



Supplementary Figure S2. Promoter methylation profile determined by GPS but not by WGBS in hepatoma cell line 97L are enriched in neuroactive ligand-receptor interaction pathway.

(A) Promoters detected by GPS and WGBS at different amount of raw sequencing data. GPS detected more promoters than WGBS with 100M, 200M and 375M paired-end reads, respectively. (B) Promoters detected by GPS, WGBS or both. Under same amount of raw sequencing data of 375M paired reads, 99.4% (28525/28699) of WGBS detectable promoters can be detected by GPS. Moreover, GPS uniquely detected 4,030 promoters, while WGBS only uniquely detected 174 promoters. (C) KEGG analysis of 4,030 genes which were enriched in neuroactive ligand-receptor interaction pathway. (D) Promoters uniquely detected by GPS with higher GC-content. A, B and C represent promoters uniquely detected by GPS, commonly detected and uniquely detected by WGBS, respectively. (E) Covered CpG number plotted as a function of coverage with 375M bisulfite-converted reads. The number of GPS-detected CpGs is higher than WGBS except 1x coverage in whole genome and CpG islands.