

Report

	final.contigs
# contigs (>= 1000 bp)	3
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	15418
Total length (>= 5000 bp)	12069
Total length (>= 10000 bp)	12069
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	12
Largest contig	12069
Total length	22083
Reference length	3576081
GC (%)	55.84
Reference GC (%)	51.82
N50	12069
N75	954
L50	1
L75	5
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 7 part
Unaligned length	16969
Genome fraction (%)	0.099
Duplication ratio	1.446
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2856.33
# indels per 100 kbp	367.65
Largest alignment	1345
Total aligned length	3770
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

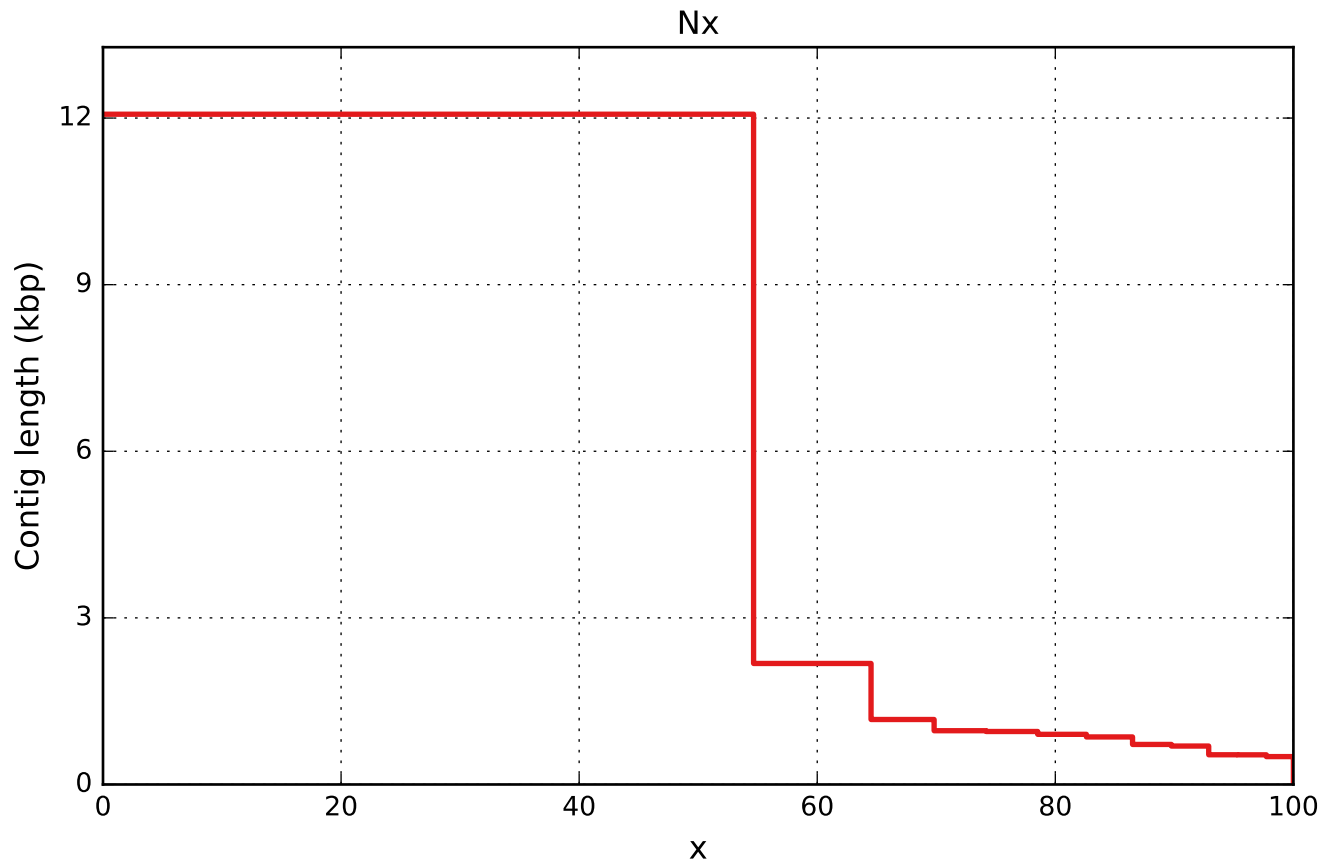
	final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	1
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	1
# possible misassemblies	1
# local misassemblies	0
# structural variations	0
# unaligned mis. contigs	0
# mismatches	101
# indels	13
# indels (≤ 5 bp)	13
# indels (> 5 bp)	0
Indels length	19

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

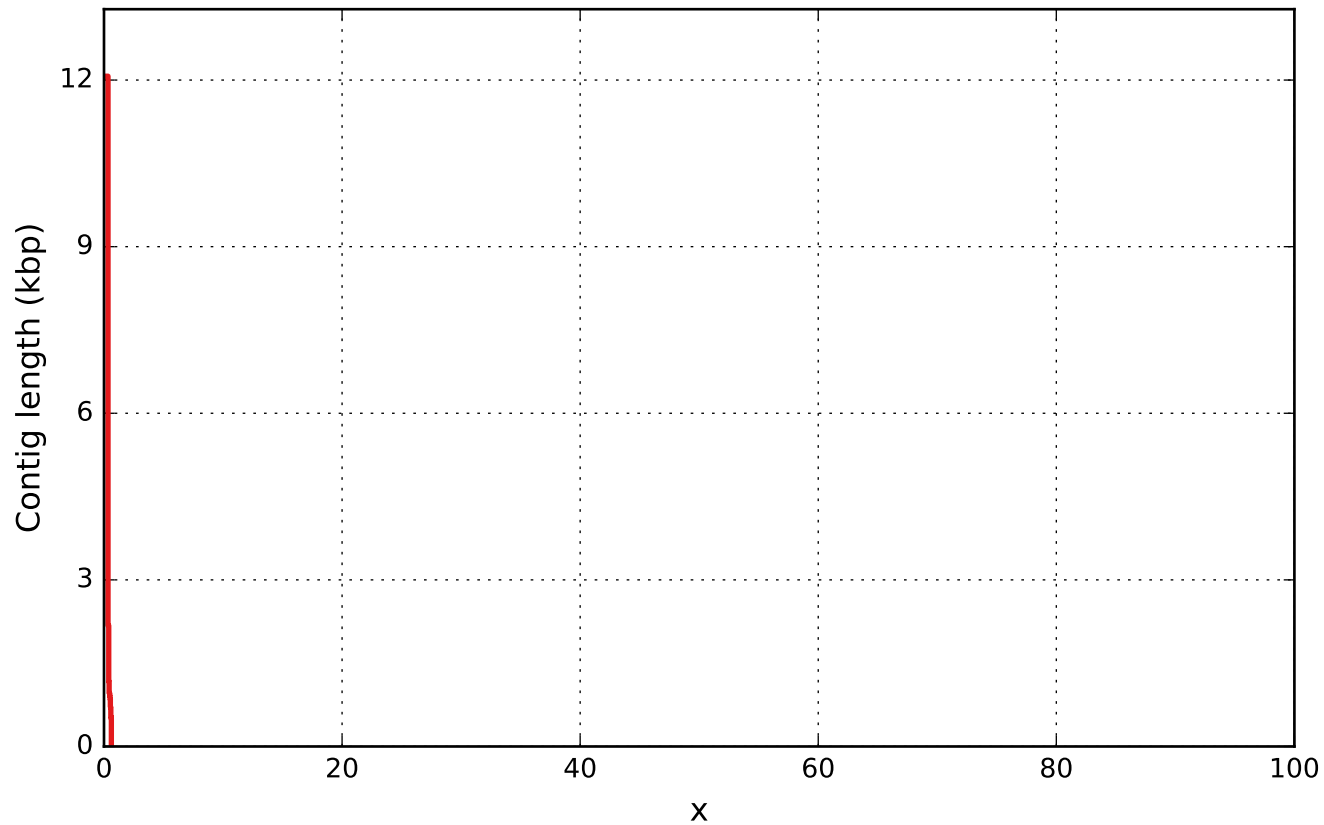
	final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	7
Partially unaligned length	16969
# N's	0

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).

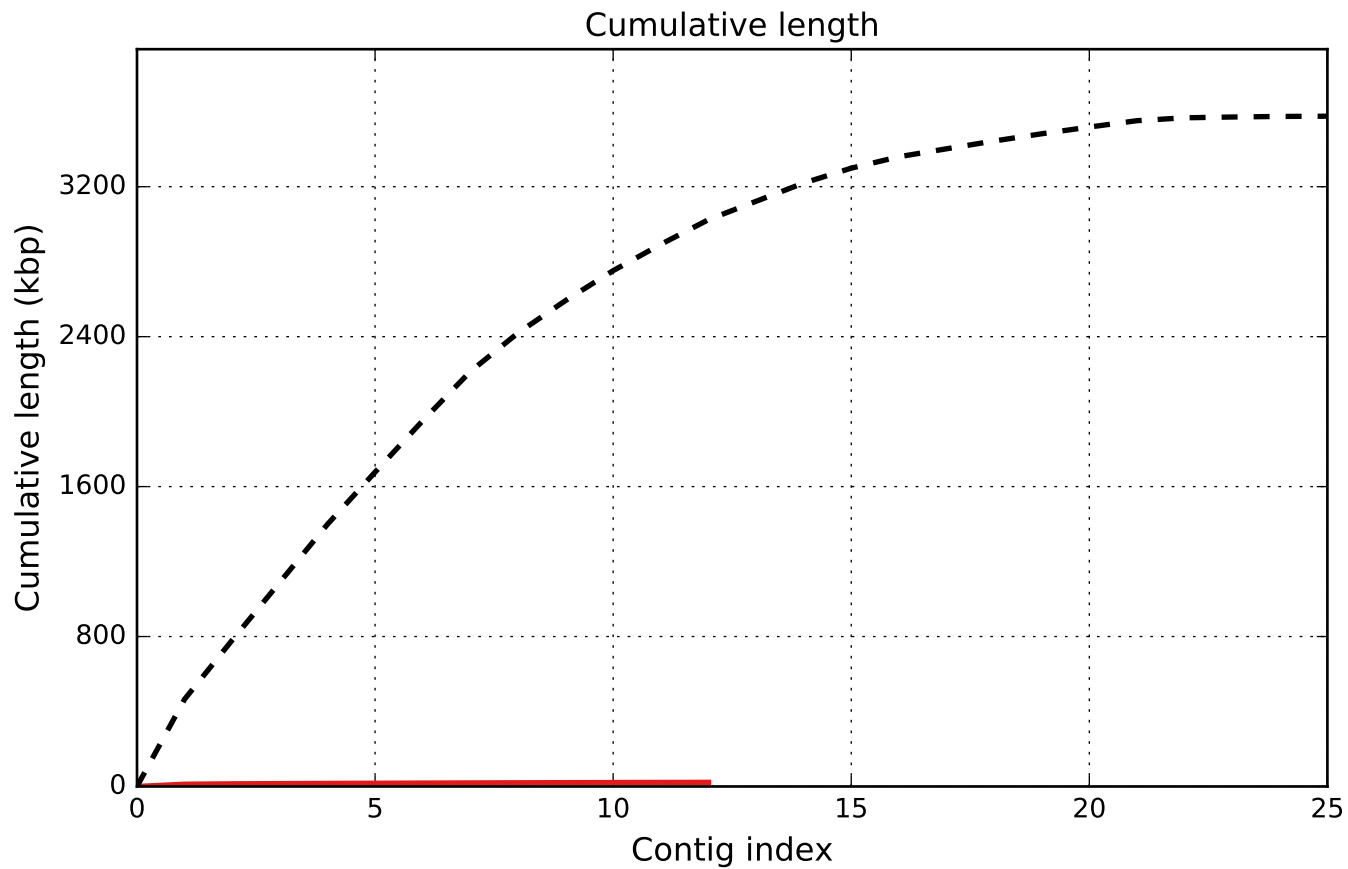


— final.contigs

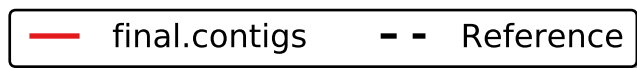
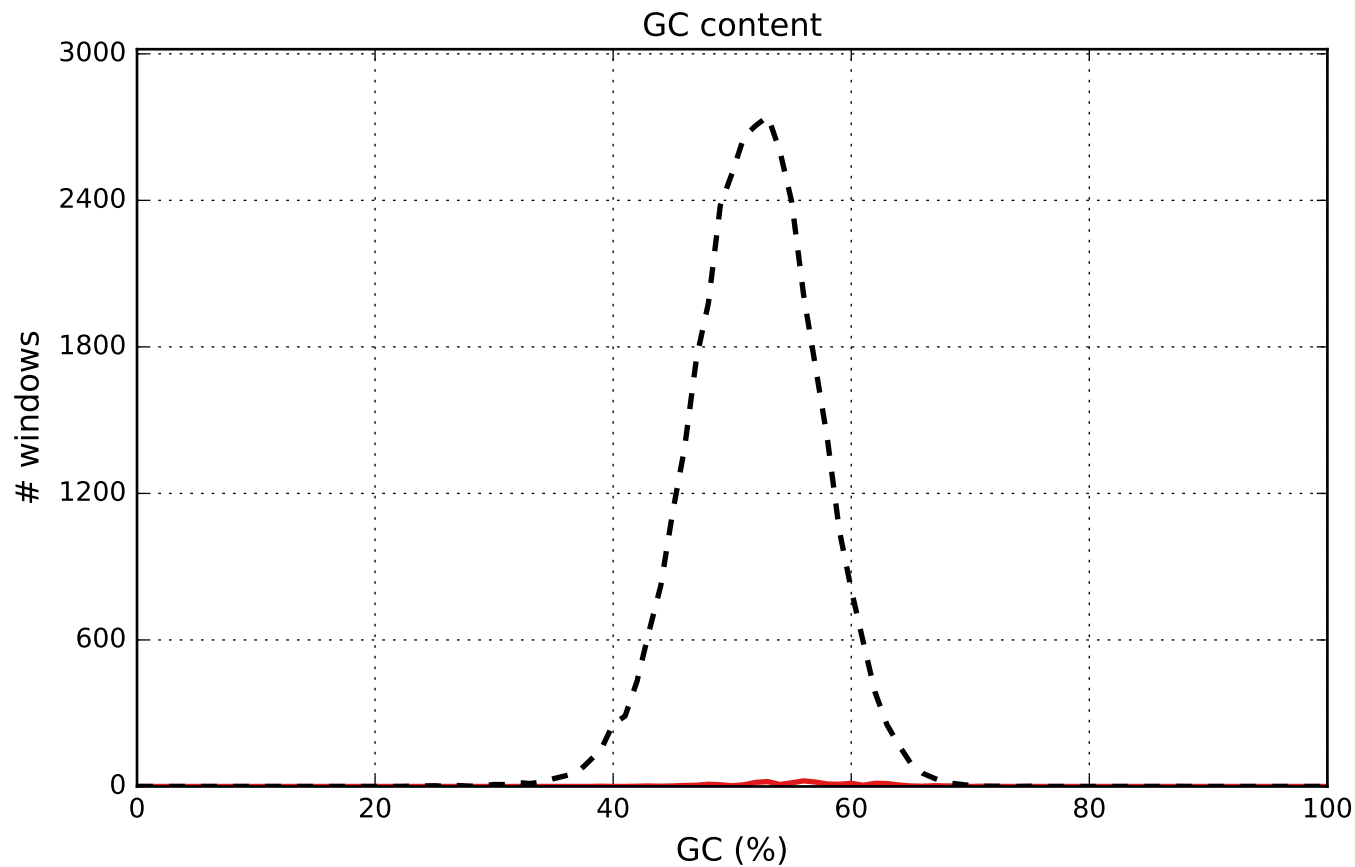
NGx

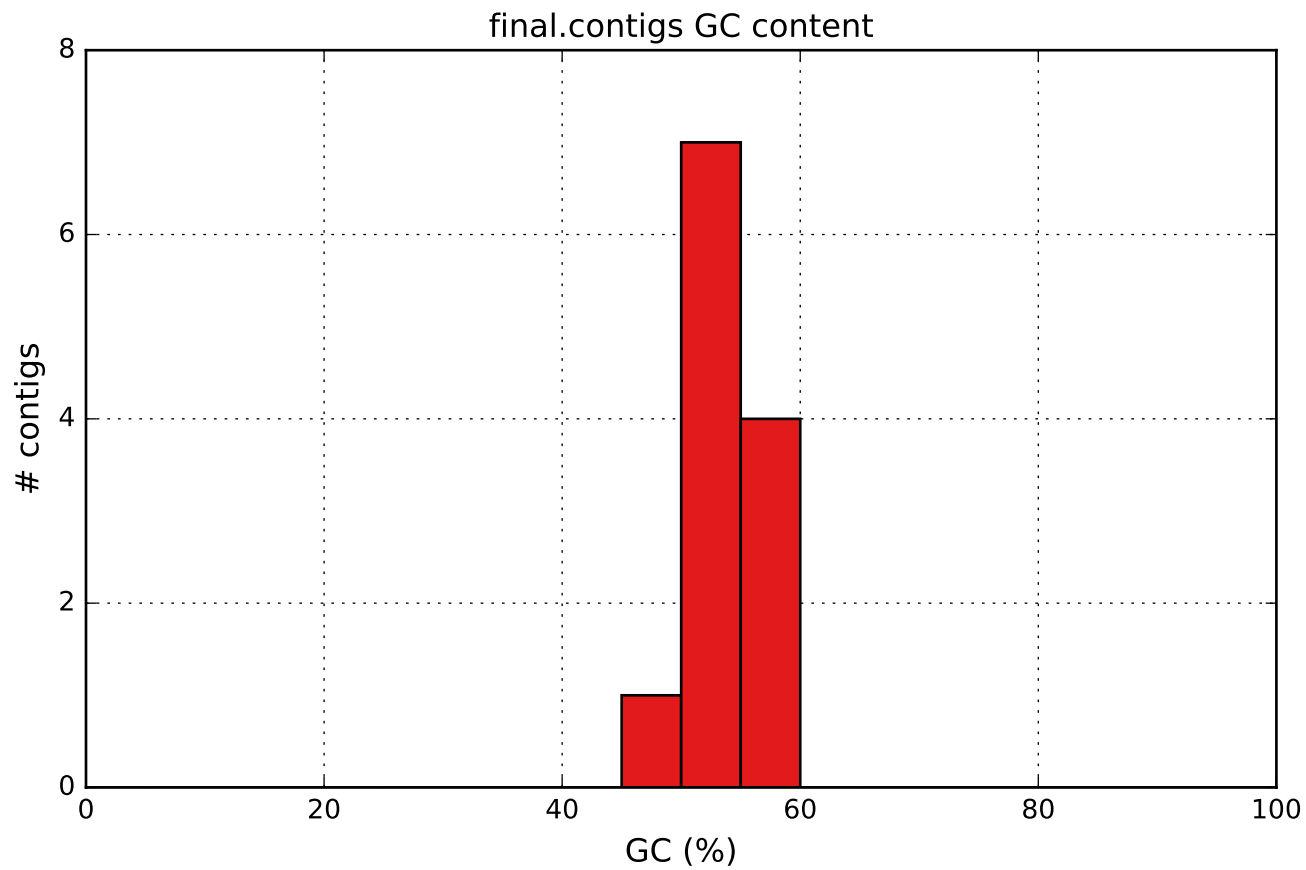


— final.contigs

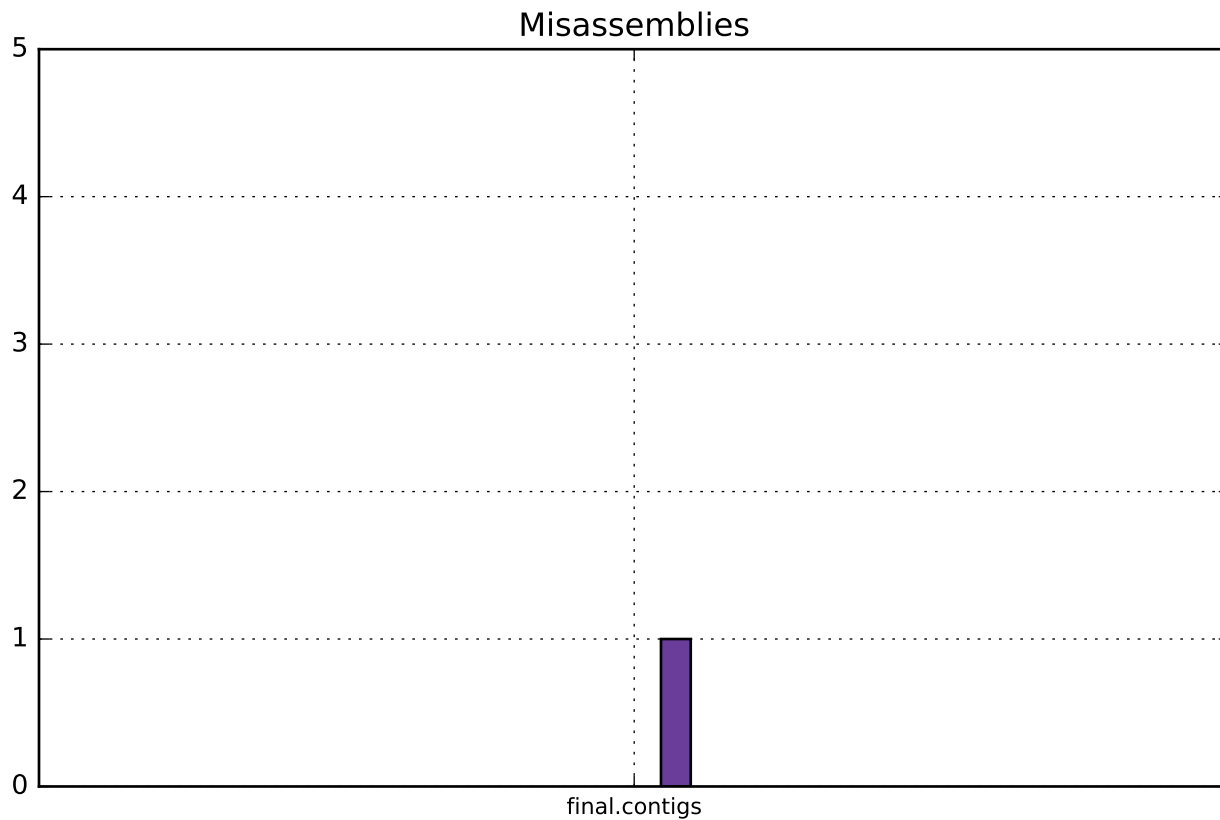



— final.contigs - - Reference



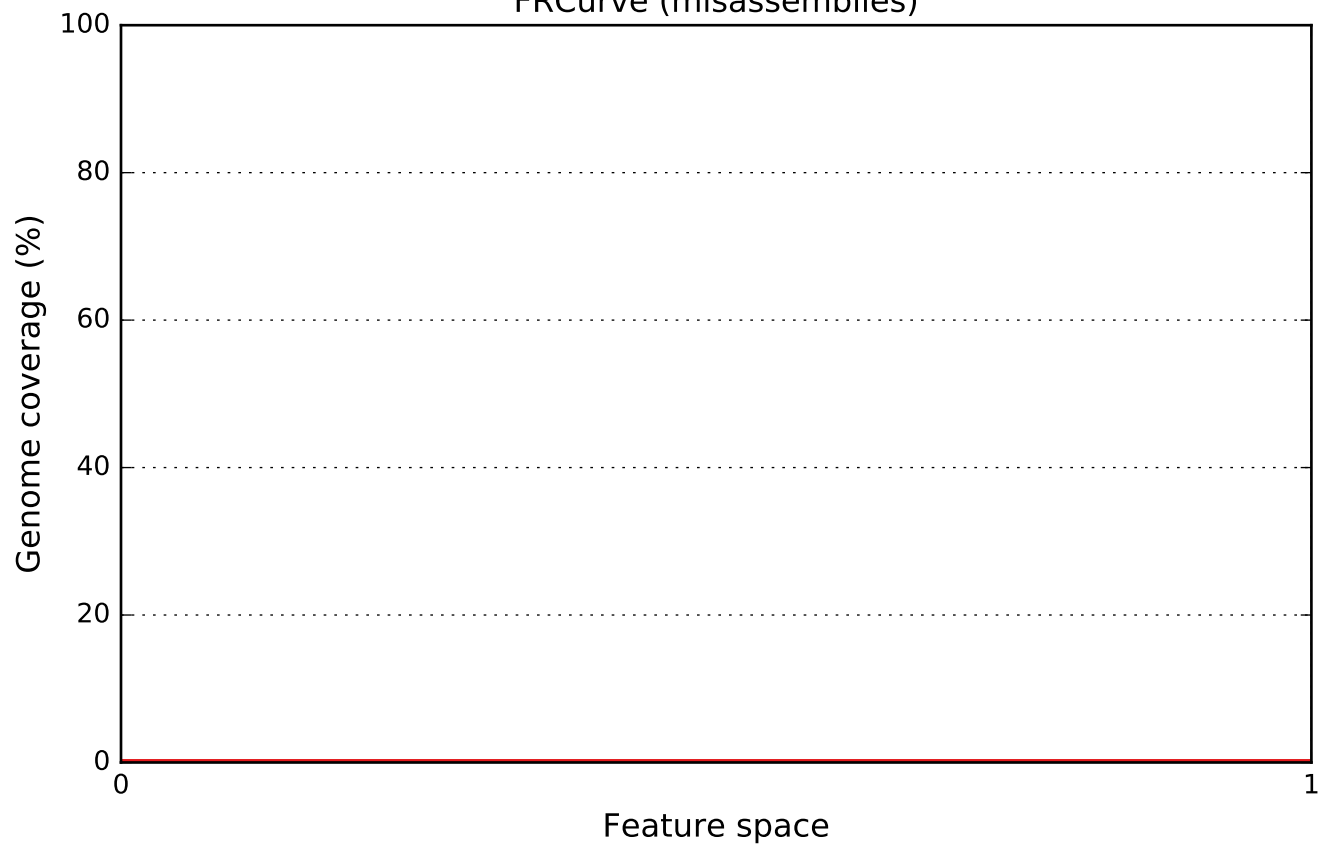


 final.contigs



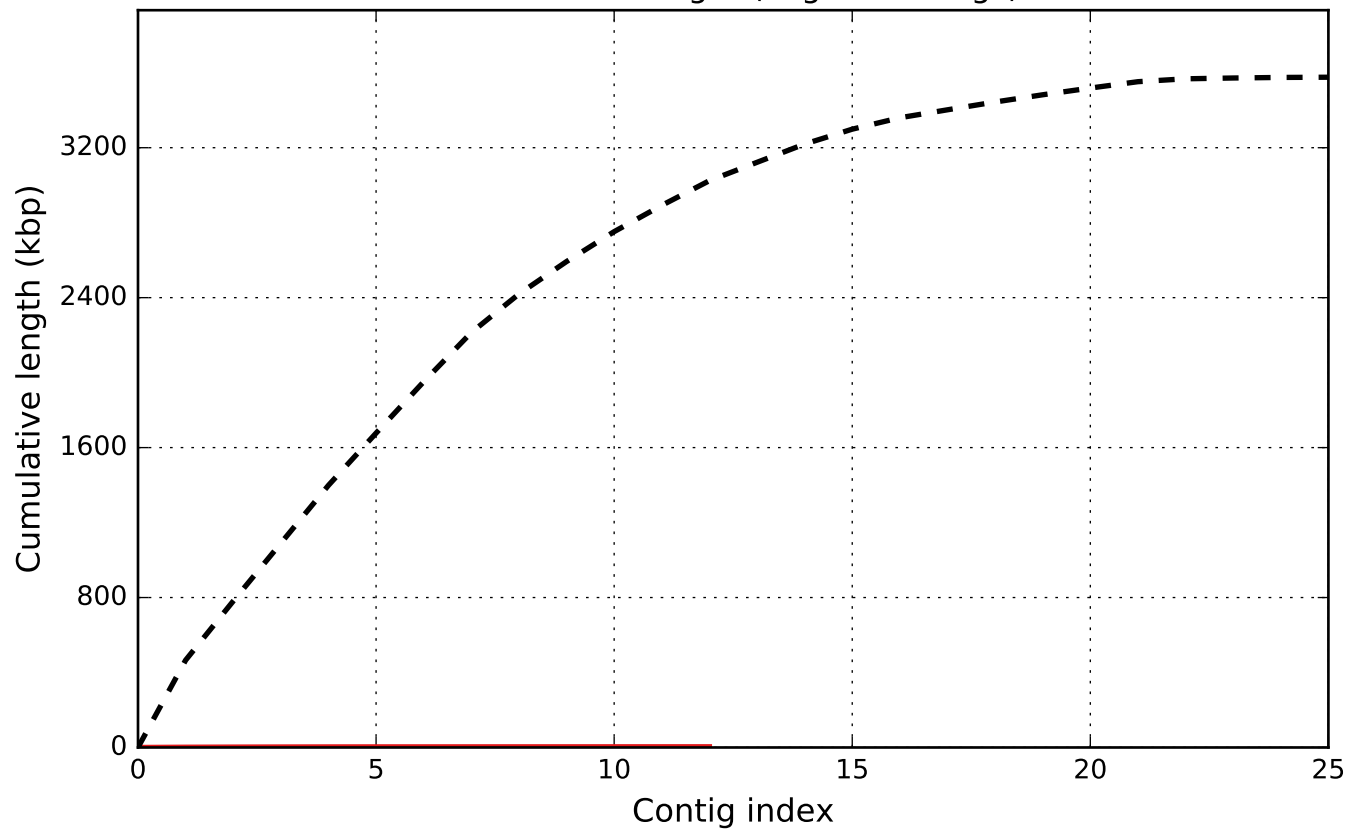
 # interspecies translocations

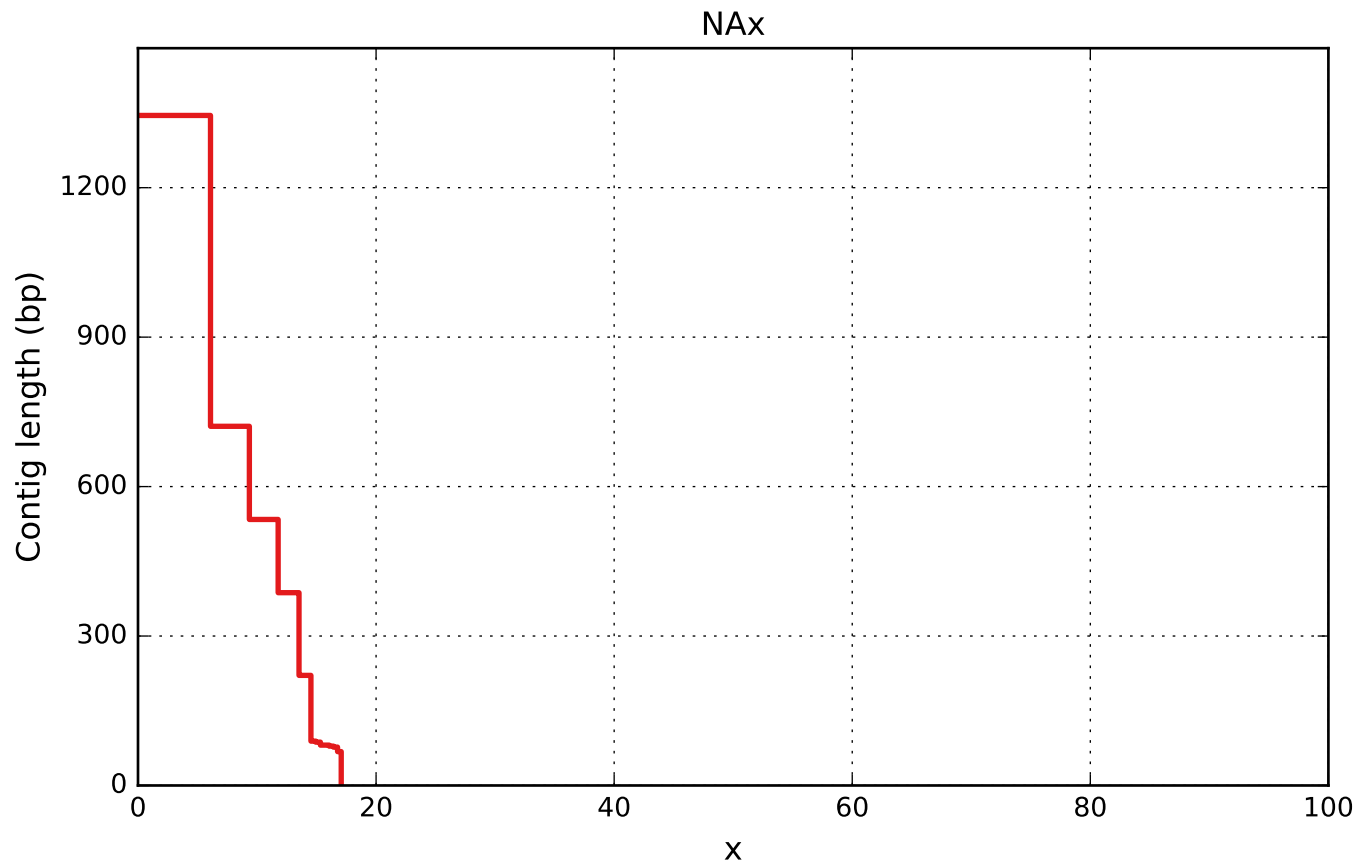
FRCurve (misassemblies)



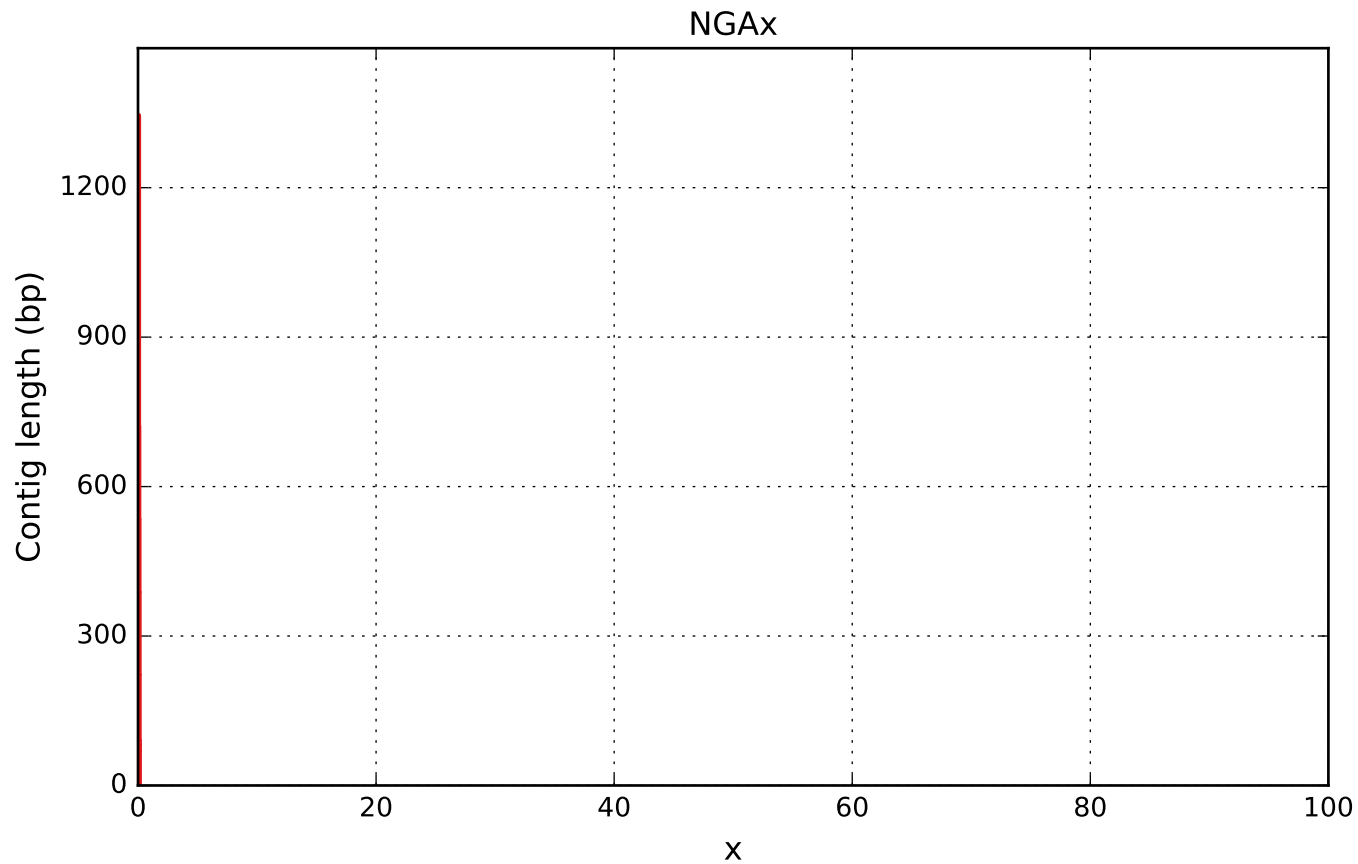
— final.contigs

Cumulative length (aligned contigs)





— final.contigs



— final.contigs