Science Advances

AAAS

advances.sciencemag.org/cgi/content/full/4/4/eaar8187/DC1

Supplementary Materials for

Low-input and multiplexed microfluidic assay reveals epigenomic variation across cerebellum and prefrontal cortex

Sai Ma, Yuan-Pang Hsieh, Jian Ma, Chang Lu

Published 18 April 2018, *Sci. Adv.* **4**, eaar8187 (2018)
DOI: 10.1126/sciadv.aar8187

The PDF file includes:

Other Supplementary Material for this manuscript includes the following:
(available at advances.sciencemag.org/cgi/content/full/4/4/eaar8187/DC1)

Supplementary Figures and Tables

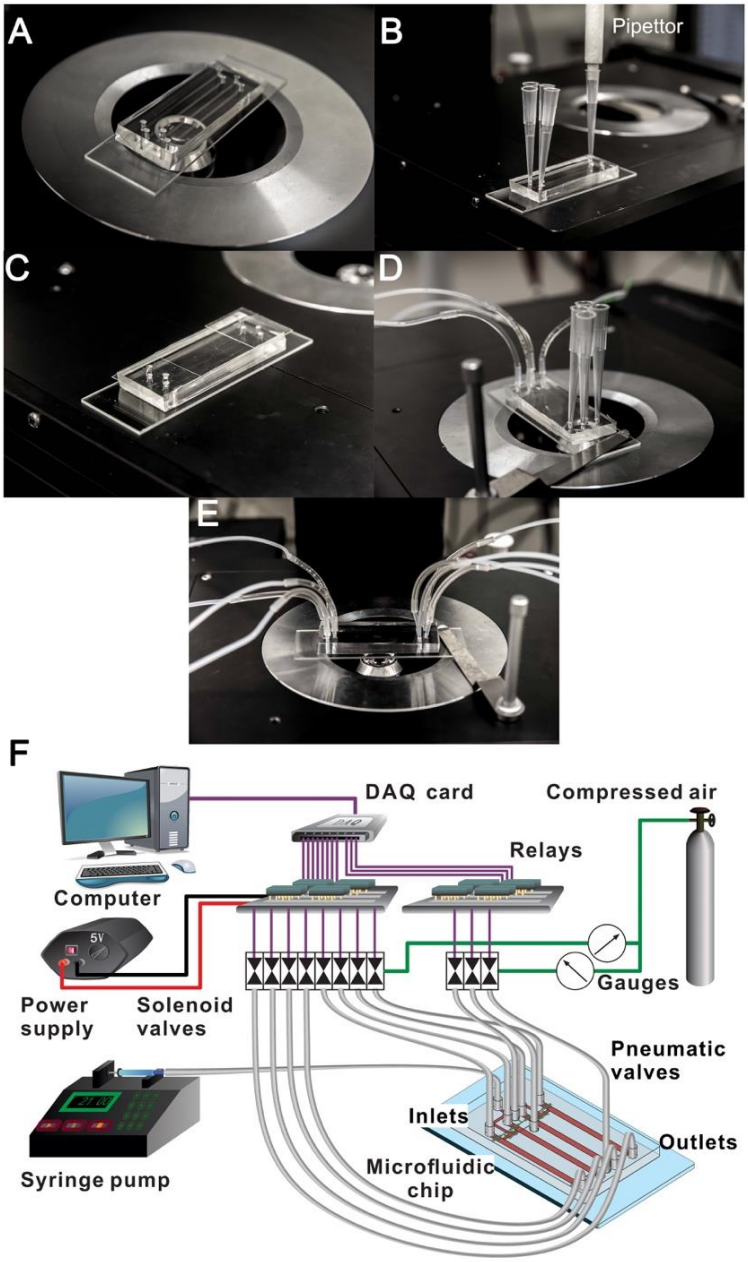

fig. S1. Fabrication, operation, and setup of the SurfaceChIP microfluidic device. We routinely operated 4 single-channel devices simultaneously as shown in (**A**-**E**). (A) A chip with four single-channel devices. (B) Flowing solution (stored in pipette tips) through a channel by aspiration using a pipettor on the other end during antibody coating and DNA elution steps. (C) Sealed chip during incubation steps. (D) Chromatin solution (in the tubing) flowed through the devices during immunoprecipitation step. Waste was hold in pipette tips. (E) Oscillatory washing of the devices. (**F**) A schematic of the ancillary system for control and liquid delivery of the microfluidic device (a 4-channel device). There were two groups of solenoid valves: the group of 8 was connected with channel inlets and outlets for oscillatory washing and the group of 3 controlled on-chip pneumatic valves.

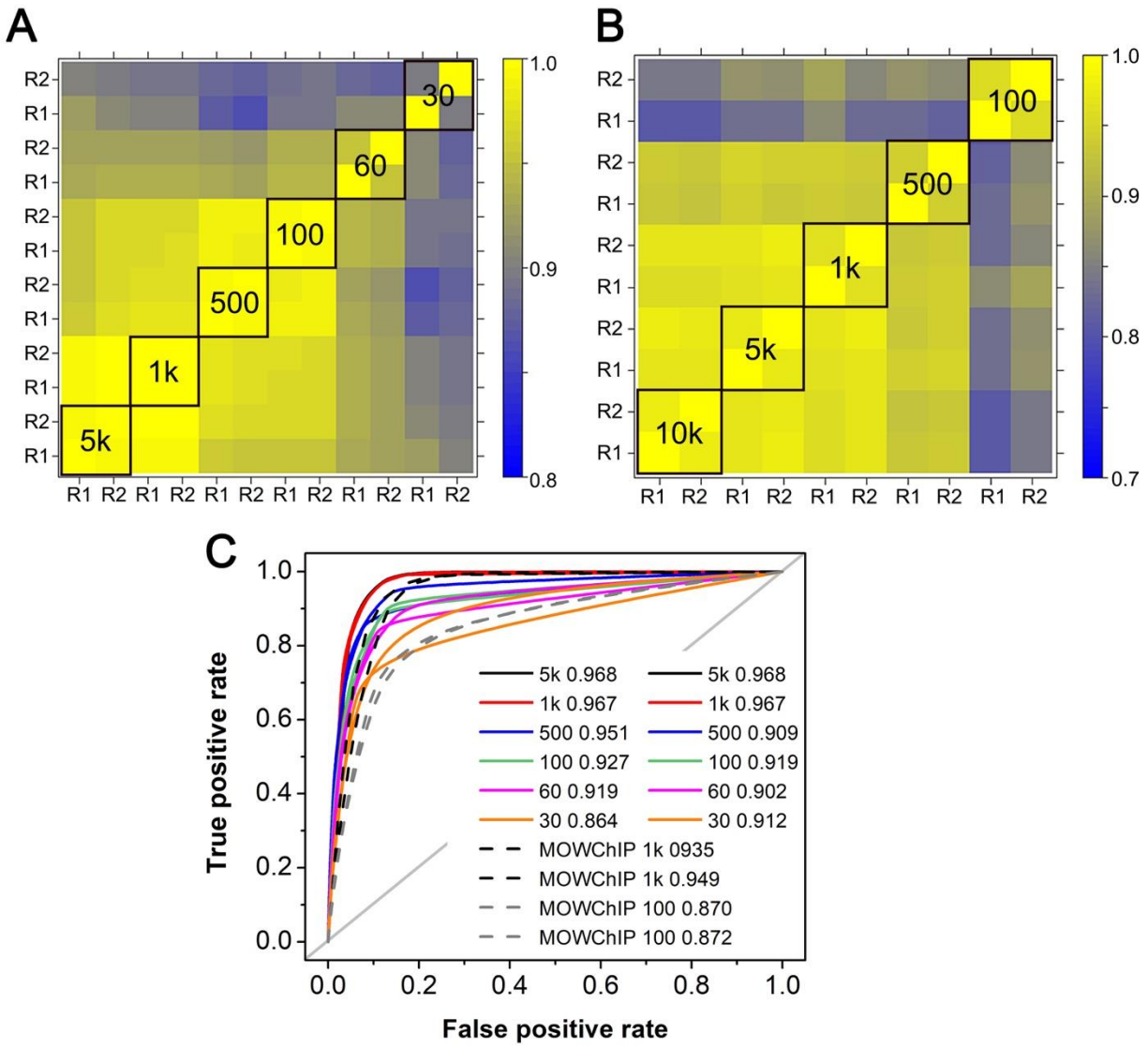

fig. S2. Data quality of SurfaceChIP-seq. Pearson's correlations of SurfaceChIP-seq signals in promoter regions among samples containing various numbers of GM12878 cells: 30-5k per assay for H3K4me3 (**A**), 100-10k per assay for H3K27me3 (**B**). R1 and R2 are replicates. (**C**) Receiver operating characteristic (ROC) curves for H3K4me3 SurfaceChIP-seq data on GM12878 cells in comparison to MOWChIP-seq data. ROC curves were constructed by comparing SurfaceChIP-seq (or MOWChIP-seq) data to published gold-standard data generated using conventional protocols with millions of cells. Values shown are the number of cells used per assay followed by area under the ROC curve (AUC). Each dataset has two replicates.

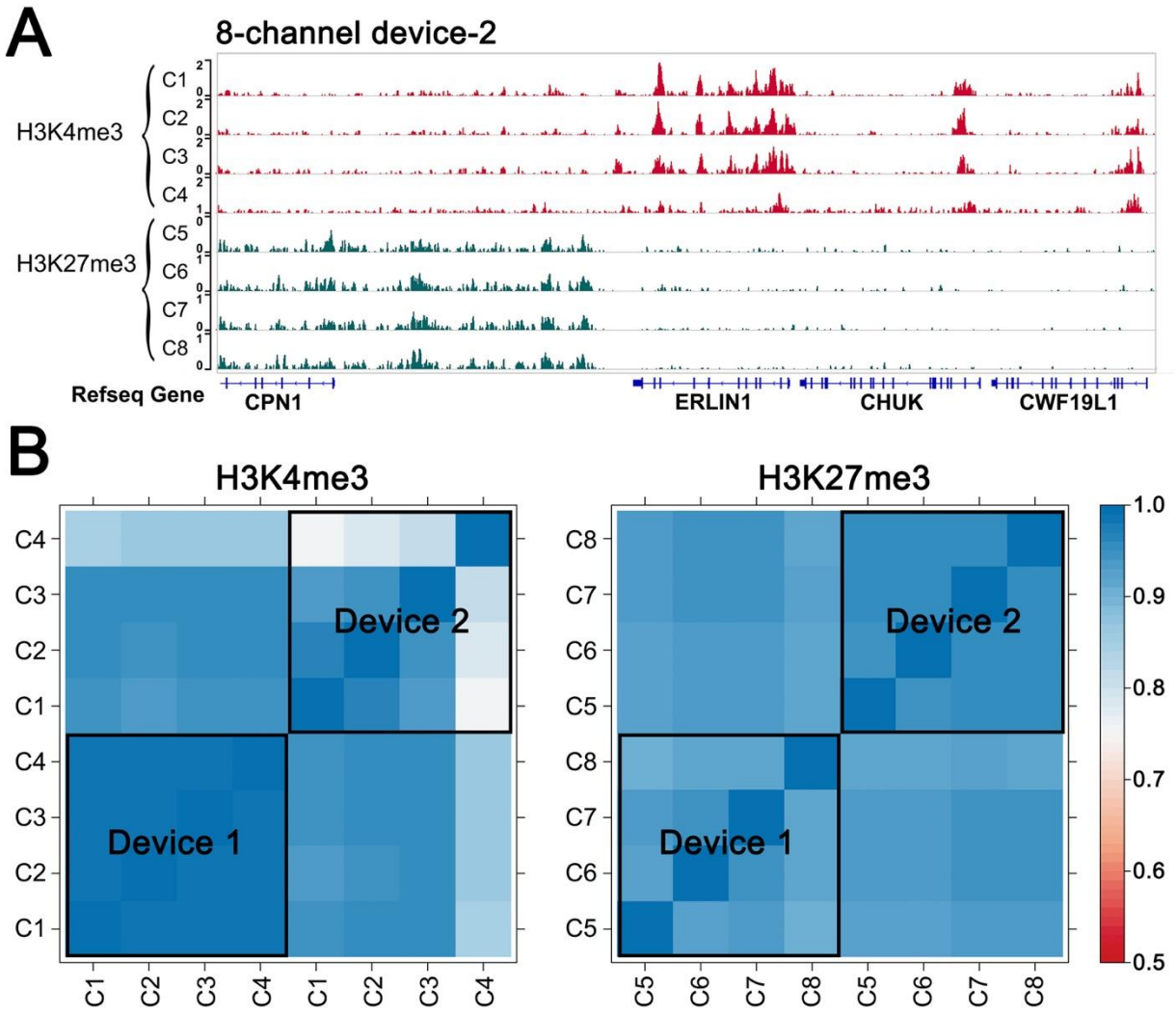

fig. S3. Reproducibility of SurfaceChIP-seq data by eight-channel devices produced in different batches. (**A**) Normalized ChIP-seq data on H3K4me3 and H3K27me3 generated using 8-channel device (No. 2, 100 cells per assay/channel for the 8 channels C1-C8). (**B**) Pearson's correlations among datasets generated by devices No. 1 and 2.

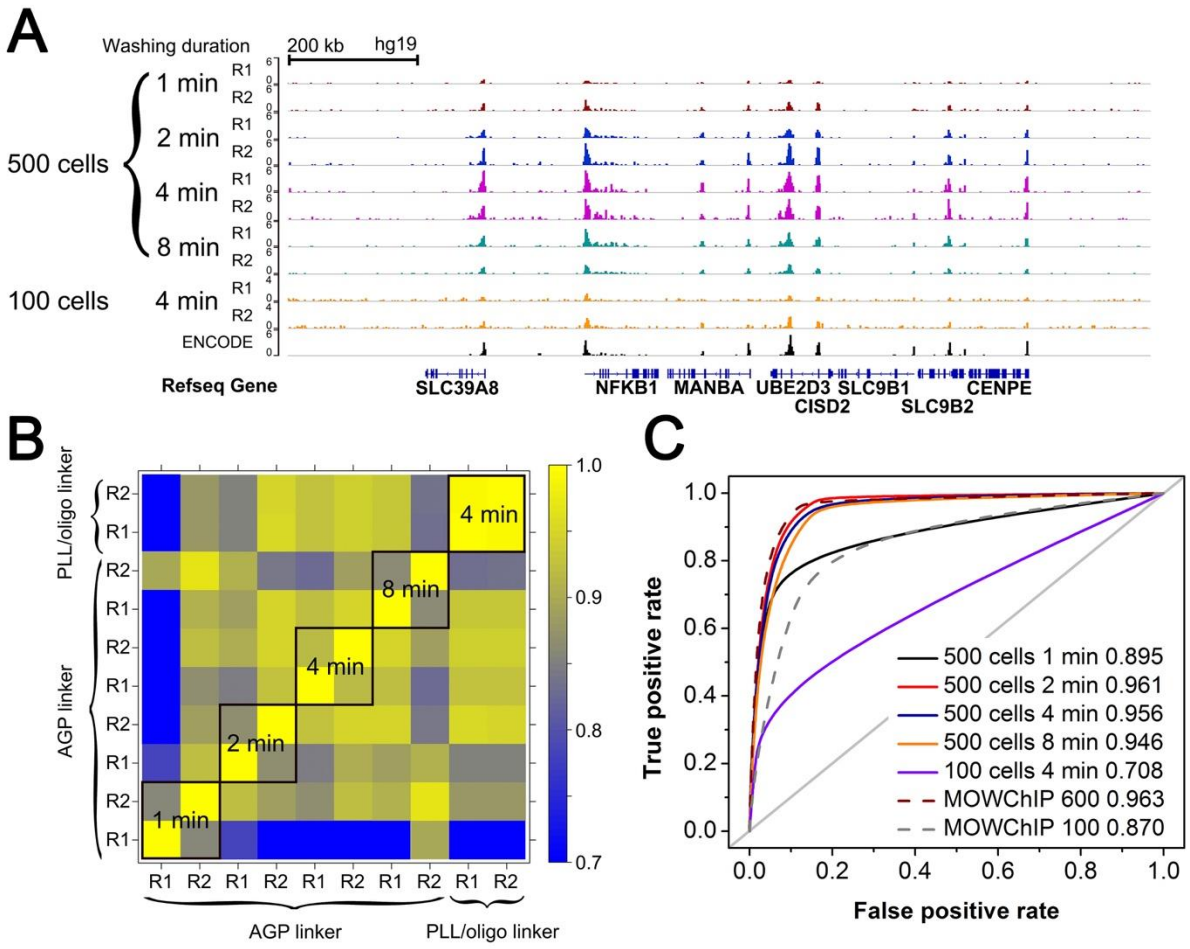

fig. S4. SurfaceChIP-seq with AGP linker. (**A**) Normalized H3K4me3 signals of GM12878 cells with 100 or 500 cells per assay under various washing durations by AGP linker SurfaceChIP-seq. R1 and R2 are replicates. (**B**) Pearson's correlations among AGP linker SurfaceChIP-seq data using various washing durations (500 cells per assay), in comparison to data generated using PLL/oligo linker. The normalized signals from promoter regions were used in calculations. (**C**) ROC curves of AGP linker SurfaceChIP-seq data on H3K4me3, in comparison to MOWChIP-seq data.

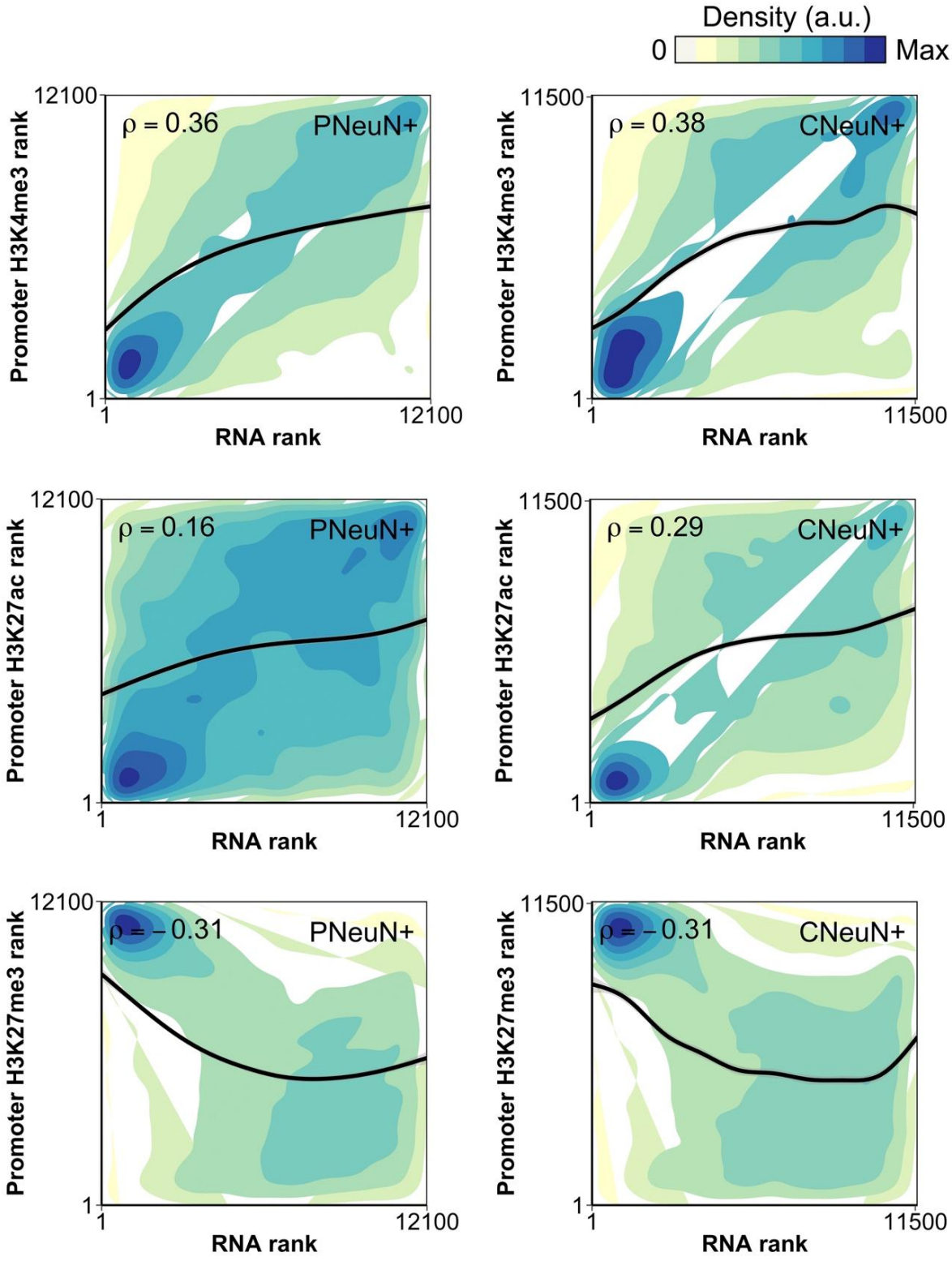

fig. S5. Rank of H3K4me3, H3K27ac, and H3K27me3 signals at promoters plotted against mRNA rank (generated by mRNA-seq). Grey area represents s.e.m. The data generated with 1k nuclei per assay using samples from mouse M3 were used in the analysis. ρ represents Spearman correlation coefficient.

table S1. Metadata of SurfaceChIP-seq and mRNA-seq. (see attached excel file)

table S2. A list of genes with differential H3K4me3 mark at promoters across PNeuN+ and CNeuN+ populations. (see attached excel file)

table S3. A list of genes with differential H3K27ac mark at promoters across PNeuN+ and CNeuN+ populations. (see attached excel file)

table S4. A list of genes with differential H3K27me3 mark at promoters across PNeuN+ and CNeuN+ populations. (see attached excel file)

table S5. A list of differentially expressed genes (fold change > 4; $P < 0.05$, *t* test) with correlated differential histone modification in H3K4me3 or H3K27me3 at promoters across PNeuN+ and CNeuN+ populations. (see attached excel file)