

Supplemental Figure S1.

AHA2	587	GDGVNDAPALKKA	599
MpHA1	118*	GDGVNDAPALKKA	130*
MpHA2	594	GDGVNDAPALKKA	606
MpHA3	593	GDGVNDAPALKKA	605
MpHA4	587	GDGVNDAPALKKA	599
MpHA5	99*	GDGVNDAPALKKA	111*
MpHA6	647	GDGVNDAPALKKA	659
MpHA7	582	GDGVNDAPALKKA	594
MpHA8	600	GDGVNDAPALKKA	612

Supplemental Figure S1. Alignment of conserved segments in the catalytic domain of H⁺-ATPase from *M. polymorpha* and *A. thaliana* with ClustalW (Thompson et al., 1994). Black blocks indicate highly conserved residues. Asterisks mean that the proteins were not full-length and N-terminal information was not acquired.