

Report

	spades_scf	mulksq_scf
# contigs (>= 0 bp)	306	305
# contigs (>= 1000 bp)	99	98
# contigs (>= 5000 bp)	71	70
# contigs (>= 10000 bp)	61	61
# contigs (>= 25000 bp)	44	44
# contigs (>= 50000 bp)	34	34
Total length (>= 0 bp)	4943957	4943249
Total length (>= 1000 bp)	4899764	4899046
Total length (>= 5000 bp)	4835293	4834575
Total length (>= 10000 bp)	4767398	4772442
Total length (>= 25000 bp)	4477870	4482914
Total length (>= 50000 bp)	4110195	4110195
# contigs	114	113
Largest contig	353048	353048
Total length	4909888	4909170
Reference length	4967469	4967469
GC (%)	65.10	65.10
Reference GC (%)	64.92	64.92
N50	117399	117399
NG50	117399	117399
N75	66058	66058
NG75	63515	63515
L50	14	14
LG50	14	14
L75	27	27
LG75	28	28
# misassemblies	36	37
# misassembled contigs	16	17
Misassembled contigs length	2455313	2496677
# local misassemblies	479	487
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	1	1
# unaligned mis. contigs	26	25
# unaligned contigs	51 + 57 part	51 + 57 part
Unaligned length	2241004	2240813
Genome fraction (%)	53.670	53.670
Duplication ratio	1.001	1.001
# N's per 100 kbp	2.02	2.02
# mismatches per 100 kbp	4206.37	4210.79
# indels per 100 kbp	51.31	51.39
Largest alignment	111601	111601
Total aligned length	2666668	2666672
NA50	1902	1956
NGA50	1733	1820
LA50	176	169
LGA50	191	184

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

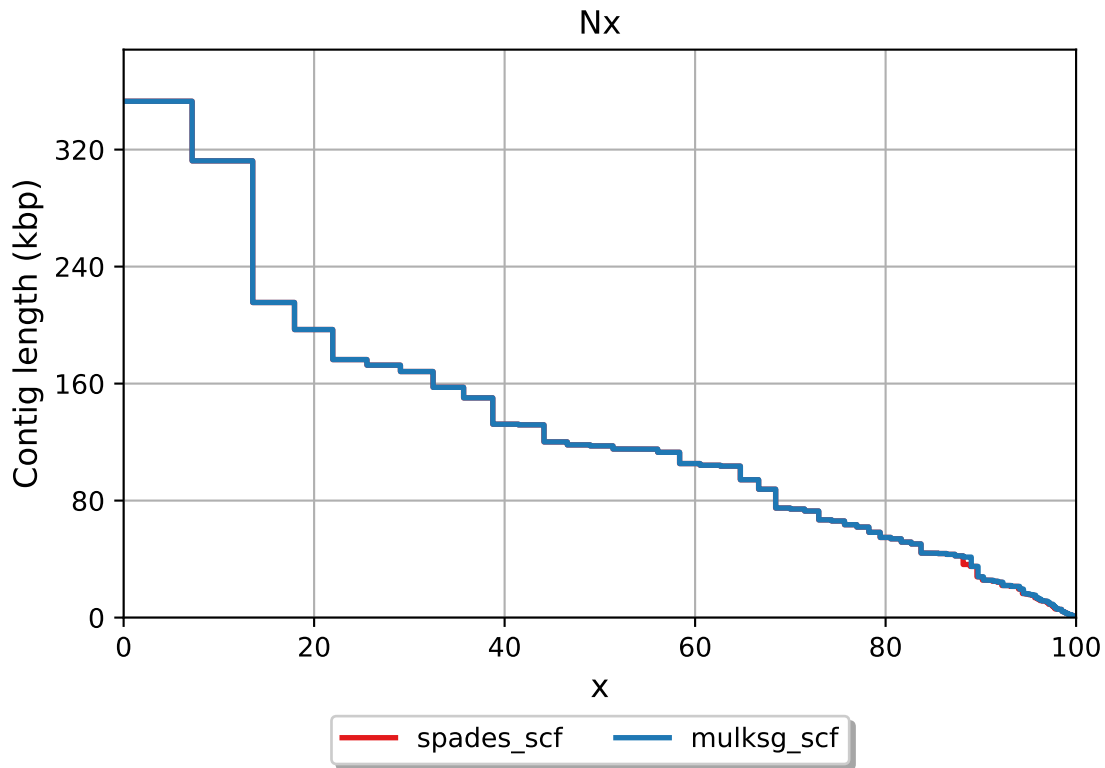
	spades_scf	mulksf_scf
# misassemblies	36	37
# contig misassemblies	36	37
# c. relocations	36	37
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	16	17
Misassembled contigs length	2455313	2496677
# local misassemblies	479	487
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	1	1
# unaligned mis. contigs	26	25
# mismatches	112143	112261
# indels	1368	1370
# indels (<= 5 bp)	1232	1234
# indels (> 5 bp)	136	136
Indels length	3804	3810

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).

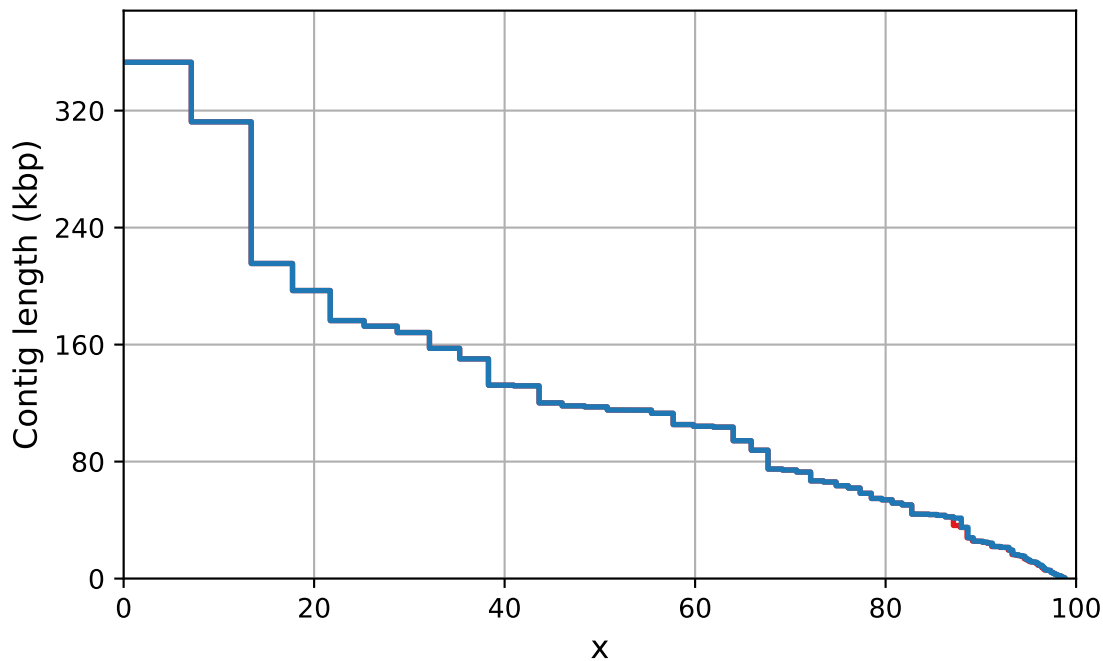
Unaligned report

	spades_scf	mulksg_scf
# fully unaligned contigs	51	51
Fully unaligned length	157831	157831
# partially unaligned contigs	57	57
Partially unaligned length	2083173	2082982
# N's	99	99

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).

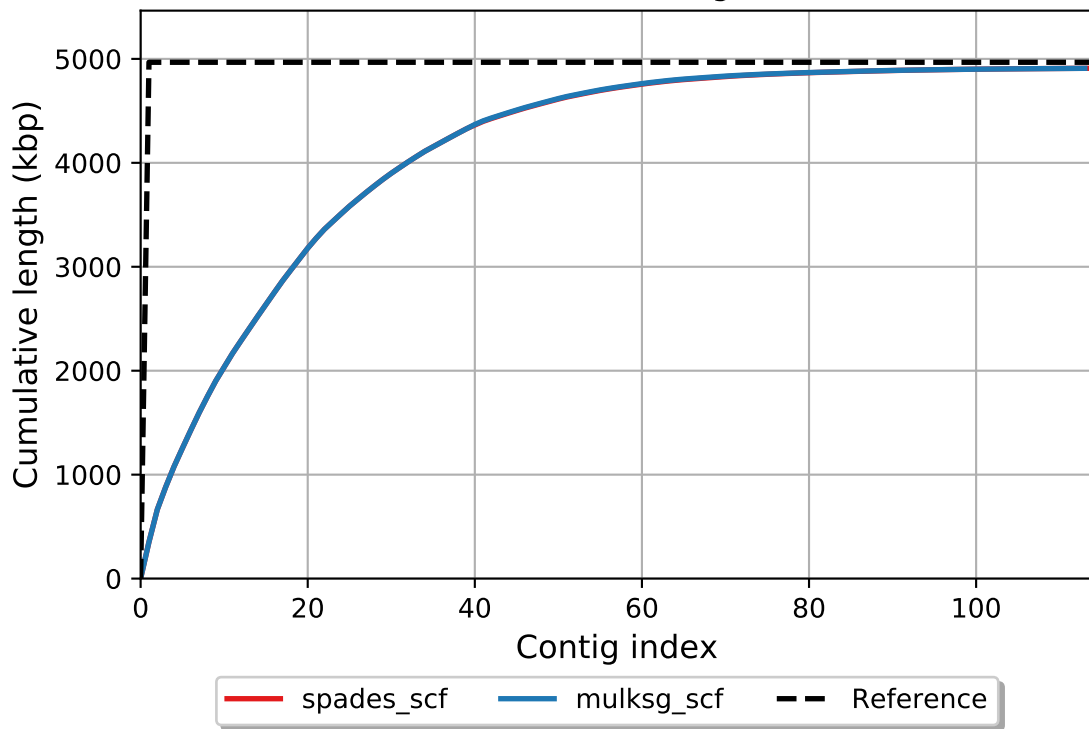


NGx

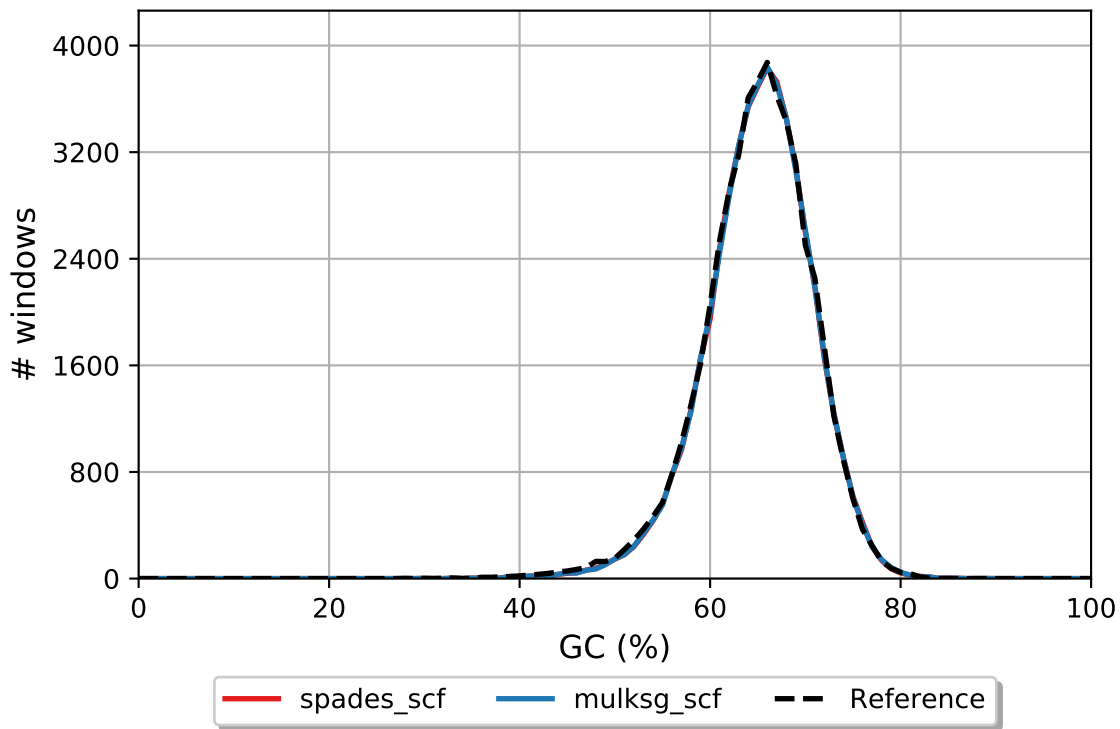


spades_scf mulksg_scf

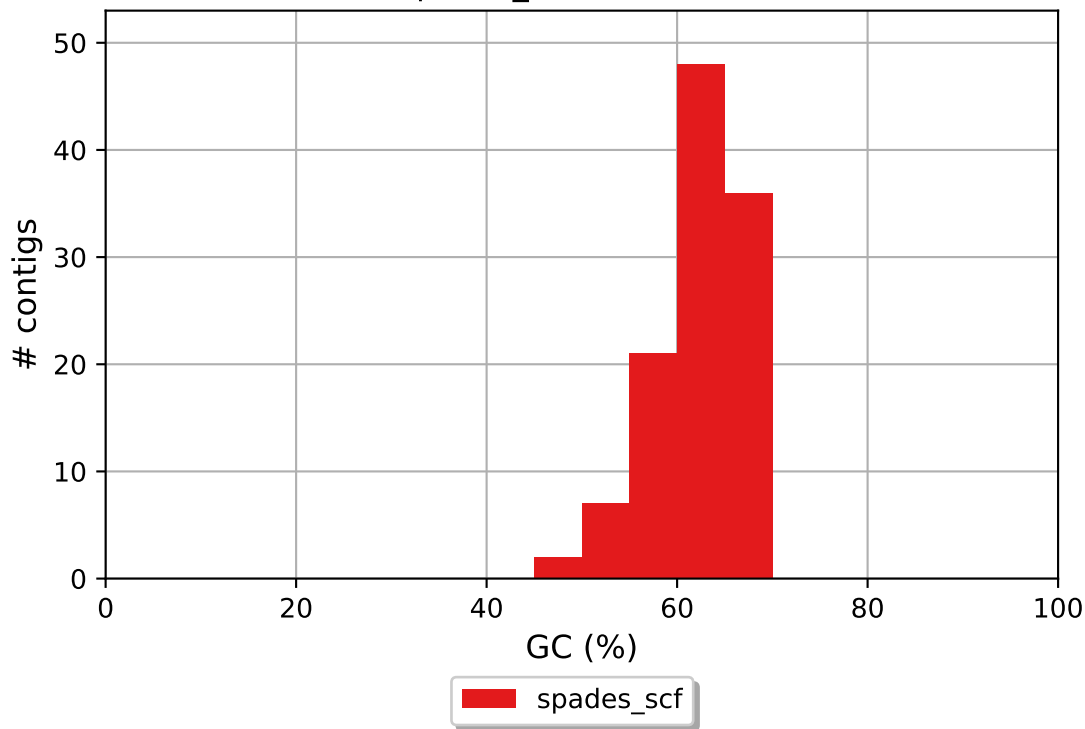
Cumulative length



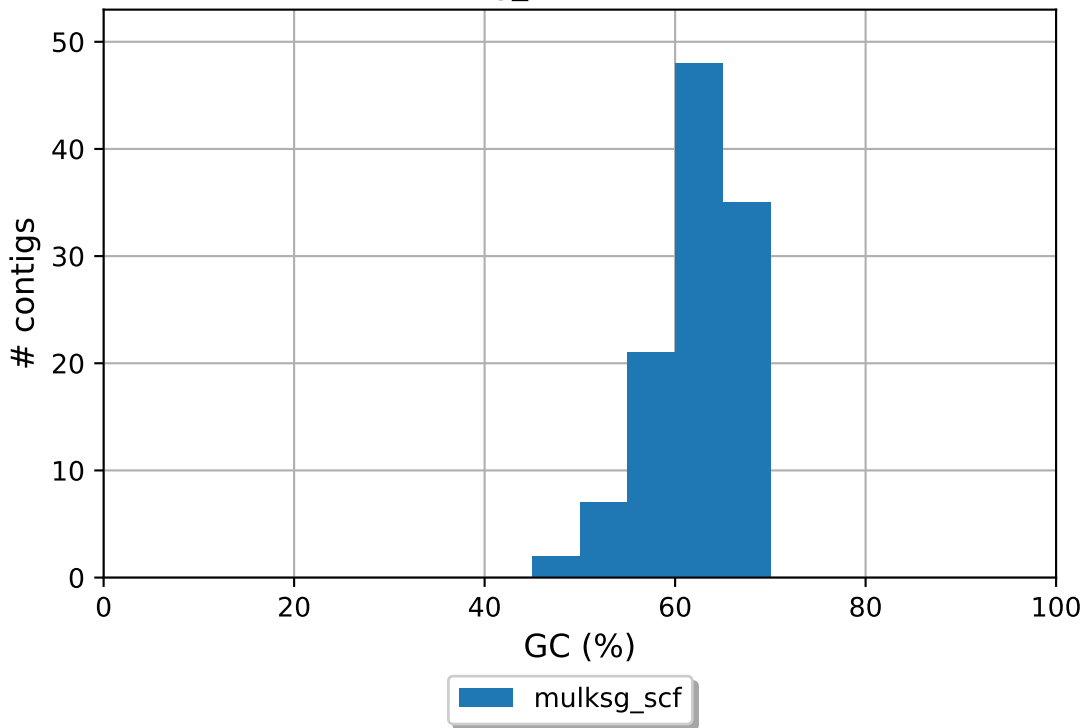
GC content



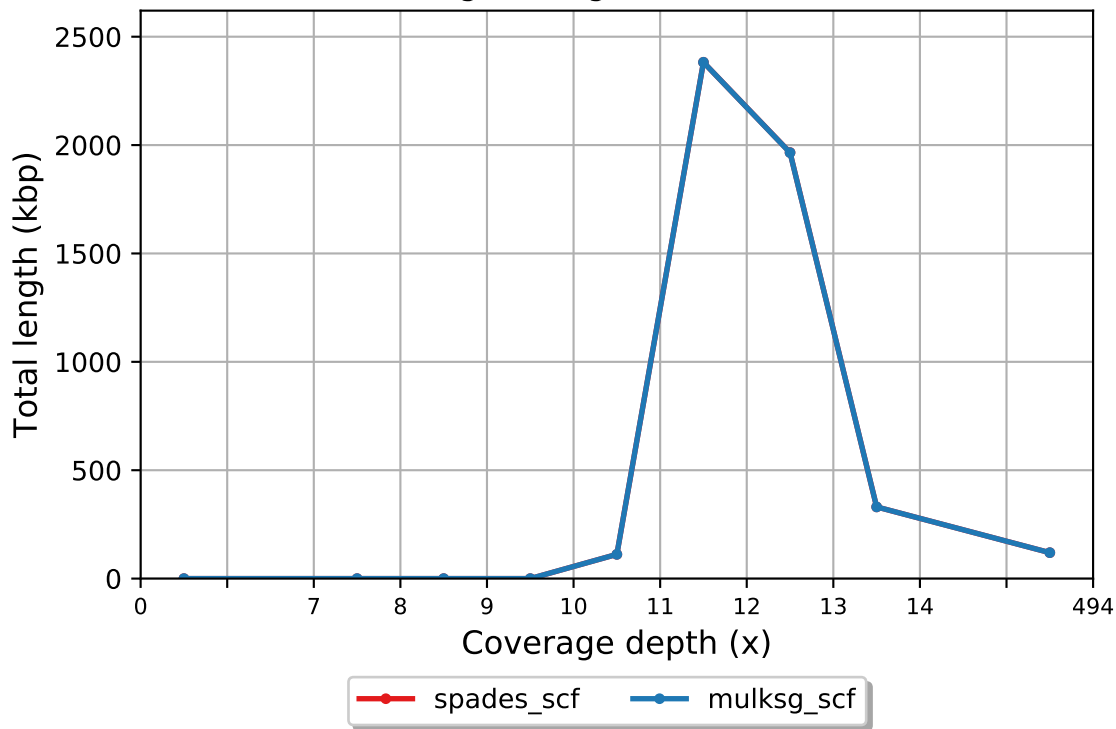
spades_scf GC content



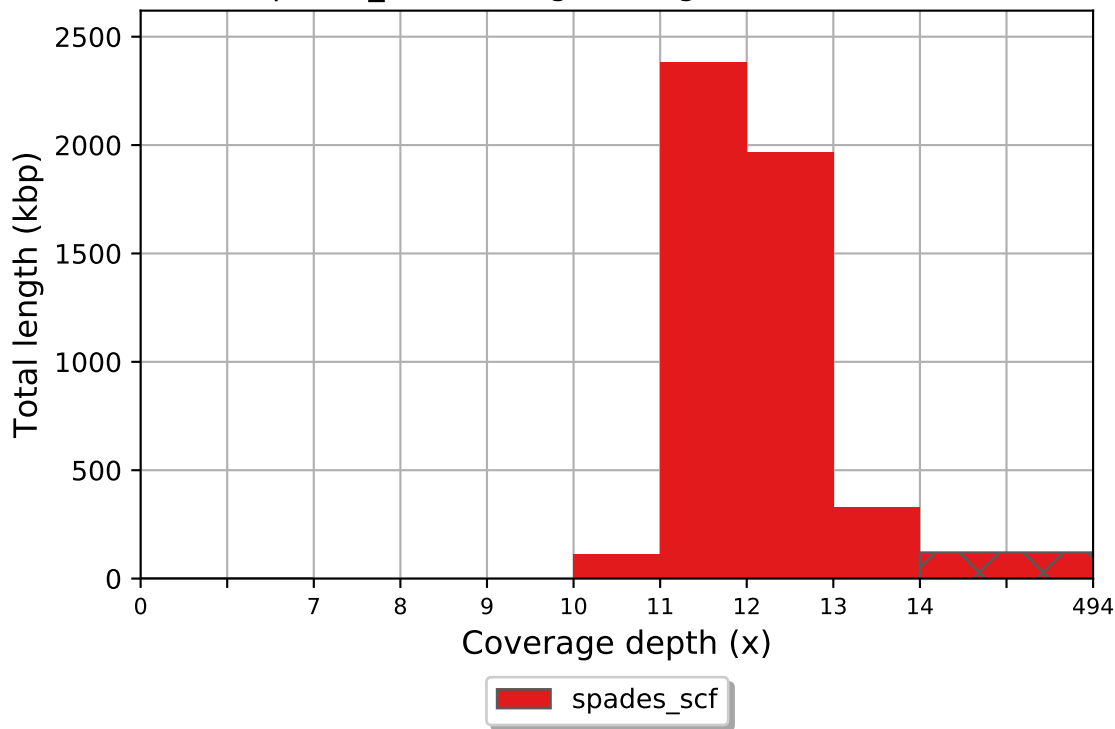
mulksg_scf GC content



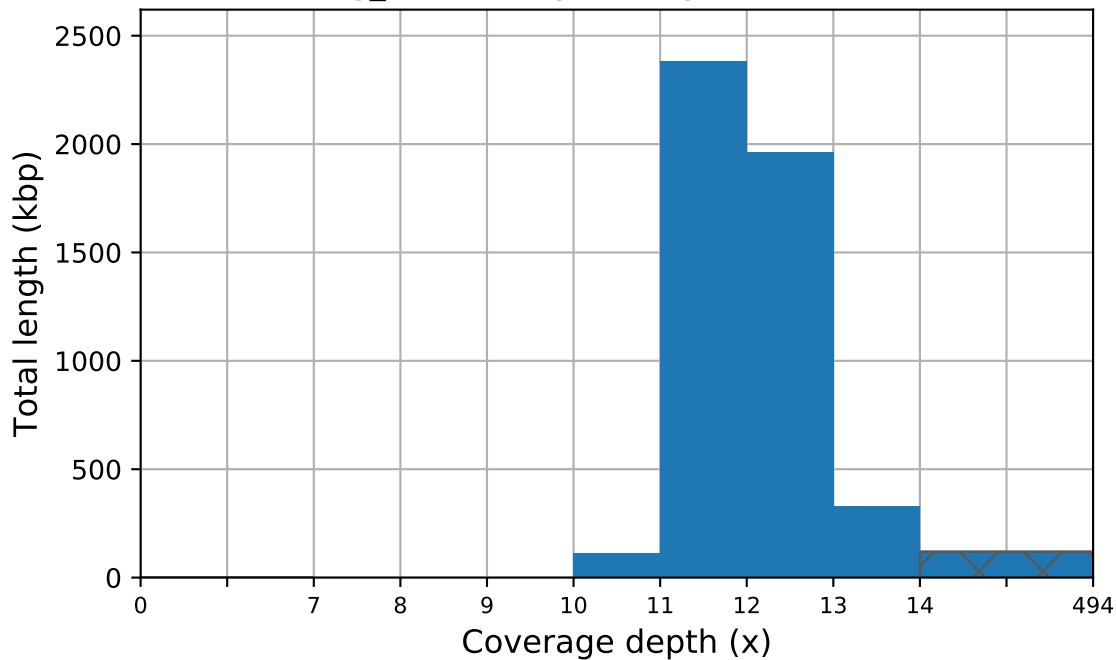
Coverage histogram (bin size: 1x)



spades_scf coverage histogram (bin size: 1x)

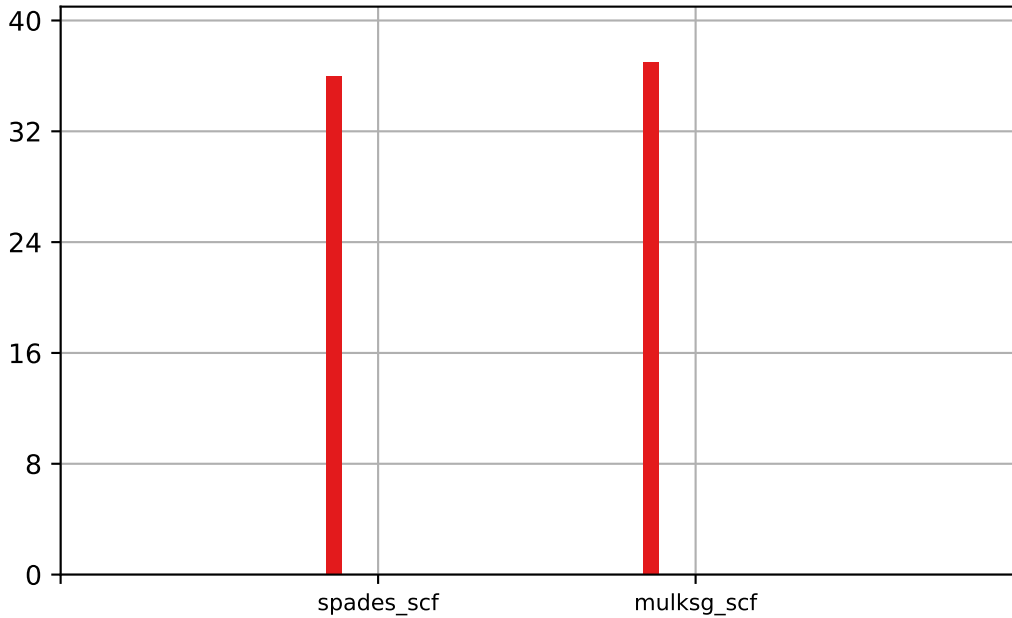


mulksg_scf coverage histogram (bin size: 1x)



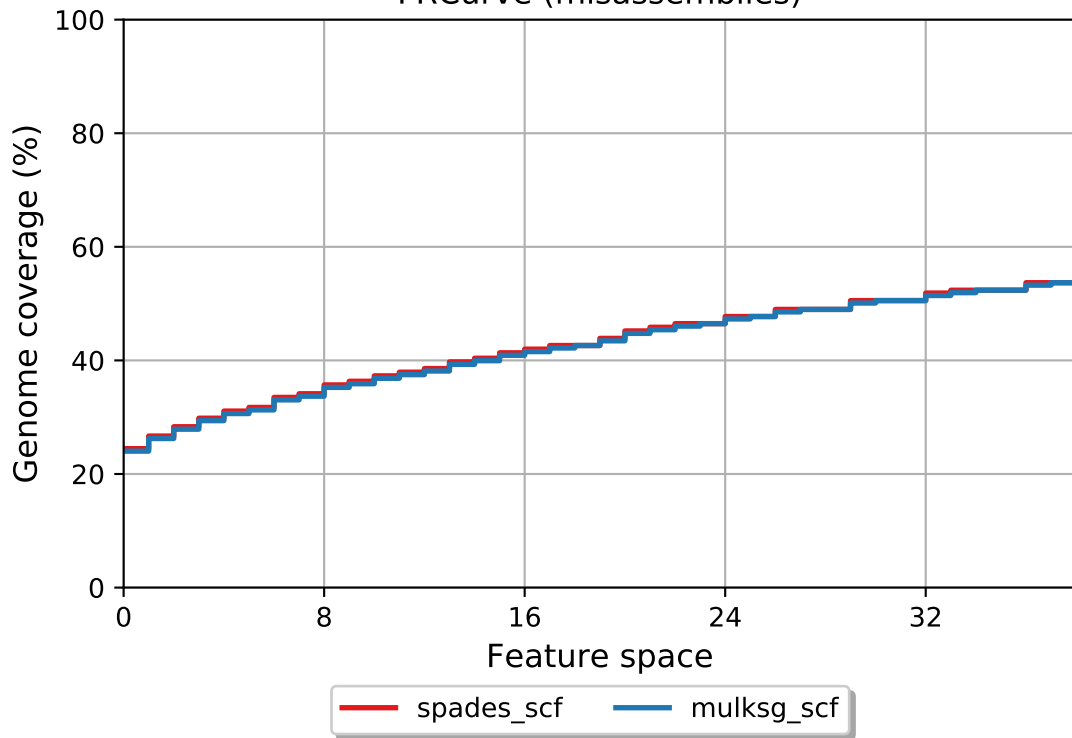
mulksg_scf

Misassemblies

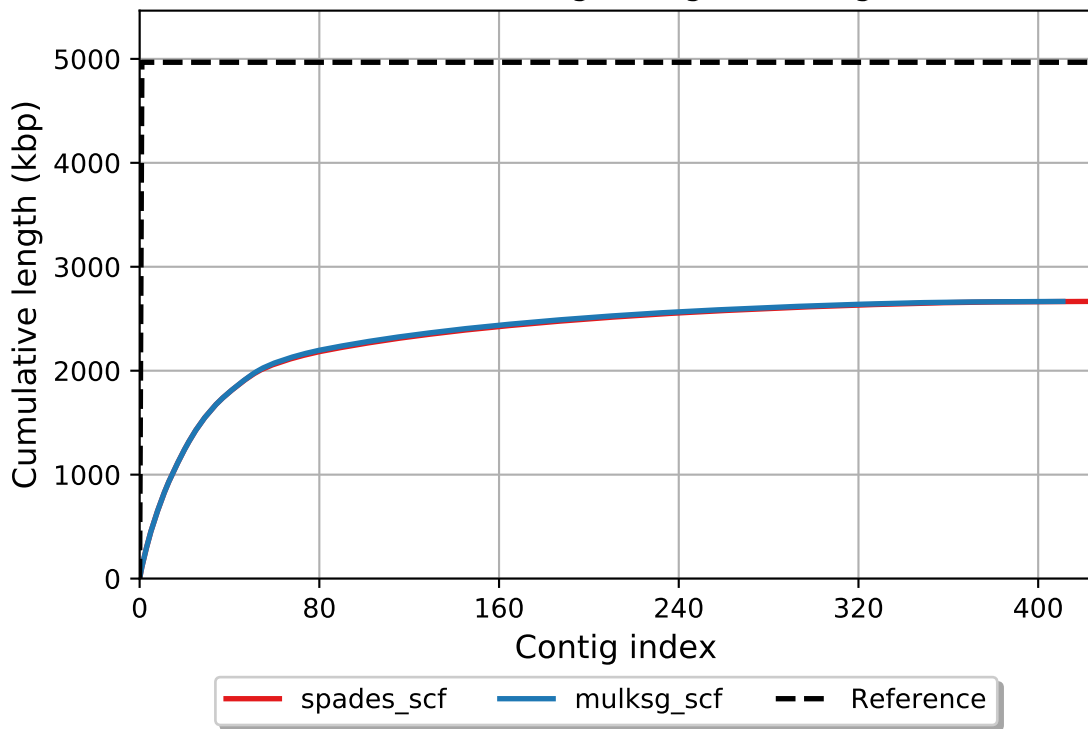


 # relocations

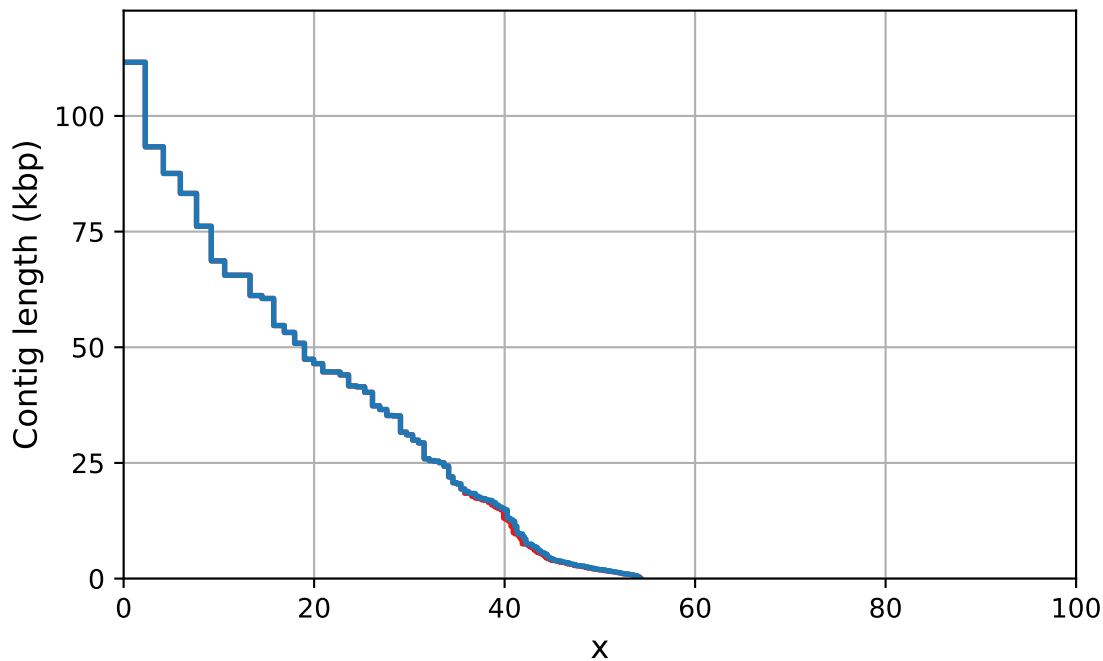
FRCurve (misassemblies)



Cumulative length (aligned contigs)

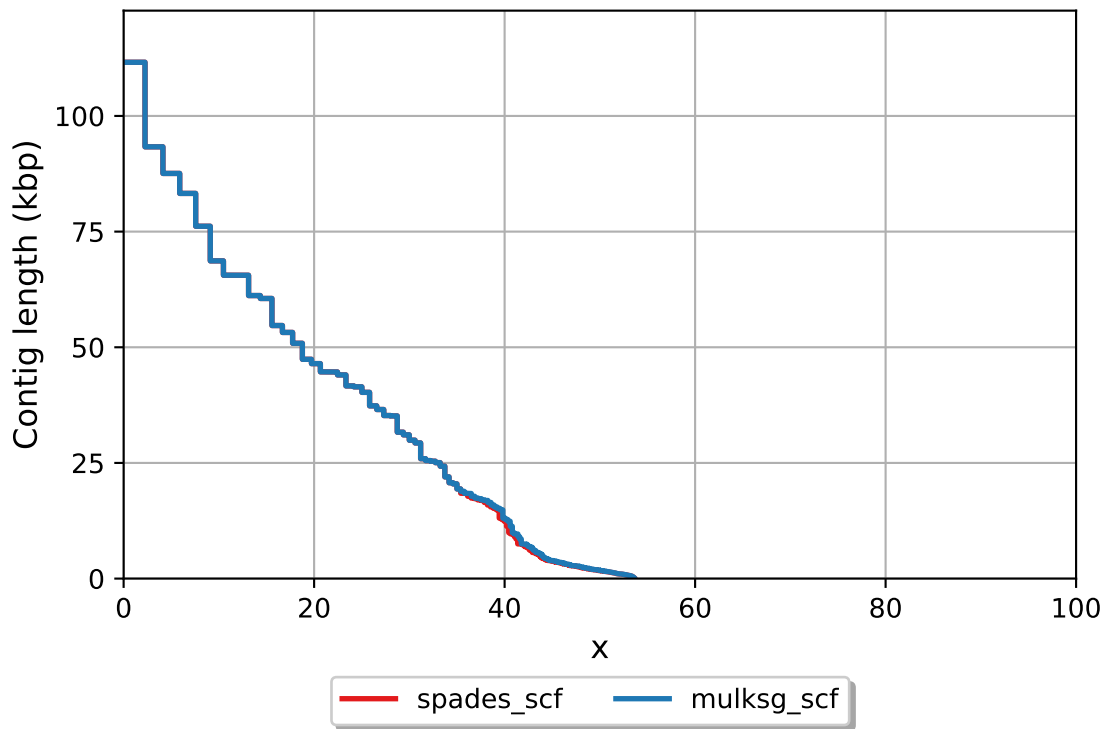


NAx

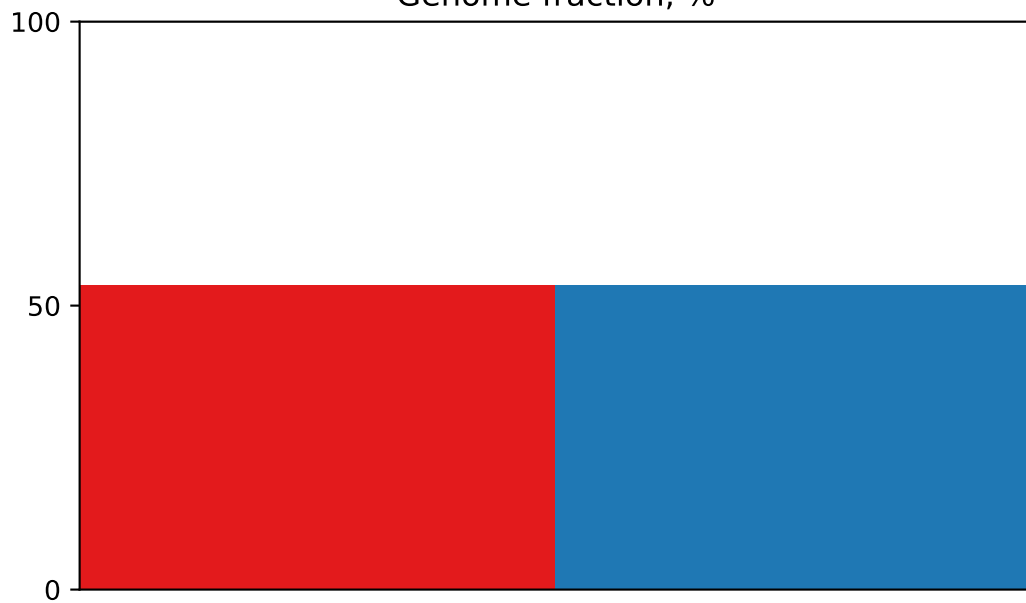


spades_scf mulksg_scf

NGAx



Genome fraction, %



spades_scf



mulksg_scf