

## Electronic Supplementary Material

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

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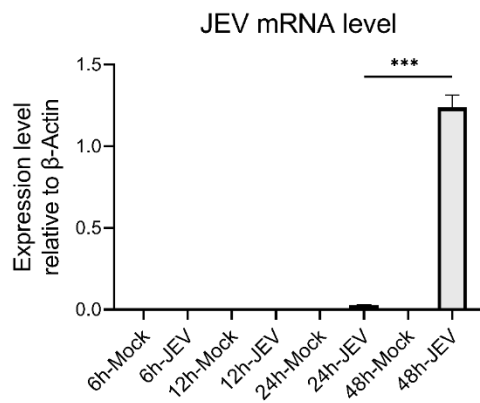
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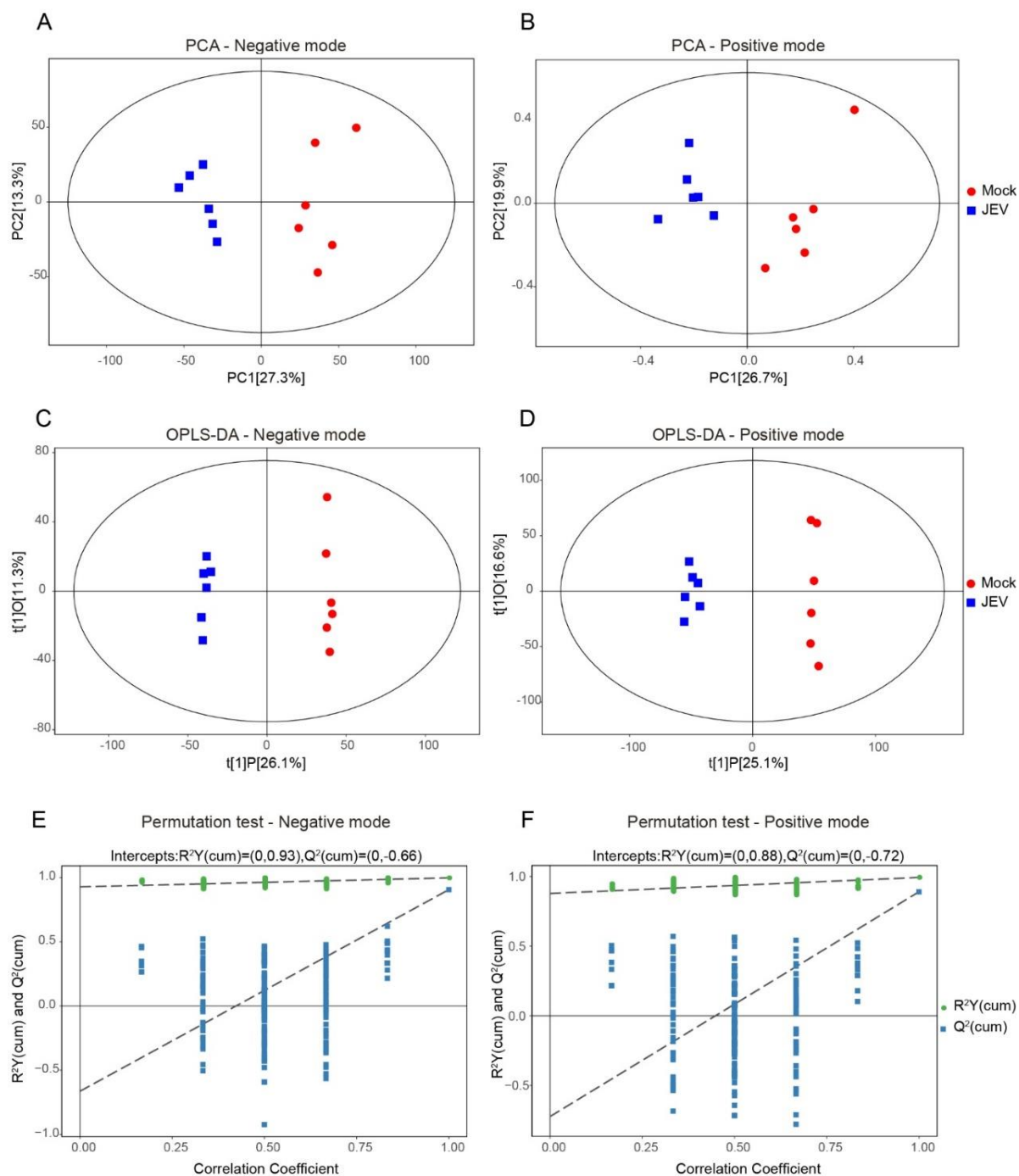
# Mengyuan Li and Jiali Yang contributed equally to this work.

**Table S1** Primer list for RT-qPCR

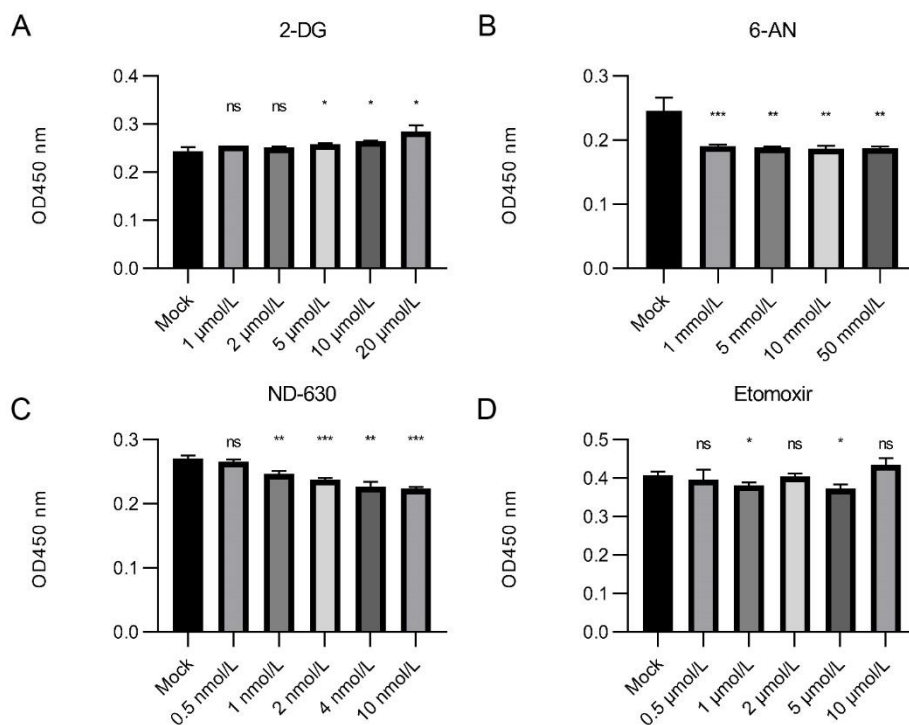
| Gene                 | Primer sequence (5'–3') |                        |
|----------------------|-------------------------|------------------------|
|                      | Forward                 | Reverse                |
| JEV                  | AGACAAGCAGATCAACCACCATT | CCCTCCAATAGAGCCAAAGTCC |
| $\beta$ -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  $\beta$ -actin. \*\*\*,  $P < 0.001$ .

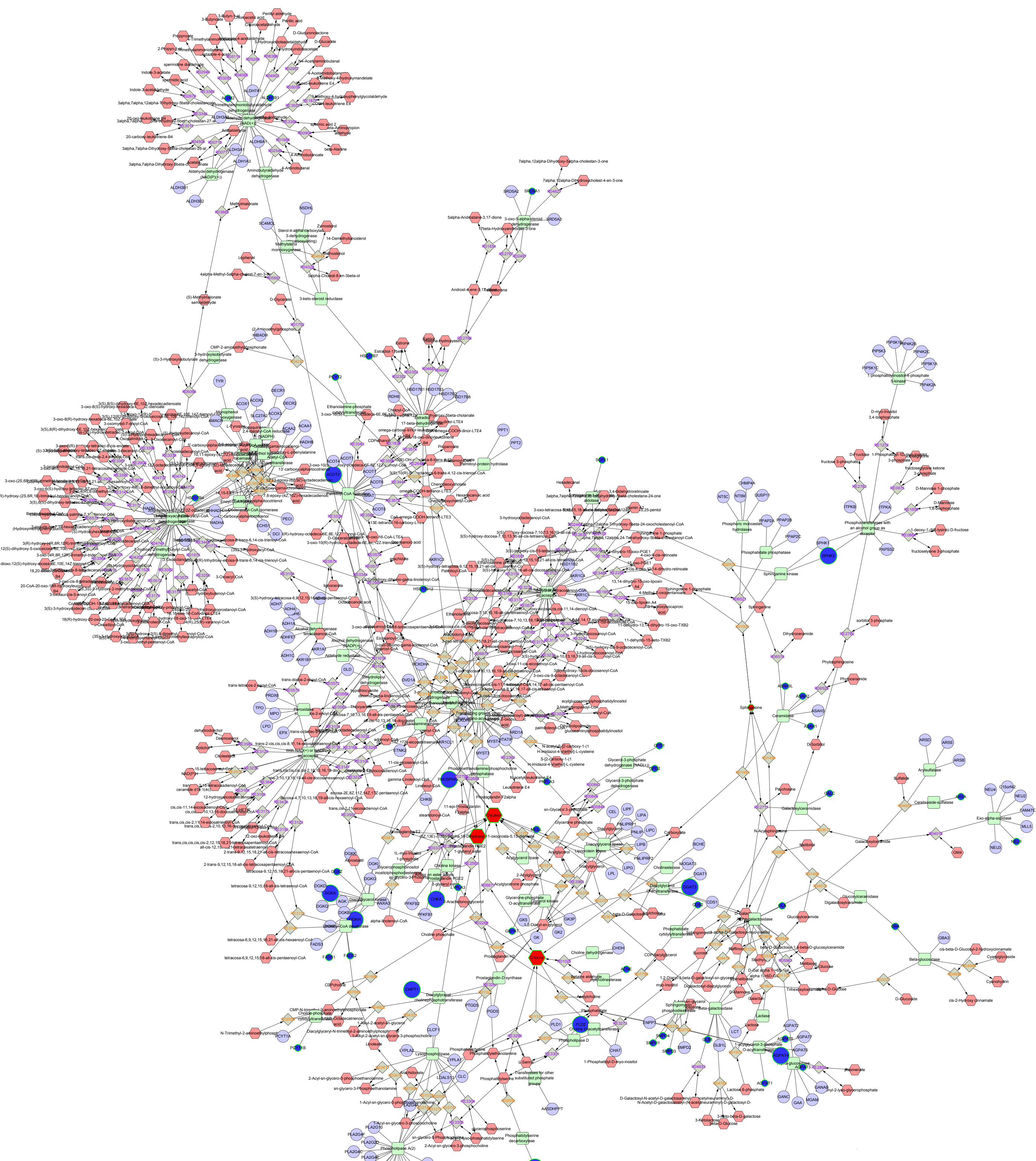


**Fig S2** Multivariate data analysis and permutation test of the metabolomic changes induced by JEV infection: score scatter plot of PCA model for JEV (blue squares) vs mock (red dots) in negative ion mode (NEG) (A) and positive ion mode (POS) (B). Score scatter plot of OPLS-DA model for JEV vs mock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

