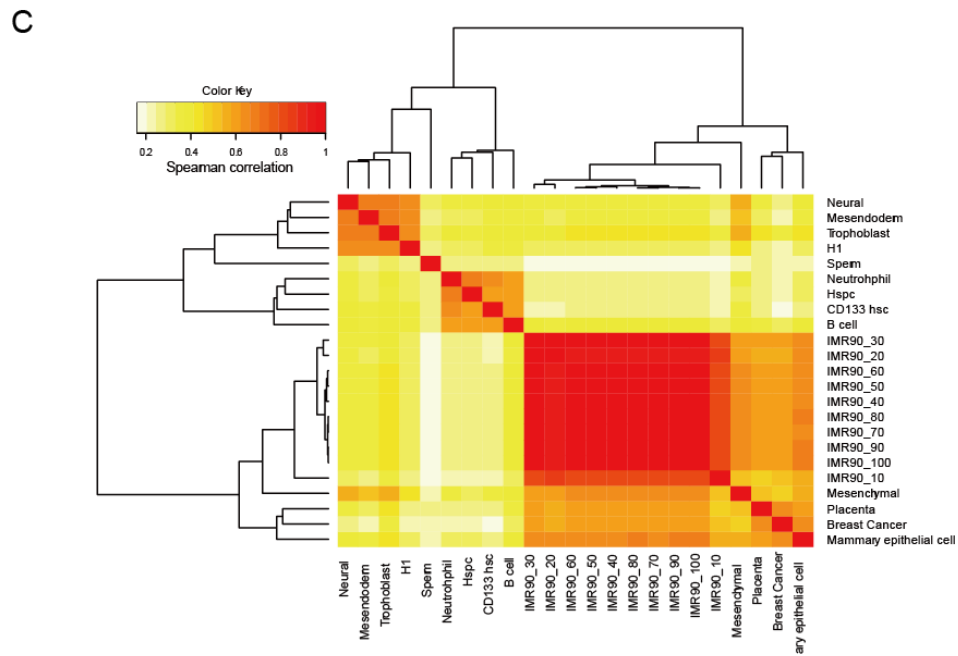
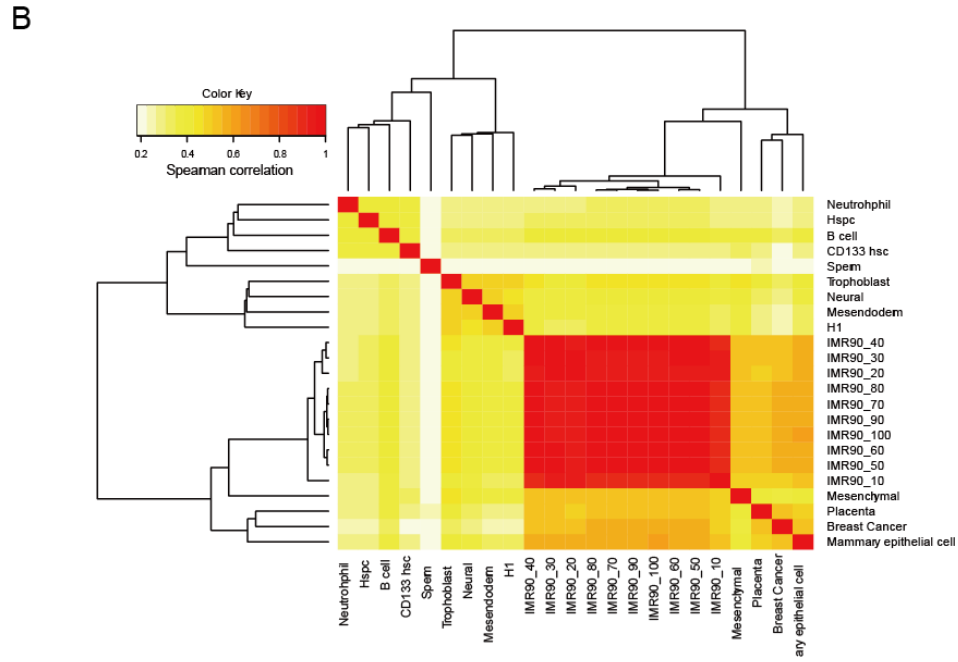


A

Sample name	Cell type	Mean depth	Number of domains (length > 10 bp)
H1	ESC or ESC-derived	33.3	71,283
Mesenchymal stem cell	ESC or ESC-derived	55.5	170,898
Mesendoderm	ESC or ESC-derived	31.3	99,353
Neural progenitor cell	ESC or ESC-derived	38.9	139,413
Trophoblast-like cell	ESC or ESC-derived	40.6	142,294
IMR90_10	PMD-positive	4.1	50,383
IMR90_20	PMD-positive	8.1	144,499
IMR90_30	PMD-positive	12.1	208,981
IMR90_40	PMD-positive	16.2	250,546
IMR90_50	PMD-positive	20.3	278,634
IMR90_60	PMD-positive	24.4	295,620
IMR90_70	PMD-positive	28.4	305,316
IMR90_80	PMD-positive	32.5	313,744
IMR90_90	PMD-positive	36.4	318,776
IMR90_100	PMD-positive	40.5	324,456
Placenta	PMD-positive	9.3	308,166
Mammary epithelial cell	PMD-positive	20.1	292,602
Breast cancer	PMD-positive	31.7	316,413
B cell	Hematopoietic	12.3	229,717
CD133 hsc	Hematopoietic	10.6	212,253
Hspc	Hematopoietic	31.7	333,716
Neutrophil	Hematopoietic	10.0	256,623
Sperm	Sperm	7.3	162,496



### Additional file 6 – Unsupervised clustering of MDL plots

(A) List of WGBS data used for the unsupervised clustering of MDL plots in Figure 4A. (B and C) Ward's clustering of the same WGBS data as (A) using the Spearman's rank-order correlation of the methylation levels of individual CpG sites (B) or sliding windows (window size, 1000 bp; step size, 1000 bp) (C).