

Supplemental data

Residues 155 and 348 contribute to determination of P2X₇ receptor function via distinct mechanisms revealed by single nucleotide polymorphisms

Helen J Bradley, Jocelyn M Baldwin*, G Ranjan Goli*, Brian Johnson, Jie Zou, Asipu Sivaprasadarao, Stephen A Baldwin, and Lin-Hua Jiang[†]

From Institute of Membrane and Systems Biology, Faculty of Biological Sciences, University of Leeds, Leeds LS2 9JT, United Kingdom

*These two authors contributed equally.

[†]Correspondence: Dr Lin-Hua Jiang at the above address. Email: l.h.jiang@leeds.ac.uk

Short title: Expression and function of P2X₇ receptors

Fig.S1 Effects of Y155H and T348A mutations on ATP-induced currents mediated by the rP2X₇ receptor

A. Representative ATP-induced current densities in cells expressing the rP2X₇ WT, Y155H or T348A mutant receptors in normal extracellular solution. The dotted line denotes the maximal current for the WT rP2X₇ receptor. B. ATP concentration-current density curves from recordings shown in A. The smooth lines represent the best fits to the Hill equation. C. Mean maximal current density in parallel experiments. The cell number in each case is indicated. ***, $p < 0.001$, the maximal current density compared to WT receptor (*t*-test).

Fig.S2 Effects of reciprocal mutations of residues 155 and 348 on BzATP-induced currents mediated by the human and rat P2X₇ receptors

A. Representative BzATP-induced current densities in cells expressing the hP2X₇ WT, H155Y or A348T mutant receptors in low divalent cation extracellular solution (top), and BzATP concentration-current density curves (bottom). B. Representative BzATP-induced current densities in cells expressing the rP2X₇ WT, Y155H or T348A mutant receptors in low divalent cation extracellular solution (top), and BzATP concentration-current density curves (bottom). In these experiments, the normal extracellular solution was used to wash off BzATP, and then extracellular was returned to the low divalent cation solution, before applications of the following concentrations of BzATP. The dotted line denotes the currents for the WT P2X₇ receptors. The smooth lines represent the best fits to the Hill equation. The cell number in each case is indicated in brackets. ***, $p < 0.001$, **, $p < 0.01$, *, $p < 0.05$, the maximal current density compared to the WT receptors (*t*-test).

Fig.S3 Representative ATP-induced current densities in cells expressing hP2X₇ mutant receptors

Mutations were introduced into positions surrounding residue 155 (A-B) and residue 348 (C). The dotted line denotes the maximal current for the WT hP2X₇ receptor.

Fig.S4 Effect of mutation of residues at position 155 on cell surface and total expression level of hP2X₇ receptors

Representative Western blots showing biotin-labelling or surface expression of the indicated WT and mutant hP2X₇ receptors (top), and total protein expression for P2X₇ receptor and GFP in whole cell lysate (bottom). -ve denotes the cells that were transfected with the empty vector.

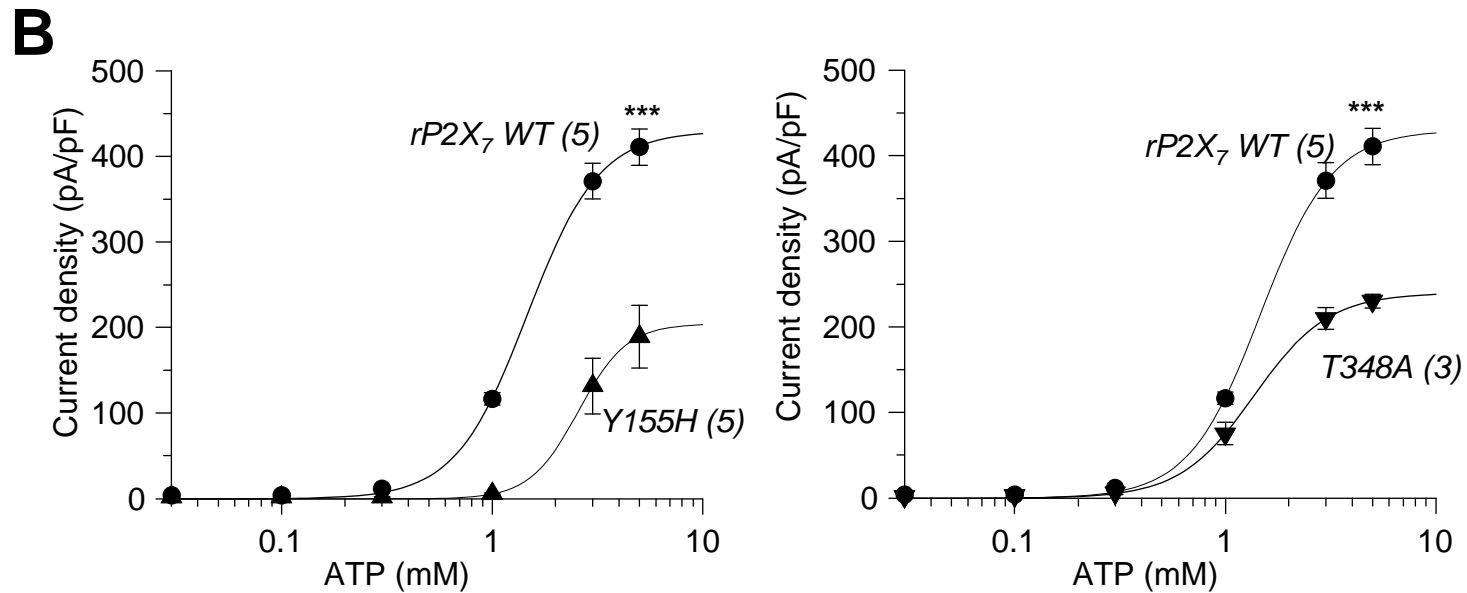
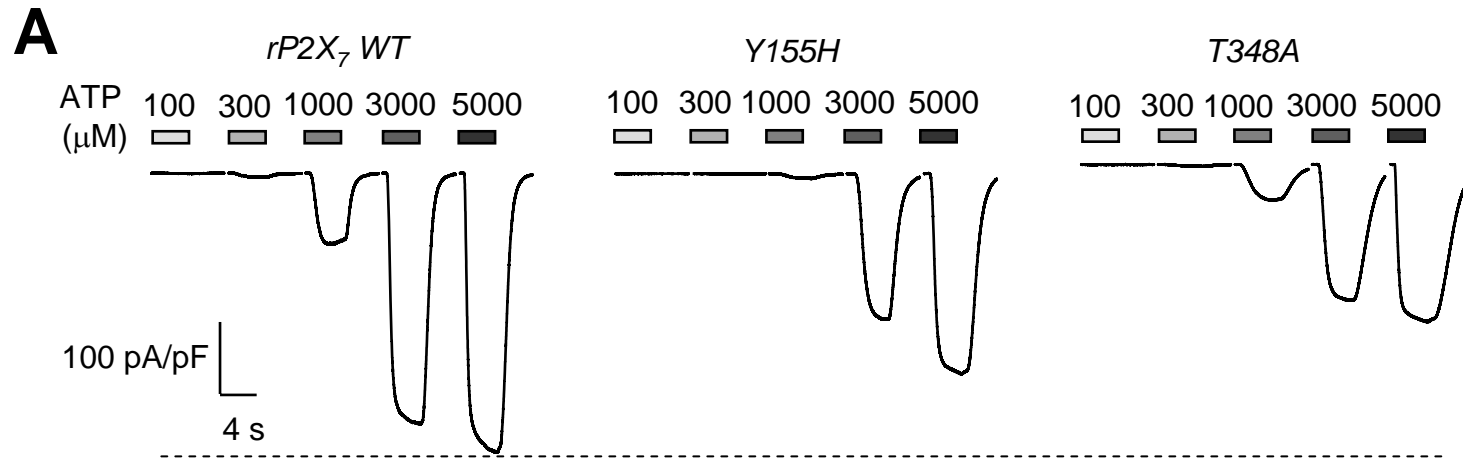
Fig.S5 Inhibition of hP2X₇ WT and H155Y mutant receptors by antagonist KN-62

ATP concentration-current density curves before (control) and after 4 min exposure to 100 nM KN-62 for the hP2X₇ WT (A) and H155Y mutant receptors (B) (n = 6 for each case). The dotted line denotes the currents for the receptors before applications of KN-62.

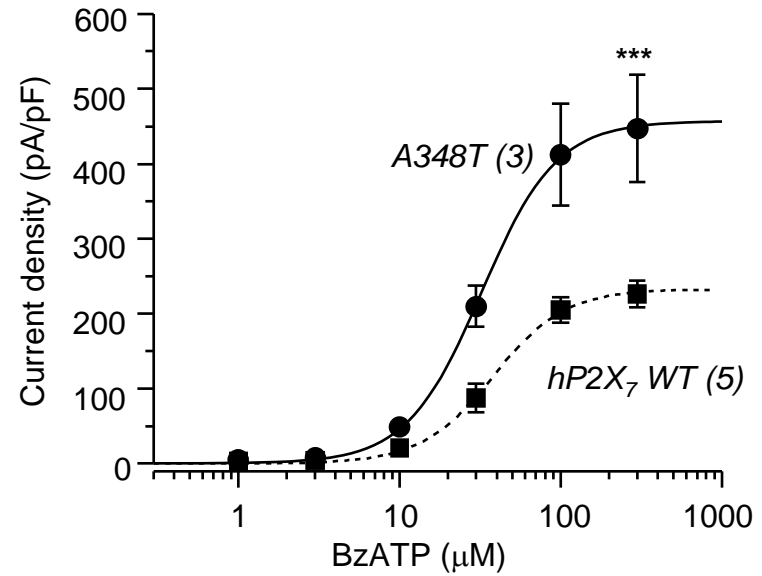
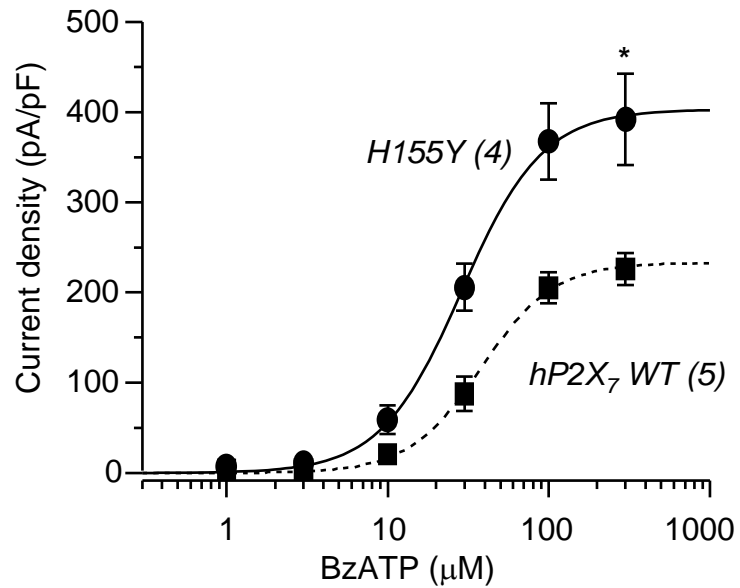
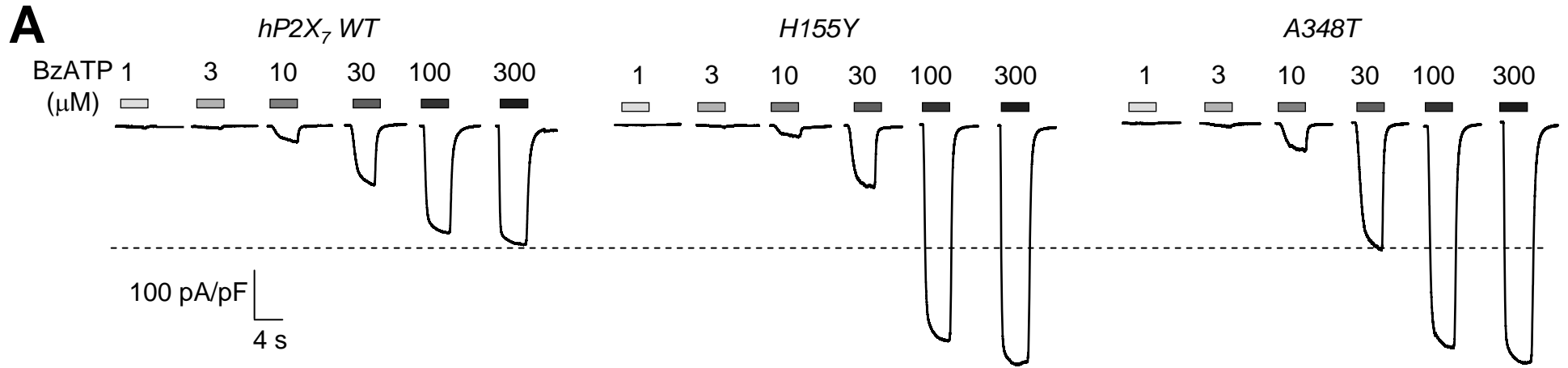
Fig.6S Location of intracellular hP2X₇ proteins and GFP-LAMP1

Representative confocal images of HEK293 cells co-expressing hP2X₇ WT receptor (red) and GFP-tagged LAMP1 (green), a protein located to the late endocytic organelles. Scale bar is 10 μ m.

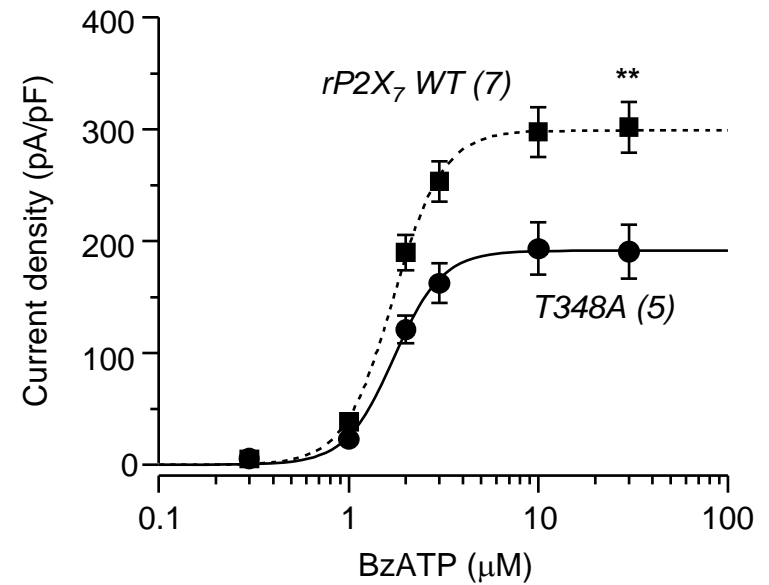
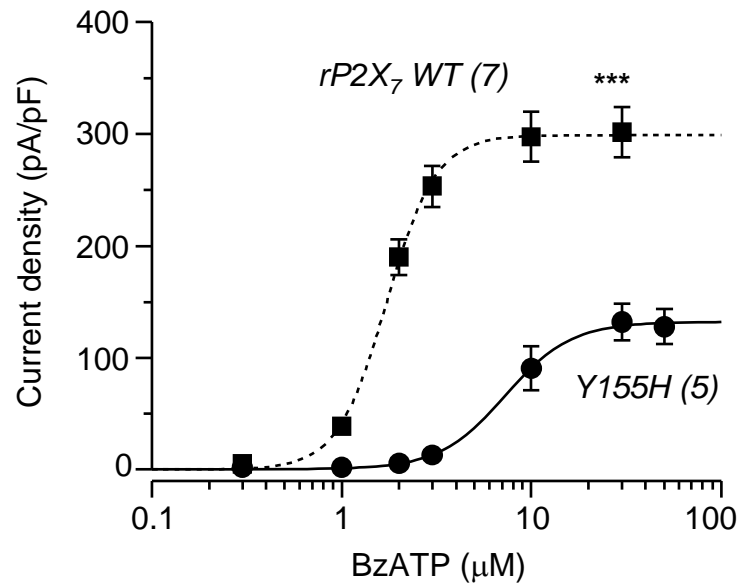
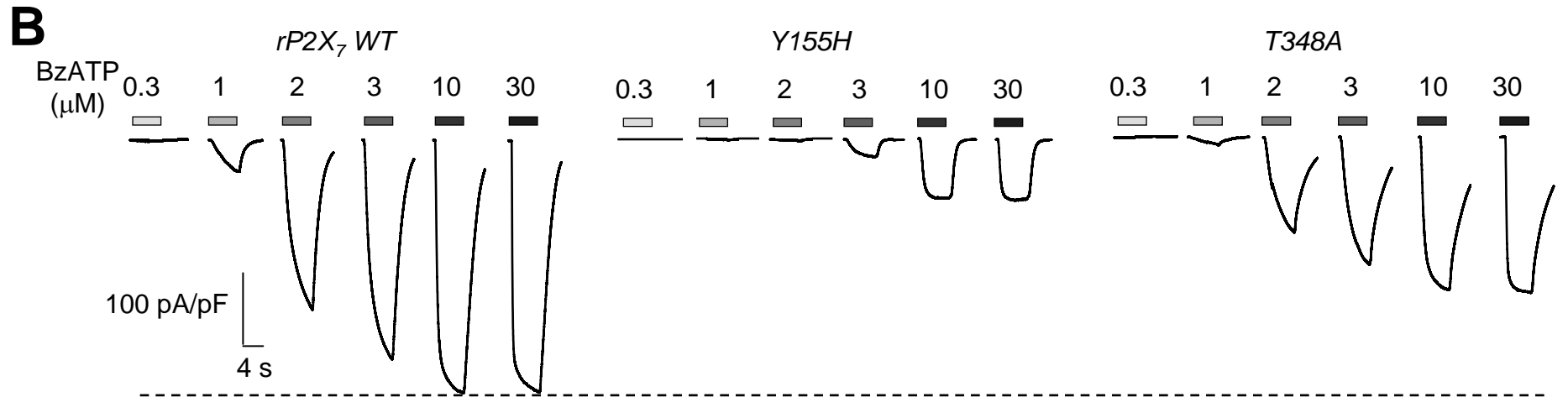
Supplemental Fig.1



Supplemental Fig.2A

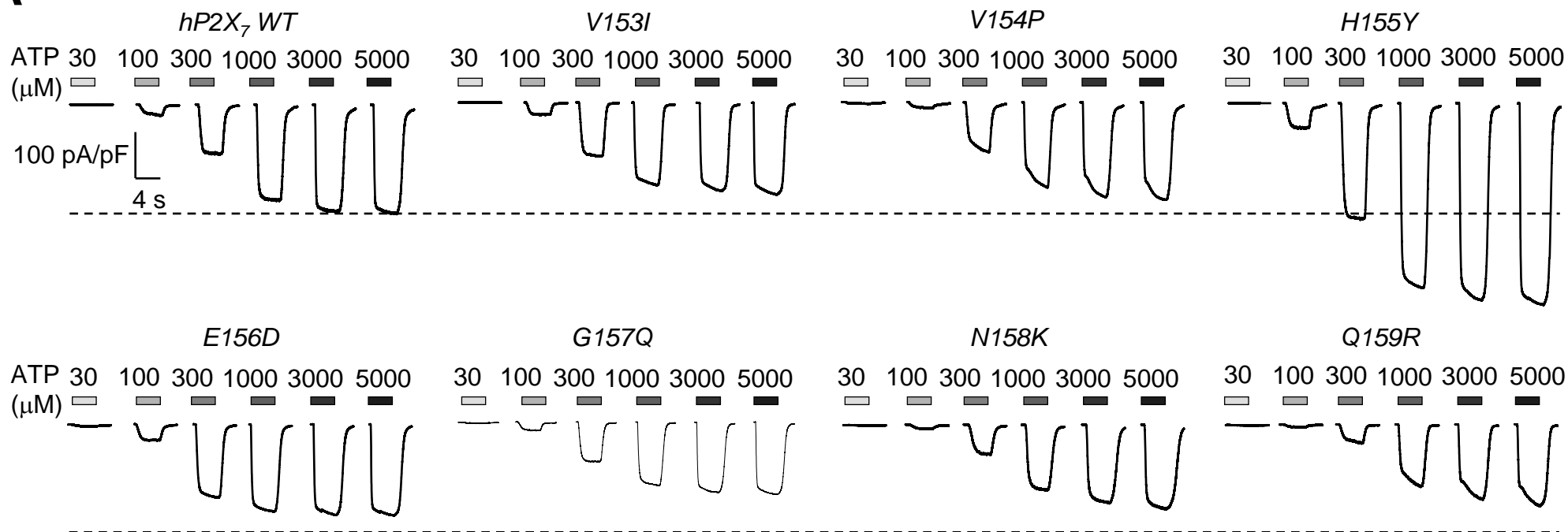


Supplemental Fig.2B

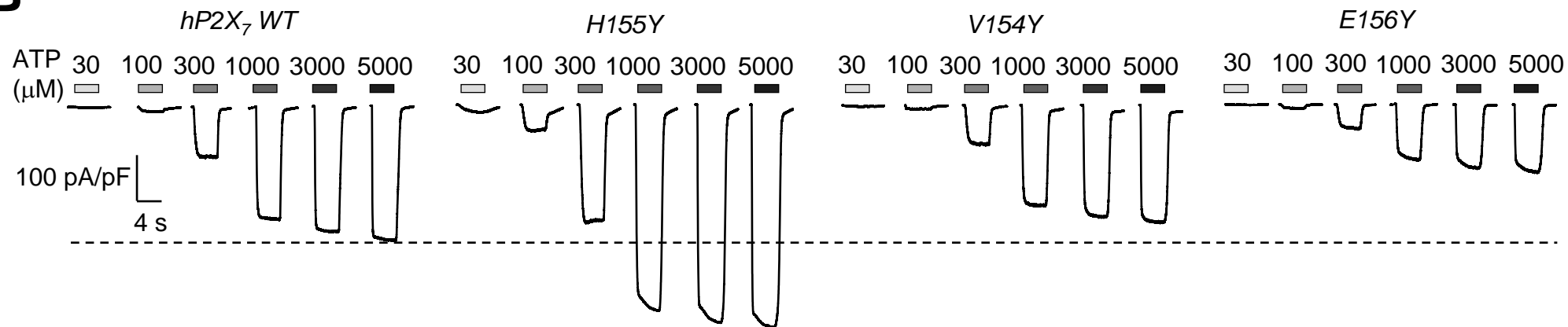


Supplemental Fig.3A-B

A

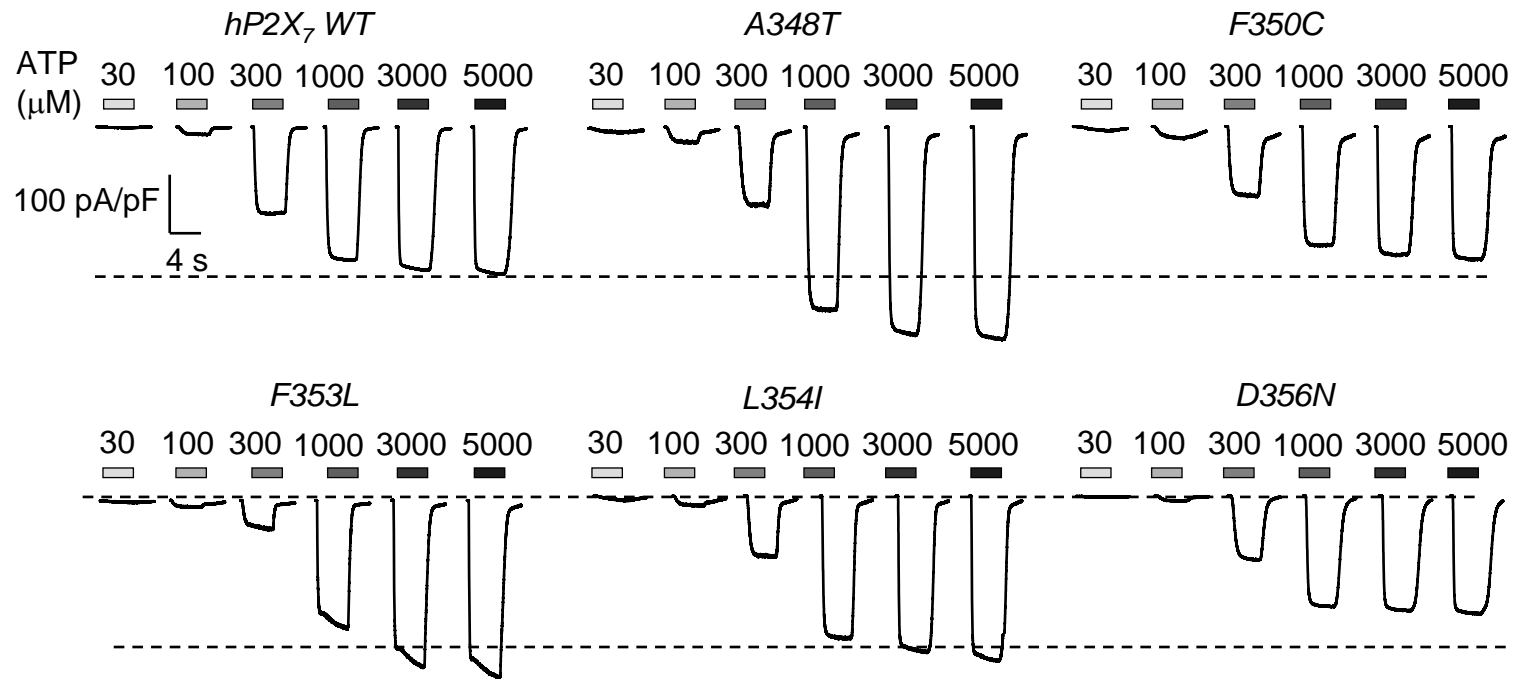


B

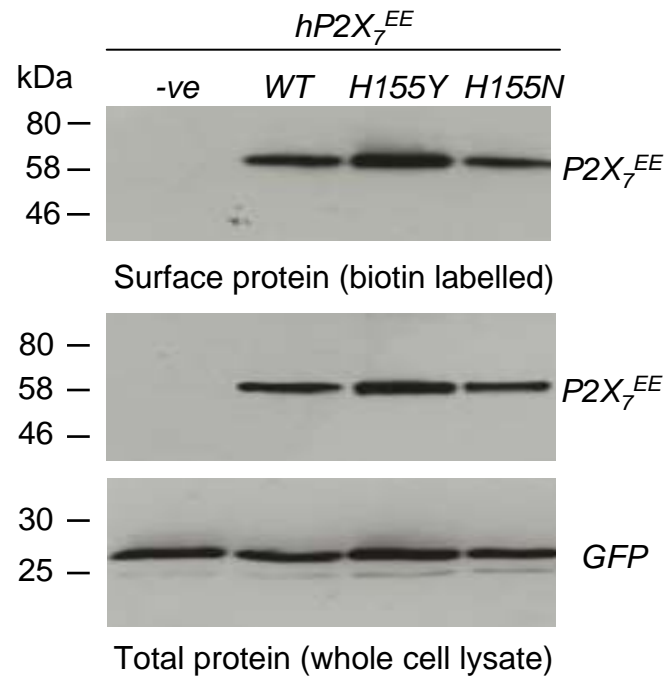


Supplemental Fig.3C

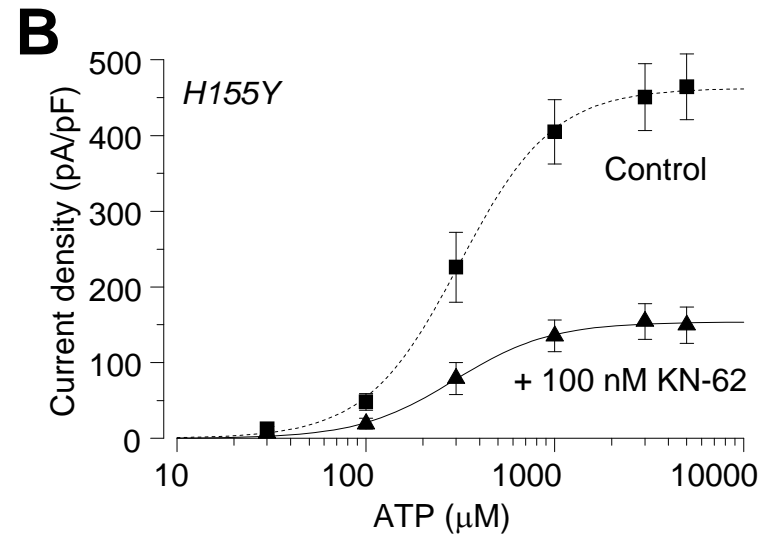
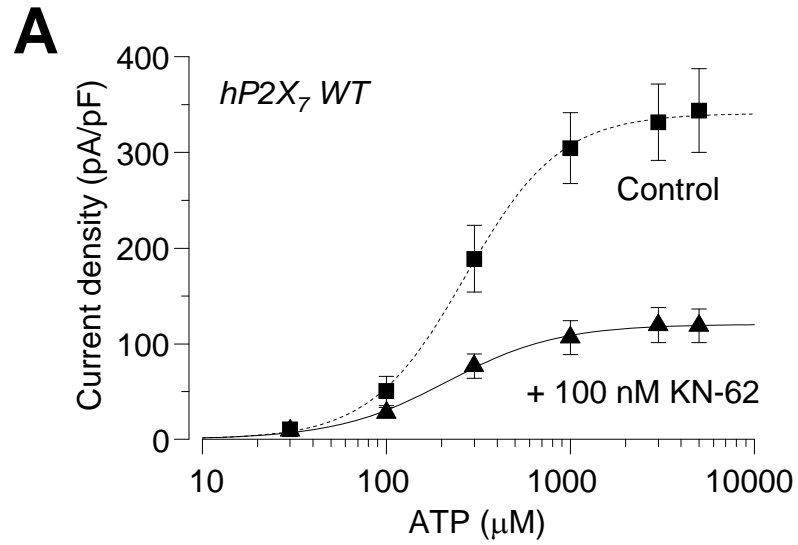
C



Supplemental Fig.4



Supplemental Fig.5



Supplemental Fig.6

