TBC1D8B mutations implicate RAB11-dependent vesicular trafficking in the pathogenesis of nephrotic syndrome. Kampf et al.

Supplemental Information

- Supplemental Figure 1. Additional information concerning patients with mutations of *TBC1D8B*.
- Supplemental Figure 2. TBC1D8B does not co-localize with RAB11 but affects RAB11 function.
- Supplemental Figure 3. Localization of TBC1D8B protein in cultured cell lines and secretory GFP upon CRISPR/Cas-mediated loss of TBC1D8B.
- Supplemental Figure 4. TBC1D8B and nephrin trafficking.
- Supplemental Figure 5. Tb1d8b and Rab11 in Drosophila.
- Supplemental Table 1: Primer sequences



Supplemental Figure 1. Additional information concerning patients with mutations of TBC1D8B.

(A) Renal histology (Periodic acid Periodic acid-Schiff's base staining) of patient B931_21 with the Thr780Ser mutation of *TBC1D8B* shows segmental glomerulosclerosis. Shown are Sanger chromatograms of the respective regions of *TBC1D8B* in which the individual mutation of each of the five families is located.

(B) Shown are Sanger chromatograms of the respective regions of *TBC1D8B* in which the mutation T780S of family B931 is located for each of the family members. The mutation segregates according to the disease state. The mother (B931_12) is confirmed as conductor for the mutation. Consistent with this, a marginally elevated protein excretion (150 mg/die) is documented for individual B931_12.

(C-G) Respective pedigrees of the families with mutations of *TBC1D8B* and nephrotic syndrome. All pedigrees are compatible with an an X-linked inheritance, but parental DNA was not available for families from (D-G), the parental mutational status thus is unknown in this families.



Supplemental Figure 2. TBC1D8B does not co-localize with RAB11 but affects RAB11 function.

(A-A") Overexpressed wild type murine Tbc1d8b carrying an N-terminal mCherry tag localizes to the cytosol in podocytes. Co-localization with endogenous RAB11 is not observed while endogenous RAB11 seems reduced in transfected cells.

(B-B") Overexpressed Myc-tagged human TBC1D8B does not show colocalization with GFP-RAB11^{constitutively active} in podocytes.

(C) Immunoblotting reveals reduction of endogenous TBC1D8B but increase of LC3B as indicator of autophagy. GAPDH serves as loading control.

(D) Schematic showing the secretory form of GFP that is generated by introducing the signal peptide of IFNA2 into the N-terminus. The signal peptide directs GFP towards the secretory pathway while being subject to cleavage during the process. Endogenous RAB11 promotes GFP exocytosis. If TBC1D8B is a RAB11-GAP, loss of endogenous TBC1D8B will disinhibit endogenous RAB11 which in turn increases GFP secretion.

(E) Western blot shows increased delivery of GFP to the supernatant (above) upon expression of RAB11A^{constitutively} active and CRISPR/Cas9-mediated silencing of *TBC1D8B* in HEK293T for gRNA 1 but not gRNA 2. The amount of inctracellular GFP (lysates) remains constant.

(F) Quantitation of densities from (L) confirms a significant increase of the GFP secretion for one gRNA directed against *TBC1D8B*. Density results are expressed a ratio of GFP signal in the supernatant to GFP within the lysates (N=3, p<0.05).



Supplemental Figure 3. Localization of TBC1D8B protein in cultured cell lines and secretory GFP upon CRISPR/Cas-mediated loss of *TBC1D8B*.

(A) CRISPR/Cas9 mediated silencing of TBC1D8B in human podocytes is marked by coexpression of GFP (inset). Loss-of-function does not affect the signal from *rabbit* anti-TBC1D8B antibody.

(B) CRISPR/Cas9 mediated silencing of TBC1D8B in human podocytes is marked by coexpression of GFP (inset). Loss-of-function does not affect the signal from *mouse* anti-TBC1D8B antibody.

(C) CRISPR/Cas9 mediated silencing of TBC1D8B in HEK293T cells is marked by coexpression of GFP (inset). Lossof-function does not affect the signal from *rabbit* anti-TBC1D8B antibody.

(D-I) Overexpressed wild type murine Tbc1d8b carrying an N-terminal GFP-tag localizes to the cytosol in cultured podocytes (D) and HEK293T cells (I). Mutant Tbc1d8b with indicated mutations does not show any overt mislocalization in podocytes (E-H).



Supplemental Figure 4. TBC1D8B and nephrin trafficking.

(A) Upon overexpression in HEK293T cells and co-IP, GFP-tagged murine Tbc1d8b precipitates with Myc-tagged nephrin.

(B) Upon overexpression in HEK293T cells and co-IP, the GFP-tagged intracellular domain of nephrin (ICD, aa1084-1241) precipitates with Myc-tagged TBC1D8B.

(C) Overexpressed GFP-nephrin and Myc-TBC1D8B (human) co-localize in HEK293T cells in vesicles.

(D) Overexpressed GFP-Tbc1d8b and Myc-nephrin co-localize in MDCK cells in subapical vesicles.

(E) MDCK cells transfected with the nephrin cDNA construct described in (Figure 3G) lacks basolateral delivery with and without co-expression of Tbc1d8b.

(F) Quantitation of results from (E) confirms low signal for basolateral delivery. The minimal basolateral protein is not affected by co-expression of GFP or Tbc1d8b constructs. Shown is the fluorescence intensity from the extracellular HA-staining in ratio to total nephrin (mCherry).



Supplemental Figure 5. Tb1d8b and Rab11 in Drosophila.

(A-A") Equatorial cross section of a garland cell nephrocyte expressing *Tbc1d8b-RNAi* co-stained for the nephrin ortholog Sns (green) and the KIRREL/NEPH1 ortholog Kirre(red). Slit diaphragm proteins localize at the cell periphery in a fine line that shows gaps, corresponding to localized loss of slit diaphragm proteins from the surface. Insets show a membrane detail from another cell showing a solitary linear protrusion of slit diaphragm protein from the membrane. Scale bar represents 5 µm throughout the figure.

(B)Surface section from garland cell nephrocyte expressing *Tbc1d8b-RNAi* reveals gaps in the fingerprint-like staining pattern.

(C-C") Equatorial and surface section (inset) from garland cell nephrocytes where expression of *Rab11*-RNAi is suppressed by GAL80^{ts} at a non-permissive temperature of 22 °C shows a regular staining pattern of the slit diaphragm proteins.

NPH5 full length human Forward S-ATGGCCCTGGGGACGACG NPH5 full length human Forward S-CTACCCCAGTATTGCCCTCAGCT NPH5 full call point Forward S-CTACCCAGAGACACCCTCCTCTG NPH5 full call point Forward S-CTACCCAGTAGACACCCTCCTGTG NPH5 full call point Forward S-CTACGCAGACACACCCTCGTGGGTCCATCCAGTTGGCTGAGCCCGAGGA Tbc18bb mouse Forward S-CTACGTATAGACACCCTGGGTCCTATCCACTTGGTTCTAGACCTTAG Tbc18bb Hanouse (1) Forward S-CATGGTGAGCGGCGGCCCCCCTGGGTCGTCATCACCCTAGGCCTAGGC Tbc18bb Hanouse (2) Forward S-CATCGTCATAGGCAGCGTGCACCCCGTGGGTGAACCCCGAGGA Tbc18bb Hanouse (2) Forward S-CATCGTCATAGGCAGCGGCTGCACCCG Tbc18bb Hanouse (2) Forward S-CATCGTCATAGGAGGGTGCACCCG Tbc18bb Hanouse (2) Forward S-CATCGTCATAGCAGGGTGCACCG Tbc18bb Hanouse (2) Forward S-CATCGTCATAGCAGGGTGGACCCG Tbc18bb Hanouse hot softer Forward	Construct	direction	Primer sequence
NPH51-LDB all length human Percess 9-CTTGGCGCGGAGACTCA NPH51-LDB all Sel start Invavad 5-CTTGGCGCGGAGACTCA NPH51-LDB all Sel start Invavad 5-CTTGGCGCGGGAGACTCA NPH51-LDB all Sel start Invavad 5-CTTGGCAGGGAGACTCA Tbc1dBb mouse Invavad 5-CCAGGTTCACCAGGGGAGACTCA Tbc1dBb-Max Invavad 5-CCAGGTAGACCCCGATGTGGCTCACCCTGTTGCCTTAGACCTTAG Tbc1dBb-Max Invavad 5-CCAGGGTAGACCCTCACTTGGCTCALCTGGGTGGAGCCCGAGGA Tbc1dBb-Max Invavad 5-CATGGTAGAGCCTCACTTGGCCTGAGCCCGAGGA Tbc1dBb-Max Invavad 5-CATGGTAGAGCCTCACTTGGCCTGAGCCCGAGGA Tbc1dBb-Max Invavad 5-GTTGGTAGAGCTGCAGTGGCTGAGCCCGAGGA Tbc1dBb-Max Invavad 5-GTTGGTAGAGCTGCAGGTGAACTTCGCCATGGCTGCACCTGGCACTGGGCGCATTAGCGCATGGGCGCATTAGAGCTGGCGTCATTAGAGCAGCGGCTCACC Tbc1dBb (D.m.) pCFD4 Invavad 5-GTTGGTAGAGCAGGGTCCACC Tbc1dBb-Max Invavad 5-GTAGAAAAAGCGGGTCTCACC RAB11 A Invavad 5-GTAGAAAAAGCGGGTCTCACC RAB11 A A Invavad 5-GTAGCAAAAAGCGGGTCTCACC RAB11 A A Invavad 5-GTAGAAAAAGCGGGTCTCACC	NPHS1 full length human	forward	5'-ATGGCCCTGGGGACGACG
NPR54:CDa a1064 start Forward S-CTCIGGCAGCGGCAACCTCA NPR57:CDa a1160 start forward S-CCAGGATTACACAGCTCCTCTGT NPR57:CDa a1160 start forward S-CCAGGATTACACAGCTCCTCTGTG NPR57:CDa a1160 start forward S-CCAGGATTACACAGTCGGCTCCTATCCCATGTGGCCCGAGGA Tbc188b mouse inward S-CTTGTGTACAGCAGCGCTCACCCATCTGGCTCAGCCCGAGGA Tbc188b Mouse (1) inward S-CATGGTGAACCGCGCCTCTCTGGCTCTGGCTCAGCCCGAGGA Tbc188b Mouse (2) inward S-CATGGTGAAGCGCGGCTCCCCC Tbc188b Mouse (2) inward S-CATCGTCATAGCGGGTGAACTCGCCCCCGGAGGA Tbc188b Manuse (2) inward S-CTTGTCAAGCAGGGGTCACCC Tbc188b Manuse (2) inward S-CTTGTCAAGCAGGGTGGACCTGGGTCATCTCCCATGGCCACGGGGGGAACTTCGCCCATGGCCACGCGGGGGGGG	NPHS1 full length human	reverse	5'-CTACACCAGATGTCCCCTCAGCT
WPB51: CD at 169 step SecTAGAATAAGAACCTCCTCCTCTG WPB51: CD at 169 step forward S-CAGAGTTCACAGGTGAAGTG Tbe188 mouse forward S-CATAGAAAAACGTGGGTCTCACCATGTGGCTGAAGCCCGAGGA Tbe188 mouse forward S-CATGTGAAAAAACGTGGGTCTCATCACATGTGGCTGAAGCCCGAGGA Tbe188-Manuae (1) forward S-CATGGTAAACCTGGCTTCACCATGTGGCTGAAGCCCGAGGA Tbe188-Manuae (2) forward S-CATGGTAAAGCCTGCTTTTTGTAC Tbe188-Manuae (2) forward S-CATGGTAAAGAAGAGCTGGGTCT Tbc188-Manuae (2) forward S-CATGGTAAAGAAAGCTGGGTCT Tbc188-Manuae (2) forward S-CTTGTAAAAAAGCAGGTCT Tbc188-Manuae (2) forward S-CTTGTAAAAAACCTGGGTCT Tbc188-Manuae (2) forward S-CTTGTAAAAAACCTGGGTCT Tbc188-Manuae (2) forward S-CTTGTG	NPHS1-ICD aa 1084 start	forward	5'-CTCTGGCAGCGGAGACTCA
WPM5-LCD as 1160 start Svavad 5-CCA3GTTTCACAGTGAGAGAG DEctdBb mouse reverse 5-CTTTGTCAAGACCAGCTGGGTCCTATCACATCTTGGTTCTAAGCCTTAG DEctdBb-Mause (1) reverse 5-CATGGTGAAGACCAGCTGGGTCCTATCACATCTTGGTTCTAAGCCTTAG DEctdBb-Mause (1) reverse 5-CATGGTGAAGCCTGGGTCACCATGTGGGTCAAGCCCGAGCAG DEctdBb-Mause (2) reverse 5-GATGGTCATAGGCAGCGGTCACCC DEctdBb-Mause (2) reverse 5-GATGGTCATAGGCAGCGGGTCACCC TBC1DBb-Mause hort softorm reverse 5-GATGGTCATAGGCAGCGGGTCACCC TBC1DBb-Mause hort softorm reverse 5-GATGGTCATAGGCAGGGTGCACCC TBC1DBb-Mause hort softorm reverse 5-GATGGTCATAGGCAGGGTGCACCC TBC1DBb-Mause hort softorm reverse 5-GATGGTCATAGGCAGGGTGCACCC TBC1DBb-Mause hort softorm reverse 5-GATGGTCATAGGCAGGGGTCACCC TBC1DBb-Mause hort softorm reverse 5-GATGGTCATAGGCGGGTGGGTCATTCGCATGTCCCCATGGGGCGCATGGGCGCCATGGCGGCGCGGGCGG	NPHS1- ICD aa 1160 stop	reverse	5'-CTAGGAATAAGACACCTCCTCCTG
The fells mouse Inverse 6:	NPHS1- ICD aa 1160 start	forward	5'-CGAGGTTTCACAGGTGAAGATG
The table mouse Processor Processor The table HA mouse (1) forward 5: CCASGCTCTATCCCTATGCC The table HA mouse (1) reverse 5: CCASGCTCATAGCCACCCTATGCC The table HA mouse (2) reverse 5: CCASGCTCATAGCCACCCTATGGCATCTCGCTCAGGCCTAGCCCTAGCC The table HA mouse (2) reverse 5: GACCAAAAAGCCAGGCTCACCC The table HA mouse (2) reverse 5: GACCAAAAAGCCAGGCTCACCC TBC1DBB human shott isoform reverse 5: CTATCTAAGCAAAGCCAGGCTCACCC TBC1DBB human shott isoform reverse 7: TATTAAGCAAGCAGC 7: TATTAAGCAAGCAGGCTCACCCGTGATCTCGCCACGCGCACGCGCAGCGCGCAGCGCGCAGCGCGGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	Tbc1d8b mouse	forward	5'- GTACAAAAAAGCAGGCTTCACCATGTGGCTGAAGCCCGAGGA
The table HA modes (1) Invarid S: CATGGTGARCCTCATTGACC The table HA modes (2) Invarid S: CATGGTGARCCTGACTTTTTTGAC The table HA modes (2) Invarid S: GATGGTARAGCCTGCATTTTTGAC The table HA modes (2) Invarid S: GATGGTARAGCCTGGATCTTGGCTGACCCTTGGTCTGAGCCTTAGC TBC1BB human short isoform Invarid S: GTTGTAGAGAAAGCAGGGTCACC TBC1BB human short isoform Invarid S: GTTGTAGAGAAAAGCAGGGTGCACC TBC1BB human short isoform Invarid S: GTTGTAGAGAAAAGCAGGGTGACCC TBC1BB human short isoform Invarid S: GTTGTAGAAAAGCAGGCTGCACC RAB11A Invarid S: GTTGTAGAAAAGCAGGCTCACCC RAB11A Invarid S: GTGTGTAGAAAAGCAGGGTGCACC RAB11A Invarid S: GTGTGTAGAAAAGCAGGGTCCACCTGCAGACTGCCA RAB11A dominant negative S2BN (1) Invarid S: GGAGATTCGGTGTGGGTCCTATAGATGTCCTGACCAGCACCGCA RAB11A dominant negative S2BN (2) Invarid S: GGAGATTCGGGGTCCCATAGGGTACCCGCGGGACCGCA RAB11A consistuality active G70. (1) Invarid S: GTAGGTAGAAAGCCTGGGGTCCCTATAGACGGTATCGGGCACCGCGGACCGCA RAB11A consistuality active G70. (1) Invarid S: GTAGGTAGAAAGCTGGGGTCCTATAGACGGACCGCGGACCGCA RAB11A consistuality active G70. (1)	Tbc1d8b mouse	reverse	5'- CTTTGTACAAGAAAGCTGGGTCCTATCACATCTTGGTTCTAGACCTTAG
Tect89-H mouse (1) everse 5: GATGGTGAAGCCTGCTTTTTGTAC Tect89-H mouse (2) everse 5: GACGTCATAGGATAGAAGCCTGCCCATGTGGCTGAAGCCCGAGGA Tect89-H mouse (2) everse 5: GTACGAAAAGCAGCCTGCCCATGTGGTCAGACCCGAGGA Tect89-H mouse (2) everse 5: GTACGAAAAGCAGCCTGGCCC TECT08 human short isoform forward 5: GTACGAAAAGCAGGCTGGCC TeCt88 (D.m.) pCFD4 forward 6: GTACGAAAAGCAGGCTGCACC Tect88 (D.m.) pCFD4 forward 6: GTACGAAAAGCAGGCTGCACCGCGGTGACCTCGCATGGCGACGCACGC	Tbc1d8b-HA mouse (1)	forward	5'- GCAGGCTTCTATCCCTATGAC
The disp.HA modes (2) Inverse 5: GACCTCACAGCTECACCTTGGCTGAAGCCTAGC The disp.HA modes (2) Inverse 5: GACCTCACAGCTEGCATCTGGTTCTAGCCTTGGT TBC DBB human shot isoform Inverse 5: CTTTGTACAAGAAAGCTGGGTCCT TBC DBB human shot isoform Inverse 5: CTTTGTACAAGAAAGCTGGGTCCT TBC DBB human shot isoform Inverse 5: CTTTGTACAGAAAATATCCGGGGTGAACCTCGCACCAAGGGGCACCGGGGGGCCCCATGCAAGGGGGGCCCATGCAAGGGGGGCCCATGCAAGGGGGGCCCATGGGGGCCCATGGGGGCCCATGGGGGCCCATGGGGGCCCATGGGGGCCCATGGGGGGCCCATGGGGGGCCCATGGGGGGCCCATGGGGGGCCCATGGGGGGCCCATGGGGGGCCCATGGGGGGCCCATGGGGGGCCCATGGGGGGGCCCATGGGGGGGG	Tbc1d8b-HA mouse (1)	reverse	5'- CATGGTGAAGCCTGCTTTTTGTAC
Tect3bs/Hamas for isoform forward 5: GFACGTATAGGGATIGAAGCCTGCCATCTTGGTTCTAGACCTTAGC TBC1DBs human short isoform forward 5: GTACAMAMAGCAGGTCTCACC TBC1DBs human short isoform feverse 5: CTTTGTACAAGAAAGCTGGGTCCT TaC1Bs human short isoform feverse 5: CTTTGTACAAGAAAGCTGGGTCCT TATATAGGAAAGCATCCGGGTGAACTTCGCTACCAAGGATAAAGTGGGTTTTAG AGCTAGAAAAAGCAGG 5: TTTTATAGGAAAGCATCCGGGTGCTATAGAGTCCCCATGGCCCACGGCGCCCGGGCGCCATGGCGCCACGGCGCCGCGGGGCGCCTATGGATTCCCCATGGCCACGGCGCCGGG RAB11 A forwinant negative S25N (1) reverse 5: TTTCTTGCAAGGAGTGGGGTCCTATTAGATGTTCTGGACGACGCCGGA RAB11 A dominant negative S25N (2) reverse 5: CTTTGTACAAGAAGCTGGGGTCCTATTAGATGTTCTGACAGCACTGCA RAB11 A dominant negative S25N (2) reverse 5: CTTTGTACAAGAAGCTGGGGTCCTATTAGATGTTCTGGACGACGCCCGGA RAB11 A dominant negative S25N (2) reverse 5: ACCCTGCTGTGTCGCATATCACCTGCGACGACCACCCACA RAB11 A dominant negative S25N (2) reverse 5: ACCCTGCTGTGTCGCATATCCCCCTGGACGACCGCACGCA	Tbc1d8b-HA mouse (2)	forward	5'- GTACAAAAAAGCAGGCTTCACCATGTGGCTGAAGCCCGAGGA
TBC1DBB human shot leform forWard 5: CTTGTACAAAAAGCAGGCTTCACC TBC1DBB human shot leform reverse 5: CTTGTACAAAAACCAGGCTCACC TBC1DBB human shot leform reverse 5: CTTGTACAAAAACCAGGCTCACC Tbc1dBb (D.m.) pCFD4 forward 5: CTTGTACAAAAACCGGGCTCACC TBC1dBb (D.m.) pCFD4 forward 5: GTACAAAAAGCAGGCTCACC RAB11 A forward 5: CTTGTACAAAAAGCTGGGTCCTATTAGATGTTCTGACAAGCACTGCA RAB11 A forward 5: CTTGTACAAAAAAGCTGGGTCCTATTAGATGTTCTGACAAGCACTGCA RAB11 A dominant negative S25N (1) reverse 5: CTTGTACAAAAAAGCTGGGTCCTATTAGATGTTCTGACAAGCACTGCA RAB11 A dominant negative S25N (2) reverse 5: CTTGTACAAGAAAGGCTGGGTCCTATTAGATGTTCTGACAGCACGCAGCAGCA RAB11 A constitutively active C70L (2) reverse 5: CTTGTACAAGAAGGGCTTCACCATGGGTCCTATAAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	Tbc1d8b-HA mouse (2)	reverse	5'- GACGTCATAGGGATAGAAGCCTGCCATCTTGGTTCTAGACCTTAGC
TBC1D8B human short isoform reverse 5: CTTTGTACAAGAAGCTGGGTCCT Statut 5: ATATAGGAMGATATCCGGGTGACTTCGCTACTACAAGGATAAAGTGGGTTTTAG AGCTAGAAATAGCAAG S: AGCTAGAAATAGCAAG Tbc1d8b (D.m.) pCFD4 forward For TAGAATAGCAAG S: AGCTAGAAATAGCAAG Tbc1d8b (D.m.) pCFD4 reverse RAB11 A forward For TGTGTACAAGAAGCGGTCCACC RAB11 A RAB11 A forward S: CTTTGTACAAGAAGCGTGGCTCCTATAGATGTTCGACAGCACTGCA RAB11 A forward RAB11 A constitutively active 250L (1) forward RAB11 A constitutively active 270L (2) forward RAB11 A constitutively active 070L (2) forward RAB11 A constitutively active 070L (2) forward RAB11 B constitutively active 070L (2) forward RAB11 B constitutively active 070L (2) forward<	TBC1D8B human short isoform	forward	5'- GTACAAAAAAGCAGGCTTCACC
111 1111 111 111 111 <td>TBC1D8B human short isoform</td> <td>reverse</td> <td>5'- CTTTGTACAAGAAAGCTGGGTCCT</td>	TBC1D8B human short isoform	reverse	5'- CTTTGTACAAGAAAGCTGGGTCCT
That TAGGAAAGATATCCGGGTGAACTTCGCTACTACAAGGATAAAGTGGGTTTTAG AGCTAGAAATAGCAAG Strint Acting Construction That TagGAAAGATAGCAAG Strint Acting Construction That TagAtaATAGGTC RAB11 A Inoward Strint Acting Construction RAB11 A dominant negative S25N (2) RAB11 A dominant negative S25N (2) RAB11 A constitutively active O7DL (2) RAB11 B dominant negative S25N (1) RAB11 A constitutively active O7DL (2) RAB11 B dominant negative S25N (1) RAB11 B dominant negative S25N (2) RAB11 B dominant negative S25N (1) RAB11 B dominant negative S25N (2) RAB11 B dominant negative S25N (2) RAB11 B consti		1010.00	5'-
Tbc1d8b (D.m.) pCFD4 forward ASCTAGAAATAGCAAG St TTTTACTTGCTATTTCTAGCTCTAAAACCGTGATTCCCCATGGCCACGCACG			
S ¹ ATTITACTIGCTATTITCTAGCTCTAAAACCGTGGTTCCCCCATGGCCACGCGACGGT TAATTGAAAATAGGTC Thotd8b (D.m.) pCFD4 froward S ² GTACAAAAAGCGAGCTTCACCC RAB11 A froward S ² GTACAAAAAGCGAGGCTTCACCC RAB11 A froward S ² GTTTTGCAAGAAAGCGAGGCTCCACTATTAGATGTTCGTGACAGCACGCAC	Tbc1d8b (D.m.) pCFD4	forward	AGCTAGAAATAGCAAG
ATTITACTTGCTATTCTAGCTCTAAAACCGTGATTCCCCATGGCCACGCACG			5'-
The class (D.m.) pCFD4 reverse TAAATTGAMAATAGGTC RAB11 A forward S - GTACAMAMAAGCAGGCTTCACC RAB11 A driverse S - CTITGTACAAGAAAGCTGGGTCCTATTAGATGTTCTGACAGCACTGCA RAB11 A driverse S - GTACAMAAAGCAGGCTTGGGTCCTATTAGATGTTCTGACAGCACTGCA RAB11 A driverse S - GTACAACAACAGCAGGGTCCTATTAGATGTTCTGACAGCACTGCA RAB11 A driverse S - GTACAAAAAAGCAGGGTCGGTCATATGAGGACCCGGACGAGCGAG			
RAB11 A forward S: GTACAMAMACCAGGCTTCACC RAB11 A freverse S: CTTGTACAAGAAGCTGGGTCCTATAGAGTGTCTGACAGCAGCAGCA RAB11 A dominant negative S25N (2) forward S: GGACATTCTGGTTGGAAAGACTGCTGCTGCTGTGCAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	Tbc1d8b (D.m.) pCED4	reverse	TAAATTGAAAATAGGTC
AB11 A forward 5 CTITIGTACAAGAMAGCTGGGTCCTATTAGATGTTCTGACAAGACACTGCA RAB11 A dominant negative S25N (2) forward S GGAATTCTGCTITGGAAGAATATCTCCC RAB11 A dominant negative S25N (2) forward S GGAATTCTGGTTGGAAGAATATCTCCCTGTCTGGATGACAGCACTGCA RAB11 A dominant negative S25N (2) forward S GGAATTCTGGTTGGCAGGGTCCTATTAGATGCCCGCAGGACGACGA RAB11 A constitutively active Q70L (2) freverse S ACCCTGGTGTCCCCAGGGGTCAAGACCGACGAGCTAACACCT RAB11 A constitutively active Q70L (2) freverse S CGTTTGTACAAGAAGCTGGGTCCTATAGATGGAGCTAAACCCGGGGCGAGAGC RAB11 B dominant negative S25N (1) forward S GTACAAGACGGGGTCCAACGCGGGGGGGCCTAAGACGCGGGGGGGG	RAB11 A	forward	
AB11 A dominant negative S25N (1) feverse S- TITCITICCAACACAGAATCITCC RAB11 A dominant negative S25N (2) feverse S- CITCITICCAACCAGAATCACCACACCCCGCGCCGCACACACACCACCCCGCA RAB11 A dominant negative S25N (2) feverse S- CATCAAAAAGCCGGGTCCACCATGGGTACCCCGCGACGAG RAB11 A constitutively active Q70L (1) feverse S- AGCCCTGCTGTCCCCATTG RAB11 A constitutively active Q70L (2) feverse S- AGCCCTGCTGTCTCCCATTGC RAB11 A constitutively active Q70L (2) feverse S- AGCCGCGCGGCTGACCCGGGGCCCGGGACGACC RAB11 A constitutively active Q70L (2) feverse S- GACAAAAAGCAGCTGGGTCCCCATGGGGACCCGGGACGAC RAB11 A constitutively active Q70L (1) feverse S- GACAAAAAGCAGCTGGGTCCCATGGGGACCCGGGACGAC RAB11 B dominant negative S25N (1) feverse S- GACACAAAAAGCAGGCTGCACCTGGGGACCCGGGACGAC RAB11 B dominant negative S25N (2) feverse S- GACACAGCAGCGACGGGTCTCACCCATGGGGACCCGGGACGAC RAB11 B dominant negative S25N (2) feverse S- CTTCGTACAAGAAGCCTGGGGTCCTATCACAGGGGACCCGGGACGAC RAB11 B dominant negative S25N (2) feverse S- CTTCGTACAAGAAGCCGGGGTCCCACCGCGGGGGGCCACC RAB11 B constitutively active Q70L (1) feverse S- CTTCGACGACGCCTCCCAGGCGCTCCCCAGGGGGTCCCCCGGACGAC RAB11 B constitutively active Q70L (1) feverse S- TGGCGCGGTCCCCCCCCAGGCCGCCCCCAG RAB11 B constitutively active Q70L (2) feverse S- CTTCGTACAAGAAGCGGGCTCCACCCAGGGGTGTCCCAGA RAB11 B constitutively active Q70L (2) feverse S- CTTCGACAGCAGCTTACCACGGCGCCCCGCAC RAB4 dominant negative S27N (2) feverse S- CTTCGTACAGGCGCTCCCCACGCCCCA RAB4 dominant negative S27N (2) feverse S- CTTCGTACAGGCGCTCCCCACGCCCCAG RAB4 dominant negative S27N (2) feverse S- CTTCGTACAGGCGCTCCCCACGCCCCCAG RAB4 dominant negative S27N (2) feverse S- CTCCAAGAAAGCCGGGCTCCACCCACACCCCAGGTCCCCCAGG RAB4 dominant negative S27N (2) feverse S- CTCCAAGAAAGCCTGGGTCCCACACGCACCCCAGGTCCCCCAGG RAB4 dominant negative S27N (2) feverse S- CTCGTGTCCCACACGCCGCGTGCCCACGCCAGGTCCCCCCGGGTCCTACCACACCCCGGGCCCACGCCAGGCCCCCCGGGTCCTACCACACCCCGGGCCCACGCCAGGCCCCCGGGTCCTACCACACCCGGGCCCACGCCGCGCCCCCGGGTCCCTGCCCGGGTCCTACCACACGCGGCCCCCGCGGTCCCTGCCCGGGTCCTACCACACGCGGCCCCCGCGCCCCGGGTCCTTCCCC			
International regative S28N (2) Forward 5° - GGAGATTCTGGTGTGGAAGGATAATCTCCTGTCTGAAGGACAGCTCCCGG RAB11 A dominant negative S28N (2) reverse 5° - CTTTGTACAAGAAGGACTGGGTCCTATTAGATGTTCTGAAGGACAGCACGCAGGAGGAGGCTACCACCACGGGAGGAGGACGACGACGACGACGAGGAGGACGAC	PAB11 A dominant negative S25N (1)	reverse	
AND THADMINIAN regative S25N (2) reverse S-CITTGTACAAGAAAGCTGGGTCCTATTAGATGTTCTGACACCTGCA RAB11 A constitutively active Q70L (1) forward S-CITTGTACAAGAAAGCTGGGTCCTATTAGATGTTCTGACACGACGGA RAB11 A constitutively active Q70L (2) forward S-CITTGTACAAGAAAGCAGGGTCTAGACGCATATCCACGCGACAGCAGGACGACGAC RAB11 A constitutively active Q70L (2) forward S-CITTGTACAAGAAGCAGGGGTCTAGACGCATATCGAGCATAACACC RAB11 A constitutively active Q70L (2) reverse S-CACCTGCTGTGTCCCATATC RAB11 A constitutively active Q70L (2) reverse S-CACACAGCGTGTGTGGGGTCCTATTCACGGGACCCGGGACGACCAC RAB11 B dominant negative S25N (1) reverse S-CAAGCGCGCTGCGGGGTCCTATCACAGGGTCCGGGACCACCACCAC RAB11 B constitutively active Q70L (1) forward S-CACACCTGCGTCGCGCCCCCAGCGGGTGTCTGGCCAGAC RAB11 B constitutively active Q70L (1) forward S-CTTCGACGCCTACACCGCGCCACACCACCACCACCACCACCACCACCACCA	RABIT A dominant negative S25N (1)	forward	
RAB11 A dominant negative S201 (2) forward 5: CTTCATACAAGAYAGC TOGGTCCCATGGGTACCCCGCGACCAGCAG RAB11 A constitutively active Q70L (1) forward 5: AGCCCTGCTGGTGTCCCCATAGGGTACCCCGCGACCAGCAG RAB11 A constitutively active Q70L (2) forward 5: AGCCCTGCTGGTGTCCCCATAGGGGACCTCGAGGGTACAGCAGCGAC RAB11 A constitutively active Q70L (2) forward 5: GATAGGAGACAGCAGGGGTTCACCATGGGGACCCGGGAGCGAC RAB11 B dominant negative S25N (1) reverse 5: CATAGAGAAGAGGGTTCACCATGGGGACCCGGGAGCGAC RAB11 B dominant negative S25N (1) reverse 5: CAAGCCGCGACAGCAGCGTTCACCATGGGGACCCGGGAGCGAC RAB11 B dominant negative S25N (1) reverse 5: CTTGTACAAGAAGCGGGTCCTATCACAGGGTTCGGCAGCAC RAB11 B constitutively active Q70L (1) forward 5: CTTGGACGCGCTCCCAGCGCCCCAGGGGCTCCACCAGCGGACCCAG RAB11 B constitutively active Q70L (2) forward 5: CTTGACAGAAGCGGGTCCCAAGCCAGGGTTCGCAGCAGC RAB11 B constitutively active Q70L (2) forward 5: CTTGACAGAAGCGGGTCCCACCACGGGGCCCCAGGGACCCCA RAB11 B constitutively active Q70L (2) forward 5: CTTGACAGAAGCGGGGTCCTACCACCAGCGGTCCCACAGGCCCAGGCCATGC RAB4 dominant negative S27N (1) forward 5: CTTGACAGAAAGCGGGGTCCTACTACCACAGGGCCCATGCC RAB4 dominant negative S27N (2) reverse 5: CTTGACAGAAAGCGGGGTCCTACCACAGGCCCAGGCCCATGCC RAB4 dominant negative S27N (2) reverse 5: CTTGACAGAAAAGCGGGGTCCACATGCAAGCACACCACCCCCGCACCTCCCGAGACGCCCCCCCC	RABITA dominant negative S25N (2)		
RAB11 A constitutively active Q70L (1) reverse 5- GAZAWAWGEGAGGGCT TCACCAGGCATATCGAGACTATACACTC RAB11 A constitutively active Q70L (2) forward 5- GATATGGGACACAGCAGGCTATACC RAB11 A constitutively active Q70L (2) forward 5- GATATGGGACACAGCAGGGCTCATATGGAGCACGAGCACGAGCACGACAGCACTGCA RAB11 B dominant negative S25N (1) forward 5- GAAGCGCGACACAGCAGGTCTTTGTGCCCACAGCAGGTC RAB11 B dominant negative S25N (2) forward 5- CATACAAAAAAGCAGGTCTTCACCAGGGGACCCAGGCACGCCAGGCACACGACAGCAGCA	RABITA dominant negative S25N (2)	feverse	
RAB11 A constitutively active Q70L (2) forward 5: Add/CCTGGTGTGCACAGCAGCCTAGAGCGATATCGAGCTATAACATC RAB11 A constitutively active Q70L (2) forward 5: CTTTGTACAAGAAACCTGGGTCTATACATGTGAGCACAGCAGCAGCACAGCAGCACAGCAGCACAGCAGCA	RAB11 A constitutively active Q70L (1)	forward	
RAB11 A constitutively active Q7DL [2] forward 5- GATAIGGARAGCAGGGTCCTATTAGAGCAGCAGCAGCACCAGCAGCAC RAB11 A constitutively active Q7DL [2] forward 5- GTTGTACAAGAAAGCAGGGTCCTATTAGAGTAGCAGCAGCAGCAGC RAB11 B dominant negative S25N [1] forward 5- GAAGCAGCAGCAGGTGTGTTCTGGCAGCCCGGGAGCGAC RAB11 B dominant negative S25N [2] forward 5- ACAACCTGCTGTGCGCGGGTCTACCATGGGAGCCCGGGAGCAC RAB11 B dominant negative S25N [2] forward 5- CTTGTGACAAGAAGCTGGGGTCTACCATGGGAGCCCGGAGCAC RAB11 B dominant negative S25N [2] forward 5- TTGACAAGAAGCTGGGGTCTACCCATGGGGACCCGGGACCAC RAB11 B constitutively active Q70L [1] forward 5- TTGGACGCTACCCCAGGGGTCCCAGCGGAC RAB11 B constitutively active Q70L [2] forward 5- TTGGACGCTACCCGGGCCCTGCCCAGCGGGCCTTGCCCAGCCGCAC RAB11 B constitutively active Q70L [2] forward 5- TTCGATACAAAGCTGGGTCCTACCAGGTCCCAGCACCACCACCCCGGAC RAB4 dominant negative S27N [1] forward 5- ATCCATACAAAAGCTGGGTCCTACCAAGCAGCAGCCAGTGTC RAB4 dominant negative S27N [2] forward 5- ATTCGCTACTACTACCAGGTGCTCACCAGCAGCAGCCAGC	RAB11 A constitutively active Q70L (1)	reverse	
RRAB11 a constitutively active Q7/L [2] reverse 5- CTTIGTACAAGAAGCIGGGTCTACCCATGGGGACCGGGAC RAB11 B dominant negative S25N [1] reverse 5- GAACGAAAAAGCAGGGTTCACCATGGGGACCCGGGAC RAB11 B dominant negative S25N [2] forward 5- ACAACCTGCTGGCGCCTCACCGCCGGACGCCGGGACGAC RAB11 B dominant negative S25N [2] forward 5- GTACAAAAAAGCAGGCTTCACCATGGGGACCCGGGACGAC RAB11 B dominant negative S25N [2] forward 5- GTACAAAAAAGCAGGCTTCACCATGGGGACCCGGGACGAC RAB11 B constitutively active Q7DL [1] forward 5- TTGGAGGCGTACCGCGGCCCA RAB11 B constitutively active Q7DL [2] forward 5- TTGGAGGCGTACCGCGCCCA RAB11 B constitutively active Q7DL [2] forward 5- TTTGAAAAAAGCAGGGTTCACCATGGGACGCTGCAGAGCACC RAB4 dominant negative S27N [1] forward 5- TTTGATACAAGAAGCTGGGGTCCTACCACAGGCACCAGGACCACCCGGAGCACC RAB4 dominant negative S27N [2] forward 5- CATTGCTACAAGAAGCTGGGTCCTACCACAGCACCACCCCGGACCACCCCGGAGCACCCCCAGCACCCCCC	RAB11 A constitutively active Q70L (2)	forward	
RAB11 B dominant negative S25N (1) forward 5- GTACAAAAAGCAGGCT ICTACCATGGGGACCCGGGACGAGC RAB11 B dominant negative S25N (2) forward 5- ACAGCCGACAGCAGGCAGCTGTGTCTTCCCCCACGCTGAGTC RAB11 B dominant negative S25N (2) forward 5- CTTTGTACAAAGAAGCAGGGTTCTACCATGGGGACCCAGGGACGACGAGCAGCAGCAGCAGCAGCAGCA	RAB11 A constitutively active Q70L (2)	reverse	
RAB11 B dominant negative S25N (1) reverse 5: AGAAGCGCGACAGCAGGTGTTCTTGCCCCCGCGCCTC RAB11 B dominant negative S25N (2) reverse 5: CTTTGTACAAGAAAGCTGGGTCCTATCACAGGTCTGGCAGCAC RAB11 B dominant negative S25N (2) reverse 5: CTTTGTACAAGAAAGCTGGGTCCCAAGCGGGTCCCAGCGGACGAC RAB11 B constitutively active Q70L (2) forward 5: TTGGAGCGGTACGCCTCCAAGCCAGCGGTGCCCCAGA RAB11 B constitutively active Q70L (2) forward 5: CTTTGTACAAGAAAGCAGGCTTCCACAGCGGTCTGGCACACC RAB41 B constitutively active Q70L (2) forward 5: CTTTGTACAAGAAAGCAGGCTTCCACAGCGCGAGCGCCACCCCCAGA RAB41 dominant negative S27N (1) reverse 5: CTTTGTACAAGAAAGCAGGCTTCACCACAGCAGCGCCACGGCACCCCCAGACGCACC RAB4 dominant negative S27N (2) forward 5: AATTGCTTACTTCATCAGTTATTGAA RAB4 dominant negative S27N (2) forward 5: AATTGCTTACTCAGTTGACTACACACACACACACCACCACTCTCGAG RAB4 constitutively active Q72L (1) forward 5: ACTCTGCTATCACAGAGAGCTGGGTCTACCATGCCACACCACCCGGGC RAB4 constitutively active Q72L (2) forward 5: CATCTATACACAGAAGCAGGGCTCACACTATACAACACACAC	RAB11 B dominant negative S25N (1)	forward	
RAB11 B dominant negative S25N (2) forward 5'- ACAACCTGCTGTCGCCGGGTCCTATCACAGGTTCTGCAGCACC RAB11 B constitutively active Q70L (1) forward 5'- GTACAAAAAAGCAGGCTTCACCATGGGGACCCAGGGACGAC RAB11 B constitutively active Q70L (1) forward 5'- GTACAAAAAAGCAGGCTTCACCATGGGGACCCAGCGACGAC RAB11 B constitutively active Q70L (2) reverse 5'- CTTTGTACAAGAAAGCGGGCCCACCGCACCAGGGTCCCACGGACGACC RAB11 B constitutively active Q70L (2) reverse 5'- CTTTGTACAAGAAAGCTGGGTCCTATCACAGGATCCGCAGCACC RAB4 dominant negative S27N (1) forward 5'- GTACAAAAAAGCAGGCTCACCCATGTCGCAGCACCACGTCCTGCAGACCAC RAB4 dominant negative S27N (2) forward 5'- ATTGCTTACTACAGGTAGCAGCACTTCACCACGCCACTCCTGAG RAB4 dominant negative S27N (2) reverse 5'- CTTTGTACAAGAAAGCTGGGCTCACCATGTCCACACACCACCACCACCTCCTGAG RAB4 dominant negative S27N (2) reverse 5'- CTTGTACAAAAAGCAGCGGCTTACCACATACACACCACACCACCACCACGGCCATGTC RAB4 constitutively active Q72L (1) freverse 5'- CTTGTACAAAAAGCAGCGGCTCACCATGAACACCACACACCACACCACGGCCATGGC RAB4 constitutively active Q72L (2) forward 5'- CTTGTACAAAGAAGCTGGGTCCTACAACAACCACACACAC	RAB11 B dominant negative S25N (1)	reverse	5'- GAAGCGCGACAGCAGGTTGTTCTTGCCCACGCCTGAGTC
RAB11 B constitutively active Q70L (1) forward 5- GTITGTACAAGAAGCTGGGTCCTATCACCAGGGACGAC RAB11 B constitutively active Q70L (1) forward 5- GTICAAAAAAGCAGGCTTCACCATGGGGACCACCAC RAB11 B constitutively active Q70L (2) forward 5- TTGGAGCGCTACCGCGCCA RAB11 B constitutively active Q70L (2) forward 5- TTGGAGCGCTACCGCGCCA RAB1 B constitutively active Q70L (2) forward 5- GTICACAAGGAGCTGGCTCCACCAGTGCCAGACCACCAC RAB1 metatore active S27N (1) forward 5- GTIACAAAAAAGCAGCTGGGTCCTATCACCAGGTCCTGGCAGCACCAC RAB4 dominant negative S27N (1) forward 5- GTIACAAAAAAGCAGCTTCACCATGTCGCAGACCGCCCATGTC RAB4 dominant negative S27N (2) forward 5- GTICACAAGAAAGCTGGGTCCTACTAACAACCACACTCCTGAG RAB4 dominant negative S27N (2) forward 5- ATTGCTTACTACAGTTTATGAA RAB4 dominant negative S27N (2) forward 5- CTITGTACAAGAAAGCTGGGTCCTACTAACAACCACACTCCTGAG RAB4 constitutively active Q72L (1) forward 5- GTIACAAAAAAGCAGGCTTGACCATGTCGCAGAGCGGCCATGTC RAB4 constitutively active Q72L (2) forward 5- CAAATATGGGATACAGCAGGCTGAGACCAGACGAGCGCCAGTGC RAB4 constitutively active Q72L (2) forward 5- CAAATATGGGATACAGCAGGCGCAGACTGAGACCAGCCGCGCGAGC RAB4 constitutively active Q72L (2) forward 5- CAAATATGGGATACAGCAGGCGCAGCAGCAGCAGCAGCAGCACCAGGCCGCC	RAB11 B dominant negative S25N (2)	forward	5'- ACAACCTGCTGTCGCGCTTC
RAB11 B constitutively active Q7DL (1) forward 5'- GTACAAAAAAGCAGGCTTCACCATGGGGACCCAGC RAB11 B constitutively active Q7DL (2) forward 5'- TTGGAGCGCTCCAAGCCGCCACAGGGTGTCCACAGGAGCAGCCAGC	RAB11 B dominant negative S25N (2)	reverse	5'- CTTTGTACAAGAAAGCTGGGTCCTATCACAGGTTCTGGCAGCAC
RAB11 B constitutively active Q70L (1) reverse 5' TGGCGCGGTAGCCGCGCAACCCAGCGGTGTCCCAGA RAB11 B constitutively active Q70L (2) reverse 5' CTTGAACAGAAAGCTGGGTCCTATCACAGGTTCTGGCAGCAC RAB4 dominant negative S27N (1) forward 5' GTACAAAAAAGCAGGCTTCACCATGTCGCAGCACCACGTCCTGCCAGAGCACCACGTCTCACAGTTCTGGCAGCACCACGTCCTGCAGAGCAGCACCACGTCCTGCAGAGAGAG	RAB11 B constitutively active Q70L (1)	forward	5'- GTACAAAAAAGCAGGCTTCACCATGGGGACCCGGGACGAC
RAB11 B constitutively active Q70L (2) forward 5'- TTGGAGGGCTACCGGGCCAC RAB11 B constitutively active Q70L (2) freverse 5'- CTTGTACAAGAAGCTGGGTCCTATCACAGGTTCTGGCAGCAC RAB4 dominant negative S27N (1) forward 5'- GTACAAAAAGCTGATGAGGAGCAACTTTTTGCCAGACGCCCATGTC RAB4 dominant negative S27N (2) forward 5'- ATTGCTTACTTCATCAGTTATTGAA RAB4 dominant negative S27N (2) forward 5'- CTTGTACAAGAAGCTGGGTCCTACTACAAACACCCACACTCCTGAG RAB4 dominant negative S27N (2) forward 5'- CTTGTACAAGAAAGCTGGGTCTACTACAAACACACACACA	RAB11 B constitutively active Q70L (1)	reverse	5'- TGGCGCGGTAGCGCTCCAAGCCAGCGGTGTCCCAGA
RAB11 B constitutively active Q70L (2) reverse 5: CTTTGTACAAGAAAGCTGGGTCCTATCACAGGGTCTGGCAGCAC RAB4 dominant negative S27N (1) forward 5: GTACAAAAAAGCAGGCTTCACCATGTGCGCAGACGGCCATGTC RAB4 dominant negative S27N (2) forward 5: ATTGCATAAACTGATGAGTAGCAGGTTCCACCATGTCGCAGTCCTGCAGATGCGAGTCCTGCAGA RAB4 dominant negative S27N (2) forward 5: ATTGCATAAACTGATGAGTAGCAGGCTTCACCATGTCGCAGACGGCCATGTC RAB4 dominant negative S27N (2) reverse 5: CTTTGTACAAGAAAAGCAGGCTTCACCATGGCGCAGCGCATGTC RAB4 constitutively active Q72L (1) forward 5: GTACAAAAAAGCAGGGTTCACCATGTCGCAGACGGCCATGTC RAB4 constitutively active Q72L (2) forward 5: CTTTGTACAAGAAAAGCAGGGCTCAACTGAACGACGACCCCGTGGAC RAB4 constitutively active Q72L (2) reverse 5: CTTTGTACAAGAAAGCTGGGTCCTACTAACAACACCACCACCCCCGGAGCACCAGGCCCCCGGGCCCCCGGGCCCCCGGGCCCCCGGGCCCCCGGGCCCC	RAB11 B constitutively active Q70L (2)	forward	5'- TTGGAGCGCTACCGCGCCA
RAB4 dominant negative S27N (1) forward 5: OTACAAAAAAGCAGGCTTCACCATGTCGCAGAGCGACAGTC RAB4 dominant negative S27N (2) forward 5: ATTACTAAAAAGCAGAGCTGAAGCAAGTTTTTGCACAGTTATTCAA RAB4 dominant negative S27N (2) forward 5: ATTGCTTACTCATCAAGTTAATGAA RAB4 dominant negative S27N (2) feverse 5: OTTTGTACAAGAAGCAGGCTCACCACACCACCACCCTGAG RAB4 constitutively active 072L (1) forward 5: AGTCCTGCTGTATCCCATATTTG RAB4 constitutively active 072L (2) forward 5: OTTGTACAAAAAAGCAGGCTTCACCAGAGCAGAGCCAGACCAGGCCCGGAC RAB4 constitutively active 072L (2) forward 5: CAAATATGGGATACAGCAGGAGCACTAGAACCAACCACCACCCCGGAGC RAB4 constitutively active 072L (2) reverse 5'- CTTTGTACAAGAAAGCTGGGTCCTACTACAACACCACACCCCCGGAGCCCCCGGAGCCCCCGGAGCCCCCC	RAB11 B constitutively active Q70L (2)	reverse	5'- CTTTGTACAAGAAAGCTGGGTCCTATCACAGGTTCTGGCAGCAC
RAB4 dominant negative S27N (1) reverse 5'- TTCAATAAACTGATGAGTAAGCAATTTTTGCCAGTTCCTGCATTTCCA RAB4 dominant negative S27N (2) forward 5'- ATTGCTTACTCATCAGTTTATTGAA RAB4 dominant negative S27N (2) reverse 5'- CTTTGTACAAGAAAGCTGGGTCCTACTAACAACACCACACTCCTGAG RAB4 constitutively active Q72L (1) forward 5'- GTACAAAAAAGCAGGCTTCACCATGTCGCAAGCAGGCCATGTC RAB4 constitutively active Q72L (2) forward 5'- CAAATATGGGATACAGCAGGACTAGAACGATCCAGGTCCGTGAC RAB4 constitutively active Q72L (2) forward 5'- CAAATATGGGATACAGCAGGACTAGAACGACCACACCAC	RAB4 dominant negative S27N (1)	forward	5'- GTACAAAAAAGCAGGCTTCACCATGTCGCAGACGGCCATGTC
RAB4 dominant negative S27N (2) forward 5'- AATTGCTTACTTCATCAGTTTATGAA RAB4 dominant negative S27N (2) reverse 5'- CTTTGTACAAGAAAGCTAGCTGCACCAACAACACCACACTCCTGAG RAB4 constitutively active Q72L (1) forward 5'- GTACAAAAAGCAGGCTTCACCATGTCGCAGACGCCATGTC RAB4 constitutively active Q72L (2) forward 5'- CAAATATGGGATACAGCAGGACTAGAACGACTCAGGTCCTGAGC RAB4 constitutively active Q72L (2) forward 5'- CATTGTACACAAGAAGCTGGGTCCTACTAGAACACACACA	RAB4 dominant negative S27N (1)	reverse	5'- TTCAATAAACTGATGAAGTAAGCAATTTTTGCCAGTTCCTGCATTTCCA
RAB4 dominant negative S27N (2) reverse 5'- CTTTGTACAAGAAGCTGGGTCCTACTAACAACACACACTCCTGAG RAB4 constitutively active Q72L (1) forward 5'- GTACAAAAAAGCAGGCTTCACCATGTCGCAGACGGCCATGTC RAB4 constitutively active Q72L (2) forward 5'- CAATATGGGATACACACAGAGCATGACAGAGCACTCAGGACCGGGTCCGTGAC RAB4 constitutively active Q72L (2) forward 5'- CATTGGACAAGACAGGGGTCCTACTAACAACCACACTCCTGAG RAB4 constitutively active Q72L (2) reverse 5'- CTTTGTACAAGAAAGCTGGGGTCCTACTAACAACCACACTCCTGAG Secretable GFP forward 5'- CTTGGTGCACAGCTGGAGGGCCCACCAGTAAAGCAAAGGTCAAGGCCA Secretable GFP reverse forGGTGAGCCTGCTGTGTGGAGCCACCAGGAAGGCCACCAG 5'- CTTGACTTGCAGCTGGAGCCACCAGGAGGGCCACCAGTAAAGCAAAGGTCAAGGCCA 5'- CTTGACTTGCAGCTGGAGCACCAGGAGGCCACCAGTAAAGCAAAGGTCAAGGCCA Secretable GFP reverse forward 5'- CTGGTGAGGCACCAGGAGGCCACCAGGAGCCACCA 5'- Dc1d8b mutation R64C mouse feverse 5'- CTGGTGTAGGATGCAAAATGGAGCACCA 5'- CTTGGTCAGCACCAGGAGCACACACAGACAGGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGAGCACCAGGGGTCCAAGCAGGGTCCAAGCAGGGTCCAGGGTCCAGGGTCCAGGGTCCAGACATAGGGACCTAGGGTCCAGAGAAGCTGGGTCCAGACATGGGTCCAGGACATAGGGGTCCAGGACATAGGGTCCAGACATAGGGACCTAGGGTCCAGACATAGGGACCTAGGGTCCAAGACACTGGGTCCAAGACACTGGGTCCAGACACACAC	RAB4 dominant negative S27N (2)	forward	5'- AATTGCTTACTTCATCAGTTTATTGAA
RAB4 constitutively active Q72L (1) forward 5'- GTACAAAAAAGCAGGCTTCACCATGTCGCAGACGGCCATGTC RAB4 constitutively active Q72L (2) forward 5'- AGTCCTGCTGTATCCCATATTCG RAB4 constitutively active Q72L (2) forward 5'- CAAATATGGGATACAGCAGGACTAGAACGACTCAGGCTCGGACC RAB4 constitutively active Q72L (2) reverse 5'- CTTTGTACAAGAAAGCTGGGTCCTACTAACAACACACCACACTCCTGAG Scretable GFP forward 5'- CCTGGTGCTCAGCAGGAGCACCAGGAGGGCCACCAGTAAAGGCAAGGGCCAAGGGCCA Secretable GFP reverse TGGTGAAGCCTGCTTTTTTGCAC CTTGACTTGCAGCTGAGCACCAGGAGGGCCACCAGTAAAGCAAAGGCCAAGGCCA Secretable GFP reverse forward 5'- TAGCTCCATTTTGCATCCTACAACAGAAGCCAGACCAA GCTTTGACATGCAAGACCAGAGCACCAGAGACCCA Tbc1d8b mutation R64C mouse forward 5'- CTGGTGTAGGATGCAAAATGGAAGCCTGCTTTTAGCAGTGG Tbc1d8b mutation F438C mouse (1) reverse 5'- CTGGTGTAGAATCGGAAAATGGAAAATCGTGAAAATGTGGAAAATCTGG Tbc1d8b mutation F438C mouse (2) feverse 5'- CTTGTACAAGAAAAGCTGGGTCCTATCACATCTGGACACTTAG Tbc1d8b mutation T79S mouse forward 5'- CAGATTGCAAAGCAGAAGCAGGACCTAGTGCTACGTGGATCACATA Tbc1d8b mutation T79S mouse forward 5'- CACCTGCAGCAGAAGAAGCTGGGTCCTATCACAGGGTGGATCACATA TBC1D8B gRNA A feverse 5'- AAACTCCTTCGAAGCAGCAGGAACTGCGGGGCCCACATA Tbc1d8b mutation T79	RAB4 dominant negative S27N (2)	reverse	5'- CTTTGTACAAGAAAGCTGGGTCCTACTAACAACCACACTCCTGAG
RAB4 constitutively active Q72L (1) reverse 5'- AGTCCTGCTGTATCCCATATTTG RAB4 constitutively active Q72L (2) forward 5'- CAAATATGGGATACAGCAGCAGCAGTACAACCAATCCAGGTCCGTGAC RAB4 constitutively active Q72L (2) reverse 5'- CTTTGTACAAGAAAGCTGGGTCCTACTAACAACCAACCACACCCCTGAG Secretable GFP forward GCTTTCTTGTACAAAG Secretable GFP reverse TGGTGAAGCTGCTGCAGCAGCAAGCAAGCAAGCAAAGGTCAAAGGTCAAGGCCA Secretable GFP reverse TGGTGAAGCCTGCTTTTTGCACACCAGGAGGGCCACCAGTAAAGCAAAGGTCAAGGCCA Tbc1d8b mutation R64C mouse forward 5'- TAGCTCCATTTTGCAACCAAGCAAGCAACACA Tbc1d8b mutation R64C mouse reverse 5'- CTGGTGTAGAGATGCAAAAGTGGAGCAACTTTAGCAGTGG Tbc1d8b mutation F438C mouse (1) reverse 5'- CAGATTTTGAGGGGAGCAACTGAAATCTGCAATACTGCAGGTGTTC Tbc1d8b mutation F438C mouse (2) forward 5'- CAGATTTGACAGAAAGCTGGGTCCTATCAAGATCTTGGTTCAGACCTTAG Tbc1d8b mutation F438C mouse (2) reverse 5'- CTTTGTACAAGAAAGCTGGGTCCTATCATGATGTCTCAGGTTCAACACTTAG Tbc1d8b mutation T779S mouse reverse 5'- CACGATGCAAGAGAAGCTGAGAAGGAA Tbc1d8b mutation T779S mouse forward 5'- CACCGACGAGGATTGGAAAGGA Tbc1d8b mutation T779S mouse forward 5'- CACCGCACGCAGGATTGGAAGGA Tbc1d8b gRNA	RAB4 constitutively active Q72L (1)	forward	5'- GTACAAAAAAGCAGGCTTCACCATGTCGCAGACGGCCATGTC
RAB4 constitutively active Q72L (2) forward 5'- CAAATATGGGATACAGCAGGACTAGAACGATTCAGGTCCGTGAC RAB4 constitutively active Q72L (2) reverse 5'- CTTTGTACAAGAAAGCTGGGTCCTACTAACAACACACCACCTCCTGAG Scretable GFP forward 6'- Secretable GFP forward 5'- CTTGACTTGCAGCTGAGCACCAGGAGGGCCACCAGTAAAGCAAAGGTCAAGGCCA Secretable GFP Tbc1d8b mutation R64C mouse forward 5'- CAGGTGAGCACCAGGAGGGCCACCAGGACGACCAGGAGGGC Tbc1d8b mutation R64C mouse reverse 5'- CAGGTGAGGAGCACAAATGGAGCTACTTTAGCAGTGG Tbc1d8b mutation R64C mouse forward 5'- CAGGTGTGAGCACACCAGAAATGGAGCTACTTTAGCAGTGG Tbc1d8b mutation F438C mouse (1) reverse 5'- CAGGTATGTACCCCTCAAAATGGAGCTACTTTAGCAGTGG Tbc1d8b mutation F438C mouse (2) forward 5'- CAGTATGTCACCCTCAAAATGGAGCTCATTTAGGAGTGTTCAGGTTCTAGACCTTAG Tbc1d8b mutation F438C mouse forward 5'- CAGTATGTCACCCTCAAAATGGGGTCCTATCACATCTTGGTTCTAGACCTTAG Tbc1d8b mutation F438C mouse forward 5'- CAGTATGTCACCCTCAAAATGGAGCTCATCACACACACAC	RAB4 constitutively active Q72L (1)	reverse	5'- AGTCCTGCTGTATCCCATATTTG
RAB4 constitutively active Q72L (2) reverse 5'- CTTTGTACAAGAAAGCTGGGTCCTACTACAACAACCACACTCCTGAG Secretable GFP forward 5'- Secretable GFP forward 5'- CTTGACTGCAGCTGCAGCACCAGGAGGGCCACCAGTAAAGCAAAGGTCAAGGCCA GCTTTCTTGTACAAAG Secretable GFP reverse TGGTGAAGCCTGCTTTTTGTAC Tbc1d8b mutation R64C mouse forward 5'- CTGGTGTAGGATGCAAAATGGAGCTACCAGAGCAGCAG Tbc1d8b mutation R64C mouse reverse 5'- CTGGTGTAGGATGCAAAATGGAGCTACTTTAGCAGTGG Tbc1d8b mutation F438C mouse (1) reverse 5'- CAGATTTTGAGGGTGACATACTGTCATTAGGAGTGCAATCTGT Tbc1d8b mutation F438C mouse (2) forward 5'- CAGATTTGTACACCTCAAAATCTGGAAAATCTTG Tbc1d8b mutation F438C mouse (2) reverse 5'- CAGATTTGTACACCTCAAAATCTGGAAAATCTTG Tbc1d8b mutation F438C mouse (2) reverse 5'- CTTTGTACAAGAAAGCTGGGTCCTATCACATCAGATGTGCTCTTCAGACCTTAG Tbc1d8b mutation T779S mouse reverse 5'- CACATTCTGCTTGATGAAAGCAAATCTGGAGA Tbc1d8b mutation T779S mouse forward 5'- CACCGCATGCAGGTTCTTTGCAGGGTCTGGATCACATA TBC1D8B gRNA A forward 5'- CACCGCATGCAGGTTCCTTTCCAAGGGATCACAAGA TBC1D8B gRNA B forward 5'- CACCGGACGGGTTCCTTTGCAGGGT TBC1D8B gRNA B	RAB4 constitutively active Q72L (2)	forward	5'- CAAATATGGGATACAGCAGGACTAGAACGATTCAGGTCCGTGAC
Secretable GFP forward 5'- CCTGGTGCTCAGCTGCAGCTGCAGCTGCGCTCTGTGGGCTGTGATCTGCCTGACCCA GCTTTCTTGTACAAAG Secretable GFP reverse TGGTGAAGCCTGCTGTAGCAGCGAGGGGCCACCAGTAAAGCAAAGGTCAAGGCCA Tbc1d8b mutation R64C mouse forward 5'- CTTGGTGTAGGATGCAAAATGGAGCACCAGGAGAGCACCA Tbc1d8b mutation R64C mouse reverse 5'- CTGGTGTAGGATGCAAAATGGAGCTACTTTAGCAGTGG Tbc1d8b mutation F438C mouse (1) reverse 5'- CAGATTTTGAGGGTGACATACTGTCATTAAGGCTTCAGTGTTC Tbc1d8b mutation F438C mouse (2) forward 5'- CAGATTTTGACAAGAAAGCTGGGTCCTATCACACTTTGGAAGACCTTAG Tbc1d8b mutation F438C mouse (2) reverse 5'- CTTGTGTACAAGAAAGCTGGGTCCTATCACATCTTGGTTCAGACCTTAG Tbc1d8b mutation F438C mouse (2) reverse 5'- CTTGTGTACAAGAAAGCTGGGTCCTATCACATCTTGGTTCAGACCTTAG Tbc1d8b mutation F438C mouse reverse 5'- CTTTGTACAAGAAAGCTGGGTCCTATCACATCTTGGTTCAGACCTTAG Tbc1d8b mutation F438C mouse forward 5'- CGTTGTACACCTTACAGGTGGTCTATCACATCTTGGTTCAGACCTTAG Tbc1d8b mutation T779S mouse reverse 5'- CACATTCTGCATTTGGAAGGAA TGTGAAGAGACA TBC1D8B gRNA A forward 5'- CACCGGACGAGGTTACTGCATGC TGTGAGAAGAGACCGAGGGT	RAB4 constitutively active Q72L (2)	reverse	5'- CTTTGTACAAGAAAGCTGGGTCCTACTAACAACCACACTCCTGAG
Secretable GFP forward CCTGGTGCTCAGCTGCAAGTCAAGCTGCTCTGTGGGGCTGTGATCTGCCTGACCCA GCTTTCTTGACAAAG Secretable GFP reverse TGGTGAAGCCTGCTTTTTGTAC Tbc1d8b mutation R64C mouse forward 5'- TAGCTCCATTTTGCATCCTACCAGGACACCA Tbc1d8b mutation R64C mouse reverse 5'- CAGGTGTAGGATGCAAAATGGAGCTACTTTAGCAGTGG Tbc1d8b mutation F438C mouse (1) reverse 5'- CAGGTATGTCACCCTCAAAATGGAGCTACTTTAGCAGTGG Tbc1d8b mutation F438C mouse (2) forward 5'- CAGGTATGTCACCCTCAAAATCTGGAAAATCTTGG Tbc1d8b mutation F438C mouse (2) reverse 5'- CTTTGTACAAGAAAGCTGGGTCCTATCACATCATGGTTCTAGACCTTAG Tbc1d8b mutation F438C mouse (2) reverse 5'- CTTTGTACAAGAAAGCTGGGTCCTATCACATCTTGGTTCTAGACCTTAG Tbc1d8b mutation F438C mouse (2) reverse 5'- CTTTGTACAAGAAAGCTGGGTCCTATCACATCTTGGTTCTAGACCTTAG Tbc1d8b mutation F438C mouse (2) reverse 5'- CTTTGTACAAGAAAGCTGGGTCCTATCACATCATGATTGCTCCTTCAGACCTTAG Tbc1d8b mutation T779S mouse reverse 5'- CACATTCTGCTTGATGTACTTCCAGGGTCTAGGATCACATA TBC1D8B gRNA A forward 5'- CACCGCATGCAGCTTTTTGGAAGGA TBC1D8B gRNA B forward 5'- CACCGGCACGACTCCTTCAGGGT TBC1D8B gRNA B forward 5'- CACCGGACGGGTTCCTTGC			5'-
Secretable GFP forward GCTTTCTTGTACAAAG Secretable GFP reverse TGGTGAAGCCTGAGCACCAGGAGGGCCACCAGTAAAGCAAAGGTCAAGGCCA Tbc1d8b mutation R64C mouse forward 5'- TAGCTCCATTTTGCATCCTACACCAGACACCA Tbc1d8b mutation R64C mouse reverse 5'- CTGGTGTAGGATGCAAAATGGAGCTACACCAGGGG Tbc1d8b mutation R64C mouse reverse 5'- CTGGTGTAGGATGCAAAATGGAGCTACAGTGGG Tbc1d8b mutation F438C mouse (1) reverse 5'- CAGATTTTGAGGGTGACATACTGTCATTAAGGCTTCAGTGTTC Tbc1d8b mutation F438C mouse (2) forward 5'- CAGTATGTCACCCTCAAAATCTGGAAAATCTTGG Tbc1d8b mutation F438C mouse (2) reverse 5'- CTTTGTACAAGAAAGCTGGGTCCTATCACATCTTGGTTCTAGACCTTAG Tbc1d8b mutation F438C mouse (2) reverse 5'- CTTTGTACAAGAAAGCTGGGTCCTATCACATCTTGGTTCTAGACCTTAG Tbc1d8b mutation F438C mouse (2) reverse 5'- CTTTGTACAAGAAAGCTGGGTCCTATCACATCATGATCTCAGACCTTAG Tbc1d8b mutation T779S mouse forward 5'- CTTTGTACAAGAAAGCTGGGTCCTATCACAGTGTGTAA Tbc1d8b mutation T779S mouse reverse 5'- CACCTTCCATTTTGGTAGCAGGA TBC1D8B gRNA A forward 5'- CACCGGCATGCAGTTATTGGAAAGGA TBC1D8B gRNA B forward 5'- CACCGGACGGTTCCTTGTCAGGGT TBC1D8B gRNA C forward 5'- CACCCGACGAGCGCTCCT			CCTGGTGCTCAGCTGCAAGTCAAGCTGCTCTGTGGGCTGTGATCTGCCTGACCCA
5'- CTTGACTTGCAGCTGAGCACCAGGAGGGCCACCAGTAAAGCAAAGGTCAAGGCCA Secretable GFP reverse TGGTGAAGCCTGCTTTTTGTAC Tbc1d8b mutation R64C mouse forward 5'- TAGCTCCATTTGCATCCTACACCAGACACCA Tbc1d8b mutation R64C mouse reverse 5'- CTGGTGTAGGATGCAAAATGGAGCTACTTTAGCAGTGG Tbc1d8b mutation F438C mouse (1) reverse 5'- CAGATTTTGAGGGTGACATACTGTCATTAAGGCTTCAGTGTTC Tbc1d8b mutation F438C mouse (2) forward 5'- CAGTATGTCACCCTCAAAATCTGGAAAATCTTG Tbc1d8b mutation F438C mouse (2) reverse 5'- CAGTATGTCACCCTCAAAATCTGGAAAATCTTG Tbc1d8b mutation F438C mouse (2) reverse 5'- CATTGTCACAGAAAGCTGGGTCCTATCACATCTTGGTTCTAGACCTTAG Tbc1d8b mutation F438C mouse (2) reverse 5'- CTTTGTACAAGAAAGCTGGGTCCTATCACATCATGACTTGGTTCTAGACCTTAG Tbc1d8b mutation T779S mouse reverse 5'- CTTGTACAAGAAAGCTGGGTCCTATCACAGGTGTGGATCACATA Tbc1d8b mutation T779S mouse forward 5'- CACCGCATCGCAGGATCATCAAGGAACGTGGGTCTGGATCACATA TBC1D8B gRNA A forward 5'- CACCGCATCGCAGTTATTGGAAAGGA TBC1D8B gRNA B forward 5'- CACCGGACGGGTCCTTGCAGGGT TBC1D8B gRNA B forward 5'- CACCGGACGACTCCTGCAGGGT TBC1D8B gRNA C forward 5'- CACCGACGACTACTTCGTGCAGG	Secretable GFP	forward	GCTTTCTTGTACAAAG
Secretable GFPreverseCTTGACTTGCAGCTGAGCACCAGGAGGGCCACCAGTAAAGCAAAGGTCAAGGCCATbc1d8b mutation R64C mouseforward5'- TAGCTCCATTTTGCACTbc1d8b mutation R64C mousefeverse5'- CTGGTGTAGGATGCAAAATGGAGCTACTTTAGCAGTGGTbc1d8b mutation R64C mousereverse5'- CAGATTTTGAGGGTGCAAAATGGAGCTACTTTAGCAGTGGTbc1d8b mutation F438C mouse (1)reverse5'- CAGATTTTGAGGGTGACATACTGTCATTAAGGCTTCAGTGTTCTbc1d8b mutation F438C mouse (2)forward5'- CAGTATGTCACCCTCAAAATCTGGAAAATCTTGTbc1d8b mutation F438C mouse (2)reverse5'- CTTTGTACAAGAAAGCTGGGTCCTATCACATCTTGGTTCTAGACCTTAGTbc1d8b mutation F438C mouse (2)reverse5'- CTTTGTACAAGAAAGCTGGGTCCTATCACATCTTGGTTCTAGACCTTAGTbc1d8b mutation T799S mouseforward5'- TGGAAGAGACATCAAAGCAGAAATGTGCTACCGTGGTTGTATbc1d8b mutation T779S mousereverse5'- CACATTCTGCTTTGATGTCTTCCAGGGTCTGGATCACATATBC1D8B gRNA Aforward5'- CACCGCATGCAGTTATTGGAAAGGATBC1D8B gRNA Aforward5'- CACCGGACGGGTCCTTGCAGGGTTBC1D8B gRNA Bforward5'- CACCGACGACTCGAAGGAACCCGTCCTBC1D8B gRNA Cforward5'- CACCGACGACTACTTCGTGCTGCAGGTBC1D8B gRNA Cforward5'- CACCGACGACTACTTCGTGCTGCAGGTBC1D8B gRNA Cforward5'- CACCGACGACTACTTCGTGCTGCAGGTBC1D8B gRNA Cforward5'- CACCGACGACTACTTCGTGCTGCAGGTBC1D8B gRNA Cforward5'- CACCGACGACTACTTCGTGCTGCAGG			5'-
Secretable GFPreverseTGGTGAAGCCTGCTTTTTGACTbc1d8b mutation R64C mouseforward5'- TAGCTCCATTTTGCATCCTACACCAGACACCATbc1d8b mutation R64C mousereverse5'- CTGGTGTAGGATGCAAAATGGAGCTACTTTAGCAGTGGTbc1d8b mutation F438C mouse (1)reverse5'- CAGATTTTGAGGGTGACATACTGTCATTAAGGCTTCAGTGTTCTbc1d8b mutation F438C mouse (2)forward5'- CAGTATGTCACCCTCAAAATCTGGAAAATCTTGTbc1d8b mutation F438C mouse (2)reverse5'- CTTTGTACAAGAAAGCTGGGTCCTATCACATCTTGGTTCTAGACCTTAGTbc1d8b mutation F438C mouse (2)reverse5'- CTTTGTACAAGAAAGCTGGGTCCTATCACATCTTGGTTCTAGACCTTAGTbc1d8b mutation F438C mouse (2)reverse5'- CTTTGTACAAGAAAGCTGGGTCCTATCACATCTTGGTTCTAGACCTTAGTbc1d8b mutation F438C mouse (2)reverse5'- CTTTGTACAAGAAAGCTGGGTCCTATCACATTGGTTCTAGACCTTAGTbc1d8b mutation T79S mouseforward5'- TGGAAGAGACATCAAAGCAGGAGCTGTGCTACGTGTTGTATbc1d8b mutation T779S mouseforward5'- CACCTGCAGCAGTTATTGGAAAGGATBC1D8B gRNA Aforward5'- CACCGCATGCAGTTATTGGAAAGGATBC1D8B gRNA Areverse5'- AAACTCCTTTCCAATAACTGCATGCTBC1D8B gRNA Bforward5'- CACCGGACGGGTTCCTTGTCAGGGTTBC1D8B gRNA Breverse5'- AAACACCCTGACAGGAACCCGTCCTBC1D8B gRNA Cforward5'- CACCGACGACTACTTCGTGCTGCAGTBC1D8B gRNA Cforward5'- CACCGACGACTACTTCGTGCTGCAGTBC1D8B gRNA Cforward5'- CACCGACGACTACTTCGTGCTGCAGTBC1D8B gRNA Cforward5'- CACCGACGACTACTTCGTGCTGCAG			CTTGACTTGCAGCTGAGCACCAGGAGGGCCACCAGTAAAGCAAAGGTCAAGGCCA
Tbc1d8b mutation R64C mouse forward 5'- TAGCTCCATTTTGCATCCTACACCAGACACCA Tbc1d8b mutation R64C mouse reverse 5'- CTGGTGTAGGATGCAAAATGGAGCTACTTTAGCAGTGG Tbc1d8b mutation F438C mouse (1) reverse 5'- CAGATTTTGAGGGTGACATACTGTCATTAAGGCTTCAGTGTTC Tbc1d8b mutation F438C mouse (2) forward 5'- CAGTATGTCACCCTCAAAATCTGGAAAATCTTG Tbc1d8b mutation F438C mouse (2) reverse 5'- CATTGTCACACGAGGGTCCTATCACACTTGGTTCTAGACCTTAG Tbc1d8b mutation F438C mouse (2) reverse 5'- CTTTGTACAAGAAAGCTGGGTCCTATCACACTTGGTTCTAGACCTTAG Tbc1d8b mutation F438C mouse (2) reverse 5'- CTTTGTACAAGAAAGCTGGGTCCTATCACATTGGTTCTAGACCTTAG Tbc1d8b mutation F438C mouse (2) reverse 5'- CTTTGTACAAGAAAGCTGGGTCCTATCACATCACATCAGACCTTAGACCTTAGACCTTAGACCTTAGACCTTAGACCTTAGACCTTAGACCCTTAGACACACAC	Secretable GFP	reverse	TGGTGAAGCCTGCTTTTTTGTAC
Tbc1d8b mutation R64C mouse reverse 5'- CTGGTGTAGGATGCAAAATGGAGCTACTTTAGCAGTGG Tbc1d8b mutation F438C mouse (1) reverse 5'- CAGATTTTGAGGGTGACATACTGTCATTAAGGCTTCAGTGTTC Tbc1d8b mutation F438C mouse (2) forward 5'- CAGTATGTCACCCTCAAAATCTGGAAAATCTTG Tbc1d8b mutation F438C mouse (2) reverse 5'- CTTTGTACAAGAAAGCTGGGTCCTATCACATCTTGGTTCTAGACCTTAG Tbc1d8b mutation F438C mouse (2) reverse 5'- CTTTGTACAAGAAAGCTGGGTCCTATCACATCTTGGTTCTAGACCTTAG Tbc1d8b mutation F438C mouse (2) reverse 5'- CTTTGTACAAGAAAGCTGGGTCCTATCACATCTTGGTTCTAGACCTTAG Tbc1d8b mutation F438C mouse (2) reverse 5'- CTTTGTACAAGAAAGCTGGGTCCTATCACATCACATCTTGGACCTTAGACCTTAG Tbc1d8b mutation T779S mouse reverse 5'- CACATTCTGCTTTGATGTCTCTTCCAGGGTCTGGATCACATA Tbc1d8b mutation T779S mouse reverse 5'- CACCGCATGCAGTTATTGGAAAGGA TBC1D8B gRNA A forward 5'- CACCGCATGCAGTTATTGGAAAGGA TBC1D8B gRNA A reverse 5'- AAACTCCTTTCCAATAACTGCATGC TBC1D8B gRNA B forward 5'- CACCGGACGGGTTCCTTGTCAGGGT TBC1D8B gRNA B reverse 5'- AAACCCCTGACAGGAACCCGTCC TBC1D8B gRNA C forward 5'- CACCGACGACTACTTCGTGCAG TBC1D8B gRNA C forward 5'- CACCGACGACTACTTCGT	Tbc1d8b mutation R64C mouse	forward	5'- TAGCTCCATTTTGCATCCTACACCAGACACCA
Tbc1d8b mutation F438C mouse (1) reverse 5'- CAGATTTTGAGGGTGACATACTGTCATTAAGGCTTCAGTGTTC Tbc1d8b mutation F438C mouse (2) forward 5'- CAGTATGTCACCCTCAAAATCTGGAAAATCTTG Tbc1d8b mutation F438C mouse (2) reverse 5'- CTTTGTACAAGAAAGCTGGGTCCTATCACATCTTGGTTCTAGACCTTAG Tbc1d8b mutation F438C mouse (2) reverse 5'- CTTTGTACAAGAAAGCTGGGTCCTATCACATTTGGTTCTAGACCTTAG Tbc1d8b mutation W460* mouse reverse 5'- CTTTGTACAAGAAAGCTGGGTCCTATCATGATTGCTCCTTCATCATCATCTTTTC Tbc1d8b mutation T779S mouse forward 5'- TGGAAGAGACATCAAAGCAGAATGTGCTACGTGTTGTA Tbc1d8b mutation T779S mouse reverse 5'- CACATTCTGCTTTGATGTCTCTTCCAGGGTCTGGATCACATA TBc1D8B gRNA A forward 5'- CACCGCATGCAGTTATTGGAAAGGA TBC1D8B gRNA A reverse 5'- AAACTCCTTTCCAATAACTGCATGC TBC1D8B gRNA B forward 5'- CACCGGACGGGTTCCTTGTCAGGGT TBC1D8B gRNA B reverse 5'- AAACCCCTGACAGGAACCCGTCC TBC1D8B gRNA C forward 5'- CACCGACGACTACTTGTCAGGGT TBC1D8B gRNA C forward 5'- CACCGACGACTACTTGTCAGGGT TBC1D8B gRNA C forward 5'- CACCGACGACCACCGACCGCTCC TBC1D8B gRNA C forward 5'- CACCGACGACTACTTCGTGCAGG TBC1D8B gRNA C	Tbc1d8b mutation R64C mouse	reverse	5'- CTGGTGTAGGATGCAAAATGGAGCTACTTTAGCAGTGG
Tbc1d8b mutation F438C mouse (2) forward 5'- CAGTATGTCACCCTCAAAATCTGGAAAATCTTG Tbc1d8b mutation F438C mouse (2) reverse 5'- CTTTGTACAAGAAAGCTGGGTCCTATCACATCTTGGTTCTAGACCTTAG Tbc1d8b mutation W460* mouse reverse 5'- CTTTGTACAAGAAAGCTGGGTCCTATCACATGTGCTCCTTCATCATCATCATCATCATCATCATCATCATCATC	Tbc1d8b mutation F438C mouse (1)	reverse	5'- CAGATTTTGAGGGTGACATACTGTCATTAAGGCTTCAGTGTTC
Tbc1d8b mutation F438C mouse (2) reverse 5'- CTTTGTACAAGAAAGCTGGGTCCTATCACATCTTGGTTCTAGACCTTAG Tbc1d8b mutation W460* mouse reverse 5'- CTTTGTACAAGAAAGCTGGGTCCTATCATGATTGCTCCTTCATCATCTTTC Tbc1d8b mutation T779S mouse forward 5'- TGGAAGAGACATCAAAGCAGAATGTGCTACGTGTTGTA Tbc1d8b mutation T779S mouse reverse 5'- CACATTCTGCTTTGATGTCTCTTCCAGGGTCTGGATCACATA Tbc1d8b mutation T779S mouse reverse 5'- CACATTCTGCTTTGATGTCTCTTCCAGGGTCTGGATCACATA TBc1D8B gRNA A forward 5'- CACCGCATGCAGTTATTGGAAAGGA TBC1D8B gRNA A reverse 5'- AAACTCCTTTCCAATAACTGCATGC TBC1D8B gRNA B forward 5'- CACCGGACGGGTTCCTTGTCAGGGT TBC1D8B gRNA B reverse 5'- AAACCCCTGACAGGAACCCGTCC TBC1D8B gRNA B reverse 5'- AAACACCCTGACAGGAACCCGTCC TBC1D8B gRNA C forward 5'- CACCGACGACTACTTCGTGCTGCAG TBC1D8B gRNA C forward 5'- CACCGACGACTACTTCGTGCTGCAG	Tbc1d8b mutation F438C mouse (2)	forward	5'- CAGTATGTCACCCTCAAAATCTGGAAAATCTTG
Tbc1d8b mutation W460* mouse reverse 5'- CTTTGTACAAGAAAGCTGGGTCCTATCATGATTGCTCCTTCATCTTTTC Tbc1d8b mutation T779S mouse forward 5'- TGGAAGAGACATCAAAGCAGAATGTGCTACGTGTTGTA Tbc1d8b mutation T779S mouse reverse 5'- CACATTCTGCTTTGATGTCTCTTCCAGGGTCTGGATCACATA TBc1D8B gRNA A forward 5'- CACCGCATGCAGTTATTGGAAAGGA TBC1D8B gRNA A reverse 5'- AAACTCCTTTCCAATAACTGCATGC TBC1D8B gRNA B forward 5'- CACCGGACGGGTTCCTTGTCAGGGT TBC1D8B gRNA B forward 5'- CACCGGACGGGTTCCTTGTCAGGGT TBC1D8B gRNA B forward 5'- CACCGGACGGGTTCCTTGTCAGGGT TBC1D8B gRNA B forward 5'- CACCGGACGGCTCCTTGTCAGGGT TBC1D8B gRNA A reverse 5'- AAACCCCTGACAGGAACCCGTCC TBC1D8B gRNA C forward 5'- CACCGACGACTACTTCGTGCTGCAG TBC1D8B gRNA C forward 5'- CACCGACGACTACTTCGTGCTGCAG	Tbc1d8b mutation F438C mouse (2)	reverse	5'- CTTTGTACAAGAAAGCTGGGTCCTATCACATCTTGGTTCTAGACCTTAG
Tbc1d8b mutation T779S mouse forward 5'- TGGAAGAGACATCAAAGCAGAATGTGCTACGTGTTGTA Tbc1d8b mutation T779S mouse reverse 5'- CACATTCTGCTTTGATGTCTCTTCCAGGGTCTGGATCACATA TBC1D8B gRNA A forward 5'- CACCGCATGCAGTTATTGGAAAGGA TBC1D8B gRNA A reverse 5'- AAACTCCTTTCCAATAACTGCATGC TBC1D8B gRNA B forward 5'- CACCGGACGGGTTCCTTGTCAGGGT TBC1D8B gRNA B forward 5'- CACCGGACGGGTTCCTTGTCAGGGT TBC1D8B gRNA B reverse 5'- AAACCCCTGACAGGAACCCGTCC TBC1D8B gRNA C forward 5'- CACCGACGACTACTTCGTGCTGCAG TBC1D8B gRNA C forward 5'- CACCGACGACTACTTCGTGCTGCAG	Tbc1d8b mutation W460* mouse	reverse	5'- CTTTGTACAAGAAAGCTGGGTCCTATCATGATTGCTCCTTCATCTTTTC
Tbc1d8b mutation T779S mouse reverse 5'- CACATTCTGCTTTGATGTCTCTTCCAGGGTCTGGATCACATA TBC1D8B gRNA A forward 5'- CACCGCATGCAGTTATTGGAAAGGA TBC1D8B gRNA A reverse 5'- AAACTCCTTTCCAATAACTGCATGC TBC1D8B gRNA B forward 5'- CACCGGACGGGTTCCTTGTCAGGGT TBC1D8B gRNA B forward 5'- CACCGGACGGGTTCCTTGTCAGGGT TBC1D8B gRNA B reverse 5'- AAACCCTGACAGGAACCCGTCC TBC1D8B gRNA C forward 5'- CACCGACGACTACTTCGTGCTGCAG TBC1D8B gRNA C forward 5'- CACCGACGACTACTTCGTGCTGCAG	Tbc1d8b mutation T779S mouse	forward	5'- TGGAAGAGACATCAAAGCAGAATGTGCTACGTGTTGTA
TBC1D8B gRNA A forward 5'- CACCGCATGCAGTTATTGGAAAGGA TBC1D8B gRNA A reverse 5'- AAACTCCTTTCCAATAACTGCATGC TBC1D8B gRNA B forward 5'- CACCGGACGGGTTCCTTGTCAGGGT TBC1D8B gRNA B reverse 5'- AAACCCCTGACAAGGAACCCGGTCC TBC1D8B gRNA C forward 5'- CACCGACGACTACTTGTCAGGGT TBC1D8B gRNA C forward 5'- CACCGACGACTACTTCGTGCTGCAG TBC1D8B gRNA C forward 5'- CACCGACGACTACTTCGTGCTGCAG	Tbc1d8b mutation T779S mouse	reverse	5'- CACATTCTGCTTTGATGTCTCTTCCAGGGTCTGGATCACATA
TBC1D8B gRNA A reverse 5'- AAACTCCTTTCCAATACTGCATGC TBC1D8B gRNA B forward 5'- CACCGGACGGGTTCCTTGTCAGGGT TBC1D8B gRNA B reverse 5'- AAACACCCTGACAAGGAACCCGTCC TBC1D8B gRNA C forward 5'- CACCGACGACTACTTCGTGCTGCAG TBC1D8B gRNA C forward 5'- CACCGACGACTACTTCGTGCTGCAG	TBC1D8B gRNA A	forward	5'- CACCGCATGCAGTTATTGGAAAGGA
TBC1D8B gRNA B forward 5'- CACCGGACGGGTTCCTTGTCAGGGT TBC1D8B gRNA B reverse 5'- AACACCCTGACAAGGAACCCGTCC TBC1D8B gRNA C forward 5'- CACCGACGACTACTTCGTGCTGCAG TBC1D8B gRNA C reverse 5'- AACCCTGCAGCACGACTACTCGTGCTGCAG	TBC1D8B gRNA A	reverse	5'- AAACTCCTTTCCAATAACTGCATGC
TBC1D8B gRNA B reverse 5'- AAACACCCTGACAAGGAACCCGTCC TBC1D8B gRNA C forward 5'- CACCGACGACTACTTCGTGCTGCAG TBC1D8B gRNA C reverse 5'- AAACCTGCAGCACGAGGAGTAGTCGTC	TBC1D8B gRNA B	forward	5'- CACCGGACGGGTTCCTTGTCAGGGT
TBC1D8B gRNA C forward 5'- CACCGACGACGACGACGACGACGACGACGACGACGACGAC	TBC1D8B gRNA B	reverse	5'- AAACACCCTGACAAGGAACCCGTCC
	TBC1D8B gRNA C	forward	
	TBC1D8B gRNA C	reverse	5'- AAACCTGCAGCACGAAGTAGTCGT

Supplemental Table 1: Primer sequences