

## Supplementary file 13

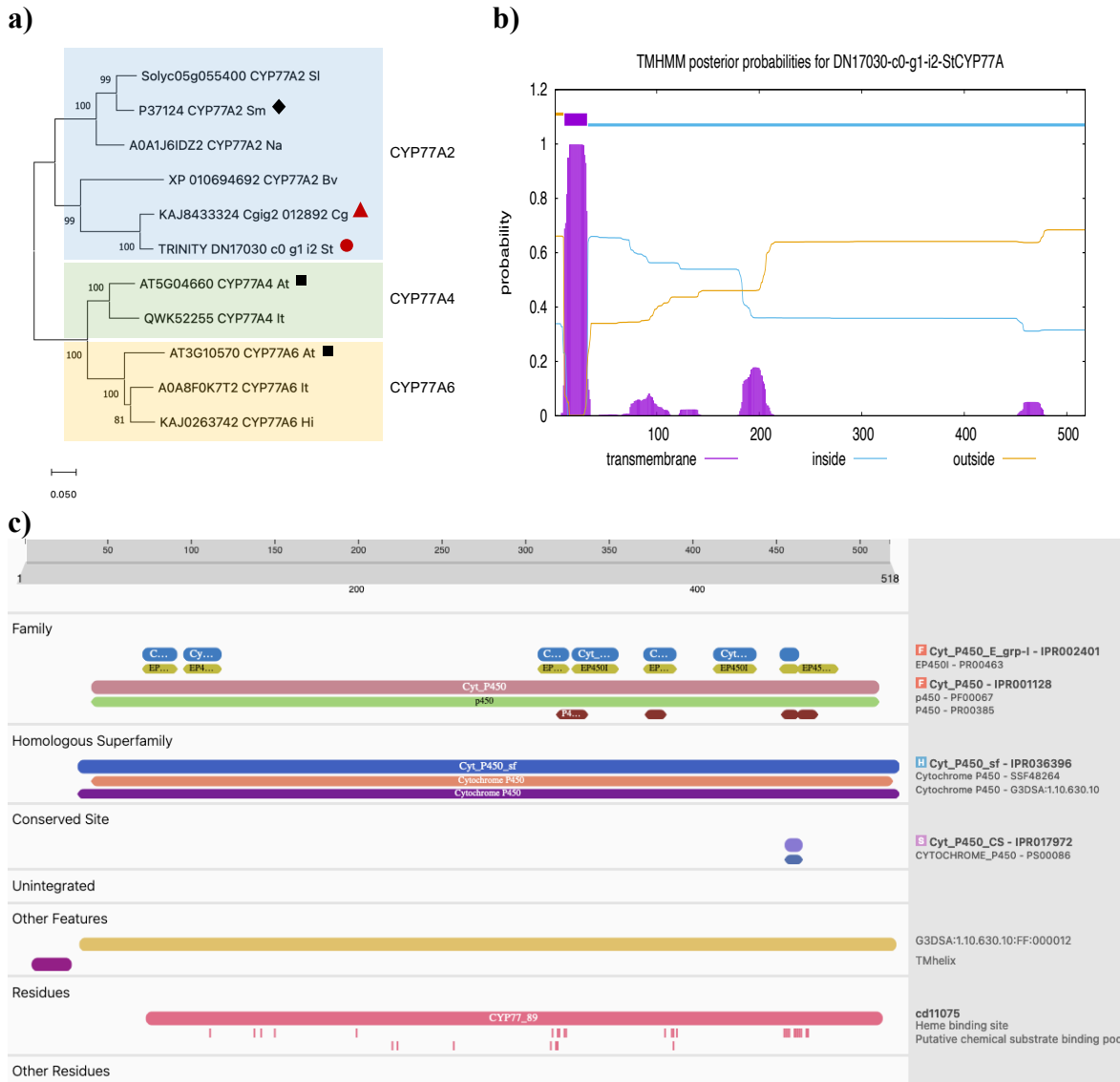


Figure S4. Analysis of the predicted protein StCYP77A from *Stenocereus thurberi*. **(a)** Phylogenetic tree of StCYP77A and related proteins of the subfamily CYP77A (CYP77A2, CYP77A4, and CYP77A6) from *Solanum lycopersicum* (Sl), *Solanum melongena* (Sm), *Nicotiana attenuata* (Na), *Beta vulgaris* (Bv), *Carnegiea gigantea* (Cg), *Arabidopsis thaliana* (At), *Isatis tinctoria* (It), and *Hirschfeldia incana* (Hi). The database accession number is included next to the protein name. The scale bar of 0.05 represented a sequence divergence of 5%. The number in the branches is the percentage bootstrap value of 1000 replicates. The highest percentages represent more significant results. The black square shows AtCYP77A4 and AtCYP77A6 from *A. thaliana*. The black diamond shows the homologous SmCYP77A2 from *S. melongena*. The red circle and red triangle show StCYP77A from *S. thurberi* and a protein from the closest related species *C. gigantea*, respectively. Neighbor-joining (NJ) phylogenetic tree constructed by MEGA11 software. **(b)** The predicted membrane-spanning region of StCYP77A. The probability of membrane insertion (Y-axis) and transmembrane region represented by purple color was determined by TMHMM software. **(c)** Predicted protein domains contained in StCYP77A amino acid sequences determined by InterProScan.