Figure 4. Multi-omics analysis in flc- mutant using MixOmics software. (A) sPLS-DA analysis in each –omic. (B) Heatmap correlation plot of most discriminant features selected from phenomics, ionomics, transcriptomic and metabolomics datasets. Omics are represented in columns and treatments are represented in rows. (C) Loading plot of each feature selected having the maximal discrimination ability on the first and second components in each -omics datasets. Color indicates the stress treatment applied. CBP1: CCG-binding protein1; SnRK2.4 sucrose non-fermenting related protein kinases 2.4; KAT1 K+ transporter: GTF: Glycosyltransferase; Grx: glutaredoxin.