

Supplementary S1

Table S1. Used primers in this study:

Primer name	Primer sequences	Working state	Comments
28ff or 25f1	5`-GACCCCAGGTCAGGCGGGACTACC-3`	OK	Universe primers for
28rr1 or 25r1	5`-GCTATCCTGAGGGAAACTTCGGAGG-3`	OK	amplification of 25S rRNA gene
9con8F2, or 98f2	5`-CGCACCGTTCGAACTGTAGTC-3`	OK	Specificity primer for RC2
9con8rev2, or 98rev2	5`-GTTACAGCGTGGCACCCCAAGG-3`	OK	Specificity primer for RC2
9con8F2cy5, or 98f2cy5	5`-CGCACCGTTCGAACTGTAGTC-3`	OK	CY5 labelled for cDNA T-RFLP
9con8F, or 98f	5`-GTGAGCGAACTGGGAGATGCTC-3`	X	
9con8rev, or 98rev	5`-CCGGGTTTCAGAGCACATTATCTC-3`	X	
9con8rev3, or 98rev3	5`-CGATTGACGTCAGTATTGCTTTG-3`	X	
9con14F, or 914f	5`-GCCCAACGTGAAAATCGGGCAG-3`	OK	Specificity primer for RC3
9con14rev2, or 914rev2	5`-GTATCACTTTGAGCCTCCACC-3`	OK	Specificity primer for RC3
9con14rev, or 914rev	5`-GGCCAGCGATGCGGCCCATG-3`	X	
9con31f, or 931f	5`-CCCTAATAACCGAATTGTAGTCTGG-3`	OK	Specificity primer for RC1
9con31rev, or 931rev	5`-CTAGATGGTTCGATTGGTCTCATCC-3`	OK	Specificity primer for RC1
283fcy5	5`-GCA (AG) CCCAAAT (CT) (AG) GG (ACT) G (AG) TAAAC-3`	OK	Forward sequencing primer
367rcy5	5`-CTTTCCTC (AG) (CT) GGT (AG) CTGT (CT) (AG) C-3`	OK	Reverse sequencing primer
406rcy5	5`-CA (AC) GCACT (GCT) TTGACTCTTTTC-3`	OK	Reverse sequencing primer
887revcy5	5`-GCCTCCA (CT) (CT) AGA (GT) TTT (CT) CT (AC) TG-3`	OK	Reverse sequencing primer
648r	5`-GCGGCGTCTATGGGGTGCCT-3`		
18S primer	NS1	5`-GTAGTCATATGCTTGTCTC-3`	Cy5 labelled sequencing primer
	NS2	5`-GGCTGCTGGCACCAGACTTGC-3`	Cy5 labelled sequencing primer
	NS3	5`-GCAAGTCTGGTGCCAGCAGCC-3`	Cy5 labelled sequencing primer
	NS4	5`-CTTCCGTCAATTCCTTTAAG-3`	Cy5 labelled sequencing primer
	NS5	5`-AACTTAAAGGAATTGACGGAAG-3`	Cy5 labelled sequencing primer
	NS6	5`-GCATCACAGACCTGTTATTGCCTC-3`	Cy5 labelled sequencing primer
	NS7	5`-GAGGCAATAACAGGTCTGTGATGC-3`	Cy5 labelled sequencing primer
	NS8	5`-TCCGCAGGTTACCTACGGA-3`	Cy5 labelled sequencing primer
ITS primer	ITS1	5`-TCCGTAGGTGAACCTGCGG-3`	
	ITS2	5`-GCTGCGTTCTTCATCGATGC-3`	
	ITS3	5`-GCATCGATGAAGAACGCAGC-3`	
	ITS4	5`-TCCTCCGCTTATTGATATGC-3`	
	ITS5	5`-GGAAGTAAAAGTCGTAACAAGG-3`	Cy5 labelled sequencing primer

A

	48	32	P-site	49
Tradescantia	AGCGCGAGTCATCAGCTCGCGTTGACTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTCCTACCGATTGAA			
Arabidopsis
Acorus
Sparganium
Zea
Triticum
Oryza
RDF2 Oryza
	49			
Tradescantia	TGGTCCGGTGAAATGTTCGGATCGCGGCACGGGGCGGTTTCGCCG-----CCCGCGACGTCGC			
Arabidopsis	..A.....G.....T..T.....			
AcorusG.....A.....			
SparganiumG.....C.....T.....			
ZeaG.....G.T...CG.ACC..TTCGC...C-----GA.CGTCCGC.			
TriticumG.....			
OryzaG.....			
RDF2 OryzaA.....G...T..T..A.....TT.....AATCCTACCGATTGAHTG.TCCA...CA			

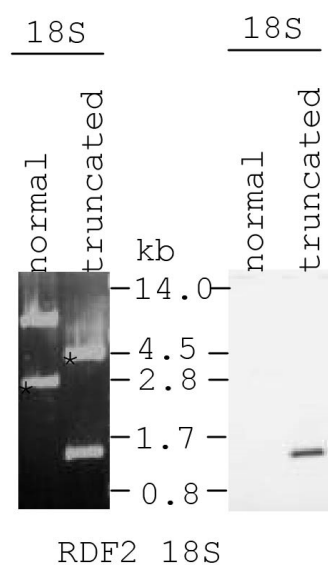
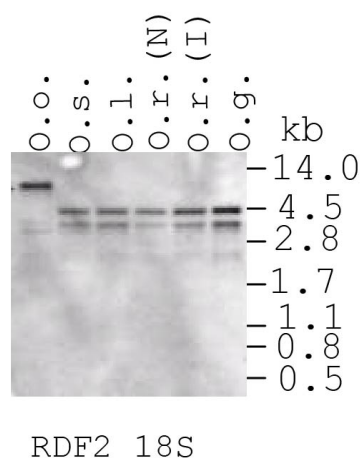
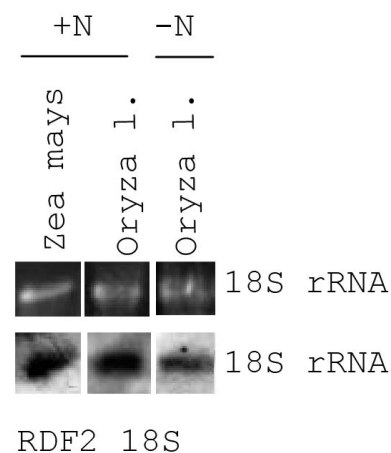
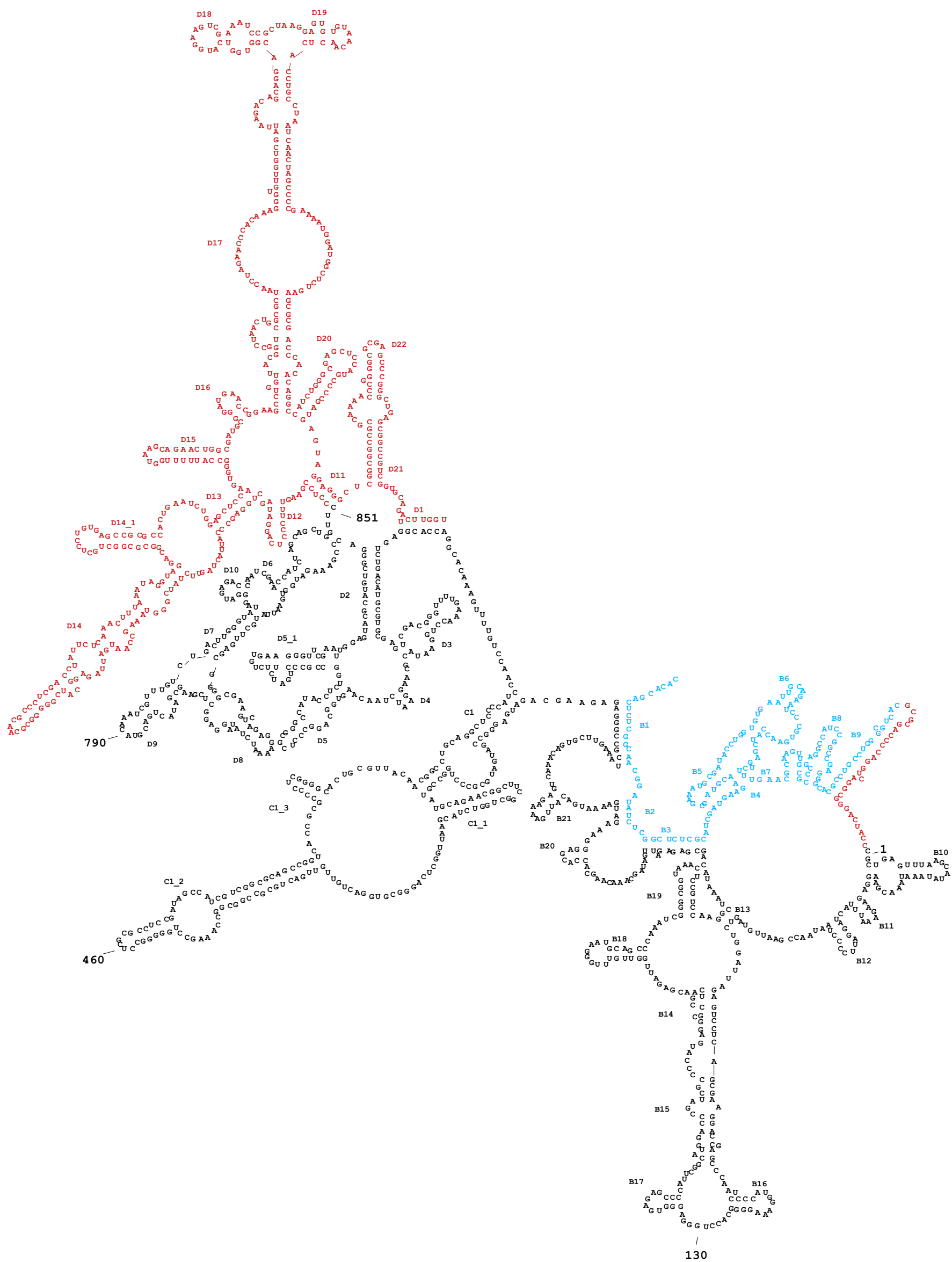
B**C****D**

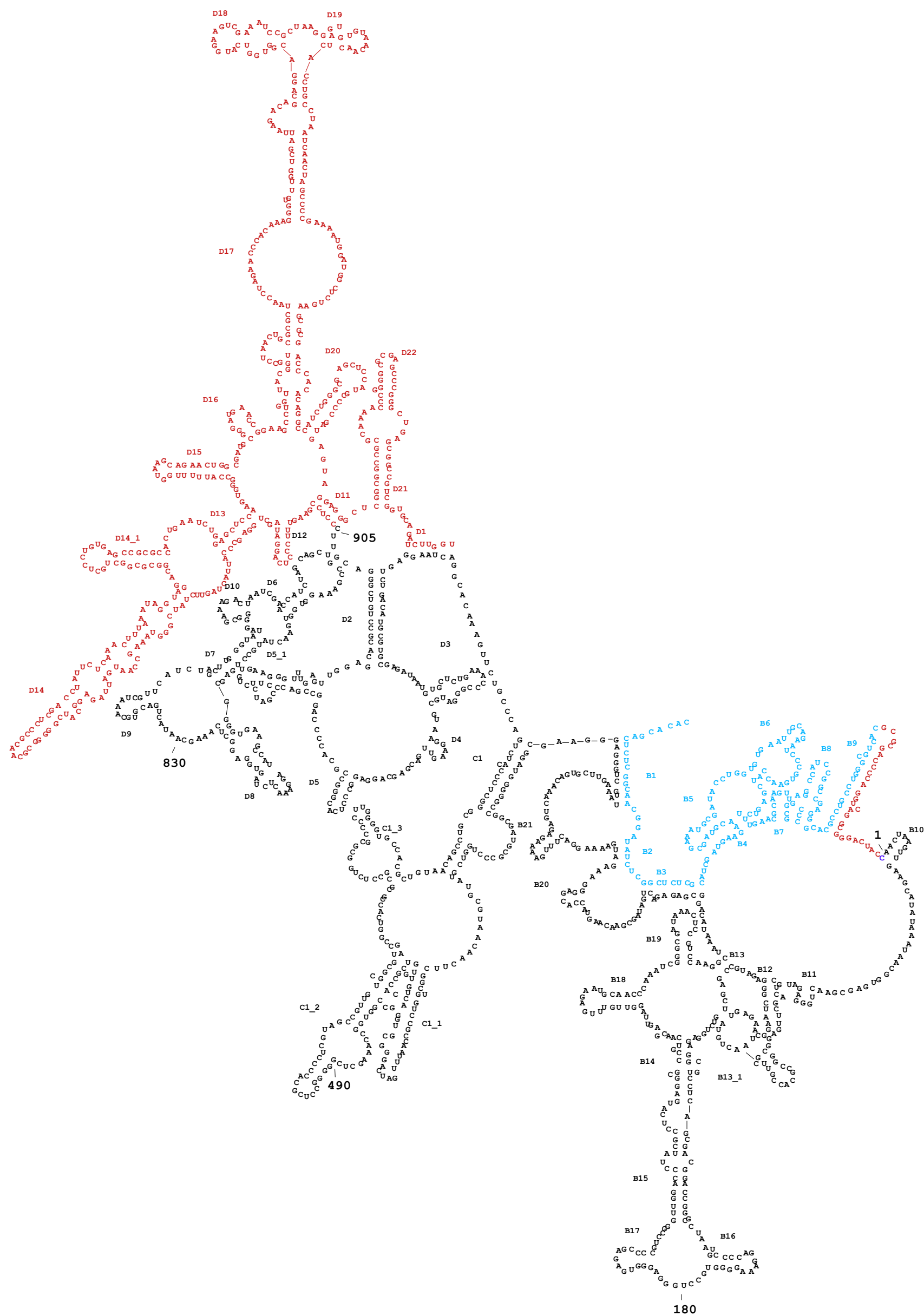
Figure S1. Codominant expression of RDF1-3 in rice. Presence of truncated RDF2 18S in ribosome preparations. (A) The portion of the aligned matrix from a unique truncated *O. officinalis* 18S ribosomal gene linked to RDF2 28S rRNA (AY097331) shows two INDELs in the decoding region that distinguishes it from other 18S rRNA genes. Dots indicate nucleotides identical to the top sequence, and dashes indicate gaps. The deleted and a putative alternative P-site are labeled. (B-D) Occurrence of the truncated 18S rRNA gene in rice. (B) Control Southern blot of *EcoR* I digested from rDNA clones with normal and truncated 18S rRNA genes (AY097331) hybridized with the

RDF2 18S probe. Vector labeled with a star. (C). Presence of the truncated 18S rRNA in ribosome preparations from leaves of *Zea mays* and *O. longistaminata* (*Oryza l.*) grown in soil fertilized (+N) or not fertilized (-N) with combined nitrogen (D). Agarose gels (upper panel) and Northern blots (lower panel).

— 5.8S rRNA M16845
— LSU rRNA M11585
— LSU rRNA AF363841



— 5.8S rRNA M16845
— LSU rRNA M11585
— LSU rRNA AF363902



Partial LSU secondary structures from rRNA families of *Oryza* spp.

5.8S rRNA M16845
LSU rRNA M11585
LSU rRNA AF363882 RC3 *O. officinalis*

