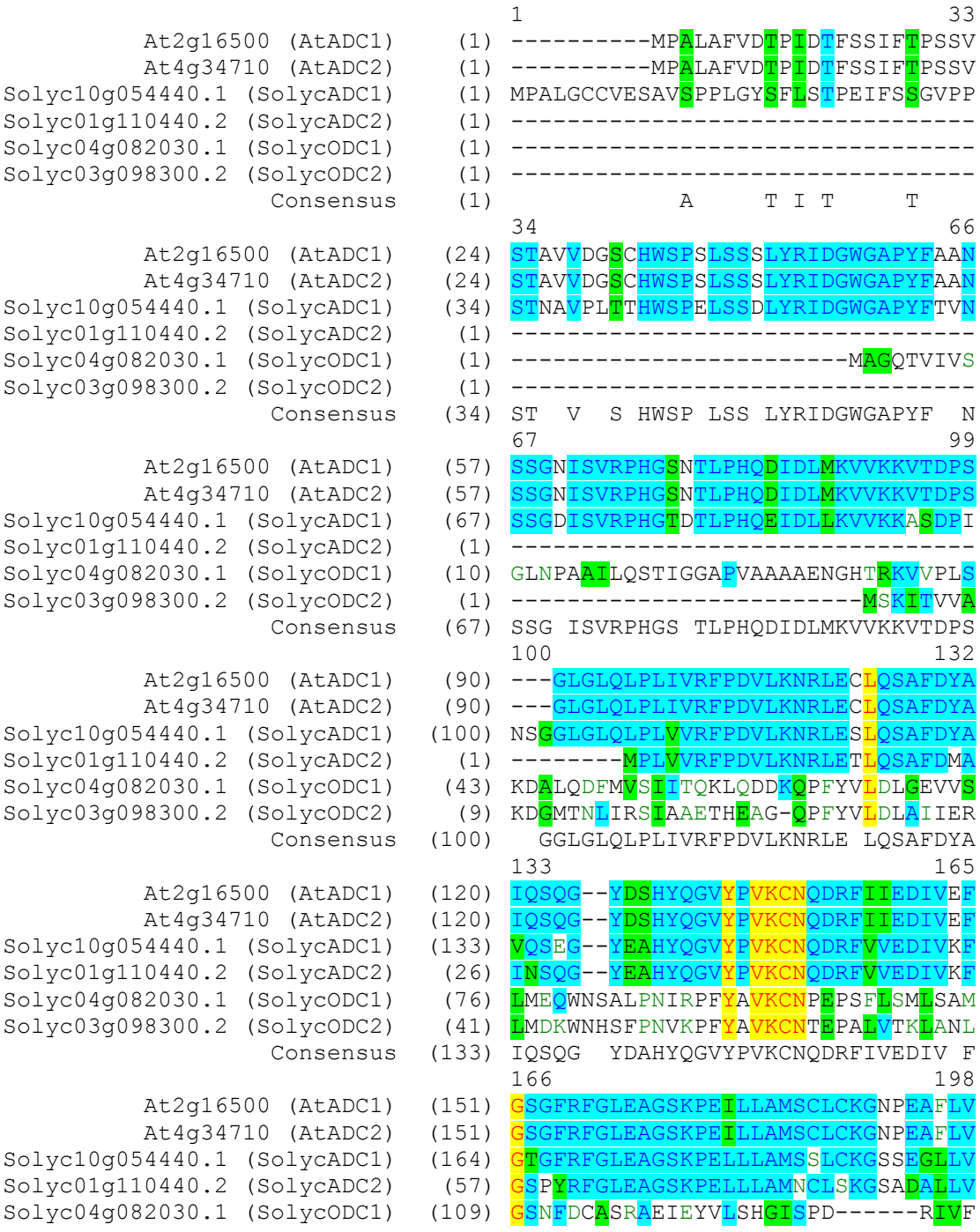
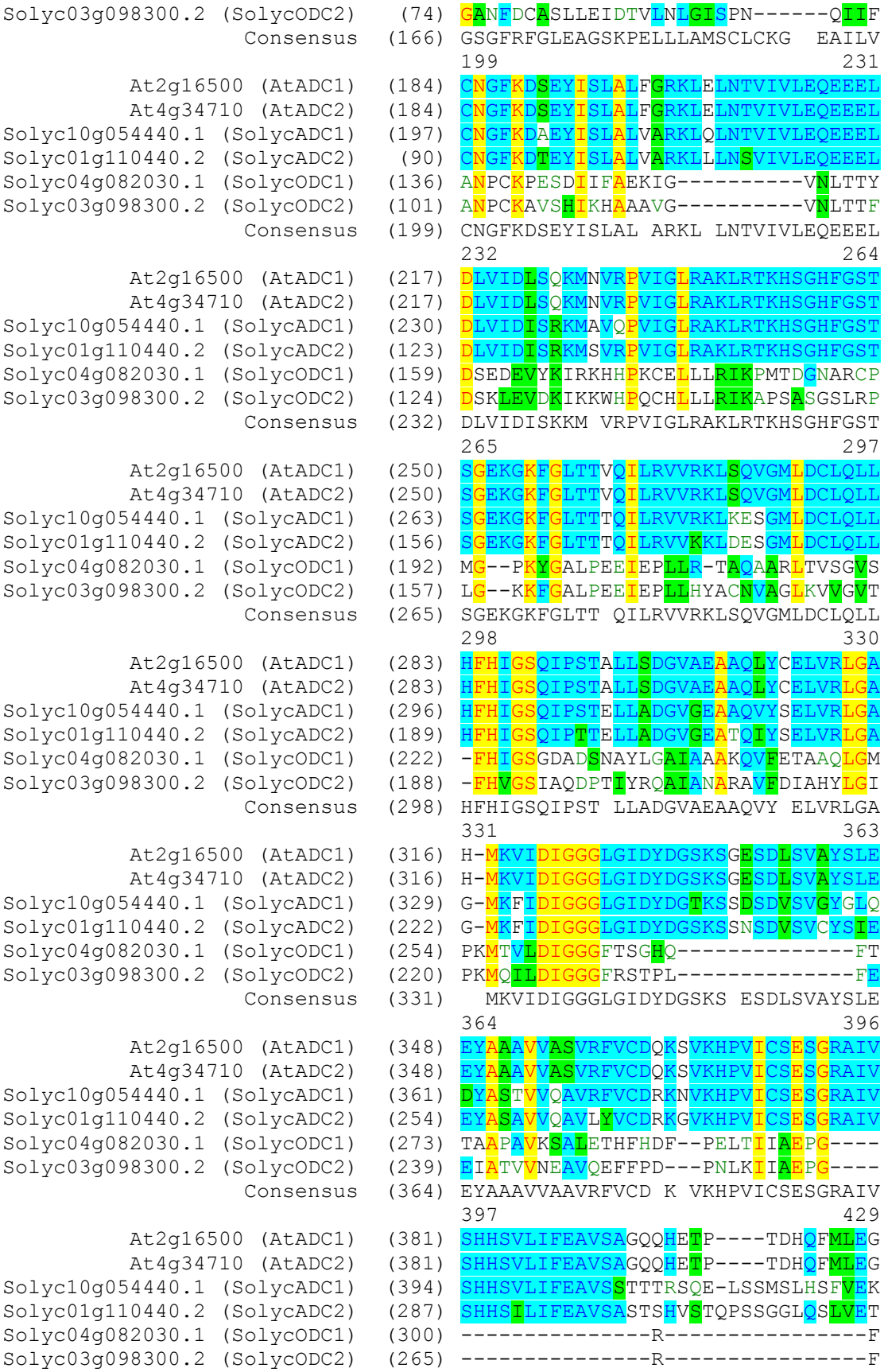
SUPPLEMENTARY

Supplementary Figure 1: **Multiple sequence alignment of protein sequences of polyamine biosynthetic genes**. At; *Arabidopsis* and Solyc; Tomato. Blue represent conserved sequences; Yellow representing identical sequences. Multiple sequence alignment of full-length proteins was performed using ClustalW.

A) Sequence alignment of ADC and ODC.

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199 231
At2g16500 (AtADC1) (184) CNGFKDSEYISLALFGRKLELNTVIVLEQEEEL
At4g34710 (AtADC2) (184) CNGFKDSEYISLALFGRKLELNTVIVLEQEEEL
Solyc10g054440.1 (SolycADC1) (197) CNGFKDAEYISLALVARKLQLNTVIVLEQEEEL
Solyc01g110440.2 (SolycADC2) (90) CNGFKDTEYISLALVARKLLLNSVIVLEQEEEL
Solyc04g082030.1 (SolycODC1) (136) ANPCKPESDIIFAEKIG----------VNLTTY
Solyc03g098300.2 (SolycODC2) (101) ANPCKAVSHIKHAAAVG----------VNLTTF
Consensus (199) CNGFKDSEYISLAL ARKL LNTVIVLEQEEEL
232 264
At2g16500 (AtADC1) (217) DLVIDLSQKMNVRPVIGLRAKLRTKHSGHFGST
At4g34710 (AtADC2) (217) DLVIDLSQKMNVRPVIGLRAKLRTKHSGHFGST
Solyc10g054440.1 (SolycADC1) (230) DLVIDISRKMAVQPVIGLRAKLRTKHSGHFGST
Solyc01g110440.2 (SolycADC2) (123) DLVIDISRKMSVRPVIGLRAKLRTKHSGHFGST
Solyc04g082030.1 (SolycODC1) (159) DSEDEVYKIRKHHPKCELLLRIKPMTDGNARCP
Solyc03g098300.2 (SolycODC2) (124) DSKLEVDKIKKWHPQCHLLLRIKAPSASGSLRP
Consensus (232) DLVIDISKKM VRPVIGLRAKLRTKHSGHFGST
265 297
At2g16500 (AtADC1) (250) SGEKGKFGLTTVQILRVVRKLSQVGMLDCLQLL
At4g34710 (AtADC2) (250) SGEKGKFGLTTVQILRVVRKLSQVGMLDCLQLL
Solyc10g054440.1 (SolycADC1) (263) SGEKGKFGLTTTQILRVVRKLKESGMLDCLQLL
Solyc01g110440.2 (SolycADC2) (156) SGEKGKFGLTTTQILRVVKKLDESGMLDCLQLL
Solyc04g082030.1 (SolycODC1) (192) MG--PKYGALPEEIEPLLR-TAQAARLTVSGVS
Solyc03g098300.2 (SolycODC2) (157) LG--KKFGALPEEIEPLLHYACNVAGLKVVGVT
Consensus (265) SGEKGKFGLTT QILRVVRKLSQVGMLDCLQLL
298 330
At2g16500 (AtADC1) (283) HFHIGSQIPSTALLSDGVAEAAQLYCELVRLGA
At4g34710 (AtADC2) (283) HFHIGSQIPSTALLSDGVAEAAQLYCELVRLGA
Solyc10g054440.1 (SolycADC1) (296) HFHIGSQIPSTELLADGVGEAAQVYSELVRLGA
Solyc01g110440.2 (SolycADC2) (189) HFHIGSQIPTTELLADGVGEATQIYSELVRLGA
Solyc04g082030.1 (SolycODC1) (222) -FHIGSGDADSNAYLGAIAAAKQVFETAAQLGM
Solyc03g098300.2 (SolycODC2) (188) -FHVGSIAQDPTIYRQAIANARAVFDIAHYLGI
Consensus (298) HFHIGSQIPST LLADGVAEAAQVY ELVRLGA
331 363
At2g16500 (AtADC1) (316) H-MKVIDIGGGLGIDYDGSKSGESDLSVAYSLE
At4g34710 (AtADC2) (316) H-MKVIDIGGGLGIDYDGSKSGESDLSVAYSLE
Solyc10g054440.1 (SolycADC1) (329) G-MKFIDIGGGLGIDYDGTKSSDSDVSVGYGLQ
Solyc01g110440.2 (SolycADC2) (222) G-MKFIDIGGGLGIDYDGSKSSNSDVSVCYSIE
Solyc04g082030.1 (SolycODC1) (254) PKMTVLDIGGGFTSGHQ--------------FT
Solyc03g098300.2 (SolycODC2) (220) PKMQILDIGGGFRSTPL--------------FE
Consensus (331) MKVIDIGGGLGIDYDGSKS ESDLSVAYSLE
364 396
At2g16500 (AtADC1) (348) EYAAAVVASVRFVCDQKSVKHPVICSESGRAIV
At4g34710 (AtADC2) (348) EYAAAVVASVRFVCDQKSVKHPVICSESGRAIV
Solyc10g054440.1 (SolycADC1) (361) DYASTVVQAVRFVCDRKNVKHPVICSESGRAIV
Solyc01g110440.2 (SolycADC2) (254) EYASAVVQAVLYVCDRKGVKHPVICSESGRAIV
Solyc04g082030.1 (SolycODC1) (273) TAAPAVKSALETHFHDF--PELTIIAEPG----
Solyc03g098300.2 (SolycODC2) (239) EIATVVNEAVQEFFPD---PNLKIIAEPG----
Consensus (364) EYAAAVVAAVRFVCD K VKHPVICSESGRAIV
397 429
At2g16500 (AtADC1) (381) SHHSVLIFEAVSAGQQHETP----TDHQFMLEG
At4g34710 (AtADC2) (381) SHHSVLIFEAVSAGQQHETP----TDHQFMLEG
Solyc10g054440.1 (SolycADC1) (394) SHHSVLIFEAVSSTTTRSQE-LSSMSLHSFVEK
Solyc01g110440.2 (SolycADC2) (287) SHHSILIFEAVSASTSHVSTQPSSGGLQSLVET
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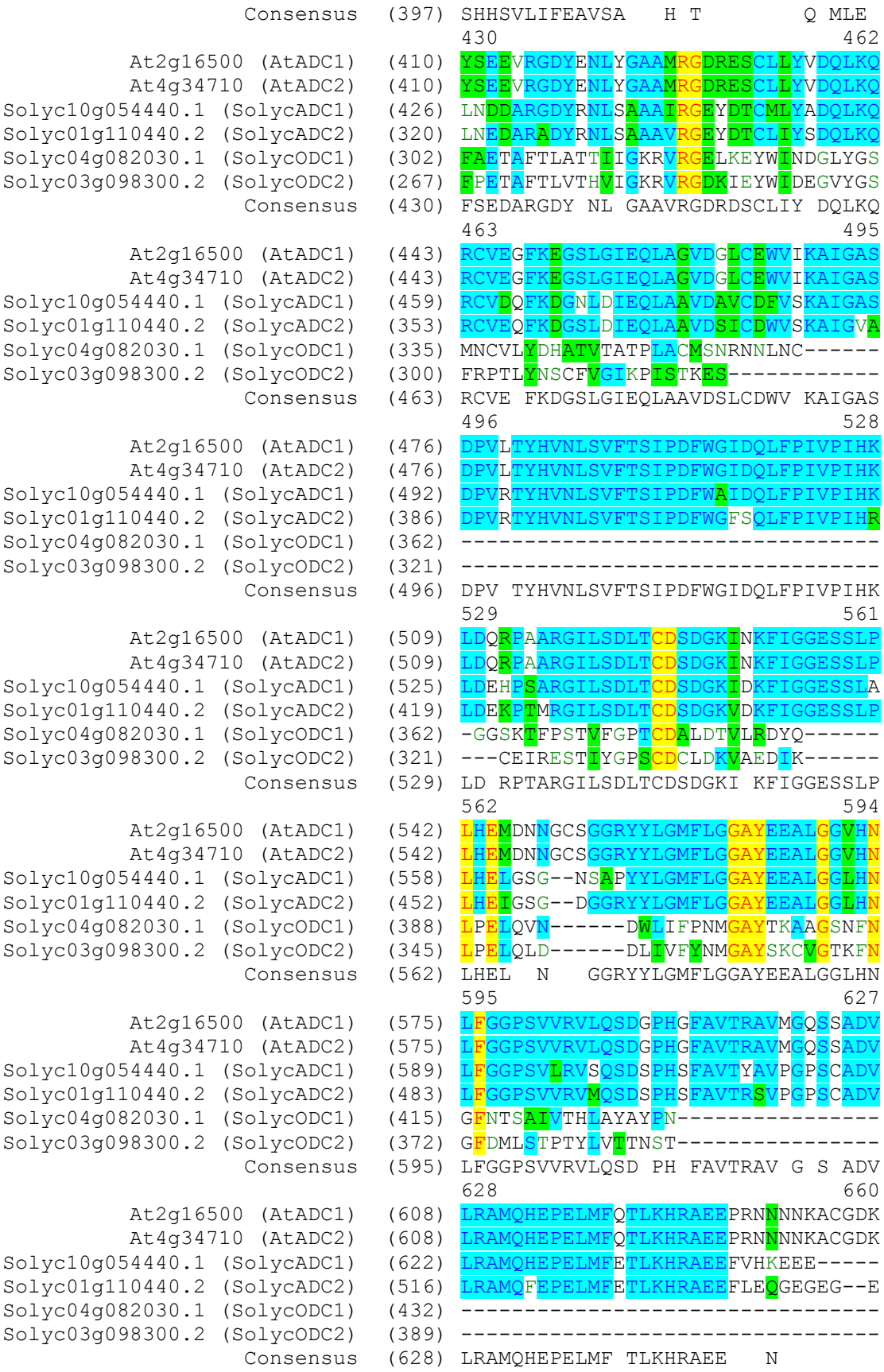
Solyc03g098300.2 (SolycODC2) (265) ---------------R----------------F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At4g34710 (AtADC2) (410) YSEEVRGDYENLYGAAMRGDRESCLLYVDQLKQ
Solyc10g054440.1 (SolycADC1) (426) LNDDARGDYRNLSAAAIRGEYDTCMLYADQLKQ
Solyc01g110440.2 (SolycADC2) (320) LNEDARADYRNLSAAAVRGEYDTCLIYSDQLKQ
Solyc04g082030.1 (SolycODC1) (302) FAETAFTLATTIIGKRVRGELKEYWINDGLYGS
Solyc03g098300.2 (SolycODC2) (267) FPETAFTLVTHVIGKRVRGDKIEYWIDEGVYGS
Consensus (430) FSEDARGDY NL GAAVRGDRDSCLIY DQLKQ
463 495
At2g16500 (AtADC1) (443) RCVEGFKEGSLGIEQLAGVDGLCEWVIKAIGAS
At4g34710 (AtADC2) (443) RCVEGFKEGSLGIEQLAGVDGLCEWVIKAIGAS
Solyc10g054440.1 (SolycADC1) (459) RCVDQFKDGNLDIEQLAAVDAVCDFVSKAIGAS
Solyc01g110440.2 (SolycADC2) (353) RCVEQFKDGSLDIEQLAAVDSICDWVSKAIGVA
Solyc04g082030.1 (SolycODC1) (335) MNCVLYDHATVTATPLACMSNRNNLNC------
Solyc03g098300.2 (SolycODC2) (300) FRPTLYNSCFVGIKPISTKES------------
Consensus (463) RCVE FKDGSLGIEQLAAVDSLCDWV KAIGAS
496 528
At2g16500 (AtADC1) (476) DPVLTYHVNLSVFTSIPDFWGIDQLFPIVPIHK
At4g34710 (AtADC2) (476) DPVLTYHVNLSVFTSIPDFWGIDQLFPIVPIHK
Solyc10g054440.1 (SolycADC1) (492) DPVRTYHVNLSVFTSIPDFWAIDQLFPIVPIHK
Solyc01g110440.2 (SolycADC2) (386) DPVRTYHVNLSVFTSIPDFWGFSQLFPIVPIHR
Solyc04g082030.1 (SolycODC1) (362) ---------------------------------
Solyc03g098300.2 (SolycODC2) (321) ---------------------------------
Consensus (496) DPV TYHVNLSVFTSIPDFWGIDQLFPIVPIHK
529 561
At2g16500 (AtADC1) (509) LDQRPAARGILSDLTCDSDGKINKFIGGESSLP
At4g34710 (AtADC2) (509) LDQRPAARGILSDLTCDSDGKINKFIGGESSLP
Solyc10g054440.1 (SolycADC1) (525) LDEHPSARGILSDLTCDSDGKIDKFIGGESSLA
Solyc01g110440.2 (SolycADC2) (419) LDEKPTMRGILSDLTCDSDGKVDKFIGGESSLP
Solyc04g082030.1 (SolycODC1) (362) -GGSKTFPSTVFGPTCDALDTVLRDYQ------
Solyc03g098300.2 (SolycODC2) (321) ---CEIRESTIYGPSCDCLDKVAEDIK------
Consensus (529) LD RPTARGILSDLTCDSDGKI KFIGGESSLP
562 594
At2g16500 (AtADC1) (542) LHEMDNNGCSGGRYYLGMFLGGAYEEALGGVHN
At4g34710 (AtADC2) (542) LHEMDNNGCSGGRYYLGMFLGGAYEEALGGVHN
Solyc10g054440.1 (SolycADC1) (558) LHELGSG--NSAPYYLGMFLGGAYEEALGGLHN
Solyc01g110440.2 (SolycADC2) (452) LHEIGSG--DGGRYYLGMFLGGAYEEALGGLHN
Solyc04g082030.1 (SolycODC1) (388) LPELQVN------DWLIFPNMGAYTKAAGSNFN
Solyc03g098300.2 (SolycODC2) (345) LPELQLD------DLIVFYNMGAYSKCVGTKFN
Consensus (562) LHEL N GGRYYLGMFLGGAYEEALGGLHN
595 627
At2g16500 (AtADC1) (575) LFGGPSVVRVLQSDGPHGFAVTRAVMGQSSADV
At4g34710 (AtADC2) (575) LFGGPSVVRVLQSDGPHGFAVTRAVMGQSSADV
Solyc10g054440.1 (SolycADC1) (589) LFGGPSVLRVSQSDSPHSFAVTYAVPGPSCADV
Solyc01g110440.2 (SolycADC2) (483) LFGGPSVVRVMQSDSPHSFAVTRSVPGPSCADV
Solyc04g082030.1 (SolycODC1) (415) GFNTSAIVTHLAYAYPN----------------
Solyc03g098300.2 (SolycODC2) (372) GFDMLSTPTYLVTTNST----------------
Consensus (595) LFGGPSVVRVLQSD PH FAVTRAV G S ADV
628 660
At2g16500 (AtADC1) (608) LRAMQHEPELMFQTLKHRAEEPRNNNNKACGDK
At4g34710 (AtADC2) (608) LRAMQHEPELMFQTLKHRAEEPRNNNNKACGDK
Solyc10g054440.1 (SolycADC1) (622) LRAMQHEPELMFETLKHRAEEFVHKEEE-----
Solyc01g110440.2 (SolycADC2) (516) LRAMQFEPELMFETLKHRAEEFLEQGEGEG--E
Solyc04g082030.1 (SolycODC1) (432) ---------------------------------
Solyc03g098300.2 (SolycODC2) (389) ---------------------------------
Consensus (628) LRAMQHEPELMF TLKHRAEE N

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                                    661                                 693
          At2g16500 (AtADC1)  (641) GNDKLVVASCLAKSFNNMPYLS----METSTNA
          At4g34710 (AtADC2)  (641) GNDKLVVASCLAKSFNNMPYLS----METSTNA
Solyc10g054440.1 (SolycADC1)  (650) --VEVSLANSLNQSFHNMPYLAPHSSCCFSGYY
Solyc01g110440.2 (SolycADC2)  (547) GVAFGSLTSSLAQSFHNMPYLS---SCCFTAEA
Solyc04g082030.1 (SolycODC1)  (432) ----------------------------------
Solyc03g098300.2 (SolycODC2)  (389) ----------------------------------
                  Consensus   (661) G   L LAS LA SF NMPYLS       S  A
                                    694                                 726
          At2g16500 (AtADC1)  (670) LTAAVNNLGVYYCDEAAAGGGGKGKDENWSYFG
          At4g34710 (AtADC2)  (670) LTAAVNNLGVYYCDEAAAGGGGKGKDENWSYFG
Solyc10g054440.1 (SolycADC1)  (681) YCNDENIVGVG-------AECAIGEEEFWPYCV
Solyc01g110440.2 (SolycADC2)  (577) TANANTNTNNGGYYYYSEDNAAAEEDEIWSY--
Solyc04g082030.1 (SolycODC1)  (432) ----------------------------------
Solyc03g098300.2 (SolycODC2)  (389) ----------------------------------
                  Consensus   (694)    A NNLGV      A G GA G DE WSY
                                    727
          At2g16500 (AtADC1)  (703) --
          At4g34710 (AtADC2)  (703) --
Solyc10g054440.1 (SolycADC1)  (707) A-
Solyc01g110440.2 (SolycADC2)  (608) --
Solyc04g082030.1 (SolycODC1)  (432) --
Solyc03g098300.2 (SolycODC2)  (389) --
                  Consensus   (727)
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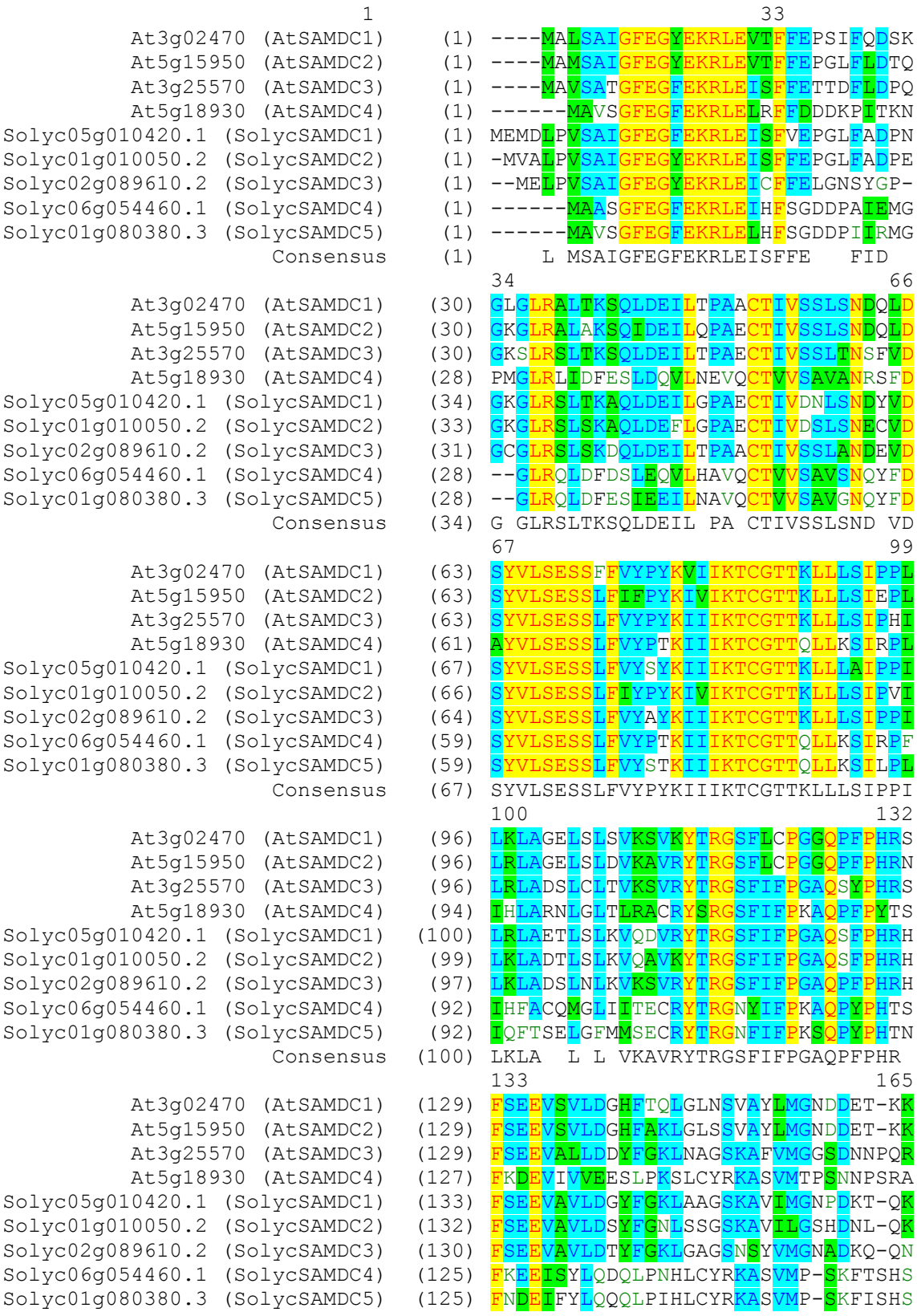
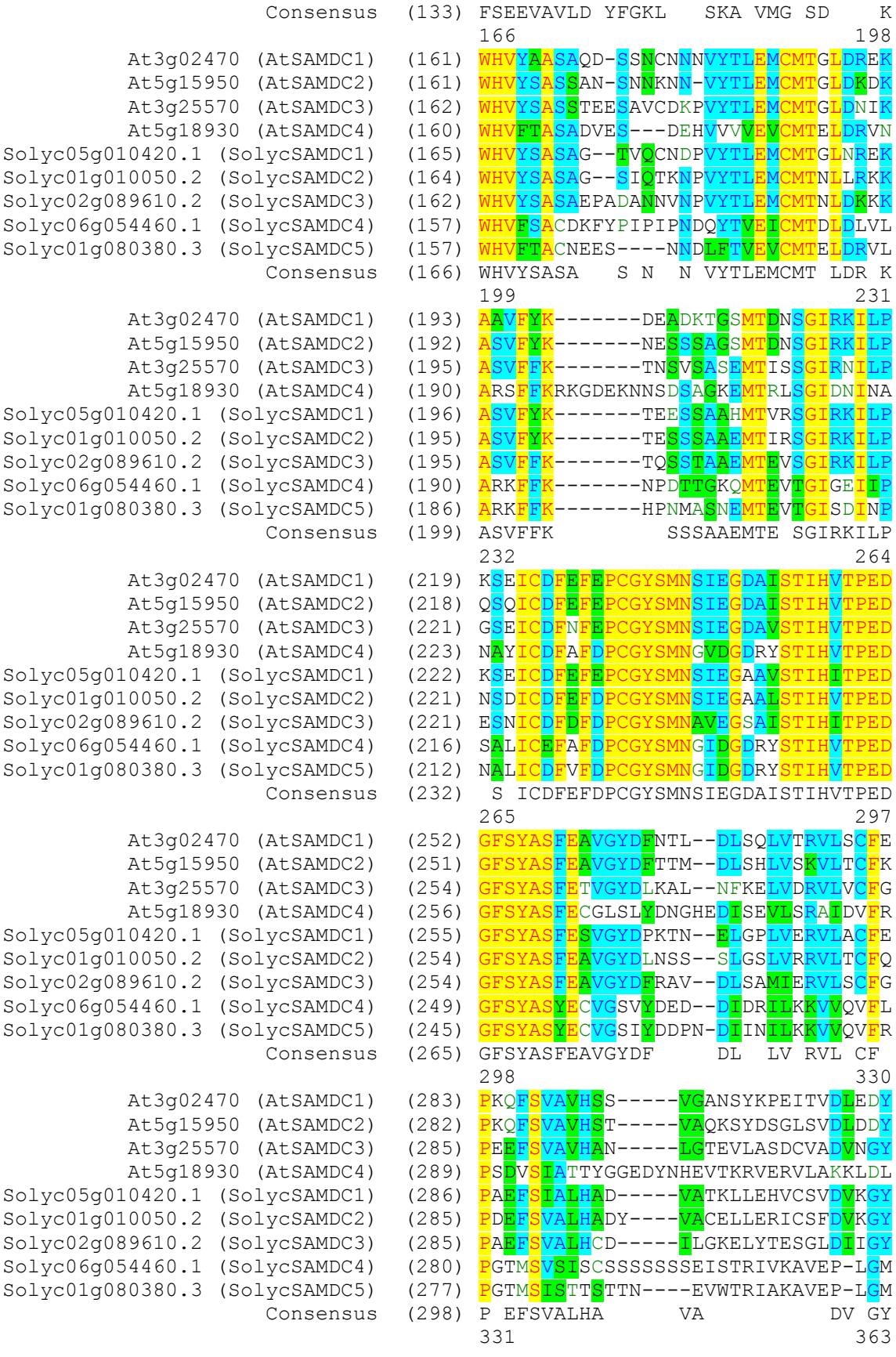
B. Multiple sequence alignment of SAMDC.




Consensus (133) FSEEVAVLD YFGKL SKA VMG SD K
166 198
At3g02470 (AtSAMDC1) (161) WHVYAASAQD-SSNCNNNVYTLEMCMTGLDREK
At5g15950 (AtSAMDC2) (161) WHVYSASSAN-SNNKNN-VYTLEMCMTGLDKDK
At3g25570 (AtSAMDC3) (162) WHVYSASSTEESAVCDKPVYTLEMCMTGLDNIK
At5g18930 (AtSAMDC4) (160) WHVFTASADVES---DEHVVVVEVCMTELDRVN
Solyc05g010420.1 (SolycSAMDC1) (165) WHVYSASAG--TVQCNDPVYTLEMCMTGLNREK
Solyc01g010050.2 (SolycSAMDC2) (164) WHVYSASAG--SIQTKNPVYTLEMCMTNLLRKK
Solyc02g089610.2 (SolycSAMDC3) (162) WHVYSASAEPADANNVNPVYTLEMCMTNLDKKK
Solyc06g054460.1 (SolycSAMDC4) (157) WHVFSACDKFYPIPIPNDQYTVEICMTDLDLVL
Solyc01g080380.3 (SolycSAMDC5) (157) WHVFTACNEES----NNDLFTVEVCMTELDRVL
Consensus (166) WHVYSASA S N N VYTLEMCMT LDR K
199 231
At3g02470 (AtSAMDC1) (193) AAVFYK-------DEADKTGSMTDNSGIRKILP
At5g15950 (AtSAMDC2) (192) ASVFYK-------NESSSAGSMTDNSGIRKILP
At3g25570 (AtSAMDC3) (195) ASVFFK-------TNSVSASEMTISSGIRNILP
At5g18930 (AtSAMDC4) (190) ARSFFKRKGDEKNNSDSAGKEMTRLSGIDNINA
Solyc05g010420.1 (SolycSAMDC1) (196) ASVFYK-------TEESSAAHMTVRSGIRKILP
Solyc01g010050.2 (SolycSAMDC2) (195) ASVFYK-------TESSSAAEMTIRSGIRKILP
Solyc02g089610.2 (SolycSAMDC3) (195) ASVFFK-------TQSSTAAEMTEVSGIRKILP
Solyc06g054460.1 (SolycSAMDC4) (190) ARKFFK-------NPDTTGKQMTEVTGIGEIIP
Solyc01g080380.3 (SolycSAMDC5) (186) ARKFFK-------HPNMASNEMTEVTGISDINP
Consensus (199) ASVFFK SSSAAEMTE SGIRKILP
232 264
At3g02470 (AtSAMDC1) (219) KSEICDFEFEPCGYSMNSIEGDAISTIHVTPED
At5g15950 (AtSAMDC2) (218) QSQICDFEFEPCGYSMNSIEGDAISTIHVTPED
At3g25570 (AtSAMDC3) (221) GSEICDFNFEPCGYSMNSIEGDAVSTIHVTPED
At5g18930 (AtSAMDC4) (223) NAYICDFAFDPCGYSMNGVDGDRYSTIHVTPED
Solyc05g010420.1 (SolycSAMDC1) (222) KSEICDFEFEPCGYSMNSIEGAAVSTIHITPED
Solyc01g010050.2 (SolycSAMDC2) (221) NSDICDFEFDPCGYSMNSIEGAALSTIHVTPED
Solyc02g089610.2 (SolycSAMDC3) (221) ESNICDFDFDPCGYSMNAVEGSAISTIHITPED
Solyc06g054460.1 (SolycSAMDC4) (216) SALICEFAFDPCGYSMNGIDGDRYSTIHVTPED
Solyc01g080380.3 (SolycSAMDC5) (212) NALICDFVFDPCGYSMNGIDGDRYSTIHVTPED
Consensus (232) S ICDFEFDPCGYSMNSIEGDAISTIHVTPED
265 297
At3g02470 (AtSAMDC1) (252) GFSYASFEAVGYDFNTL--DLSQLVTRVLSCFE
At5g15950 (AtSAMDC2) (251) GFSYASFEAVGYDFTTM--DLSHLVSKVLTCFK
At3g25570 (AtSAMDC3) (254) GFSYASFETVGYDLKAL--NFKELVDRVLVCFG
At5g18930 (AtSAMDC4) (256) GFSYASFECGLSLYDNGHEDISEVLSRAIDVFR
Solyc05g010420.1 (SolycSAMDC1) (255) GFSYASFESVGYDPKTN--ELGPLVERVLACFE
Solyc01g010050.2 (SolycSAMDC2) (254) GFSYASFEAVGYDLNSS--SLGSLVRRVLTCFQ
Solyc02g089610.2 (SolycSAMDC3) (254) GFSYASFEAVGYDFRAV--DLSAMIERVLSCFG
Solyc06g054460.1 (SolycSAMDC4) (249) GFSYASYECVGSVYDED--DIDRILKKVVQVFL
Solyc01g080380.3 (SolycSAMDC5) (245) GFSYASYECVGSIYDDPN-DIINILKKVVQVFR
Consensus (265) GFSYASFEAVGYDF DL LV RVL CF
298 330
At3g02470 (AtSAMDC1) (283) PKQFSVAVHSS-----VGANSYKPEITVDLEDY
At5g15950 (AtSAMDC2) (282) PKQFSVAVHST-----VAQKSYDSGLSVDLDDY
At3g25570 (AtSAMDC3) (285) PEEFSVAVHAN-----LGTEVLASDCVADVNGY
At5g18930 (AtSAMDC4) (289) PSDVSIATTYGGEDYNHEVTKRVERVLAKKLDL
Solyc05g010420.1 (SolycSAMDC1) (286) PAEFSIALHAD-----VATKLLEHVCSVDVKGY
Solyc01g010050.2 (SolycSAMDC2) (285) PDEFSVALHADY----VACELLERICSFDVKGY
Solyc02g089610.2 (SolycSAMDC3) (285) PAEFSVALHCD-----ILGKELYTESGLDIIGY
Solyc06g054460.1 (SolycSAMDC4) (280) PGTMSVSISCSSSSSSSEISTRIVKAVEP-LGM
Solyc01g080380.3 (SolycSAMDC5) (277) PGTMSISTTSTTN----EVWTRIAKAVEP-LGM
Consensus (298) P EFSVALHA VA DV GY
331 363

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          At3g02470 (AtSAMDC1)   (311) GCRERTFESLGEESGTVMYQTFEKLGKYCGSPR
          At5g15950 (AtSAMDC2)   (310) GCKESTMESLGEERGTVMYQRFEKLGRYCGSPR
          At3g25570 (AtSAMDC3)   (313) FSQERELEELGL-GGSVLYQRFVKT-VECCSPK
          At5g18930 (AtSAMDC4)   (322) KCRSRLMDEFPG-SGTVVYQSFTPRRK------
Solyc05g010420.1 (SolycSAMDC1)   (314) SLAEWSPEEFGK-GGSIVYQKFTRT-PYCESPK
Solyc01g010050.2 (SolycSAMDC2)   (314) SHAEWSPEELGK-GGLIVYRKFTRS-SLCGSPK
Solyc02g089610.2 (SolycSAMDC3)   (313) VSGEKTTEMLGK-GGSLTYLTFSSG-GSCGSPR
Solyc06g054460.1 (SolycSAMDC4)   (312) KRRNCTIDEFPA-AGTVVFQTFTLTGNR-----
Solyc01g080380.3 (SolycSAMDC5)   (305) KCRSCTMDDFPS-TGSVVFQTFTSCRK------
                     Consensus   (331)   RE TMEELG  GGSVVYQTFTK    C SPK
                                       364                 387
          At3g02470 (AtSAMDC1)   (344) STLKCEWSSNNSCSSEDEKDEGI-
          At5g15950 (AtSAMDC2)   (343) STLKCEWSSNSSCNSEDEKE----
          At3g25570 (AtSAMDC3)   (344) STLGFC------------------
          At5g18930 (AtSAMDC4)   (348) ------------------------
Solyc05g010420.1 (SolycSAMDC1)   (345) SVLKGCWKEEEK--EGKE------
Solyc01g010050.2 (SolycSAMDC2)   (345) SVLQDCWNEEEKRNEVKEVC----
Solyc02g089610.2 (SolycSAMDC3)   (344) SILNNCWSENEDEEMEKIC-----
Solyc06g054460.1 (SolycSAMDC4)   (339) ------------------------
Solyc01g080380.3 (SolycSAMDC5)   (331) ------------------------
                     Consensus   (364) S L   W
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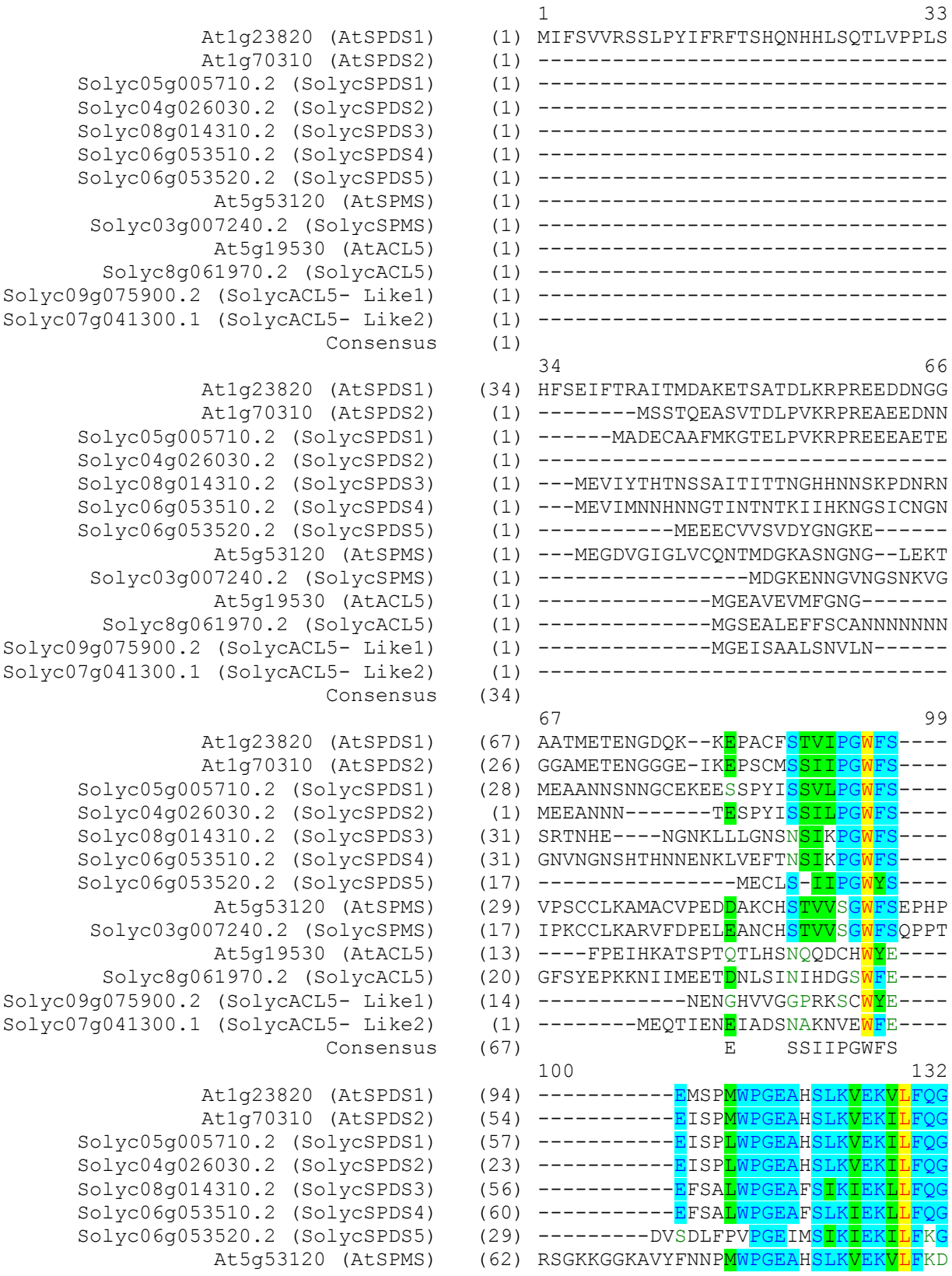
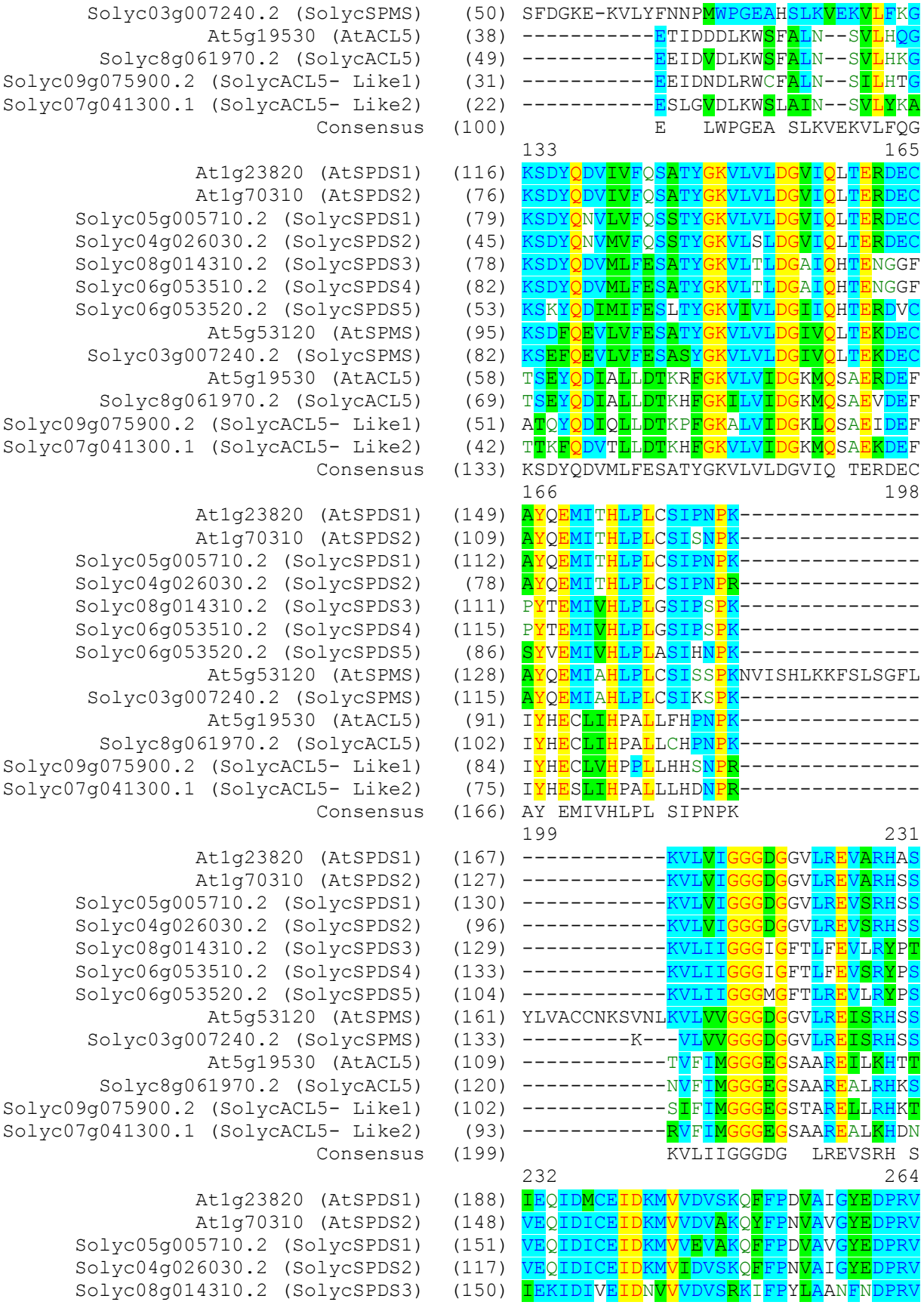
C. Multiple sequence alignment of SPDS, SPMS and ACL5.

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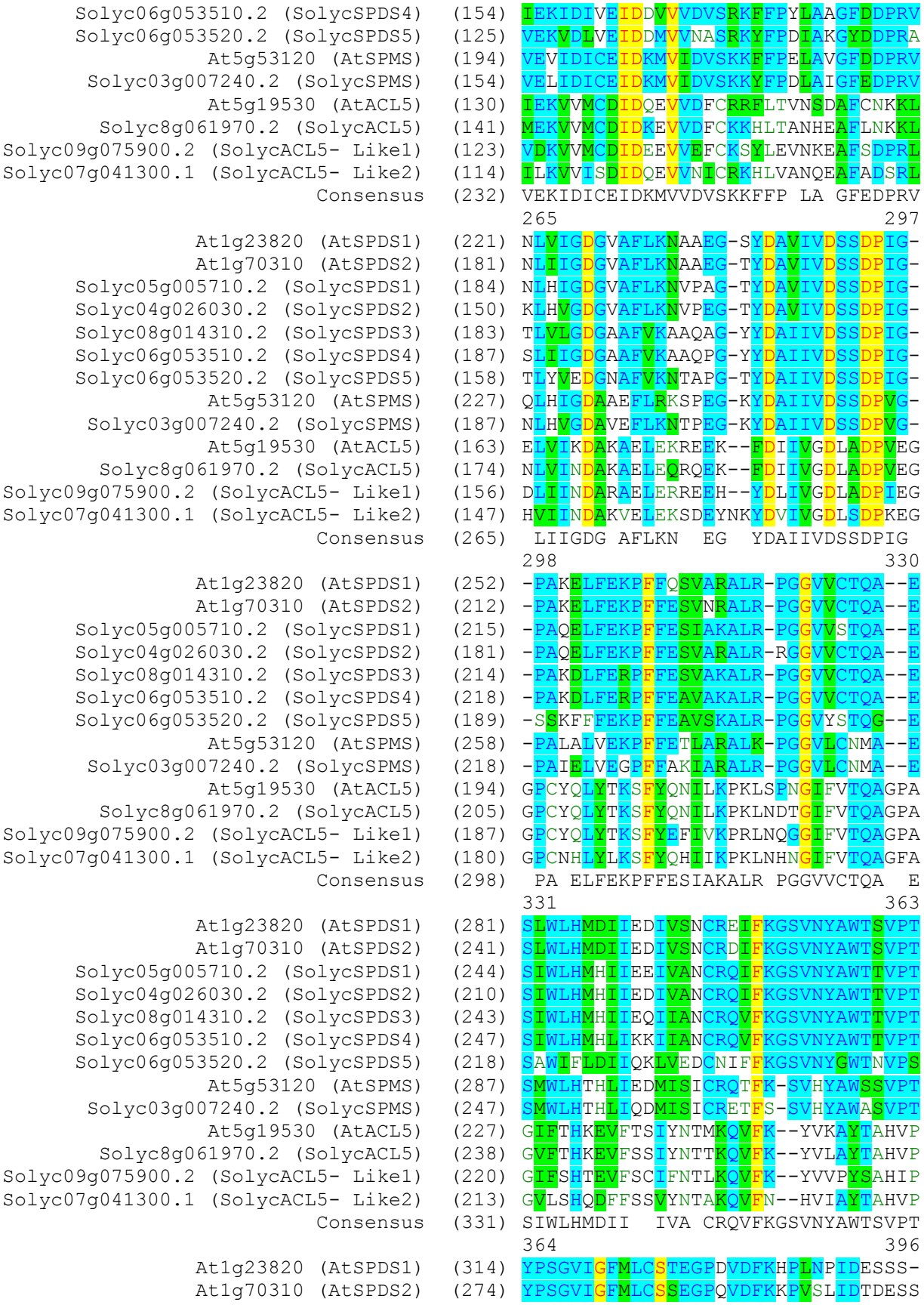
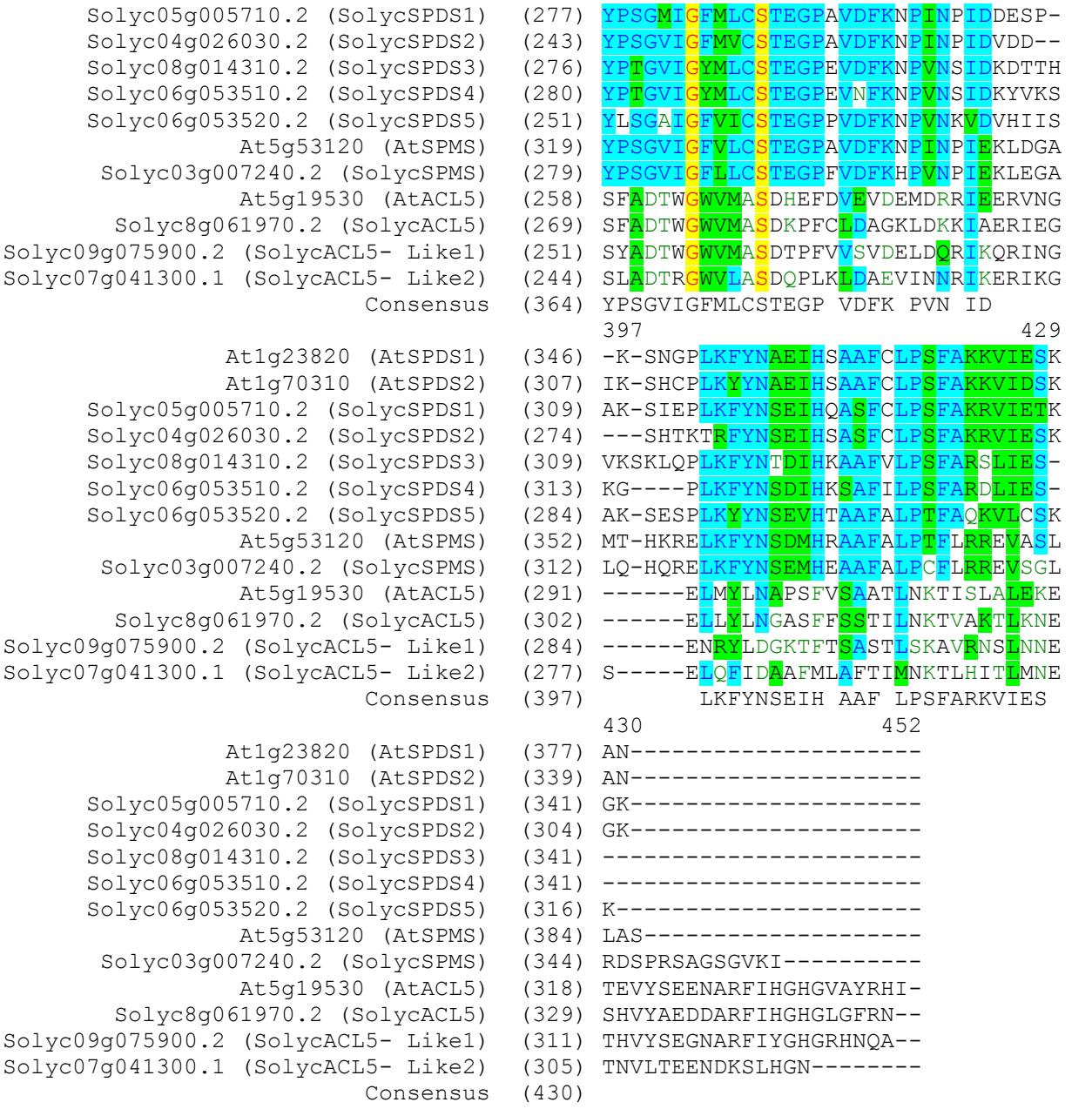
At5g19530 (AtACL5) (38) ----------ETIDDDLKWSFALN--SVLHQG
Solyc8g061970.2 (SolycACL5) (49) ----------EEIDVDLKWSFALN--SVLHKG
Solyc09g075900.2 (SolycACL5- Like1) (31) ----------EEIDNDLRWCFALN--SILHTG
Solyc07g041300.1 (SolycACL5- Like2) (22) ----------ESLGVDLKWSLAIN--SVLYKA
Consensus (100) E LWPGEA SLKVEKVLFQG
133 165
At1g23820 (AtSPDS1) (116) KSDYQDVIVFQSATYGKVLVLDGVIQLTERDEC
At1g70310 (AtSPDS2) (76) KSDYQDVIVFQSATYGKVLVLDGVIQLTERDEC
Solyc05g005710.2 (SolycSPDS1) (79) KSDYQNVLVFQSSTYGKVLVLDGVIQLTERDEC
Solyc04g026030.2 (SolycSPDS2) (45) KSDYQNVMVFQSSTYGKVLSLDGVIQLTERDEC
Solyc08g014310.2 (SolycSPDS3) (78) KSDYQDVMLFESATYGKVLTLDGAIQHTENGGF
Solyc06g053510.2 (SolycSPDS4) (82) KSDYQDVMLFESATYGKVLTLDGAIQHTENGGF
Solyc06g053520.2 (SolycSPDS5) (53) KSKYQDIMIFESLTYGKVIVLDGIIQHTERDVC
At5g53120 (AtSPMS) (95) KSDFQEVLVFESATYGKVLVLDGIVQLTEKDEC
Solyc03g007240.2 (SolycSPMS) (82) KSEFQEVLVFESASYGKVLVLDGIVQLTEKDEC
At5g19530 (AtACL5) (58) TSEYQDIALLDTKRFGKVLVIDGKMQSAERDEF
Solyc8g061970.2 (SolycACL5) (69) TSEYQDIALLDTKHFGKILVIDGKMQSAEVDEF
Solyc09g075900.2 (SolycACL5- Like1) (51) ATQYQDIQLLDTKPFGKALVIDGKLQSAEIDEF
Solyc07g041300.1 (SolycACL5- Like2) (42) TTKFQDVTLLDTKHFGKVLVIDGKMQSAEKDEF
Consensus (133) KSDYQDVMLFESATYGKVLVLDGVIQ TERDEC
166 198
At1g23820 (AtSPDS1) (149) AYQEMITHLPLCSIPNPK----------
At1g70310 (AtSPDS2) (109) AYQEMITHLPLCSISNPK----------
Solyc05g005710.2 (SolycSPDS1) (112) AYQEMITHLPLCSIPNPK----------
Solyc04g026030.2 (SolycSPDS2) (78) AYQEMITHLPLCSIPNPR----------
Solyc08g014310.2 (SolycSPDS3) (111) PYTEMIVHLPLGSIPSPK----------
Solyc06g053510.2 (SolycSPDS4) (115) PYTEMIVHLPLGSIPSPK----------
Solyc06g053520.2 (SolycSPDS5) (86) SYVEMIVHLPLASIHNPK----------
At5g53120 (AtSPMS) (128) AYQEMIAHLPLCSISSPKNVISHLKKFSLSGFL
Solyc03g007240.2 (SolycSPMS) (115) AYQEMIAHLPLCSIKSPK----------
At5g19530 (AtACL5) (91) IYHECLIHPALLFHPNPK----------
Solyc8g061970.2 (SolycACL5) (102) IYHECLIHPALLCHPNPK----------
Solyc09g075900.2 (SolycACL5- Like1) (84) IYHECLVHPPLLHHSNPR----------
Solyc07g041300.1 (SolycACL5- Like2) (75) IYHESLIHPALLLHDNPR----------
Consensus (166) AY EMIVHLPL SIPNPK
199 231
At1g23820 (AtSPDS1) (167) ----------KVLVIGGGDGGVLREVARHAS
At1g70310 (AtSPDS2) (127) ----------KVLVIGGGDGGVLREVARHSS
Solyc05g005710.2 (SolycSPDS1) (130) ----------KVLVIGGGDGGVLREVSRHSS
Solyc04g026030.2 (SolycSPDS2) (96) ----------KVLVIGGGDGGVLREVSRHSS
Solyc08g014310.2 (SolycSPDS3) (129) ----------KVLIIGGGIGFTLFEVLRYPT
Solyc06g053510.2 (SolycSPDS4) (133) ----------KVLIIGGGIGFTLFEVSRYPS
Solyc06g053520.2 (SolycSPDS5) (104) ----------KVLIIGGGMGFTLREVLRYPS
At5g53120 (AtSPMS) (161) YLVACCNKSVNLKVLVVGGGDGGVLREISRHSS
Solyc03g007240.2 (SolycSPMS) (133) ---------K---VLVVGGGDGGVLREISRHSS
At5g19530 (AtACL5) (109) ----------TVFIMGGGEGSAAREILKHTT
Solyc8g061970.2 (SolycACL5) (120) ----------NVFIMGGGEGSAAREALRHKS
Solyc09g075900.2 (SolycACL5- Like1) (102) ----------SIFIMGGGEGSTARELLRHKT
Solyc07g041300.1 (SolycACL5- Like2) (93) ----------RVFIMGGGEGSAAREALKHDN
Consensus (199) KVLIIGGGDG LREVSRH S
232 264
At1g23820 (AtSPDS1) (188) IEQIDMCEIDKMVVDVSKQFFPDVAIGYEDPRV
At1g70310 (AtSPDS2) (148) VEQIDICEIDKMVVDVAKQYFPNVAVGYEDPRV
Solyc05g005710.2 (SolycSPDS1) (151) VEQIDICEIDKMVVEVAKQFFPDVAVGYEDPRV
Solyc04g026030.2 (SolycSPDS2) (117) VEQIDICEIDKMVIDVSKQFFPNVAIGYEDPRV
Solyc08g014310.2 (SolycSPDS3) (150) IEKIDIVEIDNVVVDVSRKIFPYLAANFNDPRV


Solyc06g053510.2 (SolycSPDS4) (154) IEKIDIVEIDDVVVDVSRKFFPYLAAGFDDPRV
Solyc06g053520.2 (SolycSPDS5) (125) VEKVDLVEIDDMVVNASRKYFPDIAKGYDDPRA
At5g53120 (AtSPMS) (194) VEVIDICEIDKMVIDVSKKFFPELAVGFDDPRV
Solyc03g007240.2 (SolycSPMS) (154) VELIDICEIDKMVIDVSKKYFPDLAIGFEDPRV
At5g19530 (AtACL5) (130) IEKVVMCDIDQEVVDFCRRFLTVNSDAFCNKKL
Solyc8g061970.2 (SolycACL5) (141) MEKVVMCDIDKEVVDFCKKHLTANHEAFLNKKL
Solyc09g075900.2 (SolycACL5- Like1) (123) VDKVVMCDIDEEVVEFCKSYLEVNKEAFSDPRL
Solyc07g041300.1 (SolycACL5- Like2) (114) ILKVVISDIDQEVVNICRKHLVANQEAFADSRL
Consensus (232) VEKIDICEIDKMVVDVSKKFFP LA GFEDPRV
265 297
At1g23820 (AtSPDS1) (221) NLVIGDGVAFLKNAAEG-SYDAVIVDSSDPIG-
At1g70310 (AtSPDS2) (181) NLIIGDGVAFLKNAAEG-TYDAVIVDSSDPIG-
Solyc05g005710.2 (SolycSPDS1) (184) NLHIGDGVAFLKNVPAG-TYDAVIVDSSDPIG-
Solyc04g026030.2 (SolycSPDS2) (150) KLHVGDGVAFLKNVPEG-TYDAVIVDSSDPIG-
Solyc08g014310.2 (SolycSPDS3) (183) TLVLGDGAAFVKAAQAG-YYDAIIVDSSDPIG-
Solyc06g053510.2 (SolycSPDS4) (187) SLIIGDGAAFVKAAQPG-YYDAIIVDSSDPIG-
Solyc06g053520.2 (SolycSPDS5) (158) TLYVEDGNAFVKNTAPG-TYDAIIVDSSDPIG-
At5g53120 (AtSPMS) (227) QLHIGDAAEFLRKSPEG-KYDAIIVDSSDPVG-
Solyc03g007240.2 (SolycSPMS) (187) NLHVGDAVEFLKNTPEG-KYDAIIVDSSDPVG-
At5g19530 (AtACL5) (163) ELVIKDAKAELEKREEK--FDIIVGDLADPVEG
Solyc8g061970.2 (SolycACL5) (174) NLVINDAKAELEQRQEK--FDIIVGDLADPVEG
Solyc09g075900.2 (SolycACL5- Like1) (156) DLIINDARAELERREEH--YDLIVGDLADPIEG
Solyc07g041300.1 (SolycACL5- Like2) (147) HVIINDAKVELEKSDEYNKYDVIVGDLSDPKEG
Consensus (265) LIIGDG AFLKN EG YDAIIVDSSDPIG
298 330
At1g23820 (AtSPDS1) (252) -PAKELFEKPFFQSVARALR-PGGVVCTQA--E
At1g70310 (AtSPDS2) (212) -PAKELFEKPFFESVNRALR-PGGVVCTQA--E
Solyc05g005710.2 (SolycSPDS1) (215) -PAQELFEKPFFESIAKALR-PGGVVSTQA--E
Solyc04g026030.2 (SolycSPDS2) (181) -PAQELFEKPFFESVARALR-RGGVVCTQA--E
Solyc08g014310.2 (SolycSPDS3) (214) -PAKDLFERPFFESVAKALR-PGGVVCTQA--E
Solyc06g053510.2 (SolycSPDS4) (218) -PAKDLFERPFFEAVAKALR-PGGVVCTQA--E
Solyc06g053520.2 (SolycSPDS5) (189) -SSKFFFEKPFFEAVSKALR-PGGVYSTQG--E
At5g53120 (AtSPMS) (258) -PALALVEKPFFETLARALK-PGGVLCNMA--E
Solyc03g007240.2 (SolycSPMS) (218) -PAIELVEGPFFAKIARALR-PGGVLCNMA--E
At5g19530 (AtACL5) (194) GPCYQLYTKSFYQNILKPKLSPNGIFVTQAGPA
Solyc8g061970.2 (SolycACL5) (205) GPCYQLYTKSFYQNILKPKLNDTGIFVTQAGPA
Solyc09g075900.2 (SolycACL5- Like1) (187) GPCYQLYTKSFYEFIVKPRLNQGGIFVTQAGPA
Solyc07g041300.1 (SolycACL5- Like2) (180) GPCNHLYLKSFYQHIIKPKLNHNGIFVTQAGFA
Consensus (298) PA ELFEKPFFESIAKALR PGGVVCTQA E
331 363
At1g23820 (AtSPDS1) (281) SLWLHMDIIEDIVSNCRELFKGSVNYAWTSVPT
At1g70310 (AtSPDS2) (241) SLWLHMDIIEDIVSNCRDIFKGSVNYAWTSVPT
Solyc05g005710.2 (SolycSPDS1) (244) SIWLHMHIIEEIVANCRQIFKGSVNYAWTTVPT
Solyc04g026030.2 (SolycSPDS2) (210) SIWLHMHIIEDIVANCRQIFKGSVNYAWTTVPT
Solyc08g014310.2 (SolycSPDS3) (243) SIWLHMHIIEQIIANCRQVFKGSVNYAWTTVPT
Solyc06g053510.2 (SolycSPDS4) (247) SIWLHMHLIKKIIANCRQVFKGSVNYAWTTVPT
Solyc06g053520.2 (SolycSPDS5) (218) SAWIFLDIIQKLVEDCNIFFKGSVNYGWTNVPS
At5g53120 (AtSPMS) (287) SMWLHTHLIEDMISICRQTFK-SVHYAWSSVPT
Solyc03g007240.2 (SolycSPMS) (247) SMWLHTHLIQDMISICRETFS-SVHYAWASVPT
At5g19530 (AtACL5) (227) GIFTHKEVFTSIYNTMKQVFK--YVKAYTAHVP
Solyc8g061970.2 (SolycACL5) (238) GVFTHKEVFSSIYNTTKQVFK--YVLAYTAHVP
Solyc09g075900.2 (SolycACL5- Like1) (220) GIFSHTEVFSCIFNTLKQVFK--YVVPYSAHIP
Solyc07g041300.1 (SolycACL5- Like2) (213) GVLSHQDFFSSVYNTAKQVFN--HVIAYTAHVP
Consensus (331) SIWLHMDII IVA CRQVFKGSVNYAWTSVPT
364 396
At1g23820 (AtSPDS1) (314) YPSGVIGFMLCSTEGPDVDFKHPLNPIDESSS-
At1g70310 (AtSPDS2) (274) YPSGVIGFMLCSSEGPQVDFKKPVSLIDTDESS


Solyc05g005710.2 (SolycSPDS1) (277) YPSGMIGFMLCSTEGPAVDFKNPINPIDDESP-
Solyc04g026030.2 (SolycSPDS2) (243) YPSGVIGFMVCSTEGPAVDFKNPINPIDVDD--
Solyc08g014310.2 (SolycSPDS3) (276) YPTGVIGYMLCSTEGPEVDFKNPVNSIDKDTTH
Solyc06g053510.2 (SolycSPDS4) (280) YPTGVIGYMLCSTEGPEVNFKNPVNSIDKYVKS
Solyc06g053520.2 (SolycSPDS5) (251) YLSGAIGFVICSTEGPPVDFKNPVNKVDVHIIS
At5g53120 (AtSPMS) (319) YPSGVIGFVLCSTEGPAVDFKNPINPIEKLDGA
Solyc03g007240.2 (SolycSPMS) (279) YPSGVIGFLLCSTEGPFVDFKHPVNPIEKLEGA
At5g19530 (AtACL5) (258) SFADTWGWVMASDHEFDVEVDEMDRRIEERVNG
Solyc8g061970.2 (SolycACL5) (269) SFADTWGWVMASDKPFCLDAGKLDKKIAERIEG
Solyc09g075900.2 (SolycACL5- Like1) (251) SYADTWGWVMASDTPFVVSVDELDQRIKQRING
Solyc07g041300.1 (SolycACL5- Like2) (244) SLADTRGWVLASDQPLKLDAEVINNRIKERIKG
Consensus (364) YPSGVIGFMLCSTEGP VDFK PVN ID
397 429
At1g23820 (AtSPDS1) (346) -K-SNGPLKFYNAEIHSAAFCLPSFAKKVIESK
At1g70310 (AtSPDS2) (307) IK-SHCPLKYYNAEIHSAAFCLPSFAKKVIDSK
Solyc05g005710.2 (SolycSPDS1) (309) AK-SIEPLKFYNSEIHQASFCLPSFAKRVIETK
Solyc04g026030.2 (SolycSPDS2) (274) ---SHTKTRFYNSEIHSASFCLPSFAKRVIESK
Solyc08g014310.2 (SolycSPDS3) (309) VKSKLQPLKFYNTDIHKAAFVLPSFARSLIES-
Solyc06g053510.2 (SolycSPDS4) (313) KG----PLKFYNSDIHKSAFILPSFARDLIES-
Solyc06g053520.2 (SolycSPDS5) (284) AK-SESPLKYYNSEVHTAAFALPTFAQKVLCSK
At5g53120 (AtSPMS) (352) MT-HKRELKFYNSDMHRAAFALPTFLRREVASL
Solyc03g007240.2 (SolycSPMS) (312) LQ-HQRELKFYNSEMHEAAFALPCFLRREVSGL
At5g19530 (AtACL5) (291) ------ELMYLNAPSFVSAATLNKTISLALEKE
Solyc8g061970.2 (SolycACL5) (302) ------ELLYLNGASFFSSTILNKTVAKTLKNE
Solyc09g075900.2 (SolycACL5- Like1) (284) ------ENRYLDGKTFTSASTLSKAVRNSLNNE
Solyc07g041300.1 (SolycACL5- Like2) (277) S-----ELQFIDAAFMLAFTIMNKTLHITLMNE
Consensus (397) LKFYNSEIH AAF LPSFARKVIES
430 452
At1g23820 (AtSPDS1) (377) AN----------
At1g70310 (AtSPDS2) (339) AN----------
Solyc05g005710.2 (SolycSPDS1) (341) GK----------
Solyc04g026030.2 (SolycSPDS2) (304) GK----------
Solyc08g014310.2 (SolycSPDS3) (341) ----------
Solyc06g053510.2 (SolycSPDS4) (341) ----------
Solyc06g053520.2 (SolycSPDS5) (316) K----------
At5g53120 (AtSPMS) (384) LAS----------
Solyc03g007240.2 (SolycSPMS) (344) RDSPRSAGSGVKI----------
At5g19530 (AtACL5) (318) TEVYSEENARFIHGHGVAYRHI-
Solyc8g061970.2 (SolycACL5) (329) SHVYAEDDARFIHGHGLGFRN--
Solyc09g075900.2 (SolycACL5- Like1) (311) THVYSEGNARFIYGHGRHNQA--
Solyc07g041300.1 (SolycACL5- Like2) (305) TNVLTEENDKSLHGN--------
Consensus (430)

Supplementary Table 1: Putative cis-regulatory elements identified in the 1 kb promoter regions of polyamine biosynthetic genes of tomato

Cis - element	Function	Number of cis- element																	
		ADC1	ADC2	ODC1	ODC2	SAMDC1	SAMDC2	SAMDC3	SAMDC4	SAMDC5	SPDS1	SPDS2	SPDS3	SPDS4	SPDS5	SPMS	ACL5	ACL5 - Like1	ACL5 – Like2
AAAC-motif	light responsive element	1	1	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0
AAGAA-motif	-	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
ARE	cis-acting regulatory element essential for the anaerobic induction	4	4	1	0	1	0	4	1	1	0	1	0	0	0	1	1	0	1
Box 4	part of a conserved DNA module involved in light responsiveness	1	1	7	1	1	3	0	0	0	1	1	4	1	4	2	3	4	5

CAAT-box	common cis-acting element in promoter and enhancer regions	12	12	25	22	8	26	11	26	30	19	35	24	23	18	26	20	28	27
ELI-box3	elicitor-responsive element	1	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
GATA-motif	part of light responsive element	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
GCN4_motif	cis-regulatory element involved in endosperm expression	1	1	1	0	1	1	2	1	0	0	0	0	0	0	0	0	0	0
GT1-motif	light responsive element	1	2	1	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0

HSE	cis-acting element involved in heat stress responsiveness	1	1	1	0	1	0	0	3	0	3	0	0	2	0	0	2	2	3
I-box	part of a light responsive element	1	1	0	1	1	0	1	0	0	0	0	1	0	0	0	2	0	0
LTR	cis-acting element involved in low-temperature responsiveness	1	1	1	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0
Skn-1_motif	cis-acting regulatory element required for endosperm expression	1	1	2	0	0	1	1	0	1	1	2	2	1	1	1	5	2	0

TATA-box	core promoter element around -30 of transcription start	72	72	106	73	16	82	25	36	63	129	57	74	81	106	105	95	96	67
TC-rich repeats	cis-acting element involved in defense and stress	1	1	0	1	1	2	1	2	1	1	2	1	0	3	0	2	1	1
TCA-element	cis-acting element involved in salicylic acid responsiveness1	1	1	0	0	3	2	0	1	1	1	1	0	0	1	1	0	0	0
TCT-motif	part of a light responsive element	1	1	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	1
TGA-element	auxin-responsive element	1	1	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0

Unnamed__4	-	1	1	2	3	8	1	5	3	1	1	2	6	3	1	2	1	1	3
chs-CMA1a	part of a light responsive element	1	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
5UTR Py-rich stretch	cis-acting element conferring high transcription levels	0	0	1	1	1	0	0	0	1	1	2	2	0	1	1	0	0	0
ABRE	cis-acting element involved in the abscisic acid responsiveness	0	0	1	1	0	0	0	0	0	0	1	0	1	0	1	0	0	0
AC-I	-	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ACE	cis-acting element involved in light responsiveness	0	0	1	2	0	1	0	0	0	1	0	0	1	2	1	0	0	1
AT-rich element	binding site of	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	1	0	0

	AT-rich DNA binding protein (ATBP-1)																		
ATCT-motif	part of a conserved DNA module involved in light responsiveness	0	0	1	0	2	0	0	1	1	0	0	0	0	0	0	1	0	0
Box-W1	fungal elicitor responsive element	0	0	1	2	0	0	0	0	2	2	0	0	0	0	0	0	0	0
G-Box	cis-acting regulatory element involved in light responsiveness	0	0	2	2	1	0	2	2	0	0	2	2	0	1	2	4	2	1
MBS	MYB binding site involved in drought-inducibili	0	0	1	0	1	1	1	0	2	0	0	0	0	1	0	0	1	1

	ty																		
Unnamed__1	60K protein binding site	0	0	1	0	0	0	0	1	0	0	0	0	1	0	1	0	0	1
W box	-	0	0	1	2	0	0	0	2	0	2	0	0	0	0	0	0	0	0
AAGAA-motif	-	0	0	0	2	0	0	0	0	0	0	0	0	0	1	0	0	1	0
AE-box	part of a module for light response	0	0	0	1	0	0	0	2	0	0	0	0	0	2	0	0	0	0
ATGCAAAT motif	cis-acting regulatory element associated to the TGAGTCA motif	0	0	0	1	0	0	0	0	0	0	0	1	0	0	1	0	1	0
Box I	light responsive element	0	0	0	1	0	0	0	1	1	1	1	0	0	2	1	2	1	1
GARE-motif	gibberellin-responsive element	0	0	0	1	1	0	1	1	0	0	0	0	0	0	0	0	0	1
MNF1	part of a light responsive element	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0
O2-site	cis-acting	0	0	0	1	0	0	0	0	0	0	1	1	1	0	0	0	1	0

	regulatory element involved in zein metabolism regulation																		
TCCC-motif	part of a light responsive element	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TGA-element	-	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
as-2-box	involved in shoot-specific expression and light responsiveness	0	0	0	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0
CATT-motif	part of a light responsive element	0	0	0	0	2	0	1	0	0	0	0	1	0	0	0	0	0	0
CGTCA-motif	cis-acting regulatory element involved in the MeJA-	0	0	0	0	1	2	0	1	1	0	0	0	1	0	0	0	0	0

	responsiveness1																		
EIRE	elicitor-responsive element	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0
GA-motif	part of a light responsive element1	0	0	0	0	1	1	0	0	1	0	1	0	0	0	0	0	1	0
GTGGC-motif	part of a light responsive element	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0
P-box	gibberellin-responsive element	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
TGACG-motif	cis-acting regulatory element involved in the MeJA-responsiveness	0	0	0	0	1	2	0	1	1	0	0	0	1	0	0	0	0	0
Box E		0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
chs-CMA2a	TCACTTGApart of a light responsive element	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0

circadian	cis-acting regulatory element involved in circadian control	0	0	0	0	1	0	0	2	0	1	1	1	2	0	1	1	1	0
AT1	part of a light responsive module	0	0	0	0	0	1	0	0	0	0	0	1	1	1	0	0	0	1
ATGCAAAT motif	cis-acting regulatory element associated to the TGAGTCA motif 2	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
CAT-box	cis-acting regulatory element related to meristem expression	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0
Sp1	light responsive element	0	0	0	0	0	1	1	2	1	1	0	1	0	0	0	0	0	0
TATC-	cis-acting	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0

box	element involved in gibberellin-responsiveness																		
Unnamed__11	-	0	0	0	0	0	1	0	1	0	0	0	0	1	0	0	0	1	0
Unnamed__13	-	0	0	0	0	0	1	0	0	0	1	1	0	0	0	0	0	1	0
Unnamed__6	SEF4 factor binding site	0	0	0	0	0	2	0	0	0	1	0	0	0	0	0	0	0	0
AC-II	-	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
AT-rich sequence	-	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	1
ATCT-motif	part of a conserved DNA module involved in light responsiveness	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0
CCAAT-box	MYBHv1 binding site	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
ERE	E thylene-	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0

	responsive element																		
WUN-motif	wound-responsive element	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0
chs-CMA2b	part of a light responsive element	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
AE-box	part of a module for light response 1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
Unnamed__3	-	0	0	0	0	0	0	0	1	1	0	0	0	1	0	1	0	0	0
Unnamed__8	-	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
3-AF1 binding site	light responsive element	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	4	0	0
Box II	part of a light responsive element	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0
Box III	protein binding site	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
TATCCAT/C-motif	-	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
GAG	part of	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0

motif	light responsive element																		
F-box	-	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
AuxRR-core	Cis-acting regulatory element involved in Auxin responsiveness	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
CCGTCC-box	Cis acting regulatory element related to meristem specific activation	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0
HD-Zip 1	Element involved in differentiation of the palisade mesophyll cells	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
HD-Zip 2	Element involved in the control of	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0

	leaf morphology development																		
A-Box	Cis-acting regulatory element	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0
TA-Rich region	enhancer	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0