

Supporting Information

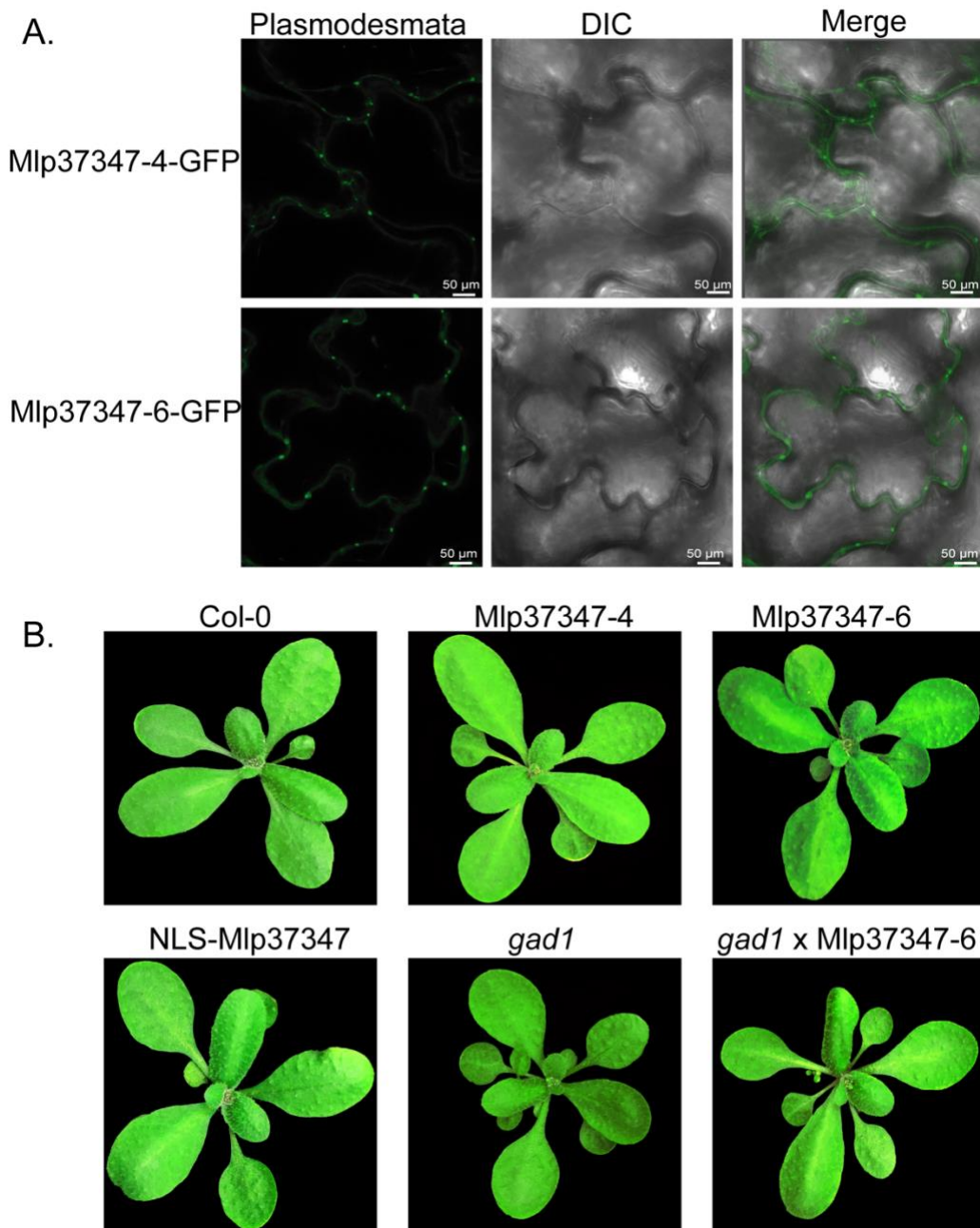


Figure S1: title Mlp37347 localizes at plasmodesmata and phenotype comparison of different transgenic lines.

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                20          40          60          80
PtGAD1  MVL SKT SSES  DDSVHSTFAS  RYVRASLPRF  KMPENSIPKE  AAFQI INDEL  MLDGNPRLNL  ASFVTTWMEP  ECDKLI MASI  NKNYVDMDEY  90
AtGAD1  MVL SHAVSES  DVSVHSTFAS  RYVRTSLPRF  KMPENSIPKE  AAFQI INDEL  MLDGNPRLNL  ASFVTTWMEP  ECDKLI MSSI  NKNYVDMDEY  90
NbGAD1  MVL SKT SSES  DVSVHSTFAS  RYVRTSLPRF  EMAENSIPKE  AAFQI INDEL  MLDGNPRLNL  ASFVTTWMEP  ECDKLI MDSI  NKNYVDMDEY  90
Consensus  MVL SKT SSES  DVSVHSTFAS  RYVRTSLPRF  KMPENSIPKE  AAFQI INDEL  MLDGNPRLNL  ASFVTTWMEP  ECDKLI MSSI  NKNYVDMDEY

                100          120          140          160          180
PtGAD1  PVTTELQNRG  VN I I A H L F N A  P L G D S E T A I G  V G T V G S S E A I  M L A G L A F K R R  W Q N K M K A E G K  P Y D K P N I V T G  A N V Q V C W E K F  A R Y F E V E L K E  180
AtGAD1  PVTTELQNRG  V N M I A H L F N A  P L E E A E T A V G  V G T V G S S E A I  M L A G L A F K R K  W Q N K R K A E G K  P V D K P N I V T G  A N V Q V C W E K F  A R Y F E V E L K E  180
NbGAD1  P - - - - - N R C  V N M I A R L F N A  P L E E E E T A I G  V G T V G S S E A I  M L A G L A F K R I  W Q N K R K A E G K  P H D K P N I V T G  A N V Q V C W E K F  A N Y F E V E L K E  174
Consensus  P V T T E L Q N R C  V N M I A H L F N A  P L E E X E T A I G  V G T V G S S E A I  M L A G L A F K R X  W Q N K R K A E G K  P X D K P N I V T G  A N V Q V C W E K F  A R Y F E V E L K E

                200          220          240          260
PtGAD1  V K L R D G Y Y V M  D P E K A V K M V D  E N T I C V A A I L  G S T L N G E F E D  V K L L N D L L V E  K N K E T G W D T P  I H V D A A S G G F  I A P F L Y P E L E  W D F R L P L V K S  270
AtGAD1  V K L S E G Y Y V M  D P Q Q A V D M V D  E N T I C V A A I L  G S T L N G E F E D  V K L L N D L L V E  K N K E T G W D T P  I H V D A A S G G F  I A P F L Y P E L E  W D F R L P L V K S  270
NbGAD1  V K L R E G Y Y V M  E P Y K A V E M V D  E N T I C V A A I L  G S T L N G E F E D  V K L L N D L L I E  K N K L T G W N T P  I H V D A A S G G F  I A P F L Y P E L E  W D F R L P L V K S  264
Consensus  V K L R E G Y Y V M  D P X K A V X M V D  E N T I C V A A I L  G S T L N G E F E D  V K L L N D L L V E  K N K E T G W D T P  I H V D A A S G G F  I A P F L Y P E L E  W D F R L P L V K S

                280          300          320          340          360
PtGAD1  I N V S G H K Y G L  V Y A G I G W V V W  R N K E D L P E E L  I F H I N Y L G A D  Q P T F T L N F S K  G S S Q V I A Q Y Y  Q L I R L G Y E G Y  K N V M E N C R D N  M M V L K Q G L E N  360
AtGAD1  I N V S G H K Y G L  V Y A G I G W V I W  R N K E D L P E E L  I F H I N Y L G A D  Q P T F T L N F S K  G S S Q V I A Q Y Y  Q L I R L G H E G Y  R N V M E N C R E N  M I V L R E G L E K  360
NbGAD1  I N V S G H K Y G L  V Y A G I G - - - -  - - - - - - - - -  - - - - - - - - -  - - - - - - - - -  - S S Q V I A Q Y Y  Q L I R L G Y E G Y  R N V M E N C R E N  A I V L R E G L E K  319
Consensus  I N V S G H K Y G L  V Y A G I G W V X W  R N K E D L P E E L  I F H I N Y L G A D  Q P T F T L N F S K  G S S Q V I A Q Y Y  Q L I R L G Y E G Y  R N V M E N C R E N  M I V L R E G L E K

                380          400          420          440
PtGAD1  T G K F N I V S K D  N G V P L V A F S L  K D N S S H K E F E  V S E M L R R F G W  I V P A Y T M P P D  A Q H V T V L R V V  I R E D F S R T L A  E R L V L D I E K V  L H E L D T L P X R  450
AtGAD1  T E R F N I V S K D  E G V P L V A F S L  K D S S C H T E F E  I S D M L R R Y G W  I V P A Y T M P P N  A Q H I T V L R V V  I R E D F S R T L A  E R L V I D I E K V  M R E L D E L P S R  450
NbGAD1  T G R F N I V S K D  E G V P L V A F S L  K D N S H H N E F E  V S E T L R R F G W  I V P A Y T M P A D  A Q H V T V L R V V  I R E D F S R T L A  E R L V L D I V K V  L H E L D T L P A R  409
Consensus  T G R F N I V S K D  E G V P L V A F S L  K D N S X H X E F E  V S E M L R R F G W  I V P A Y T M P P D  A Q H V T V L R V V  I R E D F S R T L A  E R L V L D I E K V  L H E L D T L P X R

                460          480          500
PtGAD1  I S T K I A L A N E  E K E A A A N K - -  - - - E K R D L E K  T R E I T T V W R K  F V M Q R K M - N G  V C  496
AtGAD1  V I H K I S L G Q E  K S E S N S D N L M  V T V K K S D I D K  Q R D I I T G W K K  F V A D R K K T S G  I C  502
NbGAD1  L S A K L - - - E  E V K L V K N G - -  - - - K K S E V E V  Q R E V T N Y W K K  F V L A R K A P - -  V C  450
Consensus  X S X K I X L X X E  E X E X X X N X - -  - - - K K S D X E K  Q R E I T T X W K K  F V X X R K X X X G  V C

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Figure S2: Sequence alignment of NbGAD1, AtGAD1, and PtGAD1

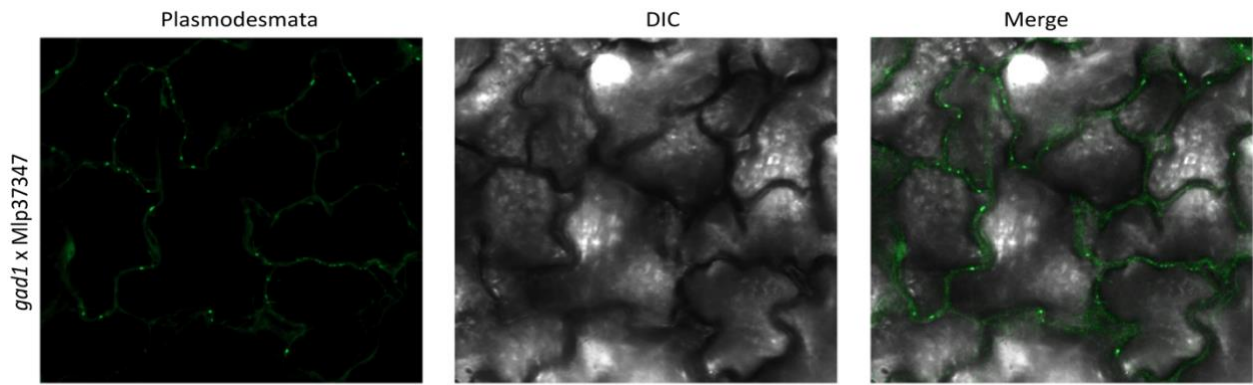


Figure S3: Localization of Mlp37347-GFP in *gad1*.