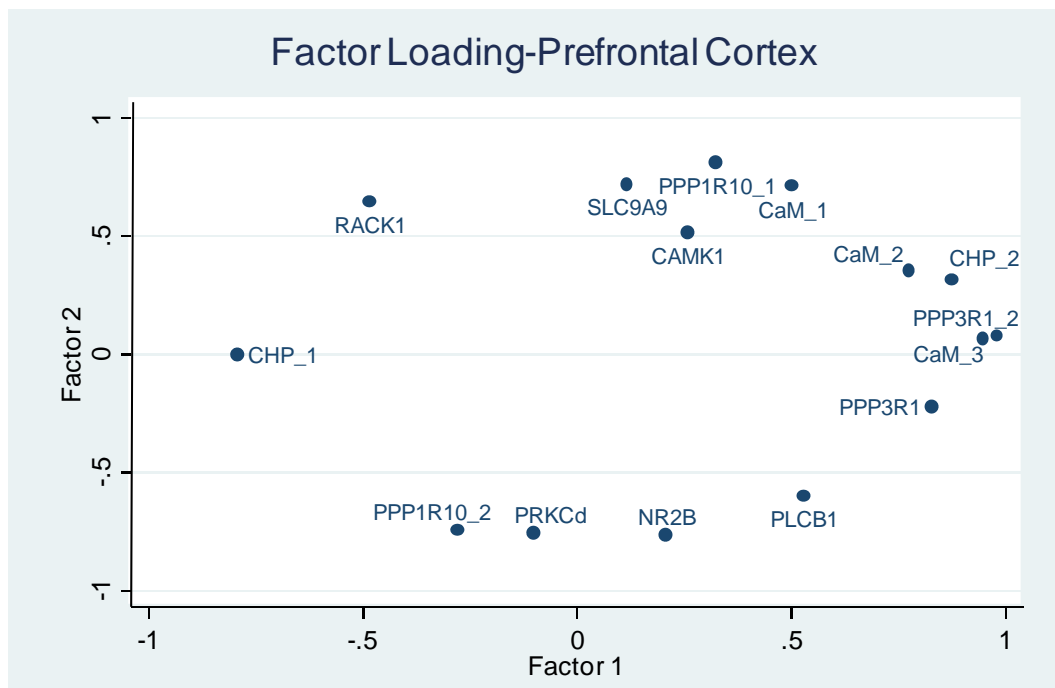


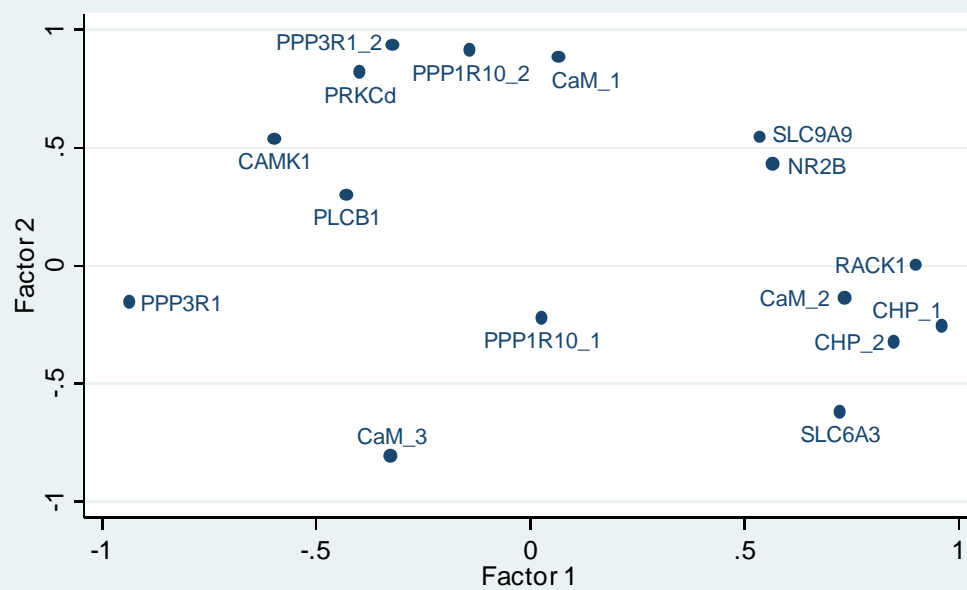
**Supplementary Table 1. Primer sequences.**

<b>Gene</b>	<b>Forward Primer</b>	<b>Reverse Primer</b>
<b><i>CycA</i></b>	AGCACTGGGGAGAAAGGATT	AGCCACTCAGTCTTGGCAGT
<b><i>Ywhaz</i></b>	TTGAGCAGAAGACGGAAGGT	GAAGCATTGGGGATCAAGAA
<b><i>Hprt1</i></b>	GCAGACTTTGCTTTCCTTGG	CGAGAGGTCCTTTTCACCAG
<b><i>RACK1</i></b>	GTGCTCTTCGAGGTCACTCC	CGGTTGTCAGAGGAGAAAGC
<b><i>CaMK1</i></b>	TCCCTGAAGGACATGAGACC	GACTTCTCCCCAGCCCTAAC
<b><i>CHP</i></b>	GAAC TTGCCATCAACCCACT	TCCGGTCCATTACATCTTT
<b><i>PPP1R10</i></b>	GGCTGAAGCTGAGTTCTGGA	ATGGCTGTAGGCAAGAGTGG
<b><i>PKCm</i></b>	GGCATCTCGTTCCATCTGC	TAAGATCGCCCTCCTGAATG
<b><i>PPP3R1</i></b>	GGTGCTTGGTGTCTTTGCAT	GAACTGGGACAGATCACACC
<b><i>PLCB1</i></b>	ATGCCATGTGCTTTGGTTTT	GGCGAGAATCACAATGTTCA
<b><i>CaM</i></b>	CCTCTTCAAGTGCCCCAAT	GGTGTGCTCAAGTCCACAGA
<b><i>NR2B</i></b>	TCTGCCTTCTTAGAGCCATT CAG	AGACAGCCACCGCAGAAAC
<b><i>SLC9A9</i></b>	TGGAGAAGATGACGTTTGACC	GAGATGGCTGTTCCCAAGAA

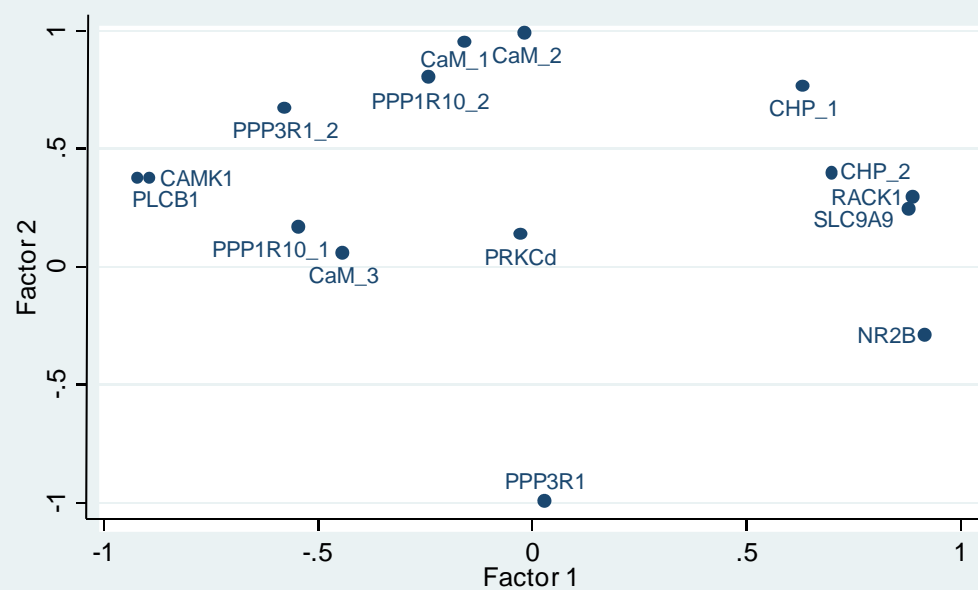
**Supplementary Figure 1. Principal Factors Factor Analysis of microarray data from three brain regions: Prefrontal cortex, substantia nigra and vental tegmental area (SN\_VTA) and hippocampus. or three brain region combined.** Ovals group the genes with factor loading predominantly in one of the two factors in the combined brain region analysis. Notice that *SLC9A9* loads equally on both factors, and appears most closely associated with NR2B, CAMK1, PPP1R10, and PRKCd across the three brain regions combined, although there were differences in the loadings within each region. Some of the genes were represented by multiple probes in the array, which were denoted by ‘\_’ followed by a number.



### Factor Loading-SN\_VTA



### Factor Loading-Hippocampus



Factor Loading-Three Brain Regions

