Supplementary Fig. 1

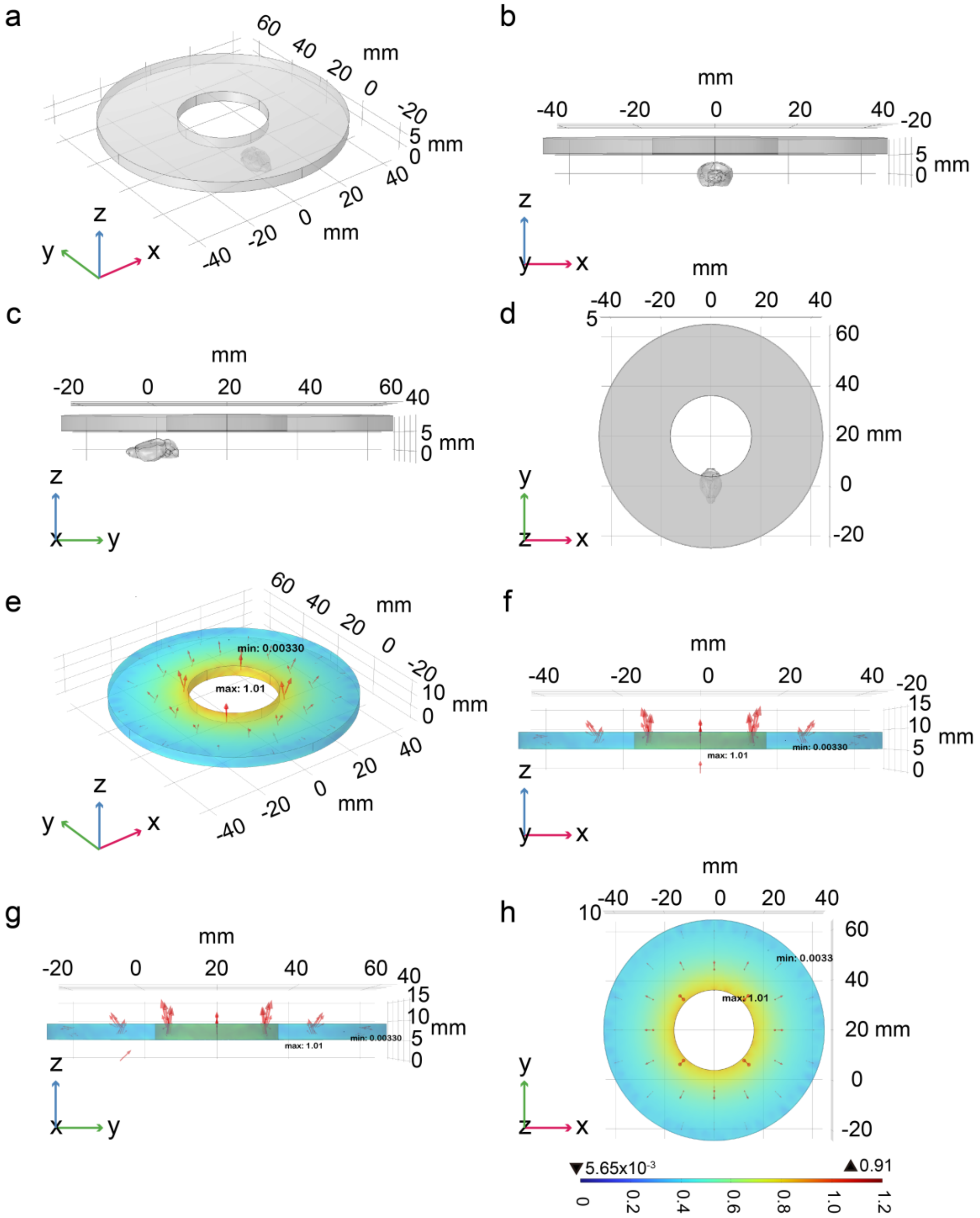


Fig. S1 Schematic representation of magnetic field simulation. Relative positioning of the coil and mouse head model (**a-d**), and the magnetic flux density distribution (**e-h**).

Supplementary Fig. 2

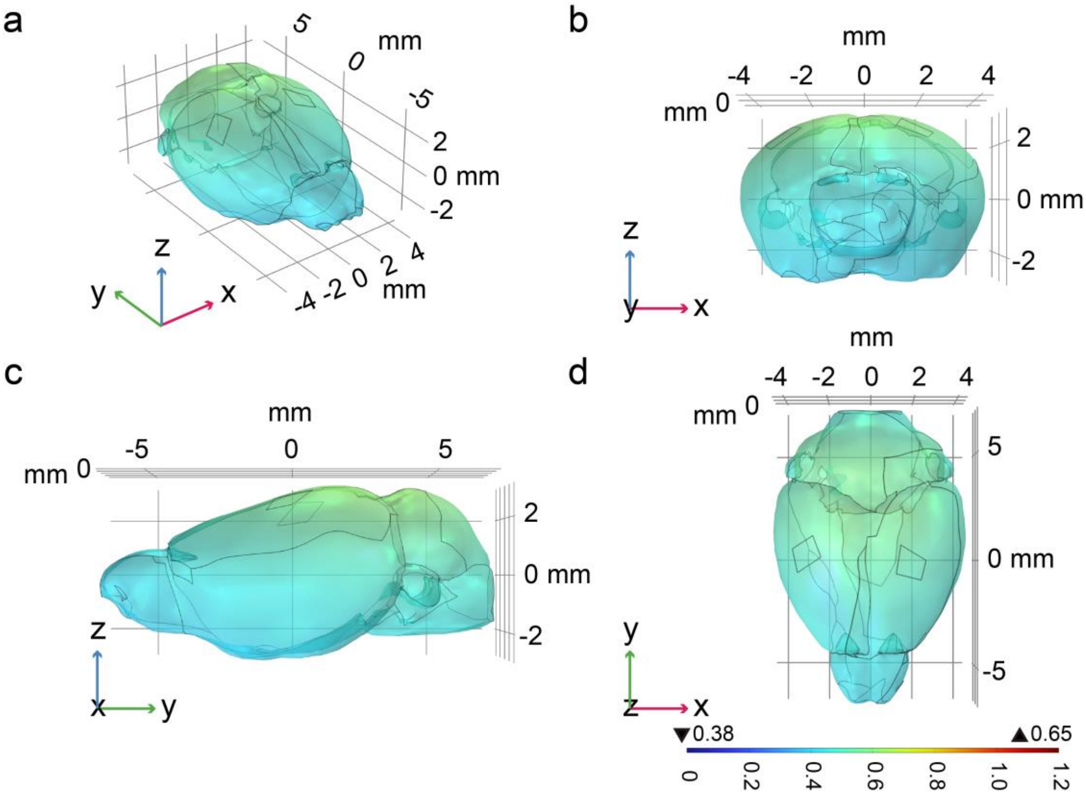
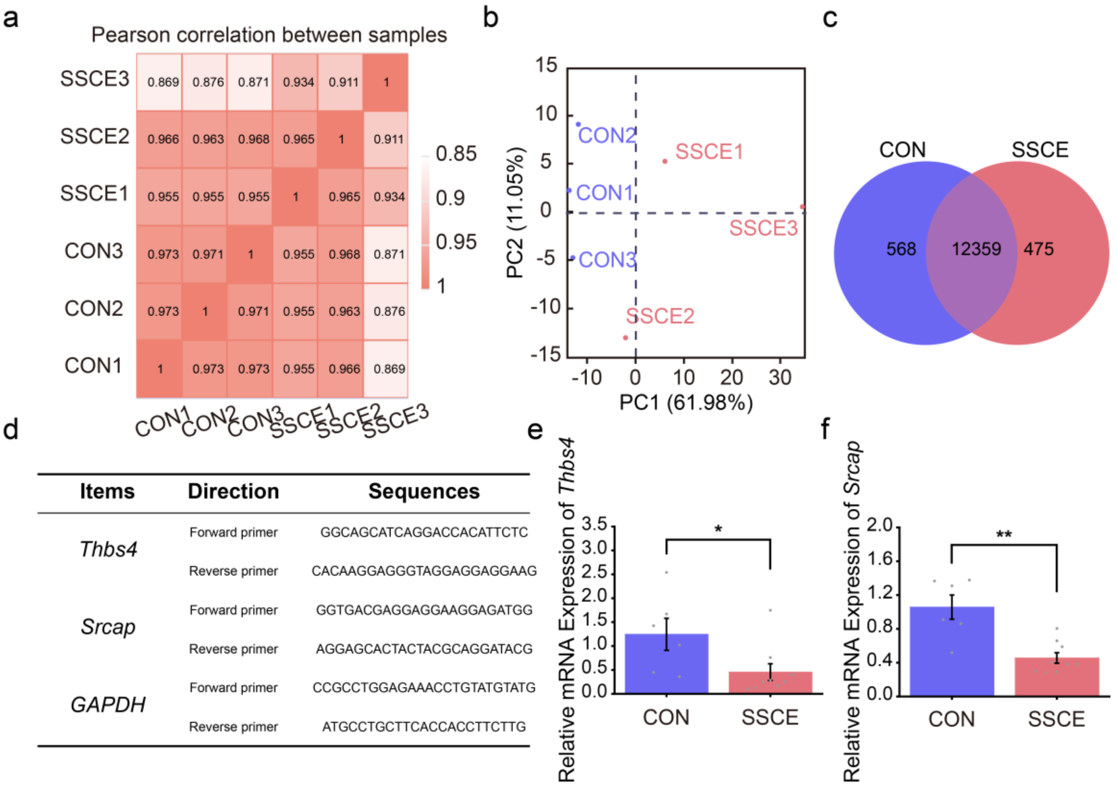


Fig. S2 Magnetic flux density (**a-d**) is shown on the anatomically accurate mouse brain model.

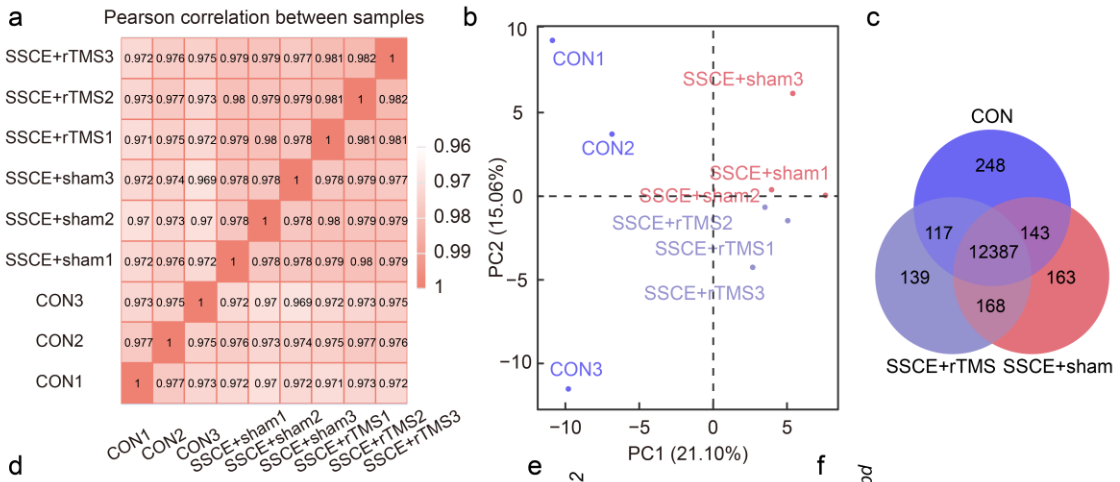
Supplementary Fig. 3



Items	Direction	Sequences
Thbs4	Forward primer	GGCAGCATCAGGACCACATTCTC
	Reverse primer	CACAAGGAGGGTAGGAGGAGGAAG
Srcap	Forward primer	GGTGACGAGGAGGAAGGAGATGG
	Reverse primer	AGGAGCACTACTACGCAGGATACG
GAPDH	Forward primer	CCGCCTGGAGAAACCTGTATGTATG
	Reverse primer	ATGCCTGCTTCACCACCTTCTTG

Fig. S3 DEGs analysis of the prefrontal cortex in mice following short-term of SSCE exposure. **a.** Correlation analysis between samples. **b**. Principal component analysis (PCA) of samples. **c**. Venn diagram of co-expressed genes between the CON and SSCE groups. **d**. Primer sequences used for RT-qPCR experiments. **e, f**. Relative expression levels of genes *Thbs4* (**e**) and *Srcap* (**f**) in the PFC of mice after short-term SSCE.

Supplementary Fig. 4



	CON1	CON2	CON3	SSCE+sham1	SSCE+sham2	SSCE+sham3	SSCE+rTMS1	SSCE+rTMS2	SSCE+rTMS3
SSCE+rTMS3	0.972	0.976	0.975	0.979	0.979	0.977	0.981	0.982	1
SSCE+rTMS2	0.973	0.977	0.973	0.98	0.979	0.979	0.981	1	0.982
SSCE+rTMS1	0.971	0.975	0.972	0.979	0.98	0.978	1	0.981	0.981
SSCE+sham3	0.972	0.974	0.969	0.978	0.978	1	0.978	0.979	0.977
SSCE+sham2	0.97	0.973	0.97	0.978	1	0.978	0.98	0.979	0.979
SSCE+sham1	0.972	0.976	0.972	1	0.978	0.978	0.979	0.98	0.979
CON3	0.973	0.975	1	0.972	0.97	0.969	0.972	0.973	0.975
CON2	0.977	1	0.975	0.976	0.973	0.974	0.975	0.977	0.976
CON1	1	0.977	0.973	0.972	0.97	0.972	0.971	0.973	0.972

d

Items	Direction	Sequences
Lcn2	Forward primer	TTTCACCCGCTTTGCCAAGTCTC
	Reverse primer	ATCCCTTCCCTGTCTCCTCAACTG
Cebpd	Forward primer	TGCCCAGCCCGCCTTTCC
	Reverse primer	CTCGCAGGTCCCAAAGAAACTAGC
Hba-a2	Forward primer	AGCAGAGGCATCAGGGTGTCC
	Reverse primer	GGTGAAATCGGCAGGGTGGTG
Lrg1	Forward primer	GGTCCCATGTCAGTGTGCAGATTC
	Reverse primer	AGAGTTGTGGCGAGTGGAGAGG
GAPDH	Forward primer	CCGCCTGGAGAAACCTGTATGTATG
	Reverse primer	ATGCCTGCTTCACCACCTTCTTG

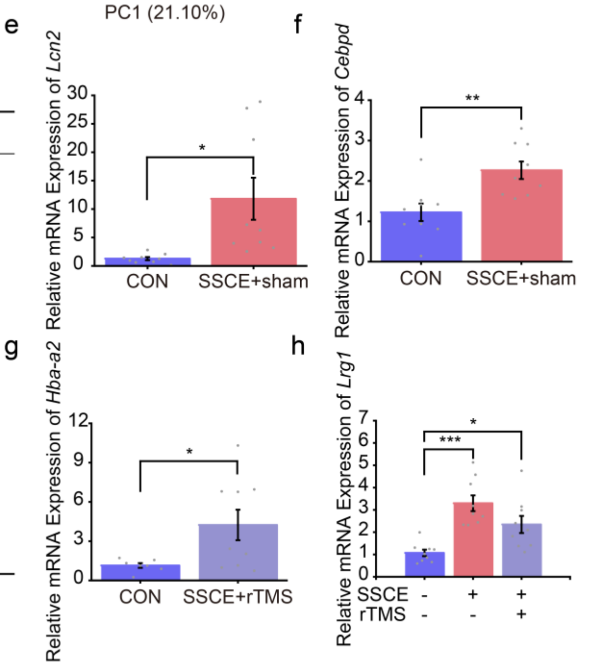


Fig. S4 DEGs analysis of the prefrontal cortex in mice following long-term of SSCE exposure. **a.** Correlation analysis between samples. **b**. Principal component analysis (PCA) of samples. **c**. Venn diagram of co-expressed genes between the CON, SSCE+sham and SSCE+rTMS groups. **d**. Primer sequences used for RT-qPCR experiments. **e-h**. Relative expression levels of genes *Lcn2* (**e**), *Cebpd* (**f**), *Hba-a2* (**g**) and *Lrg1* (**h**) in the PFC of mice after long-term SSCE.

Supplementary Fig. 5

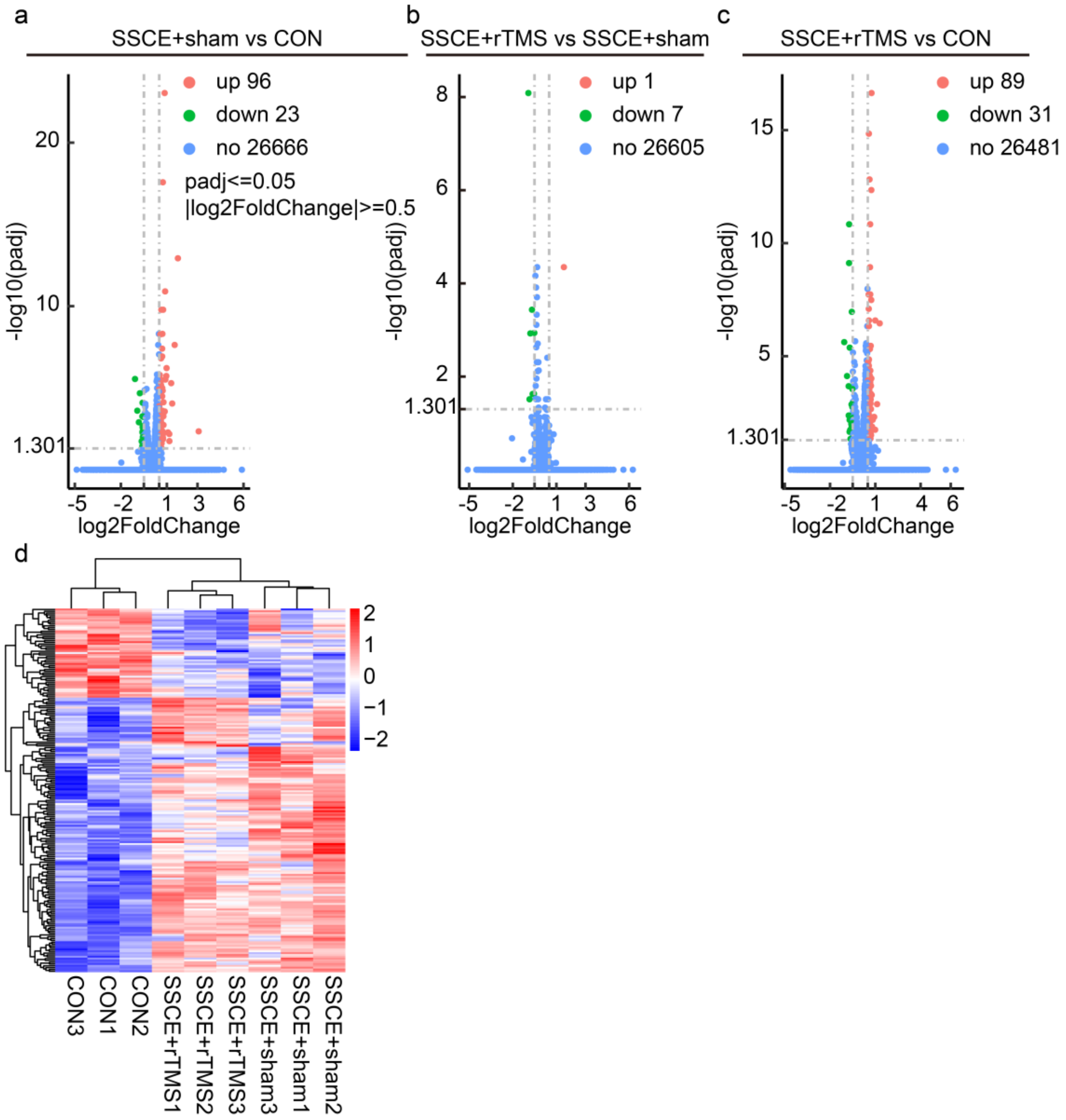


Fig. S5 RNA-seq analysis of the prefrontal cortex in mice following long-term of SSCE exposure. a-c. Volcano plot for the PFC RNA-seq analysis of mice exposed to long-term SSCE (CON: n = 6 mice, SSCE+sham: n = 6 mice, SSCE+rTMS: n = 6 mice). Differentially expressed genes (DEGs), defined by padj ⩽ 0.05, | log2FC| ⩾0.5. FC, foldchange. The complete lists of the RNA-seq analysis and DEGs are provided in **Supplementary Tables 3, 4**. **d**. Hierarchical cluster analysis of DEGs among samples in the CON and SSCE groups exposed to long-term SSCE, respectively (red, up-regulated; blue, down-regulated).

Supplementary Fig. 6

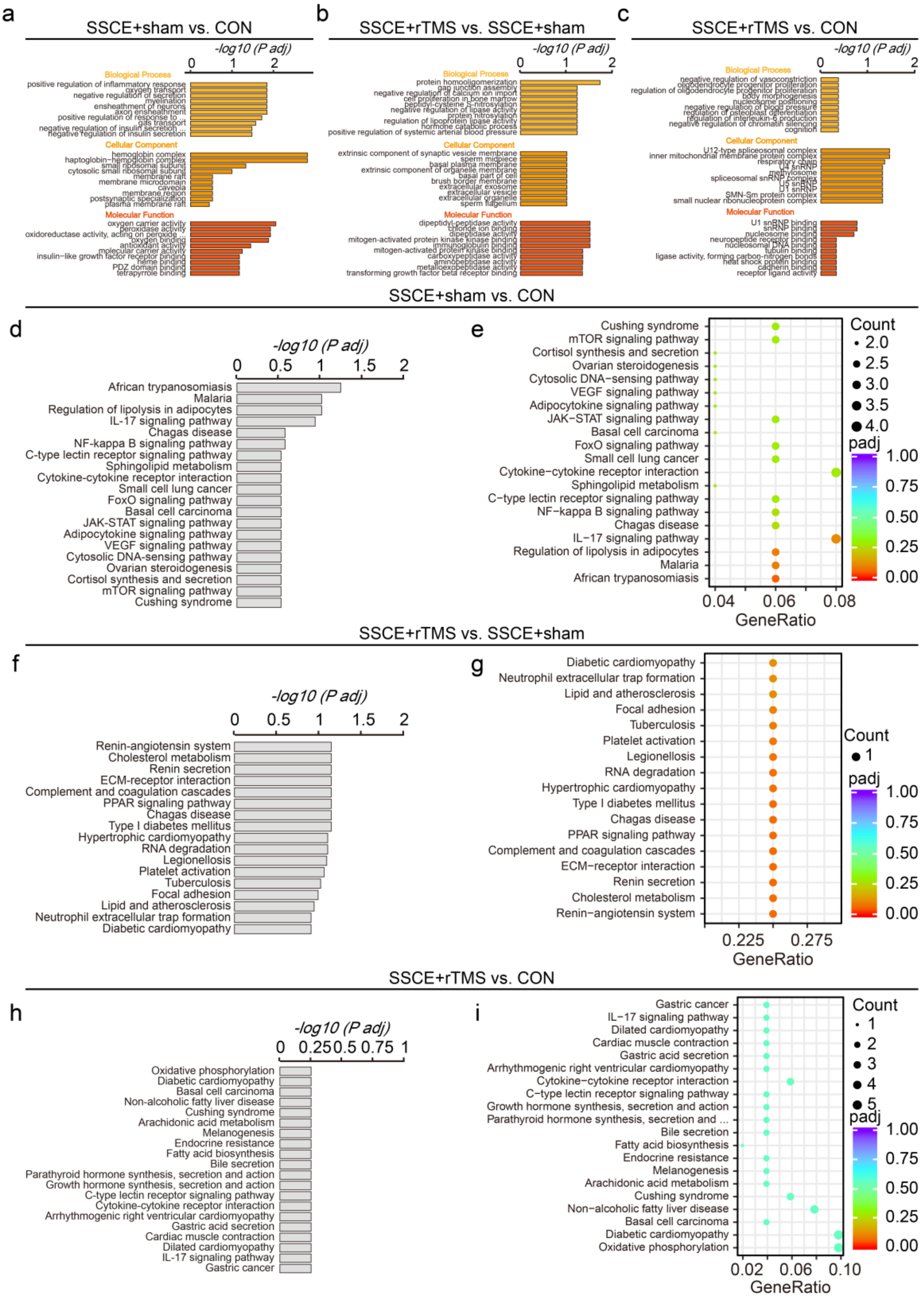
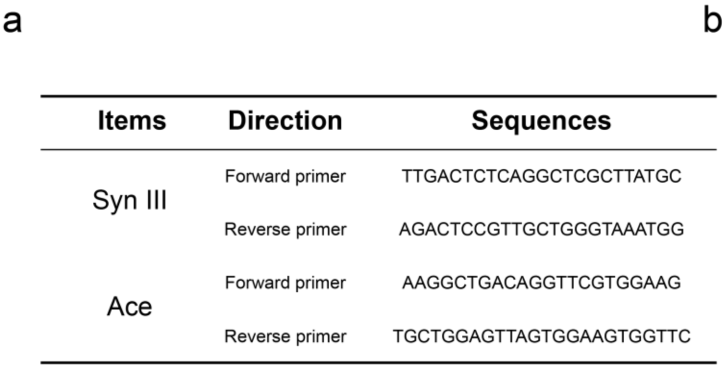
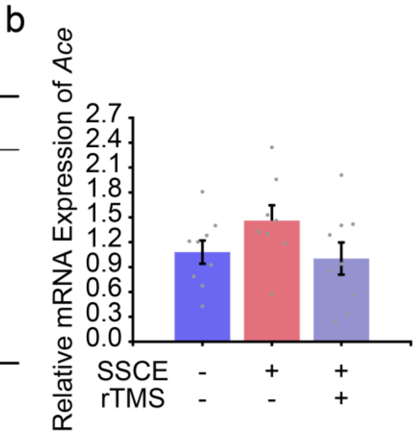


Fig. S6 GO and KEGG pathway analyses of PFC DEGs in mice exposed to long-term SSCE. a-c. All significantly enriched GO categories of biological process, cellular component, and molecular function terms between CON, SSCE+sham and SSCE+rTMS groups exposed to long-term SSCE (**a**. SSCE+sham vs CON, **b**. SSCE+rTMS vs SSCE+sham, **c**. SSCE+rTMS vs CON). **d-i**. All significantly enriched KEGG signaling pathways between CON, SSCE+sham and SSCE+rTMS groups exposed to long-term SSCE (**d, e**. SSCE+sham vs CON, **f, g**. SSCE+rTMS vs SSCE+sham, **h, i**. SSCE+rTMS vs CON).

Supplementary Fig. 7



Items	Direction	Sequences
Syn III	Forward primer	TTGACTCTCAGGCTCGCTTATGC
	Reverse primer	AGACTCCGTTGCTGGGTAAATGG
Ace	Forward primer	AAGGCTGACAGGTTCGTGGAAG
	Reverse primer	TGCTGGAGTTAGTGGAAGTGGTTC



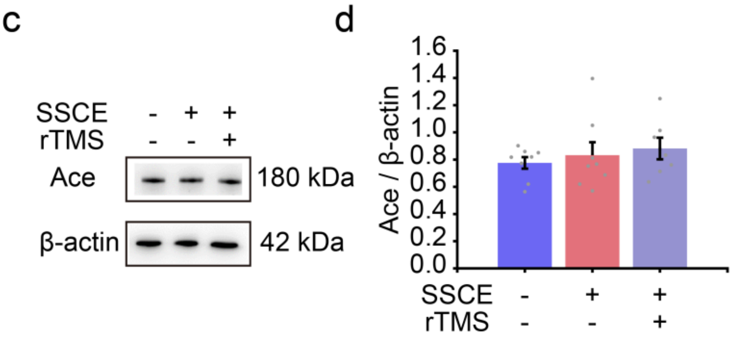


Fig. S7 Quantitative real-time PCR and Western blot verification for the Ace in the PFC of mice exposed to long-term SSCE in Figure 7. a. Primer sequences used for RT-qPCR experiments. **b**. Relative expression levels of genes *Ace* in the PFC of mice after long-term SSCE. **c**. Representative western blot bands using total protein extracts from the PFC region. **d**. Quantification of protein expression levels in the PFC among the CON, SSCE+sham and SSCE+rTMS group (from three mice in each group).

Supplementary Fig. 8

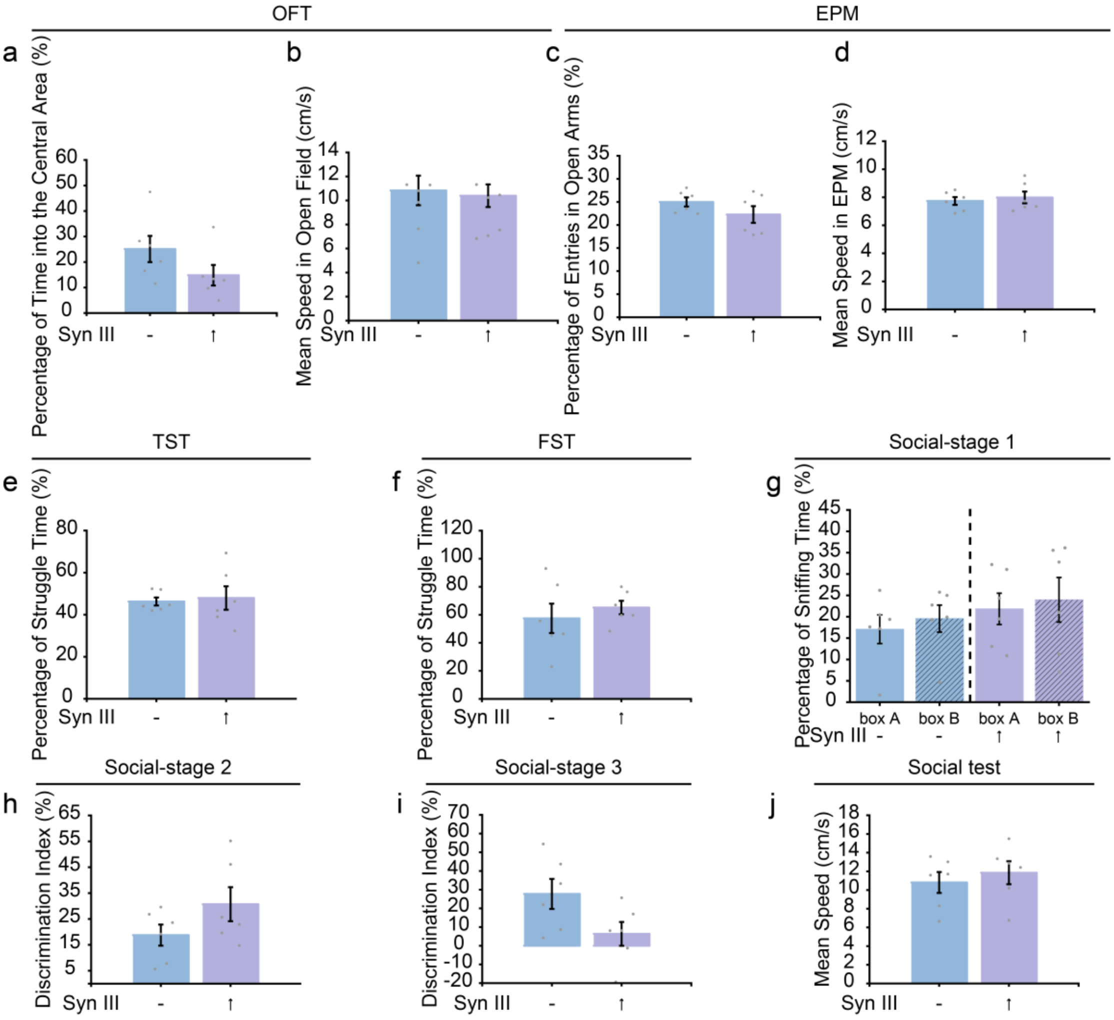


Fig. S8 Behavioral performance of mice injected with the pcAAV-CMV-Syn3-3xFLAG-P2A-GdGreen-WPRE virus into the mPFC. a, b. The percentage of time spent in the center zone (**a**) and the average speed (**b**) during the OFT, respectively. **c, d**. The percentage of time spent in the open arms (**c**) and the average speed (**d**) during the EPM, respectively. **e, f**. Percentage of time spent struggling during the TST (**e**) and FST (**f**), respectively. **g**. Percentage of time spent sniffing the empty box during Stage 1 of the SDT. **h, i**. The discrimination index during Stage 2 (**h**) and Stage 3 (**i**) of the SDT. **j**. Average speed during the SDT.

Supplementary Fig. 9

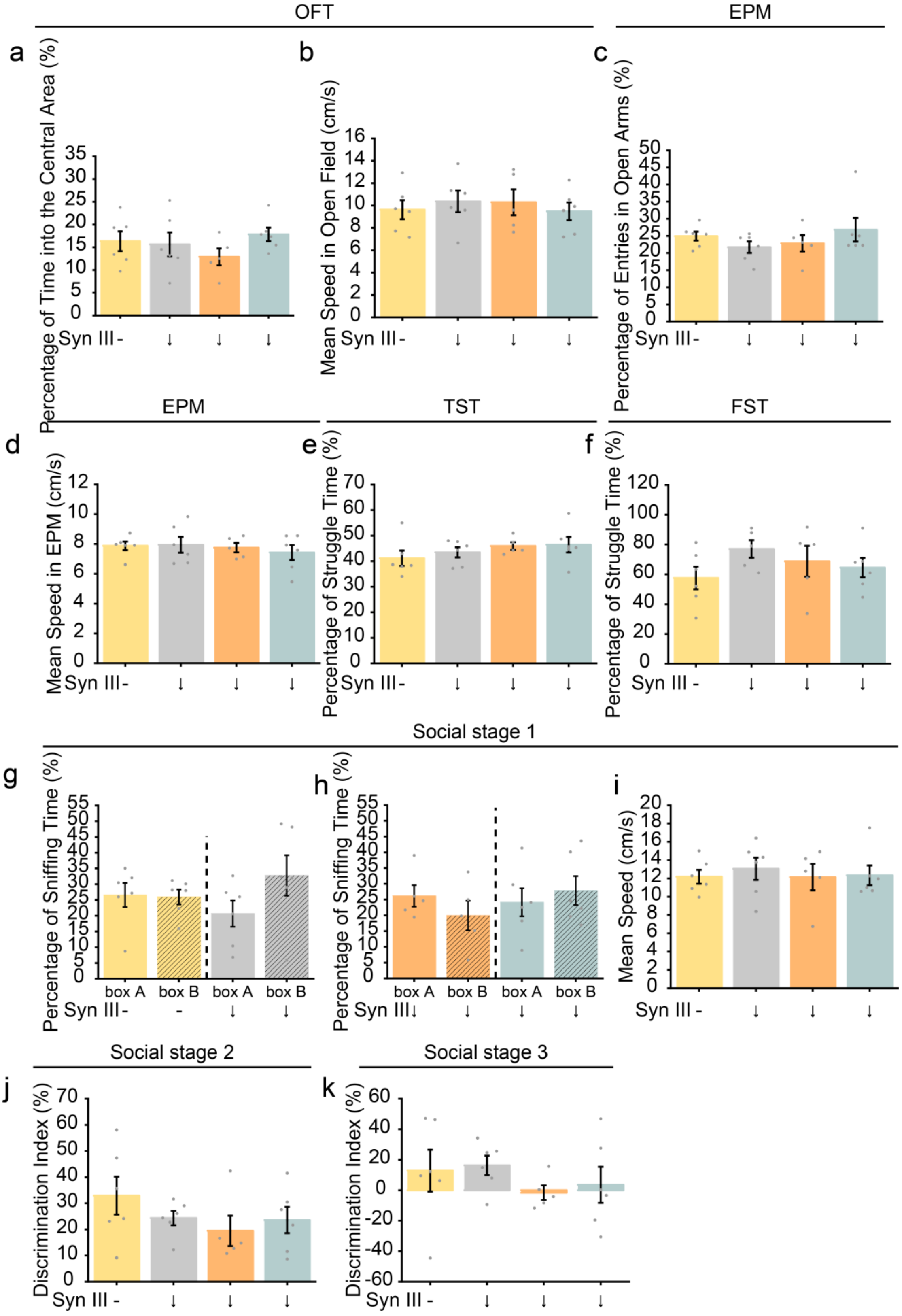
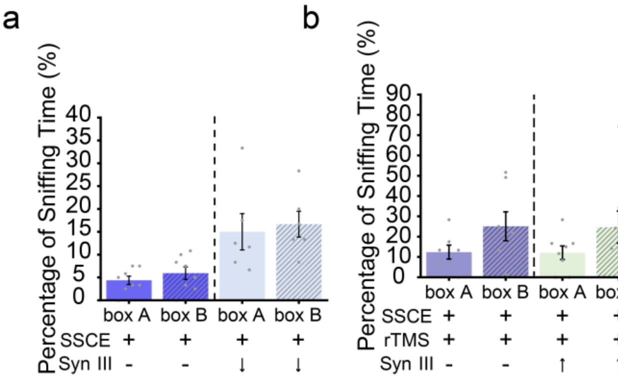


Fig. S9 Behavioral performance of mice injected with the pAAV-U6-shRNA (Syn3)-CMV-mScarlet-WPRE virus into the mPFC. a, b. The percentage of time spent in the center zone (**a**) and the average speed (**b**) during the OFT, respectively. **c, d**. The percentage of time spent in the open arms (**c**) and the average speed (**d**) during the EPM, respectively. **e, f**. Percentage of time spent struggling during the TST (**e**) and FST (**f**), respectively. **g, h**. Percentage of time spent sniffing the empty box during Stage 1 of the SDT. **j, k**. The discrimination index during Stage 2 (**j**) and Stage 3 (**k**) of the SDT. **i**. Average speed during the SDT.

Supplementary Fig. 10



c

Items	Direction	Sequences
NR2A	Forward primer	CCTTCCTTCCTTCCTTCCTTCCTTC
	Reverse primer	TGCCATTATGTCCTTGCTACCAGAG
NR2B	Forward primer	GTGACGGAGGAGGAGGAGGAG
	Reverse primer	GGAAGCAGGAGTCTAGTGGAATGG
PSD95	Forward primer	TGTCTGTCCTCTGTCCGTCCTC
	Reverse primer	CGAAAGGTGAAAGTGGAGCAAAGG
MAPK	Forward primer	GCAATCTTAACCGCTGAACCATCTC
	Reverse primer	TCTGTATGCTGCTGTGCTTCCTG
GAPDH	Forward primer	CCGCCTGGAGAAACCTGTATGTATG
	Reverse primer	ATGCCTGCTTCACCACCTTCTTG

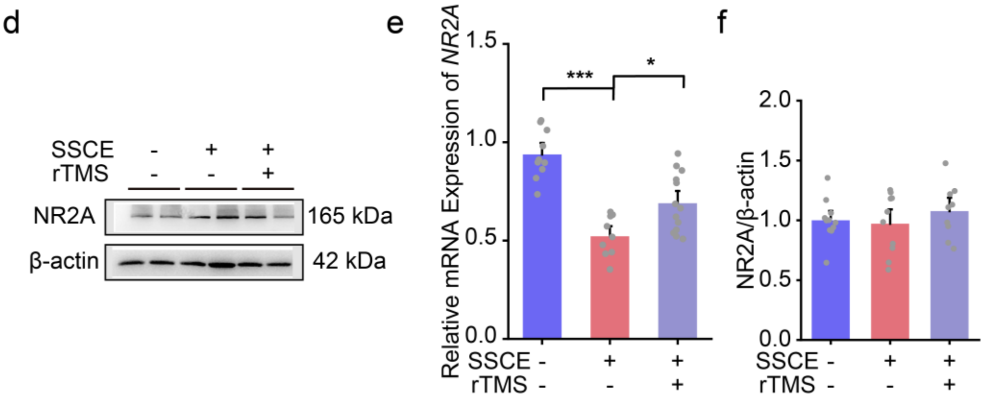


Fig. S10 Behavioral performance during the SDT and molecular expression validation. a, b. Percentage of time spent sniffing the empty box during Stage 1 of the SDT. **c**. Primer sequences used for RT-qPCR experiments. **d**. Representative western blot bands using total protein extracts from the PFC region. **e**. Relative expression levels of genes *NR2A* in the PFC of mice after long-term SSCE. **f**. Quantification of protein expression levels in the PFC among the CON, SSCE+sham and SSCE+rTMS group (from three mice in each group).

Supplementary Table. 1

Isocortex			
Region	**t**	**df**	**p value**
FRP	0.4177	4	0.6976
MOs	1.261	4	0.2759
MOp	1.152	4	0.3136
SSs	0.2604	4	0.8074
SSp	0.06931	4	0.9481
GU	1.338	4	0.2518
VISC	0.4232	4	0.6939
AUD	0.8802	4	0.4285
ACA	0.316	4	0.7678
PL	5.209	4	0.0065
ILA	1.409	4	0.2315
ORB	5.434	4	0.0056
AI	0.3646	4	0.7339
RSP	0.41	4	0.7028
PTLp	0.2188	4	0.8375
TEa	0.3907	4	0.7159
PERI	0.4357	4	0.6855
ECT	0.5447	4	0.6149
OLF			
Region	**t**	**df**	**p value**
AOB	0.1144	4	0.9144
AON	6.843	4	0.0024
COA	0.2521	4	0.8134
DP	2.189	4	0.0938
MOB	23.99	4	<0.0001
NLOT	0.0006482	4	0.9995
PAA	0.4664	4	0.6652
PIR	2.078	4	0.1062
TR	18.23	4	<0.0001
TT	0.7228	4	0.5098
HPF			
Region	**t**	**df**	**p value**
APr	2.508	4	0.0662
CA	0.0546	4	0.9591
DG	0.9513	4	0.3953
ENT	0.2511	4	0.8141
FC	1.809	4	0.1447
HATA	0.8442	4	0.4461
IG	0.3691	4	0.7308

PAR	1.184	4	0.3018
POST	0.07197	4	0.9461
PRE	2.89	4	0.0446
ProS	0.3032	4	0.7768
SUB	1.709	4	0.1627
CTXsp			
Region	**t**	**df**	**p value**
BLA	0.4007	4	0.7091
BMA	0.1144	4	0.9144
CLA	0.2664	4	0.8031
EP	2.912	4	0.0436
LA	2.281	4	0.0847
PA	4.285	4	0.0128
STR			
Region	**t**	**df**	**p value**
CP	0.596	4	0.5833
AAA	0.1623	4	0.879
ACB	0.07455	4	0.9442
CEA	0.7631	4	0.4879
FS	0.8725	4	0.4322
IA	1.053	4	0.3517
LS	0.4668	4	0.6649
MEA	0.4712	4	0.662
OT	0.6031	4	0.579
SF	0.9819	4	0.3818
PAL			
Region	**t**	**df**	**p value**
BST	0.5524	4	0.6101
PALd	0.2416	4	0.821
SI	0.7534	4	0.4931
HY			
Region	**t**	**df**	**p value**
LZ	2.938	4	0.0425
MEZ	6.858	4	0.0024
PVR	5.428	4	0.0056
PVZ	0.6275	4	0.5644
TH			
Region	**t**	**df**	**p value**
ATN	0.1119	4	0.9163
EPI	1.007	4	0.3708
GENd	1.849	4	0.1381
GENv	7.492	4	0.0017
ILM	0.7218	4	0.5103

LAT	1.843	4	0.1391
MED	0.634	4	0.5605
MTN	0.0671	4	0.9497
RT	1.248	4	0.28
SPF	2.081	4	0.106
VENT	0.9512	4	0.3954
MB			
Region	**t**	**df**	**p value**
MBmot	1.199	4	0.2967
MBsen	3.489	4	0.0251
MBsta	2.405	4	0.074
HB			
Region	**t**	**df**	**p value**
MY-mot	1.075	4	0.3429
MY-sat	5.076	4	0.0071
MY-sen	2.334	4	0.0799
P-mot	4.07	4	0.0152
P-sat	0.3226	4	0.7632
P-sen	1.791	4	0.1477
CB			
Region	**t**	**df**	**p value**
CBN	0.367	4	0.7322
CBX	0.6265	4	0.565

Supplementary Table. 2, 3

Table S2 The total RNA detection information for the PFC region after two weeks of SSCE.

Sample ID	Concentration (ng/ul)	Volume (ul)	Total amount (ug)	Integrity value	Conclusion
CON1	121.00	35.00	4.235	7.00	pass
CON2	31.00	35.00	1.085	6.70	pass
CON3	171.00	35.00	5.985	7.80	pass
SSCE1	238.00	35.00	8.330	8.30	pass
SSCE2	191.00	35.00	6.685	7.80	pass
SSCE3	96.00	35.00	3.360	7.90	pass

Table S3 Evaluation and statistics of RNA sequencing valid data after two weeks of SSCE.

Sample ID	Raw Reads	Clean Reads	Clean Ratio	GC content	Mapping Ratio
CON1	43847738	41321266	94.24%	48.70%	96.11%
CON2	45842460	42511298	92.73%	48.23%	96.0%
CON3	44218322	41111864	92.97%	48.53%	96.42%
SSCE1	40859454	37822860	92.57%	48.61%	95.12%
SSCE2	46217266	43541708	94.21%	49.55%	95.59%
SSCE3	45691830	42850474	93.78%	49.63%	94.3%

Supplementary Table. 4, 5

Table S4 The total RNA detection information for the PFC region after four weeks of SSCE.

Sample ID	Concentration (ng/ul)	Volume (ul)	Total amount (ug)	Integrity value	Conclusion
CON1	567.00	35.00	19.845	7.60	pass
CON2	495.00	35.00	17.325	7.80	pass
CON3	376.00	35.00	13.160	8.00	pass
SSCE+sham1	644.00	35.00	22.540	7.90	pass
SSCE+sham2	588.00	35.00	20.580	8.30	pass
SSCE+sham3	522.00	35.00	18.270	8.10	pass
SSCE+rTMS1	825.00	35.00	28.875	8.10	pass
SSCE+rTMS2	578.00	35.00	20.230	8.50	pass
SSCE+rTMS3	488.00	35.00	17.080	7.90	pass

Table S5 Evaluation and statistics of RNA sequencing valid data after four weeks of SSCE.

Sample ID	Raw Reads	Clean Reads	Clean Ratio	GC content	Mapping Ratio
CON1	45026542	43213944	95.97%	48.23%	96.59%
CON2	45446802	44256808	97.38%	48.44%	96.87%
CON3	45116404	43386640	96.17%	47.94%	96.52%
SSCE+sham1	44111382	41581056	94.26%	49.32%	96.33%
SSCE+sham2	41896984	39897884	95.23%	49.78%	96.14%
SSCE+sham3	45371310	43605772	96.11%	49.77%	96.29%
SSCE+rTMS1	45275668	43552104	96.19%	49.69%	96.17%
SSCE+rTMS2	45378108	43298678	95.42%	49.4%	96.43%
SSCE+rTMS3	44116184	41925346	95.03%	49.25%	96.07%