

Fig. S1 Mapman analysis of DEMRNAs in leaves (a, b, c, d) and roots (e, f, g, h) under salt stress. DEMRNAs mapping to Regulation_overview in leaves (a) and roots (e); DEMRNAs mapping to Cellular_response_overview in leaves (b) and roots (f); DEMRNAs mapping to Large_enzyme_families in leaves (c) and roots (g); DEMRNAs mapping to transcription in leaves (d) and roots (h). Each square represents a DEMRNA mapping to a specific metabolic pathway, with red being up-regulated and blue being down-regulated.

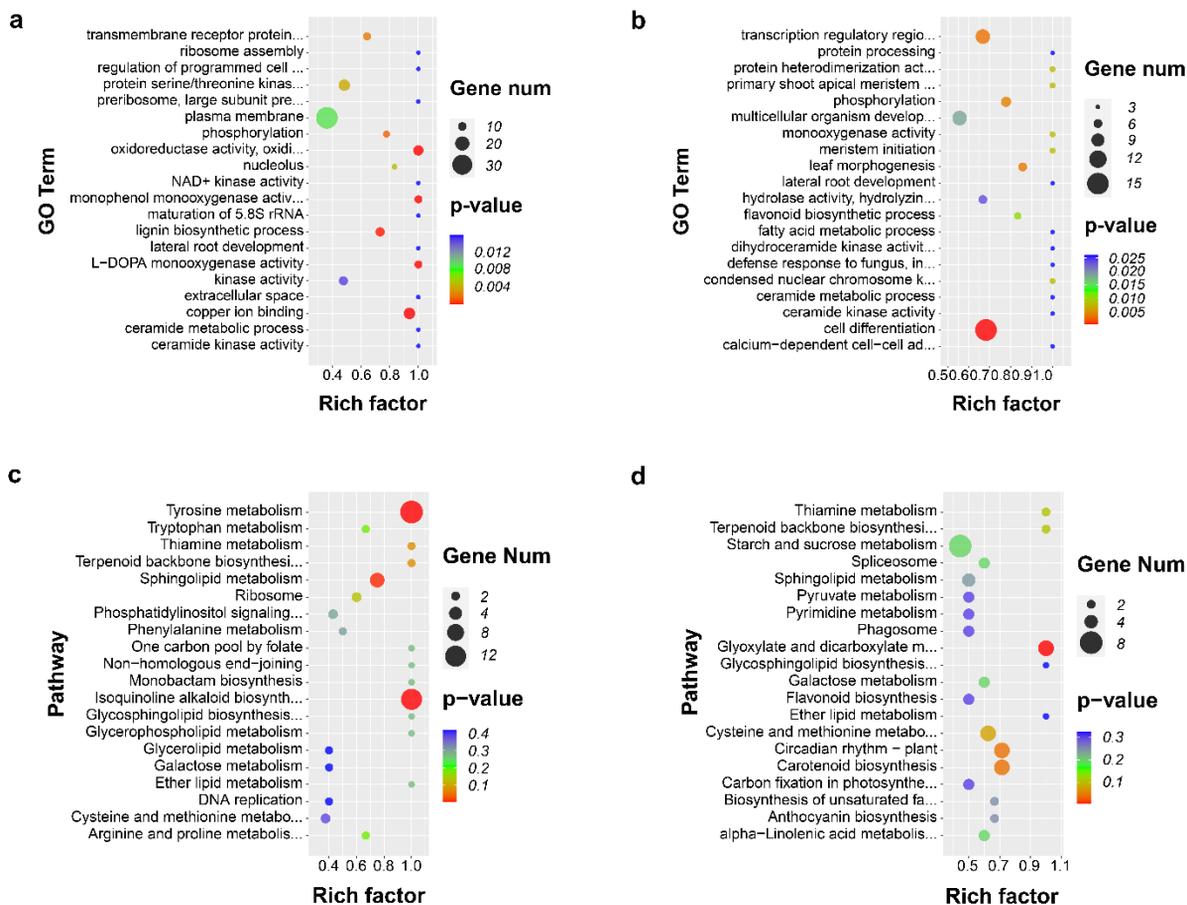


Fig. S2. GO and KEGG enrichment analysis of DEmRNAs targets. (a) GO enrichment analysis of targets of DEMiRNAs in leaves; (b) GO enrichment analysis of targets of DEMiRNAs in roots; (c) KEGG enrichment analysis of targets of DEMiRNAs in leaves; (d) KEGG enrichment analysis of targets of DEMiRNAs in roots.

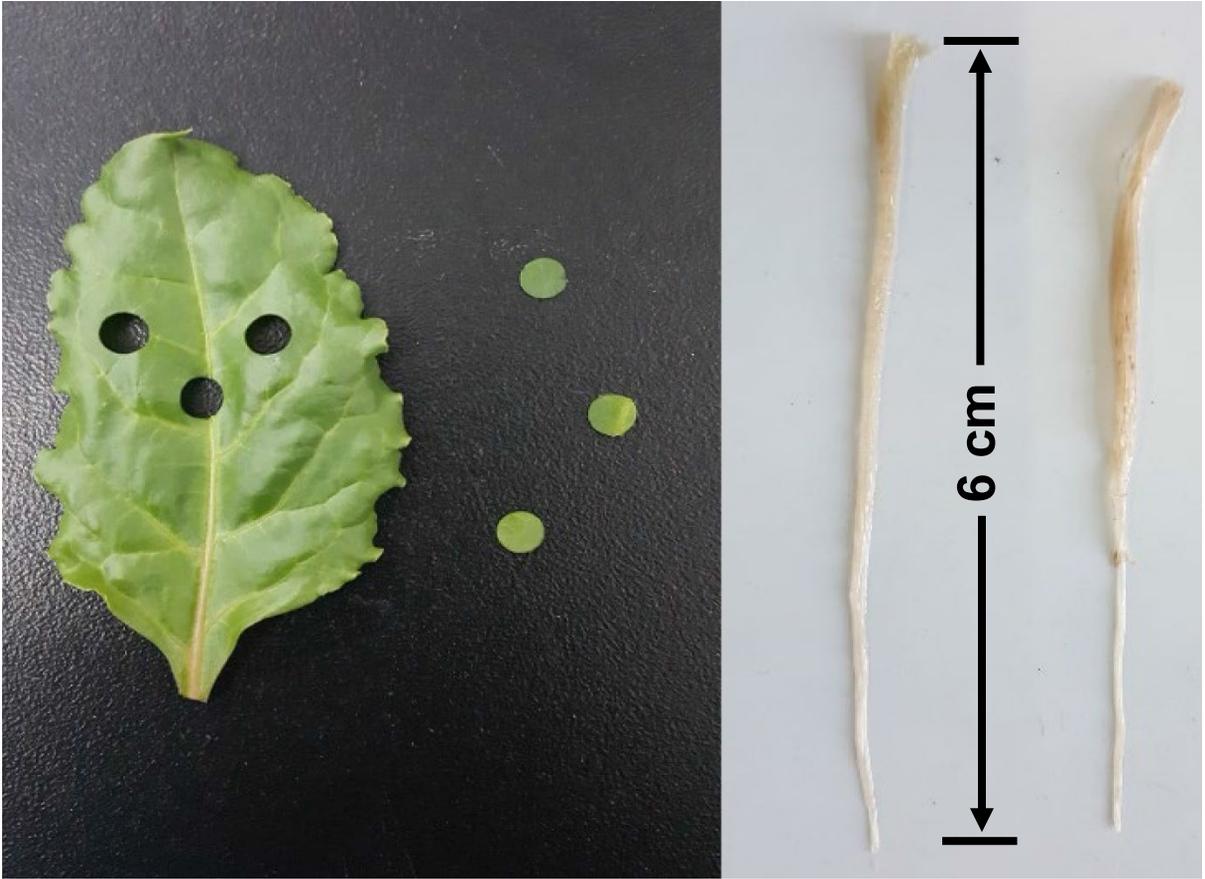


Fig. S3. Sampling location. Left: the third-pair of euphylla from six plants were taken and mixed for leaf sequencing. Right: a length of 6 cm from the root tip was collected from six plant samples and mixed for root sequencing.