



Supplemental Figure S1. Sequence comparisons between the aquaporins *McPIP2;1*, *SoPIP2;1*, *ZmPIP2;1* and *PvTIP3;1*. The alignment of loops B and D (with 6 amino acid residues from helix 5) together with parts of the N- and C-terminal regions is shown. The first two letters of each AQP name refer to the plant species (*Mc*, *Mesembryanthemum crystallinum*; *So*, *Spinacia oleracea*, spinach; *Zm*, *Zea mays*, corn; *Pv*, *Phaseolus vulgaris*, bean). Amino acid residues are colored according to their side chain: large aliphatic (green), small aliphatic (gray), basic (blue), acidic (red), hydroxyl non-aromatic (orange) and aromatic (royal). Amino acid residues involved in anchoring of loop D to loop B and the N-terminus are evinced. Putative phosphorylation sites, Ser¹²³ and Ser²⁸², are also shown. Sequence alignment was done by using CLC Sequence Viewer application.