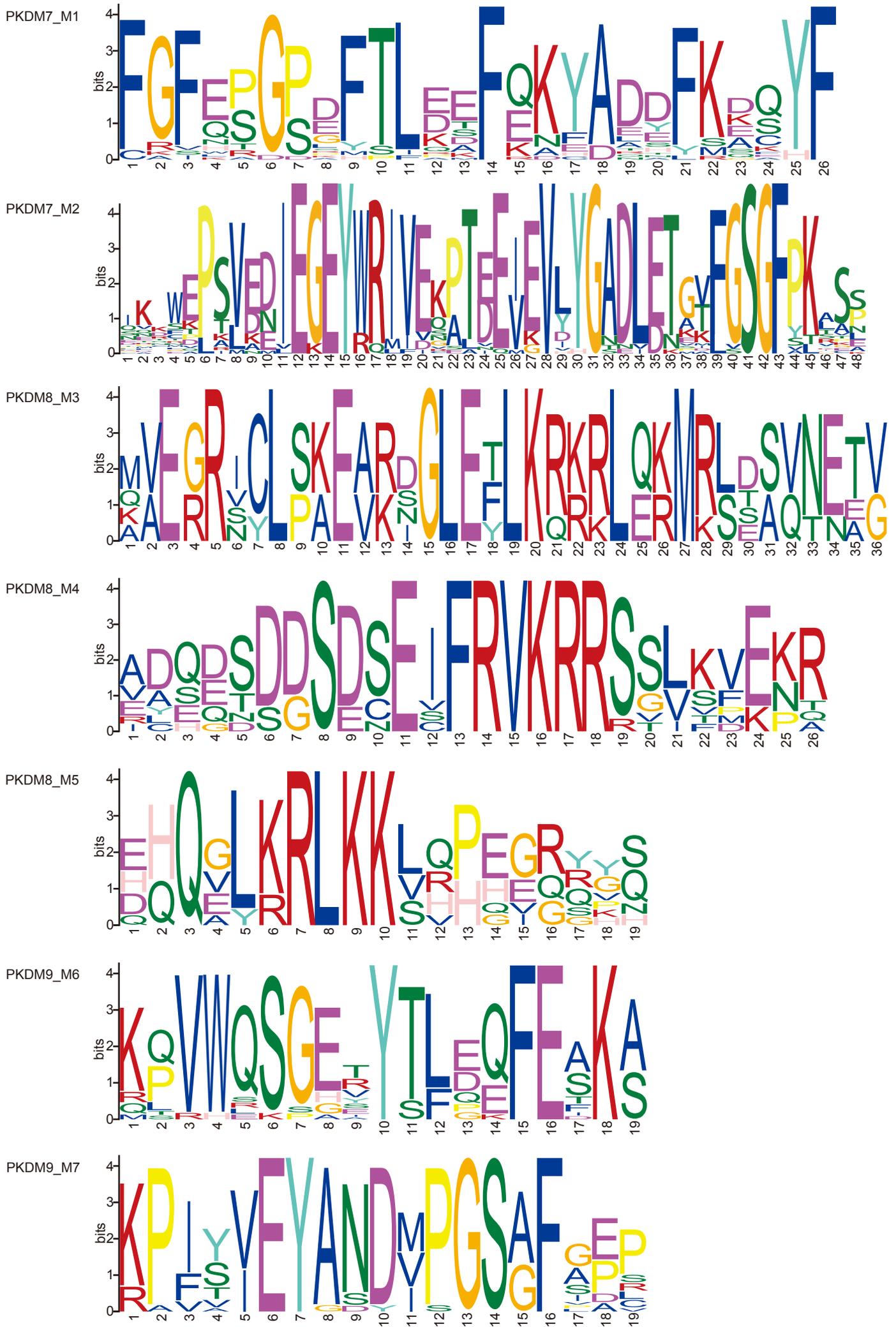
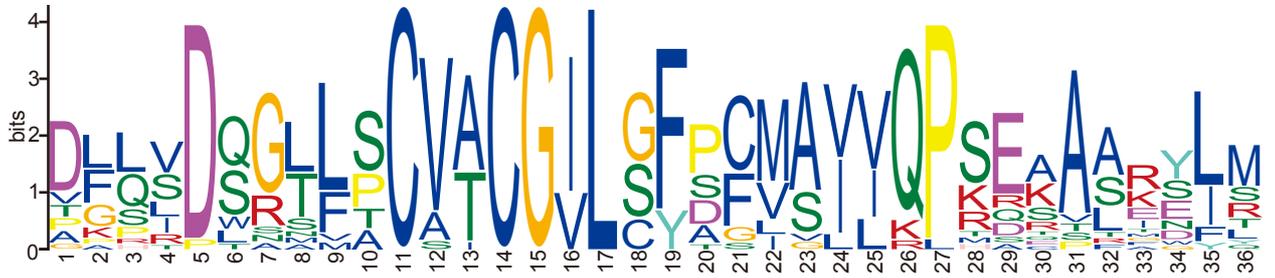


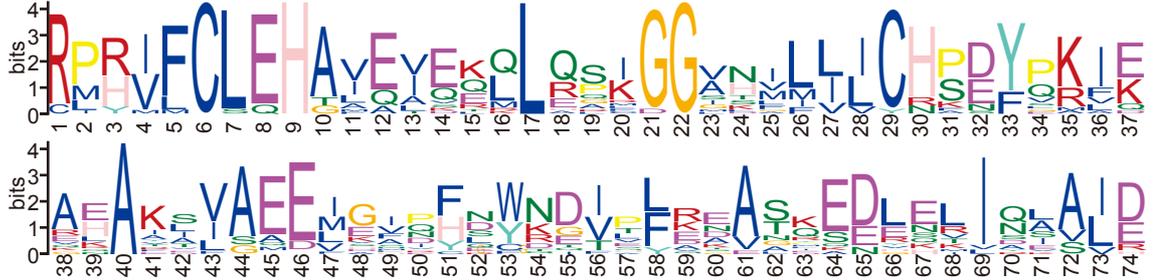
A

B

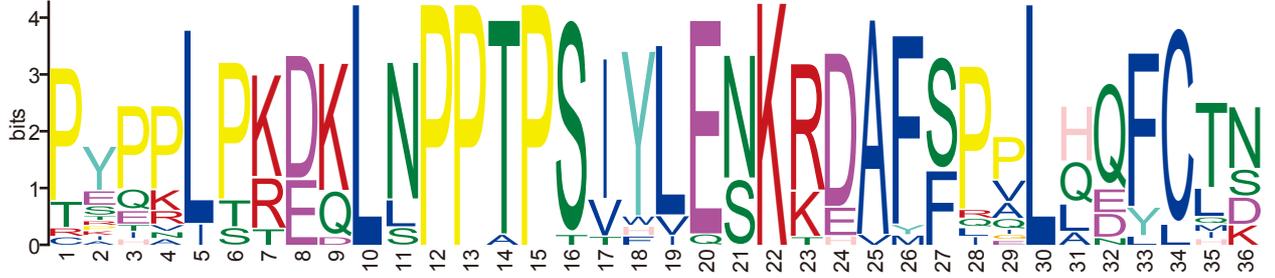
PKDM9_M8



PKDM9_M9



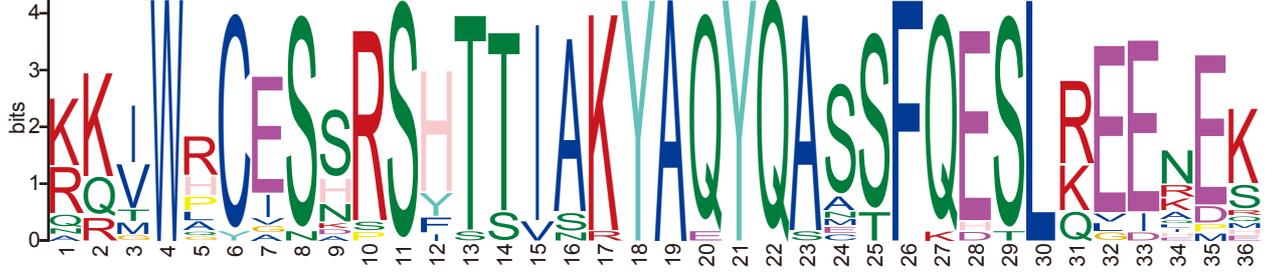
KDM6_M10



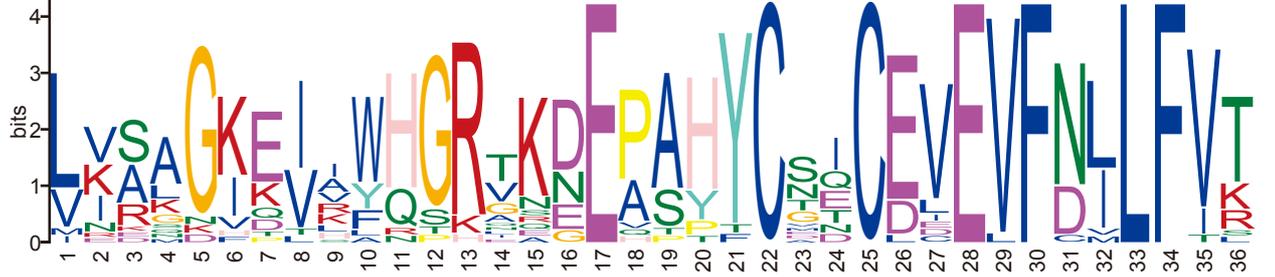
KDM6_M11



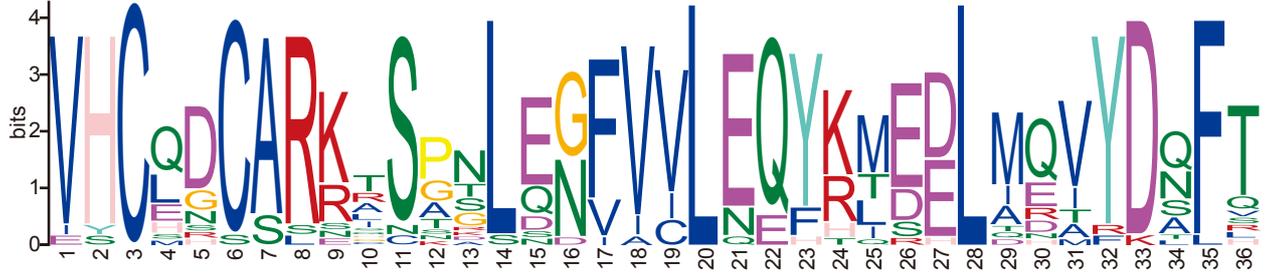
KDM6_M12



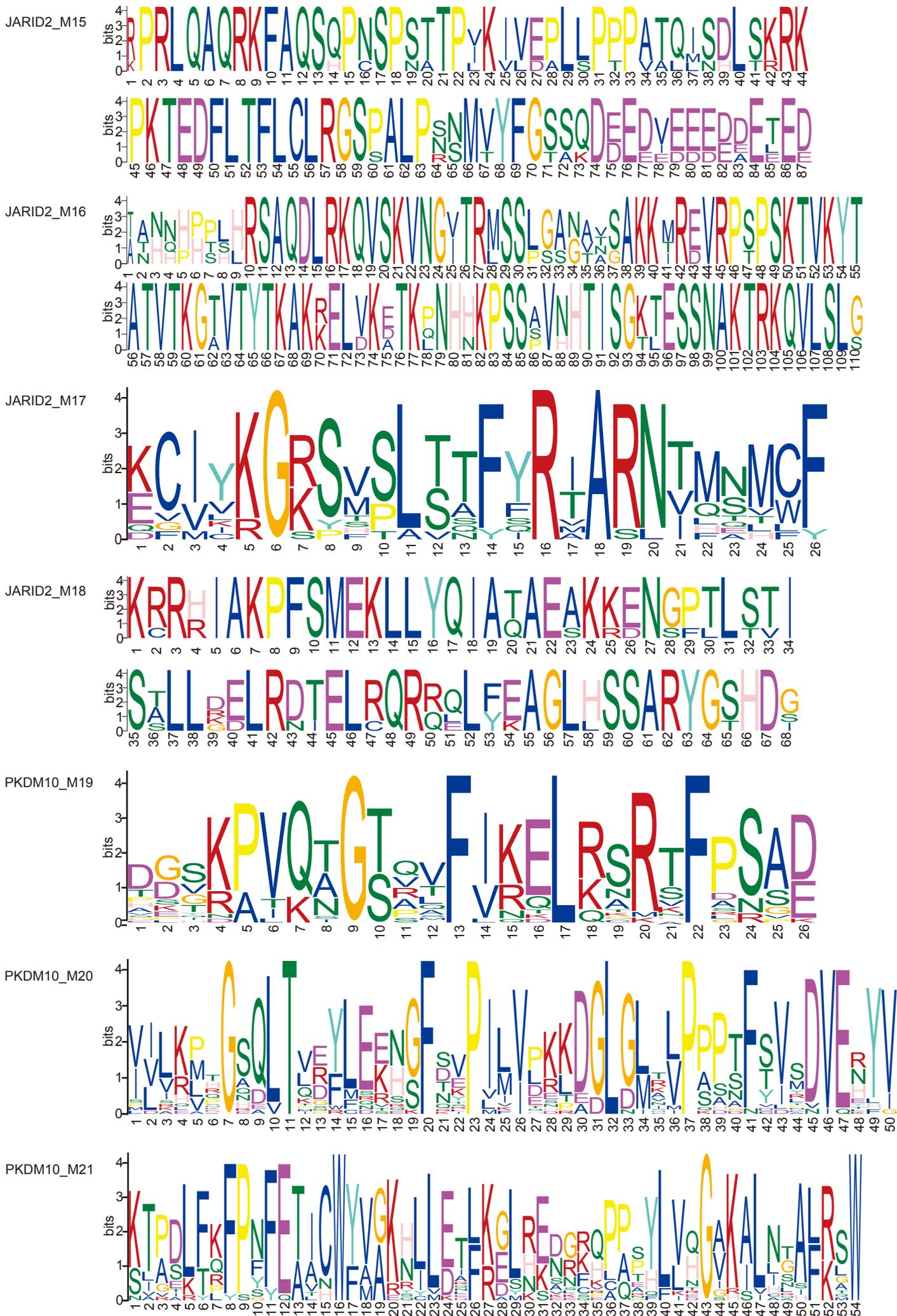
KDM6_M13



KDM6_M14



C

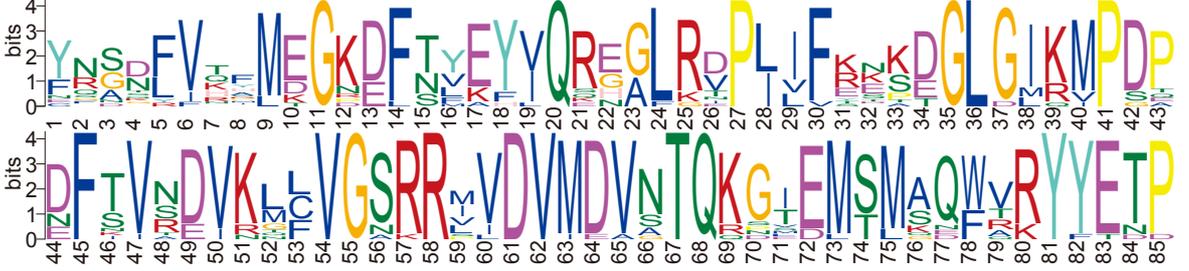


D

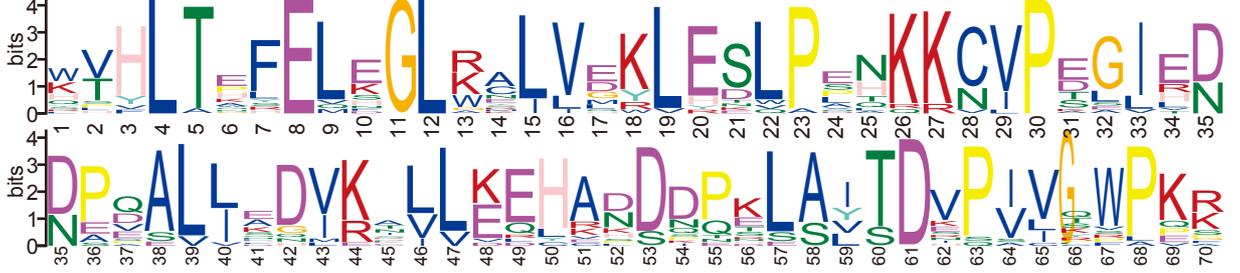
PKDM10_M22



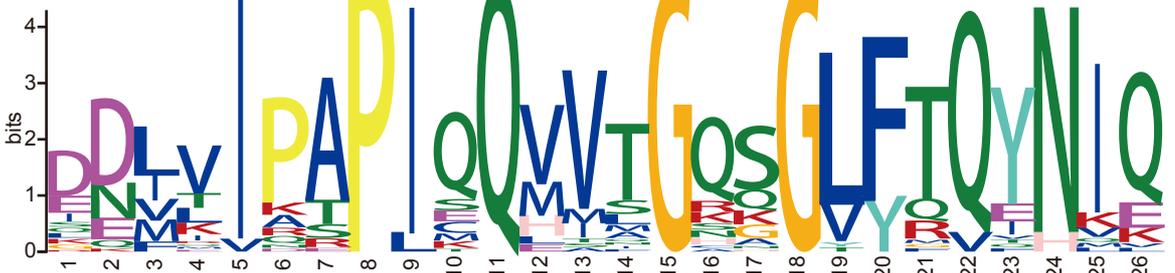
KDM2_M23



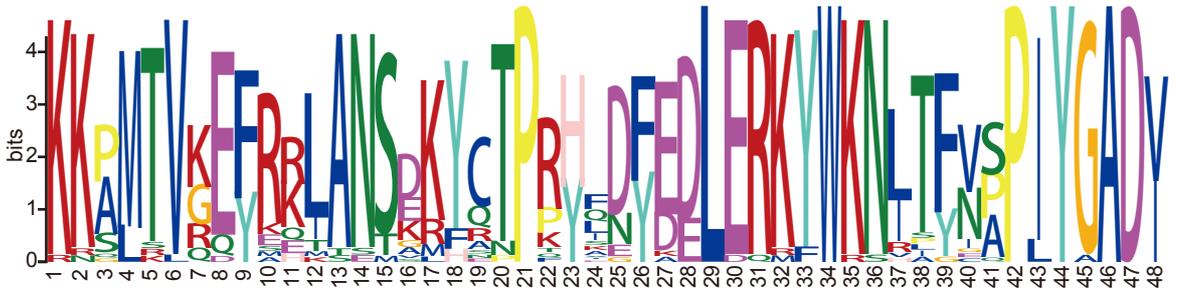
KDM2_M24



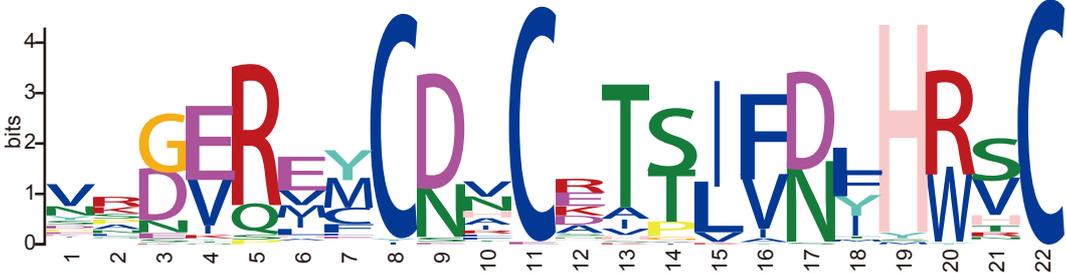
KDM4_M25



KDM4_M26



KDM3_M27

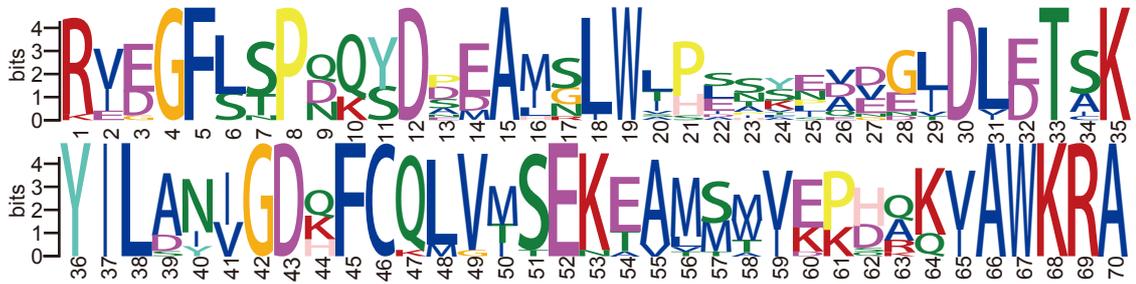


KDM3_M28

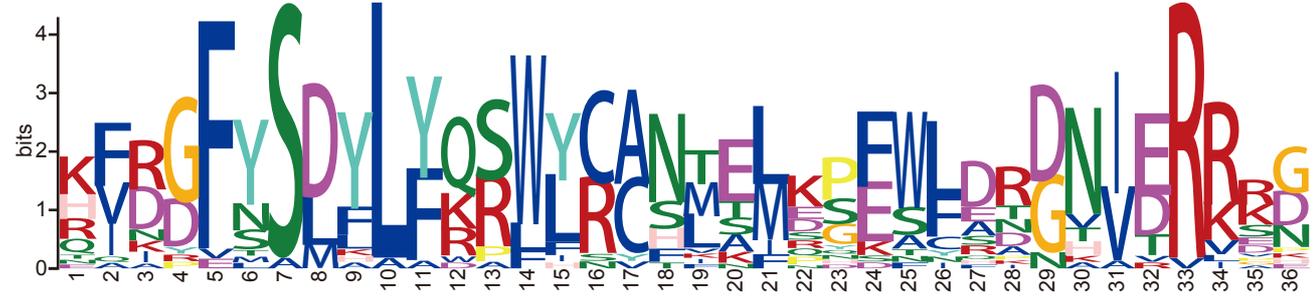


F

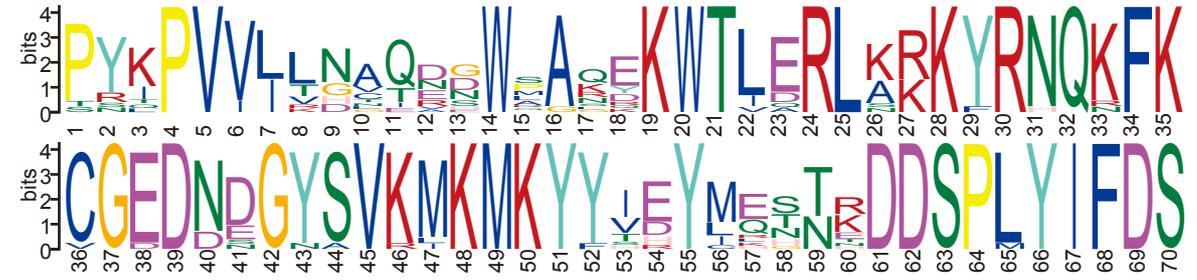
KDM3_M29



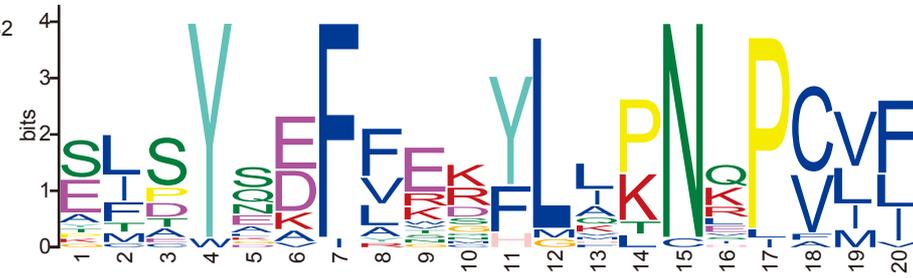
JMJD6_M30



JMJD6_M31



PKDM11_M32



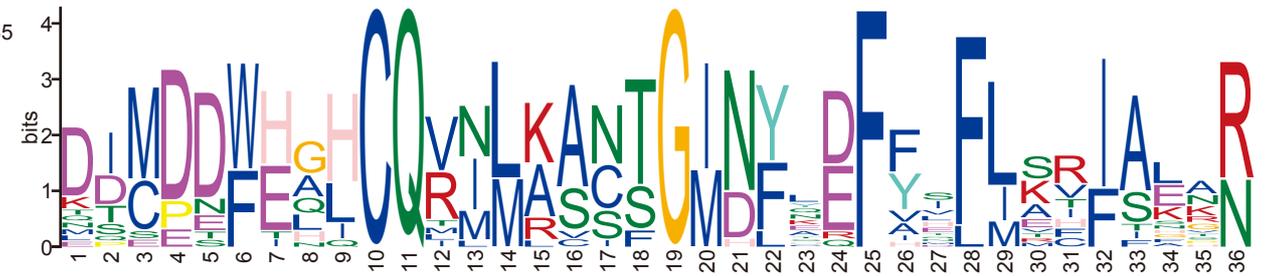
PKDM11_M33



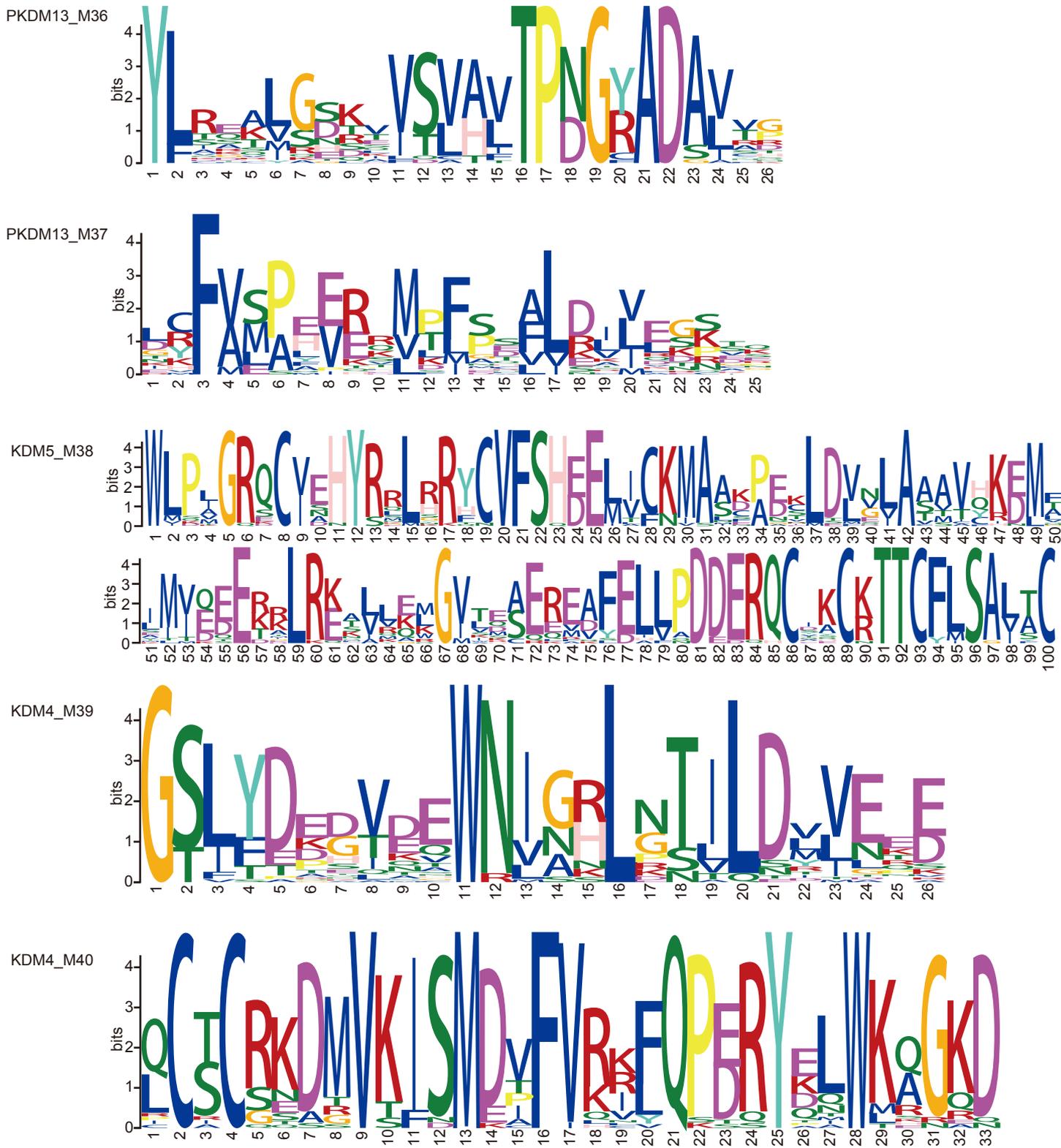
PKDM11_M34



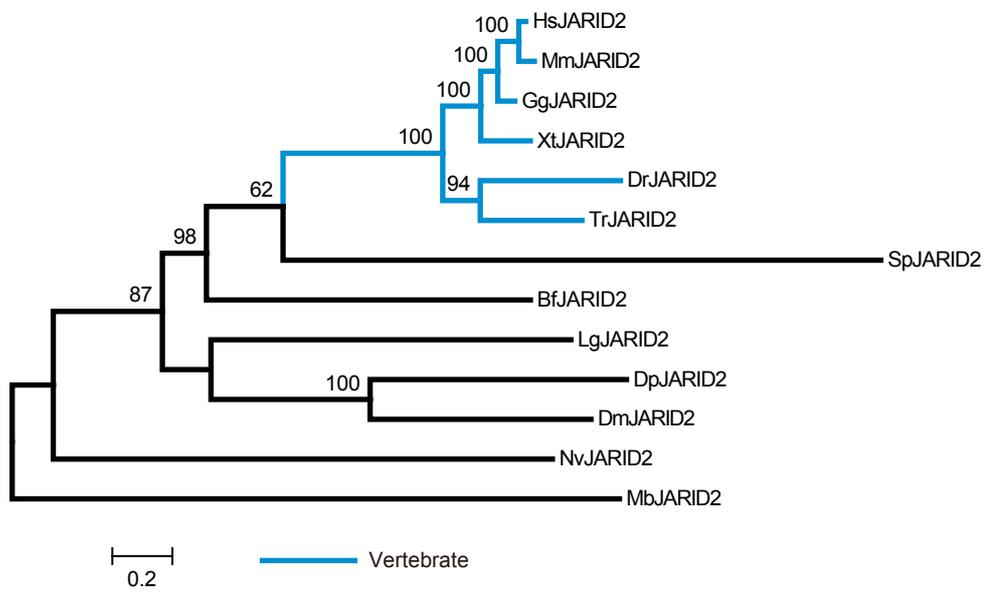
PKDM11_M35



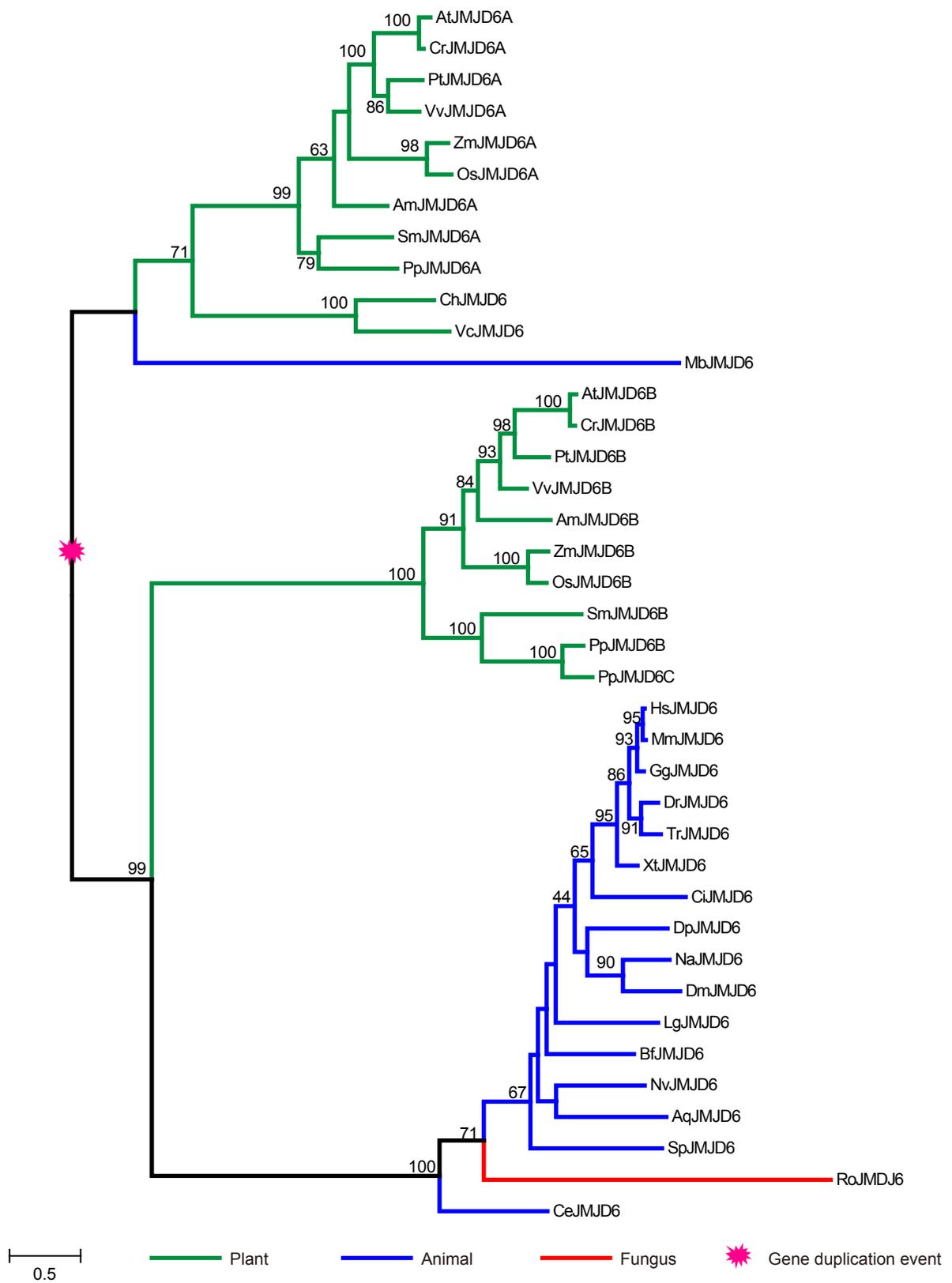
F



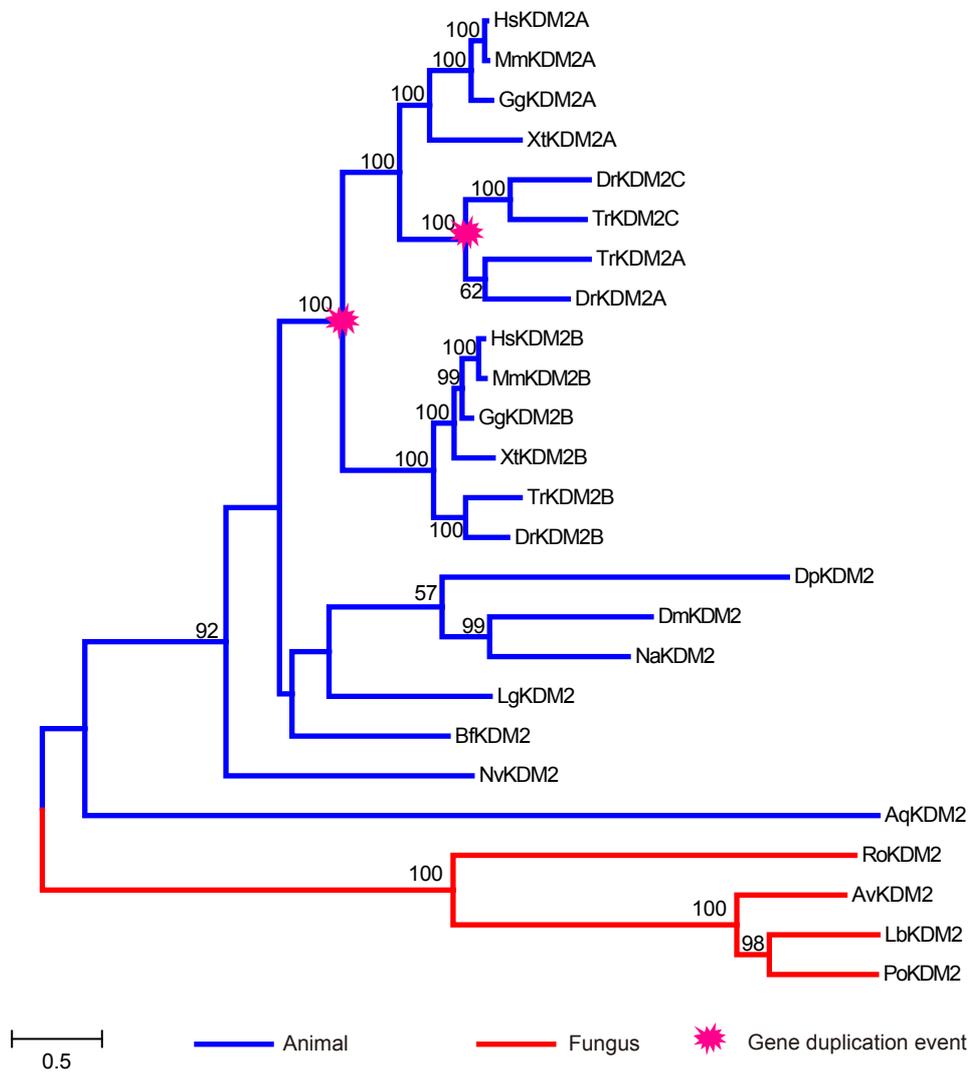
Supplemental Figure S1. Logos representing conserved motifs within different subfamilies.



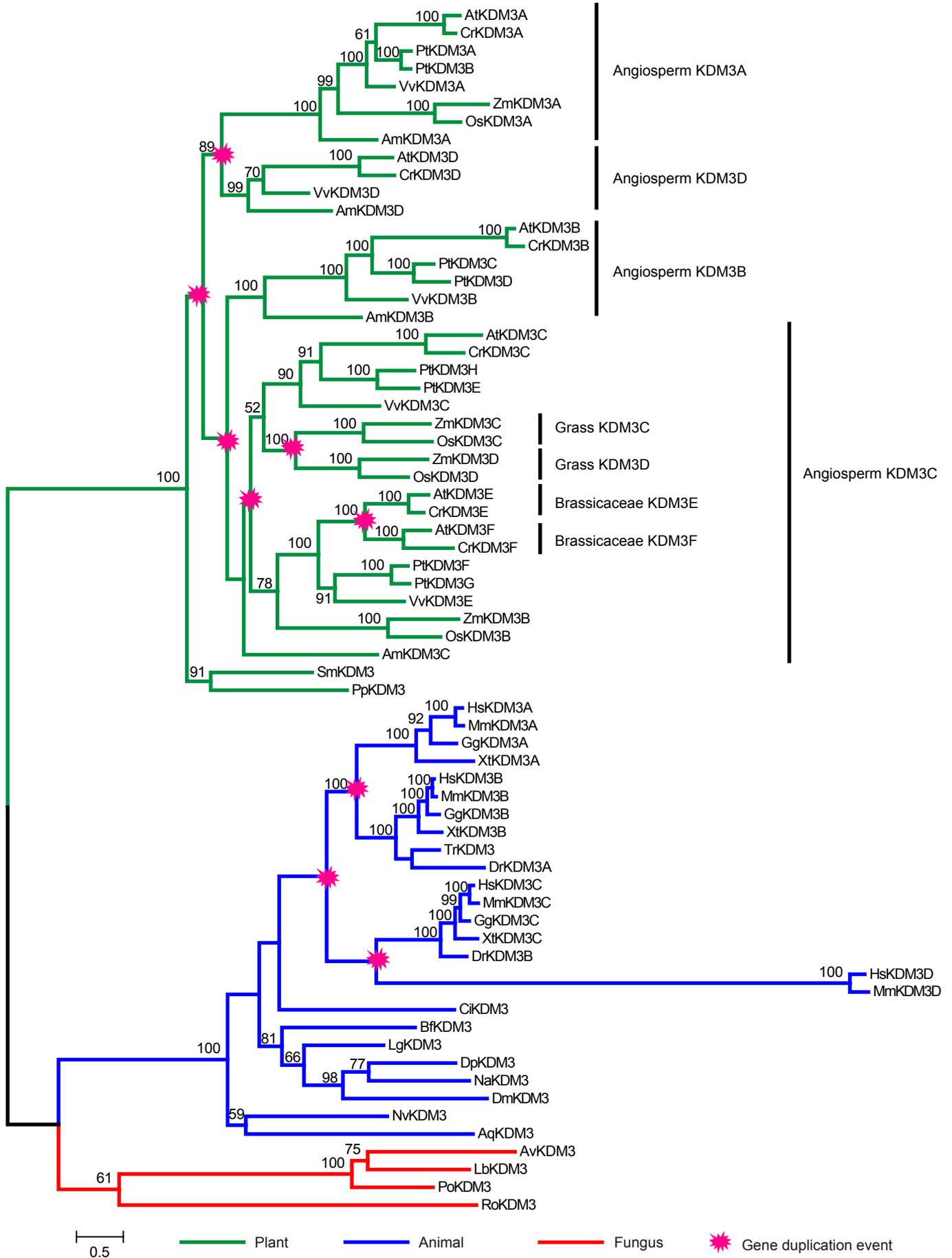
Supplemental Figures S2. The ML trees generated by RAxML of each of *JARID2*. ML bootstrap values above 50% are shown.



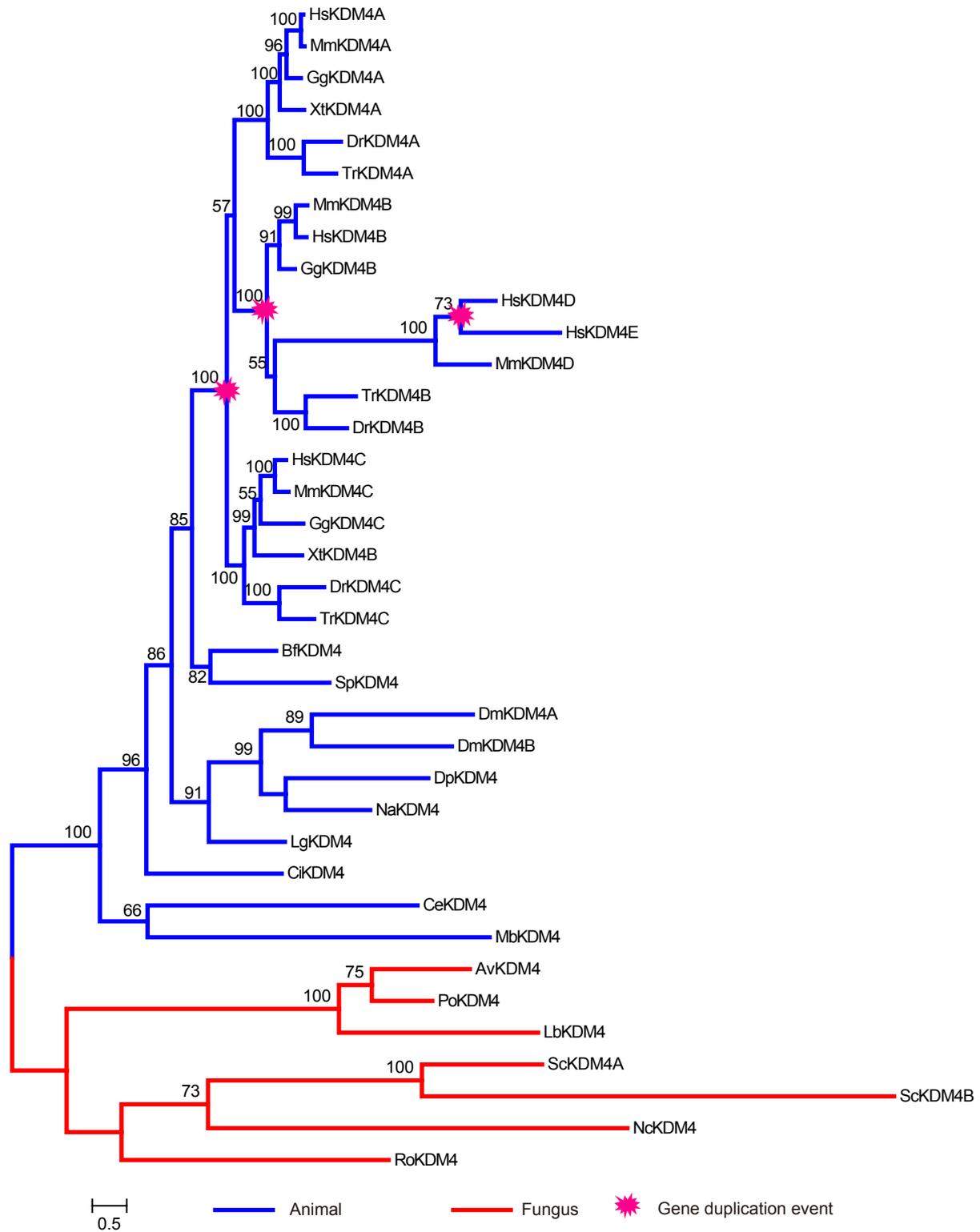
Supplemental Figures S3. The ML trees generated by RAxML of each of *JMJD6*. ML bootstrap values above 50% are shown.



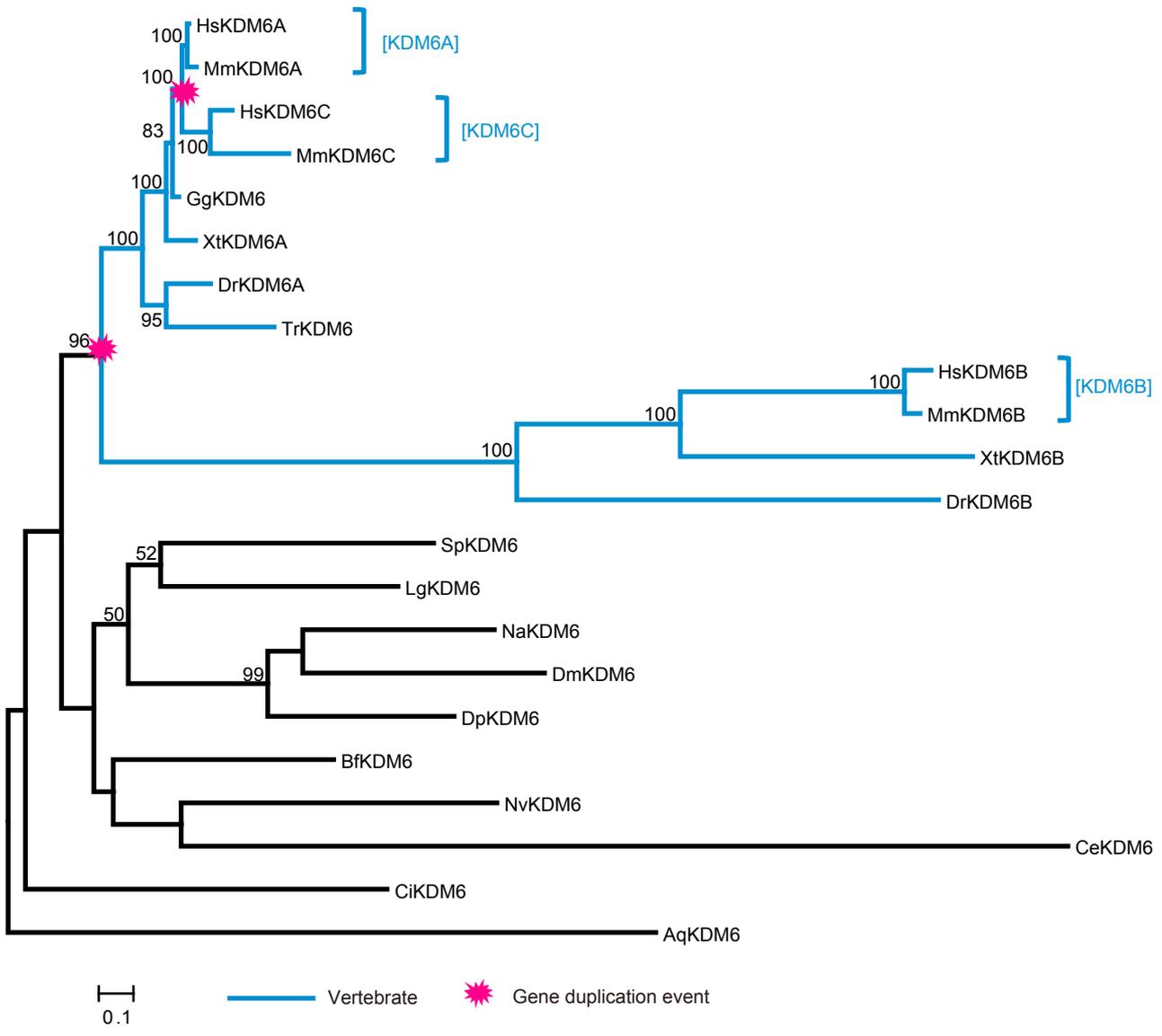
Supplemental Figures S4. The ML trees generated by RAxML of each of *KDM2*. ML bootstrap values above 50% are shown.



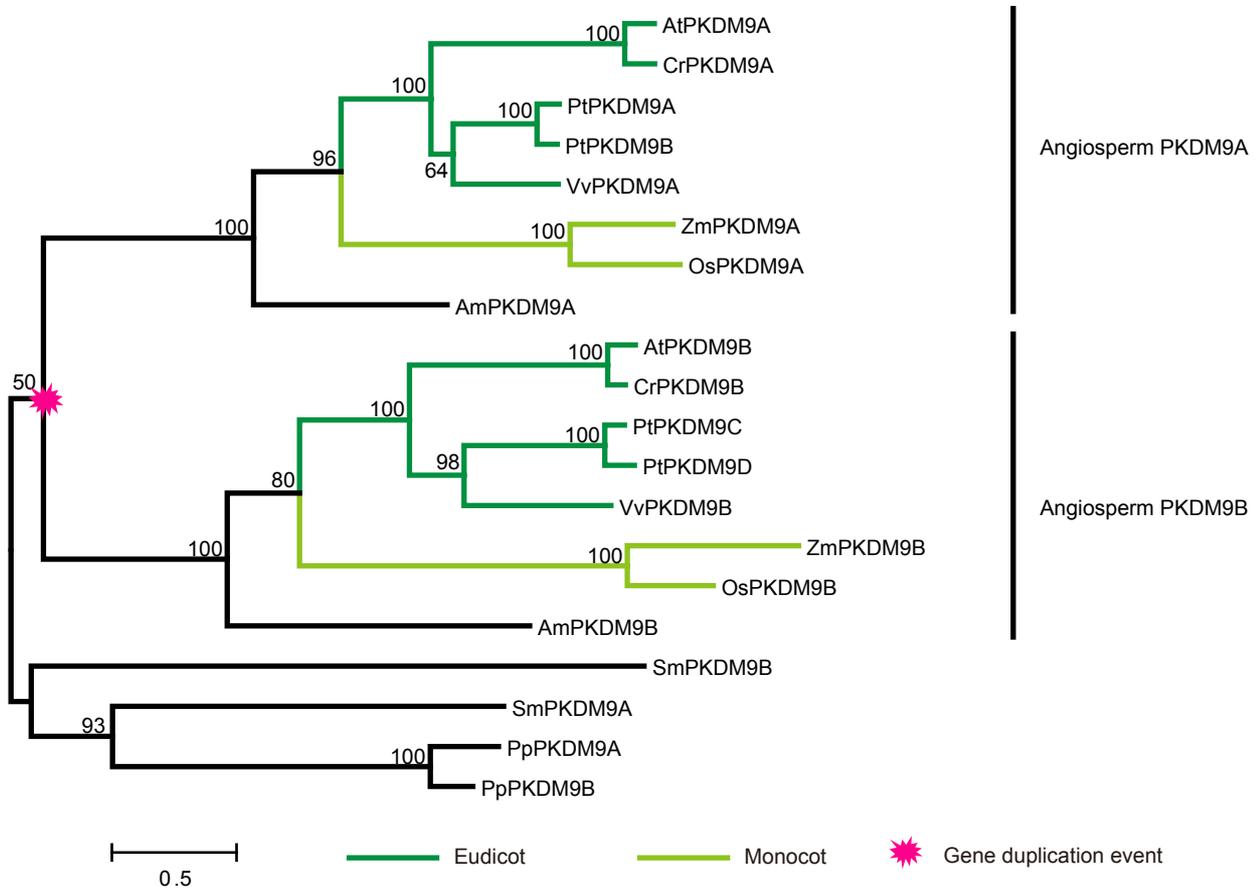
Supplemental Figures S5. The ML trees generated by RAxML of each of *KDM3*. ML bootstrap values above 50% are shown.



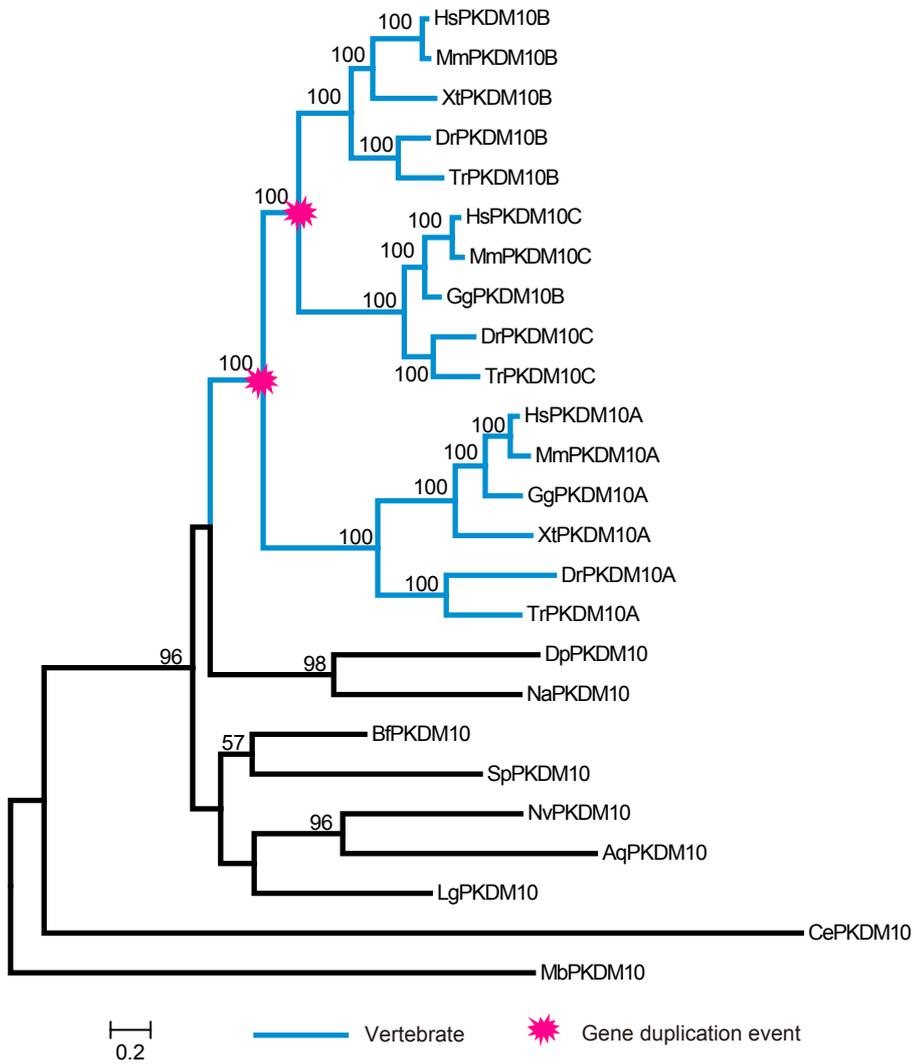
Supplemental Figures S6. The ML trees generated by RAxML of each of *KDM4*. ML bootstrap values above 50% are shown.



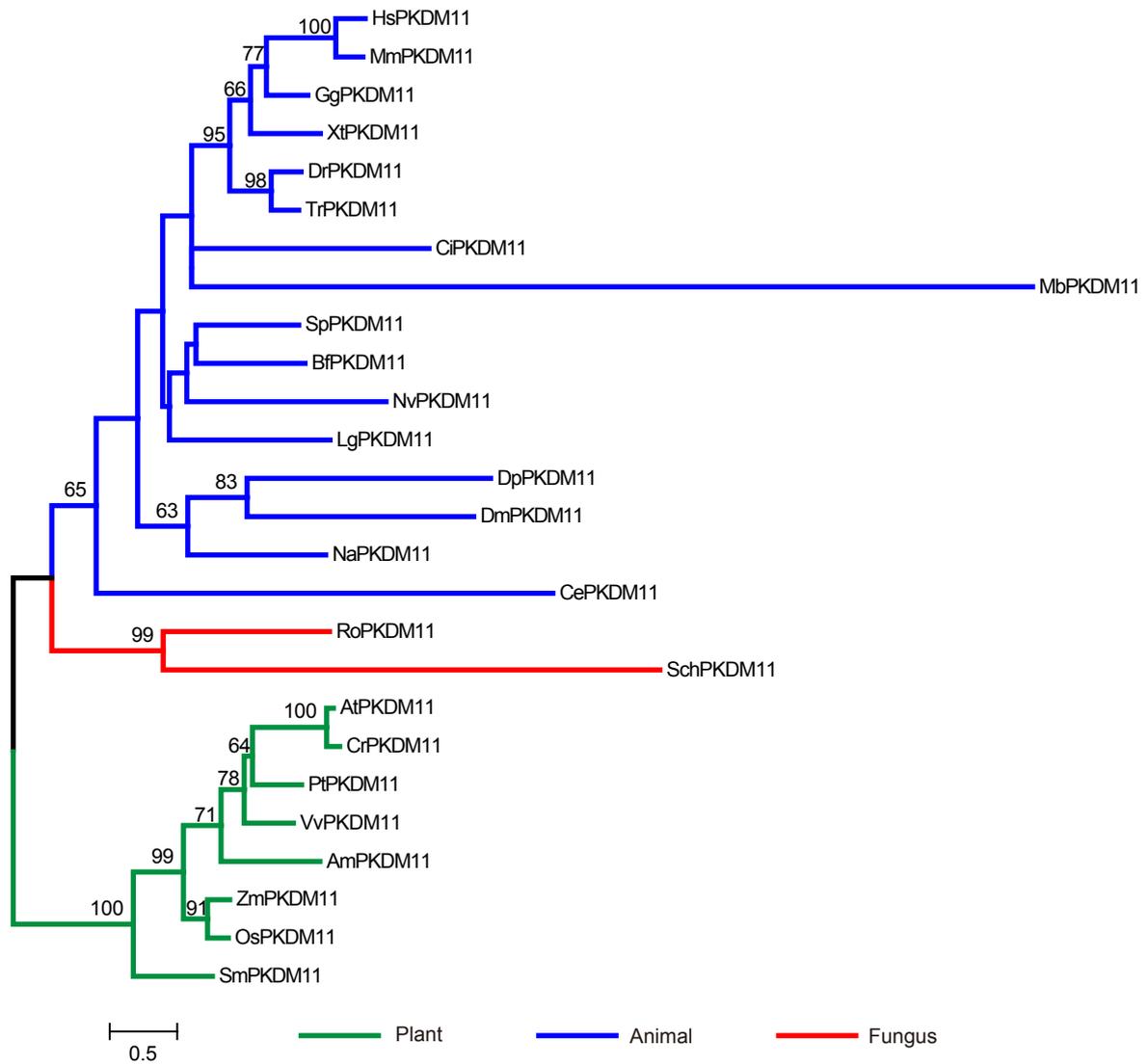
Supplemental Figures S7. The ML trees generated by RAxML of each of *KDM6*. ML bootstrap values above 50% are shown.



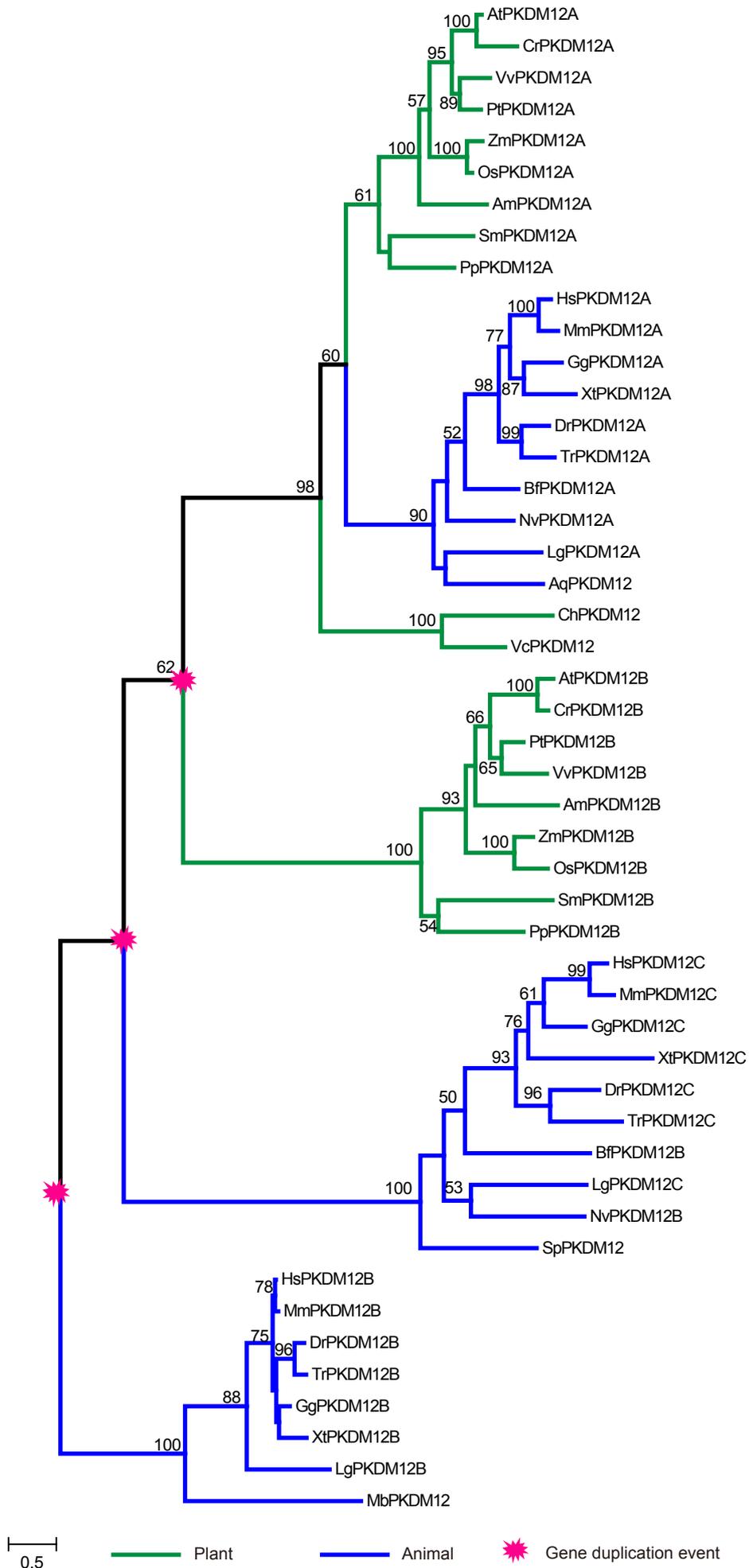
Supplemental Figures S8. The ML trees generated by RAxML of each of *PKDM9*. ML bootstrap values above 50% are shown.



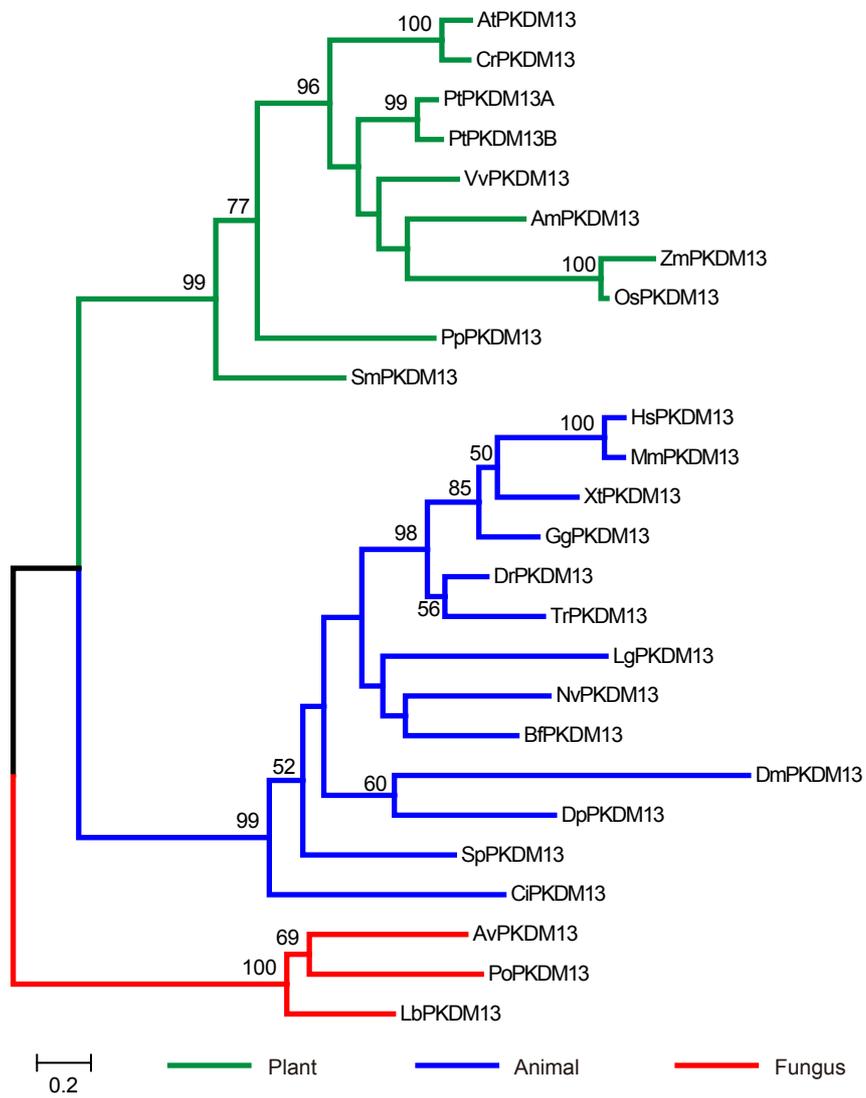
Supplemental Figures S9. The ML trees generated by RAxML of each of *PKDM10*. ML bootstrap values above 50% are shown.



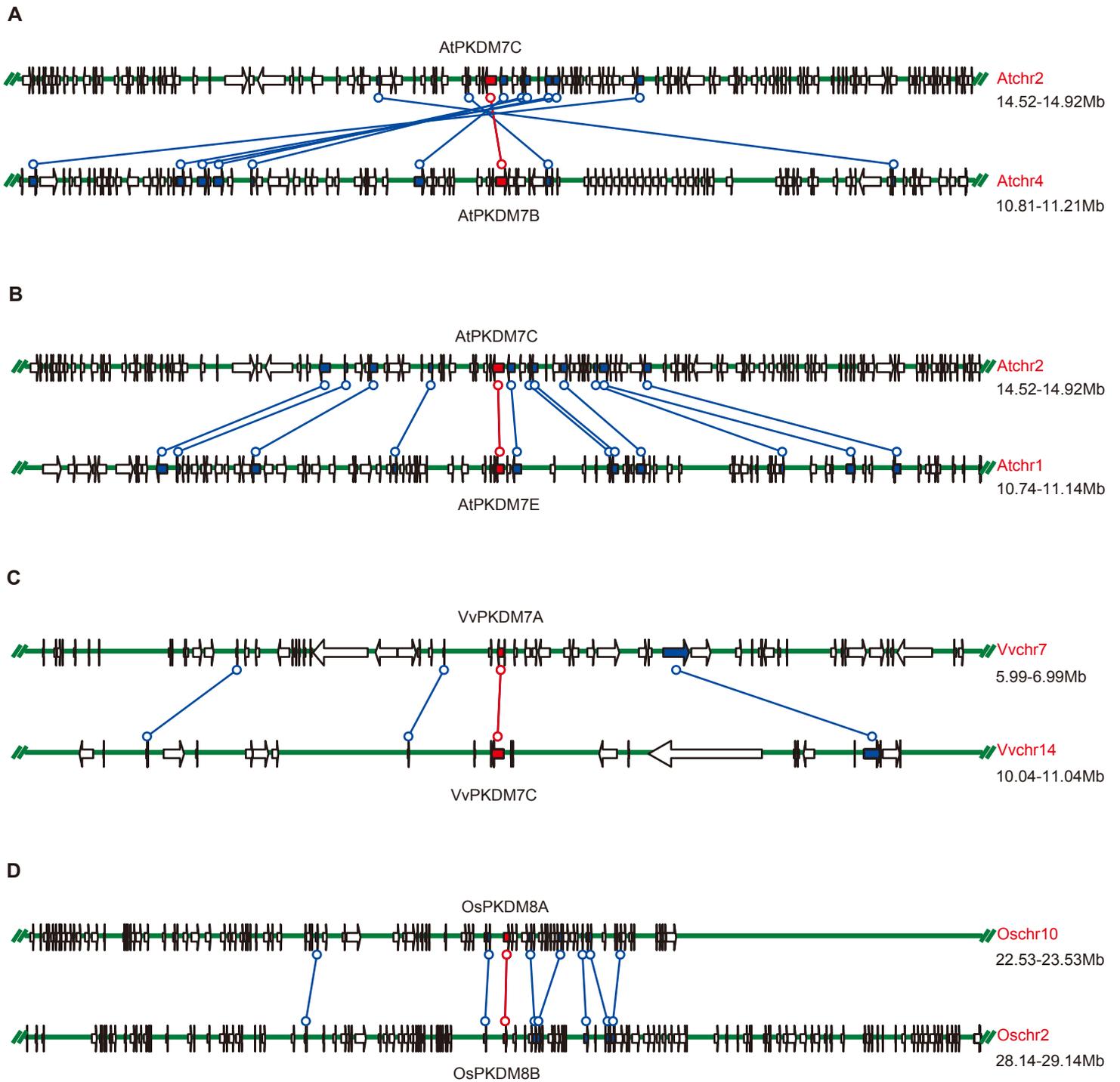
Supplemental Figures S10. The ML trees generated by RAxML of each of *PKDM11*. ML bootstrap values above 50% are shown.



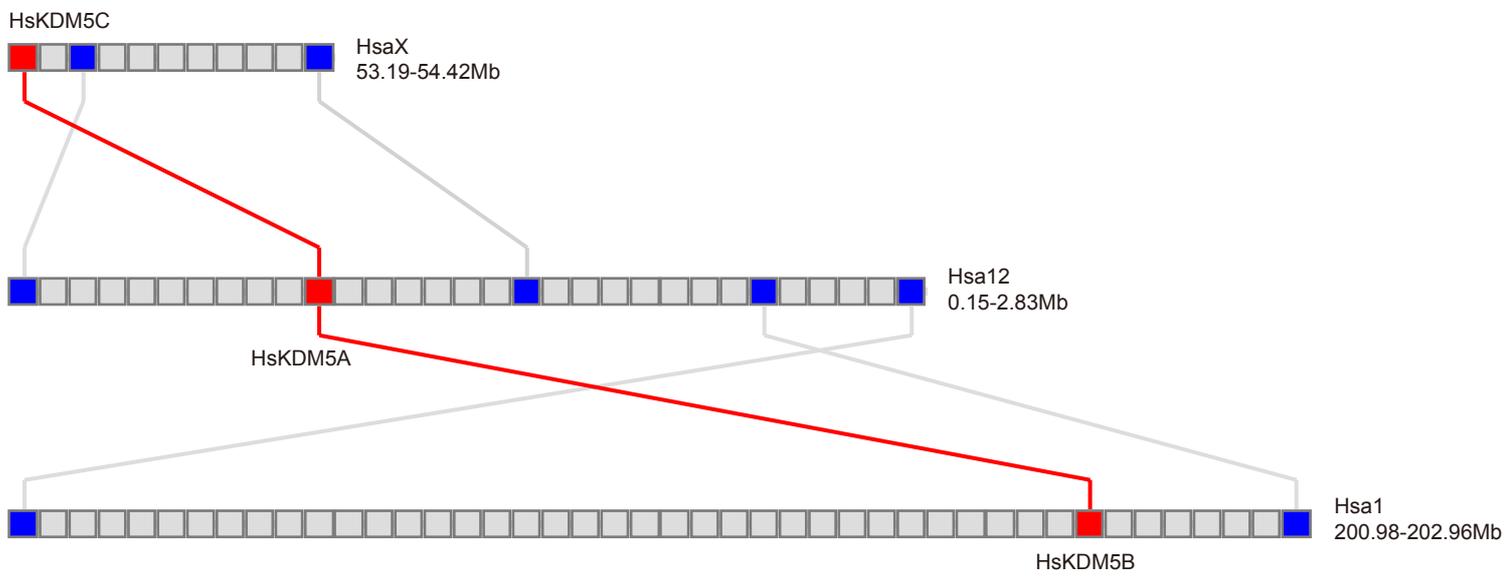
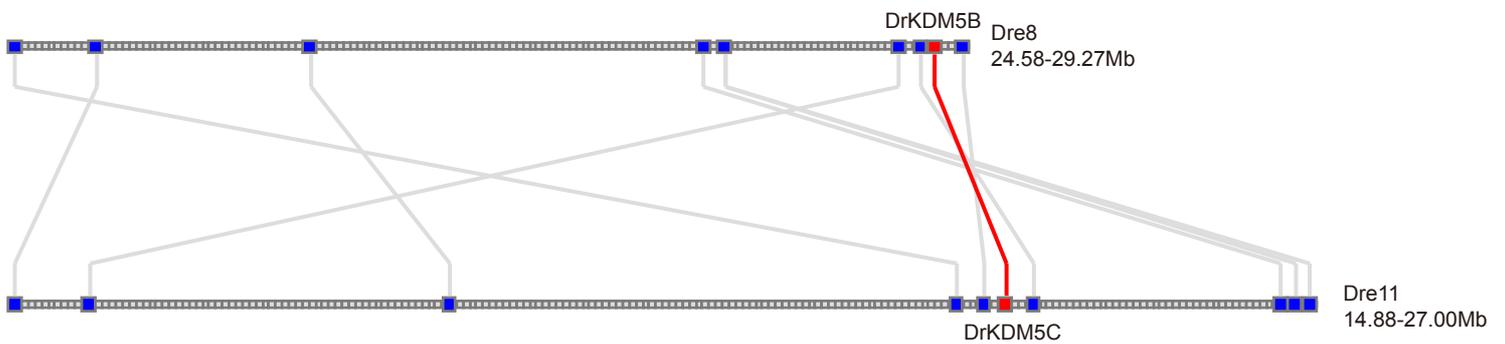
Supplemental Figures S11. The ML trees generated by RAXML of each of *PKDM12*. ML bootstrap values above 50% are shown.



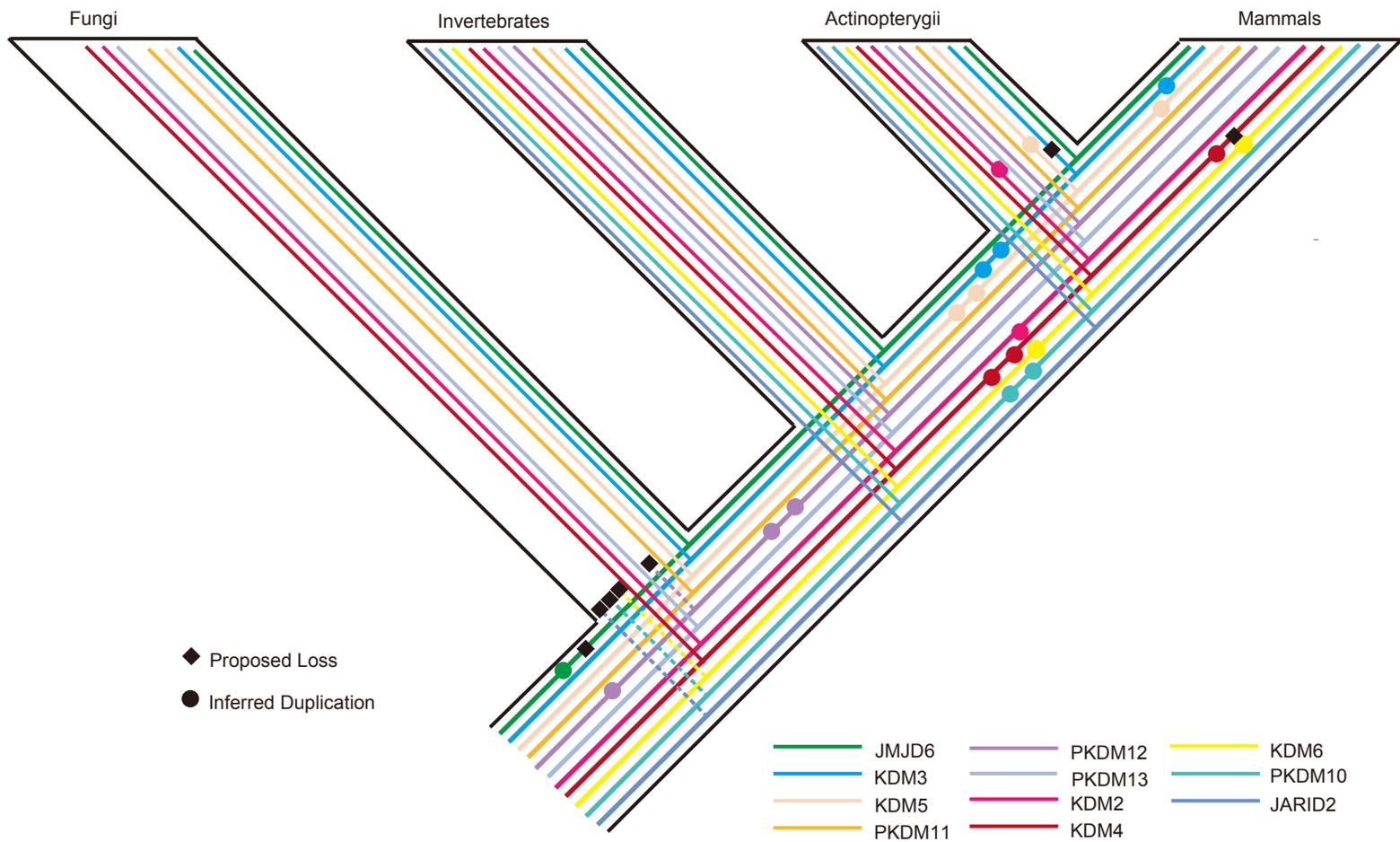
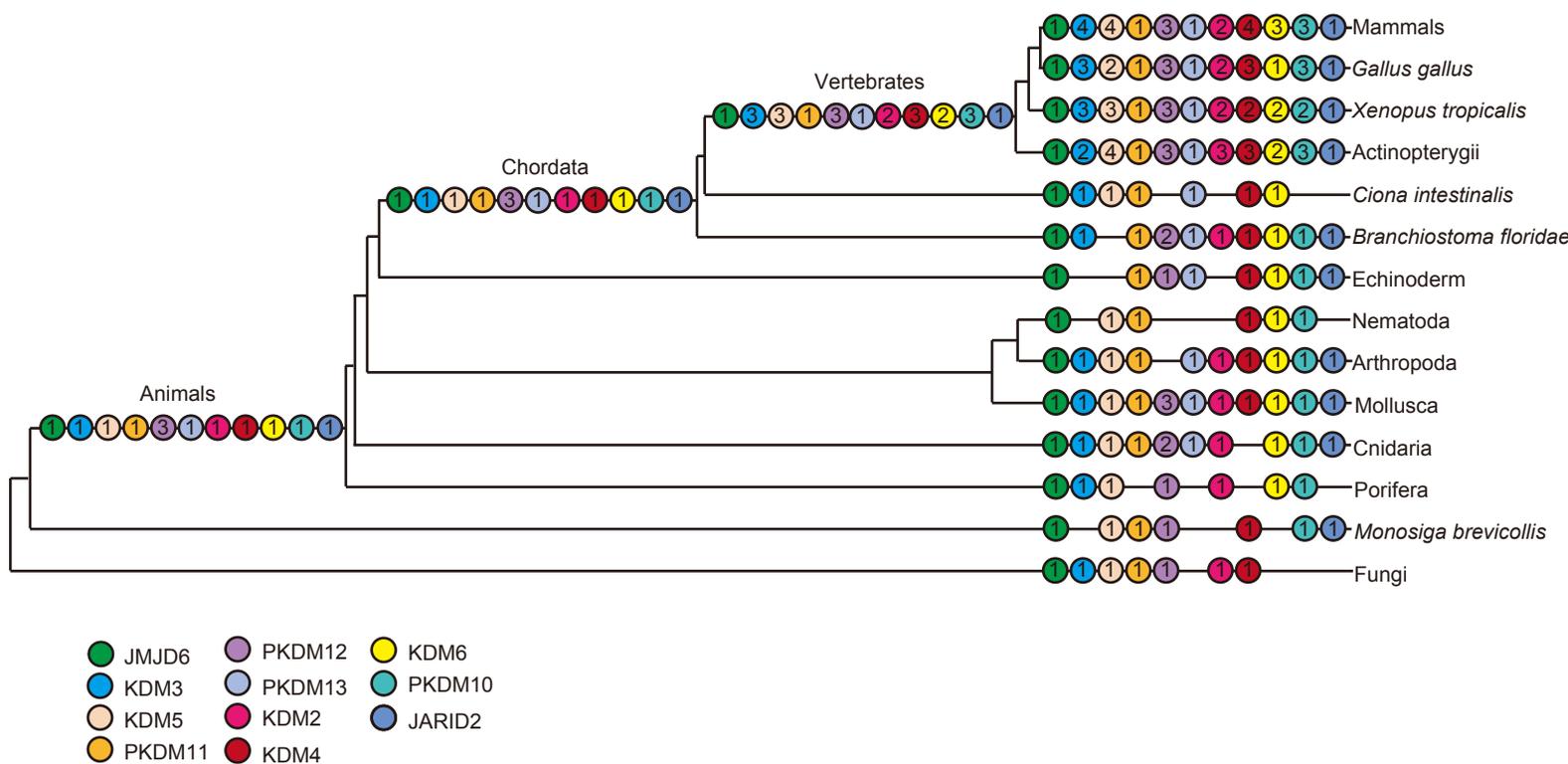
Supplemental Figures S12. The ML trees generated by RAxML of each of *PKDM13*. ML bootstrap values above 50% are shown.



Supplemental Figure S13. Representative plants with the syntenic regions containing representative duplicated gene pairs from recent polyploidy events. Species designations: At, *Arabidopsis thaliana*; Vv, *V. vinifera*; Os, *O. sativa*; chr is short for chromosome. Arrows illustrate the presence and orientation of syntenic paralogous genes, which are connected by lines. Syntenic regions include (A) *AtPKDM7C* and *AtPKDM7B*, (B) *AtPKDM7C* and *AtPKDM7E*, (C) *VvPKDM7A* and *VvPKDM7C*, (D) *OsPKDM8A* and *OsPKDM8B*.

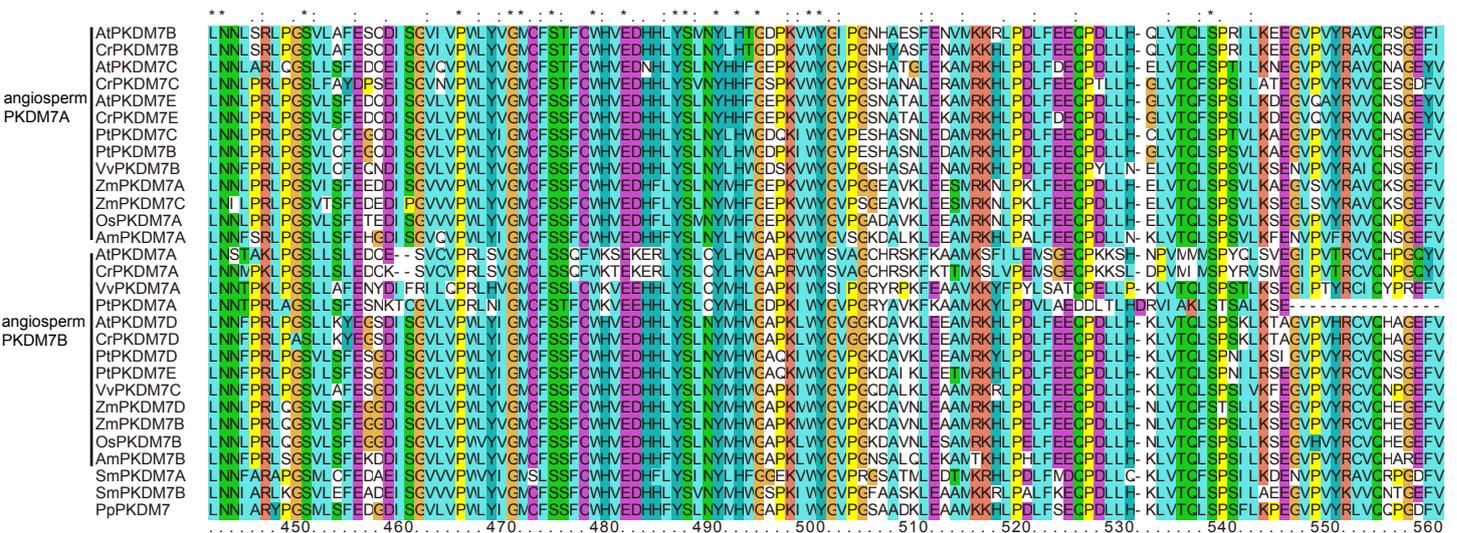
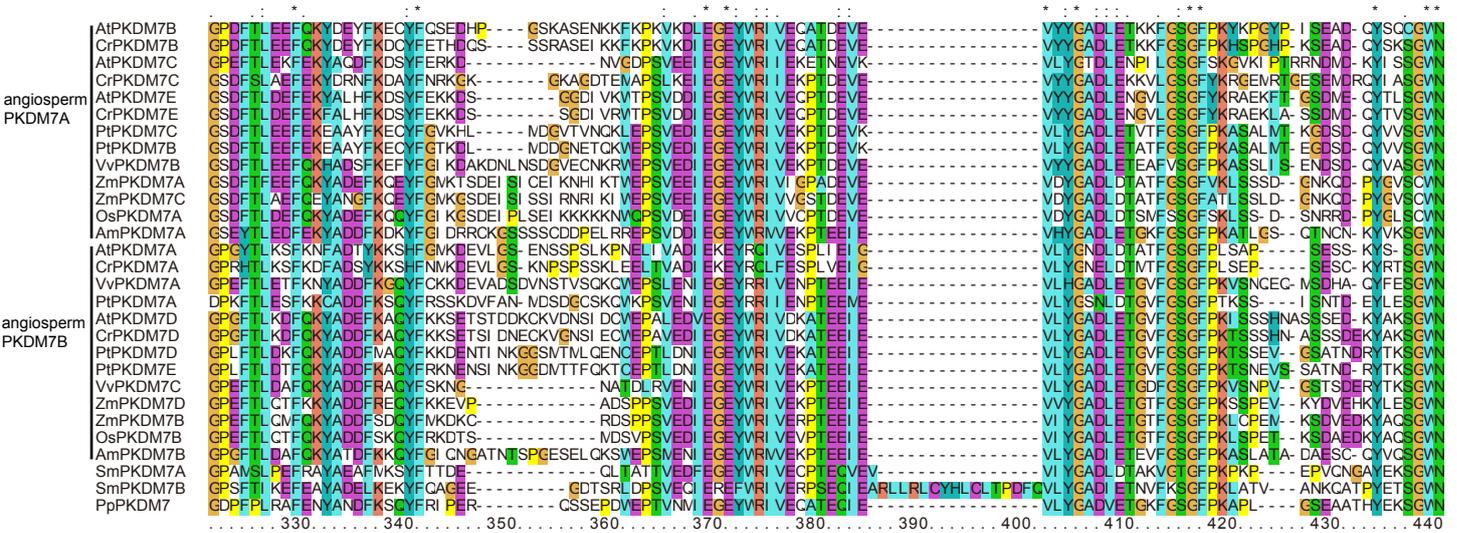
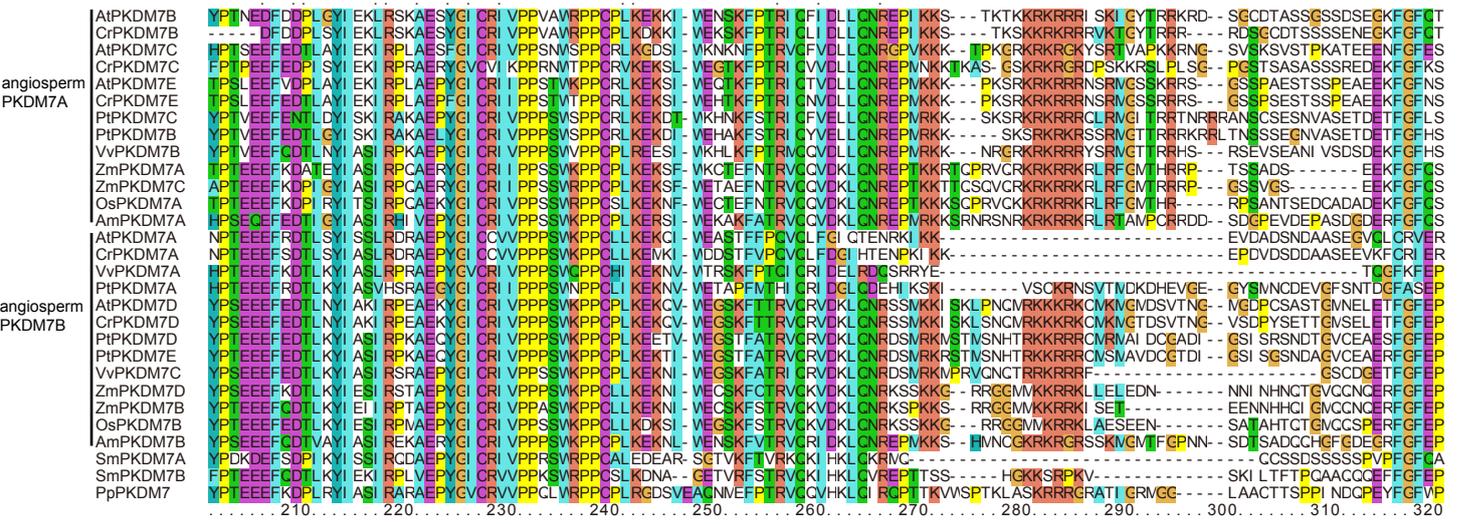
A**B**

Supplemental Figure S14. Representative animals with duplicated gene pairs generated by recent polyploidy events. Species designations: Hs, *Homo sapiens*; Dr, *Danio rerio*; chr is short for chromosome. Syntenic paralogous genes are connected by lines. Syntenic regions include (A) *HsKDM5A*, *HsKDM5B* and *HsKDM5C*, (B) *DrKDM5B* and *DrKDM5C*.

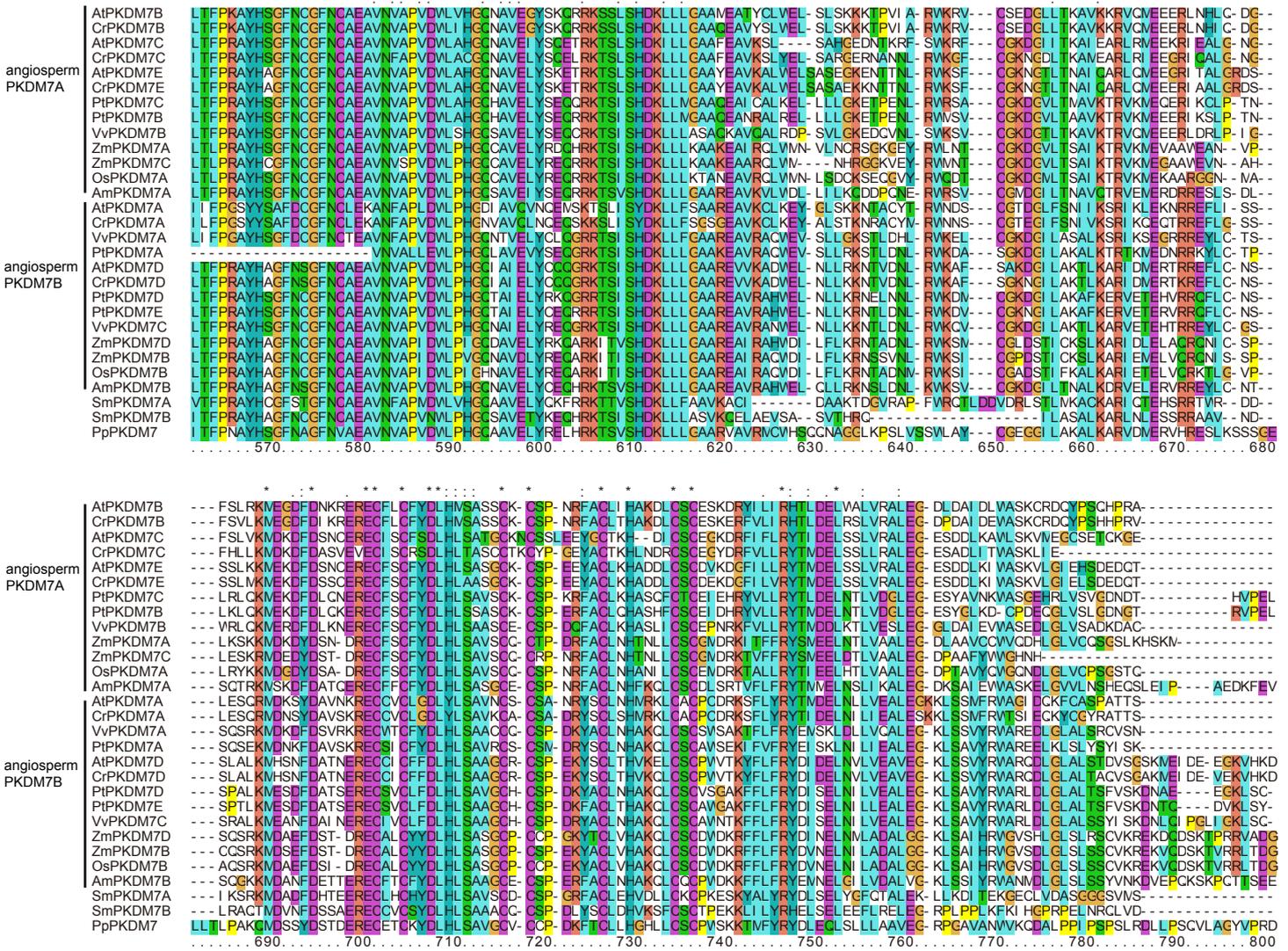
A**B**

Supplemental Figure S15. Duplication events in the JmjC protein family inferred from amino acid level analyses. (A) Schematic depicting the inferred history of gene duplication and loss within the animals and fungi. (B) Schematic depicting the complement of JmjC genes in major animal groups. The numbers in circle represents the number of genes in each *JmjC* subfamily.

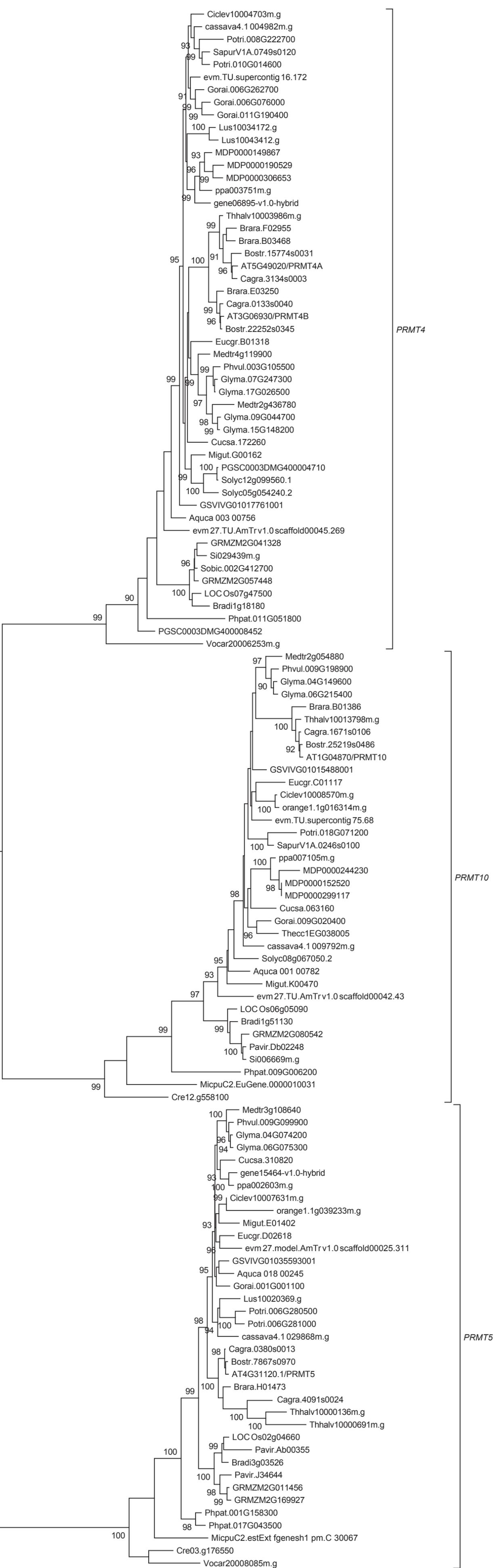
A



B



Supplemental Figure S16. Multiple sequence alignments of Angiosperm *PKDM7A* and *PKDM7B*.



Supplemental Figure S18. A ML tree of PRMT4, PRMT5 and PRMT10 in green plants.