

lurap1^{sdu20/+} (CZRC catalog ID: CZ420)

Nature of the mutation

Between 34 bp to 40 bp of the wild-type *lurap1* coding sequence, CCTGATT is mutated to GAAAGTGAAAAG in exon 2. The mutated *lurap1* codes for a truncated protein containing 254 aa, of which 286 aa are identical to wildtype *lurap1*.

Sense Strand Sequence

ctgtaacgcagaatgactgctatgtgtttacaataaccacaatgttacataagacttttgaggcataataaagcaaatatcag
cggggcgcaaaataaaacttcaataaataaaatttccttctttttactcattttctttttctttatgtagaccgtttctaatacA
TGGAGGAGAGT**AATAATACCTGTGAG**TCAGTTCCTGATTTGAA**AGATCTGG**
AGTTGAAAGTGGGTAGAAAGACCCCAGAAGGGCTCCTGAAGTGGATGAG
AGAAGAGCACAAGATGATCTCTCATCATCAGACTGACAATAATGAGACTGA
GAAGAAAGGTCTCGATGGGAAGATACGAAAACCTTAAAATGGAGATGGTAA
GAGTCAAATCTATGCATTGCACATTAACGATTATTCGAGCATAAATTA
ATTCATAATTTTAAACACAATTTCAATAAATTCACATTTAGACATCTAAGTG
CAGATTAATTGCATTAATGAAAGAAA**GCTGTGACAACCTAAAGGGCT**

Uppercase: Exon/coding sequence

Lowercase: intron/noncoding sequence

atcg: Forward/Reverse primer

atcg: TALENs target site

Genotyping assay

Primers:

sdu20_forward: 5' CTGTAACGCAGAATGACTGTC 3'

sdu20_reverse: 5' AGCCCTTTAGTTGTACAGC 3'

PCR program:

95°C 5min

95°C 30 sec

58°C 30 sec

72°C 30 sec

72°C 8min

4°C hold

} 30 Cycles

Product size: 529 bp

The sequencing results of the CZ420:

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

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WT          ATGGAGGAGAGTAATAATACCTGTGAGTCAGTT-----CCTGATTGAAAGATCTGGAGT
sdu20       ATGGAGGAGAGTAATAATACCTGTGAGTCAGTTGAAAGTAAAAGTAAAGATCTGGAGT
*****
WT          TGAAAGTGGGTAGAAAAGACCCAGAAAGGGCTCCTGAAGTGGAT
sdu20       TGAAAGTGGGTAGAAAAGACCCAGAAAGGGCTCCTGAAGTGGAT
*****
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Reference:

None