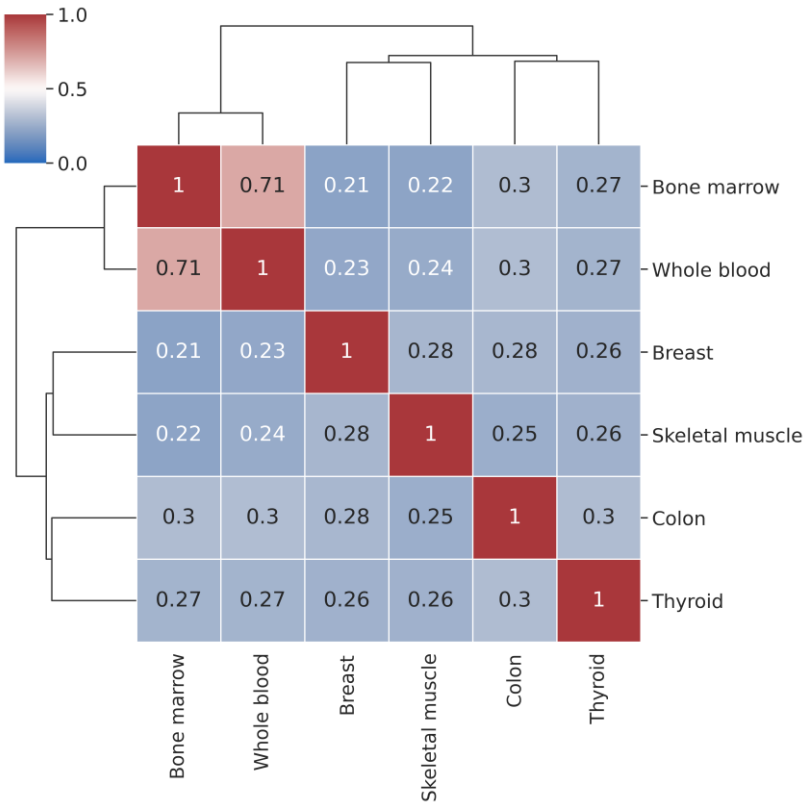
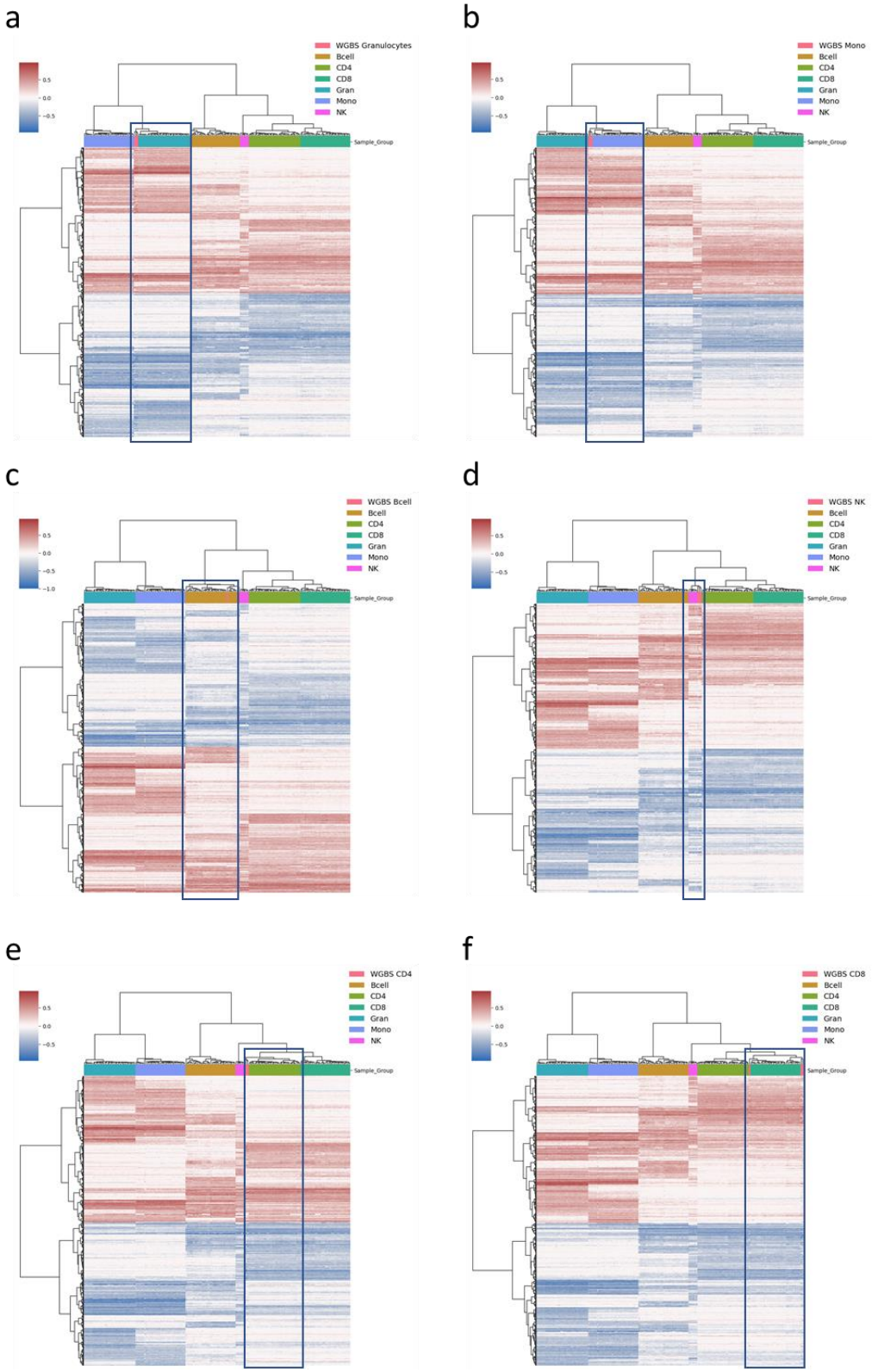
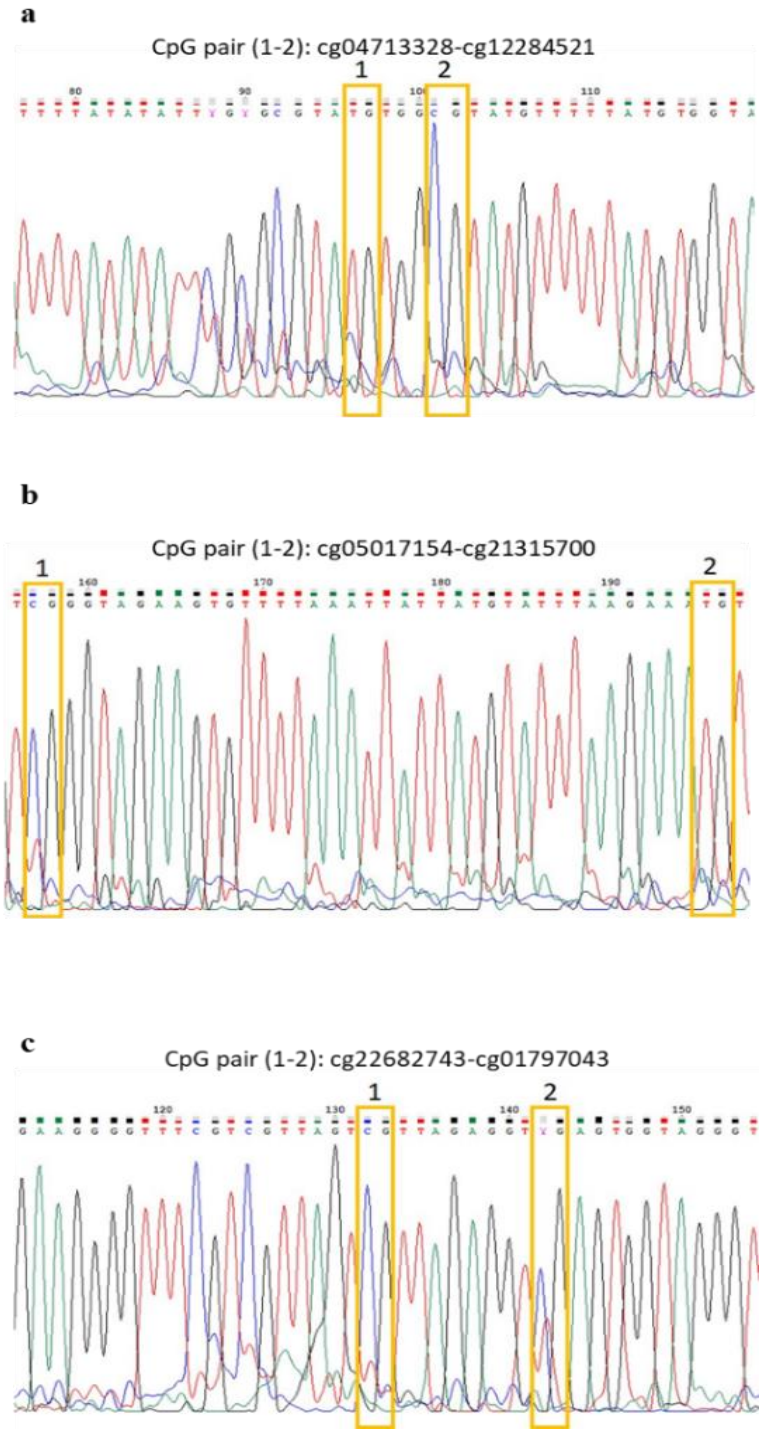


Supplementary Fig. 1. Pairwise comparison of adjacent CpG loci with discordant methylation status between each two types of different tissues, including, thyroid, bone marrow, colon, breast, skeletal muscle and whole blood. Boxes represent the Jaccard similarity index between the cell types.



Supplementary Fig. 2. Comparison of methylation patterns at “discordantly methylated cell specific” loci obtained using EPIC array and WGBS data. Unsupervised hierarchical clustering of white blood cell samples based on methylation level difference between base and consecutive CpG site. Boxes indicate methylation pattern of a cell type, for which EPIC array and WGBS data were compared, including (a) granulocytes (b) monocytes (c) B cell (d) NK (e) CD4T, and (f) CD8T and show that in each of the analyses, the samples clustered by cell type, regardless of the platform type.



Supplementary Fig. 3. Sanger sequencing chromatograms (Chromas 2.6.6) depicting discordant methylation status of adjacent CpG loci. Base CpG loci is marked as 1, and consecutive as 2 in the chromatogram. (a) Loci, in which thymine (T) originating from not methylated cytosine (C) is present at cytosine within base CpG site, while cytosine that must have been methylated before bisulfite modification is present within consecutive CpG site. (b) Loci with C which must have been methylated before bisulfite modification in base CpG site, and T originating from not methylated C in consecutive CpG site. (c) Loci with C which must have been methylated before bisulfite modification in base CpG site, and Y, originating from partially methylated C in consecutive CpG site.