

Report

	spades_scf	mulksg_scf
# contigs (>= 0 bp)	3726	3979
# contigs (>= 1000 bp)	36	37
# contigs (>= 5000 bp)	17	17
# contigs (>= 10000 bp)	17	17
# contigs (>= 25000 bp)	14	14
# contigs (>= 50000 bp)	13	13
Total length (>= 0 bp)	6203035	6291814
Total length (>= 1000 bp)	4911542	4912423
Total length (>= 5000 bp)	4884523	4884523
Total length (>= 10000 bp)	4884523	4884523
Total length (>= 25000 bp)	4823200	4823200
Total length (>= 50000 bp)	4777123	4777123
# contigs	422	440
Largest contig	1079605	1079605
Total length	5150754	5163104
Reference length	4744448	4744448
GC (%)	61.63	61.65
Reference GC (%)	61.55	61.55
N50	656974	656974
NG50	656974	656974
N75	289572	289572
NG75	491389	491389
L50	3	3
LG50	3	3
L75	6	6
LG75	5	5
# misassemblies	6	6
# misassembled contigs	3	3
Misassembled contigs length	366493	366493
# local misassemblies	45	45
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	14	14
# unaligned contigs	399 + 18 part	418 + 17 part
Unaligned length	3314893	3327363
Genome fraction (%)	38.682	38.677
Duplication ratio	1.000	1.000
# N's per 100 kbp	5.73	5.71
# mismatches per 100 kbp	4036.37	4036.73
# indels per 100 kbp	38.09	38.09
Largest alignment	61358	61358
Total aligned length	1835757	1835637
NGA50	-	-

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

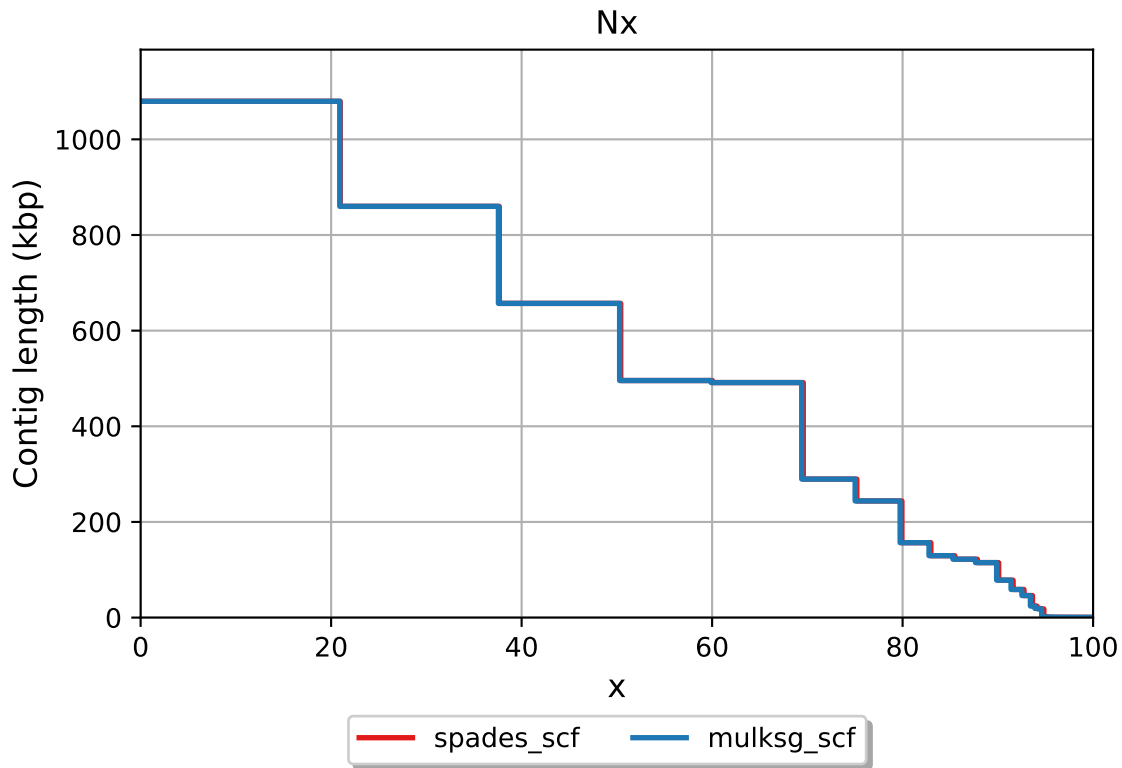
	spades_scf	mulksg_scf
# misassemblies	6	6
# contig misassemblies	6	6
# c. relocations	6	6
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	3	3
Misassembled contigs length	366493	366493
# local misassemblies	45	45
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	14	14
# mismatches	74077	74075
# indels	699	699
# indels (<= 5 bp)	637	637
# indels (> 5 bp)	62	62
Indels length	2021	2021

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).

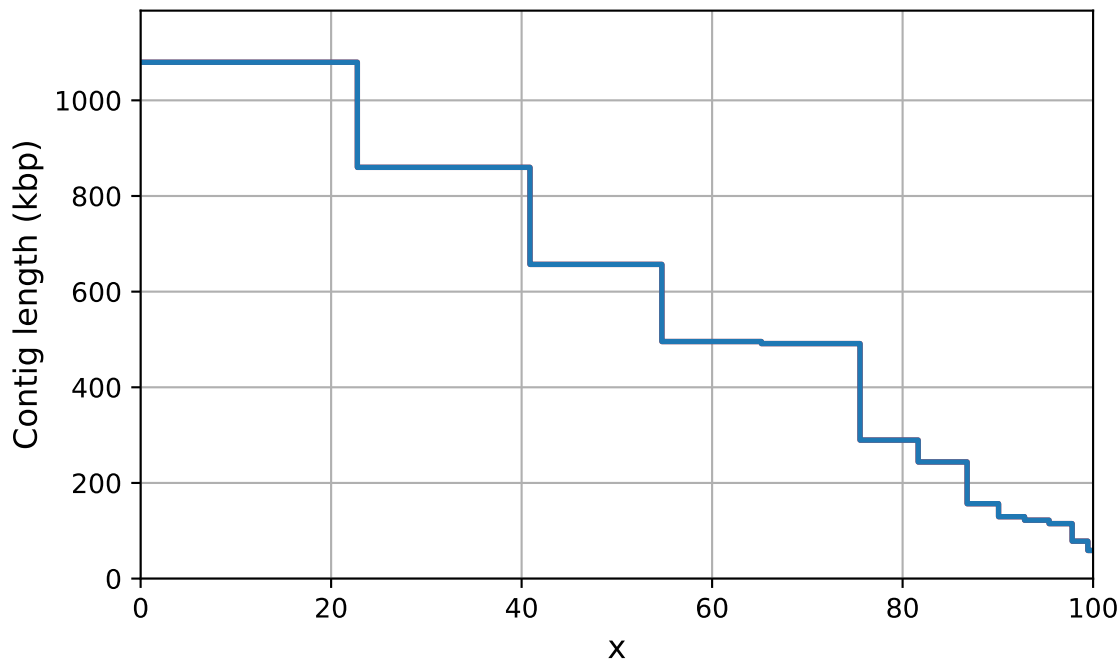
Unaligned report

	spades_scf	mulksf_scf
# fully unaligned contigs	399	418
Fully unaligned length	259180	272307
# partially unaligned contigs	18	17
Partially unaligned length	3055713	3055056
# N's	295	295

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).

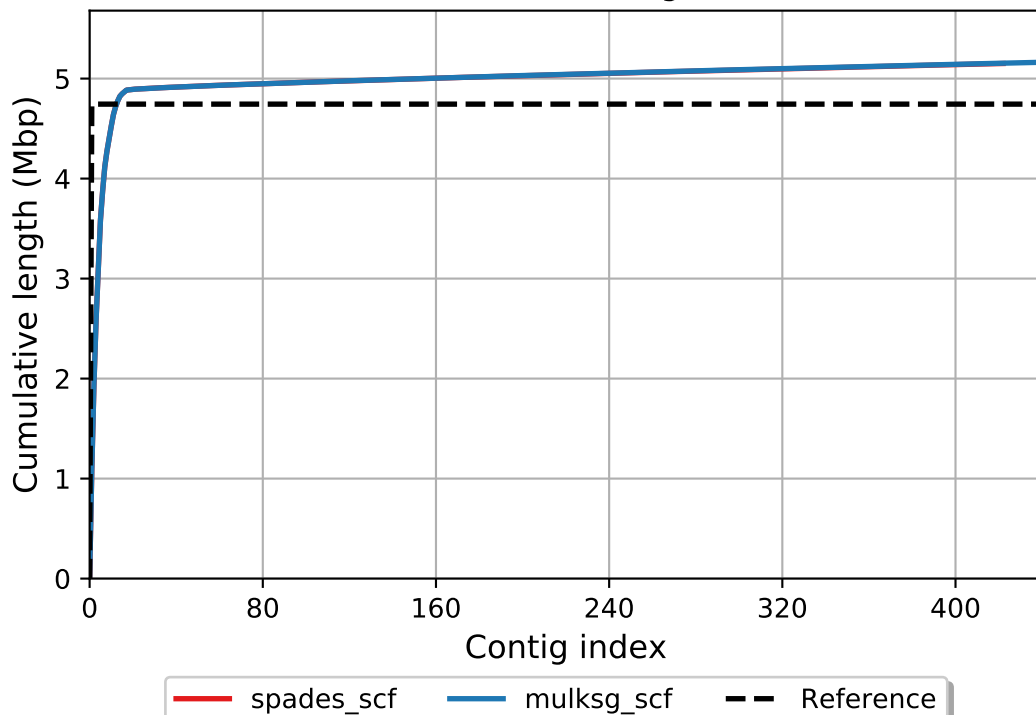


NGx

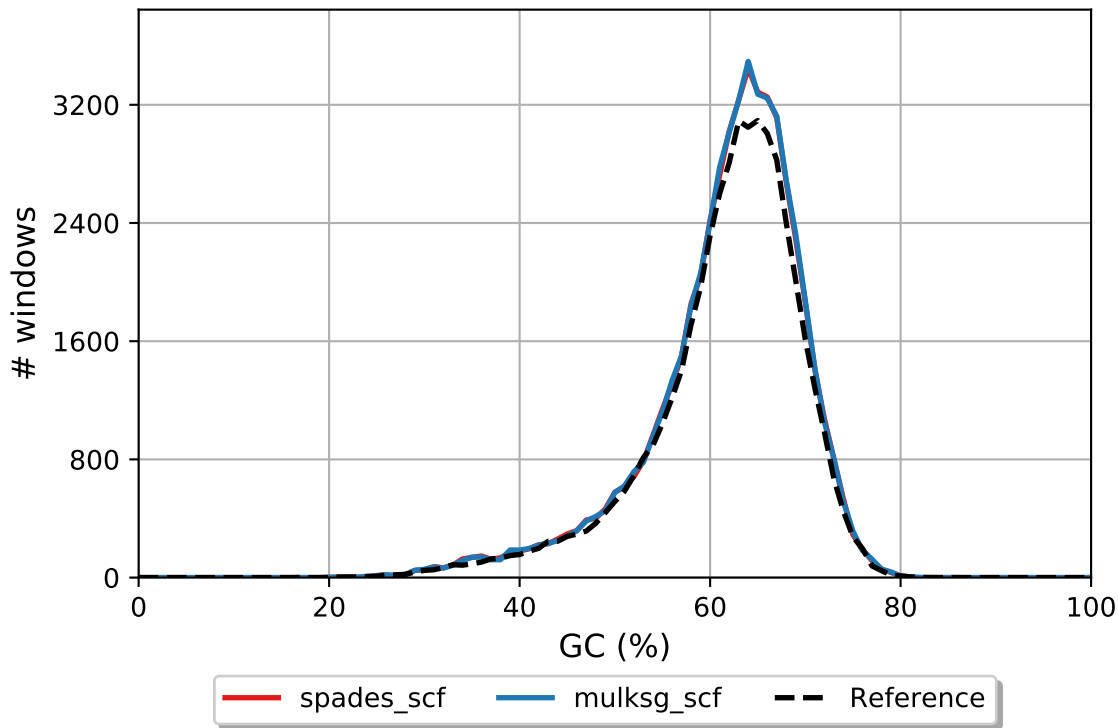


spades_scf mulksg_scf

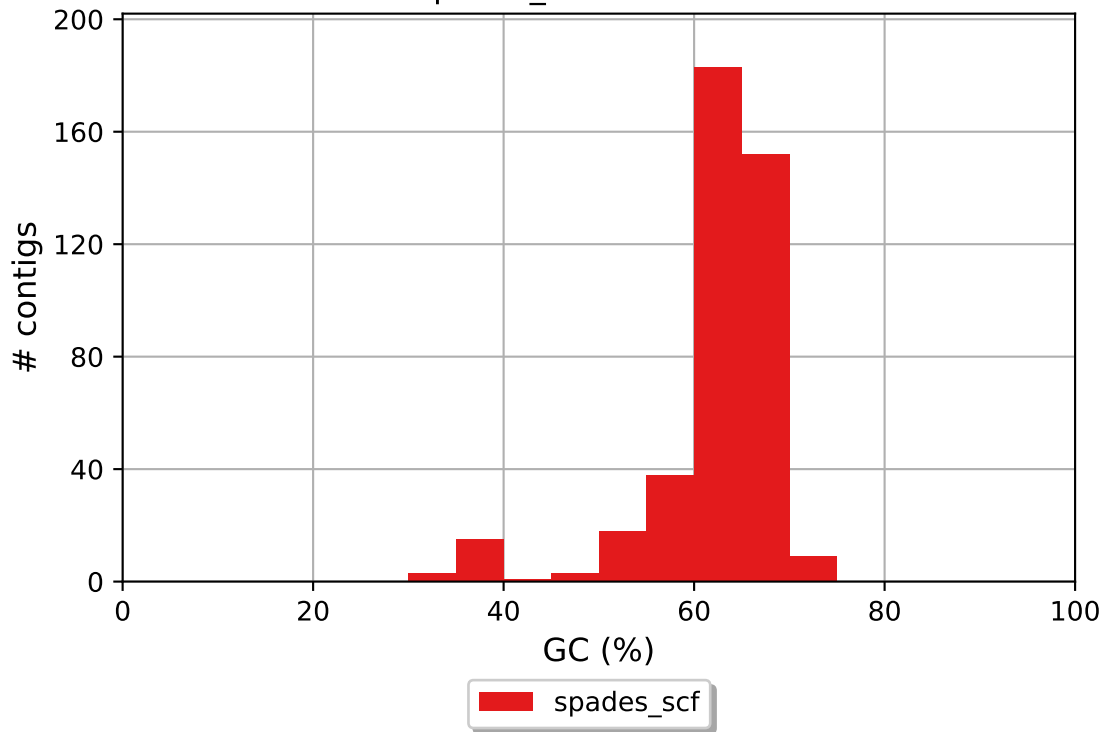
Cumulative length



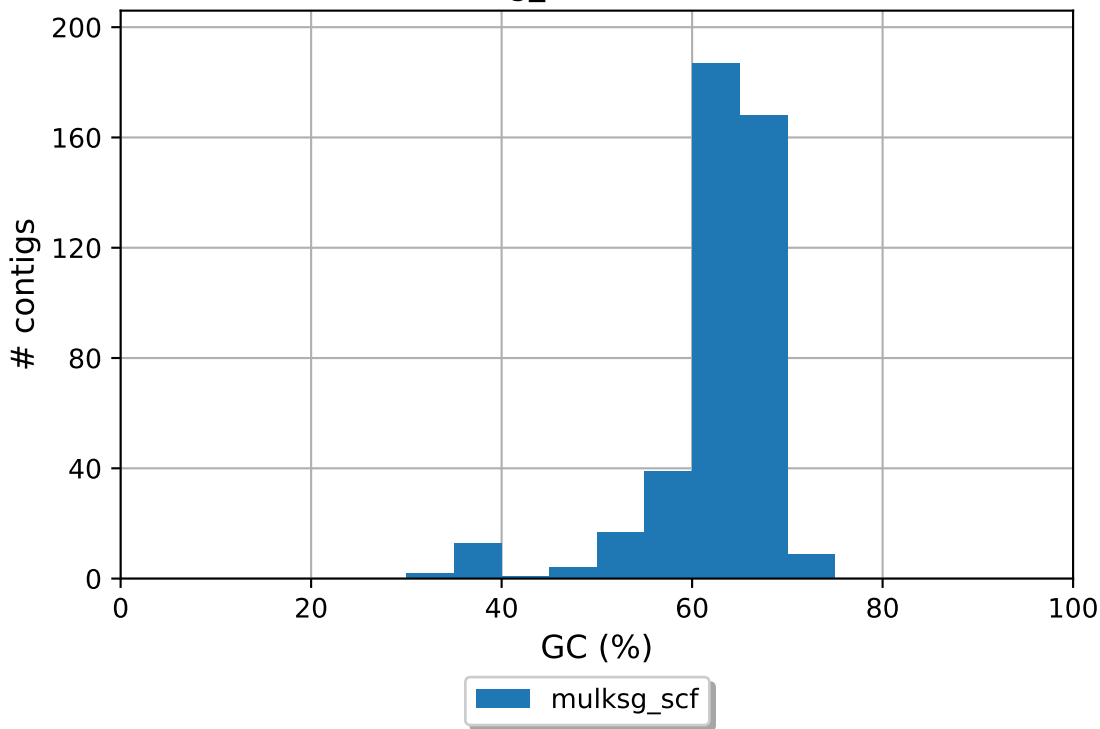
GC content



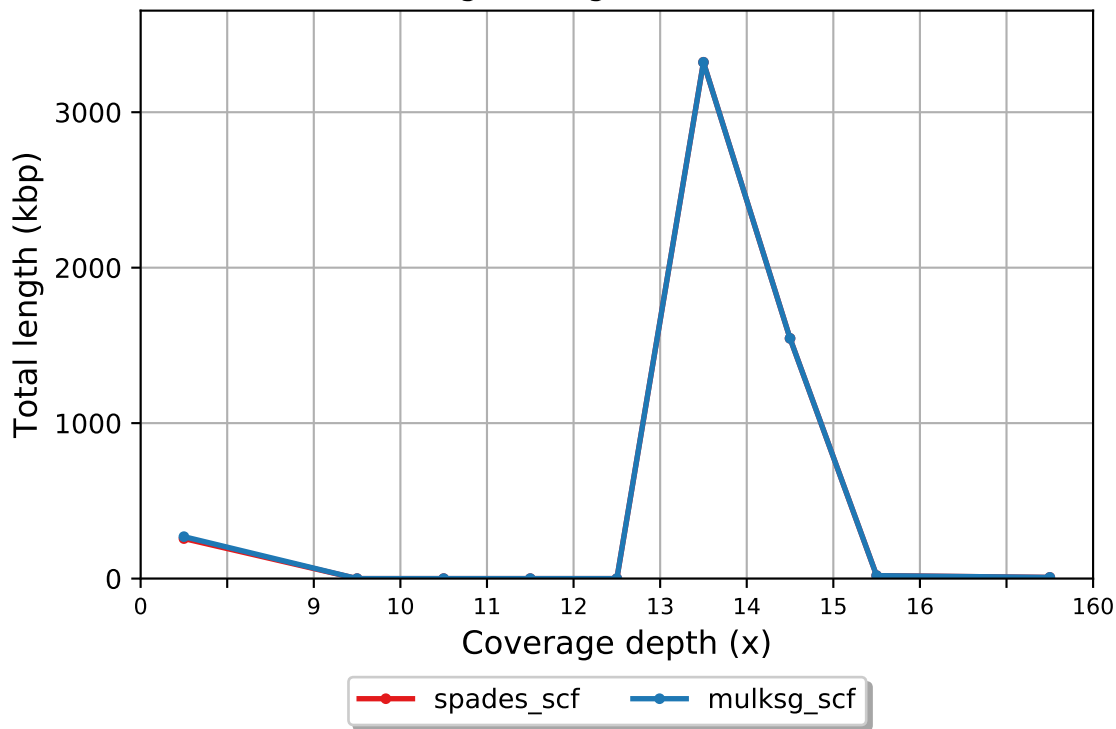
spades_scf GC content



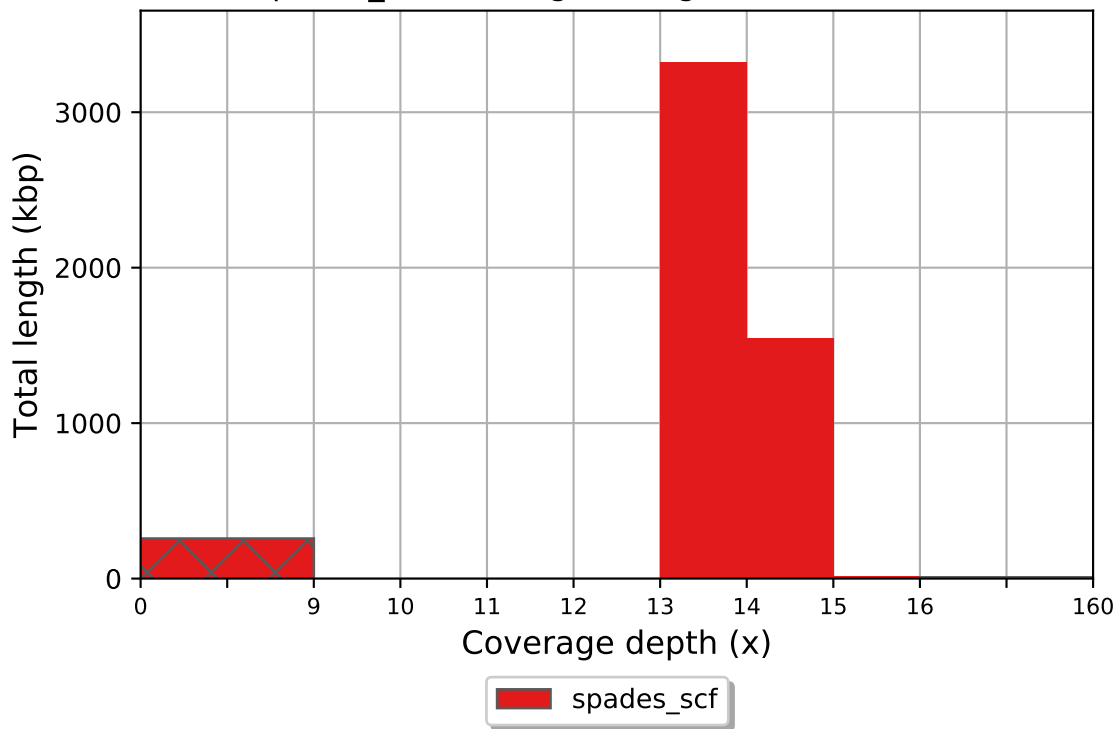
mulksg_scf GC content



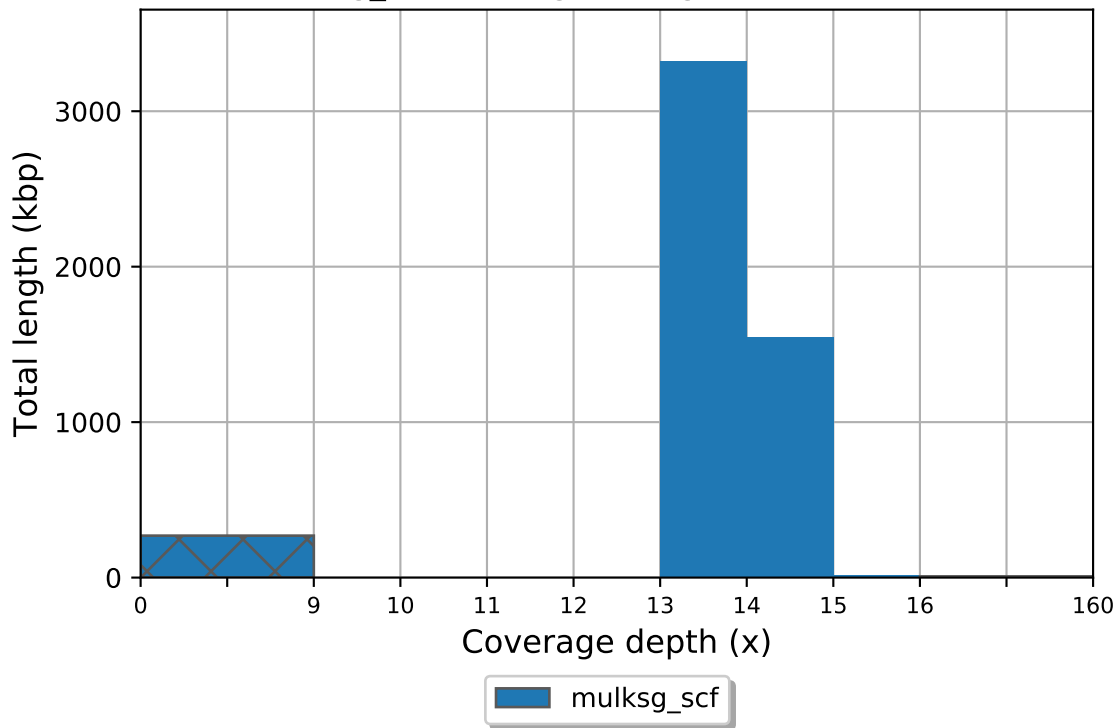
Coverage histogram (bin size: 1x)



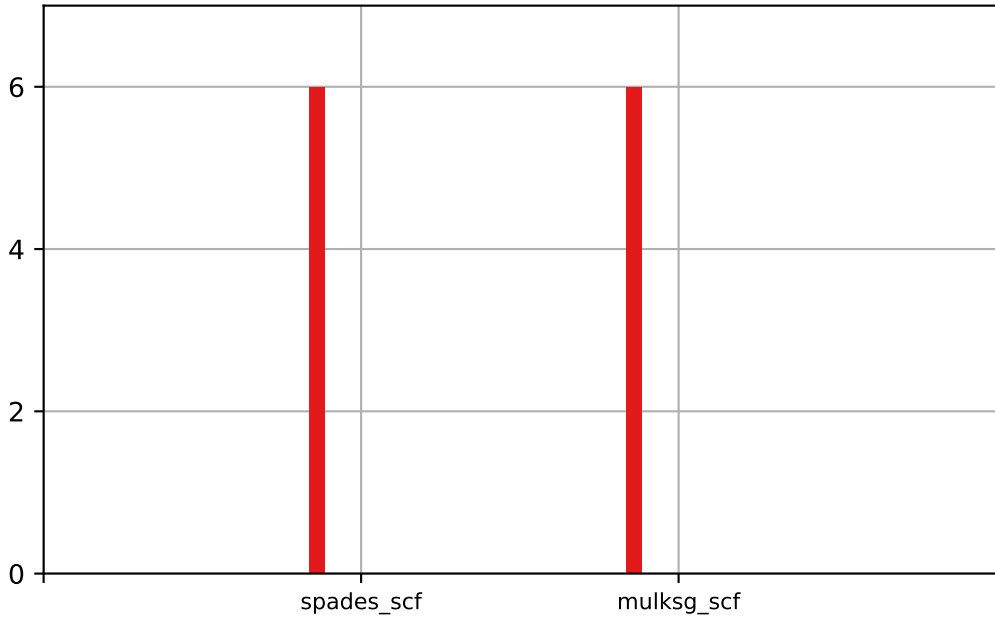
spades_scf coverage histogram (bin size: 1x)



mulksg_scf coverage histogram (bin size: 1x)

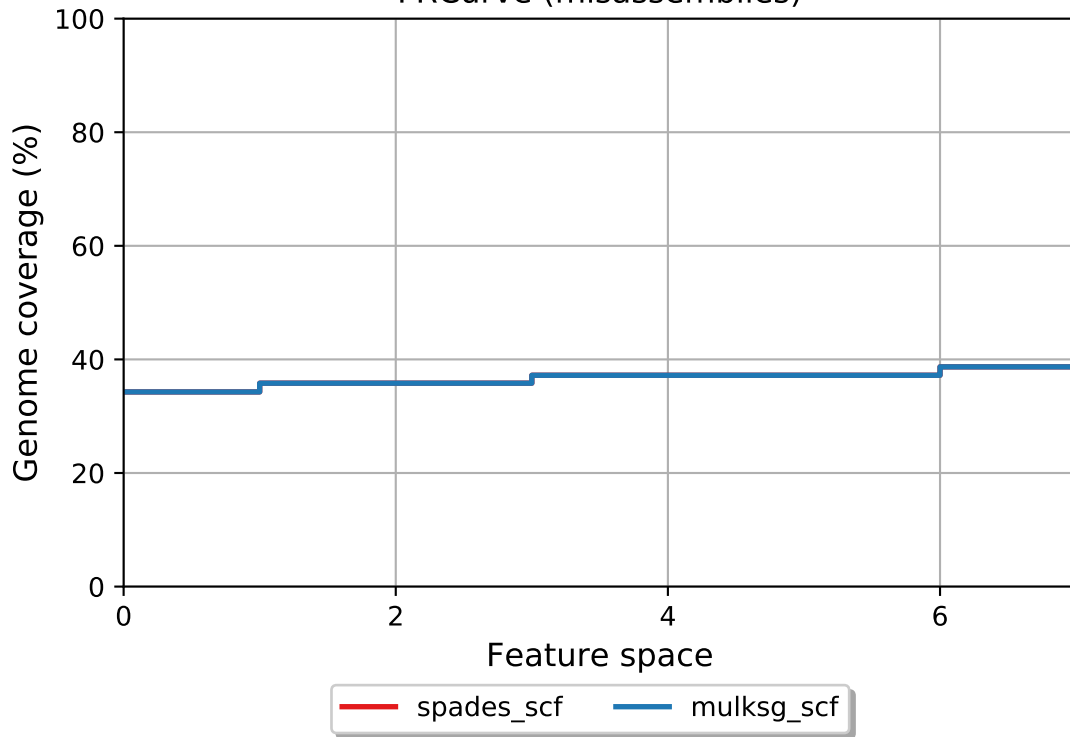


Misassemblies

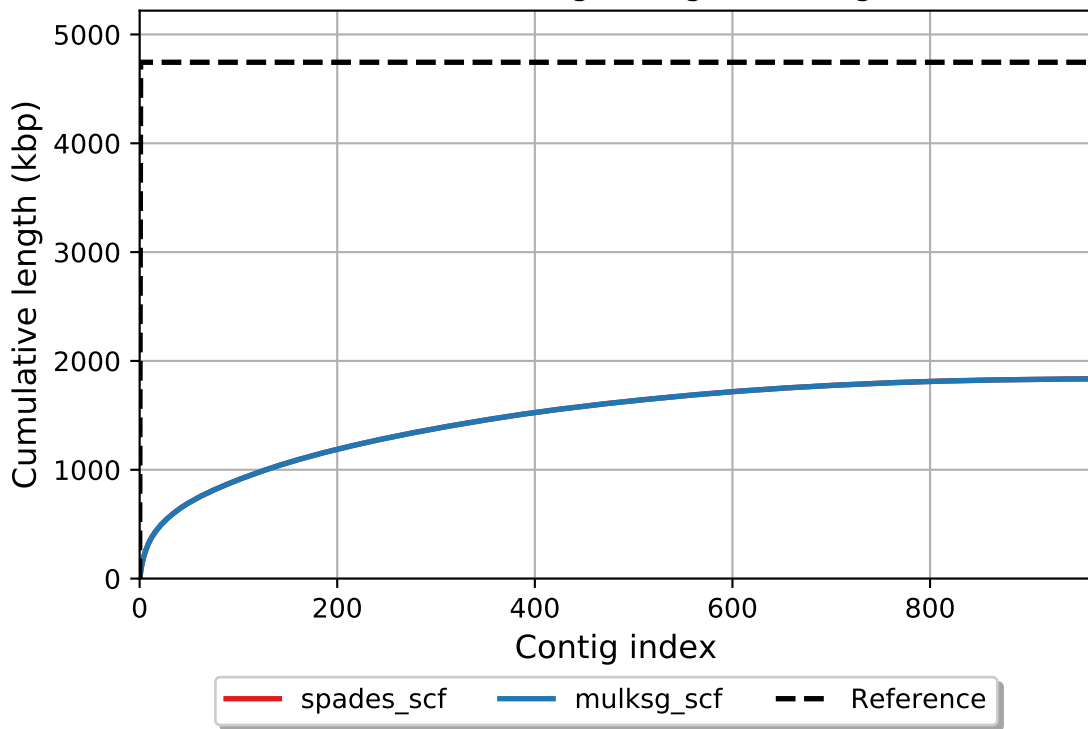


 # relocations

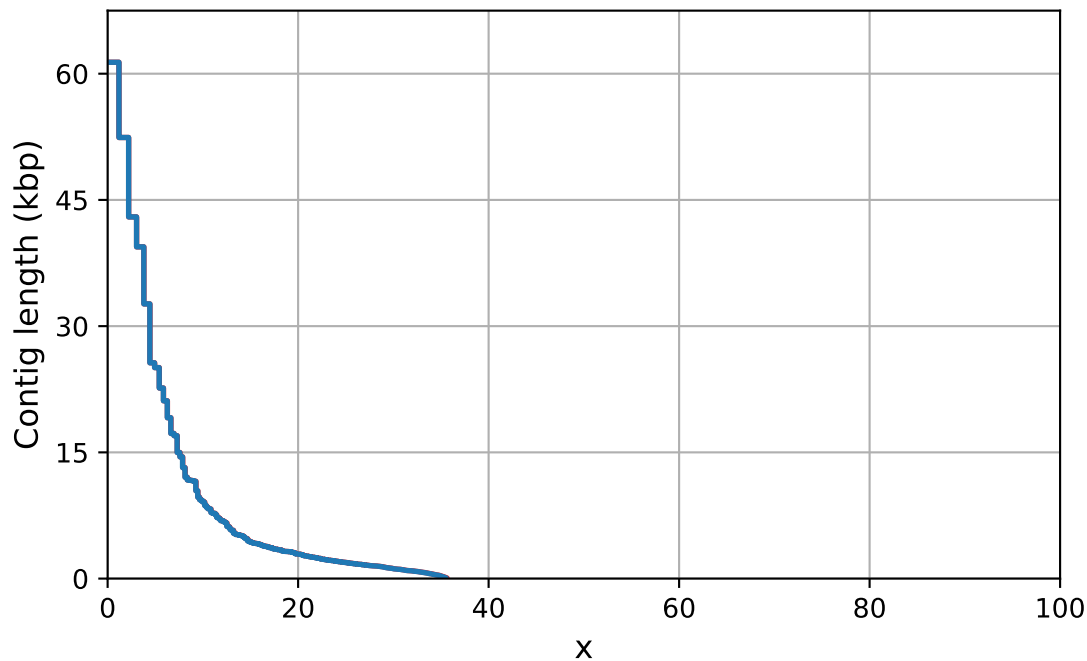
FRCurve (misassemblies)



Cumulative length (aligned contigs)

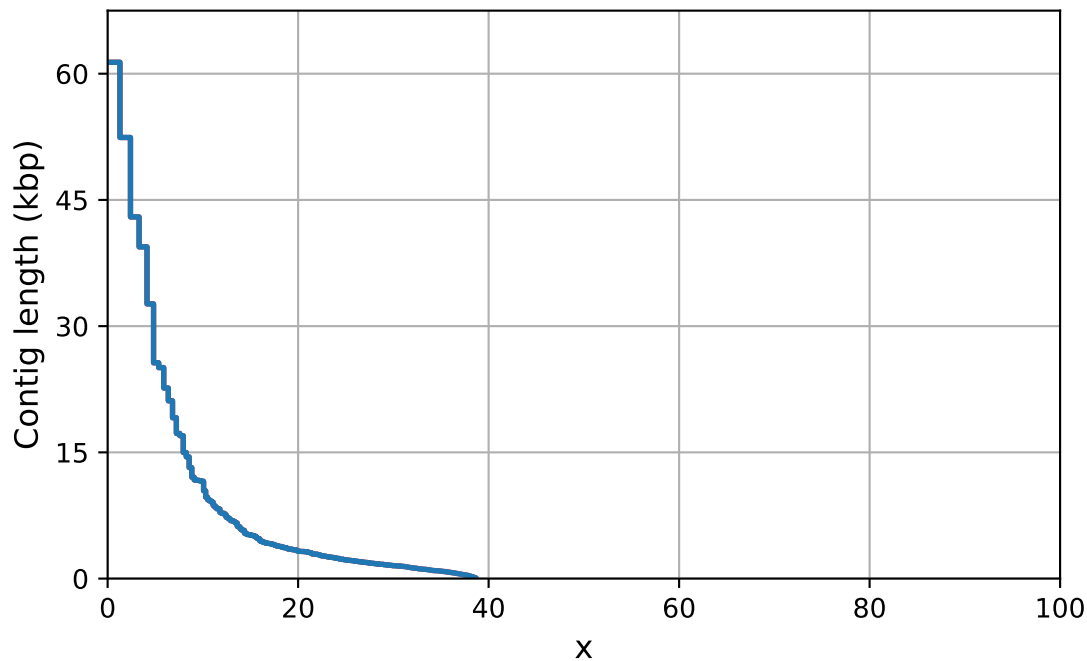


NAx



spades_scf mulksg_scf

NGAx



spades_scf mulksg_scf

Genome fraction, %

100

50



spades_scf



mulks_g_scf