



Figure 7. DEGs and DAMs in cysteine and methionine metabolism. CpNIFS3: L-cysteine desulfhydrase; ASP1: aspartate aminotransferase, mitochondrial; SAT1: serine O-acetyltransferase; CYSD1: cysteine synthase; METE: 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase; MGL: methionine-gamma-lyase; TAT: tyrosine aminotransferase; SAM3: S-adenosylmethionine synthetase; MET2A: DNA (cytosine-5)-methyltransferase 1; SAHH: adenosylhomocysteinase; ACS: 1-aminocyclopropane-1-carboxylate synthase; SAMDC: S-adenosylmethionine decarboxylase; ACO: aminocyclopropanecarboxylate oxidase; BCAT2: branched-chain amino acid aminotransferase. The relative expression levels of DEGs and the accumulation of DAMs were calculated using the Log₂FC.