Table S1. Primers used for *ZmSPS* gene amplification

Primer name	Sequence (5'–3')
ZmSPS1-F	GGTTAAGGAACCCGAGGTGG
ZmSPS1-R	GACGACAATGGGTCGTTGGT
ZmSPS2-F	CCCTAAGCACCACAAGCAGA
ZmSPS2-R	TCTATGAGGGTGAGGCCGAA
ZmSPS3-F	CGGGAACGACTGGATCAACA
ZmSPS3-R	CCTCCTCGACGAAGTATCGC
ZmSPS4-F	AGTGGCATACCCCAAGCATC
ZmSPS4-R	CCGCAATGGCATTCTGATTAATTT
ZmSPS5-F	CGACCTCTACAAGACCTGGC
ZmSPS5-R	CTCTAGACGGCGTTTGGACA
ZmSPS6-F	CATGGACGCTGAAGGAAAGC
ZmSPS6-R	TCTTTGATGAGGAACGCGACA
ZmSPS7-F	CCTACGGTGACAGCACAACT
ZmSPS7-R	TCTCTCCACGTATCAGGCCA
ZmActin1-F	TACGAGATGCCTGATGGTCAGGTCA
ZmActin1-R	TGGAGTTGTACGTGGCCTCATGGAC
ZmSPS3-BD-EcoRI-F	CATGGAGGCCGAATTCATGGCCGGGAACGACT
ZmSPS3-BD-BamHI-R	GCAGGTCGACGGATCCGTCTTTCAATATACCAAATT GCCGTAGAG
Zm00001eb129820-AD-EcoRI-F	GGAGGCCAGTGAATTCATGGTGCTTGAGTTTGTCAA CGG
Zm00001eb129820-AD-BamHI-R	CGAGCTCGATGGATCCGAACCCAGATAGAGGGAAC GC
Zm00001eb356710-AD-EcoRI-F	GGAGGCCAGTGAATTCATGAATCCCGAGTACGACTA CCT
Zm00001eb356710-AD-BamHI-R	CGAGCTCGATGGATCCAGAGCAGCAGCTGCTTTG
Zm00001eb426160-AD-EcoRI-F	GGAGGCCAGTGAATTCATGGGCCACTCCCCCT
Zm00001eb426160-AD-BamHI-R	CGAGCTCGATGGATCCTGGTGGCAGAGGATTGCCA
Y2H-F	ATGGAGTACCCATACGACGTAC
Y2H-R	TTGAGATGGTGCACGATGC

Table S2. ZmSPS exon and intron number

gene	Exon_number	Intron_number
ZmSPS1	12	11
ZmSPS2	12	11
ZmSPS3	14	13
ZmSPS4	13	12
ZmSPS5	14	13
ZmSPS6	12	11
ZmSPS7	13	12

Table S3.ZmSPS Ka/Ks

Seq_1	Seq_2	Ka	Ks	Ka_Ks
ZmSPS1	ZmSPS6	0.022307252028157386	0.19301713365525938	0.11557135683094086
ZmSPS1	ZmSPS2	0.3855549751507449	1.377887836605377	0.2798159363251326
ZmSPS2	ZmSPS6	0.37476303983622294	1.4126720970925195	0.2652866440892679
ZmSPS3	ZmSPS5	0.2511442822858324	1.31704874932356	0.19068715749118686
ZmSPS3	ZmSPS4	0.23962980055680025	1.5559342442677049	0.15401023625492682
ZmSPS3	ZmSPS7	0.2610182289778366	1.4540227522700244	0.17951454237585637
ZmSPS4	ZmSPS5	0.0964930612925454	0.8385810242736045	0.11506706984710226
ZmSPS4	ZmSPS7	0.10068342239982052	0.8885365285001565	0.11331376839371302

Table S4. Synteny analysis of the ZmSPS gene family based on MCScanX

Species	Chromosome	Gene ID	Corresponding species	Chromosome	Orthologous gene ID
Zea mays	chr3	*ZmSPS1*	*Oryza sativa*	chr1	*Os01t0919400-01*
	chr4	*ZmSPS2*		chr11	*Os11t0236100-01*
	chr6	*ZmSPS5*		chr2	*Os02t0184400-01*
	chr6	*ZmSPS5*		chr6	*Os06t0643800-01*
Zea mays	chr6	*ZmSPS5*	*Arabidopsis thaliana*	chr5	*AT5G11110.1*
Zea mays	chr3	*ZmSPS1*	*Hordeum vulgare*	chr3	*HORVU.MOREX.r3.3HG0309930.1*
	chr4	*ZmSPS2*		chr4	*HORVU.MOREX.r3.4HG0344630.1*
	chr6	*ZmSPS5*		chr6	*HORVU.MOREX.r3.6HG0568070.1*
	chr6	*ZmSPS5*		chr7	*HORVU.MOREX.r3.7HG0745120.1*

Table S5. Functional annotation of genes identified from yeast library screening of ZmSPS3

transcriptName	Pfam	GO	Annotation
Zm00001eb356710_T001	PF00025	GO:0003924; GO:0005525	Ras-related protein RABD2C
Zm00001eb035570_T001			
Zm00001eb299760_T001	PF01789; PF20928	GO:0005509; GO:0009523; GO:0009654; GO:0015979; GO:0019898	Oxygen-evolving enhancer protein 2-1
Zm00001eb202760_T001	PF00227; PF10584	GO:0005839; GO:0006511; GO:0019773; GO:0051603	20S proteasome subunit alpha 4
Zm00001eb407630_T001	PF01419		Jacalin-related lectin 19
Zm00001eb319820_T001	PF00388	GO:0006629; GO:0008081	Phosphatidylinositol phospholipase C
Zm00001eb145440_T001	PF16544	GO:0003676; GO:0003723	GH05812P-related protein
Zm00001eb336580_T001	PF02605	GO:0009522; GO:0009538; GO:0015979	Photosystem I subunit XI (psaL)
Zm00001eb168670_T001	PF00454; PF21245		Phosphatidylinositol 4-kinase
Zm00001eb363610_T001			Heparan-alpha-glucosaminide N-acetyltransferase
Zm00001eb022980_T001	PF01619		Proline dehydrogenase
Zm00001eb106460_T001	PF00125; PF16211	GO:0000786; GO:0003677; GO:0030527; GO:0046982	Histone H2A
Zm00001eb230760_T001			Protein LPA2
Zm00001eb143640_T001	PF04398		
Zm00001eb168890_T001			
Zm00001eb306790_T001	PF01255	GO:0016765	Dehydrodolichyl diphosphate synthase
Zm00001eb129820_T001	PF00069; PF03822	GO:0004672; GO:0004713; GO:0005524; GO:0006468; GO:0007165	Protein kinase (Pkinase / NAF domain)
Zm00001eb268360_T001	PF13473	GO:0005507; GO:0009055	Plastocyanin (petE)
Zm00001eb061730_T001			
Zm00001eb212520_T001	PF02531	GO:0009522; GO:0009538; GO:0015979	Photosystem I subunit II (psaD)
Zm00001eb233170_T001	PF00504		Light-harvesting complex I chlorophyll a/b binding protein 1
Zm00001eb426160_T001	PF12937	GO:0005515	F-box protein SKIP2
Zm00001eb426150_T001	PF18511	GO:0005515	F-box protein SKIP2
Zm00001eb421460_T001	PF00355; PF02921	GO:0008121; GO:0016020; GO:0051537	Quinol--cytochrome c reductase
Zm00001eb098610_T001			Expressed protein

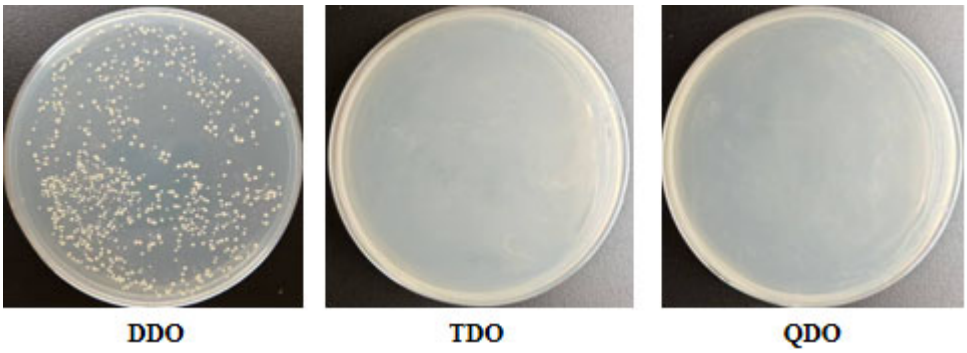


Figure S1. Verification of auto-activation of the tested constructs in the yeast two-hybrid system.