

## *trpv1*<sup>ihb141/+</sup> (CZRC catalog ID: CZ268)

### Nature of the mutation

4 bp deleted between 719 bp to 722 bp of the wild-type *trpv1* coding sequence, AGAG, is deleted in exon 5. The mutated *trpv1* codes for a truncated protein containing 250 aa, of which 813 aa are identical to wildtype *trpv1*.

### Sense Strand Sequence

**gacgacttccactactgaga**aaccaggaaatgtgaaaagggttattgctctcaatgattgtgactcatcactgttgataacttaa  
gcttacctttgtccacag**GTGAGCTGCCCTTGTC**ACTGGCTGCTTGCACTAATCA  
**GCAAGACATTGTGGACTTTCTTATGGAAAACCCTCACCA****GGCGGTGGA**  
**TGTCAGGGAGA**GGGACTGTCATGGAAACACCGTGCTTCACGCTTTAG  
TATCCGTAGCTGATAATAGCCCTGAAAACACAGAGTTCGTCATCGCCAT  
GTATGACCACATCCTAATCAAAGCTGACCAACTTCACCCCAAGACCAA  
GTTGGAGGAAATTGAAAATAATGAGGGACTGACCCCAATCACACTCGC  
TGCCAAAAAGGGAAAAGTGGGtaactatTTTTctgatTTTTctgaattttaaatgtttagaatatga  
aagctatggtttgcaaatcagtttatttgaagaagtgactcatttgaagtagtctgcatgctttacgttctgtattttggtttgtagt  
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'

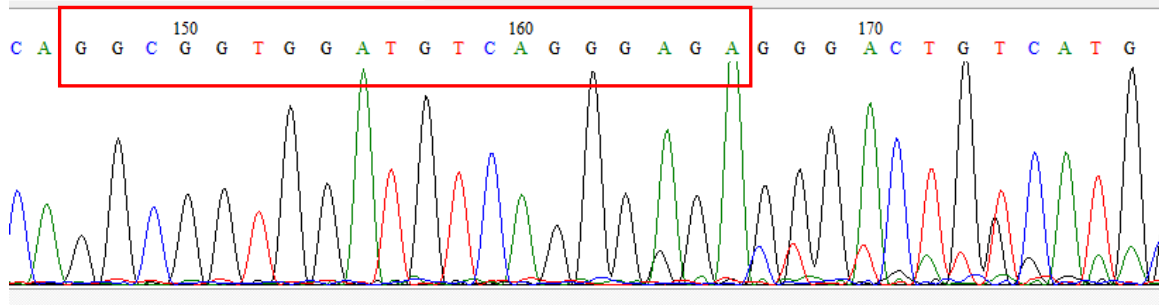
**trpv1\_reverse**: 5' GGACTACTCATCTCTACAAA 3'

#### 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 CZ268(+/-):**



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

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WT          GTGAGCTGCCCTTGTCAGCTGGCTGCTTGCCTAATCAGCAAGACATTGTGGACTTTCTTA
CZ268      GTGAGCTGCCCTTGTCAGCTGGCTGCTTGCCTAATCAGCAAGACATTGTGGACTTTCTTA
*****

WT          TGGAAAACCCCTCACCAGCGGTGGATGTCAGGGAGAGGGACTGTCATGGAACACCGTGC
CZ268      TGGAAAACCCCTCACCAGCGGTGGATGTCAGG----GGGACTGTCATGGAACACCGTGC
*****

WT          TTCACGCTTTAGTATCCGTAGCTGATAATAGCCCTGAAAACACAGAGTTCGTCATCGCCA
CZ268      TTCACGCTTTAGTATCCGTAGCTGATAATAGCCCTGAAAACACAGAGTTCGTCATCGCCA
*****

WT          TGTATGACCACATCCTAATC
CZ268      TGTATGACCACATCCTAATC
*****
    
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**Reference:**

None