

# Report

	spades_scf	mulksq_scf
# contigs (>= 0 bp)	177	185
# contigs (>= 1000 bp)	39	39
# contigs (>= 5000 bp)	31	31
# contigs (>= 10000 bp)	29	29
# contigs (>= 25000 bp)	25	25
# contigs (>= 50000 bp)	20	20
Total length (>= 0 bp)	5386862	5390680
Total length (>= 1000 bp)	5358705	5358705
Total length (>= 5000 bp)	5338085	5338085
Total length (>= 10000 bp)	5323010	5323010
Total length (>= 25000 bp)	5252280	5252280
Total length (>= 50000 bp)	5066290	5066290
# contigs	45	48
Largest contig	1202231	1202231
Total length	5362660	5364573
Reference length	5224283	5224283
GC (%)	35.33	35.33
Reference GC (%)	35.58	35.58
N50	275327	275327
NG50	275327	275327
N75	143218	143218
NG75	196834	196834
L50	4	4
LG50	4	4
L75	10	10
LG75	9	9
# misassemblies	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	5	5
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	5	5
# unaligned mis. contigs	0	0
# unaligned contigs	0 + 5 part	3 + 5 part
Unaligned length	196944	198857
Genome fraction (%)	98.810	98.810
Duplication ratio	1.001	1.001
# N's per 100 kbp	14.58	14.58
# mismatches per 100 kbp	1.84	1.86
# indels per 100 kbp	2.13	2.13
Largest alignment	1202022	1202022
Total aligned length	5164750	5164750
NA50	275327	275327
NGA50	275327	275327
NA75	143218	143218
NGA75	196834	196834
LA50	4	4
LGA50	4	4
LA75	10	10
LGA75	9	9

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

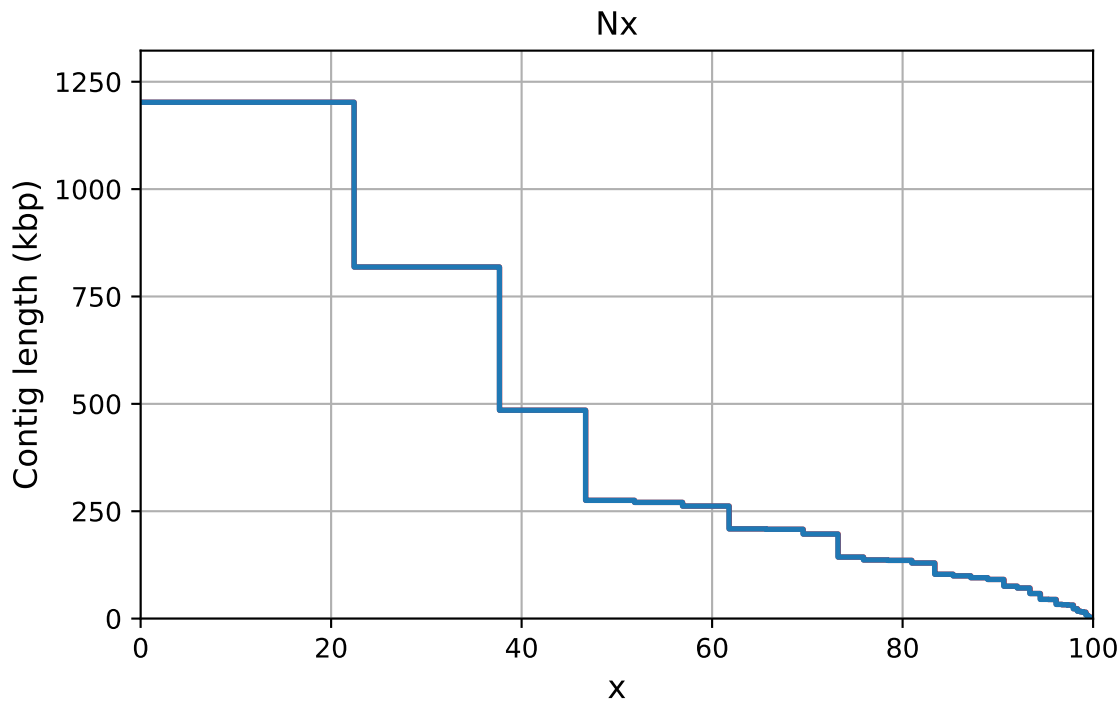
	spades_scf	mulksg_scf
# misassemblies	0	0
# contig misassemblies	0	0
# c. relocations	0	0
# c. translocations	0	0
# c. inversions	0	0
# scaffold misassemblies	0	0
# s. relocations	0	0
# s. translocations	0	0
# s. inversions	0	0
# misassembled contigs	0	0
Misassembled contigs length	0	0
# local misassemblies	5	5
# scaffold gap ext. mis.	0	0
# scaffold gap loc. mis.	5	5
# unaligned mis. contigs	0	0
# mismatches	95	96
# indels	110	110
# indels (<= 5 bp)	98	98
# indels (> 5 bp)	12	12
Indels length	720	720

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

## Unaligned report

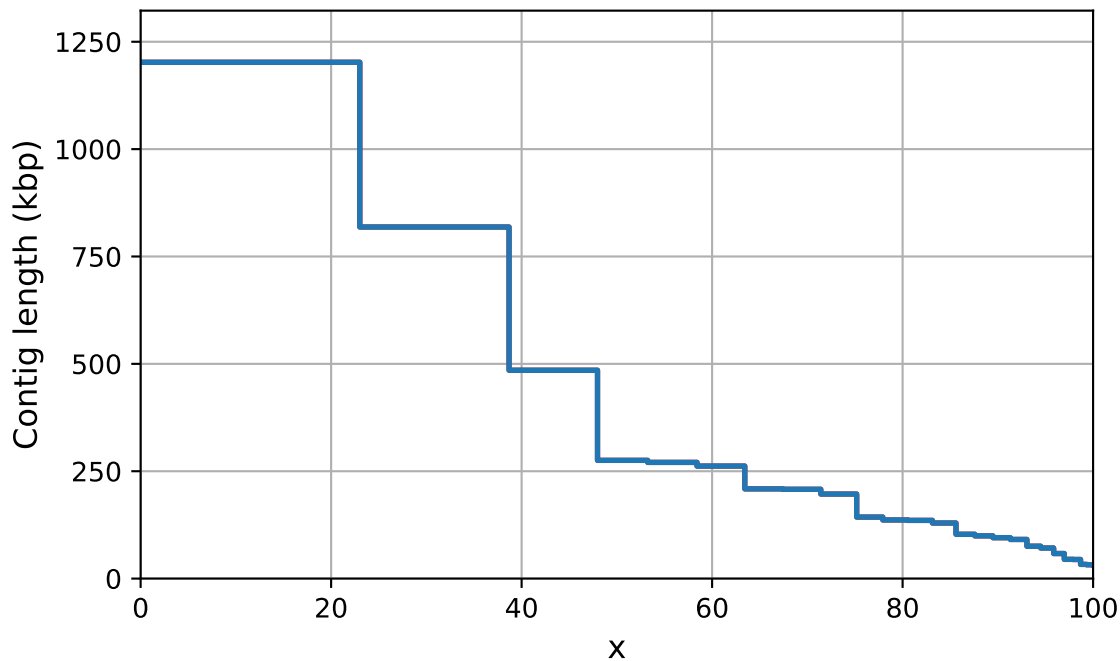
	spades_scf	mulks_g_scf
# fully unaligned contigs	0	3
Fully unaligned length	0	1913
# partially unaligned contigs	5	5
Partially unaligned length	196944	196944
# N's	782	782

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



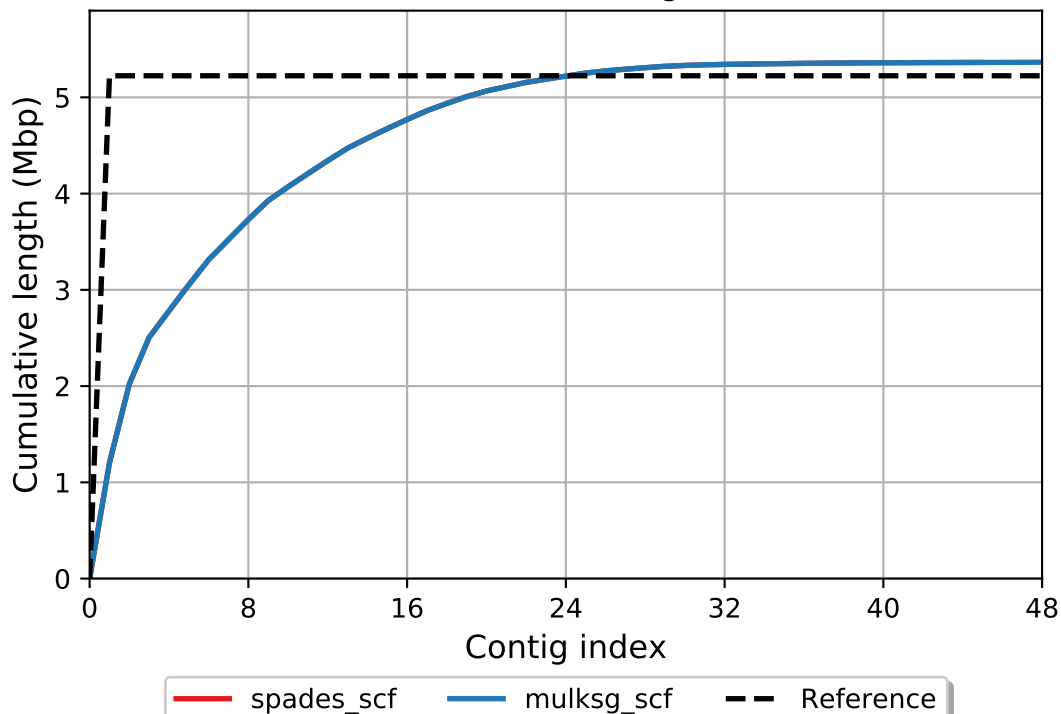
spades\_scf   mulksg\_scf

## NGx

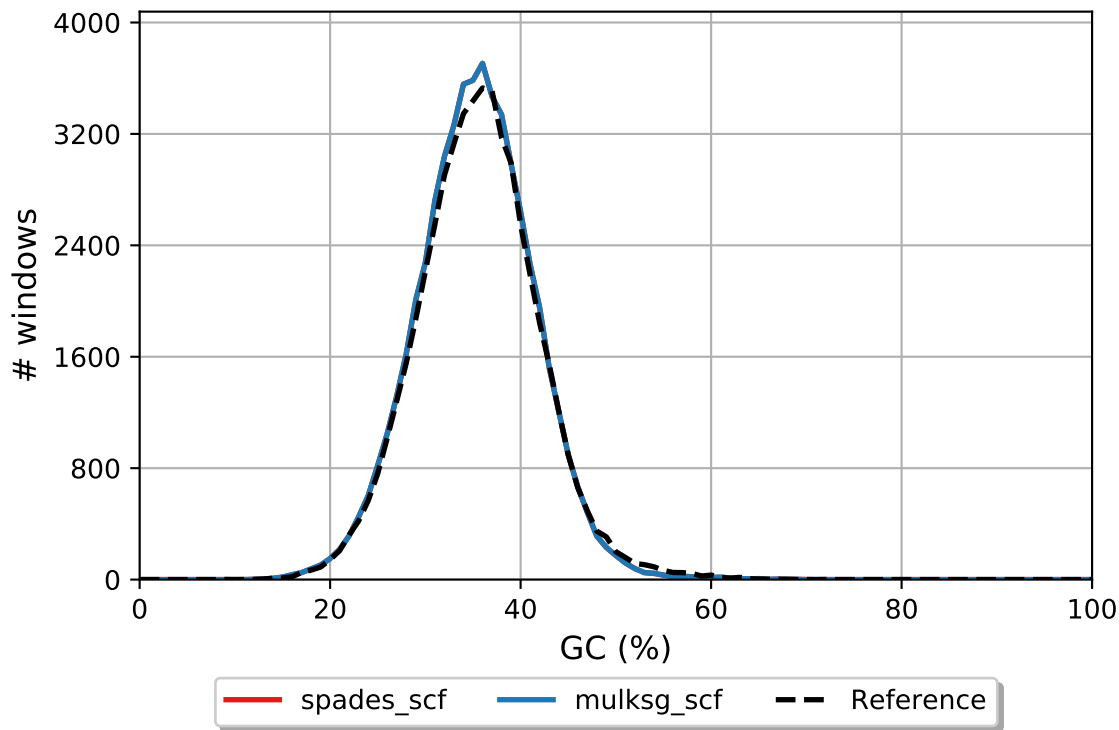


spades\_scf mulksg\_scf

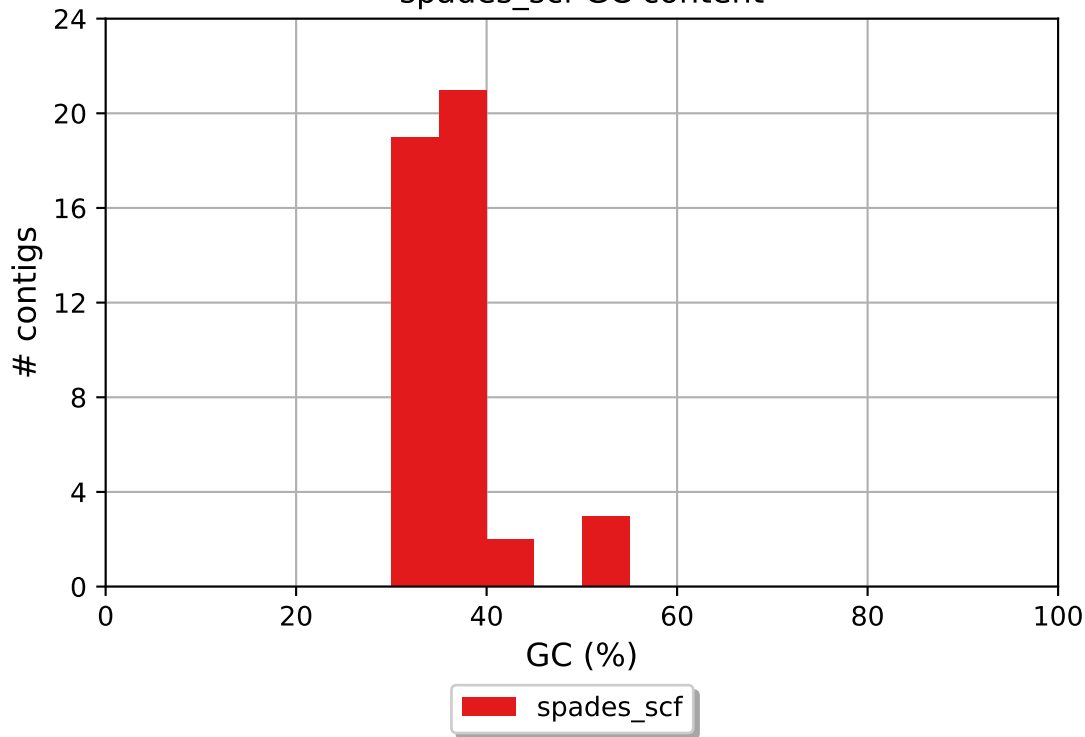
Cumulative length



GC content

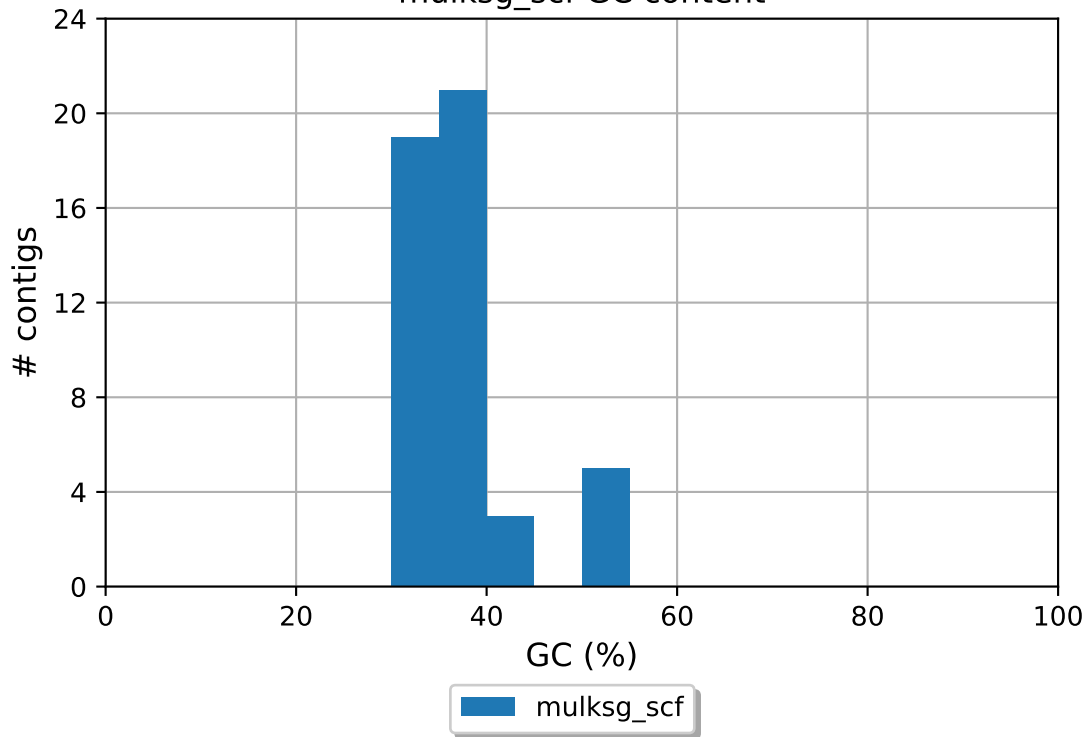


spades\_scf GC content

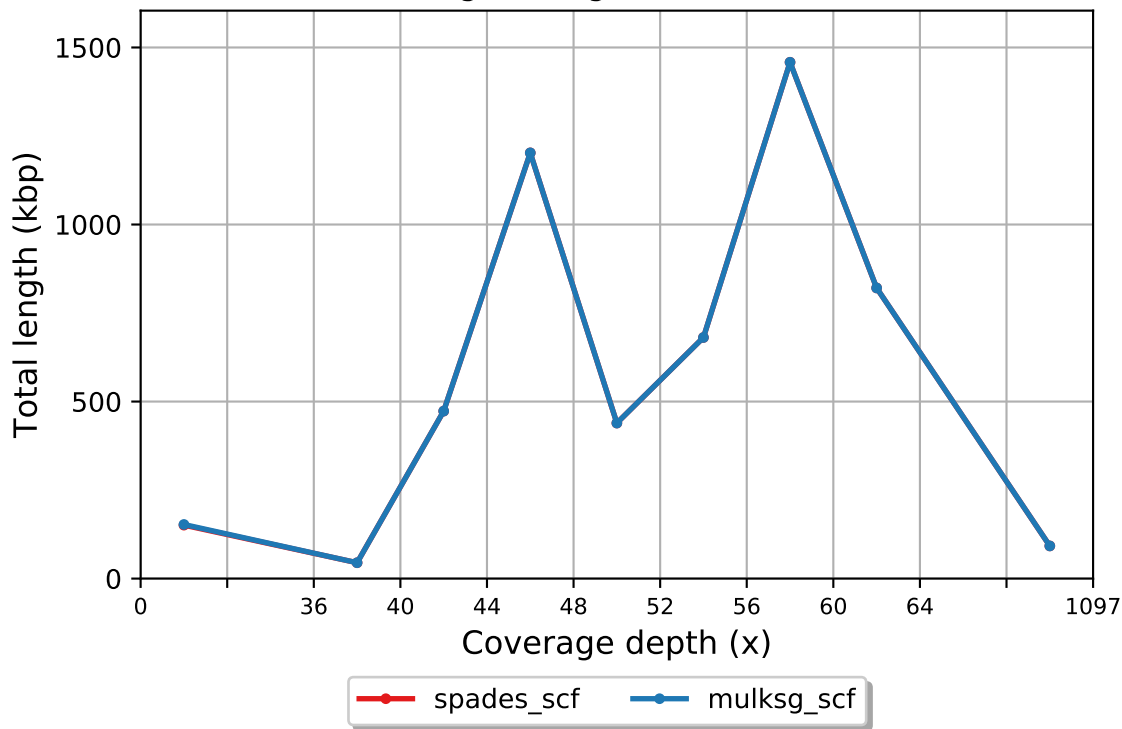




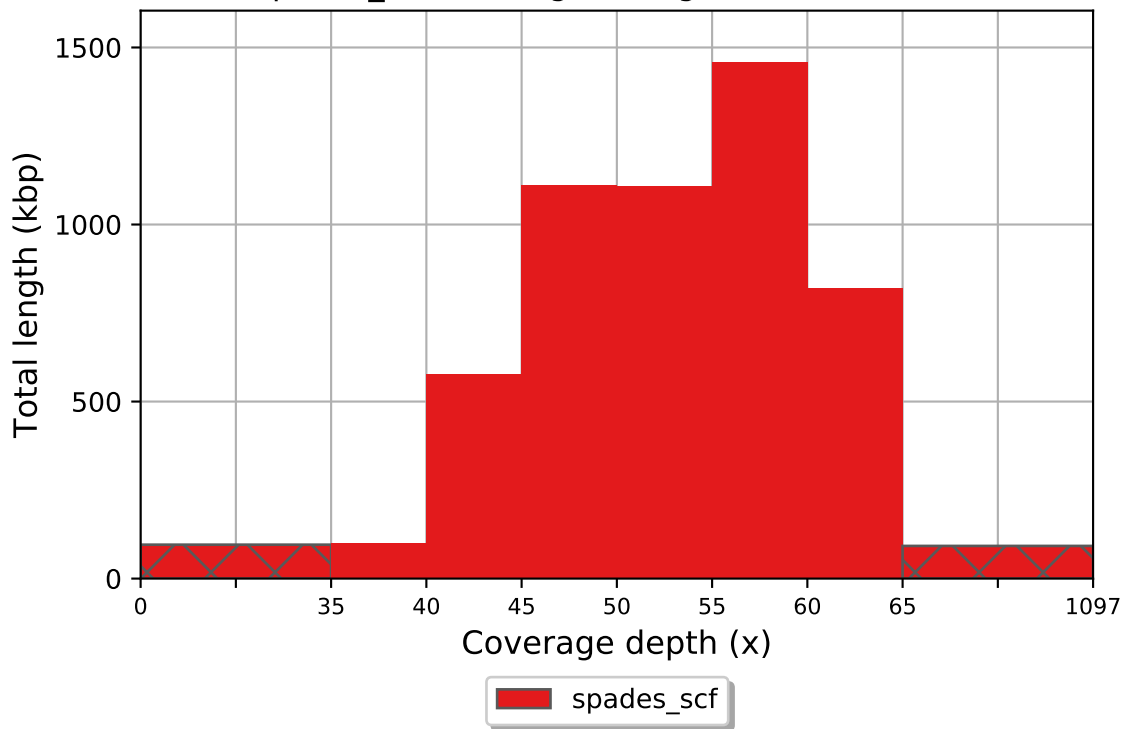
mulksg\_scf GC content



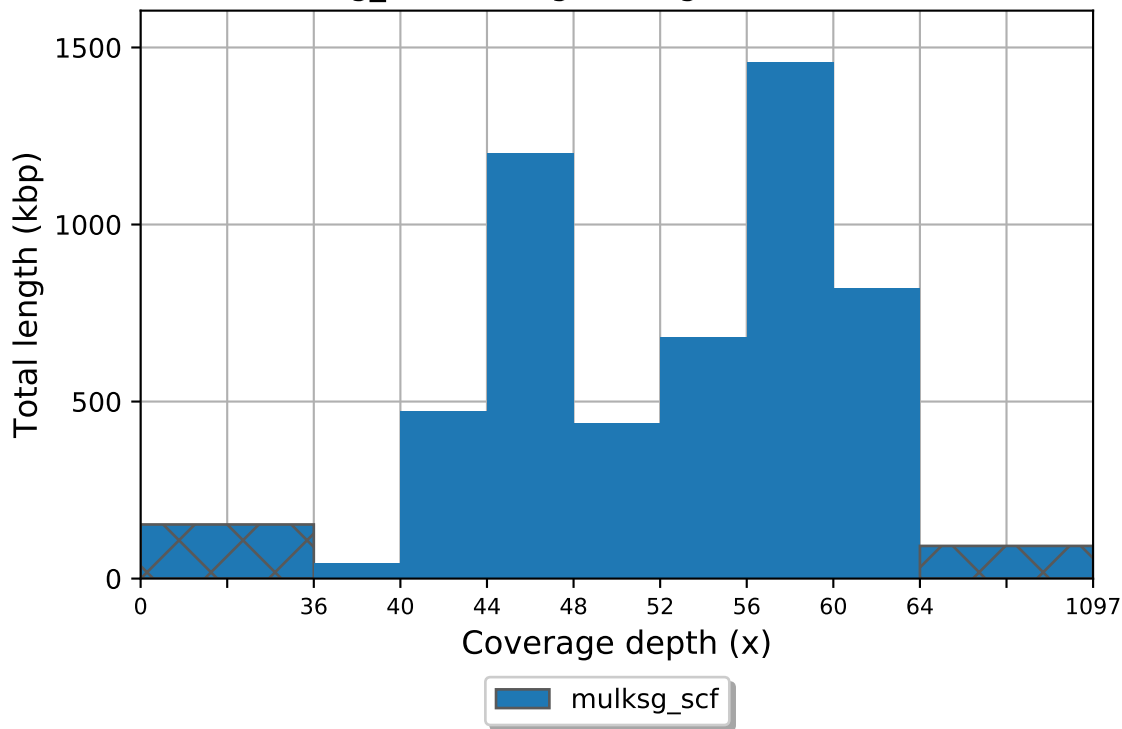
Coverage histogram (bin size: 4x)



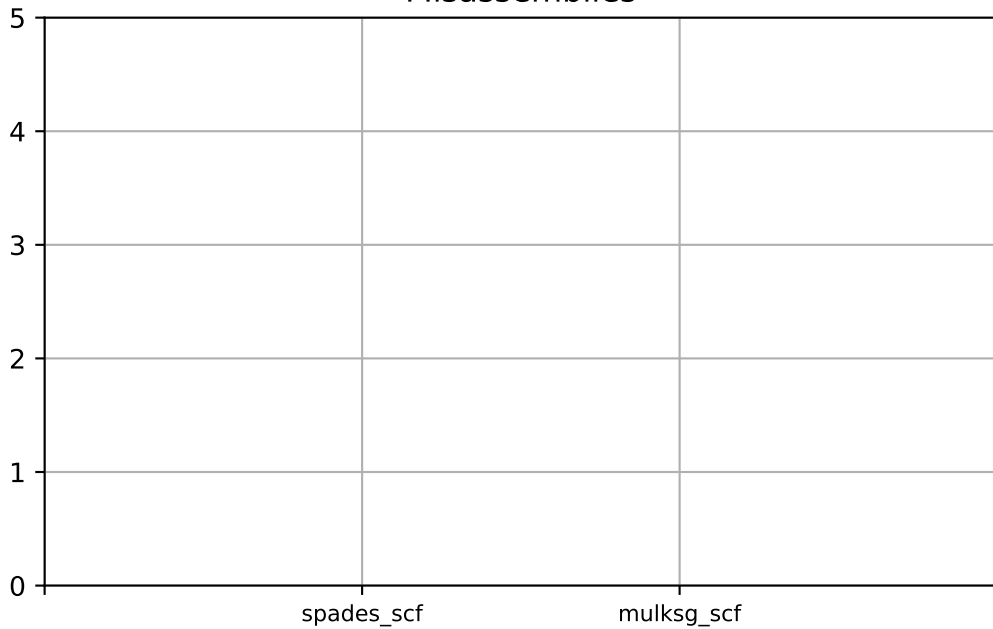
spades\_scf coverage histogram (bin size: 5x)



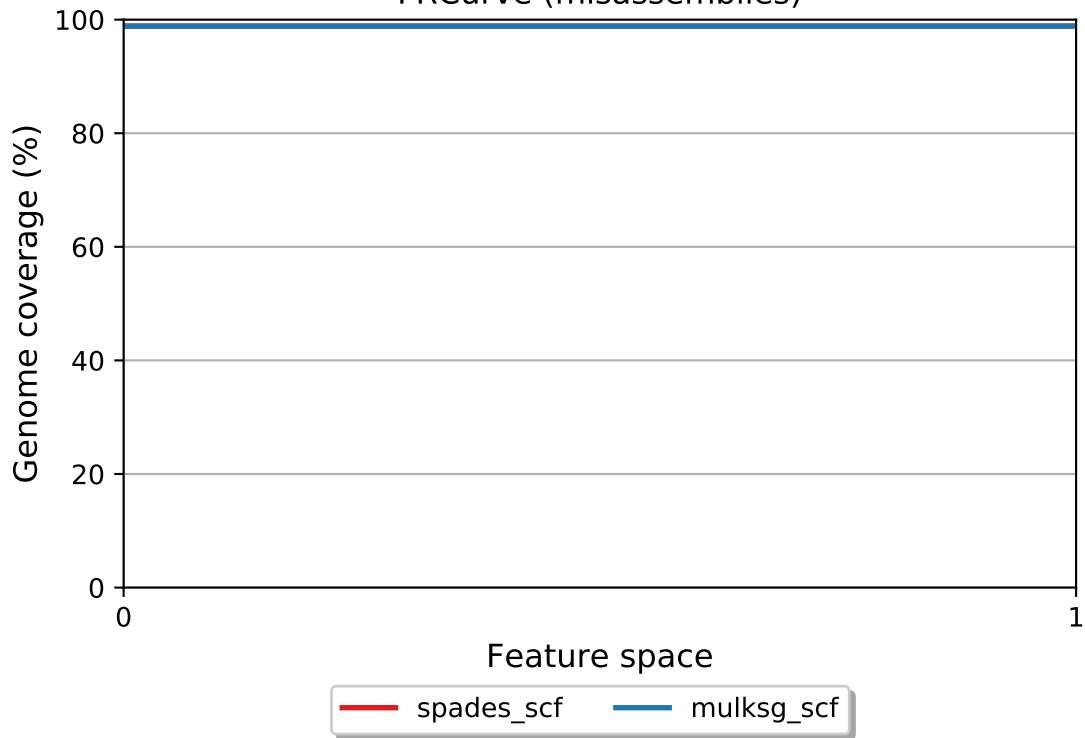
mulksg\_scf coverage histogram (bin size: 4x)



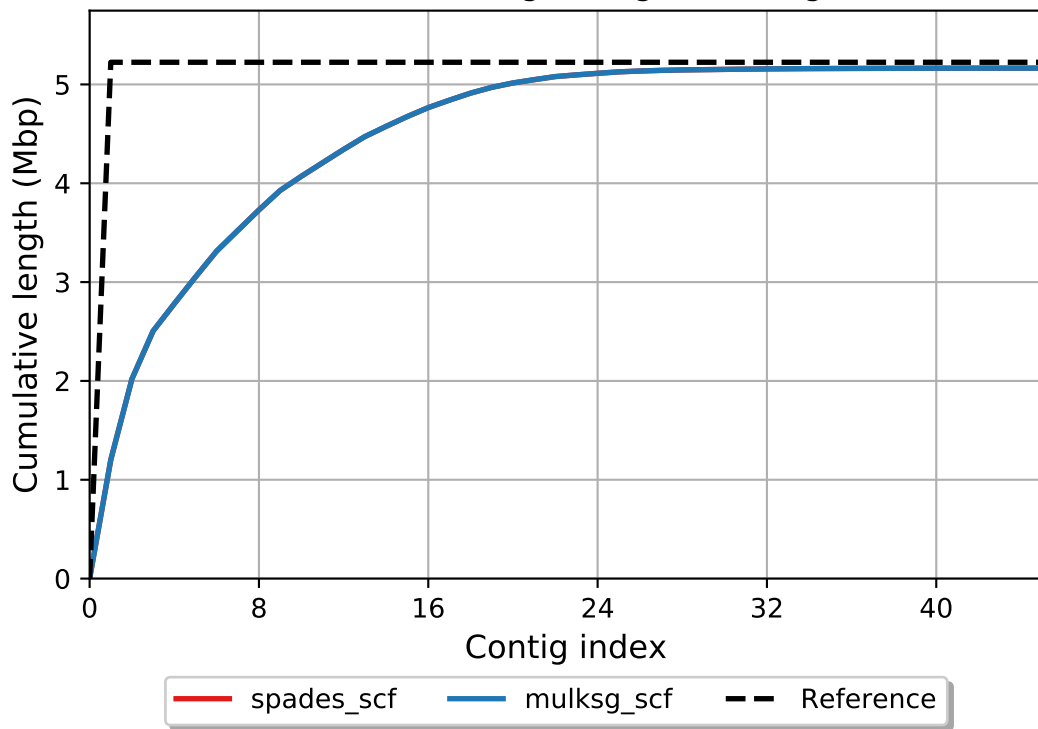
## Misassemblies



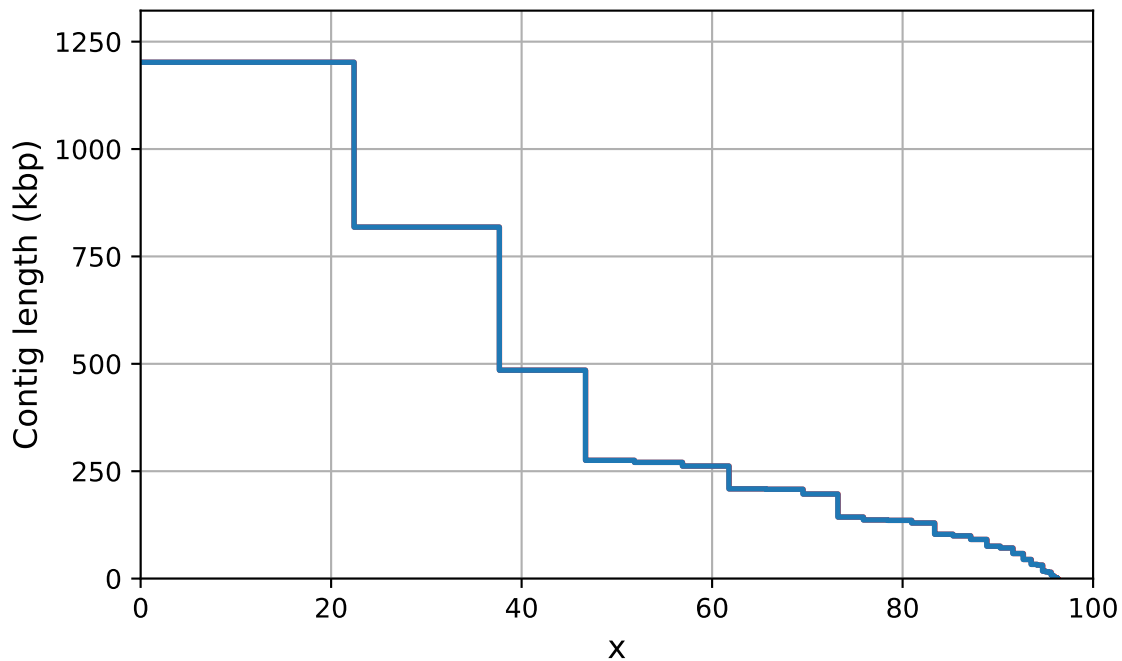
FRCurve (misassemblies)



Cumulative length (aligned contigs)



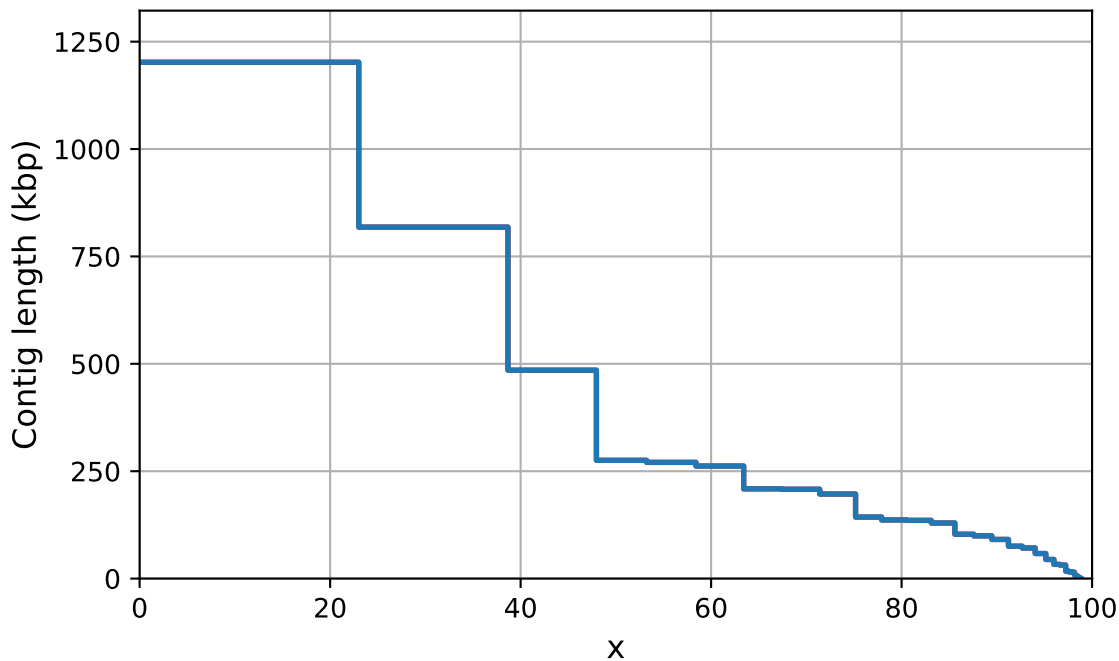
NAx



spades\_scf mulksg\_scf

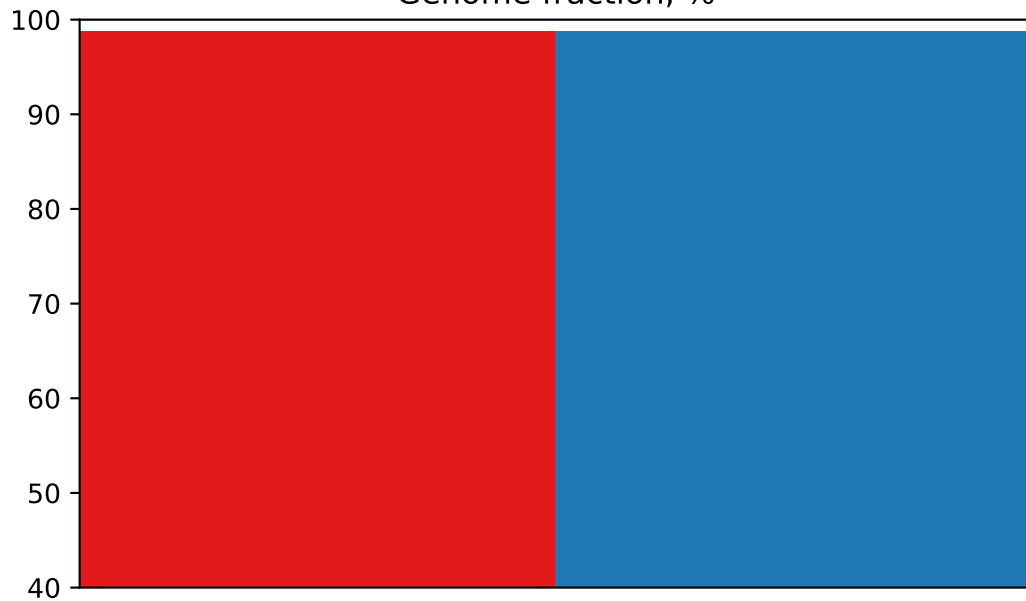


# NGAx



spades\_scf mulksg\_scf

Genome fraction, %



spades\_scf



mulksg\_scf