The same OD of *P.* *acidipropionici* CGMCC 1.2230 and *P. acidipropionici* WSH1105 were collected at the middle exponential phase, late exponential phase, and the end of fermentation. To capture accurate snapshots of the metabolome, we quenched cell metabolism by immediately adding a threefold volume of pre-chilled 60% (v/v) methanol solution containing 70 mM 4-(2-hydroxyethyl)-1-piperazine ethanesulphonic acid. After quenching at –40°C, the cells were pelleted in a centrifuge (4,000 × *g*, −4°C, 10 min). The pellets were washed with methanol solution and resuspended in 1 mL 35% perchloric acid to extract the metabolites from the cells. The mixture was frozen in liquid nitrogen and thawed three times. The supernatant was neutralized by adding K2CO3 solution with an initial concentration of 5 M, and an extract containing all metabolites was collected via centrifugation at 10,000 × *g* for 5 min at –4°C.

LC-MS analysis was performed to detect the metabolites in the samples. Ten microliters of sample was injected into an LC-MS ion trap time-of-flight spectrometer (Shimadzu, Kyoto, Japan) equipped with a Shim-Pack VP-ODS 150 L × 2.0 high-performance liquid chromatography column (Shimadzu). The samples were eluted at a flow rate of 0.2 mL/min with a gradient of 1 mM ammonium formate (A) and 80% methanol (v/v) containing 1 mM ammonium formate (B) as follows: 2% to 60% B for 15 min, 60% to 76% B for 15 min, and 76% to 2% B for 5 min. An ion trap time-of-flight detection (LCMS-IT-TOF, Shimadzu) by using an electrospray ionization source was performed in both positive and negative ion mode by using optimized conditions: detector voltage, 1.70 kV; nebulizing gas (N2) flow, 1.5 L/min; drying gas (N2) flow, 200 kPa; ion accumulation time, 30 ms; collision energy, 40% for MS2; mass acquisition at *m/z* 50–1000 for MS and MS2.