

Report

	spades_scf	mulksq_scf
# contigs (>= 0 bp)	634	625
# contigs (>= 1000 bp)	66	56
# contigs (>= 5000 bp)	38	29
# contigs (>= 10000 bp)	30	23
# contigs (>= 25000 bp)	22	19
# contigs (>= 50000 bp)	20	16
Total length (>= 0 bp)	4174333	4174432
Total length (>= 1000 bp)	3939294	3938252
Total length (>= 5000 bp)	3872333	3875816
Total length (>= 10000 bp)	3812943	3834948
Total length (>= 25000 bp)	3681650	3781002
Total length (>= 50000 bp)	3592797	3656854
# contigs	157	149
Largest contig	384004	573239
Total length	3996348	3996360
Reference length	2961149	2961149
GC (%)	47.33	47.33
Reference GC (%)	47.70	47.70
N50	243364	350399
NG50	262473	508069
N75	105216	132765
NG75	216166	350399
L50	7	5
LG50	5	3
L75	13	9
LG75	8	5
# misassemblies	1	1
# misassembled contigs	1	1
Misassembled contigs length	166802	166802
# local misassemblies	1	1
# scaffold gap ext. mis.	1	1
# scaffold gap loc. mis.	1	1
# unaligned mis. contigs	2	2
# unaligned contigs	110 + 15 part	112 + 13 part
Unaligned length	1077789	1079151
Genome fraction (%)	98.284	98.288
Duplication ratio	1.003	1.002
# N's per 100 kbp	12.39	12.39
# mismatches per 100 kbp	10.27	9.86
# indels per 100 kbp	2.10	2.10
Largest alignment	383873	573239
Total aligned length	2917031	2916589
NA50	215940	246267
NGA50	262398	350300
NGA75	115075	229773
LA50	7	5
LGA50	5	4
LGA75	9	6

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

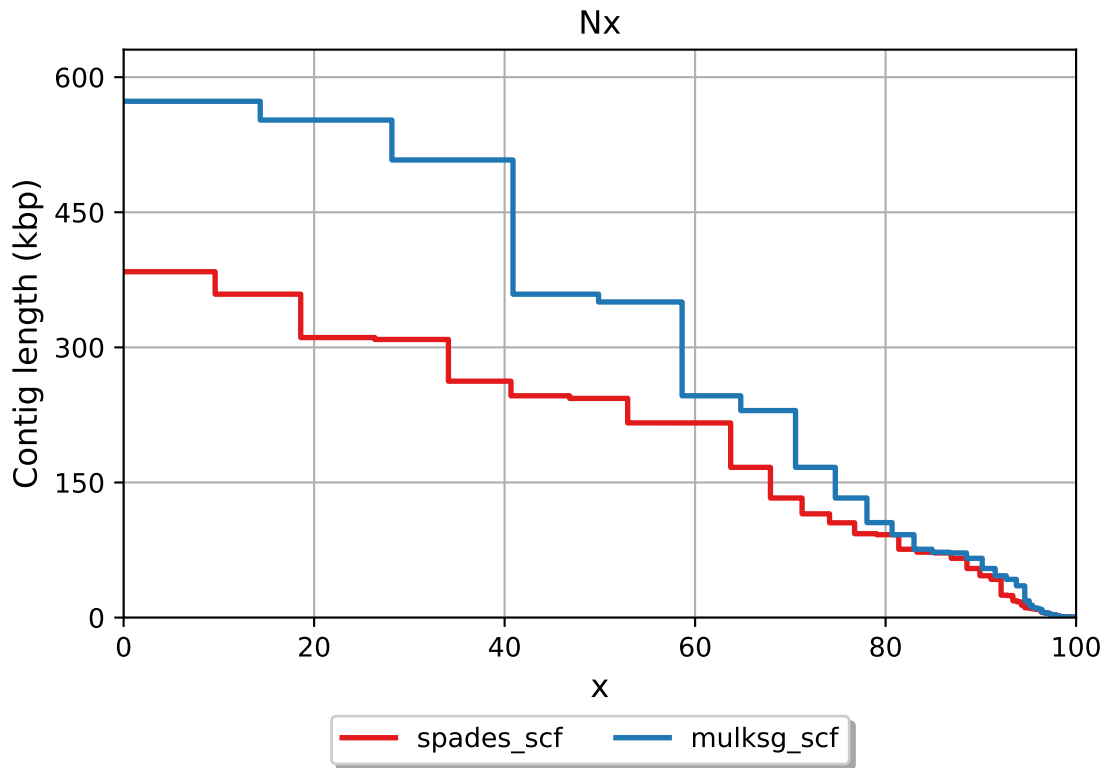
	spades_scf	mulksf_scf
# misassemblies	1	1
# contig misassemblies	1	1
# c. relocations	1	1
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	1	1
Misassembled contigs length	166802	166802
# local misassemblies	1	1
# scaffold gap ext. mis.	1	1
# scaffold gap loc. mis.	1	1
# unaligned mis. contigs	2	2
# mismatches	299	287
# indels	61	61
# indels (<= 5 bp)	56	56
# indels (> 5 bp)	5	5
Indels length	268	268

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).

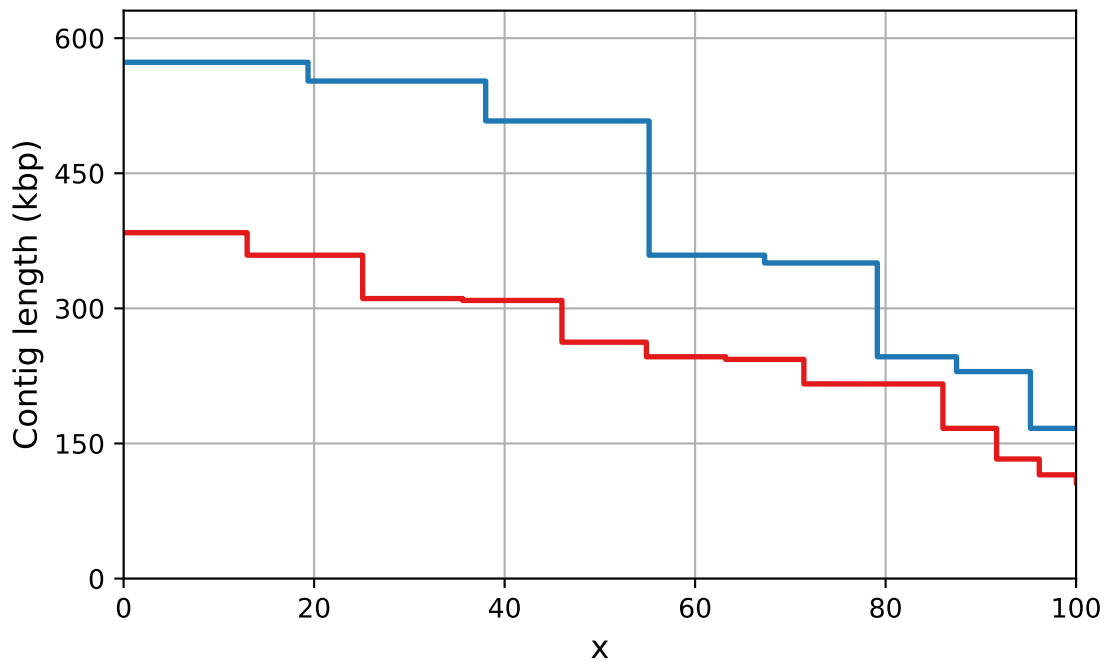
Unaligned report

	spades_scf	mulksg_scf
# fully unaligned contigs	110	112
Fully unaligned length	196614	197677
# partially unaligned contigs	15	13
Partially unaligned length	881175	881474
# N's	495	495

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).

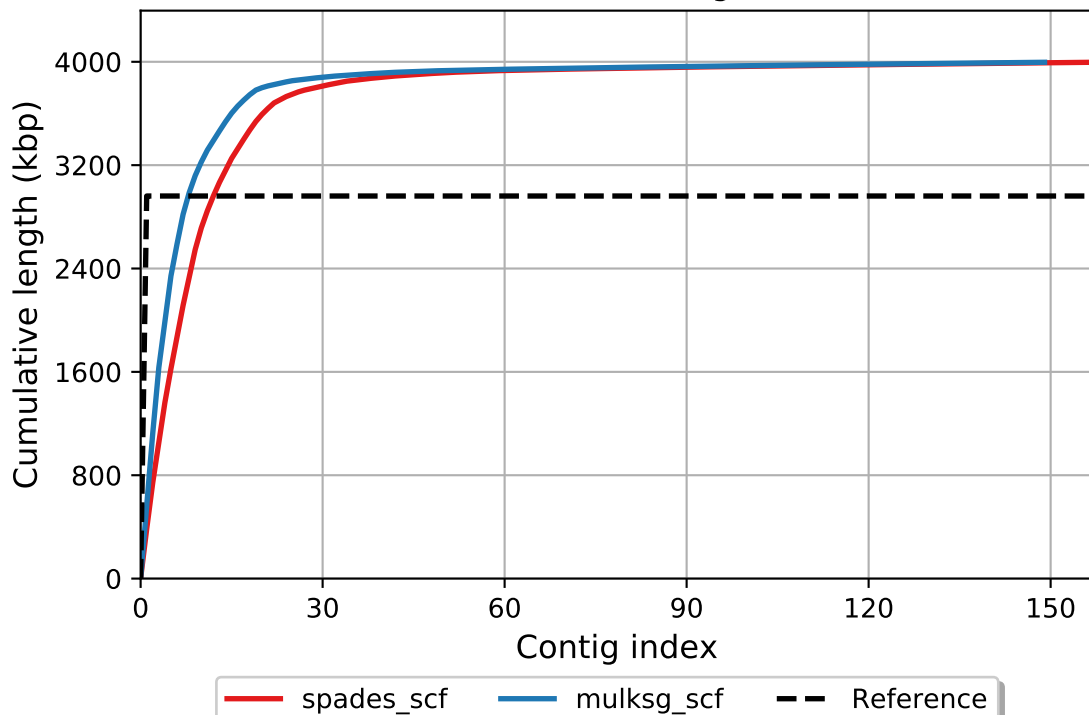


NGx

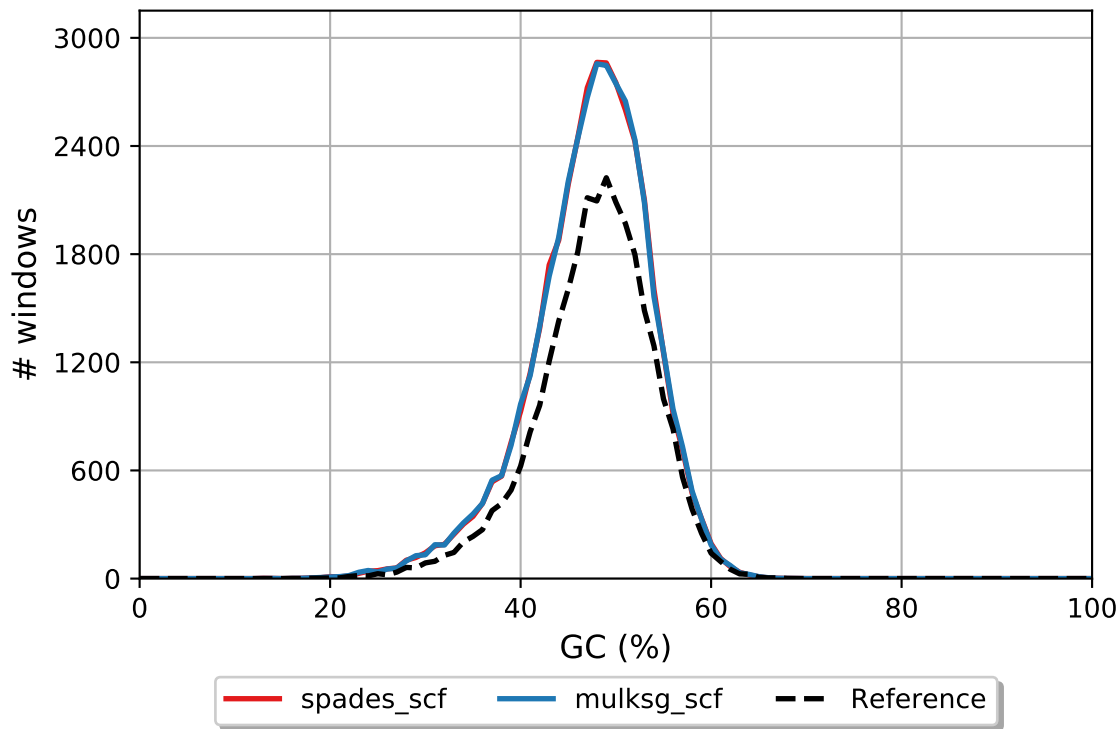


— spades_scf — mulksg_scf

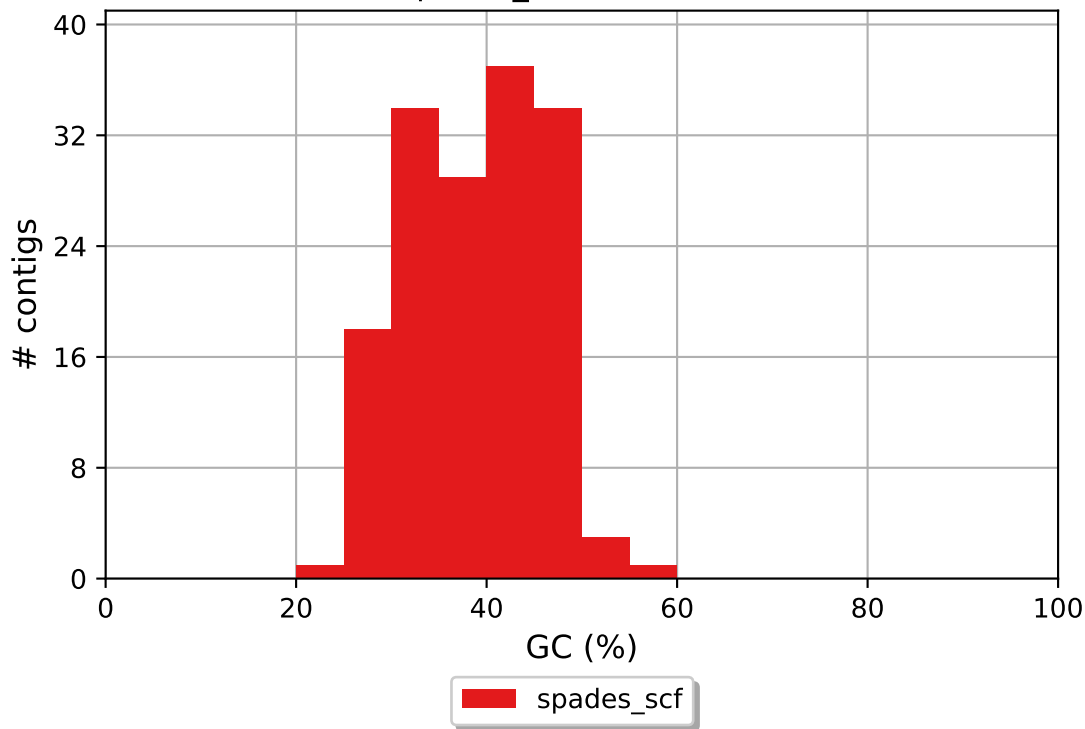
Cumulative length



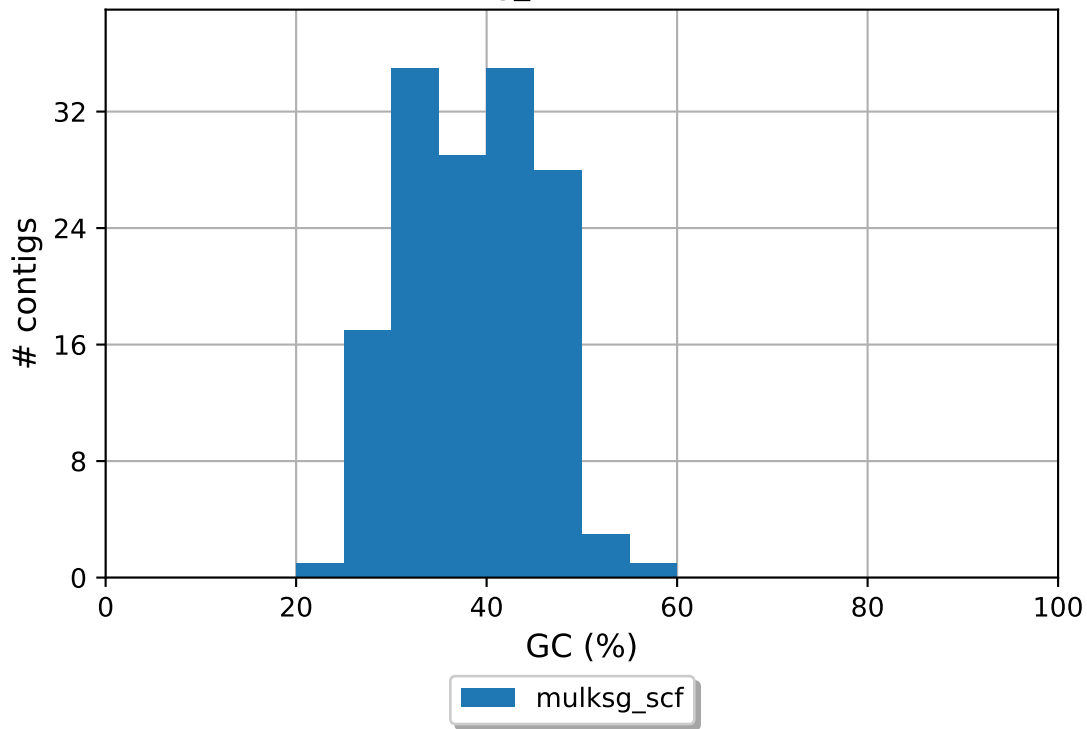
GC content



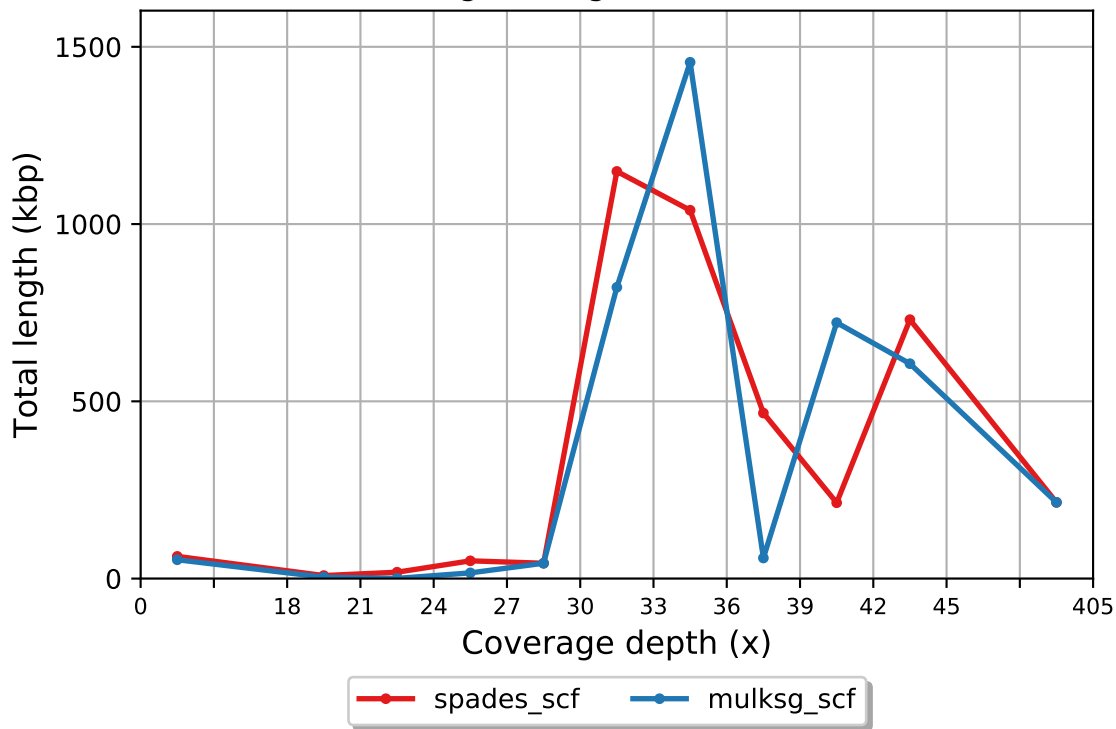
spades_scf GC content



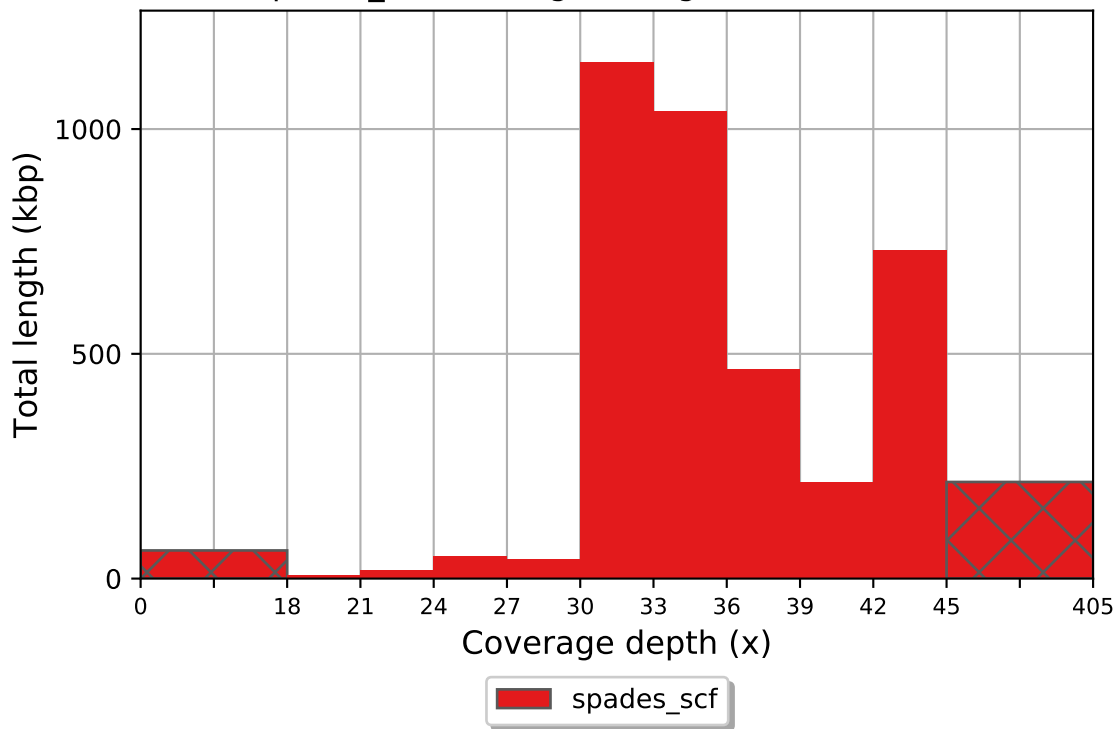
mulksg_scf GC content



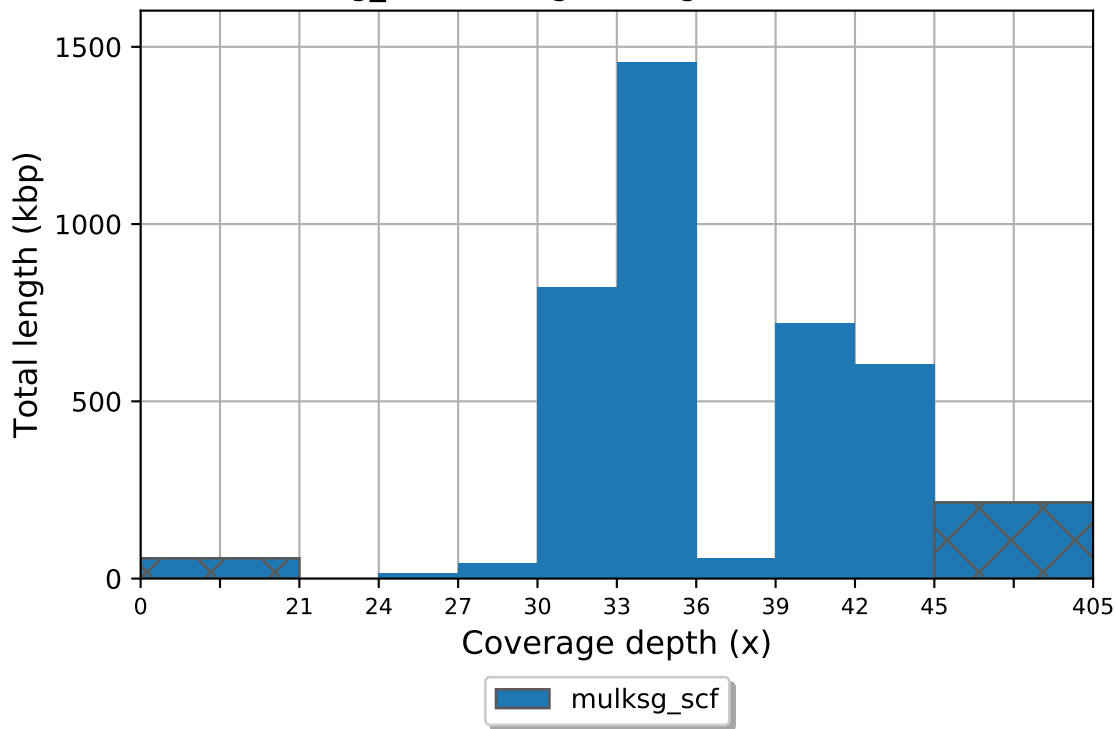
Coverage histogram (bin size: 3x)



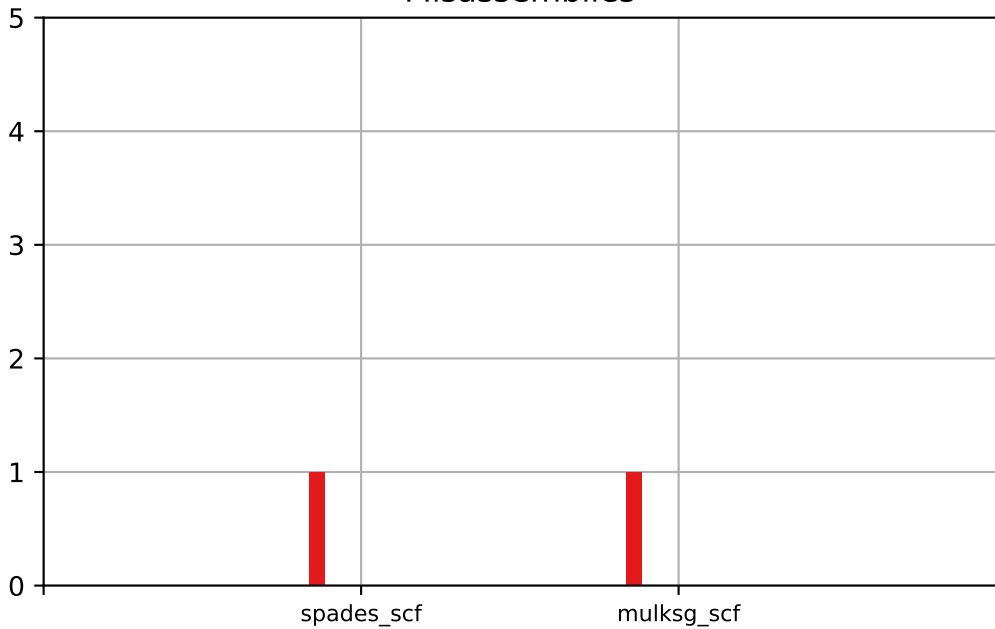
spades_scf coverage histogram (bin size: 3x)



mulksg_scf coverage histogram (bin size: 3x)

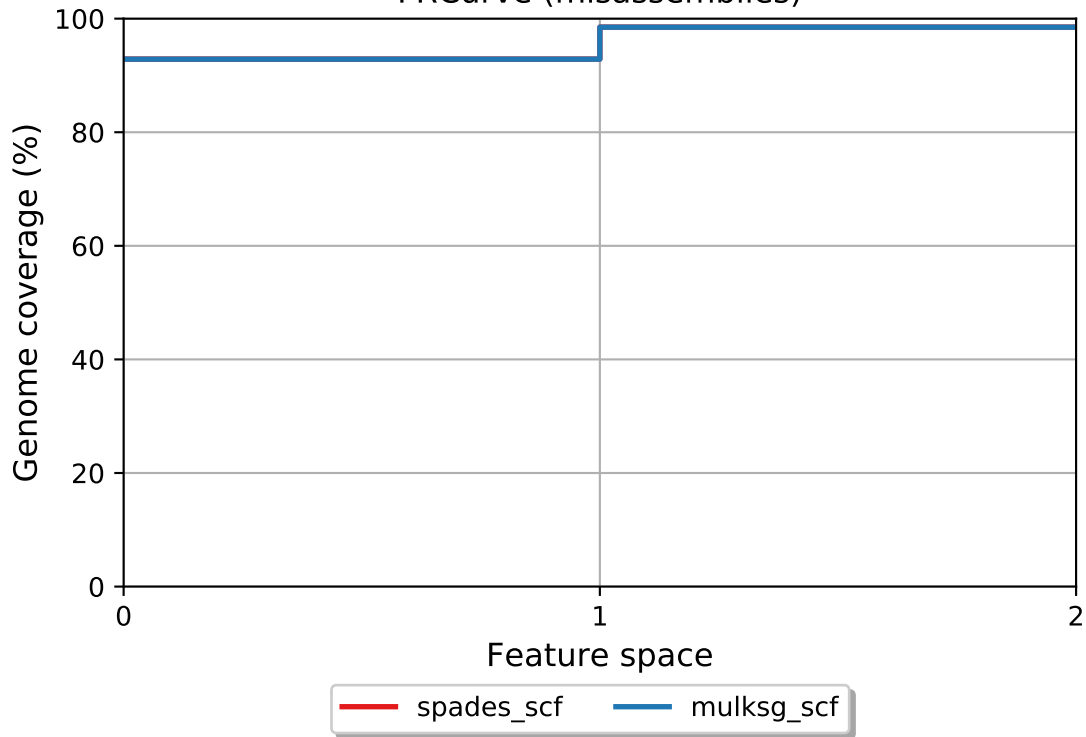


Misassemblies

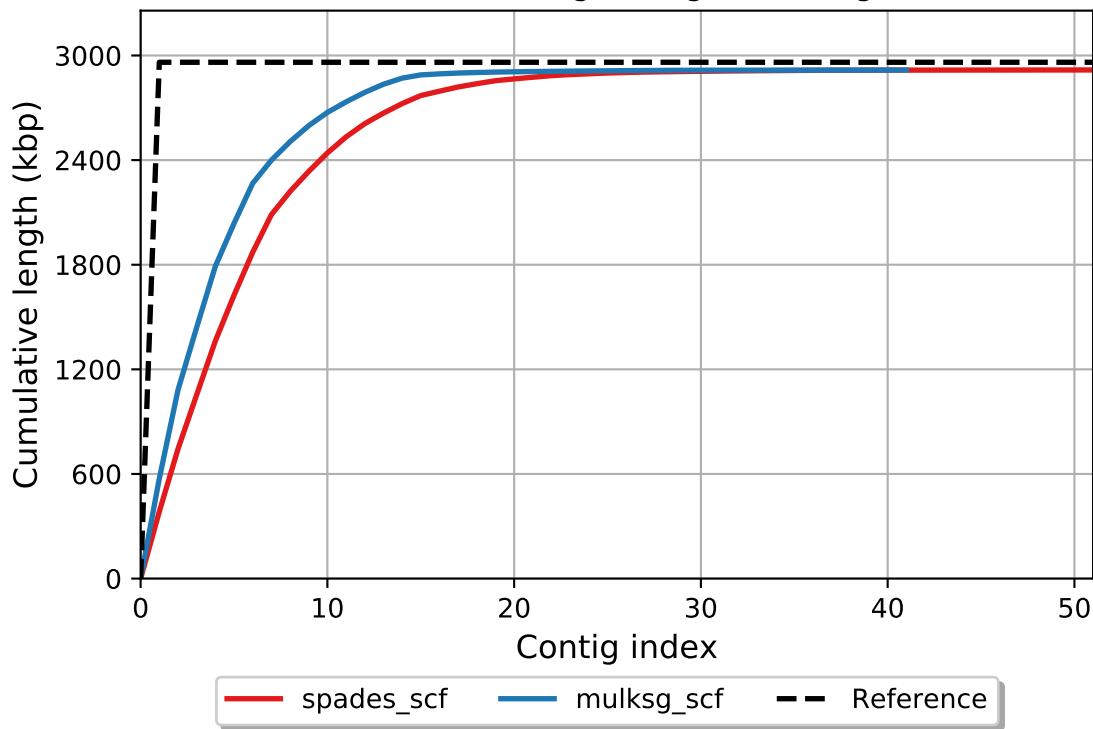


 # relocations

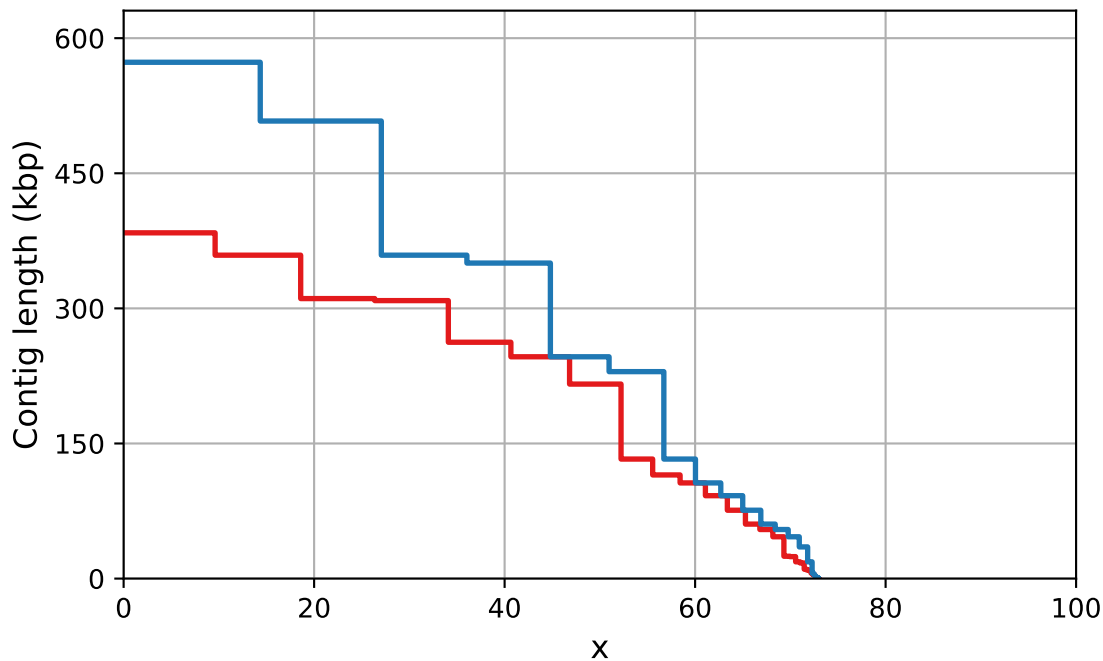
FRCurve (misassemblies)



Cumulative length (aligned contigs)

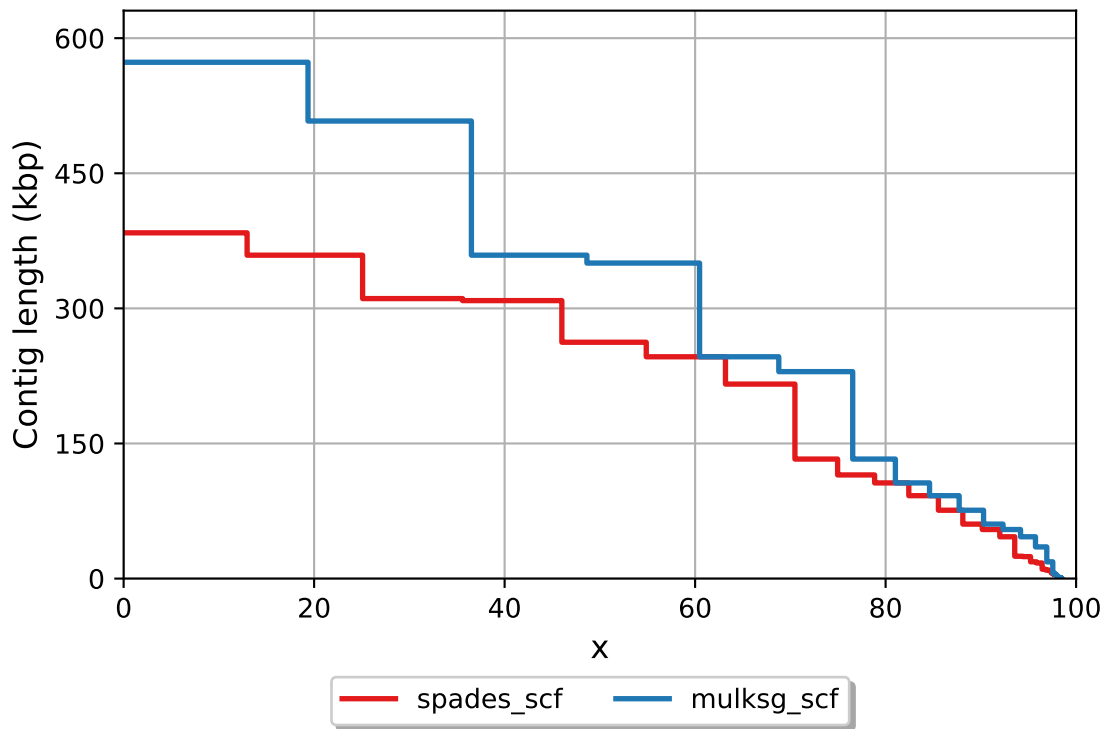


NAx

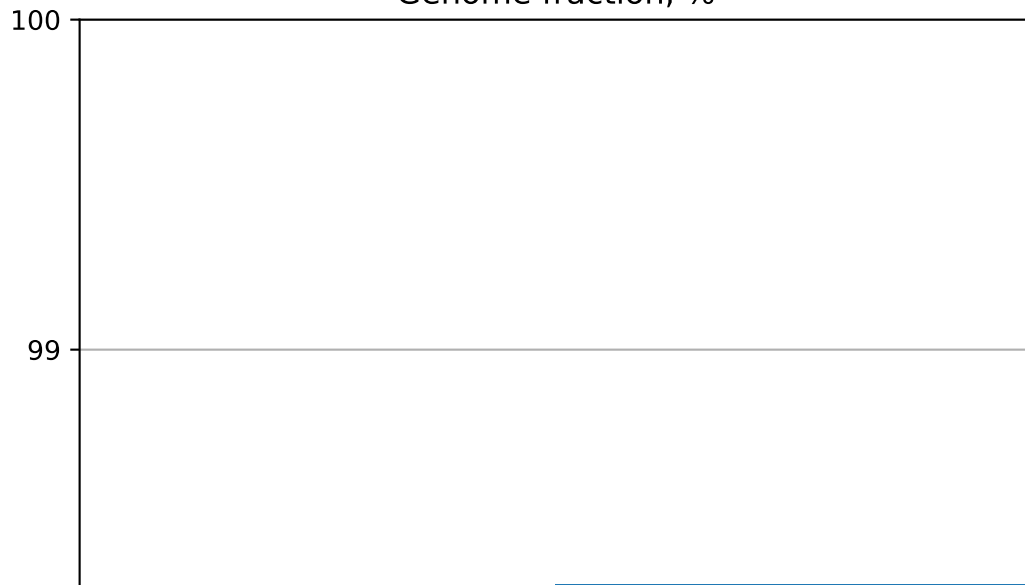


— spades_scf — mulksg_scf

NGAx



Genome fraction, %



spades_scf



mulks_g_scf