

## Report

	spades_ctg	mulksq_ctg
# contigs (>= 0 bp)	307	306
# contigs (>= 1000 bp)	100	99
# contigs (>= 5000 bp)	72	71
# contigs (>= 10000 bp)	62	62
# contigs (>= 25000 bp)	45	45
# contigs (>= 50000 bp)	35	35
Total length (>= 0 bp)	4943886	4943178
Total length (>= 1000 bp)	4899693	4898975
Total length (>= 5000 bp)	4835222	4834504
Total length (>= 10000 bp)	4767327	4772371
Total length (>= 25000 bp)	4477799	4482843
Total length (>= 50000 bp)	4110124	4110124
# contigs	115	114
Largest contig	312314	312314
Total length	4909817	4909099
Reference length	4967469	4967469
GC (%)	65.10	65.10
Reference GC (%)	64.92	64.92
N50	117399	117399
NG50	117399	117399
N75	66058	66058
NG75	63515	63515
L50	15	15
LG50	15	15
L75	28	28
LG75	29	29
# misassemblies	36	37
# misassembled contigs	17	18
Misassembled contigs length	2455242	2496606
# local misassemblies	479	487
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	26	25
# unaligned contigs	51 + 58 part	51 + 58 part
Unaligned length	2241032	2240841
Genome fraction (%)	53.670	53.670
Duplication ratio	1.001	1.001
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	4206.37	4210.79
# indels per 100 kbp	51.31	51.39
Largest alignment	93507	93507
Total aligned length	2666668	2666672
NA50	1902	1956
NGA50	1733	1820
LA50	177	170
LGA50	192	185

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

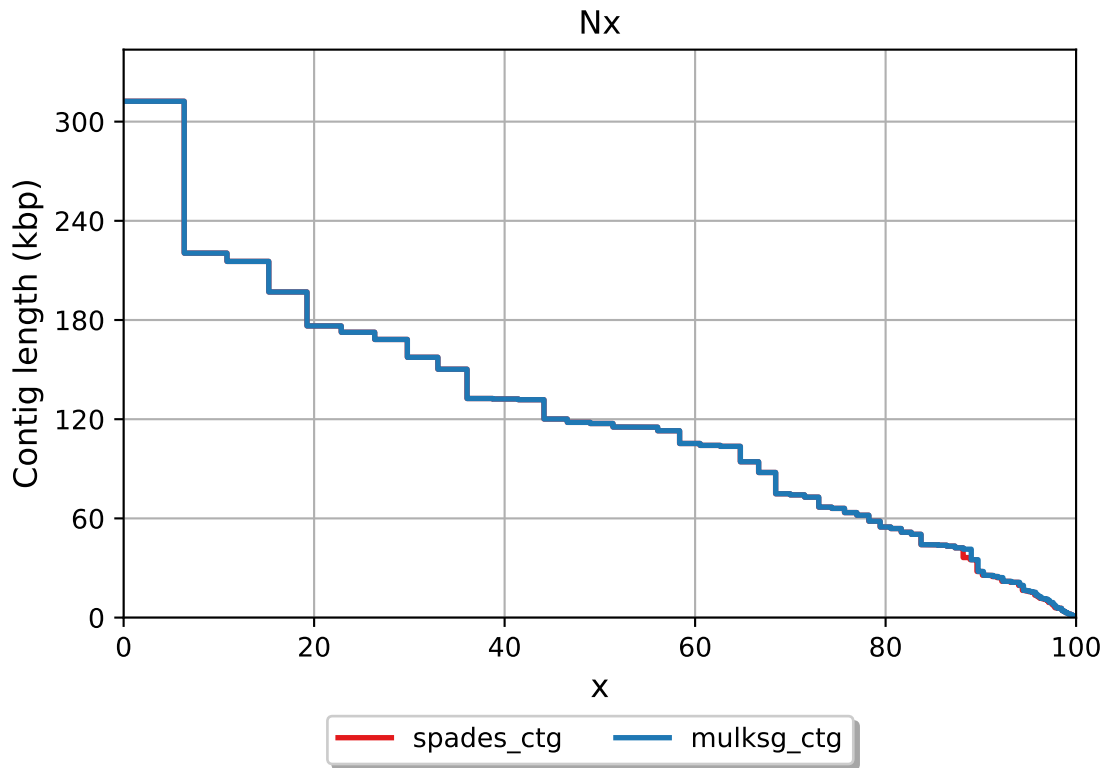
	spades_ctg	mulksq_ctg
# misassemblies	36	37
# contig misassemblies	36	37
# c. relocations	36	37
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	17	18
Misassembled contigs length	2455242	2496606
# local misassemblies	479	487
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	26	25
# mismatches	112143	112261
# indels	1368	1370
# indels (<= 5 bp)	1232	1234
# indels (> 5 bp)	136	136
Indels length	3804	3810

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).

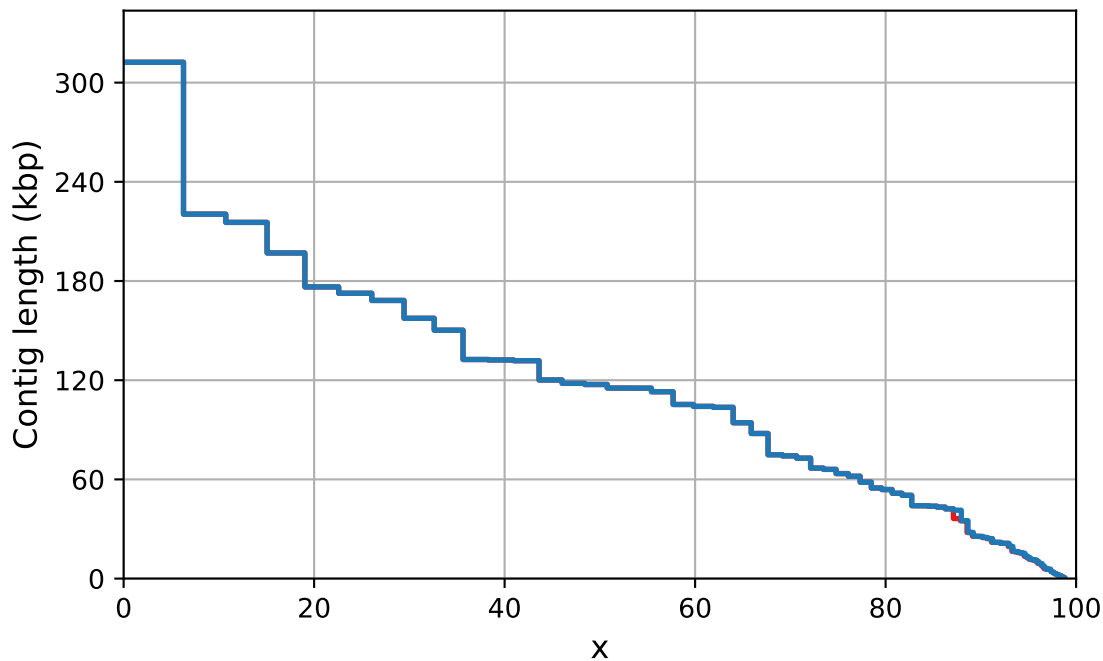
## Unaligned report

	spades_ctg	mulks_g_ctg
# fully unaligned contigs	51	51
Fully unaligned length	157831	157831
# partially unaligned contigs	58	58
Partially unaligned length	2083201	2083010
# 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).

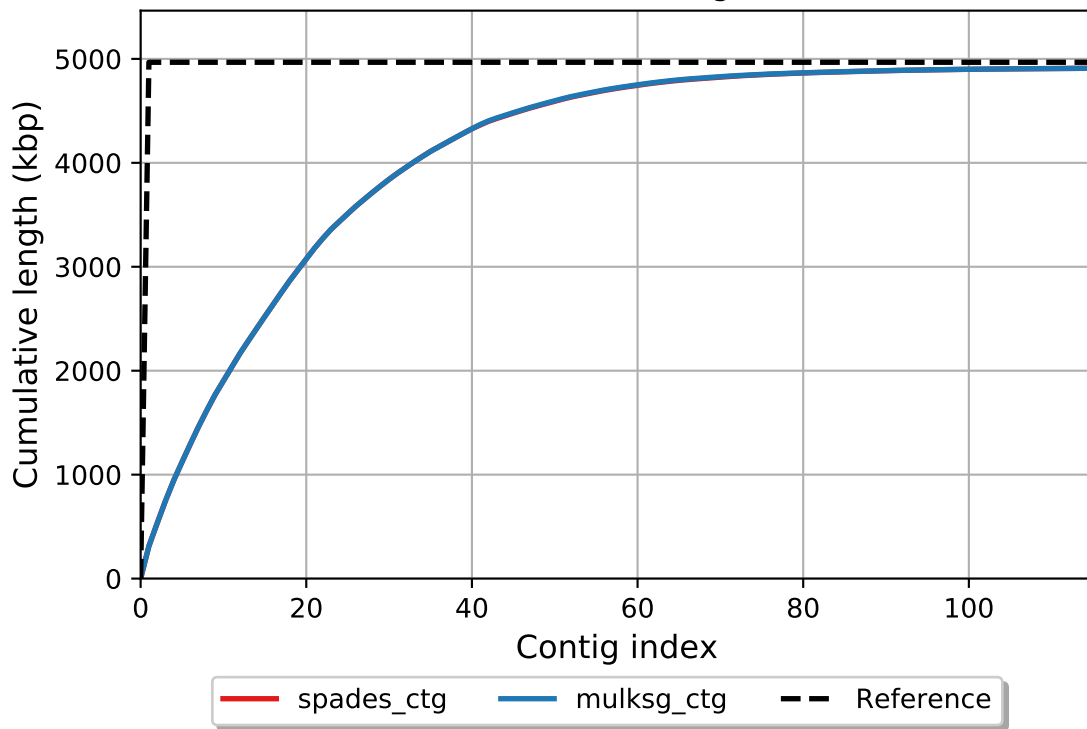


## NGx

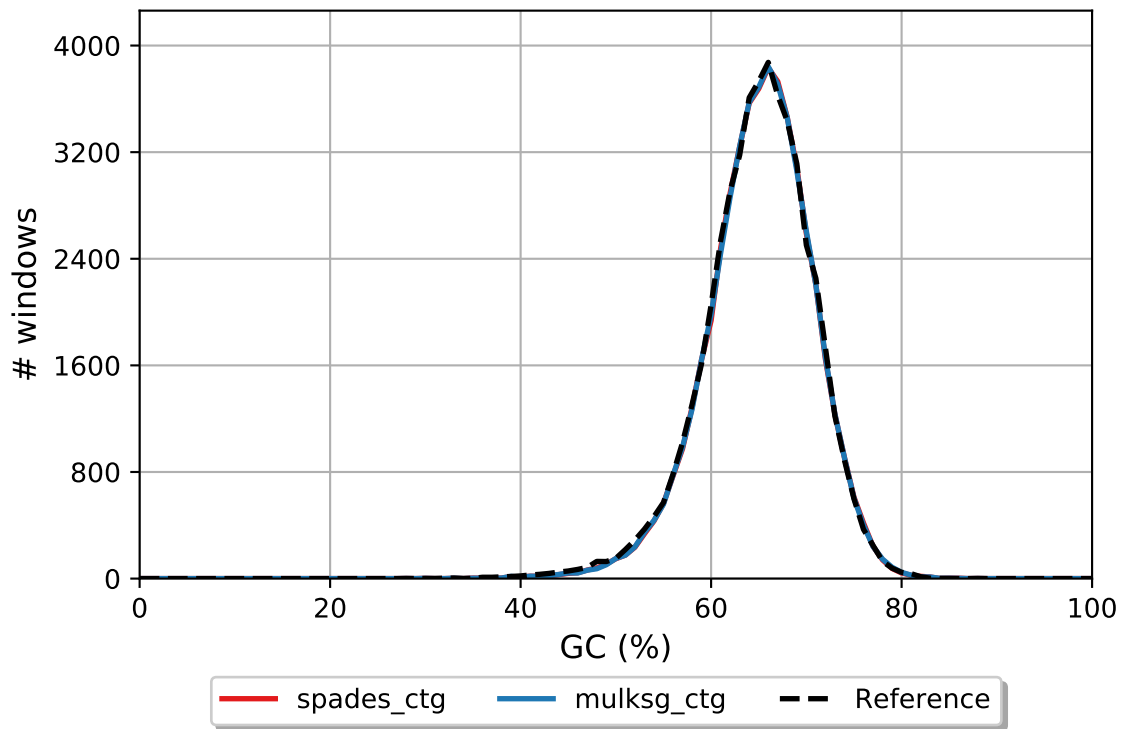


spades\_ctg   mulksg\_ctg

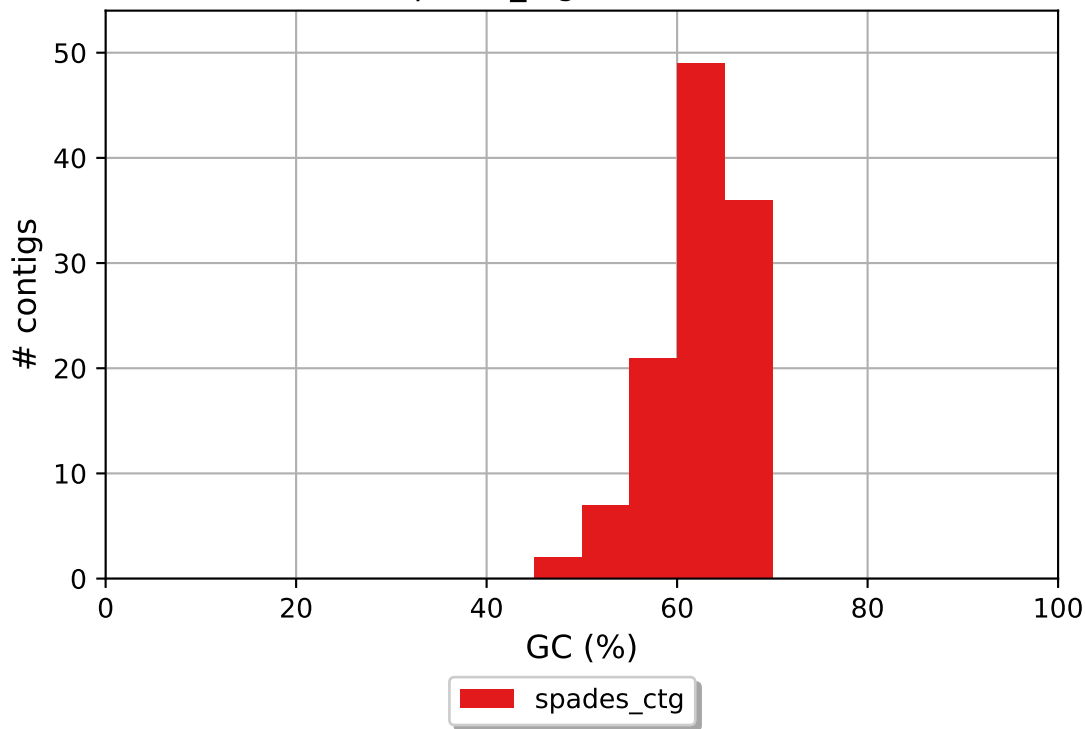
Cumulative length



GC content

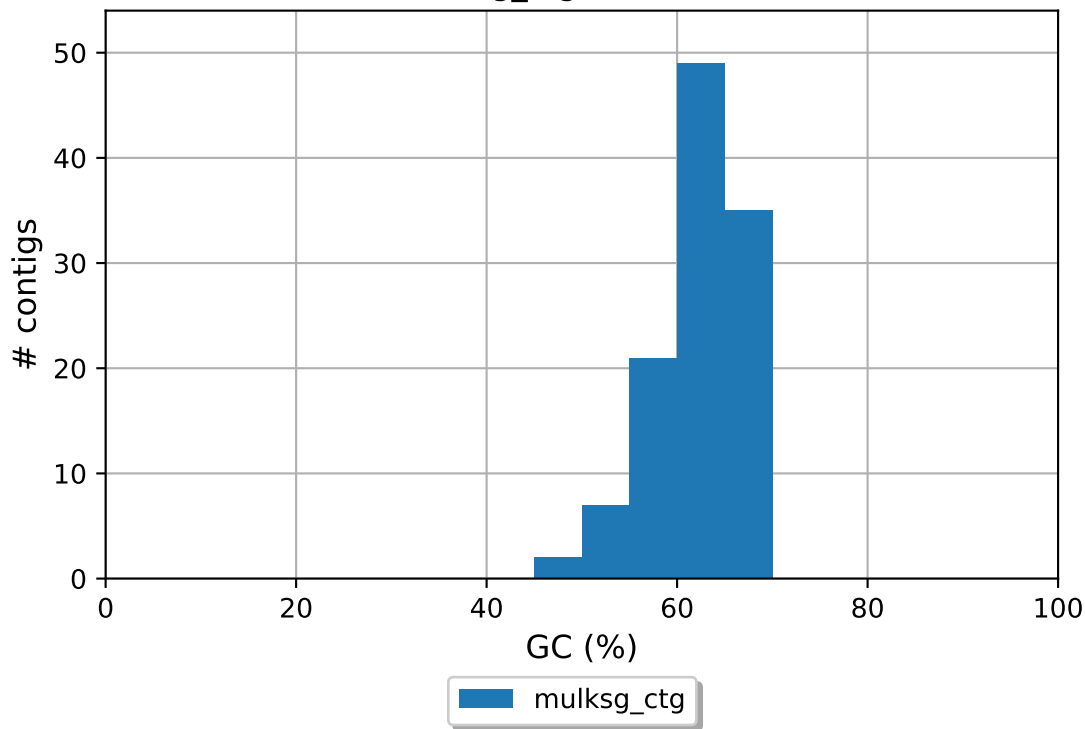


spades\_ctg GC content

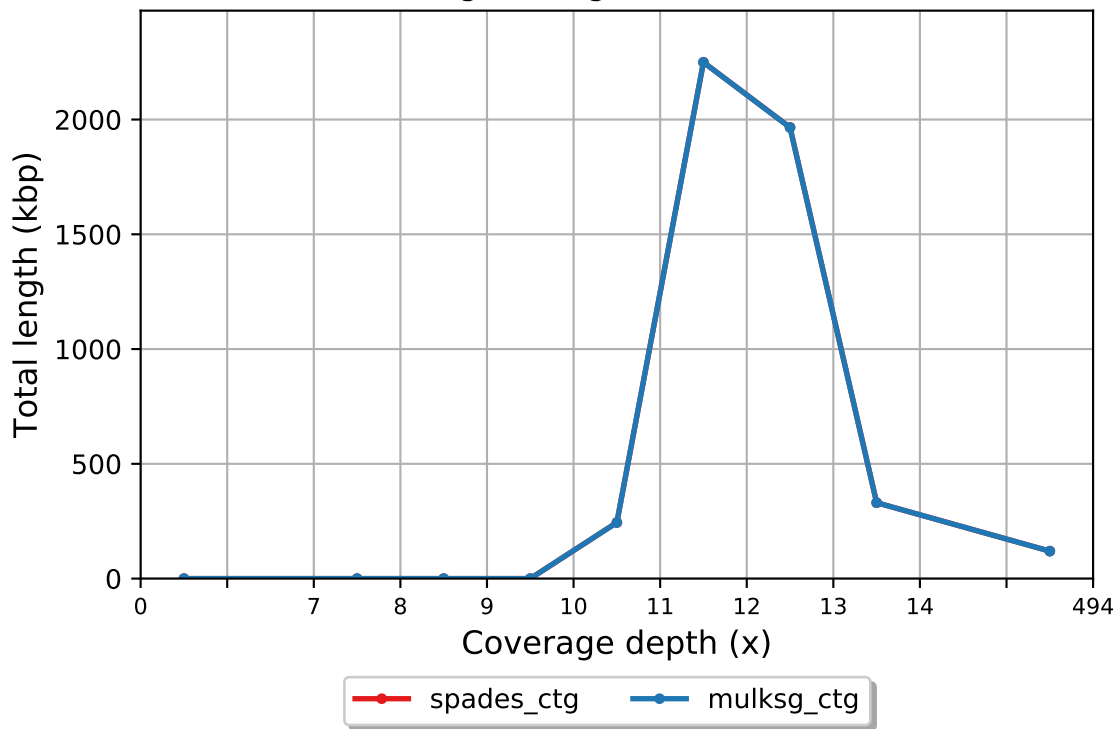




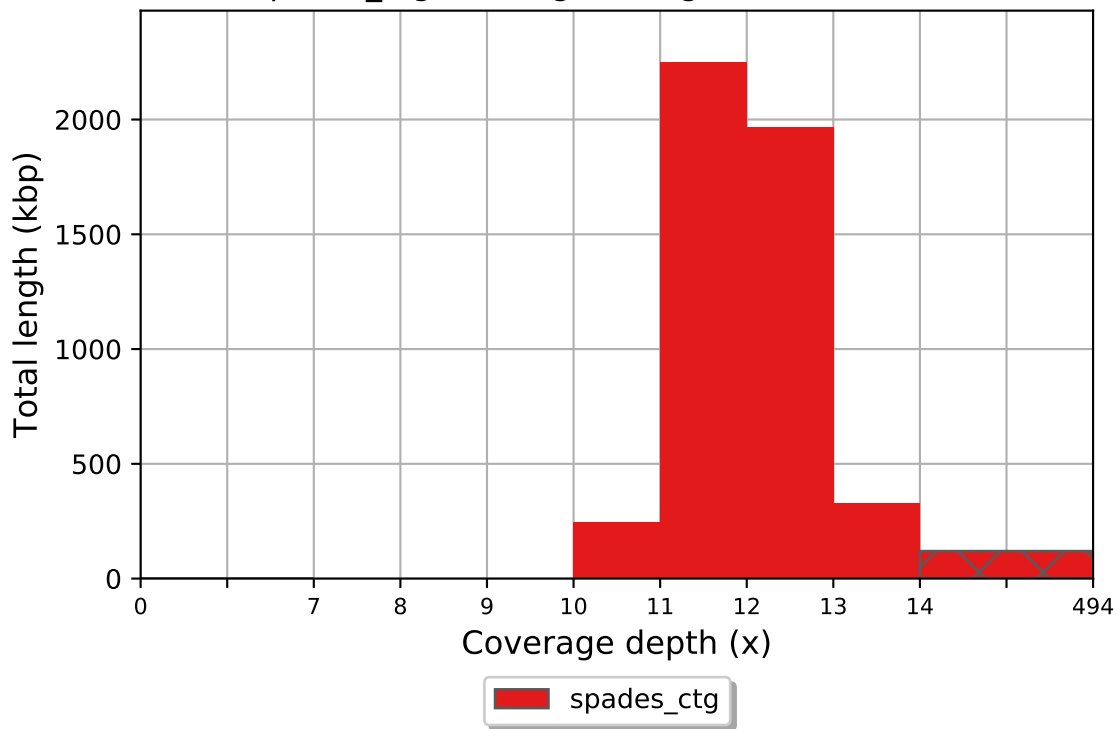
mulksg\_ctg GC content



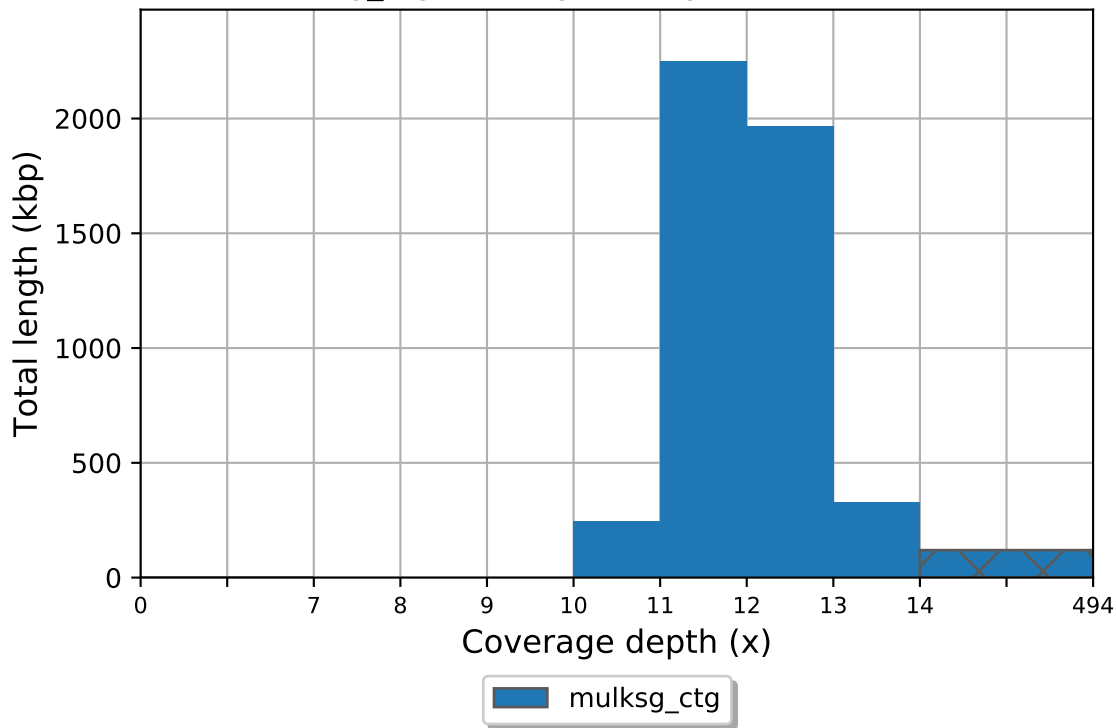
Coverage histogram (bin size: 1x)



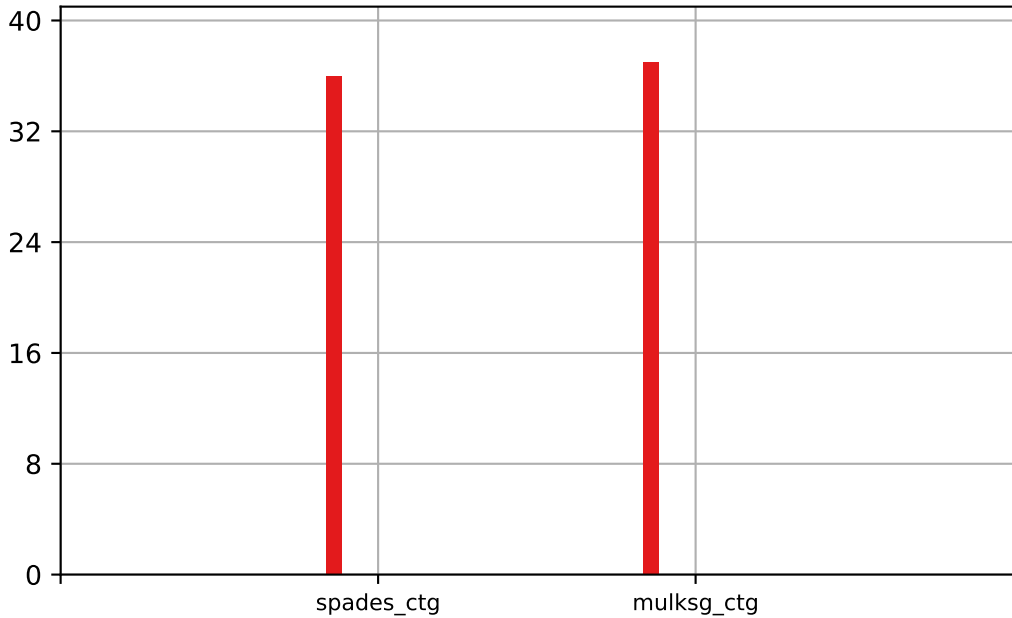
spades\_ctg coverage histogram (bin size: 1x)



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

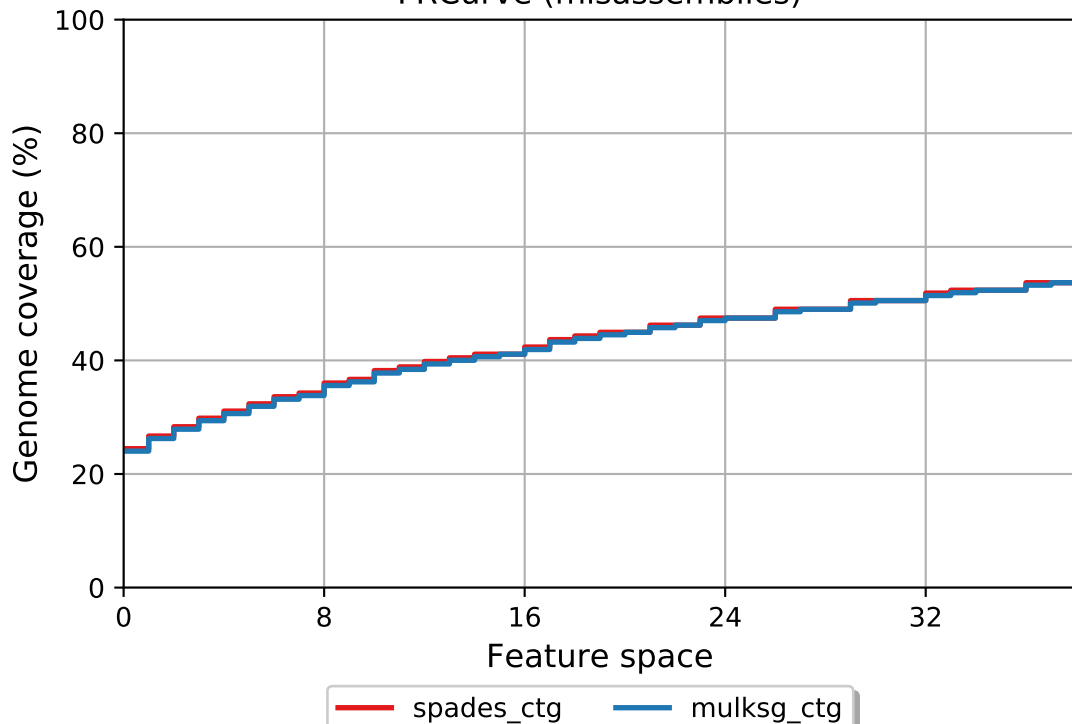


## Misassemblies

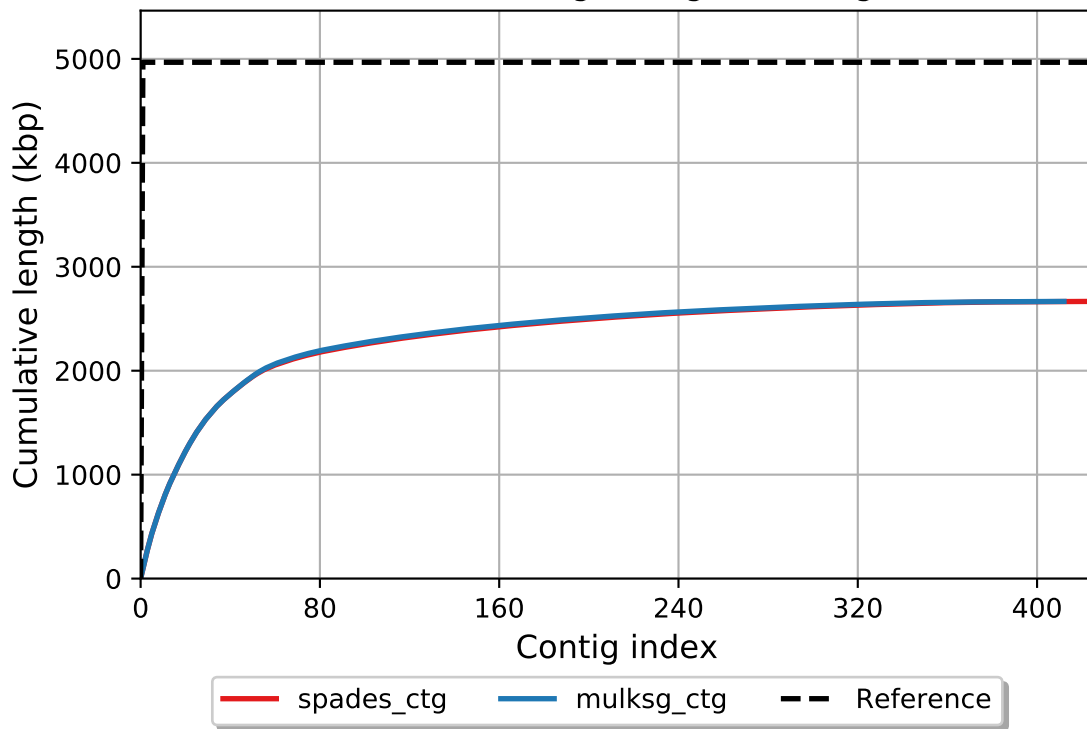


 # relocations

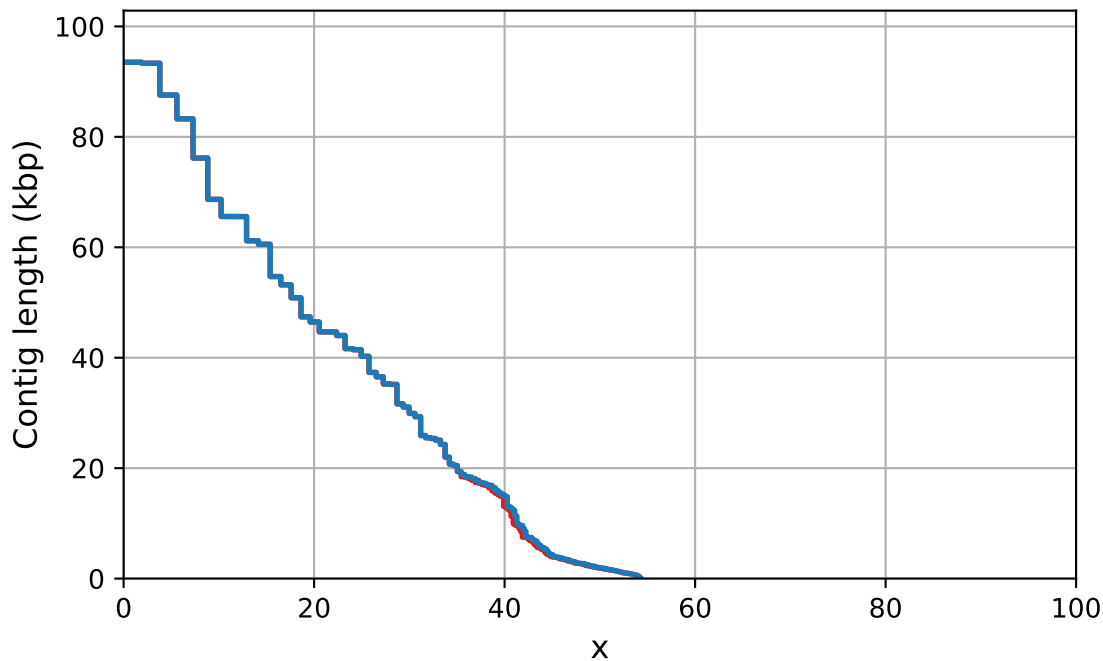
FRCurve (misassemblies)



Cumulative length (aligned contigs)



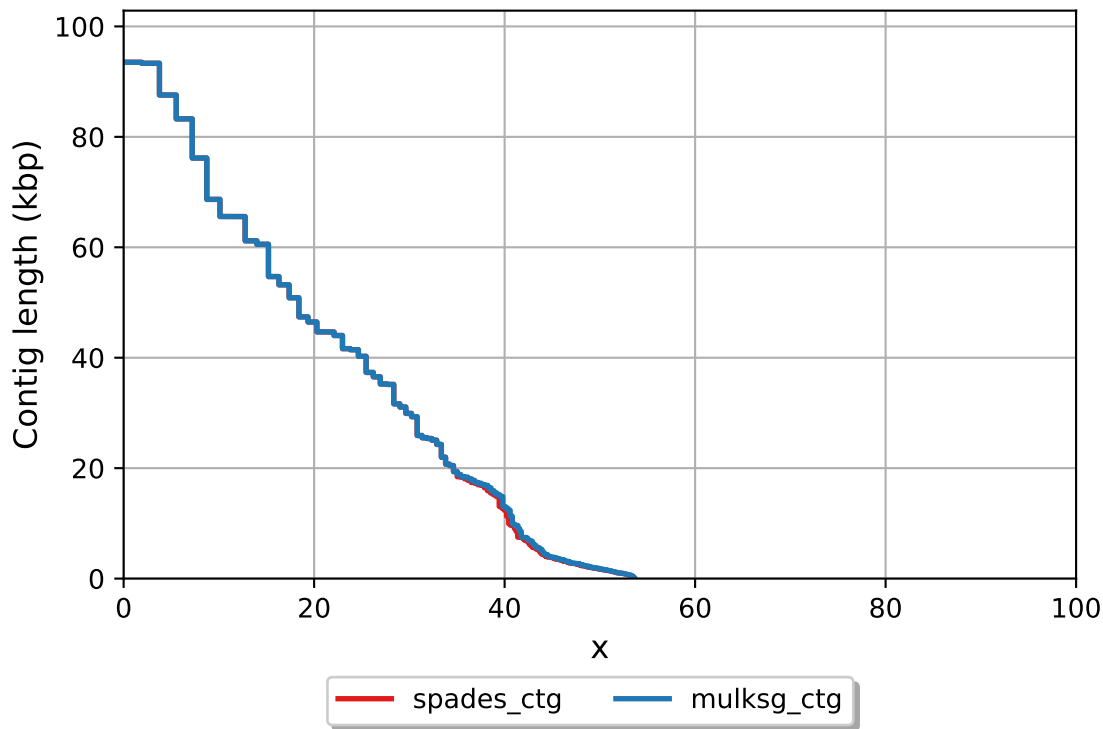
NAx



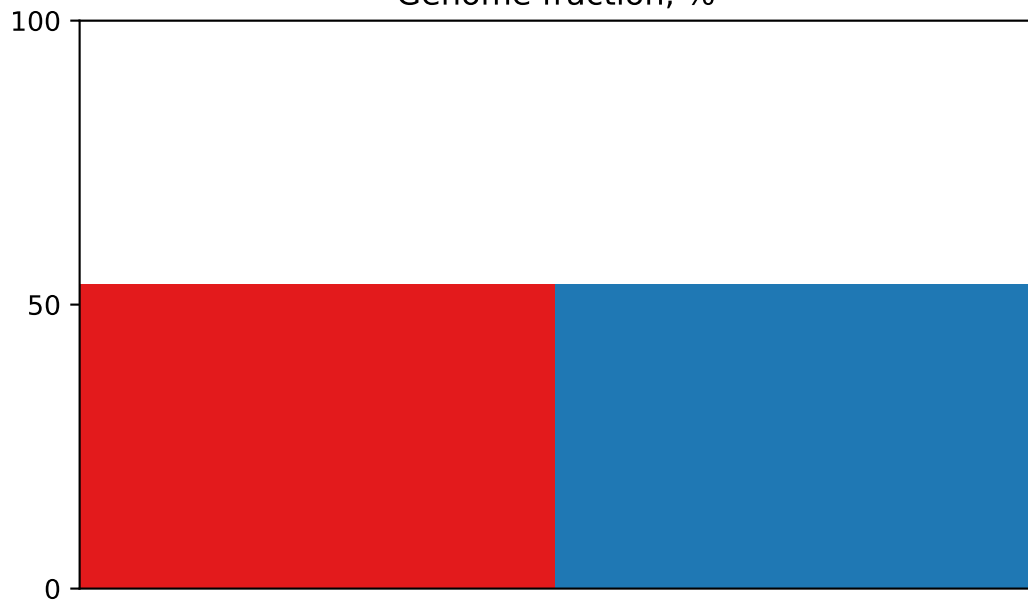
spades\_ctg mulks\_g\_ctg



# NGAx



Genome fraction, %



spades\_ctg



mulksg\_ctg