



Figure S1. Phylogenetic relationships of IPT gene family from several species. Phylogenetic relationships of *IPT* gene family from several species. Trees were constructed using the NJ method by the MEGA program. The phylogenetic tree of *IPT* gene family contained two kinds of bacteria *Agrobacterium tumefaciens* (IPTZ AGRT5, IPTZ AGRT7, MIAA.RHIRD, and IPT RHIAD) and *Dictyostelium discoideum* (IPT DICDI, MIAA DICDIb, MIAA DICDIc1, and MIAA DICDIc2); two kinds of algae *Volvox carteri* (alVctIPT I) and *Micromonas pusilla* (alMptIPT I and alMptIPT P); *Physcomitrella patens* (PpIPT1-6); two kinds of monocots *Zea mays* (5 ZmIPT genes) and *Oryza sativa* (OsIPT1-10); five kinds of dicots *Arabidopsis thaliana* (AtIPT1-9), *Brassica rapa* (13 BrIPT genes), *Populus trichocarpa* (9 PtIPT genes), *Solanum lycopersicum* (SlIPT1-6) and *Camellia sinensis* (13 CsIPT genes). The *IPT* genes were divided into four groups indicated by differently colored dots. CsIPT genes were highlighted by brown rectangles.



Figure S2. The multiple sequence alignment of tea plant *CsIPT* sequences with *Arabidopsis AtIPTs*.