

Report

	final.contigs
# contigs (≥ 1000 bp)	8
# contigs (≥ 5000 bp)	5
# contigs (≥ 10000 bp)	3
# contigs (≥ 25000 bp)	2
# contigs (≥ 50000 bp)	0
Total length (≥ 1000 bp)	113039
Total length (≥ 5000 bp)	107631
Total length (≥ 10000 bp)	94028
Total length (≥ 25000 bp)	74007
Total length (≥ 50000 bp)	0
# contigs	11
Largest contig	37300
Total length	114852
Reference length	3464554
GC (%)	57.07
Reference GC (%)	65.06
N50	36707
N75	20021
L50	2
L75	3
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 8 part
Unaligned length	112391
Genome fraction (%)	0.016
Duplication ratio	4.379
# N's per 100 kbp	0.00
# mismatches per 100 kbp	177.94
# indels per 100 kbp	711.74
Largest alignment	89
Total aligned length	890
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

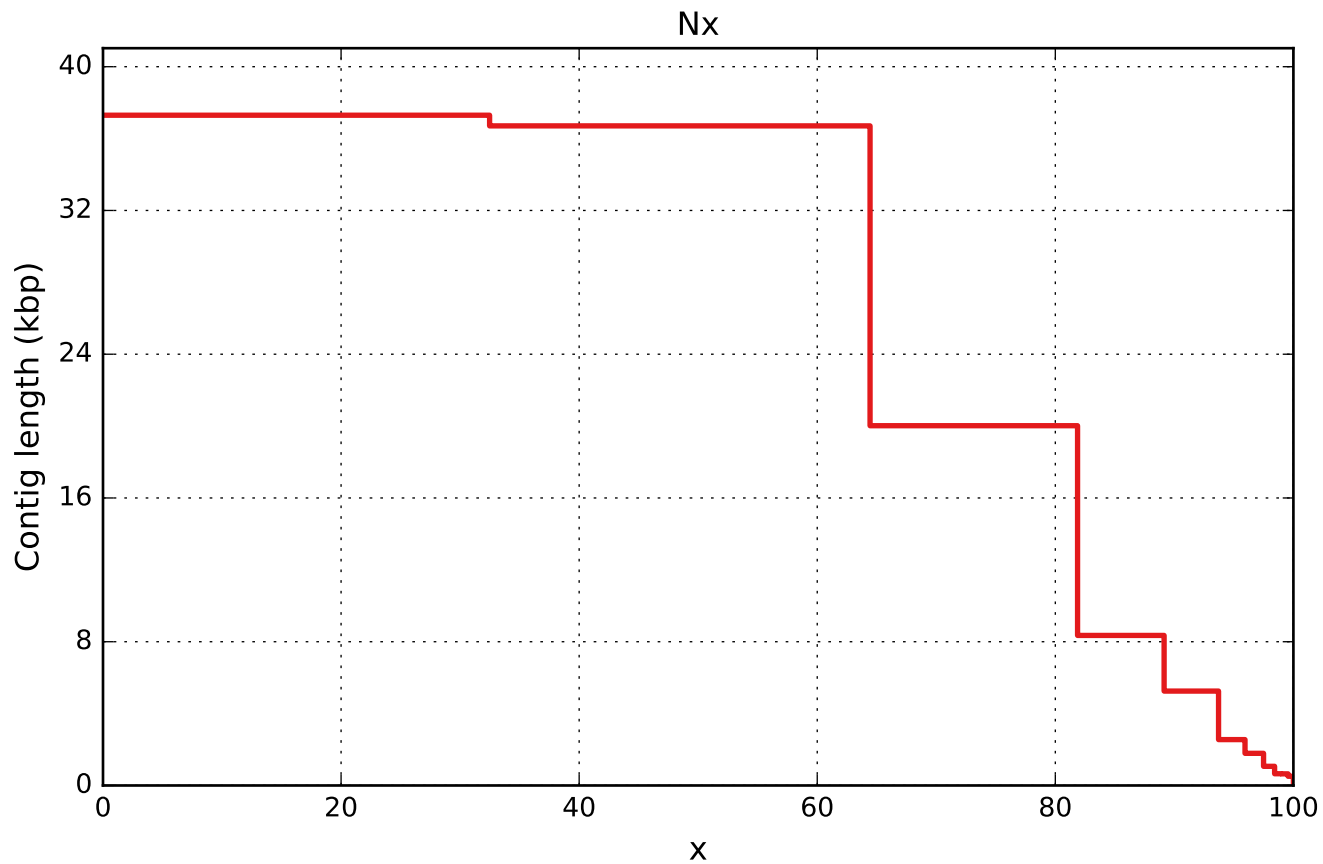
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	1
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	1
# indels	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

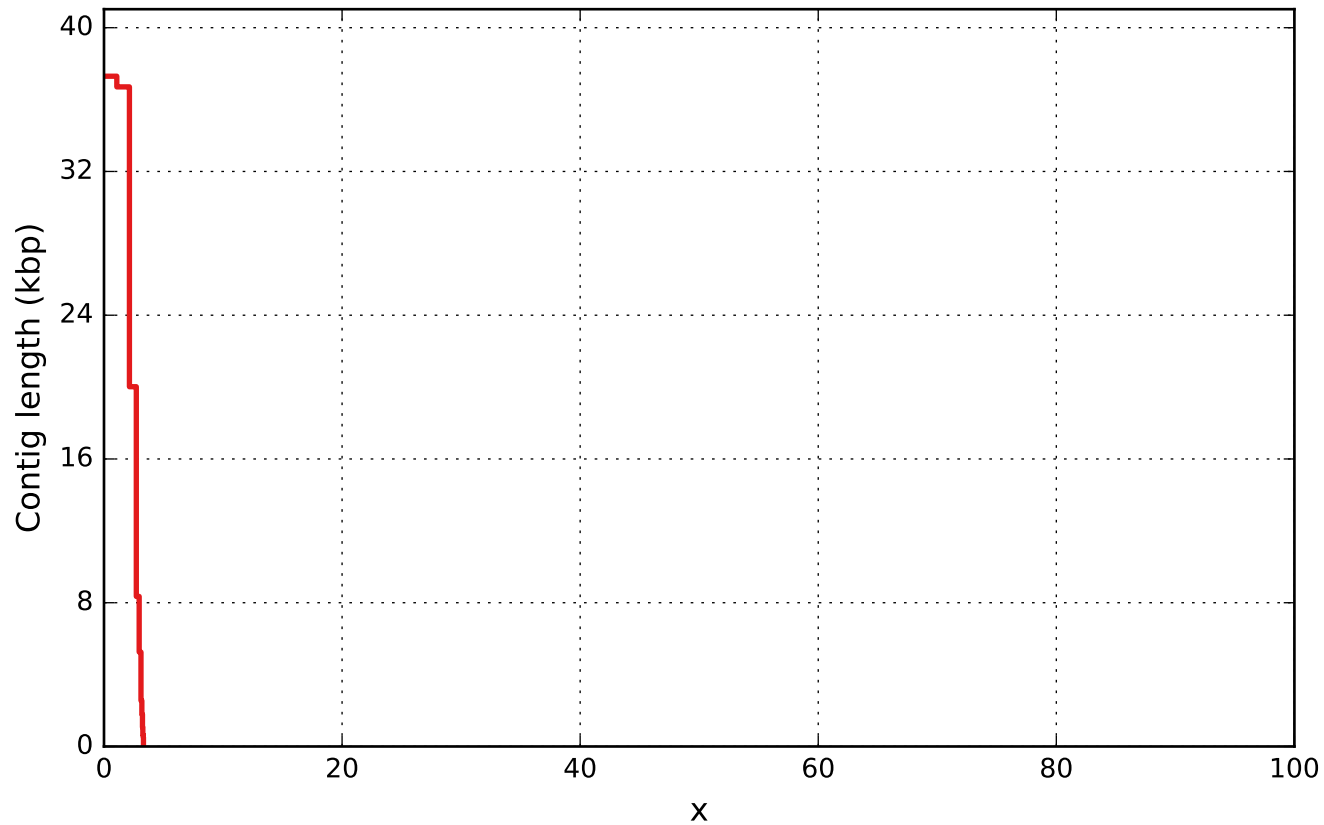
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	8
Partially unaligned length	112391
# N's	0

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).

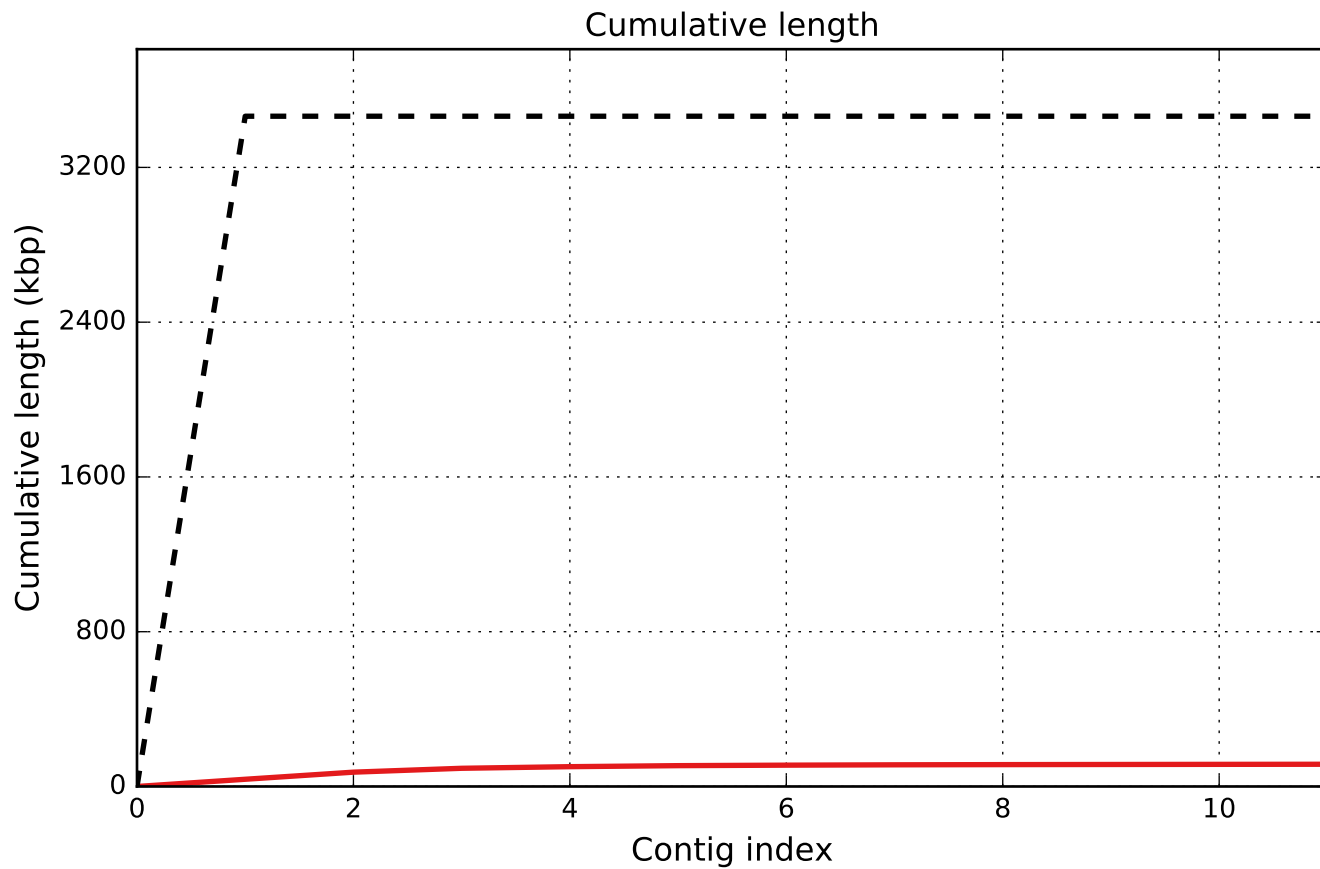


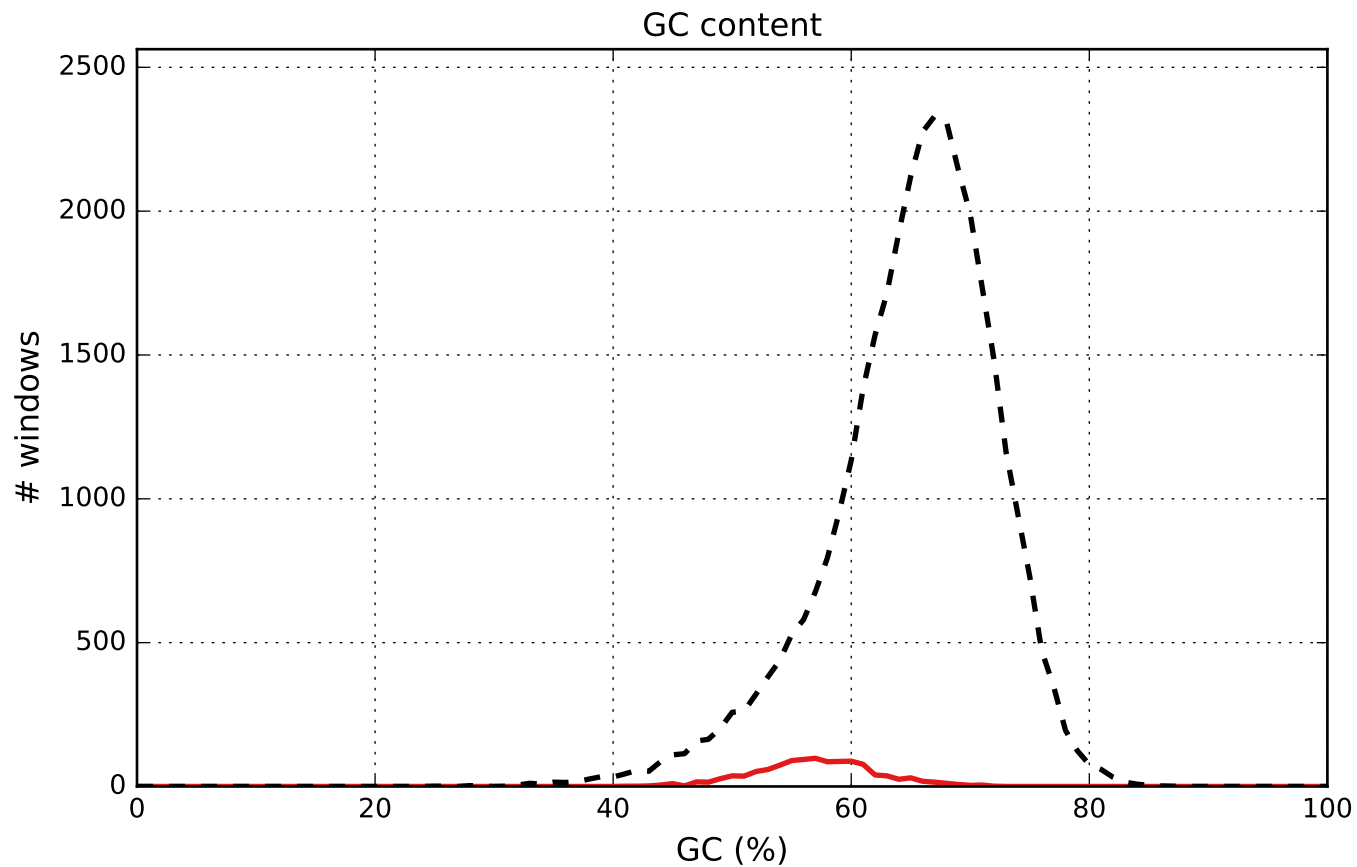
— final.contigs

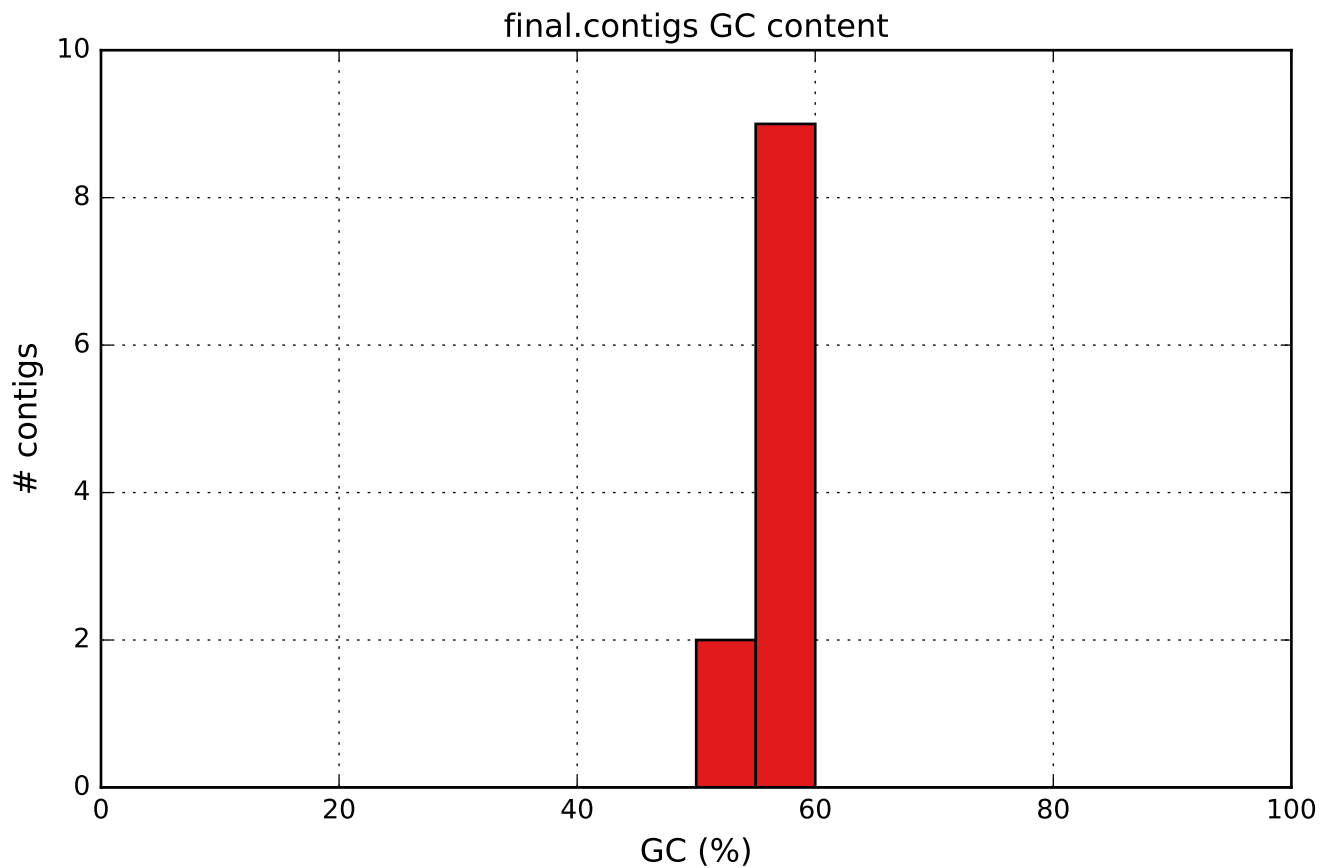
NGx



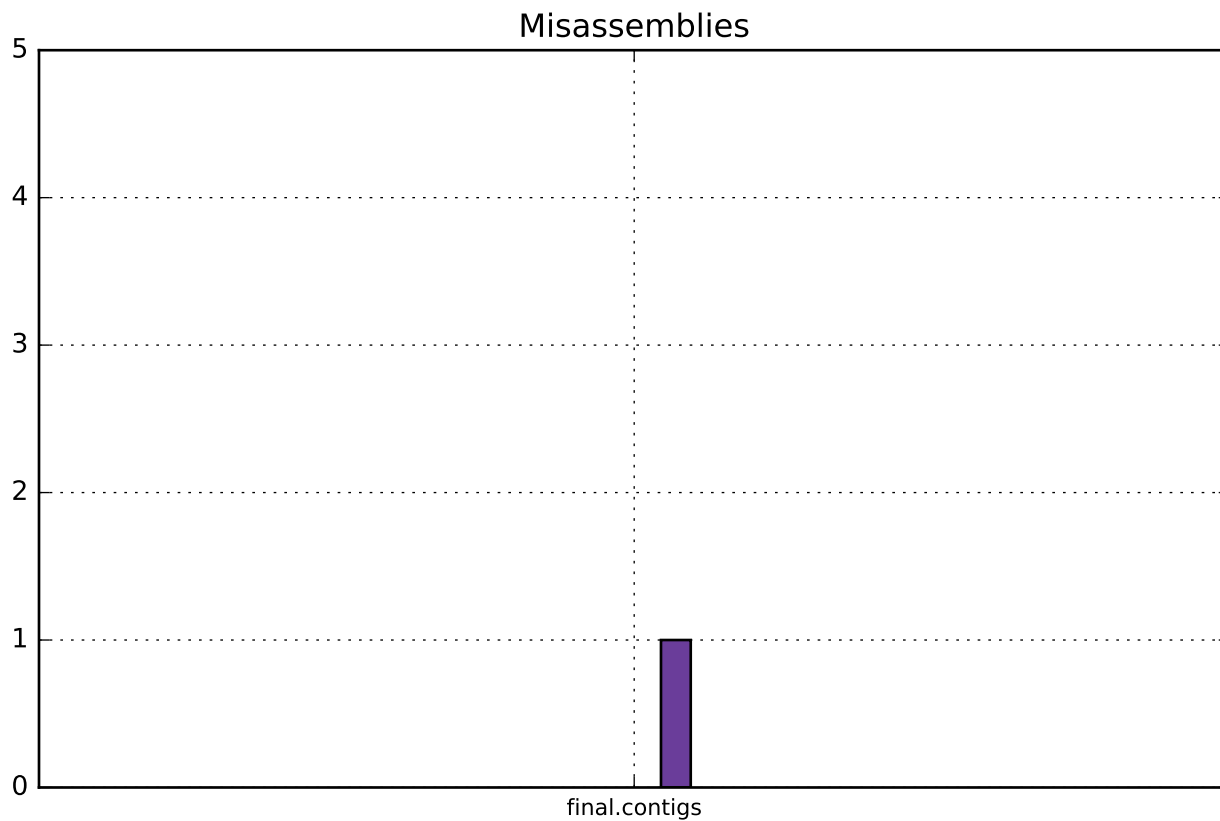
— final.contigs






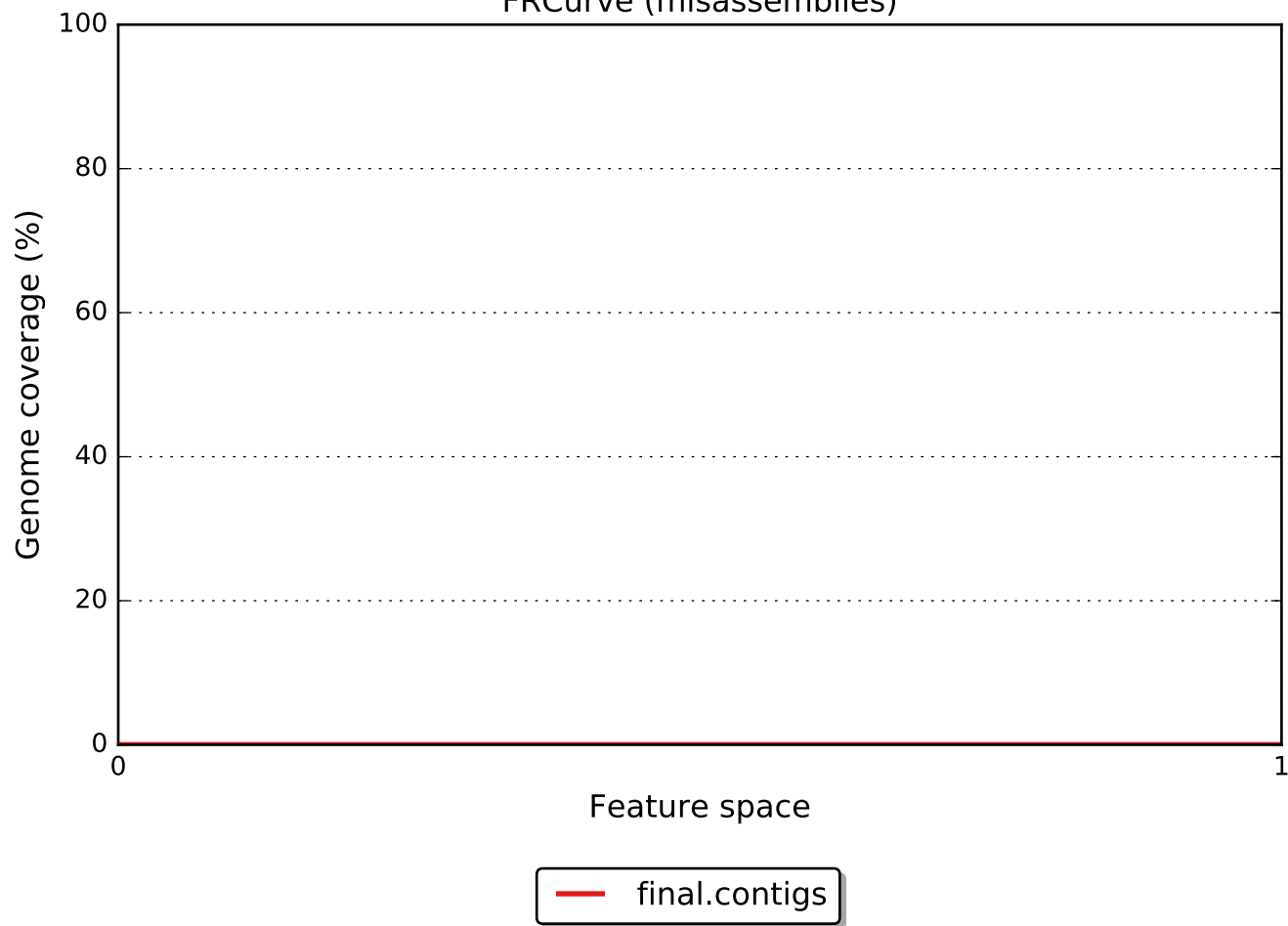


final.contigs

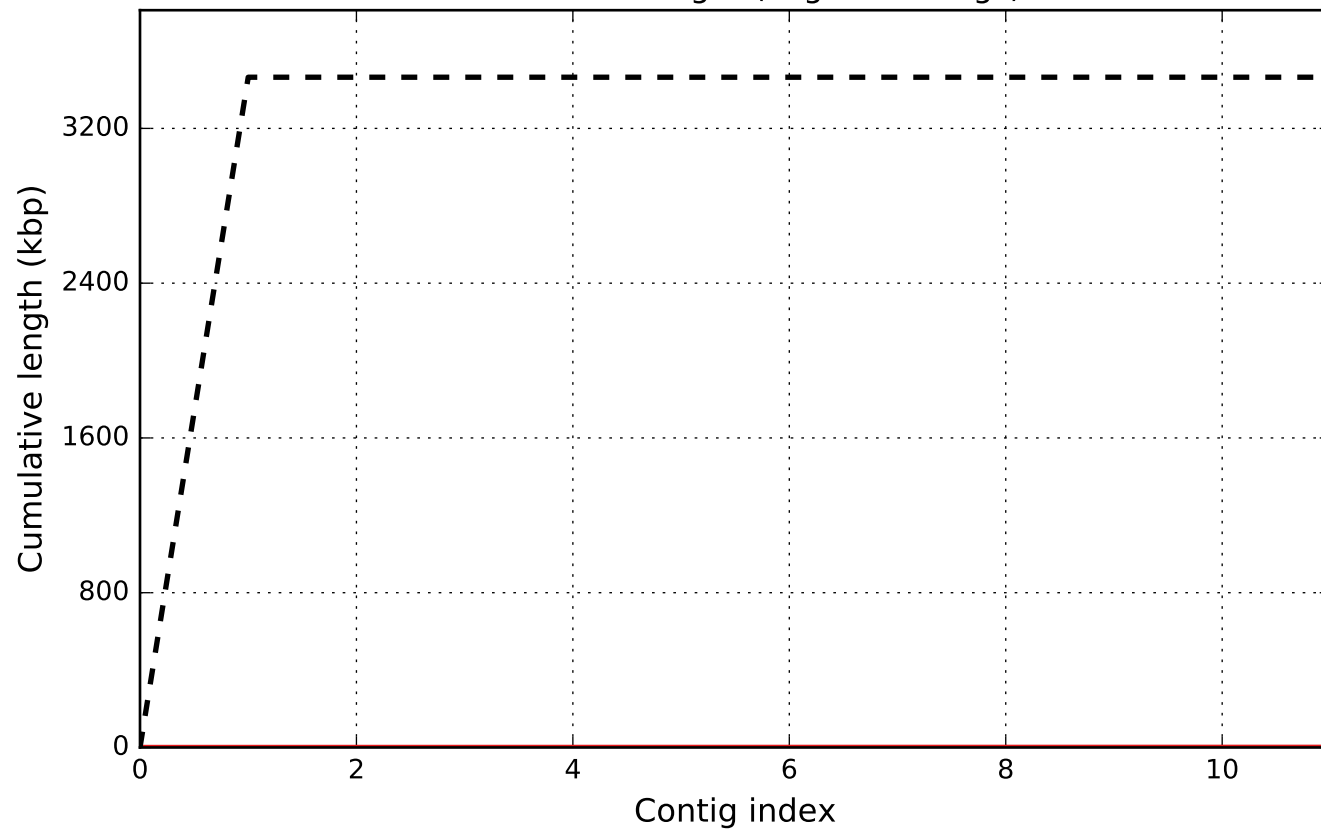


 # interspecies translocations

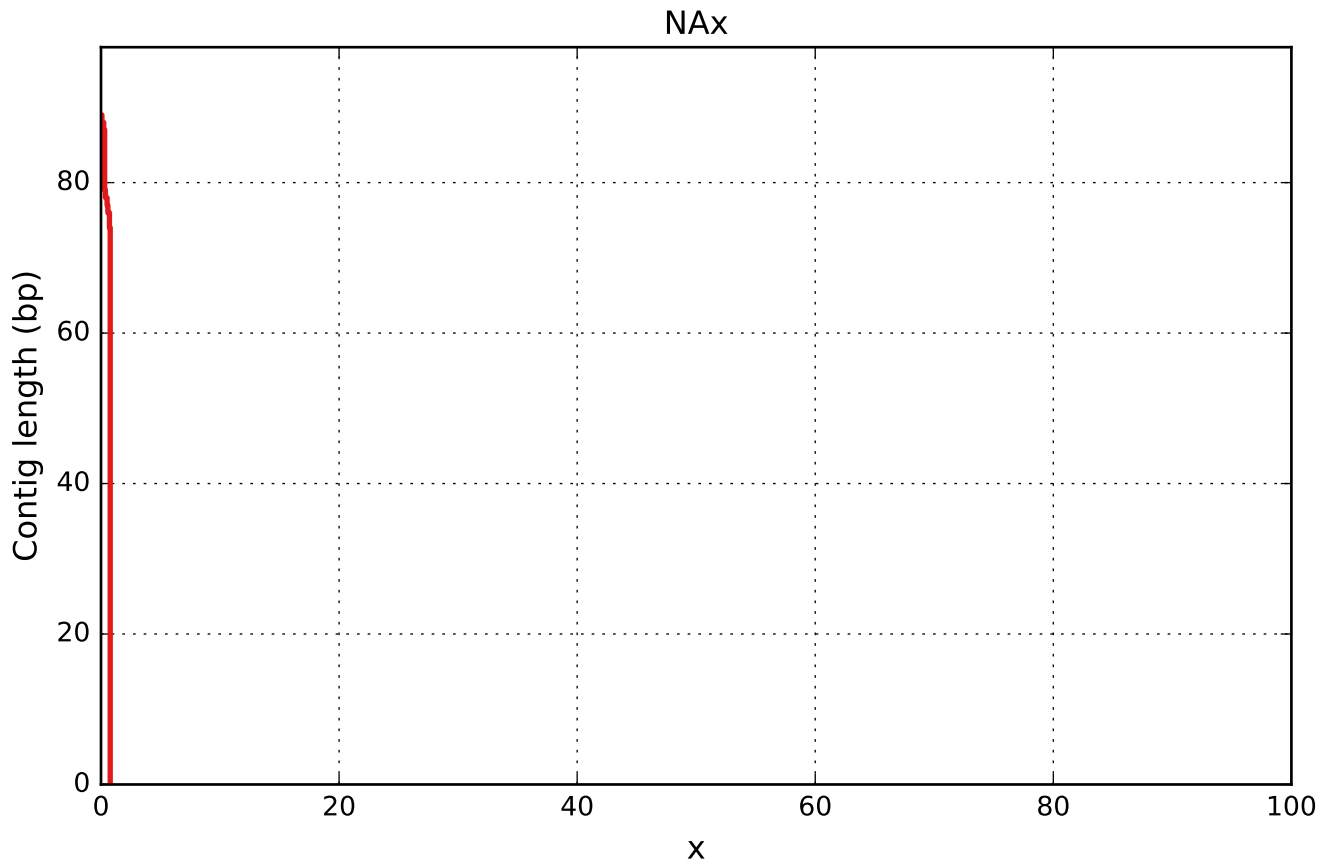
FRCurve (misassemblies)



Cumulative length (aligned contigs)

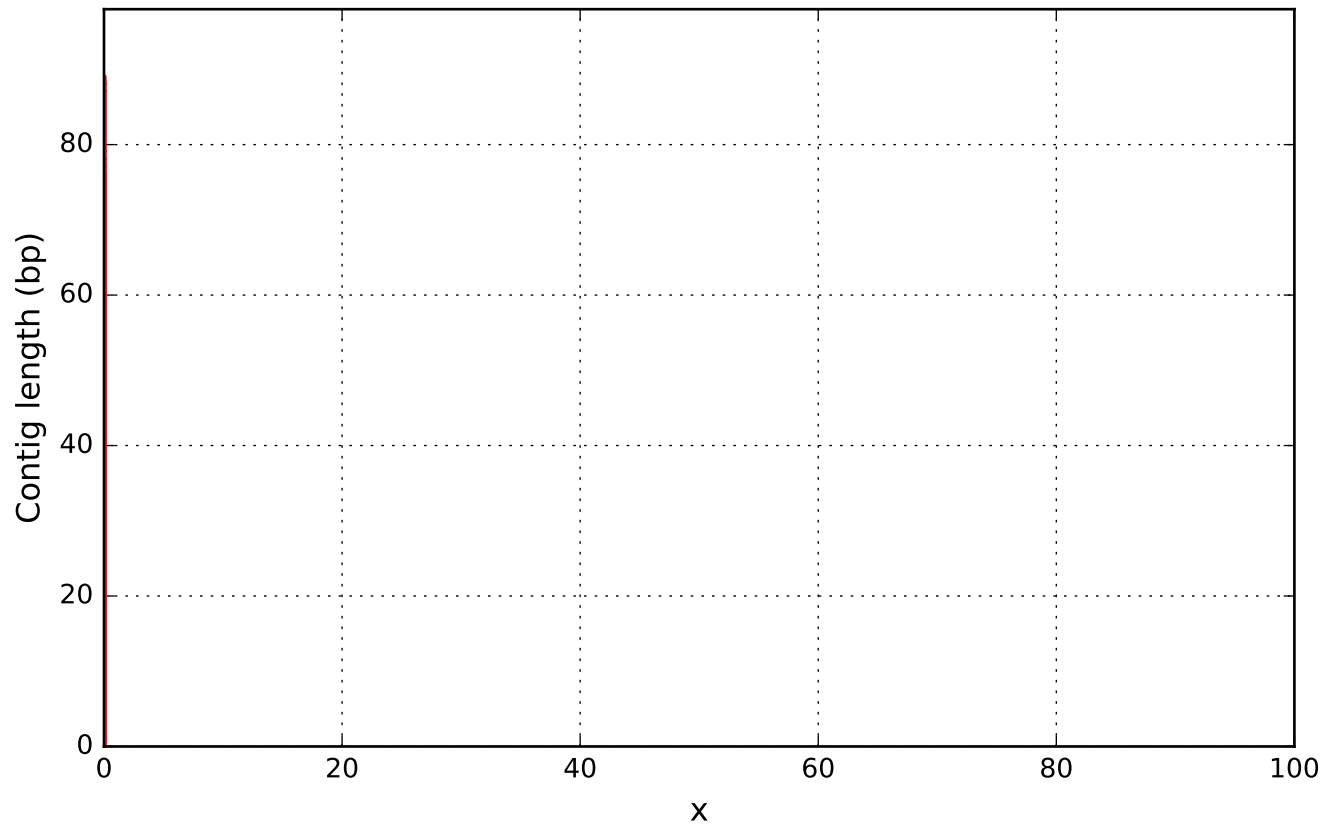


— final.contigs - - Reference



— final.contigs

NGAx



— final.contigs