



Fig. S1

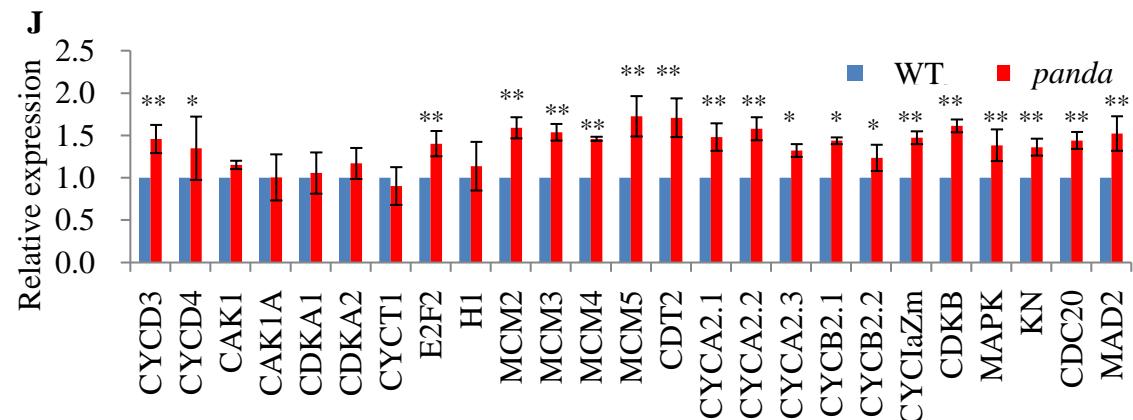
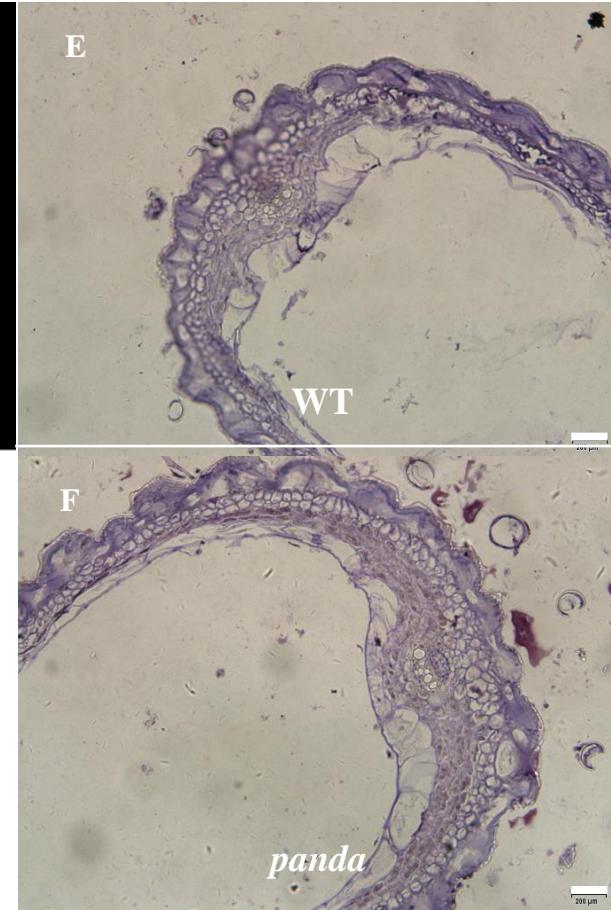
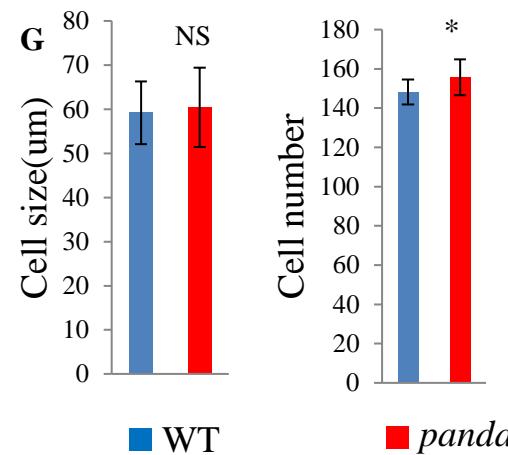
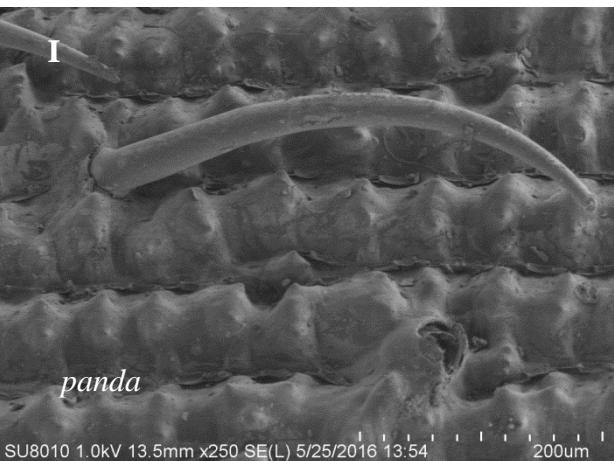
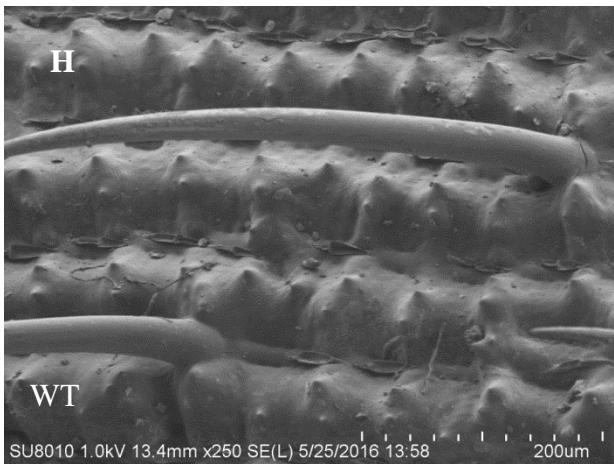
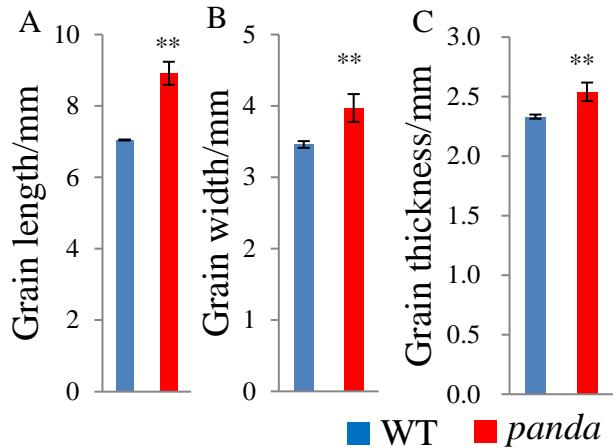


Fig. S2

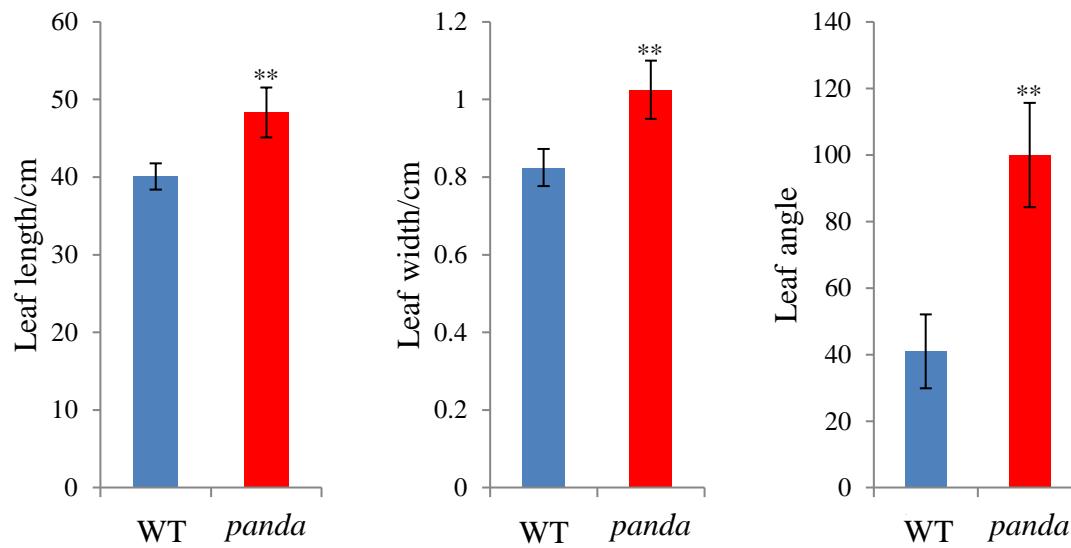


Fig. S3

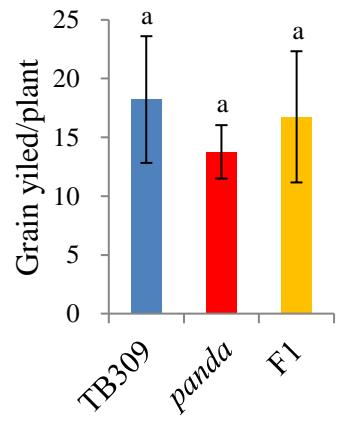
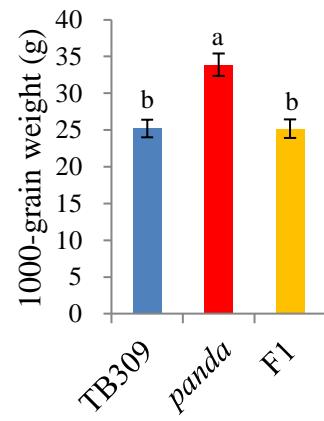
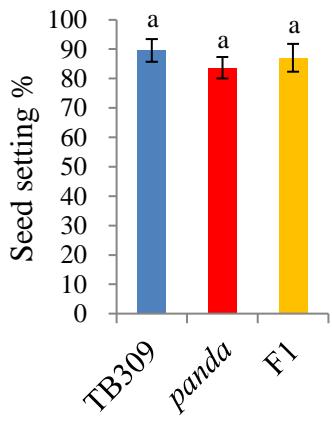
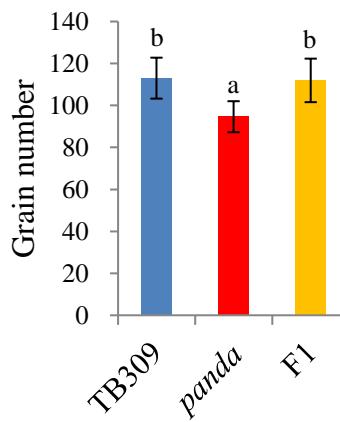
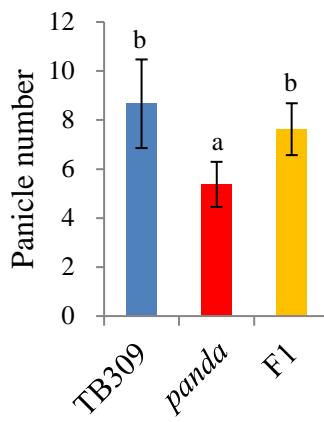
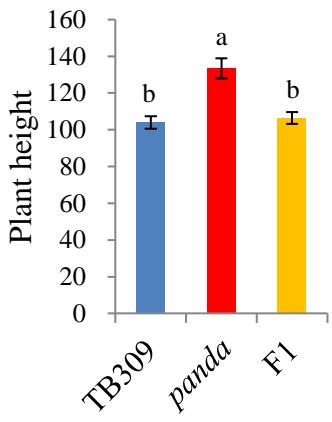


Fig. S4

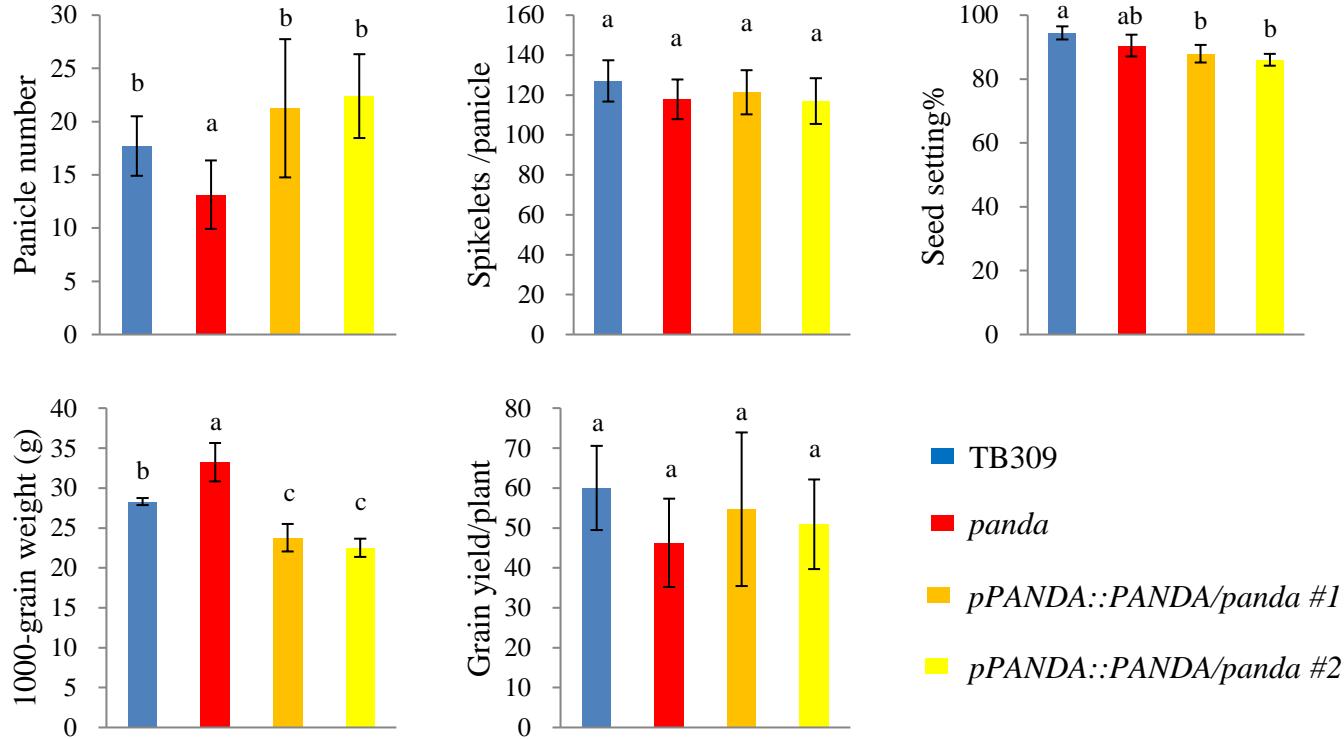
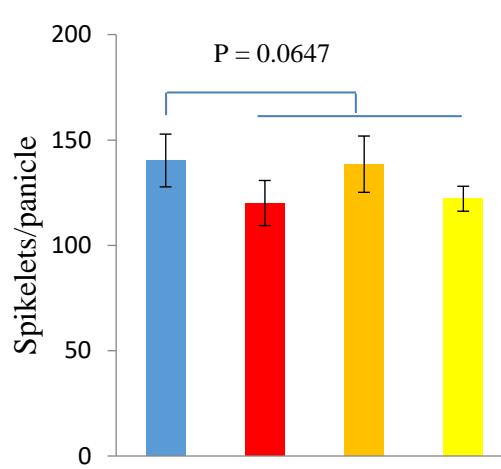
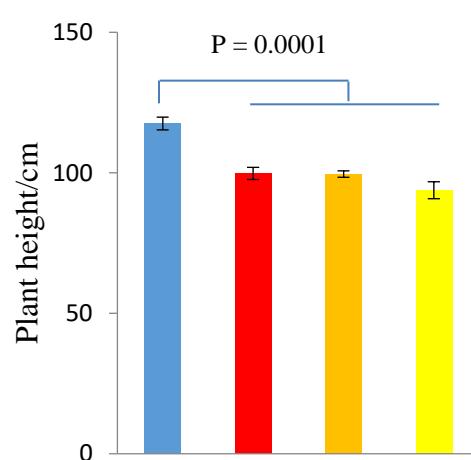
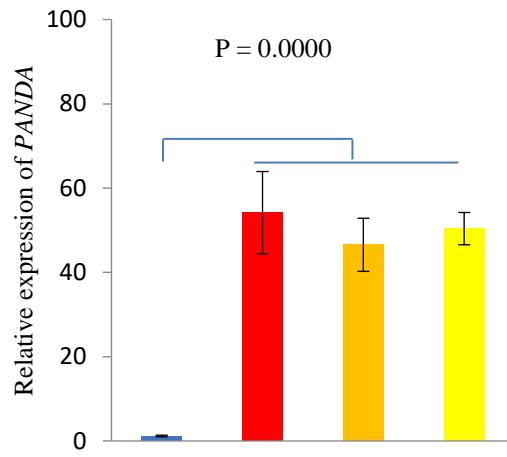


Fig. S5



- TB309
- *pUBI::PANDA-Flag #1*
- *pUBI::PANDA-Flag #2*
- *pUBI::PANDA-Flag #3*

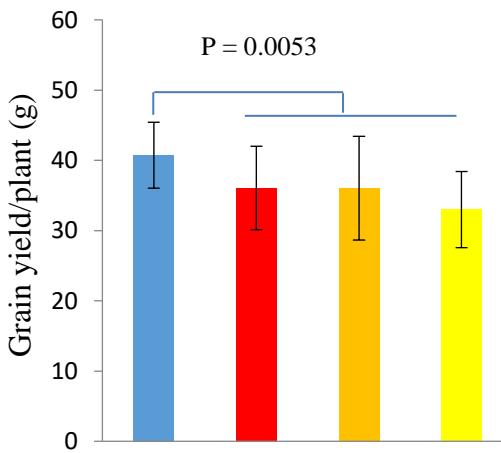
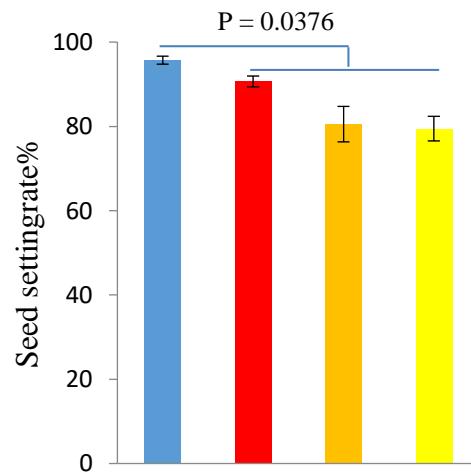


Fig. S6



- Genit (*indica*)
- *pPANDA::PANDA/Genit #1*
- *pPANDA::PANDA/Genit #2*
- *pPANDA::PANDA/Genit #3*

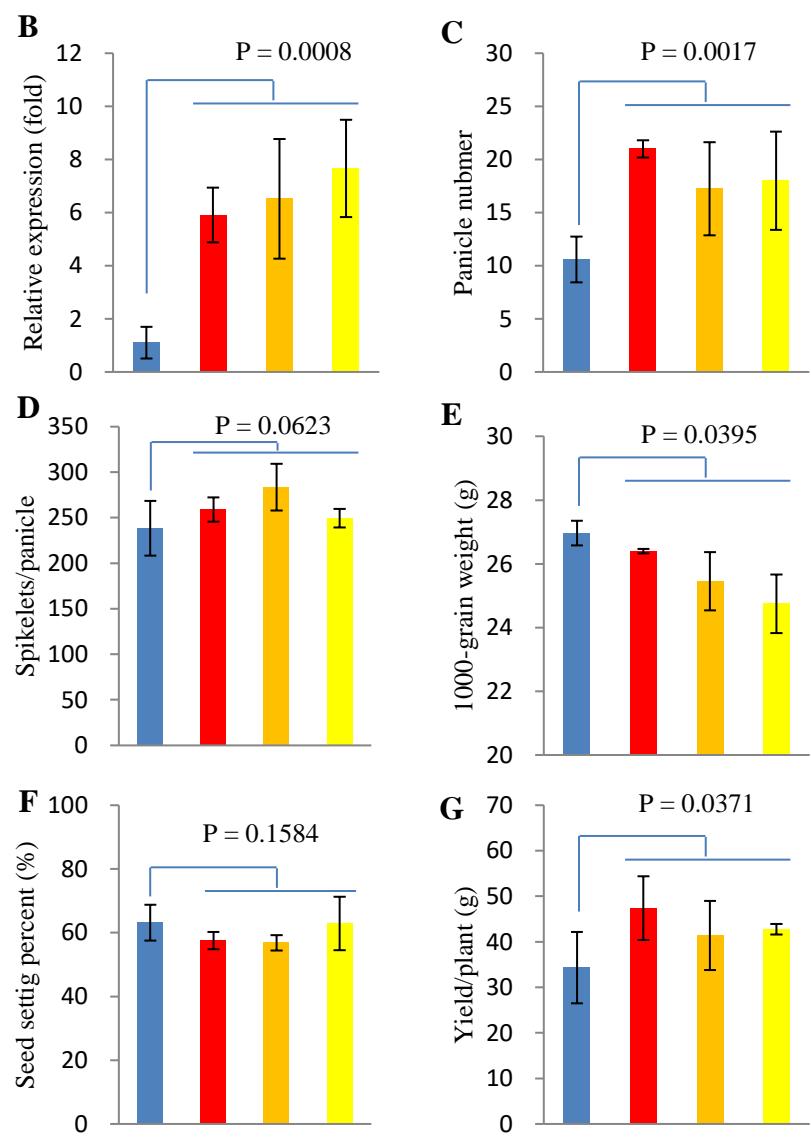


Fig. S7

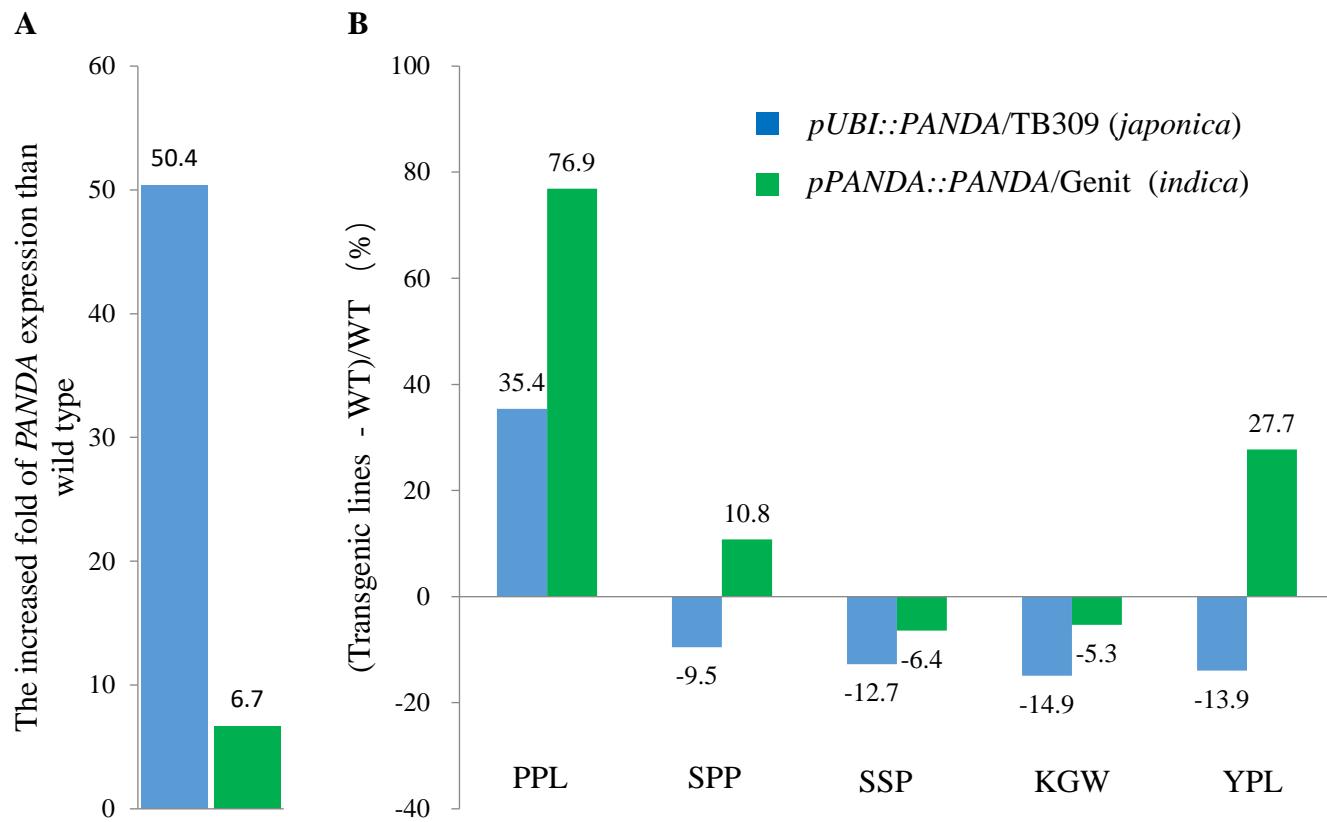


Fig. S8

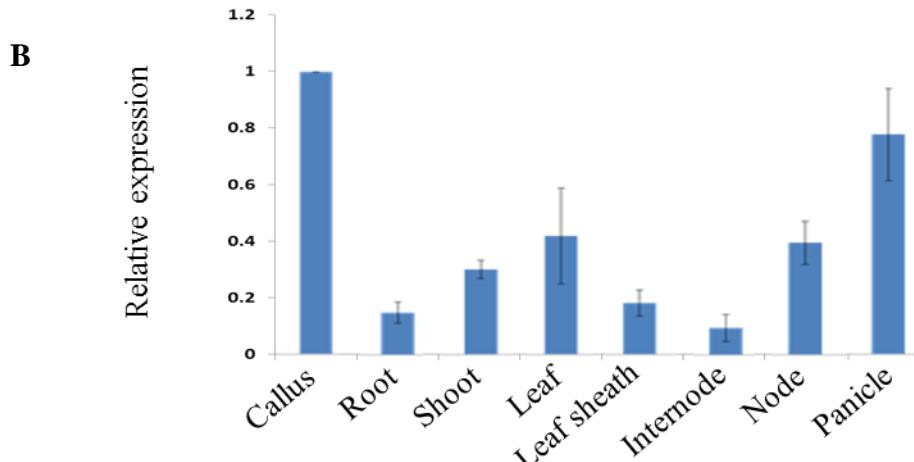
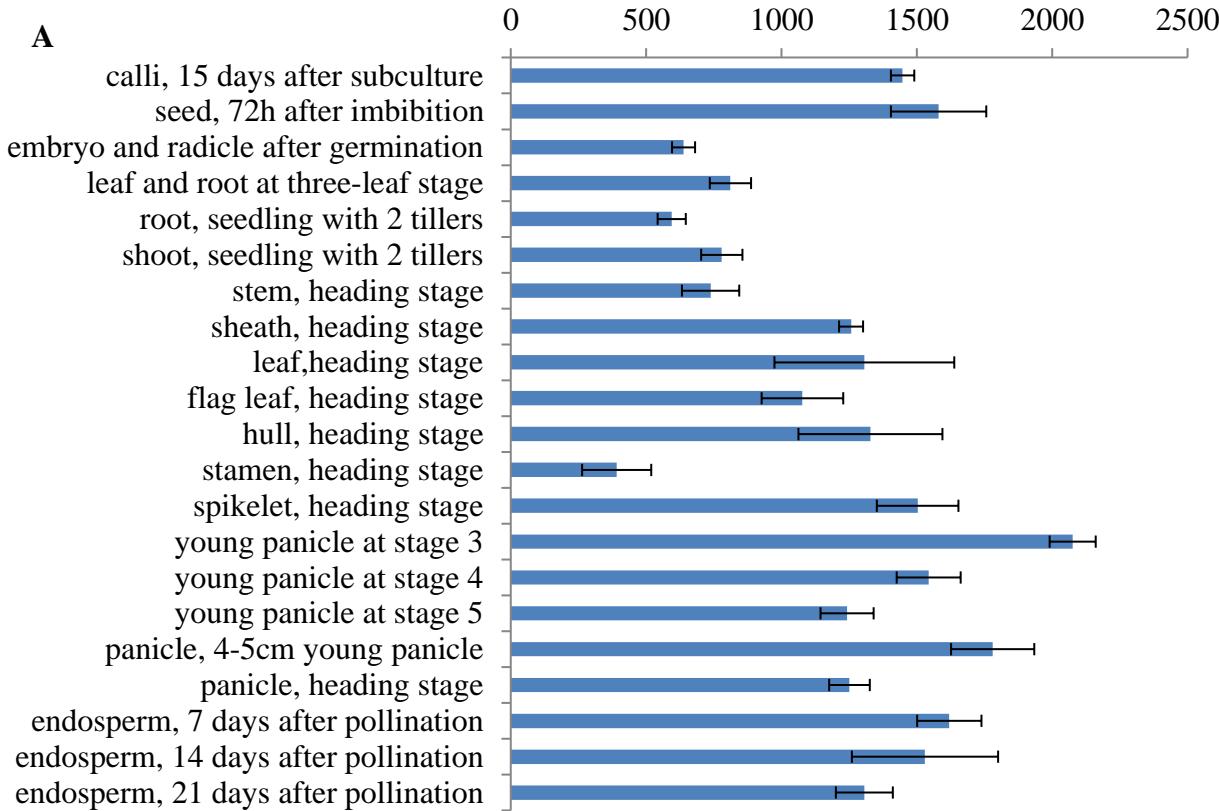


Fig. S9

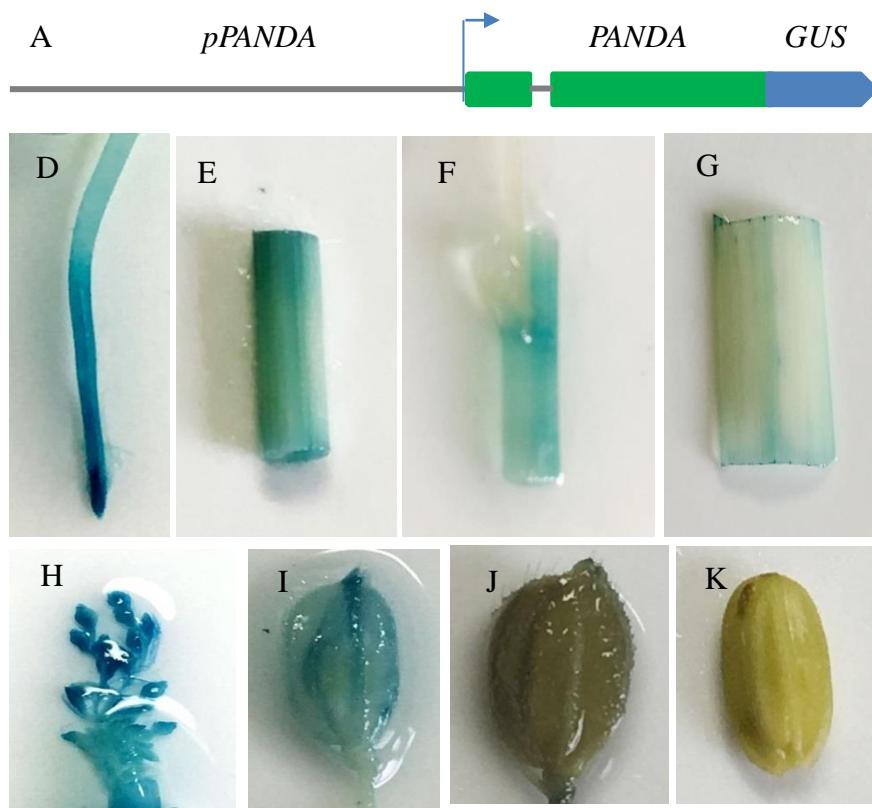
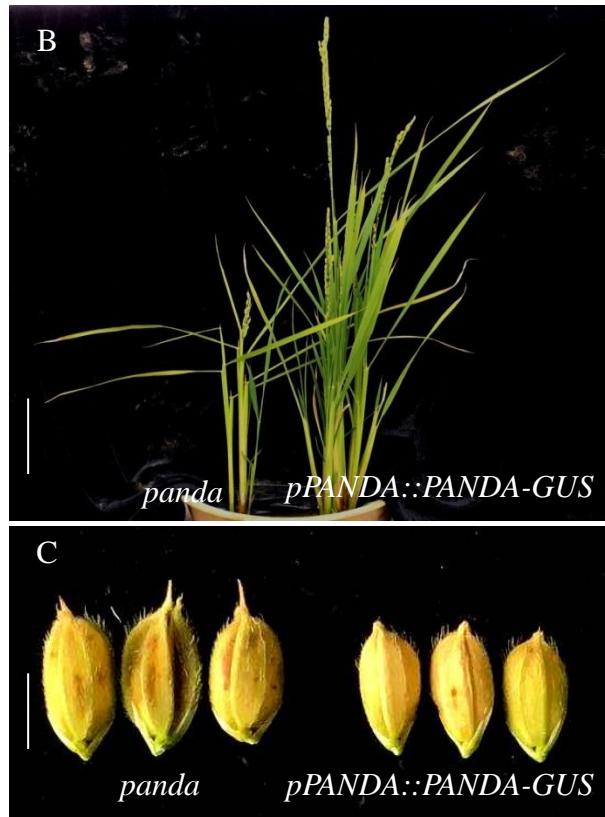


Fig. S10

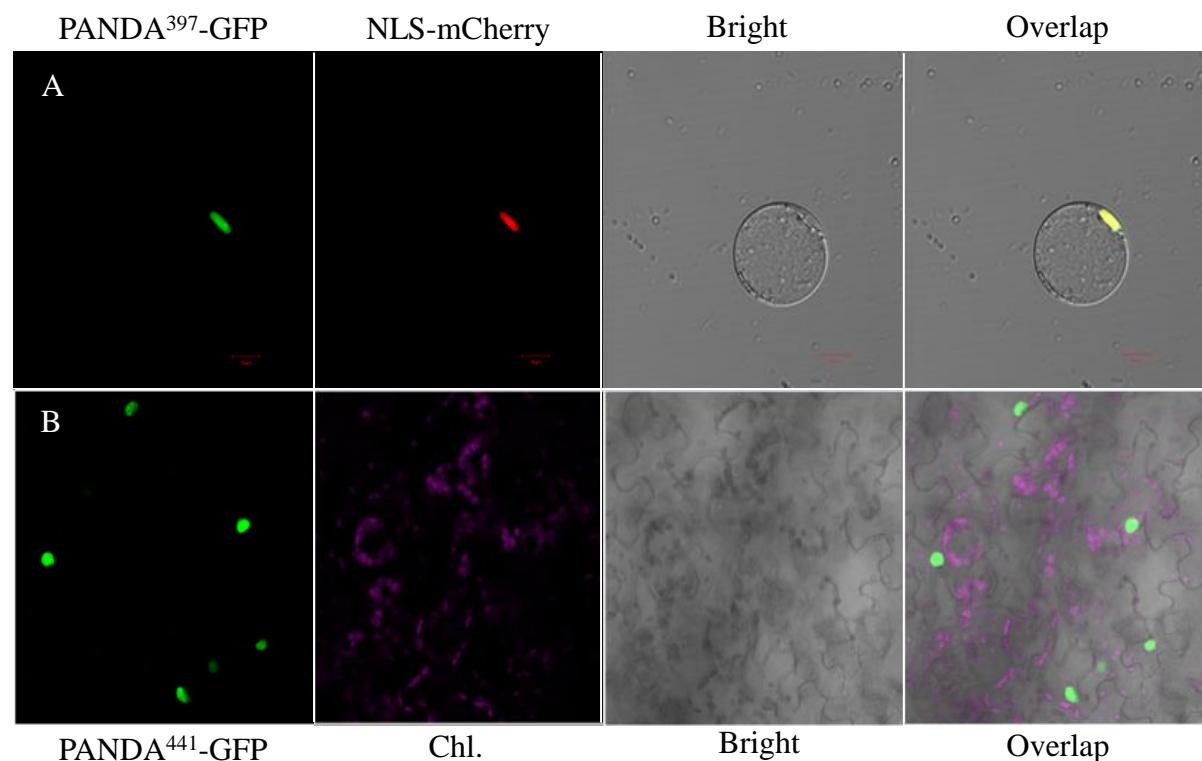


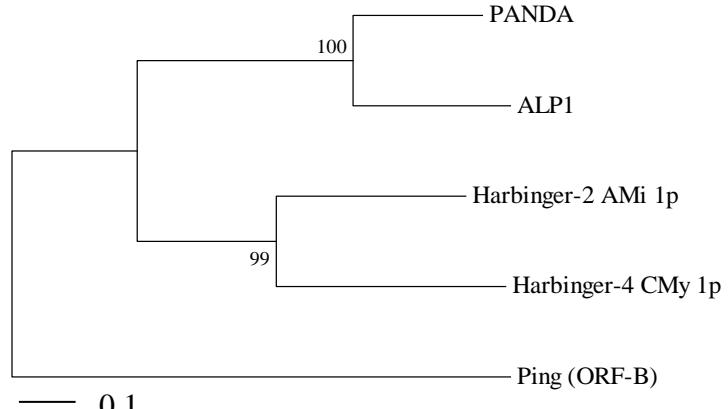
Fig. S11

A

Query ID	Subject ID	Cover %	Identify %	E value
PANDA	ALP1_Arabidopsis	83.0%	64.4%	2.00E-180
PANDA	Harbinger-4_CMy_1p	55.0%	36.1%	3.00E-47
PANDA	Harbinger-2_AMi_1p	62.0%	31.1%	3.00E-34
PANDA	Ping (ORF-B)	57.0%	23.4%	4.00E-09

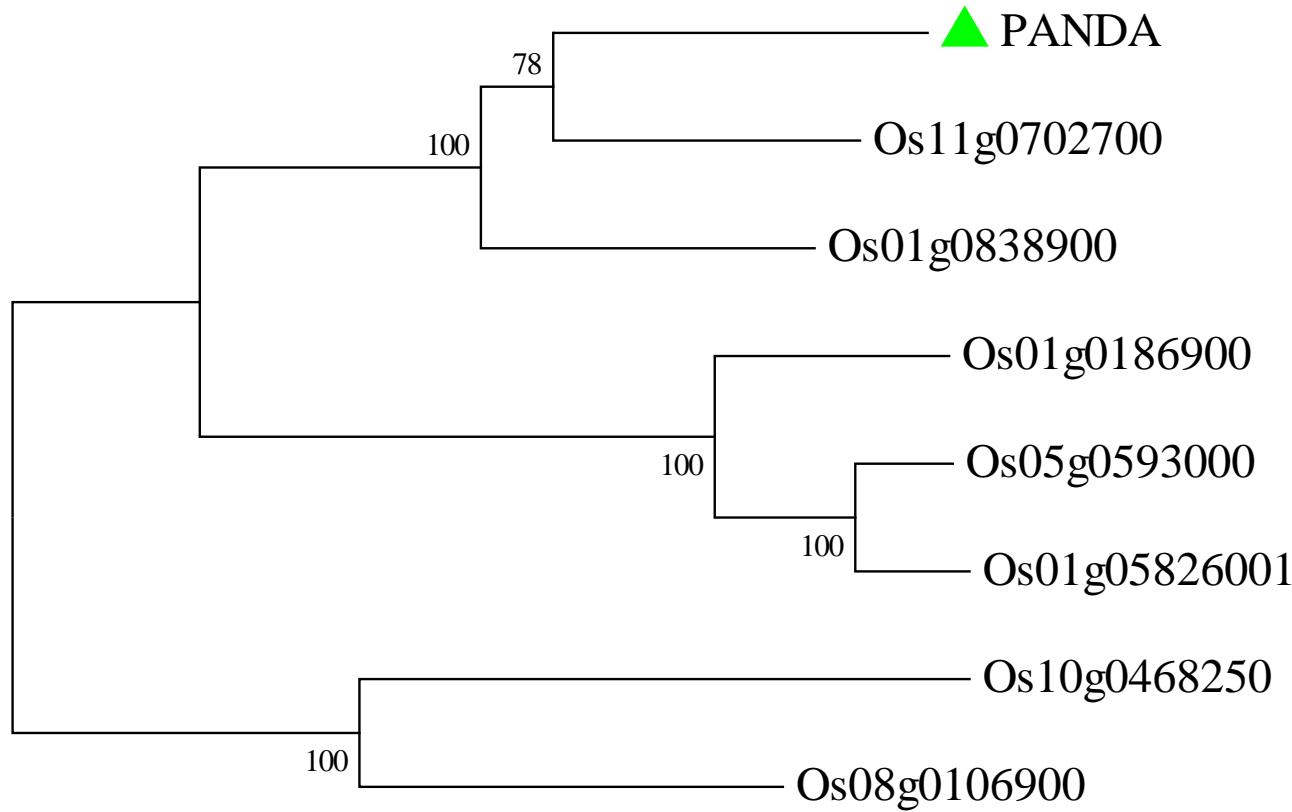
B

PING IFRRRFRMYRPLFLRIVDALGQWSD-YFTQRVDAAGRQGLSPLQKCTAAIRQLATGSGAD 144
 PANDA AFRYFFRTSRTFDYICSIVREDLISRPSSGLINIEGRLLSVEKQVAIAMRRLASGDSQV 168
 Harbinger-2_AMi_1p RWTQTFRMSRGTFMHLVAQVAPNIERQ----DTVMRPALTPEKRVIAIMRLATPASLR 187
 : ** * * : : *: :: *: ::**: .
 PING ELDEYLKIGETTAMDAMKNFKVGIREVFGERYLRRPTVEDTERLLELGERRGPGMFCSI 204
 PANDA SVGAAGVGQSTVSQVTWRFIESMEERARHHLVWPQERMEQIKARFEAESGLPNCCGAI 228
 Harbinger-2_AMi_1p YVAHSFGVGKSTAGQAVIDVCGAIQDTLADRVRILAD—PGEVVAGF-GALGFPNCVGAL 244
 : : ::*:: : : : : : *: *: *:
 PING DCMHWQWERCPATAWKQQFTRGDQKVPTLILEAVASHDLWIWAFFGVAGSNNDINVLSRS 264
 PANDA DATHTIIMTLPAVESSEDWC-DPAKNYSMFLQGIVDDEMRFIDIVTGWPGSMMPSRLLKCS 287
 Harbinger-2_AMi_1p DGTHIPILRPPG-GGRQYI-NRRGSNSVVLLEAVVDHRGRFTHYITGWAGSARDAHVLRS 302
 * * : : . . : . *: . . : . * * * . : * *
 PING TVFINEL-KGQAPRVQYMVNQNYNEGFLADGIYPEWKVFAKSYRLPIT-EKEKLYAQH 322
 PANDA GFFKHCDAGTRLDPVMVSAENGIREYIIVGNNCYPLLWLMTPYEGESLSAPMASFNAR 347
 Harbinger-2_AMi_1p PLPGLMQARTFAPGIQDLTIGDVSIIPPVIVADAAYPLLWLMRPFPGPLD-ARQQRYNEA 361
 . : : . : . *: : : : :
 PING QEGARKDIERAFGVLRQRFICILRKPARLYDRGVLRDVLCIILHNMIVEDEKEARL-- 379
 PANDA QKAARTLQPRALSRLKGWSRILNKVMWRPDKNKLPSIILVOCLLHNIIIDCEDELLPDVQ 407
 Harbinger-2_AMi_1p LARCRCCTVEQAFGHLKGRWRSLATRLE-AAPQHIPCIIAACVLHNVCESRGEVFEPQ-- 418
 . * : *: . *: : * : : : : : *: ***: . .

D**C**

PANDA	#1	GGAGAAGCAG	GTGGCGATTG	CCATGAGGAG	GCTGG:C:GT
Harbinger-2_AMi	#1	GGAGAAGCGT	GTGCCCATAG	CCATCATGAG	GCTGGCACAC
		* * *	*	*	* ***
PANDA	#41	CGGGCGATTTC	GCAGGTGTCG	GTGGGGCGG	CTTTGGTGT
Harbinger-2_AMi	#41	CCTGCCAGCC	TCAGGTAT::	GTGGCCCACT	CCTTGGGGT
		* * * * *	* ***	*****	* *
PANDA	#81	CGGGCAGTC	ACCGTCTCG:	CAGG:TGACT	TGGAGGTTCA
Harbinger-2_AMi	#81	GGGAAAGTCC	ACCG:CTGGC	CAGGCTGTCT	TGGATG:T:A
		* *	* * *	* *	* * *
PANDA	#121	T:CGAGTCGA	TGGAAGAGCG	GGCTCGGCAT	CATCTGGTGT
Harbinger-2_AMi	#121	TGTGGGGCCA	TCCAGGA:CA	CCCT:AGC::	CGAC:CGAGT
		* * * * *	* * * * * * *	* * * * *	* * * * *
PANDA	#161	GGCCCGGGCA	GG:AGAGGAT	GGAGCAGATC	AAGGCAGGTT
Harbinger-2_AMi	#161	CATCC:GGCT	GGCCGACCCA	GG:GGAGGTG	GTGGCAGGGT
		* * * * *	* * * * * * *	* * * * *	* * * * *
PANDA	#201	TCGAGGCCGA	GTCCGGTCTG	CCGAA:T:TG	TTGCGGGGCC
Harbinger-2_AMi	#201	TTGGGGCC::	CTTGGGT:TC	CCCAACTGTG	TAGGGGCC:C
		* * *	* * * * *	* * * *	* * *
PANDA	#241	ATCGATGCGA	CCCACAT		
Harbinger-2_AMi	#241	:TCGATGGGA	CCCACAT		
		*	*		

Fig. S12



0.10

Fig. S13

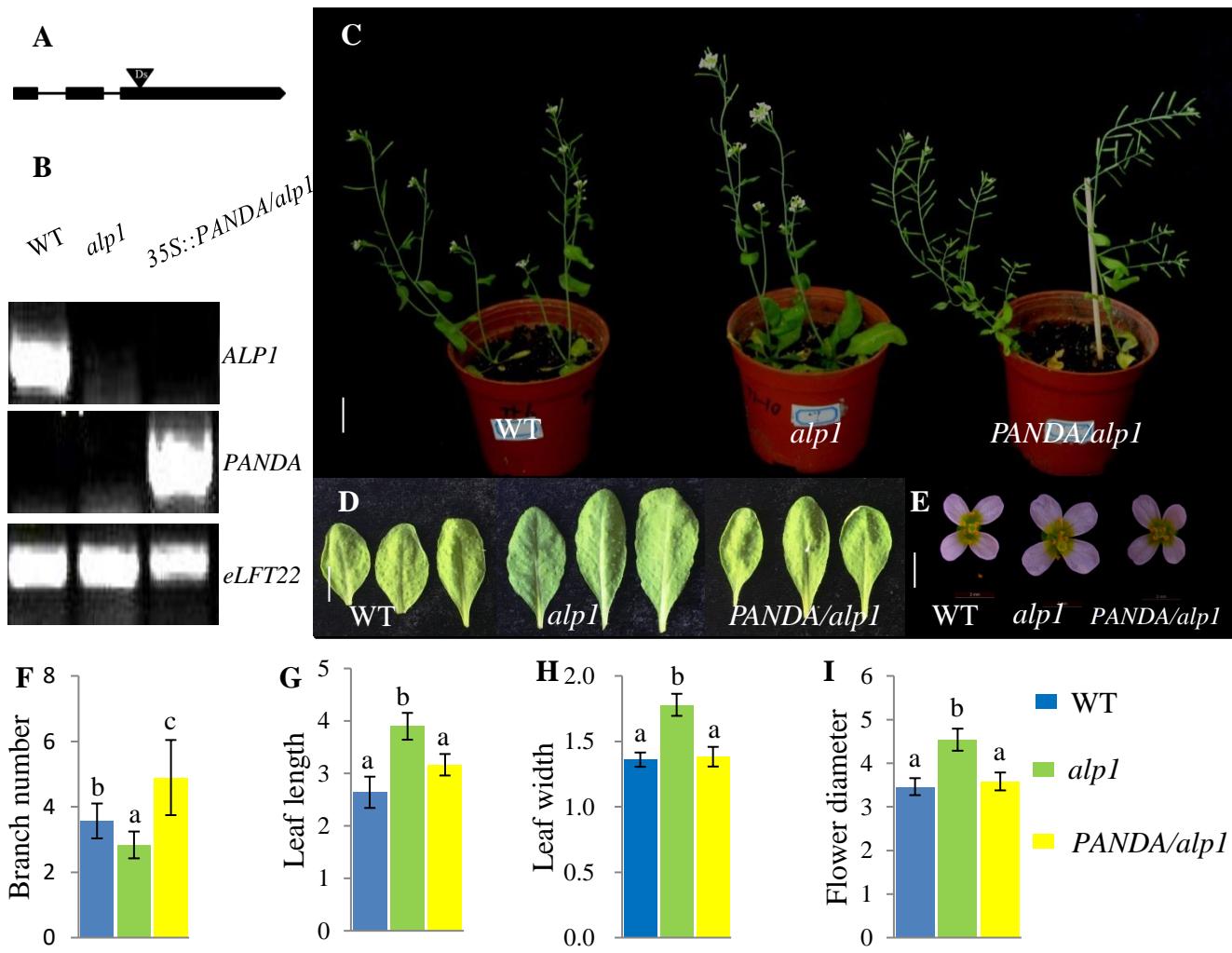


Fig. S14

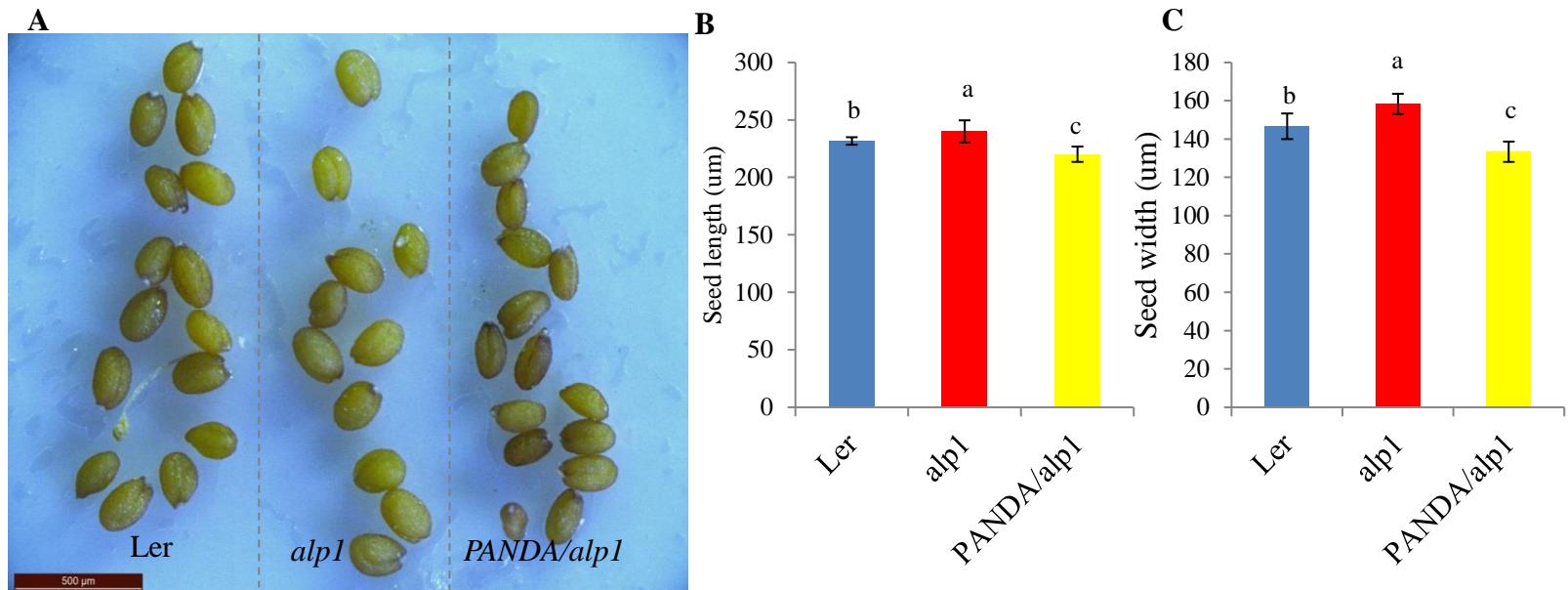
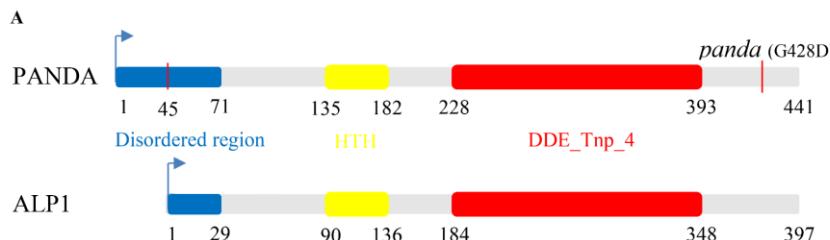


Fig. S15



B

ALP1		MAPVRQQKKKKPLD	16
PANDA	MPKKTRKKNPKSRRGRKRGGRGGREKKVEEISSSSSSRGRGRRRMAPYVKSKKGRKSKL		60
	*****. .**. *;: * *		
ALP1	EAKKLAKNKKKKVNAVPLDPEAIDCDWWDTFWLRNSS--PSVPSDEDYAFKHFFRASKT		74
PANDA	SGK-LKIVKYGGQAPPLPPPELRGLDTEWWYTFLHKHSELGLSAPSDEGEAFRYFFRTSR		119
	. . * * . * . : * : . . * ; ** ** : . : . * . ****. * . : ; *** : * :		
ALP1	TFSYICSLVREDLISRPPSGLINIEGRLLSVEKQVAIALRRLASGDSQVSFGAAFGVGQS		134
PANDA	TFDYICSLVREDLISRPPSGLINIEGRLLSVEKQVAIAMRRLASGDSQVSFGAAFGVGQS		179
	. **;*****;*****;*****;*****;*****;*****;*****;		
ALP1	TVSQVTWRFIEALEERAKHHLRWPDSDRIEEIKSKFEEMYGLPNCCGAIDITHIIMTLPA		194
PANDA	TVSQVTWRFIESMEERARHHLVWPQMERMEQIKARFEAESGLPNCCGAIDATHIIMTLPA		239
	*****;*****;*** . * . ; * : * ; * ; * . *****;*****;		
ALP1	VQASDDWCQEKNSMFLQGVFDHEMRFLNMTGPGGMVTSKLLKGFFKLCEAQI		254
PANDA	VESSEDWCDAKNSMFLQGIVDDEMRFIDIVTGWPMSMFSRLLKGCGFFKHCDAGTRL		299
	*. : *;****. ****;*. *, ****; : ; *****, * . *. ; *** **** * : . *		
ALP1	DGNPKTLSQGAQIREYVVGGISYPILLPWLITPHDSHPSDSMVAFNERHEKVRSAATAF		314
PANDA	DGPVMVSAENGIREYIVGNNCYLLPWLMTPYEGESLSAPMASFNARQKAARTLGPRAL		359
	** . . : . : * ; * . . * ; * ; * ; * . : * . ; * ; . * ; :		
ALP1	QQLKGWSRILSKVMWRPDRRKLPSTILVCCLLHNIIIDCGDYLQEDVPLSGHHDGYADR		374
PANDA	SRLKGWSRILNKVMWRPDKNKLPSIILVCCLLHNIIIDCEDELLPDVQLPDHHDTGYSEE		419
	. ;*****;*****; . ;*****;***** * * ** * , ***;*:..		
ALP1	YCKQTEPLGSELRGCLTEHLLR	396	
PANDA	KCEQVDPNGKIMRDVITGYLQI	441	
		

Fig. S16

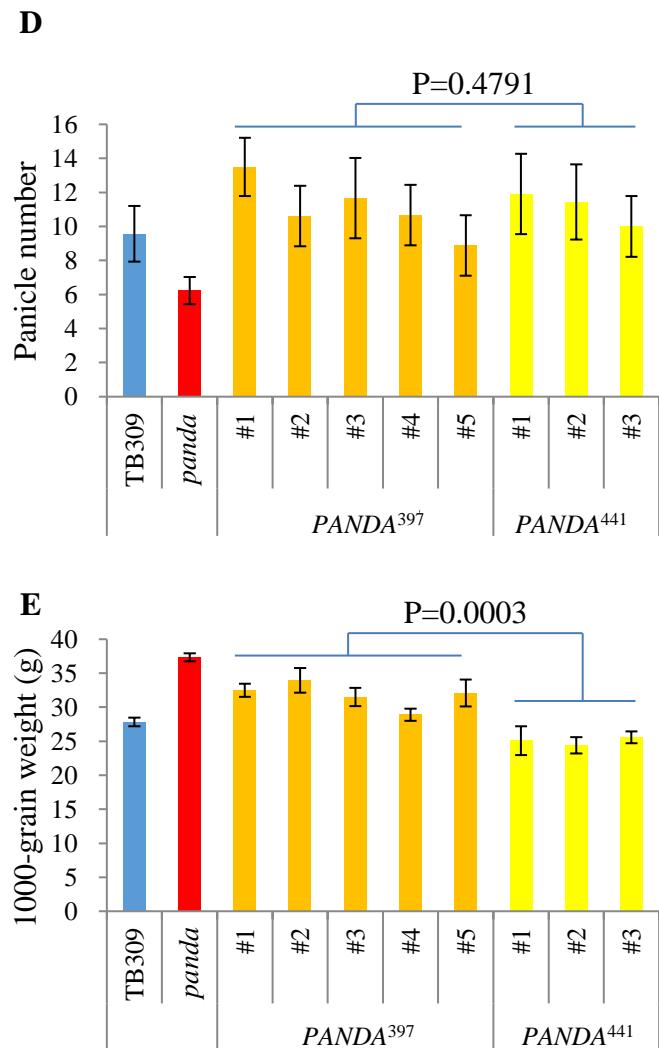
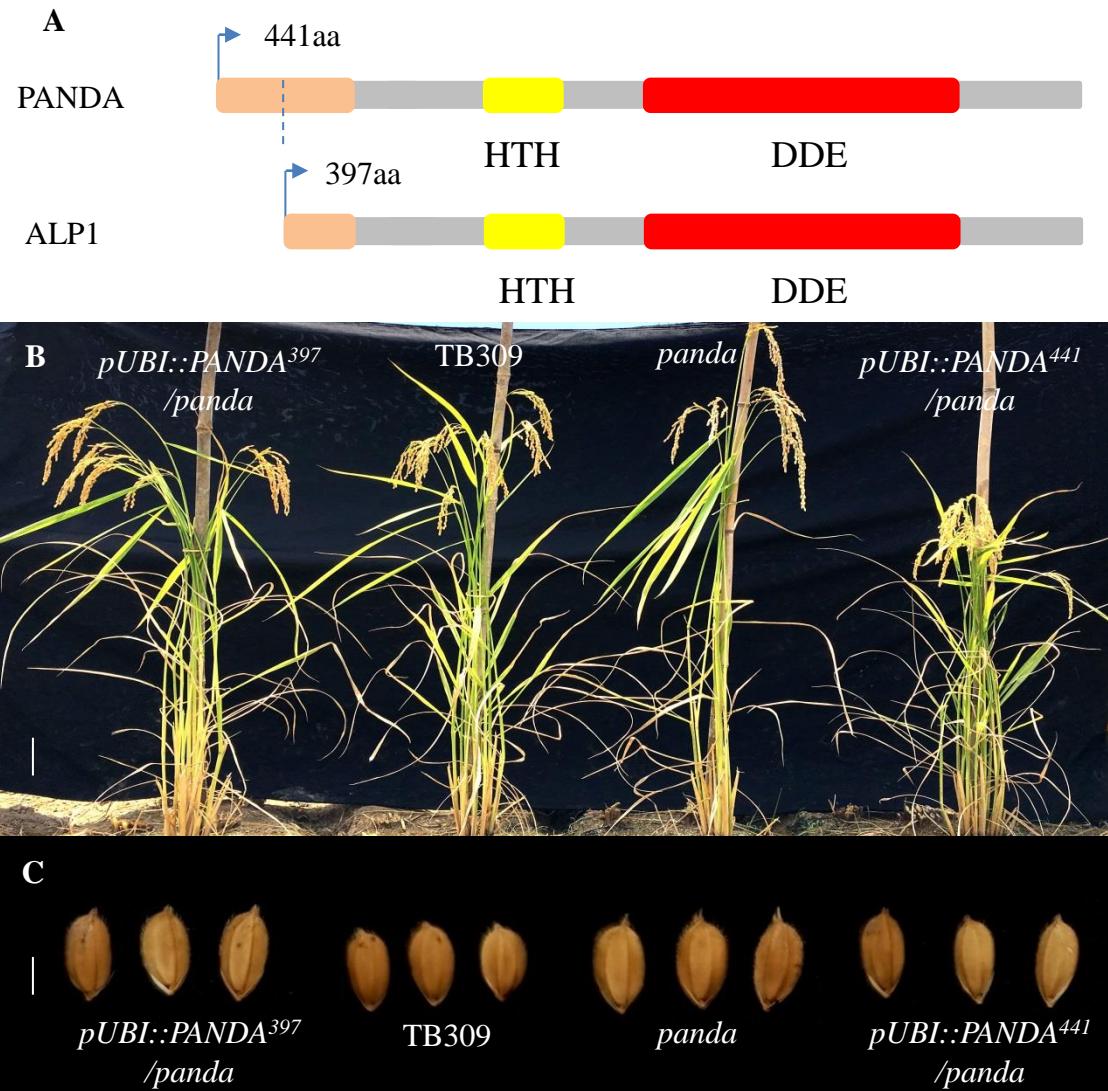


Fig. S17



Fig. S18

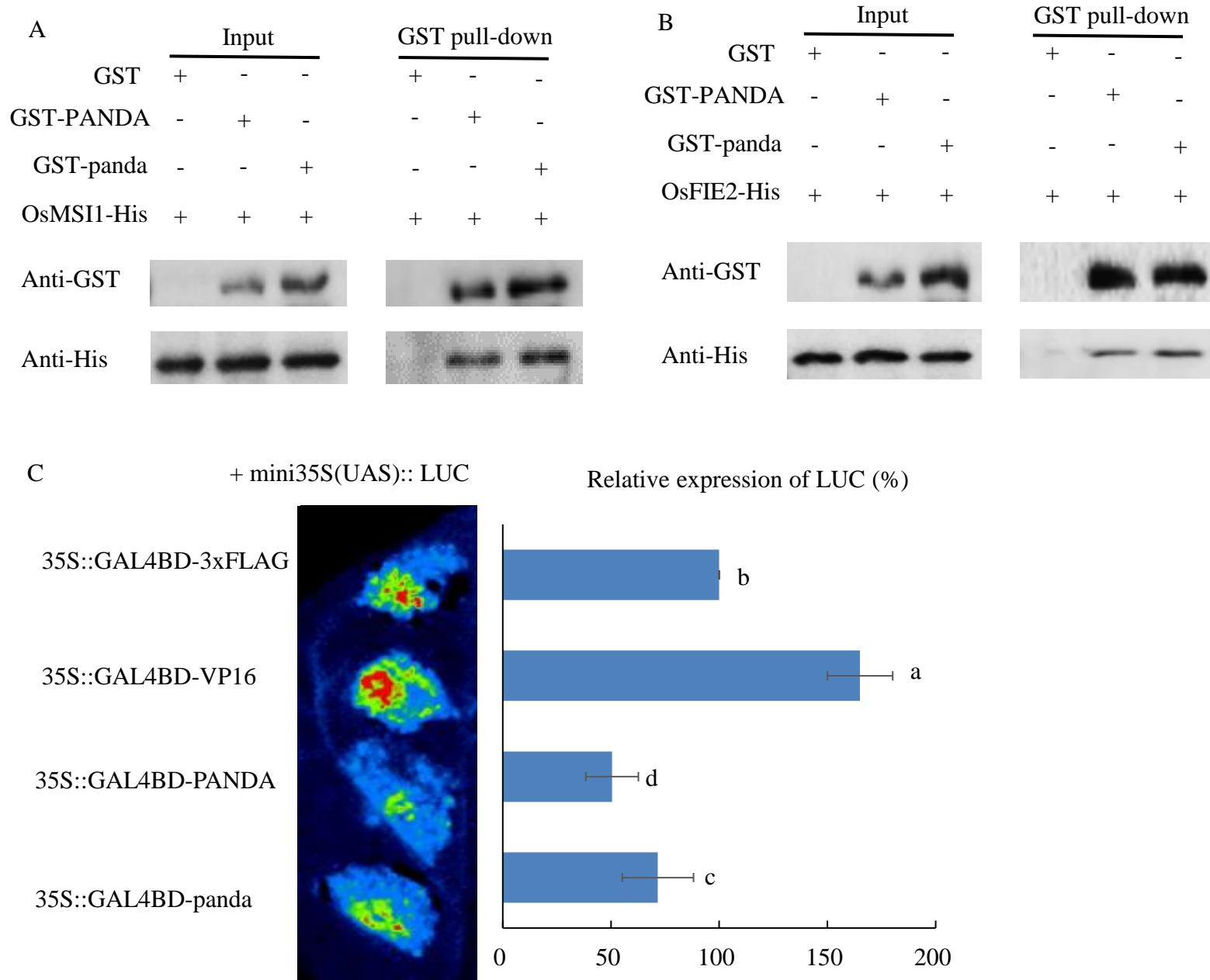


Fig. S19

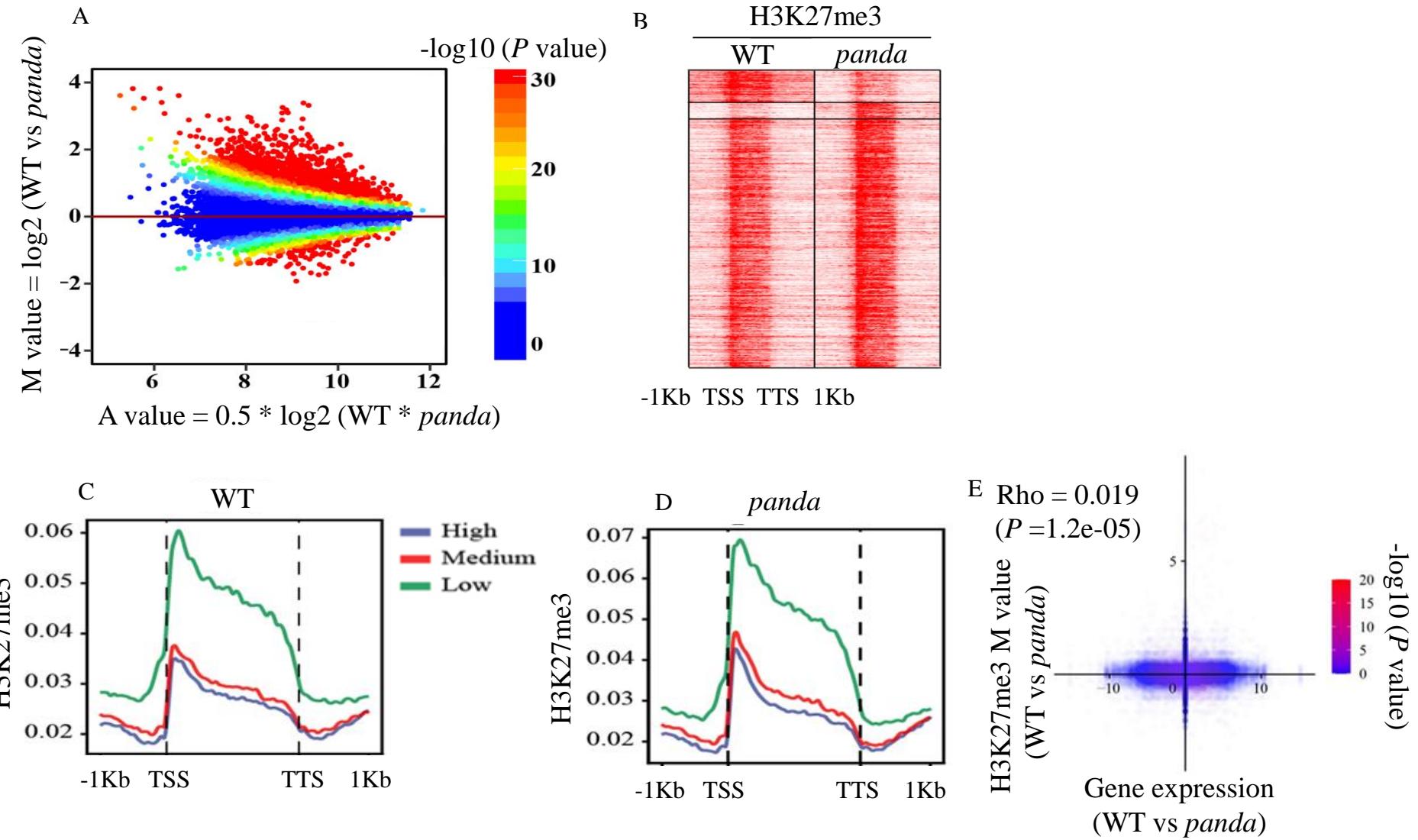


Fig. S20

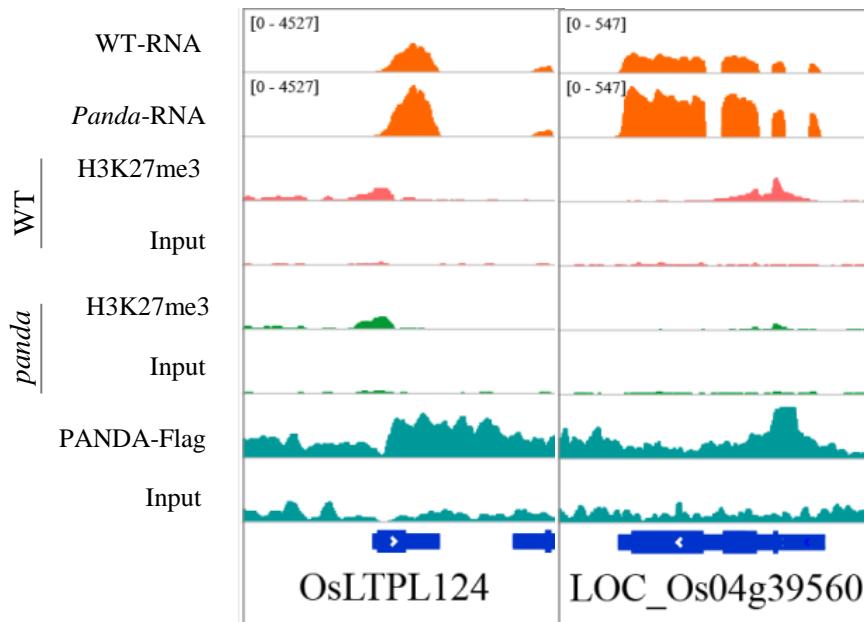
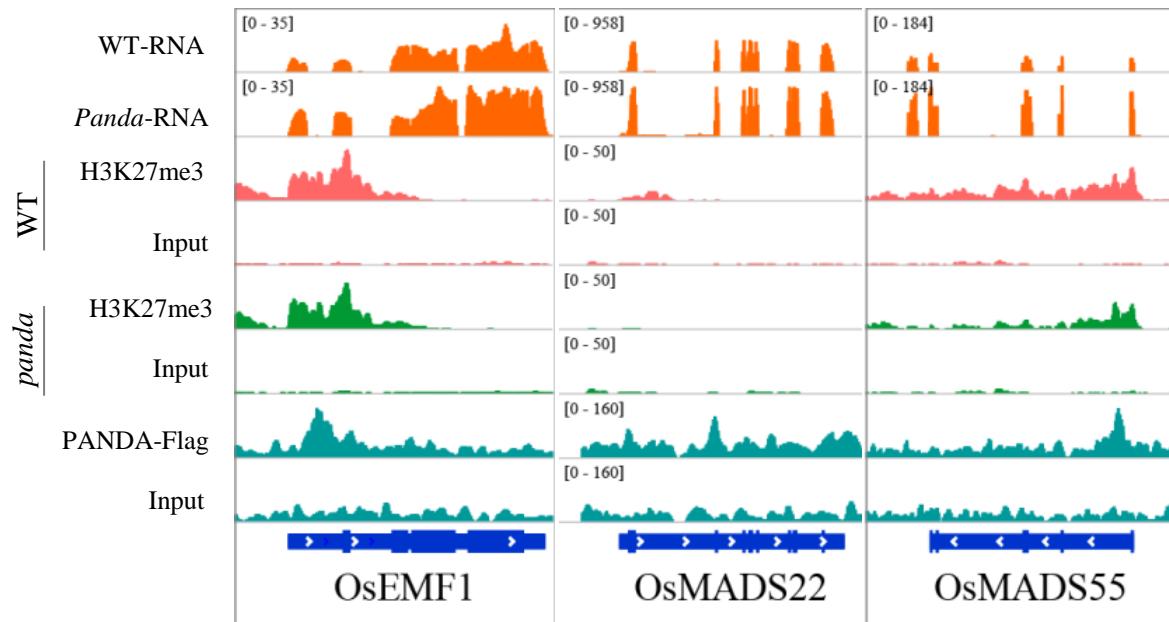


Fig. S21

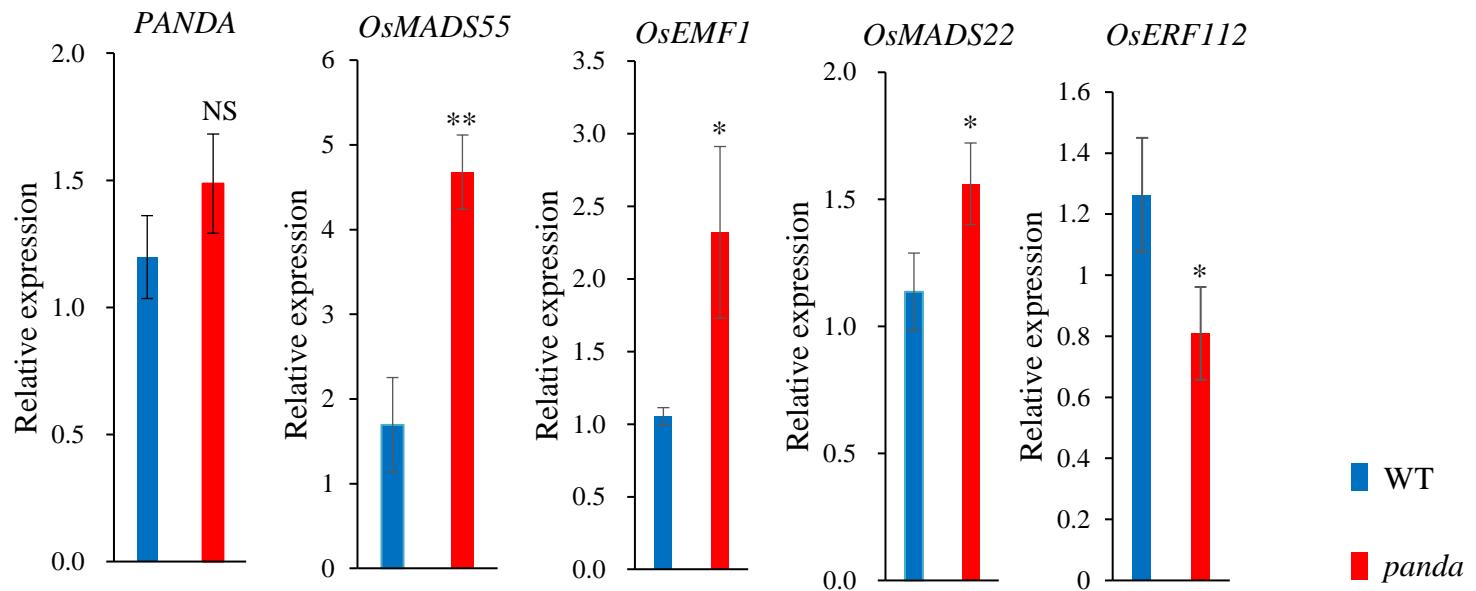


Fig. S22

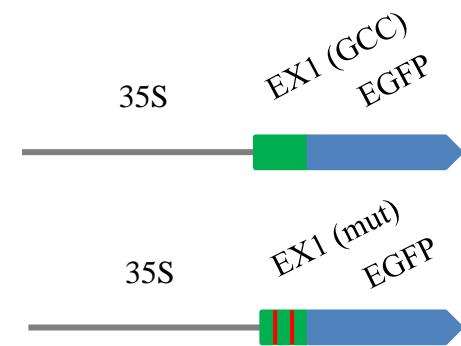
A

Exon1 (GCC): ATG ... GCG GCG GCG CGG ... CGG CGG CGG GGG...
Met ... Ala Ala Ala Arg ... Arg Arg Arg Gly ...

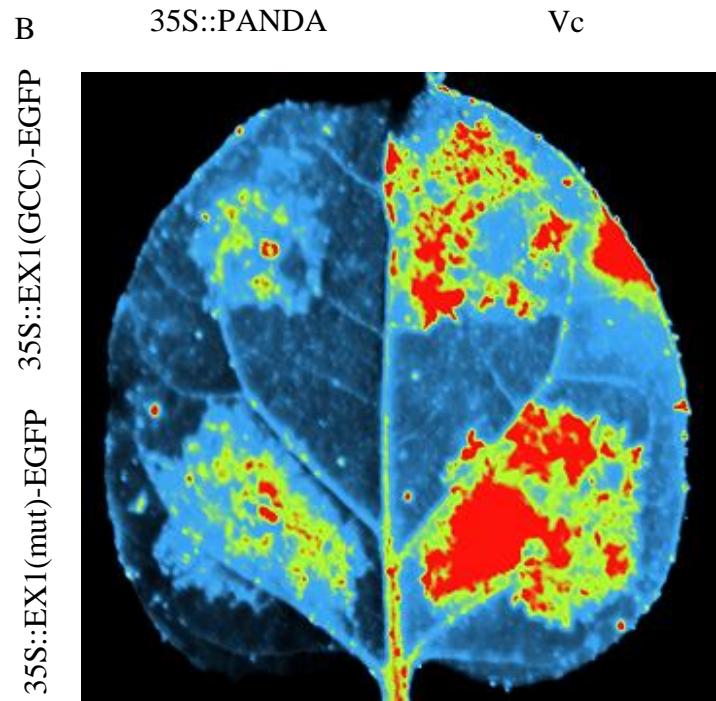
GGC motif GGC motif

Exon1 (mut): ATG ... GCT GCA GCT CGT CGG ... CGT CGA CGT GGG...
Met ... Ala Ala Ala Arg ... Arg Arg Arg Gly ...

mutation mutation



B



35S::EX1(mut)-EGFP 35S::EX1(GCC)-EGFP

C

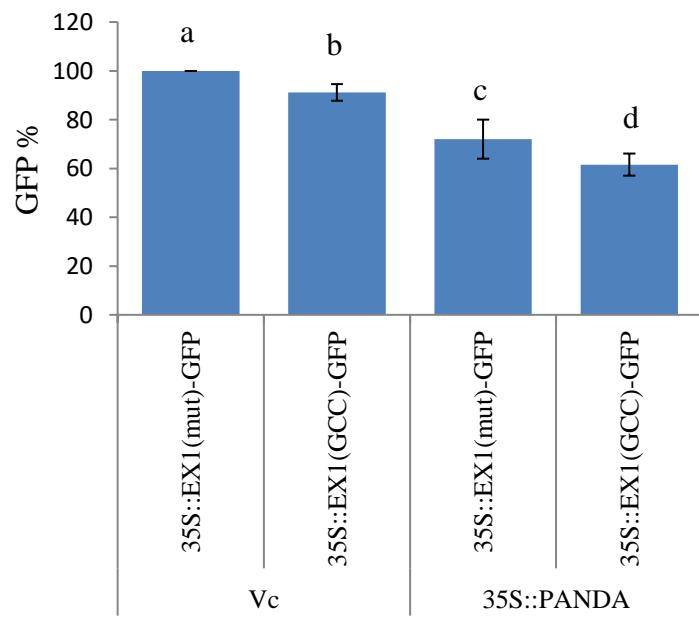


Fig. S23

PANDA	-	+	+	+	-	-	+
GCC motif- FITC	+	+	+	+	-	-	-
GCC motif	-	-	+	-	+	-	-
GCC motif with mutation	-	-	-	+	-	+	-
	-	-	-	-	-	-	-

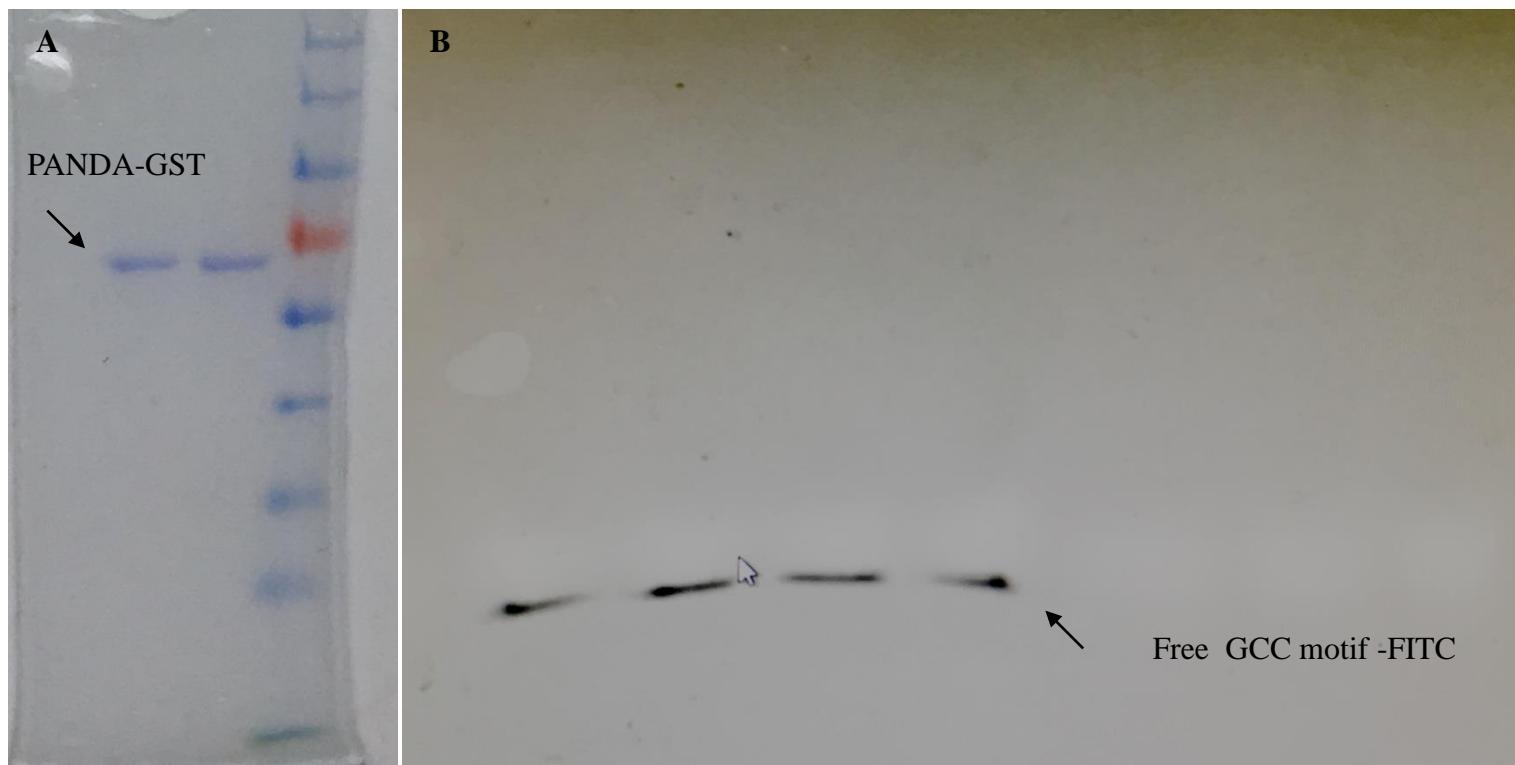


Fig. S24

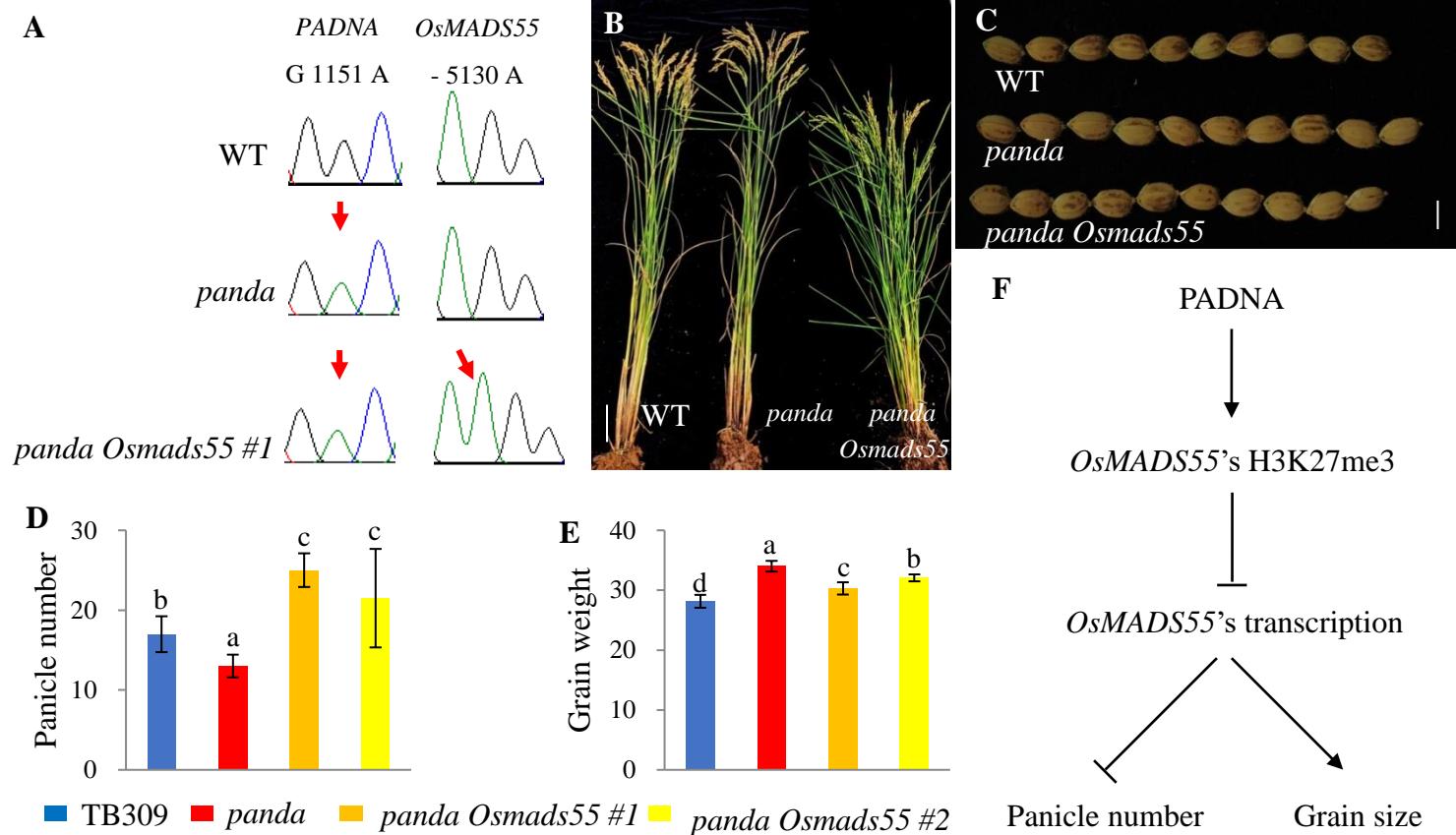


Fig. S25

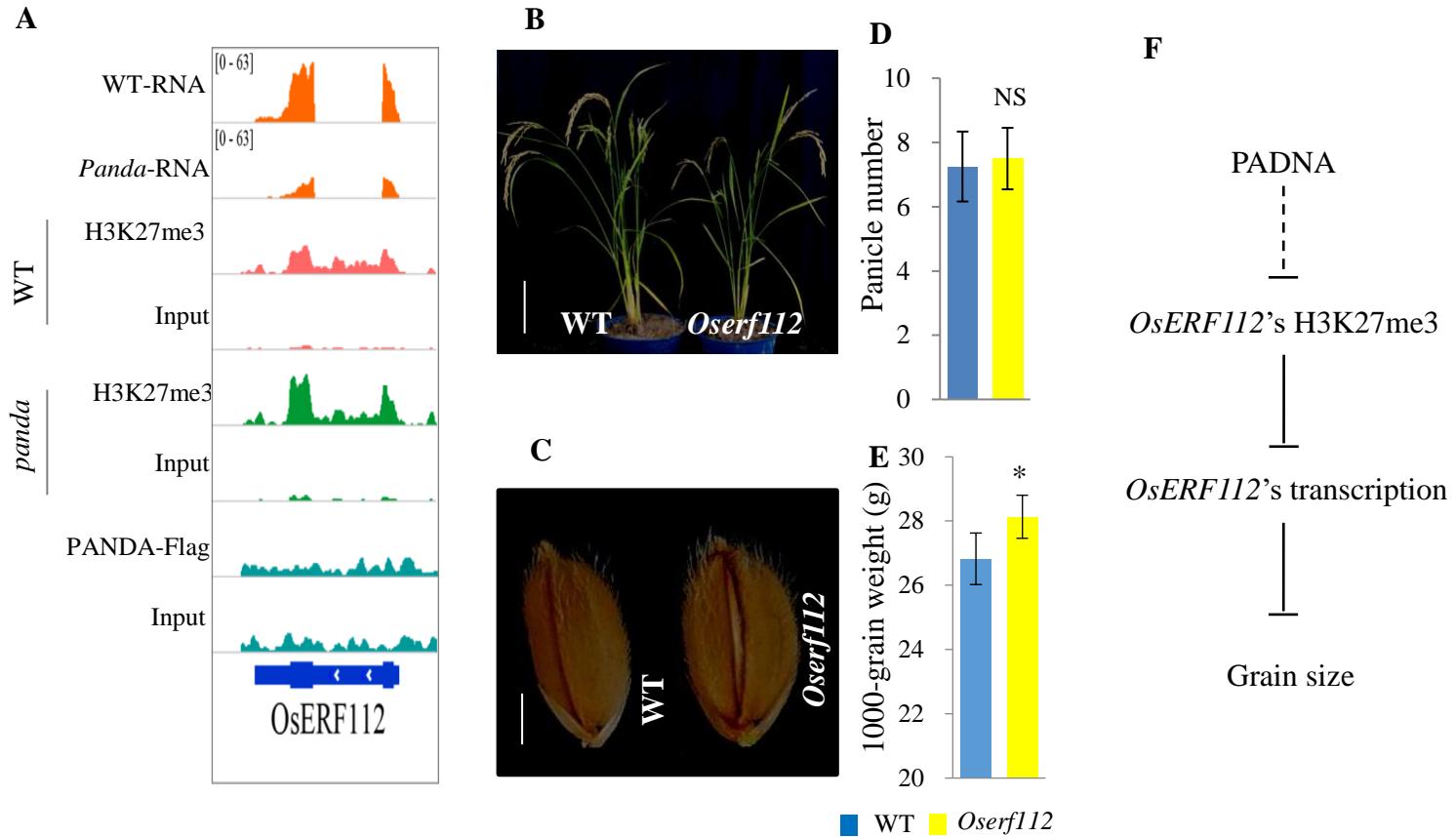


Fig. S26