



Figure S4-f: error distributions (as defined by alignment to the reference sequence) for the simulated-read assemblies of the *Neisseria meningitidis* 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.