

Report

	final.contigs
# contigs (>= 1000 bp)	6
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	39659
Total length (>= 5000 bp)	32249
Total length (>= 10000 bp)	32249
Total length (>= 25000 bp)	32249
Total length (>= 50000 bp)	0
# contigs	13
Largest contig	32249
Total length	44433
Reference length	4984172
GC (%)	55.98
Reference GC (%)	64.67
N50	32249
N75	2184
L50	1
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	4 + 6 part
Unaligned length	42021
Genome fraction (%)	0.015
Duplication ratio	3.137
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2990.90
# indels per 100 kbp	0.00
Largest alignment	105
Total aligned length	769
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	2
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	23
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

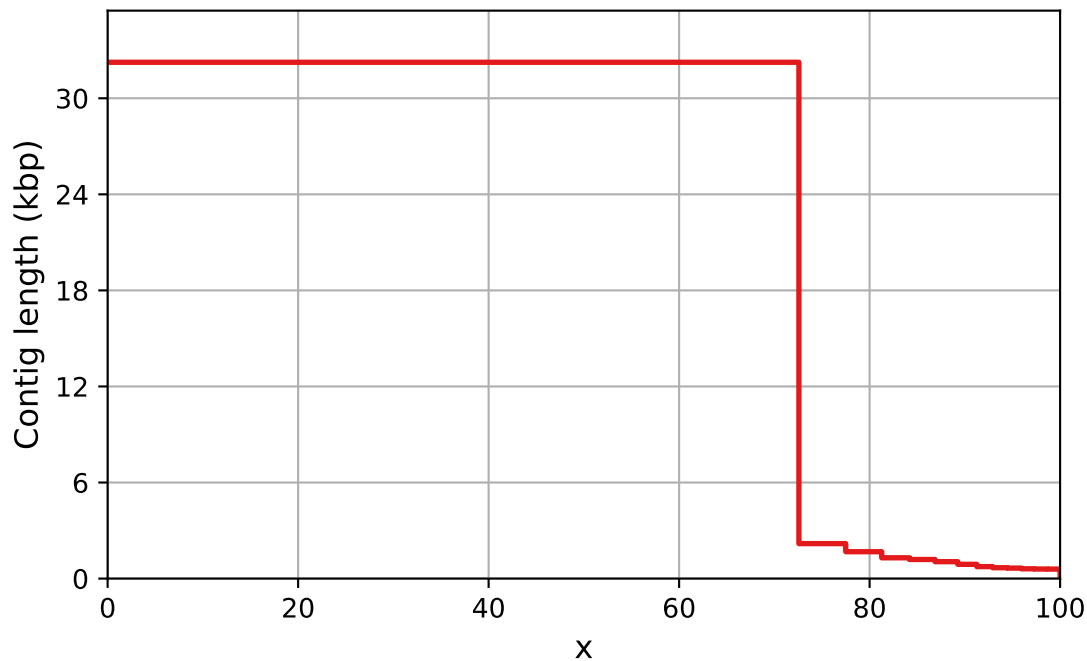
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	final.contigs
# fully unaligned contigs	4
Fully unaligned length	4630
# partially unaligned contigs	6
Partially unaligned length	37391
# N's	0

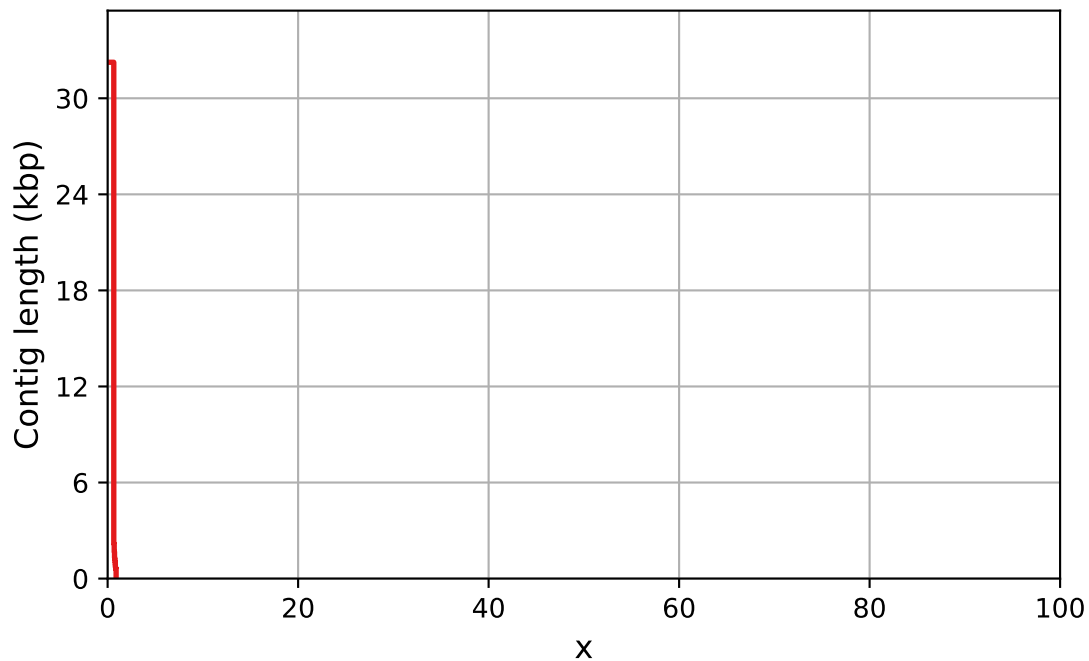
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

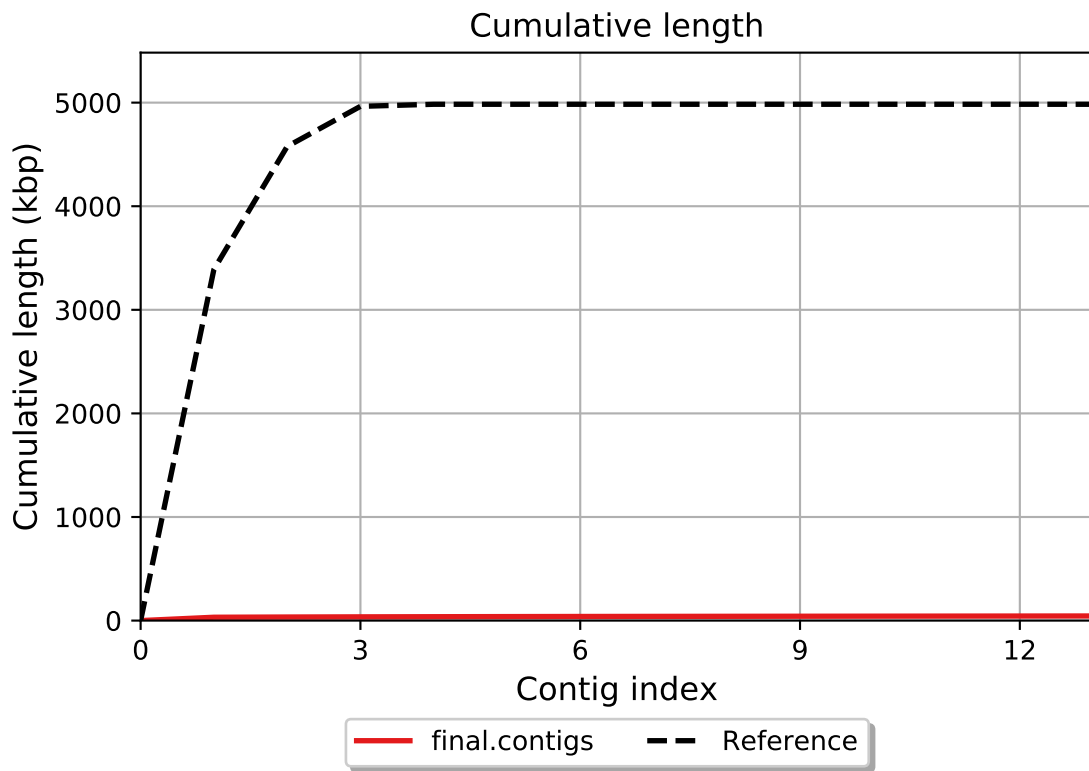


— final.contigs

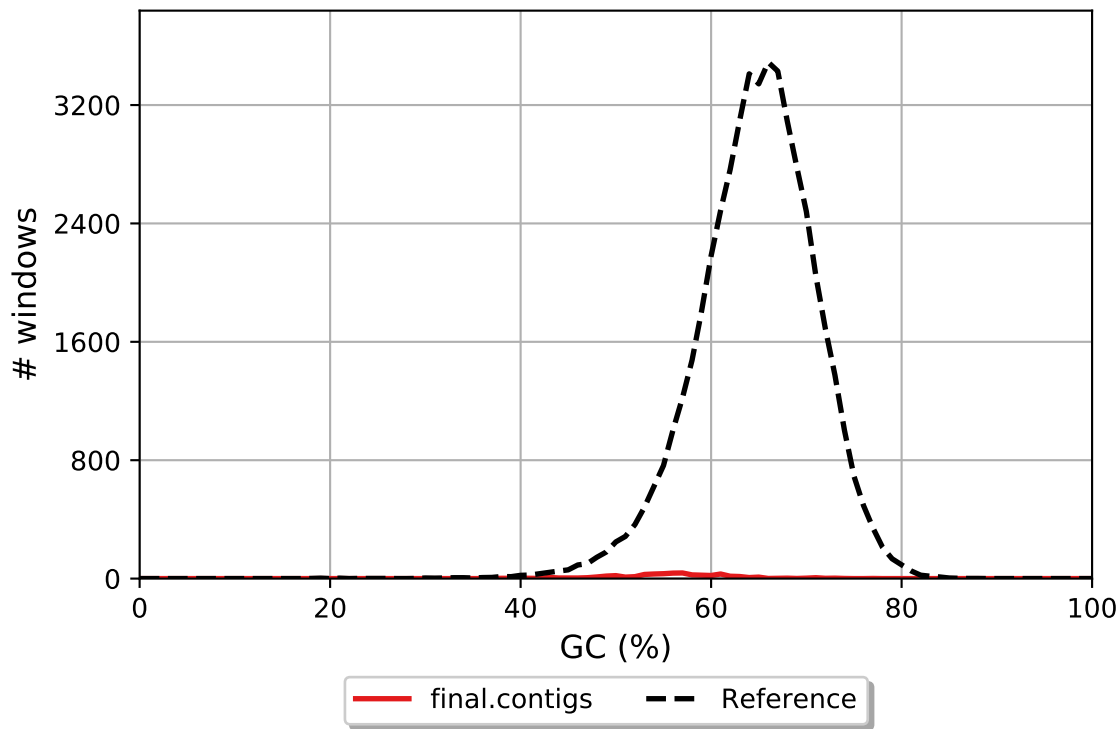
NGx



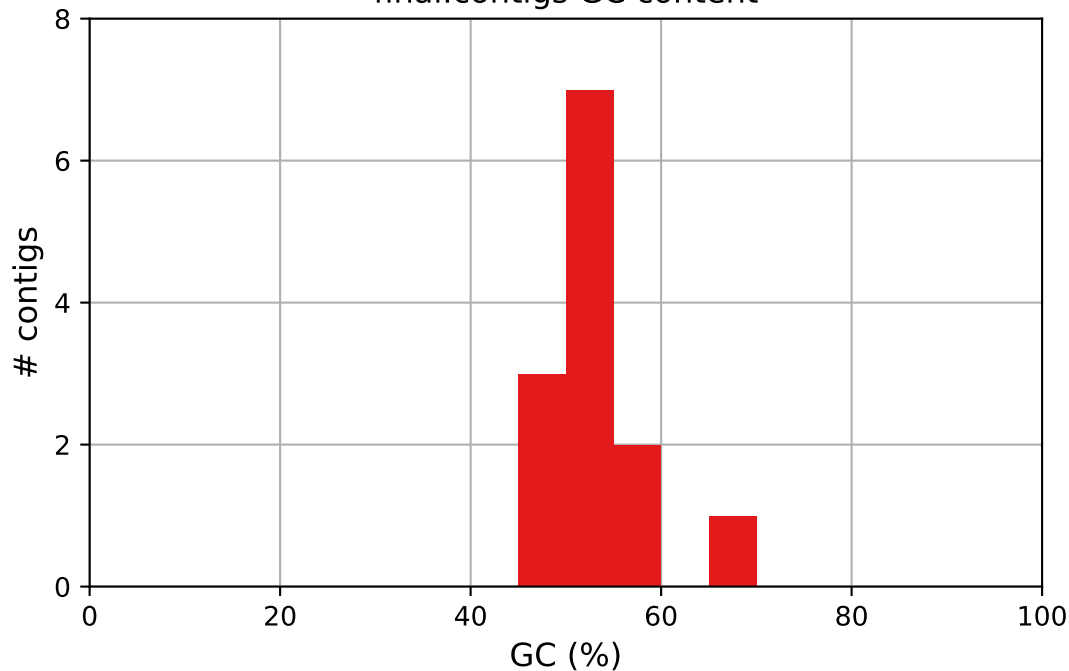
— final.contigs



GC content



final.contigs GC content



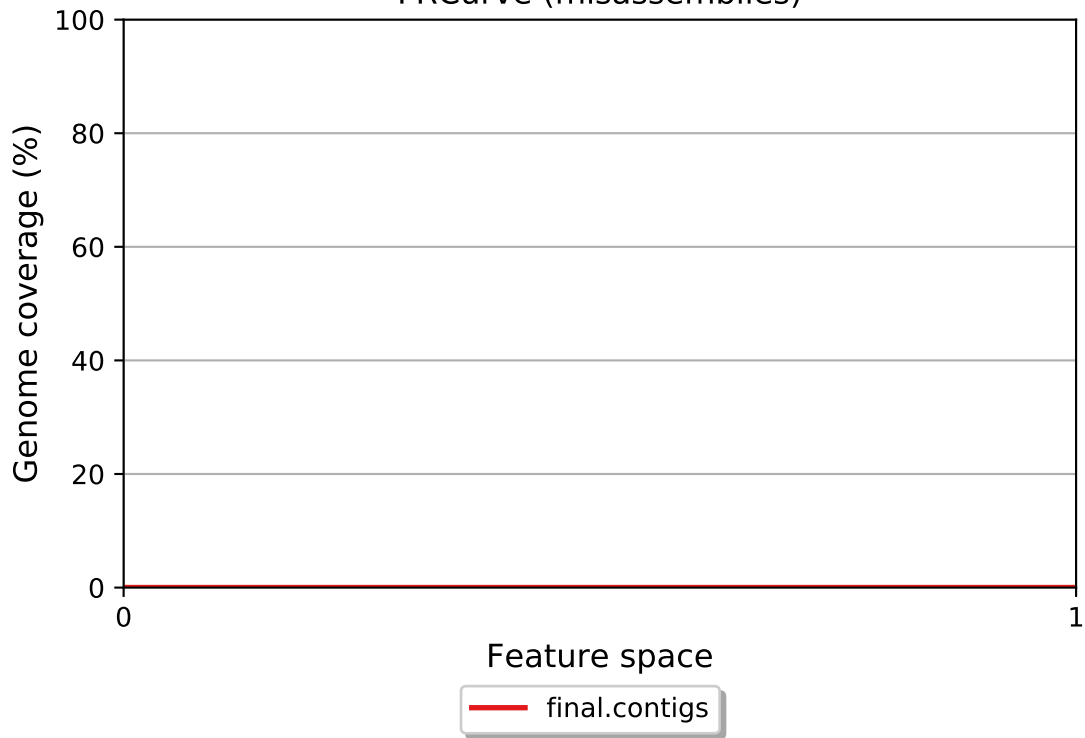
final.contigs

Misassemblies

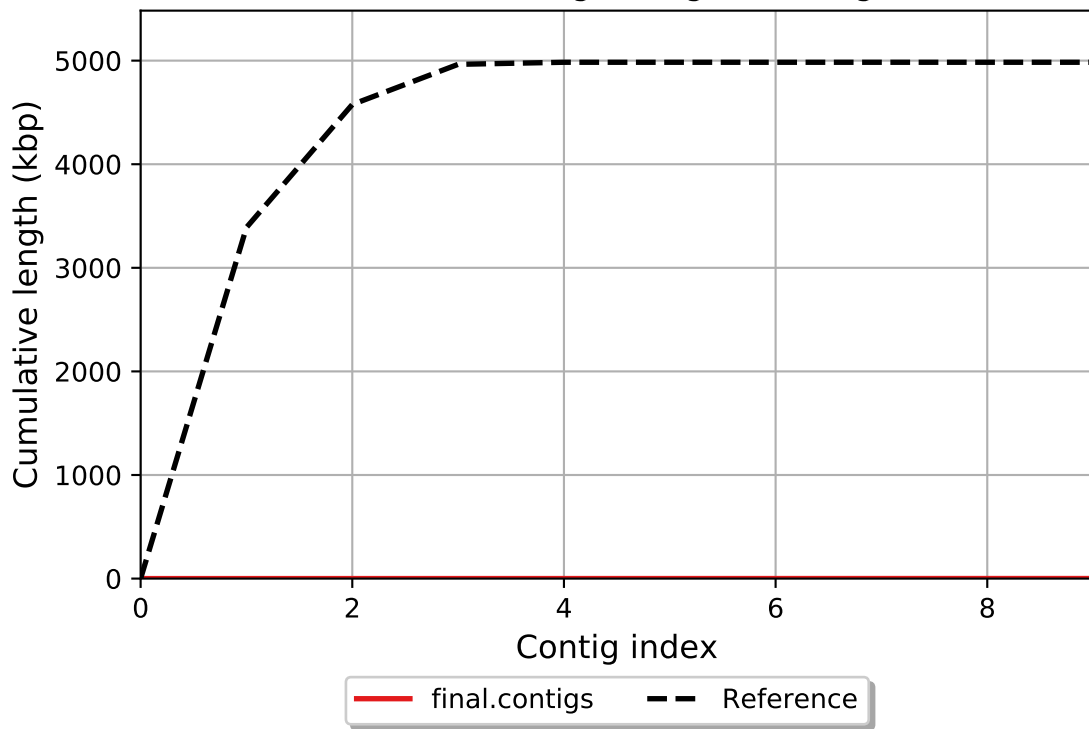


interspecies translocations

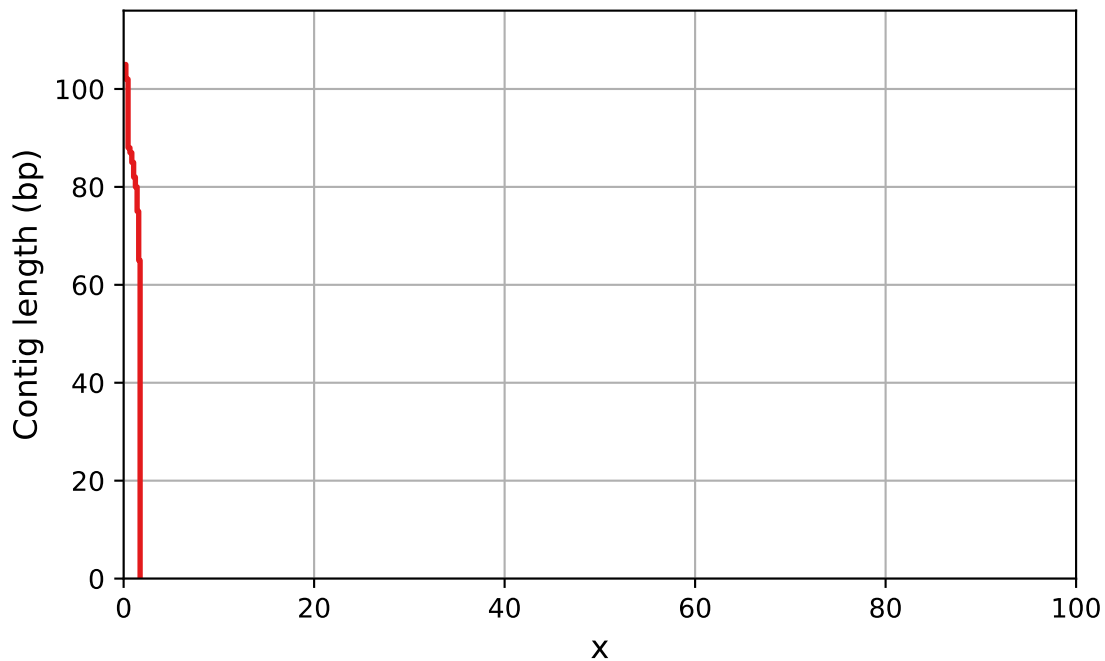
FRCurve (misassemblies)



Cumulative length (aligned contigs)

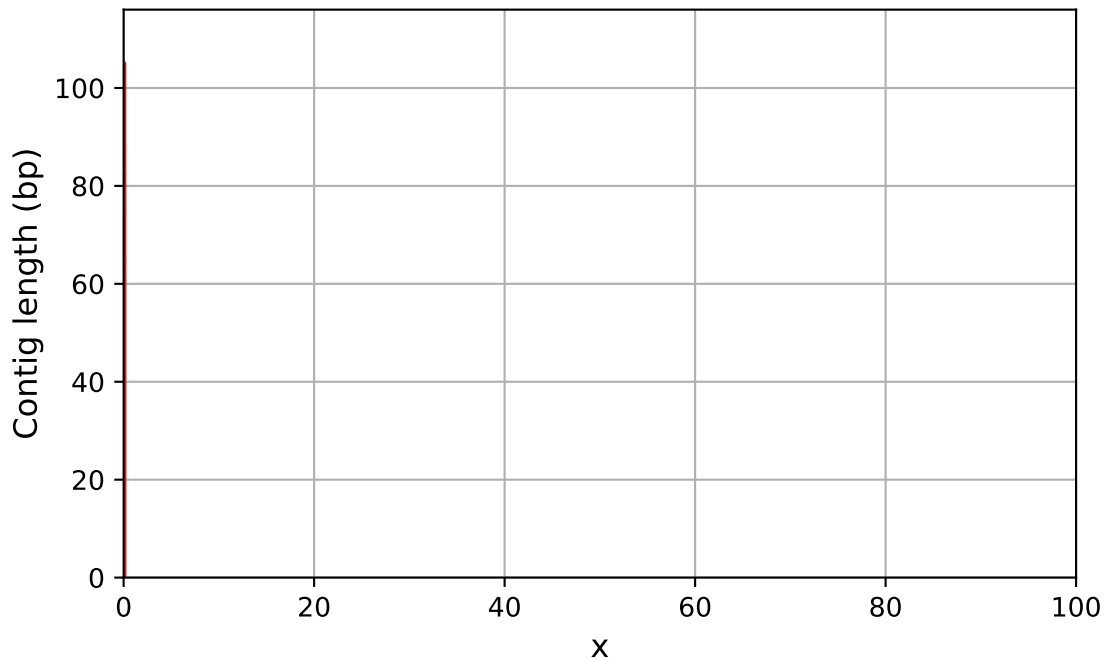


NAx



— final.contigs

NGAx



— final.contigs