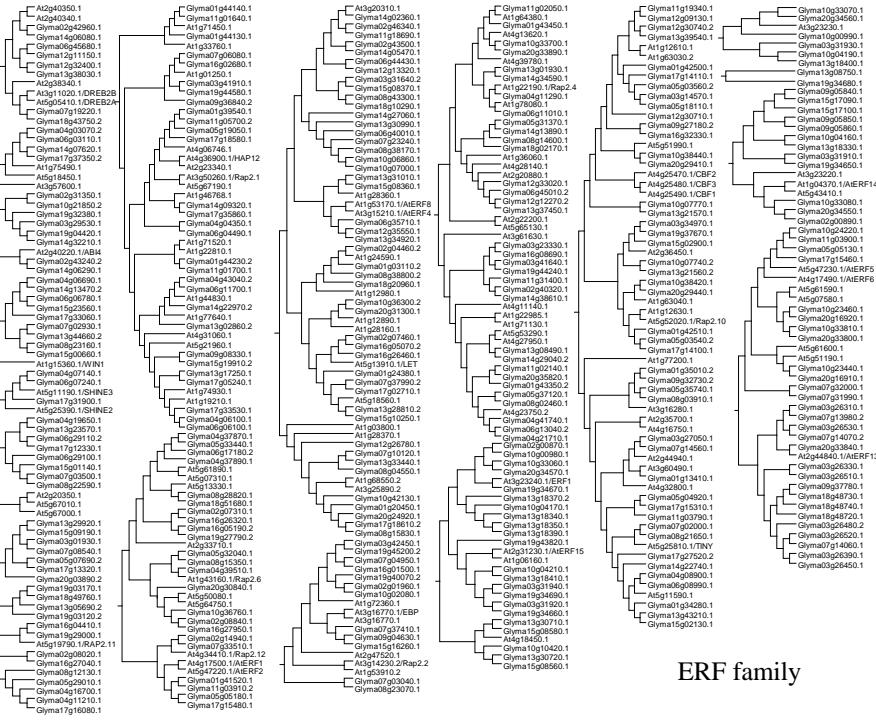


## **Supporting Information**

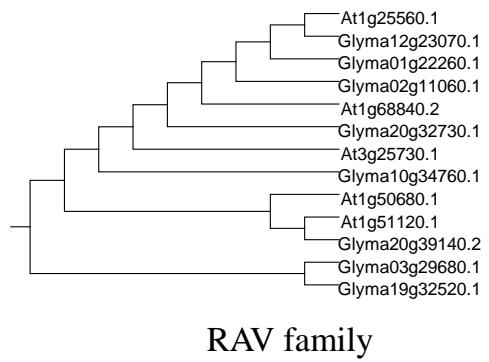
**Supplementary Table S1.** Sequence identities (%) of nine AP2 proteins of *G. max*.

**Supplementary Table S2.** The primer sequences used in the present study

Purpose	Primer name	Primer sequences (5'-3')
For gene cloning	GmAP2-1F	CACCATGTGGGATCTGAATGACTC
	GmAP2-1R	TCATGAGGGTCTCATGAGAGA
	GmAP2-2F	CACCATGTGGGATCTCAACGACTCA
	GmAP2-2R	TCATGAGGGTCTCATGAGACTG
	GmAP2-3F	CACCATGTTGGATCTTAATCTGAATG
	GmAP2-3R	TCAGAACTTGTGGTGGCTAC
	GmAP2-4F	CACCATGTTGGATCTTAATCTGACTG
	GmAP2-4R	CTAGGACGGTGGCTCGGGGACTT
	GmAP2-5F	CACCATGAGTAACTGGTTGGGTTCT
	GmAP2-5R	TCATTCAATTCCACAAAGCAAACA
	GmAP2-6F	CACCATGGCTGGTGCCACGAATTGG
	GmAP2-6R	TCAGTAGGACTGGTGAGGCCATA
	GmAP2-7F	CACCATGAAGAGGTCTCCAGCATCTTC
	GmAP2-7R	TCATAGATCTAGAGCATAGTCAC
For qRT-PCR analysis	qGmAP2-1F	AGGTGGAAGCAGAACATTGGATA
	qGmAP2-1R	ACTGTCATCATGAGCTACAGAG
	qGmAP2-2F	CTTCCTTCGATGGAGATGATGAC
	qGmAP2-2R	CTGTCCATGGACTCTTCTTCATT
	qGmAP2-3F	CCCGCTGGATCATAAAACGGT
	qGmAP2-3R	CGGTCCCTCTGTAGAAAGTGA
	qGmAP2-4F	AGTCACCTCTACCGAAGAACCC
	qGmAP2-4R	TAGATCCTCCTCATATAATCAACG
	qGmAP2-5F	GGCACCAAGCTTTGCACCAA
	qGmAP2-5R	CAAGGAAGAAGGATTGTGAGAT
	qGmAP2-6F	GGACCAACTCGGGTCCGA
	qGmAP2-6R	GTCAAAGCTGATCCTTACAATT
	qGmAP2-7F	AGAAGGGTCGACAAGTTATTG
	qGmAP2-7R	TTCCGCATACTCTCCAATTCGT
	qPP2A-F	TATCGGATGACGATTCTCGTGCAG
	qPP2A-R	GCTTGGTCGACTATCGGAATGAGAG
	qSUB3-F	GTGTAATGTTGGATGTGTTCCC
	qSUB3-R	ACACAATTGAGTTCAACACAAACCG



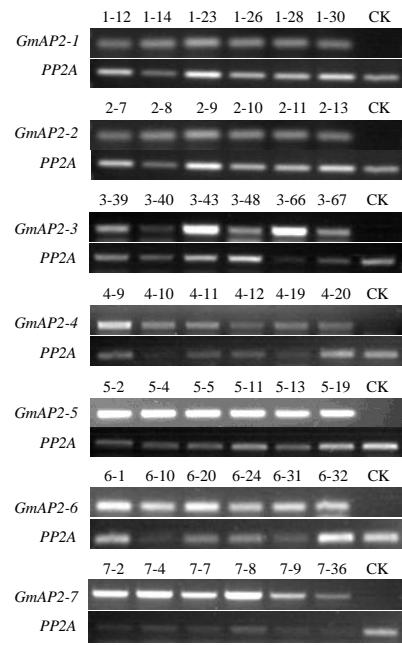
**Figure. S1. Phylogenetic analysis of the ERF family members in soybean and *Arabidopsis*.** The neighbor-joining (NJ) method was applied to construct trees using MEGA X software. Bootstrapping with 500 replications was performed.



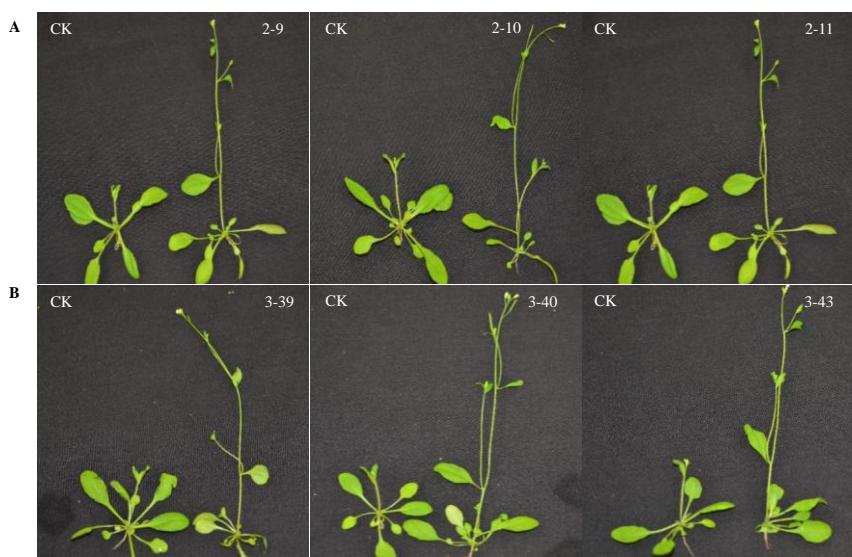
**Figure. S2. Phylogenetic analysis of the RAV family members in soybean and *Arabidopsis*.** The neighbor-joining (NJ) method was applied to construct trees using MEGA X software. Bootstrapping with 500 replications was performed.

GmAP2-1	M W D L N D S P D Q R Q T O R E E E S E - - - - -	G S F C Y S S P S K R V G S F S N S S S S A V V I E D G S D D D E L N E V R - - - - -	55
GmAP2-2	M W D L N D S P D Q R K R E E E S E E - - - - -	G S S S L Y D D K G K R V R V G S V S N S S S S A V V I G D G S E E E Y E E D E E - - - - -	56
GmAP2-3	M L D L N L N A E S T Q - - - N N E S L - - - - -	G D D D N N N N K G K R V R V G S V S N S S S S A V V I G D G S E E E Y E E D E E - - - - -	73
GmAP2-4	M L D L N L N A E S T Q - - - N D E L L - - - - -	V L L D K F F P E A S - - - - - L G T S N S S S V V N A E G G S S N - - - E D S C S - - - - -	48
GmAP2-5	M A M N W L Q S T L T P H L R I D D E F E R E N Q E R G G Y H H M S P S P H L S V M P E R D G S L C D S F S N A A S Q E W Y D S A I G G G N	G Y H H M S P S P H L S V M P E R D G S L C D S F S N A A S Q E W Y D S A I G G G N	77
GmAP2-6	M A G A T N W L T F S T - - - - - H M E M Q Q F G P Y D T T T H S H C F N D S N F V G W T N S K S V M D S Q S S E T Q Q L A V P K M E D F Y F G G N	G P Y D T T T H S H C F N D S N F V G W T N S K S V M D S Q S S E T Q Q L A V P K M E D F Y F G G N	67
GmAP2-7	M L D L N L N A E W T D S F S N G D S P - - - - -	L P S S Q K F F E G S R N Q M A E S G T S N S S V V N A D G S S N G G G D E D S C S - - - - -	0
GmNNC1	M L D L N L N A E W T D S F S N G D S P - - - - -	L P S S Q K F F E G S R N Q M A E S G T S N S S V V N A D G S S N G G G D E D S C S - - - - -	61
AtAP2	- -	- P P N P L V T H Q F F P E M D S - - - - -	71
GmAP2-1	- -	- D S D H P P V T H Q F F P E M D S E L P - - - - -	97
GmAP2-2	- -	- G F G S V Q N E S M D S E L P - - - - -	123
GmAP2-3	- -	- T R A G D V E F A S - - - - - V R K V E G A N E V V A T A T K E L F P V S S E N - - - - -	85
GmAP2-4	- -	- D H Q D L K A M I V P G F K A S G T N S K I T R V A P A A L G - - - - -	111
GmAP2-5	S N E E G P K L E D F L G C Y S N S P A K V F C Q D S Q P D Q N Q S Q D N V S K I N V N V N A P S F C T N N S E I E T G D S L T P S S L L H S F H A Y N D N S H	N Q S Q D N V S K I N V N V N A P S F C T N N S E I E T G D S L T P S S L L H S F H A Y N D N S H	157
GmAP2-6	- -	- T R A D D V Y V T F N F D I L K V E G A N D V Y T - - - - -	0
GmAP2-7	- -	- K E L F P V M S E G - - - - -	0
GmNNC1	- -	- T R A D D V Y V T F N F D I L K V E G A N D V Y T - - - - -	0
AtAP2	- -	- N Q G V V A S G F P R A H W F G V K F C Q S D L A T G S S A G K A T N V A A A V V E P A Q P L K K S R R	123
GmAP2-1	- -	- V T A A A A A G S S S - - - - - E T P G A G - - - - - E T P G A G - - - - - E T P G A G - - - - -	142
GmAP2-2	- -	- V A T A G G G T G V F R A H W V G V K F C Q S - - - - - E T L G T G K S S V E V S Q P M K K S R R	171
GmAP2-3	- -	- W W Q G S S T S S S Q A R K N L M D L P L D H Q M G E V E V V V V Q P Q P Q - - - - - V R K V E G A N E V V A T A T K E L F P V S S E N - - - - -	129
GmAP2-4	A L I P T T N G M Y K S W L A Q T Q F S S D G K P S D G K P S E A N G G N F Q S L S L T M S P S V Q N G V G A I G A H S G E S N C K G S A L T L C D V V A A N G S D D N S N K A V V A V G F D T R - - - - -	N Q S Q D N V S K I N V N V N A P S F C T N N S E I E T G D S L T P S S L L H S F H A Y N D N S H	237
GmAP2-5	- -	- M K R S P A S S G S S T S S V S Y G F E A P I E K E P R K H P R R R N L S Q C K - - - - - K V A H	156
GmAP2-6	- -	- M K R S P A S S G S S T S S V S Y G F E A P I E K E P R K H P R R R N L S Q C K - - - - - K V A H	46
GmAP2-7	- -	- M K R S P A S S G S S T S S V S Y G F E A P I E K E P R K H P R R R N L S Q C K - - - - - Q N Q T T	149
GmNNC1	- -	- M K R S P A S S G S S T S S V S Y G F E A P I E K E P R K H P R R R N L S Q C K - - - - - K V A H	149
AtAP2	G P R S R S S Q R R G V T F Y Y R T G R W S S H I W D C G - - - - -	K Q V Y L G G F D T A H A A B A D R A A I K F R G E V A D I N F N I E D Y E E D	193
GmAP2-1	G P R S R S S Q R R G V T F Y Y R T G R W S S H I W D C G - - - - -	K Q V Y L G G F D T A H A A B A D R A A I K F R G E V A D I N F N I E D Y E E D	241
GmAP2-2	G P R S R S S Q R R G V T F Y Y R T G R W S S H I W D C G - - - - -	K Q V Y L G G F D T A H A A B A D R A A I K F R G E V A D I N F N I E D Y E E D	241
GmAP2-3	G P R S R S S Q R R G V T F Y Y R T G R W S S H I W D C G - - - - -	K Q V Y L G G F D T A H A A B A D R A A I K F R G E V A D I N F N I E D Y E E D	199
GmAP2-4	G P R S R S S Q R R G V T F Y Y R T G R W S S H I W D C G - - - - -	K Q V Y L G G F D T A H A A B A D R A A I K F R G E V A D I N F N I E D Y E E D	199
GmAP2-5	T F G Q R T R V T R H W T G Y Y A H L L W D N S C R E K E G Q T R X K G Q V Y V G G Y D R E E K A A A A Y D R A A I K F R G D A D I N F N I L V D Y E E E	T F G Q R T R V T R H W T G Y Y A H L L W D N S C R E K E G Q T R X K G Q V Y V G G Y D R E E K A A A A Y D R A A I K F R G D A D I N F N I L V D Y E E E	317
GmAP2-6	T F G Q R T R V T R H W T G Y Y A H L L W D N S C R E K E G Q T R X K G Q V Y V G G Y D R E E K A A A A Y D R A A I K F R G D A D I N F N I L V D Y E E E	T F G Q R T R V T R H W T G Y Y A H L L W D N S C R E K E G Q T R X K G Q V Y V G G Y D R E E K A A A A Y D R A A I K F R G D A D I N F N I L V D Y E E E	236
GmAP2-7	T F G Q R T R V T R H W T G Y Y A H L L W D N S C R E K E G Q T R X K G Q V Y V G G Y D R E E K A A A A Y D R A A I K F R G D A D I N F N I L V D Y E E E	T F G Q R T R V T R H W T G Y Y A H L L W D N S C R E K E G Q T R X K G Q V Y V G G Y D R E E K A A A A Y D R A A I K F R G D A D I N F N I L V D Y E E E	236
GmNNC1	G P R S R S S Q R R G V T F Y Y R T G R W S S H I W D C G - - - - -	K Q V Y L G G F D T A H A A B A D R A A I K F R G E V A D I N F N I E D Y E E D	298
AtAP2	D K Q T N L T K E E F V H V L R Q Q P F P R G S S Q S - - - - -	P Q D H N L D L S L G N S A N S K H S Q D M R L R M N Q Q D S L H S F N E V L - - - - -	339
GmAP2-1	D K Q M T N L T K E E F V H V L R Q Q P F P R G S S Q S - - - - -	P Q D H N L D L S L G N S I S R H N Q D S L H S F N E V L - - - - -	355
GmAP2-2	D L K Q M S N L T K E E F V H V L R Q Q P F P R G S S Q S - - - - -	P Q D H N L D L S L G N S T S N P G D N Q A L S R N P A V T H D Q H M P P S E S - - - - -	320
GmAP2-3	D L K Q M K N L S K E E F V H V L R R Q H S R G Q S S N Y R Q V G T L L K R K C G R W E A A R M Q F L G K V V Y Y L G L F D T E I V A A R Y D D A A I K C N R I	P Q D H N L D L S L G N S T S N P G D N Q A L S R N P A V T H D Q H M P P S E S - - - - -	278
GmAP2-4	D L K Q M K H M K H T R R H Q H O Q W O R V T R H W T G Y Y A H L L W D N S C R E K E G Q T R X K G Q V Y V G G Y D R E E K A A A A Y D R A A I K C N R I	P Q D H N L D L S L G N S T S N P G D N Q A L S R N P A V T H D Q H M P P S E S - - - - -	345
GmAP2-5	E L E E M E H A G R Q E F I A S L L R R Q S G F S G L S K G R A S S G R V T R H W T G Y Y A H L L W D N S C R E K E G Q T R X K G Q V Y V G G Y D R E E K A A A A Y D I I A A I K F R G	P Q D H N L D L S L G N S T S N P G D N Q A L S R N P A V T H D Q H M P P S E S - - - - -	316
GmAP2-6	E L E E M D W N S R Y E E T F Y Y A H L L W D N S C R E K E G Q T R X K G Q V Y V G G Y D R E E K A A A A Y D I I A A I K F R G	P Q D H N L D L S L G N S T S N P G D N Q A L S R N P A V T H D Q H M P P S E S - - - - -	206
GmAP2-7	E L E E M D W N S R Y E E T F Y Y A H L L W D N S C R E K E G Q T R X K G Q V Y V G G Y D R E E K A A A A Y D I I A A I K F R G	P Q D H N L D L S L G N S T S N P G D N Q A L S R N P A V T H D Q H M P P S E S - - - - -	206
GmNNC1	D L K Q M N U L S K E E F V H V L R Q Q P F P R G S S Q S - - - - -	P Q D H N L D L S L G N S T S N P G D N Q A L S R N P A V T H D Q H M P P S E S - - - - -	298
AtAP2	D Q V T N E D P I Y D P L L E L L N A E S S G N P T T - - - - -	P Q D H N L D L S L G N S A N S K H S Q D M R L R M N Q Q D S L H S F N E V L - - - - -	435
GmAP2-1	K E A V T N E D P S I Y D P L L E L L N A E S S G N P T T - - - - -	P Q D H N L D L S L G N S I S R H N Q D S L H S F N E V L - - - - -	502
GmAP2-2	K E A V T N E D P S I Y D P L L E L L N A E S S G N P T T - - - - -	P Q D H N L D L S L G N S T S N P G D N Q A L S R N P A V T H D Q H M P P S E S - - - - -	533
GmAP2-3	P E E A V T N E E P S T Y E S E S M K P E A I N E - - - - -	P Q D H N L D L S L G N S T S N P G D N Q A L S R N P A V T H D Q H M P P S E S - - - - -	384
GmAP2-4	P E E A V T N E E P S T Y E S E S M K P E A I N E - - - - -	P Q D H N L D L S L G N S T S N P G D N Q A L S R N P A V T H D Q H M P P S E S - - - - -	345
GmAP2-5	T S A V T N E D P S I Y D P L L E L L N A E S S G N P T T - - - - -	P Q D H N L D L S L G N S T S N P G D N Q A L S R N P A V T H D Q H M P P S E S - - - - -	345
GmAP2-6	T S A V T N E D P S I Y D P L L E L L N A E S S G N P T T - - - - -	P Q D H N L D L S L G N S T S N P G D N Q A L S R N P A V T H D Q H M P P S E S - - - - -	461
GmAP2-7	T S A V T N E D P S I Y D P L L E L L N A E S S G N P T T - - - - -	P Q D H N L D L S L G N S T S N P G D N Q A L S R N P A V T H D Q H M P P S E S - - - - -	346
GmNNC1	T N -	P Q D H N L D L S L G N S T S N P G D N Q A L S R N P A V T H D Q H M P P S E S - - - - -	273
AtAP2	- G L G -	P G G Q D N Q D L L N L G L A T P G P G P K E N W Q Q L H F P S I P Y N T H G G R S S K M E	365
GmAP2-1	- G L G -	P G G Q D N Q D L L N L G L A T P G P G P K E N W Q Q L H F P S I P Y N T H G G R S S K M E	435
GmAP2-2	- G L G -	P G G Q D N Q D L L N L G L A T P G P G P K E N W Q Q L H F P S I P Y N T H G G R S S K M E	502
GmAP2-3	- G L G -	P G G Q D N Q D L L N L G L A T P G P G P K E N W Q Q L H F P S I P Y N T H G G R S S K M E	533
GmAP2-4	- G L G -	P G G Q D N Q D L L N L G L A T P G P G P K E N W Q Q L H F P S I P Y N T H G G R S S K M E	485
GmAP2-5	- G L G -	P G G Q D N Q D L L N L G L A T P G P G P K E N W Q Q L H F P S I P Y N T H G G R S S K M E	476
GmAP2-6	- G L G -	P G G Q D N Q D L L N L G L A T P G P G P K E N W Q Q L H F P S I P Y N T H G G R S S K M E	574
GmAP2-7	- G L G -	P G G Q D N Q D L L N L G L A T P G P G P K E N W Q Q L H F P S I P Y N T H G G R S S K M E	447
GmNNC1	- G L G -	P G G Q D N Q D L L N L G L A T P G P G P K E N W Q Q L H F P S I P Y N T H G G R S S K M E	493

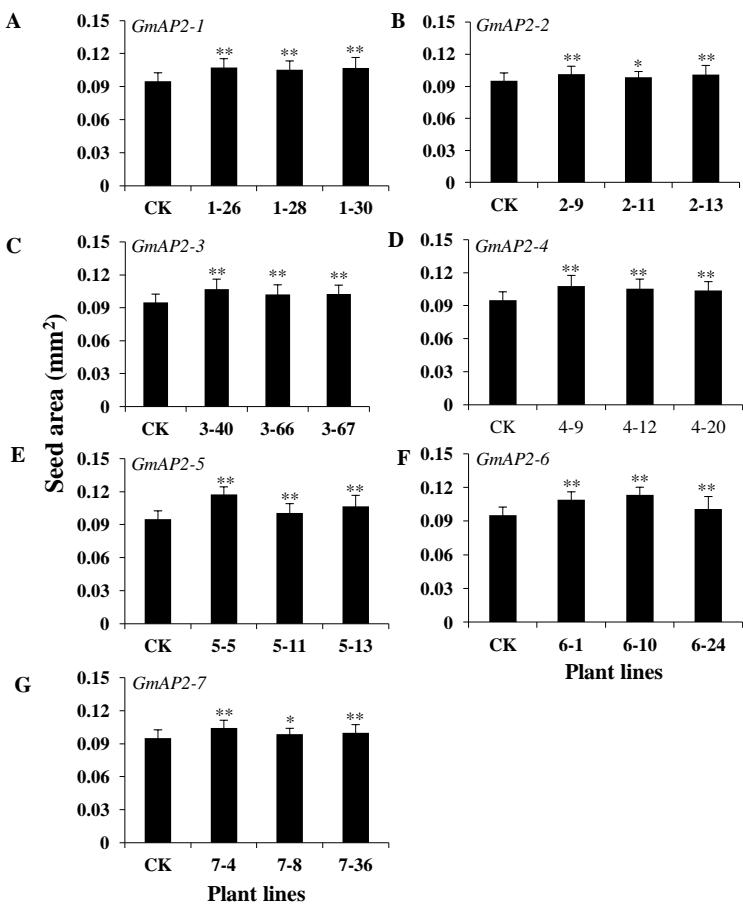
**Figure. S3. Sequence alignment of the candidate AP2 proteins in soybean with those from *Arabidopsis*.** The alignment was performed by using software DNAMAN. The two AP2 domains were boxed with red color. All the sequences for soybean used in the figure are retrieved from the Soybean Database (<http://soykb.org/>) and AtAP2 are retrieved from the Arabidopsis Database (<https://www.arabidopsis.org/>). The accession number are as followed (shown in parenthesis): *Arabidopsis thaliana*: AtAP2 (At4g36920); *Glycine max*: GmAP2-1 (Glyma01g39520.3), GmAP2-2 (Glyma05g18041.1), GmAP2-3 (Glyma15g04930.1), GmAP2-4 (Glyma13g40470.1), GmAP2-5 (Gm16g00950.2), GmAP2-6 (Glyma08g38190.2), GmAP2-7 (Glyma15g34770.1) and GmNNC1 (Glyma12g07800.1).



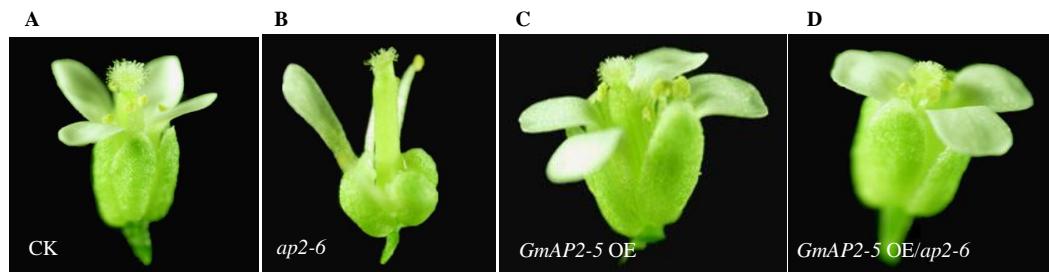
**Figure. S4. Relative transcript levels of the candidate *GmAP2* genes in the transgenic *Arabidopsis* lines detected by RT-PCR.** CK represents *Arabidopsis* wild type, the other numbers represent different transgenic lines in T<sub>1</sub> generation (*GmAP2-1*, *GmAP2-2*, *GmAP2-3*, *GmAP2-4*, *GmAP2-5*, *GmAP2-6*, *GmAP2-7*). The *PP2A* gene (At1g13320) was used as the reference gene.



**Figure. S5. Representative early flowering of the *GmAP2* over-expression lines in *Arabidopsis*.** All plants were grown in the same tray to ensure the same growth condition (16-h light/8-h dark) at 22 °C. The 30-day-old plants were photographed. (A) The *GmAP2-2* over-expression lines (2-9, 2-10 and 2-11) in *Arabidopsis*. (B) The *GmAP2-3* over-expression lines (3-39, 3-40 and 3-43) in *Arabidopsis*. CK, the wild type *Arabidopsis* as control.



**Figure. S6. Seed area of the transgenic lines over-expressing seven individual *GmAP2* genes in the *Arabidopsis* wild type.** Seeds were harvested from 10 plants each line, and 40 seeds each line were photographed. ImageJ software was used to calculate the seed area. CK indicates the wild type *Arabidopsis*. Data are presented as mean  $\pm$  SD, Student's t test ( $n=40$ , \* $P < 0.05$ , \*\* $P < 0.01$ ). (A-G) The over-expression lines for *GmAP2-1* (A), *GmAP2-2* (B), *GmAP2-3* (C), *GmAP2-4* (D), *GmAP2-5* (E), *GmAP2-6* (F), *GmAP2-7* (G).



**Figure. S7. Representative flower structure of the *GmAP2* over-expression lines in *Arabidopsis*.** All plants were grown in the same tray to ensure the same growth condition (16-h light/8-h dark) at 22 °C. The flowers of the 42-day-old plants were photographed. (A) CK, the wild type *Arabidopsis* as control. (B) The *ap-6* mutant line. (C) The transgenic lines over-expressing *GmAP2-5* in the wild type. (D) The transgenic lines over-expressing *GmAP2-5* in the *ap-6* mutant background.