



Supplemental Figure 2a. Stacked barplots displaying the proportion (X-axes) of three gene subtypes, viz., protein-coding (green), long-noncoding (pink), and short-noncoding (blue) before and after applying a filtration step (Y-axes) to MethExp genes, that discards all loci that contain a neighboring gene spanning the region between them and their associated upstream CGIs. Application of the filter resulted in no differences in the proportions of these gene subtypes across all 34 tissue types.