

Description of Additional Supplementary Files

File name: Supplementary Data 1

Description: Chinese yew seed gene sequence at transcripts level.

File name: Supplementary Data 2

Description: Transcripts annotation of dormancy seed.

File name: Supplementary Data 3

Description: Transcripts annotation of germinating seed.

File name: Supplementary Data 4

Description: Transcription factors prediction.

File name: Supplementary Data 5

Description: Gene expression at transcripts level (FPKM).

File name: Supplementary Data 6

Description: Differentially expressed genes (transcripts level) between dormant and germinating seed.

File name: Supplementary Data 7

Description: GO analysis of DEGs (at transcripts level).

File name: Supplementary Data 8

Description: Peptides detected in Chinese-yew seed.

File name: Supplementary Data 9

Description: Quantitative proteome dataset of Chinese-yew seed.

File name: Supplementary Data 10

Description: Differentially expressed genes (protein level) between dormant and germinating seed.

File name: Supplementary Data 11

Description: Domain and subcellular localization and KEGG pathway analysis of DEGs (at proteins level).

File name: Supplementary Data 12

Description: List of genes expressed both at transcripts and proteins level.

File name: Supplementary Data 13

Description: Ion signal detected by LC-MS.

File name: Supplementary Data 14

Description: Statistical analysis result for LC-MS.

File name: Supplementary Data 15

Description: Metabolites identification of LC-MS.

File name: Supplementary Data 16

Description: KEGG pathway analysis of differentially expressed metabolites.

File name: Supplementary Data 17

Description: Ion signal detected and identification result for MALDI-MS.

File name: Supplementary Data 18

Description: Primes of mRNA used for qRT-PCR analysis.