

trpv1^{ihb142/+} ZRC catalog ID: CZ269)

Nature of the mutation

In 704 bp of the wild-type *trpv1* coding sequence, C, is mutated into GAG in exon 5. The mutated *trpv1* codes for a truncated protein containing 252 aa, of which 813 aa are identical to wildtype *trpv1*.

Sense Strand Sequence

gacgacttccactactgagaaaccaggaaatgtgaaaagggttattgctctcaatgattgtgactcatcactgttgataacttaa
gcttacctttgtccacag**GTGAGCTGCCCTTGCTACTGGCTGCTTGCACTAATCA**
GCAAGACATTGTGGACTTTCTTATGGAAAACCCTCACCAGGCGGTGGA
TGTCAGGGAGAGGGACTGTCATGGAAACACCGTGCTTCACGCTTTAG
TATCCGTAGCTGATAATAGCCCTGAAAACACAGAGTTCGTCATCGCCAT
GTATGACCACATCCTAATCAAAGCTGACCAACTTCACCCAAGACCAA
GTTGGAGGAAATTGAAAATAATGAGGGACTGACCCAATCACACTCGC
TGCCAAAAGGGAAAAGTGGGgtaactatTTTTctgatgtttctgaatttaaattgtttagaatatga
aagctatggtttgcaaatcagtttatttgaagaagtgactcattgaagtagtctgcatgctttacgttctgtattttggtttgtagt
tcctttttgtagagatgagtagtcc

Uppercase: Exon/coding sequence

Lowercase: intron/noncoding sequence

atcg : Forward/Reverse primer

atcg : Crispr-Cas9 target site

Genotyping assay

Primers:

trpv1_forward: 5' GACGACTTCCACTACTGAGA 3'

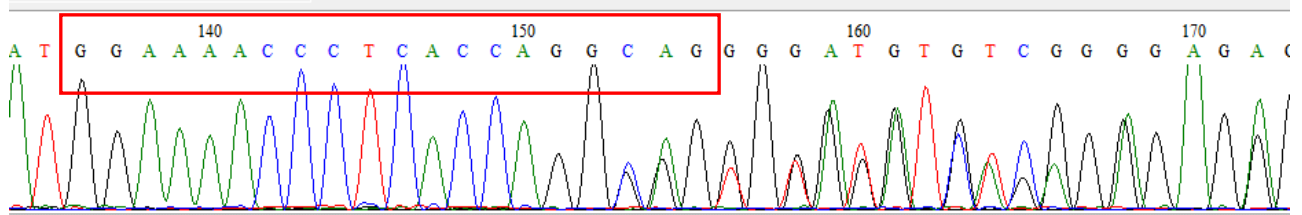
trpv1_reverse: 5' GGACTACTCATCTCTACAAA 3'

PCR program:

95°C 5min
95°C 30 sec
60°C 30 sec
72°C 30 sec } 30 Cycles
72°C 8min
4°C hold

Product size: 570 bp

The sequencing results of the CZ269(+/-):



CLUSTAL format alignment by MAFFT FFT-NS-i (v7.215)

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WT          GTGAGCTGCCCTTGTCACCTGGCTGCTTGCACCTAATCAGCAAGACATTGTGGACTTTCTTA
ZKD269     GTGAGCTGCCCTTGTCACCTGGCTGCTTGCACCTAATCAGCAAGACATTGTGGACTTTCTTA
*****

WT          TGGAAAACCCTCACCAGG--CGGTGGATGTCAGGGAGAGGGACTGTCATGGAACACCCGT
ZKD269     TGGAAAACCCTCACCAGGGAGGGTGGATGTCAGGGAGAGGGACTGTCATGGAACACCCGT
*****

WT          GCTTCACGCTTTAGTATCCGTAGCTGATAAATAGCCCTGAAAACACAGAGTTCGTCATCGC
ZKD269     GCTTCACGCTTTAGTATCCGTAGCTGATAAATAGCCCTGAAAACACAGAGTTCGTCATCGC
*****

WT          CATGTATGACCACATCCTAATC
ZKD269     CATGTATGACCACATCCTAATC
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Reference:

None