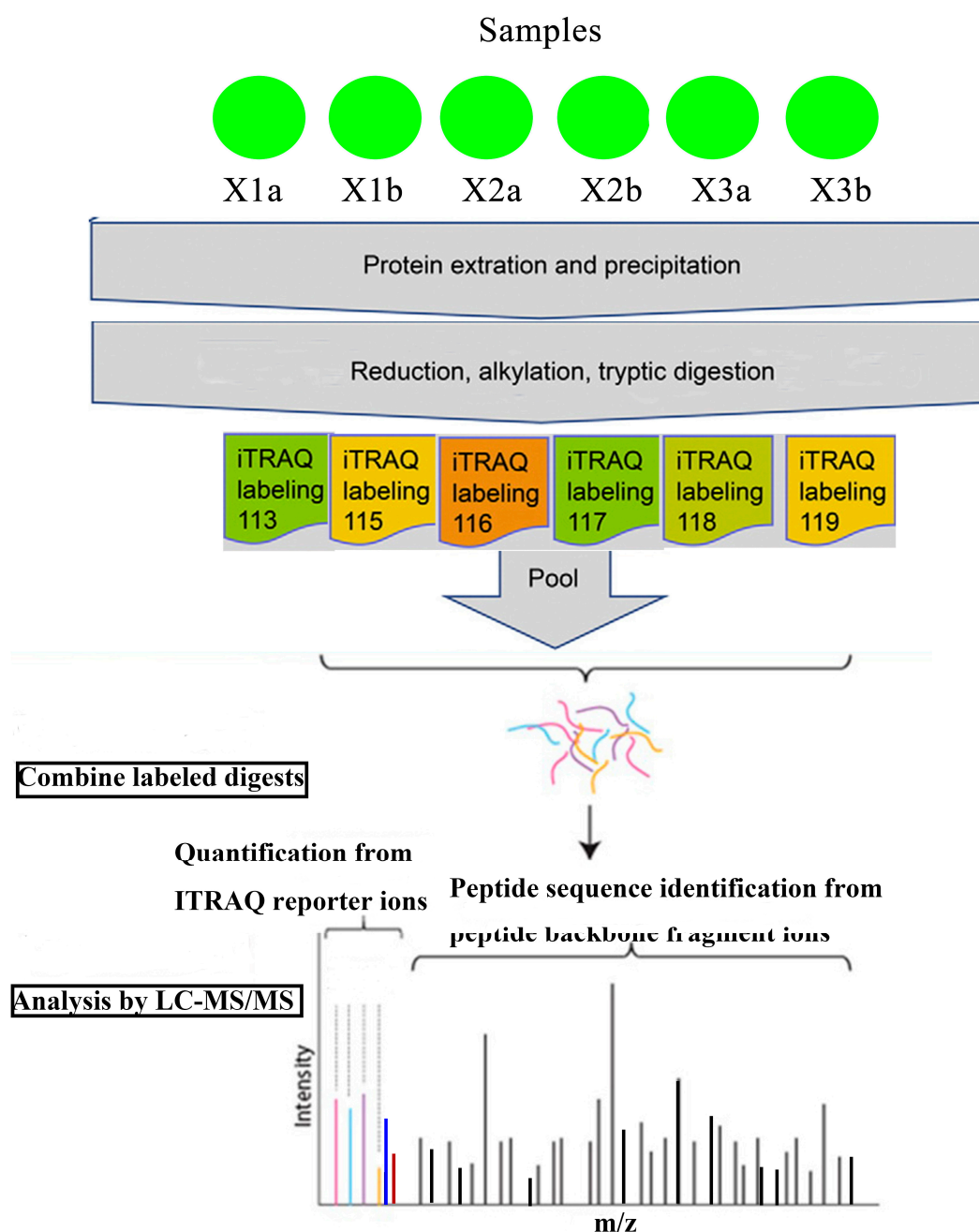
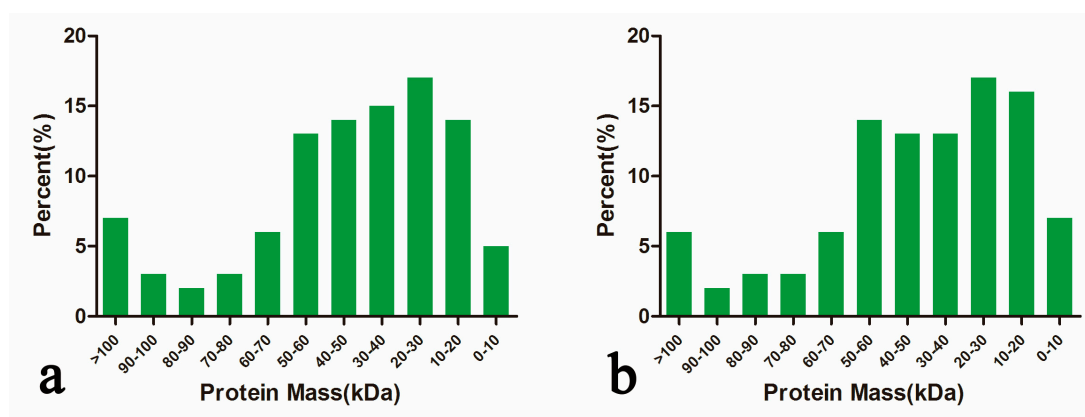


# Supplementary Materials: Isobaric Tags for Relative and Absolute Quantitation (iTRAQ)-Based Comparative Proteome Analysis of the Response of Ramie under Drought Stress

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**Figure S1.** A flow chart of the iTRAQ experiment for quantitative proteome analysis [1]. X means leaves or roots of ramie. X1 means L1 or R1; X2 means L2 or R2; X3 means L3 or R3; a and b represent two repeats, respectively.



**Figure S2.** Protein mass distribution in ramie **a** in leaves; **b** in roots.

**Table S1.** Details for 44 important functional groups.

**Table S2.** All leaf proteins and root proteins were classified into 22 COG subcategories and 21 subcategories, respectively.

**Table S3.** Details for hierarchical display of data from differentially expressed protein of leaves under drought stress.

**Table S4.** Details for hierarchical display of data from differentially expressed protein of roots under drought stress.

**Table S5.** Differentially expressed proteins of leaves and roots under drought stress.

**Table S6.** Alternative bioenergetic pathways in stressed organisms.

**Table S7.** qPCR data values for Figure 9 and 10.

## References

- 1 Wang, Z.Q.; Xu, X.Y.; Gong, Q.Q.; Xie, C.; Fan, W.; Yang, J.L.; Lin, Q.S.; Zheng, S.J. Root proteome of rice studied by iTRAQ provides integrated insight into aluminum stress tolerance mechanisms in plants. *J. Proteom.* **2014**, *98*, 189–205.