

Report

	spades se	spades pe	spades mp
# contigs (>= 0 bp)	64	73	63
# contigs (>= 1000 bp)	12	13	10
# contigs (>= 5000 bp)	9	9	7
# contigs (>= 10000 bp)	7	7	6
# contigs (>= 25000 bp)	3	3	2
# contigs (>= 50000 bp)	0	0	1
Total length (>= 0 bp)	214660	215089	218546
Total length (>= 1000 bp)	201501	201948	209550
Total length (>= 5000 bp)	189883	189686	203029
Total length (>= 10000 bp)	174094	174649	194103
Total length (>= 25000 bp)	93271	92926	107427
Total length (>= 50000 bp)	0	0	79147
# contigs	16	18	12
Largest contig	36582	36522	79147
Total length	204733	205715	210874
Reference length	325724	325724	325724
GC (%)	35.07	35.03	35.00
Reference GC (%)	32.97	32.97	32.97
N50	24323	24323	28280
NG50	16447	17326	20692
N90	7061	7061	17591
NG90	-	-	-
auN	23372.7	23239.2	43018.5
auNG	14690.9	14677.0	27850.2
L50	4	4	2
LG50	7	7	5
L90	9	9	6
LG90	-	-	-
# misassemblies	4	4	6
# misassembled contigs	2	2	4
Misassembled contigs length	40770	41649	145131
# local misassemblies	1	2	1
# scaffold gap ext. mis.	7	7	7
# scaffold gap loc. mis.	10	9	7
# unaligned mis. contigs	0	0	0
# unaligned contigs	0 + 0 part	0 + 0 part	0 + 0 part
Unaligned length	0	0	0
Genome fraction (%)	62.175	62.459	62.991
Duplication ratio	1.002	1.001	0.994
# N's per 100 kbp	1318.79	1312.50	3101.38
# mismatches per 100 kbp	4.44	3.93	6.37
# indels per 100 kbp	4.93	5.40	6.86
Largest alignment	36482	36422	44291
Total aligned length	202908	203652	203946
NA50	20246	20246	20246
NGA50	7766	7951	8728
NA90	4107	4286	4293
NGA90	-	-	-
auNA	21043.3	20833.6	23458.2
auNGA	13226.7	13157.7	15186.9
LA50	4	4	4
LGA50	8	8	7
LA90	12	12	11
LGA90	-	-	-

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 se	spades pe	spades mp
# misassemblies	4	4	6
# contig misassemblies	3	3	5
# c. relocations	3	3	5
# c. translocations	0	0	0
# c. inversions	0	0	0
# scaffold misassemblies	1	1	1
# s. relocations	1	1	1
# s. translocations	0	0	0
# s. inversions	0	0	0
# misassembled contigs	2	2	4
Misassembled contigs length	40770	41649	145131
# local misassemblies	1	2	1
# scaffold gap ext. mis.	7	7	7
# scaffold gap loc. mis.	10	9	7
# unaligned mis. contigs	0	0	0
# mismatches	9	8	13
# indels	10	11	14
# indels (<= 5 bp)	1	1	1
# indels (> 5 bp)	9	10	13
Indels length	784	819	1410

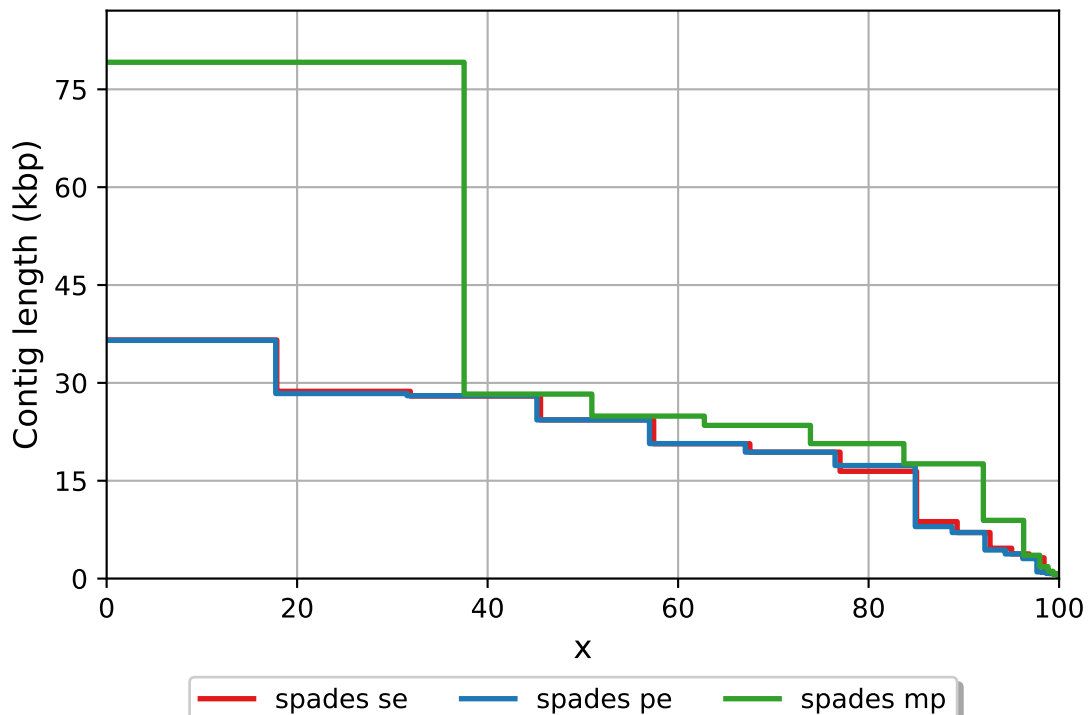
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

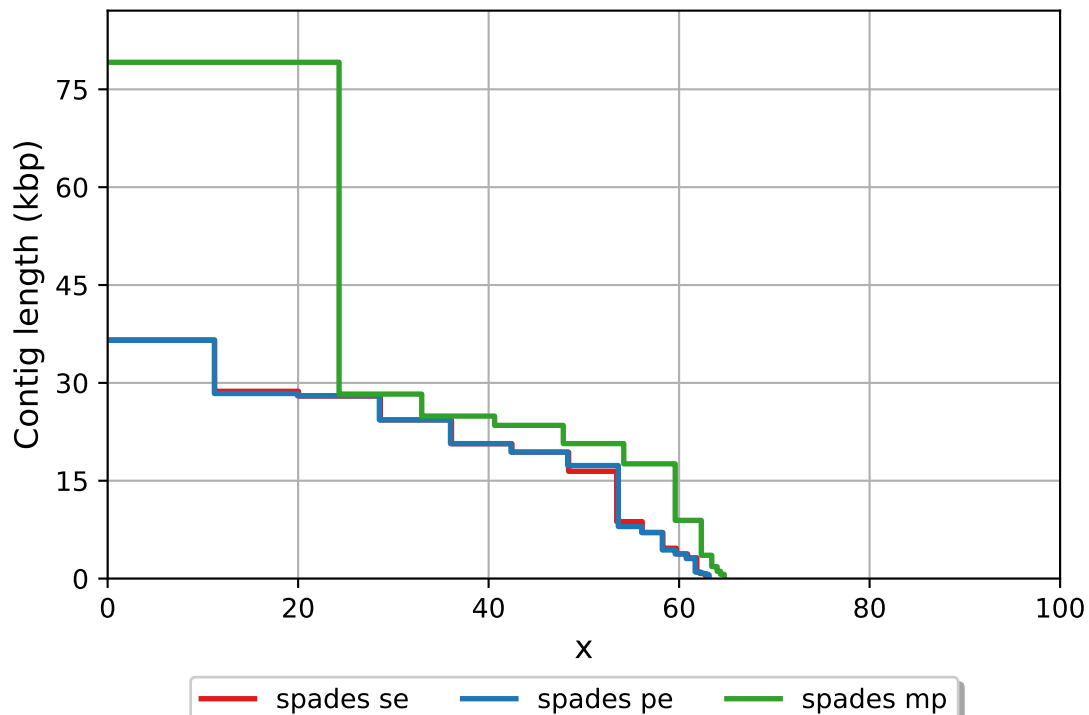
	spades se	spades pe	spades mp
# fully unaligned contigs	0	0	0
Fully unaligned length	0	0	0
# partially unaligned contigs	0	0	0
Partially unaligned length	0	0	0
# N's	2700	2700	6540

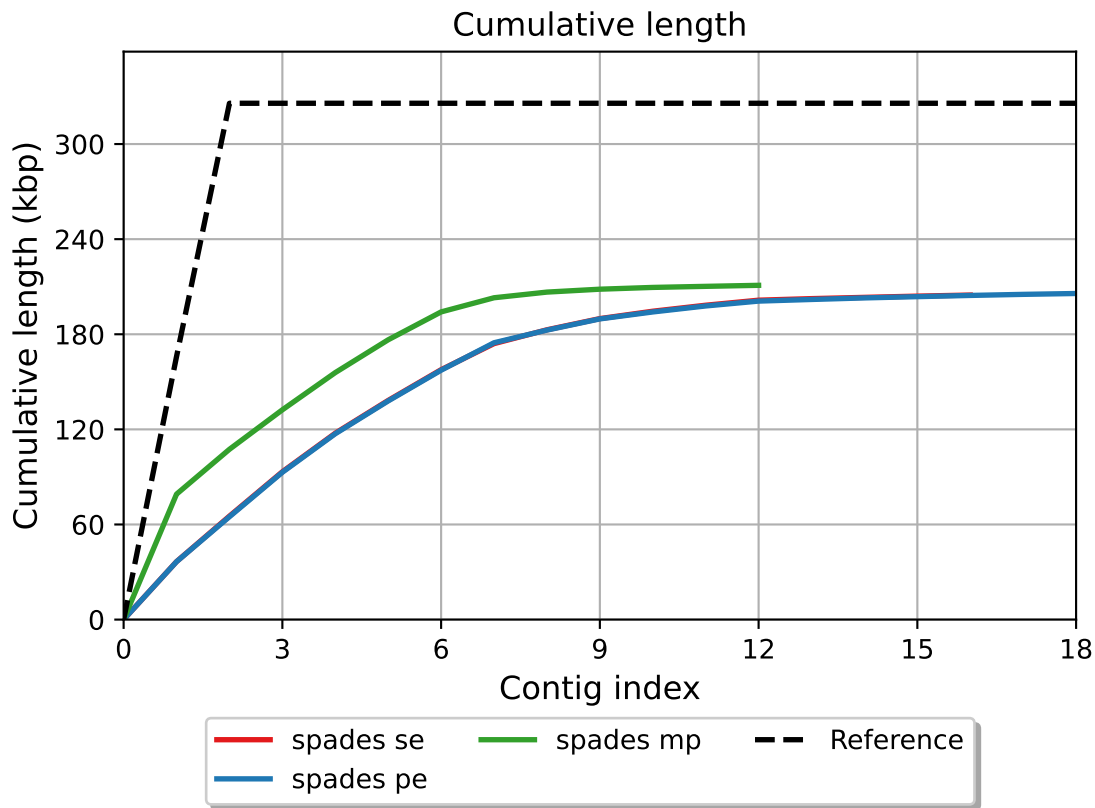
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

Nx

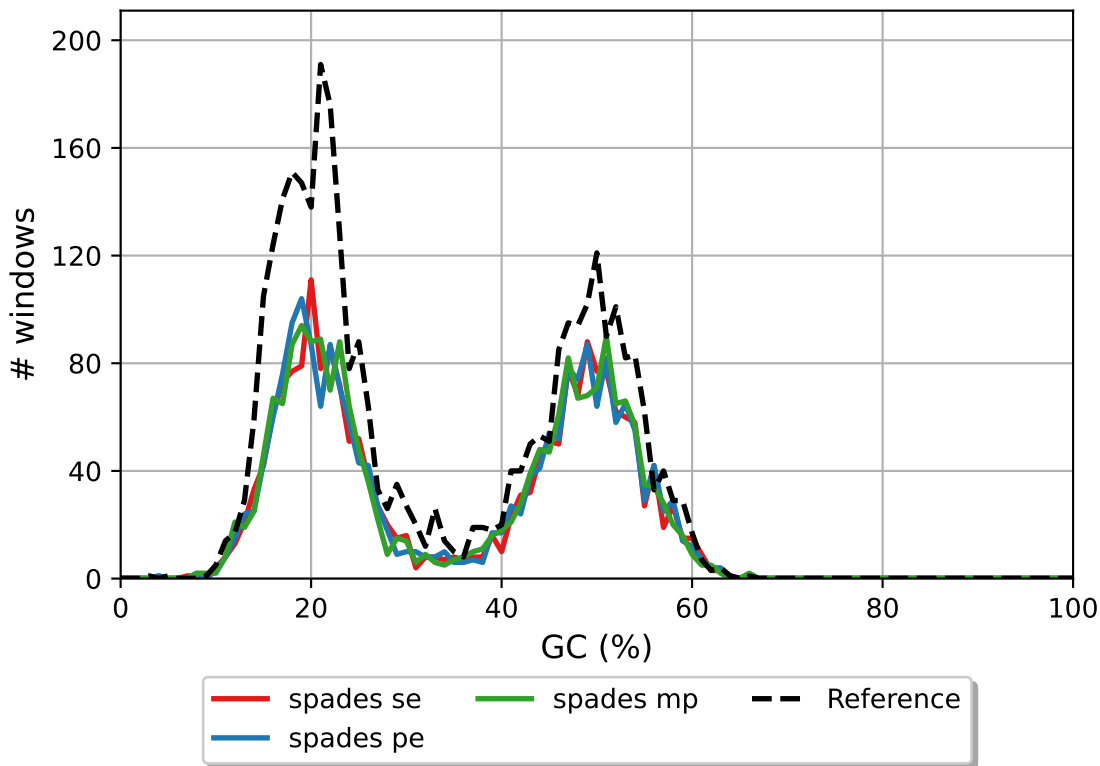


# NGx

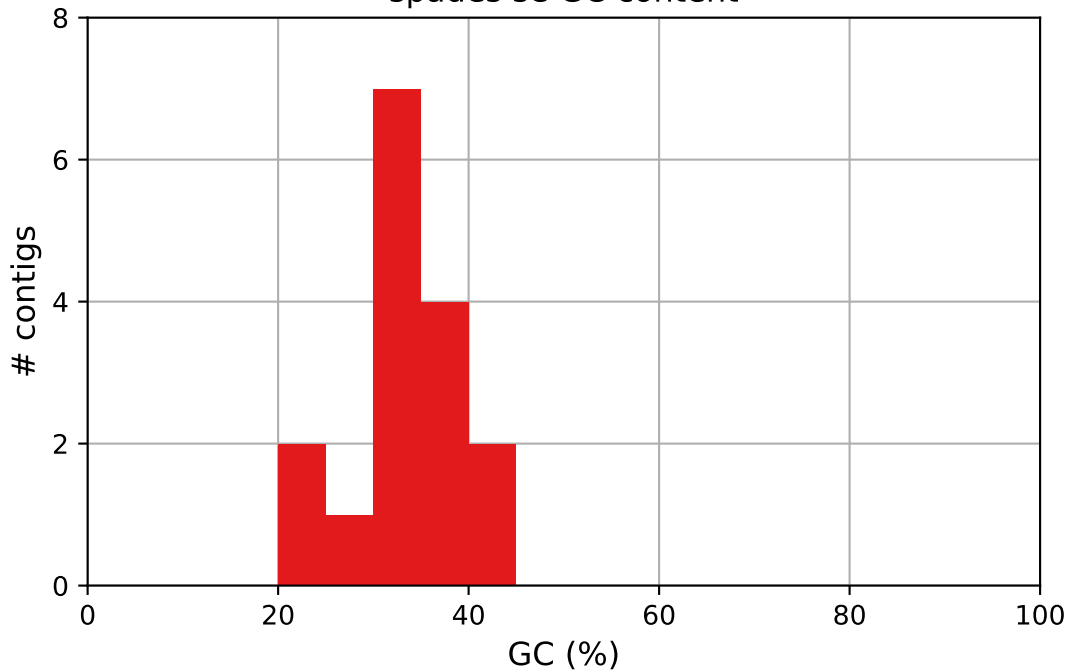




## GC content



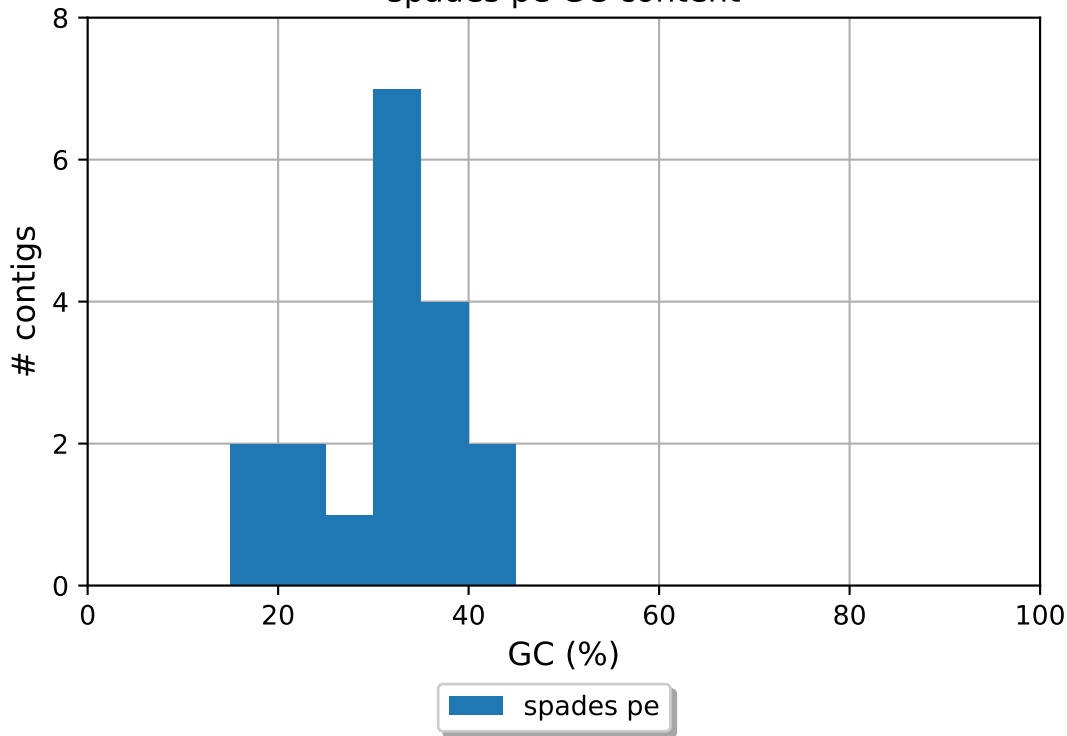
spades se GC content



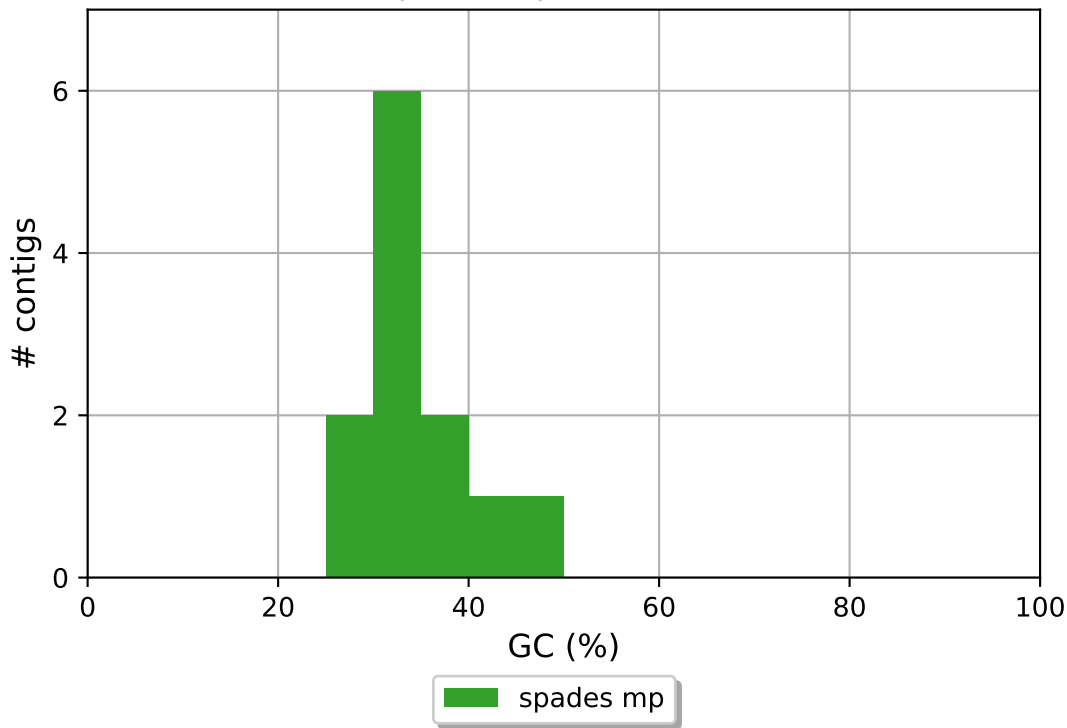
spades se



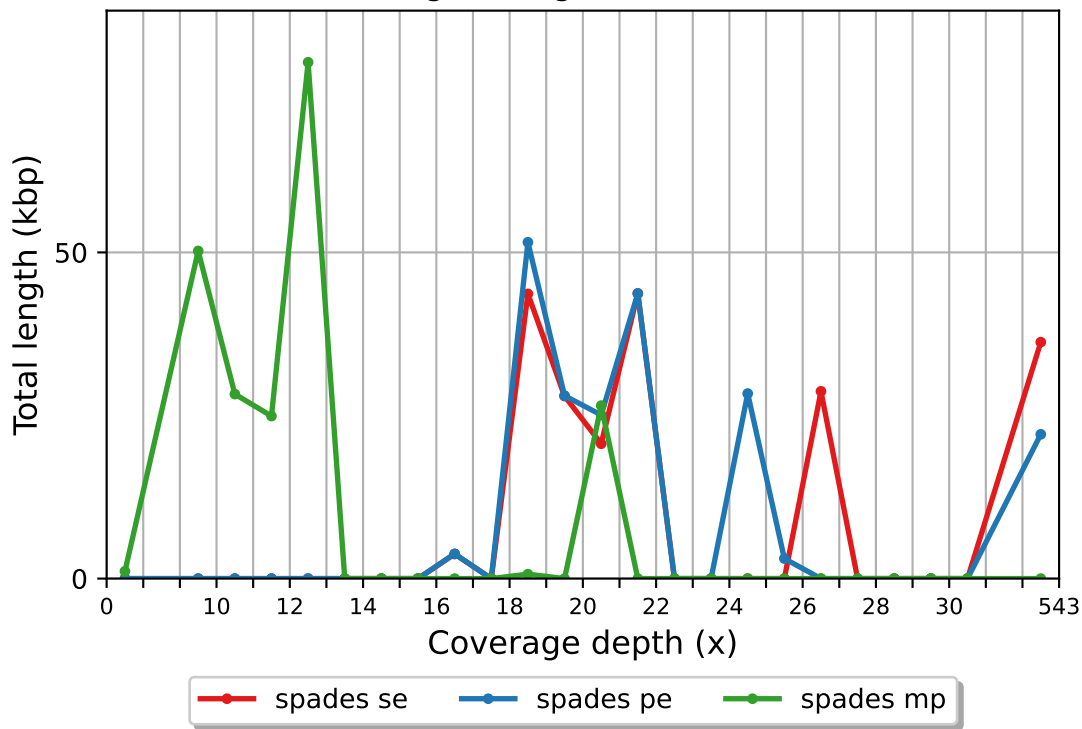
spades pe GC content



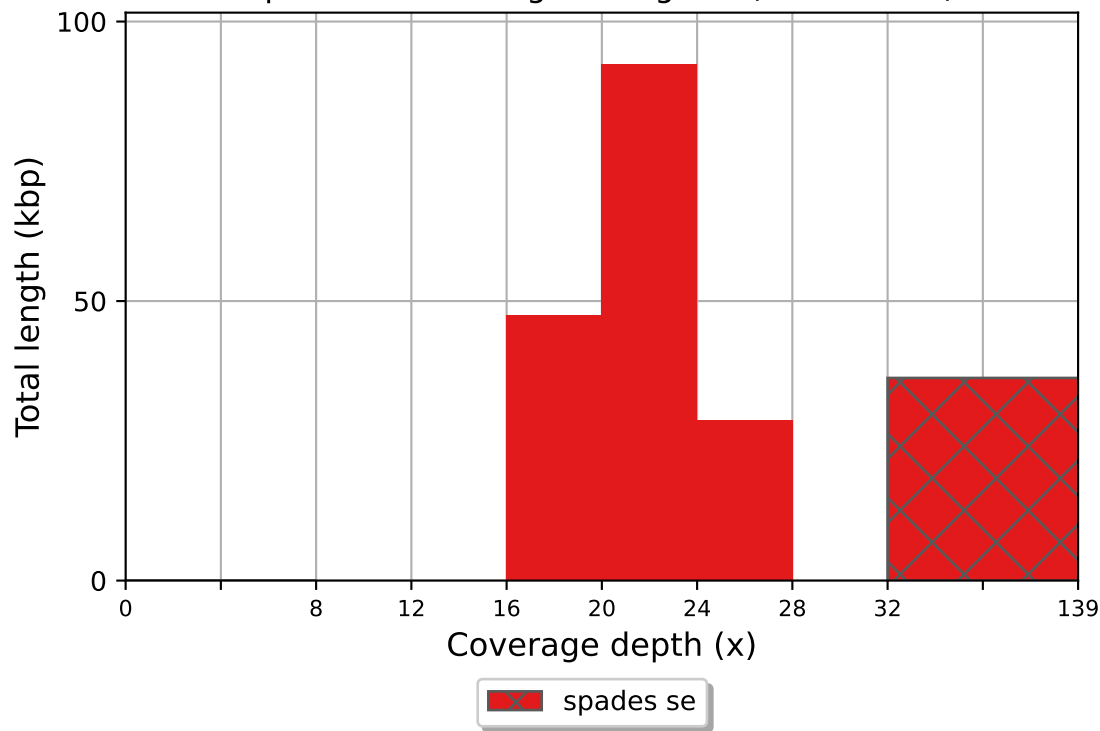
spades mp GC content



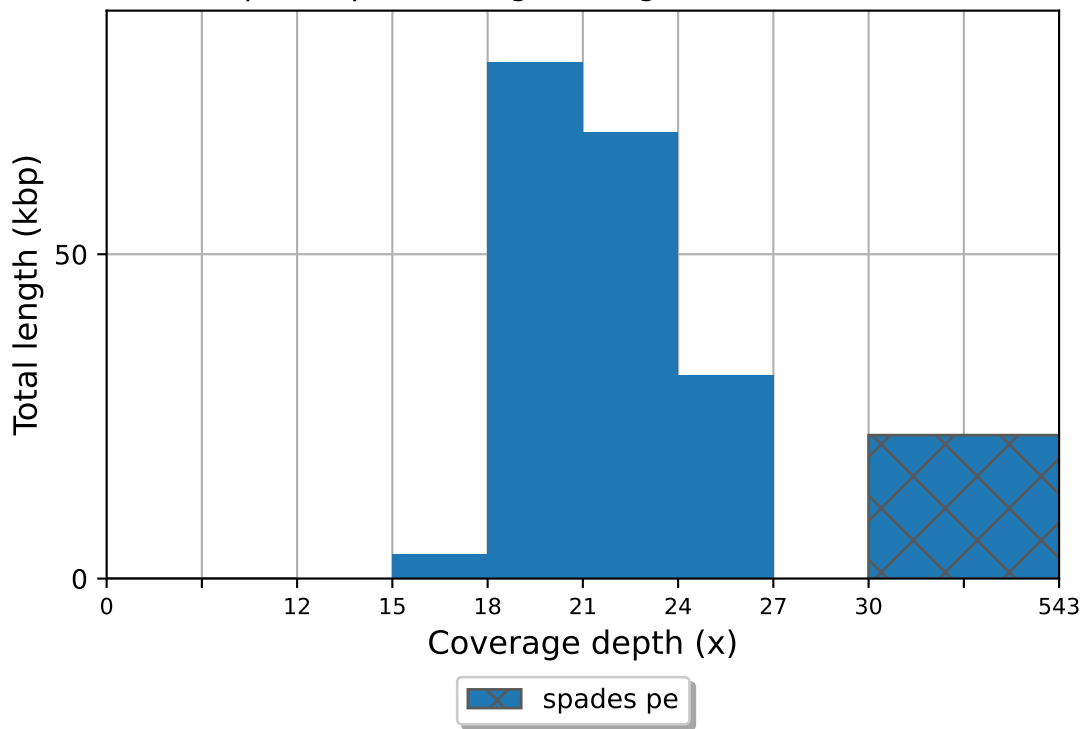
Coverage histogram (bin size: 1x)



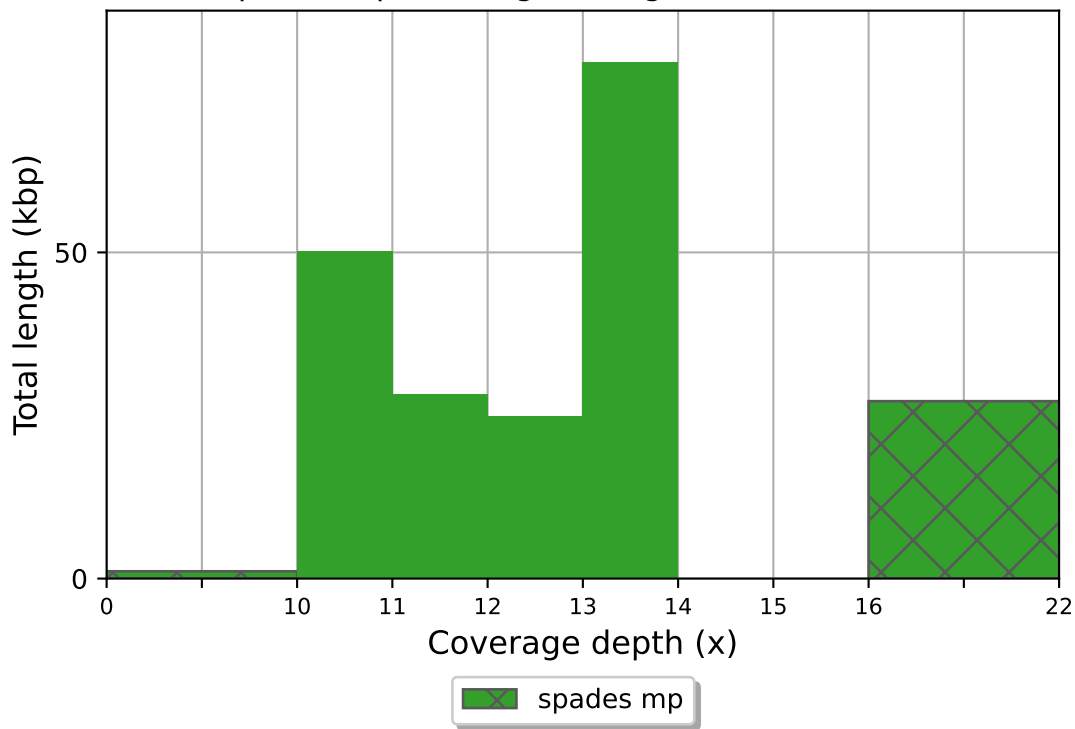
spades se coverage histogram (bin size: 4x)



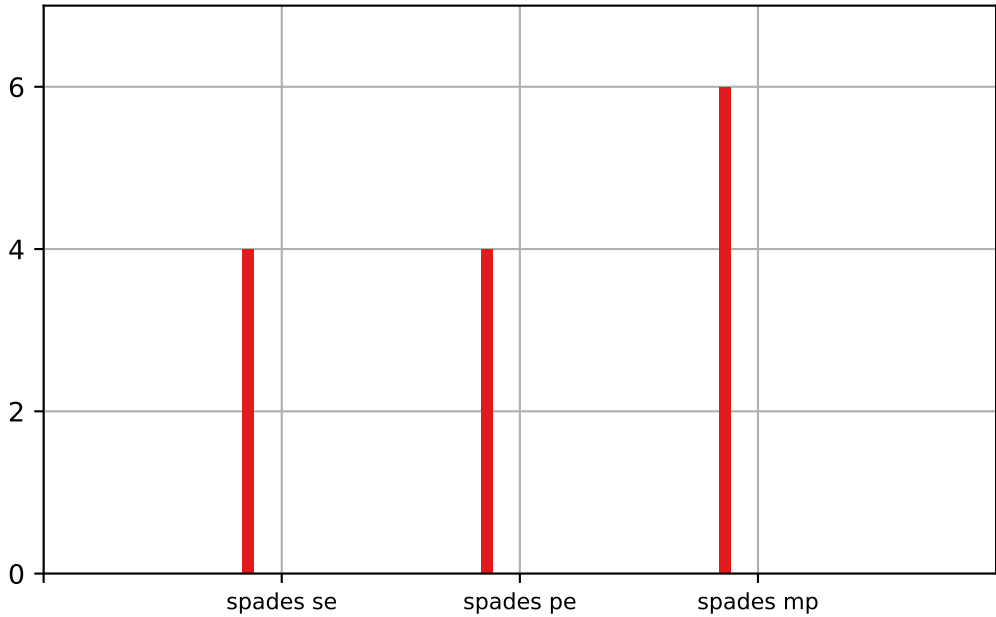
spades pe coverage histogram (bin size: 3x)



spades mp coverage histogram (bin size: 1x)

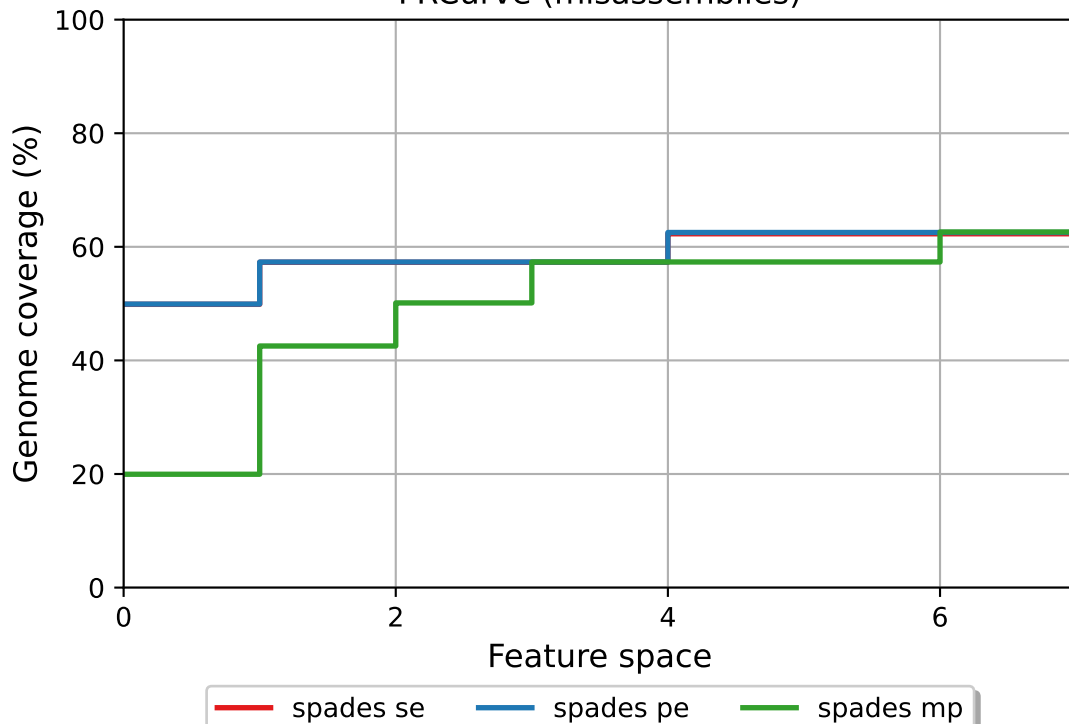


## Misassemblies



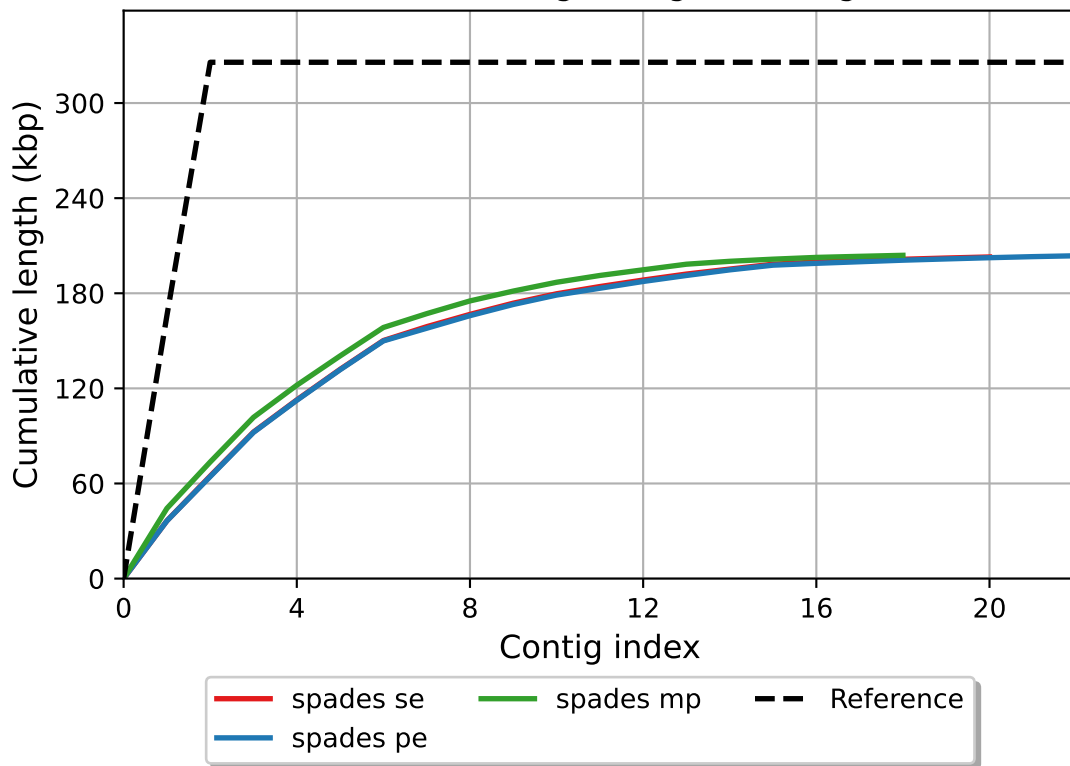
 # relocations

FRCurve (misassemblies)

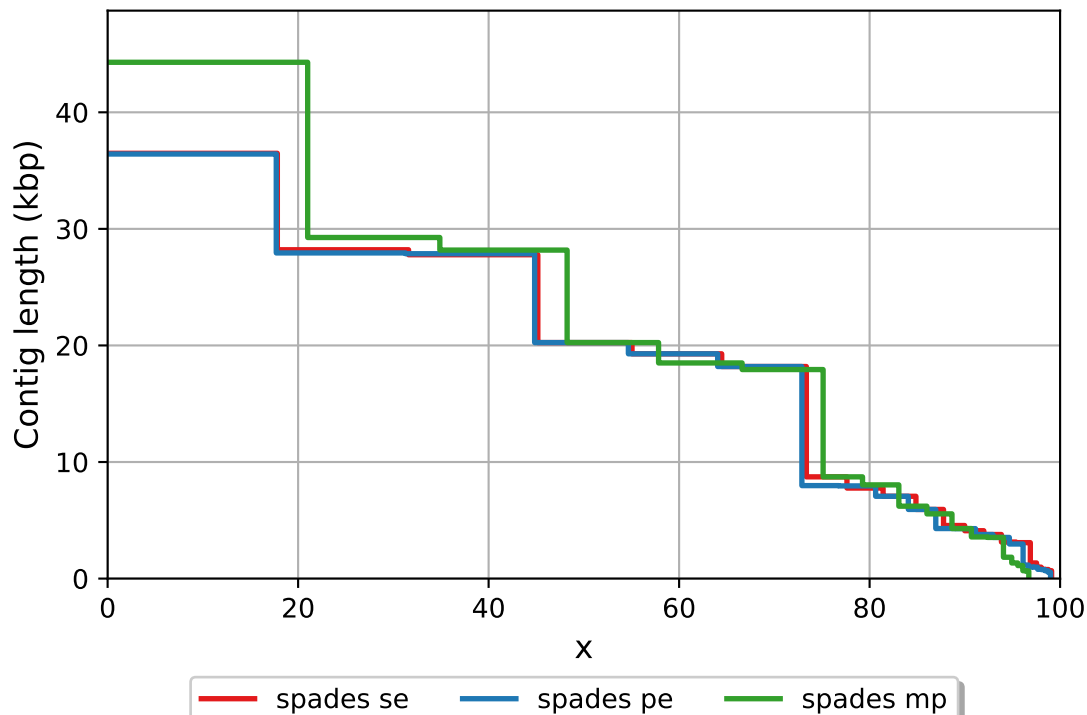




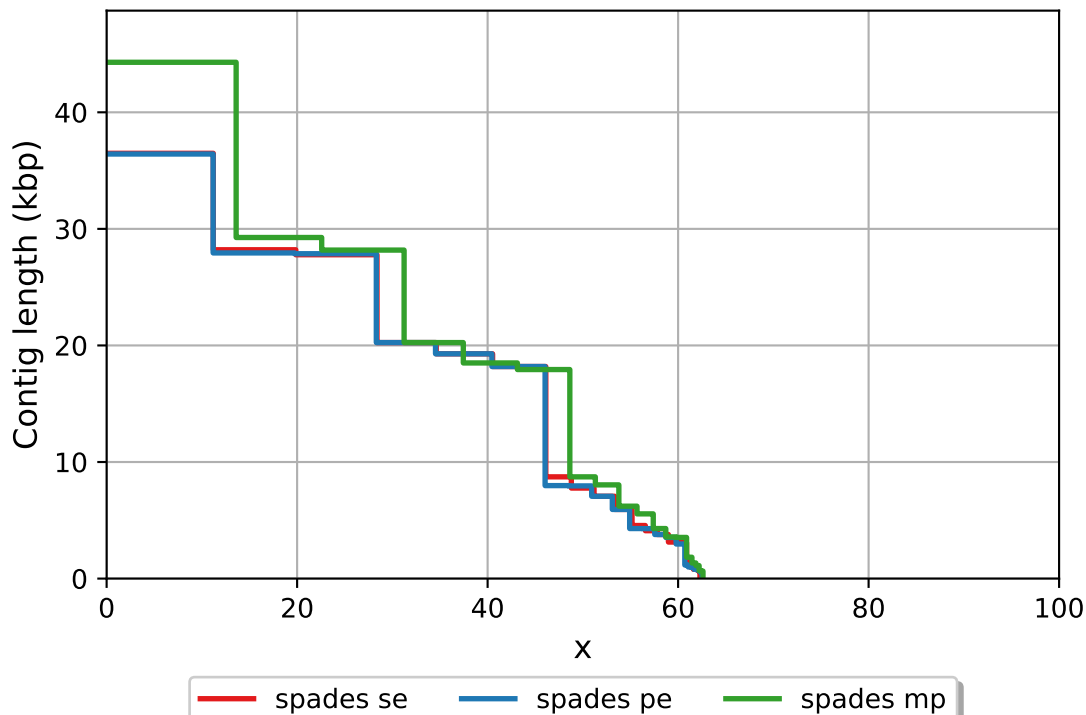
Cumulative length (aligned contigs)



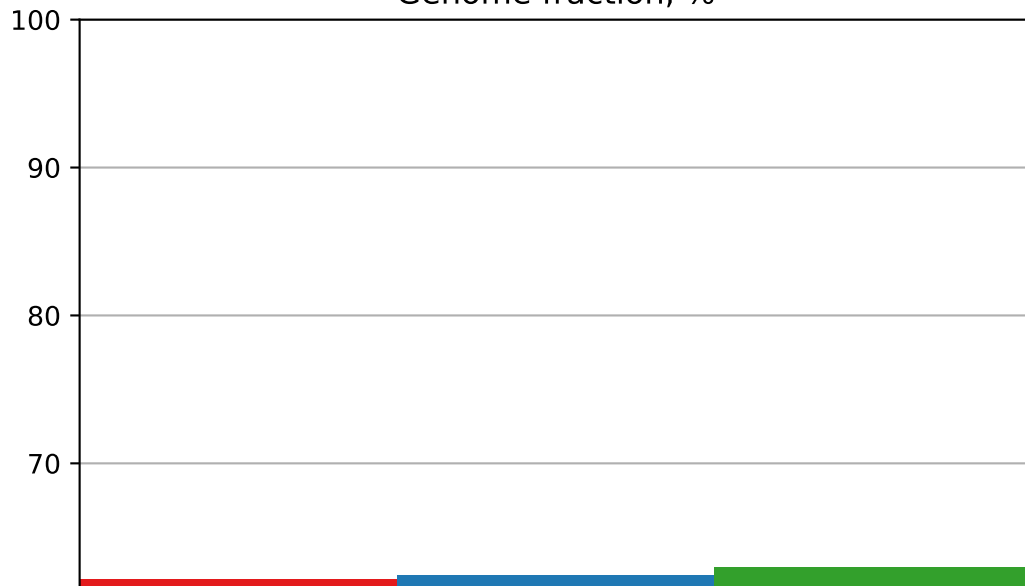
# NAx



# NGAx



Genome fraction, %



spades se



spades pe



spades mp