

## *fzd8b*<sup>sdu22/+</sup> (CZRC catalog ID: CZ422)

### Nature of the mutation

Between 414 bp to 422 bp of the wild-type *fzd8b* coding sequence, GGATCCGAA is mutated to TACTGGG in exon1. The mutated *fzd8b* codes for a truncated protein containing 149 aa, of which 576 aa are identical to wildtype *fzd8b*.

### Sense Strand Sequence

ACCACGACAACCAGGATGAAGCCGGACTTGAGGTGCACCAGTTCTGGCCCCTCGTGG  
AGATCCAGTGTTCCCCTGACCTGCGCTTCTTTTTGTGCAGTATGTACACGCCTATTTGCT  
TGGAGGATTATAAGAAACCTTTGCCGCCGTGCAGGAGTGTGTGCGAGCGGGCGAAAG  
CGGGATGCGCGCCGCTGATGAGGCAGTACGGGTTCCCGTGGCCGGACAGAATGAGGT  
GCGATCTTCTACCTGTGCAGGGGGATCCGAACACTCTGTGTATGGACTACAACAGGAC  
TGATGCCACATCATCTCCAGCTGCTCCAAAAACAACAAGCCGACCAGGGAAACCATTC  
AAACGGAAAAATAAAAGCAGTCCTGGATCTTCATCTTGTGAACCGGAGTGTTACTGTC  
GCGCGCCGATGGTGCCCGTGCACAGTGACCACATCCGCTGTATA

Uppercase: Exon/coding sequence

Lowercase: intron/noncoding sequence

atcg : Forward/Reverse primer

atcg : TALENs target site

### Genotyping assay

#### Primers:

sdu22\_forward: 5' ACCACGACAACCAGGATGA 3'

sdu22\_reverse: 5' TATACAGCGGATGGTGGT 3'

#### PCR program:

95°C 5min

95°C 30 sec

58°C 30 sec

72°C 30 sec

72°C 8min

4°C hold

} 30 Cycles

Product size: 450 bp

The sequencing results of the CZ422:

CLUSTAL format alignment by MAFFT FFT-NS-i (v7.397)

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WT          AGAATGAGGTGCGATCTTCTACCTGTCAGGGGGATCCGAACTCTGTGTATGGACTAC
sdu22       AGAATGAGGTGCGATCTTCTACCTGTCAGGGTA--CTGGGCACTCTGTGTATGGACTAC
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**Reference:**

None