

## Report

	spades_ctg	mulksq_ctg
# contigs (>= 0 bp)	615	624
# contigs (>= 1000 bp)	40	40
# contigs (>= 5000 bp)	25	25
# contigs (>= 10000 bp)	23	23
# contigs (>= 25000 bp)	19	19
# contigs (>= 50000 bp)	12	12
Total length (>= 0 bp)	3019386	3020413
Total length (>= 1000 bp)	2837255	2836692
Total length (>= 5000 bp)	2806166	2806166
Total length (>= 10000 bp)	2794542	2794542
Total length (>= 25000 bp)	2718783	2718783
Total length (>= 50000 bp)	2450070	2450070
# contigs	72	72
Largest contig	381434	381434
Total length	2857560	2856759
Reference length	27041	27041
GC (%)	32.77	32.76
Reference GC (%)	30.52	30.52
N50	242064	242064
NG50	381434	381434
N75	122619	122619
NG75	381434	381434
L50	5	5
LG50	1	1
L75	9	9
LG75	1	1
# misassemblies	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	0	0
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	2	2
# unaligned contigs	70 + 2 part	70 + 2 part
Unaligned length	2848095	2847294
Genome fraction (%)	31.897	31.897
Duplication ratio	1.097	1.097
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	2469.57	2469.57
# indels per 100 kbp	92.75	92.75
Largest alignment	4181	4181
Total aligned length	9465	9465
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

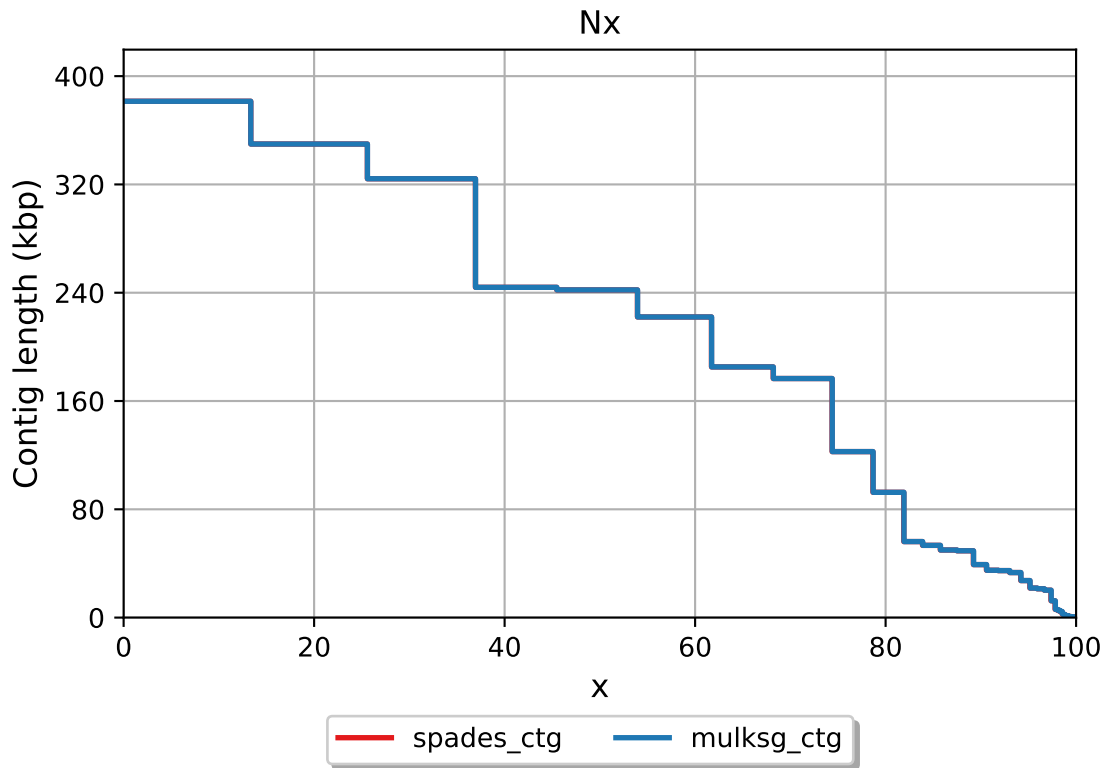
	spades_ctg	mulksq_ctg
# misassemblies	0	0
# contig misassemblies	0	0
# c. relocations	0	0
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	0	0
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	2	2
# mismatches	213	213
# indels	8	8
# indels (<= 5 bp)	6	6
# indels (> 5 bp)	2	2
Indels length	47	47

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).

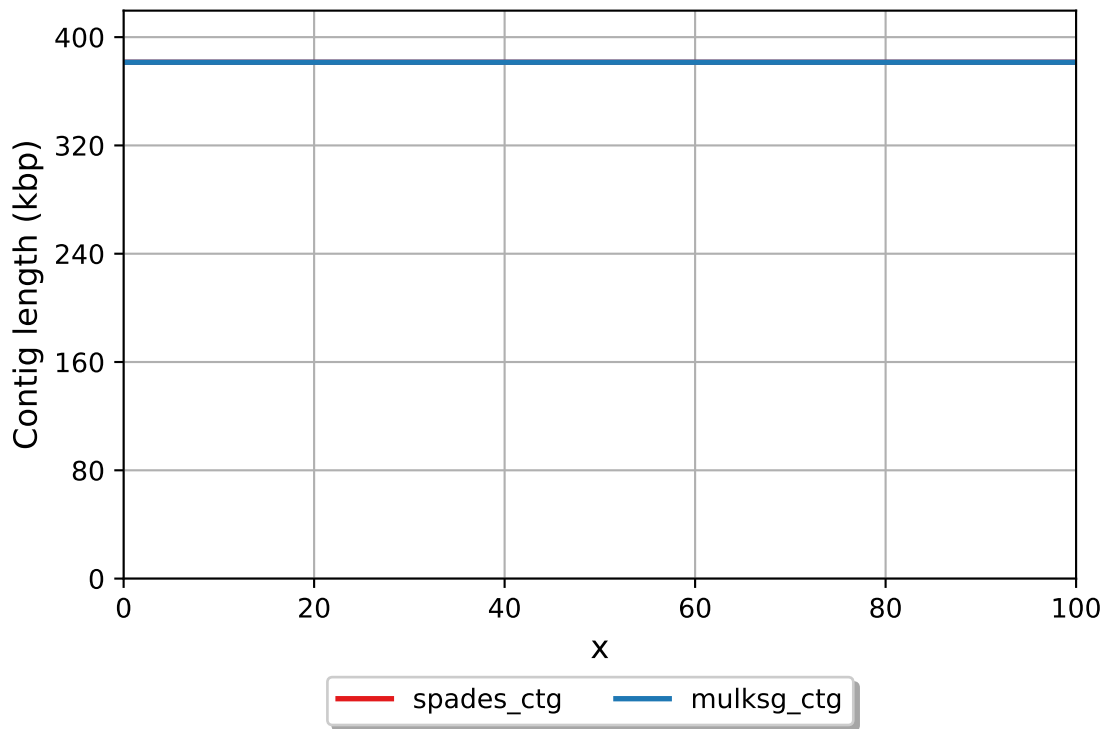
## Unaligned report

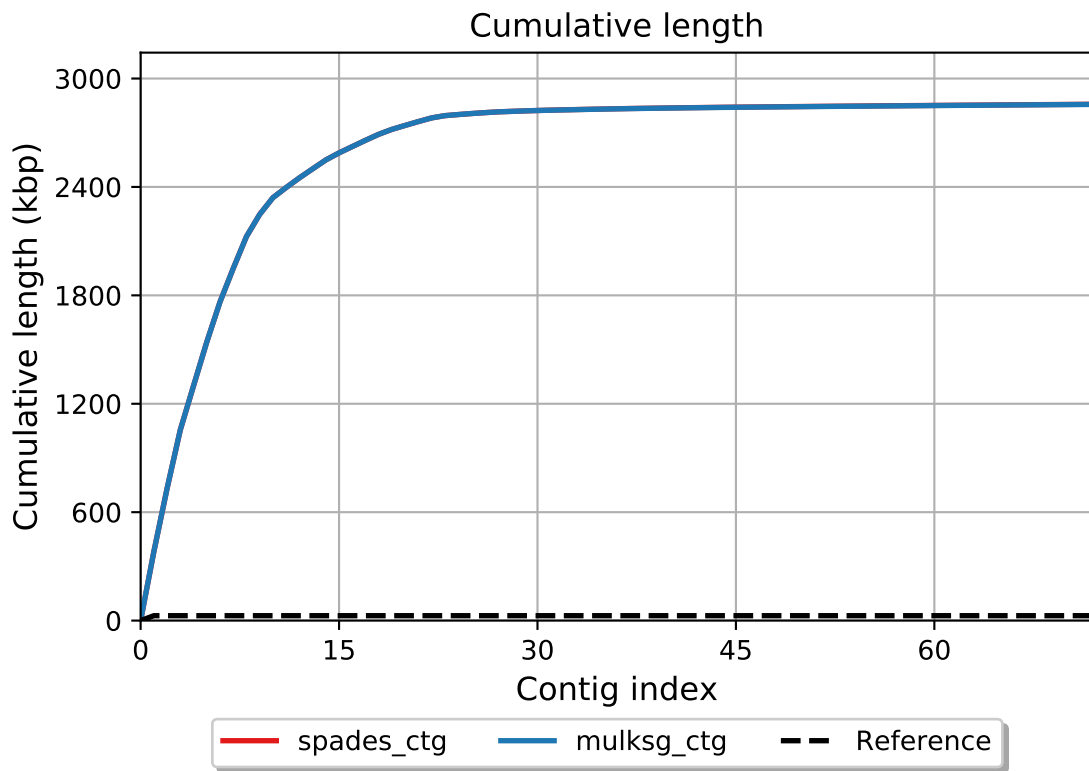
	spades_ctg	mulks_g_ctg
# fully unaligned contigs	70	70
Fully unaligned length	2448780	2447979
# partially unaligned contigs	2	2
Partially unaligned length	399315	399315
# N's	0	0

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).

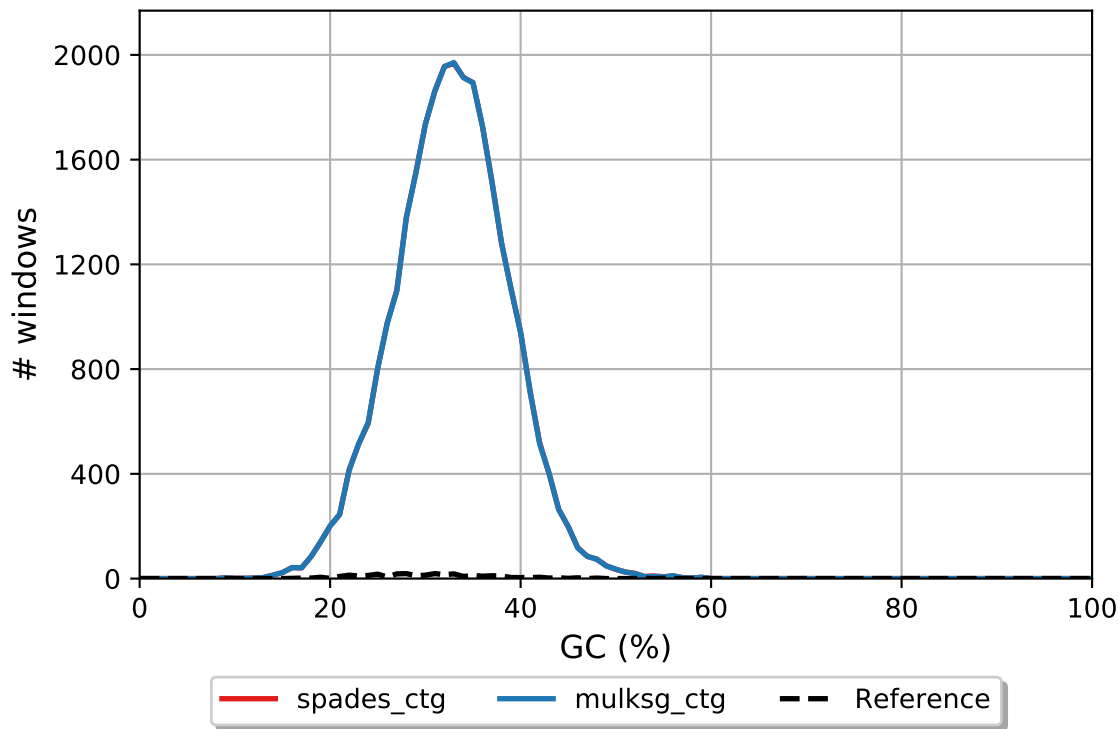


# NGx

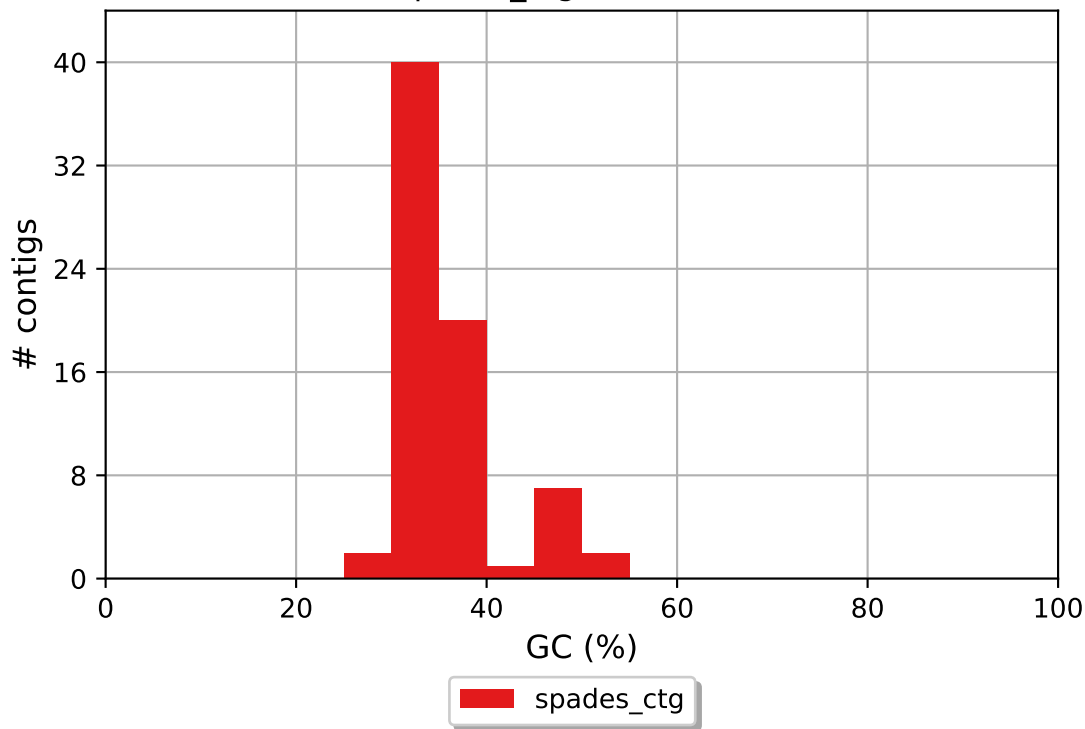




GC content

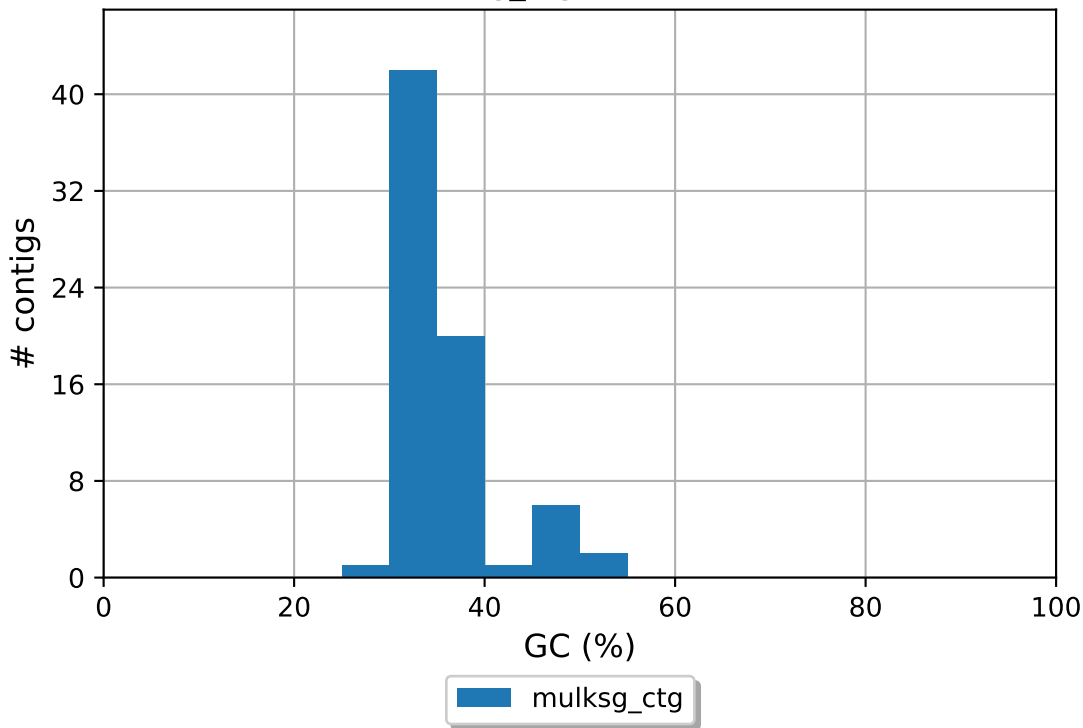


spades\_ctg GC content

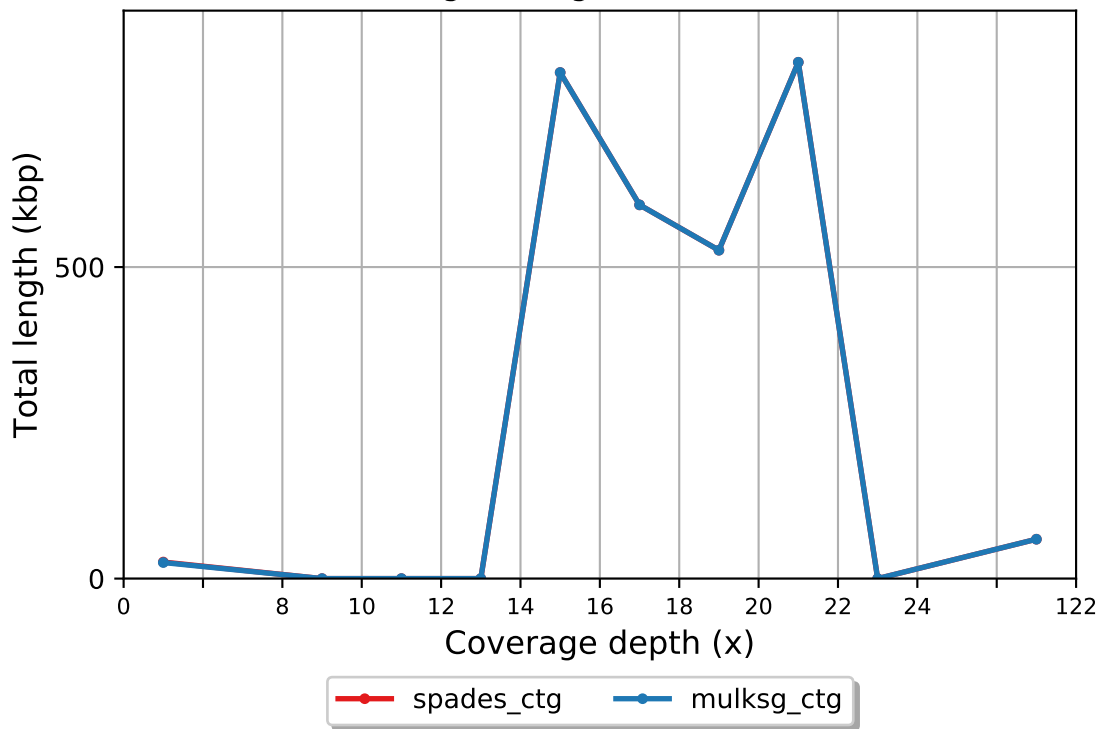




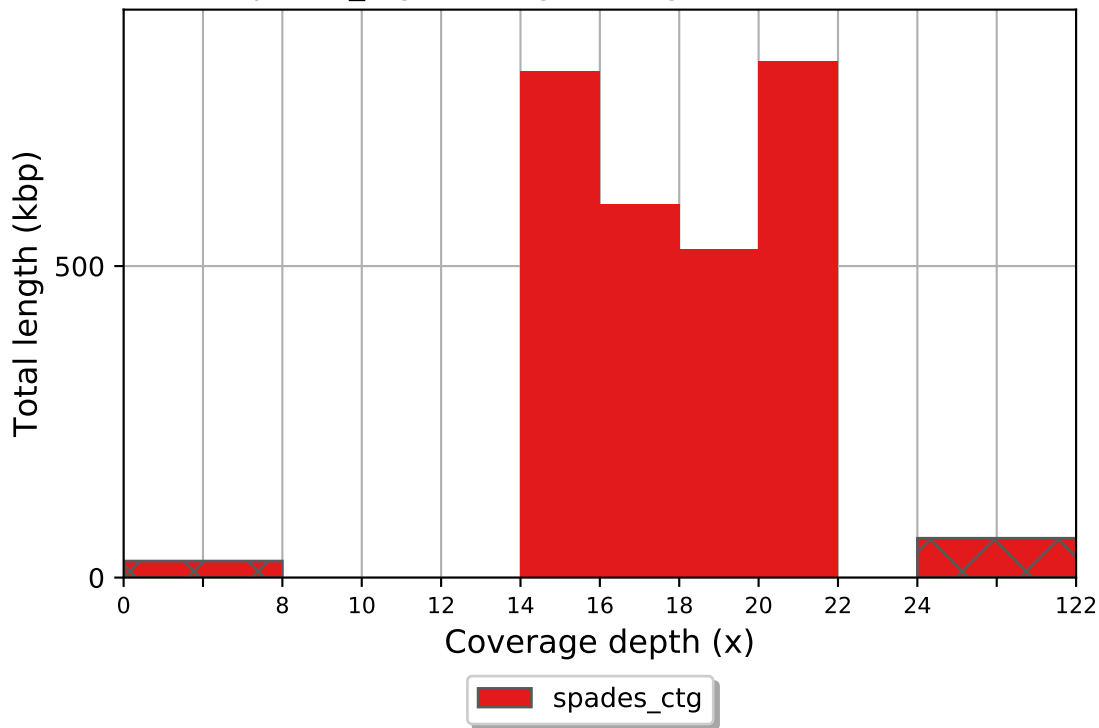
mulksg\_ctg GC content



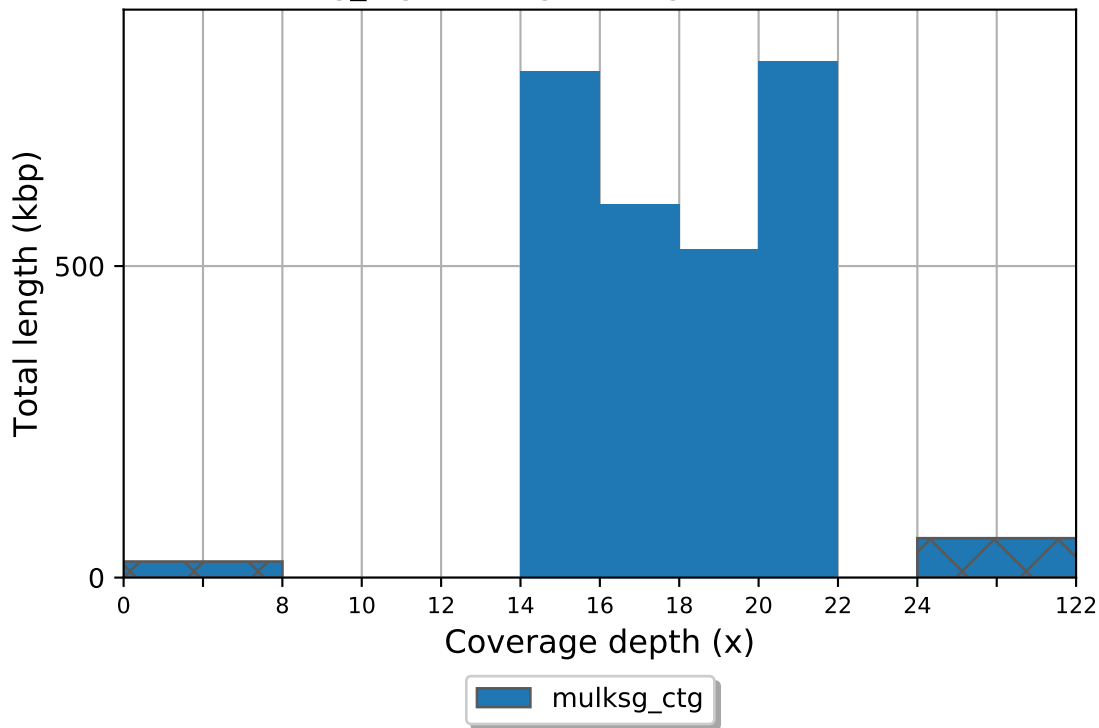
Coverage histogram (bin size: 2x)



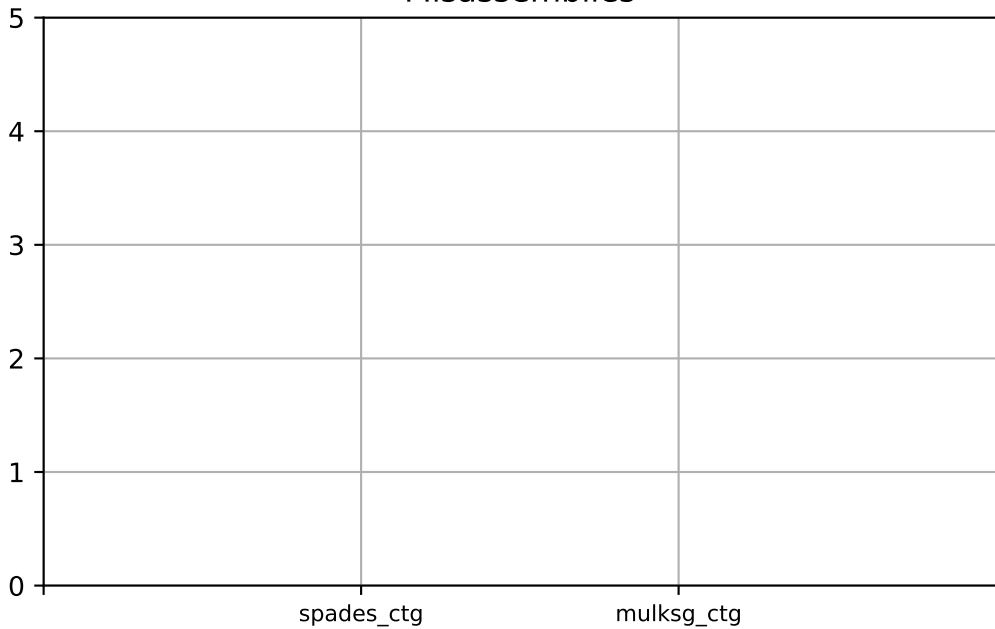
spades\_ctg coverage histogram (bin size: 2x)



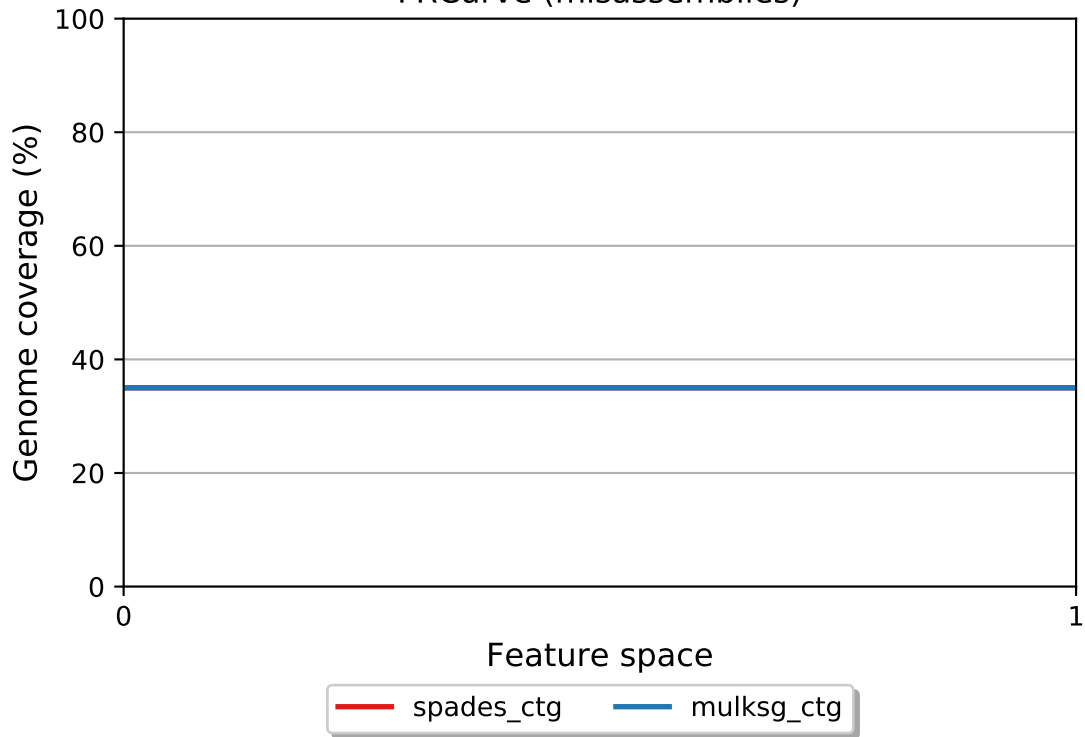
mulksg\_ctg coverage histogram (bin size: 2x)



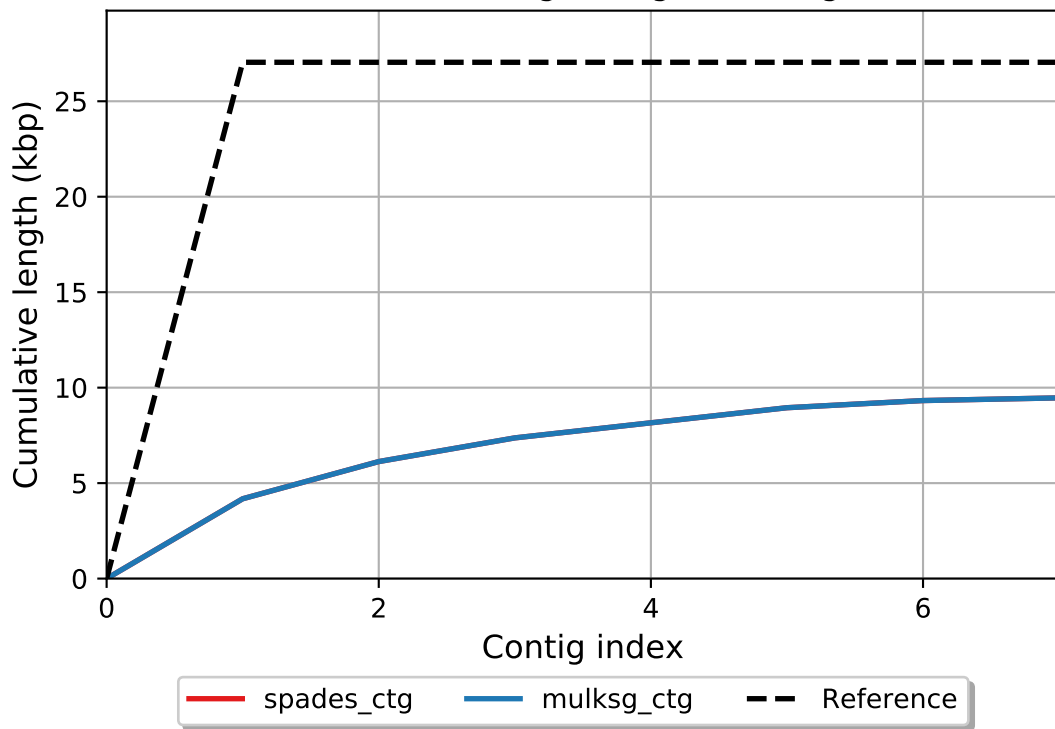
## Misassemblies



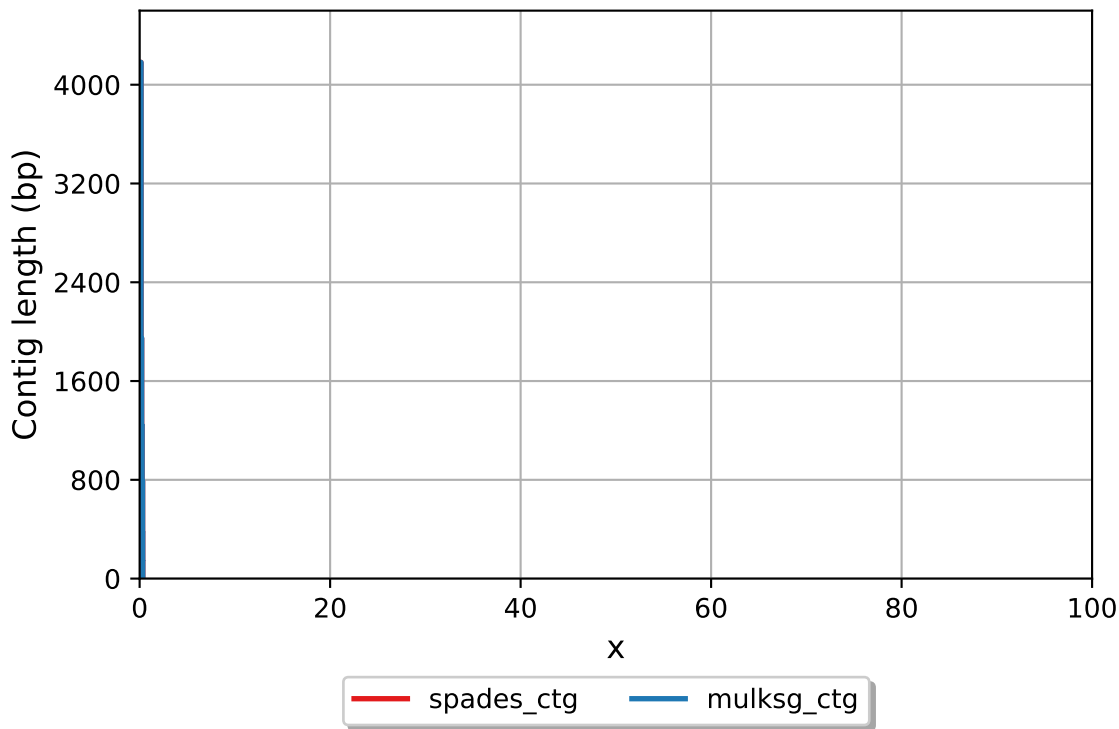
FRCurve (misassemblies)



Cumulative length (aligned contigs)

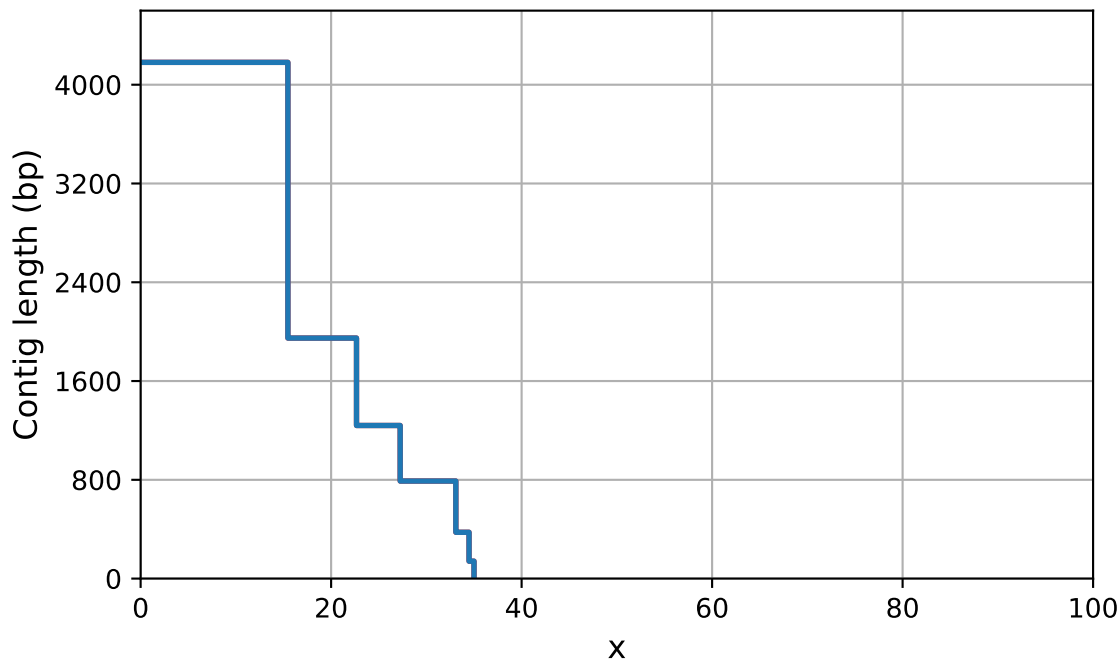


NAx



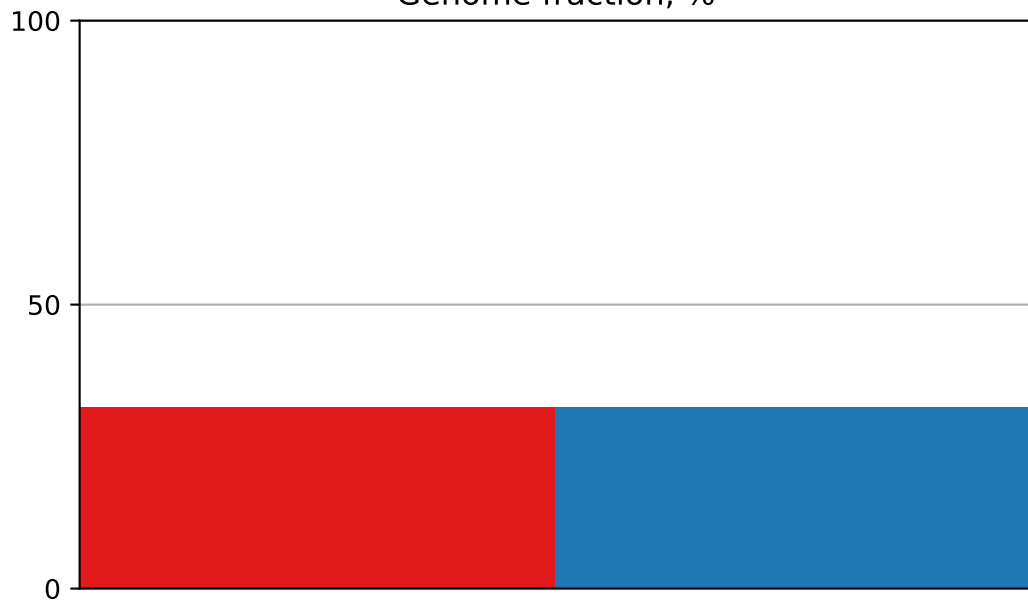


# NGAx



spades\_ctg   mulksg\_ctg

Genome fraction, %



spades\_ctg



mulksg\_ctg