Figure S1. Multiple alignments of amino acid sequences of ZmSAPs
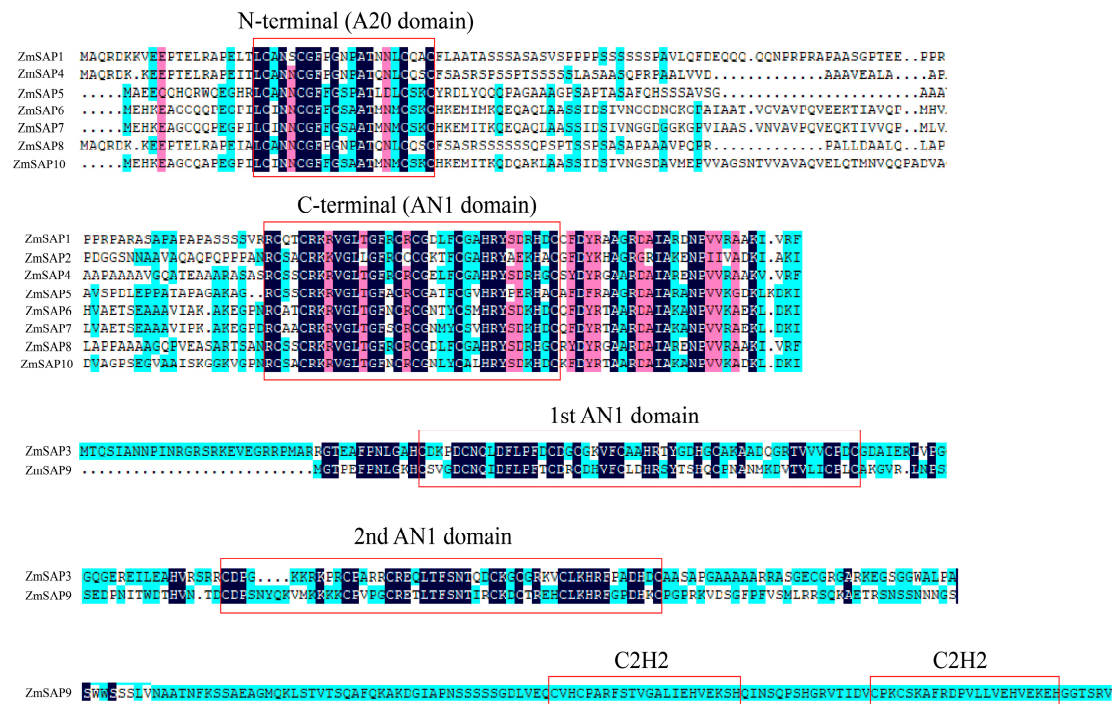
N-terminal (A20 domain)

```
ZmSAP1   MAQRDKKVEEPTELRAPELTLCANSCGFPGNPATNNIGQAGFLAATASSSASASVSPPPPSSSSSSPAVLQFDEQQQ.QQNPRPRPAASGPTEE..PPR
ZmSAP4   MAQRDK.KEEPTELRAPEITLCANCGFPGNPATQNLGQSCFSASRSPSSPTSSSSSLASAASQPRPAALVVD............AAAVEALA....AP.
ZmSAP5   .....MAEECQHQRWQEGHRLCANCGFPGSPATLDLICSKCYRDLYQCCPAGAAAGFSAPTASAFQHSSSAVSG.....................AAA
ZmSAP6   .....MEHKEAGCQQFEGFILCINACGFFGSAATMNMCSKCHKEMIMKQEQAQLAASSIDSIVNCGDNCKCTAIAAT.VCVAVDQVEEKTIAVQT..MHV
ZmSAP7   .....MEHKEAGCQQFEGFILCINACGFFGSAATMNMCSKCHKEMITKQEQAQLAASSIDSIVNGGDGGKGFVIAAS.VNVAVPQVEQKTIVVQP..MLV
ZmSAP8   MAQRDK.KEEPTELRAPFIALCANCGFPGNPATQNLGQSCFSASRSSSSSQPSPTSPSASAPAAAVPQPR............PALLDAALQ..LAP
ZmSAP10  .....MEHKEAGCQAPEGFILCINACGFFGSAATMNMCSKCHKEMITKQDQAKLAASSIDSIVNGSDAVMEPVVAGSNTVVAVAQVELQTMNVQQPADVA
```

C-terminal (AN1 domain)

```
ZmSAP1   PPRPARASAPAFAPASSSSVRRGQTCRKFVGLIGFRCRCGDLFCGAHRYSDRHICRDYRAAGRDAIARDNEVVRAAGI.VRF
ZmSAP2   PDGGSNNAAVAQAQFQPPPANRCSACRKFVGLIGFRCCCKTFCGAHRYAEKFACGFDYKFACRGRFIAKDNFIIVADKI.AKI
ZmSAP4   AAPAAAAAVGCATEAAARASASRCSSCRKFVGLIGFRCRFCGELFCGAHRYSDRHCSYDLYRGAHFDAIARDNEVVRAAKV.VRF
ZmSAP5   AVSPDLEFFATAPAGAKAG..RGSSCRKFVGLIGFRCRCGATFCGVHRYFERHACAHDFRAAGRDAIARANEVVKGDGLKDKI
ZmSAP6   HVAETSEAAAVIAK.AKEGPNRGATCRKFVGLIGFRCNCGNTYGSMRYSDRHICRDDYRTAARDAIAKANEVVKAEKL.DKI
ZmSAP7   LVAETSEAAAVIPK.AKEGPDRGAACRKFVGLIGFSCRCGGNNYGSVHRYSDRHICRDFYRTAARDAIAKANEVVRADEKL.DKI
ZmSAP8   LAPPAAAAGQFVEASARTSANRGSSCRKFVGLIGFRCRCGDLFCGAHRYSDRHGCRYDYRGAARDAIAKANEVVRAAKI.VRF
ZmSAP10  IVAGPSEGVAAISKGGKVGFMRGSACRKFVGLIGFMGFGNLYGALHRYSDKFICGKFLYRTAARDAIAKANEVVKADEKL.DKI
```

1st AN1 domain

```
ZmSAP3   MTCSIANNPINRGRSRKEVEGRRPMARRGTEAFPNLGAHCDKFDCNCIDFLPFLCDGCGKVFCAAHRTYGDFGCAKAADCGRTVVVCEICGDAIERIVEG
ZmSAP9   .........................NGTPDFPNLGRHCSVGDCNCLDFLPFTCDRCDHVFCLDHRSYTSFCCFNANMKDVTVLICELCAKGVR.LNFS
```

2nd AN1 domain

```
ZmSAP3   GQGEREILEAHVRSRRCDFG....KKRFPRCFARRCREGLTFSNTQLDCKCGCRKVCLKHREFADHFDCAASAFGAAAAARRASGECGRGARKEGSGGWALPA
ZmSAP9   SEDPNITWDTHVN.TDCDFSNYQKVMRFKKCFVPGCRETLTFSNTIPCKLCTREHCLKHREGPDFKCFGFRKVDSGFFFVSMLRRSCKFETRSNSSNNNGS
```

C2H2   C2H2

```
ZmSAP9   SWWSSSIVNAATNFKSSAEAGMQKLSTVTSQAFQKAKDGIAPNSSSSSGDLVECCVHCPARFSTVGALIEHVEKSHQINSQPSHGRVTIDVCPKCSKAFRDPVLLVEHVEKEHGGTSRV
```

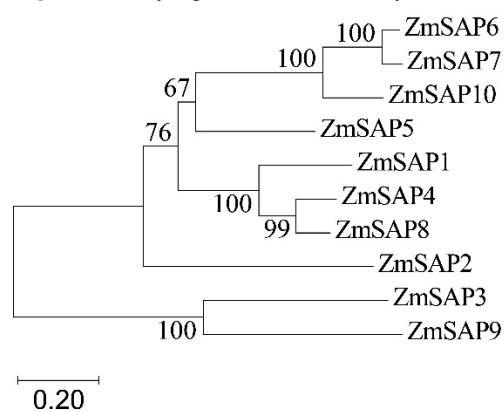**Figure S2.** Phylogenetic evolutionary tree of ZmSAPs.

0.20

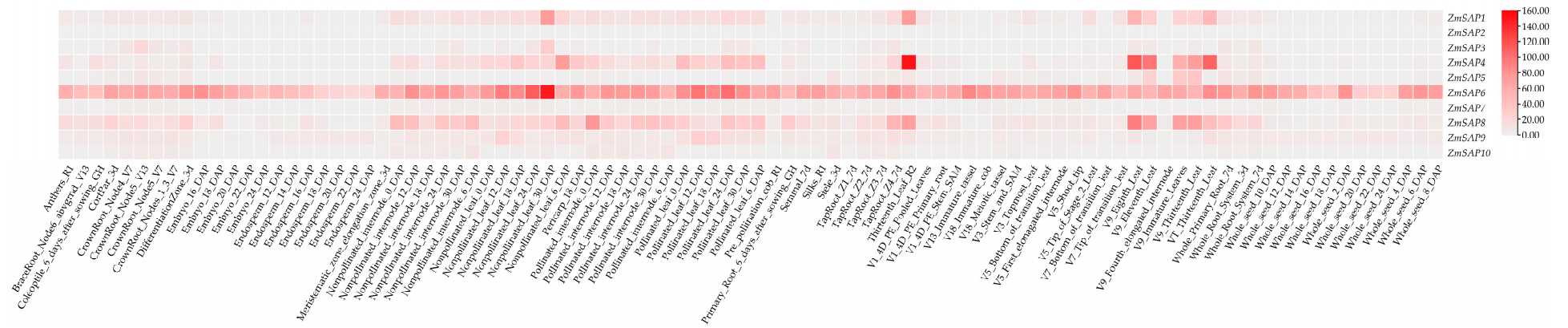**Figure S3.** Expression profiles of *ZmSAPs* in different development stages of maize.

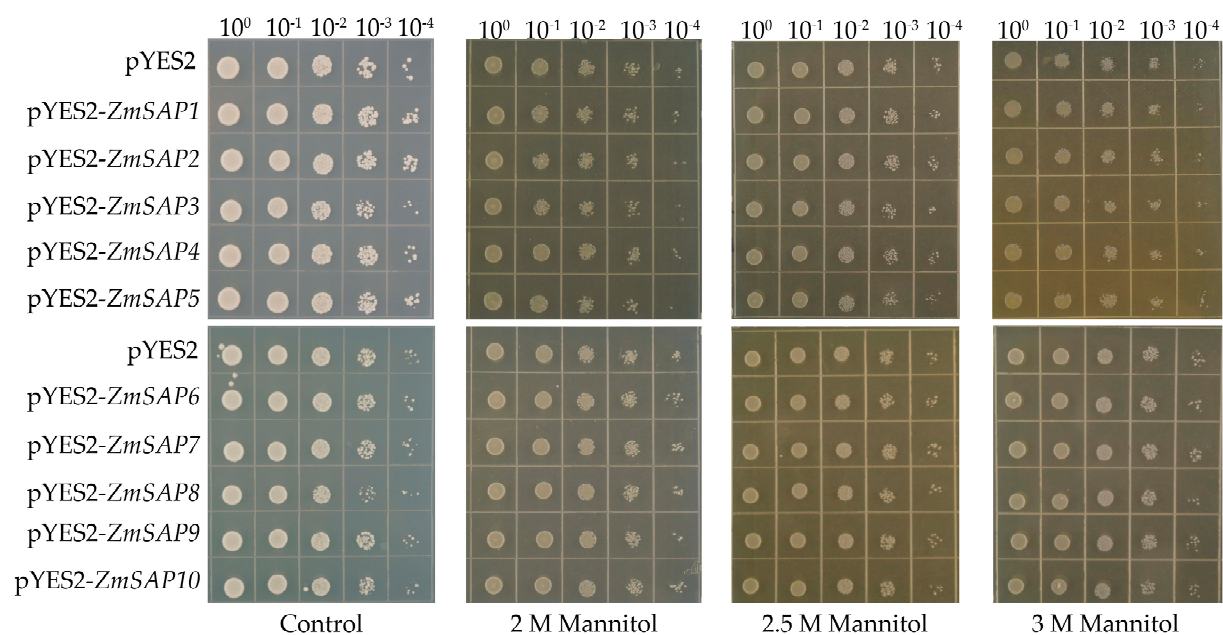**Figure S4.** Phenotype of yeast under drought stress mimicking by mannitol.

	10^0 10^{-1} 10^{-2} 10^{-3} 10^{-4}	10^0 10^{-1} 10^{-2} 10^{-3} 10^{-4}	10^0 10^{-1} 10^{-2} 10^{-3} 10^{-4}	10^0 10^{-1} 10^{-2} 10^{-3} 10^{-4}
	Control	2 M Mannitol	2.5 M Mannitol	3 M Mannitol

Table S1. Collinearity relationship between SAP genes in maize and rice

Name of *ZmSAP*	Name of *OsSAP*
ZmSAP1	*OsSAP1*
ZmSAP 1	*OsSAP5*
ZmSAP 2	*OsSAP14*
ZmSAP 3	*OsSAP17*
ZmSAP 4	*OsSAP1*
ZmSAP 4	*OsSAP5*
ZmSAP 5	*OsSAP8*
ZmSAP 6	*OsSAP8*
ZmSAP 6	*OsSAP4*
ZmSAP 7	*OsSAP8*
ZmSAP 7	*OsSAP4*
ZmSAP 9	*OsSAP16*
ZmSAP 10	*OsSAP8*
ZmSAP 10	*OsSAP4*

Table S2. Primers used in this study.

Gene	Primer sequence (5-3)	Assay
ZmSAP1	ACGACTGCTGCTTCGACTAC ATCCGAGACGCCTAGAACCT	for RT-qPCR
	CTTGGTACCGAGCTCGGATCCATGGCTCAGCGCGACAAG CCCTCTAGATGCATGCTCGAGGAACCTAACGATCTTGGCGGC	for pYES2-*ZmSAP1* construction
ZmSAP 2	CTGTTTTCGAGACAACGCCG TTATTGCTGCCTCCGTCAGG	for RT-qPCR
	CTTGGTACCGAGCTCGGATCCATGACGCAGAAGCGGAAGAG CCCTCTAGATGCATGCTCGAGAATTTTGGCGATCTTGTCGG	for pYES2-*ZmSAP2* construction
ZmSAP 3	GAAAAGAGGTAGAGGGGCGG AAGTCGAGCTGGTTGCAGTC	for RT-qPCR
	CTTGGTACCGAGCTCGGATCCATGACCCAATCAATCGCTAACAA CCCTCTAGATGCATGCTCGAGGAAGATCTTGAGGCTCCGGATG	for pYES2-*ZmSAP3* construction
ZmSAP 4	CGGACAAGGTCTTCGGTGTT CCACTGCACCACCACCATTA	for RT-qPCR
	CTTGGTACCGAGCTCGGATCCATGGCGCAGCGCGACAAG CCCTCTAGATGCATGCTCGAGGAACCTAACGACCTTGGCCG	for pYES2-*ZmSAP4* construction
ZmSAP 5	ACGGATCGTCGGATTGTACG TCAGTAAACGGCCAGCGATT	for RT-qPCR
	CTTGGTACCGAGCTCGGATCCATGGCGGAGGAGCAGCAG CCCTCTAGATGCATGCTCGAGGATCTTGTCCTTGAGCTTATCGC	for pYES2-*ZmSAP5* construction
ZmSAP 6	CCCCAGTCGAGTCACGAAAA ACGATACCGACCCAAACCAC	RT-qPCR
	CTTGGTACCGAGCTCGGATCCATGGAACACAAGGAGGCCG CCCTCTAGATGCATGCTCGAGGATCTTGTCAAGCTTCTCCGCC	for pYES2-*ZmSAP6* construction
ZmSAP 7	GTGTTTTCAGGCCACTGCTC GCAGAGGTTGCTTCCTCCTA	for RT-qPCR
	CTTGGTACCGAGCTCGGATCCATGGAACACAAGGAGGCGG CCCTCTAGATGCATGCTCGAGGATCTTGTCGAGCTTCTCCGC	for pYES2-*ZmSAP7* construction
ZmSAP 8	TAGGTTCTGATTCGACCGGC GATTTCGCATGCCTTTCCCC	for RT-qPCR
	CTTGGTACCGAGCTCGGATCCATGGCGCAGCGCGACAAG CCCTCTAGATGCATGCTCGAGGAACCTAACGATCTTGGCCGC	for pYES2-*ZmSAP8* construction
ZmSAP 9	TCACGGTCTCACTCTCACCT AAACGGACGGGACACGAAAT	for RT-qPCR
	CTTGGTACCGAGCTCGGATCCATGGGCACGCCGGAGTTC CCCTCTAGATGCATGCTCGAGCACTCTTGACGTTCCTCCATGC	for pYES2-*ZmSAP9* construction
ZmSAP 10	CTTTATCTCTCTCCCCACGCC CGATTCCTCTCCGACGATCC	for RT-qPCR
	CTTGGTACCGAGCTCGGATCCATGGAGCACAAGGAGGCTGG CCCTCTAGATGCATGCTCGAGGATCTTGTCGAGCTTGTCTGCC	for pYES2-*ZmSAP10* construction