

## *fzd3a*<sup>sdu21/+</sup> (CZRC catalog ID: CZ421)

### Nature of the mutation

Between 759 bp to 761 bp of the wild-type *fzd3a* coding sequence, CTT is mutated to TCTTGGGCATATTCTTGGG in exon 4. The mutated *fzd3a* codes for a truncated protein containing 271 aa, of which 2058 aa are identical to wildtype *fzd3a*.

### Sense Strand Sequence

AGTTCAACGGGATTATGGCTTTTGGTGCCCGCGAGAGTTGAAGATCGAGCCCGACCTG  
GGTACTCCTTCATGGGCGTCCGTGACTGCTCTCCTCCCTGCCCAACATGTACTTCCG  
CAAAGACGAGCTCATCTTCGCCGCTATTCATCGGCGTCATTTCCATCGTCTGCCTATC  
TGC GACTCTGTTACACCTTCTTGACTTTTCTCATCGATGTGGGTCGCTCCGCTACCCCG  
AGCGTCCCATCATCTTCTACGCTGTC TGCTATATGATGGTATCTCTGGTCTTCTTCTTGGG  
CTTCTGTTGGAGGATCGTGTCTCATGTAACACAGCAAGCCCGGGTCGTTTCCGAGCC  
TCCACCATACCCAAGGCTCCCAACAATAAAGCATGCACCCACTCTTCATGACCCTCTA  
CTTCTTACCATGGCAGGAAGTGTGGTGGGTCATTCTCACCATCACCTGGTTCCTAG  
CAGCAGTCCCAAATGGGGAAGCGAGGCC ATCGAGAAGAAGGCTTTGCT

Uppercase: Exon/coding sequence

Lowercase: intron/noncoding sequence

atcg : Forward/Reverse primer

atcg : TALENs target site

### Genotyping assay

#### Primers:

sdu21\_forward: 5' AGTTCAACGGGATTATGGCT 3'

sdu21\_reverse: 5' AGCAAAGCCTTCTTCTCGAT 3'

#### PCR program:

95°C 5min  
95°C 30 sec  
58°C 30 sec } 30 Cycles  
72°C 30 sec  
72°C 8min  
4°C hold

Product size: 522 bp

The sequencing results of the CZ421:

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

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WT          CTGGTCTT-----CTTCTTGGGCTTCCTGTTGGAGGATCGTGTCTCATG
sdu21       CTGGTCTTGGGCATATTCTTGGGCTTCTTGGGCTTCCTGTTGGAGGATCGTGTCTCATG
***.      *                               *****
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**Reference:**

None