**Additional file 5: Table S3** The amino acid sequences encoded by genes involved in cancer-related signaling pathways in *P. brassicae*

|  |  |
| --- | --- |
| **Gene ID** | **Amino acid Sequence** |
| **>PlasB\_04559 (PbPI3K-1)** | MSVKMGDADADDQDAWWENELQAYHETSKDRGDNIFDAHPSVTAAPLSMADSVDGGMKTGGSNSSAESDDDDDEMKSLSNLVDDDNTNNQGDGGTESRRLQRHISIEETVEMIQTPEHVLAALNRMIEEVTRMSNQAFVSDEARHGLAEAKEALEKVATILEDDDRKDAKTDVDVLLNFDHLPWYFDNPGVAAYRARAYQFPHVQYQQQDSHIPRYLTAGVLPKNTPDSLRCNVVVMQNKRPQTLQMTISSTIWGTADSWKTSDACTGHDTAATLMVKIYDQFETRAEAIRILGDPSQNMLKFVGFDEYIHGTETLYCYETIRASLRNRASVDLCLIQRPIPRVLTESAARHPEIYKERVDPAVPILTIDDFTETRATSTMQWDAMTYFPLRSLQQEFRYRVRGIEGVSESVLPRLDSTHTHLRVRVFLFHGTEIIKHSDMTTTDAPRCQSPRWSRWLTPPDGVPHILASNIPREARISILLYGKRSYTKDEDLLSWVNVPLVDEFGHVRSGMMHLKMWTIDTNIKQGHLDALTFVFRGTTVENLTRGANHQPVSVCIEFEQRALSVTAPIVEVYREPDVAKIGEKQLWKKLSKEVRTNLDILIKTDPLYVLTPKDKEIFWTTRHHLLPYPLALPKFLQSVDWTSVDHRNEAHRLLSNWTPPLNPVSALELLDARYADYKVREYAVNCLRVLPDDELQLFLLQLAQSIKNEPYHDSPLTRFLVERALRNPHSIGHSLFWHLKAELHSPFHCERYAMILEEYLFHSGWHAAELRKQYEIVQRLQRISGKVVARKHAKDMTDDEIQAEYLAALHKFNENYLSTNESTQIPLNPKWLVTTLVVEKCRFMSSKMAPLWLVFKNADPLGDNIIIMFKSGDDLRQDILTLQLLKVMDKIWVSEDLDMRLIPYNCVSTGINAQGKGVGLIEIVLNSDTTSGIQLKYGGGALGALKLDPLHKFIADHNKEPDQYESAKDNFIKSCAGYCVATYVLGIGDRHNGNIMLTKDGRLFHIDFGHFLGNFKSKFGIKRERAAFVLTPEMAFVMGGKNYKKAKEFRVFTDLSAQAFTILRNHASLFINLFSLMVSAQMPELMFQEDIHYLRDKFFLQDSEKGAVERLRKEIQKSLNTTYRQFDNLIHNIKHK\* |
| **>PlasB\_04589 (PbPI3K-2)** | MGDQIADDAATAASPWIEAVNEDGHVYWYNVETQMSTWDNPFVDETVADELESDSLSVFGQFDAHDVSRARGLSDSISGETEFLVDSGTFSAFVTQPVRRRGSVKAPSDGVPVDDSAGCTSVHSVQNGVHSGGADVGSMSSHSERYHRHDYIAIPENANERRTRMSLTTDPWVECREVVSGRTLFYHRVTKEVVFDVSPSAIDSAAIKTANAIDDAAIESGSGAFPSYFRPAVPSSVPPSDAPVSSNAASVPHKYGPSSMMTMKGDVFNEPVGSYTPLIPDALSQLHSIPIVGELLETQSLPWNFSNPMAQHYRAVALAHPLNEHVPPPQAMMYPRYFSTIPIPAQRHIVCTVKLPESGVKSSMSYTKIHCSATDSANDMVWKALKKCDGRNFEPEKCILKAIGTEEYIYGTASVLDFEYIRVCINSHVEIRLCLLYIDDIQARVESVNDEMRVDEESDRYPADDAFDQVAIYNDGDYQEACNTDAVPVERLRVLPIKALTIPLRFQVCDLENIQLCPRFEPLIYAVCVEIKLMLGSVTLPNTTVRTRFRRPREGLLFLQDITLPNIDLSTLPSGTVIVFAAYGVRLEQKEVLLSYVKQPVVEFNGCLVAGRKCLPMWIVPNDDKGALDDINFARATCRPNLSVVDAPTLNVRFDSYLCPVLCPVAQPPIPLDTQLGGPVSLNTMNAKIRNRLEGIVSRDALYEFDSEEKEILWMARYNYMNDASVLPKLMRCVDWLSPQQAAEAYHLLYAWAKPEHPLHALALLDVHYADYRVREYAVSILEELSDSDLQQVLLQLVQVLKFELNHDSPLARFLLRRGIKNPYQIGHFLFWHLKAEIHNPDVCERFALLLENYLVNIKRHARELLSQDYVIKQLQAVAEQVQFQKTKELMADVECKELLRENLGKLNRLFPERWQIPLNPKWQVRALKPQFCKYMSSKKVPLWLCFANSDPDGGDIRVIFKTGDDLRQDLLTLQLFRIMDRTWLRQGKDMALKPYTCVATGVTRENEGVGMIEVVGDSATISDIQIEEGGGALGAFKNKTLVKWLQKHNRGTPEFNAAVDNFMRSCAGYCVATFCLGIGDRHNDNIMLTKDGHLFHIDFGHFLGNFKSKYGFKRERFPFVFTPEMAQVMGGLKSHEYKEFVALCCSAFNILRKEASLFLNLFSLMIPAGMPELSCTEDIHYLRDQLLLTLSDDAASKAFKKEIKKTISDFYRRVDNSIHILVKH\* |
| **>PlasB\_01656 (PbRas)** | MDAAKDGKPGSPALPVKIVVVGDGAVGKTTLLLRYVENRFPETYVPTVFENYYRDVVVEGIAVNMGLWDTAGQEDFDRLRSLSYNDTDLVLIVFSIDAPTSLANVSSKWVPEIQHHCEGVPFLLVGTKSDLRNDEQTLEKLRARNQKVVELSDANAVGKEIGAQAILECSALTGAGIKEVFDQALKVVLVKKGLLKTEKPQSTSCCTLM\* |
| **>PlasB\_04173 (PbMEK)** | MAPPNTRANTRSRQQQPGLTSRRQSGRNNKPGFRRRRPPALCVDENDVDDVLKSQVRVAIRLWNEPRAFVIGDFQIDGKGFTLGPSVKAAGLTSLVDSSRPVSDADVVDGHQTTRVDIQISGINELEVFAVCGVGSTSRVRIVRHKATRQLLALKQVDLDTSAERVQPIIAELRALHECNSPSIVSFHGAFYSNSCASIVMEYMDSGSLKDLATRSLNSSIPEYIISAIAKQILHGLVYLHCSKGIIHRDLKPSNILLNSMGRVKLADFGVSGKVSNVTRNRHTFVGTVSYMSPERIMGENHTVSSDIWSFGITLMECALGYFPFTQTAFRSRSKPAFWDMLDTVSTCPTPRLPGNMFSNEFNDFVSSWYINNVSSVKHDILDVRNLDCVPVPVEAATVRTFTFA\* |
| **>PlasB\_00238 (PbERK1)** | MSDSTPAVDETVTGSTSRPTLSNAAEPSTGGASPPAATPNWNERHQFSASGTQFLVDKQYTPVKSIGSGAYGIVCSAMDTVTQKKIAIKKISAAFDDLIDAKRILREIKLLSHFKHDNVIRLVDMVNPLTAAQFDDVYMVMECMETDLHKIIYSKNELTDEHCQYFIYQILRAMKYVHSSNVIHRDLKPSNLLLNGNCDLKVCDFGLARGTNDKDDYELTEYVVTRWYRAPEIMCACQDYDRKIDVWSIGCIFGEILGRKPLFPGDNYIHQLNLIFGTLGTPSDADLDWITNAKALQYIKNLKKKPSMPFERVYPKAPPQAIDLLSKMLVFNPANRISVEDALAHPYLKALHNPKDEPICPTTFDFEFEKQANTKVGIQKLMFEEIEKFRPGVVNPIL\* |
| **>PlasB\_02211 (PbERK2)** | MRTGDDRRRPSQASEAEREAAMRSRPVSTVTPGGTRSFMVLGNRFNVRDRYKLIRVLGFGAFGVVCAADDTWTRTQVAIKKISNAFSNLIHTKRILREVRLMRYFCHDNIIKILDLMRPTGDVADADDIYIVTELMETDLHQIIVSPQKLTIEHVQYFLYQILRGLRCIHSAGVLHRDLKPSNLLLNSNCDLKIADFGLARMASAEDDTNAFMTEYVATRWYRAPEIMLSWKEYSKAIDMWSVGCIFAELLGRRPLFQGRDYMHQLHLITDVLGTPSFADTEYIASPKAKEYIRSLPIKPRIPLQSLYPGAPADALDLLQKMLMFSPEKRISVDEALTHPFLASLHDPTDEPTASGAFDFSFESVDLDVDTLRDLLWNEAEQYEKSDPAGHVDASITPMSY\* |
| **>PlasB\_05287 (PbSGK)** | MLRPHHDQALPTVTATPGQTFAIDRAGCRSVHRTADDFEAIRRVLQTRYDFREPILSAGSGAAVGMQAWLQKALTSPLTRSSPELRRFLEPDSADSEDDIDADLDDALGNLSVDEDLDKEIKQSLSVPTVPASLDDFQLLKVIGKGAFGKVMLVRSKSDPKQLFALKQLDKSKVRNKGQSEHAMTERNILEYIRHPFIVTMRGAFQTESKLFIVLDYCAGGELFFHLQRMGTFSEELARFYTAQLVLAIEYLHELGIVFRDLKLENVLLDAKGNIQLTDFGLSKEGVADNVSARSFCGTPEYLAPEVLTGTGYGRAADWWSLGTLLFEMLTGLPPFYAKDSKQLFQRILTSRLRLPYHVSPEAGDLLQRLLSRNVESRIGSSDDDAREIKQHCFFAGIDWDLLLAKEVPPPFNPCDGLAPDDTSNFDIDFTNLPVASTDLASGSFVKDVDPDLSNSLSDFPFPLNPASGQR\* |
| **>PlasB\_03214 (PbCDK)** | MAGDGERPESQQYAGLGRYQKIEKIGEGTYGVVYKARDRVTGESIALKKIRLDSEDEGIPSTAIREISLLKELQHPNVVSLRDVVHHDFKKLYLVFEYLDQDLKKYMDSQTAPLDLMLVKSYMQQLLKGIAFCHSHRTLHRDLKPQNLLIDRQGALKLADFGLARAFGVPVRPYTHEVVTLWYRAPEILLGTKEYSTPVDIWAAGCIFAELVTKQPLFPGDSEIDELFRIFRALGTPNETTWPRVTSMPDYKSTFPKWDPRPLSTCVPGLDRVGLDLLGKMLRYEPGKRISAKQALEHAYFDDLYDLQR\* |
| **>PlasB\_10022 (PbCyclin1)** | MTRARPSERLAPAVASTPSASSKASTAMPISPLATRPPSLNLIDEFSNMLVNEQKFHAEMSYVDDYRQFSYDMRSRLLGWIVEVLSYVDASEQTLFLAAAIFDRFFRLGGCHKALWALLAGTSIFIASKYYQISAVRVRLITEALHNTYTRQDVYDMEMAVLGRLDFNISLVTAWDFAVFFLSRLPSLPQDGETVIRSMTSYLLELALVDRMHFDMRPSSLAASCIALAVHHHLYTIGADAPLRDQVVTDLERAVSARHCFLVDGMRSLYRLHDGRSPADPVPKKYASDAYHNVSKAQLRCPTRY\* |
| **>PlasB\_07777 (PbCyclin2)** | MSRRAKRNRDAAADAAGDLSRRHRVQANAVAVGKVLLCRELDDGAGACMTRWIEPDVCRGALLDTTTTMIERMRTRQSTYDTNLNPNYLTGHPCLRPKMRSIVVDWMQQVCQEYGLSRETCHLATNYFDRYVCGQLATPPTRLQLVAVTALLIASKLEDVNVPTVADFAYTCAGSYAAAEILRTELDMVKALGWMLRPHSPSTWARLFLLRGIDQATPGSKPGRDLLRSDRFVRVMEVIDAARLYVKSLQYSPYVLAASVLFHVFDGYADLIGLATGMDRAQCAECMEWIALLDDCIPRVGLHSILDRGYRPPDMHVRQVYNPHALQVCLDDTRHN\* |
| **>PlasB\_00247 (PbPKA1)** | MSFLFKPKRRRNNSGTSEDADLNLSPETTKIREYLASRENLSLSTFTIGATLGTGTFGRVRLATIAIDGKPKYMALKMLKKTEIIRLKQVEHIKDEKRILSAICHPFIVNFFGSFQDEKRLYMIMEYVIGGELFSQLRRARRFTNDASRFYAVEIVLALEFCHERNIVYRDLKPENILIDKEGHVKITDFGFAKFVEDRTWTLCGTPEYLAPEIIQSKGHGKAVDWWALGVLIFEMCAGYPPFYDENPFGIYQKILDGTIDFPKHFDPNAKDLVRRLLTADRTKRYGCLKNGVDDIKEHRWFKGIDWDAALQRKLTPPFIPTAMSENDTTNFDKYPDSVERGHPPEISAADAALFEAF\* |
| **>PlasB\_07097 (PbPKA2)** | MEWVEERTRGTPPPLRNSHRQASWGSKSVIYGGRGASSVLDDVFTIDMGSDGTWKEMVINGGFIPPARENHALVVVGDRMIVFGGSEYGRLSNEVYELSLSTCTWKKIETSGKPPSARERHTMTIVDNVAYIFGGQSAECEFLNDLYALDFSTWTWSLLNPPKAPTPRNHHSAVAVDTRIYVFGGKSHNGYFNDVHYYDISTRQWHQPQLQGISPAGRWGHTSIAFDRRIVIFGGWNGTWCFNDLNLLDTVTKAWTRLTTTTSGPSARAYHSASVYGGHSMMMFGGRNGLRRMDDTFTLELKESLGKAGSVEAMQALKNLWKLSDFELRETLGTGSFGRVRFAKHIPSGKFYAIKILKKAEILRLKQVDHILSEKTILQAINHPFIVNMFASFQDKKYLYLAMEYVVGGEFFTHLRRAGRFNNDSSCFYAAQIVLIFQYLHSKDIVYRDLKPENLLLDAKGNIKMTDFGFAKKVEFRTWTLCGTPEYIAPEILLNKGHGKPVDWWALGILIYEMLAGAPPFVDDDPMGIYQKILAGRIEYPAHFNRHAKDLISRLLTPDITNRLGNLKNGVEDIKRHKWFANINWTKLYNRKMLTPFVPKVRGDDDTHNFDHFPDSAEPPADVVLENDPFENF\* |
| **>PlasB\_01916 (PbGβγ)** | MTTKEKIEKCKKEIEDLKATIRDLRGDSDSADQPLQRVAREQGVSPGTCSIKQRRILKGHFGKIYAMHWSDDSRHLVSASQDGKLIVWNAFSTNKVHAIPLRSSWVMTCAYSPQGTFVACGGLDNLCSVYKLSNKAEGQQRTHCELAQHEGYLSCCRFINEGEIITSSGDSTCILWDIEQKQPKNTFSDHAGDVMSVSIFGPEGKTFVSGSCDATAKLWDTRADGKSAVKTFPGHESDINSVMFFPDGNAFGTGSDDSSCRLFDIRAYRQLNKYSSDKILCGITSVAFSKTGKMLFAGYDDYNCYVWDTLLGSNPSQLSGHENRVSCLGVAADGKALCTGSWDTFLKIWA\* |
| **>PlasB\_02182 (PbCaM)** | MATPDKQLTDEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGNGTIDFPEFLTMMARKMKDTDSEDEIREAFKVFDKDGNGFISAAELRHVMTNLGEKLTDEEVDEMIREADVDGDGQINYEEFVKMMMAS\* |
| **>PlasB\_06593 (PbRaf-1)** | MDEASRDLAPPSATMNASEQSSVNDIRKAGHLKKQGGARGGRKNWKRRWVVLKSEYICYFGEKENGTSEDGPCLGVVPLRGAKIVSVEAIADETQLASDTPQSSSAAQLPTTCYQCHKANSSRIHCKSCQNVFCEACAAENQMIGDKATRVCSFCRHRHADEDTIAMAATASNMEIGSVVEVVYREAKNTVFFKKEKPQYLFAIRTKERELWLAAEDAQEKAAWVTAISEVIVSYKKAFNNANSATAGNQAEKEQKQDGKATGSPSQQWEIDYNQITILEKIGDGAFGEVFKGRLWGTDVAVKTIKADQVTESVVDDLKKEVAILSQLRHPNVVLYIGACTKPPNVCIVTEWCDKGSLHDVLHDSSIPLDIQRIVSLSVGIAQGINYLHSLERRIIHRDLKSHNVLVDRNFNVKVADFGLSHVRESLTQQNGTSALNNDTNGRTRANAFTAAAPQQLGAPADFQSMKINSESMGGHYGVFGTPEWMAPEIMEGTAYNQKVDVYSFGIMMSEILTRKLPFRDQYKIKSYMDVVDAVLDDGAMPTLPGWIGLRLKRLIESCLSRNSSARPSFMSIILKLRSMFSASPAELFQTYDLPRLHDMLATPDRHNQALAAKEIASFKFEQEACPAGCDDDIVIREIDMAKRVCARCRYSAAHHQKLDDAVVTQFIGKLTDMLASSSGKVVLPAVEALERLITGGQRKSSTKLRQENLSIIKERNGIERLLGLVSSRSPQLSEAASSCLMLLIEDLPVDDSSYKQLKGTSLHVLSAMMEKDIAQRRDENAQMTEQLRNKVKTFETLQRLVQAAQIQQQPPSSSENVLEDRPMLSSSQRRRPKSPVQVPVNPAATLATAAVTDQWSDQGTVVAAVAAVPAPVITVQKPPDAPARPDPGPRFTSKGTTAVVRPPARETAPDDMPIVALDETPTNNLDTASSSAVPSASVPSTPGPSDPADDDGAGSPRNTAPEAVQQLVRPQTPDVPLPGRFQRISPANGDWVFVHDAQLGEWILKYVIVTPSMICVFRSYDDVEQTRPPEATVNASVPPGKRLKFKTGRKFRQPWCFHLCSQGQKWWFSLRSSQHTEIWSDVIVRPLLPDALREAFGATQQTLLRPGGNSPQLSPRLDEMSADDAVNIEGPNRTQSAQSIAALAPGVASPGTVDQATSAVDQPIPATEQPGSPAVAVEQPAPAVEQPAPVVEQPAPVVEQPAPVVEEPAPVVEQPVPVIEQPEPVAEVASPAVVEAPRTMRTSVPVVPAMEAALDARGTSLVSRGSAEHPVVEFEEADTSTTQLLDIPMLEAEAEPLVMQSPVSMAAHLESATSAFGSTLSLDALAKADQGPPESEAQGSSKAPADAGATKRLSTVAATDTGDKSPPVALPTSSDRPQVINQAPEPTPSGAPATRRDTSPARDVPTQELVSEQTTTSEAAGVPPSTEPRSVEVSPVPLSSEPVAALSSSPNRQLEPASAVARAHGVEPASRDSPVVSPKEVAAGKFVKRYIETTGARSPMLKPNQRLLSLRPGNELSRGNAALRLAAMPEVTSLPPTFVEQFGRRDCWHYSYLIMPDRLSQQWVAKFVVLLGAQPIRLMVYNSHNDPPQKPISEHLLEEASAATSQAVEACLGFPVEYDEKIALVVKEKPAQANTTEPSRPLLFLCASETDRHKWLSLIQRVVALSRV\* |
| **>PlasB\_09434 (PbRaf-2)** | MSLSLSATDDTAAPDRLSAEPIWEGYLMKQGGARGGFKNWKKRWFRLDAENLCYYKERPRAPTDAKSNDADTSSSIAEPAVLGVLPIRNATIVDLQGADDVAVKAVELPPAWDVGATACHDCKKEFSGSVRRRFCRACGLAHCSPCSPRSVLQSRIGFAEPVRVCNSCFNGITSAGGFKNADGGSRLDDGIIIVQTEQKKSKGFEWRSKKHLFILNSAELQMYLQAETSTVKLEVMTAIRSVVLYHQRKAQRATTGSAVTVAEPESSNNRPHKLDRQMSASSQWNIDFKAIKILHEIGEGSTGMVYKGRLWGTDVAVKTIRNATMADDLQKEVAILSQLRHPNVVLYIGACLEKPNVAVVTEWCDRGSLFDLLYDDSPGCCNLDFQSIITIAIGIAQGMNYLHSLNQKIIHRDLKSHNILIDSHFTPKVADFGLSKVKEPTRLGDNIDPQIVTESLAIGHQKALRAHAAAKKKAAEDSKEAQSEVPGGTAEWMAPEVMEGAPYNQSVDVYSYGIVLSELLSRRLPFRDKYTITGYADVVEAVLDDGATPTIPEWCGAKMQKLVADCLSRNAEARPTFNEIILRLRSFYPLDPADVFQKFDIPRLLSMLDSPDRTEQFRAVRELSDMAVDLTDLCHVCGHTPLKYAQMGEATVVKFVARLTTMLLSPHADIIQHAMLALRAMIDESEAALRPTLFGAIRESGGVQRIALHLKSDKEDMANAAALLLSRIIADPGTVDNPATLMGLSPEVMAELLAIAKQEVSTLKKKIEGNEGSLSRKVELSTWISNRLRQAEFGLSDAQTALASIATPRTIIANVASPSPEGGSFEGKDLPVQLRAEMGRGAQCWGWLGLLDPAGEQWIDVYAVLRNATICIFDSEESRPETIRYIIRIRLGNVSAKFRAGRKRGRHNCLQIALSQELLPVAVDPKTPPIRRVFINVGSHERFAFWVRHINEHLDIPVPLDFAPDETMT\* |
| **>PlasB\_01538 (PbEif4E)** | MPGPAKRRNLFTTDGSDDESDADPFQTLLSSLKVDQKYEGMLKRRKLEEDGADQSEDDDDDTSVEDGERVLMSTEEIVEFQRKHGDAFEVAEDGEEDDSEQGDDESSDDGVADSNDDGDDNVPSDESEDDEDVANNDNDDSIAADPKDEYSDLDDGKPQGEDPVLPYHTRMFSNESASALQAKAPFANVSGGPPQWRVTMRRLAEDENESVWQLSPSTGDIQKSWPGNVVRGVEPEPSPLQPVVSRYQDLVYTCRKPGDDRATSDLYLRHVVRHVLRTLRTISDNDATLGSDPTFEARDQGFTHPTVLIMCPFRSSAHRIVNRVLELLPSKFTRQVSNIKRFNEEFGPPEPDAEEKDRFNRKPSLYKDVFSGNFDDNFRLGIKLGKRSVKLFADFYASDIIIASPLGLRMIVGGEGDLQSERDYDFLSSIEVAVLDQADVFMMQNWEHLQAVLSCMNLIPNDSSHSDFSRLRSWNLDGLAAHHRQMLIFASHGFPELNALSSKHCLSLAGCVRIRRHEFPGVLEQVVLPIRQQFQRFHHGDTPTDASEARFKWFAEEILPQLKTNLSSHILLFVPSYFDYVRIRNLLRSQKVKVALCSEYTKKGSVARARSRFFHGEQKFLLCTERFHFFRRYCIRGAHTIFFYGLPQEPTFYLDFVNAIEPGSHQTTIALFSRFDALALERVVGSSRAARLLSAHKDLHMFC\* |
| **>PlasB\_01918 (PbMOB1)** | MKGIFGMGQKTFKPTKSHEKGSKRDEMHLKAQATLGSGDMAMAVKLPKGEDMNEWLAVNTVDFYKYISLLYGTIAEFCTAESCPAMSAGDAFQYLWADGVKIKKPIKCSAPEYVDHLMSWVESQLNDEHIFPLQIGAPFPKNFQTQIIPTLFKRLFRVYAHLYHEHFTKMQALGAEAHLNTCFKHFMFFVREFNLIDKKEQEPLKDLIENLVSQ\* |