

Report

	spades_scf	mulksq_scf
# contigs (>= 0 bp)	181	176
# contigs (>= 1000 bp)	109	101
# contigs (>= 5000 bp)	77	69
# contigs (>= 10000 bp)	70	64
# contigs (>= 25000 bp)	50	44
# contigs (>= 50000 bp)	34	27
Total length (>= 0 bp)	4580979	4578907
Total length (>= 1000 bp)	4555691	4551511
Total length (>= 5000 bp)	4475742	4471944
Total length (>= 10000 bp)	4414933	4431621
Total length (>= 25000 bp)	4050646	4072537
Total length (>= 50000 bp)	3493993	3459938
# contigs	120	117
Largest contig	292708	292708
Total length	4563290	4562515
Reference length	114179	114179
GC (%)	68.82	68.82
Reference GC (%)	70.07	70.07
N50	84722	111873
NG50	292708	292708
N75	51238	55037
NG75	292708	292708
L50	16	13
LG50	1	1
L75	33	27
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	112 + 4 part	111 + 4 part
Unaligned length	4448536	4447781
Genome fraction (%)	100.000	100.000
Duplication ratio	1.005	1.005
# N's per 100 kbp	0.00	0.00
# mismatches per 100 kbp	7.01	7.01
# indels per 100 kbp	2.63	2.63
Largest alignment	58318	112704
Total aligned length	114662	114642
NGA50	58318	112704
NGA75	36015	112704
LGA50	1	1
LGA75	2	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

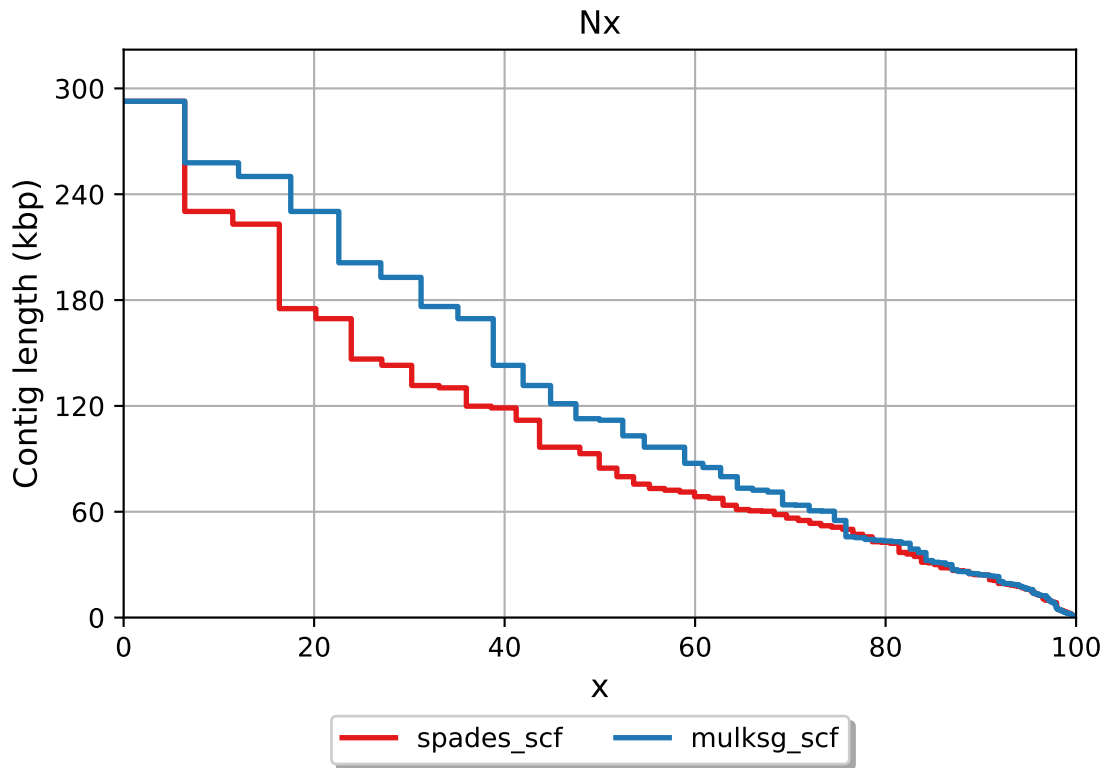
	spades_scf	mulksg_scf
# misassemblies	0	0
# contig misassemblies	0	0
# c. relocations	0	0
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	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).

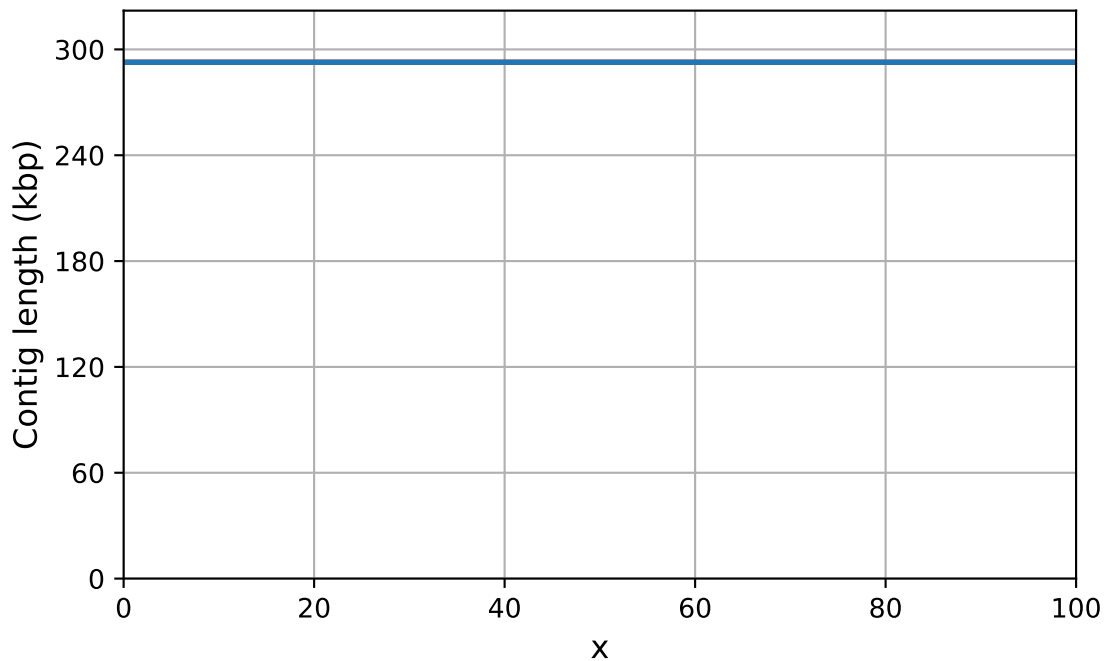
Unaligned report

	spades_scf	mulks_g_scf
# fully unaligned contigs	112	111
Fully unaligned length	4261003	4260303
# partially unaligned contigs	4	4
Partially unaligned length	187533	187478
# N's	0	0

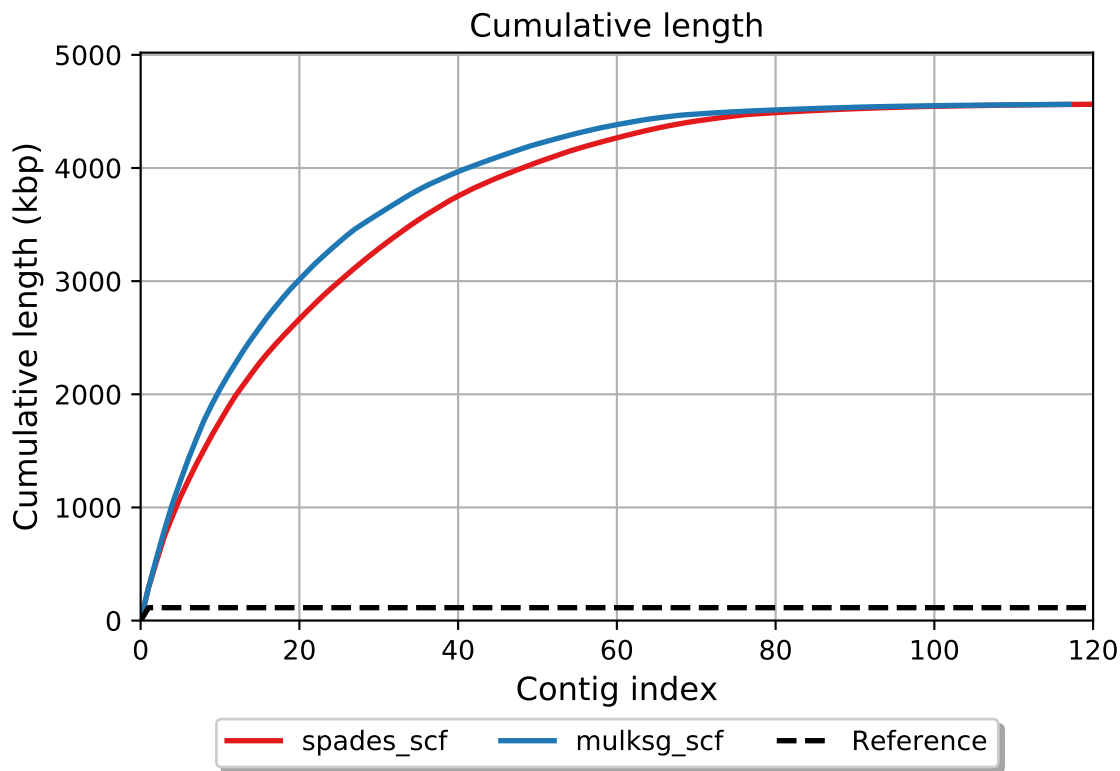
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



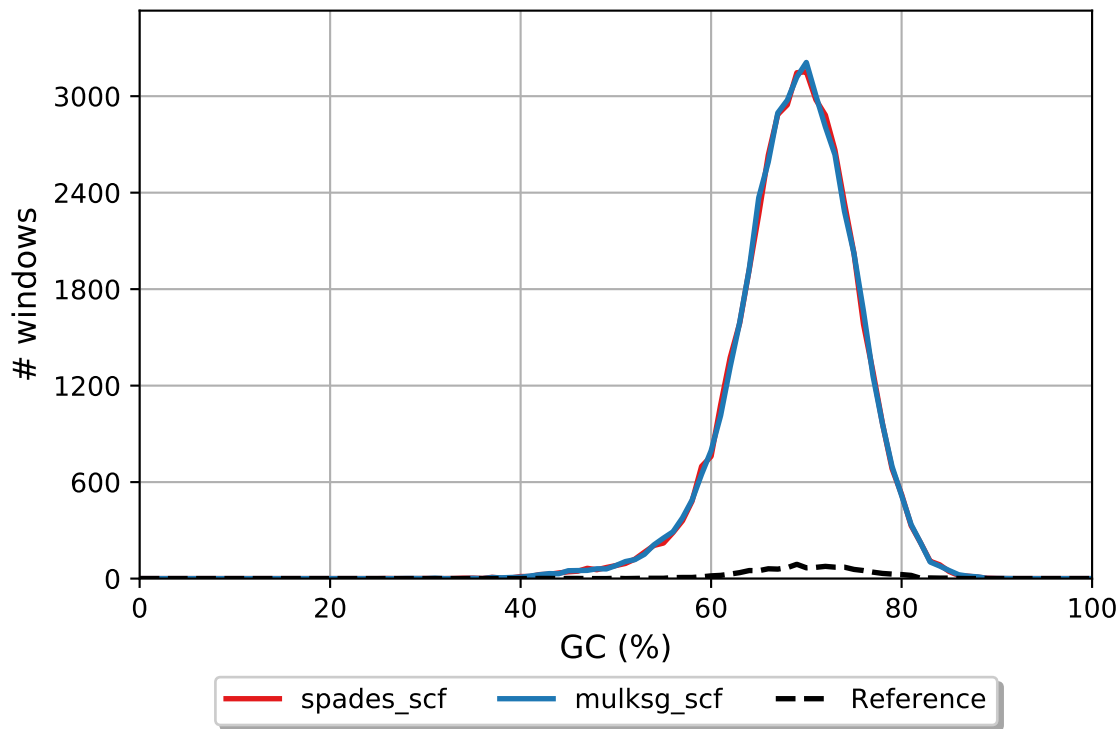
NGx



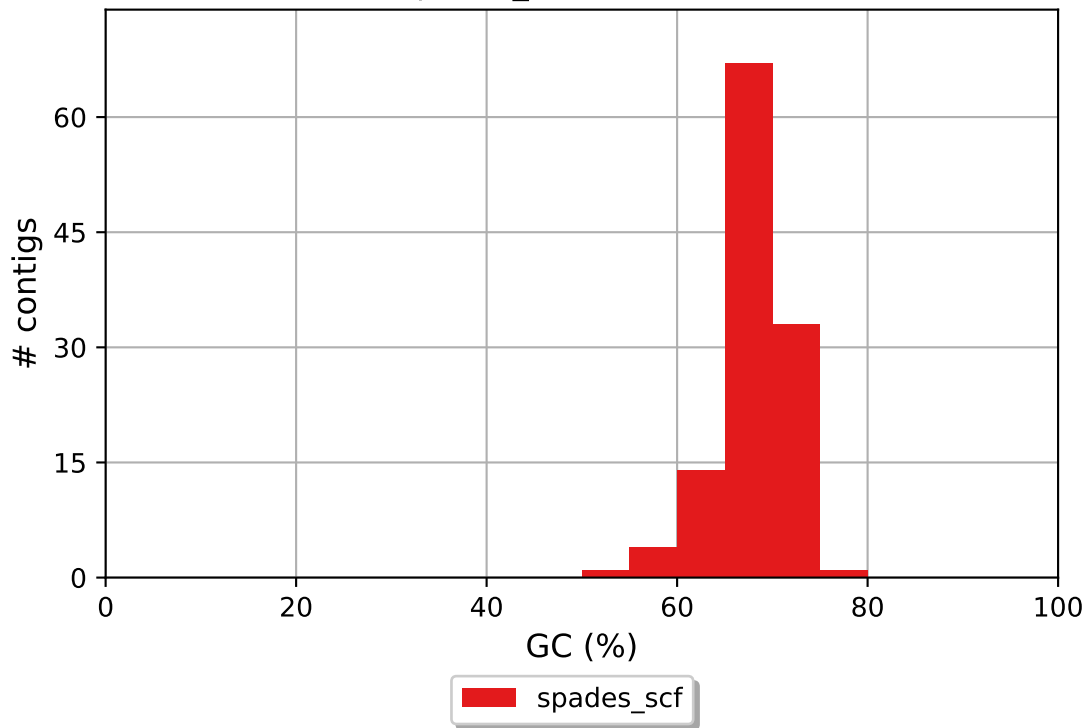
spades_scf mulksg_scf



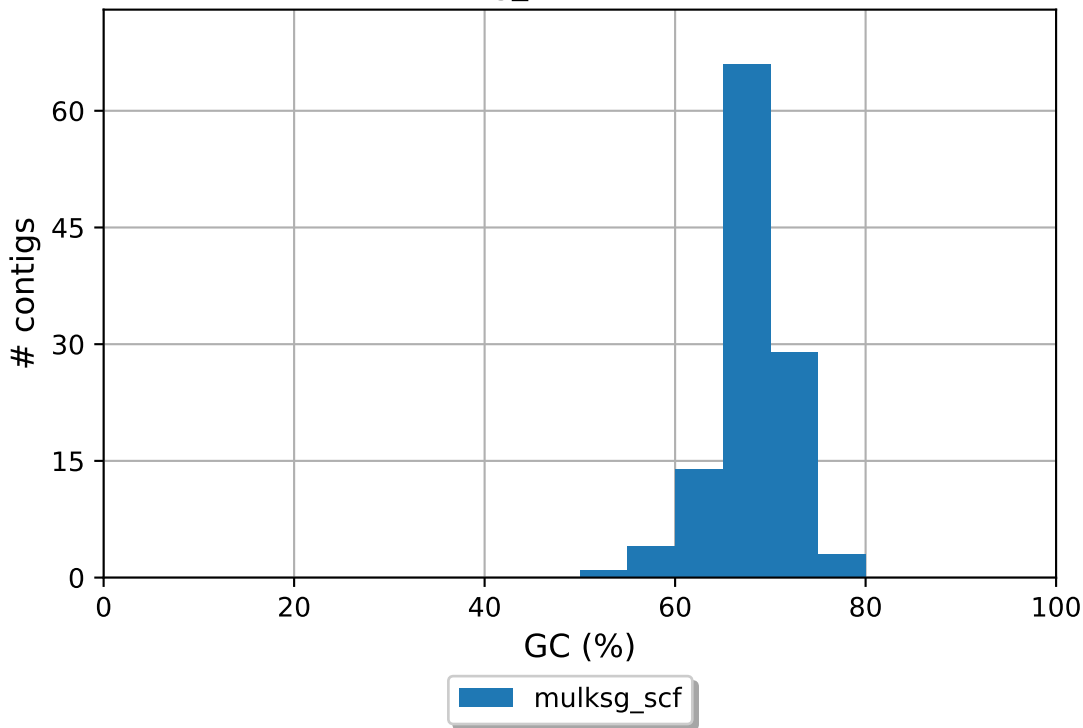
GC content



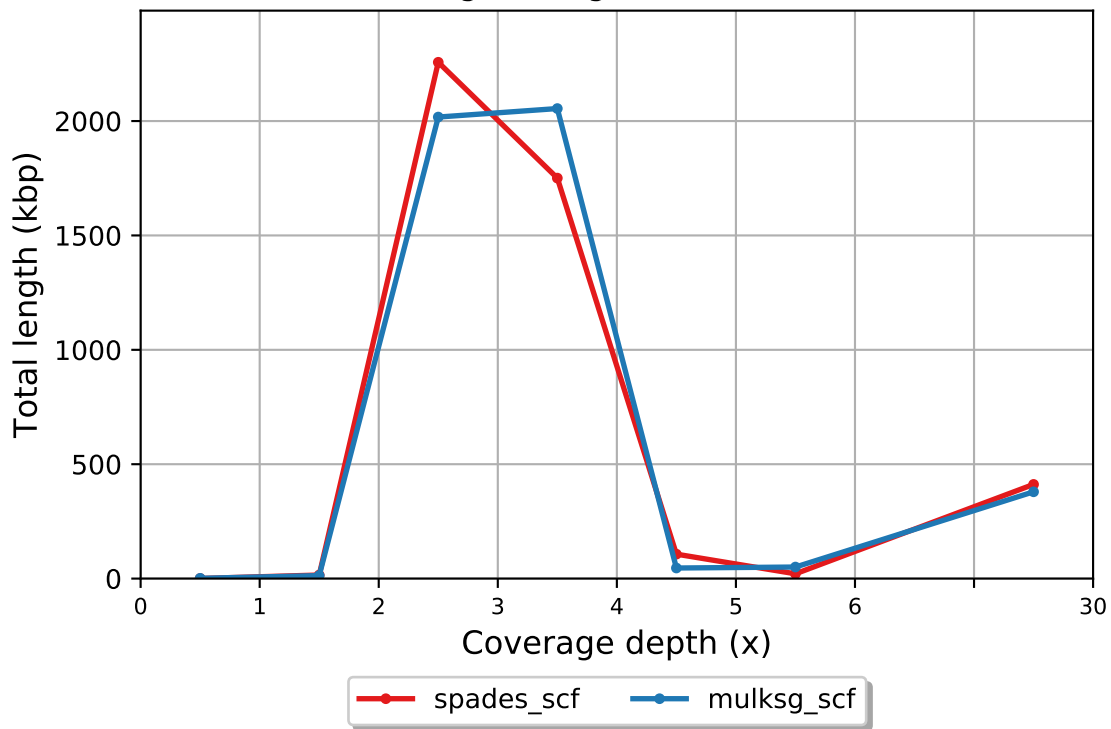
spades_scf GC content



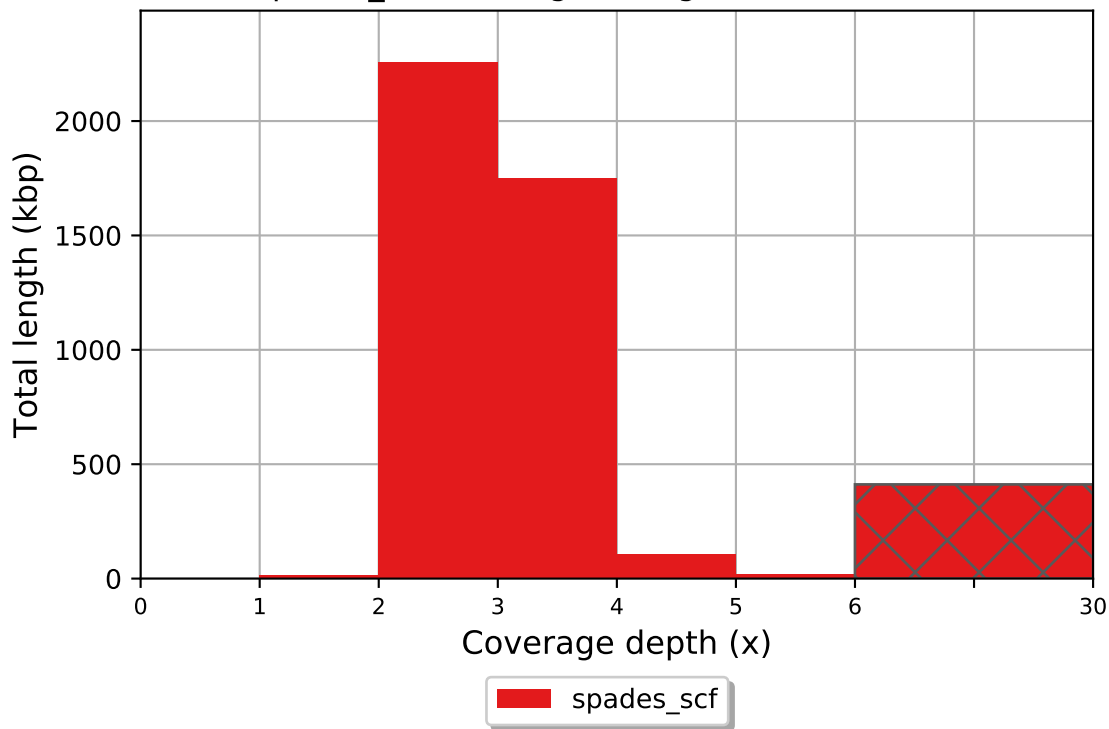
mulksg_scf GC content



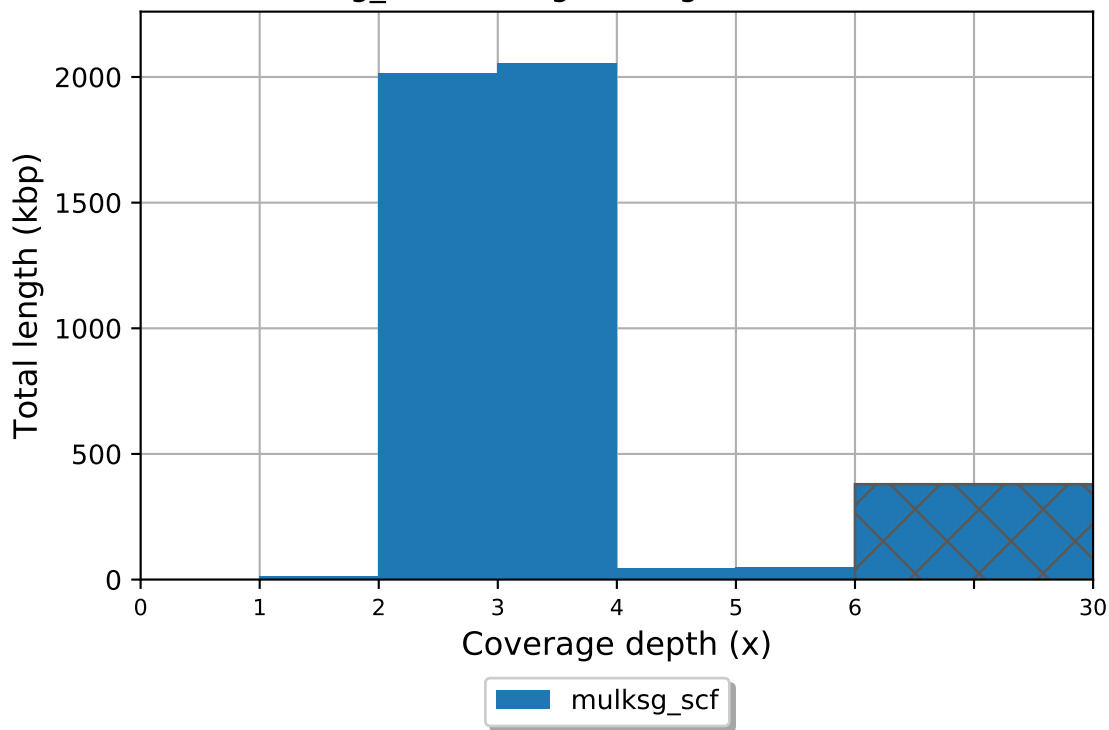
Coverage histogram (bin size: 1x)



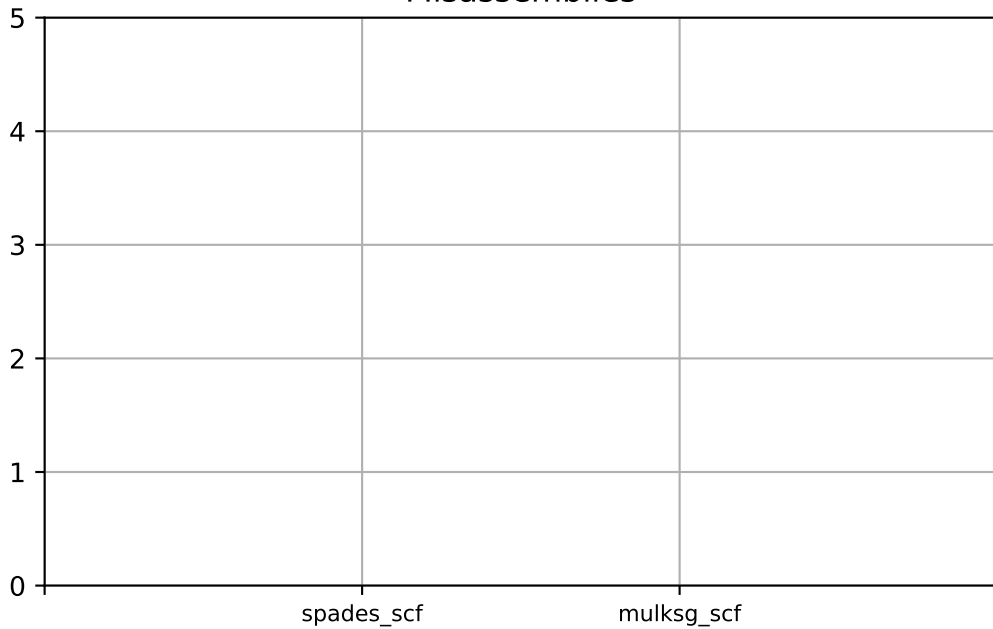
spades_scf coverage histogram (bin size: 1x)



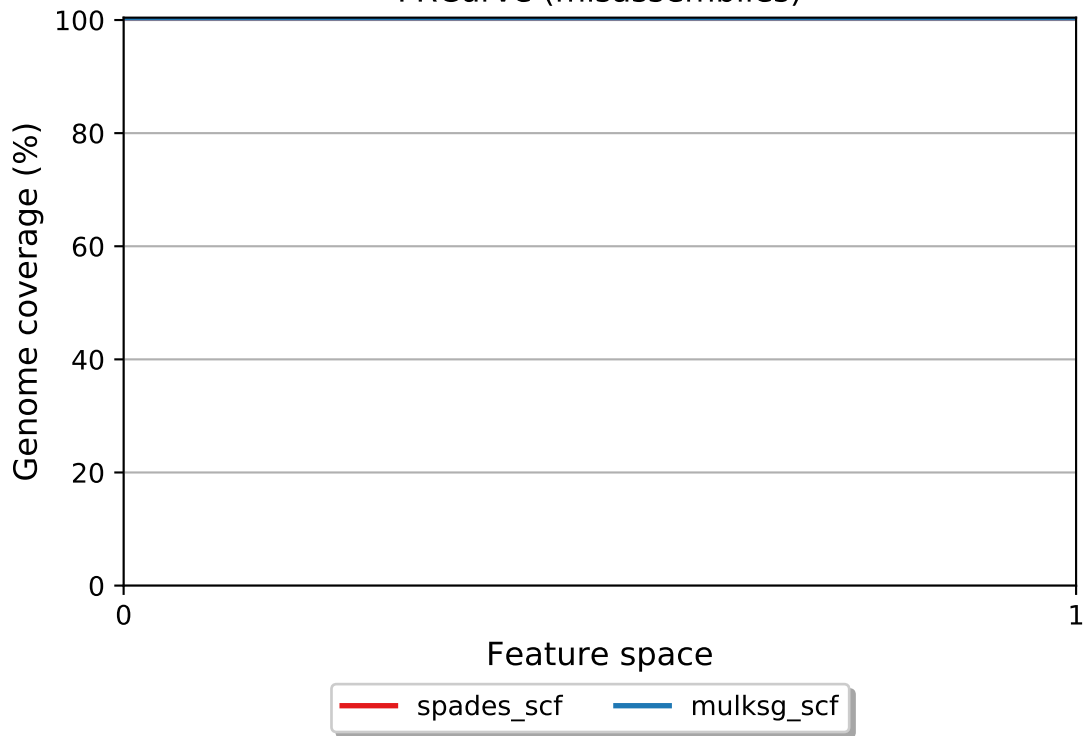
mulksg_scf coverage histogram (bin size: 1x)



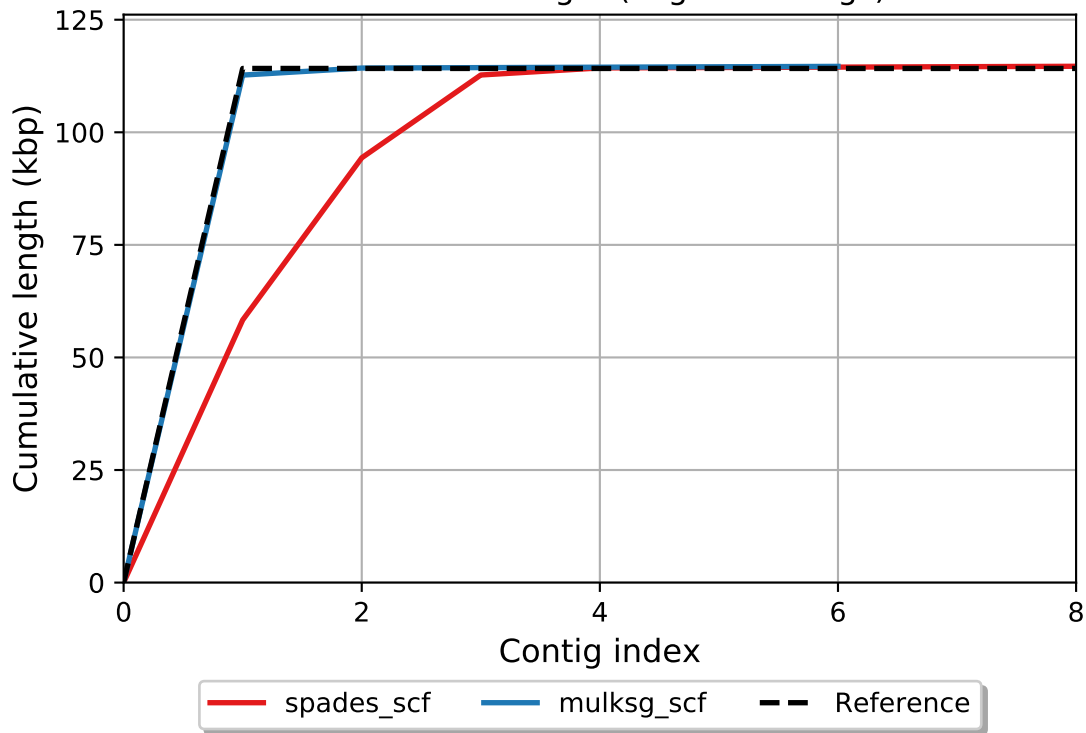
Misassemblies



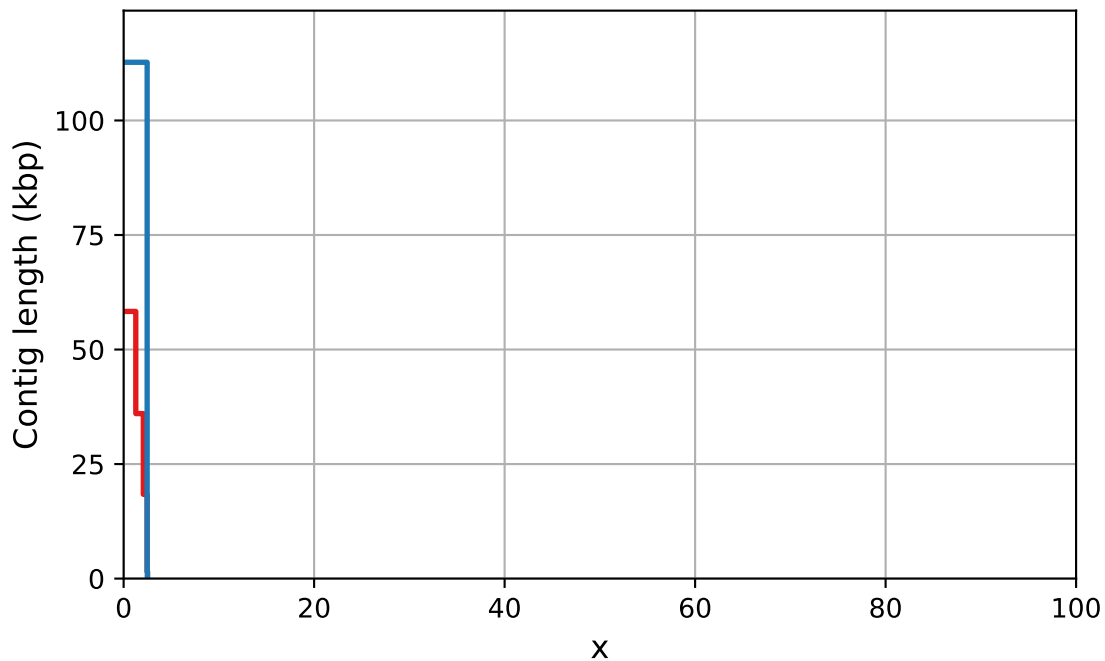
FRCurve (misassemblies)



Cumulative length (aligned contigs)

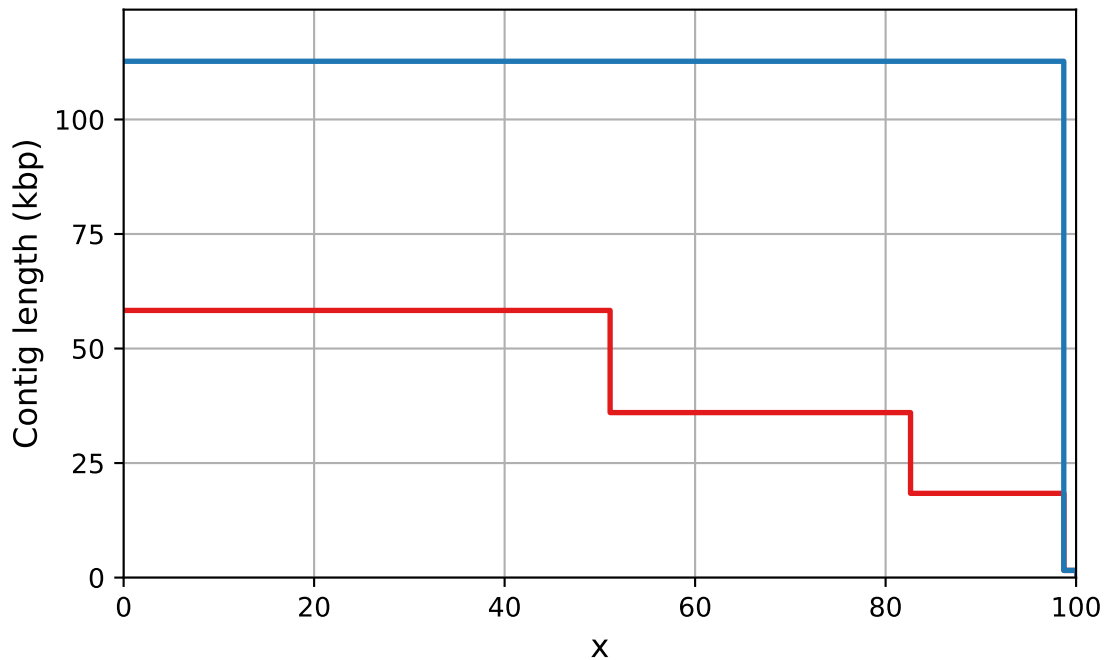


NAx



spades_scf mulksg_scf

NGAx



— spades_scf — mulksg_scf

Genome fraction, %

