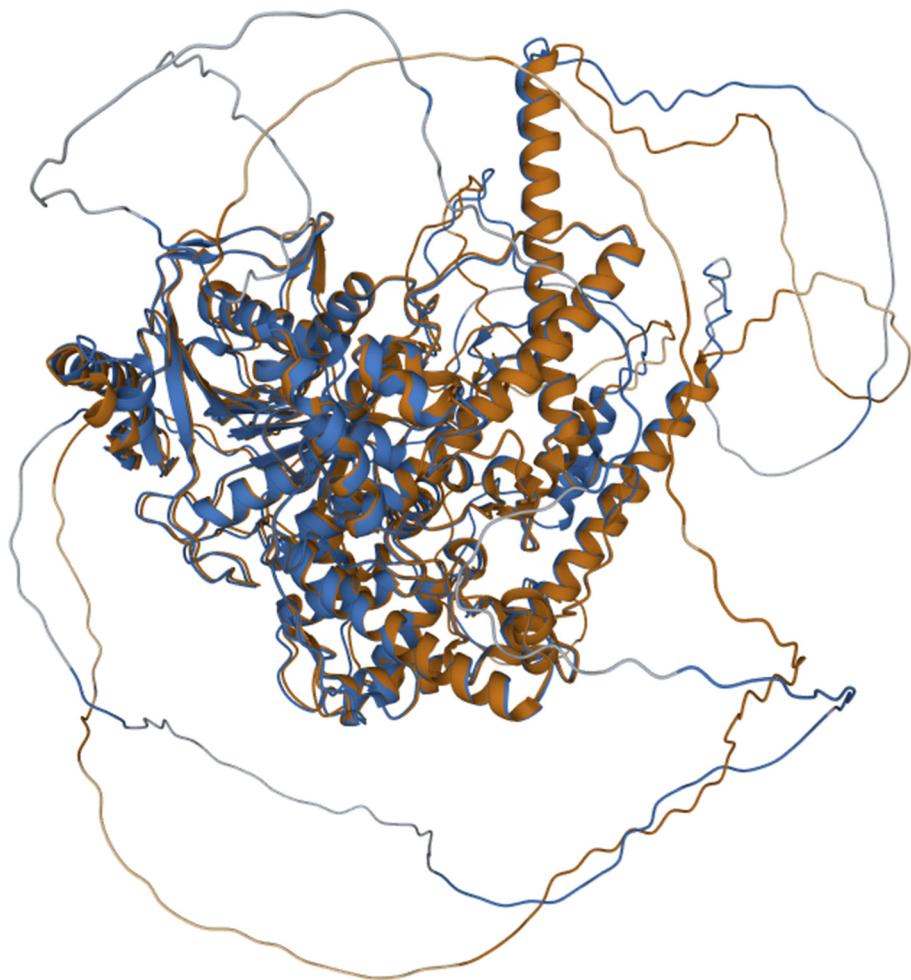
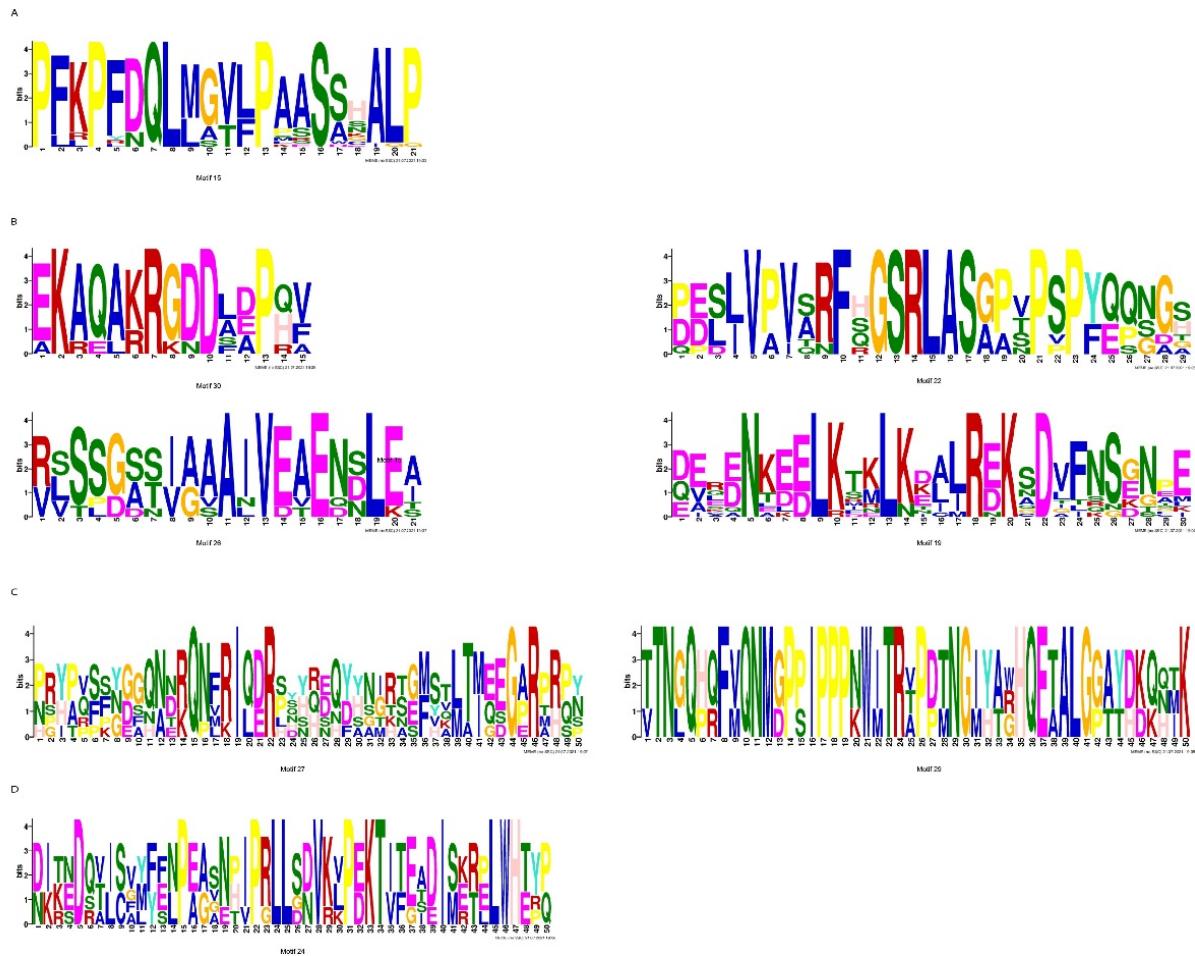


RMSD	TM-score	Score	SI%	SS%	Length
3.19	0.72	1738.79	52	63	777



**Figure S1.** The pairwise structure alignment of two plant XRN proteins. The pairwise structure alignment of AtXRN3 (Orange) and OsXRN3 (Blue), displaying high similarity in the domains of alpha-helices and beta-sheets. The root mean square deviation (RMSD), TM-score, Score for structural similarity, sequence identity percentage (SI%), sequence similarity percentage (SS%) and the length of residue pairs structurally equivalent in the alignment were showed.

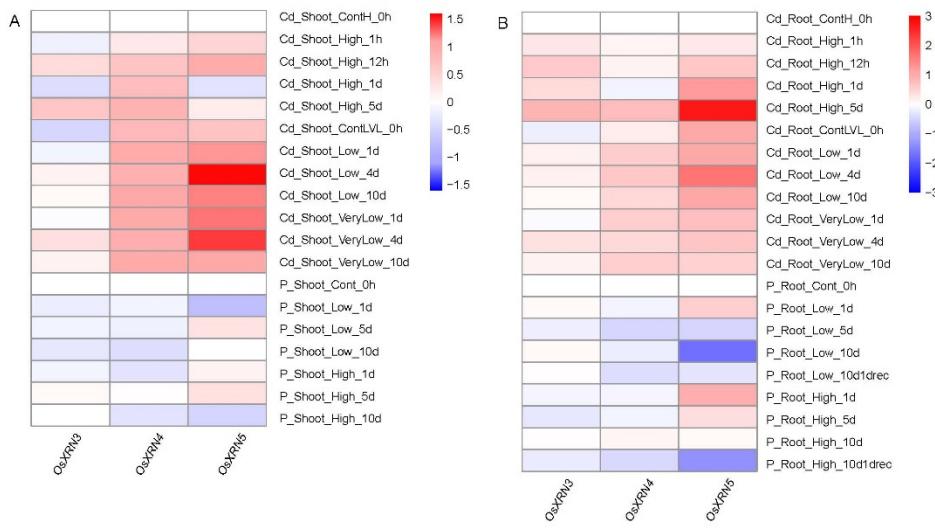


**Figure S2.** Visualization of the selected conserved motif sequences. (A) Motif 15, shared among all 23 XRN s. (B) Motifs 30, 22, 26 and 19 that were frequently lost in XRN4, XRN5 and a few of XRN3. (C) Motifs 27 and 29 specifically detected in XRN4 proteins. (D) Motif 24 specifically detected in XRN5 proteins.

	14	7	
5FIR_C	2 GVPATFRWLTKYpatvnaNEDqrqdqgNRVpdctgnPNFQ-EFDONLYLDKNGI1HPCThpe-----	66	
XP_001610853	1 ----FYWLLDNNgsfksgl-----ekvierPVDHYLMDMNAVINHVAThgni-----	44	
Q4U127	79 GVRPLRYGMMEWFsdrvip1D-----D-----SEISKGVUDYFVDMNAVINHSAThgni-----	126	
EFC46364	2 GVPFLFSFLSSECpemikeIPS-----SSASS----SNTTMTIDHLYLMMGIIHTFKdtnlgtkllerlvssss	69	
Q55506	2 TVPGLSGFINSKF-----QG-----TCIke-----rGNGKixVDBHFVDVNINLLYRKYky-----	46	
EGC39673	2 GVEGLQVFICKRKYlykp-----lpnnfHTDHYIDIVNVNLHKITkk-----	44	
XP_004029912	2 GVPGVFGWICRKYpckrykiY-----Q-----SGKKKxVDCYLIDVSFCYQVtkddln-----	50	
WGS:AAGF:cds.TTHERM_00663830A	2 GVPGVFSWIHRKyqvkrV-----R-----NGRKxHDLCLIDVNGCYQArdehg-----	50	
A0CLH9	2 GVPNFYSWLSKRYpmckypfT-----R-----HHGhxDIFLYLDMNQV1YKAAtngtl-----	49	
A0CZ91	2 GVPNFYSWLMRRPcl-----yht-----RaQRDVYFLDMNQI1YKAAtdpctyl-----	48	
5FIR_C	67 drapAKNEDEXFALIIFYEDRITYSIVRPPRLLYXAIDGVAPRAKXNQRSRRFASREXAEK-----	128	
XP_001610853	45 -----spvVQANEQRLRRTSAIEMMFDIVRPPRKMLYMAVGVCPTAKINQQRGRFLTSKNDPLadicsav	113	
Q4U127	127 pflIMQEDQRMQRMRVIAALLNTFLVLPKPKMMyIYGVCPGCSAKINQQRTRFLYKSNSNdeeykev	195	
EFC46364	70 sssssssssnneeve-----IPKTFNLLVLPKPKMMyIYGVCPGCSAKINQQRTRFLYKSNSNdeeykev	149	
Q55506	47 -----xKTPDRTLFDIVNLQIYSLFDKDVKEKS1FFAVDGPPIKSFSEOKDRFKNDALPNFLhklntkk	113	
EGC39673	45 -----piQANRNLKRKHFNEIYSTKIRHPIFFSVDPGPGRSKMTTQEERRLKNLNLHLLyjinknr	112	
XP_004029912	51 -----gylNQPSLQIYQNLTHIESIOLIEPOQSQVYLMMDGTCPRAKMNQQRORRFHAQMNLNQ-----	113	
WGS:AAGF:cds.TTHERM_00663830A	51 -----yndl1KPKS1FQVLDHIDS1IELVEPQLQVYLMMDGPGSAPCAKINQQRERRWVSFNNHSGLpkrhhh	114	
A0CLH9	50 -----1kdyn1EKSIESLWTS1LNyIDT1LNLDQVLQVYLMMDGPGSAPCAKINQQRERRWVSFNNHSGLpkrhhh	120	
A0CZ91	49 -----fkdq1LERDFDT1VS1LDM1I1NLVNPQQLFLAFQDVAFRAKMNQQRQRFQSQRKRYK1qlkql	119	
5FIR_C	129 -----S-IEEQRNRLXAEGLAVPpkkEEAHFDNSC1TPGTPIFARLADALRYIH-----RVTndr-----	187	
XP_001610853	114 saEdgytyiaakRLPFDNEYDONS-----FNPNY1SPGTDPMK1VDSE1SNWLAL-----KTegf-----	167	
Q4U127	196 dgxKjykvnk1KRNQVQNS-----FPNSY1SPGTDPMK1VDSE1SNWLALLgnyETw-----	248	
EFC46364	150 hgqGnhhgeQhDLHGEENRKKKED-----ESLFDSI1STS1GSMKELS1EHPF1K1-----KLQddp-----	209	
Q55506	114 lnQeqdenksDLQLVED5WFDQ5ST-----VEDKCYTSDFGFTSGD1TGYVRAK1Y1S1T1K1fkwKGyF-----	177	
EGC39673	113 deTgendi1NLKHHDYDYLEG1EL-----NVNGFSTLNFTPG1S1FMGLL1SFPIY1YTKN-----KLSf-----	169	
XP_004029912	114 --KE-----DFKQNg1lKEQ1TVPSNSVSPGTPMFFELNK1R1REHEFK-----K1Qeepplne-----	164	
WGS:AAGF:cds.TTHERM_00663830A	115 -----KD-----ELKKHgfDVKET1TVPNNS1IARG1P1MYELNEQ1L1R1Y1ET-----R1alsnkamtgead	171	
A0CLH9	121 d1EQN-----hFKNQ1TAGTE1P1M1YELNEQ1KF1N1R-----KFKe-----	160	
A0CZ91	120 g1FOQ-----etYKNNQ1SPGTE1TVQ1LNQ1KF1Y1ER-----K1Sed-----	159	
5FIR_C	188 -----swAN-IE1ILSDANVPGCEEHK1XDYVRKQRQgnPAHDPTN-----HLCGADADLIXLGI1ATHAEANF1 251		
XP_001610853	168 -----fgK-----CMVTINGVTPVGEGEHK1FQCIKRMN-----VCKCRSR1d-----H1VYGLADAMLMSMVA1KMPN1KV	230	
Q4U127	249 -----NcY1VYNGT1DVPGEGEHK1YD1T1R1M1-----ELDPDVR1st-----H1VYGLADAMVMSL1T1KLPKNY1 310		
EFC46364	210 -----nvRN1EN1IFSDSVFGEGEHK1MSH1RK1VQ-----Q1PNR1Se1kPM1YGMDS1L1LLSL1V1HED1IV	273	
Q55506	178 -----EDLENVY1SPHOR1YRGCEGEW1FEMINNS-----IKPREP-----IL1YSSDSDV1F1LS1LA1KNS1I 236		
EGC39673	170 -----aK-----NVF1SA1DRMGCEGEW1K1FQH1NN1N-----Y1LND1-----ITIAS1NSD1M1L1F1C1L1SKYNN1Q1	226	
XP_004029912	165 -----kttdt1YKR-LH11SD1SCNCGEGEHK1LEV1RKHK-----NFKLT-----HC1V5PDAD1L1L1S1A1GR1L1 227		
WGS:AAGF:cds.TTHERM_00663830A	172 kehqvsyKK-LQF1LSD1SNAPGEGEHK1LEV1RKHT-----NLQ1T-----HC1VGDAD1L1L1SLA1T1G1R1L1 235		
A0CLH9	161 -----kyAN-LQV1FSGSDVPGEGEHK1LEFMRG1K1qQN1NP1DWT-----H1C1Y1SAD1D1L1M1L1G11HL1KV1S1 224		
A0CZ91	160 -----kfKN-1K1FSGCDVPGEGEHK1L1S1F1R1NLQ-----CDP1NSV-----H1M1Y1G1AD1L1M1L1G11T1Q1LN1V1 219		



**Figure S3.** The conceived protein sequences of XRN 5'-3' exonuclease N-terminus. (A) The protein alignment of XRN 5'-3' exonuclease N-terminus that possess 5'-3' exonuclease activity, showing 10 most diverse species. The number ID of identified motif corresponding to the conserved sequences were marked. (B) The motifs 14, 7, 4, 9, 21, 6, 18 and 1 in XRN 5'-3' exonuclease N-terminus domain.



**Figure S4.** Cluster analysis of the OsXRNs expression pattern response to nutrition. Heatmaps demonstrate the expression profiles of OsXRNs in response to Cd and P in rice shoot (A) and root (B).