

```

          10         20         30         40         50
...|...|...|...|...|...|...|...|...|...|
Fv EWG40990.1  MCRETITITIAQCAPEVSPVLAFYCAKLHLVAKDRIICDATKGKCICFFGSC 50
Ff KLP03525.1  MCSETITITVAQCAPKVSPVLAFYCAKLHLVAKERIVCEAAKGKCICFFFGSC 50
Fo EWZ36701.1  MCRETITITIAQCAPEVAPVLAFYCAKLHLVAKDRTVCDAARGKCICFFFGSC 50
Fg ESU17197.1  MCVETITITIALCAPQSAPRLSFTCGNLHLVAENHVVCDSAVGNCICYFGTC 50
Fl KPA39364.1  MCVETITITIALCAPESSPHLSFTCGKLHLVAGRRTVCDKASGRCVCYFFGTC 50
Nh XP_003053980.1  MCHEVITITIALCAPTKAPSLSFTCGKLHMIAQRHVCDRARGSCVCFFFGTC 50
Tv XP_013952680.1  MCKEFLTITIAICAPQKAPSMSSFTCGQLHLVAERRQVCDKATGACLCFVGTC 50
Ac KFH42786.1  MCSEDIAVALCAPVERRALSYTCSKLHLIASNRHVCFRAKGNCVCFFGTC 50
Th KKO99655.1  MCKEYTTTITIAICAPQKAPSMSSFTCGQLHQVVDRRQVCDKATGSCICFVGTC 50

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          60         70         80         90        100
...|...|...|...|...|...|...|...|...|...|
Fv EWG40990.1  GTIEREIPTKGINLGEVVKARCAECTPREHRVRD-IPAQEILESVLLR-S 98
Ff KLP03525.1  GAIDREIPTKGINLSDIVKARCAECTPREHRVGNGIPAQQILESVLLR-S 99
Fo EWZ36701.1  GTIDREIPTKGINLGDVVKVRCAECTPREHRVGNGLKAQQILESVLLR-S 99
Fg ESU17197.1  GKVIREVPTGGIDFSAISKVRCTTCTAREDEVGDARKDREILESVLLGRP 100
Fl KPA39364.1  GNAGRAALTDGIDFSAISKVRCTSCTAREDAVGDRRKNQEVLESVLLDPS 100
Nh XP_003053980.1  GTVEKNASTSGIDLSAIEKIRCAECTTREDNVGDRRDAKQIESPLLQRI 100
Tv XP_013952680.1  GVLESVPSTQGLRMSSVKSIRCAACTSREEEVGDRRTNELIESPLLTRT 100
Ac KFH42786.1  GTVERTFDS-VFDLTDLPKVRCSVCTVREDDVGHSSAAREILESPVPTRK 99
Th KKO99655.1  GVLETIPSTLAIPIASLKSIRCVACTTREEIGDRRSNELIDSPLLTRA 100

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          110        120        130        140        150
...|...|...|...|...|...|...|...|...|...|
Fv EWG40990.1  TDGQNG--WEERSKLLSELWLNKTACPYHVDTSAEP--VAPVINITES 142
Ff KLP03525.1  ADAQNG--WEERSKLVSELWLNKTACPYHVDTSAEPATPVAEVINITEH 146
Fo EWZ36701.1  VDARNG--WEERSKLISELWLNKPACPYHVETSTEPAGPITGAINITQH 146
Fg ESU17197.1  ATNDAD--WDQTSKRLQQLWQKSACPYHVQGSVRK--AKATVNKPAK 144
Fl KPA39364.1  AVHYVD--VDRKVKLLSQLWHQKSDCPYHAEG----- 130
Nh XP_003053980.1  PIEPTDDFVNKKHSAMLHELWGGARTCPFHLQPDRPR----- 137
Tv XP_013952680.1  AIKSSEQ--KIKFDEIIKDLWNGKEDCPYHVLSTVRE----- 135
Ac KFH42786.1  AIPEEG--LERYMRTLKSMWGSMDHCPYHVTEHENQ-----EMAAH 138
Th KKO99655.1  AVKSTED--MQHFKAIIKSLWNGEDECPYHTMLTTRE----- 135

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          160        170        180        190        200
...|...|...|...|...|...|...|...|...|...|
Fv EWG40990.1  IHLDTEVGHYGTGLSAESAGPTDSTPESAL-----ELKPAFEATVGKD 185
Ff KLP03525.1  IHLDTEVGHTGTGLSAESVVPTDPASESP-----ELKPGFEAAVQKD 188
Fo EWZ36701.1  VHFDADAGRSGVGLTAELAGPTKPTHEHAFDPTTESAELKPGFEAAVEKN 196
Fg ESU17197.1  EQVQAQVDIKSAVPSAPSKASFGKVVIDKD-----DLHQSATTD 183
Fl KPA39364.1  -----PVIDSASAEASFDEVSIEKQ-----GPVQSATTD 159
Nh XP_003053980.1  ---QPSASTVNVQTKRFDERPVTPQTNDES-----VTKSHSMSRD 174
Tv XP_013952680.1  ---GSNSFPVTSKNLSDMEMDKEEDKDG-----VEKSLTAS 168
Ac KFH42786.1  HQGDAETNENESEFYDQHDNGSRQPNDDGD-----VDTKPRNDNENE 180
Th KKO99655.1  ---TSEDTPVIPKLVSVADMNTNESIS-----KEVPIAD 166

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          210        220        230        240        250
...|...|...|...|...|...|...|...|...|...|
Fv EWG40990.1  VGEFSSSDNAAMKDASSSSVGTVFTEPIFTDSLVAEPASTLADEWTANAG 235
Ff KLP03525.1  FGDFSSSDNAAMKDASSSLVG-----PVFTDSFVAEPASSLVDEWT---- 229
Fo EWZ36701.1  FSGFSSSEHAALKDASSPVE-----PIFTDSLVAEPASSPADEWT---- 237
Fg ESU17197.1  ASEHSEADSASAVDPWT-----GAPVIAEPVTAEPAGFDSPSVK---- 222
Fl KPA39364.1  VFEHNEADSASAVDAWT-----SAPVSVNTDITEIADFDSPSDK---- 198
Nh XP_003053980.1  SVDKGWTSQAATNNSSKS-----KLSRKSSASPTGIAS---- 207
Tv XP_013952680.1  SGEDAISDNVSEASSNAT-----HGSNGSLNSNAS----- 198

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Ac KFH42786.1      TSEPPKEESPRTYDPVKG-----ELRTDDENKASETTNHNKCP---- 218
Th KKO99655.1     VHEKVADDNVSEASSNAT-----HGSNGSLASNLS----- 196

          260          270          280          290          300
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Fv EWG40990.1     TVNTADEWNTNTAPTGEQDGNANNHASDSGAKNILDPEVGIISTSRWAPG 285
Ff KLP03525.1     -----TNTAPGGGGHGDNTENHSSDSGVKDILDPEEVGIISTSRWAPG 270
Fo EWZ36701.1     -----TNTAPTGEQRDNADNHGFDSGVKNILDPEVGIISTSRWAPG 278
Fg ESU17197.1     -----DDVTTVIAND-----NDGGTSVKTGSDAGKGGHNGLEG 255
Fl KPA39364.1     -----DHASIVGDGNDVTTGFINDDGASVKAGSDTDKGVQNGLEG 239
Nh XP_003053980.1 -----VDSAVGLGSSRWAPKNLEEEAARSVKNQSPPTQKRPSPLQK 248
Tv XP_013952680.1 -----QESKKKDTID--LGRKVG LQASIWANAPDKSPKGIKHTSSP 237
Ac KFH42786.1     -----QNNNVVNGDDGIEDASDEVEAASGAEDSPKTSDSASRPMTG 259
Th KKO99655.1     -----QESSKKKNEDSGLGRKVG LQASIWANAPAKTPERKKHNGSP 237

          310          320          330          340          350
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
Fv EWG40990.1     NSPT-ASKPTNPVAVDFKEPESGEEHNQAQEQAQTPVVAPSRRRAVNFVSYNP 334
Ff KLP03525.1     NSPTNSTKPTKPAVDFKDNESGEER----EKVQTPVVAVSRRRAVNFVSYNP 316
Fo EWZ36701.1     NSPSNSSQPAELAFEVRDNEKQEQ-----EQTPVVAVSRRRAVNFVSYDP 322
Fg ESU17197.1     DVDTKLGHDA PKSID-----GATPVSRRAVNFVAFSA 286
Fl KPA39364.1     -----GTTLVTRRAVNFVSYSA 255
Nh XP_003053980.1 QSSP-----PSQKRIVPAAAPVVFVADP 270
Tv XP_013952680.1 QVQS-----PVKRQKAATPQG----- 253
Ac KFH42786.1     IEASQWAPRNEAPNAD-----LHVQAPADSTPPSPAPKAI 294
Th KKO99655.1     KSQS-----PVKRQKPVVPPQGRKPAV 258

          360          370
.....|.....|.....|.....|.....|.....|
Fv EWG40990.1     SNAEKLME TAEIIFANLKKAF LMGKA- 359
Ff KLP03525.1     DNAEKLLE TAE MFANVKKAF LMGKA- 341
Fo EWZ36701.1     NNAEKLLE TAEKFANVK- AFLMAKA- 346
Fg ESU17197.1     EAADKLRD TTAKFASL KSSFLMGKPI 312
Fl KPA39364.1     EAADKLRD ATSKFASL KSGFLMGKAT 281
Nh XP_003053980.1 GNASKVRH ATKKMANMKAF LSGT PMPF 296
Tv XP_013952680.1 ---PKTRMNL PQIAAKN FLREGSA- 275
Ac KFH42786.1     AASRPPTL TAEKIASMK EFLRMN--- 317
Th KKO99655.1     ALVKKTKF NL PQIAAKS FLKATMV- 283

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Figure S4 Sequence alignment of putative Fveg_03194 homologs A BLASTP search of NCBI's non-redundant protein database was performed with the sequence of *F. verticillioides* Fveg_03194. The sequences of eight putative homologs were downloaded, imported into Bioedit 7.2.5, and aligned with Clustal W. Columns were shaded according to the BLOSUM62 similarity matrix. Each sequence is specified by its accession number: EWG40990.1 (*Fveg_03194*), *F. verticillioides*; KLP03525.1, *F. fujikuroi*; EWZ36701.1, *F. oxysporum*; ESU17197.1, *F. graminearum*; KPA39364.1, *F. langsethiae*; XP_003053980.1, *Nectria haematococca*; XP_013952680.1, *Trichoderma virens*; KFH42786.1, *Acremonium chrysogenum*; KKO99655.1, *Trichoderma harzianum*.