

Report

	run_25_velvet_contigs	run_25_spades_contigs	run_25_unicycler_contigs
# contigs (>= 0 bp)	34	123	104
# contigs (>= 1000 bp)	28	26	54
# contigs (>= 5000 bp)	11	13	3
# contigs (>= 10000 bp)	7	7	0
# contigs (>= 25000 bp)	0	0	0
# contigs (>= 50000 bp)	0	0	0
Total length (>= 0 bp)	161875	186971	147655
Total length (>= 1000 bp)	158001	176528	128940
Total length (>= 5000 bp)	110708	138975	17294
Total length (>= 10000 bp)	88022	94893	0
Total length (>= 25000 bp)	0	0	0
Total length (>= 50000 bp)	0	0	0
# contigs	32	30	69
Largest contig	17457	18288	5867
Total length	161492	179079	139556
Reference length	197205	197205	197205
GC (%)	33.26	33.06	32.88
Reference GC (%)	33.00	33.00	33.00
N50	10045	10045	2539
NG50	5732	9300	1932
N90	2273	3184	1074
NG90	-	680	-
auN	8902.8	10050.1	2846.4
auNG	7290.5	9126.4	2014.3
L50	7	7	19
LG50	9	8	32
L90	21	19	51
LG90	-	28	-
# misassemblies	0	0	0
# misassembled contigs	0	0	0
Misassembled contigs length	0	0	0
# local misassemblies	0	0	0
# 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 (%)	81.840	90.813	70.765
Duplication ratio	1.001	1.000	1.000
# N's per 100 kbp	6.19	0.00	0.00
# mismatches per 100 kbp	7.43	3.35	5.02
# indels per 100 kbp	2.48	1.68	0.00
Largest alignment	17457	18288	5867
Total aligned length	161478	179008	139552
NA50	10045	10045	2539
NGA50	5732	9294	1932
NA90	2273	3184	1074
NGA90	-	680	-
auNA	8902.6	10046.8	2846.4
auNGA	7290.4	9123.4	2014.3
LA50	7	7	19
LGA50	9	8	32
LA90	21	19	51
LGA90	-	28	-

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

	run_25_velvet_contigs	run_25_spades_contigs	run_25_unicycler_contigs
# misassemblies	0	0	0
# contig misassemblies	0	0	0
# c. relocations	0	0	0
# 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	0	0	0
Misassembled contigs length	0	0	0
# local misassemblies	0	0	0
# scaffold gap ext. mis.	0	0	0
# scaffold gap loc. mis.	0	0	0
# unaligned mis. contigs	0	0	0
# mismatches	12	6	7
# indels	4	3	0
# indels (<= 5 bp)	4	1	0
# indels (> 5 bp)	0	2	0
Indels length	7	129	0

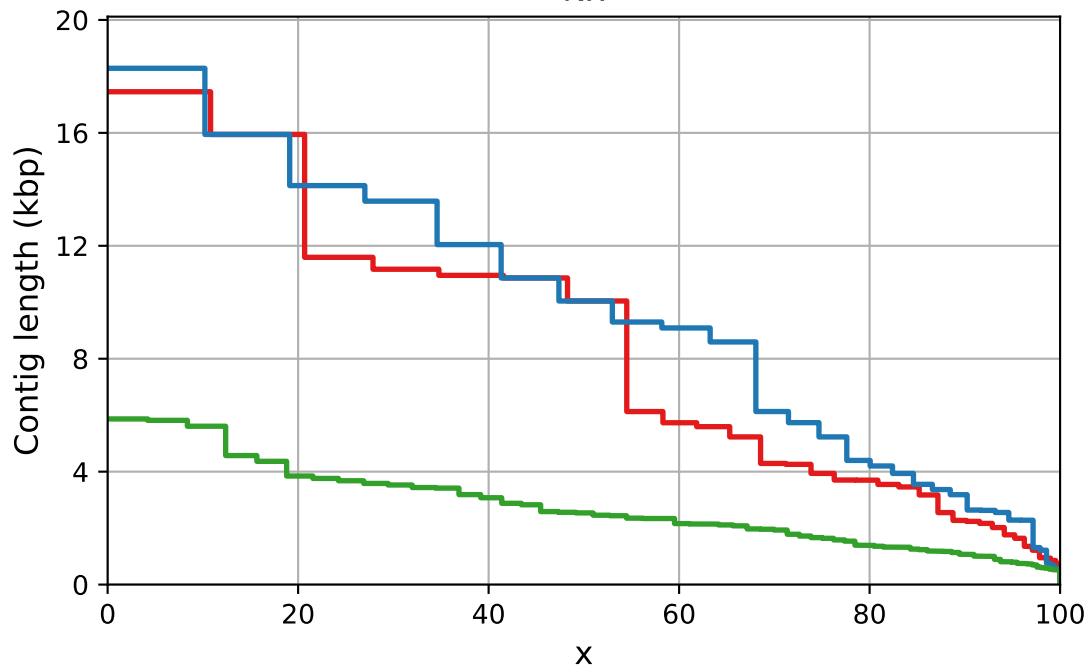
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	run_25_velvet_contigs	run_25_spades_contigs	run_25_unicycler_contigs
# 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	10	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).

Nx

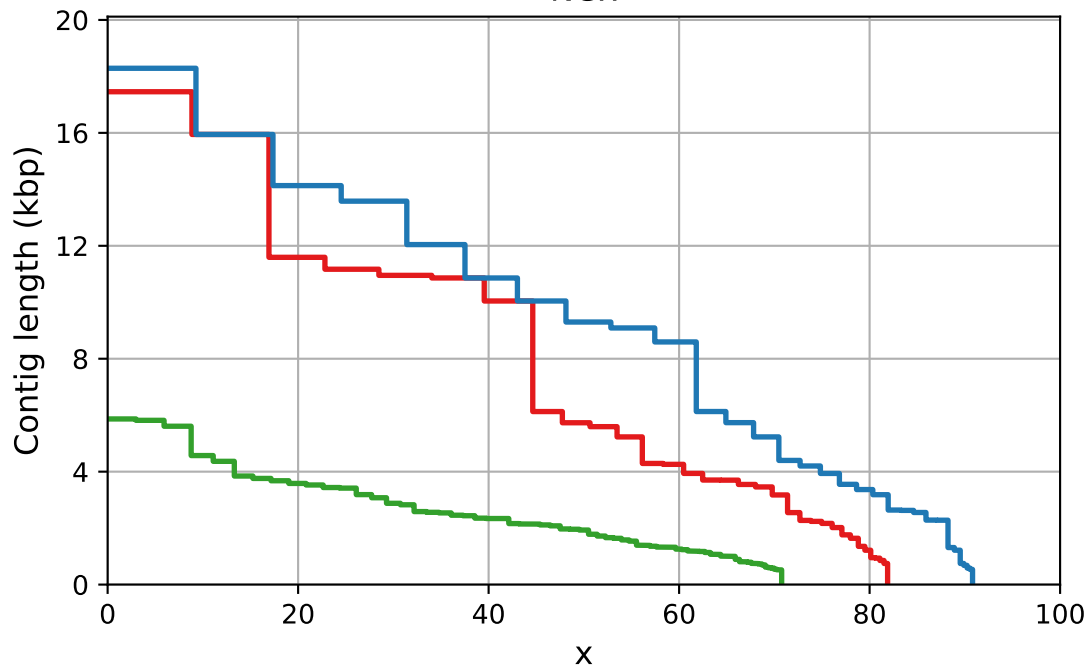


run_25_velvet_contigs

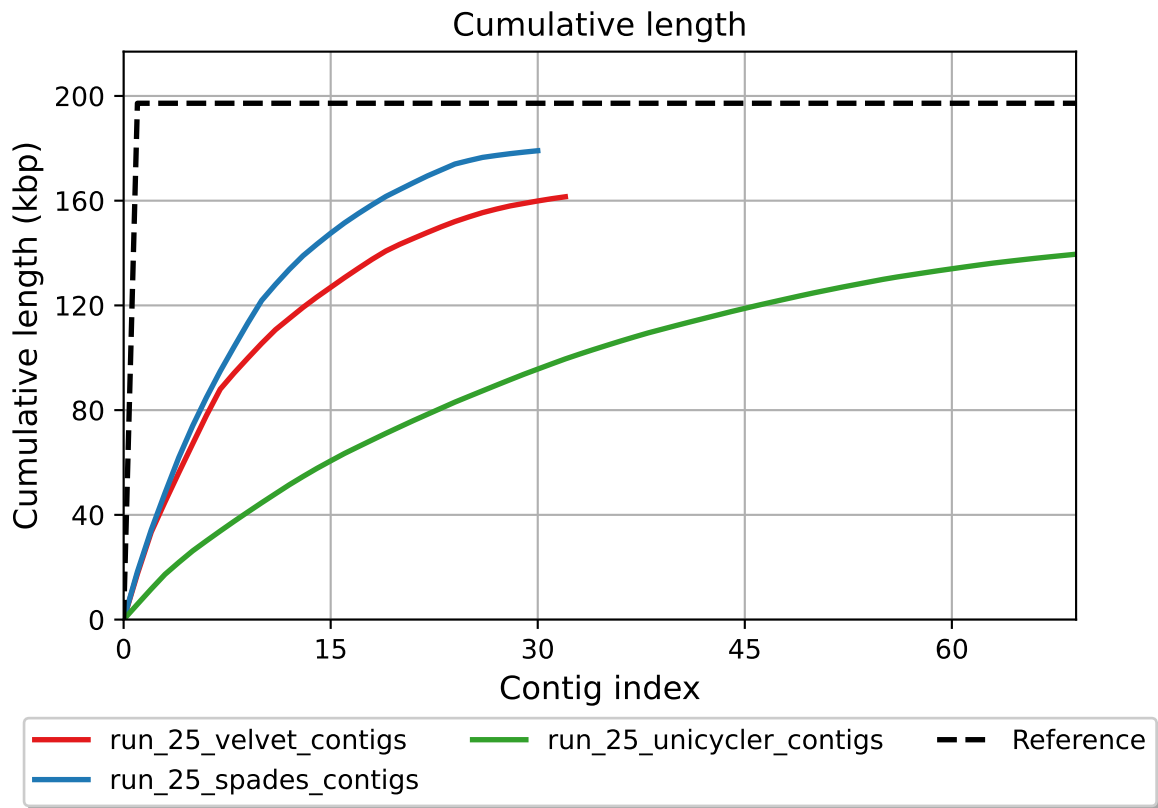
run_25_spades_contigs

run_25_unicycler_contigs

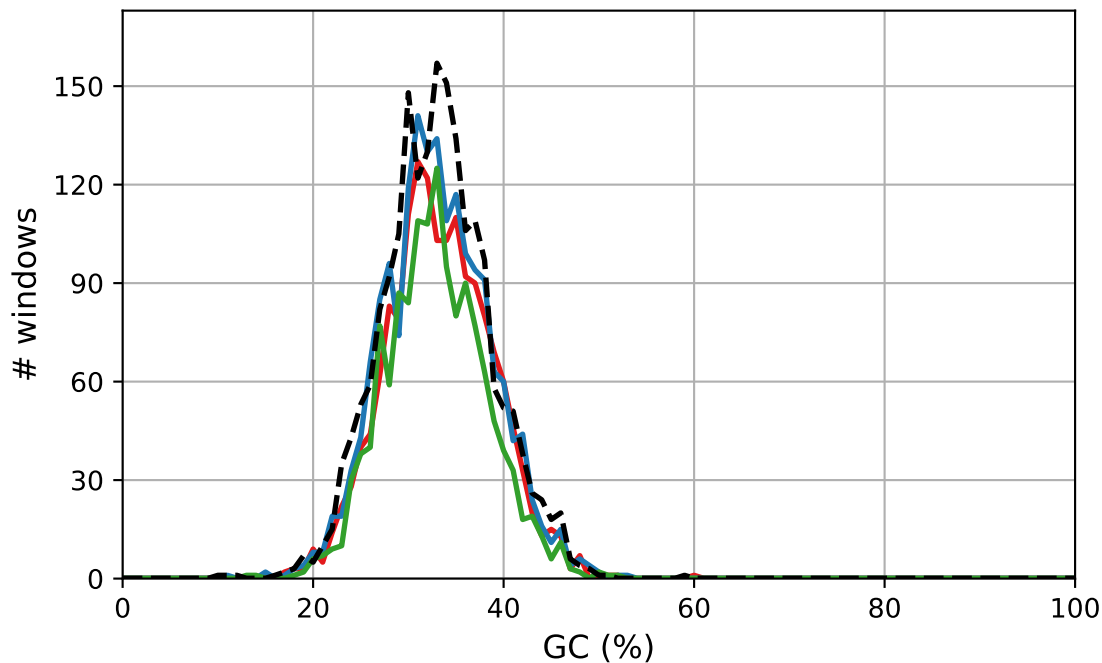
NGx



run_25_velvet_contigs run_25_spades_contigs run_25_unicycler_contigs

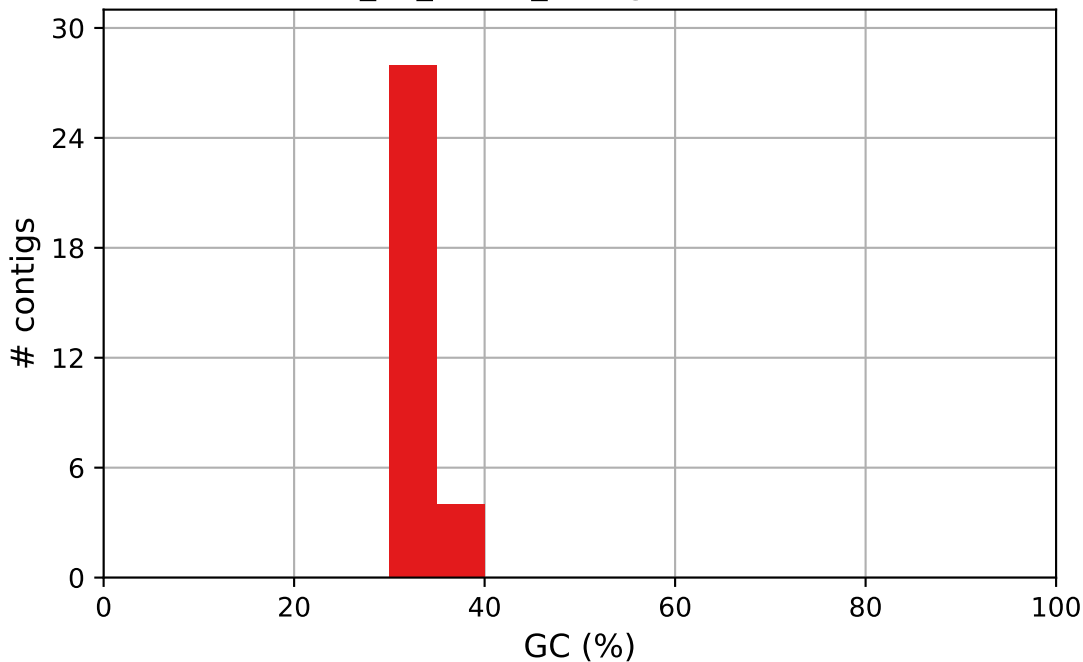


GC content



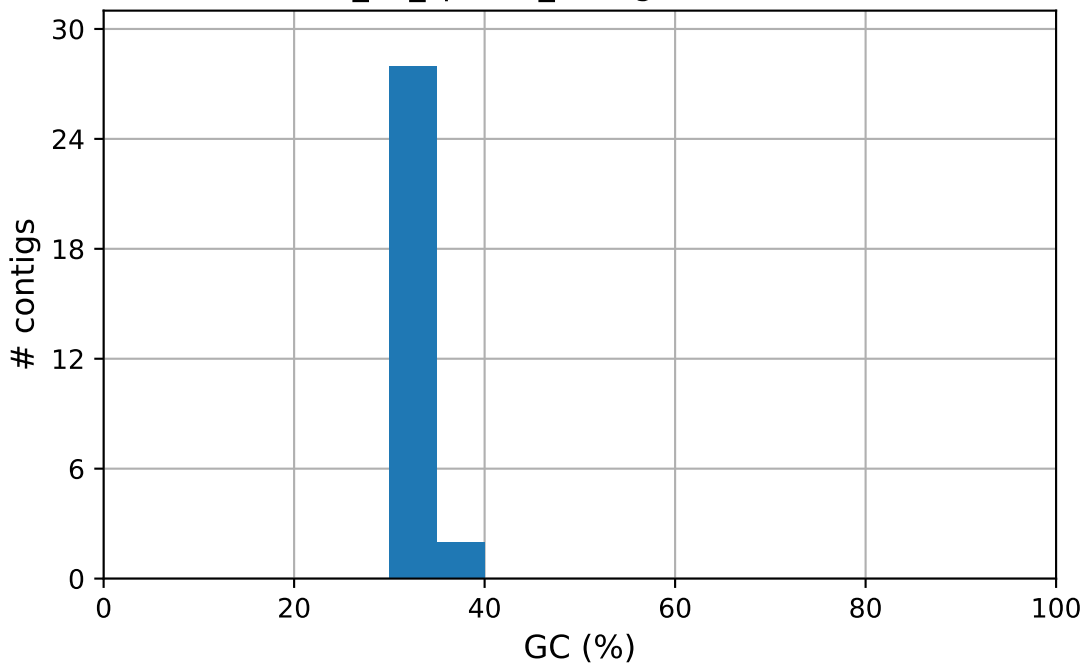
run_25_velvet_contigs run_25_unicycler_contigs Reference
run_25_spades_contigs

run_25_velvet_contigs GC content



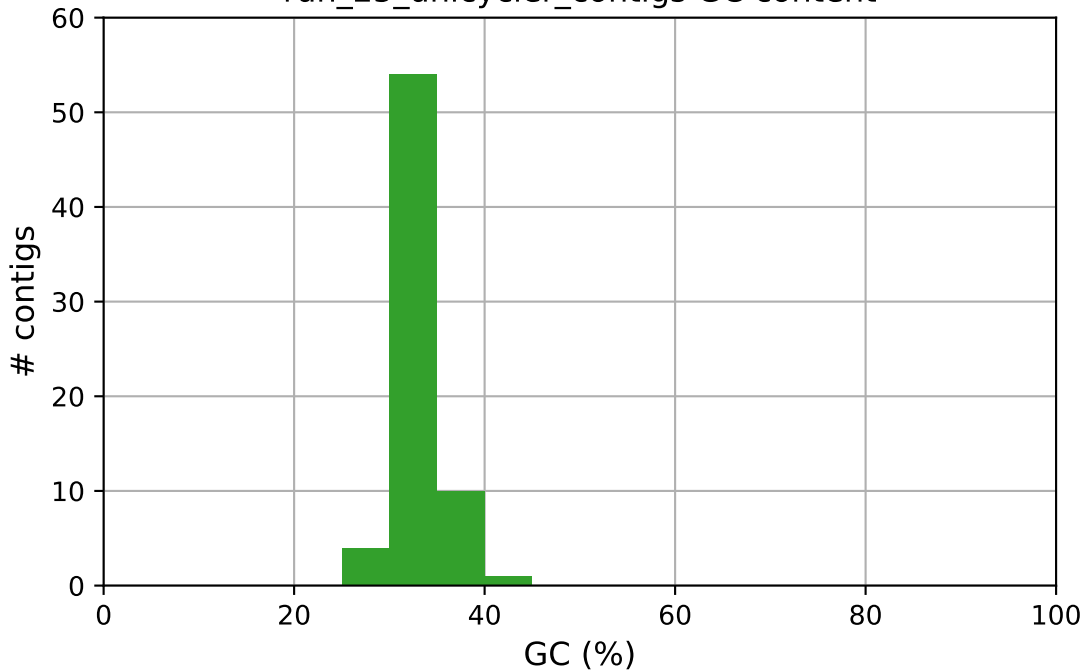
run_25_velvet_contigs

run_25_spades_contigs GC content



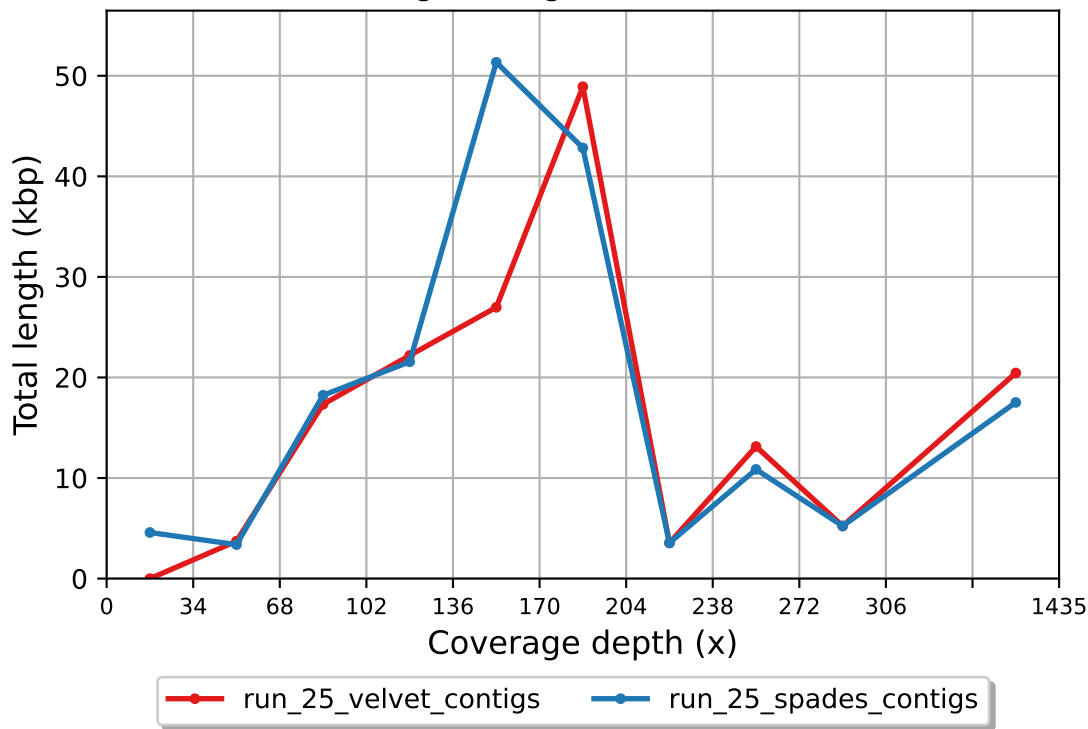
run_25_spades_contigs

run_25_unicycler_contigs GC content

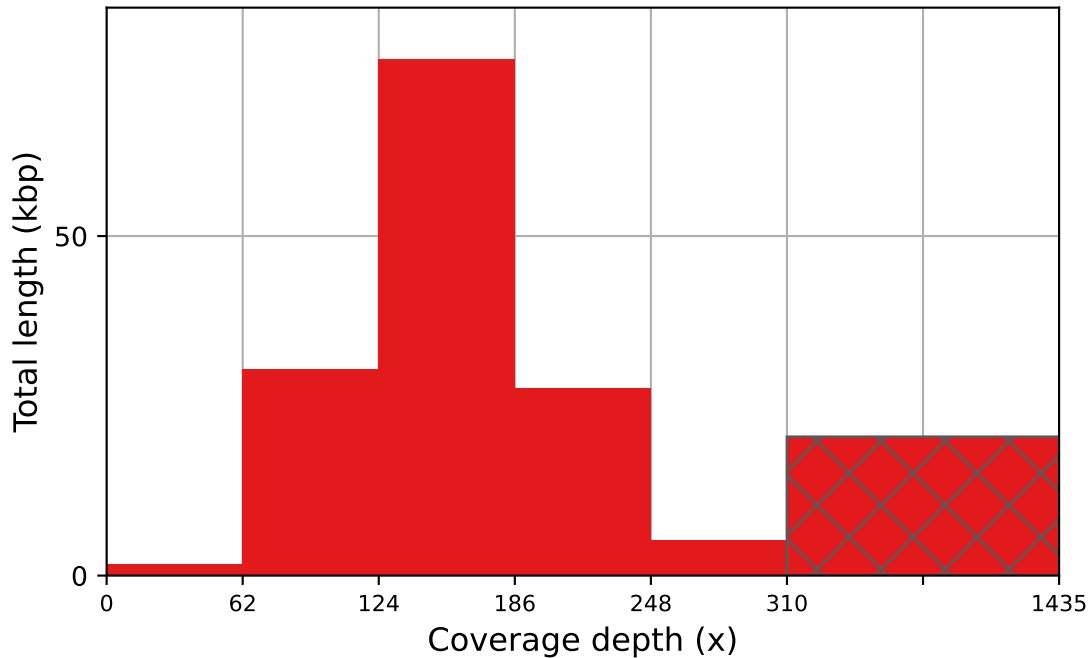


run_25_unicycler_contigs

Coverage histogram (bin size: 34x)

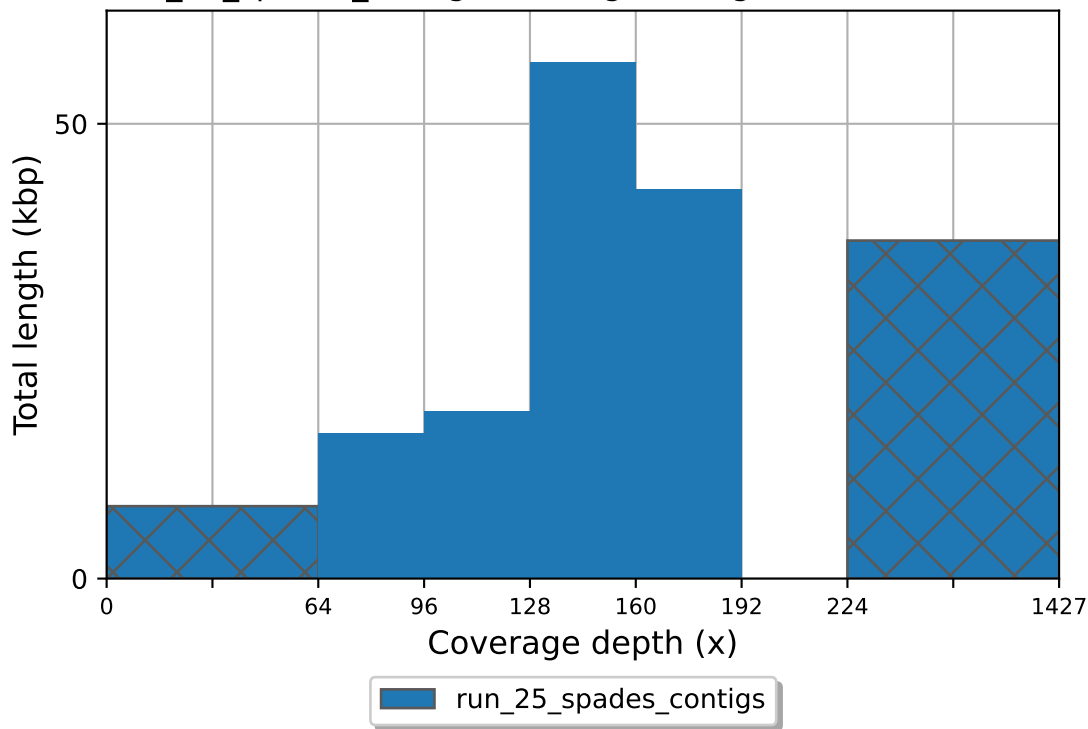


run_25_velvet_contigs coverage histogram (bin size: 62x)

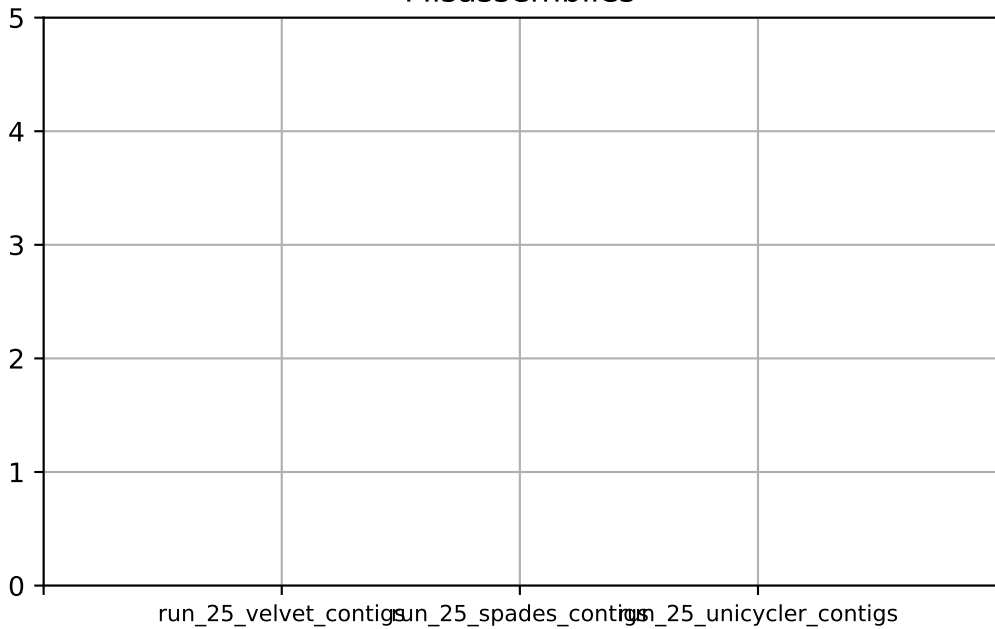


run_25_velvet_contigs

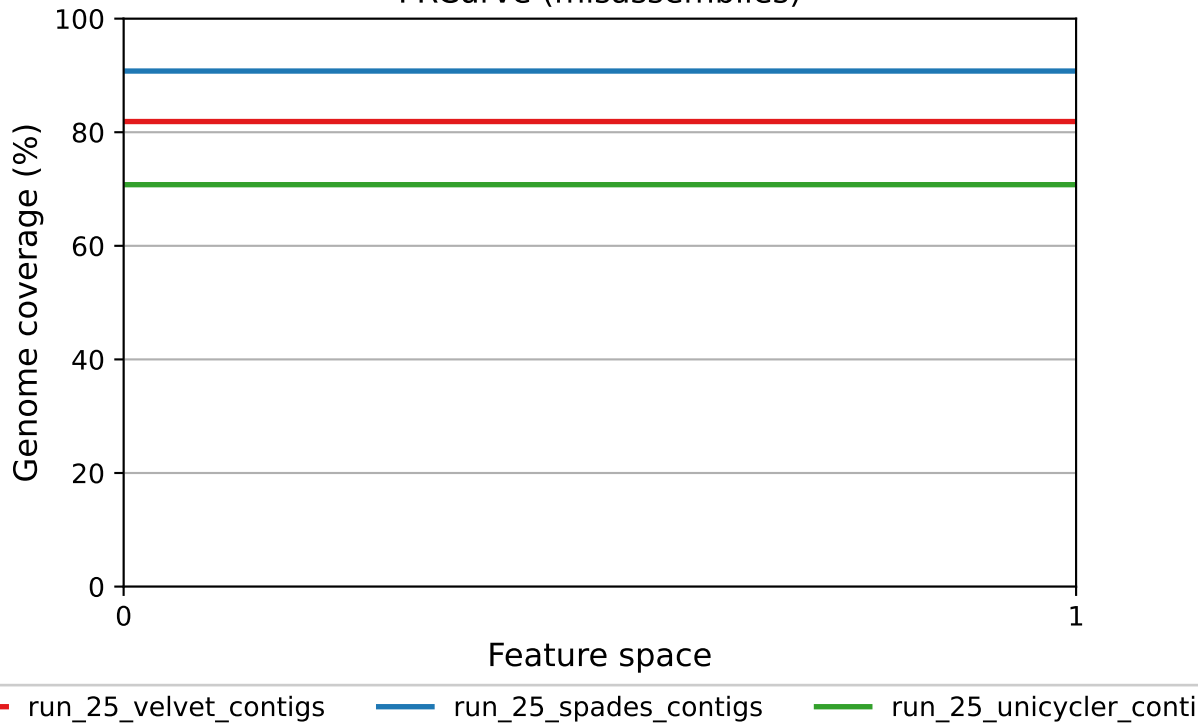
run_25_spades_contigs coverage histogram (bin size: 32x)



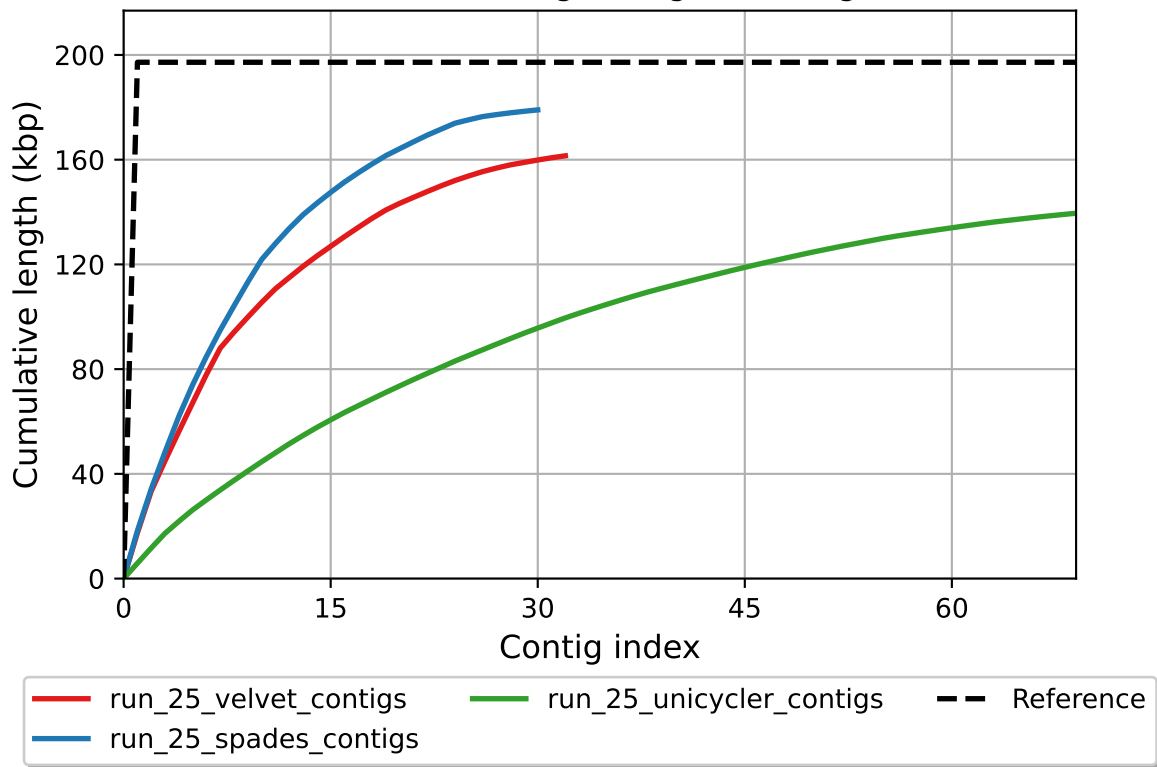
Misassemblies



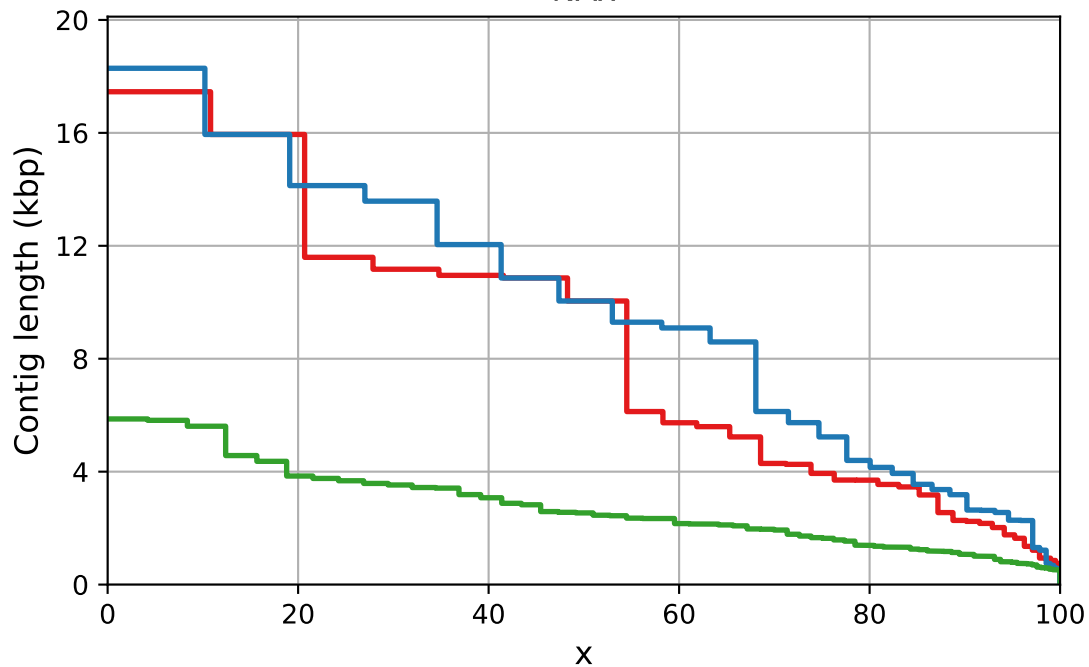
FRCurve (misassemblies)



Cumulative length (aligned contigs)

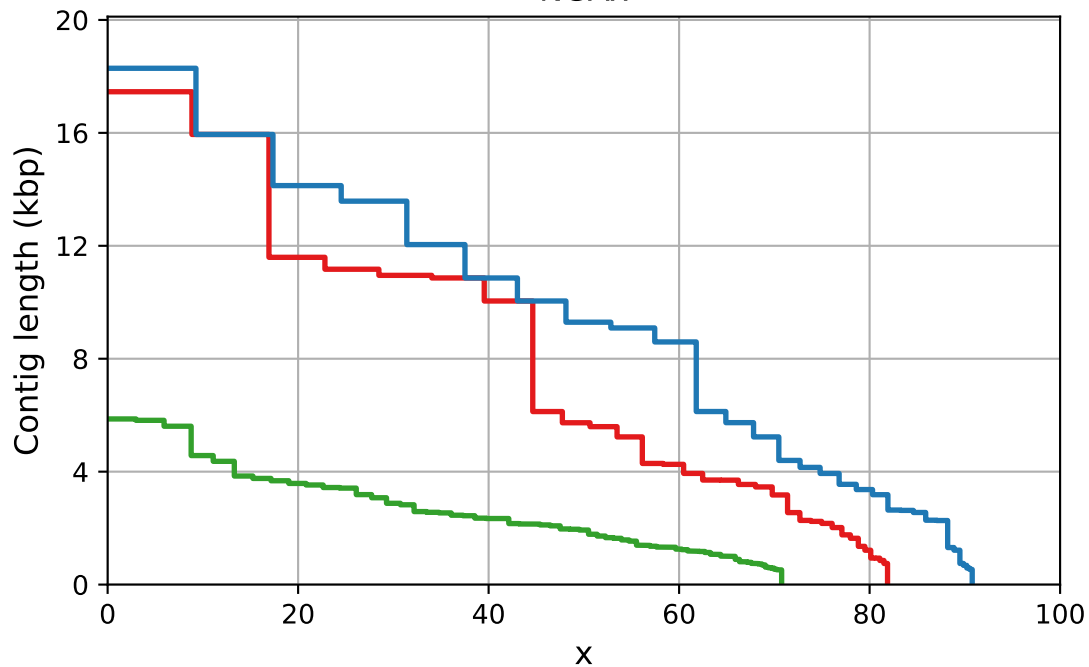


NAx



run_25_velvet_contigs run_25_spades_contigs run_25_unicycler_contigs

NGAx



run_25_velvet_contigs run_25_spades_contigs run_25_unicycler_contigs

Genome fraction, %

100

50

run_25_velvet_contigs run_25_spades_contigs run_25_unicycler_contigs

