

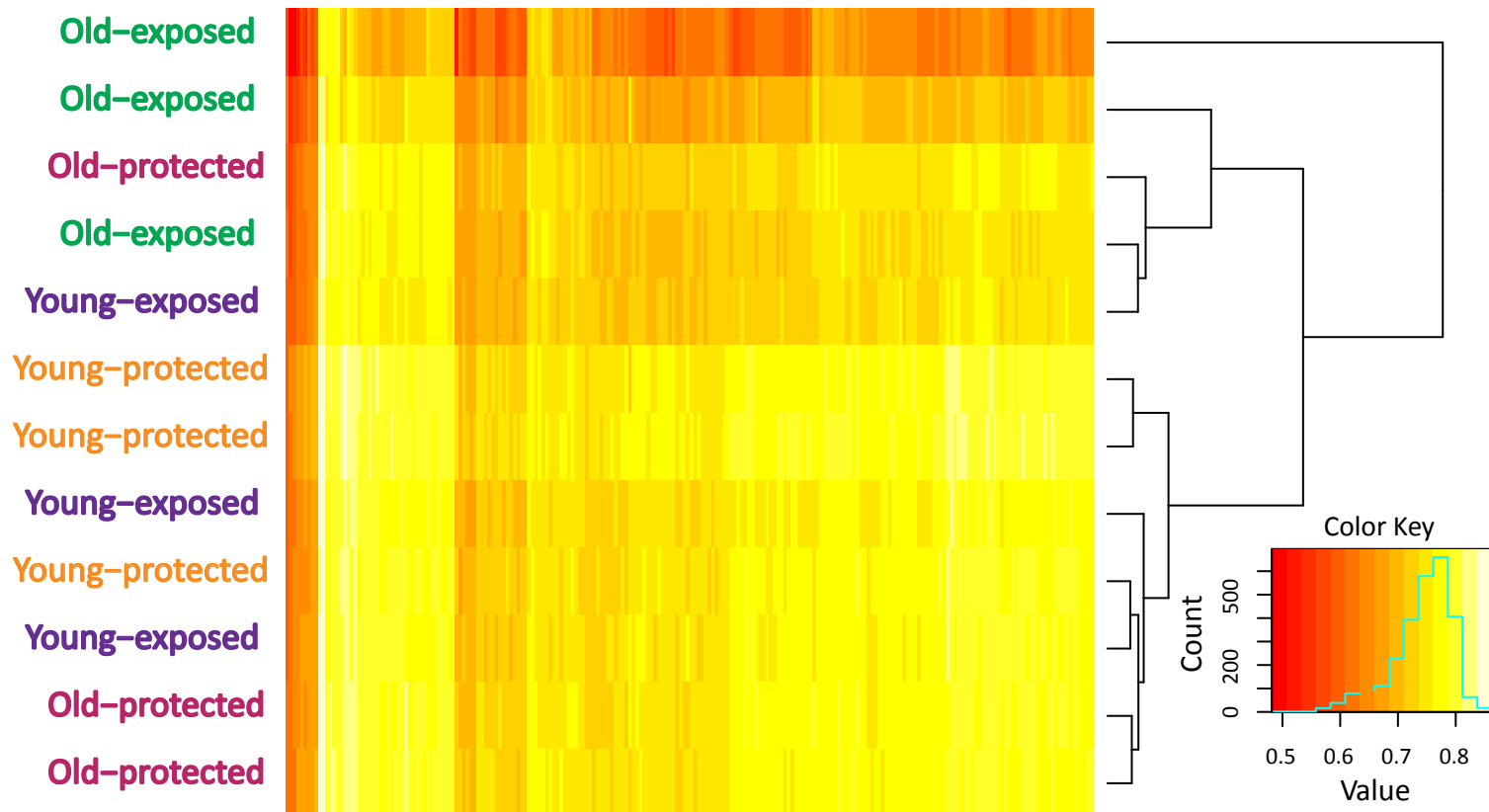


Figure S3. Hypomethylated blocks identified in 450k data separate O-exp and Y-pro samples analyzed using WGBS. Heatmap showing mean methylation from WGBS data in regions identified as blocks i comparing O-exp and Y-pro epidermis in 450k Data. Samples and blocks are ordered by hierarchical clustering. Yellow/red indicate higher/lower methylation, respectively.