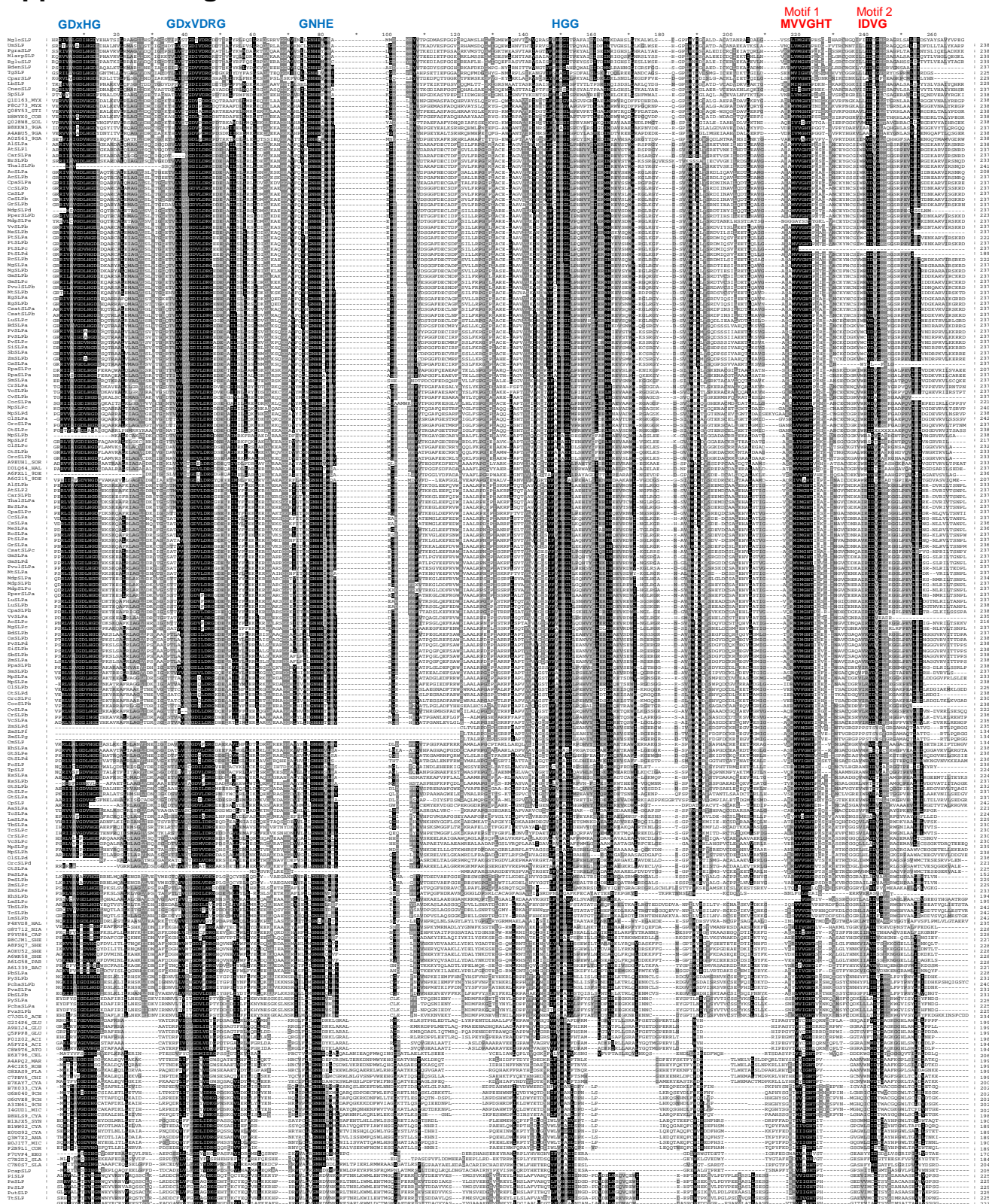
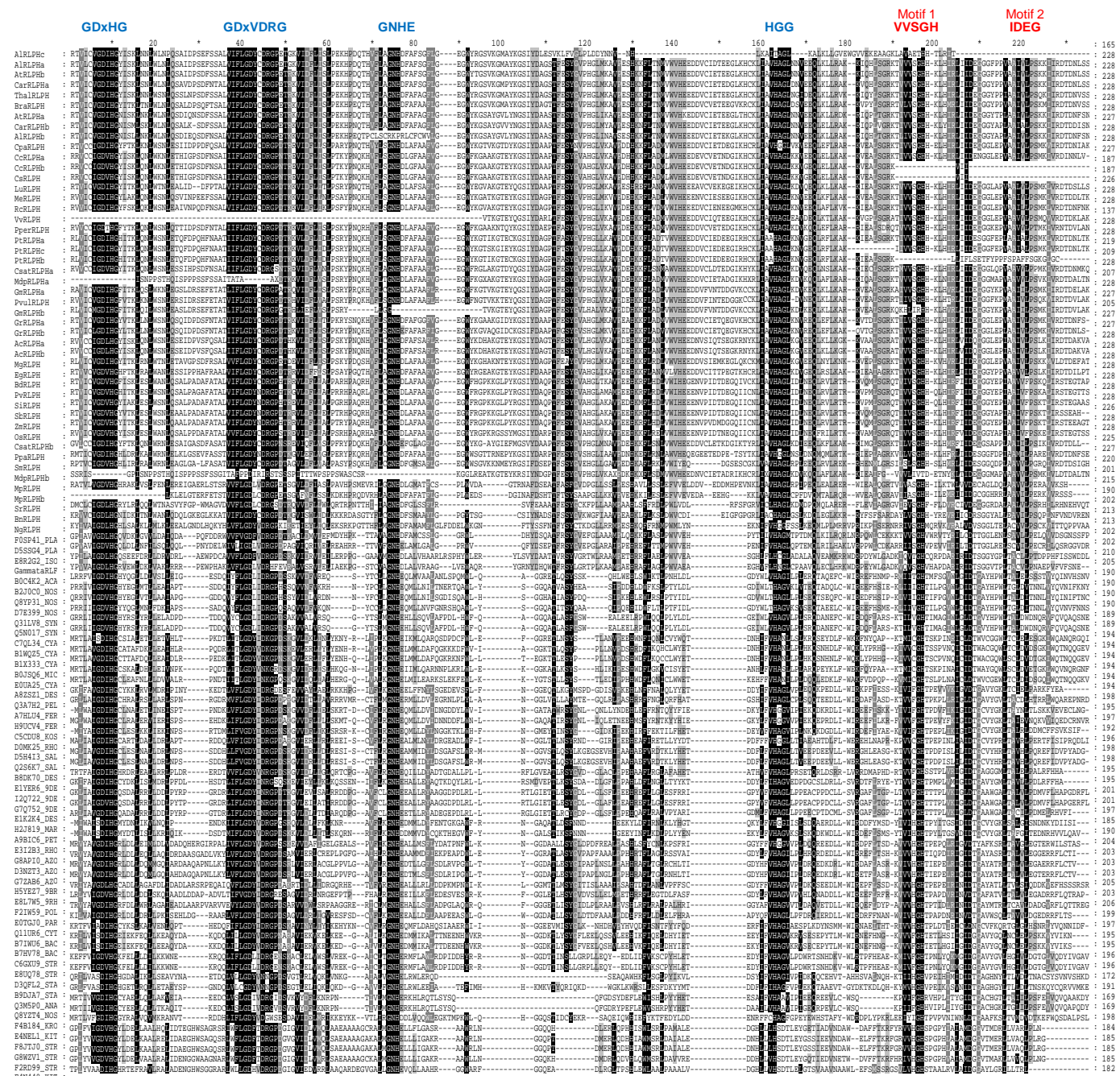


Supplemental Figure S1



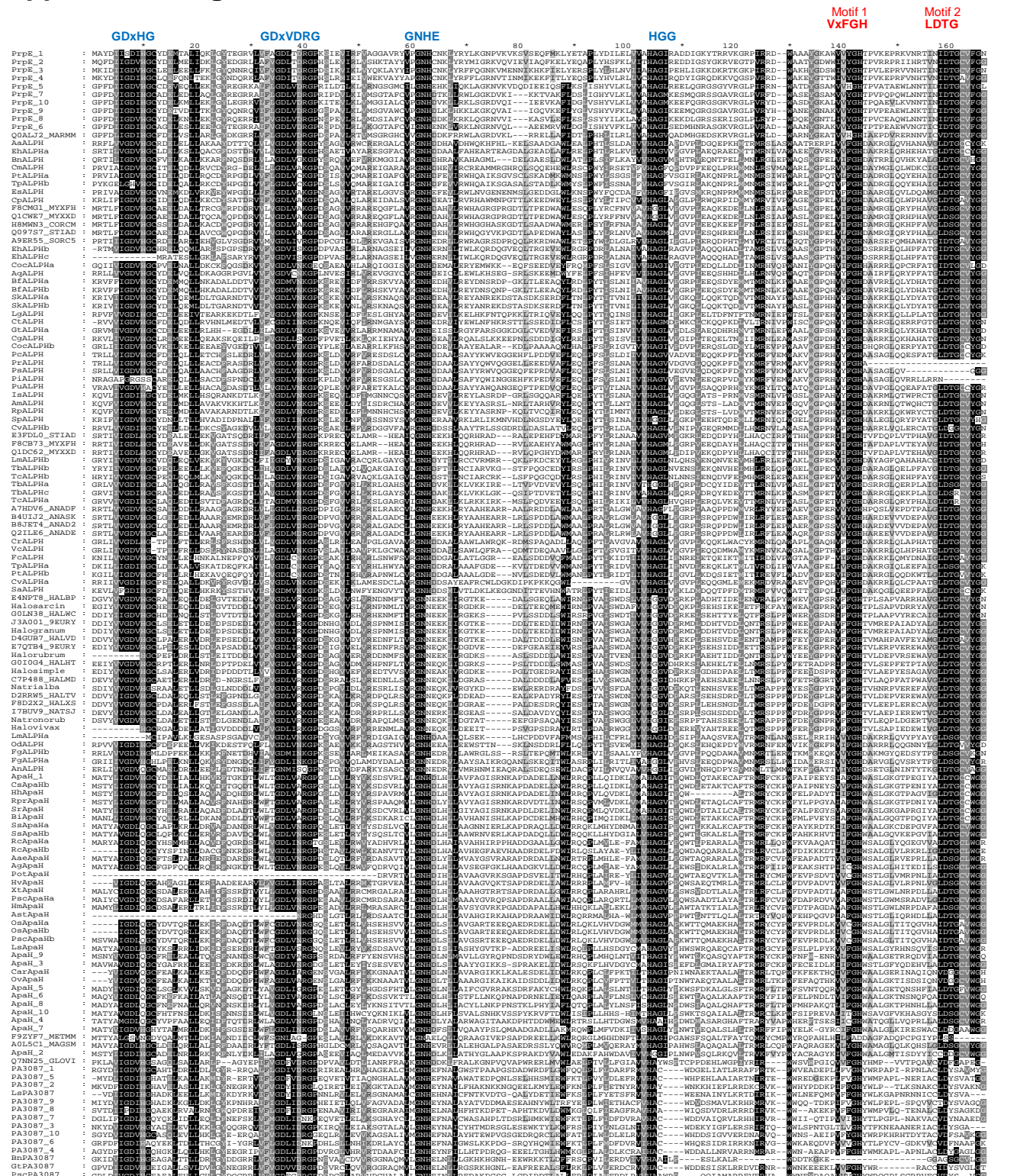
Supplemental Figure S1: Alignment of the phosphatase domain of SLP protein phosphatases from both Prokaryotes and Eukaryotes. Candidate SLP phosphatase sequences identified as detailed in Materials and Methods were aligned using MAFFT. The alignment was visualized in GeneDoc and manually edited to remove the extreme N- and C-terminal regions outside the protein phosphatase domain, plus poorly aligned regions, prior to phylogenetic tree inference. Two conserved bacterial-like phosphatase motifs (orange) were identified in addition to the known canonical PPP-family protein phosphatase motifs (blue). Of the two bacterial-like PPP-phosphatase motifs, Motif 1 represents a novel region of conservation. Motif 2 was previously reported (Andreeva and Kutuzov, 2004). The gene identifiers of each sequence used here are located in Supplemental Table S1.

Supplemental Figure S2



Supplemental Figure S2: Alignment of the phosphatase domain of RLPH protein phosphatases from both Prokaryotes and Eukaryotes. Candidate RLPH phosphatase sequences identified as detailed in Materials and Methods were aligned using MAFFT. The alignment was visualized in GeneDoc and manually edited to remove the extreme N- and C-terminal regions outside the protein phosphatase domain, plus poorly aligned regions, prior to phylogenetic tree inference. Two conserved bacterial-like phosphatase motifs (orange) were identified in addition to the known canonical PPP-family protein phosphatase motifs (blue). Of the two bacterial-like PPP-phosphatase motifs, Motif 1 represents a novel region of conservation. Motif 2 was previously reported (Andreeva and Kutuzov, 2004). The gene identifier of each sequence used here are located in Supplemental Table S1.

Supplemental Figure S3

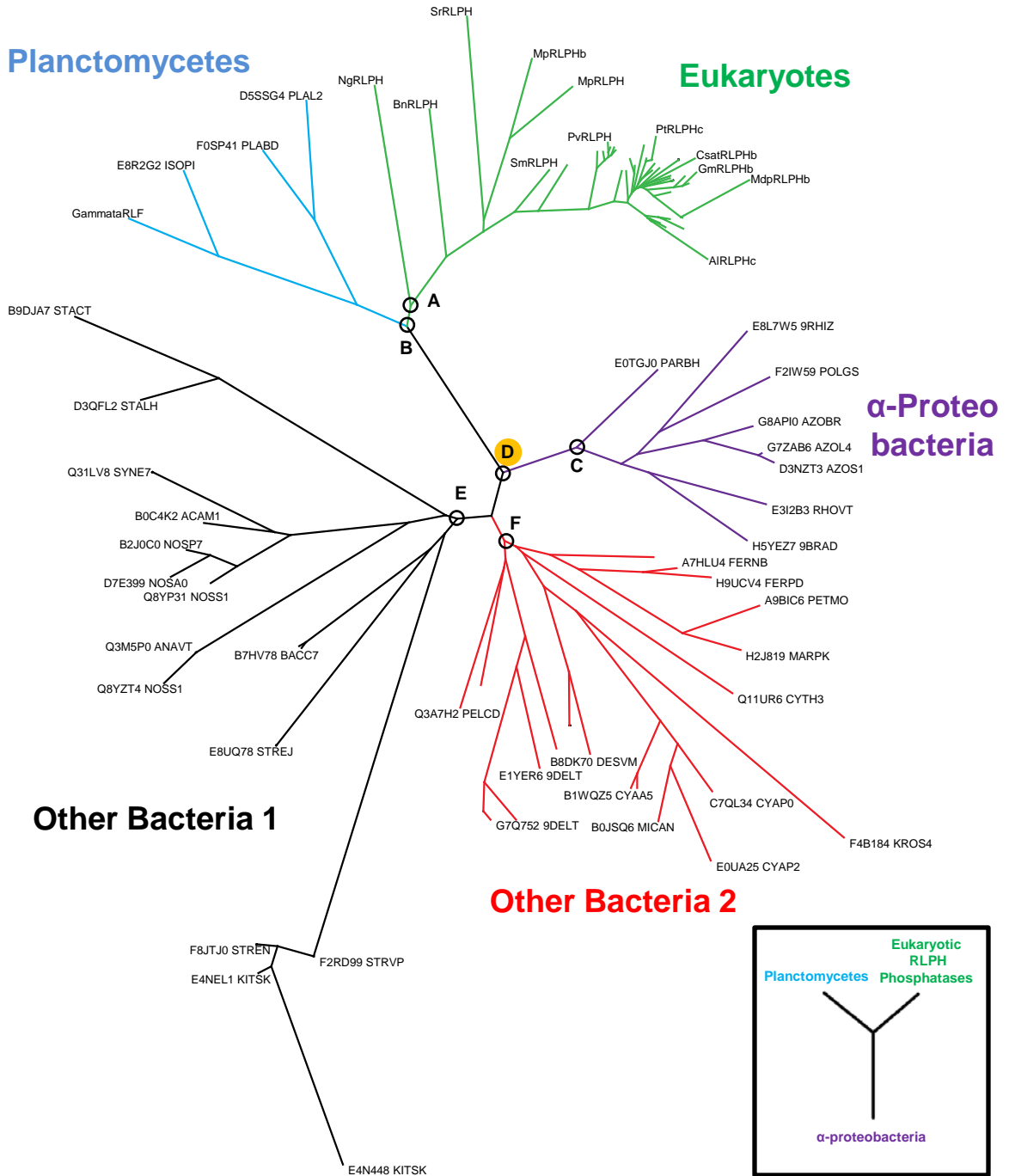


Supplemental Figure S3: Alignment of the phosphatase domain of ALPH protein phosphatases from both Prokaryotes and Eukaryotes. Candidate ALPH phosphatase sequences identified as detailed in Materials and Methods were aligned using MAFFT. The alignment was visualized in GeneDoc and manually edited to remove the extreme N- and C-terminal regions outside the protein phosphatase domain, plus poorly aligned regions, prior to phylogenetic tree inference. Two conserved bacterial-like phosphatase motifs (orange) were identified in addition to the known canonical PPP-family protein phosphatase motifs (blue). Of the two bacterial-like PPP-phosphatase motifs, Motif 1 represents a novel region of conservation. Motif 2 was previously reported (Andreeva and Kutuzov, 2004). The gene identifiers of each sequence used here are located in Supplemental Table S1.

Supplemental Figure S5

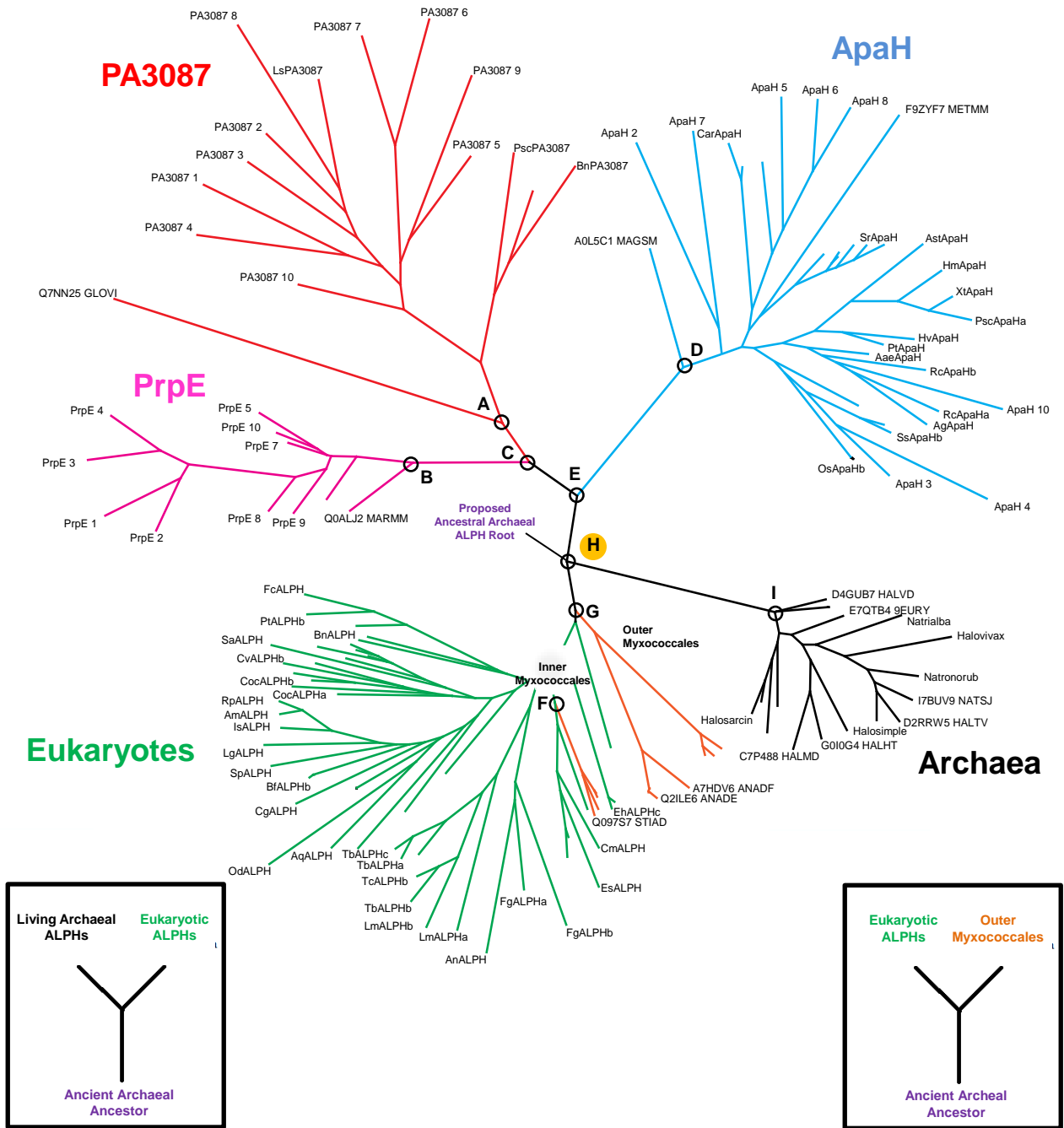
Planctomycetes

Eukaryotes



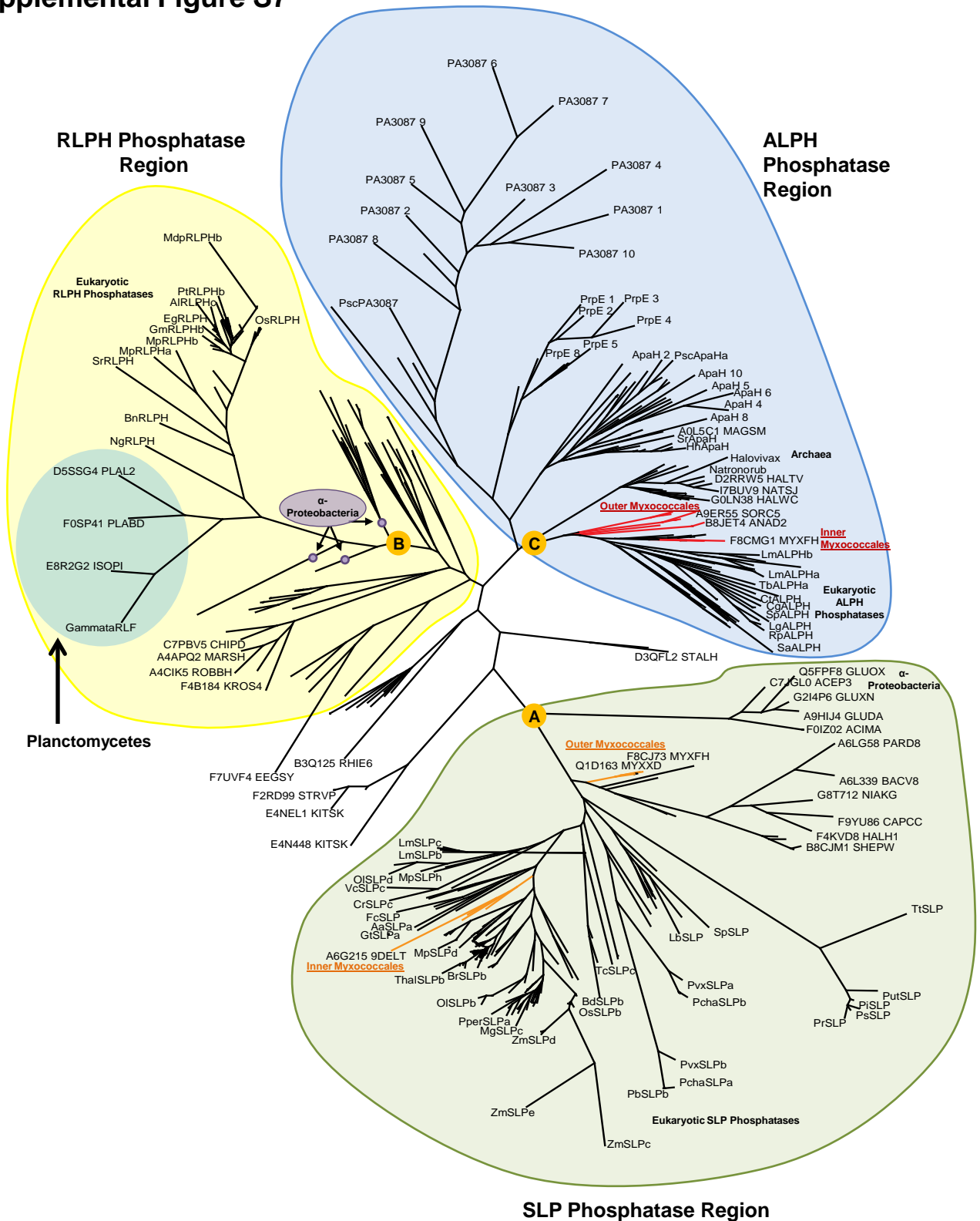
Supplemental Figure S5: Phylogenetic radial tree depicting RLPH protein phosphatase distribution and interrelationships across both Eukaryotes and Bacteria. A radial depiction of the orthogonal tree presented in Figure 2. Insets highlight key evolutionary nodes depicted within the tree. Sequences from eukaryotic ALPH phosphatases (green), α -Proteobacteria (purple), Planctomycetes (blue), and other bacteria (red and black) are highlighted. Sequences used in multiple sequence alignment and phylogenetic tree generation are listed in Supplemental Table S1.

Supplemental Figure S6



Supplemental Figure S6: Phylogenetic radial tree depicting ALPH protein phosphatase distribution and interrelationships across Eukaryotes, Archaea and Bacteria. A radial depiction of the orthogonal tree presented in Figure 3. Insets highlight key evolutionary nodes depicted within the tree. Sequences from eukaryotic ALPH phosphatases (green), Archaea (black), PrpE (pink), PA3087 (red) and ApaH (blue) groups are highlighted. "Outer Myxococcales" and "Inner Myxococcales" are highlighted in orange and are explicitly labeled on the tree. Sequences used in multiple sequence alignment and phylogenetic tree generation are listed in Supplemental Table S1.

Supplemental Figure S7



Supplemental Figure S7: Phylogenetic radial tree depicting SLP, RLPH and ALPH protein phosphatase distribution and interrelationships across Eukaryotes, Archaea, and Bacteria. A radial depiction of a maximum-likelihood phylogenetic tree (PhyML, 5 random starts) inferred from a combined sequence set composed of all three classes of bacterial-like phosphoprotein phosphatase sequences. The eukaryotic SLP region is colored green, and the associated α -proteobacterial sequence cluster is labeled ' α -Proteobacteria'. The eukaryotic RLPH region is colored yellow, and the associated α -proteobacterial sequence cluster is labeled ' α -Proteobacteria', with branches denoted with purple circles. The eukaryotic ALPH region is colored blue, and the associated archaeal sequence cluster is labeled 'Archaea'. Support for the labeled nodes (aBayes support) is as follows: Node A (0.997) [α -Proteobacteria plus SLP radiation]; Node B (1.00) [α -Proteobacteria plus RLPH radiation]; Node C (0.999) [Archaeal ALPHs plus ALPH radiation]. In the SLP sequence region and the ALPH sequence region, "Outer Myxococcales" and "Inner Myxococcales" are both clearly indicated in orange and red, respectively. In the RLPH sequence region the associated Planctomycetes bacteria are highlighted in green. Sequences used in multiple sequence alignment and phylogenetic tree generation are listed in Supplemental Table S1.