

Supplemental Figures S1, S2, and S3

TITLE: The Trehalose Pathway in Maize: Conservation and Gene Regulation in Response to Diurnal Cycle and Extended Darkness

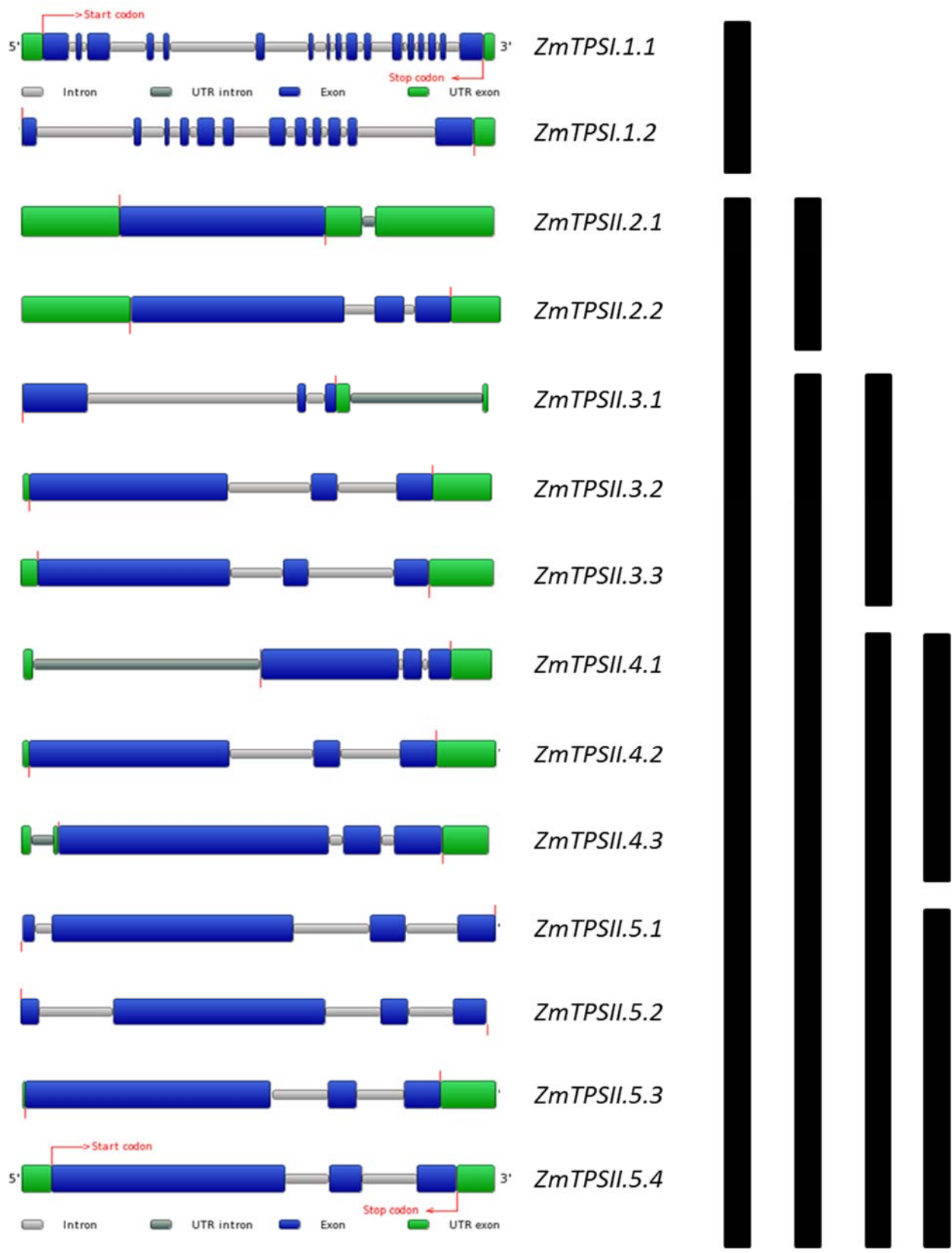
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Supplemental Figure Legends

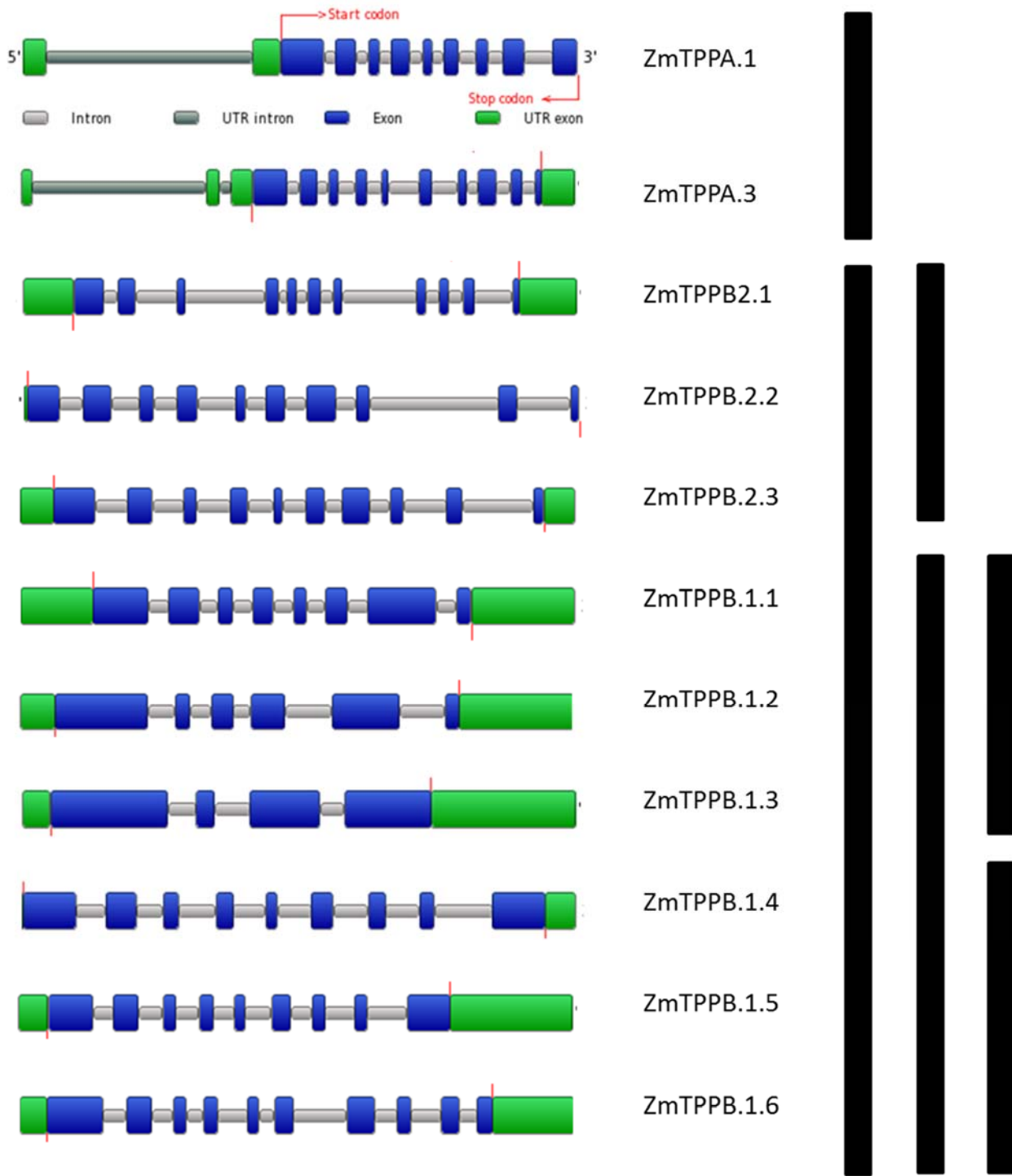
Figure S1. Gene structures with introns for maize TPS I and II genes (A) and TPP genes (B). Graphical representation of maize TPS genes showing exons (blue), introns (gray), and non-coding sequences (green).

Figure S2. Predicted enzymatic domains for maize TPS (A) and TPP (B) genes. Conserved residues for substrate binding are highlighted in red.

Figure S3. Expression of Arabidopsis (A) class I TPS genes, (B) class II TPS genes, (C) TPP genes, (D) SNRK1 (inducible) targets, (E) SnRK1 (repressible) targets in mature leaf tissue throughout the diurnal cycle and after 4 h extended night.



Supplemental Figure S1A: Gene structures with introns for maize TPS class I and class II genes.



Supplemental Figure S1B: Gene structures with introns for maize TPP class A and class B genes.

Supplemental Figure S2A: Predicted enzymatic domains for TPS proteins.

TPS predicted domain; Conserved residues **UDPG (donor)** & **G6P (acceptor)** binding

TPP predicted domain; Conserved motifs **HAD phosphatases**

ZmTPSI.1.1_tps1/1-960 MSSDAARGQ-----RGINCTRGDAAAMPTSSPFVGDGSGGAGSPIRVERMVRERSRR
ZmTPSI.1.2/1-576 -----
ZmTPSII.2.1/1-888 ---MVSRSY-----SNLLELA-----AGGSGGEP-LPSLG--RRRIPRV
ZmTPSII.2.2/1-863 ---MASRSY-----SNLLDLA-----TGAADQAPAVAALGALRRRLPRV
ZmTPSII.3.1/1-912 ---MMSRSY-----TNLLDLAEGNFAALGP---VGGSGRQR-HGSFG--LRRMSRV
ZmTPSII.3.2/1-912 ---MMSRSY-----TNLLDLAEGNFAALGP---AGGSGRQR-HGSFG--LRRMSRV
ZmTPSII.3.3/1-912 ---MMSRSY-----TNLLDLAEGNFAALGPAAGAGGGGRQR-QGSFG--LRRMSRV
ZmTPSII.4.1/1-864 ---MVLKSH-----TNLLDMCCE-----DVFDQQP-----LRSRPHV
ZmTPSII.4.2/1-865 ---MVSKEY-----SNLLDLTSG-----DGFDFRQP-----FKSLPRV
ZmTPSII.4.3/1-868 ---MVSKEY-----SNLLDMTPG-----DGFDFRRP-----FKSLPRV
ZmTPSII.5.1/1-953 MEAGASSRYPLWTRGGVQTRMEGMGGVWKRARM--EGRRRRMAVGFAGGDLGRGARE
ZmTPSII.5.2/1-860 -----MTCLGHSCGPR-----ASGPCRAAIWPFVG--VQQINLK
ZmTPSII.5.3/1-986 ---MPSFPR-----ANVVDKTRGPSPCAHAVTPPTLTSGSPRCPFLPRSDTHT
ZmTPSII.5.4/1-851 ---MPSISC-----HNLLDLA-----AADDVPLP-----SPTPLRLPRV

ZmTPSI.1.1_tps1/1-960 YDIFASDAMDTDAEAAFALDGVQSPGRA-----SPAN
ZmTPSI.1.2/1-576 -----
ZmTPSII.2.1/1-888 -----VTASGIV-----PDLD
ZmTPSII.2.2/1-863 -----VTPGLI-----DD--
ZmTPSII.3.1/1-912 -----MTVPGTL-----TELD
ZmTPSII.3.2/1-912 -----MTVPGTL-----SELD
ZmTPSII.3.3/1-912 -----MTVPGTL-----SELD
ZmTPSII.4.1/1-864 -----VNSPGII-----SDPD
ZmTPSII.4.2/1-865 -----VTSPGII-----SDTD
ZmTPSII.4.3/1-868 -----VTSPSII-----SDHD
ZmTPSII.5.1/1-953 GGHRALCAYLENKKSGPGWKIPLPACCAPALPSRGGPRPAVKYYDPIPRFQPHENPKSQ
ZmTPSII.5.2/1-860 -----ATTGEVM-----
ZmTPSII.5.3/1-986 HIQLAIFVPPVLLPCPRPTSAFLSPETS-----AKVIDPSPTPTPTDRPPNE
ZmTPSII.5.4/1-851 -----MSVA-----

ZmTPSI.1.1_tps1/1-960 MEDAGGAAA-----
ZmTPSI.1.2/1-576 -----
ZmTPSII.2.1/1-888 VSD-----
ZmTPSII.2.2/1-863 -----
ZmTPSII.3.1/1-912 GEDESEPAA-----
ZmTPSII.3.2/1-912 GEDESEPAA-----
ZmTPSII.3.3/1-912 GEDESEPAA-----
ZmTPSII.4.1/1-864 WES-----
ZmTPSII.4.2/1-865 WDT-----
ZmTPSII.4.3/1-868 WDS-----
ZmTPSII.5.1/1-953 TKRPNPCAA-----
ZmTPSII.5.2/1-860 -----

ZmTPSII.5.3/1-986 P DTPRRVAALLFSSCAIAAVSTSATPTDRQEEDDEEAMP SLSCHNLLDLAAAEVPLPSPT
ZmTPSII.5.4/1-851 -----

ZmTPSI.1.1_tps1/1-960 -----ARPLAGSRSGFRRLGLRGMKQRLLVVANRLPVSANRRGED-----HWSL
ZmTPSI.1.2/1-576 -----
ZmTPSII.2.1/1-888 -----AASAADQSS-----HAPRERVIIVANQLPVRASRRRAAGAGGGWDF
ZmTPSII.2.2/1-863 -----SPASPS-----TPPRPTIIVANQLPIRSHRPESEE---P WTF
ZmTPSII.3.1/1-912 -----TSSVASDVPS-----SVAADRILIVVSNQLPIVARRRPDGR----GWSF
ZmTPSII.3.2/1-912 -----TSSVASDVPS-----SVAADRILIVVSNQLPIVARRRPDGR----GWSF
ZmTPSII.3.3/1-912 -----TSSVASDAPS-----SVAADRILIVVSNQLPIVARRRPDGR----GWSF
ZmTPSII.4.1/1-864 -----SNDGNSVGS-----MPFCFKRKIIIVANFLPVICAKNEATG----EWSF
ZmTPSII.4.2/1-865 -----ISDGDSVGS-----ASSTERKIIIVANFLPLNCTRDET G----VLSF
ZmTPSII.4.3/1-868 -----ISDGDSVGS-----AFSIERKIIIVANFLPLNCTRDET G----ELSF
ZmTPSII.5.1/1-953 -----QAAAMLSV SASDGRSPCV EARRIVVTHRLPLHAEPNPDAPY---GFDF
ZmTPSII.5.2/1-860 -----VSKTSSPSASNGELSTSPVEARRIVVTYRLPLRAEPNLDSPH---GFDF
ZmTPSII.5.3/1-986 PLRLPRVMSVASPASPTSPS-----PPAPRRRIVSHRLPLRASPDPSAPF---GFRF
ZmTPSII.5.4/1-851 -----SPASPTSP-----APAPRRRIVSHRLPLRASPDPAAPF---GFAF

ZmTPSI.1.1_tps1/1-960 EISAGGLV SALL-----GVKDVDAKWIGWAGVNV PDEVGQRALTKALAEK-RCIPVFL
ZmTPSI.1.2/1-576 -----
ZmTPSII.2.1/1-888 AWDQDSLLLQVKDSLRAHHGRADVEFVYVGGLRDDVPP-AEHDQVAHDLLEGFRCVPTFL
ZmTPSII.2.2/1-863 EWEDDSLRLHLH-----HSSSPLMEFIYIGCLRDDIPQ-AEQDAVAQALLETHNCVPAFL
ZmTPSII.3.1/1-912 SWDDDSL LQLR-----DGIPDEMEVLFVGS LRADVPA-AEQDAVSQALLDRFRCAPVFL
ZmTPSII.3.2/1-912 SWDGSLLLQLR-----DGIPDEMEVLFVGS LRADVPA-AEQDEVSQTL LDRFRCAPVFL
ZmTPSII.3.3/1-912 VWDDDSL LQLR-----DGIPDEMEVLFVGS LRADVPV-AEQDEVSQALLDRFRCAPVFL
ZmTPSII.4.1/1-864 AMDNQLLVQLK-----DGFPIGNEVIYVGS LNVQVDP-IEQDRVSQKLFKEHRCVPTFL
ZmTPSII.4.2/1-865 SLDHDALLMQLK-----DSFSNETDVVYVGS LKVQVDP-GEQDQVAQKLLREYRCIPTFL
ZmTPSII.4.3/1-868 SLDHDSLLMQLK-----DGFSNETDAVYVGS LKVHVDP-REQDQVAQKLLREYRCIPTFL
ZmTPSII.5.1/1-953 SLDADALPLQLA-----RGLPR--PVVFGALPSAAASISASEE LADLLARFGCSPVFL
ZmTPSII.5.2/1-860 SLDADALPLQCT-----RGLPR--PVVFGALPSAAASISESDDLADL FTRFACSPVFL
ZmTPSII.5.3/1-986 SVDAGTVAYQLR-----SGLPTNAPVLHIGTLPASAAE-AASDELSNYLLANFSCLPVYL
ZmTPSII.5.4/1-851 SVDAGTVAYQLR-----SGLPANAPVLHIGTLPAAAAE-AASDELSDYLLANFSCLPVYL

ZmTPSI.1.1_tps1/1-960 DEEIVHQY YNGYCNNILWPL--FHYLGLPQEDRL-----ATTRNFESQF
ZmTPSI.1.2/1-576 -----
ZmTPSII.2.1/1-888 PADLRSRFYHGFCCKQLWPL--FHYM-LPLSPEL-----GGRFDRLW
ZmTPSII.2.2/1-863 PTDIAERY YHGFCCKQHLWPL--FHYM-LPLSPDL-----GGRFDRLW
ZmTPSII.3.1/1-912 PDHLNDRFYHGFCCKRQLWPL--FHYM-LPFSSPASASAAATSSSVATSSPGNGCFDRSAW
ZmTPSII.3.2/1-912 PDHLNDRFYHGFCCKRQLWPL--FHYM-LPFSSPASASAAATSSSVATSSPGNGFRDRSAW
ZmTPSII.3.3/1-912 PDRLNDRFYHGFCCKRQLWPL--FHYM-LPFSSA---SAAGTTSSSAATCNGRFRDRSAW
ZmTPSII.4.1/1-864 PAELQHQFYHIFCKQHLWPL--FHYM-LPVCHDK-----DELFD RSLF
ZmTPSII.4.2/1-865 PSDLQQQFYHGFCCKQLWPL--FHYM-LPICLDK-----GELFD RSLF
ZmTPSII.4.3/1-868 PSDLQQQFYHGFCCKQLWPL--FHYM-LPICLDK-----GELFD RTLF
ZmTPSII.5.1/1-953 DPGLHKDFYDGFCKRYLWPM--LHYL-LPFTLTP-----FFGSGGLKFKANLY
ZmTPSII.5.2/1-860 DPSLHNDFYNSFCCKRYLWPILQLQYL-LPFTRSS-----DSGCLSFNEDLY
ZmTPSII.5.3/1-986 PTDLHHRFYHGFCCKHYLWPL--LHYL-LPLTPSS-----LGGLPFQRTLY

ZmTPSII.5.4/1-851 PTDLHHRFYHGFKHYLWPL--LHYL-LPLTPSS-----LGGLPFQRTLY

ZmTPSI.1.1_tps1/1-960 DAYKRANQMFAADVVEHYQ-DGDVIWCHDYHLMFLPKCLKDHDINMKVGWFLHTPFPSSE

ZmTPSI.1.2/1-576 -----

ZmTPSII.2.1/1-888 QAYVSVNKIFADKILEVISPEDEFVWVHDYHLMVLPFTFLRKRFRNRVKLGFFLHSPFPSSSE

ZmTPSII.2.2/1-863 QAYVSANKIFADKVLEVINPDDDFVWVHDYHLMVLPFTFLRKRFRNRKLGFFLHSPFPSSSE

ZmTPSII.3.1/1-912 EAYVLANKFFFEKVVEVINPEDDYVWVHDYHLLALPTFLRRRFRNLRIGFFLHSPFPSSSE

ZmTPSII.3.2/1-912 EAYVLANKFFFEKVVEVINPEDDYVWVHDYHLLALPTFLRRRFRNLRIGFFLHSPFPSSSE

ZmTPSII.3.3/1-912 EAYVLANKFFFEKVVEVINPEDDYVWVHDYHLMALPTFLRRCFNLRIGFFLHSPFPSSSE

ZmTPSII.4.1/1-864 QAYVRANKIFADKIVEAVNSDDDCVWVHDYHLMLIPTLLRKKLHRIKVGFFLHSPFPSSSE

ZmTPSII.4.2/1-865 QAYVRANKLIFADKVMEAINADDFVWVHDYHLMMLPTFLRKRRLHRIKIGFFLHSPFPSSSE

ZmTPSII.4.3/1-868 QAYVRANKLIFADKVMEAINDDDYVWVHDYHLMMLPTFLRKRRLHRIKIGFFLHSPFPSSSE

ZmTPSII.5.1/1-953 RAYLTANTQYAEVLEQLNPEDELVFIHDYHLLALPTILRHKSPRARIGFFLHTPFPTSE

ZmTPSII.5.2/1-860 RAYLTANTQYADRVFEHLNTEDELVLIHDYHLFALPTILRHKSPRARIGFFLHSPFPPTSE

ZmTPSII.5.3/1-986 HSFLSANRAFADRLTEVLSPEDELVWIHDYHLLALPTFLRKRFPRAKVGFFLHSPFPSSSE

ZmTPSII.5.4/1-851 HSFLSANRAFADRLTEVLCPEDELVWIHDYHLLALPTFLRKRFPRAKVGFFLHSPFPSSSE

ZmTPSI.1.1_tps1/1-960 IYRTLPSRLELLRSVLCADLVGFHTYDYARHFVSACTRILGLEGTPE---GVEDQGRLT

ZmTPSI.1.2/1-576 -----

ZmTPSII.2.1/1-888 IYKTLPVREELLRSLNADLIGFHTFDYARHFVLSCCSRMLGLKYESQRYIALEYGRTV

ZmTPSII.2.2/1-863 IYKTLPVREELLRALLNSDLIGFHTFDYARHFVLSCCGRMLGLSYESKRGHICLEYGRTV

ZmTPSII.3.1/1-912 IYRTLPRDEILKALLNCDLIGFHTFDYARHFVLSCCSRMLGIEYQSKRGYIGLDYFGRTV

ZmTPSII.3.2/1-912 IYRTLPRDEILKALLNCDLIGFHTFDYARHFVLSCCSRMLGIEYQSKRGHIGLDYFGRTV

ZmTPSII.3.3/1-912 IYRTLPREEILKALLNCDLIGFHTFDYARHFVLSCCSRMLGIEYQSKRGYIELDYFGRTV

ZmTPSII.4.1/1-864 IYRTLPRDEILKSLNADLIGFQTFDYARHFVLSCCSRLGLNYESKRGHIGIEYFGRTV

ZmTPSII.4.2/1-865 IYRTLPRDEILKSLNADLIGFQTFDYARHFVLSCCSRLGLHYESKRGYIGIEYFGRTV

ZmTPSII.4.3/1-868 IYRTLPRDEILKSLNADLIGFQTFDYARHFVLSCCSRLGLHYESKRGYIGIEYFGRTV

ZmTPSII.5.1/1-953 LFRTPVREDLLRSLLNADLVGFHNYDYARHFVLSACTRLLGVTSHTRGYISIDYCGRAV

ZmTPSII.5.2/1-860 LFRAPVREELLRALLNADLVGFQNYDYGCHFISACSTLLGITSAHGDYICIDYFGRAV

ZmTPSII.5.3/1-986 IFRTIPVRDDLVRALLNADLVGFHTFDYARHFVLSACSRLGLDYQSKRGYIGIEYGRTV

ZmTPSII.5.4/1-851 IFRTIPVRDDLVRALLNADLVGFHTFDYARHFVLTACSRLGLDYQSKRGYIGIEYGRTV

ZmTPSI.1.1_tps1/1-960 RVAAPFPIGIDSDRFKRALELPAVKRHVSELTERF--AGRKVMLGVDRLDMIKGIKIPQKILA

ZmTPSI.1.2/1-576 -----MLGVDRLDMIKGIKIPQKILA

ZmTPSII.2.1/1-888 TIKILPVGVHLEQLRSVLNLPGLVGVKVAELLKQFCHRNRLLLGLVDDMDIFKGISLKLLA

ZmTPSII.2.2/1-863 SIKILPVGVMHLEQLKTVLGLPETEAKVSELMEMYSKGRVVMGLVDDMDIFKGISLKLLA

ZmTPSII.3.1/1-912 GIKIMPVGVMHMQLESGLRLPDREWRLSELQQQF--QGKTVLLGVDDMDIFKGINLKLLA

ZmTPSII.3.2/1-912 GIKIMPVGVMHMQLESGLRLPDREWRLSELQQQF--QGKTVLLGVDDMDIFKGINLKLLA

ZmTPSII.3.3/1-912 GIKIMPVGVMHMQLELGLRLPDREWRLSELQRQF--QGKTVLLGVDDMDIFKGINLKLLA

ZmTPSII.4.1/1-864 SLKILAGVHVGRLEATLRLPATIKKVEIESRY--SGKLVILGVDDMDIFKGISLKLLG

ZmTPSII.4.2/1-865 SLKILSVGVHIGRLESVLKLPATVSKVQIEQRY--KGKILMLGVDDMDIFKGISLKFLG

ZmTPSII.4.3/1-868 SLKILSVGVHVGRLESVLKLPATVSKVEEIEQRY--KGKILMLGVDDMDIFKGISLKLLA

ZmTPSII.5.1/1-953 SVKILAGGVDIGQLREVLSPEEAKAKEVATK--AGRQLLLGVDDVDFKIGIGLKLLA

ZmTPSII.5.2/1-860 VVKILSVGDMVRLREVLSPEEAKAKEVATK--AGRQVLIGVDDVDFNRIDVKLLA

ZmTPSII.5.3/1-986 TVKILPVGIDMQLRVSVSAPETEDAVRRVTEAY--KGRRLMVGVDVDFKIGIGLKFLA

ZmTPSII.5.4/1-851 TVKILPVGIDMQLRVSVSAPETEDAVRRVTEAY--KGRRLMVGVDVDFKIGIGLKFLA

ZmTPSI.1.1_tps1/1-960 FEKFL EENPDWNNKVLLQIAVPT**R**TDVPEYQKLT SQVHEIVGRINGRFGTL-TAVPIHH
ZmTPSI.1.2/1-576 FEKFL EENPDWNDKVVLLQIAVPT**R**TDVPEYQKLT SQVHEIVGRINGRFGTL-TAVPIHH
ZmTPSII.2.1/1-888 FEQLLMQHPEWRGRVVLVQIANPA**R**GRGKD VREVQEESDAMVRRINDAFGQP-GYQPVIL
ZmTPSII.2.2/1-863 MEELLRQHPEWRGKLVLVQIANPA**R**GRGKDVAEVQETETYAMVRRINEVYGEP-GYEPVVL
ZmTPSII.3.1/1-912 FENMLRTHPKWQGRAVLVQIANPA**R**GRGKDLEAIQAEIEESCQRINVDGFGS-GYSPVVF
ZmTPSII.3.2/1-912 FENMLRTHPKWQGRAVLVQIANPA**R**GRGKDLEAIQAEIEESCQRINGDFGQS-GYSPVVF
ZmTPSII.3.3/1-912 FENMLRTHPKWQGRAVLVQIANPA**R**GRGKDLEAIQAEIEESCQRINGDFGQS-GYSPVVF
ZmTPSII.4.1/1-864 LELLLERTPKLRGKVVLVQIVNPA**R**SIGKDIEEAKYEASVAQRINDKYGSA-NYKPVVL
ZmTPSII.4.2/1-865 LELLLDRNPKLREKVVVLVQIINPA**R**STGKDVQEAIT EAVSVAERINTNYGSS-SYKPVVL
ZmTPSII.4.3/1-868 LELLLDRNPKLREKVVVLVQIINPA**R**STGKDVQEAIT EAVSVAERVNTKYGSS-SYKPVVL
ZmTPSII.5.1/1-953 MERLLESQPELHGQVVLVQINNPA**R**SPGYDTDEICAE LQAMKRINARFATPAGYEP IVI
ZmTPSII.5.2/1-860 MERLLESRPELIGQVVLVQINNPA**R**SPGRD TDVLAEVQLLMDRINARFAKP-GYDPIVM
ZmTPSII.5.3/1-986 MEQLLVEHRELGRVVLVQIANPA**R**SEGRDVQGVQDEARAI SARVNARFGTP-GYTPIVL
ZmTPSII.5.4/1-851 MEQLLVEHRELGRHAVLVQIANPA**R**SEGRDVQGVQDEARAI SARVNARFGTP-GYTPIVL

ZmTPSI.1.1_tps1/1-960 LDRSLDFHALCALYAVTDVALVTS**LDGMNLV**SYEYVACQGS-----KKG
ZmTPSI.1.2/1-576 LDRSLDFHALCALYAVTDVALVTS**LDGMNLV**SYEYVACQGS-----KKG
ZmTPSII.2.1/1-888 IDQ**PL**QFYERMAYYVAECCLVAVR**DGMNL**IPY**EY**VIARQGNERIDSILGLGPASRKKS
ZmTPSII.2.2/1-863 IDE**PL**QFYERVAYYVIAEVCVAVR**DGMNL**IPY**EY**IVSRQNEKLD RMLRQKPEEKKS
ZmTPSII.3.1/1-912 INRDVSSVEKVA YYTIAECVVAVR**DGMNL**TPY**EY**IVCRQGAPGSES VSEVSGP--KKS
ZmTPSII.3.2/1-912 IDRVDVSSVEKIA YYTIAECVVAVR**DGMNL**TPY**EY**IVCRQGAPGSES VSEVSGP--KKS
ZmTPSII.3.3/1-912 IGRDVSSVEKIA YYTIAECVVAVR**DGMNL**TPY**EY**VVCRQGAPGQS SVSEVSGP--KKS
ZmTPSII.4.1/1-864 IDYSIPFYEKIAFYAASDCCIVNAVR**DGMNL**IPY**EY**TVCRQGN EELDKLRGLNKSSSHTS
ZmTPSII.4.2/1-865 IDHHIPFYEKIAFYAASDCCIVNAVR**DGMNL**VPY**EY**TVCRQGN EIDKLRGLGKDTHTS
ZmTPSII.4.3/1-868 IDNRIPFYEKVAFYAASDCCIVNAVR**DGMNL**VPY**EY**TVCRQGN EIDRVRGLDKDTHTS
ZmTPSII.5.1/1-953 IEDPMTMHEK LAFYTSADICLVAVR**DGLN**RTPYIYTVCRQEGP ISSGVVAGP----KEG
ZmTPSII.5.2/1-860 IDDP**L**TMHEK LAFYTSADICIVAVR**DGLN**RTPYIYTVCREHGP ISSGVVAGP----RES
ZmTPSII.5.3/1-986 IDGPVTPQEKAAAYYAAAECCVLSAVR**DGLN**RIPYIYTVCRQES-----TALGDDAPKRS
ZmTPSII.5.4/1-851 IDAPVTPQEKAAAYYAAAECCVLSAVR**DGLN**RIPYIYTVCRQES-----TALGDDSPKRS

ZmTPSI.1.1_tps1/1-960 VLILSEFAGAAQSLGAGAILVNPWNITEVADSI RHALTMPSDEREKRHRHNYAHVTHTTA
ZmTPSI.1.2/1-576 VLILSEFAGAAQSLGAGAILVNPWNITEVADSI RHALTMPSDEREKRHRHNYAHVTHTTA
ZmTPSII.2.1/1-888 MLVVSEFIGCSPSLS-GAIRVNPWNIDS VADAMDYALEMPEGEKVL RHEKHRYVSTHDV
ZmTPSII.2.2/1-863 MLVVSEFIGCSPSLS-GAIRVNPWNIEAVADAMETALVLPEN EKRLRHDKHFVSTHDV
ZmTPSII.3.1/1-912 MLVVSEFIGCSPSLS-GAIRVNPWNIEATAEAMNEAISMPEQEKQLRHEKHRYVSSH DV
ZmTPSII.3.2/1-912 MLVVSEFIGCSPSLS-GAIRVNPWNIEATAEAMNEAISMPEQEKQLRHEKHRYVSSH DV
ZmTPSII.3.3/1-912 MLVVSEFIGCSPSLS-GAIRVNPWNIEATAEAMNEAISMPEQEKQLRHEKHRYVSSH DV
ZmTPSII.4.1/1-864 TLIVSEFVGCSPSLS-GAFRVNPWSMEDVADALYSVTDLTRY EKNLRHEKHRYVSSH DV
ZmTPSII.4.2/1-865 TLIVSEFVGCSPSLS-GAFRVNPWSVDDVADALCRATDLTSEKRLRHEKHRYVSTHDV
ZmTPSII.4.3/1-868 TLIVSEFVGCSPSLS-GAFRVNPWSVDDVADALCRATDLSESEKRLRHEKHRYVSTHDV
ZmTPSII.5.1/1-953 AIVLSEFVGCATSLG-GAVHINPWNVDVAE GMMALRFNGREKQVRQEKHYRFVSTHDI
ZmTPSII.5.2/1-860 AIVLSELVGCSTFLR-GAVRVNPWNVDVVEGMSSALRLNERDKKILHAKHYMYVKHDI
ZmTPSII.5.3/1-986 AIVLSEFVGCSPSLS-GAIRVNPWSVESVAEAMNAALRMPAEQRLRHEKHRYVSTHDV
ZmTPSII.5.4/1-851 VIVLSEFVGCSPSLS-GAIRVNPWSVESVAEAMNAALRMPAEQRLRHEKHRYVSTHDV

ZmTPSI.1.1_tps1/1-960 QDWAETFFVFLNDTVAEAL-----LRTRQVPPG---LPSQMAIQYLRSKNRL
ZmTPSI.1.2/1-576 QDWAETFFVFLNDTVAEAL-----LRTRQVPPG---LPGQTAIQQYLRSKNRL
ZmTPSII.2.1/1-888 GYWANSFLQDLERICLDHNRRCWIGFGLKFRVVALDPNFKKLAVEHLVLAYRRTKRV
ZmTPSII.2.2/1-863 GYWANSFLDLERTCKYHSQKRCWIGFGLRFRVSLDLTFRKLSLENILMAYRRAKTRA
ZmTPSII.3.1/1-912 AYWSKSFILDLERACRDHFKRTCWIGLGFGRVVALDPHFRLNMDSIVNAYEISESRA
ZmTPSII.3.2/1-912 AYWSKSFILDLERACRDHFKRTCWIGLGFGRVVALDAHFRKLNMDSIVNAYEISGSRA
ZmTPSII.3.3/1-912 AYWSKSFIDLERVCKDHFKRTCWIGLGFGRVVALDPHFRTKLNMDSIINAYEISESRA
ZmTPSII.4.1/1-864 AYWARSFQDLKACIEQYSQRCWTTGFGLNFRVIALSPGFRRLSLEHLASSYKKANRRM
ZmTPSII.4.2/1-865 AYWARSFQDLERACKDHSRRCWAIGFGLNFRVIALSPGFRKLSSEHFVSSYNKASRRA
ZmTPSII.4.3/1-868 AYWAHSFAQDLERACRDHYSRRCWAIGFGLNFRVIALSPGFRKLSSEHFVSSYNRASRRA
ZmTPSII.5.1/1-953 AYWGRSLDQLQRASKDHASMKFMSVGLAMSYHIVVLSPNFQKLSPEHINPSYQRAGNRL
ZmTPSII.5.2/1-860 AYWGRSLDQNLQKASMDHASMNFLSVGLAMNFRIVVLDPNFQKLSPEHINPSYHRTGNRL
ZmTPSII.5.3/1-986 AYWARSFSDQLQRACKDHSRHHWIGFMSFKVVALGPNFRRLSVEHIVPSYRRTENRL
ZmTPSII.5.4/1-851 AYWARSFSDQLQRACKDHSRHHWIGFMSFKVVALGPNFRRLSVEHIVPSYRRTDNRL

MOTIF I

MOTIF II

ZmTPSI.1.1_tps1/1-960 LILGFNS**TL**TEPVESSGRRGGDIKEMELKLPDLKGPLRALCEDERTTVIVL**SGS**DRSV
ZmTPSI.1.2/1-576 LILGFNS**TL**TEPVESSGRRGGDIKEMELKLPDLKGPLGALCEDERTTVIVL**SGS**DRSV
ZmTPSII.2.1/1-888 ILL**DYD**GTLM-PQ**T**SLGKSPTSRTIDM-----LNSLCRDRNMVFLV**SAKSRMT**
ZmTPSII.2.2/1-863 ILL**DYD**GTLM-PQ-AINKSPSTESVRI-----LNSLCRDKDNVVYLC**SGYDRRT**
ZmTPSII.3.1/1-912 ILL**DYD**GTLV-PQ**T**SINKEPSPEVLNI-----INTLCSDSRNIVFLV**SGRDKDT**
ZmTPSII.3.2/1-912 ILL**DYD**GTLV-PQ**T**SINKEPSPEVLNI-----INTLCSDSRNIVFLV**SGRDKDM**
ZmTPSII.3.3/1-912 ILL**DYD**GTLV-PQ**T**SLNKEPSPQVLSI-----INTLCSDSRNIVFLV**SGRDKDT**
ZmTPSII.4.1/1-864 I**F**LD**DYD**GTLV-PQ**T**SHDKSPSAELIST-----LNSLCSMDKNTVFIV**SGRGRDS**
ZmTPSII.4.2/1-865 I**F**LD**DYD**GTLV-PQ**S**SINKAPSEEVISV-----LNTLCNDPKNIVFIV**SGRGRDS**
ZmTPSII.4.3/1-868 I**F**LD**DYD**GTLV-PQ**S**SINKAPSEEVISI-----LNTLCNDPKNVFIV**SGRGRDS**
ZmTPSII.5.1/1-953 ILL**DYD**ETVMFHPGLLDRHPSQRLIGI-----LNELCSDPKNTVFVV**SGRSKDE**
ZmTPSII.5.2/1-860 ILL**DYD**GTVMVP**Q**GLITRHPSEQELVSV-----LNELCSDPMNTVFVV**SGRSKDE**
ZmTPSII.5.3/1-986 ILL**DYD**GTVM-PENSIDRTPSSEVISV-----LNRLCEDPKNRVFIV**SGRGKDE**
ZmTPSII.5.4/1-851 ILL**DYD**GTVM-PENSIDRTPSSEVISV-----LNRLCEDPKNRVFIV**SGRGKDE**

ZmTPSI.1.1_tps1/1-960 LDENFGEF-KMWLAAEHGMFLR-PTYGEWMTTMEHLNMDWVDSVKHVFEYFTERTPRSH
ZmTPSI.1.2/1-576 LDENFGEF-KMWLAAEHGMFLR-PTYGEWMTTMEHLNMDWVDSVKHVFEYFTERTPRSH
ZmTPSII.2.1/1-888 LNEWFLPCESLGLAAEHGCFRLRLRDAEWETCVPV-IDCSWKQIAEPVMKTYTETTDGST
ZmTPSII.2.2/1-863 LHEWF-PCENLGLIAAEHGYFLRCKRDAEWKTCVAA-TDCSWKQIAEPVMCLYRETTDGST
ZmTPSII.3.1/1-912 LGKWFSSCPKLGIAAEHGYILRWSSEEWQ**TCTQA**-MDFGWMQMAKPVMNLYTEATDGSY
ZmTPSII.3.2/1-912 LGKWFSSCPKLGIAAEHGYFLRWSSEEWQ**TCTQA**-MDFGWMQMAKPVMNLYTEATDGSY
ZmTPSII.3.3/1-912 LGKWFSSCPRLGIAAEHGYFLRWSREEEWQ**TCTQA**-LDFGWMQMAKPVMNLYTEATDGSY
ZmTPSII.4.1/1-864 LSEWFASCENLGLIAAEHGYFIRWNKAAEWETSFSG-IYSEWKLADPIMHVYMETTDGSF
ZmTPSII.4.2/1-865 LDEWFSPEKLGIAAEHGYFIRWSKEAAWESSYR-PQE**W**KHIAEPVMQVY**TET**TDGSS
ZmTPSII.4.3/1-868 LDEWFSPEKLRLLAAEHGYFIRWSKEAAWESSYSS-PRQ**E**W**K**HIAEPVMQVY**TET**TDGSS
ZmTPSII.5.1/1-953 LARWLEPCERLGLIAEHGYFTRWSRYPWESPDLK-VDY**G**W**K**MVEPVMDLYAV**TD**GSS
ZmTPSII.5.2/1-860 LAGWLAPCEKLGISAEHGYFTRWSRDPWESP**KL**L-LDNDWKNIVEPVMKYCDV**TD**GSY
ZmTPSII.5.3/1-986 LSRWFAPCEKLGIAAEHGYFTRWSRDPWEASALA-ADLDWKN**T**AEPVMRLY**TEAT**DGSY
ZmTPSII.5.4/1-851 LSRWFAPCEKLGIAAEHGYLTRWSRDPWD**T**SGLA-ADFDW**K**TAEPVMQ**LYTEAT**DGSY

ZmTPSI.1.1_tps1/1-960 FEHRETSFVWNYKYADVEFGRLQARDMLQHLWTGPISNAAVDVVQGSRSVEV--RSVG-V
ZmTPSI.1.2/1-576 FEHRETSFVWNYKYADVEFGRLQARDMLQHLWTGPISNAAVDVVQGSRSVEV--RSVG-V
ZmTPSII.2.1/1-888 IEDKETAIVWCYEDADPDFGSCQAKELHDHL-ESVLANEPVSVKAGPNLVEV--K**P**Q**G**-V

ZmTPSII.2.2/1-863 IEDRETVLVWNYEDADPDFGSSQAKELVDHL-ESVLANEVPSVKTPHSVEV--KPQG-V
 ZmTPSII.3.1/1-912 IERKESALVWHHQDADPDFGSSQAKELLDHL-ESVLANEVPSVKSGQFIVEV--KPQG-V
 ZmTPSII.3.2/1-912 IETKESALVWHHQDADPDFGSSQAKELLDHL-ESVLANEVPSVKSGQFIVEV--KPQG-V
 ZmTPSII.3.3/1-912 IEAKESALVWHHQDADLDFGSSQAKEMLDHL-ESVLANEVPSVKSGQFIVEV--KPQG-I
 ZmTPSII.4.1/1-864 IEPKESALVWHYQNTDHDGFGSCQAKELVSHL-ERVLSNEPVVRRGHQIVEV--KPQG-V
 ZmTPSII.4.2/1-865 IESKESALVWHYLDADHDGFGSFQAKELQGH-ERVLSNEPVVVKCGHYIVEV--KPQG-V
 ZmTPSII.4.3/1-868 VESKESALVWHYLDADHDGFGSFQAKELKDHL-ERVLSNEPVVVKCGHYIVEV--KPQG-V
 ZmTPSII.5.1/1-953 VETKETALVWHYEGTDPVFGPSQAKELRDHL-SDVLAKEPVSVRSYNIIVEV--NPQE-V
 ZmTPSII.5.2/1-860 IEAKETALVWHYEEADPDFGPRQAKELQYHL-RDVLSEEPVYKSGHQIVEVNGNPQEVV
 ZmTPSII.5.3/1-986 IEHKESGMVWHHDEADPDFGSSQAKELLDHL-ENVLANEVPSVKRGQHIVEV--NPQG-I
 ZmTPSII.5.4/1-851 IEHKESAIVWHHDEADPDFGSSQAKELLDHL-ENVLANEVPSVKRGQHIVEV--NPQG-I

MOTIF III

ZmTPSI.1.1_tps1/1-960 TKGAAIDRILGEIV-HSENMITP-IDYVLCIGHFLGKDEDIYVFFDPEYPSSESKVKPEGG
 ZmTPSI.1.2/1-576 TKGAAIDRILGEIV-HSENMITP-IDYVLCIGHFLGKDEDIYVFFDPEYPSSESKVKPEGG
 ZmTPSII.2.1/1-888 SKGLVAKRILSTTQ-ERGDADDDLPDFVLCVGD-DRSDEDMF-----EVIAAAAA-
 ZmTPSII.2.2/1-863 SKGLVARRMLVSMK-ERGQC---PDFVLCIGD-DKSDEDMF-----QLIATAAC-
 ZmTPSII.3.1/1-912 SKGIVAERILASVK-ERGGKQ---ADFVLCIGD-DRSDEDMF-----ENIADI IK-
 ZmTPSII.3.2/1-912 SKGIVAERILASVK-ERGGKQ---ADFVLCIGD-DRSDEDMF-----ENIADI IK-
 ZmTPSII.3.3/1-912 SKGIVAERILASVK-ERGGKQ---ADFLLCIGD-DRSDEDMF-----ENIADI IG-
 ZmTPSII.4.1/1-864 SKGISVDKIIRTLV-SKGEV---PDLMLCIGN-DRSDEDMF-----ESINRATS-
 ZmTPSII.4.2/1-865 SKGLAVNKLIIHTLV-KNGKA---PDFLMCVGN-DRSDEDMF-----ESINGMTS-
 ZmTPSII.4.3/1-868 SKGRAVDKLIQALANNNGKA---QDFLMCVGN-DRSDEDMF-----ECINGMAS-
 ZmTPSII.5.1/1-953 DKGTAVQRIIAAMR-DRGRM---PDFILCVGD-DASDEDMF-----KAVTAPSN-
 ZmTPSII.5.2/1-860 GKGTAVQGLIAALG-ARGRM---PDFILCVGD-DVSDEDMF-----EAISAPSS-
 ZmTPSII.5.3/1-986 SKGVVVDLSSMV-RTGKP---PDFVLCIGD-DRSDEDMF-----ESIVCPAS-
 ZmTPSII.5.4/1-851 SKGVVVDLSSMV-RTGKP---PDFVLCIGD-DRSDEDMF-----ESIVCPAS-

MOTIF III

ZmTPSI.1.1_tps1/1-960 SASLDRRPNGRPPSNGRSNSRNPQSRTPQKAQQAASERSSSSSSSTSSNHDWREGSSVLD
 ZmTPSI.1.2/1-576 SASLDRRPNGRPA SNGRSNSRNPQSRPQKAQQAASERSSSSSSSTSSNHDWREGSSVLD
 ZmTPSII.2.1/1-888 -----ARGVSSLQ
 ZmTPSII.2.2/1-863 -----G---DSLA
 ZmTPSII.3.1/1-912 -----R---NMVA
 ZmTPSII.3.2/1-912 -----R---NMVA
 ZmTPSII.3.3/1-912 -----R---NLVA
 ZmTPSII.4.1/1-864 -----LSELP
 ZmTPSII.4.2/1-865 -----N---AVLS
 ZmTPSII.4.3/1-868 -----N---DVSS
 ZmTPSII.5.1/1-953 -----K---SAFP
 ZmTPSII.5.2/1-860 -----KF---AFP
 ZmTPSII.5.3/1-986 -----SSGGVRLP
 ZmTPSII.5.4/1-851 -----NSG-VKLP

ZmTPSI.1.1_tps1/1-960 LKGENYFSCAVGRKRSNARYLLSSSEEVVSFLKELATA-----TA
 ZmTPSI.1.2/1-576 LKAENYFSCAVGRKRSNARYLLSSSEEVVSFLKELATE-----TA
 ZmTPSII.2.1/1-888 AEA-EVFACTVGRKPSKAKYYLDDPADIVRLVQGLASV-----SDDQTHAPPPPPP
 ZmTPSII.2.2/1-863 SKA-EVFACTVGRKPSKAKYYLDDAAEVVRLMQGLSYV-----SEELANQRD

ZmTPSII.3.1/1-912 PRT-SLFACTVGGQKPSKAKFYLDLDTF EVVAMLSALADATGAELKSDSADELAASISSLDI
 ZmTPSII.3.2/1-912 PRT-SLFACTVGGQKPSKAKFYLDLDTF EVVAMLSALADATGAELKSDSADELAASISSLDI
 ZmTPSII.3.3/1-912 PRT-ALFACTVGGQKPSKAKFYLDLDTF EVVIMLSALADATGPELETDSADEVAYISSLDI
 ZmTPSII.4.1/1-864 AAP-EVFACSVGPKASKANYVVDGCE EVIRLLKGVTA-----SLQKDTA
 ZmTPSII.4.2/1-865 PTMPELFACTSVGGQKPSKAKFYLDLDTF EVIRLLKKNVTRI-----PSQRQDVSA
 ZmTPSII.4.3/1-868 TTVPEVFACSVGQKPSKAKFYLDLDTF EVIRLLRDATRF-----SSSQREDVNA
 ZmTPSII.5.1/1-953 EDA-EVFACTIGTKPSLAKYYLDLDPV EVLSMLKGLIKS-----SVEERP
 ZmTPSII.5.2/1-860 EAA-EIFACTVGNKPSLAKYYLEDPD EVLKMLKGLIDS-----FEE
 ZmTPSII.5.3/1-986 ASS-EVFACTVGGKPSMAKYYLDLDTV DVVKMLDGLASA-----PSPRRPG
 ZmTPSII.5.4/1-851 ASS-EVFACTVGGKPSMARYLDLDTV DVVKMLDGLASA-----PSQQR

ZmTPSI.1.1_tps1/1-960 GFQATCADYMHVLG-
 ZmTPSI.1.2/1-576 GFQSSCADYMFLLDRQ
 ZmTPSII.2.1/1-888 SAATTAADTVPR---
 ZmTPSII.2.2/1-863 EDEDSSLDDVWE---
 ZmTPSII.3.1/1-912 GDEQSESDTPIGGS
 ZmTPSII.3.2/1-912 GDEQSETSDTPIGGS
 ZmTPSII.3.3/1-912 GDEQSESSDKPVEGS
 ZmTPSII.4.1/1-864 GHSHAAFEDTLEVVS
 ZmTPSII.4.2/1-865 SHGRVTFRGVLDYVD
 ZmTPSII.4.3/1-868 SRGRVTFRDALDYVD
 ZmTPSII.5.1/1-953 GDGEGPSRVSFD---
 ZmTPSII.5.2/1-860 NHSTVEANK-----
 ZmTPSII.5.3/1-986 PAAAVQLRVSFEGSL
 ZmTPSII.5.4/1-851 SRPAVQLRVSFEGSL

Supplemental Figure S2B. Predicted enzymatic domains for TPP proteins.

TPP predicted domain; Conserved motifs **HAD phosphatases**

ZmTPPA.1/1-388 --MDLKTGLNS---PVIADHLPTLALPAA-VMTFTTPTSFP---SP-----
ZmTPPA.3/1-369 --MDMGSG-SS---PVITDPISISPLLGLTSLNLMFVSVM---SG-----
ZmTPPB.1.1/1-367 --MTKQGMVVPV--PEAAVAVPPNSAP---LFQYPPRAAP---GV-----
ZmTPPB.1.2/1-384 MPMAKPSVAEASGVPAQASCSCPCPGTTLFPYPPPRGASGIAAA-----
ZmTPPB.1.3/1-370 --MAKPSVAVPEV-GVPAAQA-SCTCPGT-LLAYPPRGAG--VAA-----
ZmTPPB.1.4/1-357 -MTNQDQVVVSEM-GIAAGAALPGPSPA--LLAC---RGAA---AG-----
ZmTPPB.1.5/1-356 --MTNQDQVVVSEM-GIAAGTALPGSSPA--LLAC---RGAA---AG-----
ZmTPPB.1.6/1-384 --MTNQDQVVVSDM-GIAAAAALP--PPG--LFACRGVAGAVSSLRGTYSGLGLPGGAAAD
ZmTPPB.2.1_ramosa3/1-361 --MTKHAAYSSED-VVAVAAPA--PAGRHTSFQALKGAP---L-----
ZmTPPB.2.2/1-327 --MTKHTAFAGADGGTTAAAA-----VTLCAPRA----RG-----
ZmTPPB.2.3/1-357 --MTKRFAFAADD-AIIAAAAVTSQPGRRTSYPPARA----RG-----

ZmTPPA.1/1-388 GLCLNTTKKIPLPGKIEEVRAAG-W-LDLMKASSPTRKRQIKDVICDAQSD---LDLQYC
ZmTPPA.3/1-369 GCSSSPSMSASSRRKIEEVLVNG-L-LDAMKSSSPRKKHNL-AFGQDNSPD---EDPAYT
ZmTPPB.1.1/1-367 AVRKKCLQMGAGAGRI-----GGW-VESMRASSPTHAKAAAALAGV-----EEERYA
ZmTPPB.1.2/1-384 AVRRKCLQAEVGGGAC-----WGVESMRASSPTHARAAAALAGAGAD---EEEERA
ZmTPPB.1.3/1-370 AVRRKCLQVELGAGAG-LLGGAGAWGVESMRASSPTHARAAAALAGGGVDVDVDEERAA
ZmTPPB.1.4/1-357 AMSLRYLDLAAAAARS---ASGTW-ADAMRASSPTRSRAA-----DEFT
ZmTPPB.1.5/1-356 AMSLRYLDLAAAAARS---ASCTW-VEAMRASSPTRSRAAADV-----DELT
ZmTPPB.1.6/1-384 GGEFRSPVAAAANAPPGRSCTSRV-VEAIRASSPARCPAV-----DEYD
ZmTPPB.2.1_ramosa3/1-361 DCKKHAVDLSASGAAVV--GGGPW-FESMKASSPRRAADA-----EHG
ZmTPPB.2.2/1-327 -----ARRV---AAGSL-PELVRRHA-----DLD
ZmTPPB.2.3/1-357 GCRLAPAVAAAAARQATDDPGAAGSW-PELV---VPRHA-----DFD

MOTIF I

ZmTPPA.1/1-388 NWTVNYPALISFEAISDLAGSKRLALFLDYDGTLSPIVDNPNALMSDEMRAAVRHAAS
ZmTPPA.3/1-369 AWLSKCPALASFKQIVANAQGRRIAVFLDYDGTLSPIVDDDPKAFMSPVMRAAVRNVAK
ZmTPPB.1.1/1-367 AWMVKHPSALAMFDQLVAASKGKQIVVFLDYDGTLSPIVDDPDAAYMSDTMRRAVRSVAK
ZmTPPB.1.2/1-384 AWMARHPSALGKFERIVAASEGRRIVMFLDYDGTLSPIVDDPDAAFMSETMRMAVRSVAK
ZmTPPB.1.3/1-370 SWMARHPSALGRFERIVAAEGRKIVMFLDYDGTLSPIVDDPDAAFMSETMRMAVRSVAK
ZmTPPB.1.4/1-357 AWRKHPSALGKFEQIASASKGKVVVMFLDYDGTLSPIVADPDAAYMSDAMRAAVRDVAK
ZmTPPB.1.5/1-356 AWMRKHPSALGKFEQIASASQGGKVVVMFLDYDGTLSPIVADPDAAYMSDVMRAAVRDVAK
ZmTPPB.1.6/1-384 AWTRKHPSALGSFDQIAAAAKGKRIVMFLDYDGTLSPIVADPDMAFMTPEMRAAVRNVAK
ZmTPPB.2.1_ramosa3/1-361 DWMEKHPSALAQFEPLLAAAKGKQIVMFLDYDGTLSPIVEDPDRVMSEEMREAVRRVAE
ZmTPPB.2.2/1-327 DWMEKHPSALAGFESVLAEEGKQVVMFLDYDGTLSPIVKDPDSAVMSEEMRDVAVRVAE
ZmTPPB.2.3/1-357 DWMEKHPSALAAFESVLAEEGKQIVMFLDYDGTLSPIVRDPDSAVMSEEMRDVAVRVAE

MOTIF II

ZmTPPA.1/1-388 LFPTAII SGRSRDKVDFVFKLNELYYAGSHGMDIMGP--VRKTTDSNGVEICIRSTDVHGK
ZmTPPA.3/1-369 YFPTAIVSGRSRKKVFEFVKLTELYYAGSHGMDIVTS-----AAAHATEKC-----K
ZmTPPB.1.1/1-367 HFPTAIVSGRCRDKVFEFVKLAELYYAGSHGMDIKGP---AKGSRHT-KA-----KG
ZmTPPB.1.2/1-384 HFPTAIVSGRCRDKVGFVVKLAELYYAGSHGMDIKGP--AKASSRHE-KA-----KA
ZmTPPB.1.3/1-370 HFPTAIVSGRCRDKVFEFVKLAELYYAGSHGMDIKGPAAAKASSSRH-AA-----KA
ZmTPPB.1.4/1-357 HFPTSIVSGRCRDKVRNFVALSELYYAGSHGMDIKGP-----SS-----NP
ZmTPPB.1.5/1-356 HFPTAIVSGRCRDKVRSFVLDLSELYYAGSHGMDIEGP-----SS-----NP

ZmTPPB.1.6/1-384 RFPTAIV**TGR**CIEKVCFSVGLPELYYAGSHGMDIKGP-----NS-KE-----DK
ZmTPPB.2.1_ramosa3/1-361 HFPTAIV**SGR**CRDKVLNFVKLTELYYAGSHGMDIQGP--AACRQPNHVQQA-----EA
ZmTPPB.2.2/1-327 HFPTAIV**SGR**CRDKVFNFKLAELYAGSHGMDIKGP----TAQSKHT-KA-----KA
ZmTPPB.2.3/1-357 HFPTAIV**SGR**CRDKVFNFKLAELYAGSHGMDIKGP----TAQSKHT-KA-----KA

ZmTPPA.1/1-388 EVNLFQP--ASEFLPMITEVYKLGESVKDIDGARMEDNKFCVSVHYRNVAEDDYKVKVFH
ZmTPPA.3/1-369 EANLFQP--ACEFLPMINEVSKCLVEVTSSIEGARVENNKFCVSVHYRNVAEKDWKVVAG
ZmTPPB.1.1/1-367 GGVLFPQ--ASQFLPMIEQVHDSLVEKTKCIPGAKVENNKFCVSVHFRCVDEKSWITLAD
ZmTPPB.1.2/1-384 KGVLFQPATASEFLPMIEAVHERLVETTRSIPGAKVENNRFCVSVHFRCVDEKMWGELWE
ZmTPPB.1.3/1-370 KGVVFPQ--ASEFLPMIEEVHERLVQTRCIPGAKVENNRFCVSVHFRRVDEKMWGELSE
ZmTPPB.1.4/1-357 ESVLCQP--ASEFLPMDEVYKALVEKTKSTPGAKVEHNKFCVSVHFRCVDEKRWGLAE
ZmTPPB.1.5/1-356 ESVLCQP--ASEFLPVIDEVYKALVEKTKSTPGAKVENNKFCVSVHFRCVDEKRWNALAE
ZmTPPB.1.6/1-384 TVLLLPQ--AREFLPVIDKAYKALVEKTKDTTGARVENNKFCVSVHFRCVDEKSWSSLAE
ZmTPPB.2.1_ramosa3/1-361 AAVHYQA--ASEFLPVIEEVFRTLAKMESIAGARVEHNKYCLSVHFRCVREEEWNVA
ZmTPPB.2.2/1-327 EAVLCQP--ASAFLPVIDEAYRALTARTAPIPGATVENNKFCVSVHFRCVQEEKWRALEE
ZmTPPB.2.3/1-357 GAVLCQP--ARAFLPVIEEVYRALTASTAPIPGATVENNKFCVSVHFRCVQEEKWRALEE

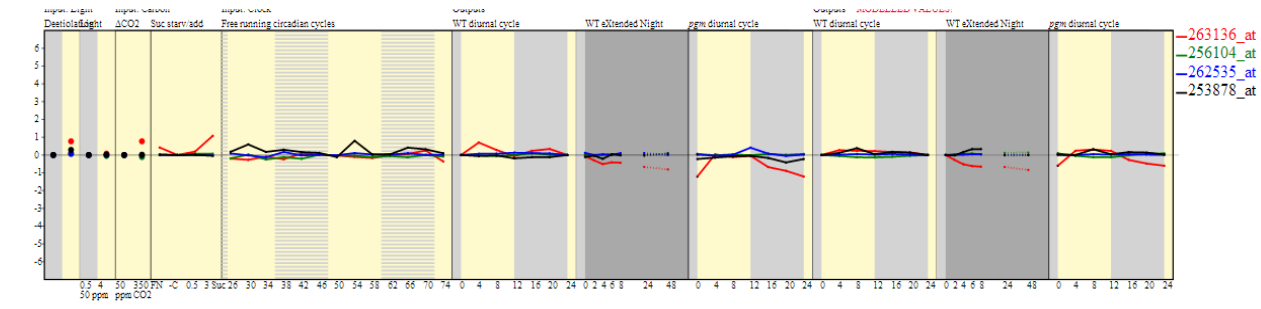
MOTIF III

ZmTPPA.1/1-388 RVTAVLEGYPCRLRLTHGRKVFVVRPVIDW**NK**GKAVEFLLESLGL-SESEDVLPVIYV**GDDR**
ZmTPPA.3/1-369 LVKQVLEAFPRRLKVTNGRMVLEVRPVIDW**DK**GKAVEFLRLSLGL-SDSEDVVPVIYI**GDDR**
ZmTPPB.1.1/1-367 MVKSVLKDYPKLKLTKQGRMVFEVRPTIKW**DK**GKALEFLLESLGY-ADCTDVLVPVIYI**GDDR**
ZmTPPB.1.2/1-384 SVKGVLRREYPRRLTLQGRMVLEVRPTIKW**DK**GKALEFLLESLGF-AGCTNVLPVYI**GDDR**
ZmTPPB.1.3/1-370 SVRGVLRGYPKRLTLTHGRMVLEVRPSIKW**DK**GKALEFLLESLGF-ADCSSVLPVYI**GDDR**
ZmTPPB.1.4/1-357 QVKAVIDKYPKLKLTHGRKVLIRPSIMW**DK**GKALEFLLESLGF-ANRSDVLPVYI**GDDR**
ZmTPPB.1.5/1-356 QVKAVIDKYPKLKLTKQGRKVLIRPSIMW**DK**GKALEFLLESLGF-ASCSDALPVYI**GDDR**
ZmTPPB.1.6/1-384 KVKAVLRDFPELELTEGRKVVVEVRPSIMW**DK**GKAVEFLRLSLGFDDRTNVLPVYI**GDDR**
ZmTPPB.2.1_ramosa3/1-361 EVRSVLRREYPNKLTLTHGRKVLIRPSIKW**DK**GKALEFLKLSLGY-AGRNDVFPVIYI**GDDR**
ZmTPPB.2.2/1-327 QVRSVLRKEYPDLRLTKGRKVLIRPSIKW**DK**GNAIQFLLECLGF-ADSNNVFPVIYI**GDDR**
ZmTPPB.2.3/1-357 QVRSVLRKEYPDLRLTKGRKVLIRPSIKW**DK**GNALQFLLESLGF-AGSNSVFPVIYI**GDDS**

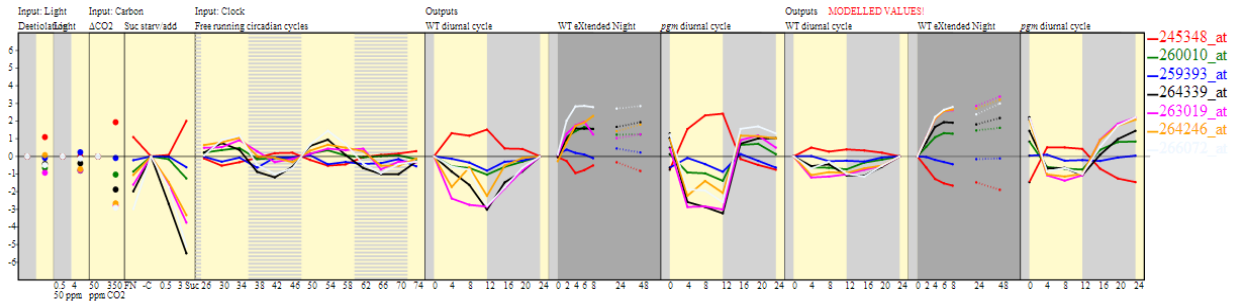
ZmTPPA.1/1-388 **TDEDAFKVLKASN--R**GFILVSSIPKESDAFYSLRDP**AEV**THSTVATTNFCFEYFLGQ
ZmTPPA.3/1-369 **TDEDAFKVLRERS--**CGYGILVSQVPKDTEAFYSLRDP**SEVMG**-----FLNSLVR
ZmTPPB.1.1/1-367 **TDEDAFKVLRKRG--**QGVGILVSKHKPDTCASYS**LQEP**AEVME-----FLLRLVE
ZmTPPB.1.2/1-384 **TDEDAFRALRRRGQDQ**GVGILVSKHPKETSASYS**LQEP**AEVME-----FLLRLVE
ZmTPPB.1.3/1-370 **TDEDAFKVLRRRGQDQ**GVGILVSKHPKETSASYS**LQGP**AEVRA-----
ZmTPPB.1.4/1-357 **TDEDAFKVLRKRG--**QGIGILVSKCPKETNASYS**LQDP**GEVMD-----FLLRLVD
ZmTPPB.1.5/1-356 **TDEDAFKVLRKRG--**QGVGILVSKCPKETNASYS**LQDP**GEVMD-----FLLRLVE
ZmTPPB.1.6/1-384 **TDEDAFKVLRERG--**QGIGILVSKCPKETDATYS**LQDP**TEVME-----FLVRLGQ
ZmTPPB.2.1_ramosa3/1-361 **TDEDAFKVLRNMG--**QGIGILVSKLPKETAASYS**LSDP**AEVKE-----FLRKLAN
ZmTPPB.2.2/1-327 **TDEDAFKVLRGMG--**QGIGILVSKIPKETSASYS**LR**EPS**EVKE**-----FLHMLVR
ZmTPPB.2.3/1-357 **TDEDAFKVLRNLG--**QGIGILVSKIPKETRASYS**LR**EPS**EV**EE-----FLRKLVS

ZmTPPA.1/1-388 KEN-----
ZmTPPA.3/1-369 WKKHPL-----
ZmTPPB.1.1/1-367 WERLSKARPKW-----
ZmTPPB.1.2/1-384 WKRLSRLSRTQ-----

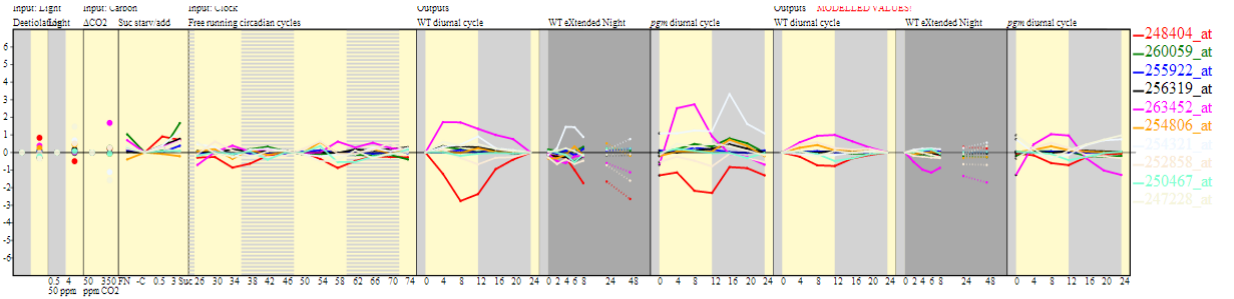
ZmTPPB.1.3/1-370	-----
ZmTPPB.1.4/1-357	WKRKSSAAPMVRPRV---
ZmTPPB.1.5/1-356	WKRKSTTRPPV-----
ZmTPPB.1.6/1-384	WNPLRSPSPAARPRGRKQ
ZmTPPB.2.1_ramosa3/1-361	KKGARQP-----
ZmTPPB.2.2/1-327	SKQR-----
ZmTPPB.2.3/1-357	WSKESRQRD-----



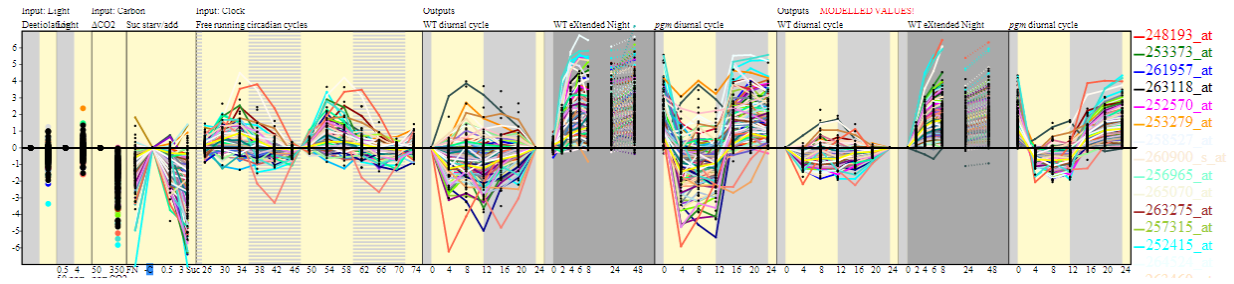
A



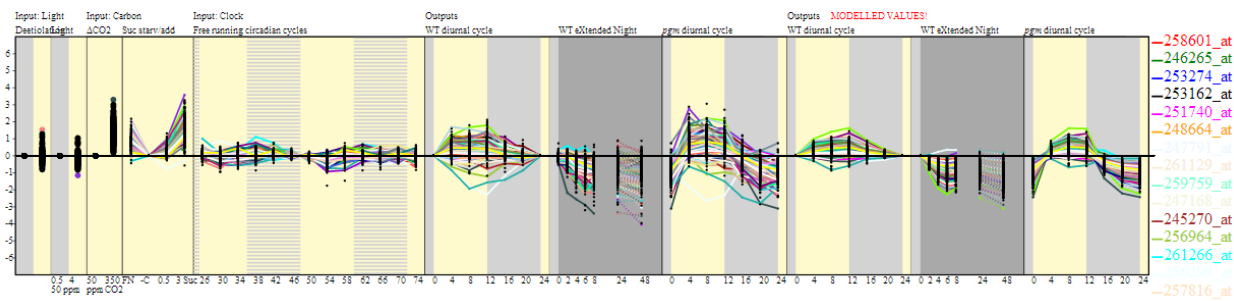
B



C



D



E

Supplemental Figure S3. Expression of Arabidopsis (A) class I TPS genes, (B) class II TPS genes, (C) TPP SNRK1 (inducible) targets, (E) SnRK1 (repressible) targets in mature leaf tissue throughout the diurnal cycle after 4 h extended night.

