

Report

	spades_ctg	mulksq_ctg
# contigs (>= 0 bp)	639	630
# contigs (>= 1000 bp)	71	61
# contigs (>= 5000 bp)	43	34
# contigs (>= 10000 bp)	35	28
# contigs (>= 25000 bp)	25	22
# contigs (>= 50000 bp)	22	18
Total length (>= 0 bp)	4173918	4174017
Total length (>= 1000 bp)	3938879	3937837
Total length (>= 5000 bp)	3871918	3875401
Total length (>= 10000 bp)	3812528	3834533
Total length (>= 25000 bp)	3650695	3750047
Total length (>= 50000 bp)	3524724	3588781
# contigs	162	154
Largest contig	359056	552381
Total length	3995933	3995945
Reference length	2961149	2961149
GC (%)	47.33	47.33
Reference GC (%)	47.70	47.70
N50	216078	246267
NG50	220074	344139
N75	105216	132765
NG75	157031	229841
L50	8	5
LG50	6	4
L75	15	11
LG75	10	6
# misassemblies	1	1
# misassembled contigs	1	1
Misassembled contigs length	155353	155353
# local misassemblies	0	0
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	2	2
# unaligned contigs	110 + 16 part	112 + 14 part
Unaligned length	1077655	1079017
Genome fraction (%)	98.289	98.290
Duplication ratio	1.003	1.002
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	10.14	9.79
# indels per 100 kbp	2.06	2.06
Largest alignment	359056	536021
Total aligned length	2917047	2916604
NA50	151655	163761
NGA50	215940	246267
NGA75	115075	151655
LA50	9	7
LGA50	6	4
LGA75	11	8

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

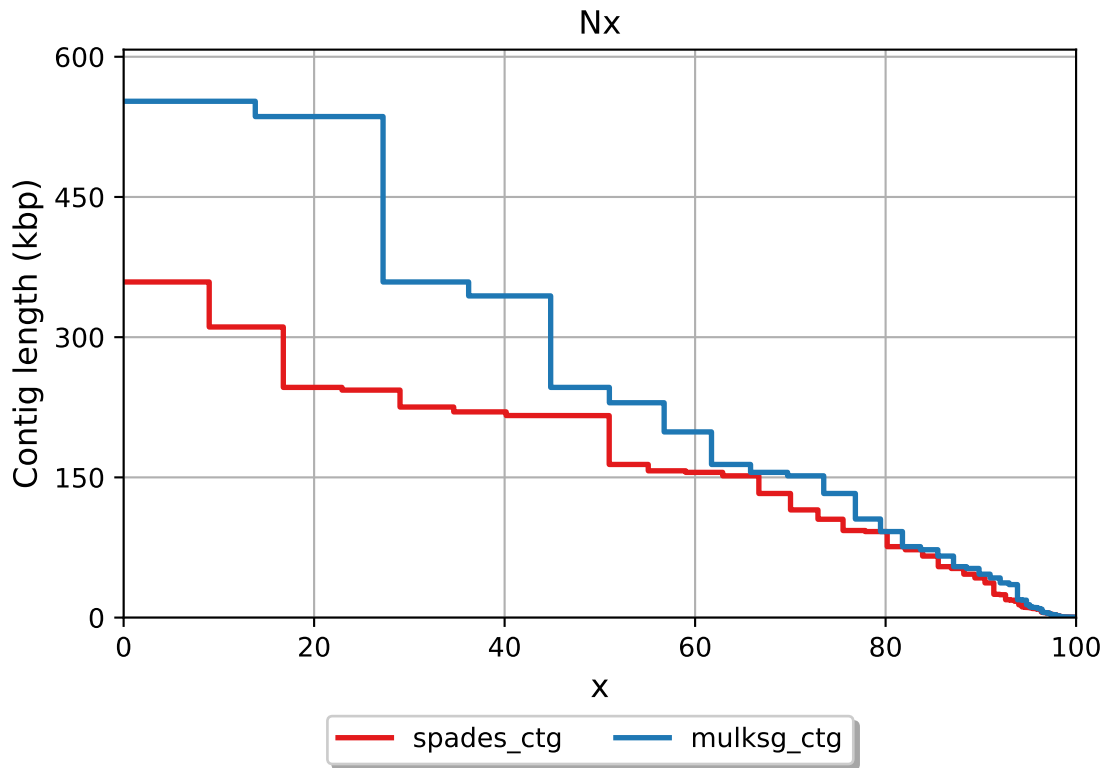
	spades_ctg	mulksq_ctg
# misassemblies	1	1
# contig misassemblies	1	1
# c. relocations	1	1
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	1	1
Misassembled contigs length	155353	155353
# local misassemblies	0	0
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	2	2
# mismatches	295	285
# indels	60	60
# indels (<= 5 bp)	57	57
# indels (> 5 bp)	3	3
Indels length	82	82

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).

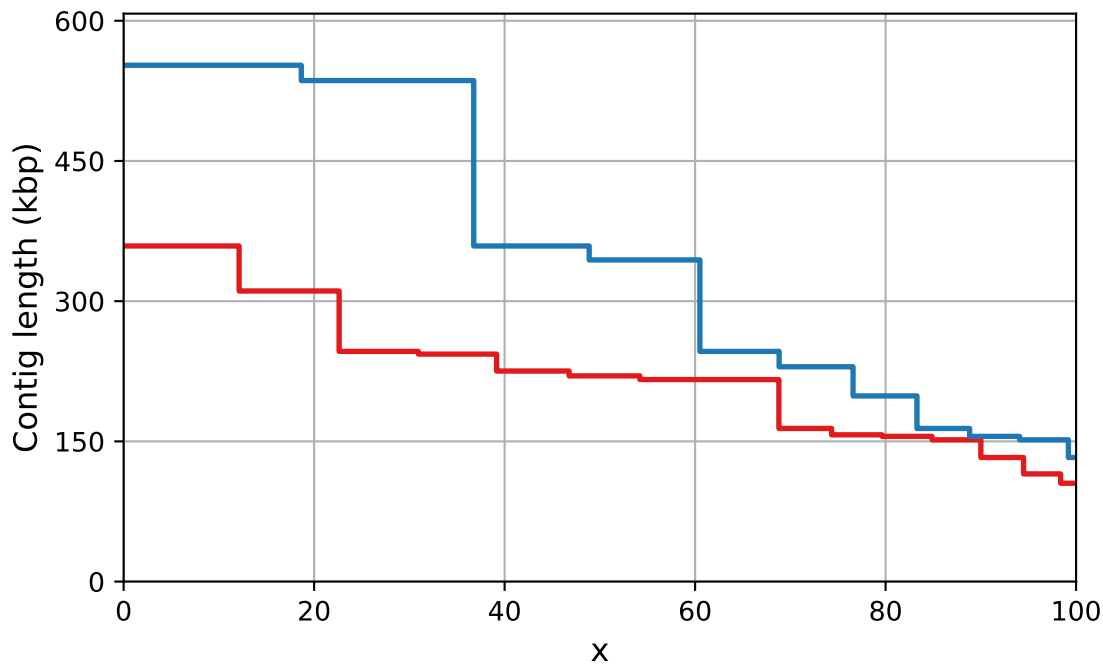
Unaligned report

	spades_ctg	mulksg_ctg
# fully unaligned contigs	110	112
Fully unaligned length	196614	197677
# partially unaligned contigs	16	14
Partially unaligned length	881041	881340
# N's	0	0

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).

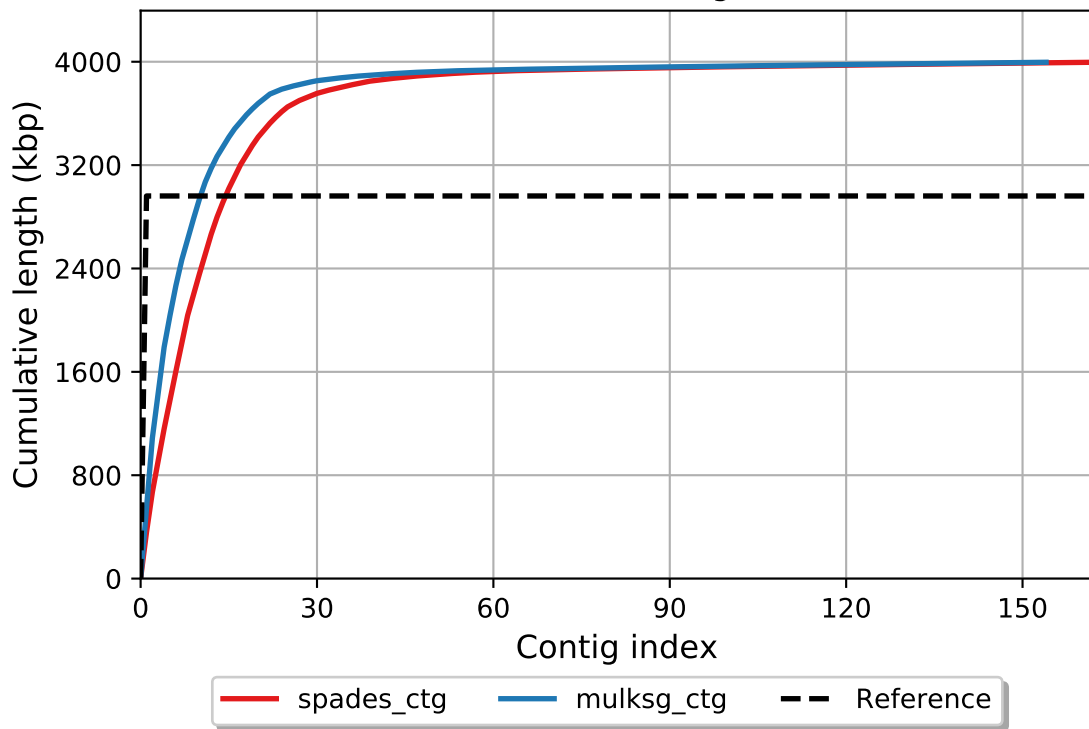


NGx

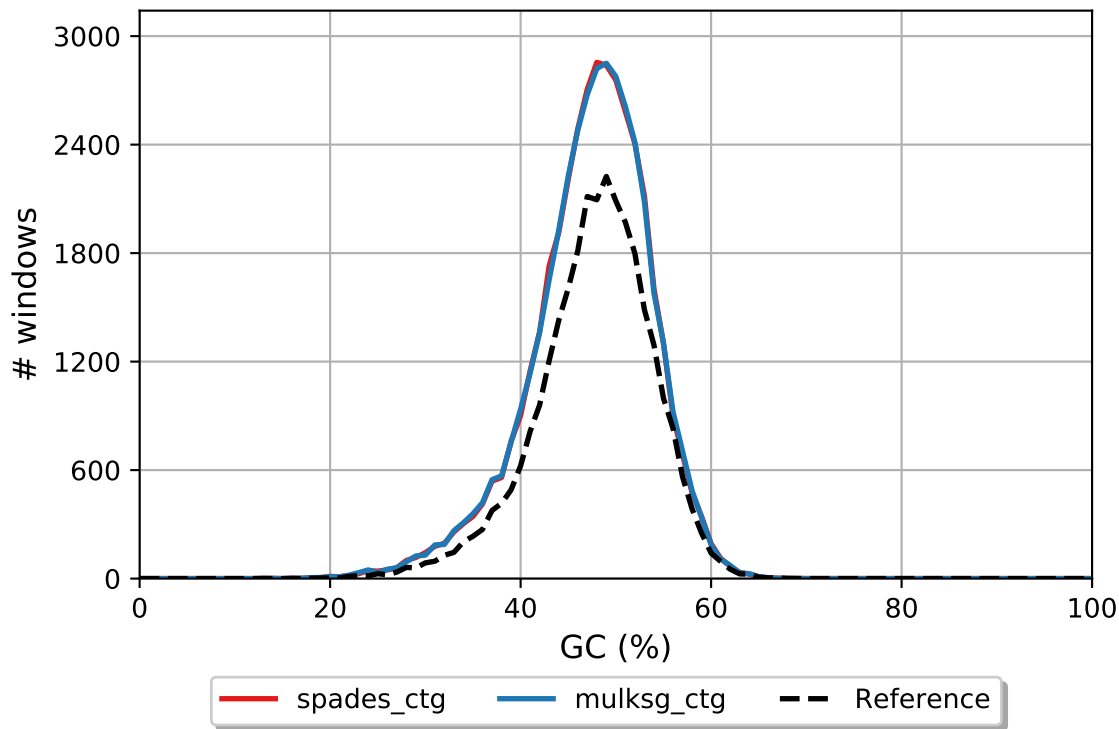


— spades_ctg — mulksg_ctg

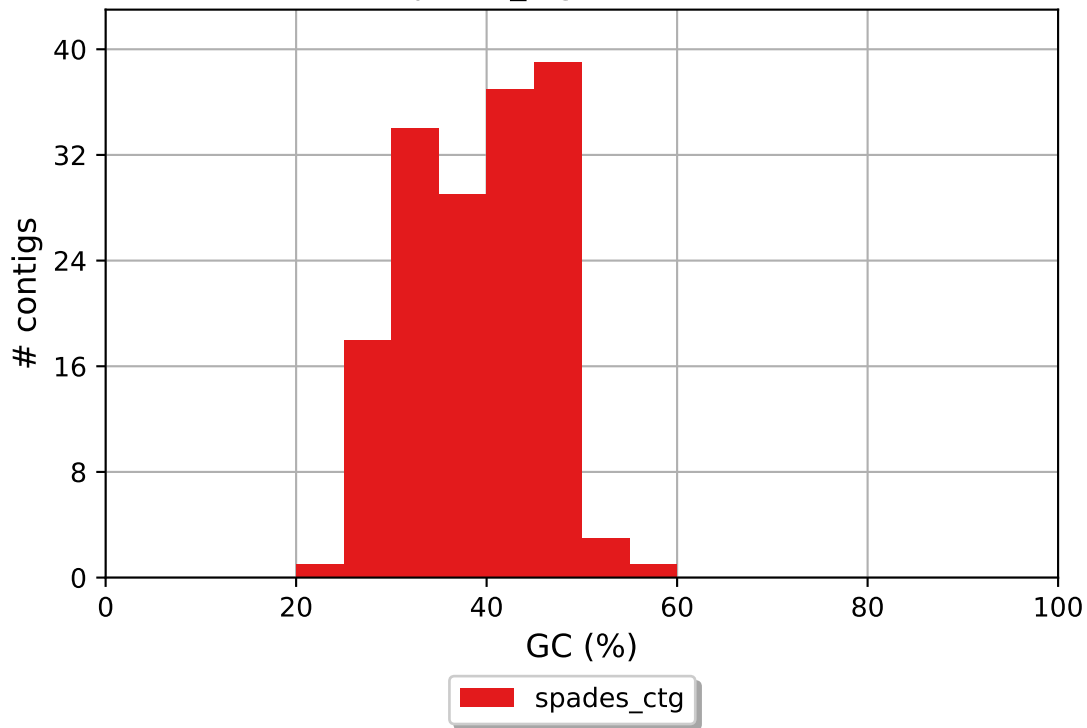
Cumulative length



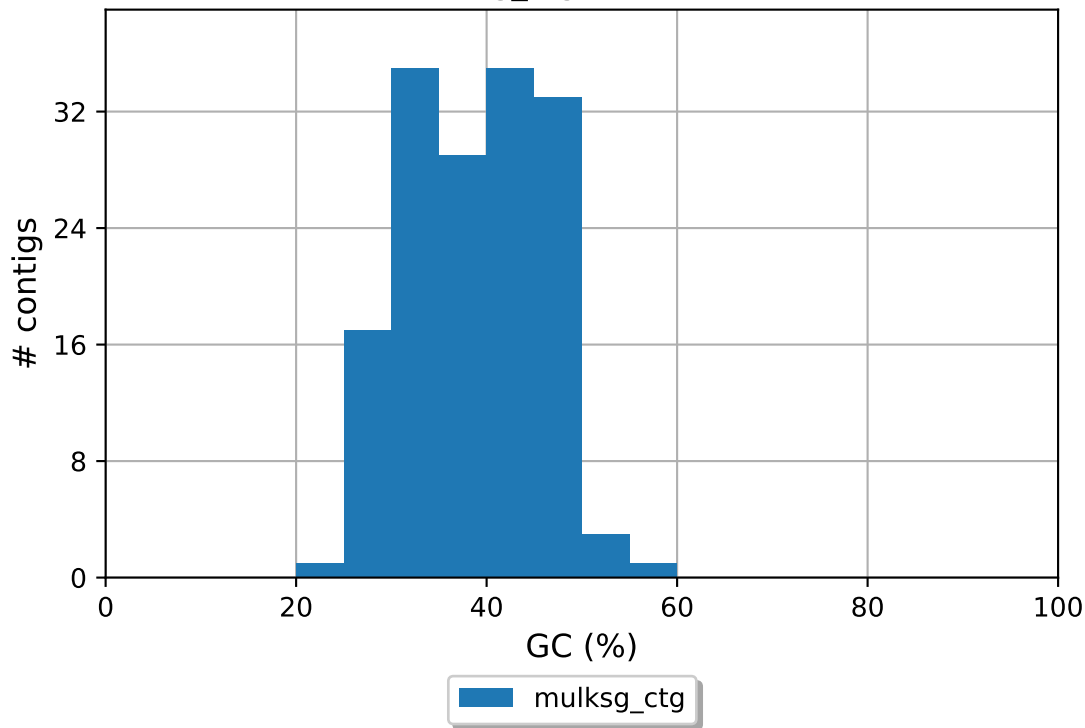
GC content



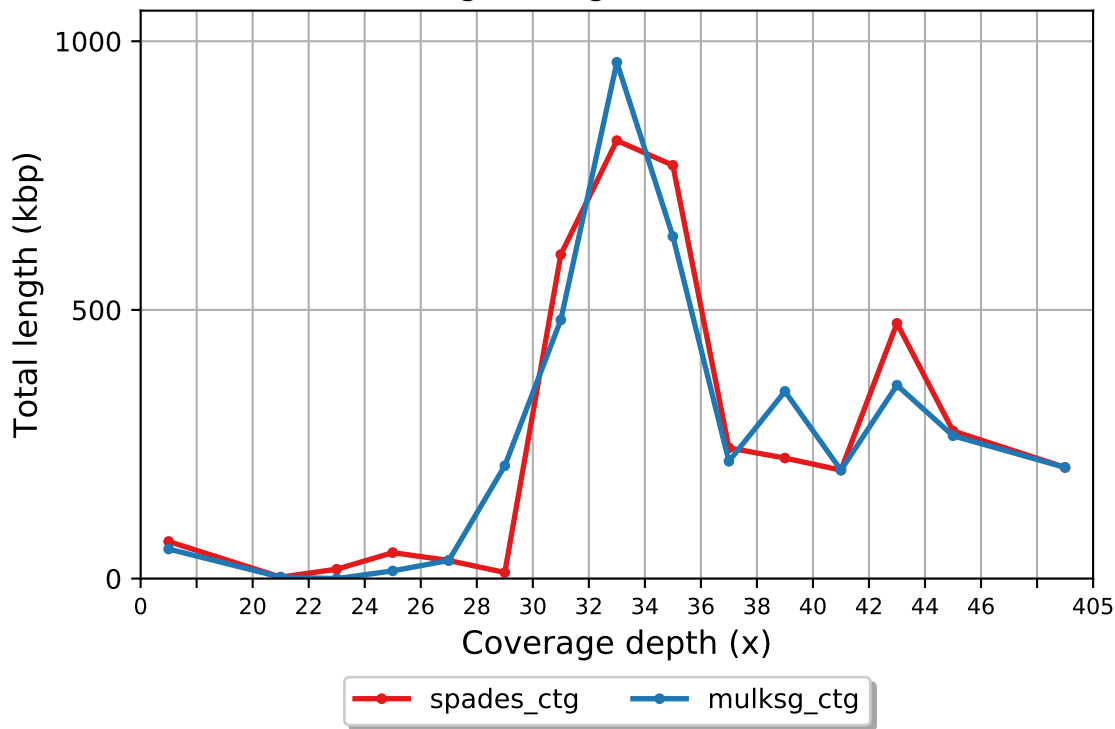
spades_ctg GC content



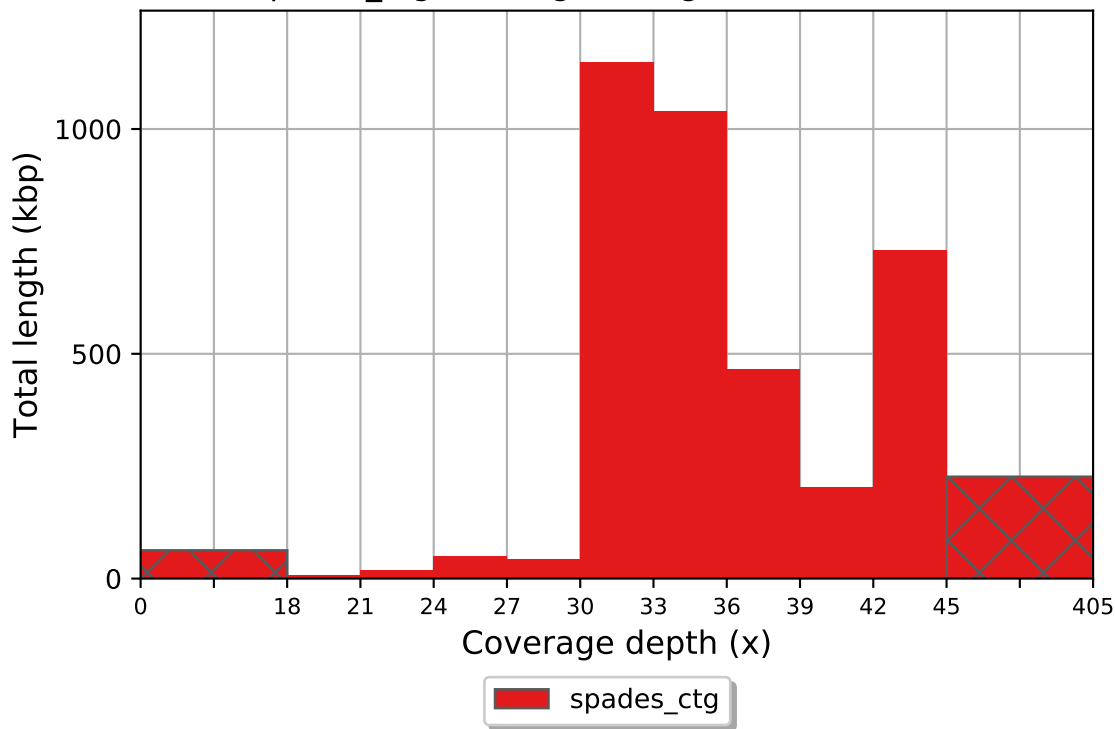
mulksg_ctg GC content



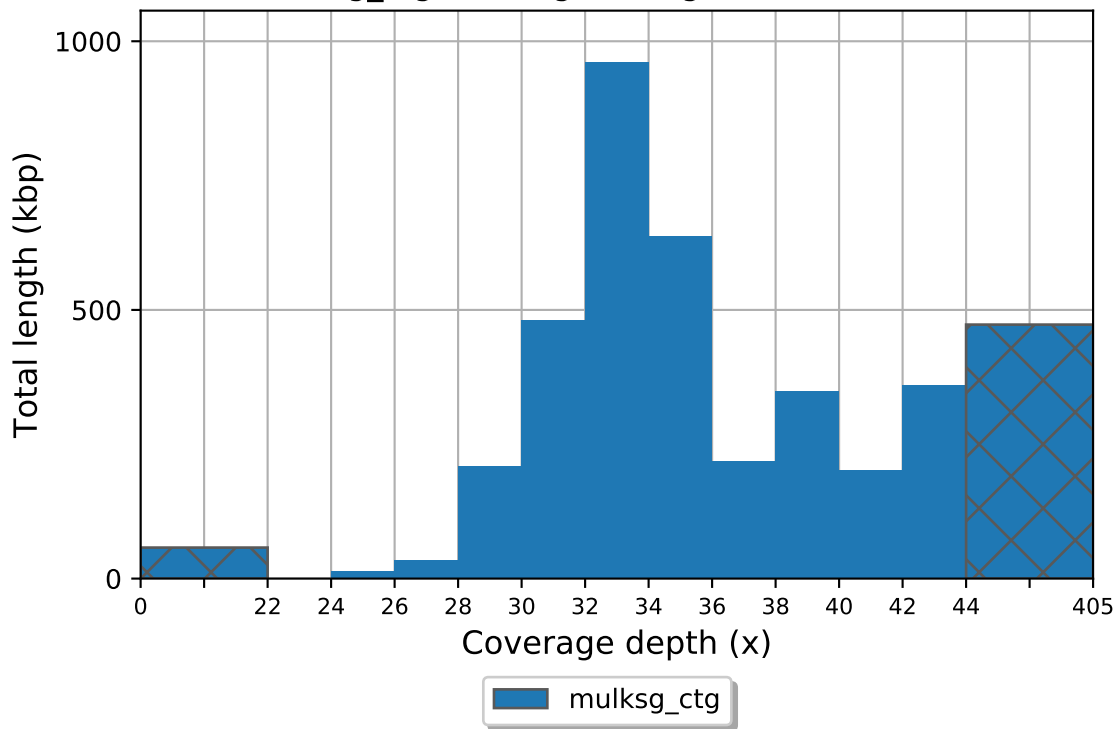
Coverage histogram (bin size: 2x)



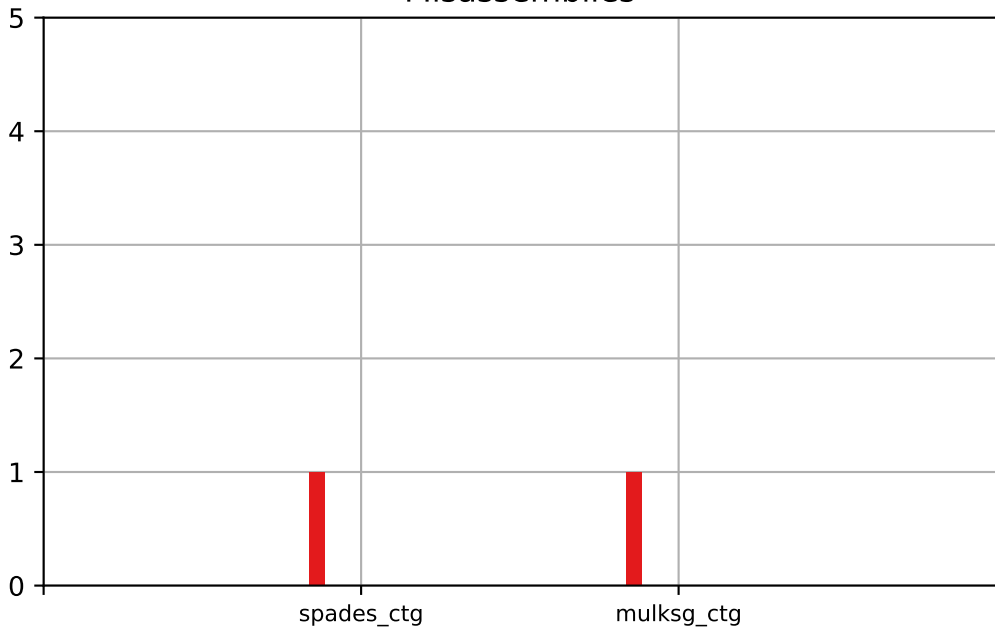
spades_ctg coverage histogram (bin size: 3x)



mulksg_ctg coverage histogram (bin size: 2x)

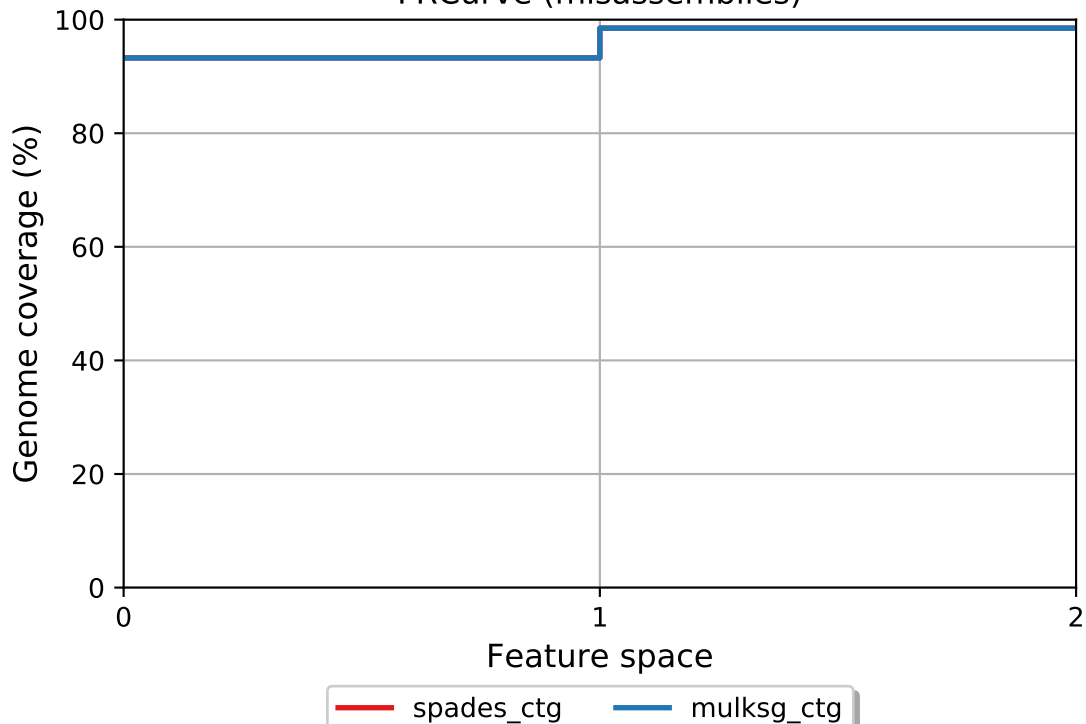


Misassemblies

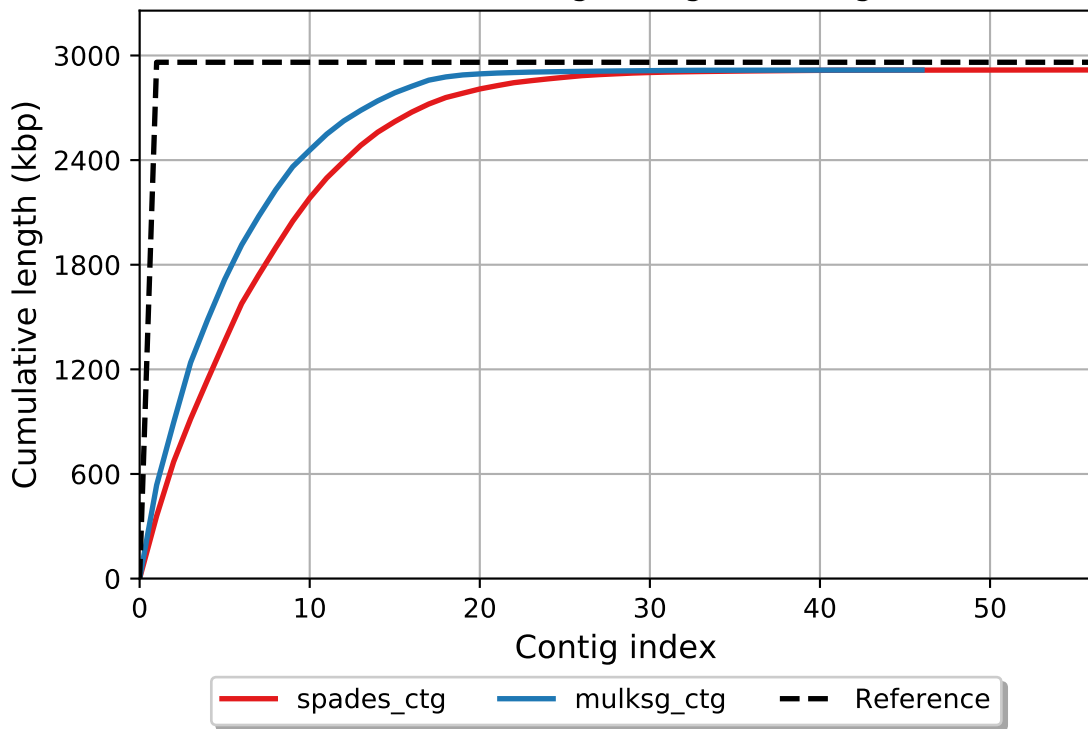


 # relocations

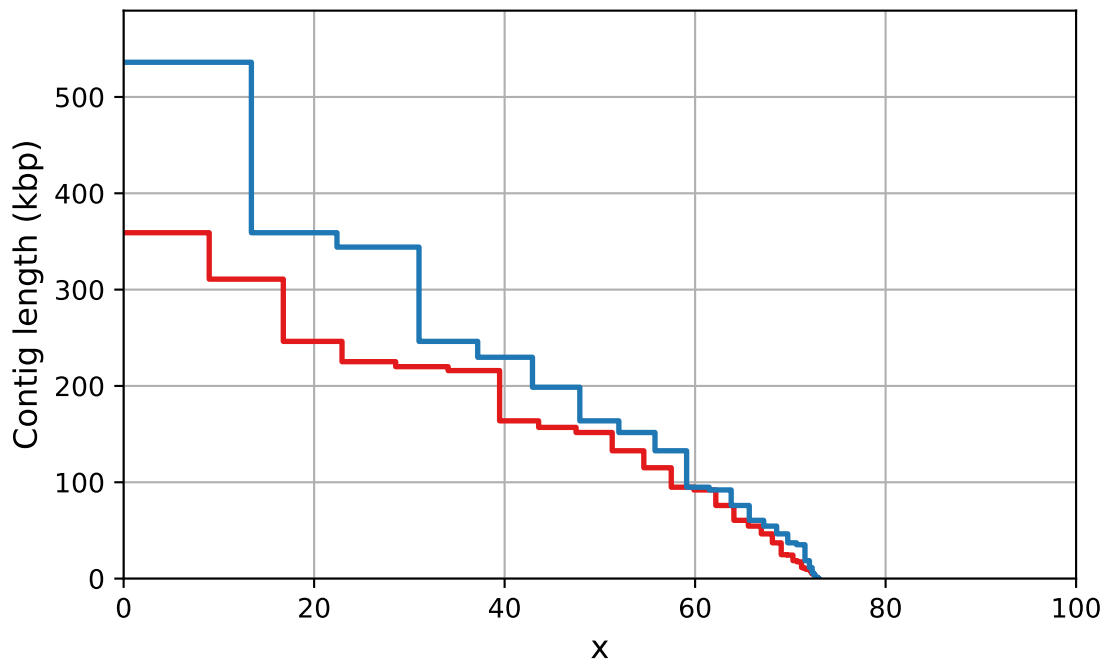
FRCurve (misassemblies)



Cumulative length (aligned contigs)



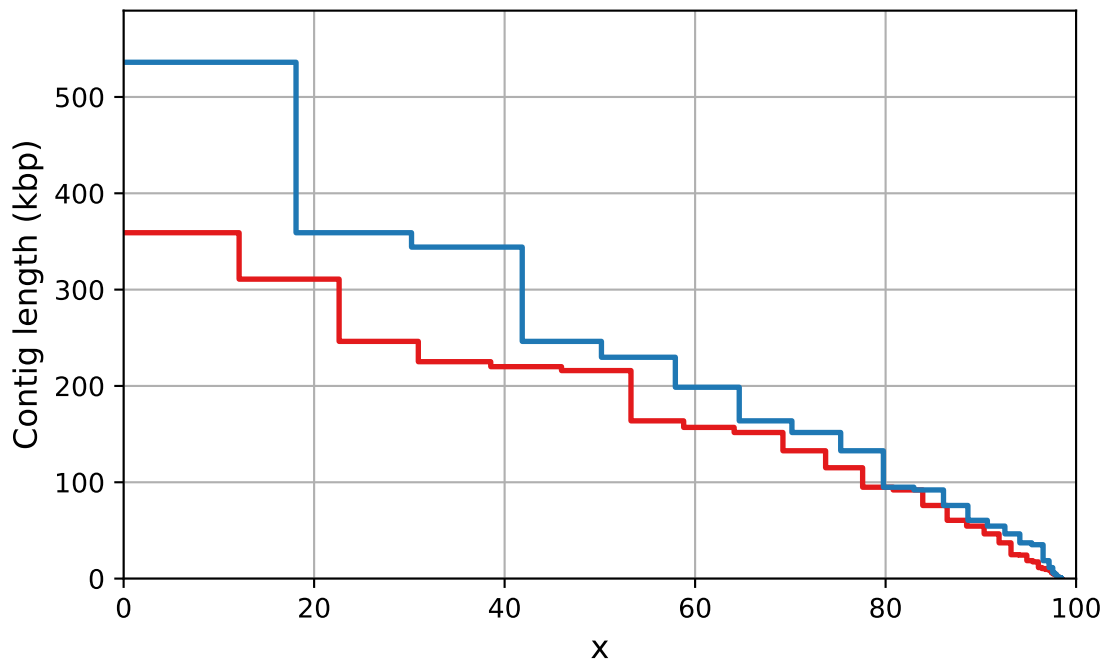
NAx



— spades_ctg

— mulksg_ctg

NGAx



— spades_ctg — mulksg_ctg

Genome fraction, %

100

99



spades_ctg



mulks_g_ctg