

Tree scale: 0.1

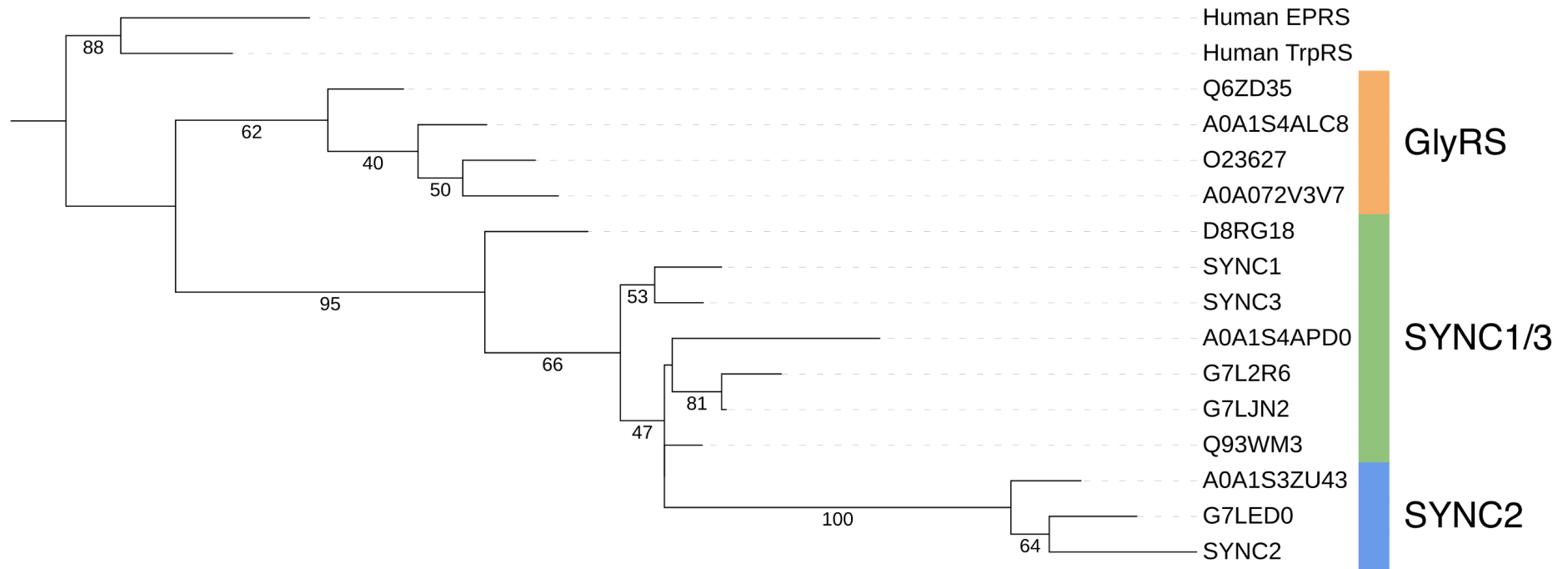


Fig. S1. Phylogenetic tree of WHEP domain sequences from human aaRSs and plant AsnRS and GlyRS obtained using maximum likelihood method. Plant AsnRSs are denoted SYNC1, 2, and 3. WHEP domain from human TrpRS and GluProRS (EPRS) are included. Others indicate accession numbers assigned in UniProt database. Bootstrap values from 1,000 replicates are shown in percentage. The major branches such as between human aaRSs, plant GlyRS, SYNC1/3, and SYNC2 show significant bootstrap values indicating a clear distinction between these categories. On the other hand, branches within each categories show relatively low values, such as in GlyRS and SYNC1/3.