Figure 1. DNA methylation haplotype in human genome and the conservativity between tissues and stability in different methylation platform

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(A) DNA methylation blocks were inferred with genome-wide bisulfite-sequencing.The pearson correlation was calculated and empirical threshold were appled for the methylation block inference genome-widely. (B) The distribution charactersitics of the methylation blocks in human genome. The left and right were showed with or without intergenic regions. (C) Methylation block regions identified by BS-seq data of normal tissues were significantly over-represented in different platforms such as Methylation 450K microarray and RRBS. the right figure showed the regions from methylation 450K and RRBS within the methylation blocks shown higher correlation compared with regions without the methylation block regions. (D) Methylation blocks were shown highly conversive in 11 normal tissues from methylation 450K array. (D). large number of dataset from GEO also validated the conservative of methylation blocks. Meanwhile (D and E) shown the conservativity of methylation blocks were not influenced by CpG or not.