

SI Figure 1. Disruption of the *IAMH1* gene does not dramatically affect either Arabidopsis development or auxin reporter expression. A) No obvious phenotypes were observed in the *iamh1-1* mutant. B) Expression of the auxin reporter *DR5:GUS* was not altered in the *iamh1-1* mutant.



**SI Figure 2. Phylogenetic analysis of IAMH1 proteins across plant species**. The tree was generated using Clustal Omega online program. The shown tree is a Neighbour-joining tree without distance corrections.

Zea	-MAPLTPRLVVPIDVKKQPWEQKVPLHNRWHPDIPPVADVTEGELFRVEMVDWTGGRVRD	59
Solanum	-MAPPTPRLVIPIDLKKKPWOOKLPLHNRWHPEIPPVTEIKTGEMFRIEMVDWTAGSIOD	59
Arabidongia		5.0
Receive		59
Brassica	-MAPATPRVVVKVDLKKRPWEQEQPLHNRWHPEIQPVGEVKAGEFFRVEMVDWTGGAVKD	59
Selaginella	-MAPRTPKSVVKVDVTKQPWEQDSPLHNRWHPDIPPVAQVSVEELFRVETIDWTGGQILD	59
Physcomitrella	MAPIKTPRAIVTVNPNKRPWEQTVPLHNRWHPDIPAVGEVEEGEVFRVETVDWTGRQILN	60
Chlamydomonas	-MPPRTPIPVVKMDPKKAPWEQEKKPHNRWHPDIPPVAEVKTGDLFRVETIDWTGGQIKD	59
-	:* :: :: .* **:* ****** * :: :.**:* :* . : :	
Zea	DNSADDIKSI.DI.TTTHYI.SGPLRIVDSEGVPASPGDIJ.AVETCNLGPI.PGDEWGYTATFE	119
Solanum		110
Buchidaucia		119
Arabidopsis	NDSASDIKNLVLTTTHHLSGPIKVVDEEGVAARAGDLLAVEICNLGPLPGDEWGFTGSFD	119
Brassica	DDSAEDIKSLDLSTVHYLSGPIKVVDEEGVAAKPGDLLAVEICNLGPLPGDEWGFTASFD	119
Selaginella	NDSAEDVKNMDLSRVHYLSGPIRVMDEAGKPAIPGDILVVEICNLGPLPGDEWGFTGTFD	119
Physcomitrella	NDSAEDMKNIDLTLVHNLSGPIRVNDTEGKPAMPGDLLVVEILNLGPLPGDEWGFTGIFD	120
Chlamydomonas	DDSADDIKHVDLSCCHYLSGPIRITDEKGEPARPGDLLVVELCNLGPLPGDEWGYTGTFD	119
	**** *** * ** * ******* * * * *********	
Zea	RENGGGFLTDHFPTARKAIWYFEGIYAYSPQIPGVRFPGLTHPGIVGTAPSAELLNIWNE	179
Solanum	RENGGGFLTDHFPRATKAIWYFEGIYAYSPHIPGVRFPGLIHPGIIGTAPSKELLNIWNE	179
Arabidonsis	PENCECET TOHEDCATKATWYFECTYAYSOOTDCVPEDCLTHDCVTCTADSNELLPTWND	179
Arabidopsis Draggina		170
Brassica	RENGEGF LTDHFPCATRAIWIF EGI MISPUTPGVRFPGLTHPGI I GTAPSRELLKI WRE	179
Selaginella	RENGGGFLTDHFPSATKAIWHFDGIFAYSRHIPGVRFPGLIHPGLIGTAPSKELLDIWNS	179
Physcomitrella	RENGGGFLTDHFPNACKAIWDFEGIWASSRHIPGVRFPGLIHPGLIGTAPSKELLDIWNK	180
Chlamydomonas	RDNGGGFLTDHFPEATKAIWYFDGIYASSRHIPGVRFAGLIHPGLIGTAPSHELLKIWNE	179
Zea	REKRLAETSPOTLKLCEVLHORPLANLPTPENCLLGKIOEGTAGWHKVANEAARTIPGRE	239
Solanum	RERKLEETGPRSLKLCEVLHSRPLANLPSTKGCTLGKTODGTPEWTRTANEAARTTPGRE	239
Arabidongia		220
Alabidopsis		239
Brassica	RERQLEESGLSSLTLCEVVHQRPLANLPIAKGCLLGNMEEGTPEWERIAKEAARTIPGRE	239
Selaginella	RERLLVEET-PSLTLCSSLHTRPLANLPLAKGALLGKIPPGSSQWQAIANEAARTIPGRE	238
Physcomitrella	REKALVDDGENALTLGKHLHTRPLALLPQTQGALLGKVEKGSKDWKRIAAEACRTIPGRE	240
Chlamydomonas	REGALVEAGENSTTLGGVLHTRPLALLPEPKGALLGDIPADSPQWSKVAGEAARTIPGRE	239
	** * : : .* :* *** ** ::**.: .: * :* **.******	
Zea	NGGNCDIKNLSRGSKVYLPVFVEGANLSTGDMHFSQGDGEVSFCGAIEMSGFLELKCEII	299
Solanum	NGGNCDTKNLSRGSKTYLPVFVEGANLSTGDMHFSOGDGEVSFCGATEMSGFLELKCETT	299
Arabidonsis		299
Readian Braddian		200
Brassica	NGGNCDINNESRGSNI LEVY VEGANLS IGDMIF SOBJELIST CATEMSOF LELACETT	299
Selaginella	NGGNCDIKNLSRGCKVYFPVFVEGANLSMGDMHFSQGDGEVSFCGAIEMSGFLELRCEIL	298
Physcomitrella	NGGNCDIKNLSRGCRVYFPVFIEGANLSMGDMHFSQGDGEVSFCGAIEMSGFLELKCSII	300
Chlamydomonas	NGGNCDIKNLSRGCKVYFPVFVEGANLSMGDMHFSQGDGEVSFCGAIEMSGFLEIKTEII	299
	***************************************	
Zea	RGGMKEYLTPVGPTPLHVNPIFEIGPVEPRFSEWLVFEGISVDESGKQHFLDASVAYKRA	359
Solanum	RNGMKEYLTPMGPTSLHVNPIFEIGPMEPRFSEWLVFEGISVDESGQQHYLDASVAYKRA	359
Arabidopsis	RNGMOEYLTPMGPTPLHVNPIFEIGPVEPRFSEWLVFEGISVDESGKOHYLDATVAYKRA	359
Brassica	RNGMKEVI. TPMGPTPI. HVNPIFEIGPVEPRFSEWI. VFEGISVDETGROHVI. DATVAVKRA	359
Selaginella	PCCMEPYMTPTCPTKI, HVHDI, FFTCPI, FDFFSFWI, VFFCVSVDFSCKOHFT, DASTAVKPA	358
Dhug gemitus 11.		200
Physcomitrella	RGGMEQYLTPMGPTKLHVNPIFEIGPLEPKFSEWLVFEGLSVDEDGKQHYLDASIAYKKA	360
Chlamydomonas	KGGMEQYLTPMGFTKLHVHPIFEIGFLEFKISEWLVFEGISVDESGKQHYLDATVAYKKA *.**:.*:*** ***************************	359
_		
Zea	VLNAIEYIARFGYSKEQVYLLLSCCPCEGRISGIVDSPNAVATIAIPTAIFDQDIKPKHL	419
Solanum	VLNAIDYLSKFGYSKEQVYLLLSCCPCEGRISGIVDAPNAVATLAIPTAIFDQDIRPKVN	419
Arabidopsis	VLNAIDYLFKFGYSKEQVYLLLSCCPCEGRLSGIVDSPNAVATLAIPTAIFDQDIRPKNR	419
Brassica	VLNAIDYLFKFGYSKEQVYLLLSCCPCEGRISGIVDSPNALATLAIPTSIFDQDIRPKTQ	419
Selaginella	VLNAIHYFSNFGYSKEQVYLLLSCCPCEGRISGIVDAPNAVATLAVPTAIFDQDVRPKRG	418
Physcomitrella	VLNCIDYLSKFGYSKFOVYLLLSCCPCEGRISGIVDVPNACATLAIPVNIFDODIRPKKG	420
Chlamydomonas		410
	VLNCIDYLSKFGYTKOOVYLLLSCCPCEGRISGIVDVPNAVATLAIPIAIFDODIRPKAG	4 1 4
	VLNCIDYLSKFGYTKQQVYLLLSCCPCEGRISGIVDVPNAVATLAIPIAIFDQDIRPKAG ***.*.*: .***:*:***********************	419
7.02	VLNCIDYLSKFGYTKQQVYLLLSCCPCEGRISGIVDVPNAVATLAIPIAIFDQDIRPKAG ***.*.*: .***:*:***********************	419
Zea	VLNCIDYLSKFGYTKQQVYLLLSCCPCEGRISGIVDVPNAVATLAIPIAIFDQDIRPKAG         ***.*.*:         ***.*.*:         ***.**:         ***         RGRPGPKLIRLPDLLSCSNNGHIPVTQDQSGTRAS         454         KVPLGPRLIRNPGTPOCTYDGNLPTKNPLLHOOGSSCNMPASS         463	419
Zea Solanum Arabidonsis	VLNCIDYLSKFGYTKQQVYLLLSCCPCEGRISGIVDVPNAVATLAIPIAIFDQDIRPKAG ***.*.*: .***:*:***********************	419
Zea Solanum Arabidopsis Brassica	VLNCIDYLSKFGYTKQQVYLLLSCCPCEGRISGIVDVPNAVATLAIPIAIFDQDIRPKAG         ****.*:.******************************	412
Zea Solanum Arabidopsis Brassica Solaginollo	VLNCIDYLSKFGYTKQQVYLLLSCCPCEGRISGIVDVPNAVATLAIPIAIFDQDIRPKAG         ****.**:         ****.**:         RGRPGPKLIRLPDLLSCSNNGHIPVTQDQSGTRAS         454         KVPLGPRLIRNPGIPQCTYDGNLPITKNPLLHQQGSSCNMDASS         463         KVPVGPRVVRKPDVLKSTYDGKLPITKNPSSSS         452         KVPAGPRIVRKPDVMKSTYDGKLETTRNPSSSYS         454	412
Zea Solanum Arabidopsis Brassica Selaginella Bhugacmitaria	VLNCIDYLSKFGYTKQQVYLLLSCCPCEGRISGIVDVPNAVATLAIPIAIFDQDIRPKAG****.**:***.*:***:*:***:*:***:*:***:*:***:*:***:*:***:*:***:*:***:*:***:*:***:*:***:*:*:***:*:*:***:*:*:***:*:*:****:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:	413
Zea Solanum Arabidopsis Brassica Selaginella Physcomitrella	VLNCIDYLSKFGYTKQQVYLLLSCCPCEGRISGIVDVPNAVATLAIPIAIFDQDIRPKAG***.*.*:***:*:*******************************	417
Zea Solanum Arabidopsis Brassica Selaginella Physcomitrella Chlamydomonas	VLNCIDYLSKFGYTKQQVYLLLSCCPCEGRISGIVDVPNAVATLAIPIAIFDQDIRPKAG***.*.*:***:*:*******************************	417

**SI Figure 3. IAMH1 is highly conserved.** The multiple sequence alignment was generated using the Clustal Omega program (https://www.ebi.ac.uk/Tools/msa/clustalo/)

## GTCCTCTTCCAGGAGATGAATGGGGATTCAC WT



**SI Figure 4. Sequence analysis of** *iamh2* **CRISPR mutants**. The *iamh2-2* contained an T insertion. The *iamh2-3* had a 20-bpo deletion.



