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Supplementary Data

Molecular cloning and characterization of two Trithorax-Group genes from *Phaseolus vulgaris* roots and symbiotic nodules.

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Supplementary figures.

	_	AWS DOMAIN	SET DOMAIN
Glyma20g30870 Glyma10g36720 PvuASH1h ASHH1/NP_974158	FW MDLHTEELPQYIHMNONEFCIRRHKKOKEEDIAICECKYDADDPDNACGDSCLNVLTSTECTPGYCPCGYLCKNOKFOKCEYAKTKLFKTEGRGWGLLADEDIKAGGFYIEYCG 114 MOPHTEELPDYIHINONEFCIRRHKKOKEEDIAICECKYDADDPDNACGDSCLNVLTSTECTPGYCPCDILCKNOKFOKCEYAKTKLFKTEGRGWGLLADEDIKAGGFYIEYCG 114 MOPSCHPDGEGELPYYHIYONDFFYRHKKOKEEDIAICECKYDANDTDSACGDSCLNVLTSTECTPGYCPCDILCKNOKFOKCEYAKTKLFKTEGRGWGLLAGEDIKAGGFYHEYCG 114 MOFSCHPDGEGELPYYHIYONDFFYRHKKOKEEDIAICECKFDFGDPBSACGERCLNVITNTECTFGYCPCGYYCKNOKFOKCEYAKTKLFKTEGRGWGLVALEEIKAGGFTMEYCG 120		
SET DOMAIN			
Glyma20g30870 Glyma10g36720 PvuASH1h ASHH1/NP_974158	EVISWKEAKRRSQAYENQGLKDAFIIFLNVSESIDAT EVISWKEAKRRSQAYENQGLKDAFIICLNASESIDAT EVISWKEAKKRAQTYETHGVKDAYIISLNASEAIDAT	RKGSLARFINHSCOPNCETRKWNVLGEIRVGIFAKHDIPIGNELAYDYNFEW RKGSLARFINHSCOPNCETRKWNVLGEIRVGIFAKHDIPIGTELAYDYNFEW RKGSLARFINHSCRPNCETRKWNLGEIRVGIFAKHDVPIGTELAYDYNFEW KKGSLARFINHSCRPNCETRKWNVLGEVRVGIFAKESISPRTELAYDYNFEW	FGGAKVRCLCGALKCSGFLGAKSRGFQEDTY 234 FGGAKVRCLCGALKCSGFLGAKSRGFQEDTY 234 YGGAKVRCLCGAVACSGFLGAKSRGFQEDTY 240
Glyma20g30870 Glyma10g36720 PvuASH1h ASHH1/NP_974158	LWEDDDGRYSVEKIPVYDSAEDEPVSNFNGRTE LWEDDDDRYSVEKIPVYDSAEDEPVSNVNGRTE VWEDGDDRYSVDKIPVYDSAEDELTSEPSKNGESNTN	SPSLDVMVKAEQLLESTAFHVOPLDSVOMKDLDVKKIKTDVADEHMALLYY SPSLDVIVKAEQLSESTAFHVOPLDSVOMKDLDVKKIKTDVADEDMNFYS SSPLDVMLKOEQLSESTOFNVOSLDSVOMKGLDVKKIKTEVTDEDMHLYN SEEKEKDISTENHLESTALNIQQOSDSTPTPMEEDVVTETVKTETSEDMKLLSS	QDSEHTLSQKN-AISHIRSNTAGRNYCLGPR 346 HDTEQTLSQKNAMISRIRSNAAGRNYHIGPR 347 QNSQEDSSPKTAIVSRVHGNISKIKSE 356
Glyma20g30870 Glyma10g36720 PvuASH1h ASHH1/NP_974158	SMSTKRSRAYNGGRFKNLIEKKIDVKFAAALLASKEA SMSTKRSRAYNGGRFKNLVEKKIDAKFAAGLLASKEA SLPKKRGRPFSGGKTKNVAQKHVDIANVVQLLATKEA	QEEILNCEKIKDDATSALDSLYDEIRPAIEEHERDSQDSVSTTVAEKWIQAC QEEIFNCEKMKDDATSALDSLYDEIRPAIEEHERDSQDSVSTTVAEKWIQAC QEEILNCEKRKDDATSTLOSLYDEIRPAIEEHERDSQDSVSTTVAEKWIQAC QEVELKYEEVKERAVRLSSLYDEIRPAIEEHERDSQDSVATSVAEKWIQAS	CLKLKABFDLYSSIVKNVACTAQRAS-GQVK 465 CLKLKABFDLYSSIVKNVACTAQRAP-GQAK 466 CNKLKABFDLYSSVIKNIASTPIKPQDTKTK 476
Glyma20g30870 Glyma10g36720 PvuASH1h ASHH1/NP_974158	Rev PTEVINENEIKLLTG- PTEVINENEIKLLTG- PTEVINENEIKLLTG- PTEVINENEIKLLTG- VAEAQNEDHIKLLEAK 492		

Fig S1. Multiple sequence alignment of TRX proteins. Alignment of the Arabidopsis cDNA *ATX1* sequence (At2g31650) with two predicted soybean (*Glycine max*) Trithorax sequences (Glyma08g29010.1 and Glyma18g51890.1) and the *P. vulgaris PvuTRX1h* sequence. Consensus sequences used to design consensus primers to amplify an internal fragment from the *P. vulgaris PvuTRX1h* are shown inside rectangles as "Fw" and "Rev". Protein domains are indicated in red letters with the name of the conserved domains above the sequences.

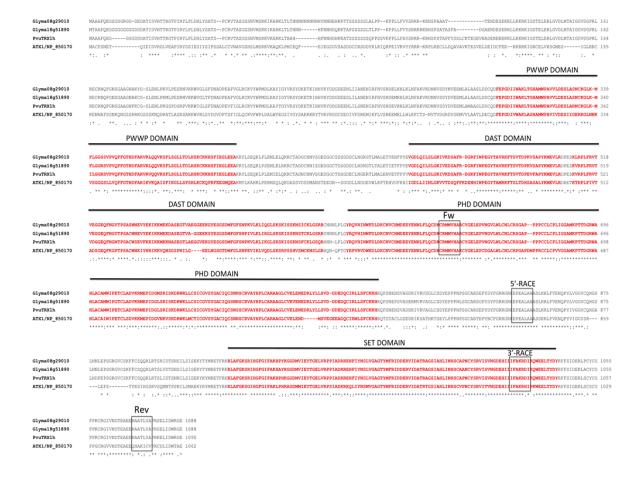


Fig S2. Multiple sequence alignment of Ash1 proteins. Alignment of the Arabidopsis ASHH1 sequence with two homologous soybean sequences, Glyma20g30870.1 and Glyma10g36720.1, and the *P. vulgaris PvuASH1h* sequence. Consensus sequences used to design consensus primers to amplify an internal fragment from the *PvuASH1h* sequence are shown inside rectangles as "Fw" and "Rev". Protein domains are indicated in red letters with the name of the conserved domains above the sequences.