ONLINE SUPPLEMENTAL MATERIAL

Cherny et al., http://www.jgp.org/cgi/content/full/jgp.201511456/DC1



Figure S1. Sequence of the S4 segment in hH_V1 , kH_V1 , and EhH_V1 . The signature sequence that defines H_V1 (together with Asp in the S1 helix) encompasses RxWRxxR. The three species studied are *Homo sapiens* (hH_V1), *Karlodinium veneficum* (kH_V1), and *Emiliania hux-leyi* (EhH_V1).



Figure 52. Saturation of the Δ pH dependence of WT kH_Vl and of W176F mutant of kH_Vl. The voltage at which g_H is 10% maximal is plotted as a function of pH_o (A and C) or pH_i (B), with lines connecting measurements in the same cell. In whole-cell measurements, pH_i is color coded, as indicated. In inside-out patches, pH_o is color coded, as indicated. For reference, the dashed gray line in each graph shows the slope of the ubiquitous 40-mV/U Δ pH shift in the g_H-V relationship; the position of this line is arbitrary. C illustrates that saturation occurs at lower pH_o in W176F.



Figure S3. Saturation of the ΔpH dependence of WT EhH_V1 and of W278X mutants of EhH_V1. The voltage at which g_{H} is 10% maximal is plotted as a function of pH_o (A and C) or pH_i (B and D), with lines connecting measurements in the same cell. In whole-cell measurements, pH_i is color coded, as indicated. C includes three W278A, one W278F, and one W278S; D includes one W278A, one W278F, and three W278S. In inside-out patches, pH_o is color coded, as indicated. For reference, the dashed gray line in each graph shows the slope of the 40-mV/U ΔpH shift in the $g_{H-}V$ relationship; the position of this line is arbitrary.