



Figure 3. Differential accumulated metabolites (DAMs) in *flc-* mutants under control, salinity, heat and the combination of salinity+heat, and biosynthetic pathway analysis. (A) Venn diagrams of the overlap between DAMs in each treatment. (B) Biosynthetic pathway enrichment. (C) Secondary metabolite biosynthetic pathways analysis. (D) Hormone biosynthetic pathways enrichment. (B, C and D were performed using PlantCyc software). Data were normalized against Wt control ($p < 0.05$; $FC > 2$). AA: amino acids; Ncl: nucleo; FA: fatty acids; Lip: lipids; Carbh: carbohydrates; Second: secondary metabolites; Co: cofactors; Horm: hormones; Cell str: cell structure; Reg: regulatory; N-cont: N-containing; Polyket: polyketides; S-cont: S-containing; Sug-der: sugar derivatives; Terp: terpenoids; Terphe: terpenophenolics; Pheprop: phenylpropanoids; AUX: auxins; CK: cytokinins; GB: gibberellins; ABA: abscisic acid; Jas: jasmonates; BR: brassinosteroids; SA: salicylic acid.