

Number of ope site/Mb

Figure S9. Relationship of CpG density and hypomethylated DMFs. The y-axis shows the DMF density score, which was generated by dividing the number of DMFs by the number of analysed fragments for each 1 Mb window across the human genome. Tiling windows with at least three analysed fragments were considered for this analysis. The x-axis shows the number of CpG sites in each 1 Mb window.