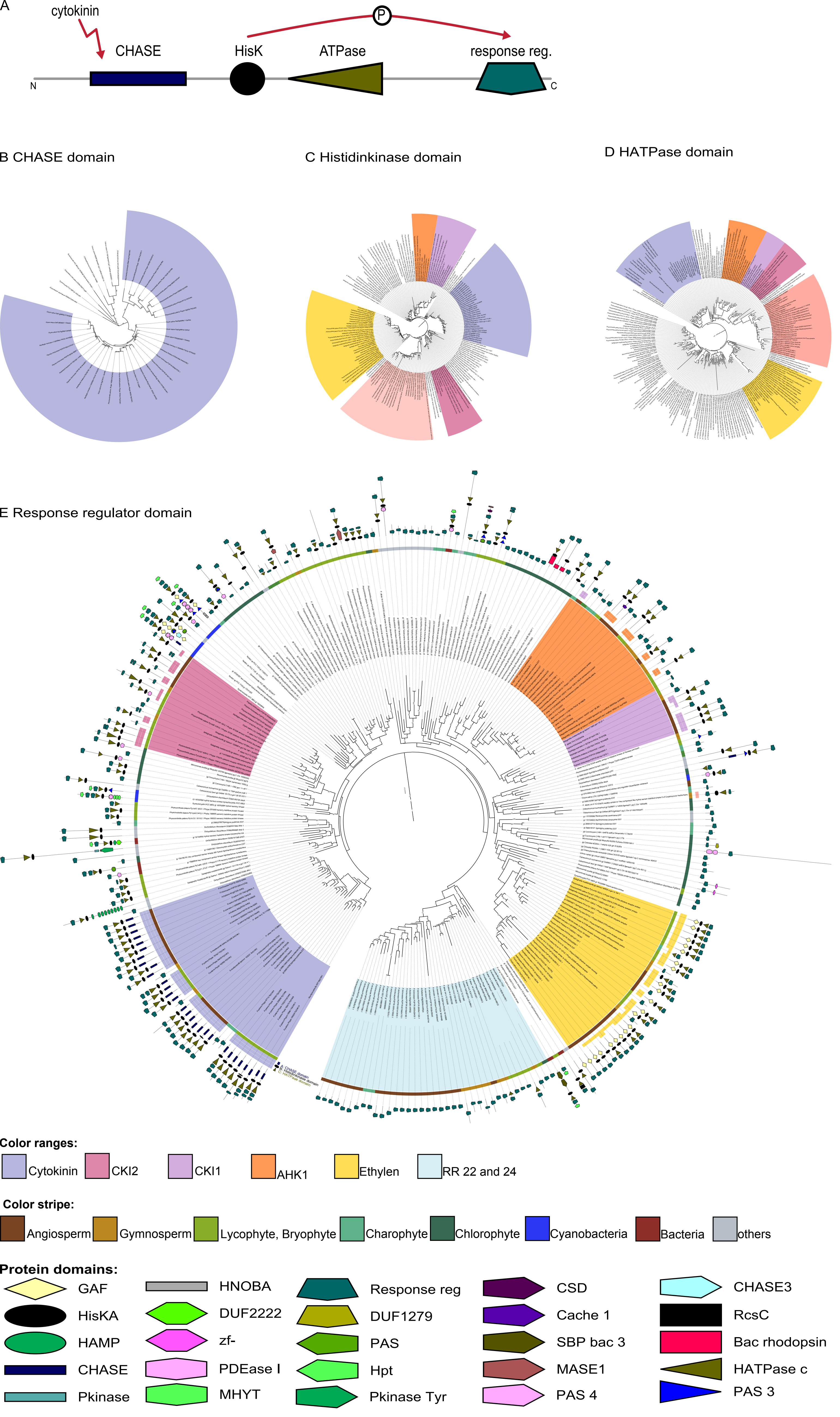

Supplemental Figure S2. Phylogenetic sub-trees for different domains of hybrid histidine kinases. (A) Schematic overview of the domain composition of a cytokinin receptor. For each sequences set of the (B) CHASE, (C) HisK, (D) HATPase or (E) response regulator domains were aligned and a maximum likelihood tree was calculated. In these trees clades were colored according to known plant gene functions associated with the respective protein. Sub-trees with the relevant clades are shown. For coloring the clades, the least internal node of a colored clade was defined by: the node where only plant genes derived from, no other sequences are part of the colored clades or where two functional annotations met.