



Supplemental Figure S2. Full length sequence alignment of *McPIP2;1* and *SoPIP2;1*. Putative transmembrane domains are marked by double arrows above the sequences. The signature motifs (NPA) for aquaporins are shown in pale blue background. Amino acid residues identity between *McPIP2;1* and *SoPIP2;1* is shown as a conservation bar graph below the sequences. Sequence alignment was done by using CLC Sequence Viewer application.