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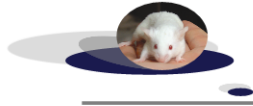
Email: [ics@igbmc.fr](mailto:ics@igbmc.fr)

Web site: <http://www.phenomin.fr/en-us/>

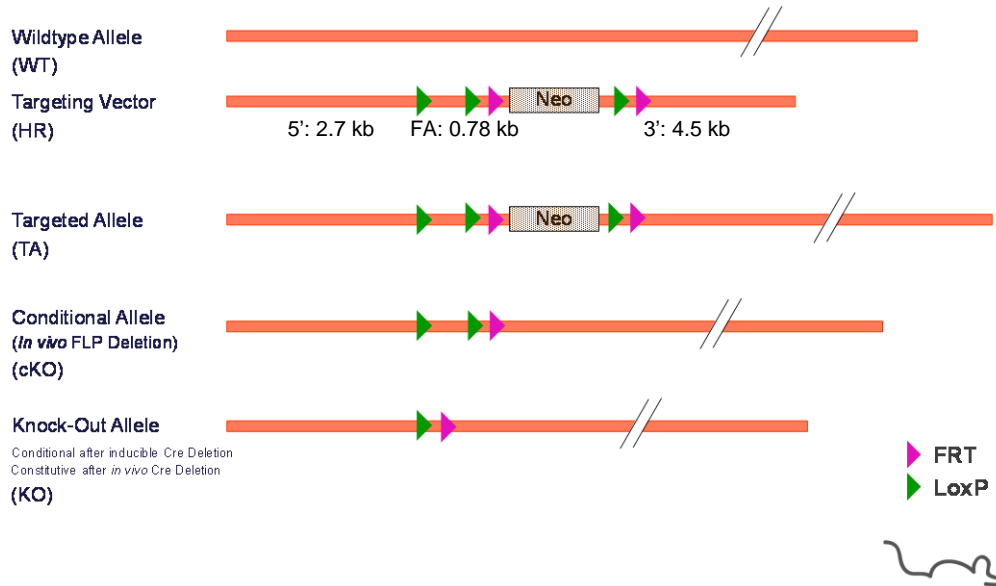
This protocol has been prepared by Claudia Caradec, Engineer  
This protocol has been validated by Sylvie Jacquot, Ph.D., Project Manager

1. Schematic representation of the locus

1.1. Overview



## Overview Targeting Strategy



Legend:

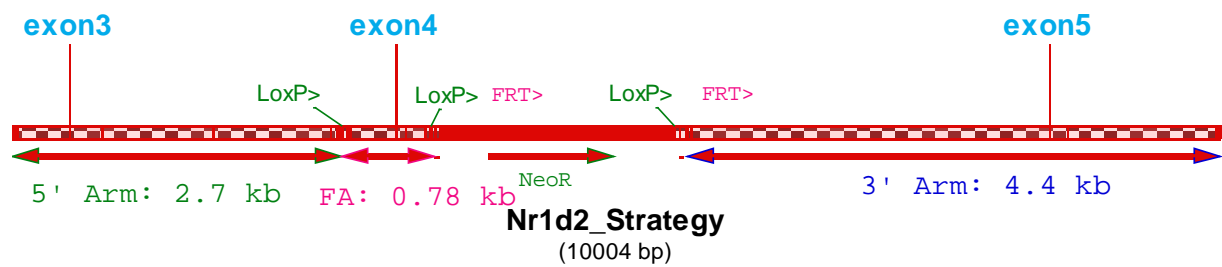
5': 5' homology arm;    FA: floxed fragment;    3': 3' homology arm  
 This schematic representation is not on scale

**1.2. Strategy chosen: flox of exon 4**

Nr1d2 gene (also named RevErb beta) is a member of the nuclear receptor family. Additional information on this gene can be accessed at

<http://www.informatics.jax.org/javawi2/servlet/WIFetch?page=markerDetail&key=86572>

**Strategy used to generate the conditional knock out model**



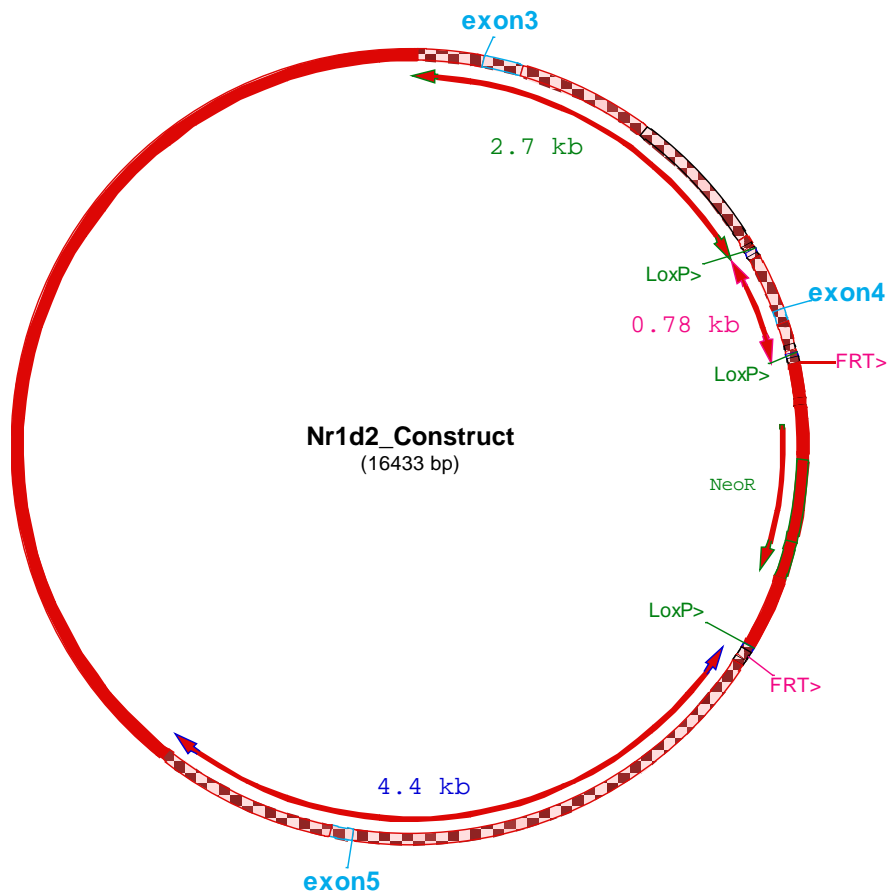
2. Construct used for homologous recombination in ES cells: Nr1d2 project

**2.1. Legend**

loxP sites are indicated in green ; FRT sites are indicated in purple; *Mus musculus* sequences are indicated in uppercase ; exogenous sequences are marked in lowercase.

The targeting vector was generated in 129Sv/Pas and was not fully sequenced.

**2.2. Map of targeting vector plasmid**





attctaccgggtaggggagggcgcttttcccaaggcagctctggagcatgcgcttttagcagccccgctgggcacttg  
gcgctacacaagtggcctctggcctcgcacacattccacatccaccggtaggcgccaaccggctccgttctttgg  
tggcccccttcgcgccacccttctactcctcccctagtcaggaagtcccccccgccccgagctcgcgctcgtag  
gacgtgacaaatggaagtagcacgtctcactagctctcgtgcagatggacagcaccgctgagcaatggaagcgggt  
aggcctttggggcagcggccaatagcagctttgctccttcgctttctgggctcagaggctgggaaggggtgggtc  
cgggggccccgctcaggggccccggttcaggggccccggtggcggaaggtcctattgtgagcgtcacaatccccgc  
attctcgaagcttcaaaagcgcacgtctgccgcgctattgtgagcgtcacaattccgggctttcgagaagga  
gccaatatgggatcggccattgaacaagatggattgcacgcaggttctccggcgcgttgggtggagaggctattc  
ggctatgactgggcacaacagacaatcggctgctctgatgccgcgctgtccggctgtcagcgcaggggccccg  
gttctttttgtcaagaccgacctgtccgggtgccctgaatgaactgcaggacgaggcagcgcggctatcgtggctg  
gccacgacgggcttcccttgcgcagctgtgctcgacgttctcactgaagcgggaagggactggctgctattgggc  
gaagtgcggggcaggatctcctgtcatctcacttgcctcctgccgagaaagatccatcatggctgatgcaatg  
cggcggctgcatacgttctgacggctacctgcccattcgaccaccaagcgaacatcgcatcgagcagcagcgt  
actcggatggaagccggctcttctgctcagcaggtgatctggacgaagagcatcaggggtcgcgcccagccgaactg  
ttcgccaggctcaaggcgcgcagctcccgcagggcagggatctcgtcgtgacctatggcgatgctgcttgcgcaat  
atcatggtggaataatggcgcgctttctggattcatcgactgtggcggctgggtgtggcggaccgctatcaggac  
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atcgcgctcccgatcgcagcgcacgccttctatcgcttcttgacgagttcttctgaggggacgatccgct  
gtaagtctgcagaaattgatgatctattaacaataaagatgtccactaaaatggaagttttcctgtcactactt  
tgtaagaaggtgagaacagagtagctacattttgaatggaaggattggagctacgggggtgggggtgggggtgg  
gattagataaatgctgctctttactgaaggctctttactattgctttatgataatgtttcatagttggatatca  
taatttaacaagcaaaaccaaattaagggccagctcattcctcccactcatgatctatagatctatagatctct  
cgtgggatcattgtttttctcttgattcccactttgtggttctaagtagctgtggtttccaatgtgtcagtttca  
tagcctgaagaacgagatcagcagcctctgttccacatacacttcatctcagtagttgttttgcaagttcta  
tccatcagaagctgactctagatctggatccataacttcgtataatgtatgctatacgaagttatctcgaggaag  
ttcctattctctagaaagtaggaacttcaaggtcctcgcctctgctcgtccggtgagct

### 2.6. 3' homology arm (4.5 kb)

GGCCAGCTAGGCCGAGCAGTTCAGTTCTAGTTTCATTCCTCTCCAGTCAGGTACAGGCCTTGATGGTCAGGAAACA  
GGTATGAGCCAGAGAGATAGGGCAGTGCCTACTACCTTGTGGAGCACTTCTTTTCTTCTTTTGGAAACAGAGTC  
TGAGGTAGTCTATGACTGGCCAGAACTTGCTGTGTATGACAGTGGAGGATGACCTAGTACTTGTATGTATAGC  
AGTGAAGATGACCTAGCGTTTTTGTATCCTGCTTCTGCCAAGGGCTGGGATTATAGGCATAGGCCTGTGCATG  
TAAACCAAGATTTGAGTTAAGTTTTTGTCTGTTTTGCTCAAGCTGATCACACCACAGGTGGAGAAAATTTGAAAATT  
AATTTGCTTTCAGCAGTTTGAAGACTAGGGGCTGCATCTTGGGAGGCCTTTCTGTTGGAGGATGGAAGGCATTGAA  
TAGAAACATCATGCTCATGTGTAAGAATGTGAACATAAGTGTGTATAGAAATGAGCCCAGCCACATTTTTTGT  
TTGTTTTAGGCAGGGTTTTTCTGTGTAGCCATGGTACTATGTAGCTATGTAGAGCAACCAGGCTGGCCTCAA  
CACAGAGGTCTACCTGCCTCTGCTGGGATTAAGGCATGCACCATCATGCCTGACTCCTAATGTATTCATAACAA  
ATTCATTTTCATATTAACATTAGCCAATTCAGAAAGCAGACACCCTATGACACATGCAGCACTGTGTATAGG  
GGTGTAGTTTTCTAGAACATGATCCTTGGGGAACATAGACCACATTAGCTCTTATCCTGTAGTACTGTGGAC  
TCGGAATAACTGCTAAGTGTATTTAATAATGTAGTGTGCTGAGAAAATAATGCTTGGGCAAGGATGTGTGATG  
CTAAGCTAGCCTGAGCTACTTAGCAAGATCTTATCTCAAACACAAAACAAAATAATAGCAACAAAACAGTA  
GAATACAAATGAGTCAGATCATTAAGTAGAACACACAGGAAAGAGTTAATTTCTAGTGTATGCAACCAGAACTCT  
AGGTAAGCTCTTTGAGGTGGCCCCGCCTCCTCACGTACATCCAGAATCTCTCTTAAATCTGACACAACTCTTTTT  
TTCTGTAACCAACAAGATCAACATGTGTTCTTGTTTTTCTCACTGTAGGCGAGAGTAAACAACCAAAATGGCAGG  
ATGTGACAGGGTGAATAAGATAAGAAAAATAAGTCTCTCCTGGGACAAAATCTGAAGAAGTTGAGTCTGGGAGTT  
TTAATGACTAGTAAGTGTTTTTTTCTGTAGACGTAGCTCTTTTTCTATTGTCTTAGAGAATGTATATATATTTT  
AAAGAAAATGTAAAGTATTTTAAAGTTAAATTCATGCTCAGTTTTGCAGTTAGATAATATAACAACAATTTGAATG  
AAATGTATTATATATTTCTTTTTAAAAGTATCTTTTTAAATGTGTATTACTGGTTTTGCCTGGATGTGTGTCTATG  
TACCACTTGAGTTCTGGTGGCCATGGAGTCTAGAAGAGGGCGTCAGATCTACTACAGCAAGAGCTACAAATGGT  
TGTAAGCTGCCATGTGGGTGCTGGAGAGCAGCTGGTGTCTTCAACCACTGAGCCATCTCTCATCACTATATTTGAT  
AAATACAAATAATTGATCAATATCTTGGTAGTATTTGTTTTGAGACAGGGTCTTCTGAAAGTAGCCAGGCTGGCTT  
AGACTCAAAATCTGCCTTAGCTTTTCAAGTTACTGTGATTACTTGGAAATCAAGTAATGTAAACCATGCTAAATG  
CATACTTTTGGGGTAGTGTGTGCTGGGAATGAGACCAAGGTCTAACAAGTTTAGGCAAAATACTTTACCTTGAT  
CCACCTCATAGATTCTAGTACCCTCTTTTTACTTGTTTTTGTTTTGTTTTGCTTGTTTGTTTTATTTTTTAGTCCGG  
GTTTTCTTTGGGTGGTGTGGCTATCCTGGAACCTCGCTCTATAGCCCAGGCTGGCAGAACTCACAGAGATCCACCT  
ACCTCTGCCTCCAGAGTGTGGGATTCGAAGCATGACACCACCAAGTCTCAGTCTCTTAAAAATG  
CATTTTTCTTAGCTTTGCATAATTTAAAACAAGTATATAGTATCATAAACAGTAAAATGCAAAAGTGTATATCT  
GGTCAATATTTAATAAGATGTATCGTGTAGTCAGTTATAATATTAAGGGGATATGCAGTTTGAAGTGAATTTTTA  
GTTGTTTTTTCTTGAGTTTTGTGTTTTTTCTTAGGAAAATTGAGCTTGGGGTAGATGAAGATCTGGCAGATAGAGCAT







3. ES cell lines targeted and validation data:

**3.1. ES cell lines targeted**

The targeting vector was electroporated in P1 ES cells [MCI-129Sv/Pas background]

Number of clones screened: ~ 300

Number of positives: 3

Reference of clone used to generate the mouse line:

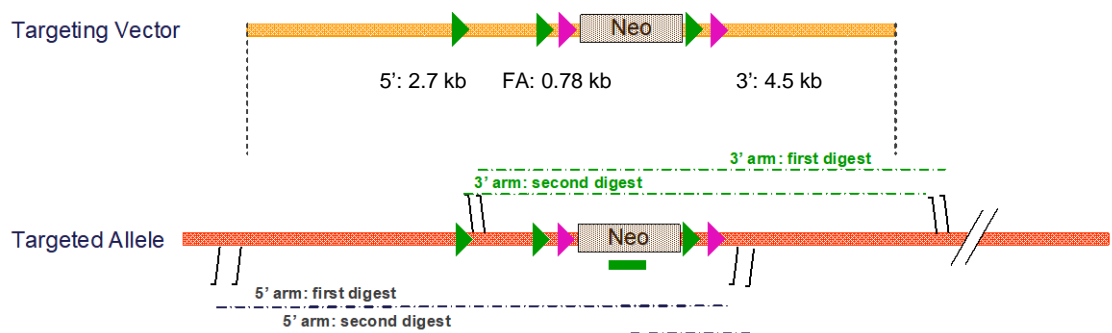
- clone **DG5-162**

**3.2. Southern data on positive clone**

**3.2.1. Neo Southern strategy**



## Southern Screening Strategy



■ Neo probe  
▲ FRT  
▲ LoxP

Digestions used to validate the 5' and 3' insertion

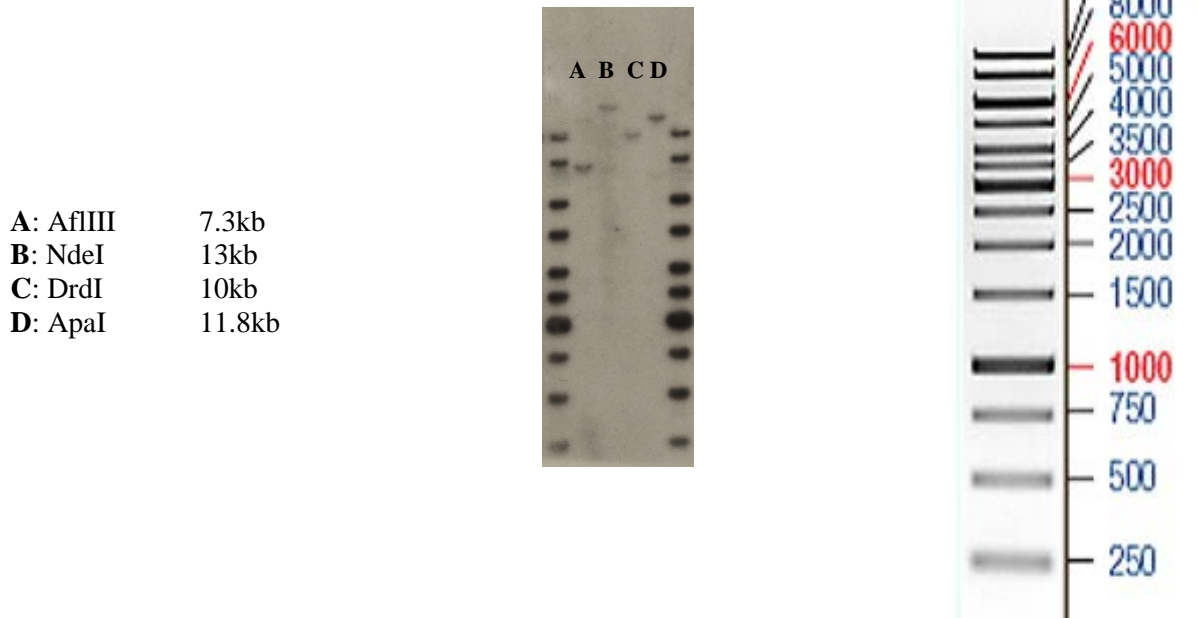
| Probe | Name                 | Genomic DNA digest | WT allele (kb) | Targeted Allele (kb) |
|-------|----------------------|--------------------|----------------|----------------------|
| Neo   | 5' arm first digest  | AflIII             | /              | 7.3                  |
|       | 5' second digest     | NdeI               | /              | 13                   |
|       | 3' arm first digest  | DrdI               | /              | 10                   |
|       | 3' arm second digest | Apal               | /              | 11.8                 |

Four different digests are used to validate correct HR event. Two digests validate the 5' insertion, 2 other digests validate the 3' insertion

**3.2.2. Picture of Neo Southern**

Neo southern blot: 5' and 3' arm validation

ladder



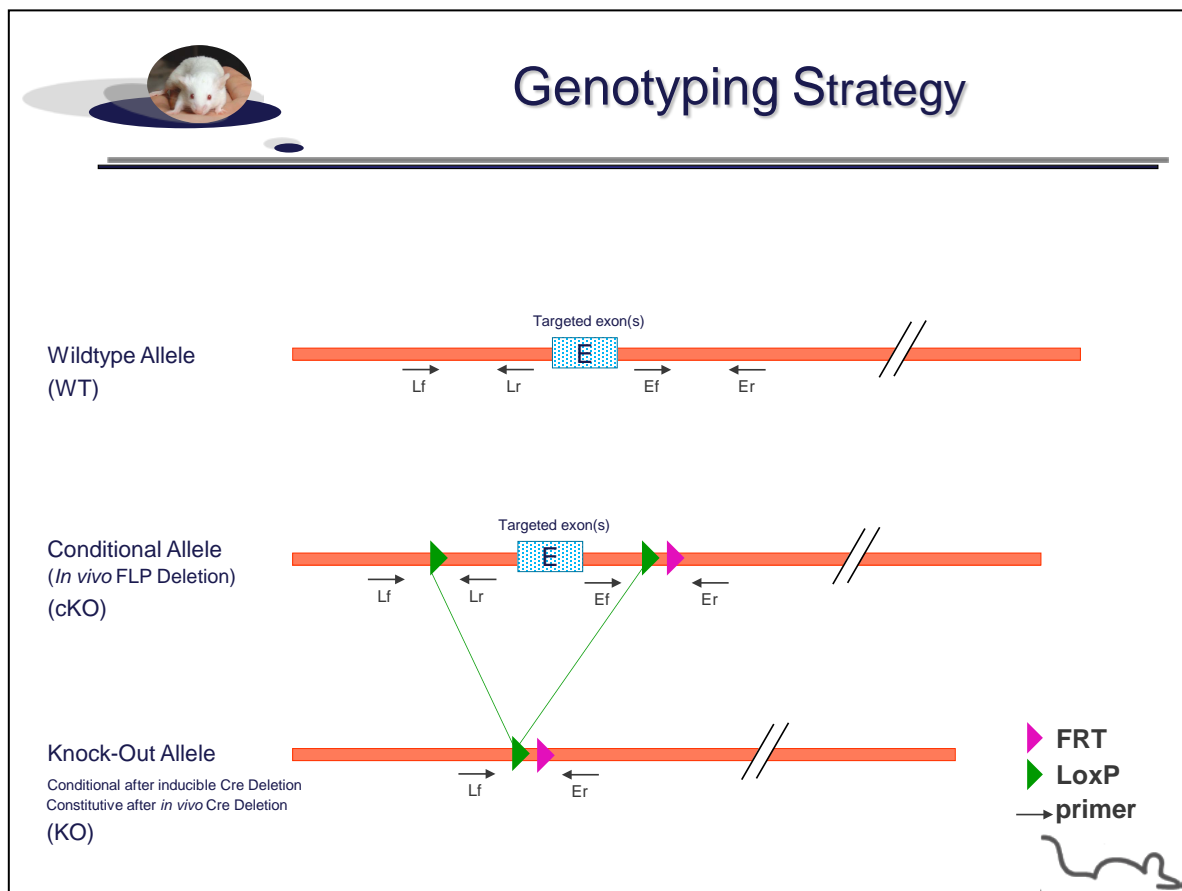
4. Data on conditional and knock-out animals

**Both conditional and knock-out mouse models were backcrossed in C57BL/6J background.**

**4.1. Genotyping protocol and data**

**4.1.1. Genotyping strategy**

The map below describes the position of the primers used for genotyping for each possible allele.



Sequence of primers used for genotyping

| Primers | Sequence                   |
|---------|----------------------------|
| Lf      | TCATCGCTCCAGTCTCCTACATTTTC |
| Lr      | ACCAGGCAAGTGCACCAAACACTGC  |
| Ef      | GGTTAGGTTTGTGAGTGTCCACAGC  |
| Er      | GGAAGTGCTCCAACAAGGTAGTGCA  |



**Molecular Biology Data**  
**Nr1d2 conditional knock out model**

PCR fragments expected size (bp):

| Region analyzed   | Primers used | Position on the primer (see the map above) | Conditional allele (L2) | Knock-Out allele (L-) | WT allele (WT) |
|---|--------------|--|-------------------------|-----------------------|----------------|
| Presence of the distal 5'LoxP                                   | 24-25        | Lf / Lr                                    | 489                     | ---                   | 431            |
| Excision of the selection marker                                | 26-27        | Ef / Er                                    | 376                     | ---                   | 237            |
| Total Excision (Excision of the floxed exon(s), i.e. knock out) | 24-27        | Lf / Er                                    | 1182                    | 443                   | 983            |

\* This PCR product will not be observed using our PCR genotyping conditions (see description below)  
--- No Amplicon should be obtained

#### 4.1.2. PCR protocol

This section describes the composition of the mix and cycling conditions used for genotyping.

| Reagents:                          | Volume:     |
|------------------------------------|-------------|
| -10x Buffer (Roche)                | 2.5µl       |
| -dNTPs 10mM (Amersham Biosciences) | 0.5µl       |
| -Taq DNA Polymerase (Roche)        | 0.2µl       |
| -DNA (50ng/µl)                     | 3µl         |
| -5' primer (100 µM)                | 0.125µl     |
| -3' primer (100 µM)                | 0.125µl     |
| -Sterile H2O                       | up to 25 µl |

Cycling conditions:

| Temp | Time | #Cycles |
|------|------|---------|
| 94°C | 3min | 1       |
| 94°C | 1min | 2       |
| 62°C | 1min |         |
| 72°C | 1min |         |
| 94°C | 30s  | 30      |
| 62°C | 30s  |         |
| 72°C | 30s  |         |
| 72°C | 3min | 1       |
| 4°C  | ∞    |         |

**NB: These PCR conditions have been optimized for high-throughput genotyping. Adaptation to small-scale may be required.**

**4.1.3. Picture of genotyping with various alleles**

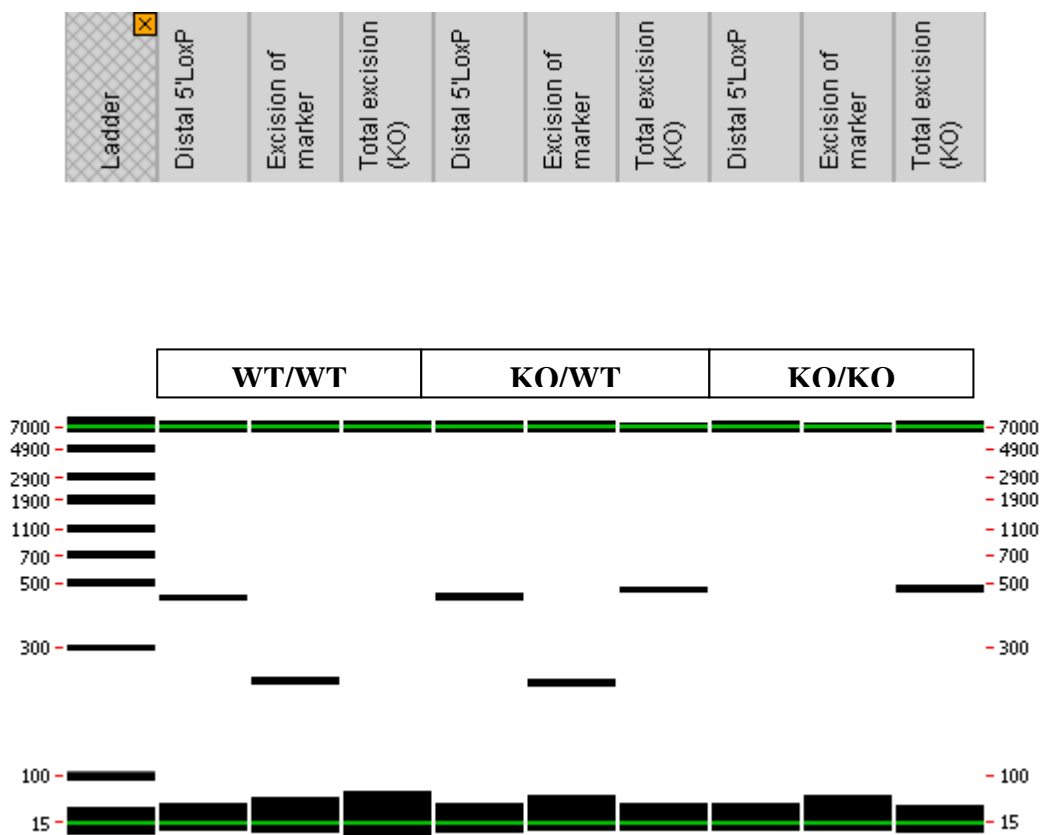
- Picture of genotyping with conditional knock-out (cKO) allele

Data not shown.

- Picture of genotyping with knock-out (KO) allele

Analysis of PCR products pattern was not done by gel electrophoresis but using LabChip® 90 microfluidic apparatus. PCR products were run on the HT DNA 5K LabChip® 90 Assay Kit.

Representative genotyping picture



Note that as this technology is more sensitive than gel analysis, non specific signals and/or primer dimers may be visible on the picture.