

Table S1. Secondary data set for stress responsive enzymes and factors of *R. solanacearum* using KO orthologs.

Sl. No.	Enzyme/Name	Coded by	KO No.	Quarry Sequence from <i>Ralstonia solanacearum</i> strain GMI1000
1	Catalase	katE	K03781	MSFPSRLRVSLALAAALTAFAHAGAVTLTRDNGAPVGDNQNSQTAGPNGPVLLQDV QLIQKLQRFDRERIPERVVHARGTGAHGTVFVASKDISDLTRAKVFTPGEEPVFVRFS SVIHSGHSPETLRDPRGFATKFYTREGNWDLVGNLNPVFFIRDAMKFPDMVHSLKPS PDSNVQDPNRFDFFSHQPESTHMLTRVYTDYGTPTSIREMDGNSVHAYKFVNAKG EVHYVKFWKSLQGGKGLSAKEVEAIQGGKDFNHMTRDLIANIDKGNYPKWDLYIQ VLKPEQLAKDFDPLDATKVWPDVPEVKVGTMTLNKNPENVFQETEAALAPSNLV PGIEPSEDRLQGRIFSYADTQLYRVGTNGLQLPVNRPRTSAANYNQDGLNAGARK GSVNYQPSAHADLSDAATVKYSQLPVSGTTQQQRIARTQNFKAQAGDYRSLTAKEQ ANLVSNLAGDLGQVKDDGVKYTMLSYFQKADAGYGRALAAQAVKADPARVESLAA KLQD
2	Catalase	katG	K03782	MGPEPEAAGIEEQGLGWSSRFGTGKGTDAITSGLEVTWTTPTQWSNNFFQNLFGE WELTKSPAGAHQWVAKDAAETIPDAHDPKSAKHLPTMLTTDLRLDFPAYEKISRRFY EHPEQFADAFARAWFKLTHRDMGPRARYLGPVPAEALIWQDPIPAVDHKLIDTQDI AALKARILASGLSVSQLVSTAWASASTFRGSDMRGGANGARIRLAPQKDWANQPA QLAKVLETLESIQGAFFGAQSGGKKVSLADLIVLAGCAGVEQAANKAGHAEVFPFT PGRMDAAQAQTDVESFAVLEPIADGFRNYQKGYTLPAEALLVDKAQLLTAPEM TVLVGGLRVLDTNIGQTRHGVFTQRPESLTNDFVNLDMGTVEWDRKDRDVFEGR DRATGALKWTGTRVDLVFGSHSQLRALAEVYGSADAQAKFVRDFVAWWDKVMNL DRFDLA
3	Nitric-oxide reductase	norB	K04561	MNTNHLRWRLGLIFVLSFGALGYLGRQIYLAAPPQAVVTTAGDVLFTGEQIQRG QQAWLAAGGQQLGTWVGHGSYVAPDWSADWLHREATALQAIHTQQQFSAASLT AAQQAADVTVTKKEEMRRNTYDAARDSITVSKERARAIHGVQAQHFALFGTDPSLAT LRDQYAMATGALPDQADREALAAFFFWTSWAAATDRPGETDVSYSNWPHEPLVG NTMTSDAAMWSMVSIILLAGIAAMLWLHGSGKHEEDAKPLPADPFLNVVATPSMK ATRYFFAVIGLILVQIGMGAITAHYAVEGEAFFGIPLAQVLPYVISRTVHTQLGLVL IATAWLATGLYIAPLLSGREPQFKLGVDLFWALIFIVVGSIAATGWLTGLQHRGADF GFWIGNQGLEYSMGRVWQLLLFVGLFWVALLGRALWPALKTPSESRLIAMVFL SATCIGGFYSTSLVWQHTHYSMIEYWRWWLVHLWVEGFVEVFATAVVALLFTL GLVRAASANRAIVAEIVFLFGGILGLTHHLIFTGTPTSISVGAVFSALEVVPLTLIGL EALQTYRRMRGTPWLGAYKWPVLCFVAVGFVWNTVAGGLGFAINPPASLYYVQGL NMTAAHGHAAALFGVYGMGLGIGLMLFCLRGYARSLHADRLKPAYWGLNIGLAM MVFMSLLPAGIYQAWASITKGMWYARSPEVHVKLMETLVWLRVPGDIVFAGGAFI LALYALRLRRPPSRQAATAPATATR
4	Superoxide dismutase	sodB	K04564	MAHTLPPLPYALDALPHISKETLEFHYGKHHQTYVTNLNNLIPGTEFENLSLEDIVK KSSGGLFNNAQVWNHTFYWNLKPNGGGAPAGALADAINAKWGSFDFKKEEFTK VAIGTFSGWAWLVKKADGSLDLVSTNAATPLTTDAKPLLTCDVWEHAYYIDYRN ARPKYVEAFWSLVNWDVFNFA
5	Superoxide dismutase	sodC	K04565	MKQLVIGLAAIGLMAGCASNAGTGASTGAPAAAGTSALATLAPKSGSNVQGTIKLLQ QGDSRVAMAVDIAGLPPNGMFGFHVHEKGDCSSPDGMSAGGHFNPTGQPHGDPRS GPHHAGDIPMLQSDASGKAVGSIVLNGVTLTPGATSLVGRAVIVHAGMDDYKTQPT GNSGGRVACGVIVAN
6	Hydrogen peroxide-inducible genes activator	oxyR	K04761	MIAMTLTELKYIVAVARERHFGRAAEACFVSQPTLSVAIKKLEDELAVQIFERGASEV SVTPVGEQIVTQAQHVLEQTMAIREIAKQGMPLAGPLRLGVITYTIGPYLLPALVKQ MIDTVPQMPLMLQENFTARVELLKQGEIDCAIMAEPFPEAGLMTVPLYDEPFVAV PRGHALAGSSAVDPEALKQQTMLLLGNGHCFRDHVLNVCPELSRFSQADGIQKTF EGSSLETIRHMASVGITVLPRTSVVPMQPAADLLAYVPFQEPVDRRVVLAWRKS FTRVAAIEAVAKAVACSLPGIKPLPVTPLVH
7	dnak suppressor protein	dksA	K06204	MSSKKLLEAEILKMGDKDYMNQAQLAFFKDRLEKLRDDILKNAGQTTEHLRETVI VPDPADRATIEEEHALELRTRDRERKLLKKVEQSIARIDEGNYGYCDETGEPIGIPRL ARPTATLLEAQERREKQKLFGD
8	nitric oxide-sensitive transcriptional repressor	nsrR	K13771	MRLTDYTDYSLRTLIYVAVHPDVLVTIQIADAFGIPKNHLLIKIVQGLGQNGFLAHTVR GAGTYTLGRPAVEINIGDVVRATEPDSFSLVECFVNLNATRTLKKNDEEITLTTEGFSVLK AYFEVLDITYTLQDLIERPAALNRVLAEGVAVPMPQSGKGRTPKAAPAAGSRTKSG
9	dissimilatory nitrate respiration regulator	DNR	K21563	MHETRDIGDLLKHSPLFEGLDAEDLATLARDSHQIRLARHDFVFHRGDCADGFYVV AVGTIKLVLPAGHGHNVIEFFGPGEYFGEFPMFLNQPHAADAQALEDSSLIRIGKPTI DAALDIHPTLARRMLTGLSSRLHTLMCDIETVNLQSASQRLIGYLLMLPRKLDRARFP CSKTLVASKLGLAPATLSRVLQQLIRDGLILVEGRDVVHSAAALQRLRAG
10	oxidative stress resistance two-component response regulator	ompR	K07659	MENSGHKILVDDDDPRLRDLRLRYLGEQGTVLVAENATAMNKLWLRRERFDLLVL DLMMPGEDGLSICRRLRGANDQTPHIMLTAKGEDVDRIVGLEMAGDDYLPKPFNP LIARIHVLRRRGPAEIPGAPSETPETFAFGDFVLNLAATRLKKNDEEITLTTEGFSVLK VFARHPRQPLSREKLMEMARGREYEVFDRSLDVQISRLRKLIEPDASNPRFIQTVWGL GYVFIPDGAK
11	two-component response regulator	baeR	K07664	MILIVEDEPKLAALMADYLRAAHYETEWDGTRAVQVRVRETSPELVLLDMLPGK DGLEICREVRAFSDLPVMTARVEEIDRLGLGELGADDYICKPFSRELVARIKTILR RVQRSGAQSDSLLQIDNTAYSATLRGQRLDTPVEFRLLSALANAPGRILSRANLLEQ IYDDHRVVDTRVDTHVKNLRRKMELVSPGTIELHSVYGVGYRLDA
12	Histidine kinase	baeS	K07642	MRLSFGITSKLFAALFALSVMVVALAMGAARVWFDTNFDYVNNAREAMAVFAQ SIESVYAEHGNWGVLRNDRQAWYRLIRREIGRTHAGPFGGPRGDAEPVPPFAPPPGD VPPGGLPPPPDAGDRPPQHPPEGPGMHPIWLLDAGRVPVIGDGPVPGSGQWHL HHNGQTVGWLATPQRMHVPEGADQAFQAQLRATWIIAALSVLLAAGVAAILLARG

				VLAPMRRLAHATRRMAEGDYAARVDVHSGDEIGHLADDFNRLAETLEANQKMRR QLTADISHELRTPLAVLRGELEALEDGVRALTPASLTSLQAEVGTLSKLIDDLIELSL ADVGAALAFHMESIDLADTVCSAAQGFPTRLMDKRIALQLDLPTGPSRDAAIQGGDPQR LRQLMQNLLENTLRYTDAGGTLRIHVHRAGAWWCLDPVQDSAPGVPEAMLPRVDFDR LFRADPSRGRAGQGAGLGLSLCQTIVQTHGGTIDARSPSLGGLWAIARLPAANSSVAD HDPDR
13	periplasmic protein	cpxP/ spy	K06006	MFAVTPRRSLAAVAAGLLLSCAVAYAQSSAPEASPRPPMAPHGMHPMPGGPGFMGP HHGGLFLHGLKLTEAQRDKVFAIEYAQMPELREQRKAIEHARRDLREMVVSGQYDE ARSRALTDALGRAVARETQLRAQADAKILQVLTPEQRKQISDREAQRVAAMEEEAG PPPQPM
14	captular synthesis response regulator	rcsB	K07687	MQAPVRFIAADHDPGVVAAVRHLCRVEGFEVVGEATSADGLLALLGRVHCDVVIT DYAMPASRHGDGIVLLEFLRRHPGVRVVVLTMLETHAVVDRMLRAGIRVIAKAD SPHHILEGVHAALAGRAYLSPRFGPRLDSAHPGHAPDDHGALDRLGKREVLRLMY VGGETVSEIARRLNRSVKTISAQKQKSMRKLRLATEAALDFAAQHGLLGTGR
15	histidine kinase	rcsC	K07677	MPQRLTKTGRYSRRVLYGCTAALSIAIVGAVLLGRGIIDQYGRQVAVFVTSGE VRTEVDGLSARLAQFADLYEGVWNLQNDVVPTRRYAGKLAADRATVTGADLT ATPVTLISSLDRLPADGARLAMALRVLRDVSGAPLMDAQKLGVTLDGFLYTPDATFL AAPALRPADLRSAREQGPQPFIRERIAAVEQRIASSAPEAVRGRRLWYPADETNGH ASVSQILVPMYRDNRVLTIALTLPDAQFTRFFLRKESRRPGFFLLSQTGQSRSLGDL ADLEERRLLDTVLANADWSRQAGAEPTTFYKDGVEFVSRRRAGPDWIAVYAYRWQ DVWSDQLQHEFFAGMVFCVLVLGLLWATAAYFDLRVTRPLLSDAKKLIEAEHFSKAI DTLPIGIGVYSPETDSILLENSAVRMLGNVSNEQRLRFYRVVMHERDAEPVPGARH SFIEVRWERAEGQSSYIGVASSWTRFGGRSAVLLGLVDMNERKANEILLMEAKQTA DEANRAKSMFLAIVGHEIRTPLHGAMGHLELLARSALSLEQREWVDMTSRSFDALLT LVNDLLDSTKLEANALQISPVMPNEVLERCARSFGAIVQGGVAFHCITDPDLDL VVDGDDQRLTQILQNLLSNAKFTERTGITIASRCLKEAPVGRRLDGLGILLHLKRELD AMQSTIFNPLAQADDSISRRFGGTGLGLFLCRNLAHLMGGRISVRSEPGIGSAFRVDL PFAQNTAPAPPPVLTGLSVELLCPVSQWRGMLAERLRRWG ATVRPAEASAAEPLHIRLAVEADGRAWHAADLGTVPLLGTVFVTAKGPLHAHRDGO KIEVSSFTREGLLAALTELTGAARPAETPVSMVDEGLGADLDLVAEDDAVNRTL RHQLAALGCQRVRVAVDGVEALEMWLERRADLVITDLGMPRLDGLLHLKRELD PRARVIATSASVSAEIKADVEQFSSLLQKPVSLGDLRRLRQEMLSRTASPTPAVAEPV RADALDALLRQAFRTEWNERKKSIEQALAGKMDALRRRVHRLQGALMALGADA LVEELRGLQDIYSRADWALIAIRCHQLLAHVDASVG
16	RNA polymerase sigma-70 factor	rpoE (σE)	K03088	MTIAPEQLDALRPHLLRFAQLQLRDPALEDVADTVLAVLEHPERFAGNASLKTY VIGILKHKIIDAIRSGRREVRVSLLAGGASDETDQRTDEAVFDALFAADGHYLTTPSD WGNPDAAALSRRFEFDILQMCVDRLPPRVGRVFMREWLELETDEICQLEITATNA WELFYARMRLRACLDLHWFNGQAAA
17	sigma-E factor negative regulatory protein	rseA	K03597	MEFWYREGMQAQMQAADAGFAERISALMDGEVAAHEAAAVELAKDGEGAGHW REYQLIGDALRSEDLLGAHSTEAFLGRFSAKLDAEPHLLVPAVAQRAQTEERHRLV RPSWVRRVVPSTAVAAA VAAVSWVVPQLRGPTGSGDASPALVAKAQQGAGAQA VTVSAAENTPMIRDARLDEYLSAHRQSATNGVVVPYLRAVANGAASTQDSSQE
18	serine protease	degQ (degS)	K04772	MLRRFWLFFAQAVTVVLAVVFWIATLKPEWLQRGKVAVQSGSPIVALKEVAPLGHS GTTSNSYAEAAKVAMPVAVNIFSSKNAPKRNNPQANADPWFRFFFGDRLPEQRQEP TASLGSGVIVSPEGYILTNNHHVVDGADEIEVALTDGRKANAKVVGTDPEITDLAVLKI SLTNLPAITLGRLENVRVGDVLAIGNPFGVGQTVTMGIVSALGRSHLGINTESIIFQ TDAAINPGNSGGALVDAEENLLGINTAIYRSRGGSLGIGFAIPVSLAKQVMFENISTGS VVRGWIGVEPQDVTPEIAESFGLSRKDGALIAAVVQGGPADRAGLRPGDILINVGES IQDTTALLNSIAQLKPSTEAKVTVSRKGKPVELTIMVGKRPVPVRNVPMPSPEDQEP Q
19	recombination protein	recA	K03553	MEDGKKAASMSAEKQKALAAALAQIEKQFGKGSIMKMGDAEVEPVQVVSTGSLGL DVALGVGGLPRGRVVEIYGPESGKTTLTLQVVAEMQKLGGTCAFIDAHEHALDVTY ADKLGKVPDILLISQPDTEQALEIADALVRSGVDLIVDSVAAVLPKAEIEGEMGD ALPGLQARLMSQALRKLTGTIKRTNCLVIFINQIRMKIGVMFGSPETTTGGNALKFYA SVRLDIRRIGSIKKGDEVVGNETKVKVKNKVAPPFREAIFDILYAGVVSREGEIIDL VEAKVVEKSGAWYSYNGERICQGRDNCREFLRENAELAREIENKVREHLGVTMPMA VTLAEVEED
20	recA repressor	lexA	K01356	MATLTTRQQIYDLIHQTIQRTGFPPTRAEIAAEFGFSSPNAAEEHLRALARKGVIELT PGASRGIRLRAEGGASPHQFSLPSMGLMQLTLPLVGRVAAGSPILAAEHIDRQYQVD PSLFSSRPDFLLKVRGMSMRDAGILDGDLAVQRAAEANGKIVVARLGDDVTVKR FQRKGRQVELIAENPDFEPIHVDLDRDEFQLEGLAVGLIRPAAP
21	rna polymerase sigma (sigma-38) factor	rpoS (σS)	K03087	MPRQKAATSANPADETIGAVDGNAPNGRSGRARGAAPASDDVEVVDPLIDEAP AAEPADIADTSDANDSADSEDEEDGEEAAPEEDFRTVLQAEAAADTVQHYNLRIS IKPLLTAEELHFSTLAKAGEFAARQVMIERNLRLVVSIAKGYLNRGVPLLDLIEEGN LGLMHAIEKFDPERGFRFSTYATWWIRQSIERAIMNQARTVRLPVHVIRELNVQLRA KRHLEKSGIDGRDASIEDIAHLLGKTTEEVDVLSNEHTTSLDTPFDLPDGTSLDLFL SDEHGASPDQEVARELSQLMKSWLARLSDKHRYVVERRFGLNHIEPATLEELAAE MGLTRERVRQIQEALVKLRHFASQGVKDAVL
22	fructose operon transcriptional repressor	fruR	K03435	MTVRKDVAAAAGVSVATVSRALAGGPVSEALRRKRVDAVAASGYRPNLSARRLR SQAQTVGLIVSDIRNPFPTSVSRAVEDAAAYAGLRVILCNSDEDPDKEAMYLRIME EERTVTGVLSPTRRIAESPAPVVLGFPVVLIDRAGPACGVDAVVLDNQAAQALAEH LAQHGYRRIGGLFGRTSSTGAERHAGVAAGLARHGLAIDARFILPTAEAAEAETLAW LASGERPDALVASNAQSLGLVLRAIRRLSLDVPGDIAVAGDFNEPWEITAGPGVTVI EQPVYDIGRLAMTMLQERLAQPELPTRRVLLTGRLVARGSTPQRRM
23	GTP diphosphokinase	spot	K01139	MFGPTSQPAAPPRQVVSIAGLTEKLSYLKPADIKLVKEAFHFSDEAHLGQYRQSSEP YITHPVAVAEICAGWKLDVQSIMAALLHDVIEDQGVTKSELAEEKFGPKVAELVDGLT KLDKLEFQSREQAQAESFRKMLLAMARDVRVILVKLADRTHNMRTLDHVPPEKRRR IAGETMEIYAPIAHLRLGLNTTYRELQELSFRIGSPFRYATLEKAVKAARGNRREVVSRI

				LEAAQRALGDAGVSAELTGREKTLYSIYRKMHDKQLSFSQVLDVYGFRVVVETQM HCYMAVGALHGLYKPMMPGKFKDYIAIPKINGYQSVHTTLVGPFGTPVEFQIRTREMN QIAEAGVAAHWMYKQHHDEPDRAQQQAHQWLQSLLDIQSQSGDSQEFLHVKIDL FPDAVYVFTPKGEIRALPRGATALDFAYAVHSDLGNCQVAVKINNALLPLRTELKNG DIVEVVTAPYSKPNPAWLTFVRTGKARAAIRHFLKTAKLDEAIQLGERLLEQALRQL GIDMKAVPAQVWERIVQWTGNGKAREDFADLALGRRVAAVVARRIEIGLQEGGHEG DEALIAAVHAFAGEEAPAVTVSGDEGMAMVFSPPCRPIPGDPIVGYIGKGEGQLQIHVE ECRVAKRLHGKDPEHWIDVMWAEHTTTRAFDVSIKVLVRNTKGILARVAADLTSA ANVAHVSMQEGGGQEATYMTFLIQVHDRVHLADVMRALRRNLDVIRIARDRGGE
24	ferric uptake regulator	fur (ZUR)	K03711	MNSPAPRDVPTTSHPDAPAAAARARLRGLGSRVTEPRVRVLAALMQGDAPLSHQAV CDALPADAGIDRVTVYRVLDWLVAGGIVHKTAGADRVRFRSLAEHDAAREAHHRA HSHFCTQCGRDFCLETATPPAVPTPALPAGFAADHAELTIKCCADCAARHQTGNA PCPN
25	dna protection during starvation	Dps	K04047	MAKKNGGAAAAAQINIGIAEKDRKKIAEGLSRLLADTYSLYLKTNNFHWNVTPMF NTLHLMFETQYNELWTAVDSSAERIRALGYAPGSYSEFARLSSIPEAKGVPAAEDM IRELVAGHESVTRTARSLFPDVKAADEPTADLLTQRMIDIHEKTAWMLRSLLA
26	assimilatory nitrate respiration regulator	Fnr	K21563	MHETRDIGDLLKHSPLFEGLDAEDLATLARDSHQIRLARHDFVFHGRDCADGFYVV AVGTIKLVLPAGAHGHNKVIEFFGPGGEYFGEPPMFLNQPHAADAQALEDSSLIRIGKPTI DAALDIHPTLARRMLTGLSSRLHTLMCDIETVNLQSASQRLIGYLLMLPRKLDRARFP CSKTLVASKLGLAPATLSRVLQQLIRDGLILVEGRDVVIHSAAALQRQLRAG
27	anaerobic regulatory protein	Fnr	K01420	MIPSTLKAQTSADVTRPTPLQLKLVRDATQARQTVSPALSSQCANCMMHWVCIAG AVPSTQQERVDRMVHTWRKVKGGEALFRAGDTFHLYAIRSGSFKTVVSHPNGSSH VTGFQLAGETLGLDGIADRHCTDAIALEDSTVCSMPFHCVEDLCQAIRPLQHRLHQ LLAEEIVRESGLMLLLARLTAEARVATFLLNLSSRMQDRGYSGCFTLRMTREEIGSY LGMQLETVSRALSRFQREGWISVNGKQIELANKAALSEL
28	transcription regulator protein	H-NS	K03746	MATYKDLLSQKAKLEEQLAARQKELAEITAQVRQVVQEYGLTAEDIGLAPKRGGK RAPKAAPVPKYRDPKTGATWTGRGRAPAWIGKNRDKYLIA

Table S2. Secondary data set for stress responsive enzymes and factors of *R. solanacearum* using KO orthologs derived from STRING results

Sl. No.	Enzyme/Name	Coded by	KO No.	Quarry Sequence from <i>Ralstonia solanacearum</i> strain GMI1000
1	lipoprotein	nlpD	K06194	MNPPSPARAGRLAVAMVSAALLAACASSGNQAPVLDRTSRAGSAPAAPLEPPPPGY YRVKRGDTLYSIALRNGQAPRDLVTWNNIPNPNQIEVDQLIRVVPPNADASATGAVA TPVRPPNTTTPIDAAPAAPTPPVVSSGASAGATDGAIALAWPAHQVIGRFDDKANK GIDIGGKRGDVTAADDGKVIHVGLRGYGNLVIKHNDTFLTAYGNNDKVLVTEQS TVKKGQKIAEMGSTDADRVKLHFEVRRNGKPVDPMRFLPPQ
2	serine protease	degQ	K04772	MLRRFWLFFAQAVTVVLAVVFIATLKPEWLQRGKAVVQSGSPIVALKEVAPLGHS GTTNSYAEAAKVAMPAVVNIFSSKNAPKRNNPQANADPWFRFFFGDRLPEQRQEP TASLGSGVIVSPEGYILTNHHVVDGADEIEVALTDGRKANAKVVGTDPETDLAVLKI SLTNLPAITLGRLENVRVGDVVLAIKNPFGVGQTVTMGIVSALGRSHLGINTFENFIQ TDAAINPGNSGGALVDAEENLLGINTAIYSRSGSLGIGFAIPVSLAKQVMESIISTGS VVRGWIGVEPQDVTPEIAESFGLSRKDGALIAAVVQGGPADRAGLRPGDILINVNGES IQDTTALLNSIAQLKPSTEAKVTVSRKGKPVELTIMVGKRPVPVRRNVMPSPEDQEP Q
3	sigma-E factor negative regulatory protein	rseB	K03598	MRESMSKVWHPVAGAGARKLQAVRRSVFLLLCVSALSVAQAQQPEPMRKEAAS WLTKIHRAALKQNYVGTLYQRGSGMHSTRIQHYTDLFNNEYERVEALDGKQREM LRQNDVVRNLIYEVKLVVTEKQENKDSFPALLATTNGDVLDQYDMRHLPAERVAG MDCEVFQLDPKDGFYAYRIWAERSSGLLIRAQTIGEDGKVLQVAFSQVEVGVPS KQKILAAALKSVTGWNQYEVVSQPTNLAEQGWAITSPIKGFQKIREVRRPLGDIAPAG KSSSGFEVQVVFSDGLAGLSLFIQVSEKRSRREGFISQGATHVMVRRADFWLTVV GEVFPATIKQFGAAVDYKPVSAANAASRPASTP
4	DNA repair and recombination protein	recX	K03565	MALPROPLSLKARALGYLSRREHSRAELRRKLAPHAESVDEVEALLDWLEGENWLS NTRFAESVVHRRASRYGTARLMQELKTHELGDDALGEVKAQLQASEMARAKAVW ERRFRPPADMAERAKQVRFMVARGFSRAVVSRIQGADALLDDGDEPV
5	osmolarity sensor histidine kinase	ompR	K07638	MRIPRPAALRRLISVFGSLFWRTFMLIALLIAISLGAWFQSFRIREFEPRAQQIAMQIV SVVKLTRAALLYSDPARRRFLLDLVQNEGKIVPREKEDEYRTPQANPYLTQLVQR EIRNRLGQDVTIATAVNDIPGVVVSFQIEGDDYVVAISPDRFEHVPGQLWLWWSIAA LVLSVLGAAFITSRVNQPLKRLADTARAISAGDDPKSLPEGGGTEVAQANHSFNQMV RDLKQLEADRAVMLAGISHDLRTPLTRLRLETEMSPVDDQTRELMVADIEQMDAIIG QFLDYARPSGEMLEAVDLTELVRDTPVYSAHDDIDLTLKLAPEAIARCNRMETQRI LDNLIENARRYGKTHDTGRAEITVSTALQGNEVVLCAVDRGAGVPADQLALLTRPF YRLESARSEAKGAGLGMSIVSRILQRSGGRLTLENRTPPETGLVVSACYARG
6	sensor histidine kinase transcription regulator protein	envZ	K07638	MRIPRPAALRRLISVFGSLFWRTFMLIALLIAISLGAWFQSFRIREFEPRAQQIAMQIV SVVKLTRAALLYSDPARRRFLLDLVQNEGKIVPREKEDEYRTPQANPYLTQLVQR EIRNRLGQDVTIATAVNDIPGVVVSFQIEGDDYVVAISPDRFEHVPGQLWLWWSIAA LVLSVLGAAFITSRVNQPLKRLADTARAISAGDDPKSLPEGGGTEVAQANHSFNQMV RDLKQLEADRAVMLAGISHDLRTPLTRLRLETEMSPVDDQTRELMVADIEQMDAIIG QFLDYARPSGEMLEAVDLTELVRDTPVYSAHDDIDLTLKLAPEAIARCNRMETQRI LDNLIENARRYGKTHDTGRAEITVSTALQGNEVVLCAVDRGAGVPADQLALLTRPF YRLESARSEAKGAGLGMSIVSRILQRSGGRLTLENRTPPETGLVVSACYARG
7	catalase hydroperoxidase hPII oxidoreductase protein	kata	K03781	MSFPSRSLRVSLALAAALTAHAGAVTLTRDNGAPVGDNQNSQTAGPNPVLQDV QLIKLQRFDRERIPERVHARGTGAGHVFAVASKDISDLTRAKVFTPGETPVFVRF SVIHSGHSPETLRDPRGFATKFTYREGNWDLVGNLNPVFFIRDAMKFPDMVHSLKPS PDSNVQDPNRRFFDFSHQPESTHMLTRVYTDYGTPTSIREMDGNSVHAYKFVNAKG EVHYVKFHWKSLQGQKGLSAKEVEAIQKGFNMTDLIANIDKGNYPKWDLYIQ VLKPEQLAKFDFDPLDATKVWPDVPEVKVGTMTLNKNPENVFQETEQAALAPSNLV PGIEPSEDRLQGRIFSADTQLYRVGTNGLQLPVNRPTSAANYNQDGDNLNAGARK GSVNYQPSAHADLSAATVKYSQPLVSGTTQQQRIARTQNFQAGDYRSLTAKEQ ANLVSNLAGDLGQVKDDGVKYTMSYFQKADAGYGRALAQAVKADPARVESLAA KLQD

Table S3. Normalised (10%) pBLAST 2.2.26 score for the SRGs of *R. solanacearum*.

	FJAT15252	FJAT1458	FJAT1458	FJAT1463	FJAT1463	FJAT15249	FJAT15252	FJAT15249	T78	EP1	T60	FJAT454	FJAT448	FJAT448	SL3882
katE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
katG	98.71	98.71	98.71	98.71	98.71	98.71	98.71	98.71	98.82	98.39	98.82	98.71	98.71	98.71	98.82
norB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sodB	81.73	81.73	81.73	81.73	81.73	81.73	81.73	81.73	81.73	81.73	81.73	81.73	81.73	81.73	81.73
sodC	86.63	86.63	86.63	86.63	86.63	86.63	86.63	86.63	86.63	87.19	86.63	86.63	86.63	86.63	86.63
oxyR	96.11	96.11	96.11	96.11	96.11	96.11	96.11	96.11	96.11	95.65	96.11	96.11	96.11	96.11	96.11
dksA	90.32	90.32	90.32	90.32	90.32	90.32	90.32	90.32	90.32	89.61	90.32	90.32	90.32	90.32	90.32
nsrR	100	100	100	100	100	100	100	100	100	100	100	100	100	100	100
dnr	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ompR	92.18	92.18	92.18	92.18	92.18	92.18	92.18	92.18	92.18	92.18	92.18	92.18	92.18	92.18	92.18
baeR	35.31	35.31	35.31	35.31	35.31	35.31	35.31	35.31	35.31	35.08	35.31	35.31	35.31	35.31	35.31
baeS	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
gmK	100	100	100	100	100	100	100	100	99.34	99.34	99.34	99.34	99.34	99.34	99.34
rcsB	99.32	99.32	99.32	99.32	99.32	99.32	99.32	99.32	99.32	99.54	99.32	99.32	99.32	99.32	99.32
rcsC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
rpoE	90.27	90.27	90.27	90.27	90.27	90.27	90.27	90.27	90.27	90.52	90.27	90.27	90.27	90.27	90.27
rseA	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.7	60.23	60.7	60.7	60.7	60.7	60.7
degS	94.42	94.42	94.42	94.42	94.42	94.42	94.42	94.42	94.42	94.42	94.42	94.42	94.42	94.42	94.42
recA	82.15	82.15	82.15	82.15	82.15	82.15	82.15	82.15	82.15	82.15	82.15	82.15	82.15	82.15	82.15
lexA	99.77	99.77	99.77	99.77	99.77	99.77	99.77	99.77	99.77	99.77	99.77	99.77	99.77	99.77	99.77
rpoS	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82
fruR	85.03	85.03	85.03	85.03	85.03	85.03	85.03	85.03	85.03	85.03	85.03	85.03	85.03	85.03	85.03
spoT	98.48	98.48	98.48	98.48	98.48	98.48	98.48	98.48	98.48	98.35	98.48	98.48	98.48	98.48	98.48
fur	71.22	71.22	71.22	71.22	71.22	71.22	71.22	71.22	71.22	71.22	71.22	71.22	71.22	71.22	71.22
dps	88.92	88.92	88.92	88.92	88.92	88.92	88.92	88.92	89.21	88.92	89.21	88.92	88.92	88.92	89.21
fnr	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
rpoA	88.87	88.87	88.87	88.87	88.87	88.87	88.87	88.87	88.87	88.87	88.87	88.87	88.87	88.87	88.87
h-ns	96.34	96.34	96.34	96.34	96.34	96.34	96.34	96.34	92.15	96.34	96.34	96.34	96.34	96.34	96.34
katA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
envZ	93.26	93.26	93.26	93.26	93.26	93.26	93.26	93.26	93.26	93.26	93.26	93.26	93.26	93.26	93.26
ompR	93.26	93.26	93.26	93.26	93.26	93.26	93.26	93.26	93.26	93.26	93.26	93.26	93.26	93.26	93.26
nlpD	78.34	78.34	78.34	78.34	78.34	78.34	78.34	78.34	78.34	78.34	78.34	78.34	78.34	78.34	78.34
degQ	94.42	94.42	94.42	94.42	94.42	94.42	94.42	94.42	94.42	94.42	94.42	94.42	94.42	94.42	94.42
recX	96.21	96.21	96.21	96.21	96.21	96.21	96.21	96.21	96.21	97.16	96.21	96.21	96.21	96.21	96.21
rseB	92.84	92.84	92.84	92.84	92.84	92.84	92.84	92.84	92.84	93.24	92.84	92.84	92.84	92.84	92.84

Table S3. (Cont.)

	FJAT454	SEPPX05	MAFF 211471	MAFF 211472	RS24	HA4- 1	FJAT91	FJAT91	FJAT91	SL3300	FJAT15353	FJAT15353	FJAT15353	FJAT1303	FJAT1303
katE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
katG	98.71	98.28	98.82	98.82	98.39	98.82	98.82	98.82	98.82	98.82	98.39	98.39	98.39	98.39	98.39
norB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sodB	81.73	80.96	81.73	81.73	81.73	81.98	81.73	81.73	81.73	81.73	81.73	81.73	81.73	81.73	81.73
sodC	86.63	86.63	86.07	86.07	87.19	86.63	86.07	86.07	86.07	86.63	86.63	86.63	86.63	86.63	86.63
oxyR	96.11	96.11	96.11	96.11	95.65	96.11	96.11	96.11	96.11	96.11	96.11	96.11	96.11	96.11	96.11
dksA	90.32	90.32	90.32	90.32	90.32	90.32	90.32	90.32	90.32	90.32	90.32	90.32	90.32	90.32	90.32
nsrR	100	99.72	100	100	100	99.72	100	100	100	100	99.72	99.72	99.72	100	100
dnr	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ompR	92.18	92.18	92.18	92.18	92.18	92.18	92.18	92.18	92.18	92.18	92.18	92.18	92.18	92.18	92.18
baeR	35.31	35.31	35.31	35.31	35.08	35.08	35.31	35.31	35.31	35.31	35.31	35.31	35.31	35.08	35.08
baeS	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
gmK	99.34	100	99.34	99.34	99.34	99.34	99.34	99.34	99.34	99.34	99.34	99.34	99.34	99.34	99.34
rcsB	99.32	98.63	99.77	99.77	98.86	99.77	99.77	99.77	99.77	99.32	99.77	99.77	99.77	99.77	99.77
rcsC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
rpoE	90.27	90.27	90.27	90.27	90.52	90.52	90.27	90.27	90.27	90.27	89.03	89.03	89.03	89.03	89.03
rseA	60.7	60	60.7	60.7	60.23	60	60.7	60.7	60.7	60.7	60.23	60.23	60.23	60.23	60.23
degS	94.42	94.42	94.42	94.42	94.42	94.17	94.42	94.42	94.42	94.42	94.42	94.42	94.42	94.42	94.42
recA	82.15	82.15	82.15	82.15	82.15	82.15	82.15	82.15	82.15	82.15	82.15	82.15	82.15	82.15	82.15
lexA	99.77	100.7	99.77	99.77	99.77	99.77	99.77	99.77	99.77	99.77	99.77	99.77	99.77	99.77	99.77
rpoS	82	76.08	82	82	82	82	82	82	82	82	82	82	82	82	82
fruR	85.03	85.03	85.03	85.03	85.03	85.03	85.03	85.03	85.03	85.03	85.03	85.03	85.03	85.03	85.03
spoT	98.48	98.48	98.48	98.48	98.48	98.48	98.48	98.48	98.48	98.48	98.48	98.48	98.48	98.48	98.48
fur	71.22	71.22	71.22	71.22	71.22	71.22	71.22	71.22	71.22	71.22	71.22	71.22	71.22	71.22	71.22
dps	88.92	89.21	89.21	89.21	88.92	88.92	89.21	89.21	89.21	89.21	89.21	89.21	89.21	89.21	89.21
fnr	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
rpoA	88.87	88.87	88.87	88.87	88.87	88.87	88.87	88.87	88.87	88.87	88.87	88.87	88.87	88.87	88.87
h-ns	96.34	96.34	96.34	96.34	96.34	97.91	96.34	96.34	96.34	96.34	96.34	96.34	96.34	92.15	92.15
katA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
envZ	93.26	93.04	93.26	93.26	93.26	92.93	92.93	92.93	92.93	92.93	92.93	92.93	92.93	92.93	92.93
ompR	93.26	93.04	93.26	93.26	93.26	92.93	93.26	93.26	93.26	93.26	93.26	93.26	93.26	93.26	93.26
nlpD	78.34	78.34	78.34	78.34	78.34	78.34	78.34	78.34	78.34	78.34	78.34	78.34	78.34	78.34	78.34
degQ	94.42	94.42	94.42	94.42	94.42	94.17	94.42	94.42	94.42	94.42	94.42	94.42	94.42	94.42	94.42
recX	96.21	97.16	96.21	96.21	97.16	96.21	96.21	96.21	96.21	96.21	97.16	97.16	97.16	97.16	97.16
rseB	92.84	93.37	92.84	92.84	93.24	90.19	92.84	92.84	92.84	92.84	93.24	93.24	93.24	93.24	93.24

Table S3. (Cont.)

	YC40-M	SL3822	RUN2279	CQPS-1	B2	MAFF 301560	MAFF 241647	204	203	202	FJAT15244	RSCM	FJAT15244	FJAT15244	SL3755
katE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
katG	98.71	98.82	97.42	98.49	98.6	98.39	98.71	98.49	98.49	98.49	98.82	98.39	98.82	98.82	98.92
norB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sodB	81.73	81.73	81.98	81.73	81.73	81.73	81.73	81.73	81.73	81.73	81.73	81.73	81.73	81.73	81.73
sodC	86.63	86.63	86.07	87.19	85.52	87.19	86.63	87.19	87.19	87.19	86.07	87.19	86.07	86.07	86.63
oxyR	95.65	96.11	95.33	67.19	96.11	95.65	95.65	96.11	96.11	96.11	96.11	96.11	96.11	96.11	96.11
dksA	90.32	90.32	90.32	90.32	90.32	90.32	90.32	90.32	90.32	90.32	90.32	90.32	90.32	90.32	90.32
nsrR	99.72	100	97.44	100	100	100	99.72	100	100	100	100	100	100	100	99.72
dnr	0	0	10.46	0	10.71	0	0	0	0	0	0	0	0	0	0
ompR	92.18	92.18	91.77	92.18	92.18	92.18	92.18	92.18	92.18	92.18	92.18	92.18	92.18	92.18	92.18
baeR	35.08	35.31	35.08	35.08	35.31	35.08	35.08	35.08	35.08	35.08	35.08	35.31	35.08	35.08	35.08
baeS	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
gmk	99.34	99.34	100	100	99.34	99.34	99.34	100	100	100	99.34	100	99.34	99.34	100
rcsB	99.77	99.32	96.13	98.18	99.32	98.86	99.77	97.49	97.49	97.49	99.77	99.77	99.77	99.77	99.77
rcsC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
rpoE	90.27	90.27	87.78	88.53	89.03	90.52	90.27	88.53	88.53	88.53	89.03	90.52	89.03	89.03	89.03
rseA	60.7	60.7	58.84	60.23	60	60.23	60.7	60.23	60.23	60.23	60.23	60.23	60.23	60.23	60.23
degS	94.42	94.42	93.8	94.42	94.42	94.42	94.42	94.42	94.42	94.42	94.42	94.42	94.42	94.42	94.42
recA	82.15	82.15	81.02	82.15	82.15	82.15	82.15	82.15	82.15	82.15	82.15	82.15	82.15	82.15	82.15
lexA	99.77	99.77	97.91	99.77	99.77	99.77	99.77	99.77	99.77	99.77	99.77	0	99.77	99.77	99.77
rpoS	82	82	80.55	82	82	82	82	82	82	82	82	23.92	82	82	82
fruR	85.03	85.03	84.88	85.03	85.03	85.03	85.03	85.03	85.03	85.03	85.03	85.03	85.03	85.03	85.03
spoT	98.48	98.48	98.15	98.48	98.41	98.48	98.48	98.48	98.48	98.48	98.48	98.48	98.48	98.48	98.48
fur	70.93	71.22	69.48	70.64	71.22	71.22	70.93	70.64	70.64	70.64	71.22	71.22	71.22	71.22	71.22
dps	88.92	89.21	89.21	89.21	88.92	88.92	88.92	89.21	89.21	89.21	89.21	89.21	89.21	89.21	88.92
fnr	0	0	10.46	0	10.71	0	0	0	0	0	0	0	0	0	0
rpoA	88.87	88.87	88.87	88.87	88.87	88.87	88.87	88.87	88.87	88.87	88.87	88.87	88.87	88.87	88.87
h-ns	96.34	96.34	96.34	90.05	92.15	96.34	96.34	95.81	95.81	95.81	96.34	91.1	96.34	96.34	96.34
katA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
envZ	92.93	92.93	93.04	93.04	92.93	93.26	93.26	93.26	93.26	93.26	93.26	93.26	93.26	93.26	92.93
ompR	93.26	93.26	93.04	93.26	92.93	93.26	93.26	93.26	93.26	93.26	93.26	93.26	93.26	93.26	92.93
nlpD	78.34	78.34	78.7	78.34	78.34	78.34	78.34	78.34	78.34	78.34	78.34	0	78.34	78.34	78.34
degQ	94.42	94.42	93.8	94.42	94.42	94.42	94.42	94.42	94.42	94.42	94.42	94.42	94.42	94.42	94.42
recX	97.16	96.21	95.9	97.16	95.58	97.16	97.16	97.16	97.16	97.16	97.16	97.16	97.16	97.16	97.16
rseB	92.84	92.84	93.77	93.24	90.19	93.24	92.84	93.24	93.24	93.24	93.24	93.1	93.24	93.24	92.97

Table S3. (Cont.)

	YQ	MAFF 241648	MAFF 211479	MAFF 211491	UW763	FJ1003	T117	362200	T42	SL3730	SL2729	RUN2474	FJAT442	FJAT442	FJAT1452
katE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
katG	98.82	98.28	98.28	98.82	98.71	98.39	98.82	98.82	98.82	98.82	98.82	97.42	98.71	98.71	98.71
norB	0	0	0	0	0	0	79.56	0	0	0	0	0	0	0	0
sodB	81.73	81.98	81.98	81.73	81.73	81.73	81.73	81.98	81.73	81.73	81.73	80.96	81.73	81.73	81.73
sodC	86.07	87.19	87.19	86.07	86.63	87.19	86.63	86.63	86.63	86.63	86.63	86.07	86.63	86.63	86.63
oxyR	96.11	96.11	96.11	96.11	96.11	96.11	96.11	96.11	96.11	96.11	96.11	95.33	95.65	95.65	95.65
dksA	90.32	90.32	90.32	90.32	90.32	90.32	90.32	90.32	90.32	90.32	90.32	90.32	90.32	90.32	90.32
nsrR	100	100	100	100	99.72	100	100	99.72	100	100	100	97.44	99.72	99.72	99.72
dnr	0	0	0	0	0	0	11.57	0	0	0	0	10.46	0	0	0
ompR	92.18	92.18	92.18	92.18	92.18	92.18	92.18	92.18	92.18	92.18	92.18	91.77	92.18	92.18	92.18
baeR	35.31	35.31	35.31	35.31	35.76	35.08	35.31	35.08	35.31	35.31	35.31	35.08	35.08	35.08	35.08
baeS	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
gmK	99.34	100	100	100	100	99.34	99.34	99.34	99.34	99.34	99.34	100	99.34	99.34	99.34
resB	99.77	98.63	98.63	98.63	99.77	99.77	99.32	99.77	99.32	98.41	99.32	96.13	99.77	99.77	99.77
resC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
rpoE	90.27	90.52	90.52	90.52	90.52	89.03	90.27	90.52	89.53	89.53	89.53	87.78	99.27	99.27	99.27
rseA	60.7	60.23	60.23	60.23	60.7	60.23	60.7	60	60.7	60.7	60.7	58.84	60.7	60.7	60.7
degS	94.42	94.42	94.42	94.42	94.42	94.42	71.34	94.17	94.42	94.42	94.42	93.8	94.42	94.42	94.42
recA	82.15	82.15	82.15	82.15	82.15	82.15	82.15	82.15	82.15	82.15	82.15	81.02	82.15	82.15	82.15
lexA	99.77	99.77	99.77	99.77	99.77	99.77	99.77	99.77	99.77	99.77	99.77	97.91	99.77	99.77	99.77
rpoS	82	82	82	82	82	82	82	82	81.6	82	82	80.55	80.55	80.55	80.55
fruR	85.03	85.03	85.03	85.03	85.03	85.03	85.03	85.03	85.03	85.03	85.03	84.88	85.03	85.03	85.03
spoT	98.48	98.48	98.48	98.48	98.48	98.48	98.48	98.48	98.48	98.48	98.48	97.09	98.48	98.48	98.48
fur	71.22	71.22	71.22	71.22	71.22	71.22	71.22	71.22	71.22	71.22	71.22	69.77	70.93	70.93	70.93
dps	89.21	89.21	88.92	88.92	89.21	89.21	89.21	88.92	89.21	89.21	89.21	89.21	88.92	88.92	88.92
fnr	0	0	0	0	0	0	0	0	0	0	0	10.46	0	0	0
rpoA	88.87	88.87	88.87	88.87	88.87	88.87	88.87	88.87	88.87	88.87	88.87	88.87	88.87	88.87	88.87
h-ns	96.34	98.95	98.95	98.95	100	96.34	96.34	97.91	96.34	96.34	96.34	90.58	96.34	96.34	96.34
katA	0	0	0	0	0	0	39.54	0	0	0	0	0	0	0	0
envZ	93.26	93.26	93.26	93.26	93.15	93.26	93.26	92.93	93.26	93.26	93.26	93.04	93.26	93.26	93.26
ompR	93.26	93.26	93.26	93.26	93.15	93.26	93.26	93.93	93.26	93.26	93.26	93.04	93.26	93.26	93.26
nlpD	78.34	78.34	78.34	78.34	78.34	78.34	78.34	78.34	78.34	78.34	78.34	78.7	78.34	78.34	78.34
degQ	94.42	94.42	94.42	94.42	94.42	94.42	94.42	94.17	94.17	94.17	94.17	93.8	94.42	94.42	94.42
recX	96.21	95.58	95.58	95.58	96.53	97.16	96.21	96.21	96.21	96.21	96.21	95.9	97.16	97.16	97.16
rseB	92.84	92.97	92.97	92.97	93.1	93.24	92.84	90.19	92.84	92.84	92.84	93.77	92.84	92.84	92.84

Table S3. (Cont.)

	FJAT1452	FJAT445	FJAT 445	SY1	MAFF 311693	SL2330	FJAT1 5304	FJAT15 340	FJAT 1530 4	FJAT15 340	FJAT15 304	FJAT1534 0	UW386	Rs-SY1	FJAT1303
katE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
katG	98.71	98.71	98.71	98.82	98.28	98.92	98.39	98.39	98.39	98.39	98.39	98.39	97.53	98.39	98.39
norB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
sodB	81.73	81.73	81.73	81.73	81.98	81.73	81.73	81.73	81.73	81.73	81.73	81.73	81.73	81.73	81.73
sodC	86.63	86.63	86.63	86.63	87.19	86.63	86.63	86.63	86.63	86.63	86.63	86.63	86.07	86.63	86.63
oxyR	95.65	95.65	95.65	96.11	96.11	96.11	96.11	96.11	96.11	96.11	96.11	96.11	95.65	96.11	96.11
dksA	90.32	90.32	90.32	90.32	90.32	90.32	90.32	90.32	90.32	90.32	90.32	90.32	90.32	90.32	90.32
nsrR	99.72	99.72	99.72	99.72	100	99.72	100	100	100	100	100	100	97.72	100	100
dnr	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ompR	92.18	92.18	92.18	92.39	92.18	92.18	92.18	92.18	92.18	92.18	92.18	92.18	92.18	92.18	92.18
baeR	35.08	35.08	35.08	35.08	35.31	35.08	35.08	35.08	35.08	35.08	35.08	35.08	32.57	35.08	35.08
baeS	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
gmk	99.34	99.34	99.34	100	100	100	99.34	99.34	99.34	99.34	99.34	99.34	99.56	99.34	99.34
rcsB	99.77	99.77	99.77	99.77	98.63	99.77	99.77	99.77	99.77	99.77	99.77	99.77	97.04	99.77	99.77
rcsC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
rpoE	99.27	99.27	99.27	90.52	90.52	89.03	89.03	89.03	89.03	89.03	89.03	89.03	88.53	89.03	89.03
rseA	60.7	60.7	60.7	60	60.23	60.23	60.23	60.23	60.23	60.23	60.23	60.23	59.77	60.23	60.23
degS	94.42	94.42	94.42	94.17	94.42	94.42	94.42	94.42	94.42	94.42	94.42	94.42	94.42	94.42	94.42
recA	82.15	82.15	82.15	82.15	82.15	82.15	82.15	82.15	82.15	82.15	82.15	82.15	82.15	82.15	82.15
lexA	99.77	99.77	99.77	99.77	99.77	99.77	99.77	99.77	99.77	99.77	99.77	99.77	95.59	99.77	99.77
rpoS	80.55	80.55	80.55	81.47	82	82	82	82	82	82	82	82	81.08	82	82
fruR	85.03	85.03	85.03	85.03	85.03	85.03	85.03	85.03	85.03	85.03	85.03	85.03	85.19	85.03	85.03
spoT	98.48	98.48	98.48	98.48	98.48	98.48	98.48	98.48	98.48	98.48	98.48	98.48	97.09	98.48	98.48
fur	70.93	70.93	70.93	70.64	71.22	71.22	71.22	71.22	71.22	71.22	71.22	71.22	68.19	71.22	71.22
dps	88.92	88.92	88.92	89.21	89.21	89.21	89.21	89.21	89.21	89.21	89.21	89.21	88.63	89.21	89.21
fnr	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
rpoA	88.87	88.87	88.87	88.87	88.87	88.87	88.87	88.87	88.87	88.87	88.87	88.87	88.87	88.87	88.87
h-ns	96.34	96.34	96.34	96.34	98.43	96.34	92.15	92.15	92.15	92.15	92.15	92.15	96.34	96.34	92.15
katA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
envZ	93.26	93.26	93.26	92.93	93.26	92.93	93.26	93.26	93.26	93.26	93.26	93.26	92.83	93.26	93.26
ompR	93.26	93.26	93.26	92.93	93.26	92.93	93.26	93.26	93.26	93.26	93.26	93.26	92.83	93.26	93.26
nlpD	78.34	78.34	78.34	78.34	78.34	78.34	78.34	78.34	78.34	78.34	78.34	78.34	78.34	78.34	78.34
degQ	94.42	94.42	94.42	94.17	94.42	94.42	94.42	94.42	94.42	94.42	94.42	94.42	94.42	94.42	94.42
recX	97.16	97.16	97.16	96.21	95.58	97.16	97.16	97.16	97.16	97.16	97.16	97.16	96.85	97.16	97.16
rseB	92.84	92.84	92.84	90.19	92.97	92.97	93.24	93.24	93.24	93.24	93.24	93.24	92.84	93.24	93.24

Table S3. (Cont.)

	MAFF 211491	Rs5	T95	SL2064	KACC 10722	SL3175	T98	T11	SL23 12	T82	T101	T12	T51	UW163	SL3103
katE	0	0	39.41	39.41	39.41	39.41	39.41	39.41	39.51	39.51	39.51	39.51	39.41	0	0
katG	98.28	90	91.29	91.29	91.29	91.61	91.61	91.29	91.51	91.51	91.51	91.51	91.29	89.46	98.82
norB	0	0	79.56	79.56	79.56	79.37	79.37	0	79.83	79.83	79.83	79.83	0	0	0
sodB	81.98	82.99	80.2	80.2	80.2	80.2	80.2	81.73	80.2	80.2	80.2	80.2	80.2	82.99	81.73
sodC	87.19	82.45	84.68	84.68	84.68	84.96	84.96	84.68	84.96	84.96	84.96	84.96	84.68	81.34	86.63
oxyR	96.11	92.22	94.56	94.56	94.56	94.56	94.56	96.11	94.56	94.56	94.56	94.56	94.56	93.62	96.11
dksA	90.32	88.17	84.59	84.59	84.59	84.59	84.95	84.59	84.59	84.59	84.59	84.59	84.59	88.17	90.32
nsrR	100	90.03	91.17	91.17	91.17	86.04	86.04	100	91.17	91.17	91.17	91.17	91.17	92.69	100
dnr	0	0	11.57	11.57	11.57	11.66	11.66	0	11.57	11.57	11.57	11.57	11.57	0	0
ompR	92.18	92.18	92.18	92.18	92.18	92.18	92.18	92.18	92.18	92.18	92.18	92.39	92.18	92.39	92.18
baeR	35.31	35.54	35.31	35.31	35.31	35.31	35.31	35.31	35.31	35.31	35.31	35.31	35.31	35.54	35.31
baeS	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
gmK	100	99.56	98.25	98.25	98.25	98.25	98.25	94.09	98.25	98.25	98.25	98.25	98.25	99.78	99.34
rcsB	98.63	81.32	89.29	89.29	89.29	88.84	88.84	68.11	89.75	89.75	89.75	89.75	89.29	81.32	99.77
rcsC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
rpoE	90.52	84.04	85.04	85.04	85.04	85.04	85.04	90.27	85.04	85.04	85.04	85.04	85.04	84.29	90.27
rseA	60.23	57.91	56.51	56.51	56.51	56.05	56.05	27.67	56.51	56.51	56.51	56.51	56.51	57.91	60.7
degS	94.42	91.44	91.19	91.19	91.19	90.94	90.94	94.42	90.94	63.77	63.77	63.77	91.19	91.69	94.42
recA	82.15	81.16	78.61	78.61	78.61	78.47	78.47	82.15	78.61	78.61	78.61	78.61	78.61	78.61	82.15
lexA	99.77	96.52	93.97	93.97	93.97	93.97	93.97	51.74	93.97	93.97	93.97	93.97	93.97	96.29	99.77
rpoS	82	80.29	81.21	81.21	81.21	81.21	81.21	81.21	81.21	81.21	81.21	81.21	81.21	79.76	82
fruR	85.03	85.95	84.41	84.41	84.41	84.1	84.1	85.03	84.41	84.41	84.41	84.41	84.41	83.8	85.03
spoT	98.48	95.24	95.38	95.38	95.38	96.3	96.3	95.38	95.24	95.24	95.24	95.24	95.38	95.9	98.41
fur	71.22	66.86	68.6	68.6	68.6	69.19	69.19	68.6	68.6	68.6	68.6	68.6	68.6	68.02	71.22
dps	89.21	89.21	89.21	89.21	89.21	89.21	89.21	89.21	89.21	89.21	89.21	89.21	89.21	89.21	88.63
fnr	0	0	11.57	11.57	11.57	11.66	11.66	11.57	11.57	11.57	11.57	11.57	11.57	0	0
rpoA	88.87	88.72	88.57	88.57	88.57	88.57	88.57	88.87	88.57	88.57	88.57	88.57	88.57	88.57	88.87
h-ns	98.95	90.58	96.34	96.34	96.34	87.43	87.43	67.02	72.77	72.77	72.77	72.77	13.93	91.1	13.51
katA	0	0	39.54	39.54	39.54	39.54	39.54	0	39.64	39.64	39.64	39.64	39.54	0	0
envZ	93.26	90.54	91.09	91.09	91.09	90.76	90.76	93.26	83.04	91.09	91.09	83.04	91.09	89.89	93.26
ompR	93.26	90.54	91.09	91.09	91.09	90.76	90.76	93.26	83.04	91.09	91.09	83.04	91.09	89.89	93.26
nlpD	78.34	74.91	75.09	75.09	75.09	75.09	75.09	75.09	75.09	75.09	75.09	75.09	75.09	75.09	78.34
degQ	94.42	91.44	91.19	91.19	91.19	90.94	90.94	73.82	90.94	63.77	63.77	63.77	91.19	91.69	94.42
recX	95.58	91.8	94.01	94.01	94.01	94.95	94.95	94.01	94.64	94.64	94.64	94.64	94.01	92.43	97.16
rseB	92.97	90.98	92.57	92.57	92.57	92.57	92.57	92.57	92.31	92.31	92.31	92.31	92.57	91.91	92.84

Table S3. (Cont.)

	CIAT_078	IBSBF 2571	KACC107 09	IBSBF15 03	UY031	RS 488	RS 489	GMI10 00	FJAT- 1458	FJAT- 91	PSI07	OE1-1	Po82	RS10	YC45
katE	0	0	0	0	0	0	0	0	0	0	39.41	0	0	0	0
katG	89.46	89.46	98.82	89.46	89.57	89.57	89.14	99.89	98.71	98.82	91.94	98.39	89.46	98.49	98.28
norB	0	0	0	0	0	0	0	0	0	0	79.37	0	0	0	0
sodB	82.99	82.23	81.73	82.99	82.99	82.99	82.99	81.73	81.73	81.73	80.2	81.73	82.99	81.98	81.98
sodC	81.34	81.34	86.63	81.34	83.57	83.57	84.12	87.74	86.63	86.07	84.96	87.19	81.34	87.19	87.19
oxyR	93.62	93.62	96.11	93.62	93	93	92.22	96.11	96.11	96.11	94.56	95.65	93.62	96.11	96.11
dksA	87.81	88.17	90.32	88.17	88.17	88.17	88.17	90.32	90.32	90.32	84.95	90.32	88.17	90.32	90.32
nsrR	92.59	92.59	99.43	92.59	91.17	91.17	82.34	100	100	100	86.04	100	92.59	100	100
dnr	0	0	0	0	0	0	0	0	0	0	11.66	0	0	0	0
ompR	92.39	92.39	92.18	92.39	92.39	92.39	92.18	92.18	92.18	92.18	92.18	92.18	92.39	91.36	92.18
baeR	35.54	35.76	35.31	35.54	35.31	35.31	35.08	35.31	35.31	35.31	35.31	35.08	35.54	35.31	32.12
baeS	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
gmk	99.78	99.34	99.34	98.78	99.34	99.34	99.56	100	100	99.34	98.03	99.34	99.78	100	100
rcsB	81.55	81.32	99.77	81.32	82.69	82.69	80.18	99.77	99.32	99.77	88.84	98.86	81.32	98.41	27.56
rcsC	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
rpoE	84.29	84.29	90.27	84.29	84.54	84.54	83.29	90.52	90.27	90.27	85.04	90.52	84.29	90.52	90.52
rseA	57.91	57.91	60.7	57.91	57.67	57.67	57.67	60.7	60.7	60.7	56.05	60.23	57.91	60.23	60.23
degS	91.69	91.69	94.42	91.69	91.56	91.32	91.56	94.42	94.42	94.42	90.94	94.42	91.69	94.42	94.42
recA	78.61	51.98	82.15	78.61	81.16	81.16	80.74	82.15	82.15	82.15	78.47	82.15	78.61	78.61	82.15
lexA	96.29	96.29	99.77	96.29	96.29	96.29	96.52	100.46	99.77	99.77	93.97	99.77	96.29	99.77	99.77
rpoS	73.32	79.76	82	79.76	79.89	79.89	80.16	82	82	82	81.21	82	79.76	82	81.47
fruR	83.64	83.8	85.03	83.8	83.49	83.49	83.49	85.03	85.03	85.03	84.26	85.03	83.8	85.03	85.03
spoT	64.27	95.77	98.41	95.9	96.17	96.17	95.44	98.61	98.48	98.48	96.3	98.48	95.77	98.48	98.48
fur	68.02	68.02	71.22	68.02	67.73	67.73	67.15	71.22	71.22	71.22	69.19	71.22	68.02	71.22	71.22
dps	89.21	89.21	89.21	89.21	88.63	88.63	88.92	89.21	88.92	89.21	89.21	88.92	89.21	89.21	89.21
fnr	0	0	0	0	0	0	0	0	0	0	11.66	0	0	0	0
rpoA	88.57	88.57	88.87	88.57	88.72	88.72	88.72	88.87	88.87	88.87	88.57	88.87	88.57	88.87	88.57
h-ns	93.19	92.15	89.01	92.15	13.93	13.93	13.93	100	96.34	96.34	95.81	96.34	82.15	97.91	98.95
katA	0	0	0	0	0	0	0	0	0	0	39.54	0	0	0	0
envZ	89.89	89.89	93.26	89.89	90.54	90.54	90.22	93.15	93.26	93.26	90.54	93.26	89.89	93.15	93.26
ompR	89.89	89.89	93.26	89.89	90.54	90.54	90.22	93.15	93.26	93.26	90.54	93.26	89.89	93.15	93.26
nlpD	75.09	75.09	78.34	75.09	75.09	75.09	75.09	78.34	78.34	78.34	75.09	78.34	75.09	78.34	78.34
degQ	91.69	91.69	94.42	91.69	91.56	91.32	91.56	94.42	94.42	94.42	90.94	94.42	91.69	94.42	94.42
recX	92.43	93.38	97.16	91.48	93.06	92.74	90.85	96.53	97.16	97.16	94.95	97.16	92.43	97.16	95.58
rseB	91.91	91.91	92.84	91.91	91.64	91.64	90.85	93.37	93.24	93.24	92.57	93.24	91.91	93.37	92.97

Table S3. (Cont.)

	T25	T110	SL3022	CFBP 8695	CFBP 8697
katE	0	0	39.51	0	0
katG	98.92	59.14	54.52	86.27	85.27
norB	0	0	79.63	0	0
sodB	81.73	80.46	80.2	82.99	81.98
sodC	86.63	86.63	84.68	83.57	81.34
oxyR	67.19	96.11	94.56	93	93
dksA	90.32	90.32	84.59	88.17	88.17
nsrR	100	99.72	91.17	91.17	91.17
dnr	0	0	11.57	0	0
ompR	92.18	90.74	92.18	92.39	92.39
baeR	35.08	26.65	35.31	35.31	35.31
baeS	0	0	0	0	0
gmk	100	94.09	98.25	99.34	99.34
rcsB	99.77	68.11	89.75	82.69	82.92
rcsC	0	0	0	0	0
rpoE	90.27	89.03	85.04	84.54	84.54
rseA	60.23	27.67	37.44	57.67	57.91
degS	94.42	73.82	91.32	91.56	91.56
recA	82.15	82.15	78.61	81.16	81.16
lexA	99.77	51.74	93.97	96.29	96.29
rpoS	82	82	81.21	78.98	79.24
fruR	85.03	85.03	84.41	83.49	83.95
spoT	98.48	98.48	95.38	96.17	96.17
fur	71.22	71.22	68.6	67.73	67.73
dps	48.98	88.63	89.21	88.63	89.21
fnr	0	0	11.57	0	0
rpoA	88.87	88.87	88.57	88.72	88.72
h-ns	96.34	96.34	66.49	13.93	13.93
katA	0	0	0	0	0
envZ	92.93	92.93	91.09	90.54	90.43
ompR	92.93	92.93	91.09	90.54	90.43
nlpD	78.34	73.83	75.09	75.09	75.09
degQ	94.42	73.82	91.32	91.56	91.56
recX	97.16	35.65	94.64	93.06	93.06
rseB	90.98	49.34	65.92	91.64	92.18

Table S4. Bacterial secretion systems of *R. solanacearum*

Sl. No.	Secretion system	Gene	KO No.
1	Tat	TatA/ TatA/E	K00832
2	T1SS	LipA/LipC	K01046
3	T1SS	CyaB	K01768
4	T5SS	AspA	K01744
5	T4SS	Alr	K01775
6	T1SS	HlyD	K01993
7	T1SS	HlyD	K02005
8	T1SS	HlyD	K02022
9	T1SS	ABC transporter	K02056
10	T1SS	ABC transporter	K02057
11	T1SS	ABC transporter	K02058
12	Tad	Flp/ Fap/ PilA/ CpaB	K02279
13	T3SS	CpaC/RcpA	K02280
14	T4P	PilV/ CpaD	K02281
15	Tad	TadZ/CpaE	K02282
16	Tad	TadA/CpaF	K02283
17	T4SS	Alr	K02314
18	Flg	FlGB	K02387
19	Flg	FlGC	K02388
20	T3SS	FlhB	K02401
21	Flg	FliE	K02408
22	T3SS	FliH	K02411
23	T2SS	GspN/XcpP	K02452
24	T2SS	GspD	K02453
25	T2SS	GspE/HxcR/XcpR/PilB	K02454
26	T2SS	GspF/PilC/XcpS	K02455
27	T2SS	GspG/XcpT	K02456
28	T2SS	GspH/XcpU	K02457
29	T2SS	GspI/XcpV	K02458
30	T2SS	GspJ/XcpW	K02459
31	T2SS	GspK/XcpX	K02460
32	T2SS	GspL/XcpY	K02461
33	T2SS	GspM/XcpZ	K02462
34	T2SS	GspN	K02463
35	T4P	PilA/Flp	K02650
36	T4P	PilA/Flp	K02651
37	T4P	PilB/ GspE	K02652
38	T2SS	GspF/PilC/XcpS	K02653
39	T2SS	GspO	K02654
40	T4P	PilN	K02663
41	T4P	PilT	K02669
42	T4P	PilU	K02670
43	T9SS	SprT	K02742
44	Sec-SRP	SecA	K03070

45	Sec-SRP	SecB	K03071
46	Sec-SRP	SecD	K03072
47	Sec-SRP	SecE	K03073
48	Sec-SRP	SecF	K03074
49	Sec-SRP	SecG	K03075
50	Sec-SRP	SecY	K03076
51	T5SS	LepB/IepB	K03100
52	Sec-SRP	Ffh/Srp54	K03106
53	Sec-SRP	FtsY	K03110
54	T2SS	DamX	K03112
55	Tat	Tat A	K03116
56	Tat	TatB	K03117
57	Tat	TatC	K03118
58	T4SS	VirB1/ AvhB1	K03194
59	T4SS	VirB10/ AvhB10	K03195
60	T4SS	VirB11/ AvhB11	K03196
61	T4SS	VirB2/ AvhB2	K03197
62	T4SS	VirB3/ AvhB3	K03198
63	T4SS	VirB4/ AvhB4	K03199
64	T4SS	VirB5/ AvhB5	K03200
65	T4SS	VirB6/ AvhB6	K03201
66	T4SS	VirB7/ AvhB7	K03202
67	T4SS	VirB8/ AvhB8	K03203
68	T4SS	VirB9/ AvhB9	K03204
69	Sec-SRP	YajC	K03210
70	Sec-SRP	YidC/Oxa1	K03217
71	T3SS	PscC/YscC/EscC/HrcC	K03219
72	T3SS	PscD	K03220
73	T3SS	PscF	K03221
74	T3SS	PscJ/YscJ/EscJ/HrcJ	K03222
75	T3SS	PscL	K03223
76	T3SS	PscN/YscN/EscN/HrcN/FilI	K03224
77	T3SS	PscQ/RhcQ	K03225
78	T3SS	PscR/YscR/EscR/HcrN	K03226
79	T3SS	YscS/EscS/HcrS	K03227
80	T3SS	PscT/YscT/EscT/HcrT	K03228
81	T3SS	PscU/YscU/EscU/HcrU	K03229
82	T3SS	PscV/RhcV/PcrD	K03230
83	T4SS	TraG/ VirD4	K03250
84	Tat	TatD/MttC	K03424
85	T1SS	HlyD	K03543
86	T5SS	LepA	K03596
87	T5SS	SspA	K03599
88	T5SS	SspB	K03600
89	T4SS	MobB	K03753
90	T3SS	PscB	K04049
91	T3SS	PscE	K04050
92	T3SS	PscG	K04051

93	T3SS	PscH	K04052
94	T3SS	PscI	K04053
95	T3SS	PscK	K04054
96	T3SS	PspO	K04056
97	T3SS	PscP	K04057
98	T3SS	PscW/PopN	K04058
99	T3SS	PscX	K04059
100	T3SS	PscY	K04060
101	T3SS	FlhB	K04061
102	T6SS	ImpA/ OstA/ LptA	K04744
103	T1SS	HlyB/ CyaB/ MsbA	K06147
104	T1SS	HlyB/ CyaB/ MsbA	K06148
105	T4SS	TraR/DksA/DnaK	K06204
106	Tat	TatE	K06886
107	T6SS	HcpA	K07126
108	T4SS	TrbL	K07344
109	T5SS	AlpA	K07733
110	T1SS	HlyD	K07798
111	T6SS	ImpA/ OstA/ LptA	K09774
112	T1SS	HlyD	K11003
113	T1SS	HlyB/ CyaB/ MsbA	K11004
114	T1SS	MsbA	K11085
115	T6SS	ImpM/TssM	K11890
116	T6SS	ImpL/TssL	K11891
117	T6SS	ImpK/TssK/DotU	K11892
118	T6SS	ImpJ/TssJ	K11893
119	T6SS	ImpI/TssI	K11894
120	T6SS	ImpH/TssH	K11895
121	T6SS	ImpG/TssG	K11896
122	T6SS	ImpF/TssF	K11897
123	T6SS	ImpC/TssC	K11900
124	T6SS	ImpB/TssB	K11901
125	T6SS	HcpA	K11902
126	T6SS	Hcp	K11903
127	T6SS	ImpA/VgrG/VasJ/TssA	K11904
128	T6SS	VasG	K11907
129	T6SS	ImpA/VgrG/VasJ/TssA	K11910
130	T1SS	TolC	K12340
131	Tad	TadB	K12510
132	Tad	TadC	K12511
133	T1SS	AprD/HasD	K12536
134	T1SS	AprE	K12537
135	T1SS	AprF	K12538
136	T1SS	HlyD	K12542
137	T1SS	TolC	K12543
138	T1SS	AprA/HasA	K12545
139	T4SS	Tral/LasI	K13060
140	T5SS	IscA	K13628

141	T1SS	HlyD	K15549
142	T1SS	HlyD	K15727
143	T1SS	HlyD	K18901
144	T4SS	TraR/ DksA	K19732
145	T4SS	TrbJ	K20266
146	T4SS	TrbB	K20527
147	T4SS	TrbC	K20528
148	T4SS	TrbD	K20529
149	T4SS	TrbE	K20530
150	T4SS	TrbF	K20531
151	T4SS	TrbG	K20532
152	T4SS	TrbI	K20533
153	T3SS	RetS	K20972
154	T1SS	HlyD	K21136

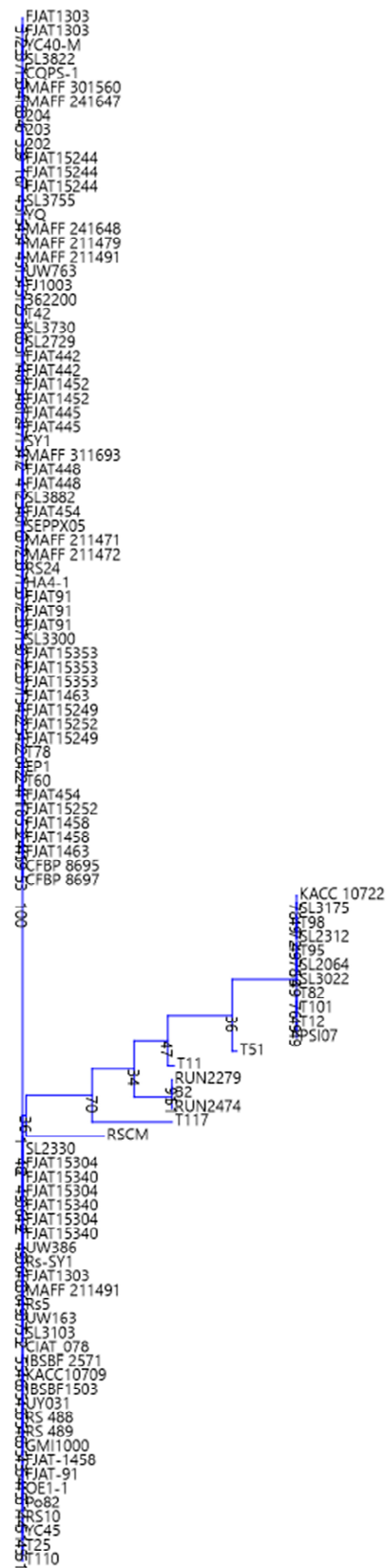


Figure S1. Cluster dendrogram based on distribution of stress responsive genes within *R. solanaceum* species complex.