

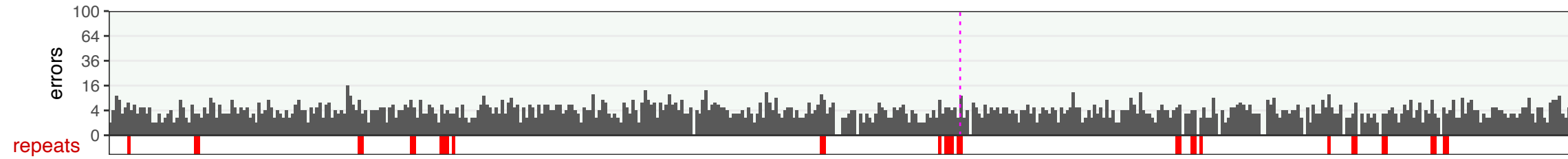
Salmonella enterica (simulated reads)

Unicycler
hybrid



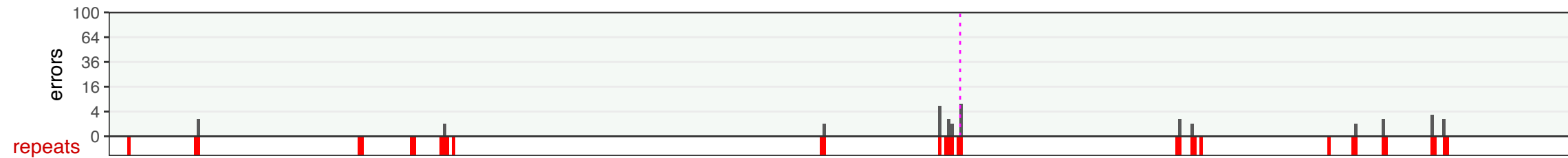
non-repeats (4.8 Mbp)	repeats (98 kbp)	error types
25 errors Q52.8	114 errors Q29.4	ins: 26 del: 28 sub: 85

Flye



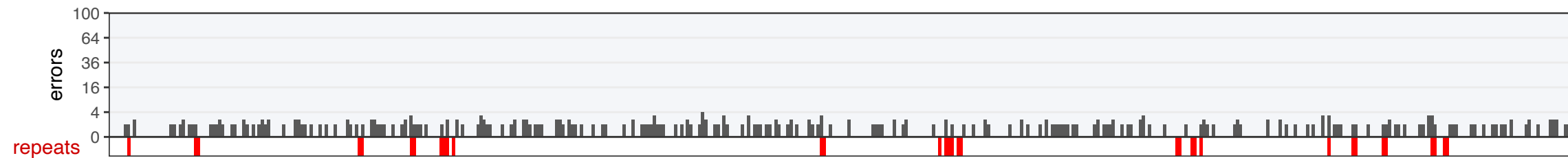
1953 errors Q33.9	57 errors Q32.4	ins: 0 del: 2010 sub: 0
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Flye
+Pilon



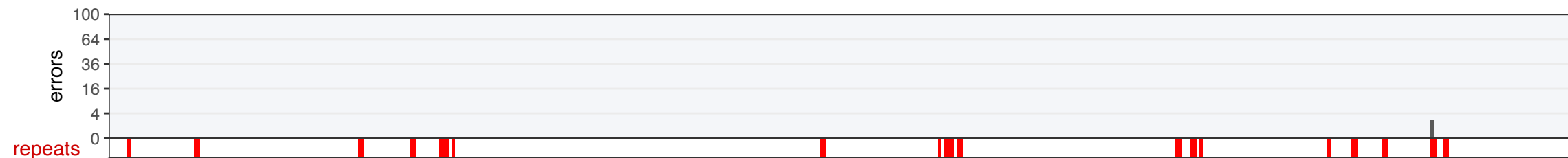
6 errors Q59.0	25 errors Q36.0	ins: 0 del: 31 sub: 0
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Tracycler



278 errors Q42.3	7 errors Q41.5	ins: 0 del: 285 sub: 0
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Tracycler
+Pilon



0 errors Q ∞	2 errors Q46.9	ins: 0 del: 2 sub: 0
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Figure S4-h: error distributions (as defined by alignment to the reference sequence) for the simulated-read assemblies of the *Salmonella enterica* 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.