

Supplemental Figure S1. Maximum likelihood phylogenetic tree of Pet127 orthologs listed in Supplemental Table S1. The amino acid sequences were aligned using muscle (Edgar, 2004) and analyzed in SeaView v. 5 (Gouy et al., 2021). For phylogenetic analysis the alignments were trimmed to remove noninformative regions in BMGE (Criscuolo and Gribaldo, 2010), using the BLOSUM30 similarity matrix. Phylogenetic tree was inferred using IQ-TREE (Nguyen et al., 2015) under the LG+F+R3 model. Branch support was assessed using the ultrafast bootstrap approximation (Hoang et al., 2018) with 1000 repeats and the nearest neighbor interchange (NNI) search.

