

## Report

	spades_ctg	mulksq_ctg
# contigs (>= 0 bp)	67	65
# contigs (>= 1000 bp)	50	50
# contigs (>= 5000 bp)	30	31
# contigs (>= 10000 bp)	26	26
# contigs (>= 25000 bp)	22	22
# contigs (>= 50000 bp)	22	22
Total length (>= 0 bp)	3944058	3944128
Total length (>= 1000 bp)	3935796	3937016
Total length (>= 5000 bp)	3890786	3894557
Total length (>= 10000 bp)	3862605	3861317
Total length (>= 25000 bp)	3794239	3799144
Total length (>= 50000 bp)	3794239	3799144
# contigs	57	56
Largest contig	382053	382053
Total length	3941039	3941468
Reference length	2961149	2961149
GC (%)	47.50	47.50
Reference GC (%)	47.70	47.70
N50	199447	199447
NG50	260649	260649
N75	141668	141668
NG75	192074	192074
L50	7	7
LG50	5	5
L75	13	13
LG75	8	8
# misassemblies	3	2
# misassembled contigs	2	2
Misassembled contigs length	522287	516808
# local misassemblies	3	3
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	3	3
# unaligned contigs	24 + 11 part	23 + 10 part
Unaligned length	1026247	1026471
Genome fraction (%)	98.282	98.292
Duplication ratio	1.002	1.002
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	9.35	8.66
# indels per 100 kbp	2.37	2.37
Largest alignment	382053	382053
Total aligned length	2914799	2914599
NA50	152282	152375
NGA50	192074	192074
NGA75	110108	126528
LA50	9	9
LGA50	6	6
LGA75	11	11

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

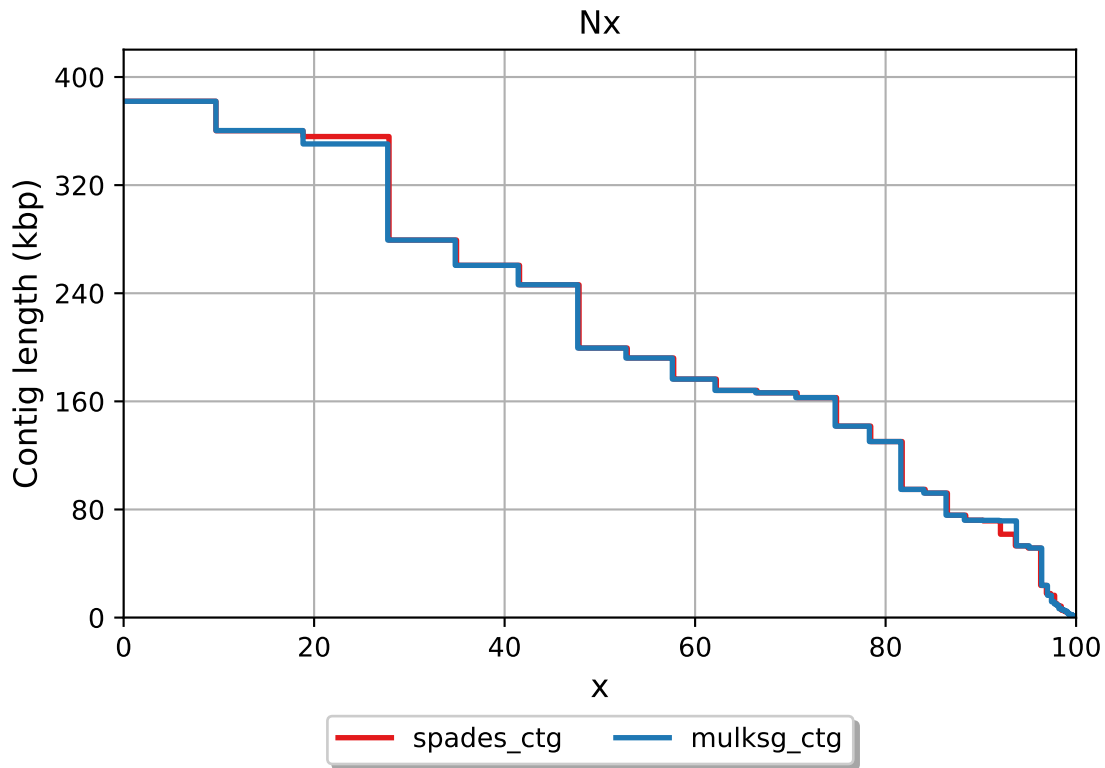
	spades_ctg	mulksq_ctg
# misassemblies	3	2
# contig misassemblies	3	2
# c. relocations	3	2
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	2	2
Misassembled contigs length	522287	516808
# local misassemblies	3	3
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	3	3
# mismatches	272	252
# indels	69	69
# indels (<= 5 bp)	65	65
# indels (> 5 bp)	4	4
Indels length	110	110

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).

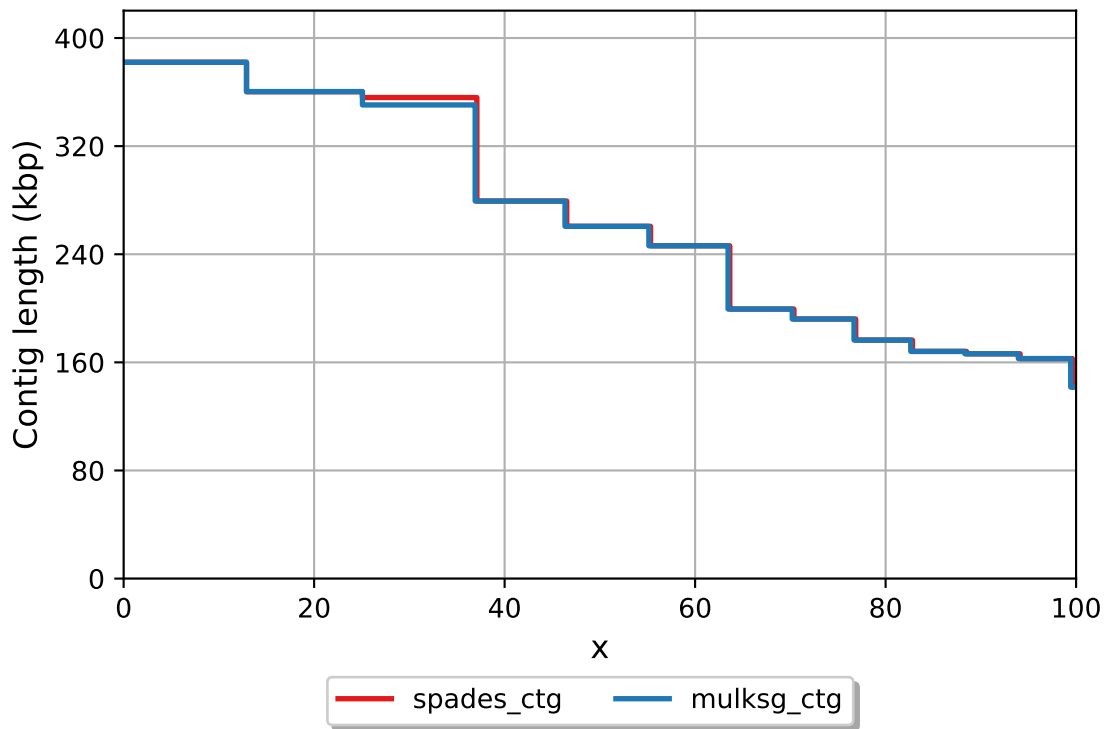
## Unaligned report

	spades_ctg	mulksg_ctg
# fully unaligned contigs	24	23
Fully unaligned length	54997	66415
# partially unaligned contigs	11	10
Partially unaligned length	971250	960056
# N's	0	0

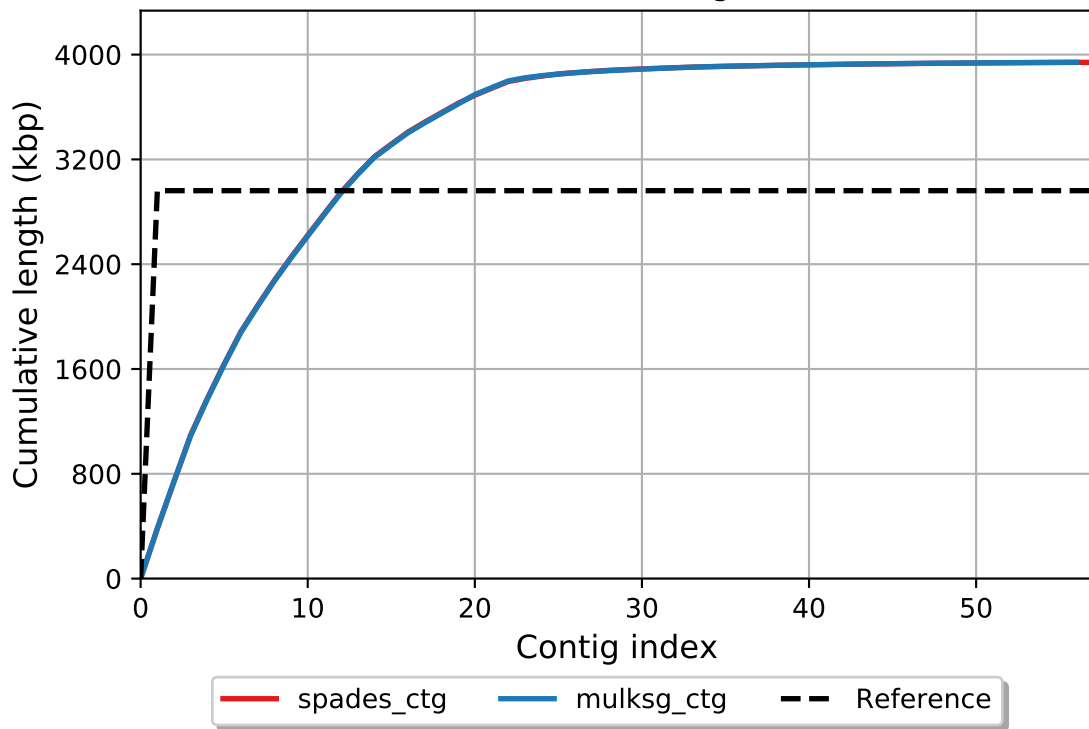
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



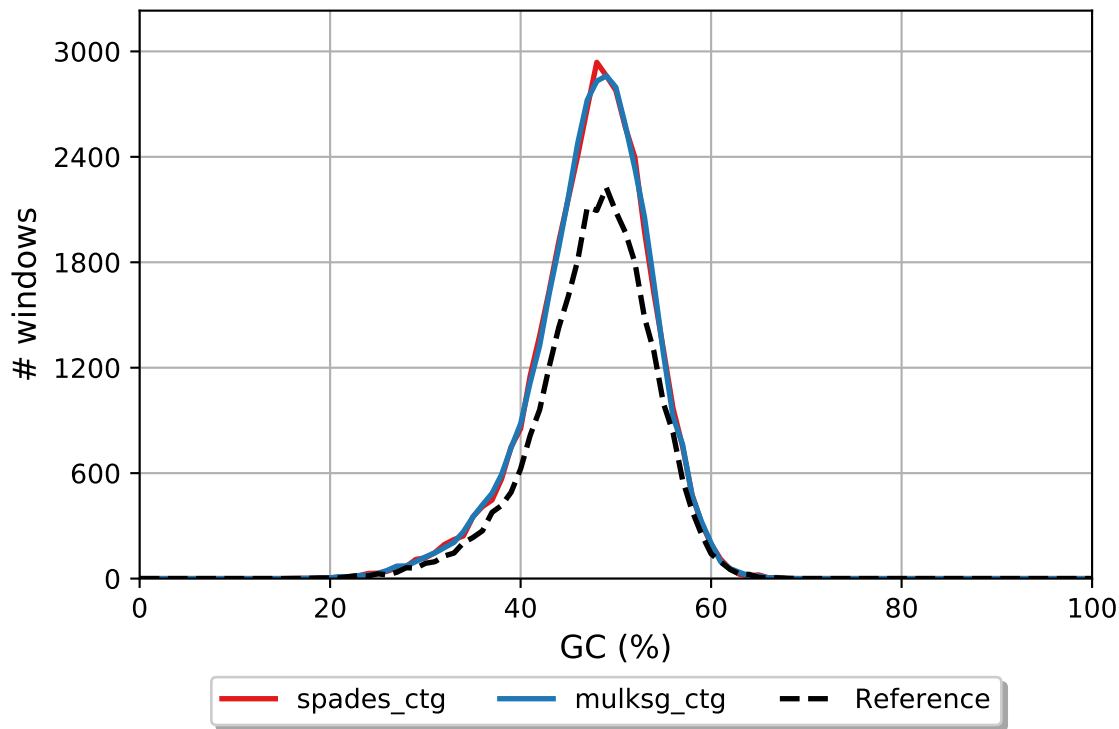
# NGx



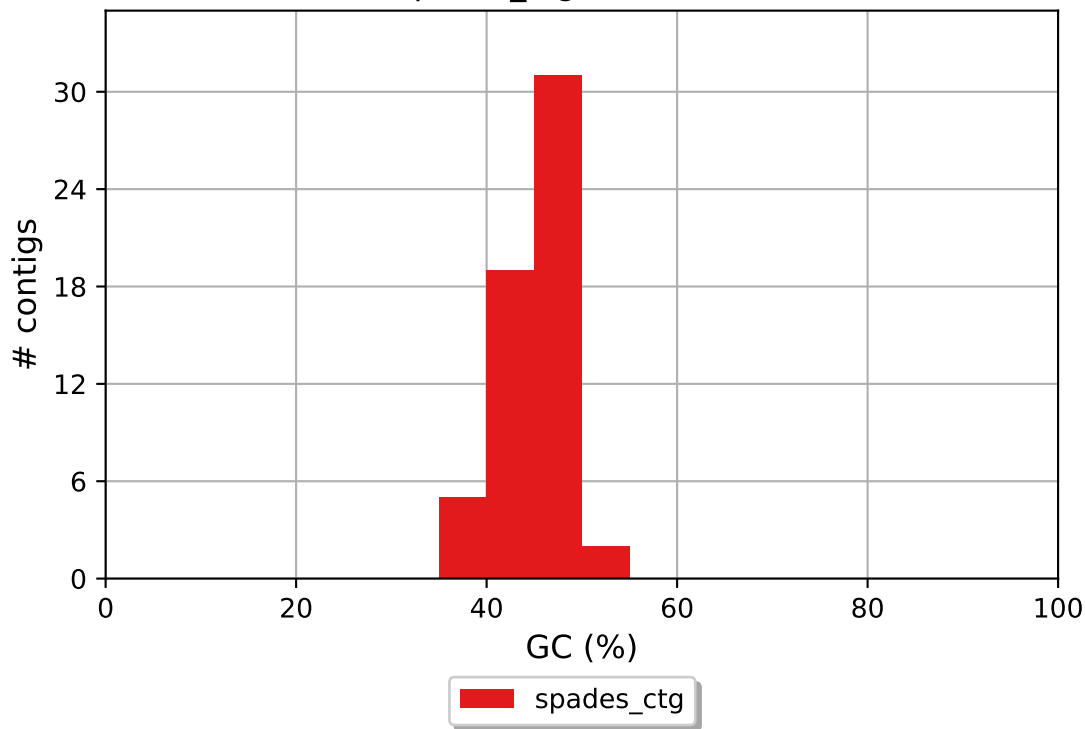
Cumulative length



GC content

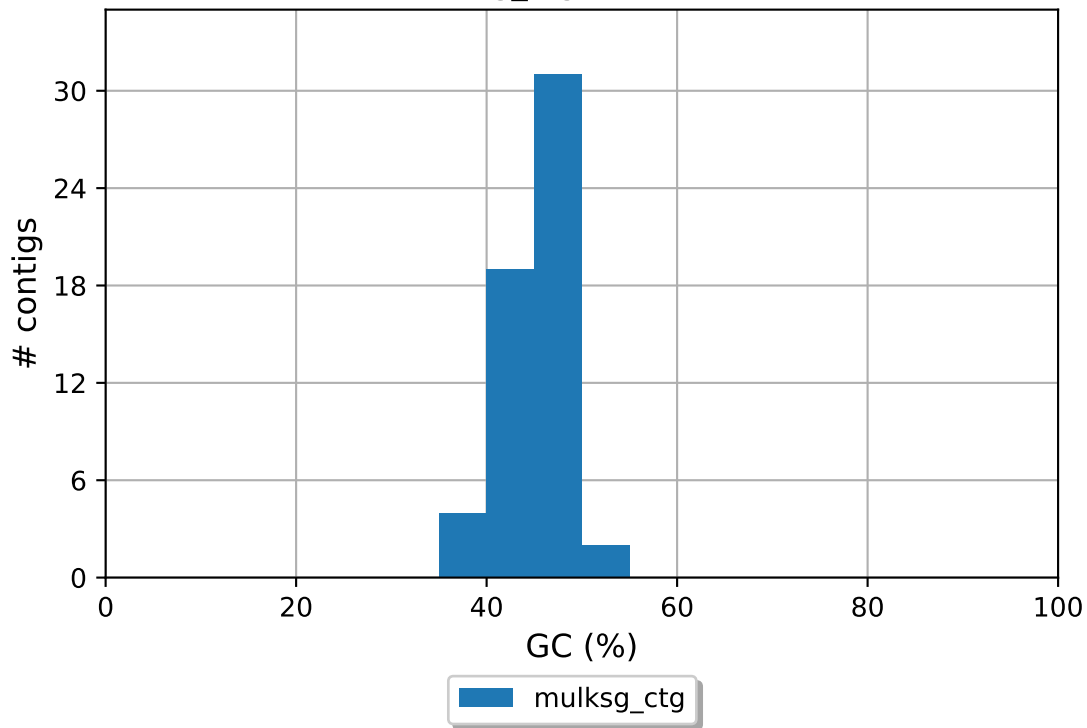


spades\_ctg GC content

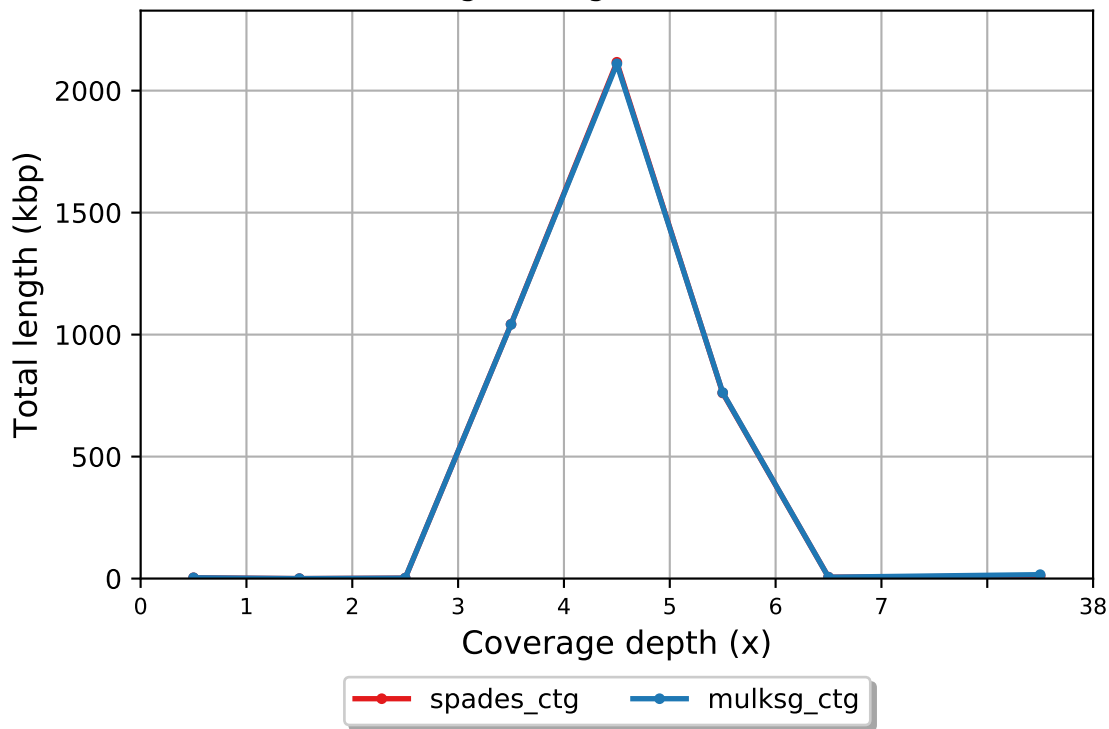




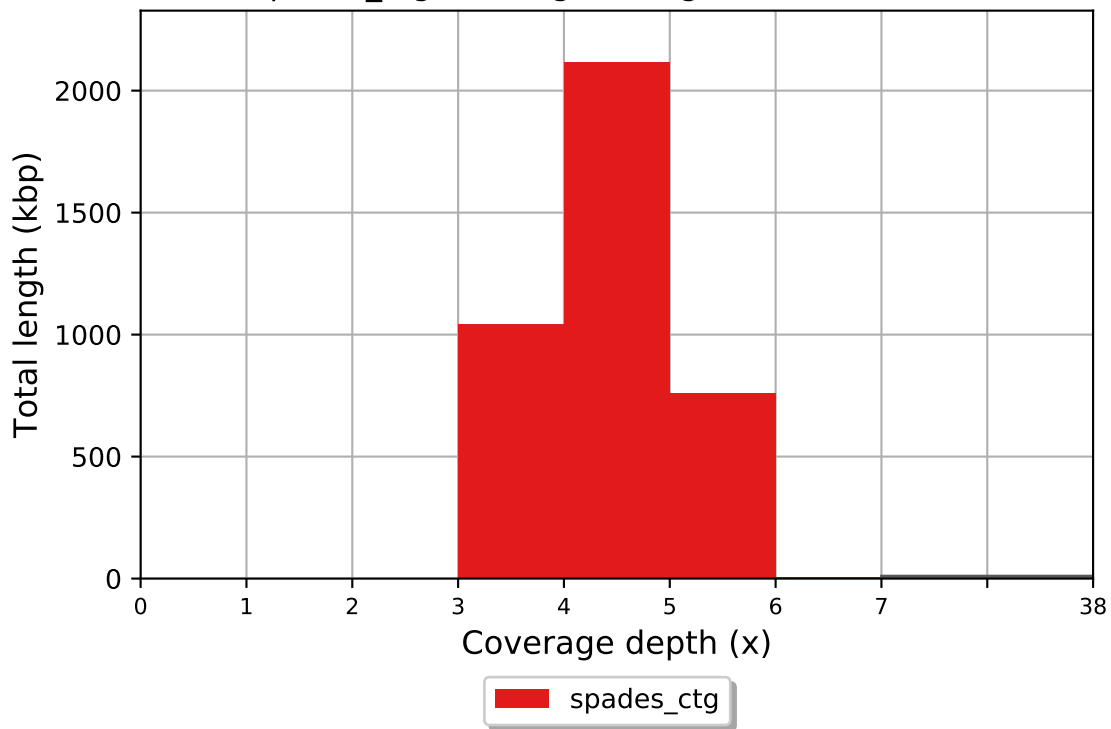
mulksg\_ctg GC content



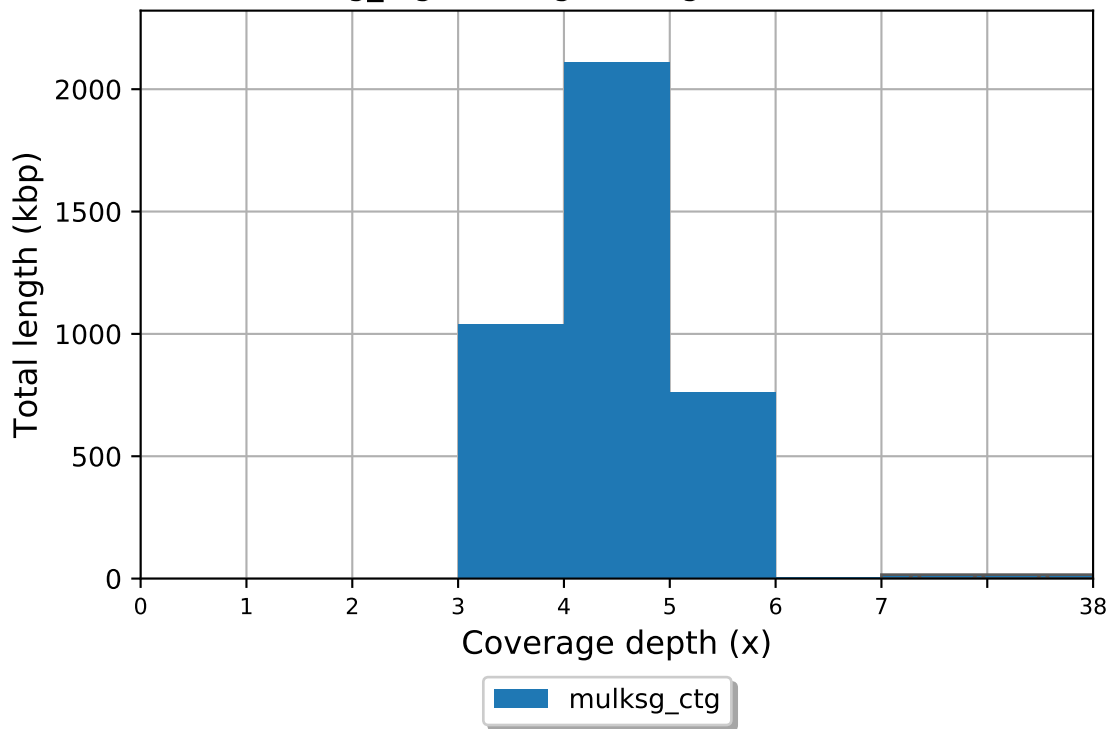
Coverage histogram (bin size: 1x)



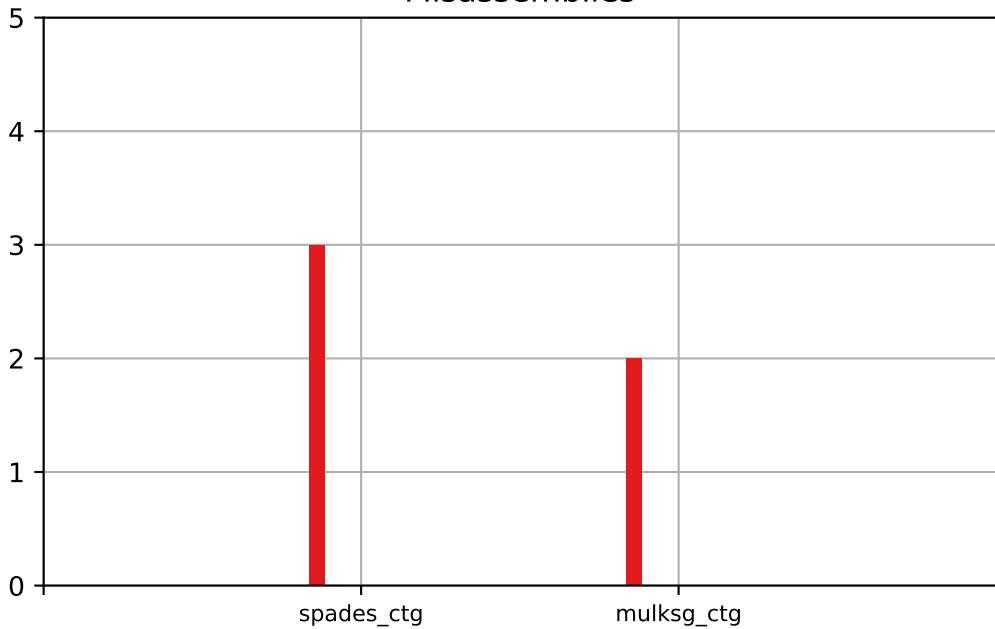
spades\_ctg coverage histogram (bin size: 1x)



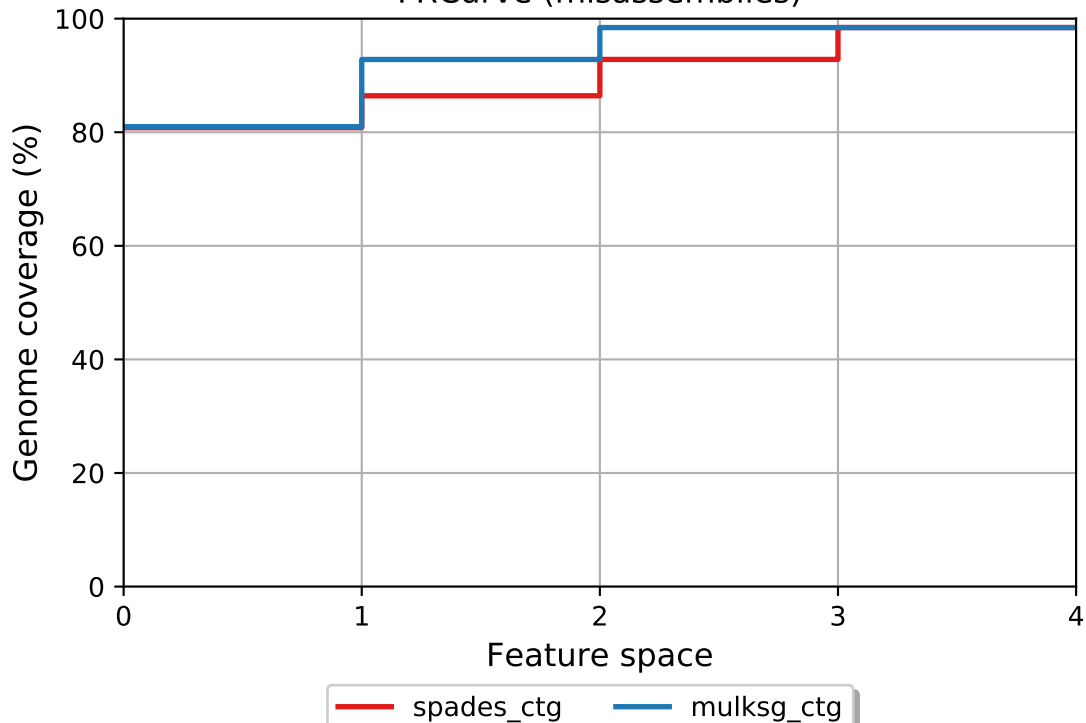
mulksg\_ctg coverage histogram (bin size: 1x)



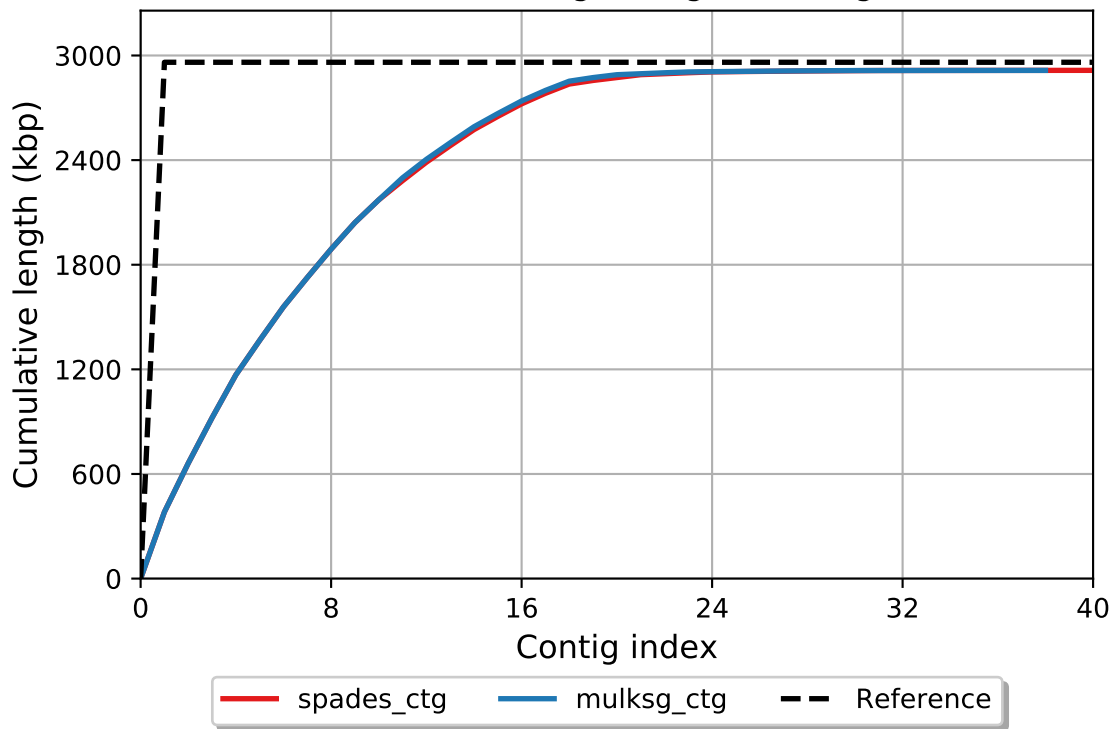
## Misassemblies



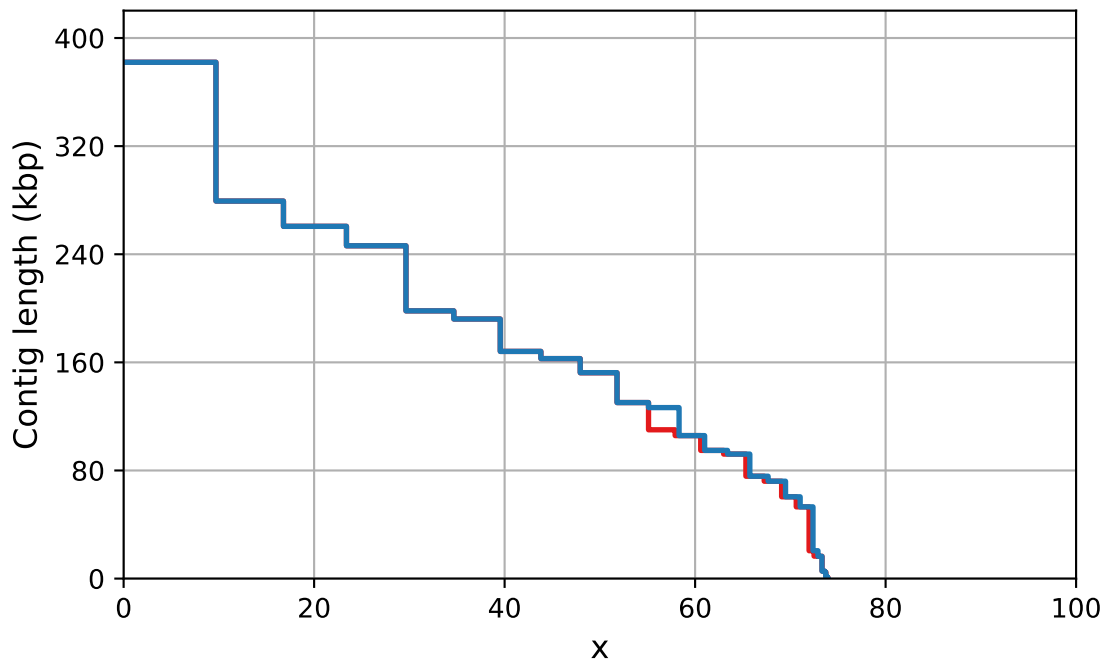
FRCurve (misassemblies)



Cumulative length (aligned contigs)



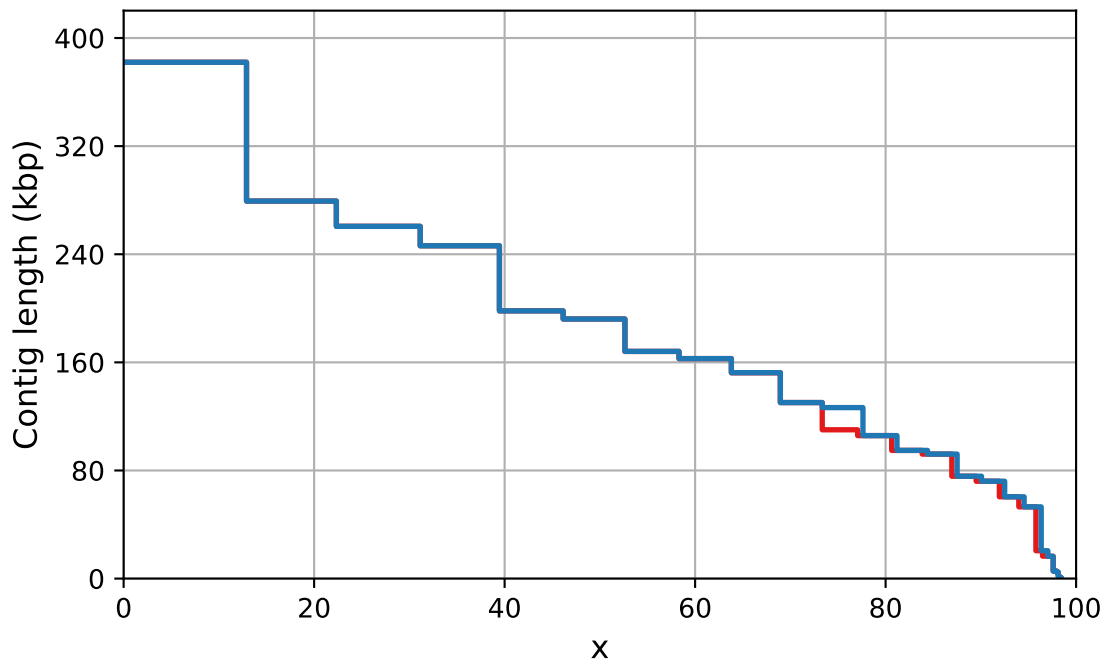
NAx



spades\_ctg mulksg\_ctg

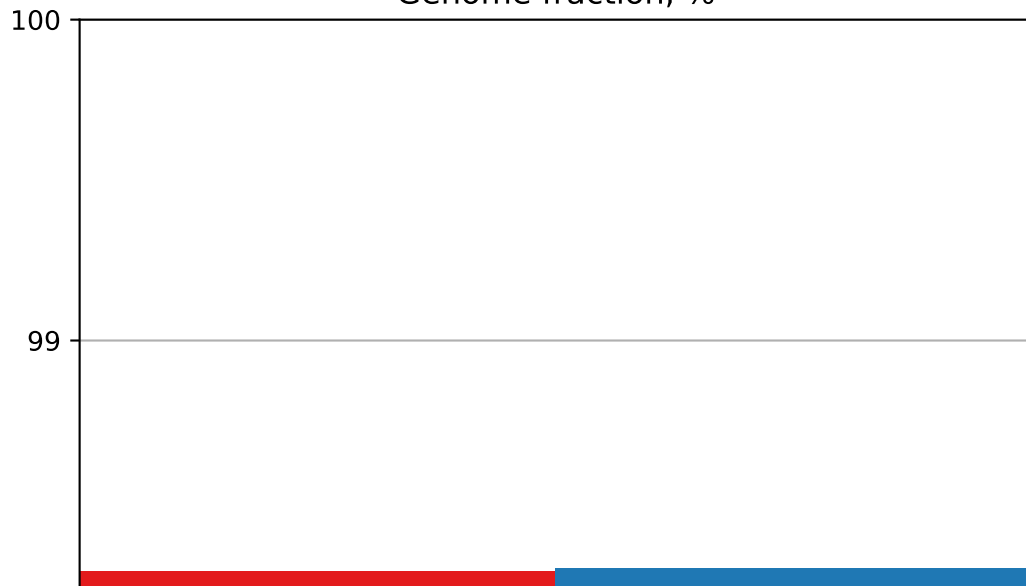


# NGAx



spades\_ctg mulksg\_ctg

Genome fraction, %



spades\_ctg



mulksg\_ctg