

MsNRAMP2	MSGFSEEDNSKEEVREEDGNRLLEVDEGEGLSTSEEAAMESEKIVVDFEFG..TVDDSTWPFPSWKLMFTGEG	78
MtNRAMP2	MSGFSEEDNSKEEVREEDGNRLLEVVEGE..SSSEEAAMESEKIVVDFEFG..TVDDSTWPFPSWKLMFTGEG	76
AtNRAMP2ENIVVENLPEEDRLPPPPPSCLPSTISEEAAPETNEKILLVDFEFPDDPTTGDPFPPFSWKLMFTGEG	75
Consensus	e ke ee se eaa e eki vdfe t ppsfw klw ftgpg	
MsNRAMP2	FLMSIAFLDPGNLEGDLQAGAIAGYSLIWLWMWATL MGLLICSL SARVGVATGRHLAELCRDEYFWARYVLWMAELAL	158
MtNRAMP2	FLMSIAFLDPGNLEGDLQAGAIAGYSLIWLWMWATL MGLLICSL SARVGVATGRHLAELCRDEYFWARYVLWMAELAL	156
AtNRAMP2	FLMSIAFLDPGNLEGDLQAGAIAGYSLIWLWMWATL MGLLICSL SARVGVATGRHLAELCRDEYFWARYVLWMAELAL	155
Consensus	flmsiafldpgnlegdlqagaiagysllwllmwat mgllicl sarvgvatgrhlaelc eyp waryvlw maelal	
MsNRAMP2	IGADIQEVIGSAIAIQILSRGLPLWAGVITASDCFLFLFLENYGVKLEAF FAVLIATMLSFAMWFGDACPSGKEIV	238
MtNRAMP2	IGADIQEVIGSAIAIQILSRGLPLWAGVITASDCFLFLFLENYGVKLEAF FAVLIATMLSFAMWFGDACPSGKEIV	236
AtNRAMP2	IGADIQEVIGSAIAIQILSRGLPLWAGVITASDCFLFLFLENYGVKLEAF FAVLIATMLSFAMWFGDACPSGKEIV	235
Consensus	igadiqevigsaiaiqilsrg lplwagv itasdcf flflenygvrklea favliatm lsfamwfg dacpsgkel	
MsNRAMP2	GFILPFRSSKTHQAVGVVGCVMFHNVLHSAIVQSRKIDENKRRVQEALNYYIESVALSVTFMINLFVTTVFAK	318
MtNRAMP2	GFILPFRSSKTHQAVGVVGCVMFHNVLHSAIVQSRKIDENKRRVQEALNYYIESVALSVTFMINLFVTTVFAK	316
AtNRAMP2	GFILPFRSSKTHQAVGVVGCVMFHNVLHSAIVQSRKIDENKRRVQEALNYYIESVALSVTFMINLFVTTVFAK	315
Consensus	gil pr sskti qavgvvgcvimphnvlhsalvqsrkidp k rvqealnyy ies val fminlfvttvfak	
MsNRAMP2	GFYGTICANSIGLVNAGCYLDERGGGLPILYINGIGLLAAGQSSTITGTYAGQFIMGGFLNRLKKNRAITRSCAI	398
MtNRAMP2	GFYGTICANSIGLVNAGCYLDERGGGLPILYINGIGLLAAGQSSTITGTYAGQFIMGGFLNRLKKNRAITRSCAI	396
AtNRAMP2	GFYGTICANSIGLVNAGCYLDERGGGLPILYINGIGLLAAGQSSTITGTYAGQFIMGGFLNRLKKNRAITRSCAI	395
Consensus	gfygt an iglvnagqyl ek gggl pilyingigllaagqsstittgtyagqfimggflnrlkkn ra itrscai	
MsNRAMP2	VPTIIVAIVNRSASLDVLNWLNVLQSQIPFALLPLTLVSKERIMGSFKGFLERVAWTVAALIIINGYLLVDF	478
MtNRAMP2	VPTIIVAIVNRSASLDVLNWLNVLQSQIPFALLPLTLVSKERIMGSFKGFLERVAWTVAALIIINGYLLVDF	476
AtNRAMP2	VPTIIVAIVNRSASLDVLNWLNVLQSQIPFALLPLTLVSKERIMGSFKGFLERVAWTVAALIIINGYLLVDF	475
Consensus	vpt i vaiv n seasldvlnewlnvlqs qipfal plltivske img fk gp l r awtvaal ingyll df	
MsNRAMP2	FLSEVNSVLFQVACSTVYIAFIVYLISSGALPSALVDR...LPKGFCSSE	529
MtNRAMP2	FLSEVNSVLFQVACSTVYIAFIVYLISSGALPSALVDR...LPKGFCSSE	527
AtNRAMP2	FLSEVNSVLFQVACSTVYIAFIVYLISSGALPSALVDR...LPKGFCSSE	529
Consensus	f sev lfg c t yiafivylis s ps lpk s	

Figure S1. *MsNRAMP2* , *MtNRAMP2*(XM_013606289.3) and *AtNRAMP2*(NM_103618.3) amino acid sequence alignment.

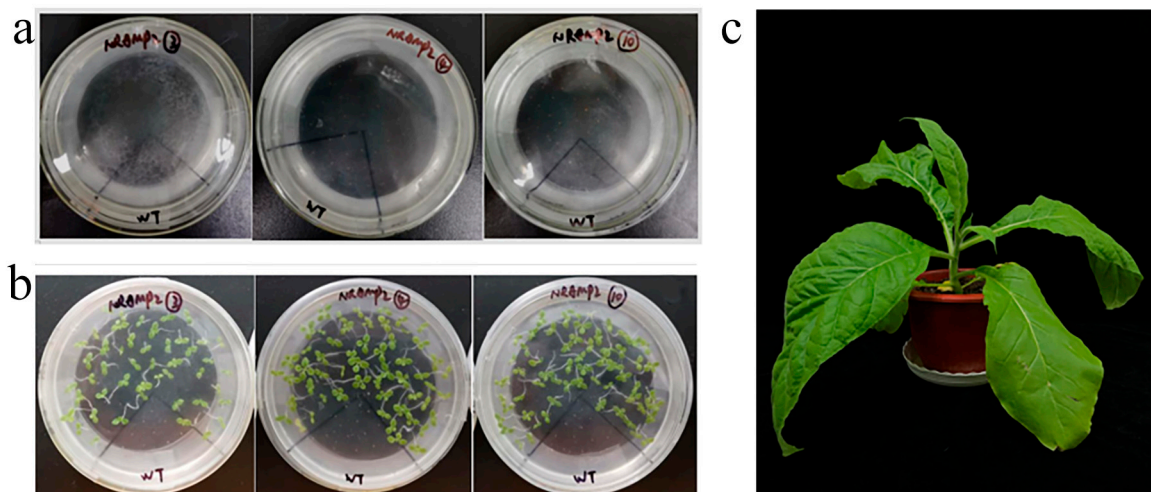


Figure S2. *MsNRAMP2* transgenic tobacco: (a) Germination of *MsNRAMP2* overexpression transgenic tobacco; (b) Screening and culture of *MsNRAMP2* transgenic tobacco; (c) *MsNRAMP2* transgenic tobacco positive plant.

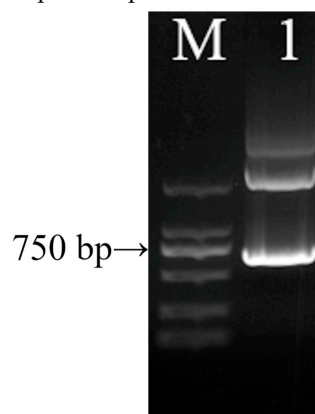


Figure S3. PCR amplification of *MsMYB* CDS fragment: M: DL2000 Marker; 1: *MsMYB* fragment.