



Figure S3. (a) The numbers of available pores after every 6-hour (*i.e.* mux scan) are shown above a percentage of the maximum pore number (*i.e.* 2048). Length and quality score distributions were similar between the three protocols (b) as well as their sequencing speed (c). Plots (b) and (c) were created by NanoPlot (de Coster 2018). Each loaded library was equivalent to DNA from 3 million GM12878 cells.