

Csa6M512870.1	MAFVSQFNQLPCKTLALNPPQPQLTSKPSVFPIASIGATARAAAGKSL
Cucsa.044900.1	MAFVSQFNQLPCKTLALNPPQPQLTSKPSVFPIASIGATARAAAGKSL
	*****.*****
Csa6M512870.1	LNDDEWGEDKDEKYGDDSSVAVAEKEEEKPLEPSEIYKLKKALVDSFYGTDRGLRVSRDT
Cucsa.044900.1	LNDDEWGEDKDEKYGDDSSVAVAEKEEEKPLEPSEIYKLKKALVDSFYGTDRGLRVSRDT

Csa6M512870.1	RAEIVELITQLESKNPTPAPTEALTLLNGKWILAYTTFAGLFPLLSRNPLVKVEEISQT
Cucsa.044900.1	RAEIVELITQLESKNPTPAPTEALTLLNGKWILAYTTFAGLFPLLSRNPLVKVEEISQT

Csa6M512870.1	IDSENLTVQNSVQFSGPLATTSITTNAKFEVRSPLRVHIKFEEGVIGTPQLTDSIVIPDN
Cucsa.044900.1	IDSENLTVQNSVQFSGPLATTSITTNAKFEVRSPLRVHIKFEEGVIGTPQLTDSIVIPDN

Csa6M512870.1	VDFLGQKIDFTPFNGIISLQDTASNVAKTISSQPPIKFSISNTRVESWLLTTYLDEDLR
Cucsa.044900.1	VDFLGQKIDFTPFNGIISLQDTASNVAKTISSQPPIKFSISNTRVESWLLTTYLDEDLR

Csa6M512870.1	ISRGDGGSVFVLLKEGSSFLSL
Cucsa.044900.1	ISRGDGGSVFVLLKEGSSFLSL

Figure S1. Comparison of deduced amino acid sequences of CsaFBN1 (Csa6M512870.1) in var. Chinese long with that (Cucsa.044900.1) in var. Gy14. A different amino acid residue is indicated by red letter. The deduced amino acid sequences were aligned using ClustalW (<http://www.genome.jp/tools/clustalw/>) with default parameters.

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Csa6M108600.1    MAKSLSLPSLPFIFPSSITSHLSHLPKISCSSISFQSQSAKRQLLT LISDQQRGLKTQKN
Cucsa.120630.1    MAKSLSLPSLPFISPSSITTHLSHLPKISCSSISIQSQSAKRQLLT LISDQQRGLKTQKN
                  *****:*****:*****
Csa6M108600.1    PQKLASIVKSIDHLASLGRNSVTDDSLSATWRLWLTTEKEQLFIEKAHLFGTRAGDVL
Cucsa.120630.1    PQKLASIVKSIDHLASLGRNSVTDDSLSATWRLWLTTEKEQLFIEKAHLFGTRAGDVL
                  *****
Csa6M108600.1    QVIDVEKKSLNNVITFPPDGVFFVRSNIEVASSQRVNFRFTSAVLRGKNWEIPLPPFGQG
Cucsa.120630.1    QVIDVEKKSLNNVITFPPDGVFFVRSNIEVASSQRVNFRFTSAVLRGKNWEIPLPPFGQG
                  *****
Csa6M108600.1    WFDTVYLDDEIRVVKDIRGDYLIVERAPYSWTE
Cucsa.120630.1    WFDTVYLDDEIRVVKDIRGDYLIVERAPYSWTE
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Figure S2. Comparison of deduced amino acid sequences of CsaFBN9 (Csa6M108600.1) in var. Chinese long with that (Cucsa.120630.1) in var. Gyl4. Three different amino acid residues are indicated by red letters. The deduced amino acid sequences were aligned using ClustalW (<http://www.genome.jp/tools/clustalw/>) with default parameters.

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AtSPS1.pro MA-TSCRNIDLGTAAG---CGCG---RR-QPESLRKTVCKETSSNRSYGGLV---GSCSAVPEKSKEDISLINGIGQSQTVS 71
AtSPS2.pro MA-TSCRNIDLGTSVLD---HSCSSSTSRRTFGNSSKTVCMI-GGRSCVGNLVFLERDLATCRVAPAKSKENSLINGIGQOTVM 82
CsaSPS1.pro MS-VHCQSLEDEGSHVLDYA-CGCSSTPFLDPHTVRSYVRLSTKGRKRHQARTLICSQRKNG-CRWFTST-TKEETVLNCTINGGPQPF 85
OsaSPS2.pro MLSVSCPRVYMSFNG-LDFGQLASCRCRWAGRS-----GQVAFRRRFGCNCFTASPSQPGLAADVPAEAS 67

AtSPS1.pro FDLK-QESKQPISLVTLFPIVADLQSLNINLLSIVGAENPVLSAADQIFGAGGKMRPGLVFLVSRATAELAGLKELTVEHRRLA 158
AtSPS2.pro LALR-QESRPISLETDFEVWADDLQSLNINLLSIVGAENPVLSAADQIFGAGGKMRPGLVFLVSRATAELAGLKELTVEHRRLA 169
CsaSPS1.pro LDRKEESRPISSTSLFEVWADDLQSLNINLLSIVGLENELVSAALDFGAGGKMRPGLVFLVSRATAELAGLKELTVEHRRLA 173
OsaSPS2.pro SARTTMIPEFTSVSLLEVVSDDLKLNINLLSIVGAENPVLSAADQIFGAGGKMRPGLVFLVSRATAELAGLKELTVEHRRLA 155

AtSPS1.pro IIEMIHTASLIHDDVLDSDMRGKETVHELPGTRVAVLAGDFMFAQASWYLANLENLEVIKLSQVIKDFASGEIKQASSLFDCE 246
AtSPS2.pro IIEMIHTASLIHDDVLDSDMRGKETVHELPGTRVAVLAGDFMFAQASWYLANLENLEVIKLSQVIKDFASGEIKQASSLFDCE 257
CsaSPS1.pro IIEMIHTASLIHDDVLDSDMRGKETVHELPGTRVAVLAGDFMFAQASWYLANLENLEVIKLSQVIKDFASGEIKQASSLFDCE 261
OsaSPS2.pro IIEMIHTASLIHDDVLDSDMRGKETVHELPGTRVAVLAGDFMFAQASWYLANLENLEVIKLSQVIKDFASGEIKQASSLFDCE 243

AtSPS1.pro LDEYLLKSYKTSASLVAASTKGAAIFSRVESVDVTEQMYEFGKNLGLSPQVDDIILDFTQSTEDLGKPGASDLAKGNLTAPVIFALERE 334
AtSPS2.pro LDDYLLKSYKTSASLVAASTKGAAIFSRVESVDVTEQMYEFGKNLGLSPQVDDIILDFTQSTEDLGKPGASDLAKGNLTAPVIFALERE 345
CsaSPS1.pro LDEYLLKSYKTSASLVAASTKGAAIFSRVESVDVTEQMYEFGKNLGLSPQVDDIILDFTQSTEDLGKPGASDLAKGNLTAPVIFALERE 349
OsaSPS2.pro LDDYLLKSYKTSASLVAASTKGAAIFSRVESVDVTEQMYEFGKNLGLSPQVDDIILDFTQSTEDLGKPGASDLAKGNLTAPVIFALERE 331

AtSPS1.pro PSLREITIESEFSGSLEPAIDVVRNGGKIRAGELAKEDIALNLQCLPSSGFRSALEDMVNLERID 406
AtSPS2.pro PSLREITIESEFSGSLEPAIDVVRNGGKIRAGELAKEDIALNLQCLPSSGFRSALEDMVNLERID 417
CsaSPS1.pro PKLREITIESEFSGSLEPAIDVVRNGGKIRAGELAKEDIALNLQCLPSSGFRSALEDMVNLERID 421
OsaSPS2.pro PKLREITIESEFSGSLEPAIDVVRNGGKIRAGELAKEDIALNLQCLPSSGFRSALEDMVNLERID 403

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Figure S3. Protein sequence alignment among Arabidopsis SPS1, SPS2, cucumber SPS1, and rice SPS2. The deduced amino acid sequences were aligned using ClustalW (<http://www.genome.jp/tools/clustalw/>) with default parameters.

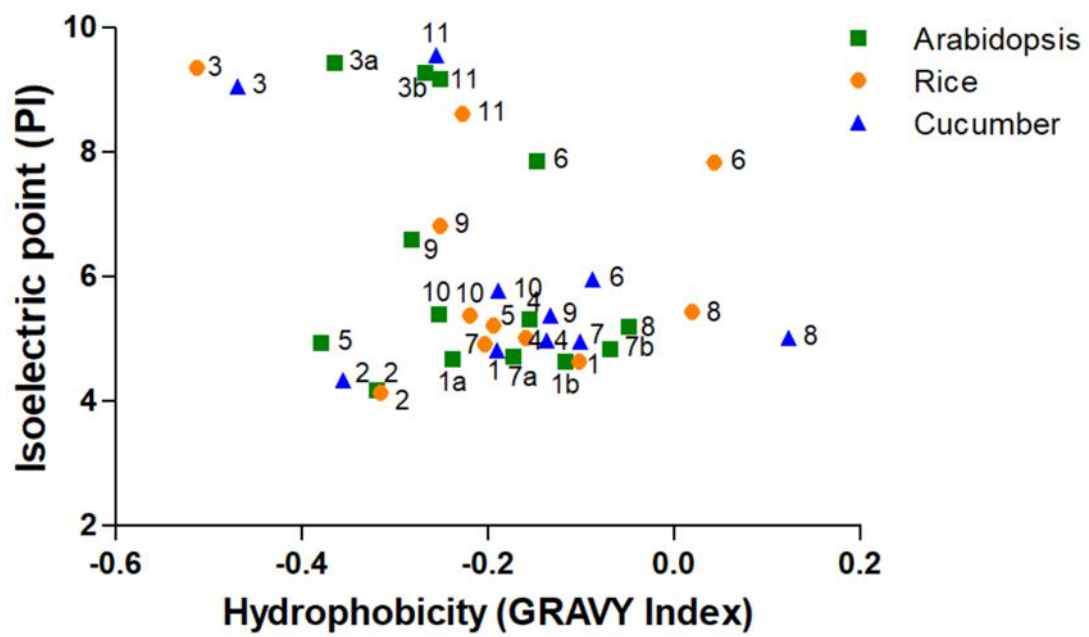


Figure S4. Physicochemical properties of FBN proteins from Arabidopsis, rice and cucumber. PI and hydrophobicity (GRAVY index) were measured for each FBN after removal of the chloroplast transit peptide using the ProtParam tool (ExpPASy).

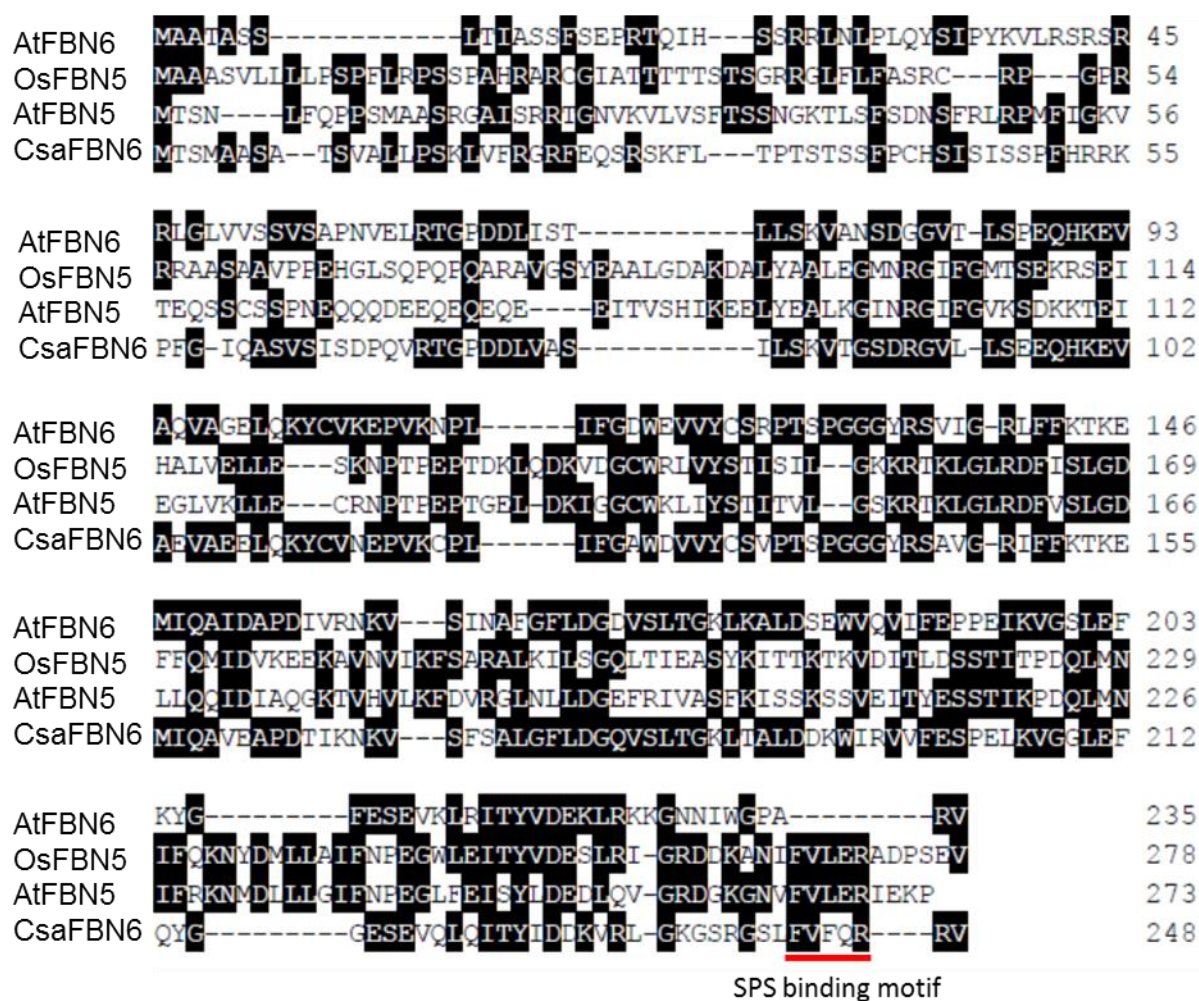


Figure S5. Protein sequence alignment among Arabidopsis FBN6, rice FBN5, Arabidopsis FBN5, and cucumber FBN6. The deduced amino acid sequences were aligned using ClustalW (<http://www.genome.jp/tools/clustalw/>) with default parameters. Possible SPS binding motif was underlined with red color.