

## Metabolomics

MDA-MB-231 cells or HEK293T cells were transfected with  $\Delta$ ATG1+2 or Flag-hSPAR for 48 hours. The metabolites were extracted for metabolite quantification by LC/MS analysis at PTMBio (HangZhou, CHINA).

### 1. Chemicals and reagents

HPLC-grade acetonitrile (ACN) and methanol (MeOH) were purchased from Merck (Darmstadt, Germany). MilliQ water (Millipore, Bradford, USA) was used in all experiments. All of the standards were purchased from Sigma-Aldrich (St. Louis, MO, USA). Ammonium acetate and formic acid were bought from Sigma-Aldrich (St. Louis, MO, USA). The stock solutions of standards were prepared at the concentration of 1 mg/mL in MeOH. All stock solutions were stored at  $-20^{\circ}\text{C}$ . The stock solutions were diluted with MeOH to working solutions before analysis.

### 2. Sample preparation and extraction

The sample was thawed on ice, 100  $\mu\text{L}$  of ultrapure water extract (containing protease inhibitors, PMSF and EDTA) was added to resuspend the cell pellet. Divide 50  $\mu\text{L}$  cell suspension and add 200  $\mu\text{L}$  of methanol (precooled at  $-20^{\circ}\text{C}$ ) and vortexed for 2 min under the condition of 2500 r/min. The sample was frozen in liquid nitrogen for 5 min, removed on ice for 5 min, after that, the sample was vortexed for 2 min. The previous step was repeated for 3 times. The sample was centrifuged at 12000 r/min for 10 min at  $4^{\circ}\text{C}$ . Take 200  $\mu\text{L}$  of supernatant into a new centrifuge tube and place the supernatant in  $-20^{\circ}\text{C}$  refrigerator for 30 min. Then the supernatant was centrifuged at 12000 r/min for 10 min at  $4^{\circ}\text{C}$ . After centrifugation, transfer 180  $\mu\text{L}$  of supernatant through Protein Precipitation Plate for further LC-MS analysis. The left 50  $\mu\text{L}$  cell suspension was frozen and thawed for 3 times, centrifuged at 12,000 r/min for 10 min, and the supernatant was taken to determine the protein concentration by BCA Protein Assay kit.

### 3. UPLC Conditions

The sample extracts were analyzed using an LC-ESI-MS/MS system (UPLC, ExionLC AD, <https://sciex.com.cn/>; MS, QTRAP® 6500+ System, <https://sciex.com/>). The analytical conditions were as follows, HPLC: column, ACQUITY BEH Amide (i.d.2.1 $\times$ 100 mm, 1.7  $\mu\text{m}$ ); solvent system, water with 2 mM ammonium acetate and 0.04% formic acid (A), acetonitrile with 2 mM ammonium acetate and 0.04% formic acid (B); The gradient was started at 90% B (0-1.2 min), decreased to 60% B (9 min), 40% B (10-11 min), finally ramped back to 90% B (11.01-15 min); flow rate, 0.4 mL/min; temperature,  $40^{\circ}\text{C}$ ; injection volume: 2  $\mu\text{L}$ .

### 4. ESI-MS/MS

AB 6500+ QTRAP® LC-MS/MS System, equipped with an ESI Turbo Ion-Spray interface, operating in both positive and negative ion modes and controlled by Analyst 1.6 software (AB Sciex). The ESI source operation parameters were as follows: ion source, turbo spray; source temperature 550°C; ion spray voltage (IS) 5500 V(Positive) , -4500 V(Negative); curtain gas (CUR) were set at 35.0 psi; DP and CE for individual MRM transitions was done with further DP and CE optimization. A specific set of MRM transitions were monitored for each period according to the amino acid eluted within this period.

#### 5. Detection of Amino acid and its metabolites

Amino acid and its metabolites were detected by (<http://www.metware.cn/>) based on the AB Sciex QTRAP 6500 LC-MS/MS platform.