

ybx1^{tsu27/+} (CZRC catalog ID: CZ412)

Nature of the mutation

Between 89 bp to 91 bp of the wild-type *ybx1* coding sequence, GGG is mutated to TCATC in exon 1. The mutated *ybx1* codes for a truncated protein containing 43 aa, of which 309 aa are identical to wildtype *ybx1*.

Sense Strand Sequence

TAGATTGGGGAATGGGTGGA GAGATGTGACAGAATATCGTCCGGCATT TTTACTCAGTC
CGTCCAGTTCGATCGGCAACGGGAGCGGAGAAAGGAAAGCGGAGAGCCCGAAGGCA
GCAGCCCCACCACCGCCGGCCAGGTTACCATCTAGCACCGGAAAACACACTAGA
GAGCCACCGCCGGCTTTACCAACAAGAAAACAACATGAGCAGCGAGGCCGAGACACA
ACAGCCGCCGCAGCCTGCCGCCGACGCGGAGAGCCCGTCCAGCCCGGCAGCCGCAGC
TACCGCGGGGATAAGAAGGTCATCGgtaagcttgcggcgaaaccaagccccctggcctgcggtcgtttaagttt
cggataatacattttctaaacgtccagggttatttcagttatgttacaaaatgtatgtcagttcaagaaaggccacgctgtctgcgactgtct
gtcgttattccgtaccaacttaattgtgtctgtaccggtggcgtcctgcctggattttgtttggagctgtccggttatttaccacatgtaagatt
tacgtacattaacttgagacgttaaacggtttcaccagtttgaatgtaac

Uppercase: Exon/coding sequence

Lowercase: intron/noncoding sequence

atcg: Forward/Reverse primer

Genotyping assay

Primers:

CZ412_forward: 5' TAGATTGGGGAATGGGTGGA 3'

CZ412_reverse: 5' GTTAACATTCAAACCTGGGTG 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:617 bp

The sequencing results of the CZ412:

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

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WT          ACGCGGAGAGCCCGTCCAGCCCGGCAGCCGCAGCTACCGCGG--GGGATAAGAAGGTCAT
CZ412       ACGCGGAGAGCCCGTCCAGCCCGGCAGCCGCAGCTACCGCGGTCATCATAAGAAGGTCAT
*****.*****
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WT          CG
CZ412       CG
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Reference:

None