SUPPLEMENTARY DATA

Table S1 Primer sequences used for quantitative real-time PCR.

Gene	Forward primer (5’-3’)	Reverse primer (5’-3’)
GmSPX1-RT	CCAAACGAGGAAGCAACACAATG	TTCTGGATGAACGGCAAACGC
GmSPX2-RT	TTGATTCAAACGCGGAGT	AAGACCAGTCGTTGGTG
GmSPX3-RT	ACTATAGTGCCCTTAACTACATAGG	AAGCATCACATCCCTCCTCA
GmSPX4-RT	GCTTAACCACTTCCTTCGCCT	CACTAATTGAAGGCCAGTCATTGTT
GmSPX5-RT	GCAGACGCTGCCTGATTGGCG	TGAATTCACAGCTTCTACAACTCTG
GmSPX6-RT	TCAATCACTACCGCCATCACT	ACTAGTCCTGCAAAGTTTAATGAAC
GmSPX7-RT	GCAAACGCCTCAAGTCCGAC	TCTCTTCACTTGAATCCTTAACTTTG
GmSPX8-RT	CAAGCGCCTCAAGACCGAC	TTCATCATCTCTTCCCGCGA
GmSPX9-RT	CGAAGATGGCCAAGCTCTGC	GAAGGGCTGGTTCACCACAGA
GmPT2-RT	GACATAGCGCGAAATCTGTC	CAAACACGGCCGCAATGAAG
GmPT7-RT	TGACCACAAGTACGATCTTCC	CGCCAATAGTAGGTAAGAGCA
GmHAD1-6-RT	GTGACAACTGGGTCGTCGATGAT	CAGGTATAACTCTGGGGTGCAAG
GmALMT1-RT	GAGCACTTACTCGGGAATGTG	GGACTTTGGCAGTTG ATGGG
GmPAP21-RT	GCTGATGGTGTTTGGATTG	TGTTGGGTGTCAAAGTTGAG
GmIPS1-RT	TGATAGTACCGGATTATCAAGG	CTGATAGGCATAGTTTGCAG
GmRNS1-RT	CATCTGGGATTTCTGATCTCAC	TTGTAAGAGCTTGGAGGAGG
TefS1-RT	TGCAAAGGAGGCTGCTAACT	TGCAAAGGAGGCTGCTAACT

Table S2 Primer sequences used for transient expression and *GmSPX3* over-expression.

Gene	Forward primer (5’-3’)	Reverse primer (5’-3’)
GmSPX1-GFP	TCTAGAGATGAAGTTTGGGAAGAG	GGATCCCGGACAATAGGAACTGCAGC
GmSPX2-GFP	TCTAGAGATGAAGTTCTGGAAGATC	GGATCCCGGTTATGCAAAGGAGGC
GmSPX3-GFP	TCTAGAGATGAAATTCGGAAAGAG	GGATCCCGCTTGGCTGTTTGTTCC
GmSPX4-GFP	TCTAGAGATGAAGTTCTGGAAGATC	GGATCCCGGTTATGCAAAGGAGGCA
GmSPX5-GFP	TCTAGAGATGAAGTTTGAGAAGATCC	GGATCCCGGTTGTGTGGAGAAGATGG
GmSPX6-GFP	GGTACCGATGAAATTTGGGAAAGAG	GGATCCCGCACAGAATCAGTTTCCT
GmSPX7-GFP	TCTAGAGATGAAATTCGGAAAGAGC	GGATCCCGCTTGGCTGTTTGTTCC
GmSPX8-GFP	TCTAGAGATGAAATTCGGGAAGAG	GGATCCCGCTTGGCTGCTTGTTCC
GmSPX9-GFP	TCTAGAGATGAAGTTTGACAAGAT	GGATCCCGGGTTGCTTTCTCTAG
GmSPX3-OX	TCTAGAATGAAGTTTGGGAAGAG	TCTAGATTACTTGGCTGTTTGTTCC

Fig. S1. Multiple alignment of the GmSPX family members in soybean. The alignment was created by the ClustalX program. Black lines indicate three sub domains of the SPX domain.

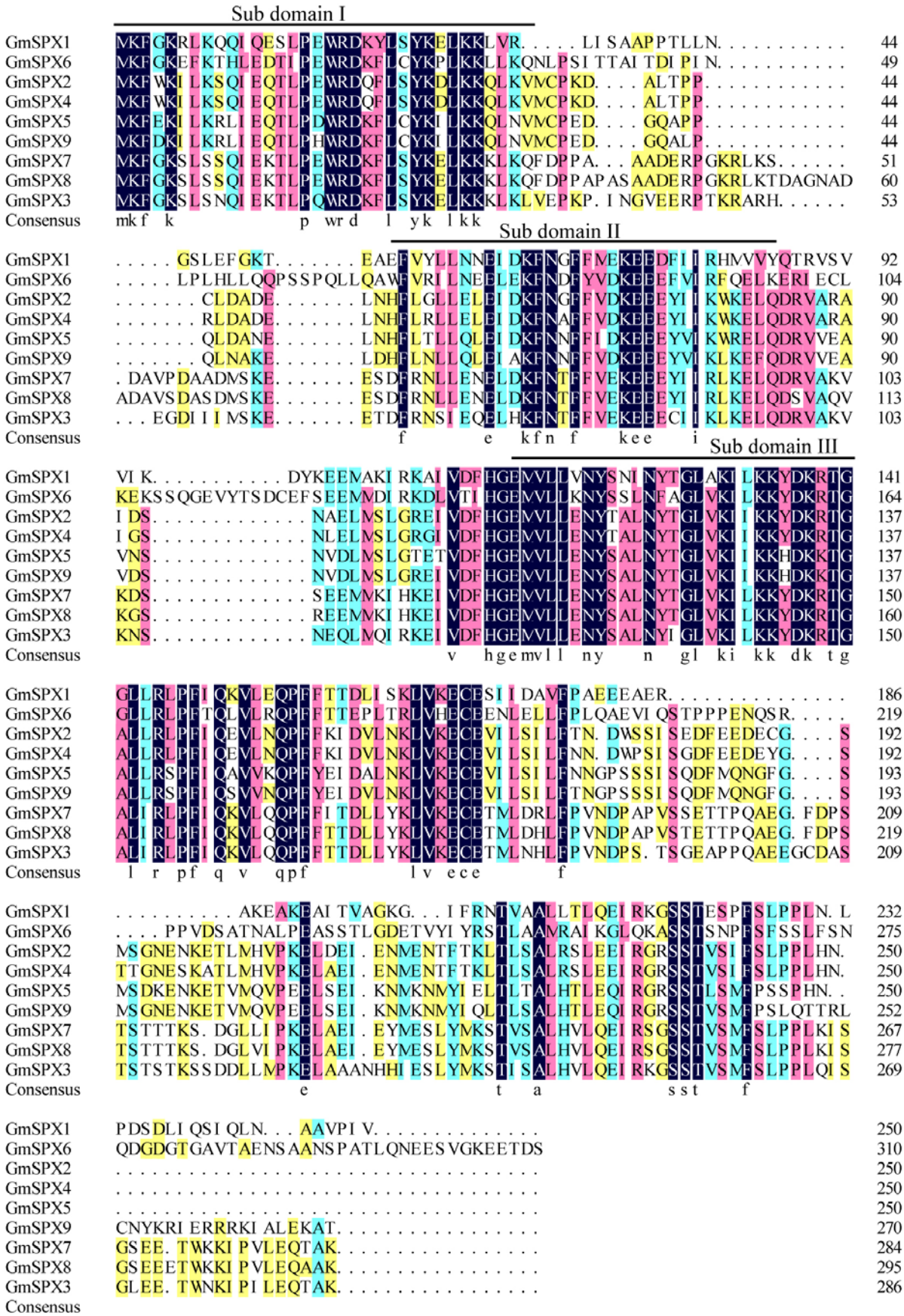

Fig. S2. Expression of *GmSPX3* in transgenic soybean hairy roots. Soybean composite plants were grown in nutrient solution containing 500 μM (+P) phosphorus for 21 d. Transcripts of *GmSPX3* in hairy roots were determined by qPCR analysis. CK represents soybean hairy roots transformed with the empty vector; OX means transgenic soybean hairy roots with overexpressing *GmSPX3*. Each bar is the mean of four replicates with standard error. Asterisks indicate significant differences in *GmSPX3* expression between OX and CK. ***, $P < 0.001$.