

Supplementary Figure S1. The red root and white root from the same *S.miltiorrhiza* plant after grown for 2 months. The liquid in the sample bottle was the extract from the root of *S.miltiorrhiza*, which has grown for 6 months.

Supplementary Figure S2. Expression of lncRNAs (Right) and miRNAs (Left) in phloem and epidermis of red roots (RZP, black) and white roots (WZP, white) of a *S. miltiorrhiza* plants. Expression levels were quantified by qRT-PCR. The level of transcripts in RZP was arbitrarily set to 1, and the level in WZP was given relative to this. *SmActin* was used as the internal control gene, and three biological replicates were used.

Supplementary Table S1. Summary of known and predicted miRNA in this study.

Supplementary Table S2. Expression profiles of DEGs and DE-ncRNAs in different tissues.

Supplementary Table S3. Functional annotation of target genes of DEGs and DE-ncRNAs.

Supplementary Table S4. Go enrichment analysis of targets of differentially expressed ncRNAs.

Supplementary Table S5. KEGG analysis of targets of differentially expressed ncRNAs.

Supplementary Table S6. ncRNAs that may regulate key enzyme genes of tanshinone biosynthesis and metabolism pathway.