TNXB MUTATIONS IS A CAUSE OF VESICOURETERAL REFLUX (VUR)

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SUPPLEMENTARY MATERIALS

SUPPLEMENTARY METHODS

Scratch wound healing assay

Fibroblast cell line was established by culturing skin biopsy samples in modified DMEM. Cells were seeded on collagen-1 coated plates and allowed to grow to confluence prior to scratch wound creation. Scratch wounds were applied using 1000 µL pipet tip. Fibroblasts were treated with platelet derived growth factor (PDGF) (Cell Signaling, Inc.; Beverly, MA) at a concentration of 50 ng/ml or vehicle prior to being returned to 37^oC growth conditions for incubation for 15 hours. Fibroblast wound healing images at 0 and 15 hours were obtained using an EVOS® microscope and wound healing was guantified in 4 experiments as the % wound closure.

Immunoblotting and reagents

Following treatment, human epidermal fibroblast cultures were washed with PBS. Cells were harvested in RIPA buffer (Cell Signaling Technologies, Boston, MA, USA). Cell lysates were subjected to SDS-polyacrylamide gel electrophoresis. Protein immunoblotting was performed using rabbit polyclonal anti-FAK antibody or rabbit polyclonal anti-phospho-FAK (Tyr 397) antibody, or rabbit polyclonal TNXB antibody (Proteintech, Inc; Chicago, IL). Immunolabeled proteins were detected using a chemiluminescence detection system (Pierce Biotechnology, Rockford, IL, USA) on Kodax BioMax film (VWR Scientific).

Immunohistochemical and Immunofluorescence staining of the UVJ junction

Paraffin embedded human tissue samples were obtained from the pathology department at the University of Iowa under approval of Institutional Board Review protocol # 200901770. Normal controls were obtained from autopsy specimens and

compared to specimens isolated from individuals with radiographically demonstrated reflux who underwent surgical re-implantation. Block samples were sectioned via microtome into 5-7 micron sections and affixed to microscopy slides. Immunohistochemistry and Immunofluorescence was performed on slide sections that had undergone heating to 55°C and allowed to cool to room temperature. Slides were cleared twice with xylene for 5 minutes. Slide samples were hydrated through a reducing ethanol bath series and rinsed with distilled water and PBS. Slides were then submerged in boiling citrate buffer (10 mM, Ph 6.0), allowed to cool for 1 minute, resubmerged and allowed to cool for 20 minutes to room temperature in antigen retrieval solution. A.) For Immunohistochemistry: Slides were rinsed with distilled water and endogenous peroxidase activity was blocked with 3% hydrogen peroxidase in PBS for 20 min. Slide sections were then rinsed with PBS and incubated with 5% normal goat serum/5% Bovine Serum Albumin for 1 hr at room temp. Avidin-Biotin activity was blocked using a kit: (Invitrogen, Avidin/Biotin Blocking Kit, Cat#: 00-4303) as described by the manufacturer. Slides were subsequently incubated with rabbit anti-tenascin-XB antibody (Proteintech, Inc; Chicago, IL), 1:50 diluted in 1% blocking solution) at 4°C overnight, rinsed in PBS and Incubated with Biotinylated Anti-Rabbit IgG 1:200 (Vector Lab, BA-1000), (7.5ug/ml) diluted in 2% NGS/ PBS 60min at RT and rinsed with PBS. Sections were incubated with VECTASTAIN Elite ABC Reagent per manufacturer's guidelines for 1 hr and rinsed with PBS. Antibody staining was revealed using the DAB Peroxidase Substrate Kit (Vector lab, SK-4100) per manufacturer's guidelines. Sections were rinsed with distilled water, dehydrated through an ethanol/xylene series, coverslipped and visualized under light microscopy. Images are captured using the image capture software in the Microscopy core at the University of Iowa. B.) For Immunofluorescence: slide sections were then rinsed with distilled water, PBS and incubated with 5% normal goat serum/5% Bovine Serum Albumin for 1 hr at room temp.

Slides were incubated with primary antibody (rabbit anti-tenascin-XB, 1:50 diluted in 1% blocking solution) at 4°C overnight, rinsed with PBS and incubated with Dilute Fluorescent 2nd antibody with 1% blocking solution (Alexa Fluor® goat anti-Rabbit 568 1:200) for 1.5 - 2hr at RT, covered from the light. Slides were rinsed with PBS and underwent aqueous mounting, with removal of any remaining buffer and application of 2-3 drops of VECTASHIELD® Mounting Medium (Catalog # H-1000) and coverslipped and allowed to dry for 20 minutes in the dark. Confocal images were obtained immediately using the equipment available in the University of Iowa Microscopy core.

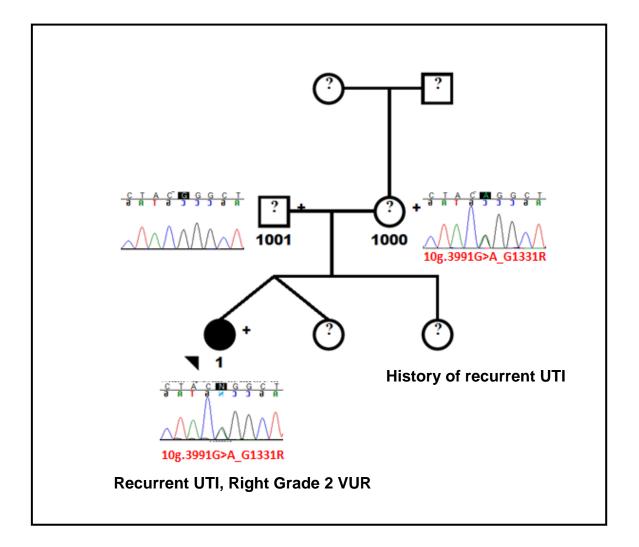


Figure S1: Pedigree of second family with G1331R mutation. Squares are males and circles are females. Filled shape denote affected individuals, shapes with question mark denote unknown phenotype. The proband (individual 1) has right grade 2 VUR, her mom (Individual 1000) never had VCUG done. The proband and her mom have the G1331R change.

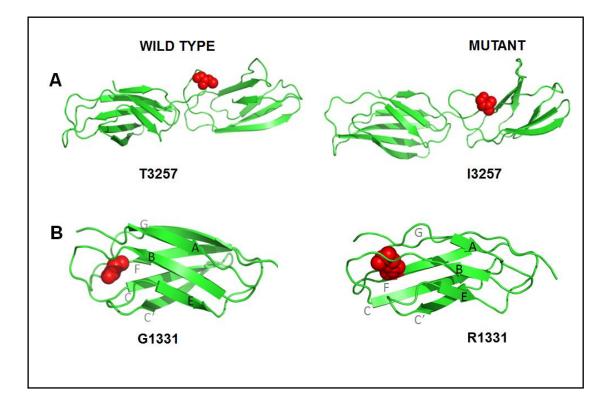


Figure S2: Location of TNXB mutations in three-dimensional models of the TNXB fibronectin Type III (FnIII) domains. (A) I-TASSER was used to model the structure of TNXB FnIII domains 23 and 24. Residue T3257 (in red) is predicted to reside in the linker between the two fibronectin domains, modeling the T3257I mutation results in some structural changes. (B) The structure of the 5th FnIII domain of human TNXB was predicted using the I-TASSER server for homology modeling. The beta strands are labeled as designated by Leahy et al. and residue G 1331 is shown as a space-filling model highlighted in red. Structural modeling of the 5th FnIII domain containing the G1331R mutation (again highlighted in red) resulted in, perturbation of the secondary structure of the protein.

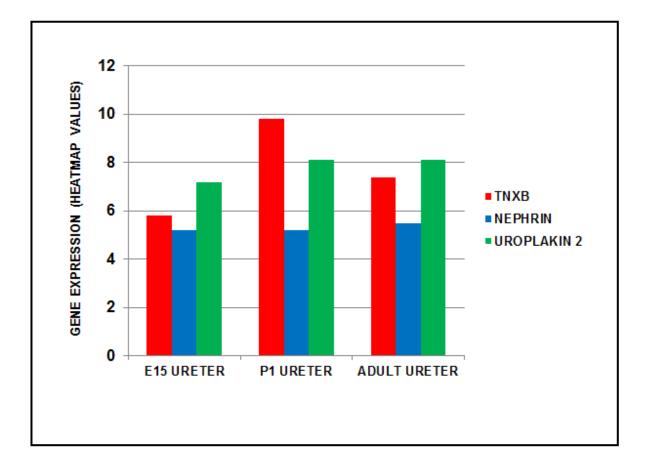


Figure S3: Microarray expression data for TNXB, nephrin and uroplakin II in mouse ureter. TNXB is expressed from E15 (Embryonic day 15) and is persistent post natally (P1: postnatal day1) and also in adult ureter, it is relatively more abundant than nephrin a key podocyte gene at every time point but similar to uroplakin II a gene that is enriched in the developing lower genitourinary tract. Relative expression of each gene in Heatmap value is derived from average of three different data set. Data is derived from the publicly available Genitourinary Molecular Anatomy Project (<u>www.gudmap.org</u>).

LOCI	MLOD SCORE IN FAMILY 6606
Chromosome 1p13	-9.7
SOX11 Chrom2	-8.3
ROBO2 Chrom3	-11.0
FRAS1/SPRY1 Chrom4	-9.1/-0.54
GDNF Chrom5	-10.0
CDC5L Chrom6p21	3.3*
TOP1MT/SOX17/Chrom8q24	-8.2/-1.1/-8.3
Chrom10q26	-16.3
EMX2	-15.6
PAX2	-16.4
RET	-14.8
NAT10 Chrom11	-11.8
Chromosome12p11	-9.1
FREM2 Chrom13	-8.9
ANGEL1 Chrom14	-4.5
HNF1B Chrom17	-14.7
USF2 Chrom19	-8.5
UPK3A	-12.4

Table S1: Exclusion of previously reported loci for VUR/CAKUT in family 6606

*Mutations in CDC5L was excluded in family 6606 by direct exon sequencing

Table S2: Primer sequences for TNXB

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TNN8-12F GGAGGATTAAAGGGGTCAAGG TNN8-12R GGTACACAGCGAACATCCATC TNN8-13F CAGGTGGACAAAGGGAAGAC TNN8-13R CCCCATTCCATTCATCCATC TNN8-13R CCCCATTCAGTCAATCAGGC TNN8-14R CCGGTGGACAAGGGAACAC TNN8-14R CCGGTGGACAAGGACAGGCAATATGGTAA TNN8-14R CCGGTGGCAATTATGGTAA TNN8-14R CCGGTGGCAAGGACAGGCAATATGGTAA TNN8-14R CCGGTGCAGGACAGGACAAGGACAGGAC TNN8-14F TTGCGATGCTGGCTGG TNN8-14F ACGGACGCGGGGGA TNN8-14F CCGTGCAGGGGGGA TNN8-14F CCGGTGCGGGGGGA TNN8-14F CCGGCGGGGGGA TNN8-14F CCGGTGCGGGGGGA TNN8-14F CCGGTGCGGGGGGA TNN8-14F CCGGTGCGGGGGGA TNN8-14F CCGGTGCGCTGGGGGGA TNN8-14F CCGGTGCGCGGGGGGA TNN8-14F CCGGTGCGCGGGGGGA TNN8-14F CCGGTGCGCGGGGGGA TNN8-14F CCGGTGCGCGGGGGGA TNN8-14F CCGGTGCGCGGGGGGA TNN8-14F CCGGTGCGCGGGGGGA <t< td=""><td></td><td></td></t<>		
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TNN8-13F CAGGTGGACAAGGGAAGAC TNN8-13F CCCCATCTACATGCTAA TNN8-14F CTGGGCCAATATGGTAA TNN8-14F CCAGTTCTGGGTAA TNN8-14F CCCAGTTCTGCTAA TNN8-14F CCCAGTTCTGCTAA TNN8-15F CCCAGTTCTGCTTCGCAGAAACAGC TNN8-15F CCCAGTTCTGCAGAAACAGC TNN8-15F CCCAGTTCTGCAGGAAGAGG TNN8-15F CCCAGTGCTGCAGGAGGGTGTA TNN8-15F CCCAGTGCTGCAGGAGGGTGTA TNN8-17R CTTTCAGATGGCTGGGGAGGGTGTA TNN8-18F CCAGTGCATGCGGGGGGGGTGTA TNN8-18F CCCAGTGCATGGGGGGGGTGA TNN8-18F CCCAGTGCAGGGGGGGTGA TNN8-18F CCCAGTGCAGGGGGGGTGA TNN8-18F CGTGCAGCAGGGGGGTGA TNN8-18F CGTGCAGCAGGGGGGTGA TNN8-18F CGTGCAGCAGGGGGTGA TNN8-18F CGTGCAGCAGGGGGTGA TNN8-18F CGTGCAGCAGGGGGTGA TNN8-18F CGTGCAGCAGGGGGTGA TNN8-20F CGTGCAGCAGGGGGTGA TNN8-20F CGTGCCACTGGGGGGGGGTGA TNN8-22F CGTGCAGCCAGGGGGGTGA <td></td> <td></td>		
TNN8-19R CCCCATCTCAGTTCAGTCAGC TNN8-14F CTGGGGCCANTATAGGTA TNN8-14F GCAGTTCTGGGTTTTCCAG TNN8-15F AMAGGGCACACAGAGGAACTT TNN8-15F CCCATCTGGGTTTTCCAG TNN8-15F CCCATCTTCCAGAACAGC TNN8-15F CCCATCTTCCAGAACAGC TNN8-16F TTCGAAGGCTTCCCTCCTC TNN8-16F TTCGAAGGCTTCCCTCCTC TNN8-16F CCCATCTTCCAGAACAGC TNN8-16F CCCATCTAGCTGCTGC TNN8-16F CCCATCTCCTCCTCC TNN8-16F CCCATCTAGCGGCTGGCTGC TNN8-16F CCCATCTAGCCCAGCAGAA TNN8-16F CCCATCTAGCCTGGCTGC TNN8-16F CCCATCAGCCCCAGCAGAA TNN8-16F CCCATCAGCCCCAGCAGAA TNN8-16F CCCATCAGCCCCAGCAGAA TNN8-16F CCCATCAGCCCCAGCAGAA TNN8-16F CCCATCAGCCCCAGCAGAA TNN8-16F CCCATCAGCCCAGCAGAA TNN8-16F CCCACCACCTCAGCAGAA TNN8-17F CCCACCACCTACAGCAGAA TNN8-28F CCCCACCACCTACAGCAGCAGGT TNN8-28F CCCGCACCTAGCAGCAGCAGCAGAA		
TNR8-14F CTGGGCCAATATGGTAA TNR8-14F CCACATTCTGCATTTTCCAG TNR8-15F AAAGGGCCCAAGGAACTT TNR8-15F AAAGGGCCACAGGAAACAGC TNR8-15F CCCACATTCTGCATCCTC TNR8-16F TTCTGAAGGCTGCTGCCTCG TNR8-16F TTCGAAGGCTGGGAAG TNR8-17F ACCAAAGGCAGGGGGGAG TNR8-17F ACCAAGGCTGGGCAGA TNR8-17F ACGAAGGCTGGGAGAG TNR8-17F ACGAAGGCCTGGGCTGA TNR8-17F AGGTGATCCTGGGCAGA TNR8-17F AGGTGAAGCCTGGGCTGA TNR8-18F AGGTGATCCTGGGCTGA TNR8-18F CCACGACCAGCGGGGAGG TNR8-28F GCACCAAGGGGAAGGGT TNR8-28F CCACGACCCTACGCACCC TNR8-28F ACCAAAGGCATCCCC TNR8-28F ACCAAAGGCAGAAGGGTAA TNR8-28F CCACGACCTACGCACCCACAGAGA TNR8-28F CCACGAGCCAGAGAGGGTA TNR8-28F CCACGAGCCTACGCACAGAGAGA TNR8-28F CCACGAGCACGCAGAGAGG TNR8-28F CCACGAGCACGAGAGAGG TNR8-28F CCACGAGCAGGAGAGGG		
TNR8-14R GCASTTCTGGGTTTTCCAG TNR8-15F MAGGGGCACAAGGAAACTT TNR8-16R CCCAGTCTTCCAGAAACGC TNR8-16R TTCTGAAGGCTTGCCTCC TNR8-16R TTCTGAAGGCTGCAGAGGCTGG TNR8-17F ACCAAAGACAGAGAGGGTGA TNR8-17F CCCAGTCGCCGCGGGGGGGGGGGGGGGGGGGGGGGGGGG		
TNNB-19F AAAGGGGCACAGGAAAGCTT TNNB-19F CCCARCTTCCCAGAAACAGC TNNB-16F TTCGAAGCCTTCCCTC TNNB-16F TTCGAATGCTTGCACTGCTTG TNNB-17F ACCAAAGAGCAGAGGGGGA TNNB-17F CCTTCGAGTGCTGGAGGGGGA TNNB-17F CCTTCGAGTGCTGGAGGGGGA TNNB-17F ACGAAGAGCCTGGGGGGGA TNNB-17F CCCAGTCATAGCCTGGAGGGGGA TNNB-17F ACGAAGAGCCTGGAGGGA TNNB-17F ACGAAGGCCTGGAGGGA TNNB-17F ACGAAGGCCTGGAGGGAA TNNB-18F CCCAGTCCTGGAGGGGAA TNNB-19F ACGAAGGCCTGCGAGA TNNB-21F CCCGCAGCTCCTCTGGAG TNNB-21R CCCGACGACTGAGGGAAAGGT TNNB-22R ACCAAAGGCAGGGGGAGA TNNB-22F ACCAAAGGCAGGGGGA TNNB-22F ACCAAAGGCAGGAGGGGA TNNB-22F ACCAAAGGCAGGAGGGGA TNNB-22F ACCAAAGGCAGGCGGAAGAG TNNB-22F ACCAAAGGCAGAGGGGA TNNB-22F ACCAAAGGCAGAGGGGA TNNB-22F ACCAAAGGCAGAGGGGAAAGC TNNB-22F CCCATGGAGACTGCAAGAGGGAAAGC		
TNR8-15R CCCAGTCTTCCAGAAAGC TNR8-16F TTCCAAGACCTTCTCCTCCT TNR8-17R ACCAAAGACGACAAGAGGGTGA TNR8-17R CTTCAAGTCGCTGGAGCCTGTA TNR8-17R CTTCAAGTCGCTGGAGGAC TNR8-17R CTTCAAGTCGCTGGAGGAC TNR8-17R CTTCAAGTCGCTGGAGGAC TNR8-17R CCCAACACCTCGGAGGAC TNR8-18R CCCAACACCTCCTGGAGCTTC TNR8-19F AGTCAACCCTGCGAGCA TNR8-19F CCCAACACACCACCAGCAGAC TNR8-20F CCCAACACACCCCTCCAAGCAGCAGCAC TNR8-21F CGCAACCACCCCATCCAAGCTGA TNR8-21F CGCAACCACCCCATCCAAGCTGA TNR8-21F CGCAACCACCCCATCAAGCTGA TNR8-21F CGCAACCACCCATCCAAGCTGA TNR8-21F CGCAACCACCCATCAAGCTGA TNR8-21F CGCAACCTACCCACTGAAGCTGA TNR8-22F ACGGAACTTGCTTTGTTGTA TNR8-24F CTTGGAAACGTGGCAAGAGA TNR8-24F CTGGAAACGTGCAAGAGCA TNR8-24F CTGGAAACGTGGCAAGAGA TNR8-24F CCACCAGTCAAGCACCACCC TNR8-24F CTGGAAACGTGGCAAGAGA TNR8-24F		
TNR8-16F TTCGAAGGCTTCCTC NR8-16R TTCGAATGCTCCTCC NR8-17F ACCAAAGAGCAAGACGCTGGAGAG NR8-17F CTCTCGACGGGGAGA NR8-17F AGGACATGCGTGGGGAGA NR8-18F AGGACATGCGGGGGGGA NR8-18F AGGCAAGCACGCTGCTC NR8-19F AGTGAAGGCACCAGGGGGA NR8-19F AGTGAAGGCACCAGGGGGA NR8-19F CCTCCAACACCTCCTTGCAG NR8-20F CCCCAGCACCAGCGGGGA NR8-20F CCACCCCATGAGGCAACCCCC NR8-20F CCACGCACTCAGAGCAAGTGC NR8-21F GGTACCCCTAGAGGAAGGTGA NR8-22F ACCCAAGAGCCCACACCC NR8-22F ACCCAAGAGCAGCAGACGCC NR8-22F ACCCAAGAGCAGCAGAGTGCC NR8-22F ACCCAAGAGCCCAAGCCC NR8-22F ACCAAGAGCCCAAGCAGCACCC NR8-22F ACCAAGAGCCCAAGCAGCGGGGGA NR8-22F ACCAAGAGCCCAAGCCC NR8-22F ACCAAGAGCCCAAGCCC NR8-22F ACCAAGAGCCCAAGCCC NR8-22F CCAGGCACCCCGCAAGCAGCA NR8-22F CCAGCAGCCCCAAGCCC NR8-22F CCAGCGCAAGCCCGAGGAGGGGA NR8-22F <td></td> <td></td>		
TNR-16R TTICGATTGCTGATCGTTG NNR-17F ACCAAGAGGCAGAGCAGAGGGTGA NNR-17R CTITCAGATGCTGGAGGCAGA NNR-17R CCAGTCATAGCCTTGGAGGCTA NNR-18R CCAGTCATAGCCTTGCGTGA TNNR-19F AGGAGTCGTGAGGCTGA NNR-19R CCCAGCACAGCAGAA NNR-19R CCTCAACACCTCCTGCGAG TNNR-19R CCTCAACACCTCCTGCGAG NNR-19R CCCAGAGCATCAGCGTGA TNNR-19R CCCAGGACGTAGCACAGCGTGA TNNR-19R CCCAGGACGTAGCACAGCGTGA TNNR-19R CCCAGGACGTAGCACACCTCC TNNR-22F GGTACCCUTCAGGGGAAAGGT TNNR-22F CCCAGGACGTAGCACAGCC TNNR-22F AGCGACGTTAGCCCCATCAGAGG TNNR-22F AGCGACGTAGCACAGCC TNNR-22F AGCGACGTGTGGTGA TNNR-22F AGCGACGTGTGGGCGTGA TNNR-22F AGCGACGTGGAGGGAA TNNR-22F CCTGGGACGGAGAAGCG TNNR-22F CTTGAGACCTGAGGAGAA TNNR-22F GTGAGACTGAGAGGGAAAGCG TNNR-22F GTGAGACTGAGAGAGAGGA TNNR-22F CCAGCACGTGAGAGAGAA TNNR-22F CCAGCACGTGAGAGAGAA TNNR-22F CCAGCACGTGAGGAGAAGCA TNNR-22F CCAGCACGTGAGGGAGAGAA TNNR-22F CCAGCACGTGAGGAGAGAAGCAGCA		
TNRB-17F ACCAAAGACCAACAGCGTGA TNRB-17F CTTCTCAGACGGTGGGAGA TNRB-18F AGGACATGCTGGAGAG TNRB-18F CCAGTCATAGCCTTGGCTTC TNRB-18F CCCATCATAGCCTTGGCTGAGA TNRB-19F AGTGAAGCCACAGCAGA TNRB-19F CCTCAAACACCTCCTTGCAG TNRB-20F ACCAAAGACCATCCAGCTTA TNRB-21F GGTACCCATGAGGCATACAGCTGA TNRB-21F GGTACCCATGAGGCAACTCC TNRB-22F ACCTAGAGCAACTTCGC TNRB-22F ACCTAGAGCAACTTCGCCCTTA TNRB-22F ACCCAAAGCACCTGAGCGCAACTCC TNRB-22F ACCCAAAGCACCTGACGCCATAGCAACC TNRB-22F ACCCAAAGCACCAAGCTGCCCTTA TNRB-22F ACCCAAAGCACCAAGCTGCCCTTA TNRB-22F ACCCAAAGCACCAAGCTGCCCTTA TNRB-22F ACCAAAGCACCTGCCTTA TNRB-22F ACCCAAAGCACCTGCCCTTA TNRB-22F ACCCAAGCCCTAGCGCGGGGA TNRB-22F CCATGGACCCAAGCCCTAGCCCTTA TNRB-22F CCATGCAAGCCCTAGCGCGGGAAGCACC TNRB-22F CCATGCAAGCCCTAGCGGGGAAGCACC TNRB-22F CCATGCAAGCCCCAAGCACCCCCCAAGCACCC		
TNRB-17RCTTTCAGATGCTGGAGAGTNRB-18FAGGAGATGCTGGAGAGCTGTATNRB-18RCCAGTCATAGCCTGGAGATNRB-19FAGTGAAGGCACCAGCAGAATNRB-19RCCTCAACACCTCTGCAGTNRB-20RGCACCAGCAGCAGCTGATNRB-21FGGTACCCATGAGGGTAATNRB-22RGCACCAGCAGCAGCTGATNRB-22RCCACCAGCATGAGGGTAATNRB-22RACCTAAGCCTCCATGAGGGTAATNRB-22RACCTAGAGCCCCATGAGGGTAATNRB-22FACCTAGAGCCCCATGAGGGTAATNRB-22FACCTAGAGCCCCATGAGGGTAATNRB-22FACCTAGAGCCCCATGAGGGTAATNRB-22FACCTAGAGCCCCATGAGGGTAATNRB-22FCAGGCACTTTGCCTTATNRB-22FCAGGCACTTTGCCCTATNRB-22FCAGGCACTTTGCCCTATNRB-22FCATGGAAGCGTGCAAAGGGTGAATNRB-22FCTTGAGAGCCCCACGCAGGAGAATNRB-22FCTTGAGAGACGTCCCACACACCCTNRB-22FCTTGCAGAGAGCCCAGGGGGGTNRB-22FCCAGCCCCAGGAGAGAATNRB-22FCCAGCACTGCCGAGGAGAATNRB-22FCCAGCACTGCCCAGGCAGGAGAATNRB-22FCCAGCACTGCCCAGGCAGGAGAATNRB-22FCCAGCCCCAGCACGCAGGAGAATNRB-22FCCAGCCCCAGCACGCAGGAGAATNRB-22FCCACCCCTGCTCCCCAAAAGGCCTNRB-22FCCAGCCCTGAGAACCCCAAATNRB-22FCCACCCCTGCTCCCCAAATNRB-22FCCACCCCCCCCAAGAACCCCAAATNRB-22FCCACCCCTGGCTCCCCAAAATNRB-22FCCACCCCTGGCTCCCCAAAATNRB-23FCCACCCCCCAAGAACCCCAAATNRB-23FCCACCCCTGGCTCCCCAAAATNRB-23FCCACCCCCCCAAGACCCCAAA <td></td> <td></td>		
TNR-18F AGGAGATGCTGGAGGCTGTA TNR-18F CCAGTACACCTTGCTTC TNR-19F AGTGAAGGCACACAGAA TNR-19F AGTGAAGGCACACACAGAA TNR-19F ACCAAAGGCACACACAGAA TNR-19F ACCAAAGGCACACACAGAA TNR-20F ACCAAAGGCACACACCTCAGACTGT TNR-20F GGTACCCATGAGGCACAGA TNR-21F GGTACCCATGAGGCACAGAGAGGT TNR-22F ACCAAAGCACACTCCC TNR-22F ACCAAGCCATAGGCACAGAGGGTGA TNR-22F ACCAAGCCATGAGCACCCC TNR-22F ACCAAGCCAGAGGGTGA TNR-22F ACCAAGCCAGAGGGTGA TNR-22F ACCAAGCCAGAGGGTGA TNR-22F ACCAAGCCAGAGCGGCAA TNR-22F ACCAAGCCAGAGCAGGGTGA TNR-22F ACCAAGCCAGAGGGTGA TNR-22F ACCAAGCCAGCAGGGTAA TNR-22F CATGGAACGTGCAAGGGGTGA TNR-22F CATGGAACGTGCAGAGGGGGAA TNR-22F CATGGAACGTGCAAGACGCA TNR-22F CCATGCCAGAGACGGGAA TNR-22F CCATGCTCACAGAGACGCAA TNR-22F CCACAGTCATTGCCCAAGAGCCAA <t< td=""><td></td><td></td></t<>		
TNB-19R CCAGTCATAGCCTIGGCTTC TNB-19F AATGAAGGCAACCAGCAGA TNB-19R CCCTCAACACCTCTGCAG TNB-20F ACCAACACCTCTGCAG TNB-21F GCACCAGCATCTGCAGCTGT TNB-22F ACCAACGCCCAGCATGCAGCTGT TNB-22F ACCAACGCCCCATCAAGACGTT TNB-22F ACCAACGCCCCCATCAAGAC TNB-22F ACCAACGCCCCCATCAAGAC TNB-22F ACCAACGCCCCCATCAAGAC TNB-22F ACCAACGCCCCATCAAGAC TNB-22F ACCAACGCCCCATCAAGAC TNB-22F ACCAACGCCCCATCAAGAC TNB-22F ACCAACGCCCCATCAAGAC TNB-22F ACCAACGCCCCCCTTA TNB-22F ACCAACGCCCCACCAAGAC TNB-22F CTGCAGCCCTGCGACCCACCC TNB-22F CTGCAGCCCCGCGACGAAGCGG TNB-22F CTGCAGCCCCGCAGCAAGCAC TNB-22F CCACCCACCCCCCCCCACGAGCAC TNB-22F CCACCGCCCCCCCACGAGCACC TNB-22F CCACCGCCCCCCCACGAGCACC TNB-22F CCACCGCCCCCCACGAGCACC TNB-22F CCACCGCCCCCCACGAGCACC TNB-22F CCACCGCCCCCCACGAGCACC TNB-22F CCACCGCCCCCCACGAGCACC		
TNBs-19F AGTGAAGGCACCAGCAGAA TNBs-19F ACTCAACACCTCCTTGCAG TNBs-20F ACCAACACCTCCTTGCAG TNBs-20F GCACCCAGCATCCAGACTGT TNBs-21F GGTACCCATGAGGGAAAGGT TNBs-21F CCACCAGCGTAAGCACTCC TNBs-22F ACTGTGAGCCCATCAGAGC TNBs-22F ACCTAACGAGGTAAGCACTCC TNBs-22F ACCAACGAGGTGGAAGCACTCC TNBs-22F ACCAACGAAGTGCCCTTA TNBs-23F ACCAACGAAGTGCCCTTA TNBs-24F CATGGAAACGAAGTGGCCATC TNBs-24F CATGGAACCTGCAAAGAGG TNBs-24F CATGGAAACGAAGTGCCCTTA TNBs-24F CATGGAAACGAAGTGCCAAGAGA TNBs-24F CATGGAAACGTGAGAAGACC TNBs-24F CATGGAAACGTGAGAAGACC TNBs-24F CATGGAAACGTGAGAAGACC TNBs-24F CCAGGAAACTGGAGAAGCCAA TNBs-24F CCAGCAGTCACAAGAGACCCAAC TNBs-24F CCAGCAGTCAACCCAAG TNBs-24F CCACCAGTCATACCCAAGA TNBs-24F CCACCAGTCAACCCAAC TNBs-24F CCACCAGTCAACCCAAC TNBs-24F CCACCAGTCAACCCAAC TNBs-24F CCACCAGTCACCCAAC TNBs-24F CCACCAGTCACCCAAC TNBs-24F CCACCAGTCAACCCAAC TNBs-24F CCACCAGTCAACCCAAC		
TNB-19RCCTCAACACCTCCTTGCAGTNB-92PACCAACAAGAGCAACAGGGTGATNB-20RGCACCAGCATCCAGACTGTTNB-21FGGTACCCATGAGCAAAGGCAAGCGTNB-21RCCACGACGTAAGCACATCCTNB-22FACCTGGACCCCCCTAGAGCTNB-23FACCAAAGACAGATGCCCTTATNB-23FACCAAAGACCAGTGCCCTTATNB-24RCGTGAACCCCCCTAGAGCTNB-24RCGTGAACCCCCCTAGAGCTNB-25FACCAAAGACAGAGGGTGATNB-24FCATGGAAAGCAGTGCAAAGAATNB-25FGTGCAACCCTGACCCCCCCCCCCCCCCCCCCCCCCCCCC		
TNB-20FACCAAAGAGCAGTGATNB-20RGCACCAGCATCCAGGATCAGAGAGGTTNB-21FGGTACCCATGAGGAAAGGTTNB-21FCCACGAGGTAAGCAGTCCTNB-21RCCACGAGGTAAGCAGTCCTNB-22FACTGTGAGCCCCATCAAGACTNB-23FACCAAGAGAGTGCCCTTATNB-24RCCATGGAAGCGTGCCATCAAGACTNB-24FCATGGAAACGTGCCAAGAAGAGGGTGATNB-25FGGGCACTTTGTTTTGTGATNB-28RGCGCACTTGTGTGAGCACAGTGCTNB-28RCCTGGAGACGTGCAAAGAGGGGGAATNB-28FCCATGGGCAGAGAGGGGGAATNB-28FCCAGCCTCTCAGCGAAGTGGCAAAGAGTNB-28FCCACAGTCCTCAGGCAAGTGGTNB-28FCCACAGTCGTAGCACAGCATNB-28FCCACAGTCGTAGCACAGCATNB-28FCCACAGTCGTAGCCAAGGCTNB-28FCCAGAGCTGGCGAGAACGCATNB-28FCCAGGCATGCCCAAGCCCAAGTNB-28FCCACGTCATCACCAAAGCCCAAGTNB-28FCCAGGTGCTGGCAGGCCCAAGACTNB-28FCCAGTCATCACCCAAGACCCAAGTNB-28FACAGGTGCCAAGCCCCAAGATNB-28FCCAGTGATGCCTGGCTTGCTNB-28FACAGGTGCCCAAGCACGCTTNB-28FACAGGTGCCCAAGGCTTNB-28FACAGGGTGCTGGGGGGGCTGCCAAGATNB-28FCCAGTGATGCCTGCCAAAGCCTTNB-28FACAGGGTGCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGG		
TNXB-20RGCACCAGCATCCAGACTCTTNXB-21FGCACCACCATCAGCAAAGCTTNXB-21RCCACCACCATAGCAAAGCATNXB-22FACTGTGAGCCCATCAAAGACTNXB-22FACGTGTGAGCCCATCAAAGACTNXB-22FACCCAAAGAGCAGGGTGATNXB-22FACCCAAAGAGCAGGGTGATNXB-22FACCCAAAGAGCAAGGCGTGATNXB-22FACCCAAAGAGCAAGGCGTGATNXB-22FCTGGAAACGTGCCAAAGACTNXB-22FCCCAAAGAGCAGGGTGATNXB-22FCCTGGAAGACGTGCAAAGAATNXB-22FCCTGGAAGACGTCCAAGAGCATNXB-22FCCTGGAAGACGTCCAAGGCAACACCTNXB-22FCCTGGAAGACGTCGAGGAACACCTNXB-22FCCTGGGGAAGCGGGAACACCTNXB-22FCCTGAGCCTCGGGGAGAACGCGATNXB-22FCCGACAGTCGGGAGAACGCCATNXB-22FCCGACAGTCGGAGAGCAGCATNXB-22FCCGACAGTCCCCGAGGAGATNXB-22FCCCACCAGTCATCACCCAAGATNXB-22FCCCCCTGTCTCGCAAGACCCAAGTNXB-22FCCCCCTGTCTCTGCGAGGACCACATNXB-22FCCCCGTCACGAGATCCAAATNXB-22FCCCGCTACTCCCCAAGGACTTNXB-29FAAGAGGTCCCAAGATCCAAATNXB-29FACAGCGCCCCCGCGAGGACTTNXB-29FGCCCGTAGGACTTNXB-30PGACGCCCCCGCTCAGGACTTNXB-31FTTGTCTTCGCACATCCCCCCTCGCATTNXB-32RGCCCAGCCCGGGAAGATCAAATNXB-32RGCCCAGCCCGGGAGATAAATNXB-33FCCCCCTGCTGTCCTCTCAATNXB-33FCCCCCTGCTGTCCCCTCTCCAATNXB-33FCCCCCTGCCTGCGCAAAGCCCCCCTCTCCTCAATNXB-33GFCCCCCCTGCGTGTCCCTCTCCAATNXB-33GFGCCCCCC		
TNXB-21F GGTACCCATAGAGGGAAAGGT TNXB-21R CCCACCATAGCACATCC TNXB-22F ACTGTGAGCCCATCAGAC TNXB-22F ACCAAAGAGCAAGTGCCCTTA TNXB-23F ACCAAAGAGCAAGGTGA TNXB-23F ACCAAAGAGCAAGGGTGA TNXB-23F CACGAACGCCAAAGAA TNXB-24F CATGGAAACGTGCAAAGAA TNXB-24F CATGGAAACGTGCAAAGAA TNXB-24F GTCACGTCCTCAGGACAACC TNXB-25F GTCACGTCCTCAGGACAACC TNXB-28F GCCACTGCGACGACGAC TNXB-28F CCACGTCCTCAAGGACACACA TNXB-28F CCACGTCCTCAAGGACACACA TNXB-28F CCACCACTCCTCAAGGACCAAG TNXB-28F CCACCACTCCTCAAGGACACACA TNXB-28F CCACCACTCACAAGACCCAAG TNXB-28F CCACCACTCACAAGACCCAAG TNXB-28F CCACCACTCACAAGACCCAAG TNXB-28F CCACCACTCACAGACCCAAGA TNXB-28F CCACGCTCACAGACTCCAAA TNXB-29F AGAGGGTCCCAAGATCCAAA TNXB-29F CCACCTCAGCACTCCAAGACT TNXB-29F CCACGCTAAGACCCAAGCT TNXB-29F CCACGCTAAGGCACACT TNXB-30F CCCCGCTAAGGAATCCCAAT		
TNRB-21RCCACGACGACTAGCACATCCTNRB-22FACTGTGAGCCCACACAGACTNRB-22FACCAAAGACGACATGCCCTAAGACTNRB-23FACCAAAGACGACATGCCCTTATNRB-23FACCAAAGACGACATGCCCTTATNRB-24FCATGGAAAGCGGCAACACCTNRB-24FCATGGAAACCTGCAAAGAGATNRB-24FCTTGAAGACCTGCGAGAGGAGTNRB-25FGTCAGTCCCCGAGGAGATNRB-26FCCGACGACTGCCGAGGAGATNRB-26FCCGACGACTGGGAGAGACCCAAGGTNRB-26FCCGACGACTGCGAGAGACCCAAGGTNRB-27FCCCCCCGTGCTCACCAAGACCCAAGGTNRB-28FCCTTCCTCACAAGACCCAAGGATNRB-28FCCCCCCCAGGACACCCCAAGGATNRB-28FCCCCCTTGCTCACCAAGACCCAAGGATNRB-28FCCCCCTTGCCCAAGATCCCAAGATNRB-28FCCCCCTTGCCCAAGATCCCAAGATNRB-28FCCCCCTTGCCCAAGATCCCAAGATNRB-28FCCCCCTTGCCCAAGATCCCAAGATNRB-28FCCCCCTTGCCAAGATCCCAAGATNRB-28FCCCCCTTGCCTGGACGACTTNRB-28FCCCCCTTGCCTGGACGACTTNRB-28FGCCCCCTAGCCTTGGAGGACTTNRB-28FGCCCCCCCTGGAGGACTTNRB-30FGCCCCCCCGAGAGCACACCCCTNRB-31FTTGTCTCCACCCCCAAGGCCACTTNRB-31FTTGTCTCCCCCCCCCAAGGCCACTTNRB-31FTGTCTCCCCCCCCCAAGGCCACTTNRB-32FGCCAAGCCTGAGAGCAAGACCACCCTNRB-33FCCCCCCCCTCAAGCCCCCCCCCAAGCCCCTNRB-33FCCCCCCCCCTCCCCCCCCAAGCCCCCCTTNRB-33FCCCCCCCCCTCTCTCTTNRB-33SRCCCCCCCCCCTCCCCCCCCCCCCCCCCCCCCCCCCCC		
TNRB-22FACTGTGAGCCCATCAAGACTNRB-22RACGCAAGACCCATCACAGACTNRB-23FACCAAAGACCATCCCCTTATNRB-23FACCAAAGAGCAAGAGGGTGATNRB-23FCATGGAAACGTGCCAAAGAATNRB-24FCATGGAAACGTGCAAAGAATNRB-24FCATGGAAACGTGCAAAGAATNRB-23FGTCAGTCCTCAGGCAACTCCTNRB-23FGTCAGTCCTCAGGCACATCCTNRB-23FGTCAGTCCTCAGGCACATCGTNRB-25FCCAACACTGGCAGACAGCACACCTNRB-26FCCAACACTGGCAGACAGCACACACTNRB-26FCCCTCCTCACAAGACCCAAAGATNRB-27FCCCCCCTCTCTCCCCACAGACCCAAAGATNRB-28RCCCGCTAGTCATCACCAAAGATNRB-28RCCCGCTAGGCCTGGCTTCTNRB-29RCCCGCTAAGAACTGCGCACTTTNRB-29RGCCCGCTAAGAACTGCCCACATCTNRB-30FGACGGCACTCACTTCCGCCTCTNRB-31FTTGTCTCACGCCCAGAGCCAAAGCTNRB-32RGCCAAGCCCAAGGCCAAGCTNRB-32FGCCCAGCTGGAGGCACCTNRB-33FCCCCCCTGGGTGCTGCAGAGACCTNRB-33FCCCCCGTGGAGGCACCTNRB-33FCCCCCGTGGAGGCACCTNRB-33FCCCCCGTGGAGGTAAAAATNRB-33FCCCCCGTGGGTGCCTTCGTCATNRB-33FCCCCCGTGGGTGCTTCCGCACTNRB-33FCCCCGTGGGTGCTTCCGCACTNRB-33FCCCCGTGGGGTGTGTAAAAATNRB-33FCCCCGTGGGGGGTGAATNRB-33FCCCCGTGGGGGTGTGAAAAAATNRB-33FCCCCGTGGGGGTGTGAAAAAATNRB-33FCCCCGTGGGGGGTGAAATNRB-33FCCCCGTGGGGGGTGAAAAAAAAAAAAAAAAAAAAAAAAA		
TNRB-22RAGCAAAGCAGTTGCCCTTATNRB-23FACCAAAGAGCAGTGGATNRB-23FGGGCACTTTGTGTTTTGTGATNRB-23RCATGGAAACGTGCAAAGAGAGTGATNRB-24FCATGGAAACGTGCAAAGAGAGAAGAAGAATNRB-24RCTTGAAGACCTGAGACACTCCTNRB-25FGTCACTCCTGAGCACATCCTNRB-25FGTCACTCCAGGAAAGTGGTNRB-26FCGAAGACTGCGCAGGAGAGAGAGAAGAAGAAGAATNRB-26RCCATCCTCACACAGACCCAAGACCAAGATNRB-27FCCACCGTCATCACCAAAGACTCCAAGACTNRB-28FAGGAGGTGCCAAGAGCCCAAGACTNRB-28FCCACGTCATCACCAAGACCCAAGATNRB-28FAGGAGGTGCCAAGAGCCCAAGACTNRB-28FAGGAGGTGCCAAGAGCCCAAGACCTNRB-29FATCACTGGCCTGAGCACCCAAGACCTNRB-29FATCACTGGGCCCTGAGGACTTNRB-29FATCACTGGGCCCAGGACGCCTNRB-30RGCCGCTTTCGCCAAGAGCCCAGATCTNRB-30PGGAGGACCTCACATTTCGGCAGTTNRB-30PGGCAGCCCAGGAAGCTCTNRB-31FTTGCTCTAGCCCAAGGAGCGCTNRB-31RCTCGGTACCACCACGAGAGGCTNRB-32FGGCAGCCTAGCAAGCAGCACACACACACACACACACACAC		
INXB-23RGGCACTTIGTGTTTTGTGAINXB-24FCATGGAAAGGTGCAAAAGAAINXB-24FCITGAAGACCTGACACATCCINXB-25FGTCAGTCCTCAGGGAAGTGGINXB-25FAACAAAAGATGGCAGAGACAGCAINXB-25RAACAAAAGATGGCAAGACAGAAINXB-26FCGAAGACTGGAAGACAGCAINXB-27FCCACCAGTCATCACCAAGACCCAAGAINXB-27FCCACCAGTCATCACCAAGACCCAAGAINXB-28FAAGAGGTGCCAAGATCCAAAAINXB-28FAAGAGGTGCCAAGATCCAAAINXB-28FAAGAGGTGCCAAGATCCAAAINXB-28FACCGCTAGCCAAGATCCAAAINXB-28FCCACTCATCACCAAGATCCCAAAINXB-29FATCAGTGGCTGAGGAGCTINXB-30FGGCGCTAAGAAATGCTCACTINXB-30RATGCAGCCCCAGGAAGCTCINXB-31FTTGCTCACCCAGGAAGCTCINXB-32FGGCAGACTAAAGCCINXB-33RCTCGATCACACGCAGGAAGCTINXB-33FCCCCGTGAAGAAGACCACTINXB-33FCCCCCGTGAAGACAGACAINXB-33FCCCCCGTGAAGCACACTCACTINXB-33FCCCCCCTCGACGAAGCCINXB-33FCCCCCCTCTCCTCTCAAINXB-33FCCCCCCTCGAAGACACACACCINXB-33FCCCCCCTCTCCTCAAINXB-33FCCCCCCTCCTCCTCAAINXB-33FCCACCCGTGTGCTCTCTCAAINXB-33FCCCCCCTCCTCCCCACAINXB-33FCCCCCCCTCCTCCAACACACCCINXB-33SCCCCCCTCTTCCAAINXB-34.35FCCCCCCCCCCCCCCCCCCACAINXB-338CAGCCGCATGAGCAGACACACACACCINXB-34.35FCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC		
INXB-23RGGGCACTTGTGTTTTGTGAINXB-24FCATGGAAAGCTGACAAGAAINXB-24FCTTGAAGACCTGAGCAAGACAINXB-25FGTCAGTCCTCAGGGAAGTGGINXB-25RAACAAAAGATGGCGAGGAGAINXB-26FCGAAGACTGGAGAAGACACAINXB-26RCCTTCCTCACAGAGACCAAGACCCAGACACTINXB-28RCCACCCAGCCAGGCCCGAGGACCTINXB-29FATCAGTGGCGCGAGGGCCCAGACTINXB-29RGCCCCTAAGAAAGCCCCACTINXB-30RGAGGGACCCACTTCGGCTGAGGACTINXB-30RGCAGGCCCAGGAAGCCCINXB-31FTTGCTCACCCCAAATGCINXB-32FGGCCAGCCCAGCAAGCCINXB-33RCCCCAGCTAAGCCCACGAGACCCINXB-33FCCCCCGTGAAGACACAGCCINXB-33FCCCCCCTCTCCTCTCAINXB-33FCCCCCCTCCTCCTCCACAINXB-33FCCCCCCCTCGAAGACCACCINXB-33FCCCCCCCTCCTCCTCCACACCINXB-33FCCCCCCCTCCTCCTCCACACCINXB-33SCAAGCGGGAGCACACCINXB-34, 35FCCCCCCCTCCTCCCCCAGACCACCINXB-34, 35FCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	TNXB-23F	ACCAAAGAGCAAGAGGGTGA
TNXB-24RCTTGAAGACCTGAGCACATCCTNXB-25FGTCAGTCCTCAGGGAGGGGTNXB-25RAACAAAGATGCGAGGAGATNXB-26FCGAAGACTGGAGAGACAGCATNXB-26RCCTTCCTACACAAGACCCAAGTNXB-27FCCACCAGTCATCACAAGAGATNXB-28FGTCCTGTTGTGGGCACTTTTNXB-28FAAGAGGTGCCAAGAACAGCATNXB-28FCCATCATAGCGTGCTGAGGAACTTNXB-28FCCACTCATAGCCTTGGGCACTTCTNXB-28FCCAGTCATAGCCTTGGGTGCTGAGGACTTNXB-29FATCAGTGGGTGCTGAGGACTTNXB-30FGAGGGACTCACTTCCGCTTCTNXB-30RATAGCAGCCCAGGAAGCTCTNXB-31RTTGCTCAGCCCAAGGACTTNXB-32FGCCAGGCCTAGGAAGCTCTNXB-31RCTCGATCACAGCGGGAGGTNXB-32FGCCAGGCCTAGGAAGCCTNXB-33FCCCCCTGGAAGAACACCTNXB-33FCCCCCTGGAAGTACAAAGACCTNXB-33FCCCCCTGGAAGTACAAGACCTNXB-33FCCCCCTGGAAGTACAAGACCTNXB-33FCCCCCTGGAAGTACAAGACCTNXB-33FCCCCCTGGAAGTACAAGACCTNXB-33FCCCCCTGGTGTCTTGCTNXB-33FCCCCCTGTGACTCATTNXB-33FCCCCCTGTGACTCATTNXB-33FCCCCCTGTGAGTACAAGACCTNXB-34.35FCCCTCCTCTTCAATNXB-338ATGCGAAAGCAGGAGGGGTNXB-34.35FGCCACGCCTGTGGTGTGTGTNXB-338,37FGCAGGCACTCCATTNXB-34.35FGTCGCAAAGCAGGAGGAGGGGTNXB-34.35FGTCGCGCTGTGTGGTGGTGTGTTNXB-33,39FATGCCCAAAGCAGGAGGGGGGAATNXB-34.35FGTCGCGCCTCTTCAATNXB-34.35FGCCCCCCTCTTCCCCTNXB-	TNXB-23R	GGGCACTTTGTGTTTTGTGA
TNX8-25FGTCAGTCCTCAGGGAAGTGGTNX8-26FCGAAGACTGGCGAGGAGATNX8-26FCGAAGACTGGCGAGCACACATNX8-26FCCCTCCTCACAAGACCCAAGATNX8-27FCCCACCAGTCATCACAAGACCCAAGATNX8-27RGTCCTGTTCTTGGGCACTTTTNX8-28FAGAGGTGCCAAGATCCAAAATNX8-28FCCAGTCATCACAAGACCCAAGATNX8-28FCCAGTCATAGCCTTGGCTTCTNX8-28FCCAGTCATAGCCTTGGCTTCTNX8-28RCCCGTAGGGTGCTGAGGACTTNX8-29FATCCAGTGGGTGCTGAGGACTTNX8-29FGCCGCTAAGAATGCTCACTTNX8-30FGCAGGCCCAGGAAGCCCTNX8-30FGCGGATCCCAAGGCCCTNX8-31FTTGTCTCAGCCCAAGGCCTNX8-31FTTGTCTCAGCCCAAGGCCCCTNX8-32FGGCGAAGCTCACTTTCAGCCCAAGCCTNX8-33FCCCCGTGAAGGACGCCTNX8-33FCCCCGTGAAGTACAAGACCTNX8-34.35FCCCCGTGAAGTACAAGACCTNX8-34.35FCCCCCTCCGGTGAGCTCTGTCTNX8-34.35FCCCCTCTCGTTCTCTCCAATNX8-34.35FCCCCTCCCGTGAAGCACGAGGAGTNX8-34.35FCCCCTCCCGTGAAGCGCACTTNX8-34.35FCCCCTCCCGTCCTCTCTCAATNX8-34.35FACGGAAACGAGGAGGGGTGAATNX8-38.37FAGGGAAACGAGGAGGGGTGAATNX8-38.37FGCAGGCTCTGTGCTNX8-38.37FCCAGCGCCAGGGGTGAATNX8-38.38RATGTCGCAAAGCAGGAGGGGTGAATNX8-38.39FATGTCGCACACTTCACTNX8-34.35FCCCCCCTCTCTCTCTNX8-44FCAGGGCCTGGGGACTACTNX8-44FAAGGGCCTGGCGGACTAC	TNXB-24F	CATGGAAACGTGCAAAAGAA
TNXB-25RAACAAAAGATGGCGAGGAGATNXB-26FCGAAGACTGGAGAGACAGCATNXB-26RCCTTCCTCACAAGACCCAAGTNXB-27FCCACCAGTCATCACCAAGAGATNXB-27FGTCCTGTTCTGGGCACTTTTNXB-28FAAGAGGTGCCAAGACCCAAATNXB-28FAAGAGGTGCCAAGACCTGGCTTCTNXB-29FATCAGTGGGTGCTAGGGACTTNXB-29RGCCGCTAAGAAATGCTCACATTNXB-30FGAGGACTCACTTCGGGAGTTTNXB-30RATGAGCCCAAGGAGGCTTNXB-31FTTGTCTTCAGCACCAAGAGCCTNXB-32FGGCCAAGCCCAAGGAGGCTNXB-31FTTGTCTTCAGCAGCAAGGGAGTNXB-32FGGCCAAGCCTAGCAGGAGGAGTNXB-33RCCCAGCCTGGAAGAAAATNXB-33RCCCCGTGGAAGTAAAAATNXB-33RCCCCCGTGGAAGTAAAAATNXB-33RCCCCCCTCGTCTCTCTCAATNXB-34, 35FCCCCCCTCGTCTCTCTCTCAATNXB-34, 35FCCCCCCTCCTCTTCTCTCAATNXB-34, 35FCCAAGCCTGCAGCTTCGTTNXB-36, 37FAGGAAACCAGGAAGGAGGGGGGAAGATNXB-38, 39FATGCGCAAAGCAGGAGGGGGGAATNXB-38, 39FATGCGCCAAGCAGGAGGGGGGAATNXB-38, 39FATGTCGCCAAGCACGACGTCACTNXB-38, 39FATGTCGCCAAGCACGAGGGGGGAAGATNXB-38, 39FATGTCGCCAAGCACGAGGGGGGGAAGATNXB-38, 39FATGTCGCCACTTCTCCCCTNXB-34, 35FCCCCCCCCTCTGGGGGGTGGATNXB-34, 39FCTAGGGTCTGTGGGGGTGGAATNXB-34, 39FATGTCGCCAAGCACGAGGAGGGGGAAGATNXB-34, 39FCTAGGGTCTGTGGGGGTGGATNXB-34, 39FCTAGGGTCTGTGGGGGTGGAATNXB-34, 39FCTAGGGCCCTGCCCTTCTCCCTNXB-34, 39F	TNXB-24R	CTTGAAGACCTGAGCACATCC
TNXB-26FCGAAGACTGGAGACAGCATNXB-27FCCACCAGTCATCACCAAGATNXB-27FCCACCAGTCATCACCAAGATNXB-27FCCACCAGTCATCACCAAAGATNXB-28FACAGGGTGCCAAGAGTCCAAATNXB-28FCCAGTCATAGCCTTGGCTTCTNXB-29RCCCAGTCATAGCCTTGGCACTTNXB-30FGCCGCTAAGAATCCTCACTTNXB-31FTTGCTTCACGCCAAGAGCCTNXB-32FGCCCAGCCAAGAGCCTNXB-30RATAGCAGGCCAGGGACTTNXB-31FTTGCTTCACCCCAAATGCTNXB-32FGGCAGCCAGAGCCCAAGGCAAGCCCTNXB-33FCCCGCTAGAAAAGGCCACTTNXB-32FGGCAAGCCTAGAGGCCAAGGCAAGCCCTNXB-31FTTGCTTCACCCCAGAGGAAGCTNXB-32FGGCCAGCGCAAGAGCCAAGGCAAGCCCTNXB-33FCCAGCCTGGAAGTACAAGACCCTNXB-33RCCAGCCTGGTTCTCTCCCTNXB-33RCCAGCCTGGTTCTCTCCCTNXB-34.35FCCCCCTCCTCGTTCCTCCCAATNXB-34.35FCCAGCCTGGTGCTCTCTCCTNXB-34.35FCCAGCCTGCTCGTCCCCCTNXB-34.35FCCAGCCGGAGGAGAGTNXB-34.35FCCAGCCTGCTCCTCCCAATNXB-34.35FCCAGCCTGCTCCTCCCAATNXB-34.35FCCAGCCTGCCGTTCTCTCCTNXB-36.377AGGGAAACCAGGAGAGAGAGTNXB-38.397GAGAAACCAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGA		
TNXB-26RCCTTCCTCACAAGACCCAAGTNXB-27FCCACCAGTCATCACCAAGATNXB-27RGTCCTGTTCTGGCCATTTTNXB-28FAAGAGGTGCCAAGATCCAAATNXB-29FATCAGTGGGCCGCGAGGACTTNXB-29FATCAGTGGGCCGCGAGGACTTNXB-30RGAGGGACTCACTTTCGGAGTTTNXB-31FTTGTCTTCAGCCAAGATCCAATGCTNXB-32FGGCAGCGCAAGAATGCCCTNXB-31FTTGTCTTCAGCCAAGAGCCTCTNXB-32FGGCAGGCCTAAGAAATGCTCTNXB-31FTTGTCTTCAGCCCAAGAGCCTCTNXB-33FCCCCGTGAAGGAGGAGGTNXB-33FCCCCGTGAAGGATAAAATNXB-33FCCCCCGTGAAGACCCTNXB-33SFCCCCCCGTGAGGATCAAAAATNXB-34.35FCCCCCCCTGATCTCTCTCAATNXB-36.37FAGGGAAAGCAGGAAGGGGAGTNXB-38.39FATGTCGCAAAACCGGTGAATNXB-38.39FATGTCGCAAAACCGGTGAGTNXB-38.39FATGTCGCAAAACCGGTGGTGTTNXB-38.39FATGTCGCAAAACCGTTGACTNXB-38.39FATGTCGCAAAACCGTTGAGCTNXB-38.39FATGTCGCAAAACCGTTGAGCATNXB-38.39FATGTCGCAAAACCGTTGAGCATNXB-38.39FATGTCGCAAAACCGTTGAGCATNXB-38.39FATGTCGCAAAACCGTTGAGCATNXB-38.39FATGTCGCAAAACCGTTGAGCATNXB-42.43FCTGTTCACCTTTCACCTNXB-42.43FCTGTTCACCTGGGGACTACTNXB-44FAAGGACCTGGCTGTGCTCTCT		
TNXB-27FCCACCAGTCATCACCAAAGATNXB-27RGTCCTGTTCTTGGGCACTTTTNXB-28FAAGAGTGCCAAGATCCCAAATNXB-28FATCAGTGGGTGCTGGCGCAGGATCCAAATNXB-29RGCCGCTAAGAATGCTCACTTNXB-30FGAGGGACTCACTTTCGGAGTTTNXB-30FTTGCTCTCAGCCAAAATGCCTNXB-31FTTGCTCTCAGCCAAATGCTNXB-32FGGCAGAGGCCAGGGAGGTNXB-31FTTGCTTCTCGCCAAATGCTNXB-32FGGCAGAGCTCAATGCTNXB-31FTTGCTCTCGGCAAATGCTNXB-32FGGCAGAGCTAAAGGCCACTTNXB-33FCCCGGTAGAGGCACTTNXB-33FCCCCGTGGAGGTAAAGGCCACTTNXB-33FCCCCGTGGAAGTACAAAGACCTNXB-33FCCACGCGTGTGCTCTGTCTNXB-33FCCACCGTGTGCTCTGTCTNXB-33SFCCACCCGTGTGCTCCTCTAATNXB-33.3FATCTGCAGAGCAGGAAGGAGTNXB-36.37FAGGAAACGAGGAAGGAGGAGTNXB-38.39FATGTCGCAAAACAGGGGAGTNXB-38.39FATGTCGCAAAACACGTCAGTNXB-38.39FATGTCGCAAAACACGTCAGTNXB-38.39FATGTCGCAAAACACGTCAGTNXB-38.39FATGTCGCAAAACACGTCAGTNXB-38.39FATGTCGCAAAACACGTCAGTNXB-38.39FATGTCGCAAAACACGTCAGTNXB-38.39FATGTCGCAAAACACGTCAGTNXB-38.39FATGTCGCAAAACACGTCAGTNXB-38.39FATGTCGCAAAACACGTCAGTNXB-42.43FCCTGTTACACTTTCACCTNXB-42.43FCACAGGGACTGGGGACTACTNXB-42.43RCACAGGGACTGCGCTTTCCTTNXB-42.44FAAGGACCCTGGCTCTTCCT		
TNXB-27RGTCCTGTTCTTGGCACTTTTNXB-28FAAGAGGTGCCAAGATCCAAATNXB-28RCCAGTCATAGCTTGGCTTCTNXB-29FATCAGTGGGTGCTGAGGACTTNXB-29RGCCCCAGCAAAGCCTTNXB-30FGAGGACTCACTTTCGGAGTTTNXB-30FGAGGACTCACTTTCGGAGTTTNXB-30FGAGGACTCACTTTCGGAGTTTNXB-31RCTCGATCACGCAGGAGGCTNXB-32FGGCCAGGAGCCACGCAGAAGCCCTNXB-32FGGCCAGGCTGGAAGGCCACTTNXB-33FCCCCGTGAAGCTCAGACGCCACCTNXB-33FCCCCGTGAAGCTCACACCTNXB-33FCCCCCTGGAAGCTCAGACCACCTNXB-33FCCCCCTGGAAGCTCAGACCACCTNXB-33FCCCCCTGTCTCTCTCTCAATNXB-34.35FCCCCCTCGTTCTCTCCTAATNXB-36.37FAGGGAAAGCAGGAAGGAGGAGTNXB-36.37FAGGGAAAGCAGGAAGGAGAGAGAAGAAGACCTNXB-38.39FATCTGCCAAAACACCTTCATTNXB-38.39FATCTGCGCAAACACGTCAGATNXB-38.39RGTAGGGTCTTGTGGGGTGTTTNXB-38.39FATCTGCCAAAACACCTTCAGATNXB-38.39FATCTGCCAAAACACCTTCAGATNXB-34.35FCTCGCCAAAACACCTTCAGATNXB-38.39FATCTGCGAAAACACCTCCATTNXB-38.39FATCTGCGCAAACACCTTCAGATNXB-38.39FATCTGCGCAAAACACCCTTCAGATNXB-38.39FATCTGCCAAAACACCTTCAGATNXB-34.35FCTCGCCCTCTTCACCTNXB-34.35FCTCGCCCTCTTCACCTNXB-38.39FATCTGCGCAAACACCTTCAGATNXB-38.39FATCTGCCAAAACACCTTCAGATNXB-38.39FATCTGCGCAAACACCCTTCACCTNXB-42.43FCCCGCCTCTTCACCTNXB-42.43FCACAGGGACTACC<		
TNXB-28FAAGAGGTGCCAAGATCCAAATNXB-28RCCAGTCATAGCCTTGCTTCTNXB-29FATCAGTGGGTGCTGAGGACTTNXB-30FGCCGCTAAGAAATGCTCACTTNXB-30FGAGGGACTCACTTTCGGAGTTTNXB-30RATAGCAGCCCAGGAAGCTCTNXB-31FTTGTCTTCAGCCCAAATGCTNXB-31RCTCGATCACAGGAGGCAGTNXB-32RGGCAAGCCTGGAAGAAAAAATNXB-33RCCCCGTGAAGACACAGCCTNXB-33RCCCCTGTGAAGACAAAGACCTNXB-33AFCCCCTCCTTCTCTCTCAATNXB-34.35FCCCTCCGTTCTCTCTCAATNXB-34.35FCCCTCCGTTCTCTCTCAATNXB-337FGGGAAGCAGGAGAGAGAAAATNXB-33.37FGGGAAGCAGGAGAGAGAAAATNXB-38.37FGGGAAGCAGGAGAGAAAAATNXB-38.39FATGTCGCAAACACGTTCAGTNXB-38.39FGAGGAACCAGGAAGGAAAATNXB-38.39FATGTCGCAAAACACGTTCAGTNXB-38.39FATGTCGCAAAACACGTTCAGTNXB-38.39FATGTCGCAAAACACGTTCAGTNXB-38.39FATGTCGCAAAACACGTTCAGTNXB-38.39FATGTCGCAAAACACGTTCAGTNXB-38.39FATGTCGCAAAACACGTTCAGTNXB-38.39FATGTCGCAAAACACGTTCAGTNXB-42.43FCGTGTCACCCTCTTCAATNXB-42.43FCTGTTACACCGGGGTGAATNXB-42.43FAAGGCCCTGGCTGATNXB-42.44FAAGGACCTGCTCTCTCT		
TNXB-28RCCAGTCATAGCCTTGGCTTCTNXB-29FATCAGTGGTGCTGAGGACTTNXB-29RGCCGCTAAGAAATGCTCACTTNXB-30FGAGGGACTCACTTTCGGAGTTTNXB-30RATAGCAGCCCAGGAAGCTCTNXB-31RTTGTCTCAGCCCAATGCTNXB-31RCTCGATCACACGCAGGAAGTNXB-32FGGCAGAGCTAAAGACCTNXB-32RCCCCGTGAAGTAAAAATNXB-33RCCCCGTGGAAGTAAAAATNXB-33RCCCCGTGGAAGTAAAAATNXB-33RCCCCGTGGAGTACAAAGACCTNXB-33RCCCCTCCTCTTCTCCAATNXB-34.35FCCCCTCCTCGTTCTCTCCAATNXB-34.35FCCCCTCCCTCGTTCTCTCCAATNXB-34.35RATCTGCAGAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAG		
TNXB-29FATCAGTGGGTGCTGAGGACTTNXB-29RGCCGCTAAGAAATGCTCACTTNXB-30FGAGGGACTCACTTTCGGAGGTTTNXB-30RATAGCAGCCCAGGAAGCTCTNXB-31FTTGTCTTCAGCCCAAGAGGGAGTNXB-31RCTCGATCACAGCAGGGAAGTNXB-32FGGCAGACCTAAAGGCCACTTNXB-33RCCCCGTGAAGTACAAGAGCCTNXB-33RCCCCGTGAAGTACAAGAGCCTNXB-33RCCCCCTCGTGTCTCTCTCTTNXB-34.35FCCCCCCCTCGTTCCTCTCAATNXB-36.37FAGGAAAGCAGGAAGAGGAGTNXB-36.37RGAGAGACGGAAGGAGGAGTNXB-36.37RGAGAGACGGAAGGGGGGGAGTNXB-38.39FATGTCGCAAAACCGGTGAATNXB-38.39FATGTCGCAAAACCGGTGAATNXB-38.39FATGTCGCAAAACCGGTGAATNXB-38.39FATGTCGCAAAACCAGGTAGCAATNXB-38.39FATGTCGCAAAACCAGGTCAGTNXB-38.39FCTAGGTCTGTGGGGTGGATNXB-38.39FCTAGGCTCGTGGGGTGGATNXB-38.39FCTAGGGTCGTGGGGAGACTCAGTNXB-38.39FCTAGGGTCGTGGGGAAACAACACGTTCAGTNXB-34.44FAAGACCCTGGGGCTGATNXB-44.44FAAGACCCTGGCCTCTCCT		
TNXB-30RGCCGCTAAGAAATGCTCACTTNXB-30FGAGGGACTCACTTTCGGGAGTTTNXB-30RATAGCAGCCCAGGAAGCTCTNXB-31FTTGTCTCAGCCCAAATGCTNXB-31RCTCGATCACAGCAGGGAAGTNXB-32RGCCAAGCCTGAAATACACTNXB-33FCCCCGTGAAGTACAAAGACCTNXB-33RCAAGCTGGTGTGCTTCTGTCTNXB-33FCCCCCGTGAAGTACAAAGACCTNXB-34.35FCCCCTCCTCGTTCTCTCTCAATNXB-34.35FCCCTCCTCGTTCTCTCTCAATNXB-34.35FCCCTCCTCGTTCTCTCCATTNXB-34.35FCCCTCCTCGTTCTCTCAATNXB-34.35FCCCTCCTCGTTCTCTCAATNXB-36.37FAGGAAAGCAGGAGGAGTNXB-36.37FGAGGAAACCAGGAGGAGATNXB-38.39FATCTGCCAAAACCAGTTCAGTNXB-38.39FATGTGCCAAAACCAGTTCAGTNXB-38.39FGTAGGGTCTGTGGGGTGTTNXB-30.41FACGCGCATGGAGTAGTCACTNXB-40.41FCGTGTCCACCTCTTTCACCTNXB-40.41FCGTGTCCACCTCTTTCACCTNXB-42.43FCTGTTACACTGTGGGGCTGATNXB-44FAAGGACCCTGGCGTACC		
TNXB-30FGAGGGACTCACTTTCGGAGTTTNXB-30RATAGCAGCCCAGGAAGCTCTNXB-31FTTGTCTTCAGCCAAATGCTNXB-31RCTCGATCACAGCAGGGAAGTNXB-32FGGCAGAGCTAAAGGCCACTTNXB-32RGCCAACCCTGGAAGATAAAATNXB-33FCCCCGTGAAGTACAAAGACCTNXB-34.35FCCCCCGTGAAGTACAAAGACCTNXB-34.35FCCCCCCTCCTCGTTCTCTCTCAATNXB-34.35FCCCCCCTCCTCGTTCTCTCTCAATNXB-36.37FAGGGAAAGCAGGAGGAGGAGTNXB-36.37FGGGAAAGCAGGAGGGGGGAATNXB-38.39FATCTGCCAAAACCGGTCAGTNXB-38.39FATGTCGCAAAACCAGGGAGGGGGAATNXB-36.37RGAGGGACTCCATTNXB-36.37RGTAGGCTCTGTGGGGTGTTNXB-38.39FATGTCGCCAAAACCAGTCAGTNXB-38.39FCTAGGCTCTGTGGGGGTGAATNXB-38.39FCTAGGGTCTGTGGGGGTGAATNXB-38.39FGTAGGGTCTGTGGGGGTGTTNXB-34.41FCCGTGTCCACCTCTTTCACCTNXB-42.43FCACAGGGACTGGGGGAATNXB-444FAAGGACCCTGGCTCTCTCT		
TNXB-30RATAGCAGCCCAGGAAGCTCTNXB-31FTTGTCTTCAGCCCAAATGCTNXB-31RCTCGATCACAGCAGGAAGTNXB-32FGGCAGACTAAAGGCCACTTNXB-32RGCCAAGCCTGGAAGATAAAATNXB-33RCCCCGTGAAGATACAAAGACCTNXB-33RCCAGCTGGTGTGCTTCTGTCTNXB-34.35FCCCCCCTCGTTCTCTCTCAATNXB-34.35FCCCCCCCCGAAGAAGAGAGAGAGAGAGAGAGAGAGAGAG		
TNXB-31FTTGTCTTCAGCCCAAATGCTNXB-31RCTCGATCACAGCAGGGAAGTNXB-31RGGCAGAGCTAAAGGCCACTTNXB-32FGGCAAGCCTGGAAGATAAAATNXB-32RGCCAAGCCTGGAAGATAAAATNXB-33FCCCCGTGAAGTACAAAGACCTNXB-33RCAAGCTGGTGTGCTTCTGTCTNXB-34.35FCCCTCCTCGTTCTCTCAATNXB-34.35FCCCTCCTCGTTCTCCATTNXB-34.35FATCTGCAGAGCAGAGAGAGGAGTNXB-36.37FAGGGAAAGCAGGAGGGGGAATNXB-36.37RGAAGAGAAGCAGGAGGGGGAATNXB-38.39FATGTCGCAAAACACGTTCAGTNXB-38.39FGTAGGGTCTGTGGGGGTGTTNXB-38.39FATGTCGCAAAACACGTTCAGTNXB-38.39FGTAGGGTCTGTGGGGGTGTATNXB-40.41FACGCGCATGGAGTAGTCACTNXB-40.41FCGTGTCCACCTCTTTCACCTNXB-42.43FCTGTTACACTGTGGGGCTGATNXB-42.43FCACAGGGACTGGGGAACTACTNXB-444FAAGGCCCTGGCTCTTCTCT		
TNXB-31RCTCGATCACAGCAGGGAAGTNXB-32FGGCAGACCTAAGGCCACTTNXB-32RGCCAAGCCTGGAAGTAAAATNXB-33FCCCCGTGAAGTACAAAGACCTNXB-33RCAAGCTGGTGTGCTTCTGTCTNXB-34.35FCCCCTCCTCGTTCTCTCCAATNXB-34.35FCCCCTCCTCGTTCTCTCCATTNXB-34.35RATCTGCAGAGCGACTTCCATTNXB-36.37FAGGGAAAGCAGGAGGGGGGAATNXB-36.37FGAGGAAACCAGGAGGGGGGGAATNXB-38.39FATGTGCGCAAAACCAGTTCAGTNXB-38.39FGTAGGGTCTGTGGGGGTGTTNXB-38.39RGTAGGGTCTGTGGGGGGTGAATNXB-30.41FACGCGCATGGAGTAGTCACTNXB-40.41FCGTGTCCACCTCTTTCACCTNXB-42.43FCTGTTACACTGTGGGGGAATNXB-42.43FCACAGGGACTGGGGAACTACTNXB-44FAAGGACCCTGGCTTCTCT		
TNXB-32FGGCAGAGCTAAAGGCCACTTNXB-32RGCCAAGCCTGGAAGATAAAATNXB-32RGCCAAGCCTGGAAGATAAAATNXB-33FCCCCGTGAAGTACAAAGACCTNXB-33RCAAGCTGGTGTCTTCTGTCTNXB-34.35FCCCCCTCCGTGTTCTCTCCAATNXB-34.35RATCTGCAGAGCGACTTCCATTNXB-34.35RATCTGCAGAGCGAGCGGAGAGAGGGGAGTNXB-36.37FGAGGAAAGCAGGAGGAGGAGAGAGGGAGTNXB-36.37FGAGAGAACGAGGAGGGGGGAATNXB-38.39FATGTCGCAAAACCAGTCAGTNXB-38.39FGTAGGTCTGTGGGGTGTTTNXB-30.41FACGCGCATGGAGTAGTCACTNXB-40.41FCGTGTCCACCTCTTTCACCTNXB-42.43FCTGTTTACACTGTGGGGCTGATNXB-42.43FCACAGGGACTGGGGAACTACTNXB-44FAAGGACCCTGGCTCTCTCT		
TNXB-32RGCCAAGCCTGGAAGATAAAATNXB-33FCCCCGTGAAGTACAAAGACCTNXB-33FCCACGTGGTGTCTTCTGTCTNXB-34.35FCCCTCCTGTTCTCTCCAATNXB-34.35FCCCTCCCGTTCCTCCAATNXB-34.35RATCTGCAGAGGCGACTTCCATTNXB-36.37FAGGAAAGCAGGAGGGGGAGATNXB-36.37RGAGAGACGAGGAGGGGAATNXB-38.39FATGTCCCAAAACACGTCAGTNXB-38.39RGTAGGGTCTGTGGGGTGTGTTNXB-38.39RGTAGGGTCTGTGGGGTGGTTNXB-38.39RGTAGGGTCTGTGGGGTGGTTNXB-40.41FACGCCATGGAGTAGTCACTNXB-40.41RCGTGTCCACCTCTTTCACCTNXB-42.43FCTGTTACACTGTGGGGCTGATNXB-42.44FAAGGACCCTGGGGACTAGC		
TNXB-33FCCCCGTGAAGTACAAAGACCTNXB-33RCAAGCTGGTGTGCTTCTGTCTNXB-34.35FCCCTCCTGTTCTCTCAATNXB-34.35RATCTGCAGAGCGACTTCCATTNXB-36.37FAGGGAAAGCAGGAAGAGGAGTNXB-36.37RGAGAGAACGAGGAGGGTGAATNXB-38.39FATGTCGCAAAACACGTTCAGTNXB-38.39RGTAGGGTCTGTGGGGGTGTTTNXB-40.41FACGCGCATGGAGTAGTCACTNXB-40.41RCGTGTCCACCTCTTTCACCTNXB-42.43FCTGTTACACTGTGGGGCTGATNXB-42.43FCACAGGGACTGGGGGAATNXB-444FAAGACCCTGGCTCTTCCT		
TNXB-33.RCAAGCTGGTGTGCTTCTGTCTNXB-34.35FCCCTCCTGTTCTCTCTCAATNXB-34.35RATCTGCAGAGCGACTTCCATTNXB-36.37FAGGGAAAGCAGGAGGAGGGGGATNXB-36.37RGAGGAAACCAGGAGGGGGGAATNXB-38.39FATGTGCGAAAACCACTTCAGTNXB-38.39RGTAGGGTCTGTGGGGGTGTTNXB-30.41FACGCGATGGAGTAGTCACTNXB-40.41FCGTGTCCACCTCTTTCACCTNXB-42.43FCTGTTCACCGGGGGAATNXB-42.43FCACAGGGACTGGGGGAATNXB-42.44FAAGACCCTGCGCTTCTC		
TNXB-34.35F CCCTCCTGTTCTCTCTCAA TNXB-34.35R ATCTGCAGAGCGACTTCCAT TNXB-36.37F AGGAAAAGCAGGAGGGGGAA TNXB-36.37R GAGAGAAGGAGGAGGGTGAA TNXB-38.39F ATGTCGCAAAACCAGTCAG TNXB-38.39F ATGTCGCAAAACCAGTCAG TNXB-38.39F GTAGGTCTGTGGGGTGTGT TNXB-30.41F ACGCGCATGGAGTAGTCAC TNXB-40.41R CGTGTCCACCTCTTTCACC TNXB-42.43F CTGTTACACTGTGGGGCTGA TNXB-42.43R CACAGGGACTGGGGCTAC TNXB-42.44F AAGGACCCTGGCTCTCTCT		
TNXB-34.35RATCTGCAGAGCGACTTCCATTNXB-36.37FAGGGAAAGCAGGAGGAGGAGTNXB-36.37RGAAGAACGAGGAGGGGGAATNXB-38.39FATGTCGCAAAACACGTTCAGTNXB-38.39RGTAGGCTCTGTGGGGTGTGTTNXB-40.41FACGCGCATGGAGTAGTCACTNXB-40.41RCGTGTCCACCTCTTCACCTNXB-42.43FCTGTTACACTGTGGGGCTGATNXB-42.43FCACGGGACTGGGGGACTACTNXB-42.44FAAGGCCCTGGCGACTAC		
TNXB-36.37F AGGGAAAGCAGGAAGAGGAG TNXB-36.37R GAGAGAACAGGAGGAGGGTGAA TNXB-38.39F ATGTCGCAAAACACGTTCAG TNXB-38.39R GTAGGGTCTGTGGGGGTGTGT TNXB-40.41F ACGCGCATGGAGTAGTCAC TNXB-40.41F CGTGTCCACCTCTTTCACC TNXB-40.41R CGGTGTCGTGGGGGTGA TNXB-42.43F CTGTTACACTGTGGGGCTGA TNXB-42.43F CACAGGGCTACGGGGAACTAC TNXB-44F AAGACCCTGGCTCTTCTCT		
TNXB-36.37R GAGAGAACGAGGAGGGTGAA TNXB-38.39F ATGTCGCAAAACACGTTCAG TNXB-38.39R GTAGGGTCTGTGGGGTGT TNXB-40.41F ACGCGCATGGAGTAGTCAC TNXB-40.41F CGTGTCCACCTCTTTCACC TNXB-40.41F CGTGTCCACCTCTTTCACC TNXB-42.43F CTGTTACACTGTGGGGCTGA TNXB-42.43R CACAGGGACTGGGGGAACTAC TNXB-44F AAGGACCCTGGCTTCTCT		
TNXB-38.39F ATGTCGCAAAACACGTTCAG TNXB-38.39R GTAGGGTCTGTGGGGTGTGT TNXB-40.41F ACGCGCATGGAGTAGTCAC TNXB-40.41R CGTGTCCACCTCTTCACC TNXB-42.43F CTGTTACACTGTGGGGCTGA TNXB-42.43F CACAGGACTGGGGCTAC TNXB-42.43F CACAGGGACTACTCAC TNXB-42.43F CACAGGGACTAC TNXB-42.43F CACAGGGACTAC TNXB-42.43F CACAGGGACTAC TNXB-44F AAGGACCCTGGCTCTTCTCT		GAGAGAACGAGGAGGGTGAA
TNXB-38.39R GTAGGGTCTGTGGGGTGTGT TNXB-40.41F ACGCGCATGGAGTAGTCAC TNXB-40.41R CGTGTCCACCTCTTCACC TNXB-42.43F CTGTTACACTGTGGGGCTGA TNXB-42.43R CACAGGACTAGGGGAACTAC TNXB-44F AAGGACCCTGGCTCTTCTCT		
TNXB-40.41F ACGCGCATGGAGTAGTCAC TNXB-40.41R CGTGTCCACCTCTTTCACC TNXB-42.43F CTGTTACACTGTGGGGGCTGA TNXB-42.43R CACAGGGACTGGGGGAACTAC TNXB-44F AAGGACCCTGGCTCTTCTCT		
TNXB-40.41R CGTGTCCACCTCTTTCACC TNXB-42.43F CTGTTACACTGTGGGGCTGA TNXB-42.43R CACAGGGACTGGGGGAACTAC TNXB-44F AAGGACCCTGGCTTCTCT		
TNXB-42.43F CTGTTACACTGTGGGGCTGA TNXB-42.43R CACAGGGACTGGGGAACTAC TNXB-44F AAGGACCCTGGCTCTTCTCT		
TNXB-44F AAGGACCCTGGCTCTTCTCT		
TNXB-44R CAGAGGGAGCTGGAGTTGAT		
	TNXB-44R	CAGAGGGAGCTGGAGTTGAT

Table S3: Known and n	new TNXB variants in	patients with VUR
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RS number	Exon/Intron	Nucleotide	Amino Acid Change
rs41270461	3	607G>A	V203M
rs1150752	3	904A>G	T302A
rs204896	3	1532G>A	R511H
rs41270458	3	1734C>T	None
rs17201602	3	1949G>A	R650H
rs204900	6	2761T>G	S921A
rs185819	9	3482A>G	H1161R
rs12211410	10	3764G>A	R1255H
rs61735731	10	4010G>A	R1337H
New	14	5155G>A	V1719M
rs17207923	16	5713G>A	E1905K
rs3749962	17	6030C>T	None
rs1150756	18	6288G>A	None
rs9469081	18	6379G>A	V2127M
rs150379644	Intron 18	(+)8A>T	None
rs9469080	Intron 18	(+)11T>C	None
rs204883	19	6696C>T	None
rs2239689	Intron 20	(-)24C>T	None
rs204885	Intron 20	(+)5G>A	None
rs204886	21	7251A>G	None
rs204887	21	7440T>C	None
rs1150757	21	74612C	None
rs2269429	21	7483G>A	G2495S
rs1009382	22	7553G>T	G2518V
rs12196385	22	7680C>T	None
rs2066982	22	7790G>A	R2597Q
rs369637	22	7797G>A	None
rs440160	24	8192C>G	P2731R
rs17207895	26	9050A>G	K3017R
rs41258944	28	9562G>A	V3188I
rs61740331	28	9672G>A	None
rs61740337	28	9699T>C	None
rs142041833	32	10723T>C	S3575P
rs12208609	32	1072312C	None
rs141851943	32	107820>1	None
rs374698	33	11142G>A	None
rs2856449	33	11088T>A	None
New	33	1184G>A	None
rs397948	Intron 35	(-)45T>C	None
rs143318192	Intron 35	(-)451>C (-)9A>G	None
rs2894232	35		None
rs2395085	35	114121>C	Q3806R
rs75024733	36	11547A>G	None
rs78089407	36	11548C>A	Q3850K
rs28361049	36	11616G>A	None
	36		V3877I
rs28361048		11629G>A	
rs2734313	Intron 36	(+)10G>C 11921A>C	None N3974T
rs1135809	38		
rs7742632	<u>39</u> 39	11962C>A	L3988I M4004T
rs10456399		12011T>C	
rs113312810	40	12156C>G	None
rs114988582	40	12170A>T	N4057I
rs4959086	40	12180C>G	C4060W
rs4959085	40	(+)5C>T	None
rs6457477	41	12224G>A	R4075H
rs4959084	43	12520G>A	D4174N
rs4959083	43	12530G>A	S4177N