

## Report

	spades_ctg	mulksq_ctg
# contigs (>= 0 bp)	1492	1840
# contigs (>= 1000 bp)	95	95
# contigs (>= 5000 bp)	53	53
# contigs (>= 10000 bp)	47	47
# contigs (>= 25000 bp)	40	40
# contigs (>= 50000 bp)	31	31
Total length (>= 0 bp)	5729346	5840711
Total length (>= 1000 bp)	5285055	5285194
Total length (>= 5000 bp)	5195684	5195684
Total length (>= 10000 bp)	5153756	5153756
Total length (>= 25000 bp)	5055953	5055953
Total length (>= 50000 bp)	4767400	4767400
# contigs	177	187
Largest contig	639080	639080
Total length	5337364	5343981
Reference length	5373121	5373121
GC (%)	43.40	43.40
Reference GC (%)	43.42	43.42
N50	157629	157629
NG50	157629	157629
N75	86927	86927
NG75	86927	86927
L50	9	9
LG50	9	9
L75	20	20
LG75	20	20
# misassemblies	98	98
# misassembled contigs	25	25
Misassembled contigs length	4146068	4146068
# local misassemblies	55	55
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	3	3
# unaligned contigs	123 + 41 part	134 + 40 part
Unaligned length	1018305	1025010
Genome fraction (%)	80.292	80.292
Duplication ratio	1.001	1.001
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	649.35	649.32
# indels per 100 kbp	20.17	20.17
Largest alignment	189113	189113
Total aligned length	4315940	4315852
NA50	44793	44793
NGA50	44793	44793
NA75	14269	13503
NGA75	13436	13436
LA50	35	35
LGA50	35	35
LA75	84	85
LGA75	86	86

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

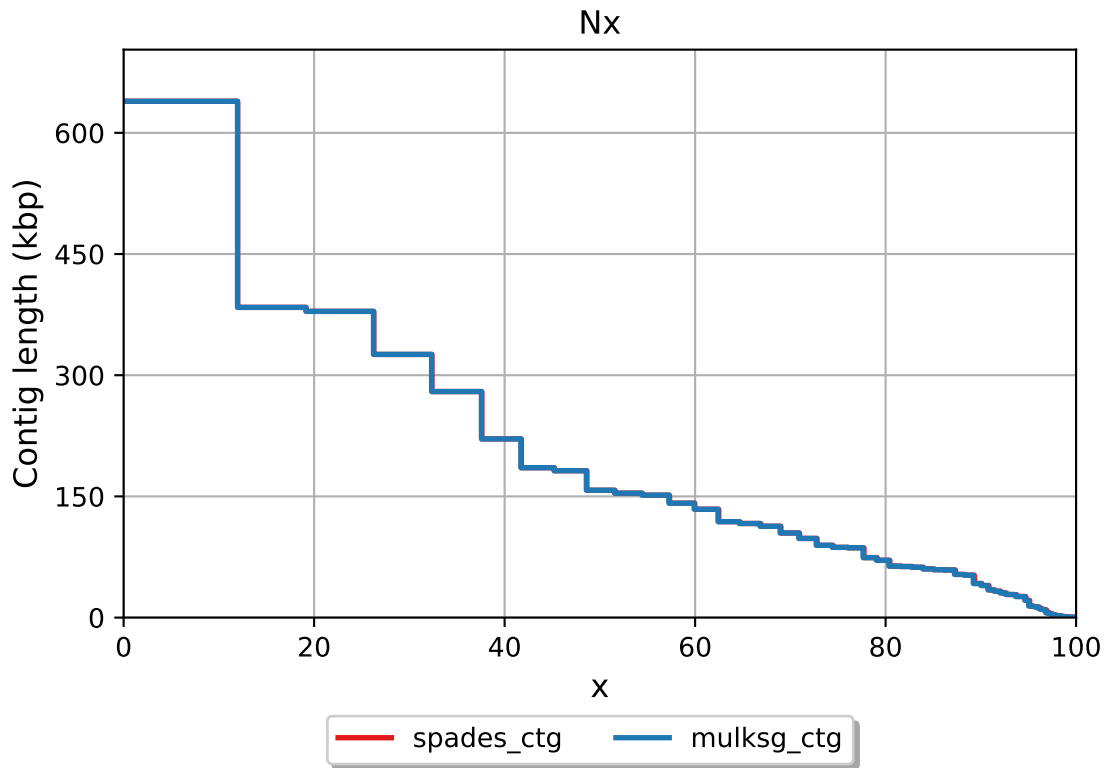
	spades_ctg	mulksg_ctg
# misassemblies	98	98
# contig misassemblies	98	98
# c. relocations	97	97
# c. translocations	0	0
# c. inversions	1	1
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	25	25
Misassembled contigs length	4146068	4146068
# local misassemblies	55	55
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	3	3
# mismatches	28014	28013
# indels	870	870
# indels (<= 5 bp)	744	744
# indels (> 5 bp)	126	126
Indels length	3753	3753

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).

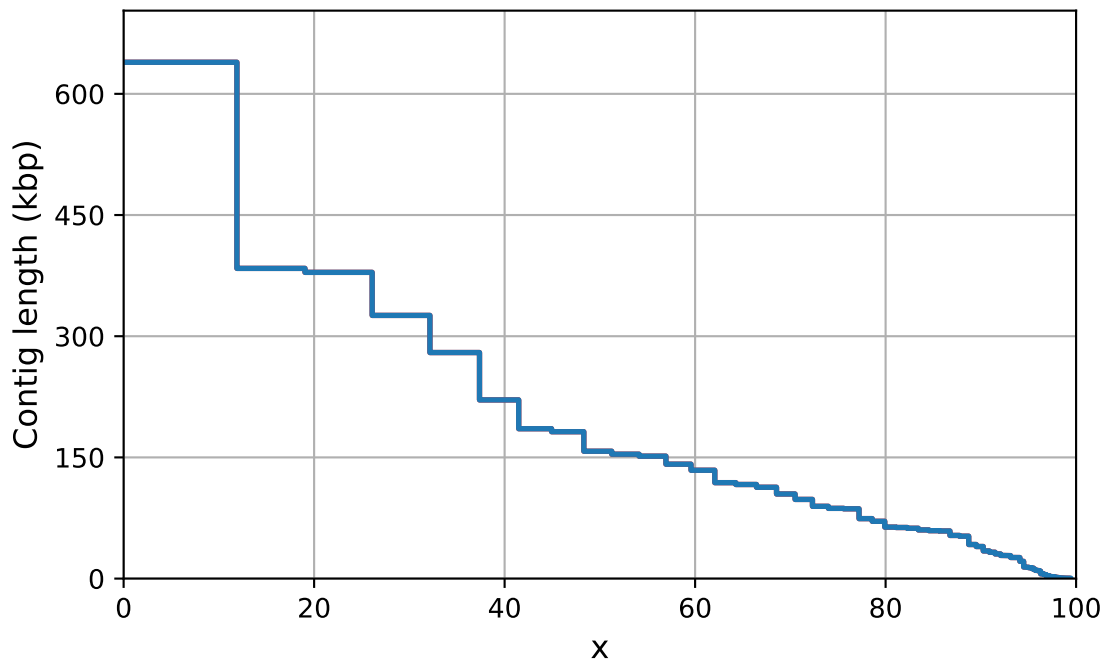
## Unaligned report

	spades_ctg	mulks_g_ctg
# fully unaligned contigs	123	134
Fully unaligned length	288246	299009
# partially unaligned contigs	41	40
Partially unaligned length	730059	726001
# N's	0	0

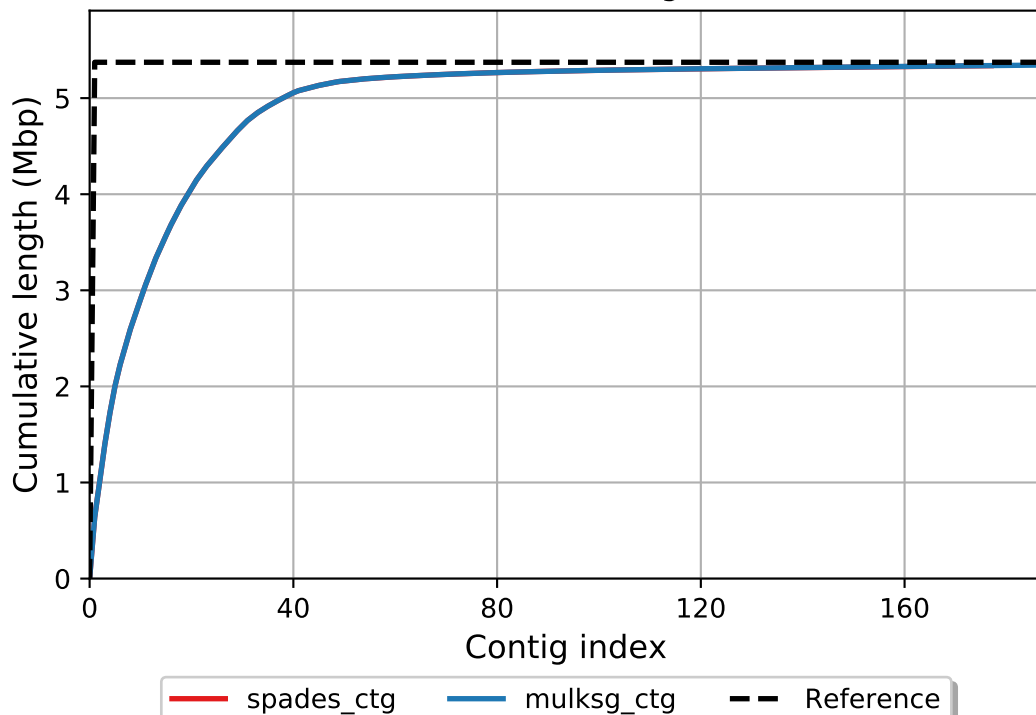
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



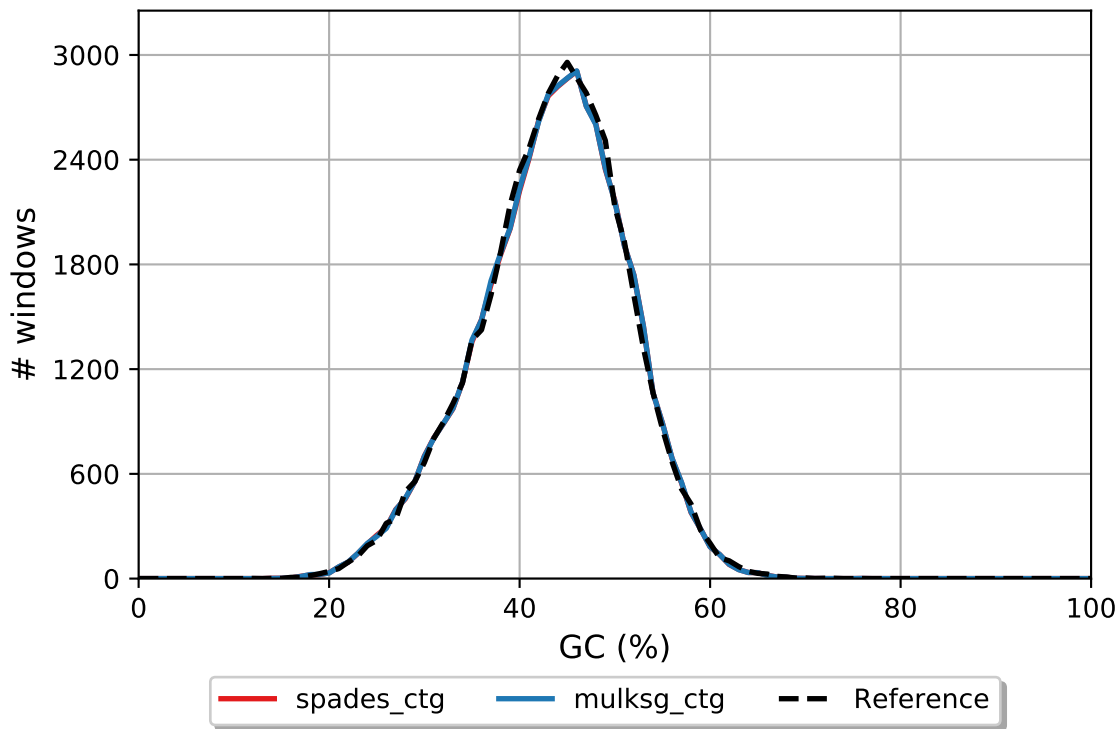
# NGx



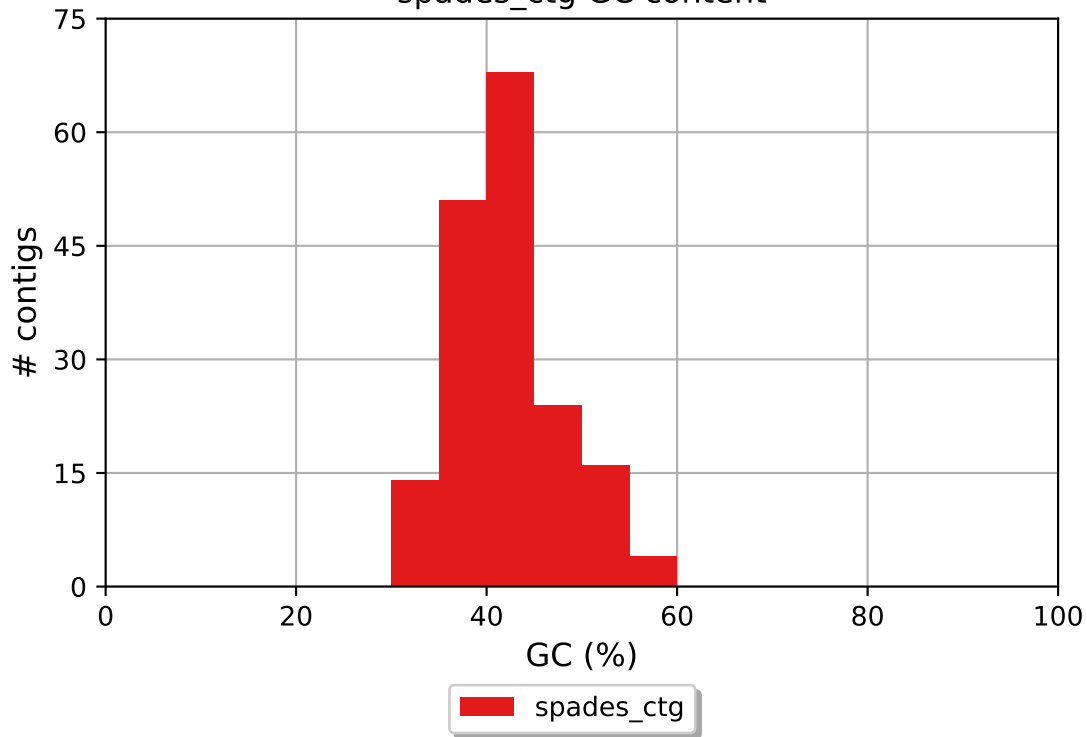
Cumulative length



GC content

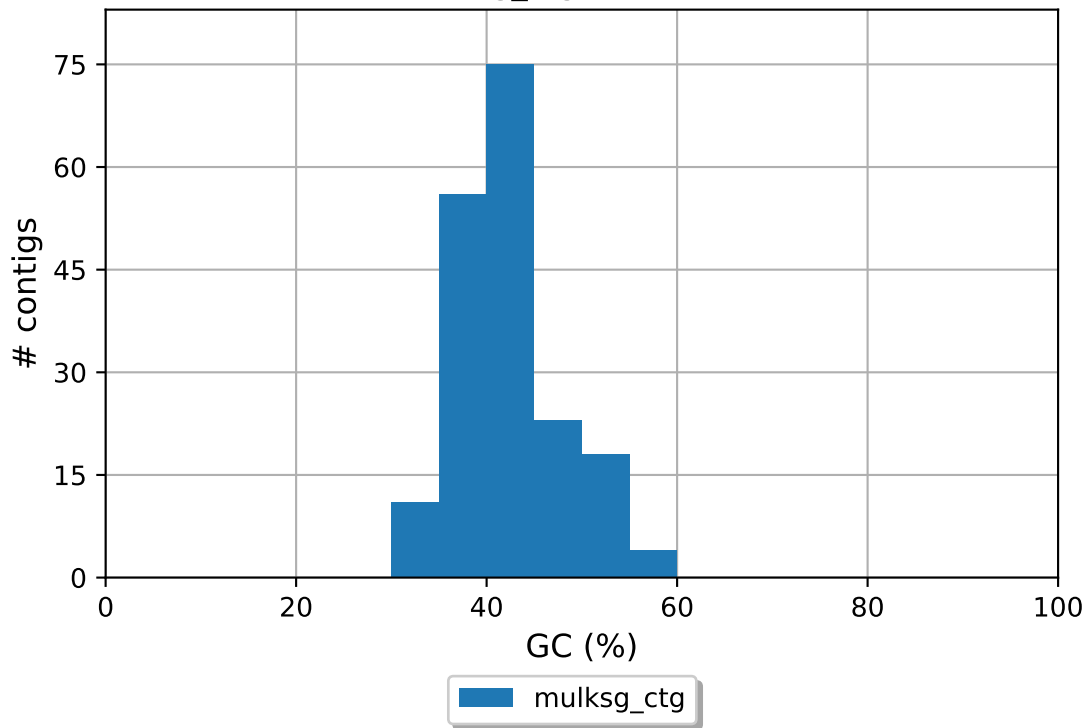


spades\_ctg GC content

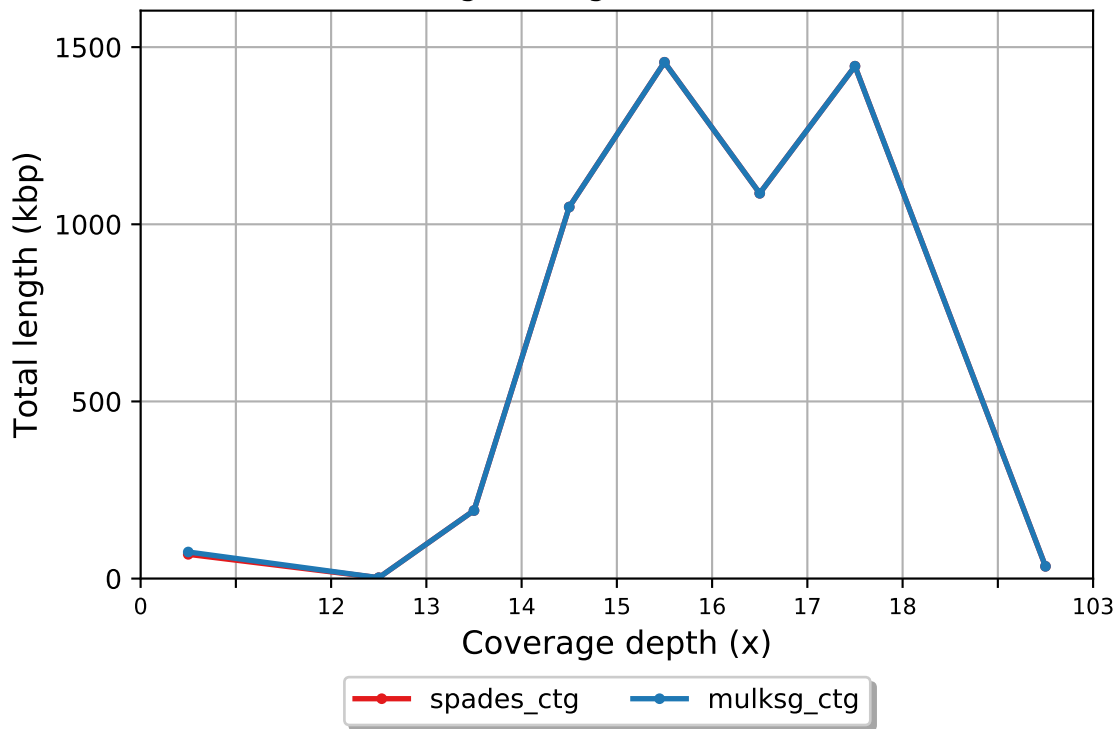




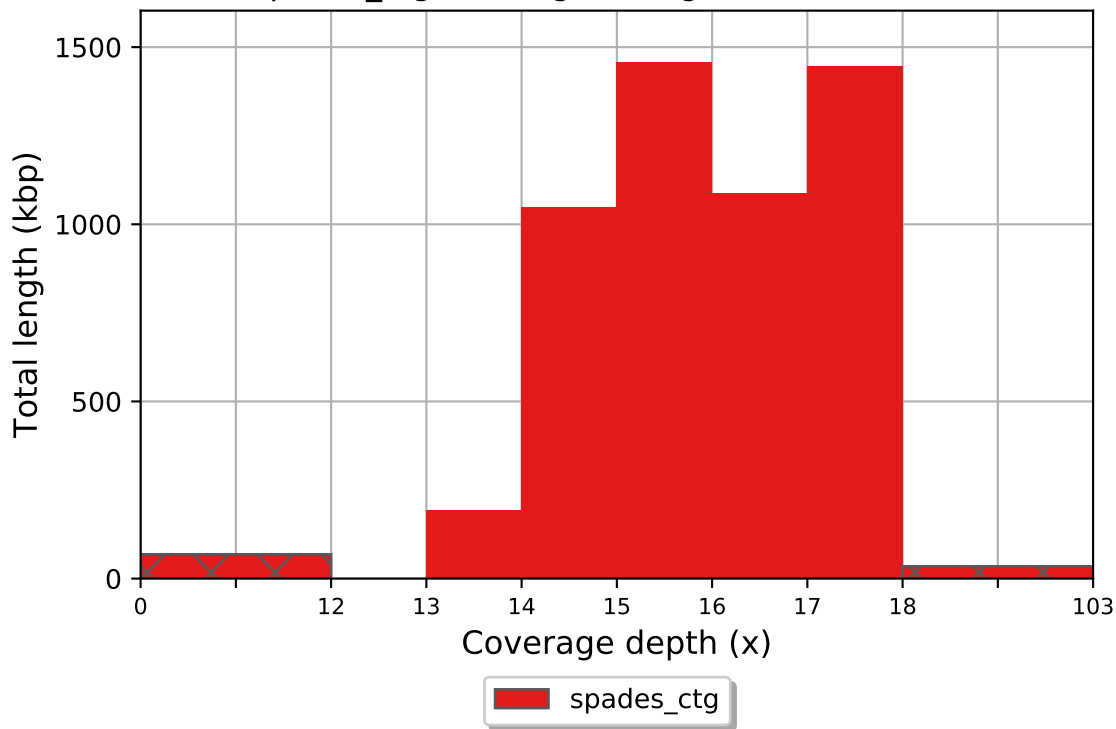
mulksg\_ctg GC content



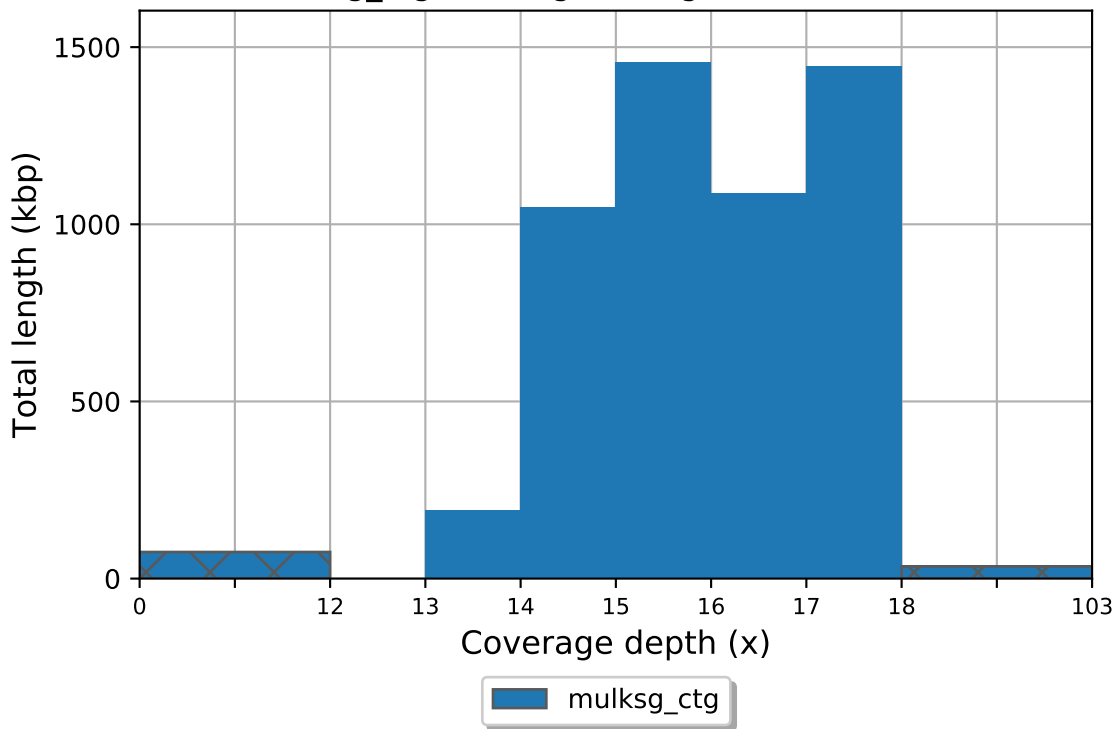
Coverage histogram (bin size: 1x)



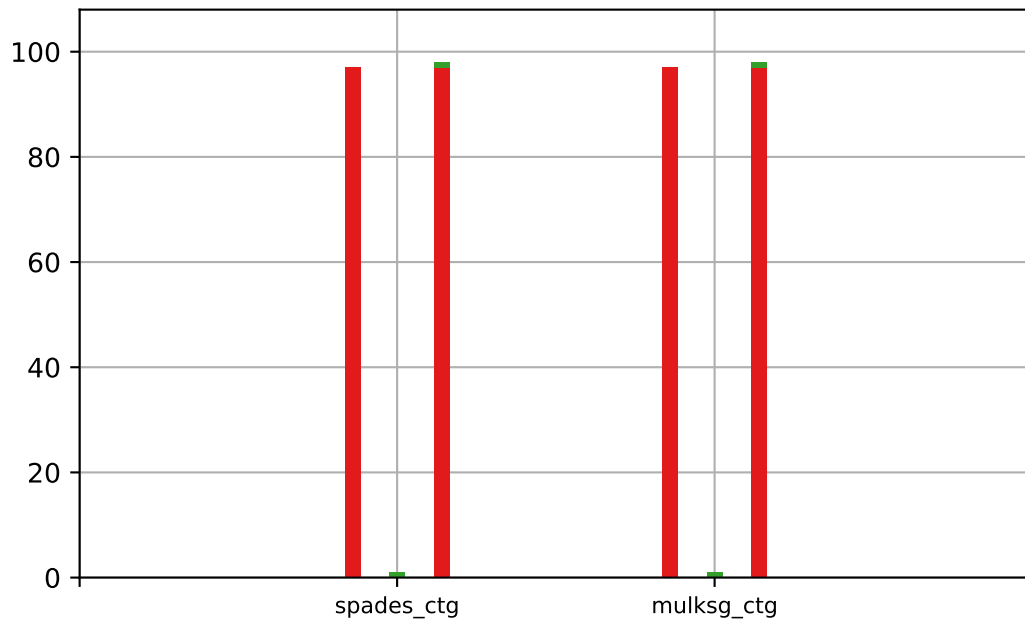
spades\_ctg coverage histogram (bin size: 1x)



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



## Misassemblies

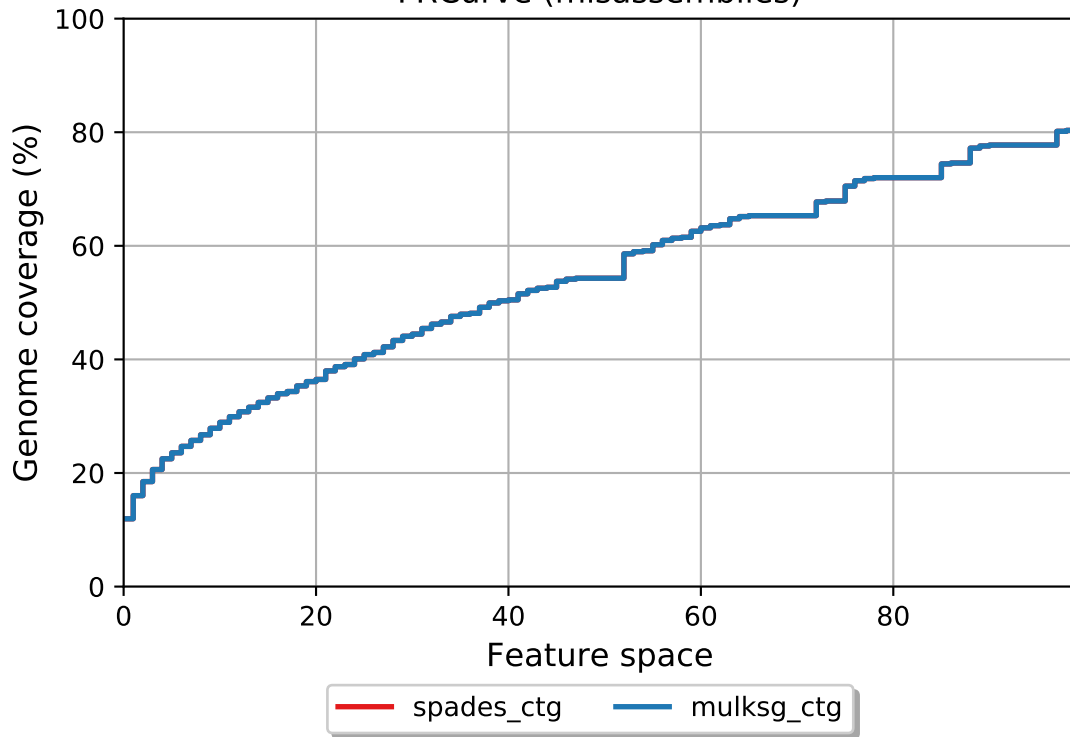


# relocations

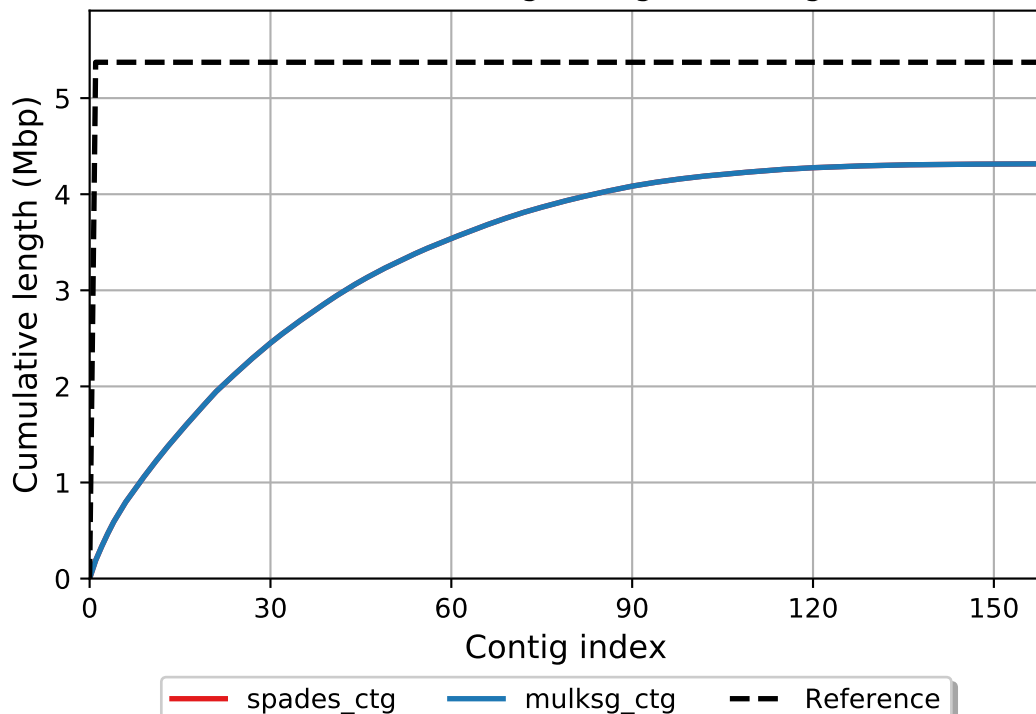


# inversions

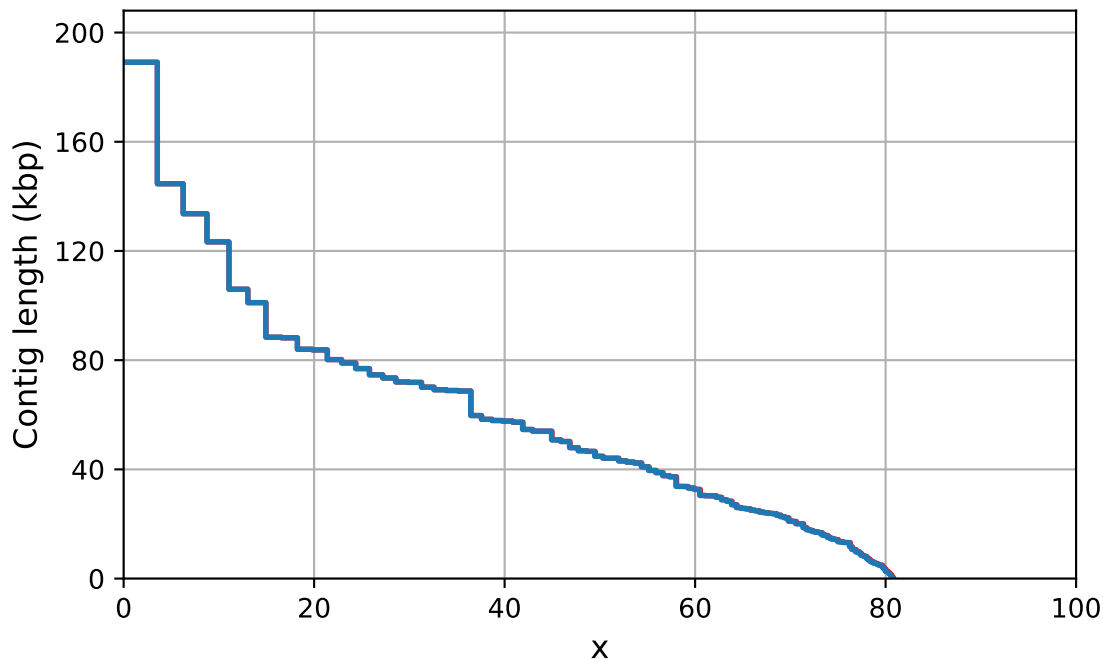
FRCurve (misassemblies)



Cumulative length (aligned contigs)



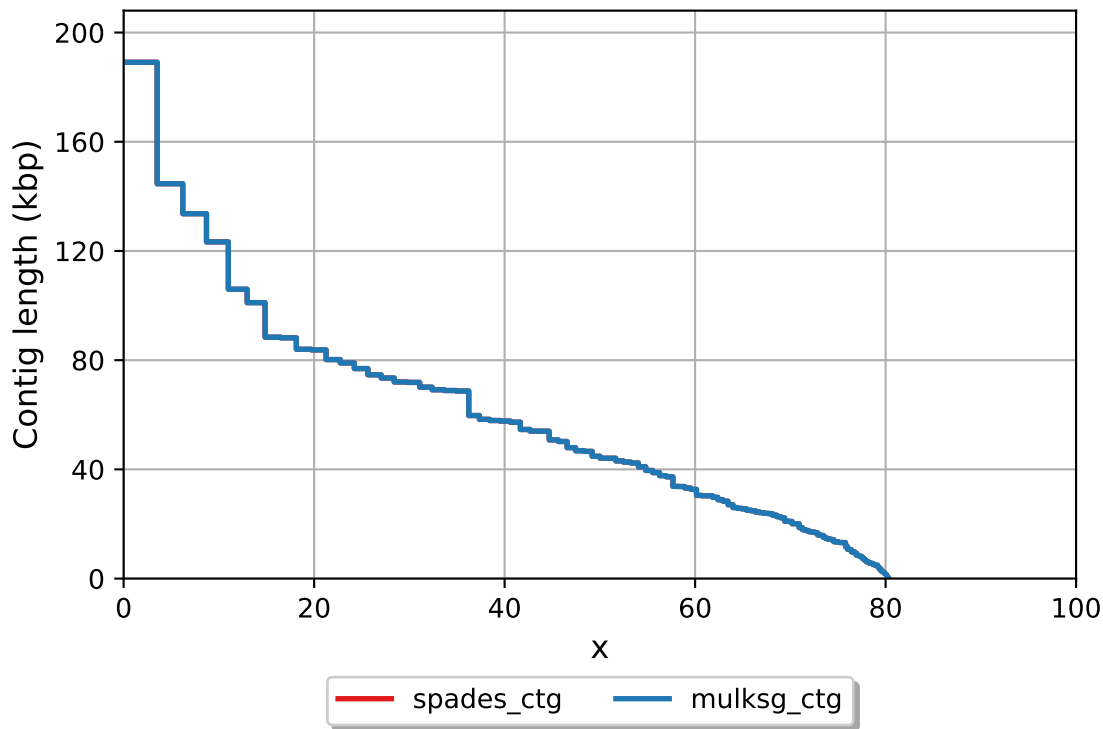
# NAx



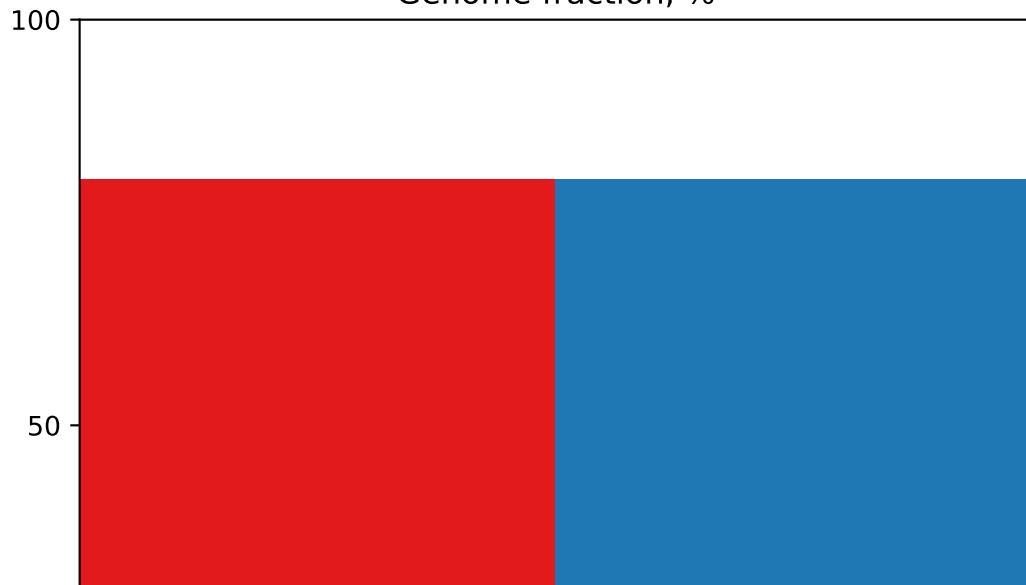
spades\_ctg mulksg\_ctg



## NGAx



Genome fraction, %



spades\_ctg



mulksg\_ctg