



## *pdgfrb*<sup>ihb440/+</sup> (CZRC catalog ID: CZ1390)

### Nature of the mutation

Between 703 bp and 707bp of the wild-type *pdgfrb* coding sequence, TTCTC are deleted in exon 4.

### Sense Strand Sequence

**gctccgctatctgccaatca**tcataaacgagccaagtctgccataaacgcatcagatgattgtttcaatgaacaatggcgttttgtt  
ctctcacatgtgttcagCTCCCGAGGCTCTGGATCCCTACATCAACGCCTCCAAAACGGTC  
CTAAAGCAGGGCGAGACGCTCAACGTCAACTGCACCGTTCACGGCGT**GGAGCTG**  
**GTCTTCTTCTCT**GGGATTTCCCAACAAAGACgtgagtgggctggaataaacgctttgtttcattact  
ccccatcggagcctcatgagaagagctgaatgagctcaagatgtgaaccacacctcactgtcacgaccagcagcgttttattaaga  
gatgcatcagaatagtacgaagtaatacagttgaagtcataagttctatatttctaacaaaataactcatttctaataactaattacgtt  
atctttccatgatgacagctgcagaatattaacttccaagacactagtatttagctcaaagt**gacatttagaggcttaatt**

Uppercase: Exon/coding sequence

Lowercase: intron/noncoding sequence

**atcg** : Forward/Reverse primer

**atcg** : Crispr/cas9 target site

### Genotyping assay

#### Primers:

*pdgfrb* \_forward: 5' GCTCCGCTATCTGCGAATCA 3'

*pdgfrb* \_reverse: 5' AATTAAGCCTCTAAATGTCA 3'

#### PCR program:

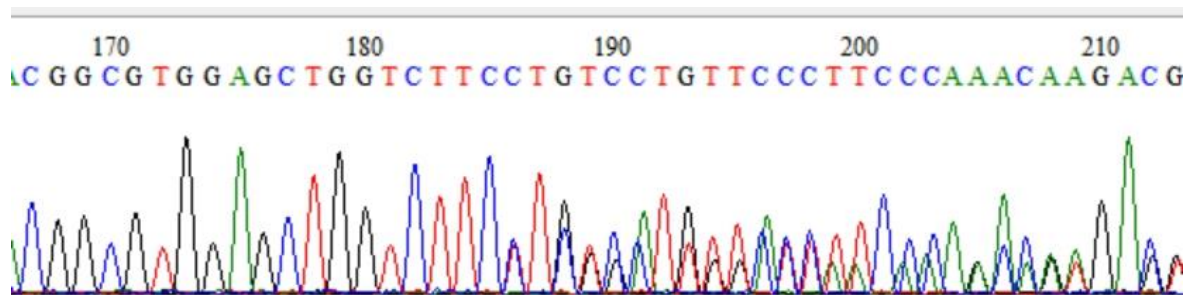
95°C	5min	} 30 Cycles
95°C	30 sec	
55°C	30 sec	
72°C	30 sec	
72°C	8min	
4°C	hold	

Product size: 551 bp





The sequencing results of the CZ1390(+/-):



WT	GGCTCTGGATCCCTACATCAACGCCTCCAAAACGGTCCTAAAGCAGGGCGAGACGCTCAA
CZ1390	GGCTCTGGATCCCTACATCAACGCCTCCAAAACGGTCCTAAAGCAGGGCGAGACGCTCAA
	*****
WT	CGTCAACTGCACCGTTCACGGCGTGGAGCTGGTCTTCTTCTCCTGGGATTTCCCAACAA
CZ1390	CGTCAACTGCACCGTTCACGGCGTGGAGCTGGTCT-----TCCTGGGATTTCCCAACAA
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