Report

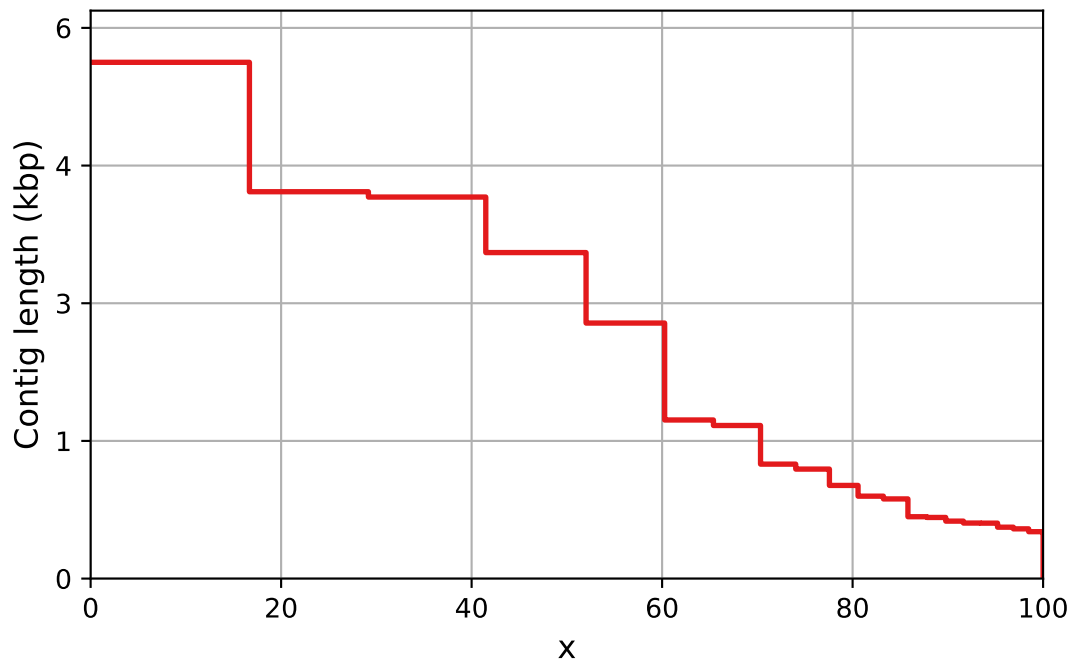|	final.contigs
# contigs (>= 1000 bp)	10
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	27184
Total length (>= 5000 bp)	5625
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	20
Largest contig	5625
Total length	33738
Reference length	4000057
GC (%)	43.75
Reference GC (%)	40.23
N50	3552
N75	1193
L50	4
L75	9
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# unaligned contigs	3 + 13 part
Unaligned length	29530
Genome fraction (%)	0.046
Duplication ratio	2.280
# N's per 100 kbp	0.00
# mismatches per 100 kbp	4875.41
# indels per 100 kbp	54.17
Largest alignment	272
Total aligned length	2656
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	2
# possible misassemblies	3
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	90
# 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
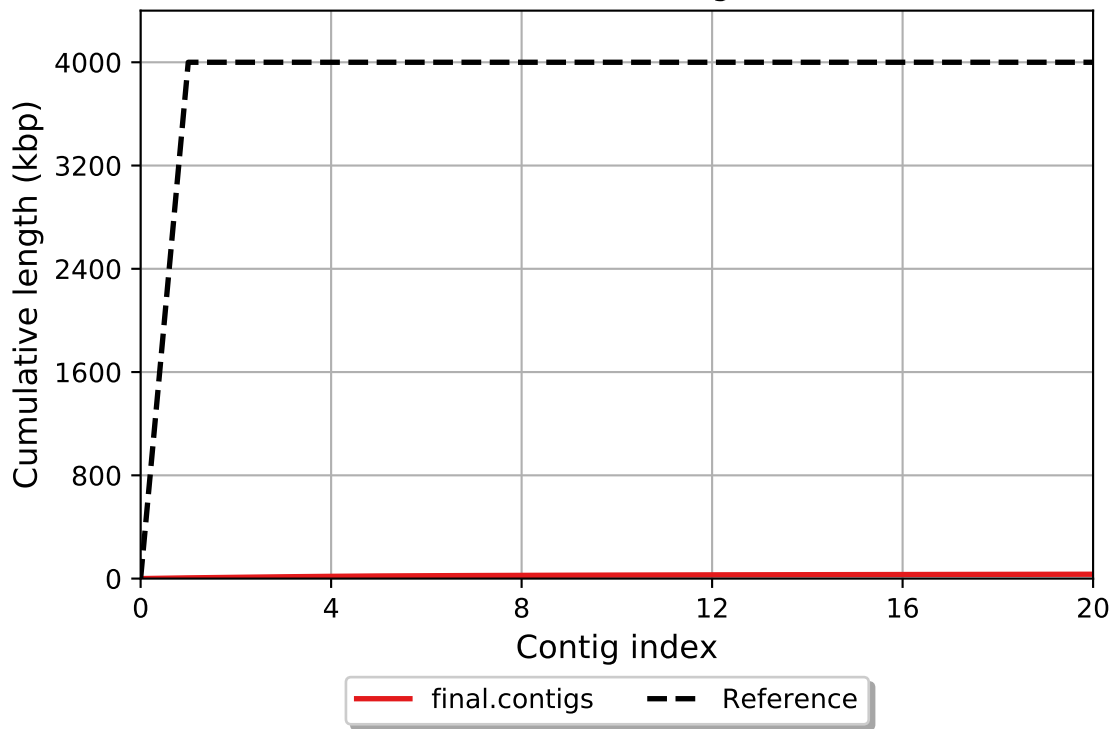
	final.contigs
# fully unaligned contigs	3
Fully unaligned length	2962
# partially unaligned contigs	13
Partially unaligned length	26568
# N's	0

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).
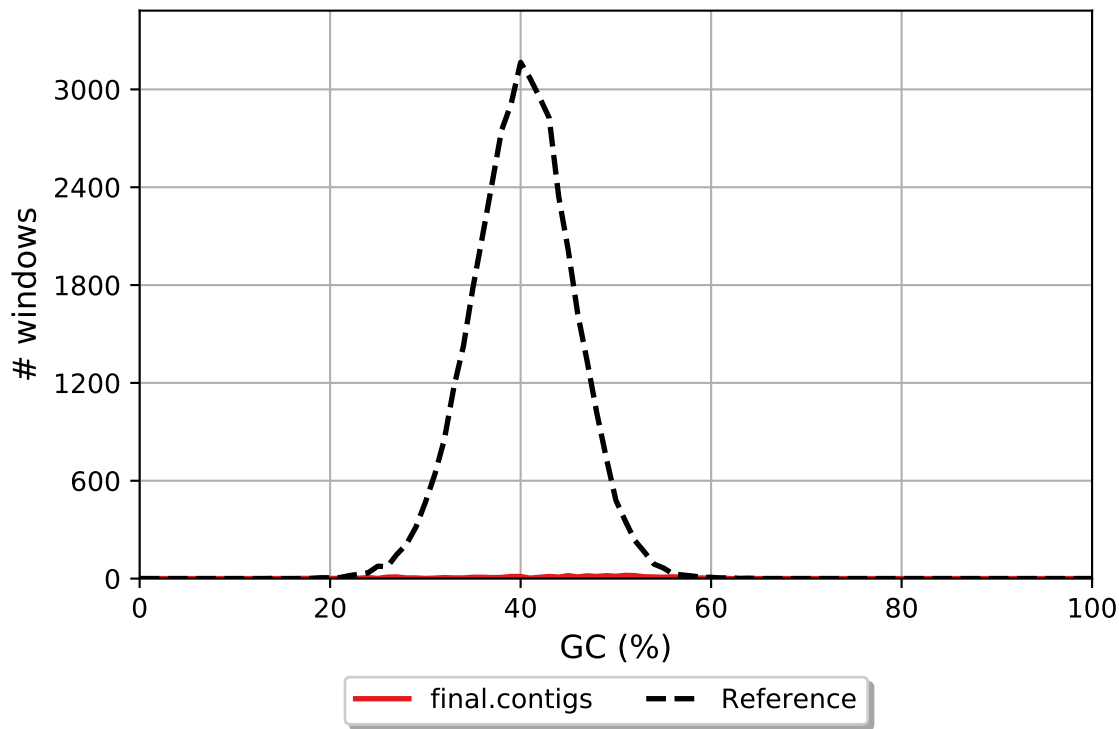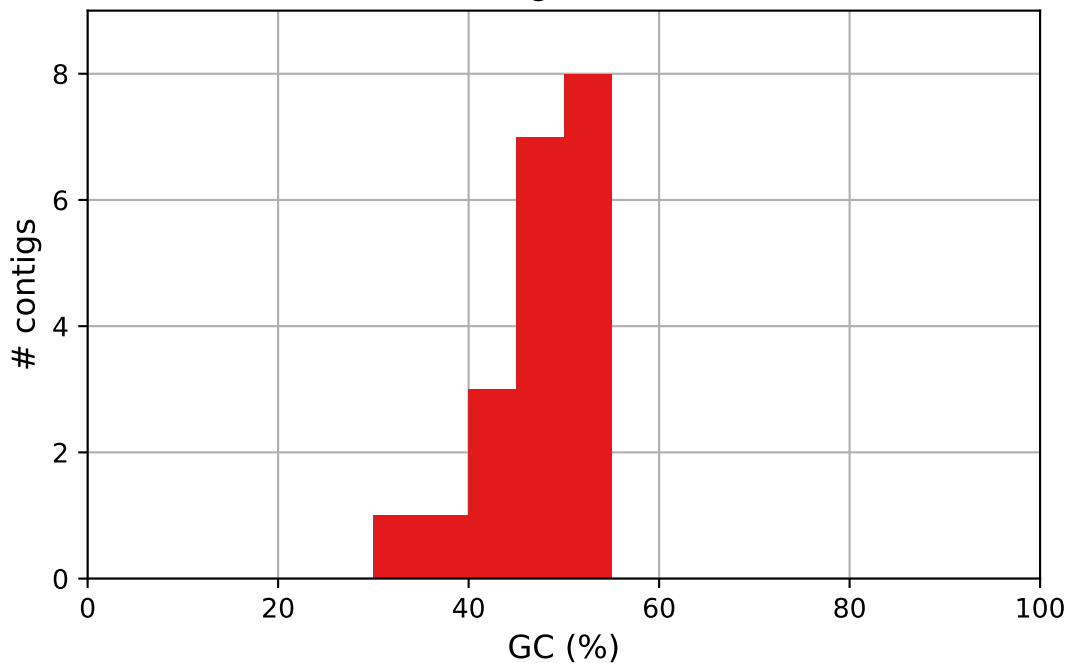
Nx

NGx
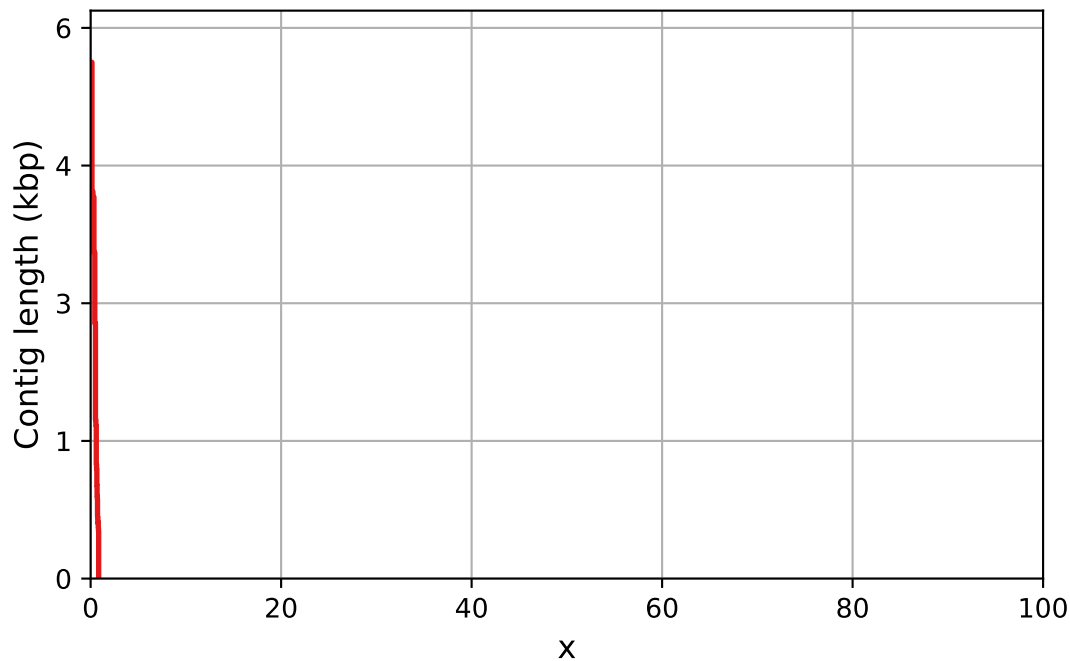
final.contigs

Cumulative length

GC content

final.contigs GC content

Misassemblies
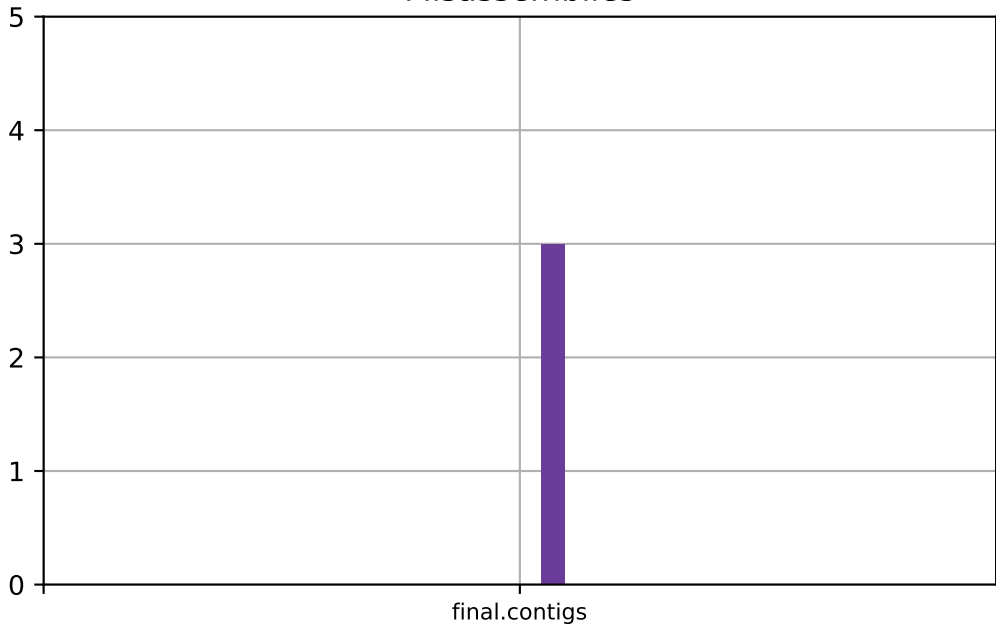
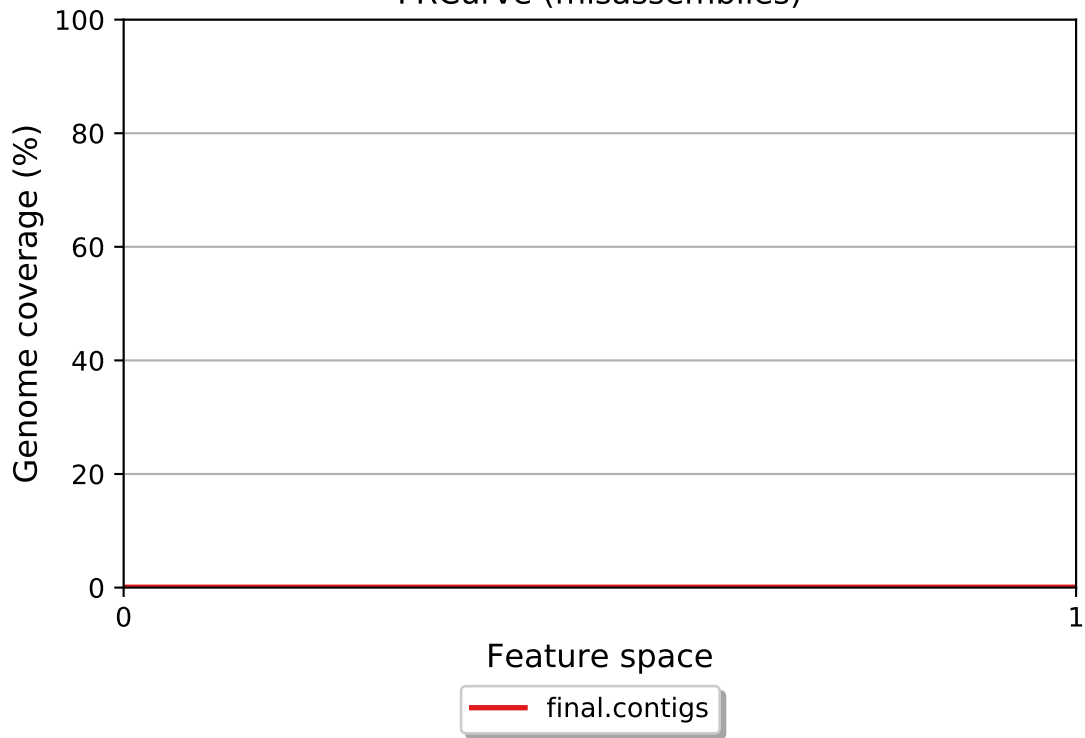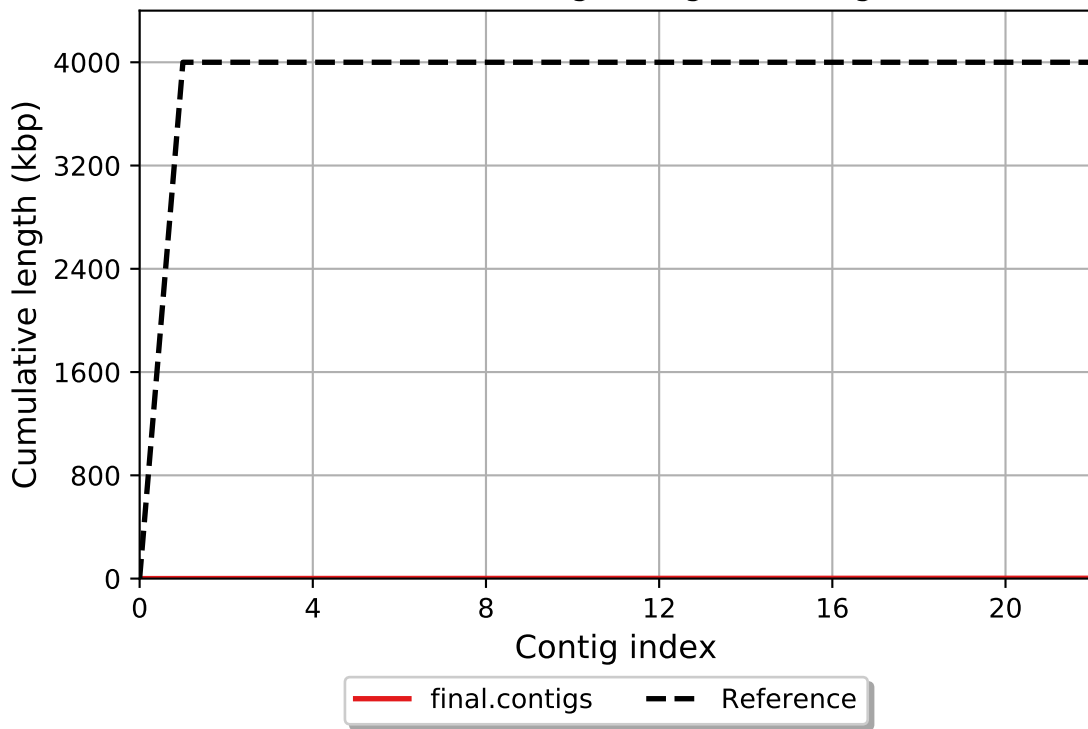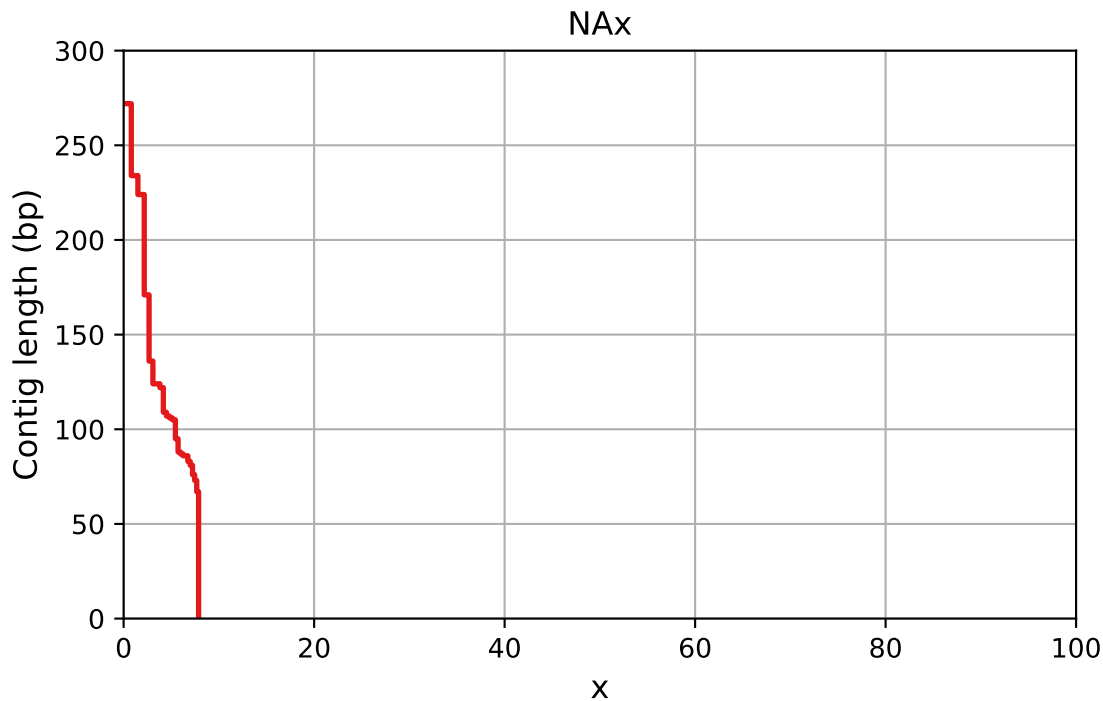|	final.contigs

■ # interspecies translocations

FRCurve (misassemblies)

Cumulative length (aligned contigs)

NAx

NGAx