Report

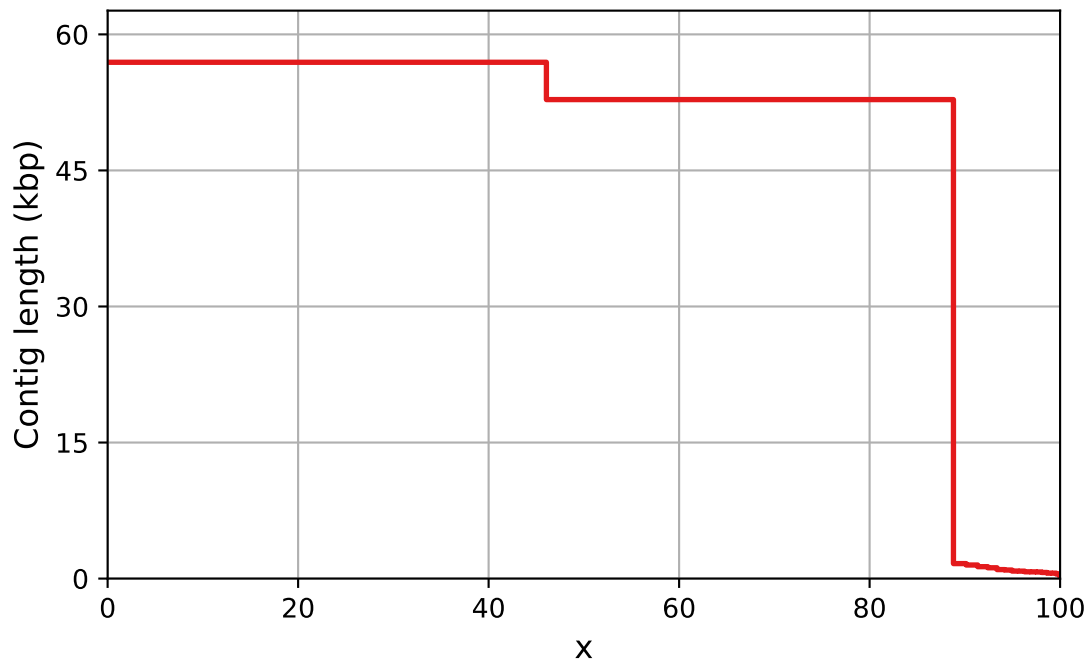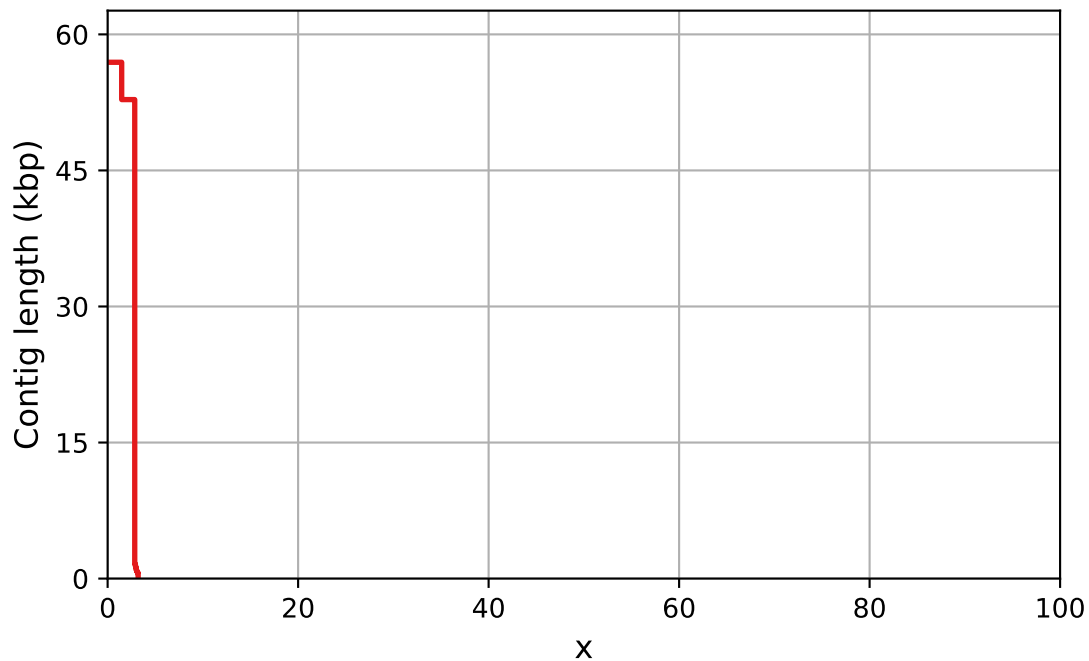|	final.contigs
# contigs (>= 1000 bp)	6
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	2
# contigs (>= 50000 bp)	2
Total length (>= 1000 bp)	115392
Total length (>= 5000 bp)	109736
Total length (>= 10000 bp)	109736
Total length (>= 25000 bp)	109736
Total length (>= 50000 bp)	109736
# contigs	17
Largest contig	56925
Total length	123571
Reference length	3854463
GC (%)	57.88
Reference GC (%)	45.75
N50	52811
N75	52811
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	1
# unaligned contigs	2 + 10 part
Unaligned length	118869
Genome fraction (%)	0.041
Duplication ratio	2.946
# N's per 100 kbp	0.00
# mismatches per 100 kbp	6015.04
# indels per 100 kbp	125.31
Largest alignment	376
Total aligned length	2455
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	5
# possible misassemblies	5
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	96
# indels	2
# indels (<= 5 bp)	2
# indels (> 5 bp)	0
Indels length	2

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).
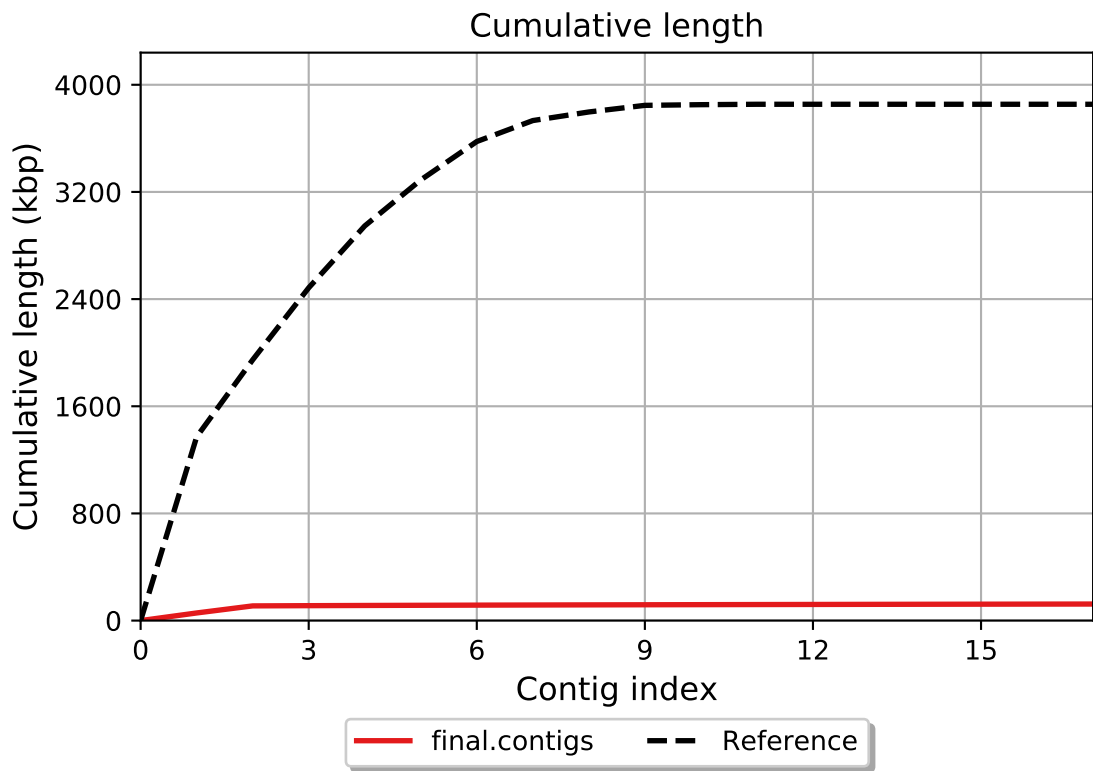
Unaligned report
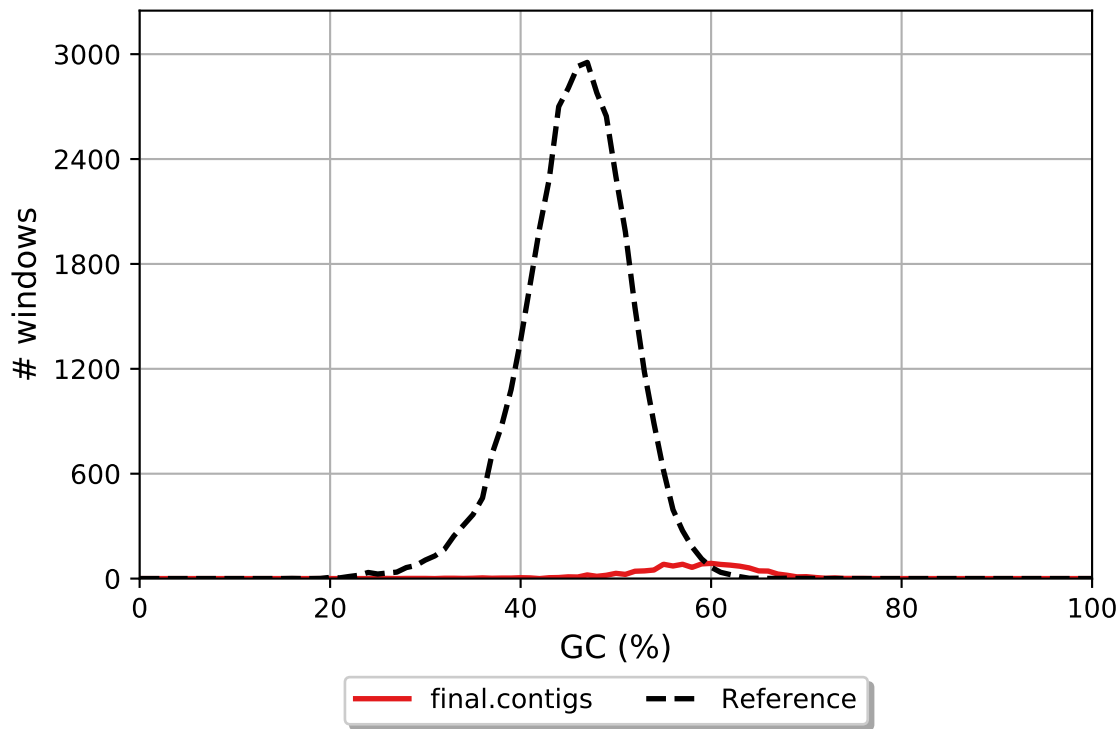
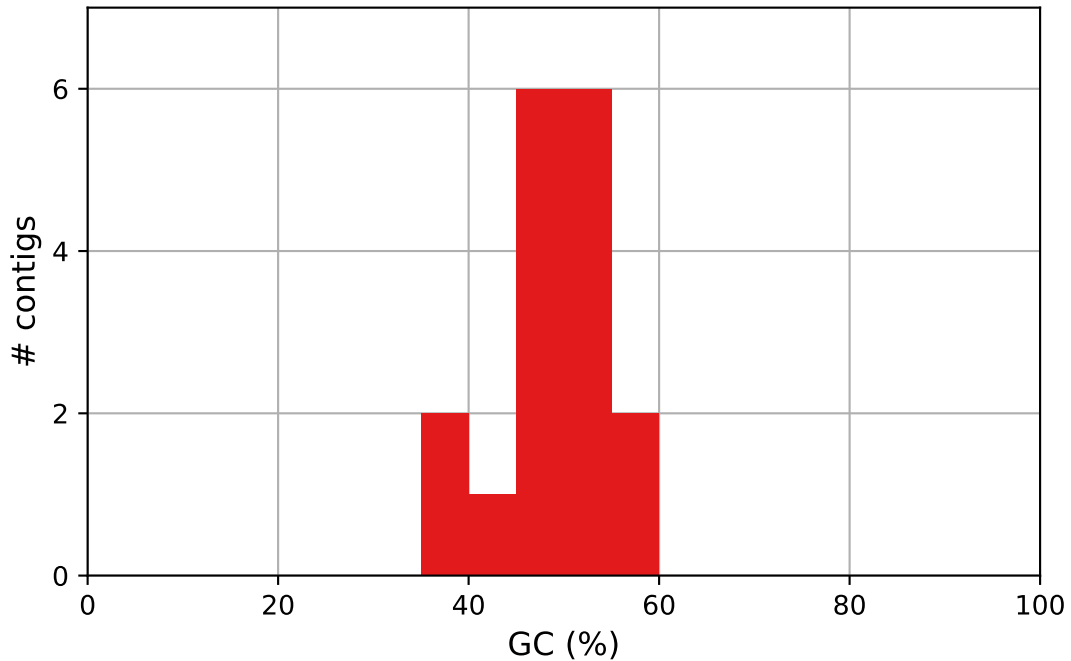|	final.contigs
# fully unaligned contigs	2
Fully unaligned length	1422
# partially unaligned contigs	10
Partially unaligned length	117447
# N's	0

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

NGx

Cumulative length

GC content
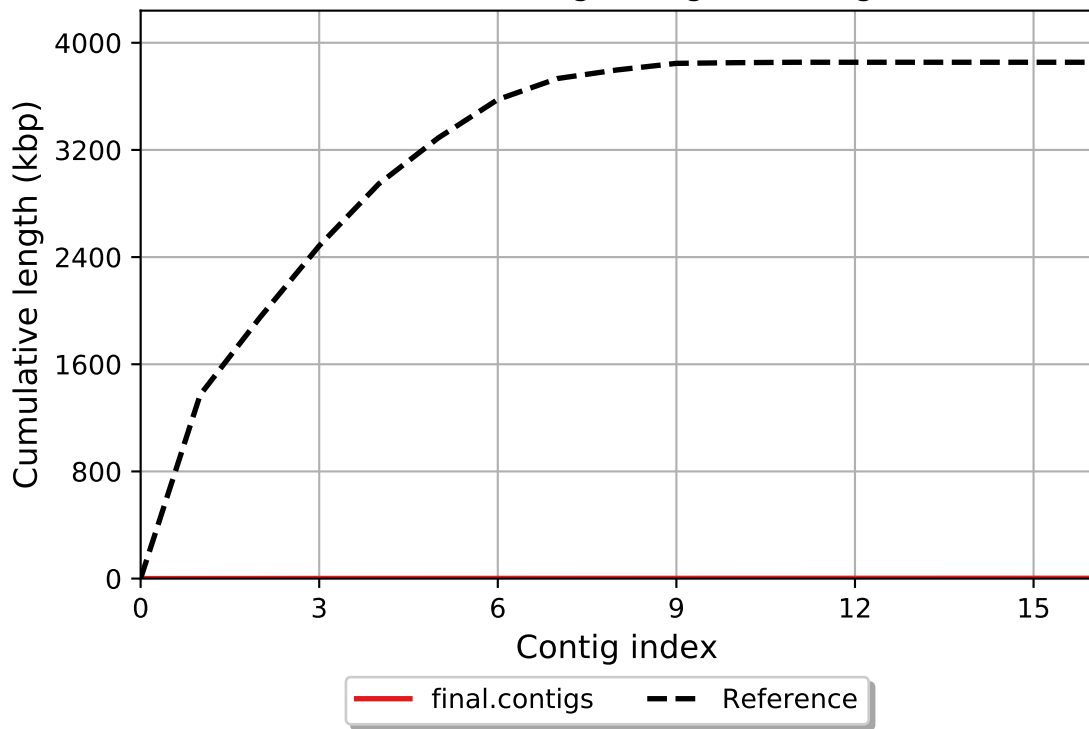
final.contigs GC content

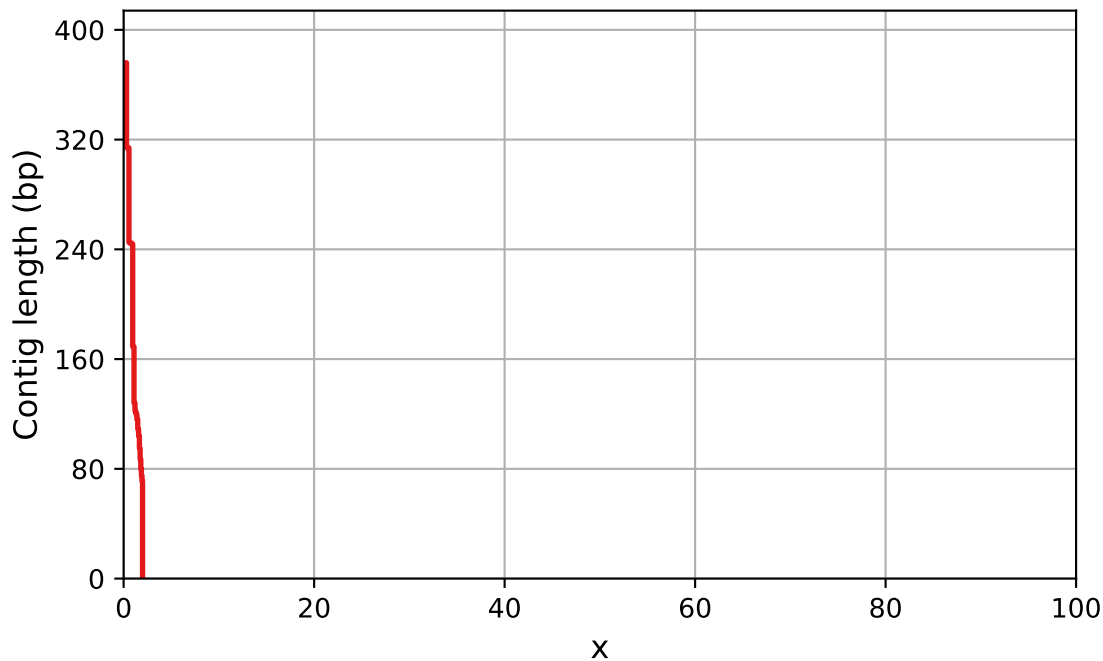# Misassemblies

final.contigs

interspecies translocations

FRCurve (misassemblies)
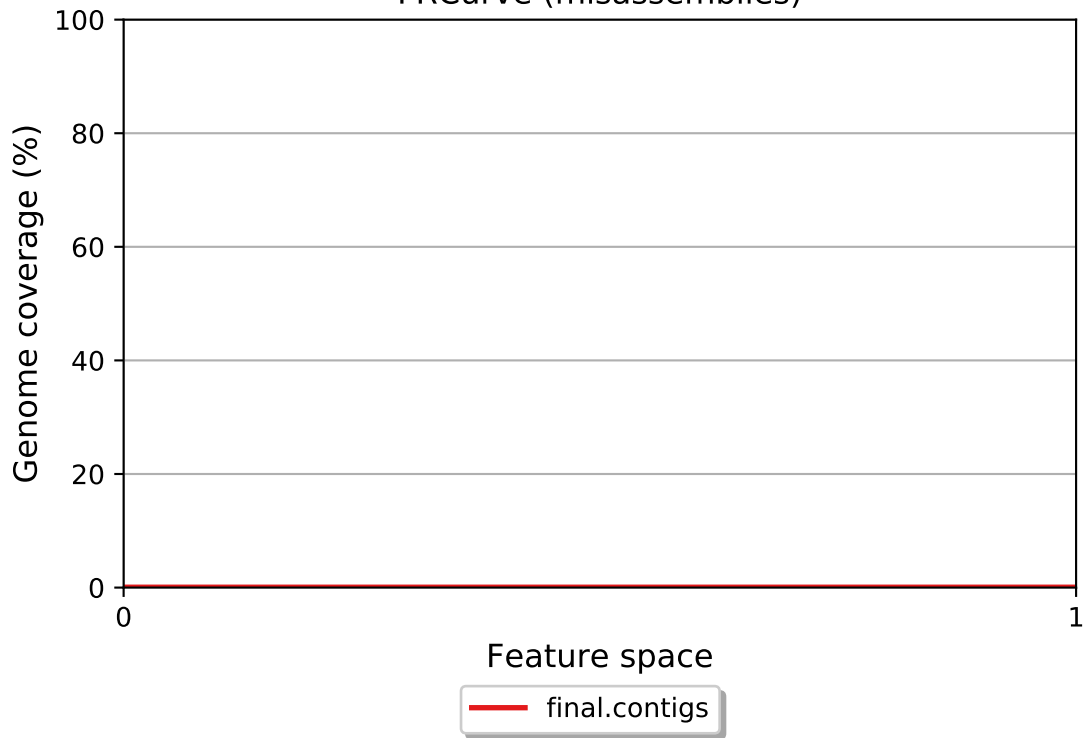
Cumulative length (aligned contigs)

NAx

final.contigs

NGAx