Report

	combined.final.contigs
# contigs (>= 1000 bp)	4
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	0
# contigs (>= 50000 bp)	0
Total length (>= 1000 bp)	32212
Total length (>= 5000 bp)	29461
Total length (>= 10000 bp)	29461
Total length (>= 25000 bp)	0
Total length (>= 50000 bp)	0
# contigs	10
Largest contig	16895
Total length	36895
Reference length	3633537
GC (%)	33.27
Reference GC (%)	32.71
N50	12566
N75	12566
L50	2
L75	2
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 7 part
Unaligned length	33929
Genome fraction (%)	0.043
Duplication ratio	1.903
# N's per 100 kbp	0.00
# mismatches per 100 kbp	3014.75
# indels per 100 kbp	128.29
Largest alignment	654
Total aligned length	1881
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

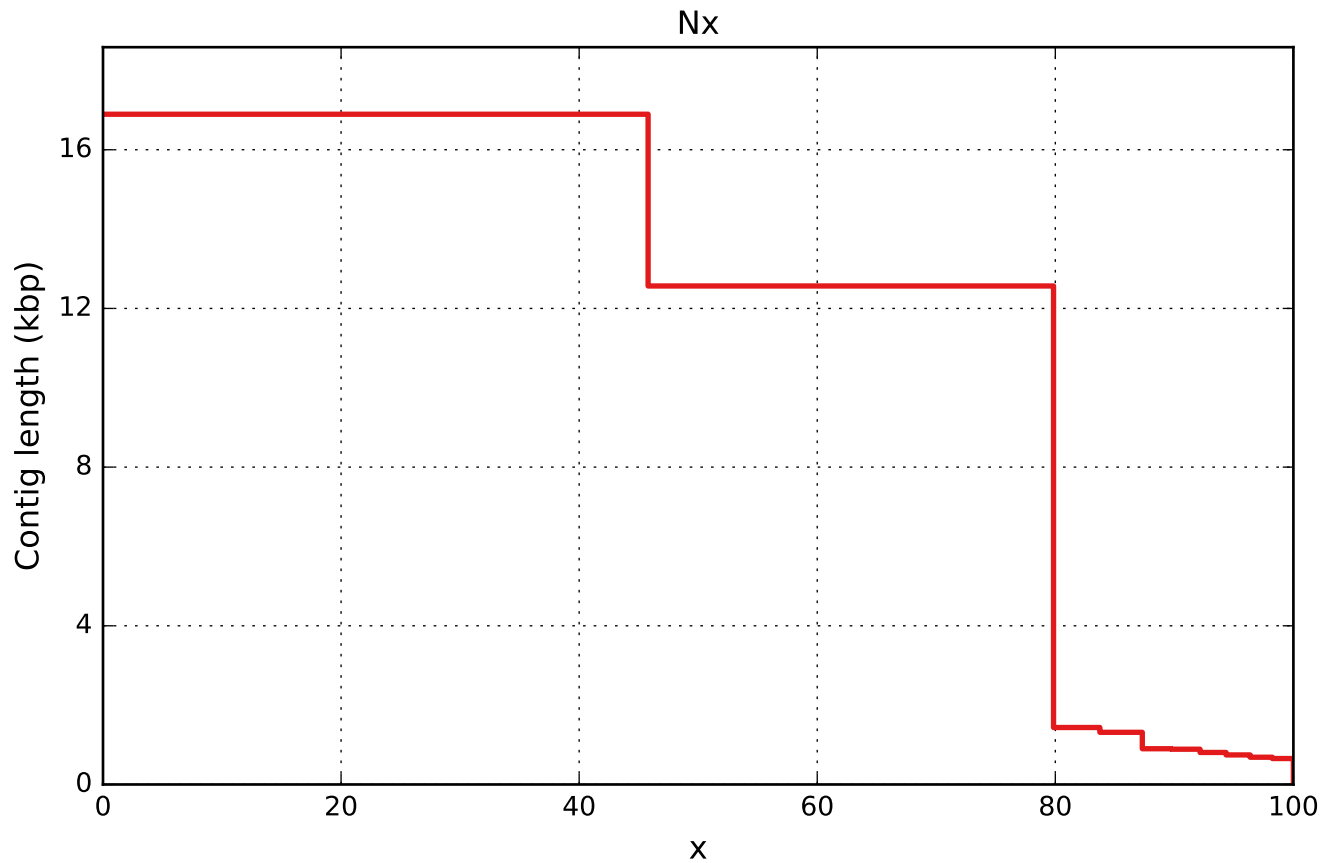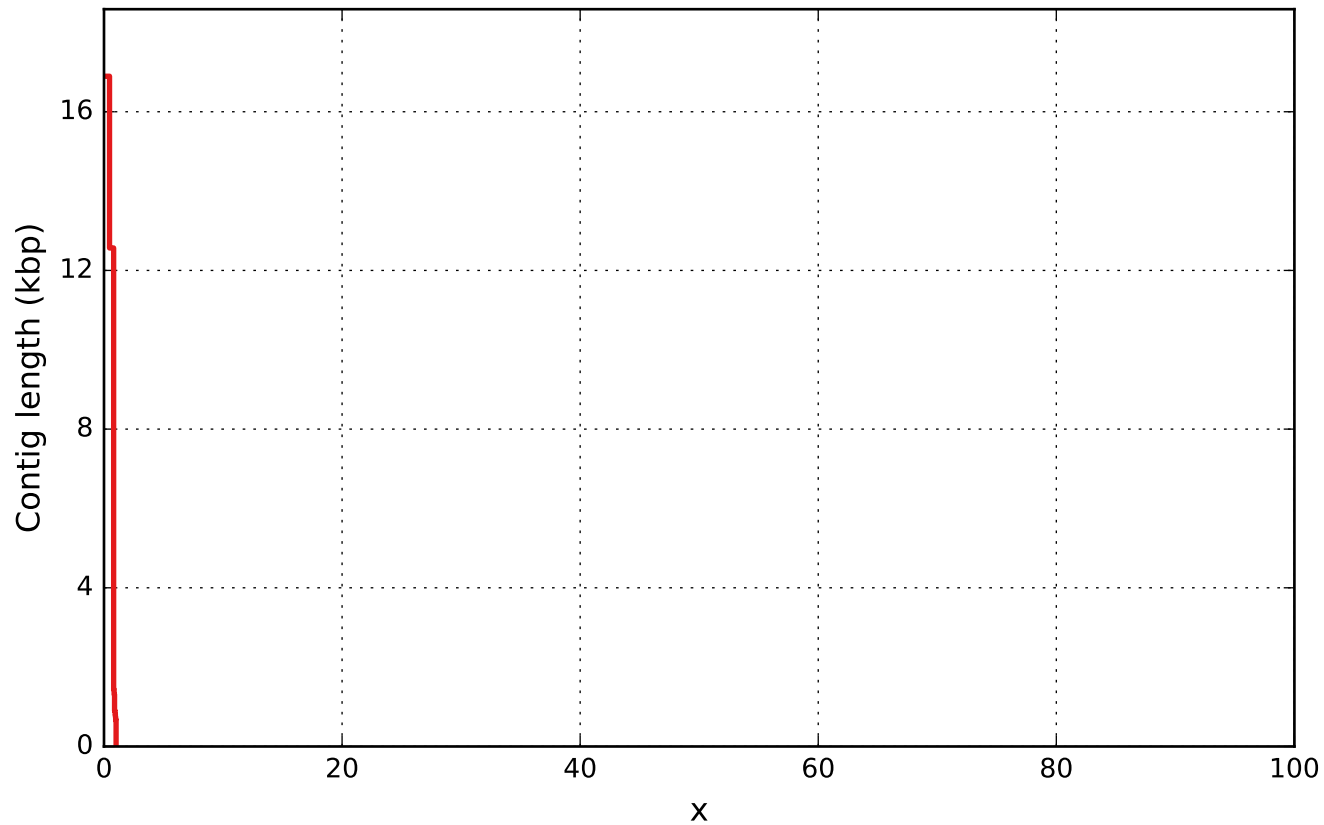|	combined.final.contigs
# misassemblies	0
# relocations	0
# translocations	0
# inversions	0
# interspecies translocations	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	0
# unaligned mis. contigs	0
# mismatches	47
# 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
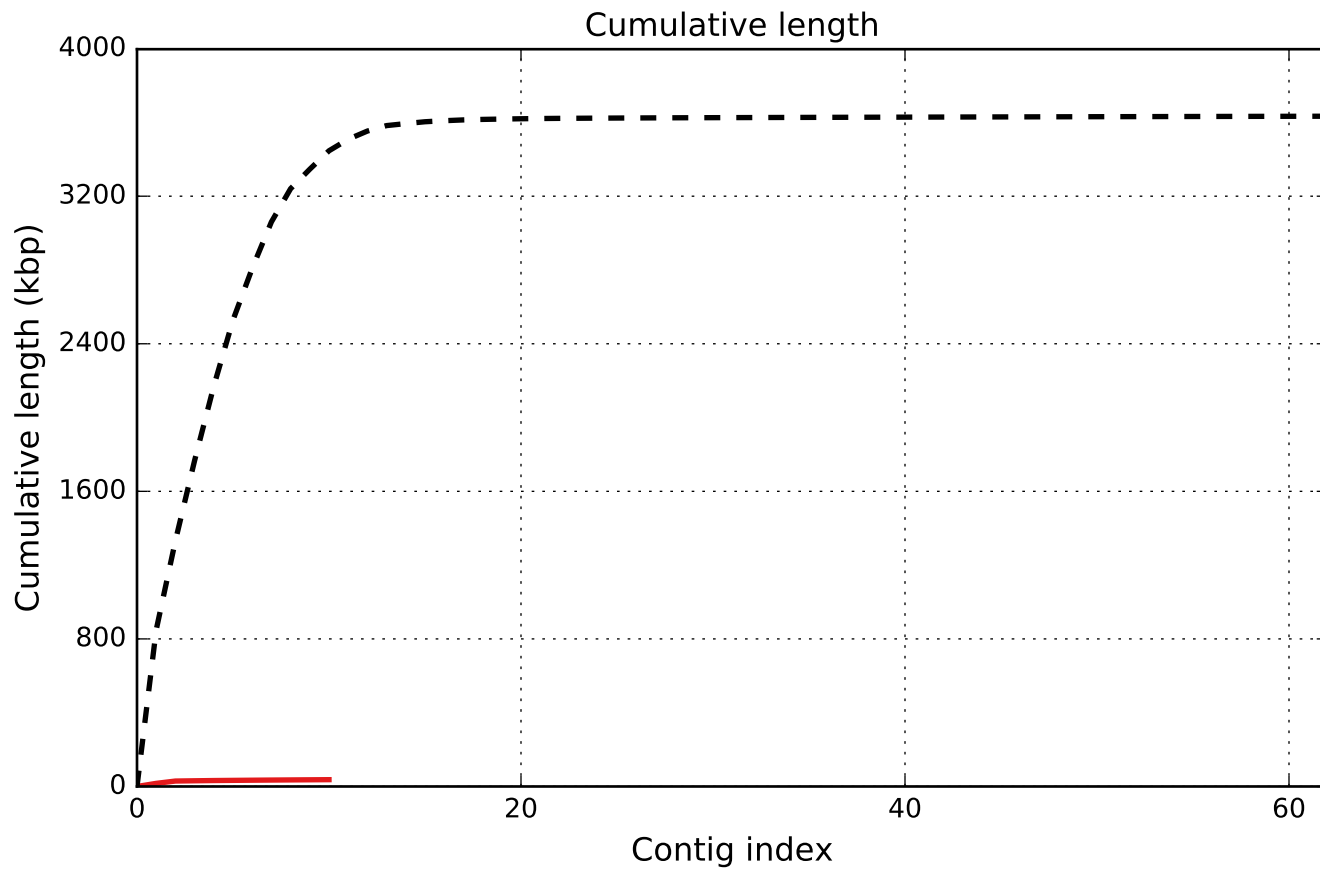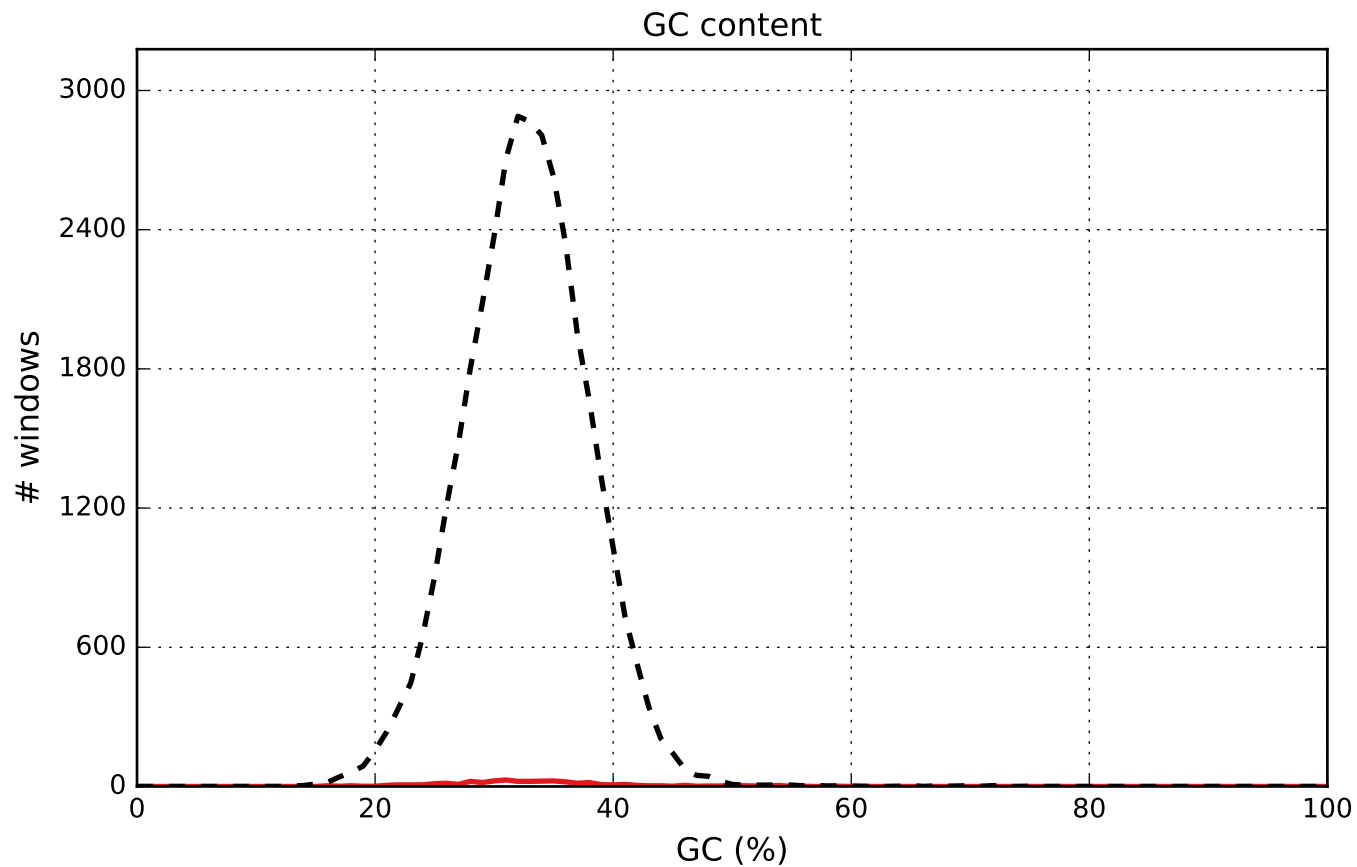
	combined.final.contigs
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	7
Partially unaligned length	33929
# N's	0

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

4000

3200

2400

1600

800

0

Cumulative length (kbp)

0   20   40   60

Contig index

───── combined.final.contigs   ─ ─ ─ Reference
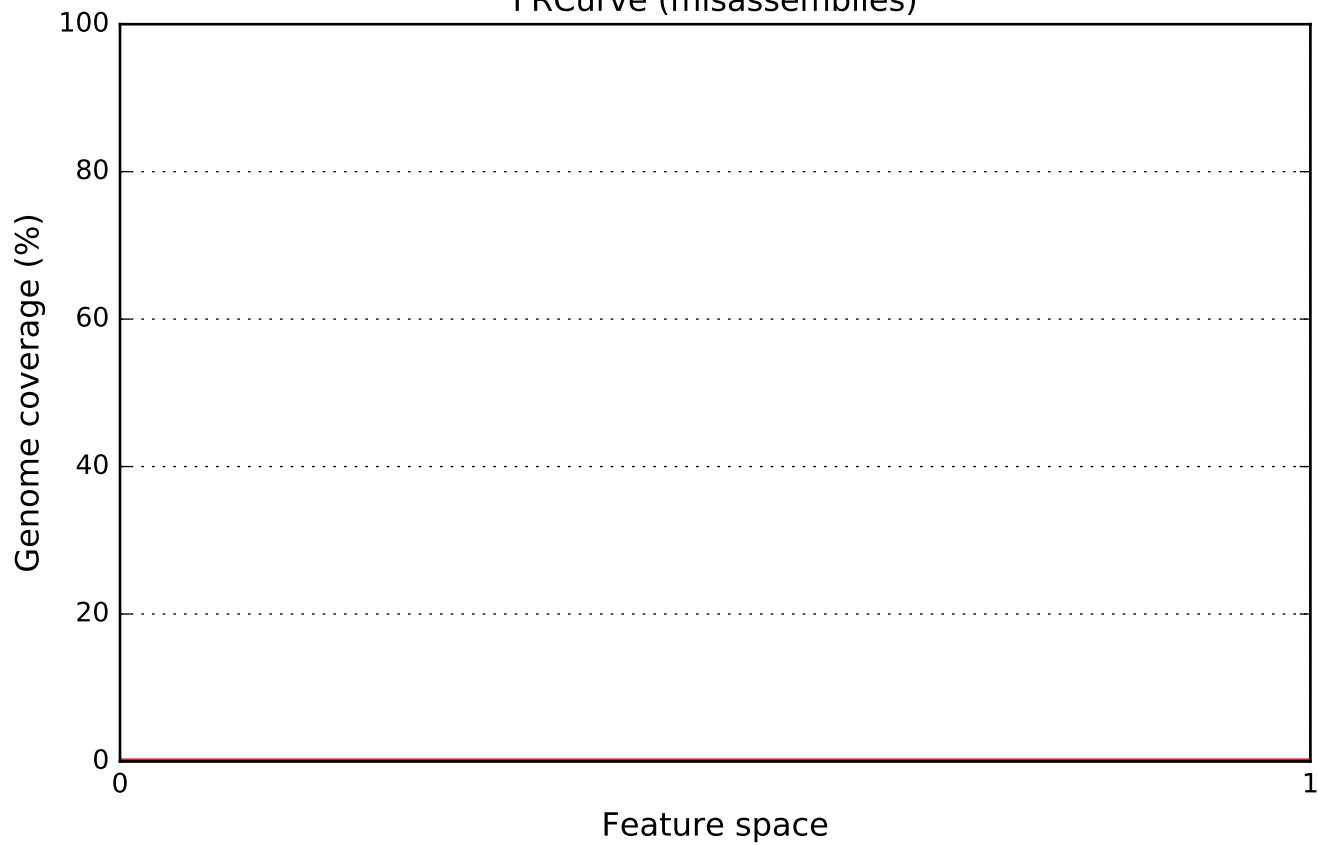
GC content

combined.final.contigs GC content
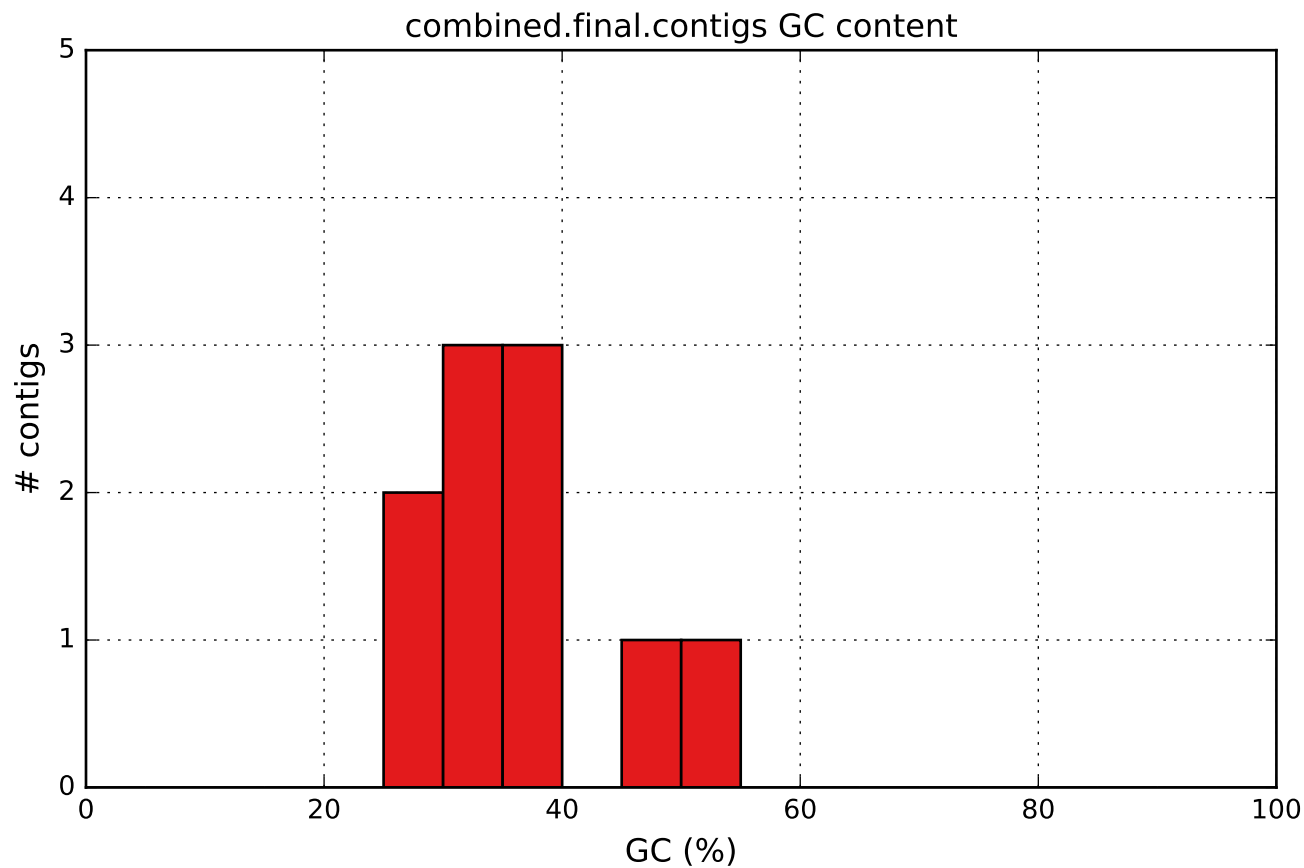
Misassemblies

combined.final.contigs
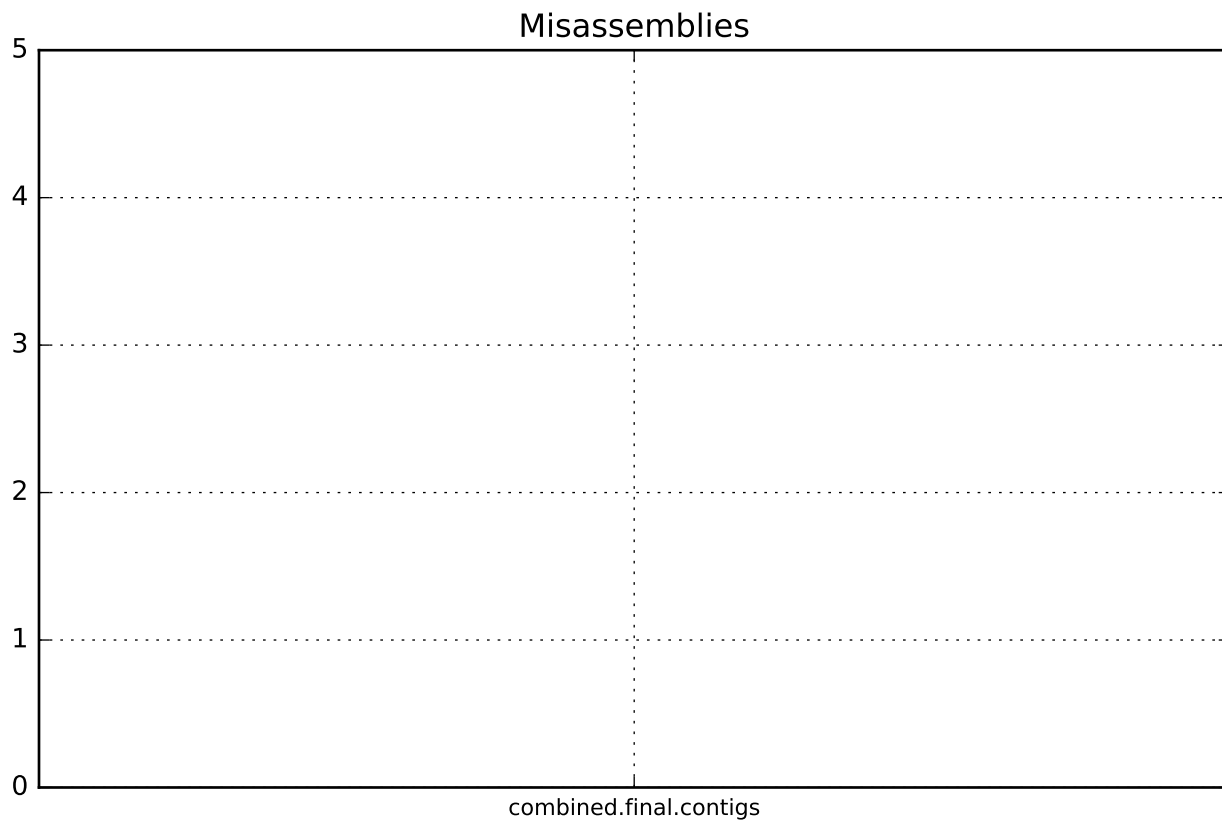
FRCurve (misassemblies)

Cumulative length (aligned contigs)
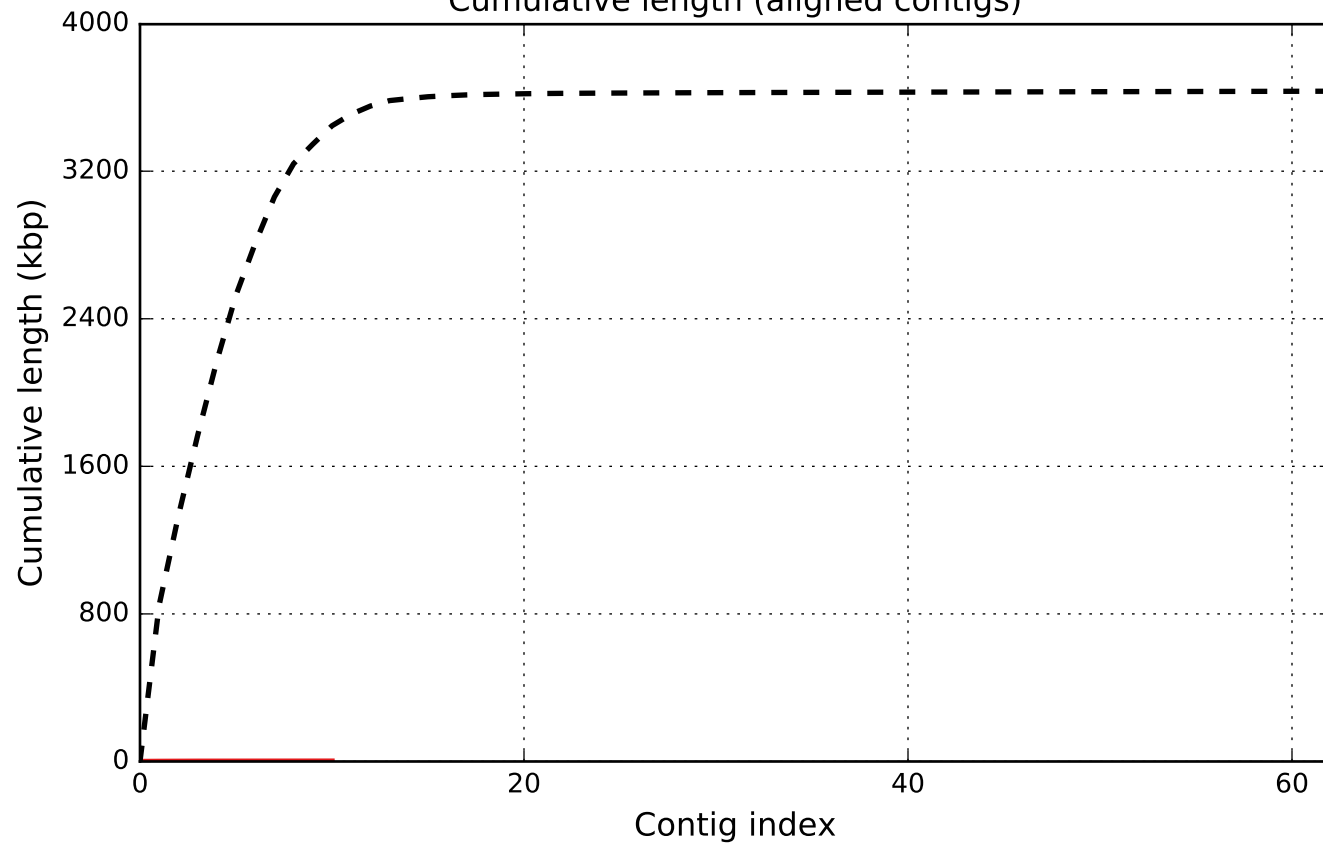
Legend: combined.final.contigs —— Reference - - -

NAx

Contig length (bp)

x
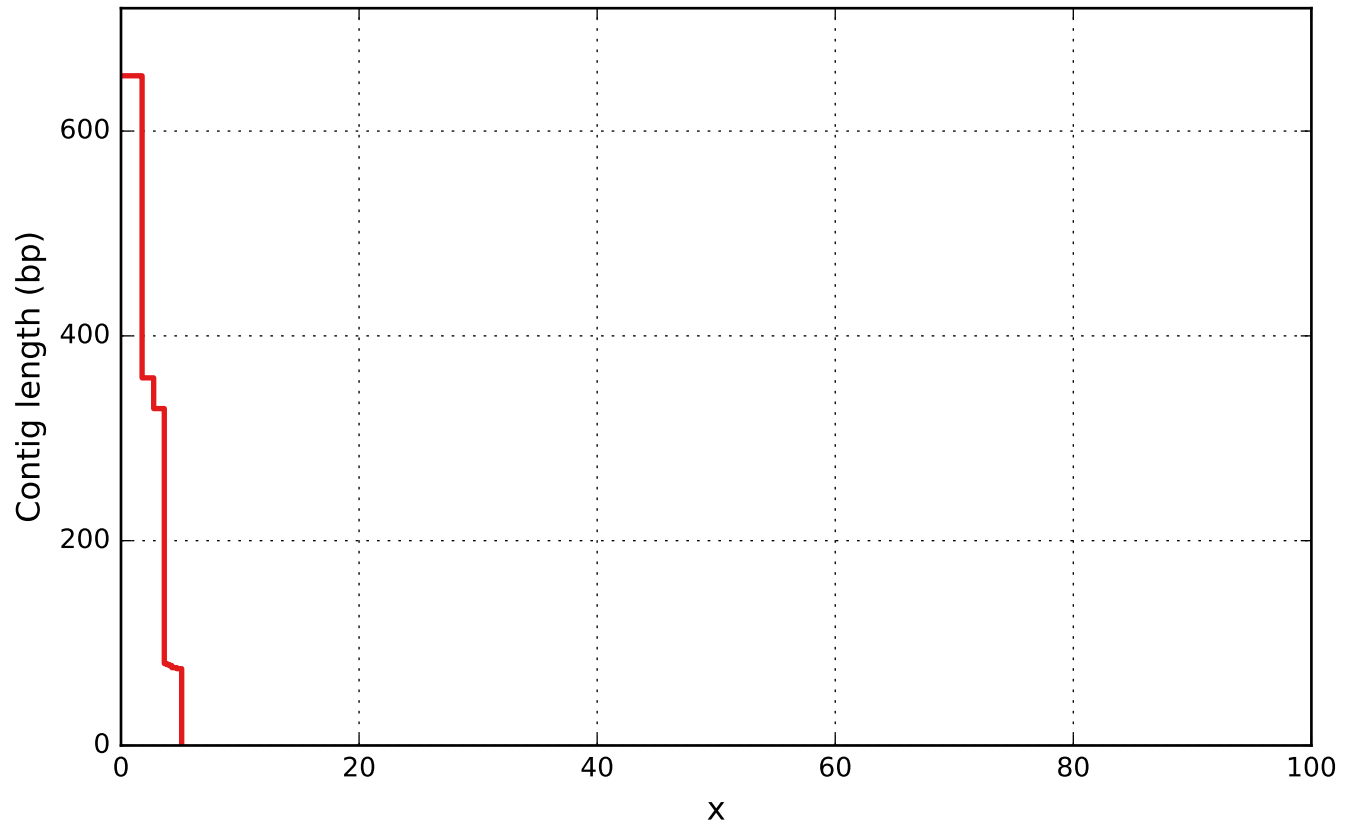
combined.final.contigs

NGAx

Contig length (bp)

x

combined.final.contigs