

Report

	final.contigs
# contigs (>= 1000 bp)	212
# contigs (>= 5000 bp)	0
# contigs (>= 10000 bp)	0
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	294163
Total length (>= 5000 bp)	0
Total length (>= 10000 bp)	0
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	742
Largest contig	2966
Total length	671221
Reference length	5047152
GC (%)	51.80
Reference GC (%)	50.59
N50	918
NG50	-
N90	595
NG90	-
auN	1062.1
auNG	141.3
L50	256
LG50	-
L90	619
LG90	-
# misassemblies	4
# misassembled contigs	3
Misassembled contigs length	1786
# local misassemblies	3
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# unaligned contigs	1 + 70 part
Unaligned length	60981
Genome fraction (%)	10.682
Duplication ratio	1.012
# N's per 100 kbp	0.00
# mismatches per 100 kbp	7298.89
# indels per 100 kbp	182.58
Largest alignment	2964
Total aligned length	545521
NA50	726
NGA50	-
NA90	-
NGA90	-
auNA	771.2
auNGA	102.6
LA50	310
LGA50	-
LA90	-
LGA90	-

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

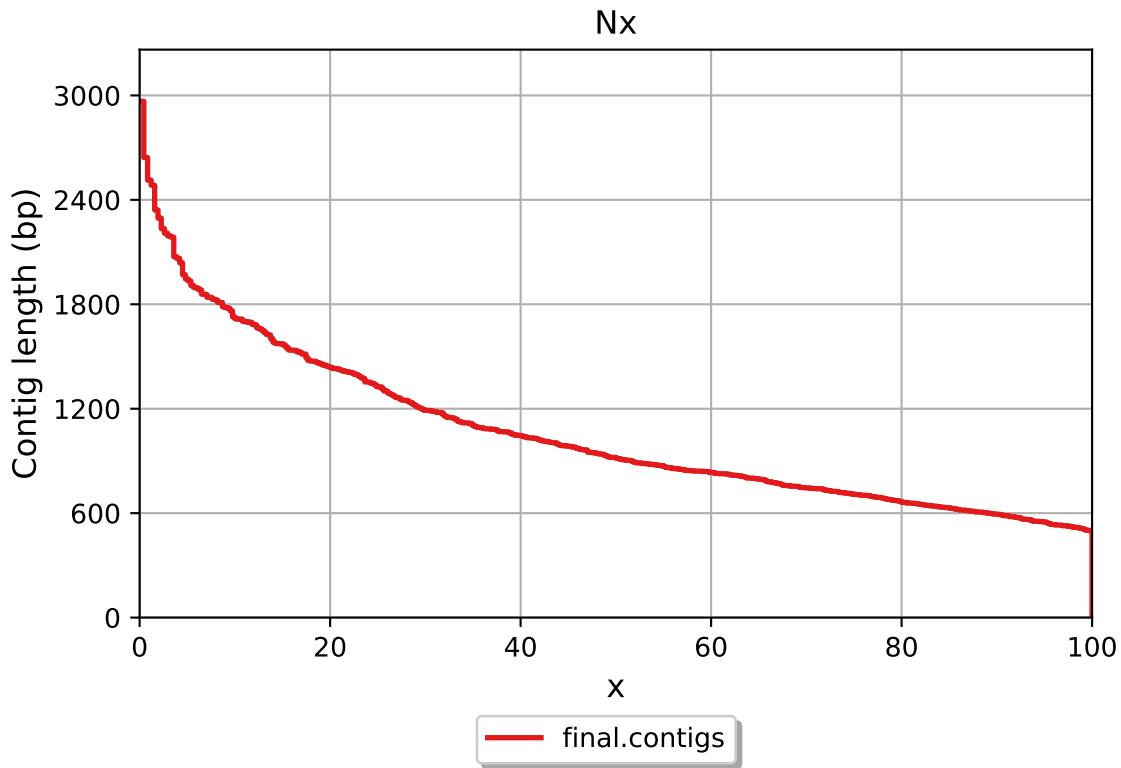
	final.contigs
# misassemblies	4
# contig misassemblies	4
# c. relocations	4
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	3
Misassembled contigs length	1786
# possibly misassembled contigs	47
# possible misassemblies	47
# local misassemblies	3
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	3
# mismatches	39817
# indels	996
# indels (<= 5 bp)	939
# indels (> 5 bp)	57
Indels length	2762

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).

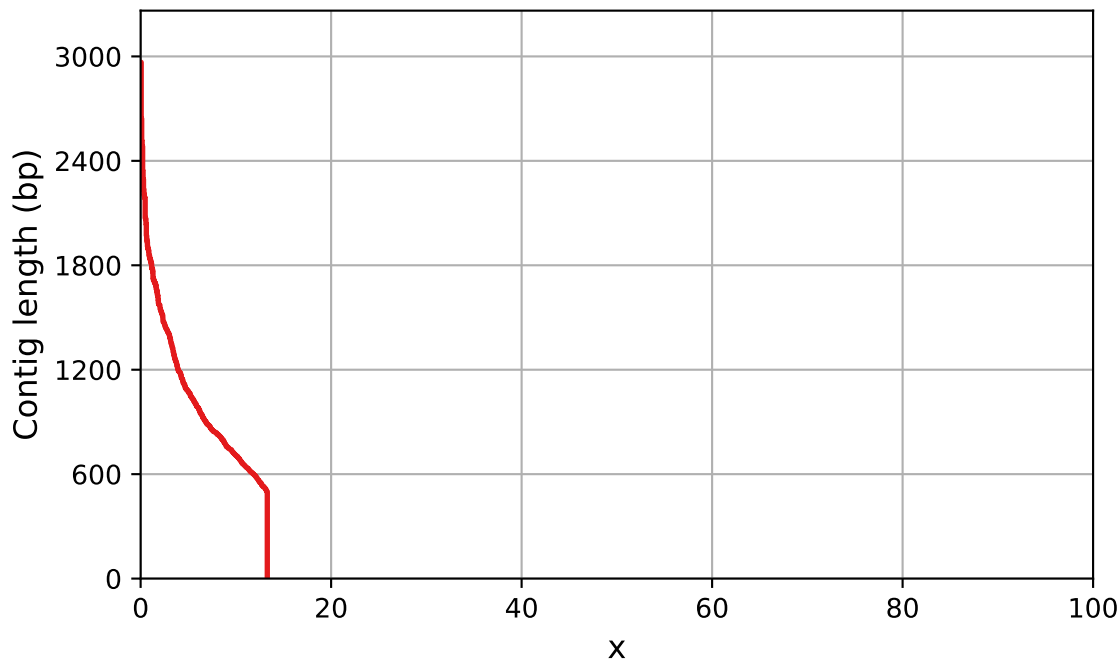
Unaligned report

	final.contigs
# fully unaligned contigs	1
Fully unaligned length	2208
# partially unaligned contigs	70
Partially unaligned length	58773
# 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).

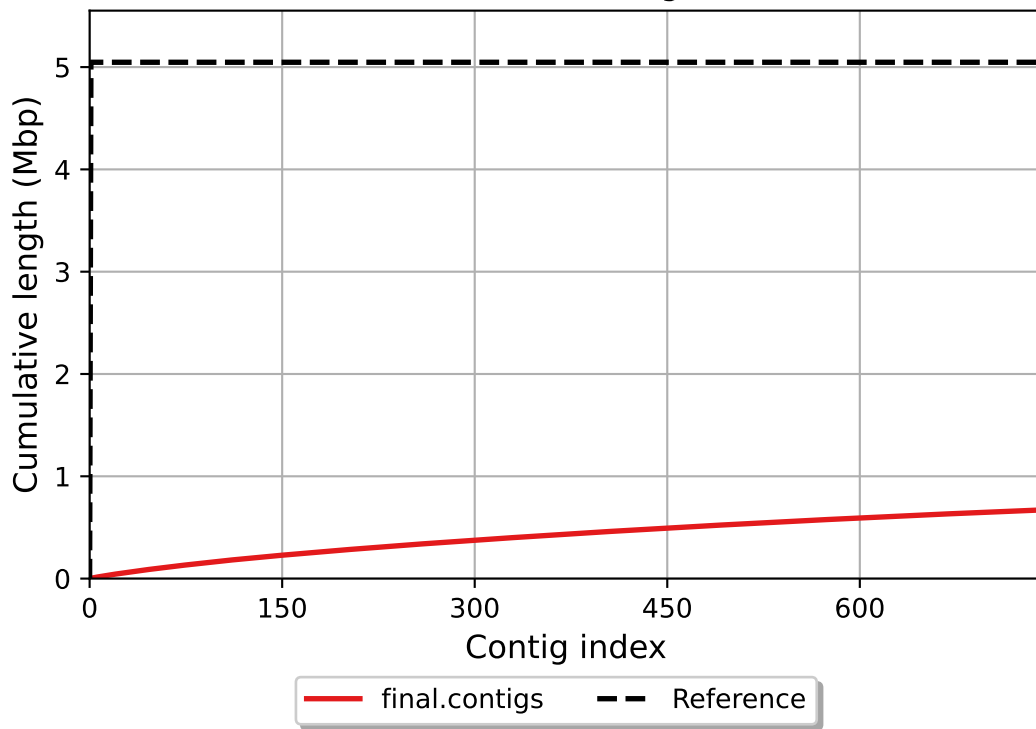


NGx

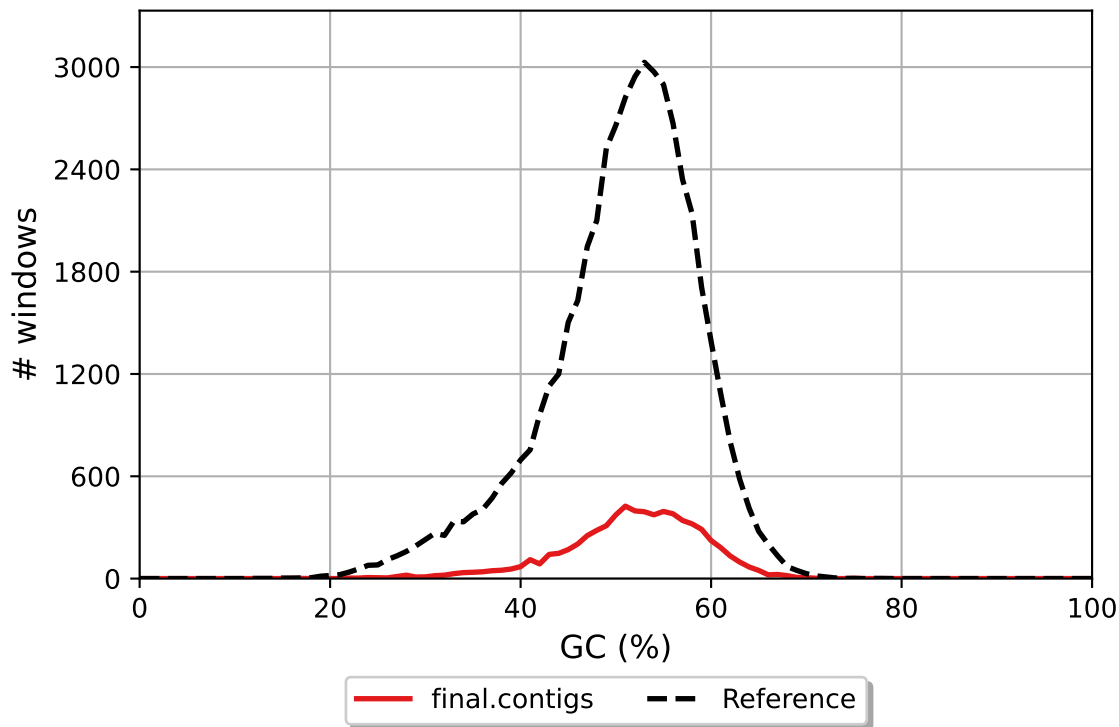


— final.contigs

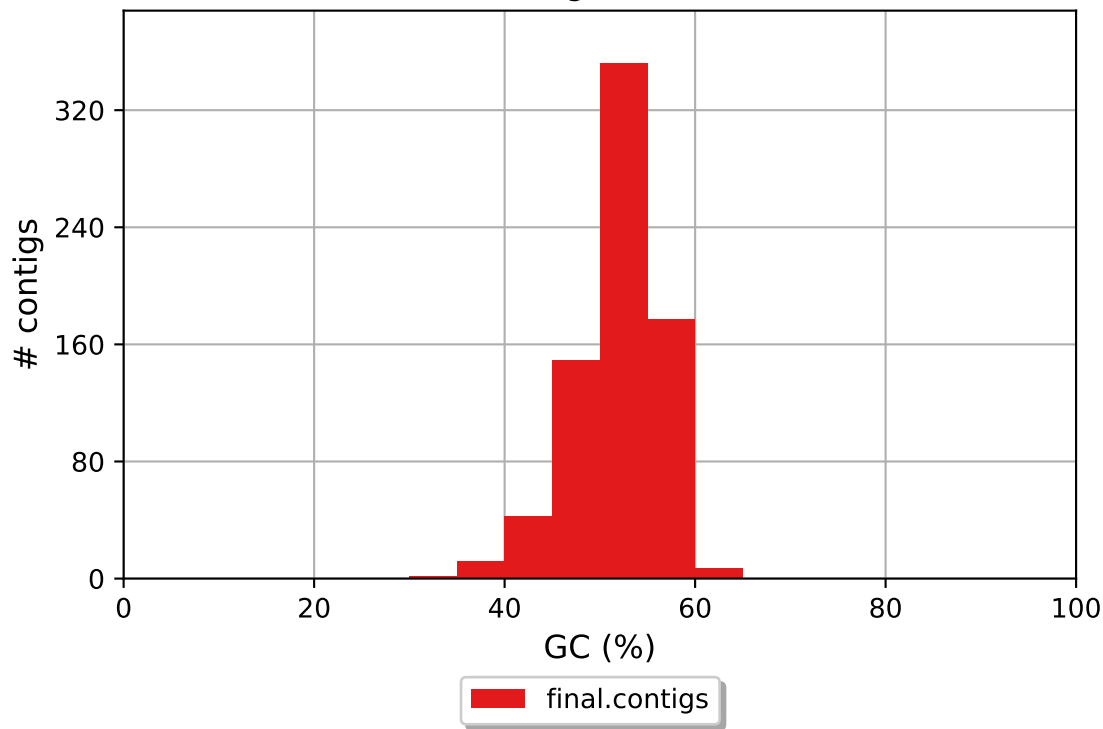
Cumulative length



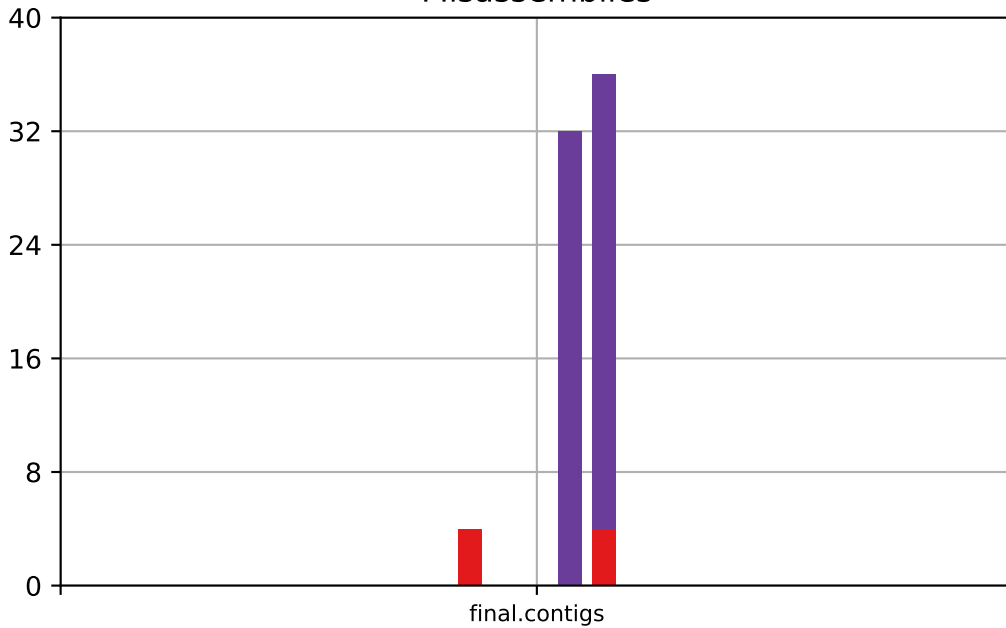
GC content



final.contigs GC content



Misassemblies



relocations

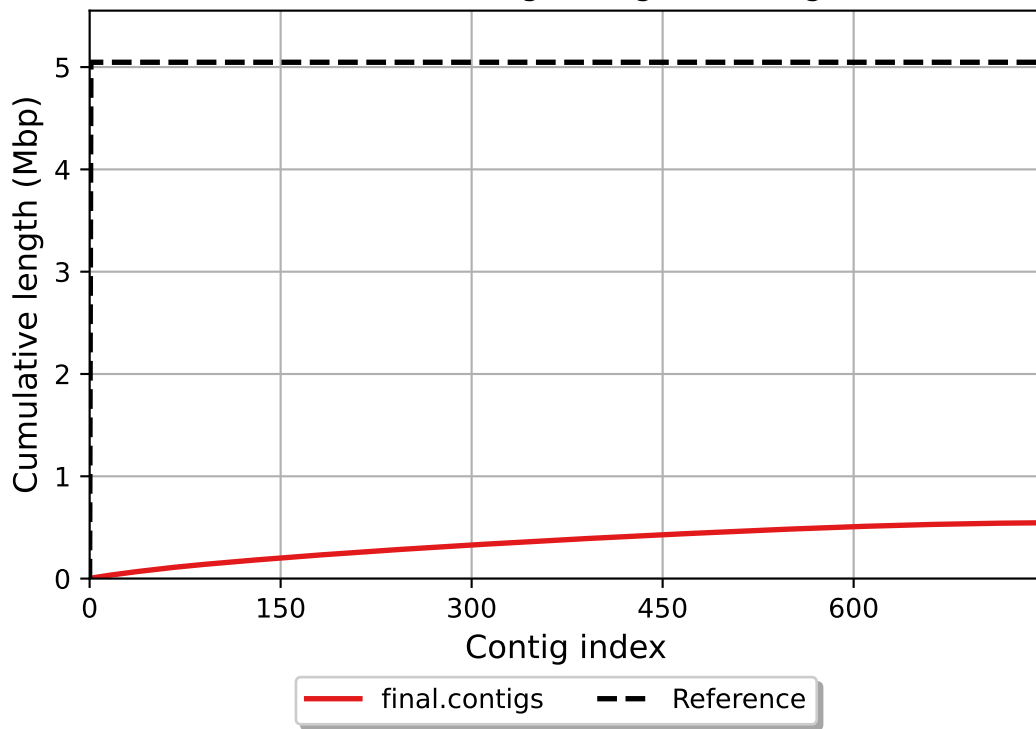


interspecies translocations

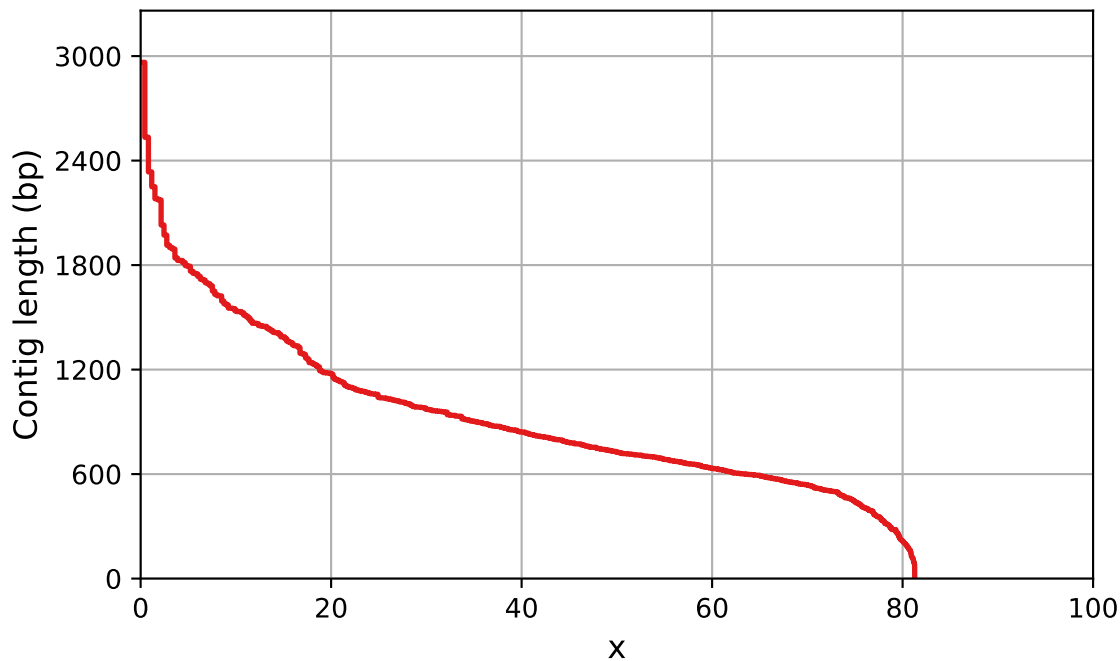
FRCurve (misassemblies)



Cumulative length (aligned contigs)

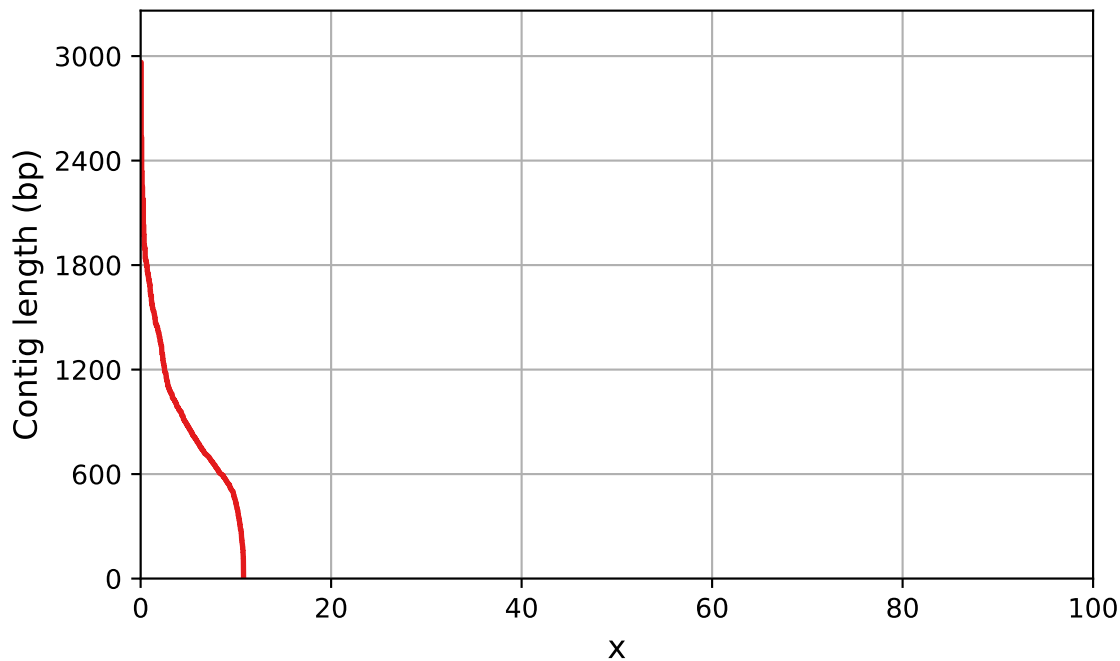


NAx



— final.contigs

NGAx



— final.contigs