The extracted metabolites were analyzed on an Ultimate 3000 HPLC system (Dionex, Germering, Germany) coupled to a Q Exactive HF mass spectrometry. The mass spectrometry was performed in a data dependent acquisition mode (Top10) ranging from m/z 70 to m/z 1000 with a 60000 resolution in both positive and negative modes simultaneously. Data acquisition and monitoring were performed through Xcalibur software (version 2.0.7, ThermoFisher Scientific, Bremen, Germany). UPLC-HRMS data were analyzed using MS-DIAL software after conversion to mzML file format using MSConvert (Version 3.0, ProteiWizard).