

*File S4.* smMIP coverage of single- and multiple-timepoint datasets. (a) Average smMIP coverage over the entire CH-panel for both technical replicates per individual in the single-timepoint dataset (N=1050). (b) Average smMIP coverage over the entire CH-panel for both technical replicates per DNA sample in the multiple-timepoint dataset (N DNA samples=180). In both (a) and (b) the error bars represent the standard deviation.