

## Supplementary Information

### Therapeutic effects of a novel electrode for transcranial direct current stimulation in ischemic stroke mice

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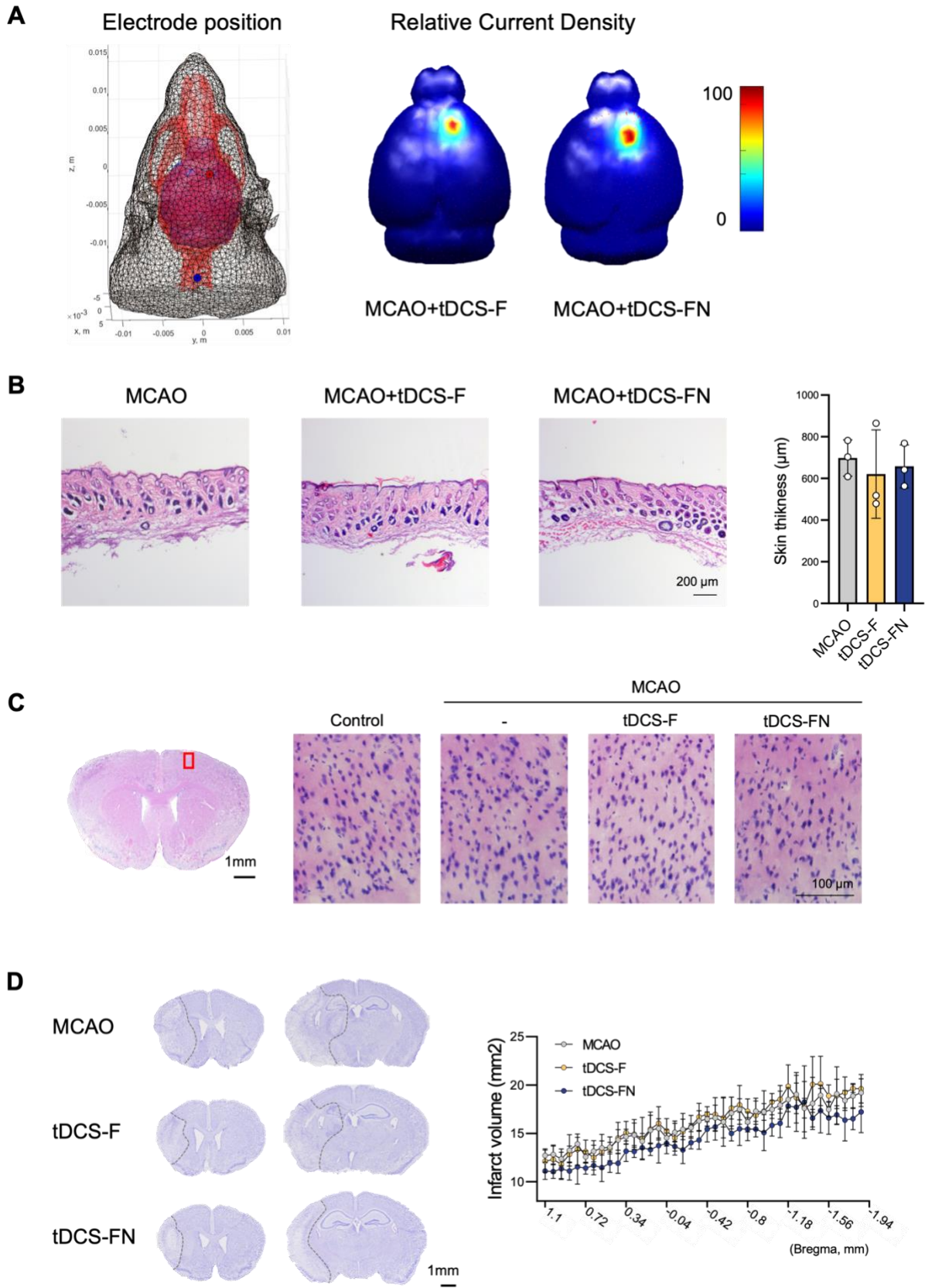
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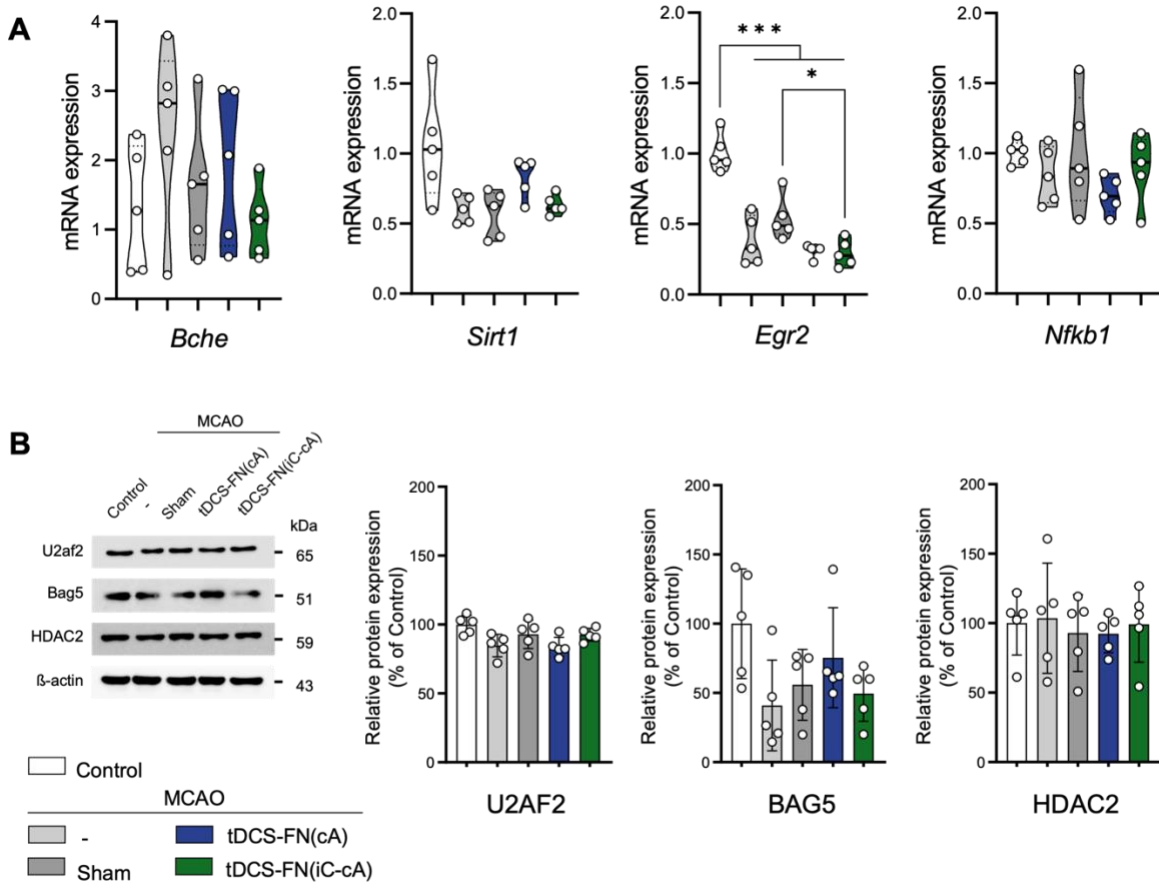
#### **This PDF file includes:**

Figures S1- S2

Table S1



**Figure S1. The 3D simulation of HD-tDCS and histological examination of the scalp. (A)** 3D simulation of HD-tDCS. Higher relative electrical fields and spatial focality were predicted in the motor cortex using the new HD electrode compared with the conventional HD electrode. **(B)** Histological examination and bar chart of the scalp by hematoxylin–eosin (H&E) staining. No pathological injuries were observed in the HD-tDCS-treated groups compared with the non-treated group (n=3/group). **(C)** Histological examination of the cerebral cortex by H&E staining. There were no pathological injuries by conventional or new HD electrode stimulation. **(D)** Representative brain images (0.98 mm and -1.58 mm from bregma) and quantification of the relative infarct volume. Borders to the healthy tissue are indicated with a dot line. Nissl staining: In total, 40 brain sections were identified every 75  $\mu\text{m}$  at 1.1 mm to -1.9 mm from the bregma (n=5/group). Data are presented as means $\pm$ SEMs. Magnification:  $\times 25$ ; scale bar=200  $\mu\text{m}$ . HD-tDCS, high-definition transcranial direct current stimulation; MCAO, middle cerebral artery occlusion. F, conventional electrode; FN, new needle-conjugated electrode.



**Figure S2. Verification of the potential signaling pathway of the therapeutic effects of HD-tDCS using the newly-designed electrode, based on the transcriptome analysis. (A)** Bar charts of the gene expressions of *Bche*, *Sirt1* and *Nfkb1*, and *Egr2* in the peri-infarct region using qPCR. **(B)** Representative western blots for U2AF2, BAG5, and HDAC2. In all groups, no significant changes were induced in gene or protein expression. All samples were obtained from the peri-infarct region (n=5/group). tDCS, transcranial direct current stimulation; FN, new needle-conjugated electrode.

**Table S1. GO and KEGG pathways according to the electrode configuration of the new HD-tDCS application.**

List	Count	%	-log (Pvalue)	Genes	Fold Enrichment
vs. tDCS-FN(cA)					
<b>UP regulation genes in DEG</b>					
<b>GO_Biological process</b>					
GO:0032933~SREBP signaling pathway	2	2.11	1.38	<i>INSIG1, EIF2A</i>	46.25
GO:1903351~cellular response to dopamine	2	2.11	1.34	<i>HDAC2, GABPA</i>	42.39
GO:2000736~regulation of stem cell differentiation	2	2.11	1.13	<i>HDAC2, SMYD5</i>	25.44
GO:0045737~positive regulation of cyclin-dependent protein serine/threonine kinase activity	2	2.11	1.03	<i>CDK5RAP1, MNAT1</i>	20.35
GO:0016575~histone deacetylation	3	3.16	1.78	<i>HDAC2, BCL6, MSL3</i>	14.96
GO:0006260~DNA replication	3	3.16	1.09	<i>RRM2B, POLD2, DONSON</i>	6.25
GO:0006281~DNA repair	6	6.32	1.77	<i>MSH6, DCLRE1A, RRM2B, POLD2, MNAT1, RNF111</i>	3.97
GO:0006974~cellular response to DNA damage stimulus	6	6.32	1.32	<i>MSH6, DCLRE1A, BCL6, RRM2B, POLD2, RNF111</i>	3.00
GO:0006357~regulation of transcription from RNA polymerase II promoter	15	15.79	2.48	<i>ZFP799, HDAC2, EGR2, ZFP935, ZFP438, ZFP426, ZBTB2, MED23, BCL6, ZFP40, MNAT1, ZFP212, ZFP300, ZFP9, GABPA</i>	2.38
<b>GO_Cellular component</b>					
GO:0005657~replication fork	3	3.16	2.29	<i>HDAC2, BCL6, DONSON</i>	27.73
GO:0016234~inclusion body	2	2.11	1.07	<i>PSMC6, BAG5</i>	22.34
GO:0005654~nucleoplasm	28	29.47	4.23	<i>DCLRE1A, HDAC2, IPO11, GTF3C5, SPATA7, ZBTB2, COIL, TATDN1, MKNK2, POLD2, POLR2H, EXOSC2, RNF111, GABPA, EGR2, ZFP438, PLEKHA5, TTI2, MED23, MSH6, TBL3, RRM2B, BCL6, DNAJC7, NUP98, SRSF5, MNAT1, ZFP212</i>	2.18
GO:0005794~Golgi apparatus	10	10.53	1.11	<i>MSH6, SLC35A1, RAB30, PRRC1, RAB40B, BCL6, ATLI, COPG2, GBA2, CLN5</i>	1.88
GO:0005634~nucleus	35	36.84	2.05	<i>DCLRE1A, HDAC2, IPO11, GTF3C5, ZFP426, COIL, TATDN1, BAG5, RAVER1, MKNK2, POLD2, POLR2H, ZFP300, EXOSC2, RPS10, RNF111, GABPA, ZFP799, EGR2, ZFP438, DONSON, MSL3, MED23, MSH6, TBL3, PSMC6, RRM2B, BCL6, DNAJC7, ZFP40, AKT1S1, NUP98, SRSF5, MNAT1, BRDT</i>	1.46
GO:0005829~cytosol	22	23.16	1.10	<i>IPO11, PIGN, ZFP438, PLEKHA5, MYO19, GBA2, SPATA7, TTI2, CLN5, MSH6, PEX7, BAG5, AP5M1, DNAJC7, RRM2B, AKT1S1, CDK5RAP1, COPG2, SRSF5, EXOSC2, RPS10, RNF111</i>	1.41
<b>GO_Molecular function</b>					

GO:0031072~heat shock protein binding	3	3.16	1.39	<i>HDAC2, BAG5, DNAJC7</i>	9.23
GO:0003729~mRNA binding	4	4.21	1.02	<i>RAVER1, SRSF5, NUP98, EIF2A</i>	3.62
GO:0000978~RNA polymerase II core promoter proximal region sequence-specific DNA binding	10	10.53	1.36	<i>EGR2, HDAC2, BCL6, ZFP935, ZFP40, ZFP426, ZFP212, ZFP300, GABPA, ZBTB2</i>	2.11
GO:0016787~hydrolase activity	13	13.68	1.59	<i>DCLRE1A, HDAC2, ENTPD1, ATLI, PTPRO, GBA2, NT5C3B, TATDN1, PDE7B, NUP98, MEST, GDPGP1, TRABD2B</i>	1.99
GO:0000166~nucleotide binding	13	13.68	1.40	<i>ENTPD1, MARS2, ATLI, GTPBP8, MYO19, MSH6, NT5C3B, RAB30, PSMC6, RAB40B, MKNK2, MAP3K6, GDPGP1</i>	1.86
GO:0046872~metal ion binding	24	25.26	1.96	<i>ZFP799, DCLRE1A, HDAC2, EGR2, ZFP935, SMYD5, ZFP426, GTPBP8, NT5C3B, TATDN1, RRM2B, BCL6, ZFP40, ZFYVE19, MKNK2, CDK5RAP1, PDE7B, MAP3K6, MNAT1, ZFP212, ZFP300, ZFP9, TRABD2B, RNF111</i>	1.65
<b>KEGG pathway</b>					
mmu03430:Mismatch repair	2	2.11	1.07	<i>MSH6, POLD2</i>	22.09
mmu00240:Pyrimidine metabolism	3	3.16	1.68	<i>NT5C3B, ENTPD1, RRM2B</i>	13.02
mmu01232:Nucleotide metabolism	3	3.16	1.35	<i>NT5C3B, ENTPD1, RRM2B</i>	8.68
mmu05168:Herpes simplex virus 1 infection	8	8.42	2.70	<i>ZFP799, ZFP935, ZFP40, ZFP426, SRSF5, ZFP212, ZFP300, ZFP9</i>	4.24
<b><u>Down regulation genes in DEG</u></b>					
<b>GO_Biological process</b>					
GO:0002764~immune response-regulating signaling pathway	2	1.41	1.90	<i>LAT2, CTSH</i>	158.22
GO:1904431~positive regulation of t-circle formation	2	1.41	1.73	<i>SLX1B, ERCC1</i>	105.48
GO:1990410~adrenomedullin receptor signaling pathway	2	1.41	1.60	<i>RAMP3, ADM</i>	79.11
GO:0000720~pyrimidine dimer repair by nucleotide-excision repair	2	1.41	1.60	<i>ERCC1, SIRT1</i>	79.11
GO:0090656~t-circle formation	2	1.41	1.51	<i>SLX1B, ERCC1</i>	63.29
GO:0031102~neuron projection regeneration	2	1.41	1.51	<i>ULK1, ADM</i>	63.29
GO:0071322~cellular response to carbohydrate stimulus	2	1.41	1.43	<i>RPS6KA2, NFKB1</i>	52.74
GO:0035166~post-embryonic hemopoiesis	2	1.41	1.43	<i>MYO1E, ERCC1</i>	52.74
GO:0097647~amylin receptor signaling pathway	2	1.41	1.37	<i>RAMP3, ADM</i>	45.21
GO:0001936~regulation of endothelial cell proliferation	2	1.41	1.26	<i>KDR, TEK</i>	35.16
<b>GO_Cellular component</b>					
GO:0000506~glycosylphosphatidylinositol-N-acetylglucosaminyltransferase (GPI-GnT) complex	2	1.41	1.33	<i>PIGC, PIGA</i>	41.37
GO:0031201~SNARE complex	3	2.11	1.46	<i>STX2, SYN2, VAMP3</i>	10.13
GO:0005902~microvillus	3	2.11	1.00	<i>MYO1E, PDGFA, TEK</i>	5.58

GO:0008021~synaptic vesicle	5	3.52	1.62	<i>GRIN2A, PSEN2, HAP1, STX2, SYN2</i>	4.55
GO:0005769~early endosome	9	6.34	3.05	<i>PSEN2, KDR, AP1S3, ACKR1, HAP1, TM9SF4, RAB22A, FGD2, VAMP3</i>	4.49
GO:0005765~lysosomal membrane	5	3.52	1.14	<i>ABCA2, LAPTM5, PSEN2, AP1S3, WDR24</i>	3.16
GO:0005764~lysosome	8	5.63	1.67	<i>ABCA2, RAMP3, LAPTM5, CTSH, ARSG, HAP1, WDR24, SGSH</i>	2.87
GO:0031410~cytoplasmic vesicle	13	9.15	2.18	<i>ABCA2, PANK1, WFS1, LAPTM5, RAB22A, MYO1E, GRIN2A, KDR, AP1S3, HAP1, ADGRL4, STX2, VAMP3</i>	2.45
GO:0030054~cell junction	12	8.45	1.57	<i>CAMSAP3, MYO1E, GRIN2A, MAST2, NPHP1, KDR, TEK, HAP1, SYN2, GABRG1, SNTA1, VAMP3</i>	2.10
GO:0009986~cell surface	9	6.34	1.03	<i>GRIN2A, RAMP3, PSEN2, KDR, PDGFA, TEK, STX2, VAMP5, VAMP3</i>	1.93
<b>GO_Molecular function</b>					
GO:0017176~phosphatidylinositol N-acetylglucosaminyltransferase activity	2	1.41	1.38	<i>PIGC, PIGA</i>	46.90
GO:0008484~sulfuric ester hydrolase activity	2	1.41	1.12	<i>ARSG, SGSH</i>	25.25
GO:0004521~endoribonuclease activity	3	2.11	1.72	<i>ZC3H12C, YBEY, LACTB2</i>	14.07
GO:0004518~nuclease activity	6	4.23	2.91	<i>ISG20, ZC3H12C, YBEY, SLX1B, LACTB2, ERCC1</i>	7.46
GO:0004519~endonuclease activity	4	2.82	1.70	<i>ZC3H12C, YBEY, SLX1B, LACTB2</i>	6.91
GO:0008168~methyltransferase activity	5	3.52	1.62	<i>METTL25, PRDM4, METTL8, TRMT61A, METTL17</i>	4.53
GO:0005516~calmodulin binding	5	3.52	1.50	<i>CAMSAP3, MYO1E, WFS1, PHKA2, SNTA1</i>	4.17
GO:0016740~transferase activity	23	16.20	3.10	<i>PRDM4, PANK1, MAST2, NSMCE2, IBA57, DTX4, PIGV, FHIT, SIRT1, PAFAH2, TRIT1, PAPSSI, METTL25, PIGA, RPS6KA2, KDR, ULK1, IDNK, TEK, METTL8, TRMT61A, METTL17, TGM2</i>	2.14
GO:0016787~hydrolase activity	18	12.68	1.79	<i>USP36, HDDC2, SLX1B, PSEN2, DUSP18, HEXDC, FHIT, PAFAH2, ISG20, ZC3H12C, YBEY, LACTB2, HMCES, AFMID, CTSH, ARSG, HIBCH, TGM2</i>	1.84
GO:0000166~nucleotide binding	16	11.27	1.03	<i>ABCA2, PANK1, MAST2, FHIT, GTPBP1, RAB22A, TRIT1, PAPSSI, MYO1E, RPS6KA2, KDR, ULK1, IDNK, TLL12, TEK, TGM2</i>	1.53
<b>KEGG pathway</b>					
mmu00563:Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	3	2.11	1.83	<i>PIGC, PIGA, PIGV</i>	15.72
mmu04130:SNARE interactions in vesicular transport	3	2.11	1.63	<i>STX2, VAMP5, VAMP3</i>	12.39
mmu04142:Lysosome	6	4.23	2.55	<i>ABCA2, LAPTM5, CTSH, AP1S3, ARSG, SGSH</i>	6.06
mmu04722:Neurotrophin signaling pathway	5	3.52	1.95	<i>PRDM4, RPS6KA2, ARHGDI, PSEN2, NFKB1</i>	5.63
mmu00230:Purine metabolism	4	2.82	1.14	<i>HDDC2, PGM2, FHIT, PAPSSI</i>	4.07
mmu04015:Rap1 signaling pathway	5	3.52	1.16	<i>GRIN2A, KDR, PDGFA, TEK, SIPA1L2</i>	3.18
mmu04014:Ras signaling pathway	5	3.52	1.05	<i>GRIN2A, KDR, PDGFA, TEK, NFKB1</i>	2.90

	mmu01100:Metabolic pathways	19	13.38	1.45	<i>HDDC2, GLDC, PANK1, HEXDC, PIGV, FHIT, SIRT1, PAFAH2, TRIT1, PAPSS1, SGSH, PIGC, ALDH3B1, PIGA, AFMID, PGM2, IDNK, L2HGDH, HIBCH</i>	1.60
vs. tDCS-FN(iC-cA)	<b>UP regulation genes in DEG</b>					
	<b>GO_Biological process</b>					
	GO:0006850~mitochondrial pyruvate transport	2	1.08	1.78	<i>MPC1, MPC2</i>	119.61
	GO:0098942~retrograde trans-synaptic signaling by trans-synaptic protein complex	2	1.08	1.39	<i>FARP1, NLGN1</i>	47.84
	GO:0097114~NMDA glutamate receptor clustering	2	1.08	1.31	<i>NLGN1, HTR1A</i>	39.87
	GO:0060527~prostate epithelial cord arborization involved in prostate glandular acinus morphogenesis	2	1.08	1.25	<i>FRS2, IGF1</i>	34.17
	GO:1903608~protein localization to cytoplasmic stress granule	2	1.08	1.19	<i>DHX9, DCP1A</i>	29.90
	GO:0061732~mitochondrial acetyl-CoA biosynthetic process from pyruvate	2	1.08	1.19	<i>MPC1, MPC2</i>	29.90
	GO:2000726~negative regulation of cardiac muscle cell differentiation	2	1.08	1.19	<i>HDAC3, FRS2</i>	29.90
	GO:0006625~protein targeting to peroxisome	2	1.08	1.10	<i>ZFAND6, LONP2</i>	23.92
	GO:0046620~regulation of organ growth	2	1.08	1.10	<i>LATS1, SAV1</i>	23.92
	GO:0009312~oligosaccharide biosynthetic process	2	1.08	1.06	<i>MGAT2, ST6GALNAC6</i>	21.75
	<b>GO_Cellular component</b>					
	GO:0072487~MSL complex	2	1.08	1.41	<i>MSL3, MSL3L2</i>	50.43
	GO:0005641~nuclear envelope lumen	2	1.08	1.01	<i>BCHE, CACYBP</i>	19.39
	GO:0000118~histone deacetylase complex	3	1.62	1.33	<i>HDAC2, HDAC3, RCOR2</i>	8.60
	GO:0032391~photoreceptor connecting cilium	3	1.62	1.29	<i>CETN2, CEP290, SPATA7</i>	8.22
	GO:0022627~cytosolic small ribosomal subunit	3	1.62	1.24	<i>RPS27, RPS21, RPS10</i>	7.72
	GO:0019005~SCF ubiquitin ligase complex	4	2.16	1.76	<i>FBXW11, CACYBP, FBXO32, FBXO33</i>	7.31
	GO:0022626~cytosolic ribosome	4	2.16	1.58	<i>RPS27, RPS21, RPL9, RPS10</i>	6.23
	GO:0005762~mitochondrial large ribosomal subunit	3	1.62	1.07	<i>MRPL20, MRPL1, MIEF1</i>	6.10
	GO:0017053~transcriptional repressor complex	3	1.62	1.04	<i>HDAC2, HDAC3, C1D</i>	5.91
	GO:0098982~GABA-ergic synapse	5	2.70	1.96	<i>NLGN1, RPS27, GLRB, HTR1A, NR3C2</i>	5.78
	<b>GO_Molecular function</b>					
	GO:0046972~histone acetyltransferase activity (H4-K16 specific)	2	1.08	1.49	<i>MSL3, MSL3L2</i>	60.76
	GO:0050833~pyruvate transmembrane transporter activity	2	1.08	1.49	<i>MPC1, MPC2</i>	60.76
	GO:0001069~regulatory region RNA binding	2	1.08	1.40	<i>DHX9, IREB2</i>	48.61
	GO:1902388~ceramide 1-phosphate transporter activity	2	1.08	1.25	<i>CPTP, MTPP</i>	34.72
	GO:0005548~phospholipid transporter activity	2	1.08	1.15	<i>PITPNM1, MTPP</i>	27.00



GO:0032041~NAD-dependent histone deacetylase activity (H3-K14 specific)	2	1.08	1.10	<i>HDAC2, HDAC3</i>	24.30
GO:0033558~protein deacetylase activity	2	1.08	1.03	<i>HDAC2, HDAC3</i>	20.25
GO:0005212~structural constituent of eye lens	4	2.16	2.92	<i>CRYGS, CRYBA2, CRYBB2, CRYBA4</i>	18.69
GO:0051059~NF-kappaB binding	4	2.16	2.65	<i>HDAC2, HDAC3, FAF1, COMMD6</i>	15.19
GO:0031072~heat shock protein binding	6	3.24	3.30	<i>HDAC2, PACRG, BAG5, GPR37, DNAJC7, FAF1</i>	9.11
<b>KEGG pathway</b>					
mmu03420:Nucleotide excision repair	3	1.62	1.22	<i>RFC4, CETN2, POLD1</i>	7.38
mmu03010:Ribosome	6	3.24	1.59	<i>MRPL20, MRPL1, RPS27, RPS21, RPL9, RPS10</i>	3.55
<b>Down regulation genes in DEG</b>					
<b>GO_Biological process</b>					
GO:0031587~positive regulation of inositol 1,4,5-trisphosphate-sensitive calcium-release channel activity	2	0.64	1.26	<i>HTT, HAP1</i>	35.88
GO:0018193~peptidyl-amino acid modification	2	0.64	1.26	<i>ASPHD1, ASPHD2</i>	35.88
GO:0051386~regulation of neurotrophin TRK receptor signaling pathway	2	0.64	1.26	<i>DOK5, ULK1</i>	35.88
GO:0001998~angiotensin-mediated vasoconstriction involved in regulation of systemic arterial blood pressure	2	0.64	1.26	<i>G6PDX, AGT</i>	35.88
GO:2001170~negative regulation of ATP biosynthetic process	2	0.64	1.26	<i>FLCN, PARP1</i>	35.88
GO:0071205~protein localization to juxtaparanode region of axon	2	0.64	1.17	<i>NFASC, CNTN2</i>	28.71
GO:0032929~negative regulation of superoxide anion generation	2	0.64	1.17	<i>PON3, AKT1</i>	28.71
GO:0014873~response to muscle activity involved in regulation of muscle adaptation	2	0.64	1.17	<i>SRL, AGT</i>	28.71
GO:0099504~synaptic vesicle cycle	2	0.64	1.17	<i>SYN2, SYN1</i>	28.71
GO:0048858~cell projection morphogenesis	2	0.64	1.09	<i>CAMK2B, CSPG5</i>	23.92
<b>GO_Cellular component</b>					
GO:0089701~U2AF	3	0.96	2.45	<i>U2AF2, U2AF1L4, SF1</i>	31.96
GO:0098984~neuron to neuron synapse	2	0.64	1.19	<i>ATP1A3, ATP1B2</i>	29.83
GO:0060203~clathrin-sculpted glutamate transport vesicle membrane	2	0.64	1.05	<i>OTOF, SYN1</i>	21.31
GO:0033018~sarcoplasmic reticulum lumen	2	0.64	1.05	<i>CALU, SRL</i>	21.31
GO:0071004~U2-type prespliceosome	3	0.96	1.72	<i>U2AF2, SNRNP70, SNRPB</i>	13.98
GO:0005774~vacuolar membrane	4	1.29	2.41	<i>NAPA, SLC22A17, ATP6V0C, WDR24</i>	12.43
GO:0048787~presynaptic active zone membrane	3	0.96	1.63	<i>OTOF, APBA1, STX2</i>	12.43
GO:0033268~node of Ranvier	3	0.96	1.54	<i>NFASC, KCNQ2, CNTN2</i>	11.19
GO:0035371~microtubule plus-end	3	0.96	1.43	<i>DCTN1, CLIP4, SLAIN1</i>	9.73
GO:0030285~integral component of synaptic vesicle membrane	6	1.93	3.36	<i>SYNGR1, SLC6A7, ATP6V1G2, SLC30A3, SV2A, VAMP3</i>	9.32

<b>GO_Molecular function</b>					
GO:0033897~ribonuclease T2 activity	2	0.64	1.56	<i>RNASET2B, RNASET2A</i>	72.53
GO:0004376~glycolipid mannosyltransferase activity	2	0.64	1.39	<i>PIGB, PIGV</i>	48.35
GO:0047179~platelet-activating factor acetyltransferase activity	2	0.64	1.27	<i>PAFAH1B3, PAFAH2</i>	36.27
GO:0003847~1-alkyl-2-acetylglycerophosphocholine esterase activity	3	0.96	2.30	<i>PLA2G6, PAFAH1B3, PAFAH2</i>	27.20
GO:0030628~pre-mRNA 3'-splice site binding	2	0.64	1.03	<i>U2AF2, U2AF1L4</i>	20.72
GO:0004708~MAP kinase kinase activity	3	0.96	1.70	<i>MAP2K3, MAP2K2, MAP2K7</i>	13.60
GO:0004712~protein serine/threonine/tyrosine kinase activity	5	1.61	3.20	<i>PRKCG, CLK1, MAP2K2, AKT1, DYRK1B</i>	12.51
GO:0004521~endoribonuclease activity	5	1.61	2.89	<i>RCL1, YBEY, AGO2, RNASET2B, RNASET2A</i>	10.36
GO:0042054~histone methyltransferase activity	3	0.96	1.48	<i>SUV39H1, CARM1, SMYD1</i>	10.36
GO:0016409~palmitoyltransferase activity	3	0.96	1.37	<i>ZDHHC12, ZDHHC6, ZDHHC4</i>	9.07
<b>KEGG pathway</b>					
mmu00563:Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	3	0.96	1.28	<i>PIGB, GPAAI, PIGV</i>	8.04
mmu04721:Synaptic vesicle cycle	6	1.93	2.33	<i>NAPA, SLC6A7, ATP6V1G2, STX2, ATP6V0C, CPLX1</i>	5.43
mmu04961:Endocrine and other factor-regulated calcium reabsorption	4	1.29	1.25	<i>PRKCG, ATP1A3, ATP1B2, SLC8A2</i>	4.57
mmu04664:Fc epsilon RI signaling pathway	4	1.29	1.17	<i>MAP2K3, MAP2K2, AKT1, MAP2K7</i>	4.22
mmu04012:ErbB signaling pathway	5	1.61	1.50	<i>PRKCG, CAMK2B, MAP2K2, AKT1, MAP2K7</i>	4.15
mmu04261:Adrenergic signaling in cardiomyocytes	9	2.89	2.84	<i>CAMK2B, CACNB1, TPM2, AKT1, ATP1A3, ATP1B2, ADRA1B, AGT, SLC8A2</i>	4.13
mmu04722:Neurotrophin signaling pathway	7	2.25	2.12	<i>CAMK2B, MAPK7, MAP2K2, PRDM4, PSEN2, AKT1, MAP2K7</i>	4.03
mmu04260:Cardiac muscle contraction	5	1.61	1.45	<i>CACNB1, TPM2, ATP1A3, ATP1B2, SLC8A2</i>	4.01
mmu04912:GnRH signaling pathway	5	1.61	1.41	<i>CAMK2B, MAP2K3, MAPK7, MAP2K2, MAP2K7</i>	3.87
mmu04918:Thyroid hormone synthesis	4	1.29	1.05	<i>PRKCG, ATP1A3, ATP1B2, TTF1</i>	3.77