

Fig. S1.

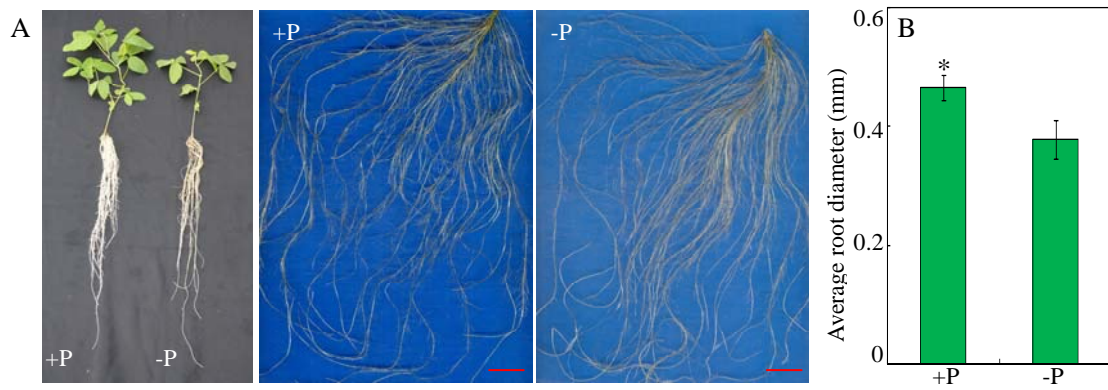


Figure S1. Phenotype and average root diameter of soybean subjected to P sufficient and deficient conditions. (A) Phenotype of soybean plants under +P (250  $\mu\text{M}$   $\text{KH}_2\text{PO}_4$ ) and -P (5  $\mu\text{M}$   $\text{KH}_2\text{PO}_4$ ) conditions. Scale bars: 2 cm; (B) Average root diameter under +P and -P conditions. Data represents the means of four replicates with standard error. Asterisks indicate significant differences between two P treatments. \*:  $P < 0.05$ .

Fig. S2.

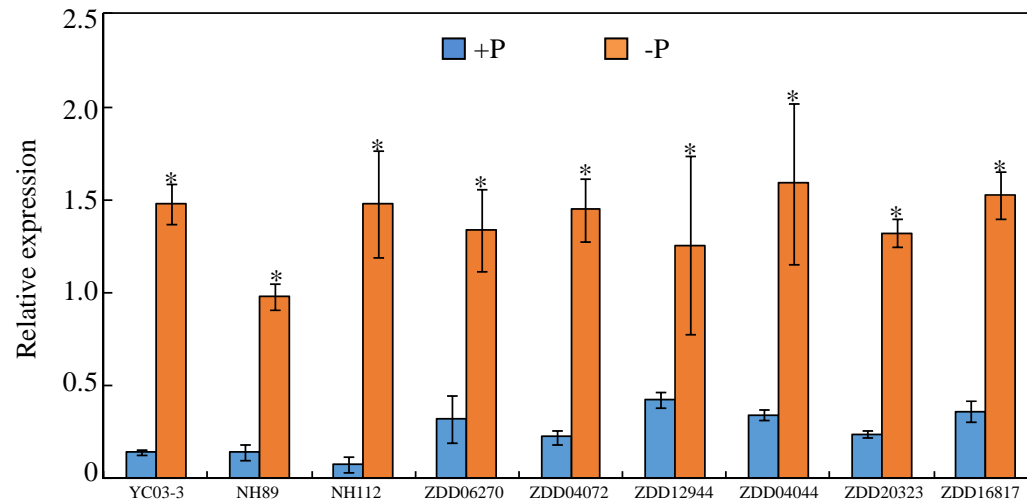


Figure S2. Expression patterns of *GmPAP1-like* in response to Pi starvation among different soybean genotypes. After germination, the uniform seedlings of nine soybean genotypes were subjected to +P (250  $\mu\text{M}$   $\text{KH}_2\text{PO}_4$ ) and -P (5  $\mu\text{M}$   $\text{KH}_2\text{PO}_4$ ) treatments for 10 days. qRT-PCR was conducted to analyze *GmPAP1-like* expression in soybean roots. Data represent the means of four replicates with standard error. Asterisks indicate significant differences between two P treatments. \*:  $P < 0.05$ .

Fig. S3.

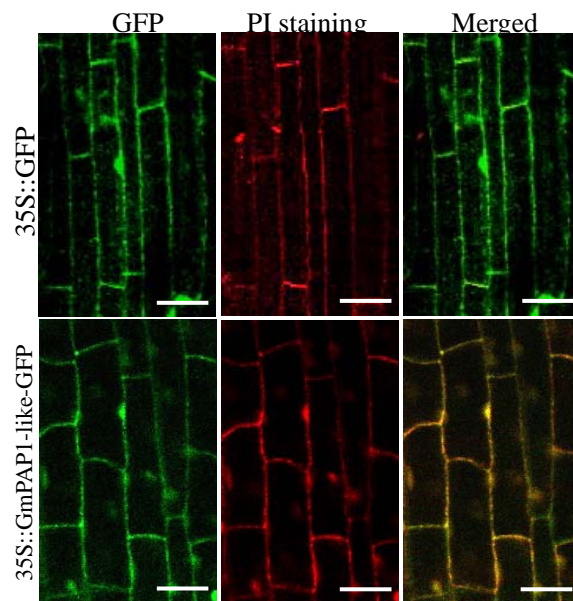


Figure S3. Subcellular localization of GmPAP1-like in transgenic bean hairy roots overexpressing *GmPAP1-like*. Bean hairy roots expressing *35S::GFP* (upper layer) and *35S::GmPAP1-like-GFP* (lower layer) were observed by confocal laser scanning microscopy. Red fluorescence derived from propidium iodide (PI) staining was used to indicate cell walls. Scale bars: 20  $\mu\text{m}$ .

Fig. S4.

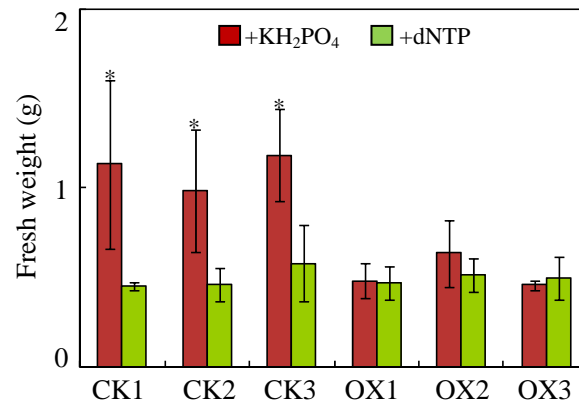


Figure S4. Growth of transgenic bean hairy roots was affected by *GmPAP1-like* overexpression. Data represent the means of four replicates with standard error. Asterisks indicate significant differences between the two P treatments. \*:  $P < 0.05$ .