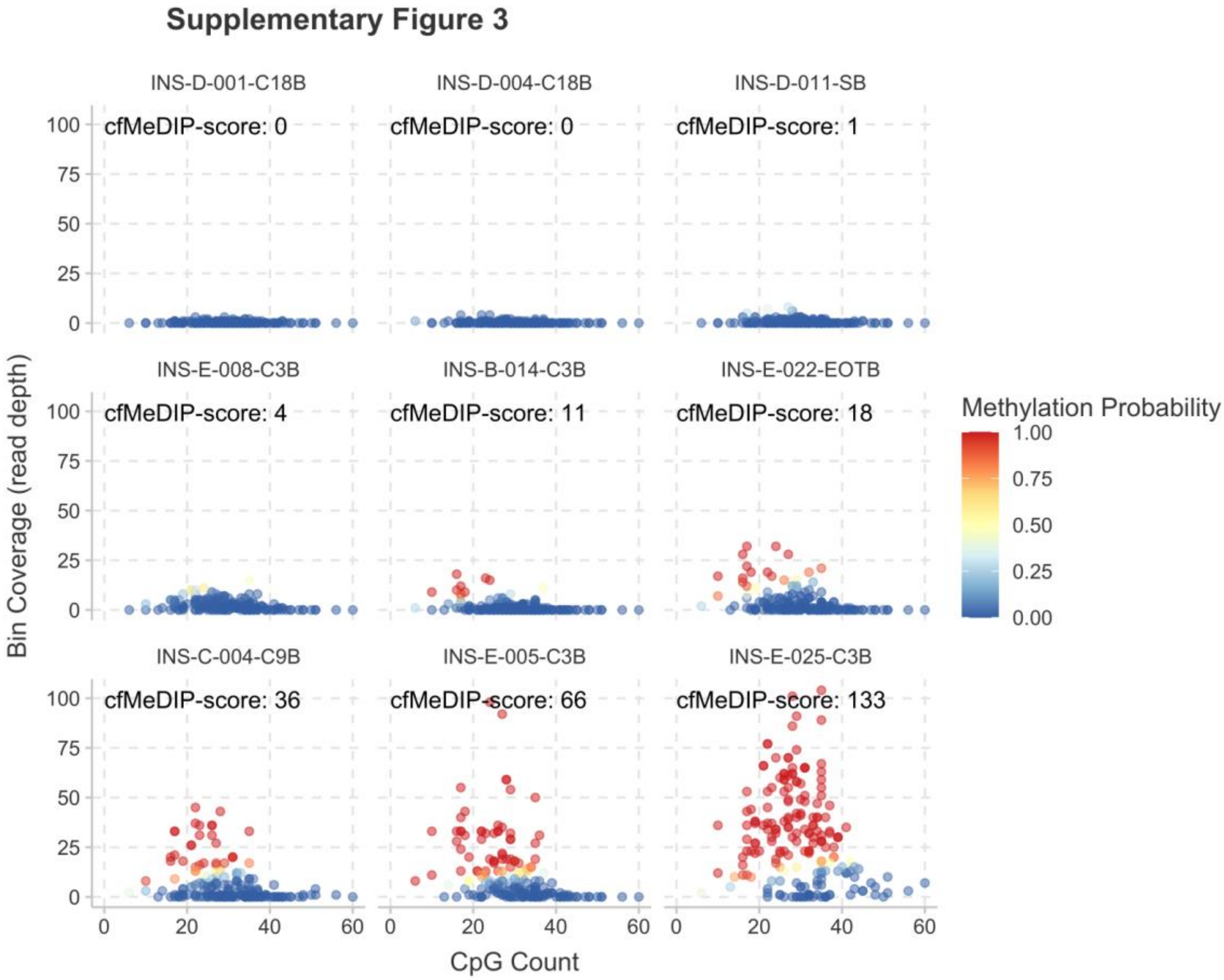

Supplementary Figure 3. Examples of cancer-specific methylation score calculation. Cancer-specific methylation scores were computed using the sum of inferred absolute methylation values for all reads overlapping an independently-trained cancer-specific signature. Here, we show examples illustrating how absolute methylation levels are inferred from coverage depths in 300 bp bins while adjusting for the density of CpGs.