Accessory Publication

Table S1. SSL proteins sequences used for phylogenetic analysis

Protein sequences were obtained from the following sources: *Arabidopsis* (http://www.ncbi.nlm.nih.gov/ or http://compbio.dfci.harvard.edu/tgi/cgi-bin/tgi/gimain.pl?gudb=arab); poplar (http://genome.jgi-psf.org/annotator/servlet/jgi.annotation.Annotation?pDb=Poptr1_1); rice (http://rapdb.dna.affrc.go.jp/tools/blast); *Aureococcus anophagefferens* (http://genome.jgi-psf.org/annotator/servlet/jgi.annotation.Annotation?pDb=Auran1). Other sequences were from National Center for Biotechnology Information (NCBI; http://www.ncbi.nlm.nih.gov/). Signal peptides were predicted by http://www.cbs.dtu.dk/services/SignalP/

Name	Accession number	Mature protein sequence (secretion signal removed)	Representative SSL in tree (Fig. 2*b*)
AtSSL1	At2g41300	EYKINADQSENSNVGRFGGNYGRLGRLSGSIHHWTGEYRGLEKRPNHS EDNPPSRGWTGEPGLDPRGEGPYVGVTDGRILKWSGEDLGWIEFAYSSPHRKNCSSHKVEPACGRPLGL SFEKKSGDLYFCDGYLGVMKVGPKGGLAEKVVDEVEGQKVMFANQMDIDEEEDAIYFNDSSDTYHFGRD VFYAFLCGEKTGRAIRYDKKTKEAKVIMDRLHFPNGLALSIDGSFVLSCEVPTQLVHRYWAKGPNAGTR DIFAKLPGYADNIRRTETGDFWVALHSKKTPFSRLSMIHPWVGKFFIKTLKMELLVFLFEGGKPHAVAV KLSGKTGEIMEILEDSEGKNMKFISEVQERDGRLWFGSVFLPSVWVLDRQ	
AtSSL2	At2g41290	EGPKHGGESMLTVQIPDFRLIPTTGALGPESFVFDFFGDGPYTGLS DGRIVKWLANESRWIDFAVTTSAREGCEGPHEHQRTEHVCGRPLGLAFDKSTGDLYIADAYMGLLKVGP TGGVATQVLPRELNEALRFTNSLDINPRTGVVYFTDSSSVYQRRNYIGAMMSGDKTGRLMKYDNTKQVT TLLSNLAFVNGVALSQNGDYLLVVETAMCRILRYWLNETSVKSQSHDNYEIFAEGLPGFPDNIKRSPRG GFWVGLNTKHSKLTKFAMSNAWLGRAALGLPVDWMKVHSVWARYNGNGMAVRLSEDSGVILEVFEGKNE NKWISISEVEEKDGTLWVGSVNTPFAGMYKI	

AtSSL3	At1g08470	SISKFPDFKTYKIDMPPLSSLPKERDRQNLLQNSEIRFLNEVQG PESIAFDPQGRGPYTGVADGRILFWNGTRWTDFAYTSNNRSELCDPKPSLLDYLKDEDICGRPLGLRFD KKNGDLYIADAYLGIMKVGPEGGLATSVTNEADGVPLRFTNDLDIDDEGNVYFTDSSSFFQRRKFMLLI VSGEDSGRVLKYNPKTKETTTLVRNLQFPNGLSLGKDGSFFIFCEGSIGRLRKYWLKGEKAGTSEVVAL LHGFPDNIRTNKDGDFWVAVHCHRNIFTHLMAHYPRVRKFFLKLPISVKFQYLLQVGGWPHAVAVKYSE EGKVLKVLEDSKGKVVKAVSEVEEKDGKLWMGSVLMSFIAVYDLP	
AtSSL4	At3g51420	ITLYQLDSFEPASLPADSLITSPTSIPPLLNDRFLTGAEFIGVGLLNN PEDIAYHKDSNLIYTGCVDGWVKRVSVHDSANDSIVEDWVNTGGRPLGIAFGLHGEVIVADANKGLLSI SDGGKKTELLTDEADGVRFKLTDAVTVADNGVLYFTDASSKYDFYQFIFDFLEGKPHGRVMSFDPTTRA TRVLLKDLYFANGISMSPDQTHFVFCETIMRRCSKYYISEERVEVFIQGLPGYPDNIRYDGDGHYWIAL ISEVTTSWKLSMKYLFLRKLIYMAAKYGVELLSIKNAAVLQVDLDGNPIAMYHDHPFSHITSGVKIGNH LYFGSLLHSYITRLDLLKYPAQKKL	
AtSSL5	At3g51430	LYQLDTFDPAPVPSEAYASSTTSIPPLISDKYLTGAEFIGVGLLDK PEDIAYHQDSNLIYTGCIDGWVKRVSVHDSANDSVVEDWVNTGGRPLGIAFGVHGEVIVADAYKGLLNI SGDGKKTELLTDQAEGVKFKLTDVVAVADNGVLYFTDASYKYTLHQVKFDILEGKPHGRLMSFDPTTRV TRVLLKDLYFANGVSMSPDQTHLIFCETPMRRCSKYYINEERVEVFIQGLPGYPDNIRYDGDGHYWIAM VSGASTLWRLSMKYPFLRKITAIAAKYGVELMFMKNAGVLQVDLDGNPIAYYHDQRLSHITTGIKIGNY LYCGNILHSYIIRLDLLKYPAQKKKL	
AtSSL6	At3g51440	ITLYQLDTFDPAHHPADSLISSTASIPPLINERFLTGAEFIGVGLLNS PEDIAYHEDSGFIYTGCVDGWVKRVKVAESVNDSLVEDLVNTGGRPLGIAFGIHGEVIVADAYKGLLNI SGDGKKTELLTEEADGVRFKLPDAVTVADNGVLYFTDGSYKYNLHQFSFDILEGKPHGRLMSFDPTTKV TRVLLRDLYFANGVSLSPDQTHLVFCETPIRRCSKYYINGGRVELFIQGLPGYPDNIRYDGDGHYWIAM PSGVTTLWKLSMKYPFLRKITAMAAKYGYEPMFMENAGVLQVDLDGNPIAYYHDQALSHITTGVKIGNY LYCGSLWHSHILRLDLLKYPAQNKKL	
AtSSL7	At3g51450	KLDTFDPAIVPSDAFTSSATSLPPLINDEFLTGAEFIGVGLLNI PEDIAYHKESNLIYTGCVDGWVKRVKVADSVNDSVVEDWVNTGGRPLGIAFGIHGEVIVADVHKGLLNI SGDGKKTELLTDEADGVKFKLTDAVTVADNGVLYFTDASYKYTLNQLSLDMLEGKPFGRLLSFDPTTRV TKVLLKDLYFANGITISPDQTHLIFCETPMKRCSKYYISEERVEVFTQSLPGYPDNIRYDGDGHYWIAL PSGVTTLWNISLKYPFLRKLTAMVAKYGVDLMFMENAGVLQVDLDGNPIAYYHDPKLSHIATCDKIGKY LYCGSLSQSHILRLDLLKYPAQNKKL	
AtSSL8	At3g57010	PDNLKGTKHVLQDAKTIPLPVDGPESLEFDPQGEGPYV	

		GVTDGRILKWRGEELGWVDFAYTSPHRDNCSSHEVVPSCGRPLGLSFERKTGDLYICDGYFGVMKVGPE GGLAELVVDEAEGRKVMFANQGDIDEEEDIFYFNDSSDTYHFRDVFYVSLSGTKVGRVIRYDMKKKEAK VIMDKLRLPNGLALSKNGSFVVTCESSTNICHRIWVKGPKSGTNEVFATLPGSPDNIRRTPTGDFWVAL HCKKNLFTRAVLIHTWVGRFFMNTMKMETVIHFMNGGKPHGIVVKLSGETGEILEILEDSEGKTVKYVS EAYETKDGKLWIGSVYWPAVWVLDTSVYDSI	
AtSSL9	At3g57020	TLIVPENLEGAKNVLTMAKTIPIPVAGPESIEFDPKGEGPYAA VVDGRILKWRGDDLGWVDFAYTSPHRGNCSKTEVVPTCGRPLGLTFEKKTGDLYICDGYLGLMKVGPEG GLAELIVDEAEGRKVMFANQGDIDEEEDVFYFNDSSDKYHFRDVFFVAVSGERSGRVIRYDKKTKEAKV IMDNLVCNNGLALNKDRSFLITCESGTSLVHRYWIKGPKAGTRDIFAKVPGYPDNIRLTSTGDFWIGLH CKKNLIGRLIVKYKWLGKLVEKTMKLEYVIAFINGFKPHGVAVKISGETGEVLELLEDKEGKTMKYVSE AYERDDGKLWFGSVYWPAVWVLDRK	
AtSSL10	At3g57030	ILVKNSQTGSGIFAPPEISGSRDVFPSAKVVNLTGASGPESIAFDPAGEGP YVGVSDGRILKWRGEPLGWSDFAHTSSNRQECARPFAPELEHVCGRPLGLRFDKKTGDLYIADAYFGLL VVGPAGGLAKPLVTEAEGQPFRFTNDLDIDEQEDVIYFTDTSARFQRRQFLAAVLNVDKTGRFIKYDRS SKKATVLLQGLAFANGVALSKDRSFVLVVETTTCKILRLWLSGPNAGTHQVFAELPGFPDNIRRNSNGE FWVALHSKKGLFAKLSLTQTWFRDLVLRLPISPQRLHSLFTGGIPHATAIKLSESGKVLEVLEDKEGKT LRFISEVEEKDGKLWIGSVLVPFLGVYDL	
AtSSL11	At1g74000	TKKSSFQKLPVPGNRTGPEAFAFDSTGKGFYTGVTGGKILKYLPKKG YVDFAQITNSSKSSLCDGALGTTNVEKCGRPAGIAFNTKTGDLYVADAALGLHVIPRRGGLAKKIADSV GGKPFLFLDGLDVDPTTGVVYFTSFSSTFGPRDVLKAVATKDSTGKFFKYDPSKKVVTVLMEGLSGSAG CAVSSDGSFVLVGQFTKSNIKRYWIKGSKAGTSEDFTNSVSNPDNIKRIGSTGNFWVASVVNSATGPTN PSAVKVSSAGKVLQTIPLKDKFGDTLVSEVNEYKGQLYIGALFGPFAGILKL	
AtSSL12	At1g74020	DDASFQKLPVPETRSGPEAFAFDSTGKGFYTGVSGGKILKYLPETGY VDFAQITESSNSSWCDGTIGTALAGRCGRPAGIAFNEKTGDLYVADAPLGLHVISPAGGLATKITDSVD GKPFKFLDGLDVDPTTGVVYFTSFSSRFSPIQVLIALGLKDATGKLYKYDPSTKVVTVLMEGLSGSAGC AVSSDGSFVLVSQFTKSNIKRYWIKGPKAGSSEDFTNSVSNPDNIKRIGSTGNFWVASVVNKIIVPTNP SAVKVNSNGEVLQTIPLKDKFGDTLLSEVNEFEGNLYIGTLTGPFAGILKLEKGSCPAT	
AtSSL13	TC287152	FHMSPIGGREFKPVKHEVAPYKEVMGSWPRDNLSR LGNHGKLEFVDQVFGPESLEFDSLGRGPYTGLADGRVVRWMGEAIGWETFSVVTSKWSEEACVRGVDST TNKQWKHEKLCGRPLGLRFHKETGNLYIADAYYGLLVVGPEGGIATPLATHVEGKPILFANDLDIHRNG SIFFTDTSKRYDRANHFFILLEGESTGRLLRYDPPTKTTHIVLEGLAFPNGIQLSKDQSFLLFTETTNC	PtSSL8

		RLVKYWLEGPKMGEVEVVADLPGFPDNVRINEEGQFWVAIDCCRTPAQEVLTNNPWIRSIYFRLPIPMK LLAKTMGMRMYTVISRFDEEGKVLEVLEDRQGKVMKLVSEVREVQGKLWIGTVAHNHIATLPYPLTMNQ	
AtSSL14	At1g74010	DDASFQKLPVPDKRSGPESFAFDSTGGFYTGVSGGKILKYVPGKGYVD FAQITDSSNSAWCNGALGTAFAGKCGRPAGIALNSKTGDLYVADAPLGLHVISPAGGLATKLADSVDGK PFKFLDGLDVDPTTGVVYFTSFSSKFGPREVLIAVGLKDASGKLFKYDPATKAVTELMEGLSGAAGCAV SSDGSFVLVSEFIKSNIKKYWIKGPKAGTIEDFSSLVSNPDNIRRVGSTGNFWVASVVNKVVMPTDPRA VKLDANGKVLQTIFLKNEFGNTLLSEVNEFNGHLYIGTLTGPFAGVMKL	
AtSSL15	At5g22020	LYCSIDPFHHCAISDFPNFVSHEVISPRPDEVPWERDSQNSLQKSKILFF NQIQGPESVAFDSLGRGPYTGVADGRVLFWDGEKWIDFAYTSSNRSEICDPKPSALSYLRNEHICGRPLG LRFDKRTGDLYIADAYMGLLKVGPEGGLATPLVTEAEGVPLGFTNDLDIADDGTVYFTDSSISYQRRNFL QLVFSGDNTGRVLKYDPVAKKAVVLVSNLQFPNGVSISRDGSFFVFCEGDIGSLRRYWLKGEKAGTTDVF AYLPGHPDNVRTNQKGEFWVALHCRRNYYSYLMARYPKLRMFILRLPITARTHYSFQIGLRPHGLVVKYS PEGKLMHVLEDSEGKVVRSVSEVEEKDGKLWMGSVLMNFVAVYDL	
DmHmu	NP_477159	LPPRTTFPFKDYIVTPPKDLKGALESNFHLEGAERLLEGRVYG PECLIARNNEIYTGIHGGEVIKLTSNHVTHVTKIGQPCEDIYEESRCGRPLGLAFDTQGNNLIIADAYY GLWQVDLGTNKKTLLVSPAQELAGKSINRPAKIFNGVTVSKEGDVYWTDSSSDFTIEDLVFASFANPSG RLFKYNRSKNVSEVLLDELAFANGLALSPNEDFIVVAETGAMRLTKYHLKGAKAGQSEVFVDGLPGLPD NLTPDAEGIWVPLVQSADSEHPNGFTLFTRFPSVRLFLARMLALFELPFRYLNSVYPNKFSQRFIHFVG HMESITVLAPKRTTVVRVDWNGNIVGSLHGFDKSAATISHVLEFQDFLFLGSPTNQYLARVKSPKAKQP TLKVRNVRVEGEGLEASIGPPSKATPKPKAAPSTTTPKPTTTTTTTTPKPTTKTTTTTTTTPKPTTTTT TKKPTTTTTTTTTTTPKPTTTKPPTAKPSTTTTPTTTPKPTTTTTPTTPTTPTPEPSKPKVKRTVPEKPA PVEEEIPSDTQPPKKEKLKVINKQGVNVEL	
DmSSL	NP_651656	FPFEQYFIKPARDLNGTLELNNHLNGARKLWKDQIFG PECLIVLEDKIYTGIHSGEVIRLNNEESVQPITKIGQPCDYIFDDELCGYPVGLALDTQGNNLIVSDAY YGIWQVDLETKKKTVLVPAEQILPGKGANRRAKLFNSLVISRQGDIFWTDSFSEDFVFAAFANPSGRYD RVKKTNEVLLDELSFANGLALSPSEDFIILAETTAMRLRRYYLKGSRAGESEVFVEGLPGCPDNLTADE EGIWVPLSVASDSQNPNLFAVLAPYPRLRSFLARLVALMRLPLRVLNHIYPNDIAARLFHSFNDLVIRN APKRSTVVRVDWNGNIVRSLHGFDRSASGISHVLEVKGHLYLGSPFNHYVAKVKLPEEGLKSVKGN	
RsSTR1	CAA44208	SPILKEILIEAPSYAPNSFTFDSTNKGFYTSVQDGRVIKYEG PNSGFVDFAYASPYWNKAFCENSTDAEKRPLCGRTYDISYNLQNNQLYIVDCYYHLSVVGSEGGHATQL ATSVDGVPFKWLYAVTVDQRTGIVYFTDVSTLYDDRGVQQIMDTSDKTGRLIKYDPSTKETTLLLKELH	

		VPGGAEVSADSSFVLVAEFLSHQIVKYWLEGPKKGTAEVLVKIPNPGNIKRNADGHFWVSSSEELDGNM HGRVDPKGIKFDEFGNILEVIPLPPPFAGEHFEQIQEHDGLLYIGTLFHGSVGILVYDKKGNSFVSSH	
OpSTR1	BAB47180	SPEFFEFIEAPSYGPNAYAFDSDGELYASVEDGRIIKYDKPSNK FLTHAVASPIWNNALCENNTNQDLKPLCGRVYDFGFHYETQRLYIADCYFGLGFVGPDGGHAIQLATSG DGVEFKWLYALAIDQQAGFVYVTDVSTKYDDRGVQDIIRINDTTGRLIKYDPSTEEVTVLMKGLNIPGG TEVSKDGSFVLVGEFASHRILKYWLKGPKANTSEFLLKVRGPGNIKRTKDGDFWVASSDNNGITVTPRG IRFDEFGNILEVVAIPLPYKGEHIEQVQEHDGALFVGSLFHEFVGILHNYKSSVDHHQEKNSGGLNASF KEFSSF	
CrSTR1	CAA71255	SPILKKIFIESPSYAPNAFTFDSTDKGFYTSVQDGRVI KYEGPNSGFTDFAYASPFWNKAFCENSTDPEKRPLCGRTYDISYDYKNSQMYIVDGHYHLCVVGKEGGY ATQLATSVQGVPFKWLYAVTVDQRTGIVYFTDVSSIHDDSPEGVEEIMNTSDRTGRLMKYDPSTKETTL LLKELHVPGGAEISADGSFVVVAEFLSNRIVKYWLEGPKKGSAEFLVTIPNPGNIKRNSDGHFWVSSSE ELDGGQHGRVVSRGIKFDGFGNILQVIPLPPPYEGEHFEQIQEHDGLLYIGSLFHSSVGILVYDDHDNK GNSYVSS	
Ch.rSSL1	XP_001694117	TLNPTLPYPAQRFGFAHIDPATLPLDNSPLEGVYARNEVLRKAHKLFDGVI ASAETVAVSPEGNLTLVDKHGFVYEAEPATKVPGAVFTGEWALDLPATYYLGPGRPLGFHHDAAGNLVIA DTLKGLIRLDRTTGAVELLTARVSADSALAPDTPLAYVNDLDIDHDTGVIYFTDSQSIPVYPDRETGTFY DTFQSYLLGFIGGDVAGRLCRYDPATLRTDVLLTGLWFANGVALAADKSYVAVVETNRLRVHRYWLSGP KAGTSDLLIERLPGFPDGMSRAPDGNMWLAIVAPVTGLPKLLKSKVTRFLLAYLPAWARPRIPRWGAALKI SPTGQPLQLLMDPDGSHIAFVSSVTEVAGRLYFGNVRMNYVSYLDLKDV	
PpSSL1	XP_001769001	WFLGTDPLEVSMGRGIVEFDPQHVPPPPMHQFKNFPRDTQNKLQKGEVKWQGQFLGPESLTFDSQGRGPYTGV SDGRIVRYNGPQAGWSTFAYTSRNWSEACTPLSLTTPNHALEHVCGRPLGLRFHKGTGELWIADAYLGIMK VGAQGGQAEVVLSEIDGVPMKFVNDLDFDNDGNLYFTDSSTHWQRRQFLLCLMEADDTGRFIKYNPTTKETEI LIDKLRFSNGVAVSKDGMFVLVAEGRLGRLLRYWVKGGKAGTYEVFADLPGWPDNVRRNEAGDFWIAFHCPRR KLEMILSRYPLLRTLIIRLPISSKNVYWMLAGKPHGMLRYGPDGDFKEILEDQEGKVAKMLSEAEEHDGKLY LGSVLLPQIVVYTLENKS	
PpSSL2	XP_001762386	EWCWWLCGNVIWSPSTLPVGGHHSKCGSLILAQSDKCKLGYYQIHLIVDPLSAHSGRRLERVSRSEVLAWFLA SDPLEFSTLSGIDDFHAQYVALPPFNPLTKITPDAENKLQASAVIGTGDIFGPESIVFDAQGKGPYTGLSDGR IVCYDGPELGWSTFATTSKNRLLRYWIKGPSANTWEVVWIDLPGIPDNVRRNNNCEFWVGFHGKRTFVEMH SGAVPWFRHFVAKLPIPSNYLYKIVAPKAHALIVRYSPEGQVLEVLEDQTGKVVKVVSEVEEHDGKLYIGTVL FPQIDIYTLPT	

PpSSL3	XP_001773641	NRKLECVEKLGEGLVLGPEDVVVARDGSLVVATRDGWVKKVWPRNGTVENWKRVGGYPCGLALGVHGEI LVADPLQGLLNVTDDDEVRCITSTAEGTPITFPDSVTVSGKGQIYFTDASTKHLLHFWHLDVLESRPHGRVLN FDPTTGRTTVLMKGLAFANGIALSPTEDFLVVCESWKYRCVRYWLEGEFKGTLETFIDNLPGLPDNIHLHAPS QTFWLGLVGGRSWLTDLTLKSALLKHFFAKFWHHVTPFNFERGELIAINLHGQVIVSYQDPRGARFSFATGAV IQDNYLYIGSLTEPFLGRLNL	
PpSSL4	XP_001766712	FYSYVDRKSPIDAVPIILAPFPKAEGVYAPNTLLQSVEKLGTGKLLQPEDIIVDPSGKFLYVSTSDGWIKKLY LADGSVEDWKHVGGRPLGLAVGNDGEVLVCEPSTGLLKVTDEGVEVLVTEVEGTKLNFVDAVAVAKDGLIYFT DASTKYPLDDFVLDNLESRPHGRLLVYNPEDKTSRILRKDLYMANGITLSKDDEYLVFAETVAARISKYYLKG NKKGSIEIINENLPGFPDNVHYDSERELLYIGIVGQRDAALDVFLKTPWLKKFVALYESVRGAVDNSNKMGRV LVIDNNGTPVKSYQDPTGKVVGFTTGGVEVDGYVYVGGLRDDYVGRVKL	PpSSL3
PpSSL6	XP_001768837	VHNKLLHGLAKLGDGQLLQPEDMVADPTEMFLYTTNSDGWIKKYYLSNGSVENWVNVGGRPLAIALGNE GEVLVCEPVQGHVQVDKLGTKEILATEAGGIEFGLIDAVTVSSNGLIYFTDASTKHPLGTWHFDMLEGQVSGR IAVYNPEDKSTRVLLDELYFPNGIALSKSEDHFINCETTVARCMKFFLRGEKEGTIKTFIENLPGHPDNIHRN LKNGRFYIGIPGNRNGLTDFVARTPVAKQILAFSPVLYKLLDMRKMGRVFEVDPSGKPLQVYEDPTGEVIGFV TTVVEVDWYLYVGGFRDSFAGRIKVH	PpSSL3
PpSSL7	XP_001759191	WDPPLIGPLAGLNFDWSNWNSSDIRPMLGINEWPCDPDNKLLQAQKLILQDASGPESLAFDSTGAGPYTGVSD GRILRWDGDEARWHTFGVTSSIRTEVCDVHPPLVRNEPVCGRPLGLRFDKHDNLYIADAYFGLLVMGPQGGVA KPVSTQAEGVPFRFVNDLDLDENGTVYFTDSSSRRPRSQCNIVTFEQDRSGRVLRYDPKTQQTTVLARELFYP NGIAVSLDSSFMLLSHTSKSRIGKYWLKGPKLGTLEEFAEVPGFPDNIRRTKEGDFWVALHSRVTKLQNFLAN HWYLLRILYSLPLRFDFISWLTTGTPDAMVIKFNPNGEAIEAFEDRKGQNARLLSFADERDGVLWMSSVFMPS IWTLPLNASAASHL	
PpSSL8	XP_001783026	DPLELSSLSGIEDFQAQYVAPPPYNPLSGISRDVESKLQAAEILGQGEIFGPESLAFDAQGNGPFTGLSDGRI VRYDGPELGWTSFATTSKNRSAICDYNHIPEAKLDYEHICGRPLGLRFDKRTGELYIADAYLGILKVGPQGGL AEPVVTGFNGESFKLCNDLDFDEDGNLYFTVSSTKYQRRQFFLSRLELDNTGRFFKYDPVSKETTVLIQGLRF PNGVAVSKDGTFVVIAESNMARLLRYWLKGPKASTWEVVWMDLPGVPDNVRRNENGDFWVAFHNKRTFME MYTGALPWLRHLVAKLPIPSKYLYAMLAPKPHALILRYSSEGQLLETLEDQPGKVVKVVSEVEEHDGKLYIGT VLFPQVAMYALSSSA	PpSSL2
PpSSL9	XP_001783886	MGRGISHFNPQYVEPTPAHVFKDFPRDNQNKLQNGEIVGRGQFLGPESLTFDAQGRGPYTGVSDGRILR YDGPERGWTTFAYTSKNRSEVCAPKTSLAPNFAFEHVCGRPLGLRFHKETGDLWIADAYLGILKVGPEGGHAE VVLNEIEGVPMKFLNDLDFDDEGNLYFTDSSTRWQRRQFLHSVMEADDTARFIKYNLATKEATVLIDHLRFSN	PpSSL1

		GVAVSKDGTFVVVAECRTGILWRYWLKGSKAGTHELFADLPGWPDNVRCNEAGDFWVALHARRCWSEEFLTKH PWIRYLIIRLPVPVQYVYKLLTGKPSGMILRYGPDGAVKEVLEDQEGKVVKMVSEVEEHDGKLYIGSVLLPYI VIYTLPPPATPATTPAEESTPLSSE	
PpSSL10	XP_001753951	EKLGEGNLVWPEDLVLGPDGKFLYVSCAGSGWIKKLHLADHSVEDWQHVGGVPLGLALGPDGEVLVADA LQGLVKVTDEGVEVLASEVDGSKITFADGVAVDRDGLIYLSDVSFKYNVSAHWFEFWEGKPNGRLIVYDPKAK SSRLLLDNIYSPTGLTLTKDEDALIFTENVVARITKYYVKGDKKGTMEIMNENLPGHPDNIHYNYDEGVYYVG IVGQRSALFDLIWKTPFLKKLVMVLPEAVRLSLDAAARTARLLIIDDSGRALRQYQDPDAKAVGIVTGGIKVG DYLYVSSMKETFVGRIKL	PpSSL3
PtSSL1	LG_VIII000978	MCDGSTNTKLEPVCGRPLGLKFNSATCDLYIADAYYGLLVVGPEGGVATQLAASAEGVPFRFMNALDVDS RTGVVYFTDSSIYFQRREYLLAIISADKTGRLMKYDPNSKKVTVLLKGLAFPNGVAISKDNSFILVAESFTMRI LKFYLVGSEIHGQETFIQLGRFPDNIKRTANGEFWVALNTGRGKIRRLDSTKLQQETSIDWFVDDPVAVRLTSG GKVVNVLDGNGGNALDSVSEVEEYSGLLWLGSSMKPYVGYIKNKK	
PtSSL2	gw1.VI.1078.1	KKVPIVGAFGPESFAFDSLGKGPYASLSDGRIVKWQGNRKGWTDFAVASPNRYACKQQPFAHTEHICGRPL GLCFDETHGDLYIADAYMGLLRVGTQGGLATKIVTHAQGIPLRFTNGLDIDQSSGAIYFTDSSSQYQRRQYLSV VLSGDKSGRLMKYDPVNKQVRVLLSNLTFPNGVALSKDGNFILLAETTRCRILRYWIKTSKAGTVEVFAQLQGF PDNIKRSPRGGYWVGMNSRREKLSELLFSYPWIGNVLLKLPLDIAMLQSTLSKYRGSGLAVRLSENGDILEVFE DNDGDGLKSISEVMEKDGRLWIGSIALPFAGRY	
PtSSL3	gw1.XII.136.1	AFGPESIAFESPGGAFYTGVSDGHIFKYIXQPLTGWTVFAFTSPNRSVAFCDGTTDPNKGPICGRPFGLAYNS FTRLLYIADAYYGLLVADSNGRLAKQIATSAEGQPFVFHNAIDIDPVTGNVYFTDASAVYDLRSISAQVNDSTA RLLKYDPRTSQVTVLLRNLSRAVGLAVSPDGSFLLVSEAIGNRIRRYWLTGPKANTAEIFLSNINVVRPQNIKR TPSGGFWIAAASVK	
PtSSL4	gw1.V.3580.1	FTVLLTILSPVLVATLVFQLDSFEPAPLPIHELTQPPLKALKKNDHMLQGSELVGFKQLIGPEDIAYDSSSGVI YTSCADGWVKRVTINDSVADTIVESWVNTGGRPLGLALGHDNEVIVADAFKGLLKISGEGKVELLADEAEGVKL KLTDAVDIAEDGTIYFTDASYKYNLLEFFWDFLEGKPYGRAISYDPVTKETKVLAHDLYFANGVAVSPDQQYVV FCETFIKYYIQGKKKGSLETFIDNLPGLPDNIHHDGHGHYYIALASGITVALDLALKHPFLRKLMGIYTKYIGE INVVKNSGVFIVDLEGKPTEHYYDPGLALISSGIRIGNHIYCGSVVSPYIVRLDVTKHPAR	
PtSSL5	gw1.I.9767.1	ILAGLFLLLTLYCGIDPWKQSAISGFPDFKSYKVEMPPWSILPKEKDEENLLQRSEIKFLNQIQGPESMAFDPL GRGPYTGVADGRILFYDGQKWTDFAYTSSNRSEICNPQPSPLSYLKNEHICGRPLGLRFDKKTGDLYIADAYFG LMKVGPEGGLATSLSNEAEGIPLRFTNDLDIDDEGNIYFTDSSTTYQRRNFMQLVFSGENSGRVLKYNPTTKET TVLVRNLQFPNGVSLSKDGSFFVFCEGSIGRLRKYWLKGEKAGTSEVLAILPGFPDNVRTNEEGNFWVAIHCRR	

		SFYTHINAQYPNLRTFLLKLPIPMKIQYLLQIGGWPHGLVVKYSPEGKLLQILEDSQGKVVKAISEVEEKDGKL WMGSVLMRFVGVYNL	
PtSSL6	gw1.XVI.1318.1	IPIVGAIGPESFAFDSLGEGPYTSLSDGRIIKWQGDKKRWIDFAVTSPNRDGCGGPHDHHQMEHVCGRPLGS CFDETHGDLYIADAYMGLLRVGPEGGLATKIATHAQGIPFRFTNSLDIDQSSGAIYFTDSSTQYQRRDYLSVVL SGDKSGRLMKYDTASKQVTVLLKNLTFPNGVALSTDGSFVLLAETTSCRILRYWIKTSKAGALEVFAQLQGFPD NIKRSPRGGYWVGINSKREKLSELLFSYPWIGKVLLKLPLDITKFQTALAKYRGGGLAVRLSENGDIVEVFEDR DGNRLKSISEVMEKDGKLWIGSIDLPFAGRFKL	PtSSL2
PtSSL7	eugene3.00150409	ESFRQIFLPPTGFGPESLAFESPGGAFYTGVNDGRVLRYQPPTGSWTSFAITSPNRTIALCDGTTDPDKGPICG RPLGLAYSPSTKLLYIADAYYGLFVADSNGRLAKQIATSAEGQRFVACNALDIDPITGNIYFTDASAVYDLRNS SKALLANDSTGRLMKYDVRKNQVTVLLRNLSVAVGVAVSKDGGFVLVSEFVGNRIRRYWLTGRDAGTSDIFLSN LNIVRPNNIKRTSLGDFRIAAATVRQDSQTLVPIRVRVDEHGRISETVSLEAQYGSTPISEVQQSGLSL YVSSRGVNFVGVYTP	PtSSL3
PtSSL8	LG_VII000152	FVIMDPFKMGPLGHHDFKPVKHDLAPYKQVMENWPRDNKSRLGSGNLEFANEVFGPESLEFDSLGRGPYAGLAD GRVVRWMGEDVGWETFALVSTNWSEKLCARGVDSTTSKQWKHEKLCGRPLGLRFHKESGNLYIADAYYGLLVVG PEGGLATPLATHVRGEPILFANDLDIHKNGSIFFTDTSKRYDRVDHFFILLEGESTGRLLRYDPPTKTTHIVLD GLAFPNGVQLSKDQTFLVFTETTNCRIMKYWLEGPKTGKVELVANLPGFPDNVRLNEKGQFWVAIDCCRTAAQE VLTNNPWVKSVYFRLPIRMRYLAWLMGMKMYTVVSLFNENGEILEVLEDPKGVVMKLVSEVREVEGKLWIGTVA HNHIATLPYP	
PtSSL9	LG_XVI0104	LGPPTIPTSNDHLHSAKILHVSGAVGPESLVFDPNGEGPYTGVADGRVLKWIAGDDGSGSWTDFATTSSNRNEC VRPFAPEMEHVCGRPLGLRFDKKTGNLYIADAYLGLQVVGPTGGLATPVVTELEGQPMRFTNDLDIDEQEDVIY FTDTSMVFQRRQFILSLLTKDKTGRLLKYDKSSKEVTVLARGLAFANGVALSKDSTFLLVAETTTCRILRFWLH GPNAGKSDVFTELPGFPDNIRRNSKGEFWVALHSKKGLFAKVVLSNSWIGKTLLKFPLSFKQLHSLLVGGKAHA TAIKLSEEGKVLDVLEDCDGKTLRFISEVEEKDGKLWIGSVLMPFLGTYNL	
Os01g0698200		QQIKTTDTRWSYHLPLPDGVSGAE SLAFDGKDGLYTGVSDGRVLKWGGSAAGWTTFAYNANYRKIPLCSSSEVP PEERESICGRPLGIRLFRKTGELYIADAYKGLMKVGPDGGEAQVVATEAD GVPFHFLNGLDVDQATGDAYFTDSSSTYTRRFNGEITMNADATGRLLKYD ARTRRVTVLKTDLPYPNGVAVSRDRTHLVVAHTVPCQAFRYWLRGTKAGE YELFADLPGYPDNGGYWVALNQERMRLGAAPAAKHLVGVRLNPDGVEVEE LTAAKGVTLSEVAEQKGKLWLGSVELDYIGMFA	

Os03g53950		MVQGCRCEVVDACVREVRLASPYRIHQIFRFTTPRRLALAHRGDTYKARDEGQCHWRDKA GSATRREGGESEGGERRRRLMASPAVVAFAVAVAVAALAAFCGTDPLRTGSMVDFPGFV PHVVELPDASEMPPHADTRERLRGAEIRFRGEVQGPESVAFDPLGRGPYTGVADGRVVRW DGARWVYFAHSSPNWTAELCGHKASPLDYLKDEHICGRALGLRFDRRTGDLYIADAYFGL LKVGPDGGLATPLATEAEGVRFNFTNDLDLDDDGNVYFTDSSIHYQRRHFMQLVFSGDPS GRLLKYDPNTKKATVLHRNIQFPNGVSMSKDGLFFVFCEGSRGRLSRYWLKGEKAGTVDL FAILPGFPDNVRTNDKGEFWVAIHCRRSIYARMVSRNVRLRKFLLSLPIPAKYHYLMQIG GKLHALIIKYNPEGEVLDILEDTTGQVVRAVSEVEEKDGKLWIGSVLMPFIAVFDYANAS	
Os03g0750700		DPFHLGPLAGVDYRPVRHELAPYR EVMARWPRDNGSRLRHGRLEFVGEVFGPESIEFDRHGRGPYAGLADGRVVRWMGEDAGWE TFAVMSPDWSEKVCANGVESTTKKQHEMERRCGRPLGLRFHGETGELYVADAYYGLMSVG PNGGVATSLAREVGGSPVNFANDLDIHRNGSVFFTDTSTRYNRKDHLNVLLEGEGTGRLL RYDPETKAAHVVLSGLVFPNGVQISDDQQFLLFSETTNCRIMRYWLEGPRAGQVEVFADL PGFPDNVRLSSGGGGGRFWVAIDCCRTAAQEVFAKRPWLRTLYFKLPLTMRTLGKMVSMR MHTLVALLDGEGDVVEVLEDRGGEVMRLVSEVREVGRKLWIGTVAHNHIATIPYPLEEQS SSNVLGD	
Os06g41830		ATARMFKTIDARRSQHLDLTGSLVGPESVAF DGKGHGPYSGVSDGRVMRWNGEAAGWSTYTYSPSYTNNKCAASTLPTVQTESKCGRPLGL RFHFKTGNLYIADAYMGLMRVGPGGGEATVLATKADGVPLRFTNGVDIDQVTGDVYFTDS SMNYQRSQHEQVTATKDSTGRLMKYDPRTNQVTVLQSNITYPNGVAIGVDRTHLIVALTG PCKLMRYWIQGSKAGKSEPFAELPGYPDNVRPDGKGGYWVALHREKYELPFGPDNHLVAM RVSAGGKLVQQMRGPKSLRPTEVMGEEGW	
Os06g41850		ATATTRMFKTIDARRSQHLDLGGSLVGPES VAFDGKGRGPYSGVSDGRIMRWNGEAAGWSTYTYSPSYTKNKCAASTLPTVQTESKCGRP LGLRFHYKTGNLYIADAYMGLMRVGPKGGEATVLAMKADGVPLRFTNGVDIDQVTGDVYF TDSSMNYQRSQHEQVTATKDSTGRLMKYDPRTNQVTVLQSNITYPNGVAMSADRTHLIVA LTGPCKLMRHWIRGPKTGKSEPFVDLPGYPDNVRPDGKGGYWIALHREKYELPFGPDSHL VAMRVSAGGKLVQQMRGPKSLRPTEVMERKDGKIYMGNVELPYVGVVKSS	
Os07g0543600		AAVAKDTSATLVETLPL PTTLVGPESVAFDKFGDGPYSGVSDGRILRWDGADKGWTTYSHAPGYNVA KCMAPKLHPAELTESKCGRPLGLRFHNTSGNLYIADAYKGLMRVGPRGGE ATVLATEADGVPFKFTNGVDVNQVTGEVYFTDSSTRFQRSQHEMVTATGD	

		STGRLMKYDPTTGYLDVLQSGMTYPNGLAISADRSHLVVALTGPCKLVRH WIEGPKAGTSEPFAELPGYPDNVRPDGKGGYWVALHREKTETPYGSDTHL LAVRIGRKGKILQELRGPKNVRPTEKI	
Os07g0614000		CPIQPLAPPPARPPAAARFPPNNLLQNLEKLGEGMLSA PEDVYVDDAGGEVFTATRDGWVRRMQANGSWERWGLVGGTGLLGVAPSADGAMLVCDADK GLLKVDENGRVTLLASTVEGSTIRFADAAIEASDGTVYFSDASTRFSFDNWFLDFFEYRF TGRLLKYDPRTGEASVVLDGLGFANGVALPPDEAFVVVCETMRFRCLRVWLKGEKAGEAE IFVDNLPGNPDNIRLGSDGHFWIALLQVRSPWLDLISRWSLTRRVIASFPALVERTKATL KGAVVAQVSLNGEIVRVLGDSEGNVINMVTSVTEFNGDLFLGSLATNFIGKLSLAKVTRE QEDAVPS	
Os08g07810		QQVKTSHAQFAFHLPLPDGVTGAE SLAFDSSNHGPYTGVSDGRVLRWGGAAAGWTTFAHHENYRKIPMCTTPVAPAEETESMCG RPLGLAFHDRTGDLYIADAYKGLMRVGPRGGEAEVLAAGADGVPFNFVNGIDVDQATGDV YFTDSSTTYPRRFNSEIMMNADATARLLKYDAATKRVTVLRAGLPYANGVAVSRDGSHAV VAHTVPCQAFRYWIKGPNAGEYELLADLPGYPDNVRRDANGGYWVALNQEKARLDATAAA AVAPPAKHLVGVRLDGDGVEVEELTAAKGVTLSEVVERGGKLWLGSVELDFIGLMQ	
Os08g0442200		QRVICEAPPCTTASQVKTTPTNRASHVRLPEGVTGAES LAFDSSNRGPFTGVSDGRVLKWGGDSAGWTTFAYNRNYRSNPTCASSSEETESTCGRPLG LAFHLKTGILYFADAYKGLMRVGPRGGQADVLATEADGVPFNYLNGVDVDQDTGDVYFTD SSTTITRRYQENIMRNRDATARLMKYDAKTKQVTVLKDRLPYANGVAVSHDGRYLVVAHT GPAQVFRYWLKGAKAGQYELFADLPGYPDNVRRDAKGGYWVGLNREKITFNVPAAASPAK HLVGVRLNGDGVEVEELTAASRAVTLSEVVERDRKLWLGSVDLDYVGLLQ	
Os09g0373200		ATTSAGGGDEPTYETKSI DPSLAVMTLPAPVTGPESLAFDGRGDGPYTGGSDGRILRWRGGRLGWTEF AYNSRHKSVGVCSPEKKLVVPESVCGRPLGLQFHHASGDLYVADAYLGLL RVPARGGLAEVVATEAAGVPFNFLNGLDVDQRTGDVYFTDSSTTYRRSQY LLVVAMGDETGRLLRYDARRRRVTVLHSGLPYPNGVAVSDDGTHVVVAHT GLCELRRYWLRGPRAGKSETFAEVPGYPDNVRRDGDGGYWVALSRGADND DVAPTVAVRVTAAGKKKGGGAAVVAEALAGFSFVTVSEVAEQNGTLWIGS VDTPYAGAAVRGRR	Os06g41830
Os09g0374900		AAAAAAGGHGEEMKSIYAGPKVVPVRLGRPAFGPESL	Os06g41850

		AFDHRGGGPYTGVSNGRVLRWRADRRRPGWTEFAHNYKHATVAECAARKKAAAAAESVCG RPLGVQFDRRTGEMYIADAYLGLMRVGRRGGMAEVVAAEAGGVALNFANGVDVDQATGDV YFTDSSTTYKRSDYLLVVLSGDATGRLLRYEPRTGNVTVLESGLAFPNGVAVSADGTHLV VAETASCRLLRHWLRGSNAGATEVLADLPGYPDNVRHAAADGGRGASYWVALNRDKAWTV NGTTPASVAAVRVVVDDGGSKVDVALRGFGGATVSEVVERNGSLWFGSVDTPYVGLLKLT SL	
Os10g39710		LYSPEGFSPAPMPPEYSYGAPVSAPRHEPRALAASER VGEGRLPAPEDLAYDAAGGWLYTGCGDGWVRRVSVSSGDVEDWARTGGRPLGVALTADGG LVVADADIGLLKVSPDKAVELLTDEAEGVKFALTDGVDVAGDGVIYFTDASHKHSLAEFM VDVLEARPHGRLMSFDPSTRRTTVLARGLYFANGVAVSPDQDSLVFCETVMRRCSRYHIN GDKAGTVDKFIGDLPGFPDNIRYDGEGRYWIAISAGRTLQWDVLTRSPFVRKLVYMVDRF VVAVPHNLKNAGAMSVTLAGEPVSMYSDPGLALTTGWLKVGDYLYYGSLTKPYLSRIDLA KSPAEKAQE	
Os11g04660		AILSLDSRSDVRQLEIRDGDVELIPLLDGAAGPESIVFGDAGDG PYTSVSDGRILKWLPPPERRWVEHSCSVPELLDSCRGSKDTKREQECGRPLGLKFNSKTG ELYVADAYLGLRVVSPGENVSRPLVPKRTGSPFSFSNGVEIDHETGVIYFTETSTRFQRR EFLNIVITGDNTGRLLKYDPKENKVEVLVDGLRFPNGLAMSIDGSYLLLAETTTGKILRY WIKTPKASTIEEVAQLPGFPDNIKMSPRGGFWVGLHAKRGKIAEWSISYPWLRKLIFKLP AQRIQRITSFLTGFGRQVIALRLSEDGKTIEAMSVHGDVRKLFKSISEVEEKDGNLWIGS VLSPFLGLYRI	
Os12g04424		MIWWNIMSRSKCDKAINHISTLHKQIRSRSRVAISLIAVTISLIAVIHIGSGLLVPMKAR LVVLAAAVAAAALLVSLDPRSDDVPVLEIWERDVELITVDAGGAVGPESVAFDGDGDGPY TGVSDGRVLKWLPLERRWVEHSSAVIEPHMLDSCRGSKDTKREQECGRPLGLKFNSKTGE LYVADAYLGLRVVSPGENVSRPLVPKWTESPFSFSNGVEIDHETGVIYFTETSTRFQRRE FLNIVITGDNTGRLLKYDPKENKVEVLVDGLCFPNGLAMSNDGSYLLLAETTTGKILRYW IKTPKASTIEEVVQLHGFPDNIKMSPRGGFWVGLHAKRGKIAEWSISYPWLRKVILKLPA QRIQRITSFLTGFGRQVIALRLSEDGKTIEAMSVHGDVRKLFKSISEVEEKDGNLWIGSV LSPFLGLYRI	Os11g04660
cyanobact Am	YP_001522267.1	WPVPIEPVAWEAPSNPGYSGAFESNQRLKDIQKLPLRDNHGPEDIALDSQGRIYASTHEGRIVRLLPDGSSSQ NWVETGGRPLGIDFDKSGHLIIADAFRGLLSIAEDKTITVLATEADGVPISYANDVDIADDGKIYFSDASTKF GAKEWGGTYEASLLDLMEHGGHGRLLVFNPTDGSVQTLLDDLNFANGVALSHDQTYVLVNETGNYRVIRYWLN GPQKGQSETFLKDLPAFPDNISTGLGNRFWVALVSPRSAVLDQLSNKPFMRKVIQRLPAFLRPKAQPYGHIIA	

		VDGSGNVVQNLQDPQGTYPLNTAITETEEYLYIGSLVAPNIGRLSKPDDF
proteobact Hc	YP_431405.1	VINPEAYDAPSAPDLEGSYAPNQRLLEAELIGQGRLDGPEDVAQDA DGAIYAGLANGDIVRINKDGELKVLANTGGRPLGLEFNPAGDLIVADAAKGLLQLDKEGKLTVLTSKADN LPFGVADDVDVGEDGVIYFSDASWRWGVHEHRLDLIESRPHGRLLRYDPGAGVTTVLLEDLYFANGVALS QNEDFVAVCETGRYRVRRYWLQGPKQGTSDILIENLPGFPDGVSSNGAGEFWIALIAPRNGVLDFMHSFP WLKSRMSKLPEALQPQAERYGFVLGVNEQGEILHNLQDPEGERLHTITSVEQVGDVLLFGTLTGDWIGRL SLTREESESPEL
Agla Aa	estExt_fgenesh2_ kg.C_120003	MPPPYDGVAASAVSAADLDLYPGQPGGTPIPPVLEGAWAPNDRLRAATRLFEGIVAGSESVATLDGGDLLLVD KFGWVWISAGGTATPTRTWYVGPGRPLGFHAHRGKLLVACSTKGLLELDLESGALRILANVATDTREPLNYVN DLAVDGATGDVYFSSSTELGVRRDGTRGFYDTMQGYLMNLMRGDHSGRLLKYDARTGATTTLAAGLAYANGVA LSPDASFAVVAETNRARLMRVDLATGEMSVFVDGLPALPDGVTAAADGFWIAGIARPAPVAAKLAPYPALRTL AAHVAPYVFPVFAKPWAGALKVGFDGAPLDALYDPTGERVSTMSCVVQHGARLYLGNLAGDFVSVVDLGS

Table S2. Primers and optimal acquisition temperatures used in Q-PCR

Gene	Forward primer (5′–3′)	Reverse primer (5′–3′)	PCR size (bp)	Acquisition temperature (°C)
GAPDH	TGGTTGATCTCGTTGTGCAGGTCTC	GTCAGCCAAGTCAACAACTCTCTG	262	77
Actin	GAGTTCTTCACGCGATACCTCCA	GACCACCTTTATTAACCCCATTTACCA	180	76
Cyclophilin	TGGCGAACGCTGGTCCTAATACA	CAAAAACTCCTCTGCCCCAATCAA	223	79
Tubulin	ATGTGGGTGAGGGTATGGAA	CCGACAACCTTCTTAGTACTCCTCT	143	78
AtSsl4	GAGCCTCTTGCATTCCTACATTACTAG	TGATGTGCCAGGGACGAAG	127	75
AtSsl5	CACAAAAATGGTAAACGTATCGTCCC	TTGGAATGGCTTGTATGGTTGA	116	72
AtSsl6	TATGGCGGCTAAGTACGGCTAT	GGTGGTTATGTGAGAGCGC	121	77
AtSsl7	ATCGCGTACTACCATGATCCAAA	TCAGGAGATCAAGTCGGAGGATA	115	72

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                                                    C89         C101
CrSTR1    49  AFTFDSTDKGFYTSVQDGRVIKYEGPNSGFTDFAYASPFWNKAFCENSTDPEKRPLCGRTYDISYDYKNS
AtSSL14   40  SFAFDSTG-GFYTGVSGGKILKY-VPGKGYVDFAQITDSSNSAWCNGALGTAFAGKCGRPAGIALNSKTG
AtSSL7    61  FIGVGLLNIPEDIAYHKESNLIYTGCVDGWVKRVKVADSVNDSVVEDWVNTG-----GRPLGIAFG-IHG
Consensus     ......  ......  .....*  ..  *..... ....  * .... .. .**. .*.. . .

                                      W149
CrSTR1   119  QMYIVDGHYHLCVVGKEGGYATQLATSVQGVPFKWLYAVTVDQRTGIVYFTDVSSIHDDSPEGVEEIMNT
AtSSL14  108  DLYVADAPLGLHVISPAGGLATKLADSVDGKPFKFLDGLDVDPTTGVVYFTSFSSKFG  PREVLIAVGL
AtSSL7   125  EVIVADVHKGLLNISGDGKKTELLTDEADGVFKLTDAVTVADN-GVLYFTDASYKYT--LNQLSLDMLE
Consensus     ......  .* . .*  ...*.. .**......*..**.....* . .*..***. *... . .

                                V208              F266
CrSTR1   188  SDRTGRLMKYDPSTKETTLLLKELHVPGGAEISADGSFVVVAEFLSNRIVKYWLEGPKKGSAEFLVTIP-
AtSSL14  176  KDASGKLFKYDPATKAVTELMEGLSGAAGCAVSSDGSFVLVSEFIKSNIKKYWIKGPKAGTIEDFSSLVS
AtSSL7   192  GKPFGRLLSFDPTTRVTKVLLKDLYFANGITISPDQTHLIFCETPMKRCSKYYIS--EERVEVFTQSLPG
Consensus     . .*.*...**.. ...*..* ..*  .* .* *....... *...  .. **.  ... ...  ...

                                M276          H277
CrSTR1   157  NPGNIKRN-SDGHFWVSSSEELDGGQ-------------HGRVVSRGIKFDGFGNILQVIPLPPPYEG-
AtSSL14  246  NPDNIRRVGSTGNFWVAS---VVNKV-------------VMPTDPRAVKLDANGKVLQTIFLKNEFGN-
AtSSL7   260  YPDNIRYD-GDGHYWIALPSGVTTLWNISLKYPFLRKLTAMVAKYGVDLMFMENAGVLQVDLDGNPIAYY
Consensus     .*.**.. ..*..*..* .              .. .......... ...**.... . ....

                     HFE309           LF324
CrSTR1   312  -----EHFEQIQEHDGLLYIGSLFHSSVGILVYDDHDNKGNSYVSS
AtSSL14  298  -----TLLSEVNEFNGHLYIGTLTGPFAGVMKL-------------
AtSSL7   329  HDPKLSHIATCDKIGKYLYCGSLSQSHILRLDLLKYPAQNKKL---
Consensus     ...  ...  . **.*.*. . ..... .
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Fig. S1. Alignment of CrSTR1, AtSSL7 (class A) and AtSSL14 (class B). Numbering of conserved residues above the alignment refers to *Rauvolfia* STR (Ma *et al.* 2006).
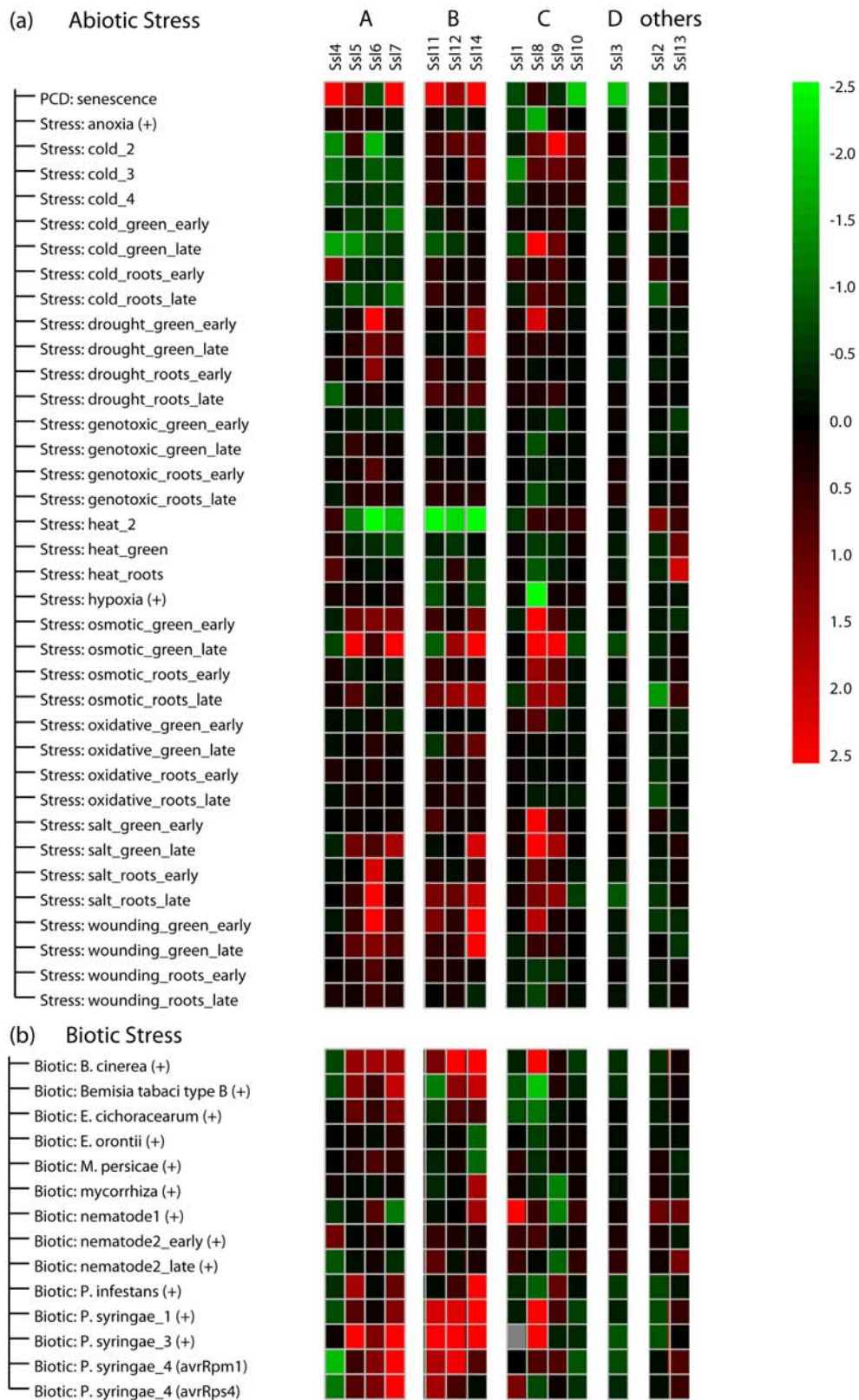
Fig. S2. *In silico* analysis using Genevestigator (Zimmermann *et al*. 2005) showing the response of *AtSsl* genes to a variety of (*a*) abiotic and (*b*) biotic stresses.

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