**Supplementary Text**

**Data processing and analysis**

Adapter trimming was done with Trimmomatic (v 0.32) with default parameters. For mapping, we used Bowtie2. For paired-end reads, we used parameters as in Denny et al (2016)[1]. For single-end reads, no additional parameters were set. Picard was used for removing duplicates with *lenient* stringency level. For peak analysis, we tested three parameter sets with two peak calling mode, *broad* and *narrow*, as below:

1. Default parameters: shift 0, extsize 200, default FDR cutoff (0.01)
2. ENCODE parameters: shift -37, extsize 73, p-value cutoff (0.01)
3. BAMPE parameters: BAMPE mode for paired ends, default FDR cutoff (0.01)

Samples sequenced with single-end reads were excluded in BAMPE parameters. The number of peaks greatly varies across different parameters (**Figure S1**). Peak mode affected in the peak numbers to some degree. ENCODE parameters produced much higher number of peaks and showed different pattern to the number of reads. When we added the same level of FDR filtering, however, the trend in regard to the number of reads became consistent across different parameters.

**RNA expression variability test of commonly accessible genes**

We assigned the rank of mean expression, *r(gene)*, to the commonly accessible genes. Then we generated the control set by randomly selecting genes ranked closest to the genes within the commonly accessible gene set (e.g., *r(gene)+1* or *r(gene)-1*), excluding genes within the set. The direction of selecting the closest ranked gene was determined randomly. The Wilcoxon rank sum test was applied between the commonly accessible gene set and the control set.

**Mouse brain sample description**

Among various types of neurons in the CeA, somatostatin-positive neurons (SOM+) are long-range projection neurons and are one of the major populations of the CeA, whose synaptic plasticity plays a role in fear learning [2]. In stark contrast, SOM+ neurons in the cortex are local interneurons that have distinct functions and developmental origin compared with SOM+ neurons in the CeA [3, 4]. Interestingly, the Tyrosine Kinase-Type Cell Surface Receptor HER4 (*ErbB4*), which plays important roles in neuronal development and function, is largely excluded from SOM+ cortical neurons but is highly expressed in SOM+ CeA neurons [5, 6]. Therefore, SOM+ neurons in the CeA and those in the cortex are ideally suited to the test of epigenetic changes in the contexts of fear memory formation and the manipulation of ErbB4 content. Here we assayed global changes in chromatin accessibility in the SOM+ CeA neurons versus SOM+ cortical neurons in fear-conditioned mice and mice in which *Erbb4* is selectively deleted in SOM+ cells (*SOMErbb4-KO* mice) that could lead to differentially regulated gene expression. For the purposes of the current analysis, this variation is matched between amygdala and cortex samples and we focus only on the top-level brain-region analysis within this paper.

Male and female mice bred onto the C57BL/6J background with the age of 2-3 months were used for the experiments. Fear conditioning procedures were performed following Penzo et al (2014) [7] with modifications; 2 tones during habituation and the shock intensity at 0.7 mA. Control mice were under the same condition except for foot shock.

**Preparation of nuclei from brain tissue**

24 hours after fear conditioning, animals were deeply anesthetized and rapidly decapitated. Brains were dissected and sectioned at 500m on ice in a stainless steel brain matrix (EMS 69090-C). PFC or CeA was microdissected in ice-cold PBS with 1x protease inhibitors (Roche) under a stereomicroscope. The tissue was resuspended in 500µl homogenization buffer containing 300mM sucrose, 60mM KCl, 15mM NaCl, 15mM Tris-HCl, 5mM MgCl2, 0.1mM EGTA, 1 mM DTT, 0.1mM PMSF and 1x protease inhibitors, EDTA-free (Roche), and disrupted using a cordless pestle motor homogenize tissue with 4 bursts of 5 seconds. Nuclei were prepared by a seven minute detergent lysis with the addition of IGEPAL CA-630 (Sigma) to a final concentration of 0.2%, followed by pelleting at 1500rcf and gentle resuspension in PBS containing 2% FBS for FACS sorting. Nuclei were filtered through 40 m cell strainers and NucBlue was added to SOMErbb4-KO nuclei, while SOMH2B-GFP were gated on GFP. Nuclei were sorted into technical replicates of 50,000 nuclei and immediately proceeded to the ATAC-seq transposition reaction.

**ATAC-seq library preparation**

For each library, 50,000 sorted nuclei were resuspended in Transposition Reaction Mix then incubated at 37° C. Using Qiagen MinElute Kit we purified 50uL reaction volume. Transposed DNA were stored at -20C. We used the primers in Buenrostro et al (2013) for library construction. ATAC-seq library quality was assessed on an agarose gel with 1X SYBR Gold to view banding. Libraries were quantified by both Bioanalyzer High Sensitivity Chips and the KAPA Illumina Library Quantification kit.

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