

## Report

	Spades_Assem_contigs	Spades_h_Assem_contigs	velvet_Assem_contigs	velvet_h_Assem_contigs
# contigs (>= 0 bp)	128	1	305	16
# contigs (>= 1000 bp)	4	1	0	7
# contigs (>= 5000 bp)	0	1	0	7
# contigs (>= 10000 bp)	0	1	0	4
# contigs (>= 25000 bp)	0	1	0	1
# contigs (>= 50000 bp)	0	1	0	0
Total length (>= 0 bp)	49819	100000	56973	100309
Total length (>= 1000 bp)	5313	100000	0	99584
Total length (>= 5000 bp)	0	100000	0	99584
Total length (>= 10000 bp)	0	100000	0	81134
Total length (>= 25000 bp)	0	100000	0	33235
Total length (>= 50000 bp)	0	100000	0	0
# contigs	20	1	11	7
Largest contig	1737	100000	998	33235
Total length	15923	100000	7243	99584
Reference length	4639675	4639675	4639675	4639675
GC (%)	51.21	52.59	50.71	52.58
Reference GC (%)	50.79	50.79	50.79	50.79
N50	718	100000	632	19911
N75	635	100000	542	13440
L50	8	1	5	2
L75	13	1	8	4
# misassemblies	1	0	0	0
# misassembled contigs	1	0	0	0
Misassembled contigs length	1084	0	0	0
# local misassemblies	0	0	0	0
# unaligned contigs	0 + 0 part	0 + 0 part	0 + 0 part	0 + 0 part
Unaligned length	0	0	0	0
Genome fraction (%)	0.343	2.155	0.156	2.145
Duplication ratio	1.000	1.000	1.000	1.001
# N's per 100 kbp	0.00	0.00	0.00	0.00
# mismatches per 100 kbp	31.40	0.00	0.00	0.00
# indels per 100 kbp	0.00	0.00	0.00	0.00
Largest alignment	1737	100000	998	33235
Total aligned length	15923	100000	7243	99584
NA50	715	100000	632	19911
NGA50	-	-	-	-
NA75	587	100000	542	13440
LA50	8	1	5	2
LA75	14	1	8	4

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_Assem_contigs	Spades_h_Assem_contigs	velvet_Assem_contigs	velvet_h_Assem_contigs
# misassemblies	1	0	0	0
# relocations	1	0	0	0
# translocations	0	0	0	0
# inversions	0	0	0	0
# misassembled contigs	1	0	0	0
Misassembled contigs length	1084	0	0	0
# local misassemblies	0	0	0	0
# mismatches	5	0	0	0
# indels	0	0	0	0
# short indels	0	0	0	0
# long indels	0	0	0	0
Indels length	0	0	0	0

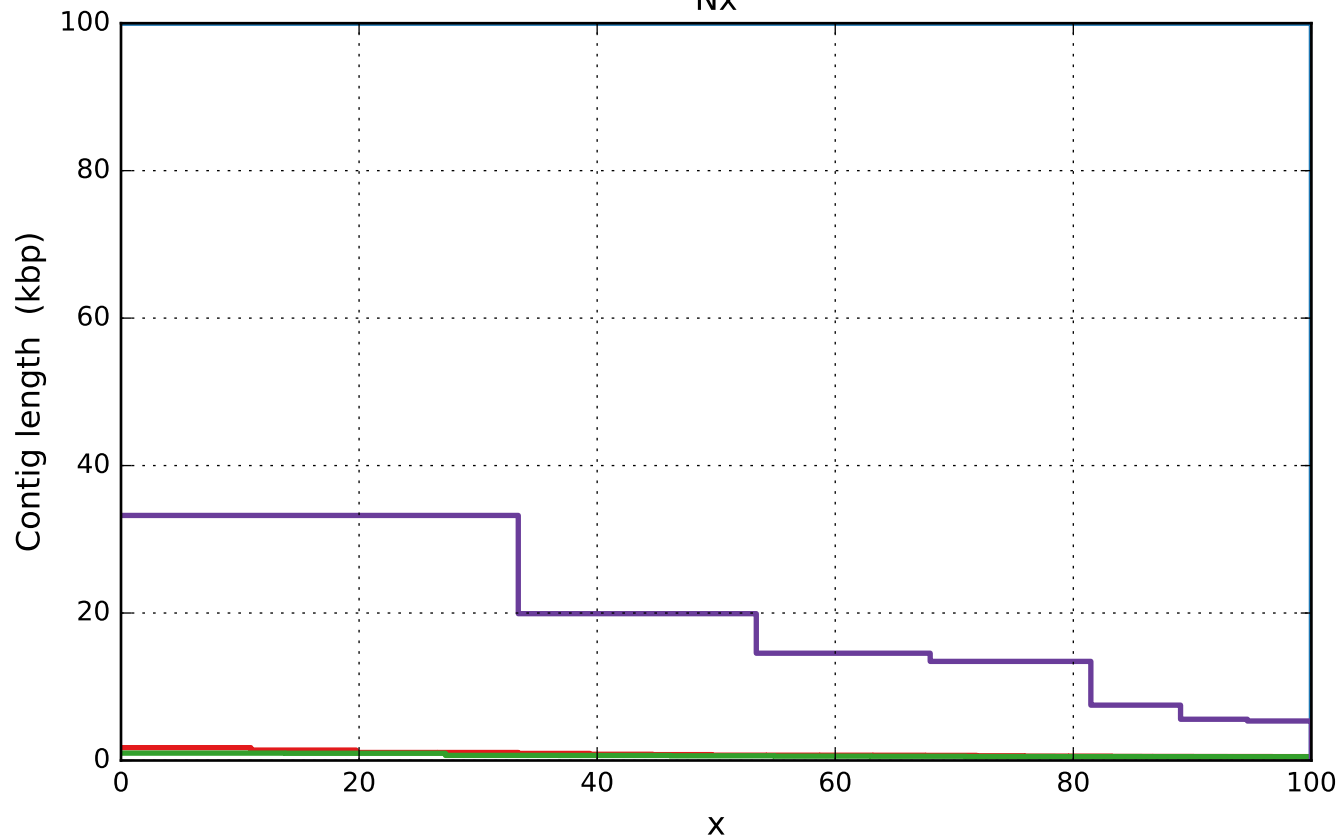
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

## Unaligned report

	Spades_Assem_contigs	Spades_h_Assem_contigs	velvet_Assem_contigs	velvet_h_Assem_contigs
# fully unaligned contigs	0	0	0	0
Fully unaligned length	0	0	0	0
# partially unaligned contigs	0	0	0	0
# with misassembly	0	0	0	0
# both parts are significant	0	0	0	0
Partially unaligned length	0	0	0	0
# N's	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).

Nx



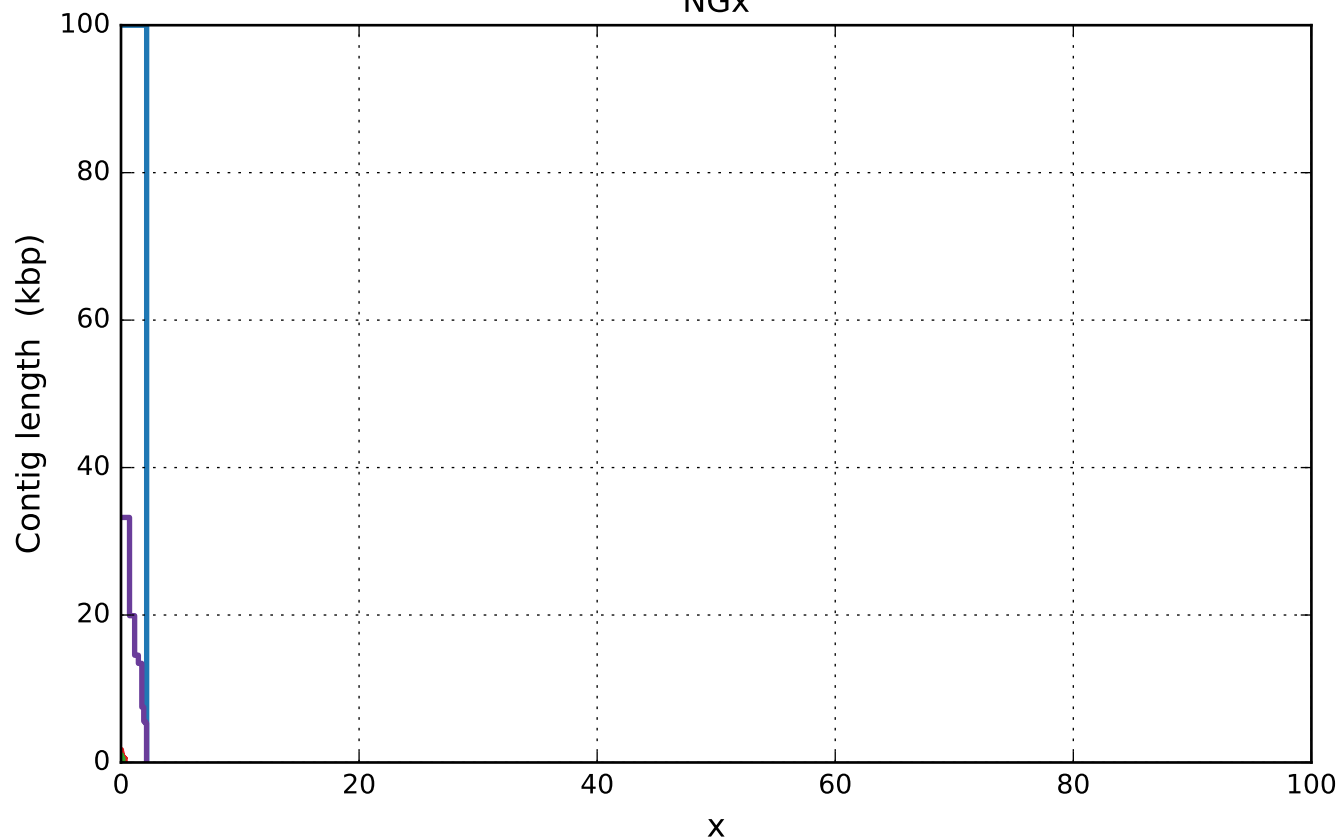
Spades\_Assem\_contigs

velvet\_Assem\_contigs

velvet\_h\_Assem\_contigs

Spades\_h\_Assem\_contigs

NGx

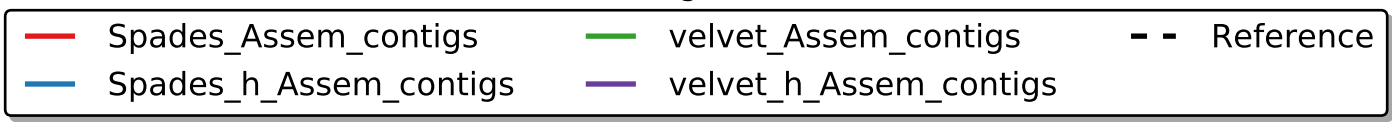
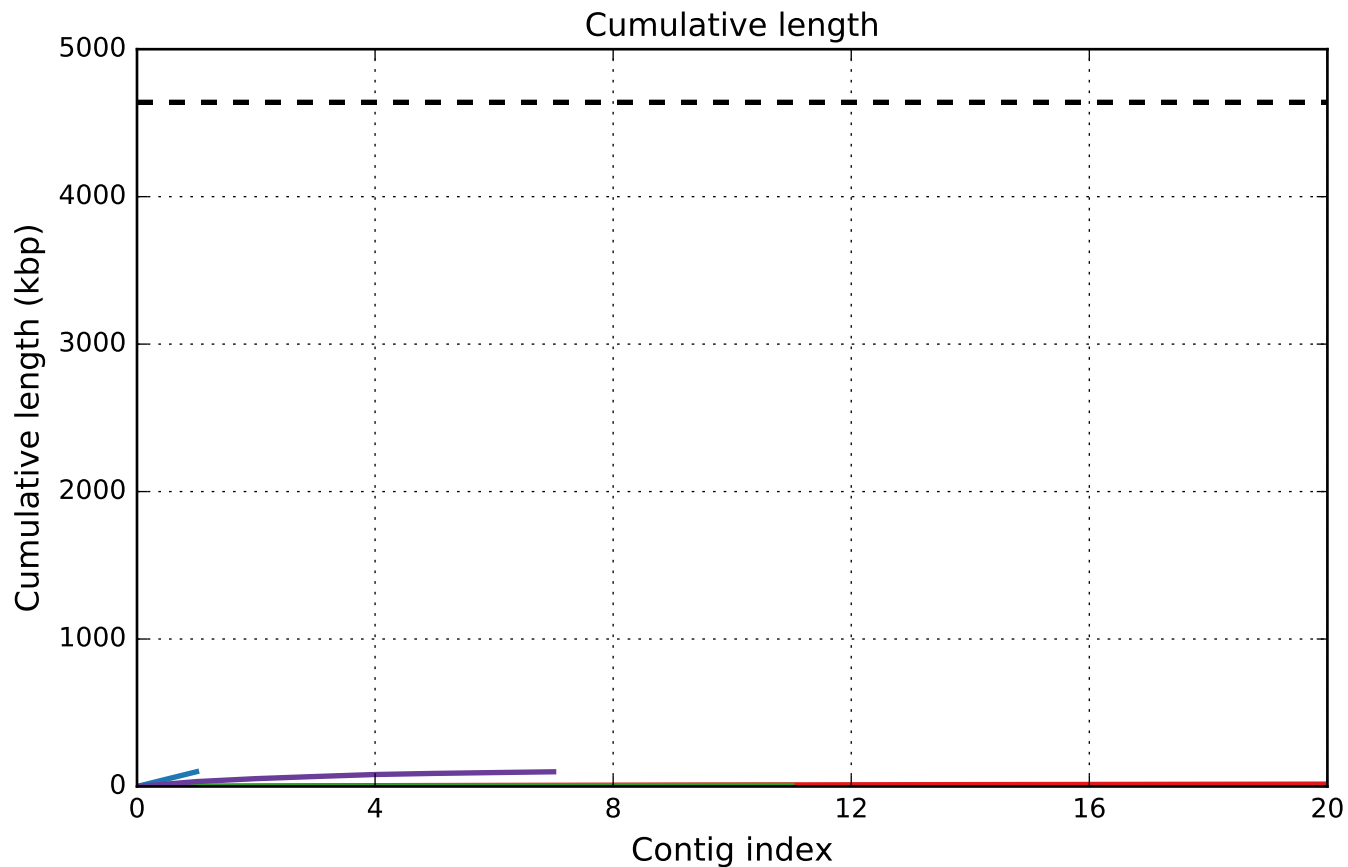


Spades\_Assem\_contigs

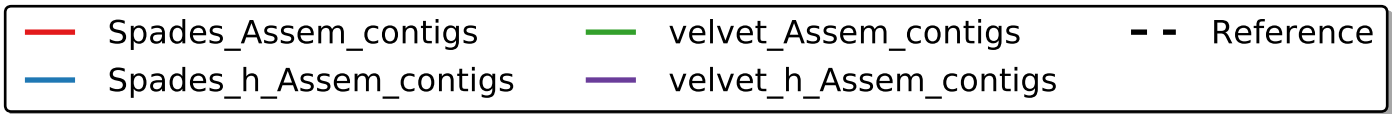
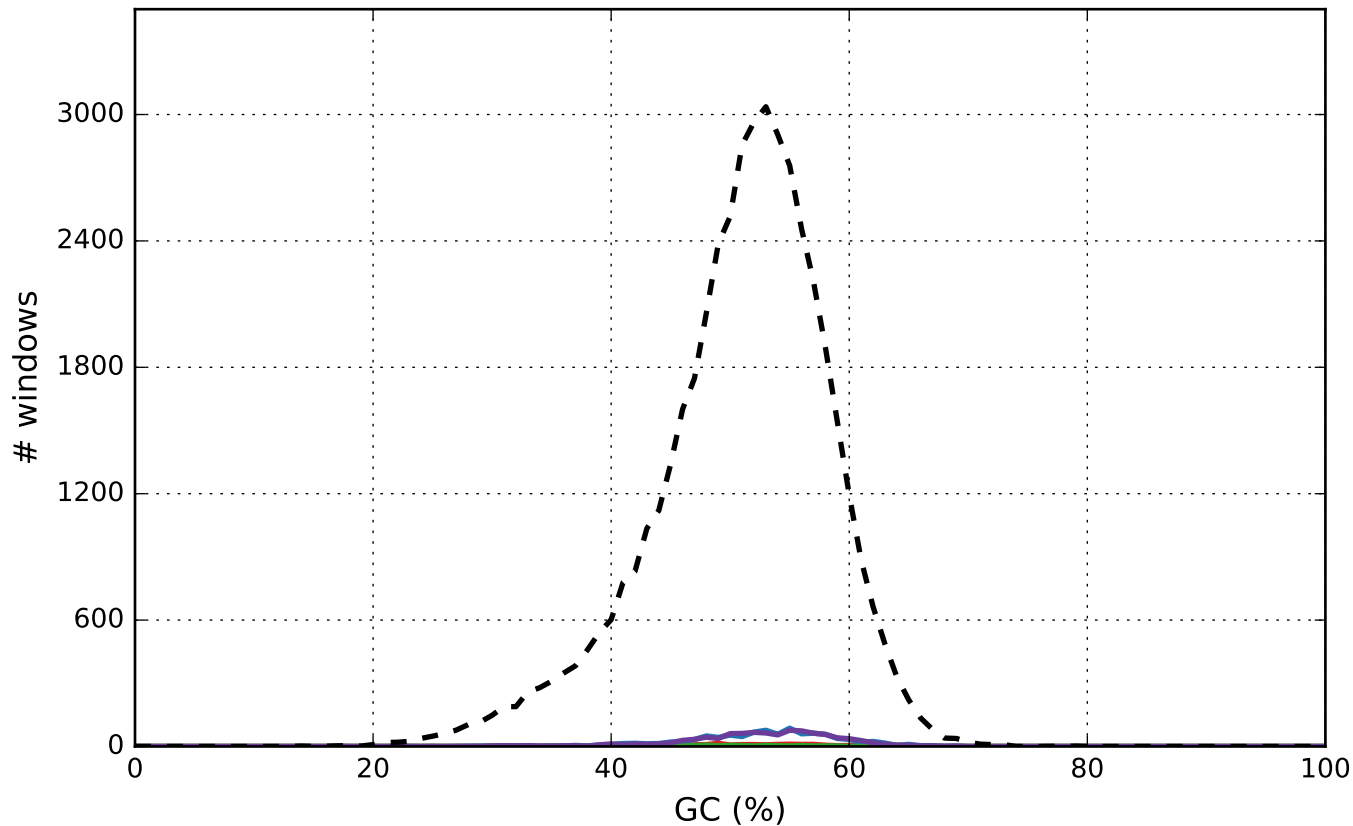
velvet\_Assem\_contigs

velvet\_h\_Assem\_contigs

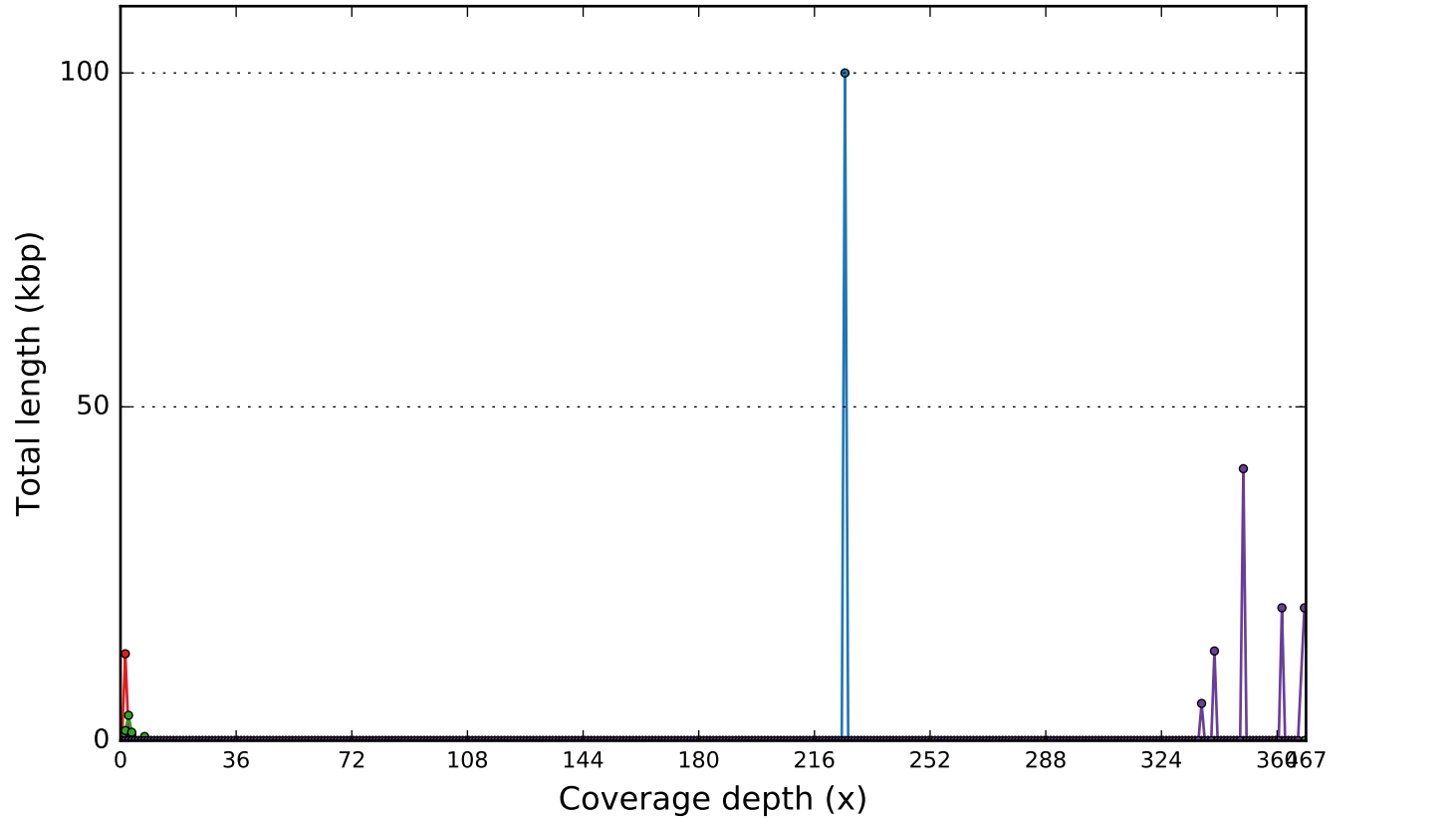
Spades\_h\_Assem\_contigs



# GC content

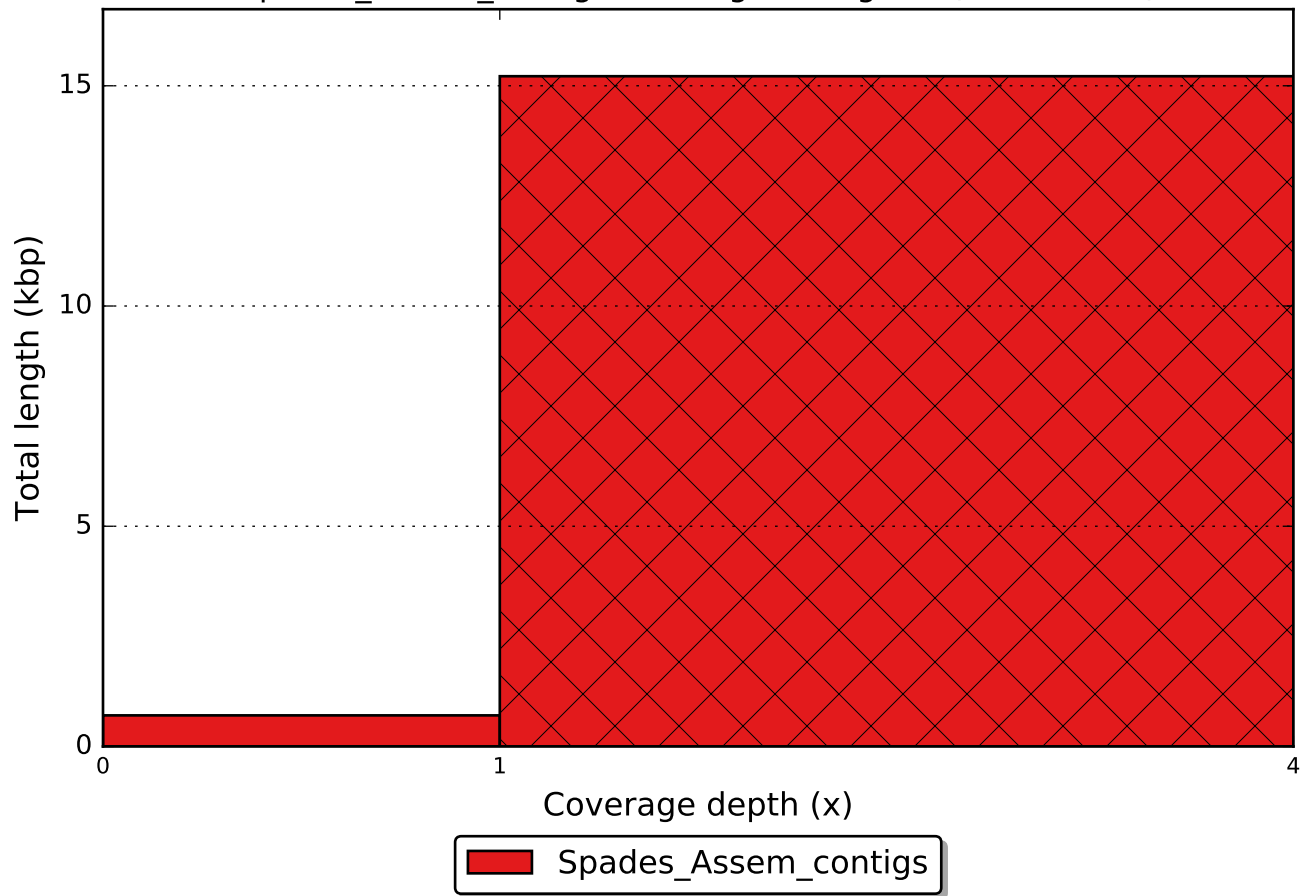


Coverage histogram (bin size: 1x)

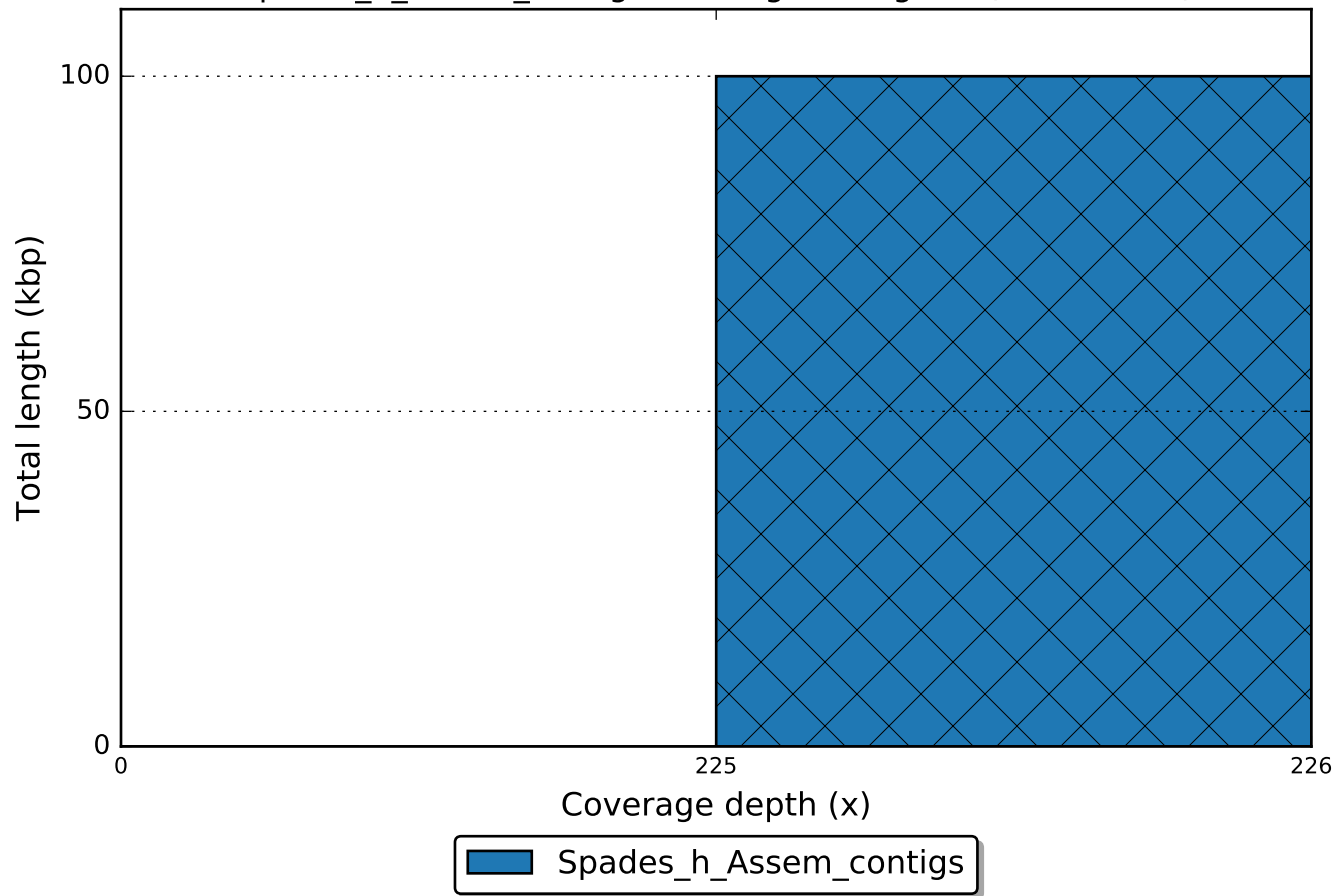




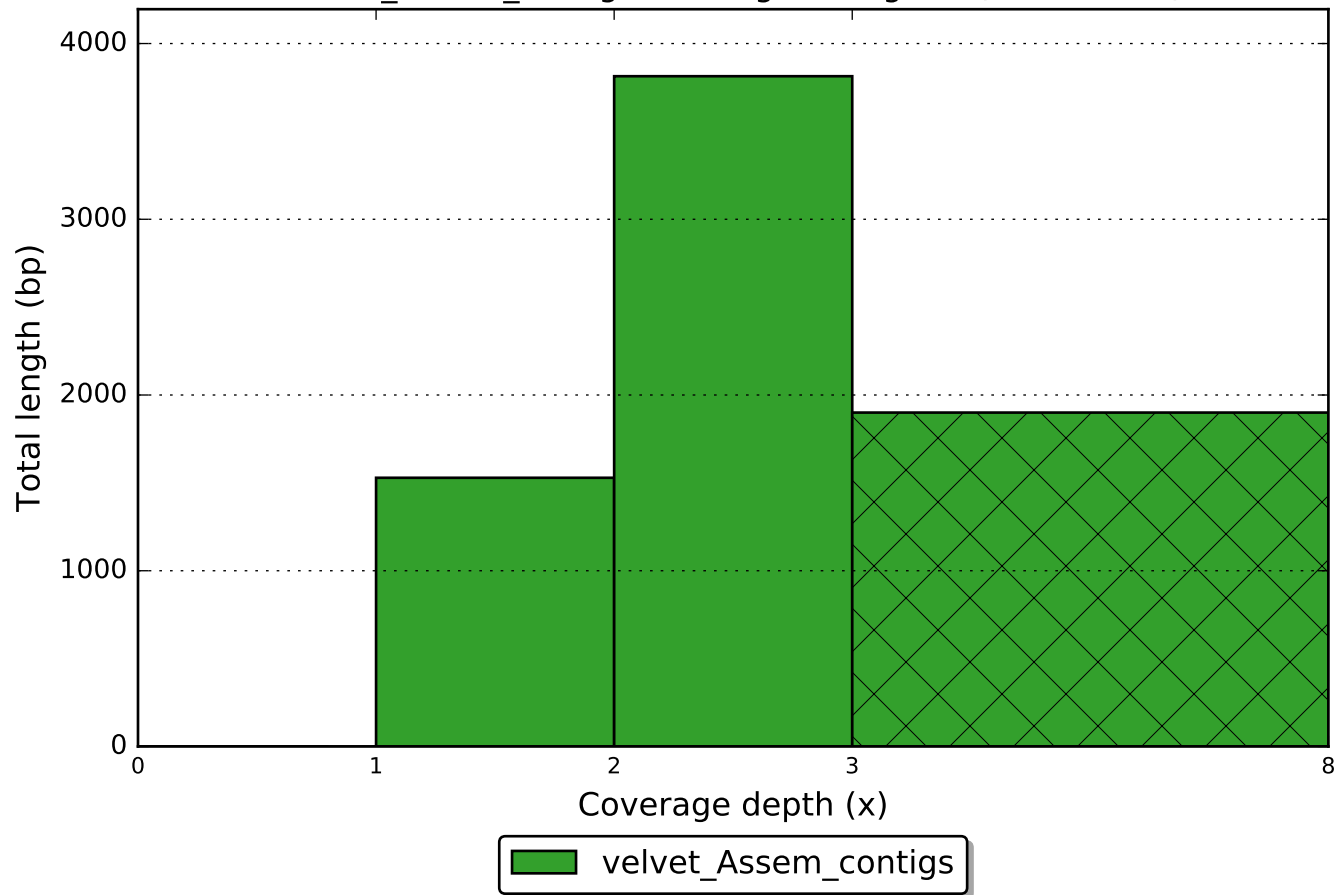
Spades\_Assem\_contigs coverage histogram (bin size: 1x)



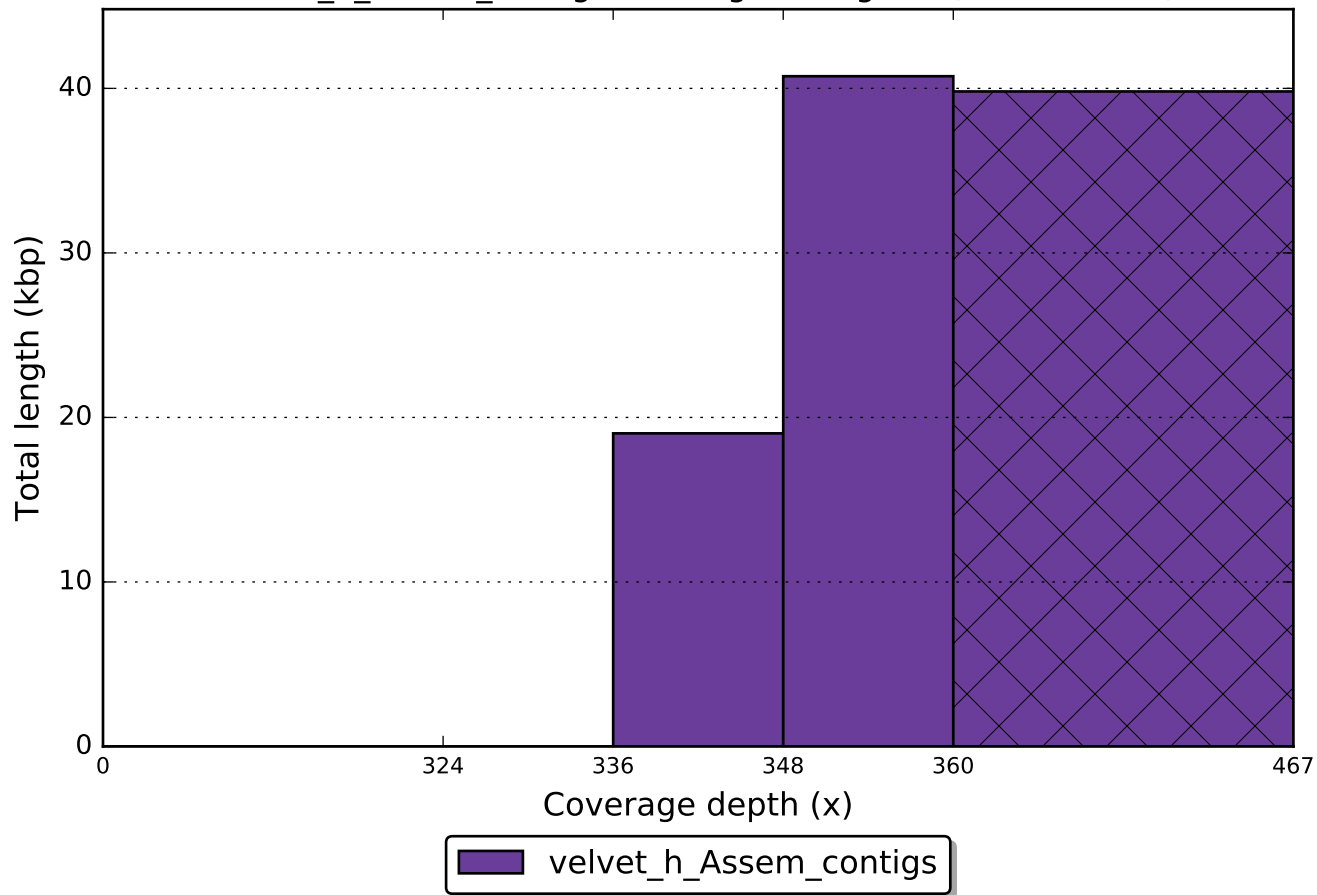
Spades\_h\_Assem\_contigs coverage histogram (bin size: 1x)

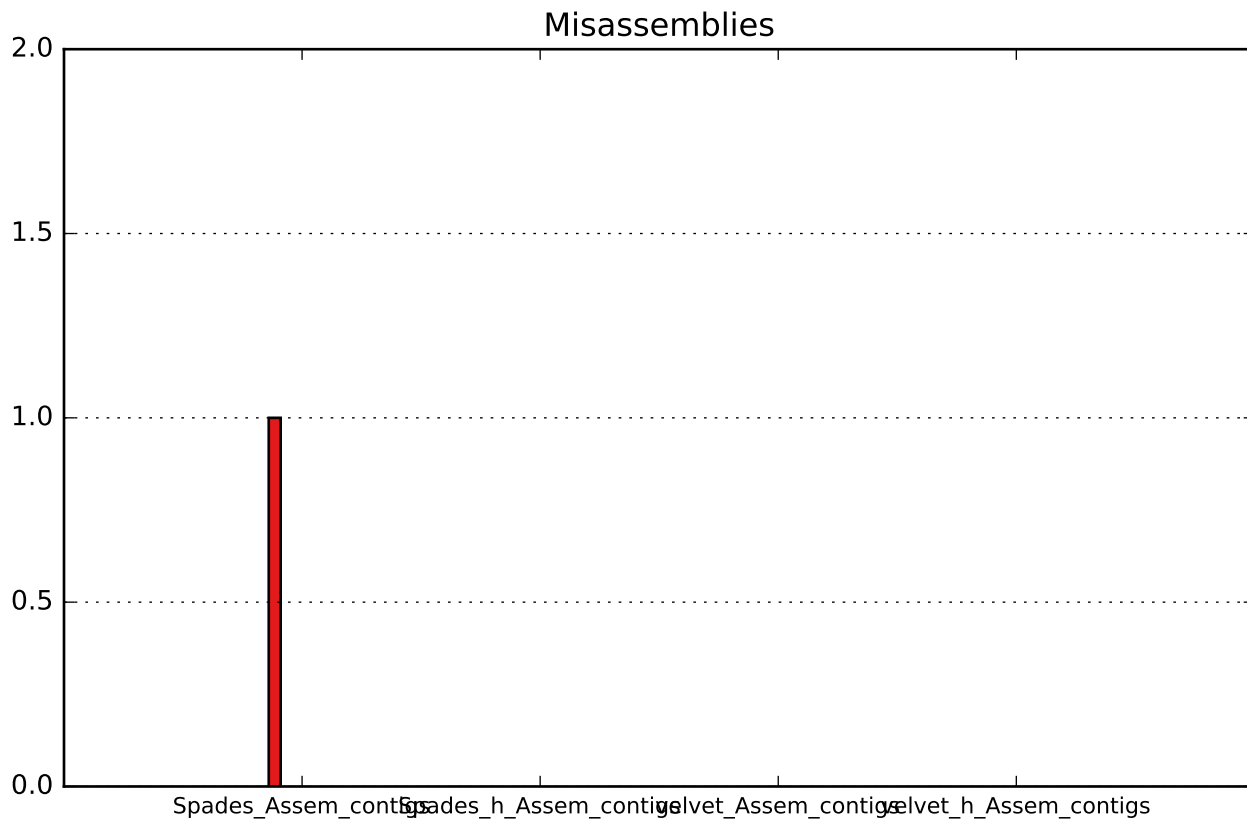


velvet\_Assem\_contigs coverage histogram (bin size: 1x)

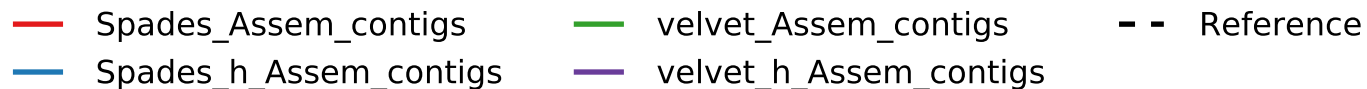
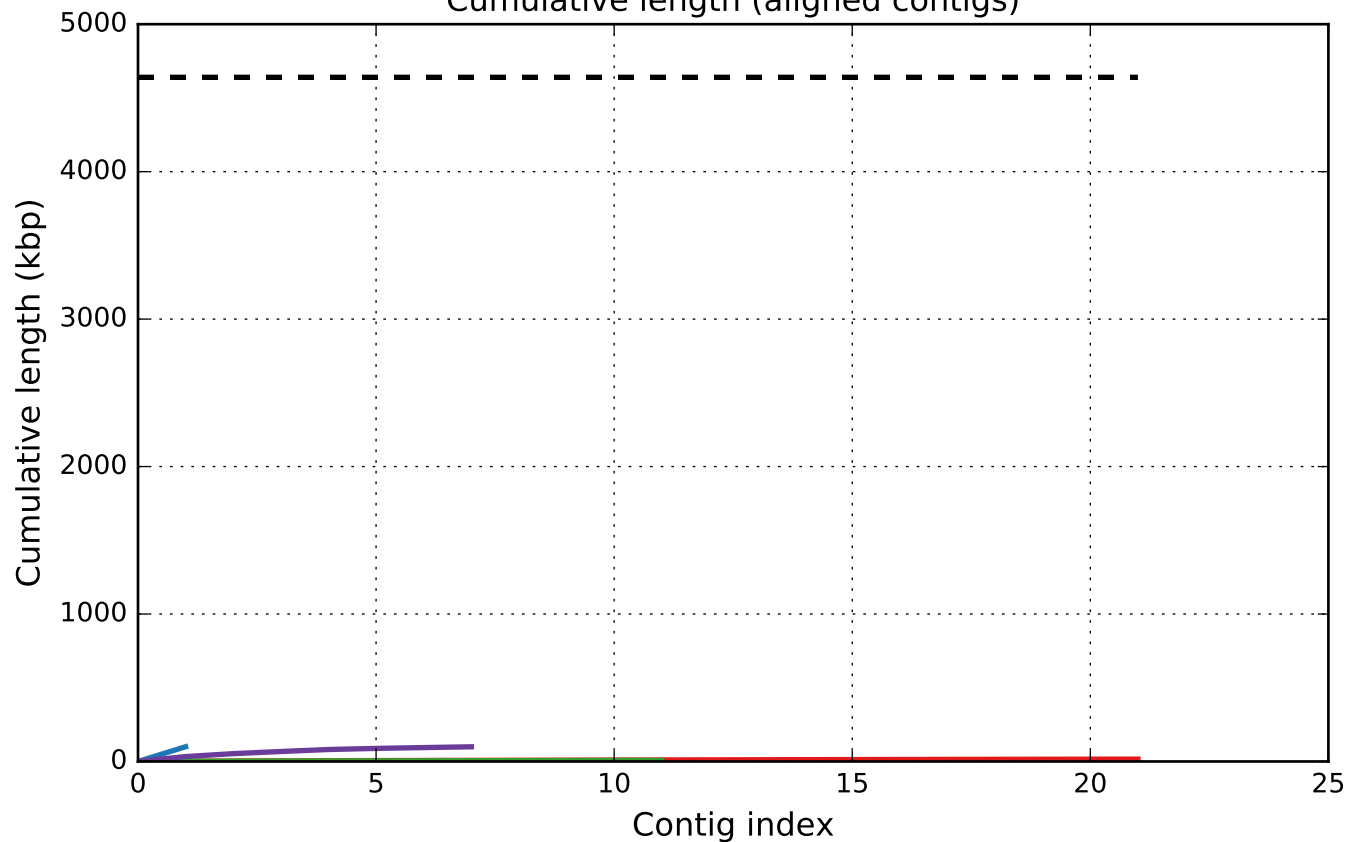


velvet\_h\_Assem\_contigs coverage histogram (bin size: 12x)

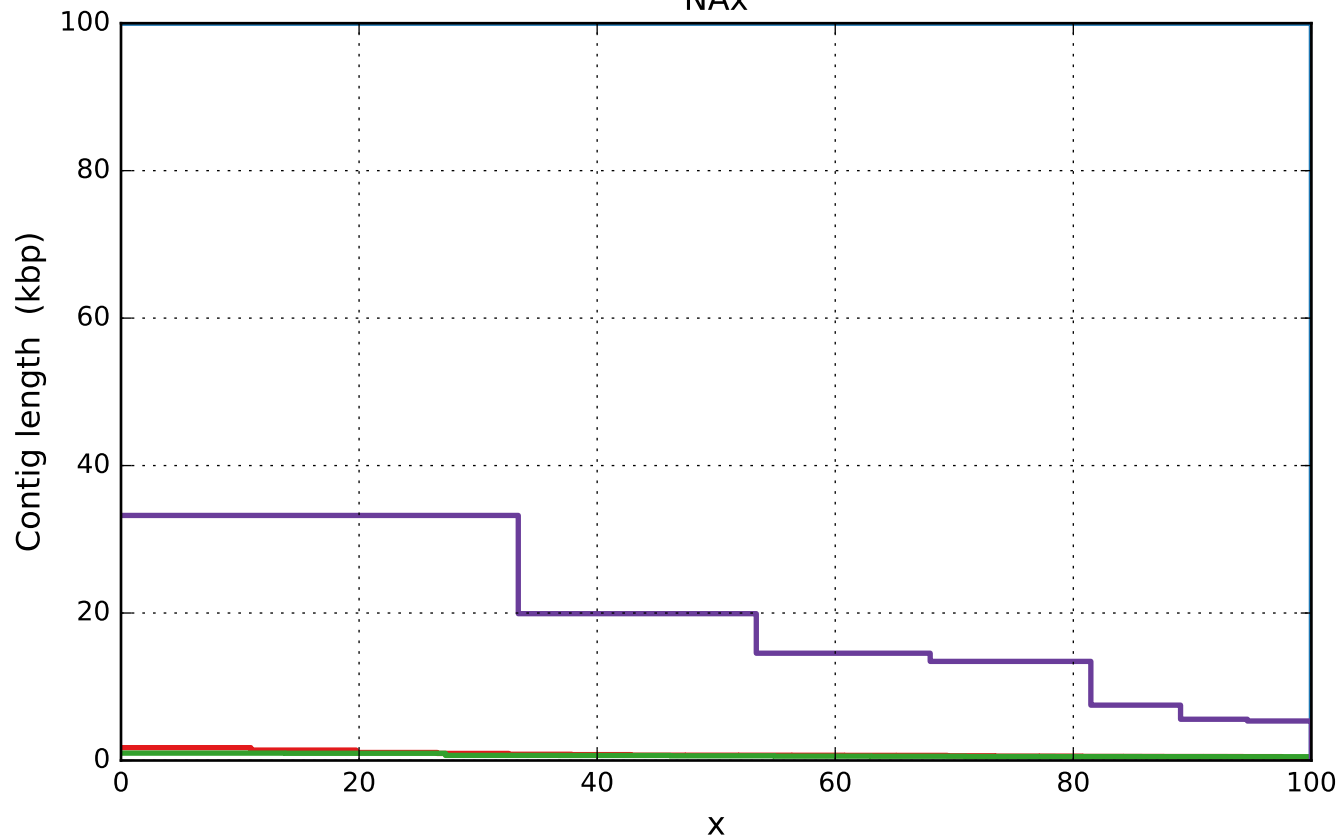




Cumulative length (aligned contigs)



NAx



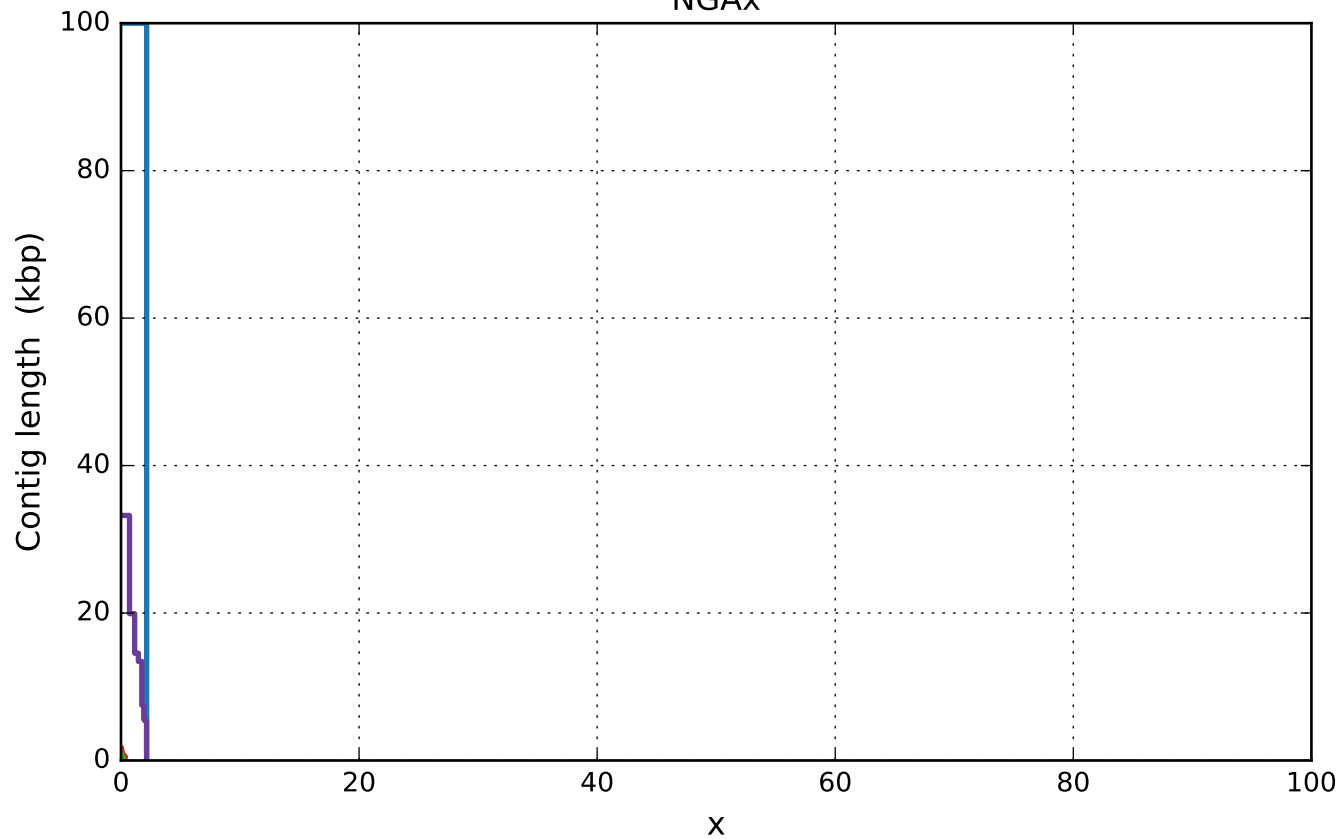
Spades\_Assem\_contigs

velvet\_Assem\_contigs

velvet\_h\_Assem\_contigs

Spades\_h\_Assem\_contigs

NGAx



Spades\_Assem\_contigs

velvet\_Assem\_contigs

velvet\_h\_Assem\_contigs

Spades\_h\_Assem\_contigs



