Supplementary Table S1. Experimental groups and exposure to microwave radiation

Group	Average power density of L-band microwaves	Average power density of C-band microwaves	SAR (W/kg)
S[*]	0 mW/cm^2	0 mW/cm^2	0
L10	10 mW/cm^2 for 6 min	0 mW/cm^2	3.7
C10	0 mW/cm^2	10 mW/cm^2 for 6 min	3.3
LC10[#]	10 mW/cm^2 for 6 min	10 mW/cm^2 for 6 min	3.7 for 6 min + 3.3 for 6 min

Note. [*]The rats in the sham radiation group were placed in polypropylene cages and placed on the radiation table for 6 min without microwave exposure. [#]The rats in the LC10 groups were first radiated with L-band microwave radiation for 6 min and then immediately radiated with C-band microwave radiation for 6 min. The sham group and exposure group. The sham group and exposure groups adopt the same settings, and the sham group did not give microwave exposure. The experiment of the sham group and exposure groups were not conducted in parallel.

Supplementary Table S2. Primer sequences of differentially expressed lncRNAs and mRNAs

Transcripts and gene names		Primer sequences
MSTRG.1068.1 (NA)	Forward (F)	CTCGGGAGAAAGGGTATGTGAG
	Reverse (R)	TGGTGAGCGGGCATTTTAG
ENSRNOT00000002044 (Napa)	Forward (F)	TGAAGGAGTGGGTGCAATGT
	Reverse (R)	ATAAATGGCGGGGTGAAGG
MSTRG.27033.1 (Slc24a2)	Forward (F)	GTGTGTGTGTGTGTTCAAGGAATAA
	Reverse (R)	AGCAAGCCAGTCCCTATTAAGAAA
ENSRNOT00000083373 (Slc24a2)	Forward (F)	GTCCACACCCAGTCCACCTT
	Reverse (R)	GGCATCAAACCCTATCAAATCTTC
MSTRG.31953.1 (Pdgfb)	Forward (F)	AGACGCTTGGAGTAGAGACAGGA
	Reverse (R)	TACGTGAGTCTGGGAGGGGTAG
ENSRNOT00000023196 (Pdgfb)	Forward (F)	GAATACTTTCAGGCAGGCTAGGG
	Reverse (R)	AAGGGACAGGGAGAGATGAGTG
ENSRNOT00000023066 (Syngr1)	Forward (F)	TGTCAAGGACCGCAAGAAAG
	Reverse (R)	CAGAAACCCACGAACCAGAAG
MSTRG.35922.1 (Dlgap1)	Forward (F)	GCACCATCGCTCACAGACA
	Reverse (R)	CCTTGTAAACCCCTCCTCCAC
ENSRNOT00000022351 (Dlgap1)	Forward (F)	TCACCAAAGTTCCGCTCCA
	Reverse (R)	CTGTCCGTTCACCTCCATCTC

Supplementary Table S3. GO analysis of differentially expressed lncRNAs and corresponding mRNAs after microwave exposure

Groups	mRNA (transcripts, genes)	lncRNA (transcripts, genes)	BP	CC	MF
L10 *vs.* S	ENSRNOT00000000117, Cplx2	MSTRG.14373.2, Cplx2	neurotransmitter transport, synaptic vesicle exocytosis, positive regulation of synaptic plasticity, regulation of neurotransmitter secretion and et al.	Dendrite, SNARE complex, mast cell granule, neuronal cell body, terminal bouton, synapse, and et al.	SNARE binding, syntaxin-1 binding, syntaxin binding, calcium-dependent protein binding
	ENSRNOT00000083373, Slc24a2	MSTRG.27033.1, Slc24a2	calcium ion transport, cellular calcium ion homeostasis, learning, memory, long-term synaptic potentiation, long term synaptic depression, calcium ion transmembrane transport	integral component of plasma membrane, membrane, integral component of membrane, intrinsic component of plasma membrane	calcium channel activity, calcium, potassium: sodium antiporter activity, symporter activity, antiporter activity, protein dimerization activity
C10 *vs.* S	ENSRNOT00000002044, Napa	MSTRG.1068.1	brain development, regulation of synaptic protein transport, vesicle-mediated transport, neuron differentiation, glutamatergic, SNARE complex disassembly	SNARE complex, terminal bouton, myelin sheath, synaptobrevin 2-SNAP-25-syntaxin-1a complex, presynapse, postsynapse and et al.	SNARE binding, syntaxin binding, protein-containing complex binding
	ENSRNOT00000072973, Vbp1	MSTRG.2384.1	protein folding, microtubule-based process, tubulin complex assembly	Cytoplasm, polysome, prefoldin complex	tubulin binding
	ENSRNOT00000031230, ENSRNOT00000084012, Agap2	MSTRG.31244.1	positive regulation of phosphatidylinositol 3-kinase signaling, negative regulation of apoptotic process, negative regulation of neuron apoptotic process and et al.	Nucleus, nucleolus, cytoplasm, mitochondrion, cytosol	GTPase activity, GTPase activator activity, protein binding, GTP binding, metal ion binding and et al.
	ENSRNOT00000023196, Pdgfb	MSTRG.31953.1, Pdgfb	positive regulation of MAPK cascade, positive regulation of ERK1 and ERK2 cascade, positive regulation of calcium ion import and et al.	Intracellular, membrane	growth factor activity, superoxide-generating NADPH oxidase activator activity, identical protein binding and et al.
	ENSRNOT00000073079, Tbcc	MSTRG.34726.1, Bicral	cell morphogenesis, protein folding, tubulin complex assembly, post-chaperonin tubulin folding pathway	Cytoplasm, cytosol, photoreceptor connecting cilium	nucleotide binding, GTPase activity, GTP binding, tubulin binding
	ENSRNOT00000022351, Dlgap1	MSTRG.35922.1, Dlgap1	chemical synaptic transmission, signaling, protein localization to synapse, regulation of proteasomal protein catabolic process, maintenance of postsynaptic density structure and et al.	postsynaptic density, synapse, postsynaptic membrane, glutamatergic synapse, postsynaptic density, intracellular component and et al.	protein binding, protein domain specific binding, protein-containing complex binding, structural constituent of postsynaptic density

Continued

Groups	mRNA (transcripts, genes)	lncRNA (transcripts, genes)	BP	CC	MF
C10 *vs.* S	ENSRNOT00000012533, Ccdc47	MSTRG.6501.2, Limd2	ER overload response, endoplasmic reticulum organization, post-embryonic development, ubiquitin-dependent ERAD pathway, calcium ion homeostasis	endoplasmic reticulum, rough endoplasmic reticulum, membrane, integral component of membrane)	calcium ion binding
	ENSRNOT00000002906, Atg3	MSTRG.7482.1	autophagosome assembly, autophagy of mitochondrion, autophagy, macroautophagy	cytoplasmic ubiquitin ligase complex, cytoplasm, cytosol	transferase activity, Atg8 ligase activity, Atg12 transferase activity, ubiquitin-like protein transferase activity, enzyme binding
LC10 *vs.* S	ENSRNOT00000023066, Syngr1	MSTRG.31953.1, Pdgfb	regulation of long-term neuronal synaptic plasticity, regulation of short-term neuronal synaptic plasticity, synaptic vesicle membrane organization and et al.	synaptic vesicle, membrane, integral component of synaptic vesicle membrane, synaptic vesicle membrane, cytoplasmic vesicle, synapse and et al.	
	ENSRNOT00000023196, Pdgfb	MSTRG.31953.1, Pdgfb	positive regulation of MAP kinase activity, positive regulation of calcium ion import, positive regulation of reactive oxygen species metabolic process and et al.	Intracellular, membrane	identical protein binding, protein homodimerization activity, protein heterodimerization activity, platelet-derived growth factor binding
	ENSRNOT00000010827, Slc24a2	MSTRG.27033, Slc24a2	calcium ion transport, cellular calcium ion homeostasis, learning, memory, long-term synaptic potentiation, long term synaptic depression and et al.	integral component of plasma membrane, membrane, integral component of membrane, intrinsic component of plasma membrane	calcium channel activity, calcium, potassium: sodium antiporter activity, and et al.
	ENSRNOT00000018190, Rala	MSTRG.14864.1	Ras protein signal transduction, exocytosis, regulation of exocytosis and et al.	cell surface, membrane, cleavage furrow, myelin sheath, Flemming body	GTPase activity, protein tyrosine kinase activity, GTP binding, myosin binding, GDP binding, ATPase binding
	ENSRNOT00000019340, Rap2b	MSTRG.19020.1, MSTRG.19019.1	Rap protein signal transduction and et al.	bicellular tight junction, membrane, recycling endosome, extracellular exosome	nucleotide binding, GTP binding, GDP binding, protein domain specific binding
LC10 *vs.* L10	None	None	None	None	None
LC10 *vs.* C10	None	None	None	None	None
L10 *vs.* C10	ENSRNOT00000043627, Map2	MSTRG.35424.1	Axonogenesis, microtubule binding, dendrite development, central nervous system neuron development, establishment of cell polarity, negative regulation of axon extension, neuron projection development, dendrite morphogenesis, regulation of axonogenesis	Microtubule, postsynaptic density, dendrite, nuclear periphery, axon initial segment, dendritic shaft, axon hillock, cell body, CA3 pyramidal cell dendrite, proximal neuron projection	dystroglycan binding, tubulin binding

Supplementary Table S4. KEGG pathways of differentially expressed lncRNAs and corresponding mRNAs after microwave exposure

Groups	**mRNA (transcripts, genes)**	**lncRNA (transcripts,genes)**	**KEGG pathways**
L10 *vs.* S	ENSRNOT00000000117, Cplx2	MSTRG.14373.2, Cplx2	Synaptic vesicle cycle
C10 *vs.* S	ENSRNOT00000002044, Napa	MSTRG.1068.1	Synaptic vesicle cycle
	ENSRNOT00000031230, Agap2	MSTRG.31244.1	FoxO signaling pathway, Endocytosis
	ENSRNOT00000084012, Agap2	MSTRG.31244.1	FoxO signaling pathway, Endocytosis
	ENSRNOT00000022351, Dlgap1	MSTRG.35922.1, Dlgap1	Glutamatergic synapse
LC10 *vs.* S	ENSRNOT00000023196, Pdgfb	MSTRG.31953.1, Pdgfb	MAPK signaling pathway, Ras signaling pathway, Rap1 signaling pathway, PI3K-Akt signaling pathway, and et al.
	ENSRNOT00000018190, Rala	MSTRG.14864.1	Ras signaling pathway, Rap1 signaling pathway and et al.
LC10 *vs.* L10	None	None	None
LC10 *vs.* C10	None	None	None
L10 *vs.* C10	None	None	None

Supplementary Table S5. Differential genes for validation after microwave exposure

lncRNA					**mRNA**				
transcripts	genes	$\log_2$ (FC) L10 *vs.* S	$\log_2$ (FC) C10 *vs.* S	$\log_2$ (FC) LC10 *vs.* S	transcripts	genes	$\log_2$ (FC) L10 *vs.* S	$\log_2$ (FC) C10 *vs.* S	$\log_2$ (FC) LC10 *vs.* S
MSTRG.1068.1	NA	−0.4	−0.46	−0.69	ENSRNOT00000002044	Napa	−0.17	−0.28	−0.2
MSTRG.27033.1	Slc24a2	0.43	0.38	0.61	ENSRNOT00000083373	Slc24a2	−0.36	−0.66	−0.47
MSTRG.31953.1	Pdgfb	−0.52	−0.73	−0.84	ENSRNOT00000023196	Pdgfb	−0.2	−0.32	−0.29
MSTRG.31953.1	Pdgfb	−0.52	−0.73	−0.84	ENSRNOT00000023066	Syngr1	0.31	−1.01	−1.68
MSTRG.35922.1	Dlgap1	0.05	0.45	0.42	ENSRNOT00000022351	Dlgap1	−0.24	−0.33	−0.17

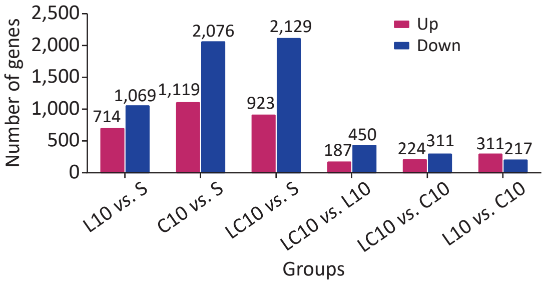
Note. NA meant not available in the datebase.

Supplementary Table S6. Statistical analysis of differential gene validation results

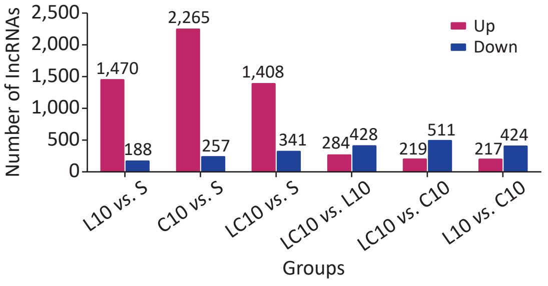
Differential gene	Comparison	Significantly different?	F value	*P* value
MSTRG.1068.1	L-band main effect	No	F (1,12) = 1.681	0.204
	C-band main effect	No	F (1,12) = 4.107	0.051
	Interaction effect	No	F (1,12) = 0.799	0.378
	S *vs.* L10	No		0.133
	S *vs.* C10	Yes		0.048
	S *vs.* LC10	No		0.194
ENSRNOT00000002044	L-band main effect	No	F (1,12) = 0.240	0.628
	C-band main effect	No	F (1,12) = 1.533	0.225
	Interaction effect	No	F (1,12) = 1.304	0.262
	S *vs.* L10	No		0.684
	S *vs.* C10	No		0.946
	S *vs.* LC10	No		0.231
MSTRG. 27033.1	L-band main effect	No	F (1,12) = 0.035	0.853
	C-band main effect	Yes	F (1,12) = 10.011	0.004
	Interaction effect	No	F (1,12) = 0.918	0.358
	S *vs.* L10	No		0.577
	S *vs.* C10	Yes		0.010
	S *vs.* LC10	Yes		0.016
ENSRNOT00000083373	L-band main effect	Yes	F (1,12) = 4.592	0.040
	C-band main effect	No	F (1,12) = 3.211	0.083
	Interaction effect	No	F (1,12) = 1.67	0.206
	S *vs.* L10	Yes		0.018
	S *vs.* C10	No		0.043
	S *vs.* LC10	Yes		0.007
MSTRG.31953.1	L-band main effect	Yes	F (1,12) = 10.307	0.004
	C-band main effect	Yes	F (1,12) = 46.186	0.000
	Interaction effect	No	F (1,12) = 2.877	0.102
	S *vs.* L10	Yes		0.002
	S *vs.* C10	Yes		0.000
	S *vs.* LC10	Yes		0.000
ENSRNT00000023196	L-band main effect	No	F (1,12) = 3.601	0.067
	C-band main effect	Yes	F (1,12) = 4.326	0.046
	Interaction effect	No	F (1,12) = 1.391	0.248
	S *vs.* L10	Yes		0.032
	S *vs.* C10	Yes		0.033
	S *vs.* LC10	Yes		0.007

Continued

Differential gene	Comparison	Significantly different?	F value	*P* value
ENSRNOT000000023066	L-band main effect	Yes	F (1,12) = 5.545	0.025
	C-band main effect	No	F (1,12) = 3.244	0.081
	Interaction effect	No	F (1,12) = 2.9	0.099
	S *vs.* L10	Yes		0.007
	S *vs.* C10	Yes		0.021
	S *vs.* LC10	Yes		0.006
MSTRG. 35922.1	L-band main effect	No	F (1,12) = 2.366	0.134
	C-band main effect	No	F (1,12) = 0.395	0.534
	Interaction effect	No	F (1,12) = 0.087	0.770
	S *vs.* L10	No		0.204
	S *vs.* C10	No		0.519
	S *vs.* LC10	No		0.135
ENSRNOT00000022351	L-band main effect	No	F (1,12) = 3.709	0.065
	C-band main effect	Yes	F (1,12) = 23.21	0.000
	Interaction effect	No	F (1,12) = 4.142	0.052
	S *vs.* L10	No		0.932
	S *vs.* C10	No		0.060
	S *vs.* LC10	Yes		0.000



Supplementary Figure S1. Differentially expressed mRNAs in the sham and microwave exposure groups.



Supplementary Figure S2. Differentially expressed lncRNAs in the sham and microwave exposure groups.