

Figure S1. Molecular weight (kDa) vs. isoelectric point plots of TaPIN genes.

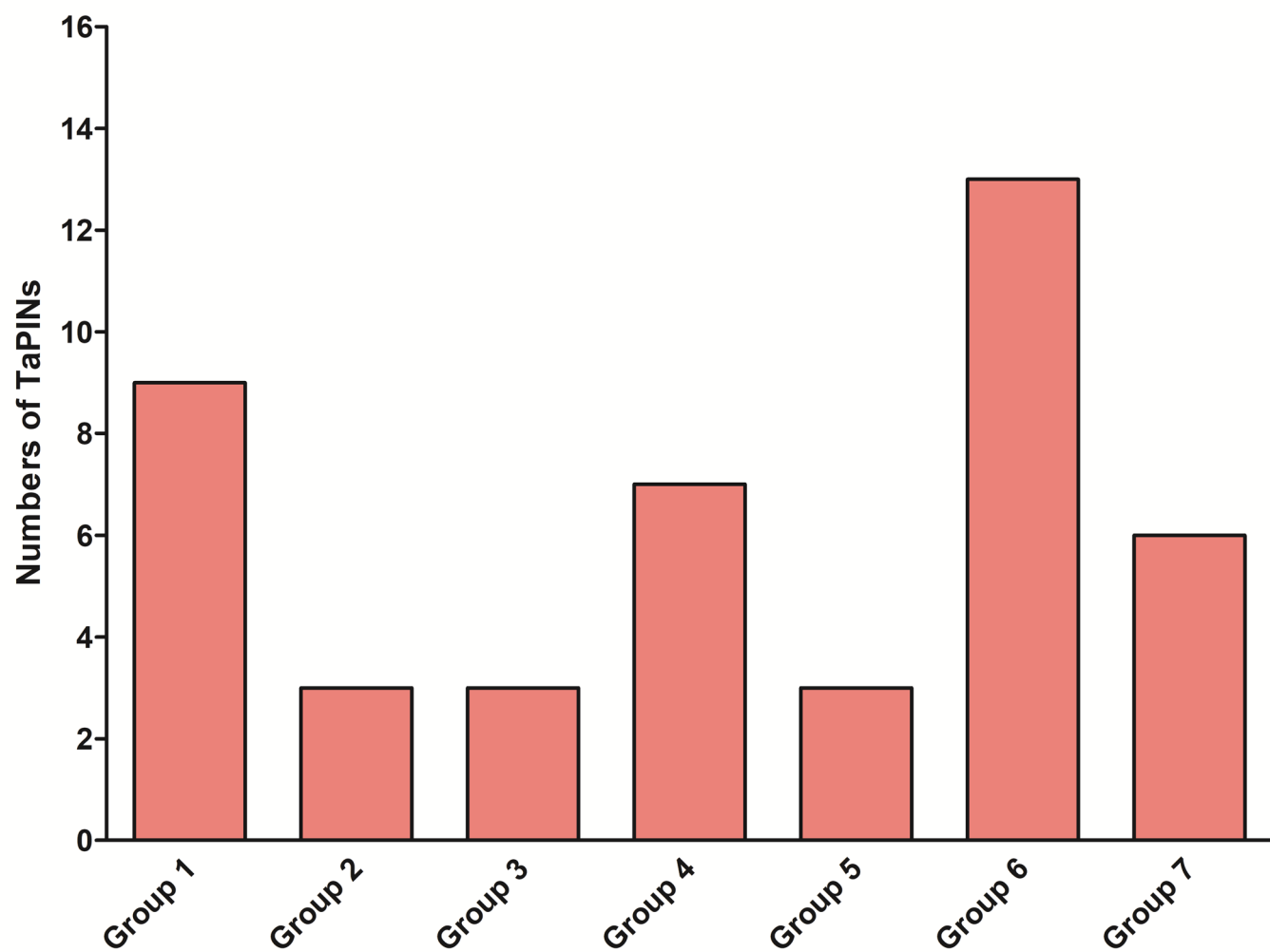


Figure S2. Distribution of TaPINs in different group of phylogenetic tree.

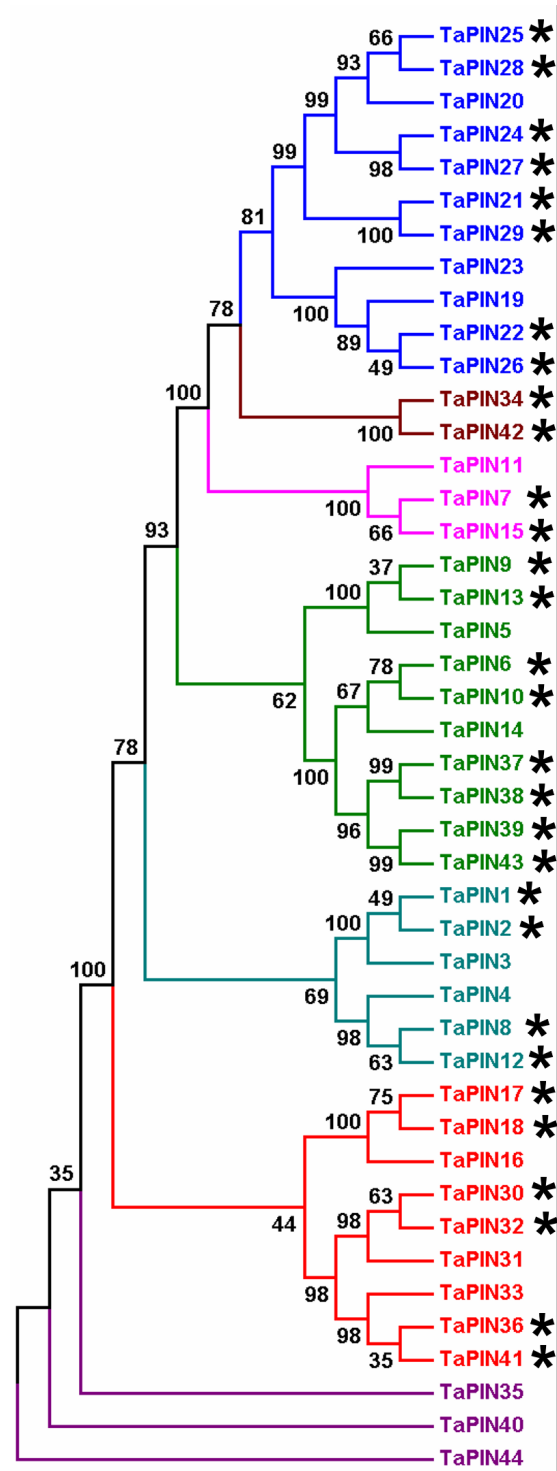


Figure S3: Phylogenetic analysis of TaPIN genes. A phylogenetic tree was constructed using MEGAX with the neighbor-joining (NJ) method and 1000 bootstrap replications. Black asterisk indicate the duplicated genes.

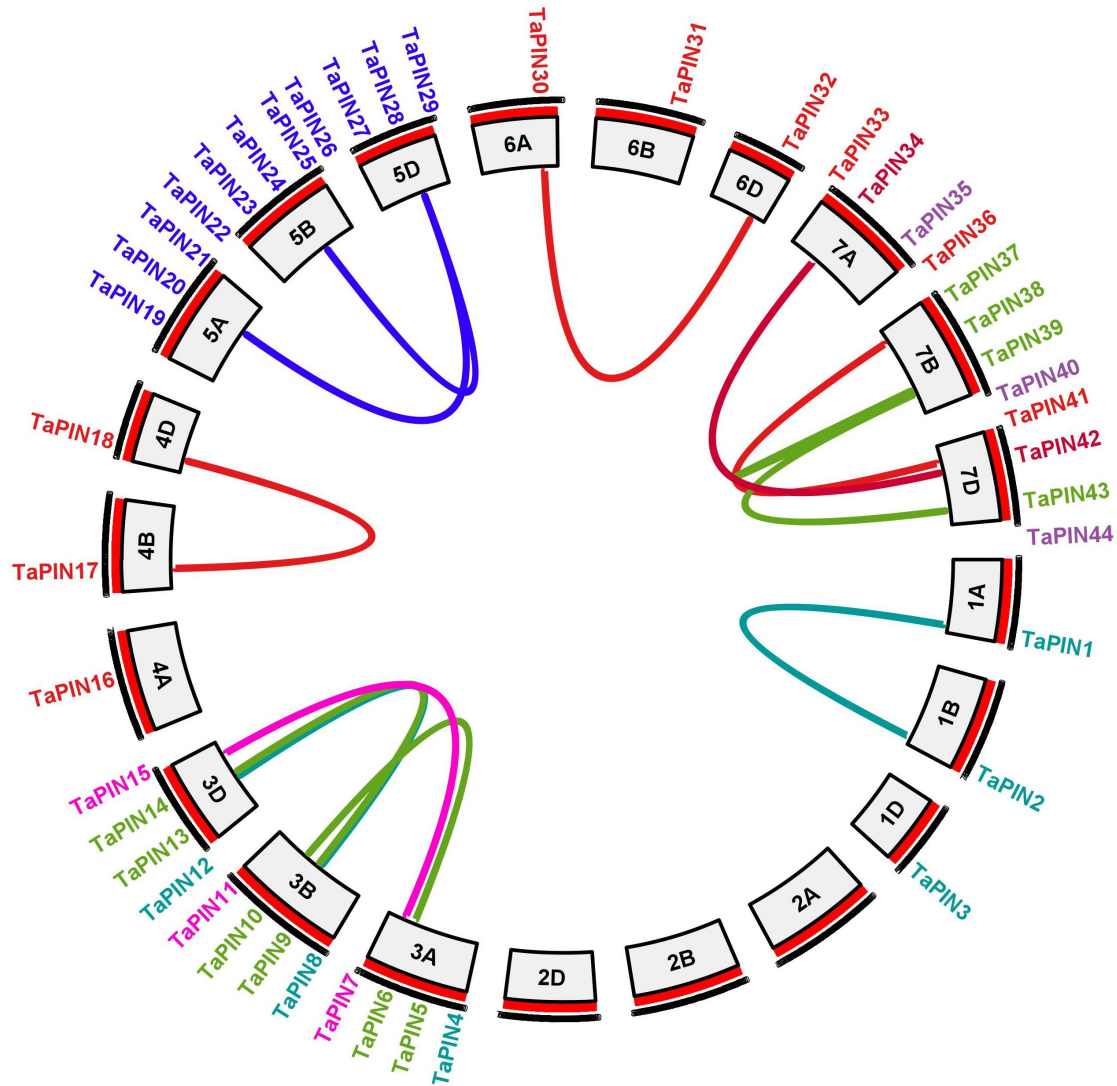


Figure S4: Chromosomal distribution and duplicated PIN gene pairs in wheat. Duplicated PIN gene pairs are connected with lines with distinct colors. The figure was generated using TBtools.

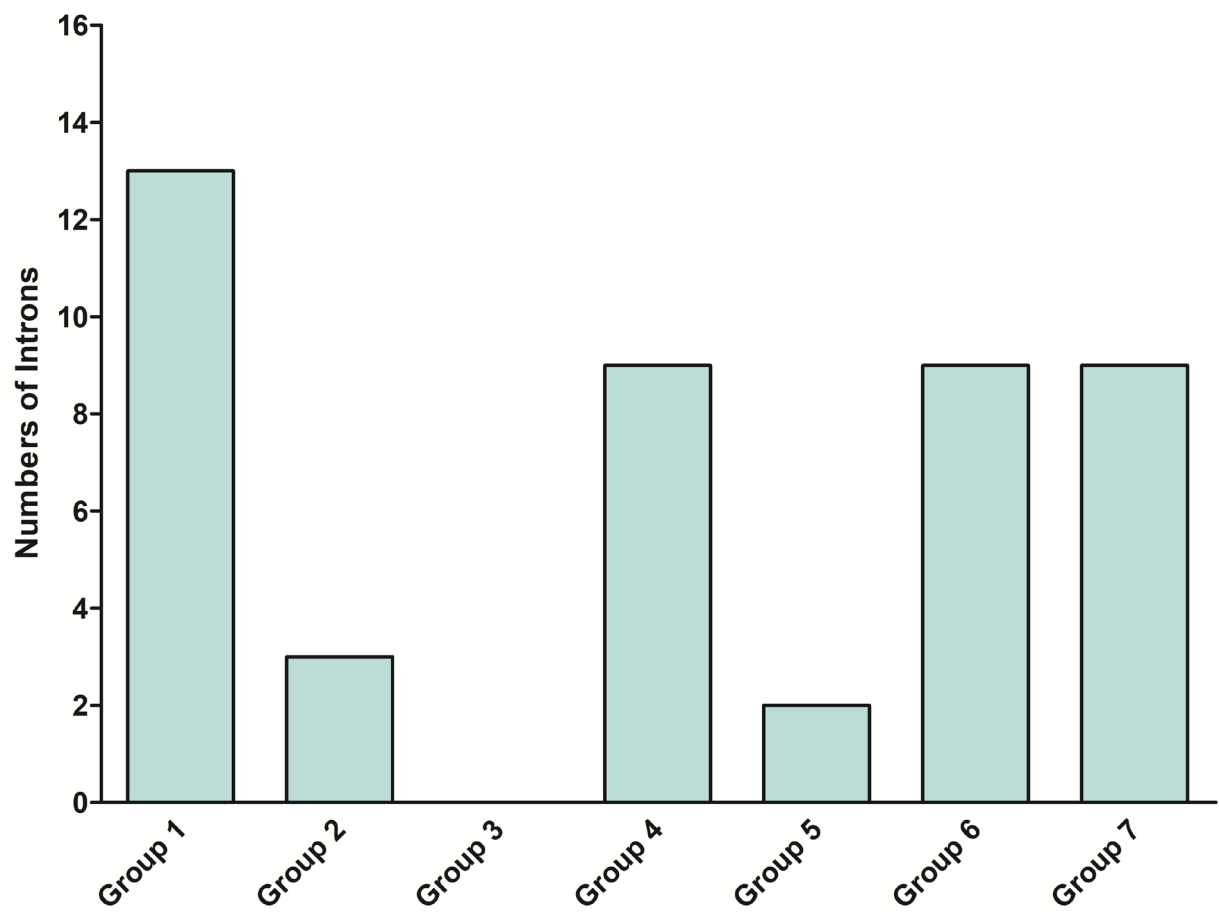
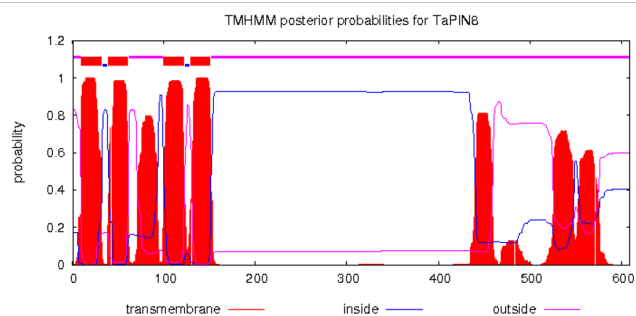
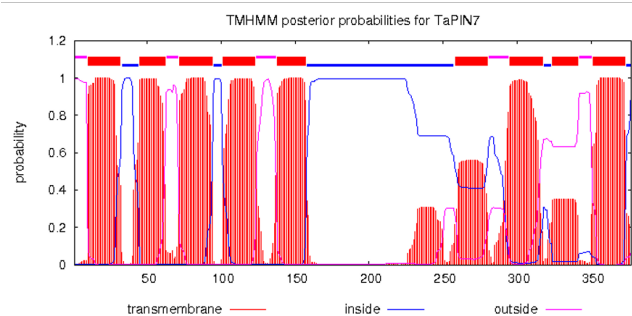
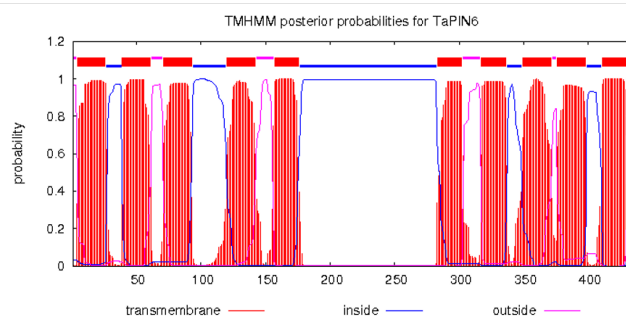
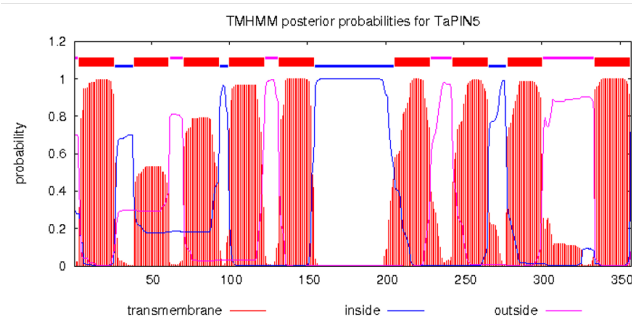
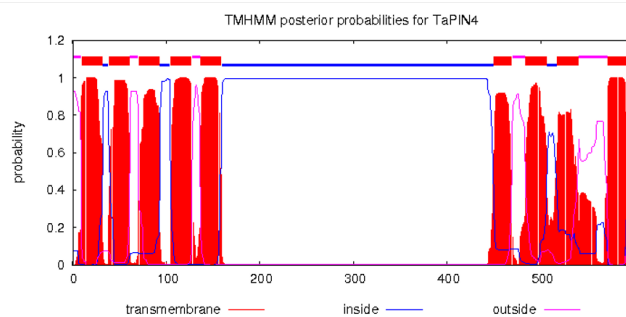
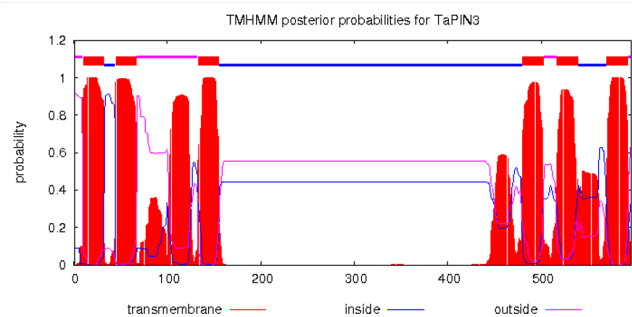
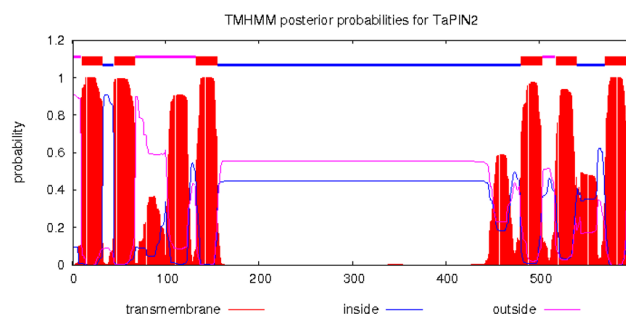
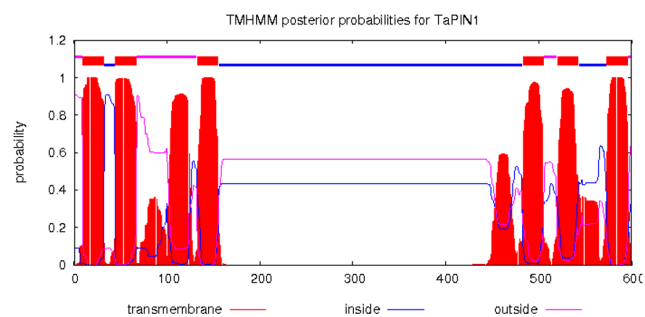
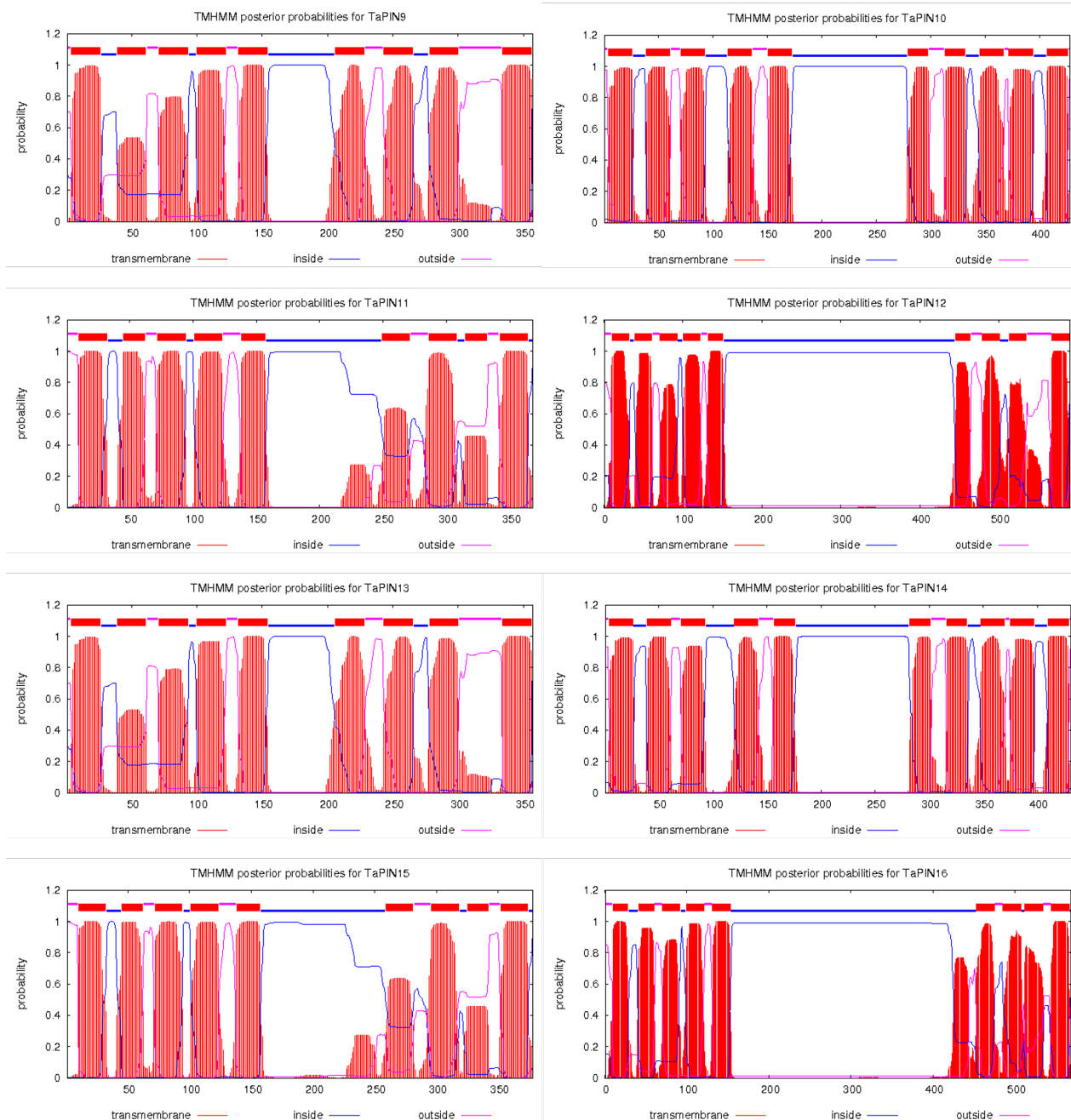
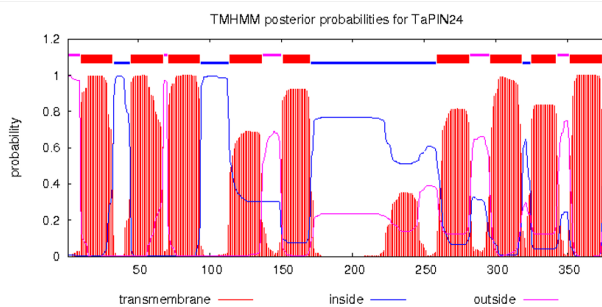
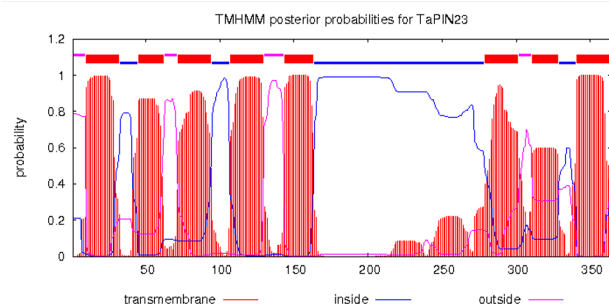
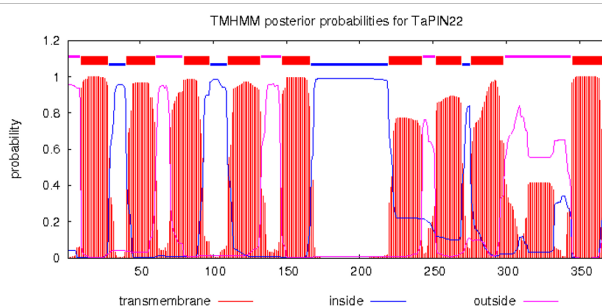
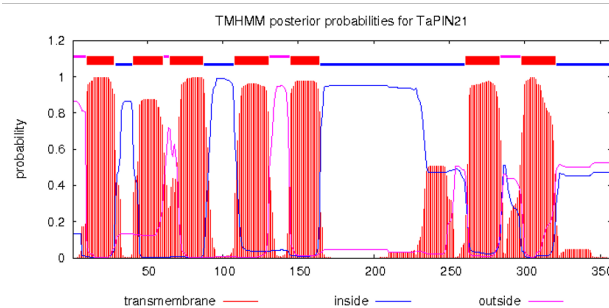
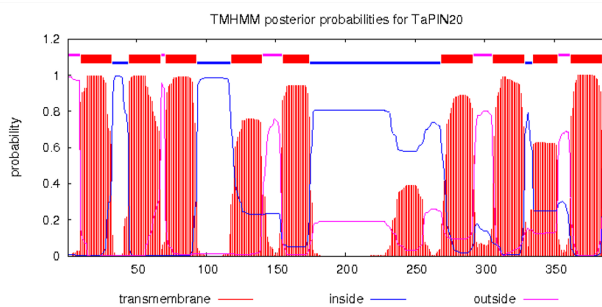
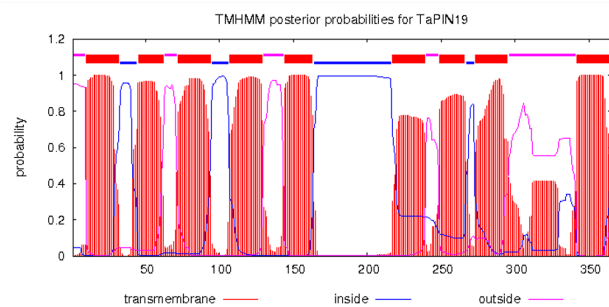
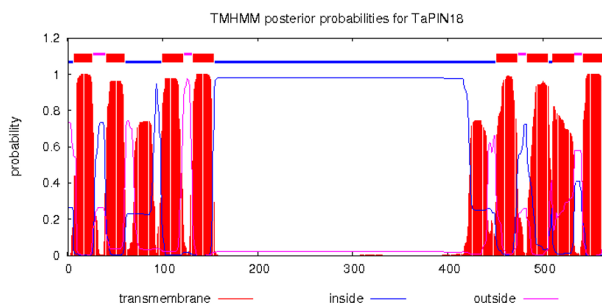
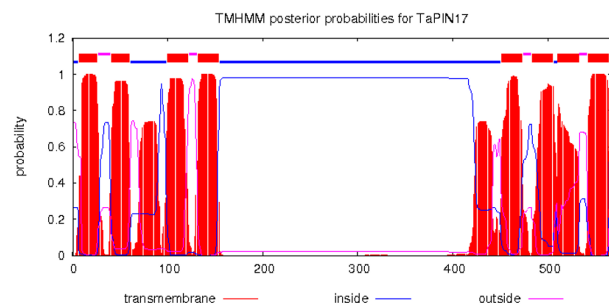
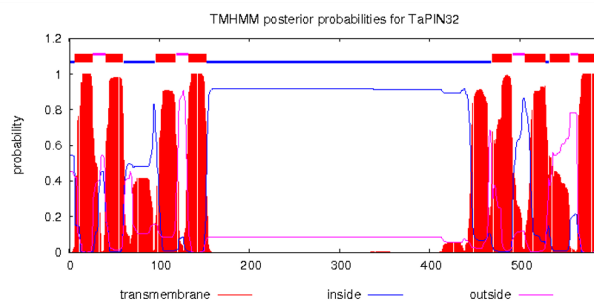
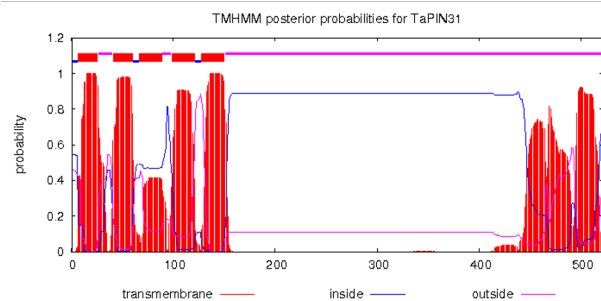
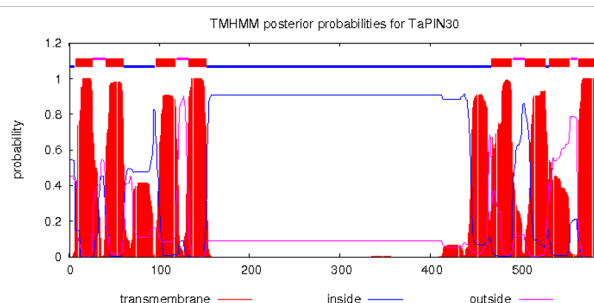
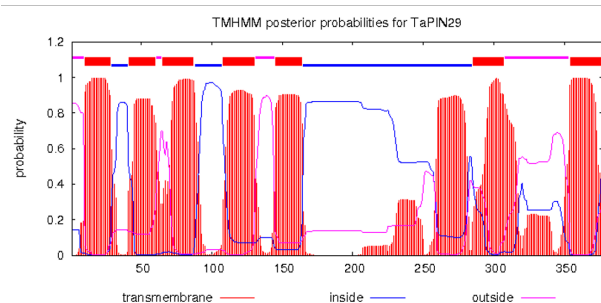
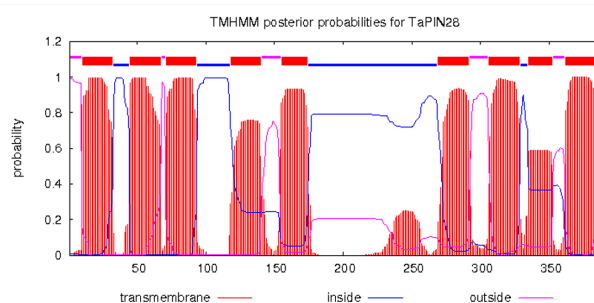
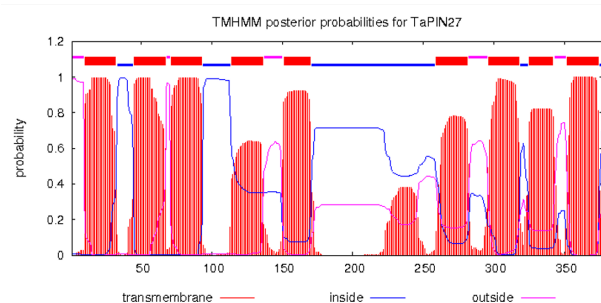
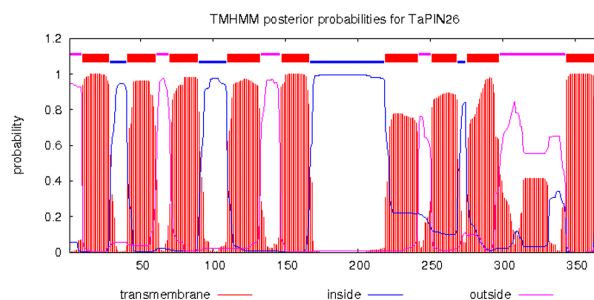
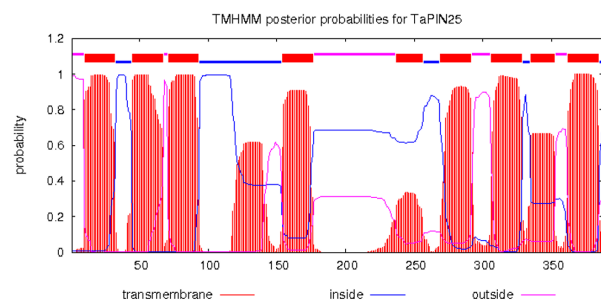


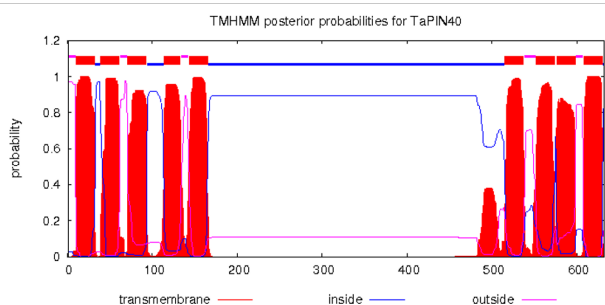
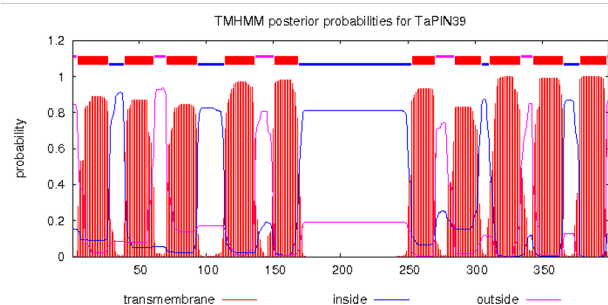
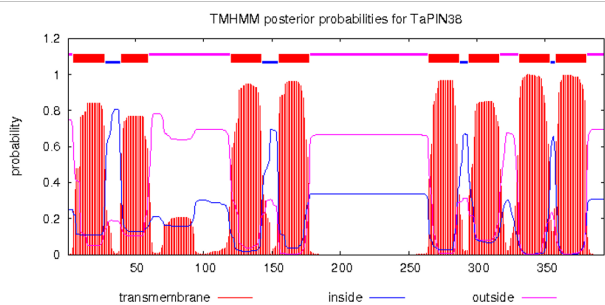
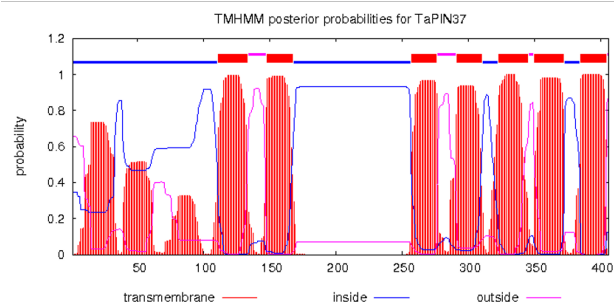
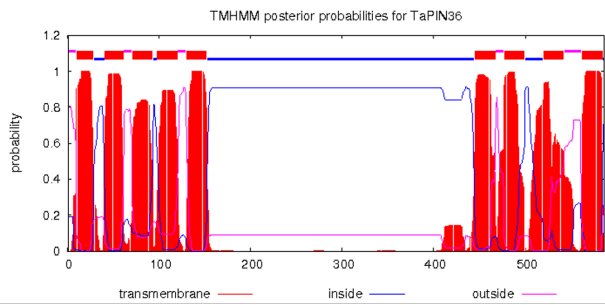
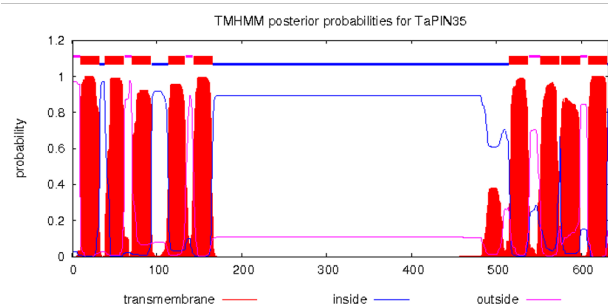
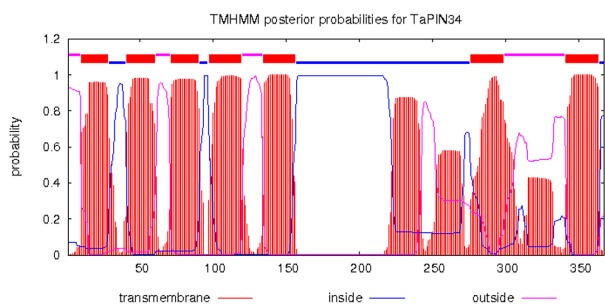
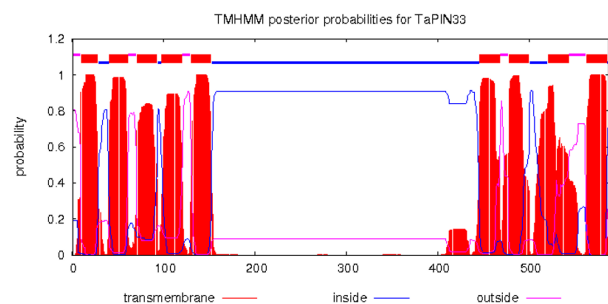
Figure S5. Distribution of number of introns of TaPINs genes in different group of phylogenetic tree.











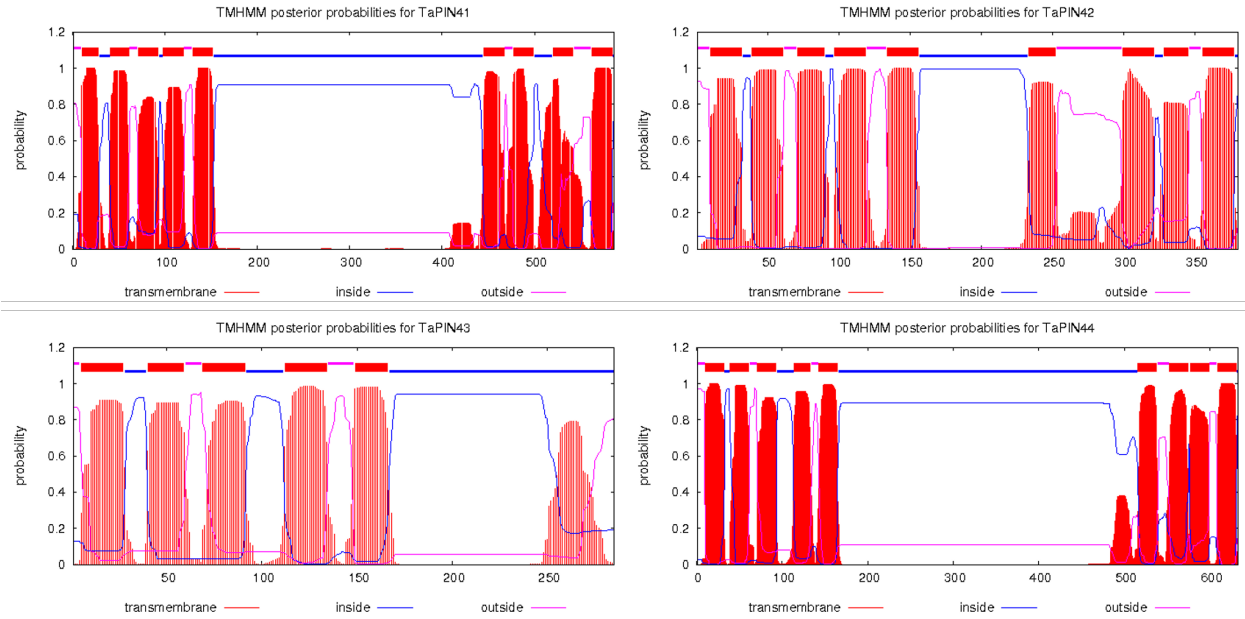


Figure S6. The Predicted Transmembrane Helices of the TaPIN Proteins. The transmembrane domains were identified using TMHMM2: (www.cbs.dtu.dk/services/TMHMM/) and SOSUI software tools (<http://www.cbs.dtu.dk>, <http://harrier.nagahama-i-bio.ac.jp>). The red peaks representing the predicted transmembrane domain and blue color line indicate the central hydrophobic loop of proteins.

TaPIN1 : GSHAEACAEAPDGSMEVVRSSAASLSRRSLNGAAAGMPS-----FARESSVTGVEIFSVSSSNHTPRGSSFTHGDFSATTGGGGGAAAFALPP---PPFP : 281
TaPIN2 : GSHAEACAEAPDGSMEVVRSSAASVSRRSLHNGAAAGMS-----PPRGSNLTGMEIYSVSSSNHTPRGSSFTHGDFSATTGGGG-CAAFALPP---PPFP : 279
TaPIN3 : GSHAEACAEAPDGSMEVVRSSAASVSRRSLHNDAAAGMS-----PPRGSNLTGMEIYSVSSSNHTPRGSSFTHGDFSATTGGGG-AAAFALPP---PPF : 278
TaPIN4 : GGHAEAESEADGRLHVTVRRSSVS-RRSTLL-----VTPRPSNLTGAEIYSLSSCNPTPRGN-FNQADFFAVVVG-----AP : 264
TaPIN5 : -----EEAGTLG-----ATQQTQYQEGQSGVSAARC----- : 198
TaPIN6 : ---NDEAVVAAKRAHEVTVNIEIT-----EVAFASTAQKDLADNTTTVAKETADA----- : 255
TaPIN7 : ---KADAEAPT-----AV-----AVLVVGVEEVGGKPS----- : 214
TaPIN8 : GGRAETSEADGRLHVTVRRSSVS-RRSTLL-----VTPRPSNLTGAEIYSLSSCNPTPRGN-FNQADFFAVVVG-----AP : 258
TaPIN9 : -----EEAGTLG-----ATQQTQYQEGQSGVSAARC----- : 198
TaPIN10 : ---NDEAVVAAKRAHEVTVNIEIT-----EVAASASTAQKDLADNTTTVAKETADA----- : 251
TaPIN11 : ---KADAEAPT-----GAEEVGGKPS----- : 205
TaPIN12 : GGRAETSEADGRLHVTVRRSSVS-RRSTLL-----ATPRPSNLTGAEIYSLSSCNPTPRGN-FNQADFFAVVVG-----AP : 258
TaPIN13 : -----EEAGTLG-----ATQQTQYQEGQSGVSAARC----- : 198
TaPIN14 : ---NDEAVVAAKRAHEVTVNIEIT-----EVAFASTVQKDLADNTTTVAREMTADA----- : 255
TaPIN15 : ---KADAEAGGG-----AV-----AVLVVGGAEEVGGKPS----- : 215
TaPIN16 : GADLQAEAEGEDGFMVTVRKSTS--SRSEAACSHSHSHSH--SQSMQPRVSNLSGVEIYSLQSSNPTPRGS-FNHAEFFNIVG-----GA : 272
TaPIN17 : GADLQAEAEGEDGFMVTVRKSTS--SRSEAACSHSHSHSH--SQSMQPRVSNLSGVEIYSLQSSNPTPRGS-FNHAEFFNIVG-----GA : 272
TaPIN18 : GADLQAEAEGEDGFMVTVRKSTS--SRSEAACSHSHSHSH--SQSMQPRVSNLSGVEIYSLQSSNPTPRGS-FNHAEFFNIVG-----GA : 272
TaPIN19 : -----VEDGG-----AEGRRREF----- : 202
TaPIN20 : ---QAVPGSDDVDR-----FAAAGDGKMAATGWA----- : 224
TaPIN21 : ---EAPGSDVHR-----FAAAGDGKMAATGCA----- : 216
TaPIN22 : -----VEDGG-----AEGRRREF----- : 205
TaPIN23 : -----VEDGG-----AEDSRQR----- : 201
TaPIN24 : ---CAAGSDD-----GDGKTAATGCA----- : 214
TaPIN25 : ---CAAPGSDVDR-----FAAAGDGKMAATGWA----- : 224
TaPIN26 : -----VEDGG-----AEGRRREF----- : 204
TaPIN27 : ---CAAGSDD-----GDGKTAATGCA----- : 214
TaPIN28 : ---CAAPGSDVDR-----FAAAGDGKMAATGWA----- : 224
TaPIN29 : ---EAPGSDVHR-----FAASRDGKMAATGCA----- : 213
TaPIN30 : SNAIETAEKEDGKIHVTVRRSSA--SRSDIYSRRSMGFS----STTPRPSNLTNAEIYSLQSSNPTPRGS-FNHTDFYSMVGRSSNFGAADAYG--IRTGA : 283
TaPIN31 : SNAIETAEKEDGKIHVTVRRSSA--SRSDIYSRRSMGFS----STTPRPSNLTNAEIYSLQSSNPTPRGS-FNHTDFYSMVGRSSNFGAADAYG--IRTGA : 283
TaPIN32 : SNAIETAEKEDGKIHVTVRRSSA--SRSDIYSRRSMGFS----STTPRPSNLTNAEIYSLQSSNPTPRGS-FNHTDFYSMVGRSSNFGAADAYG--VRTGA : 283
TaPIN33 : RDMIETAEKEDGKIHVTVRRSSA--SRSDIYSRRSMGFS----STTPRPSNLTNAEIYSLQSSNPTPRGS-FNHTDFYSMVGRSSNFAAGDAFGEVVRTGA : 285
TaPIN34 : ---TSDDRAQHE-----MDVEAAPPTGGRRIR----- : 205
TaPIN35 : REALHADAEGRDGFVHVIRRSASG--STTGGHGAGRSIYRGASNAMTPRASNLTGVEIYSLQSSNPTPRGS-FNQSDFYSMFNGSKLASPKGQPP--VAGTF : 301
TaPIN36 : RDMIETAEKEDGKIHVTVRRSSA--SRSDIYSRRSMGFS----STTPRPSNLTNAEIYSLQSSNPTPRGS-FNHTDFYSMVGRSSNFAAGDAFGEVVRTGA : 285
TaPIN37 : ---EKRAIAAVERVHVTVNVVEST-----EHTRQQ--GMVAGQQAALTEVCAGE----- : 228
TaPIN38 : ---EKRAIAAVERVHVTVNVVEST-----EHTRQQ--GMVAGQQAALTEVCAGE----- : 236
TaPIN39 : ---EASPE-----NVEST-----EVQAAQQGMAAASQTTIAVVGEAETHGA----- : 221
TaPIN40 : REALHADAEGRDGFVHVIRRSASG--STTGGHGAGRSIYRGASNAMTPRASNLTGVEIYSLQSSNPTPRGS-FNQSDFYSMFNGSKLASPKGQPP--VAGGG : 301
TaPIN41 : RDMIETAEKEDGKIHVTVRRSSA--SRSDIYSRRSMGFS----STTPRPSNLTNAEIYSLQSSNPTPRGS-FNHTDFYSMVGRSSNFAAGDAFGEVVRTGA : 285
TaPIN42 : ---SSDDARFARFEVSHSDEVV-----DLDEVAAPPTGGRRIR----- : 216
TaPIN43 : ---EASPE-----NVGST-----EVAAPQPGMAVASQTTIAVVGEVETHAA----- : 219
TaPIN44 : REALHADAEGRDGFVHVIRRSASG--STTGGHGAGRSIYRGASNAMTPRASNLTGVEIYSLQSSNPTPRGS-FNQSDFYSMFNGSKLASPKGQPP--VAGGG : 301

TaPIN1 : HGAVRASSFGAADLFLSHSSRQHTP-RFSASYDEHAFPRGRSTAAVAFAVEDPKD--NVHMFWDSSGASGASEVSG-LEVLRS--AKESGRRRTFSDATSTNSDS : 379
TaPIN2 : HGAVRASSFGAADLFLSHSSRQHTP-RFSASYDEHAFPRGRSAAAFAVEDPKD--NVHMFWDSSGASGASEVSG-LEVFRSS--TKESGRRRAPSDTTSINSDS : 377
TaPIN3 : HGAVRASSFGAADLFLSHSSRQHTP-RFSASYDEHAFPRGRSAAAFAVEDPKD--NVHMFWDSSGASGASEVSG-LEVFRSS--AKESGRRRAPSDATSTNSDS : 376
TaPIN4 : FARVDGSSFGASEHYSLQSSQGPTPRESNLDEHSAAPK--CAMTDAGAQNHNDAKELHMFVWSSSAFFVSEVVGLEVFVSGG--TGAHLDAAAKEIRMVVFADFP : 366
TaPIN5 : -----AFR----- : 201
TaPIN6 : ----- : -
TaPIN7 : ----- : -
TaPIN8 : FARVGDSSFGASEHYSVQSSQRPTPRESNLEHSAAGPK--CAMTDAGAQNHNDAKELHMFVWSSSAFFVSEVVGLEVFVSGG--TDAHLDAAAKEIRMVVFADFP : 360
TaPIN9 : -----AFR----- : 201
TaPIN10 : ----- : -
TaPIN11 : ----- : -
TaPIN12 : FARVGGSSFGASEHYSLQSSQGPTPRESNLDEHSAAGPK--BATTDAGAQNHNDAKELHMFVWSSSAFFVSEVVGLEFMFTGG--AGAHLDAAAKEIRMVVFADFP : 360
TaPIN13 : -----AFR----- : 201
TaPIN14 : ----- : -
TaPIN15 : ----- : -
TaPIN16 : K---GDEEKGSAGAGNGTGGHSP-QPLP-CALAGKR-----KD---LHMFVWSSSAFFVSEVVGLEFMFTGG--GGADHGDVL-AKGAQAYDEY : 352
TaPIN17 : K---GDEEKGSAGAG--NGTGGHSP-QPLP-CALAGKR-----KD---LHMFVWSSSAFFVSEVVGLEFMFTGG--GGADHGDVL-AKGAQAYDEY : 350
TaPIN18 : K---GDEEKGSAGAG--NGTGGHSP-QPLP-CALAGKR-----KD---LHMFVWSSSAFFVSEVVGLEFMFTGG--GGADHGDVL-AKGAQAYDEY : 350
TaPIN19 : ----- : -
TaPIN20 : ----- : -
TaPIN21 : ----- : -
TaPIN22 : ----- : -
TaPIN23 : ----- : -
TaPIN24 : ----- : -
TaPIN25 : ----- : -
TaPIN26 : ----- : -
TaPIN27 : ----- : -
TaPIN28 : ----- : -
TaPIN29 : ----- : -
TaPIN30 : TPRPSNYEEDAPKPKHFAFGAGHYF-AFNP-AVAAAPKPGPKKFAANGCAKGED--LHMFVWSSSAFFVSDVFGGGAPDYN--AAAASPRK-MDGAKERDDY : 379
TaPIN31 : TPRPSNYEEDAPKPKHFAFGAGHYF-AFNP-AVAAAPKPGPKKFAANGCAKGED--LHMFVWSSSAFFVSDVFGGGAPDYN--AAAASPRKSMDGAKERDDY : 380
TaPIN32 : TPRPSNYEEDAPKPKHFAFGAGHYF-AFNP-AVAAAPKPGPKKFAANGCAKGED--LHMFVWSSSAFFVSDVFGGGAPDYN--AAAASPRK-MDGAKERDDY : 379
TaPIN33 : TPRPSNYEEDAKAGNNNNNNKYGQYP-AFNP-AMAAAPQK-FAKKAANGCAKGEDGDKLHMFVWSSSAFFVSDVFGNGTEAYND--AAAKDVRVA--AASPRKAD : 381
TaPIN34 : ----- : -
TaPIN35 : GARGQGLDEQVANKFKGGEAAAFYP-AFNPMMMEAPR-KKELGGSNSNSNKE--LHMFVWSSSAFFVSEANLNAVNHAASTDFAAAPFAAATPRDGATPRGVS : 402
TaPIN36 : TPRPSNYEEDAKAGNNNNNNKYGQYP-AFNP-AMAAAPQK-FAKKAANGCAKGEDGDKLHMFVWSSSAFFVSDVFGNGTEAYND--AAAKDVRVA--AASPRKAD : 380
TaPIN37 : ----- : -
TaPIN38 : ----- : -
TaPIN39 : ----- : -
TaPIN40 : GARGQGLDEQVANKFKGGEAAAFYP-AFNPMMMEAPR-KKELGGSNSNSNKE--LHMFVWSSSAFFVSEANLNAVNHAASTDFAAAPFAAATPRDGATPRGVS : 402
TaPIN41 : TPRPSNYEEDAKAGNNNNNNKYGQYP-AFNP-AMAAAPQK-FAKKAANGCAKGEDGDKLHMFVWSSSAFFVSDVFGNGTEAYND--AAAKDVRVA--AASPRKAD : 380
TaPIN42 : ----- : -
TaPIN43 : ----- : -
TaPIN44 : GARGQGLDEQVANKFKGGEAAAFYP-AFNPMMMEAPRKKELGGSNSNSNKE--LHMFVWSSSAFFVSEANLNAVNHAASTDFAAAPFAAATPRDGATPRGVS : 403

TaPIN1 : SR---INRTGAAGVERVISEAAQESLERLEAGTEATEKEQEQDE-----TKKVGDD--EVGKPFASVLRLLITVWRRLRNFNWASVGLWSLIDEPY : 471
TaPIN2 : SR---SNRPGATGGERVVKSEAAATQESLERLEAGTEAAEKEQEQDE-----TKKDDGG--EVGKPFASVLRLLITVWRRLRNFNWASVGLWSLIDEPY : 469
TaPIN3 : SR---SNRPGATGGERVVKSGAAQESLERLEAGTEATGKEQEQDE-----TKKDDGG--EVGKPFASVLRLLITVWRRLRNFNWASVGLWSLIDEPY : 468
TaPIN4 : QNGSCKENGSGYTAARGGCRKRAVEHDG-DAVQAGPDRLTFRINSSP-----GDEDGAETGRARQHCMPFASVLRLLITVWRRLRNFNWASVGLWSLIDEPY : 466
TaPIN5 : -----FUIVGMKRLNENITVCIIGLWAMTSSPC : 232
TaPIN6 : -----EAEQGSPPFAKSTAPSVTHIALAGKRVRIENWASVGLWSLIDEPY : 305
TaPIN7 : -----WR-LVKTAAEKIARNENWASVEVGIWACVANEL : 248
TaPIN8 : QNGSCKDNGGYTAAARGGGKAVEDDG-DAVQAGPDRPTAKINSSP-----GDEDGAETG---KHQMPFASVLRLLITVWRRLRNFNWASVGLWSLIDEPY : 457
TaPIN9 : -----FUIVGMKRLNENITVCIIGLWAMTSSPC : 232
TaPIN10 : -----EAEKASPPFAKSTAPSVRHHGLAGKRVRIENWASVGLWSLIDEPY : 301
TaPIN11 : -----WR-LVKTAAEKIARNENWASVEVGIWACVANEL : 239
TaPIN12 : QNGSCKENGSGYTAARGGGGKAVEDDGDAAVQAGPDRILAAKINSSP-----GDEDGAESGRARQHCMPFASVLRLLITVWRRLRNFNWASVGLWSLIDEPY : 461
TaPIN13 : -----FUIVGMKRLNENITVCIIGLWAMTSSPC : 232
TaPIN14 : -----EAS-PPFAKSTAPSVTHIALAGKRVRIENWASVGLWSLIDEPY : 304
TaPIN15 : -----WR-LVKTAAEKIARNENWASVEVGIWACVANEL : 249
TaPIN16 : G---RGGGDDFSFFNKNGGVANVDGPTIAKLGSNSTAQLHPKDD-----GEER---AAAMPFASVLRLLITVWRRLRNFNWASVGLWSLIDEPY : 441
TaPIN17 : G---RGGGDDFSFFNKNGGVANVDGPTIAKLGSNSTAQLHPKDD-----GEER---AAAMPFASVLRLLITVWRRLRNFNWASVGLWSLIDEPY : 439
TaPIN18 : G---RGGGDDFSFFNKNGGVANVDGPTIAKLGSNSTAQLHPKDD-----GEER---AAAMPFASVLRLLITVWRRLRNFNWASVGLWSLIDEPY : 439
TaPIN19 : -----WF-LVRAWIRVARNENWASVGLVWACVINE : 236
TaPIN20 : -----FWAPDRITGLRVGENVVASLGVWASVANE : 259
TaPIN21 : -----FWAPDRITGLRVGENVVASLGVWASVANE : 251
TaPIN22 : -----WF-LVRAWIRVARNENWASVGLVWACVINE : 239
TaPIN23 : -----WF-LVRAWIRVARNENWASVGLVWACVINE : 235
TaPIN24 : -----FWAPDRITGLRVGENVVASLGVWASVANE : 249
TaPIN25 : -----FWAPDRITGLRVGENVVASLGVWASVANE : 259
TaPIN26 : -----WF-LVRAWIRVARNENWASVGLVWACVINE : 238
TaPIN27 : -----FWAPDRITGLRVGENVVASLGVWASVANE : 249
TaPIN28 : -----FWAPDRITGLRVGENVVASLGVWASVANE : 259
TaPIN29 : -----FWAPDRITGLRVGENVVASLGVWASVANE : 248
TaPIN30 : N---VER-DDFSFGNRGALDRDAEA-----GDEKAMTADFNN-----AMGAG---PTAMPPTSVLRLLITVWRRLRNFNWASVGLWSLIDEPY : 461
TaPIN31 : N---VER-DDFSFGNRGALDRDTEA-----GDEKAMTADFNN-----AMGAG---PTAMPPTSVLRLLITVWRRLRNFNWASVGLWSLIDEPY : 462
TaPIN32 : N---VER-DDFSFGNRGALERDAEA-----GDEKAMTADFNN-----GMGAG---PTAMPPTSVLRLLITVWRRLRNFNWASVGLWSLIDEPY : 462
TaPIN33 : G---VER-DEFSFGNK---ERDAEA-----GDEKAA-AEQGTA-----GLVAA---PTVMPPTSVLRLLITVWRRLRNFNWASVGLWSLIDEPY : 460
TaPIN34 : -----WF-LVRAWIRVARNENWASVGLVWACVINE : 239
TaPIN35 : GSVTFVLKKDASSGAVEVEIEDGMMKSEATGLGAKFFVSGSPYVAPRKKGADVPGLEEA---AHMPPFASVLRLLITVWRRLRNFNWASVGLWSLIDEPY : 505
TaPIN36 : G---VER-DEFSFGNK---ERDAEA-----GDEKAA-AEQGTA-----GLVAA---PTVMPPTSVLRLLITVWRRLRNFNWASVGLWSLIDEPY : 459
TaPIN37 : -----DDESAEAEEDSLFASPSMRHIAFTGKRVRIENWASVGLWSLIDEPY : 279
TaPIN38 : -----DDEGAEAEEDSLFASPSMRHIAFTGKRVRIENWASVGLWSLIDEPY : 287
TaPIN39 : -----DAEVAEAEEDVALPPFMSHIAFTGKRVRIENWASVGLWSLIDEPY : 272
TaPIN40 : GSVTFVLKKDASSGAVEVEIEDGMMKSEATGLGAKFFVSGSPYVAPRKKGADVPGLEEA---AHMPPFASVLRLLITVWRRLRNFNWASVGLWSLIDEPY : 505
TaPIN41 : G---VER-DEFSFGNK---ERDAEA-----GDEKAA-AEQGTA-----GLVAA---PTVMPPTSVLRLLITVWRRLRNFNWASVGLWSLIDEPY : 459
TaPIN42 : -----NL-NASTGMKIARNENWASVGLVWACVINE : 250
TaPIN43 : -----DAEVAEAEEDVALFAPPSMSHIAFTGKRVRIENWASVGLWSLIDEPY : 269
TaPIN44 : GIVTFVLKKDASSGAVEVEIEDGMMKSEATGLGAKFFVSGSPYVAPRKKGADVPGLEEA---AHMPPFASVLRLLITVWRRLRNFNWASVGLWSLIDEPY : 506

TaPIN1 : HVTMEATVAKSISILSDAGLGV MFSLG-----LEMAQCR TACGKSNASTV VREIAGVIA : 532
TaPIN2 : HVTMEATVAKSISILSDAGLGV MFSLG-----LEMAQCR TACGKSNASTV VREIAGVIA : 530
TaPIN3 : HVTMEATVAKSISILSDAGLGV MFSLG-----LEMAQCR TACGKSNASTV VREIAGVIA : 529
TaPIN4 : HVSMTVVEKISISILSDAGLGV MFSLG-----LEMAQCR TACGKSNASTV VREIAGVIA : 527
TaPIN5 : QCLPLVNSISIRLSDAGLGV MFSLG-----LEMAQCR TACGKSNASTV VREIAGVIA : 293
TaPIN6 : GUKMERLDDSLFTQTITVGTSMFSG-----LEMAQCR TACGKSNASTV VREIAGVIA : 366
TaPIN7 : HVELSVENSVLIMSRTGLGCMFSGM-----LEMAQCR TACGKSNASTV VREIAGVIA : 309
TaPIN8 : HVSMTVVEKISISILSDAGLGV MFSLG-----LEMAQCR TACGKSNASTV VREIAGVIA : 563
TaPIN9 : QCLPLVNSISIRLSDAGLGV MFSLG-----LEMAQCR TACGKSNASTV VREIAGVIA : 293
TaPIN10 : GUKMERLDDSLFTQTITVGTSMFSG-----LEMAQCR TACGKSNASTV VREIAGVIA : 362
TaPIN11 : HVELSVENSVLIMSRTGLGCMFSGM-----LEMAQCR TACGKSNASTV VREIAGVIA : 300
TaPIN12 : HVSMTVVEKISISILSDAGLGV MFSLG-----LEMAQCR TACGKSNASTV VREIAGVIA : 522
TaPIN13 : QCLPLVNSISIRLSDAGLGV MFSLG-----LEMAQCR TACGKSNASTV VREIAGVIA : 293
TaPIN14 : GUKMERLDDSLFTQTITVGTSMFSG-----LEMAQCR TACGKSNASTV VREIAGVIA : 365
TaPIN15 : HVELSVENSVLIMSRTGLGCMFSGM-----LEMAQCR TACGKSNASTV VREIAGVIA : 310
TaPIN16 : GUEMPEATVAKSISILSDAGLGV MFSLG-----LEMAQCR TACGKSNASTV VREIAGVIA : 502
TaPIN17 : GUEMPEATVAKSISILSDAGLGV MFSLG-----LEMAQCR TACGKSNASTV VREIAGVIA : 500
TaPIN18 : GUEMPEATVAKSISILSDAGLGV MFSLG-----LEMAQCR TACGKSNASTV VREIAGVIA : 500
TaPIN19 : HVTESLDEGSVILMSRTGLGCMFSGM-----LEMAQCR TACGKSNASTV VREIAGVIA : 297
TaPIN20 : HPEMPEATVAKSISILSDAGLGV MFSLG-----LEMAQCR TACGKSNASTV VREIAGVIA : 320
TaPIN21 : HPEMPEATVAKSISILSDAGLGV MFSLG-----LEMAQCR TACGKSNASTV VREIAGVIA : 312
TaPIN22 : HVTESLDEGSVILMSRTGLGCMFSGM-----LEMAQCR TACGKSNASTV VREIAGVIA : 300
TaPIN23 : HPEMPEATVAKSISILSDAGLGV MFSLG-----LEMAQCR TACGKSNASTV VREIAGVIA : 296
TaPIN24 : HPEMPEATVAKSISILSDAGLGV MFSLG-----LEMAQCR TACGKSNASTV VREIAGVIA : 310
TaPIN25 : HPEMPEATVAKSISILSDAGLGV MFSLG-----LEMAQCR TACGKSNASTV VREIAGVIA : 320
TaPIN26 : HVTESLDEGSVILMSRTGLGCMFSGM-----LEMAQCR TACGKSNASTV VREIAGVIA : 299
TaPIN27 : HPEMPEATVAKSISILSDAGLGV MFSLG-----LEMAQCR TACGKSNASTV VREIAGVIA : 310
TaPIN28 : HPEMPEATVAKSISILSDAGLGV MFSLG-----LEMAQCR TACGKSNASTV VREIAGVIA : 320
TaPIN29 : HPEMPEATVAKSISILSDAGLGV MFSLG-----LEMAQCR TACGKSNASTV VREIAGVIA : 309
TaPIN30 : NPTMEATVAKSISILSDAGLGV MFSLG-----LEMAQCR TACGKSNASTV VREIAGVIA : 522
TaPIN31 : NPTMEATVAKSISILSDAGLGV MFSLG-----LEMAQCR TACGKSNASTV VREIAGVIA : 513
TaPIN32 : NPTMEATVAKSISILSDAGLGV MFSLG-----LEMAQCR TACGKSNASTV VREIAGVIA : 523
TaPIN33 : NPTMEATVAKSISILSDAGLGV MFSLG-----LEMAQCR TACGKSNASTV VREIAGVIA : 521
TaPIN34 : RUMPEATVAKSISILSDAGLGV MFSLG-----LEMAQCR TACGKSNASTV VREIAGVIA : 300
TaPIN35 : NQUMETVAKSISILSDAGLGV MFSLG-----LEMAQCR TACGKSNASTV VREIAGVIA : 566
TaPIN36 : NPTMEATVAKSISILSDAGLGV MFSLG-----LEMAQCR TACGKSNASTV VREIAGVIA : 520
TaPIN37 : GUKMERLDDSLFTQTITVGTSMFSG-----LEMAQCR TACGKSNASTV VREIAGVIA : 340
TaPIN38 : GUKMERLDDSLFTQTITVGTSMFSG-----LEMAQCR TACGKSNASTV VREIAGVIA : 348
TaPIN39 : RUMPEATVAKSISILSDAGLGV MFSLG-----LEMAQCR TACGKSNASTV VREIAGVIA : 333
TaPIN40 : NQUMETVAKSISILSDAGLGV MFSLG-----LEMAQCR TACGKSNASTV VREIAGVIA : 566
TaPIN41 : NPTMEATVAKSISILSDAGLGV MFSLG-----LEMAQCR TACGKSNASTV VREIAGVIA : 520
TaPIN42 : RUMPEATVAKSISILSDAGLGV MFSLG-----LEMAQCR TACGKSNASTV VREIAGVIA : 311
TaPIN43 : ---QVE-----SFCSS----- : 277
TaPIN44 : NQUMETVAKSISILSDAGLGV MFSLG-----LEMAQCR TACGKSNASTV VREIAGVIA : 567


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TaPIN1 : VSS--AAVGLRCTLRLIAVVQATLPQGI VPFVFAKEYNLHAAILCTGVIFGMLIALPITVLLYYIILGL- : 599
TaPIN2 : VSS--AAVGLRCTLRLIAVVQAALPQGI VPFVFAKEYNLHAAILCTGVIFGMLIAVPTVLLYYIILGL- : 597
TaPIN3 : VSS--AAVGLRCTLRLIAVVQAALPQGI VPFVFAKEYNLHAAILCTGVIFGMLIALPITVLLYYIILGL- : 596
TaPIN4 : AAS--AAVGLRCTLRLKVAIVQAALPQGI VPFVFAKEYNVPEILSTAVIFGMLIALPITITAYYALLGLVH : 595
TaPIN5 : ISS--YAVGMRCTLLKVAIVQAALPQGI VPFVFAKEYNVPEILSTAVIFGMLIAVEAATAYYFVIT---- : 357
TaPIN6 : IAS--IAIGMHCTLLHIAVVQAALPLAVTSFVFAKEYNVPEILSTAVIFGMLIAVEAATAYYFVIT---- : 432
TaPIN7 : IGS--IAVGLRGDVLRLVAIIQAALPQSITSFIFFAKEYGLHADVLSAVIFGMLVSLPILLGLYIVLELIR : 377
TaPIN8 : AAS--AAVGLRCTLRLKVAIVQVTT-----HACQLKKEHACIHVKRCF-----FECMFS----- : 609
TaPIN9 : VSS--YAVGMRCTLLKVAIVQAALPQGI VPFVFAKEYNVPEILSTAVIFGMLIAVEAATAYYFVIT---- : 357
TaPIN10 : IAS--IAIGMHCTLLHIAVVQAALPLAVTSFVFAKEYNVPEILSTAVIFGMLIAVEAATAYYFVIT---- : 428
TaPIN11 : IGS--IAVGLRGDVLRLVAIIQAALPQSITSFIFFAKEYGLHADVLSAVIFGMLVSLPILLGLYIVLELIR : 368
TaPIN12 : AAS--AAVGLRCTLRLKVAIVQAALPQGI VPFVFAKEYNVPEILSTAVIFGMLIALPITITAYYALLGLVH : 590
TaPIN13 : ISS--YAVGMRCTLLKVAIVQAALPQGI VPFVFAKEYNVPEILSTAVIFGMLIAVEAATAYYFVIT---- : 357
TaPIN14 : IAS--IAIGMHCTLLHIAVVQAALPLAVTSFVFAKEYNVPEILSTAVIFGMLIAVEAATAYYFVIT---- : 431
TaPIN15 : IGS--IAVGLRGDVLRLVAIIQAALPQSITSFIFFAKEYGLHADVLSAVIFGMLVSLPILLGLYIVLELIR : 378
TaPIN16 : AAS--IAVGLRGVLLHIAIVQAALPQGI VPFVFAKEYNVPEILSTAVIFGMLIALPITITVYYIILGL-- : 568
TaPIN17 : AAS--IAVGLRGVLLHIAIVQAALPQGI VPFVFAKEYNVPEILSTAVIFGMLIALPITITVYYIILGL-- : 566
TaPIN18 : AAS--IAVGLRGVLLHIAIVQAALPQGI VPFVFAKEYNVPEILSTAVIFGMLIALPITITVYYIILGL-- : 566
TaPIN19 : AGA--VALGLRGDVLRLIAIIQAALPQSITTFVFAKEYGLHADVLSAVIFGTIASLFLVLTYYIIVLGFVG : 365
TaPIN20 : IGA--LILGLRGDLLRVAILQAALPQSVGAFIFATEYDLHADVLSAVIFGTIASLFLVLTYYIIVLGLM- : 387
TaPIN21 : AGA--LILGLRGDLLRVITLQAALPQSVATFVFAKEYDLHADVLSAVIFGTIASLFLVLTYYIIVLGLM- : 357
TaPIN22 : AGA--VALGLRGDVLRLIAIIQAALPQSITTFVFAKEYGLHADVLSAVIFGTIASLFLVLTYYIIVLGFVG : 368
TaPIN23 : AGA--VALGLHGDVLRVITLQAALPQATTFVFAKEYGLHADVLSAVIFGTIASLFLVLTYYIIVLGFIE : 364
TaPIN24 : VGA--LILGLRGDLLRVAILQAALPQSVGAFIFATEYDLHADVLSAVIFGTIASLFLVLTYYIIVLGL- : 377
TaPIN25 : IGA--LILGLRGDLLRVAILQAALPQSIGTFIFATEYDLHADVLSAVIFGTIASLFLVLTYYIIVLGLM- : 387
TaPIN26 : AGA--VALGLRGDVLRLIAIIQAALPQSITTFVFAKEYGLHADVLSAVIFGTIASLFLVLTYYIIVLGFVG : 367
TaPIN27 : VGA--LILGLRGDLLRVAILQAALPQSVGAFIFATEYDLHADVLSAVIFGTIASLFLVLTYYIIVLGL- : 377
TaPIN28 : IGA--LILGLRGDLLRVAILQAALPQSIGTFIFATEYDLHADVLSAVIFGTIASLFLVLTYYIIVLGLM- : 387
TaPIN29 : AGA--LILGLRGDLLRVITLQAALPQSVATFVFAKEYDLHADVLSAVIFGTIASLFLVLTYYIIVLGLVI : 377
TaPIN30 : AAS--FAVGLRCTLRLHVAIVQAALPQGI VPFVFAKEYSVPEILSTAVIFGMLIALPITITVYYIILGL- : 588
TaPIN31 : NS-----GLGSSC----- : 521
TaPIN32 : AAS--FAVGLRCTLRLHVAIVQAALPQGI VPFVFAKEYSVPEILSTAVIFGMLIALPITITVYYIILGL- : 589
TaPIN33 : AAS--IAVGLRCTLRLHIAIVQAALPQGI VPFVFAKEYSVPEILSTAVIFGMLIALPITITVYYIILGL- : 587
TaPIN34 : AGA--AAVGLRGDVLRLFAIIQAALPQSIAFVFAKEYGLHADVLSAVIFGTIASLFLVLTYYIIVLGLIV : 367
TaPIN35 : ATS--IAVGLRGVLLHVAIVQAALPQGI VPFVFAKEYNCPQILSTAVIFGMLIALPITITVYYIILGL- : 632
TaPIN36 : AAS--IAVGLRCTLRLHIAIVQAALPQGI VPFVFAKEYSVPEILSTAVIFGMLIALPITITVYYIILGL- : 586
TaPIN37 : IAS--IAVGMHCTLLRLIAVVQAALPLAVASFVFAKEYNVPEILSTAVIFGMLIAVEAATAYYFVIT---- : 406
TaPIN38 : IAS--IYVGMHCTLLCIAVVQAALPLVVASFVFAKEYNVPEILSTAVIFGMLIAVEAATAYYFVIT---- : 393
TaPIN39 : IAS--FAIGMQCTLLRLIAVQAALPLSVISFVFAKEYNVPEILSTAVIFGMLIAVEAATAYYFVIT---- : 399
TaPIN40 : ATS--IAVGLRGVLLHVAIVQAALPQGI VPFVFAKEYNCPQILSTAVIFGMLIALPITITVYYIILGL- : 632
TaPIN41 : AAS--IAVGLRCTLRLHIAIVQAALPQGI VPFVFAKEYSVPEILSTAVIFGMLIALPITITVYYIILGL- : 586
TaPIN42 : AGAGAAVAFGLRGDVLRLFAIIQAALPQSIAFVFAKEYGLHADVLSAVIFGTIASLFLVLTYYIIVLGLIV : 380
TaPIN43 : -----FILHLAVV----- : 285
TaPIN44 : ATS--IAVGLRGVLLHVAIVQAALPQGI VPFVFAKEYNCPQILSTAVIFGMLIALPITITVYYIILGL- : 633

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Figure S7. Alignment of the TaPINs protein sequences. The highly conserved regions of the TaPIN proteins were underlined with black color. Colored and shaded amino acids are chemically similar residues. Dashes indicate gaps introduced to maximize the alignment of homologous region.

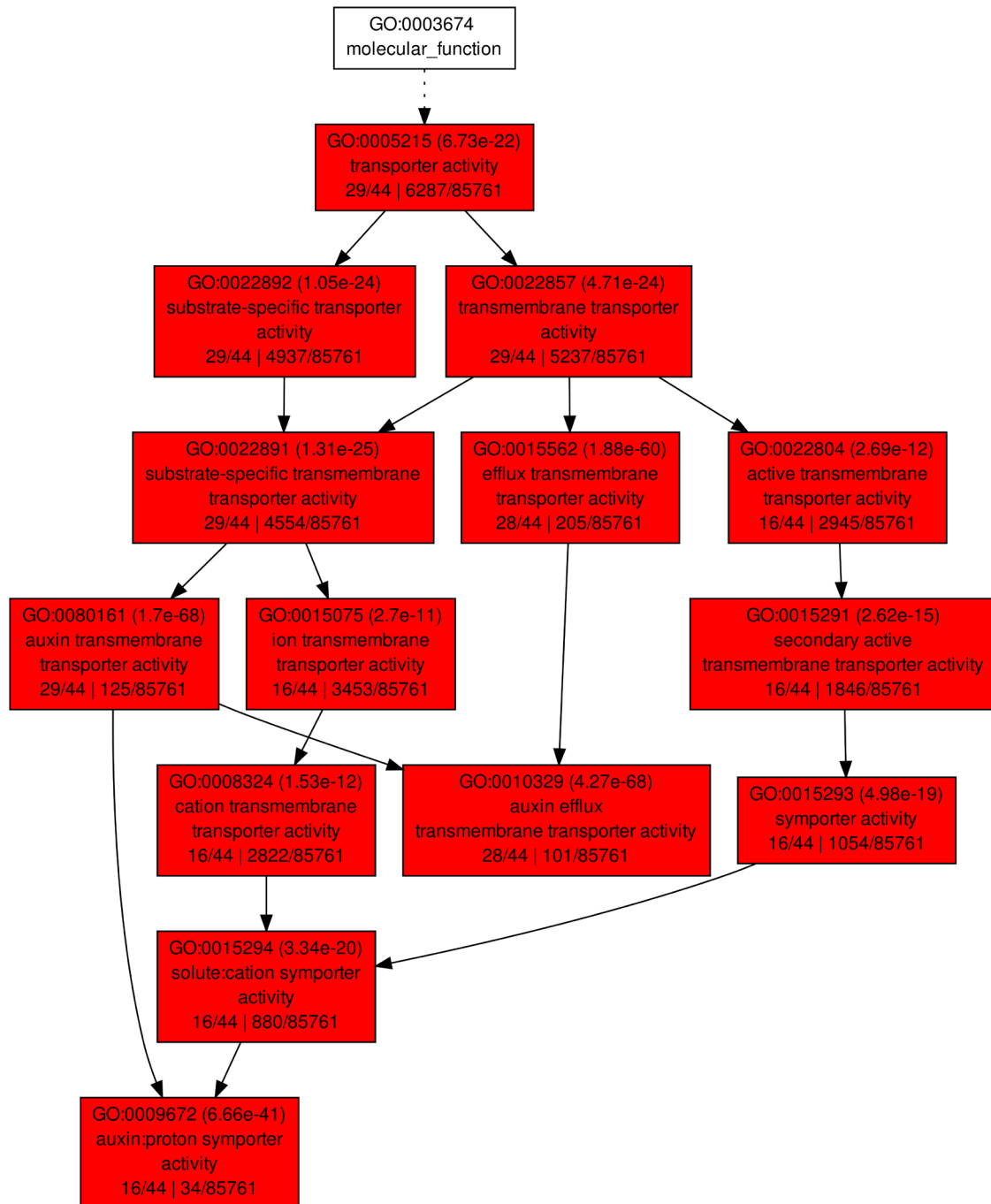


Figure S8. Gene ontology term distribution TaPIN gene family predicted using AgriGO
A. Biological Process. **B.** Cellular component. **C.** Molecular function.

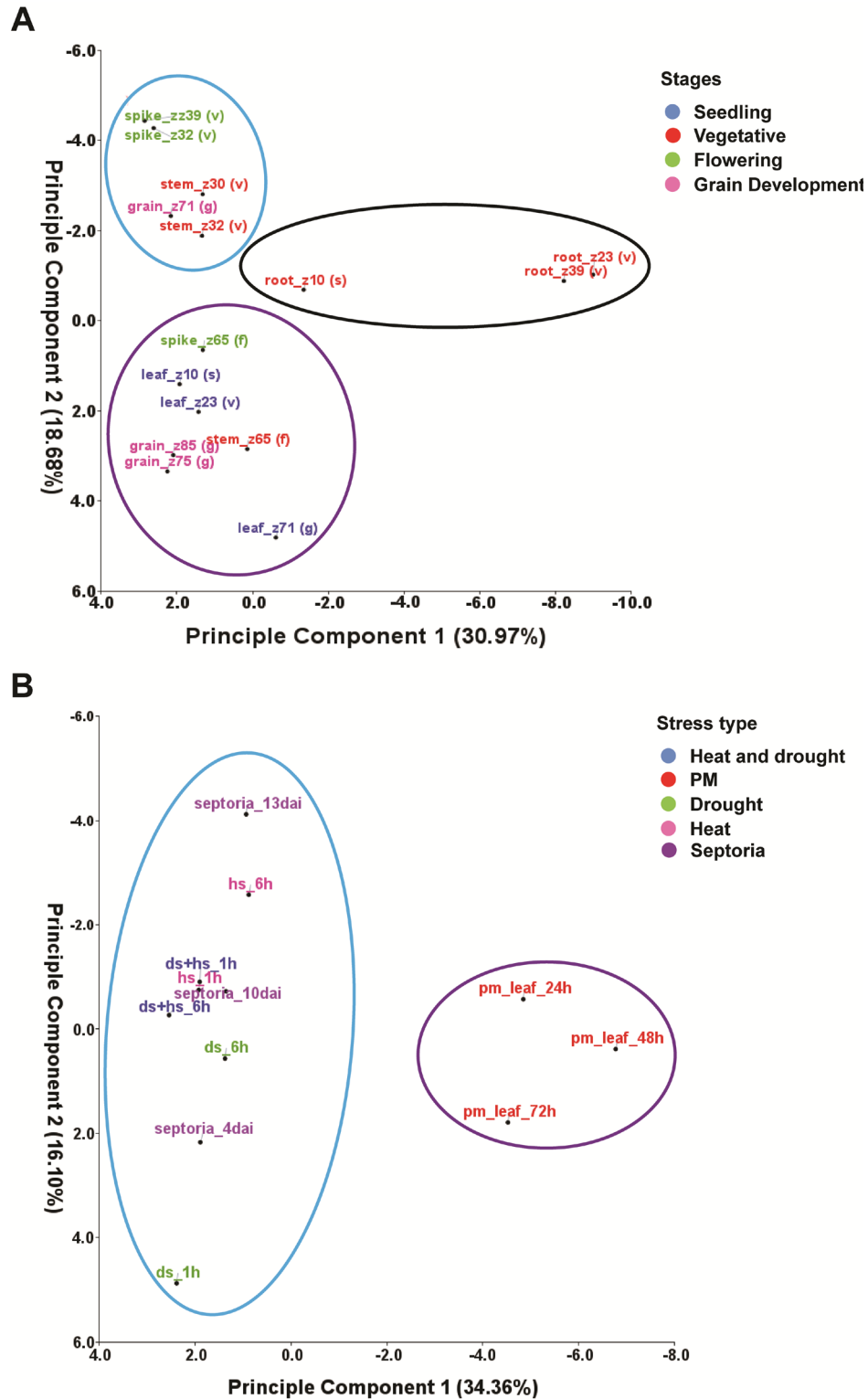


Figure S9: PCA plots displaying grouping of different (A) Developmental stages (B) Biotic and abiotic stress conditions based on the TaPIN expression pattern.

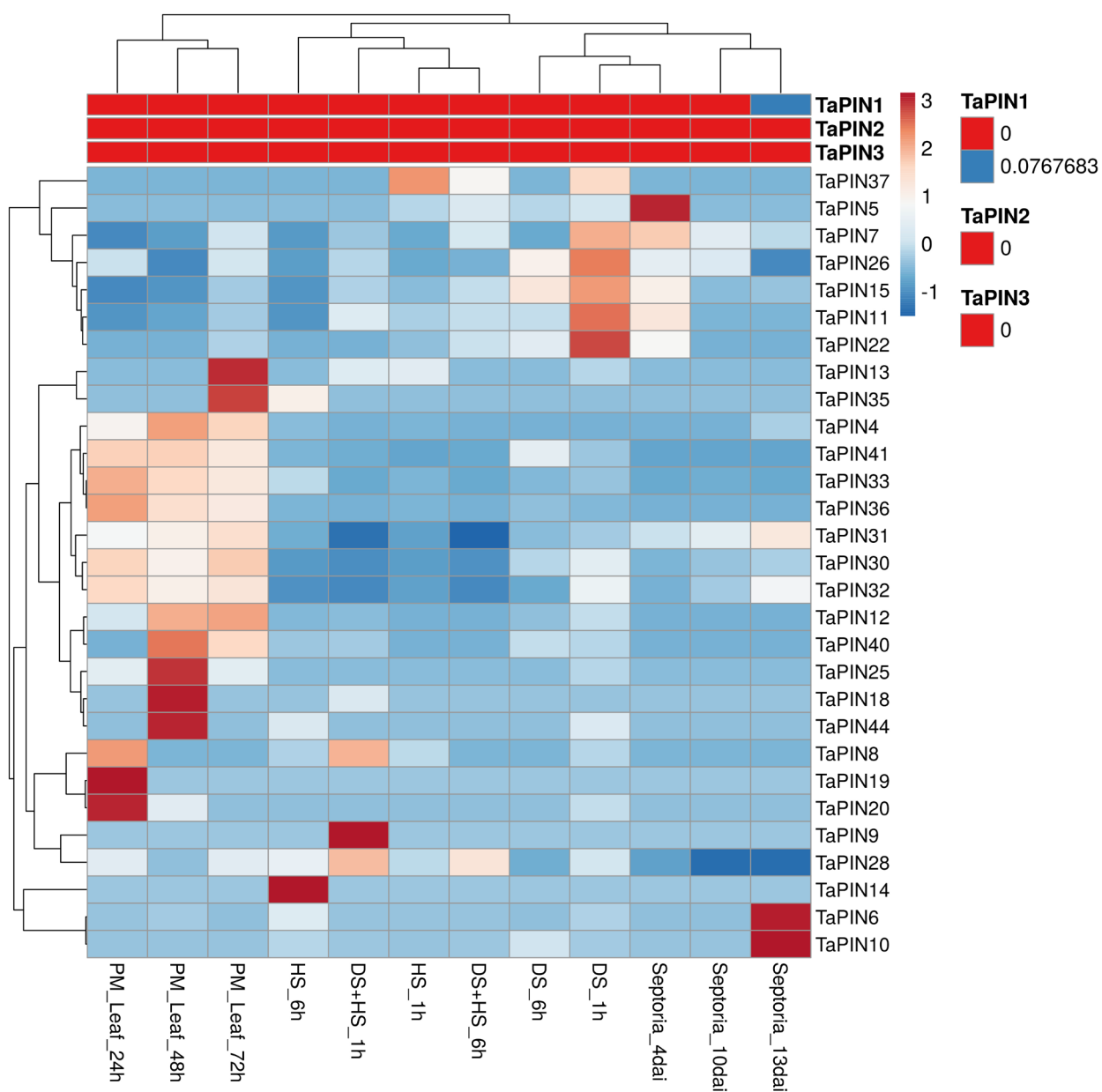


Figure S10: Heatmaps representing the expression pattern of TaPIN genes in different stress conditions. TPM values were directly used to construct the heatmaps. FPKM values were directly used to create the heatmaps. DS: Drought stress, HS: Heat stress, h: hour, d: days. PM: Powdery mildew.

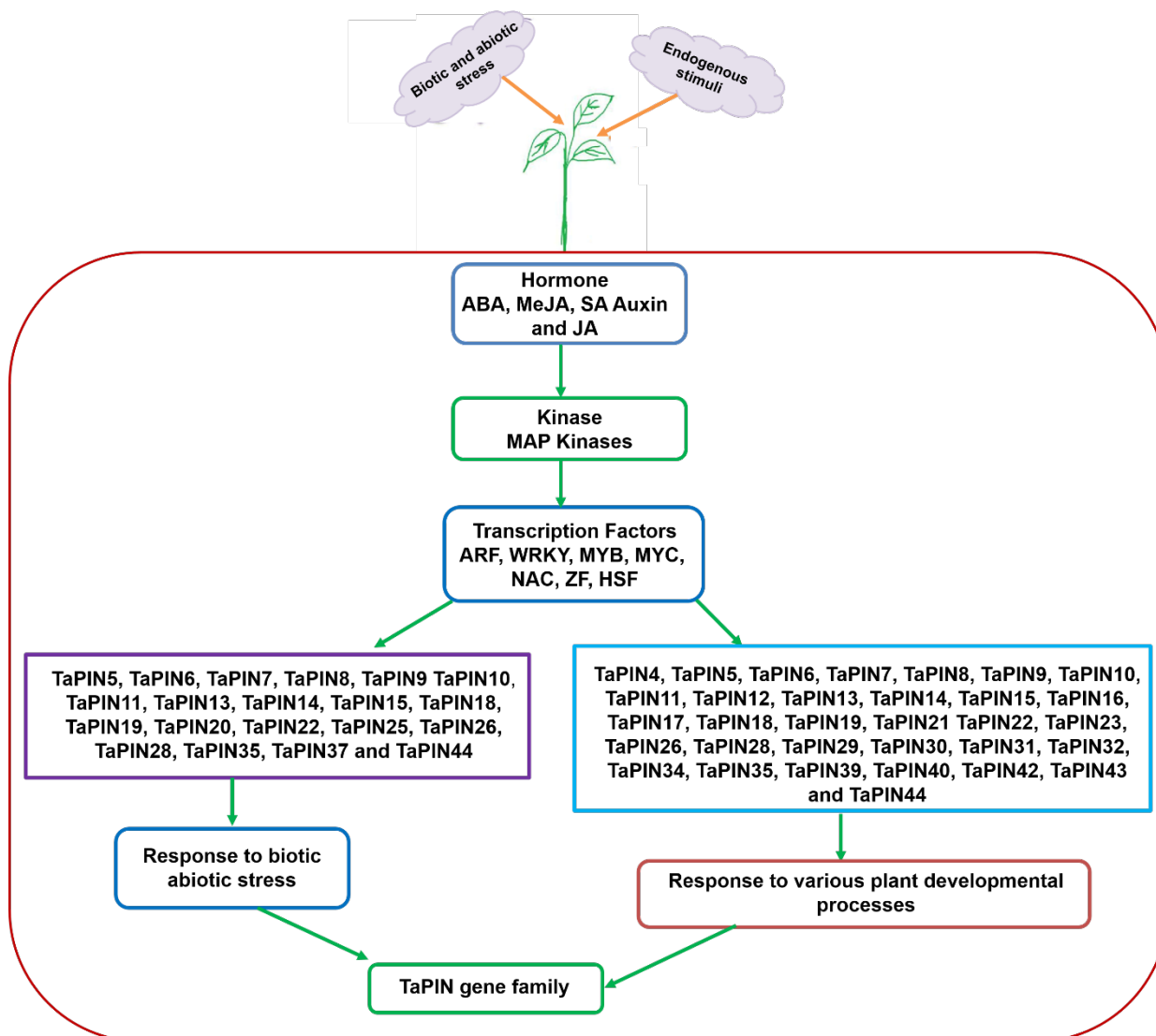


Figure S11. A possible function of TaPIN gene family in various plant developmental processes and diverse stress conditions. ABA: Absciscic acid; MeJA: Methyl jasmonate; SA: Salicylic acid; JA: Jasmonic acid; MAP: Mitogen-activated protein kinase; ARF: Auxin response factors; MYB: Myeloblastosis; NAC: No apical meristem; ZF: Zinc Finger and HSF: Heat shock factors.