Supplementary Materials: Rat Aquaporin-5 Is pH-Gated Induced by Phosphorylation and Is Implicated in Oxidative Stress

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rAQP5 hAQP5	1020304050MKKEVCSLAFFKAVFAEFLATLIFVFFGLGSALKWPSALPTILQISIAFGMKKEVCSVAFLKAVFAEFLATLIFVFFGLGSALKWPSALPTILQIALAFG*******:**:***
rAQP5 hAQP5	60708090100LAIGTLAQALGPVSGGHINPAITLALLIGNQISLLRAVFYVAAQLVGAIALAIGTLAQALGPVSGGHINPAITLALLVGNQISLLRAFFYVAAQLVGAIA***
rAQP5 hAQP5	110120130140150GAGILYWLAPLNARGNLAVNALNNNTTPGKAMVVELILTFQLALCIFSSTGAGILYGVAPLNARGNLAVNALNNNTTQGQAMVVELILTFQLALCIFAST******:**********:********
rAQP5 hAQP5	
rAQP5 hAQP5	
rAQP5 hAQP5	 260 DHREERKK <mark>T</mark> I EL T AH EQREERKK <mark>T</mark> M EL T TR ::******: ***::

Figure S1. Sequence alignment of the full-length amino acid sequences of *Rattus norvegicus* AQP5 and human AQP5. The alignment was generated with CLUSTAL W (using BioEdit software). The amount of conservation of each amino acid is represented by symbols ('*', exact match in all sequences; ':', conserved substitution; '.', semi-conserved substitution). The two conserved NPA signature motifs are underlined. Ser152, S156, Ser231, Ser233, Thr242, Thr259 and Thr263 (**colored green**) are consensus phosphorylation sites of hAQP5; His173 and Ser183 (**colored yellow**) are the residues involved in the switch between narrow and wide conformations in the gating mechanism of human AQP5 proposed by Janosi et al. (doi:10.1371/journal.pone.0059897).