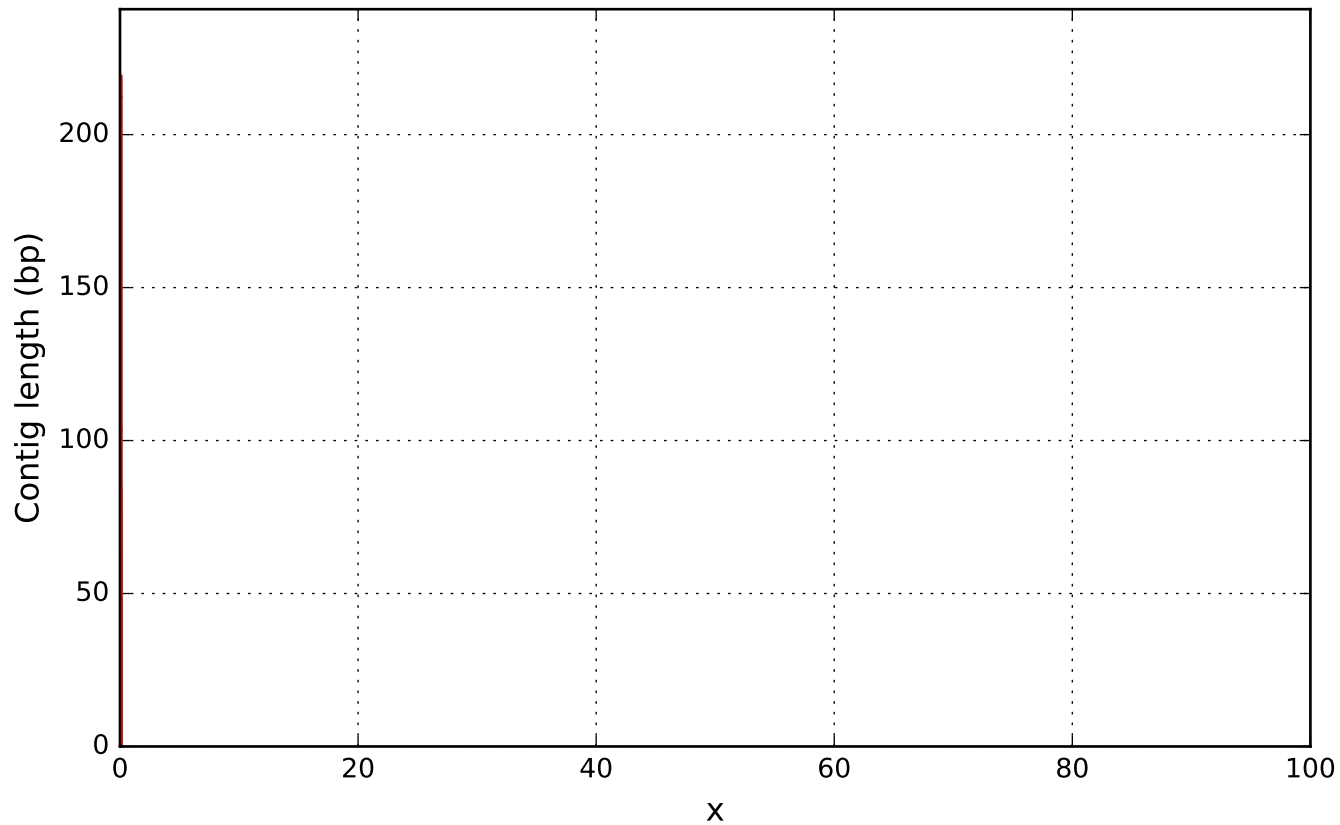
— combined.final.contigs - - Reference

NAx



— combined.final.contigs

NGAx



— combined.final.contigs