

Report

	spades se	spades pe	spades mp
# contigs (>= 0 bp)	693	826	1199
# contigs (>= 1000 bp)	42	35	36
# contigs (>= 5000 bp)	11	14	10
# contigs (>= 10000 bp)	3	4	5
# contigs (>= 25000 bp)	0	0	1
# contigs (>= 50000 bp)	0	0	0
Total length (>= 0 bp)	319865	330163	358676
Total length (>= 1000 bp)	183193	197523	188106
Total length (>= 5000 bp)	98223	137011	132118
Total length (>= 10000 bp)	45672	62461	92571
Total length (>= 25000 bp)	0	0	34829
Total length (>= 50000 bp)	0	0	0
# contigs	71	62	62
Largest contig	20266	21407	34829
Total length	202009	215416	206827
Reference length	838112	838112	838112
GC (%)	36.60	36.42	36.61
Reference GC (%)	36.41	36.41	36.41
N50	4996	7268	9117
NG50	-	-	-
N90	1271	1539	1066
NG90	-	-	-
auN	6805.5	8511.5	12355.3
auNG	1640.3	2187.7	3049.0
L50	12	10	7
LG50	-	-	-
L90	41	33	35
LG90	-	-	-
# misassemblies	3	4	8
# misassembled contigs	3	3	5
Misassembled contigs length	32938	37770	87200
# local misassemblies	10	6	9
# scaffold gap ext. mis.	9	8	9
# scaffold gap loc. mis.	7	12	4
# unaligned mis. contigs	0	0	0
# unaligned contigs	0 + 0 part	0 + 0 part	0 + 0 part
Unaligned length	0	0	0
Genome fraction (%)	23.593	25.349	24.226
Duplication ratio	1.001	0.997	0.998
# N's per 100 kbp	2425.63	1903.29	2130.77
# mismatches per 100 kbp	19.20	35.87	29.60
# indels per 100 kbp	15.16	14.63	16.77
Largest alignment	19450	20699	21501
Total aligned length	197921	211876	202725
NA50	4603	6156	6106
NGA50	-	-	-
NA90	914	917	860
NGA90	-	-	-
auNA	5968.6	7303.9	7462.8
auNGA	1438.6	1877.3	1841.7
LA50	14	12	11
LGA50	-	-	-
LA90	47	39	47
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	3	4	8
# contig misassemblies	2	3	6
# c. relocations	2	3	6
# c. translocations	0	0	0
# c. inversions	0	0	0
# scaffold misassemblies	1	1	2
# s. relocations	1	1	2
# s. translocations	0	0	0
# s. inversions	0	0	0
# misassembled contigs	3	3	5
Misassembled contigs length	32938	37770	87200
# local misassemblies	10	6	9
# scaffold gap ext. mis.	9	8	9
# scaffold gap loc. mis.	7	12	4
# unaligned mis. contigs	0	0	0
# mismatches	38	76	60
# indels	30	31	34
# indels (<= 5 bp)	4	7	3
# indels (> 5 bp)	26	24	31
Indels length	1943	1655	2279

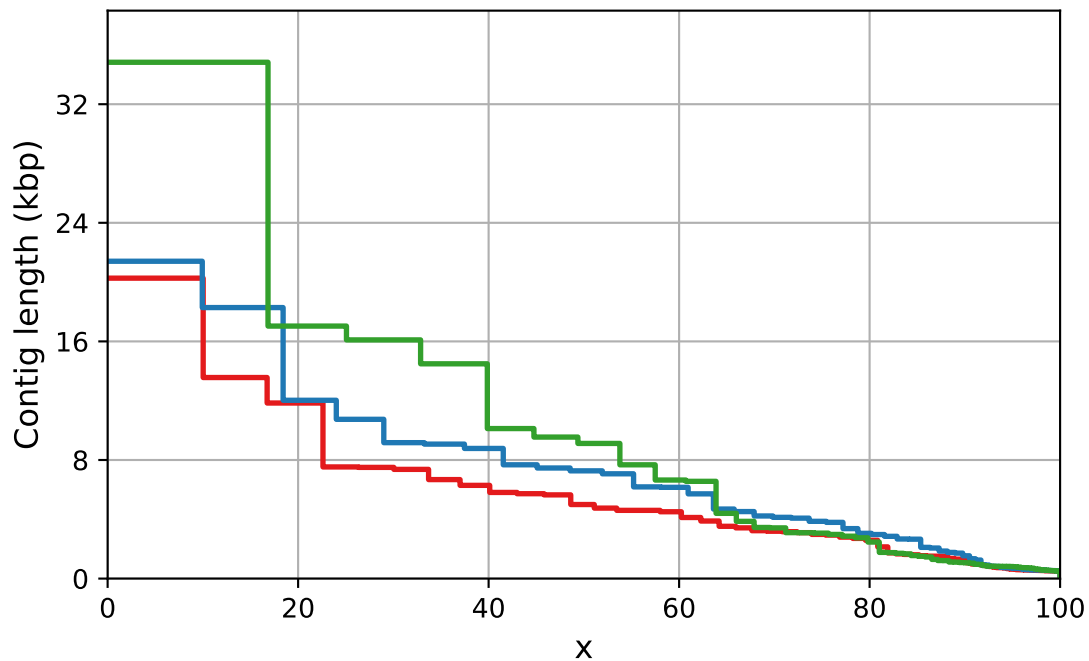
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

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	4900	4100	4407

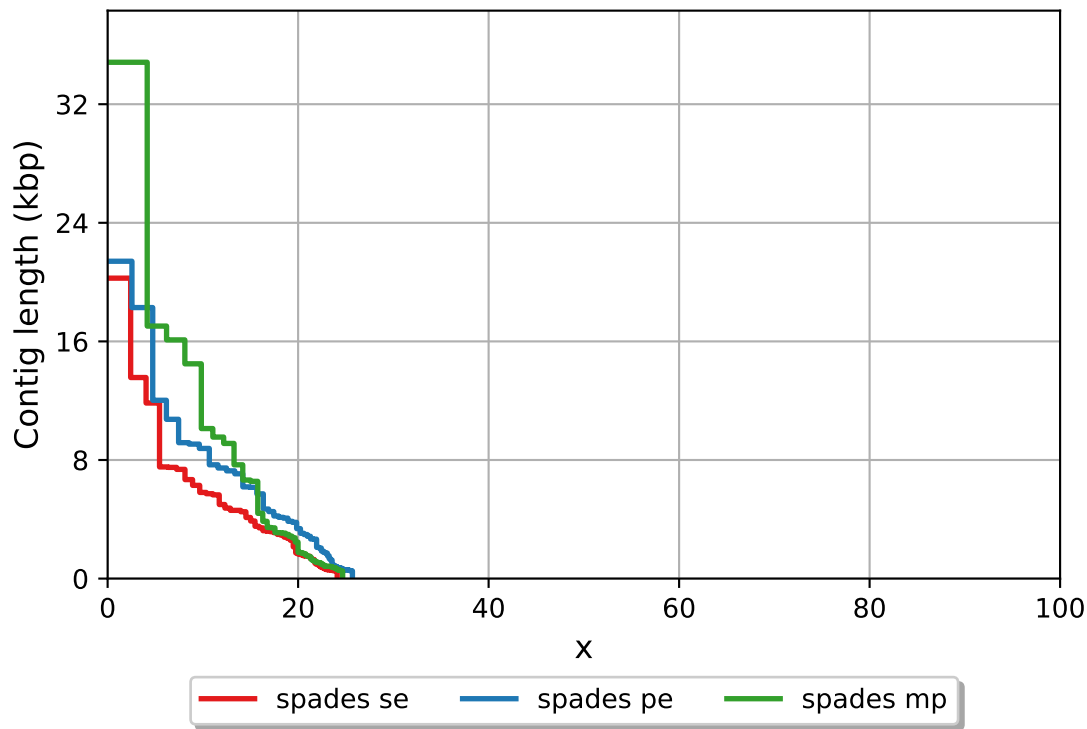
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx

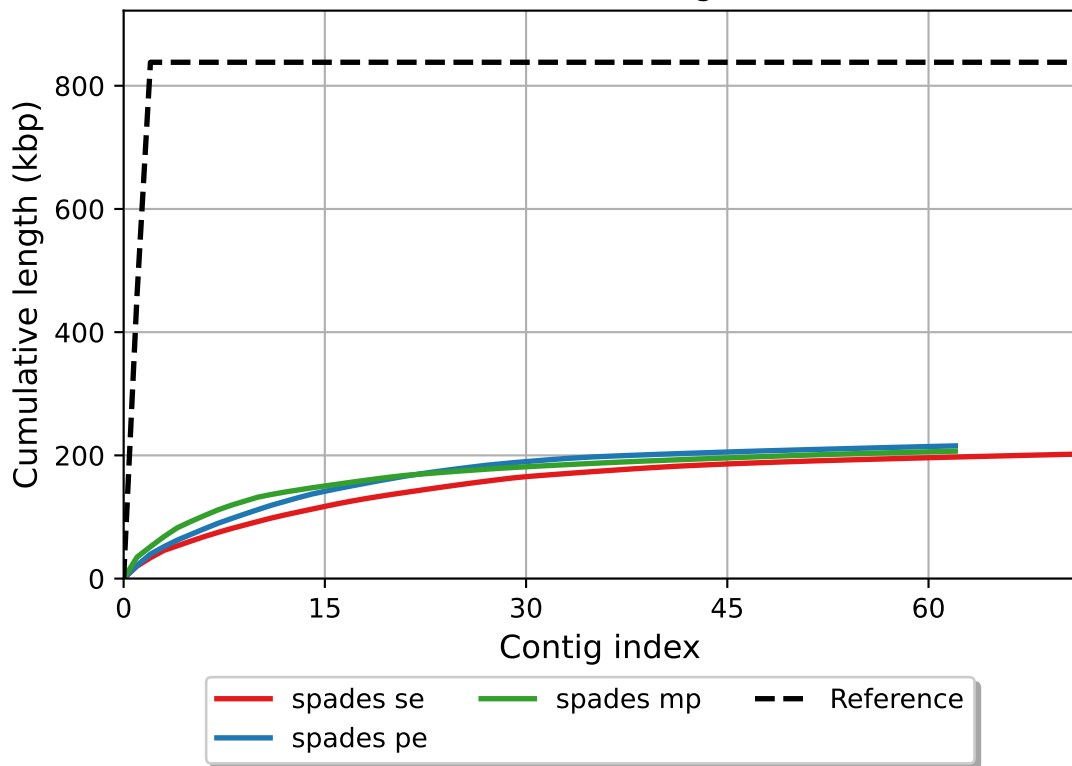


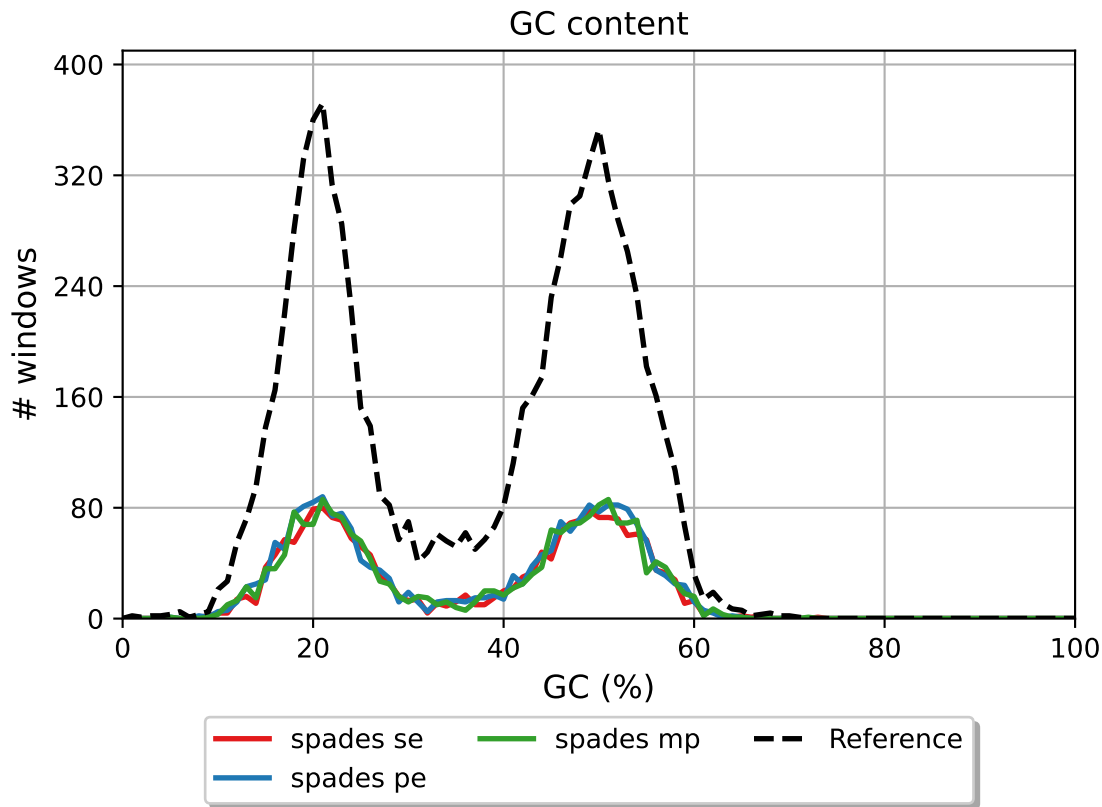
spades se spades pe spades mp

NGx

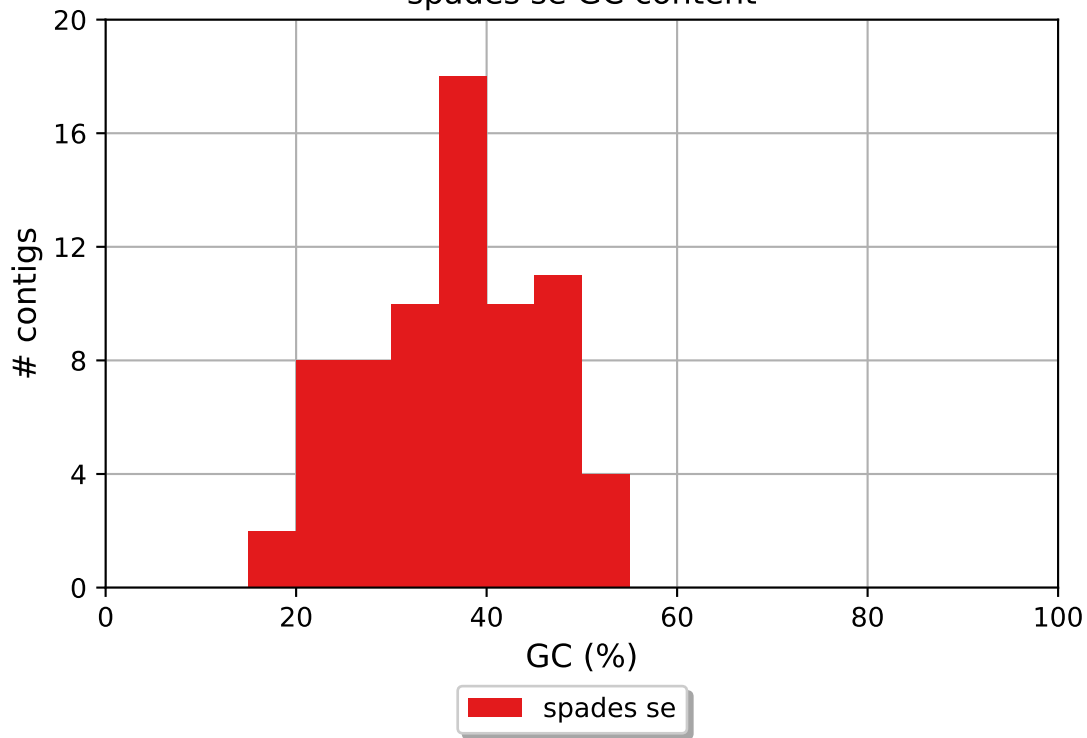


Cumulative length

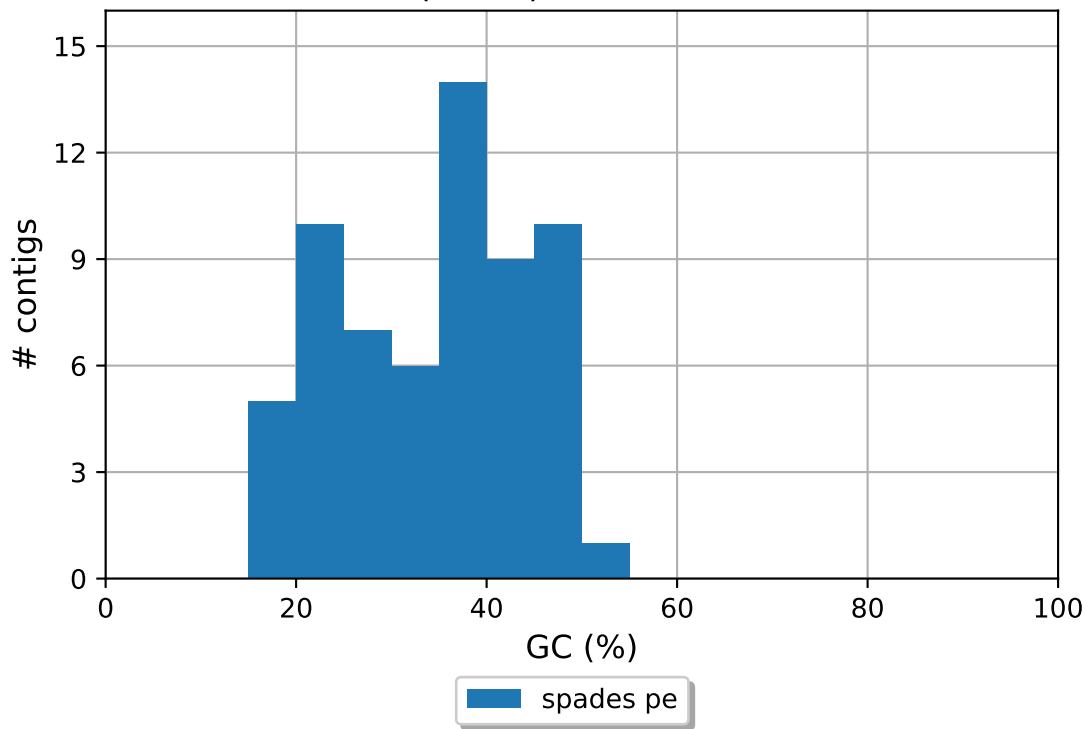




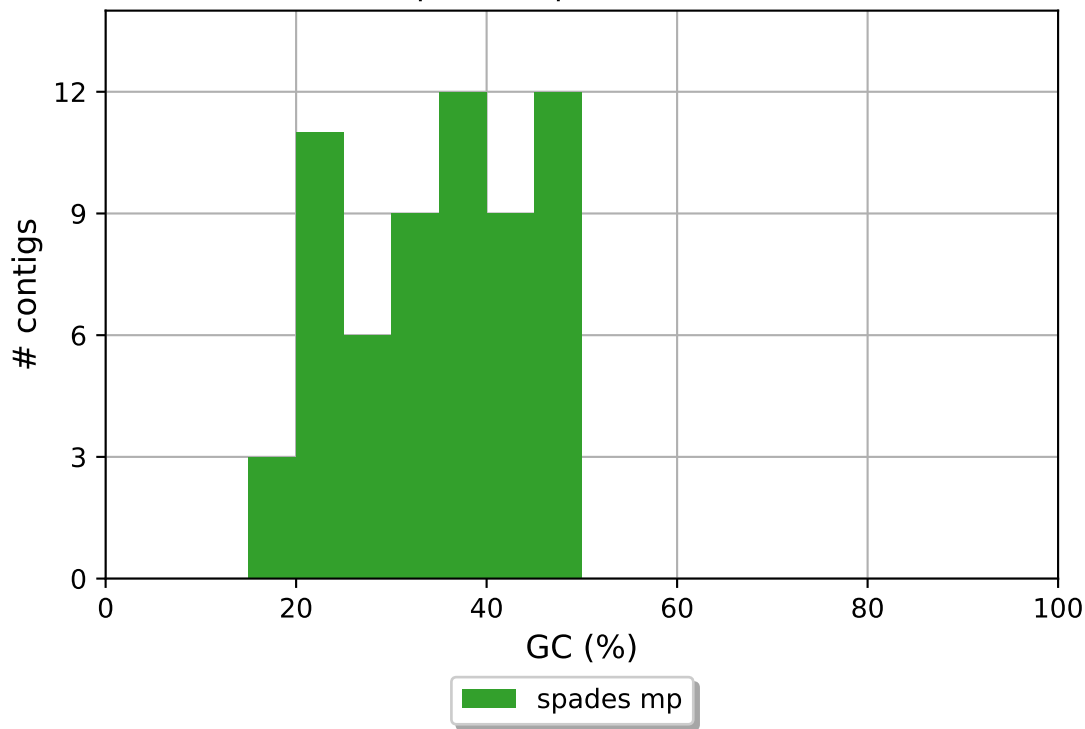
spades se GC content



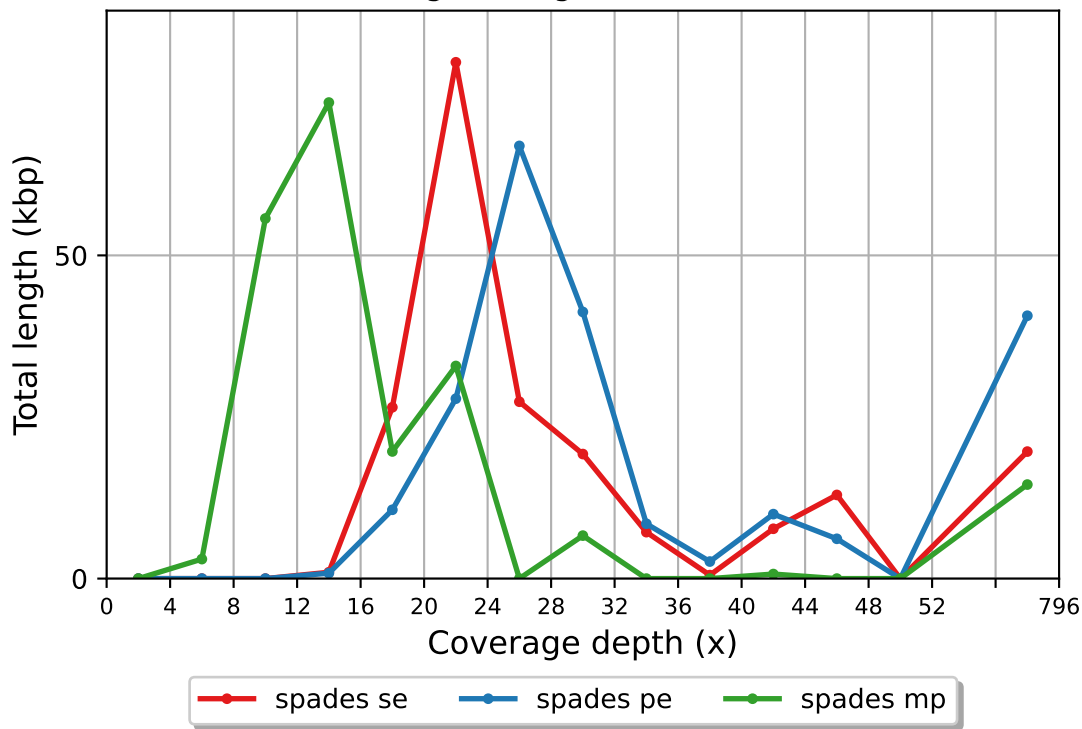
spades pe GC content



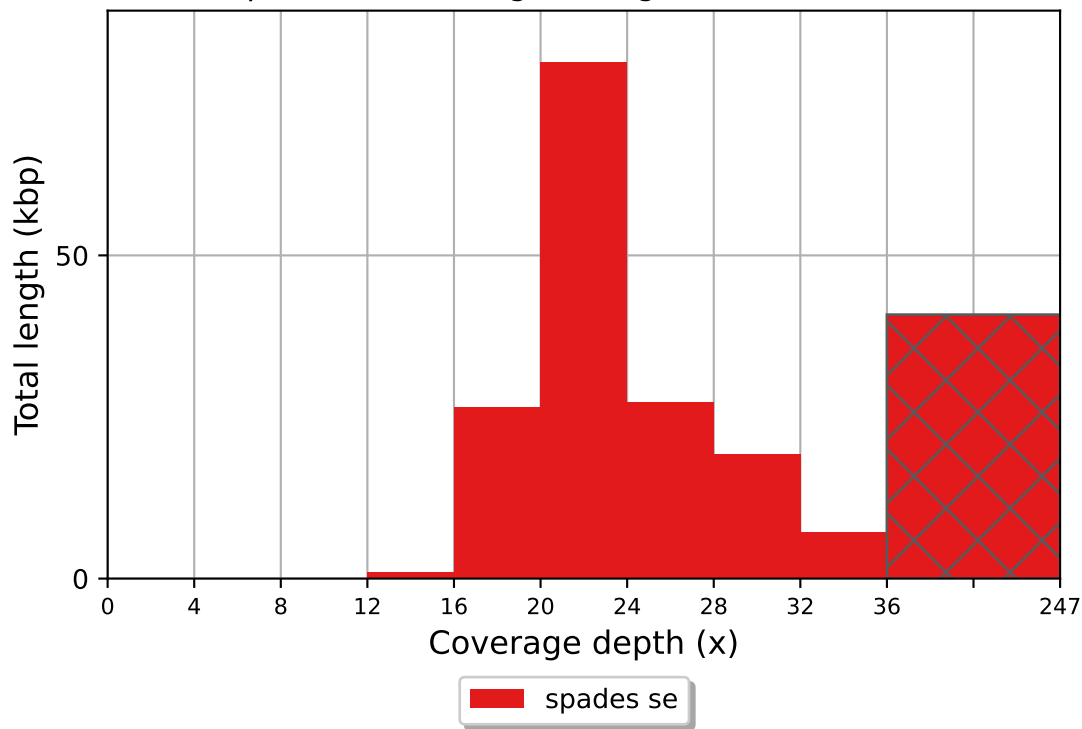
spades mp GC content



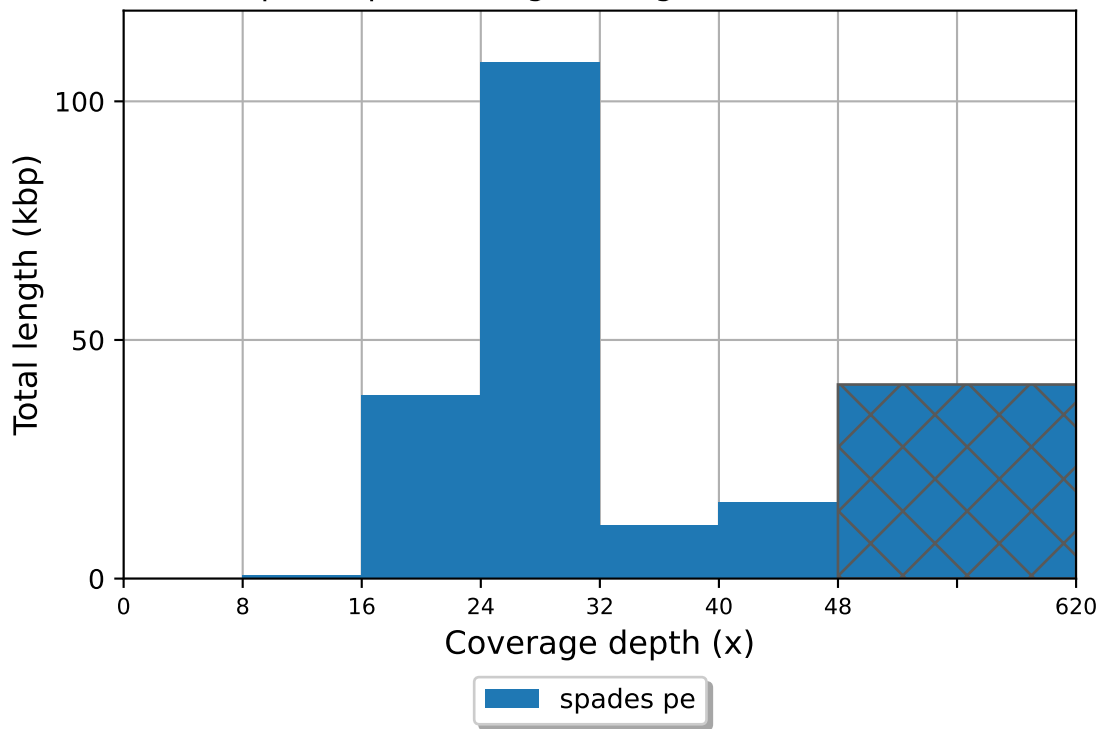
Coverage histogram (bin size: 4x)



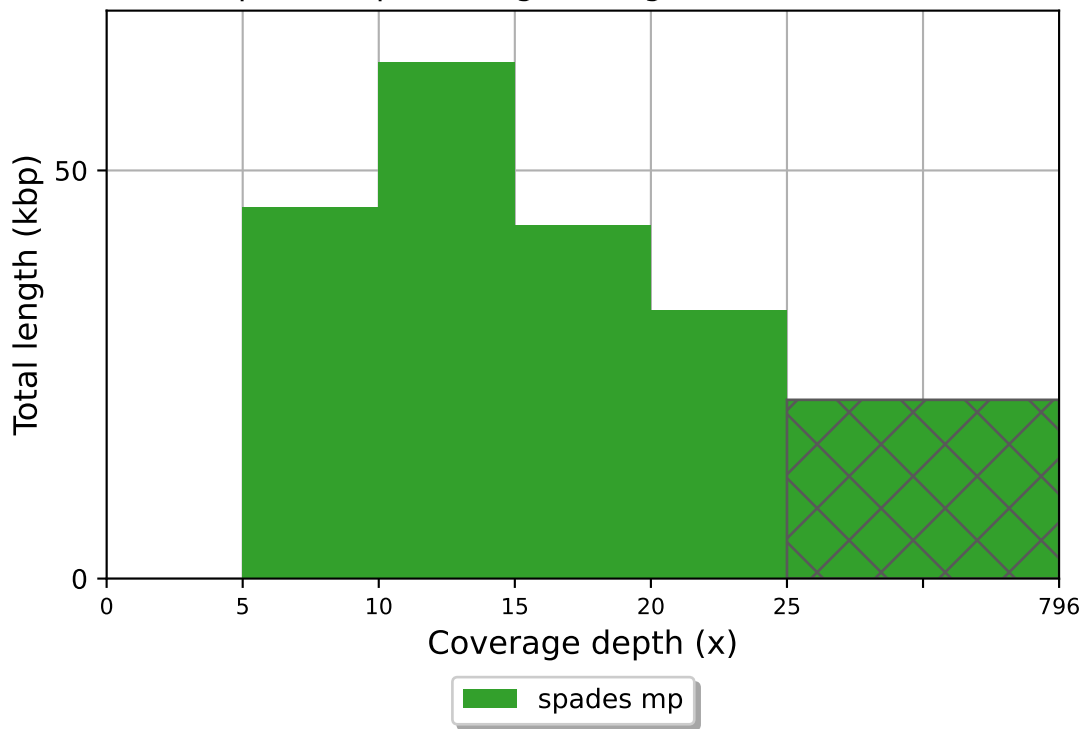
spades se coverage histogram (bin size: 4x)



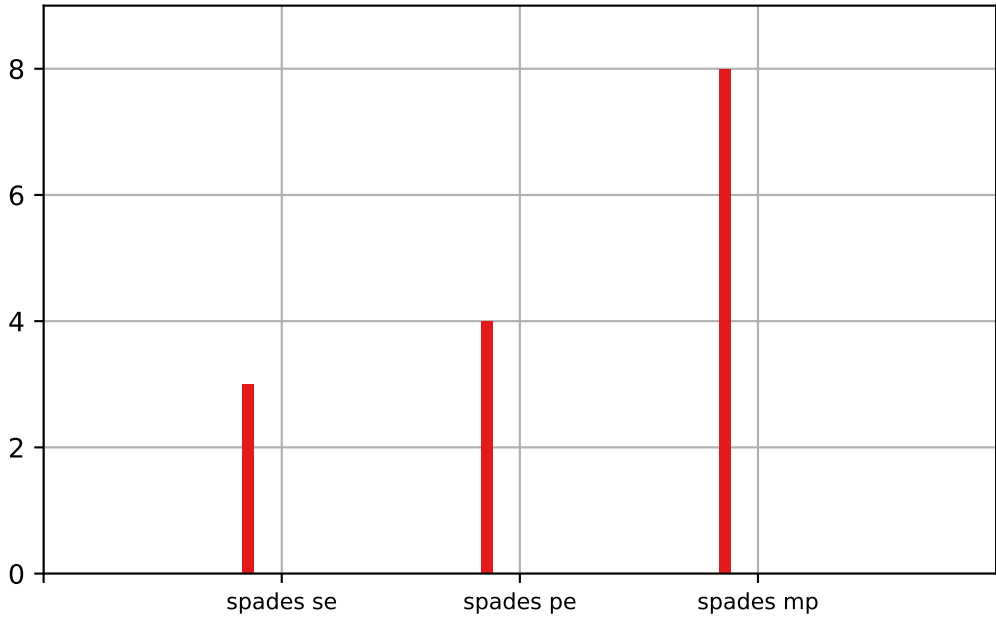
spades pe coverage histogram (bin size: 8x)



spades mp coverage histogram (bin size: 5x)

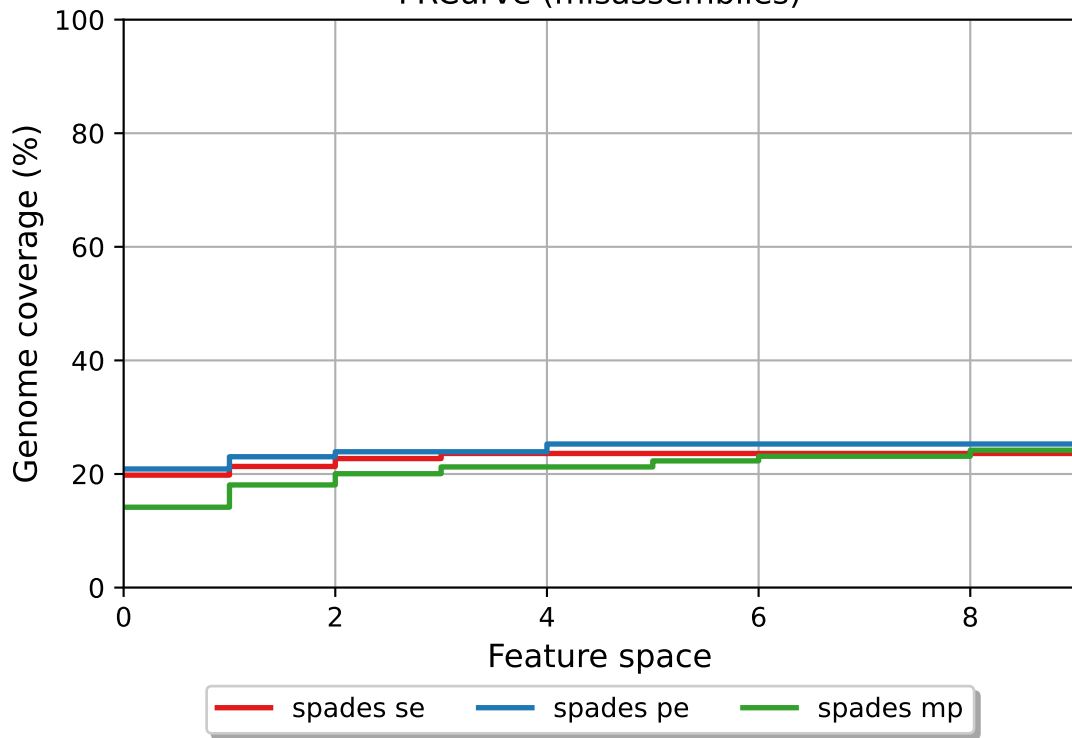


Misassemblies

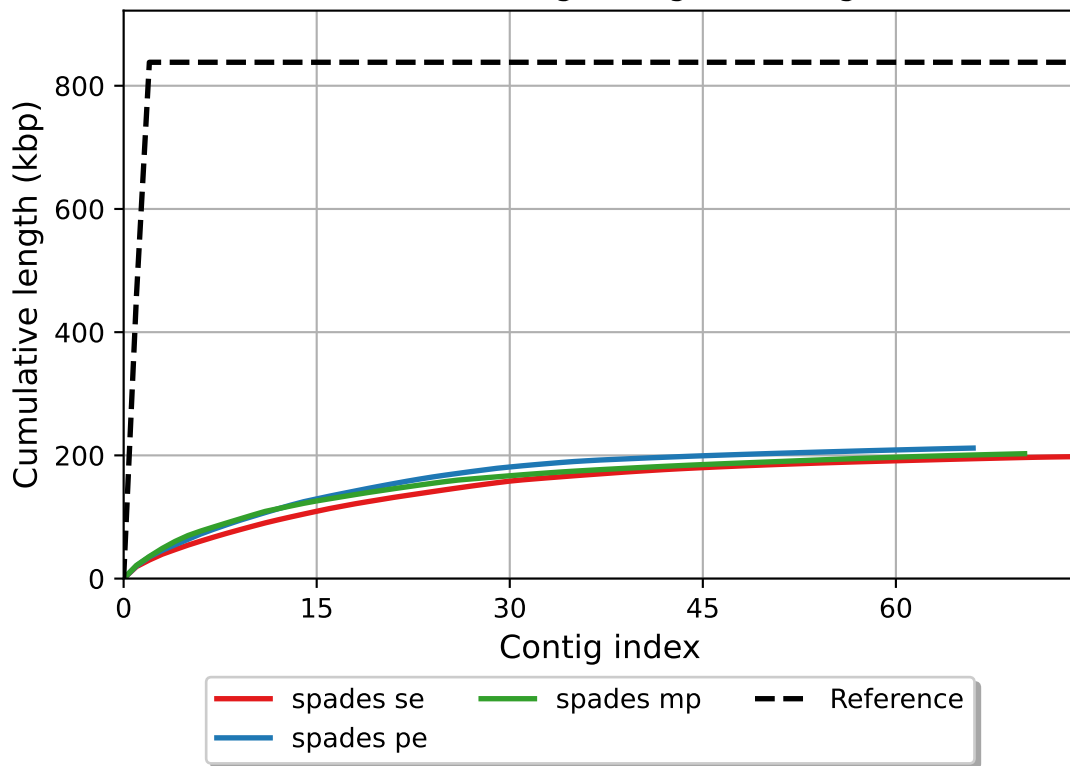


 # relocations

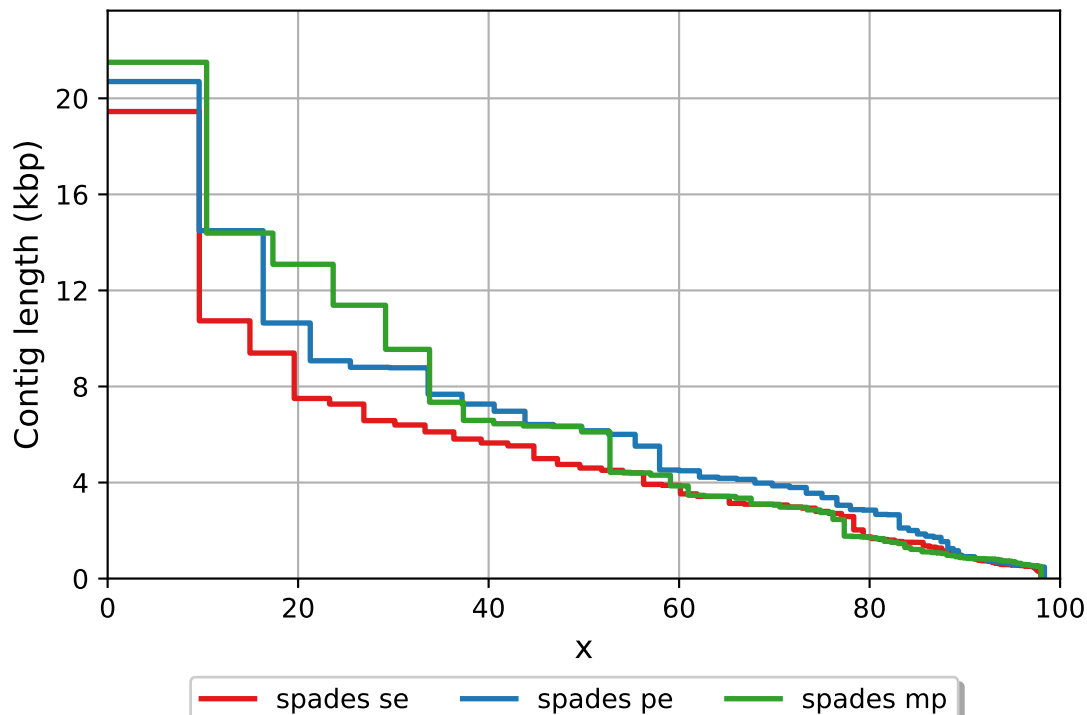
FRCurve (misassemblies)



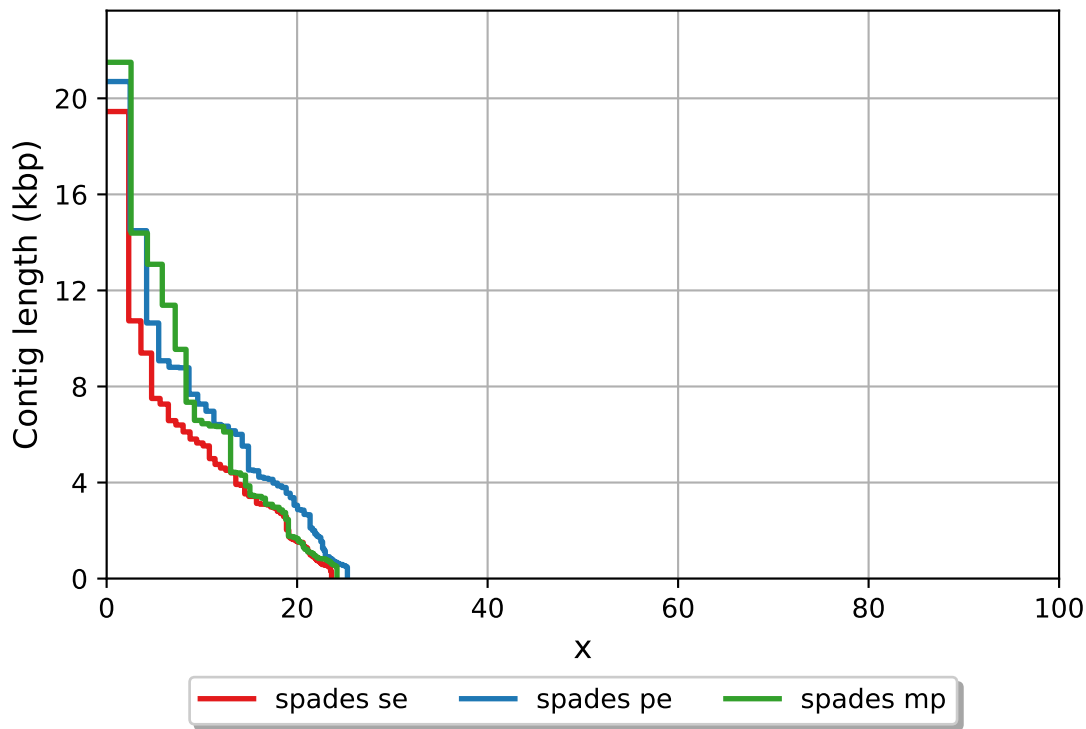
Cumulative length (aligned contigs)



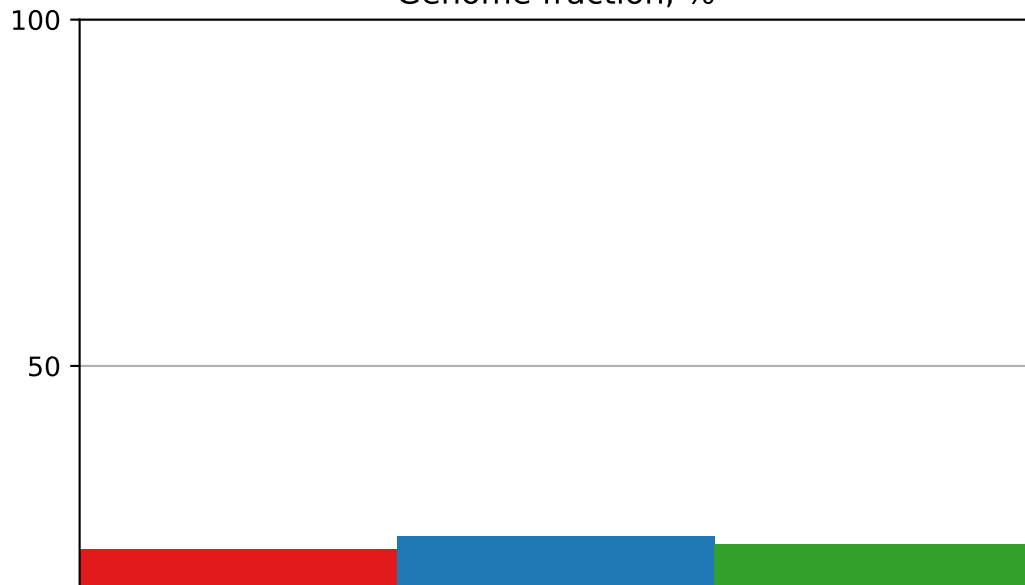
NAx



NGAx



Genome fraction, %



spades se



spades pe



spades mp