

1 SUPPLEMENTARY MATERIALS

2 **Transcriptomics integrated with metabolomics reveals the** 3 **amelioration of mussel-derived plasmalogens on high-fat** 4 **diet-induced hyperlipidemia in zebrafish**

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6 **Tables**

7 **Table S1. List of primers used in the qPCR experiments.**

8 **Table S2. Profile of 29090 transcripts and their expression levels identified in this study.**

9 **Table S3. Profile of 6161 metabolites identified based on MS/MS.**

10 **Table S4. The identified 20 potential metabolomics biomarkers based on MS/MS**

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12 **Figure S1. Validation of RNA-seq data using qRT-PCR.** These genes were randomly selected.
13 The mRNA expression level of each gene in the control group was set as 1, and those in HFD,
14 HFD_Pls and HFD_ATV groups were quantified relative to it. The results are represented as
15 average \pm SD of three biological replicates. Different letters on the data indicate significant
16 differences compared with other groups ($P < 0.05$).

17 **Figure S2. The SUS plot of the characteristic metabolites using the OPLS-DA model.**

18 **Figure S3. PLS-DA-based ROC curves of the 6 identified biomarkers. The associated AUC,**
19 **95% CI, sensitivity, and specificity were presented.**

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21 **Table S1. List of primers used in the qPCR experiments.**

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Gene Symbol	Forward Primer (5'–3')	Reverse Primer (5'–3')	Amplicon length (bp)
<i>β-Actin</i>	GATGCGGAAACTGGCAAAGG	GAGGAGGGCAAAGTGGTAAACG	115
<i>Cyp1a</i>	AGGACAACATCAGAGACATCACCG	CACTAGATAGACAACCGCCCAGG	178
<i>Cp</i>	TAAGAAGTGCTTCCCGAACG	GTCGGCCATAATCCCAAAT	88
<i>Gpx4a</i>	TGCGTTTCTTAGGGTCTGCT	TCTCAGAGTACTTGGCGTGC	223
<i>Lipca</i>	ACTGAGCCTGAAGCCAAGATGAAG	CGTCTACCGACCAGCCATGAATG	184
<i>Ndufs8b</i>	TTACCATTACAGAGGAGGCT	GGTAGTTGATCGTAGCTGGTTCT	167
<i>Pla2g12b</i>	CTGCTTGGCTTCCAGTTTGAT	TCTGCAAAGGTCTCACATGC	199
<i>Pmt</i>	AGGTGGGATTCAGTAATGTCC	TCCTGTATAAACTCGTCCTCA	108
<i>Ptgdsb</i>	TGCCTATGACTGACTTCGACCT	AGCAGGAACCATCACTCTTTAGG	185
<i>Sod3a</i>	TGAAGTCTCTCCCATCCCAA	CCCTGACTGAGGTCTCCGTA	179
<i>Sult2st3</i>	GACCACATCAAAAAGCTGGCGAAAC	GTGCTGTTACTGACGACACGATC	164

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25 **Table S4. The identified 20 potential metabolomics biomarkers based on MS/MS**

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Metabolite	p(corr)[1]	Vip
Isobutyric acid	0.99	1.57
Methylsuccinic acid	0.99	1.57
2-Methoxy-3-methyl-9h-carbazole	0.96	1.53
4-Ethylphenylsulfate	0.93	1.48
2-Hydroxyacetaminophen sulfate	0.88	1.41
Pseudouridine	0.88	1.41
Cysteinyl-lysine	0.86	1.37
Uracil	0.86	1.37
Pa(14:0/0:0)	0.85	1.36
8(s)-Hydroxy-(5z,9e,11z,14z)-eicosatetraenoic acid	0.85	1.35
Gamma-glutamylisoleucine	0.83	1.33
Gamma-glutamylphenylalanine	0.83	1.32
Indole	0.80	1.28
5-Methoxytryptophan	0.80	1.28
Cis-5,8,11,14,17-eicosapentaenoic acid (EPA)	-0.80	1.27
5-alpha-Thdoc	-0.78	1.24
5-Hydroxytryptophol glucuronide	-0.88	1.25
Gamma-glutamyltyrosine	0.76	1.23
3-Methylglutaryl carnitine	0.89	1.43
Glutaryl carnitine	0.87	1.25

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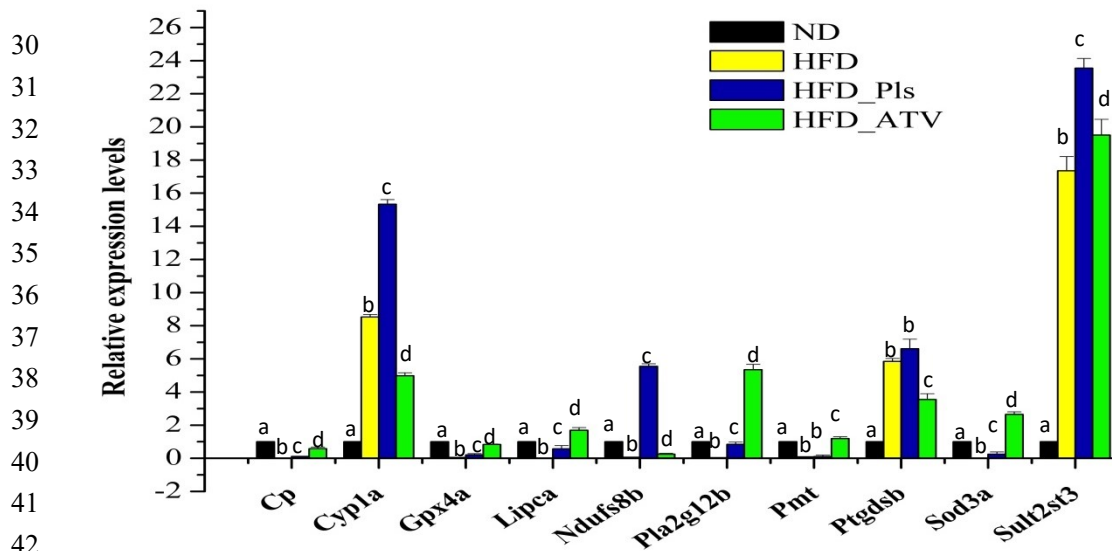


Figure S1

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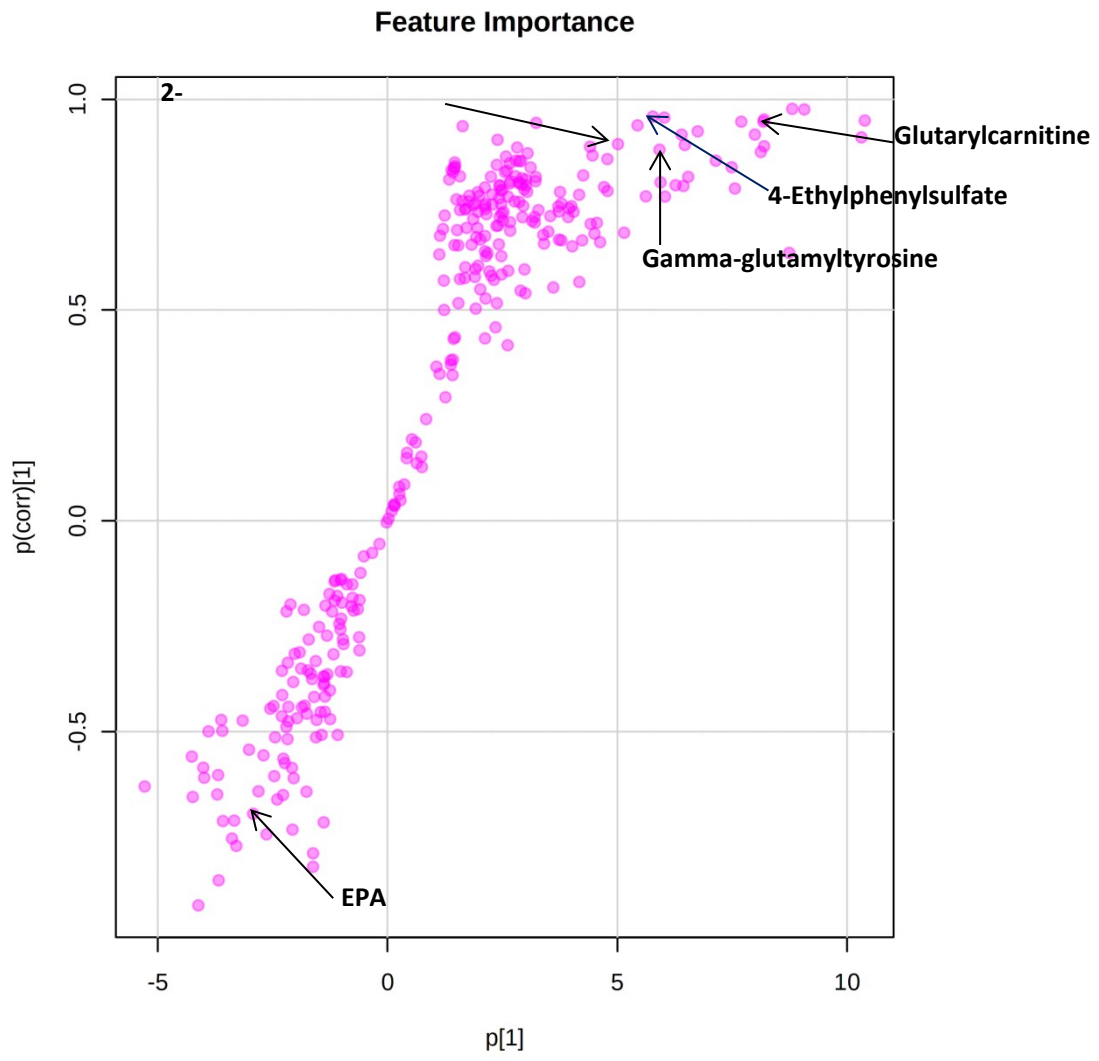


Figure S2

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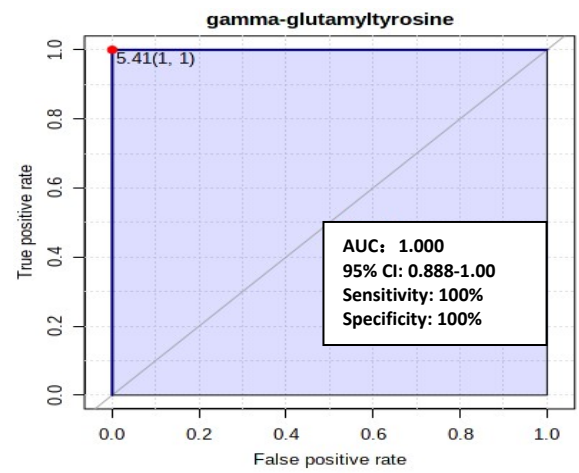
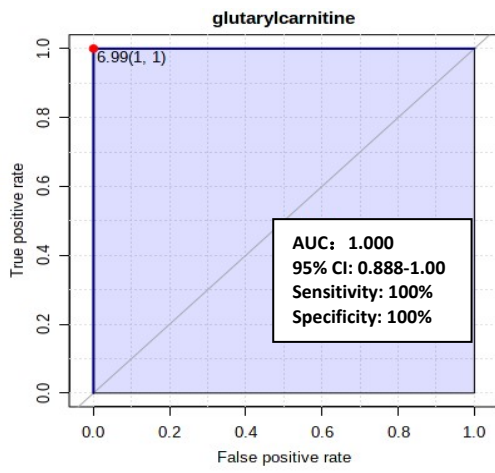
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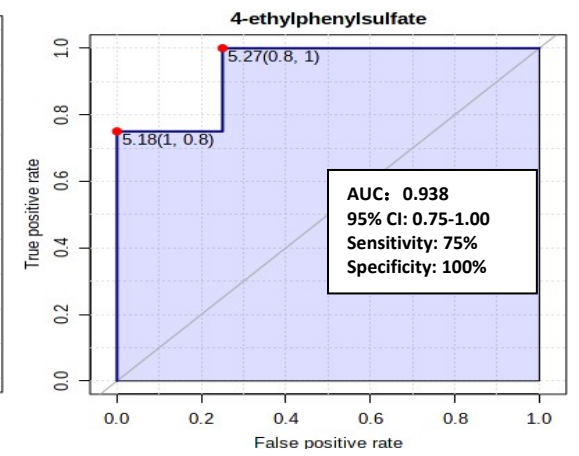
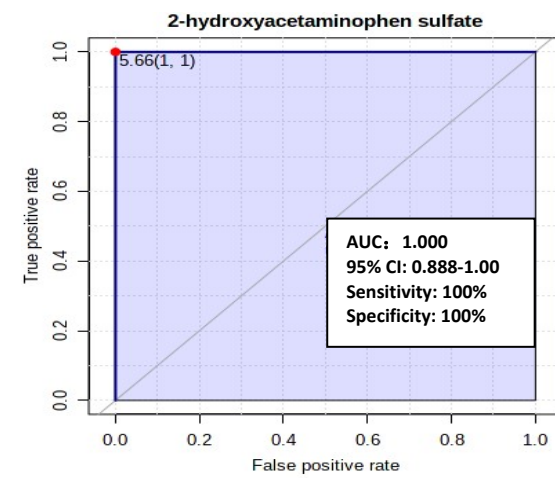
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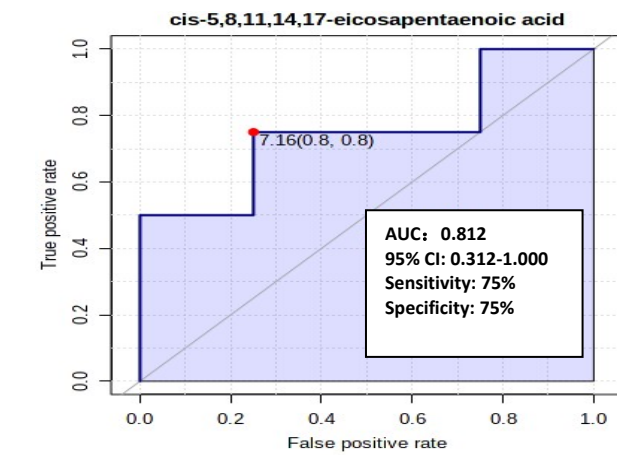


Figure S3