**Figure S1:** (**A**) Principal component analysis (PCA) and (**B**) orthogonal partial least squares discriminate analysis (OPLS-DA) score plots of metabolic profiles in wild and cultivated *T. cuspidata*.

**Figure S2:** Transcriptome PCA analysis and differential gene analysis between wild and cultivated samples of *T. cuspidata*. (**A**) PCA analysis of the differential Transcriptome identified from wild and cultivated samples. (**B**) Significant up- regulated versus significant down-regulated DEGs in the comparisons. (**C**) Volcano plot of DEGs for C vs W.

**Figure S3:** KEGG enrichment analysis of differentially expressed genes. (**A**) Up-regulated. (**B**) Down-regulated.