

# Report

	velvet_high_contigs	spades_nanopore_contigs	spades_high_contigs	velvet_low	spades_low
# contigs (>= 0 bp)	11	65	1	305	128
# contigs (>= 1000 bp)	7	20	1	0	4
# contigs (>= 5000 bp)	7	3	1	0	0
# contigs (>= 10000 bp)	4	0	1	0	0
# contigs (>= 25000 bp)	1	0	1	0	0
# contigs (>= 50000 bp)	0	0	1	0	0
Total length (>= 0 bp)	100061	72814	100000	56973	49818
Total length (>= 1000 bp)	99562	58394	100000	0	5313
Total length (>= 5000 bp)	99562	19533	100000	0	0
Total length (>= 10000 bp)	81134	0	100000	0	0
Total length (>= 25000 bp)	33235	0	100000	0	0
Total length (>= 50000 bp)	0	0	100000	0	0
# contigs	7	24	1	11	20
Largest contig	33235	6735	100000	998	1737
Total length	99562	61012	100000	7243	15922
Reference length	4639675	4639675	4639675	4639675	4639675
GC (%)	52.58	52.37	52.59	50.71	51.21
Reference GC (%)	50.79	50.79	50.79	50.79	50.79
N50	19911	3698	100000	632	718
N75	13440	1843	100000	542	635
L50	2	6	1	5	8
L75	4	12	1	8	13
# misassemblies	0	1	0	0	1
# misassembled contigs	0	1	0	0	1
Misassembled contigs length	0	1084	0	0	1084
# local misassemblies	0	0	0	0	0
# unaligned mis. contigs	0	0	0	0	0
# unaligned contigs	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part
Unaligned length	0	0	0	0	0
Genome fraction (%)	2.144	1.319	2.155	0.156	0.343
Duplication ratio	1.001	0.997	1.000	1.000	1.000
# N's per 100 kbp	0.00	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	0.00	14.70	0.00	0.00	31.40
# indels per 100 kbp	0.00	313.68	0.00	0.00	0.00
Largest alignment	33235	6735	100000	998	1737
Total aligned length	99562	61012	100000	7243	15922
NA50	19911	3698	100000	632	715
NGA50	-	-	-	-	-
NA75	13440	1843	100000	542	587
LA50	2	6	1	5	8
LA75	4	12	1	8	14

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

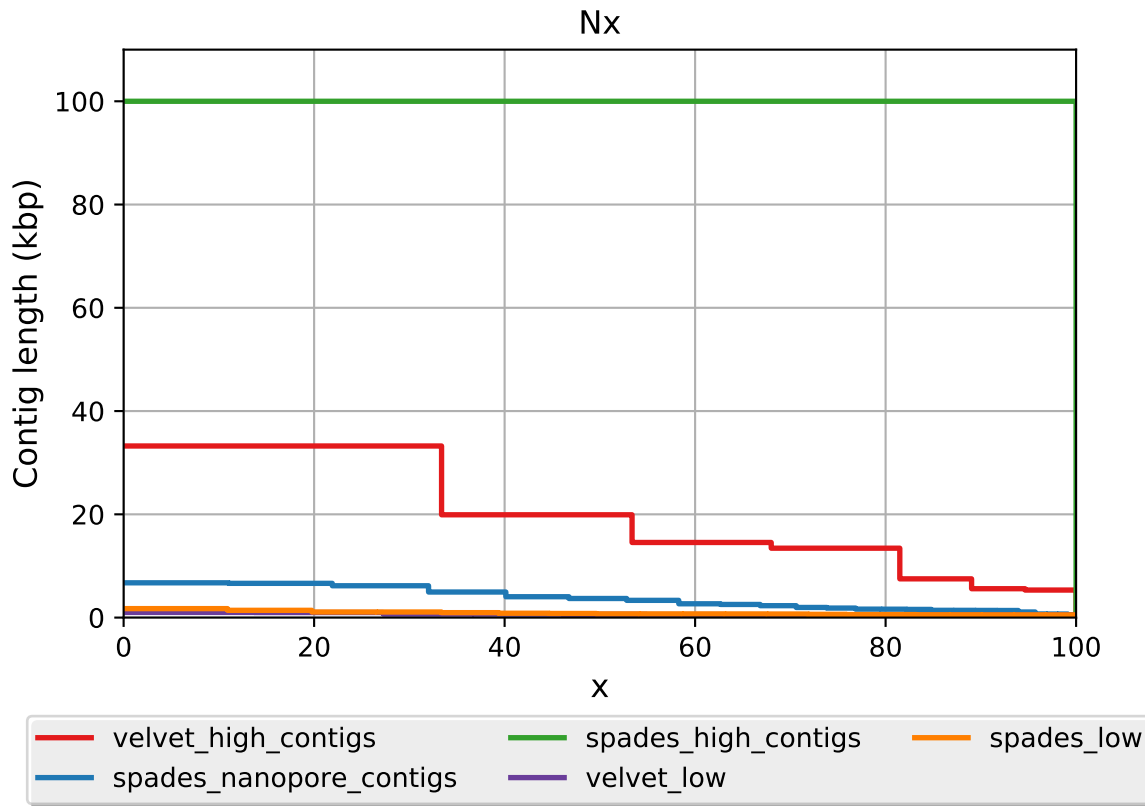
	velvet_high_contigs	spades_nanopore_contigs	spades_high_contigs	velvet_low	spades_low
# misassemblies	0	1	0	0	1
# relocations	0	1	0	0	1
# translocations	0	0	0	0	0
# inversions	0	0	0	0	0
# misassembled contigs	0	1	0	0	1
Misassembled contigs length	0	1084	0	0	1084
# local misassemblies	0	0	0	0	0
# unaligned mis. contigs	0	0	0	0	0
# mismatches	0	9	0	0	5
# indels	0	192	0	0	0
# indels (<= 5 bp)	0	192	0	0	0
# indels (> 5 bp)	0	0	0	0	0
Indels length	0	234	0	0	0

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

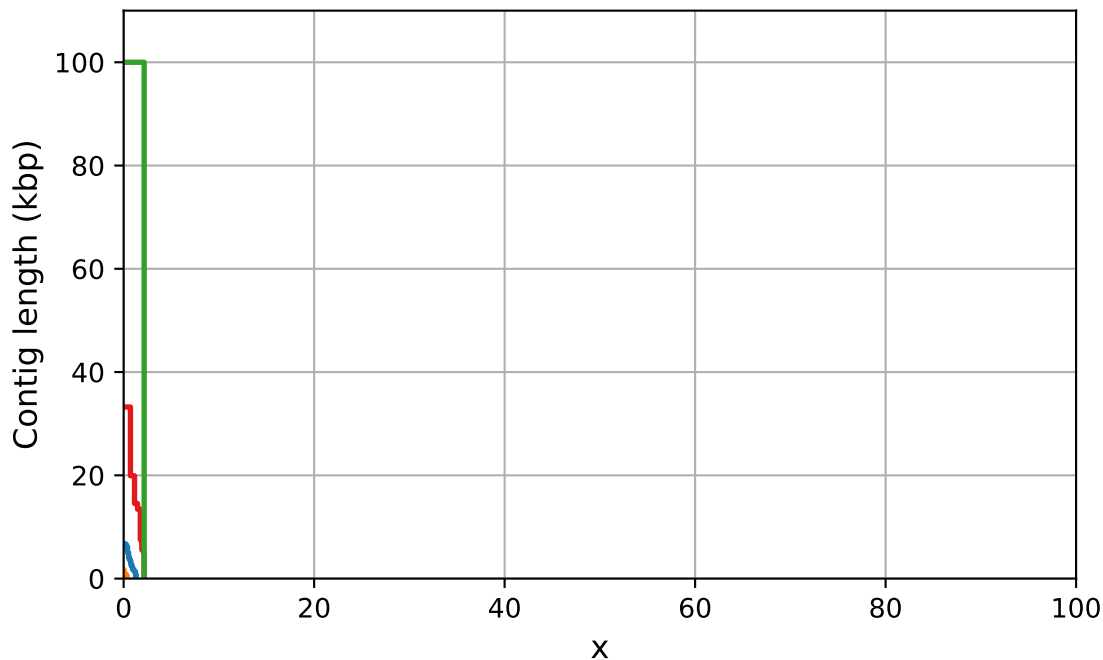
## Unaligned report

	velvet_high_contigs	spades_nanopore_contigs	spades_high_contigs	velvet_low	spades_low
# fully unaligned contigs	0	0	0	0	0
Fully unaligned length	0	0	0	0	0
# partially unaligned contigs	0	0	0	0	0
Partially unaligned length	0	0	0	0	0
# N's	0	0	0	0	0

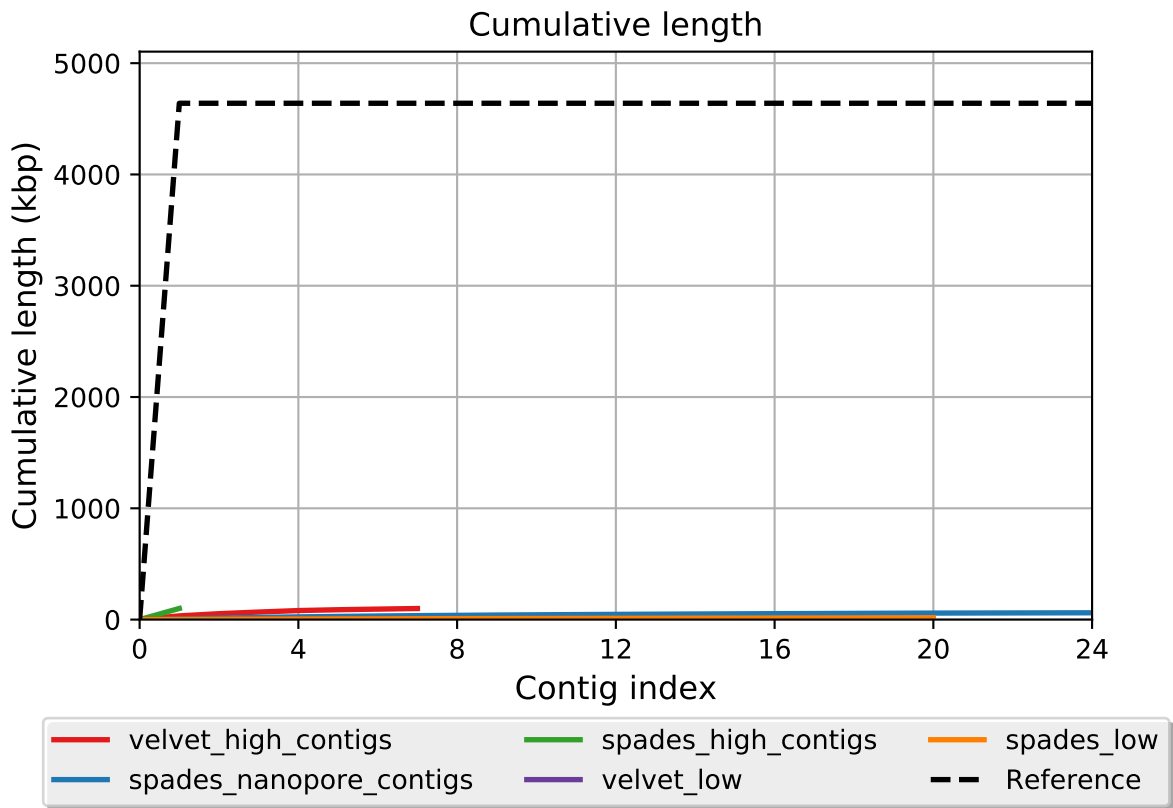
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



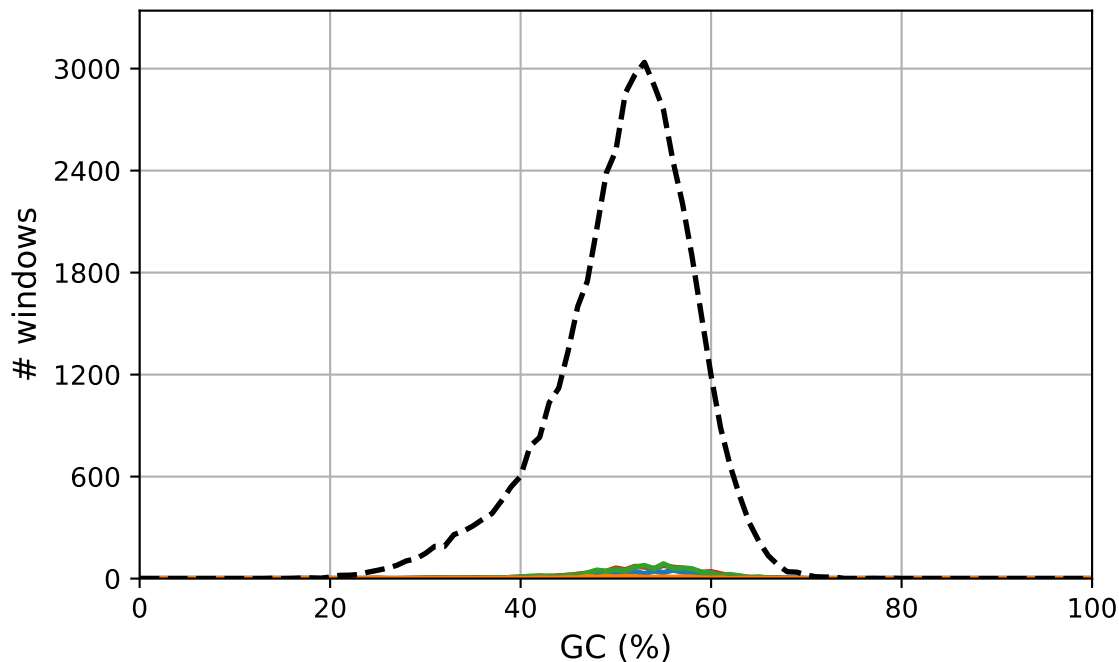
# NGx



— velvet\_high\_contigs — spades\_high\_contigs — spades\_low  
— spades\_nanopore\_contigs — velvet\_low

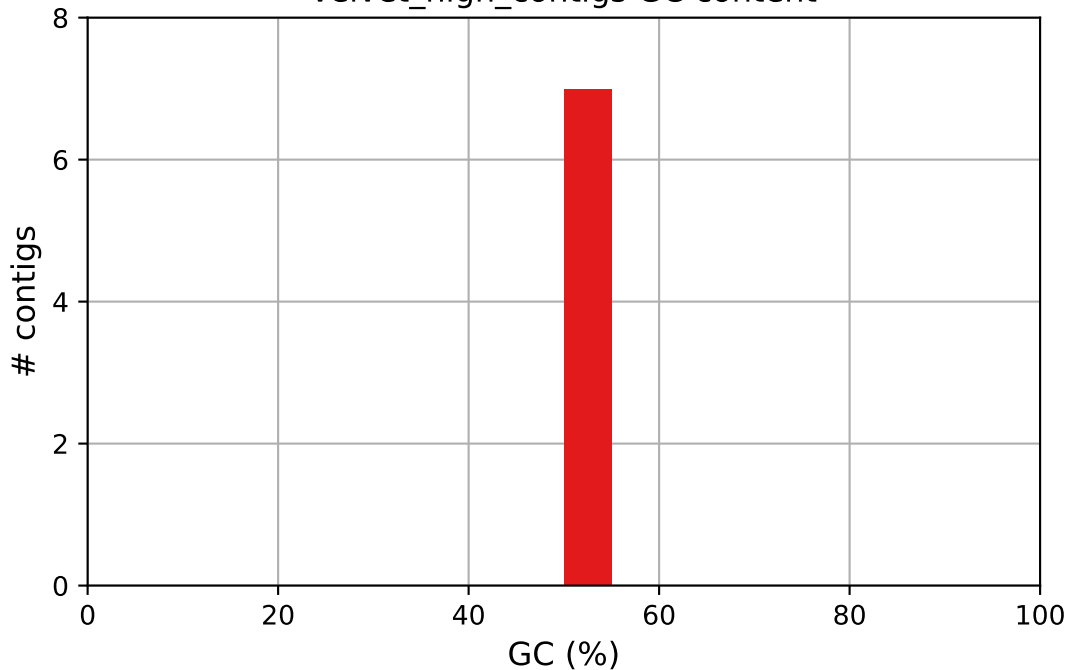


GC content



— velvet_high_contigs	— spades_high_contigs	— spades_low
— spades_nanopore_contigs	— velvet_low	— Reference

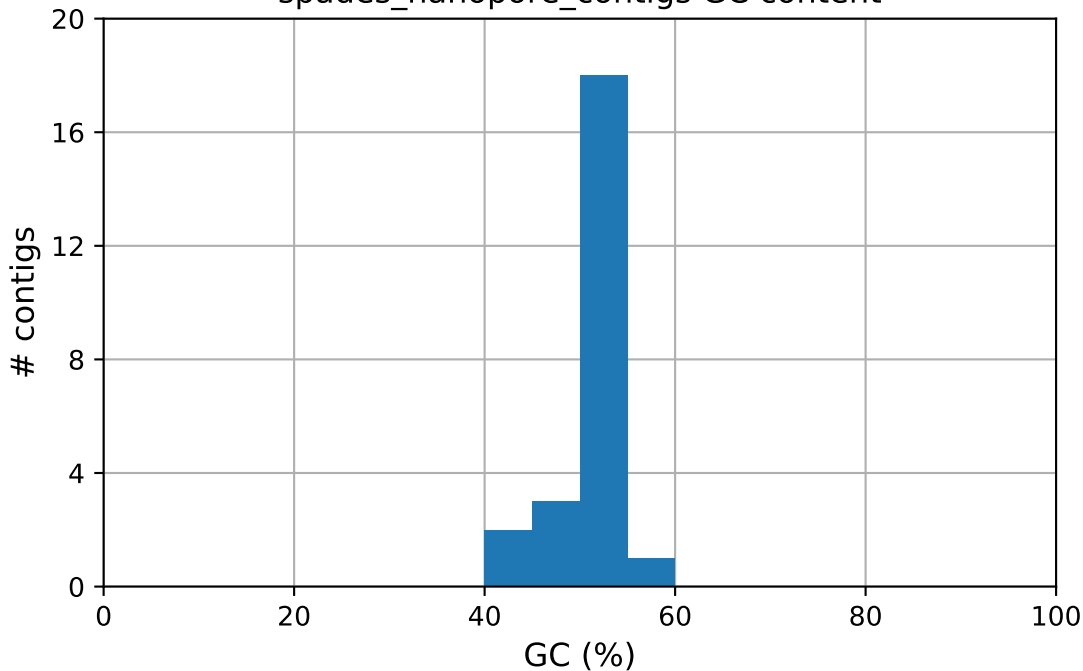
velvet\_high\_contigs GC content



■ velvet\_high\_contigs

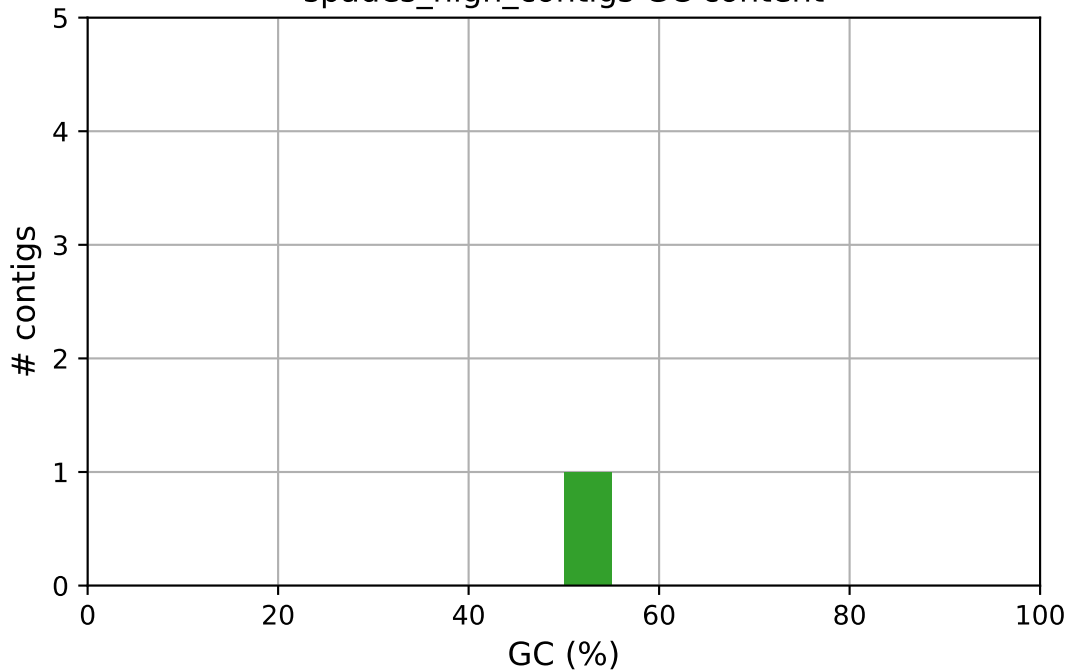


spades\_nanopore\_contigs GC content



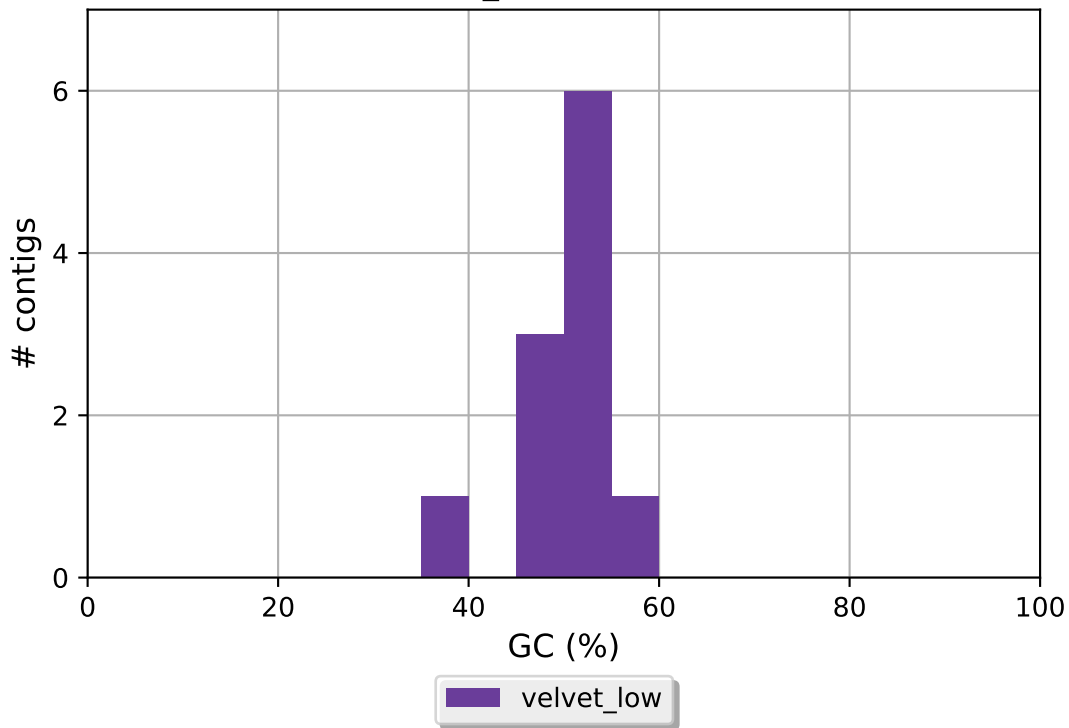
spades\_nanopore\_contigs

spades\_high\_contigs GC content

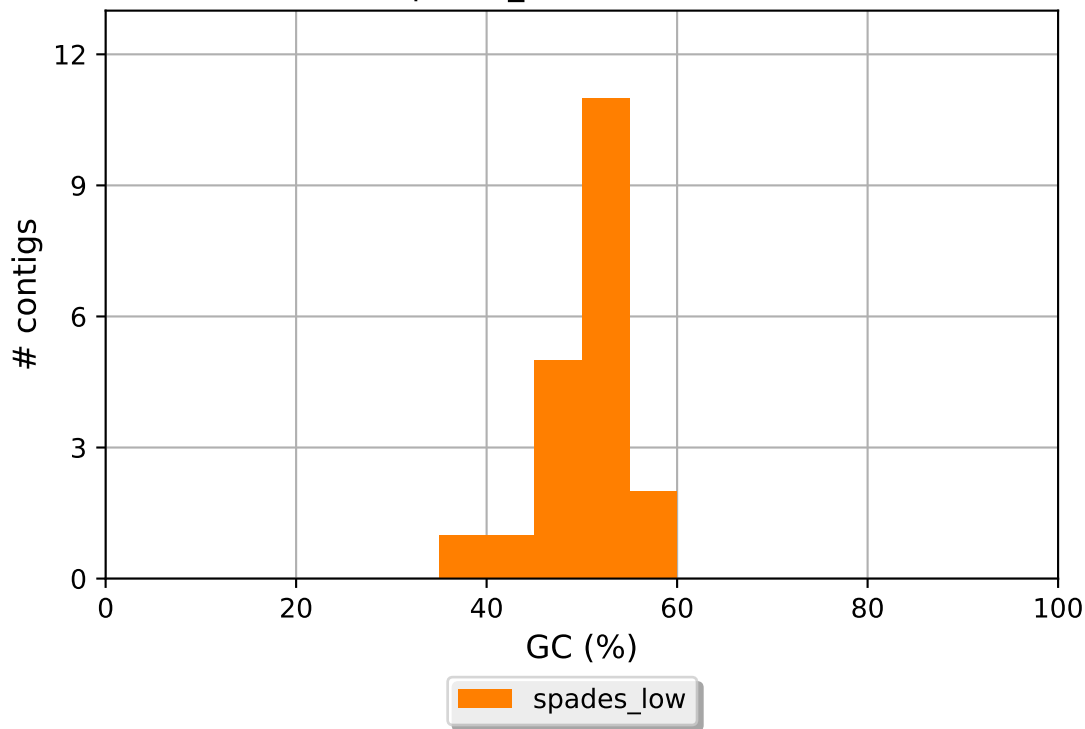


spades\_high\_contigs

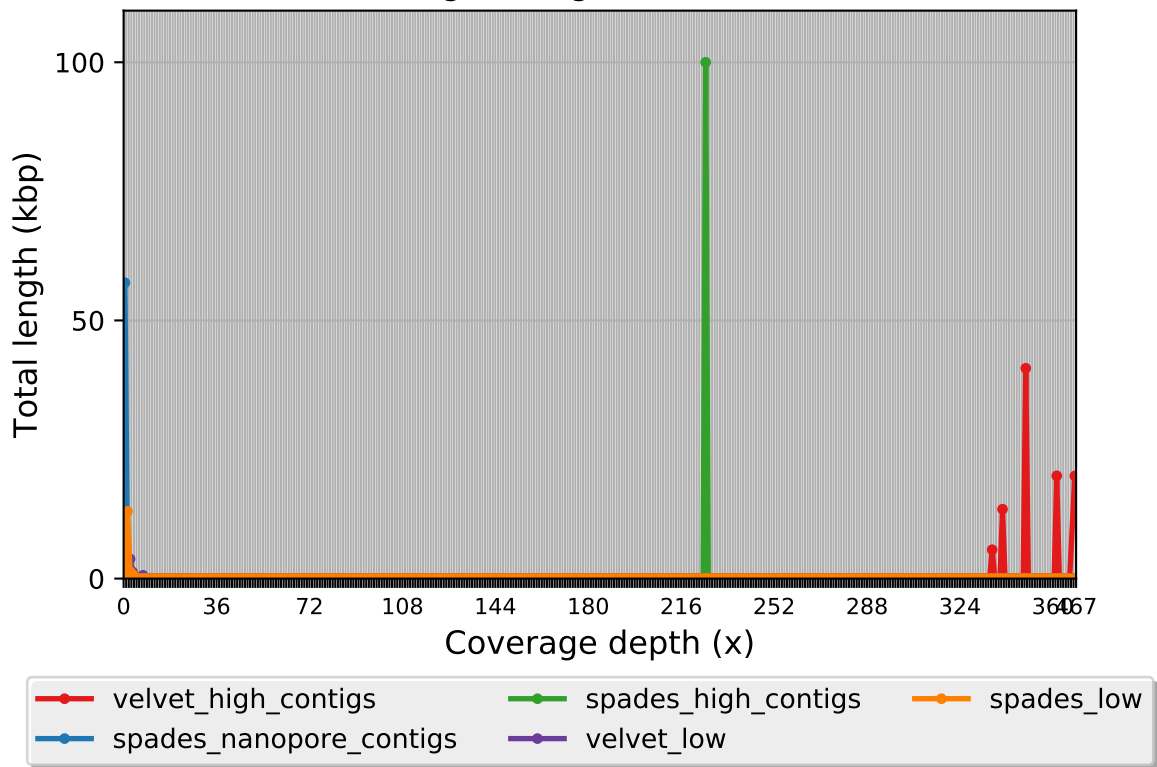
velvet\_low GC content



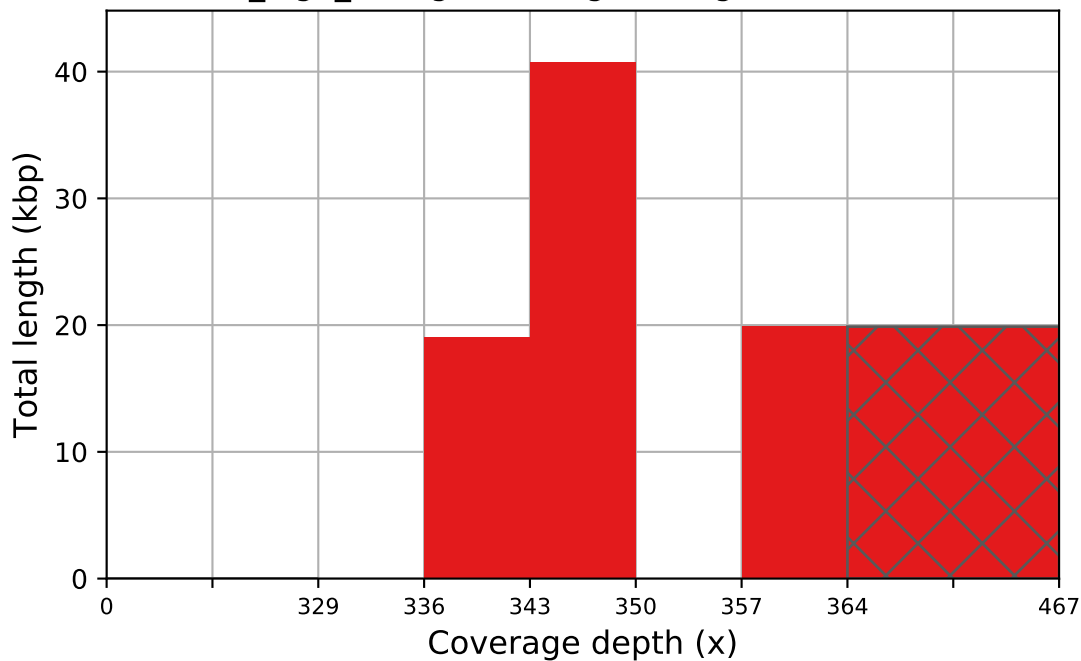
spades\_low GC content



Coverage histogram (bin size: 1x)

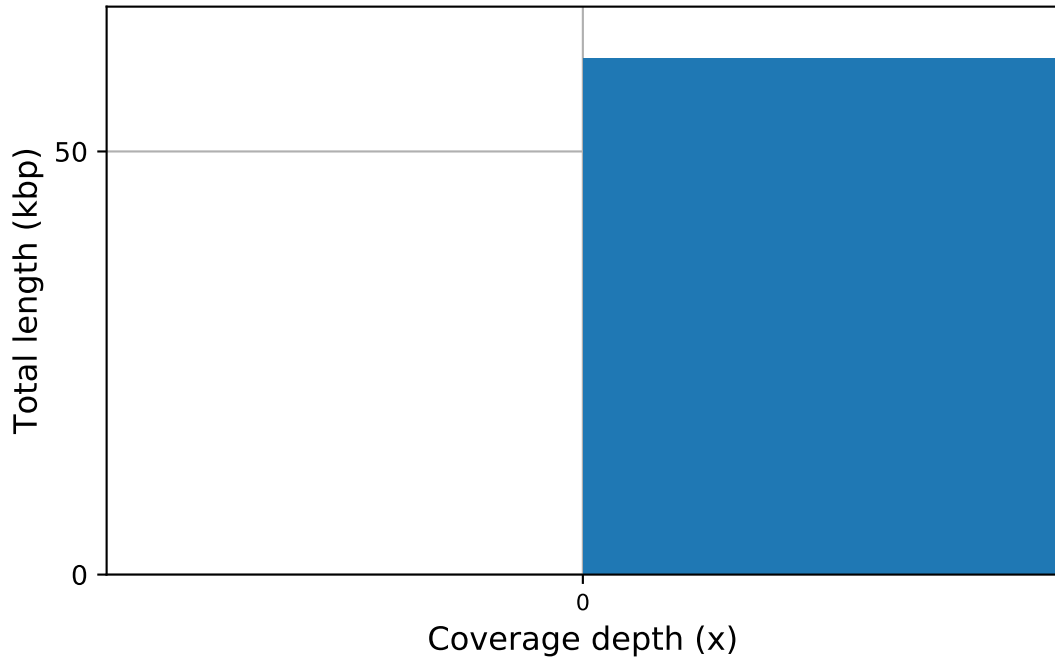


velvet\_high\_contigs coverage histogram (bin size: 7x)



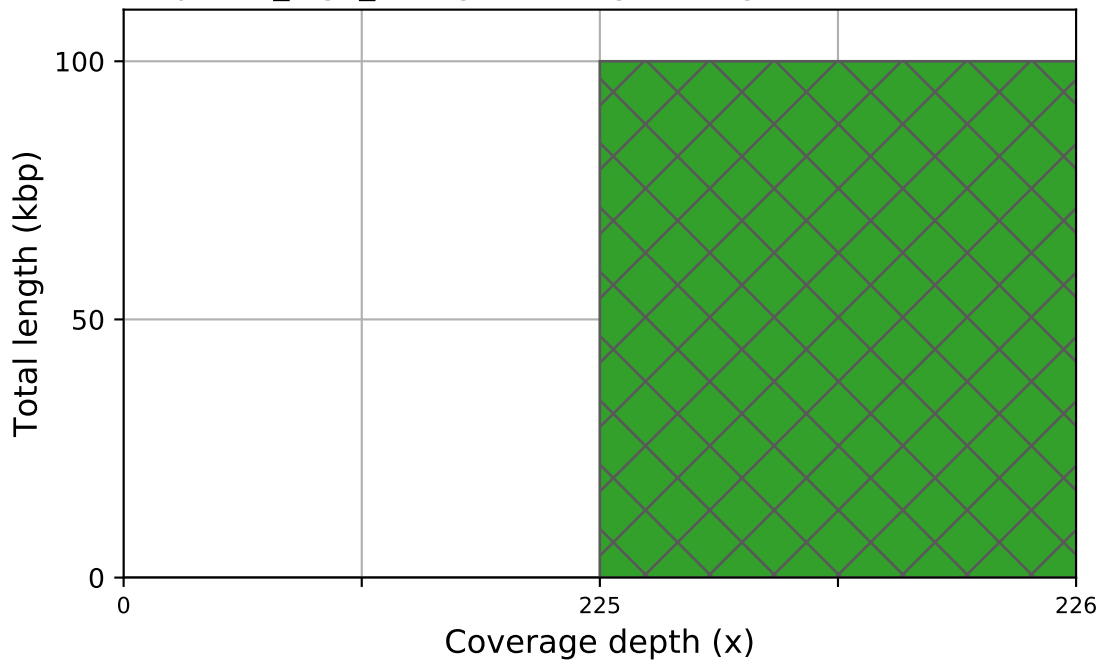
■ velvet\_high\_contigs

spades\_nanopore\_contigs coverage histogram (bin size: 1x)



spades\_nanopore\_contigs

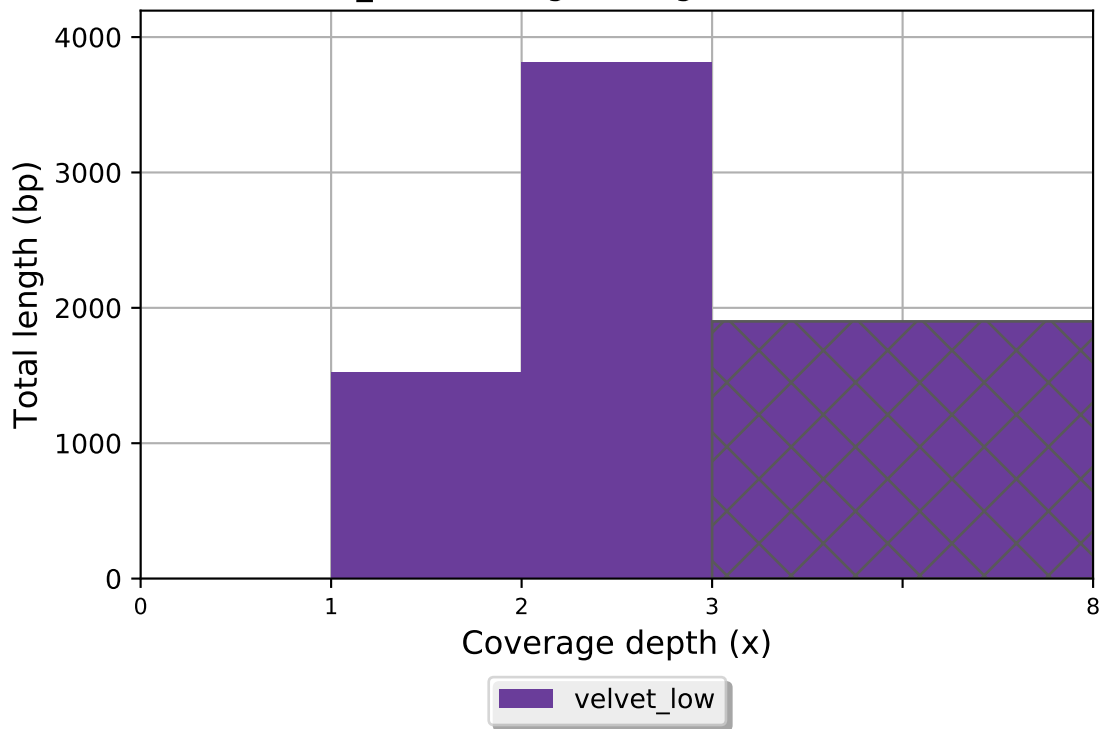
spades\_high\_contigs coverage histogram (bin size: 1x)



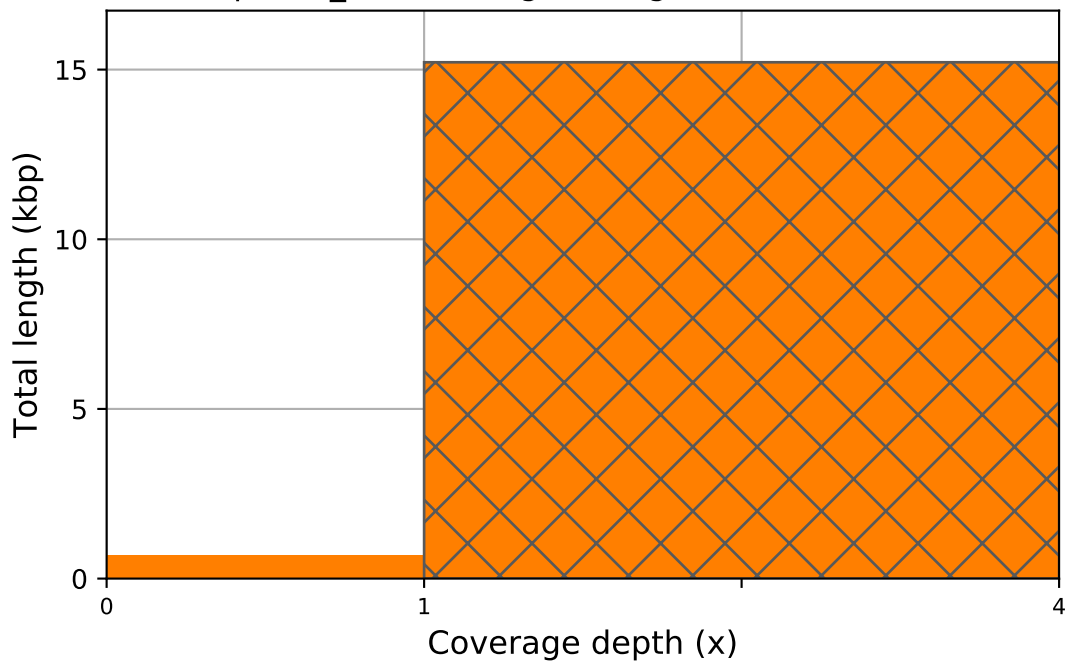
spades\_high\_contigs



velvet\_low coverage histogram (bin size: 1x)

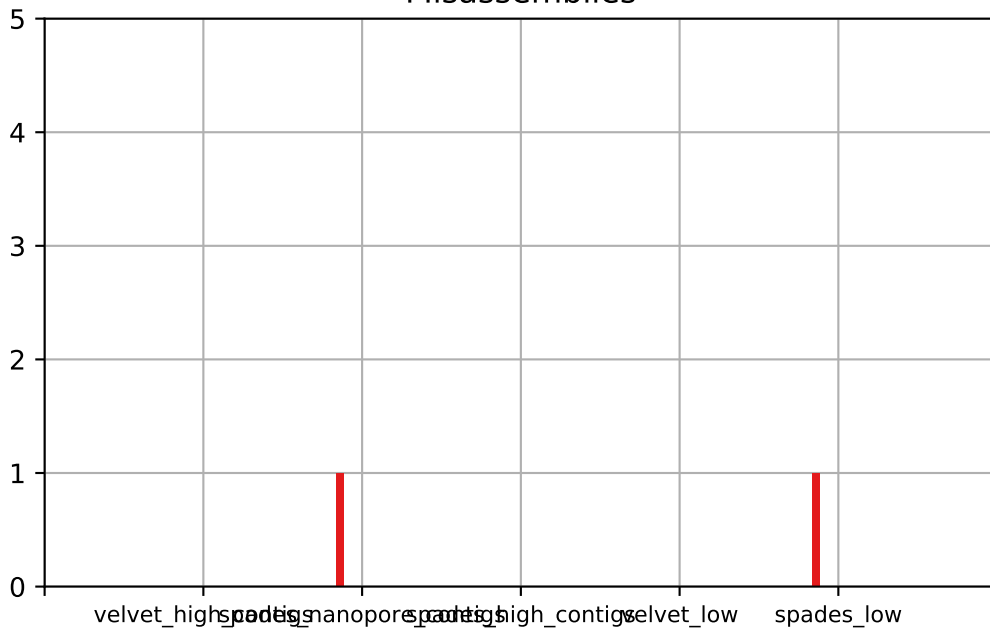


spades\_low coverage histogram (bin size: 1x)

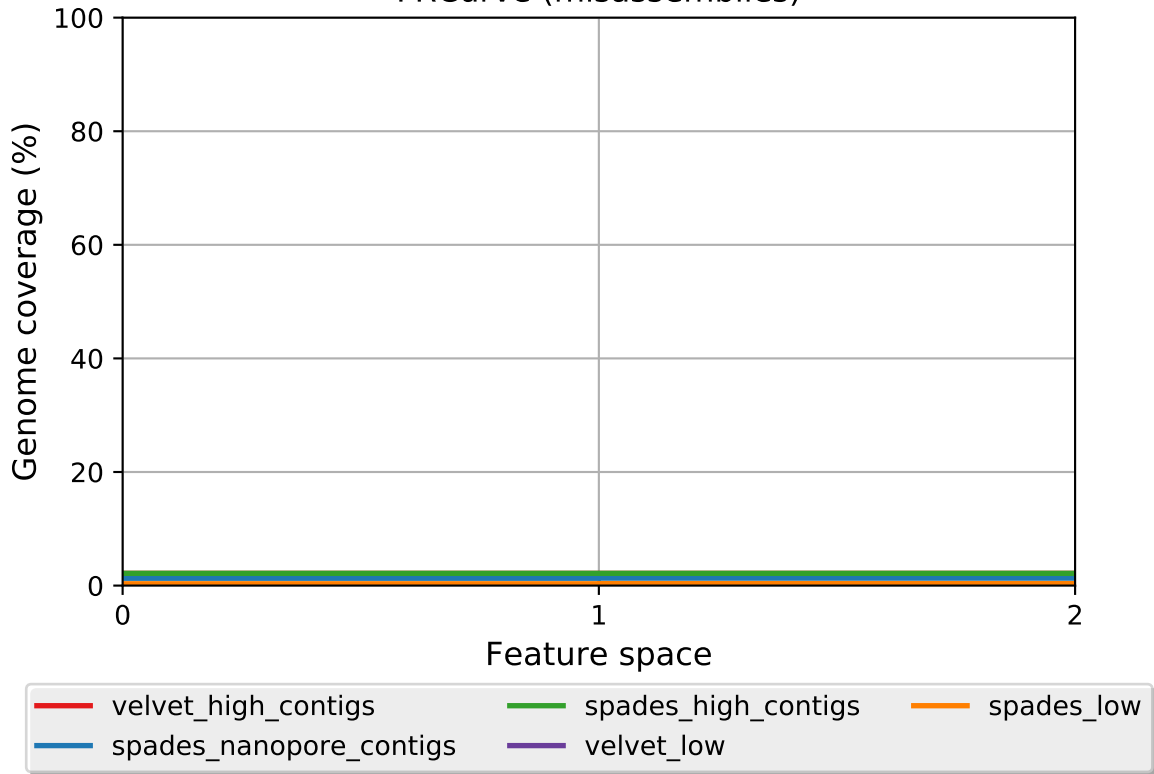


spades\_low

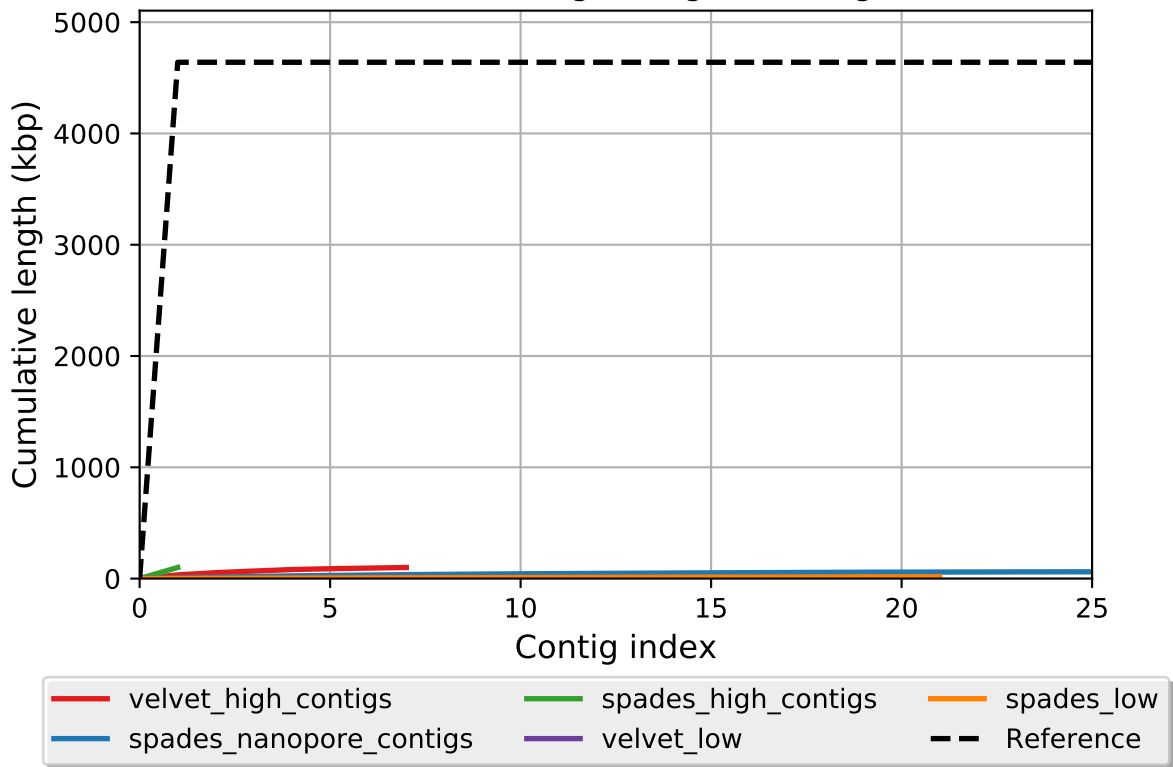
## Misassemblies



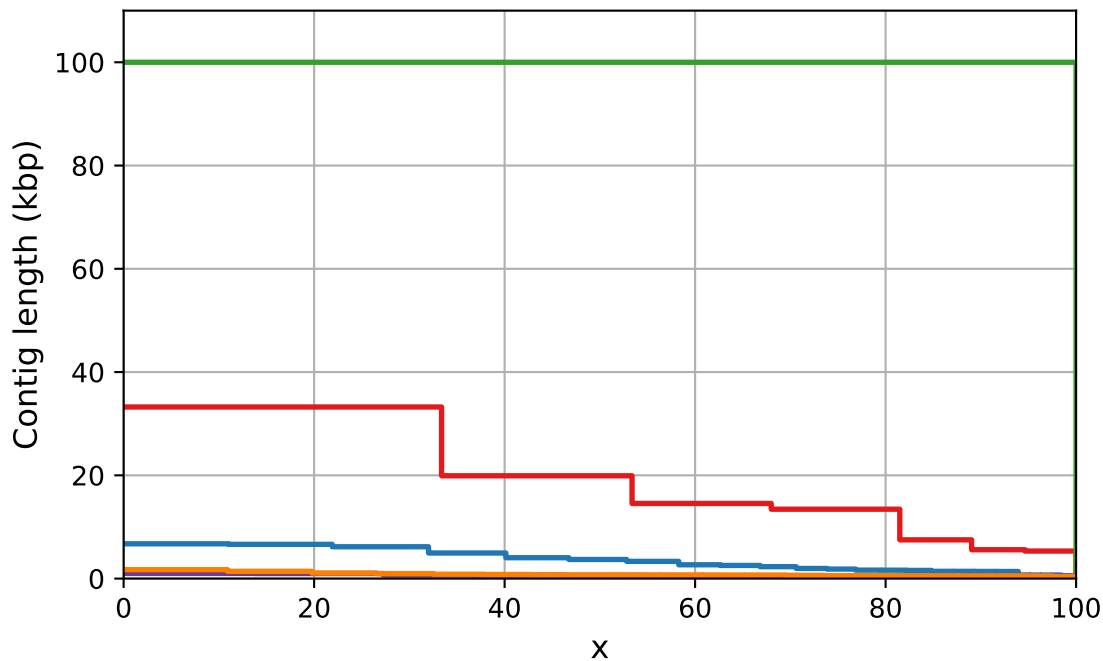
FRCurve (misassemblies)



Cumulative length (aligned contigs)

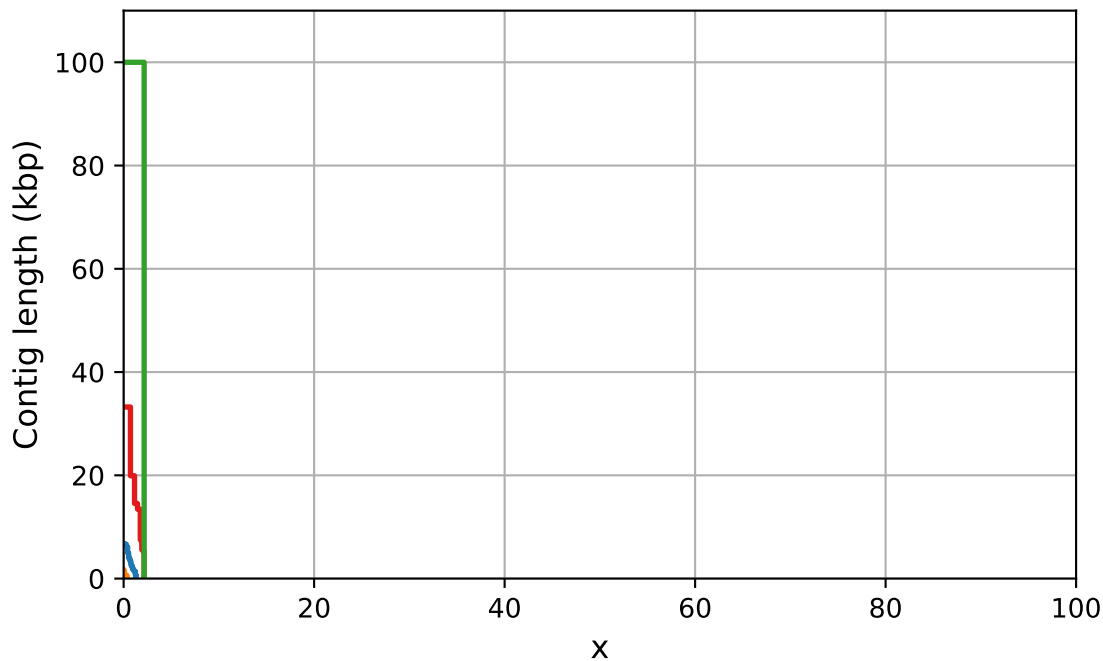


NAx



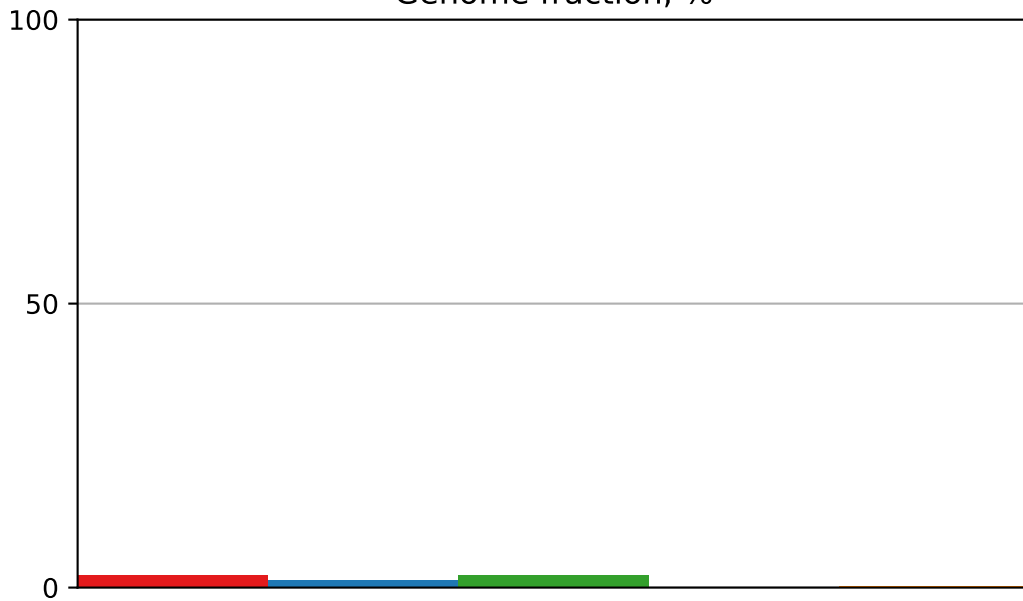
— velvet\_high\_contigs — spades\_high\_contigs — spades\_low  
— spades\_nanopore\_contigs — velvet\_low

# NGAx



— velvet\_high\_contigs — spades\_high\_contigs — spades\_low  
— spades\_nanopore\_contigs — velvet\_low

Genome fraction, %



velvet_high_contigs	spades_high_contigs	spades_low
spades_nanopore_contigs	velvet_low	