

## ***flrt2*<sup>ihb414/+</sup> (CZRC Catalog ID: CZ 1358)**

### **Nature of the mutation**

Between 286bp to 289 bp of the wild-type *flrt2* coding sequence, TACG, is deleted in exon 1.

### **Sense Strand Sequence**

GTAATGAGAGGAGCCTGACG TCTGTGCCTCTGGGGGTGCAAGAGGGATACAAGAC  
CCTCTTCCCTCCACAACAATCAGATCAATAATGCCGGCTTTCCATTGGAGCTACACAA  
TGTTGCCTCTGTAGAAACGGTTTACCTGTACGGGAATCAGCTGGATGAATTTCCC  
TTAACCTTCCGAAGAATGTCCGAGTGTTCATCTCCAGGAAAACAACATCCAGAC  
CATTCCAGGGCAGCACTTGCCCAGCTACACATGCTGGAGGAACTCCACCTGGAT  
GACAACTCCATCTCAACTGTAGGGGTAGAGGAGGGGGCTTTTAGGGAGGCTCTCA  
GTCTCAAACCTTTTTCCTCACCAAAAACCATCTAAGCAGTATCCCTATCGGATTAC  
CTGCAGACCTAAAGGAGCTGCGTTTGGATGAGAATCGAATTGCAGACATTGACGA  
GGATGCCTTTCAGAATGTCACCACCCTGCAGCGACTGTTACTGGATGGAACTTGC  
TTGAGGATGAGGCCATTGCTCCTGGTACCTTCCAGGATTTGGTCAATCTCAAAGAA  
CTGTCCCTGGCAGCAACTCCCTCACCGCTCCACCACCATTGCTCCCTAGCGTATC  
CCTAACTAAGCTCAACCTGCAGGAAAACCAGATAGACA CTATTGAAGTGACAGCC  
TTT

Uppercase: Exon/coding sequence

Lowercase: intron/noncoding sequence

atcg : Forward/Reverse primer

atcg : Crispr/cas9 target site

### **Genotyping assay**

#### **Primers:**

**flrt2\_forward:** 5' GTAATGAGAGGAGCCTGACG 3'

**flrt2\_reverse:** 5' AAAGGCTGTCACTTCAATAG 3'



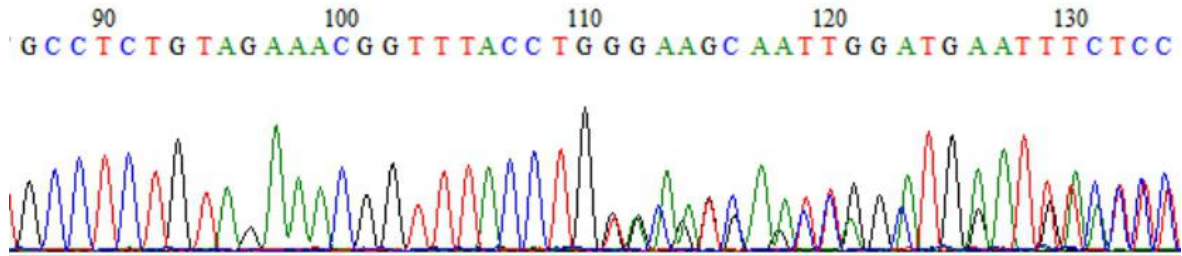


**PCR program:**

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: 671 bp**

The sequencing results of the *flrt2<sup>ihb414/+</sup>* :



WT	TCTTCCTCCACAACAATCAGATCAATAATGCCGGCTTTCCATTGGAGCTACACAATGTTG
ihb414	TCTTCCTCCACAACAATCAGATCAATAATGCCGGCTTTCCATTGGAGCTACACAATGTTG
	*****
WT	CCTCTGTAGAAACGGTTTACCTGTACGGGAATCAGCTGGATGAATTTCCCCTTAACCTTC
ihb414	CCTCTGTAGAAACGGTTTACCT----GGGAATCAGCTGGATGAATTTCCCCTTAACCTTC
	*****

**Reference:**

None

