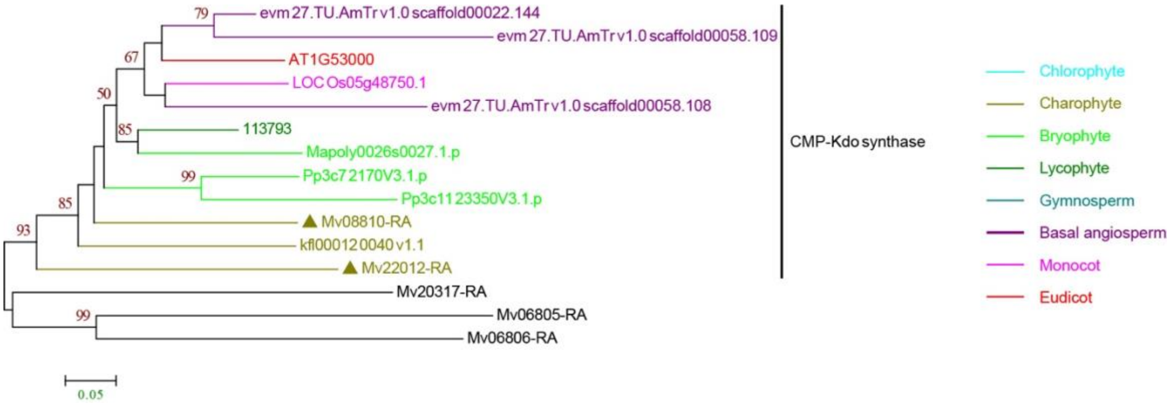
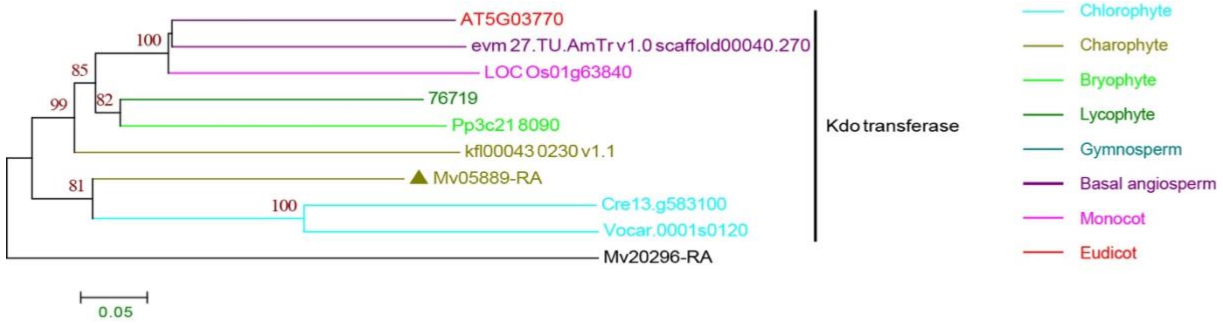
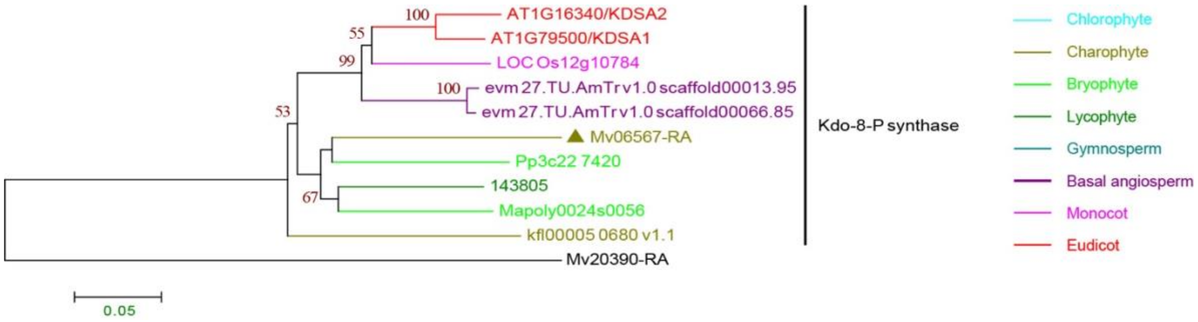
Data S1. Phylogenetic trees.



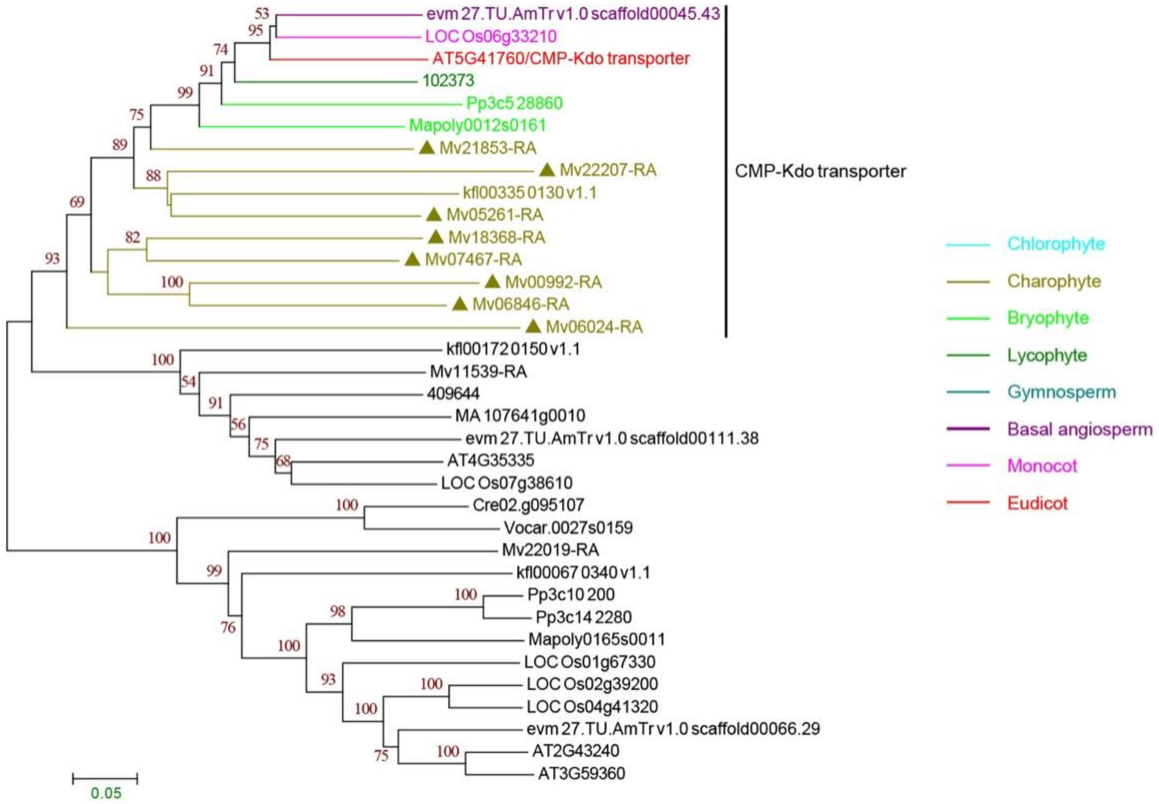
Data S1A. Phylogenetic relationships of CMP-Kdo synthetase proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequences were highlighted by triangles. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



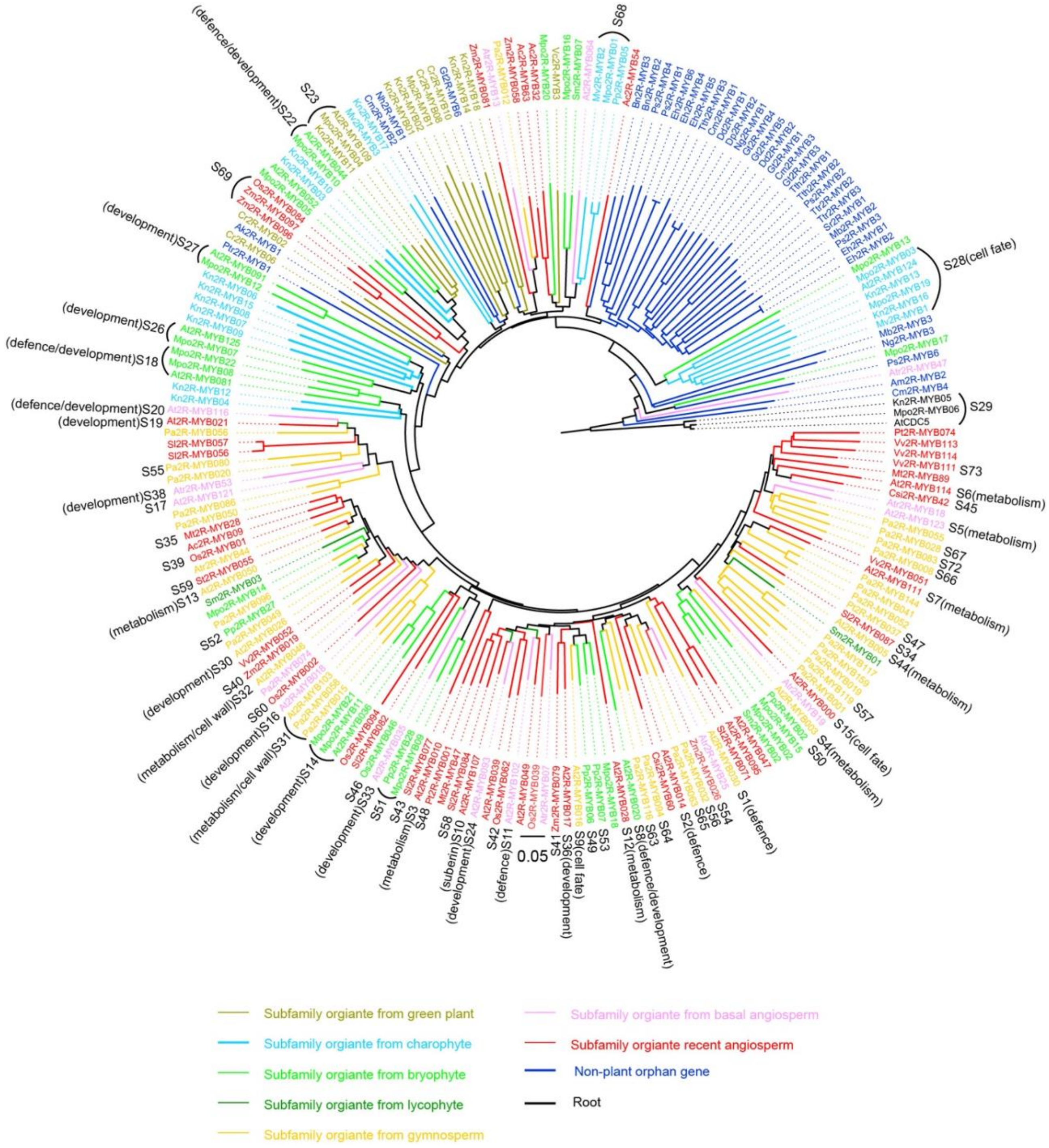
Data S1B. Phylogenetic relationships of Kdo transferase proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequences were highlighted by triangles. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



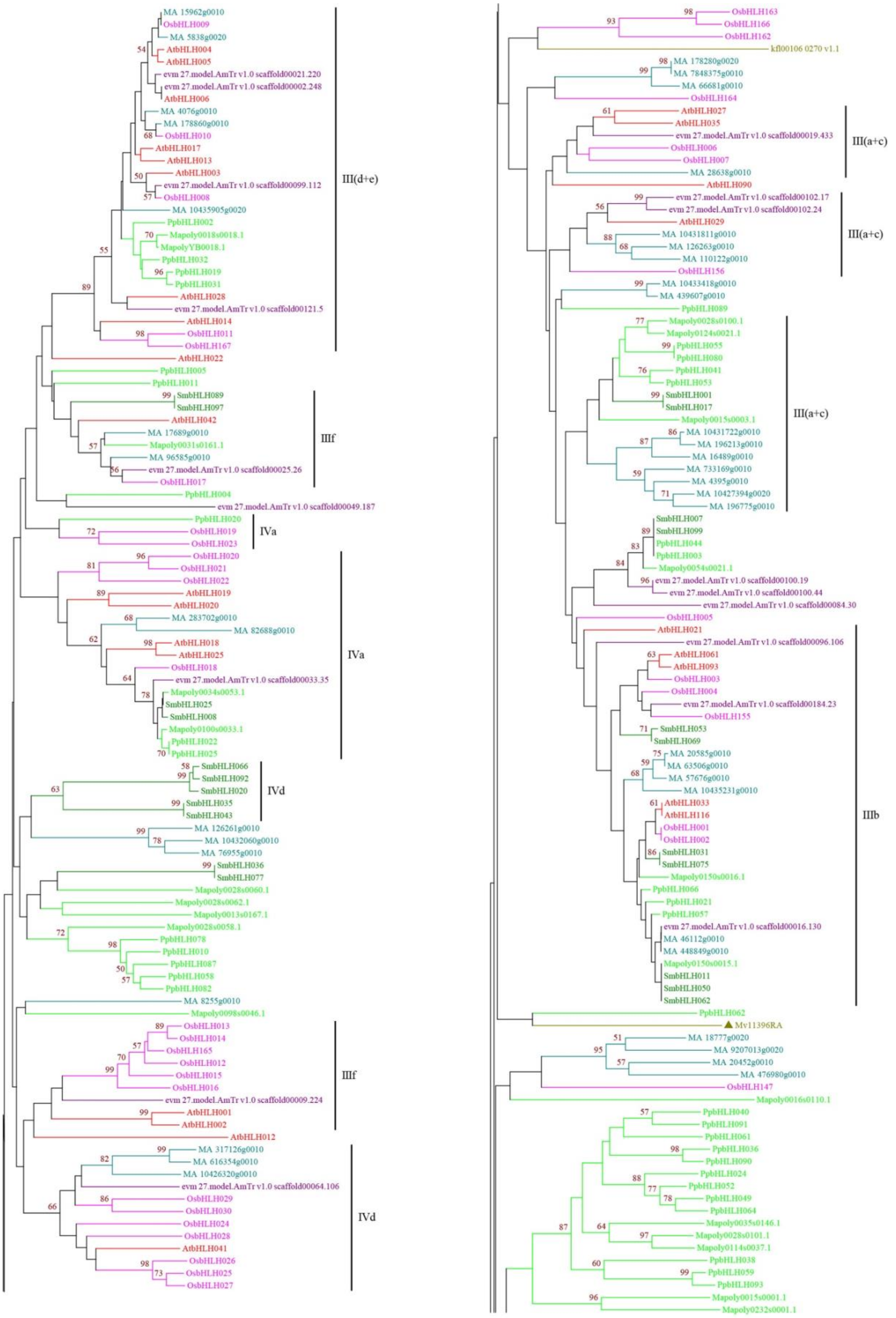
Data S1C. Phylogenetic relationships of Kdo-8-phosphate (Kdo-8-p) synthase proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequences were highlighted by triangles. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



Data S1D. Phylogenetic relationships of CMP-Kdo transporter proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequences were highlighted by triangles. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



Data S1E. Phylogenetic relationships of R2R3-MYB TFs. The R2R3-MYB neighbor-joining (NJ) phylogenetic tree includes representative sequences from previously identified 73 subfamilies and 95 non-plant orphan genes based on 50 eukaryotes,[1] and all R2R3-MYB proteins from *K. nitens*, *M. polymorpha*, and *M. viride*. The subfamily names and related functions were indicated. The three shows that *M. viride* proteins (Mv2R-MYB1-3) belong to the subfamilies of S28, S68 and one yet-to-be defined subfamily, respectively.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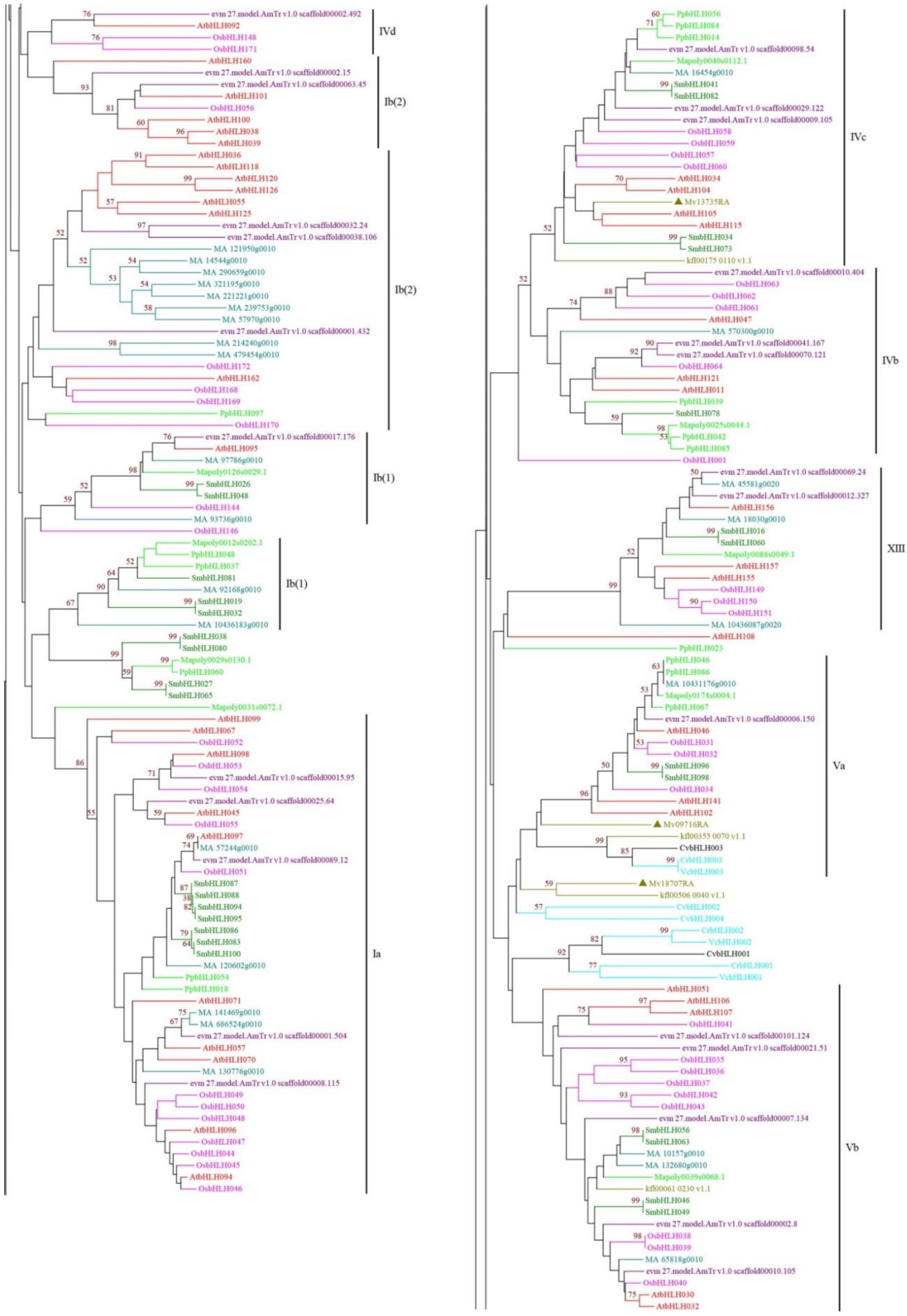
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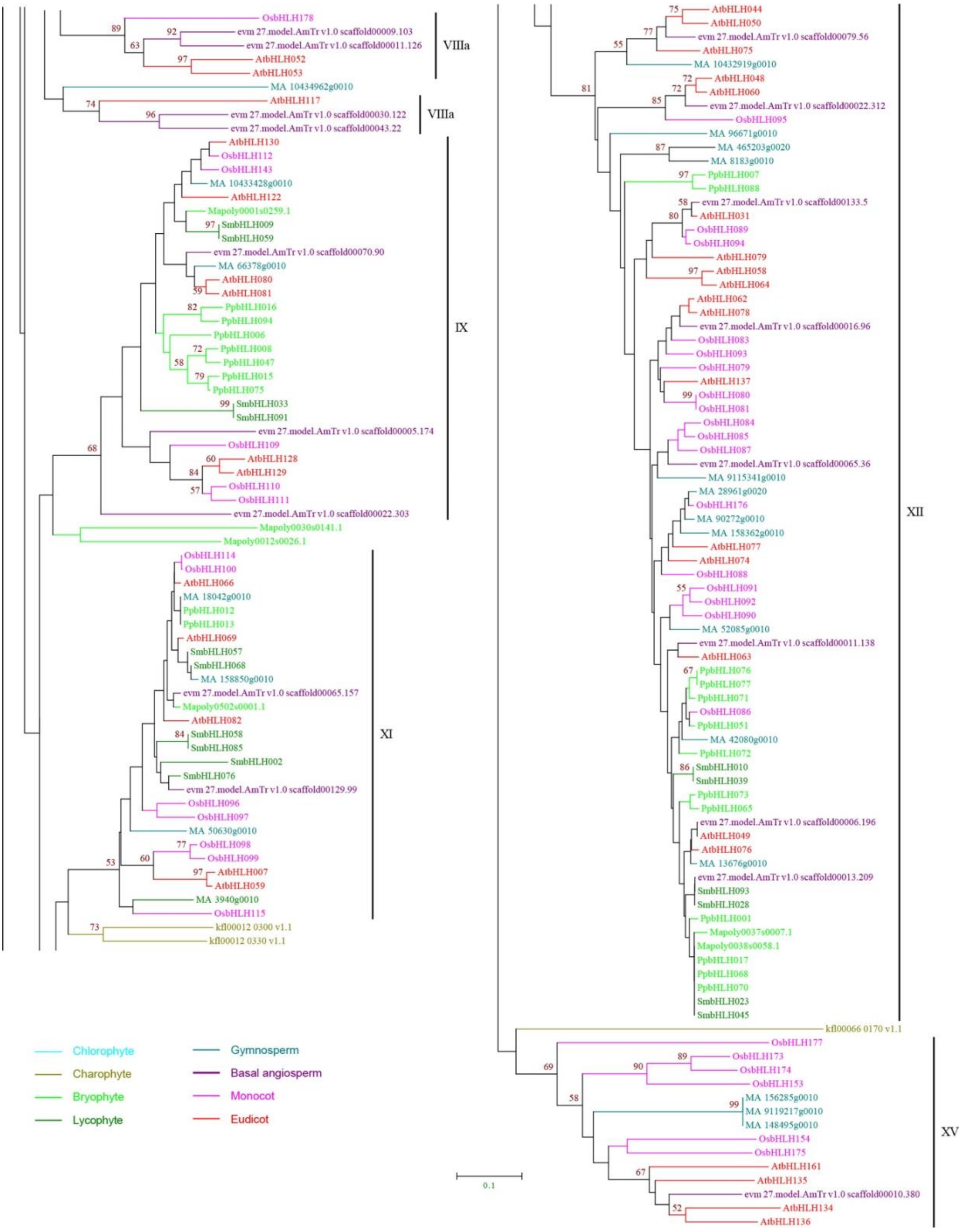
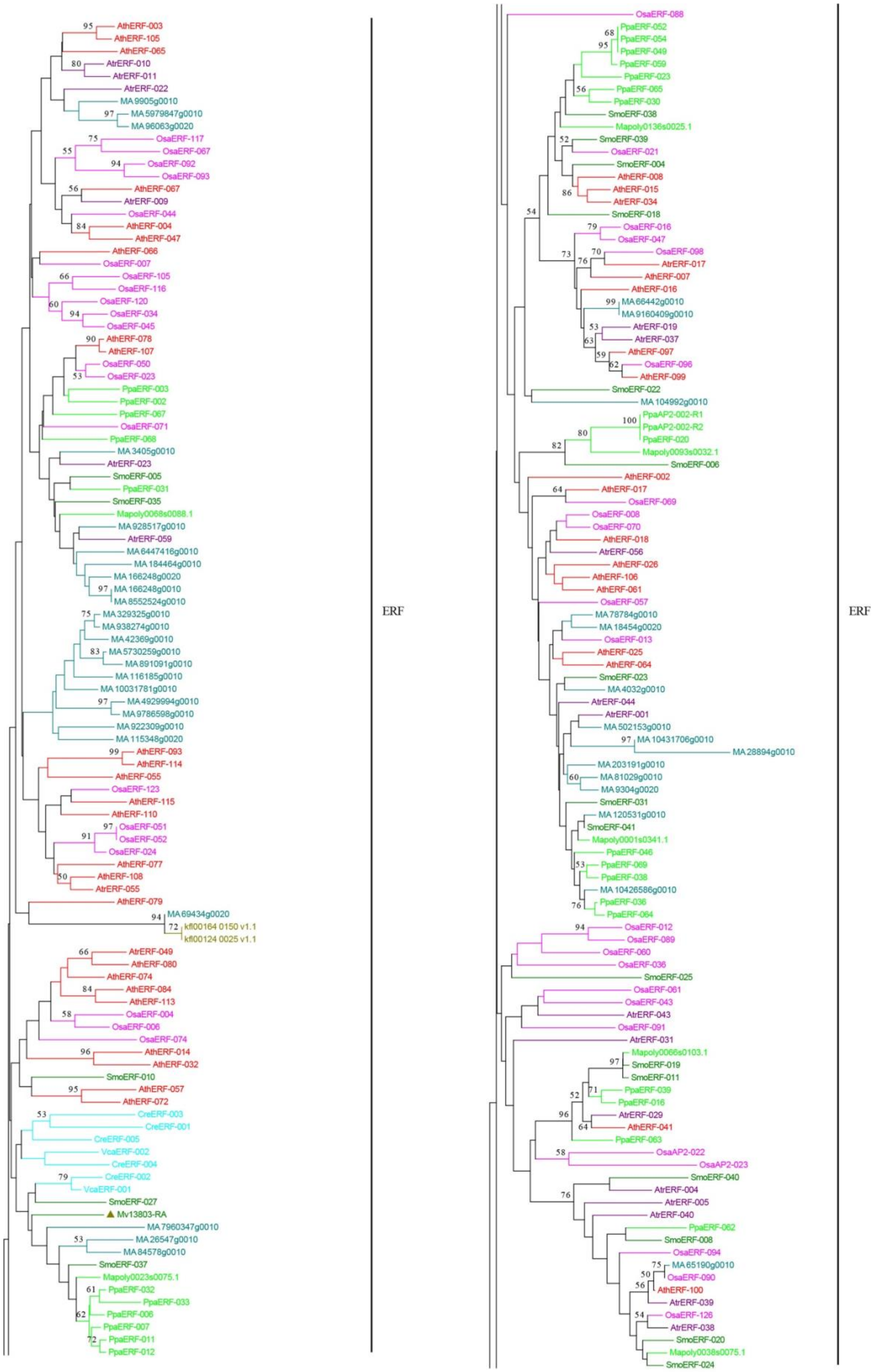


Data S1F. Phylogenetic relationships of basic helix-loop-helix (bHLH) TFs from *M. viride* and 10 evolutionarily representative species. The *M. viride* sequences were highlighted by triangles. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates. The classification/clade was named according to a previous study.[2]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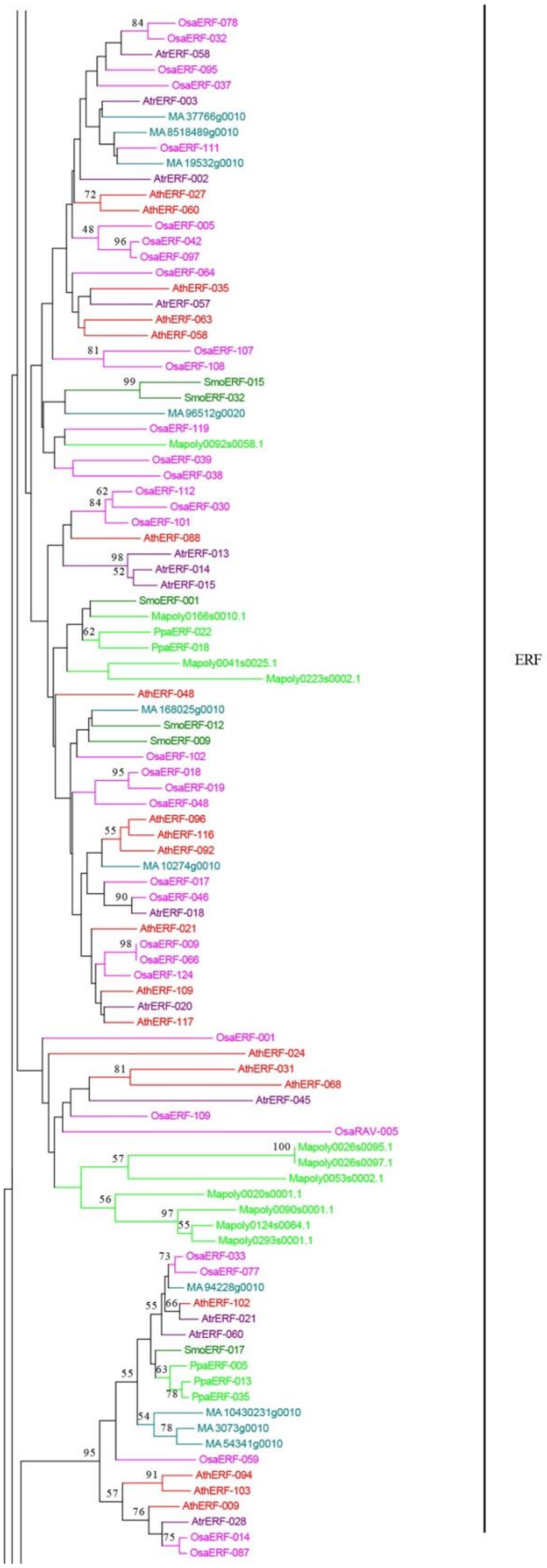
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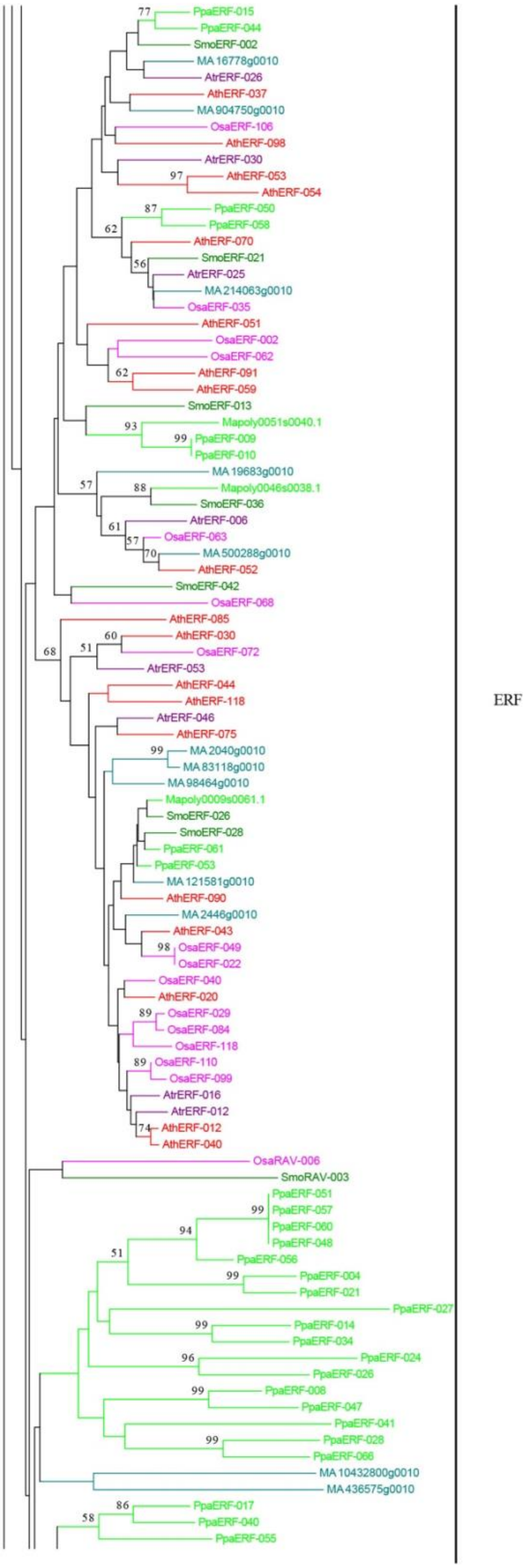
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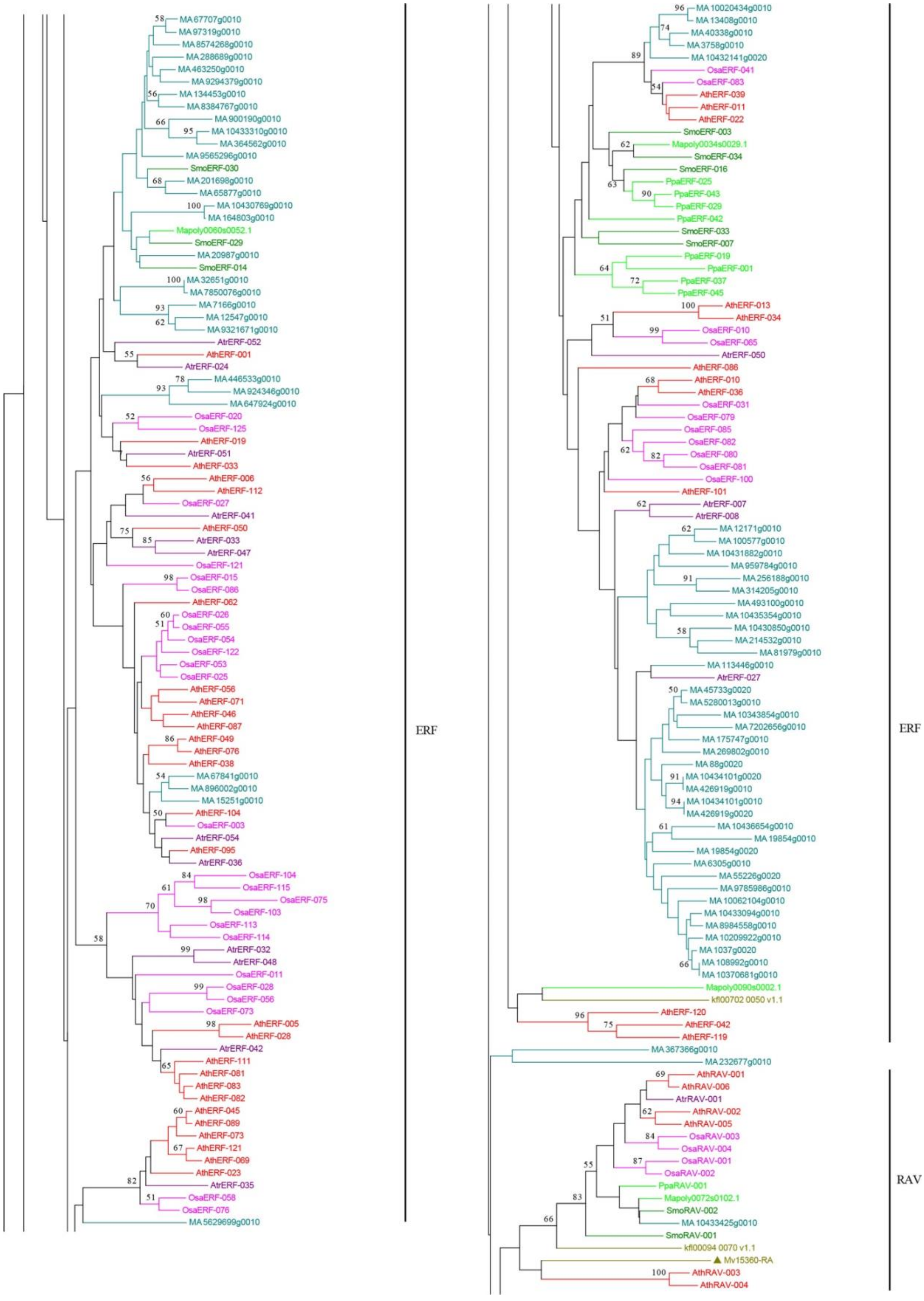
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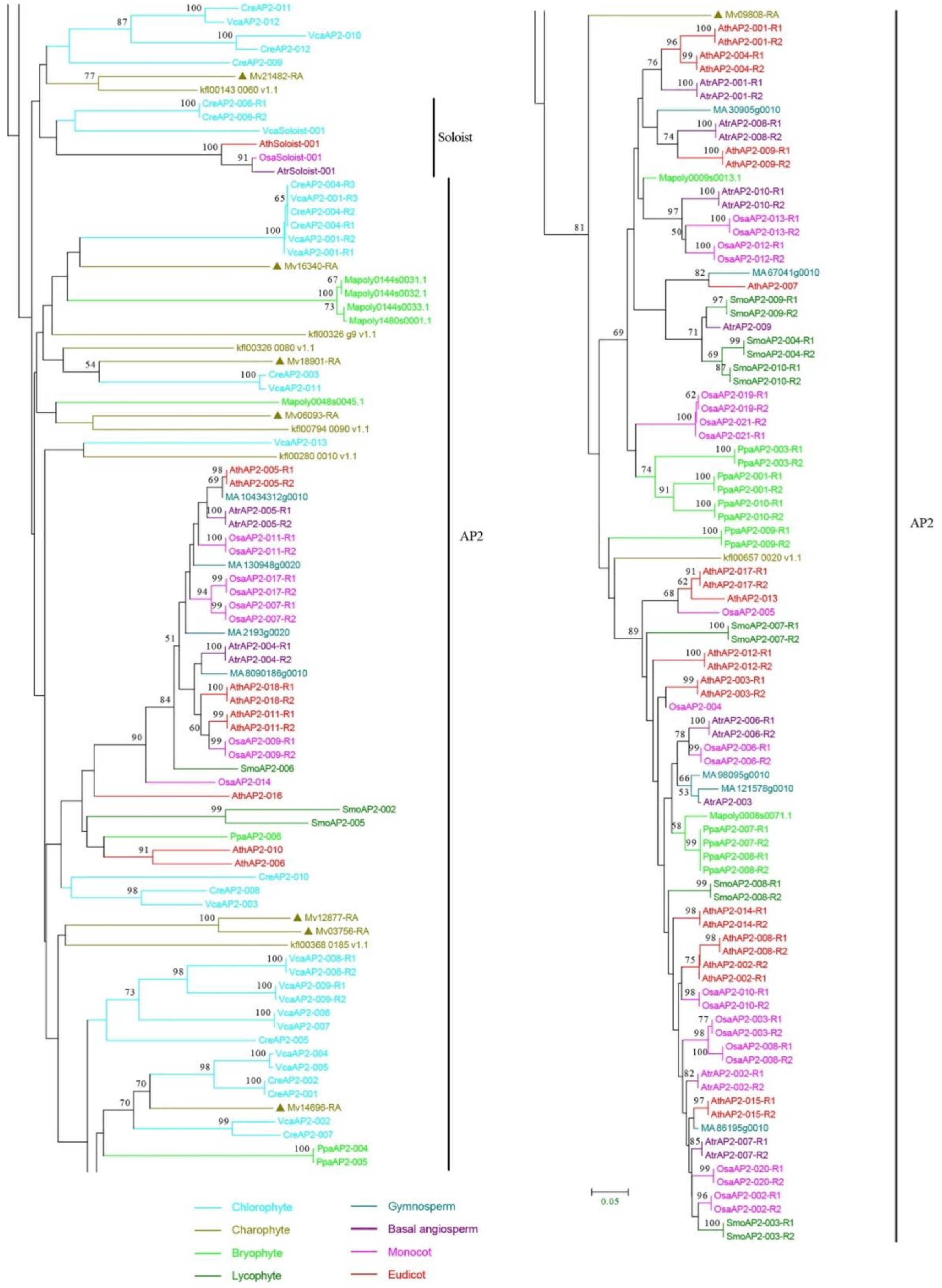
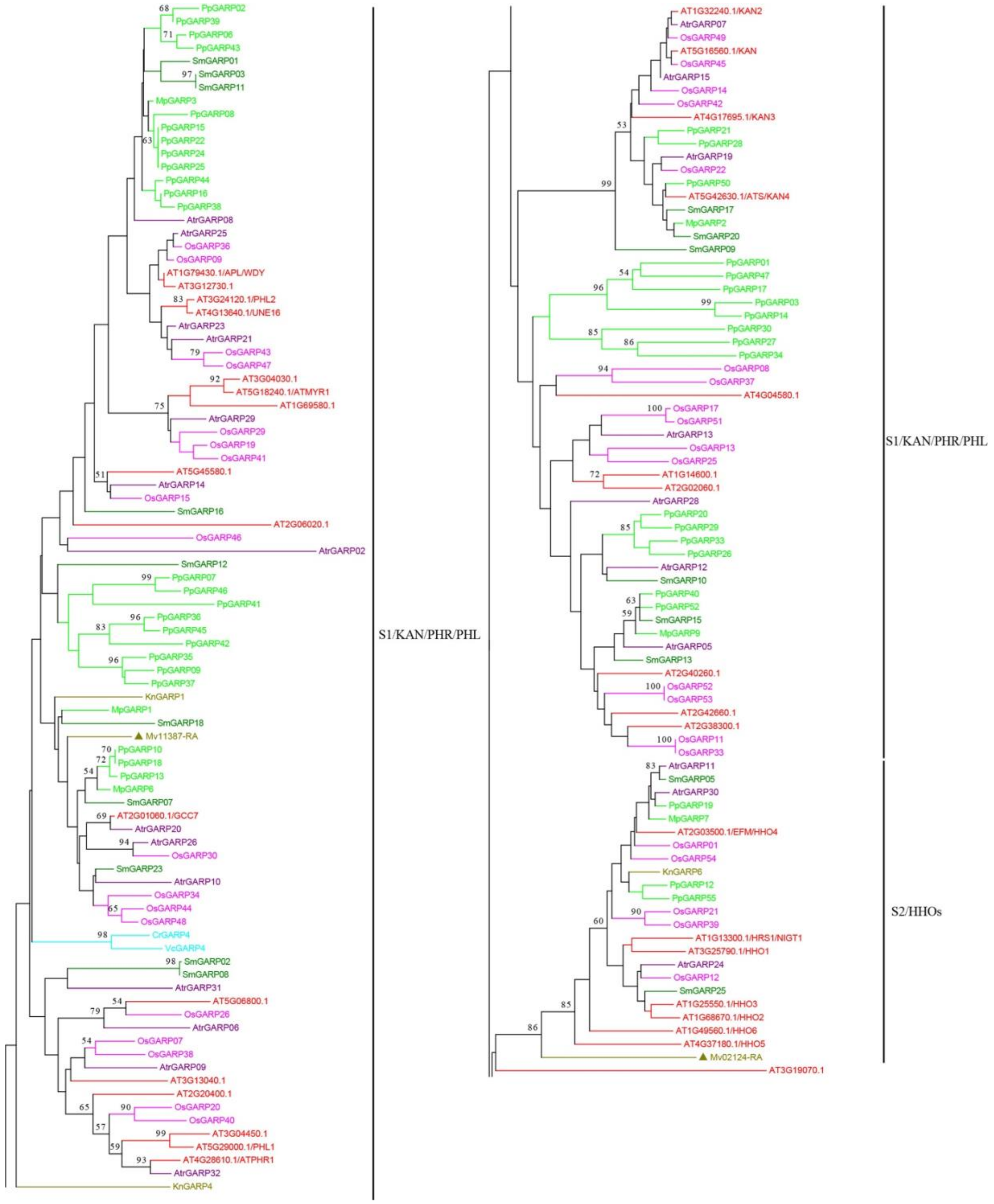


Data S1G. Phylogenetic relationships of APETALA 2/ERE binding factor (AP2/ERF) TFs from *M. viride* and 10 evolutionarily representative species. The *M. viride* sequences were highlighted by triangles. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates. The classification/clade was named based on previous studies.[3-6]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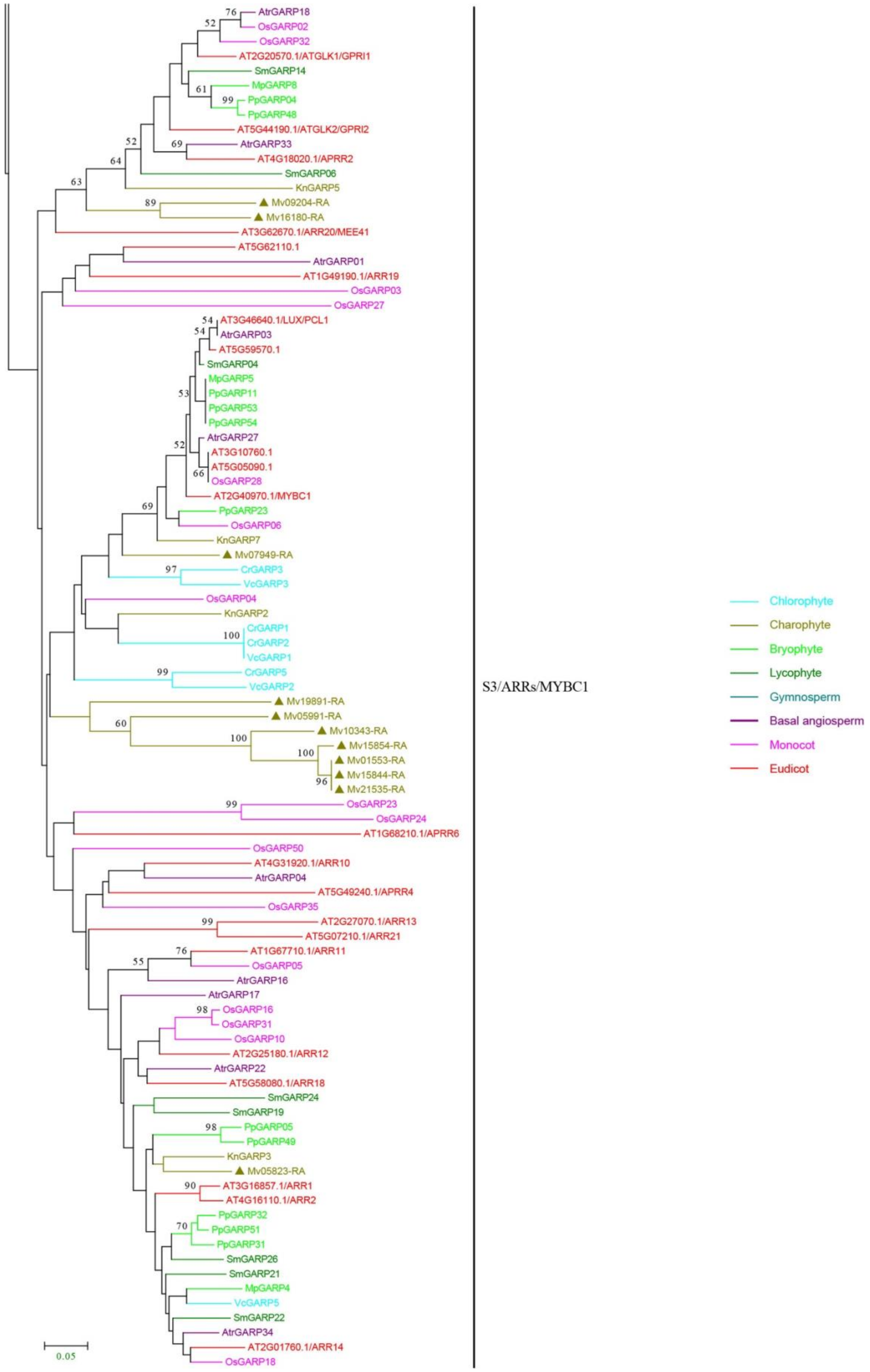
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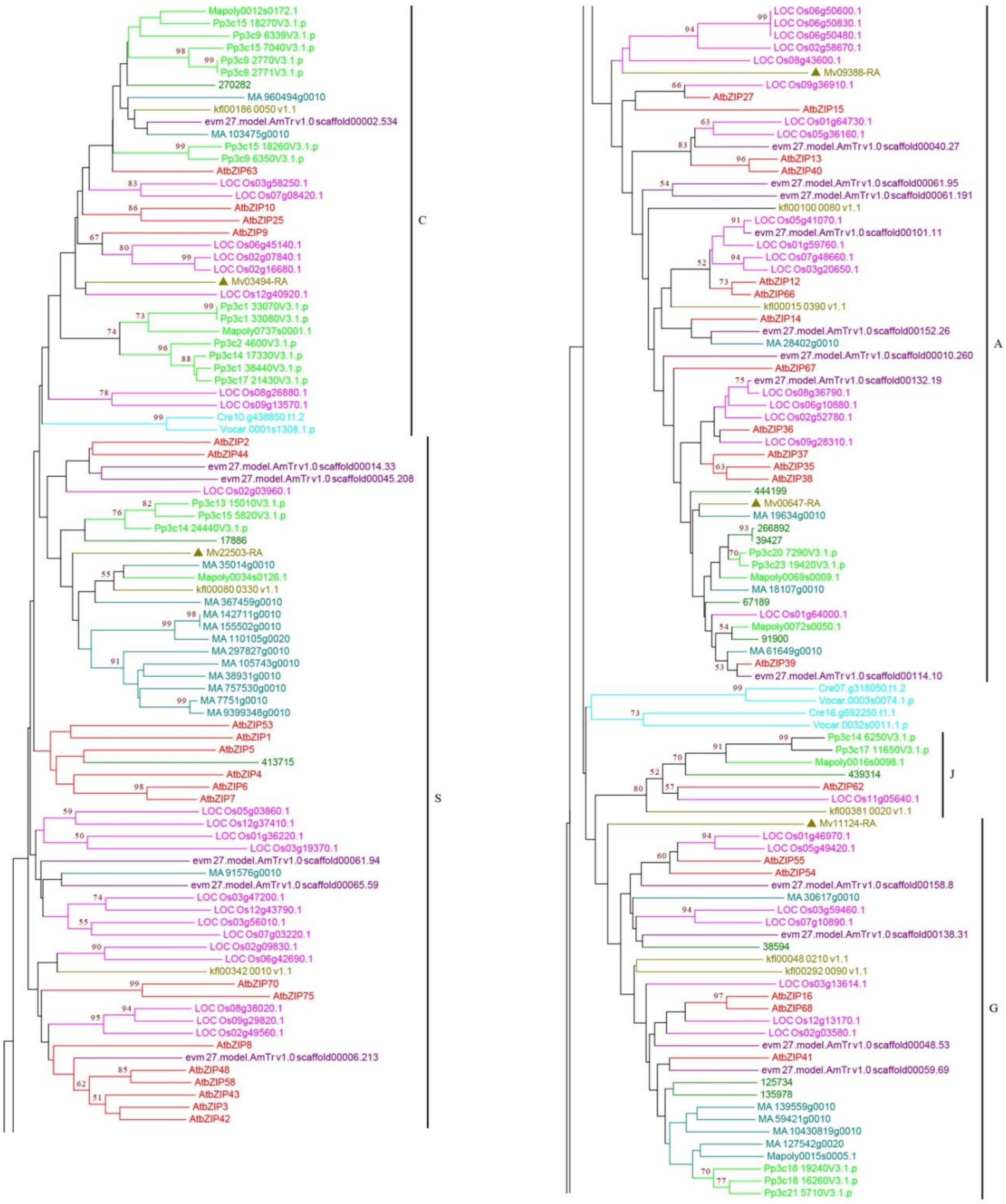
Eudicot

Data S1H. Phylogenetic relationships of GARP TFs from *M. viride* and 10 evolutionarily representative species. The *M. viride* sequences were highlighted by triangles. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates. The classification/clade was named based on a previous study.[7]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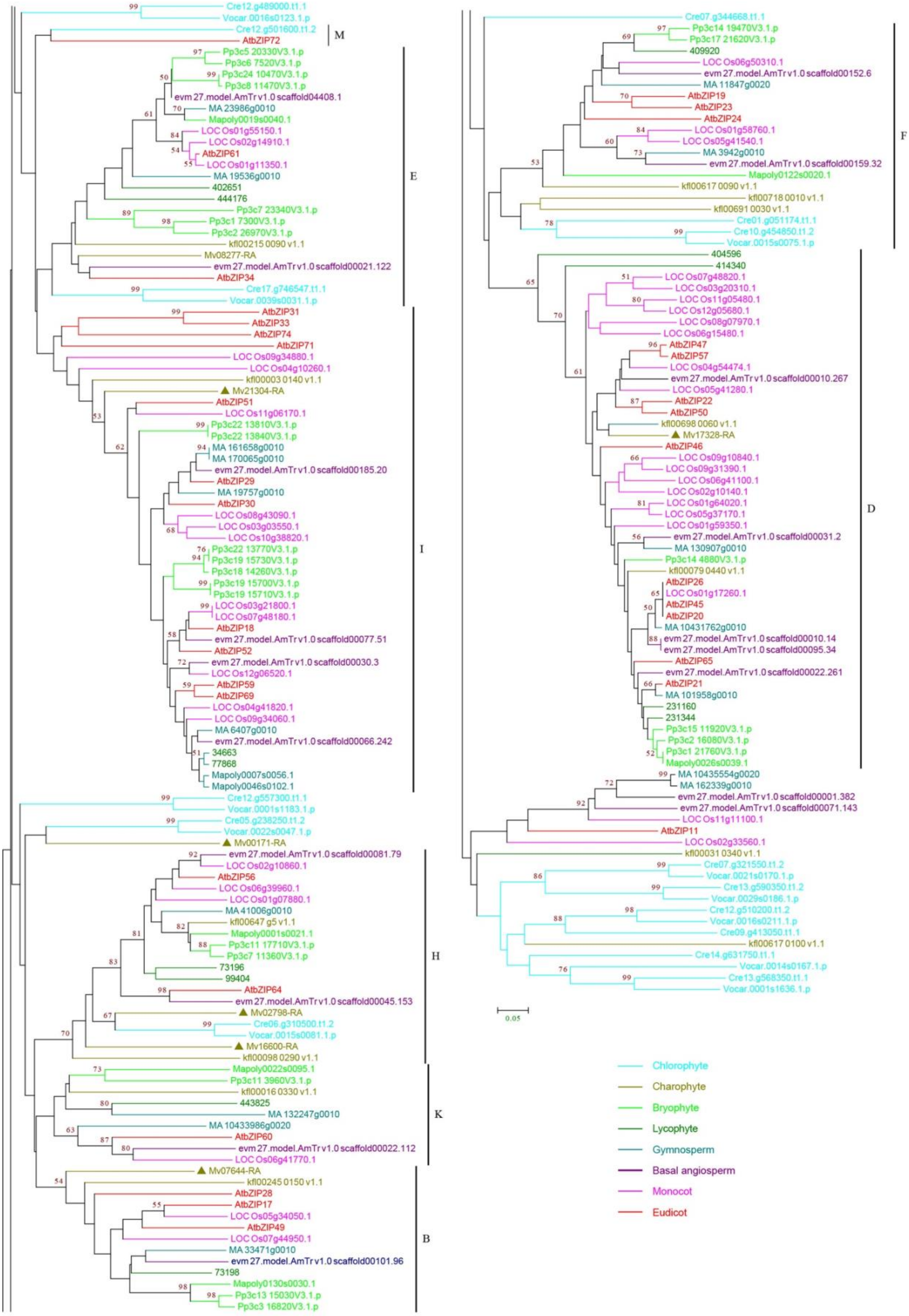
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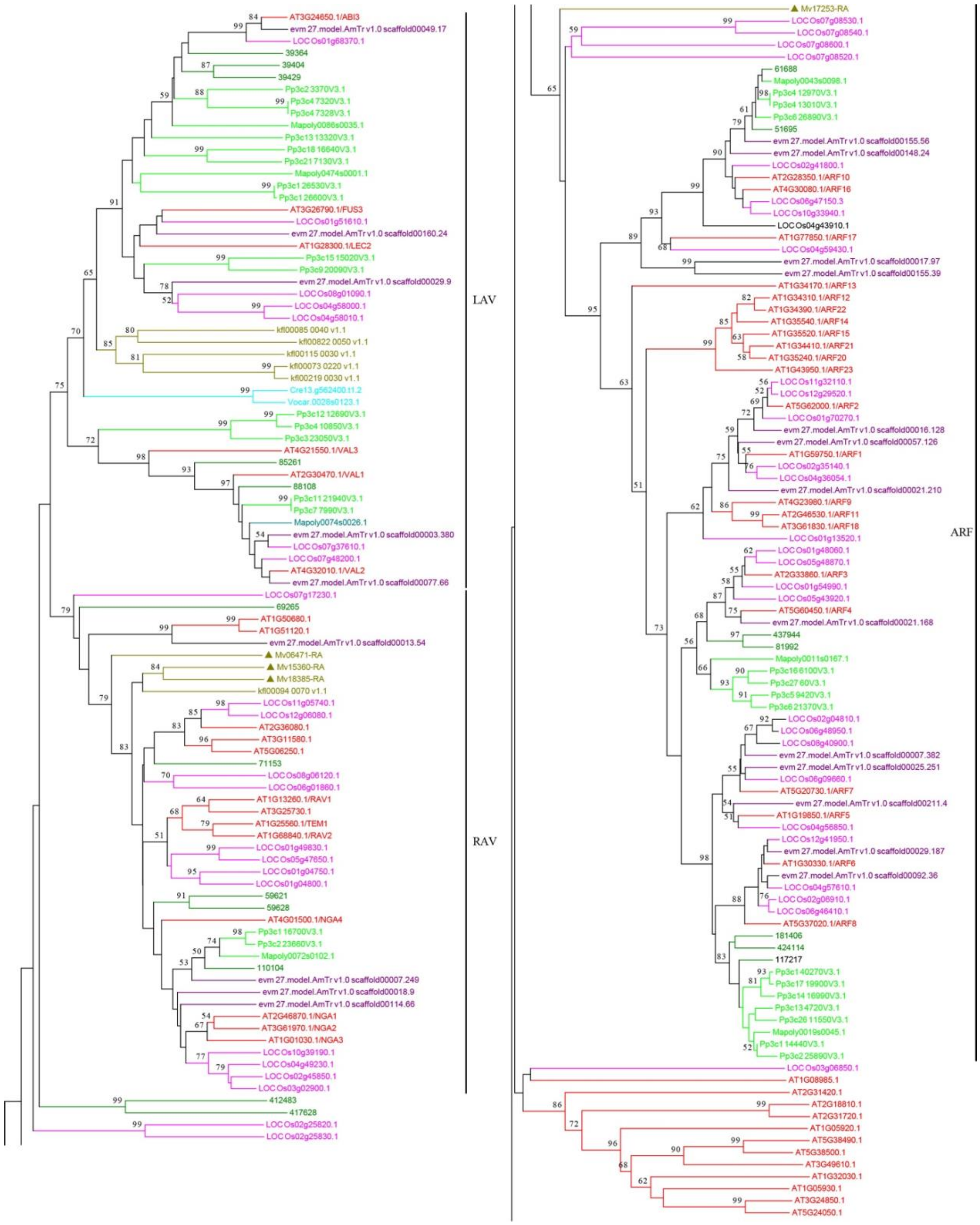
Data S1I. Phylogenetic relationships of Basic Leucine Zipper (bZIP) TFs from *M. viride* and 10 evolutionarily representative species. The *M. viride* sequences were highlighted by triangles. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates. The classification/clade was named based on previous studies.[8-9]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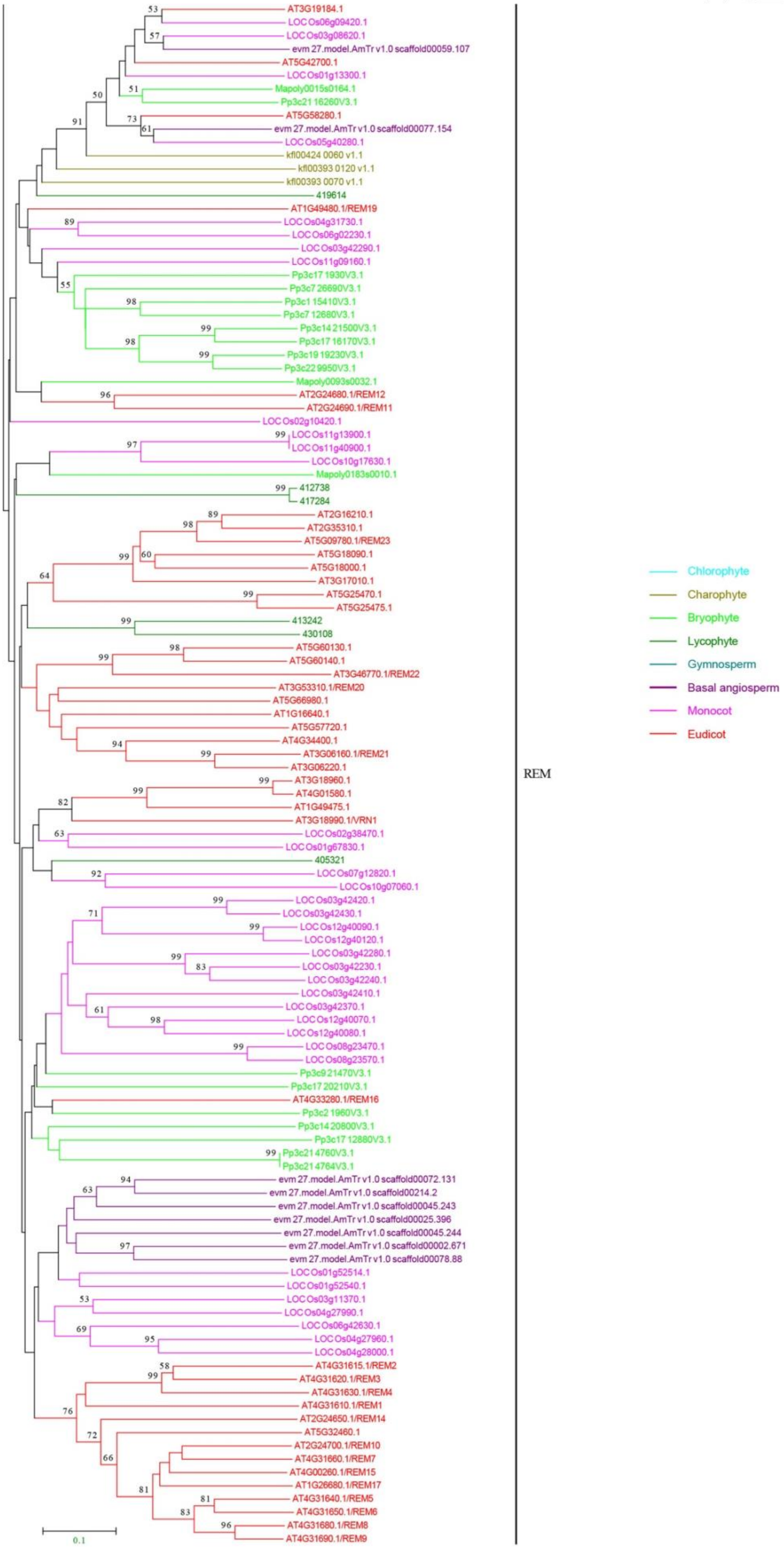
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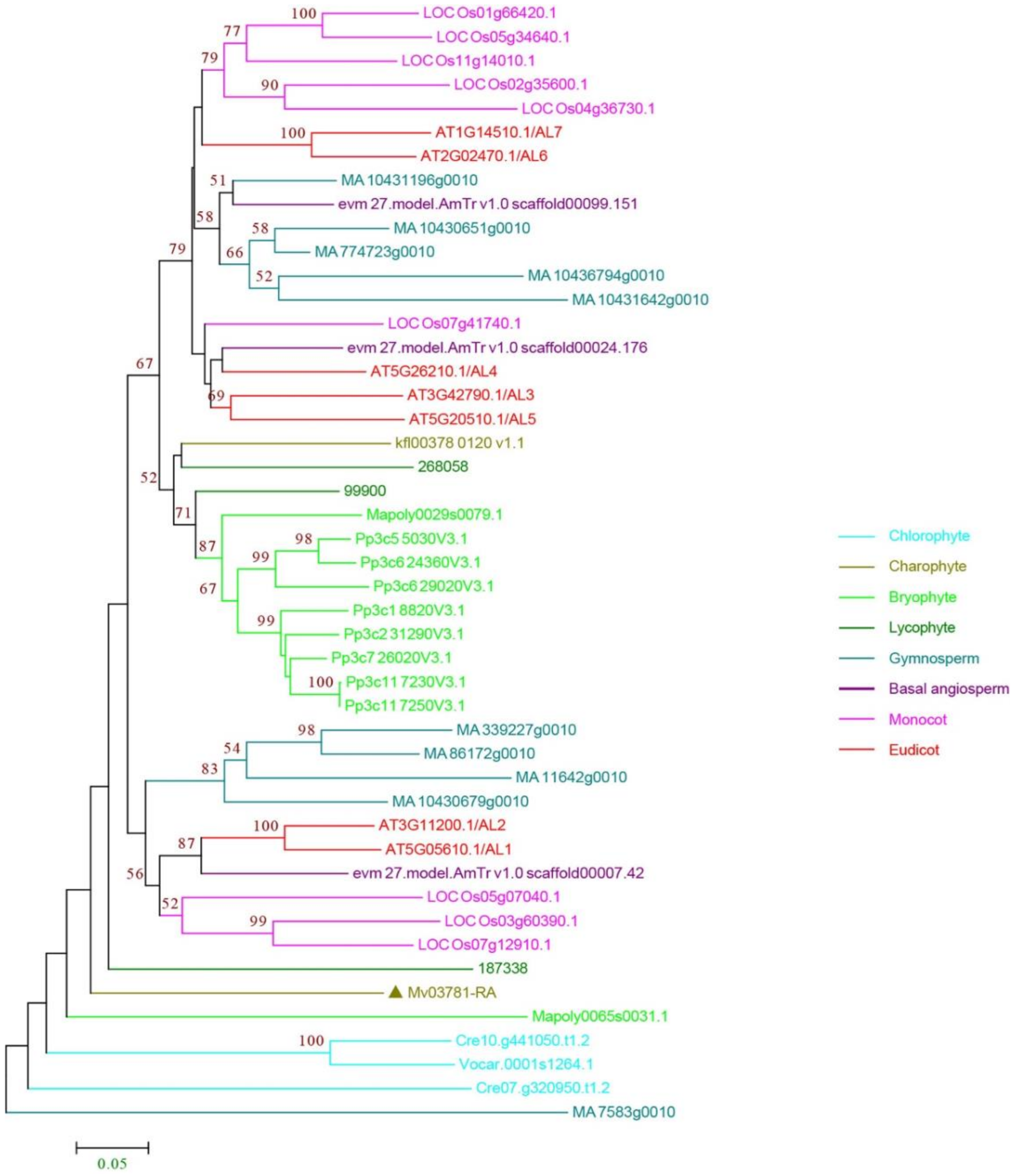
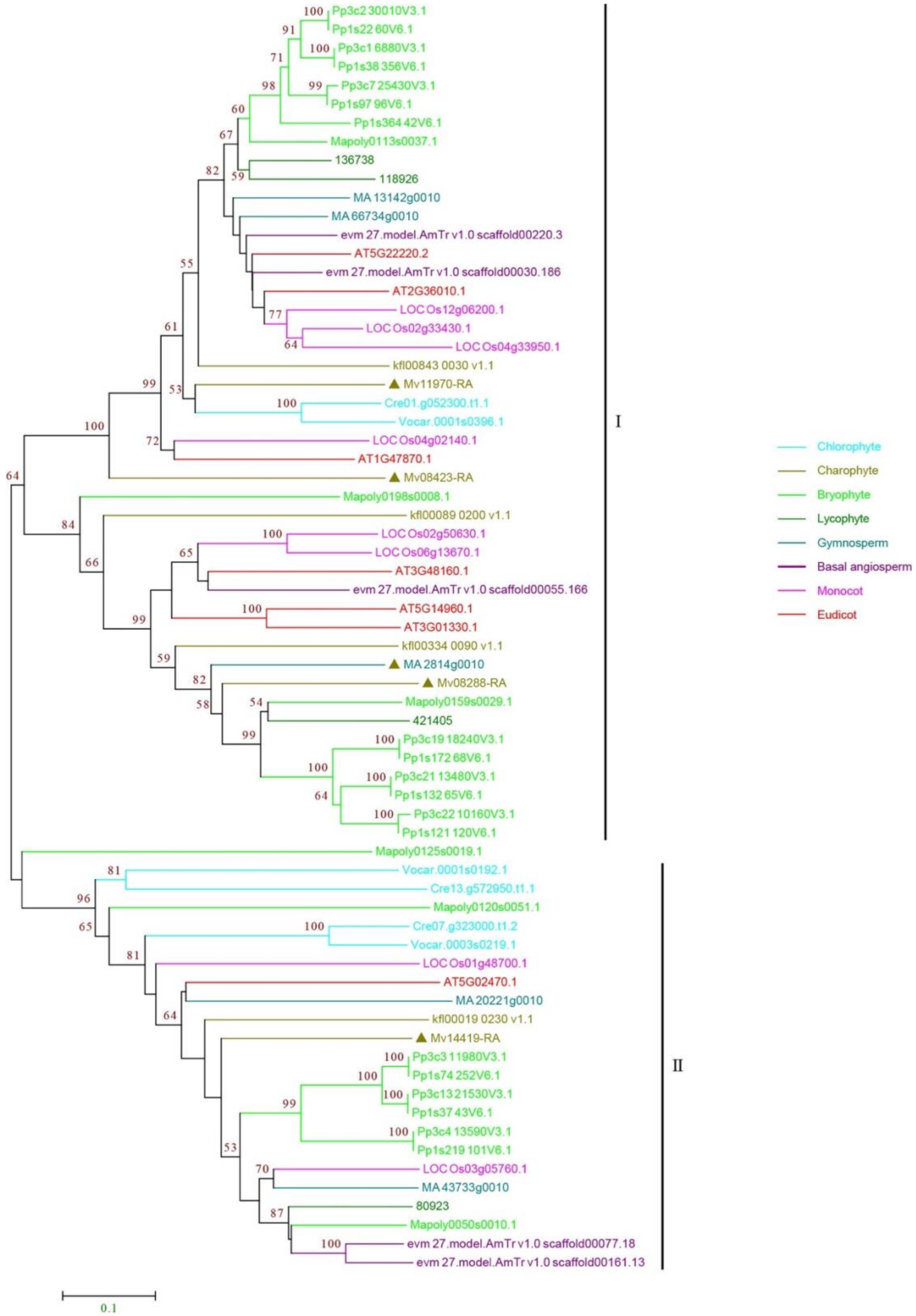
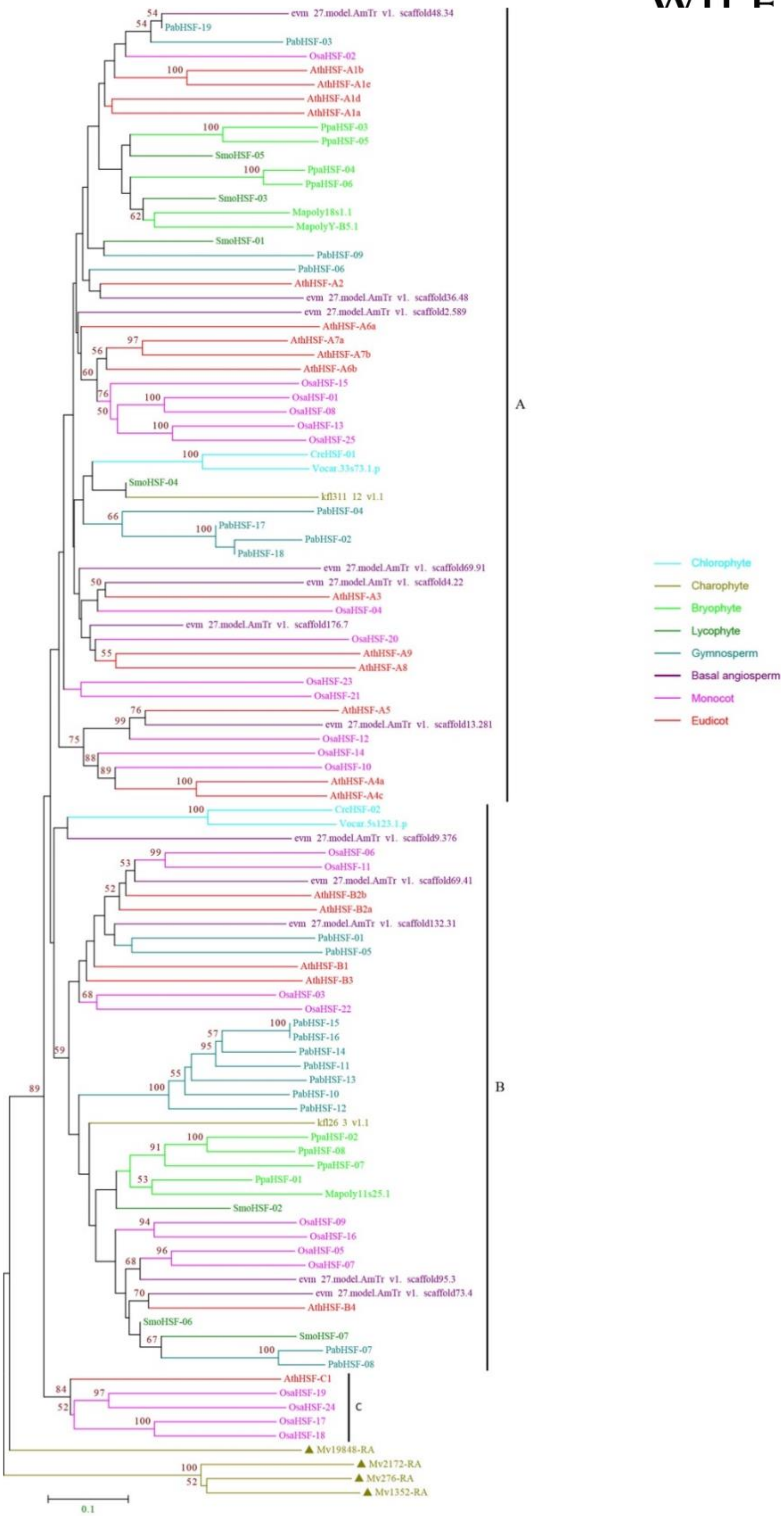
Data S1J. Phylogenetic relationships of B3 TFs from *M. viride* and 10 evolutionarily representative species. The *M. viride* sequences were highlighted by triangles. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates. The classification/clade was named based on previous studies.[10-12]



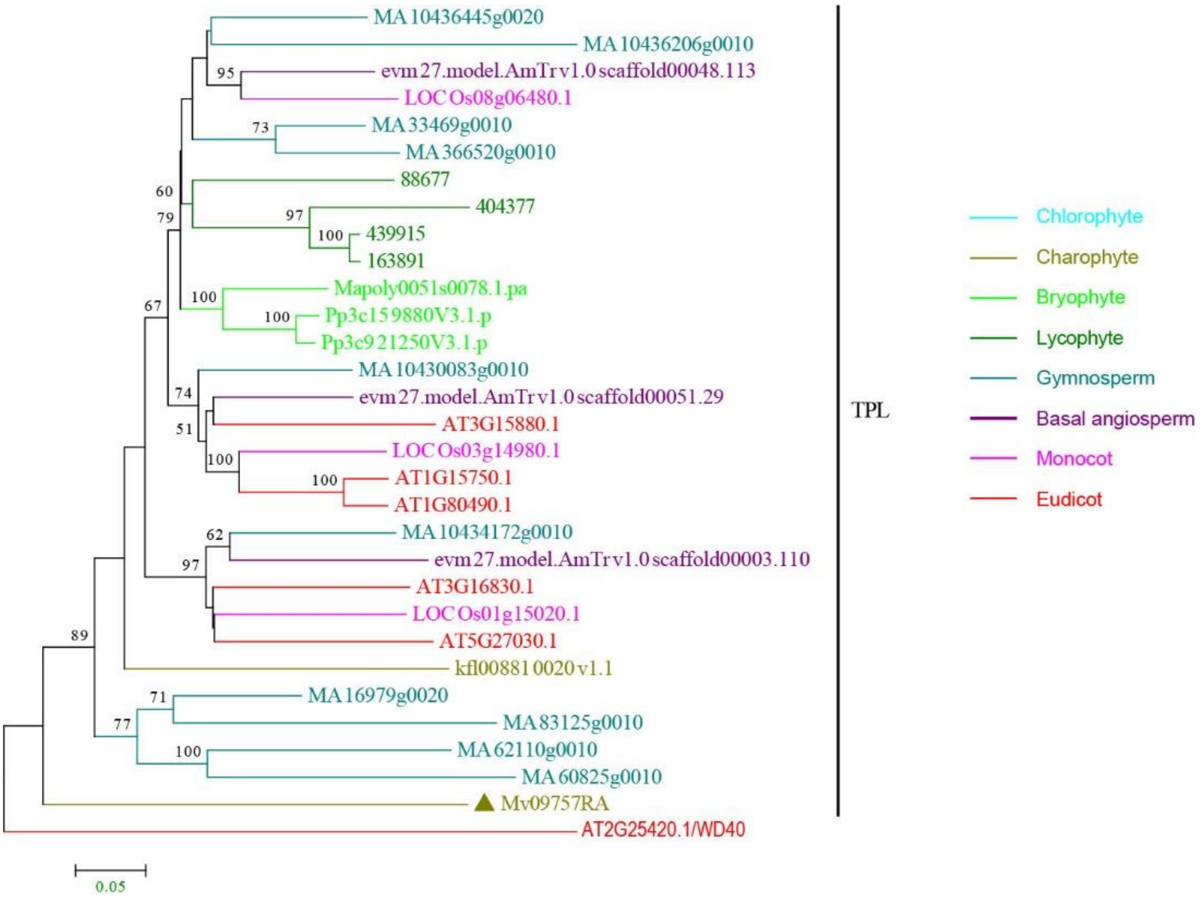
Data S1K. Phylogenetic relationships of alfin1-like TFs from *M. viride* and 10 evolutionarily representative species. The *M. viride* sequence was highlighted by a triangle. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



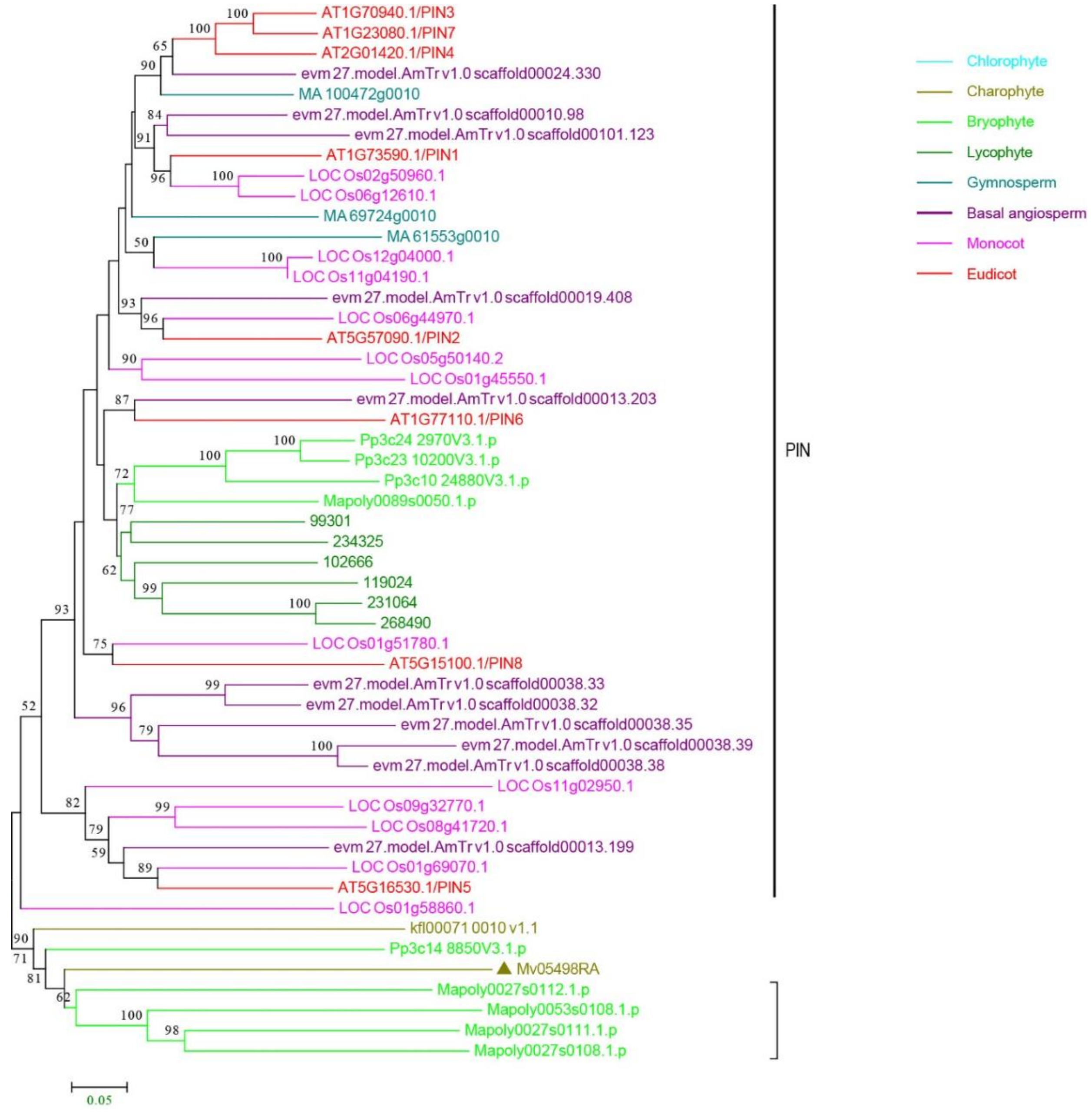
Data S1L. Phylogenetic relationships of E2 factor (E2F) TFs from *M. viride* and 10 evolutionarily representative species. The *M. viride* sequences were highlighted by triangles. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates. The classification/clade was named based on previous studies.[13-14]



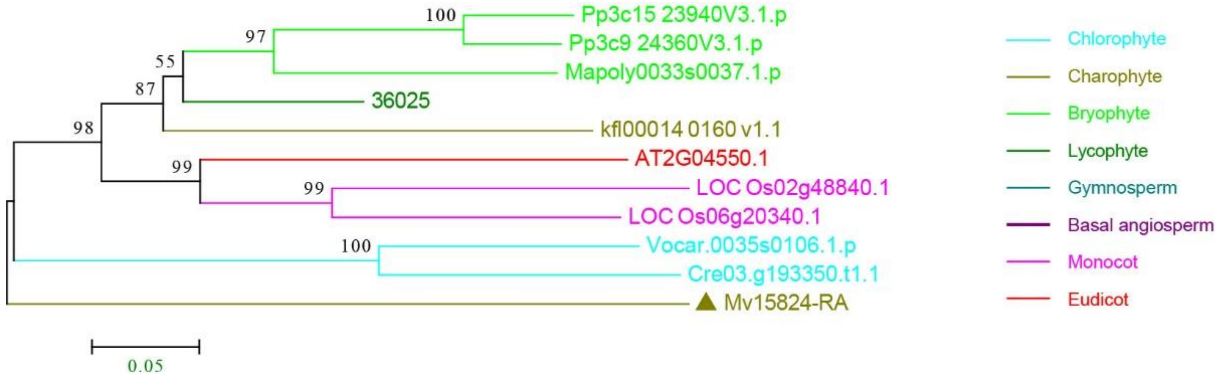
Data S1M. Phylogenetic relationships of heat shock transcription factor (HSF) TFs from *M. viride* and 10 evolutionarily representative species. The *M. viride* sequences were highlighted by triangles. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates. The classification/clade was named based on a previous study.[15]



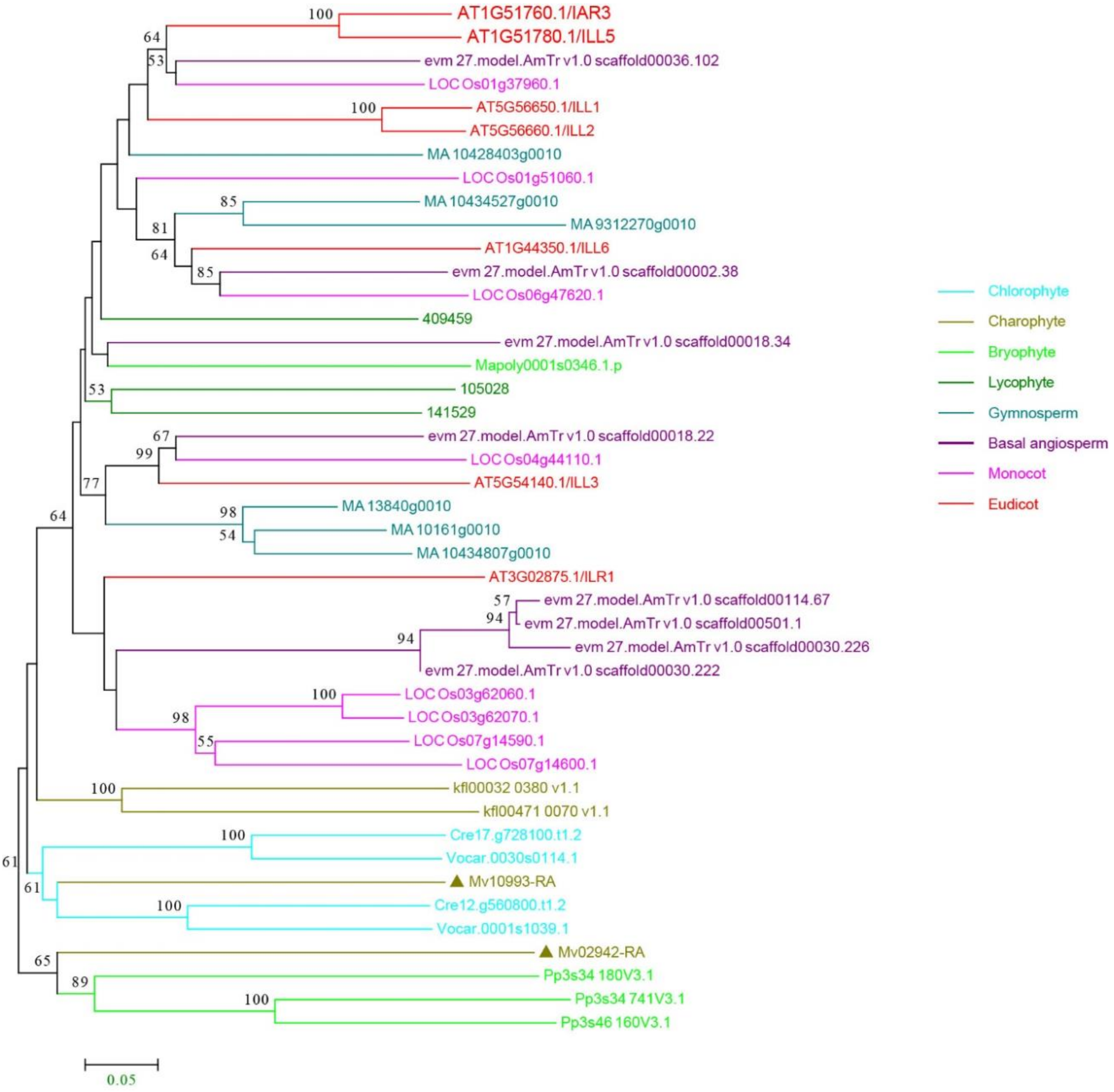
Data S1N. Phylogenetic relationships of TOPLESS (TPL) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequence was highlighted by a triangle. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



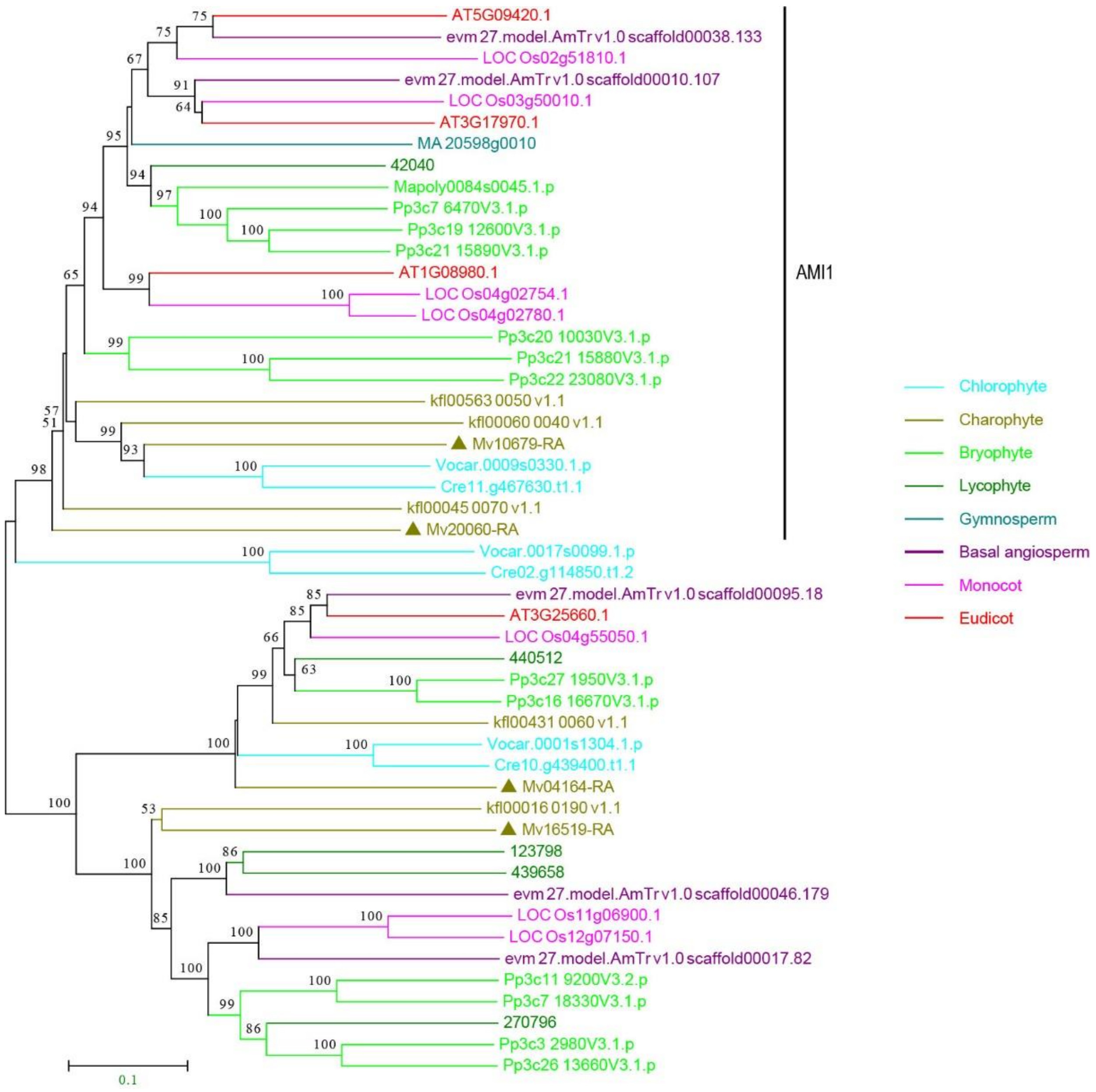
Data S1O. Phylogenetic relationships of PIN-FORMED (PIN) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequence was highlighted by a triangle. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



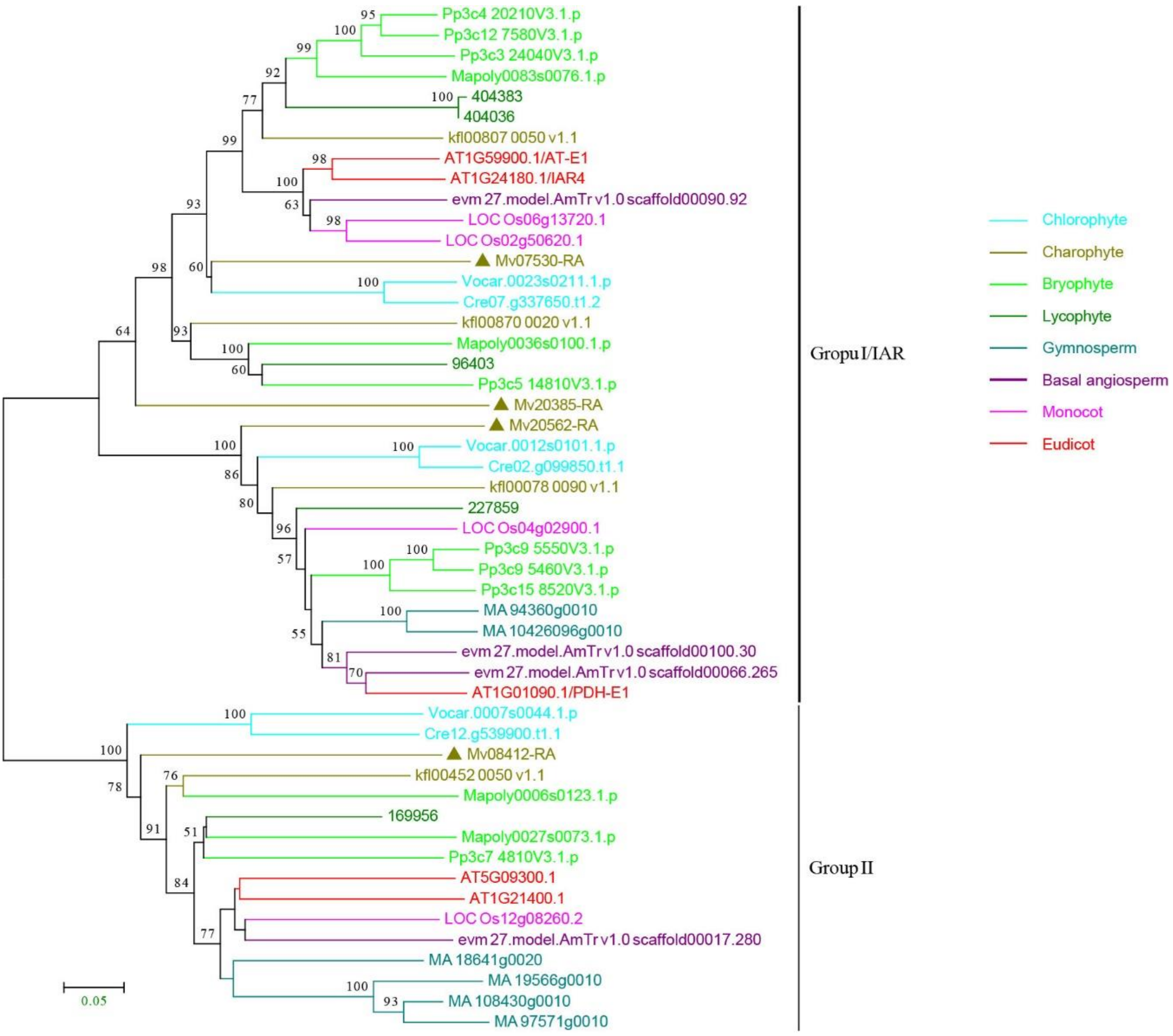
Data S1P. Phylogenetic relationships of INDOLE-3-BUTYRIC ACID RESPONSE (IBR) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequence was highlighted by a triangle. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



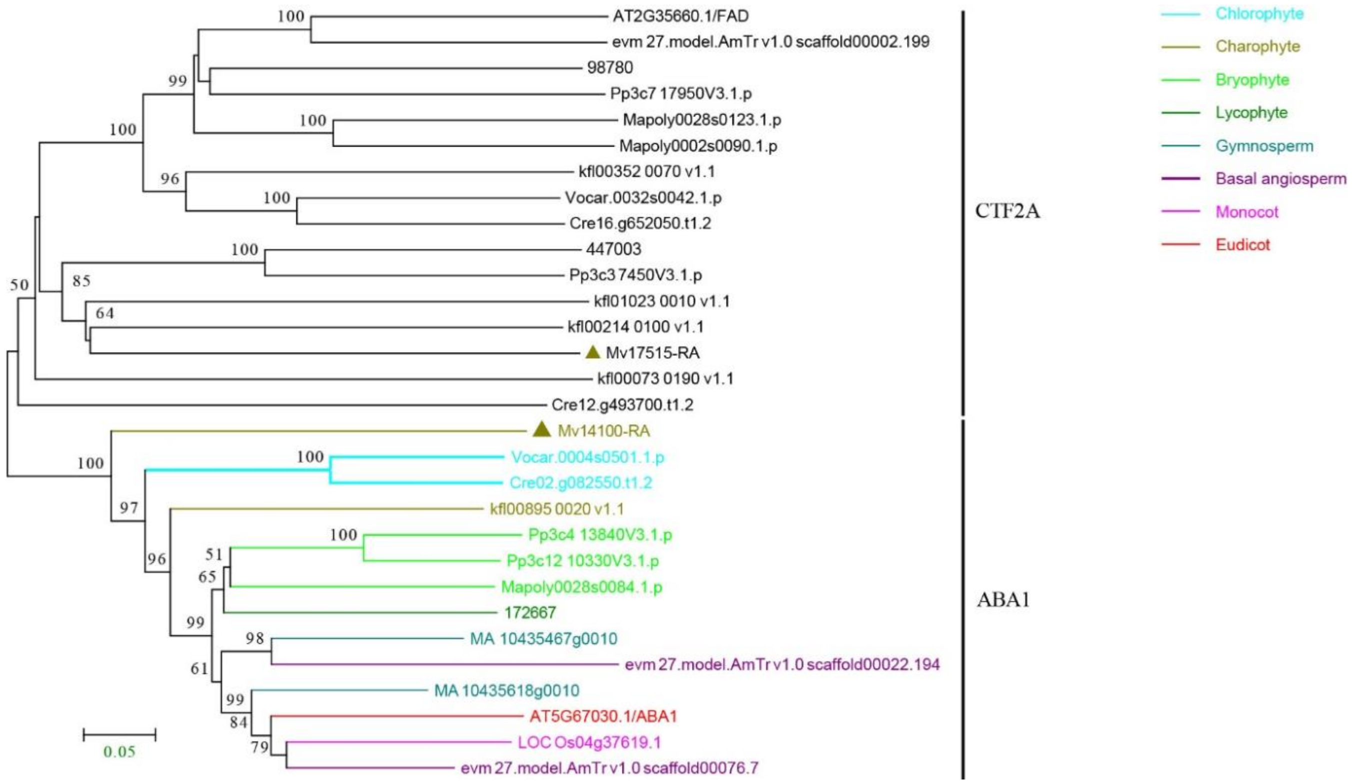
Data S1Q. Phylogenetic relationships of IAA-LEUCINE RESISTANT (ILR) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequences were highlighted by triangles. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



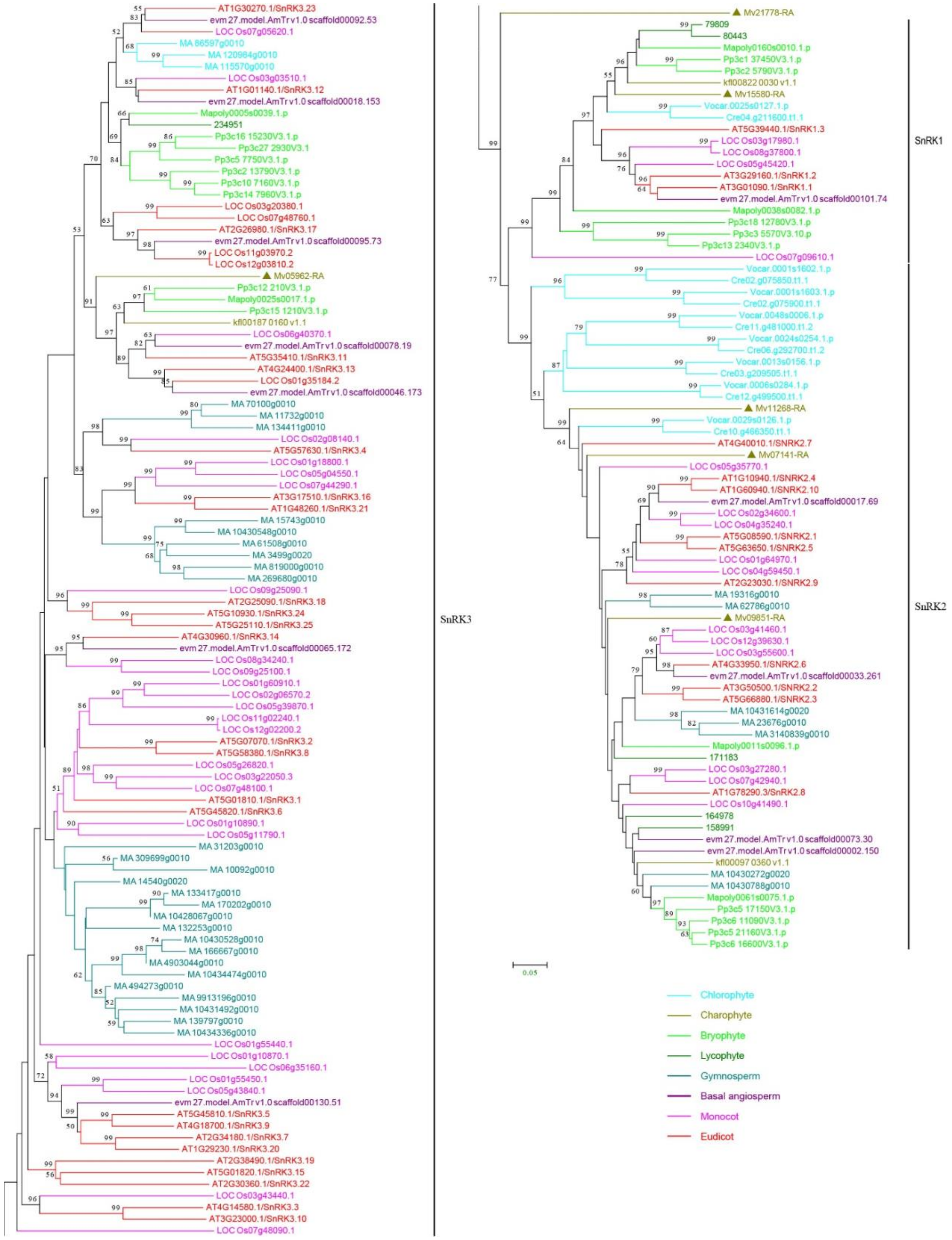
Data S1R. Phylogenetic relationships of AMIDASEA1 (AMI1) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequences were highlighted by triangles. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



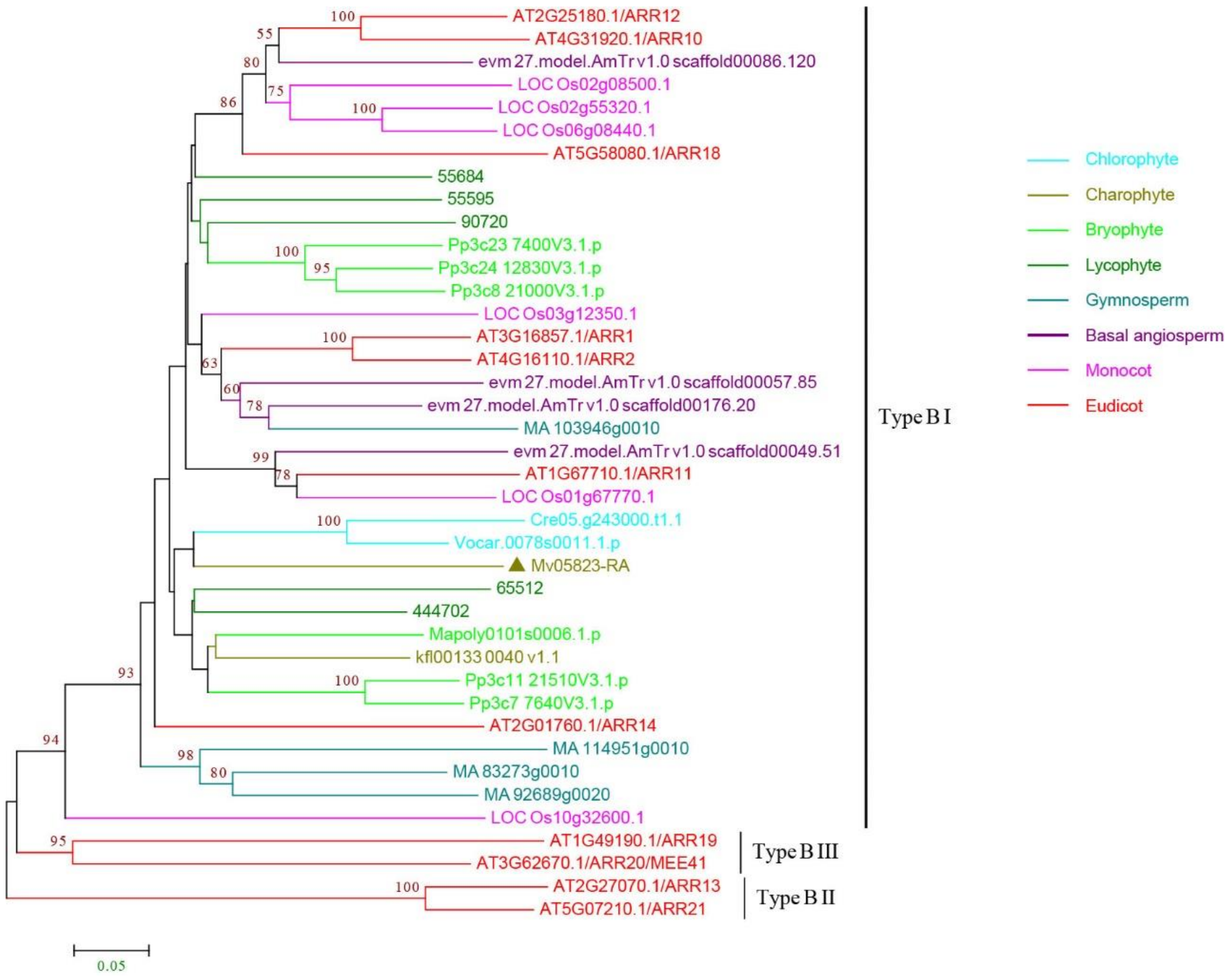
Data S1S. Phylogenetic relationships of IAA-CONJUGATE-RESISTANT (IAR) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequences were highlighted by triangles. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



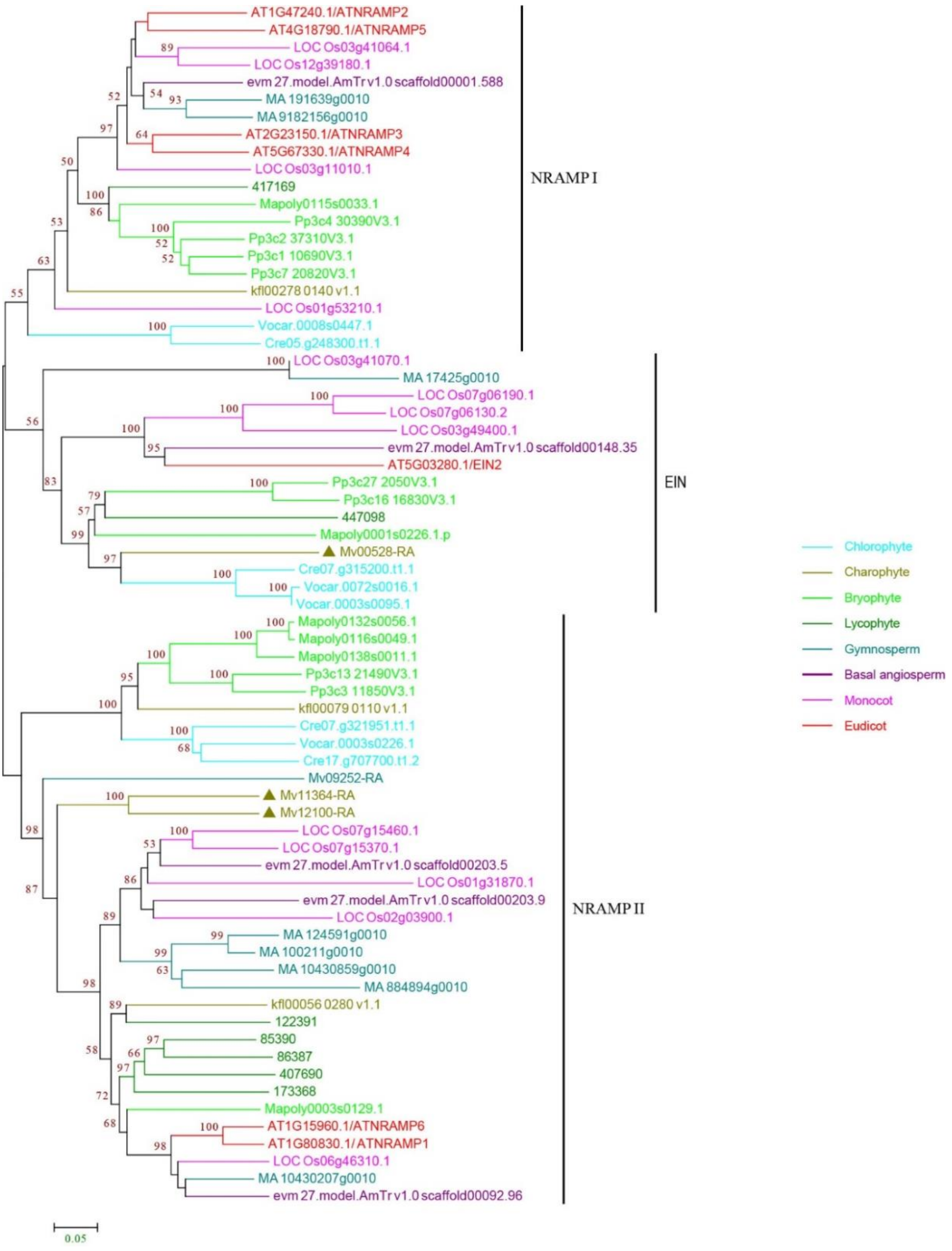
Data S1T. Phylogenetic relationships of ABA DEFICIENT 1 (ABA1) proteins from *M. viride* and other evolutionarily representative species. *M. viride* sequences were highlighted by triangles. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



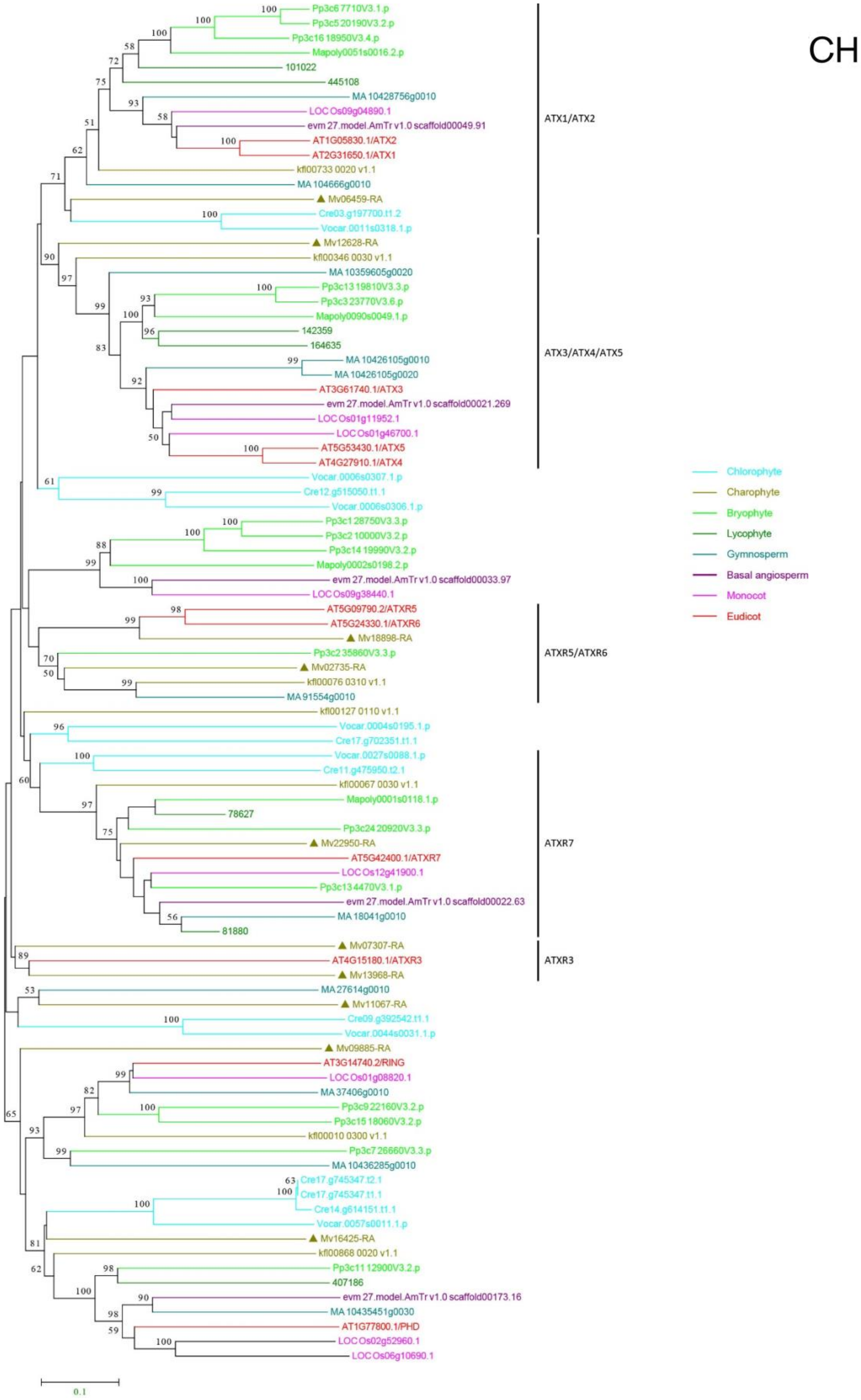
Data S1U. Phylogenetic relationships of SNF1-RELATED PROTEIN KINASE (SnRK) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequences were highlighted by triangles. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



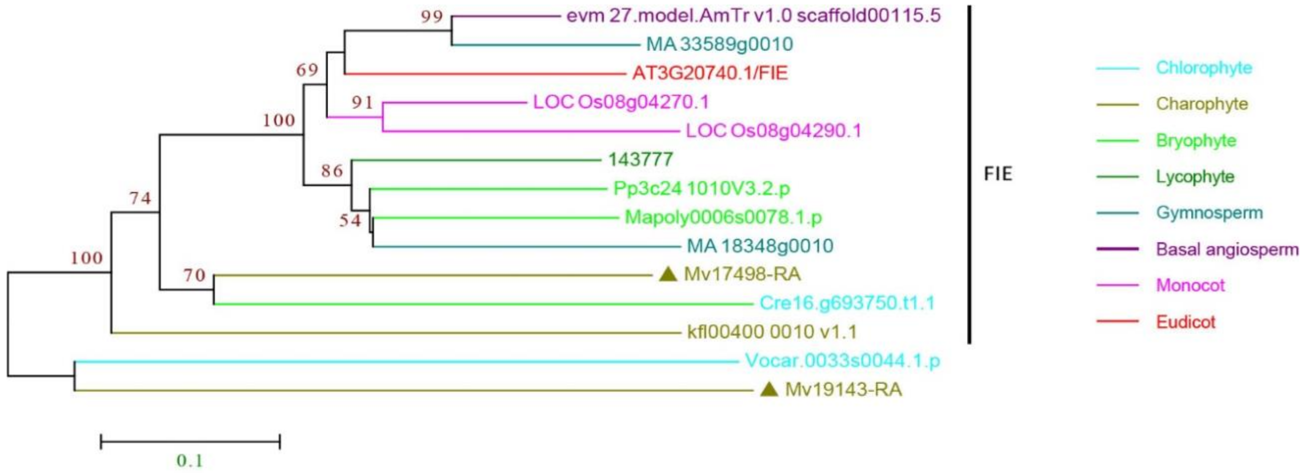
Data S1V. Phylogenetic relationships of Type B RESPONSE REGULATOR (ARR) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequence was highlighted by a triangle. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



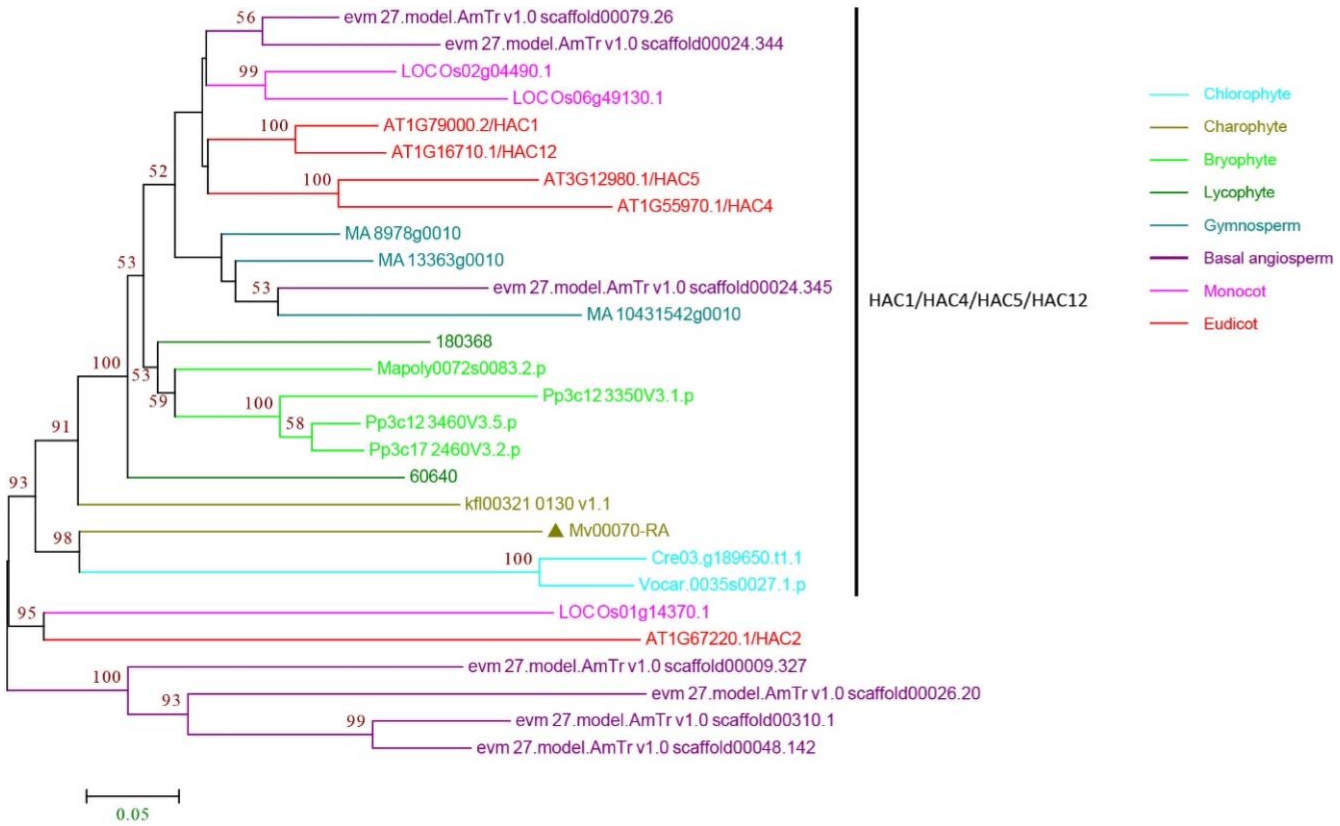
Data S1W. Phylogenetic relationships of ETHYLENE INSENSITIVE2 (EIN2) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequences were highlighted by triangles. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



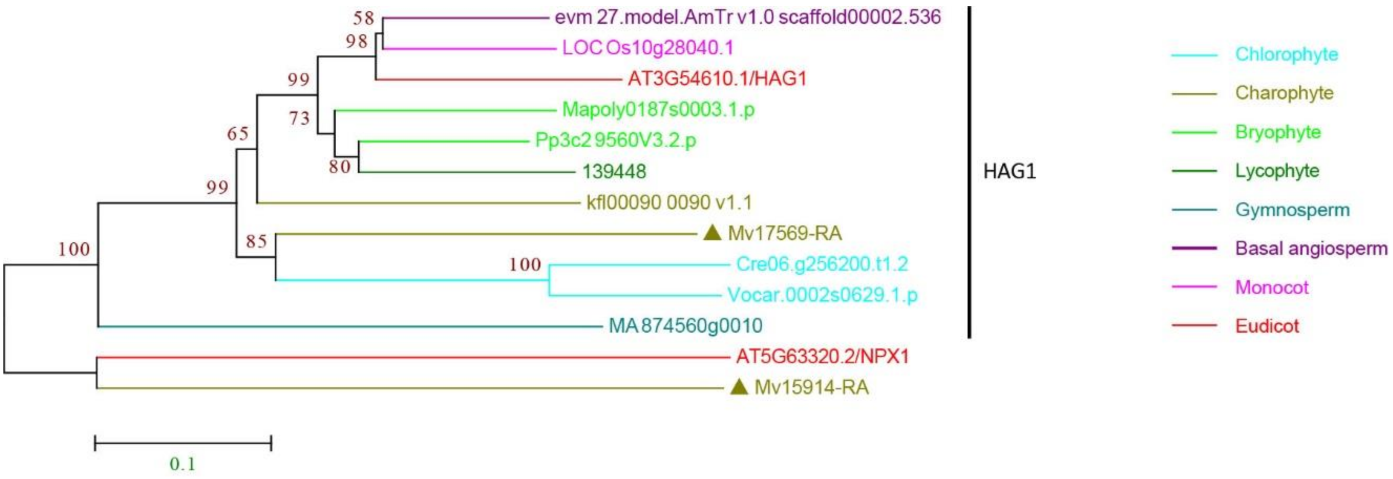
Data S1X. Phylogenetic relationships of TRITHORAX-LIKE PROTEIN (ATX) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequences were highlighted by triangles. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



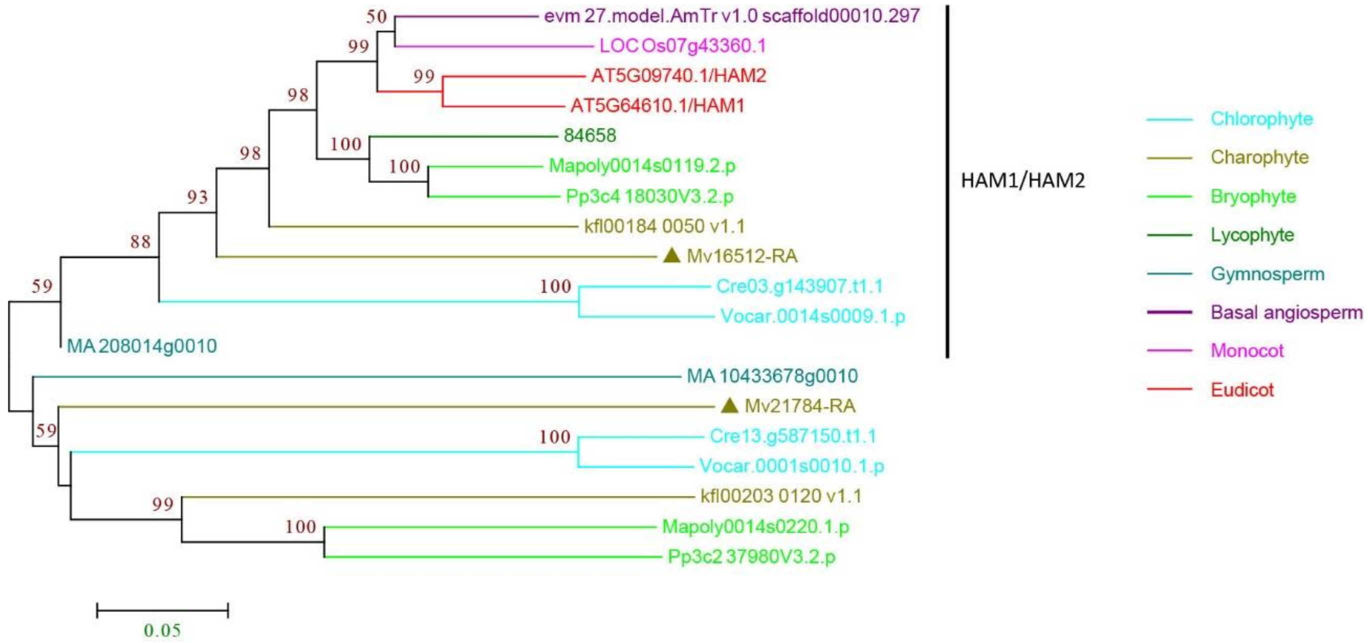
Data S1Y. Phylogenetic relationships of FERTILIZATION-INDEPENDENT ENDOSPERM (FIE) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequences were highlighted by triangles. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



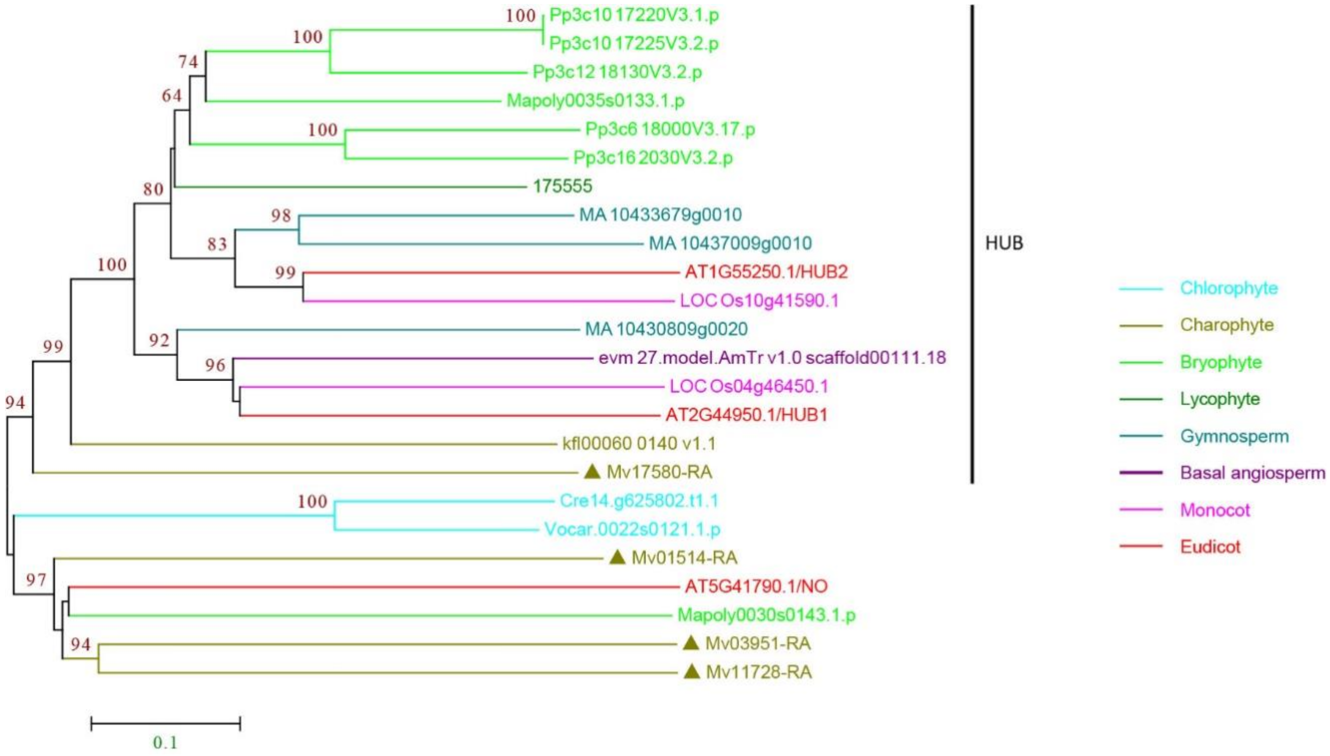
Data S1Z. Phylogenetic relationships of HISTONE ACETYLTRANSFERASE OF THE CBP FAMILY (HAC) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequence was highlighted by a triangle. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



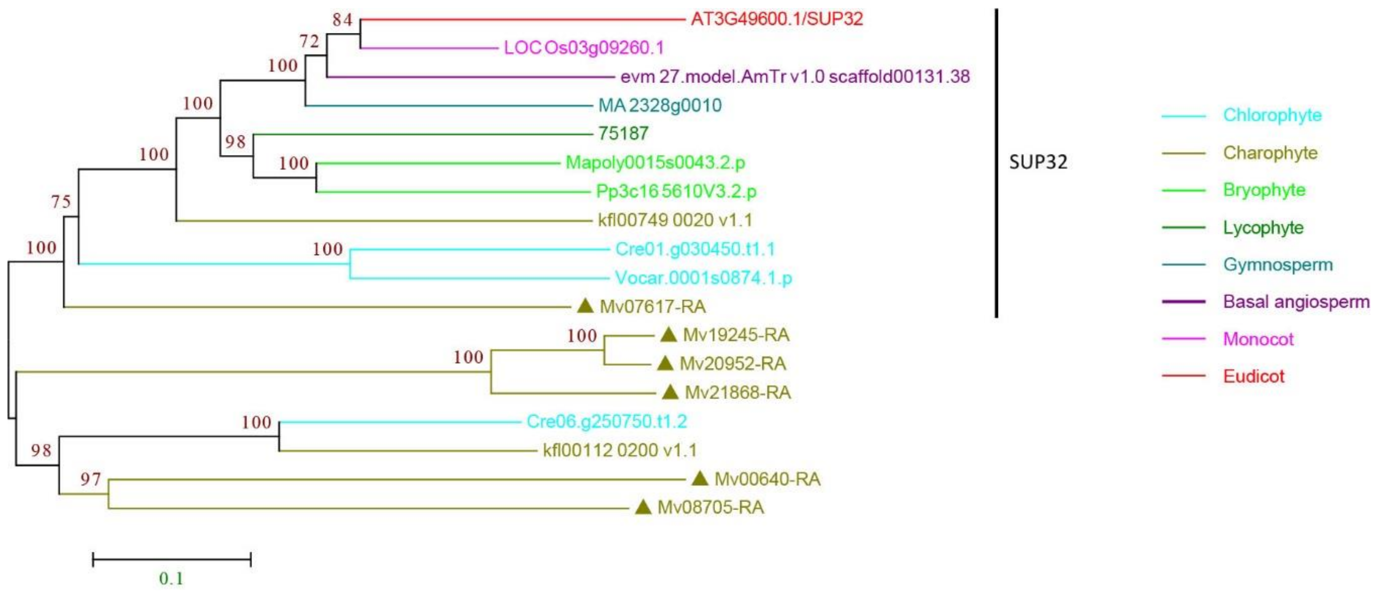
Data S1AA. Phylogenetic relationships of HISTONE ACETYLTRANSFERASE OF THE GNAT FAMILY 1 (HAG1) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequences were highlighted by triangles. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



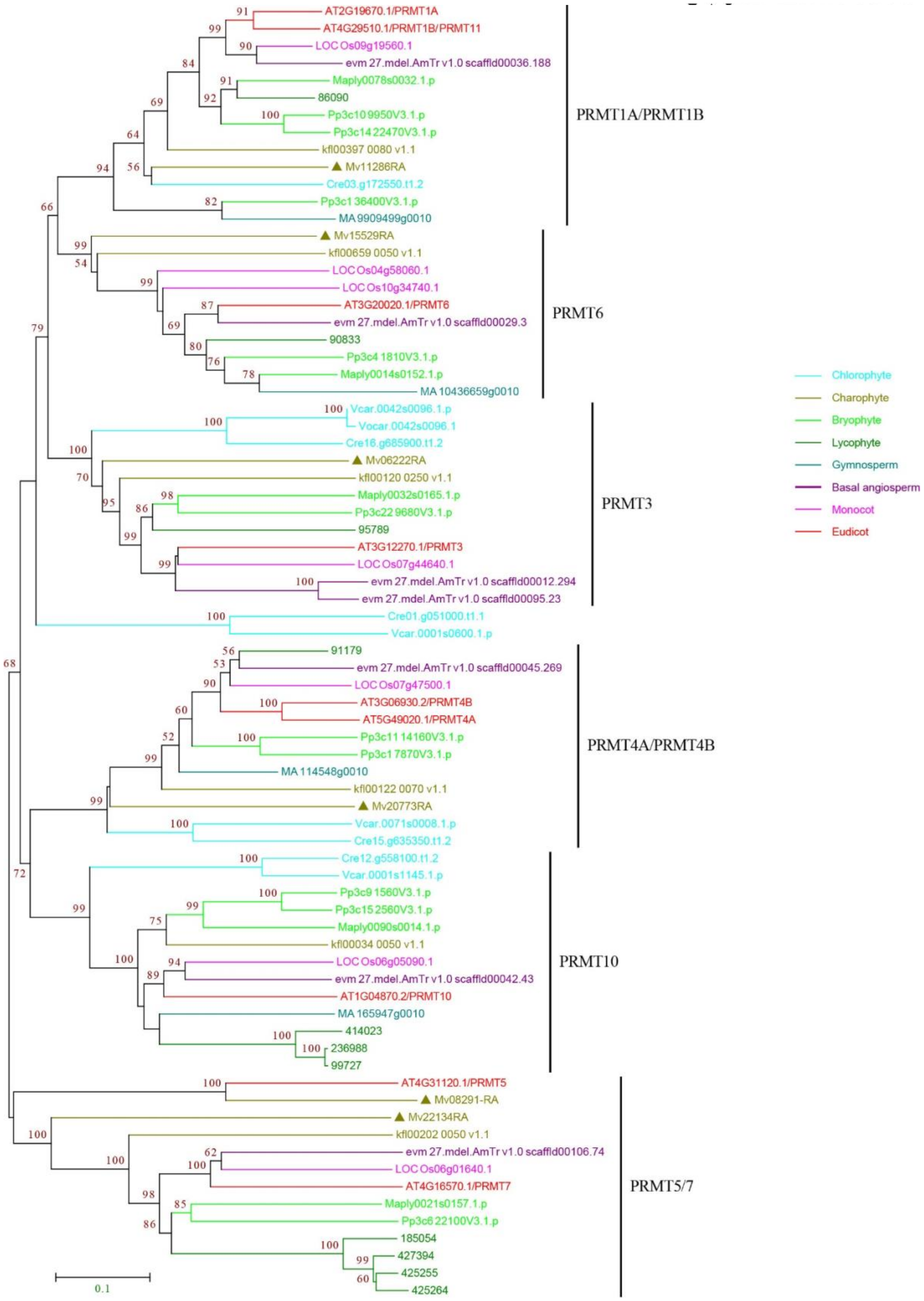
Data S1AB. Phylogenetic relationships of HISTONE ACETYLTRANSFERASE OF THE MYST FAMILY (HAM) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequences were highlighted by triangles. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



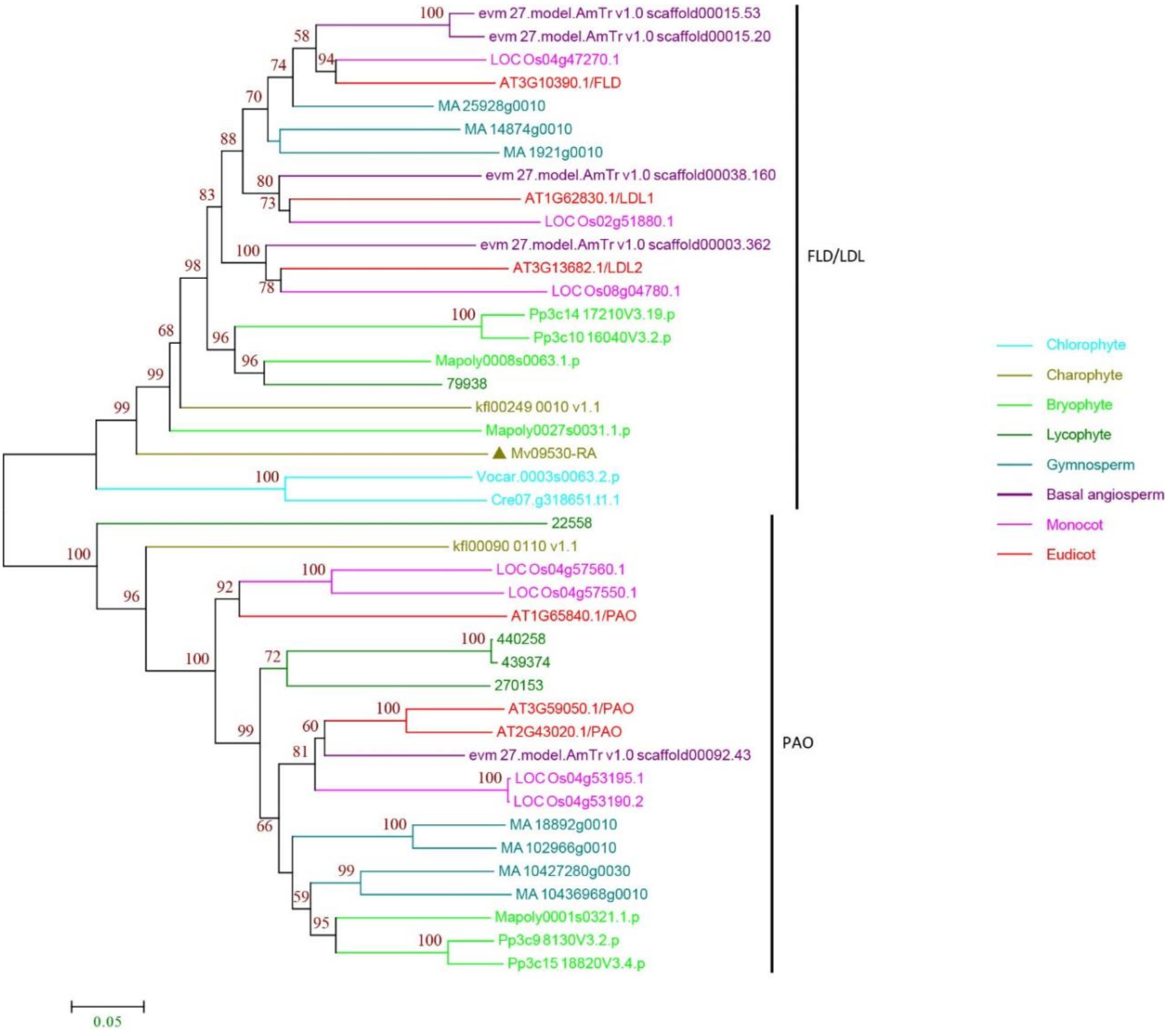
Data S1AC. Phylogenetic relationships of HISTONE MONO-UBIQUITINATION (HUB) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequences were highlighted by triangles. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



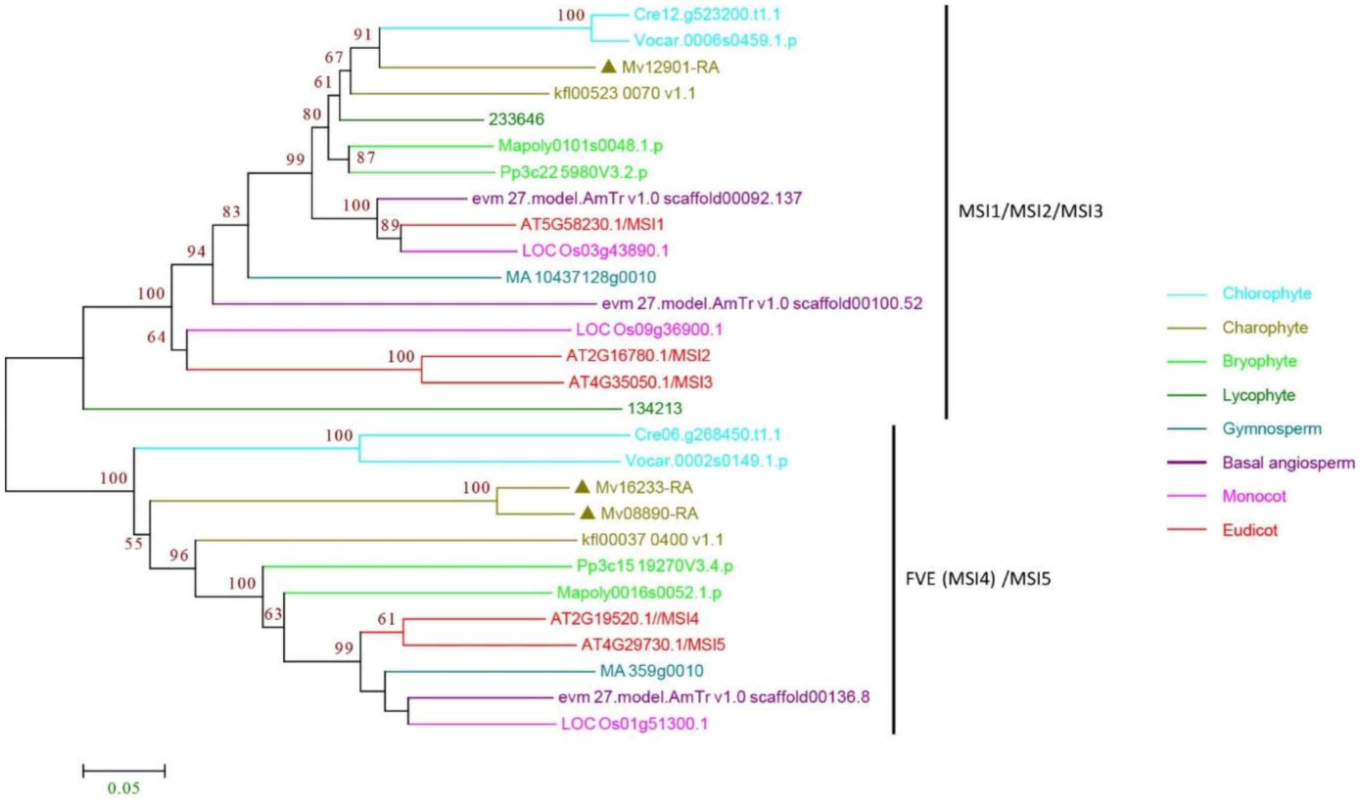
Data S1AD. Phylogenetic relationships of UBIQUITIN-SPECIFIC PROTEASE (also called SUP) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequences were highlighted by triangles. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



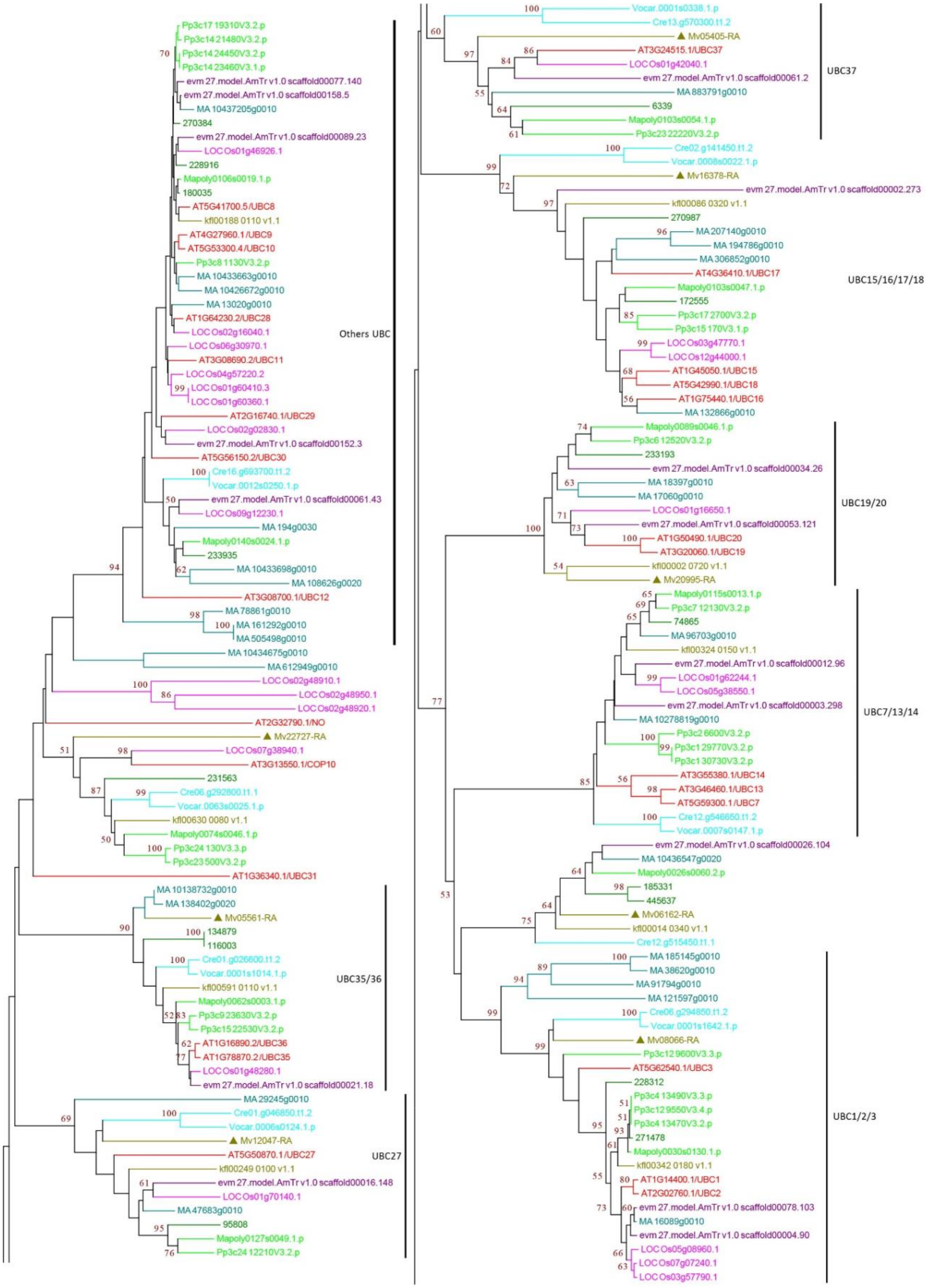
Data S1AE. Phylogenetic relationships of PROTEIN ARGININE METHYLTRANSFERASE (PRMT) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequences were highlighted by triangles. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



Data S1AF. Phylogenetic relationships of FLOWERING LOCUS D (FLD) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequence was highlighted by a triangle. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



Data S1AG. Phylogenetic relationships of MULTICOPY SUPRESSOR OF IRA (MSI) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequences were highlighted by triangles. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.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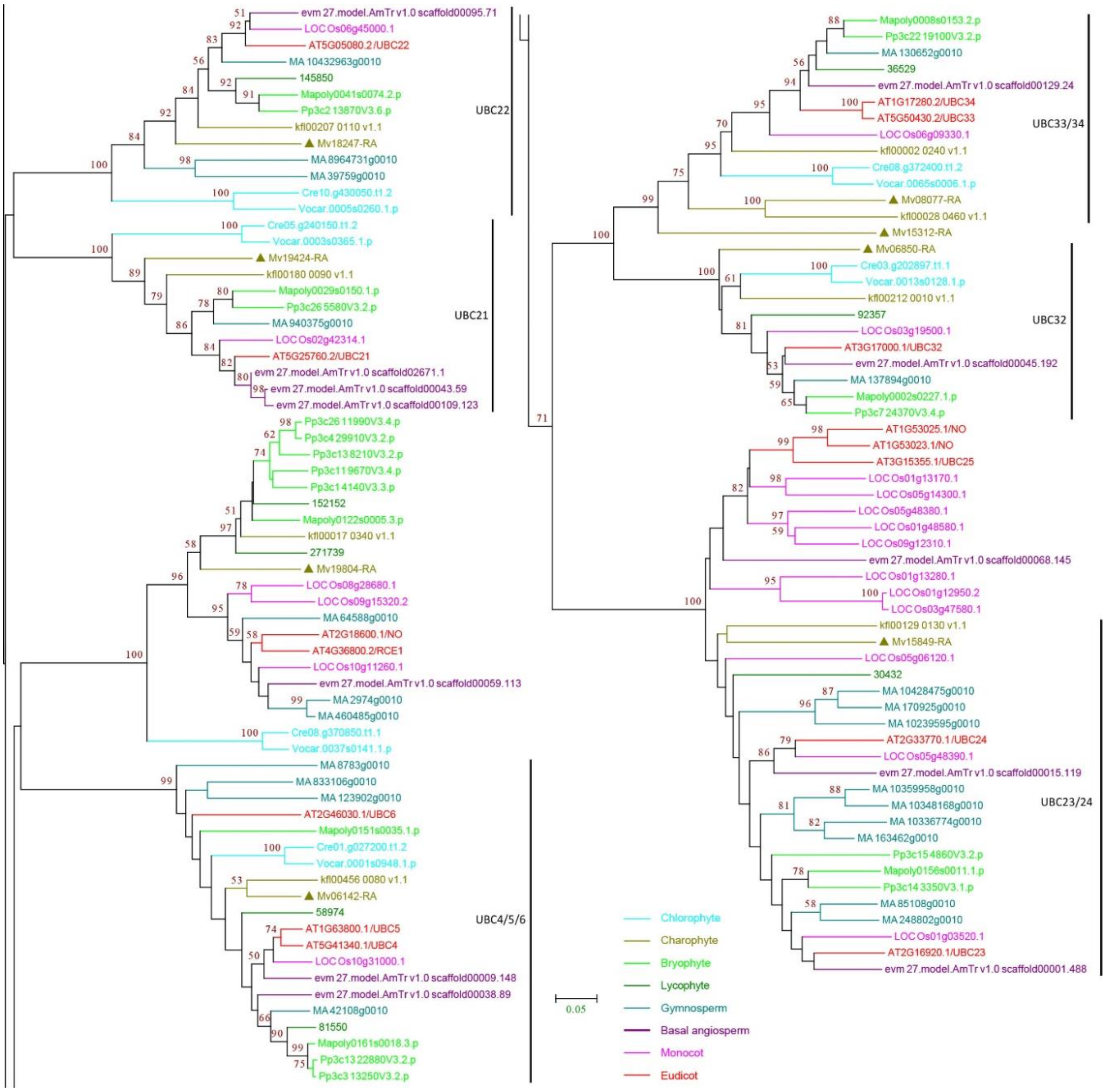
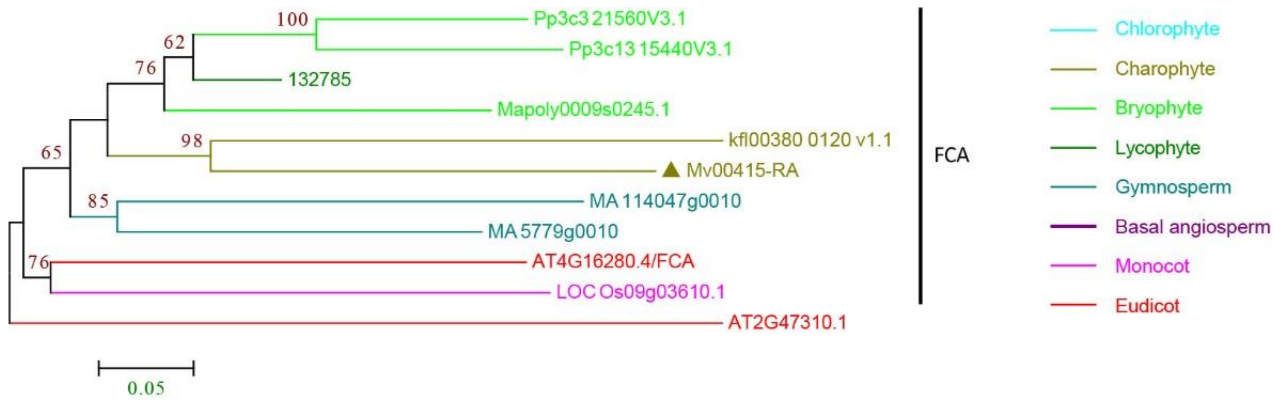
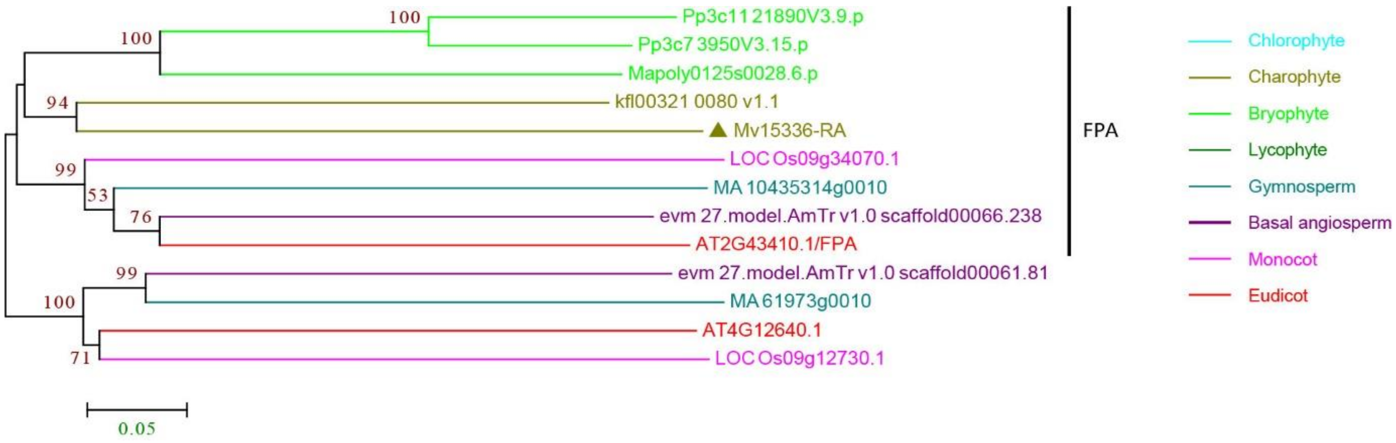


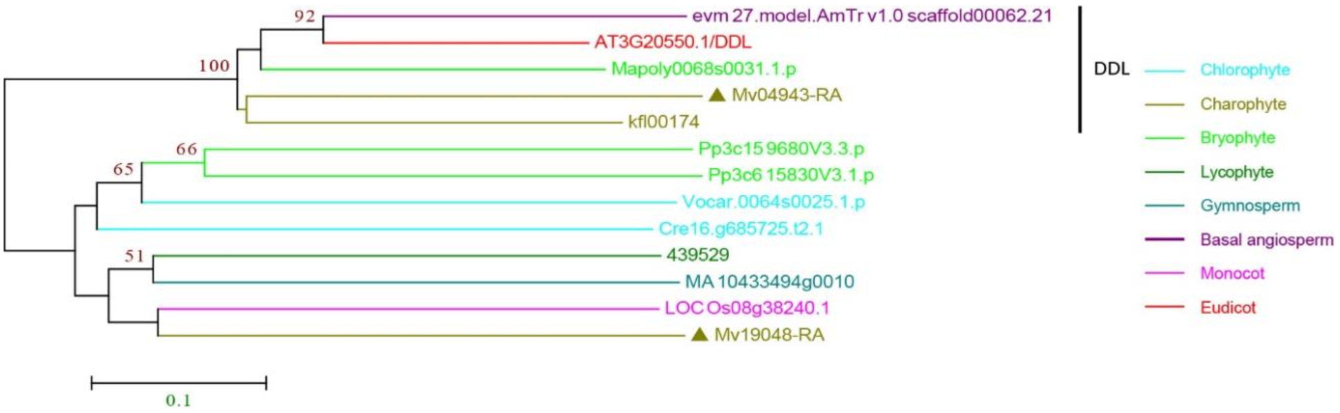
Data S1AH. Phylogenetic relationships of UBIQUITIN-CONJUGATING ENZYME (UBC) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequences were highlighted by triangles. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



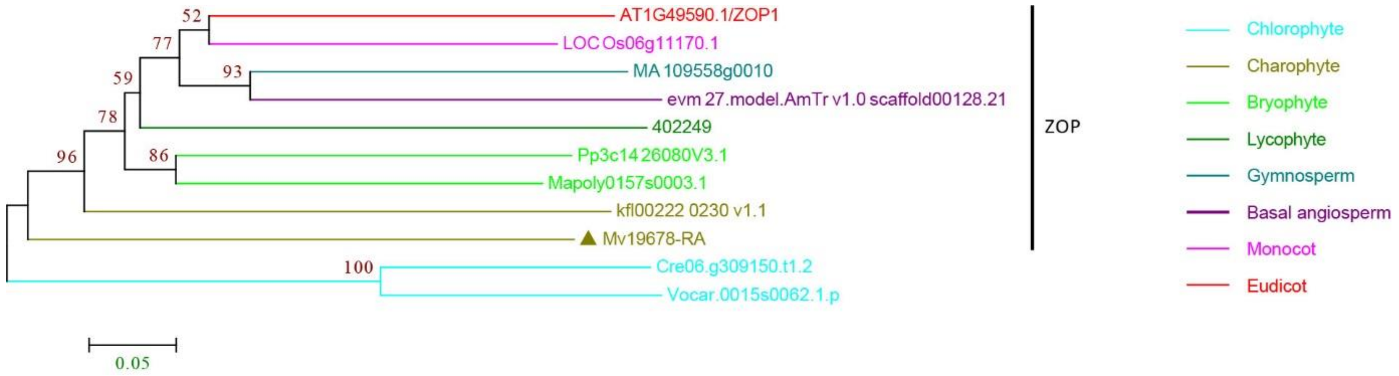
Data S1AI. Phylogenetic relationships of FLOWERING CONTROL LOCUS A (FCA) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequence was highlighted by a triangle. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



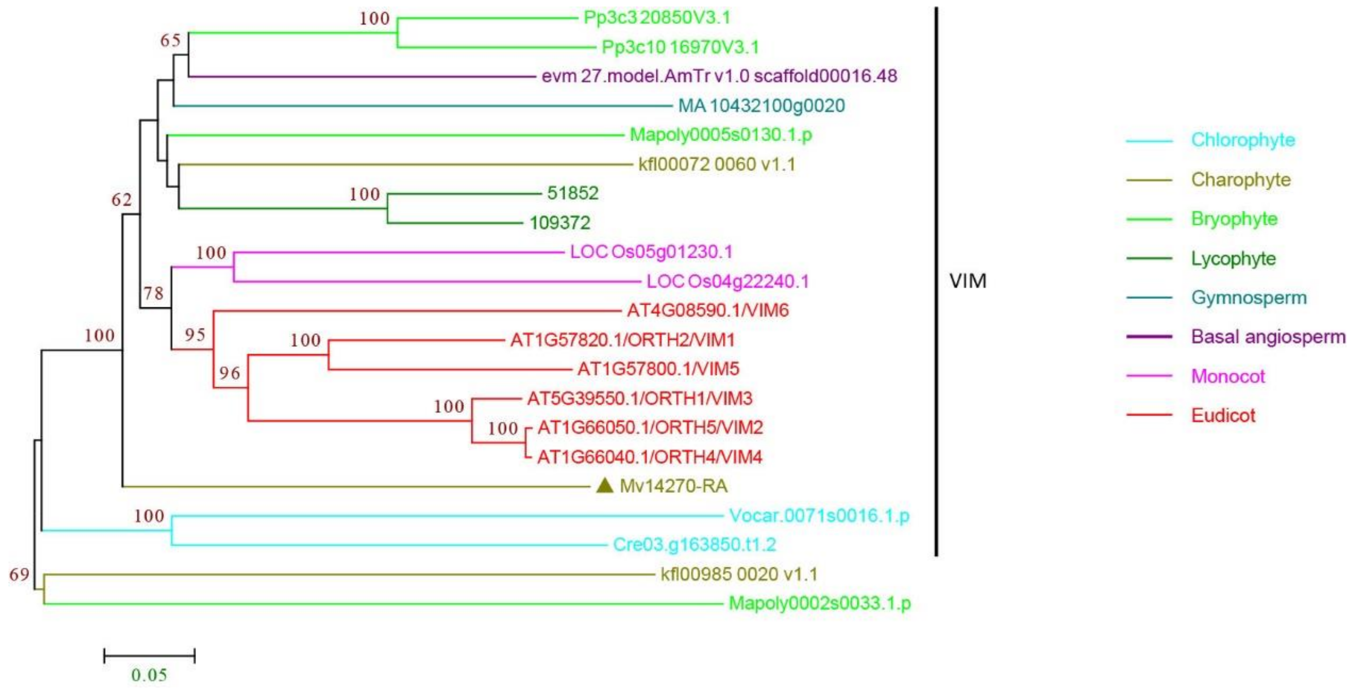
Data S1AJ. Phylogenetic relationships of FPA proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequence was highlighted by a triangle. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



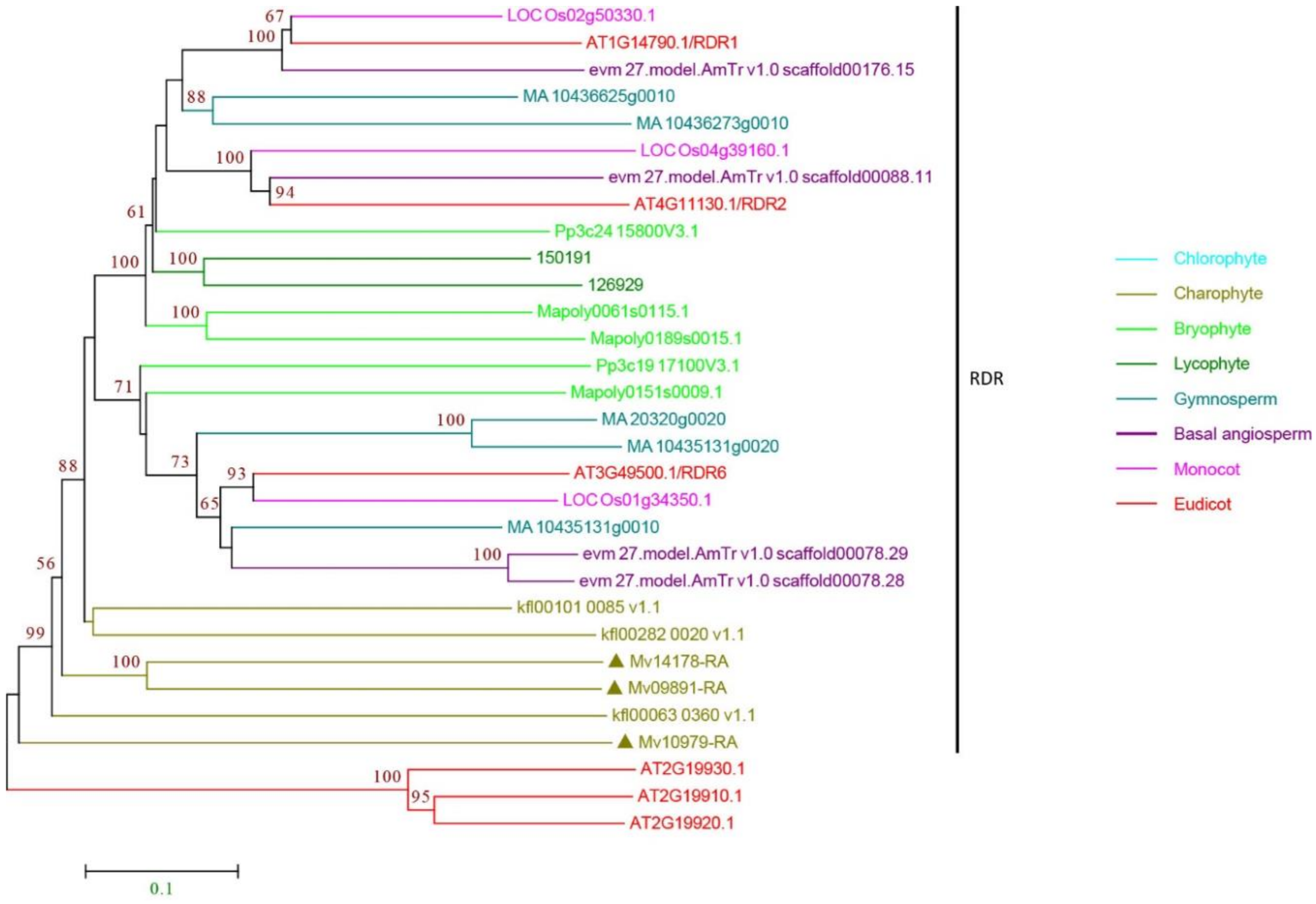
Data S1AK. Phylogenetic relationships of DAWDLE (DDL) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequences were highlighted by triangles. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



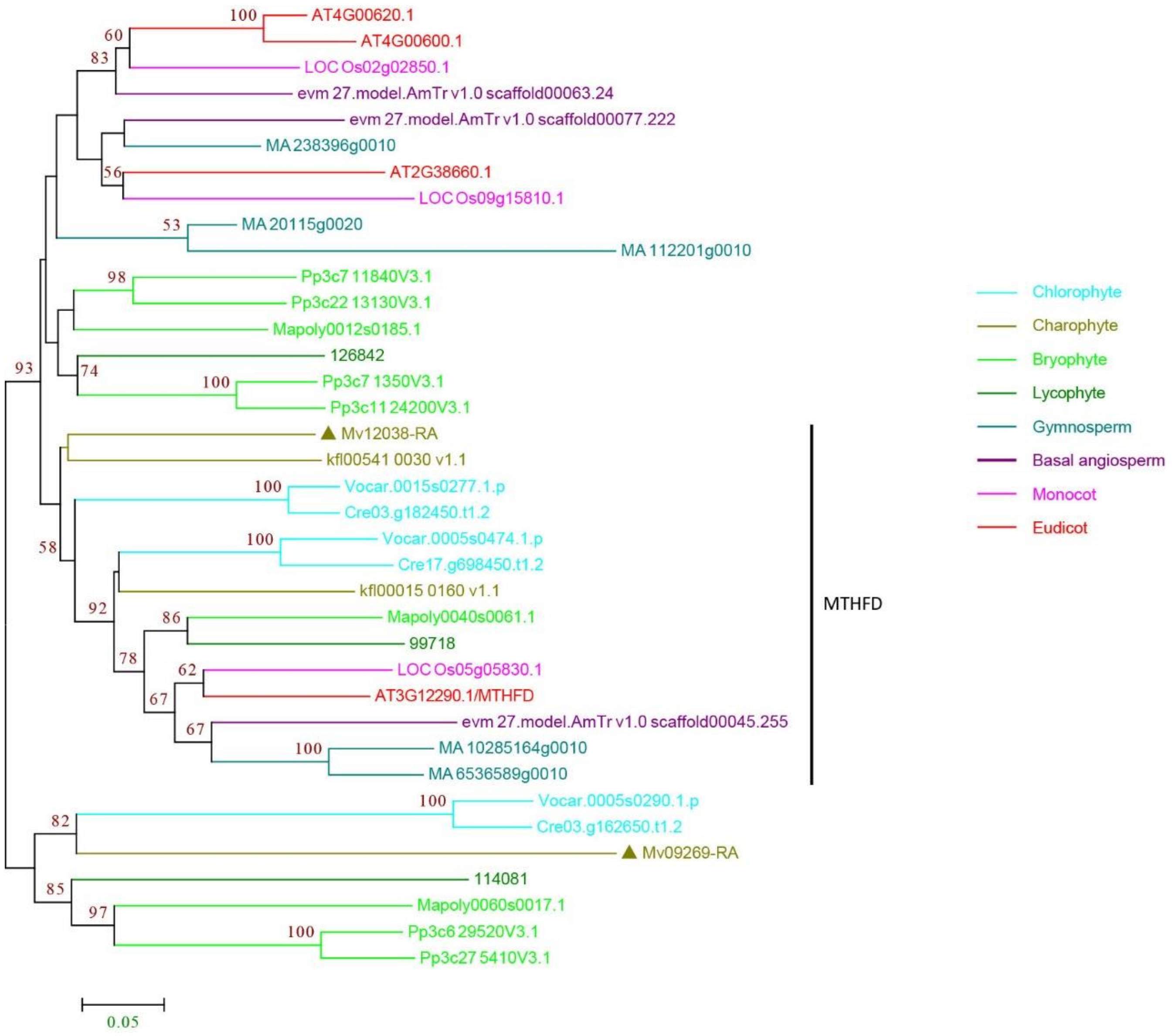
Data S1AL. Phylogenetic relationships of ZINC-FINGER AND OCRE DOMAIN-CONTAINING PROTEIN 1 (ZOP1) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequence was highlighted by a triangle. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



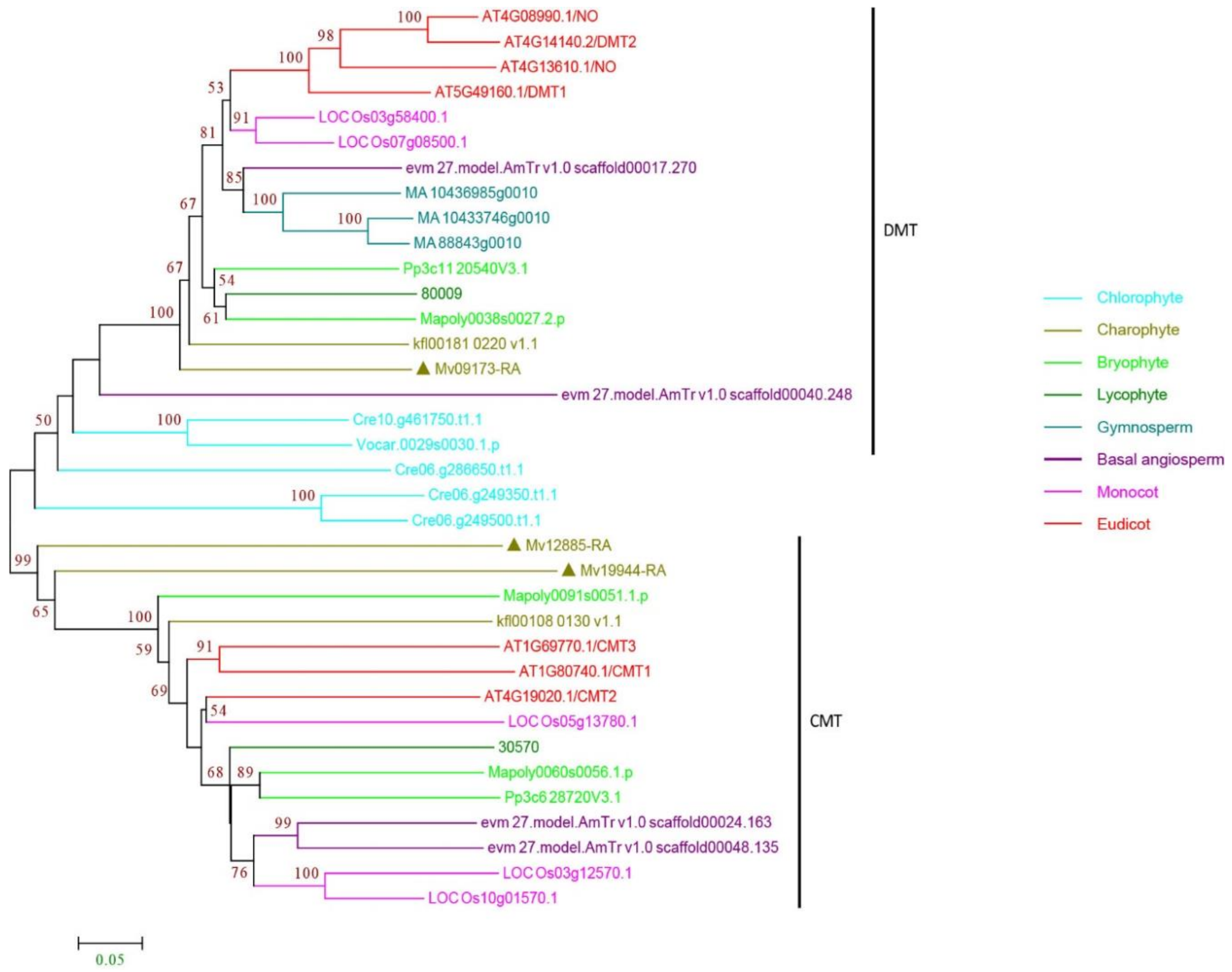
Data S1AM. Phylogenetic relationships of VARIANT IN METHYLATION (VIM) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequence was highlighted by a triangle. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



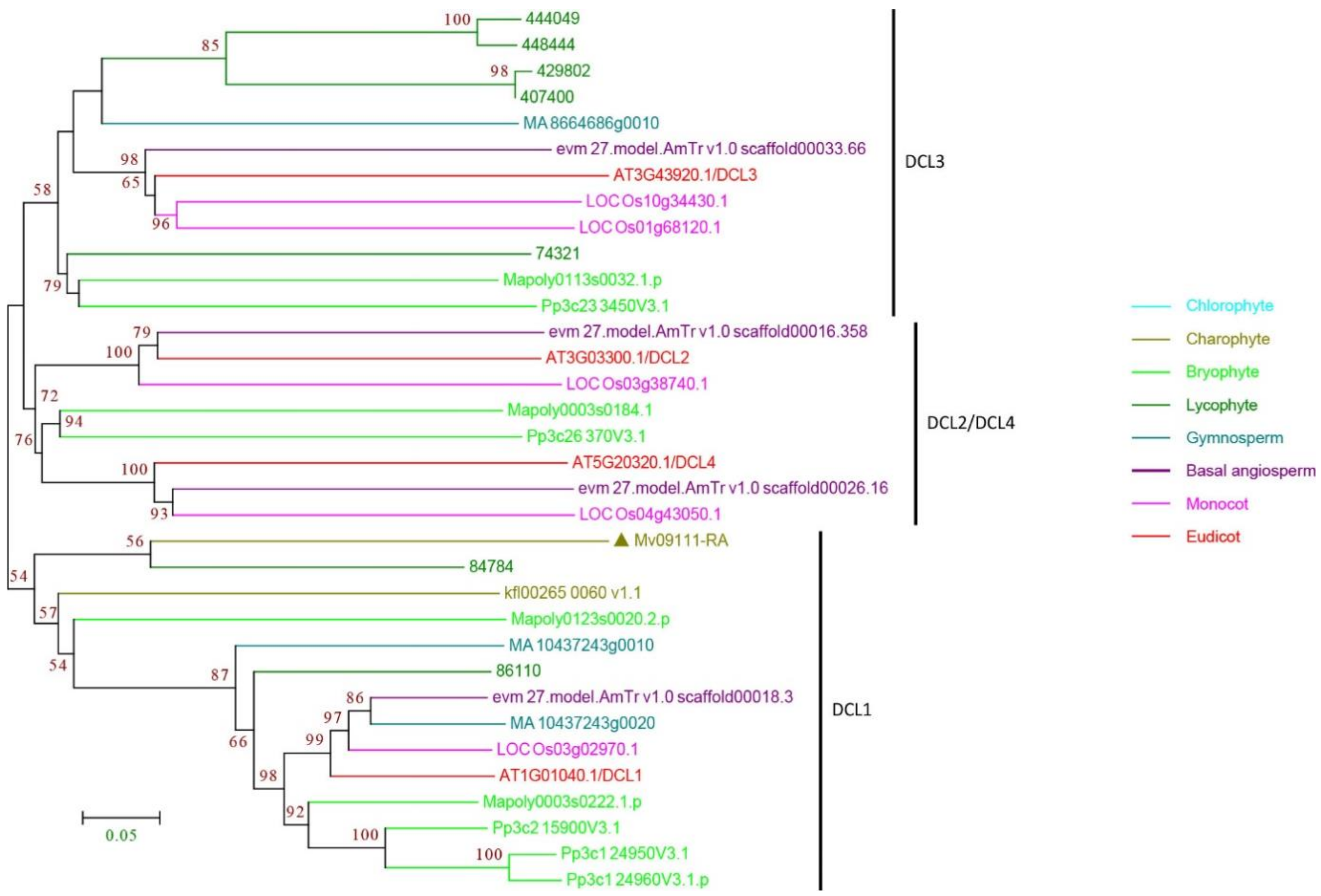
Data S1AN. Phylogenetic relationships of RNA-DEPENDENT RNA POLYMERASE (RDR) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequences were highlighted by triangles. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



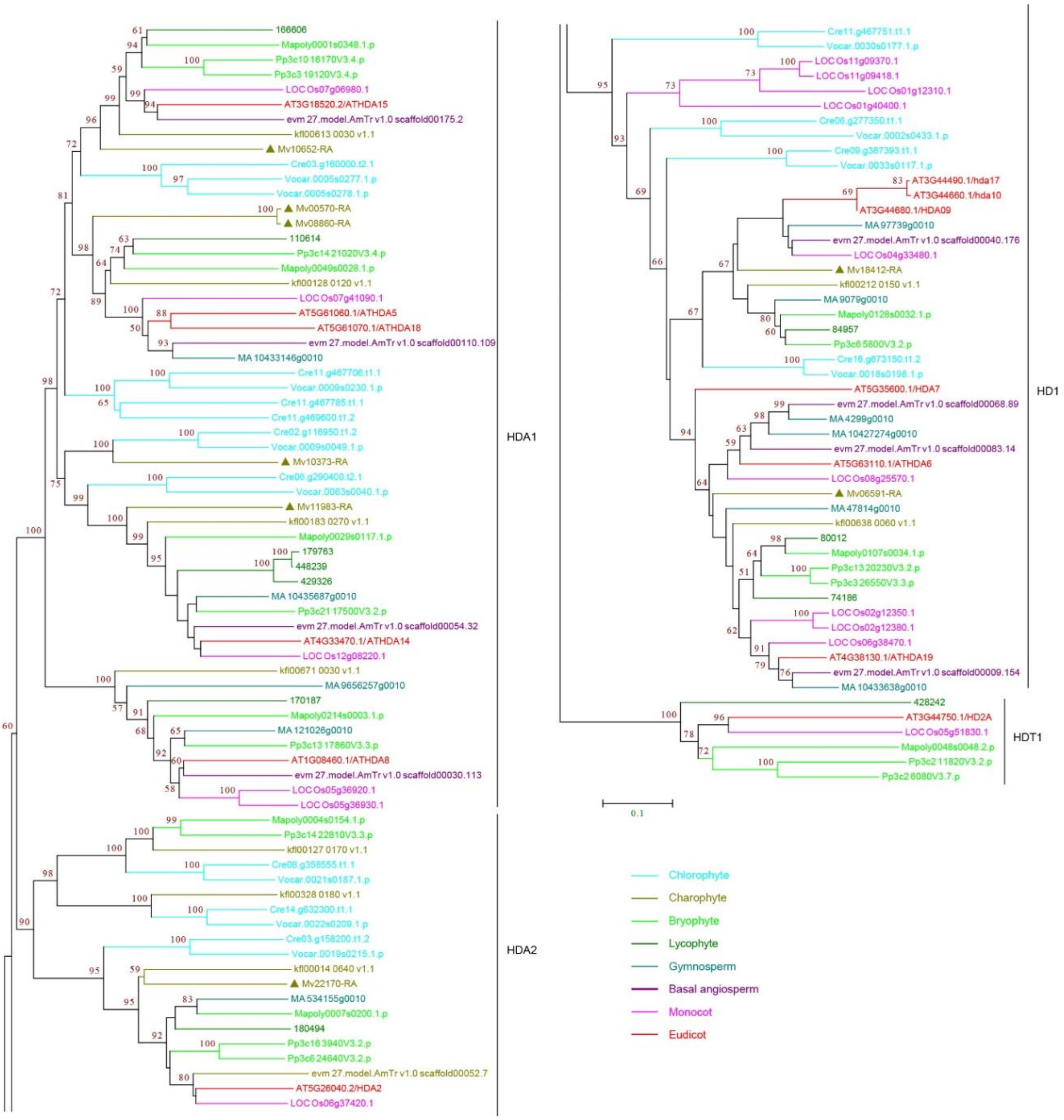
Data S1AO. Phylogenetic relationships of METHYLENETETRAHYDROFOLATE DEHYDROGENASE (MTHFD) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequences were highlighted by triangles. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



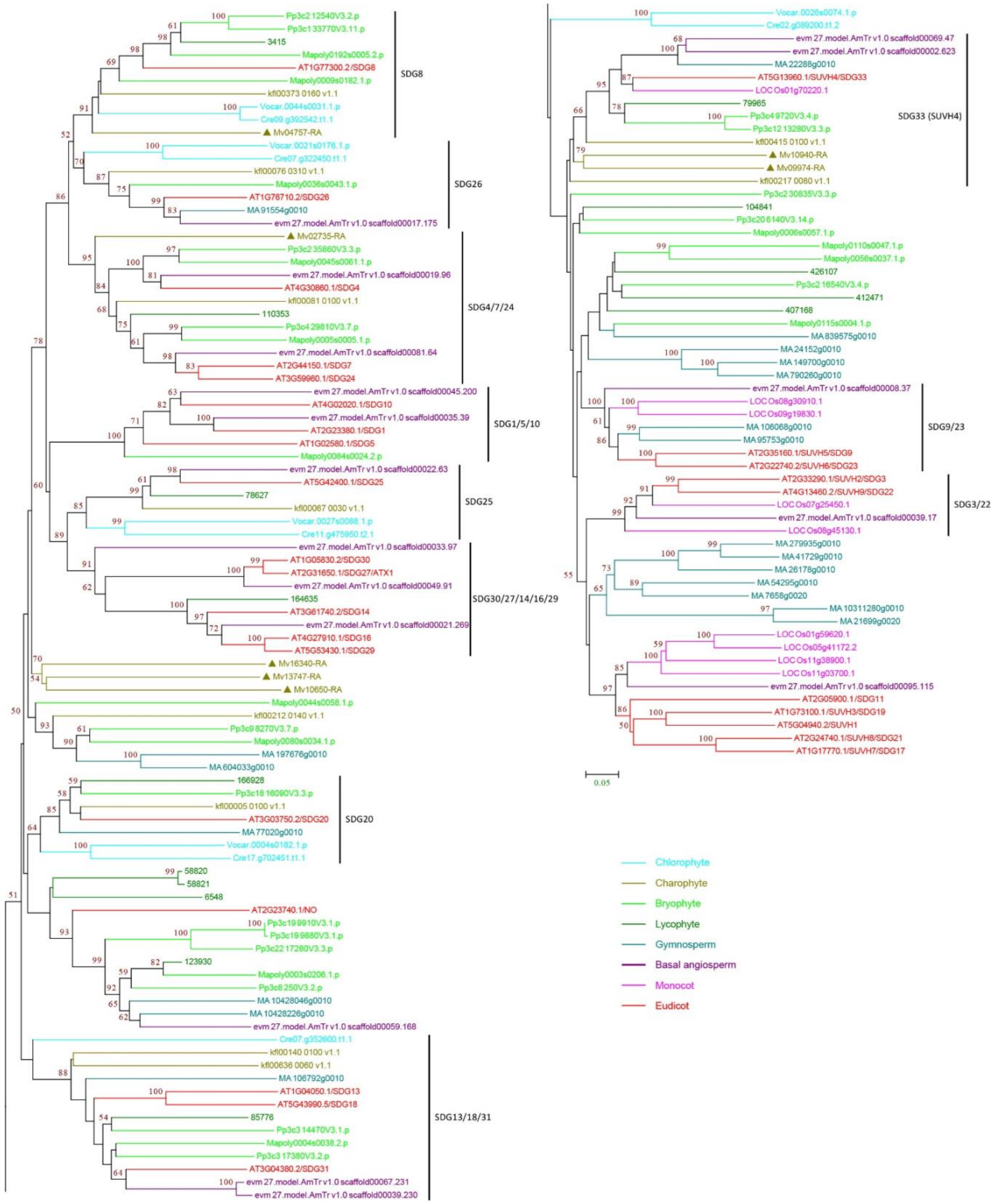
Data S1AP. Phylogenetic relationships of CHROMOMETHYLASE/DNA METHYLTRANSFERASE (CMT/DMT) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequences were highlighted by triangles. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



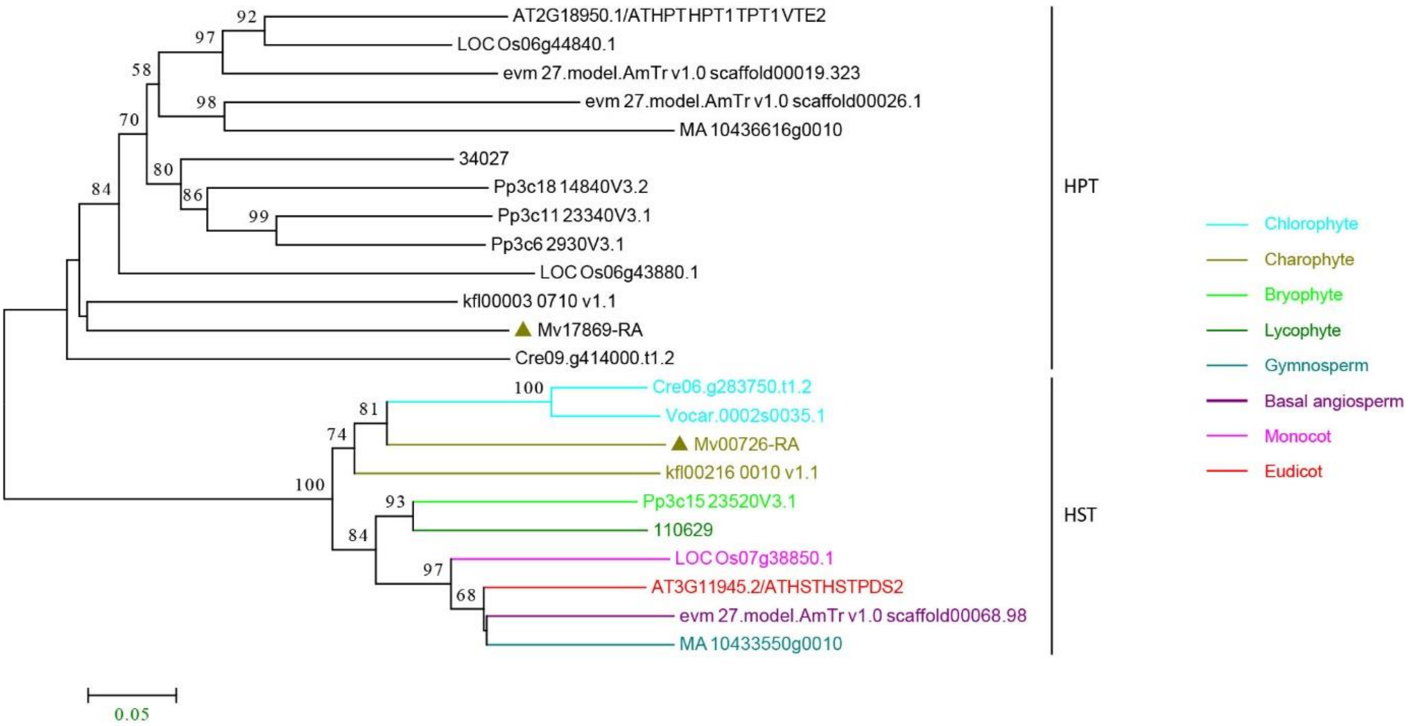
Data S1AQ. Phylogenetic relationships of DICER-LIKE (DCL) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequence was highlighted by a triangle. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



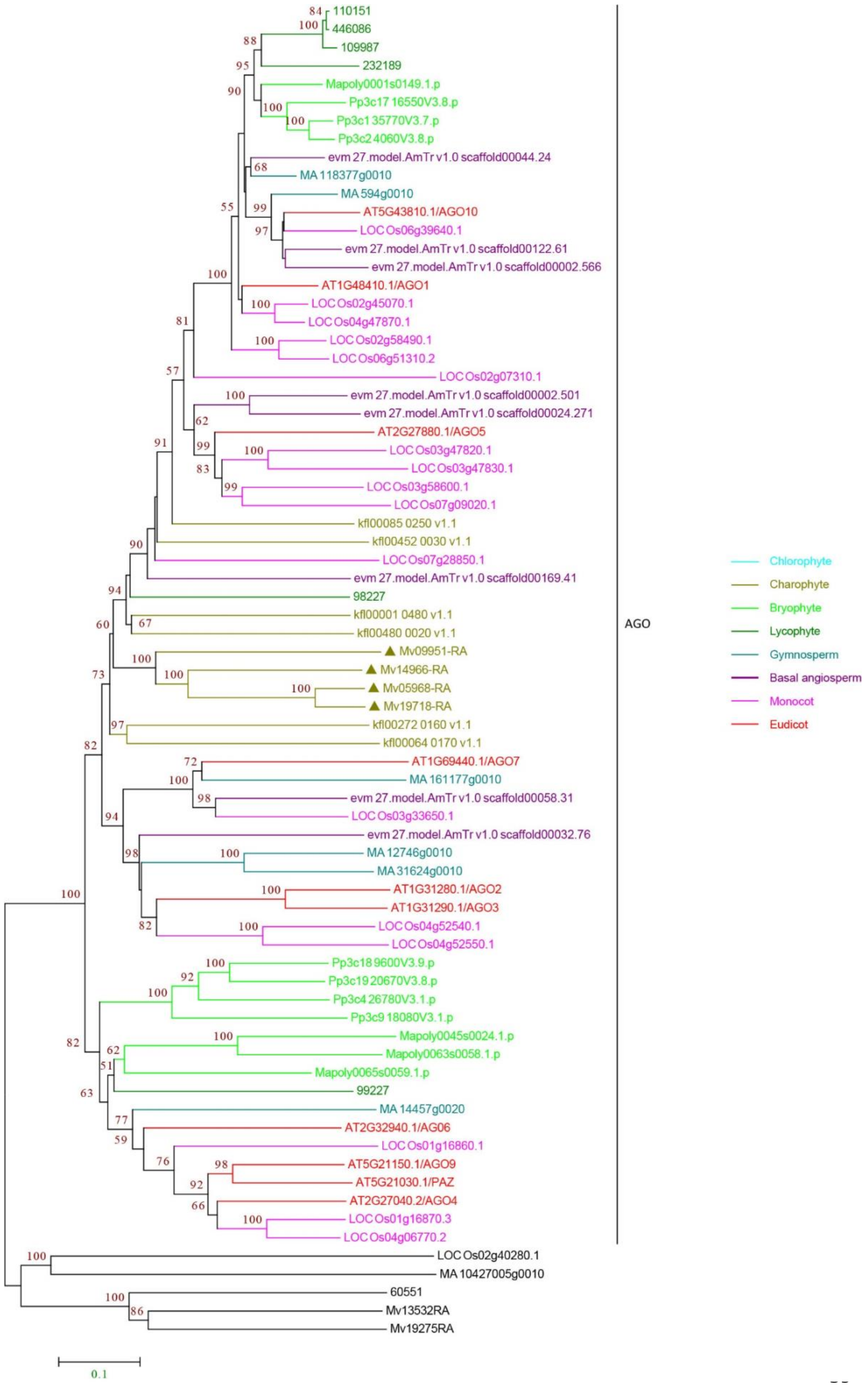
Data S1AR. Phylogenetic relationships of HISTONE DEACETYLASE (HD) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequences were highlighted by triangles. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



Data S1AS. Phylogenetic relationships of SET DOMAIN PROTEIN (SDG) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequences were highlighted by triangles. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



Data S1AT. Phylogenetic relationships of HOMOGENTISATE PRENYLTRANSFERASE (HST) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequences were highlighted by triangles. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.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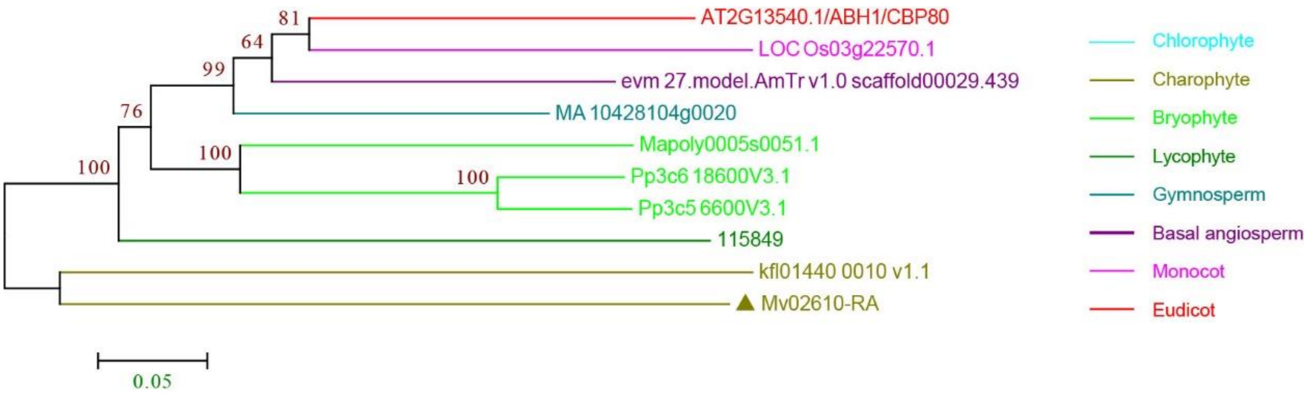
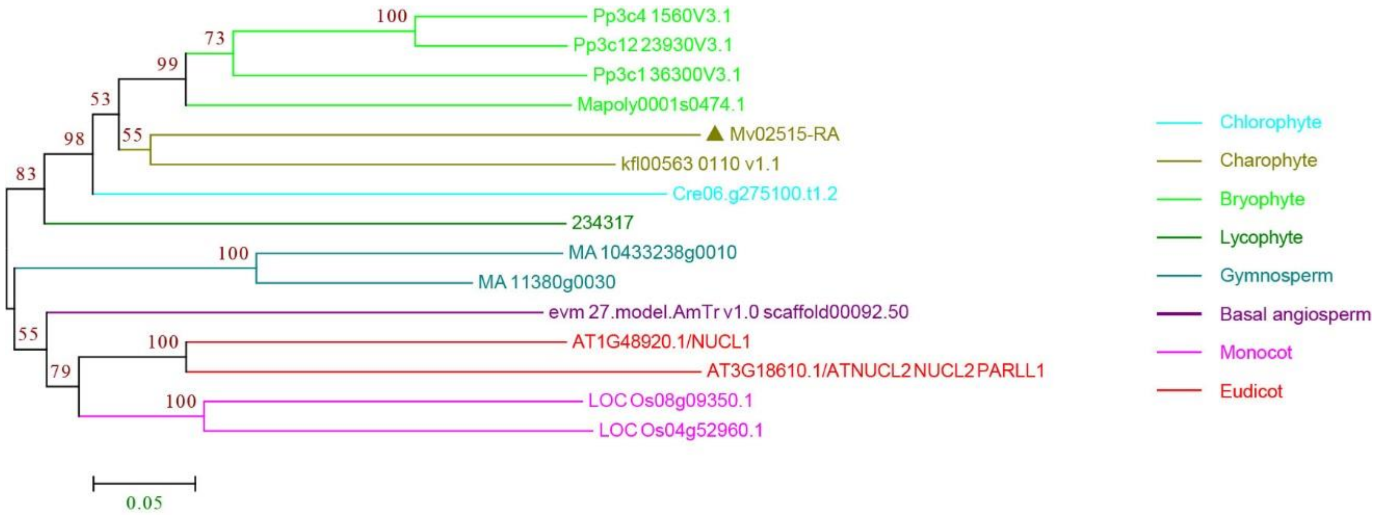
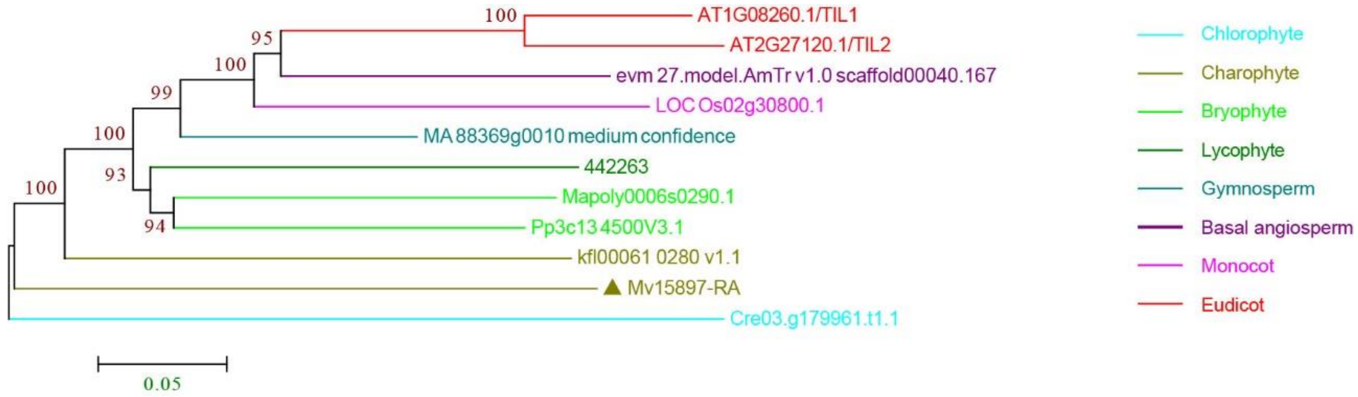
Data S1AU. Phylogenetic relationships of ARGONAUTE (AGO) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequences were highlighted by triangles. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



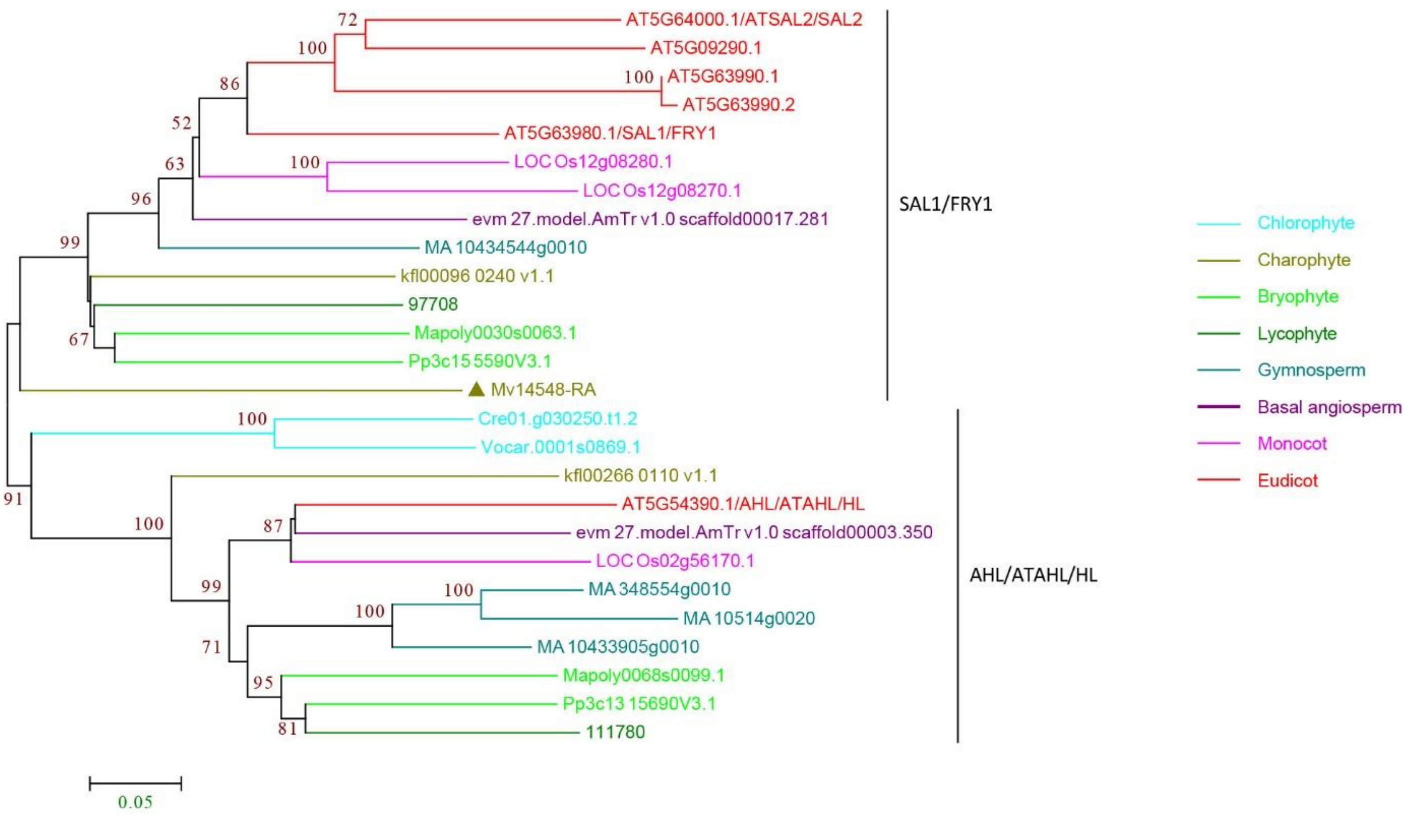
Data S1AV. Phylogenetic relationships of ABA HYPERSENSITIVE 1 (ABH1) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequence was highlighted by a triangle. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



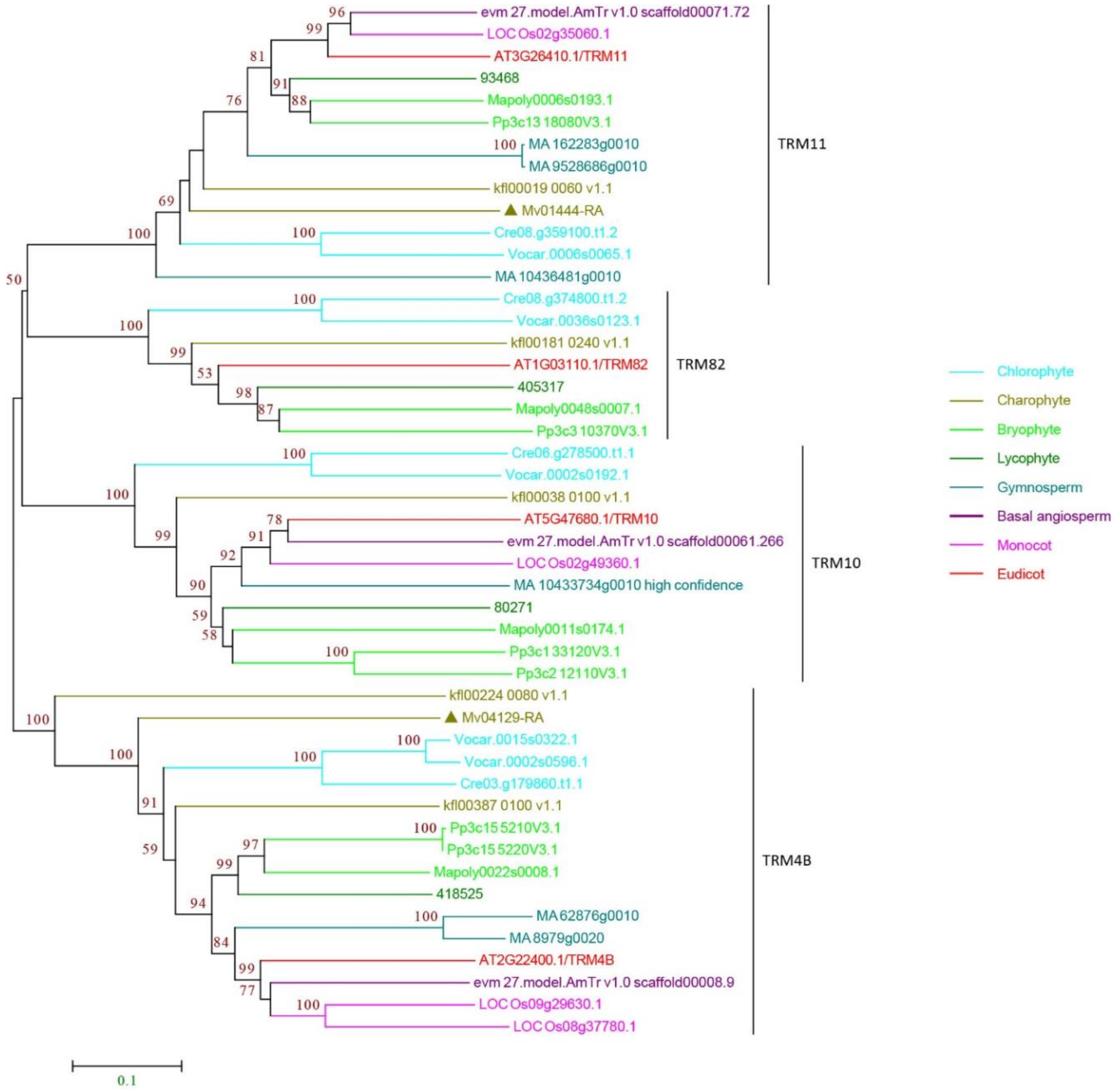
Data S1AW. Phylogenetic relationships of NUCLEOLIN-LIKE (NUCL) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequence was highlighted by a triangle. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



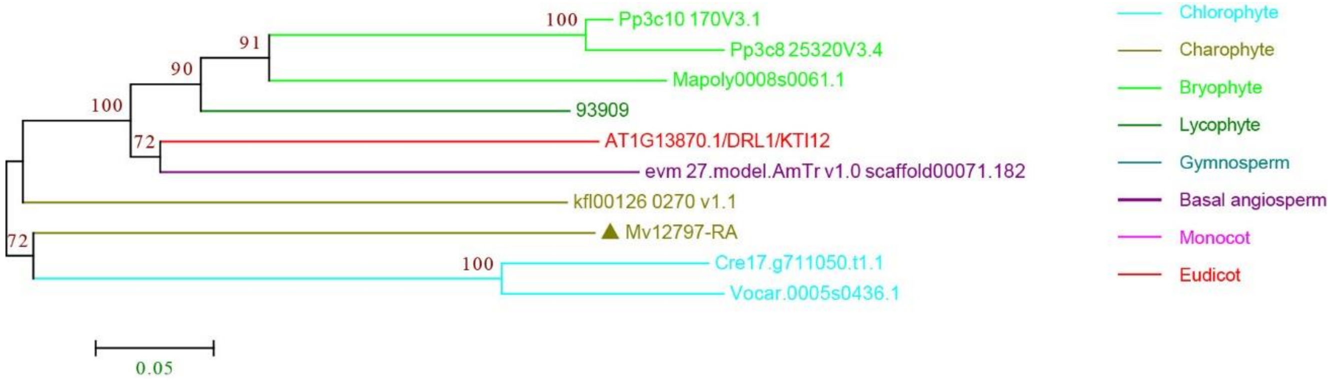
Data S1AX. Phylogenetic relationships of EARLY IN SHORT DAYS 7 (ESD7 or TIL) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequence was highlighted by a triangle. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



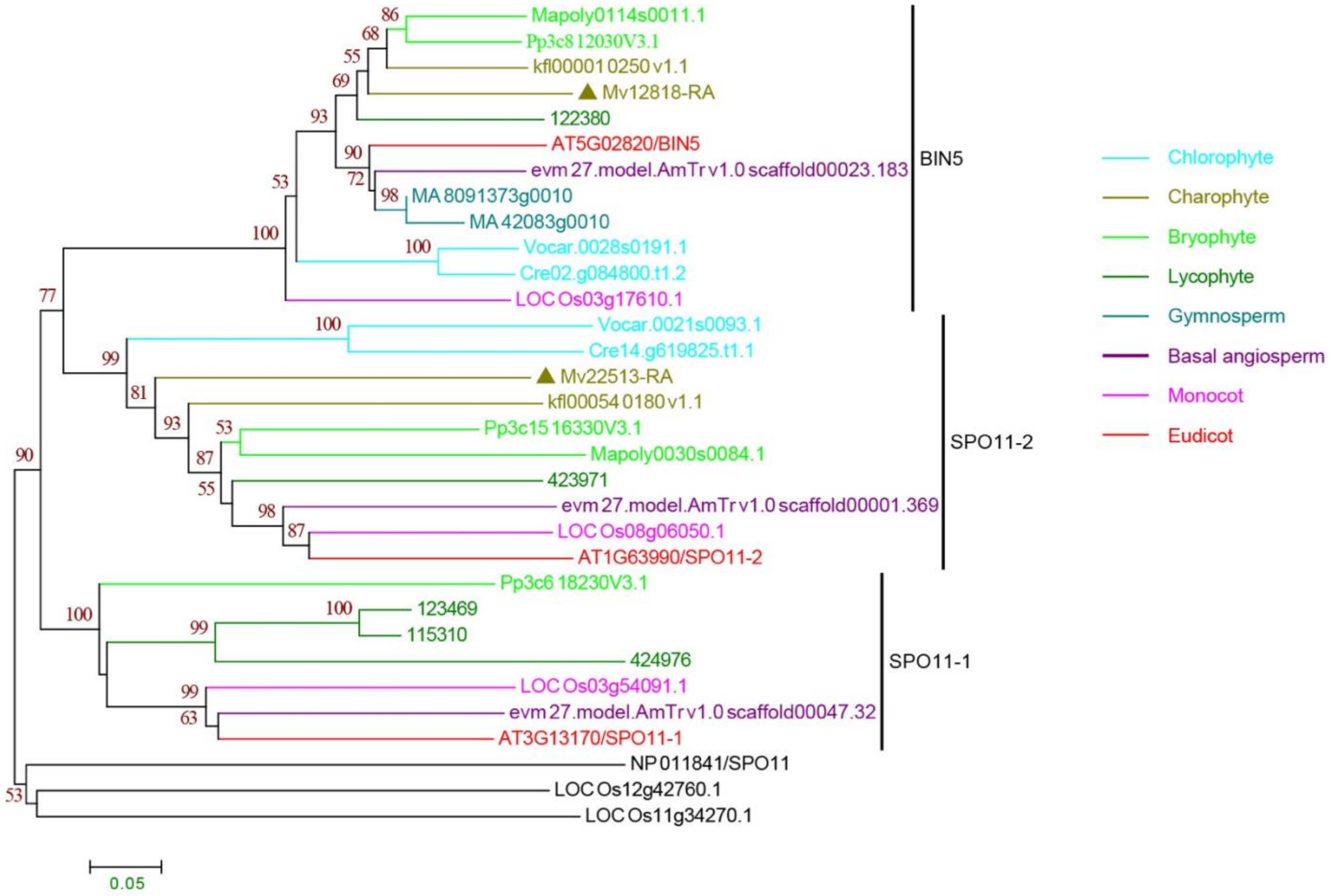
Data S1AY. Phylogenetic relationships of SAL1 proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequence was highlighted by a triangle. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



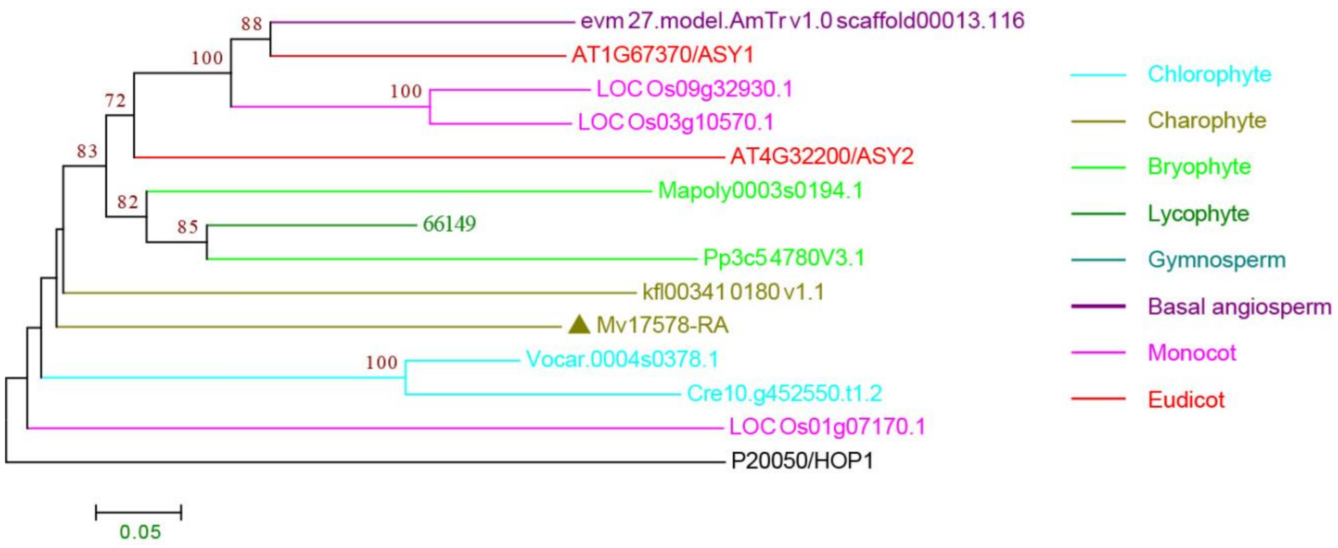
Data S1AZ. Phylogenetic relationships of TRNA MODIFICATION (TRM) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequences were highlighted by triangles. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



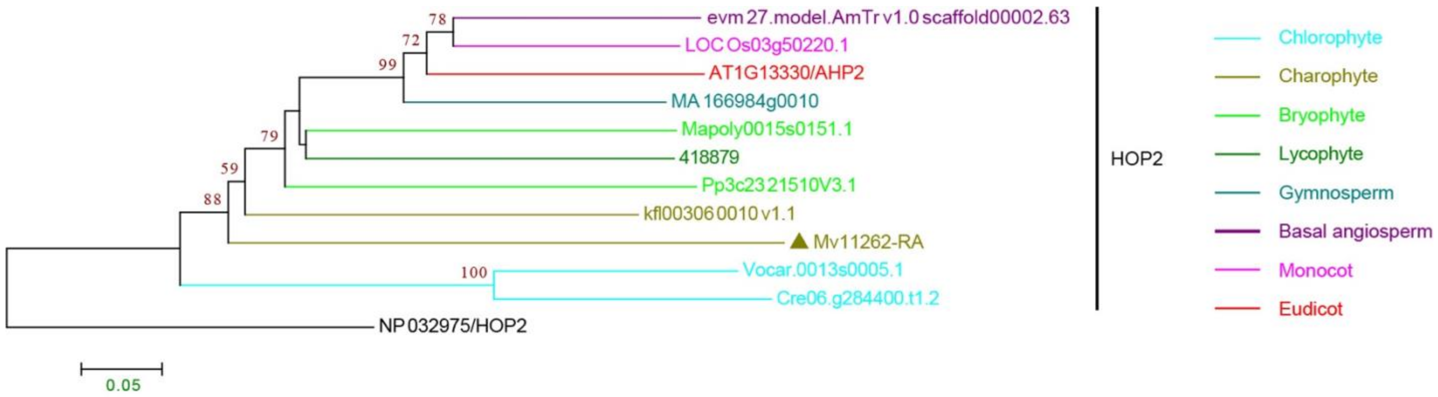
Data S1BA. Phylogenetic relationships of DEFORMED ROOTS AND LEAVES 1 (DRL1) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequence was highlighted by a triangle. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



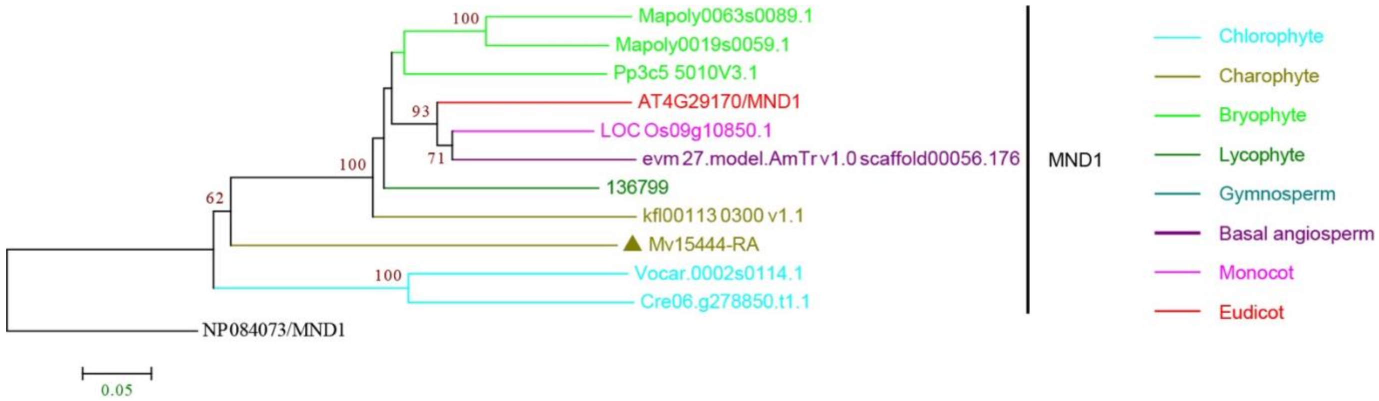
Data S1BB. Phylogenetic relationships of SPO11 proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequence was highlighted by a triangle. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



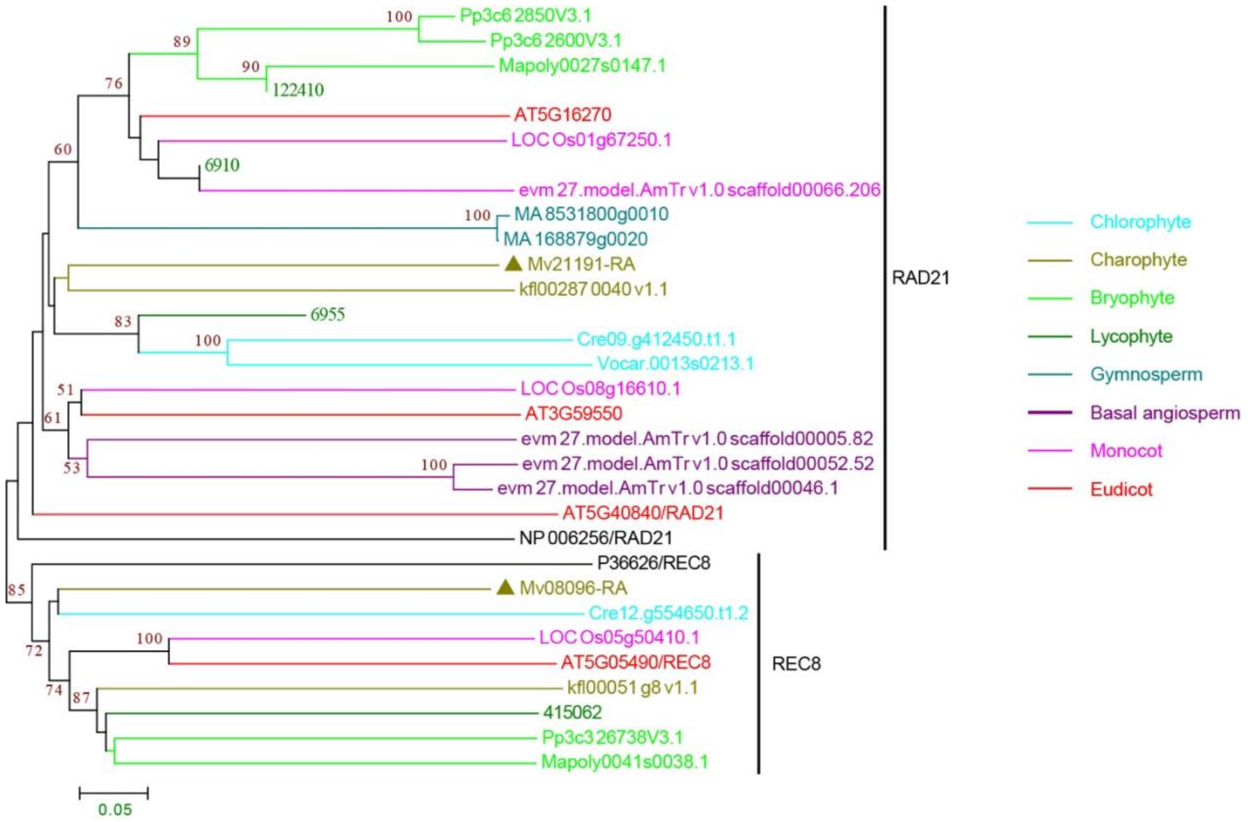
Data S1BC. Phylogenetic relationships of HOP1 proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequence was highlighted by a triangle. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



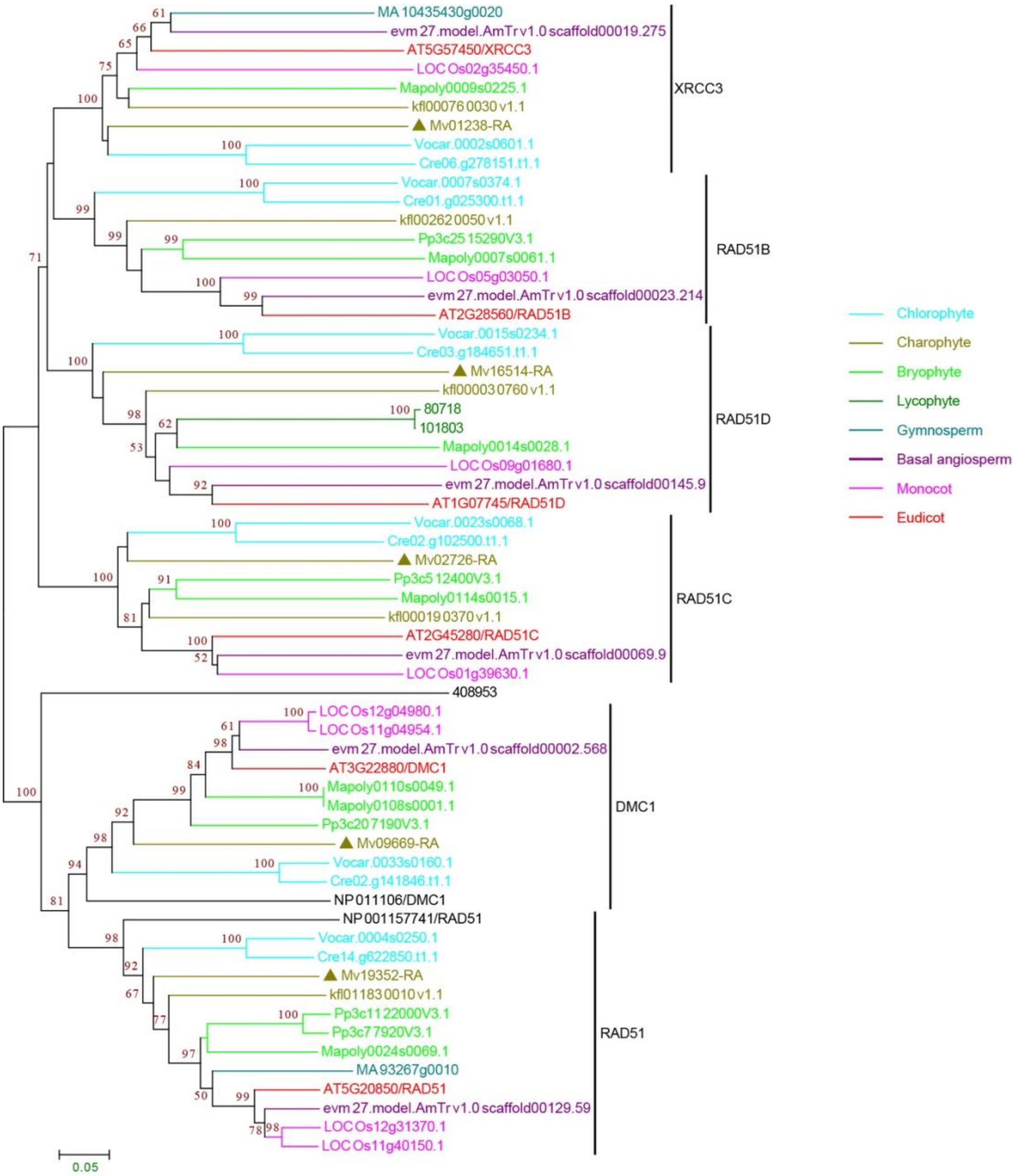
Data S1BD. Phylogenetic relationships of HOP2 proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequence was highlighted by a triangle. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



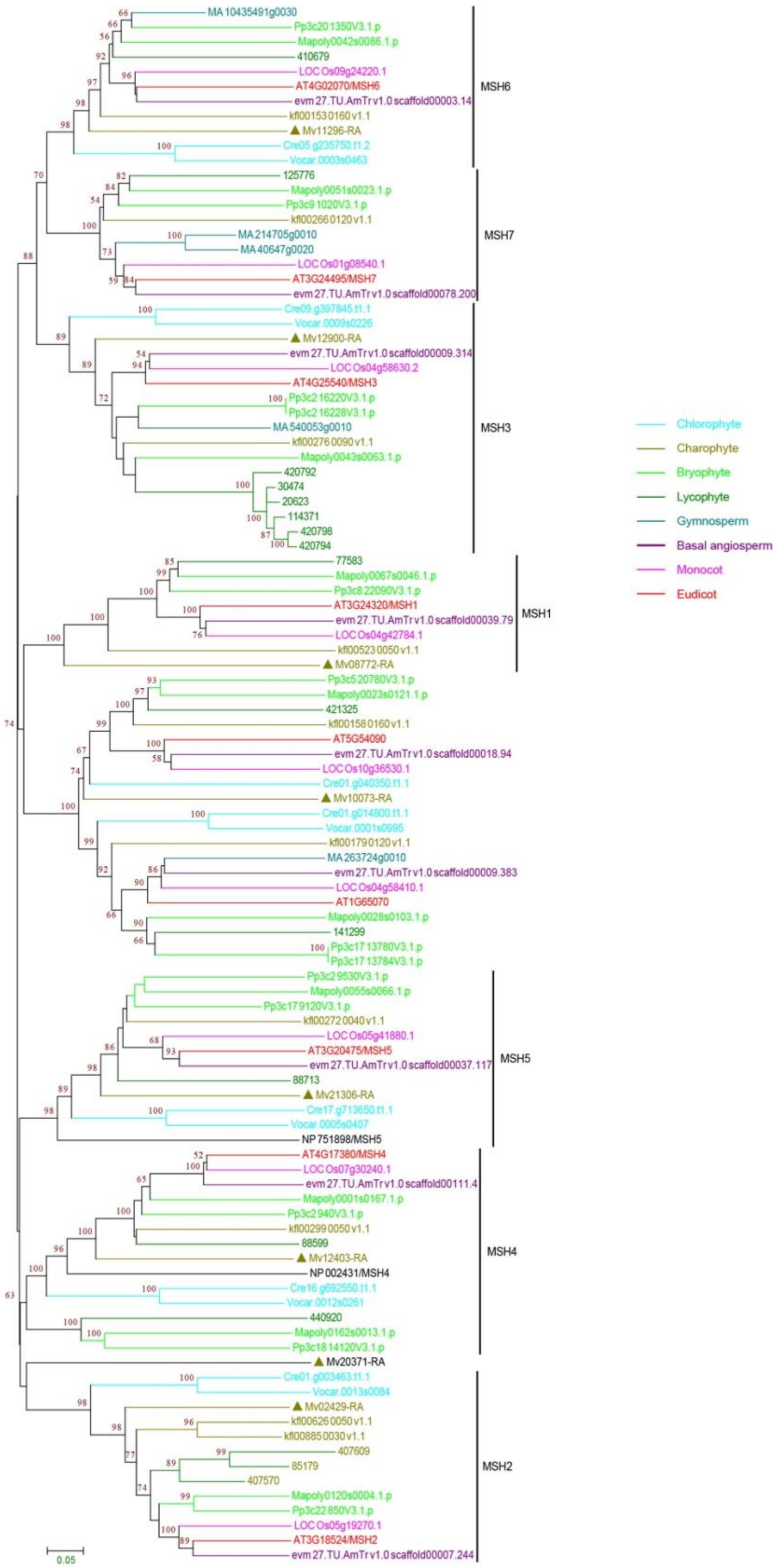
Data S1BE. Phylogenetic relationships of meiotic nuclear division protein 1 (MND1) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequence was highlighted by a triangle. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



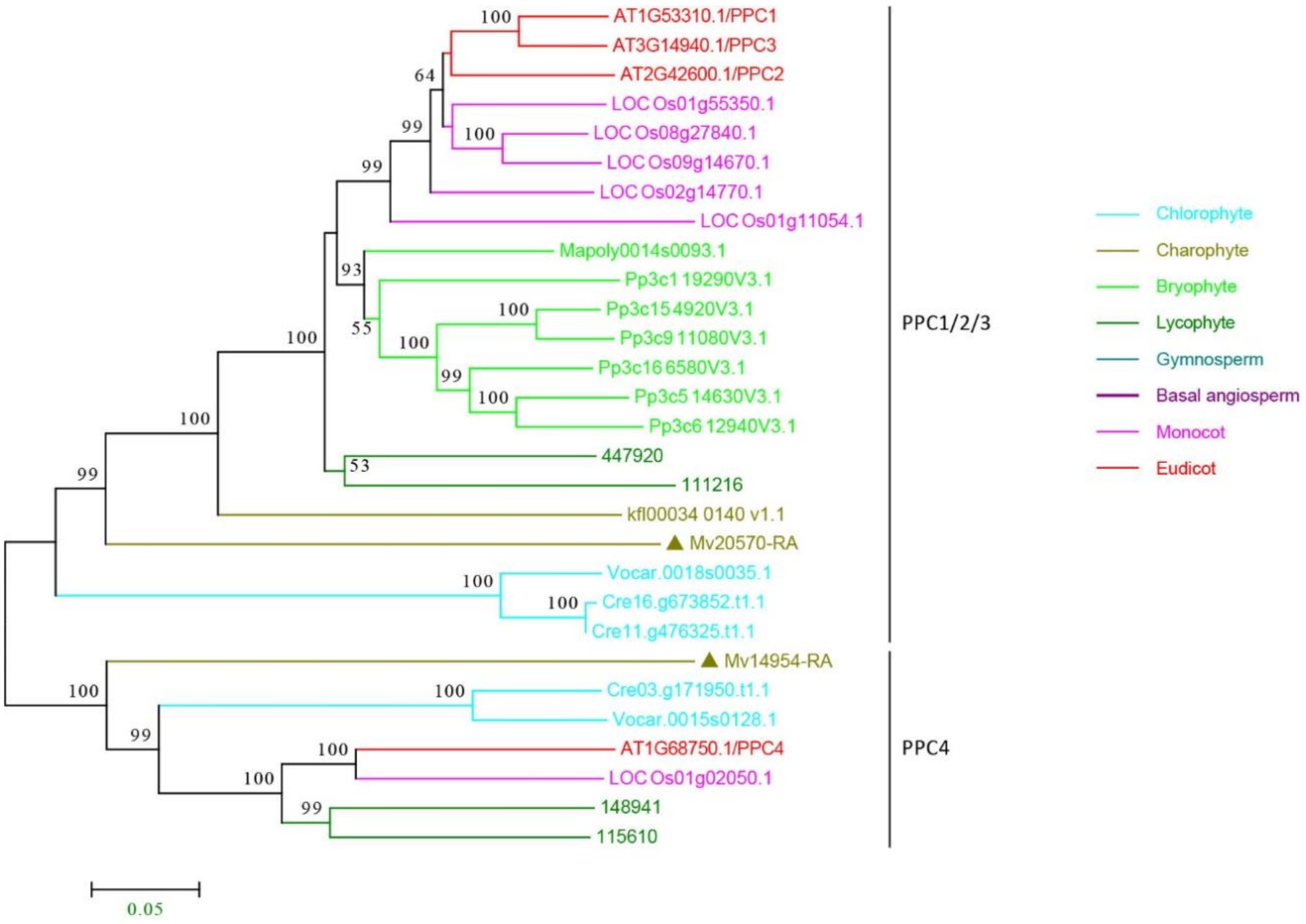
Data S1BF. Phylogenetic relationships of REC8 proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequence was highlighted by a triangle. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



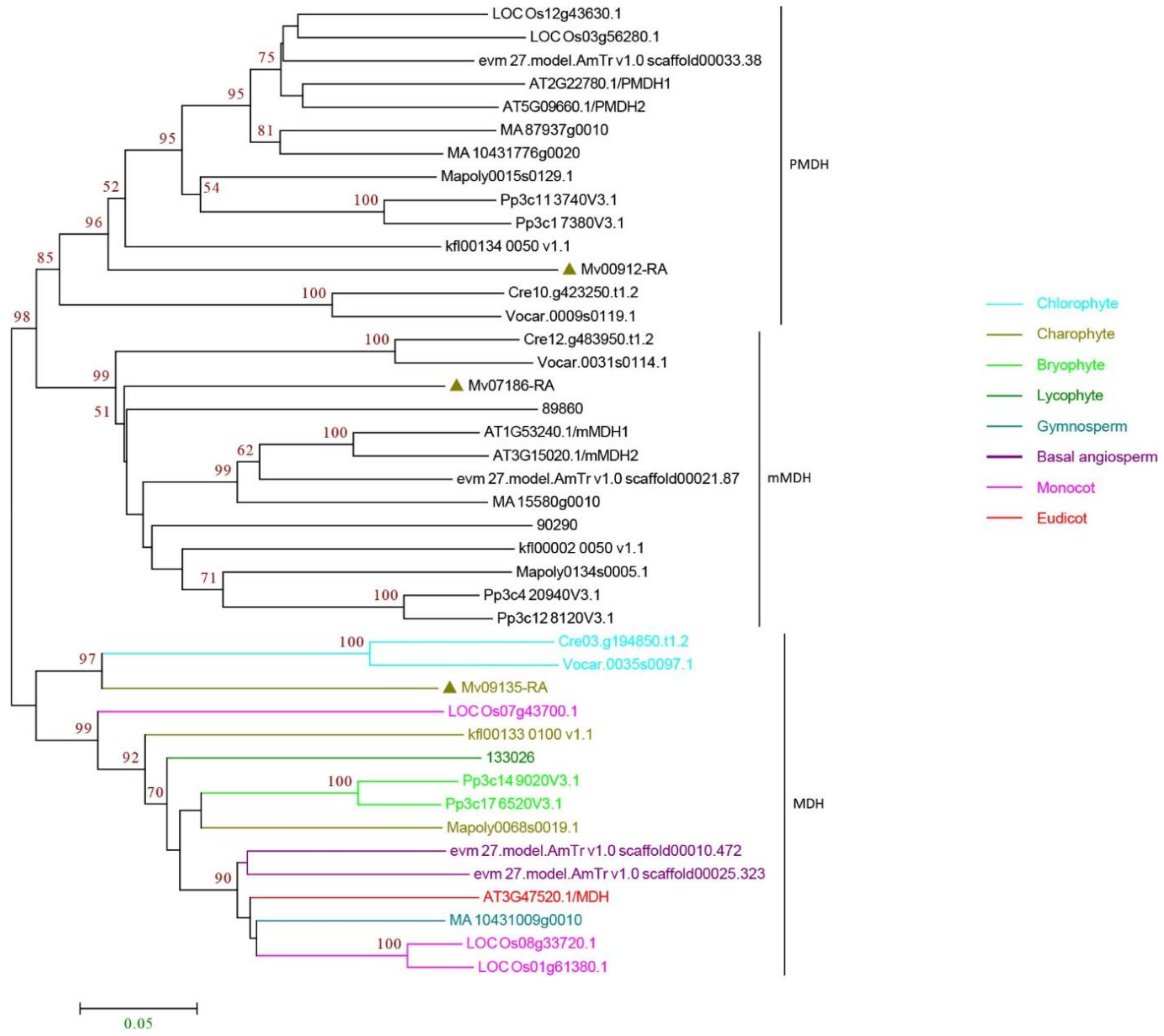
Data S1BG. Phylogenetic relationships of DMC1 proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequence was highlighted by a triangle. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



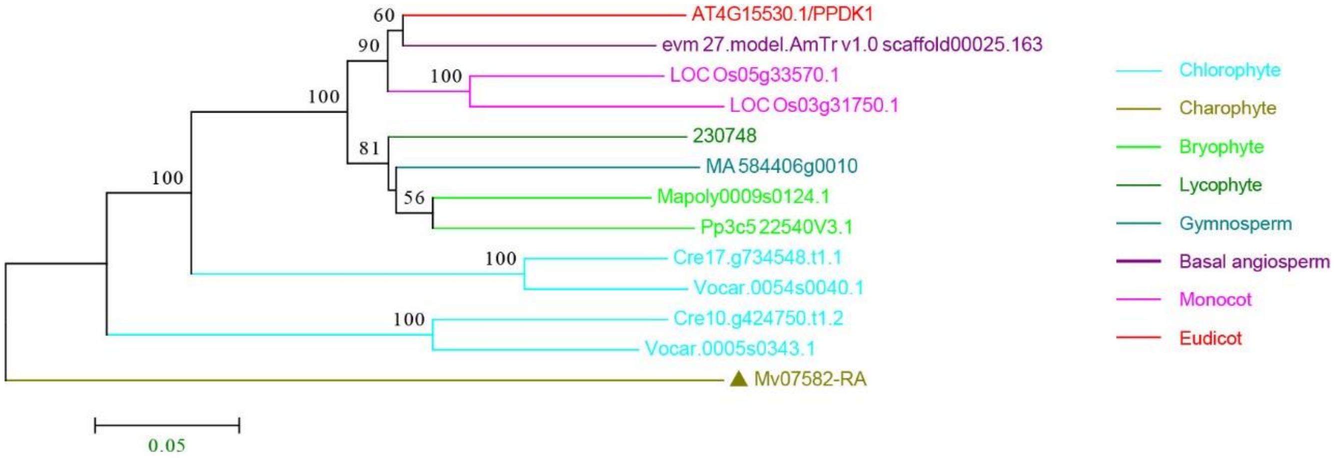
Data S1BH. Phylogenetic relationships of MutS protein homolog 4 (MSH4) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequence was highlighted by a triangle. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



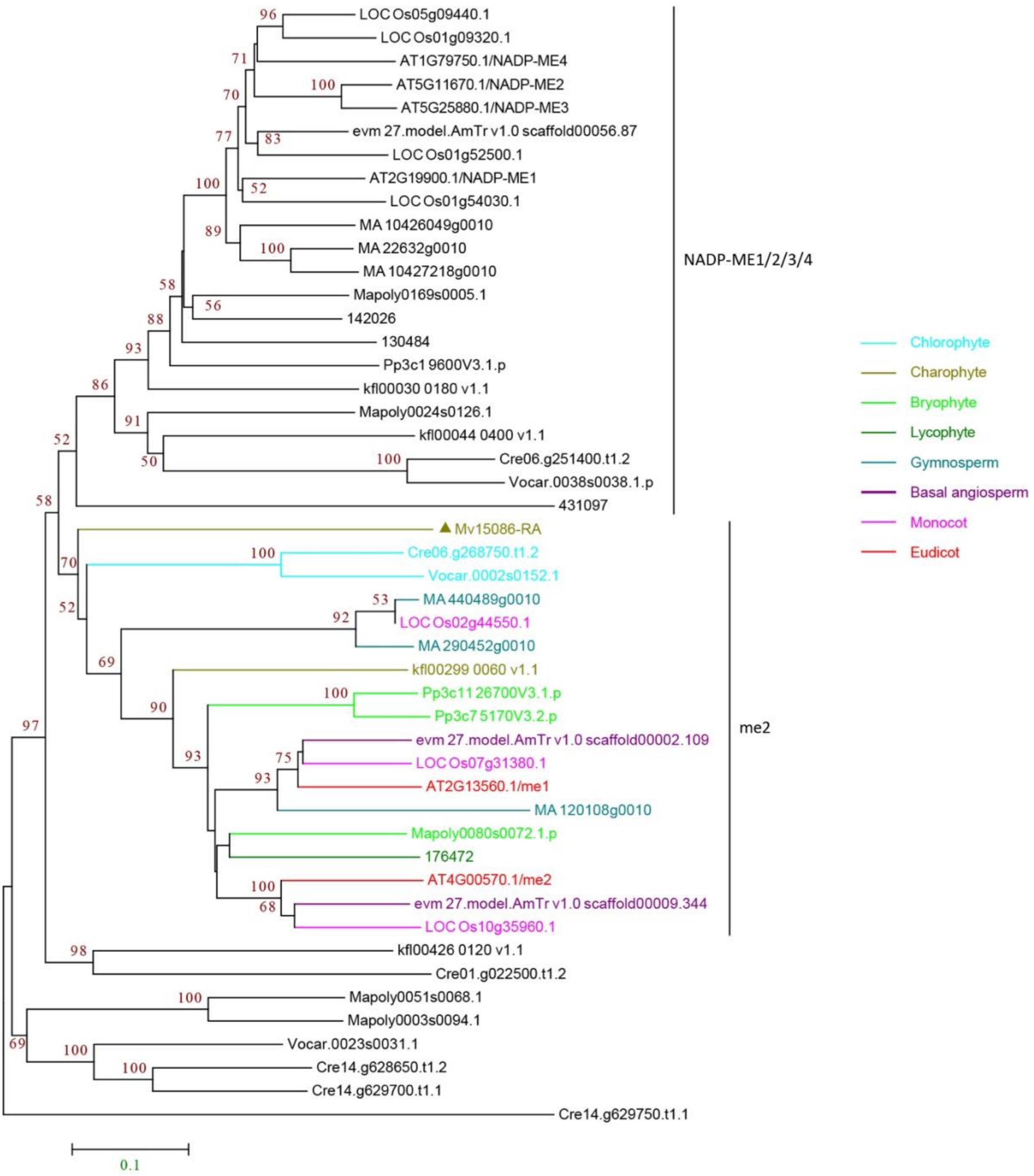
Data S1BI. Phylogenetic relationships of PHOSPHOENOLPYRUVATE CARBOXYLASE (PPC) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequences were highlighted by triangles. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



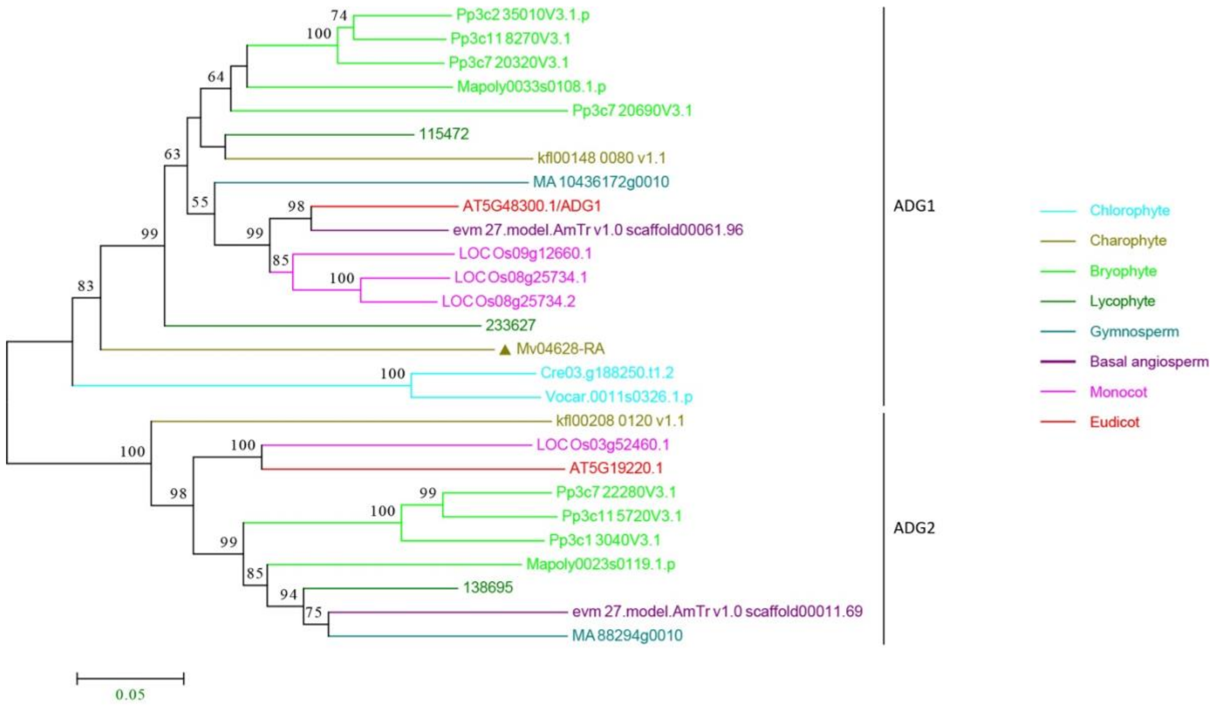
Data S1BJ. Phylogenetic relationships of MALATE DEHYDROGENASE (MDH) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequences were highlighted by triangles. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



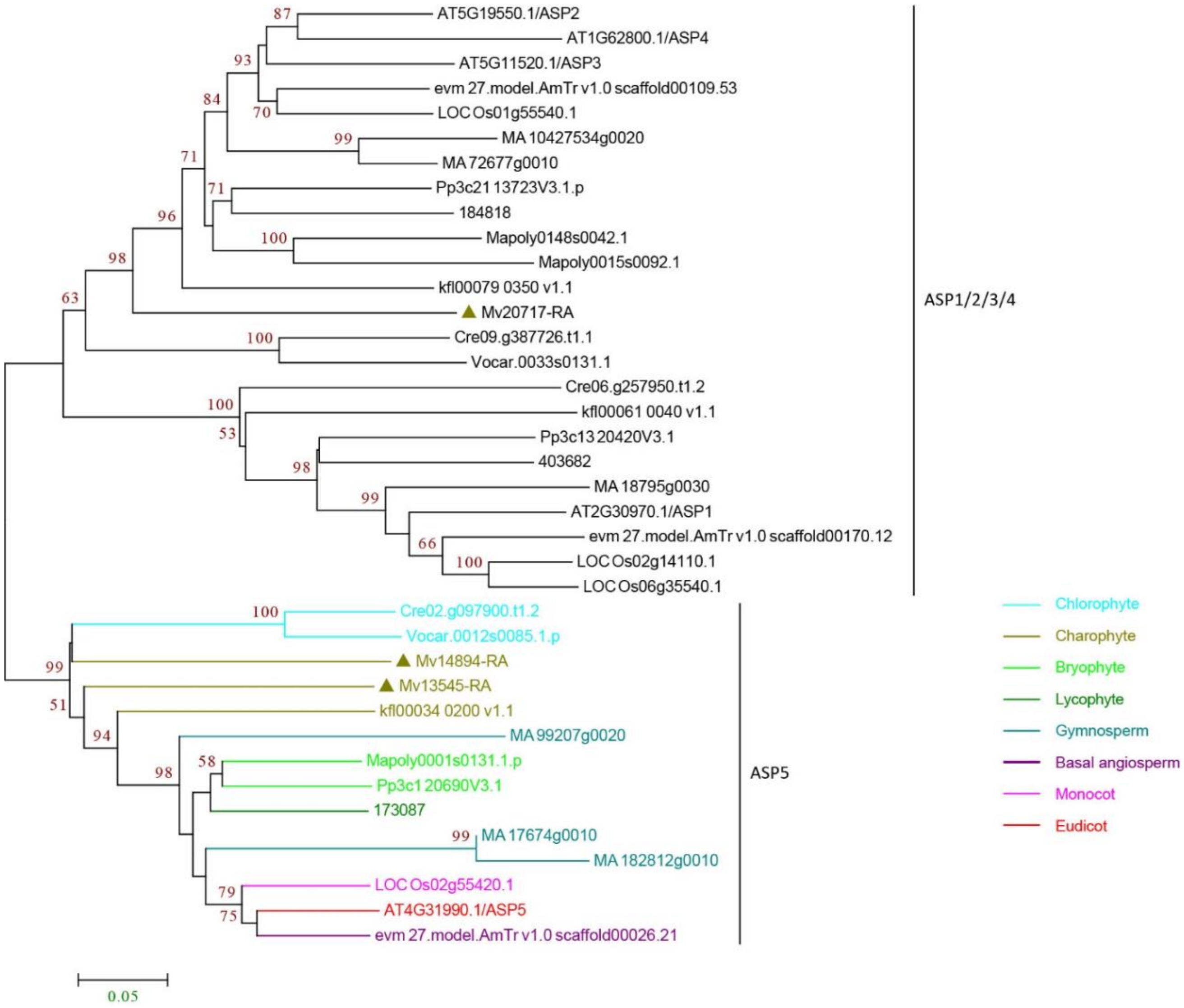
Data S1BK. Phylogenetic relationships of PYRUVATE ORTHOPHOSPHATE DIKINASE (PPDK) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequence was highlighted by a triangle. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



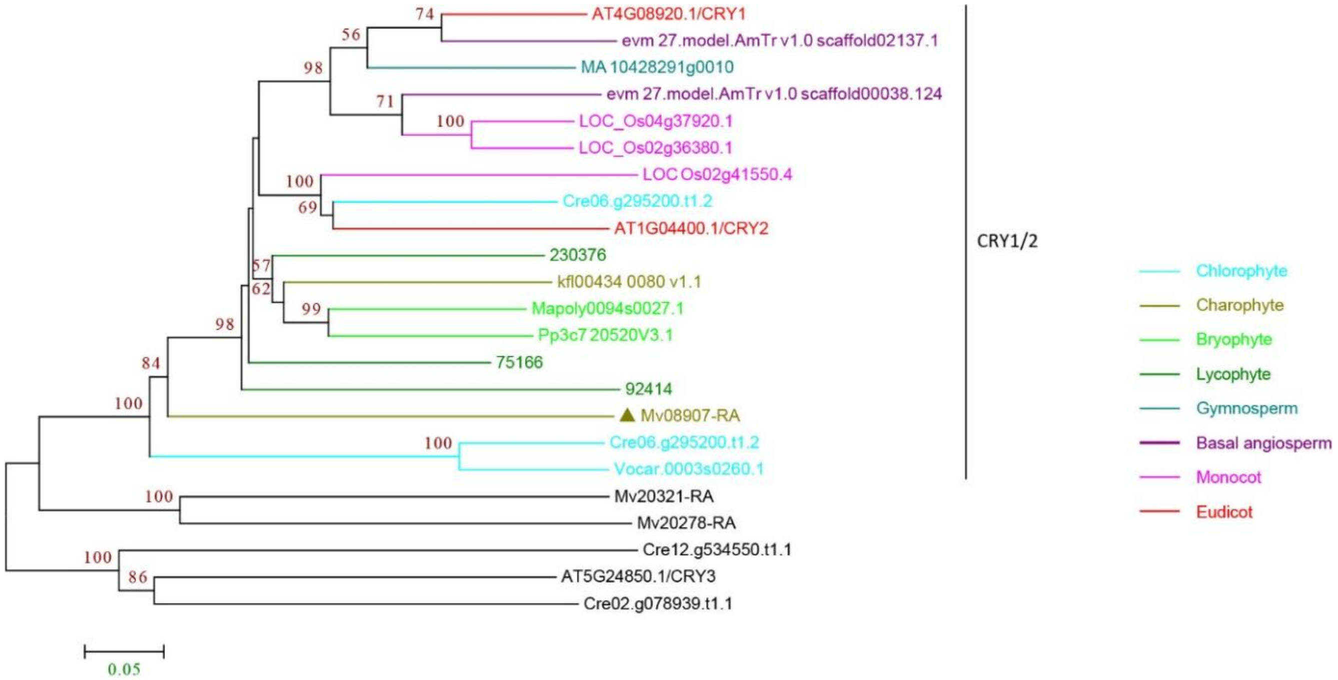
Data S1BL. Phylogenetic relationships of MALIC ENZYME 2 (me2) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequence was highlighted by a triangle. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



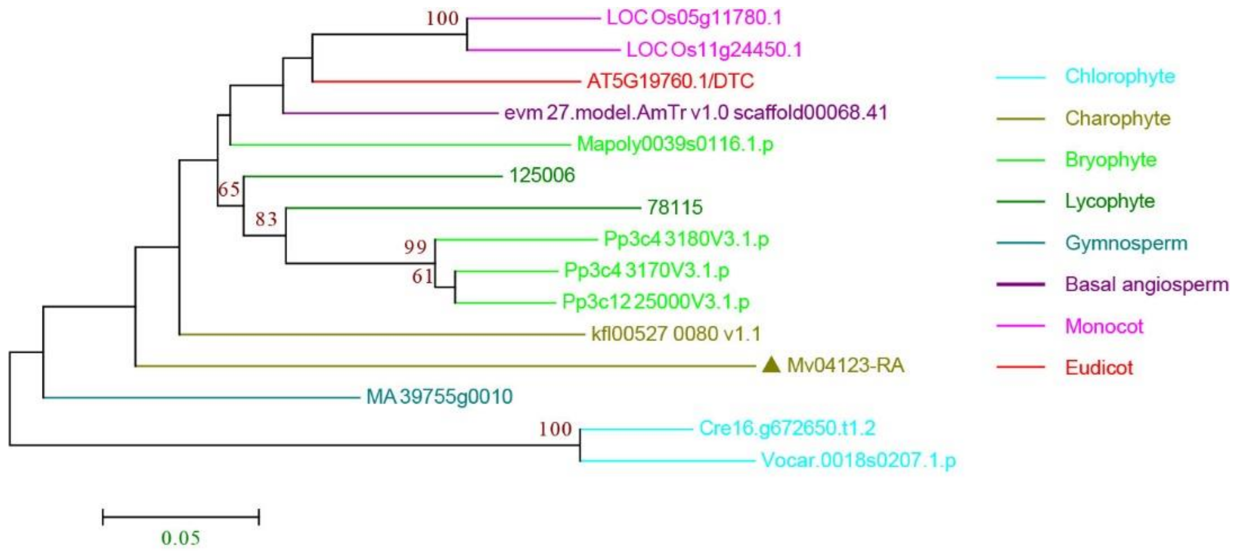
Data S1BM. Phylogenetic relationships of ADP GLUCOSE PYROPHOSPHORYLASE (ADG) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequence was highlighted by a triangle. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



Data S1BN. Phylogenetic relationships of ASPARTATE AMINOTRANSFERASE (ASP) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequences were highlighted by triangles. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.

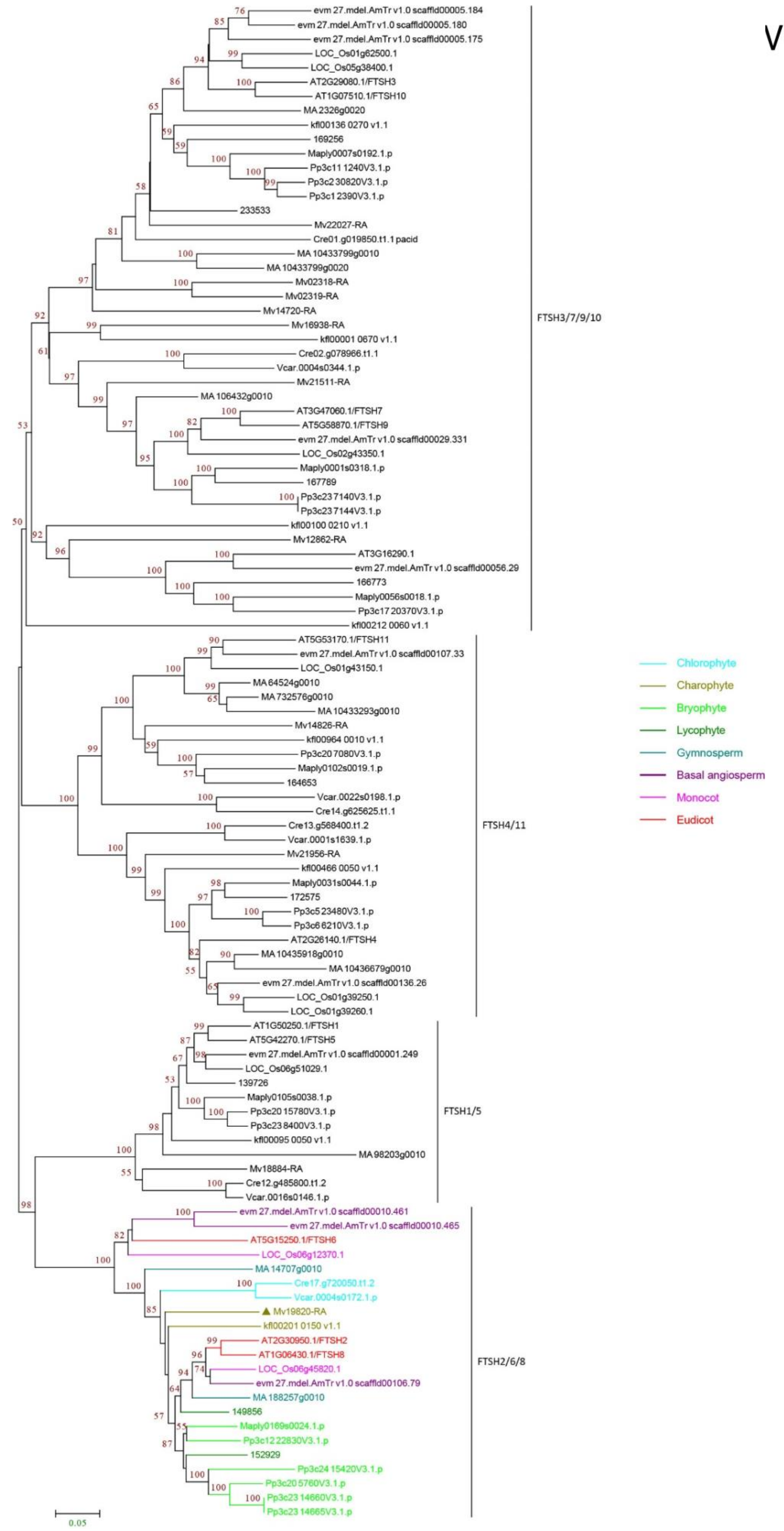


Data S1BO. Phylogenetic relationships of CRYPTOCHROME (CRY) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequence was highlighted by a triangle. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



Data S1BP. Phylogenetic relationships of DTC proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequence was highlighted by a triangle. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.

VCH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Charophyte
Bryophyte
Lycophyte
Gymnosperm
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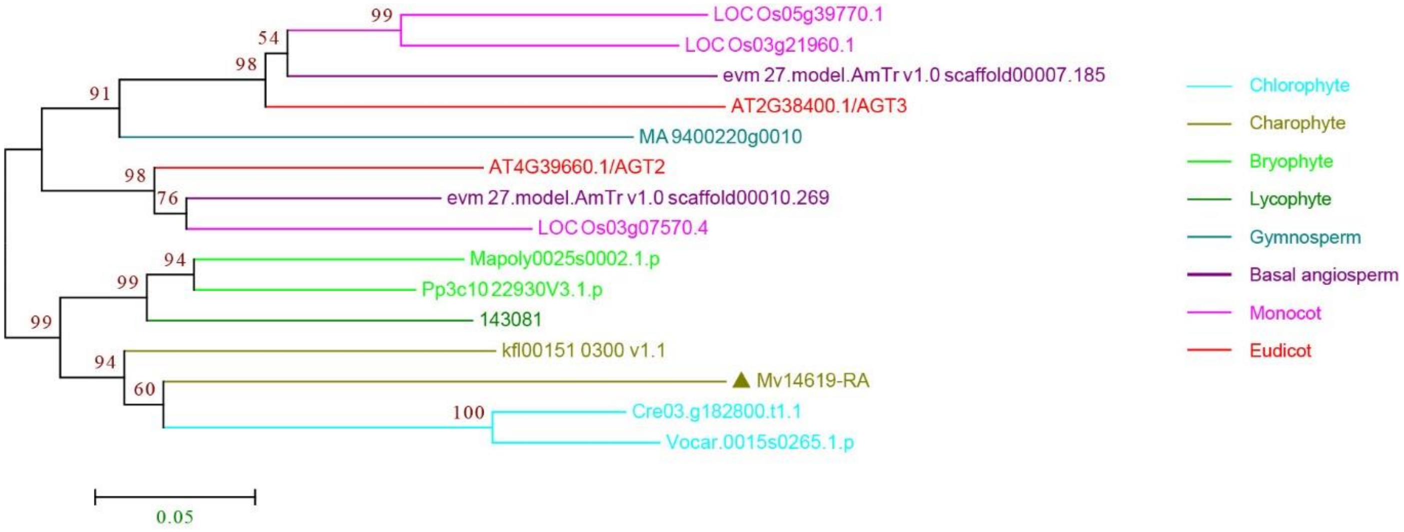
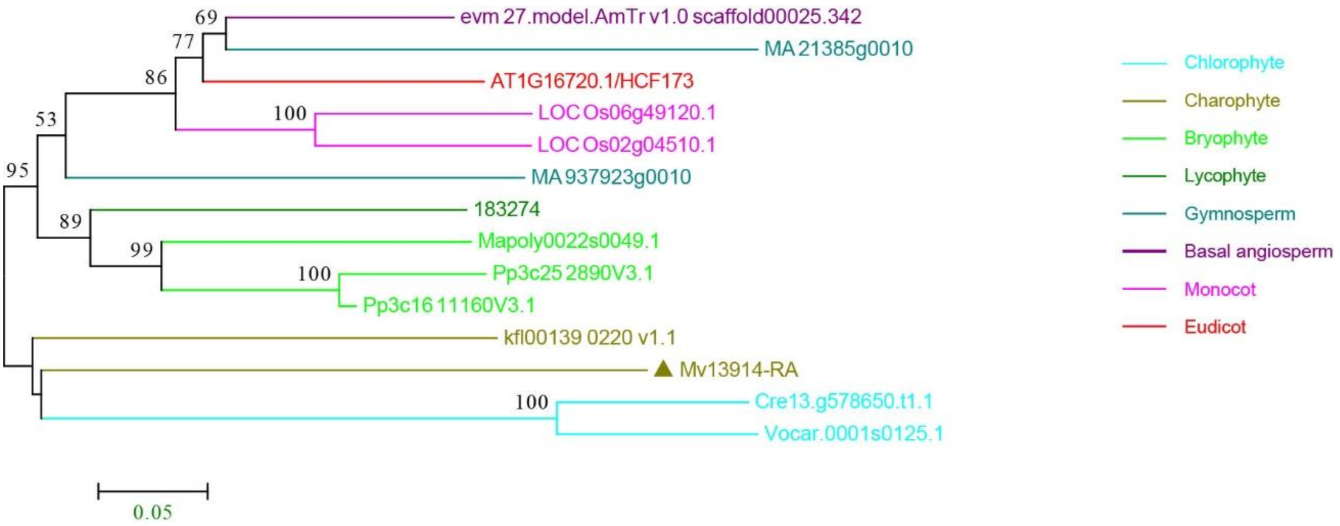
Monocot
Eudicot

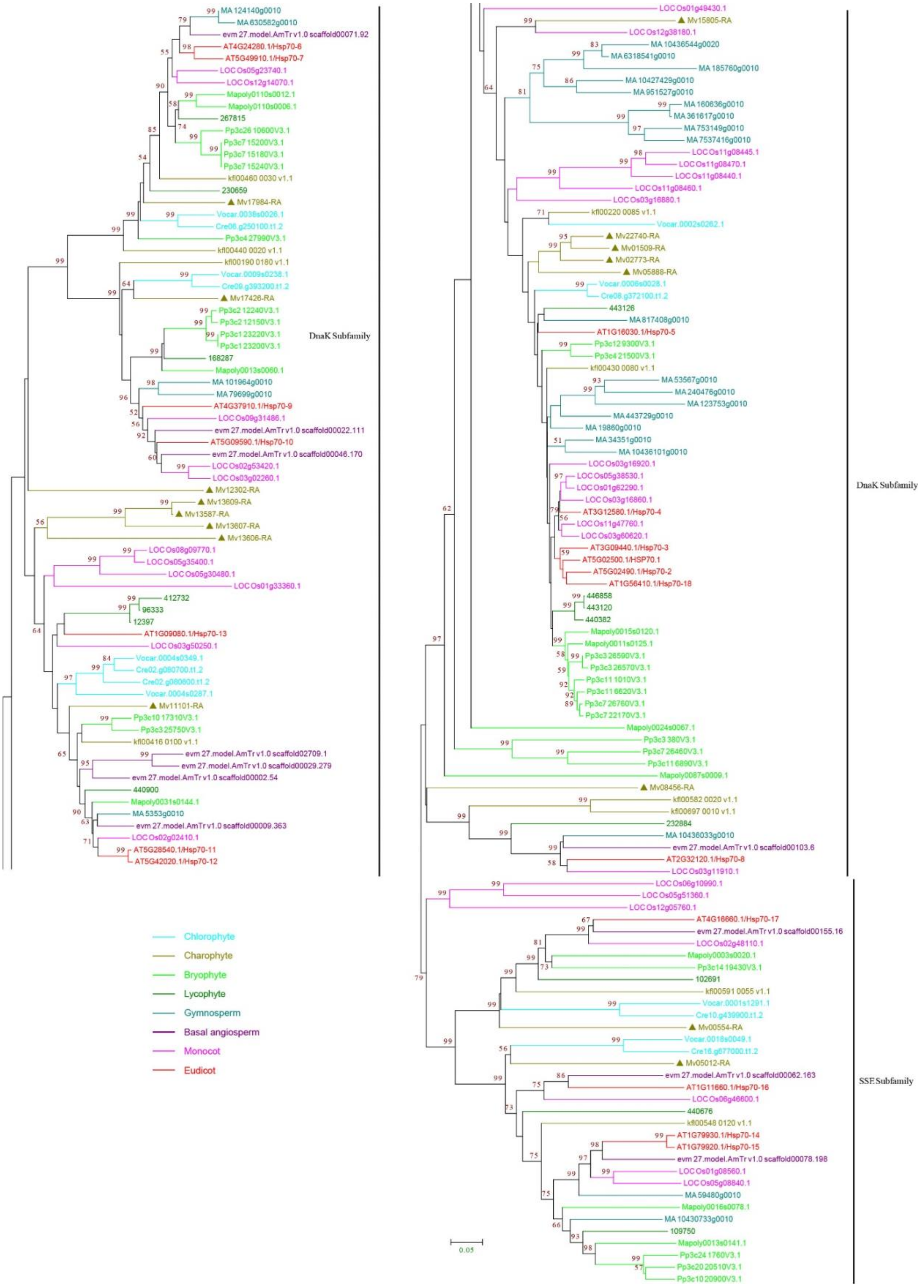
Data S1BQ. Phylogenetic relationships of FTSH proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequence was highlighted by a triangle. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



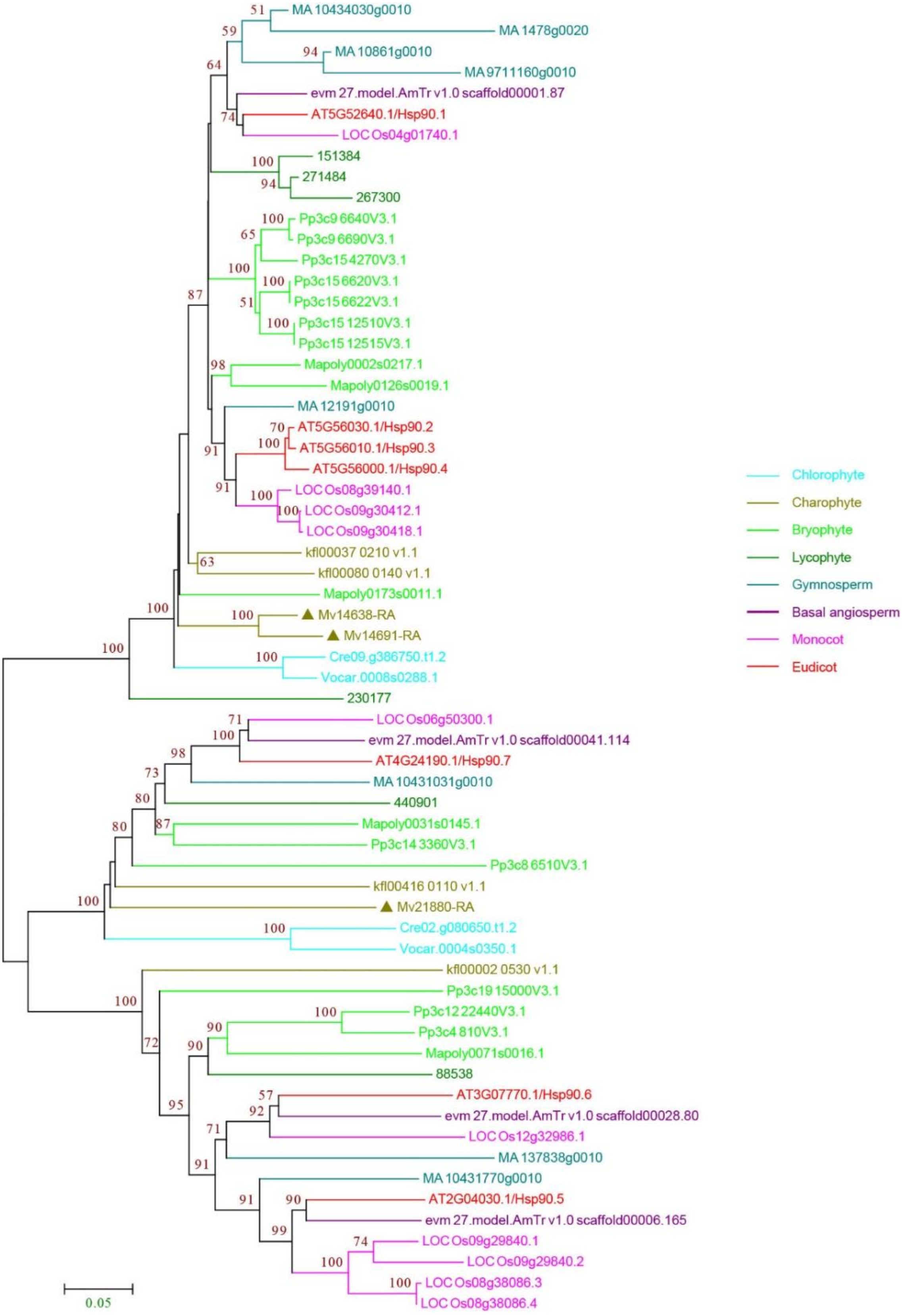
Data S1BR. Phylogenetic relationships of ALANINE:GLYOXYLATE AMINOTRANSFERASE (AGT) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequence was highlighted by a triangle. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



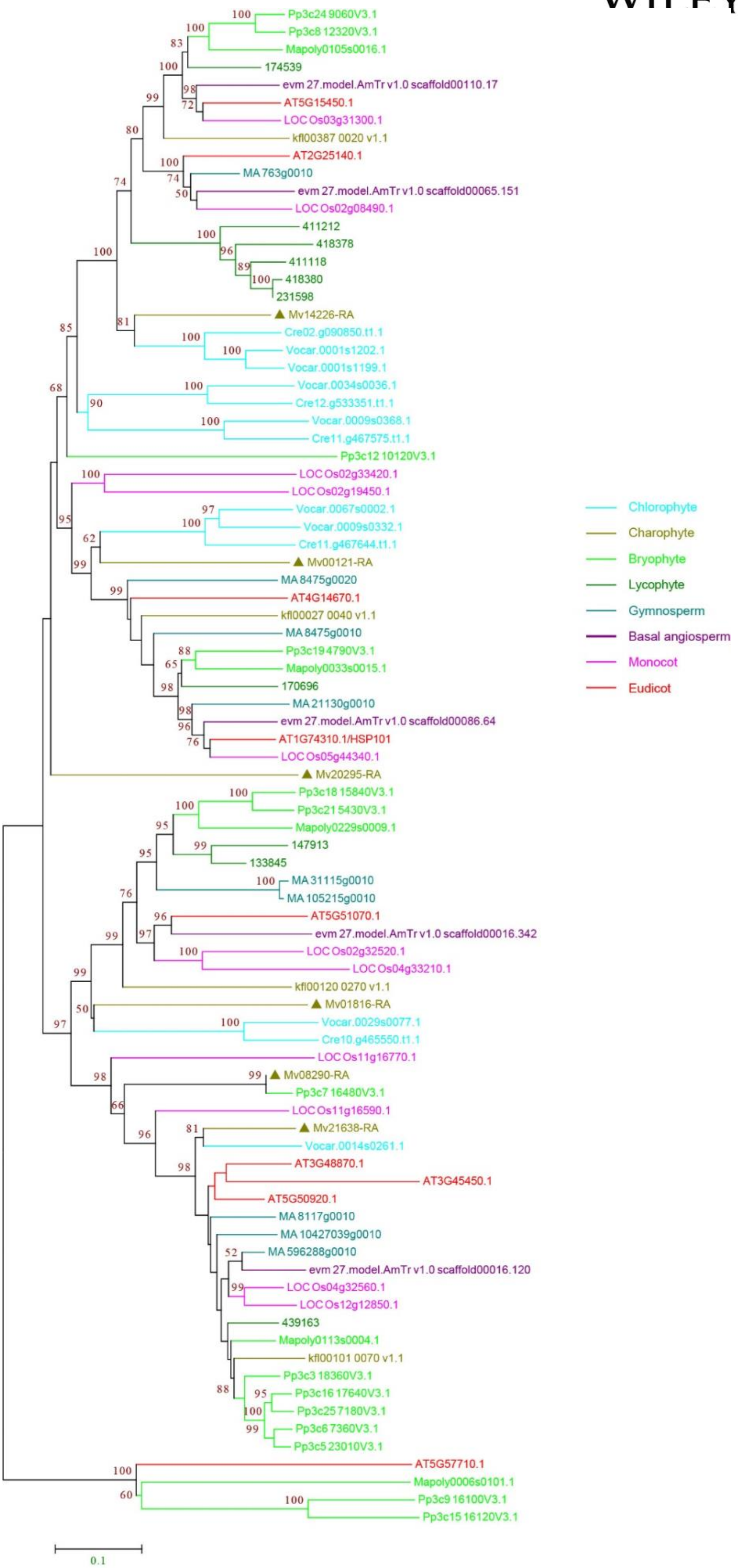
Data S1BS. Phylogenetic relationships of HIGH CHLOROPHYLL FLUORESCENCE PHENOTYPE 173 (HCF173) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequence was highlighted by a triangle. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



Data S1BT. Phylogenetic relationships of heat shock protein 70 (HSP70) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequences were highlighted by triangles. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.



Data S1BU. Phylogenetic relationships of heat shock protein 90 (HSP90) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequences were highlighted by triangles. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.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Monocot
Eudicot

Data S1BV. Phylogenetic relationships of heat shock protein 100 (HSP100) proteins from *M. viride* and other evolutionarily representative species. The *M. viride* sequences were highlighted by triangles. Numbers on the major branches indicate bootstrap values (> 50%) in 1,000 replicates.

References

[1] H. Du, Z. Liang, S. Zhao, M. G. Nan, L. S. Tran, K. Lu, Y. B. Huang, J. N. Li, *Sci. Rep.* **2015**, *5*, 11037.

[2] N. Pires, L. Dolan, *Mol. Biol. Evol.* **2010**, *27*, 862.

[3] J. K. Okamuro, B. Caster, R. Villarroel, M. Van Montagu, K. D. Jofuku, *Proc. Natl. Acad. Sci. USA* **1997**, *94*, 7076.

[4] F. Licausi, M. Ohme-Takagi, P. Perata, *New Phytol.* **2013**, *199*, 639.

[5] K.-J. Dietz, M. O. Vogel, A. Viehhauser, *Protoplasma* **2010**, *245*, 3.

[6] T. Nakano, K. Suzuki, T. Fujimura, H. Shinshi, *Plant Physiol.* **2006**, *140*, 411.

[7] A. Safi, A. Medici, W. Szponarski, S. Ruffel, B. Lacombe, G. Krouk, *Curr. Opin. Plant Biol.* **2017**, *39*, 159.

[8] M. Jakoby, B. Weisshaar, W. Dröge-Laser, J. Vicente-Carbajosa, J. Tiedemann, T. Kroj, F. Parcy, *Trends Plant Sci.* **2002**, *7*, 106.

[9] W. Dröge-Laser, B. L. Snoek, B. Snel, C. Weiste, *Curr. Opin. Plant Biol.* **2018**, *45*, 36.

[10] K. Swaminathan, K. Peterson, T. Jack, *Trends Plant Sci.* **2008**, *13*, 647.

[11] Y. Wang, D. Deng, R. Zhang, S. Wang, Y. Bian, Z. Yin, *Mol. Biol. Rep.* **2012**, 39, 6267.

[12] F. Y. Peng, R. J. Weselake, *Theor. Appl. Genet.* **2013**, *126*, 1305.

[13] E. Morgunova, Y. Yin, A. Jolma, K. Dave, B. Schmierer, A. Popov, N. Eremina, L. Nilsson, J. Taipale, *Nat. Commun.* **2015**, *6*, 10050.

[14] R. Rauber, C. Cabreira, L. B. de Freitas, A. C. Turchetto-Zolet, M. Margis-Pinheiro, *Mol. Phylogenet. Evol.* **2016**, *99*, 225.

[15] P. von Koskull-Doring, K. D. Scharf, L. Nover, *Trends Plant Sci.* **2007**, *12*, 452.