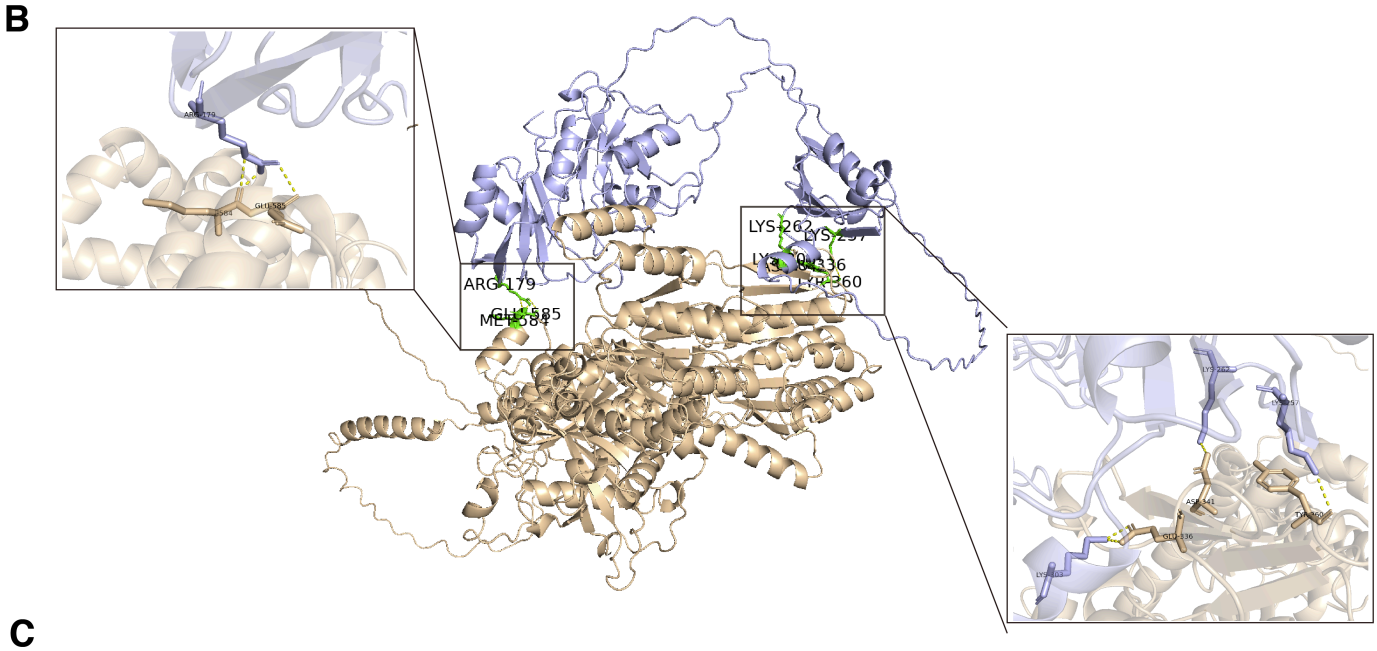
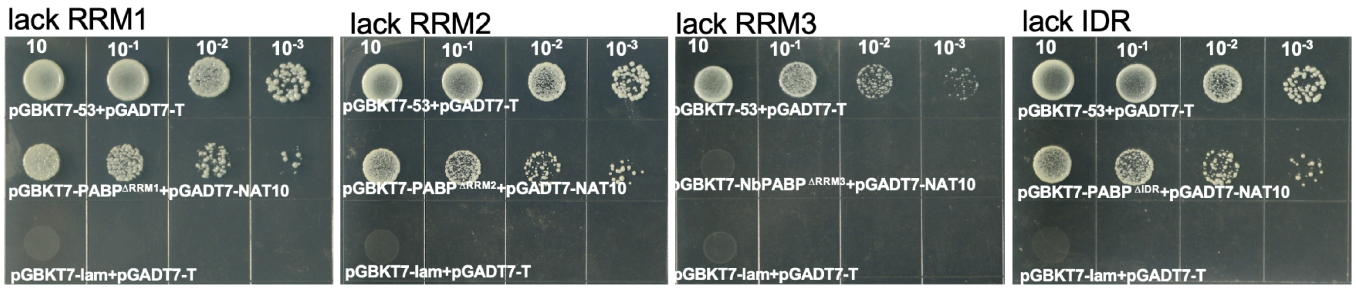
A

Gene ID	Appearance	Annotation
Niben101Scf08566g05001.1	3	Serine/arginine-rich splicing factor SC35-like
Niben101Scf00691g03001.1	2	Anthranilate synthase beta subunit 1
Niben101Scf04528g11009.1	1	Glycine-rich RNA-binding protein
Niben101Scf08859g00009.1	2	Polyadenylate-binding protein
Niben101Scf01406g03019.1	1	Fructose-1,6-bisphosphatase
Niben101Scf00132g01002.1	1	RNA polymerase II transcriptional coactivator KELP
Niben101Scf16657g00010.1	1	Protein TIFY 10A/NtJAZ3 mRNA for jasmonate ZIM-domain protein 3
Niben101Scf10448g00020.1	2	Vacuolar protein sorting-associated protein 55 homolog

B



C



Extended Data Fig. 2 Supporting evidence for the interaction between NbNAT10 and PABP, as a supplement to Fig. 2.

a. The list of several potential interacting proteins was identified from the *N. benthamiana* cDNA library using yeast two-hybrid (Y2H) screening with NbNAT10 as bait.

b. Predicted interactions between PABP and NbNAT10 analyzed using AlphaFold3. The predicted model identified multiple potential binding residues between PABP (blue) and NbNAT10 (yellow) and reveals docking sites within the RNA recognition motifs (RRMs) of PABP, as delineated by red solid line boxes. The yellow dashed lines represent hydrogen bonds (<4 Å).

c. The yeast two-hybrid (Y2H) assay was utilized to ascertain the interaction between NbNAT10 and four structural domains of PABP and NbNAT10. pGBKT7-53 and pGADT7-T were employed as positive controls, while pGBKT7-lam and pGADT7-T were used as negative controls.