



**Figure S4-k:** error distributions (as defined by alignment between two independent assemblies) for the real-read assemblies of the *Acinetobacter baumannii* 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.