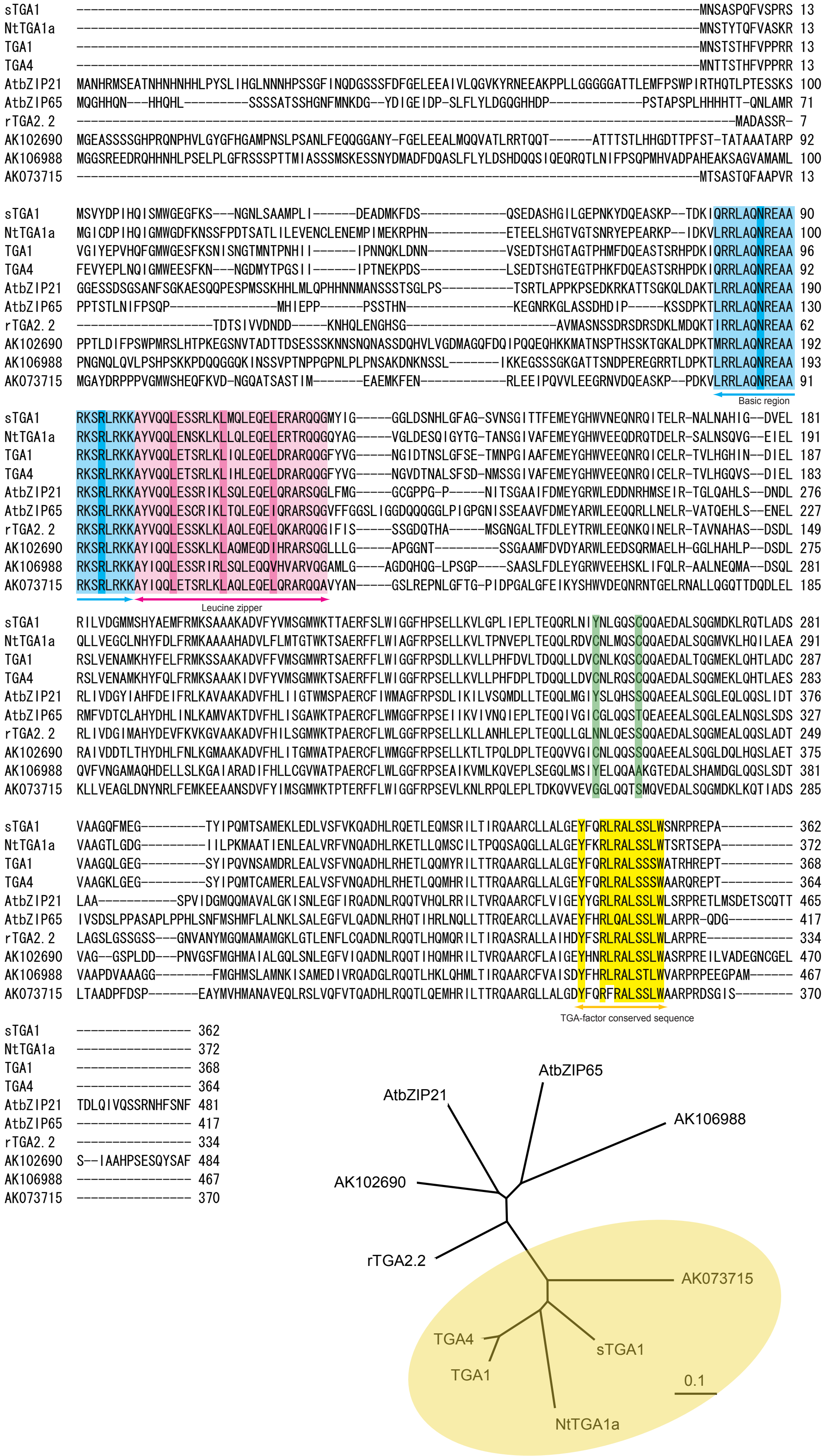
Fig. S1



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sTGA1      ---------------------------------------------------------------------------------------MNSASPQFVSPRS 13
NtTGA1a    ---------------------------------------------------------------------------------------MNSTYTQFVASKR 13
TGA1       ---------------------------------------------------------------------------------------MNSTSTHFVPPRR 13
TGA4       ---------------------------------------------------------------------------------------MNTTSTHFVPPRR 13
AtbZIP21   MANHRMSEATNHNHNHHLPYSLIHGLNNNHPSSGFINQDGSSSFDFGELEEAIVLQGVKYRNEEAKPPLLGGGGGATTLEMFPSWPIRTHQTLPTESSKS 100
AtbZIP65   MQGHHQN---HHQHL---------SSSSATSSHGNFMNKDG--YDIGEIDP-SLFLYLDGQGHHDP-------------PSTAPSPLHHHHTT-QNLAMR 71
rTGA2.2    --------------------------------------------------------------------------------------------MADASSR- 7
AK102690   MGEASSSSGHPRQNPHVLGYGFHGAMPNSLPSANLFEQQGGANY-FGELEEALMQQVATLRRTQQT------ATTTSTLHHGDTTPFST-TATAAATARP 92
AK106988   MGGSREEDRQHHNHLPSELPLGFRSSSPTTMIASSSMSKESSNYDMADFDQASLFLYLDSHDQQSIQEQRQTLNIFPSQPMHVADPAHEAKSAGVAMAML 100
AK073715   ---------------------------------------------------------------------------------------MTSASTQFAAPVR 13

sTGA1      MSVYDPIHQISMWGEGFKS---NGNLSAAMPLI------DEADMKFDS------------QSEDASHGILGEPNKYDQEASKP--TDKIQRRLAQNREAA 90
NtTGA1a    MGICDPIHQIGMWGDFKNSSFPDTSATLILEVENCLENEMPIMEKRPHN-----------ETEELSHGTVGTSNRYEPEARKP--IDKVLRRLAQNREAA 100
TGA1       VGIYEPVHQFGMWGESFKSNISNGTMNTPNHII------IPNNQKLDNN-----------VSEDTSHGTAGTPHMFDQEASTSRHPDKIQRRLAQNREAA 96
TGA4       FEVYEPLNQIGMWEESFKN---NGDMYTPGSII------IPTNEKPDS------------LSEDTSHGTEGTPHKFDQEASTSRHPDKIQRRLAQNREAA 92
AtbZIP21   GGESSDSGSANFSGKAESQQPESPMSSKHHLMLQPHHNNMANSSSTSGLPS----------TSRTLAPPKPSEDKRKATTSGKQLDAKTLRRLAQNREAA 190
AtbZIP65   PPTSTLNIFPSQP---------------MHIEPP------PSSTHN---------------KEGNRKGLASSDHDIP-----KSSDPKTLRRLAQNREAA 130
rTGA2.2    ------------------TDTSIVVDNDD-----KNHQLENGHSG----------------------AVMASNSSDRSDRSDKLMDQKTIRRLAQNREAA 62
AK102690   PPTLDIFPSWPMRSLHTPKEGSNVTADTTDSESSSKNNSNQNASSDQHVLVGDMAGQFDQIPQQEQHKKMATNSPTHSSKTGKALDPKTMRRLAQNREAA 192
AK106988   PNGNQLQVLPSHPSKKPDQQGGQKINSSVPTNPPGPNLPLPNSAKDNKNSSL-------IKKEGSSSGKGATTSNDPEREGRRTLDPKTLRRLAQNREAA 193
AK073715   MGAYDRPPPVGMWSHEQFKVD-NGQATSASTIM-------EAEMKFEN------------RLEEIPQVVLEEGRNVDQEASKP--PDKVLRRLAQNREAA 91

sTGA1      RKSRLRKKAYVQQLESSRLKLMQLEQELERARQQGMYIG-----GGLDSNHLGFAG-SVNSGITTFEMEYGHWVNEQNRQITELR-NALNAHIG--DVEL 181
NtTGA1a    RKSRLRKKAYVQQLENSKLKLLQLEQELERTRQQGQYAG-----VGLDESQIGYTG-TANSGIVAFEMEYGHWVEEQDRQTDELR-SALNSQVG--EIEL 191
TGA1       RKSRLRKKAYVQQLETSRLKLIQLEQELDRARQQGFYVG-----NGIDTNSLGFSE-TMNPGIAAFEMEYGHWVEEQNRQICELR-TVLHGHIN--DIEL 187
TGA4       RKSRLRKKAYVQQLETSRLKLIHLEQELDRARQQGFYVG-----NGVDTNALSFSD-NMSSGIVAFEMEYGHWVEEQNRQICELR-TVLHGQVS--DIEL 183
AtbZIP21   RKSRLRKKAYVQQLESSRIKLSQLEQELQRARSQGLFMG-----GCGPPG-P-----NITSGAAIFDMEYGRWLEDDNRHMSEIR-TGLQAHLS--DNDL 276
AtbZIP65   RKSRLRKKAYVQQLESCRIKLTQLEQEIQRARSQGVFFGGSLIGGDQQQGGLPIGPGNISSEAAVFDMEYARWLEEQQRLLNELR-VATQEHLS--ENEL 227
rTGA2.2    RKSRLRKKAYVQQLESSKLKLAQLEQELQKARQQGIFIS-----SSGDQTHA-----MSGNGALTFDLEYTRWLEEQNKQINELR-TAVNAHAS--DSDL 149
AK102690   RKSRLRKKAYIQQLESSKLKLAQMEQDIHRARSQGLLLG-----APGGNT---------SSGAAMFDVDYARWLEEDSQRMAELH-GGLHAHLP--DSDL 275
AK106988   RKSRLRKKAYIQQLESSRIRLSQLEQQVHVARVQGAMLG----AGDQHQG-LPSGP----SAASLFDLEYGRWVEEHSKLIFQLR-AALNEQMA--DSQL 281
AK073715   RKSRLRKKAYIQQLETSRLKLAQLEQELQRARQQAVYAN-----GSLREPNLGFTG-PIDPGALGFEIKYSHWVDEQNRNTGELRNALLQGQTTDQDLEL 185

sTGA1      RILVDGMMSHYAEMFRMKSAAAKADVFYVMSGMWKTTAERFSLWIGGFHPSELLKVLGPLIEPLTEQQRLNIYNLGQSCQQAEDALSQGMDKLRQTLADS 281
NtTGA1a    QLLVEGCLNHYFDLFRMKAAAAHADVLFLMTGTWKTSAERFFLWIAGFRPSELLKVLTPNVEPLTEQQLRDVCNLMQSCQQAEDALSQGMVKLHQILAEA 291
TGA1       RSLVENAMKHYFELFRMKSSAAKADVFFVMSGMWRTSAERFFLWIGGFRPSDLLKVLLPHFDVLTDQQLLDVCNLKQSCQQAEDALTQGMEKLQHTLADC 287
TGA4       RSLVENAMKHYFQLFRMKSAAAKIDVFYVMSGMWKTSAERFFLWIGGFRPSELLKVLLPHFDPLTDQQLLDVCNLRQSCQQAEDALSQGMEKLQHTLAES 283
AtbZIP21   RLIVDGYIAHFDEIFRLKAVAAKADVFHLIIGTWMSPAERCFIWMAGFRPSDLIKILVSQMDLLTEQQLMGIYSLQHSSQQAEEALSQGLEQLQQSLIDT 376
AtbZIP65   RMFVDTCLAHYDHLINLKAMVAKTDVFHLISGAWKTPAERCFLWMGGFRPSEIIKVIVNQIEPLTEQQIVGICGLQQSTQEAEEALSQGLEALNQSLSDS 327
rTGA2.2    RLIVDGIMAHYDEVFKVKGVAAKADVFHILSGMWKTPAERCFLWLGGFRPSELLKLLANHLEPLTEQQLLGLNNLQESSQQAEDALSQGMEALQQSLADT 249
AK102690   RAIVDDTLTHYDHLFNLKGMAAKADVFHLITGMWATPAERCFLWMGGFRPSELLKTLTPQLDPLTEQQVVGICNLQQSSQQAEEALSQGLDQLHQSLAET 375
AK106988   QVFVNGAMAQHDELLSLKGAIARADIFHLLCGVWATPAERCFLWLGGFRPSEAIKVMLKQVEPLSEGQLMSIYELQQAAKGTEDALSHAMDGLQQSLSDT 381
AK073715   KLLVEAGLDNYNRLFEMKEEAANSDVFYIMSGMWKTPTERFFLWIGGFRPSEVLKNLRPQLEPLTDKQVVEVGGLQQTSMQVEDALSQGMDKLKQTIADS 285

sTGA1      VAAGQFMEG---------TYIPQMTSAMEKLEDLVSFVKQADHLRQETLEQMSRILTIRQAARCLLALGEYFQRLRALSSLWSNRPREPA---------- 362
NtTGA1a    VAAGTLGDG---------IILPKMAATIENLEALVRFVNQADHLRKETLLQMSCILTPQQSAQGLLALGEYFKRLRALSSLWTSRTSEPA---------- 372
TGA1       VAAGQLGEG---------SYIPQVNSAMDRLEALVSFVNQADHLRHETLQQMYRILTTRQAARGLLALGEYFQRLRALSSSWATRHREPT---------- 368
TGA4       VAAGKLGEG---------SYIPQMTCAMERLEALVSFVNQADHLRHETLQQMHRILTTRQAARGLLALGEYFQRLRALSSSWAARQREPT---------- 364
AtbZIP21   LAA-----------SPVIDGMQQMAVALGKISNLEGFIRQADNLRQQTVHQLRRILTVRQAARCFLVIGEYYGRLRALSSLWLSRPRETLMSDETSCQTT 465
AtbZIP65   IVSDSLPPASAPLPPHLSNFMSHMFLALNKLSALEGFVLQADNLRHQTIHRLNQLLTTRQEARCLLAVAEYFHRLQALSSLWLARPR-QDG--------- 417
rTGA2.2    LAGSLGSSGSS---GNVANYMGQMAMAMGKLGTLENFLCQADNLRQQTLHQMQRILTIRQASRALLAIHDYFSRLRALSSLWLARPRE------------ 334
AK102690   VAG--GSPLDD---PNVGSFMGHMAIALGQLSNLEGFVIQADNLRQQTIHQMHRILTVRQAARCFLAIGEYHNRLRALSSLWASRPREILVADEGNCGEL 470
AK106988   VAAPDVAAAGG--------FMGHMSLAMNKISAMEDIVRQADGLRQQTLHKLQHMLTIRQAARCFVAISDYFHRLRALSTLWVARPRPEEGPAM------ 467
AK073715   LTAADPFDSP-------EAYMVHMANAVEQLRSLVQFVTQADHLRQQTLQEMHRILTTRQAARGLLALGDYFQRFRALSSLWAARPRDSGIS-------- 370

sTGA1      ---------------- 362
NtTGA1a    ---------------- 372
TGA1       ---------------- 368
TGA4       ---------------- 364
AtbZIP21   TDLQIVQSSRNHFSNF 481
AtbZIP65   ---------------- 417
rTGA2.2    ---------------- 334
AK102690   S--IAAHPSESQYSAF 484
AK106988   ---------------- 467
AK073715   ---------------- 370
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Fig. S1. Comparison of the amino acid sequences of AK073715, AK102690, and AK106988 to those of plant TGA factors, including sTGA1 (soybean TGA1, AAA75414), NtTGA1a (tobacco TGA1a, S17715), TGA1, TGA4, AtbZIP21, AtbZIP65 (Arabidopsis TGA factors, Q39237, Q39162, CAC40022, CAC40649, respectively), and rTGA2.2 (rice TGA factor, BAB72062). Basic regions, leucine zippers, and the TGA-factor conserved sequences are colored (blue, red, and yellow, respectively). Positions of cysteine residues that are involved in redox status of Arabidopsis TGA1 are also colored in green boxes. Asterisks indicate the signal peptide for nuclear localization (bipartile pattern). These amino acid sequences were compared using the program CLUSTALW. Phylogenetic tree was generated from the resulting alignment using the program TREEVIEW.