

Supplementary Information for

Pannexin 1 involvement in bladder dysfunction in a multiple sclerosis model

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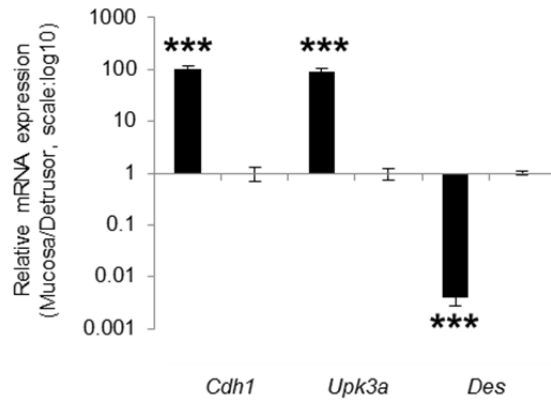
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Supplementary Information includes:

Supplementary Figures S1 to S10

Supplementary Table S1

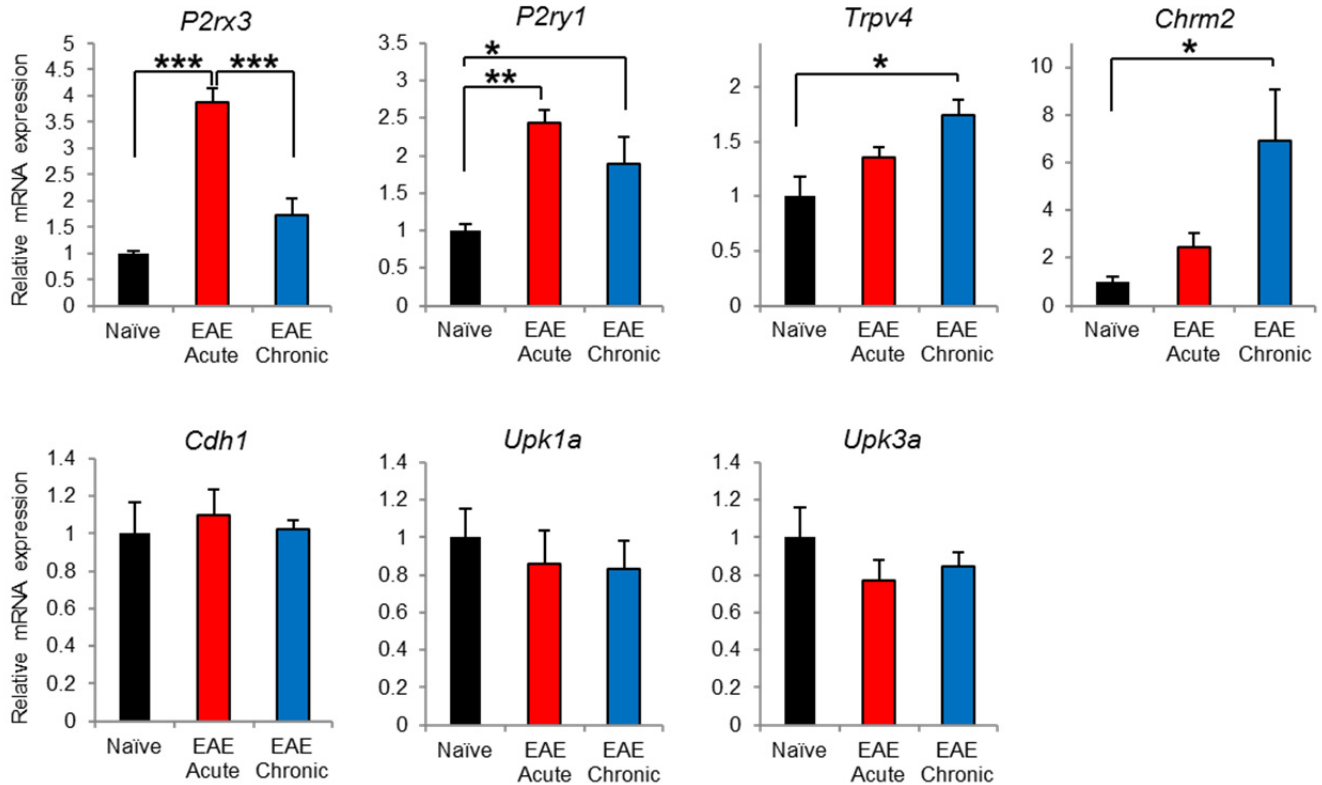
Supplementary Figure S1



Supplementary Figure S1 | Validation of proper separation of bladder mucosa from detrusor muscle. Real time RT-PCR showing mRNA of *Cdh1* and *Upk3a* detected in bladder mucosa and *Des* in bladder detrusor (***) $P < 0.0001$ by paired Student *t*-test, $n=5$). Error bars indicate SEM. For the relative expression, the values of detrusor were set as 1.

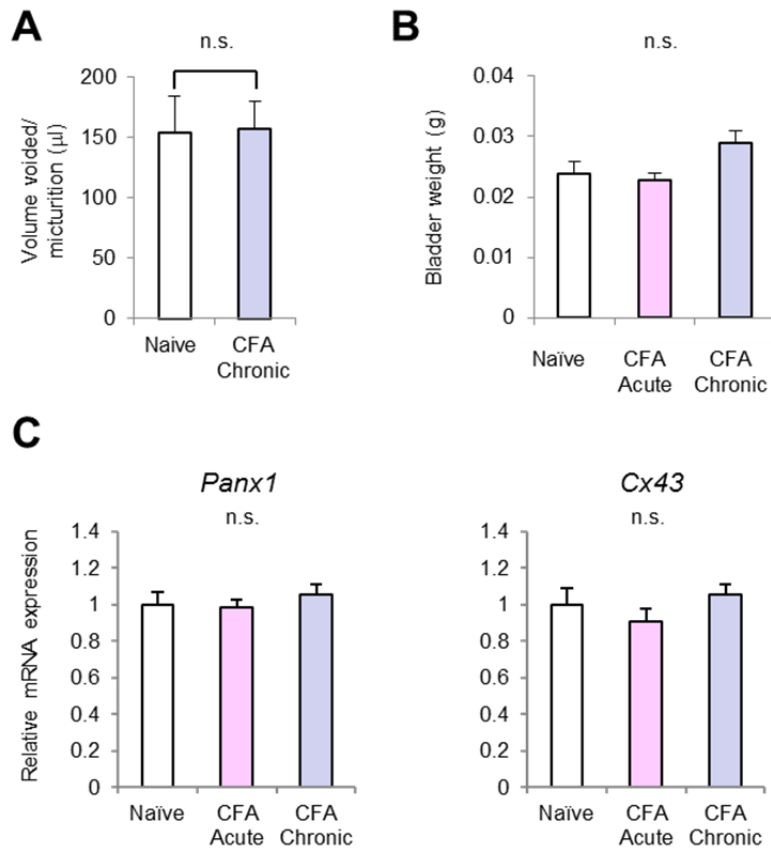
Supplementary Figure S2

Mucosa



Supplementary Figure S2 | mRNA expression levels in bladder mucosa of naive mice, and EAE mice at the acute and chronic phases of the disease. * $P < 0.05$ and ** $P < 0.01$ and *** $P < 0.001$ by one-way ANOVA followed by Tukey's *post-hoc* test ($n=5, 3$ and 3 , respectively). All error bars represent SEM. For the relative expression, the values of naive mice were set as 1. Note that certain genes associated with the bladder mechanosensory, transduction and signaling systems, such as the purinergic receptors *P2rx3* and *P2ry1*, *Trpv4* (*transient receptor potential cation channel, subfamily V, member 4*) and *Chrm2* (*cholinergic receptor, muscarinic type 2*) were significantly upregulated, while urothelial marker genes were unchanged as *Cdh1*, *Upk1a* and *Upk3a*. *P2rx1*, *P2rx2*, *P2rx4*, *P2ry2*, *P2ry6* and *Chrm3* were not significantly changed (data not shown).

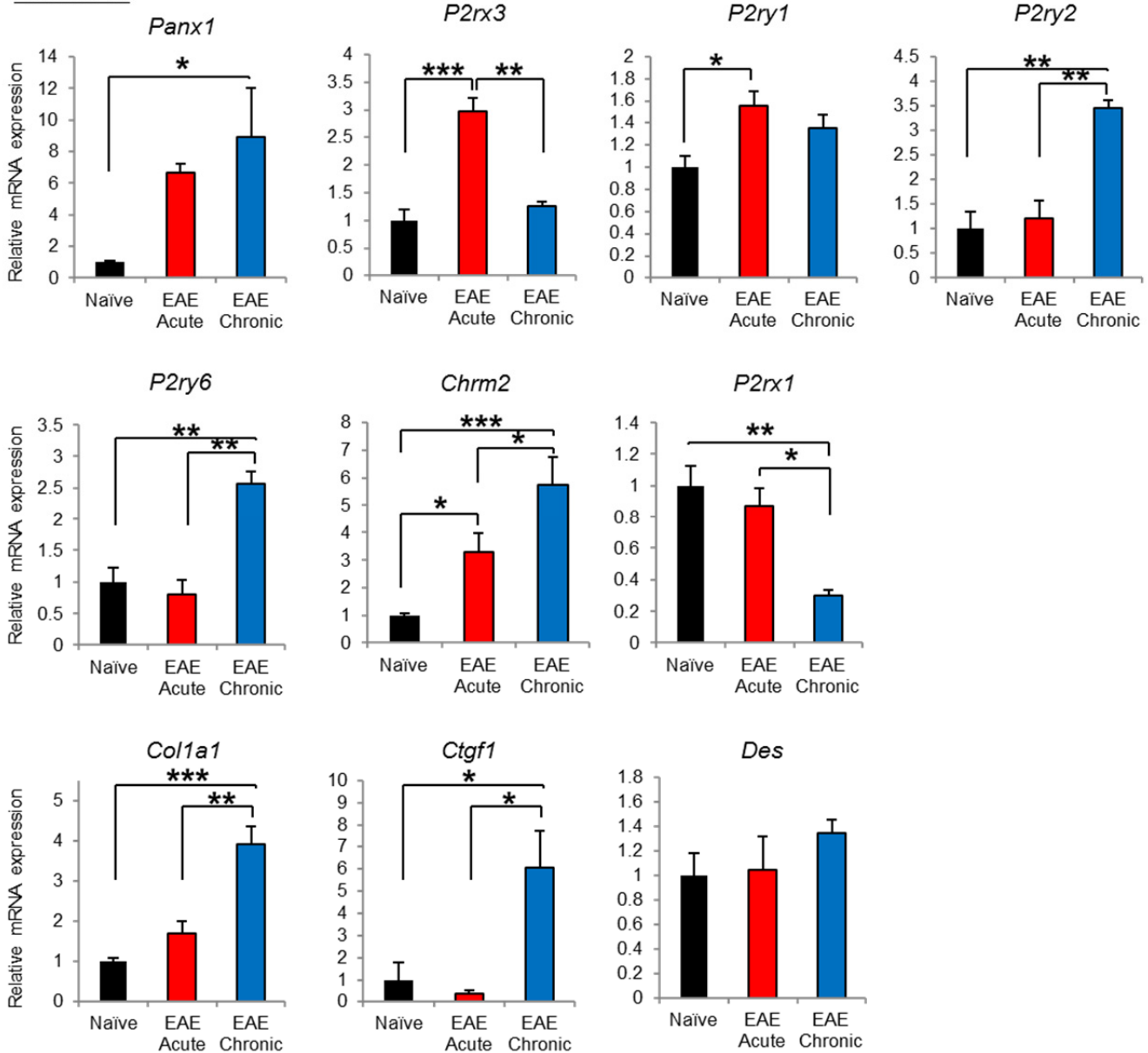
Supplementary Figure S3



Supplementary Figure S3 | Additional control experiments using CFA-only treated mice. (A) Average UVVM was not significantly different in naïve mice and in mice treated only with CFA when compared at 35 days post CFA injection, a time point which would correspond to the chronic phase of EAE (n=4 and 3, unpaired *t*-test). (B, C) Bladder weight in B and mRNA expression levels of *Panx1* and *Cx43* in bladder mucosa in C were not significantly different in naïve mice and CFA-only treated mice (n=4, 4 and 3, one-way ANOVA). All error bars indicate SEM.

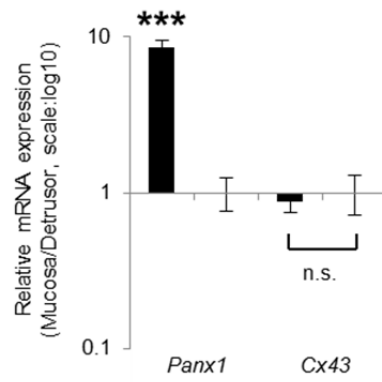
Supplementary Figure S4

Detrusor



Supplementary Figure S4 | mRNA expression levels in the bladder detrusor of naive mice, and EAE mice at the acute and chronic phases of the disease. * $P < 0.05$ and ** $P < 0.01$ and *** $P < 0.001$ by one-way ANOVA followed by Tukey's *post-hoc* test ($n=5, 3$ and 3 , respectively). All error bars represent SEM. For the relative expression, the values of naive were set as 1. Note that some of genes associated with the bladder mechanosensory, transduction and signaling systems, such as *Panx1*, *P2rx3*, *P2ry1*, *P2ry2*, *P2ry6* and *Chrm2* were upregulated but *P2rx1*, a major purinergic receptor in detrusor, was down-regulated. Genes associated with fibrosis were upregulated as *Col1a1* and *Ctgf1*. *Des* (*Desmin*), a muscle marker, was relatively unchanged. *Cx43*, *P2rx2*, *P2rx4*, *Trpv4* and *Chrm3* were not significantly changed (data not shown).

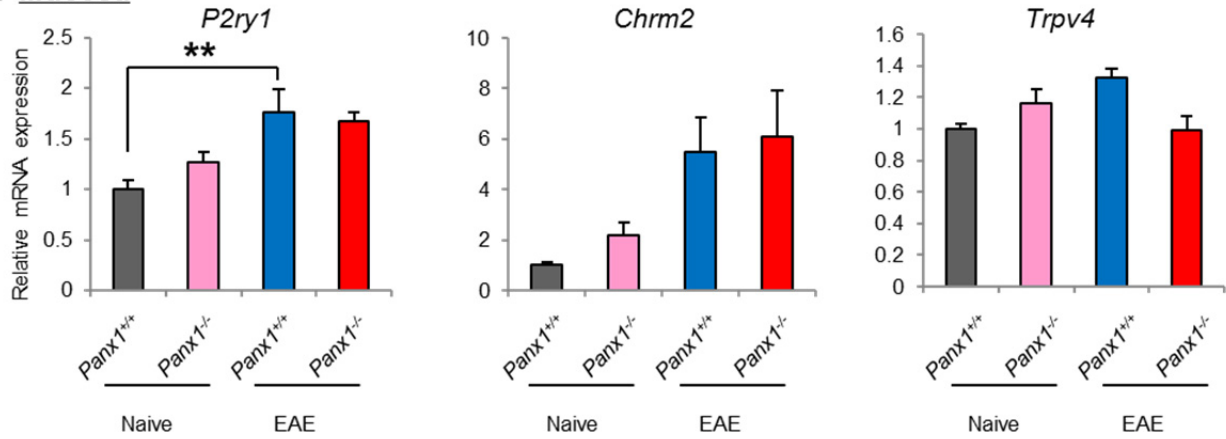
Supplementary Figure S5



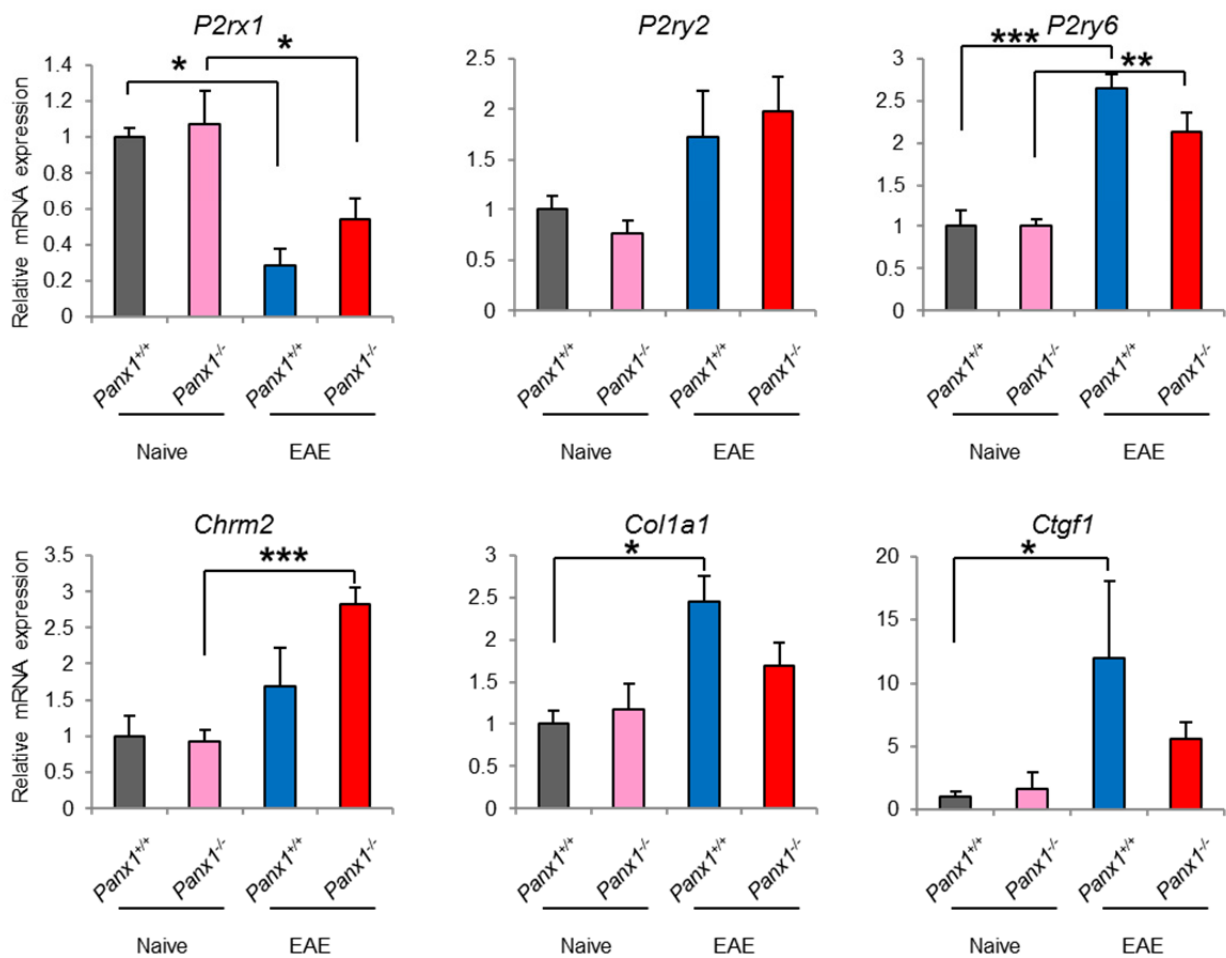
Supplementary Figure S5 | Differences in *Panx1* and *Cx43* mRNA expression levels between the bladder mucosa and detrusor. *** $P < 0.0001$ by paired t -test ($n=5$). All error bars represent SEM. For the relative expression, the values of detrusor were set as 1.

Supplementary Figure S6

A Mucosa



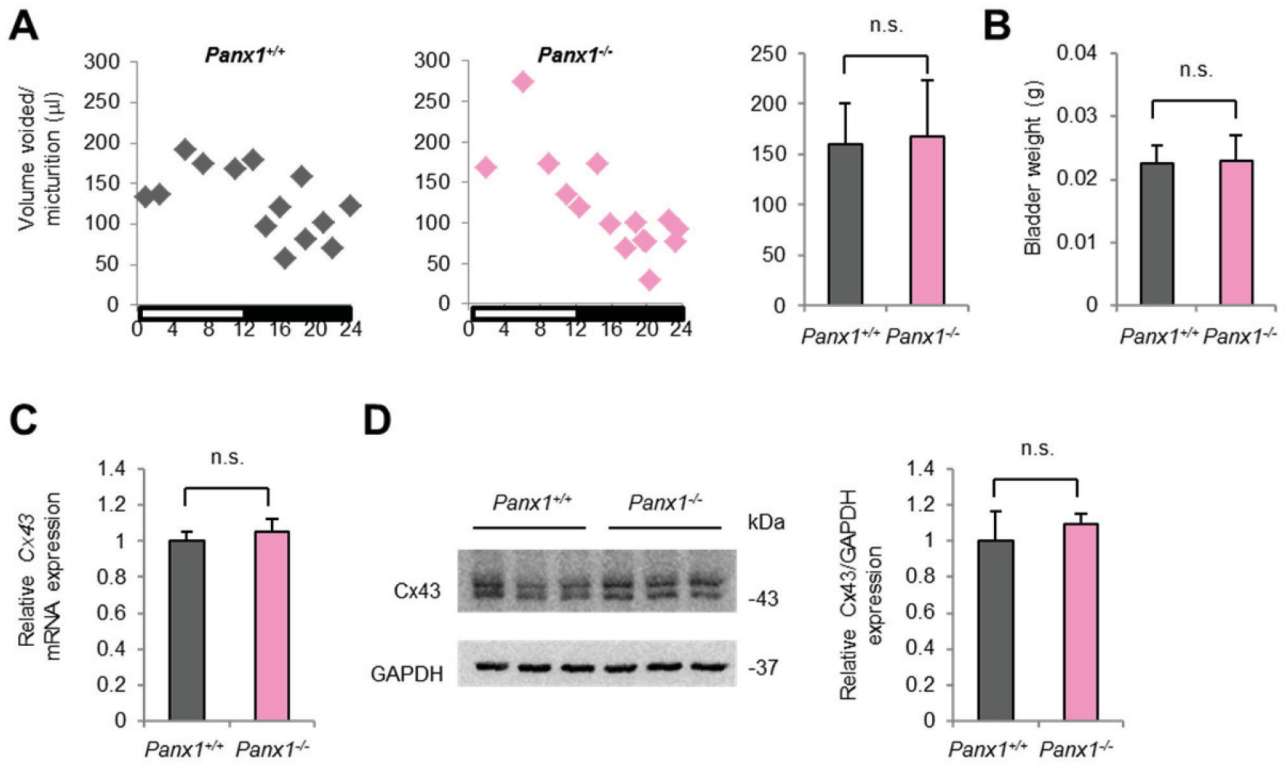
B Detrusor



Supplementary Figure S6 | mRNA levels for some of the genes associated with the bladder mechanosensory, transduction and signaling systems expressed in the bladder mucosa (A) and detrusor (B) of *Panx1*^{+/+} and *Panx1*^{-/-} naïve and EAE mice. Upregulation of *P2y1* and *Chrm2* in mucosa, and *P2ry2* and *P2ry6* in detrusor observed in *Panx1*^{+/+} EAE mice were also detected in *Panx1*^{-/-} EAE mice. Upregulation of *Trpv4* in mucosa, and genes associated with fibrosis as *Col1a1* and *Ctgf1* in detrusor observed in *Panx1*^{+/+} EAE mice was not or less detected in *Panx1*^{-/-} EAE mice, although they are not significantly different. **P* < 0.05 and ***P* < 0.01 and ****P* < 0.001 by one-way ANOVA followed by Bonferroni's *post-hoc* test (n=5, 4, 3 and 8, respectively). All error bars indicate SEM.

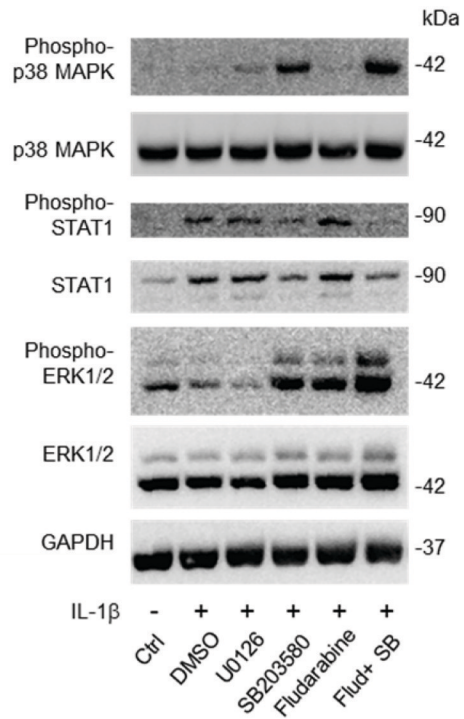
Supplementary Figure S7

Naive



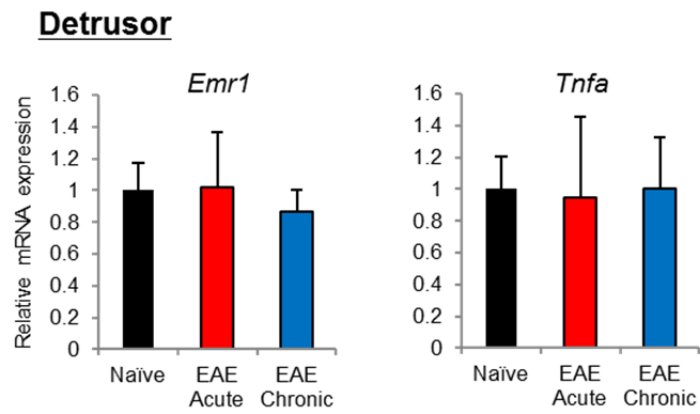
Supplementary Figure S7 | *Panx1*^{+/+} and *Panx1*^{-/-} naïve mice display similar phenotypes in terms of micturition and Cx43 expression in the bladder mucosa. (A) Representative charts of urine volume voided per micturition (UVVM) from *Panx1*^{+/+} (left panel) and *Panx1*^{-/-} naïve mice (middle panel), and corresponding average UVVM (n=3 each genotype). No significant difference (n.s.) by unpaired *t*-test. (B) Bladder weight was not significantly different by unpaired *t*-test (n=3). (C, D) Expression levels of Cx43 mRNA in C and its protein in D in the bladder mucosa of *Panx1*^{+/+} and *Panx1*^{-/-} naïve mice were not significantly different by unpaired *t*-test (n=3). All error bars indicate SEM. Full-length blots are presented in Supplementary Fig. S17.

Supplementary Figure S9



Supplementary Figure S9 | Effects of U0126, SB203580 and Fludarabine on expression and phosphorylation of target proteins in TRT-HU1 cells. U0126 inhibited phosphorylation of ERK1/2. SB203580 inhibits p38 catalytic activity, therefore did not inhibit p38 phosphorylation. Fludarabine increased STAT1 phosphorylation. Full-length blots are presented in Supplementary Fig. S18.

Supplementary Figure S10

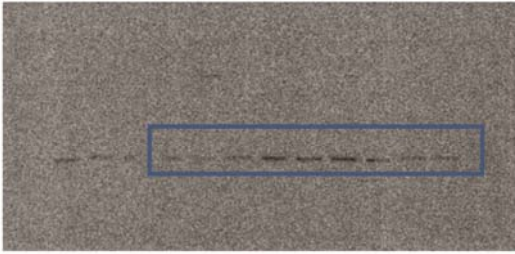


Supplementary Figure S9 | mRNA expression levels of *Emr1* and *Tnfa* in the bladder detrusor of naïve mice, and EAE mice at acute and chronic phases of the disease. No significant differences in naïve, EAE acute and chronic phases by one-way ANOVA (n=5, 3 and 3, respectively). All error bars indicate SEM.

Supplementary Figure S11

Figure 2C

Panx1



GAPDH

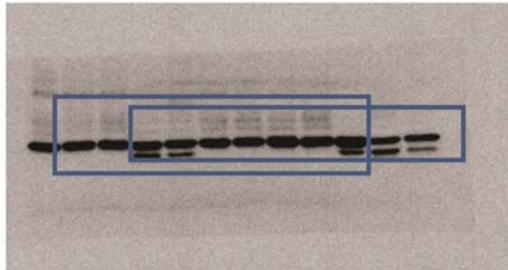
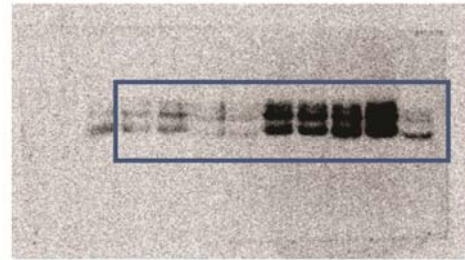


Figure 2D

Cx43



GAPDH is common in 2C and 2D

Panx1



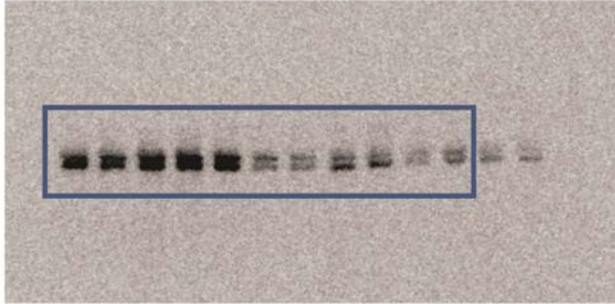
GAPDH



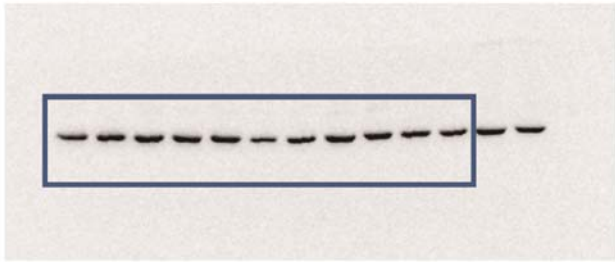
Supplementary Figure S11 | Full-length unedited blots for Figures 2C and 2D.

Supplementary Figure S12

Cx43



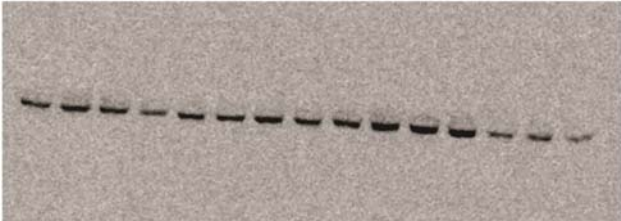
GAPDH



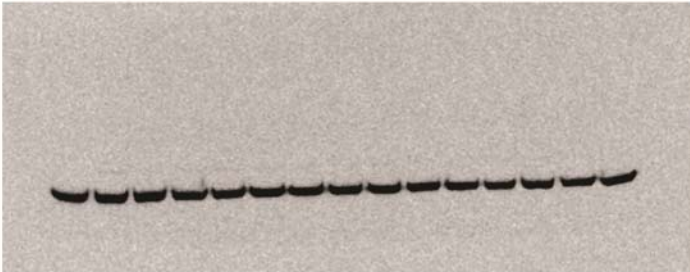
Supplementary Figure S12 | Full-length unedited blots for Figure 3E.

Supplementary Figure S13

Cx43

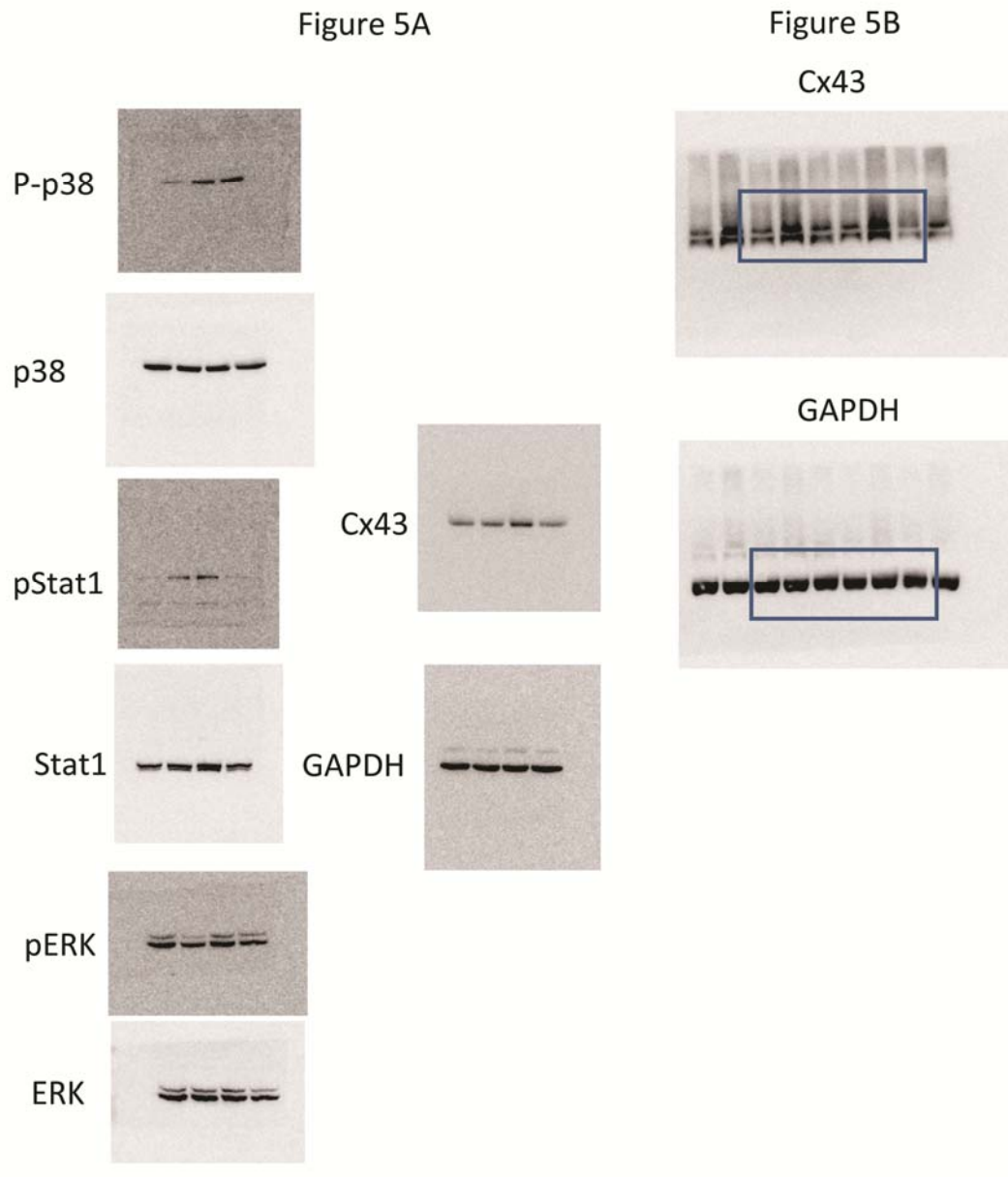


GAPDH



Supplementary Figure S13 | Full-length unedited blots for Figure 4C.

Supplementary Figure S14



Supplementary Figure S14 | Full-length unedited blots for Figures 5A and 5B.

Figure 6B

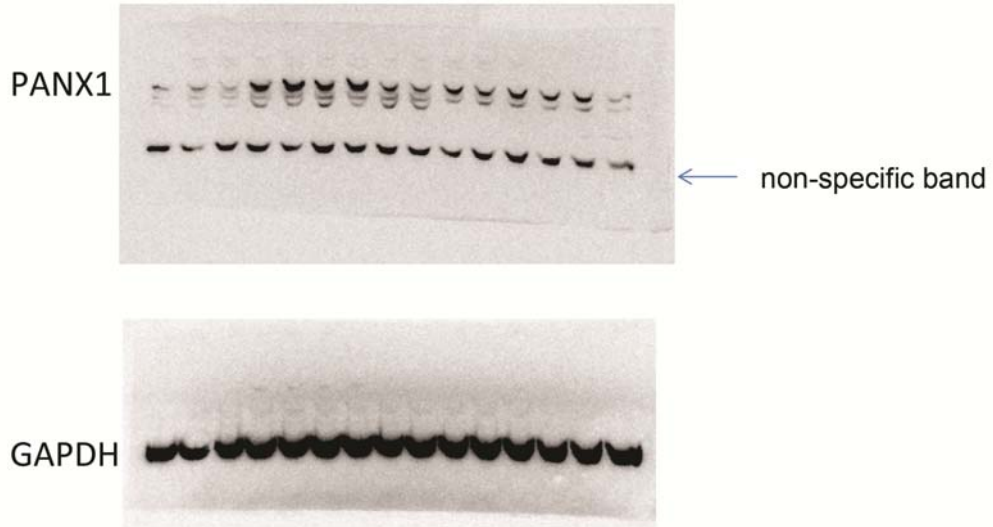
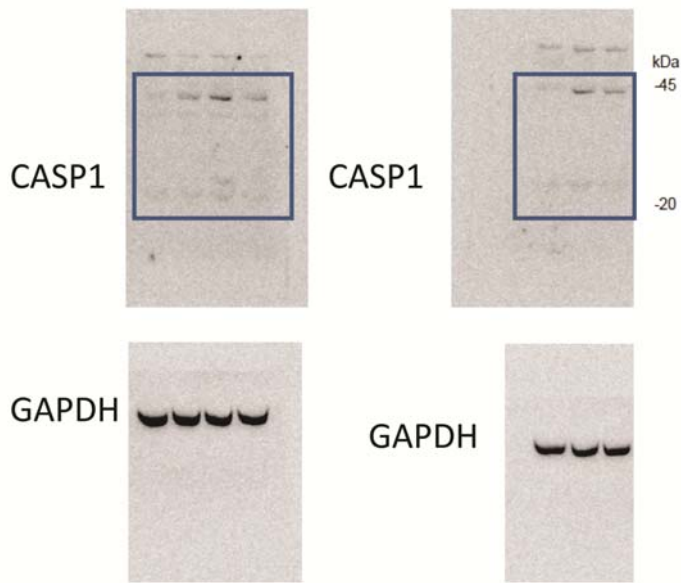
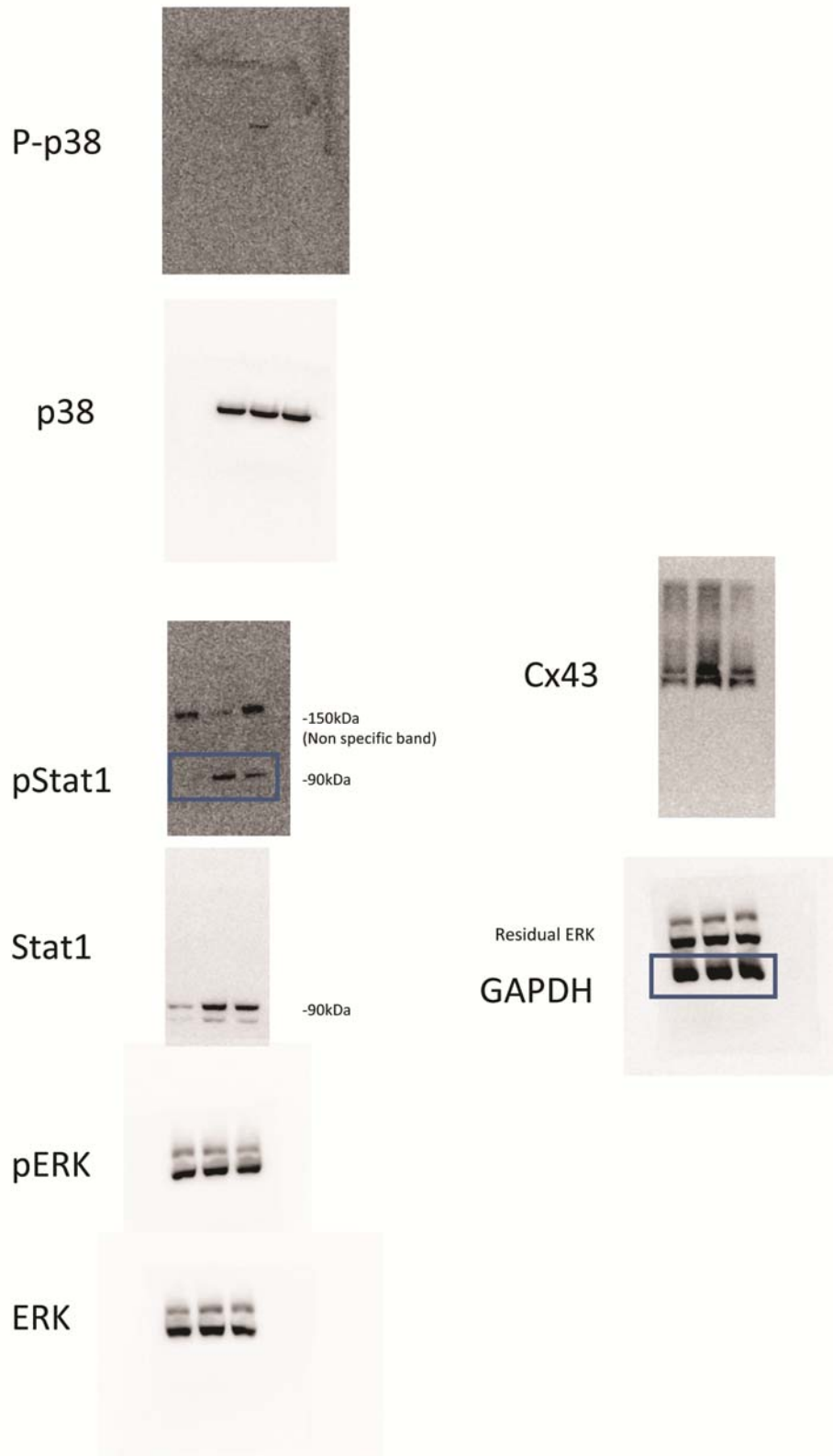


Figure 6D

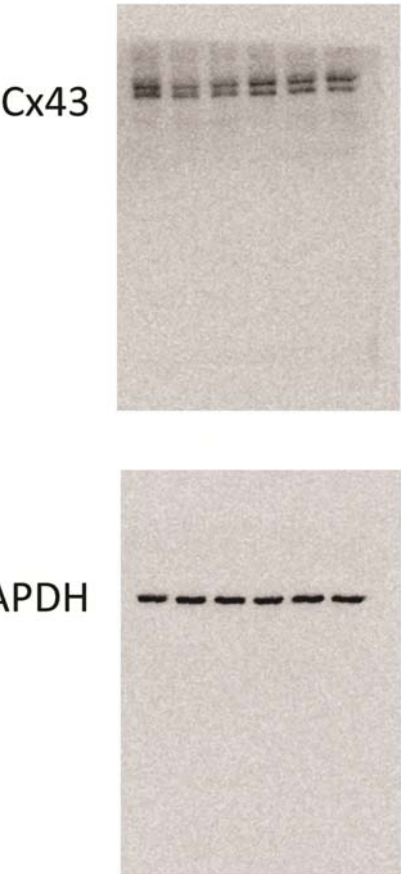


Supplementary Figure S16



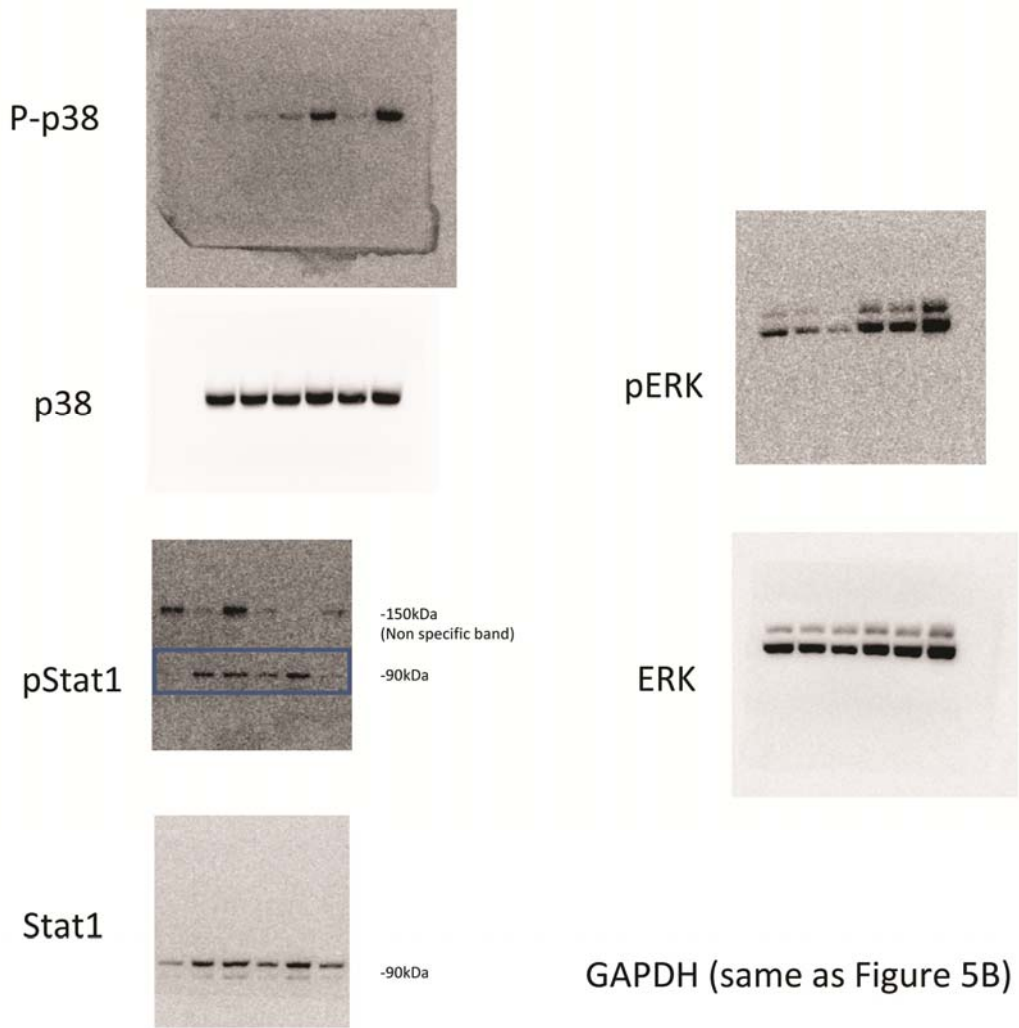
Supplementary Figure S16 | Full-length unedited blots for Figure 7B.

Supplementary Figure S17



Supplementary Figure S17 | Full-length unedited blots for Supplementary Figure S7 D.

Supplementary Figure S18



Supplementary Figure S17 | Full-length unedited blots for Supplementary Figure S9.

Supplementary Table S1

Primers for real-time RT-PCR

Species	Gene name	Accession	Forward (5'→3')	Reverse (5'→3')	Amplicon size (b.p.)
Mouse	<i>Panx1</i>	NM_019482	AGCCAGAGAGTGGAGTTCAAAGA	CATTAGCAGGACGGATTCAGAA	104
	<i>Cx43</i>	NM_010288	CCATCCAAAGACTGCGGAT	GTAATTGCGGCAGGAGGAA	138
	<i>P2rx1</i>	NM_008771	AGCCCAAGGTATTCGCACA	ACAGGACACCAGCCAAAGATC	81
	<i>P2rx2</i>	NM_001164833	AAAACAAGCTCTACAGCCATAAGAAGT	TCAAAGTTGGGCCAAACCTT	140
	<i>P2rx3</i>	NM_145526	GCCCAACAGTGAGCTTTCTC	ATTTCCCTGGGCTCTCCTAA	58
	<i>P2rx4</i>	NM_011026	CACAACGTGCTCCTGGCTA	GCCTTTCCAAACACGATGAT	125
	<i>P2ry1</i>	NM_008772	AGGAAAGCTTCCAGGAGGAG	CGTGTCTCCATTCTGCTTGA	95
	<i>P2ry2</i>	NM_008773	CGTGCTTACTTCGTACCA	AAAAGCAGACCCAGCATGAC	102
	<i>P2ry6</i>	NM_183168	CATTAGTTCAGCGCTACC	CTCCACACACTACCCAAGCA	91
	<i>Trpv4</i>	NM_022017	CACCCAGTGACAACAAGAGA	CGATTGAAGACTTTGAGGATGG	107
	<i>Chrm2</i>	NM_203491	CATTGCGGCTTTCTATCTGC	TCTGGATCTTGTGTGCTCCA	212
	<i>Chrm3</i>	NM_033269	ACACCTTCTGTGACAGCTGCA	TCGCTTGTGAAAAATGACGG	212
	<i>Upk1a</i>	NM_026815	CCTCCTGCATCACATCCTACA	CCACAACACTCTTGCTCAATCA	157
	<i>Upk3a</i>	NM_023478	CATCATCCTCAGCTTTGTGGA	GAGAACACCTCTGTCTGTCTAGG	159
	<i>Cdh1</i>	NM_009864	GAGGAGAACGGTGGTCAAAGA	AGCTGGCTCAAATCAAAGTCC	120
	<i>Col1a1</i>	NM_007742	GCAACAGTCGCTTCACCTACA	CAATGTCCAAGGGAGCCACAT	137
	<i>Ctgf1</i>	NM_010217	AGAACTGTGTACGGAGCGTGAC	CACCATCTTTGGCAGTGCA	107
	<i>Des</i>	NM_010043	AAGGCCAAACTACAGGAGGAAA	TACGAGCTAGAGTGGCTGCATC	97
	<i>IL-1β</i>	NM_008361	CAGGCAGGCAGTATCACTCA	TGTCCTCATCCTGGAAGGTC	90
	<i>IL-6</i>	NM_031168	CCGGAGAGGAGACTTCACAG	TCCACGATTTCCAGAGAAC	102
<i>Tnfa</i>	NM_013693	ACGGCATGGATCTCAAAGAC	GTGGGTGAGGAGCACGTAGT	116	
<i>Nfkb1</i>	NM_008689	GGAAAAAACATCCACCTGCAC	TGCAAAGCCAACCACCAT	105	
<i>Emr1</i>	NM_010130	TCAGTCTCGCAACATCAAGA	ACCAGCAGCGATTATGCATC	123	
<i>IL-1R-1</i>	NM_008362	TACCCGAGGTCCAGTGGTATAAG	AGCCACATTCTCACCAACAG	98	
Human	<i>Cx43</i>	NM_000165	AGCAAAAAGAGTGGTGCCCA	TTGTCAAGGAGTTTGCCTAAGG	63
	<i>IL-1β</i>	NM_000576	TTATGTGCACGATGCACCTG	AGGACATGGAGAACACCACCTTG	149
	<i>IL-1R-1</i>	NM_000877	AGAGGAAAACAAACCCACAAGG	AACTGGCCGGTGACATTACAG	108
	<i>STAT1</i>	NM_007315	ATCTGTCTTCTTCTGACTCCA	CCTTACAAAACCTCGTCCACG	186
	<i>PANX1</i>	NM_015368	GGCAGAGCTCAAAGGTATGAA	GCAAACCAGCTGTGAAACCA	186
	<i>CASP1</i>	NM_033294	GGAAACAAAAGTCGGCAGAGA	GATAATGAGAGCAAGACGTGTGC	72

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	<i>Trpv4</i>	NM_022017	CACCCCAGTGACAACAAGAGA	CGATTGAAGACTTTGAGGATGG	107
	<i>Chrm2</i>	NM_203491	CATTGCGGCTTTCTATCTGC	TCTGGATCTTGTTGTGCTCCA	212
	<i>Chrm3</i>	NM_033269	ACACCTTCTGTGACAGCTGCA	TCGCTTGTGAAAAATGACGG	212
	<i>Upk1a</i>	NM_026815	CCTCCTGCATCACATCCTACA	CCACAACACTTTGCTCAATCA	157
	<i>Upk3a</i>	NM_023478	CATCATCCTCAGCTTTGTGGA	GAGAACACCTCTGCTCTGTCTAGG	159
	<i>Cdh1</i>	NM_009864	GAGGAGAACGGTGGTCAAAGA	AGCTGGCTCAAATCAAAGTCC	120
	<i>Col1a1</i>	NM_007742	GCAACAGTCGCTTACCTACA	CAATGTCCAAGGGAGCCACAT	137
	<i>Ctgf1</i>	NM_010217	AGAAGTGTGTACGGAGCGTGAC	CACCATCTTTGGCAGTGCA	107
	<i>Des</i>	NM_010043	AAGGCCAAACTACAGGAGGAAA	TACGAGCTAGAGTGGCTGCATC	97
	<i>IL-1β</i>	NM_008361	CAGGCAGGCAGTACTCACTCA	TGTCCTCATCCTGGAAGGTC	90
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