Citrobacter koseri MINF 9D (real reads)

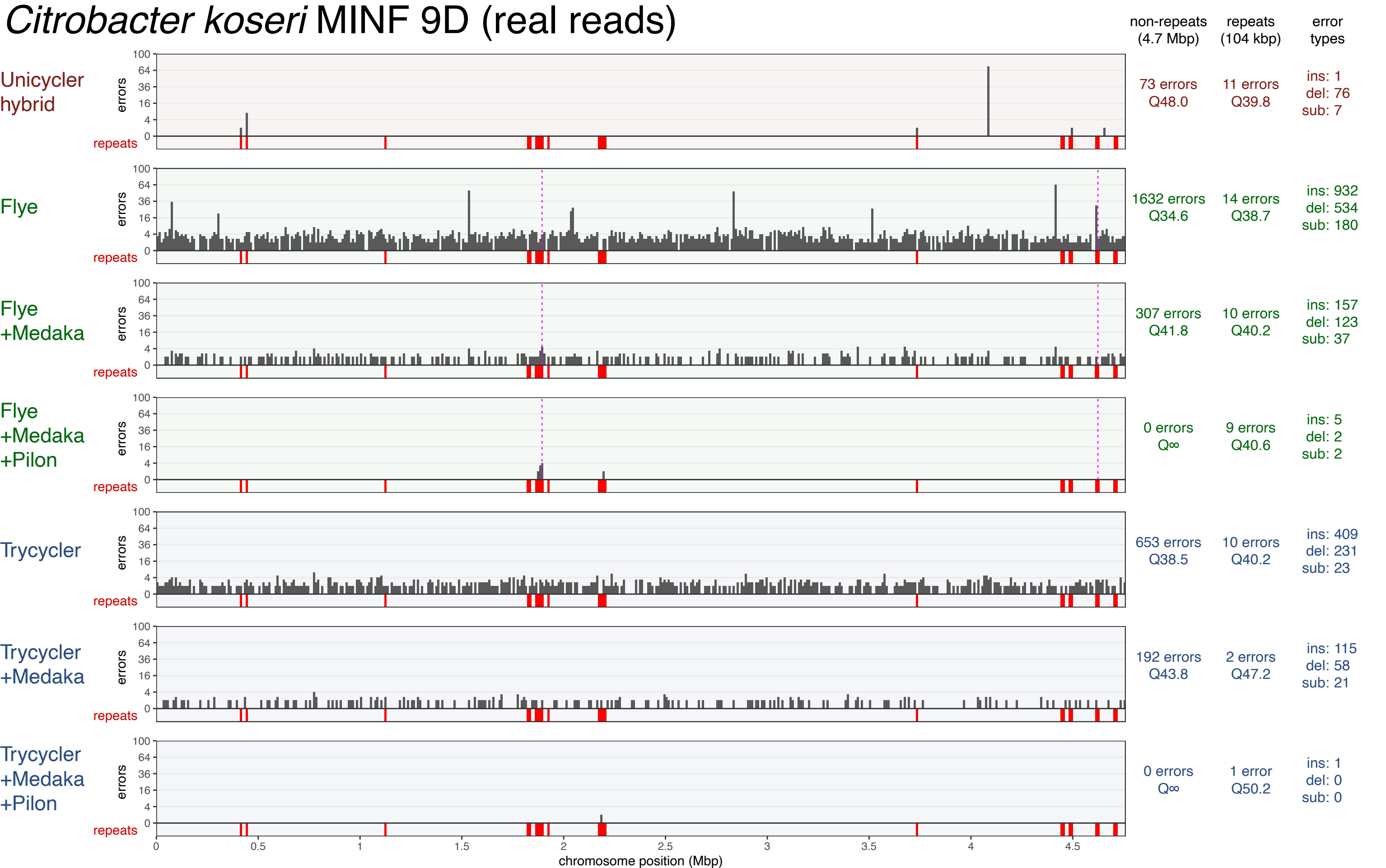|	non-repeats (4.7 Mbp)	repeats (104 kbp)	error types
Unicycler hybrid	73 errors Q48.0	11 errors Q39.8	ins: 1 del: 76 sub: 7
Flye	1632 errors Q34.6	14 errors Q38.7	ins: 932 del: 534 sub: 180
Flye +Medaka	307 errors Q41.8	10 errors Q40.2	ins: 157 del: 123 sub: 37
Flye +Medaka +Pilon	0 errors Q∞	9 errors Q40.6	ins: 5 del: 2 sub: 2
Trycycler	653 errors Q38.5	10 errors Q40.2	ins: 409 del: 231 sub: 23
Trycycler +Medaka	192 errors Q43.8	2 errors Q47.2	ins: 115 del: 58 sub: 21
Trycycler +Medaka +Pilon	0 errors Q∞	1 error Q50.2	ins: 1 del: 0 sub: 0

Figure S4-l: error distributions (as defined by alignment between two independent assemblies) for the real-read assemblies of the *Citrobacter koseri* chromosome. Repetitive regions of the genome are shown as red blocks at the bottom of each plot. For Flye assemblies, the contig start/end positions (where the sequences began before they were rotated to be consistent with the reference) are shown by the dashed lines.