DRAWINGS

Fig. 1

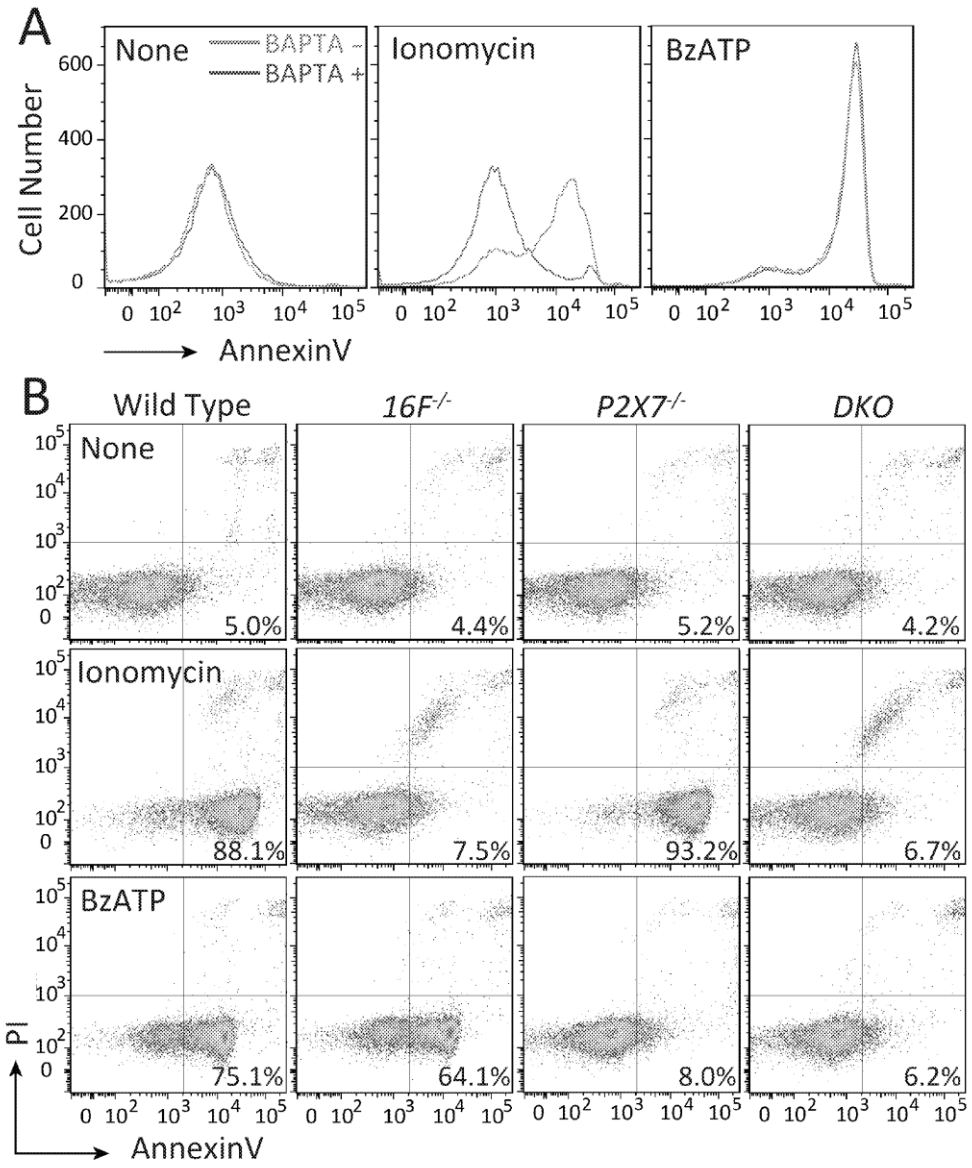


Fig. 2

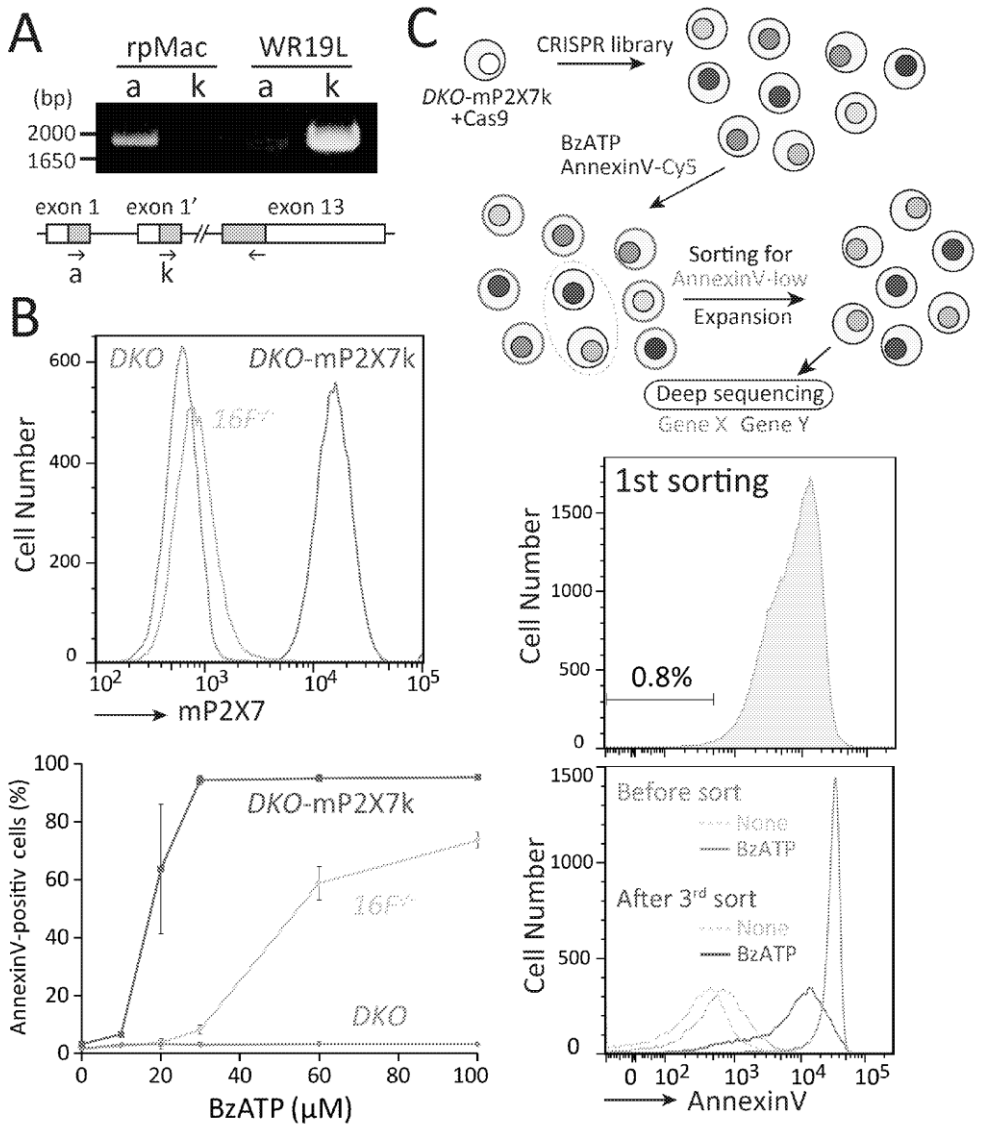

A
rpMac
WR19L
a
k
a
k
(bp)
2000
1650
exon 1
exon 1'
exon 13
a
k
B
DKO
DKO-mP2X7k
16F7
Cell Number
mP2X7
AnnexinV-positiv cells (%)
DKO-mP2X7k
16F7
DKO
BzATP (μM)
C
DKO-mP2X7k
+Cas9
CRISPR library
BzATP
AnnexinV-Cy5
Sorting for
AnnexinV-low
Expansion
Deep sequencing
Gene X Gene Y
1st sorting
0.8%
Cell Number
Before sort
None
BzATP
After 3rd sort
None
BzATP
Cell Number
AnnexinV

Fig. 3

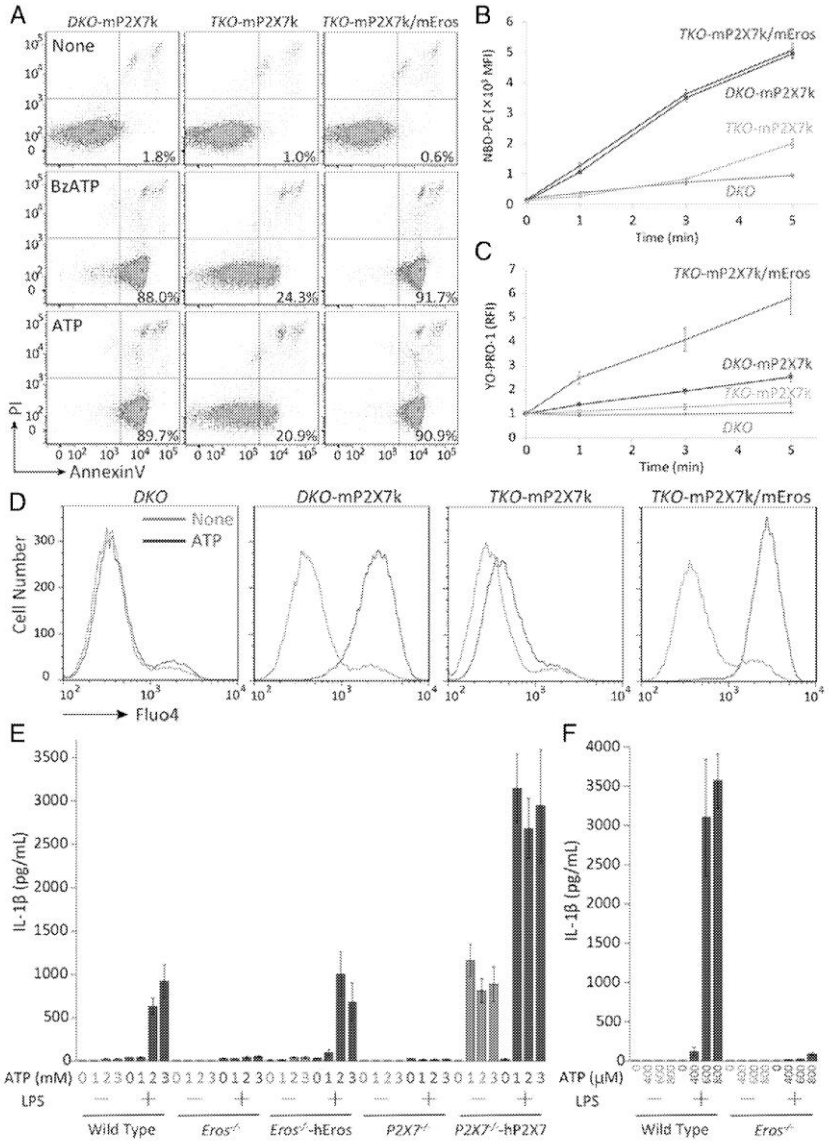
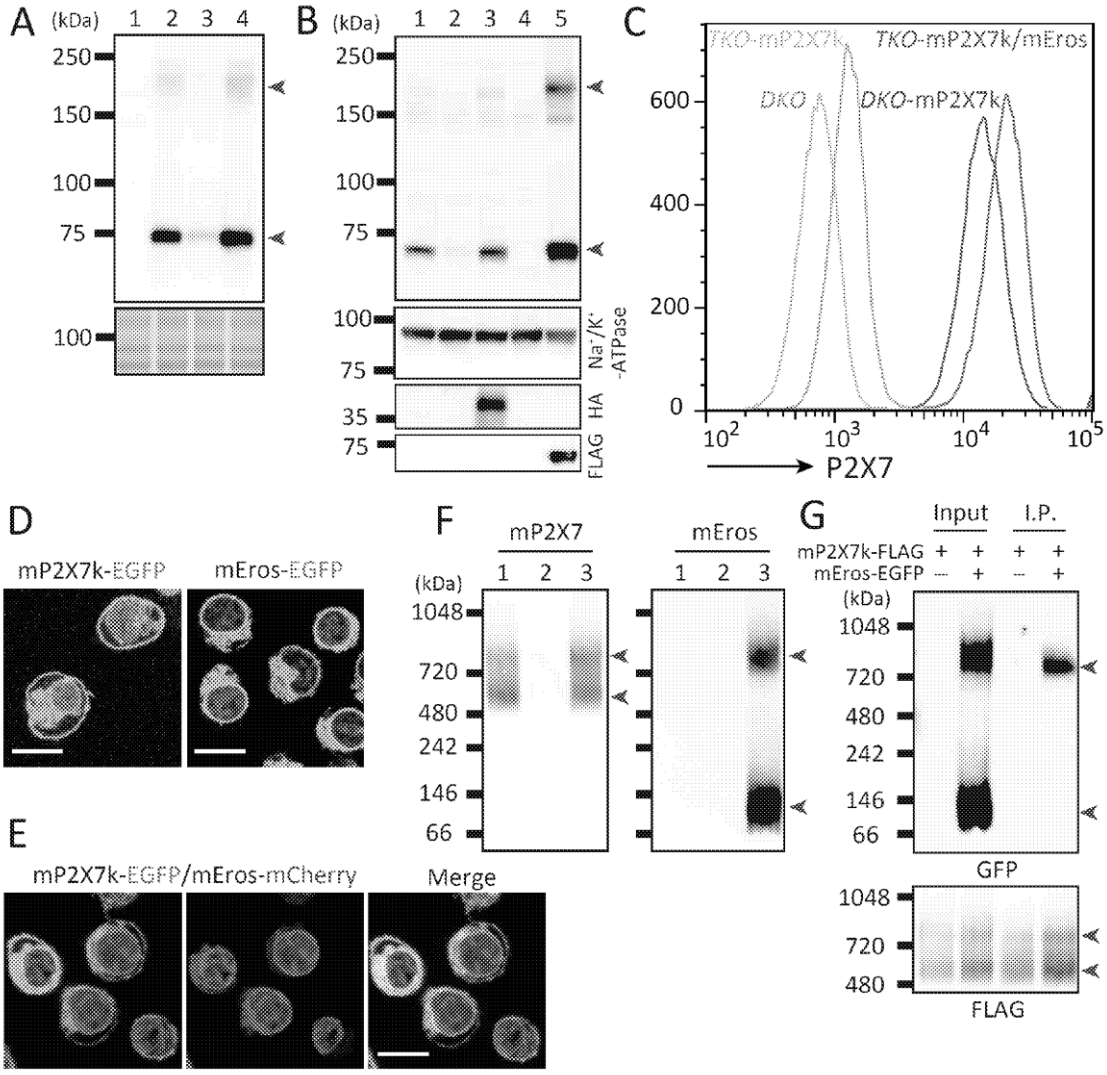

A
DKO-mP2X7k
TKO-mP2X7k
TKO-mP2X7k/mEros
None
BzATP
ATP
1.8%
1.0%
0.6%
88.0%
24.3%
91.7%
89.7%
20.9%
90.9%
PI
AnnexinV
B
NBD-PC (×10³ MFI)
Time (min)
C
YO-PRO-1 (RFI)
D
Cell Number
Fluo4
E
IL-1β (pg/mL)
ATP (mM)
LPS
Wild Type
Eros-/-
Eros-/--hEros
P2X7-/-
P2X7-/--hP2X7
F
ATP (μM)

Fig. 4


A
(kDa)
1 2 3 4
250
150
100
75
100
B
(kDa)
1 2 3 4 5
250
150
100
75
100
75
35
75
Na+/K+-ATPase
HA
FLAG
C
TKO-mP2X7k
TKO-mP2X7k/mEros
DKO
DKO-mP2X7k
600
400
200
0
10^2
10^3
10^4
10^5
P2X7
D
mP2X7k-EGFP
mEros-EGFP
E
mP2X7k-EGFP/mEros-mCherry
Merge
F
mP2X7
mEros
1 2 3
(kDa)
1048
720
480
242
146
66
G
Input
I.P.
mP2X7k-FLAG + + + +
mEros-EGFP – + – +
(kDa)
1048
720
480
242
146
66
GFP
1048
720
480
FLAG