VIROLOGICA SINICA

Electronic Supplementary Material

Integrated Metabolomics and Transcriptomics Analyses Reveal Metabolic Landscape in Neuronal Cells during JEV Infection

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Supporting information to DOI: 10.1007/s12250-021-00445-0

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Table S1 Primer list for RT-qPCR

Gene	Primer sequence (5′–3′)	
	Forward	Reverse
JEV	AGACAAGCAGATCAACCACCATT	CCCTCCAATAGAGCCAAAGTCC
β-Actin (Mus)	TGACGGGGTCACCCACACTG	AAGCTGTAGCCGCGCTCGGT

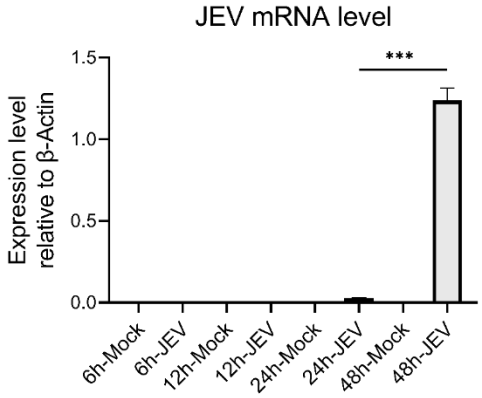


Figure S1 JEV proliferation in Neuro2a cell line. JEV RNA levels were detected by qPCR analysis. The level of mRNA expression was normalized with β-actin. ***, $P < 0.001$.

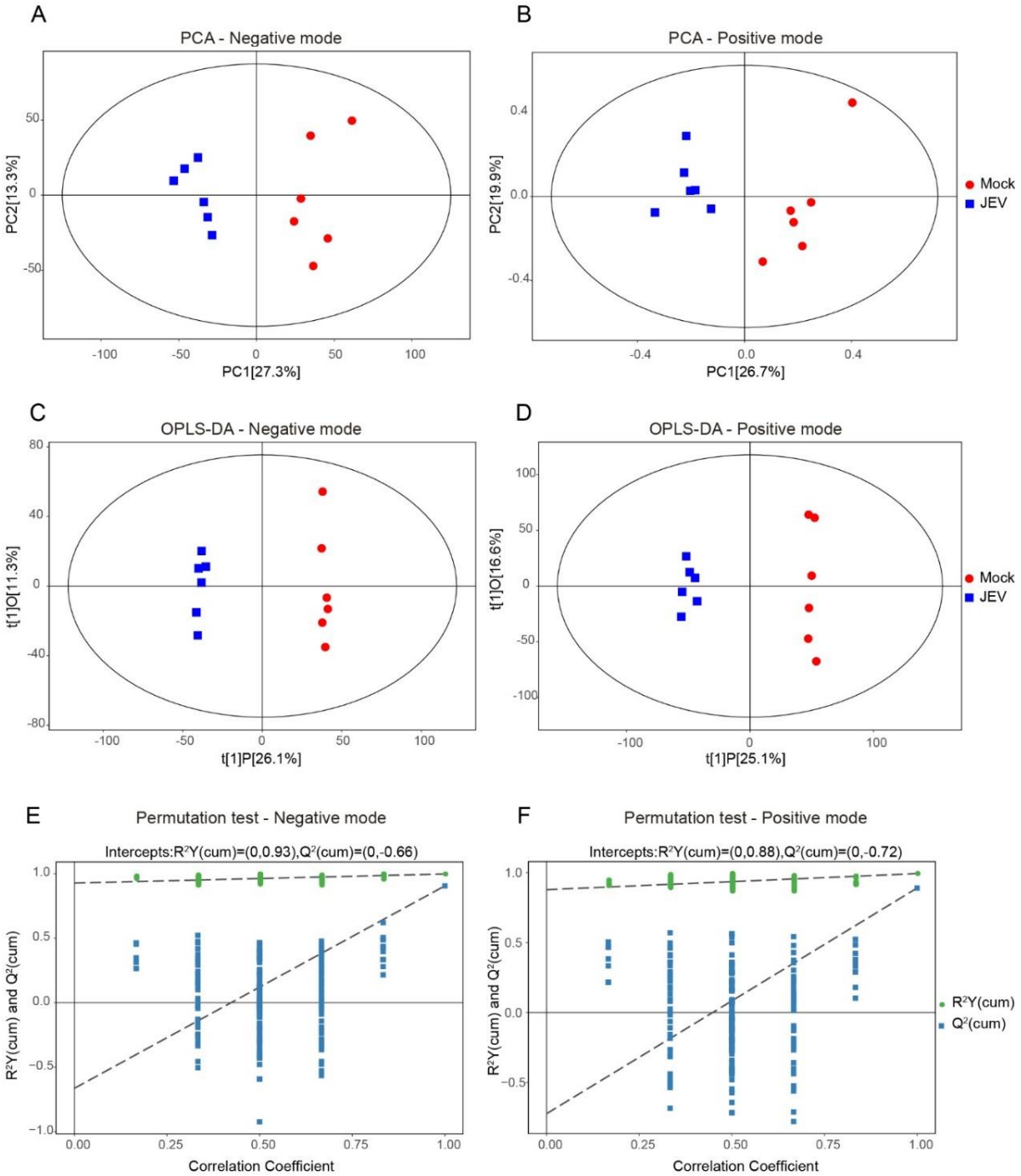


Fig S2 Multivariate data analysis and permutation test of the metabolomic changes induced by JEV infection: score scatter plot of PCA model for JEV (blue squares) vs mock (red dots) in negative ion mode (NEG) (**A**) and positive ion mode (POS) (**B**). Score scatter plot of OPLS-DA model for JEV vs mock in NEG (**C**) and POS (**D**). Permutation test of OPLS-DA model for JEV vs mock in NEG (**E**) and POS (**F**).

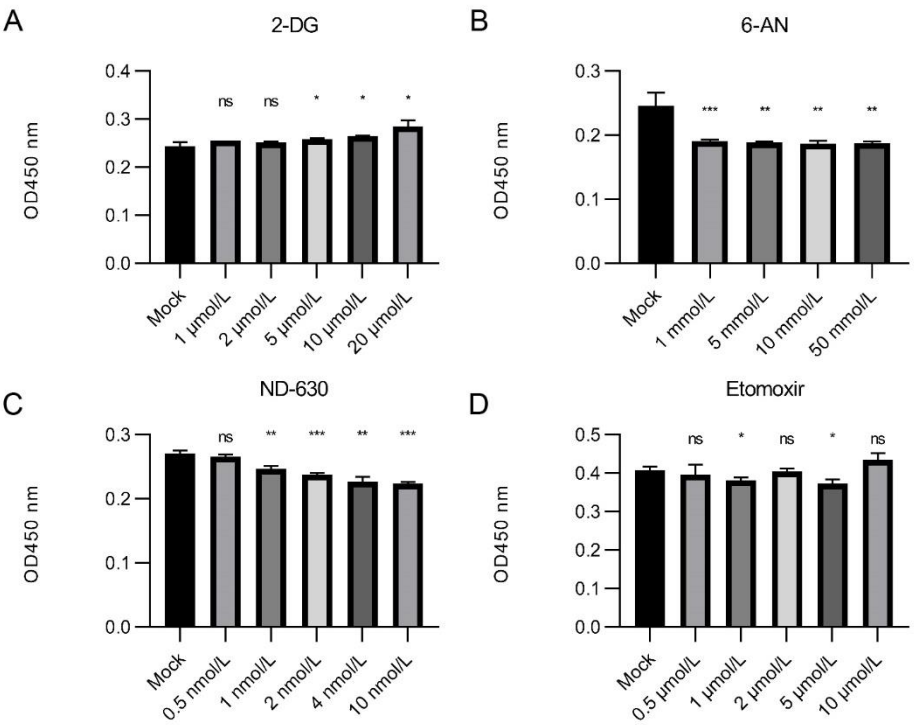
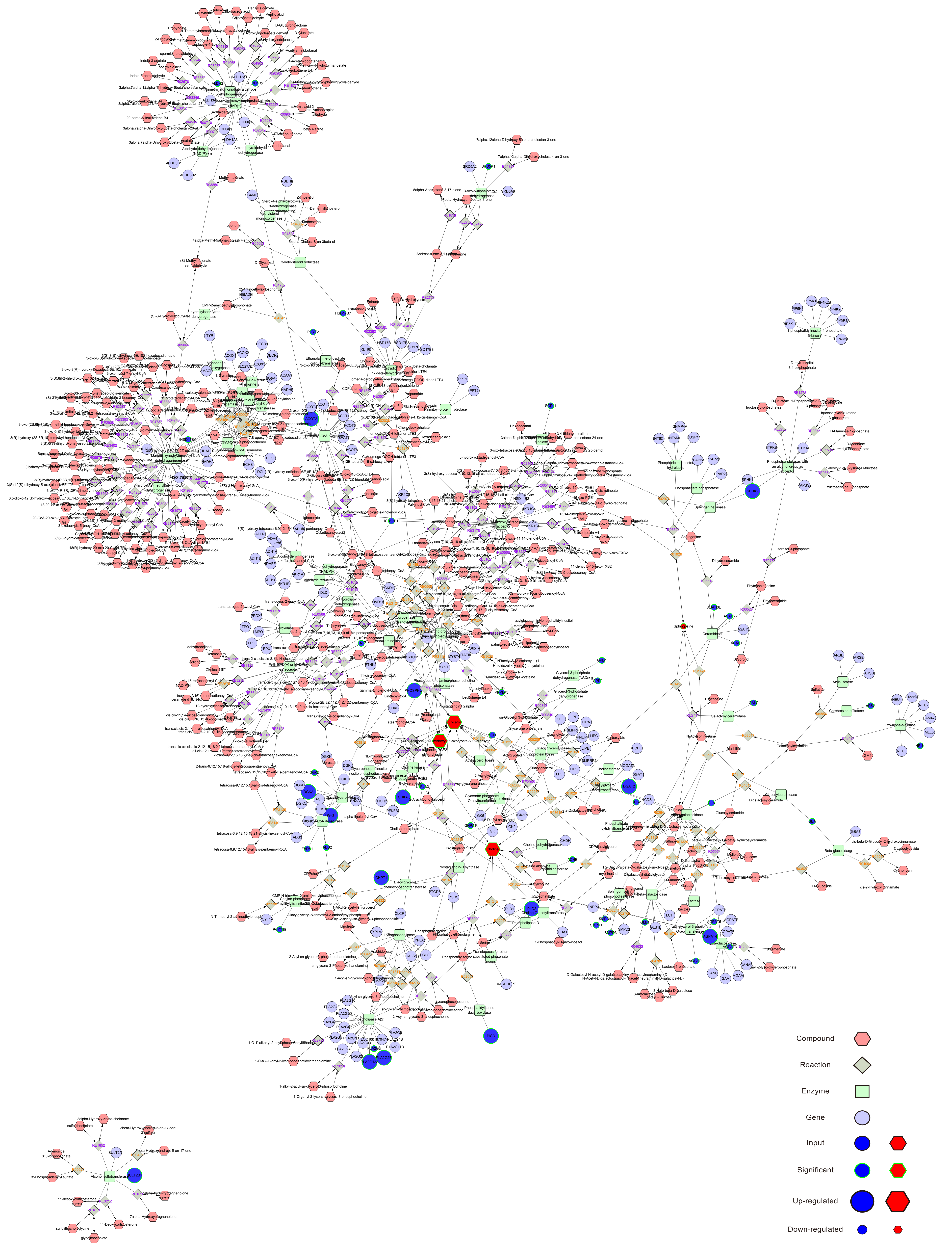


Figure S3 CCK-8 Cell viability assay of Neuro2a cells. Neuro2a cells were treated with different concentration of 2-DG (**A**), 6-AN (**B**), ND-630 (**C**) and Etomoxir (**D**) for 24 h and CCK-8 cell viability assays were then performed. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$; ns, not significant.

Figure S4 Integrated network analysis of metabolomic and transcriptomic profiling specifically associated with lipid metabolism


Compound
Reaction
Enzyme
Gene
Input
Significant
Up-regulated
Down-regulated