

Table S1 The specific information of differential metabolites in the control and berberine intervention groups

Metabolite	Concentration of control group (nmol/g) ($\bar{x}\pm s$)	Concentration of berberine group (nmol/g) ($\bar{x}\pm s$)	VIP	P value	Fold change
Adenosine triphosphate	36.1962±7.9391	23.7059±2.3780	2.0389	0.0105	0.6549
Adenosine diphosphate	125.2872±22.5679	98.4104±10.8903	1.8762	0.0253	0.7855
3-Ureidopropionate	0.7737±0.1545	0.9973±0.1483	1.9136	0.0285	1.2891
Homogentisate	1.8871±0.4883	3.5096±1.3418	1.2919	0.0303	1.8597
Quinolinic acid	1.9753±0.7372	3.8185±1.6866	1.0896	0.0341	1.9332
Methylmalonic acid	3.0574±0.5149	4.7761±0.7285	1.9536	0.0008	1.5621
Picolinic acid	2.0575±0.5053	3.5255±1.3317	1.2519	0.0301	1.7135
Indole-3-acetate	2.7891±0.8002	3.7268±0.9009	1.3375	0.0857	1.3362
Phosphoenolpyruvate	4.9968±1.4483	3.5420±0.7703	1.3399	0.0550	0.7089
Cis-aconitate	3.1221±0.7210	4.1294±0.9637	1.3752	0.0675	1.3226
Isocitrate	2.2362±1.0196	3.4015±1.0348	1.5761	0.0778	1.5211
L-cysteate	0.4205±0.0828	0.5530±0.1369	1.1637	0.0700	1.3151

VIP, variable importance of projection.

Table S2 The specific information of the enriched pathways

Pathway	Total	Hits	P	−log ₁₀ (P)	Impact
Citrate cycle (TCA cycle)	20	3	0.000409	3.3884	0.0950
Glyoxylate and dicarboxylate metabolism	32	2	0.025286	1.5971	0.0238
Taurine and hypotaurine metabolism	8	1	0.062136	1.2067	0
Ubiquinone and other terpenoid-quinone biosynthesis	9	1	0.069649	1.1571	0
Purine metabolism	66	2	0.09408	1.0265	0.028
Nicotinate and nicotinamide metabolism	15	1	0.11358	0.9447	0
Pantothenate and CoA biosynthesis	19	1	0.1418	0.8483	0.0286
Beta-alanine metabolism	21	1	0.1556	0.8079	0.1045
Pyruvate metabolism	22	1	0.16243	0.7894	0
Glycolysis/gluconeogenesis	26	1	0.18922	0.7230	0.1055
Cysteine and methionine metabolism	33	1	0.23422	0.6304	0
Pyrimidine metabolism	39	1	0.27096	0.5671	0.0132
Valine, leucine, and isoleucine degradation	40	1	0.27692	0.5576	0.0226
Tryptophan metabolism	41	1	0.28284	0.5485	0
Tyrosine metabolism	42	1	0.28871	0.5395	0.0647

TCA, tricarboxylic acid.

Table S3 The 13 common metabolic pathways between transcriptome sequencing and central carbon metabolism

Pathways	
1	Citrate cycle (TCA cycle)
2	Glyoxylate and dicarboxylate metabolism
3	Taurine and hypotaurine metabolism
4	Purine metabolism
5	Nicotinate and nicotinamide metabolism
6	Pantothenate and CoA biosynthesis
7	Beta-alanine metabolism
8	Pyruvate metabolism
9	Glycolysis/gluconeogenesis
10	Cysteine and methionine metabolism
11	Pyrimidine metabolism
12	Valine, leucine, and isoleucine degradation
13	Tryptophan metabolism

TCA, tricarboxylic acid.

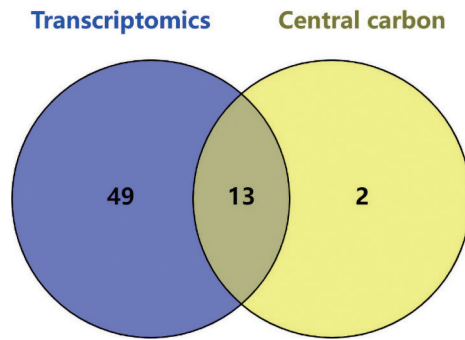


Figure S2 The intersection of the metabolic pathways obtained by transcriptome sequencing and central carbon metabolism.

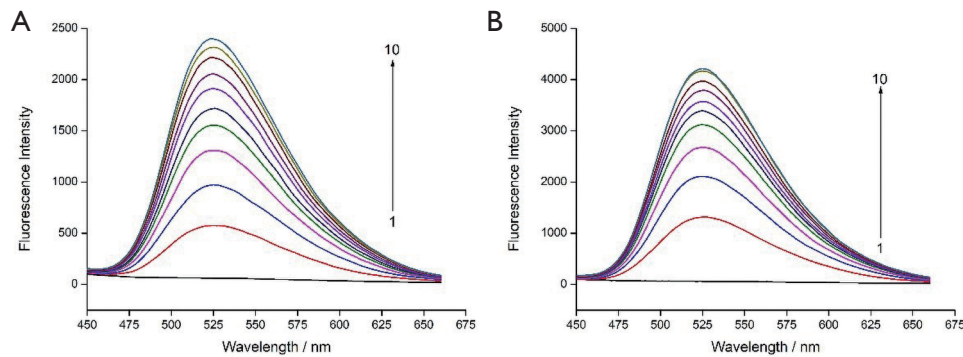


Figure S1 Fluorescence emission spectra of berberine binding with different concentrations of *c-MYC* and *HIF1α* G-quadruplexes, respectively, at 313K. (A) Fluorescence emission spectra of berberine binding with different concentrations of *c-MYC* G-quadruplexes at 313 K. (B) Fluorescence emission spectra of berberine binding with different concentrations of *HIF1α* G-quadruplexes at 313 K. From 1 to 10, the concentrations of G-quadruplex were 0.4, 0.8, 1.2, 1.6, 2.0, 2.4, 2.8, 3.2, 3.6, and 4.0 μM , respectively. *HIF1α*, hypoxia inducible factor 1-alpha.