

## *esr1<sup>ihb248/+</sup>* (CZRC catalog ID: CZ455)

### Nature of the mutation

Between 580 bp to 581 bp of the wild-type *esr1* coding sequence, TG is mutated to CGAC in exon 4.

### Sense Strand Sequence

actcttggctgtgacggaacagttttacattttgctaatacaaaagtttctgaaggaaaacctctctgaaagctgagctgaagaagatctgg  
catgagtttctactgtgcattttggttgagcatgattgcttaagaatgatgaaaaacaagcactgctttatttccaccttagGTCACAA  
TGACTATGTTTGTCCAGCGACCAACCA**GTGCACTATTGACAGAAACC**GTCGAAAGAGC  
TGCCAAGCATGCAGACTGCGCAAGTGTTATGAAGTAGGCATGATGAAAGGAGgtacattttat  
atatatataatactattttttctctccatctatatgtaaatatcatctgctcattgatcatgattaaagcagcctctgtagagtttctccagtg  
tcaagaattgagcaaaattcgaattaaaggatcttctccaaaattatcctctgctgactgtatatattatattacataaatatgattaga  
catatacaaaagtaacttatagaagtgagtac**agccctcacattttgtaaa**

Uppercase: Exon/coding sequence

Lowercase: intron/noncoding sequence

**atcg** : Forward/Reverse primer

**atcg** : Crispr/cas9 target site

### Genotyping assay

#### Primers:

**esr1\_forward**: 5' ACTCTTTGTTGCTTGTGACG 3'

**esr1\_reverse**: 5' TTTACAAAAATGTGAGGGCT 3'

#### PCR program:

95°C 5min

95°C 30 sec

60°C 30 sec

72°C 30 sec

72°C 8min

4°C hold

} 30 Cycles

**Product size: 572 bp**

### The sequencing results of the CZ455:

```
WT      caagcactgctttatttctccaccttagGTCACAATGACTATGTTTGTCCAGCGACCAA
CZ455   caagcactgctttatttctccaccttagGTCACAATGACTATGTTTGTCCAGCGACCAA
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WT      CCACTG--CACTATTGACAGAAACCGTCGAAAGAGCTGCCAAGCATGCAGACTGCGCAAG
CZ455   CCACCGACCACTATTGACAGAAACCGTCGAAAGAGCTGCCAAGCATGCAGACTGCGCAAG
***.* *****
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### Reference:

None