

Report

	spades_scf	mulks_g_scf
# contigs (>= 0 bp)	1491	1839
# contigs (>= 1000 bp)	94	94
# contigs (>= 5000 bp)	52	52
# contigs (>= 10000 bp)	46	46
# contigs (>= 25000 bp)	39	39
# contigs (>= 50000 bp)	30	30
Total length (>= 0 bp)	5729366	5840731
Total length (>= 1000 bp)	5285075	5285214
Total length (>= 5000 bp)	5195704	5195704
Total length (>= 10000 bp)	5153776	5153776
Total length (>= 25000 bp)	5055973	5055973
Total length (>= 50000 bp)	4767420	4767420
# contigs	176	186
Largest contig	639080	639080
Total length	5337384	5344001
Reference length	5373121	5373121
GC (%)	43.40	43.40
Reference GC (%)	43.42	43.42
N50	157629	157629
NG50	157629	157629
N75	97991	97991
NG75	89451	89451
L50	9	9
LG50	9	9
L75	19	19
LG75	20	20
# misassemblies	99	99
# misassembled contigs	26	26
Misassembled contigs length	4276309	4276309
# local misassemblies	55	55
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	3	3
# unaligned contigs	123 + 40 part	134 + 39 part
Unaligned length	1018227	1024932
Genome fraction (%)	80.292	80.292
Duplication ratio	1.001	1.001
# N's per 100 kbp	1.84	1.83
# mismatches per 100 kbp	649.35	649.32
# indels per 100 kbp	20.17	20.17
Largest alignment	189113	189113
Total aligned length	4315940	4315852
NA50	44793	44793
NGA50	44793	44793
NA75	14269	13503
NGA75	13436	13436
LA50	35	35
LGA50	35	35
LA75	84	85
LGA75	86	86

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

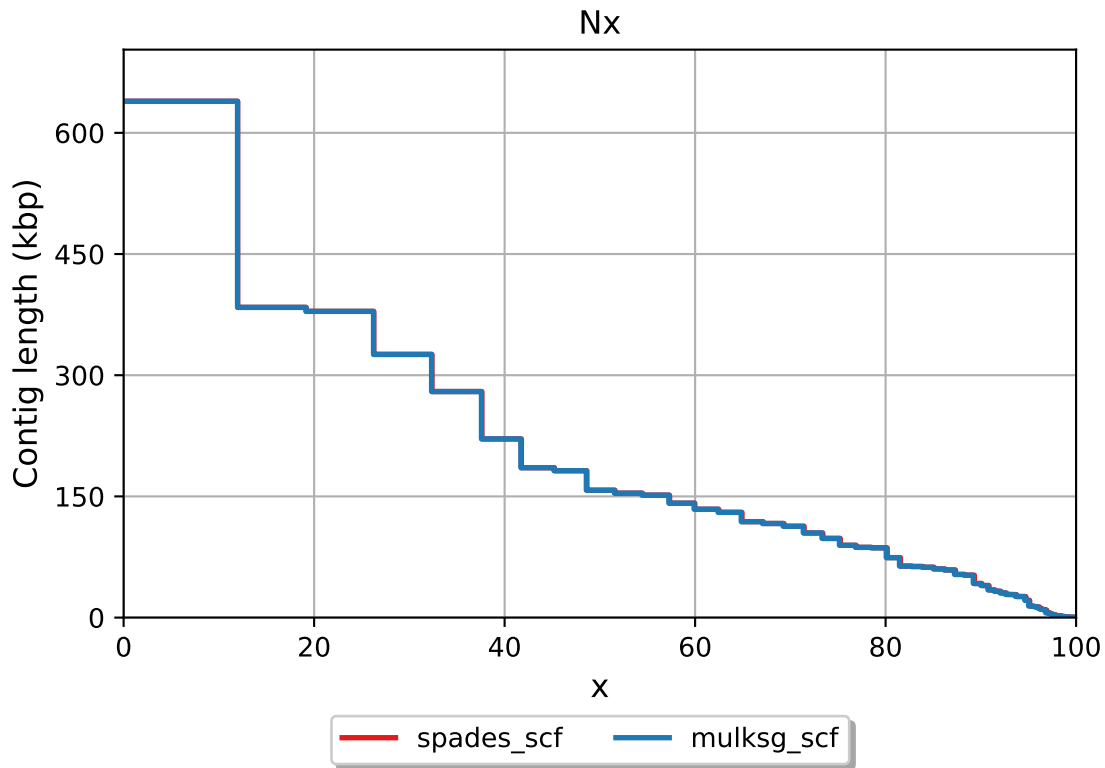
	spades_scf	mulksg_scf
# misassemblies	99	99
# contig misassemblies	98	98
# c. relocations	97	97
# c. translocations	0	0
# c. inversions	1	1
# scaffold misassemblies	1	1
# s. relocations	1	1
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	26	26
Misassembled contigs length	4276309	4276309
# local misassemblies	55	55
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	0	0
# unaligned mis. contigs	3	3
# mismatches	28014	28013
# indels	870	870
# indels (<= 5 bp)	744	744
# indels (> 5 bp)	126	126
Indels length	3753	3753

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).

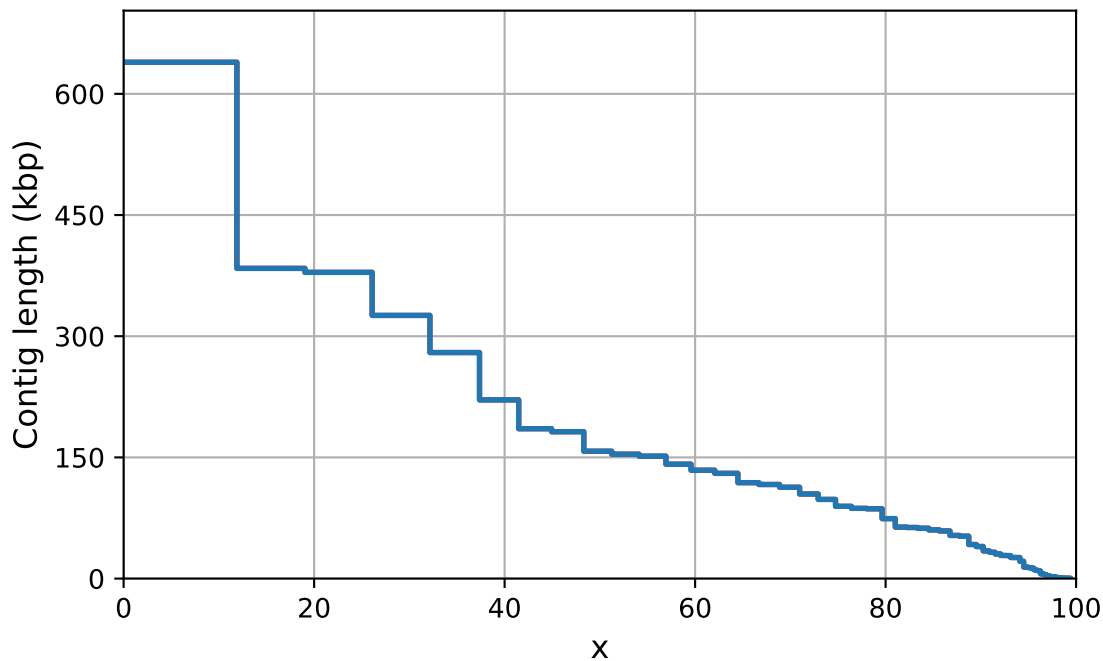
Unaligned report

	spades_scf	mulks_g_scf
# fully unaligned contigs	123	134
Fully unaligned length	288246	299009
# partially unaligned contigs	40	39
Partially unaligned length	729981	725923
# N's	98	98

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).

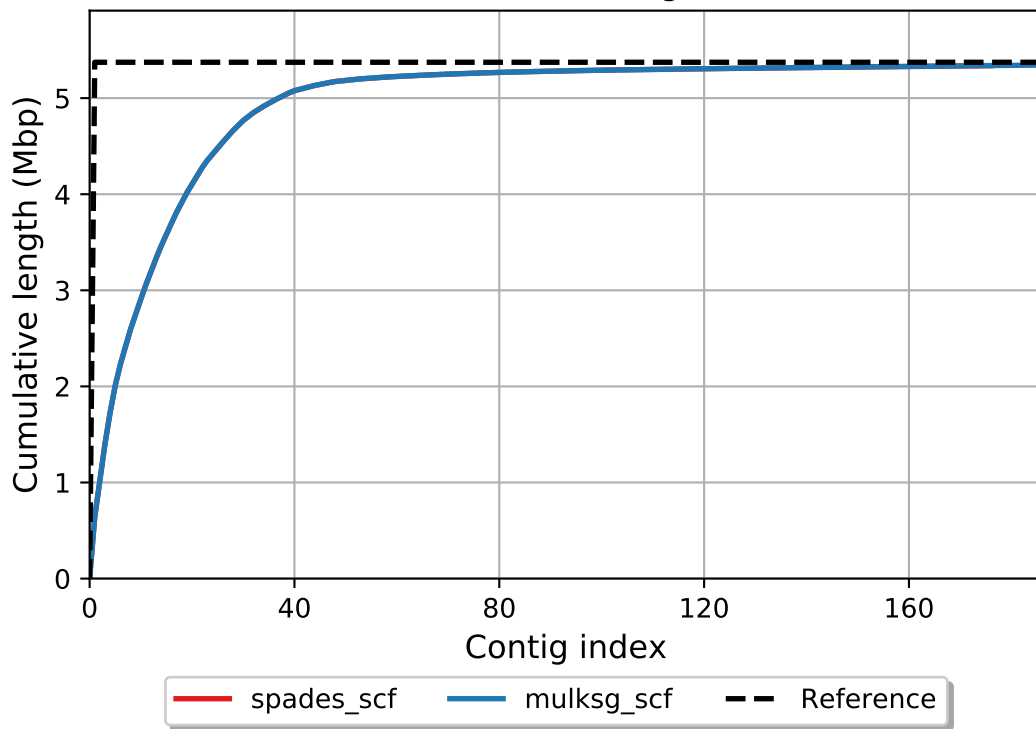


NGx

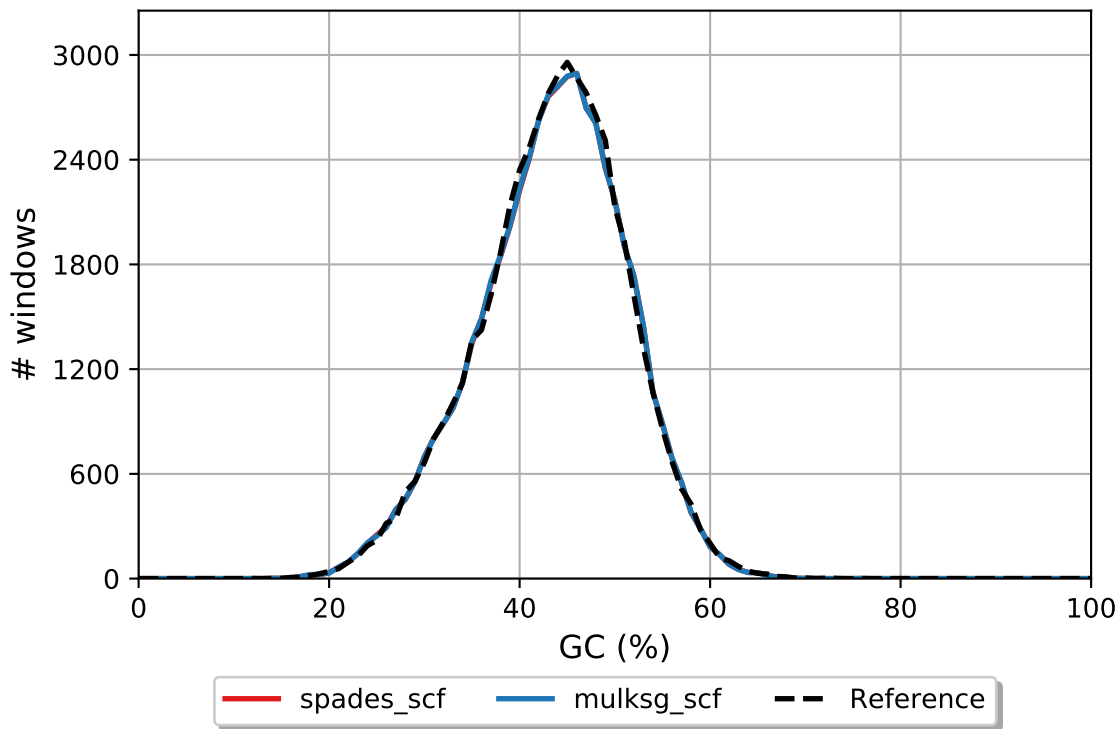


spades_scf mulksg_scf

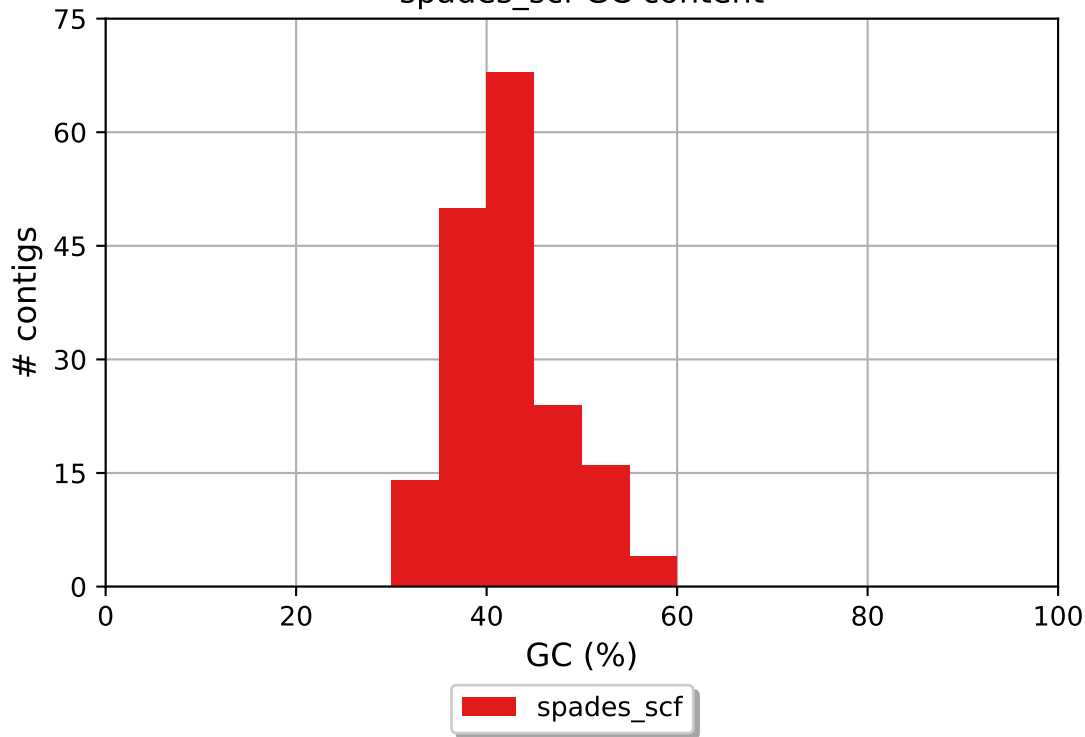
Cumulative length



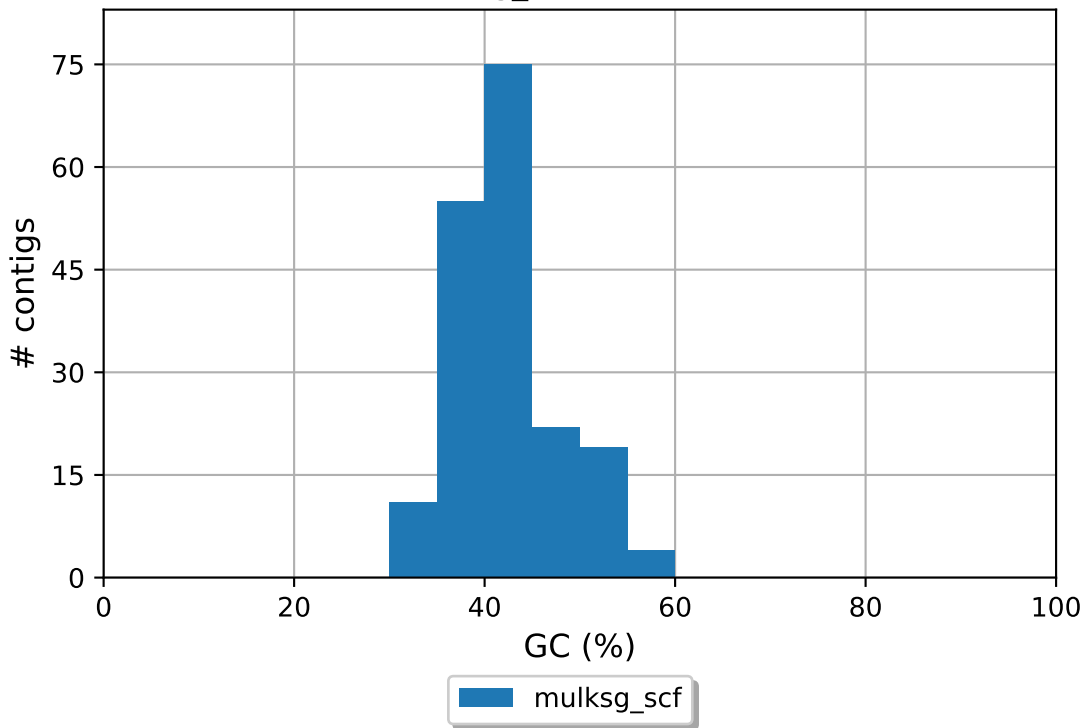
GC content



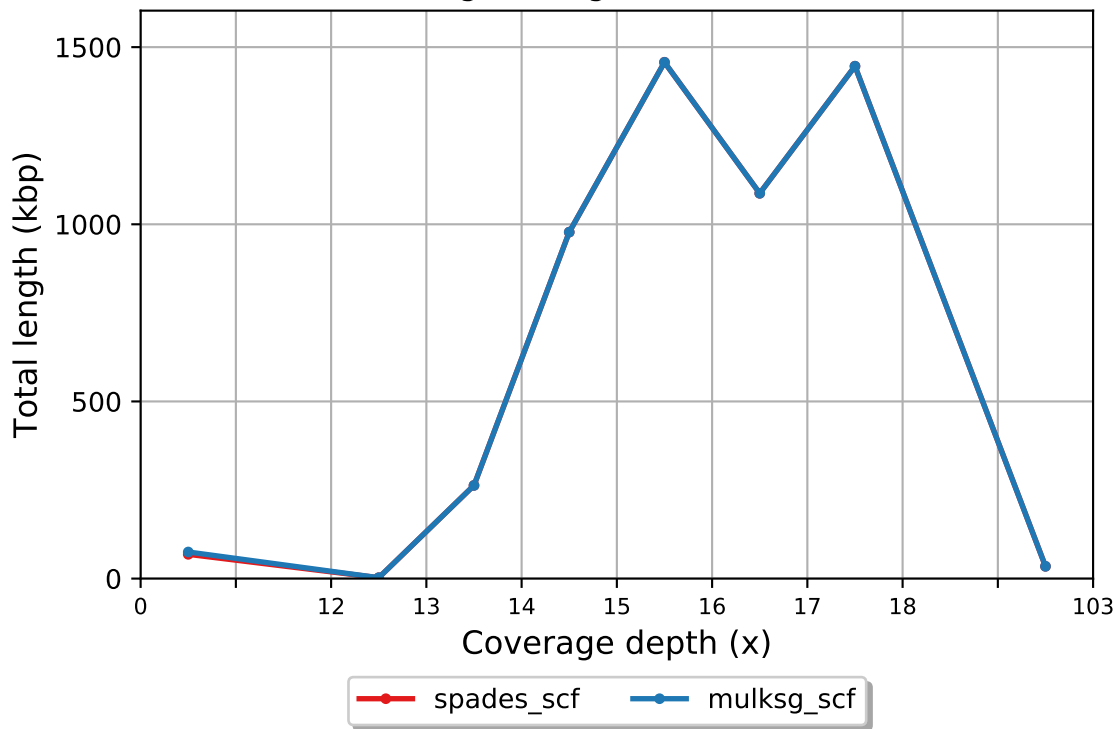
spades_scf GC content



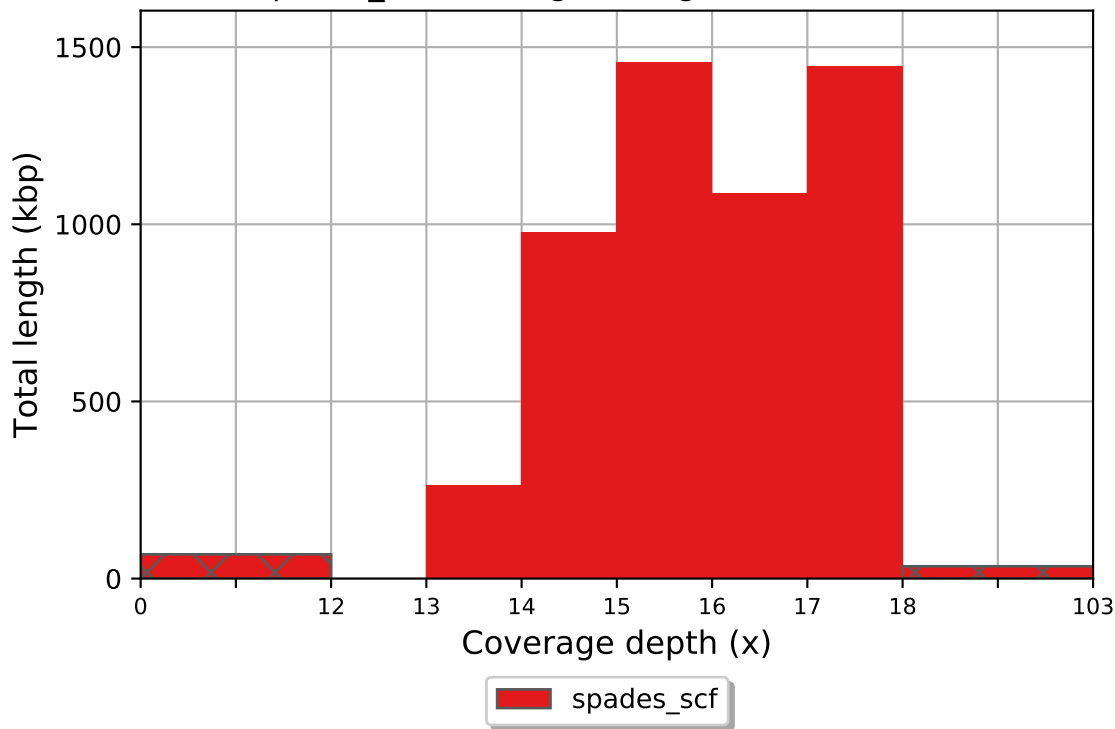
mulksg_scf GC content



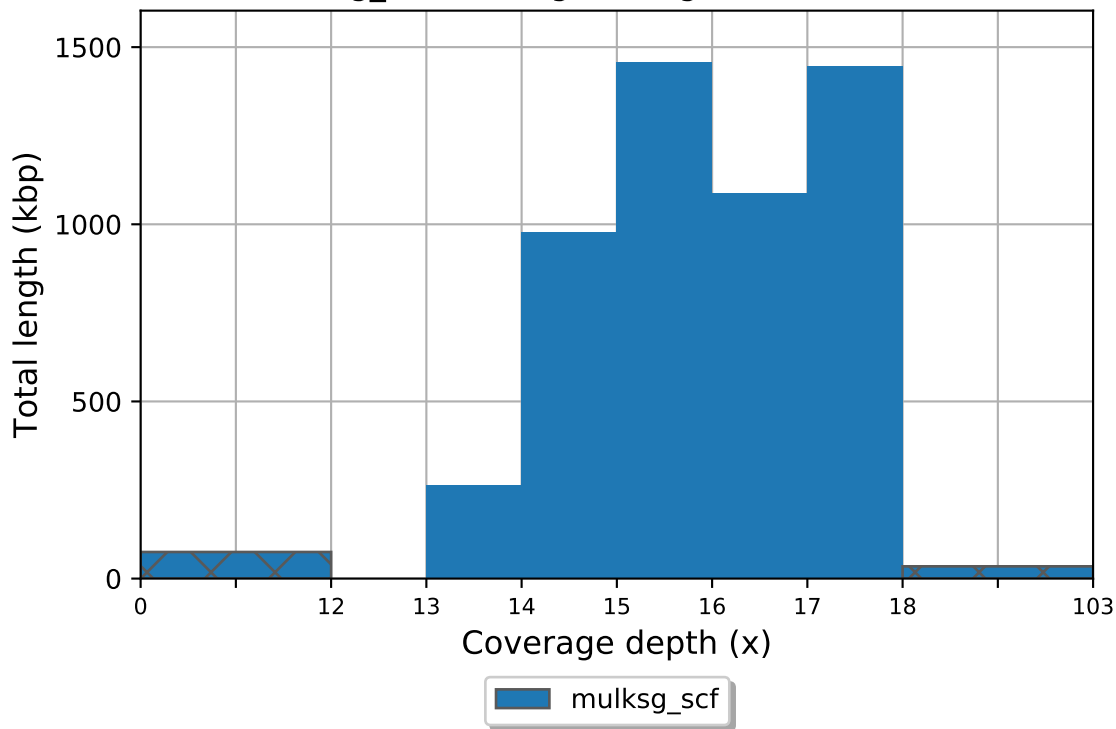
Coverage histogram (bin size: 1x)



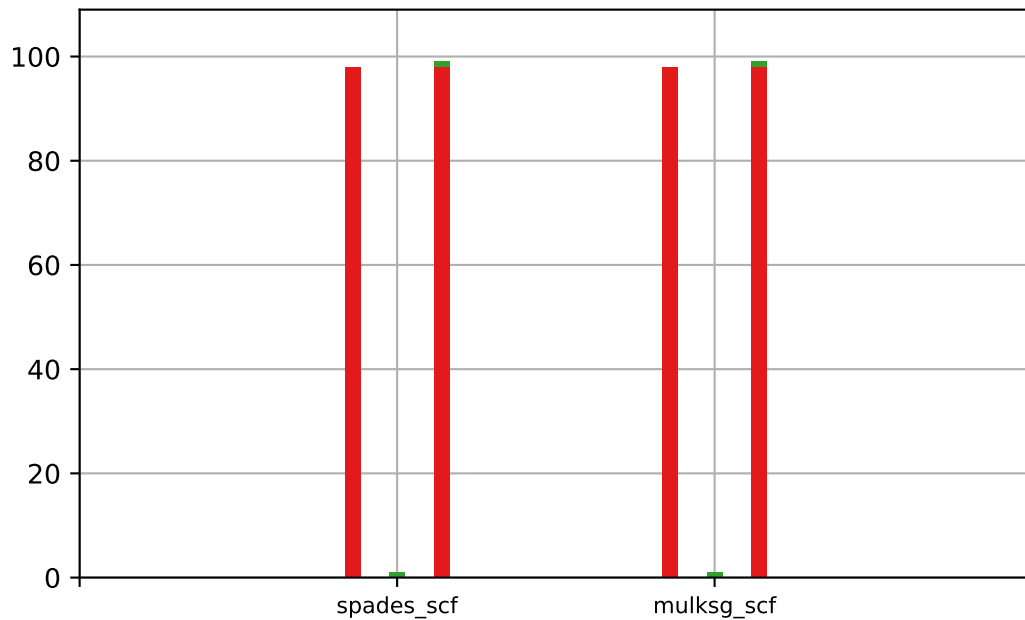
spades_scf coverage histogram (bin size: 1x)



mulksg_scf coverage histogram (bin size: 1x)



Misassemblies

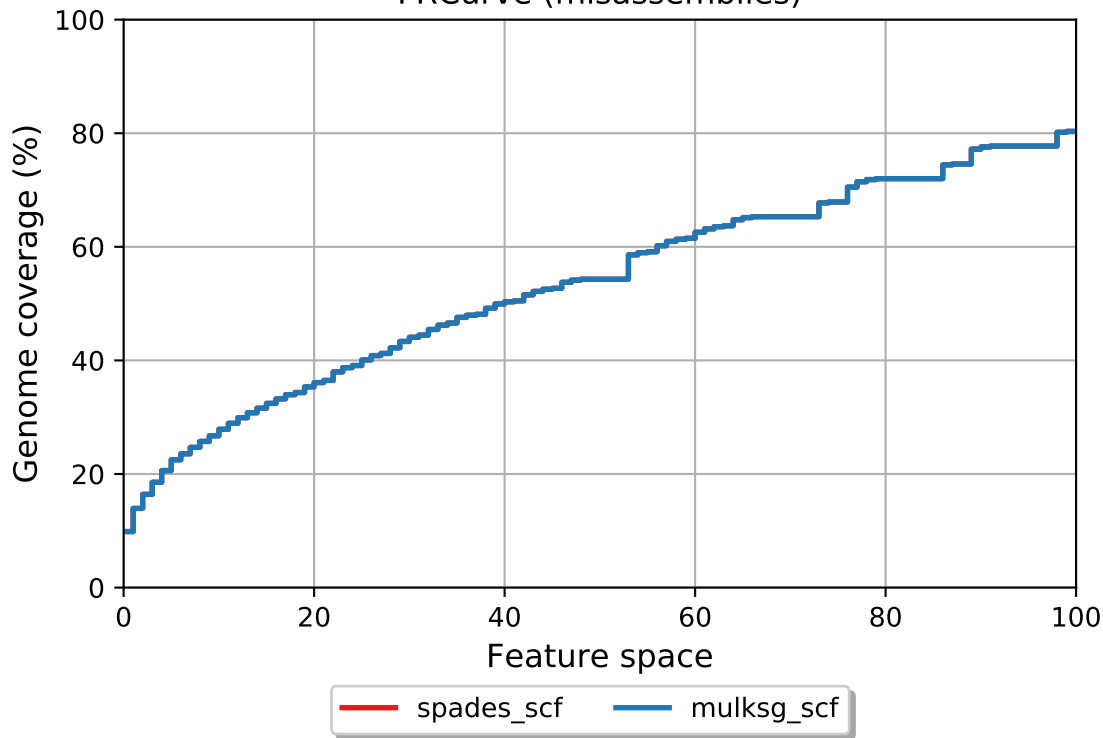


relocations

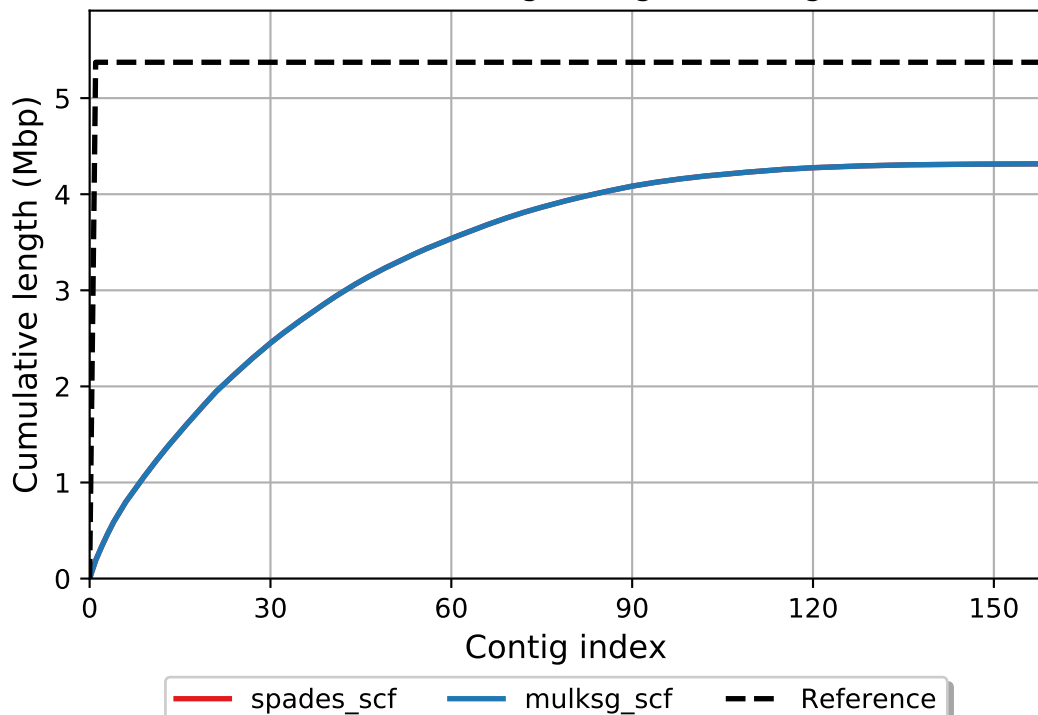


inversions

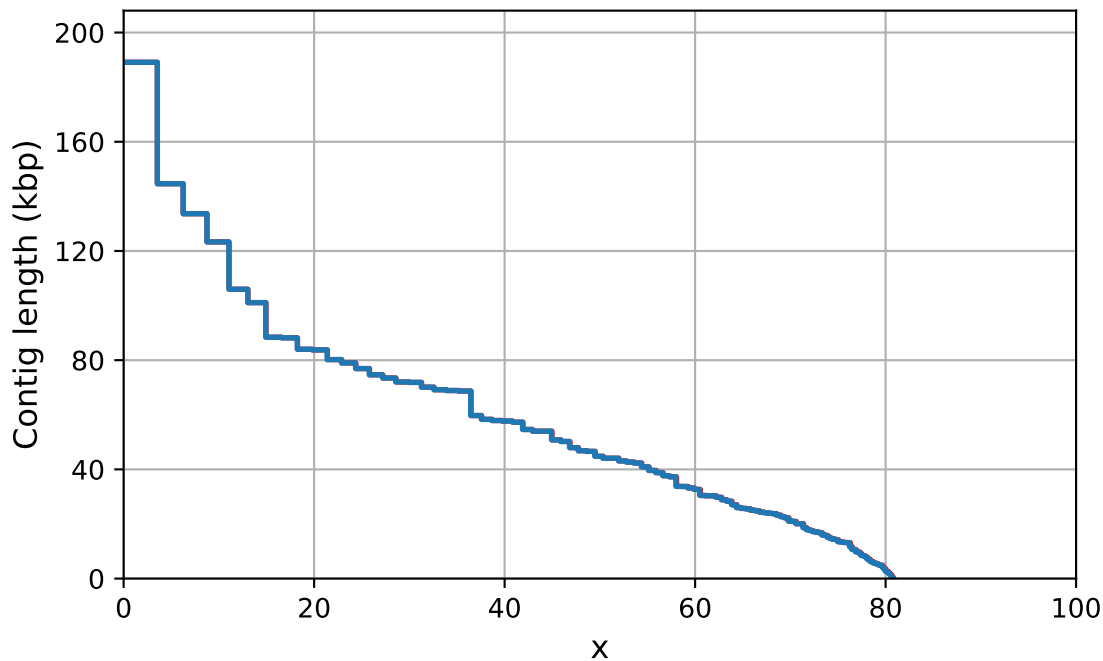
FRCurve (misassemblies)



Cumulative length (aligned contigs)

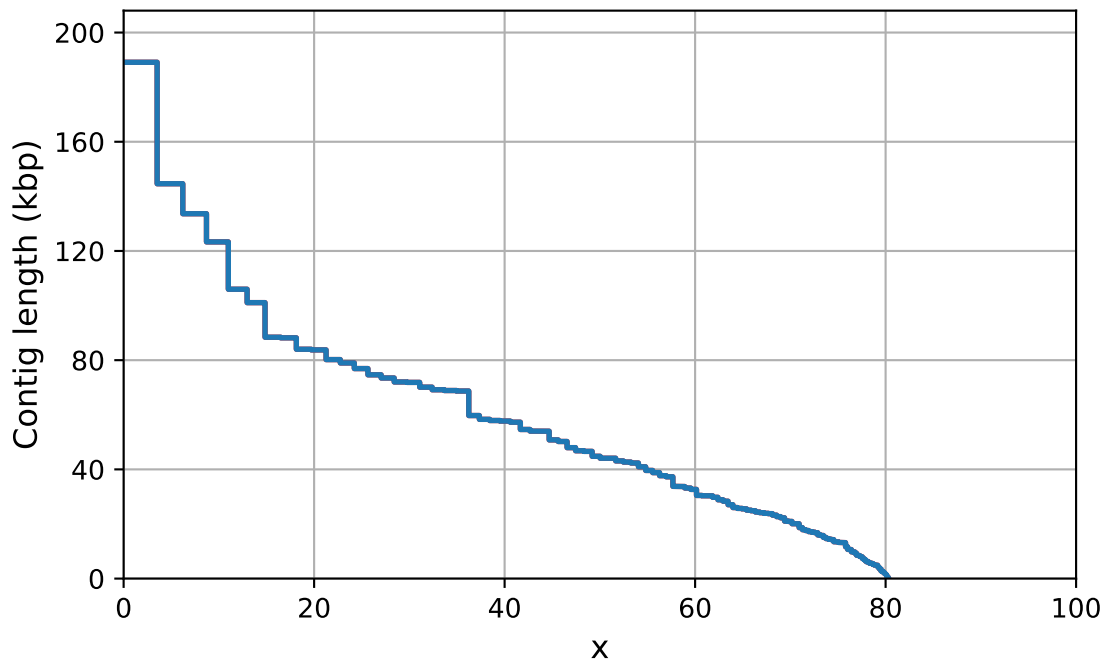


NAx



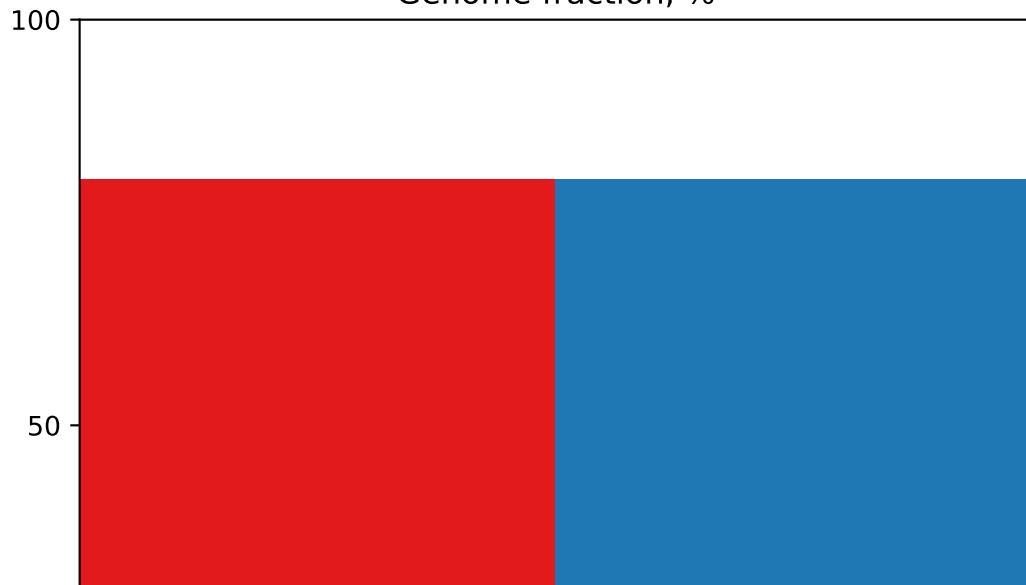
spades_scf mulksg_scf

NGAx



— spades_scf — mulksg_scf

Genome fraction, %



spades_scf



mulksg_scf