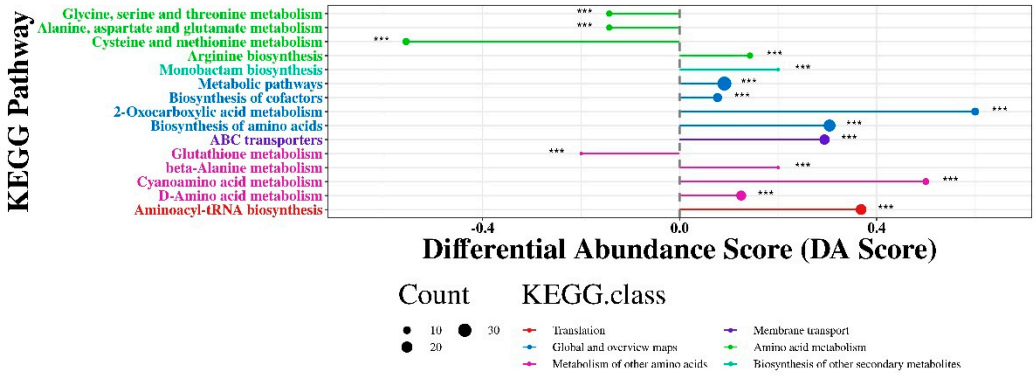
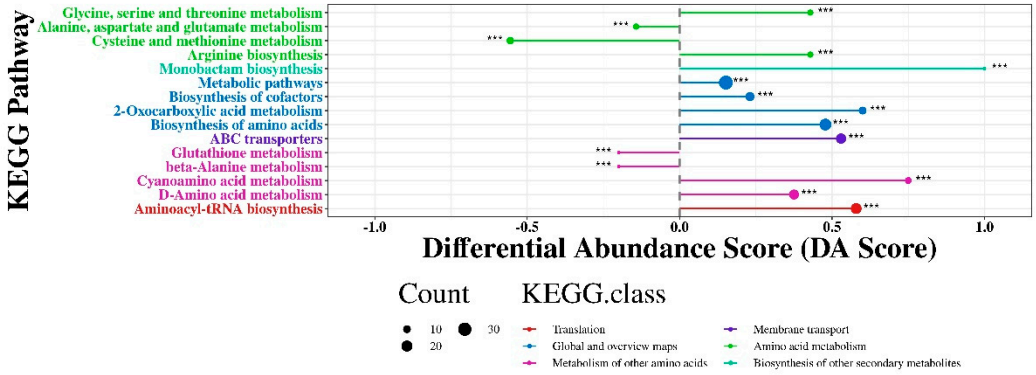
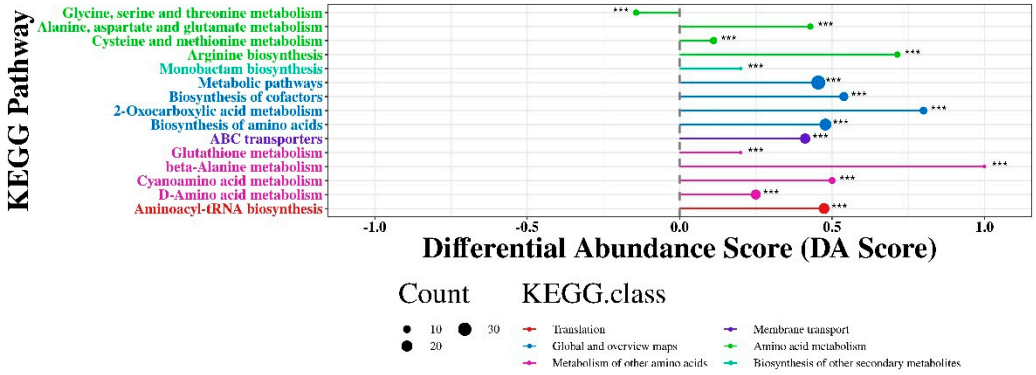
P1_Leaf_7d-P31_Leaf_7d



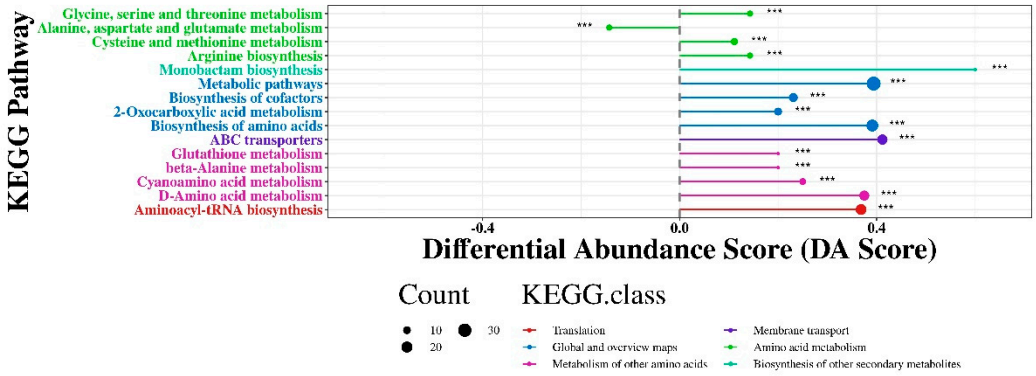
P1_Leaf_14d-P31_Leaf_14d



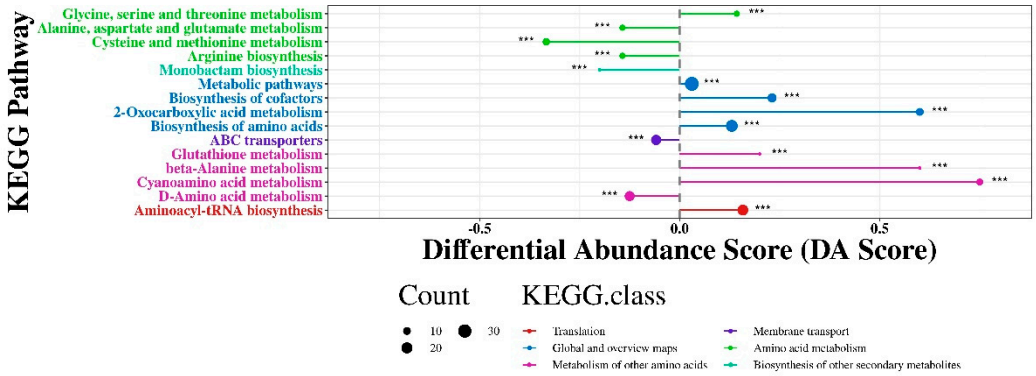
P1_Leaf_21d-P31_Leaf_21d



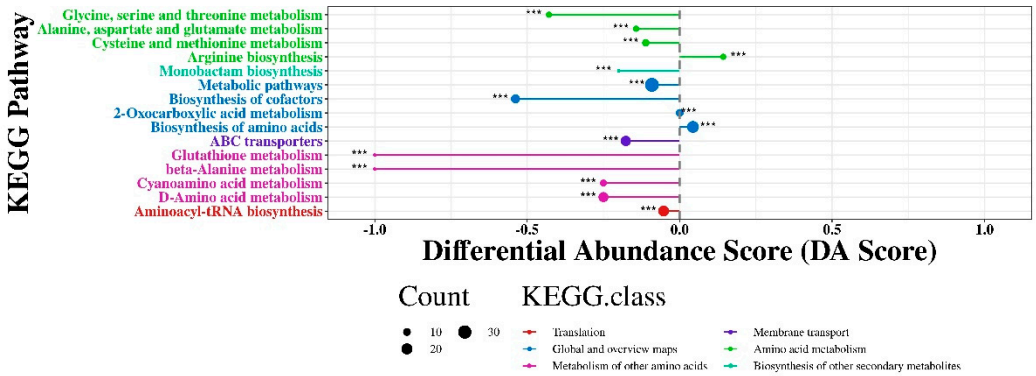
P1_Root_7d-P31_ Root_7d



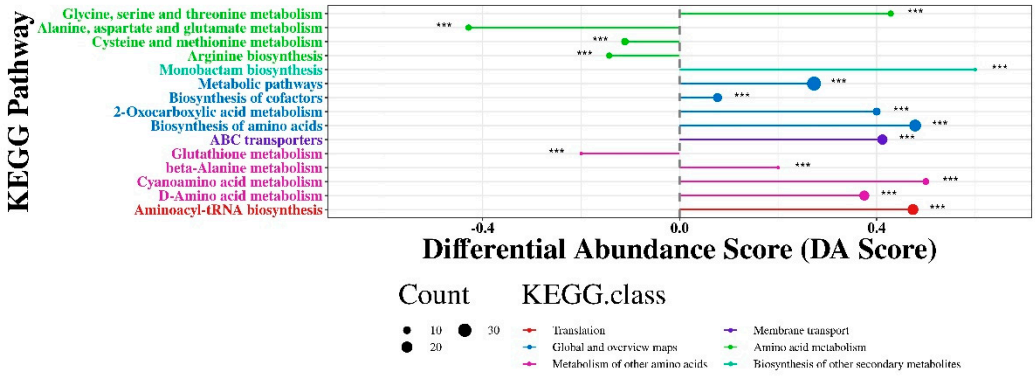
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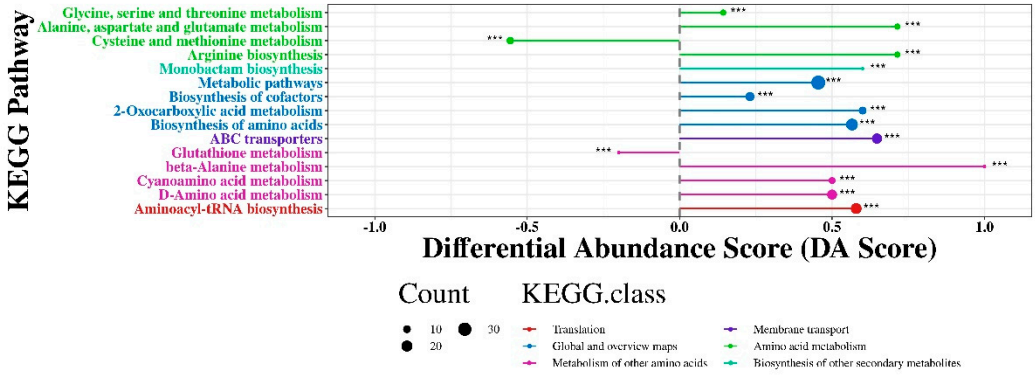
P1_Root_21d-P31_ Root_21d



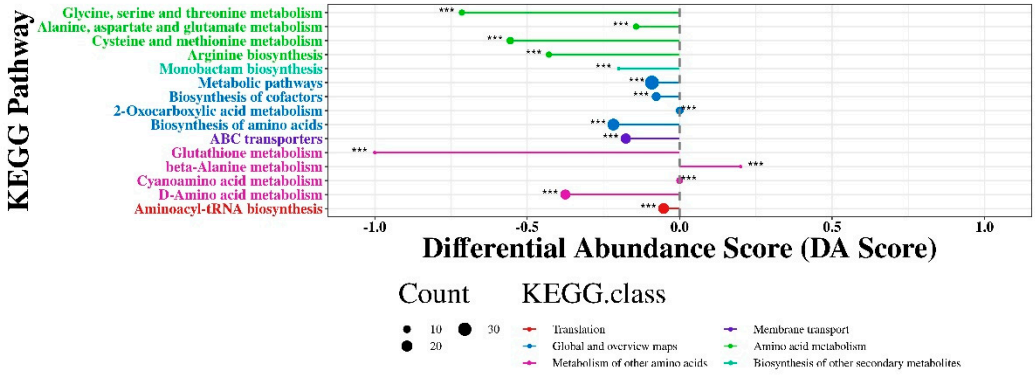
P1_Nodule_7d-P31_ Nodule_7d



P1_Nodule_14d-P31_ Nodule_14d



P1_Nodule_21d-P31_ Nodule_21d



The horizontal axis represents the differential abundance score (DA Score), and the vertical axis represents the KEGG metabolic pathways.

The DA score reflects the overall changes in all metabolites of the metabolic pathway. A score of 1 indicates an upregulation in the expression trend of all annotated differential metabolites in the pathway, -1 indicates a downregulation, and the length of the line segment represents the absolute value of the DA Score. The size of the dots indicates the number of differential metabolites

annotated in the pathway, with larger dots indicating more differential metabolites in the pathway.