

S3 File. DNA and protein alignments built to determine intron landscapes.

Alignments were performed using Muscle as described in the materials and methods section. Exonic sequences from *Passalora* species were aligned to the previous DNA alignment using Muscle and new alignment was manually edited in GeneDoc. All names are as described in Figure 3 and S4 File.

DNA alignments: introns are highlighted in yellow. Four-level shade indicates nucleotide conservation over 90%, 80%, 60%, and under 60%. In D, two-level shade indicates nucleotide conservation over and lower than 65%. In B, insertion of a single nucleotide in the sequence of *Lentfl* makes it a pseudogene.

Protein alignments: positions of RSIs, previously identified ILEs and novel ILEs are indicated in yellow, orange and red, respectively. For novel ILEs, the position is indicated within the sequence of the two most closely related fungal species. Numbers indicate phase 0, 1 or 2. Numbering of intron positions in Figure 3 corresponds to the position in the corresponding alignment below, minus the number of upstream intron positions. Four-level shade indicates amino acid identity of 100%, over 80%, over 60%, and under 60%.



Protein alignment for Figure 3A

Fulfu193200 -----MTLSNFQLGASLVSAGLAVWQAVIAA1IILGKFIIAAVAVTNG-YLGAE-WHIGFPVVSRYVW-GIYGOHYVALVQRVILSLVWFHAVQSWTGGLGVQNIILAAIFPSYQNMGNVFPASANMNAKQ1FIGWVLFNVLIIPLLYIRPEKIQVW 143
Dotse126132 MGLQQFIDFIRIPSNERSVANVWINEIDLRLPPWRRTWTRWAYISFWAINQMTLSNFQLGASLVSAGLAVWQAVIAA1IILGKFIIAAVAVTNG-YVGAE-WHIGFPVVSRYVW-GVYGOHYVALVQRVVLSLVWFHAVQSWTGGLCVQNIILAAIFPSYQHMDSVFPASANMNAKQ1FIGWVIFNIIIVPILLYIRPEKIKVW 194
Sphmu82757 MSFCAIIDYCRSPNARSVANVWINEIDLRLPPHRRTWTRWAYISFWAINQMCLSNWQLGASLVAAGLSVWQAVIA-TFIGKLIIAMVAVANG-YVGAE2WHIGFPVVSRYIW-GMYG-HYIALFQRILLSLVWFSVQSWTGGLCVQNIILASMFPSYQHMGNHFPASANMNTKQ0FIGWVVENVIMVPIIYVKPEKMQVW 194
Sphpo39262 MSFCAIIDYCKLPSNARSVANVWINEIDLRLPPHRRTWTRWAYISFWAINQMCLSNWQLGASLVAAGLSVWQAVIA-TMIGKVIIAMVAVANG-YVGAE2WHIGFPVVSRYIW-GMYG-HYIALFQRILLSLVWFSVQSWTGGLCVQNIILASMFPSYQHMGNHFPASANMNTKQ0FIGWVVENVIMVPIIYVKPEKMQVW 194
Cerzm42490 MAFRDILDVRLPSDSRSVTNVWINEIDLRLPPHRRTWTRWAFASFWAINQLTLSNWQLGASLVSAGLSVWQAVIA-TVIGKVIIAMVAVANG-YVGAE-WHIGFPVVSRYIW-GMYG-HYIALIQRIVLSLWFSVQSWTGGLCVQNIILAAIFPSYQYMPNHFASADMTTKQ-FIGWVIFNLIIMPIIYIKPERIQVW 194
Psefi36375 MGLGRVLEIIRLPTNSRSVVSEFWINEIDLRLPPSRRTWTRWAYISFWAINQICLSNFQLGASLVSAGLAVWQAVIA-VIIGKFIIAAVAIANG-YVGAE-WHIGFPVVSRYIW1GMYG-SYLAIVQRILLSLVWFSVQSWTGGLCVQNIILCAIFPSYQNLKNPFESAKMCAKQ-FVGVWIFENVIMIPILYVVRPEKMKWI 194
Zymtr50149 MFVGSFLESIRLPSNDRSVANVWINEIDLRLPPNRRTWTRWAYVSWFAINQIALGNFQLGASLVSTGLSVWQAVIA-VLVGKIIIAVAVANG0TVGAE-WHIGFPVVSRYIW-GIYG-HYIALIQRILLSLVWFSVQSWTGGLCVQNIILAAIFPSYQHMKNHFPASAHMDTRQ-FIGWVIFNLIIMPIIYVVRPEKMKVW 194
Glotr82366 --MESGLRFLQVHSSGDE-TSVWINDIRPLPPSRRTWDKIAFISFWAINQIALSNWQGTGSSLVAVGLSVWQTMIA-VIVAKIISLVAIYNG-YVGAE-WHIGFPVVSRYVW-GVYG-SYLSLILQRILLSLVWFSVQSWTGGLCITAIISSEIFPSYQHMGNTMFASTHMTTKQ-FVGVWVYVNVVTVEMLYIPPEKTKRL 191

Fulfu193200 VLGMINIVTAITLLSIVIWVLSAAGGGGPLLTPAETTTSSSELGWAIIVHGVTTVIGGIAVGLTNQMDYSRFARRPGDQVF-GQWFSIIVFGAIMPVSLGCFASASQEVYGEAI-WNPPDLVQKWLDTDYNPKSRSAAFFAGCGLLICQLAINTVDNAFSAAGMDMAGLAPSEFINIRRGAYIGLVLSIAMCPWQLLSAASTFV 341
Dotse126132 VLGMINIVTAITLLSMVIWVLSAAGGGGPLLTPAGTTTSSSELGWAIIVHGVTTVIGGIAVGLTNQMDYSRFARRPGDQVF-GQWFSIIVFGVIMPALGCLAASASQGVYGEAI-WNPPNLVQKWLDTDYNKSRRAAFFAGCGLLTCQLAINTVDNAFSAAGMDMAGLAPSEFINIRRGAYIGLVLSIAMCPWQLLSAASTFI 392
Sphmu82757 VAGNMVTAITLLISMCIWIMVTAGGGGPLLSPATALLSNWDLGWSMVHGVTTVIGGIAVGLTNQMDYSRFARRPGDQVM-GQWLSIIVLGVIMPALGCLASASQGVYGEAI2WNPPNLVQKWLDTDYNRSRRAAGFFAGCGLVIICQLAINTVDNAFSTGMDMAGLFPSEFINIRRGAYIGLILSIAMCPWQLLSAASTFI 392
Sphpo39262 VAGNMVTAITLLISMCIWIMVTAGGGGPLLSPATTLLSNWDLGWSMVHGVTTVIGGIAVGLTNQMDYSRFARRPGDQVM-GQWLSIIVLGVIMPALGCLASASQGVYGEAI2WNPPNLVQKWLDTDYSSRRAAGFFAGCGLVIICQLAINTVDNAFSTGMDMAGLFPSEFINIRRGAYIGLILSIAMCPWQLLSAASTFI 392
Cerzm42490 VLWFNFITAITLLISMVWIMAKAGGGGPLLSPAAALSSELGWMVHGVTTVIGGIAVGLTNQMDYSRFARRPGDQVM-GQWLSIIVLGVIMPVSLGCLASASQKVYGEAI2WNPPNLIQKLLDTSYTPGARAAFFAGCGLVIICQLAINTVDNAFATGMDMAGLFPSEFINIRRGAYVGIALS IAMCPWKLLSAASTFI 392
Psefi36375 ILIFNIISALTLLSMVIWVMNEAGGGGPLLSPAKATSSWDLGWSIVHGVTTVIGGIAVGLSNQMDYSRFARRPGDQVF1GQWFSIIVLGSIMPALGCLGASASQAVYGEAI-WNPPNLVQKWLDTDYNPKSRAAFFAGFGLVICQLAINTVDNAFSAAGMDTAGLFPSEFINIRRGAYIGLVLSIAMCPWELLASASTFI 392
Zymtr50149 VLWMNAVSVFTLLAMTIWLLAEGAGPLLKQFATVKSSSALAWSITSGVTTVIGGIAVGLTNQMDYSRFARRPGDQVI-GQWVSIIFAGTIMPFLGCLCASASVTVYGEPI2WNPPNLVQKWLDTDYTAKSRAAFFAGIGLVVCQLAINTVDNAFSTGMDMAGLFPSEFINIRRGAYVGLVLSIAMCPWELLASAGTFI 392
Glotr82366 FIVMNVISFFTLLISMMIWALSQAAGGGGPLLSPAAVSSSELGWAIIVSGITTVIGGIAVGLTNQFDYSRFARKPGDQIF-GQWFSIIFFGTIMPFLGCLTSASVAIYGEAL-WNPPDIVLQKWLDTDYTAKSRAAFFAGVGLVVCQLAINTVDNAFSAAGMDLAGLFPKYINIRRGAYIGLVLSIIMQWQLLSAAGTFI 389

Fulfu193200 SVLSAY1SVFLGPMVGIMVCDYWTLRHRRIKLSLDLYHP-GQDGLYYFWHGINWRAFAIAWAVGWSYLLPGFAHAVTFRVIVPEACTN-LYYLAFPLGFVSTVYWCINQVWTLDDGFGVKDEIDYYGTFTEEEAAKLGVAMMETIEGEVDRDGVSVFEEEMGKDEKFFVAGSMNVTAV 512
Dotse126132 SVLSAY1SVFLGPMVGIMVCDYWILRHRVVKLSLDLYHP-GKDGLYYFWHGVNWRFAFAIAWAVGWSYLLPGFAHAVTPKVLVPEACTH-LYYLAFPLGFVSTVYWSLNKIWTAGFGVKDDIDYYGTFTEEEAAKLGVAMTETIEGEARERVSIEQDMHKDDKFAAGLTDIRAV 563
Sphmu82757 SVLSAY-SVFLGPMVGIMICDYFILRKRVRKLSLDLYHP-GKDGLYYFWNGINWRSEFVSWAIGWSYLLPGFAHAVTFSIKVPEACTN-LYYLAFPLGFVSTVYHFCINTAFPPVGLQEIDDVDYFGTFTEETEAAMGVAVSETIESEDGGSPNLDKGG----AGLTQVRSV 558
Sphpo39262 SVLSAY-SVFLGPMVGIMICDYFILRKRVRKLSLDLYHP-GKDGVYYFWNGINWRSEFVSWAVGWSYLLPGFAHAVTPIVKVPEACTN-LYYLAFPLGFVSTVYHFCINTAFPPRGLQEIDDVDYFGTFTEETEAATRMGVAVPETIESEDGGSPNLDKGG----AGWTQVRRV 558
Cerzm42490 SVLSAY-SVFLGPMVGIMICDYWVLRKRVRKLSLDLYHP-GKDGIYYFESHGINWRSEFAWITGWSYSLPGFVHAVNSEIAVPEACTN-LYYLAFPLGFVSTVYHFCINTAFPPVGLREADDVDYFGTFTEGEEAARLGVALPEMLDGLDHSPEVRVEKTG----SGYVKEWQE 558
Psefi36375 SVLSAY-SVFLGPMVGIMTCDYWILRKRVRKLSLDLYNP-HKEGVYYYWRGINWRSEFASWVIGWAYLLPGFAHAVTFSIKVPEACTN2LYYLAFPLGFVSTVYHAIKLVPPFGLGKDDDEDYFGTFTEEEAARLGVAATLYTIDGEER--PEDEIVKSK----ASKAKLV- 555
Zymtr50149 SVLGAY-GVFLGPMVGIMVCDYFVLRKRVRKLSLDLYHP1GKDGLYYFWYGINWRSEFAWVIGWCYLLPGFAHAVTENVKVPPEAWNH-LYYLAFPLGFVSTVYHAIKLVPPFGLGKDDDEDYFGTFTEDEARRLSFDKPSVIEKLV----- 537
Glotr82366 SVLSAY-SVFLGPMVGMQVCDYWLVGRKIKLSLDLYSS-SPEGIYYYSRGNWRAFAAWIVGWASQIPGFVNAVNEDIKVPVGSQH-LYYLAFPAGEFCISELVFYALNRLAPFAGLGEVDDVDYFGTFDEEEADKMGIRPAEDSDSSGADVEVDEKRLDL----ERTVSVDKL 555

Protein alignment for Figure 3B

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Sphmul65575
Aciril12790
Zasce69443
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Didex5051
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Bipvil05691
Bipzel01154
Phlgi131735

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-----MVGDRDFAEMKRADRLVARI-----PGDAASCF-FNPDHKGAEFYSKPYFCGAK-NGAPGYQICANNKVPADLDTAHRFIAPCPNDIRG-P-CPGL-NT-AAN-HG-FLSRDGIIVTFAELTDTQQNVYGVGYDLAVLLAV-LGVGLDGD2PI-TTKLSLGCDATSRT 151
-----MVDDRDFAEMKRADDLVARQ-----PGDAASCF-FNSKHKGAEFYSKPYFCGAK-NGAPGDQACANNLVFAK1GDTAHQFMAPCAEDIRG-P-CPGL-NT1AAN-HG-FLSRDGIIVTFAELTCAQQNVYGVGYDLAVLLAV2LGVGLDGD2PI-TTKLSLGCDATSRT 151
-----MDPVEMAERLALVVRQ-----APGSNVCF-FNPDHRGAVFENPKPYFCGAQ-NGAPGFQICANNRVFAROGDTAHAYQAPCPNDIRG-P-CPGL-NT-AAN-HG-FLSRDGIIVTFAELTCAQQNVYGVGYDLAVLLAV-LGVGLDGD-PI-TTKLSLGCDATSRT 148
-MLKRFLLAGLIASQGYAFPWVARHVRDPEMKASNRNLSRRTYPGAGTGYGDYDGESEATCF-YNADHVFAAANPKPYFCGAR-DGLPGYQVCKNNQVFAPOGDTAHQYQAFSSDIRG-P-CPGL-NT-AAN-HN-FLARDGITTEVELVDAQQNVYGVGYDLAVLLAV-LGVGLDGD-PIGIEKMSIGCDATSRT 188
MPQNSIFTALLWTGFAAGYPWVVDHAALDPRRVDNRQLRLRQ-----SPSAANCF-NPNHTGAVPYSDPYFCGAR-NGKPGSTRCVGNIVFAPOGDNHYFVFPFLDIRG2F-CPGL-NV-AAN-HN-FLSHDGIITNTELILAQQNVYGVGYDLAVLLAV-LGVGDGD-PLGTTKLSIGCDATSRT 176
MKSFSLLIILSQVPSIIAWPWIANVPGVDSLAMHAHPENFAKQRRQ-----TGLDPTCF-FNPDHTGAAFDPOQPYTGSIDGLPGTGV-GGVQVFA-P-GDTAHEFTAPCPNDIRG-F1CPGM-NT-AAN-HN0FLSHDGIITNLAELVSAQQNLYNLHFDIATFIAV-RGIALDGD-VV-TTKLSIGCDATSRT 177
-MQTSLLL-LSASAVSAYPWVANQPGVDSSLPRNRNV-----KRQDNCF-FNSNHQPAAPYNSQPYTGAR-NGARGTGK-GGIKVPAD-GDTAHAFQAPCPNDIRG-P-CPGL-NA-AAN-HN-FLARDGITTEVELVDAQQNLVNDWDIATLLAT-LGVVADGD-IL-TGKLSIGCDATSRT 167
-MTEDRLTA-----LSTPITNQPLRTTFASPT-----FARGTVQDELGK-----GGIRVFAH-GDTAHAFKAPTSKDIRG-P-CPGL-NA-AAN0HN-FLARDGITTEVELMDAQQNLVNVYDLALILAV-LGVVQDGD-II-TGKLSIACDATSRT 132
-MLTLPSSL-LFASSAAAFPWVAGSPGVDSLRFREAREAVT-----QKRQACE-FNANHQFAAPYAPTYVYGAK-NGRPGTGK-GGIKVPAD-GDTAHRFVPEPKDIRG-P-CPGL-NA-AAN-HN-FLAHDGVVTEVELVDAQQNVYGVGYDLAVLLAV-LGIEAGGD-VV-TGKLSIGCDATSRT 172
-MHSLSLL-LQASFATAYPWVAGETGVNSGLFRQARQV-----EKRQENCF-YNPFVHKGAAPTYAPTYAGAK-NGVPCNGK-GGIKVPAD-GDTAHAYTEPCPNDIRG-P-CPGL-NA-AAN0HN-FLSHDGIITNFEIVDMQQNVYVNGYDLSVLLTV-LGIQAGGD-VV-TGKLSIGCDATSRT 168
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-MHVLPPLV-IHATSIVAFPWIGTPPGVSSSFFKDAHTV-----GKRQEKCF-FNPVHKGAAPTYEPYTYTGAK-NGHPSQI-GGIKVPAD-GDTAHAFTEPCPNDIRG-P-CPGL-NA-LAN0HN-FLSHDGIITNCELVDAQQNVFNVDLSDILHAV-LGIQAGGD-PI-TGRLSIACDATSRT 168
-MYILPILLSIYVTSTVAEPWIANQPGVNPISIFRNAHPV-----EKRQENCF-FNPDHKGAAPTYEPYTYTGAK-NGVPCNQR-GGIKVPAD-GDTAHAYTEPCPNDIRG-P-CPGL-NA-LAN0HN-FLSHDGIITNCELVDAQQNVFNVDLSIVHTV-LGMQAGGD-FI-TGRLSIACDATSRT 169
-MYILPILLSIHVTSTVAEPWIGNQPGVNPISIFRNAHPV-----EKRQENCF-FNPHHKGAAPTYEPYTYTGAK-NGAPCNQR-GGIKVPAD-GDTAHAYTEPCPNDIRG-P-CPGL-NA-LAN0HN-FLSHDGIITNCELVDAQQNVFNVDLSVHTV-LGMQAGGD-FI-TGRLSIACDATSRT 169
-MYILPILLSIHATSTVAEPWIGNQPGVNPISIFRNAHSV-----EKRQEKCF-FNPDHKGAAPTYEPYTYTGAK-NGAPCNQR-GGIKVPAD-GDTAHAYTEPCPNDIRG-P-CPGL-NA-LAN0HN-FLSHDGIITNCELVDAQQNVFNVDLSIVHTV-LGMQAGGD-FI-TGRLSIACDATSRT 169
-MYILPILLSIHAASTVAEPWIGNQPGVNPISIFRNAHPV-----EKRQENCF-FNPDHKGAAPTYEPYTYTGAK-NGAPCNQR-GGIKVPAD-GDTAHAYTEPCPNDIRG-P-CPGL-NA-LAN0HN-FLSHDGIITNCELVDAQQNVFNVDLSVHTV-LGMQAGGD-FI-TGRLSIACDATSRT 169
-MYILPILLSIHAASTVAEPWIGNQPGVNPISIFRNAHPV-----EKRQENCF-FNPDHKGAAPTYEPYTYTGAK-NGAPCNQR-GGIKVPAD-GDTAHAYTEPCPNDIRG-P-CPGL-NA-LAN0HN-FLSHDGIITNCELVDAQQNVFNVDLSVHTV-LGMQAGGD-FI-TGRLSIACDATSRT 169
-MARFNLIALL-----PWITFALAFPRPIMNTLSK-----RRAVLQEGARLSRRAAAPTAAQFFYGGAKIDGLPGSQQ-GGFQVFA-P-GDTAHAFQSPFAGAERG-P-CPGL-NT-MAN0HG-FLSRDGIITTEDELVAAQQNAFNIAVDLAVLLAT-LGVALDGD-II-TEKVSIGGDAIART 161

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Lentfl317754
Didex5051
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Pyrtr150011
Altbr3820
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Bipmall64970
Bipso346574
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Phlgi131735

220 240 260 280 300 320 340 360 380 400

-ATP---G-LGPELGLDGNKFEAGDTSLTRNDYFT-AGG0DNFKENNTIYTDI---INNYCKDQ---CN-RDHVALYRKARYDWSVQH-NGNFYFGPK-SVLLFGAASSFL-YELFPSLGEF-GTANPTIMS-YFF-----QK-EQLPPN-WFSRVDPYSPILVAEIIHAYQYLHEV-AFGGNTGAP-NTFV 314
-ATP---G-LGPELGLDGNKFEAGDTSLTRNDYFT-ANG0DNFKENNTIYTDI---INNYCKDN---CG-RAHIAKYRKARYDWSLNH-NGNFYFGPK0SLLLYGAASFL-YELFPSLGEF-GTANPTIMS-YFF-----QK-EELPPN-WFSRVDPYTIPDVANEIIHAYQYELYEV-AFGGNTGKPN-NTFV 314
-ATP---G-LGPEGLLSTENKFEAGDTSLTRNDYFL-ANG-DNFRFNRTLYNMI---SQTGGGL---HN1RENIALYRFQRYQOQLNE-NGNFYFGPK-SVLLFGAASFL-YELFPSLGGF1GTPDQTIMD-FFF-----IK-EQLPPN2WFSRVDPYTIPLIAEIIHAYQYFLHEV-AFGGNTGKPN-NTFV 310
SSSE---G-TTNELGLDGNKFEAGDTSLTRNDYFLADG-DNYSEFNQTLFNMSDAD---GN---FD-LTALANYRYQRYQOQLSE-NGNFYFGVK-SVLLFGAASFL2YELFPSLGEF-GSPNCAIMD-SYF-----QK-EELPPN2WFSRVDPYTLLDVADQINCMYAAHEV-AFGGNTGSP-NSFV 351
SSTG---F---SEFGLNGH1KFEAGDSSLTRNDYFLIDNG-DNYSEFNSSLYEMSEVARSVSNGI---EN-RKALATYFAQRHAQSIHE-NGNFYEDPK-SVLLYGAAATFL2YELFPSGGPS-GVADQTIMN-YFF-----LQ-EQLPPN-WFSRSEKFSLLDVVTEIILAMYQEDFV-FEGANAGVP-DSEV 341
SIDFTG-T-LGREPGLNANFKFEAGDSSLTRNDYFL-NNG-DAFTFQGMFADMYRVANETSNGV---FD-RDTISVYRSRRYDESVAE-NPNFYFGPK-ALLLYGAASFL-YEVEVFGPE-GLANFDIVS-TEYGAV---PNDSGSYDHP-ERIPEN-WFNRAAYGLLEIGNEIIHAYQYGRFVK-LFGGNVG-A-GNEL 357
ATLG---GVLGRQFGLNGH1KFEAGDSSLTRNDYFT-NHG-DNYSEFNGLFKRMKDVADRVSNG---FD-RNTLAAYRSQRYDESVAE-NGNFYFGPL-ALLLYGAASFL-YELFASYGPE-GTADLKIIS-SFEGTTQDSN--GNWQAGP-ERIPDN-WFNRTSYTNNDVTEIILAQYVQYVK-LFGGNVG-T-NNED 346
AALGGLNL-LGRQFGLNLSRFEADSSLTRNDYFT-HGG-DNYSEFNGLFARMKEVADRVSNG---FD-QKAMAAYRSQRYDESVAE-NGNFYFGPL-AILLYGASSFV-YELFAPYG---GQADIASVS-SFEGTTQDSN--GEWQHTA-ERIPDG-WHNRYPYTTASGVTEIILAQYLAYPK-FFGGNG-P-NNEN 311
ALLP---I-LGRQFGLNTRKFEADSSLTRNDYFL-NNG-DNYSEFNGLFASMKSVADRVSNG---FD-LNALAAYRSQRYDESVAE-NDNFFFGPL-SVLLYGAAATFL-YELFPSYGPE-GVADLTKM-SFFGAVEDLSAPGGWRHVA-EQIPSN-WFNRRSPYSHVNTTQTILAMYAQYVK-LFGGNVG-K-KNEN 352
ALLP---L-LGRQFGLNGH1KFEADSSLTRNDYFT-SNG-DNYSEFNGLFANMKNVADRVSNG---FD-RNALAAYRSQRYDESVAE-NDNFFFGPL-SVLLYGAAATFL-YELFPSYGPE-GTADLTKM-SFFGAVEDLSAPGGWRHVA-EQIPSN-WFNRRSPYSHVNTTQTILAMYAQYVK-LFGGNVG-K-KNEN 352
ALLP---L-LGREPGLNGH1KFEADSSLTRNDYFT-SGG-DNYSEFNGLFANMKNVADRVSNG---FD-RNTLSVYRSQRYDESVAE-NGNFYFGPL-SVLLYGAAATFL-YELFPSYGPE-GTADLTKM-SFFGAVEDLSAPGGWRHVA-EQIPSN-WFNRRSPYSHVNTTQTILAMYAQYVK-LFGGNVG-K-KNEN 352
ATLP---L-LGKQFGLNGH1KFEADSSLTRNDYFT-ANG-DNYSEFNGLFQAQKAVADKVSNG---FD-RNALAAYRSQRYDSDVQENASEFFFGPL-SVLLYGAAATFL-YELFPSYGDK-GVPDIAITM0SFFGAVEDSSAPGGWRHVP-ERIPEN-WFSRVEPYNNPDVTEIIVALYIKYK0LFGGNVG-K-NNED 348
AFSE---L-LGRQGLNANFKFEADSSLTRNDYFL-ADG-DNYSEFNGLFQAQKAVADEVSGK---FD-RNALAKYRSRYDSDVANONPNFFSPY-SLILYGAAAFI-YELFPSHGK-GTPDLETK-SFFGAVEDPSAPGGWRHVP-ERIPEN-YVSRVQPYTVPLAAGEIILAMYLYQYVK-LFGGNVG-T-NNEN 348
ALLP---A-IARQFGLNANFKFEADSSLTRNDYFL-ADG-DNYSEFNGLFQAQKAVADEVSGK---FD-RNALAKYRSRYDSDVANONPNFFSPL-AIILYGAAAFI-YELFPSYGNK-GTPDLETK-TFFGAVEDPSAPGGWRHVP-ERIPEN-WFSRVEPYTVPLAAGEIILAMYLYQYVK-LFGGNVG-T-NNEN 349
ALLP---A-IARQFGLNANFKFEADSSLTRNDYFL-ADG-DNYSEFNGLFQAQKAVADEVSGK---FD-RNALAKYRSRYDSDVANONPNFFSPL-AIILYGAAAFI-YELFPSYGNK-GTPDLETK-TFFGAVEDPSAPGGWRHVP-ERIPEN-WFSRVEPYTVPLAAGEIILAMYLYQYVK-LFGGNVG-T-NNEN 349
ALLP---A-IARQFGLNANFKFEADSSLTRNDYFL-ADG-DNYSEFNGLFQAQKAVADEVSGK---FD-RNALAKYRSRYDSDVANONPNFFSPL-AIILYGAAAFI-YELFPSYGNK-GTPDLETK-TFFGAVEDPSAPGGWRHVP-ERIPEN-WFSRVEPYTVPLAAGEIILAMYLYQYVK-LFGGNVG-T-NNEN 349
ALLP---A-IARQFGLNANFKFEADSSLTRNDYFL-ADG-DNYSEFNGLFQAQKAVADEVSGK---FD-RNALAKYRSRYDSDVANONPNFFSPL-AIILYGAAAFI-YELFPSYGNK-GTPDLETK-TFFGAVEDPSAPGGWRHVP-ERIPEN-WFSRVEPYTVPLAAGEIILAMYLYQYVK-LFGGNVG-T-NNEN 349
AALGALQGL-LGPEGLLDTENTFEADTSLTRNDYFL-ANG-DNYSEFNGLFAMTETVASTSSTDDPLYD-RTGIALYRFQRYQOQSRAE-NEHFFYFGPK-ATHIYGAAASFL-YCAFPSQANN-LKPLKATMM-SFFGAVEFAAGEFAFGFQ-ERFPDN-WFNRETPYTILEIATEIILAQYLAHEV-LFGGNVG-P-DDFD 348

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420 440 460 480 500

GIGELGPSISNSSINGN-----AAGVVCILYQ-IATENTESAIGGG---TLSSQSAQWAAKMLNPIHGGNGT--AAQFGCPLNYNNA----- 391
GIGQYGPSISNSSFNGT-----AAGIACILYQ-FATENAPSSLGGG---TLSSQSAQWAASKLNPIHSGNGT--AAQYSCPIFNNA----- 391
GVGTQGPYISNNTIPGS-----FAGVACILYQ-IATENIPSAIGGGGAANDAIPASSINEMRNTLNPIHTNSSLSGAAAFGCPHVTGTAS----- 394
GFGETGFTTSSSTFNGT---TAAGTACILYQ-IATGSIAGELGGD---VTPAANYAASKLNPLIAGLDELVGTCPLNYSNN----- 432
GIGTSGITTSNSTKAT-----FAGIACILYQ-IITENIEAGGGSN---VPLARLAWVNVNINPIHGLGT--LGSIACPILVTV----- 416
AINTTFGIIQNGTLPDE---VTAKDFVCILYQ-LAVDNVPGTVANEAE---ELPLQVITWVLTQLNPIHQNNG---CPIKIT----- 428
ALSSPFGVIRDGKLPLA---ATASDLLCILYQ-LGTQPVFSSLSVVT---TLPLSLNWSVGLNPIHFKNAG-----CALRPDQTAPIA----- 423
ALN--FGVIRDGKLPDS---ATAGDILCILYQ-LATSQVENTLTGVL---ALPINLVKWSASKLNPIHFDNAG-----GALAPL----- 380
ALPGAIGLADGKLPTE---ATESDLLCILYQ-LGTGVVFASLSTVT---DITGSLNFGVAKLNPIHVRNVG-----CALKPDQTFPGN----- 429
ALGTPFNVIKDGILPSS---AKLECFILYQ-LATSPVFGMLSTVT---DITGSLNDFALAKLPIHFKNTG-----CLVKSQGGSSGGGLIGLLNG 432
ALSTPFDIKNGKLPST---ANLGCFLYQ-LATGVPVSMSTVT---DITGALLDFALTKLNPIHFKNTG-----CPLKSQGGSSGGGLLDGLLNG 432
ALSTPFDIKVDGKLPD---VTAAQATCILYQ-LGVMAVSTLSTVT---DITDAVDFGVGLNPIHFKNAG-----CPIMVS----- 419
ALNTPFGIVRDGRLPDG---VTAKDLMCILYQ-LTVSPLFGVLGPVG---DLTDAVINFAFSKLNPIHFAFNNSG-----CPLRIN----- 419
ALSTPFDIKVDGKLPDE---VTVKLMMCLYQ-LAVSPVGMFGAVT---DITGAVINFAFSKLNPIHFAFNNTG-----CPLKVG----- 420
ALSTPFGIKVDGKLPDE---VTVKDVLCLYQ-LAVSSVGMFGAVT---DIAGAVINFAFSKLNPIHFAFNNTG-----CPLRVG----- 420
ALSTPFDIKVDGKLPDE---VTVKLMMCLYQ-LAVSPVGMFGAVT---DITGAVINFAFSKLNPIHFAFNNTG-----CPLRVG----- 420
ALSTPFGIKVDGKLPDE---VTVKDLMCLYQ-LAVSPVGMFGAVT---DVTGAVINFAFSKLNPIHFAFNNTG-----CPLRVG----- 420
ALSTPFGIKVDGKLPDE---VTVKDLMCLYQ-LAVSPVGMFGAVT---DVTGAVINFAFSKLNPIHFAFNNTG-----CPLRVG----- 420
ALGA-FGIISNGQGGNGSTISANDVACILYQVFAFEAVPDSVSGLL---TLPIELNWIITKILPLSQGLG-----CPIATNS----- 423

Protein alignment for Figure 3C. The image shows a multiple sequence alignment of various protein sequences. The sequences are labeled on the left with identifiers such as Zasce60808, Cerzm65622, Zymtr43851, Lopma596116, Pyrtr157321, Curlu123898, Bipma1034928, Bipso218368, Bipor28457, Bipvi84790, Bipze101753, Pengl219443, Aspve124547, Aspwe173916, Penca5982, Penfe431082, Penbi454008, Penbr34900, Penca423940, PENCH69724, Colgr10528, Colgl11931734, Colfi1350467, Melva566401, Psean79378, and Psehu1241. The alignment is presented in a grid format with columns representing amino acid positions. Asterisks (*) are placed above the alignment to indicate conserved regions. The alignment is split into two main sections, with the first section covering positions 1-200 and the second section covering positions 220-400.

Continuation of the protein alignment for Figure 3C. This section shows the alignment for amino acid positions 220 to 400. The same sequence identifiers as in the first section are used on the left. The alignment continues in a grid format, with asterisks (*) marking conserved regions. The alignment is split into two main sections, with the first section covering positions 220-300 and the second section covering positions 320-400.

Continuation of the protein alignment for Figure 3C. This section shows the alignment for amino acid positions 420 to 480. The same sequence identifiers as in the previous sections are used on the left. The alignment continues in a grid format, with asterisks (*) marking conserved regions. The alignment is split into two main sections, with the first section covering positions 420-440 and the second section covering positions 460-480.



Protein alignment for Figure 3D

	*	20	*	40	*	60	*	80	*	100	*	120	*	140	*	160	*	180	*	200																																																																																																																																																																																				
Fulfu186212	M	S	T	G	Q	S	R	R	N	G	K	A	A	S	C	E	P	C	R	K	G	K	I	R	C	D	H	Q	R	P	T	C	G	R	C	Q	R	R	G	L	T	S	Q	C	F	Y	H	F	A	P	L	T	K	P	R	G	T	G	S	G	F	A	G	A	H	V	F	N	I	E	S	N	A	R	F	A	I	T	A	E	Q	R	N	L	S	H	G	L	Q	D	V	R	E	R	A	Q	A	P	D	G	S	S	H	T	S	Q	T	Y	G	F	P	W	P	S	S	W	V	A	S	P	E	T	H	G	Q	Q	S	L	Y	W	N	V	P	R	A	K	D	N	E	A	E	D	K	R	L	P	V	I	K	E	V	I	M	L	L	K	H	F	R	F	M	Q	I	L	V	E	E	Y	A	T	H	A	Q	A	S	L	V	P	Q	P	I	A	M	S	F	M	D	S	L	A	D	L	T	T	A	Y	A	S	A	
Dotse147401	M	S	A	G	Q	S	R	R	N	G	K	A	A	S	C	E	P	C	R	R	G	K	I	R	C	D	H	Q	R	P	T	C	G	R	C	Q	R	R	N	L	T	A	Q	C	F	Y	H	F	A	P	L	T	K	P	R	G	S	G	S	A	A	A	G	S	H	A	F	N	V	Q	P	A	P	R	S	E	P	V	A	D	Q	S	R	A	P	G	A	L	P	E	I	R	D	R	T	R	F	P	D	G	H	N	-	T	G	Q	T	Y	G	F	P	W	P	S	S	W	T	A	S	P	G	T	H	G	Q	Q	S	L	Y	W	S	V	P	R	A	R	D	A	E	D	Q	R	L	P	L	I	K	E	V	L	T	L	L	K	H	F	R	F	M	Q	I	L	I	E	E	Y	A	T	H	A	Q	A	S	L	V	P	Q	P	I	S	M	S	F	M	D	S	L	A	D	L	I	T	T	Y	A	S	A			
Fulfu186212	D	D	A	N	D	D	G	F	T	Q	M	A	K	N	V	L	R	A	T	S	A	P	I	E	T	P	D	D	I	A	G	F	L	A	2	M	Y	S	G	D	N	M	R	L	E	T	I	G	L	L	Y	T	T	S	A	T	A	C	L	L	G	L	A	R	D	D	D	R	H	T	E	F	V	E	A	M	Y	R	G	S	T	T	C	L	H	2	L	V	R	D	I	S	P	E	I	N	D	V	M	L	W	L	S	F	E	N	M	R	L	T	H	T	E	G	D	S	1	S	P	I	V	W	R	K	L	G	D	V	T	T	D	I	F	A	A	G	F	H	R	E	A	K	N	T	S	K	T	P	F	F	L	A	E	C	R	R	K	A	F	V	A	A	Y	Q	L	D	K	F	I	A	T	L	L	D	L	P	P	R	I	L	R	R	Y	S	D	C	K	M	P	L	E	L	T	D	E	Q	E	L		
Dotse147401	D	D	A	N	D	D	G	F	S	Q	M	V	R	S	V	F	K	A	T	S	A	P	I	E	T	P	D	D	I	A	G	F	L	A	2	M	Y	S	G	E	N	M	R	L	E	T	I	G	L	L	Y	T	M	S	A	T	A	C	H	L	G	L	A	R	D	D	D	K	H	T	E	F	I	E	A	M	Y	R	G	S	T	S	C	L	R	2	L	V	R	D	I	S	P	E	I	N	D	V	M	L	W	L	S	F	E	N	M	R	L	T	H	T	E	G	D	S	1	S	P	I	V	W	R	L	G	N	V	T	T	D	I	F	A	A	G	F	H	R	E	A	K	N	T	S	K	T	P	F	F	L	A	E	C	R	R	K	A	F	V	A	A	Y	Q	L	D	K	F	I	A	T	L	L	D	L	P	P	R	I	L	R	R	Y	S	D	C	K	M	P	L	E	L	T	D	E	Q	I				
Fulfu186212	L	S	D	A	G	E	I	A	Q	A	R	A	K	L	S	P	D	G	W	S	P	D	K	Q	Y	I	F	A	T	W	Q	R	V	R	F	Q	L	G	M	L	R	E	D	I	L	E	Y	P	F	L	P	P	T	L	E	N	N	A	A	L	2	K	N	L	A	R	R	C	H	Q	T	Y	D	S	L	F	S	H	L	K	Y	N	P	D	S	W	N	A	I	P	P	F	A	C	I	M	L	T	V	M	R	L	N	Y	L	Q	S	C	F	Q	I	Q	R	L	L	E	D	T	E	P	S	A	W	F	E	L	L	R	I	S	A	E	T	V	A	T	V	L	Q	I	G	N	S	L	N	K	A	I	F	I	R	H	D	F	P	Y	I	0	V	L	A	Y	G	L	P	S	A	V	M	L	A	Y	A	L	Q	S	T	A	R	G	N	K	R	Q	A	L	P	S	D	L	S	R	A	S	L	I	R	H	L	S
Dotse147401	L	S	D	P	E	A	I	A	Q	A	R	A	R	L	S	P	D	G	W	S	P	D	K	Q	Y	I	F	A	T	W	Q	R	V	R	F	Q	L	G	M	L	R	E	D	I	L	E	Y	P	F	L	P	P	T	L	E	N	N	A	A	L	2	K	N	L	A	Q	R	C	H	Q	T	Y	D	S	L	F	A	H	L	K	Y	N	P	D	S	W	N	A	I	P	P	F	A	C	I	M	L	T	V	M	R	L	N	Y	L	Q	S	C	F	Q	I	Q	R	L	L	Q	D	T	E	P	S	A	W	S	E	L	L	R	V	S	A	E	T	V	A	T	V	L	Q	I	G	N	S	L	N	K	A	I	F	I	R	H	D	F	P	Y	I	0	V	V	A	Y	G	L	P	S	A	V	M	L	A	Y	A	L	Q	S	T	A	R	G	N	K	R	Q	A	L	P	S	D	L	S	R	A	S	L	I	R	H	I	A
Fulfu186212	V	F	V	S	Q	L	E	S	I	C	A	F	S	E	R	N	Y	T	I	C	I	Q	A	S	K	A	I	T	R	A	L	D	E	V	L	E	M	F	A	T	F	A	A	M	S	N	E	A	P	Q	T	P	V	S	A	N	E	N	S	T	A	G	P	L	A	T	F	A	L	S	A	S	Q	P	V	M	L	D	T	A	M	N	V	C	A	D	L	I	S	G	D	L	L	D	G	F	D	L	S	S	W	V	K	N	I	D	W	T	G	T	G	G	E	W	S	T	F	--																																																																																		
Dotse147401	V	F	V	S	H	L	E	S	I	S	D	F	I	E	R	N	N	T	I	C	I	Q	A	S	K	A	I	T	R	A	L	D	E	V	L	E	M	F	A	T	F	A	A	A	-	A	S	I	A	P	Q	T	A	G	T	A	N	D	H	S	T	G	P	L	A	T	F	A	L	S	A	S	Q	P	I	L	P	D	G	N	M	N	V	C	A	D	L	E	S	G	D	L	L	D	G	F	D	L	S	S	W	V	K	N	I	D	W	T	G	T	G	G	E	W	S	T	F	--																																																																																		