

Supporting Information

Weighted gene co-expression network based on transcriptomics:

Unravelling the differentiation dynamics of 3T3-L1

preadipocytes and the regulatory mechanism of protopanaxatriol

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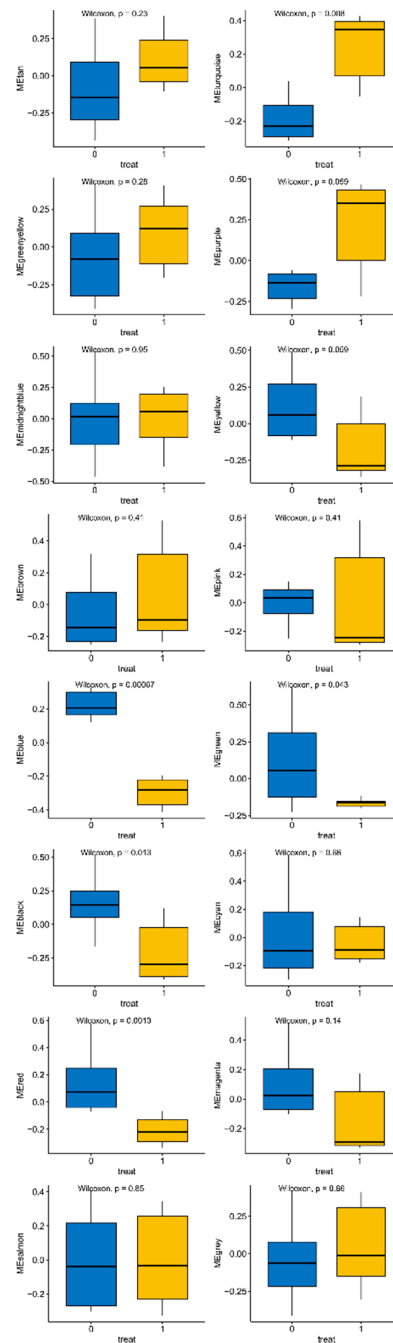
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Supplementary Figure S1A:



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Box plot illustrating the correlation between modules and phenotypic characteristics. The x-axis depicts the sample information, while the y-axis represents the module eigenvalues.