

Report

	spades_scf	mulksg_scf
# contigs (>= 0 bp)	125	128
# contigs (>= 1000 bp)	52	50
# contigs (>= 5000 bp)	44	43
# contigs (>= 10000 bp)	36	35
# contigs (>= 25000 bp)	31	28
# contigs (>= 50000 bp)	22	21
Total length (>= 0 bp)	4588927	4591033
Total length (>= 1000 bp)	4567936	4567949
Total length (>= 5000 bp)	4549496	4551578
Total length (>= 10000 bp)	4492357	4494439
Total length (>= 25000 bp)	4397996	4359024
Total length (>= 50000 bp)	4085593	4118293
# contigs	57	56
Largest contig	510758	510758
Total length	4571900	4572424
Reference length	114179	114179
GC (%)	68.82	68.82
Reference GC (%)	70.07	70.07
N50	204781	204781
NG50	510758	510758
N75	119953	130406
NG75	510758	510758
L50	8	8
LG50	1	1
L75	15	14
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	0	0
# unaligned contigs	51 + 4 part	50 + 4 part
Unaligned length	4456470	4456993
Genome fraction (%)	100.000	100.000
Duplication ratio	1.011	1.011
# N's per 100 kbp	15.22	15.24
# mismatches per 100 kbp	7.01	7.01
# indels per 100 kbp	2.63	2.63
Largest alignment	112703	112703
Total aligned length	114642	114642
NGA50	112703	112703
NGA75	112703	112703
LGA50	1	1
LGA75	1	1

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

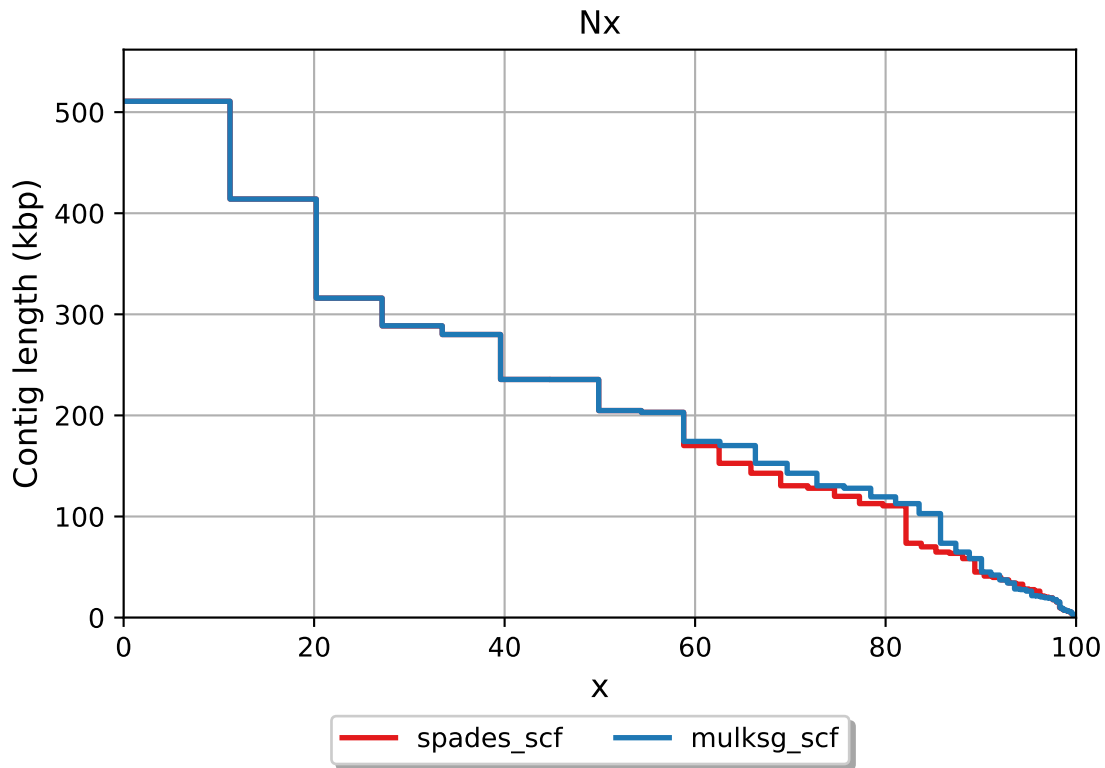
	spades_scf	mulksg_scf
# misassemblies	0	0
# contig misassemblies	0	0
# c. relocations	0	0
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	0	0
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	0	0
# mismatches	8	8
# indels	3	3
# indels (<= 5 bp)	3	3
# indels (> 5 bp)	0	0
Indels length	3	3

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).

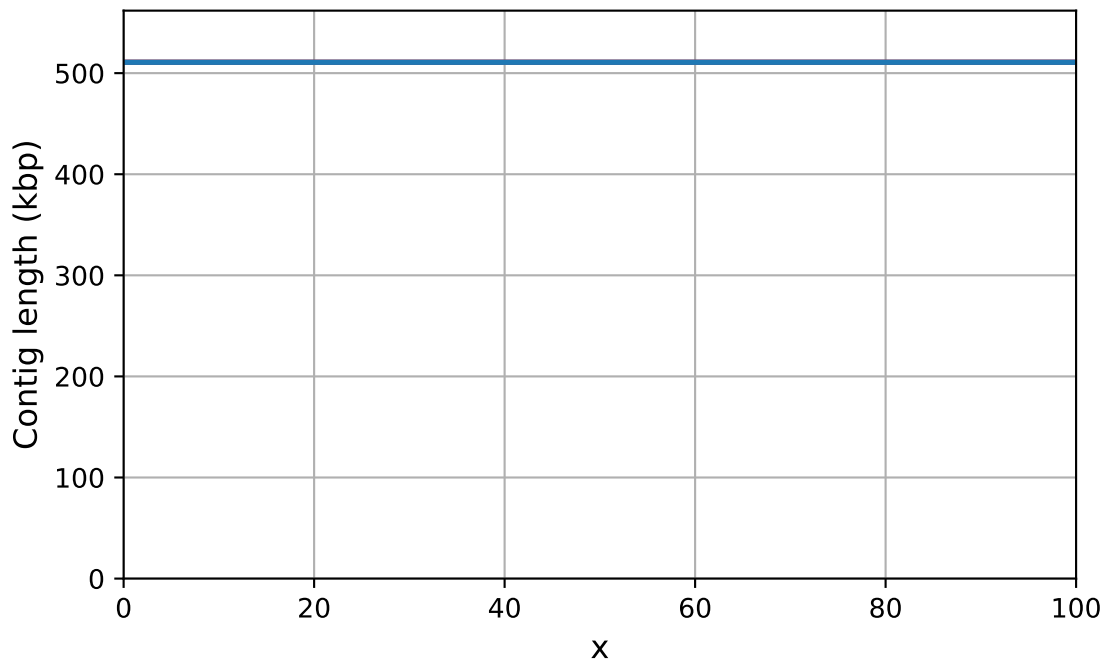
Unaligned report

	spades_scf	mulks_g_scf
# fully unaligned contigs	51	50
Fully unaligned length	3989211	3989757
# partially unaligned contigs	4	4
Partially unaligned length	467259	467236
# N's	696	697

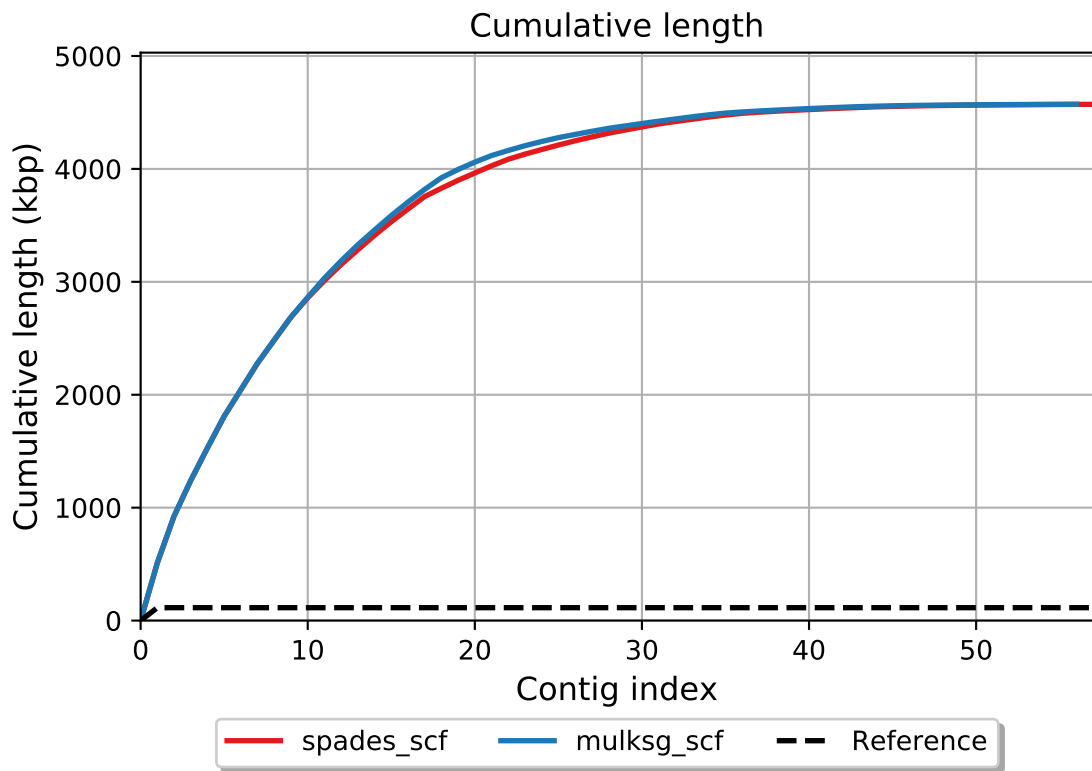
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



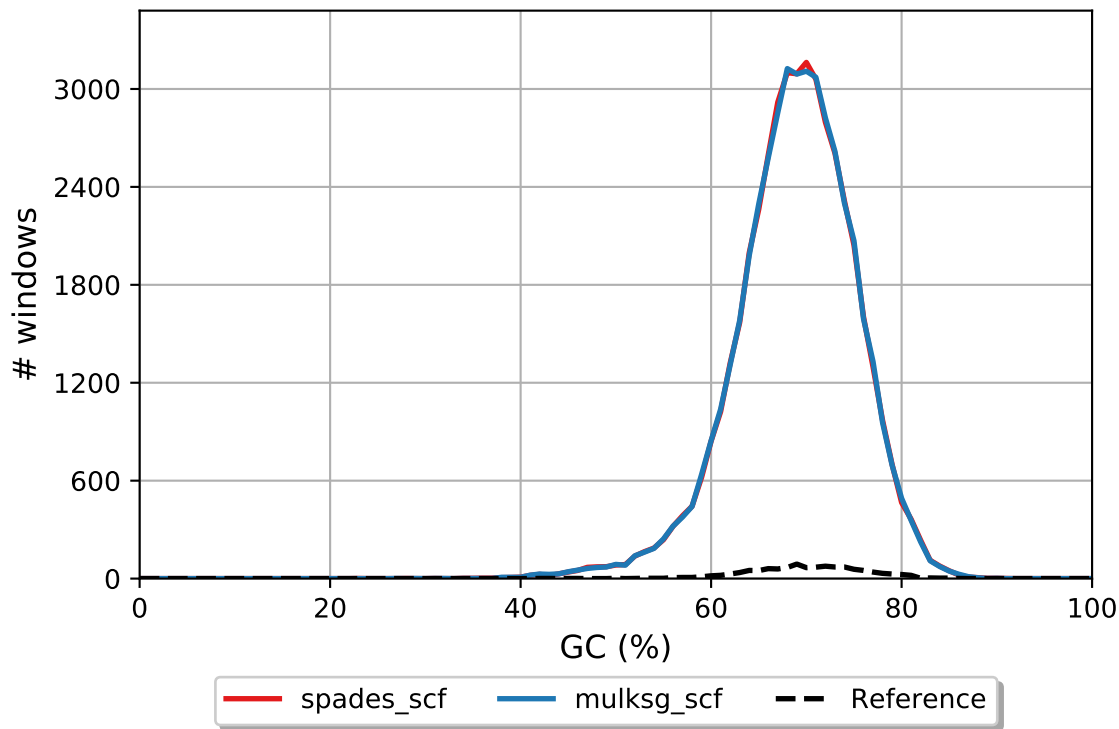
NGx



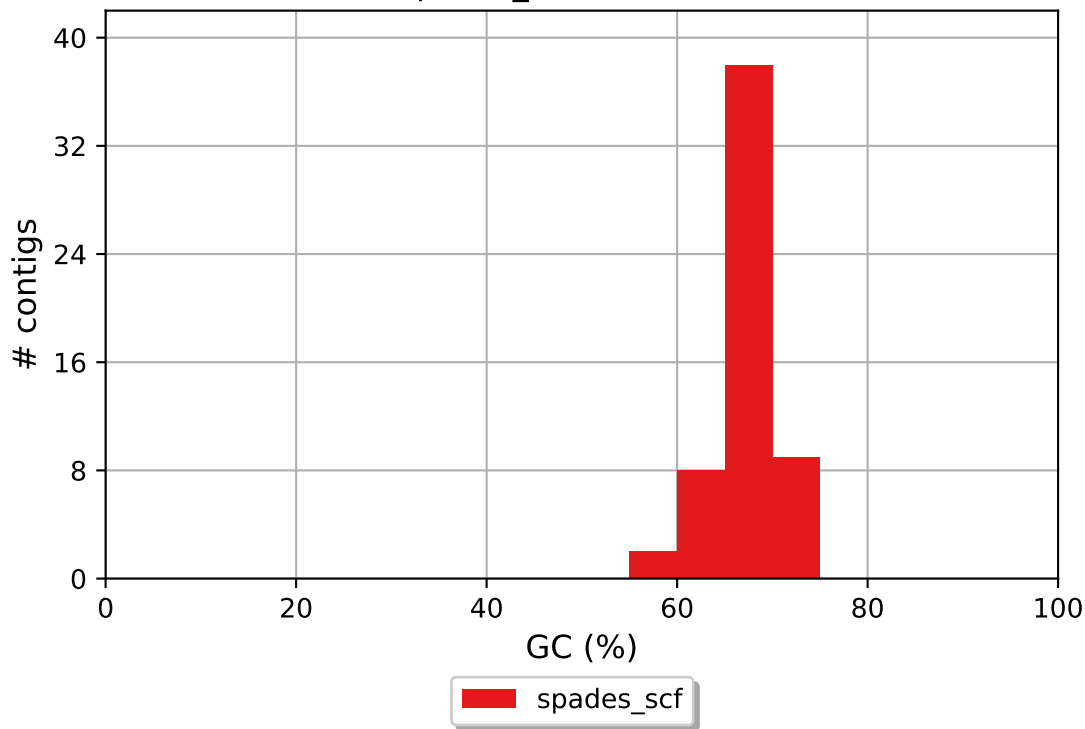
spades_scf mulksg_scf



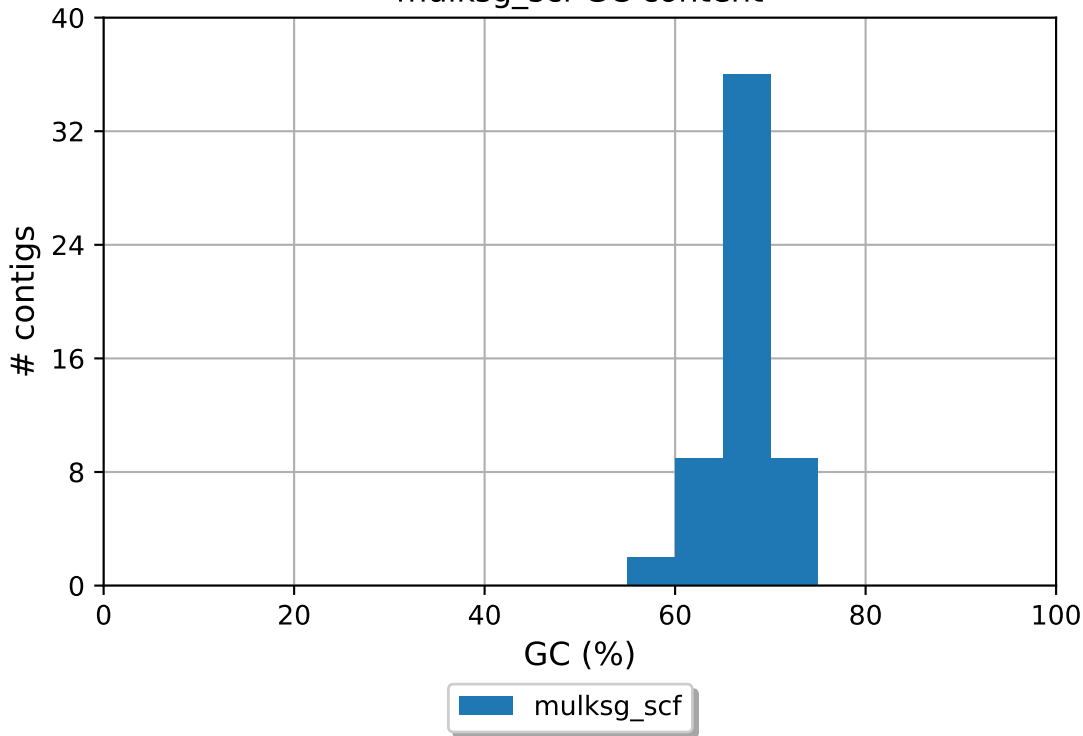
GC content



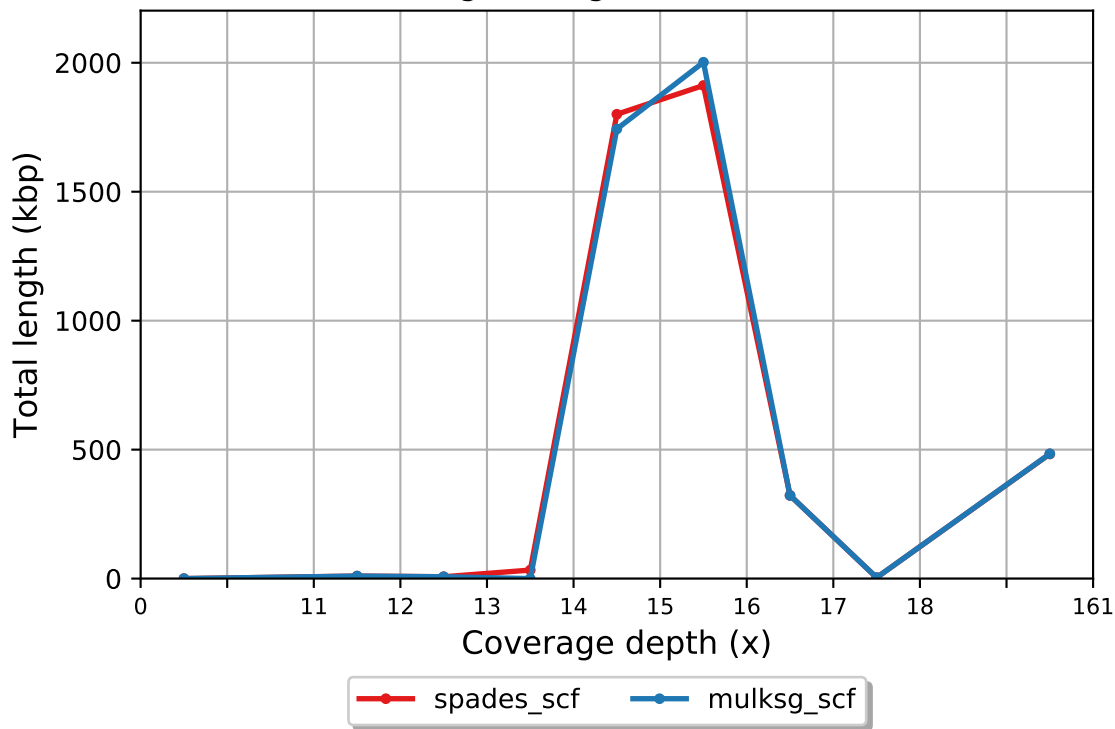
spades_scf GC content



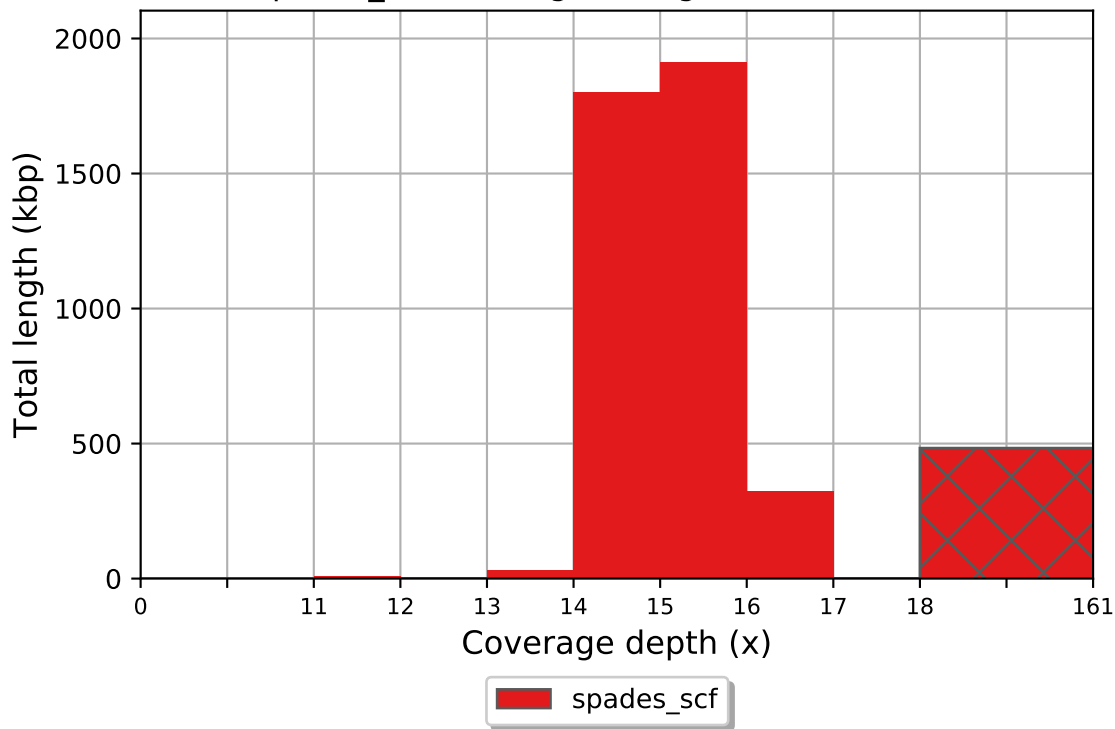
mulksg_scf GC content



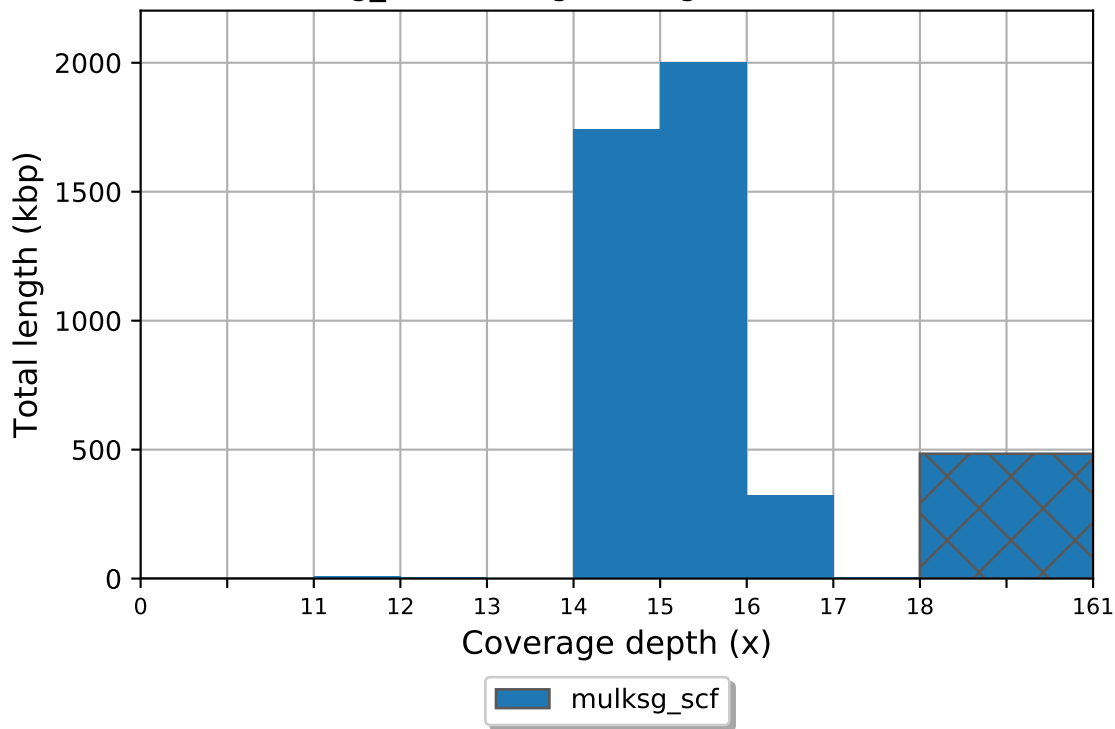
Coverage histogram (bin size: 1x)



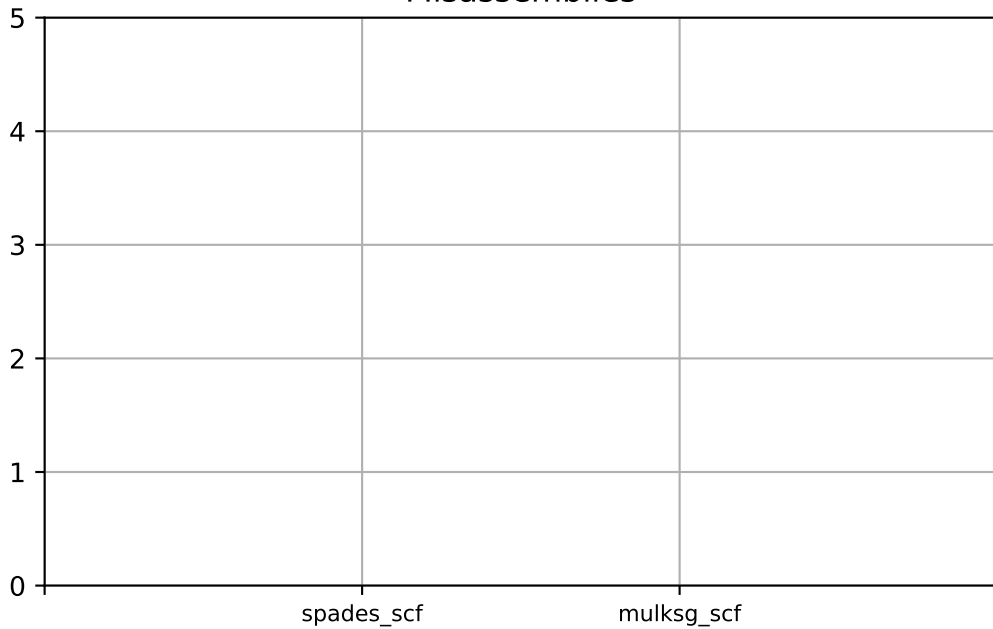
spades_scf coverage histogram (bin size: 1x)



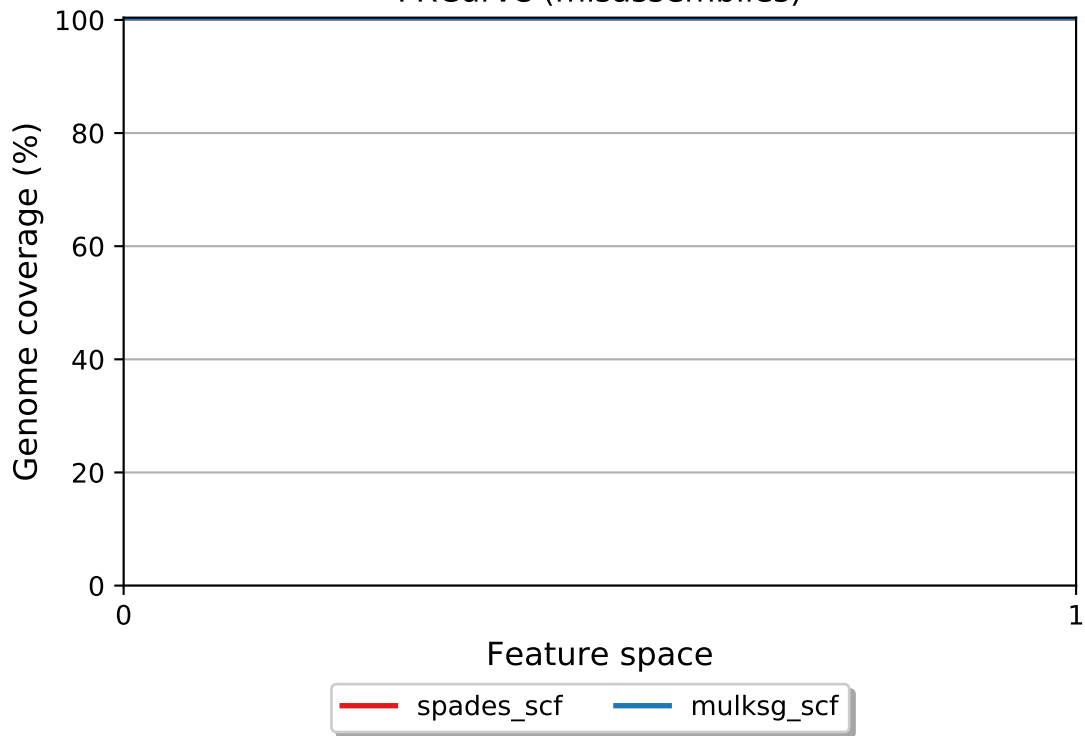
mulksg_scf coverage histogram (bin size: 1x)

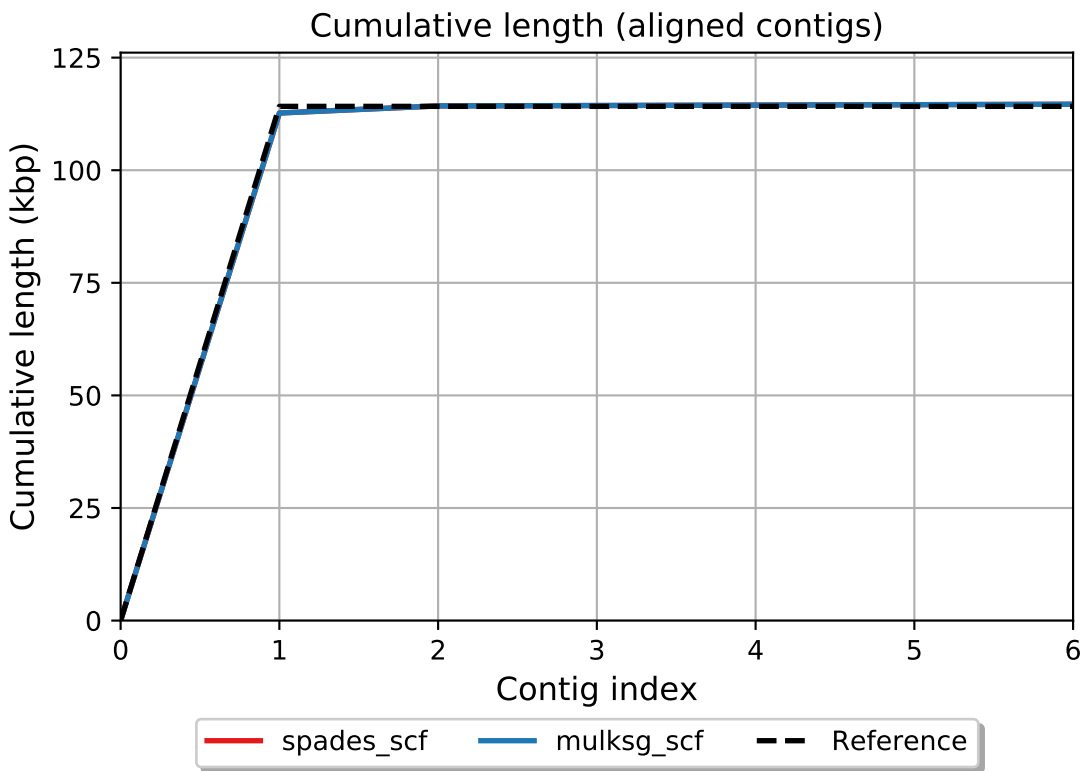


Misassemblies

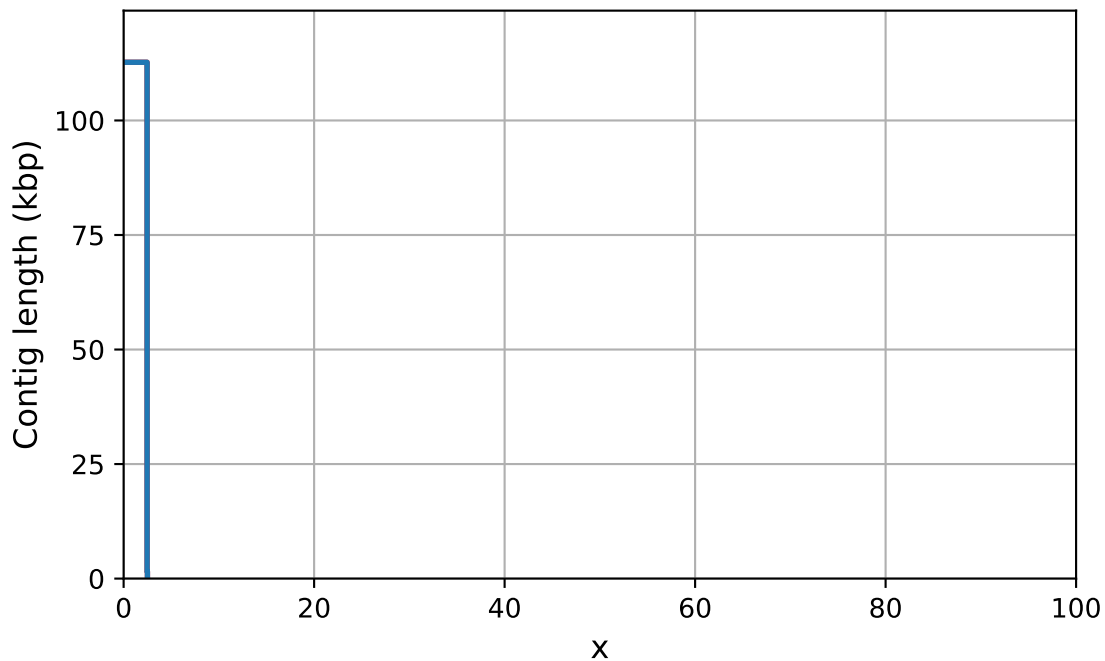


FRCurve (misassemblies)



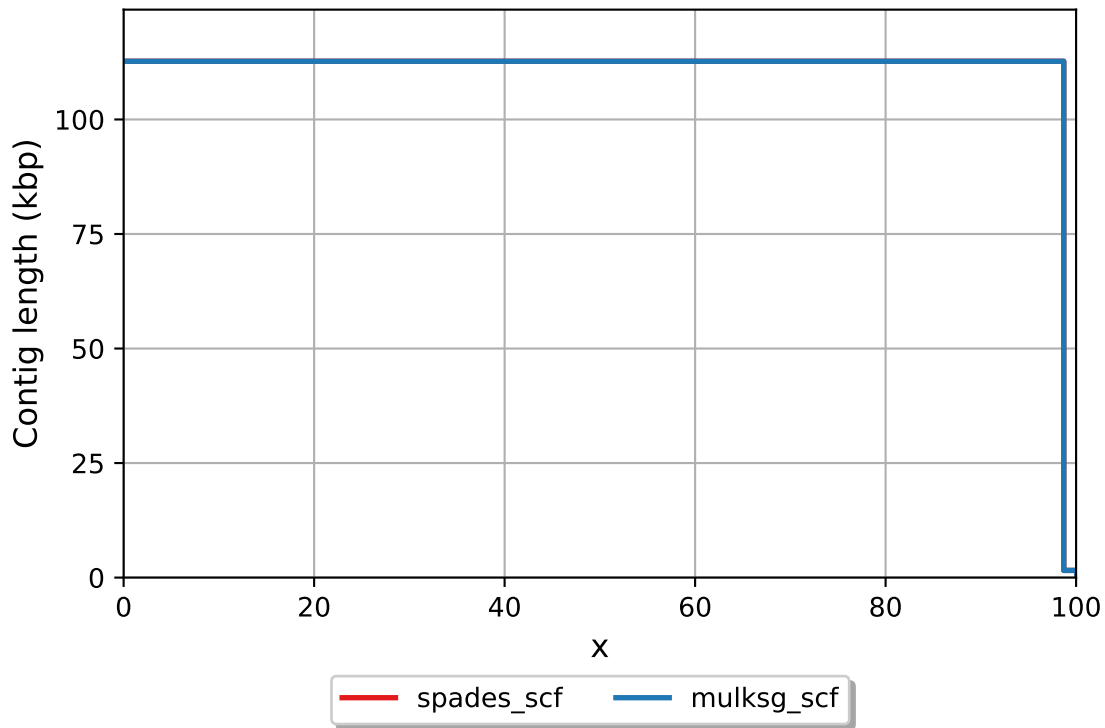


NAx



spades_scf mulksg_scf

NGAx



Genome fraction, %

