

Report

	uniq_contigs_contigs_contigs_contigs_contigs
# contigs (>= 0 bp)	865
# contigs (>= 1000 bp)	214
# contigs (>= 5000 bp)	49
# contigs (>= 10000 bp)	49
# contigs (>= 25000 bp)	42
# contigs (>= 50000 bp)	40
Total length (>= 0 bp)	56060051
Total length (>= 1000 bp)	55680580
Total length (>= 5000 bp)	55442199
Total length (>= 10000 bp)	55442199
Total length (>= 25000 bp)	55346808
Total length (>= 50000 bp)	55266602
# contigs	865
Largest contig	8114736
Total length	56060051
Reference length	59128983
GC (%)	48.37
Reference GC (%)	48.36
N50	2699428
NG50	2699428
N75	1510877
NG75	1021228
L50	7
LG50	7
L75	13
LG75	16
# misassemblies	1
# misassembled contigs	1
Misassembled contigs length	8114736
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# possible TEs	0
# unaligned mis. contigs	0
# unaligned contigs	305 + 0 part
Unaligned length	133005
Genome fraction (%)	99.890
Duplication ratio	1.003
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.28
# indels per 100 kbp	0.24
Largest alignment	6126713
Total aligned length	55926542
NA50	2522609
NGA50	2522609
NA75	1510877
NGA75	1021228
LA50	8
LGA50	8
LA75	14
LGA75	17

All statistics are based on contigs of size >= 400 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

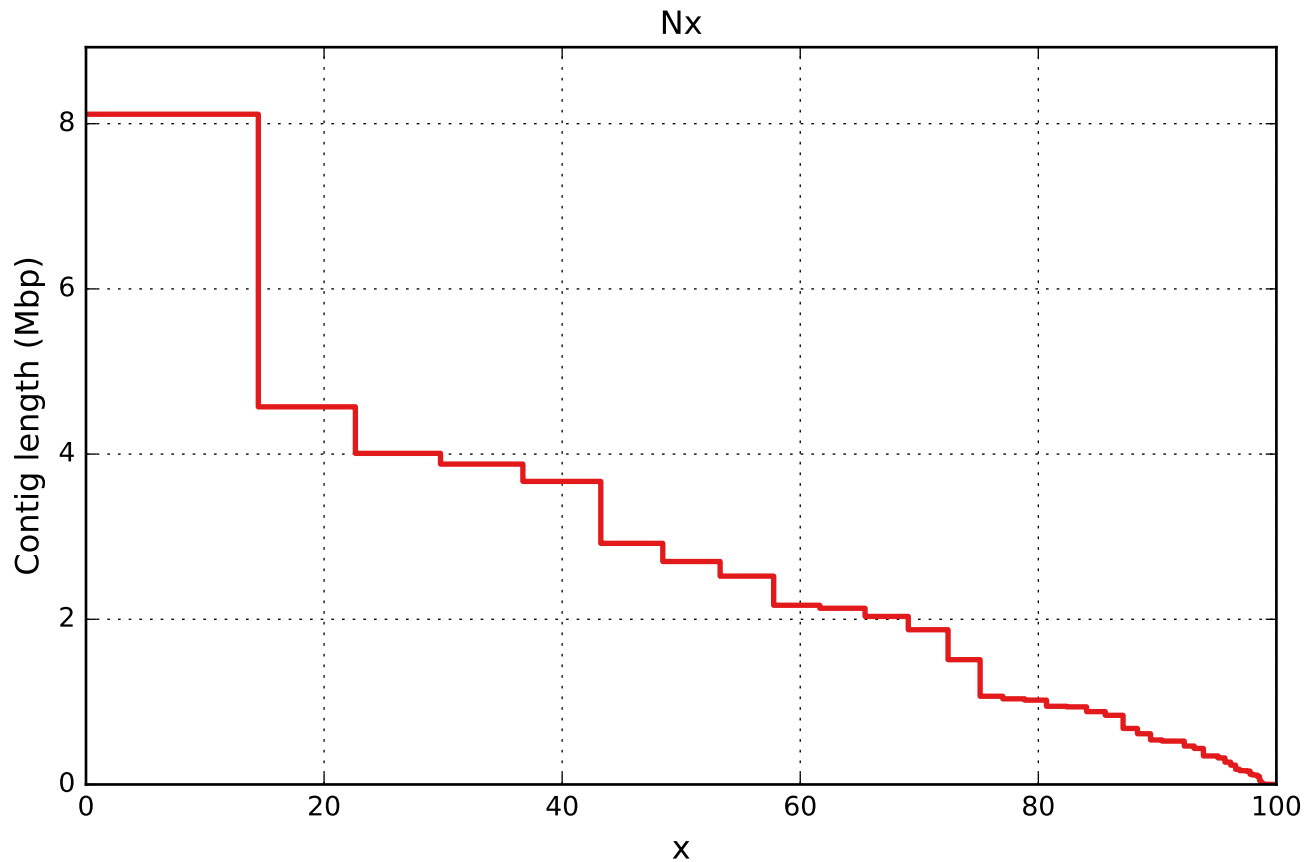
	uniq_contigs_contigs_contigs_contigs_contigs
# misassemblies	1
# contig misassemblies	1
# c. relocations	1
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	8114736
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# misassemblies caused by fragmented reference	0
# possible TEs	0
# unaligned mis. contigs	0
# mismatches	155
# indels	134
# indels (<= 5 bp)	128
# indels (> 5 bp)	6
Indels length	694

All statistics are based on contigs of size ≥ 400 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

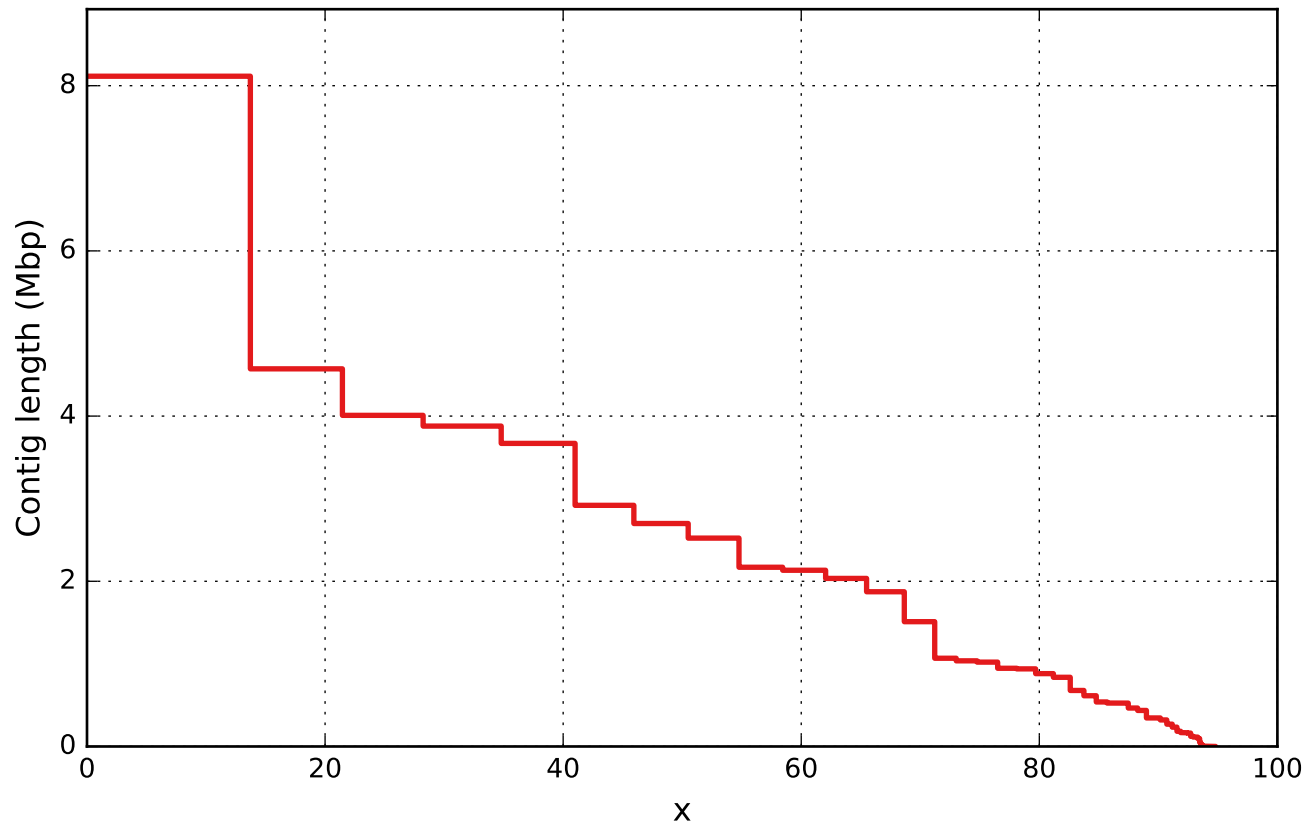
	uniq_contigs_contigs_contigs_contigs
# fully unaligned contigs	305
Fully unaligned length	133005
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

All statistics are based on contigs of size ≥ 400 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

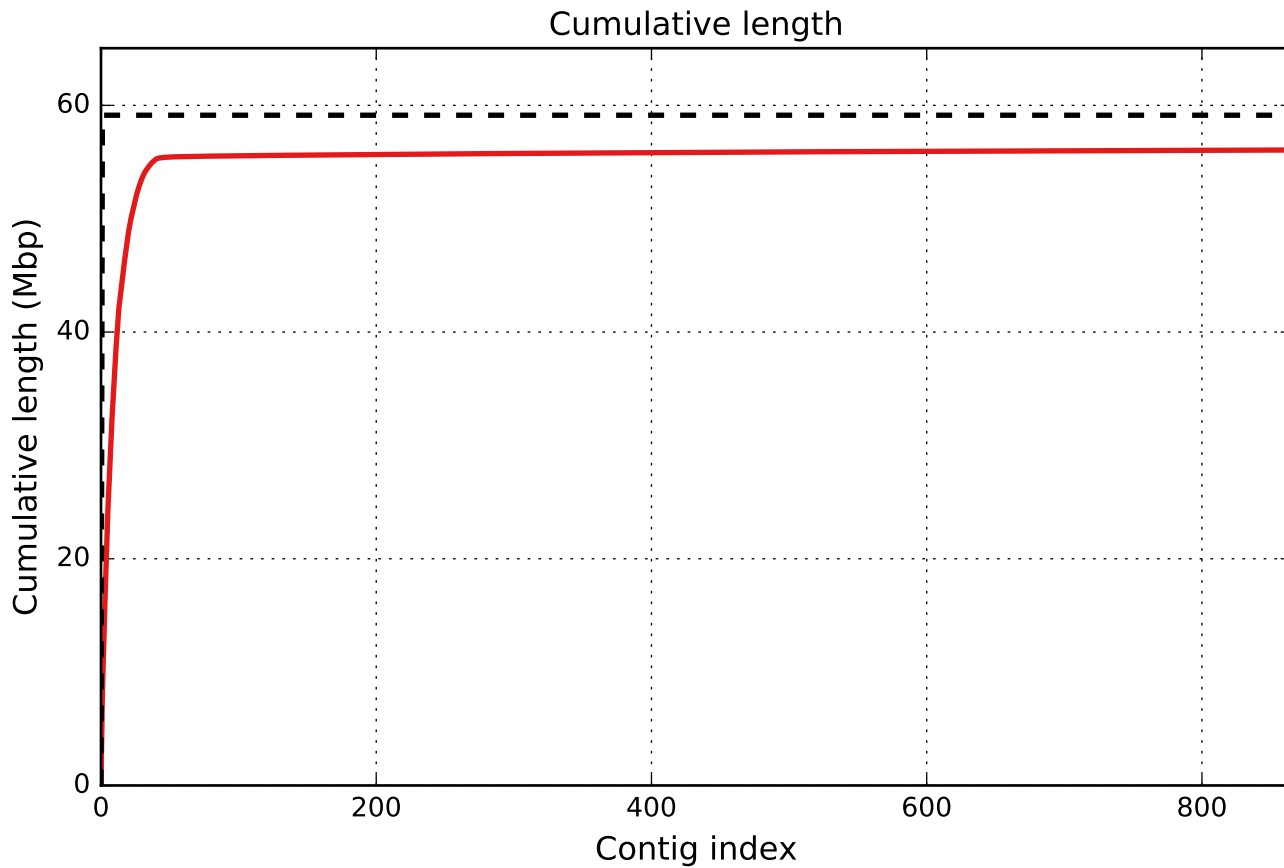


— uniq_contigs_contigs_contigs_contigs

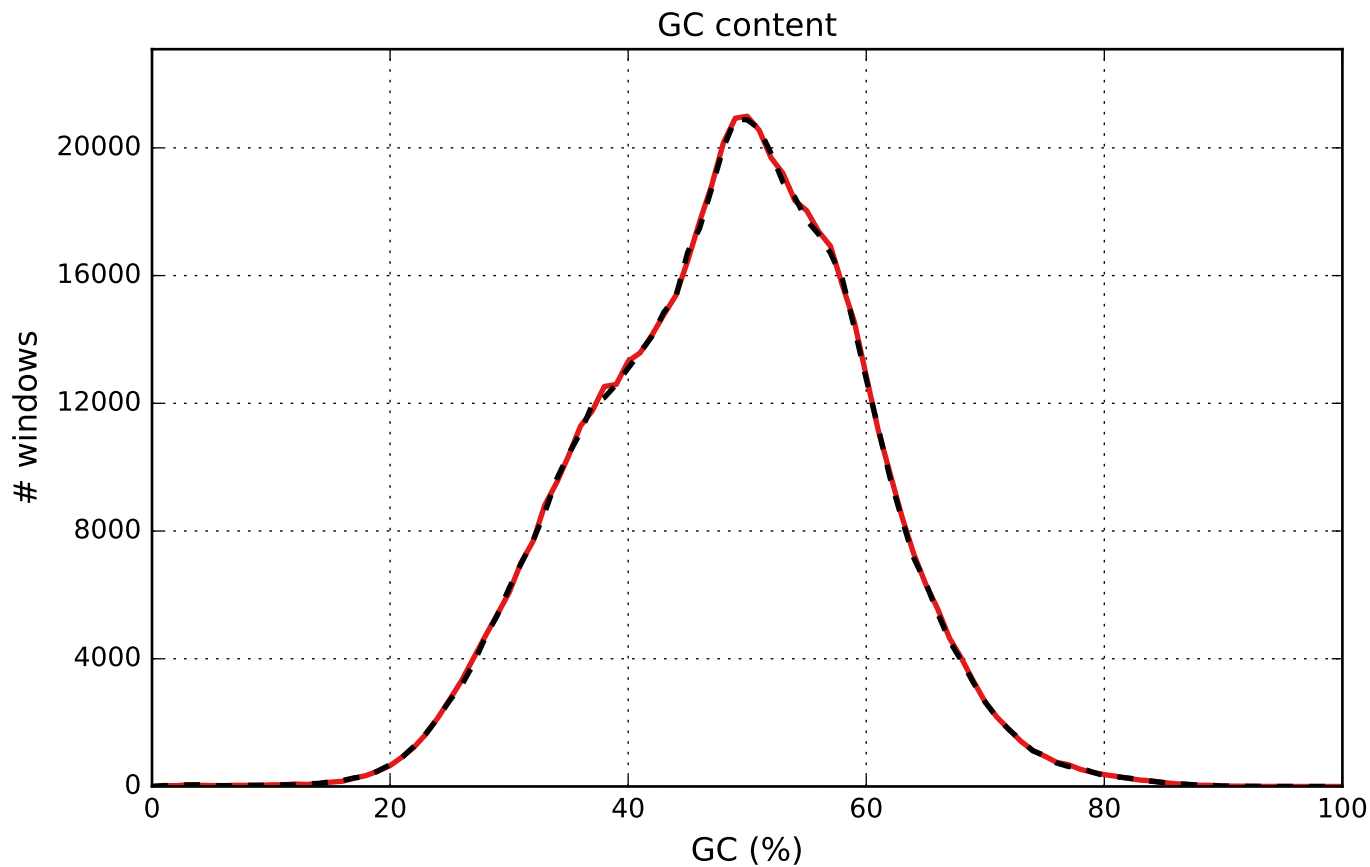
NGx



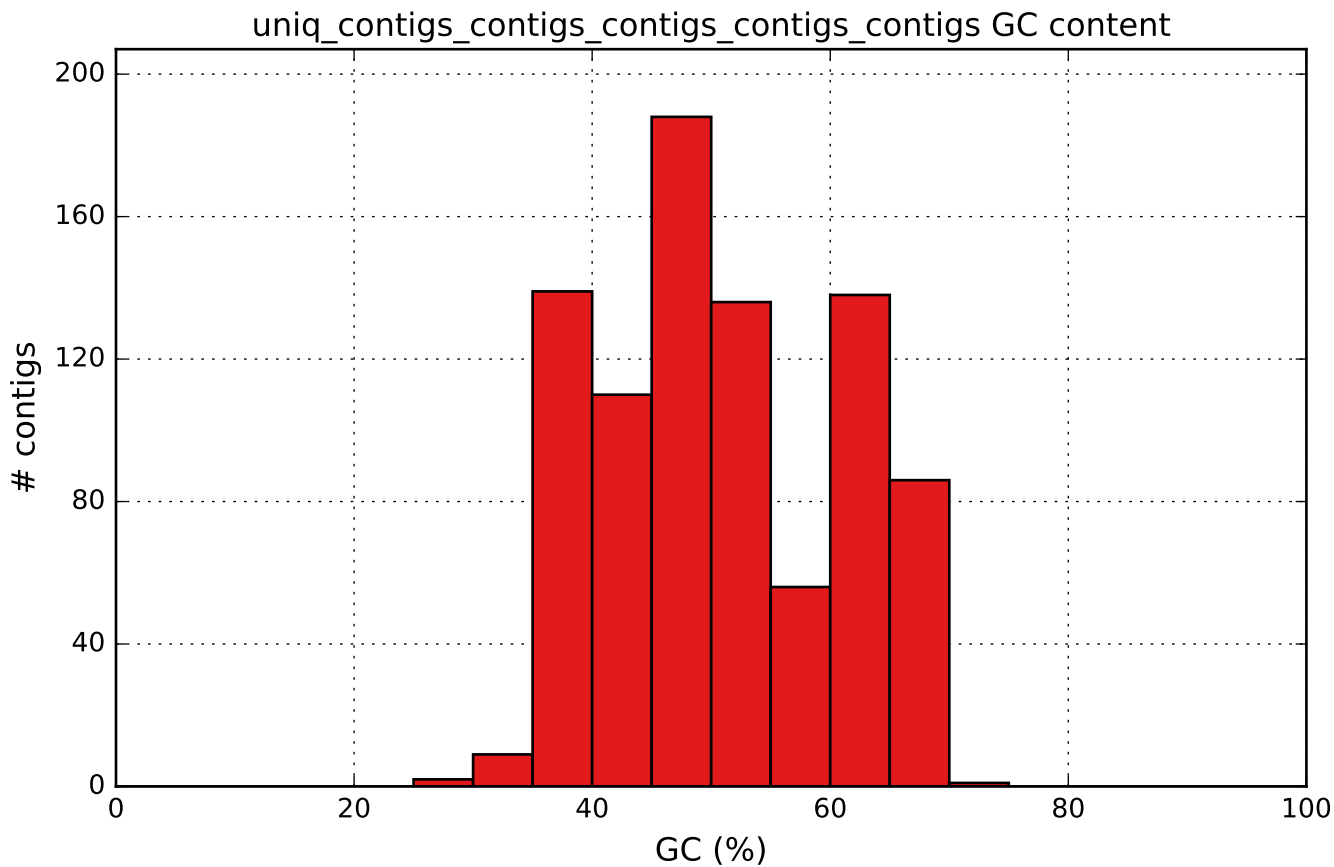
— uniq_contigs_contigs_contigs_contigs



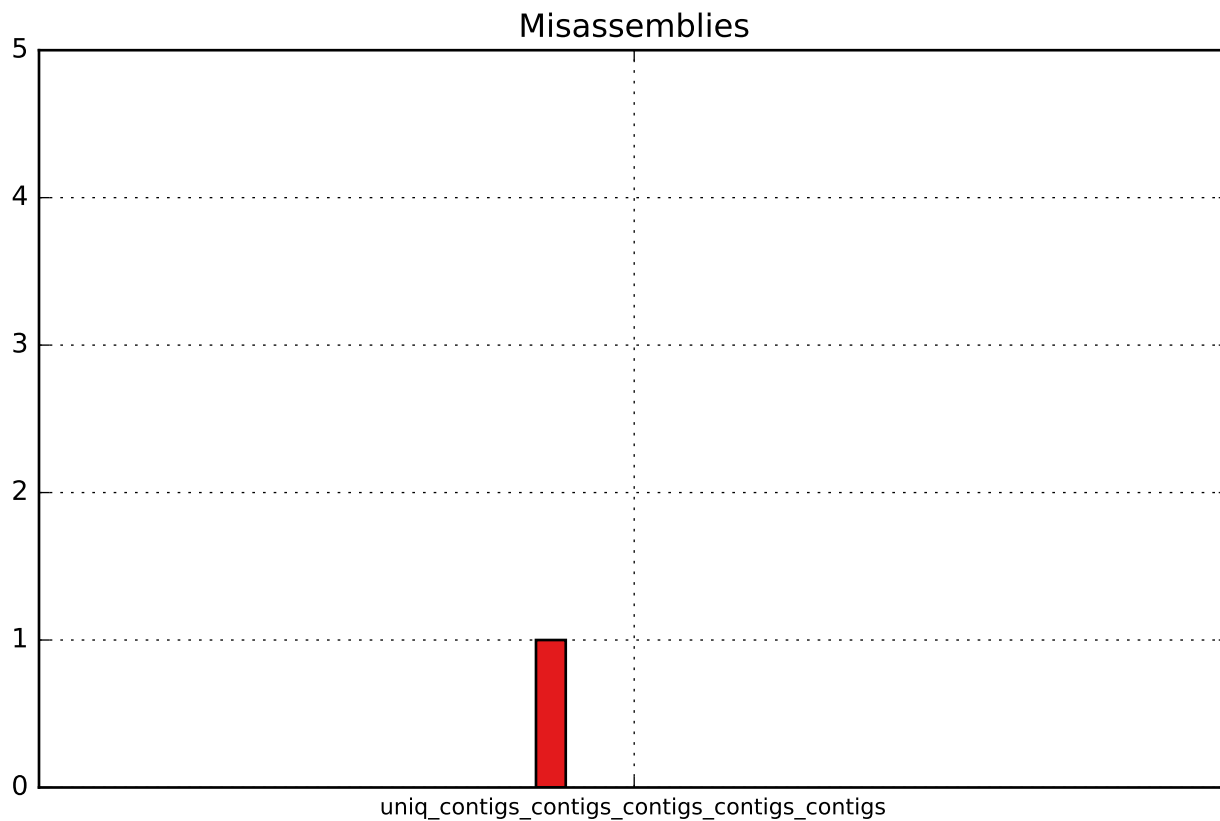
— uniq_contigs_contigs_contigs_contigs_contigs - - Reference



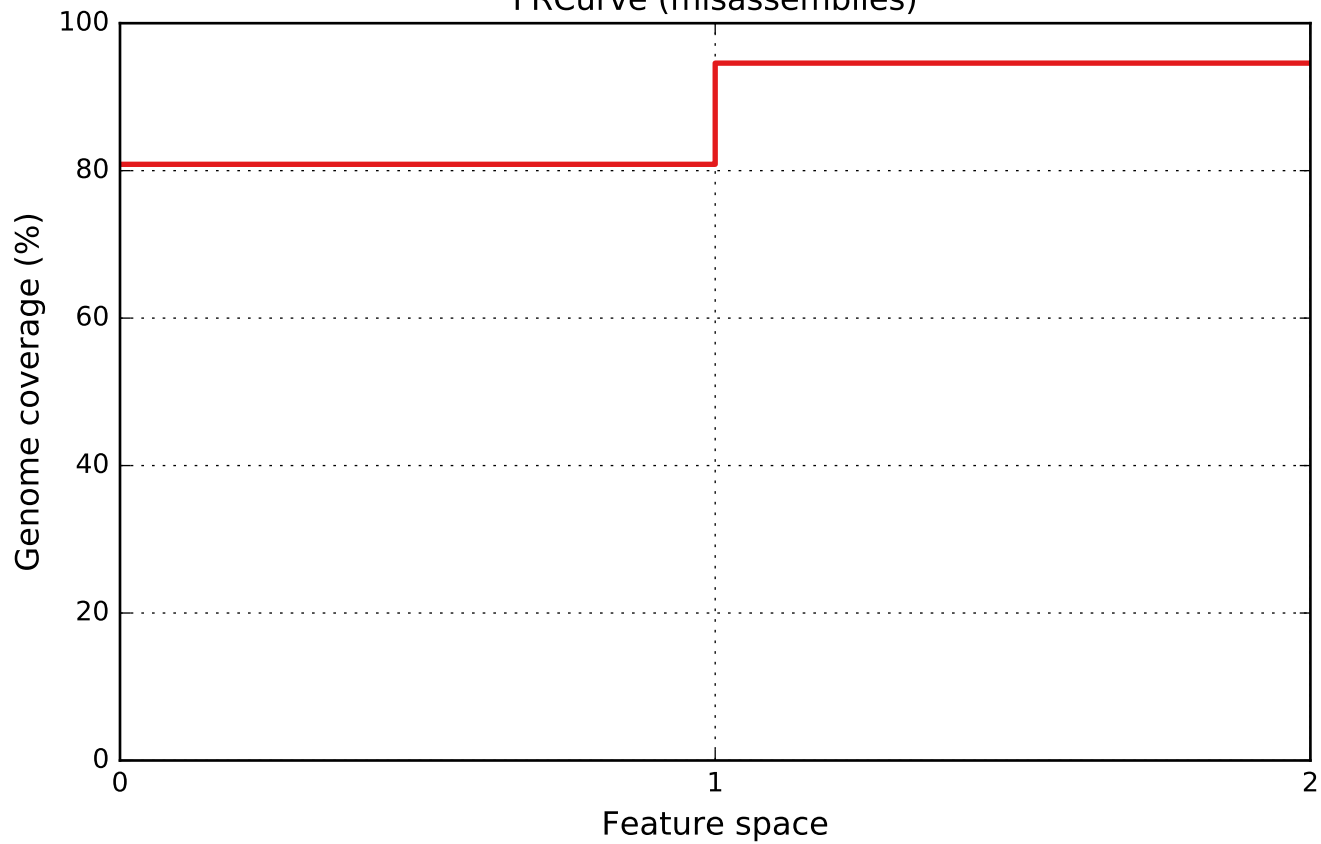
— uniq_contigs_contigs_contigs_contigs_contigs - - Reference



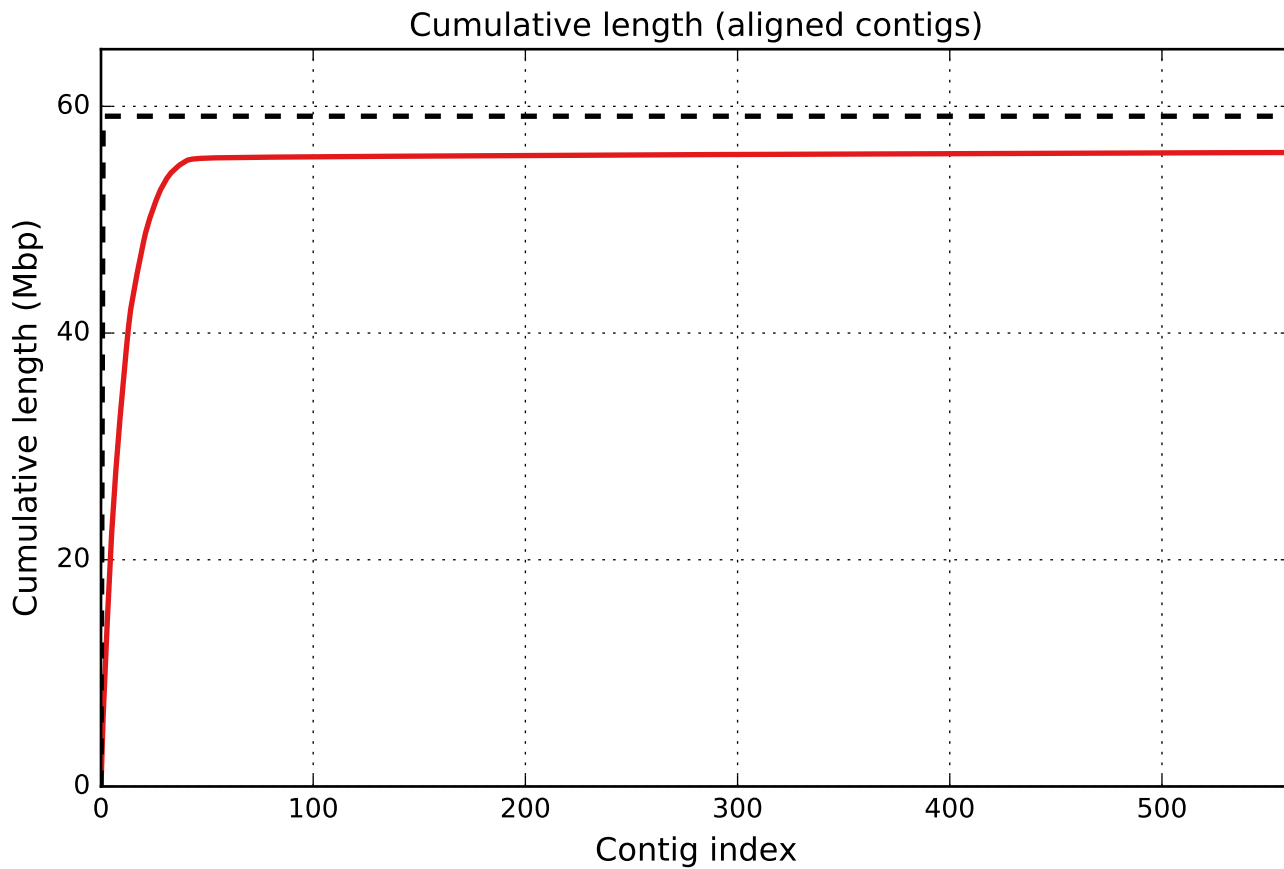
uniq_contigs_contigs_contigs_contigs_contigs



FRCurve (misassemblies)

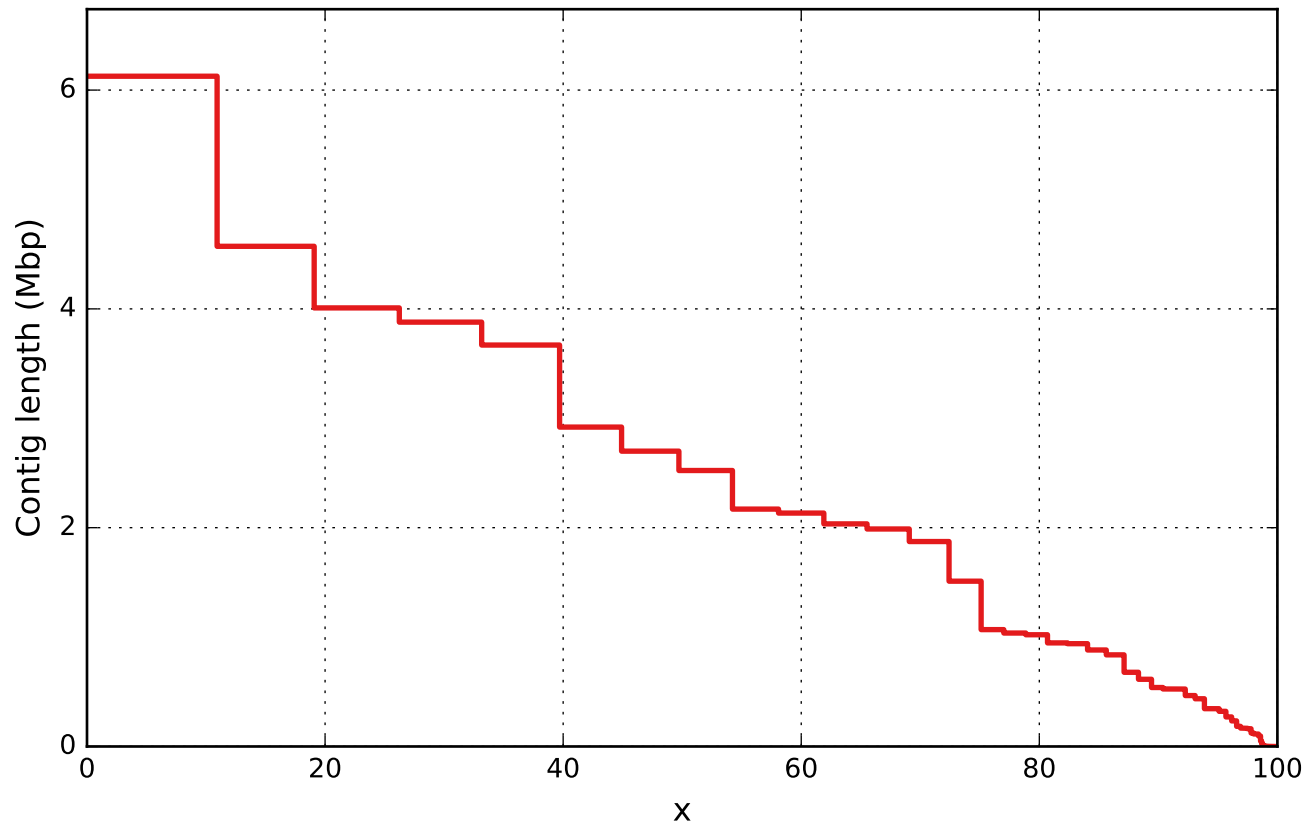


— uniq_contigs_contigs_contigs_contigs_contigs



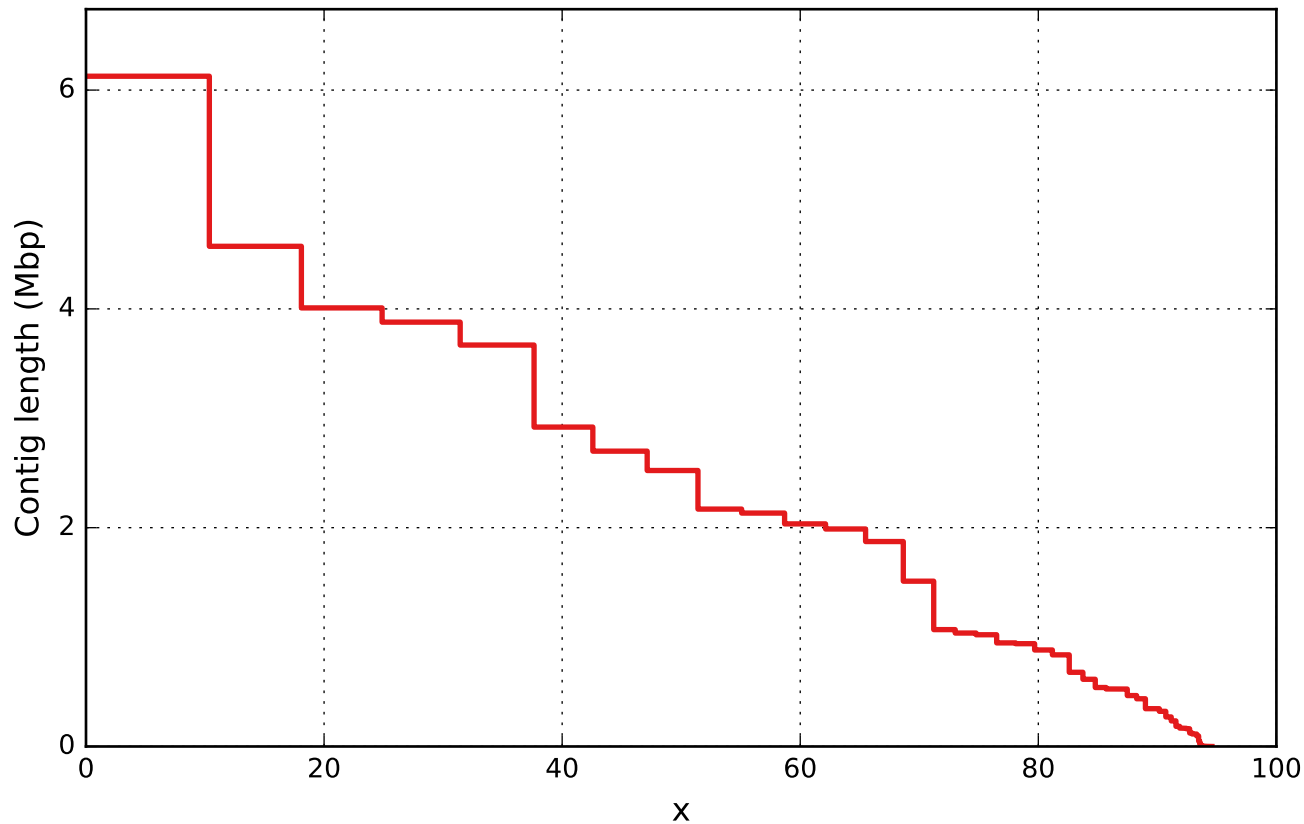
— uniq_contigs_contigs_contigs_contigs_contigs - - Reference

NAx



— uniq_contigs_contigs_contigs_contigs

NGAx



— uniq_contigs_contigs_contigs_contigs