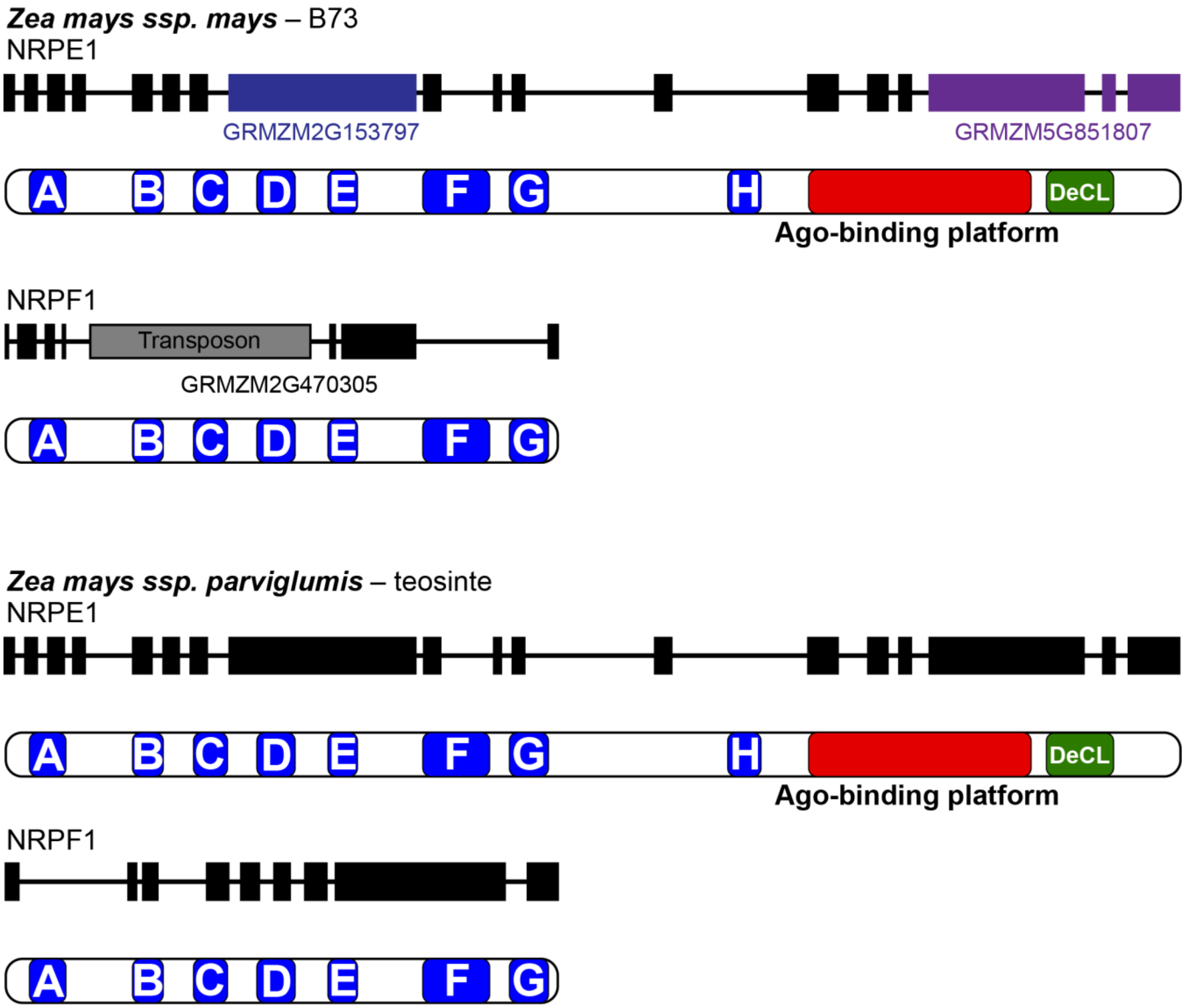
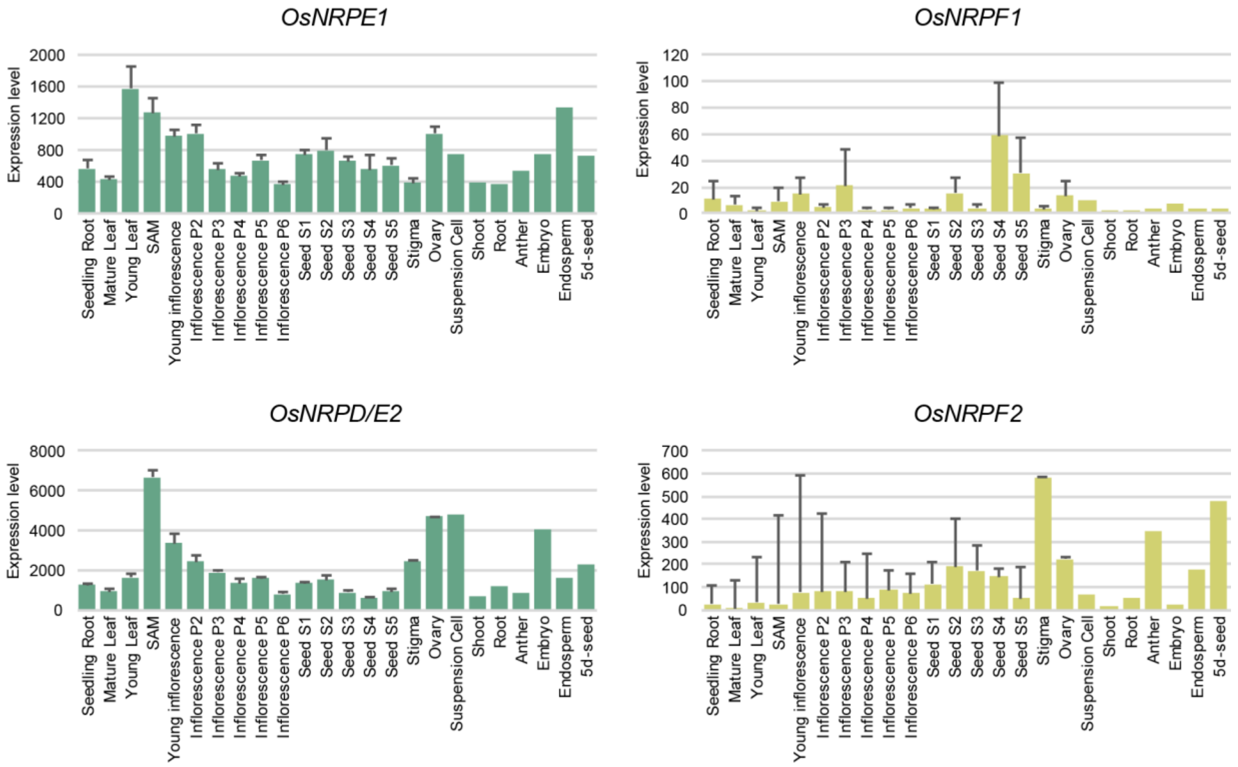
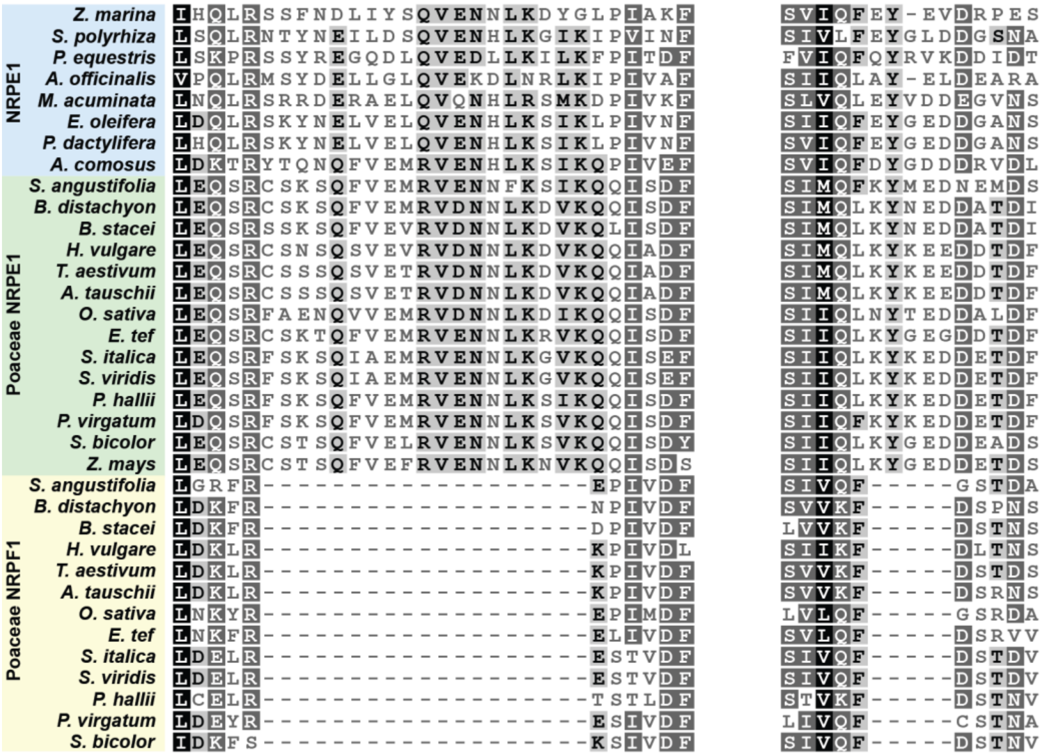


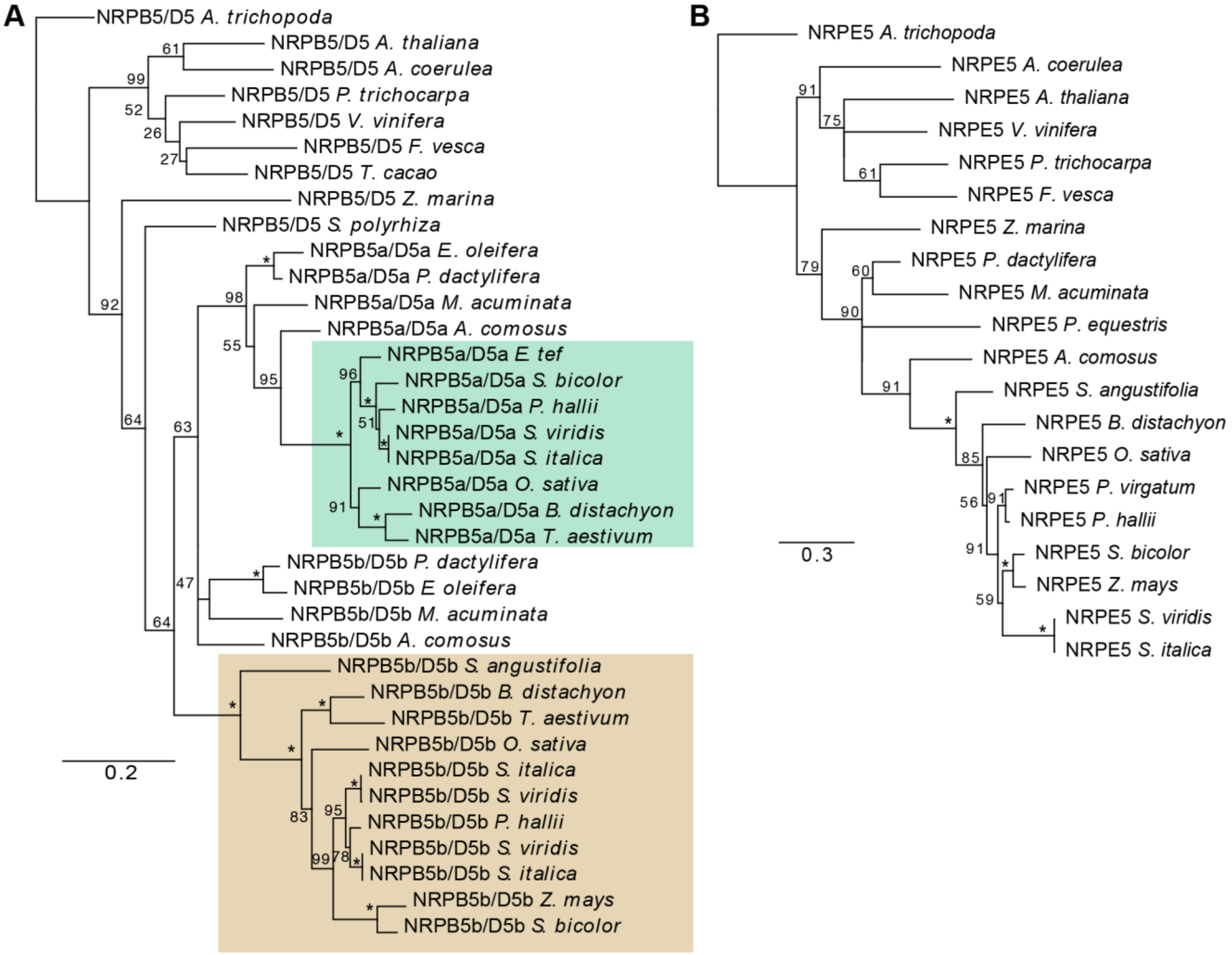
Supplemental Figure 1. Pseudogenization of *Zea mays NRPF1* locus. Domesticated *Zea mays ssp mays* and its wild progenitor *Z. mays ssp parviglumis* (teosinte) both possess a full length *NRPE1* paralog but lack an intact *NRPF1* coding sequence. In *Z. mays ssp mays* variety B73, *NRPE1* has been misannotated as two independent genes, shown in dark blue and purple. The coding region of *NRPF1* is truncated shortly after the G domain and contains a transposable element in intron 4. The teosinte *NRPF1* is also truncated after the G domain, but lacks the transposable element found within the *Z. mays ssp mays* locus.



Supplemental Figure 2. Pol V subunit paralogs are expressed in rice. Expression analysis from BAR Rice eFP (http://bar.utoronto.ca/efprice/cgi-bin/efpWeb.cgi) for rice *NRPE1*, *NRPF1*, *NRPD/E2*, and *NRPF2*.

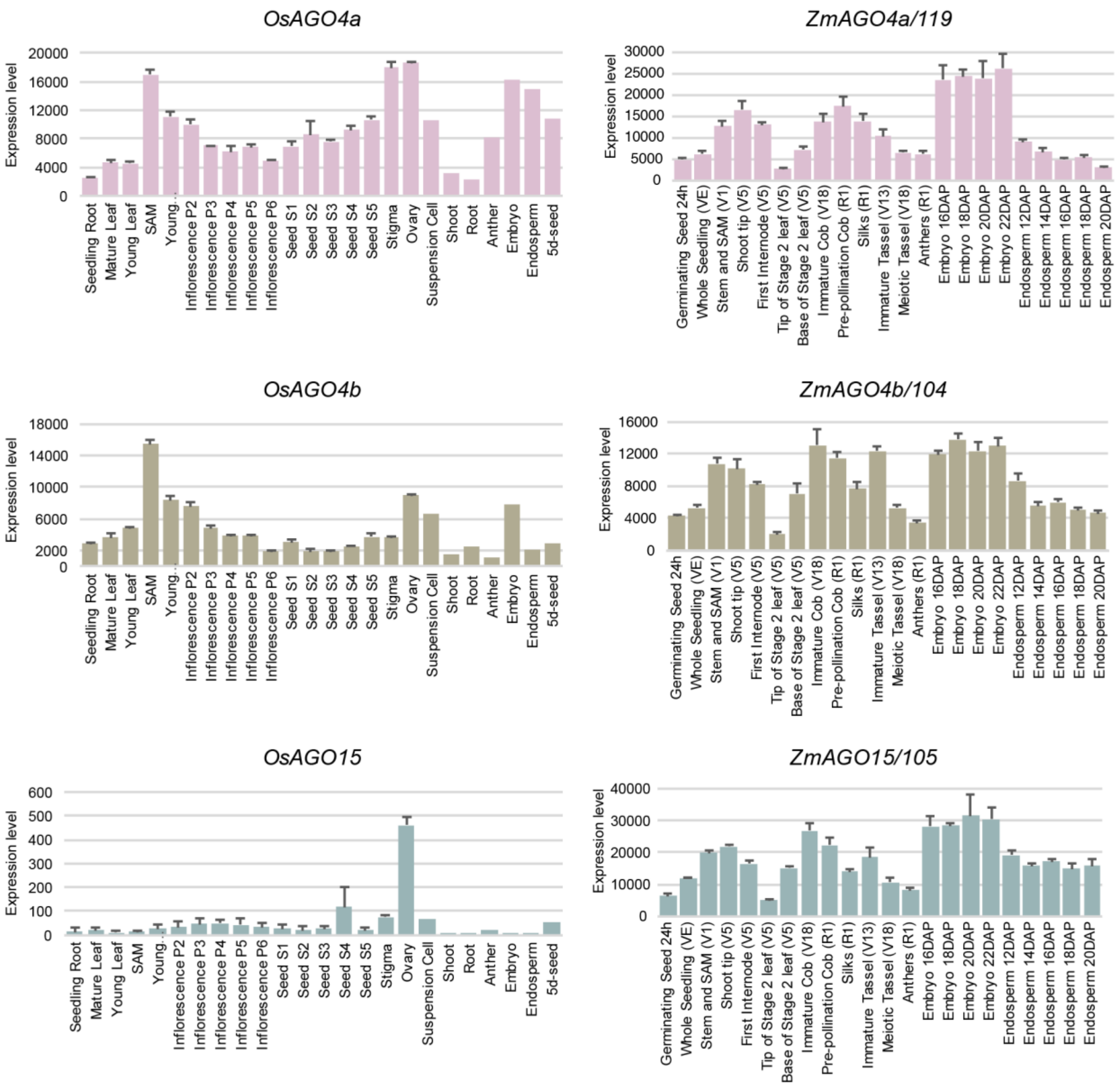


Supplementary Figure 3. Structural differences between *NRPE1* and *NRPF1*. Examples of two sequences that are present in all NRPE1 sequences, but are absent in all NRPF1 sequences.

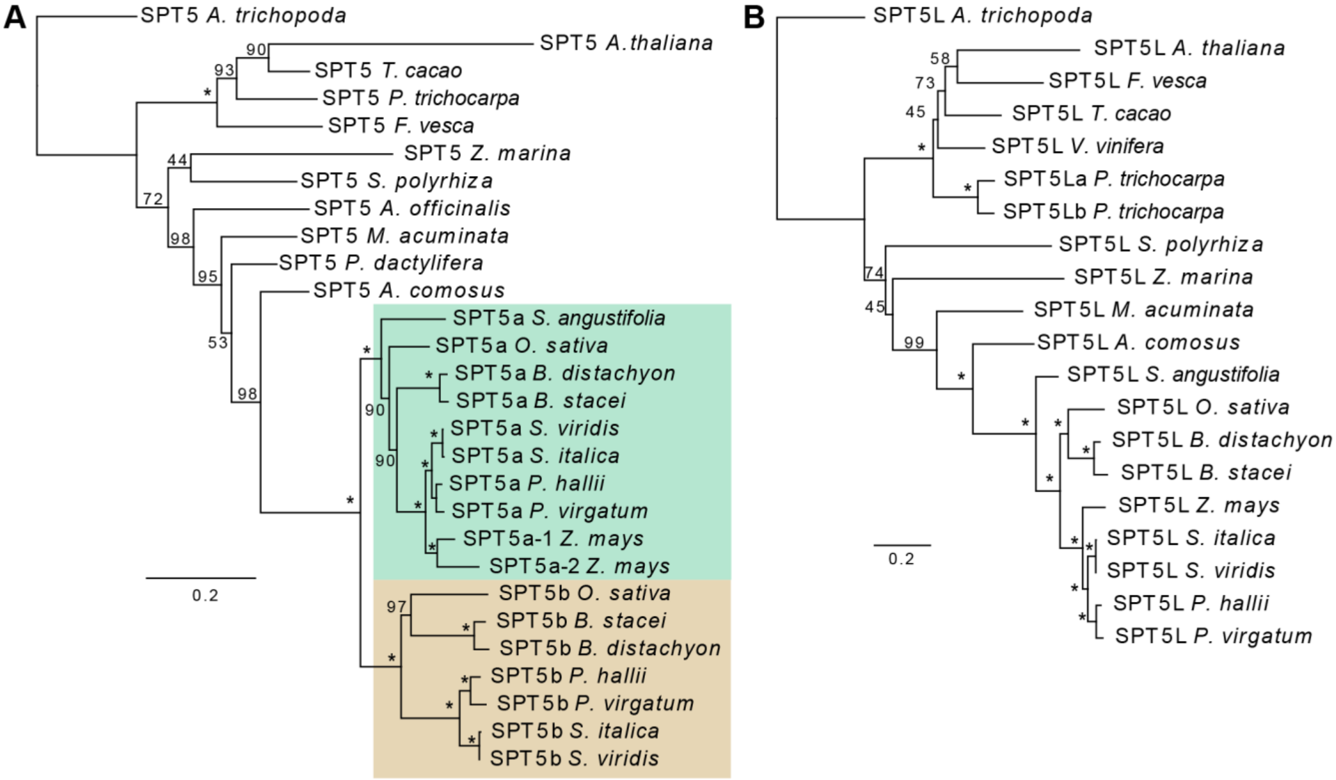


Supplementary Figure 4. Duplication of *NRPB5/D5*, but not *NRPE5*.
(A) A maximum likelihood phylogenetic tree of *NRPB5/D5* shows a duplication event early in monocot evolution. The exact placement of this duplication is unclear, but there are two highly supported clades (100% bootstrap support, colored green and brown) of Poaceae sequences, suggesting retention of multiple paralogs throughout the grass family. (B) The *NRPE5* maximum likelihood phylogenetic tree closely mirrors the species tree, indicating there has not been a duplication of the Pol V fifth subunit. Branches will 100% bootstrap support are marked with an asterisk. Lineage-specific duplications were collapsed into a single terminal branch.

Supplementary Figure 5. Multiple paralogs of NRPB/D/E9 in grasses. (A) Neighbor-joining tree and (B) alignment of monocot NRPB/D/E9 coding sequences demonstrates there are three groups of sequences in Poaceae (A, B, C). Colored residues disagree with the consensus.

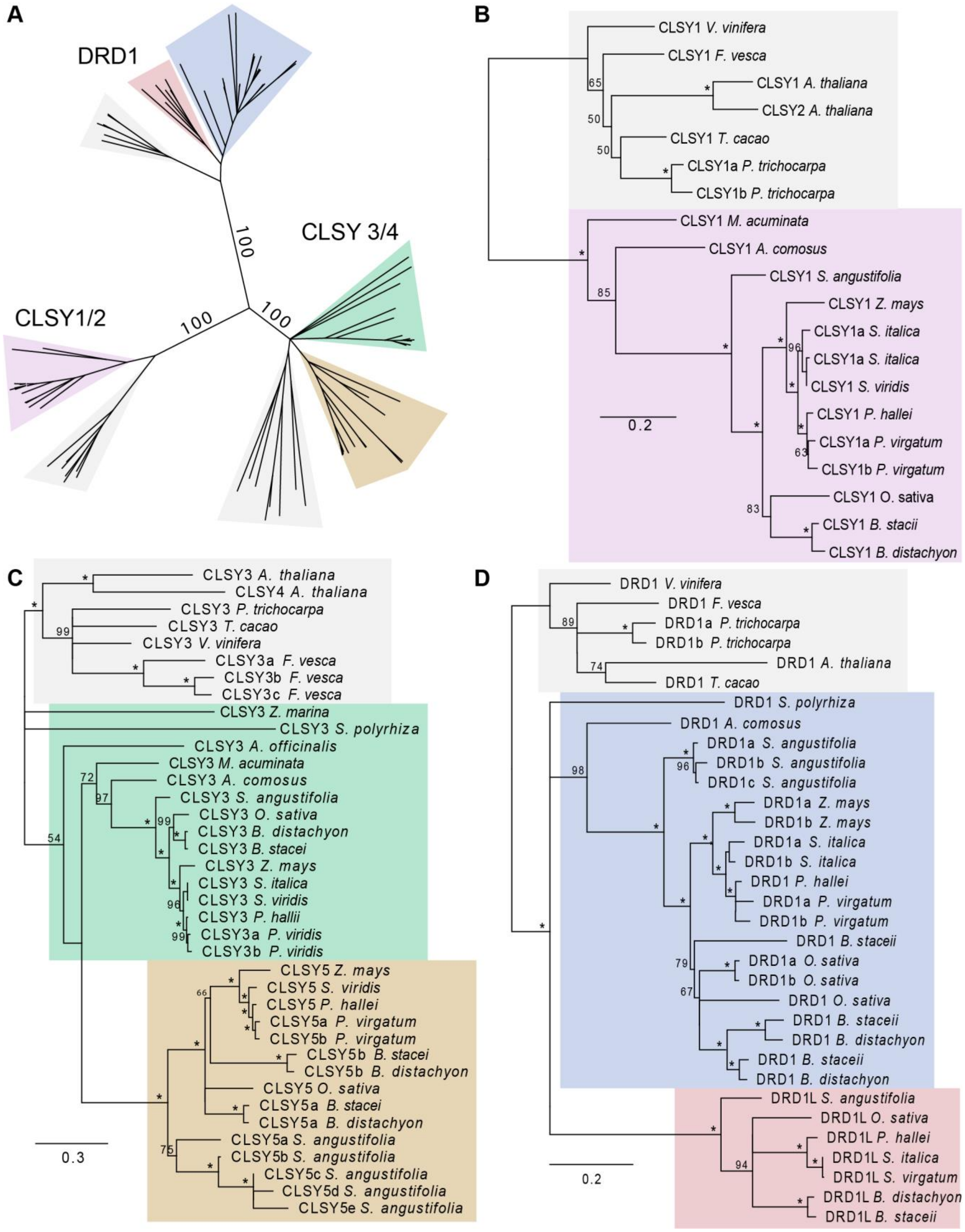


Supplemental Figure 6. Expression patterns of *AGO4* paralogs in rice and maize. BAR Rice eFP (http://bar.utoronto.ca/efprice/cgi-bin/efpWeb.cgi) and maize eFP (http://bar.utoronto.ca/efp_maize/cgi-bin/efpWeb.cgi) expression data demonstrate that *OsAGO4a* and *OsAGO4b* are expressed throughout rice development. *OsAGO15* might be more narrowly expressed, however we were unable to detect transcripts using RT-PCR in floral tissue. *ZmAGO4a/119*, *ZmAGO4b/104*, and *ZmAGO15/105* are widely expressed.



Supplemental Figure 7. *SPT5*, but not *SPT5L*, transcription elongation factors are duplicated in grasses.

Maximum likelihood phylogenetic trees of the conserved domains in *SPT5* (A) and *SPT5L* (B) families demonstrate that *SPT5* duplicated at the divergence of Poaceae. The paralogous clades are highlighted in green and brown. *SPT5L*, the paralog associated with Pol V in Arabidopsis, does not show a similar duplication. Branches will 100% bootstap support are marked with an asterisk. Lineage-specific duplications were collapsed into a single terminal branch.



Supplemental Figure 8. ***DRD1*** **and** ***CLSY3/4*****-type SWI/SNF nucleosome remodeling proteins are duplicated in grasses.**

We assessed orthologs of the DRD1-type (including *DRD1*, *CLSY1/2*, and *CLSY3/4* clades) SWI/SNF nucleosome remodeling proteins and discovered duplications of *CLSY3/4* and *DRD1* in grasses. SWI/SNF proteins were recovered from monocot and selected dicot genomes from Phytozome. Reciprocal BLAST and phylogenetic trees were used to classify these proteins and eliminate non-DRD1-type SWI/SNF proteins. (A) An unrooted neighbor-joining tree of selected peptide sequences demonstrates that all sequences are unambiguously assigned to one of three subgroups. Support values from 100 bootstrap replicates. (B-D) Coding sequences were recovered and used to build maximum likelihood phylogenetic trees of the conserved helicase domains of each SWI/SNF subclass. Branches with support values <50 were collapsed and branches with 100% support are marked with an asterisk. The *CLSY1/2* tree (B) recapitulates the expected topology with a few lineage-specific duplications. The *CLSY3/4* (C) and *DRD1* (D) trees identify deeper duplications in the monocot grouping. For both trees placement of the duplication is somewhat unresolved, probably due to errors in annotation, however the additional paralogs (*CLSY5* or *DRD1L*) are only recovered in grass species, suggesting these duplications occurred at the divergence of Poaceae.

Supplemental Table 1. List of gene sequences used in this study

Gene	Species	Gene ID
NRPE1	*A. comosus*	Aco023234
NRPE1	*A. tauschii*	F775_02057
NRPE1	*A. officinalis*	evm.model.AsparagusV1_06.200
NRPE1	*B. distachyon*	Bradi4g45065
NRPE1	*B. stacei*	Brast05G298800
NRPE1	*E. oleifera*	Unannotated, FGENESH predicted coding sequence
NRPE1	*E. tef*	snap_masked-scaffold3807-abinit-gene-1.26-mRNA-1
NRPE1	*H. vulgare*	MLOC_ 62016
NRPE1	*M. acuminata*	GSMUA_Achr3T05690/ GSMUA_Achr3T05700/ GSMUA_Achr3T05710
NRPE1	*O. sativa*	LOC_Os02g05880
NRPE1	*P. dactylifera*	PDK_30s802521L005
NRPE1	*P. equestris*	PEQU_19764 + PEQU_19766
NRPE1	*P. hallii*	Pahal.A00310
NRPE1	*P. virgatum*	Pavir.Ga01147
NRPE1	*S. angustifolia*	Unannotated, FGENESH predicted coding sequence
NRPE1	*S. bicolor*	Sobic.004G043750
NRPE1	*S. italica*	Seita.1G086100
NRPE1	*S. polyrhiza*	Spipo2G0033800
NRPE1	*S. viridis*	Sevir.7G147000
NRPE1	*T. aestivum*	Traes_6DS_43BCD40B9
NRPE1	*Z. mays*	GRMZM2G153797 + GRMZM5G851807
NRPE1	*Z. marina*	Zosma75g00810

Gene	Species	Gene ID
NRPF1	*A. tauschii*	F775_23577
NRPF1	*B. distachyon*	Bradi2g61683
NRPF1	*B. stacei*	Brast01G012100
NRPF1	*E. tef*	snap_masked-scaffold3548-abinit-gene-3.18-mRNA-1
NRPF1	*H. vulgare*	MLOC_54009
NRPF1	*O. sativa*	LOC_Os01g73430
NRPF1	*P. hallii*	Pahal.I03212
NRPF1	*P. virgatum*	Pavir.Aa03252
NRPF1	*S. angustifolia*	Unannotated, FGENESH predicted coding sequence
NRPF1	*S. bicolor*	Sobic.003G439200
NRPF1	*S. italica*	Seita.7G138600
NRPF1	*S. viridis*	Sevir.1G084000
NRPF1	*T. aestivum*	Traes_3AL_E77A5F03A
NRPF1	*Z. mays*	GRMZM2G470305

Gene	Species	Gene ID
NRPD/E2	*A. comosus*	Aco009438
NRPD/E2	*A. tauschii*	F775_01648
NRPD/E2	*A. officinllis*	evm.model.AsparagusV1_03.117
NRPD/E2	*B. distachyon*	Bradi5g23540
NRPD/E2	*B. stacei*	Brast09G228900
NRPD/E2	*E. oleifera*	Unannotated, FGENESH predicted coding sequence
NRPD/E2	*E. tef*	maker-scaffold4272-snap-gene-0.34-mRNA-1
NRPD/E2	*H. vulgare*	HORVU2Hr1G115600
NRPD/E2	*M. acuminata*	GSMUA_Achr8T17010_001
NRPD/E2	*O. sativa*	LOC_Os04g54840
NRPD/E2	*P. dactylifera*	PDK_30s897181L002
NRPD/E2	*P. equestris*	PEQU_35605
NRPD/E2	*P. hallii*	Pahal.G02501
NRPD/E2	*P. virgatum*	Pavir.Gb00384
NRPD/E2	*S. angustifolia*	Unannotated, FGENESH predicted coding sequence
NRPD/E2	*S. bicolor*	Sobic.001G448100

NRPD/E2	*S. italica*	Seita.7G258200
NRPD/E2	*S. polyrhiza*	Spipo15G0003500
NRPD/E2	*S. viridis*	Sevir.7G269600
NRPD/E2	*T. aestivum*	Traes_2DL_4FD242B37
NRPD/E2	*Z. mays*	GRMZM2G054225_T01
NRPD/E2	*Z. marina*	Zosma248g00150

Gene	**Species**	**Gene ID**
NRPF2	*A. tauschii*	F775_00990
NRPF2	*B. distachyon*	Bradi3g15852
NRPF2	*B. stacei*	Brast03G026500
NRPF2	*E. tef*	maker-scaffold17955-snap-gene-0.28-mRNA-1
NRPF2	*H. vulgare*	HORVU7Hr1G076850
NRPF2	*O. sativa*	LOC_Os08g07480
NRPF2	*P. hallii*	Pahal.F01121
NRPF2	*P. virgatum*	Pavir.Fb00476
NRPF2	*S. bicolor*	Sobic.007G056900
NRPF2	*S. italica*	Seita.6G047400
NRPF2	*S. viridis*	Sevir.6G044700
NRPF2	*T. aestivum*	Traes_7DL_222F95DC4
NRPF2	*Z. mays*	GRMZM2G133512_T01

Gene	**Species**	**Gene ID**
NRPB/D5	*A. coerulea*	Aqcoe7G260800
NRPB/D5a	*A. comosus*	Aco018959
NRPB/D5b	*A. comosus*	Aco024268
NRPB/D5	*A. thaliana*	AT3G22320
NRPB/D5	*A. trichopoda*	evm_27.model.AmTr_v1.0_scaffold00068.11
NRPB/D5a	*B. distachyon*	Bradi2g52777
NRPB/D5b	*B. distachyon*	Bradi5g13967
NRPB/D5a	*E. oleifera*	
NRPB/D5b	*E. oleifera*	
NRPB/D5	*E. tef*	maker-scaffold1292-augustus-gene-2.17-mRNA-1
NRPB/D5	*F. vesca*	mrna05314.1-v1.0-hybrid
NRPB/D5a	*M. acuminata*	GSMUA_AchrUn_randomT09620_001
NRPB/D5b	*M. acuminata*	GSMUA_Achr2T00920_001
NRPB/D5a	*O. sativa*	LOC_Os01g59140
NRPB/D5b	*O. sativa*	LOC_Os04g41040
NRPB/D5a	*P. dactylifera*	cds10971
NRPB/D5b	*P. dactylifera*	cds22816
NRPB/D5a	*P. hallii*	Pahal.E01240
NRPB/D5b	*P. hallii*	Pahal.G00686
NRPB/D5	*P. trichocarpa*	Potri.006G161600
NRPB/D5	*S. angustifolia*	STRANG_00084297-RA
NRPB/D5a	*S. bicolor*	Sobic.003G328700
NRPB/D5b	*S. bicolor*	Sobic.006G127500
NRPB/D5a	*S. italica*	Seita.5G352900
NRPB/D5b	*S. italica*	Seita.7G144900
NRPB/D5c	*S. italica*	Seita.5G051100
NRPB/D5	*S. polyrhiza*	Spipo0G0040300
NRPB/D5a	*S. viridis*	Sevir.5G358000
NRPB/D5b	*S. viridis*	Sevir.7G153500
NRPB/D5c	*S. viridis*	Sevir.5G050500
NRPB/D5a	*T. aestivum*	Traes_3B_37BBD6C41
NRPB/D5b	*T. aestivum*	Traes_2BL_1FD85D348
NRPB/D5	*T. cacao*	Thecc1EG037836t1
NRPB/D5	*V. vinifera*	GSVIVT01015349001
NRPB/D5	*Z. marina*	Zosma440g00110

NRPB/D5	*Z. mays*	GRMZM2G099183

Gene	**Species**	**Gene ID**
NRPE5	*A. coerulea*	Aqcoe2G036200
NRPE5	*A. comosus*	Aqcoe2G036200
NRPE5	*A. thaliana*	AT3G57080
NRPE5	*A. trichopoda*	evm_27.model.AmTr_v1.0_scaffold00116.10
NRPE5	*B. distachyon*	Bradi4g26550
NRPE5	*F. vesca*	mrna21892.1-v1.0-hybrid
NRPE5	*M. acuminata*	GSMUA_Achr9T19340_001
NRPE5	*O. sativa*	LOC_Os12g04510
NRPE5	*P. dactylifera*	PDK_30s65509269L001
NRPE5	*P. equestris*	PEQU_23089
NRPE5	*P. hallii*	Pahal.H00047
NRPE5	*P. trichocarpa*	Potri.001G025500
NRPE5	*P. virgatum*	Pavir.Ha01857
NRPE5	*S. angustifolia*	STRANG_00052800-RA
NRPE5	*S. bicolor*	Sobic.005G030600
NRPE5	*S. italica*	Seita.8G027200
NRPE5	*S. viridis*	Sevir.7G328000
NRPE5	*V. vinifera*	GSVIVT01033595001
NRPE5	*Z. marina*	Zosma192g00210
NRPE5	*Z. mays*	GRMZM2G162697

Gene	**Species**	**Gene ID**
NRPB/D/E9a	*A. comosus*	Aco001788
NRPB/D/E9b	*A. comosus*	Aco027798
NRPB/D/E9c	*A. comosus*	Aco009500
NRPB/D/E9	*A. officinalis*	evm.model.AsparagusV1_07.1236
NRPB/D/E9a	*B. distachyon*	Bradi4g04820
NRPB/D/E9b	*B. distachyon*	Bradi1g78509
NRPB/D/E9c	*B. distachyon*	Bradi1g20820
NRPB/D/E9a	*B. staceii*	Brast10G053700
NRPB/D/E9b	*B. staceii*	Brast02G002000
NRPB/D/E9c	*B. staceii*	Brast06G047100
NRPB/D/E9a	*M. acuminata*	GSMUA Achr10G02200 001
NRPB/D/E9b	*M. acuminate*	GSMUA Achr7T05620 001
NRPB/D/E9c	*M. acuminata*	GSMUA Achr4G24050 001
NRPB/D/E9a	*O. sativa*	LOC Os12g37370
NRPB/D/E9b	*O. sativa*	LOC Os03g01230
NRPB/D/E9c	*O. sativa*	LOC Os07g42395
NRPB/D/E9a	*P. dactylifera*	cds4303
NRPB/D/E9b	*P. dactylifera*	cds18947
NRPB/D/E9a	*P. equestris*	PEQU_29548
NRPB/D/E9b	*P. equestris*	PEQU_21523
NRPB/D/E9a	*P. hallii*	Pahal.I04586
NRPB/D/E9b	*P. hallii*	Pahal.G01696
NRPB/D/E9c	*P. hallii*	Pahal.B04703
NRPB/D/E9a	*P. virgatum*	Pavir.Ca02562
NRPB/D/E9b	*P. virgatum*	Pavir.J16609
NRPB/D/E9c	*P. virgatum*	Pavir.Ba00418
NRPB/D/E9a	*S. angustifolia*	STRANG 00026340-RA
NRPB/D/E9b	*S. angustifolia*	STRANG 00027772-RA
NRPB/D/E9c	*S. angustifolia*	STRANG 00003454-RA
NRPB/D/E9a	*S. bicolor*	Sobic.008G128900
NRPB/D/E9b	*S. bicolor*	Sobic.009G165600
NRPB/D/E9c	*S. bicolor*	Sobic.002G374200
NRPB/D/E9a	*S. italic*	Seita.3G335700

NRPB/D/E9b	*S. italic*	Seita.7G044300
NRPB/D/E9c	*S. italic*	Seita.2G388500
NRPB/D/E9	*S. polyrhiza*	Spipo2G0057100
NRPB/D/E9a	*S. viridis*	Sevir.3G350200
NRPB/D/E9b	*S. viridis*	Sevir.7G049300
NRPB/D/E9c	*S. viridis*	Sevir.2G399000
NRPB/D/E9	*Z. marina*	Zosma25g01500
NRPB/D/E9a	*Z. mays*	GRMZM2G046061
NRPB/D/E9b	*Z. mays*	GRMZM2G023028
NRPB/D/E9c	*Z. mays*	GRMZM5G898768

Gene	**Species**	**Gene ID**
AGO4	*A. comosus*	Aco017860
AGO4a	*A. tauschii*	F775_27134
AGO4b	*A. tauschii*	F775_27714
AGO4	*A. officinalis*	evm.model.AsparagusV1_07.1132
AGO4a	*B. distachyon*	Bradi2g10370
AGO4b	*B. distachyon*	Bradi2g14147
AGO4a	*B. stacei*	Brast01G298200
AGO4b	*B. stacei*	Brast08G001100
AGO4	*E. oleifera*	Unannotated, FGENESH predicted coding sequence
AGO4a	*E. tef*	maker-scaffold315-augustus-gene-0.27-mRNA-1
AGO4b	*E. tef*	snap_masked-scaffold1886-abinit-gene-0.21-mRNA-1
AGO4a	*H. vulgare*	HORVU3Hr1G038830
AGO4b	*H. vulgare*	HORVU1Hr1G095300
AGO4	*M. acuminata*	GSMUA_Achr9T05150
AGO4a	*O. sativa*	LOC_Os01g16870
AGO4b	*O. sativa*	LOC_Os04g06770
AGO4	*P. dactylifera*	cds36720
AGO4	*P. equestris*	PEQU_18408
AGO4a	*P. hallii*	Pahal.E03348
AGO4b	*P. hallii*	Pahal.C01666
AGO4a	*P. virgatum*	Pavir.Eb01138
AGO4b	*P. virgatum*	Pavir.J00737
AGO4a	*S. angustifolia*	Unannotated, FGENESH predicted coding sequence
AGO4b	*S. angustifolia*	Unannotated, FGENESH predicted coding sequence
AGO4a	*S. bicolor*	Sobic.003G129500
AGO4b	*S. bicolor*	Sobic.009G259900
AGO4a	*S. italica*	Seita.5G043300
AGO4b	*S. italica*	Seita.3G117800
AGO4	*S. polyrhiza*	Spipo3G0017600
AGO4a	*S. viridis*	Sevir.5G040900
AGO4b	*S. viridis*	Sevir.3G120100
AGO4a	*T. aestivum*	TRIAE_CS42_3AS_TGACv1_211331_AA0688710
AGO4b	*T. aestivum*	TRIAE_CS42_1DL_TGACv1_062840_AA0220790
AGO4a/119	*Z. mays*	GRMZM2G589579
AGO4b/104	*Z. mays*	GRMZM2G141818

Gene	**Species**	**Gene ID**
AGO15	*A. tauschii*	F775_02440
AGO15	*B. distachyon*	Bradi2g10360
AGO15	*B. stacei*	Brast01G298300
AGO15	*E. tef*	maker-scaffold1490-snap-gene-1.50-mRNA-1
AGO15	*H. vulgare*	HORVU7Hr1G107770
AGO15	*O. sativa*	LOC_Os01g16860
AGO15	*P. hallii*	Pahal.E03353
AGO15	*P. virgatum*	Pavir.Eb01136
AGO15	*S. bicolor*	Sobic.003G129200

AGO15	*S. italica*	Unannotated, FGENESH predicted coding sequence
AGO15	*S. viridis*	Sevir.5G041600
AGO15/105	*Z. mays*	GRMZM2G469673/GRMZM2G048335/GRMZM2G089743

Gene	**Species**	**Accession**
SPT5	*A. thaliana*	AT2G34210
SPT5	*A. trichopoda*	evm_27.model.AmTr_v1.0_scaffold00002.351
SPT5	*A. comosus*	Aco002639.1
SPT5	*A. officinalis*	evm.model.AsparagusV1_05.376
SPT5a	*B. distachyon*	Bradi1g46230.3.p
SPT5b	*B. distachyon*	Bradi3g57590.2.p
SPT5a	*B. stacei*	Brast07G070000.1
SPT5b	*B. stacei*	Brast04G034700.1
SPT5	*F. vesca*	gene30070v1.0hybrid
SPT5	*M. acuminata*	GSMUA_Achr3P08080_001
SPT5a	*O. sativa*	LOC_Os06g10620.1
SPT5b	*O. sativa*	LOC_Os02g53230.1
SPT5a	*P. hallii*	Pahal.D02854.1
SPT5b	*P. hallii*	Pahal.G02677.1
SPT5	*P. trichocarpa*	Potri.009G124200.1
SPT5	*P. dactylifera*	LOC103718524
SPT5a	*P. virgatum*	PavirDb02038.1
SPT5b	*P. virgatum*	Pavir.Aa00338.1
SPT5a	*S. angustifolia*	STRANG 00000456RA
SPT5a	*S. italica*	Seita.4G084400.1.p
SPT5b	*S. italica*	Seita.1G335500.1
SPT5	*S. polyrhiza*	Spipo10G0038700
SPT5a	*S. viridis*	Sevir.4G083700.1
SPT5b	*S. viridis*	Sevir.1G342100.1
SPT5	*T. cacao*	Thecc1EG035426
SPT5	*Z. marina*	Zosma52g01330.1
SPT5a	*Z. mays*	GRMZM2G142072_P01
SPT5a	*Z. mays*	GRMZM2G171488_T02

Gene	**Species**	**Accession**
SPT5L	*A. thaliana*	AT5G04290.1
SPT5L	*A. trichopoda*	evm_27.model.AmTr_v1.0_scaffold00002.356
SPT5L	*A. comosus*	Aco005272.1
SPT5L	*B. distachyon*	Bradi2g20517.2
SPT5L	*B. stacei*	Brast08G068300.2
SPT5L	*F. vesca*	gene23431v1.0hybrid
SPT5L	*M. acuminata*	GSMUA_Achr7P16990_001
SPT5L	*O. sativa*	LOC_Os05g43060.1
SPT5L	*P. hallii*	Pahal.C02415.2
SPT5L	*P. trichocarpa*	Potri.008G032800.1
SPT5L	*P. trichocarpa*	Potri.010G228800.1
SPT5L	*P. virgatum*	Pavir.Ca01318
SPT5L	*S. italica*	Seita.3G186400.1
SPT5L	*S. polyrhiza*	Spipo3G0088300
SPT5L	*S. viridis*	Sevir.3G191100.1
SPT5L	*T. cacao*	Thecc1EG043328t1
SPT5L	*V. vinifera*	GSVIVT01016203001
SPT5L	*Z. mays*	GRMZM2G375222_P01
SPT5L	*Z. marina*	Zosma159g00420.1

Gene	**Species**	**Accession**
CLSY1	*A. comosus*	Aco011099
CLSY1	*A. thaliana*	AT3G42670

Gene	**Species**	**Accession**
CLSY2	*A. thaliana*	AT5G20420
CLSY1	*B. distachyon*	Bradi1g16720
CLSY1	*B. stacei*	Brast06G002700
CLSY1	*F. vesca*	gene21045-v1.0-hybrid
CLSY1	*M. acuminata*	GSMUA_Achr8G01860_001
CLSY1	*O. sativa*	LOC_Os07g49210
CLSY1	*P. hallii*	Pahal.J01776
CLSY1a	*P. trichocarpa*	Potri.008G073500
CLSY1b	*P. trichocarpa*	Potri.010G183800
CLSY1a	*P. virgatum*	Pavir.Ba00302
CLSY1b	*P. virgatum*	Pavir.Bb03632
CLSY1	*S. angustifolia*	STRANG_00023332-RA
CLSY1a	*S. italica*	Seita.2G442300
CLSY1b	*S. italica*	Seita.9G461000
CLSY1	*S. viridis*	Sevir.2G454400
CLSY1	*T. cacao*	Thecc1EG042431
CLSY1	*V. vinifera*	GSVIVG01032746001
CLSY1	*Z. mays*	GRMZM2G108166

Gene	**Species**	**Accession**
CLSY3	*A. comosus*	LG08:12562121..12567155
CLSY3	*A. officinalis*	evm.model.AsparagusV1_04.2656
CLSY3	*A. thaliana*	AT1G05490
CLSY4	*A. thaliana*	AT3G24340
CLSY3	*F. vesca*	gene10657-v1.0-hybrid
CLSY3	*F. vesca*	gene10658-v1.0-hybrid
CLSY3	*F. vesca*	gene23334-v1.0-hybrid
CLSY3	*M. acuminata*	GSMUA_Achr7G06840_001
CLSY3	*O. sativa*	LOC_Os05g32610
CLSY3	*P. hallii*	Pahal.F01921
CLSY3	*P. trichocarpa*	Potri.014G050200
CLSY3a	*P. virgatum*	Pavir.J01490
CLSY3b	*P. virgatum*	Pavir.Cb01678
CLSY3	*S. angustifolia*	STRANG_00015789-RA
CLSY3	*S. italica*	Seita.3G254300
CLSY3	*S. viridis*	Sevir.3G260900
CLSY3	*S. polyrhiza*	Spipo5G0053000
CLSY3	*T. cacao*	Thecc1EG036301
CLSY3	*V. vinifera*	GSVIVG01013277001
CLSY3	*Z. marina*	Zosma89g01000.1
CLSY3/RMR1	*Z. mays*	GRMZM2G154946
CLSY5	*B. distachyon*	Bradi3g50300
CLSY5	*B. distachyon*	Bradi2g26500
CLSY5	*B. distachyon*	Bradi2g43501
CLSY5	*B. stacei*	Brast01G217700
CLSY5	*B. stacei*	Brast04G120300
CLSY5	*B. stacei*	Brast08G132400
CLSY5	*O. sativa*	LOC_Os02g43460
CLSY5	*P. hallii*	Pahal.A02764
CLSY5a	*P. virgatum*	Pavir.Aa01193
CLSY5b	*P. virgatum*	Pavir.Ab02445
CLSY5a	*S. angustifolia*	STRANG_00083573-RA
CLSY5b	*S. angustifolia*	STRANG_00018510-RA
CLSY5c	*S. angustifolia*	STRANG_00037404-RA
CLSY5d	*S. angustifolia*	STRANG_00042628-RA
CLSY5e	*S. angustifolia*	STRANG_00038294-RA
CLSY5	*S. viridis*	Sevir.1G259000

CLSY5/RMR1-like	*Z. mays*	GRMZM2G178435

Gene	**Species**	**Accession**
DRD1	*A. comosus*	Aco017413
DRD1	*A. thaliana*	AT2G16390.1
DRD1a	*B. distachyon*	Bradi2g21450
DRD1b	*B. distachyon*	Bradi3g19890
DRD1L	*B. distachyon*	Bradi1g74070
DRD1	*B. stacei*	Brast03G065000
DRD1a	*B. stacei*	Brast08G078200
DRD1b	*B. stacei*	Brast03G077600
DRD1L	*B. stacei*	Brast02G053000
DRD1	*F. vesca*	gene21858-v1.0-hybrid
DRD1	*O. sativa*	LOC_Os08g14610
DRD1a	*O. sativa*	LOC_Os07g25390
DRD1b	*O. sativa*	LOC Os06g14440
DRD1L	*O. sativa*	LOC_Os03g06920
DRD1	*P. hallii*	Pahal.B01415
DRD1L	*P. hallii*	Pahal.I00535
DRD1a	*P. tricocarpa*	Potri.004G159000
DRD1b	*P. trichocarpa*	Potri.009G120700
DRD1a	*P. virgatum*	Pavir.Bb00923
DRD1b	*P. virgatum*	Pavir.J23343
DRD1a	*S. angustifolia*	STRANG_00017656-RA
DRD1b	*S. angustifolia*	STRANG_00048730-RA
DRD1c	*S. angustifolia*	STRANG_00048722-RA
DRD1L	*S. angustifolia*	STRANG_00017091-RA
DRD1a	*S. italica*	Seita.6G109100
DRD1b	*S. italica*	Seita.9G302200
DRD1L	*S. italica*	Seita.9G529000
DRD1L	*S. viridis*	Sevir.9G533600
DRD1	*S. polyrhiza*	Spipo9G0003300
DRD1	*T. cacao*	Thecc1EG006828
DRD1	*V. vinifera*	GSVIVG01024225001
DRD1a	*Z. mays*	GRMZM2G574858
DRD1b	*Z. mays*	GRMZM2G393742

Sup. Table 2. Reverse transcriptase PCR primers

Primer	Sequence
OsE1 F	GGCCAAAGAAACAATCCTGGTAG
OsE1 R	CTCACTAGTGGTATCAACTGCAGTAGACTGTGT
OsF1 RT F	GCGAGTTGTGCTTTTACACCAGT
OsF1 R	CTCACTAGTTTTGAAGTACTTTCTGCAGAATGAATCT
OsDE2 RT F	GAGAAAGGATGACTTTGCCAGAC
OsDE2 RT R	GGTGATCGAACCTGTCTTAGAGTA
OsF2 RT F	GGAAGCAAACATGACTTTGCCAG
OsF2 RT R	CGAGCGAGTCTGTCTTAGAGTAA

Sup. Table 3. NRPE1 and NRPF1 CTD characteristics

	length[1]	Ago hooks
NRPE1, Non-Poaceae		
Ananas comosus	431	9
Asparagas officinalis	539	8
Elaeis oleiferia	291	5
Musa acuminata	375	6
Phalaenopsis equestris	471	8
Phoenix dactylifera	313	7
Spirodela polyrhiza	246	4
Zostera marina	707	23
NRPE1, Poaceae		
Aegilops tauschii	444	15
Brachypodium distachyon	513	15
Brachypodium stacei	496	15
Eragrostis tef	595	14
Oryza sativa	541	13
Panicum hallii	506	13
Panicum virgatum	526	15
Streptochaeta angustifolia	585	16
Seteria italica	541	16
Seteria viridis	541	15
Sorghum bicolor	538	14
Triticum aestivum	468	16
Zea mays	468	9
NRPF1, Poaceae		
Aegilops tauschii	314	5
Brachypodium distachyon	265	2
Brachypodium stacei	288	2
Hordeum vulgare	324	3
Oryza sativa	249	0
Panicum virgatum	241	2
Streptochaeta angustifolia	189	1
Seteria italica	242	1
Seteria viridis	242	1
Sorghum bicolor	276	2
Triticum aestivum	324	4

Sup. Table 4. Evidence of positive selection following the duplication of *NRPE1*.

NRPE1	**Position[1]**	**BEB score**	**Amino acid[1]**	**Ancestral / F1 amino acid[1]**	**Surface (S) / Interior (I)**	**Feature/Structure**
High confidence (sites on branch)	513	0.66	M	F/Y	Surface	Pore
Lower confidence (sites in clade)	1049	0.990**	G	P	Interior	Jaw

NRPF1	**Position[1]**	**BEB score**	**Amino acid[1]**	**Ancestral / E1 amino acid[1]**	**Surface (S) /Interior (I)**	**Structure / Feature in template model**
High confidence (sites on branch)	539	0.878	K	P	Surface	Pore / Near RBP 8 surface
	503	0.873	K	V/G	Surface	Pore
	742	0.845	K	V/A	Surface	Funnel-Bridge helix / RBP2 interaction site
	304	0.823	F	E/D	Surface	Clamp-Rudder
	349	0.768	E	S	Surface	Active site pocket
	1184	0.734	A	C	Surface	Clamp
	223	0.609	S	Q/K	Surface	Clamp / RPB2 interaction site
	825	0.597	I	N	Surface	Foot
	1034	0.59	A	K	Surface	Cleft
	899	0.554	H	S/P	Surface	Jaw / Near RPB2 surface
	367	0.534	A	K/N	Surface	Dock
Lower confidence (sites in clade)	226	0.985*	C	P	Surface	Clamp / Near RPB2 surface
	234	0.998**	V	V/I	Surface	Clamp
	235	0.991**	S	P	Surface	Clamp-Lid
	237	0.980*	V	I/F	Surface	Clamp-Lid
	240	0.999**	G	G	Surface	Clamp-Lid / Near RPB2 surface
	243	0.976*	F	I	Surface	Clamp-Lid
	244	0.955*	S	M	Surface	Clamp-Lid
	254	0.966*	R	K	Surface	Clamp
	259	0.976*	K	K	Surface	Clamp
	270	0.972*	S	S	Surface	Clamp
	301	0.984*	D	D	Surface	Clamp-Rudder / Near RPB2 surface
	309	0.954*	T	S	Surface	Clamp-Rudder
	319	0.995**	T	T	Surface	Clamp

	341	0.976*	G	G	Surface	Active site pocket
	360	0.999**	K	Q/R	Surface	Dock
	368	0.980*	Q	R	Surface	Dock
	371	0.994**	D	E	Surface	Dock
	382	0.991**	T	R/K	Surface	Dock
	395	0.987*	K	----	Surface	Dock / Indel relative to NRPE1
	396	0.996**	D	----	Surface	Dock / Indel relative to NRPE1
	399	0.977*	N	S	Surface	Dock / Near Rbp2 surface
	402	0.995**	H	H/Y	Surface	Dock
	420	0.991**	I	I/V	Surface	Active site pocket
	440	0.987*	Q	Y	Surface	Active site pocket
	496	0.974*	G	G	Interior	Pore
	521	0.969*	R	K	Surface	Pore
	532	0.957*	S	V/L	Interior	Pore
	556	0.992**	T	A	Interior	Pore
	557	0.993**	K	L	Surface	Pore
	558	0.998**	S	P	Surface	Pore
	678	0.999**	P	L	Surface	Funnel
	696	0.993**	L	F	Surface	Funnel / Near RPB2 surface
	718	0.989*	T	L	Surface	Funnel / Near RPB2 surface
	739	0.966*	E	S/T	Surface	Funnel-Bridge helix / Near RPB2 surface
	755	0.976*	S	T	Surface	Funnel-Bridge helix / Near RPB2 surface
	843	0.983*	A	N	Surface	Cleft / Near RPB5 surface
	861	0.999**	N	K	Surface	Cleft
	862	0.973*	E	K	Surface	Cleft
	889	0.961*	K	E	Surface	Jaw
	921	0.993**	S	E/D	Surface	Jaw
	929	1.000**	T	V	Surface	Jaw
	940	0.999**	M	L	Interior	Jaw
	949	0.977*	F	L/F	Surface	Jaw
	977	0.963*	G	D/E	Surface	Jaw
	987	0.964*	T	L/V	Surface	Jaw / Near RPB9 surface
	988	0.985*	E	E	Surface	Jaw / Near RPB9 surface
	993	0.987*	F	I/V	Surface	Jaw / Near RPB9 surface
	1025	0.991**	S	A	Surface	Cleft / Near RPB9 surface
	1054	0.978*	S	N	Interior	Cleft
	1057	0.989*	A	A	Interior	Cleft
	1078	0.991**	M	I	Surface	Cleft / Near RPB5 surface
	1087	0.957*	Q	E/D	Surface	Cleft / Near RPB5 surface
	1093	0.999**	S	C	Surface	Cleft / Near RPB5 surface
	1099	0.998**	T	V	Surface	Cleft

	1128	0.965*	Q	K	Surface	Cleft / Near RPB5 surface
	1174	0.954*	I	M	Surface	Clamp / Near RPB5 surface
	1201	0.999**	N	H	Surface	Clamp

[1] Relative to *O. sativa* paralogs

Sup. Table 5. Evidence of positive selection following the duplication of *NRPD/E2*.

NRPF2	**Position[1]**	**BEB score**	**Amino acid[1]**	**Ancestral / D2/E2 amino acid[1]**	**Surface (S) / Interior (I)**	**Feature/Structure**
High confidence (sites on branch)	747	0.989*	M	Y	Surface	Rbp2 domain 6 / Near RBP1 surface
	614	0.902	E	S	Surface	Rbp2 domain 4 / Near RPB9 surface
	299	0.864	G	Y	Surface	Rbp2 domain 2
	741	0.853	T	F	Surface	Rbp2 domain 6
	682	0.815	N	E	Surface	Rbp2 domain 5
	139	0.568	V	S	Surface	Protrusion
	383	0.51	M	L	Interior	Rbp2 domain 2
Lower confidence (sites in clade)	75	0.951*	R	N/D	Surface	Protrusion
	99	0.998**	F	F	Interior	Protrusion
	102	0.988*	L	L	Interior	Protrusion
	105	0.964*	V	V	Interior	Protrusion
	133	0.951*	E	E	Surface	Protrusion
	138	0.984*	W	W	Surface	Protrusion
	146	0.975*	V	E	Surface	Protrusion
	208	0.967*	K	R	Surface	Protrusion
	223	0.959*	L	L	Surface	Protrusion
	227	0.998**	E	D	Interior	Protrusion
	261	0.997**	S	K/R	Surface	Rbp2 domain 2
	274	0.990**	R	K	Surface	Rbp2 domain 2
	279	0.972*	S	Y	Surface	Rbp2 domain 2
	283	0.990**	Q	E/D	Interior	Rbp2 domain 2
	441	1.000**	M	R	Surface	
	442	1.000**	H	H	Surface	
	444	1.000**	Q	E	Surface	
	457	0.998**	G	G/S	Surface	
	473	0.997**	V	I/V	Interior	
	515	0.989*	M	L	Interior	Rbp2 domain 3
	522	0.999**	V	V	Surface	Rbp2 domain 3
	525	0.999**	A	A	Surface	Rbp2 domain 3
	527	0.999**	K	K	Surface	Rbp2 domain 3 / Near RPB1 surface
	599	1.000**	L	P	Surface	
	611	0.999**	D	D	Surface	Rbp2 domain 4 / Near RPB9 surface
	639	0.989*	Q	H	Surface	Rbp2 domain 4 / Near RPB1+RPB9 surfaces
	658	0.972*	I	I/V	Surface	Rbp2 domain 4

	664	0.996**	N	K	Surface	
	670	0.998**	N	G	Surface	
	699	1.000**	Y	W	Surface	Rbp2 domain 5 / Near RBP1 surface
	743	0.999**	K	R	Surface	Rbp2 domain 6 / Near RBP1 surface
	752	0.998**	I	H	Interior	Rbp2 domain 6
	761	0.986*	T	T	Surface	Rbp2 domain 6
	775	0.974*	L	L	Surface	Rbp2 domain 6
	800	0.952*	S	R	Surface	Rbp2 domain 6
	819	0.993**	I	V	Surface	Rbp2 domain 6 / Near RBP1 surface
	833	0.991**	L	M	Interior	Rbp2 domain 6
	846	0.998**	Q	E	Surface	Rbp2 domain 6
	871	0.989*	N	D	Surface	Rbp2 domain 6
	887	0.998**	I	D	Surface	Rbp2 domain 6
	916	0.997**	I	I	Surface	Rbp2 domain 6
	927	0.954*	E	Q	Surface	Rbp2 domain 6
	938	0.999**	T	K	Surface	Rbp2 domain 6
	942	0.959*	F	V	Interior	Rbp2 domain 6
	948	0.989*	T	V	Surface	Rbp2 domain 6
	1073	1.000**	H	I	Surface	Rbp2 domain 6
	1134	0.998**	V	F	Surface	Rbp2 domain 7 – Zinc finger / Near RBP1 surface
	1154	1.000**	R	R	Surface	Rbp2 domain 7 – Zinc finger
	1177	1.000**	R	N	Surface	Rbp2 domain 7 – Zinc finger / Near RBP1 surface
	1181	0.992**	V	I	Surface	Rbp2 domain 7 / Near RBP1 surface
	1196	1.000**	S	S	Surface	Rbp2 domain 7 / Near RBP1 surface
	1207	0.984*	L	V	Surface	Rbp2 domain 7 / Near RBP1 surface

[1] Relative to *O. sativa* paralog