Supplementary material

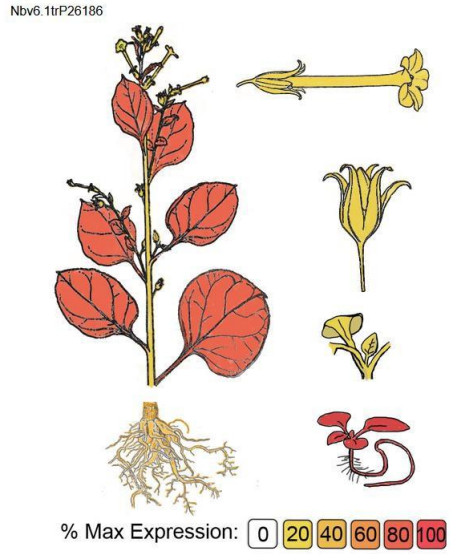

Figure S1. *NbMIG21* pattern of expression according to Version 6 Gene expression Atlas https://sefapps02.qut.edu.au/atlas/tREX6.php).

Pfam ID: UBN_AB `etllkrvkklrlkeeeeklkellekLkeaidevmpeqiekYekevaalaeakaakka.........d`

MASLQCHKPAQHAPSTLCQKTTTVTCNKANNEHHSFADKMKDMTDKMYHHDSHNHQSACHGTKTQQTAACHGTKTQQSAAC
HGTKTQQSAASHRTKTQQTACHGTSANGTKTQLSVACHGTKTQQSAASHGTKTQQTACHGTSATATHARACGKKKEGSFMH
KMRDQMRSRRNRNKDGSCSDGSDSSSSSSSDESDNENCGRTKNRGSC

Figure S2. Motif search service (https://www.genome.jp/tools/motif/) revealed that NbMIG21p fragment from 15 to 81 positions (red) contains motif corresponding to ubinuclein conserved middle domain (PF14075) (framed).

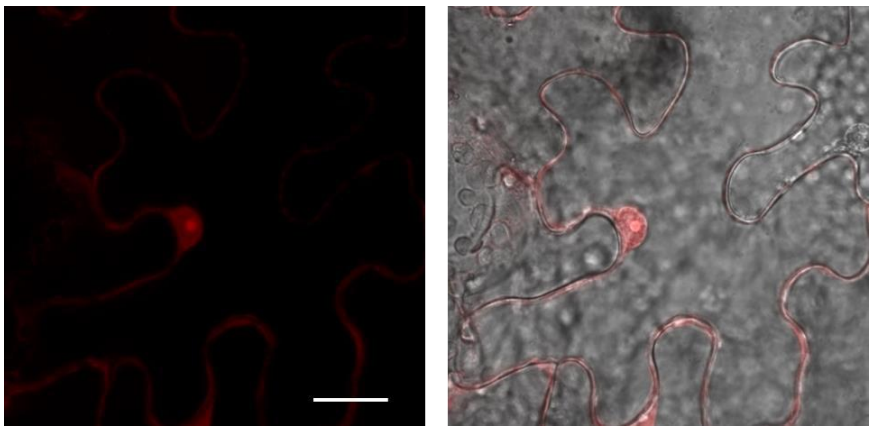

Figure S3. NbMIG21p:RFP intracellular localization. Images of 35S-NbMIG21:RFP expressing epidermal cells of *N. benthamiana* leaves 3 dpi obtained using confocal fluorescence microscopy. Projection of several confocal sections (left) superimposed on a bright field image of the same cell (right). Bar = 20 μm.

Table S1. PrMIG21 cis-acting elements analysis

Regulatory sequence	Position	Sequence	Function of site
ABRE	-1016	ACGTG	cis-acting element involved in the abscisic acid responsiveness
ARE	-944 -91	AAACCA AAACCA	cis-acting regulatory element essential for the anaerobic induction
Box 4	-235	ATTAAT	part of a conserved DNA module involved in light responsiveness [57]
MRE	-704	AACCTAA	MYB binding site involved in light responsiveness
MYB	-767 -641	CAACCA	MYB-binding site [58]
MYC	-913 -607	CAATTG	MYC-binding site [59]
MYB	-801	TAACTG	MYB-binding site [60]
TCA	-561	TCATCTTCAT	salicylic acids response motif [61]
STRE	-1008	AGGGG	present in the promoters of stress-regulated genes and is recognized by the transcription factors Msn2p/4p [62]
G-box	-1016	CACGTT	cis-acting regulatory element involved in light responsiveness

Table S2. Oligonucleotides used for qRT-PCR and cloning

Name	Sequence
qRT-NbMIG21_f	GCAAATGGCACCAAAACTC
qRT-NbMIG21_r	GTAGCAGTGGCACTTGTTC
18S rRNA_f	ACGGCTACCACATCCAAG
18S rRNA_r	ACTCATTCCAATTACCAGACTC
PP2A_f	ATTGCTGCCTGTGGTTATTAC
PP2A_r	ATAGACTGAAGTGCTTGATTGG
N-NbMIG21-Acc65I_f	**GGTACC**ATGGCATCACTTCAGTGC
N-NbMIG21-BamHI_r	**GGATCC**GCAGCTCCCTCTATTC
C-NbMIG21-BamHI_f	**GGATCC**CTGGCATCACTTCAGTGC
C-NbMIG21-SalI_r	**GTCGAC**TCAGCTCCCTCTATTCTTG
NbMIG21-NoLS-mut_f	TGGGATCAACGGGAACATCGACGGAAG
NbMIG21-NoLS-mut_r	GTTCCCGTTGATCCCACTTCCCATTTG
GFP-Acc65I_f	**GGTACC**ATGAGCAAGGGCGAGG
GFP-BamHI_r	**GGATCC**TTTCTTGTACAGCTCGTCC
GFP-PstI_r	**CTGCAG**TTACTTGTACAGCTCGTCC
YN- Acc65I_f	**GGTACC**ATGGTGGTGAGCAAGGGCG

YN- BamHI_r	**GGATCC**CATGATATAGACGTTGTGGC
YC- Acc65I_f	**GGTACC**ATGGCCGACAAGCAGAAGAAC
YC- BamHI_r	**GGATCC**TTTGGACTTGTACAGCTC
NbCoilin-Acc65I_f	**GGTACC**ATGGAGGGCGTTAGGCTTC
NbCoilin-BamHI_r	**GGATCC**AATTTTGTTCTGGGATCTTAGG
NbFib2-Acc65I_f	**GGTACC**ATGGTTGCACCAACTAGAGG
NbFib2-BamHI_r	**GGATCC**GGCAGCAGCCTTCTGCTTC
6H-NbMIG21-Acc65I_f	**GGTACC**GCATCACTTCAGTGCC
PrNtPME-HindIII_f	**AAGCTT**GCTAGCAGGAACTAATCAGG
PrNtPME- Acc65I_r	**GGTACC**GAGCTCCCGGCGAAGAAATC
PrMIG21-HindIII_f	**AAGCTT**GTTACCATGTCTATGTGGAGC
PrMIG21-NruI_r	**TCGCGA**TGAATATGTCTGAAACTGAC
PrAELP-HindIII_f	**AAGCTT**AAAAACCTAACAATCC
PrAELP-NcoI_r	**CCATGG**CTCTAGTTGTTTTAGAG
PrKPILP-HindIII_f	**AAGCTT**AAATGAGAATTTACTTAAG
PrKPILP-NcoI_r	**CCATGG**TGTTAAGGATATGGTTAATG
PrThio-HindIII_f	**AAGCTT**ACCAGCACCTAAGC
PrThio-NcoI_r	**CCATGG**AGTTACTTTGAATGAGTAAAAAAG