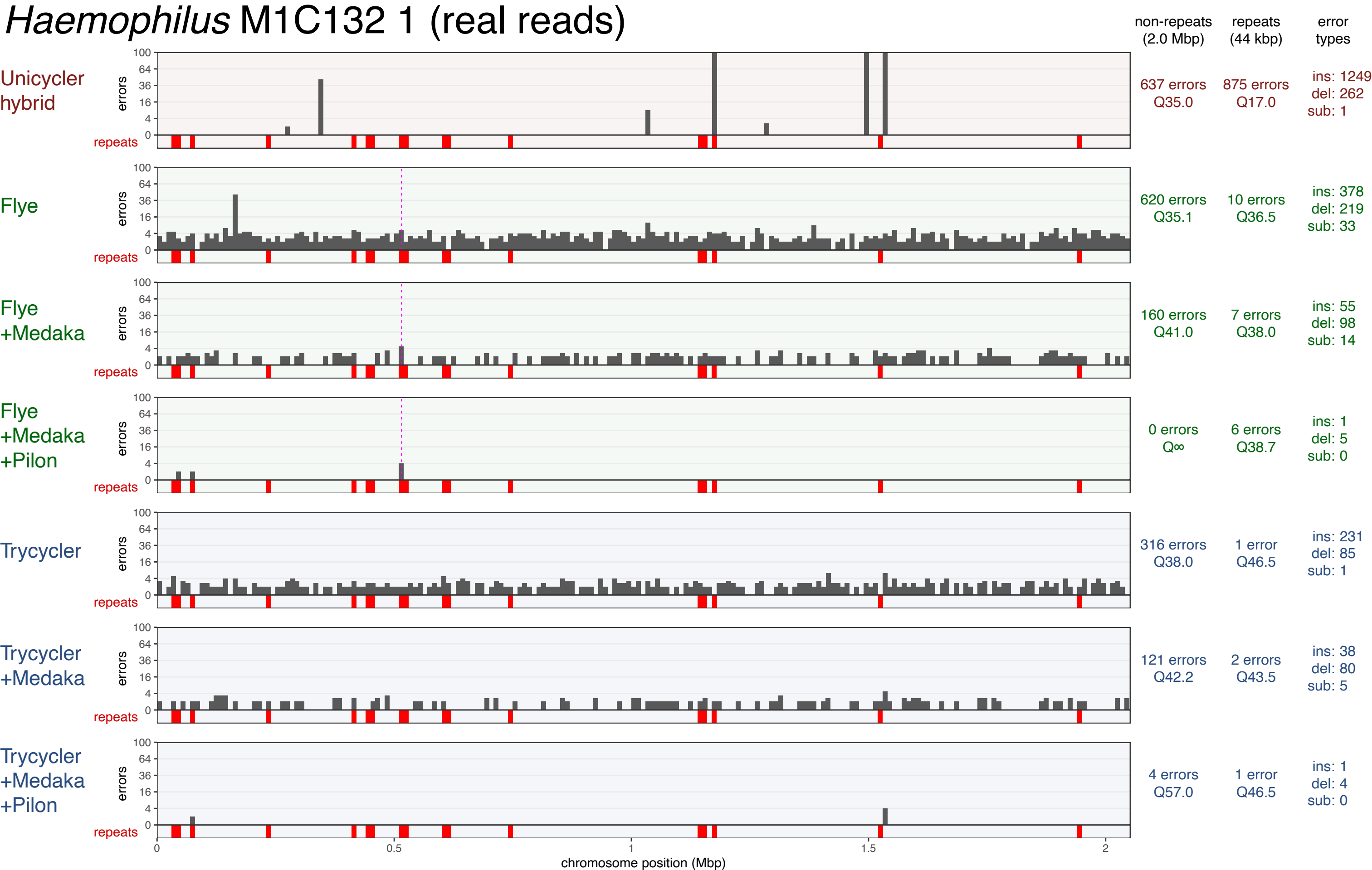


# *Haemophilus* M1C132 1 (real reads)



**Figure S6n:** error distributions (as defined by alignment between two independent assemblies) for the real-read assemblies of the *Haemophilus* 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.