***Echiniscus testudo***

**Toll Pathway**

**Spaetzle**

*>TRINITY\_DN38236\_c0\_g2\_i1.p1 TRINITY\_DN38236\_c0\_g2~~TRINITY\_DN38236\_c0\_g2\_i1.p1 ORF type:internal len:185 (+),score=37.79 TRINITY\_DN38236\_c0\_g2\_i1:3-554(+)* ***(Spz3)***

*KTLVTPFWANNSEGETLAIVNFFPFEQAVQQELCKPGRSRCLEDCFCEQTLSWHRLLALDSGDKRRGIFMDWFQFPAYCTCRCYNKLPLPKKLQPTSLPRVRKLPSSLARTSEVILSEAVQEAPARTFMNDNDDENNASPSAWVRHPAKLRHESSEKQKADIQGEFVNNNFLLTPRFSTPPVAS*

*>TRINITY\_DN44431\_c0\_g1\_i1.p1 TRINITY\_DN44431\_c0\_g1~~TRINITY\_DN44431\_c0\_g1\_i1.p1 ORF type:5prime\_partial len:164 (+),score=13.95 TRINITY\_DN44431\_c0\_g1\_i1:1-492(+)* ***(Spz4)***

*RRSYCTLPGTAYPTAQVGNYIVENLSTMKRMAGSPRIPNREEDADQRHASDGQDQRKKRLAGTGTGTRGKYLCPATEELVTPFWANNATGARLAIVNSPPFEQAVHTVKCTRGAQGRCHPTRPCWCTQEYSWFRLLAYDPTDNCKGIFMEWFKFPSSCNCMCY*

**Toll**

*>TRINITY\_DN54133\_c0\_g1\_i10.p1 TRINITY\_DN54133\_c0\_g1~~TRINITY\_DN54133\_c0\_g1\_i10.p1 ORF type:internal len:778 (+),score=223.42 TRINITY\_DN54133\_c0\_g1\_i10:3-2333(+)* ***(Toll6-LRR only)***

*LSNQWISGQLLRNLLKLEQLDLSYNQMSQVDDQMLRNLLAVRALDMRNNRLESLNTRAFEALHNLERLDLSQNQLSGLPNFNGLYKLADLNVADNVIRSLPGDFLGDSKDLVTLNLCGNQLVDLPSTLGGGQLNMQRLQTLRVCRNRFRSLPWDGFKTLKSLEELDLSGNELSAWRFPGCLPDKPQLRVLDLSNNHLSDPLYNISSLKSSNICPALESLNLAQNVLSTLPDLRGAFPTLRALNVSSNRLTTLEWSIMPAAMRSITAFSNQIVDMQGDPDSFCSNLEQLDLSSNRITRLSALPRGLRRLDARNNLISSFVGNVFESKPNLHEVHLEMNRIEQLEESDVRVTPFQNEQRPLPKLFLRDNPLQCHCTMTFLLDIGQRNSPQSQQTTNRNFDYENEIASLPPQVPGPIYMPSRSVMKNYFELADFNQLECGDIQIGEFLNAGGRQTQPRKSLALINTTDMLCHYKSECSEKCECCEYSACDCKRACPDGCACYHDRDWRTNIVDCSANVRAVGGGDAATPTAEAFKAVPGVLPIDATEVRLDGNNFRTLNERSFLAKSRLQSLYLNNSNIAEIRPQAFLGLNNLQQLDLHGNSLRELAGPEFRELEHLQRLDLGSNQLSRISPSALGNLTQLKFLSLRSNRLNDLTGVVLPEPAPSLESVMNSNNKRQKRDNNVLRVDLANNPWDCACSDEDKSSGKFQAVTAWLDKFGPNIIRFITVQCLDGAPANARSRTNSGGPIVLRALALKERRCEMNYDEALQMLNAEAAKVAAA*

*>TRINITY\_DN49023\_c0\_g1\_i7.p1 TRINITY\_DN49023\_c0\_g1~~TRINITY\_DN49023\_c0\_g1\_i7.p1 ORF type:internal len:220 (+),score=85.20 TRINITY\_DN49023\_c0\_g1\_i7:1-657(+)* ***(Toll8-TIR only)***

*YLASRDFRGNLLDSSEPSSPATTPRHLIHAAKSSEAILQGGQQSKRAIVVISTSFLQREWSQLEYRTAHQQLFKDRRQKVIFICLDDVDVERRDLDVDLRISMKRHPCLKWGEKLFWKKLYFALPDSRCANATTNCANNNAALFNGATLPHAQQNFYPYHQTNFMPFNNNNNTMMPPFNVNHQLHHLPPAYQQQAAAMMAAAAVQQQQQTMTMLPNGGA*

*>TRINITY\_DN53360\_c0\_g3\_i1.p1 TRINITY\_DN53360\_c0\_g3~~TRINITY\_DN53360\_c0\_g3\_i1.p1 ORF type:5prime\_partial len:497 (+),score=90.85 TRINITY\_DN53360\_c0\_g3\_i1:2-1492(+)* ***(Toll8-LRR only)***

*EMKTKSTFLLFLLSGTMLAFAQKEEPQPTSQSGCSLVSPFTQVVSCQSLPDGLALRFFSVRTTKNIEAVLNALGSTKVQSLTIERSPWLRDFDISRLKNVPCLAKLHALRLRQLFLQSFPQNFMVQFPTLHSLEIAFCQLGSLPEVPPRCCDGASAEGGLTSLNLTQNRIAYLHSENFARLTQLVELDLSWNMINTLPPQAFAALKNLRTLSVQGNSISDVDDTAFVECERLQYLDLSFNPIGGSNIKTSYGFSDGQPTKPAASRPPSGGRSGGSGNPTLPSLVFKPLKELISLDMRRTGIVHVPPGIGQLKKLKLLWLSQNVIQYLSTEPFQDLTSLVMLDLSYNRIQYFTAEAVSKLTDLTTLNLAANPLKELPIGMFAALKKLVQLDLRYTYIGEDTDALAAAQTNLAANNTRLLKLLIAPLNENQHHQYEPPQQQGTSAGSPPMIIPSMVPNQPHPMMPPMGPPGAVAPPFGIQPAHGGLPPRPGMMSPPTD*

**IMD Pathway**

**Tak1**

*>TRINITY\_DN55417\_c0\_g1\_i7.p1 TRINITY\_DN55417\_c0\_g1~~TRINITY\_DN55417\_c0\_g1\_i7.p1 ORF type:5prime\_partial len:890 (+),score=217.45 TRINITY\_DN55417\_c0\_g1\_i7:3-2672(+)*

*VDHLARAKHPNIVPIYGACMKIPVCLVMEYAECGSLFALLHYAENVDYTFGHALSWLLQCARGVEYLHSMKPRPVVHRDLKPPNLLLKNHCRKLLLCDFGTAVDAKTYMTNNKGSAAWMAPEVFEGVHYSEKCDVFSFGIIIWEVLSRHKPFHNVGGPALRILWLVHQGNRPPLLENCPRLLEQLMTQCWRKAAAERPSMAQAVKVLEFMVKYVSDYDVPIPWPKPHSAATGTPLPAIRTGTPDVQQREQQRQGLIQPTTPLHQQTQPDTDRQPDYSLTSTGSLYTPNLTDTQSSSTLSDSLTQTLSPENLTLSGTSAADSPESSKGVQNEAAAPEPSSSKRVVVNDVTAMPLYAVPNSGRTEPAFTPSAEKATEPPVKSTLNAAGYASARQLSRLNLSAVELTPIVSATDTIPNVYETISSSLDVAPEQAEVVATVTDAAEDDAEQQRESQYKAGGQSPAVLSNNLNIQPMQGRRPQQQQQRRQAGKFYIELPRPSQTDVEQQLQHHSSNLSLMSPDHQKQQQPRYQYGRQSSQQLAGENISPDGHHHQHIQWQIPDPVLVHAANTPPAPQDRTLFHRGAVSPAYQPQQSLTENVSENYHQQQLQQQQQSAPVRRSDSDKRHRTQLTLHVEDPVPDEENRSMLNAEEMADQRQEFPSSSGTMPLLTATHYLNTPSPNLQYRQQFYASQPDLSRTLYANQMQQPVQHFGITTTPASPRGNASSQPQQQQQQVRYVFAAQPHLYASQQQLYDNNNNVYYARPPQSPTVMYSPYSTSTGGGYVPPAPPPPQVAPSGFTLRLPSGVRLSFNVGNQQQQRSNETMTQSPAATSSGQYANYRNSPPFTGGQRFLRPNSFYIQPQQQQQEHPAASRSPSLRVIHSFVPSHQQNQQ*

**JNK Pathway**

**Hemipterous**

*>TRINITY\_DN53835\_c1\_g2\_i5.p1 TRINITY\_DN53835\_c1\_g2~~TRINITY\_DN53835\_c1\_g2\_i5.p1 ORF type:internal len:925 (+),score=242.19 TRINITY\_DN53835\_c1\_g2\_i5:3-2774(+)*

*FFFFNDTATTEIYTFRVLQSDDPLAIDPPQQLKALLTLARGRFYADKPQLSVFVEQSKIHTYNCTMPTSTVPTTATEESACHAVPSRNNSVYASKPPLTAGSMRQTHVLQPTDDSAELVKHANFNLQPRSSRKPRTLNIGQTATCGPAFGRAVSPFLASNSSADRLSNGTPVTSASPNDGALDDAENGFGAKEFRDSYRLTRRRKLELTRSQLPECLHNSFLPNDDRVMLEELQDEEKLREIMKETGILTIRGTSYVASIEDLEHVGEVGHGVCGTVVKMRFKKTGDVIAVKQMRRSGNREENKRIIRDLEVILKSNDCPHIVQCYGCFVTEAEVWICMELMTSCMEKLLHRTRRLYADDPTRGIPEPIIGTMSLAVVKALHYLKEKHGVIHRDVKPSNILVDARTGRFKLCDFGISGRLVDSKAKTRTAGCAAYMAPERISPPDPKKPDYDIRADVWSFGISLYELATGSMPYKGCQGDFEVLTKIIEDDPPLLSPDDGFSIPFCSFLQACLTKDHKHRPKYHELLQHPFIRLYELKKIDIFDFLRSVTSNTQFLYLQQEMLLKPSVQQQSPTVTPQLPGMPLYHRINRQAPPQQKPLPPPVTSFSIVPLADGELMPPVLPPKQNNVAAKNTLRQLATAPAPFFLAQPPRLPKQSFIADAGVVQHAYNNNIMPNYSNLDSNSAGPLSSRFDEPIQISMPTNVYHTTHTGVSLPHASAAPSSVSSSVSPASMTSTSSTISPFSPSNIYELIRHRYWPQHPQQPHQNPASVPKPQRQQQEYSTMSYYDWLQSTSSEQKPSATNAPFLFDNVSGPLVATGGYVPFASAAAAEPPSNAVRYTTSTGVVDDRCKEAIMLPNSNRLALGGVTDSMSAQLANLFIRSSTQQQQLMLHRLQRLPQQQPAAYVSTSSSLSRPTKMVVMPSST*

**Jnk**

*>TRINITY\_DN54832\_c0\_g1\_i1.p1 TRINITY\_DN54832\_c0\_g1~~TRINITY\_DN54832\_c0\_g1\_i1.p1 ORF type:complete len:524 (+),score=146.87 TRINITY\_DN54832\_c0\_g1\_i1:375-1946(+)*

*MNSANHTAIMTTKHPGMFYTQEVGDTRFALLKRYINLKPIGSGAQGIVCAAYDTFAKQHVAIKKLSRPFQNGTHAKRAYREFKLMNLVNHKNVIGLLNAFTPQRTFEEFTDVYLVMELMDANLCQVIQMELDHDRMSYLLYQLLCGIKHLHSAGIIHRDLKPSNIVVRSDCTLKILDFGLARSANASYMMTPYVVTRYYRAPEVILGMGYKDNVDIWSVGCIFGEMIRGGVLFPGTDHIDQWNKIIEQLGTPSQDFMRRLQPNVRNYVENRPKYAGYPFEKLFPDVLFPRDSAEHRPLRAAVARDLLSKMLVVDPEKRISVEEALRHPYINVWYEESEVNAPPAGMYDHTVEEGEHNVDEWKRLIYDEVIAYEHLHGLVAIANSGSGGGELVDGVVISDAVVPTTRTNGGSSSNNSASYDAAMVNASAVVVDDGYSMSGAGSSSGAANMQQQQQQYSSQQHHNQLSSSSSNATVNSSSALQRQPSSGGSSGGQRRGSNSDGAGANGMVTVDQRLTQQQIATHF*

**TIR-1 Pathway**

**TIR-1**

*>TRINITY\_DN55036\_c0\_g2\_i2.p1 TRINITY\_DN55036\_c0\_g2~~TRINITY\_DN55036\_c0\_g2\_i2.p1 ORF type:5prime\_partial len:985 (+),score=221.34 TRINITY\_DN55036\_c0\_g2\_i2:2-2956(+)*

*SRGLMQAMRGGNALHPSTPSIANEQRSSSSSSYHHSSSRQSKEVYESRNGKEIQNSKQILSHSDSARNRRDEIESLGPDGQRQIDAKQGFFTQSKSKSSLEELDAAGKSVKHVASSLQQLAGVKSGSFAAKGEELKQIGGETRFSGRALVTSMKTDANGETHGTVSGSSLHGGSDAAATDNHHDDPFHLITKITAFHVDPKAGDSGQPQITSSTSTTANQGSITNGKFRSGQQNAFMQPSQQFDSLRGMLQNFLTQFDEVDSNAVTHRKLNSDGITLTELSNDASPVKAMKSNNLPRLTHQMQNEGMLDALLNYADADDVDQDIKMLSMHIMDRAADDPVVLNHLSSQKRGIRNAIKFAVTKGSDESKKLGSGLLEKMLNTSEDTCSRIVDNGGLDAVLEASRSNDVETRRNCALALLNLSMFGGAENRIKMIKHRAQEWLYPLAFDQKDVCTKYFSFLALGVLIAQKELEASLAHTDTLSLVDDFVQQYKPSEVADTYKELSPFDTKQSAELLRRMLPNLESRIPQAQQLAAFHFATEAYAHAAAGSGPDAALKRAALRDMGAIDKLRWCACYPNARAAQLALEALAILHEKPPAMSPLSQQVQFWQPESVRNWCLLVGFKRLAQAFYECGVDGDLLLLLNDSILREEFRMDSLVDRRKFLRELEYVRILSDYSGCDSQRLRDLLRAISPEFVQYTYNLVHSGVDKRTLPLLTDEHLRADAQILNGIHRLHILEAIKRKYITTGNMVGAVGGTNPAMISGSQQALFSPTSNSQLQACLLQQSETDVFISYRRSTGALLASLLKVHLQMRGFAVFIDIERLEAGAFDQKLLESIRSAKHFILVLSNKALDRCLGDGDRKDWIHKEICAALENNCNIVPIIDVDFEWPRPEDLPEDMRDVVKFNGVRWIHDYQDACVDKLERFLKRQLNVNAGVEANSKTGQRLLRSSVGGSPSTVPPTQMPLSNASPSNSSGGSSQGRQSATPV*

**NSY-1**

*>TRINITY\_DN55499\_c0\_g1\_i3.p1 TRINITY\_DN55499\_c0\_g1~~TRINITY\_DN55499\_c0\_g1\_i3.p1 ORF type:3prime\_partial len:1531 (+),score=530.86 TRINITY\_DN55499\_c0\_g1\_i3:186-4775(+)*

*MAVRRELVSSMTARFEQSNAPMGAASSSNNNNAAPTAGKRLSQPIGHDRNMTIAVVVDVLQIDSGFGARQQAFDDIQRLCKTQKLTLVKIDFDRLRDNDNTTISHFYNADVAIVDLSLKNQQASLFFHIGVRENIGMRENIFIYHADAQSARDLELSSYTSQHFASNAIDSLGYSIGMSDSGKRECRVTVSWSPESGSGSSLASRLKMLLRESSQQSKAQAKEKLKDDLQKAKLLNDDLARKNELQRLRQRLDDHDMLSPDILFNFLISYRELQDWDGMVKLVEDVIRIESPAAKQCTKAPIIQHWYAFALNRRNVGSDREKALRAVNRLLKEKSNHSSELLGLCGRIYKDKYKASGYTDAESLKNAIRAYREGFKKDTSIYTGINLATLLVVSGKRFADCSELQNTANILFNLIGKKGPIAELRDYWDVATYFELSYLVDDLINACIAAECMFKLNPPPWYIKTTIQNIRMVNDAKNQQLQDRFRDGENMNMMSGSDSSASTRSWEQPSFICSSTASSHHRLPAAASRAAVSHAPPYMRARSEREDDVYQLFQWWAEFLIDAANSADCGRNSNTNSMSAAAAAALNTVPSQQPIVSFSQQPLVGTAASQLQTSPAGFLMPTNSNDPYNAAVNTFSQASAAAAPISQRTEFPILGHETLVEDDGRTQQRYIPGYISVTNMETNEGVAERSVSLRYLAKRVWNASNNSSAAAAAAAAAKTKNLALSLKSANNNRSSMPGMPRTSSDAMMMSLTPRDEAVSPVAATATAADNNDADEADDDDNEENVYEFKPDRIKGVTFVKHDDRCIYLWVITSEEFQLYFSNNAYRVRFHELYRDLMMKSSNSSGPALGAALGALDFGDGDEDEEVIDYEYVFDARGQKRLLGRGTYGTVFAARLKSTQVLIAIKEIRVSNAAQVQPLHDELKLHSRLRHKNIVHYIGSVYENNEFKIFMEQVPGGSLSALLRGPWGKLKEDGPLRHYCSQILEGLAYLHSSSIAHRDIKGDNVLINTYSGVLKISDFGTSRRLAGLTEFSDSIVGTAQYMAPEVIRRRPRSDLRAADIWSFGCTVVEMATAKPPFHDSREEFAIIFRVGENKEHPKIPDELSEVCKQFIEKCFRPEPEQRPSAAALMKHDFIVSSARQRHATATPNSRGTPVSATRSTLNVQQQQHGAGDASSSMSPFQMQNLLNRSFSVMPQQSPSSAAAAVAAAHTAQQMHAHYAHQQSYNPQNHHHNMPPPLSVAADSTDDLTGNASSSTSFMMPSSKHARLVNATGTSSTFSSEIAQSTVMSEAAINSPPAEESGGNPFFILRKQNERRNTLLDILKERQDVLVESLANTLRTRFSDKLSANVITHVDVKQLIITVIAILEQPDQKLAHIDRFASRLPSGDRGFSCFNQVRHCLFALSKALNDELKLRSGIKPHWMFNIEGLLKDASDEIIKNLPAFLRLPVEDLSAVEEEEDEQEAGENAGGGADSQMYYRHQQYIHIERREAAEDYNAAAFDDAAMSTDGDAPPSPHRVPSPHAAGAQQQQQQ*

**SEK-1**

*>TRINITY\_DN45434\_c0\_g1\_i2.p1 TRINITY\_DN45434\_c0\_g1~~TRINITY\_DN45434\_c0\_g1\_i2.p1 ORF type:complete len:400 (+),score=75.55 TRINITY\_DN45434\_c0\_g1\_i2:225-1424(+)*

*MSLAKRTKKKGIQLRLAADTIPNESDANGPIDTSMESSGYTGFNADAVPEFLLDAQATLTINGQDFRVSADDFQTLKELGRGQYGVVELKKHKGTGMEMAVKSIRYTGIQLEQRRALTDLQVSTRTGACPYLIKCYGALYRDGDVMLCMEVLDCSLDKVIAFLREQNAAGKEARIPEDILGCIAVAVVNALHFLKTELHVMHRDVKPSNILVNRAGEIKLCDFGIAGTLNESMAKTRNVGCNMYMAPERLDPSLTDIEGFDIRSDVWSLGITMLELAILKHPFRFASIFDQIKQVVNDPSPTLPPDLPYSATMKDFIDKCLIKDFNQRYKYDQLLAHPLIKKYTEHPADMASYFTRVLNAMDGVGDSAAAPASGGEPAKVSHLKKSTNTAARVSELEEL*

**PMK-1**

*>TRINITY\_DN50336\_c0\_g2\_i1.p1 TRINITY\_DN50336\_c0\_g2~~TRINITY\_DN50336\_c0\_g2\_i1.p1 ORF type:complete len:388 (+),score=97.41 TRINITY\_DN50336\_c0\_g2\_i1:192-1355(+)*

*MTEVDEKIPAEVGIVEDMDVEITRPSDNLSLHFYRTELNKTFFEIPNHYEQLLAVGVGAYGAVISAFDTVRQERVAVKKLNRPFQTAIHAKRTYREIKLLKHMNHENVIGLLDLFTPQMNVQSLNNFRDVYLVNELMGADLNQIIKSQKLSDDHVQFLVYQLLRGLKYIHSVGVIHRDLKPSNIAVNEDCGLKILDFGLARQHDEEMTGYVATRWYRAPEIMLNWMHYGESVDIWSAGCIMSELITRKPLFPGNDHIDQLTLILKVVGTPDDTFLERIPFEDARQFIRQLPRFPRKSFKDVYPTASASAVDLLEKMLDLDPESRISAVKTLEHPYLEQYHDEEDEPTGEKFDSWFEDKELTVDEWKKLVLDEIKSFAPPAPPQAEEE*

***Echiniscoides* cf. *sigismundi***

**Toll Pathway**

**Spaetzle**

*>TRINITY\_DN22736\_c0\_g1\_i1.p1 TRINITY\_DN22736\_c0\_g1~~TRINITY\_DN22736\_c0\_g1\_i1.p1 ORF type:5prime\_partial len:398 (+),score=174.96 TRINITY\_DN22736\_c0\_g1\_i1:2-1195(+)* ***(Spz3)***

*PQRPEKALHHHHPQQQQQQLPQSPPLPIPIVSQQYYPAASIQQQPQYNQWNSNNNINNKEHLLINNNSSSNIIASFINNNNNKESLQQREQLFLEAMKNPHQRDVALLFLSLLGMQTSQIQSFTNAAQFDSINNDLTAVVAAANAYKAAQRALQSPSLSKINPKSNEALQNDPATQHHHHQHQNEKKSAEQKLPPPPSTIASPCDVPAGPMHQHIDPNSQYCLLPGKQYPNSMIGSFIFEHRSTMRRMFGSISAKNLLKREEDSSDAAVGAAARLMHMDHFDHRKKRNVNLNINKKTNNSTRGKYLCPSVEELITPFWANNATGTRLAIVNSPPFEQAVHTIKCARNQQGRCHPTRPCWCTQEYSWFRLLAYDPAEDCKGIFMEWFKFPSSCNCMCY*

*>TRINITY\_DN24733\_c0\_g1\_i2.p1 TRINITY\_DN24733\_c0\_g1~~TRINITY\_DN24733\_c0\_g1\_i2.p1 ORF type:5prime\_partial len:212 (-),score=80.82 TRINITY\_DN24733\_c0\_g1\_i2:288-923(-)* ***(Spz3)***

*ANNSDGDTMAIVNFHPFEQAVQQEVCKLNAQGRCRNGCICEQKYAWYRLLAFNPKDECKGIFMDWFQFPSCCACRCYELPSLNLLFNDDQPSLSPPPTIEATPLDKNITKNVENKDEEASTNTQVITTPKSTTTTTTETFPKHFITVNVRNPGDAKSTFTQDAIKIEVEKLKRLRTSQEINGRNEFISPSSKNTLKRIQQWKHRSPKVVFD*

*>TRINITY\_DN32439\_c2\_g1\_i2.p1 TRINITY\_DN32439\_c2\_g1~~TRINITY\_DN32439\_c2\_g1\_i2.p1 ORF type:5prime\_partial len:341 (+),score=118.87 TRINITY\_DN32439\_c2\_g1\_i2:1-1023(+)* ***(Spz4)***

*ASAVTNACPSDQFVMTPFWANNSDGNTLAIVNFHPFEQAVQQEVCKNGIQGRCRDGCVCEQKHAWYRLLAFDPSEECKGIFMDWFQFPSCCSCRCYELPSSNPFKFDPIVHVVEENITKPILSIDKSNNNKVIENTDRKIDNHIFPNEEITLIEASKPLSTQPERFIEVKIQQPKSTTTSTTTTTTTEKPKTTTATTTTTTTTSTTTTEKPTTTKKTSTLSSTTATPITTTTINEKLDTKTIIIDNKDDDKTIISPRVKQILLNSRAQTLKLKDKVRDSINKKQEDQDLIQAELKKLRKLRESRNGNNYFDPFEWPTLKQLRQWSDRTAKIDDENVFVIT*

*>TRINITY\_DN27087\_c0\_g2\_i1.p1 TRINITY\_DN27087\_c0\_g2~~TRINITY\_DN27087\_c0\_g2\_i1.p1 ORF type:complete len:229 (-),score=64.09 TRINITY\_DN27087\_c0\_g2\_i1:480-1166(-)* ***(Spz4)***

*MMMKVLLIITITQIIYSYAQTRPRSQPPCDLNKESFCTSPGTNYPWLGITQFINQNLGTMRRMFGENSDPSVNEIIQGRKRIKSQQNSGGGQQHPEFRMMTTFDSNNNIDRKAINKDSTTYNPCHSEESIEQPFWIKNSRGDNRIVVNESPWDQFIHVEKCVNKLNGNTKTNSTSTSTRLLGCADGCGCFQEDRLVKLLVTDPNDLERGIFVDWVTVPGCCLCKCYSN*

**Toll**

*>TRINITY\_DN16336\_c0\_g1\_i2.p1 TRINITY\_DN16336\_c0\_g1~~TRINITY\_DN16336\_c0\_g1\_i2.p1 ORF type:internal len:406 (-),score=59.21 TRINITY\_DN16336\_c0\_g1\_i2:2-1216(-)* ***(Toll6-LRR only)***

*KIKNNTKLYNRDFFMSAAMRYFIFLVAASFQYTICQQLESCGNGEFKCDKSIDSTCLAQRFWCDGNIDCPNGRDEDVYLCNNHNIEAVASQNSPIDKMKTSVQNNFVKNEEHLNKLYQNCQLNKYPEKCSCVMYTHLYCDQLNLRSVPKAFDDILPPENLTHMRLENNNIRALPAHAFKNFTSVTLIDLRNNKLERIDVDAFSGLKDLMFLDLNENKLLNLKSYTFEELDALNFLNLSYNKLVDWEKDTFLGAHKVTWLELRHNQLTLSRFPTMFNGFKVLRTLELDDNRIVKITKDTFQGLSHLNHLFLSGNSIETIDFDTFQHLKNLSQLELRNNKIKTLLPETFQGLTNLQTLKLANNPIQSLPVTLFHDLVNLTTLDLSGVNIRNIEISMFDKLKNLKTIK*

*>TRINITY\_DN36308\_c0\_g2\_i1.p1 TRINITY\_DN36308\_c0\_g2~~TRINITY\_DN36308\_c0\_g2\_i1.p1 ORF type:internal len:637 (-),score=202.00 TRINITY\_DN36308\_c0\_g2\_i1:1-1908(-)* ***(Toll7-LRR only)***

*NYVDLSNNVIDSISEGAFKSLHRLMSVNISNNLLENLPLFEGLSSLRRFYAQNNQLKRLPNRFLEDSWRHLNYVDLCGNQLSSLPTVLGGASSELQKLTTLKLCRNKFRSLQLDGLQALEVLDLSGNELDLWRFSGCMPNKPNLKVLDLSRNHLQSLYNVSAELKSCDKLETLLINENMLTSLPDLKPAFPALKSLNLSSNQLRQLEWQKLPETLETLIMRENSLRTLIGDAMFVTIKNVDFEGNQLAQITSFPQEVEHINLRNNYITQLPKYIFQTLGRLQTVNLQNNRLEIINKTSMLISLNAPVPKFYINGNNLKCHCSMDYLLDDNTHGLPEIGDFNELECRDMRSYTYSSSRKRKMKTLNTTDMLCQYEEYCDVGCPCCEFDACDCKLTCPDGCSCYRDSNWRENIVDCSANARAFVSRSRLQDARLNQIPEMHVKSATKIYFDGNNIGTLKHPFYNYHHLRALYLNNSNINHIESGTLQKLDKLEILNLSNNKLTSLTGKEFEGLKNIKSLDLSYNKLDSISPESLSRFRKLQKLSVQGNRMRDLVDFPIPNLANLRVSIADNEWDCVCSQEDRQTGRWQALNEWLDAYRSVVKLDKVKCIDRSTGVAIARALALQGQRCDMNYIEAQEY*

*>TRINITY\_DN36010\_c0\_g1\_i2.p1 TRINITY\_DN36010\_c0\_g1~~TRINITY\_DN36010\_c0\_g1\_i2.p1 ORF type:internal len:617 (+),score=211.59 TRINITY\_DN36010\_c0\_g1\_i2:3-1850(+)* ***(Toll8-Complete)***

*LNTTDMLCQYEEYCDVSCPCCEFGACDCKLTCPDGCSCYRDSNWRENIVDCSANARAFVSRSRLQDARLNQIPEMHVKSATKIYFDGNNIGTLKHPFYNYHHLRALYLNNSNINHIESGTLQKLDKLEILNLSNNKLTSLTGKEFEGLKNIKSLDLSYNKLDSISPESLSRFHKLQKLSVQGNRMRDLVDFPIPNLANLRVSIADNEWDCVCSQEDRQTGRWQALNEWLDAYRSVVKLDKVKCIDRSTGVAIARALALQGQRCDMDYIEAQEYLARKAVQNSIRQHNYNTENRNLKPNFTQTDATSWLSGIFIGITVALIIIFAVLLFIFRYEAQVWTFSKFGCRLCASRDSFDDDDRPYDAFISYAPQDAVLVSRELAPKLDYGYPGYKLFLPTAEEKAMNEAILQGGRQSKRTIVVLSPAFLRKWATVEWSSAHKQLFKDRRQKVIFICVDDCDKRVDLDIDLRISMKRHPMLKLGERLFWKKLYFHMPDTHTNSKHNMISGSGLIGQQQQSGLAAPMMAYPHHYQAHHHTMGPANHHYHHLPTVNSATMHHHLPPHLTNGTGTLPYHHHGNPSWPTFVPTLQHPPPPIHHHNHHHHPSQQQQQHNPHQQQLYG*

*>TRINITY\_DN26122\_c0\_g1\_i2.p1 TRINITY\_DN26122\_c0\_g1~~TRINITY\_DN26122\_c0\_g1\_i2.p1 ORF type:internal len:714 (-),score=161.18 TRINITY\_DN26122\_c0\_g1\_i2:3-2141(-)* ***(Toll8-LRR only)***

*LLTVGMEFCKFYYKQTIPILFNFVIILEIFTATVQAQCPLWTNPACNCTLNAPKNYSINCNEASIIINENLINTTEYVYHLSMHNMGFQNLPTTLFQNSRNINITQFDISHNYIVTIATDALESLADTLEMFNISHNKLGRSVEPTIRLRELNQLYRVKVLDLSYNHIKQLSPFFFHNLQRLEHIYLQHNNLDYFPLRLFGELKSLKSINLANNKFVYLAEEAFYGLVKLNELDLSHNHIVKIESKTFQNTPKLRTLSLQDNKLDHIDFNLSSVIDLNLSFNLLDDLDDDDLGAIGNLEHFDLSWNKVQSLQDKTLPKSLQTLNIAGNLLQESGIPNLNNLSILKSLNLSNNFINNIGPNYFRENKHLQFIYLHNTNLTFIPYQAIVPLRKLQVLNLNDNDFFSEKIINIGRLLPTIEVLYLSNCRLYNIEISLNSVMKLLDLSHNQLDSTNIVQNSTSLQILNLSHNQFRKFPFLKHIIKLNTIIMDNNANLTTIDINKLPANALENLYVQNCAISNITGNQIMTKISNVDLKNNQLKLIPIVLQQKMPTLRKLDLSYNMINNVTTLPQLNWENLQYLDLSYNRIEKMAKNSLNQAKNLHSIFLRANQLKSLNISEFMEVENIANFDASNNEIRSLHNVHLLENMIYCNLSYNRFAVAGIQGMLKLQTLDLSYNRLTTVPIIPFNENLKRLYLSNNNITIAENKTVKHFVNS*

**IMD Pathway**

**Tak1**

*>TRINITY\_DN36670\_c0\_g8\_i1.p1 TRINITY\_DN36670\_c0\_g8~~TRINITY\_DN36670\_c0\_g8\_i1.p1 ORF type:3prime\_partial len:352 (+),score=97.46 TRINITY\_DN36670\_c0\_g8\_i1:139-1191(+)*

*MDNKFDEVEEINYDDINLVSIVGRGAFGVVWRGTWKDKEVAIKYVESESEIDSFRREVNQLIRAKQENIVHIFGVCITTPVCLVMEFAECGSLFSLLHHGNKDERVSYSLGHTISWCLQCARGVEYLHSMKPKPVVHRDLKPPNLLLTDSCRTVKICDFGTAVDAKTYMTNNKGSAAWMAPEVFEGVHYSESCDVFSFGVIFWELLARRKPFQDIGGPALRILWLVHQGSRPPTLFNCPPLMNELMTSCWRKEPELRPTMLTVVKTLEFLIRFVSGYDEAINWPPPSSGLKTPTPSRKPTVQSFPSTPANQDSTTSSDLFSSTASLDDSVNTIKALDDVDNNNDNDNSSLV*

**JNK Pathway**

**Hemipterous**

*>TRINITY\_DN34206\_c0\_g1\_i1.p1 TRINITY\_DN34206\_c0\_g1~~TRINITY\_DN34206\_c0\_g1\_i1.p1 ORF type:complete len:673 (-),score=208.82 TRINITY\_DN34206\_c0\_g1\_i1:164-2182(-)*

*MSSRRLPKLDLLCDHNAKDSIKDVKPRGERKQLSLNFMPNATCGAAIGRTIVSRLNDTNNNNTIQDQQQQAFGLKEFRDSYRITRRKKLELAREQLPPSLRSSFMPDDERIIFEEMENEEKLREIMKRTGILTIRGVKYHALPDDLEHIGEVGNGVCGTVVKMRFKKTGDVIAVKQMRRSGNREENKRIIRDLEVILKSNDCPHIVQCYGCFVTESEVWICMELMTSCMEKLLQKTALLNGRDRSRVPEEIIGKMSVSVVKALHYLKERHGVIHRDVKPSNILVDARTGKFKLCDFGISGRLVDSKAKTRTAGCAAYMAPERISPPDPNKPDYDIRADVWSFGISLYELATGDMPYKNCKGDFEVLTKIIEDDPPLLSPDQGYSVAFCSFIQACLTKDHIYRPKYRQLLDHKFVRLFELKNVDVIGWLRSVTTNTQFLNQQREMLKKPTVQKYVQVNSPPAADESCNVIYHQTPPPPLPIKVKSRKTSRERCEEILLEIRRNSATNAAVAAKNPTSNKDKHRKQSPSPARGVQNIYEMVRQRYLNKSPHHRQQSQNTYYEWLANEEAEMQAAYNRSYYNNVHDSQQLDRDNPMSSSLPSRFSWMYRSSPAKMQQQNLARRSTSAGRPRHGQKYIIPRAVLDKNRQCSPEYRNSSLNRFLTAVPGGDSNLDCF*

**Jnk**

*>TRINITY\_DN32792\_c0\_g2\_i2.p1 TRINITY\_DN32792\_c0\_g2~~TRINITY\_DN32792\_c0\_g2\_i2.p1 ORF type:3prime\_partial len:548 (+),score=175.48 TRINITY\_DN32792\_c0\_g2\_i2:207-1847(+)*

*MDAERRLQLDIKLASKHPGMFYTQEVGDTRFTLLKRYTNLKPIGSGAQGIVCAAYDTMHHQNVAIKKLSRPFQNGTHAKRAYREFKLMKLVNHKNVIGLLNAFTPQRTFDEFTDVYLVMELMDANLCQVIQMELDHERMSYLLYQLLCGIKHLHTAGIIHRDLKPSNIVVRSDCTLKILDFGLARSANASYMMTPYVVTRYYRAPEVILGMGYKDNVDIWSVGCIFGEMIRGGVLFPGSDHIDQWNKIIEQLGTPVADFMRRLQPNVRNYVENRPKYAGYAFEKLFPDVLFPRDSGEHKALRAPIARDLLAKMLVVDPEKRISVEEALRHPYINVWYEENEVNAPPAGLYDHTVEEGEHTVDEWKRLIYDEVIAYEHIHEESSPQSLSSPNNTKLPDFTNSNGNGNTTTTTNNNNNNGNGFDTPTNNDTNTLNGATSTAGSSSWMQSAAYGYTERTNRYKQTTSTTKSTLTRSLEHDQGDIIEGEPVVRENTTVTRRITPGGYGQQPLVSSSTKTYDSTIGNENISVGTDANNSSAYDVSTKVRTVE*

**TIR-1 Pathway**

**TIR-1**

*>TRINITY\_DN34988\_c0\_g1\_i3.p1 TRINITY\_DN34988\_c0\_g1~~TRINITY\_DN34988\_c0\_g1\_i3.p1 ORF type:complete len:948 (+),score=348.20 TRINITY\_DN34988\_c0\_g1\_i3:53-2896(+)*

*MNHNATFTYQPTTNNSPINHQIKRKNVQSVDRLNDRIKKMRRNKNQTRPTGVKTVIARLEKANSVEECNGSDFGNSPEPIVSEPDSPDVQSEASALRQKYPPHHSHWLSPGALVSEKRMHSTSYSSSKHRKELVEMVNGREIKSSKESSSNKRQHSREEVEQVDASGERICNSQEDFFGHSKVSSSLETLDALGKSVKQAAAHISETGGKKSATYVQNSQGDLKQIAGDAKWSGRELLSKINTDADGQIVGEITGNVIQGIGDPDDDEGELISRIATFRIPGGNADSQKLAIEDSCIGSSQGTFDYGKPQQQQTSLKSMLQDFWSQMESKDDASQISNSQQGEAMLDNLIDYVDNENMDQDVQVLSMRVLDHCADDPVILNRLSTQSKGINGAIKFAVKKGSDESKKLGSGLLEKMLNTSEDTCSRIVDSGGLDAILDASRSTSTETRRNCALALLNLAMFGGAENRLKMVKRRVQEWLYPLAFDKDECTKYFSCLTIGVLIANKELEISVAQSETLNLVDDFVCTHTPAEVADEFTKSDIDRRQSHEVLKRMLPNLESRVPQAQQLAAFHFAMEMQCEKQMSKRKQILREIDAIEKLKWCASYPNARAAELAAQALASINEKPAFQLSQCVHLWMASQVQKWCLLIEFRKLSHFIHELDIDGDILLQLTDEMLRDDLQLNSHVQRKRFIRELSHLKALCDYSSCDPARLRDFLKSIGHDYIQYTYNFIRNGVDQRNLSLLTDDHLRYDAHIANGIHRLQICESLRKKFRATSGNIDDVRSESDVFISYRRSTGSQLASLLKVHLQLRGFSVFIDIERLEAGAFDQKLLESIRVAKHFVLVLSQSALDRCIHDDEKRDWVHKEICAALENKCNIVPIVDSDFQWPKAESLPADMREILKFNGVRWIHDYQDACVEKLERFLKREININDDGSTTNNLASISRPLQGL*

**NSY-1**

*>TRINITY\_DN22172\_c0\_g1\_i1.p1 TRINITY\_DN22172\_c0\_g1~~TRINITY\_DN22172\_c0\_g1\_i1.p1 ORF type:3prime\_partial len:1050 (+),score=413.65 TRINITY\_DN22172\_c0\_g1\_i1:182-3328(+)*

*MVSPLKPSTQPLSQPIGQNRKFTIAILIDLSHSDSGICVRKQALDEITKLCKNQRVKLLKVEYDRLRETESKAINLFYNADVAIVDLSIKSQQASLFFHVGVRENIGMRENILIYHSEAQSARDLELSPPQINNAINILGYNVVVGDRGKRECKVTYGLENKNNSTTFATVLKRLLRESTHQCKAQAKTKLKDDLQKAKSLGSEGHKEELQRLRRRLDDTEMLSPDILFNFLISYRELQDYDGMIKLVDDVHQIPSPSAQQCINAIIIQHWYAFALNRRNQKGDREKALKVVLKLLDDKNNHSSELLGLCGRIYKDQYKDSDYMDSNALHQAINAYREGFKKDISIYTGINLASLLVVSGKRFADCPELQGTANILFNQIGKKGPLAELQDYWDVATYFELNYLIDDFSNACKAAECMFKLNAPPWALKTTIHNLQMVNDARQKQSIELHLSSDITPKTSIRSDLDDNTKKISEKLFHWWTEFLQDAALMNVENRIQNRVQLPILSYETLTQDDGSQVQRYIPGFVMVGKVENEGEVEKNIRLWYLPKEMWQLPKQFPVQPTQFLTNNTQQSQQYVPSSQQVAGQSSSSPINIINENDETVDTIMENVNEETNINTKNNNEPDDDDENEFEFKPENVKGVTLYKNDERCIYLWVNFGDEFQLFFAHESFRQHFYSLYRDLIETSQNNAIDFEEEPETIDYDYQFDSLQNKKLLGRGTFGNVYAARLKNNQRLIAVKEIRVENEAEVQPLHDELKLHSRLLHKNIVQYIGSTCENNVFKIFMEQVPGGSLSDLLRTQWGPLSEGAMTHYAKQILEGLDYLHSNSIAHRDIKGDNVLINSYSGVLKISDFGTSKRLAGLTYYPDSVAGTAQYMAPEVIHSKTNRRPRSDLRAADIWSFGCTCVEMATAKSPFFDLNDAYAIMYRVGENKEHPKIPDELSQICRNFIERCFLVEPDERPTACILLKDEFLCKKRSKANKDAVNTNNSNTNSVYTRSVSAIASHLCQSSFDSTDDIQAVPQTANIITNNKNNHKIIINNNNNNNNVASSSTAK*

**SEK-1**

*>TRINITY\_DN29712\_c0\_g1\_i1.p1 TRINITY\_DN29712\_c0\_g1~~TRINITY\_DN29712\_c0\_g1\_i1.p1 ORF type:complete len:363 (-),score=119.46 TRINITY\_DN29712\_c0\_g1\_i1:174-1262(-)*

*MSLPKRSNPRKKIPKLSINPTVTTINDNKSQKNETFPEKHPHEEEGHVPAFLESCANLAINGADVRVCAEDLITVKELGRGQYGIVELKKHRESGVEMAVKSIRYSGIQLEKKRALTDLHVSTKTGDCPHLIDCFGALYRDGDVMICMEVLDSSLDKIIVPLRTHQLNFPEPILGKIAYAIVTALHYLKNQLKVMHRDVKPSNILIRRNGDVKLCDFGIAGTLNESLAATRNVGCNLYMAPERLDPGLEVQGFDIRSDVWSLGITMLELCILKHPYKFKTVFDQLKQVVHNAPPTLPTESGYSADVKNFIDKCAVKDVQSRWTYDQLLEHPMVQSNKGVDCAEFFRIAIDLLDSGDDEQQQS*

**PMK-1**

*>TRINITY\_DN31287\_c0\_g1\_i1.p1 TRINITY\_DN31287\_c0\_g1~~TRINITY\_DN31287\_c0\_g1\_i1.p1 ORF type:complete len:393 (+),score=124.36 TRINITY\_DN31287\_c0\_g1\_i1:77-1255(+)*

*MADTIPANAAINQSMDCEMLRHSDKEPIKFYRTELNKTFFEIPTHYQQLQVVGVGAYGAVVSAVSNKLNTKAAIKKLNRPFQTAIHAKRTFREVSLLKHMQHENVIGLIDLFSPQIHCNNLNSFKDCYLVSELMGADLNQIVKSQRLSDDHVQFLVYQLLRGLKYIHSVGIIHRDLKPSNIAVNEDCELKILDFGLARPHDEEMTGYVATRWYRAPEIMLSWMHYKNTVDVWSAGCIMSELITGKPLFPGTDHIDQLTRILKIVGTPEDEFIDKIPYEDARQFIRQLPRYNRVNFADFYKNHAASPDAVNLLEKMLAFDAEIRITAEEALEHPYLEQYHDKDDEPIGTPFNDWFESKELTVDEWKNLVLKEIVDFVPPLLHHNVDNDEHMDH*

***Milnesium tardigradum***

**Toll Pathway**

**Spaetzle**

*>Gene.26074::GFGZ01032235.1::g.26074::m.26074 Gene.26074::GFGZ01032235.1::g.26074 ORF type:5prime\_partial len:156 (-) GFGZ01032235.1:192-659(-)* ***(Spz3)***

*YIHENHGDMKRLFDGLKDPLILANEHTAPANYHMRVSKLATTRNPCSSDSYMEQPYWSKNVNDELRVIVNQSPFEQFVQIEKCKEAPADERLKCPGDECSCMQEYRMLRLVAYDPSTKEQGIFMDYFRMASCCQCKCIVTLTNGTDLPKRGDRDL*

*>Gene.13229::GFGZ01015569.1::g.13229::m.13229 Gene.13229::GFGZ01015569.1::g.13229 ORF type:complete len:455 (+) GFGZ01015569.1:181-1545(+)* ***(Spz4)***

*MHNKPYQYNYNMYCRYDFHVSFHIHQHTNLTPYILILILIYSYICKADIFDLPKTNYVPRYRPDFDLREIPCDLGEGNACTRPGRAYPWLAMRDYIKDNQALIKRMYGDNCDAKTPSKLRAQGPLETRSQYARTALVNACPSEQFVITPFWANNSDGATLAVVNFHPFEQAVQQEICKSGVQGRCKDGCLCEQKHSWYRLLAFDPRNECRGIFMDWFQFPSCCACRCYDVPSPEGEPFVSAVDAEPKLTDLNGLYATASPQSTTQLAVTTPLSNTTEYANATLIPSTESNSTVPRVTIAARTILTTATPAVSNISTTNNLFTPYKNTTDNPAASRSYTTTRNVTLTSTQTRTSTRRRFMPVTATPTTVSTTSTTAASTTALSSFNSINISNSHNDHSTSTVHSAEEASVRPTVVEESPRSTEQMTMSQNLLRNTYSSYIISNGRPLWKAWYSKT*

**Toll**

*>Gene.19845::GFGZ01023890.1::g.19845::m.19845 Gene.19845::GFGZ01023890.1::g.19845 ORF type:3prime\_partial len:451 (+) GFGZ01023890.1:97-1446(+)* ***(Toll7-LRR only)***

*MKRITTLDIGRTDLSKSASLFGGLNGVFRIVMDSNYLADIRDTDLFGGFTGNLDTLNLEHCNLTSLPSGYFDNIVKPKLRVLNLAHNQIQFPELINPSLQSSFSGYQSLTELSLKGNQLSTFLPSLVTGLAGLNVLDLSCNAWTRISSRFFNGLKQLKLLNLDMCHDHPWSQHHVSQTVTIDDDAFDYFSGASTLSMRHGHIDNRIFRILSRMQNSAQNLLEVLDLGGNSITSLDFRSFSGFTSLKKLVLEHNQLSTLAASQFASIPNLQTLNLAYNNIAQLAVGQFNGSPQLNNLKLDSNQLASLPVGVFDSVTSLESLELQNNQLTELGPFVNRDFASLQKLDLTGNPLWRIKAYELNKFTGLKTLYLWGTKVQEIEKGAFDVLKVDTTTSVSLPRESLGCYNENLWLRDYISSNGFHEFVHVISSTDTDSRPHLYISHVPKCTAADG*

*>Gene.10506::GFGZ01012108.1::g.10506::m.10506 Gene.10506::GFGZ01012108.1::g.10506 ORF type:3prime\_partial len:496 (-) GFGZ01012108.1:1-1485(-)* ***(Toll8-complete)***

*MAVAEGSVGFCVFALTIIAMAGTHTHAQSAEPVTSDIDDVTCQDPKNQNVFKLMGTSEEVYLCQYQEQCSEECHCCEFAACDCKMTCPLNCTCFHDKNWTRNVIDCSNQLLTNTPLMIPMHSTDVFMDGNALVRLPEHTFLGRTRMTVLYLNHSQIQRLDNRTFNGLLNLRQLYLQHNQIQTLNGFEFMQLELLEYLDLSWNEISNIRAHTFTPFRRLRVLNLAGNQLRFLSNVLPLISLASHTHMLINNNLWECDCNNEHEQKVTDVMMRYASRIADLLQLQCYDRRQYPAILRDLSRPDERCTTMEALTRMESLNYANPANAHHASNSIDNYIMVIVGAILGFVCLICLLTIGLAIRYRYEIKVCLYSRFRLRLCANGDESEDKASQCYEKLFDAFISYSDLDEHLVLGELAPRLEFGSPKYKLFLHYRDHPLGMRTPESIIQGVSLSKRTILVLSENYLKREWSKLDFKTAHQQVFKDKRNKIIIVLLGDIQ*

**Imd Pathway**

**JNK Pathway**

**Hemipterous**

*>Gene.14207::GFGZ01016883.1::g.14207::m.14207 Gene.14207::GFGZ01016883.1::g.14207 ORF type:complete len:544 (+) GFGZ01016883.1:147-1778(+)*

*MDGKGLGESFDDKIRDLERRIQVENDKNGVKSTTSTETVPPAHAPFSKTAALKNFSLNLKSPMAPRKEPKHLSMATVGPSTGRSIGPQLQNGDTSPEPSLLGFRDSFRLTRQRRLELASSTMPPGINTSPSPSRPEDQNEYEDKLVEIMKLTGIMTLRGEKYPCTIDDLEHLGELGHGTCGTVVKMKFKKTGDIMAVKIMRKSGNREENKRTIRDLDVVLKSHDCPYIVQCVGCFVTDSEVWICMELMSTCLDKLLKRTEAQIPEKILGKLSVSVLKALNYLKECHGVIHRDVKPSNILLDEKGTFKLCDFGISGRLVDSKAKTRCGGCAAYMAPERICPPDPNRPDYDIRADVWSFGISLIELATGECPYRNSKTDFEVLTKILEEDSPTLPPYQGFSMDFCAFVRDCLIKDYKRRPKYRKLLDHPFIVRYELLKVDVATWFKQTYAPRPSLHSDLLLSSRHPFNALNGLSTFANIRSFYNGGSNTDLSISTNSSSSANSAPATPHKSWSIRQATRTIFRTSANIPVPNTAPLPRKNYFITN*

**Jnk**

*>Gene.19939::GFGZ01023996.1::g.19939::m.19939 Gene.19939::GFGZ01023996.1::g.19939 ORF type:5prime\_partial len:221 (+) GFGZ01023996.1:2-664(+)* ***(fragmented at N-terminal)***

*GHMVSRMHLGEMIRGAVLFPGTDHIDQWNKIIEQLGTPSTDFMRRLQPSVRQYVENRPKYSGYAFEKLFPDVLFPPDSQEHPKLKANHARDLLLQMLVIDPEKRISVDEALMHQYINVWYEETEVNGPAPGPYDHSVDEREHTVEEWKRLIYDEVSLYERQFDKNCAADLLKLQTASNNREDDHDSRNRVPSVGRSDSDSNERQSMGNNSTATSVKNSRS*

**Jra**

*>Gene.21560::GFGZ01025851.1::g.21560::m.21560 Gene.21560::GFGZ01025851.1::g.21560 ORF type:complete len:315 (-) GFGZ01025851.1:719-1663(-)*

*MDVSMSDASSNSNHTNFDKSQSKKSRPLTLDLNPKQYSTGQSLTVNPDASVKASPSFIALTSPDLQMLQLGSPELEKLIIQGLMSAQTPTPTQLIFPKNVTEEQESYAKGFVDALTALHRNGAMAYNMTPTQTGVPPFPVNGQVFPQFFVPQQQMQLLQQQMQPQQMQMQMQVSTLPVQAKQEPRESSYTPSVSPALSDPQTVPSVTSSKSSDSTASMNVGGVINLEDQSRMKVERKRERNRVAAAKCRQRKLEKISTLEERIRGIQNVNSELENSAQKLREEVQKYKQELLTHIKSGCHIDLSSQLLQSLQSL*

**Fos**

*>Gene.23370::GFGZ01028002.1::g.23370::m.23370 Gene.23370::GFGZ01028002.1::g.23370 ORF type:3prime\_partial len:301 (+) GFGZ01028002.1:377-1276(+)*

*MTSTTTTSSTTAAAADASRLGYAKILWEMANGSGSNTRESNSASTMLQPTSAHLAFPTHTNSHSSVPTSFYPVYLQQQHQPQTSQSAAIKTEPGVYQQRQPSLTHSDVSSAQNGSNNQKSSGSRGRGGRRPVRDEKLTAEEEERRKVRRERNKQAAARCRKRRLDHTNVLMEETDCLEDKQTKLKSEVEMLQNQKAELEFILECHRRNCSKMGQMSSNGSSRSATPQTATMVNASNVISAEEQSQRQSQTSMVQSQSQVTTSMTTAMLPPPPIVVTSAPVASVHSGQKHAVPYASRPTSL*

**TIR-1 Pathway**

**SEK-1**

*>Gene.7963::GFGZ01009139.1::g.7963::m.7963 Gene.7963::GFGZ01009139.1::g.7963 ORF type:complete len:350 (+) GFGZ01009139.1:360-1409(+)*

*MSLGRPKGSHRKVTPNFRFTNDTTQQNNTNHVMHGPPKAGLDVCAPMTFKGQRFNVCADDLEIISELGRGQYGVVDKVRHRPSGHVFAVKRIRSTEDAEERRRMLQDLEVNTRSGDCPYLVQSYGALFREGDLWICMEVMDTSLDYFYKTAWKYAYGMPEPICGKIAVAVISGLQFLRSELKVMHRDVKPSNILLSRDGSIKLCDFGISGRLEQSIAKTRGIGCSLYMAPERLVPPDDSEGYDIRSDVWSFGITLIEVATGSHPFKWTNLFQQMKQVVEDPPPFLNSAIDASPEFRSFIDQCVKKKSDDRPKYDELLRHDFLKKYINSDTNIGEFVTRVLDTAEQNLAS*

**PMK-1**

*>Gene.23110::GFGZ01027723.1::g.23110::m.23110 Gene.23110::GFGZ01027723.1::g.23110 ORF type:complete len:265 (+) GFGZ01027723.1:426-1220(+)* ***(fragmented at the C-terminal)***

*MEVPDRYQNLQAVGSGAYGNVCSADDKVTQQKVAIKKLARPFQTPIHAKRTYRELRLLKHMNHDNVIGLLDVFTPQTSIDEFTDVYLVTHLMGADLSQIVKTQKLTDPHIQFLVYQILRGLKYIHSAGVIHRDLKPGNIAVNEDCELRILDFGLARQAQDEMTGYVATRWYRAPEIMLNWMHYTQTVDIWSVGCIMAELITGKPLFPGSDHINQLNLILDIVGTPSADLLEKIESEDARMYIKSLPKKQPRDFRQVSLKLLTKP*

***Hypsibius exemplaris***

**Toll Pathway**

**Spaetzle**

*>BV898\_01376.p01 hypsibius\_dujardini\_nhd315\_core\_32\_85\_1 protein* ***(Spz2)***

*MKYHCQLLVFVLDISIIFYRTIFATNSNQTDKDAQNLSRDTLVTTSTANPSVAPAKLLFRGYQHNYYTYDEPLTPYAKVRPLLGHGFLSDTLAKLDPSFRTAKKAKAKRRQQQATFSGFEKYPAVVFSSSGVGTLDRMDVAASDAKLQRHLLAAQINETVGGRVGPGTKLDSVYGITMGSSYTPACVKSPLQTICLDDPFYPTDSVKEAVLQSRQDFMKLYADVAFQSADNLCDGITRQDEEKHCNVFSQIHPISSSSSWTANYAHKQGPQGGSMDLRSRSAAATTTQPPTNSPPFHGQGKGYICQSVIHYARVLRAKNHRGQWRIVVNVPGYTQTSRFEECLRPLHRCQYISSKLQTSCIQKWNFHRLMVWDKYNGFETDIFRLPIACSCFIRPKAYQVTGRFYGERGFGPDTSRQSVDLRKAPRTVPLQKKELLAPPMQISETSKRYSYMPPDGSPVDPYLYYYYLSNLLPDQSVKYVAPGTVQVGSTEYVYGNNGVTQKKSL*

*>BV898\_11103.p01 hypsibius\_dujardini\_nhd315\_core\_32\_85\_1 protein* ***(Spz2)***

*MLFPTGRVLIFAVSLFMLIGADDPAAVNNRVTLSIVPKPQCAQSTTLSFCLDDATYPNDDIQREINANYGVFYKMYADVANQSTASLVDGLGGEDEAKYDYAFYYGDRRNSLSGSTSKDRPVYSNYVFRDDYYKEGGYVCPAFIEYTSLFQATNARGEWQYIVNLKPWTQTVRLEQCFYPLAPCSFMSPSFKTQCVQKYSYQRLIAYEPHGRGLYTDIFRLPTACSCFIRPLKSSQSLGLLMSDASQSIASNSPSYAPSNAITNGFKPVRVRDPSGRSSPGYSLAASQSSNSWYPDSQPMLMASSSRSDIEAGVPPQQDSRLVERRRVRPDGLSLSDITSDPEVDLSFGNPATGDYQGTSRGGGGGGPPMSYDSPSNHGPPQTAYDSPSSYQQPRQRGGSGGPPSQFQGDESHMEPSYSNGPSPYSGMGPDNGGGGNFNGNGNGDGRGMNGNSGGPGPRMWNNNNNGPPSDNNGPPQGPPRNGQSGDYRMSPGPGYYDYNSGQRN*

*>BV898\_01649.p01 hypsibius\_dujardini\_nhd315\_core\_32\_85\_1 protein* ***(Spz2)***

*MSVIPVLLLVSSGVLAHVVFAGDDGEYYPFFNPVFQQPILSPSHRSQRMRFIPPDDDRIIARPSGYKKHGQLSPAIGAQPPFLFPGFTPVTFPSCAEGPSFAYCLTDSQYPTDLIASCIENDPETFKRLRNQVLWSCDVFPELEAPVMTEFPLEVQEEVTTESSVIPVPAEEPATTEQEVLQPMRVGGIPARGRAVQPVRPPMRERLTKAAAKAPLRVRPVVAGVASPRTKTAPSRRTRRDDTSGLQFLTQQRVAMNHSYEVCSSAVRNDLGIVRAESELGEWGWLVQTGECKQIVRSEECITVGEPCAYLCSSLKSQCTQRYSLQRLLTCTAERGLHLDWYRIPASCGCQVQFAGHTAQHTTTADPLGD*

*>BV898\_10383.p01 hypsibius\_dujardini\_nhd315\_core\_32\_85\_1 protein* ***(Spz3)***

*MADSAFVFSDTFPQAQLLHQSSSPQGKPIQPIGTACDGLTQDYCAKPGHFYPRSEISYYIEENRSIMKRMFGSVSARSLLKKDEEEAAVDNSDLRRRRQAKQLAQPAVYLCPVEEELVTPFWALNGTGTKLAIVNTPPFEQAIHTVKCARGQPGRCHPTRPCLCTQEYSWFRLLAYDSSDNCKGIFME*

*>BV898\_10371.p01 hypsibius\_dujardini\_nhd315\_core\_32\_85\_1 protein* ***(Spz4)***

*MQRREGGSLICDSERNYQIGIGEHSTHRTGDMRRDHWVLQIPLRQLWFIVLVNLLTNDSIAAQAFTSFDDSPSPSDNYIPRSRPDFNFADIPCDLKENNFCTRAGKAYPWYGIGNFIADNRAMIKRLYGSENQRGPSANHAQGPITTRQGKSVAGTGTNACPSEQFVVTPFWANNSDGNTLALVNFHPFEQAIQQEICKTGVQGRCRDGCQCEQKHAWYRLLAFDPRNECKGIFMDWFQFPSCCSCNCYDNLPVRDASSSSTTPSTSTLPTVEAKSDEGLSAKLINVSAMAEGPPTTSQLSTSSLTSQKTVSHTSSSINITTTSTSTLLPKSRTQQPSSTTTSPLLTTLPAPLNVPCLSTTASSQSATTLSHPRLSLLASAPATSRYLRLKPYLPFRRAQLLEPRLQMQSHLSPLHPNILGQED*

**Toll**

*>BV898\_02438.p01 hypsibius\_dujardini\_nhd315\_core\_32\_85\_1 protein* ***(Toll2-LRR only)***

*MPDTSKKRSEGSSIRRLFCGCISGTDQTSSEPMEEDKSIHFYSGIKDDCNYGFAGVECGSPLPHVYEEISEAEKGRLPLRYWKPHRSVPLVEPYEIIPIPTVGGPATRARTSRFDIRLSDPKMKSLFEEFLREHWVKDHAQAEGGETYGQSSNESGISVWNEEEEPRTGGASIDGSLPYCHLRVFLGLSFAMTTQVALGRDVAPHDHEAAQPTAPCLTSINFAKCNCDFIQRGYLVDCNNITWGELLQFFTAFGASSEALDIFVVLHDFSGDVDDHGFDRLEEQTLGKLAQHWKSLTITRASNVTALPNFLWATALEDIFLENLTQLSSKINDSVLPPNLSQLILDGINISQLAGWSLEGLSKLTHLEIIRYGSMNWAGRQYFTNVTTLTELHIVGGQLTGLTDSSLTGLENLQILNLSANGLKDLPGALLREMLDLEILDVSYNDLIAVPDGWLETNLELREFRARWNDIQSIPSEFFDNTQQLAQLDLTENYIHSIPAKLFKNTSKLSVLKLRDNNLASVMDGDFEHLTNLTDLDLGMNLLTSLPARAFRGLGRLVELNLTRNYIADIARDAFRDLHSVREIDLSHNRLTVLKKGMFTGLRHKLAKLDLSDNKINLVEPEALHGVNASVIDMAGSSFLCSCANILLKAYLTSPTLCVDPRDMTIHNLADIVADNCASSDEAFIKSRQEGLFFAGSVLFMATIFLLIGIVAVLSYRVSSRRVFYPSTYYDQENFTGSDFEIKTISTSL*

*>BV898\_00416.p01 hypsibius\_dujardini\_nhd315\_core\_32\_85\_1 protein* ***(Toll2-LRR only)***

*MILWLTLMFWLFLPAIRTDGDGSCPKPNSPNCRVDCTGLSYNILCVDYVHFQTLKDDFDLLASYGKKIIVNLWNLNNSALHVESNLFGKSLVLVERLSLHNNSGLILFPNLRGAKILESILIVGSPKMAEFTIETLPDSMKEIILMNTGVTRLEVETAELARNLTHMERFTLQGSNISFIQPNFFSVFPNLNRIKFASNSFLVTDQSSGVEESGSGIGNAMFTTTLPLDHFIFKDNDFSGTPQADATTFLRRTLRSLKLHGANGYTDASVVDFSGNGILIDTGTLFELTKFLREIGSLNLRANPFENSMTITDMFANFTNLRKLDLSLTNLPISRGAFSNLPQLEELYLSGNSFTDMTAVDMFERSNSTKLRILDLSNNTLTALPEGNLERINGNLQNLSLNNNMLLPAEFTPEIVGTSDFADNATFAAINNGYRATLAHWSSLRELGLSANSWTTFDGKFLAPLTVLNTVDLSSNPFVNITKEYFANMPNSIRKIDLSMHQPEDVDPATVDEDAFSTMPPNISALILIKGNFRNWIFKRLQNMTNSSLASLETLDLQDNLIRFLDGDSLNGFPNLKSLSLRGNLLQSMANASFRNLKSLVNLTVSLNQIVRIDSNDFEGLGNIKRIDLRANKIAHIESGAFDQLSTLTNLYLGENNMTDINGVFQTNNYNLIHLGLQKNNITCFNRTALDPLRGIKWLYTSLPKEVTTSIFVDPGTDDLTTNNMMAKVYANPLDSGDNLDCDVKYDSPLLHSAQLMVTDNITLWETDHVRLEVSNPWDLSTRKFIAHVAKCYIPQPRNMTIITGNLLCSMGDSKTAGGLRVSCNYFPIYSVTILVLTCRKLLF*

*>BV898\_08130.p01 hypsibius\_dujardini\_nhd315\_core\_32\_85\_1 protein* ***(Toll6-LRR only)***

*MELILRIGLVWSIYFLHAAVRTFSIRHQPDGVSEGLHEMPATSSVSFASTHSSANRTGTDGANIMHGPVAKSSSRMPEVSSCPEYCVCSQADADGALLSCNGEHVFPYPELSAFGNVSRLLLENFKKNDLRPADLAGLMATARELRLPRNGIATIRDSLFTGTKSLKRLDLSGNKLSLLTNLTFIGLGSGGLLYLDLSGNRIAAIDPGSFAYLRDLIQLDLNSNKLSQLPNDLFKGLLSLQYLNLEVNQIREIQPHALSHIPRLVHLNLAMNTQLSATSFGLVDFKDLLALQYCDLSHCGLQAVPSNLRSTIRDIRLTGNKLVNITKNSLEKYPALAVLVMDDCAIQHIAPDAFVKLTSLQRLWMNGNGLRGVPLNLPSSLKGLYLDDNNIKLLQGRDMAGLLDMEEIRLQGNQITTIESSTFRGMPHLATLDLRANRLGTLNTALFPPVNSISRLDLSLNPLRTVGRDFLQHLGALKQLEIIRTHAAATVDVPADFFSLLPQLTALDLGGSPALANRLLHEISASPNRSSVLPHLHTLSLRACELTFFETNLEDFFARVPKIKLAQNELACFRENRWLLRLIQHDQKRFYRAQDLKCSTPRHLQGRKVISVSVDTLNDTRVPIPSAALNHNSHFSPGGRQTKHITPSSPVVVVGVADTSRTWIITFIACLFTAAVVSLFFLVVLSCCDAKEARLKRASLCAKLSRFLRRKHDPFPEQMAASNRTLYRSQDDSIFMIGTSESSYPALSPYEELEQRTFRSQLEGIYENDCLSTISTLEIRV*

*>BV898\_10174.p01 hypsibius\_dujardini\_nhd315\_core\_32\_85\_1 protein* ***(Toll8-complete)***

*MLLHRQSGLFPRTSAAGSCMTCWGRLSLLRTLLWCTMAAMVMTVVADPARGQSVARVDYPYACPEECQCQTTLRNGVVVECALLSIGLWSDFRAIQSNFTQGLIIQCDARHLDSKLLEGAFTHLTDLETLSLVDCAFTKVPRDAFLGLHRLKSLTVSTRTAANQLELEEGSLRRLSNLESLDLQRSNLQRLPEGELCALTKLKTLSLQGNALASIAHLGTSAGCLGNLEKAFFDGNSLRNMDKNIGDYLGPNLKVLSLSRNKLDSFSDDSFSRLKQLTDLDLSVNHIESISDGLWQHQANLERLSLFGNQVKSLPVNAFVMLAHLRELNLSQNVLTNQWITGDLFRSLQMLQWLDVSANQLTHIDRAMLRNLLNLVKFHAGQNRIEWIEPQAFTYQHKLELLDLAQNLLPSLEDEALDGLFALTALNLSTNQLKGLTENTLADSKKLTVLDVCNNQIQQLNPAALLSVRSLQILRLCKNQLTSLQPSLLRHLSDLQTLDISENRLKALEPETLTNKPNLRLLILSNNDLTELRETVSDKPLLRLEELQLDGNLLQSVGNWTAGRFTNLLRLNVSNNQITQLSLADLPRSLLHLDGHANSILQLASSSAGGSGLEGLQLRQLDLSNNQLSALAPKDLPASLQTLNLADNRIGTIERYTFYNKPRLSAVNLMRNRLQSLDDYALRISPVEPGDQLPQFSVGQNPFLCDCQMVYLKKVNSNNFLRWYPLLADLEQLECRDQRTKSTRRLLEVPEEAFLCPYTEQCFSTCHCCDFGACDCKMTCPDNCTCYHDQKWDKNIIDCSTQQLTSIPMMLPMDATDVYLDGNVLPSMPEHALIGRTRMQALYLNNSQIQRIDNHTFNGLSHLKVLHLHHNQITVLRGHEFDQLVNLEVLDLSWNDIHSIHPATFSQLTKLRVLNIAGNQLDSLVALPLPPSLTTIQLFLANNLWECWCNDDREALLTDWLVRHSGKILDIHHLHCYDRSQYPALLRDMKKPRERCSSSTANSDTPLTGHTSRVPVSAESNDSFMIMVGVILGCVCFVVILAIALILRYRYEIQVRFYSRFRMRLCSSMSQDEDEECEYGYEKMFDAFISYSDQDEHLVLGELAPRLEYGVPKYKLFLHSRDYPLGTRTPDSVIQGVQMSKRTILFLSENYLKREWSKLDFKTAHQQVFKDKRNKIIIVLLGDIQMKDLDVDLRIYLKQNPCLHWGEKLFWKKLYYALPDPEPVLENHYSHTLSSNTLRNGHIYSYPITDL*

**Imd Pathway**

**PGRP**

*>BV898\_09012.p01 hypsibius\_dujardini\_nhd315\_core\_32\_85\_1 protein* ***(PGRP-Sc2)***

*MRTFNRTFCLFVAVIISAWTFTSALKIISRAEWGARHPLATRPLRTPASHVFIHHSDGPTSSDVKSGSEIVRSIQDCHMDERGWSDIGYHFLIGGDGSIFEGRDWSNIGAHVANHNRKGHGIVFLGNFMEVAPTEAALTAAKDLINYAVKERHLRPNYFLKGHRQMGFTDCPGDRLYKIIRSWPNFRP*

**Tak1**

*>BV898\_07869.p01 hypsibius\_dujardini\_nhd315\_core\_32\_85\_1 protein*

*MAPPSLKLAEVLLFRVICSSKPVFRPYYHSYYHSFYHSYCSVPPSFRPSILPSFFLALPLLHHFASSVHLIASSVLTSTLSSLQAIRLYVYSFFPFTTFEFDRQAAAIRSSSVSTPSILVLSAVASGFPSPATTVHLLIPCIGLSTSHSVRDSLDAMANHYHRVGPIVAVVVFLSIVPAKMGSILEEIKYHDLRFEEIVGRGSFGVVYRAKWKGQTVAVKRAETETEIQSFRIEARQLQLVSHPNIITIFGICSDDTSNPLCLIMEFAECGSLYQLLHGTEDAPQYSLAHAISWLVQCARGVAYLHTMKPKPLIHRDLKPPNMLLSDAGRKCKLCDFGTACEARTYLTNNRGSAAWMAPEVFESNKYTEKCDVFSFGIIIWEVLTRKRPYDEIGGNIYRIMWAIHRGIRPPLINGCPAILETLMTKCWAKEPYERPKMVYVVKILDRIMARLKGATQPIRFKKNPRDLARVRSIQEKSAADSLDDQFTSSGSKTDLSTVLDSPDQEKRQTVFHNRTFVSPDQAYHTNTLEILPIVEAEAEPYVRYTTLHEHTSGPVLDEEFEYPPPRYNYSSTLELGSSGNVSTDDHGFVEYNNVSAKMQPMGPILTSSASSSSILQRPVTLDFSRPSAPGLRLSFNPNPNFHIDVLTGGGGPTAVRRVQSMTLEMQSSPTTTTTTTTTTTTHKGGHGHPTTVIERHYSCPMGTSSSSHQTSDPEEYSFTEDATDEDDNSCPSSFTTHRIFSS*

**JNK Pathway**

**Hemipterous**

*>BV898\_08588.p01 hypsibius\_dujardini\_nhd315\_core\_32\_85\_1 protein*

*MDMDDVFLVKIRELEVRIQAENASAKETSEAKMAPSAREPPELPLNFNLSSPSVTRKKPRPLLMNHSTVGPAMGRALTPDTSGENAAPSLLGFRDSFRLTRQRKLELAGASLPPGVYANAAISSNKGEDHKVEYEEKLSEIIKKTNIITIRGKKYDSSIEDLESLGELGHGTCGTVIKMRFKKTGDVLAVKVMRKSGNQEENKRIIRDLDVVLKSHDCPHIVQCVGCFVTDSEVWICMELMATCLDKLLKRTKSPLPEKILGKCAVSVLKALNYLKEXXXXRSHPQRCQTLKHPNRLKSGRLVDSKAKTRCAGCAAYMAPERICPADPNRPDYDIRADVWSFGISLVELATGELPYKNCKTDFEVLTKILDDQPPALPSHRGFSMDFCAFVKDCLIKDYKRRPKYRKLLDHAFIVRYELVNVDVAAWVKQVYLYPAFHADFLTPVDSLPPTPVKSSPQTPQTPQKTWFVETTRSIFRSSANVPSTAPLPRKQYNVVRN*

**Jnk**

*>BV898\_15875.p01 hypsibius\_dujardini\_nhd315\_core\_32\_85\_1 protein description = sp|Q8QHK8|MK08\_XENLA Mitogen-activated protein kinase 8 OS=Xenopus laevis GN=mapk8 PE=2 SV=2 [Source:UniProtKB/TrEMBL;Acc:Q8QHK8]*

*MASPGKNPGQFYTIEVGDTRFCVLKRYQNLKPIGSGAQGIVCAAFDNVLQQNVAIKKLSRPFQNVTHAKRAYREFKLMNLVNHKNVIGLLNAFSPQRTFEEFCDVYLVMELMDANLCQVIQMDLDHERMSYLLYQLLCGIKHLHSAGIIHRDLKPSNIVVRSDCTLKILDFGLARSANASFMMTPYVVTRYYRAPEVILGMGYKENVDIWSVGCIFGEMIRGAVLFPGSDHIDQWNKIIEQLGTPSLEFMKRLQPSVRHYVENRPKYAGYACEKLFPDVLFPPDSQEHGKLKASQSRDLLAKMLIIDPEKRISVEDALLHPYINVWYEETEVNGPSPGPYDHIVDEREHTVEEWKRLIYDEVSIYERDFERCPTPSQLNGTGGGVQPADGASDMASRARKNAAAQQAKNGTESSDGGVSNGGGTSYSSNSSGGKSSR*

**Jra**

*>BV898\_00178.p01 hypsibius\_dujardini\_nhd315\_core\_32\_85\_1 protein*

*MDVSQGHPASSQSTTITTTSAATDRTPSSSPAKKQRGNLTLDLHGPAATAHTSGSLVIPTSSGGGVEFRPSPGFMLTSPDVQMLQLASPELEKFIIQGLMGQNTPTPTQLVFPKNVTEEQESYAKGFVDALNALHRSGMAYNVVTPGQGQGFPINNANGQNIFPQFFTMPTQQQFVQPQLMQQQPLLQIQSQQQQQPQQQQQHSLNLGGGGQIQPKMEPYSPSPSPAPSDPQTVPSDRGSSKSTNSSSAGTSPINMETQGKMKQERKRERNRLAAAKCRMRKLERISQLEERVKELKEQNAGLTETSSHLRNDLASLRQELLNHMQQGCNLSLPQHILQSLQQQQQMQE*

**Fos**

*>BV898\_05375.p01 hypsibius\_dujardini\_nhd315\_core\_32\_85\_1 protein*

*MDDGSRHDTLRGKRYAPQKIRDRVSRKIRPIFTAISATSSRVLNVSLLDRRCLSRVALTQQTLSPSLACALCSVQCIRFAMTTKHSTTPQTTTSATVTTPSSTSTATAAAATRQAAQILYRMANSGGTSTSNVVAAGTSSTTTSSSLVTEPITPVLLAAAPTMLNPASAHFAVTTTASFNQTGGSGLQQAHNFIPVYFQSPVGGGVSGQLKQDSTSTMTFQFQPQQYQVIQQQAQPLQGGRTVYQLNIGGGGGDNPQYQVARMAAVAGVNQQQQPQHQGQPQQLVGKGRAGGRKSNTKEDKLSSEEMDRRKVRRERNKQAAARCRKRRMDQTNILTDETEALEAVQNDIKSEIEKYQLEITEIQSILDTHRANCGKNIPATSVHMRVHSPPRIHVQVPPTSVNDSMIMPPPPTIVVPSSAPEPIATAAPATTDEPGAKRKTGSALQRPSNLPGPLQQLDLLAMPTPSPSKLVFNFESHTGLTPTGLTPTGLTPLIPSISSDAPEKTDTSSSAEAGASAAQQTSPNNLVSL*

**TIR-1 Pathway**

**TIR-1**

*>BV898\_01052.p01 hypsibius\_dujardini\_nhd315\_core\_32\_85\_1 protein*

*MLKSLKNAMDHRHKKKPGNEPPSPSPSAGAGSSSASATAASNGPPAFVIAPKVFDRRASAESTLNPPASSIYFAGGKGLPPKMSKSPEPQPVVTEPDSPMPVIRSRYGSQDGLLNGRSQTGSPLVERSSHSQSHHHQTSTQSVTVQQRRTVQEIVDGPNGRQVLSYSADRQNSQSKESQITSTEVNGEVKVDADHKVSSSSAGKASLEALDSMGQSLRAACAALSHSSNTTSSSFAGTSSGVGELTQTSRSETAGFQGMQNPDGTFRGATYHSKSKADGVPTVSQGVSTAAVLDQMRSDKTMASMENQVRNTLRQMAEMMDGANGTMSPMLKNKMADDGVVDLLIDNVDSSDQEVSVLSAKVLDRCMNPEAREKLLKKGVDGIVRVATIKGNAESRRVGTGLLEKMLNNSETACSEVVKHGGLDAVLEACKSQDLQTQRSSALALLNLSLYGGQFNQHQMIKQRAQDWLFPLAFGQTDPSTKYFACLCVGSLIANKELEAAVVKSGTLDLVNEFVTDNSPEIFATVYAEQLDPKQSRDVMTRLIPSLESKIAEAQQLAAFHFATEAHARQKKNDLKIFKELGIIEHLKTCASSPNDIASRLAGMALKVLGETVPHRLSQQSPLWTLQDVKHWLQQVGFPTFAKPFAESEVDGDLLLQLTDVTLQEDLKMNSRLQRQRFIRDLHQLKRISDYTSCDPYNIHSFLLGIAPEYAQYTYNLLKSGIDPSVFPFITDDHLKNDAHIENGVHRAKILDAIRKRHSLERGVVMDVRSETDVFISYRRATGSQLASLLKVHLQLRGFSVFIDIDKLDAGAFDQKLIDSVRMAKHFVLVLSPTALDRCIGDDERKDWIHREISAALACKCNIVPVTDPTFCWPSPEVLPEDMRSIGRFNGIRWIHDYQDACVDKLERFLRGDLNIKTLSAASTAAQSSAPQSGAGLSNSSIAYHGSAF*

**NSY-1**

*>BV898\_00660.p01 hypsibius\_dujardini\_nhd315\_core\_32\_85\_1 protein*

*MSASVNTTQERRLTLACVVDMEQNEGLPTRKKAYEEIMKAAKDYRILVQPIPFERLDYGESAVLDAMYSADVAIVDMSLSNQQITLSGHLGSRERFGMQGSFILYDSEMVHGLFKSNLGTDVMNSIGYALSEDGERCIVTDSWMSDSGTSLYLKLKQLLKDVQITSSTHAKEKFIDDLRKARETLSSAQLKQELDTLRHRFDADSLLISPGIVLNLLLSYRDIQGYSAMISLMEDIQSRRDQPSAQQCLQSDFMYYYAWALNRRNHAGDRAKALEVIESLCLSEPPYLHPDGICLCGRIYKDLFIQSNYSNREYIQKSIEWYRKGFTVKPNEYAGINLATLLVVSGEKVDHSTELQSLLIQLNHMIGKRGSLEQLTDYWTVATFFEMCVLARNFHKAWQAAECMYKLKPPLWHIQSTMGNIKLIDTSVKMNRSLSDGGDGDGNDSQAESMSMEDDEELYSFFLELFSDATAPKTDAIHFPVLILEDTSTRRRLVPHFVTVNADETSAGERSIKIWQTACVDGMDALFKPEHVKGAAPNKQDERCLFLYVAYNVSEGLQLYFSCGNQRDRFYQLCKEFLRSAEDFIDLDEEKSIEYDYEMDKNGQRVLLGSGTFGRVYAARDSNTQVKLAVKEIRVSNDDAVQPLHDEIKLHSKLNHKNIVQLHGSVYENGFFKIFMEQVPGGSLSDLLRGLWGPLKGNEITIAFYSRQILEGLKYLHDQKIVHRDIKGANVLVNTFSGVLKISDFGTCKRLSGLNSNASSFKGTFQYMAPEVIDAQSQRGYATPADIWSFGCTVVEMADGKPPFSEIASPMAAMFKVGKEKSHPLIPAELSELCRSFIELTFEVIPANRPTAADLLKHPFLTDTYKRKHRQSLSASLEGLLRSQSTPLDSDPFSTTEIHAKLRNVHSTNVVEGHNANVSTPSTTPAPGSPQPDSGDSTAGSHYWARKQDEAQLALLKVLSDENAALAVRMVEIFDNNNRDGQSLLGDAETDMLLKAIEQCVSRDETVGRTFAKILIEELKSGVEEADHTRLMKQLQLFLFLLKREVQDVLRKRSIKPHWMFAFDDMISRAVQTILQQMGGSFAGDDEDDTLALELDEPDRREYTSQTSTSVNSGSNAHHHQHHHLAAASVKLGKLQDTTAALMEQLIAAEVRYQELLRRTLNDKSATIRLLEAQLINNNAKDMPPNL*

**SEK-1**

*>BV898\_06639.p01 hypsibius\_dujardini\_nhd315\_core\_32\_85\_1 protein description = sp|P70236|MP2K6\_MOUSE Dual specificity mitogen-activated protein kinase kinase 6 OS=Mus musculus GN=Map2k6 PE=1 SV=1 [Source:UniProtKB/TrEMBL;Acc:P70236]*

*MSLPRKARPRPPMEKLTSSTPPRSPSVDQAPRPDLGSSAPMTFNGVTYDVSVDDLEILYSLGRGQYGHVDRVRHKKSGFEFAVKRIRSTDDPAERKAMLMDLQVNNINGGKCPYVVRSFGALFREGDLWICMEAMDISLEMFYKKAFQLKIEIPESVLAHITFAIVSGLQFLKEELNIMHRDVKPSNVLLSRKGEVKICDFGISGQLVQSMAKTRNIGCSLYMPPERVDPCAAVDDQGFDIRSDVWSVGITIIEVAIGKHPFTTWRNPFEQMKQVVSGPPPKLPDNGPFSDNFKHFVASCCQKDYLQRPKYVDLLKHPFISQFQEEVSDISEFVGRILDAPAP*

*>BV898\_06638.p01 hypsibius\_dujardini\_nhd315\_core\_32\_85\_1 protein description = sp|G5EDF7|SEK1\_CAEEL Dual specificity mitogen-activated protein kinase kinase sek-1 OS=Caenorhabditis elegans GN=sek-1 PE=1 SV=1 [Source:UniProtKB/TrEMBL;Acc:G5EDF7]*

*MSLSRIRAARGSVLEKIITPPRKPSVGESLNPDLGASATMQLNGTSYVVTVDDLQILNFLGRGQYGRVDRVRHIGSAFEFAVKRIRSTDDPAERKAMLMDLQVNSANSGQCPYVVRSFGALFHDNDWWICMEAMDISLEAFYKKAFALHINIAEDVLAHISFSIVAGLQFLKQELNIMHRDVKPSNILLSRKGEVKICDFGISGNLYKSKAKTQIGCALYMPPERVIGVTGDQGFDIRSDVWSVGITVIEVATGKHPFPGWNNQFQQMKIVVDGPAPKLPDEPFSDSLKDFVAKCCQKDFNQRPTYLELLQHPFIAKVQDDVRLTDIVAFVESILDAPTPAAS*

**PMK-1**

*>BV898\_00978.p01 hypsibius\_dujardini\_nhd315\_core\_32\_85\_1 protein* ***(with PHD\_SF, C2A\_rabphilin domains at the N-terminal)***

*MASLKPPTTPTGPSSQDPWVCPDDRQLALRGRLRTGWSVHTGKGTSAPKKSAPTTLTDEEQEAILAVIKRAETMEQQEQERIGKLVDRLDNMKKLTVGNGVTHCAFCGREFGRVLGGSPQSCKDCGQAVCSKCGVDTSDSKKRTVWLCKVCSEAREVWKKSGAWFFKGIPKHVMPEKKEGNGNIGNKRPANVEPPPIPMTSTTSTSSPAHSSPPKSPLFATPNTPSHRRPSMSMVWSFISKSKDESSAPPSPPINSNSSGTATLSLGQKQSASPEDSEDGPVVIHRSFSRRRHHESDSESGMSGRNSVDSTASDASKTVSEIRVGRSSFRRRKNTTPAARAAAAAATAAQQVADPTAPTLMPPPMPDLPPFVEPPSSSSTSIELSPARPNLSAPTPSAAVITRAQSVTSSKNKHNPQSRLNGNGIEAEESTVMDSPEDDPSSLGYLEFEIQYNSAQCTLQCNIIRARNLRAMDRNGFSDPYVKLHLLPGASRSNKQRTKTINKSLNPVFNEILTYYGITEDDINRKVLRLAVLDEDVFGHDFIGETRVILKYLPVMEWKKFDVVLEKRIPTADKTDDMLDERGRILLSLLYSAKRQALVVGIVRCAALAAMDRDGFSDPYVKIYLKPDPLKKTKNKTTVKKRTLNPEFNEEFTYPIKLGDLLKKTLEITVWDRDYGKSNDYIGGVQMSINSKGEKLKHWYEVLRNPDTAYVKWHGLVDEEFHDSIRTLRDIMNDHSARFYRVELGRTTWEVPERYEGLQAIGSGAYGSVASAKDKESKQNVAIKKLARPFQTTIHAKRTYRELRLLRHMNHDNVIGLLDVFTPERDLKDFNEVYFVTHLMGADLSSIVKSQKLTDNHVQFLIYQILRGLKYIHSAGVIHRDLKPGNIAVNEDCELRILDFGLARQAQDEMTGYVATRWYRAPEIMLNWMHYSQTVDIWSVGCIMAELIIGRPLFPGADHISQLNHILDLVGTPTETLLAKIESVDAQNYIRNLPHVDPKNFKDVFPQAKDSAIGLLKQMLELDPDVRVTAEQALAHPYLADYHDPLDEPICELPYDQAFEELEIPIDEWKKLVLAEVDTFPR*

***Ramazzottius varieornatus***

**Toll Pathway**

**Spatzle**

*>RVARI.g9821.t1 ramazzottius\_varieornatus\_v101\_core\_32\_85\_1 protein* ***(Spz2)***

*MLLASKILRDRVTGSRQQKAFNNLLATRNSFQDKSDGPRRNLSSSLGKPANIIYVAYQRNYYNYDKFPPYLSENVGLKTAKSAAENRKNYLSVTGFGPVPRLKDGNATHLYDYETVSSNRIDDRILYSEQMPPTTVPPVLPVPELTTNKPSPPSGTPTISQGSTSTAHAYTPACARSQLQTICLDDPFYPTDLVKEAVLQESEHFTKLYAEVAFQSADNLCDGLSRTDEEKYCNVFSQIHPISASNSWTVNHLNAPLNPTVASATTVDKGWQLPLPASAAEDLRMRAEASGNPAALQDPVLNSKGYVCHSVIHYARIMRAKNHRGQWRVIVNIPGHTQTSRIEECTKPLERCHYISPKLNSACIQKWNFQRLLAWDKYNGFEMDIFRLPVACSCFIRPKTASPLLQSQKFPAVTNNMAPPFVPPMSMSPPKPMPVHAPSNPVSTSIKISSGTSSNRNFNTPPDAPHNIPQQVQQKMQAQPANSWKEERPKNVLLQQGSPSLSETDHWLAMQSSLHPKQRGLSGQGNAGPIDTNAVQLYHQYLANMYPYQLQNNRQSFPSNLQMHDRKRHQRDPSGRYD*

*>RVARI.g11785.t1 ramazzottius\_varieornatus\_v101\_core\_32\_85\_1 protein* ***(Spz2)***

*MRKLWKLMVHGVWIGSWVLVIVAALSLGDDSPHSTYDETGNEVTSSRLVLAPDRPECAKATTLTFCLDDARYPSDDIQREISTNYGVFYKMYAEVSNQTTSSLVDGVAVDEEATYDYAFYYGDKMNLPTKSAARNSPAYKNYAYKNDYFKDGGYICPAFINYGSIYQAMNARGEWQYIVNLKPWTQTVRLEQCFYPHAPCSYMSTSFETRCVQKYSFQRLIAFEPQGRGLYTDIFRLPTACSCYIRPPEPQNALPALLQGDASQSLAYVDSTSSNALANGYKPIRVRNPPPNGPQSSRADYGQAASASSFNRGPSNWSPSQRGPPGKTWSADVGTPVSHANDQDSRLVERRRVRPEGLSLSDMTSDPDVGPSAFGYMDNGPPRGGPPRDRAGMYQPGRWRFGSPPPGRGPMYQGDGSQMNPTPYSDGPRGPYYQGPGPDNGPAGAAGPPPMQRDGPGQDGMWNGPPSQGPANPQNQNGQGSASAITPLQFGVQTSAGSHPDFQMRQSSGFYDYNSAHGEMNGPS*

*>RVARI.g11830.t1 ramazzottius\_varieornatus\_v101\_core\_32\_85\_1 protein* ***(Spz3)***

*MIFGDCDVGFVNDFIFLMSCTLICLTAAYEPKLATGSPLRLVDTATADTNSSLETDFFFSNTTDNLNATFDKKPTATGFLAHKIPSKLRKAIVSTFEHESIKDFIKLCLKQALCTKEQVLHGASGKDWQFRIKHRRGVMHFWQVYECIAYNRPEACPVDGHWSQWGKWSNCSVACGNGFSERHRTCDQPAPANYGKFCSGKAKERQPCNQFCPKNFTAMAGRDPLKMQALKSLHNISAAYPAVKDVCSKEHCTFNEVHHLIGDEDVADKYWLAMHCIERHVGCPIDGEWSAWQPWSSCSSDCGIGQRFRVRRCNDPPPSNGGLPCEGPMIDEEDCLGTNCGPTNESAIALFPLWTEWTDWTPCPAKTCDVYGTEYSTRKCVGLTPNEKCNVGDGTFADKLVRKRPCVKVGCLPSPTTAKPKPRYFAERKPVPVFSEFEKMVPKRYHRRRGKRALRKRRLGPHGASLRPARLRHHVRTLTVLIWLCDVIWAQLISGAHSAGASSVNLQADAPFLPYAELFSGEALQLQRPKATPFGVTCDGITQEYCTKPGQFYPRSEISFFIDENRSMMKRMFGTVSSRSLLRKDEEEVAMDNSDLRKKRMAKPPQTPQQLTTYLCPVEEELVTPFWAVNGTGVRLAIVNSPPFEQAIHTVKCARGQPGRCHPTRPCWCTQEYSWFRLLAYDATDNCKGIFMDWFKFPSHCACKCVQAAAATAENGASVPVSVAPLLPT*

**Toll**

*>RVARI.g1507.t1 ramazzottius\_varieornatus\_v101\_core\_32\_85\_1 protein* ***(Toll7-LRR only)***

*MEIQWGPNLLILLCLLSIQLVLGQYPLLDFSRPQSNGTLSPSNWTTCPGSLQTLPVSNCSCYLIDEDDLFFQCENVGWNHVQTILYHFEQSGILQEFFLYVRDFVGDMGKFAYTSAMNVTAIPGASQNDTVGLYWSGLYIDGAPEVRTIAELQWAQHLREIVLRNFPSLSAADSNVLPINLQTLVLRETAIREVDINSTLARLSNLTHLEISHSLSSLSIPSFGSDSSMAEPSFSPLHLAGIQTLILRNNSLRDLPADLLAGMSSLHSIDLSHNQLSTLPSSFFHDTFALEEVYLQNNSLSQLTSDSFHTTPYLSILDLSHNALTIPSQLINRHTRRVEIVNMRNNRIDEINEGNFAGWNSVRILNLANNTISSLRRGSFRGLHNLDMLDLSHNSISEVAAGSFEGLSSVHYIDLRSNMMRVIYAGFLEGIRLEYSGLTVDLDVSDNKIRIIEEGAANVSALSENGTHVVLHLNGNSLLCSCRNVWMGRYLSTANTSMLPVELDTGSTAMYCVDSREMMVRDITALTEDNCSVEEPRLFTTALEGIFLAGSILFLLTIVVTLAVLCISLHRRPSSSRTFYPAAYYNPDIYEPSIEIKSISTTTL*

*>RVARI.g12172.t1 ramazzottius\_varieornatus\_v101\_core\_32\_85\_1 protein* ***(Toll8-complete)***

*MFSALLICLSVITSCYAQSTRVDYPYACPEECQCQTTMRNGVFVECALLSIGVWSDFRAIQSNFTQGLLIQCDARHLDSKLLEGTFAHLAELEKLSLVDCAFTKVPKDAFRGLKSLKFLTISTRASGNVLQLEEGALKPLEQLEVLDLQRSNMQRLPANELCGLKNLKTLHLEDNALGNLASLGTSSGCLQSLQAAHLDGNAIAALGYGDVSQFLGRNLTRLSITRNKINSLSNNAFEKMDKLTELDLSENVLESIPEELWRQESKLEKLSLTGNELKSIPVNTFVLLGQLRHLNLSHNGLTNQWINGELLRNNPKIEVLDVSQNQLTHIDRSLLHNLLNLNELDLQQNRIEWIEPTAFDRQQKLETLDLSQNLLPSLEEGAFSGLYVLNRLNMSTNQLKTVSDSLLAQSKKLTGLDLSNNQINQLSATTLVGVRGLQELRLGKNQLVILPAPLLRHLSDLSILDLSENRLRSLEPDTLVNKPNLKVLILSNNDLAELREDVFERSFLRLEDIQLDGNVLQTIGNWTAARFTNLLRLNISNNQISQLRLADLPASLQLLDGHSNAIVELIAAGSESLQLRHLDLSSNQLTRLGPKDLPASLQVLDLADNNIETIERNTFSNKPRLMSVNLTRNKLHSLEDSSLKINSFSAAEKLPDFHLSRNPFLCDCQMVFLKKVTSENSLRWFPRIVDLDTLECRDMRAKSTGRLLDVPDESFLCTYEEQCSSVCHCCDFGACDCKMTCPDNCTCYHNRNWDRNIIDCSAESLTTIPIMLPMEASDVYLDGNRLPSLPEYALIGRTKMTSLYLNNSQIQRIDNHTFNGLSQLRNLHLHHNQITILRGGEFSQLVSLEVLDLSWNDIHSIHEHTFLTLTKLRVLNLAGNQLDSLITLPLPPAPTVSSLQLFLANNVWECWCNEERELGLTEWLVRFTARIQDIHHMHCYDRSQYPALLRDMKRPRERCSSLDAQNTQSSQFPVVSESAPESFMVVVGIVLGCVCFLVIVLVAFVLRYRYEIQVRLYSRFRLRLCSSMETEDEESEYGYEKICDAFISYSDLDEHLVLGELAPRLEFGSPKYKLFLHYRDHPLGMRTPESIIQGVQLSKRTILVLSENYLKREWAKLDFKTAHQQVFKDKKNKIIIVLLGDIQMKDLDVDLRIYLKQNPCLQWGEKLFWKKLYYALPDPEPILESHYSHTLSSVRNGHIYSYPITDL*

*>RVARI.g10421.t1 ramazzottius\_varieornatus\_v101\_core\_32\_85\_1 protein* ***(Toll8-LRR only)***

*MFLSVVFGSRLWIFMLLVGCGSCENGVPDTDEVLITSSTRFAENGTMPSSSSSMHHNEGALNANVIAVNRSVSSTSEVTCPEYCVVCPSMTDKTENTLLDCNGQHLFEFPYALLSLNASSIRMQNFRRNDWKQQSGLIELIDAPSGWSGLRELRLPRNNINSIKNPVFSSLTRLTRLSLDHNKLEALTNWTFIGLSRLLLLDCSYNAIASLDIAAFAPLSSLIELDMSHNLISRIPNGLFKGLLSLQHLNLDQNSIGEIQPDALTGLNLVHLNIAFNPTTESVLQELKLSELHNLQYCDLSHCKMSTIPQNLPATIRDIRLSGNNFTSLTRKCFERYLKLAVLTLDDCNIHHMEDGALGVLGSLQHLWMQNNFVRTFPKGLPSKLKGLYLDQNLIRSLRRSDFGQLFDVEEIRLQRNQISVIESCAFCDMPHLNLLDLRANRLDMLNTSLFPTDNSLSKLDLSLNPLRIINSAVFAASSMLKQLEMSRVDTLSVNSQEMLSFLPHLTALDTSGSPALAEQLLRELTASPSNTTFLLPHLHSLNIRNCGLSFVNFQLRPLFSRLNRIKMTQNNIDCSTESRWLIEMVQTHPSRFQRAQELSCSGPGALKDRKLLSVNPKVLRASQQPRPGSTTTRLFHATEGWRTRNLTRQFPVHQFGHSMGSAFDLSHYGRLAPTVDMTAGSSKSWIITAIACALTATIVSLTFVLVICCCSLKRFRDKRLSLFSKMSSFLGWTSAHTLADRAASDRTLYRSQDDSIFMIDSASPFPPLSPYEELECEQRRIANSADLRTANTEYHNDAMSLVSSVRSCPFEILV*

**Imd Pathway**

**PGRP**

*>RVARI.g4441.t1 ramazzottius\_varieornatus\_v101\_core\_32\_85\_1 protein description = sp|Q70PU1|PGSC2\_DROSI Peptidoglycan-recognition protein SC2 OS=Drosophila simulans GN=PGRP-SC2 PE=3 SV=1 [Source:UniProtKB/TrEMBL;Acc:Q70PU1]* ***(PGRP-SC2)***

*MIVSNHISQSDEDDFLMGNIVTRAQWGARPPKSAPSKLAEPVTYAFIHHSEGPSSTDLASGKKVVQGIQNYHMDSNKWDDIGYSFLIGGDGSIFEGRGWGVVGAHTQNYNSAGYGICFLGSFTSALPTAAAMNAAKALIADAVAKGHLKKAYQLKGHRQMGSTDCPGTKLYNEIKTWPQFVA*

*>RVARI.g2418.t1 ramazzottius\_varieornatus\_v101\_core\_32\_85\_1 protein description = sp|Q70PY2|PGSB1\_DROME Peptidoglycan-recognition protein SB1 OS=Drosophila melanogaster GN=PGRP-SB1 PE=2 SV=2 [Source:UniProtKB/TrEMBL;Acc:Q70PY2]* ***(PGRP-SC2)***

*MDSDAQSATSRAVKIVRRAEWGARPPQSISRLQEPVTYAFIHHSAGTEPKDLESGKRTVRSIQNYHMDTQKWSDIGYTFLIGGDGSVFEGRGWGIVGAHTMNYNSTGYGFCFLGTFTNSLPTLAARNAAKALIAEAAAAGRLKKDYKLKGHRQMGSTECPGTALYNEIKTWPHFSP*

**Tak1**

*>RVARI.g10532.t1 ramazzottius\_varieornatus\_v101\_core\_32\_85\_1 protein*

*MGSLLEDIPYRDLQFKEVVGRGSFGVVYRAKWKGQIVAIKRAETETELQSFRMEVQQLQRVCHPNIITILGVSSDESQNPLCLVMEFADCGSLYNLLHGEDIPQYSCSHAVSWLLQCARGVAYLHNMRPKPLIHRDLKPPNILLTDSGRQCKLCDFGTACEARTYLTNNRGSAAWMAPEVFESNKYTEKCDVFSFGIIIWEVLTRRRPYDEAGGNIYRIMWAIHRGIRPPLIRGCPALIETLMTQCWAKDPQERPRMIEVVKILEIVFKKLHGASLPVQWKKSNKDLPHVRSDSQVLKKRDGSLERRTIVPQSTPAQPQMETVLCRSHDAQGSSPLHKSQSDDTICHSNTLNIIPVVEAEAEPSVRYTTLHEHQPLNRSSVNRLRNHLFEMGLDEHLAELADFMQPPRYNYSSTVEFGSGNSLNDRDDHGFVEFNTVTTSSTQRGSPTRIASGGAVRPVTLDFIGPSSSGMRLSFKPSQISTQIDMRASPAVRRLQSLTLEMSSPPGSSVASPVTTVFQRHFSYGSGMPSDTDDDDTCHSISSLPPHFTVRELDHAKL*

**JNK Pathway**

**Hemipterous**

*>RVARI.g1191.t1 ramazzottius\_varieornatus\_v101\_core\_32\_85\_1 protein*

*MDVQDSFAKKIRDLEKRIAAENAARHERKPSLTRKDSFKLSLDVTPVPSSPEEVRTALTPAMPKTTPFAFDLASPSMTRKKPKPLIMNHSTVGPAMGRAMTPDINLENLPEPSLLGFRDSFRLTRQKRLELASSTMPPGVYTNATRLSQEDHLTEYEDKLGEIMKKTNIITLRGVKYESTTDDLENMGELGHGTCGTVVKMRFKKTGDVLAVKIMRKSGNREENKRIIRDLDVVLKSHDCPTIVRCLGCFVTDSEVWICMEMMTTCLDKLLKRTKTPVPERILGKMTVSVVKALHYLKEKHGVIHRDVKPSNILMDNQGNFKLCDFGISGRLVDSKAKTRCAGCAAYMAPERIVCPTDASRPDYDIRADVWSLGVSLIELATCELPYKGCKTDFEVLTKILDETAPSLPSHQGFSMDFCSFVRDCLIKDYKRRPKYRKLLEHPFVVRYELLKVDVAAWVKEVYKPLAPLLAQWETPPPSIPSLIPGEFSNGDELHKPRIPSLPKSVPPVRRNFARPAVEPTGNGTVELEVDGPAKPLTNGMDGVSTSMPTSTPIAVPSTHRTPASAFSGPRSMIQQMAAGLSSASAGVQKPAWLVKQAARSLLQRPNAATLPPANVPALPSSAPLPRKQYAFRNAV*

**Jnk**

*>RVARI.g11733.t1 ramazzottius\_varieornatus\_v101\_core\_32\_85\_1 protein description = sp|P49187|MK10\_RAT Mitogen-activated protein kinase 10 OS=Rattus norvegicus GN=Mapk10 PE=1 SV=2 [Source:UniProtKB/TrEMBL;Acc:P49187]*

*MSVPGKHPGQFYTVEVGDTRFTVLKRYQNLRPIGSGAQGIVCAALDQVIQQNVAIKKLSRPFQNVTHAKRAYREFKLMNLVNHKNVIGLLNAFTPQRTFEEFADVYLVMELMDANLCQVIQMDLDHERMSYLLYQLLCGIKHLHSAGIIHRDLKPSNIVVKSDCTLKILDFGLARSANASFVMTPYVVTRYYRAPEVILGMGYKENVDIWSVGCIFGEMIRGAVLFPGSDHIDQWNKIIEQLGTPSLDFMKRLQPSVRHYVENRPKYAGYATEKLFPDVLFPPDSQEHGKLKAGQARDLLSKMLVIDPEKRISVEDALLHPYINVWYEETEVNGPTPGAYDHVVDEREHTVEEWKRLIYDEVSIYERAFESGQHSVGGVAPPATNGNATDRLSNRRSSKSDEAHNNAEAATANSSLKNTAR*

**Jra**

*>RVARI.g6272.t1 ramazzottius\_varieornatus\_v101\_core\_32\_85\_1 protein*

*MEVSNAPNQPVISSAQPSTTSAATSTSKSGGGGKKRNLTLDLKPPDTSSSMTTTVSAASTLTVPSTSSVLNIGSSPGFVLTSPDVQMLQLASPELEKFIIQGLMGQNTPTPTQIVFPKNVTEEQESYAKGFVDALNALHRSGMAYNVNSNGNVAAFPISNVNGQNIFPQFFTMPQMAQQVQTMQPMQLQMTSQPVAGHQMVQLQMPAPMNVPKMEFNSPSVSPAPSDPQTVPSERGSTRSTNSSSGTSPINMESQSKMKVERKRERNRLAAAKCRMRKIERIAQLEERVKELKDQNGELANSRQQTQQDLANLRQELLTHLSAGCSLTIPQNLLQSIQQHQQETE*

*>RVARI.g12593.t1 ramazzottius\_varieornatus\_v101\_core\_32\_85\_1 protein*

*MHLTTMEMEVLKSGNSSLEVPESVHDIAEKKRKMTLDFAGDNNASSSTRKRRSVITSLPNVAPNSNDSASPDDDILHFLQPGNTAFLLTSPDINMLKISSPELERIIMNSWTPTSTPASFLSTLTHLPTSSSLTAKSENIMAEADVFAKFLNDLHSPTFYSLMASPSPSPGLSVSYGDPAVSTLPGPPNAAYAARDHSSTDTSLGYQHQLCLRTSSGSSSPHSGRSKSPGSRDRPPIPPIYDYVDYTTRLRRRPARGASLGRTYQERYGDGHLSASDGDQEGPCSPHSSLDSSDMSTSYTYDSIKYALRDVDEQFRLKSERKRERNRLAAAKCRKRKMDKIGTLGQQVDHMRSEVEHLEGAAAFLRRQIWHLKAELLTHLDHGCLIADVPSASASATSASNSET*

**Fos**

*>RVARI.g11692.t1 ramazzottius\_varieornatus\_v101\_core\_32\_85\_1 protein*

*MTTKQQSSSPQTVNTISTSTSTSATGSTASRAAAQILYRMPNSNGLITEPITPVLLTTPTMLNSASFTMTPQGFATSSSATGGQNASFIPVYIQQPNAGQGQPIIKQEPGTMTFQFNPQQLQQLQQQQQQQQQQQLQQGGQRVAYVVDPSQYHPNRMNSVSPVSSYHGASGQSASPTKRSGGRRPNKDERLSQEEEDRRRVRRERNKQAAARCRKRRMDQTSTLTEETEMLEEQQNKLRGEIEALQQEKTEIELLLQAHRTCCTKGIPAAMMSRDVSFSPPQVPVEQPRAPSVETTSMQPPPPPPAISLPPASVSHFDVATKAEAKRGQAAGRPVSLPVRTELTQLDLSNNLAMPTPSPSKLVFNFDHSGLTPTGLTPTGLTPLIPSISADATDKNATPQRQPTADGVSPNNLVSL*

**TIR-1 Pathway**

**TIR-1**

*>RVARI.g12715.t2 ramazzottius\_varieornatus\_v101\_core\_32\_85\_1 protein description = sp|Q9N0F3|SYSM\_BOVIN Serine--tRNA ligase, mitochondrial OS=Bos taurus GN=SARS2 PE=1 SV=1 [Source:UniProtKB/TrEMBL;Acc:Q9N0F3]* ***(class II aars-like domain at the N-terminal)***

*MAAAVEVIGTKQAFRFAPKSIETLAAGYAGSLRRTKLSLLSTDRAYILGGLFAKLEQALISFTTGFLKQRGFEFISVPDIISPEVLDGCGMERLKGRHNMIYLLDEQRHGRFALSGTSEMAIAALHRNKIIHRDQLPIKLSAMSRCYRAEVSDVQEGIYRVHEFTKVEMFGLCQPDDSKTMLEEFVTIQKDLVSTLGLHAQVLDMPKEELGLAASRKFDIEAWMPGSQRYGEISSASNCKDFQSSRLNITYQKKPQETKDTLPFVHTVNGTACAVPRMIIAILEQNQLSNVASFSLLRLKNAMDHRHKKKPAEEGTASSSTLSSSGRTPSIASQAAQPGLISLNISPKTFERRASAEPNVGSHLAAKMAKTPEPIISEPDSPLPMMKSRFASSDLLSSTRPQSPLIERSTSQQAAHNPYFDGSVTYYQPKNAMSNPALLDTEDVDMTVHSTVQASPIVQRSSHQTSSRSVMVQQQRHYQEIVDGPNGRQVRNFSDSRRDDHSKQSQIQSTEVNGQLKVEADHKVSSTSAAKATIEAMDTMGQSLRQACAALSHSSNKTSSSFAADSSGKGELSQTSQTDTYGFQGEQQPDGTFRGTTYQNSVNGPAVKHSLSTSQLLDHFDNATPKAIKNEMRKTLLQMLETFETAGNSLSTQNQLQHKINDDGIVDLLIDNVDSGDQEVSVLSTRVLDKCMDVEARDKILKKGVDGIVRVATMKGNAESRRAGTGVLGKIMNNSEMACNQVVKNGGLDAVLEACKSQDLETQRSSALALLNLSLYGGQFNQHQMIKQRAQDWLFPLAFGQTDKQTKYSACLCVGTLIANKELEAAVVKSGTLDLVNEFVTDNQPEIFATVYAELLDPKQSRDVMTRLIPSLDSHILEAQQLAAFHFATEAHARKKKNDFKIFRDLGIIEHLKTCASSPNDIASRFAAECLSLLGETVPHRLTQQSPLWTIQDVKHWLQQIGYSKESKVFSENEVDGDVLLQLTDMMLSEDLKMHSRLQRHRFLRVLQQLKRISDYASCDPFNIHSFLLQIAPEYAQYTYNLLKAGIDPSVFPFITDDHLKYDAKIDNGVHRAKILDAIRRRHSLEKGAVMEVRSENDVFISYRRSTGSQLASLLKVHLQLRGFSVFIDIDKLDAGAFDQKLIDSVRMAKHFVLILSPTALDRCIGDDDKKDWIHKEISAAISCKCNIVPITDPQFTWPSPEILPEDMRSICRFNGIRWIHDYQDACVDKLERFLRGDLNTKPSSVPSQSSSQQGHPQSLPAAISYHGAGASAF*

**NSY-1**

*>RVARI.g822.t2 ramazzottius\_varieornatus\_v101\_core\_32\_85\_1 protein*

*MSANREPARDRRLTLACVIDLVQPEGLPTRQKAYEDIVKAAKELQITLQLIQFERLDFGEAAVLDIVYSADVAIVDMSISSQQISLSGHIGSRERFEMQEAIILYHSEMVHGFRSSLGAAAMNSIGYSLSEDGERCVVTESWMADAGITLHSKIKLMLKDMKPATSTRAIQKFLEDLRKARDSLTGAELKTELDNLRHGFDSDPTLLSTETAFNLTLSFRDIQDYSSMISLIDDVKSKSEQPAAQSLLQNSDFMYWYSFALVRRNQPGDRAKALDVIEKLCSDTSYSNPDGVCLCGRIYKDMFAESKYTNRSQLLKAIEWYRKGFALKPNEFAGINLATLLVVSGERFEQSPELQSVLIQLNHMIGRKGSLDSLKEYWIVATFFEMSVLARDFKKAGQAAECMYKLKPPLWHIGSTMGNIKLIDKACGFKNGMEQNDKDGAESLDSSIVMDDDEELYQFWLELFNDALSAPHPTAVHFPVLVLEDTVSKRRLLPHYVTVNVDEDAAGERSIKIWQVSNAEDGVEVLFKQEHVKGAALNKQDERCIFLYVAYNVSEALQLYFSCGSQRDRFNQLCKAFLTSAEDFVDLDEEEASIEYDYEVDEKGQRILLGSGTFGRVYAAHNSNTQVKMAVKEIKVSNDDAVQPLHDEIKLHSKLNHKNIVQLHGSVYENGFFKIFMEQVPGGSLSVLLRSWGPLKNNETTIAYYSRQILEGLKYLHDQKIVHRDIKGGNVLVNTFNGILKISDFGTSKRLSGLNSNASSFKGTFQYMAPEVIDAQNQRGYATPADIWSFGCTVVEMAQGKPPFSDVQSPMVAMFKVGREKSHPAIPEELSDVCKNFILETFKAVPAERMAAADLLKHPFLRDTYKKKHRHSISASLDGLGRSLSVPRESGTDSVDEGNMTDRPPLKLRTAAHASMMDKGMGTPSTTPAPGSPVPDADSAGTNYWNRKQDEAQSTLLKILQDERSHLVARMQETFENNNRDGQSLLDAEASELLLKGIEKSVEKCEGDLGRIAARIVVEELKKNTPEAEHGRLFKQLQLFLFLLKREIQDVLRTRSIKPHWMFAFDDMIGRAVQIILQQMGFSFDGNESTLERREYTSQTSTSQGSSGIAHYETASARLVKLQDGSAALMEQLIQAEVRYQDLLKRSLNDKHQLIRLLEAQLMNQAKDLPHSS*

**SEK-1**

*>RVARI.g10287.t1 ramazzottius\_varieornatus\_v101\_core\_32\_85\_1 protein description = sp|O09110|MP2K3\_MOUSE Dual specificity mitogen-activated protein kinase kinase 3 OS=Mus musculus GN=Map2k3 PE=1 SV=2 [Source:UniProtKB/TrEMBL;Acc:O09110]*

*MSLGPGRKPRPVIAKISQQARTPSADHAVPHPDLDSRAAMMFDTRDTPYQVSAADLEQLGSLGRGQYGQVDRVRHKESGFEFAVKRIRSTDDPEERKRMLMDLNVNQMSCGKCPYVVRSYGALFCEGDLWICMEVMDISLEQFYKKLFAQGRTFPDEVLGFITFAIVSGLQFLKEQLNIMHRDVKPSNVLLSRKGEVKLCDFGISGQLVQSLAKTRNVGCSLYMSPERVAPSSEDSAGFDIRSDVWSVGISLIEVATGTHPYKTWKNPFQQMQQVVGGPAPSLPAEGFTDEFRDFISLCCKKKAEERPKYVDLLKHPFISRFHDAPLDISQFAISVIDG*

**PMK-1**

*>RVARI.g2471.t1 ramazzottius\_varieornatus\_v101\_core\_32\_85\_1 protein description = sp|P47812|MK14\_XENLA Mitogen-activated protein kinase 14 OS=Xenopus laevis GN=mapk14 PE=2 SV=1 [Source:UniProtKB/TrEMBL;Acc:P47812]*

*MQPHAVDHGVHQAKFYKQELGKTIWEVPERYENLVAIGSGAYGSVCSALDKETQQNVAIKKLARPFQTAIHAKRTYRELRLLRHMNHDNVVGLLDVFTPQRQLQDFNEVYFVTQLMGADLSSIVKTQKLTDNHIQFLVYQILRGLKDLKPGNIAVNEDCELRILDFGLARQAQDEMTGYVATRWYRAPEIMLNWMHYTQTVDIWSVGCIMAELITGKPLFPGSDHITQLNLILDLVGTPGETLLNKIESIDAQNYIRSLPHVDPKNFKQVFPNAKDSAIGLLKQMLELDPDVRVTAEQALAHPYLSDYHDPSDEPLCELPYDQAFEDLEIPVDEWKNLVLQEVNTFPRV*

***Mesobiotus philippinicus***

**Toll Pathway**

**Spaetzle**

*>TRINITY\_DN23652\_c0\_g1::TRINITY\_DN23652\_c0\_g1\_i1::g.19790::m.19790 TRINITY\_DN23652\_c0\_g1::TRINITY\_DN23652\_c0\_g1\_i1::g.19790 ORF type:complete len:282 (-) TRINITY\_DN23652\_c0\_g1\_i1:124-969(-)* ***(Spz3)***

*MMNFFRAFCSLIKRITFYYFSHLVVLYREGKCHQAAASPSGSILRSHSQPLSDHSLAASAVLLASNPQVQDVFSLSQNLKAPQNERLSCDGLFQDYCGKPGQLYPRSDISAFIEENKALMRRMFGSLSAKSLLRKDEEDQAALENADLRKKRMAKNPQQLTTYLCPVEEELVTPYWAVNGTGVKLAIVNNAPFEQAIHTVKCARAAQLQSNQRCHPTRPCWCTQEYSWFRLLAYDPNDNCKGIFMDWFKFPSHCACKCMQAATVLGAPVASGSATPSNPIS*

*>TRINITY\_DN12201\_c0\_g1::TRINITY\_DN12201\_c0\_g1\_i1::g.23285::m.23285 TRINITY\_DN12201\_c0\_g1::TRINITY\_DN12201\_c0\_g1\_i1::g.23285 ORF type:complete len:298 (-) TRINITY\_DN12201\_c0\_g1\_i1:140-1033(-)* ***(Spz3)***

*MWNIYALNGDGQRWIWICYVILLVYGATVSTSKQTNLTASCDLETGRHVMCFTPGENYPWYDIEVYIEDHRGTVLRMFGSETDPLRDAKDDIAKDSAAYRMREISFSKLKNPCVSDVSLEQPYWSKNQKGQLRVIVNHSPFEQFVQIEKCISTPDEQKKIGTKPQSKCPSDGCFCMQEYRSIRLVAYDPAQDEKGIFMDWFEFPCCCQCKCKPDSNSNTTFARDLEREDVLLTKVVVTPTPVAPFPTQRLETEIKIVGKDKSAGNISTSMSLPLTVSSGLVVQRDHHDQDHDLTLVV*

**Toll**

*>TRINITY\_DN4638\_c0\_g1::TRINITY\_DN4638\_c0\_g1\_i1::g.2312::m.2312 TRINITY\_DN4638\_c0\_g1::TRINITY\_DN4638\_c0\_g1\_i1::g.2312 ORF type:complete len:370 (+) TRINITY\_DN4638\_c0\_g1\_i1:102-1211(+)* ***(Toll6-LRR only)***

*MKILWNIFLLKSLFFLCLINADLCPPAASLAPSCTCTTLGEGVGITCRAVRDASDLQGALRLIGNPISEISVSDSPLMKNFALESLEEIPNAKDLQSLMLFRVMINFASSSRPLALSKLRILNISKNGIRDFPPMLLTNLTELTYLNLSHNALTTVLPSHFDTLKRLEILDLTNNKINYIPPLTFQGLTKLRLLKMGRNALRDLSAEMFKGLKVLEELDLSQNVIRYLPRDLINEFKDLKILNLHRNWIIDIPGNTFANLTQLEKLVLSGNGLKYLSADSFKGLDFLTFLDLSNNGLEFIPEGLLDSLKELEVLNVSFNRIKNMPVSLMKNLKSLRRLDIRRTLITFVPGDIYGLVSPQSNVRVLQLLS*

*>TRINITY\_DN6963\_c0\_g2::TRINITY\_DN6963\_c0\_g2\_i1::g.31630::m.31630 TRINITY\_DN6963\_c0\_g2::TRINITY\_DN6963\_c0\_g2\_i1::g.31630 ORF type:5prime\_partial len:200 (-) TRINITY\_DN6963\_c0\_g2\_i1:338-937(-)* ***(Toll8-TIR only)***

*QCYQRRVRDSRFRLRLCSSLSDEDEENGDYAYEKICDAFISYSDEDDPLVLGELAPRLEFGVPKYKLFLHYRDYPLGVRTPESIIQGVQLSRRTILILSENYLKREWAKLDFRLAHQQVFKDRRNKIIIVLVGNIQMKDLDVDLRMYLKANPCLHWGEKMFWKKLYYALPDPEPVDDQYSRTMGSVRNGHIYSYPITDL*

**Imd Pathway**

**PGRP**

*>TRINITY\_DN12590\_c0\_g1::TRINITY\_DN12590\_c0\_g1\_i1::g.24948::m.24948 TRINITY\_DN12590\_c0\_g1::TRINITY\_DN12590\_c0\_g1\_i1::g.24948 ORF type:complete len:188 (+) TRINITY\_DN12590\_c0\_g1\_i1:73-636(+)* ***(PGRP-SC2)***

*MKHVAILSLLLLAVDFSWTFPRAVSIVSRSQWGARNPRSSTTLSTPVTYAFIHHTAGAASTDLASGKRIVKGIQDYHMDSNNWDDIGYSFLIGGDGSIFEGRGWNKVGAHTAGYNANGYGIAFLGTFTSGSPTTAAVNAAKNLIKEAVSRGYLKSNYILKGHRQVGSTECPGTKLYQDIQKWTNWKP*

**Tak1**

*>TRINITY\_DN12964\_c0\_g1::TRINITY\_DN12964\_c0\_g1\_i1::g.5190::m.5190 TRINITY\_DN12964\_c0\_g1::TRINITY\_DN12964\_c0\_g1\_i1::g.5190 ORF type:complete len:523 (+) TRINITY\_DN12964\_c0\_g1\_i1:493-2061(+)*

*MGSLLEDIKYQDLQFEDIVGRGSFGVVYRAKWKGRTVAVKRAETETEIQSFKVEVRQLQRVSHPNIITIFGICSDQTTNPLCIIMEYADCGSLYQLLHGSEKAPQYSCAHAISWLLQCAQGVAYLHAMKPKPLIHRDLKPPNILLTDGGRQCKICDFGTACEARTYLTNNRGSAAWMAPEVFESNKYTEKCDVFSFGIIIWEVLTRKRPYDEIGGNIYRIMWAIHRGIRPPNIRGCPPVLETLMTKCWARLPTDRPKMTQVVKLLERVQQCLKAPSQKAVAFKRSNSNVARLRSIEEGGSRKNSSAGVNEKRISTPQTSDTVLFKGDRQLESGYATQNPASGPSSPTTFTHTSTLDILPMAAEPEPAVRYTTVHEHVPLGQEGQERFSPQFSSTLEYNSNSNTSDDHGFVEYNHPIRQVPGNYHIINRPTSLDFIRPAHAQNFSFALHPNTQIEMHITPSVRRVRSLTFNMSSPTSTSGSISFPTTVIQRHYSVRSDPDDFSYTEDATDEDDVCHSDSLYVR*

**JNK Pathway**

**Hemipterous**

*>TRINITY\_DN16187\_c0\_g1::TRINITY\_DN16187\_c0\_g1\_i1::g.14699::m.14699 TRINITY\_DN16187\_c0\_g1::TRINITY\_DN16187\_c0\_g1\_i1::g.14699 ORF type:complete len:522 (-) TRINITY\_DN16187\_c0\_g1\_i1:241-1806(-)*

*MDAGDNFADRIRDLEKRIQAENATYKMSAGSGSQENGVLQHPTTNFNLLSPSVTRKKKPPVLLPSHTTVGPQLGRAIASQISPEGDAETPTEPSLLGFRDSFRLTRQRRLELASSALPPGVFQNAAISSAKTEDHQIEYEEKLAEIMKKTNIITLRGKQYQSSIEDLENLGELGHGTCGTVVKMRFKKTGDVLAVKIMRKSGNREENKRIIRDLDVVLKSHDCQHIVQCVGCFVTDAEVWICMEMMATCLEKLLQRTGTPIPEKILGKMTVSVLKALHYLKESHGVIHRDVKPSNILLDNKGTFKLCDFGISGRLVDSKAKTRCPGCVAYMAPERVCPVDPNRPDYDIRADVWSFGISLIELATGELPYKNCKTDFEVLTKIIDDNPPSLPPHCGFSLDFCSFVKECLIKNYKQRPKYRKLLDHPFVVRYELLNVDVASWVKQLQPRLLLPPAFQAELFSPTLPPMTPKTPTKTPSPQSAPQTPQRSWFVKQATKTLFRSAANVPSTAPLPRKQYNVVNNY*

**Jnk**

*>TRINITY\_DN8090\_c0\_g1::TRINITY\_DN8090\_c0\_g1\_i1::g.20398::m.20398 TRINITY\_DN8090\_c0\_g1::TRINITY\_DN8090\_c0\_g1\_i1::g.20398 ORF type:complete len:440 (+) TRINITY\_DN8090\_c0\_g1\_i1:475-1794(+)*

*MAVTGKNPGQFYTIEVGDTRFTVLKRYQNLKPIGSGAQGIVCAAYDNVLGQNVAIKKLSRPFQNVTHAKRAYREFKLMNLVNHKNVIGLLNAFTPQRTYEEFTDVYLVMELMDANLCQVIQMDLDHERMSYLLYQLLCGIKHLHSAGIIHRDLKPSNIVVRSDCTLKILDFGLARSANASFMMTPYVVTRYYRAPEVILGMGYKENVDIWSVGCIFGEMIRGAVLFPGSDHIDQWNKIIEQLGTPSLDFMRRLQPSVRHYVENRPKYAGYPFEKLFPDVLFPPDSQEHGKLKGRRNLLPKFTNLSASHSRDLLSKMLVIDPEKRISVDEALQHPYINVWFEESEVNGPQPGPYDHIVDEREHTVDEWKRLIYDEVSMYERAFERKCASDQNGAASTTETMSDSSSKFAAGRRGSSGRSDTDLSDRNAASSSANHNKSSR*

**Jra**

*>TRINITY\_DN11325\_c0\_g1::TRINITY\_DN11325\_c0\_g1\_i1::g.259::m.259 TRINITY\_DN11325\_c0\_g1::TRINITY\_DN11325\_c0\_g1\_i1::g.259 ORF type:complete len:335 (+) TRINITY\_DN11325\_c0\_g1\_i1:354-1358(+)*

*MDDSAMSERTATSSSSVSGSSATLTESKSSVKSPKIRTNLTLDLKQSSGAPNQLLIPATSGSNELKASPGFLLTSPDVQMLQLASPDLEKLLMQGLIGGNTPTPTTTQIIFPKTVTEEQESYAKGFVDALNALHRGGMSGVAYNVVNPQGGNVAFPINQVGTQNFLPQIFTLPTQQFQLQPMTQQFQQPSQNTGYSLQQPKLEPYSPSVSPVPSDPQTVPSDRVSVKSSNSSSRTSPINMEDQGKMKMERKRERNRIAAAKCRQRKLDRISELEDKVKALKDQNSALANTASQLRNDLHALKQELMMHVSSGCHIEMSDSLMQSMHEMAEFQHS*

**Fos**

*>TRINITY\_DN7107\_c0\_g1::TRINITY\_DN7107\_c0\_g1\_i1::g.19113::m.19113 TRINITY\_DN7107\_c0\_g1::TRINITY\_DN7107\_c0\_g1\_i1::g.19113 ORF type:complete len:365 (-) TRINITY\_DN7107\_c0\_g1\_i1:585-1679(-)*

*MLQPSSSHIIQVPQQSAGNLQYTTSGGNFVPVFIGASPAGSAGIKQEPGAGLVQFQPGLQSLAPQVGGARVYLAATGAPQDNAQLHAIRMTNGTASMAPVGNNLANLTASTSGSHPTKGRSGGRRPNKDNSLTPEEDERRRIRRERNKQAAARCRKRRMDHTNVLVEETEQLEEMQSNLKADIENLQREKEEMEYLLQAHRVICSKDLHPHLAPNSPQTLTAPSDNLVSISDVQVMPPPVNVSVNAVPAANLPSVVVTTVEGSRPAKRNLDGTTKGAMRPSSLPVKNAVAAEHSLGLADPTPSPSKMVFTFDHHSGLTPTATGLTPTGLTPLIPSLPDGDQGKNPSRAPDAAAESTSPNTLVAL*

**TIR-1 Pathway**

**TIR-1**

*>TRINITY\_DN13869\_c0\_g1::TRINITY\_DN13869\_c0\_g1\_i2::g.45334::m.45334 TRINITY\_DN13869\_c0\_g1::TRINITY\_DN13869\_c0\_g1\_i2::g.45334 ORF type:5prime\_partial len:741 (+) TRINITY\_DN13869\_c0\_g1\_i2:2-2224(+)*

*IKCTFLIFNFYIFSMVAFHLVCFFCLALSHSSNVTTSNYAGSHSGMGELTQTSKTDSMGMKAVQNNDGTIRGMMFTNSGGGSNTQNLSMGDTMAQLQYKTPGAAEDQVKSTLKQMAEMMKRKDSVTPKLMDKFTDDGVMDLLIANVDSEDQEVSMLSAKVLDRCMNPEARERLLKRGLDGIVRVATIKGNTESRRAGAGLLEKILNNSEAACSQVVKQGGLDAILEACKSQDVETQRSSALALLNLSLYGGHFNQHRMIKQRAQDWLFPLAFGQNDKATKYFACLCIGSLIANKELEAAVIKSGTLDLVNDFVTENSAEEFANGFADQLDAKQSRDVLLRLLPILESRIAEAQQLAAFHYAAEAYARRKKNELKLFREIGAVEHLKNCASSPNDIASRLAGEALVVLGEQVPHRLSQQVPLWNVQDVKHWMQQVGYPNFAKVFVENEVDGDLLLRLTEKTLHDDLKMHSRILRQRFMRDLSQLKRNSDYVSCDPFNIHSLLLQIGPEYAQYTYNLLKTGIEPSVFPFITDDHLKNDAEIENGVHRTKILDALKRRSSLEKGCVMEVRSENDVFISYRRATGSQLASLLKVHLQLRGFSVFIDIDKLDAGAFDQKLIDSVRMAKHFVLILSPTALDRCVGDDERKDWIHREISAALSCKCNIVPITDPSFNWPTPETLPEDMRSICKFNGIRWIHDYQDACVDKLERFLRGDLNIKPSGPSQAGTTGSSTIQPISYHGSAF*

**NSY-1**

*>TRINITY\_DN5119\_c0\_g1::TRINITY\_DN5119\_c0\_g1\_i1::g.19683::m.19683 TRINITY\_DN5119\_c0\_g1::TRINITY\_DN5119\_c0\_g1\_i1::g.19683 ORF type:3prime\_partial len:1092 (+) TRINITY\_DN5119\_c0\_g1\_i1:45-3317(+)*

*MSVAGYSERRMTLACVVDLVVPEGLATRQKAYDDVLRAARDYKINVQHIKFDKLENSKETSVLDVMYSADVAVVDMSLSSQQIALSGHLGSRERFGMQGNFIIYNSEVVHNLFRQSIGATTMYSIGYSLSEDGERCIVTDSWMSDSGISLYSKLKQLLKDVQVTTSTHAKERFLDDLRKARESMNPGELKLELNKLRHRLDADPVLLSPETVFNLLISYRDISDHDAMIGLMDDIQLRKEQPSAQQCLQPDFLYWYCFALNRRNQSGDRAKALEVMETLCIESFVVPDGLCLCGRIYKDMFLQSDCENRALLLKAIEWYRKGFAVKPNEFAGINLATLLVVSGERFERSAELQSVLMALNHMIGRKGSISLLTDYWTVATFFEMQVLSEDFPKACQAAECMYKLKPQLWQISTTMQNIKLIDKSRRMLLKDDGTGSRSSSVVVEDDEDLYRFWTEFFEDISASRPETSHFPVLILEDNGPNRTFVPFYVTINVDEKAAGEKSIKFWQSGVSEGIEYLLKPEHVKSVAPNKQDERCLFLYVASWHVSENMQVYFSCGTQRDRFFSLCKEFLKTEDYVDLDADDIQITYDYEFDKNGQRILLGSGTYGRVYAARNSNTQVKMAVKEIRVNNDEAVQVLHDEIKLHSKLHHKNIVQYHGSVFENGFFKIFMEQVPGGSLSDLLRGLWGPLKNNEVTIAFYSKQILEGLRYLHDQKIVHRDIKGGNVLVNTFNGVLKISDFGTCKRLSGLNSNASSFKGTFQYMAPEVIDAQSQRGYAAPADIWSFGCTVIEMAEGKPPFSNLGSPMAAMFIVGRTKSHPPIPEELTDECKAFIESTFSKDPAGRLTAAELLKHPFLAQANKRRAHRHSVSQELPFSRSQSVPPADADEAPRPKYETYATTETSVGTSAPSTPVAPSSPQPTEHDTSPSYQNRKHGEAKSSMLEILRLAHDDLTSRILESFENNNKDGAALINSESADCLIRLVEKCIESEEGGRVGAKIVIDSLKDGVPAAEHHALLKQLQLFLFLLKREVQDLLRSRSIKPHWMFALDNMISQSVQIILQQMGMSFDDSDSEPEKREYTSQTSTSVNSAHFSA*

**SEK-1**

*>TRINITY\_DN10149\_c0\_g1::TRINITY\_DN10149\_c0\_g1\_i1::g.34575::m.34575 TRINITY\_DN10149\_c0\_g1::TRINITY\_DN10149\_c0\_g1\_i1::g.34575 ORF type:complete len:339 (+) TRINITY\_DN10149\_c0\_g1\_i1:260-1276(+)*

*MSLPRRAKPPKFGPIQQPTQPEAPHIAAGLDSHATMRFDMNGPDYEVAADDLDFIVTLGRGQYGQVDKVRHKESGQYIAVKRIHATDDQEERKRMLMDLQVNRLNDGRCPYVIRSFGALFREGDLWICMEVMDTSLENFYKQAFKMNSPMPEDVIAHITFAVVNGLQFLKELNIMHRDVKPSNILLSRNGDVKLCDFGISGKMEKSMAKTKKVGCELYMAPERVDPNQLTDGGFDVRSDVWSVGISLIEISTGTHPFSVWKNPFQQIQQVVNGDPPRLPDRFSPEFRDFVNVCCKKSVEERPKYLALLEHPFLKEELVKPMDISAFVQSIIGPPSNAS*

*>TRINITY\_DN14073\_c0\_g1::TRINITY\_DN14073\_c0\_g1\_i4::g.29169::m.29169 TRINITY\_DN14073\_c0\_g1::TRINITY\_DN14073\_c0\_g1\_i4::g.29169 ORF type:complete len:351 (+) TRINITY\_DN14073\_c0\_g1\_i4:96-1148(+)*

*MEKLSKSDSTSETESNVYKDAAYMQFVPDGERYLVTEADLKPVLLANEERAIIGKGKYGLVLRMKHVPSQHIFALKRIRLCDKTEEQKRCLMDQHVSLKNKINPSPYVVKCYGCYVAEGDVNICKELMDASLLQFYKKVPAGFGLPEELMFHITHSVISALQYLKSENIMHRDVKPSNILISRDGSVKLCDFGICGNLTLSRAPTNIYSPLYTPPERVNPDTTSETSGFDVRSDVWGLGVTLIEVAECRHPYQAFALEGEPGKMGFGLLSALVMGPAPSLSGRFSDNFRDFVSLCCTKELERRPKYVRYGEIPGLVDHPFYNQVANLERVAEIARAVFDGNSEHLIRIEG*

*>TRINITY\_DN14071\_c0\_g1::TRINITY\_DN14071\_c0\_g1\_i2::g.29150::m.29150 TRINITY\_DN14071\_c0\_g1::TRINITY\_DN14071\_c0\_g1\_i2::g.29150 ORF type:complete len:351 (-) TRINITY\_DN14071\_c0\_g1\_i2:338-1390(-)*

*MENSSESASTSEMGSNVYKDAAYMQFVLDGERYLVTEADLEPVLLANEERAIIGEGKYGLVLRMKHVPSQHVFALKRIRLCDEIDKQKRCLMDQHVSLKNKINPSPYVVKCYGCFVGEGDVNICMELMDASLLQFYKKVPAGFGLPEELMFHITHSVISALQYLKSENIMHRDVKPSNILISRDGSVKLCDFGICGNLTLSRAPTNIYSPLYTPPERVNPDTTSETSGFDVRSDVWGLGVTLIEVGECRHPYQAFASEGEAGKMGFGLLNALVNGPAPSLSGPFSDDFRNFVSLCCTKELERRPKYVRYGEIPGLVDHPFYNQVANLDRVAEITRAVFDGNSEHLIRVEG*

**PMK-1**

*>TRINITY\_DN7761\_c0\_g1::TRINITY\_DN7761\_c0\_g1\_i1::g.35021::m.35021 TRINITY\_DN7761\_c0\_g1::TRINITY\_DN7761\_c0\_g1\_i1::g.35021 ORF type:complete len:359 (+) TRINITY\_DN7761\_c0\_g1\_i1:114-1190(+)*

*MARGHSFQGERFVKIDLHRATWEVPERYEGLSAIGSGAYGNVASAFDRVTNQKVAIKKLARPFQTAIHAKRTFRELRLLRHMNHDNVIGLLDVFTPQHSLQDFKDVYFVSHLMGADLSSIVKTQKLTDAHIRFLIYQILRGLKYIHSAGVIHRDLKPGNIAVNEDCELRILDFGLARQAQDEMTGYVATRWYRAPEIMLNWMHYTQTVDIWSVGCIMAELITGKPLFPGADHISQLNFILELVGTPDQSLLNKIESEDARNYIASLPRSAPKDFNAVFPSAGPVAIDLLKRMLELDPDNRITAEEALAHEYLNEYHDPSDEPICTEPYDQRFEDYELSVDEWRGMILEEVESFPRPQA*

*>TRINITY\_DN10825\_c0\_g1::TRINITY\_DN10825\_c0\_g1\_i3::g.2914::m.2914 TRINITY\_DN10825\_c0\_g1::TRINITY\_DN10825\_c0\_g1\_i3::g.2914 ORF type:5prime\_partial len:415 (+) TRINITY\_DN10825\_c0\_g1\_i3:1-1245(+)*

*CKNCSLIRVNLITSTIISSIPYSFECAMEQRFYATLIEDTTFNLPERYQNLRKVGTGTYGMVVEALDVLTNWKVAIKKLSRPFDETDARAKRAYREIKLLQHMNNVHVLRLHDVITPQRDLQSFREVYLVMPYCGRDLRSWVKDQNRSFSDLDVRSLLCQILRGLKYLHSANIIHRDLKPDNIAINEFGNATILDFGMARASEKEMTGFVSVACYRAPEMYFNWRHYTEKVDMWSVGCIGAELFMGRPLLPLTVTQDNKGTVYIDNSLYLFNAIFSITGSPSEEAIRKISDAAAQTYLRQVKKTPPADLQQLCPTASAEMCQLLRQLLEFDPQLRIDAASALEGPCLGLYHKPDEEPRCSSIFDQSFENLDLCIEGWKELVWQEIIQASQQVLVPLPAPLPQFIYYAQQTQPFQ*

***Paramacrobiotus richtersi***

**Toll Pathway**

**Spaetzle**

*>Gene.48482::GFGY01017053.1::g.48482::m.48482 Gene.48482::GFGY01017053.1::g.48482 ORF type:internal len:465 (+) GFGY01017053.1:3-1394(+)* ***(Spz2)***

*LFTMTSLSLISVRLWSAKIRKKGTFAVGIVYFSLCFSLSACASAADFPSNFYNSATNDPYGNEITPYGYDNNYPSEQSTIPTVAAASQQSSQNRPQCAQATTLTFCLDDATYPSADIIKDINKNLGVFYKMYAEVTNQSTASMVEGVPASEEDKYDFAFYYGDRDRTKDTKTYGAGANPPFRADYYKDGGYVCPAFIDYTGLFQATNARGEWQYIVNIKPWLQTVRIEQCFYPQSSCSYMSKAIPTSCVQKYSYQRLIAYEPHGRGLYMDVFRLPTACSCYIRRAPRPSNPIPSASFNAPQLVGEATQNVATRAGFIPQATSQKSPLPPAVAADSSSYAPYYAPKGGYKEQNTYSDAQADSILVERRRVRPEPLSLGDMTGDQEADFNYQPNPPPWERRPPGPPPMSPHFMPAASGSRGTGMFALDEYTAAMDAEASRADPAYSPAQSNVVQPRRGPANGSGPA*

*>Gene.42643::GFGY01013912.1::g.42643::m.42643 Gene.42643::GFGY01013912.1::g.42643 ORF type:complete len:366 (-) GFGY01013912.1:237-1334(-)* ***(Spz3)***

*MDFTYNTVAVHPPATRPPPAHGAAVSRTILRLIFLLSSTGFLLQVAHADLSMFSSSNYVPRLRPEFDTADIPCDLSRPEGACALPGKAYPWLAISGYIEDNKAMLKRMYGDTCDRPGQQHARLRAQGPMRQSRGKDGDKADVGFVNACPSEQFVVTPFWANNSAGTTLAVVNFHPFEQAVQQEVCKAGTTGRCRDGCRCEQKYSWYRLLAFDPRNECRGIFMDWFQFPSCCACHCYEVDPSAKPEPHPDLPLPKMGALTTPASTSTTNATVDTEDYDNDTTEATTTATSATTPTTSVTTTTKRPRPATPPATSSSPTRPTTAPTTSRWPNQTLPATTPTLSIGLPRYRKLRPLLPFPWPPRIRVL*

*>Gene.26745::GFGY01007052.1::g.26745::m.26745 Gene.26745::GFGY01007052.1::g.26745 ORF type:complete len:279 (+) GFGY01007052.1:152-988(+)* ***(Spz3)***

*MRDSDNRHLLGRRAVVLSCLSVIVTLISFSSGMSALTAEDSPCDLQTGQMCTEPGEHYPWKQLERYIDDNRGLAYRMFGDAADPLSPLNELHLQELAEYRVPKKSQPLYRNPCVSDIALEQPYWSKNHKGQLRVIVNHTPFEQFVQLEKCLSTPDMDSRYADTEGQCPDVDCLCMQEYRTVRLVAYDPAQDEKGIFMDWFEFPCCCQCKCFQRATNDNNATAAERELDEVTSTPRTTVSTTPTTTTVKPETTPAGRTVRPSTKPTNGNGKGQAVTLVL*

**Toll**

*>Gene.6303::GFGY01001029.1::g.6303::m.6303 Gene.6303::GFGY01001029.1::g.6303 ORF type:complete len:1230 (+) GFGY01001029.1:577-4266(+)* ***(Toll8-complete)***

*MSRRKGSLTRCDMAVIIWLQLVISLAYAVSQSPTRVDYPYQCPEECHCQTTLRNGVFVECALLSIGLWSDFRAIQANFTQGLLIQCDARHLDSKLLEGAFAHLTDLEKLSLVDCAFTRIPKDAFSGLRQLKSLTISTRSPTAQMHIEAGALHRLEQLETLDLHRSNIARFPAGELCALRSLKFLHLQDNSVNNLVQLGTSGACLSSLEAVYLDGNSVRTLDSDMAEYLGTKLRFLSLSRNKLDSVSDSALARLEQLTELDLSMNQLESLSDGLLQHQTQLERLWLNGNQVKSLPVNAFVMLGQLRVLNLSQNALTNQWINGDLVRNCLQLHSLDLSHNQLTHIDRSLLRNLLNLNQLHLHHNRIEWIEPQAFAYQHKMEQLDLSQNLLAALEDEALDGLFALSLLNLSINQLKSLPERILANAKKLTVLDAGHNQIQQLPAAVFNGVRALQWLGLSRNQLTSLQPAVLRNLMDLQVLDLSDNRVKNLPAGWLNNKPNLKVLILSNNDLVDFKEDVAEGMLIRLEDLQLDGNLLQTLGNWTQSKFSNLLRLNVSNNQISQLSLADVPRSLQQLDAHSNSIVQLSLGSAASQSSHNEMNVQLRHLDVSNNQITSVGPKDLPASLQTVNLADNRIVSIERYTFNNKPRLSAVNLQRNRLESLDEYALKISPVEASEQLPEFHIGSNPFLCDCQMVYMKKMNSKNSKSYLRENPNLADLPSVECREMRSKAMRRMLDVPDEAFVCAYTEQCVPSCHCCDYAACDCKMTCPDNCTCYHDHKWEKNIIDCSARQLDTIPLMIPMDSTDVFLDGNVLPALPEHALIARSRLNALYLNNSQIQRIDNRTFNGLAHLKILHLHHNQITLLRGYEFTQLESLEILDVSWNDIHSIHPHTFAGLHKLRLVNLAGNQLDALVTLPLPVNALQLYLANNLWECWCNEDREKTLTEWLDKAAPRIIDIEQMHCYDRSQYPALLRDMKKPRDRCSSVEALTRETTQHFPVVSESSNQVLLLVGSILGCLCVVIFIAVVVVLRYRYEIQVRLHSRFRVRLCSSLSDEDEESGGDYAYEKICDAFISYSDEDDPLVLGELAPRLEFGVPKYKLFLHYRDYPLGVRTPESIIQGVQLSRRTILILSENYLKREWAKMDYRLAHQQVFKDRKNKIIIVLVGNIQMKDLDVDLRMYIKSNPCLQWGEKMFWKKLYYALPDPEPLLEDHYSRTLSSVRNGHIYSYPITDL*

*>Gene.19507::GFGY01004549.1::g.19507::m.19507 Gene.19507::GFGY01004549.1::g.19507 ORF type:complete len:374 (+) GFGY01004549.1:140-1261(+)* ***(Toll8-LRR only)***

*MISCGIYCFILISLYFADSAIADLCPPAASLAPSCSCSTASEGVAISCRAVRDVTDLQTALRLVSSPVSEIAISDSPQMKNFALESLEEIATVKDVQSLMLFRVMINFPSSTRPVNFPKLRLLNISKNGIRDIPPTLLSNLTELTYLNLSHNALTAILPSHFENMKRLESLDLTNNKLNYLPPLTFQSLTKLKNLKLGRNALRDLSAEMFRGLKILEELDLSQNVIRYLPRDLISEFKDLKFLNLHRNWIIDIPGNTFANLTQLEKLVLSGNGLKYLSADSFKGLDFLTSLDLSNNGLEYIPDGLLDNLKELEVLNVSFNRIKNMPISLMKNSKALRRLDIRRTLITFVADFDSRVTFTDWSVPNRTCASYNC*

*>Gene.13143::GFGY01002650.1::g.13143::m.13143 Gene.13143::GFGY01002650.1::g.13143 ORF type:complete len:644 (+) GFGY01002650.1:258-2189(+)* ***(Toll8-LRR only)***

*MTQLKIMNSPQLMDMPAELLPKGIESIYLYATNITSLINDFAETDTITSLRNFTYIRGALRYIQPHFFALFPRLTSLRISHTQFFLDAVDQQDMYPVAPLRNLSFTHNNFTGMSEERGAIVIHKLIEYTRMAPGGEVDLSGNGLAVSTEAVLALRNWRGVKSLIMRGNRFMNFTGLTGVFKEFDRLEVLDLSRTGLLKTKGAFSGLRKLHTLLLADNNFRDLTLTDIFSGSESKSLRILDLSGNRLRALPTAAGTDTFSESLEEFYLSNNDLDLDNIQDYENSSATFNDYQKLKYLDISHNRLVKFDSERLSRLKRLEKLNLACNKFLHVTKQYFNRLPATLRFLNLSFCATGENDSPRFTNDAFSGMSEKLETLIMQSGYLINTIFARFKLATKLRLKNLDLSWNLISGLPQDRETLVPLMSLITLRLRGNFFQSIGPKEFQHFPMLQRLDLSSNKIISIGGSDLDGLYNLELLDLSDNSIIQVEKGAFRNLNKLKSLYFGKNSFTGIGSLFDGMQQPKLQQLSLDGIPVGCIASDIAGVFRHLKWIYLNRSQPLYLAYGSFRQMKDDISVTPPDPFPFGDVSASEMGCDEDVPYQSIVSSYYRLMVRDGSNKISQQAVLNFPSCHVDAFRNLRELVENVIC*

*>Gene.4452::GFGY01000673.1::g.4452::m.4452 Gene.4452::GFGY01000673.1::g.4452 ORF type:complete len:523 (+) GFGY01000673.1:129-1697(+)* ***(Toll8-LRR only)***

*MVKLIYFLILAIAITSVRSKCPPPDYSLCNCTEVKPSELVVSCDGLDTLPDIKYQLDGIPIGEITELAILRSRDFRGLRPDFFKGYSKLNRLSLAANPNSNLELPVGLFDEIGKNLEALDLSTSNQTEKVLRAELFVPLGNLKHLDLSGNQISQVRPQIFENMKSLQVLDLGDNKLTDLPPYVIADLLDLKMLDLSNNQLQELPLDLFDDTQNNLKILDIGGNRISSLTSAHFVLMPNLTVLDARKNPLSSINGDMFSGTPNLARISFDGIQAAVIPPRLFDGLPLDSLDLSDLKNVRSLPEALLSKVGKTLTELHLDDNPKLLTIPNKFFRGLDKLEILDVSNTGIELLPNSFWTDLPSLRKLKISNNPWLLSLPPPKWFSPQLKFLDATNCPKFPVSVTNWIKTNFDTKSLLLDFPINIYRSVNKEIQLRHITDAPRVTQPPPGNTNDGPKPHHPHKPRPSSGSTNNNGGGNSGPNGRPDGNQGNNNNNDWQSADSNPNNNNNNNNNNGGGGWGWNIFGR*

**Imd Pathway**

**PGRP**

*>Gene.5635::GFGY01000897.1::g.5635::m.5635 Gene.5635::GFGY01000897.1::g.5635 ORF type:complete len:193 (+) GFGY01000897.1:1196-1774(+)* ***(PGRP-SC2)***

*MRSLLAGFCCIVVLGTGFAVPIARQNKAVSIVSRADWGARAAKNPVTLSKPVSYAFIHHTAGAVSTDLASGKRVVKNIQNFHIDTNKWDDIGYSFLIGGDGTIFEGRGWNRVGAHTQGYNSNGYGIAFLGTFTSQLPTAKALASAKALIADAVSRGFLKQAYTLKGHRQMGSTECPGTKLFNEIKSWKNWKA*

**Tak1**

*>Gene.32296::GFGY01009257.1::g.32296::m.32296 Gene.32296::GFGY01009257.1::g.32296 ORF type:complete len:521 (+) GFGY01009257.1:414-1976(+)*

*MLMMGSLLENINYVDLRFEEIVGRGSFGVVYRAKWKGQTVAVKRAETETEIQSFQIEVRQLQRVCHPNIITVYGVCDDQTTNPLCLVMEYADCGSLYQLLHGNENTPPYTTAHAISWLLQCAKGIAYLHAMKPKPLIHRDLKPPNILLTDAGRHCKICDFGTACEARTYLTNNRGSAAWMAPEVFESNKYTEKCDVFSFGIIIWEVLTRRRPYDEIGGNIYRIMWAIHRGIRPPKIYGCPAILETLMTKCWARLPADRPRMVQAVKILDRILQFMKQDSQQPIKWKRSQQHLSRVRSIEEGDSQSISPLPSPNPPEERHVDTVLFRGDGSSAQEANETHSHTNTLNIPFRVVKNFVEAEPEPQVRYTTLHEHIQEPPIDEDDAYFQSRYASTRVAFNAADDHGFVEYNHPAQLPQTGPCFRVTTERPSSLDFRPRGRNFQVSVPSTSSFKIEFSPAPTVRRVQSLTFNMHTTSPTGNAPKTIIQRMYSLPRDSDECITEDATDDDDGSHSDSFPIPTLYA*

**JNK Pathway**

**Hemipterous**

*>Gene.27481::GFGY01007324.1::g.27481::m.27481 Gene.27481::GFGY01007324.1::g.27481 ORF type:complete len:528 (-) GFGY01007324.1:360-1943(-)*

*MDGEDELDLAAKIRELDKRIQAENQMSENGTYKHSGENVQKPPLNFNLLSPSVTRKKVKPLLMTSHTTVGPALGRAMTPDIQNETGEPSLLGFRDSFRLTRQRRLELASSALPPGVFHNATISSAKTDDHQLEYQEKLGEIMKKTNIITIRGVKYESKTEDLENLGELGHGTCGTVMKMRFKKTGDVLAVKIMRKSGNREENRRIIRDLDVVLKSHDCPSIVQCLGCFVTDSEVWICMEMMATCLEKLLQRTHAPLPEKILGKMTVSVLKALDYLKESHGVIHRDVKPSNILLDSRGIFKLCDFGISGRLVDSKAKTRCAGCVAYMAPERICPADPNRPDYDIRADVWSFGISLVELATGELPYKDCKTDFEVLTRIIEDPPPSLPPHQGYSMDFCAFVKDCLIKDYKRRPKYRKLLDHPFVVRYELLHVDVASWVKNMQPRLVVPLAFQAALLSPSPTAALPPHNPPKTNTPQSAPQTPQKSWFVKQATKSIFRSAANVPSVAQKKLFAPSTAPLPRKQYNVVNNY*

**Jnk**

*>Gene.24224::GFGY01006149.1::g.24224::m.24224 Gene.24224::GFGY01006149.1::g.24224 ORF type:complete len:433 (-) GFGY01006149.1:741-2039(-)*

*MAVTAKNPGQFYTIEVGDTRFTVLKRYQNLKPIGSGAQGIVCAAYDNVIGQNVAIKKLSRPFQNVTHAKRAYREFKLMNLVNHKNVIGLLNAFTPQRTYEEFTDVYLVMELMDANLCQVIQMDLDHERMSYLLYQLLCGIKHLHSAGIIHRDLKPSNIVVRSDCTLKILDFGLARSANASFMMTPYVVTRYYRAPEVILGMGYKENVDIWSVGCIFGEMIRGAVLFPGSDHIDQWNKIIEQLGTPSLEFMKRLQPSVRHYVENRPKYTGYPFEKLFPDVLFPPDSQEHGKLKASYSRDLLSKMLVIDPEKRISVEDALQHPYINVWFEESEVNGPQPGPYDHIVDEREHTVDEWKRLIYDEVSLYERLFERPVTGVPEQPKSNGGTVAQDNADSSRLRRNSSGRVDGEGSERTTSNNNAASSSSNSVHKNSR*

**Jra**

*>Gene.2641::GFGY01000350.1::g.2641::m.2641 Gene.2641::GFGY01000350.1::g.2641 ORF type:complete len:338 (-) GFGY01000350.1:4827-5840(-)*

*MSETSQNPSNPSAASVSGAHPPAKSPAGGHKKRNLTLDLKSGPSGGTQLLSVPATSGASEQVKTSPGFLLTSPDVQMLQLASPDLEKFIIQGLMGANTPTPTQLVFPKNVTEEQESYAKGFVDALNSLHRNGTVGMAYNVLPTNSGNVAFNLGQVNGQNVFPQFFTLNHSNQLLQPLQTPQQQHQQQQQSLPMTLQMSAPHGGHLALQQPKPEPYSPSVSPAPSDPQTVPSDARSTGSSTGGTPPINMDHQHKLKVERKRERNRLAAAKCRQRKLARIAELEEKVREIKEMNAGLEATAQGLRGDLGMLRQELLMHLQSGCSIDMSQNLLATLQRHS*

**Fos**

*>Gene.26012::GFGY01006794.1::g.26012::m.26012 Gene.26012::GFGY01006794.1::g.26012 ORF type:complete len:360 (-) GFGY01006794.1:1123-2202(-)*

*MLQSGSNHNPQYSTASFNQNVGSMINVSGGQIINSIPPHSVIPLYIPSGGTTTTTTHIKQEPGILQFQNLQNLHQSGPRLLLTTGPPEGVPLYQGQRMANGSLMMNPQSDSPGPSGSVTGSTGNPRGRGGRKAARDDKLTPEEEERRKVRRERNKQAAARCRKRRMDHTNVLVEEVEGLEEAGNQIKAEIEEMQREKEEIEYLLQTHRATCSKEFELPPPPPPPAVETDVEMESAEPVPVPQEPAVIMPPPPPAPVVPVINVVPPKVPEKKAAAATRPVSLPFKSTLPTGNLLDLAMPTPSPTKLFFNFDHSGLTPTGLTPTGLTPLIPSCSTDTPQNKSPPRPVDAAGDSVSPNLVSL*

**TIR-1 Pathway**

**TIR-1**

*>Gene.1051::GFGY01000117.1::g.1051::m.1051 Gene.1051::GFGY01000117.1::g.1051 ORF type:complete len:941 (-) GFGY01000117.1:218-3040(-)*

*MLKSLKSAMDRSSHKKKSDSSSTSFDSTPRSSHGDIIPPVAFQAVKTFERRVSADAANVHSTSNLHSNLIPSGLPPKMSFSHAKSPEPIISEPGSPVIPLTKHRFGSTDLLSNGRASSPHVERKHHQSSSQSVTVHQSRQYQEIVDGKQVMSYSASRQNSQQKESKIQSSEINGEVKVDADHKVSSSQAAKASIEALDSMGQSLRAACAALSHSSNSSNSAYTGSHSGIGELTQTSKSETLGARAVQNPDGTVQSITYSNAGGNNPVSVQKRSISGLMEDLRSTPGQLENQVRSTLKQMVEMMEEQTTITPMLKNKLDNDGVVDLLIENVDSQDQEVSMLSAKMLDKCMNMDARERLLKRGIDGIVRVATIKGNPESRRAGAGLLEKILNNSEAACTEVVNHGGLDAVLEACKSTDVETQRSSALALLNLSLYGGQFNQHRMIKQRAQDWLFPLAFGQQDQTTKYFACLCVGSLIANKELEAAVVKSGTLDLVNDFVTENTPEEFATKYAEQLDAKQSKDIIIRLLPILESRIAEAQQLAAFHFATEAYARKKRNELKLFREVGAIEHLKNCASSPNDIASRFAAEALAVLGEAIPHRLSQQVPLWTVQDVKQWLQQVGYTSVAKSFVEKEVDGDLLLQLTEQTLRDDLNMHSRILRQRFLRDLLQLKRIADYTSCDPFNIHSLLLQIGLEYAQYTYNLLKAGVDPSVFPFISDEHLKNDAWIENGVHRAKILDAIGKRRSLEKGTVMEVRSENDVFISYRRATGSQLASLLKVHLQLRGFSVFIDIDKLDAGAFDQKLIDSVRQAKHFVLILSPSALDRCINDTERKDWIHREISAALSYKCNIVPITDPTFIWPNPDALPEDMRSVCKFNGIRWIHDYQDACVDKLERFLRGDLNLKPAHPTATSQTGAGAASQISASAQSIAPSTGTPAISYHGSAF*

**NSY-1**

*>Gene.1452::GFGY01000176.1::g.1452::m.1452 Gene.1452::GFGY01000176.1::g.1452 ORF type:complete len:1150 (-) GFGY01000176.1:3155-6604(-)*

*MSLGNQTERRLTLAIVIDLLVPEGLSARQKAYDDILRAAKDYKINTYRVEYDKLERSKETAVLDLMYSADVAIVDMSLSNQQIGLSGHLGARERFGMQGNFVIYNSEYIHGLFKSTGGSGMNSIGYSLSEDGERCIVTDSWMADSGVSLYAKLKQLLKDVQVTTSTHAKEKFLDDLRKVREMPHDQLKPELDKLRQRLNKDFLLLSPEIIFNLLMSYRDIQDHDAMISIMEEVQSHQDQPNAQQCLQPDFMYWYCFALNRRNRPGDRDKALHMMENICTDLYVVPDALCLCGRIYKDMFVESECKNRTYIVKATEWYRKGFAVKPNEFAGINLATLLVVSGEKFENSNELQTVLMQLNHMISRKGNLELLDDYWTAATFFEMQVLSDDFRKACQAGECMYRLKPQGWMIRTTMQNIKLIDQAKRTIAKGIDSVPSSRSSSIAVEDDEEVYRFWLEFFEDSYIPRPDTSHFPVLILDDNSGDRHFIAFYVTINVSEEIAGDKTIKFWQAGCTEGIEYLLKPEHVKSAAPNKQDERCLFLYVAYPFSENLQVYFSSGNQRDRFYALCKEFLSSTDDYVDLDDEGPAMVYDYDYDKNGQRVLLGSGTFGRVYAAKNANTQVKMAVKEIRVNNDAAVQLLHDEIKLHSKLHHKNIVQYHGSVYENGFFKIFMEQVPGGSLSDLLRGWGPLKGSEVTIAFYSRQILEGLRYLHDQKIVHRDIKGGNVLVNTFSGVLKISDFGTSKRLSGLNSNANSFKGTFQYMAPEVIDAQGQRGYAAPADIWSFGCTVIEMAQGKPPFSEIQPMAAMFLVGRNRSHPMLPEELSAECREFILCTFCSEPAERWTAAGLLKHPFLRDSKKRQRNNSVTSLNGAMSRSHSVPPGADSMDMASTLEAHILVEKGVGTSSPSTAAAPTSPQPEQEASGSYWRRKHNETQSALLALLDSEHRTLIDRMMESFENNNKDGGTLIDTACTETLIKLVEKCIHSEEGGRIGAKIVIEDLKGTIAPTEHNRLLKQLQLFLFLFKREVQDVLRTRSIKPHWMFAFDDMISRSVQIILQQMGMSFDDSDSEPEKREYTSQTSTSPGSYCQAPYEQALARFIKLQYGTTEIFELLIKAEERYQSVLRQLLEEKNRAIMLAENQRFGSTGSMGSQ*

**SEK-1**

*>Gene.43657::GFGY01014429.1::g.43657::m.43657 Gene.43657::GFGY01014429.1::g.43657 ORF type:complete len:345 (-) GFGY01014429.1:281-1315(-)*

*MPPNPRRAALPKLNQKAPEPKPDEAHSPAPGIDTRAVMRFDPEGRDYEVAADDLDFVRSLGRGQYGSVDEYKHISSGYVFAVKRIRSTDDPEERKRMLMDLNVNKLSEGKCPYVVRSFGALFREGDLWICMEIMDISLEMFYKKVFSLNQTIPEGVIAHIAYAMISGLVFLKNTLNIMHRDVKPSNILLSRRGDVKLCDFGISGQLVQSMAKTKIGCSFYLPPERVDPMASGEGGGYDIRSDVWSCGITLIEIAIGRLPYKSWKSLFQQISEVVHGPPPTLPDDSPYSQDFRDLVNSCCQKDVTHRPKYPELLAKPFLTNEEANPQNICAYVVEILDAAIPNPA*

*>Gene.47046::GFGY01016228.1::g.47046::m.47046 Gene.47046::GFGY01016228.1::g.47046 ORF type:complete len:345 (+) GFGY01016228.1:264-1298(+)*

*MAMAEESEEFVFGPQYPALDLITPRAMMQFEEDGAEHEVSLDTMTCLEYLDKGTYGTVSRYQHRPSGYTMAVKRINFNNDNSDNPAEMRKRLFMDVDVNQRIMSQSRRERCPYLIRSFGTILTENEVWICMELMDISLEKFYKKVYKLGHRLPEYVIANILYAVICGLSFLKDHCVIMHRDVKPSNILLSKNGAVKICDFGISAELEKSRTRSNIGCQFYKAPERVDPDSTNCPVEGFDVRSDIWSLGITAMEIAIGNLPFKNTSLFGVIREILDPTPPTLPSDAPYSREFRDFVNACCRRDYQERPRYADLLRMPFMVKEAASRHDISRYVQQVMDTPVINSC*

*>Gene.33313::GFGY01009662.1::g.33313::m.33313 Gene.33313::GFGY01009662.1::g.33313 ORF type:complete len:212 (+) GFGY01009662.1:1253-1888(+)*

*MELMDTCLAKFYTKMFKLGRIFPEDILAYIAYAVVSGLKFLKHPLDIMHRDVKPSNILLSRNGDVKLCDFGISAKLIHSLAKTVIGCDLYMAPERISPVDGNGYDIRSDVWSVGVTLVEVATGHQPYANGGALFNLIKNIVDGPPPKIPDGSQYSDVFQSFIASCCEKNVENRPRYDALLTTPFLTKERIRPAAVGHVVQDVLDAAVPESS*

**PMK-1**

*>Gene.7211::GFGY01001228.1::g.7211::m.7211 Gene.7211::GFGY01001228.1::g.7211 ORF type:complete len:357 (-) GFGY01001228.1:2963-4033(-)*

*MDVDHEVQHVKFYTKELHRTTWEVPERYEGLEAIGSGAYGNVASAYDKLTKQKVAIKKLARPFQTDIHAKRTYRELRLLKHMMHENVIGLLDVFTPQRGFRELKEVYFVTHLMGADLSSIVKTQILSDSHVQFLIYQILRGLKYIHSAGVIHRDLKPGNIAVNEDCELRILDFGLARQAQDEMTGYVATRWYRAPEIMLNWMHYTQTVDIWSVGCIMAELISGRALFPGTDHISQLNLILELVGTPNSQFLEKIESDDARSYIQSLPRKAPKDFHREFPNASPAAVDMLRRMLELDPDNRITAEDGLAHEYLHDYHDPADEPVCEEPYDQHFEDLVLSIEQWREMVFQEIQTFPRQ*

*>Gene.40691::GFGY01012980.1::g.40691::m.40691 Gene.40691::GFGY01012980.1::g.40691 ORF type:complete len:257 (-) GFGY01012980.1:757-1527(-)*

*MALFYATVFTIFRRRTNFEDGEENSAELPQQRSFWDTFLQCITPASPSEGQTTAVESVHHVTQVPNFYVTELYKTTWEVPERYQGLKTVSDGAASGNVAFAFDTVKKQKVAIKKLSRCFLSDIHAKRTYREFSLLRHMQHENVVTLLDVFTPQRTHPELQHIYLVMPCMDTNLQTLIKTYRRSDEPVCLTDDYVQVITYQILCGLKYIHSAGIIHRDLKPANIAINMDSTVRILDFGLARHEQDEGSMTGYVVTRW*

*>Gene.26069::GFGY01006811.1::g.26069::m.26069 Gene.26069::GFGY01006811.1::g.26069 ORF type:complete len:201 (+) GFGY01006811.1:1083-1685(+) (fragmented at N-terminal)*

*MWLPDGKGLLPARAWKFERTRTAELVLRSLSLRYRAPEIIINWMHYTQIVDIWSVGCIMAELITGRPVFPGSDHVSQMKLMLNLVGAPSETTLNKIASDDARTYIASLSTKPPRDFAEIFPTASKDAVDLLKRMLEFDPDNRITAEQALAHGYLDLYHVPEEEPVCGTPYDHTFEGKILSTAEWREMVFHEVKAFSRPSR*

***Richtersius* cf*. coronifer***

**Toll Pathway**

**Spaeztle**

*>TRINITY\_DN25694\_c0\_g1\_i3.p1 TRINITY\_DN25694\_c0\_g1~~TRINITY\_DN25694\_c0\_g1\_i3.p1 ORF type:complete len:449 (-),score=47.23 TRINITY\_DN25694\_c0\_g1\_i3:383-1729(-)* ***(Spz3)***

*MMPFYRTLFFIINLGAFGLGVMRGDVFDLPSSNYIPRSRPDFDLADIPCDLSDTTNTCGRPGPSYPWSGMHSYIRDNQGMIKRMYGDTCDRSPDQRAQGPNYGLRQAKQVEKHSTPIVNACPSDQFVITPFWANNSEGMTLAVVNFHPFEQAVQQEVCKPGQTGRCRDGCLCDQKYSWYRLLAFDPRNECKGIFMDWFQFPSCCACHCFELPPEPMSGVVTNVTNDSGPFDILSPRGGTLNFSSTEPSTASVAPTTSPTLTDQGETATATETETEAVSNSTTRSESTTVAVPTTTSPPSTKVTVNSRQTLQATTSRKPLPLPVSSSPAPAAVPASAQANGVLYFPYAPYRPPDRQYVRVVADKIINRTAVSVSSTTNKPFRPHFLTVSKTKTTASLPTSATSTVTATATSTLVTSAGLSEVIERAFLDPSANLLRIVPAVRKNRVARI*

*>TRINITY\_DN11947\_c0\_g1\_i1.p1 TRINITY\_DN11947\_c0\_g1~~TRINITY\_DN11947\_c0\_g1\_i1.p1 ORF type:complete len:322 (+),score=54.26 TRINITY\_DN11947\_c0\_g1\_i1:624-1589(+)* ***(Spz3)***

*MDRYGMGAGRESWERMNTSRARMPLLVAMMLMKSNSGRSQLLTFSGAPPAPSLSASLSMFAQQTLADHSVSGSLVGGPVGSNIAQDLYAPAHSHLGFKSSFQENNQLNCDGHGASQDYCAKPGLFYPRNDIGFFIDENKALMKRMFGSVSAKSLLRKDEEDQAAVDNTDLRKKRMAKAPQQLTVYLCPVEEELVTPFWAVNGTGIKLAIVNTPPFEQAIHTVKCSAHMARASGTASAGGQQLLVTSQKCHTTRPCWCQQEYSWFRLLAYDPNDNCKGIFMDWFKFPSHCACKCVQAATVNSVAAAVAAASHQSSSPTALPP*

*>TRINITY\_DN52457\_c0\_g1\_i1.p1 TRINITY\_DN52457\_c0\_g1~~TRINITY\_DN52457\_c0\_g1\_i1.p1 ORF type:3prime\_partial len:188 (-),score=27.37 TRINITY\_DN52457\_c0\_g1\_i1:1-561(-)* ***(Spz3)***

*MLSVKKIGSRVAVSWLMAFYHVASPLQIPCDLEKSVSGMCMVPGQQYPWKEIEHYIEDNLGLTSRIFGASALPPDLQLEFVANRSANYRMRSVGSPMARINPCVTEVSLEQPYWSKNMKGQLRVIVNHSPFEQFVQVEKCNAVPSMVASRCPGENCYCMQEYRSIRLVAYDPAEDSKGIFMDWFEFP*

**Toll**

*>TRINITY\_DN23852\_c0\_g1\_i1.p1 TRINITY\_DN23852\_c0\_g1~~TRINITY\_DN23852\_c0\_g1\_i1.p1 ORF type:complete len:555 (+),score=40.75 TRINITY\_DN23852\_c0\_g1\_i1:82-1746(+)* ***(Toll-LRR only)***

*MFSERPNLFRVIALLFWLSTLRSTASAENVEEDCPSVLNFGGCTCSTVATSRYLLDCRGLQWKELKFILSTYSHADLDLDLSLVLRDYQGNFSDWRESLGIDTLDVLKNHLHSLSLWRMPTLQQSPDFSWASGMVELILSGMSALSNHALTSSILPPHLQRLRLSSTRLTKIDHEMLNGLYNLTTLELEGHASIELIGQPFQDLRNLTALSIIGGLSSFSDNASLGLENLKFLNLSHNELPSVPKDVFTDMLQLEVLDLSHNEIQSLPANLLGNKPNLHYISLAYNNLEEIPAQLFHSSRNLTEIDLSHNNMASLSFGLLDYSNRLVVIDLSHNSLVVFPTDVLHAQNSLVNLYLSGNLIETLDGDLLQGLSSLQSLDLSSNLVTSIPAPLFSHAGNLTLLNVSNNRIQVVRKVVLEALNGTRVDFSGNALTCTCNNLALAEYLTIPGNYPTGDIHCVDPRSFKIYSLLKLNSTNCMQPTTVRIFSTALEALFFVGTILFLLSLIIAIGSSCAYSRQSSRRQSFYPGMEIPSGPHAYGVPVETKTHKVDLTTVL*

*>TRINITY\_DN15330\_c0\_g2\_i2.p1 TRINITY\_DN15330\_c0\_g2~~TRINITY\_DN15330\_c0\_g2\_i2.p1 ORF type:complete len:370 (+),score=46.41 TRINITY\_DN15330\_c0\_g2\_i2:132-1241(+)* ***(Toll6-LRR only)***

*MMNPLFVICLPILLWIHEATSDLCPPAASLAPSCLCTTLAEGVGVSCRALRDVADLQGALRLIDGSINQISISDSPQMKNFGLEALEEVPGLSNVQILMLFRVIINFPSSPKPLGFSKLRILNISKNGIRDFPQIILTNLTELTYLNLSHNALTAVFPSHFDTLKKLETLDLTNNKLNYLPPTTFQGLTKLKTLKLGRNALRDLSADMFRGMKLLEELDLSQNVIRYLPRDLINEFKDLKILNLHRNWIIDIPGNTFGNLTQLEKLVLSGNGLKYLSADSFKGLDYLTHLDLSNNGLEFIPEGLLDSLKELEVLNVSFNRIKNMPVTLLKNLKSLRRLDIRRTLITFVPGDIYGLVSPQSNVRVLQLLS*

*>TRINITY\_DN25515\_c0\_g1\_i1.p1 TRINITY\_DN25515\_c0\_g1~~TRINITY\_DN25515\_c0\_g1\_i1.p1 ORF type:complete len:1226 (+),score=171.87 TRINITY\_DN25515\_c0\_g1\_i1:420-4097(+)* ***(Toll8-Complete)***

*MVCRHVRSPARCDMPLLAALLWLLCVFPLVSPQLTRVDYPYACPEECRCHTTLRNGVYVECALLSIGLWSDFRAIQPNFTQGLIIQCDARHLDSKLLEGAFAHLTDLEKLSLVDCAFTKIPKDAFLGLKKLKTLTISTQVMKEPLLVEEGSLRRLENLETLDFHRSNLVKFPPNELCGLKQLKFLRLEDNNVNNMAQIGTSGGCLTSLEAVYLDGNSLRILDKDVAEYLSSKLRILSLSRNKIDSLSDDAFSRLEFLTDLDLSENQLESISDGLLQNQVRLERLWLNGNLVKSLPVNAFVMLNHLRQLNLSQNSLTNQWINGDLLRNCLQLHLLDLSQNQLTHIDRSLLRNLLNLNQLTLQQNRIEWIEPQAFTYQHKMELLDLSQNLLPSLEEDAFDGLFALTKLNLSTNQLKSLSENVLADSKKLSVLDLSSNQIQQLSPSVFLPVRSLQFLGLNRNQLTLIQGSLLRNLIDLQILDLSENRLKNLEQGFLSNKPNLKMLILSNNDLVELNEDFSEGALMRLEDLQLDGNLLQKLGNWSLSKFSNLLRLNVSNNQINQLHLSDLPRSLLHLDAHSNSIVQLSLGITTGTNDANLQLRHLDLSRNRITAIGAKDLPASLHVLNLSDNRLDTIERYTFYNKPRLSTVSLQRNRLESLDDYALRISPVEAGEKLPEFHIGSNPFLCDCQMVYMKKVNSNNFLRWYPILADLAELECREMRTKSNRRILDVSDDAFLCPYTEQCSSVCHCCDWGACDCKMTCPDNCTCFHDQKWEKNIIDCSARQLDTIPLMVPMDSTDVYLDGNILPVLPEHALIARKRMYALYLNNSQIQRIDNRTFNGLDHLRILHLHHNQISVLRGYEFTQIGELEILDLSWNDIRSVHPHTFIQLTKLKVLNLAGNQLDSLTLLPLPEGSPGTQLFLANNLWDCWCNEDRERTLTEWLLKHSSKVADISNMHCYDKSQYPALLRDMKKPRERCSSVEALSRDTVQNFPVVSESTNSQVLLLVGAILGCFCVVVFIAVAVVLRYRYEIQVRLYSRFRLRLCSSLSEEDEESGDYAYEKICDAFISYSDLDEQLVLGELAPRLEFGVPKYKLFLHYRDHPLGVRTPESIIQGVQLSRRTILVLSENYLKREWAKMDYRLAHQQVFKDRKNKIIIVLVGNIQMKDLDVDLRVYLKSNPCLQWGEKLFWKKLYYALPDPEPLEDHYSRTLSTARNGHIYSYPITDL*

*>TRINITY\_DN14447\_c0\_g1\_i1.p1 TRINITY\_DN14447\_c0\_g1~~TRINITY\_DN14447\_c0\_g1\_i1.p1 ORF type:complete len:555 (+),score=96.33 TRINITY\_DN14447\_c0\_g1\_i1:395-2059(+)* ***(Toll8-LRR only)***

*MRRHEELGFAIVIFCLNSINFVSAKCPSPSFSSCNCSDTKDPARIVVSCDGLASVPDLKWQLDGLPAGEISELAILRTKNFNGIRPDFFDLFKILKRLSLAANPLSNLKLPIGLFSKIGATLEALDLSTSNQTEKDLPPGLFEPLVNLKHLDLSNNQIAQIRPQVLASLKSLKVLDLGDNKLTSLPASPFAALTNLEMLDLNDNMLTELPLDLFDDVQKSMRILDVGGNKIQSLTADHLVLMPNLEVLDVRKNQINPLNSDVFSKSPKLARISLDGLQAAVIPPRVFDKLPLESVDLSDCVNVRALPESLFSNVGQTLKELHLDDNPKILSLPKAFFHGLDKLEILDLSNMGLELLPNAFWSDLPALKKLKVSDNPFLWSLPKPTSYSLDLKNVDAGNCPKMPSKVIAWIKQNFDTRSLMLDFPINIYRSINHEIQMFHVTMLPTEATTRMVTGRRPPMQGGGDNNNGGGGGRGNSNGGYNNNNNNGYNNGGPNNGGGNGNSQPGNNDGWEAAPENDNNNNNGNNGNNGNNNNNNNNNNNNGGGGGWGWGWGRR*

**IMD Pathway**

**Tak1**

*>TRINITY\_DN25374\_c0\_g1\_i3.p1 TRINITY\_DN25374\_c0\_g1~~TRINITY\_DN25374\_c0\_g1\_i3.p1 ORF type:complete len:511 (-),score=66.83 TRINITY\_DN25374\_c0\_g1\_i3:551-2083(-)*

*MGSLLEDIGYHDLQFEEIVGRGSFGVVYRAKWKGQTVAVKRAETETEVQSFRVEVRQLQRVCHPNIITIFGVSADETNPLCLIMEYADCGSLYQLLHGSENSPQYTCAHAINWLVQCAKGVAYLHSMKPKPLIHRDLKPPNILLTDSGRHCKICDFGTACEARTYLTNNRGSAAWMAPEVFESNKYTEKCDVFSFGIIIWEVLTRRRPYDEIGGNIYRIMWAIHRGIRPPSIRGCPAILETLMTKCWARLPGDRPRMVQAVKVLERVLKFMKGDEQPIRWKRSNQNISSLRSIEENSSSSRSKSTERAGIAMPTTPTSNVDTVLFRGDAMNDPGGVQSHSSTLNILPMVAAEPEPYVRYTTLIEHLNKPAQKDDHVSSSSHFSSTLEFNNSDPLTHSDDPGFVECAHPQAQQNLRFFARPSSLDVIRHPDLSFMHPNIQIEMRHTPAVHHVRSLTFNMSSDSGHAPATVIQRHYRIRSDPDEYSYTEDAGTDEDDACQTESFPSQTLFAR*

**JNK Pathway**

 **Hemipterous**

*>TRINITY\_DN67322\_c0\_g1\_i1.p1 TRINITY\_DN67322\_c0\_g1~~TRINITY\_DN67322\_c0\_g1\_i1.p1 ORF type:complete len:514 (-),score=79.62 TRINITY\_DN67322\_c0\_g1\_i1:477-2018(-)*

*MKMDAGDDFCDRIRDLEKRIIAENATYKRNTENAPDLSPSSLNFNLMSPSVTRKKPKPFTMTHTTVGPAMGRAISSQSSDGESESTEPSLLGFRDSFRLTRQRRLELAGSALPPGVHHNAAISSAKPEDHQVEYEEKLKEIMKKTNIITVRGKKFESSIEDLENLGELGHGTCGTVVKMRFKKTGDVLAVKIMRKSGNREENKRIIRDLDVVLKSHDCPHIVQCVGCFVTDAEVWICMELMVTCLEKLLTRTRTPIPEKILGKMAVSVLKALNYLKESHGVIHRDVKPSNILLDGKGTFKLCDFGISGRLVDSKAKTRCAGCVAYMAPERICPVDPNRPDYDIRADVWSFGISLVELATGELPYKSCKTDFEVLTKVLEDVAPSLPPHCGFSMDFCAFVKDCLIKDFKRRPKYRKLLDHPFIVRYELLHVDVGAWVKQVLPRLVLPPAFQVDLLSPLSKLPPLPVKTPSPQSAPQTPQKSWFVKQASKSIFRSAANVPSTAPLPRKQYNIVNY*

**Jnk**

*>TRINITY\_DN18814\_c0\_g3\_i1.p1 TRINITY\_DN18814\_c0\_g3~~TRINITY\_DN18814\_c0\_g3\_i1.p1 ORF type:3prime\_partial len:321 (-),score=40.29 TRINITY\_DN18814\_c0\_g3\_i1:1-960(-)*

*MAVTAKHPGQYYTIEVGDTRFTVLKRYQNLKPIGSGAQGIVCAAFDNVLNQNVAIKKLSRPFQNVTHAKRAYREFKLMNLVNHKNVIGLLNAFTPQRTYEEFTDVYLVMELMDANLCQVIQMDLDHERMSYLLYQLLCGIKHLHSAGIIHRDLKPSNIVVRSDCTLKILDFGLARSANASFMMTPYVVTRYYRAPEVILGMGYKENVDIWSVGCIFGEMIRGAVLFPGSDHIDQWNKIIEQLGTPSLEFMKRLQPSVRHYVENRPKYSGYPFEKLFPDVLFPPDSQEHGKLKGLTASHSRDLLCKMLVIDPEKRISVDDA*

**Jra**

*>TRINITY\_DN4480\_c0\_g1\_i1.p1 TRINITY\_DN4480\_c0\_g1~~TRINITY\_DN4480\_c0\_g1\_i1.p1 ORF type:complete len:336 (-),score=57.26 TRINITY\_DN4480\_c0\_g1\_i1:467-1474(-)*

*MDDASMSDMTTVSAAVSGVSSSEKGVIQLTNNKKRALTLDLKSSSSLLTVPATSGVCGPLAELKTPGFMLTSPDVQMLQLASPDLEKFIIQGLMGQNTPTPTQIVFPKNVTEEQESYAKGFVDALNALHRTGVTGIQTVNGMAYNVVNSNNGNMAFPLNQVNGQNLFPQFFTLPNQQFLQPIQAQIQQSTNNPNIQIHVTPAKPEPYSPSVSPVPSDPQTVPSERGSTRSTNSSSGTSPINMDDQHKMKVERKRERNRLAAAKCRQRKLERISQLEERVKELKDQNTALSETANHLRDDLSGLRQELLAHLTSGCNIEVSPNLLQTLQQMQNMQS*

*>TRINITY\_DN26203\_c0\_g1\_i1.p1 TRINITY\_DN26203\_c0\_g1~~TRINITY\_DN26203\_c0\_g1\_i1.p1 ORF type:complete len:464 (-),score=88.23 TRINITY\_DN26203\_c0\_g1\_i1:388-1779(-)*

*MPPRQRKNDKKLADAAVSVMSAENTPPMAAGNDATSHSTSTFRVTHPVNTDQSDVSSIASRKRRLTLDLPAFSSIPTRVSNSTPYVAKAGSANSPVSGPFLLTSPDMQMLKISTPELDRLLLQSLFSGRALMTPSTPVSSQNAYSKTADEAKDSYTKGYVDCIHSMQNSVAQYNMNLGSAIPYQFPMTMNVPMGMPFQLVAGTTQLDQNTGGNVGVTSKTQTSSQVATTTTGVLYRPQLPVPLPAHTQPFHTNLPIPVQLFPQLMLPRSPLPNNIPAPADLRINNTTSPNYLVSSPKPDTNYSDSNSITTLKKNTTRNPRKRPLDRSSYSPLSGTSDGQRVPSRTSCSSSNDEIINVDDPLVGLDQDSREKQERKRERNRLAAAKCRQRKMDKIAVLDEQIVRLKEGNEELERKAEKLRKEVEELRMEAISHKRAGCDLKLPEGLERRIAAMEMSSTAAQTDL*

**Fos**

*>TRINITY\_DN25370\_c0\_g1\_i3.p1 TRINITY\_DN25370\_c0\_g1~~TRINITY\_DN25370\_c0\_g1\_i3.p1 ORF type:complete len:418 (-),score=47.64 TRINITY\_DN25370\_c0\_g1\_i3:402-1655(-)*

*MTTKQISTSASTTSASTGTSSAAATSNATTAAHILYRMANLTSGGSNHIVTSHYGMNTVTEPITPVTPMIFSATMLQQGGAHFPNFSSNNAIPLTVQSSMAPHTTTSGNFIPVFIGSGGTTTIKQEPGEAPQVHTVRMSNVMNNSNPTMAGIGSPSSMNGGSSSGNHSSKGRSGGRRPNKQEKLTPEEDERRKVRRERNKQAAARCRKRRMDHTNILTEETDGLQDIQNQLKTDIEELQREKAEIEFLLQSHRAICSREVQLDPDVTMTPPRPSSQTMKSFLPDSQNMSPANPPNATSSPPAPMTVPTINITCANSGEHSSLLRKGGLGNAATRPASLSVKPTMASIDCGNSSLPTPSPTKLLFNFEHCGLTPTGLTPTGLTPLIPSCSAEVGVHNRSPPRPTDPTGDISPNTLASL*

**TIR-1 Pathway**

**TIR-1**

*>TRINITY\_DN13462\_c0\_g2\_i1.p1 TRINITY\_DN13462\_c0\_g2~~TRINITY\_DN13462\_c0\_g2\_i1.p1 ORF type:5prime\_partial len:378 (+),score=53.25 TRINITY\_DN13462\_c0\_g2\_i1:2-1135(+)*

*KLFREIGAVERLKNCASSPNDIASRLAGEALIVLGESVPHRLSQQIPLWTVQDVKHWMQQIGYVSLAKVFVENEVDGDLLLQLTDQTLRDDLKMHSRLQRQRFLRDLHQLKRISDYNSCDPFNIHSFLLQISPEYAQYTYNLLKAGVDPTVFPFITDDHLKNDAVIENGVHRAKIMDAVRRRHNLEKGAVAEVRSETDVFISYRRATGSQLASLLKVHLQLRGFSVFIDIDKLDAGAFDQKLIDSVRMAKHFVLILSPSALDRCIGDDERKDWIHKEITAALACKCNVVPITDPAFNWPTPETLPEDMRAVCKYNGIRWIHDYQDACVDKLERFLRGDLNIKPSLATSQPGTGQIAQVHSSSSPLPHNSAAHHHSAF*

**NSY-1**

*TRINITY\_DN26026\_c0\_g1\_i1.p1 TRINITY\_DN26026\_c0\_g1~~TRINITY\_DN26026\_c0\_g1\_i1.p1 ORF type:complete len:1162 (+),score=221.04 TRINITY\_DN26026\_c0\_g1\_i1:264-3749(+)*

*MGAIGNPERRLTLACVLDLVCPEGLKTRQKAYTDILRAADDYKIHVHHIEFDRLETNKITAVLDLMYNADVAIVDMSLSSQQIGLSGHLGSRERFGMQGNIILYHSEMVHGLFKGSIGTASMNTLGYSLSEDGERCVVTDSWMADAGIGLFSKLKQLLKDVQVTTSTHAKEKFLDDLRKARETLSNDQLKPELDKLRLRLDMDSMLLSPETVFNLLISYRDIQDHTAMISLMDRIQQKKDEGNAAQCLQPDFMYWYCFALNRRNGPGDRGKALEVMEKLCMGVFAVPDGLCLLGRIYKDMFNESNHENRDYLLKSIEWYRKGFCEKPNEFAGINLSTLLVVSGERFEHSIELQSVLMQLSHMLNRKGSLEILKDYWTVATCFEMAVLAEDFKKACLAAECMYKLKPQTWMIRSTMGNIALIEKSRKLQRTRSSSGESSRSSSVAVEDDEELYQFWIEFFDNGLTAPRPDSAHFPVLILQDDALVRHLVPFFVTISMAEETMEERTIKIWQASTVDGVEYLLKPEHVKSAAPNKQDDRCLFFYVAYHVSENLQVYFSSTDQRDRFYQLCKDFLRMTDDFVDLEDEEPPLEYDYENDNNGQRKLLGSGTYGRVYAAKNSNTQVKLAVKEMRVNDDAAVQLLHDEIKLHSKLHHRNIVQYHGSVYEGGFFKIFMEQVPGGSLSDLLRTWGPLKGNEITIAYYSKQILEGLRYLHDQKIVHRDIKGGNVLVNTFNGVLKISDFGTSKRLSGLNANASSFKGTFQYMAPEVIDSQSQRGYGAPADIWSFGCTVIEMAEGKPPFSDMFSPLAAMFVVGREKSHPPIPVELGEDCREFILATFRVNPALRLSAAELLKHQFLSIAAYKKRHRLSLTRPEDGTPRSQSVPLGVDPPAANGTVMSWNIETFATEDRGVGASLPSSNVTAPSSPEVDQETTGSFWKRKRNETQVELIQILQSERVHLTQRMMESFENNNKDGASLITPQSTEMILKGIEKCVDSQEAAKHVAEVIIEEMKGNVGVADHGRLLKQLQLFLFLLKREIQDVLRNRSIKPHWMFALDDMISKAVQAILQQMGMSFDDEGEPEKREYTSQTSTSAGSSGRVNFVYDNALVKLAKVQGGNAELLNMLIMAEERYQNLLKQTLGDRQQQIRLLELQHGGSVDLAVSK*

*>TRINITY\_DN27106\_c0\_g1\_i1.p1 TRINITY\_DN27106\_c0\_g1~~TRINITY\_DN27106\_c0\_g1\_i1.p1 ORF type:complete len:1304 (-),score=246.89 TRINITY\_DN27106\_c0\_g1\_i1:268-4179(-)*

*MGAIGNPERRLTLACVLDLVCPEGLKTRQKAYTDILRAADDYKIHVHHIEFDRLETNKITAVLDLMYNADVAIVDMSLSSQQIGLSGHLGSRERFGMQGNIILYHSEMVHGLFKGSIGTASMNTLGYSLSEDGERCVVTDSWMADAGIGLFSKLKQLLKDVQVTTSTHAKEKFLDDLRKARETLSNDQLKPELDKLRLRLDMDSMLLSPETVFNLLISYRDIQDHTAMISLMDRIQQKKDEGNAAQCLQPDFMYWYCFALNRRNGPGDRGKALEVMEKLCMGVFAVPDGLCLLGRIYKDMFNESNHENRDYLLKSIEWYRKGFCEKPNEFAGINLSTLLVVSGERFEHSIELQSVLMQLSHMLNRKGSLEILKDYWTVATCFEMAVLAEDFKKACLAAECMYKLKPQTWMIRSTMGNIALIEKSRKLQRTRSSSGESSRSSSVAVEDDEELYQFWIEFFDNGLTAPRPDSAHFPVLILQDDALVRHLVPFFVTISMAEETMEERTIKIWQASTVDGVEYLLKPEHVKSAAPNKQDDRCLFFYVAYHVSENLQVYFSSTDQRDRFYQLCKDFLRMTDDFVDLEDEEPPLEYDYENDNNGQRKLLGSGTYGRVYAAKNSNTQVKLAVKEMRVNDDAAVQLLHDEIKLHSKLHHRNIVQYHGSVYEGGFFKIFMEQVPGGSLSDLLRTWGPLKGNEITIAYYSKQILEGLRYLHDQKIVHRDIKGGNVLVNTFNGVLKISDFGTSKRLSGLNANASSFKGTFQYMAPEVIDSQSQRGYGAPADIWSFGCTVIEMAEGKPPFSDMFSPLAAMFVVGREKSHPPIPVELGEDCREFILATFRVNPALRLSAAELLKHQFLSIAAYKKRHRLSLTRPEDGTPRSQSVPLGVDPPAANGTVMSWNIETFATAKKQKRKREDSRNGTEIKRKQNSKKPPELVSGRKRKDCGDALDHEAKKFIRRSSTDLLPIRRCPKNIENSLIDPRCKRKDYDDAFERESKKFGEYDACFVSPLCTPVTTKDFEEVVIQTASSACPLLVYVCGCMLPAFAVCTEDRAVGASLPSSNVTAPSSPEVDQETTGSFWKRKRNETQVELIQILQSERVHLTQRMMESFENNNKDGASLITPQSTEMILKGIEKCVDSQEAAKHVAEVIIEEMKGNVGVADHGRLLKQLQLFLFLLKREIQDVLRNRSIKPHWMFALDDMISKAVQAILQQMGMSFDDEGEPEKREYTSQTSTSAGSSGRMNFVYDNALVKLAKVQGGNAELLNMLIMAEERYQNLLKQTLGDRQQQIRLLELQHGGSVDLAVSK*

**SEK-1**

*>TRINITY\_DN13655\_c0\_g2\_i1.p1 TRINITY\_DN13655\_c0\_g2~~TRINITY\_DN13655\_c0\_g2\_i1.p1 ORF type:complete len:343 (-),score=52.46 TRINITY\_DN13655\_c0\_g2\_i1:506-1534(-)*

*MPPRKIKLEPIKFSPNVAQEAAPPGLDSHARMKFDANGPDYEVTASDLELLRQLGRGQYGYVEEYRHLESGYVFAVKRIRCTDDPEERKRMLMDMQVNESNGGRCPYVVRSFGALFREGDIWICMEVMDASLEKFYKDLFTAKLTFPEEVLAHIAFAVVSGLKFLKDQLKVMHRDVKPSNILLSRRGEVKLCDFGVSGQLVQSMAKTNVGCSAYMPPERVNPLVVSEGYDIRSDVWSFGVTMIEVATGKHPYAKWKNAFQQMQQVVVGAAPSLPEGPFSDVFREFIDWCCQKDLEHRPKYERLLEHEFLRRDREHPTDISTFVKTVLDGNCIIDGAPQEAGA*

**PMK-1**

*>TRINITY\_DN25063\_c0\_g1\_i2.p1 TRINITY\_DN25063\_c0\_g1~~TRINITY\_DN25063\_c0\_g1\_i2.p1 ORF type:complete len:412 (-),score=63.65 TRINITY\_DN25063\_c0\_g1\_i2:725-1960(-)*

*MTEHRLSGRFYKVDLHRSSWEVPERYEGLAAIGSGAYGNVASAYDKVTKQKVAIKKLARPFQTAIHAKRTYRELRLLRHMKHDNVIGLLDVFTPEESFRDFKQVFFVTHLMGADLSSIVKTQPLTEQHVQFLIYQILRGLKYIHSAGVIHRDLKPGNIAVNEDCELRILDFGLARQAQDEMTGYVATRWYRAPEIMLNWMHYTQTVDIWSVGCIMAELLSGKALFPGADHITQLNLILDLVGTPGEKLLNKIESDDARQYIGSLPLCPPKDFHKVFPKTGKPAIDLLKKMLELDPDERITAEEALAHPYLAEYHDPADEPVCTEPYDQAFEDLDISIDEWRGAFSVQSKFRSKLLVDEAEVPESNGVHGSSTNSCAEGVRRWTCAVPINLGRNLLSSFVDDQFSVHLFVPL*

***Epiperipatus sp***

**Toll Pathway**

**Spaetzle**

*>TRINITY\_DN60536\_c0\_g1::TRINITY\_DN60536\_c0\_g1\_i1::g.34653::m.34653 TRINITY\_DN60536\_c0\_g1::TRINITY\_DN60536\_c0\_g1\_i1::g.34653 ORF type:complete len:219 (+) TRINITY\_DN60536\_c0\_g1\_i1:104-760(+)* ***(Spz3)***

*MMRYAKKSEIILIVILLELFFICNGNYEGNYADNDQSSEEADVFYYTDPSYSQHNTYKYSTKLNKNLMYSIVPGPHYPMVAICAFIDDNKALMRRMYGTLPPHDLFNNKILPGPKRRIRQTSPEGDNLCSSKKELVTPFWANNASEYRLAIVNFPPFQQAIHIETCRENRSCGGQTNCSCSQDDTWHRLLAYDAKDNCRGIFMEWFKFPSCCKCKCFN*

*>TRINITY\_DN65515\_c1\_g3::TRINITY\_DN65515\_c1\_g3\_i10::g.27351::m.27351 TRINITY\_DN65515\_c1\_g3::TRINITY\_DN65515\_c1\_g3\_i10::g.27351 ORF type:complete len:255 (+) TRINITY\_DN65515\_c1\_g3\_i10:126-890(+)* ***(Spz3)***

*MLIELSKMITLEYLVLIATTLLPVHYANYNSFNDIPQNSTRIRFPPNFNNKLERDKVYPSVKFRPPMSFLPMPPLIYTDYLKPVEEPIIVHSKYIIDTPYSNYKGNDYPDYEINAFLDDNKAMMRRMHGSINPMYYYNPTPNSQARYSKQRYSRQVSEEQELGSNFCPSQKETVSPYWAFNASNYKFAIVNQEPFTQAIHIEKCLQAKNCGQSNCRCAQEYTWIRLLALDPNGGCQGIFM*

*EWFKFPSCCICKCF*

*>TRINITY\_DN70147\_c6\_g1::TRINITY\_DN70147\_c6\_g1\_i3::g.11181::m.11181 TRINITY\_DN70147\_c6\_g1::TRINITY\_DN70147\_c6\_g1\_i3::g.11181 ORF type:3prime\_partial len:159 (+) TRINITY\_DN70147\_c6\_g1\_i3:126-599(+)* ***(Spz3)***

*MLLQIVAVNGFSLSSSISIRNLSNEEYYSRLKRFLNENAEEIMPIYYQLMPLLRRPKRKEFRPACPYKISVLSPFKLVNIDKKLRMVINTEPIFQTVEQEICSEHEQTFCPRGCNCKQQNKTVTLLASSVESNEETLRVFTDVFSLFYFCSCTCQFSR*

*>TRINITY\_DN67460\_c1\_g2::TRINITY\_DN67460\_c1\_g2\_i2::g.6933::m.6933 TRINITY\_DN67460\_c1\_g2::TRINITY\_DN67460\_c1\_g2\_i2::g.6933 ORF type:complete len:281 (+) TRINITY\_DN67460\_c1\_g2\_i2:87-929(+)* ***(Spz4)***

*MDAAVITQMHFGLLLGFITVVYSESNYTAPCNLNLDSYCSIPGPYYPWDNIGIFIKGNLGTTKRLFGDSKKKMLSFRRDDFGYNPCPSIMEAAQPYWARNIDGKLRAIINYEPFTQFIQVERCYDAFTGLPNKCDTDCGCYQDYRLQRLLVSDPHSENGGIFMDWFNLPFCCMCKCSVNNFINTTDTSEDFLTPKVSNNSNINGTENMDPLESDAIDPTLQDSSEVNVTTFESNISSTAKPQIKWNHTHLHSNNSQRVHFYYTKKQNITFKKKKRNKNND*

*>TRINITY\_DN21288\_c0\_g1::TRINITY\_DN21288\_c0\_g1\_i2::g.18606::m.18606 TRINITY\_DN21288\_c0\_g1::TRINITY\_DN21288\_c0\_g1\_i2::g.18606 ORF type:complete len:166 (+) TRINITY\_DN21288\_c0\_g1\_i2:25-522(+)* ***(Spz4)***

*MFWFIWVTLIIAITLNKGFAKNKLPSNYPLAEIQKAINDDYDNFYRMYRSVNSELENHRYRIRRKRFRDEYSCPVEVPENYEPNTLENISGQKRFIINFPPFNQFVYRESCNISARYLCKESCSCTQQTRVVRLLAARFGETVKGLFTDHFDVPTFCACNCLPFS*

*>TRINITY\_DN68903\_c3\_g1::TRINITY\_DN68903\_c3\_g1\_i1::g.3400::m.3400 TRINITY\_DN68903\_c3\_g1::TRINITY\_DN68903\_c3\_g1\_i1::g.3400 ORF type:5prime\_partial len:154 (+) TRINITY\_DN68903\_c3\_g1\_i1:3-464(+)* ***(Spz4)***

*FFFLQDILELYPGMMNHLKNYCGLNVIRIWVILQGLFLLQSNGESSCPDDEGYCDAPGNDYPWNEMQYYIEENQDLLQRMYGHSDFKNMYRHKSSIEPRILETVENACPSEIEIVTPFWANNSEGKYLAIVNFHPFEQAVQKETCKKECYWSL*

*>TRINITY\_DN101951\_c0\_g1::TRINITY\_DN101951\_c0\_g1\_i1::g.38134::m.38134 TRINITY\_DN101951\_c0\_g1::TRINITY\_DN101951\_c0\_g1\_i1::g.38134 ORF type:complete len:160 (+) TRINITY\_DN101951\_c0\_g1\_i1:2-481(+)* ***(Spz4)***

*MISIVTSIFINPRPDEDYVWLRENTDEEYHKILKRFVHEHYDEIEPIYNLISHQREKRGRKEGPCVKYSTYMRPSSFKNVRGEERLILNVAPFLQYIDMEECNFTTGQCAAGCICEPGHKTVTLLSTYPKEEVGKFEGAFTDFFSVPVFCSCTCRRIPL*

**Toll**

*>TRINITY\_DN67928\_c1\_g3::TRINITY\_DN67928\_c1\_g3\_i1::g.31459::m.31459 TRINITY\_DN67928\_c1\_g3::TRINITY\_DN67928\_c1\_g3\_i1::g.31459 ORF type:internal len:385 (+) TRINITY\_DN67928\_c1\_g3\_i1:3-1154(+)* ***(Toll2-LRR only)***

*LNLAWSGISRIPDGELCNALNLMLLNLTGNKIKVLSELGFMELINETYRPCPSPLGSLDLSSNHITSIPATALDGLRDLIILDLSHNQISSVASTAFHDFVHLRILNLANNSLINLPGNLFQNATELTKLDLSQNRLRSLSQNSFQGLGKLEILNLSRNDLSSQQLEGSLRALFQLTVLDLSYNRLSHVNPNMFRELFGLKHIRLDHNNIAVVTKESFANMVVLQILNMDYNQLTDIETHTIQGLHVLTYFSAEHNKISHIAADSFYDNVKLQTLKLCDNFITEIPVLKRFRMIETLDICNNQISTLSSSTFTGISSLQGIRLRGNNLTTITTGTFAHLPALSIINLSKNNIKNIEKDSFQNLSSLTYLRLDDNKVSMIIGLFN*

*>TRINITY\_DN69166\_c1\_g2::TRINITY\_DN69166\_c1\_g2\_i6::g.12813::m.12813 TRINITY\_DN69166\_c1\_g2::TRINITY\_DN69166\_c1\_g2\_i6::g.12813 ORF type:5prime\_partial len:501 (+) TRINITY\_DN69166\_c1\_g2\_i6:1-1503(+)* ***(Toll2-LRR only)***

*FINQIQGPIQAMRLIKPKIQNLPENVFHGHVISDFIIEGAGLTLDPKAFDALKTNLKRVILPSNKLTDIPTLSDSQLLEDLVLHDNLISKIDENSFNNLRALKVLILSNNSIDNISDETFQSLEQLIVLSLVGNKLTQVPKGPNSLQTFLLRGNALSTINAGTFDTYPNLVHLDLADNNLKEIKKVMIPTSEKLIVLDFSNNKISSIESGAFENAKSLKSLVLARNEIGDPKPDMFNGLENLASLNLSSNQISEITSGAFAKLKGLEELDLSGNNIKNLPEDAFSGLVLLKALAIGGNPMKELQPDLLNDTPLLNSLSLANSGLTDIPEGVRKFEKLQLLELSGNNIEKLDTSMFKNFGNLKILFLDNNQLTELPQDVFSPLKSLKVLDCSFNKLSKLTTHNFDSLSESIIYINLEGNPLDCKSQETQQLMQGLITLKQKYNYMQLMMLPKIFIVDETQKERFPVKRVDILPCLPPMNPSMRSPNFNRGPSGSSRRVVNP*

*>TRINITY\_DN69045\_c0\_g5::TRINITY\_DN69045\_c0\_g5\_i1::g.37837::m.37837 TRINITY\_DN69045\_c0\_g5::TRINITY\_DN69045\_c0\_g5\_i1::g.37837 ORF type:internal len:258 (+) TRINITY\_DN69045\_c0\_g5\_i1:2-772(+)* ***(Toll6-LRR only)***

*IIGLFNHLTKLQLLNLSSNLISEIDYAMFPRELPRLDVHNNNLSLLGNAYAMEDKVQLQYLDASYNHIERLGPSAIPHSIQVLKLTHNKIINVEAFTFYLKANLTSVFLTHNQITQIPESALRFQAVPIDKSLPEFHLSSNPFFECDCTMVYLKRINRFNNMRWLPKIVDLNNIYCGSLWKKSYALLTEKPDSDFLCEYNINCYPLCHCCDFDACDCEMRCPHNCTCYHDLPWQTNIVDCTTRHLSNVPFMLPMDAT*

*>TRINITY\_DN68651\_c8\_g4::TRINITY\_DN68651\_c8\_g4\_i1::g.20083::m.20083 TRINITY\_DN68651\_c8\_g4::TRINITY\_DN68651\_c8\_g4\_i1::g.20083 ORF type:complete len:536 (+) TRINITY\_DN68651\_c8\_g4\_i1:58-1665(+)* ***(Toll6-LRR only)***

*MKSVLVLMWCMVHYGYSQTTPNSTISCPSEELMEGCSCWEDTDTQGLVVECTPCHFGIKGNYFGHDSFDLSKLTLVLQQMPGKVIHLSLKCINISEIPDHFFLNLSVPLKRLYLVSSALEHIADKAFEGLENHLEFLALYDNNITSLNWVKSLNKLKGLFLENNKLLTLPDDNFMSSLSSLEVLSLDNNQLSSSSGLNNLPSLQEINLRNNLLTFLSDDFLKGSKDTLQKLHLEGNKLTSLENLFHFKSLKELSLSGNLVESIPESLHNLGALEYLSLSFNNISTIDRKAFSNLVHLNLLDLSFNKVTNLNELSLQGLTSLTEINLQNNQIKSVPKEIFLNLLKLKRILLNDNEIISIKAEAFENLPQLLFLGLSSNNLTIVNNMFKNLDNIQILDFKDNSISTIEKEAFNPVSSLRGLYLDVNNLTTITADQFAPLTLLEFLTLCHNSITTIDEKAFSTLGKLKTLELCSNSLTGLNSEIFLGLKSLEKLDLSFNHLTMLANDTFKSLKNLKCIKFEETGVSEELASNYDFCLT*

*>TRINITY\_DN106531\_c0\_g1::TRINITY\_DN106531\_c0\_g1\_i1::g.38837::m.38837 TRINITY\_DN106531\_c0\_g1::TRINITY\_DN106531\_c0\_g1\_i1::g.38837 ORF type:internal len:374 (+) TRINITY\_DN106531\_c0\_g1\_i1:2-1120(+)* ***(Toll7-LRR only)***

*LSNNEIESIPKEVFQSMPNLGGLFLDWNKITNINDLNLESLVNLQTLKISNNNLKQMDVTTFKNFSFLMHLELQGNQISSIEQESFQRLPMLQVLHLENNLIKVIKKHTFANQKLLFELNLGDNTIENIEDDAFDGLETLQILDLHDNSMNFEQKNIFQKVTNLTKLFMPNNNMTKVSAGIFENLPFLMELDLSNNNISEIDVNAFAKLFNLHHLRLSNNKLKSINSNDFKDLINLFVLDLEYNLIHTLDVDAFSNLSRLKILSLAFNNLEQFPEGVFKYLNKVETLKLSGNKLSFVDSTSFHHMAELRQLHLSGNLIKEIPKGMFANSYELSFLYLNENEFSEIPSFLNELSNLFILDLSSNQIERNSKRLN*

*>TRINITY\_DN65336\_c3\_g1::TRINITY\_DN65336\_c3\_g1\_i3::g.12421::m.12421 TRINITY\_DN65336\_c3\_g1::TRINITY\_DN65336\_c3\_g1\_i3::g.12421 ORF type:internal len:378 (+) TRINITY\_DN65336\_c3\_g1\_i3:3-1133(+)* ***(Toll7-LRR only)***

*RNIELLREEIIDKVKNEKVIEILRVETNNIERIEHNSIKDIQHYTFDNNRKLKTITLSHNSLTYIKSRTFMNLDKVESIDLSHNNIKKLDDDMGFGLQEVKSIDFSFNKLQTLTAHLLTYYPKLEILDLSQNVIKSLSDIQFHKNNVLKEIYLEGNNIEIISENSFDNLFKIKKLNLKNNNIQLILPRAFYGLPFLKDLNLEQNKISLINTSIFNGMINLKVLNLKENQIQAIEKDSFENMFHLQELNLEKNLLQNLNDNFFNNTKSIKKLNLRQSEIVHIDPSFFDGFENLTVLDLSGNKISLIEKEYFKDLMSLNDLNLFNNHITAIKSEVFHSLVKLKTLHLNSNKLKVIENKWFLPENMLETLDLSENKINSI*

*>TRINITY\_DN131949\_c0\_g1::TRINITY\_DN131949\_c0\_g1\_i1::g.40595::m.40595 TRINITY\_DN131949\_c0\_g1::TRINITY\_DN131949\_c0\_g1\_i1::g.40595 ORF type:internal len:219 (+) TRINITY\_DN131949\_c0\_g1\_i1:2-655(+)* ***(Toll7-LRR domain only)***

*LERNLIKHIKKTDFENLINLKVLSLTYNELSSIEGKAFKDLCNLTTLNLANNKLIQIEHNYFKGLYNLSRLYLENNSISSIEPGSFQDLQNLERLFIFFNKITSISENVFWNLMNLKTLIVSENKISSLSRHSFRNLTKLSLLQLSANEITDIDFEAIVAFPSLFKLNLNNNKINRICSSAFSKLEHLSFIDISNNYLEEFPDNAFNGSHMVLHVKIE*

*>TRINITY\_DN2524\_c0\_g1::TRINITY\_DN2524\_c0\_g1\_i1::g.18407::m.18407 TRINITY\_DN2524\_c0\_g1::TRINITY\_DN2524\_c0\_g1\_i1::g.18407 ORF type:internal len:196 (+) TRINITY\_DN2524\_c0\_g1\_i1:1-585(+)* ***(Toll7-LRR only)***

*LKSLELIDIKRNKITEIQKGAFRNLPSLKEINLSENNLVFINKDAFQHLPLLTHIDLSRNILKNLSIDFFSRLPELQFLQLRQNNFETIKKNMFSNHEMLSHLDLSSSNIHVLERHSFFNFSQLKILYLCNNSISDIFTDTFTILPELRVLDLQHNKLSFLKHGMFKKLYKLVYLHLNNNKITHISNGTFDGLVN*

*>TRINITY\_DN65973\_c1\_g1::TRINITY\_DN65973\_c1\_g1\_i1::g.10474::m.10474 TRINITY\_DN65973\_c1\_g1::TRINITY\_DN65973\_c1\_g1\_i1::g.10474 ORF type:5prime\_partial len:403 (+) TRINITY\_DN65973\_c1\_g1\_i1:2-1210(+)* ***(Toll8-complete)***

*HLRELYLNNSNIYYIDNSTFNGLIELHVLHLEGNYLTILNGHEFLHLSTLQELYLNDNRIETIANTTFKDLLMLRILYLNNNHLVIIDTDIYANNMALVQLALAENPWSCSCEFLQNFWPWVLSNADIVKDLRNLQCFWNQSEPGQFLINANSTECPGHSTSIIPYWTPARIIQNYFILIVSLGASLLLILLITIVLYCHRDVLRIWIYAKCGIRFFDKTEDDSNKQYDAFVSYSSHDENFVVRELVPRLEEGNPSYKLCLHYRDFPLGICIAETIIRSIEASRRTIMVLSESYIKSEWCRLEFKTAHHQVLEDRKRRLIVIIYGDIAQDDLDPDLRLYLRTNTYVKWGDPLFWEKLRYAMPDVKRVEIKRKNRTDHKTYAKPRDQDETFIHEISKGRTCRY*

*>TRINITY\_DN66618\_c2\_g1::TRINITY\_DN66618\_c2\_g1\_i1::g.18011::m.18011 TRINITY\_DN66618\_c2\_g1::TRINITY\_DN66618\_c2\_g1\_i1::g.18011 ORF type:complete len:628 (+) TRINITY\_DN66618\_c2\_g1\_i1:91-1974(+)* ***(Toll8-LRR only)***

*MLGNINDRIPKGCYKTTSSGDNFFVTCNEVPIKHISEFLSTVPYMMKLDMRNCYIPKLPEGFFKKKRFCELQINNCQLKELSSLDLIGLEYVLEVLNLHNNLFSSIPILGFNSIKKLILSKNVIENISKISLQNFPNLTTLILDFNKIKAIDVAVFENLPNLIQLSLKGNKLLTKEISENFFASLPNLQSLNVSDTGIKSFKFPEKLRLELLYASNNEISELTQDMFKNQPNLRKLFLNGNNISEINSHALEGLSNMNVISLDNNQIDIHTHQDLLQFCINLRVVSLSRNVTIQLNTVIFSKLPFLSDLNLSHNAIEFIDENCFPYAYSDFRFLNLSHNSLSSLDRNYLKNLSTLIYLDLSYNCIIRIDYQNLKALKNLQFLILKSNQMLNLSTNTFSDLTKLEILDMSSNLLVSVSEHSINNLKNLTYLYLNSNQFSSIPFAFFNGCLHLSQICLNNNNLNEIPVALASIPNLKILDISSNPLSPLGKNSFCHVKSLYGLYISNCGLTSLPDDVFDKLIHLKVLDASINHIESISETVFQPFISSILYIDLQENCLKRDEASEWLFQFLRKLAFINAPEPDLVVLNDDIHLNEITEFTRDYVIKYSNQHSKEFIQFVVKKPGNYLD*

*>TRINITY\_DN65515\_c1\_g2::TRINITY\_DN65515\_c1\_g2\_i2::g.27343::m.27343 TRINITY\_DN65515\_c1\_g2::TRINITY\_DN65515\_c1\_g2\_i2::g.27343 ORF type:complete len:530 (+) TRINITY\_DN65515\_c1\_g2\_i2:82-1671(+)* ***(Toll8-LRR only)***

*MSTMTCLKSSILLLMVWTCAIKAAMYGGQCPQLPPGCTCAPGLSGLTLQCGSPFKAQNLFNMKCDKCLCEVPNKLECQASKNENDKFTLDKLTAVLQLIQDPLDRILVTCGNIEFIPENYFKQFNTSIKVLHIVKSGLKSLDEGSLAGLENSVTNIDFSLNNLTTMAGFSKLTRLERIQLSNNEISEISKDAFSGSANILKEIFMEYNHLETVSSFGELSIIDKIALKGNIIDSIEDNVFSNMGTLQALSLSFNPLKNIKKGSFNGLKNLYELSLDFSEMGNLESIDFVGLNNITILSMSCSKFSKLPAQTFKDIPSLRVLDLSSSNISIIEANAFEGLSKLSRLILFGNEIKSLETDVFKYCSKLDILELQTNGIESIAPGAFKSLINLQQLFINTNSLTTISADMLEGLYNLTLLDIQGNKLVNLDANVFDNLPYLQYLYLNNNNITEIKKETFSLPNLISLSLAVNQINTIESGAFDNLKAISELYLNNNQLSQDIDKSFFNNLPILRVVYLQNNPNKNLKDLNFS*

*>TRINITY\_DN20817\_c0\_g1::TRINITY\_DN20817\_c0\_g1\_i1::g.4512::m.4512 TRINITY\_DN20817\_c0\_g1::TRINITY\_DN20817\_c0\_g1\_i1::g.4512 ORF type:5prime\_partial len:173 (+) TRINITY\_DN20817\_c0\_g1\_i1:3-521(+)* ***(Toll8-LRR only)***

*LHLPFTNLTLNGTMFTNLTTLEHLSLDCNHIDTFPPKLFQPLRKLKSLFLSGNNIKTIEKGLIEGLSNLLLLDLSHNHIEEIYADAFINISALETLNLADNELFYITPGIFSSLTNLKTLFLSHNKLDTLNPGMLKNLRNLETLLLSGNKIDIVPENAFRDNPKLKNFDLRK*

*>TRINITY\_DN134823\_c0\_g1::TRINITY\_DN134823\_c0\_g1\_i1::g.38895::m.38895 TRINITY\_DN134823\_c0\_g1::TRINITY\_DN134823\_c0\_g1\_i1::g.38895 ORF type:5prime\_partial len:293 (+) TRINITY\_DN134823\_c0\_g1\_i1:2-880(+)* ***(Toll9-complete)***

*NLSELYLQNNYFTIIDYPIQNYLKNKQLISISHNPFQCDCHIFNFSQWLQSTHNIPDKKSNYYMCNDSMVSLLEITYDLACNPEFESKDLIKQQQTFNMPLALALLVVLPLFFIIGIAAFGYYYRWYLRYWYHKIHMHIKIFTGSSPTSSMSKDYDAFVSYSSKDYEWVCLVLRPKLEENASFKLCIHDRDFKLGYQITDNIVDSIESSRKIMLILSKNYIQSEWCKWEMEIARFQDNLILVFLENIPKNCMPPTLRFLARSRTYIEWKSDSQAQKLFWERIIAALHISRTL*

*>TRINITY\_DN65811\_c2\_g1::TRINITY\_DN65811\_c2\_g1\_i2::g.20960::m.20960 TRINITY\_DN65811\_c2\_g1::TRINITY\_DN65811\_c2\_g1\_i2::g.20960 ORF type:complete len:833 (+) TRINITY\_DN65811\_c2\_g1\_i2:314-2812(+)* ***(Toll9-complete)***

*MLILLILITSFLLSAVDCVTSCFSRCVCSDNKASVDCSSLGLNYSLVLPADIEKLDYSGNHFDFLNQTFFSHIPYLRILNLSNSHVFEIHEDAFNPLHELLILDLSSNFLSAFHLNLFKNMTNLQQLYLKKNFFASLPKGIFYSLQNLEFLDISHNFLKGFELWQNLVGLENLKTVYFYGNTLKKLESDTLSILWNTSLENFDLSNTNIEFIDEFAFSPLVHLRHLKLDGNAGVAAPVNQDSVLRWLPHTNVTSLSLRYVTSWEESVTWSIIRNMKSITLQTLDMSFNYLRVISEPIFQDSSKINHLILRHMQLEEIHLNAFEPLIHLEVLDLSFNNLKYLFQPVTNFTALQRLKKLDLSNNLFVSLTTVWDAHTPGLSIYGDQLILPQLEILIIENNKLLDFKQNLFNSMPKLKQLHASFAFLRELSAPDNLVLDKDTFYHENLEYIDLSRNHLKFLASETFSDCFALKKLNLADNRLGPAFSQDKLGHLFSNLSSLLSLDLSRNEIDFLPLEQFSSLSFLKVLNLNYNKIAGFPPDVFDGLNSLESFHIKTNKITVLDAGGLQLLKNLKEIDFSENPLQCQCDVIEFFHWVNFSNLTIIRWEHLDDYFCNLRNASLKEFLFTAAENECLHMESNIILICVIAISSIVIFLLLFCLALGLYRYIYVRANVEMTPKNIAISRQNKVKDYDAFISYSGKDAPWVPEVFQKHLGGERKLRLCFHDNHQHMGRTINWDMMNKIDSSYKVLFIITKNFVQAEWFQWESMMLLFQDCAILVGLEDIPTTNMAYTLQWLVRTKPFLNWPMLENDHGLFWDDLAIYIKEDSNRKSPLYI*

**Myd88**

*>TRINITY\_DN69103\_c2\_g1::TRINITY\_DN69103\_c2\_g1\_i1::g.12775::m.12775 TRINITY\_DN69103\_c2\_g1::TRINITY\_DN69103\_c2\_g1\_i1::g.12775 ORF type:complete len:427 (+) TRINITY\_DN69103\_c2\_g1\_i1:105-1385(+)*

*MAKNFADSFTEVPGRALNISTRRLLSLFLTPKSVLHTGDWQHLAEYFGFDFMAIRYLDGYKDPVNELLDLWIDKKGNKATIGQLLNGLVTIGRLDILGQIPVYLEKDVSSYYKHLEEEQRLLEELYPVQDPAVSTACDSDEETLTIDDGRIYDAFVCFAAHDLPFVKEMIKILESDKYRLKLCINVRDLLPGKSRDKTITKIIEEKCRRFIIILTPEFLASRECKFQVEFALGLSIDKERDKSKIIPILLRQCEVPRILRFITACDYTKADVREWFWDRVVAALKAPLPKEKKSIGKEELSRSSSLPSISLQSKLNSLKDQFSCKRANCDSSEEDIKSNTLMSDITIGSSSEEHNPDIASTSSYSPHSCLMSDYSEHSSASSDRDSTQTASCSTSSDSHLIKQTKNDLKHLKSNGFSFFRKKKCAF*

**Pelle**

*>TRINITY\_DN65315\_c0\_g1::TRINITY\_DN65315\_c0\_g1\_i1::g.12475::m.12475 TRINITY\_DN65315\_c0\_g1::TRINITY\_DN65315\_c0\_g1\_i1::g.12475 ORF type:3prime\_partial len:639 (+) TRINITY\_DN65315\_c0\_g1\_i1:289-2202(+)*

*MEPSDCIYIYNLPFSVIQNISVMMDIDNKWKYLGGLMEFDITTLTLFGQCLYNNRSPTEKLLLDWGNKNHTVLELFLLLEKLKYFRAMAELKPYVNSYYHYLLQQQPSPPPVHELPNSYFSTGIASNNDLPVPTFHHDEFRKSYPTSMRPCENTEIIPSSRISNNKLNTFSENNDKMFDKADFNEQFCNYYGYHDIKKNMQTFQNFTKNTVHTEQVKISNEMQRGLVDSLPSEPFNGDQVKSYMVPSYTANISYCEILEGTNHFDSSGIIGQGAFGIVYRGIWRHTTVAIKRIKIDSENIFDNANRIKQSFAELRNILLYHHDNILPLYGYSSDGREPCLIYMYMVNGSLEDRLSCKDNTPPLSWNKKYKIALGTARGLQFLHTSKPPLIHGDIKSANILLDKSFEAKIGDFGLAHIGEISPQTHITTHIARGTTSYLPPEYLRGQKLSTKVDTYSFGVVLFELATGLKAINESKRTLLRDYIFEQKDDGILKLQDNKSGEDVYHYFQAFISMGKSCSSTRKNNRPEMTEVLEYFDSIPLKIMMNTATSDAHTPQNLPIQFECDNLITPSNKILEDNFSENLQIVNENNGINKLPDGFKNTSYFGNQSVAAFVSPEINQLQHIIEMPFIKAKYKSLPF*

**Cactus**

*>TRINITY\_DN68494\_c3\_g1::TRINITY\_DN68494\_c3\_g1\_i13::g.5934::m.5934 TRINITY\_DN68494\_c3\_g1::TRINITY\_DN68494\_c3\_g1\_i13::g.5934 ORF type:3prime\_partial len:324 (+) TRINITY\_DN68494\_c3\_g1\_i13:129-1097(+)*

*MEAIDKLPSSVEEDSASIQSKQRIFAPENFVKEEFKDSEITYDSGFHSLPEKFASLEIKNESSFCSALPTLDKPTTSSHYDILNSYINRAPNFYIVSDEDGDYLLHLAVIQCDFEMVLSICQQIPKSKYLNFTNDLHQTPLHLAVLMKQPKICELLFKYGAAIDSRDRNGQTPLHIACENGSLECVTALTNSSIQIQDLEIMNYEGLTCLHLAVIGGHSEIVFHLCSLYANVNAQDGKSGRTALHYAVEGRNDNLINMLVNNFKACVNSITYAGLTAERLARGRGYWDIQKLLISLGAAVEDFDDNMSDTDSSDYDDLVNRTK*

*>TRINITY\_DN63430\_c0\_g1::TRINITY\_DN63430\_c0\_g1\_i2::g.25843::m.25843 TRINITY\_DN63430\_c0\_g1::TRINITY\_DN63430\_c0\_g1\_i2::g.25843 ORF type:complete len:374 (+) TRINITY\_DN63430\_c0\_g1\_i2:66-1187(+)*

*MVTQTVFLKTIRLCSTMSSNDIRPRRYLGKVRKKTVKTEVGNLNSKFFPRGTDNVSSDFTKTNLGIKNTLTLPLKKRKLNAYNESLKKEDCKNIEIKCNALKSDCAKESLSSKGNSDTATVNLPSSSCADLTMGQFPNQVAPSLHMYNIALKPDEDGDFPLHIATAQNHIRAMVTFINIMKSFRTSIDVFNNLRQTPLHIAAIIGCTQPTELLLAGGASPFVVTRHGDTAFHLAVMYGHLECLRILVEKIQSLDAQKIYLEDKKHLNLNLRNHEGLTPLHLAVIKRQKEILEYLCENGVNINEVDGKSGRTPLFYAVENRDKELVELLIKHNADVNVQNYSGNDPLSTAAGKKSFDIVKLLMSHGAKESINDS*

*>TRINITY\_DN69706\_c5\_g2::TRINITY\_DN69706\_c5\_g2\_i1::g.34309::m.34309 TRINITY\_DN69706\_c5\_g2::TRINITY\_DN69706\_c5\_g2\_i1::g.34309 ORF type:complete len:493 (+) TRINITY\_DN69706\_c5\_g2\_i1:633-2111(+)*

*MKKDIPVFSSVALPGDGKYEKIAAHNIALLYKNIKDGYQTHTKIITDSSQNKKDMAIKVTERIAEALSNFAFTGELHPLILVMRHLVAIQDEAGDNILCQAVLQEKVNVVKELLKVLETISSYNIINQKNNLLQTVLHLAVFTHQPEVLKDLLLNGADATIIDHHGNNPLHLASHLGDADSLNILLDFENYSVNLRPNLDSLNYDGFAPLHLAVQANSLPCVKILTLHGASSDVQDGTSGRAPLHHAVELNCKEIINHLVIENRANVNAQMYNYNTPLHIAYGQGCDSIATNLLASGADAMIENLEYLDSSSDEEYFDSNSSEKPCHTAYHMDPSLFVKHHHQVQHKSDKENSTVTQLIPSFKEHCYISPTKHSSFYPRSFSELEKPKGDLHTLPYGVKVKLSQLLDQESSDEKNWKCLARTLDLSDFIKELSKSKYSPTRTILDHYEALEGTLASLEAALIKIKRYDALKVLTDSMKEHHSSSSKTKMPSI*

**Dif/dorsal**

*>TRINITY\_DN3720\_c0\_g1::TRINITY\_DN3720\_c0\_g1\_i1::g.18::m.18 TRINITY\_DN3720\_c0\_g1::TRINITY\_DN3720\_c0\_g1\_i1::g.18 ORF type:3prime\_partial len:196 (+) TRINITY\_DN3720\_c0\_g1\_i1:68-652(+)*

*MASSSETFLYVRNTSNLWTPSDFNLTDELINSSNGDMSIETAFTSETNLLTCEPYLQIIEQPRARGLRFRYECEGPRAGSLLGENTTAETKTYPKVQIKNYRGPAVIVGSCVTKEPPHQPHPHSLVGKDCVNGVCTVKVDSSSDTDPAEDMQVRFPQLGIQCAKKKDIEEALRVRERIRVDPFNTGFQHQAGSLD*

**Imd Pathway**

**PGRP**

*>TRINITY\_DN13502\_c0\_g1::TRINITY\_DN13502\_c0\_g1\_i1::g.11282::m.11282 TRINITY\_DN13502\_c0\_g1::TRINITY\_DN13502\_c0\_g1\_i1::g.11282 ORF type:5prime\_partial len:158 (+) TRINITY\_DN13502\_c0\_g1\_i1:1-474(+)* ***(PGRP-LC)***

*FKFPLKHVVIHHTNGISCSTRVTCSAIIWNIQWEDTHARQLDDIAYNFLISTNGQVYEGRGWTRIGQHLLLGNKDALGISFIGTYNTIWPNEKSAQAARKLLFCGVKSTRLVKNYTLTGHRQWWFPEKTLQCPGESLFTEIQSWKHFWNASEIIPTT*

**Tak1**

*>TRINITY\_DN66621\_c2\_g2::TRINITY\_DN66621\_c2\_g2\_i1::g.18218::m.18218 TRINITY\_DN66621\_c2\_g2::TRINITY\_DN66621\_c2\_g2\_i1::g.18218 ORF type:3prime\_partial len:293 (+) TRINITY\_DN66621\_c2\_g2\_i1:2-877(+)*

*MEYAEGGSLYNVLHGSGSQPVYGAGHAISWALQCARGVSYLHGMKPKALIHRDLKPPNLLLIMGGTMLKICDFGTACDIQTHMTNNKGSAAWMAPEVFEGCNYSEKCDVFSWGIILWEILTRRKPFDEIGGPAFRIMWAVHNDQRPPLIKDCPKLLEILMTKCWSKEPSERPSMDEVVHIMVHLFQFFKGADEPIVYPSDSEHGTDLNNTLQESLTSASDSPIQSPSHTVNSRISDTILTKGQPVPLTPSTAAVKPIVVEVGRNTIFNSSEERRTSAPASLASSQENLVESR*

**Ird5**

*>TRINITY\_DN61106\_c0\_g1::TRINITY\_DN61106\_c0\_g1\_i1::g.4591::m.4591 TRINITY\_DN61106\_c0\_g1::TRINITY\_DN61106\_c0\_g1\_i1::g.4591 ORF type:internal len:249 (+) TRINITY\_DN61106\_c0\_g1\_i1:3-746(+)*

*RETILGSGGFGIVTQWINVDTKDTIAIKQCCLLLEASLNSKLCRRWEVEIDIMKKLNHPNVVTSKVVPVDLEVGKDDLPLMAMEYCTQGDLRKVLTRPENCCGLPEVDVLIMSKHIASAVGYLHSMRIIHRDLKPENIVLQEIDNKIVYKLIDLGYAKELDQNSVCTSFVGTLHYLAPELFGGEKYTCAVDYWSFGLIVFECITGIRPFLANDTPYHWQLKAKSKTPDDICAYNDSDGEVVFSKKLFK*

**Relish**

*>TRINITY\_DN66394\_c3\_g2::TRINITY\_DN66394\_c3\_g2\_i3::g.28933::m.28933 TRINITY\_DN66394\_c3\_g2::TRINITY\_DN66394\_c3\_g2\_i3::g.28933 ORF type:3prime\_partial len:410 (+) TRINITY\_DN66394\_c3\_g2\_i3:162-1388(+)* ***(no ankyrin)***

*MSDISELFDNLLSRSPEELLGLTCNGQLKPTVVIVEQPQSQGFRFRYKSETGSHGGLQGESSSKKHKTFPKIKVENCSAYPVKVQAMLYTNESKPRLHVHKLMGSDCDNDGIWQKTFDASVWQQDHIALQGFSILHASKRDIVSILYEREKKDKKISKTLLGAQRVLPSDVVLTKEEDDYIKKLADSKAKEFNDHLNSVKLGFTAECNGIRGPVCFTTPIFDCKSPSTCKLKICRIDHSSGSCEGGQEIFLLCEKVQKENIEVIFFEKSGDEISWSSKGIFGLHDVHKQFAIVFKTPPYERTDIEREVEVFLQLVRPSDKATSDPLHYTYTPKEDDYDQVQRKKRKKLPGIDDNFSYLLSNYASTSTMYDDTAASAQMSYLLPEHIGSLISRDASLSEDPGLCKDDSLL*

**JNK Pathway**

**Hemipterous**

*>TRINITY\_DN65946\_c4\_g2::TRINITY\_DN65946\_c4\_g2\_i3::g.10518::m.10518 TRINITY\_DN65946\_c4\_g2::TRINITY\_DN65946\_c4\_g2\_i3::g.10518 ORF type:internal len:316 (+) TRINITY\_DN65946\_c4\_g2\_i3:3-947(+)* ***(fragmented at the C-terminal)***

*NEARQRDKLPRDLSLGHSSPQNGPRRPKPLPVGEFGFPGRPSTGRIRRPLELPPSSPLHRPSDNSDIDHKLKEIMQQTGILTFDGKKYQADIADLEHQGELGNGTCGHVVKMKYKKTLHVIAVKQMRRSGNREENKRIIMDLDVVLKSHDCPFIVQCLGCFITDSDVWICMELMATCLDKLMKKLQAPIPEYILGKMAVAILKALNYLKEKHGVIHRDVKPSNILLDEKGTVKLCDFGISGRLVDSKAKTRSAGCAAYMAPERIDPPNPLKPDYDIRADVWSLGISLVELASGEFPYRDCKTDFEVLTKILHEDP*

**Jnk**

*>TRINITY\_DN64857\_c0\_g4::TRINITY\_DN64857\_c0\_g4\_i2::g.18489::m.18489 TRINITY\_DN64857\_c0\_g4::TRINITY\_DN64857\_c0\_g4\_i2::g.18489 ORF type:3prime\_partial len:268 (+) TRINITY\_DN64857\_c0\_g4\_i2:3-803(+)* ***(fragmented at the N-terminal)***

*MYLVMELMDANLCQVIQMDLDHERMSYLLYQMLCGIKHLHSAGIIHRDLKPSNIVVKSDCTLKILDFGLARTAGTTFMMTPYVVTRYYRAPEVILGMGYKENVDIWSVGCIMGEMIRGGVLFPGTDHIDQWNKIIEQLGTPSQDFMKRLQPTVRNYVENRPKYAGYPFEKLFPDVLFPAESTEHNRLKASQARDLLSKMLVIDPEKRISVDEALLHPYINVWYDESEVNAPAPSPYDYSVDEREHTVEQWKELIYKEVMEYEQTHNS*

*>TRINITY\_DN113255\_c0\_g1::TRINITY\_DN113255\_c0\_g1\_i1::g.39399::m.39399 TRINITY\_DN113255\_c0\_g1::TRINITY\_DN113255\_c0\_g1\_i1::g.39399 ORF type:3prime\_partial len:143 (+) TRINITY\_DN113255\_c0\_g1\_i1:265-690(+)* ***(fragmented at C-terminal)***

*MCRCLWLLEAEVSQTQSCWAKIHYGTLDSPSFGNTMSKQGNSGNMFYTVEVGDTKFTILKRYQNLKPIGSGAQGIVCAAYDSVTNQNVAIKKLSRPFQNVTHAKRAYREFKLMKLVNHKNIIGLLNAFTPQKSLEDFQDVYL*

**Jra**

*>TRINITY\_DN68565\_c1\_g2::TRINITY\_DN68565\_c1\_g2\_i2::g.15214::m.15214 TRINITY\_DN68565\_c1\_g2::TRINITY\_DN68565\_c1\_g2\_i2::g.15214 ORF type:complete len:270 (+) TRINITY\_DN68565\_c1\_g2\_i2:479-1288(+)*

*MEATFYDDHHHHHQSFTKENINQLKKRMTLDLQPDRAAKKPKFSLLSSPDLNMLKLASPELEKLLISSNGMVTTTPTPTQFIFPRNVTEEQEMYARGFVDALAELHKANVPNSPGMDSIPIVYVNTTANNVITSSTMHGTNNANLVSVNNPAVTTLTVTSTVSPLPTYIKDEPQTVPNLSATPPLSPIDMETQEKIKLERKRQRNRVAASKCRRRKLERIARLEDKVKQLKGENSDLANTASKLREQICHLKQQVMEHVNSGCQIMSQY*

*>TRINITY\_DN68565\_c1\_g2::TRINITY\_DN68565\_c1\_g2\_i1::g.15209::m.15209 TRINITY\_DN68565\_c1\_g2::TRINITY\_DN68565\_c1\_g2\_i1::g.15209 ORF type:5prime\_partial len:124 (+) TRINITY\_DN68565\_c1\_g2\_i1:2-373(+)* ***(with kh-1 domain instead of jun domain)***

*LVIGKGGETIKMLQERAGVNTYIKDEPQTVPNLSATPPLSPIDMETQEKIKLERKRQRNRVAASKCRRRKLERIARLEDKVKQLKGENSDLANTASKLREQICHLKQQVMEHVNSGCQIMSQY*

**Fos**

*>TRINITY\_DN67552\_c4\_g2::TRINITY\_DN67552\_c4\_g2\_i5::g.33010::m.33010 TRINITY\_DN67552\_c4\_g2::TRINITY\_DN67552\_c4\_g2\_i5::g.33010 ORF type:complete len:403 (+) TRINITY\_DN67552\_c4\_g2\_i5:70-1278(+)*

*MEDWRNCQNPSGYNRPAYCRGESFYKIQRYLPYNYRSYNTAKAIQGYNPSGAYFESMYQQRPNNVAQSQADTRLTVADILSSMANGEAVTPTTYAALQFSSGIPTATTPTLTPTTLSNIEQTFIELQSVPSHVQNQAGFVPPLIRMDSNNSEISHDSYQSSDKSDNDWNSTPSARRHPSNNIRSSLMSSITTTTTAISSTSTTKIGRNTGGRKPIKDDKLTPEEEERRRVRRERNKLAAARCRKRRLDHTNCLILETEGLEEKKASLQNEIQMLQNEKEELEFILQKHKQICKRLSNGSNPPTSTNHVLTNISRPTSLSVSSVHSSNNHGSKMSISVAEATGLSITTPSQIFSYENLIDGGTGLTPTGLTPIIPSCSSEVLKSSGSEHSSPENITSPTLVSL*

**TIR-1 Pathway**

**TIR-1**

*>TRINITY\_DN69322\_c2\_g4::TRINITY\_DN69322\_c2\_g4\_i11::g.34898::m.34898 TRINITY\_DN69322\_c2\_g4::TRINITY\_DN69322\_c2\_g4\_i11::g.34898 ORF type:complete len:772 (+) TRINITY\_DN69322\_c2\_g4\_i11:1379-3694(+)*

*MGCTRHQNHSNFSDGQSRRRCIKWSVFCGFMGCRCPAWLCFGTPNIPRSRSFNSLNLETPALNDLEPISPVTMPDFPSLEMRCRSGSGSSPTLKFSSGAPGSSIVKKQNVKTAVAKFSQILINLIAQLRSPVINEQLQALTEMCAIVKKAWESPEYGRYLAYSLCDVLRFNGGLNILIDNCSSDNNEIRFASGKVLEQCMSTENRDHVVNNGLEGVVTFACTKGDVEMSRVGMGLLESLFKHCEDTCSRVIELGGLNAVLHSCRSNDVETLRHCAMALANLALYGGSECQQNMIKARVPEWLFPLAFSKDDSVKYYACLAISCLVSNKEIEAAVLKSGTLELVEPFVTSHNPADFAKSDGSHLHGRSKGWLERLIPVLKSNREEARSLAAFHFAMEVDIKDRQDNKEVFYEIGAVEALKQVASSPNDVASRYAIQALKVIGETIPHKLSQQVPLWNVQDVEHWISQIGFPEFRENFSNCQIDGDLLLQLTDSMLRDDINIINGILRKRLLRELNNLKMTADYSSCDPSKLDTFLLSAGDELSQYTYTMLQAGVDREMLSLLNDDHLKYDCGITNGIHRMKILKDIKDKITGQPKTDNAIDAFISYRRASGSQLASLLKVHLQLRGFRVFLDVERLEAGKFDNNLLDNIRAAKHFVLVLTQNSLDRCINDNDCRDWVHKEIVAALTSSSNIVPVIDNFSFPDPETLPEDMRAICYFNGIRWIHDYQDACVDKLERFLRGEENTTMKNALMNIQSGHLQNGSNVSKKNGSPDL*

**SEK-1**

*>TRINITY\_DN65495\_c2\_g2::TRINITY\_DN65495\_c2\_g2\_i1::g.13548::m.13548 TRINITY\_DN65495\_c2\_g2::TRINITY\_DN65495\_c2\_g2\_i1::g.13548 ORF type:complete len:185 (+) TRINITY\_DN65495\_c2\_g2\_i1:202-756(+)* ***(fragmented at N-terminal)***

*MIVAIIKALHYLQFQLKVIHRDVKPSNILINRQGEIKMCDFGISGYLVDSVAKTIEAGCKPYMAPERIDPKGDQTHYDIRSDVWSLGITLIELATGRFPYSTWGTPFEQLKQVVLEDPPRLPPNEFSPEFEEVISSCLAKNYKQRAKYEQLLSHSFVVQHISKDTDTAGYVSEILDATEEKTAQ*

*>TRINITY\_DN118917\_c0\_g1::TRINITY\_DN118917\_c0\_g1\_i1::g.39841::m.39841 TRINITY\_DN118917\_c0\_g1::TRINITY\_DN118917\_c0\_g1\_i1::g.39841 ORF type:3prime\_partial len:149 (+) TRINITY\_DN118917\_c0\_g1\_i1:59-502(+)* ***(fragmented at C-terminal)***

*MPKSSKALGKMMAGNKKKPKPSPININCSSELLPPAPTIDLDSEAEFTIGDEKILVKADDLQVLELLGRGAYGVVEKMRHTKSDKVMAVKRITLTVNHQEQKRLQMDLDILMRARACPYLVQFFGALFREGDVWMCMEVMDTSLDKFY*

**PMK-1**

*>TRINITY\_DN64857\_c0\_g1::TRINITY\_DN64857\_c0\_g1\_i4::g.18482::m.18482 TRINITY\_DN64857\_c0\_g1::TRINITY\_DN64857\_c0\_g1\_i4::g.18482 ORF type:complete len:377 (+) TRINITY\_DN64857\_c0\_g1\_i4:283-1413(+)*

*MGDGIKPGFYRVELNKTIWEVHHRYQLLSPVGSGAYGQVCSASDTQTNNGTKVAIKKLARPFQSAIHAKRTYRELRMLKHMNHENVIGLLDVFTPSQTLEEFQDVYLVTHLMGADLNNIVKTQKLSDDHVQFLVYQVLRGLKYIHSAGIIHRDLKPSNIAVNEDCELKILDFGLARHADEEMTGYVATRWYRAPEIMLNWMHYNQTVDIWSVGCIMAELLTSKALFPGTDHIDQLTRIMNLVGTPDDDLLQKITSEEARNYIRSLPIMKKKNFKDYFRGANPLAIDLLEKMLELDPDRRITAEEALAHDYLRQYADPTDEPISDTYDESFEDMDLSVPEWKRLVHKEVVMFQPKVRQLQGGLSQALQNQRHSYYNP*

***Opisthopatus kwazululandi***

**Toll Pathway**

**Spaetzle**

*>TRINITY\_DN117972\_c1\_g4::TRINITY\_DN117972\_c1\_g4\_i3::g.70929::m.70929 TRINITY\_DN117972\_c1\_g4::TRINITY\_DN117972\_c1\_g4\_i3::g.70929 ORF type:complete len:217 (+) TRINITY\_DN117972\_c1\_g4\_i3:270-920(+)* ***(Spz3)***

*MLTLVLILICNGCFCSSTYYNKTLDVQEPPIVAADVSSSYRADYAYNQNNVYKYYPQKQTTTMWYNQFPGHDYPRDAICSFIDDNKALMRRMYGTMPPVKVFNNGMYSGRAGRETRQATPEGINFCSSTKEIITPYWASNSSGYRLALVNFPPFQQAVHVETCRENRACGTQSNNCFCAQDYTWHRLLAYDAAESCRGIFMEWFRFPSCCICKCVN*

*>TRINITY\_DN102666\_c0\_g1::TRINITY\_DN102666\_c0\_g1\_i6::g.17998::m.17998 TRINITY\_DN102666\_c0\_g1::TRINITY\_DN102666\_c0\_g1\_i6::g.17998 ORF type:complete len:213 (+) TRINITY\_DN102666\_c0\_g1\_i6:225-863(+)* ***(Spz3)***

*MNHHNFCRMGGIPTILSILLLIVSLVQCYVEVPCSDDIGYCDIPGKDYPLEDMQLFIHENQALFKRMYGKESNFFEKSYRNQQLWPQPRLMDEVNACPSETILITPYWANNSQGDLLAIINFHPFEQPLQRELCSTNSIGQCRHGCYCEQNYAWHRLLAFDPKDKCKGIFMDSFQFPTCCACRCYDFYSNNVENSARNEGNFVFQREARGPT*

*>TRINITY\_DN85035\_c0\_g1::TRINITY\_DN85035\_c0\_g1\_i1::g.10687::m.10687 TRINITY\_DN85035\_c0\_g1::TRINITY\_DN85035\_c0\_g1\_i1::g.10687 ORF type:internal len:182 (+) TRINITY\_DN85035\_c0\_g1\_i1:2-544(+)* ***(Spz3)***

*GLQIIKPKPIHDRGCEYFENHSHYCREPGQHYPWDQIKAFIDDNKGLIKRMYGNVSPSELYEMDKTYVYNKPMTSSVLNGHRYRRQIGEKNMCQSEIEIFSPYWALNSKKEELAIVNFSGFNQVVSKETCLHSQRSCHDNCRCAQEYKWHRLMAYDSNDTSGCKGIFMDWFKFPSCCVCRC*

*>TRINITY\_DN112233\_c4\_g3::TRINITY\_DN112233\_c4\_g3\_i2::g.40094::m.40094 TRINITY\_DN112233\_c4\_g3::TRINITY\_DN112233\_c4\_g3\_i2::g.40094 ORF type:5prime\_partial len:130 (+) TRINITY\_DN112233\_c4\_g3\_i2:2-391(+)* ***(Spz4)***

*RMYGGIKPVMDSHYVSDQDQVKSRYSRQTIDSEDKNSGVNFCPSLKESVTPYWARNNSNYKFAIVNYEPFVQSVNTETCLEVKNCGPINCRCTQDYTWHRMLAYDPEDNCRGIFMEWFKFPSCCVCKCF*

*>TRINITY\_DN106037\_c7\_g1::TRINITY\_DN106037\_c7\_g1\_i1::g.54788::m.54788 TRINITY\_DN106037\_c7\_g1::TRINITY\_DN106037\_c7\_g1\_i1::g.54788 ORF type:internal len:438 (+) TRINITY\_DN106037\_c7\_g1\_i1:3-1313(+)* ***(Spz4)***

*HKAKYCISAGTKCLFQLKIRLSNILVTFKMDIVIYVHMYIGVVFSCLMLAVMSQRNYTAPCDLNFEPYCLTPGPNYPWKSIKAFINGNLGVTKRIFGDPNNEFLIDSYRQRRRGYNPCPSIMESIQPFWFKNIEGKLRALVNYEPFSQYIQVEKCFDTTIGLPNRCDSGCNCYQEHHPVRLLVSDPSSENDGIFMDWFSIPYCCMCKCSKIVYVNITNEQEEIVPIKISHNTLMVPFNTSFNTSIMPSSTLITPSNTLITASNTLMTPFNTSMTSSNILLTPSNTSLVPFNISLVSSTLAPSLESNTFYFTDNYEFSNTTETNVTDNVIRHGENLTKKSDYYNTSVNQRRKNNKINFISLRDDLSSSLFSLPPPPLPYKIFRPRFFCVIALNDSCILIKISDFFFTFYILCSYYNKCTLLIFISNNNNNNNNNNNNN*

**Toll**

*>TRINITY\_DN103845\_c5\_g4::TRINITY\_DN103845\_c5\_g4\_i1::g.97464::m.97464 TRINITY\_DN103845\_c5\_g4::TRINITY\_DN103845\_c5\_g4\_i1::g.97464 ORF type:internal len:309 (+) TRINITY\_DN103845\_c5\_g4\_i1:2-925(+)* ***(Toll2-LRR domain only)***

*TIPHIANLEKLVSLDLSMNQIQEIRNMFYGNLGNLEIVSLQGNLISSLDSSVFRNVPSLRRLNLKDNRITYIPDDAFQGLSSLEVLDVQNNNIKHIERNAFLHLQSLGVLHLTNNSLDVLHPGTFDAMESLRVIKLNENHLRKLQVGSFQNLLTLELLDISQNRINMVDTAAFRNLPMLMTIRLDQNYITSLRSKTFLNLKALTSVNFSQNDIHDIEADTFSDATSIRELFLSDNKIKQLSMKFLEVFKNLQFFILDNNLITNLENLPISVLPSLEILSLANNNIVIFDSKSFVNSEKLIKLNIQGNK*

*>TRINITY\_DN108036\_c1\_g1::TRINITY\_DN108036\_c1\_g1\_i3::g.80428::m.80428 TRINITY\_DN108036\_c1\_g1::TRINITY\_DN108036\_c1\_g1\_i3::g.80428 ORF type:internal len:273 (+) TRINITY\_DN108036\_c1\_g1\_i3:1-816(+)* ***(Toll2-LRR domain only)***

*LKNVQDFLENVKTPIQALRLFRPVIPTLPVNAFKNSVILDVIIEGGGLKTIEAGALESLKTTLRRLILPFNQLTELPDLNGYEALEDIILHNNSVSSVNENYFQNLPALSTLILSSNGIVSVPDGIFKSLKKLGVLSLAGNKLTEVSGKLFEGLDSLQKLFLRDNALAKINPGTFDNQLKLDHLDLAGNSLTEITKSIIPKSEKLVVLDLSNNKINKVEAGAFEDLKALKSLVLAGNDINIIVEDMFTGLENLASLNMSSDKISEIPDGVFK*

*>TRINITY\_DN112799\_c0\_g3::TRINITY\_DN112799\_c0\_g3\_i2::g.86447::m.86447 TRINITY\_DN112799\_c0\_g3::TRINITY\_DN112799\_c0\_g3\_i2::g.86447 ORF type:3prime\_partial len:359 (+) TRINITY\_DN112799\_c0\_g3\_i2:145-1218(+)****(Toll2-LRR domain only)***

*MILLQPFSLVLLIMALNSAYLTKYSCPVTCTCSFDNYNVNCSHLYLKKPFLWAGATQIQSLDYSENQIEDLGILQYYNIIKLNLSFNLIENITKDTFQFLSQLQILDLQRNFLTTIPSDAFQNLTNLKNLNLHGNYLVTVPGHLLRPLTNLQILDLTSNKFPTFLIGNDTGLPNLKNLQLSYNTLGHIDENMLKPFQNTSLDFLNLTNTLITDLEPTAFKYLTNLRTLIADQVDFKMALNICQTVQYLNLNSLHLNNIELSIKQNATYILQNLNSSSLMELEFQNNQITSFNSYTNFSDEFTDNQFKLLPFTPNLRKLNLKGHNLKVLNLDIFELLPDLEVLNLGQNKIQYIHQANNS*

*>TRINITY\_DN112899\_c2\_g5::TRINITY\_DN112899\_c2\_g5\_i5::g.45678::m.45678 TRINITY\_DN112899\_c2\_g5::TRINITY\_DN112899\_c2\_g5\_i5::g.45678 ORF type:internal len:347 (+) TRINITY\_DN112899\_c2\_g5\_i5:3-1040(+)* ***(Toll6-LRR domain only)***

*QLQYLDASYNHIERLGPSAIPHSIQVLKLTHNKITNLEAFTFYLKANLTSVFLTHNQITQILESALRFQAVPIDKSLPEFHLSSNPFFECDCTMVYLKRINRFNNMRWLPKIVDLSNVYCASLWKKPFILLIEKPDSDFLCEYNINCYPLCHCCDFDACDCEMKCPYNCTCYHDLPWQTNIVDCTSRQLNNVPFMLPMDATSAYLDGNVFRNLSSHSFIGRSRLRELYLNNSNIYYIDNSTFNGLIELIVLHLEVNYLTLLNGHEFLHLGTLQELYINDNHLETIANATFKDLNLLRILHLHNNHLITIDTDMLANNVALTQLTLMENPWSCSCEFLQNFWPWVLS*

*>TRINITY\_DN116989\_c0\_g2::TRINITY\_DN116989\_c0\_g2\_i16::g.109362::m.109362 TRINITY\_DN116989\_c0\_g2::TRINITY\_DN116989\_c0\_g2\_i16::g.109362 ORF type:internal len:564 (+) TRINITY\_DN116989\_c0\_g2\_i16:1-1689(+)* ***(Toll6-LRR domain only)***

*ISTLHFVILFISFEFSNANVEGIKPCESLQNGAKWDCSFRQLHNIPTLSNPKVILILDLNNNELKSLNVEDFRPYPNLQKLNISHNLISLVHSETFQQNVFLQTLDLSFNRLLTIPSKLFSKSSNLIELDVGNNPIFDLKGSLFFGLIKLQHLNLENLYFPIHFDNDFKDLKELRTLILKKCILGNVTMATFMPFHNISLERLDISFAVMDSVAPNSLSGLQLKDLDASGLNLNLVKQLVLNLPFLKIQNLSLDEILPNHIDEITSILYSLNSDTLEKLDFSFNYVTNIDQLILRNVTKLKRLSLKGNDLQNINFDNFAYLGNLEALDLSHNYLRNLSKTRKIPAIQHLKTLDLSWNLINKLNIKPQPLNFPLLETLILDKNELNELENNSFVEMPSLKELFISSAFENIHSQISVNTFNHPNLQVIDLSNNRFQELGVWFQNVTNLTVLSLQHNDFGSLLSSGHLVDVFSHLNNLQILNLSDCNIDSIPLQQFHELHSLHTLSLANNLMGNINPAAFSNLTRLKYFYAARNNFSSLASPILEWFDSLSLIDLSDNPFHCDCS*

*>TRINITY\_DN115117\_c3\_g1::TRINITY\_DN115117\_c3\_g1\_i1::g.58368::m.58368 TRINITY\_DN115117\_c3\_g1::TRINITY\_DN115117\_c3\_g1\_i1::g.58368 ORF type:internal len:156 (+) TRINITY\_DN115117\_c3\_g1\_i1:2-466(+)* ***(Toll7-LRR domain only)***

*NQVTKLAGVHFLTSTKIRVLNISDNKITSLEQDFISSLKELAVFSLNNNQIKELPPFFFRSSAELQELLLGKNRFGRVPQALYHINLNKKQPFFTLDLSDNNISRIPDGTFSNFTQMAALYLAGNHLKDITRVFFRKIEKLRVLDLSRNEFKGLR*

*>TRINITY\_DN91630\_c0\_g1::TRINITY\_DN91630\_c0\_g1\_i1::g.1193::m.1193 TRINITY\_DN91630\_c0\_g1::TRINITY\_DN91630\_c0\_g1\_i1::g.1193 ORF type:3prime\_partial len:250 (+) TRINITY\_DN91630\_c0\_g1\_i1:186-932(+)* ***(Toll7-LRR domain only)***

*MVKTAVHEVVVWVWGTILQIYAAKILSPCIPEEMWNYCKCTYTPEMNLDCIGLNAFQMEILLSHITDSVINMHITDGSITKLSSKGFRFLKVINLNLSNNHIMFIPDSAFWGLENSLNDLSLQNNELEQIPDVISKLRNLLKLNLSNNFIKNIQNSIFHALPILQELNLKNNHIVTIEVFSFEGLENLETLILSNNKIALIEKHSFANLHKLQKLELHNNMIQQMDGEYYSNLQSLQYIYLQNNSLKYL*

 *>TRINITY\_DN62901\_c0\_g1::TRINITY\_DN62901\_c0\_g1\_i1::g.2066::m.2066 TRINITY\_DN62901\_c0\_g1::TRINITY\_DN62901\_c0\_g1\_i1::g.2066 ORF type:internal len:275 (+) TRINITY\_DN62901\_c0\_g1\_i1:3-824(+)* ***(Toll8-TIR domain only)***

*LVRDLRGLQCFWNQSEPGQLLINSNSTECPGLSTSLIPYWRPAIIIQNYYILIVSLGASLLLILIISIVLYCHRDVLRIWIYAKCGVRFLDKTEDDSNKQYDAFVSYSSHDENFVVHELVPRMEEGNLSYKLCLHYRDFPLGICIAETIIRSIEASRRTVMVLSESYIKSEWCRLEFKAAHHQVLQDRKKRLIVIIYGDIAQDDLDPDLRLYLRTNTYVKWGDPLFWEKLCYAMPDVKRVDIKRKTRTDHKTYAKPKDQDETFIHEIPKGHNCR*

*>TRINITY\_DN116821\_c1\_g2::TRINITY\_DN116821\_c1\_g2\_i13::g.109719::m.109719 TRINITY\_DN116821\_c1\_g2::TRINITY\_DN116821\_c1\_g2\_i13::g.109719 ORF type:5prime\_partial len:308 (+) TRINITY\_DN116821\_c1\_g2\_i13:1-924(+)* ***(Toll8-LRR domain only)***

*NNIEHIEAKAFQGLETLKTIILKNNNLSYLNASMFLGLDNLTTLNLTNNAINVIEIRSFEAAINLKRLHLSHNQLTELKPRIFSNLTNLTYLDLSYNLISHIHPLVFRDLPNLVYLDFSHNNITQLNGILDPLLLLTDLNLEHNLIVTLKGNEFSNLNQLKKLLLDNNFLESINFEVFYNLKHLSYLNMGKNQLHRLPDNLLMMMINLKYLYLNSNKFETVPNALRFINIMYLDLSNNYLKNLEPSSFQGMNGLQYLNLSYNIITEINDYVFFSMTSLHYLDLSYNLIKFASEETFTFLLNKTRFEL*

**Myd88**

*>TRINITY\_DN100361\_c1\_g1::TRINITY\_DN100361\_c1\_g1\_i5::g.96895::m.96895 TRINITY\_DN100361\_c1\_g1::TRINITY\_DN100361\_c1\_g1\_i5::g.96895 ORF type:3prime\_partial len:298 (+) TRINITY\_DN100361\_c1\_g1\_i5:163-1053(+)*

*MAQTCVDYFTISARALNISTRRLLSLYLNPKSPILTGDWQNLAEYLGFDIMIIRHLDTYKDPINELLDVWIDRKGPKATIGVLITALTSIGRHDILEEIPSYLDKDVANYHKKLEEERHLLEELYPVQDPEISTGYDSEEESLTLEDGRIYDAFVCFAESDLLFVKEMIHILESEKYGLKLCINVRDLLPGRSRDKAITKIIEEKCRRFIVILTPEFLVSRQCNFQAEFAFSLSVDKDRDKSKIIPIILRQCQVPRILRFITACDYTKADVREWFWDRLVAALKAPLPKCLTTPLGD*

**Pelle**

*>TRINITY\_DN115897\_c3\_g2::TRINITY\_DN115897\_c3\_g2\_i11::g.72813::m.72813 TRINITY\_DN115897\_c3\_g2::TRINITY\_DN115897\_c3\_g2\_i11::g.72813 ORF type:complete len:651 (+) TRINITY\_DN115897\_c3\_g2\_i11:251-2203(+)*

*MEVEFIFNIPYPIFQNISNMLDVNHKWRDLGGLMLYDTTTLELFGQAIFAGKSPSEKMLNDWANRNHSVLELFILLSRLQYYRAMQLLKPLVNPRYHHLLERATNPYIAENESSSYGSNDDSDDLPLPDFKPEGCKDFFTVQTTQMTPCEHNETFHLEHCRTDFQELNISPDSSPGAYYDVAMNKKPFDSLRNSIEESTLQIYDFDKNYFTNESEQYLSSSKCDYMSHKVKIDMEERGQSSLKAKQIPNKTAKEEKISLVFPHTSTIPYSEILQATNNFDSTNIIGQGSFGIVYKSNWRHTVVAIKKFITKIEDGKDNNKIKQTLTEIQSLPVYQHDNILPLYGCSIDGLEPCLIYMYMINGSLEDRLACKNNSKPLNWNLRYQIVIGTARAIQFLHTNKPSLIHGDIKSANILLDKSYEPKIGDFGLARVGETDLATHVSTKTAREITPYLPSEYLRNRQLSTKVDIYSLGVVLYEIATSLKAIVNNKQYLTDYIIDQEECDISMLSDTKAGKDIYGLFSSFIEMGKRCTSKLKRDRPDMTEVLQYFEHLPILDNISGNVLSTLTNLNQVENDNPQSDNQLTVDNIYKNDNVQQTKEKDNHQVINWSENTYIINGESQSAFSCINQEDGDSQNIIEIPYMSAKFKSLPF*

**Cactus**

*>TRINITY\_DN109248\_c2\_g3::TRINITY\_DN109248\_c2\_g3\_i6::g.85631::m.85631 TRINITY\_DN109248\_c2\_g3::TRINITY\_DN109248\_c2\_g3\_i6::g.85631 ORF type:complete len:358 (+) TRINITY\_DN109248\_c2\_g3\_i6:185-1258(+)*

*MEANKLPCDVEEDSTAIVEDYRYSKPPNCSKSDRFDSGFHSVGFDIEPVENELSDQFLSRLSIHKENVFQSAERKSPVKALTCITREEPITAANIYQDADEDGDTVFHLTVIQGNPKHVLSICSNCPDRKYLDFVNKLHQTPLHLAVLMKQPLICKYLLDFNATVDLRDRNGQTPLHIACEQGLFDCVRVLTKEQDIHFKSDNYIQDLELMNYEGFTCLHLAVIGGHLDIISYLCNLKANVNAQDGKSGRTALHYAVEAKNEELIRLLVNFNANVNQTTYSGLTPERLAKGRGYDKIHACLRELNAEIEEDDIDEDMSDADSSDYDDITYQGKSLSEVNLSNSQKQNFIRTTYSLDH*

*>TRINITY\_DN97356\_c0\_g1::TRINITY\_DN97356\_c0\_g1\_i1::g.2282::m.2282 TRINITY\_DN97356\_c0\_g1::TRINITY\_DN97356\_c0\_g1\_i1::g.2282 ORF type:internal len:325 (+) TRINITY\_DN97356\_c0\_g1\_i1:1-972(+)*

*PPKKRKLCNFSQNIQEVKNLPIVNSELKKVIVEAQSNIKLEPQPNYKIACVKNGLEHVNISDVKTVTTTTTNCASSSDKVSDLNSLPTMPPMGQLGYSAWQLYNMALIPDEDGDFPLHIATAQDNVQAVQRLIRTMEHMHSNVDVFNKLRQTPLHLAMIIGCPESAKYLLNSGASALAVTRQGDTAIHLAVMYGHLDCLKILIENYKGRLDLNLRNHEGLTPLHLAVLKREKLILDCLCENGADINALDGKSGRTPLFHAVENNEIEIVELLIHHKADVNITNYSGNDPLSTASGKGFSKMVKLLIANNADSIPDTSEITKQTN*

**Dorsal**

*>TRINITY\_DN107889\_c1\_g1::TRINITY\_DN107889\_c1\_g1\_i7::g.43688::m.43688 TRINITY\_DN107889\_c1\_g1::TRINITY\_DN107889\_c1\_g1\_i7::g.43688 ORF type:internal len:399 (+) TRINITY\_DN107889\_c1\_g1\_i7:2-1195(+)*

*LNMASNSEDDTNLQEFLDFNSPALAVNNSSPYIKIIEQPRSRGLRFRYECEGPRAGSLLGAQSTSETRTCPRIQIMNYNGPALVLVSCVTKEKPHRPHPHSLVGKDCKDGICKIPIDERNCENMVVKFPQLGIQCAKKKDIVEALSLRKSLGVDPFQVGFQYESGSLDLTVVCLCFQVLILNSDRSMYISVGTPVVSEPIFDKKALSELVICRIDKHAAPCCGGQEMFLLCDKITKDDIEIRFFEETGDGQLTWEGFGDFSPSDVHKQVAIVFKIPQYKTLTINGPVSVMVQLRRPSDKETSDPKPFQYLPLDPDPDGIERKRKKGLNTSMLNYIEDLGFKRSSSPSQSSTLPTINVFQNRTIRQPLHKIKAETATPDNCTLSSASKSFSSPISNIFS*

**Imd Pathway**

**Tak1**

*>TRINITY\_DN109069\_c0\_g1::TRINITY\_DN109069\_c0\_g1\_i5::g.74622::m.74622 TRINITY\_DN109069\_c0\_g1::TRINITY\_DN109069\_c0\_g1\_i5::g.74622 ORF type:3prime\_partial len:467 (+) TRINITY\_DN109069\_c0\_g1\_i5:116-1513(+)*

*MEDEEKNKGNFEESIDPPQSFVEEIDYKEIKLLEVVGRGAFGVVSKASWRGKVVAVKLIESELERKAFVVEVRQLSRVSHQNIVKLYGACTKQPEVCLVMEYAEGGSLYNVLHGSGSQPIYTAAHAISWALQCSRGVSYLHGMKPKALIHRDLKPPNLLLIMGGTMLKICDFGTACDIQTHMTNNKGSAAWMAPEVFEGSNYSEKCDVFSWGIILWEIITRRKPFDEIGGPAFRIMWAVHNGTRPPLIKVCPKPLEILMTRCWAKDPLQRPSMEEVVRIMTHLFQFFKGSDEPIIYPSDSEPGVDLNSTLQGDLTSTSESPVQSPSQTVNSGIIDTILSKGQPVPLTPSTATVRPVVVEDERVPYANLPEERRTSAPASLASSQENLVNPRSSNPAKDSFLKRRSADLTQLTDFEIRTAPKSLAGQGHRRSGSFGAISISGGSNSSSRTSSPGIPNVPGNTTSHIR*

**Ird5**

*>TRINITY\_DN118429\_c6\_g3::TRINITY\_DN118429\_c6\_g3\_i6::g.98922::m.98922 TRINITY\_DN118429\_c6\_g3::TRINITY\_DN118429\_c6\_g3\_i6::g.98922 ORF type:complete len:782 (+) TRINITY\_DN118429\_c6\_g3\_i6:114-2459(+)*

*MLSDKEEVGEWKKERILGSGGFGVVTQWLNQETHGTIAIKQCRLGKVGSEILMSSKLRRRWEVEVDIMKRLNHPNVVSSRDVPQVMDVGIDDMPLMAMEYCTRGDLRKVLNRPENCCGLLESEVLTMTKDIASAVEYLHSMRIIHRDLKPENIVLQEIDNKIVYKLIDLGYAKELDQNSLCTSFVGTLHYLAPELFGGQTYTCTVDYWSFGLIVFECITGIRPFLPNESPYHWQLEVRNKGPEDICAFYDPDSEGRIAFSKNLFQPNHINPILQDRFEKFLQLMFRWEPRQRGGVLDHNRRPLCFKMLDDIHRLMIVKIYSADTNEIFHIEVNERMSMNTLKEEISLRTKIPVKDLELLLPRGMPPDPNKPACQCCDLDPVHYDWLLFVFRRGKSFSTGINTLPLPRHVQYILQEPQALVQYEEKKKMWSHAVYYCRAQLEDYKYLILAKNVALMNLLYCNSALHKKKTLLRDELNKLVAESKFFTASLQVNFDLYEKQVETGFSSEKMINRWKTRLLSNKKVTDQIKIVDDLQRLGNTVNTKTLELQKSPNTKSHQPNSLEQIETDVLEEYDKLRKLSKDKQSFFTNNEIMVKFVAKIIIERKRCALVLITNLERLLNCKEEILDLNPKLDTALVDVKALSQKLLVDHQETLTDVWNLIRLLNKCNQVDSRPLSTAISPEGFHVEAPCILPQPVTPLTTIDSLDTSPLAKSSPSMVASQSYVSLSQILEKCSEESLILMANNSETCKRLQSSFVDFSLKQEQALAQTSNIDWSFLKDTNS*

**JNK Pathway**

**Hemipterous**

*>TRINITY\_DN108589\_c1\_g2::TRINITY\_DN108589\_c1\_g2\_i1::g.66586::m.66586 TRINITY\_DN108589\_c1\_g2::TRINITY\_DN108589\_c1\_g2\_i1::g.66586 ORF type:internal len:272 (+) TRINITY\_DN108589\_c1\_g2\_i1:2-814(+)*

*FPCRPITSTRVRRQFELPTSPLHRPLDNADIDHKLKEIMKQTGILTFEGQKYQADIGDLEHHGELGNGTCGHVVKMKYKRTGHVIAVKQMRRSGNREENKRIIMDLDVVLKSHDCPFIVQCLGCFITDSDVWICMELMATCLDKLMKKLRAPIPEYILGKMAVAILKALNYLKEKHGVIHRDVKPSNILLDEKGIVKLCDFGISGRLVDSKAKTRSAGCAAYMAPERIDPPDPLRPDYDIRADVWSLGISLVELASGEFPYRDCKTDFEVL*

**Jnk**

*>TRINITY\_DN107033\_c0\_g3::TRINITY\_DN107033\_c0\_g3\_i5::g.57720::m.57720 TRINITY\_DN107033\_c0\_g3::TRINITY\_DN107033\_c0\_g3\_i5::g.57720 ORF type:3prime\_partial len:266 (+) TRINITY\_DN107033\_c0\_g3\_i5:299-1093(+) (fragmented at the C-terminal)*

*MCGCSQLLEAEAHRTHPRWAETQYGTLDSPPLGNTMSKQGNSGNMFYTVEVGDTKFTILKRYQNLKPIGSGAQGIVCAAYDSVTTQNVAIKKLSRPFQNVTHAKRAYREFKLMKLVNHKNIIGLLNAFTPQKSLEDFQDVYLVMELMDANLCQVIQMDLDHERMSYLLYQMLCGIKHLHSAGIIHRDLKPSNIVVKSDCTLKILDFGLARTAGTTFMMTPYVVTRYYRAPEVILGMGYRENVDIWSVGCIMGEMIRGGVLFPGTD*

**Jra**

*>TRINITY\_DN103466\_c12\_g1::TRINITY\_DN103466\_c12\_g1\_i1::g.53396::m.53396 TRINITY\_DN103466\_c12\_g1::TRINITY\_DN103466\_c12\_g1\_i1::g.53396 ORF type:complete len:269 (+) TRINITY\_DN103466\_c12\_g1\_i1:231-1037(+)*

*METTFYDDHHHHHHQSFTKENMNMLKKRMTLDLQSDRPAKKTKFSILNSPDLSMLKLASPELEKLIRSSNGMVTTTPTPTQFIFPRDVTEEQEMYARGFVDALAELHKANVPESPEIPIVYVSTGCNVTSTSTSTTMHGNNANLVTLHHPGVNSNTVTSTLSPLPTFIKDEPQTVPNLGATPPLSPIDMETQEKIKLERKRQRNRIAASKCRRRKLERIARLEDKVKQLKGENSDLANIASKLREQICQLKQQVMEHVNSGCQIMTQY*

**TIR-1 Pathway**

**TIR-1**

*>TRINITY\_DN114873\_c2\_g1::TRINITY\_DN114873\_c2\_g1\_i2::g.52753::m.52753 TRINITY\_DN114873\_c2\_g1::TRINITY\_DN114873\_c2\_g1\_i2::g.52753 ORF type:complete len:553 (+) TRINITY\_DN114873\_c2\_g1\_i2:108-1766(+) (with HEAT EZ domain at the N-terminal)*

*MFKVSEQESLFKHCEDTCSRVIELGGLNAVLHSCRSNDVETLRHCAMALANLALYGGSECQQKMIKARVPEWLFPLAFSKDDSVKYYACLAISSLVSNKEIEAAVLKSGTLELVEPFVTCHSPSDFAKSDASHLHGRSKGWLERLIPVLRSNREEARSLAAFHFAMEVDIKSKQDSTELLSGDSVSPFQVFYEIGAVEALKQVASCPNDVASRFAIQALKIIGEKIPQKLSQQVPVWDVQDVEYWIKQVGFPQYSEKFGACQVDGDLLLQLTDEMLRVDLHMTNGIVRKRFLRELNNLKMTADYSSCDPSKLDTFLLSAGDELSQYTYTMLQAGVDREMLRMLTDEQLKEDCCVGNGIHRMKILKNIKENINNQSKVDAMDAFISYRRASGSQLASLLKVHLQLRGFRVFLDVERLEAGKFDNNLLNNIRAAKHFVLVLTPSSLDRCIDDTNLRDWVHKEIVAALESNSNIVPVIDNFCYPDPETLPEDMRAICYFNGVRWIHDYQDACVDKLERFLRGEENNVMKAALMNAHNLTSQISNSLVKKIGSPDT*

**NSY-1**

*>TRINITY\_DN68922\_c0\_g1::TRINITY\_DN68922\_c0\_g1\_i1::g.1899::m.1899 TRINITY\_DN68922\_c0\_g1::TRINITY\_DN68922\_c0\_g1\_i1::g.1899 ORF type:5prime\_partial len:157 (+) TRINITY\_DN68922\_c0\_g1\_i1:1-471(+) (PKC domain only fragmented at N-terminal)*

*LLRSKWGPLKDNEATIAFYTRQILDGLKYLHDQKIVHRDIKGDNVLVNTYSGVLKISDFGTSKRLAGLNPCTETFTGTLQYMAPEVIDKGQRGYGAAADIWSLGCTIVEMATGHPPFNELGSPQAAMFILQKFKFVIFITVLEFEIIKCRILLLVT*

**SEK-1**

*>TRINITY\_DN106815\_c11\_g1::TRINITY\_DN106815\_c11\_g1\_i10::g.59365::m.59365 TRINITY\_DN106815\_c11\_g1::TRINITY\_DN106815\_c11\_g1\_i10::g.59365 ORF type:5prime\_partial len:334 (+) TRINITY\_DN106815\_c11\_g1\_i10:1-1002(+)*

*KRRKPNLSKLPLPKDTTPSLPTINLDSEAEFSIGENKFMVRADDLQVIELLGRGAYGVVEKMRHLNTGAVMAVKRITATVNTQEQKRLQMDLDILMRARFCPYLVQFYGALFREGDVWMCMEVMDTSLDKFYKKVYEISRIPECILGKITVAVVKALHYLQSQLKVIHRDVKPSNILINRQGEVKMCDFGISGYLVDSVAKTREAGCKPYMAPERIDPNGDISHYDIRSDVWSLGITLIELATGKFPYSSWGTPFEQLKQVVLEDAPRLPPNEFSQEFEEFISQCLAKMYKQRPKYEQLLSHRFIVLNDSMDTNTAEYVCQILDASNQGNTTA*

**PMK-1**

*>TRINITY\_DN110277\_c4\_g1::TRINITY\_DN110277\_c4\_g1\_i3::g.58745::m.58745 TRINITY\_DN110277\_c4\_g1::TRINITY\_DN110277\_c4\_g1\_i3::g.58745 ORF type:5prime\_partial len:168 (+) TRINITY\_DN110277\_c4\_g1\_i3:1-504(+) (fragmented at n-terminal)*

*SVGCIMAELIQSKTLFPGTDHIDQLTRIMALVGTPDDELLAKITSEEARNYIRSLPNMKKKDFKIYFQGASQLAINLLEMMLELDPDRRITAEDALAHDYLRQYADPTDEPISDPYDQTFEDMELSVPEWKSLVHKEVVMFQRNLKQLNAGLSYTRSLSWCKKIEFK*

*>TRINITY\_DN110277\_c4\_g2::TRINITY\_DN110277\_c4\_g2\_i3::g.58749::m.58749 TRINITY\_DN110277\_c4\_g2::TRINITY\_DN110277\_c4\_g2\_i3::g.58749 ORF type:complete len:107 (+) TRINITY\_DN110277\_c4\_g2\_i3:231-551(+) (fragmented at C-terminal)*

*MGDEIRTGFYRVELNKTIWEVHQRYQMLSPVGSGAYGQVCSALDTLIQTKVAIKKLARPFQSAIHAKRTYRELRMLKHMNHENVIGLLDVFTPSLTLDDFQDVYVF*

***Paragordius varius***

**Toll Pathway**

**Toll**

*>TRINITY\_DN28158\_c0\_g1::TRINITY\_DN28158\_c0\_g1\_i1::g.21148::m.21148 TRINITY\_DN28158\_c0\_g1::TRINITY\_DN28158\_c0\_g1\_i1::g.21148 ORF type:internal len:344 (+) TRINITY\_DN28158\_c0\_g1\_i1:3-1031(+)* ***(Toll2-LRR only)***

*LVLGANSISRLPANCFLDMSSLRTLNLENNKIVDIHDDAFKGLNNSLTYLHLPGNLLSAIPKTALQGLKNLWVLNLGENVIRDVSVDDFSDSNLKNALGTLYLNGNLLVKIPGKALSGFQTLWLLDLGDNEVVSIKNVSFPQLPALEVINLEGNNIKKIELSAFAGLEKSVKKIKLGRNALTSLAVDPFVGLENLRSIDLEGNKIIGIGAEDTEALKKLRGQVRTLALSGNKIEYITPNSFTDLEPYLTAIDLSENKLKTLKTSTFVNSGSVSDINLSKNQLENIEKDTFVEMMNMKTLNVSYNQLQELHPHMFKGLQRLISLDLSYNMIASLPSLAFKFISD*

*>TRINITY\_DN33761\_c0\_g1::TRINITY\_DN33761\_c0\_g1\_i3::g.41738::m.41738 TRINITY\_DN33761\_c0\_g1::TRINITY\_DN33761\_c0\_g1\_i3::g.41738 ORF type:complete len:724 (-) TRINITY\_DN33761\_c0\_g1\_i3:403-2574(-)* ***(Toll2-LRR only)***

*MAQLSSTINGPTVSFNLLWVILIILPVMGHHEPTCPPNTSPLAEQNSKYCTCVSTHETGMEVTCSNKKSNELGEALSVYNKAPGVDLPITTLILQLNFIPTIENDTFASLQSVTDLQFKLNRIKNFSANAFRGLENSLEKLTILEFFWVSFKYKTLDQVPTSALAPLKNLKELFLSSANIRSIPPNAFESLRNLEVLKIMSFTLNKIYNDSLNGLLNLKDFSLVSNFMKDLPPMLFFPTPNLEILFFSLKSFKHIPKDLFSKLRYVREISFNNSGIDTIEDGAFDTMSNSLKFLSFKGNQLTLLPKSLENLPKLTTLDLSSNTLFEIQANSLAGLSSLEYFSLAFNIVKNIKSNVLAQSTYLKHLDLRANLLVKIPENFFSTFRNLEMLDLSKNFIAEVPDLTFYLNDKLSKLDLSNNNLKTLSATSFKSLGKSMTYLDLSHNYLPQLPAKTFSEFQNLVYLNMSHNNMTSLDIDSLQGSEDTLRFIGISDNPWHCDCKMRRFREWYKYWSTQLSHSDKYLQEKNLENAKCHTPHNLAGVPILYPPLNAFTYCAFSDYPNNTNGATYHVKGTDDAFVNDDNDVLLDKSDNWNRVENMERNPVARAAIGDSYSNPKHMEKLMRKTNAALVIAIMLSAFLCSYLIAKFLFSGTNKMVDKTGSNNSNAPDINNNNVPHTLSNGGSATRFGKFLTSFPTPLYNGQSGNVPEDRQIITNHSYPMGTVS*

*>TRINITY\_DN35121\_c0\_g1::TRINITY\_DN35121\_c0\_g1\_i1::g.55589::m.55589 TRINITY\_DN35121\_c0\_g1::TRINITY\_DN35121\_c0\_g1\_i1::g.55589 ORF type:5prime\_partial len:863 (+) TRINITY\_DN35121\_c0\_g1\_i1:3-2591(+)* ***(Toll8-complete)***

*NFNMSFNLVEKIIGPQQAFRLDGGEGMLTLDLARNLITRLNASVNLLPPTLISLNLSSNLIEGVDEDVLINLRSLEFLALDFNRLKHLTPRLFLRQDGQGNATLIMRLAENLLECDCHFTWLPKLLSRSRDNLVIVADRDKLMCHHRYYDTMIPIVEAHSNPISTYPNGIGKWLCPYSEQCFSLCPCCDFFYCDCKMICPTGCNCYRDASWTVNVVRCDSKHFLKVPENVPRYATLLRLDGNNLTTINRTVFFAFFELEYLYLNATGLVGPLGPRSLGKLPRLAVLNLSSNSITDLPTDLFYGTGALEYLDLSYNSLSYLNSQTFQGLRSLKFLDLSNNYLRRIDASLIEFVYILSRPNDLDINNVSTDNRFDMNLADNPLDCTRCDMIEFLATNFSSHMVRKRTTCLSNGAYIENAVVSDSDKTLTLNQALKRCNNVATEITTFTTESIGVSNNNNATSTYYESTAISSTLPTWWDRFLTLTETSSHVINGTISNLNTVLISRSTSILKTTPIIVPALDLDSEFEINNTHNLMPIPLKHSKYWELAGIILAIILCIVSIWILCLRCVLGTMTCTHNRRKKTKINISQKSHLFLYQCCPNNRRNSGSPTSYAASKLKNHPKSSTLFRSFKTSVCSMVPHKNTTKHFLYDIFVSYGQNEQSFVQQTLGPQLRKNRLKLCLQYPQEIYVTEAIRQSIEKSRKFLFLLPNKVYLGIGLSRNGSVLQQESLKNIIGIYNDLFINSLDGASCATPRYPDAKKVILIVVPDGGVTSQGSMKSNLSAVDILVPLMGHANQKWTFNSTRSEQDIMQKSTTSTMSQESEAVKHLLNHPIVYWTDDLFWEKLLFLIGTPLLSRKSKQPITEL*

**Imd Pathway**

**Tak1**

*>TRINITY\_DN33218\_c0\_g1::TRINITY\_DN33218\_c0\_g1\_i1::g.56696::m.56696 TRINITY\_DN33218\_c0\_g1::TRINITY\_DN33218\_c0\_g1\_i1::g.56696 ORF type:5prime\_partial len:573 (+) TRINITY\_DN33218\_c0\_g1\_i1:3-1721(+)*

*NMVLISSPVHDVMDNIAPFVEQIEISELNIFEVVGHGTYGTVHKALWKGRVVAVKMFEDKMEKTSFISEINQLSRVNHPNIIKLYGANTKSQVYLVMEYAENGSLYNVLHNKKCRPAYTAAHAMSWALQCARGVAYLHNMKPKPIIHRDLKPLNLLLIKGGTMLKICDFGTACDFHTQMTNNRGSAAWMAPEVFEGCNYSEKCDVFSWGIILWEVITRKKPFEELGGPTFRVMWAVHNGTRPPLINQCPKPIEILMIRCWDKDPGQRPSMTEVDYVMTHIFQFFKGADTPLDFNQSAGLSDAEGDKSADDTFSSYASTTSPSTSELSSLSTQNKSSNSLLNAKDTPNNSKEERSINSTFGTPKESNQNYQRPSNLDVPTMEKLSSSPLSQSPNLTPDPWLGDQQQIWDYKLDQSHRNGHRNRGYSFDSLSVKKICHRRNRSANFTNDFAPSHQILNFQKVRDMYSFEDDFNPPSIKTEHINEEGEQCPDTIEYEIHQQICAVERYIRETDVKILELQVKQENYSKVDQPDVWKDLERDYMVEELNALIIERGRLQKYYEALVRNLNRVRHLD*

*>TRINITY\_DN33450\_c0\_g1::TRINITY\_DN33450\_c0\_g1\_i5::g.19745::m.19745 TRINITY\_DN33450\_c0\_g1::TRINITY\_DN33450\_c0\_g1\_i5::g.19745 ORF type:internal len:325 (-) TRINITY\_DN33450\_c0\_g1\_i5:2-973(-)*

*WEVITRKKPFEELGGPTFRVMWAVHNGTRPPLINQCPKPIEILMIRCWDKDPGQRPSMTEVDYVMTHIFQFFKGADTPLDFNQSAGLSDAEGDKSADDTFSSYASTTSPSTSELSSLSTQNKSSNSLLNAKDTPNNSKEERSINSTFGTPKESNQNYQRPSNLDVPTMEKLSSSPLSQSPNLTPDPWLGDQQQIWDYKLDQSHRNGHRNRGYSFDSLSIKKVGQRRNRSANFTNDFNPLPPNPSLPNFQKVRDMYSFEDDFNPPTIKTEHINEGGAQCPDTIEFELHQQICAVERYIRETDVKILELQAKQENYTKVDQPDIWK*

**Relish**

*>TRINITY\_DN36908\_c1\_g1::TRINITY\_DN36908\_c1\_g1\_i1::g.18815::m.18815 TRINITY\_DN36908\_c1\_g1::TRINITY\_DN36908\_c1\_g1\_i1::g.18815 ORF type:3prime\_partial len:833 (-) TRINITY\_DN36908\_c1\_g1\_i1:1-2496(-)*

*MRHGSGYPQPFIRILEQPLERGFRFRYKSEAGAHGGLPAESSQRNSKKYPTIKIENYIGPARIEVTLMTNEPEPRLHVHKLVGKNCEDGVCHVRVNPENDMIVSFQNLGVLHVPKKEVAQIMHERLEEEYRIQRMMNNDSDSDNYEFTEVEKQMLRHNAEESAKSMELNVVRLCFQAYIIDAGGNEIPIPPVLSNPVYDSKSPNTAALKICRMDKQAGFCVGNEEIFLLCERVQKDDVSVRFFELDESGKEVWHDYGKFSIHDVHKQYAIVFRTPAFRFQNITKPAKVFIQLQKKKDGLTSEPKPFTFKPLPCYEEIGRKRQKSILNLADVEILNDALNMIHKSSSDSNIPTNSPSGLANSQHPKERCNNIVGKNNHPQVSQVLEERSMPHHRHEKVYPESMAYEKTFVIGELFPQNRVSKLYPVTRENEGVPQQEHHKQSLQYGSSKERSNPNNININYHHYQQQHFYHPSFITGPLAPPNYETQAHHPPPSHSHEHSKDSTIHEHPKFYNSRGRSAGNVNANDMHVRERMHTKNFSENDVQSSVPCNGVEHDELEYVKTKSREISNERALKESQITANNYKMSQGEVYSSGGVSSGGDNDSSIRCNSYISDGSSPQSTPPSFVRYNNPAGTGLVEGQRKCSQDDDSNNPASMINGYDDVYNHRGVPTKEDYHTSPTSYNYNVGAQHFNVTMSPNTLPYYVSNGRNEIWSRDYDQYEHTESEEVCAEAPRMLQMSQIDRDKHLYQHQPTGNMENSIRHTVHPYNLNQYDQAMEESNKRSQDLIPMLIARGHELKKPSETSLEVKTVGKVYPMLKMTGDKANSTLENIGEEF*

**JNK Pathway**

**Jnk**

*>TRINITY\_DN31909\_c0\_g1::TRINITY\_DN31909\_c0\_g1\_i1::g.7616::m.7616 TRINITY\_DN31909\_c0\_g1::TRINITY\_DN31909\_c0\_g1\_i1::g.7616 ORF type:complete len:559 (-) TRINITY\_DN31909\_c0\_g1\_i1:302-1978(-)*

*MQKNSKRPDDDKFYMLDIGDTTFTILKRYQNLKPIGSGAQGMVCAAYDNYDDRNVAIKKLSRPFQNVTHAKRAYREFVLLKLVNHKNIISLLNAFTPQNTLEDFQDVYLVTELMDANLCQVIQMDLDHERMSYLLYQMLCGIKHLHSAGIIHRDLKPSNIVVKSDCTLKILDFGLARTAGTSFLMTPYVVTRYYRAPEVILGMGYKENVDIWSIGCIMGEMIRGSVLFPGTDHIDQWSKIIEQLGTPSSDFMKKLQPTVRNYVENRPKCPGYPFDKLFPDVLFPPDSTEHSKLKASYARDLLVKMLVINPNQRITTDEAIRHPYVNVWFDDLEVNAPSPGIYDYSVDETEHTVDQWKELIFKEVVEYQRTYDARNCSNFQALSLNPVPANTTTATNNHHSSSSQKRSTSKKDNGTTANGDSCVGPKESSNHHHHRSSSNNNTNSNSNTTTTTTTNTTCSQQQPMDDSGYPPSSGGYYRGSCSRCEHRRYCRSYCSSGDHEGCKSGGCGKGGNGCGVAAKQSLSSSSTDSNFINGDAEMLSDCCDPSDSSCTCNLMNKH*

**Jra**

*>TRINITY\_DN32015\_c0\_g1::TRINITY\_DN32015\_c0\_g1\_i1::g.9552::m.9552 TRINITY\_DN32015\_c0\_g1::TRINITY\_DN32015\_c0\_g1\_i1::g.9552 ORF type:complete len:535 (+) TRINITY\_DN32015\_c0\_g1\_i1:91-1695(+)*

*MENYKQIYNNKMDYSSNQTSMMNYQLLKERRDKLKLDLTNISEKKLKFQSILTSPDLKMLKLASPELEKLILSQPSLFTPTPTQYFFPNKPATEEQELYARGFLDALTNIKQKYQTTFALNNANSNYVSFINNRTNNSNKVPSEFSTIYFPSAFITTSHSNETHINQNNETKYPESSKINGQNENFYKYANNNDIFSRIFFNNYNLPGPRNVHQDINVSTHRQIPSIPYYNWAQEQMTINQHAPQCVSVESCPQSSVCACNSINTEIATSVDILPPLHTIKSETSEPKVSDNANSQFLSSEKPVIKSHPGSACMGSPYVNDVQGTSYIPHNSDVESFNLSRQSASPYVSSMHGSDSLKRVSDSMDLDESTIATRTRRSKCQKRASDSHTRSSLDPVNCVRGARSSNVSTCSSRRSIISTDDYDENNFGEDDHAGEVEYEVDAFNATALSPINLEAQEKIKIERKRLRNRIAATKCRQRKLEKIYELEKCVAELKQINDGTQTRLQEVRARVTLLKATLKKHVETGCNIPSEYVD*

**Fos**

*>TRINITY\_DN119896\_c8\_g1::TRINITY\_DN119896\_c8\_g1\_i1::g.37979::m.37979 TRINITY\_DN119896\_c8\_g1::TRINITY\_DN119896\_c8\_g1\_i1::g.37979 ORF type:complete len:413 (+) TRINITY\_DN119896\_c8\_g1\_i1:203-1441(+)*

*MEDWRNWQNPSGYNRSEYYHGEPFYKIRKCWQQPKGLSNHRPYTSTKETQGYNPTGTNFGSMYNQRPNNVTQSHADSRLTVADILSSMANGDAVTPNTYAALQFSSGIPTATTPTLTPTTLTNIEQTFIELQSVPHHHHHVQNQAGFVPPLVRMNSNNSDISHDSYQSSDKSDENENEWVSVSSARRHSNSNFRHSSIMSTTTATGISSTTTTKSGRNTGGRKPIKDDKLTPEEEERRRVRRERNKLAAARCRKRRLDHTNCLILETEGLEEKKAALQNEIQMLQNEKEELEFILLAHKNMCKKVTNGSNPSNNHVLTSVSRPTSLSVSSVHTSISNHHSSKISVTVTDATGIPITTPSRIFSFESLVDGSSGLTPTGLTPVIPSCSSEVHRSSGSEHSSPENLTSPTLVSL*

**TIR-1 Pathway**

**SEK-1**

*>TRINITY\_DN36223\_c2\_g3::TRINITY\_DN36223\_c2\_g3\_i1::g.47671::m.47671 TRINITY\_DN36223\_c2\_g3::TRINITY\_DN36223\_c2\_g3\_i1::g.47671 ORF type:internal len:255 (-) TRINITY\_DN36223\_c2\_g3\_i1:3-764(-)*

*LRINAKSQCPYVVEFYGAMLSEGDVWICMEVMDCSLDELYKTSRNLSQNLSEIEAKEPALPEYVIRKITLCVILALRYLREELNVIHRDVKPSNVLLSREPTASGGGVKICDFGISGTLINSLAKTIDVGCQPYMAPERIDPQLIKSQAGYGYKSDVWSLGITLVEIVTGKFPYPTWKTPFDQLKSVLEDNPPSIPTTINVSDDLKNFVATCLTKDYAKRPGYPELLAHPFLQGYQPEDLDISDYLDKMLQHFP*

*>TRINITY\_DN36223\_c2\_g1::TRINITY\_DN36223\_c2\_g1\_i1::g.47667::m.47667 TRINITY\_DN36223\_c2\_g1::TRINITY\_DN36223\_c2\_g1\_i1::g.47667 ORF type:3prime\_partial len:233 (-) TRINITY\_DN36223\_c2\_g1\_i1:3-698(-) (fragmented at the C-terminal)*

*MVSEDMINDHKRPQNIKQPAAQTKEQLFLSDQDIIPNTGSVINLSVAEPKRPRGIKRPHLALSFSPQKNQILKSNEFNNGAITFHSSNNVPTNLEAEMHLNLPKETYFQNIKHSGQESFIDGSFDSCQNSNASIDLNIKAKDLIFVKTLGRGAYGVVEELRDSKSGFTLAVKRLALTSTGSTNMPTALNAERKRLLMDLRINAKSQCPYVVEFYGAMLSEGDVWICMEVMDC*

*>TRINITY\_DN36071\_c0\_g2::TRINITY\_DN36071\_c0\_g2\_i4::g.27953::m.27953 TRINITY\_DN36071\_c0\_g2::TRINITY\_DN36071\_c0\_g2\_i4::g.27953 ORF type:internal len:173 (+) TRINITY\_DN36071\_c0\_g2\_i4:1-516(+) (fragmented at the C-terminal)*

*RLSFSPQKNQILKCNEFNNGAITFHSSNNVPTNLEAEMHLNLPKETYYQNIKHFGQESFMDGSFDSCRNSDASIDLNIKAKDLIFVKTLGRGAYGVVEELRDSKSGFTLAVKRLALTSTGFTNMPTALNAERKRLLMDLRINAKSRCPYVVEFYGAMLSEGDVWICMEVMDC*

**PMK-1**

*>TRINITY\_DN30213\_c0\_g1::TRINITY\_DN30213\_c0\_g1\_i5::g.52257::m.52257 TRINITY\_DN30213\_c0\_g1::TRINITY\_DN30213\_c0\_g1\_i5::g.52257 ORF type:complete len:358 (-) TRINITY\_DN30213\_c0\_g1\_i5:60-1133(-)*

*MIYMNKFEIQKTTWYTRDNYSNLSLIGCGSFGQVCSAHDSKYDRNVAIKKLSRPFLNSYHAKRGYCEIWLLKHMNHENLINLLDLYSPDDTAESLNDIYLVTPYMGSDLCNLIKMQSLSAEHVQFLTYQIMRGLKYIHSAGILHRDLKPSNIVVNENCELKILDFGLARSYDEVEMTGYVATRWYRAPELLLNFTKYTASVDIWSVGCIMAEMLTRKVLCPGNGPLDQLMKIIEACGPPSQAFIDKVESPEAKKYLTSLHNINQMGDLSVIIEPFDANTLDLLKKMLIWDPDFRISAVDALAHPYFDYLADPEDEPACDKDLGAAINKVINDPSISLGEWKAMIFQEIANFSEPRPV*

***Priapulus caudatus***

**Toll Pathway**

**Toll**

*>XP\_014664437.1 PREDICTED: insulin-like growth factor-binding protein complex acid labile subunit [Priapulus caudatus]* ***(Toll2-LRR only)***

*MLRMMMMTIMMITRGNRTGERNSTWMEKFRTLAMEETIGLLLLLMLAIPATSSDCSRVGGALSPCECRRFRTGAVSISCRNVDAAAILPRIKAVNVSIGQLSLSASKMATIPRQAFGGLNLSKLILRDGGVERVDQLAFAGLEDSLIFLDLGDNQLRAVPRAAIRPLWMLTVLNLHDNRIEQVRKDDLAGLTELTQLRLYNNNISRIHADAFVGMRRLDFLSMYNNRLPTIRAGWFRDMANIRDVRLYGNSIGRVPDDAFRQLSSLTTLYLYANEIASVTSRSFGGLTSLTDLRLWQNNITQLPADAFDELVNLRYLDVHLNRLESIPAGIFKNQRKLNYLTLSDNNISLIEPGAFRGLDSIEFLYLFQNRLGALHADTFADVPSLVYLHLGDNAALQLRAGMFAGLRSLQHLFLTECELTHVPNGTFGGLRQLRNLHLQTNRIAAMPAGLFADTPSLVNLYLKENAIVEIASGAFVGLTTLKRLELQRNRLTRIAPDALRHLAATLEYLVASVNRLSEDAFHAVRRLARLQFLDLSYNDNIRLLPGWALSELAALQWLKLDSTDLAAVCWGGLSGPTRLLEVTLNNNLLRHVSAHALPADVDEMPQSLELDGNPLVCDCRMDWVPAAAVATNIYGKCAEPTSVSGRQLSELQLADLNCTWDYIPLHPDCDVGDVAAPTNDFAVDVGAVTDSGVSLNWNVSDDVDDVSTFQVTYTVANDSEELQVALLTNETARTYNFTNLTPQTTYYICVVMTTTTGKQRYDCLTLETRPTPTTTTTTTTTTTTTTTTTTTTTPPPPPTPKPLPKTTTAPPPTTRKPSIITRHNTAILTVFGIFFSILFVCLIVYAIYSMAENKKARELKETERLAMAQYEAMNQEVVVTV*

*>XP\_014665738.1 PREDICTED: uncharacterized protein LOC106807798 [Priapulus caudatus]* ***(Toll8-complete)***

*MSSPQSTSTKPSYLLALCIGYAWLLSGLAVSETDETGFICPTECDCWYVGDGPPGRRLICSFLTIGPNTNFTAIPAAHTLVLEIYCSSPFLFSEVDEDALRHLVELDELHIIGCKLKEIPAGFLDGLLQLRLLRIISTHLETKVAPGAFRGVPNLLSLNLTASGLSSLPRGELCALPRLLQLLLGGNNLDSWEGTGALENGTVCLPQLAYLNLERNLLASLPDSVLGSSLLHLFMRGNRIRDVRDAALDGLASLQLLDLGENEIRTISDGAFSDAAQLRVLLLDRNQLATLPAGFYELPMVAGVNVSGNSLDDEFLARMQANGIENLDASYNELTMVTRASFNGSSSLQFLSLQGNRIENIEDFAFTEQTNLQVLFLSSNLLGNLTVDVFRGLGKIRHLFLDNNTIGDIQPNAFASMKEIINVNVSRNDLRHLGFASDMVSLIQLDVSHNQITEVSQTDLFQLTNMTYLLMSYCQMKEVEPGAFDKMDLLEKLDLSYNRLTNIRSLFRYATSLQTLMLQNNRINTTLGPSTFPGSIQTIDLESNEISDISPYTFSRKPSLKTVNFRQNRLTTLRSEAIKVSVPSADAQRPAFSIGINDYFCSCDMAYLLTVNAKGSVGHASIRDLNRVYCRTYYNPTPTNWLVDVDKKDFLCPYEEQCVLCSKCDCVGRPLCDCYHVCPTGCECWRDQSWSMTNLVTCSSSGQSEIPVNVSVMVTELRLDGNNVTTIHADDLVRRHQLNALWLNNSGVRPLTEHPLHAYMTSASQRTSPPAAESSGERCELPRLQPSWLCACFGLDAAAFIFSRGITTWLTVMWIDVTPMFSMLALHGNAFSKAPEAIYGIRSSEYTLRDSGRIYVLRIHAGECNKLFSEDLRLLGDLVIEILDFEMVMYCTAPLIRVSPGFIAGFVMLGVLFLTTVLCIALTHHYQHEIKLWLFVKYGVRVFKRKDPESDKAKKYDAFISYHNSDEDIILREFVPQLEHGETPYKLCVHNRDFLAGEFIAENIVYAVENSRRTIVLLTASFIDSEWCRYEFQAAHNQAISEKVNRIILVVFEDIPKGKLDKNLEAYIKTNTYIRYDDPMFWSKLRYALPAVRAEKPLPDDPPPAYEPPTAEMAARVRHDIYLNEIVDRPGVQGSSATDDGNVNQF*

*>XP\_014665544.1 PREDICTED: insulin-like growth factor-binding protein complex acid labile subunit [Priapulus caudatus]* ***(Toll8-LRR only)***

*MLRHVAMCNTAPRVGPGAHEHINSLPLPELDAGRRERLLRRFVHVGGRDDGPSFGRLQNTTMSRLQISGFGDLTEIPAGMFSGMKIVSLTISSSSRPTMNEQSLAGIRGLTELILTSLQLTELPSVIFPSVSHVEYLHLSYNRFTTLPDRIFSPFTRLRRLFLEFGSLTTIAPNALGGLSTLEYLDLSHNKIGFIEPGLFAEMGQLYTMMLKYNNLHALEAGTFSGLRKVTSLELEYNSIGRIDAGAFENTDGITFLKLFKNKLTSIKAGAFAGLNKLEMLDIIANFVLETIEVGAFHGLPRLSIVYLHFNNLNHLEQDIFDLSLYPESWSIITSISDNPLDCSCLGWLLSKPFDVHGLCHAPADVAGEWLENIDPSDLHCPAVRRQIVH*

*>XP\_014663137.1 PREDICTED: leucine-rich repeat and immunoglobulin-like domain containing-NOGO receptor-interacting protein 4, partial [Priapulus caudatus]* ***(Toll8-LRR only)***

*YLHLSYNRFTTLPNRIFSPFTRLRRLFLEFGSLTTIAPNALEGLSTLEYLDLSHNKIGFIEPGLFAEMGQLYTMMLEYNNLHALEAGTFSGLRKVSNLDLEYNSIGRIDAGAFENTDGITFLKLFKNKLTSIKAGAFAGLNKLEMLDIIANFDLETIEVGAFHGLPRLSIVYLFYNKLSHLEQDIFDLSLYPESWSIYTDISETR*

**Pelle**

*>XP\_014663622.1 PREDICTED: calmodulin-binding receptor-like cytoplasmic kinase 2 isoform X1 [Priapulus caudatus]*

*MASAGNKLNIGQEPVCHAIDLGDLDFCILERLRKMLDGTFDFWRDLGAEMRIDKDFMAEIPIKIQQGRSPYELLHNVWKSQNKTVTDLYLVLVRTDHLRAARVLRDLVEPQYRLLCDVGSTTHLPGHQARGKPVNESDLPPPPAPPSASYYNEDIGVRFNFVPNISGSSKVGVQDTCFEMDTGYPSRPGPRPAPSETTDVWSQSDSCNITRSSSSSLDDSWNDSIAFEKRRAAAGDYYPGYASAFAMEKERRCNVHGAEGDGPQRFPVAADTCGDRSLEPSAVHSCDCALMEGSLLSCSDGRTSTTLGQQGSGREQRVCAEAESVACAIMRTQHVSYDELYEATAGFAADHELGHGEFGIVYRARVRSSAVAVKRFVKRQGLVVDDAAECKQINNVLRHLSRYQHENILQLCMYSIGGPESCLVYQYMPNGSLLDRLLFIKGYTAVLTWQQRLAIMEGTANAILFLHCSQPPLIHGNVKSANILLDKHMEPKLGDFGLAQPAPQGDATHATVSMVMGSAGYLPREYLDRRELSAEVDVYSYGVVMLEVATGRQAQEPASRKSDYLVDAVKALKKEGHSFTTIVDSHLEQSRMWLYLSEEFINLGLCCTHQVKKRRIPMQEVQNQLVKMRRQCNEL*

**Dif/dorsal**

*>XP\_014663067.1 PREDICTED: embryonic polarity protein dorsal-like [Priapulus caudatus]*

*MEQWPPYSVHQDVMTQRPGDHQWRPPLDDNANSNSPGESQEPVVIITEHPASKLRFRYECEGRAAGSIPGEHSIPEKKTFPAIQVRNVSRPFKVIVSCVSHEKPPAKPRSHPHSLVGKNCQDGVCVVSVTNPRDGRIEFPGVGIQCAKIKDRKDQLAKRQKMKIDPYKVGFTHSDQSLDVSVVRLCFQLFIPTVMDPETNQWSYAQETWKAIRPVCSQPIYDKRAVAQLNISRIDRISGPACGGQEVWLLCDKVTRDGIEVRFFEEKNGQTVWQEKAQIVLVHKQVAIVVKTPPYRDPDITSITMVKVALHRPTDMEISPAIGYKYYPSNNGEDRELAGQFPAMAPPVMMLDHLLLKQDKQHSQVHEPFRSAMIKQEIVKPVTNCPATLPGSAMAISAATAAMPPPLHPFAVSYAIEHPLVFMQDMHPAAAAAAAAACDDSNADTHMTSLASQFNSSLSFSSLSSLSELICTGDITMAPPISNSSEVEWLLKNITDMQQ*

**Imd Pathway**

**Ird5**

*>XP\_014674193.1 PREDICTED: inhibitor of nuclear factor kappa-B kinase subunit alpha-like [Priapulus caudatus]*

*MNWPTSQPCGSWEKVRVLGSGGFGAVMLWKNTGNSQEIALKECRLLDDQITEKMRRRWTLEVDIMTRLHHENVVFGISLPDDLRALTSELPFMAIEYCRGGDLRRVLIKPENCCGLQWKEALRIATHISAAVDYLHSCRIVHRDLKPENIVLQTSGEGFMYKLIDLGYAKELDQGSICNSFVGTLHYLAPELMSGQKYTCTVDYWSLGLTVFETVTGKRPFLCNLSPVQVLSTIAQKRREHICAYQDVAGEVVFSERLCYAHRLPPRAQRRVEAWLALMLDVDPATRGGGVGDDGRRRCFPLLAEVAGVRVARVRDLGSGAAWEYEVDEGTTLTQLRAWIARDAGACGDARRLLLLPGGRRVRDDANVGELCTTLHDDRTLFLLPADFPEERLPATAAPRIPEPVAAATDDAATPLRYSDAKRCWTHAVMFCQGRVDDYAEMAAGEGAAVADLASVGAAFAHDLREVVEGATVLRTLLRVFCAAAQADVGACRRACGDAGPAAAWEAAMLATQPFTALVDRANDLHRRAAALDERHCMLRQMAPQWQSHLAALTAIKGAAAEAYERLRGVPREQRAARSMDARDAARVVAACADRWRHCVDELRAHLSRVAACGRGVRDARPQLEATRRDLAAACSTLDARQRERQRDIWDLVTRCISTAAAPRPSGGLSNGVADTATRGSEGDLSVQGGRSAQGKQRRGIEDLRTDVDSGSATPDAFFAHGTREVSTTLACSETAHTELEKMFVQLQVNKERSEECDWSFMNQQHK*

**JNK Pathway**

**Hemipterous**

*>XP\_014669659.1 PREDICTED: dual specificity mitogen-activated protein kinase kinase 7-like [Priapulus caudatus]*

*MASTTSSSFQNKMSKIEARLRAENEALKRDKVQTSLDLDLHLSPRRQRPTLSLQQPYGRSSSAPSPTLNTSMGRQPRPQGLPGPIHNIHKPPDSAEIDRKLKEIMEQTGILTCNGNQKYKADIADLELLGELGNGTCGHVVKMRHKPSTQVIAVKQMRRSGNKEENKRIIMDLEVVLKSHDSPYIVQCVGVFVTDSDVWICMELMATCLDKLMKRLKAPIPEKILGKMAVAIVKALHYLKETHGVIHRDVKPSNILLDWNGTVKLCDFGISGRLVDSKAKTRSAGCAAYMAPEKYRILPDHRKTSTTSERRMSFRNSAVAEYLSLTKDYRKQQDNELLPASLREYNYERPRSMPACCMRPVSADARLQPE*

**Jnk**

*>XP\_014677598.1 PREDICTED: stress-activated protein kinase JNK-like isoform X1 [Priapulus caudatus]*

*MSRYHGNQFYSVEVGDTTFTILRRYQNLKPIGSGAQGMVCAAYDTVTATNVAIKKLSRPFQNVTHAKRAYREFVLMKLVNHKNIIGLLNAFSPQKSLEEFQDVYLVMELMDANLCQVIQMDLDHERMSYLLYQMLCGIKHLHSAGIIHRDLKPSNIVVKSDCTLKILDFGLARTAGTTFMMTPYVVTRYYRAPEVILGMGYKENVDIWSVGCIMGEMIRGSVMFPGTDHIDQWNKIIEQLGTPNPEFMKRLQPTVRNYVENRPKYNGYTFERLFPDVLFPAESTEHNRLKGKGSKASQARDLLSKMLVVDPDQRISVDEALMHPYINVWYDDGEVNAPAPAPYDHSVDEKEHTVEAWKDHIFKEVKAYELLQNSIPAGMSLHNHTGADGDVSNDCSDGHAENNTPGGSTYNRRR*

**Jra**

*>XP\_014674155.1 PREDICTED: transcription factor AP-1-like [Priapulus caudatus]*

*MTTKVEGNTVNNNRKMEQTFYDNDSAKNNDGCRMARNWTIPMSAHHNVGERSASICELKKNMTLDFSAPAGKKAKLNTVLTSPDLNLLKLGSPELERMIIAQHGMITTTPTPGQLVMFPKSVSEEQEVYAKGFADALATLQTREQRPTSQHGRDDYGGGTYSSPSYVELTMSPALPGMAHARSNGSVDAASSSSLGGHAMTSPALSSAQVKEEPQTVPCLGRSPPVSPVNMAQQEKIKLERKRLRNRLAASKCRLRKLDRIARLEEKVAGLKGQNSSLMQTATQLREQVCQLKQVVMDHRHDGCELRC*

*>XP\_014681293.1 PREDICTED: transcription factor AP-1-like [Priapulus caudatus]*

*MLEMETTMYEDDMRTTGMGKINGKTSIGRYVINHGDNPNSADMTGLKRRMTLDFNTSSKKQRITNLLTSPDMNMLKLESPELEKLIIAQHGAITTTPTPTQFVFPRSVTEEQEMYAQGFVEALANLQRQEPGSNDSRPNYTELVSMLSSPGLISLTPSSTAASLLPPPVSALLSKPLQTTVTMPVAHSLPPIKQEAPQTVPCLNGTPPVSPVNMEHQEVIKLERKRERNRVAASKCRLRKLERISQLEGVVSDLKNQNSELSQTAVSLREQVCALKRQLLQHMNSGCKIVVPTEIGI*

**Fos**

*>XP\_014677654.1 PREDICTED: fos-related antigen 1-like [Priapulus caudatus]*

*MFTQGAGNSDTGYNTGELTSRYVAGILCSMTNDNGDDSLGHVPTTYGYGSGITTATTPTLTPTTQSFVELMTLPMVSQNRVVNEHGGFTPVVSDANGYRSNNGRQYWPHSSDPITARGLVPMREGASAAGTNTRRGGRRVKYEALNPEEEAKRRVRRERNKLAAAKCRKRRLDHTNCLLMETDMLEDERSKIENEIAELQNQKEQLEFILQAHEPTCKRGGATFATSDIPLIEPKLSSCGGLSRPTTLNVTSVLTTSVKQNGGALVSLPMLTPSNVYTTPSGGTLFNFADSDFGDHSGLTPLIQPKSCADEANRGSSSDMSSPETIKSPTLVSL*

*>XP\_014670401.1 PREDICTED: fos-related antigen 1-like [Priapulus caudatus]*

*MYFQRTKSEADGETVGDARYTVAGILSSMANGASTANPVRPNSLAISSTSATTLSHDASTIPLVCGVTTVTTPTLTPTTV*

*ANIEQTFLELTSVPVTTTAQHAANQAGFVPPIYDNTTSSDMSRESFHSVEDDAIYWQHAPAQLGIPDIMIGRPADVSTIS*

*TMGTIPMPAVSRKTGGRRIKQENLTPEEEERKRVRRERNKLAAAKCRKRRLDHTNTLMQETEKLEDEKSQIEEEIHELQS*

*QKEQLEFILRAHMPICKRRNTGDTSKPFTDISQLRVATTHAHPTSVVVTSVVTQQPEKPATSTSPTTTSSSVFKLGDEAL*

*TSGARLTPVIVAPAGAYDSKRKDDSQRDLSDDVKSSASLVKL*

**TIR-1 Pathway**

**TIR-1**

*>XP\_014677545.1 PREDICTED: sterile alpha and TIR motif-containing protein 1-like [Priapulus caudatus]*

*MDEIHRLVRQAWNMPGVGRDLAYALCDVLRTSGALDTLIAHCSDPSSELRFQSARTLEQCLSTNNRDYVVETGLDGVVKVACMKGEPAMARVGTGILENLFKHSEETCTKVVRLGGLESILTQSRSNDLPTMRHCAAAFANLALYGGAENHQLMIKQNVPEWLFPLAFSKDDSTRYYACLAICSLGSNKEIEAAVKKSGTLELVEPFLTSHDPQEFARSDDAHTHGRSKDWLQLLVPSLTSSRVEARSLAAFHFAMEASIKKRQNRLEDFYEIGAIDALKRVASSPNKLASKYAGEALQIIGEEIPHKLSLQVPLWTTIDVLQWVKQIGFELFESEFTSCRVDGDLLLQLDDAMLESDICMSNGILRKRFLRELKTLKINADYSCVDPSGLDSWMLRLQTDLSQYSYSMLHQGVCMDMLPYLNDDHLRDDCGIGNGIHRLRIAGAIRNTLACFYCLLLKVHLQLRGFRVFIDVERLEVGKFDMNLLTSIRSSKNFILVLTTHALDRCLNDENCKDWVHKEVKAALECGCSIIPVHDNFEWPEAEHLPEDMRAVCHFNGIRWIHDYQEACVDKLERFLRGENAMTKSDSMAPMPPMHGAGAPKFPLPPPAIDENRSDSGGSSGSLVDEASLFRELAGSEVVRGDSAAPTKTNAMPRAPALLLPEPPRSRRVREKEGET*

**NSY-1**

*>XP\_014678005.1 PREDICTED: mitogen-activated protein kinase kinase kinase 5-like, partial [Priapulus caudatus]*

*MEVVCVIDQVVTEGIRARRLALDAIQRACTSVGATLHQVAFEKLDFGETNVLDLFYNTDMCIVDTSVMLQQSALIYQLGVRESFGNKDNILIYNMHDEQPHDVSTTMPFKMTFSGYKFIPYTISKDGTTAVYERTGIPNVSAAPAAAVDAPAEATPLQCKIRKILKDVQIDAGFVTTGHRFVSAGLILNSLIGRKGSLSSLKDYWDVATFFEISVLAEDYSKAAQAAECMYKLTPPNWYLKSTIGNISLINTFRKKAQPTEQEVPRDEEIFLFWMEFLMEATKTECTDVRFPVLILEPTKEYMPSYVTVNLEAGIWNQESSVRLWHVAPPCPNKGMHEWVFLVESIKSVSLYRRDDRCVYLYVQQNSDDFQLFFPSEVQRKRFYDLMLELTADNENCITDLDSDLYSGPITYEYEQDESGRKTVLGKGTYGVVYAARDLMTQVKIAIKEVPEKNMSGVLKIVDFGTSKRLTGMNPCTETFTGTLQYMAPEVIDKGQRGYGAAADIWSLGCTVVEMATGKPPFIEANNENCITDLDSDLYSGPIT*

**SEK-1**

*>XP\_014665640.1 PREDICTED: dual specificity mitogen-activated protein kinase kinase 6-like [Priapulus caudatus]*

*MPSVSPPSMPPYSCESHQVVKALHDLHTKLRVIHRDVKPSNILMNRASQVKMCDFGISGQLVDSLAKTVDAGCKPYMAPERINPPRDYKGYDIKSDVWSLGISMVCTQSNVLNSASFLCIICTYWDFFTRETQQYCLQKLYKDRLNYVQLLQHPFIKKHQDTDQGDVVTFVNEVLDFMEQDSAAQAAAS*

**PMK-1**

*>XP\_014676602.1 PREDICTED: mitogen-activated protein kinase 14-like [Priapulus caudatus]*

*MAGALKPGFYRIELNKTVWEMPQRYQMLSPVGSGAYGQVCSALDTKLNRKVAIKKLARPFQSAIHAKRTYREVRMLKHMDHENIIGLLDIFTPNTTLEHFSEVYLVTHLMGADLNNIIKTQKLTDDHVQFLVYQILRGLKYVHSAGIIHRDLKPANLAVSEEVELKDLKPSNIAVNEDCELKVGISILIR*