Table S1. Grouping table of CCO treated with different glutamine and SHVV. Note: Gln represents glutamine; SHVV represents snakehead vesiculovirus; + represents the component contained in the cell culture medium; - represents a component not contained in the cell culture medium.

	CCO cell line			
Treatment	GroupA	GroupB	GroupC	GroupD
Gln	+	+	-	-
SHVV	-	+	-	+

Table S2. R^2X(cum) of the Principal Component Analysis (PCA)

	Mixed ion model			
	GroupD vs B	GroupB vs A	GroupD vs C	GroupC vs A
p1	0.301	0.304	0.366	0.329
p2	0.478	0.494	0.515	0.569
p3	0.616	0.627	0.623	0.668

Table S3. R^2X(cum), R^2Y(cum), and Q^2(cum) of the orthogonal partial least square-discriminate analysis model (OPLS-DA)

	Mixed ion model		
	R^2X(cum)	R^2Y(cum)	Q^2(cum)
GroupD vs B	0.594	0.997	0.873
GroupB vs A	0.589	0.985	0.536
GroupD vs C	0.505	0.939	0.609
GroupC vs A	0.557	0.982	0.923

Table S4. KEGG enrichment pathway list of group A and group B

First category	Second category	Pathway description	Pathway_ID	p
Cellular processes	Transport and catabolism	Autophagy - animal	map04140	0.006
		Autophagy - other	map04136	0.006
Human diseases	Cancers: Overview	Choline metabolism in cancer	map05231	0.014
	Infectious diseases: Bacterial	Pathogenic Escherichia coli infection	map05130	0.003
Metabolism	Lipid metabolism	Linoleic acid metabolism	map00591	0.025
		Sphingolipid metabolism	map00600	0.028
		Ether lipid metabolism	map00565	0.028
		alpha-Linolenic acid metabolism	map00592	0.035
		Glycerophospholipid metabolism	map00564	0.004
		Arachidonic acid metabolism	map00590	0.005
	Glycan biosynthesis and metabolism	Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	map00563	0.006
Organismal systems	Nervous system	Retrograde endocannabinoid signaling	map04723	0.001

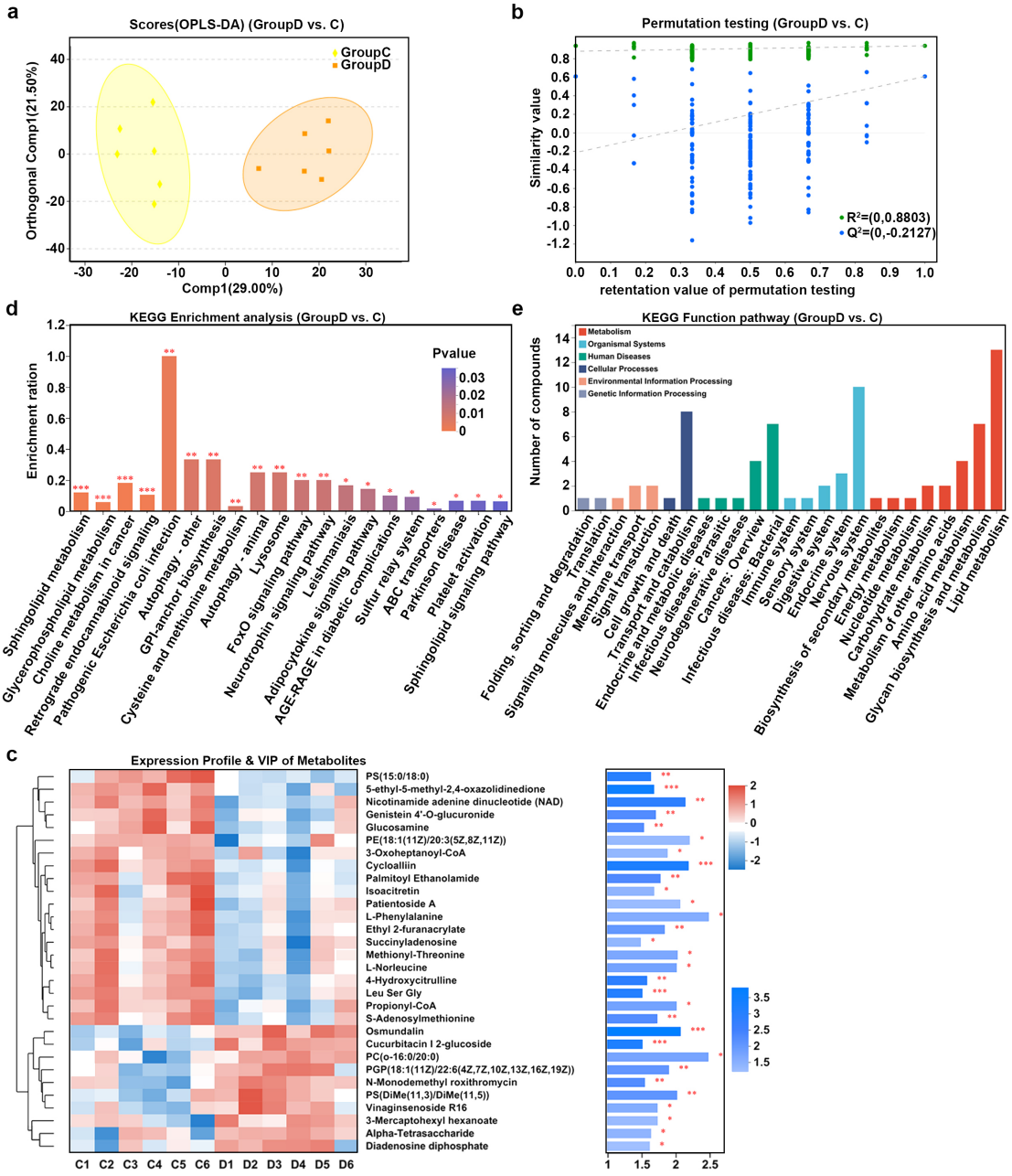

Figure S1. Orthogonal partial least squares discriminant analysis (OPLS-DA) scores of Group D and Group C, the first predicted principal component resolution of Comp1, and the first orthogonal component resolution of orthogonal comp1 (a). The permutation testing of the OPLS-DA model between Groups D vs. C (b). The variable weight (VIP) value analysis chart of GroupD and GroupC groups only shows the information of the top 30 metabolites (c). Enrichment diagram of Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway, a differential metabolite in GroupD and GroupC groups (d). Histogram of KEGG functional pathway in GroupD and GroupC groups (e). * indicates $p < 0.05$, ** indicates $p < 0.01$, and *** indicates $p < 0.001$.

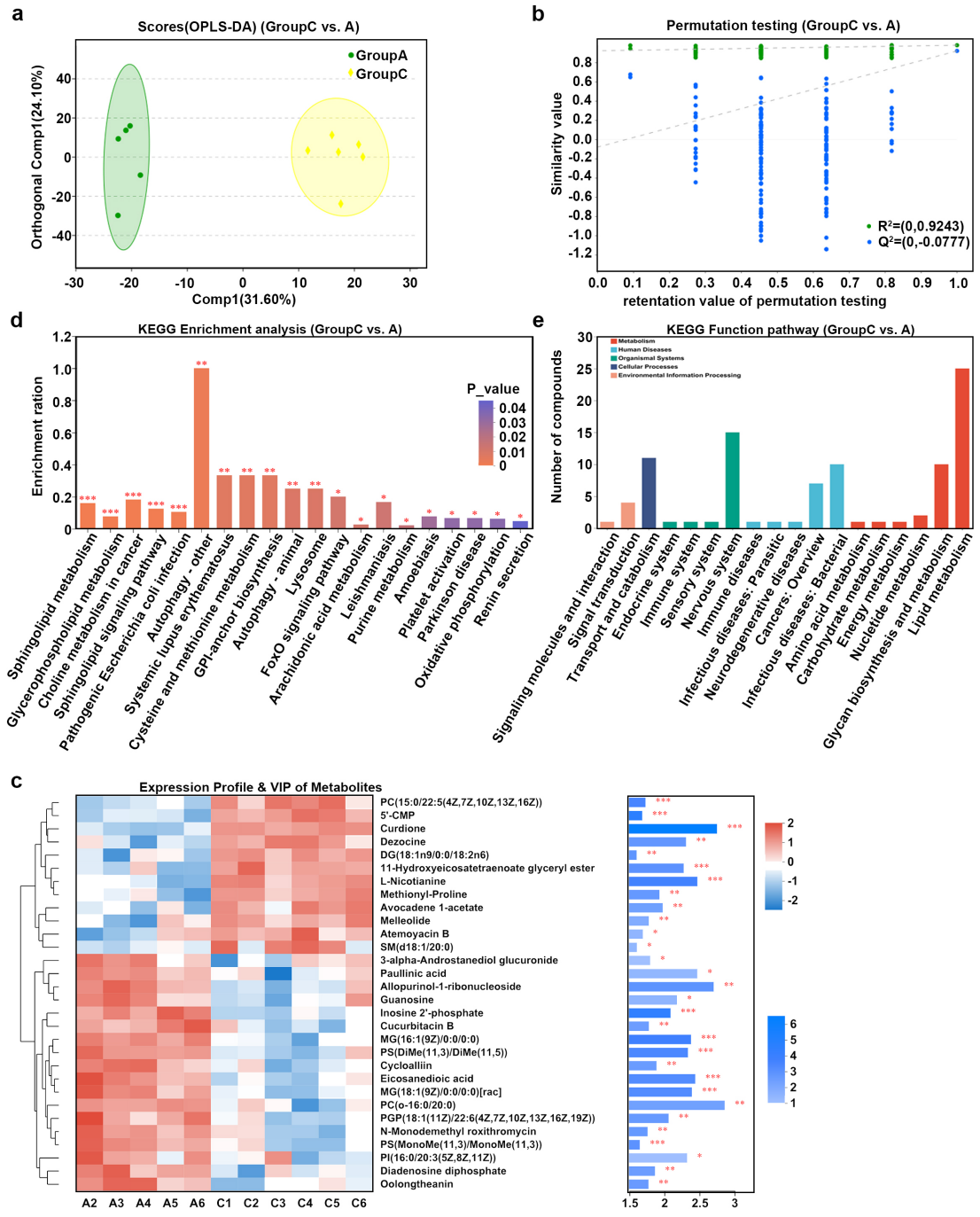

Figure S2. Orthogonal partial least squares discriminant analysis (OPLS-DA) scores of GroupC and GroupA, the first predicted principal component resolution of Comp1 and the first orthogonal component resolution of orthogonal comp1 (a). The permutation testing of the OPLS-DA model between Groups D vs. C (b). The variable weight (VIP) value analysis chart of Group C and Group A shows only the information of the top 30 metabolites (c). Enrichment diagram of Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway of differential metabolites in GroupC and GroupA groups (d). Histogram of KEGG functional pathway of differential metabolite in Group C and Group A (e). * indicates $p < 0.05$, ** indicates $p < 0.01$, and *** indicates $p < 0.001$.

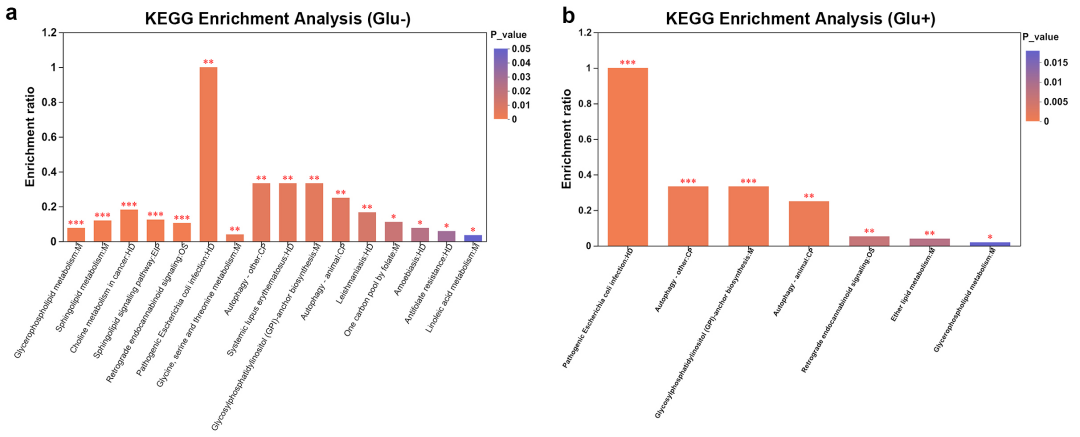

Figure S3. Under the condition of glutamine deficiency, differential metabolites were identified among Channel catfish (*Parasilurus asotus*) ovary cell line (CCO) cells and matched to pathway in Kyoto Encyclopedia of Genes and Genomes (KEGG) database (a). In the presence of glutamine, differential metabolites were identified among CCO cells and matched to pathway in KEGG database (b). * indicates $p < 0.05$, ** indicates $p < 0.01$, and *** indicates $p < 0.001$.

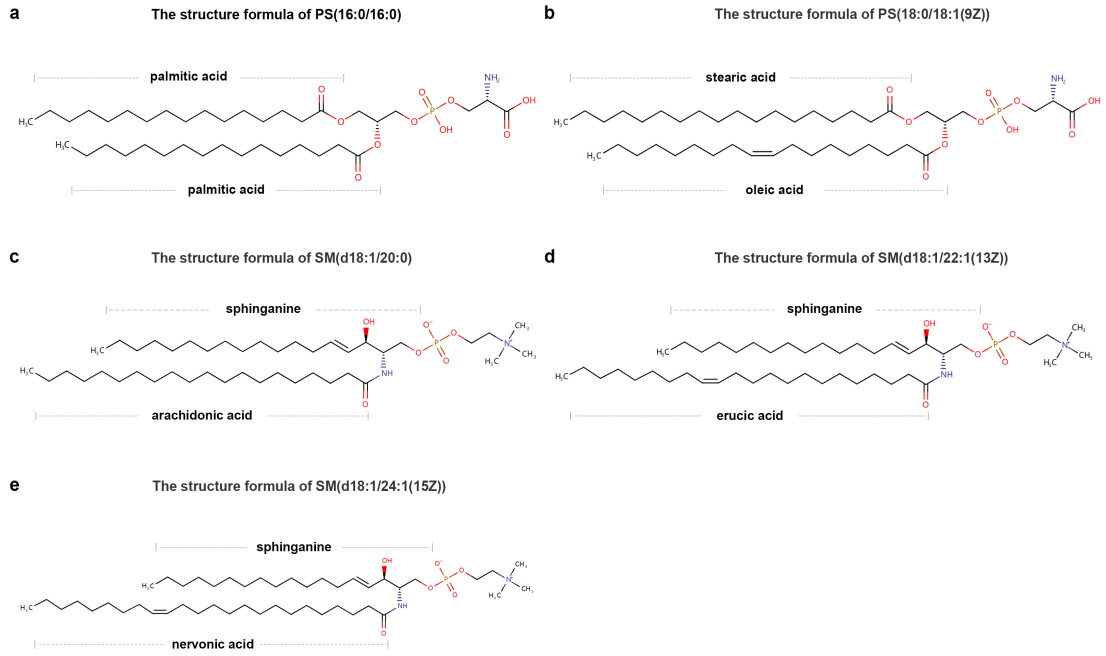

Figure S4. The structure formula of metabolites. The PS(16:0/16:0) consisted of two chains of palmitic acid (HMDB, 2005) (a). The PS(18:0/18:1(9Z)) consisted of one chain of stearic acid and one chain of oleic acid (HMDB, 2008) (b). The SM(d18:1/20:0), SM(d18:1/22:1(13Z)), and SM(d18:1/24:1(15Z)) metabolites consisted of sphinganine backbone and arachidonic acid, erucic acid, and nervonic acid chain, respectively (HMDB, 2009a; HMDB, 2009b; HMDB, 2009c) (c-e).

References

HMDB. 2005. *Showing metabocard for PS(16:0/16:0) (HMDB0000614)* [Online]. Available: https://hmdb.ca/metabolites/HMDB0000614 [Accessed].

HMDB. 2008. *Showing metabocard for PS(18:0/18:1(9Z)) (HMDB0010163)* [Online]. Available: https://hmdb.ca/metabolites/HMDB0010163 [Accessed].

HMDB. 2009a. *Showing metabocard for SM(d18:1/20:0) (HMDB0012102)* [Online]. Available: https://hmdb.ca/metabolites/HMDB0012102 [Accessed].

HMDB. 2009b. *Showing metabocard for SM(d18:1/22:1(13Z)) (HMDB0012104)* [Online]. Available: https://hmdb.ca/metabolites/HMDB0012104 [Accessed].

HMDB. 2009c. *Showing metabocard for SM(d18:1/24:1) (HMDB0012107)* [Online]. Available: https://hmdb.ca/metabolites/HMDB0012107 [Accessed].