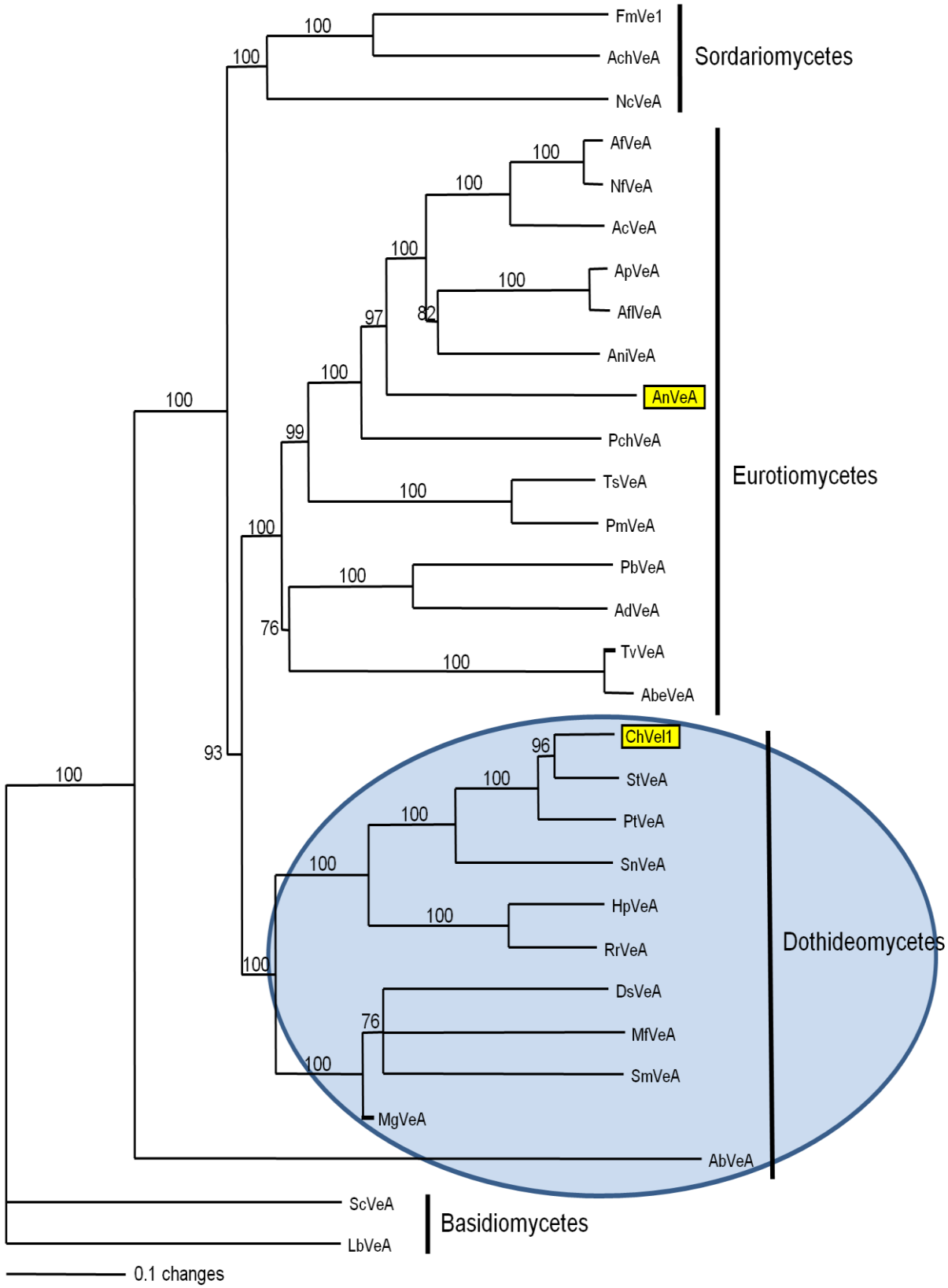
A


FmVe1
AchVeA
NcVeA
Sordariomycetes
AfVeA
NfVeA
AcVeA
ApVeA
AflVeA
AniVeA
AnVeA
PchVeA
TsVeA
PmVeA
PbVeA
AdVeA
TvVeA
AbeVeA
Eurotiomycetes
ChVel1
StVeA
PtVeA
SnVeA
HpVeA
RrVeA
DsVeA
MfVeA
SmVeA
MgVeA
AbVeA
Dothideomycetes
ScVeA
LbVeA
Basidiomycetes
0.1 changes

B

```
AfVeA   MATRPPLMPPANET--ESSVSRISREGKKITYKLSVMQQPERARACGAGAKSSADRRPVD 58
AnVeA   MATLAAPPPPLGESGNSNSVSRITREGKKITYKLNIMQQPKRARACGQGSKSHTDRRPVD 60
ChVel1  MSNIVVS----NET--KSQSVRTTKDGRQIRYNLQVIQQPERARACGSGAKSSADRRPVD 54
        *:.        .*:  ...  * :::*::* *:*.::***:****** *:** :******

AfVeA   PPPVVELRIFESDPNDDLHKTDITFAYNANFFLFATLETARPMAQGRLTGPP--TCPVLT 116
AnVeA   PPPVIELNIFESDPHDDSNKTDITFVYNANFFLFATLEPERPIATGKLMTNQ--GSPVLT 118
ChVel1  PPPIVELRVFEND-------QEITFAYNANFFLHASLENARTIAPGRAPSTAGPSFPVLT 107
        ***::**.:**.*        :***.*******.*:**  *.:* *:         ****

AfVeA   GVPVAGVAYLDRPQQAGYFIFPDLSVRHEGRYRLSFHLYEEIKDIKDADKDT-PMPDLNS 175
AnVeA   GVPVAGVAYLDKPNRAGYFIFPDLSVRNEGSYRFSFHLFEQIKDPKDATEGTQPMP---- 174
ChVel1  GTPVAGMAYLDRPTPAGYFIFPDLSVRHEGKYRLSFALFENLAEVKDLDPED-------- 159
        *.****:****:*  ************:** **:** *:*:: : **

AfVeA   STNLTKPSAPKAHLNFRLEVKSVPFTVYSAKKFPGLATSTSLSRIIAEQGCRVRIRRDVR 235
AnVeA   SPVPGKLSSPQEFLEFRLEVISNPFIVYSAKKFPGLTTSTPISRMIAEQGCRVRIRRDVR 234
ChVel1  ---PDVIYDGNHFVTHRCEVKSAPFTVFSAKKFPGLSESTALSRMVAEQGCRVRIRRDVR 216
                  : .: .* ** * ** *:********: **.:**::**************

AfVeA   MRRRGEKRTDDYDFDDERAFATR-SDRYTTPDMYAAN--SAERARSTSISTTADTSFPYG 292
AnVeA   MRRRGDKRTEDYDYDNERGYNNRRPDQYAGSDAYAN---APERPRSTSISTNMD---PY- 287
ChVel1  MRRRENKSSKEWDEYDEEGGGYDRARGTATPDNYGQAPNAPLGDRPRSLSSASN----PA 272
        **** :* :.::*  :*..     .   : .* *.    :.   *. *:*:  :

AfVeA   SDAQRRPSAGDYG--FQGAQPYQR---SMPAASAAPAPAPV------------------ 328
AnVeA   SYPSRRPSAVEYG--QPIAQPYQRPMASTPAPSSTPIPAPIPMPGPVALPPSTPSPA-SA 344
ChVel1  LAPPRRPSIEEMGHGYSASNGYQQQMPPPQTPAYAQMPSYGSNQPQYSQQYQTPQPAPMM 332
          . ****  : *     :: **:   .  :.: :  *:

AfVeA   HSPATS---------AQTSSYQSHLSFG---ATQSQYPAPQLPPTP-QSATPTNT----Y 371
AnVeA   HAPAPPSVPLAAPPPLHTPSYQSHLSFG---ATQTQYPAPQLSHIPQQTTTPTHP----Y 397
ChVel1  QPPQPPQHSTPYSQHSQHSSYSSQHQAQPPVPMNQQYGYSNYQQQPQQPQSQSQPQYDHA 392
        :.* ..          : .**.*: .     . : **  .:    * *. : ::.

AfVeA   SPHPSYSHSRNPSNGTEYDATSSGYPYPQPRLPADRPSYSKAALPPLRLEPPKAPNMQTS 431
AnVeA   SPRSSISHSRNQS-ISEYEP-SMGYPGSQTRLSAERPSYGQPSQTTS--LPPLRHSLEPS 453
ChVel1  APPRQEQMSSDYAHPSDYRRSSITQSPAQQYTASSHPVQPYHPMDQYGRSQQMSQPLHSS 452
        :*  . . * : :  ::*   *   . .*   .:.:*     .             :..*

AfVeA   TDSRSSDANAYPTLS--QPPVPRAPTPANHVTSLPPLKVLSGEYSHPSQPNAQSPHHDLG 489
AnVeA   VNSRSK------------------TPSNMITSLPPIQSLSELPSTTSQPSSAIGSSPAN 494
ChVel1  PQSYASSAPSHQSLPSLRPIVADKLEPVSPSYQSPPTSMSAAISVNSDGSNQHYALPKFN 512
         :* :.                    * .   . ** .  :     .. ..        .

AfVeA   SGKRLLWETNHTLSKRSHEETFGSDERPLHNGMRPDMDQYPSMGRKQPDYGRLPFYTDSR 549
AnVeA   EPGPRLWETNSMLSKRTYEESFGHDDRPLYNGMRPDSESYPGGMQRRPSYERSSLLDGP- 553
ChVel1  PQTQGLPPMSATSNKRSFSSTF--DSRHLNERMVAGSRPQPSGAGYSYDPGSPDMEEPMD 570
            *   .   .**:...:*  *.* * : * ..    *.      .     :

AfVeA   -DEMAYKRANGRMVMKILPALP- 570
AnVeA   -DQMAYKRANGRMVSKPATMR-- 573
ChVel1  RAAMSYRRADGTQRQRHVPEVGS 593
           *:*:**:*    :  .
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