

Genotyping protocol

Project conditional overexpression of pHsensor in
Rosa

Gt(ROSA)26Sor^{tm33Ics}/Ics

(PHENOMIN-ICS reference IR00005742 / R5742)

This report has been **prepared** by: David MOULAERT

This report has been **validated** by: Sylvie Jacquot, PhD
Head of Genotyping Service

The first version of this report was finalized the: 31 Jan 2018

The last update of this report was done the: 31 Jan 2018

For any question, please contact:

PHENOMIN-ICS

Email: mutagenesis@igbmc.fr

Web site: <http://www.ics-mci.fr/>



Table of contents

| | |
|-----------------------------------------------|----------|
| 1. Genotyping protocol and data | 3 |
| 1.1. Genotyping strategy | 3 |
| 1.2. PCR protocol | 5 |
| 2. Cre and Flp genotyping method | 5 |



1. Genotyping protocol and data

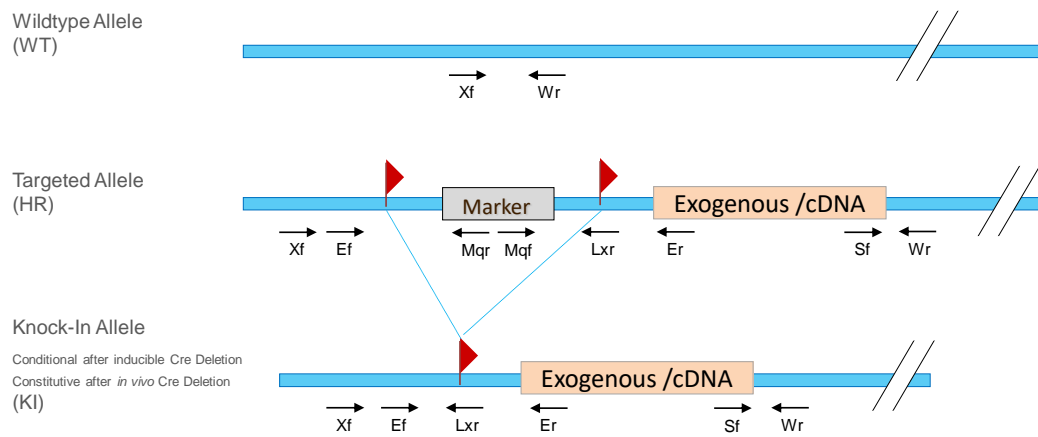
This section describes the condition used at the Mouse Clinical Institute (ICS) to genotype your **conditional overexpression of pHsensor in Rosa** Knockin (KI) project.

1.1. Genotyping strategy

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



KI Genotyping strategy



conditional overexpression of pHsensor in Rosa - Gt(ROSA)26So^{rtm33lcs}/Ics

Sequence of primers used for genotyping:

| Position | Primers | Sequence |
|-----------------|---------|------------------------------|
| Ef | 8761 | CGCAGTAGTCCAGGGTTTCCTTGATG |
| Ef ² | 8759 | CCTCCTGGCTTCTGAGGACCG |
| Er | 8763 | GTTGCATCACCTTCACCCTCTCCAC |
| Er ² | 8789 | CCATGGAACAGGTAGTTTTCCAGTAGTG |
| Lxr | 8765 | GCAGGTCGAGGGACCTAATAACTTCG |
| Mq1f | 2687 | CTGCATTCTAGTTGTGGTTTGTC |
| Mq1r | 265 | TGCTAAAGCGCATGCTCCAGACTGC |
| Sf | 8764 | CAATCTGCCCTTTCGAAAGATCCC |
| Wr | 8762 | ACCTGTTCAATCCCCTGCAGGA |
| Wr ² | 4035 | CCTTTAAGCCTGCCAGAAG |
| Xf | 8760 | CCCTCGTGATCTGCAACTCCAGTC |

²: for a selected position, a second primer was designed

PCR fragments expected size (bp):

| Region analyzed | Primers used | Position on the primer (see the map above) | Targeted allele (HR) | KI allele | WildType allele |
|--------------------------------------------------------------|--------------|-----------------------------------------------|----------------------|-----------|-----------------|
| WildType allele specific PCR (5' part of the targeted locus) | 8760-8762 | Xf / Wr | --- | --- | 111 |
| Excision of the selection marker | 8761-8763 | Ef / Er | 3034* | 365 | --- |
| Excision of the selection marker 2 | 8759-8789 | Ef ² / Er ² | 3199* | 530 | --- |
| 5' part of the selection marker | 8759-265 | Ef ² / Mq1r | 381 | --- | --- |
| 3' part of the selection marker | 2687-8763 | Mq1f / Er | 289 | --- | --- |
| cDNA 3' | 8764-4035 | Sf / Wr ² | 454 | 454 | --- |
| LoxP specific PCR | 8761-8765 | Ef / Lxr | 212 | 212 | --- |

*: this PCR product will not be observed using our PCR genotyping conditions (see description below)

---: no Amplicon should be obtained



1.2. PCR protocol

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

| Reagents: | Volume: |
|--------------------------------|-------------|
| - FastStart PCR Master (Roche) | 7.5µl |
| - DNA (50ng/µl) | 1.5µl |
| - 5' primer (100 µM) | 0.06µl |
| - 3' primer (100 µM) | 0.06µl |
| - Sterile H ₂ O | up to 15 µl |

Cycling conditions:

| Temp | Time | #Cycles |
|------|------|---------|
| 95°C | 4min | 1 |
| 94°C | 30s | 34 |
| 62°C | 30s | |
| 72°C | 1min | |
| 72°C | 7min | 1 |
| 20°C | 5min | 1 |

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

2. Cre and Flp genotyping method

You will find the genotyping protocol in the publication:

[Highly-efficient, fluorescent, locus directed cre and FlpO deleter mice on a pure C57BL/6N genetic background.](#)

Birling MC, Dierich A, Jacquot S, Hérault Y, Pavlovic G.

Genesis. 2012 Jun;50(6):482-9. doi: 10.1002/dvg.20826. Epub 2012 Mar 20.

