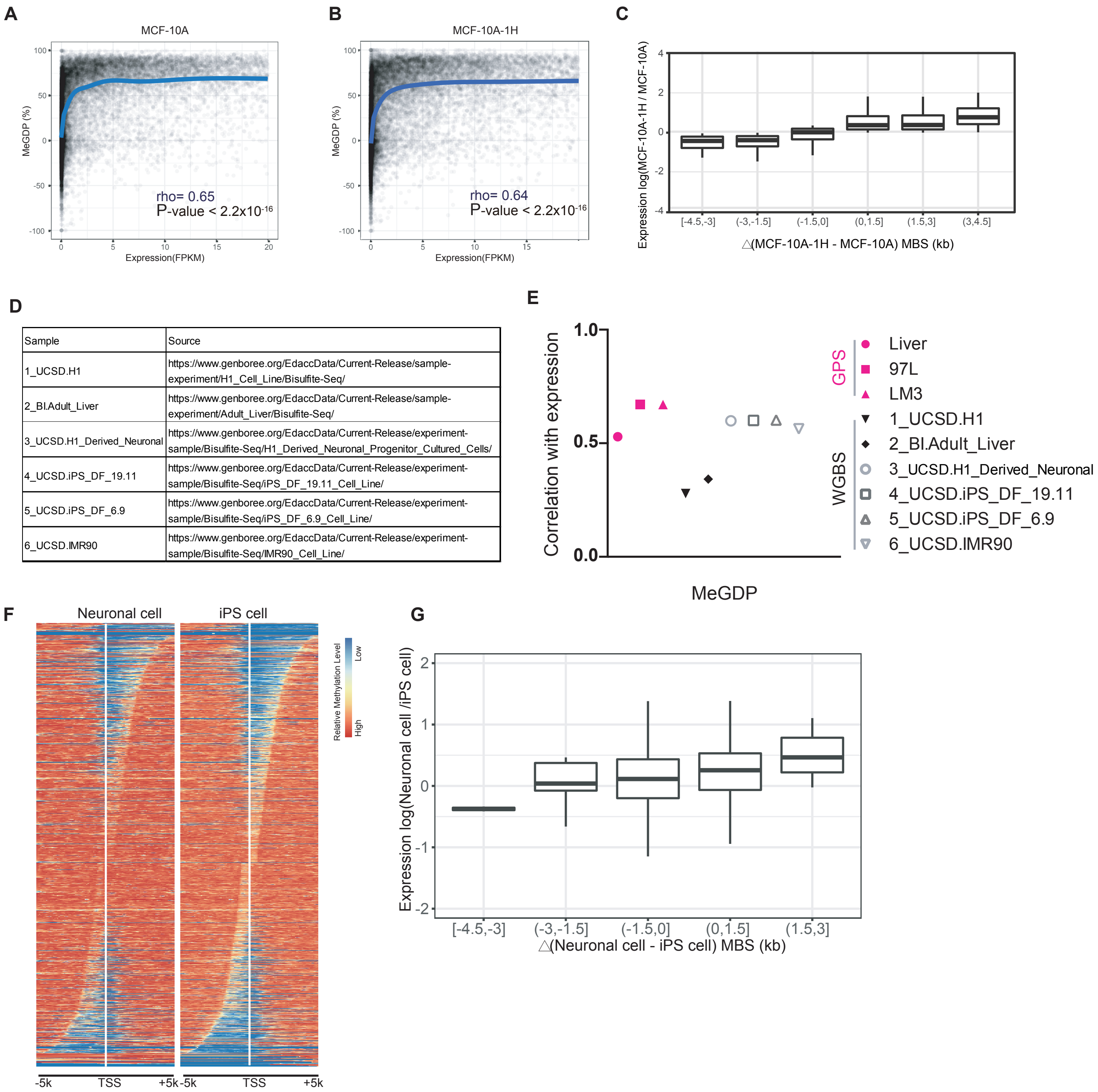

Sample	Source
1_UCSD.H1	https://www.genboree.org/EdaccData/Current-Release/sample-experiment/H1_Cell_Line/Bisulfite-Seq/
2_BI.Adult_Liver	https://www.genboree.org/EdaccData/Current-Release/sample-experiment/Adult_Liver/Bisulfite-Seq/
3_UCSD.H1_Derived_Neuronal	https://www.genboree.org/EdaccData/Current-Release/experiment-sample/Bisulfite-Seq/H1_Derived_Neuronal_Progenitor_Cultured_Cells/
4_UCSD.iPS_DF_19.11	https://www.genboree.org/EdaccData/Current-Release/experiment-sample/Bisulfite-Seq/iPS_DF_19.11_Cell_Line/
5_UCSD.iPS_DF_6.9	https://www.genboree.org/EdaccData/Current-Release/experiment-sample/Bisulfite-Seq/iPS_DF_6.9_Cell_Line/
6_UCSD.IMR90	https://www.genboree.org/EdaccData/Current-Release/experiment-sample/Bisulfite-Seq/IMR90_Cell_Line/

Supplementary Figure S13. MeGDP and MBS analysis from GPS and public WGBS datasets.

(A, B) Correlation coefficient between gene expression and MeGDP is 0.65 in MCF-10A and 0.64 in MCF-10A-1H (Spearman's rank correlation). **(C)** A positive correlation between MBS and gene expression is shown in comparison between MCF-10A and MCF-10A-1H. **(D)** Source of WGBS samples. Source of WGBS samples. DNA methylation datasets were downloaded from NIH Roadmap Epigenomics Mapping Consortium, which supplies the DNA methylation status files in Wig format, of which the raw data and mapping rate are not available. **(E)** Correlation between gene expression and MeGDP analyzed by GPS and WGBS datasets (Spearman's rank correlation). **(F)** Heatmap of DNA methylation pattern around ±5k of TSS in sample 3_UCSD_H1_Derived Neuronal (Neuronal cell for short) and 4_UCSD.iPS_DF_19.11 (iPS cell for short). **(G)** A positive correlation between MBS and gene expression is shown in comparison between Neuronal cell and iPS cell.