

## **Supplementary Material**

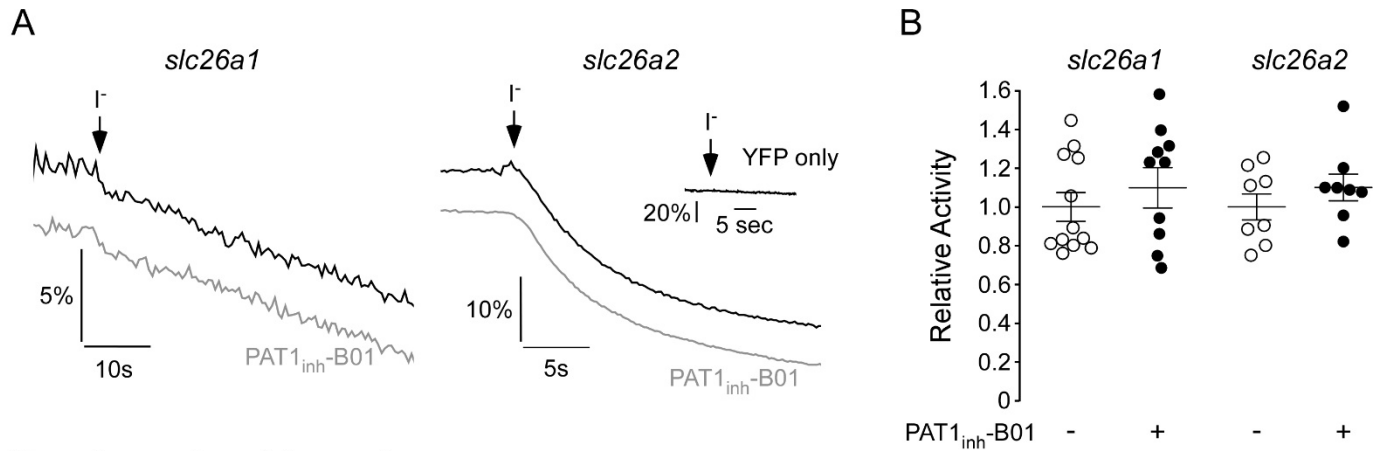
### ***Slc26a1 and slc26a2 cDNA constructs***

The complementary DNA sequences of *slc26a1* and *slc26a2* were generated using gBLOCK gene fragments (Integrated DNA technology, Coralville, IA) in the plasmid vector pIRESpuro3 (Takara, San Jose, CA). In brief, the 5' region of *slc26a1* (which consists of a ~1150 bp gBlock with a blunt 5' end and a *NheI* site at the 3' end) was cloned into pIRESpuro3 at *EcoRV* / *NheI* sites. Subsequently, the 3' end of *slc26a1* (which consists of a ~990 bp gBlock with *NheI* site at the 5' end, a silent mutation at valine 446 to remove a second *NheI* site, and a *NotI* site at the 3' end) was added to the 5' end of *slc26a1* at *NheI* / *NotI* sites. The 5' region of *slc26a2* (which consists of a ~1600 bp gBlock with a 5' *NheI* site and an *EcoRI* site at the 3' end) was cloned into pIRESpuro3 at *NheI* / *EcoRI* sites. Subsequently, the 3' end of *slc26a2* (which consists of a ~600 bp gBlock with the intrinsic *EcoRI* site at the 5' end, and a *NotI* site at the 3' end) was added to the 5' end of *slc26a2* at *EcoRI* / *NotI* sites. Full-length *slc26a2* cDNAs were subsequently transferred as *NheI* / *NotI* fragments to a modified pIRESpuro3 plasmid in which the puromycin resistance gene was replaced with the EYFP-H148Q/I152L/F46L coding sequence (pIRES-HIF, Haggie et al., JCI Insight 2018). To generate the pIRES-HIF version of *slc26a1*, a *NotI* / *XbaI* fragment in pIRES-puro3-*slc26a1* (containing the internal ribosome entry site and puromycin resistance gene) was replaced with a *NotI* / *XbaI* fragment from pIRES-HIF. cDNA constructs were confirmed by sequence analysis.

### ***Slc26a1 and slc26a2 functional assays***

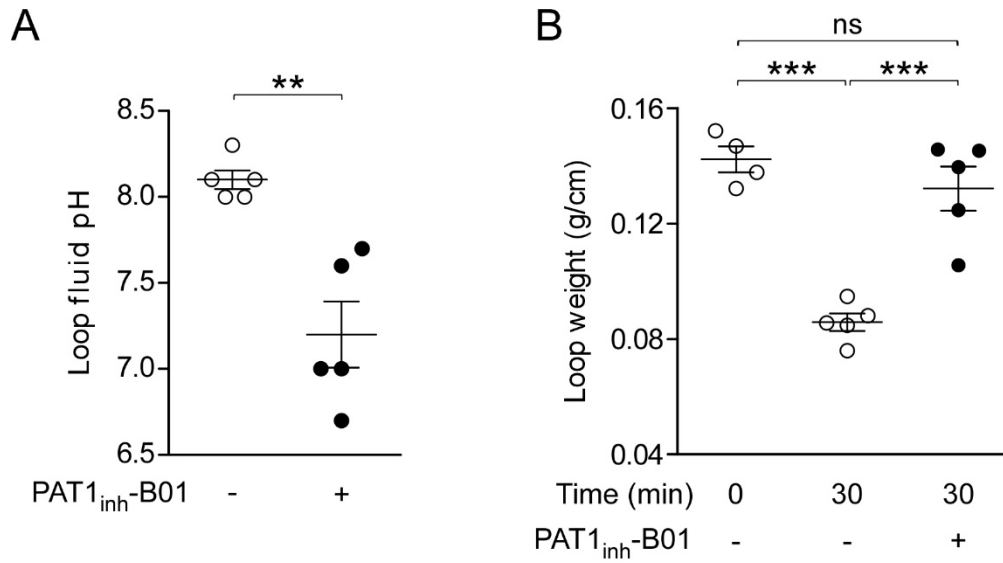
To measure *slc26a1* and *slc26a2* exchange activity, 293 T/17 cells were grown on poly-D-lysine coated 18-mm diameter glass coverslips and transiently transfected with pIRES-HIF vectors using NanoFect Transfection reagent (Alstem Cell Advancements, Richmond, CA) using manufacturer's guidelines. Two days after transfection cells were washed twice with PBS, transferred to a custom cell chamber, and bathed in 250  $\mu$ l

PBS. Cells were imaged on a stage of a TE2000 microscope (Nikon, Melville, NY) equipped with a C9100 EM-CCD (Hamamatsu, San Jose, CA), XCite light source (Excelitas, Waltham, MA), Nikon 20× NA 0.75 S Fluor objective, Uniblitz shutter (Vincent Associates, Rochester, NY) and B-2E/C filter set (Chroma, Bellows Fall, VT). To assay slc26a1 and slc26a2 function, 200-ms duration cell images were acquired continually, and exchange activity was initiated with the addition of 750  $\mu$ l sodium iodide-substituted PBS. Background-corrected, area-integrated single cell fluorescence was calculated for determination of slc26a1 / slc26a2 activity from the rate of fluorescence quenching. To test inhibitor selectivity cells were incubated with 25  $\mu$ M PAT1<sub>inh</sub>-B01 for 10 min prior to assays. Controls experiments using cells infected with EYFP-H148Q/I152L/F46L alone were used to determine intrinsic iodide leak in 293 T/17 cells.



Supplementary Figure 1

**Supplementary Figure 1.  $PAT1_{inh}-B01$  selectivity against *slc26a1* and *slc26a2*.** **A.** 293 T/17 cells were transiently transfected with a plasmid to co-express *slc26a1* or *slc26a2* and halide-sensitive YFP.  $Cl^-/I^-$  exchange activity showed without (*top*) and with (*bottom*) 25  $\mu M$   $PAT1_{inh}-B01$ . Inset (right) shows fluorescence from 293 T/17 cells expressing YFP alone. **B.** Summary data for  $PAT1_{inh}-B01$  selectivity against *slc26a1* and *slc26a2*.  $n=8-12$  experiments per condition, mean  $\pm$  S.E.M, differences not significant.



Supplementary Figure 2

**Supplementary Figure 2. A.** Loop fluid pH in ileal closed loops at 30 min after injection of 100  $\mu$ L phosphate-buffered saline (pH 7.4) without and with 30  $\mu$ M PAT1<sub>inh</sub>-B01. **B.** Loop weight/length ratio of ileal closed loops injected with 100  $\mu$ L HEPES-buffered saline at 0 min without and with 30  $\mu$ M PAT1<sub>inh</sub>-B01. n=4-5 loops per group, mean  $\pm$  S.E.M., \*\*p<0.01, \*\*\*p<0.001, ns: not significant. Student's t-test for panel A, one-way analysis of variance and post hoc Newman-Keuls multiple comparisons test for panel B.