

Report

	final.contigs
# contigs (>= 1000 bp)	4
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	35307
Total length (>= 5000 bp)	32163
Total length (>= 10000 bp)	32163
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	12
Largest contig	17842
Total length	40921
Reference length	3739502
GC (%)	39.46
Reference GC (%)	53.19
N50	14321
N75	14321
L50	2
L75	2
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	1 + 7 part
Unaligned length	37947
Genome fraction (%)	0.025
Duplication ratio	3.171
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4904.05
# indels per 100 kbp	106.61
Largest alignment	247
Total aligned length	1356
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
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	1
# possible misassemblies	2
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	46
# indels	1
# indels (<= 5 bp)	1
# indels (> 5 bp)	0
Indels length	1

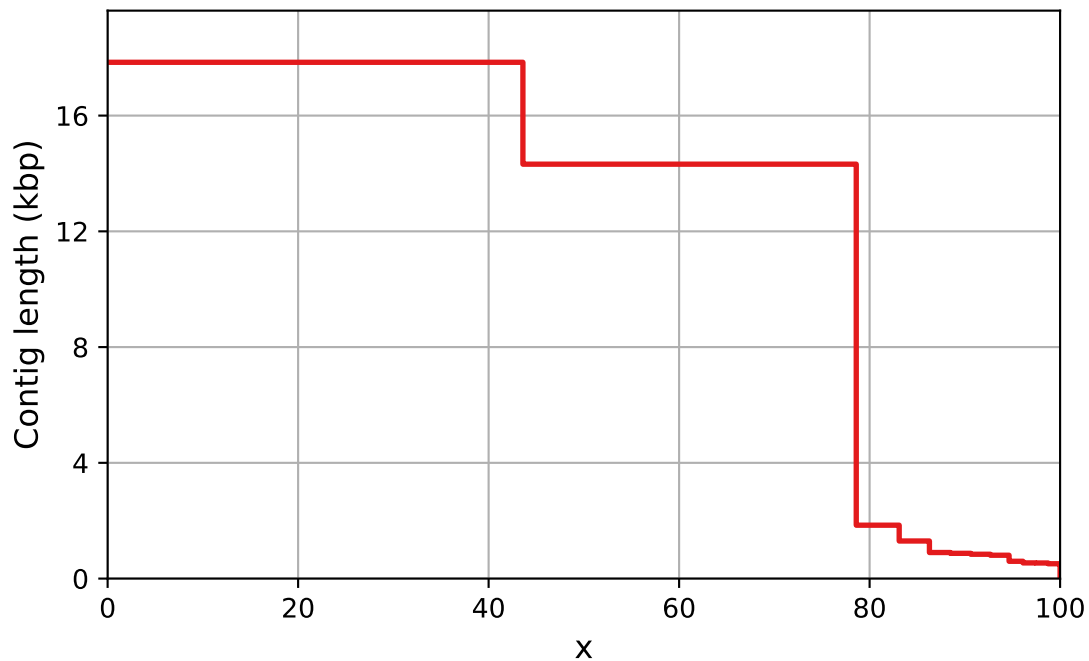
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	final.contigs
# fully unaligned contigs	1
Fully unaligned length	807
# partially unaligned contigs	7
Partially unaligned length	37140
# N's	0

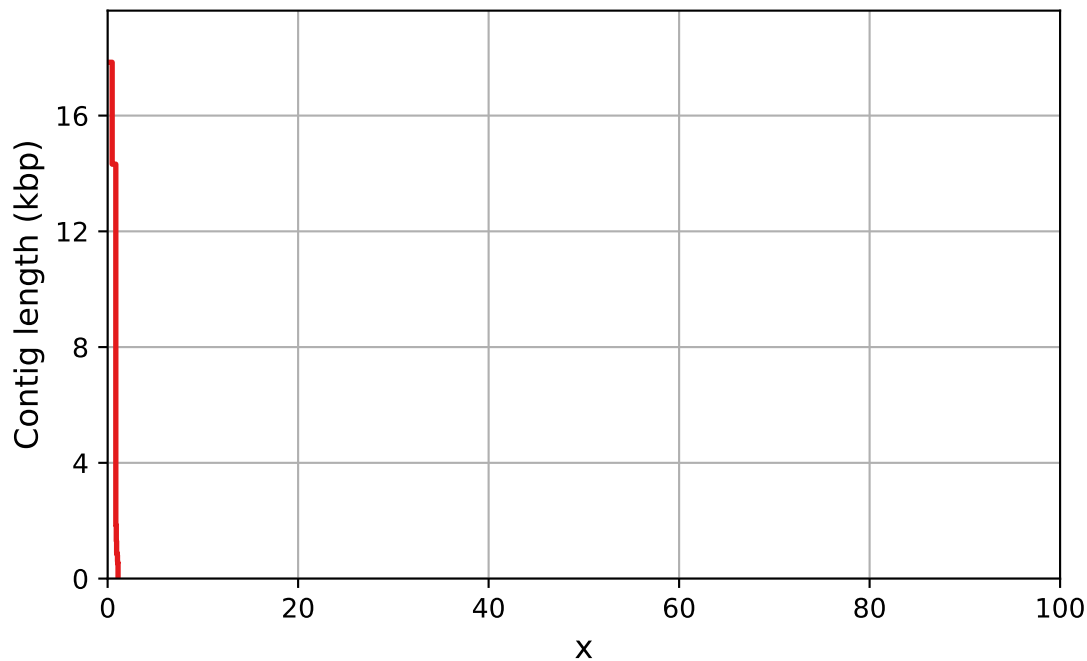
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

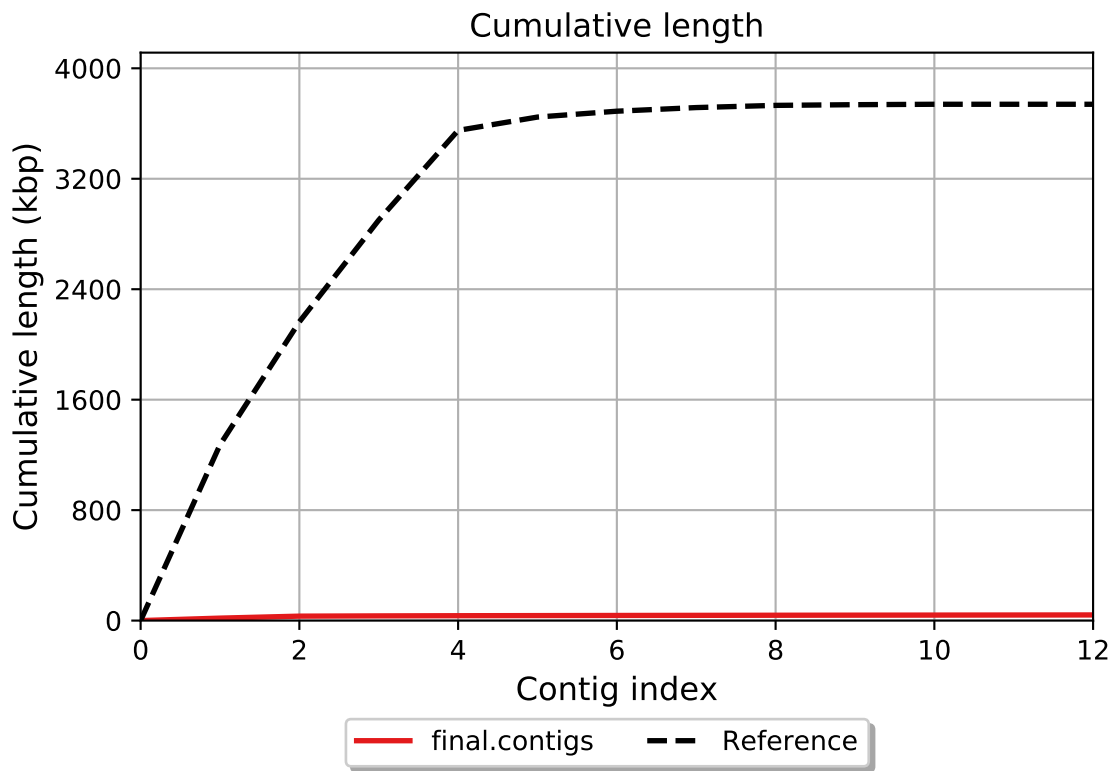


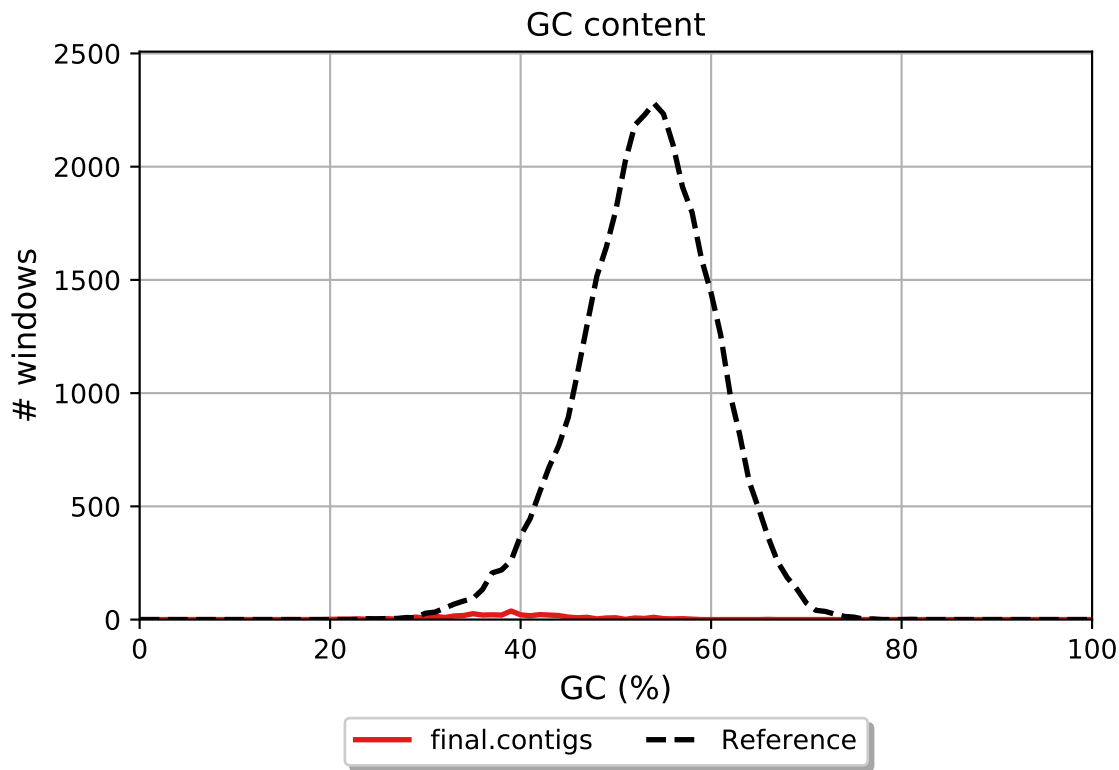
— final.contigs

NGx

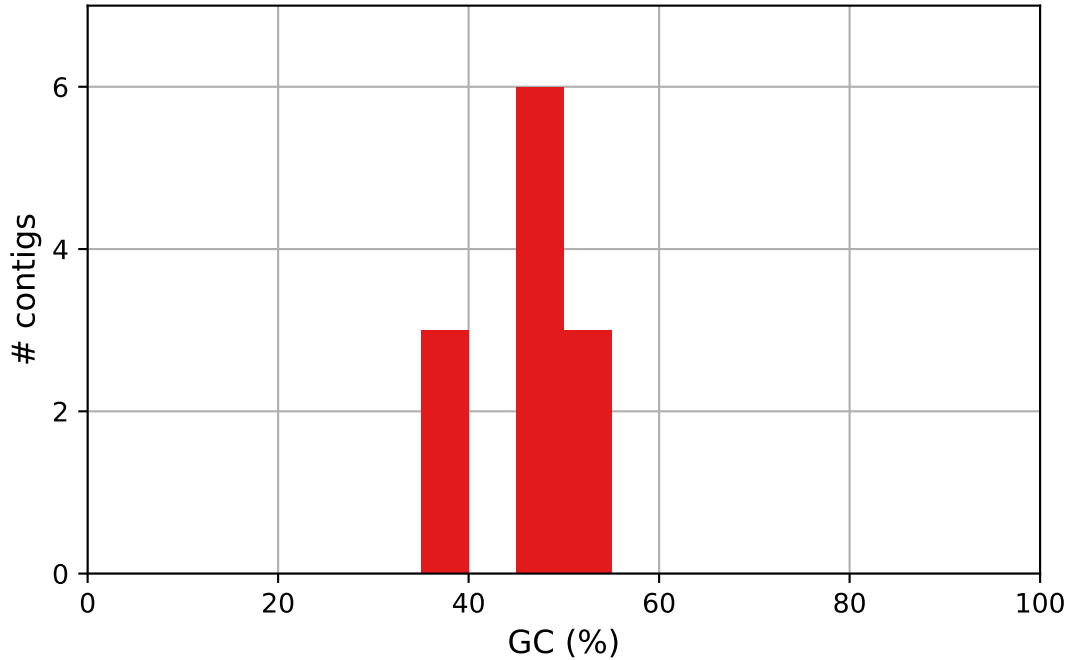


— final.contigs





final.contigs GC content



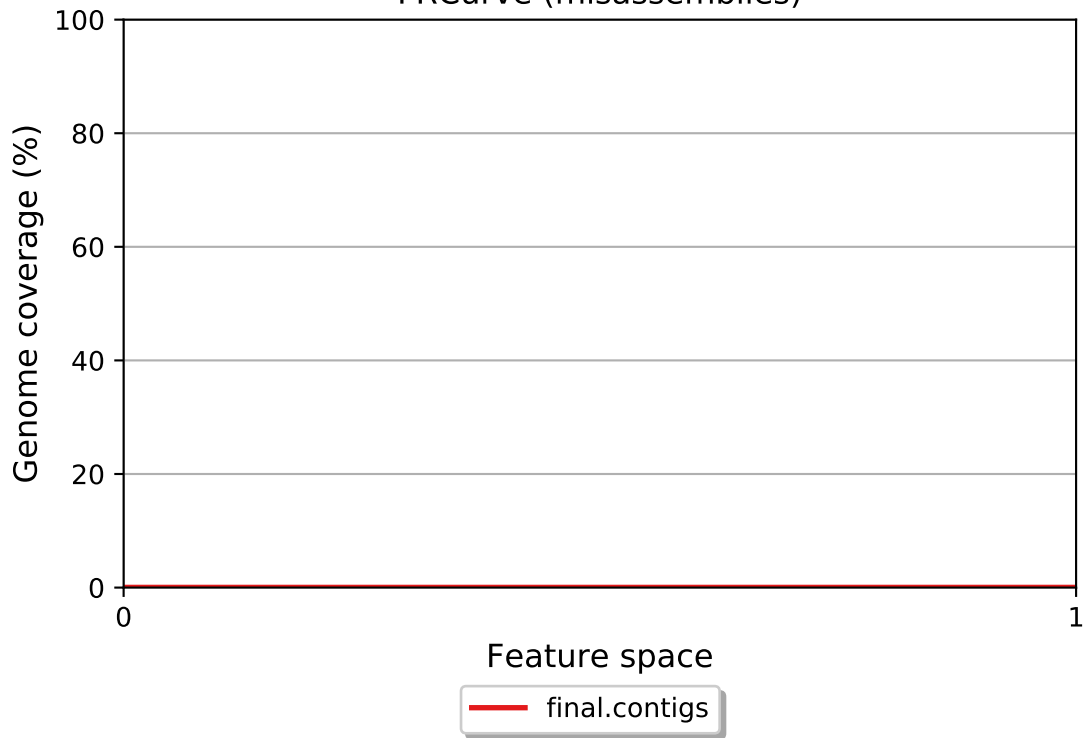
final.contigs

Misassemblies

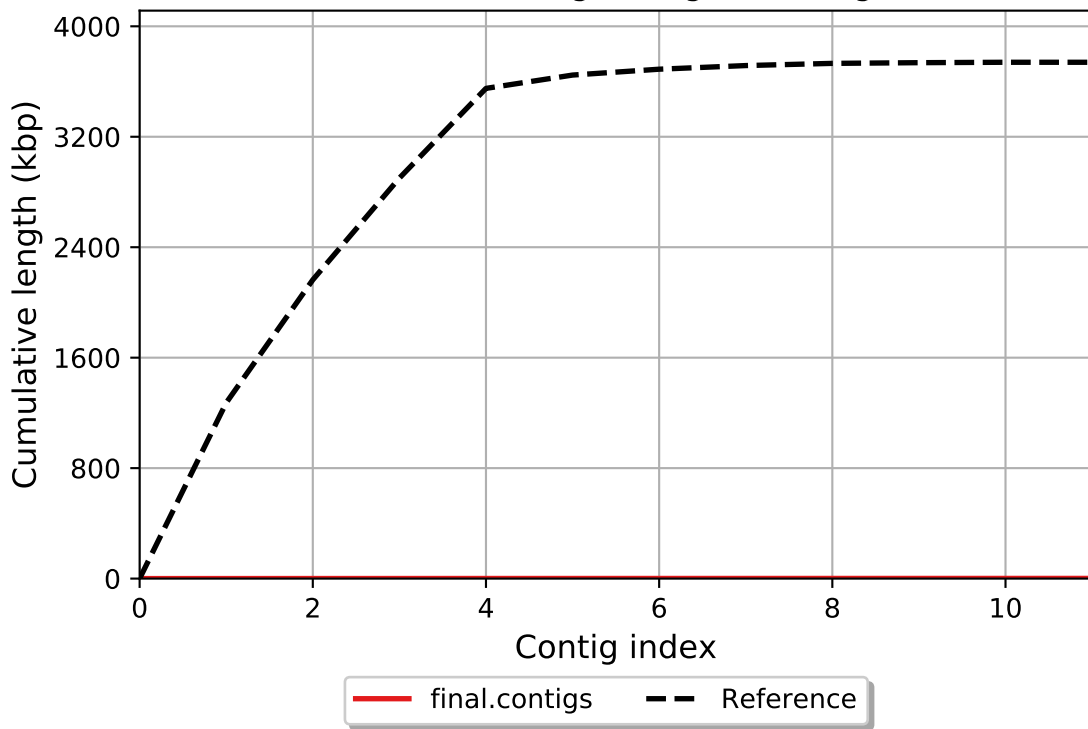


interspecies translocations

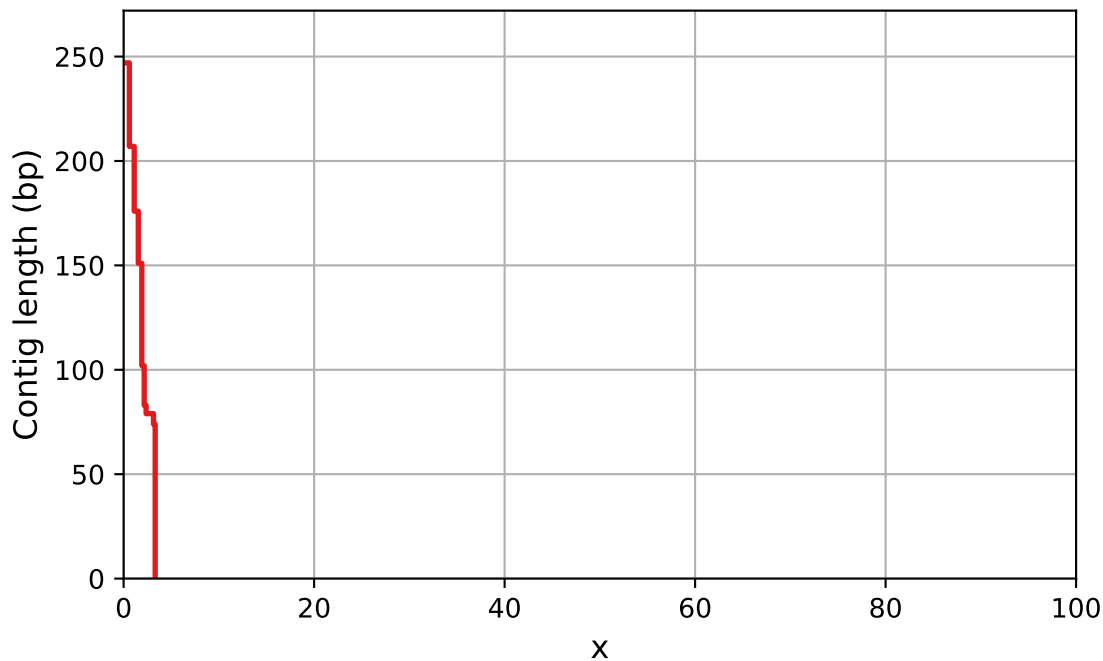
FRCurve (misassemblies)



Cumulative length (aligned contigs)

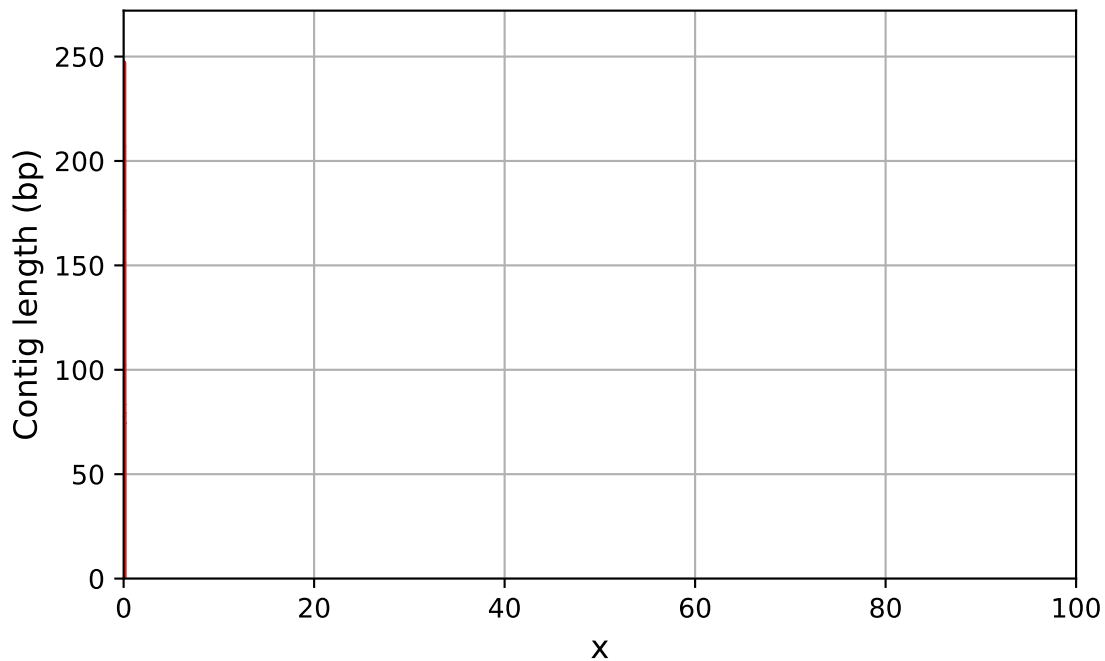


NAx



— final.contigs

NGAx



— final.contigs