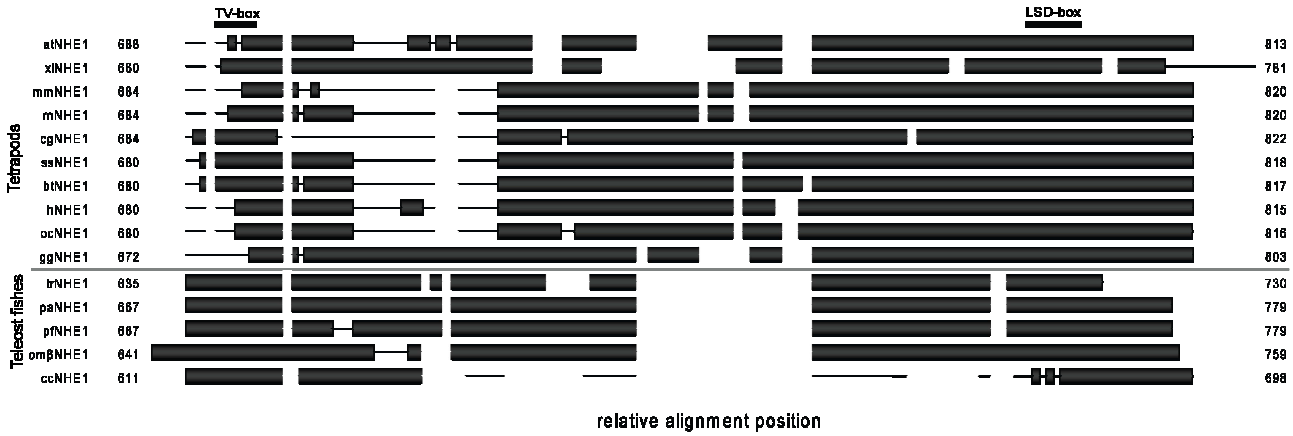
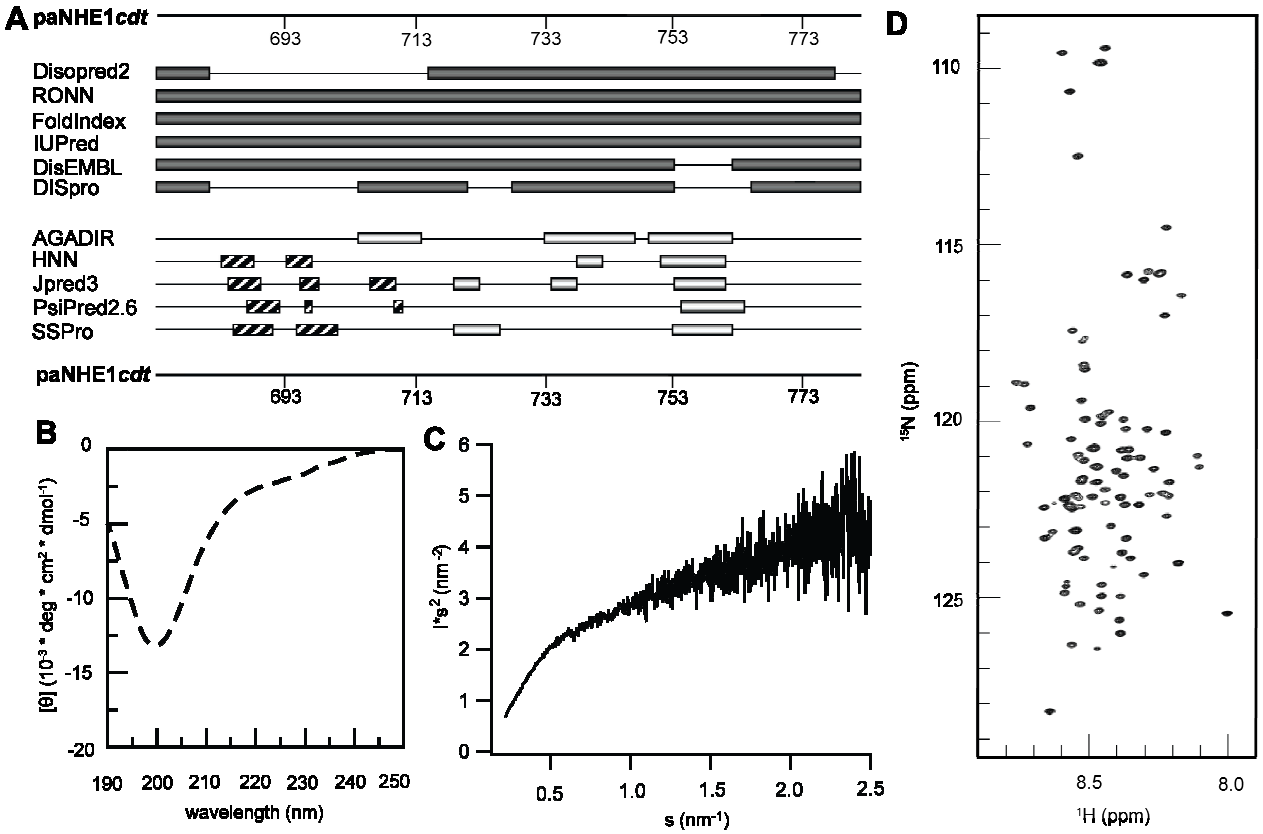
# Supplementary Figures NØRHOLM ET AL.

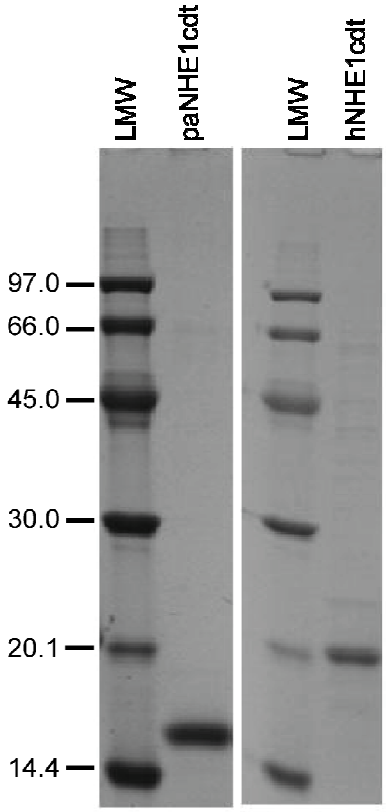



**Supplementary Figure S1** Disorder predictions of the C-terminal distal tails (*cdts*) of the 15 NHE1 homologs from the alignment in Fig. 1. The disorder and structure prediction server DisMeta which combines different algorithms was used. The figure indicates disorder when the DisMeta disorder prediction consensus was ≥ 50 % (black bars). Gaps within the *cdts* represent gaps present in the sequence alignment (Figure 1).




Supplementary Fig. S2

**Supplementary Figure S2** Bioinformatical and biophysical characterization of paNHE1 C-terminal distal tail (paNHE1*cdt*) as intrinsically disordered. (**A**) Bioinformatical structure and disorder predictions by various algorithms; disorder (black), α-helix structure (gray), extended structure (hatched), (**B**) Far-UV CD spectrum of 8 µM paNHE1*cdt* in 20mM $NaH_2PO_4$ pH 7.0 at 20ºC, (**C**) Kratky plot showing disorder, (**D**) [$^1$H, $^{15}$N]-HSQC of 1.1 mM $^{13}$C-$^{15}$N-labelled paNHE1*cdt* in PBS buffer, pH 7.0 recorded at 4ºC. Numbering as in Figure S1.




**Supplementary Figure S3** Purity of protein preparations from Coomassie brilliant blue stained SDS-PAGE gels showing that the purity of the samples is >95%. The gel is deliberately overloaded to show faint bands of impurities. The proteins migrate slower on the gel than folded proteins of the same size, which is one of the hallmarks of IDPs.