Ishida et al., http://www.jgp.org/cgi/content/full/jgp.201210930/DC1

The basic Berkeley Madonna model is available for download.

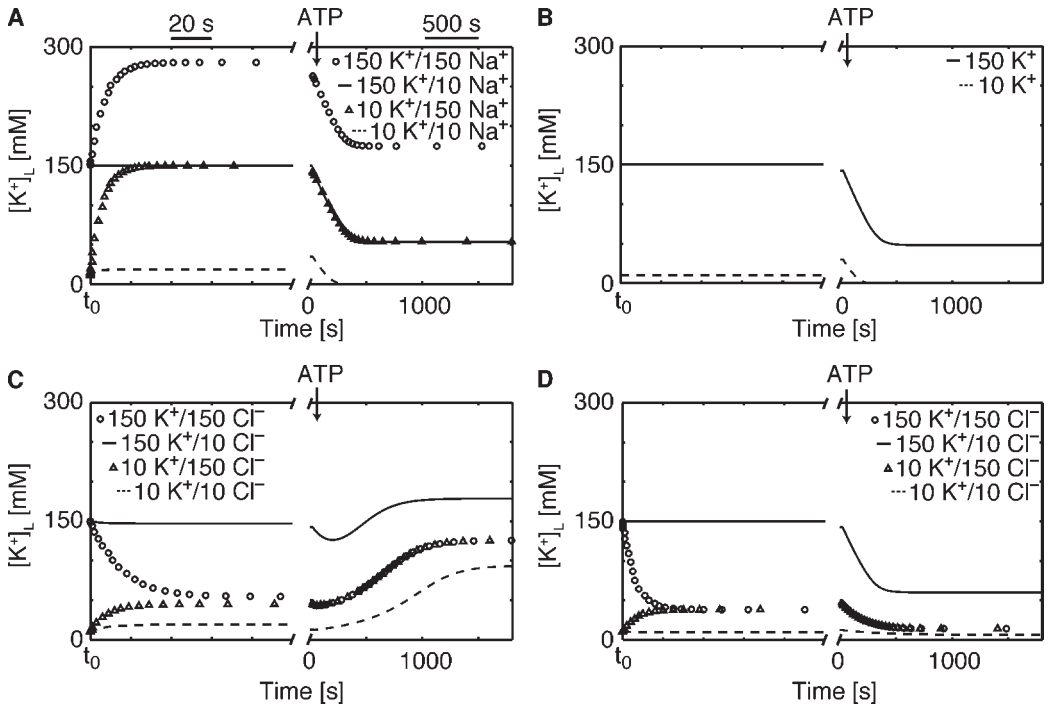

Figure S1. Luminal K^+ dynamics during acidification. Four different putative counterion pathways are explored: A model containing Na^+ channels (A), only K^+ channels (B), ClC-7 antiporters (C), and Cl^- channels (D). All simulations contain K^+ channels, V-ATPases (300 pumps), and proton leak ($P_{H+} = 6 \times 10^{-5}$ cm/s), and the simulations in A–D correspond exactly to models 1–4 in Fig. 7, respectively. Multiple curves are shown in each panel corresponding to the different starting luminal concentrations indicated in Fig. 7. V-ATPase–dependent acidification was initiated at 25 s and is indicated by the arrow in all panels. Before acidification, the system was allowed to come to steady state, which is consistent with in vitro experiments that are typically initiated sometime after isolating the lysosomes. All simulations were initiated at a time chosen to ensure that steady state was reached before acidification was started. The time scale of the left side of each panel, before time zero, is different from the scale on the right side. See A for scale bars corresponding to both regimes, which are consistent for all four panels. The left side of each panel shows the initial approach to steady state over the first 100 s, but the entire approach is not shown (break in graph), resulting in minor differences before and after each break. In some cases, the initial $[K^+]_L$ value at t_0 is significantly different from the value at 25 s when ATP is added to the system. All parameter values can be found in Fig. 7 and Table 1.