

Proteome-wide Analyses Reveal the Diverse Functions of Lysine 2-Hydroxyisobutyrylation in *Oryza sativa*

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The PDF file includes:

Figure S1. Quality control validation of MS data and distribution of Khib peptides.

Figure S2. Representative MS/MS spectra of Khib-modified peptides in rice.

Figure S3. Western blotting analysis of chloroplast proteins in rice seedling leaves.

Figure S4. GO-based enrichment analysis of identified Khib proteins.

Figure S5. KEGG pathway enrichment analysis of rice Khib proteins.

Figure S6. PPI network of all identified Khib proteins.

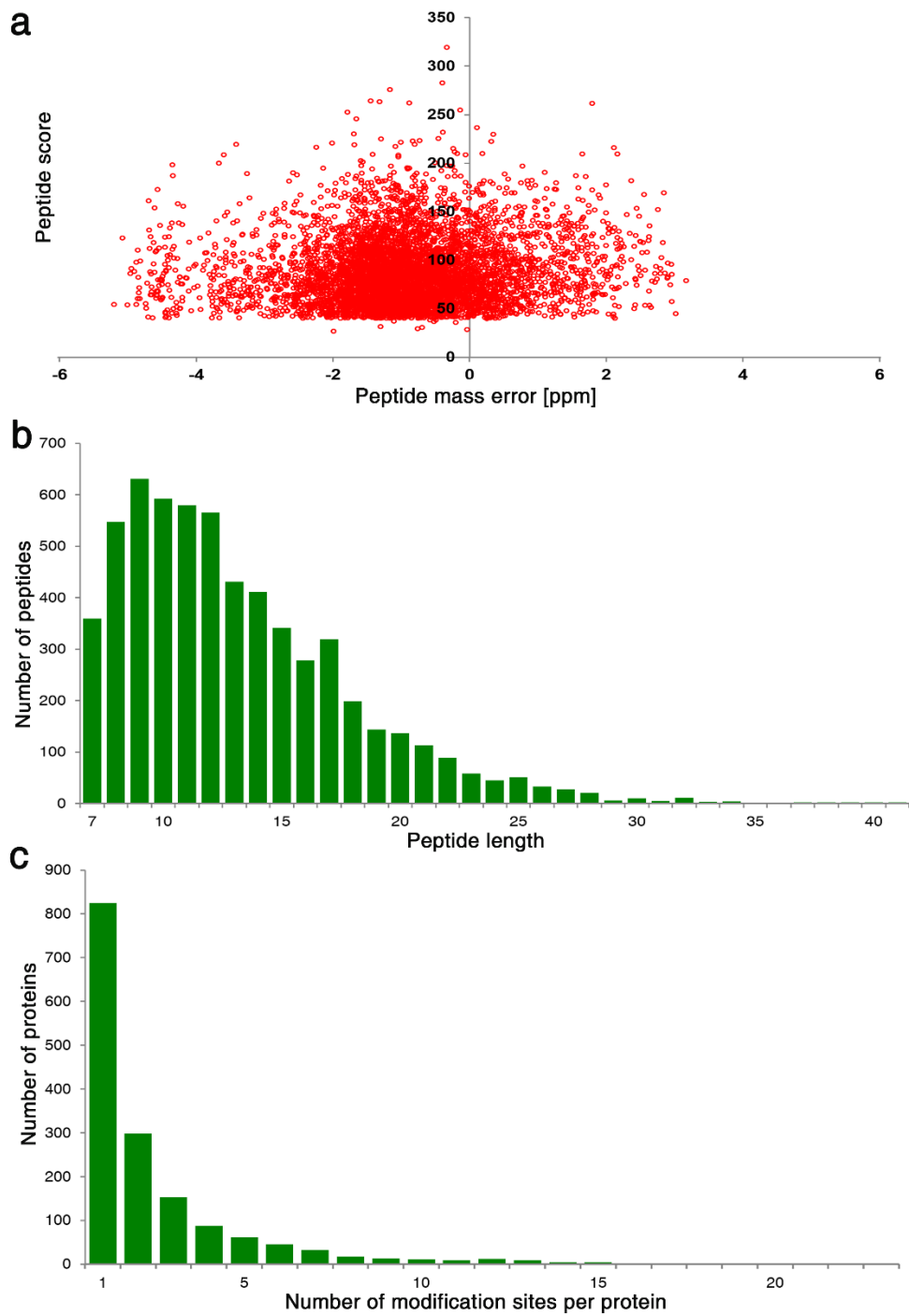


Figure S1. Quality control validation of MS data and distribution of Khib peptides. (a) The mass errors of peptides with Khib sites. (b) The lengths of all identified peptides. (c) The number of Khib sites per protein.

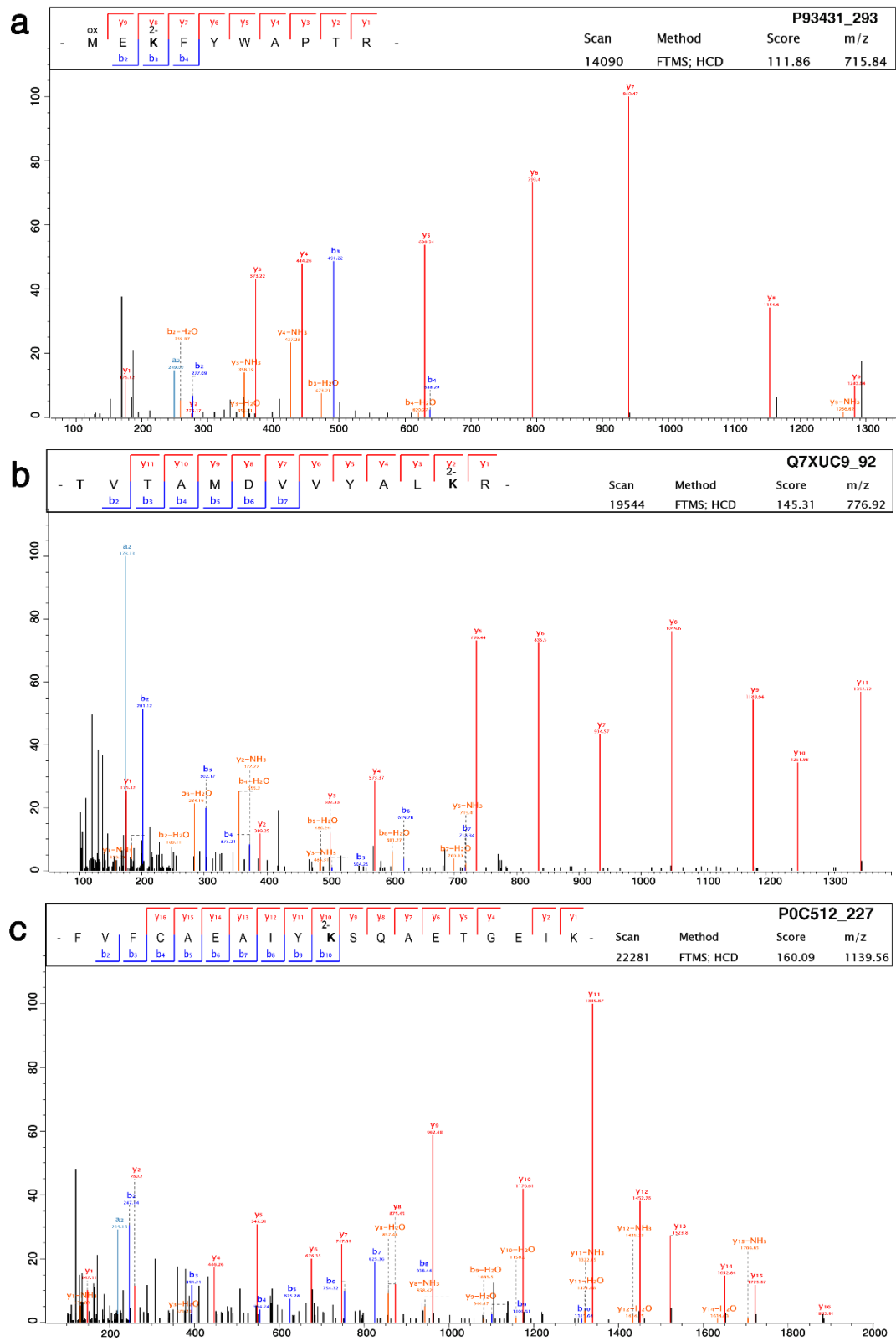


Figure S2. Representative MS/MS spectra of Khib-modified peptides in rice. **(a)** MS/MS spectrum of MEK_{hib}FYWAPTR in Rubisco activase (P93431). **(b)** MS/MS spectrum of TVTAMDVVYALK_{hib}R in histone H4 (Q7XUC9). **(c)** MS/MS spectrum of FVFCAEAIYK_{hib}SQAETGEIK in Rubisco (P0C512).

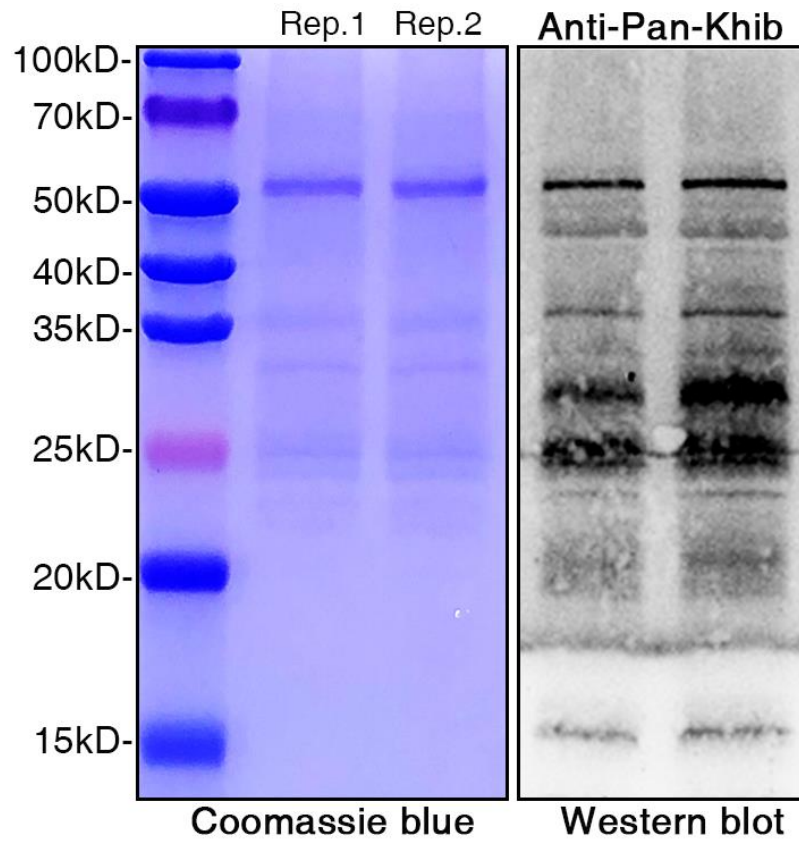


Figure S3. Western blotting analysis of chloroplast proteins in rice seedling leaves.

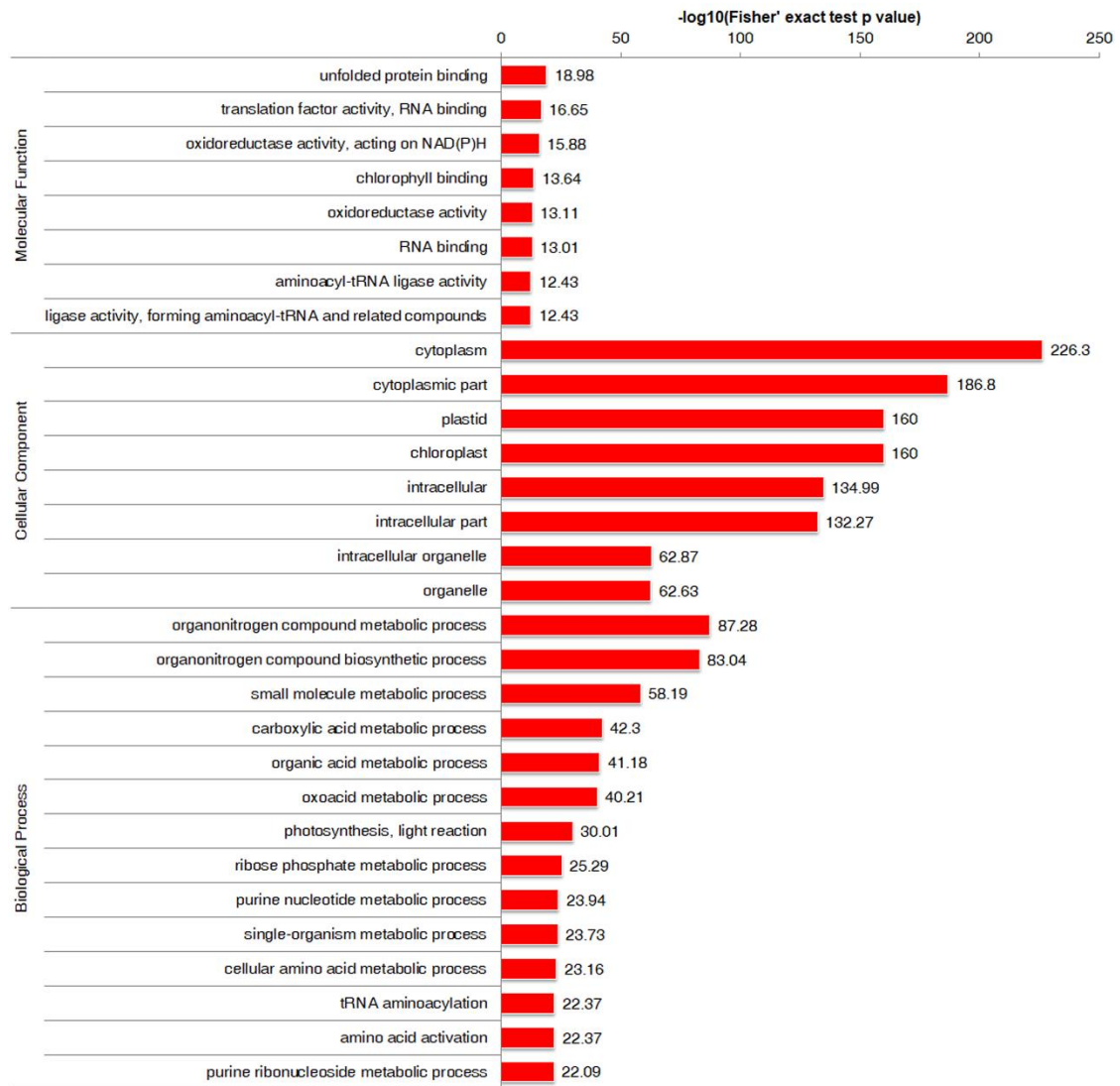


Figure S4. GO-based enrichment analysis of identified Khib proteins. The value of $-\log_{10}$ (Fisher's test p value) is shown.

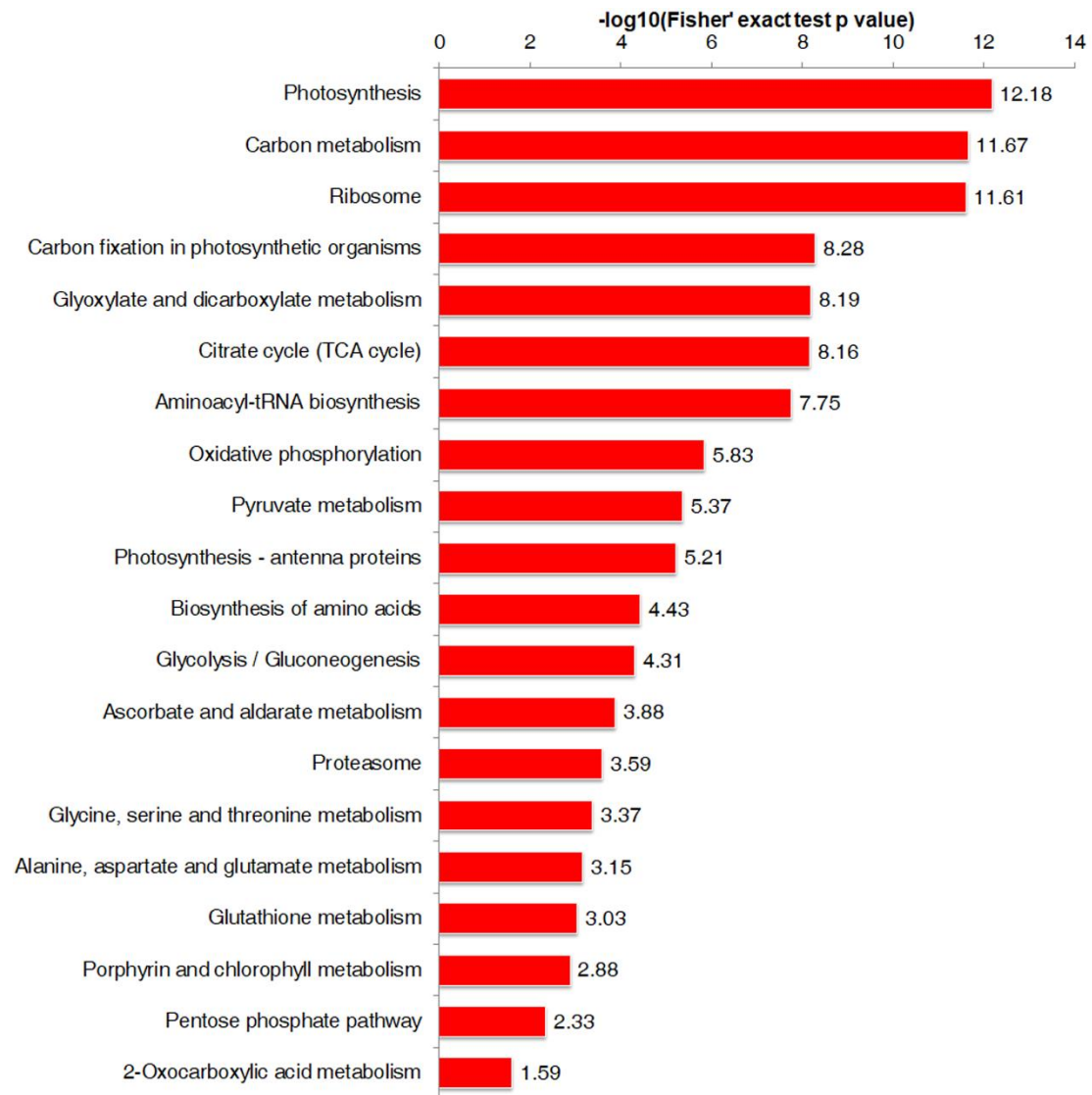


Figure S5. KEGG pathway enrichment analysis of rice Khib proteins. The value of $-\log_{10}$ (Fisher's test p value) is shown.

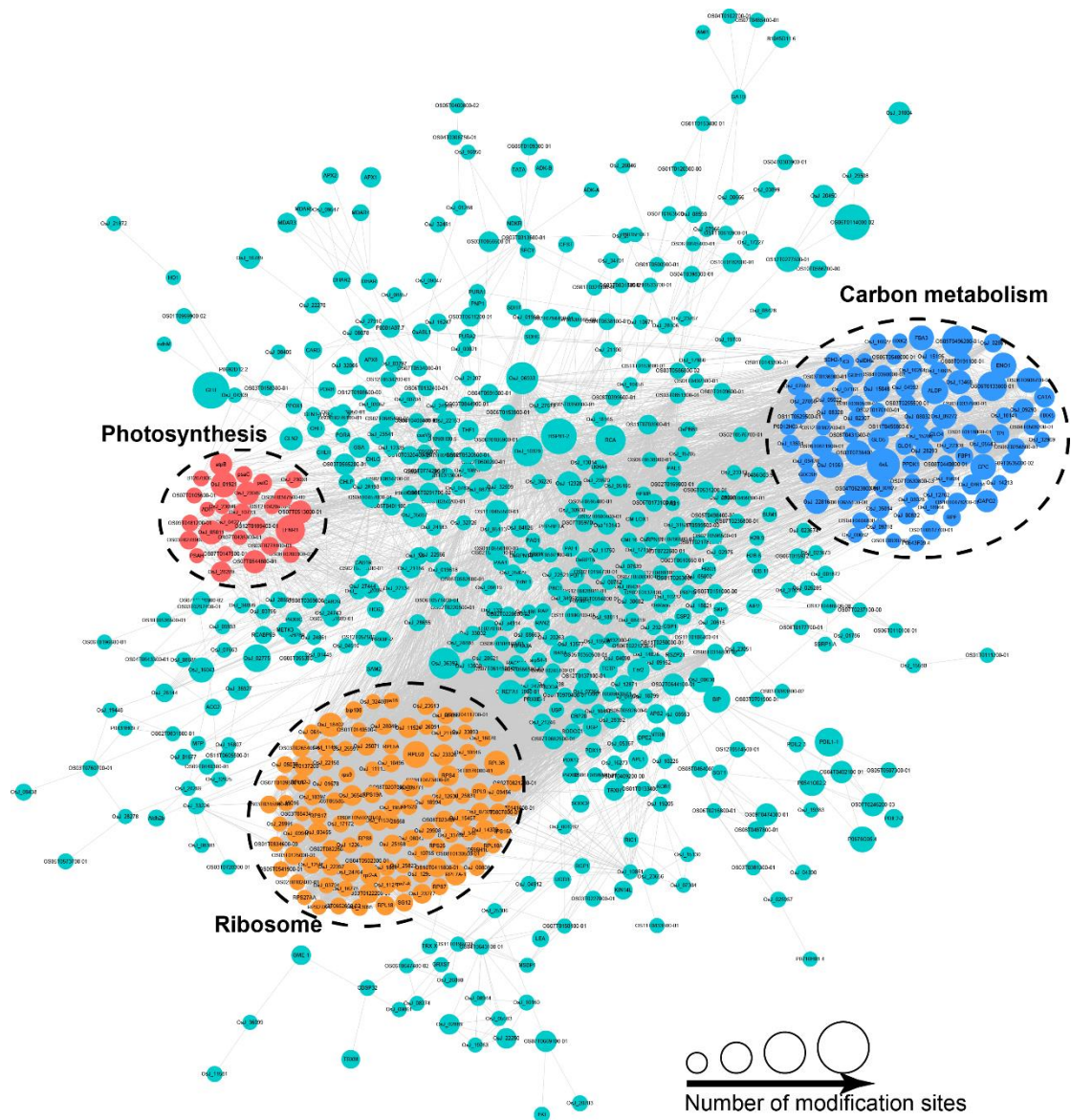


Figure S6. PPI network of all identified Khib proteins. The network of Khib protein interactions (listed with protein ID names) as analyzed using Cytoscape. The size of the dots represents the number of Khib sites.