Supplementary Material

Table S1. Primer sequence and application

Name	Forward / Reverse primer sequence（5'-3'）	Temperature/℃	Application
IlWRKY22	F:CTCCCAACAAACTCTCTCCCTAG	56℃	PCR amplification reaction
IlWRKY22	R:CAACAAAATAATCAGCTTGCCCC		
Actin	F:CTCCTTTGTTGCTGTTGACTAC	60℃	Fluorescence quantitative reference genes
Actin	R:GCACAATGTTACCGTACAGATC		
IlWRKY22	F:GATTGGAGTTGAGATGGGCTT	56℃	Fluorescence quantitative PCR reaction
IlWRKY22	R:ACTGTATAGTGGTGCTGAGGC		
IlWRKY22-BamHI	F:TTGATACATATGCCCGTCGACTTCTCTCCATCCCCTCTTT	60℃	PCR amplification reaction
IlWRKY22-SalI	R:CCCTTGCTCACCATGGATCCGCTCCCACCACCGGCAACGG		
CO	F:CACAGGTGAATACAGTCAACACC	60℃	Fluorescence quantification
CO	R:CCATGGATGAAATGTATGCGTTATGG		
GA20OX1	F:CGGTTTTGCGACGACATGAG	60℃	Fluorescence quantification
GA20OX1	R:TAGCCCCAGAAGCTCCA		

	TGA		
VRN1	F:CTGAGGGTCCCAGATAAGTTTG	60℃	Fluorescence quantification
VRN1	R:GTCAGCTTTCCTTAGTCCTACAC		
SPL3	F:CTCATGTTCGGATCTCTGGTC	60℃	Fluorescence quantification
SPL3	R:TTTCCGCCTTCTCTCGTTGTG		
FCA	F:GCTCTTGTCGCAGCAAACTC	60℃	Fluorescence quantification
FCA	R;GATCCAGCCCACTGTTGTTTAC		
SVP	F:GAAGAGAACGAGCGACTTGG	60℃	Fluorescence quantification
SVP	R:GAGCTCTCGGAGTCAACAGG		
FT	F:GGAACAACCTTTGGCAATGAGAT	60℃	Fluorescence quantification
FT	R:CTGCCAAGCTGTCGAAACAA		
SOC1	F:GATCGAGTCAGCACCAAACC	60℃	Fluorescence quantification
SOC1	R:TCCTATGCCTTCTCCCAAGA		
TPS1	F:ATTGGCATAGATTCTGATCGGT	60℃	Fluorescence quantification
TPS1	R:TCAAGACGATCAACACC		

	TAACA		
NtHAK1	F:ATCCACACCGAGCTTGTTTCAGGA	60℃	Fluorescence quantitative PCR reaction
NtHAK1	R:TGGGTCCAATTCTTCCCACCAAGA		
NtSOS1	F:GCGTGCTTATTTCCACCTTTTG	60℃	Fluorescence quantitative PCR reaction
NtSOS1	R:TTTGATGACGGCTCCCCAGT		
NtPMA4	F:TTTCCCGAGCACAAGTATGA	60℃	Fluorescence quantitative PCR reaction
NtPMA4	R:GGTAACCTCCAAGAACAACAC		
NtSOD	F:CTCCTACCGTCGCCAAAT	60℃	Fluorescence quantitative PCR reaction
NtSOD	R:GCCCAACCAAGAGAACCC		
NtCAT	F:AGGTACCGCTCATTCACACC	60℃	Fluorescence quantitative PCR reaction
NtCAT	R:AAGCAAGCTTTTGACCCAGA		
NtPOD	F:CCTCAGCTTCAAGCATTATGTCCA	60℃	Fluorescence quantitative PCR reaction
NtPOD	R:ACCTTTGTAGAAGCATCGGTCCAC		
NtActin	F:CGGAATCCACGAGACTAACATACAAC	60℃	Fluorescence quantitative PCR reaction
NtActin	R:GGTGCTGAGGGAAGCCAAGATA		

Table S2. Functional prediction of WRKY transcription factor family members in *I. lavigata*

Group	*A. thaliana*	*I. laevigata*	Function
I	*AtWRKY1* *AtWRKY2* *AtWRKY3* *AtWRKY4* *AtWRKY25* *AtWRKY26* *AtWRKY32* *AtWRKY33* *AtWRKY34* *AtWRKY44* *AtWRKY58*	isoform 3308 isoform 275946 isoform 813581 isoform 336911 isoform 460429 isoform 71297 isoform 722579 isoform 629169 isoform 239732 isoform 238068 isoform 687755 isoform 416995 isoform 342824 isoform 439137 isoform 312565 isoform 658241 isoform 7202 isoform 6445 isoform 232908 isoform 564486 isoform 298714 isoform 319525	They are involved in disease resistance, abiotic stress (salt, cold, heat) , senescence and some developmental processes (pollen development, seed coat development) . A response to a light stimulus.

Group	*A. thaliana*	*I. laevigata*	Function
IIa	*AtWRKY40* *AtWRKY60*	isoform 49561 isoform 305653 isoform 347489 isoform 63513 isoform 684413	A defensive response to bacteria or fungi.
IIb	*AtWRKY6* *AtWRKY9* *AtWRKY31* *AtWRKY36* *AtWRKY42* *AtWRKY47* *AtWRKY72*	isoform 358692 isoform 56218 isoform 320236 isoform 40279 isoform 478449 isoform 303256 isoform 14002	Defense responses to bacteria, fungi, oxidative stress; expression of genes involved in cold, leaf senescence. Root development.
IIc	*AtWRKY8* *AtWRKY12* *AtWRKY13* *AtWRKY23* *AtWRKY24* *AtWRKY28* *AtWRKY43* *AtWRKY48*	isoform 735698	They are involved in disease resistance (bacteria, fungi) , abiotic stress (salt, cadmium, drought) , senescence and some developmental processes (lignin synthesis, pollen development, florescence regulation) Auxin transport.

Group	*A. thaliana*	*I. laevigata*	Function
	AtWRKY49		
	AtWRKY50		
	AtWRKY51		
	AtWRKY56		
	AtWRKY57		
	AtWRKY59		
	AtWRKY71		
	AtWRKY75		
IId	*AtWRKY7*	isoform 352866	They are involved in plant disease resistance (bacteria, fungi) , senescence (apoptosis) and some developmental processes (flower development, florescence regulation) , regulation of jasmonic acid signaling pathway, response to light stimulation, calmodulin binding, reaction of salicylic acid.
	AtWRKY11	isoform 287969	
	AtWRKY15	isoform 241617	
	AtWRKY21	isoform 279981	
	AtWRKY39	isoform 327411	
	AtWRKY74	isoform 297487	
		isoform 410198	
		isoform 41879	
		isoform 567039	
		isoform 513126	
		isoform 286734	
		isoform 305537	
		isoform 596689	
IIe	*AtWRKY14*	isoform 561421	They are involved in disease resistance (bacteria) ,

Group	*A. thaliana*	*I. laevigata*	Function
	AtWRKY16	isoform 494831	senescence and some developmental processes (epidermis development, flower development, plant organ and root morphogenesis, florescence regulation) , auxin transport.
	AtWRKY22	isoform 588901	
	AtWRKY27	isoform 420051	
	AtWRKY29	isoform 234765	
	AtWRKY35	isoform 635473	
		isoform 51755	
		isoform 422731	
		isoform 304457	
III	*AtWRKY30*	isoform 507977	Involved in plant disease resistance (bacteria, fungi) , abiotic stress (ozone, temperature, drought) , senescence and some developmental processes (lateral root development, leaf development) ; response to salicylic acid, regulation of abscisic acid signaling pathway. Regulates Brassinosteroid, ethylene and jasmonic acid-mediated signaling pathways.
	AtWRKY38	isoform 31149	
	AtWRKY41	isoform 614906	
	AtWRKY46	isoform 69705	
	AtWRKY53	isoform 38178	
	AtWRKY54	isoform 487979	
	AtWRKY55	isoform 645693	
	AtWRKY63	isoform 629546	
	AtWRKY64	isoform 44179	
	AtWRKY66	isoform 481801	
	AtWRKY70	isoform 20352	