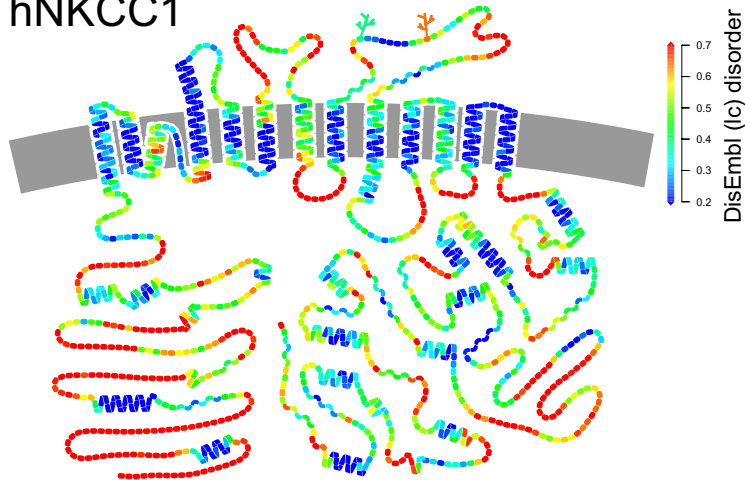
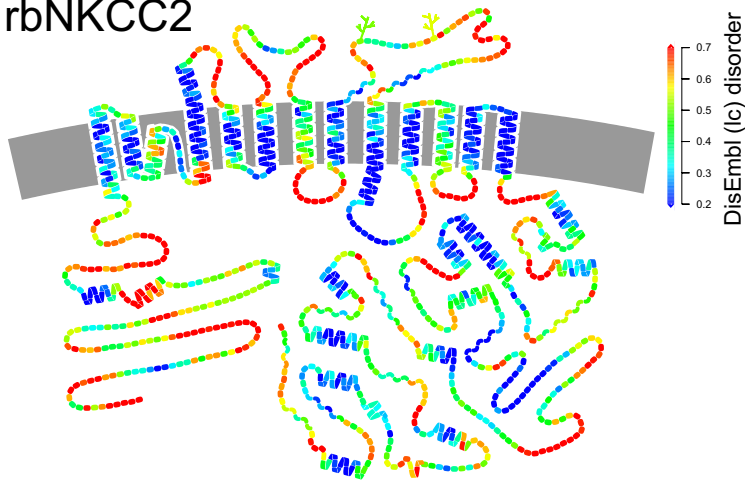


Supplemental Figure 1. Models of NKCC1 (human) and NKCC2 (rabbit), colored according to residue-by-residue similarity to one another.

hNKCC1



rbNKCC2



Supplemental Figure 2. Models of NKCC1 and NKCC2, colored by predicted disorder. The likelihood of disorder is predicted by the DisEmbl 1.5 loop-coil model (R. Linding, L.J. Jensen, F. Diella, P. Bork, T.J. Gibson and R.B. Russell. Protein disorder prediction: implications for structural proteomics. Structure Vol 11, Issue 11, 4 November 2003. <http://dis.embl.de/>

## Supplemental Table 1

### NKCC HA tag oligos

CTAGCGCCACCATGGATGTATCCATATGATGTTCCAGATTATGCTCGAGGTAGCGTAGCATTAAATA  
CCGGTATTTAAATGCTACGCTACCTCGAGCATAATCTGGAACATCATATGGATACATCCATCCTGGCG

HA for pIRES f  
HA for pIRES r

### Silent unique sites in NKCC1

GGGTCCCCGAAGACAAGCCATGAAAGAGATG  
CTTCGGGGACCCATATGTACATGGCCACAGATC

SanDI at 2475 f  
SanDI at 2475 r

GGCTGCTGGCCTAGGTCGTATGAAGCCAAACACAC  
CATACGACCTAGGCCAGCAGCCTGCATCAAATAC

AvrII at 2625f  
AvrII at 2625r

TATCTCACCTGCAGGGACAAGAAGAAATTATTGTCATCAC  
CTTGTCCCTGCAGGTGAGATATATCCAGACCTTCTTTTAG

Sbfl at 2790f  
Sbfl at 2790r

### Silent unique site in PJB

CGAGAAGCGTACGATCTTTGTGAAGGAACCTTACTTC  
CAAAGATCGTACGCTTCTCGAGGTCGACGGTATC

BsiWI for pJB cloning f  
BsiWI for pJB cloning r

### Deletion oligos NKCC1

GGGGCAAGAAGAATTATTGTCATCACAAGAGAAATCTCCGGGACTAAGGATGTGGTAGTAAGTGTGGAATA  
TAGTAAAAAGTCCGACCTAGATACTTCACGTGGGCTG  
TGAAGTATCTAGGTCGGACTTTTTACTATATTCACACTTACTACCACATCCTTAGTGCCCCGAGATTTCTCT  
TGTGATGACAATAATTCTTCTTGGCCCCTGCA

NKCC1 partA f

NKCC1 part A r

CCAAGATCTCAGAGCA  
AGCTTGCTCTGAGATCTTGGCAGCCACG

Fill part Bf  
Fill part Br

AGTGAAAAACCAATTACACACAAAGTCGAGGAAGAAGATGGCAAGACTGCAACTCAACCACTGTTGAAAAAA  
GAATCCAAGGGGCTATTGTACCTTTAAATGTAGCTGACCAA  
AGCTTTTGGTCAGCTACATTTAAAGGTACAATAGGCCCTTGGATTCTTTTTTCAACAGTGGTTGAGTTGCAG  
TCTTGCCATCTTCTCCTCGACTTTGTGTGTAATTGGTTTTTCACTCAGCCACG

NKCC1 part Bf

NKCC part Br

GGGGCAAGAAGAATTACCAAGATCTCGTGGGCTG  
AGATCTTGTAATTCTTCTTGGCCCTGCA

Fill part A f  
Fill part A r

### NKCC1 point mutants

CTCAACCAGCGCGAAAAAAGAATCCAAAGGC  
CTTTTTTCGCCGCTGGTTGAGTTGCAGTCTTG

LL/AA at aa 989-990 f  
LL/AA at aa 989-990 r

CCAAAAGGCTGCTGAAGCTAGTACACAGTTTCA  
CTAGCTTCAGCAGCCTTTTGGTCAGCTAC

LL/AA at aa 1008-1009 f  
LL/AA at aa 1008-1009 r

GTTTACAGCAACAGAAATGGCAAGACTGCAACTCAACC  
CTTGCCATCTGTTGCTGAACTTTGTGTGTAATTGG

EEED/QQQN at aa 978-981 f  
EEED/QQQN at aa 978-981 r

GACTGCAGCTGCAGCACTGTTGAAAAAAGAATCC  
CAAACGTGCTGCAGCTGCAGTCTTGCCATCCTC

TQP/AAA at aa 986-988 f  
TQP/AAA at aa 986-988 r

CAAAGGCGCCATTGTGCCTTTAAATGTAGCTGACC  
GGCACAATGGCGCCTTTGGATTCTTTTTTCAACAG

P/A at aa 988 f  
P/A at aa 988 r

### Silent sites in NKCC2

GGAACATGCTGAAAACAAGTATAACAGACAACAAAGCCGGTGC  
GCACCGGCTTTGTTGTCTGTATACTTGTTTTCAGCATGTTCC

BstZ171 at 498 f  
BstZ171 at 498 r

CCACAGTGAAGATCACGTGAAAAATTTTCAGACC  
GGTCTGAAATTTTTACGTGATCTTCCACTGTGG

PmlI at 2026 f  
PmlI at 2026 r

### Primers for NKCC2-PCR

CTTTGTGGGTCCCCGAAGCTGTGTGTTAAGG  
GGCCTCGGGCCTAGGCCGAATGAAGCCAAACAC  
CATTTCTCAGGTCTCGAGGTTCAAGAGGAATTG  
GTTCAACCAGAAGCTTGTGGAAGCCAGCACTC  
GAGCAAATCCGGATAAAATTTGCAGACATCCAC

SanDI at 2154 f  
AvrII f at 2315 f  
Sbfl f at 2478 f  
HindIII at 2676 f  
BspEI at 2896 f

in the ram UTR

CCAGGGATTACGTACGCAAGGATCAGATTTACAG

### Primers for PLAP constructs

GACATTTCTCAGAAGCTTCAGGTTCAAGAGGAAT  
GTGCTGGGTACCTACAGTTTCTGGTTGAAC  
GGTCTGGATAAAGCTTCTTCAAGGACAAGAA  
GAAACTGGGTACCAGCTTCTCATAGCTTTTGGTC

### III-IV NKCC2 primers

GGCCTCGGGCCTAGGCCGAATGAAGCCAAACAC  
CTTGAACTGCAGGACCTGAGAAATG

### IV-V NKCC2 primers

CATTTCTCAGGTCCTGCAGGTTCAAGAGGAATTG  
GTGCTGGCTTCCACAAGCTTCTGGTTGAACTC

### V-VI NKCC2 primers

GTTCAACCAGAAGCTTGTGGAAGCCAGCACTC  
ATTTTATCCGGAATTGCTCAAAGAGAAGCC

BsiWi f

NKCC2 HindIII at 2470 f  
NKCC2 KpnI with stop at 2680r  
NKCC1 HindIII at 2783 f  
NKCC1 KpnI with stop at 3038 r

AvrII at 2315 f  
SbfI at 2471r

SbfI f at 2478 f  
HindIII at 2680 r

HindIII at 2676 f  
BspeEI at 2897r