

Report

	spades se	spades pe	spades mp
# contigs (>= 0 bp)	2	2	2
# contigs (>= 1000 bp)	2	2	2
# contigs (>= 5000 bp)	2	2	2
# contigs (>= 10000 bp)	2	2	2
# contigs (>= 25000 bp)	2	2	2
# contigs (>= 50000 bp)	2	2	2
Total length (>= 0 bp)	199972	199972	199972
Total length (>= 1000 bp)	199972	199972	199972
Total length (>= 5000 bp)	199972	199972	199972
Total length (>= 10000 bp)	199972	199972	199972
Total length (>= 25000 bp)	199972	199972	199972
Total length (>= 50000 bp)	199972	199972	199972
# contigs	2	2	2
Largest contig	99993	99993	99993
Total length	199972	199972	199972
Reference length	414184	414184	414184
GC (%)	36.95	36.95	36.95
Reference GC (%)	36.48	36.48	36.48
N50	99993	99993	99993
NG50	-	-	-
N90	99979	99979	99979
NG90	-	-	-
auN	99986.0	99986.0	99986.0
auNG	48274.2	48274.2	48274.2
L50	1	1	1
LG50	-	-	-
L90	2	2	2
LG90	-	-	-
# misassemblies	33	33	33
# misassembled contigs	2	2	2
Misassembled contigs length	199972	199972	199972
# local misassemblies	10	10	10
# scaffold gap ext. mis.	0	0	0
# scaffold gap loc. mis.	0	0	0
# unaligned mis. contigs	0	0	0
# unaligned contigs	0 + 0 part	0 + 0 part	0 + 0 part
Unaligned length	0	0	0
Genome fraction (%)	48.103	48.103	48.103
Duplication ratio	0.972	0.972	0.970
# N's per 100 kbp	0.00	0.00	0.00
# mismatches per 100 kbp	300.41	300.41	301.01
# indels per 100 kbp	53.16	53.16	53.27
Largest alignment	20633	20633	20629
Total aligned length	193737	193737	193349
NA50	7604	7604	7604
NGA50	-	-	-
NA90	2456	2456	2159
NGA90	-	-	-
auNA	9685.1	9685.1	9686.2
auNGA	4676.1	4676.1	4676.6
LA50	8	8	8
LGA50	-	-	-
LA90	24	24	24
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

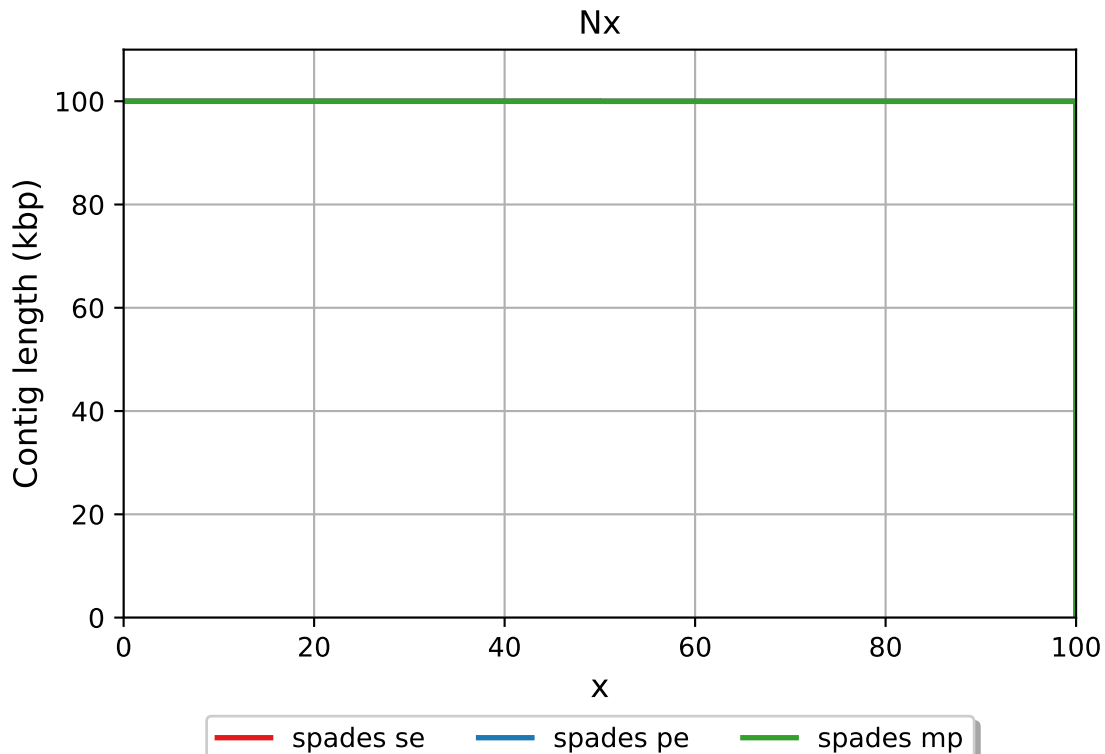
	spades se	spades pe	spades mp
# misassemblies	33	33	33
# contig misassemblies	33	33	33
# c. relocations	33	33	33
# c. translocations	0	0	0
# c. inversions	0	0	0
# scaffold misassemblies	0	0	0
# s. relocations	0	0	0
# s. translocations	0	0	0
# s. inversions	0	0	0
# misassembled contigs	2	2	2
Misassembled contigs length	199972	199972	199972
# local misassemblies	10	10	10
# scaffold gap ext. mis.	0	0	0
# scaffold gap loc. mis.	0	0	0
# unaligned mis. contigs	0	0	0
# mismatches	582	582	582
# indels	103	103	103
# indels (<= 5 bp)	34	34	34
# indels (> 5 bp)	69	69	69
Indels length	3418	3418	3418

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).

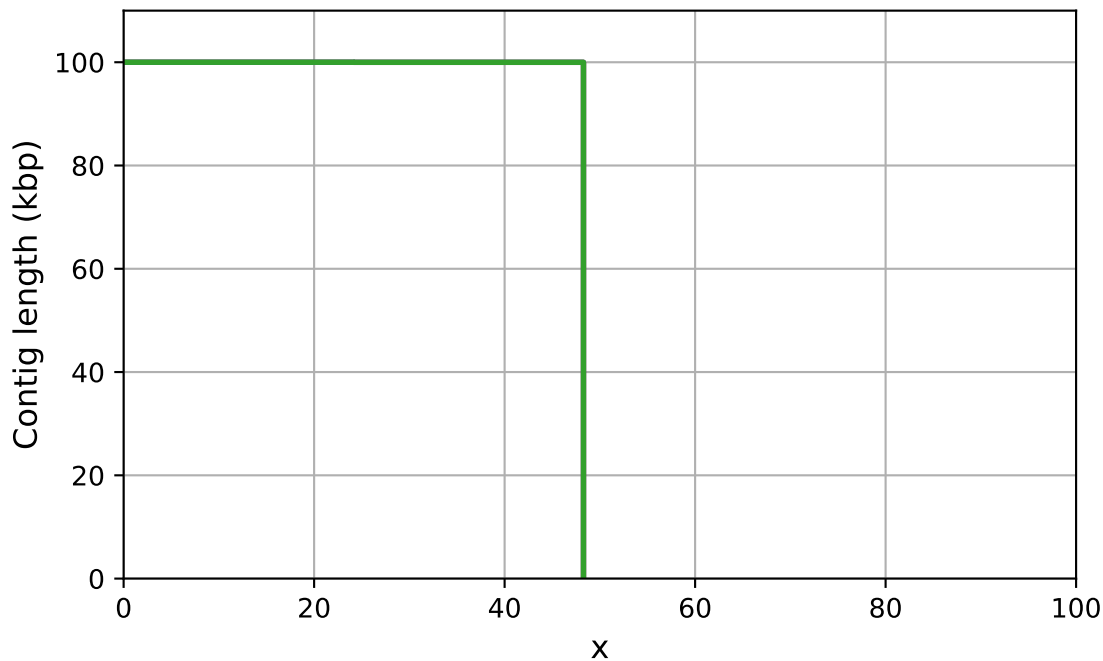
Unaligned report

	spades 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	0	0	0

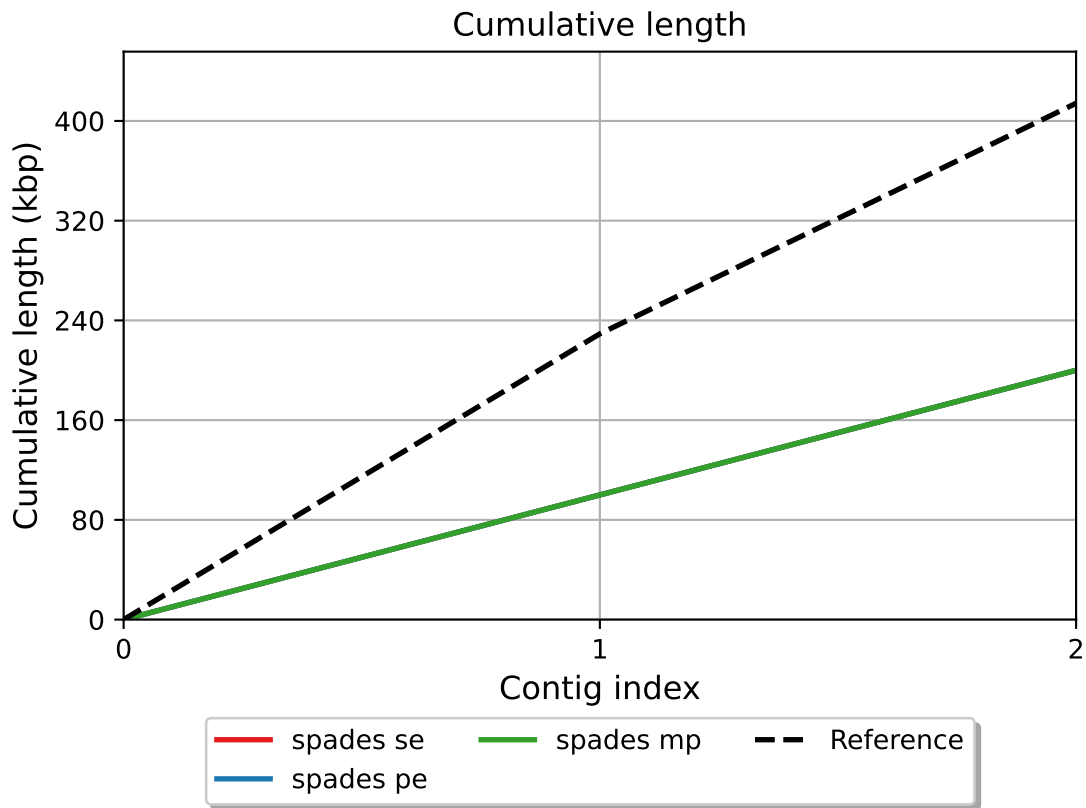
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



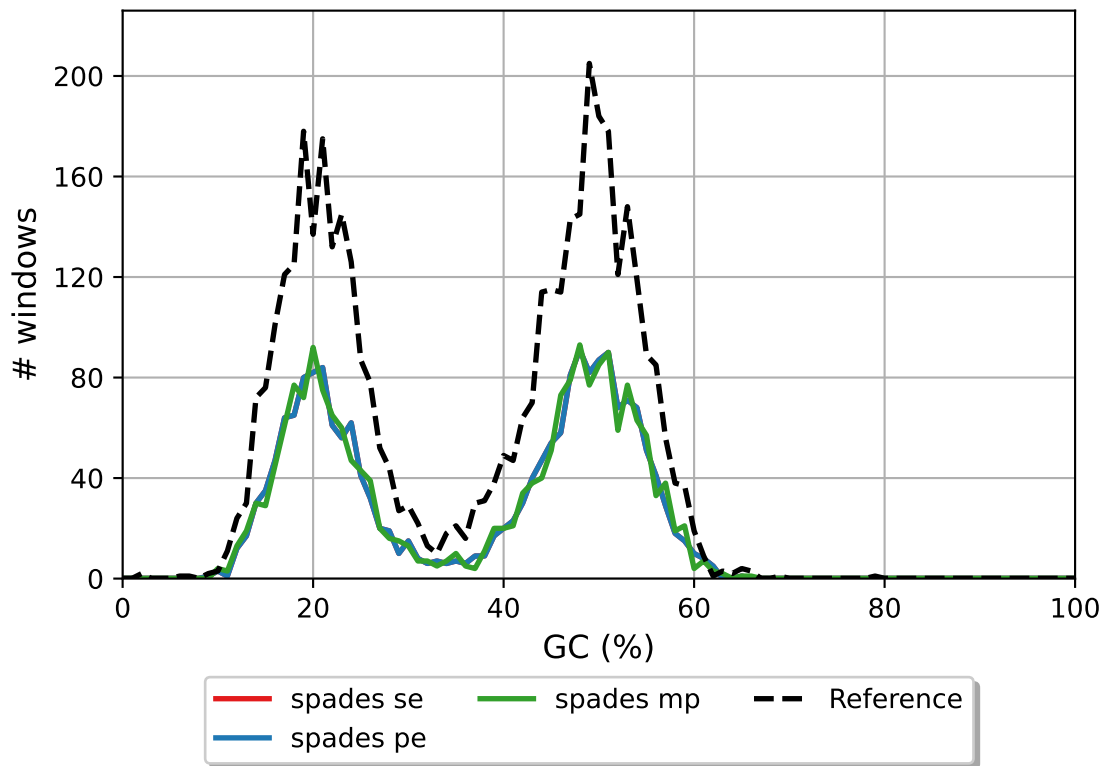
NGx



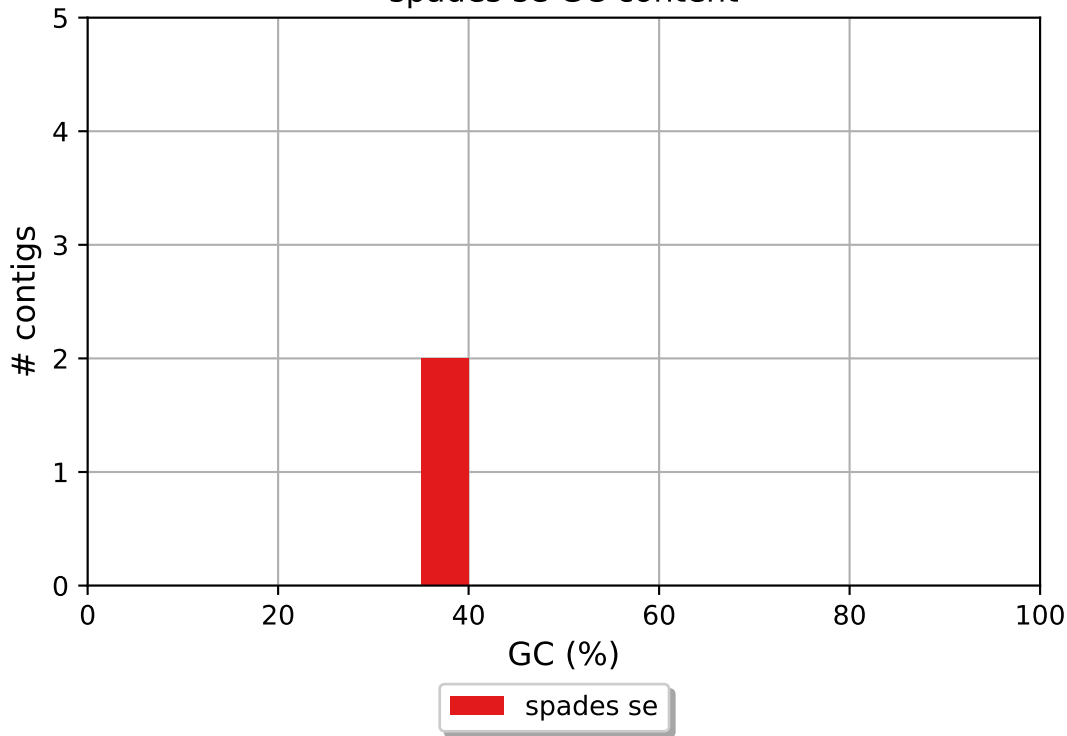
spades se spades pe spades mp



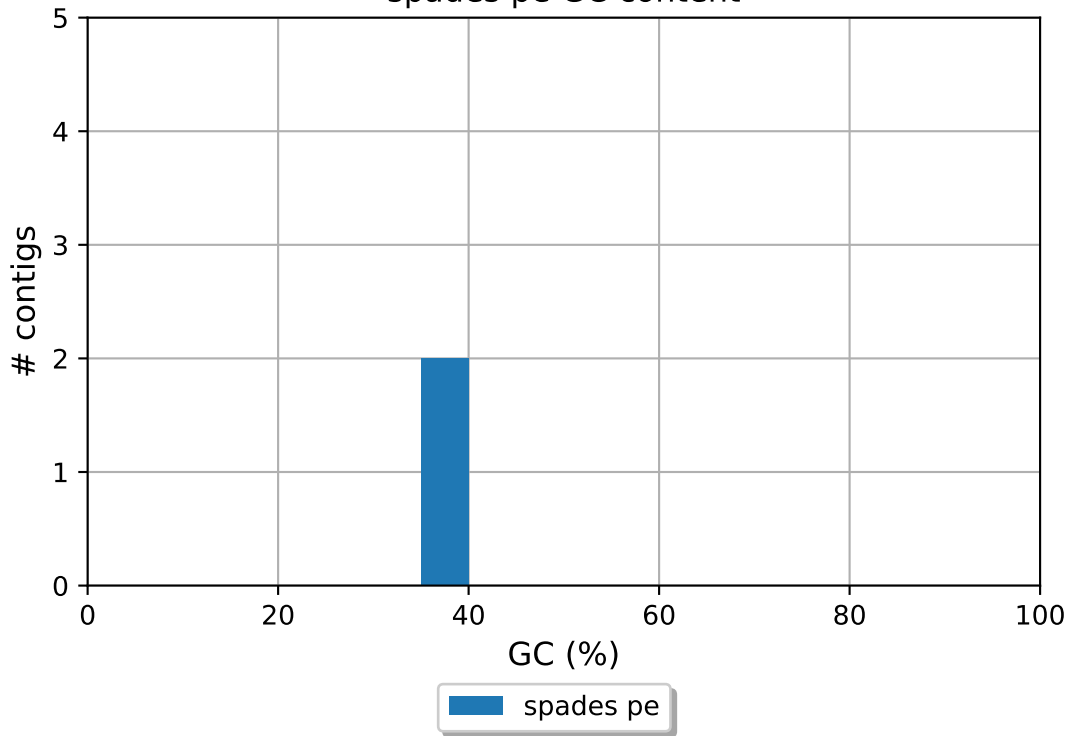
GC content



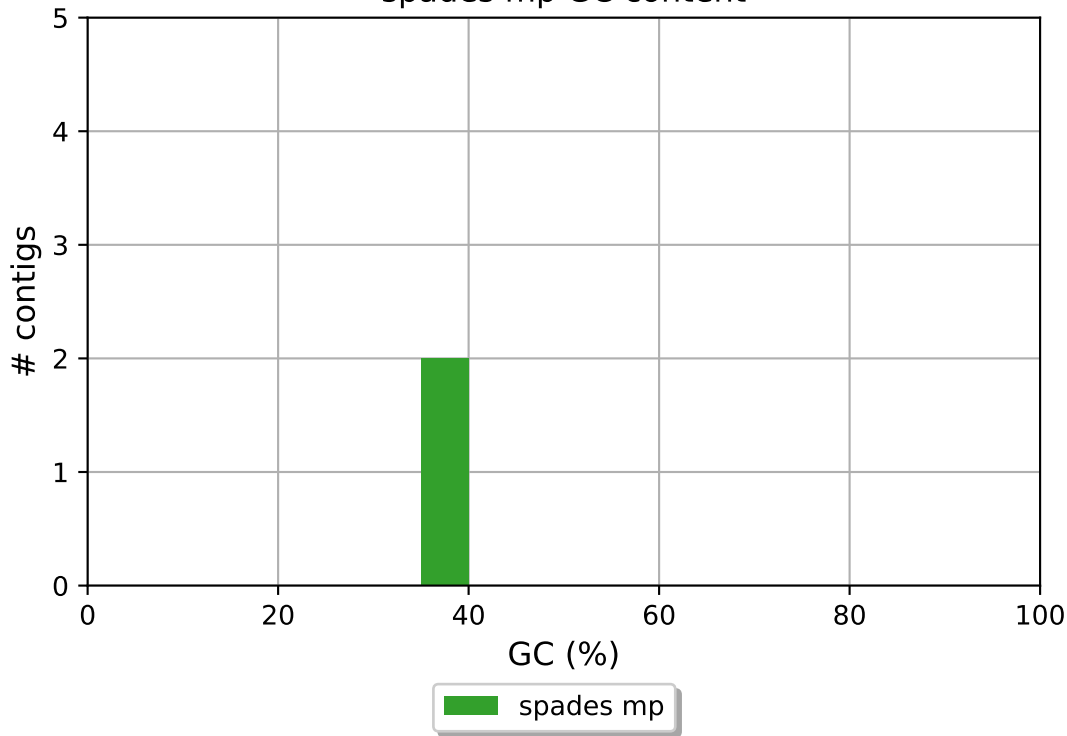
spades se GC content



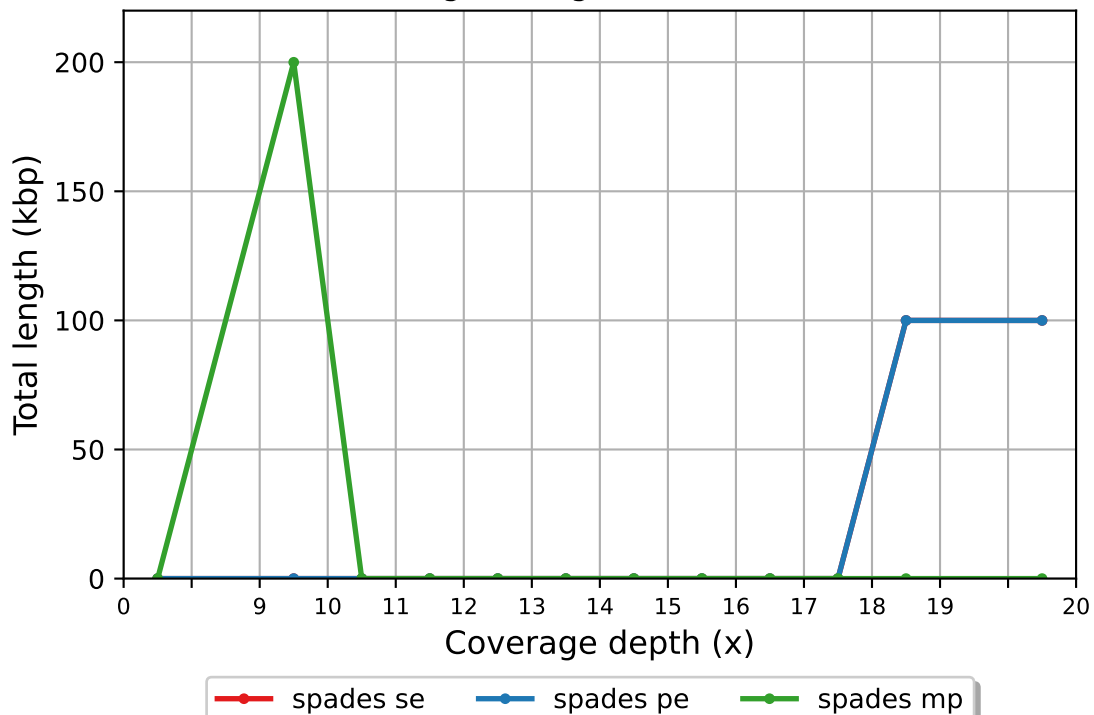
spades pe GC content



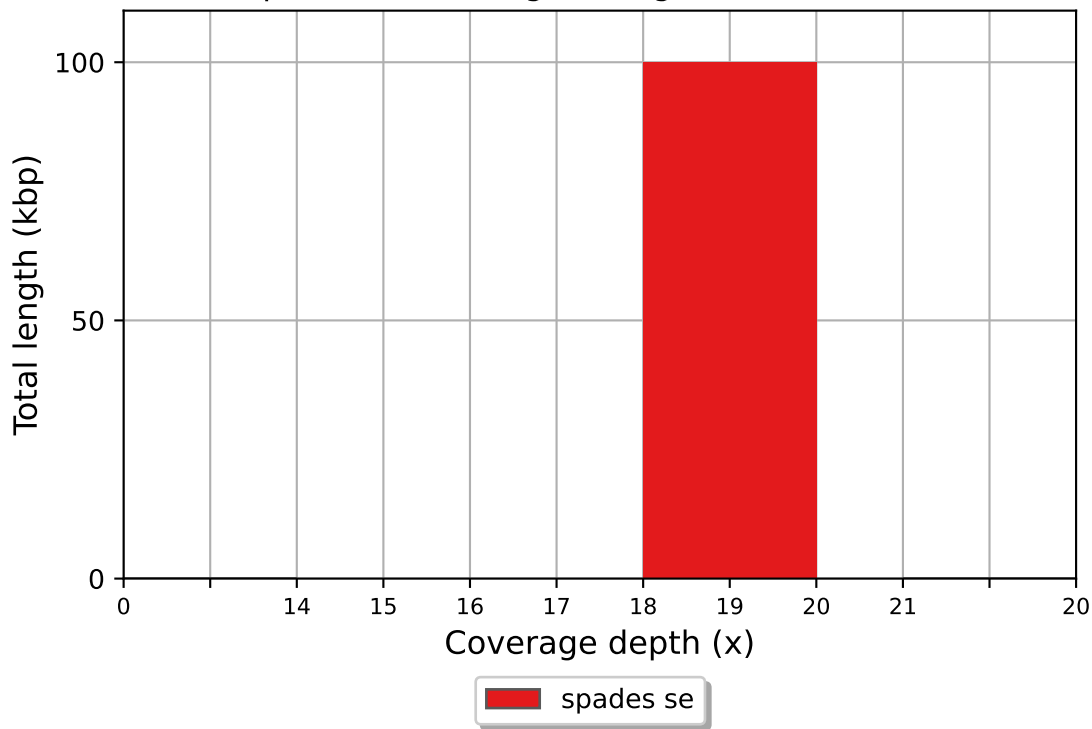
spades mp GC content



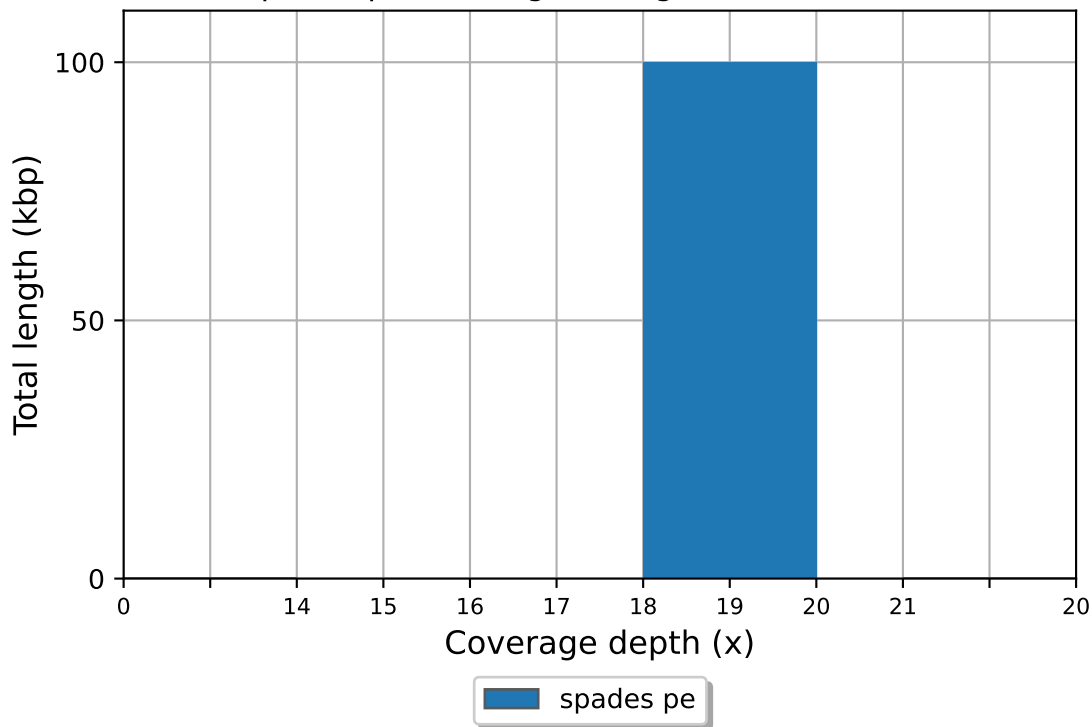
Coverage histogram (bin size: 1x)



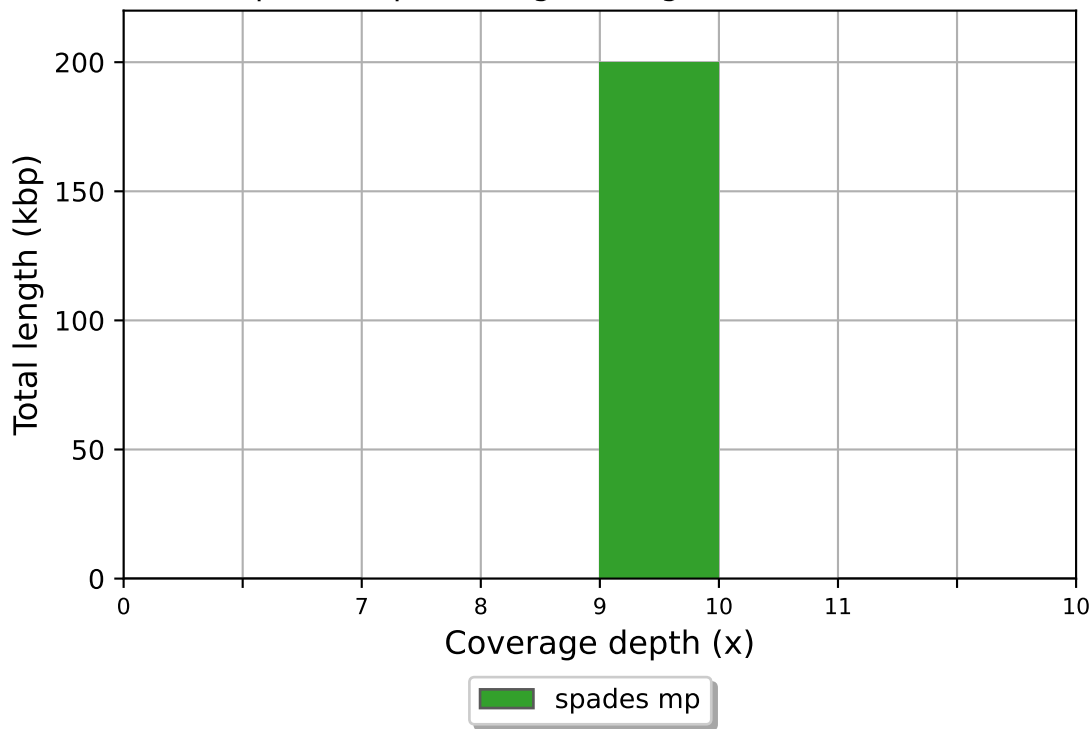
spades se coverage histogram (bin size: 1x)



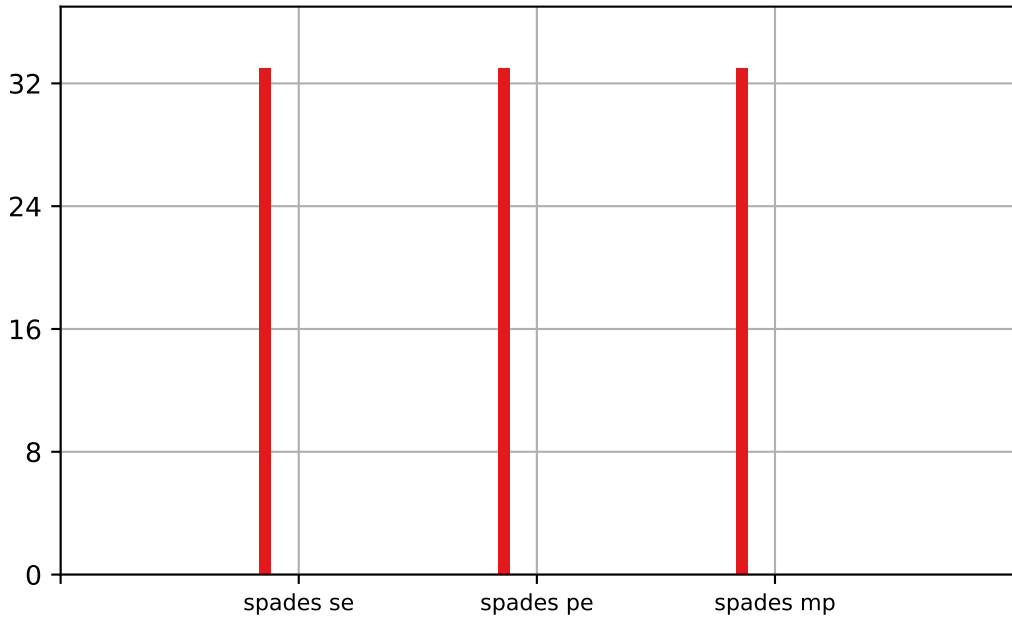
spades pe coverage histogram (bin size: 1x)



spades mp coverage histogram (bin size: 1x)

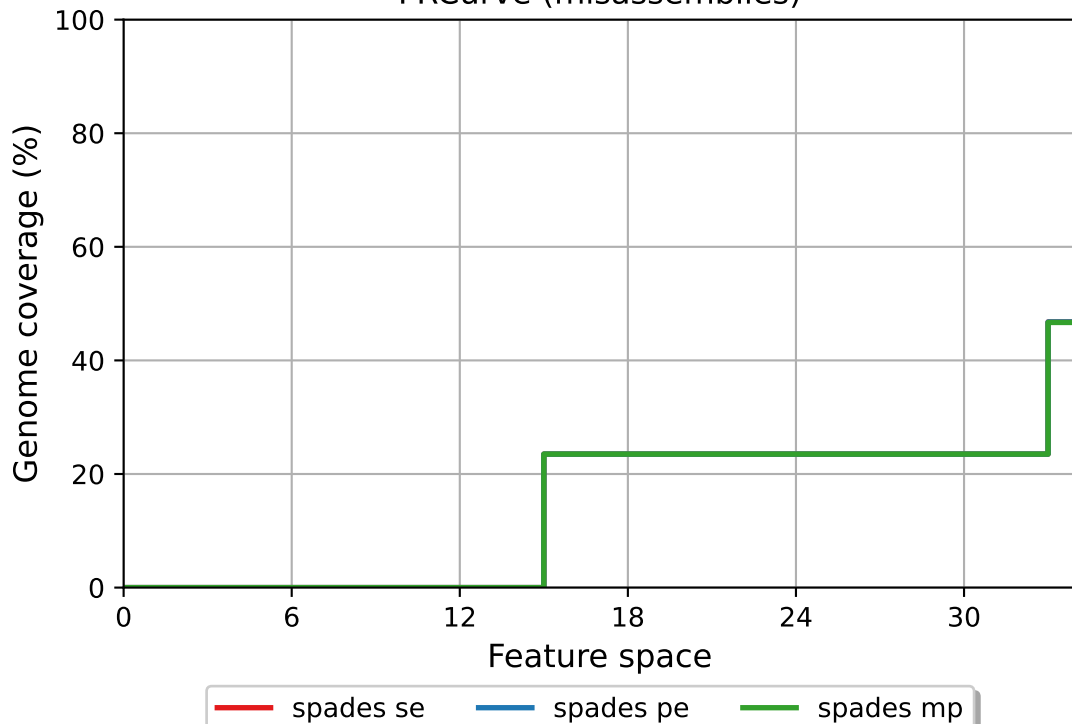


Misassemblies

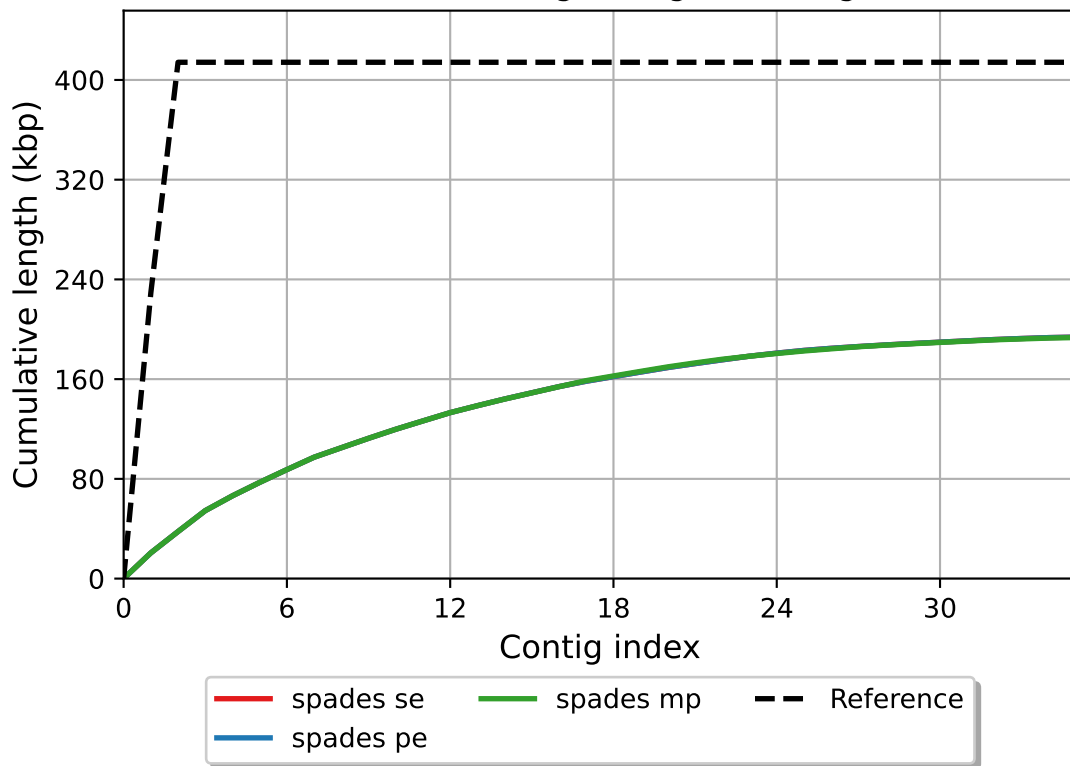


 # relocations

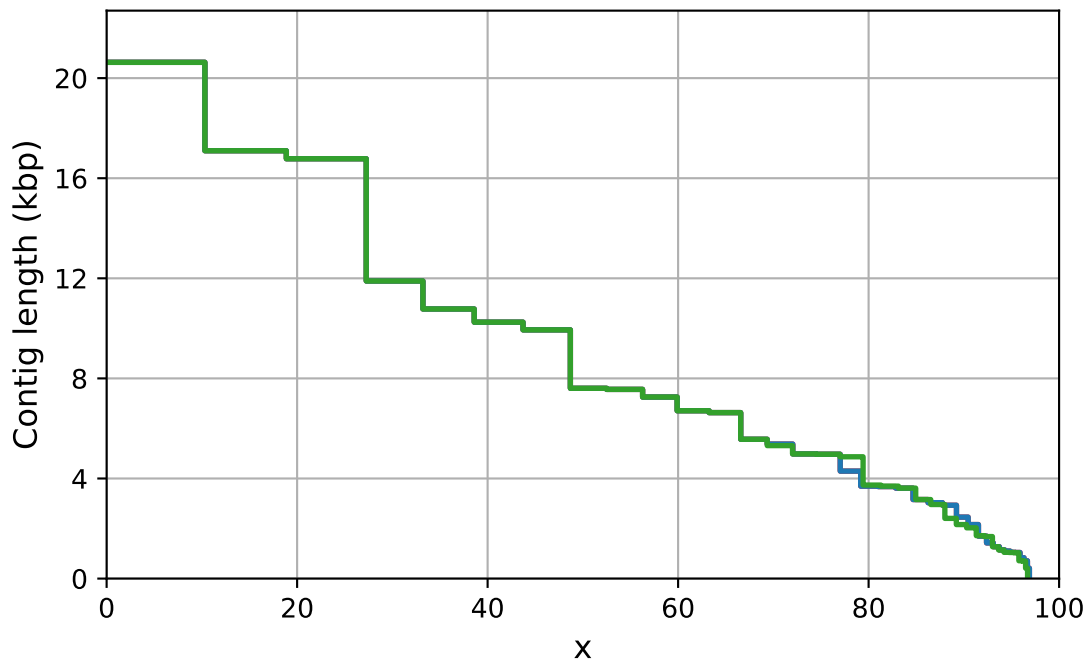
FRCurve (misassemblies)



Cumulative length (aligned contigs)

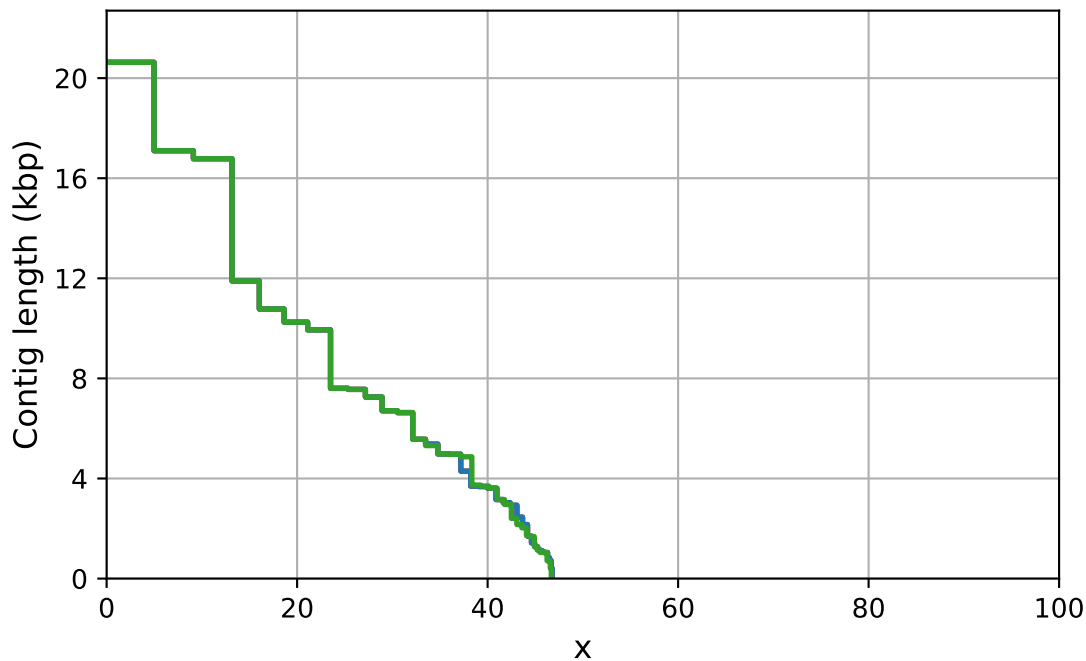


NAx



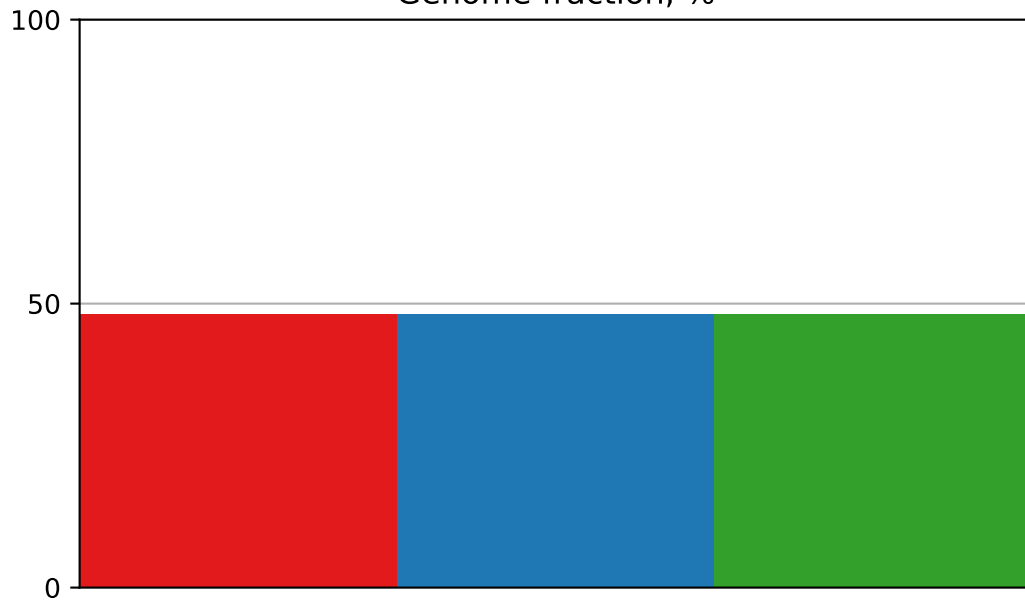
spades se spades pe spades mp

NGAx



spades se spades pe spades mp

Genome fraction, %



spades se spades pe spades mp