

Report

	mito.contigs.final
# contigs (>= 0 bp)	1
# contigs (>= 1000 bp)	1
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	1
Total length (>= 0 bp)	214261
Total length (>= 1000 bp)	214261
Total length (>= 5000 bp)	214261
Total length (>= 10000 bp)	214261
Total length (>= 25000 bp)	214261
Total length (>= 50000 bp)	214261
# contigs	1
Largest contig	214261
Total length	214261
Reference length	214261
GC (%)	30.77
Reference GC (%)	30.77
N50	214261
NG50	214261
N75	214261
NG75	214261
L50	1
LG50	1
L75	1
LG75	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	0 + 0 part
Unaligned length	0
Genome fraction (%)	100.000
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	214261
Total aligned length	214261
NA50	214261
NGA50	214261
NA75	214261
NGA75	214261
LA50	1
LGA50	1
LA75	1
LGA75	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).

Misassemblies report

	mito.contigs.final
# 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
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	0
# indels	0
# indels (≤ 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

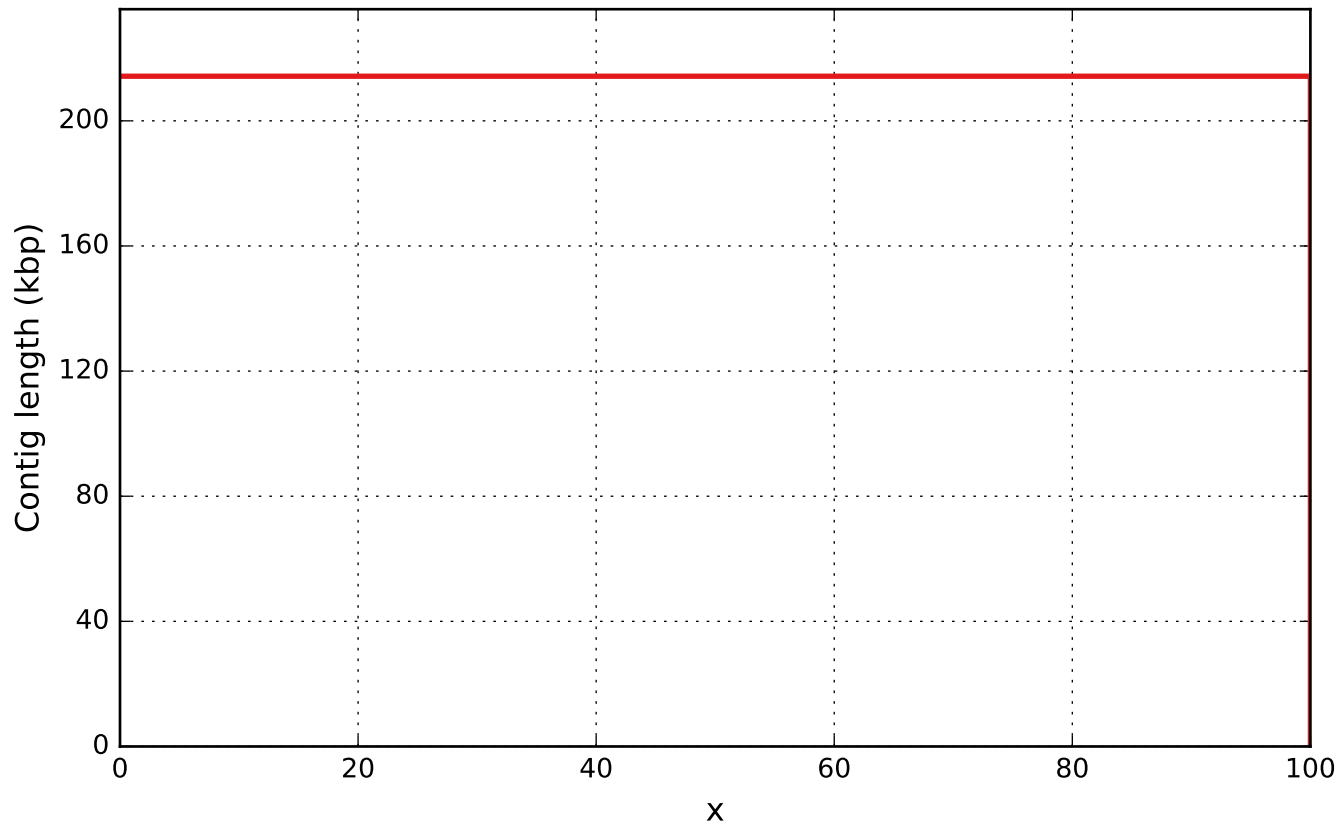
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	mito.contigs.final
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

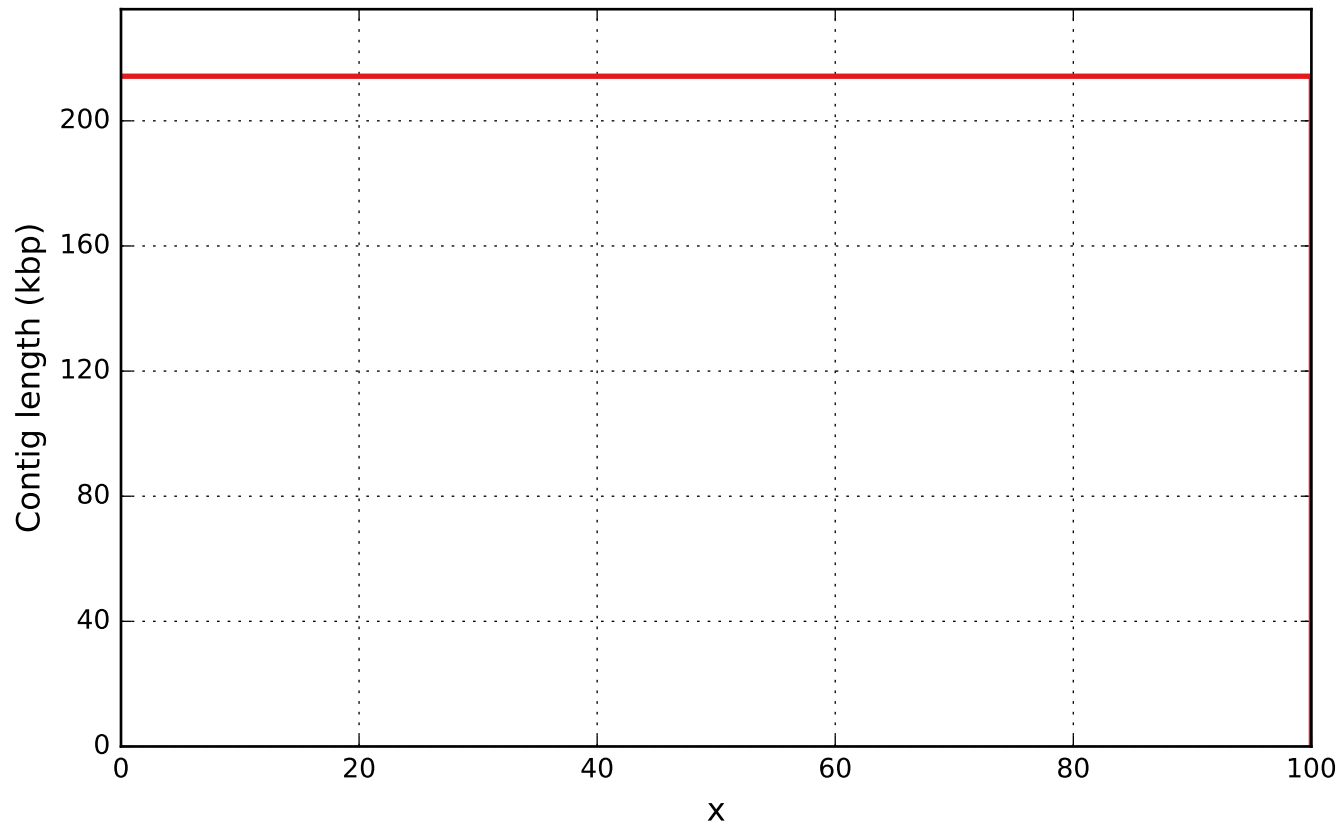
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



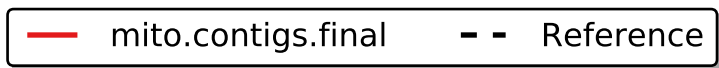
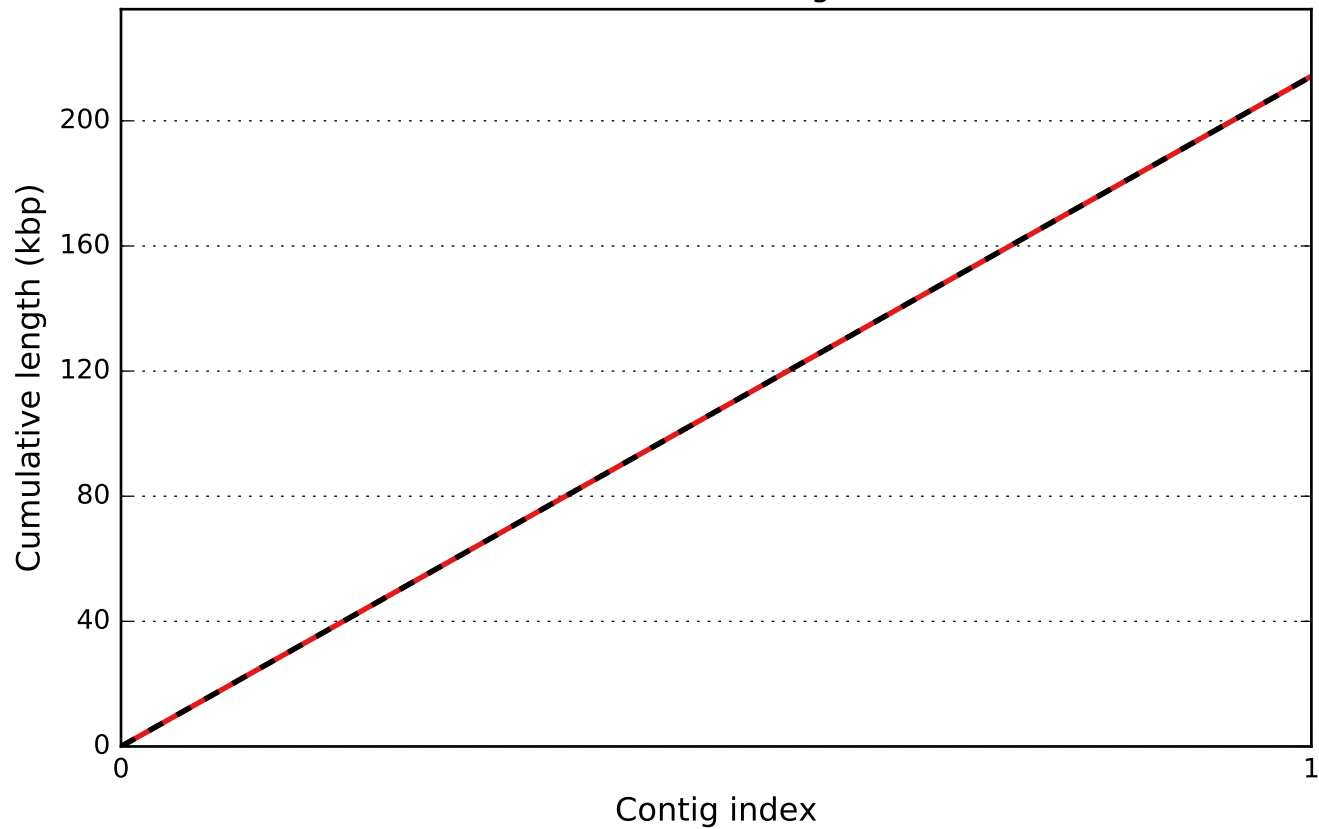
— mito.contigs.final

NGx

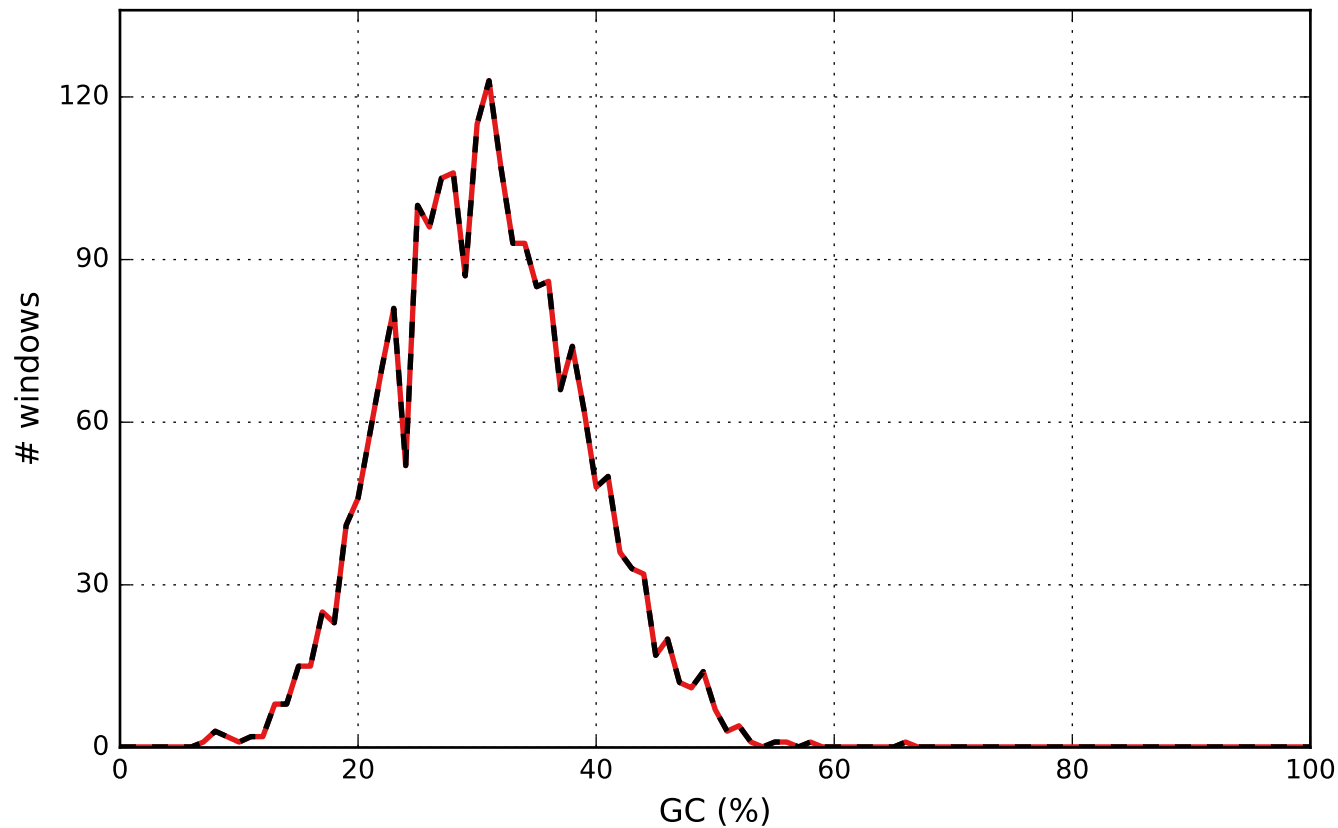


— mito.contigs.final

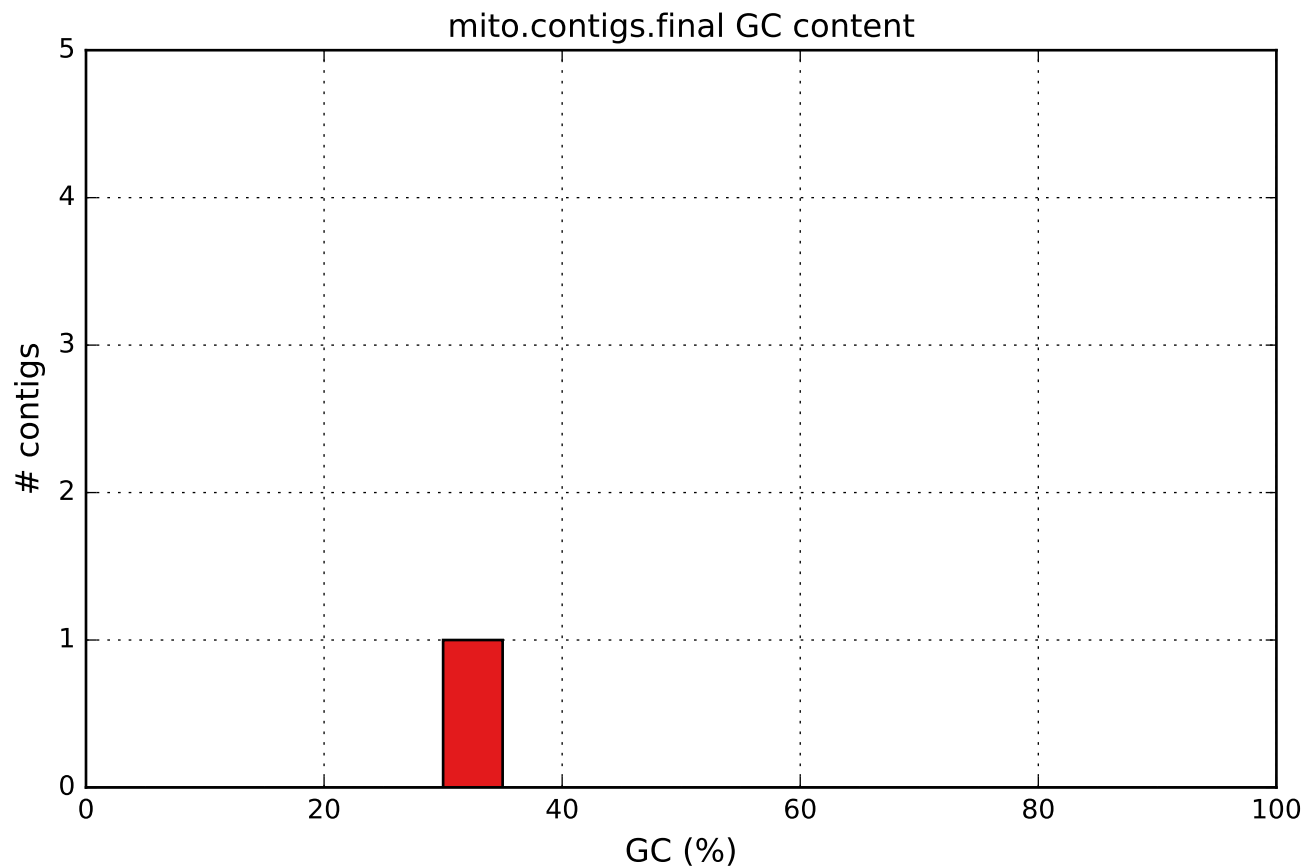
Cumulative length



GC content

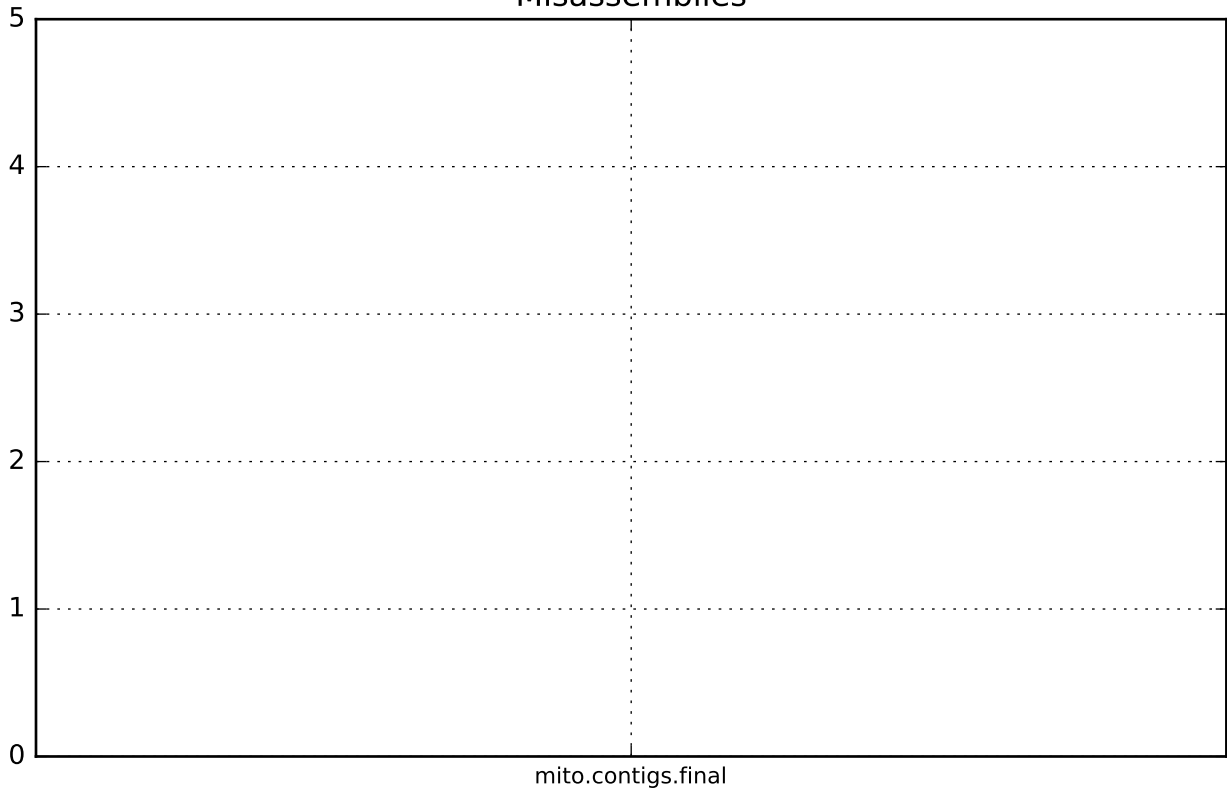


— mito.contigs.final - - Reference

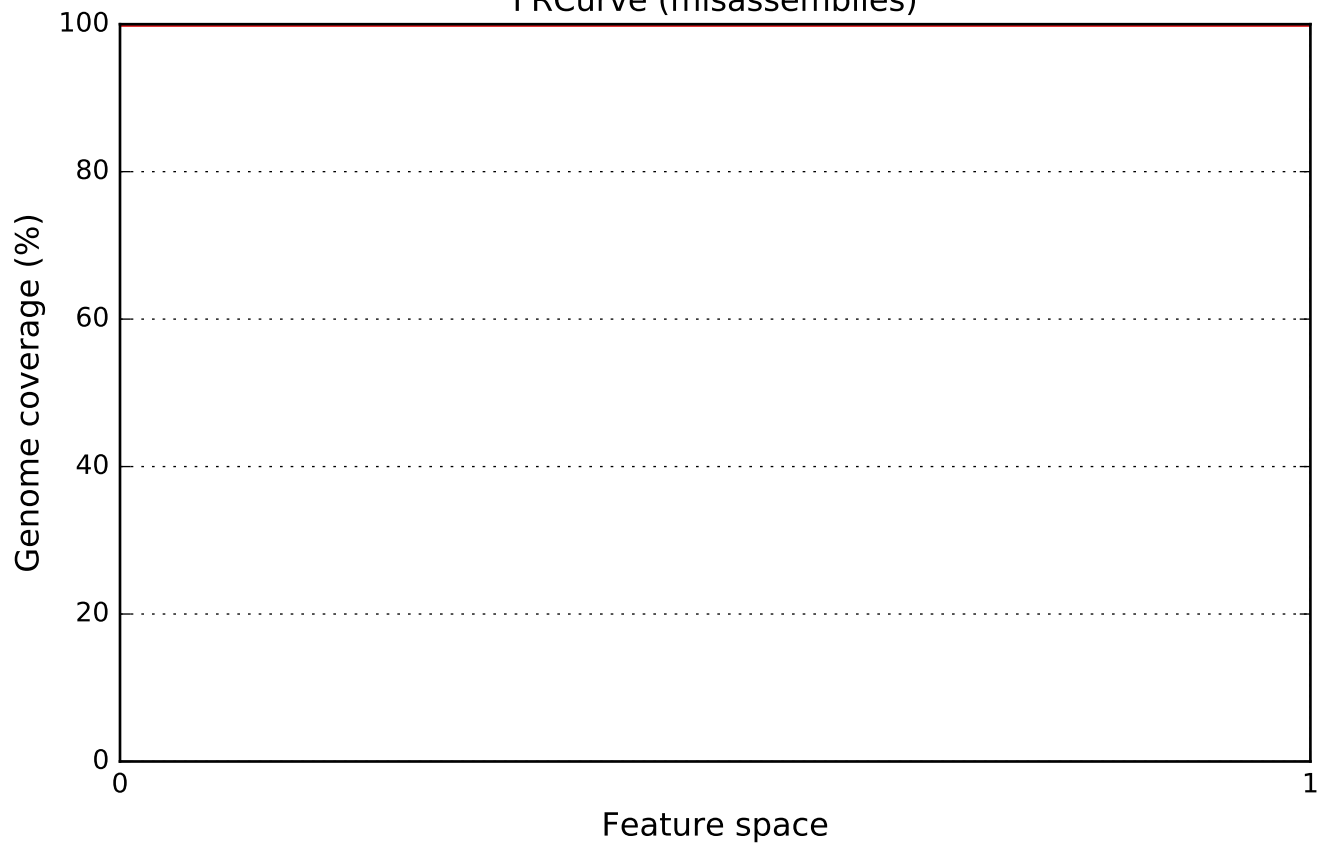


mito.contigs.final

Misassemblies

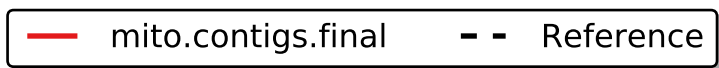
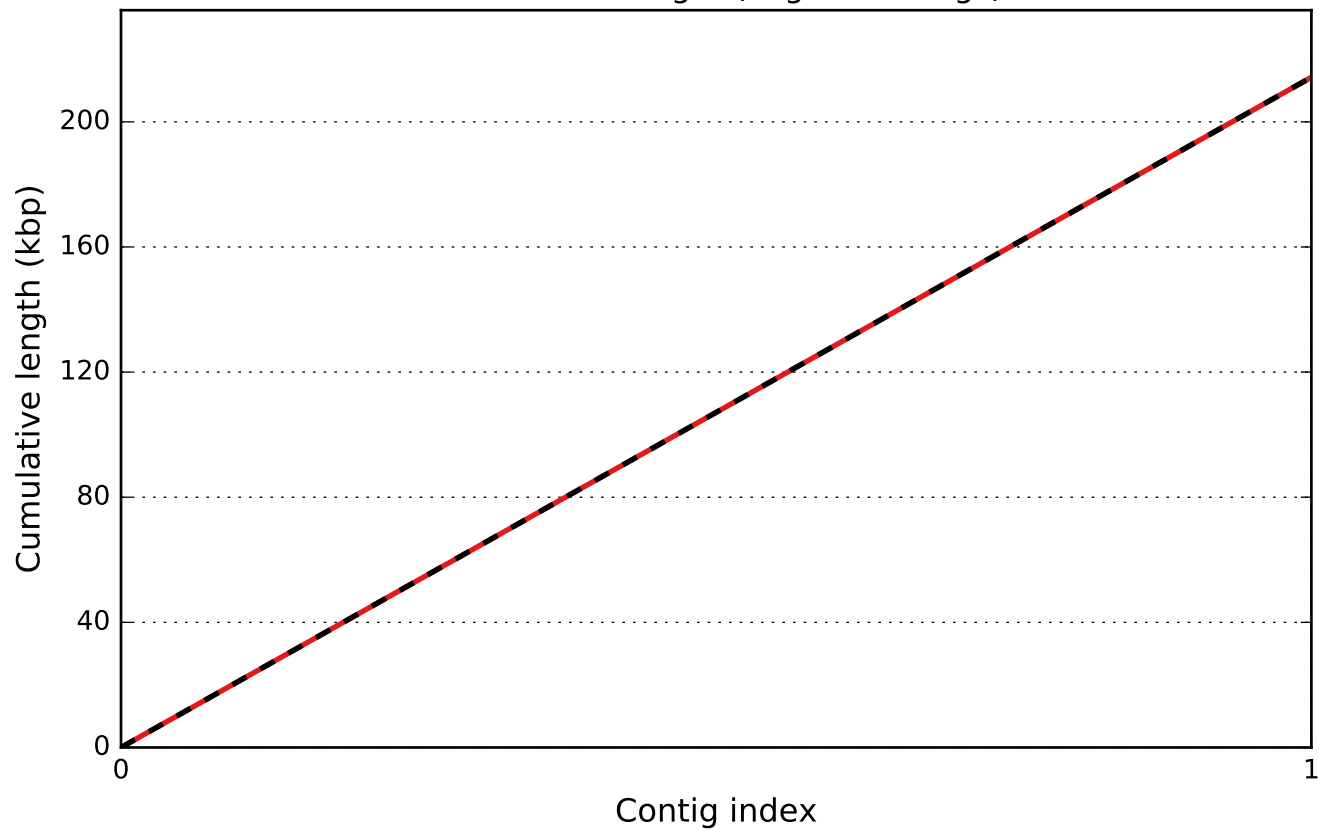


FRCurve (misassemblies)

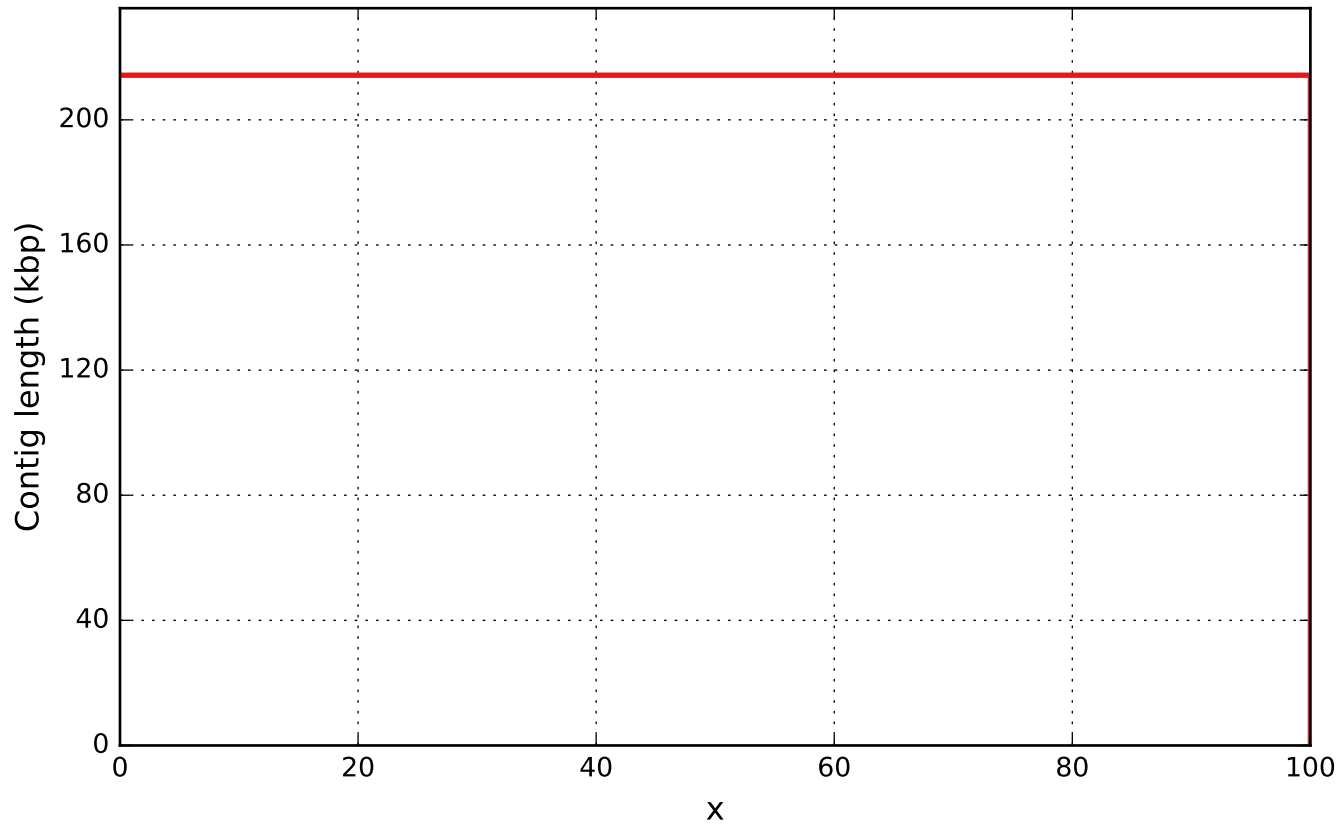


— mito.contigs.final

Cumulative length (aligned contigs)

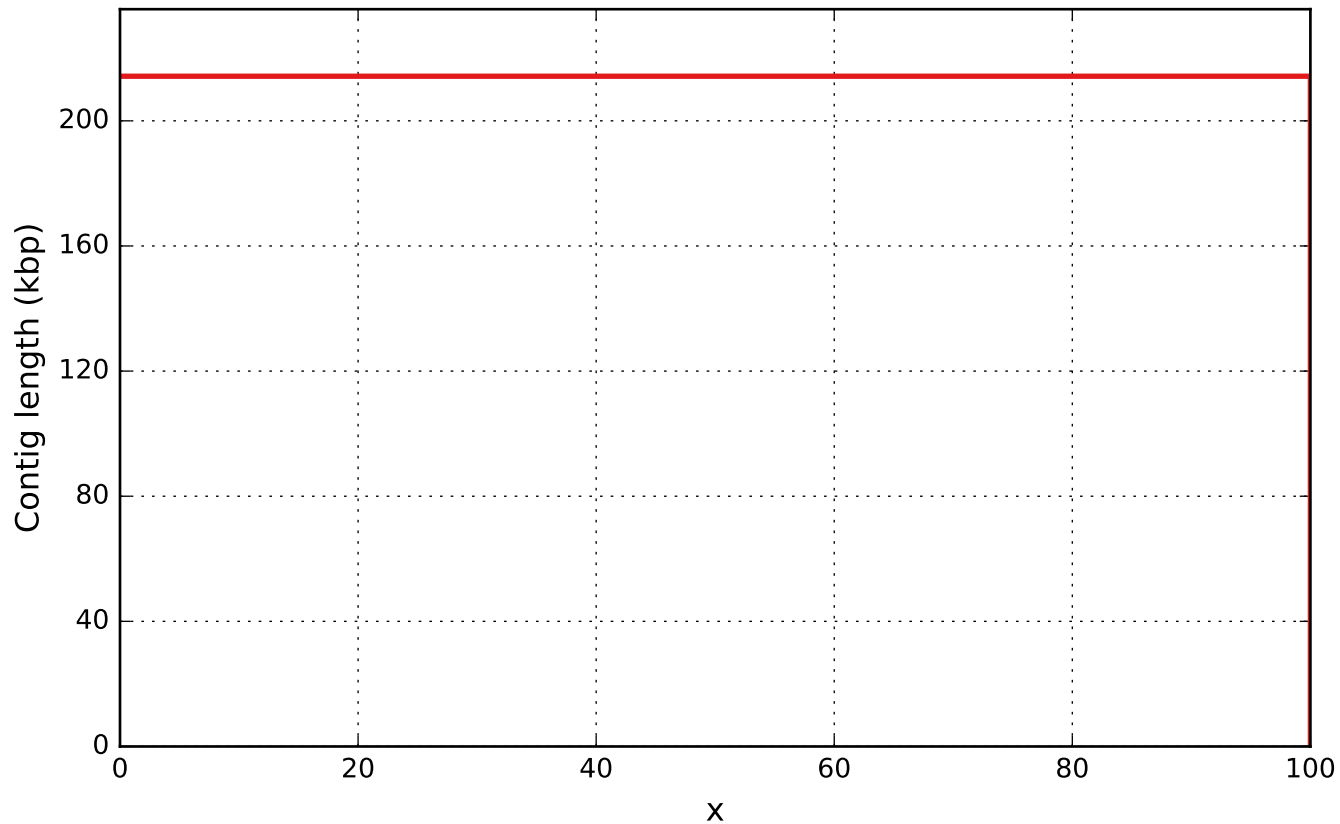


NAx



— mito.contigs.final

NGAx



— mito.contigs.final