



Figure 5-figure supplement 3:

Hypermethylation at CGs with low predicted methylation is a widespread and specific mark of cancer. Heatmap depicting the 99th percentile of methylation gain in each bin of CG density based predicted methylation for 486 human primary tissues (161 normal and 326 cancer samples) (Fernandez et al. 2012). The heatmap was subjected to hierarchical clustering, which accurately separates between normal (white) and cancer samples (black and grey) (side colorbar).