

***trpv1*^{ihb143/+} ZRC catalog ID: CZ270)**

Nature of the mutation

Between 702 bp to 703 bp of the wild-type *trpv1* coding sequence, GG, is mutated into AAA in exon 5. The mutated *trpv1* codes for a truncated protein containing 256 aa, of which 813 aa are identical to wildtype *trpv1*.

Sense Strand Sequence

gacgacttccactactgagaaaccaggaaatgtgaaaagggttattgctctcaatgattgtgactcatcactgttgataacttaa
gcttacctttgtccacag**GTGAGCTGCCCTTGCTACTGGCTGCTTGCACTAATCA**
GCAAGACATTGTGGACTTTCTTATGGAAAACCCTCACCAGGCGGTGGA
TGTCAGGGAGAGGGACTGTCATGGAAACACCGTGCTTCACGCTTTAG
TATCCGTAGCTGATAATAGCCCTGAAAACACAGAGTTCGTCATCGCCAT
GTATGACCACATCCTAATCAAAGCTGACCAACTTCACCCCAAGACCAA
GTTGGAGGAAATTGAAAATAATGAGGGACTGACCCCAATCACACTCGC
TGCCAAAAAGGGAAAAGTGGGgtaactatTTTTctgatgtttctgaattttaaatgttttagaatatga
aagctatggttgcaaatcagtttatttgaagaagtgactcattgaagtagtctgcatgctttacgttctgtattttggtttgatgt
tccttttttagagatgagtagtcc

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'

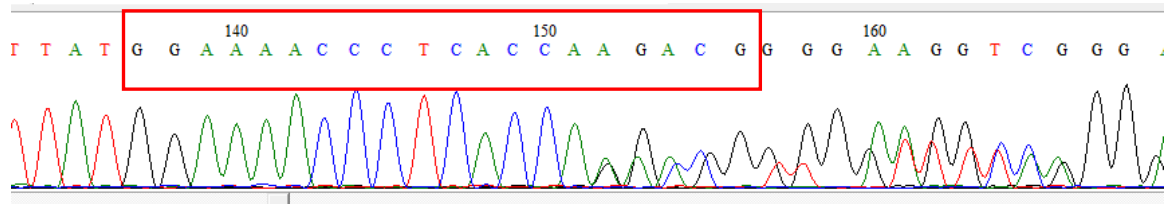
trpv1_reverse: 5' GGACTACTCATCTCTACAAA 3'

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 CZ270(+/-):



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

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WT          GTGAGCTGCCCTTGTCACTGGCTGCTTGCACTAATCAGCAAGACATTGTGGACTTTCTTA
ZK0270     GTGAGCTGCCCTTGTCACTGGCTGCTTGCACTAATCAGCAAGACATTGTGGACTTTCTTA
*****

WT          TGGAAAACCCTCACC-AGCGGTGGATGTCAGGGAGAGGGACTGTCATGGAACACCGTG
ZK0270     TGGAAAACCCTCACCAAAACGGTGGATGTCAGGGAGAGGGACTGTCATGGAACACCGTG
***** * . *****

WT          CTTCACGCTTTAGTATCCGTAGCTGATAATAGCCCTGAAAACACAGAGTTCGTCATCGCC
ZK0270     CTTCACGCTTTAGTATCCGTAGCTGATAATAGCCCTGAAAACACAGAGTTCGTCATCGCC
*****

WT          ATGTATGACCACATCCTAATC
ZK0270     ATGTATGACCACATCCTAATC
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Reference:

None