

Supplemental Figure S1

At7 MAASPKIGIGIASVSSPHRVSAASSALSPPPHLFFLTTTTTTRHGGSYLLRQPTRTRSSD 60
 At8 MAASPKIGIGIASVSSPHRVSAASSALSPPPHLFFLTTTTTTRHGGSYLLRQPTRTRSSD 60
 Os8 -MAVTRLAVAAAALSAKALRASAAP----- 23
 Hv3 -----
 Mt2 -MATAKIGLFGVATLPPTHNHRITTASSHHRFIFINS-----RRSLRTRSSS 46
 Ol -MRTHARAVAAVKVTTTTTTRASHARANRCRRSTIDAR-----ARRART 43
 Te -----
 Ns -----MFSCHSPCRS----- 10
 Pm -----
 At1 -----MCWISMSQSRFIIKSLFSTAGGFLLGSALSNPSSL 35
 At5 -----
 At2 -----MNCVSRCLKLISKARSFAR-LGGESTLSQPPSL 32
 At4 -----
 At3 -----
 At6 -----
 Mt1 -----MKFRFCPNNNWITLFNKARNLISTQ 25
 Os2 -----
 Os3 -----
 Os1 -----
 Hv2 -----
 Hv1 -----
 Ta -----
 Os4 -----
 Os5 -----
 Os6 -----MRLCSKLAALLRRSRQFAPAAAAA 24
 Os7 -----MRLCSKLAALLRRSRQFAPAAAAA 24
 Nc -----
 Pc -----
 Sc -----
 Ec -----
 Yp -----
 Hi -----



At7 SLRLRVSATANSPSSSSSGGEIIENVVIIIGSGPAGYTAAYAAANLKPVVFEQYQMGV 120
 At8 SLRLRVSATANSPSSSSSGGEIIENVVIIIGSGPAGYTAAYAAANLKPVVFEQYQMGV 120
 Os8 ---AVDEEAPASPPPSDLGKGVENLVIIGSGPAGYTAAYAAANLKPVVFEQYQVGGV 79
 Hv3 -----PGRGVENLVIIGSGPAGYTAAYAAANLKPVVFEQYQVGGV 42
 Mt2 SLTLRASSDTSSSSVAS-PGNAVENVVIIGSGPAGYTAAYAAANLKPVVFEQYQMGV 105
 Ol TTTTTTTRASAQEQUATEDAPDVENCVIIGSGPAGYTAAYAGRANLRPLMFEGFQAGGV 103
 Te -----MTPPRIENVVIIIGSGPAGYTAAYAAANLKPPLMFEGYQIGGL 43
 Ns DMLCYIKRSRYEFVINIMSNPTVENLVIIGSGPAGYTAAYAAANLKPVVFEQYQAGGL 70
 Pm -----METKVKEDNVENLVIIGSGPAGYTAAYAAANLQPLLVTGFNSGGI 47
 At1 ATAFSSSSSSSSAAAADMETHKTKVCIVGSGPAAHTAAYASRAELKPLLFEGWMANDI 95
 At5 -----LKPLLFEGWMANDI 14
 At2 A-----SAAFSSSAVMNGLETHNTRLCIVGSGPAAHTAAYAAARELKPLLFEGWMANDI 87
 At4 -----MNGLETHNTRLCIVGSGPAAHTAAYAAARELKPLLFEGWMANDI 45
 At3 -----MNGLETHNTRLCIVGSGPAAHTAAYAAARELKPLLFEGWMANDI 45
 At6 -----MNGLETHNTRLCIVGSGPAAHTAAYAAARELKPLLFEGWMANDI 45
 Mt1 RASVSSAASATAMTDTTTLPTVKTKLCIIGSGPAAHTAAVYAARELKPILFEGWMANDI 85
 Os2 -----MEGSAGAPLRTRVCIIGSGPSAHTAAYAAARELKPVLFEQWLANDI 47
 Os3 -----MEGSAGAPLRTRVCIIGSGPSAHTAAYAAARELKPVLFEQWLANDI 47
 Os1 -----MEGSAGAPLRTRVCIIGSGPSAHTAAYAAARELKPVLFEQWLANDI 47
 Hv2 -----MEGSAAAPLRTRVCIIGSGPAAHTAAYAAARELKPVLFEQWMANDI 47
 Hv1 -----MEEAAAGPLRTRVCIIGSGPAAHTAAVYAARELKPVLFEQWLANDI 47
 Ta -----MEEAAAGPLRTRVCIIGSGPAAHTAAVYAARELKPVLFEQWLANDI 47
 Os4 -----MEEAAAGPLRARVCIIGSGPAAHTAAVYAARELKPVLFEQFLANDI 47

Os5	----	CASAPSSRRCSSGGPAGPLRARVCI	I	GSGPAAHTAAVYAARAELKPVLFEGFLANDI	56	
Os6		SGSATAAAAASANGMEEAAAGPLRARVCI	I	GSGPAAHTAAVYAARAELKPVLFEGFLANDI	84	
Os7		SGSATAAAAASANGMEEAAAGPLRARVCI	I	GSGPAAHTAA-----	63	
NC		-----	MHSKVVII	I	GSGPAAHTAAIYLARAELKPVLYEGFMANGI	39
Pc		-----	MVHSKVVII	I	GSGGAGAHTAAIYLSRAELQPVLYEGMLANGT	40
Sc		-----	MVHNKVTII	I	GSGPAAHTAAIYLARAELKPVLYEGMMANGI	40
Ec		-----	MGTTKHSKLLII	I	GSGPAGYTAAVYAARANLQPVLYITGMEK---	40
Yp		-----	MSTAKHSKLIII	I	GSGPAGYTAAVYAARANLQPVLYITGMEK---	40
Hi		-----	MSDIKHAKLLII	I	GSGPAGYTAAYAAARANLQPVLYITGMEK---	40

At7		P-GGQLMTTTEVENFPGFPDGITGPDLM	MEKMRKQAERWGAELYPEDVESLSVTTAPFTVQ	179	
At8		P-GGQLMTTTEVENFPGFPDGITGPDLM	MEKMRKQAERWGAELYPEDVESLSVTTAPFTVQ	179	
Os8		P-GGQLMTTTEVENFPGFPDGVTPDLM	DKMRKQAERWGAELHQEDVEFVNVKSRPFVIR	138	
Hv3		P-GGQLMTTTEVENFPGFPDGITGPDLM	DKMRKQAERWGAELHQEDVEFVDVKSRRPFVIR	101	
Mt2		P-GGQLMTTTEVENFPGFPDGITGPDLM	DRMRQAERWGAELHHEDVEAIDVKTSPFTVQ	164	
Ol		P-GGQLMTTTEVENFPGFPDGVTPDLM	DKMRKQAERWGAVMHTEDVTVDFTSRPFVIR	162	
Te		P-GGQLMTTTEVENFPGFPDGVTPDLM	DKMRKQAERWGTEMVTEVDVIQVDFSRPFVIR	102	
Ns		P-GGQLMTTTEVENFPGFPDGVTPDLM	DKMRKQAERWGTEMVTEVDVIQVDFSRPFVIR	129	
Pm		P-GGQLMTTTFVENYPGFPDGVTPDLM	DKMRKQAERWGTEMVTEVDVIQVDFSRPFVIR	106	
At1		APGGQLTTTTDVENFPGFPDGVTPDLM	DKMRKQAERWGTEMVTEVDVIQVDFSRPFVIR	155	
At5		APGGQLTTTTDVENFPGFPDGVTPDLM	DKMRKQAERWGTEMVTEVDVIQVDFSRPFVIR	74	
At2		APGGQLTTTTDVENFPGFPDGVTPDLM	DKMRKQAERWGTEMVTEVDVIQVDFSRPFVIR	147	
At4		APGGQLTTTTDVENFPGFPDGVTPDLM	DKMRKQAERWGTEMVTEVDVIQVDFSRPFVIR	105	
At3		APGGQLTTTTDVENFPGFPDGVTPDLM	DKMRKQAERWGTEMVTEVDVIQVDFSRPFVIR	105	
At6		APGGQLNQPP-RENFPDGVTPDLM	DKMRKQAERWGTEMVTEVDVIQVDFSRPFVIR	104	
Mt1		APGGQLTTTTDVENFPGFPDGVTPDLM	DKMRKQAERWGTEMVTEVDVIQVDFSRPFVIR	145	
Os2		AAGGQLTTTTDVENFPGFPDGVTPDLM	DKMRKQAERWGTEMVTEVDVIQVDFSRPFVIR	107	
Os3		AAGGQLTTTTDVENFPGFPDGVTPDLM	DKMRKQAERWGTEMVTEVDVIQVDFSRPFVIR	107	
Os1		AAGGQLTTTTDVENFPGFPDGVTPDLM	DKMRKQAERWGTEMVTEVDVIQVDFSRPFVIR	107	
Hv2		AAGGQLTTTTDVENFPGFPDGVTPDLM	DKMRKQAERWGTEMVTEVDVIQVDFSRPFVIR	107	
Hv1		AAGGQLTTTTDVENFPGFPDGVTPDLM	DKMRKQAERWGTEMVTEVDVIQVDFSRPFVIR	107	
Ta		AAGGQLTTTTDVENFPGFPDGVTPDLM	DKMRKQAERWGTEMVTEVDVIQVDFSRPFVIR	107	
Os4		AAGGQLTTTTDVENFPGFPDGVTPDLM	DKMRKQAERWGTEMVTEVDVIQVDFSRPFVIR	107	
Os5		AAGGQLTTTTDVENFPGFPDGVTPDLM	DKMRKQAERWGTEMVTEVDVIQVDFSRPFVIR	116	
Os6		AAGGQLTTTTDVENFPGFPDGVTPDLM	DKMRKQAERWGTEMVTEVDVIQVDFSRPFVIR	144	
Os7		-----	LTTTTTDVENFPGFPDGVTPDLM	DKMRKQAERWGTEMVTEVDVIQVDFSRPFVIR	118
NC		AAGGQLTTTTTEIENFPGFPDGVTPDLM	DKMRKQAERWGTEMVTEVDVIQVDFSRPFVIR	99	
Pc		AAGGQLTTTTTEIENFPGFPDGVTPDLM	DKMRKQAERWGTEMVTEVDVIQVDFSRPFVIR	100	
Sc		AAGGQLTTTTTEIENFPGFPDGVTPDLM	DKMRKQAERWGTEMVTEVDVIQVDFSRPFVIR	100	
Ec		--GGQLTTTTTEVENWPGDNDL	TGPELLMERMHEHATKFETEIIIFDHINKVDLQNRPFRLN	98	
Yp		--GGQLTTTTTEVENWPGDNDL	TGPELLMERMHEHATKFETEIIIFDHINKVDLQNRPFRLN	98	
Hi		--GGQLTTTTTEIENWPGDNDL	TGPELLMERMHEHATKFETEIIIFDHINKVDLQNRPFRLN	98	

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At7		TSE-----	RKVKCHSIIYATGATARRLRLPRE----	EEFWSRGISACAICDGASPLFK	228
At8		TSE-----	RKVKCHSIIYATGATARRLRLPRE----	EEFWSRGISACAICDGASPLFK	228
Os8		SSD-----	REVKCHSVIIATGATAKRLRLPRE----	DEFWSRGISACAICDGASPLFK	187
Hv3		SSD-----	REVKCHSVIIATGATAKRLRLPRE----	EEFWSRGISACAICDGASPLYK	150
Mt2		SSE-----	RKVKSHTVIIATGATAKRLRLPRE----	DEFWSRGISACAICDGASPLFK	213
Ol		SSD-----	RTVKANSVIVATGATAKRLGIPAE----	ATLWSRGISACAICDGASPIFK	211
Te		SAE-----	RQVYAHSVIICTGATAKRLHLPGE----	EQYWTGKVSACAICDGATPIFK	151
Ns		SEE-----	REVKAHTIIIIATGATAKRLGLPSE----	HEFWSRGISACAICDGATPIFH	178
Pm		TLE-----	GSIKSNSIIIIATGASANRLGVINE----	DKFWSKGISACAICDGATPQFR	155
At1		TDS-----	RTVLADSVIIISTGAVAKRLSFTGSGEGNGGF	WNRGISACAVCDGAAPIFR	208
At5		TDS-----	RTVLADSVIIISTGAVAKRLSFTGSGEGNGGF	WNRGISACAVCDGAAPIFR	127
At2		TDS-----	KAILADAVILATGAVAKRLSFGVSGEASGGF	WNRGISACAVCDGAAPIFR	200
At4		TDS-----	KAILADAVILATGAVAKRLSFGVSGEASGGF	WNRGISACAVCDGAAPIFR	158
At3		TDS-----	KAILADAVILAIGAVAKRLSFGVSGEVLGGF	WNRGISACAVCDGAAPIFR	158

At6 TDS-----KAILADAVILAIGAVAKWLSFVGSGEVLGGLWNRGISACAVCDGAAPIFR 157
 Mt1 TDS-----RTVEADSVIVATGAVAKRLPFTGSGDGPNGYWNRGISACAVCDGAAPIFR 198
 Os2 SDS-----TTVLADAVVVATGAVARRLHFAGS----DAYWNRGISACAVCDGAAPIFR 156
 Os3 SDS-----TTVLADAVVVATGAVARRLHFAGS----DAYWNRGISACAVCDGAAPIFR 156
 Os1 SDS-----TTVLADAVVVATGAVARRLHFAGS----DAYWNRGISACAVCDGAAPIFR 156
 Hv2 SDS-----TTVLADTVVVATGAVARRLYFSGS----DTYWNRGISACAVCDGAAPIFR 156
 Hv1 SDD-----TVVHADSVVVATGAVARRLHFAGS----DAFWNRGISACAVCDGAAPIFR 156
 Ta SDD-----TVVHADSVVVATGAVARRLHFAGS----DAFWNRGITACAVCDGAAPIFR 156
 Os4 SGD-----TVVHADAVVVATGAVARRLHFAGS----DAFWNRGISACAVCDGAAPIFR 156
 Os5 SGD-----TVVHADAVVVATGAVARRLHFAGS----DAFWNRGISACAVCDGAAPIFR 165
 Os6 SGD-----TVVHADAVVVATGAVARRLHFAGS----DAFWNRGISACAVCDGAAPIFR 193
 Os7 SGD-----TVVHADAVVVATGAVARRLHFAGS----DAFWNRGISACAVCDGAGPIFR 167
 NC TEWSPEE---YHTADSIILATGASARRLHLPGE----EKYWQNGISACAVCDGAVPIFR 151
 Pc TEWNDEGSEPVRTADAVIIATGANARRLNLPGE----ETYWQNGISACAVCDGAVPIFR 156
 Sc TEFNEDAEP---VTTDAIILATGASAKRMHLPGE----ETYWQKGISACAVCDGAVPIFR 153
 Ec GDN-----GEYTCDALIIATGASARYLGLPSE----EAFKGRGVSA CATCDG--FFYR 145
 Yp GDG-----AEYTCDALIIATGASARYLGMASE----EAFKKGKGVSA CATCDG--FFYR 145
 Hi GDV-----QNFTCDALIIATGASARYIGLPSE----ENYKGRGVSA CATCDG--FFYR 145

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At7 GQVLAVVGGGDTATEEALYLTKYARHVHLLVRRDQLRASKAMQDRVINNP---NITVHYN 285
 At8 GQVLAVVGGGDTATEEALYLTKYARHVHLLVRRDQLRASKAMQDRVINNP---NITVHYN 285
 Os8 GQVLAVVGGGDTATEEAIYLTKYARHVHLLVRKDQLRASKAMQDRVLNPN---NITVHFN 244
 Hv3 GQVLAVVGGGDTATEEAIYLTKYACHVHLLVRRDQLRASKAMQDRVLNPN---NITVHFN 207
 Mt2 GQILAVVGGGDTATEEALYLTKYARHVHLLVRRDQLRASKAMQDRVYDNP---NVTVHFN 270
 Ol GEEVAVVGGGDTATEEAVYLTKYAKHVHLLVVRGSTMASKAMQDRVLOHK---AITVHYN 268
 Te DVELAVI GGGDSA AEEAVYLTKYGSHVHLLVRS DKMRASKAMQDRVFNPN---KITVHWQ 208
 Ns GAELAVI GAGDSA AEEESIYLTKYGSKVNLLVRS EKMASKAMQDRVLSNP---KIQVHWN 235
 Pm NEELAVI GGGDSA CEEAAYLTKYGSKVHLLVRS EKLRSAA MIDRVKANS---KIEIHWN 212
 At1 NKPLVVI GGGDSAMEEANFLTKYGSKVYI IHRRTFRASKIMQQRALSNP---KIEVIWN 265
 At5 NKPLVVI GGGDSAMEEANFLTKYGSKVYI IHRRTFRASKIMQQRALSNP---KIEVIWN 184
 At2 NKPLAVI GGGDSAMEEANFLTKYGSKVYI IHRRAFRASKIMQQRALSNP---KIDVIWN 257
 At4 NKPLAVI GGGDSAMEEANFLTKYGSKVYI IHRRAFRASKIMQQRALSNP---KIDVFWN 215
 At3 NKPLAVI GGGDSAMEEANFLTKYGSKVYI IHRRAFRASKIMQQRALSNP---KIDVIWN 215
 At6 NKPLAVI GGGDSAMEEANFLTKYGSKVYI IDRRDAFRASKIMQQRALSNP---KIDVIWN 214
 Mt1 NKPLAVI GGGDSAMEEATFLTKYGSEVYI IHRRTFRASKIMQSKALSNE---KIKVIWN 255
 Os2 NKPIAVI GGGDSAMEESNFLT KYGSHVYI IHRNTFRASKIMQARALSNP---KIQVFW 213
 Os3 NKPIAVI GGGDSAMEESNFLT KYGSHVYI IHRNTFRASKIMQARALSNP---KIQVFW 213
 Os1 NKPIAVI GGGDSAMEESNFLT KYGSHVYI IHRNTFRASKIMQARALSNP---KIQVFW 213
 Hv2 NKPIAVI GGGDSAMEEGNFLT KYGSQVYI IHRNTFRASKIMQARALSNP---KIQVWD 213
 Hv1 NKPIAVV GGGDSAMEEANFLTKYGSRVYI IHRRAFRASKIMQARALSNP---KIQVWD 213
 Ta NKPIAVV GGGDSAMEEANFLTKYGSRVYI IHRRAFRASKIMQARALSNP---KIQVWD 213
 Os4 NKPIAVV GGGDSAMEEANFLTKYGSRVYI IHRRAFRASKIMQARALSNP---KIQVWD 213
 Os5 NKPIAVV GGGDSAMEEANFLTKYGSRVYI IHRRAFRASKIMQARALSNP---KIQVWD 222
 Os6 NKPIAVV GGGDSAMEEANFLTKYGSRVYI IHRRAFRASKIMQARALSNP---KIQVWD 250
 Os7 NKPIAVV GGGDSAMEEANFLTKYGSRVYI IHRRAFRASKIMQARALSNP---KIQVWD 224
 NC NKHLVVI GGGDSA AEEAMFLTKYGSHTVLRKDKLRASSIMAHRLLNHE---KVTVRFN 208
 Pc NKPLYVI GGGDSA AEEAMFLAKYGSVTVLRKDKLRASSIMADRLLAHP---KCKVRFN 213
 Sc NKPLAVI GGGDSA CEEAQFLT KYGSKVFLVRKDH LRASTIMQKRAEKNE---KIEILYN 210
 Ec NQKVAVI GGGNTAVEEALYLSNIASEVHLIHRRDGFRAEKILIKRLMDKVENGNIILHTN 205
 Yp NQKVAVV GGGNTAVEEALYLANIAAEVHLIHRRTFRSEKILIDRLMEKVKNGNIVLHTD 205
 Hi NKPVGVI GGGNTAVEEALYLANIASTVHLIHRRDSFRAEKILIDRLYKKEEGKIVLHTD 205

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At7 TETVDVLSNTK--GQMSGILLRRL-DTGEETELEAKGLFYGIGHSPNSQLLEGQVELDSS 342
 At8 TETVDVLSNTK--GQMSGILLRRL-DTGEETELEAKGLFYGIGHSPNSQLLEGQVELDSS 342
 Os8 TEAVDVVSNPK--GQMSGIQLKRT-DTGEESVLEVKGLFYGIGHTPNSQLLQGDIDLDDA 301
 Hv3 TEAVDVVGNTK--GQMSGIQLRRI-DTGEKLVLEVKGLFYGIGHTPNSQLLEGQIELDSS 264
 Mt2 TETVDIVSNTK--GQMSGILVRKL-DSGEESVLEAKGLFYGIGHSPNTQLLKGQVELDQS 327

Ol TECVDGSPNSK--GNLGALKLRDT--NNGDERQLKVKGLFYGIGHTPNSKIFGNQIELDEA 325
 Te TEAREILGDGN---LMTGLRI INK--ATGEESLLPVRGLFYAIGHTPNTQLFKDFLELDSV 264
 Ns TEVVDVFGNG----HMDGVKVRNN--QTGEETNVHAKGLFYAIGHKPNTSLFQGGLELDEI 290
 Pm TKVEK--ANGT--DWLENVETINS--HKGN--VEIKVKGLFYAIGHTPNTKFLNNKIELDKK 266
 At1 SAVVEAYGDEN--GRVLGGLKVKNV--VTGDVSDLKVSGLFFAIGHQPATKFLDGGQLELDED 323
 At5 SAVVEAYGDEN--GRVLGGLKVKNV--VTGDVSDLKVSGLFFAIGHQPATKFLDGGQLELDED 242
 At2 SSVVEAYGDGE--RDVLGGLKVKNV--VTGDVSDLKVSGLFFAIGHQPATKFLDGGVVELDSD 315
 At4 SSVVEAYGDGE--RDVLGGLKVKNV--VTGDVSDLKVSGLFFAIGHQPATKFLDGGVVELDSD 273
 At3 SSVVEAYGDGE--RDVLGGLKVKNV--VTGDVSDLKVSGLFFAIGHQPATKFLDGGVVELDSD 273
 At6 SSVVEAYGDGE--RDVLGGLKVKNV--VTGDVSDLKVSGLFFAIGHQPATKFLDGGVVELDSD 272
 Mt1 SMVVEAFGDGE--NKKLGGLKVENV--VTKEVTDLQVSGGLFFAIGHQPATKFLDGGQLELSD 313
 Os2 SEVVEAYGGEG--GGPLAGVKVKNL--VTGKISDLQVSGGLFFAIGHQPATKFLGGQLELSD 271
 Os3 SEVVEAYGGEG--GGPLAGVKVKNL--VTGKISDLQVSGGLFFAIGHQPATKFLGGQLELSD 271
 Os1 SEVVEAYGGEG--GGPLAGVKVKNL--VTGKISDLQVSGGLFFAIGHQPATKFLGGQLELSD 271
 Hv2 SEVVEAYGGAG--GGPLAGVKVKNL--VTGEVSDLQVSGGLFFAIGHQPATKFLNGQLELHAD 271
 Hv1 SEVVEAYGGSD--GGPLAGVKVKNL--VSGEVSDVQVAGLFFAIGHQPATKFLAGQLELSD 271
 Ta SEVVEAYGGSD--GGPLGGVKVKNL--VTGEVSDFRVAGLFFAIGHQPATKFLAGQLELSD 271
 Os4 SEVVEAYGGAD--GGPLAGVKVKNL--VSGEVSDLQVAGLFFAIGHQPATKFLGGQLELSD 271
 Os5 SEVVEAYGGAD--GGPLAGVKVKNL--VSGEVSDLQVAGLFFAIGHQPATKFLGGQLELSD 280
 Os6 SEVVEAYGGAD--GGPLAGVKVKNL--VSGEVSDLQVAGLFFAIGHQPATKFLGGQLELSD 308
 Os7 SEVVEAYGGAD--GGPLAGVKVKNL--VSGEVSDLQVAGLFFAIGHQPATKFLGGQLELSD 282
 NC TVGVEVKGDDK--GLMSHLVVKDV--TTGKEETLEANGLFYAIGHDPATALVKGQLELSD 265
 Pc TVATEVIGENKPNGLMTHLRVKDV--LSNAEEVVEANGLFYAVGHDPASGLVKGQVELDDE 272
 Sc TVALEAKGDGK---LLNALRIKNT--KKNEETDLPVSGGLFYAIGHTPATKIVAGQVDTDEA 266
 Ec RTLEEVTGDQM---GVTGVRLRDTQNSDNIESLDVAGLFFAIGHSPNTAIFEGQLELEN- 261
 Yp RTLDEVLGDDM---GVTGVRLKST--HSDETEELAVAGVFIAIGHSPNTGIFSDQLALEN- 260
 Hi RTLDEVLGDNM---GVTGLRLANT--KTGEKEELKLDGLFVAIGHSPNTEIFQGGLELNN- 260

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At7 GYVLVREGT----SNTSVEGVFAAGDVQDHEWRQAVTAAGSG----CIAALSAERYLTSN 394
 At8 GYVLVREGT----SNTSVEGVFAAGDVQDHEWRQAVTAAGSG----CIAALSAERYLTSN 394
 Os8 GYILVEEGT----AKTSVDGVFAAGDVQDHEWRQAVTAAGSG----CVAALSVERYLVAN 353
 Hv3 GYILVEEGT----AKTSVDGVFAAGDVQDHEWRQAVTAAGSG----CIAALSVERYLVSS 316
 Mt2 GYLLVKEGT----AKTSVEGVFAAGDVQDHEWRQAVTAAGSG----CIAALSVERYLVSS 379
 Ol GYVVVREGT----R--T--SIEGVFSAGDLHDQEFRQAITAAGSG----CMAAISVERYLTK 376
 Te GYIVTRHG----TQTINVEGVFAAGDVQDHEWRQAVTAAGSG----CMAALDAERWLSAR 315
 Ns GYVVTKHGS----PETSVEGVFAAGDVQDHEWRQAVTAAGSG----CAAALLAERWLSAN 342
 Pm GYIACNSGR----PETSIEGIFAAGDVVDSEWRQGVTAAGTG----CMAALAAERWLAEK 318
 At1 GYVVTKPGT----TKTSVVGVFAAGDVQDKKYRQAITAAGTG----CMAALDAEHY---- 371
 At5 GYVVTKPGT----TKTSVVGVFAAGDVQDKKYRQAITAAGTG----CMAALDAEHY---- 290
 At2 GYVVTKPGT----TQTSVPGVFAAGDVQDKKYRQAITAAGTG----CMAALDAEHY---- 363
 At4 GYVVTKPGT----TQTSVPGVFAAGDVQDKKYRQAITAAGTG----CMAALDAEHY---- 321
 At3 GYVVTKPGT----TQTSVPGVFAAGDVQDKKYRQAITAAGTG----CMAALDAEHY---- 321
 At6 GYVVTKPGT----TQTSVPGVFAAGDVQDKKYRQAITAAGTG----CMAALDAEHY---- 320
 Mt1 GYVVTKPGT----TKTSVEGVFAAGDVQDKKYRQAITAAGSG----CMAALDAEHF---- 361
 Os2 GYVATKPGS----THTSVKGVFAAGDVQDKKYRQAITAAGS-----EISCFMGCYL---- 318
 Os3 GYVATKPGS----THTSVKGVFAAGDVQDKKYRQAITAAGS-----EISRFMGCYL---- 318
 Os1 GYVATKPGS----THTSVKGVFAAGDVQDKKYRQAITAAGSG----CMAALDAEHY---- 319
 Hv2 GYVATKPGS----THTSVEGVFAAGDVQDKKYRQAITAAGSG----CMAALDAEHY---- 319
 Hv1 GYVATKPGS----THTSVKGVFAAGDVQDKKYRQAITAAGSG----CMAALDAEHY---- 319
 Ta GYVATKPGS----THTSVKGVFAAGDVQDKKYRQAITAAGSG----CMAALDAEHY---- 319
 Os4 GYVVTKPGS----THTSVKGVFAAGDVQDKKYRQAITAAGSG----CMAALDAEHY---- 319
 Os5 GYVVTKPGS----THTSVKGVFAAGDVQDKKYRQAITAAGSG----CMAALDAEHY---- 328
 Os6 GYVVTKPGS----THTSVKGVFAAGDVQDKKYRQAITAAGSDRRPSQAQCLSEERVGKT 364
 Os7 GYVVTKPGS----THTSVKGVFAAGDVQDKKYRQAITAAGSDRRPSQAQCLSEERVGKT 338
 NC GYVVTKPGT----TLTSVEGVFAAGDVQDKRYRQAITSAGTG----CMAALDAEKF---- 313
 Pc GYIITKPGT----SFTINVEGVFACGDVQDKRYRQAITSAGSG----CVAALEAEKF---- 320
 Sc GYIKTVPGS----SLTSVPGFFAAGDVQDSKYRQAITSAGSG----CMAALDAEKY---- 314
 Ec GYIKVQSGIHGNATQTSIPGVFAAGDVMDHIYRQAITSAGTG----CMAALDAERY---- 313



Yp GYIKVQSGLQGNATQTSIPGVFAAGDVM¹MDHIYRQAITSAGTG----CMAALDAERY---- 312
 Hi GYIVVKSGLDGNATAISVEGVFAAGDVM¹MDHNRYRQAITSAGTG----CMAALDAERY---- 312
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At7 NLLVKFHQPQTE----EAKKEFTQRD-----VQEKFDITLTKHKGQYALRKLYHESPRV 444
 At8 NLLVEFHQPQTE----EAKKEFTQRD-----VQEKFDITLTKHKGQYALRKLYHESPRV 444
 Os8 DLLVEFHQPVRE----EKEKEITDRD-----VEMGFDISHTKHRGQYALRKVYHESPRL 403
 Hv3 DLLIEFHQPVRE----EKKKEIEGKD-----VEMGFDIHTTKHKGQYALRKLYHGSPRL 366
 Mt2 GLLIEFHQPKHE----EVKKELTDRD-----VQAGFDITLTKHKGQYALRKLYHDSPL 429
 Ol NLLVEHHQTKQRKS-VEREESVSEERAIQGEDEDSFDINVTKHYGQYALRKLYHESDRV 435
 Te GLIQEFHQQRAT----ETQPAATAKPTAS---PQQEFDPNAIKHRGSYALRKLPHESDRL 367
 Ns ALIQEFHQEATINNELETQPVA-QKTEAE---QEAGFDVNATRHHAGGYALRKLPHESDRL 398
 Pm NLSKIIIVRETSE----PEKTLSSSSFNNEEVTNEDTFNLNSEWQKGSYALRKLYHESNKP 373
 At1 -----
 At5 -----
 At2 -----
 At4 -----
 At3 -----
 At6 -----
 Mt1 -----
 Os2 -----
 Os3 -----
 Os1 -----
 Hv2 -----
 Hv1 -----
 Ta -----
 Os4 -----
 Os5 -----
 Os6 -----
 Os7 -----
 NC -----
 Pc -----
 Sc -----
 Ec -----
 Yp -----
 Hi -----

At7 ILLVLYTSPTCGPCRTLKPIILNKVVDEYNHVDVHFVEIDIEEDQEIAEAAGIMGTPCVQFFK 504
 At8 ILLVLYTSPTCGPCRTLKPIILNKVVDEYNHVDVHFVEIDIEEDQEIAEAAGIMGTPCVQFFK 504
 Os8 VCVLYTSPTCGPCRTLKPIILNKVVDEYNHVDVHFVEIDIEEDPEIAEAAGIMGTPCVQFFK 463
 Hv3 ILLVLYTSPTCGPCRTLKPIILNKVVDEYNHVDVHFVEIDIEEDPEIAEAAGIMGTPCVQFFK 426
 Mt2 ILLVLYTSPTCGPCRTLKPIILNKVVDEYNHVDVHFVEIDIEEDPEIAEAAGIMGTPCVQFFK 489
 Ol VMVMYSAPTCGPCRRLKPMPLDKVIAEYGDKVHYVEIDIAADPEIAEAAGVTGTPMTQIFY 495
 Te LLVKYVSPTCGPCRTLKPIILNKVVDEYNHVDVHFVEIDIEEDPEIAEAAGVTGTPMTQIFY 427
 Ns LIVKYVSPCGPCRTLKPIILNKVVDEYNHVDVHFVEIDIEEDPEIAEAAGVTGTPMTQIFY 458
 Pm ILLVIFSSPCGPCRRLKPMPLDKVIAEYGDKVHYVEIDIEEDPEIAEAAGVTGTPMTQIFY 433
 At1 -----LQEIGSQEGKSD----- 383
 At5 -----LQEIGSQEGKSD----- 302
 At2 -----LQEIGSQEGKSD----- 375
 At4 -----LQEIGSQEGKSD----- 333
 At3 -----LQEIGSQEGKSD----- 333
 At6 -----LQEIGSQEGKSD----- 332
 Mt1 -----LQGVGLQQDKSD----- 373
 Os2 -----LVRIAIEIVQGLSM----- 332
 Os3 -----LVRIAIEIVQGLSM----- 332
 Os1 -----LQEVGAQEGKAD----- 331
 Hv2 -----LQEVGAQEGKAD----- 331
 Hv1 -----LQEVGAQEGKAD----- 331

Ta	-----LQEVGAQEGKTD-----	331
Os4	-----LQEIGAQEDKTD-----	331
Os5	-----LQEIGAQEDKTD-----	340
Os6	-----ITEYLSFSGDTS-----	376
Os7	-----ITEYLSFSGDTS-----	350
NC	-----LSEHEETPAEHRDTSVQGNL-----	334
Pc	-----IAETET---HQEAKPVL-----	334
Sc	-----LTSLE-----	319
Ec	-----LDGLADAK-----	321
Yp	-----LDGLANDK-----	320
Hi	-----LDAQEA-----	318

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At7	NKEMLRITISGVKMKKEYREFIE-----ANK-----	529
At8	NKEMLRITISGVKMKKEYREFIE-----ANK-----	529
Os8	NKEMLRITISGVKMKKEYREFIE-----SNK-----	488
Hv3	NKEMIRTFSGVCMKKEYREFIE-----SNK-----	451
Mt2	NKENLKTIVSGVCMKREYREFIE-----ANI-----	514
Ol	QKERIEVLSGVKMKSEYRRVIDGALGASATKEVTMPAAQAGEKKESPVETSR	547
Te	NKELLEVIIVGMKPKSQYRETLQR-----YLS-----	453
Ns	DKELVKEVKGKQKSEYRLLIEG-----NL-----	483
Pm	DKLLKKQWQGVKQKSEFKEAIQN-----II-----	458
At1	-----	
At5	-----	
At2	-----	
At4	-----	
At3	-----	
At6	-----	
Mt1	-----	
Os2	-----	
Os3	-----	
Os1	-----	
Hv2	-----	
Hv1	-----	
Ta	-----	
Os4	-----	
Os5	-----	
Os6	-----	
Os7	-----	
NC	-----	
Pc	-----	
Sc	-----	
Ec	-----	
Yp	-----	
Hi	-----	

Supplemental Figure S1. Multiple alignment of primary sequences of NTRs from different sources using ClustalW. Active site and the motifs in NADP- and FAD-binding domains are marked with boxes. The region used for phylogenetic analysis is enclosed between arrows. Accession numbers in NCBI protein database are: Os, *Oryza sativa*, Os1 (NP_001047911), Os2 (EAY87270), Os3 (EAZ24372), Os4 (BAD33510), Os5 (NP_001057531), Os6 (EAZ00754), Os7 (EAZ36842), Os8 (NP_001060515); At, *Arabidopsis thaliana*, At1 (Q39242), At2 (NP_195271), At3 (1VDC), At4 (AAO42318), At5 (AAO42318), At6 (CAA80656), At7 (AAL08250), At8 (NP_565954); Hv,

Hordeum vulgare, Hv1 (EU314717), Hv2 (ABX09990), Hv3 (TC132362); Ta, *Triticum aestivum* (CAD19162); Mt, *Medicago truncatula*, Mt1 (ABH10138), Mt2 (ABH10139); Ol, *Ostreococcus lucimarinus* (XP_001422184); Te, *Thermosynechococcus elongates* (NP_682714); Ns, *Nostoc sp.* (NP_484780); Pm, *Prochlorococcus marinus* (NP_893267) ; Nc, *Neurospora crassa* (P51978); Pc, *Penicillium chrysogenum* (P43496); Sc, *Saccharomyces cerevisiae* (P29509); Ec, *Escherichia coli* (P09625); Yp, *Yersinia pestis* (NP_404967); Hi, *Haemophilus influenzae* (P43788).