Figure S55. PhyML phylogenetic relations and composition of domains for AT5G20570 homologues of representative plant species. The color legends of species and domains is given below

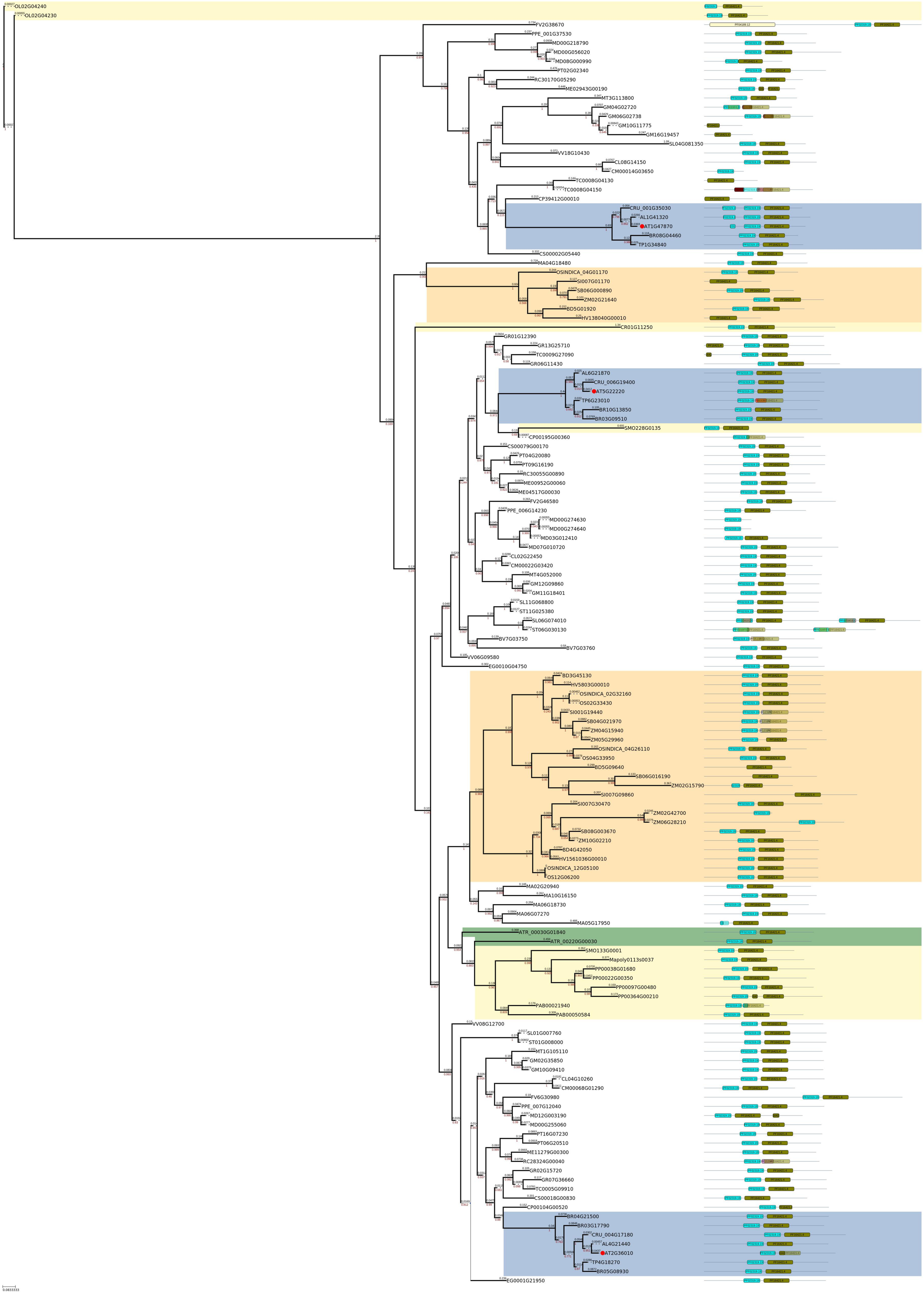
taxonpmic identity of protein

- Poaceae
- Brassicales
- Out group
- Amborella trichopoda

domain architecture

- Prokaryotic_RING_finger_family_4_PF14447_5
- Anaphase_promoting_complex_subunit_11_RING_H2_finger_PF12861_6
- Zinc_finger__C3HC4_type__RING_finger__PF00097_24
- Zinc_finger__C3HC4_type__RING_finger__PF13923_5
- Zinc_finger__C3HC4_type__RING_finger__PF13920_5
- zinc_finger_of_C3HC4_type__RING_PF15227_5
- RING_H2_zinc_finger_domain_PF12678_6
- RING_like_zinc_finger_PF17123_4
- Ring_finger_domain_PF13639_5
- zinc_RING_finger_domain_PF14634_5
- RING_type_zinc_finger_PF13445_5
- Zinc_ribbon__C4HC2_type_PF17120_4

Figure S56. PhyML phylogenetic relations and composition of domains for AT2G36010, AT1G47870, AT5G22220 homologues of representative plant species. The color legends of species and domains is given below



taxonpmic identity of protein

- Poaceae
- Brassicales
- Out group
- Amborella trichopoda

domain architecture

- E2F_transcription_factor_CC_MB_domain_PF16421_4
- E2F_DP_family_winged_helix_DNA_binding_domain_PF02319_19
- Gcd10p_family_PF04189_12
- Synaptonemal_complex_central_element_protein_1_PF15233_5
- Sugar_specific_transcriptional_regulator_TrmB_PF01978_18
- Double_strand_recombination_repair_protein_PF10376_8
- Cell_division_protein_ZapB_PF06005_11
- B_block_binding_subunit_of_TFIIIC_PF04182_11
- Uncharacterized_protein_conserved_in_archaea__DUF2250__PF10007_8
- DivIVA_protein_PF05103_12
- TATA_element_modulatory_factor_1_DNA_binding_PF12329_7
- Leucine_zipper_PF15294_5

Figure S57. PhyML phylogenetic relations and composition of domains for AT5G24310, AT5G42030, AT2G46225 homologues of representative plant species. The color legends of species and domains is given below

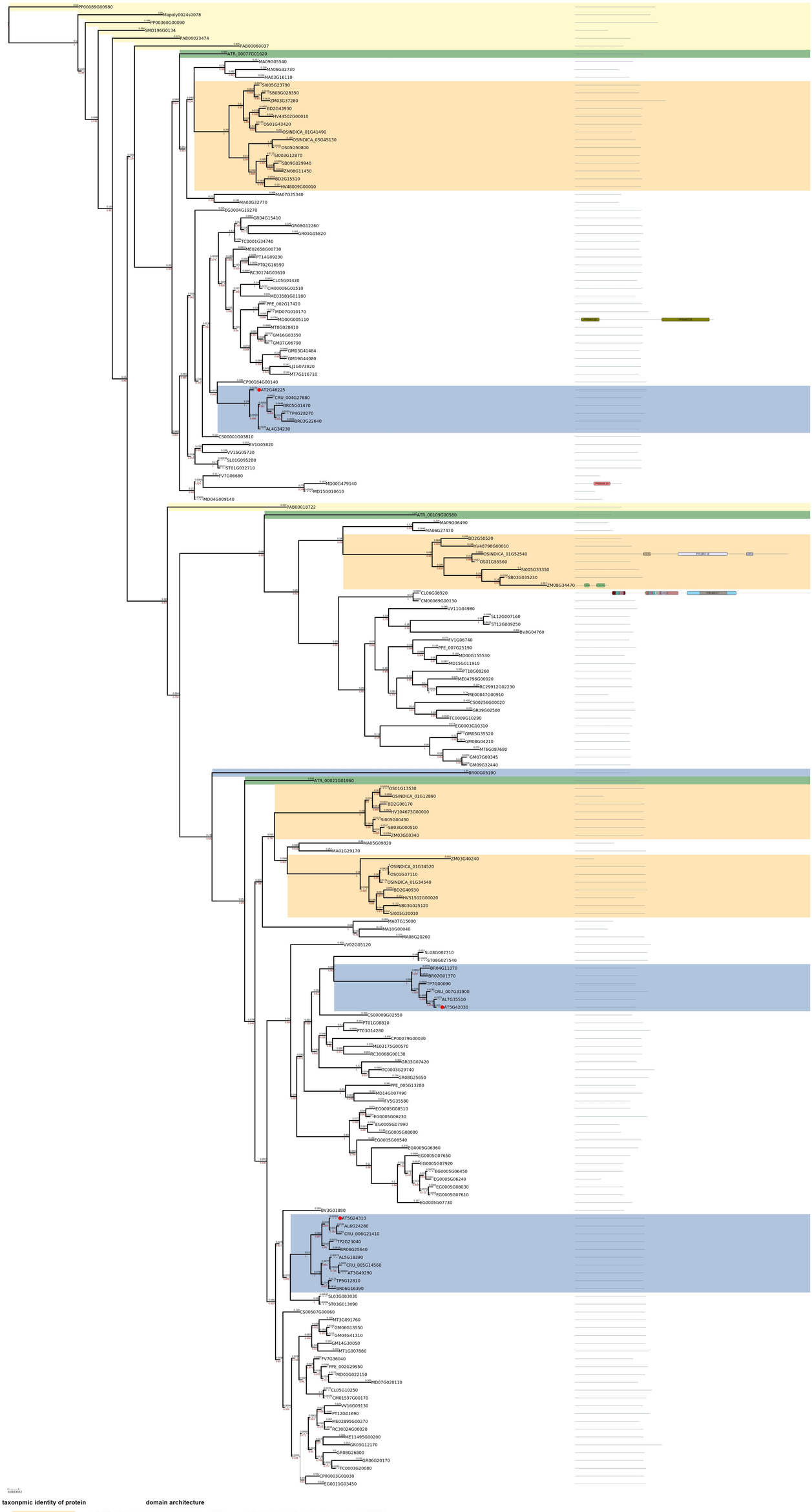
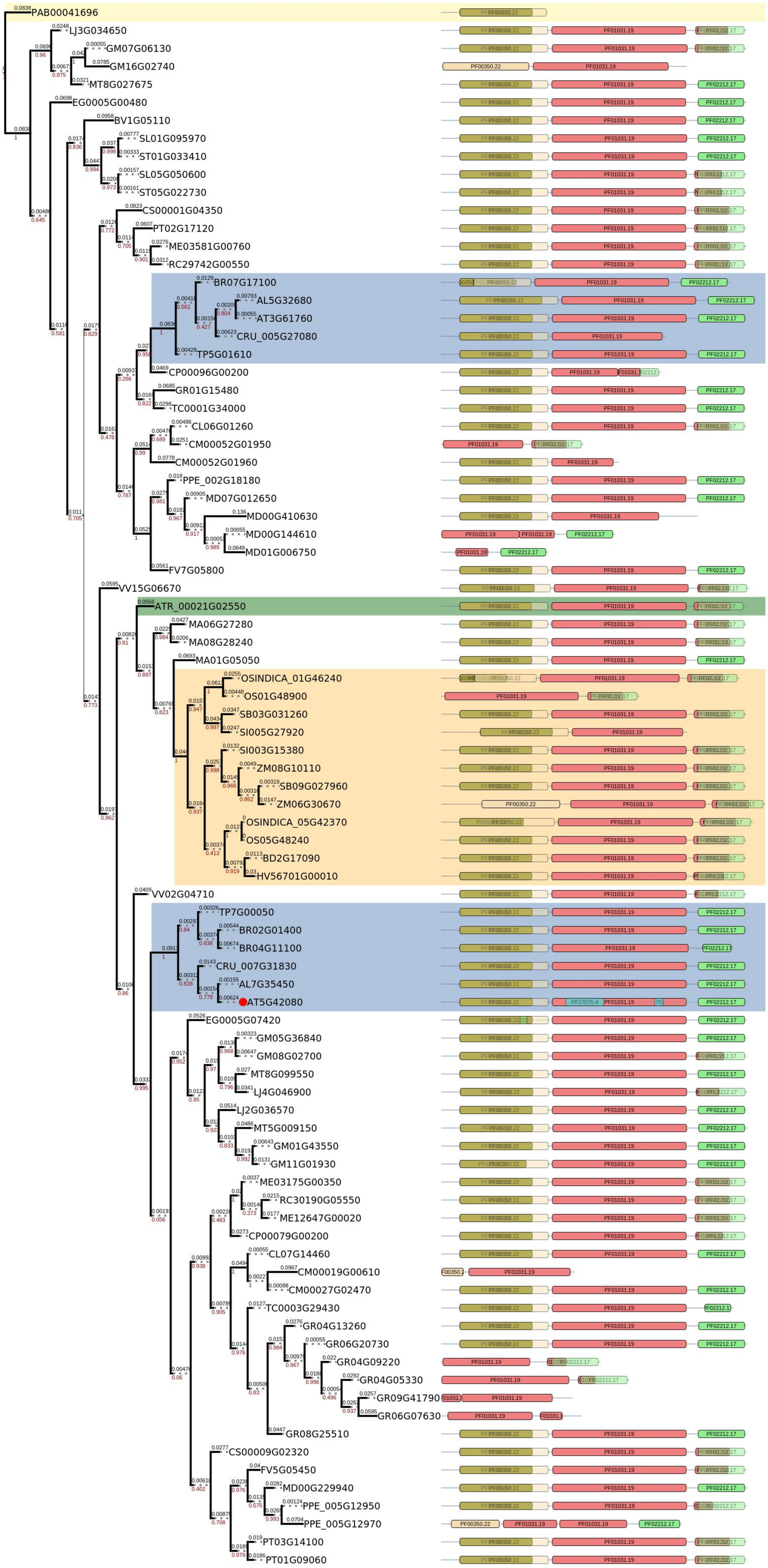


Figure S58. PhyML phylogenetic relations and composition of domains for AT5G28646 homologues of representative plant species. The color legends of species and domains is given below

taxonpmic identity of protein **domain architecture**

Poaceae	Targeting_protein_for_Xklp2__TPX2__PF06886_10
Brassicales	NPL4_family_PF05021_14
	Spectrin_binding_region_of_Ca2+_Calmodulin_PF17095_4
Out group	FAD_binding_domain_PF01494_18
	NAD_P__binding_Rossmann_like_domain_PF13450_5
Amborella trichopoda	

Figure S59. PhyML phylogenetic relations and composition of domains for AT5G42080 homologues of representative plant species. The color legends of species and domains is given below



taxonpmic identity of protein

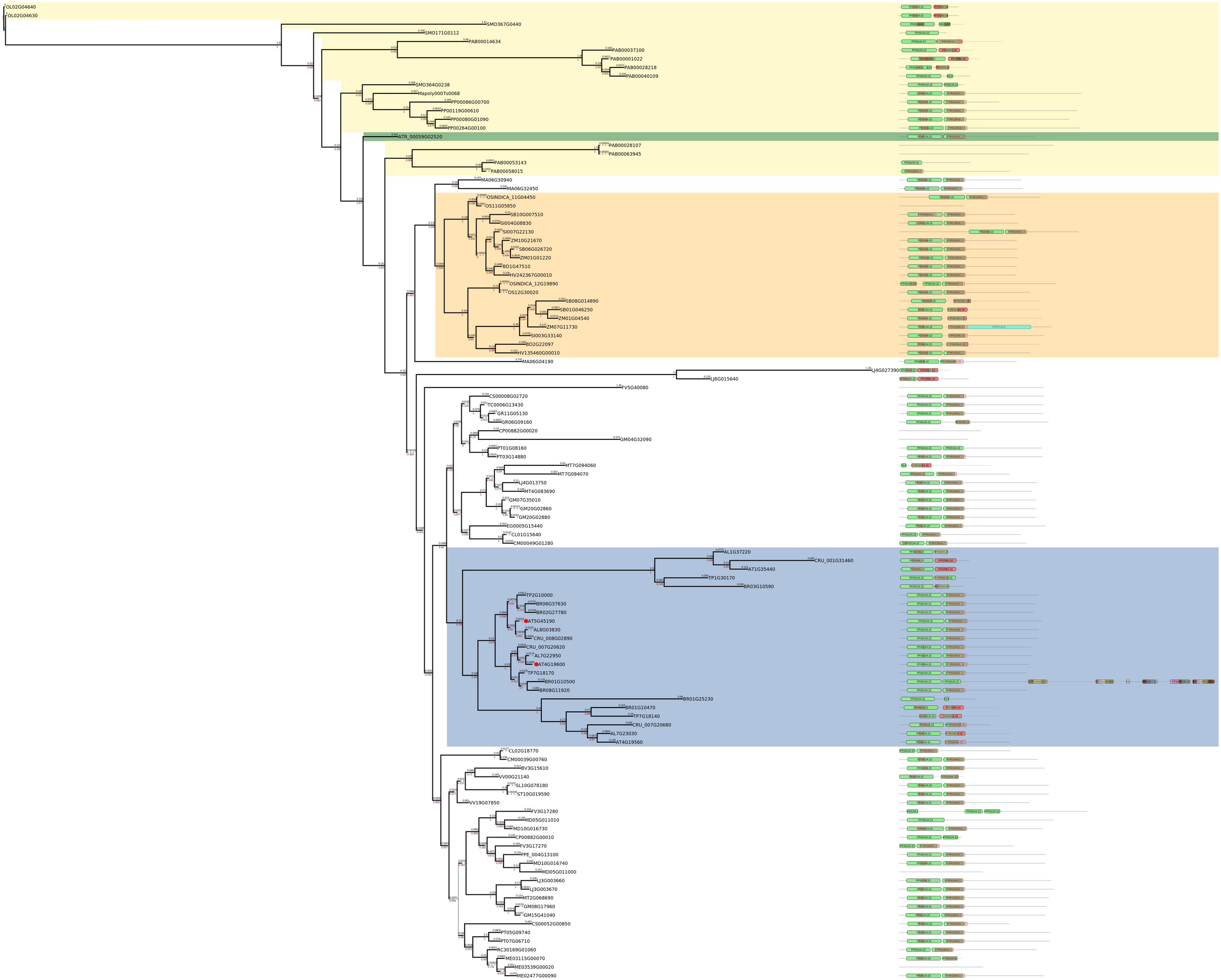
- Poaceae
- Brassicales
- Out group
- Amborella trichopoda

domain architecture

- Dynamin_family_PF00350_22
- 50S_ribosome_binding_GTPase_PF01926_22
- Dynamin_central_region_PF01031_19
- Dynamin_GTPase_effector_domain_PF02212_17
- Regular_of_rDNA_transcription_protein_14_PF17075_4

Figure S60. PhyML phylogenetic relations and composition of domains for AT5G43900 homologues of representative plant species. The color legends of species and domains is given below

Figure S61. PhyML phylogenetic relations and composition of domains for AT5G45190, AT4G19600 homologues of representative plant species. The color legends of species and domains is given below



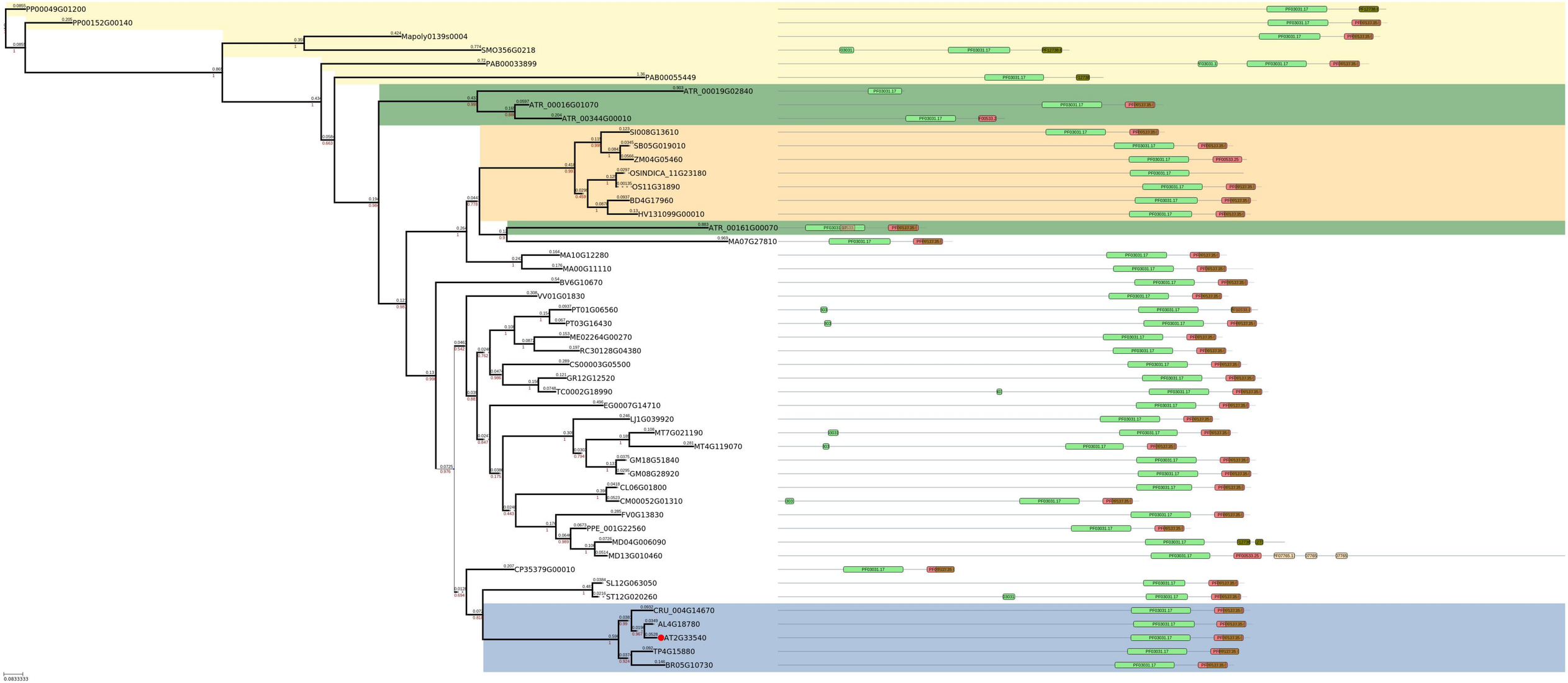
taxonpmic identity of protein

- Poaceae
- Brassicales
- Out group
- Amborella trichopoda

domain architecture

- Cyclin__C_terminal_domain_PF02984_18
- Cyclin__N_terminal_domain_PF00134_22
- Transcription_factor_TFIIB_repeat_PF00382_18
- Macoilin_family_PF09726_8
- Cyclin_C_terminal_domain_PF16899_4
- Limkain_b1_PF11608_7
- Nup53_35_40_type_RNA_recognition_motif_PF14605_5
- RNA_recognition_motif___a_k_a__RRM__RBD__or_RNP_domain__PF00076_21
- RNA_recognition_motif_PF16367_4
- Occluded_RNA_recognition_motif_PF16842_4

Figure S62. PhyML phylogenetic relations and composition of domains for AT2G33540 homologues of representative plant species. The color legends of species and domains is given below

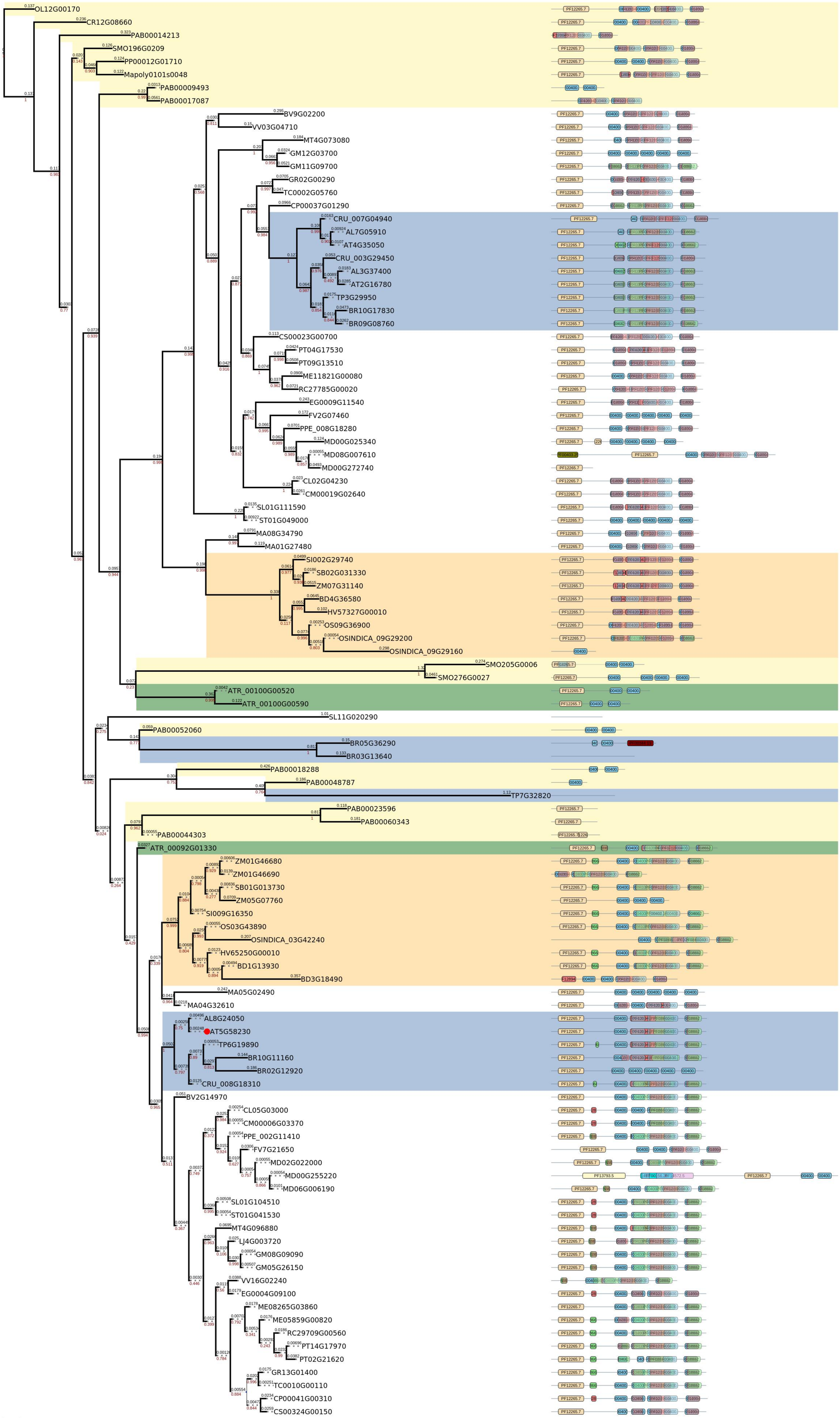


taxonpmic identity of protein domain architecture

- Poaceae
- Brassicales
- Out group
- Amborella trichopoda

- NLI_interacting_factor_like_phosphatase_PF03031_17 — PF03031.17
- twin_BRCT_domain_PF12738_6 — PF12738.6
- BRCA1_C_Terminus__BRCT__domain_PF00533_25 — PF00533.25
- KIP1_like_protein_PF07765_11 — PF07765.11

Figure S63. PhyML phylogenetic relations and composition of domains for AT5G58230 homologues of representative plant species. The color legends of species and domains is given below



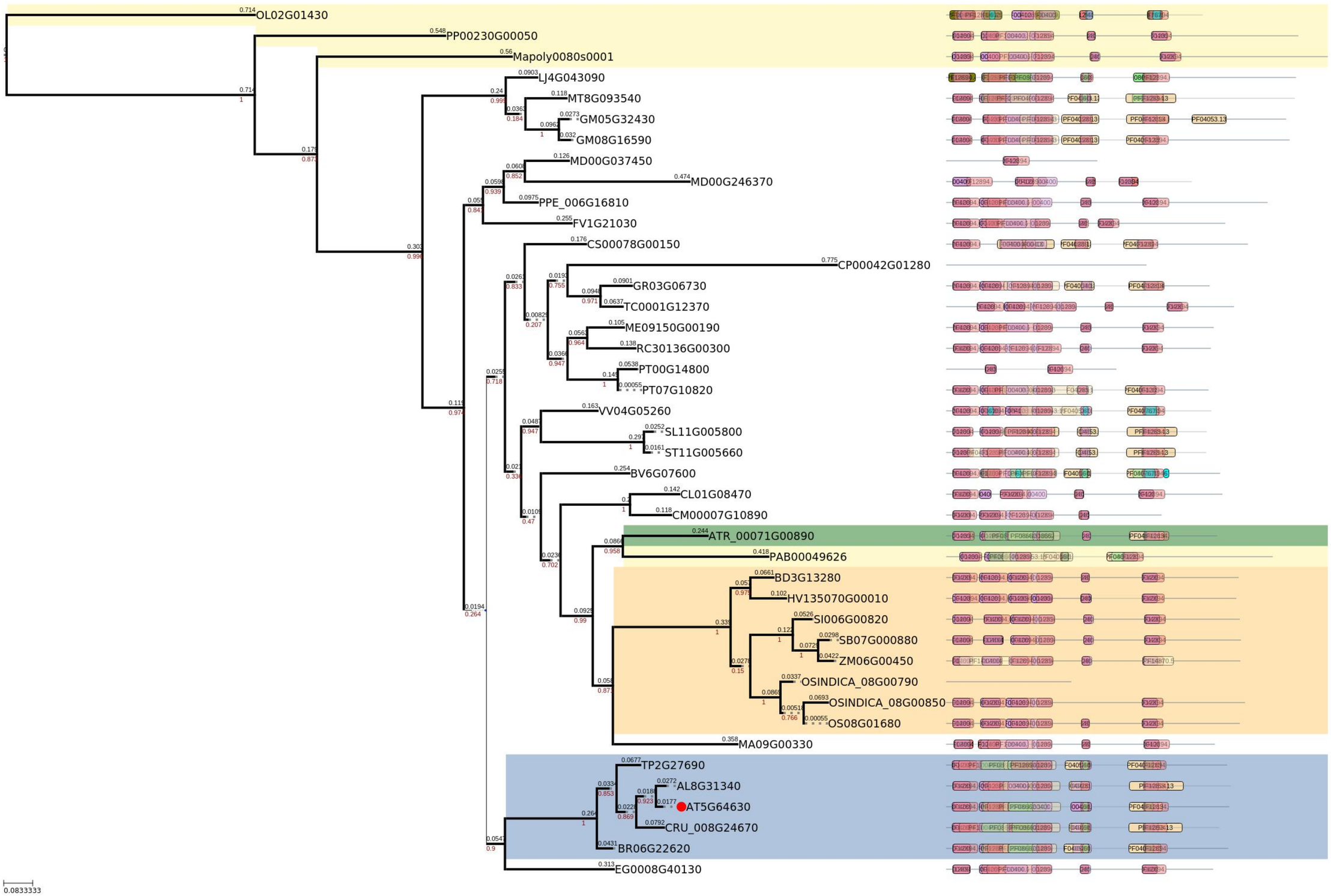
taxonpmic identity of protein

- Poaceae
- Brassicales
- Out group
- Amborella trichopoda

domain architecture

- Anaphase_promoting_complex_subunit_4_WD40_domain_PF12894_6 — PF12894.6
- Histone_binding_protein_RBBP4_or_subunit_C_of_CAF1_complex_PF12265_7 — PF12265.7
- WD_domain__G_beta_repeat_PF00400_31 — PF00400.31
- Eukaryotic_translation_initiation_factor_eIF2A_PF08662_10 — PF08662.10
- Heavy_metal_associated_domain_PF00403_25 — PF00403.25
- SecY_translocase_PF00344_19 — PF00344.19
- Phosphoribosyl_transferase_domain_PF00156_26 — PF00156.26
- N_terminal_domain_of_ribose_phosphate_pyrophosphokinase_PF13793_5 — PF13793.5
- Phosphoribosyl_synthetase_associated_domain_PF14572_5 — PF14572.5

Figure S64. PhyML phylogenetic relations and composition of domains for AT5G64630 homologues of representative plant species. The color legends of species and domains is given below



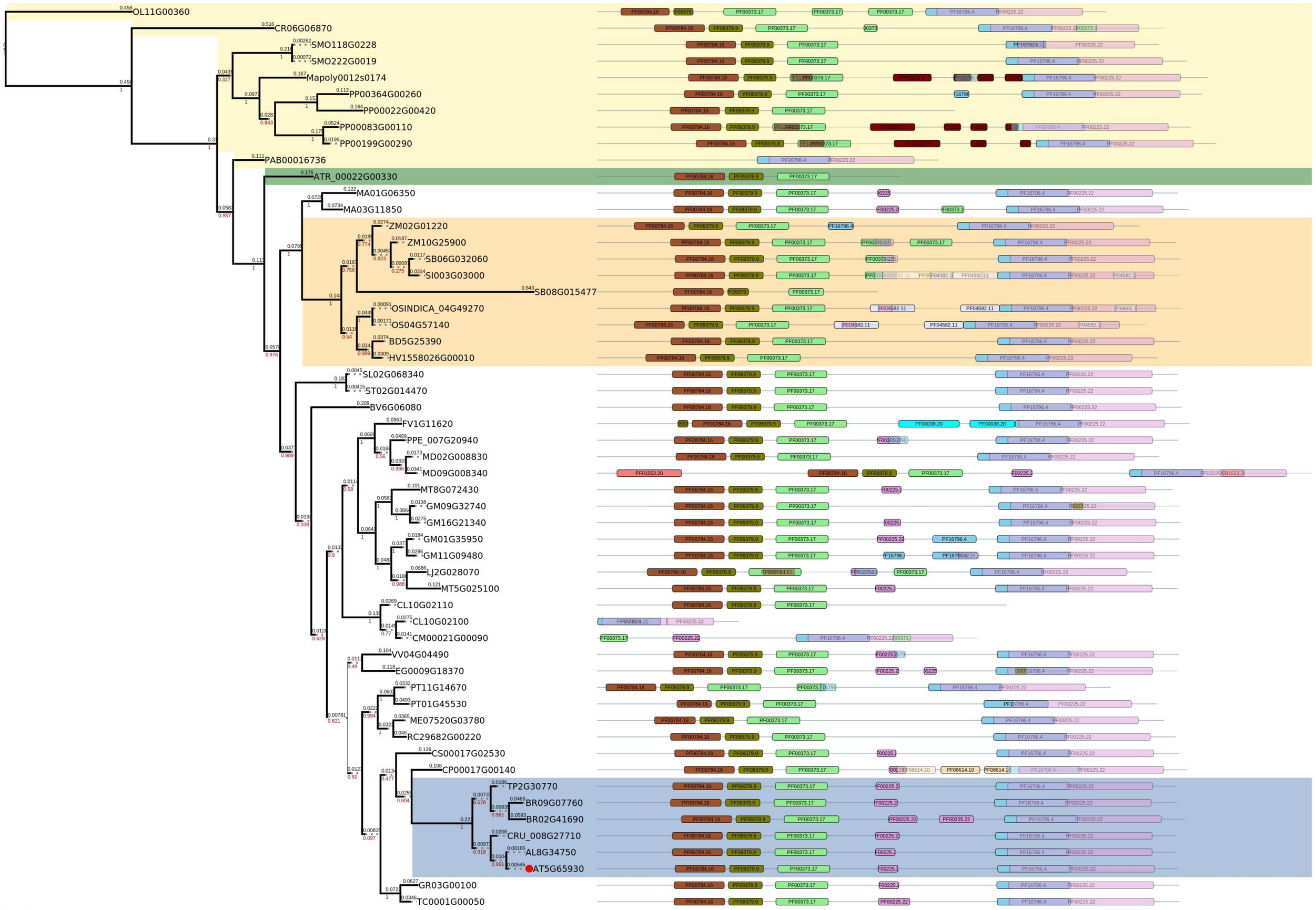
taxonpmic identity of protein

- Poaceae
- Brassicales
- Out group
- Amborella trichopoda

domain architecture

- Anaphase_promoting_complex_subunit_4_WD40_domain_PF12894_6
- WD40_region_of_Ge1__enhancer_of_mRNA_decapping_protein_PF16529_4
- WD40_like_Beta_Propeller_Repeat_PF07676_11
- WD_domain__G_beta_repeat_PF00400_31
- Eukaryotic_translation_initiation_factor_eIF2A_PF08662_10
- Coatomer_WD_associated_region_PF04053_13
- Photosynthesis_system_II_assembly_factor_YCF48_PF14870_5

Figure S65. PhyML phylogenetic relations and composition of domains for AT5G65930 homologues of representative plant species. The color legends of species and domains is given below



taxonpmic identity of protein

- Poaceae
- Brassicales
- Out group
- Amborella trichopoda

domain architecture

- FERM_central_domain_PF00373_17
- FERM_N_terminal_domain_PF09379_9
- Kinesin_motor_domain_PF00225_22
- Microtubule_binding_PF16796_4
- MyTH4_domain_PF00784_16
- Subunit_21_of_Mediator_complex_PF11221_7
- HOOK_protein_PF05622_11
- Reovirus_sigma_C_capsid_protein_PF04582_11
- Intermediate_filament_protein_PF00038_20
- Acyltransferase_PF01553_20
- Autophagy_protein_16__ATG16__PF08614_10