Supplementary Tables

Table S1 miRNA Stem-loop and TaqMan probes for miRNAs RT-qPCR

miRNAs	**Accession Number**	**Sequences**	**ID**
mmu-miR-135a-5p	MIMAT0000147	TATGGCTTTTTATTCCTATGTGA	000460
mmu-miR-28a-3p	MIMAT0004661	CACTAGATTGTGAGCTGCTGGA	002545
mmu-miR-30c-2-3p	MIMAT0005438	CTGGGAGAAGGCTGTTTACTCT	002110
mmu-miR-324-5p	MIMAT0000555	CGCATCCCCTAGGGCATTGGTGT	000539
mmu-miR-335-5p	MIMAT0000766	TCAAGAGCAATAACGAAAAATGT	000546
mmu-miR-16	MIMAT0000527	TAGCAGCACGTAAATATTGGCG	000391
snoRNA 202	AF357327	GCTGTACTGACTTGATGAAAGTACTTTTGAACCCTTTTCC ATCTGATG	001232

Table S2 Primer sequences

All primer sequences are shown from 5' to 3'.

Table S2A Primer sequences used for RNAs RT-qPCR

Name	**Accession Numbers**	**Amplicon size (pb)**	**Forward primer**	**Reverse primer**
Nr3c2 (MR)	M36074	153	ATGGAAACCACACGGTGACCT	AGCCTCATCTCCACACACCAAG
zfp36l1 (Tis11b)	NM_007564.3	100	CGACACACCAGATCCTAGTCCTT	TGCATAAAACTTCGCTCAAGTCA
*Elavl1 (*HuR*)*	NM_010485.3	87	CAGCCAATCCCAACCAGAA	TGGTGTACAGGGCCTCCAAA
*Tsc22d3 (*Gilz)	NM_010286.3	79	CTGCTGTGGAGTTTGTGACATACTAG	CCAGGCAGGCACTTCTAAGCT
Sgk1	*AF205855*	*150*	TCACTTCTCATTCCAGACCGC	ATAGCCCAAGGCACTGGCTA
18S	X00686	66	CCCTGCCCTTTGTACACACC	CGATCCGAGGGCCTCACTA
Rplp0 (36b4)	NM_007475.5	128	AGCGCGTCCTGGCATTGTCTGT	GGGCAGCAGTGGTGGCAGCAGG

Table S2B Primer sequences used for cloning the pMIR-mHuR-3'-UTR

Name	**Forward primer**	**Reverse primer**
pMIR-mHuR-3'UTR	ACGCACTAGTCGGAATAGATAATTAAGAGTGA	ACGCAGCTTCCACCTTTCTTTTTCTGA

Table S3 miRNAs Mimics & Inhibitors references for transfection

Name	ID
324-5p Mimic	MC10253
30c-2-3p Mimic	MC12646
negative control Mimic	
324-5p Inhibitor	MH10253
30c-2-3p Inhibitor	MH12646
negative control Inhibitor	

Table S4 Antibodies used for Western blot analysis

Name (Provider)	**Species**	**Protein**	**Molecular weight (kDa)**	**Dilution**
Primary antibodies				
39N	Rabbit	MR	130 kDa	1:1000 (cells) 1 :5000 (tissues)
α-Tubulin (Sigma)	Mouse	α-Tubulin	50 kDa	1:5000
Secondary antibodies				
Dylight Anti-Rabbit 800 (Fisher Scientific)	Goat	Rabbit IgG		1:10000
Dylight Anti-Mouse 680 (Fisher Scientific)	Rabbit	Mouse IgG		1:10000

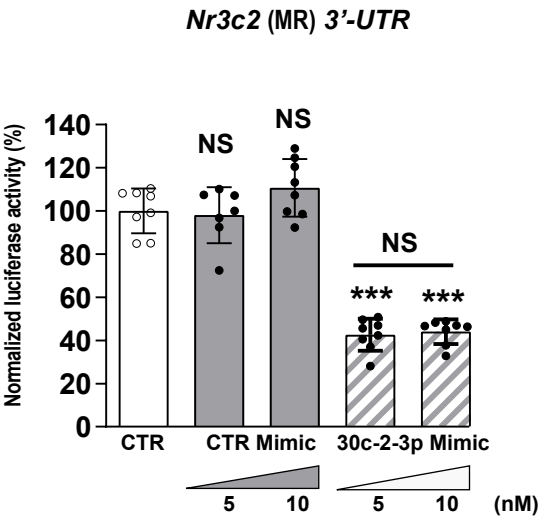
Supplementary figure legends

Supplementary Figure S1: miR-30c-2-3p functionally interacts with *Nr3c2* (MR) 3'-UTR. HEK 293T cells were transiently transfected with pMIR-mMR-3'-UTR plasmid (40 ng/well of 96-well plates) and incubated with increasing concentrations (5 or 10 nM) of negative control Mimics (CTR Mimic) or 30c-2-3p Mimics. Luciferase activities were measured 24 h after transfection and normalized to β-galactosidase activities. *** indicated *P<0.001*. NS: non-significant.

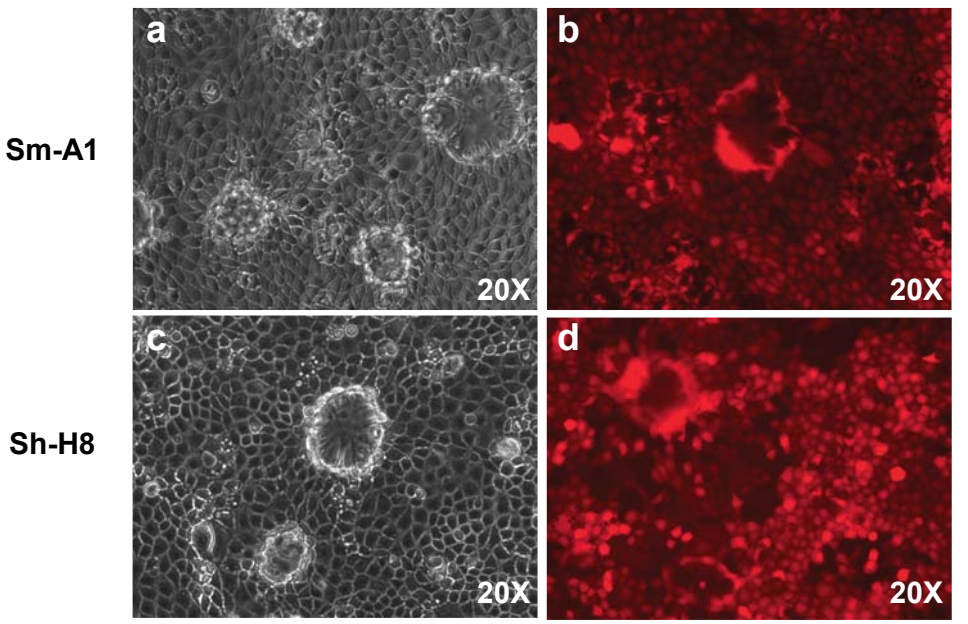
Supplementary Figure S2: Morphology of Sm-A1 and Sh-H8 clones. Cells were grown for 5 days then were stimulated with 1 µg/mL Doxycyline for 48 h. **a, c** Cellular morphology of Sm-A1 clone (**a**) and Sh-H8 clone (**c**) observed with a phase-contrast microscope. Clones maintain a cuboid shape characteristics of epithelial cells and form domes at confluency suggesting a transepithelial ionic transport. **b, d** Sh-A1 (**b**) and Sh-H8 clones (**d**) were observed with a fluorescent microscope after 48 h of doxycycline stimulation. Fluorescence of turbo Red Fluorescent Protein allowed easy identification of transduced KC3AC1 cells, which should express either scrambled miRNAs (upper panels) or miR-324-5p (lower panels).

Supplementary Figure S3: MR and miR-30c-2-3p, miR-324-5p expression in different nephron segments. **a** Schematic representation of the different nephron segments; Proximal convoluted tubules (PCT), medullary and cortical thick ascending limb of Henle's loop (mTAL and cTAL), connecting tubules (CNT), cortical and outer medullary collecting duct (CCD and OMCD). **b, c, d** Quantification by RT-qPCR of MR (**b**), miR-30c-2-3p (**c**) and miR-324-5p (**d**) expression in different nephron segments of control mice.

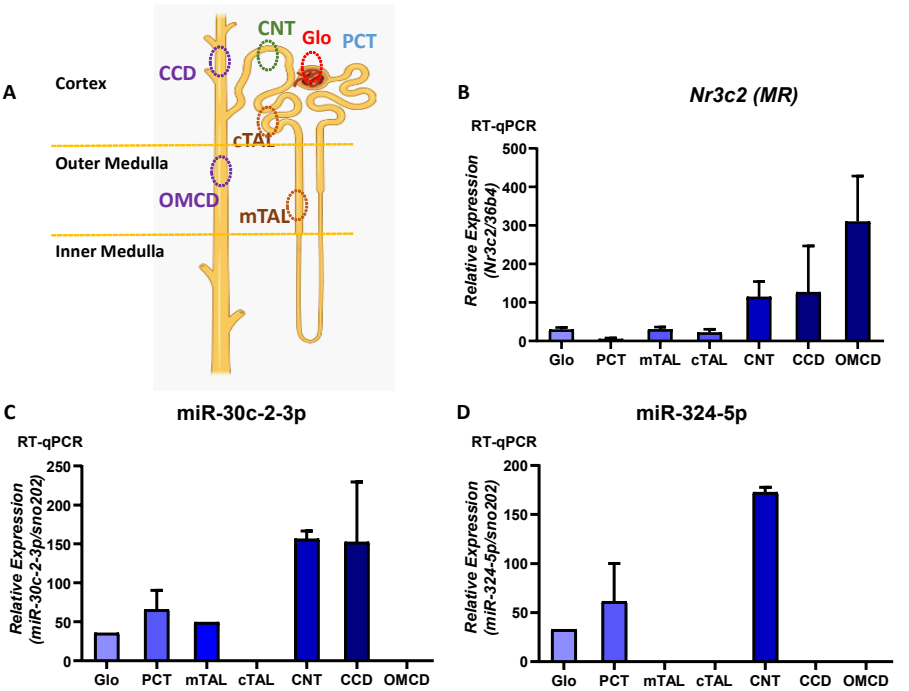
Supplementary Figure S4: Identification of half sites of Tonicity response Elements (TonEs) in regulatory sequences of miRNAs loci (red box). **a** Schematic representation of *mir30c-2* gene on murine chromosome 1 (green bar) and location of TonEs, which were identified with Jaspar software in *mir30c-2* promoter region (blue bar). **b** Schematic representation of *mir324* gene on murine chromosome 11 (green bar) and location of TonEs, which were identified with Jaspar software in *mir324* promoter region (violet bar). The bent arrow represents the transcription start site (TSS) of *mir30c-2* (**a**) and *mir324* genes (**b**), encoding miR-30c-2-3p and miR-324-5p, respectively.



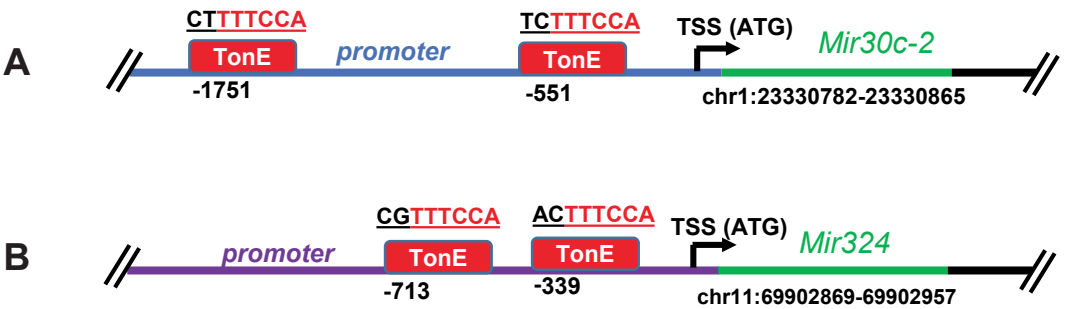
Supplementary Figure S1



Supplementary Figure S2



Supplementary Figure S3



TonE : **TGGAAANNYNY**

Supplementary Figure S4