

Supplementary Materials

Table S1. *In situ* hybridization primer sequences

Name	Sequence (5'-3')
<i>tnfaip1</i> probe F	TCTGCTGCACATCCATCGTT
<i>tnfaip1</i> probe R	TAATACGACTCACTATAGGGTCACGCAAAGTTCAAGCAGC
<i>neurod1</i> probe F	GGTGGGAATAGGCGTGAC
<i>neurod1</i> probe R	TAATACGACTCACTATAGGGACCCGAATAGTTTGAGCAG
<i>tuba1b</i> probe F	ATGCTGCTAATAACTATGCTCGTG
<i>tuba1b</i> probe R	TAATACGACTCACTATAGGGCCAACCTCCTCATAATCTTT
<i>ccnd1</i> probe F	CAACTTCATCGCAAGCCCTC
<i>ccnd1</i> probe R	TAATACGACTCACTATAGGGCGGTCATCAAAGCCACA

Table S2. *tnfaip1* sgRNA sequence and genotyping primer sequence

Name	Sequence (5'-3')
<i>tnfaip1</i> sgRNA1	AATTAATACGACTCACTATAACCAGCTTCAGCCACACACCGTTTTAG AGCTAGAAATAGC
<i>tnfaip1</i> sgRNA2	AATTAATACGACTCACTATACGCTGAACATGGATCTCAGCGTTTTAG AGCTAGAAATAGC
sgRNA scaffold	GATCCGCACCGACTCGGTGCCACTTTTTCAAGTTGATAACGGACTAG CCTTATTTTAACTTGCTATTTCTAGCTCTAAAAC
<i>tnfaip1</i> genotyping F	GGGAAATCAGACCCATCGTGT
<i>tnfaip1</i> genotyping R	AGGTTGCATCTTCTCTCAGGG

Table S3. qPCR primer sequences

Name	Sequence (5'-3')
<i>tnfaip1</i> qPCR F	GGTCTGATAGAACTGTTTATGCGTT
<i>tnfaip1</i> qPCR R	GGCTGATCGTGATGCCAAAC
<i>hsipa13</i> qPCR F	ACTCAATAAACAGGGCGGCA
<i>hsipa13</i> qPCR R	CATATTGCTGCCGAACCTCGC
<i>dhx40</i> qPCR F	AGAAGTGGGCTACCAAGTGC
<i>dhx40</i> qPCR R	AGCTGGGGTCTGCAAGAATC
<i>nppa</i> qPCR F	ATGGCCGGGGGACTAATTCT
<i>nppa</i> qPCR R	ATGCCTCTTCTGTTGCCAGG
<i>tnfrsf19</i> qPCR F	GAGAGTGCTGGAGTTGTCCC
<i>tnfrsf19</i> qPCR R	CAGCCTGCCATTGTCAGAGA
<i>clul1</i> qPCR F	CTTTGGCAGACGTGTGTTGG
<i>clul1</i> qPCR R	GACTCCCTGGCAGACTTCAC
<i>lrp2b</i> qPCR F	CGGATGGCTCACGCTATTCT
<i>lrp2b</i> qPCR R	GACGTAACTTGGGGCTCACA
<i>cryba1a</i> qPCR F	GCGCTTGCAGCTTTTTGTTG
<i>cryba1a</i> qPCR R	GCACGTTATCCATGCCACAC
<i>zbtb47a</i> qPCR F	CATGCGGACATGGCGAAAAA
<i>zbtb47a</i> qPCR R	CAGATCTGGCTGGAAGAGGC
<i>hsipb9</i> qPCR F	TGCAGAACCTGAGGAGTGAG
<i>hsipb9</i> qPCR R	GAGAAAAGCCTCGGGTGTCC
<i>adgrg4a</i> qPCR F	AGGACAGCGTACCCTGATTAC
<i>adgrg4a</i> qPCR R	GCCAAATGCAGGATCGGATT

ATGTCAGGAGAGAGCTGCCTGCACCAGCTTCAGCCAACACACCGGGCCCATC
CTGCCAGTCTCTTCAGTGGGCTACCCCAAGACTAACACCTGCACCTACCGTG
GTGTGACCGGAAATAAGTACGTTACGCTCAATGTTGGTGGAATCTGTACTA
CTCCACACTGCAGGTGCTCACTAGACAGGACACCCTGCTGAGATCCATGTTC
AGCGGCAAGATGGAGGTGCTCACAGATAAGGAAGGTTGGATCCTAAATAGAT
CGCTGTGGGAAACACTTTGGCTCCATTCTCAGCT

Figure S1. Partial sequence of the *tnfaip1* mutant related to Figure 2. Orange bases are the start codon. Red bases are the stop codon. The green nucleotide sequence in the black dashed box are the deleted 160 bases.