

Report

	spades_default	spades_kmers_careful	megahit_default	megahit_min_count_3
# contigs (>= 0 bp)	288	239	200	198
# contigs (>= 1000 bp)	132	91	156	158
# contigs (>= 5000 bp)	94	74	118	121
# contigs (>= 10000 bp)	87	67	104	108
# contigs (>= 25000 bp)	67	58	72	75
# contigs (>= 50000 bp)	51	43	49	51
Total length (>= 0 bp)	8490011	8510655	8511587	8511217
Total length (>= 1000 bp)	8447218	8472540	8492269	8493797
Total length (>= 5000 bp)	8371775	8438829	8405876	8408960
Total length (>= 10000 bp)	8324069	8384754	8296157	8308919
Total length (>= 25000 bp)	8010950	8245120	7760455	7762256
Total length (>= 50000 bp)	7438644	7723080	6917716	6910273
# contigs	132	91	156	158
Largest contig	754490	961949	539126	539126
Total length	8447218	8472540	8492269	8493797
Reference length	8605945	8605945	8605945	8605945
GC (%)	66.67	66.67	66.66	66.66
Reference GC (%)	66.61	66.61	66.61	66.61
N50	151907	217699	144335	131456
NG50	143914	217699	144335	131456
N75	85907	107910	66469	64244
NG75	79029	98944	64299	62113
L50	16	12	19	20
LG50	17	12	19	20
L75	35	26	40	42
LG75	36	27	41	43
# misassemblies	6	6	9	8
# misassembled contigs	6	6	9	8
Misassembled contigs length	1469048	1719134	1200775	1050989
# local misassemblies	9	8	4	4
# scaffold gap ext. mis.	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0
# unaligned mis. contigs	0	0	0	0
# unaligned contigs	0 + 0 part	0 + 1 part	0 + 0 part	0 + 0 part
Unaligned length	0	1317	0	0
Genome fraction (%)	98.140	98.421	98.596	98.605
Duplication ratio	1.000	1.000	1.001	1.001
# N's per 100 kbp	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	3.85	2.72	2.45	2.36
# indels per 100 kbp	0.67	0.45	0.31	0.27
# genomic features	7539 + 75 part	7563 + 62 part	7540 + 105 part	7540 + 104 part
Largest alignment	455950	505898	350746	350746
Total aligned length	8436553	8470789	8491768	8493173
NA50	143914	198969	144083	125159
NGA50	143431	198969	144083	125159
NA75	79029	103468	61973	61722
NGA75	78885	98926	61722	57545
LA50	17	13	20	21
LGA50	18	13	20	21
LA75	37	28	42	44
LGA75	38	29	43	45

All statistics are based on contigs of size >= 1000 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

	spades_default	spades_kmers_careful	megahit_default	megahit_min_count_3
# misassemblies	6	6	9	8
# contig misassemblies	6	6	9	8
# c. relocations	6	5	5	4
# c. translocations	0	1	4	4
# c. inversions	0	0	0	0
# scaffold misassemblies	0	0	0	0
# s. relocations	0	0	0	0
# s. translocations	0	0	0	0
# s. inversions	0	0	0	0
# misassembled contigs	6	6	9	8
Misassembled contigs length	1469048	1719134	1200775	1050989
# local misassemblies	9	8	4	4
# scaffold gap ext. mis.	0	0	0	0
# scaffold gap loc. mis.	0	0	0	0
# unaligned mis. contigs	0	0	0	0
# mismatches	325	230	208	200
# indels	57	38	26	23
# indels (<= 5 bp)	34	25	19	16
# indels (> 5 bp)	23	13	7	7
Indels length	833	466	341	265

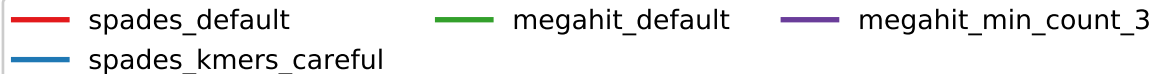
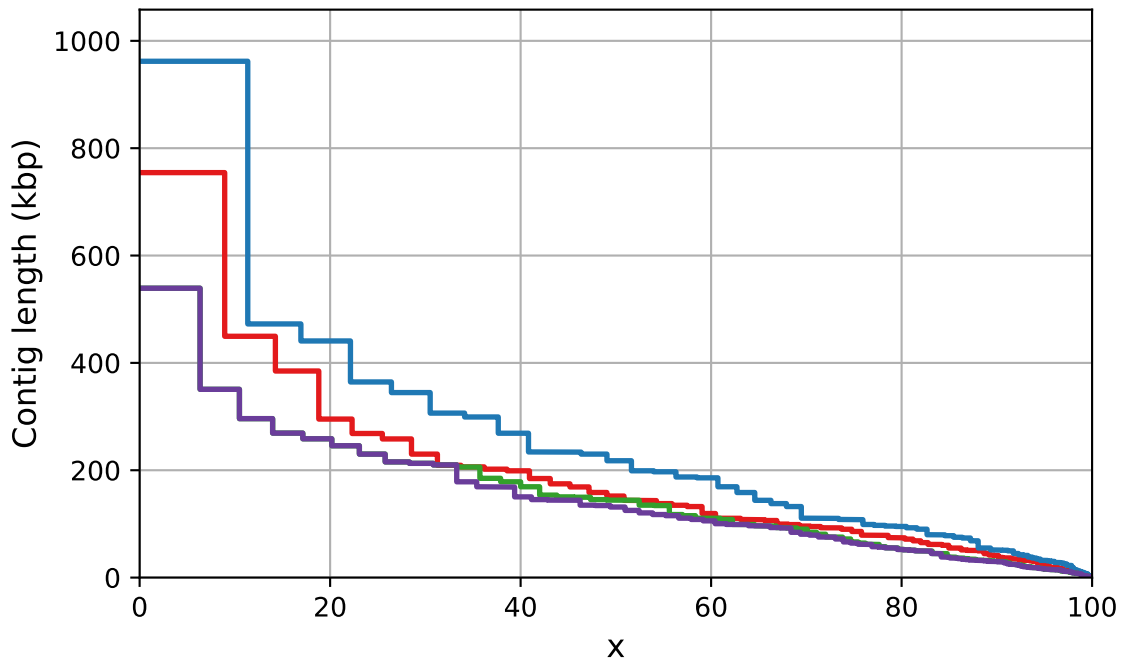
All statistics are based on contigs of size ≥ 1000 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

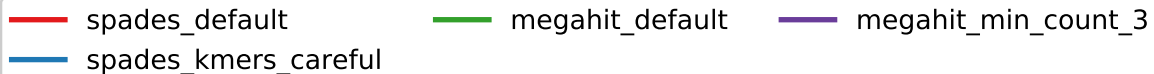
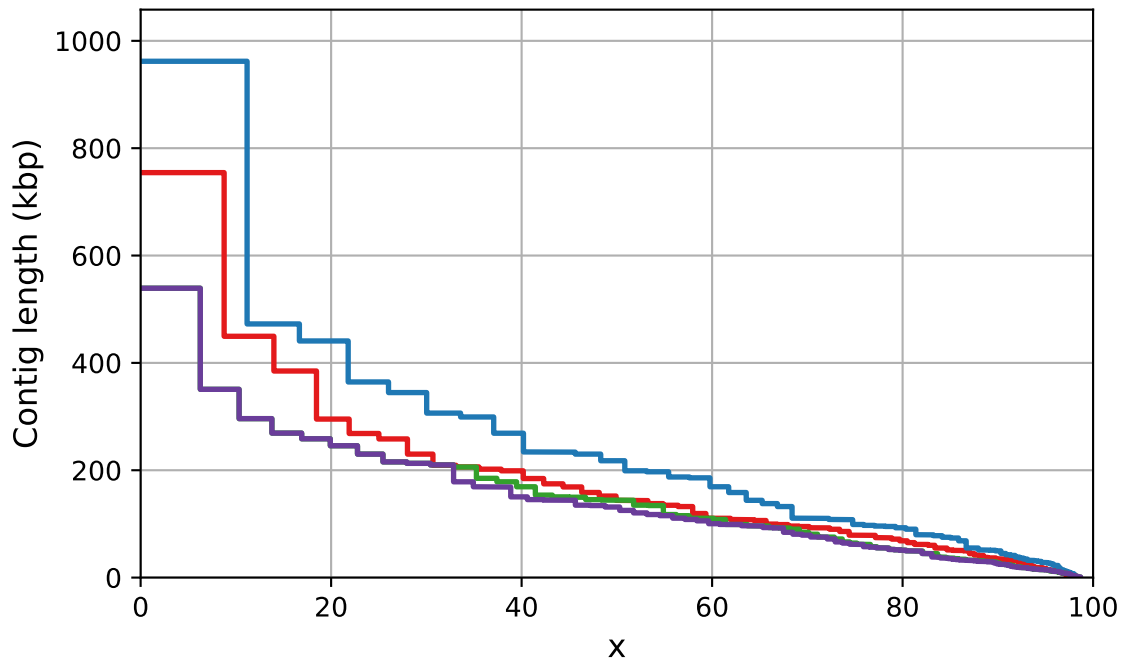
	spades_default	spades_kmers_careful	megahit_default	megahit_min_count_3
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	0	1	0	0
Partially unaligned length	0	1317	0	0
# N's	0	0	0	0

All statistics are based on contigs of size ≥ 1000 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

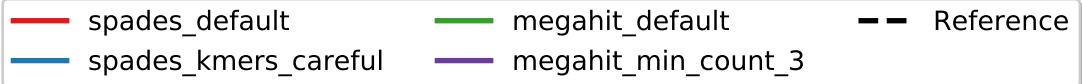
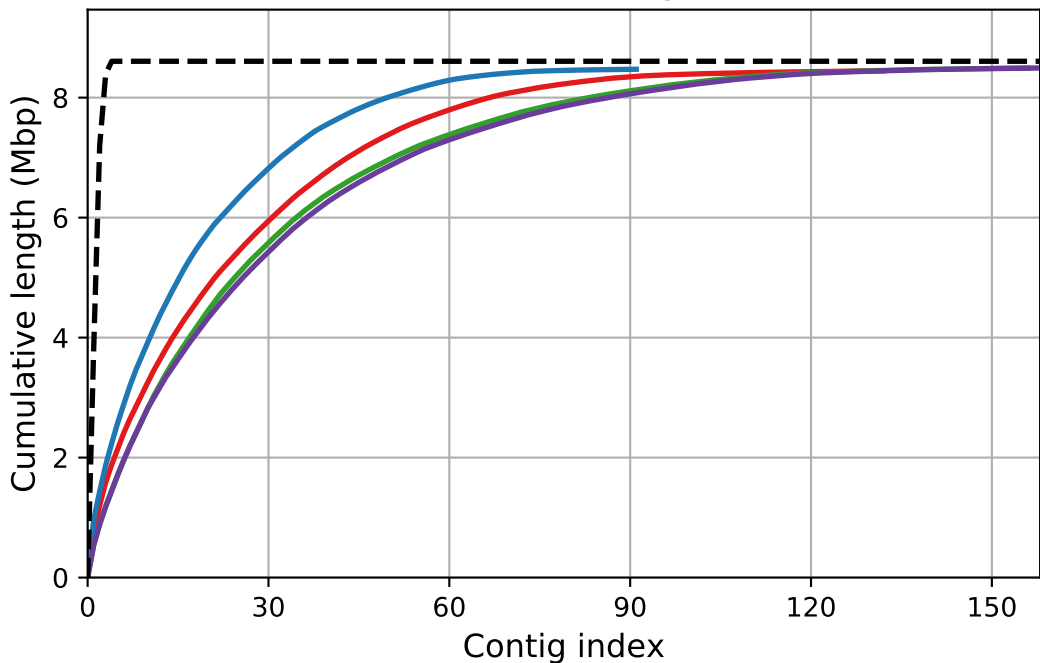
Nx



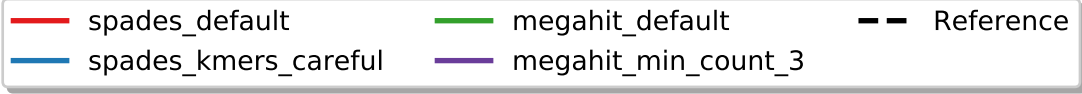
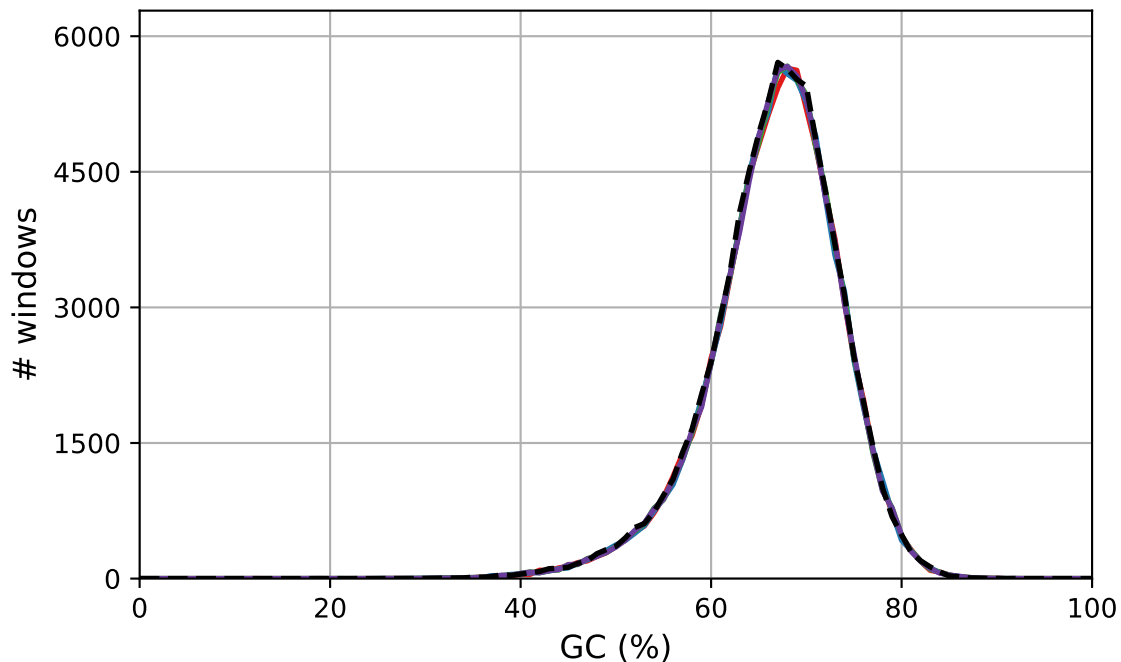
NGx



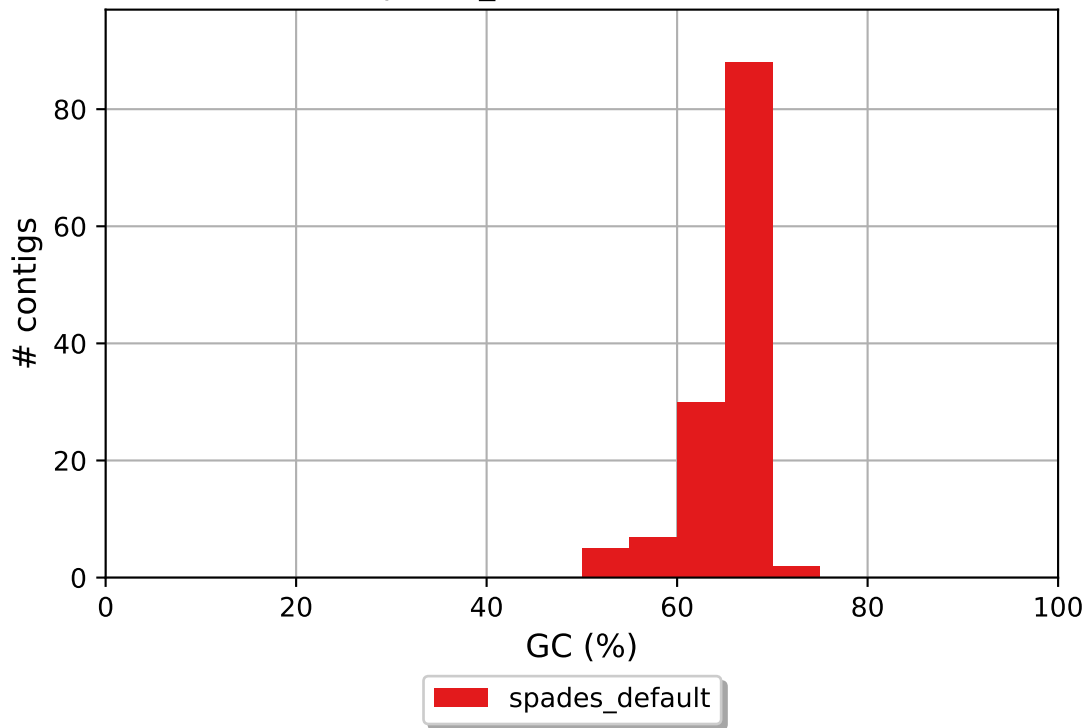
Cumulative length



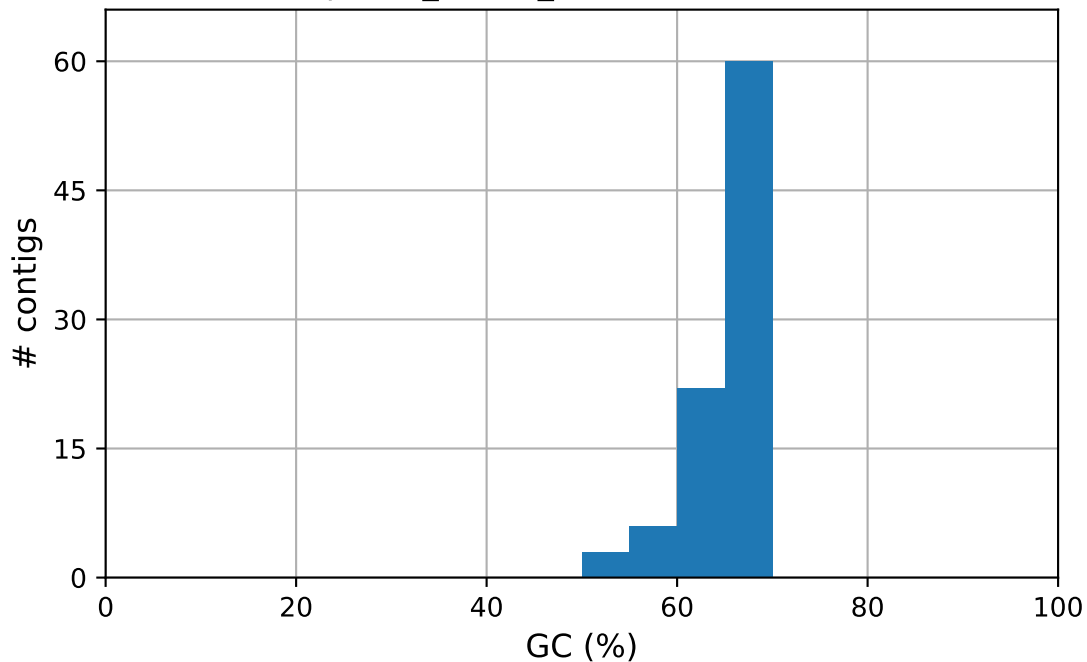
GC content



spades_default GC content

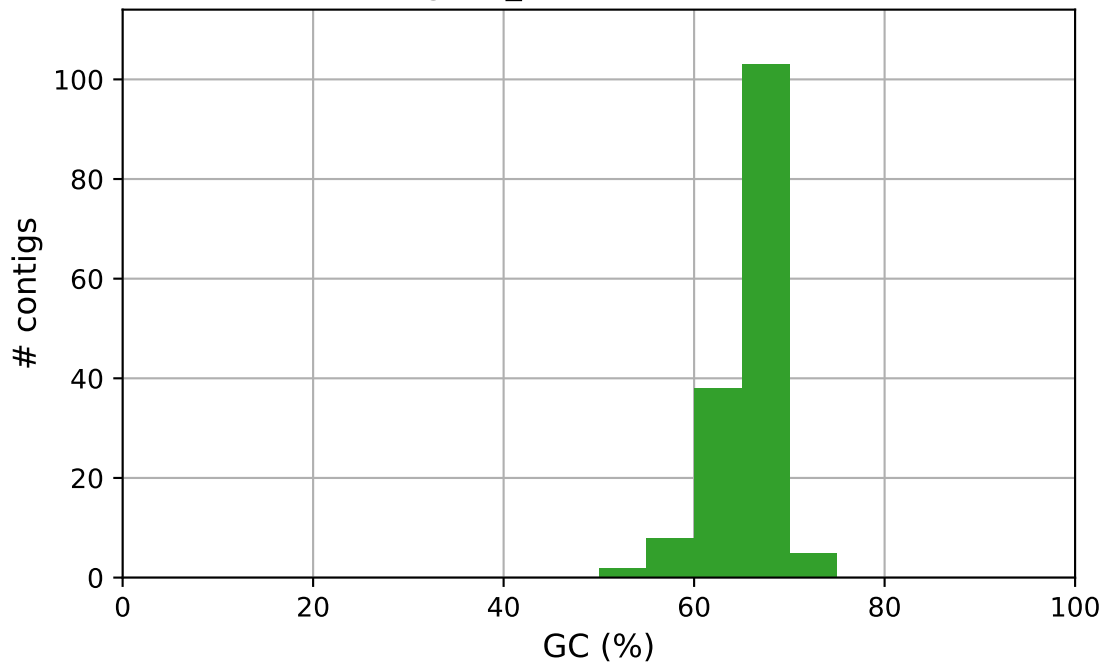


spades_kmers_careful GC content



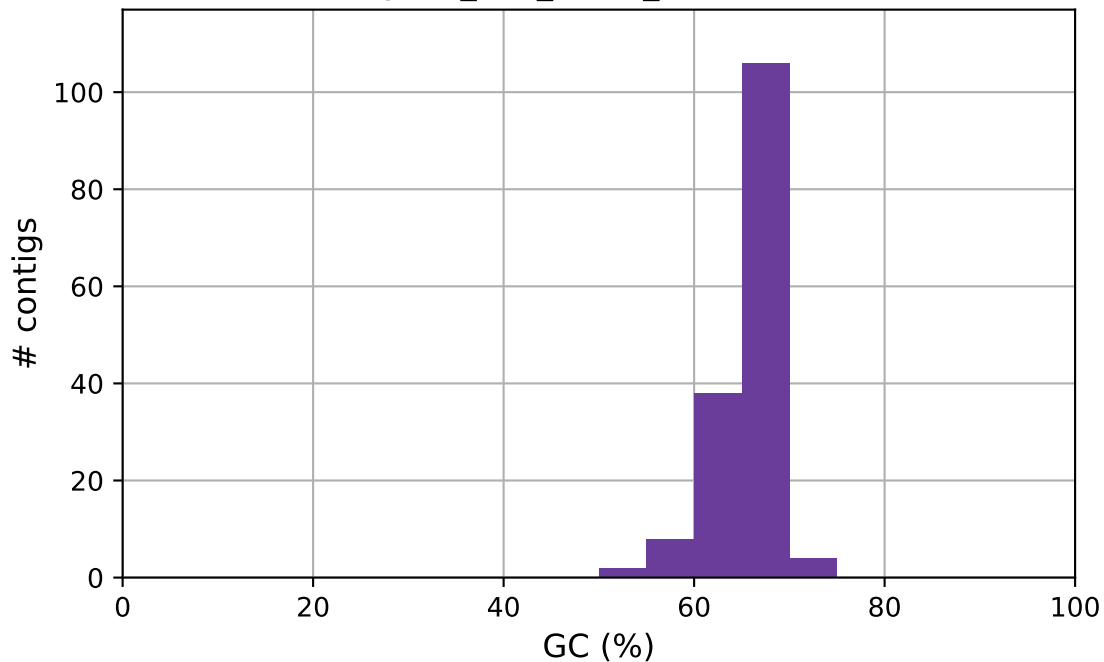
spades_kmers_careful

megahit_default GC content



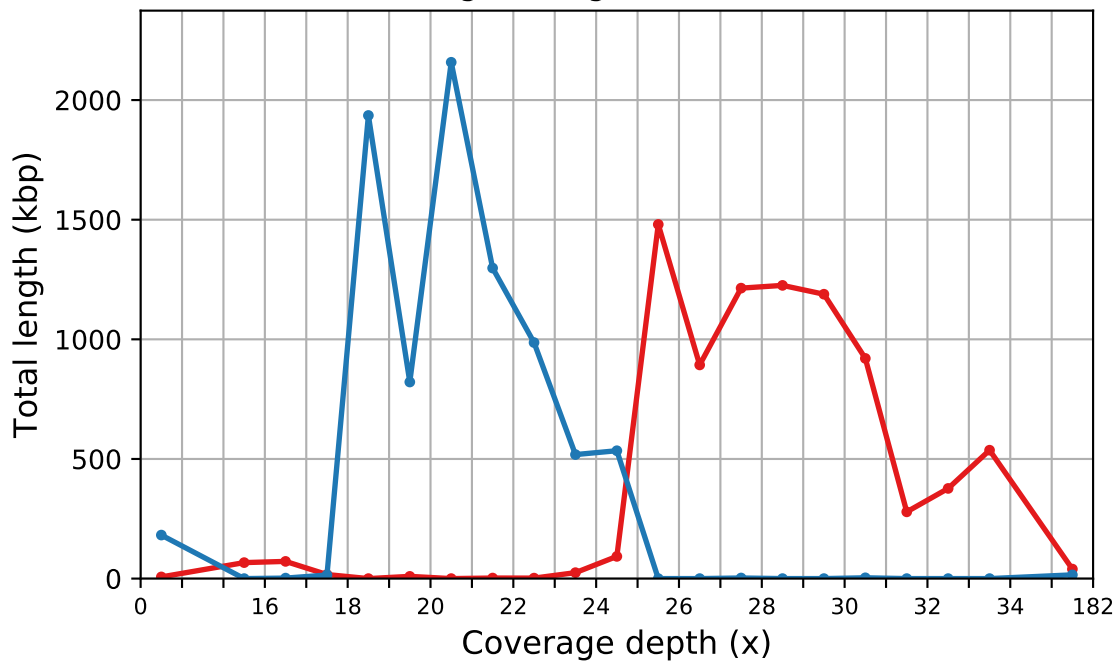
 megahit_default

megahit_min_count_3 GC content



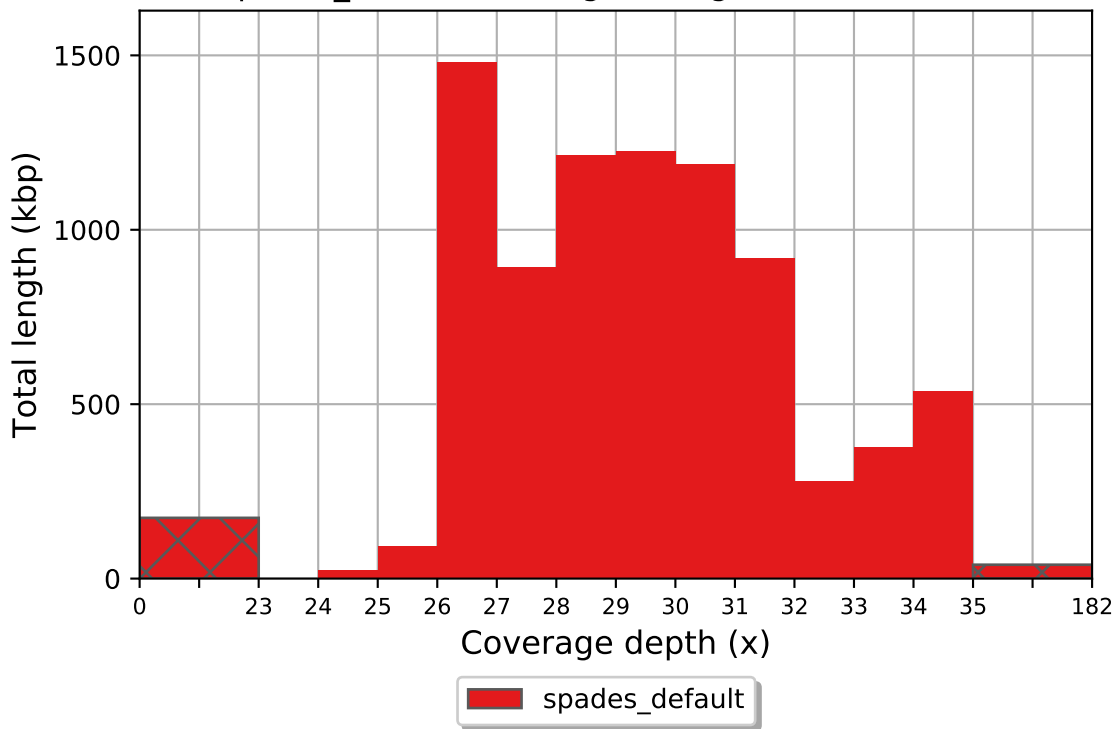
megahit_min_count_3

Coverage histogram (bin size: 1x)

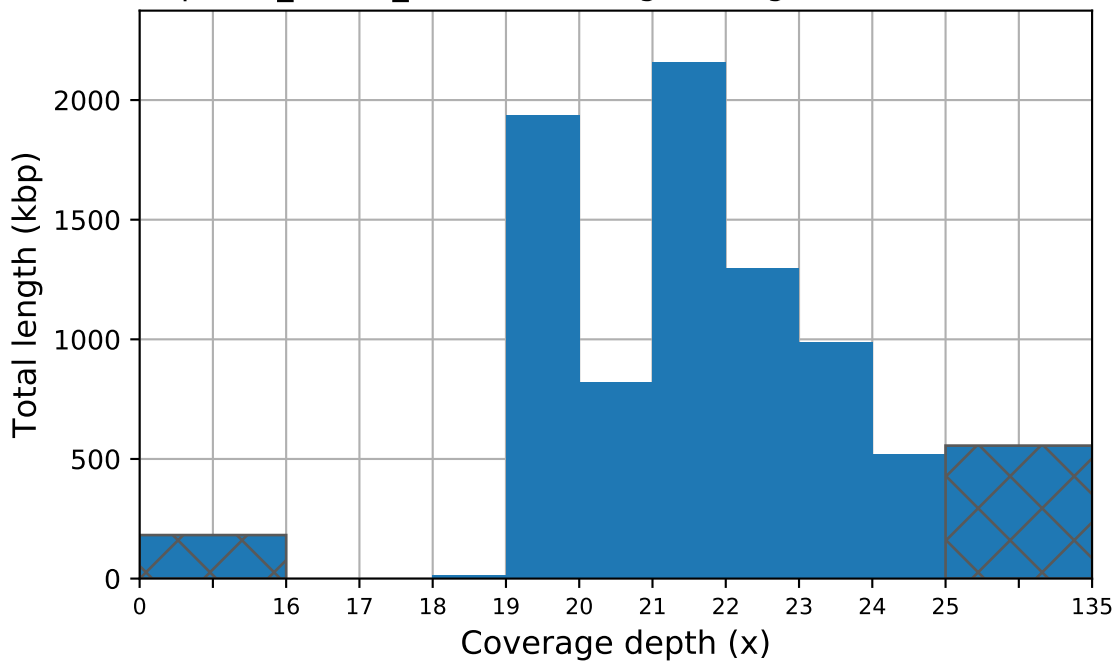


—●— spades_default —●— spades_kmers_careful

spades_default coverage histogram (bin size: 1x)

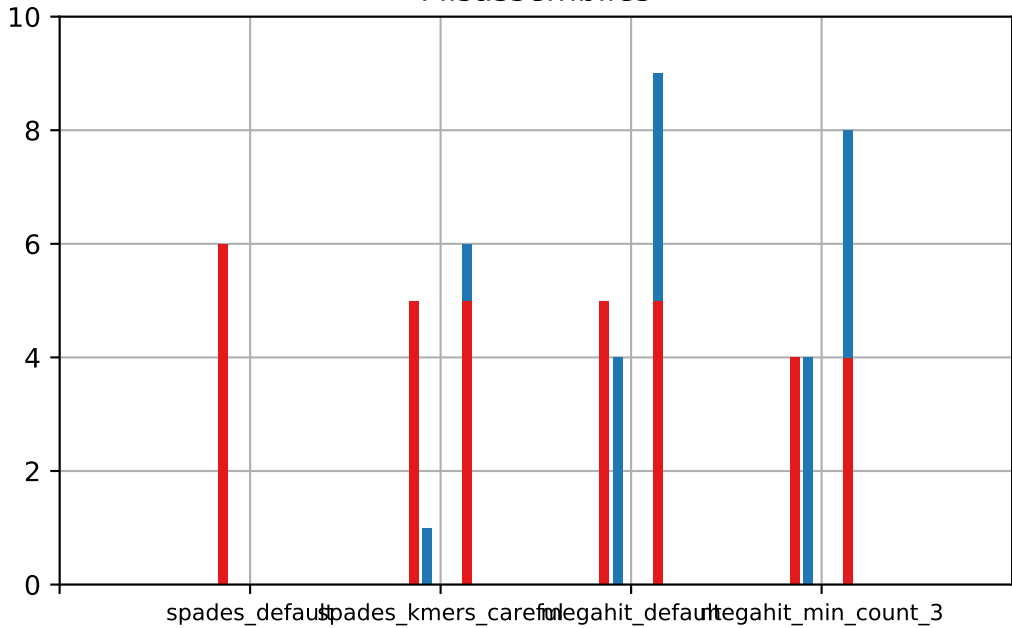


spades_kmers_careful coverage histogram (bin size: 1x)



spades_kmers_careful

Misassemblies

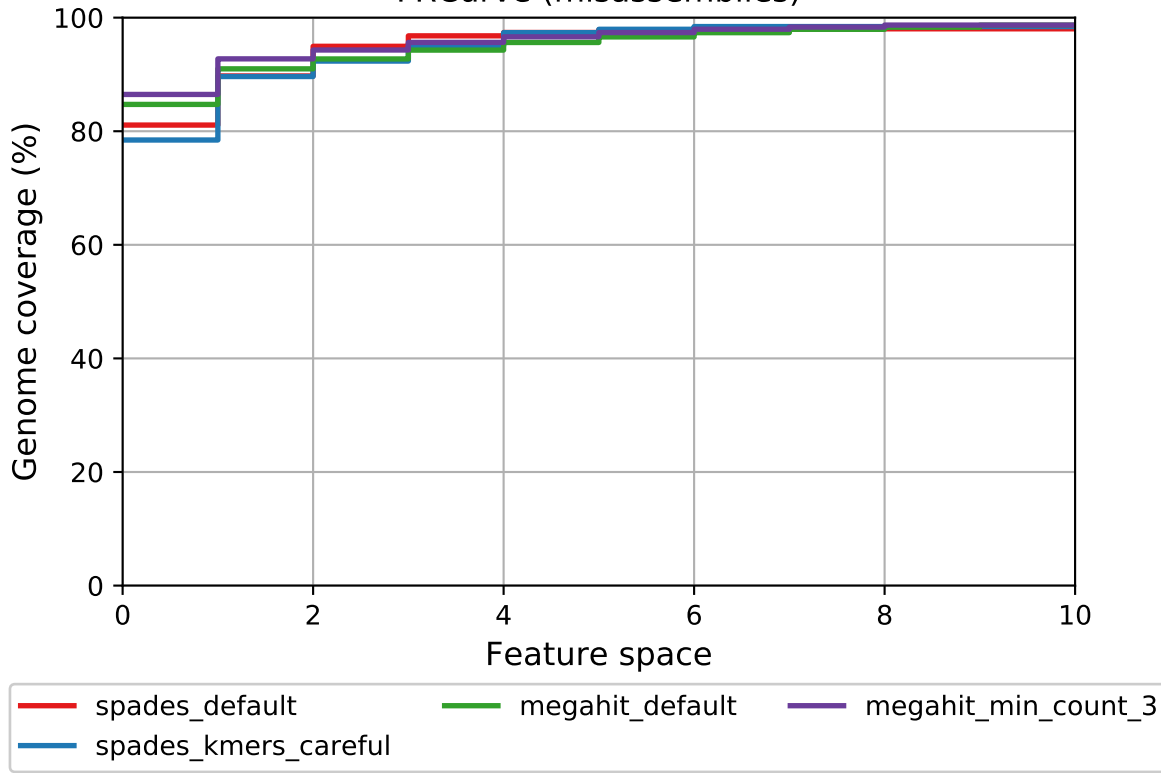


relocations

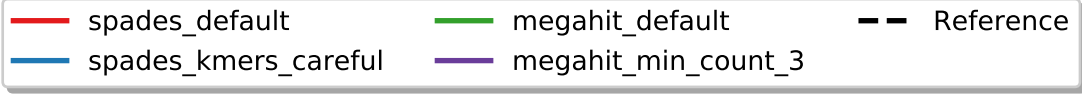
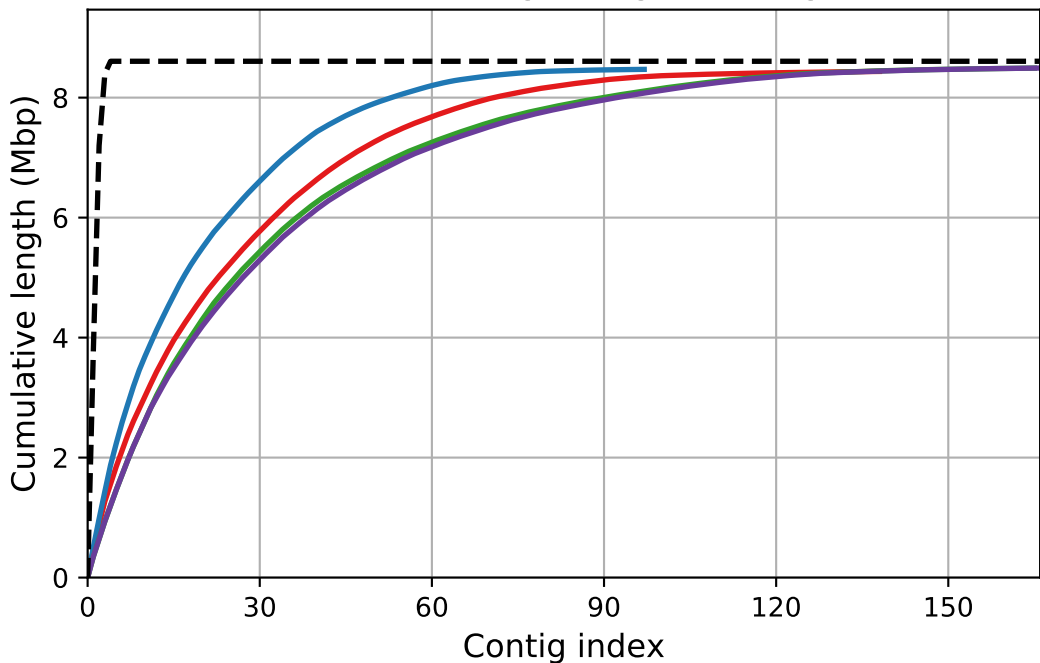


translocations

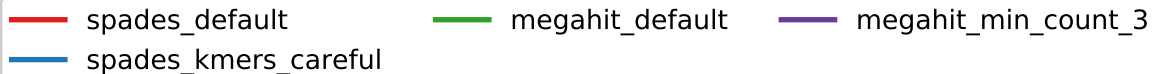
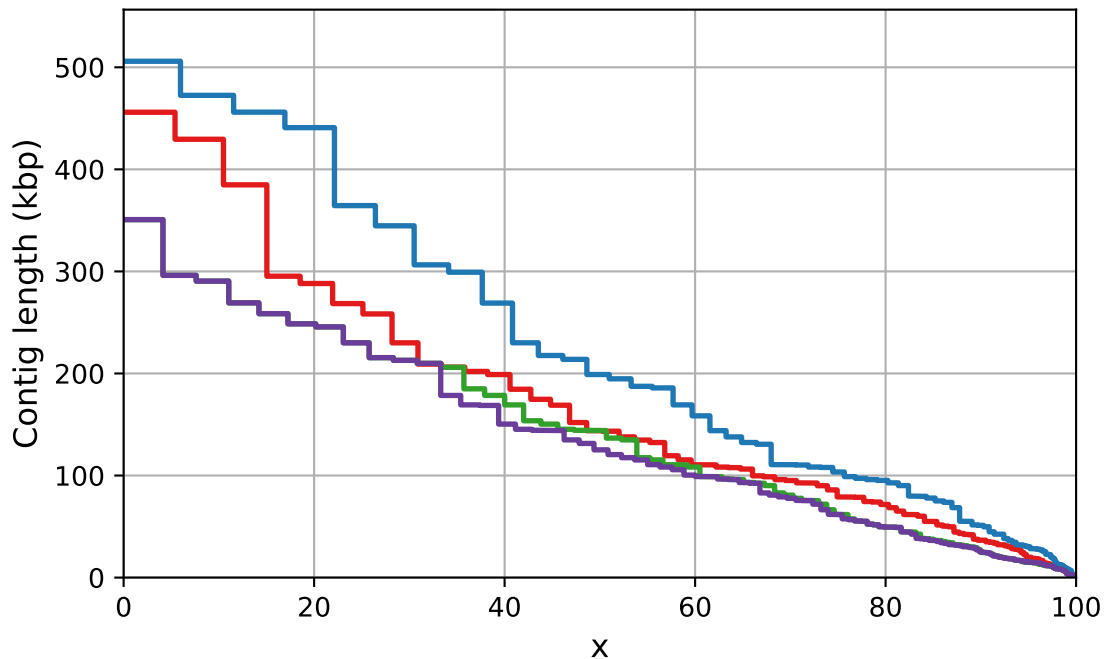
FRCurve (misassemblies)



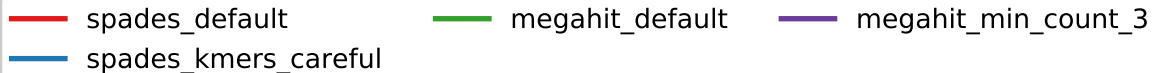
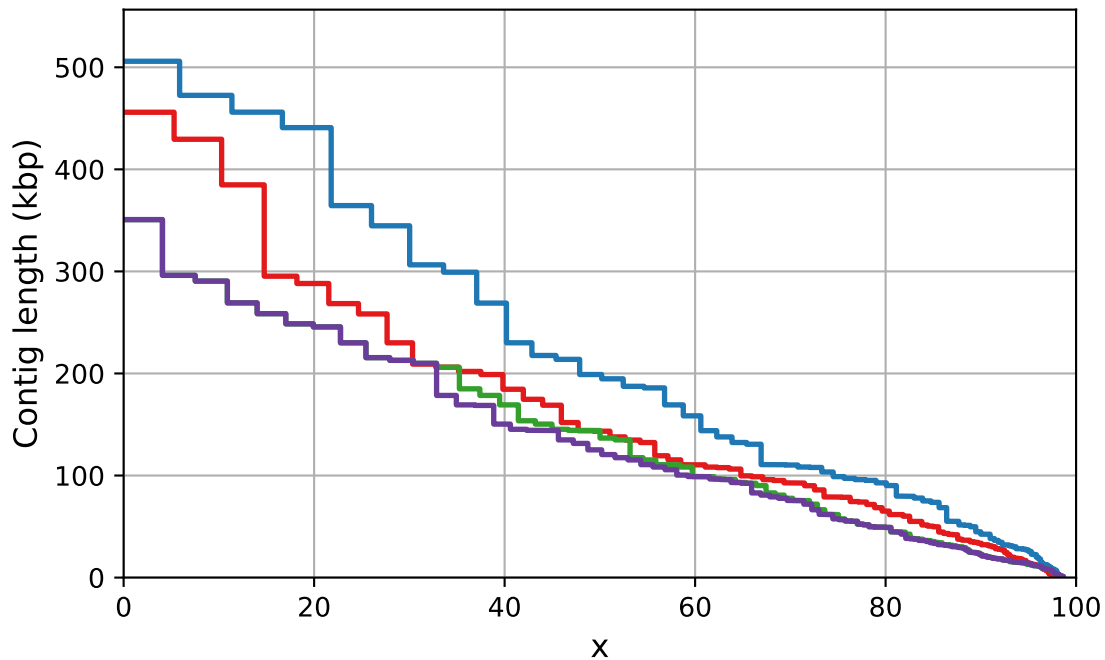
Cumulative length (aligned contigs)



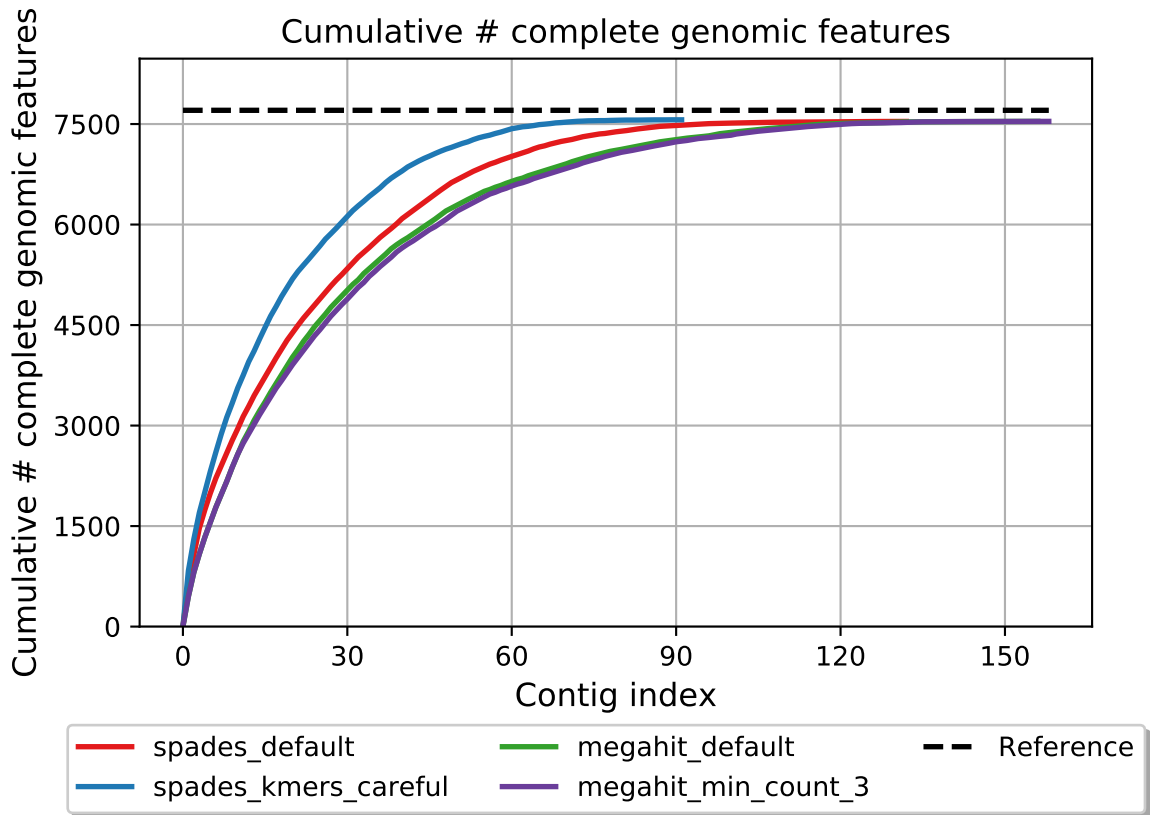
NAx



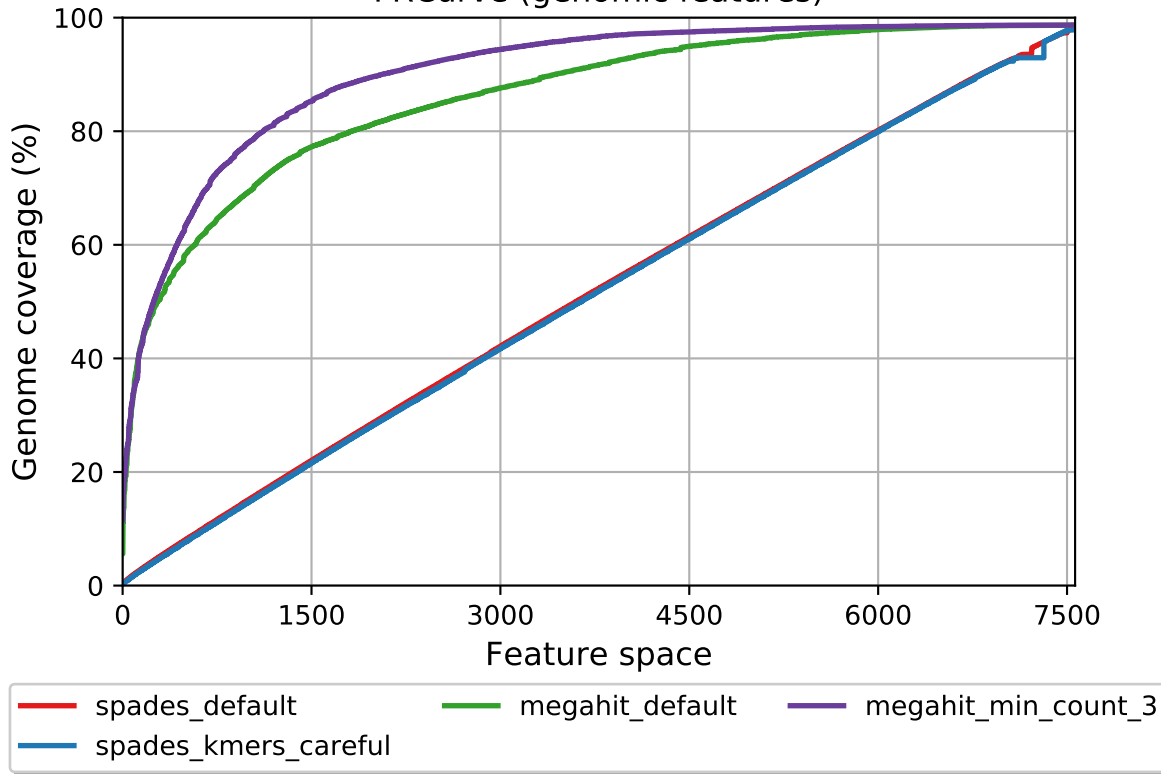
NGAx



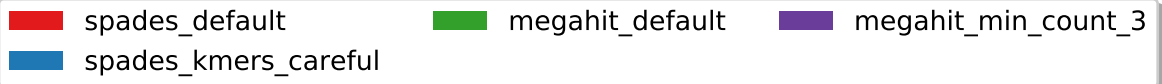
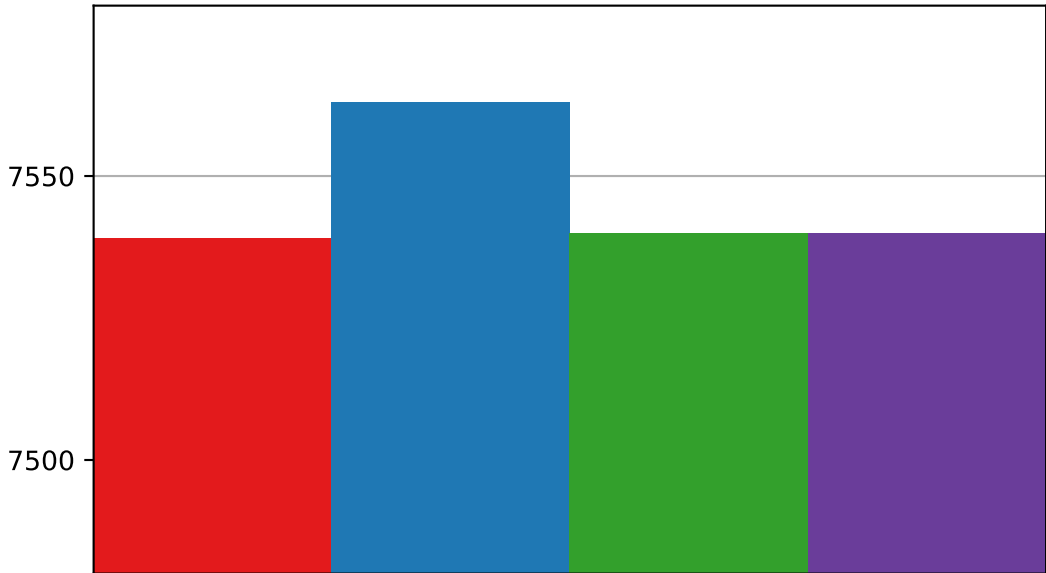
Cumulative # complete genomic features



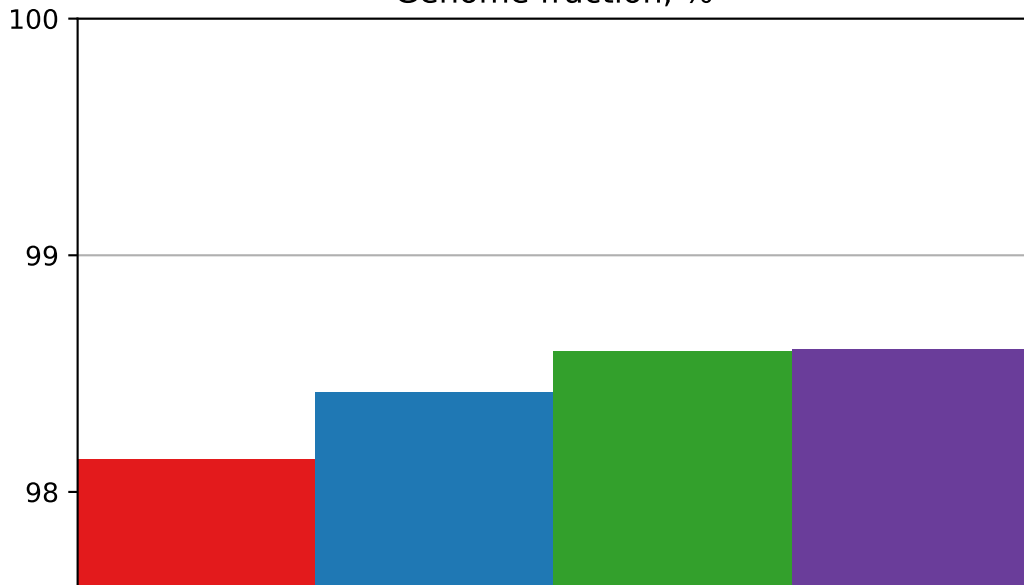
FRCurve (genomic features)



complete genomic features



Genome fraction, %



■ spades_default ■ megahit_default ■ megahit_min_count_3
■ spades_kmers_careful