

Csa6M512870.1	MAFVSQFNQLPCKTLALNPPQPQLTSKPSVFPIASIGATARAAAGKSLISVRPAFKVRAV
Cucsa.044900.1	MAFVSQFNQLPCKTLALNPPQPQLTSKPSVFPIASIGATARAAAGKSLVSVRPAFKVRAV
	*****:*****
Csa6M512870.1	LNDEWGEDKDEKYGDDSSVAVAEKEEEKPLEPSEIYKLLKALVDSFYGTDRLRVSRDT
Cucsa.044900.1	LNDEWGEDKDEKYGDDSSVAVAEKEEEKPLEPSEIYKLLKALVDSFYGTDRLRVSRDT

Csa6M512870.1	RAEIVELITQLESKNPTPAPTEALTLLNGKWILAYTTFAGLFPLLSRNLPLVKVEEISQT
Cucsa.044900.1	RAEIVELITQLESKNPTPAPTEALTLLNGKWILAYTTFAGLFPLLSRNLPLVKVEEISQT

Csa6M512870.1	IDSENLTQNSVQFSGPLATTSITTNAKFEVRSPLRVHIKFEEGVIGTPQLTDSIVIPDN
Cucsa.044900.1	IDSENLTQNSVQFSGPLATTSITTNAKFEVRSPLRVHIKFEEGVIGTPQLTDSIVIPDN

Csa6M512870.1	VDFLGQKIDFTPFNGIISLQDTASNVAKTISSQPPIKFSISNTRVESWLLTTYLDEDLR
Cucsa.044900.1	VDFLGQKIDFTPFNGIISLQDTASNVAKTISSQPPIKFSISNTRVESWLLTTYLDEDLR

Csa6M512870.1	ISRGDGGSVFVLLKEGSSFLSL
Cucsa.044900.1	ISRGDGGSVFVLLKEGSSFLSL

Supplement Fig. 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.

```

Csa6M108600.1    MAKSLSLPSLPFIFPSSITSHLSHLPKISCSSISFQSQSAKRQLLT LISDQQRGLKTQKN
Cucsa.120630.1    MAKSLSLPSLPFISPSSITTHLSHLPKISCSSISIQSQSAKRQLLT LISDQQRGLKTQKN
                  *****:*****:*****
Csa6M108600.1    PQKLASIVKSIDHLASLGRNSVTDDSLSATWRLLWTTTEKEQLFIEKAHLFGTRAGDVL
Cucsa.120630.1    PQKLASIVKSIDHLASLGRNSVTDDSLSATWRLLWTTTEKEQLFIEKAHLFGTRAGDVL
                  *****
Csa6M108600.1    QVIDVEKKSLNNVITFPPDGVEFFVRSNIEVASSQRVNFRFTSAVLRGKNWEIPLPPFGQG
Cucsa.120630.1    QVIDVEKKSLNNVITFPPDGVEFFVRSNIEVASSQRVNFRFTSAVLRGKNWEIPLPPFGQG
                  *****
Csa6M108600.1    WFDTVYLDDEIRVVKDIRGDYLIVERAPYSWTE
Cucsa.120630.1    WFDTVYLDDEIRVVKDIRGDYLIVERAPYSWTE
                  *****

```

Supplement Fig. 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.

```

AtSPS1.pro MM-TSCRNIDLGIAAG---CCCG---RR-QPESLRKTVCKETSSNRSYGGLV---GSCQAVFPKSKDISLINGIGQSQTVS 71
AtSPS2.pro MM-TSCRNIDLGISVLD---HSCSSSTSTSRFTFGNSSKTVMCI-GGRSCVGNLVFLRRDLATCRVAPAKSKENSLINGIGQSQTVM 82
CsaSPS1.pro MS-VHCQSIDEGSPVLDIYA-CGCSSTIFLDPHIVRSHVRLSTKGRKRHQARTLICSQRKNGCCRVFST-TRGETVLNCTINGGPGQFF 85
OsaSPS2.pro MLSVSCPRVMSFPG-LDFGQLASCRFWAGRS-----GKVAHRRRFGCCTFVASSPSQPGLAADVPAEANS 67

AtSPS1.pro FDLK-QESKCPISLVILFEIVADLQSLNINLLSIVGAENPVLSAADQIFGAGGKRMREPGLVFLVSRATAELAGLKELTVEHRRLE 158
AtSPS2.pro DALR-QESRCPISLETILFEVWADDLQSLNINLLSIVGAENPVLSAADQIFGAGGKRMREPGLVFLVSRATAELAGLKELTVEHRRLE 169
CsaSPS1.pro LDRKEESRSPISSTSLFEVWADDLQSLNINLLSIVGLENELVSAAGIFGAGGKRMREPGLVFLVSRATAELAGLKELTVEHRRLE 173
OsaSPS2.pro SARTTTMIFERTSVSSILFEVVSDDLKLNINLLSIVGAENPVLSAADQIFGAGGKRMREPGLVFLVSRATAELAGLKELTVEHRRLE 155

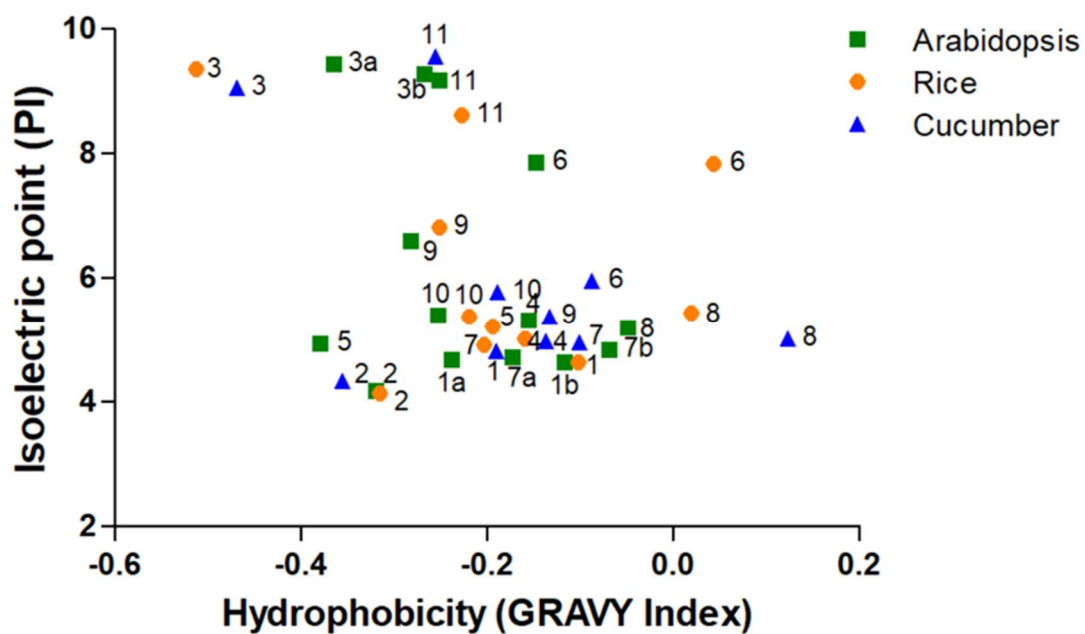
AtSPS1.pro IIEMIHTASLIHDDVLDSDMRGKETVHELPGTRVAVLAGDFMFAQASWYLANLENLEVIKLSQVIKDFASGEIKQASSLFDCTVR 246
AtSPS2.pro IIEMIHTASLIHDDVLDSDMRGKETVHELPGTRVAVLAGDFMFAQASWYLANLENLEVIKLSQVIKDFASGEIKQASSLFDCTVR 257
CsaSPS1.pro IIEMIHTASLIHDDVLDSDMRGKETVHELPGTRVAVLAGDFMFAQASWYLANLENLEVIKLSQVIKDFASGEIKQASSLFDCTVR 261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

AtSPS1.pro LDDYLLKSYKTSASLVAASTKGAAIFSVESVDVTEQMYEFGKNLGLSPQVDDIILDFTQSTEDLGKPGASDLAKGNLTAPVIFALERE 324
AtSPS2.pro LDDYLLKSYKTSASLVAASTKGAAIFSVESVDVTEQMYEFGKNLGLSPQVDDIILDFTQSTEDLGKPGASDLAKGNLTAPVIFALERE 345
CsaSPS1.pro LDDYLLKSYKTSASLVAASTKGAAIFSVESVDVTEQMYEFGKNLGLSPQVDDIILDFTQSTEDLGKPGASDLAKGNLTAPVIFALERE 349
OsaSPS2.pro LDDYLLKSYKTSASLVAASTKGAAIFSVESVDVTEQMYEFGKNLGLSPQVDDIILDFTQSTEDLGKPGASDLAKGNLTAPVIFALERE 321

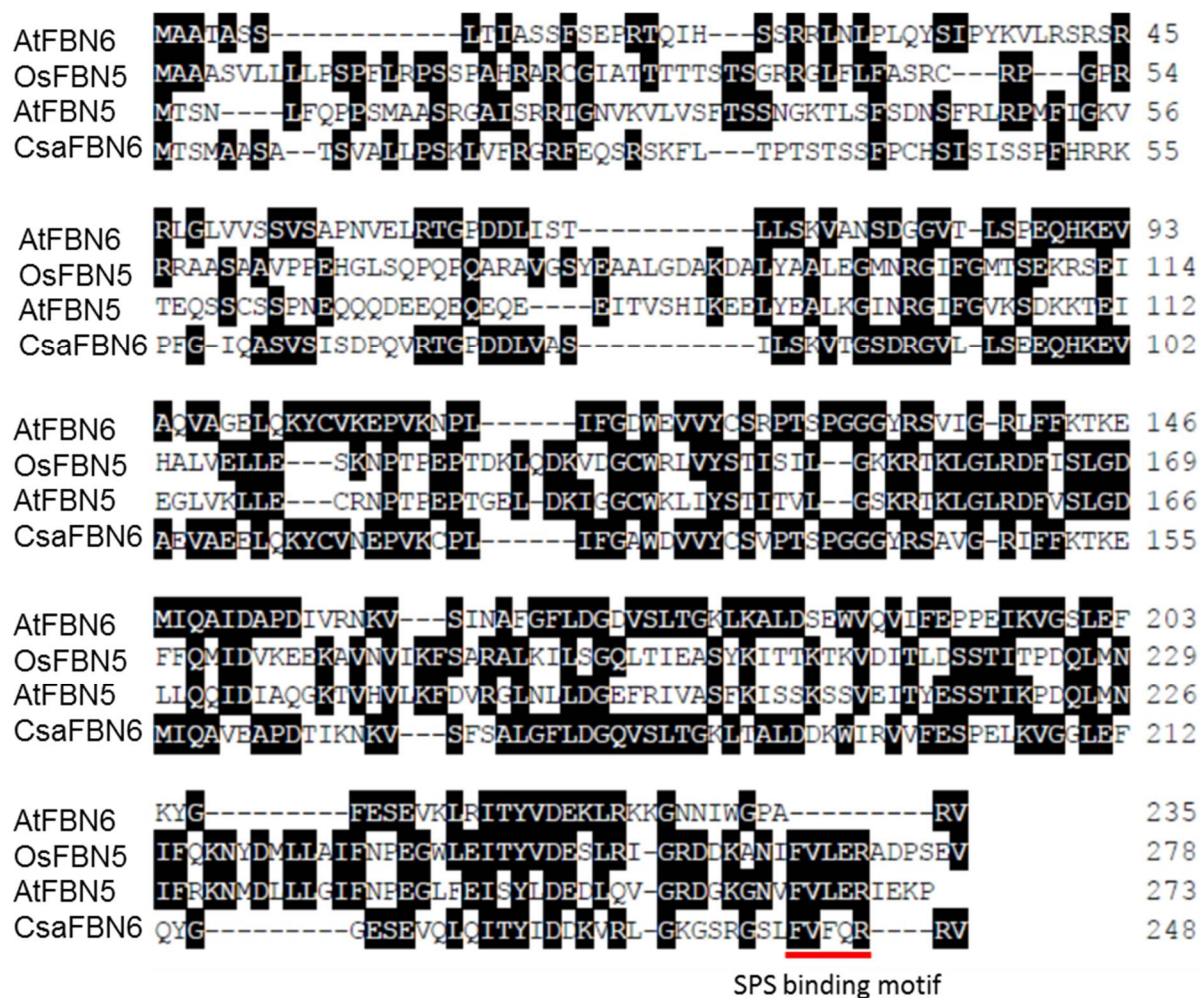
AtSPS1.pro PSLREITIESEFSGSLEPAIEPVNKGSGGIRAGELAKERKADIALNLQCLPSSGFRSALEDMVNLNLERID 406
AtSPS2.pro PSLREITIESEFSGSLEPAIEPVNKGSGGIRAGELAKERKADIALNLQCLPSSGFRSALEDMVNLNLERID 417
CsaSPS1.pro PKLRITIESEFSGSLEPAIEPVNKGSGGIRAGELAKERKADIALNLQCLPSSGFRSALEDMVNLNLERID 421
OsaSPS2.pro PKLRITIESEFSGSLEPAIEPVNKGSGGIRAGELAKERKADIALNLQCLPSSGFRSALEDMVNLNLERID 403

```

Supplement Fig. 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.



Supplement Fig. 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).



Supplementary Fig. 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.

Supplement Table S1. Oligonucleotides Used in this Study

Gene	Forward primer	Reverse primer
CsaFBN1	TCGGTTTTCCCCATCGCTTC	TTAACACCGCACGGACCTTG
CsaFBN2	ACCACTTCTCGCCCGAAGA	TTCCTTCATCGCCACCCCA
CsaFBN3	TCAACCAGGTCACAGCAGAC	GGGCTCTTCCAGGTGCTTTG
CsaFBN4	GTAGACCAGGACCTCCCACG	TTCAGCAGGAGGTAGAGGCC
CsaFBN6	CATCTCCGTTCCATCGACGC	AGAGGATGGACGCAACGAGA
CsaFBN7	CAATTCGCTCCCCTCGTTCA	GCAGAGAAGTCTCCGGCAAC
CsaFBN8	GAAACTCAACGGGGGCTTGT	GTAGTCGCCATGTGCCATCC
CsaFBN9F	CCAAACGCCAGCTTCTCACT	GGCCAAGAGAAGCCAAGTGG
CsaFBN10	CAGCAGCTCAGCAATGTCTGA	CCAAGTCCAACGTCCTTCA
CsaFBN11	AGGCATTGGCTTCAGCAGTC	CGTGAAACTGCAGGTCCTCC
CsaeIF4a	AACACACGTCGCAAGGTTGA	ACGAGACGACCCAGAACGAA

Supplement Table S2. Polymorphic sites found in genomic sequences of cucumber fibrillin genes

Gene name	Gene id	Position		Cultivar		Type
		bp	Exon/Intron	Chinese long	Gy14	
<i>CsaFBN1</i>	Csa6M512870.1	135	1st Exon	G	A	SNP
		145	1st Exon	A	G	SNP
		620	1st Intron	C	T	SNP
		719	1st Intron	G	A	SNP
		770-777*	1st Intron	-	AGGCAAAA	InDel
		780-783*	1st Intron	-	CATA	InDel
		773	1st Intron	G	T	SNP
		777	1st Intron	A	C	SNP
		789	1st Intron	G	T	SNP
		793-797*	1st Intron	-	GATAA	InDel
		1001	1st Intron	C	T	SNP
<i>CsaFBN2</i>	Csa3M008840.1	1443	2nd Intron	C	G	SNP
<i>CsaFBN3</i>	Csa1M665380.1	591	1st Intron	A	-	InDel
		601	1st Intron	A	-	InDel
<i>CsaFBN4</i>	Csa3M134880.1	not found				
<i>CsaFBN6</i>	Csa2M379140.1	not found				
<i>CsaFBN7</i>	Csa3M807340.1	not found				
<i>CsaFBN8</i>	Csa3M640570.1	685	3rd Intron	A	-	InDel
<i>CsaFBN9</i>	Csa6M108600.1	41	1st Exon	T	C	SNP
		59	1st Exon	G	C	SNP
		103	1st Exon	T	A	SNP
		1485	2nd Intron	C	T	SNP
		1816	2nd Intron	G	A	SNP
		1968	2nd Intron	C	T	SNP
		2135	2nd Intron	T	C	SNP
		2179	2nd Intron	A	T	SNP
		2210	2nd Intron	T	G	SNP
		2211	2nd Intron	G	C	SNP
		2290	2nd Intron	C	T	SNP
		2564	2nd Intron	G	A	SNP
		2666	2nd Intron	T	G	SNP
		2866*	2nd Intron	-	T	InDel
		2868	2nd Intron	C	T	SNP
		2888-2889*	2nd Intron	-	TT	InDel
		2893*	2nd Intron	-	T	InDel
		2894	2nd Intron	A	T	SNP
		2896	2nd Intron	T	A	SNP
		2897	2nd Intron	A	T	SNP
		2987	2nd Intron	G	T	SNP
<i>CsaFBN10</i>	Csa4M286330.1	not found				
<i>CsaFBN11</i>	Csa3M603030.1	117-118	1st Intron	TT	-	InDel
Total						10 InDels, 27 SNPs

* The positions were based on genomic sequences from var. Gy14 but not from var. Chinese long.