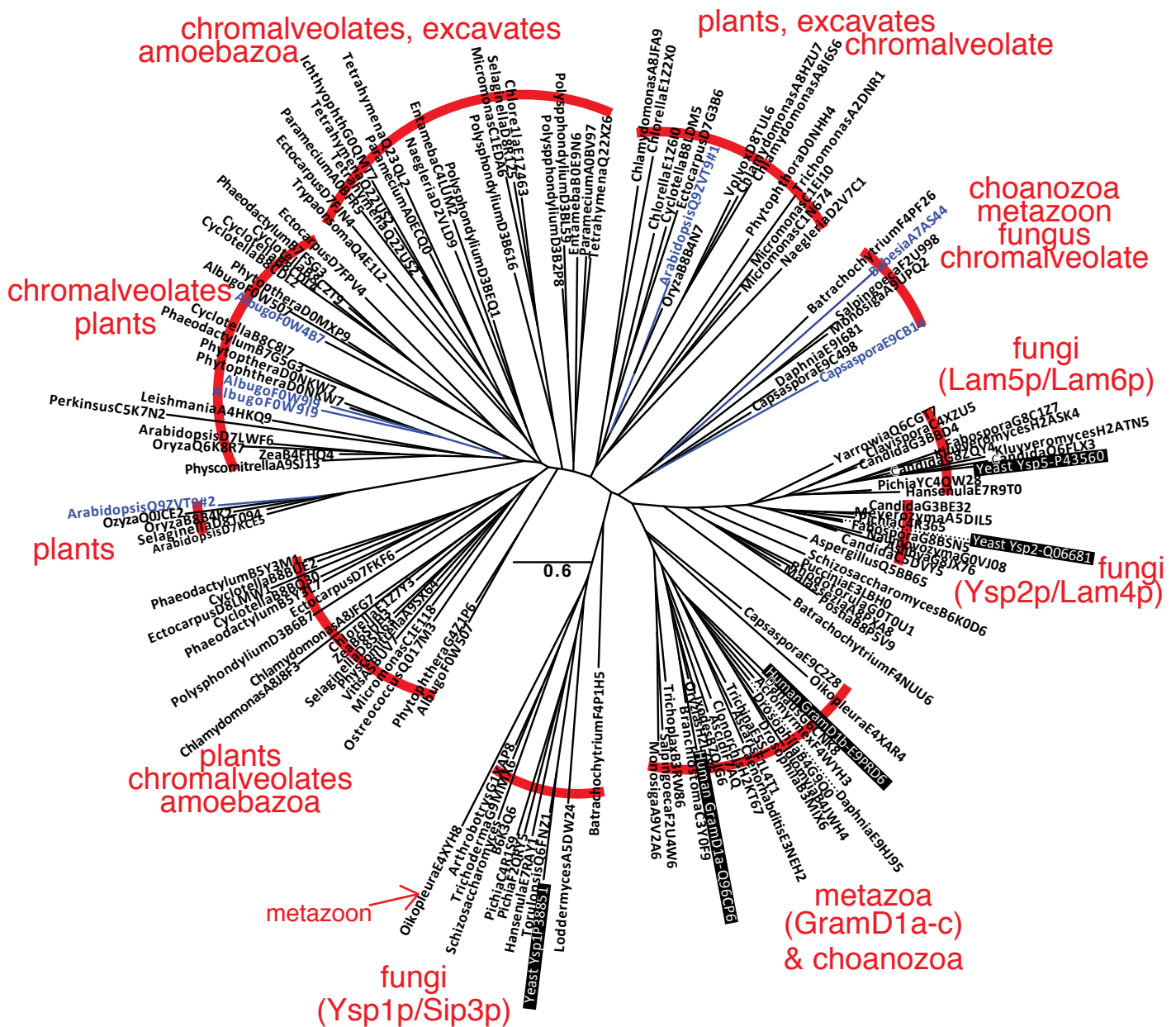


**Figure 1 - Figure Supplement 1**



**Figure 1–Figure Supplement 1: A family of StART-like domains in all eukaryotes**

An unrooted phylogenetic tree of 143 highly diverse of StART-like sequences was drawn by PHYML, showing species and Uniprot accession numbers. Ten sequence groups are bracketed to show the mixture of taxa in different parts of the tree. Four parts of the tree include yeast or human sequences (black background), showing that Ysp1p/ Sip3p are more distant from Ysp2p/Lam4–6p than are human GramD1a-c. The 7 domains labelled in blue are shown in the context of their full-length proteins in Figure 1-Figure Supplement 2C.