

Figure S2

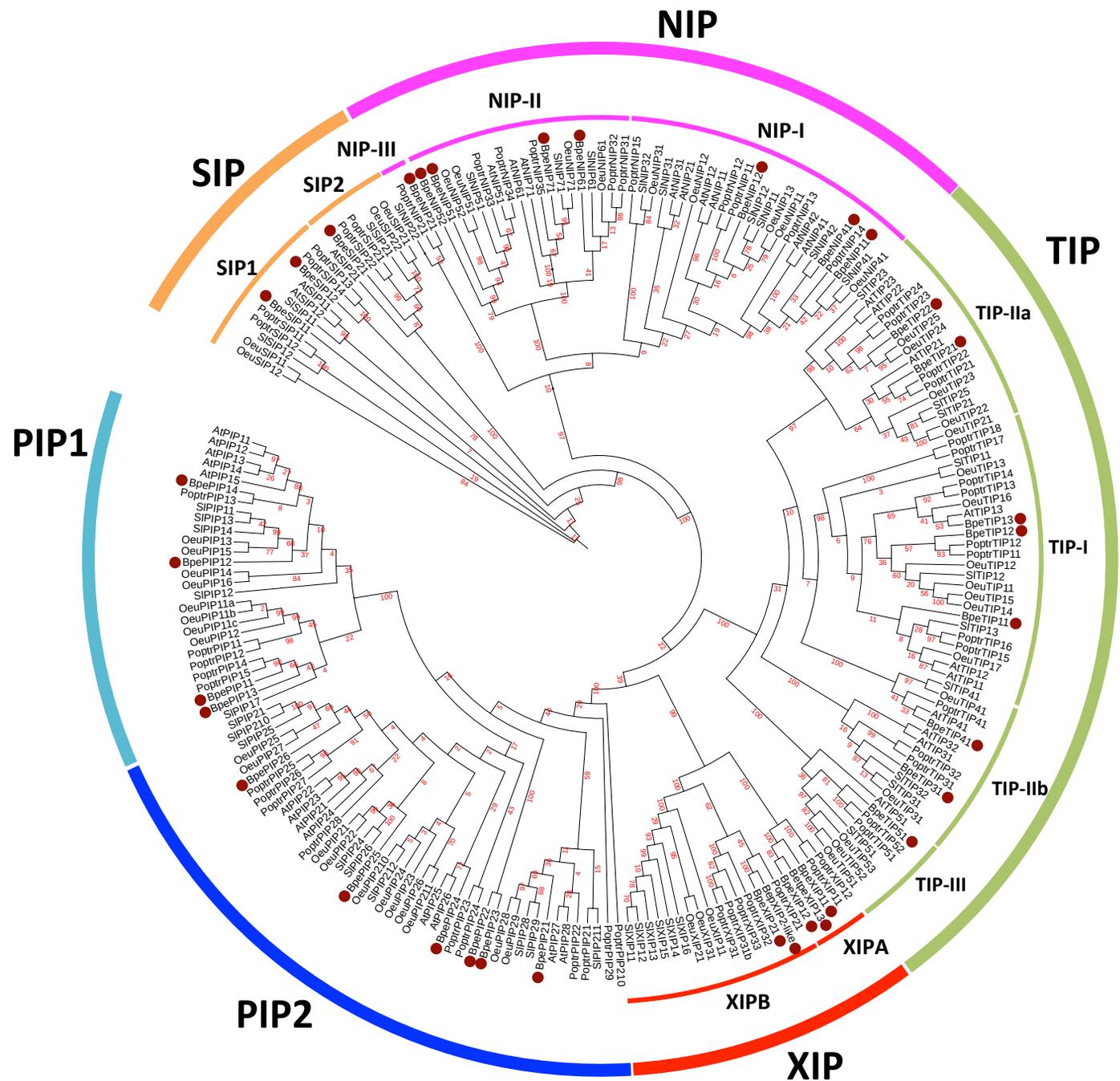


Figure S2. Phylogenetic analysis of the aquaporin family proteins of *Betula pendula* (*BpeAQPs*, filled circles), *Arabidopsis thaliana* (*AtAQPs*), *Lycopersicon esculentum* (*SIAQPs*), *Olea europaea* (*OeuAQPs*) and *Populus trichocarpa* (*PoptrAQPs*). Deduced amino acid sequences were aligned using ClustalW, and the phylogenetic tree was constructed using the maximum parsimony method. Maximum parsimony analysis was conducted using the subtree-pruning-regrafting algorithm. The number next to the branch's nodes represents bootstrap values  $\geq 50\%$  based on 5 000 resampling. The distance scale denotes the number of amino acid substitutions per site. The name of each subfamily is indicated next to the corresponding group. The *BpeAQP* accession numbers and sequences are listed in Figure S1 and Table S1.