Figure 3. Methylation haplotype load was powerful in tissue mapping and development stage mapping.
(A) Unsupervised cluster analysis shown genome-wide DNA methylation haplotype load could represent the sample relationship. the sample from same tissues were cluster together preferentially.
(B) Heatmap analysis based on genome-wide MHL shown same pattern and shown the MHL of cancer were significantly different with normal tissues, thus, providing the foundation to distinguish cancer tissues from normal tissues. (C,D,E) Tissues specific methylation haplotype regions shown advantages in tissues distinguish compared with average methylation level and total methylation level for each CpG site. (F) development specific layer specific methylation haplotype regions could separate different samples with different tissue development origin. (G) Tissue specific methylation haplotype load could be used to mapping the cancer plasma to its solid tissue origin.