

### Supplementary Materials:

Table S1. Identified differential metabolites involved in other pathways between CDA and CD on positive-ion model or negative-ion model in liver.

Metabolites	POS/NEG model	Fold change	VIP	<i>P</i> -value	Pathways
2-Hydroxyadenine	POS	0.80	1.19	0.045	Other
N6-Methyl-L-lysine	POS	0.72	1.48	0.001	Other
NG,NG-dimethyl-L-arginine(ADMA)	POS	0.72	9.26	0.008	Other
alpha-N-Acetyl-L-glutamine	POS	2.10	1.12	0.024	Other
trans-2-Hydroxycinnamic acid	POS	1.58	1.64	0.024	Other
16-Hydroxypalmitic acid	POS	0.36	1.02	0.028	Other
Isopentenyladenosine	POS	0.73	1.29	0.030	Other
EDTA	POS	0.75	1.00	0.040	Other
2-Hydroxyadenine	POS	0.80	1.19	0.045	Other
L-NG-Monomethylarginine	POS	0.80	2.08	0.053	Other
1-Palmitoyl-2-hydroxy-sn-glycero-3-phosphoethanolamine	NEG	0.47	4.65	0.002	Other
(4Z,7Z,10Z,13Z,16Z,19Z)-4,7,10,13,16,19-Docosahexaenoic acid	NEG	0.57	1.29	0.002	Other
PGA1	NEG	0.73	1.30	0.010	Other
(+)-12-HETE	NEG	0.55	2.95	0.036	Other
Myristoleic acid	NEG	0.44	1.17	0.086	Other

VIP>1 and *P* value <0.05 are regarded as significantly differential metabolites; VIP>1 and 0.05<*P* value<0.1 are regarded as differential metabolites.

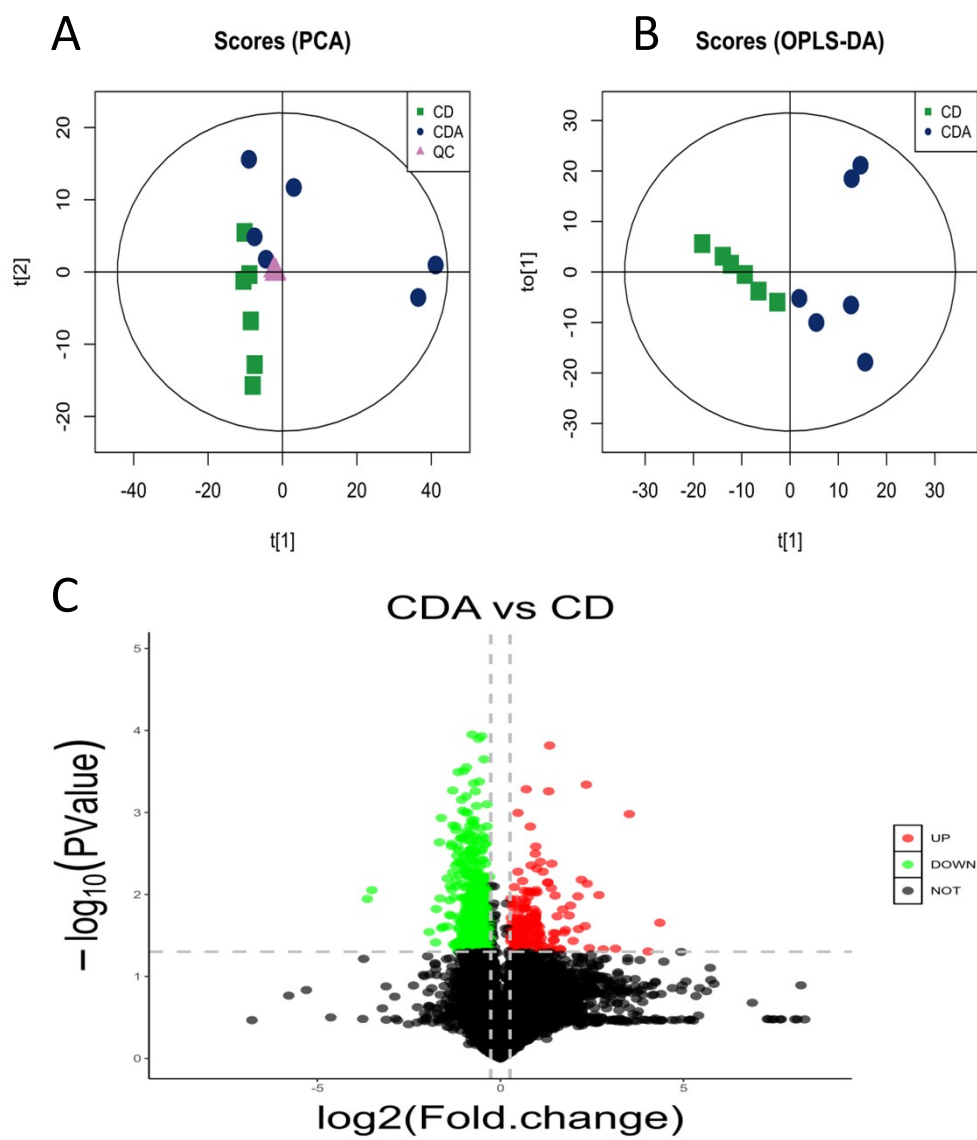


Figure S1. The PCA, OPLS-DA score plot and Volcano Plot for the metabolic profiling results of

liver tissue for CDA versus CD. A: PCA score plot.  $t[1]$  represents principal component 1, and  $t[2]$  represents principal component 2. B: OPLS-DA score plot.  $t[1]$  represents the predicted principal component and can distinguish group variations. C: Volcano Plot. The dots represents metabolites with  $FC > 1.5$  and  $P$  value  $< 0.05$ . Red dots indicate up-regulated metabolites in CDA, and green dots indicate down-regulated metabolites in CDA. Abbreviations: control diet (CD), and control diet with extra AAA (CDA); quality control (QC); principal component analysis (PCA); orthogonal partial least squares discrimination analysis (OPLS-DA); fold change analysis (FC).

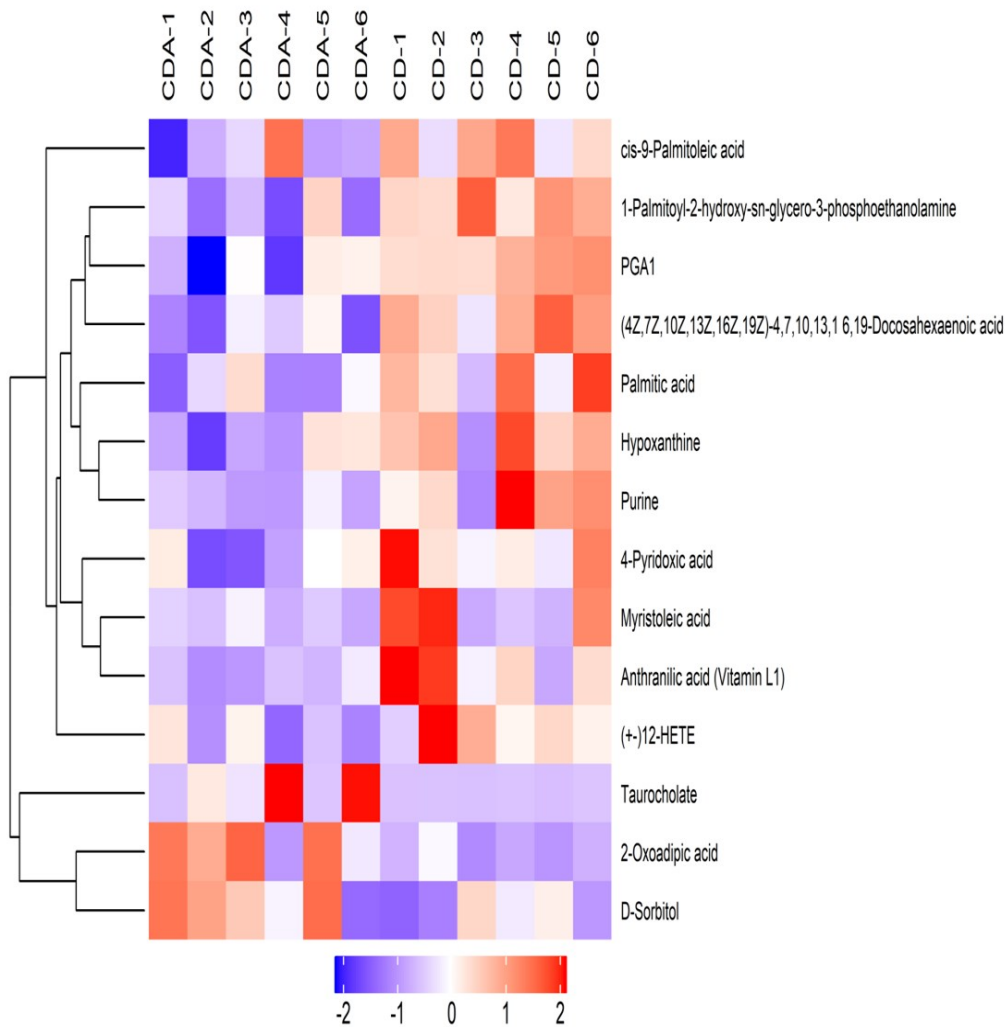


Figure S2. The Hierarchical Clustering of significant differences metabolites for CDA versus CD. Red indicates the up-regulated metabolites in CDA, and blue indicates the down-regulated metabolites in CDA. Scaled expression values are color-coded according to the legend on the

bottom. Abbreviations: control diet (CD), and control diet with extra AAA (CDA).

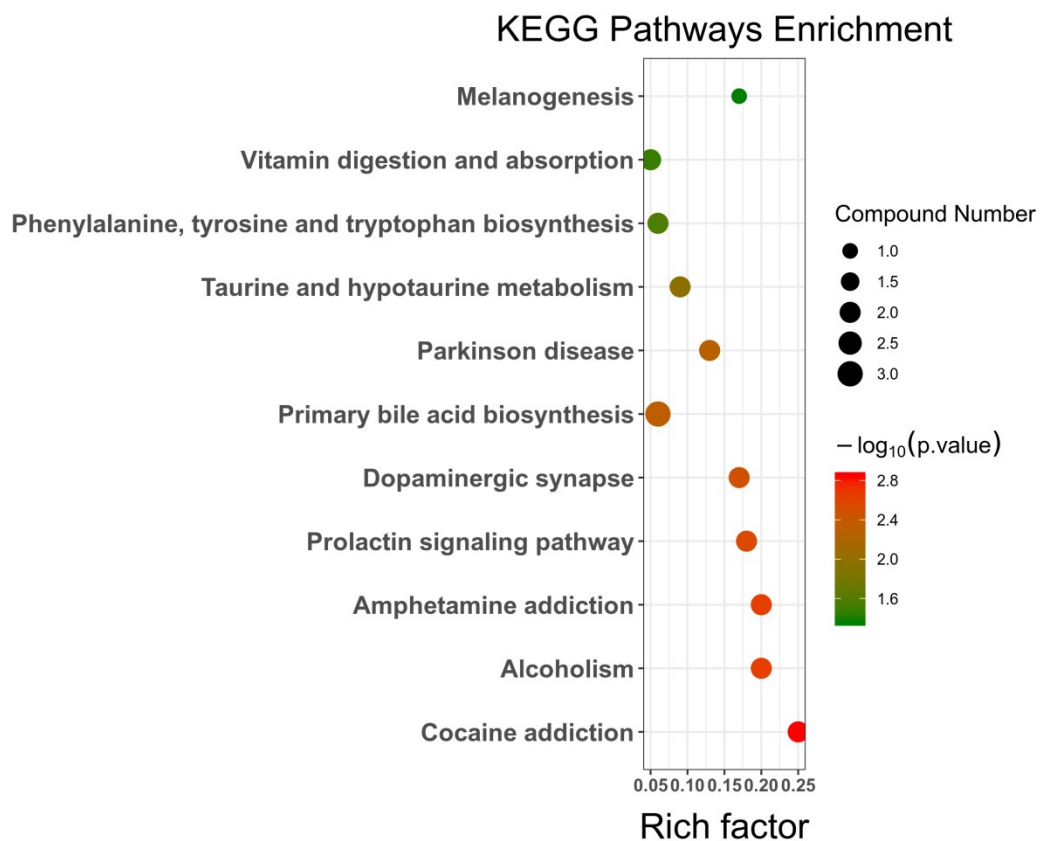


Figure S3. KEGG patCDay enrichment results based on metabolites alteration. The size of the dots represents the number of significant metabolites; the smaller  $P$  value indicates that KEGG patCDay enrichment is more significant.

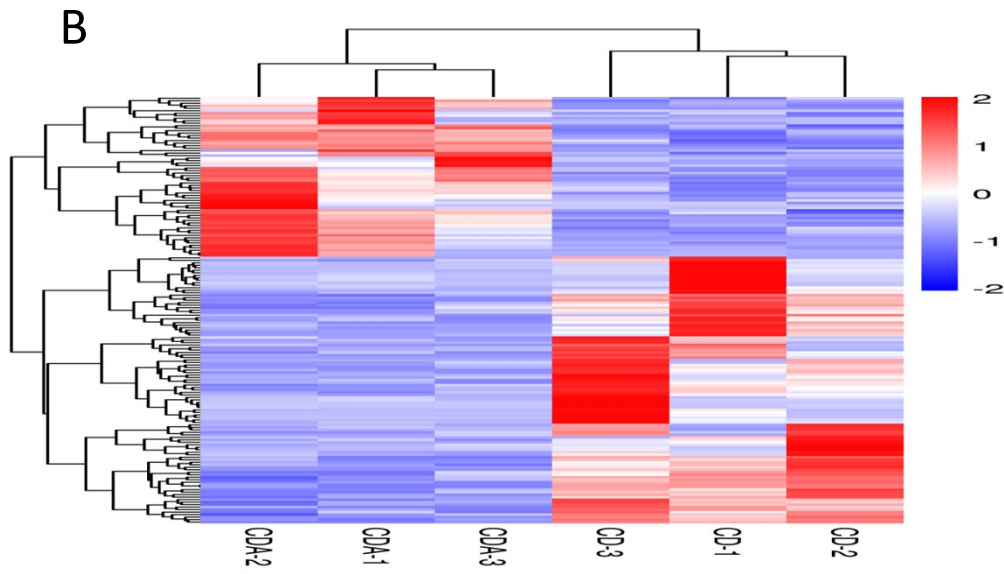
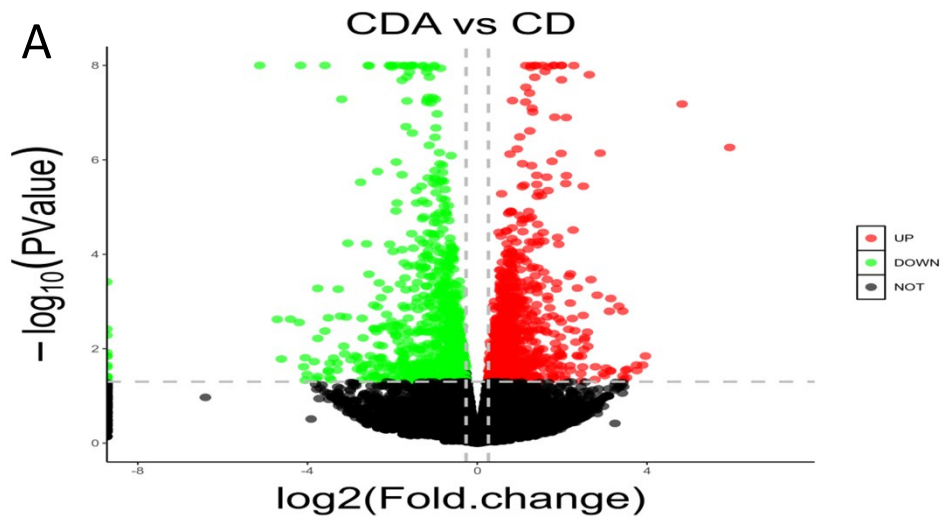


Figure S4. Volcano Plot and Hierarchical Clustering of differential genes for CDA versus CD. A: Volcano Plot. The black dots represent the genes with no significant difference, the red dots represent the up-regulated genes with significant difference, and the green dots represent the down-regulated genes with significant difference. B: The Hierarchical Clustering of differential genes. Red indicates the up-regulated genes in CDA, and blue indicates the down-regulated genes in CDA. Scaled expression values are color-coded according to the legend on the right. Abbreviations: control diet (CD), and control diet with extra AAA (CDA).

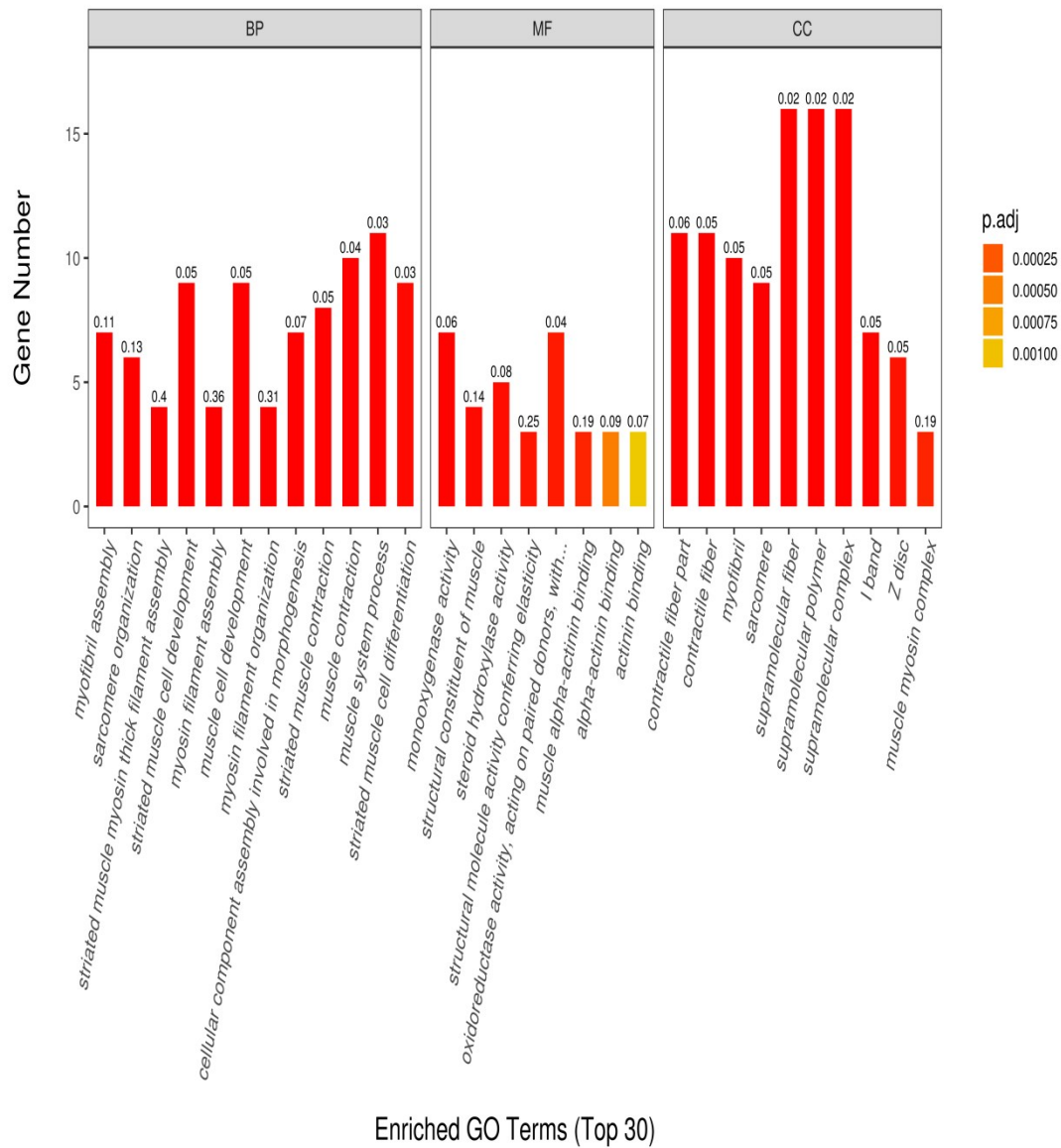


Figure S5. Gene ontology (GO) enrichment histogram of differential genes. Abbreviations of classifications: BP: biological processes; MF: molecular functions; CC: cellular components.