

Supplementary file

A

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B

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MV
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Figure S1. The nucleotide sequence of *Erianthus arundinaceus* Phosphate transporter 1;2 (EaPHT1;2). (A) The full-length CDS sequence of the EaPHT1;2 gene; (B) The ExPasy-translated protein sequence of the EaPHT1;2.

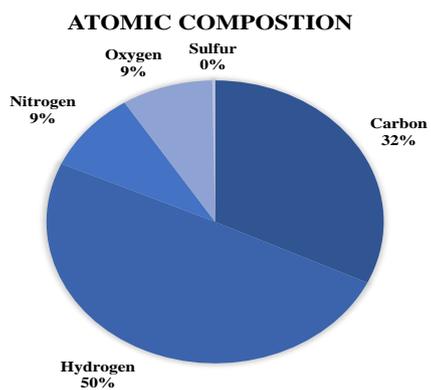
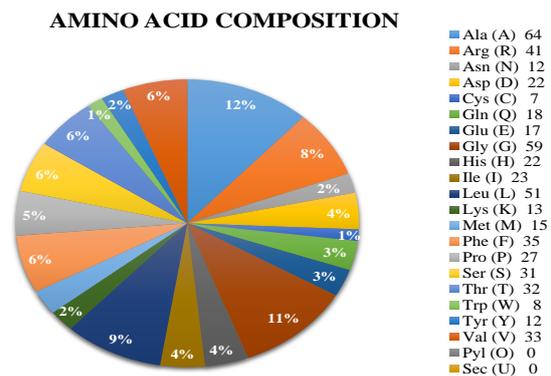
A**B**

Figure S2: Physicochemical parameters of the selected protein: (A) Atomic composition of EaPHT1;2 protein, (B) Amino acid composition of EaPHT1;2 protein

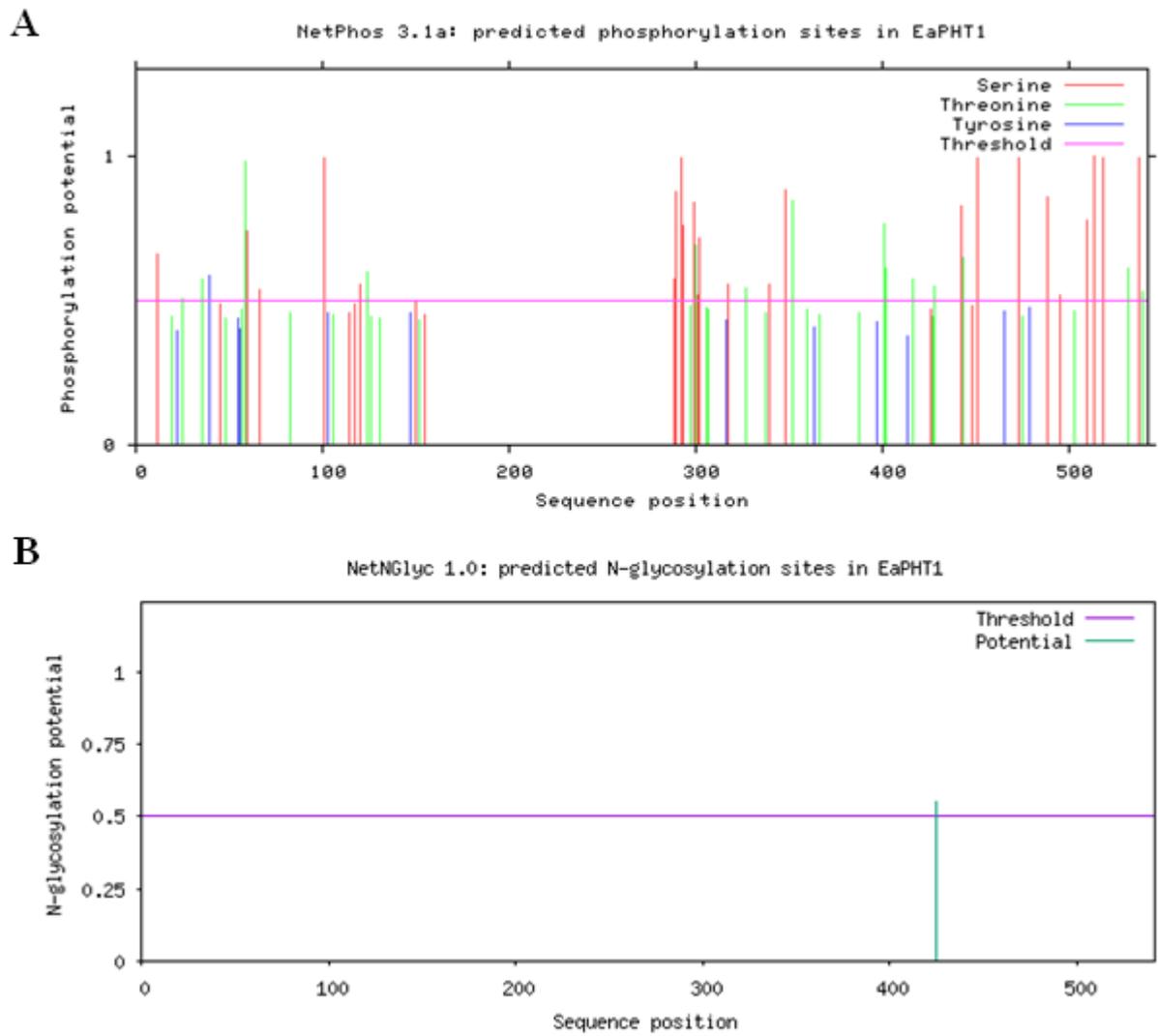


Figure S3: Post-translation modification sites of EaPHT1. (A) Phosphorylation sites. (B) Glycosylation site. The amino acids are represented in different lines at their position in the sequence and the scores higher than the threshold value are considered for posttranslational modification.

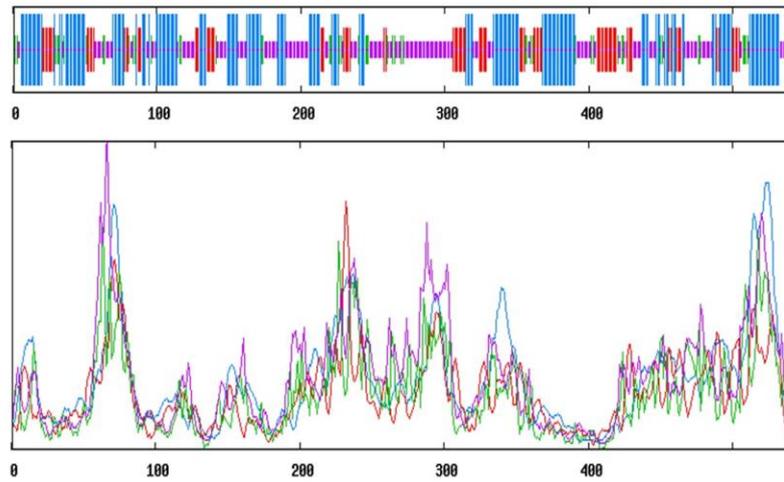
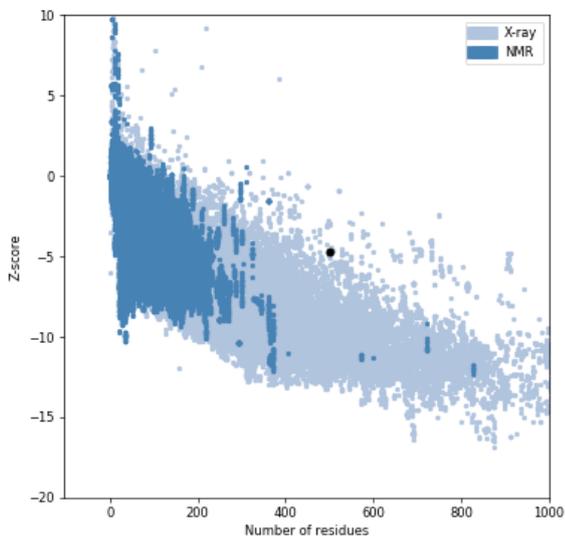
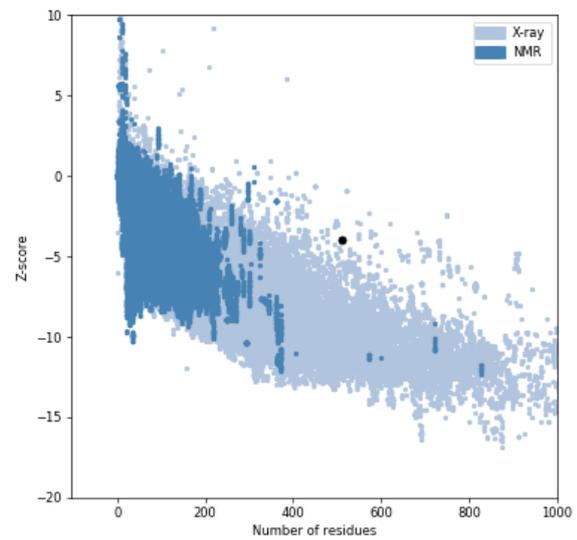
A**B****C**

Figure S4: Protein structure prediction and evaluation. (A) Secondary elements in the EaPHT1 protein predicted using the SOPMA tool. (B) Structural evaluation of EaPHT1;2 obtained through Phyre2 model; (B) EaPHT1;2 obtained through Swiss-Modelling.

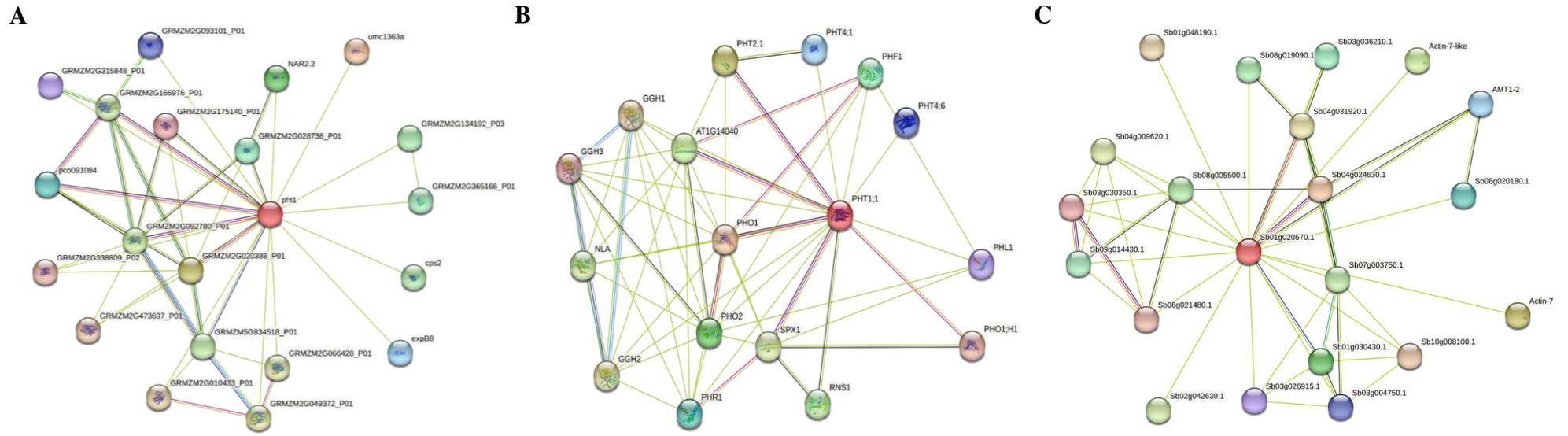


Figure S5: Protein-protein Interaction analysis of EaPHT1;2 protein. (A) PPI of EaPHT1;2 with ZmPHT1 protein. (B) PPI of EaPHT1;2 with AtPHT protein. (C) PPI of EaPHT1;2 with SbPHT protein.

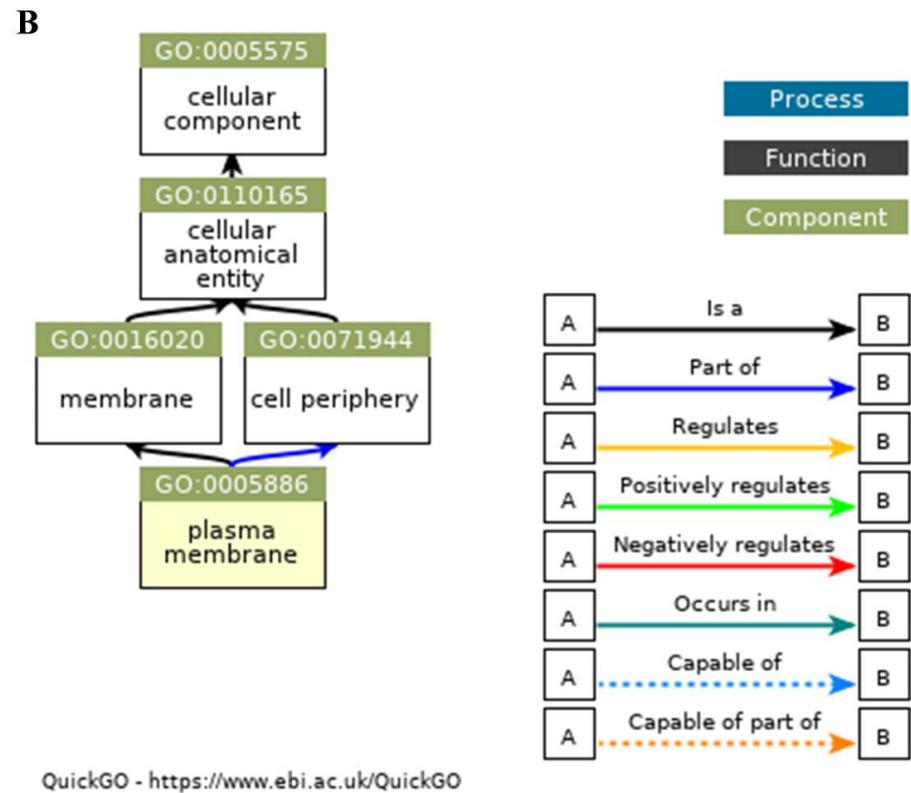
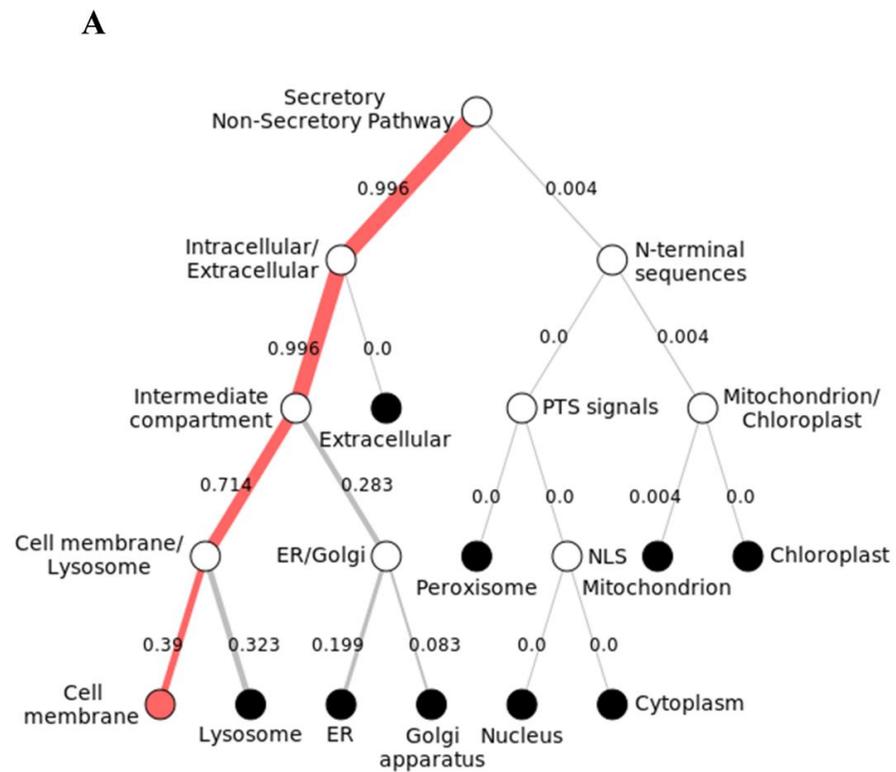
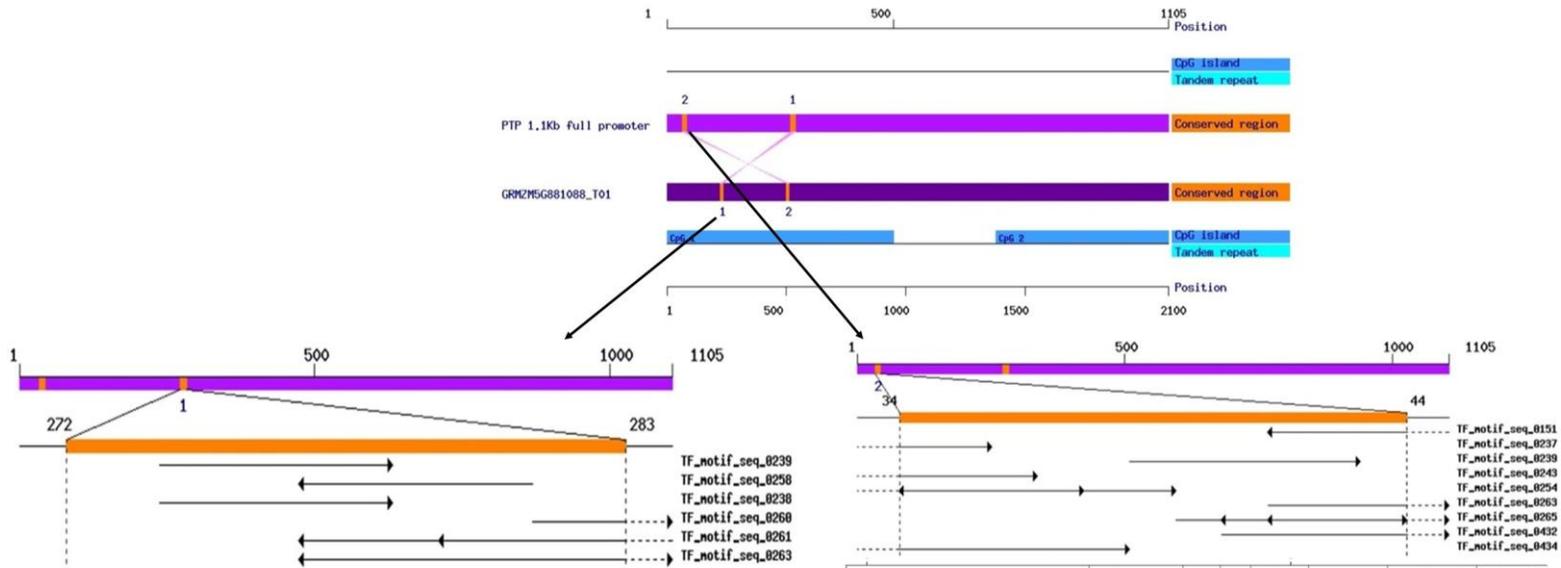


Figure S6: Subcellular Localization analysis (A) EapHT1;2 protein localization using online tools DeepLoc analysis (B) QuickGo Term analysis of EapHT1;2 protein

A



Matrix ID	Tfs/TFBSs	Position	Strand	Similarity score	Hit sequence	Located in Tandem repeat	Located in CpG island
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TF_motif_seq_0258 (/TFBSinfo.php?matrix=TF_motif_seq_0258)	U01377	277	-	0.8	GTCGC	NO	NO
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TF_motif_seq_0260 (/TFBSinfo.php?matrix=TF_motif_seq_0260)	OSE2ROOTNODULE	282	+	1	CTCTT	NO	NO
TF_motif_seq_0261 (/TFBSinfo.php?matrix=TF_motif_seq_0261)	SURECOREATSULTR11	277	-	0.8	GTCGC	NO	NO
TF_motif_seq_0263 (/TFBSinfo.php?matrix=TF_motif_seq_0263)	SORLIP1AT	277	-	0.8	GTCGC	NO	NO
		280	+	0.8	GCCTC	NO	NO

Matrix ID	Tfs/TFBSs	Position	Strand	Similarity score	Hit sequence	Located in Tandem repeat	Located in CpG island
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TF_motif_seq_0239 (/TFBSinfo.php?matrix=TF_motif_seq_0239)	AT1G29160...	39	+	1	AAGGC	NO	NO
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TF_motif_seq_0254 (/TFBSinfo.php?matrix=TF_motif_seq_0254)	AT3G14230	33	+	0.8	ATATA	NO	NO
		34	-	0.8	TATAT	NO	NO
		35	+	0.8	ATATA	NO	NO
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		41	+	0.8	GGCCC	NO	NO
		41	-	1	GGCCC	NO	NO
		42	-	0.8	GGCCC	NO	NO
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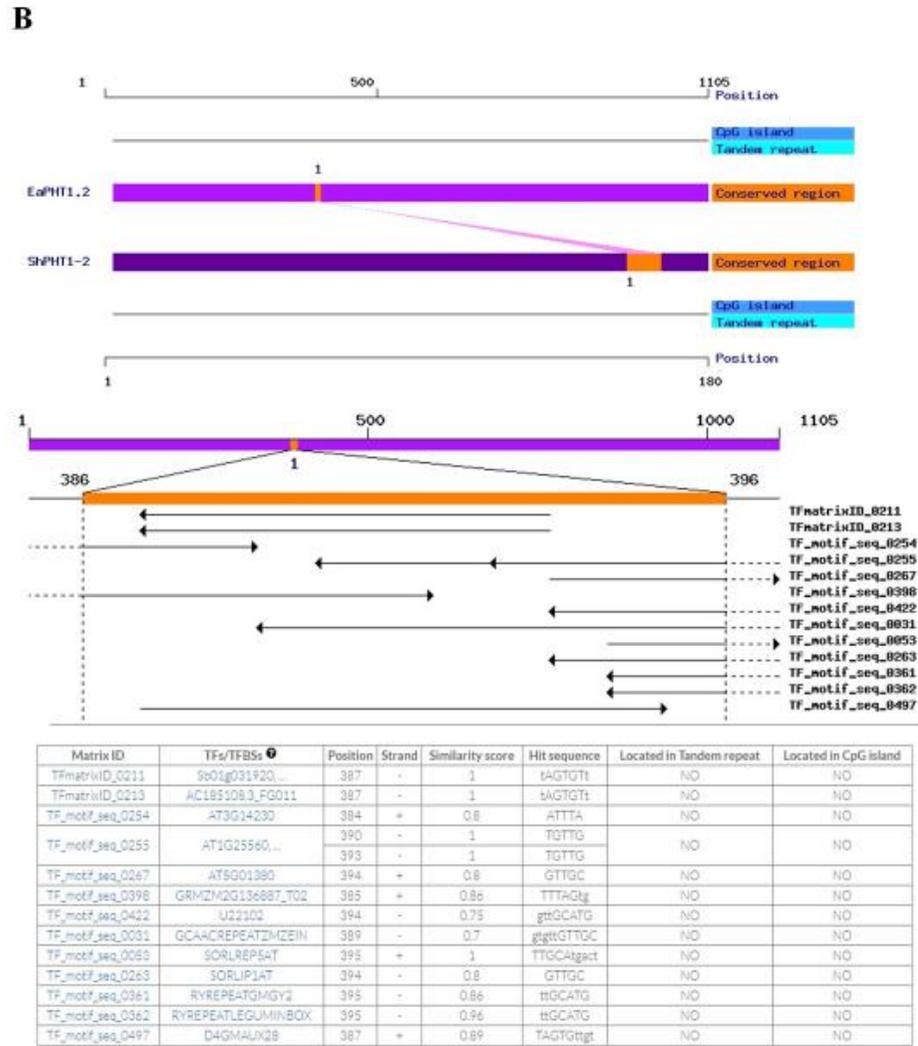


Figure S7: Comparative In-silico analysis of EaPHT1;2 promoter. (A) The EaPHT1;2 promoter conserved regions with ZmPHT1 and (B) One conserved region was ShPHT1;2 promoter regions.

Table S1: List of primer sequences used in this study for EaPHT1-2 gene isolation, promoter isolation, promoter deletion constructs, and analysis.

Primers	Name	Primer sequence
Gene Isolation Primer	GPHT1F	ATGGCGCGCGGGCGGGGACGGCCTGCA
	GPHT1R	CTACACCATCTGGGTCCCCGACGGC
Primary PCR Primer	ASP I	GGATCCTAATACGACTCACTATAGGGC
	pPHT R1	TAGTAGATGCGGCCGAGCAGC
Secondary PCR Primer	ASP II	AATAGGGCTCGAGCGGC
	pPHT R2	CCCATGCCGGCGATGACGATG
Promoter-specific primers	pFL F	CGCAAGCTTAAGGCCCCCTTAGAACGCG
	pFL R	TAAACCATGGGGTCGCTGCACC
GUS-specific Primers	GUS F	GGAATGGTGATTACCGACG
	GUSR	ATACCTGTTCACCGACGACG
Deletion Primers (For all deletion Reverse primer is the same)	EaPHT-pD1 F	CGCAAGCTTAGTGTTGTTGCATGACTG
	EaPHT-pD2 F	CGCAAGCTTAGCATCTCCATCTAACCACCA
	EaPHT-pD3 F	CGCAAGCTTAAGGCCCCCTTAGAACGCG
	EaPHT-pD4 F	CGCAAGCTTAGTGTTGTTGCATGACTG
	EaPHT-pD5 F	CGCAAGCTTAGCATCTCCATCTAACCACCA
	pFL R	TAAACCATGGGGTCGCTGCACC

Table S2: Physicochemical characteristics of the EaPHT1;2 protein

Properties	Value
No. of amino acids	542
Molecular weight	58940.73
Theoretical pI	9.8
No. of negatively charged residues (Asp + Glu)	38
No. of positively charged residues (Arg + Lys)	55
Total number of atoms	8262
Extinction Coefficient (all pairs of Cys residues form cysteines)	62255
Extinction Coefficient (all Cys residues are reduced)	61880
Half-life (in vitro) (h)	30
Instability index (II)	43.1
Aliphatic index	82.71
Grand average of hydropathicity	0.019

Table S3: Subcellular localization of EaPHT1-2 gene in different locations

Localization	Likelihood
Cell membrane	0.3897
Lysosome/Vacuole	0.31
Endoplasmic reticulum	0.2102
Golgi apparatus	0.083
Mitochondrion	0.0063
Peroxisome	0.0005
Plastid	0.0002
Nucleus	0.0001
Extracellular	0
Cytoplasm	0