

Report

	velvet_low_contigs	velvet_high_contigs	spades_low_contigs	spades_high_contigs	nanopore_spades_contigs	contigs_1	contigs_2
# contigs (>= 0 bp)	297	74	128	1	65	3	4
# contigs (>= 1000 bp)	2	32	4	1	20	3	2
# contigs (>= 5000 bp)	0	2	0	1	3	0	0
# contigs (>= 10000 bp)	0	1	0	1	0	0	0
# contigs (>= 25000 bp)	0	0	0	1	0	0	0
# contigs (>= 50000 bp)	0	0	0	1	0	0	0
Total length (>= 0 bp)	63937	100578	49818	100000	72785	6710	5870
Total length (>= 1000 bp)	2379	87881	5313	100000	58365	6710	5460
Total length (>= 5000 bp)	0	16952	0	100000	19536	0	0
Total length (>= 10000 bp)	0	10490	0	100000	0	0	0
Total length (>= 25000 bp)	0	0	0	100000	0	0	0
Total length (>= 50000 bp)	0	0	0	100000	0	0	0
# contigs	20	43	20	1	24	3	2
Largest contig	1321	10490	1737	100000	6734	3980	3360
Total length	13849	95527	15922	100000	60983	6710	5460
Reference length	10000	10000	10000	10000	10000	10000	10000
GC (%)	50.81	52.58	51.21	52.59	52.34	51.28	52.44
Reference GC (%)	52.07	52.07	52.07	52.07	52.07	52.07	52.07
N50	715	2859	718	100000	3700	3980	3360
NG50	726	10490	1083	100000	6734	1610	2100
N75	542	1726	635	100000	1839	1610	2100
NG75	679	10490	793	100000	6636	-	-
L50	8	11	8	1	6	1	1
LG50	6	1	4	1	1	2	2
L75	14	21	13	1	12	2	2
LG75	9	1	7	1	2	-	-
# misassemblies	0	0	0	0	0	1	2
# misassembled contigs	0	0	0	0	0	1	1
Misassembled contigs length	0	0	0	0	0	3980	3360
# local misassemblies	0	0	0	0	0	0	0
# unaligned mis. contigs	0	0	0	0	0	0	0
# unaligned contigs	19 + 0 part	37 + 1 part	18 + 1 part	0 + 1 part	20 + 2 part	0 + 0 part	0 + 0 part
Unaligned length	13307	86049	14936	90000	56928	0	0
Genome fraction (%)	5.420	94.420	9.860	100.000	40.660	67.100	54.600
Duplication ratio	1.000	1.004	1.000	1.000	0.997	1.000	1.000
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	0.00	0.00	0.00	0.00	0.00	0.00	0.00
# indels per 100 kbp	0.00	0.00	0.00	0.00	295.13	0.00	0.00
# genes	0 + 1 part	4 + 4 part	1 + 1 part	9 + 0 part	4 + 2 part	5 + 4 part	1 + 6 part
# operons	0 + 1 part	0 + 2 part	0 + 1 part	2 + 0 part	0 + 2 part	1 + 1 part	0 + 2 part
# predicted genes (unique)	15	91	15	77	72	7	6
# predicted genes (>= 0 bp)	15	91	15	77	72	7	6
# predicted genes (>= 300 bp)	14	86	15	74	54	6	5
# predicted genes (>= 1500 bp)	0	13	0	20	2	1	1
# predicted genes (>= 3000 bp)	0	0	0	3	0	0	0
Largest alignment	542	2849	542	10000	1521	2030	2100
Total aligned length	542	9478	986	10000	4055	6710	5460
NA50	-	-	-	-	-	1950	1471
NGA50	-	2791	-	10000	-	1610	700
NA75	-	-	-	-	-	1610	1189
NGA75	-	918	-	10000	-	-	-
LA50	-	-	-	-	-	2	2
LGA50	-	2	-	1	-	3	4
LA75	-	-	-	-	-	3	3
LGA75	-	4	-	1	-	-	-

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

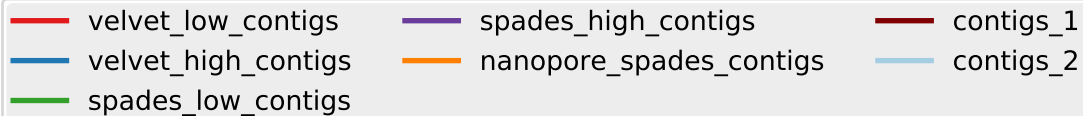
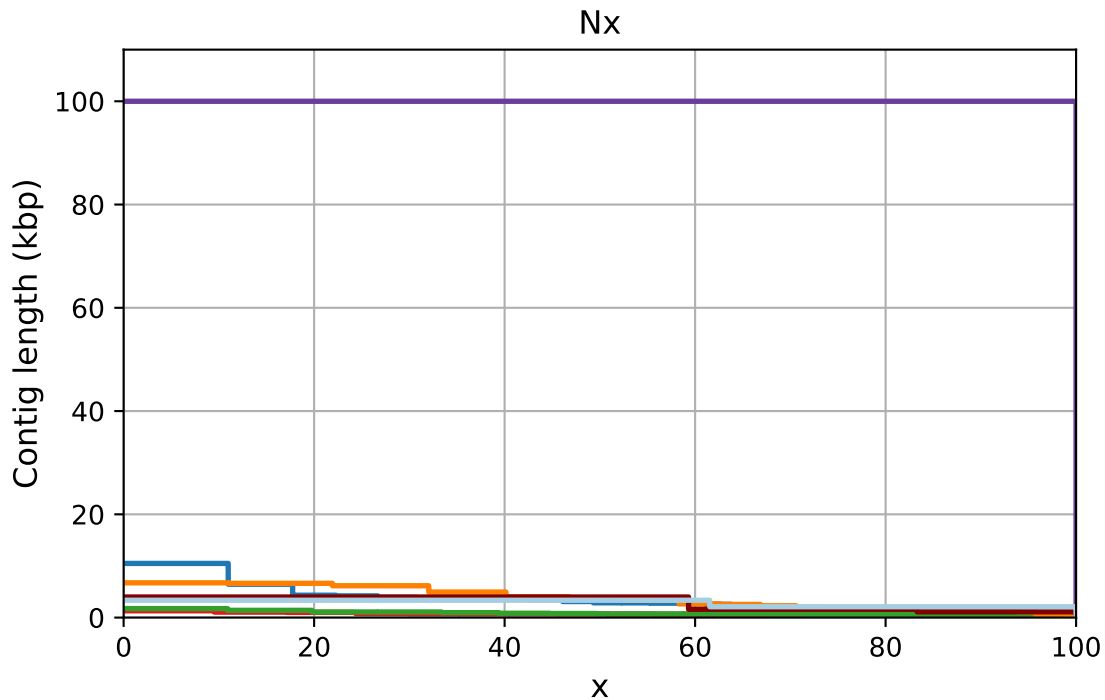
	velvet_low_contigs	velvet_high_contigs	spades_low_contigs	spades_high_contigs	nanopore_spades_contigs	contigs_1	contigs_2
# misassemblies	0	0	0	0	0	1	2
# relocations	0	0	0	0	0	1	2
# translocations	0	0	0	0	0	0	0
# inversions	0	0	0	0	0	0	0
# misassembled contigs	0	0	0	0	0	1	1
Misassembled contigs length	0	0	0	0	0	3980	3360
# local misassemblies	0	0	0	0	0	0	0
# unaligned mis. contigs	0	0	0	0	0	0	0
# mismatches	0	0	0	0	0	0	0
# indels	0	0	0	0	12	0	0
# indels (<= 5 bp)	0	0	0	0	12	0	0
# indels (> 5 bp)	0	0	0	0	0	0	0
Indels length	0	0	0	0	15	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).

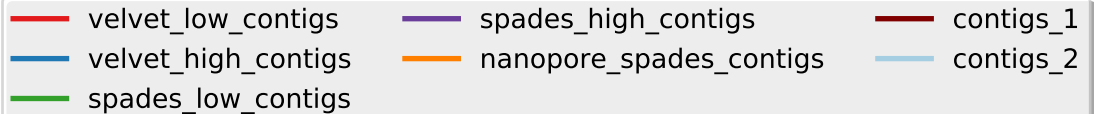
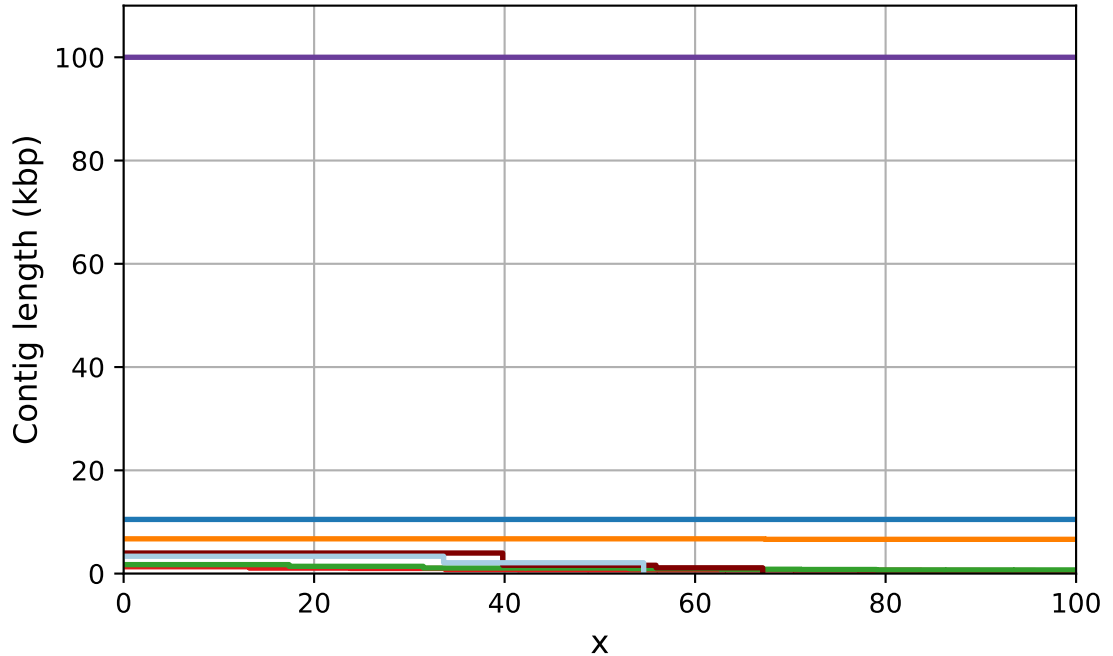
Unaligned report

	velvet_low_contigs	velvet_high_contigs	spades_low_contigs	spades_high_contigs	nanopore_spades_contigs	contigs_1	contigs_2
# fully unaligned contigs	19	37	18	0	20	0	0
Fully unaligned length	13307	84108	14296	0	51173	0	0
# partially unaligned contigs	0	1	1	1	2	0	0
Partially unaligned length	0	1941	640	90000	5755	0	0
# N's	0	0	0	0	0	0	0

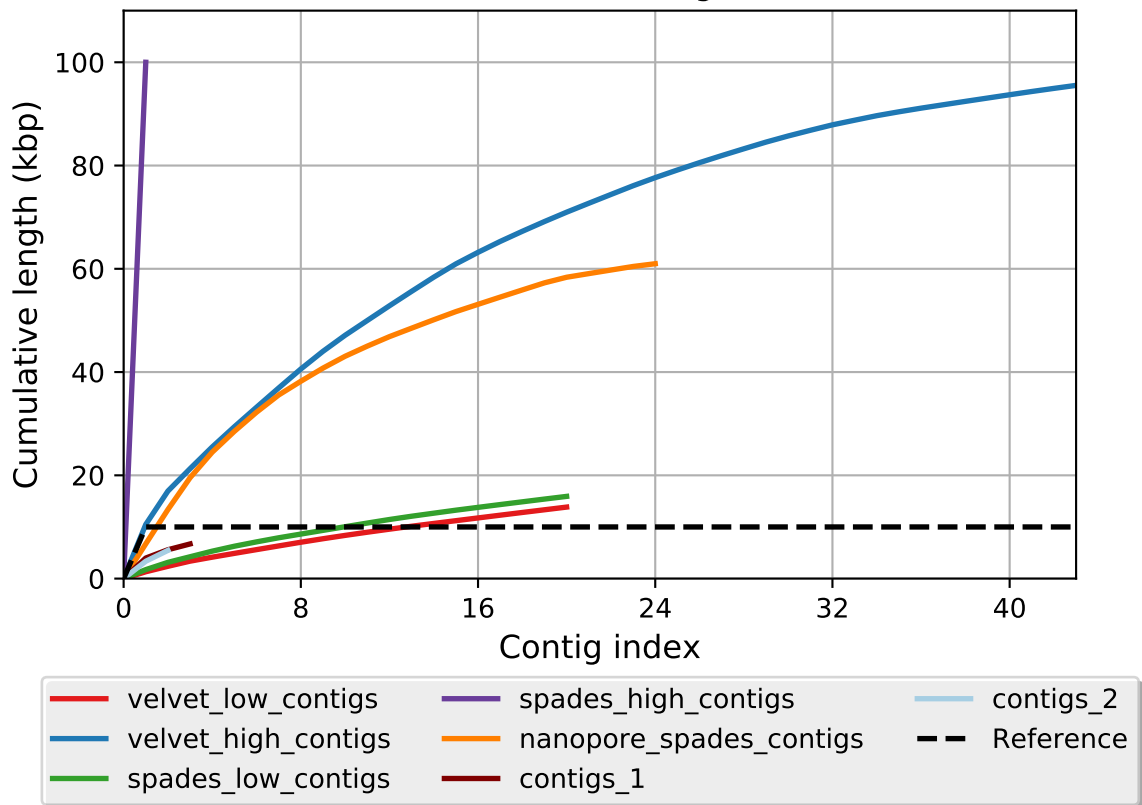
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).



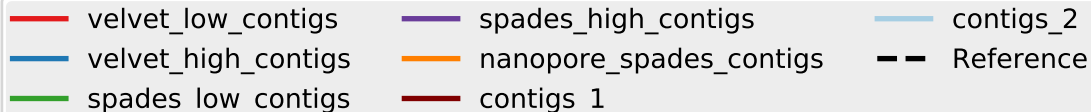
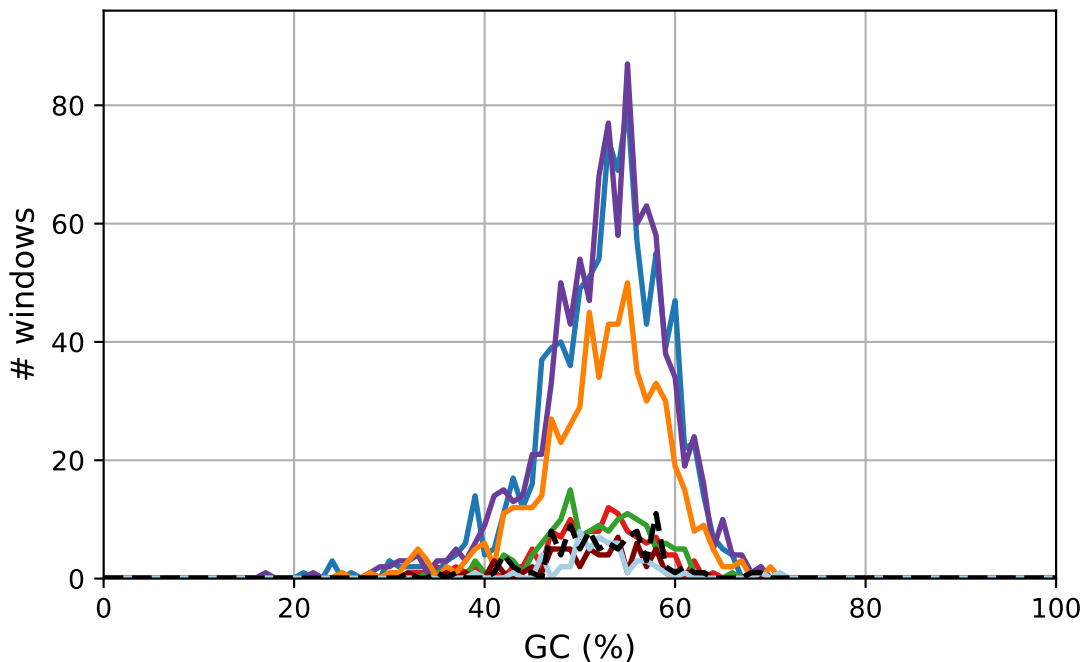
NGx



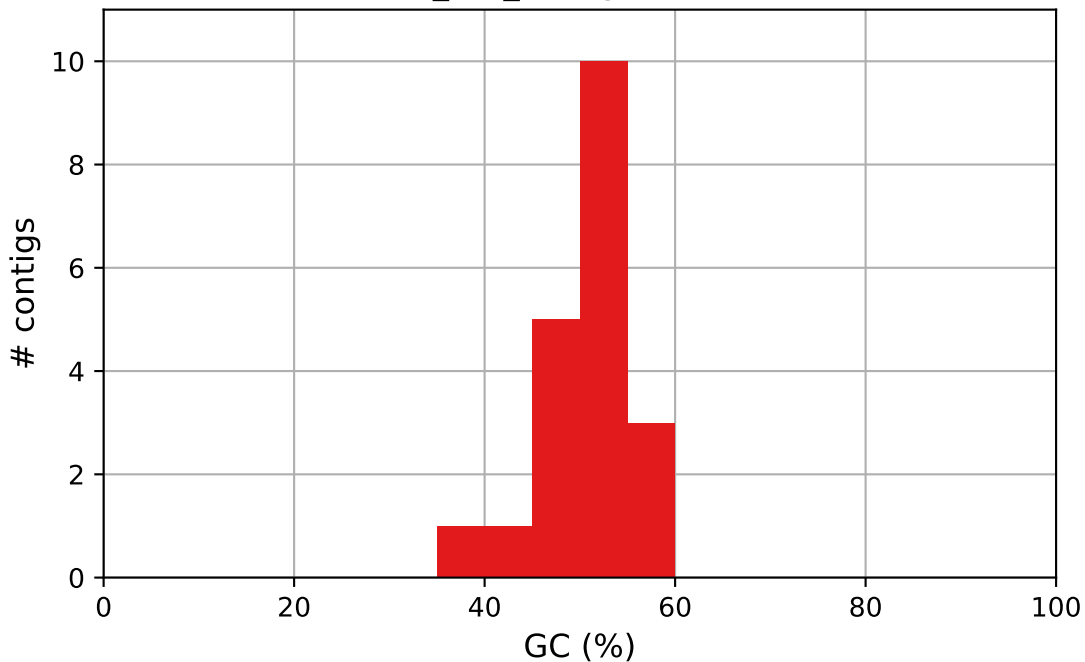
Cumulative length



GC content

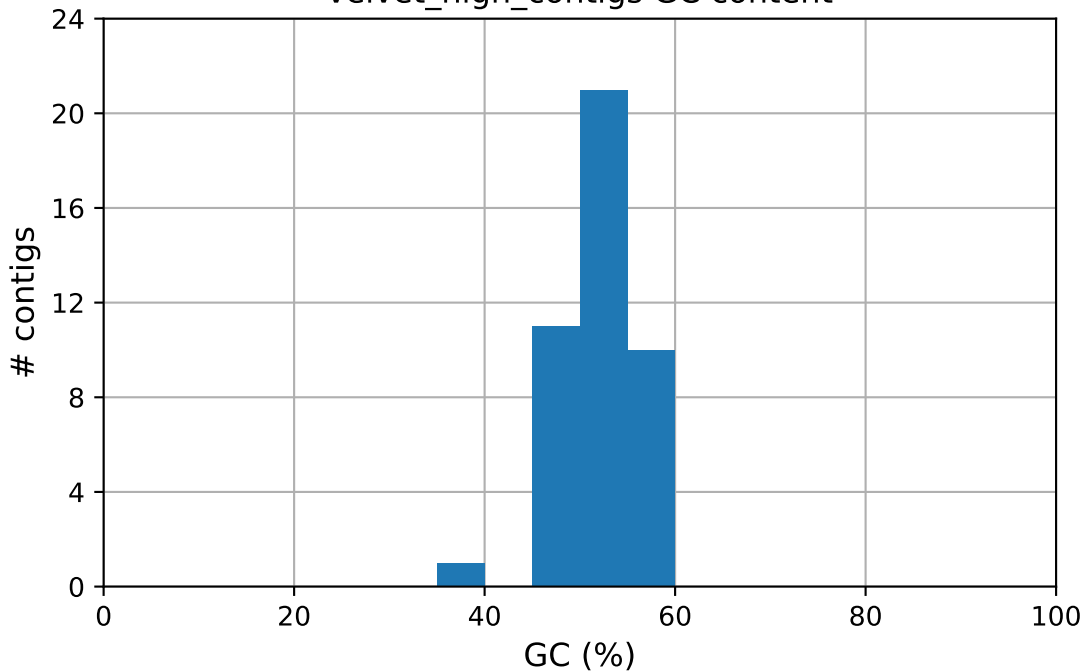


velvet_low_contigs GC content



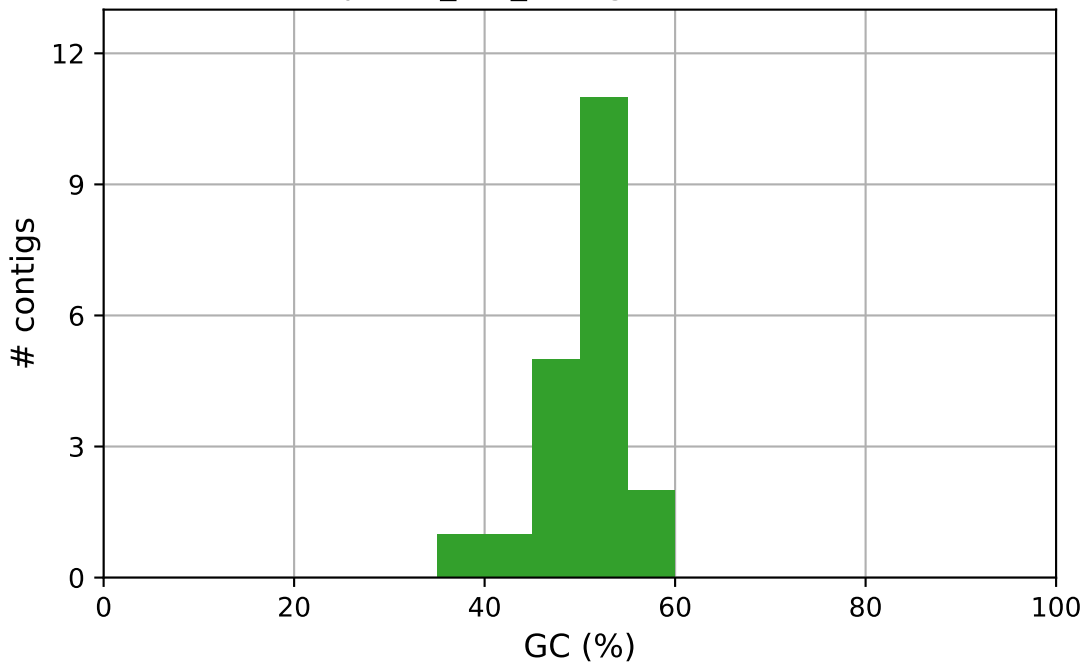
■ velvet_low_contigs

velvet_high_contigs GC content



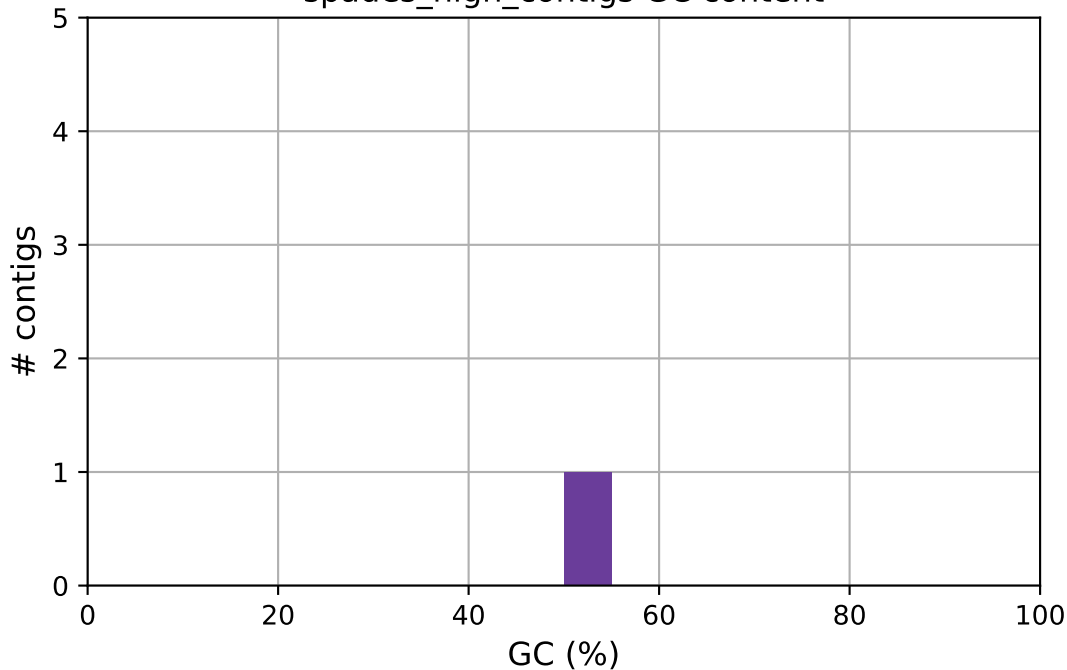
■ velvet_high_contigs

spades_low_contigs GC content



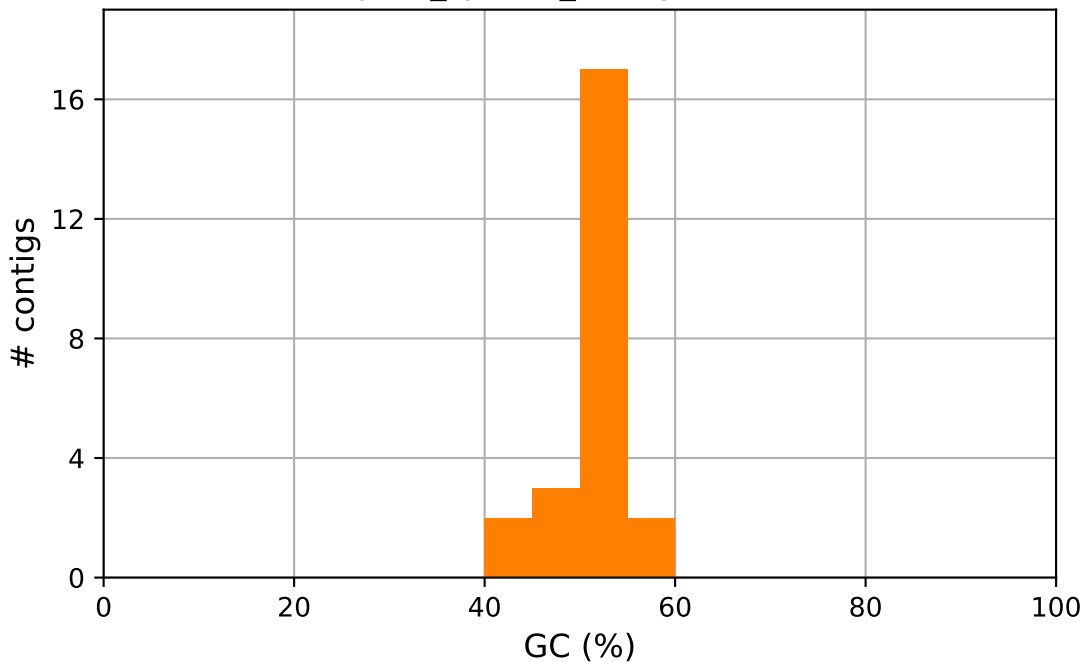
spades_low_contigs

spades_high_contigs GC content



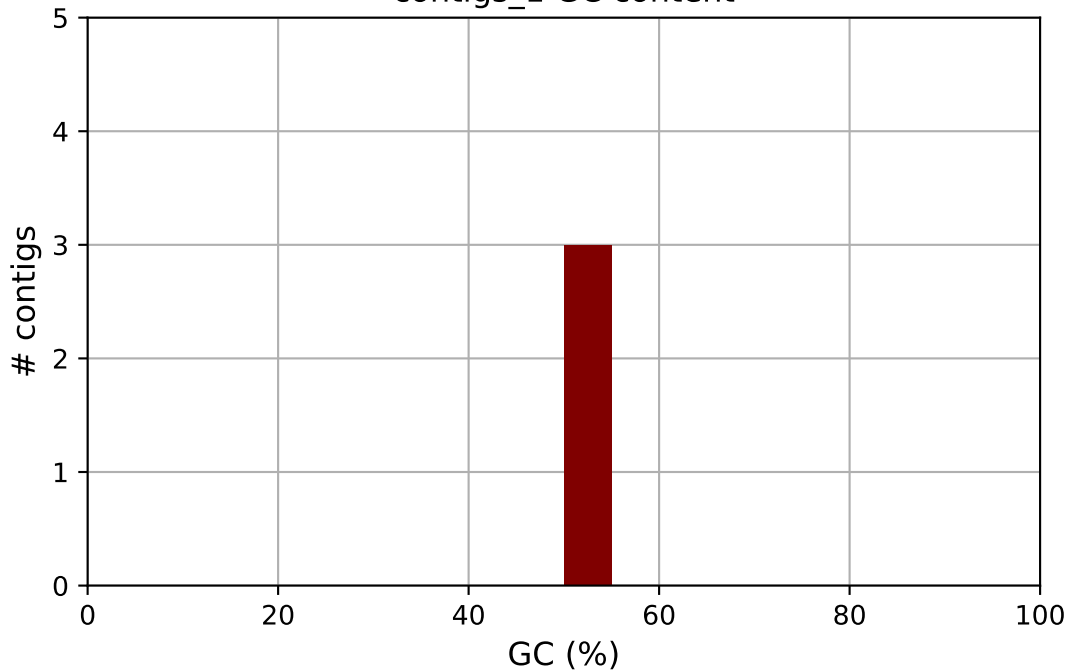
spades_high_contigs

nanopore_spades_contigs GC content



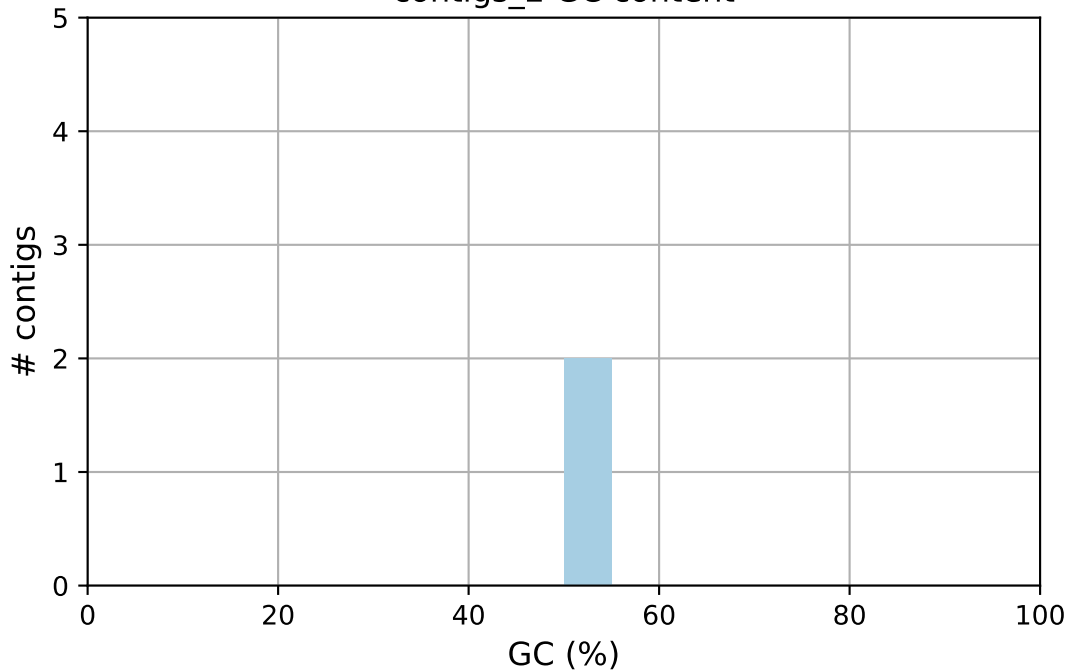
nanopore_spades_contigs

contigs_1 GC content



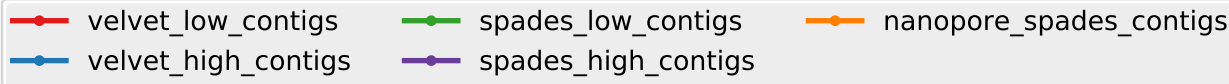
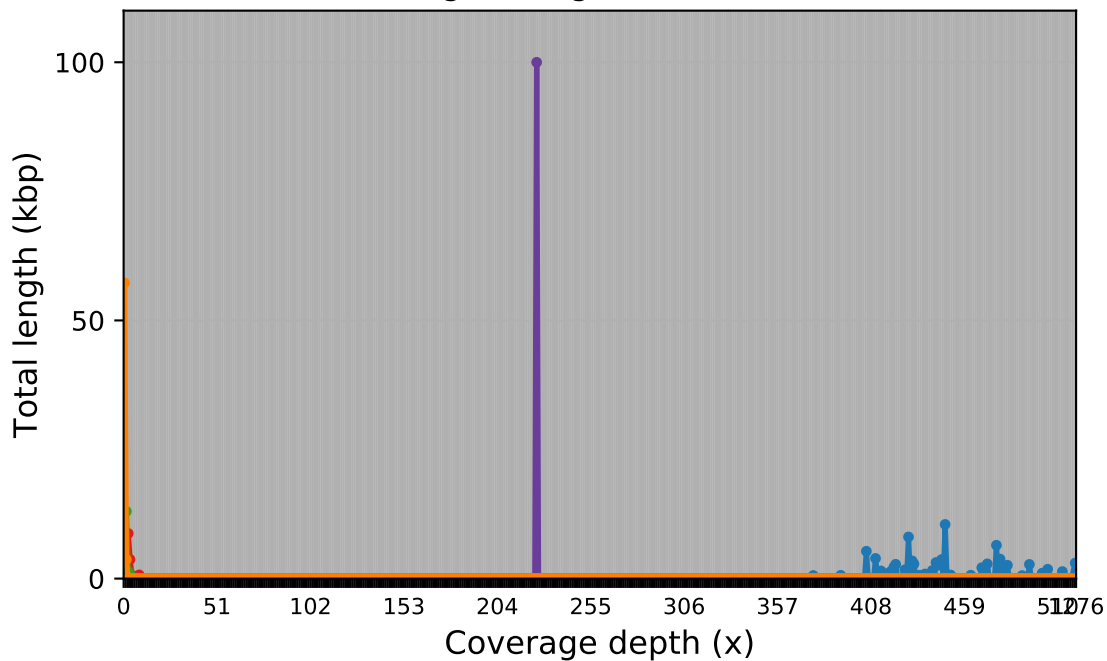
contigs_1

contigs_2 GC content

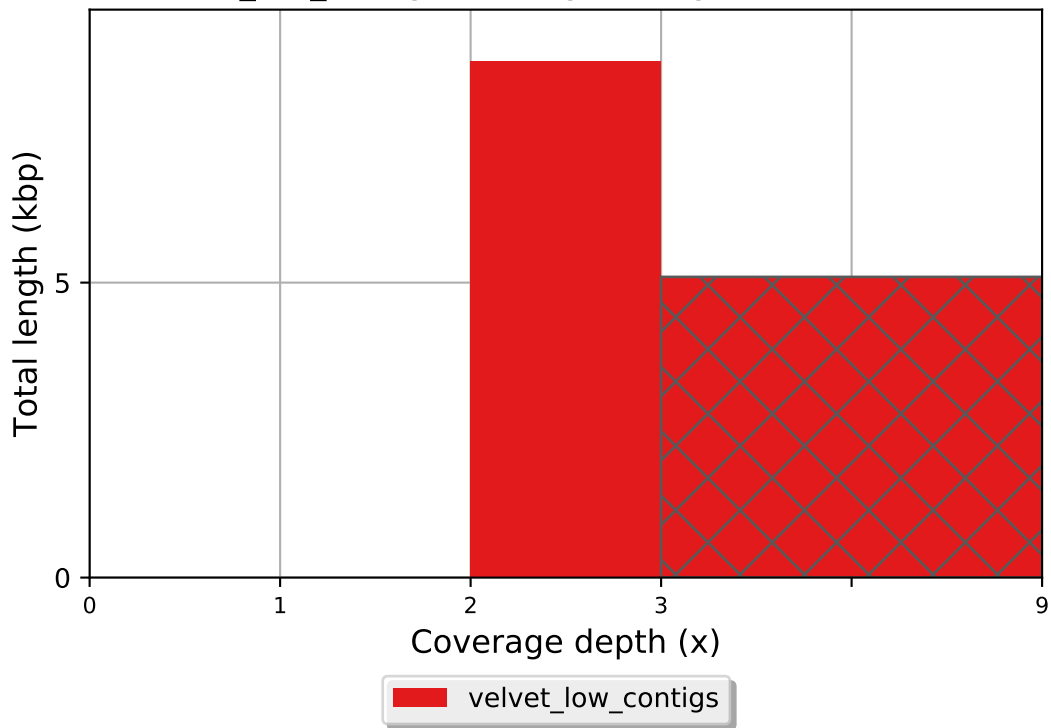


contigs_2

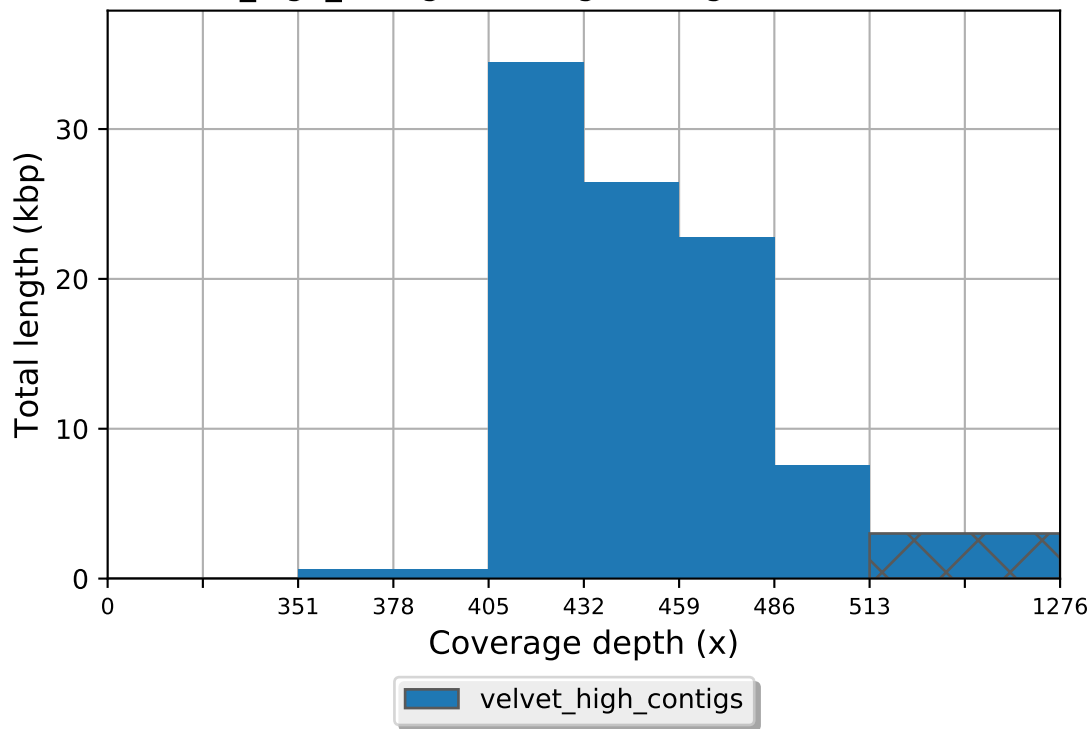
Coverage histogram (bin size: 1x)



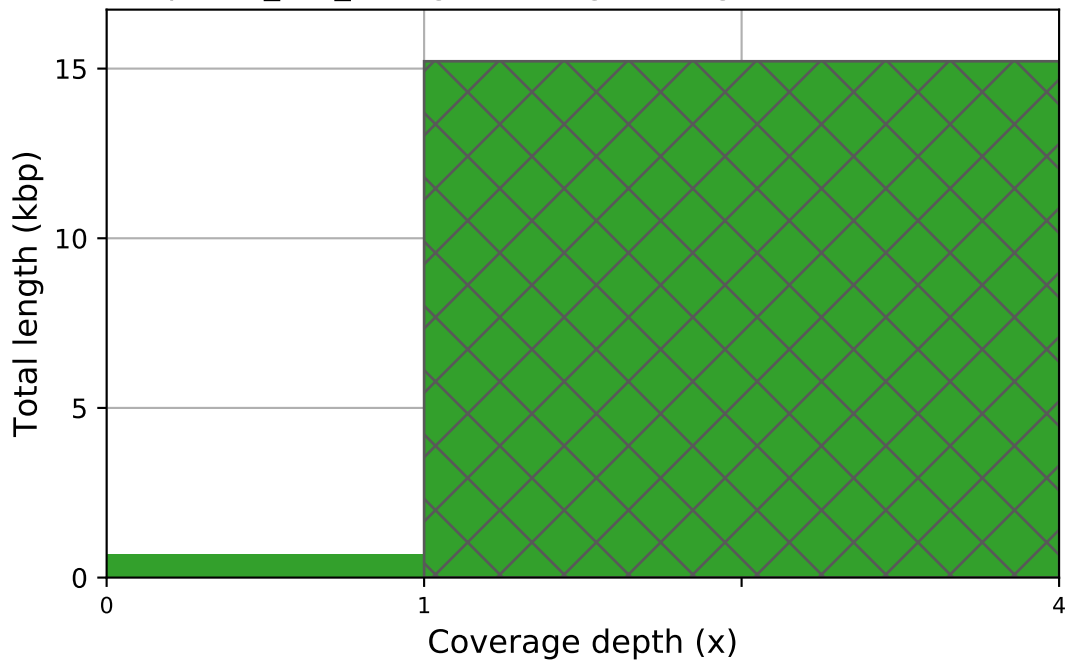
velvet_low_contigs coverage histogram (bin size: 1x)



velvet_high_contigs coverage histogram (bin size: 27x)

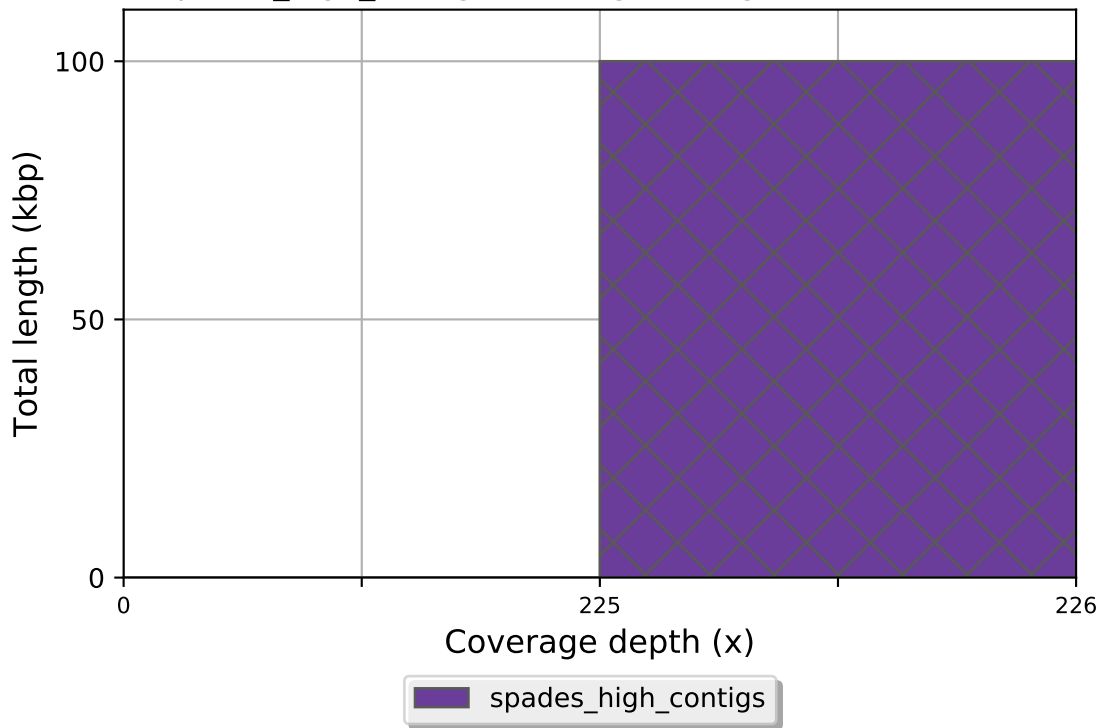


spades_low_contigs coverage histogram (bin size: 1x)

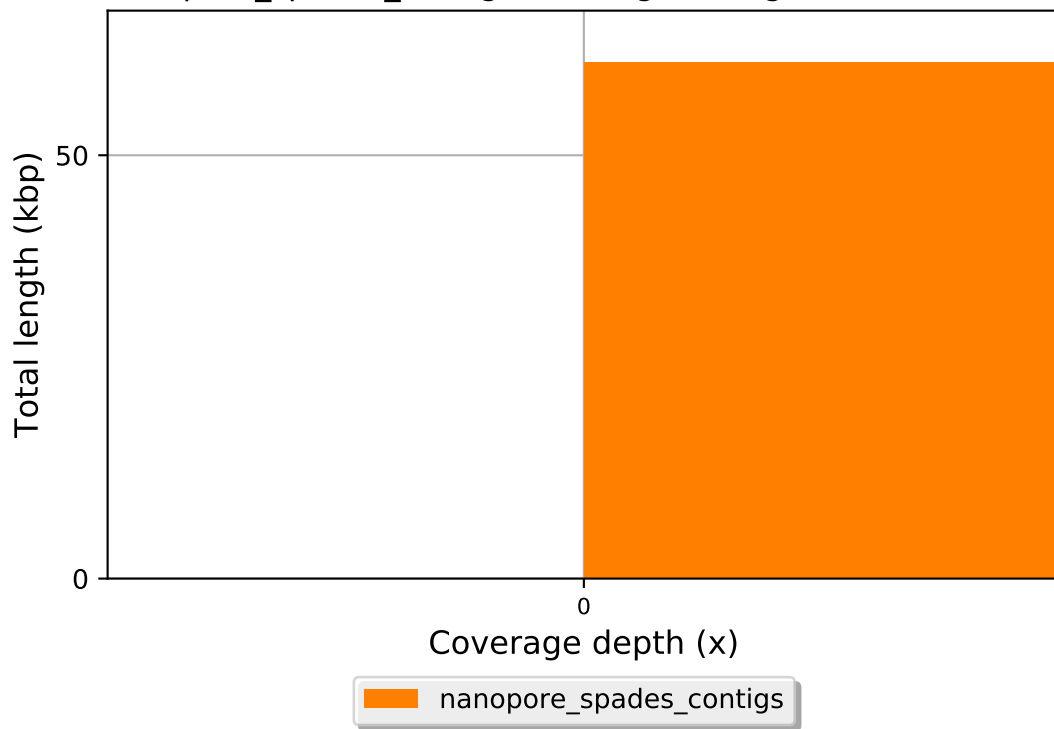


spades_low_contigs

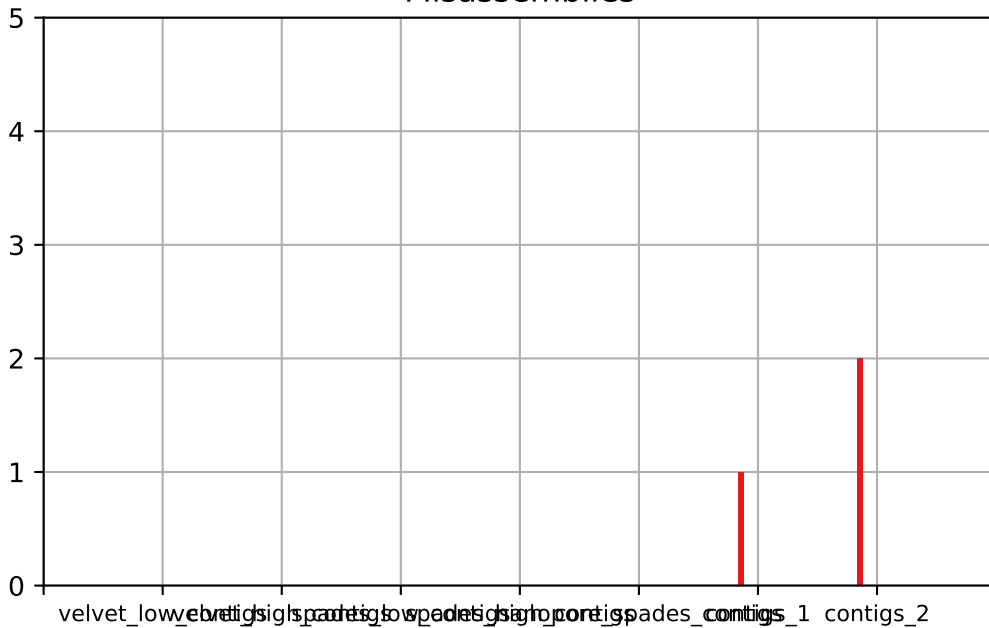
spades_high_contigs coverage histogram (bin size: 1x)



nanopore_spades_contigs coverage histogram (bin size: 1x)

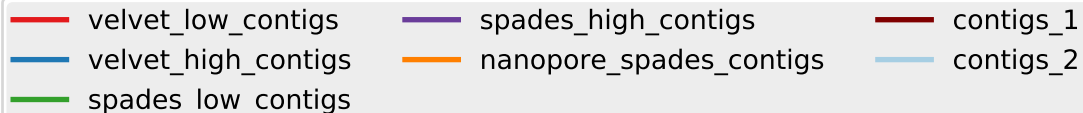
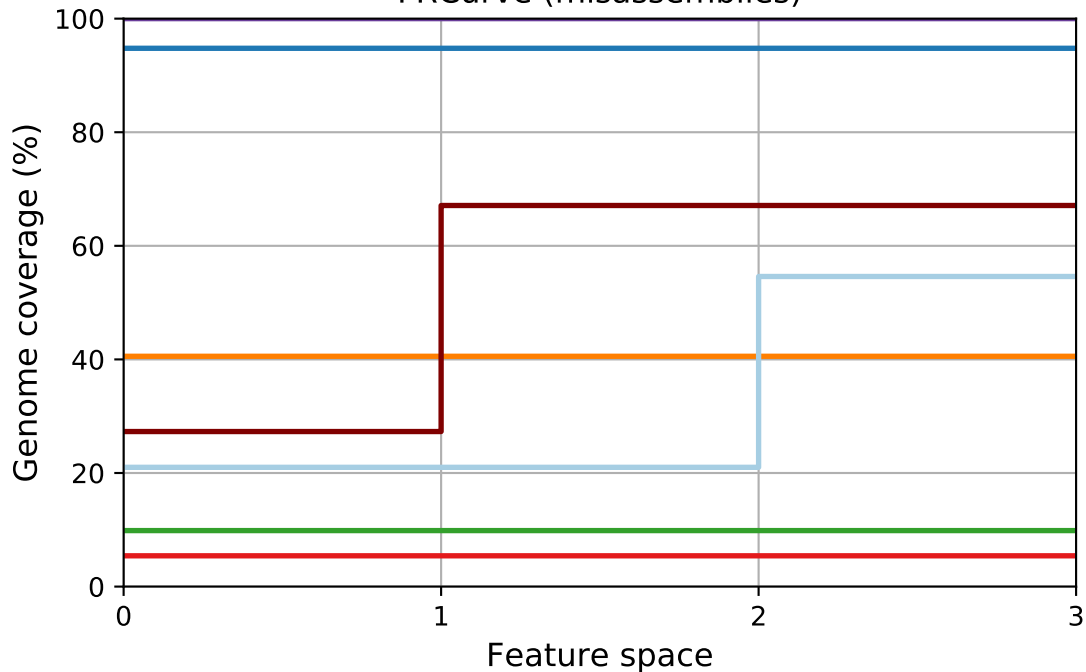


Misassemblies

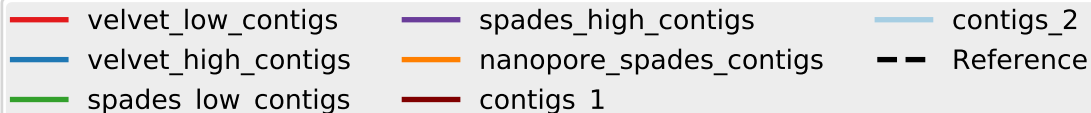
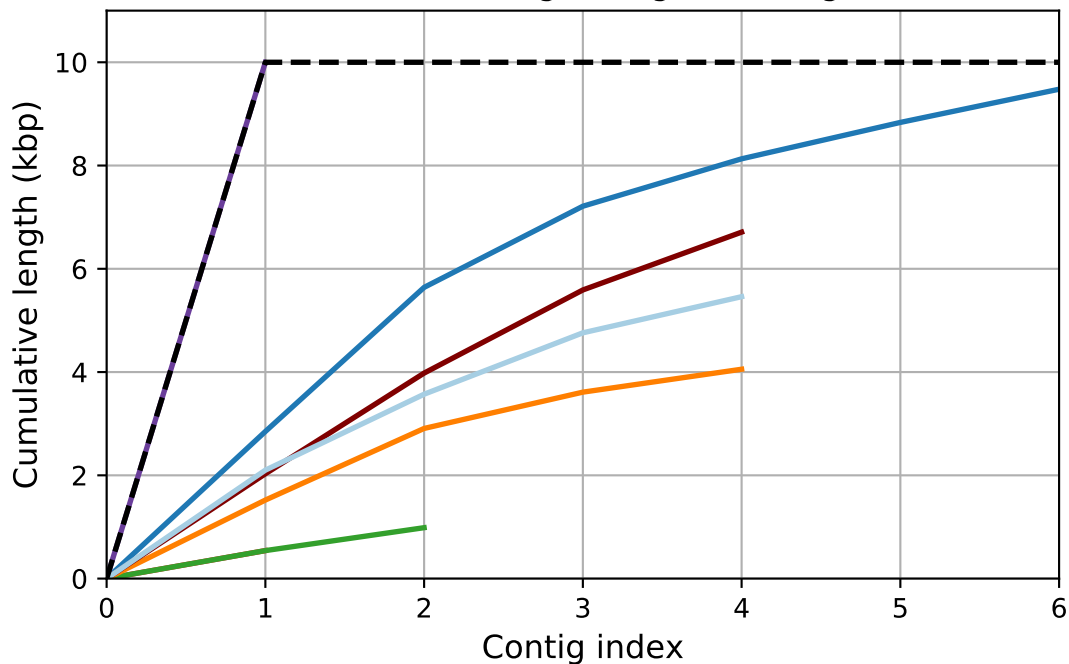


 # relocations

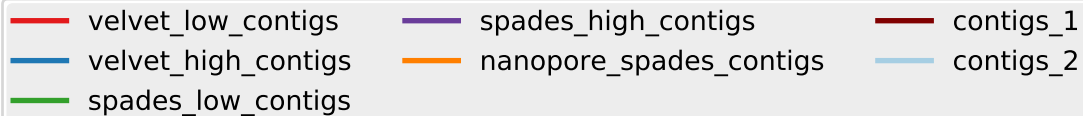
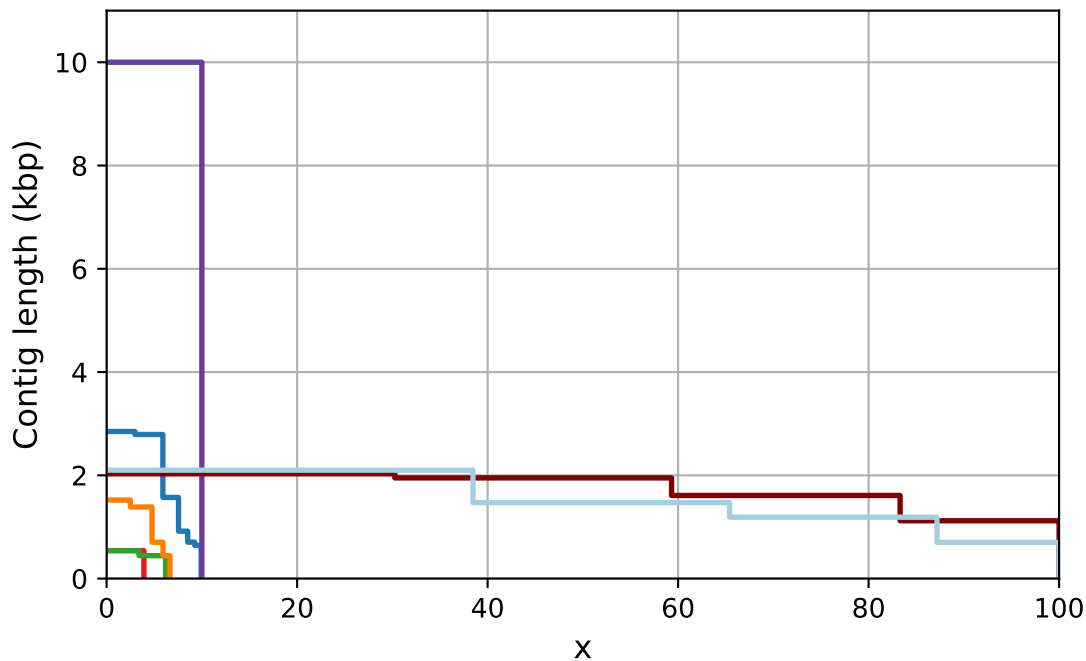
FRCurve (misassemblies)



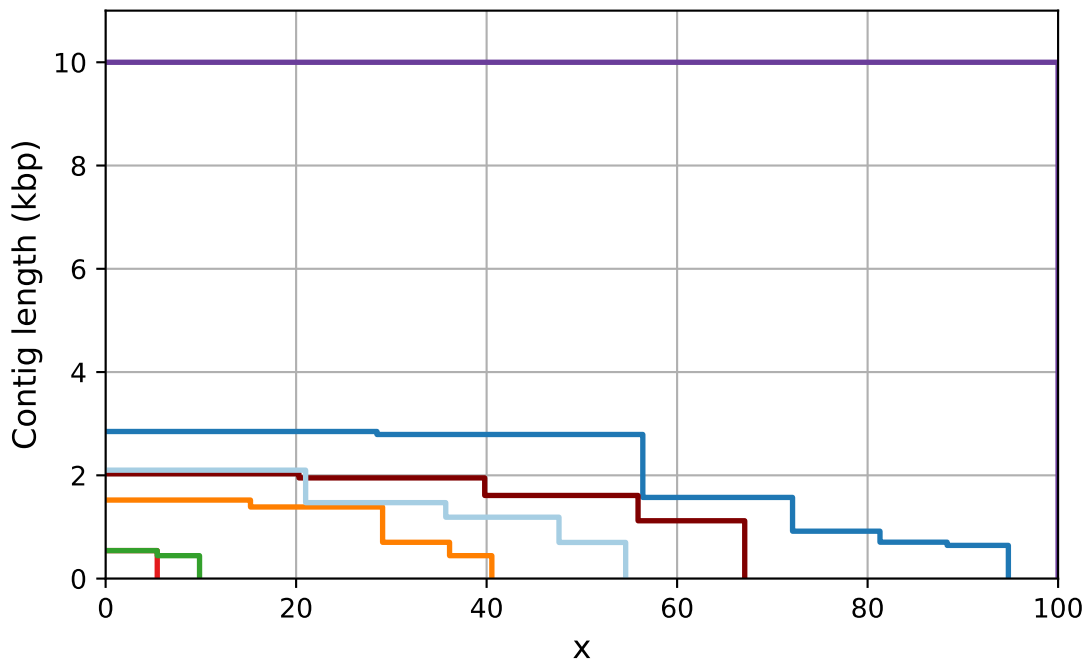
Cumulative length (aligned contigs)



NAx

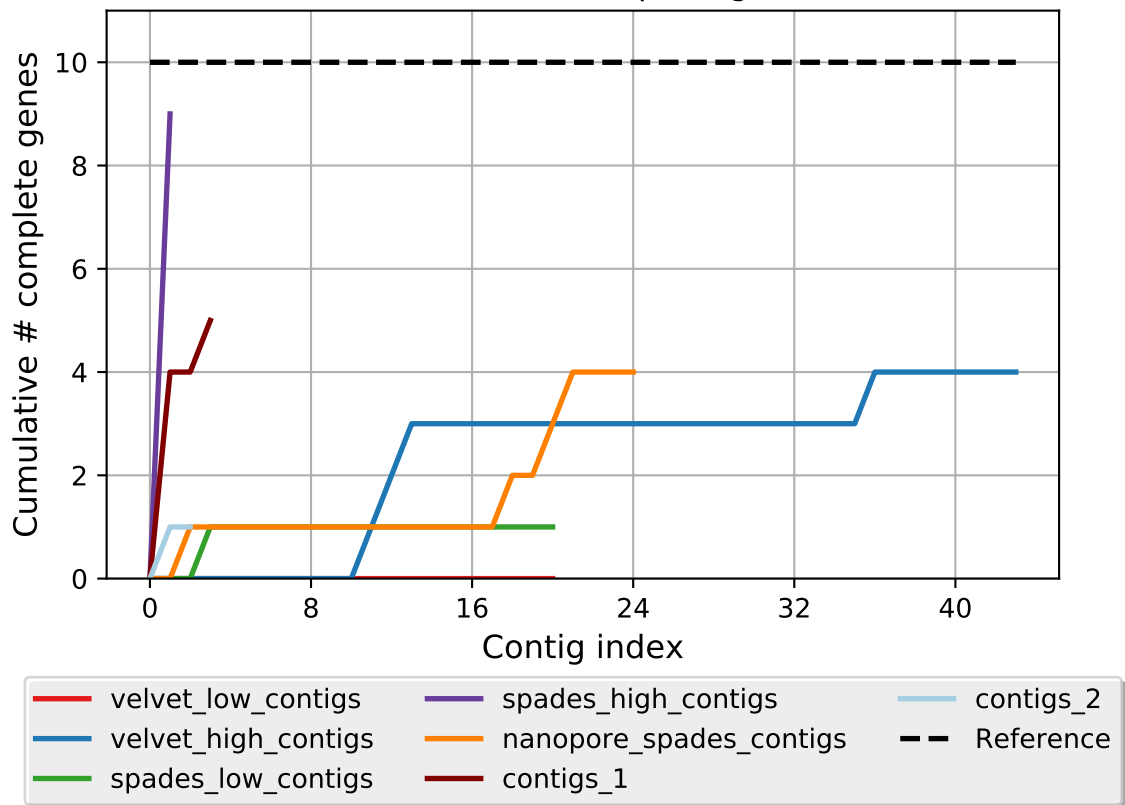


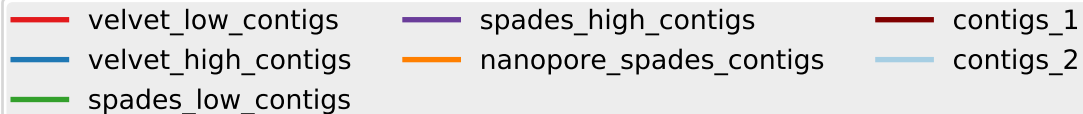
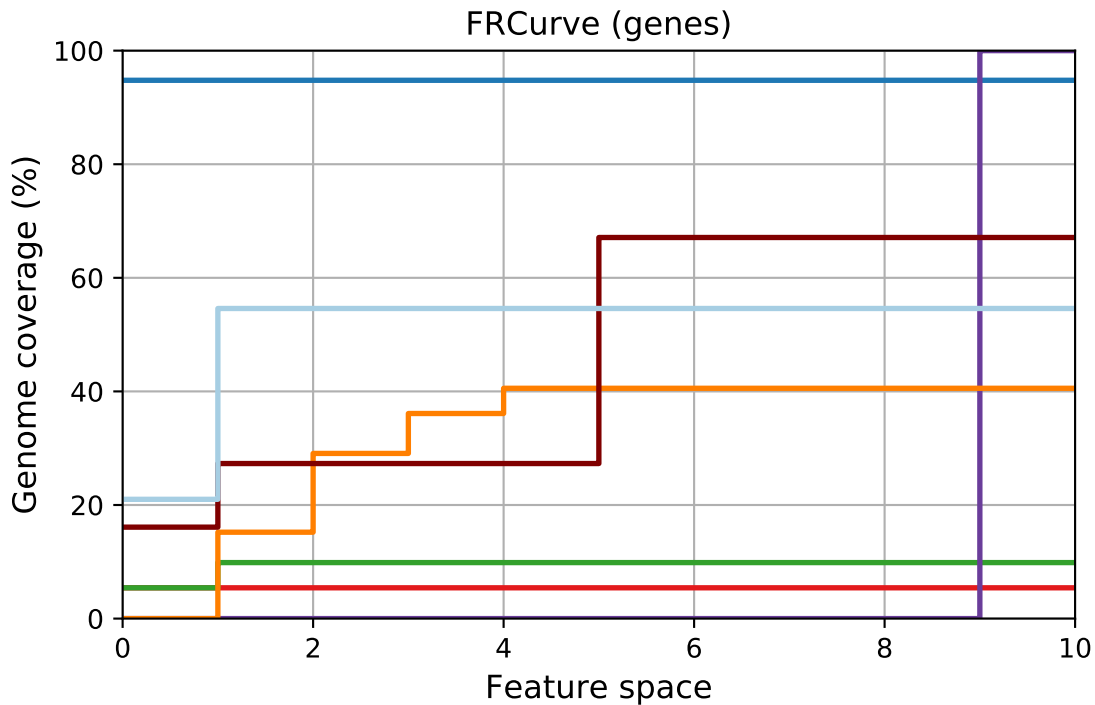
NGAx



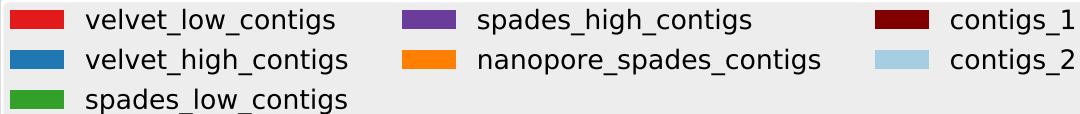
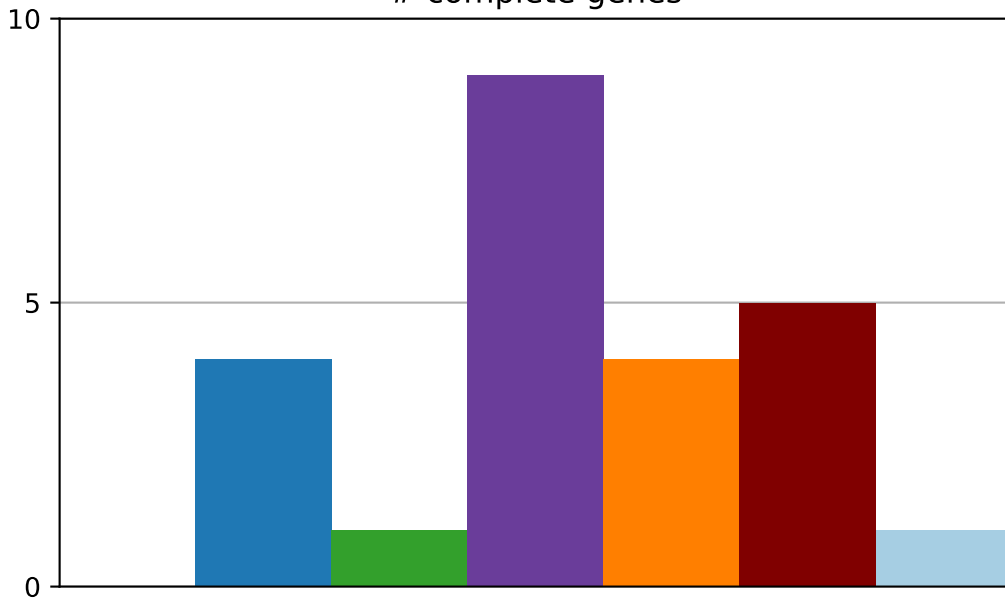
- velvet_low_contigs
- velvet_high_contigs
- spades_low_contigs
- spades_high_contigs
- nanopore_spades_contigs
- contigs_1
- contigs_2

Cumulative # complete genes

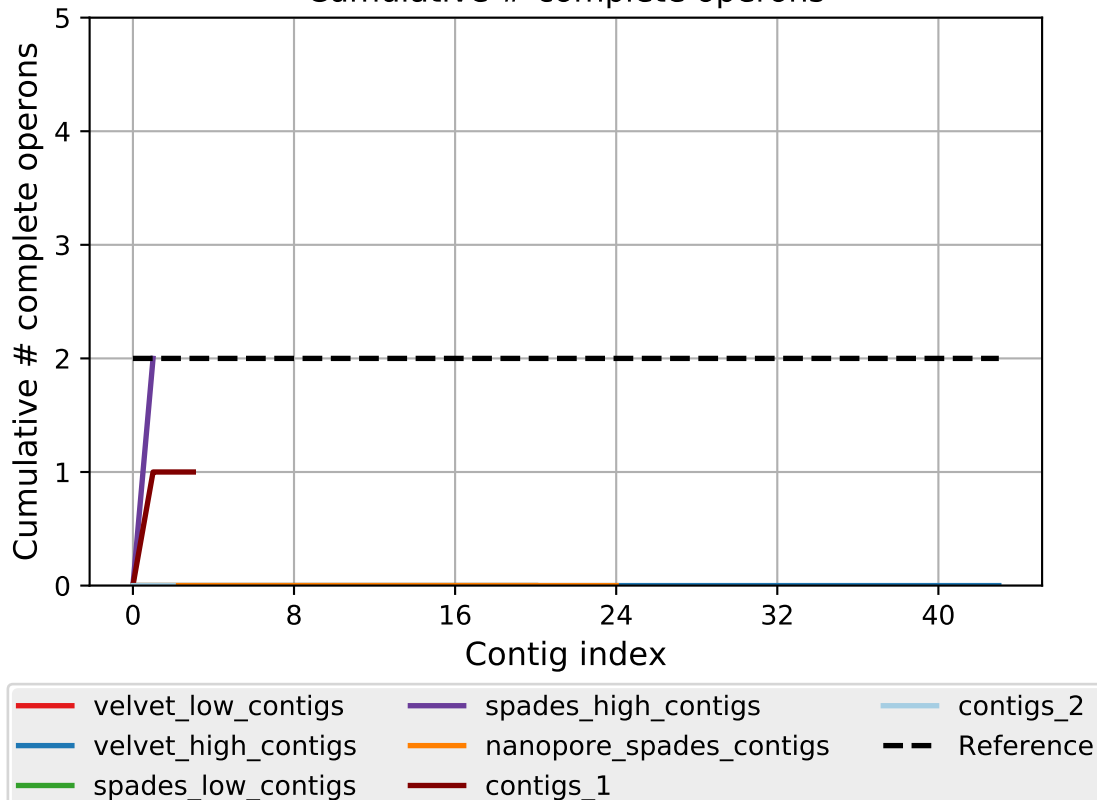




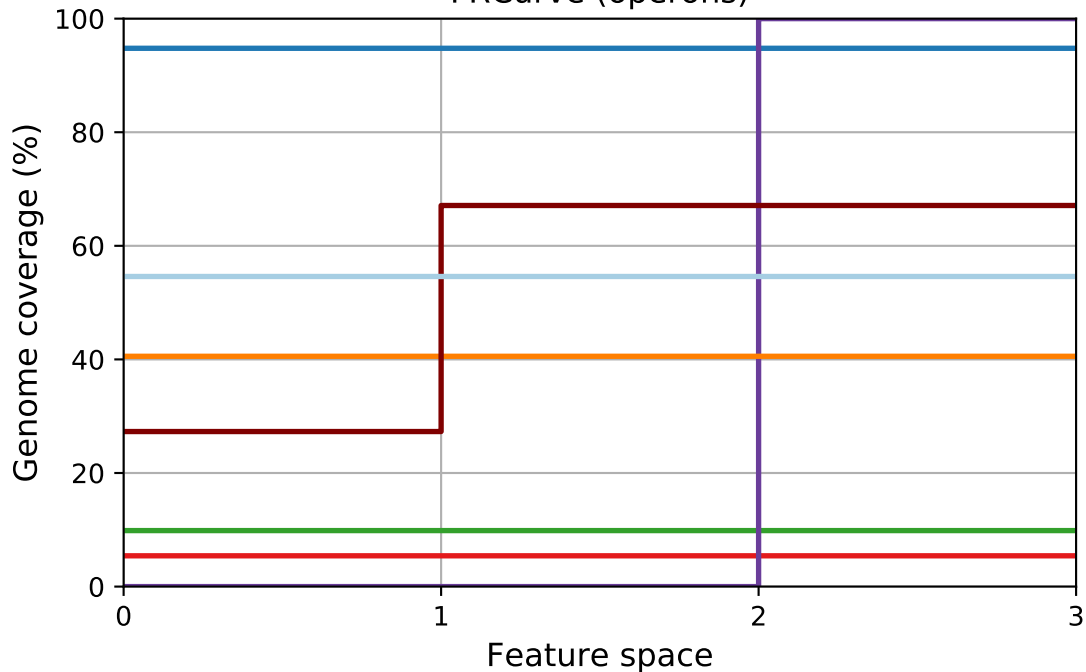
complete genes



Cumulative # complete operons

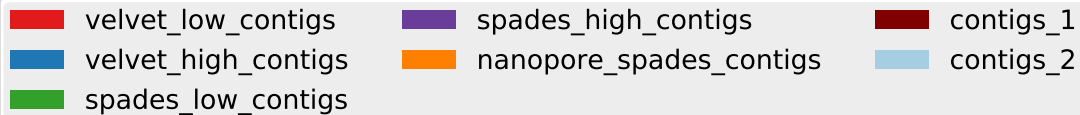
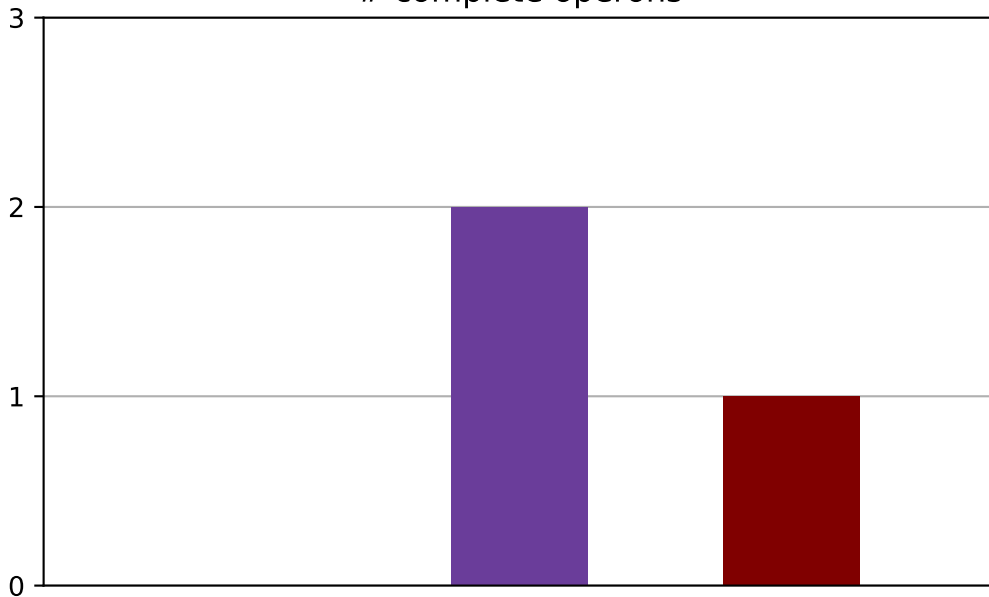


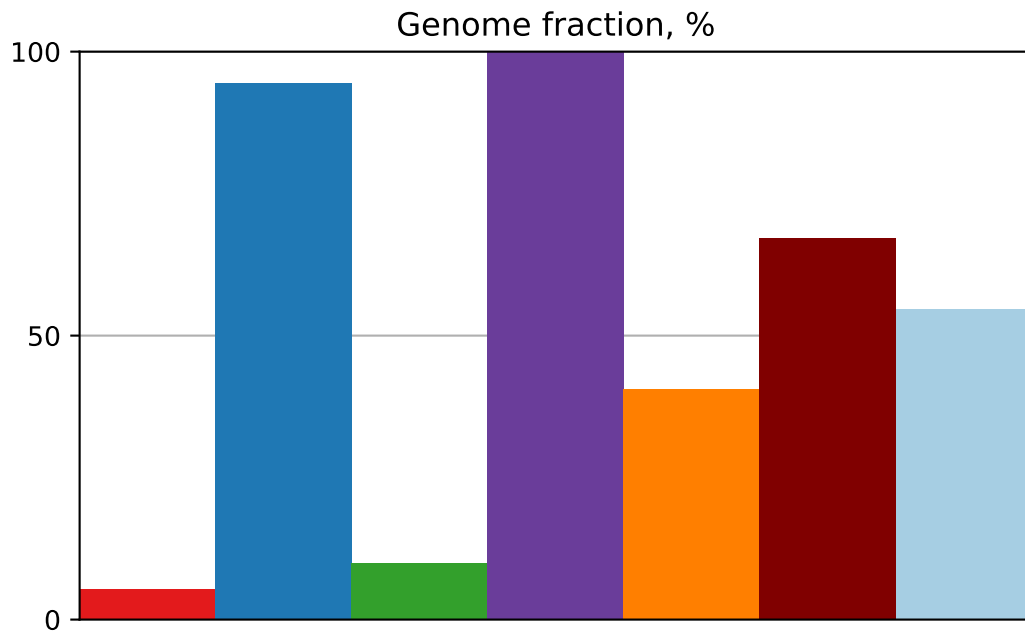
FRCurve (operons)



- velvet_low_contigs
- spades_high_contigs
- contigs_1
- velvet_high_contigs
- nanopore_spades_contigs
- contigs_2
- spades_low_contigs

complete operons





velvet_low_contigs

velvet_high_contigs

spades_low_contigs

spades_high_contigs

nanopore_spades_contigs

contigs_1

contigs_2