

Supplementary Table

Table S1 Information of *PtrAAAP* genes.

Table S2. Collinearity relationship of AAAP genes among *A. thaliana*, *P. trichocarpa*, and *O. sativa*.

Table S3. Quantitative trait locus (QTL) information for the investigated traits in the F1 population of *PtrAAAPs*.

Table S4. Primer sequences of *PtrAAAPs* for qPCR analysis and vector construction.

Supplementary Figure

Figure S1. Statistics of cis-acting elements of *PsAAAPs*, the cis-acting elements in the 2000 bp region upstream of *PtrAAAPs* are divided into 3 groups according to their function, the number of each cis-acting element of *PtrAAAPs* was marked in figure.

Figure S2. Stem phenotype of transgenic lines treated with amino acids.

Figure S3. Correlation analysis of *AAAP21* expression and amino acid content of hybrid parents. X_ represents xylem and p_ represents phloem. (* $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$).

Figure S4. Yeast two-hybrid assay.

Figure S5. Subcellular localization of *PsAAAP21*. OsART1 and HDEL are markers of the nucleus and endoplasmic reticulum, respectively.