

## Supplementary information

### Supplementary methods

#### SMRI cohort

The specimens were collected, processed, and stored in a standardized way by participating medical examiner with informed consent from next of kin. Exclusion criteria for all SMRI brain specimens: (1) significant structural brain pathology on postmortem examination by a qualified neuropathologist, or by premortem imaging; (2) history of significant focal neurological signs premortem; (3) history of central nervous system disease that could be expected to alter gene expression in a persistent way; (4) documented IQ under 70; or (5) poor RNA quality. RNA integrity and purity were determined with an Agilent 2100 Bioanalyzer (Agilent, Palo Alto, California, United States). Additional exclusion criteria for unaffected controls included age less than 30 (thus, still in the period of maximum risk) and substance abuse within 1 yr of death or evidence of significant alcohol-related changes in the liver.

**Supplementary Table 1: Primers used for quantitative real-time RT-PCR experiments.**

<b>Gene</b>	<b>Primer</b>	<b>Sequence (5'-3')</b>
miR-137	miR-137_F	TTGCTTAAGAATACGCGTAG
	Universal reverse primer	NA (Agilent Catalog # 600037)
snRNA U6	U6-snRNA_F	NA (Agilent Catalog # 600750)
	Universal reverse primer	NA (Agilent Catalog # 600037)
TCF4	TCF4_F	CCTGCATCCACATGAACG
	TCF4_R	ACATCGGAGGAAGACTGGAA
ZNF804a	ZNF804A_F	ACTCCAACGCCTGCACAAG
	ZNF804A_R	CCACTTCCAGGAGCACATAC
CACNA1C	CACNA1C_F	CCTGAGAATGAGGACGAAGG
	CACNA1C_R	GTTTTCCGGTGTGACGGACT
GAPDH	GAPDH_F	ACCCACTCCTCCACCTTTGA
	GAPDH_R	AATTCGTTGTCATACCAGGA
HPRT1	HPRT1_F	ACACTGGCAAAACAATGCA
	HPRT1_R	AGCTTGCTGGTGAAAAGGACC
SDHA	SDHA_F	TCACTGTTGATGGGAACAAG
	SDHA_R	TTTGATGCAGTGGTGGTAGG

NA Primer sequence is not available.

Supplementary Table 2: ANOVA results.

	p-value(Disease)	p-value(BP vs. CTR)	p-value(BP vs. SZ)	p-value(CTR vs. SZ)
<b>ALL</b>	0.48	0.41	0.23	0.70
<b>SMRI</b>	0.88	0.62	0.89	0.72
<b>UCI</b>	0.30	0.18	0.15	0.74