

## Report

	final.contigs
# contigs (>= 1000 bp)	5
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	47390
Total length (>= 5000 bp)	39648
Total length (>= 10000 bp)	39648
Total length (>= 25000 bp)	39648
Total length (>= 50000 bp)	0
# contigs	8
Largest contig	39648
Total length	49111
Reference length	2789967
GC (%)	48.77
Reference GC (%)	60.77
N50	39648
N75	39648
L50	1
L75	1
# 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	2 + 4 part
Unaligned length	47687
Genome fraction (%)	0.015
Duplication ratio	3.382
# N's per 100 kbp	0.00
# mismatches per 100 kbp	2850.36
# indels per 100 kbp	0.00
Largest alignment	113
Total aligned length	469
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	12
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

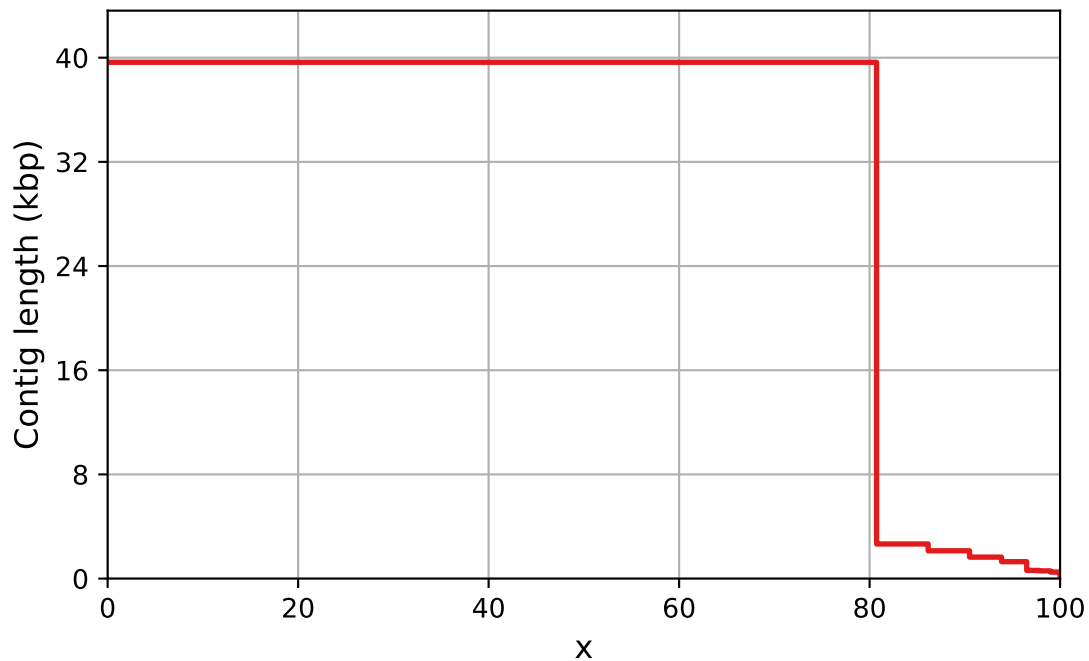
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	final.contigs
# fully unaligned contigs	2
Fully unaligned length	3958
# partially unaligned contigs	4
Partially unaligned length	43729
# N's	0

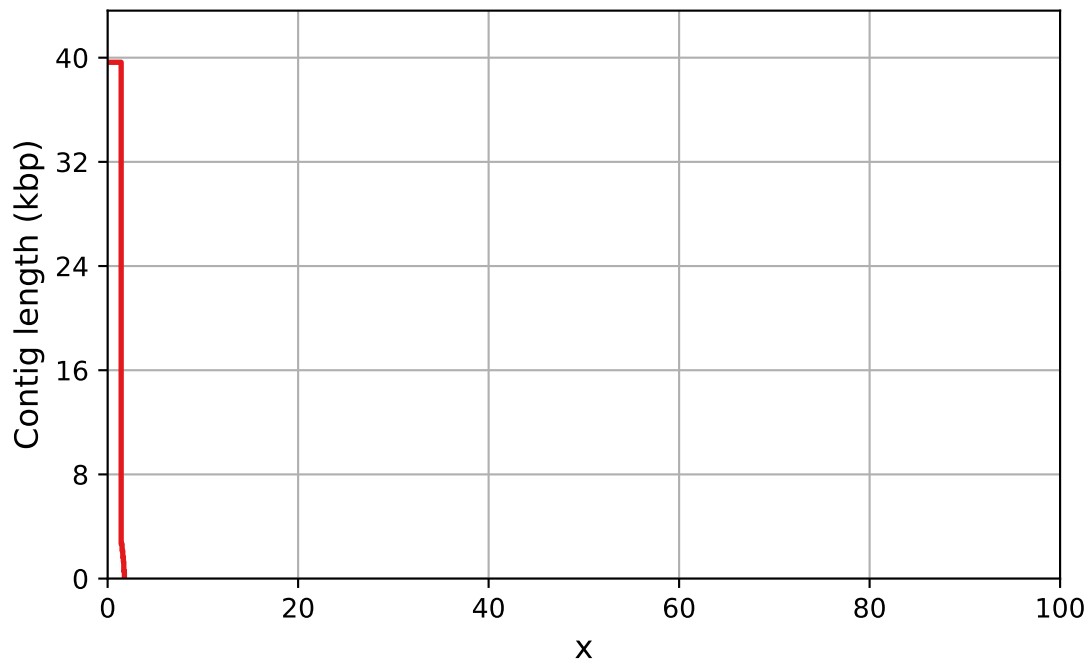
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

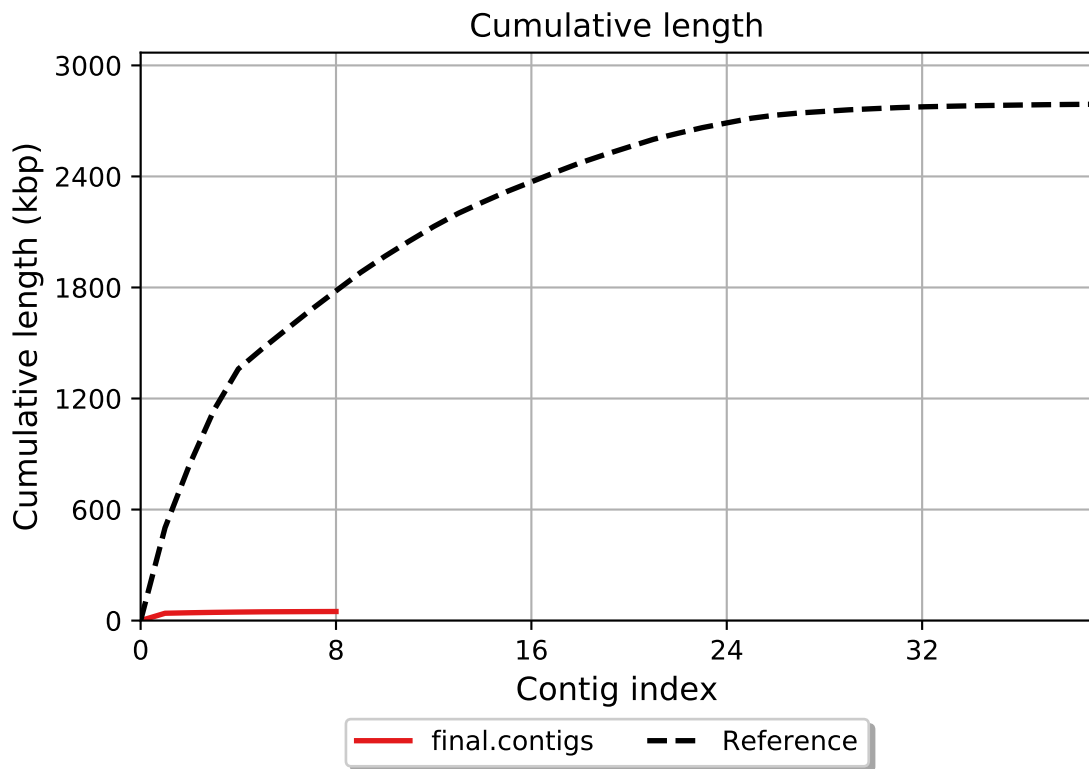


— final.contigs

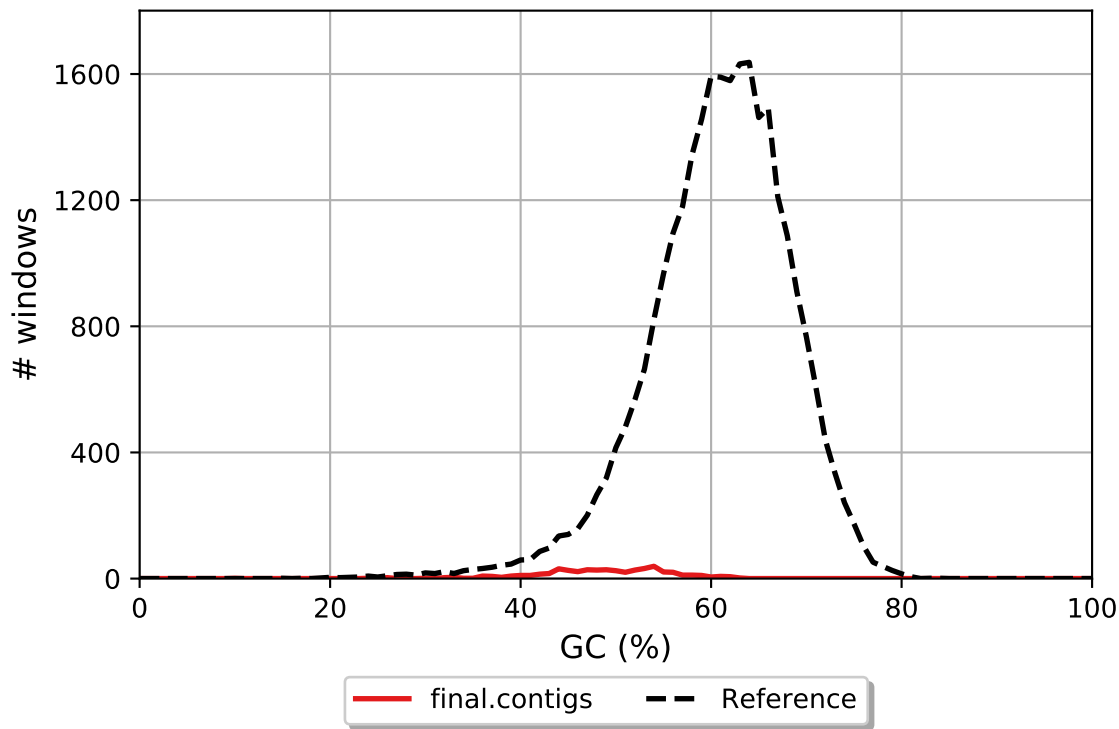
NGx



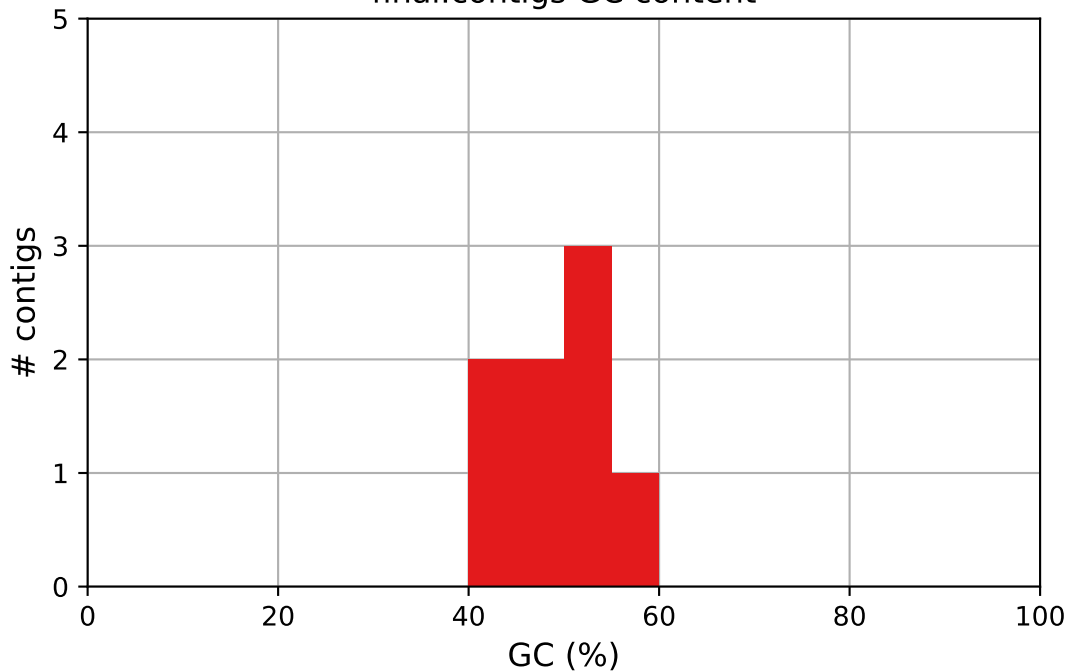
— final.contigs



# GC content



final.contigs GC content



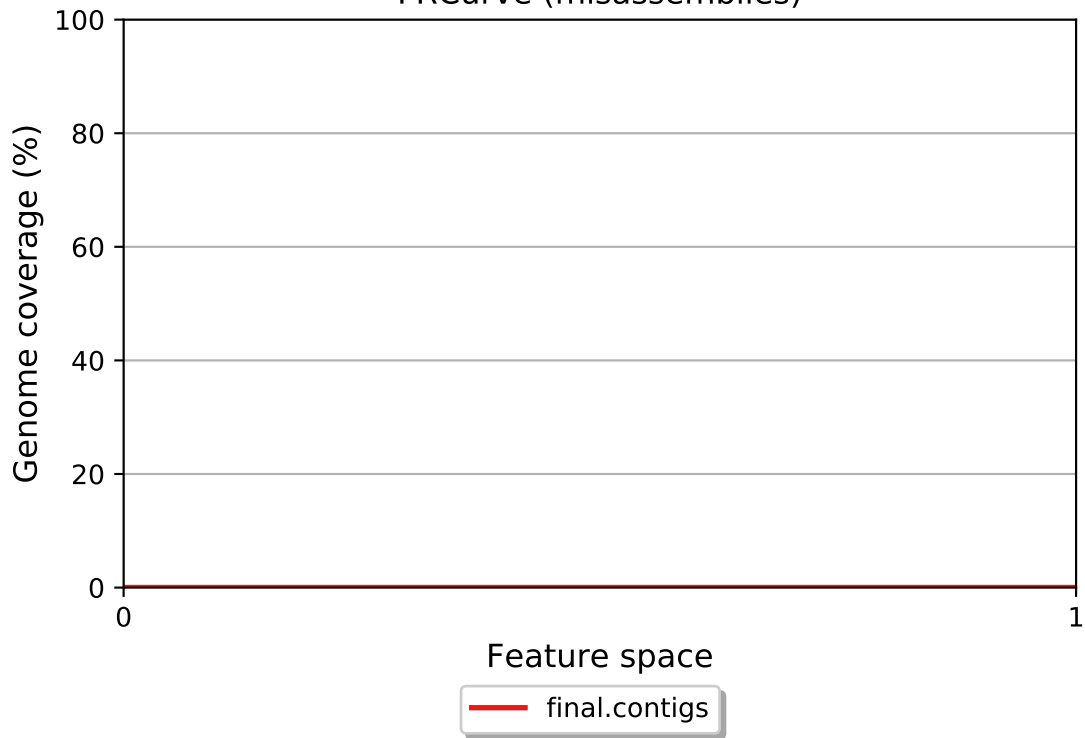
final.contigs



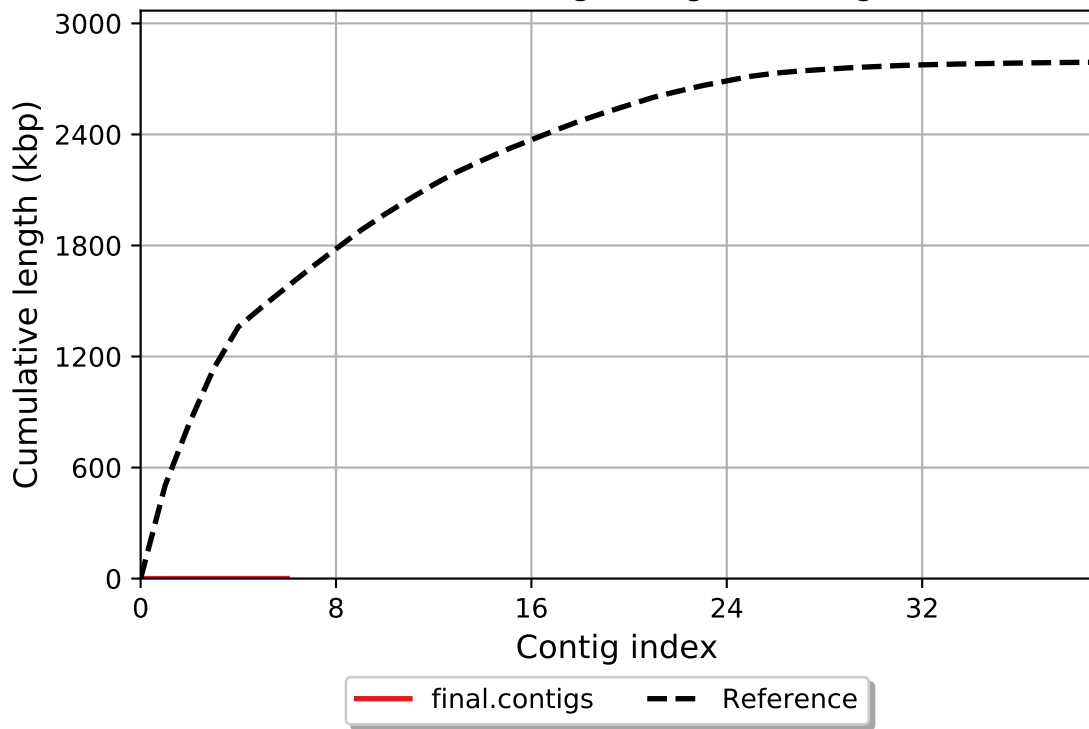
## Misassemblies

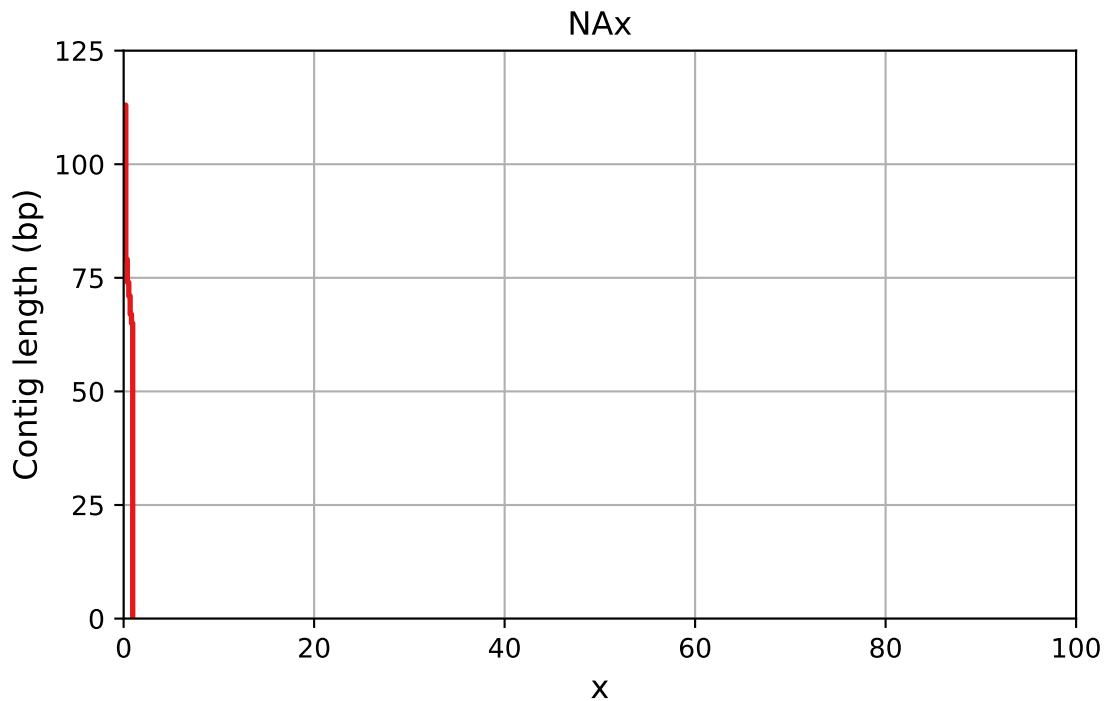


FRCurve (misassemblies)



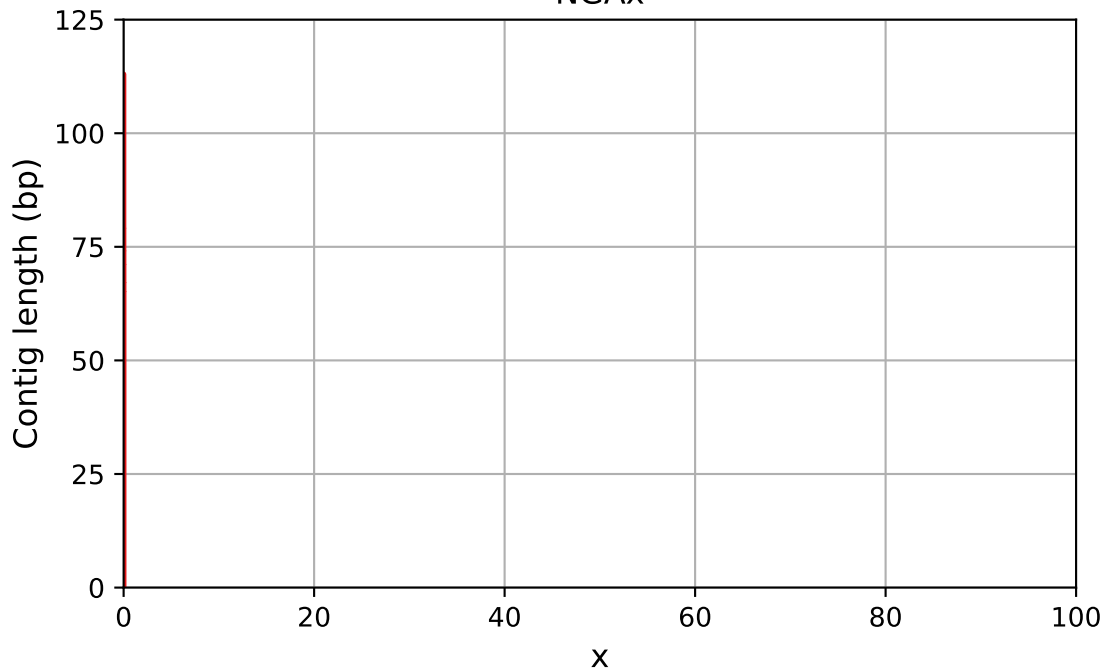
Cumulative length (aligned contigs)





— final.contigs

# NGAx



— final.contigs