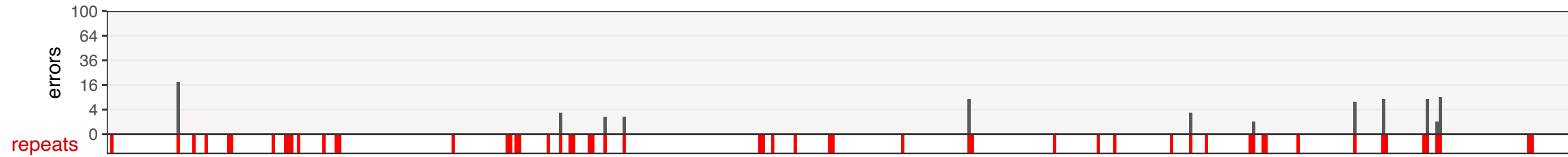


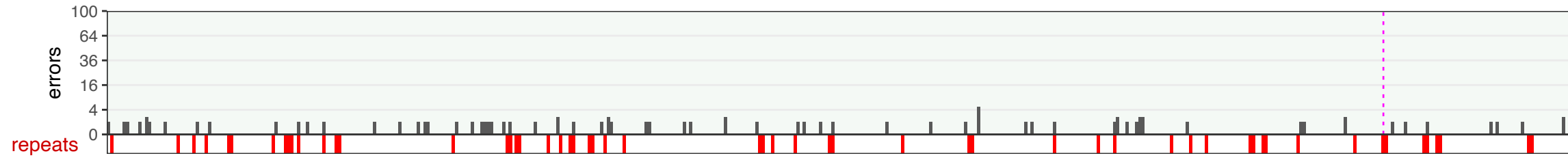
# *Escherichia coli* (simulated reads)

Unicycler  
hybrid



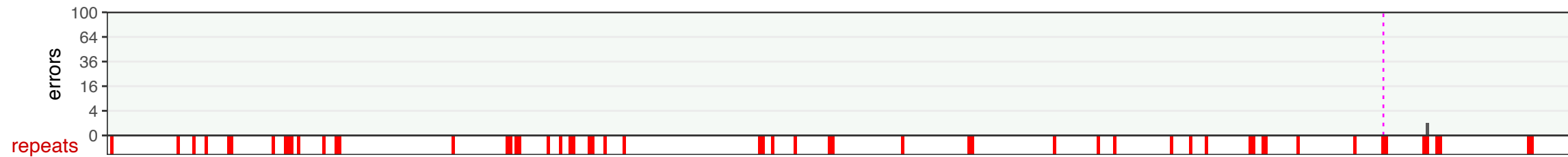
non-repeats (4.5 Mbp)	repeats (108 kbp)	error types
0 errors Q $\infty$	70 errors Q31.9	ins: 9 del: 10 sub: 51

Flye



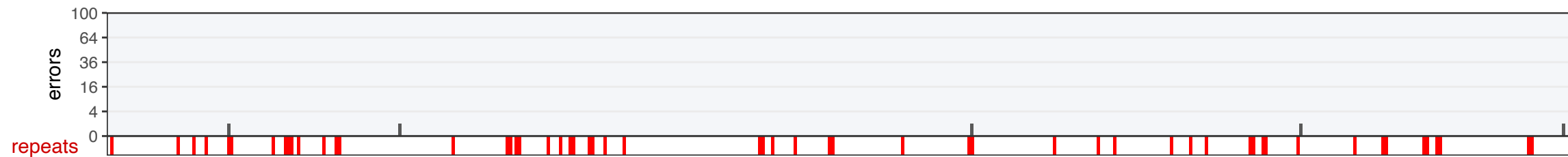
77 errors Q47.7	2 errors Q47.3	ins: 0 del: 79 sub: 0
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Flye  
+Pilon



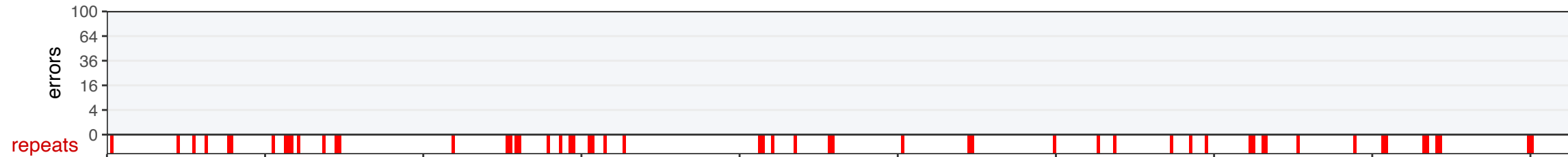
0 errors Q $\infty$	1 error Q50.3	ins: 0 del: 1 sub: 0
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Trycycler



5 errors Q59.6	0 errors Q $\infty$	ins: 0 del: 5 sub: 0
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Trycycler  
+Pilon



0 errors Q $\infty$	0 errors Q $\infty$	ins: 0 del: 0 sub: 0
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**Figure S6b:** error distributions (as defined by alignment to the reference sequence) for the simulated-read assemblies of the *Escherichia coli* chromosome. Repetitive regions of the genome are shown as red blocks at the bottom of each plot. For Flye assemblies, the contig start/end position (where the sequence began before it was rotated to be consistent with the reference) is shown by the dashed line.