



Genotyping protocol

Slc1a7

IR00003116 / E199

(ICS internal reference)

This report has been prepared by: **Valérie Rousseau**
genotyping@igbmc.fr

This report has been validated by: **Sylvie Jacquot, PhD, Head of Genotyping Service**
33 (0)3 88 65 57 44
genotyping@igbmc.fr

The first version of this report was finalized the: 07 Dec 2012

For any question, please contact:

Institut Clinique de la Souris - ICS - Mouse Clinical Institute
1 rue Laurent Fries, BP 10142
67404 Illkirch Cedex, France
Email: genotyping@igbmc.fr
Web site: <http://www-mci.u-strasbg.fr/>

TABLE OF CONTENTS

Table of contents2

1. Genotyping protocol and data2

 1.1. Genotyping strategy2

 1.2. PCR protocol4

 1.3. Picture of genotyping with various alleles4

2. Cre and Flp genotyping method5

 2.1. Cre and Flp genotyping5

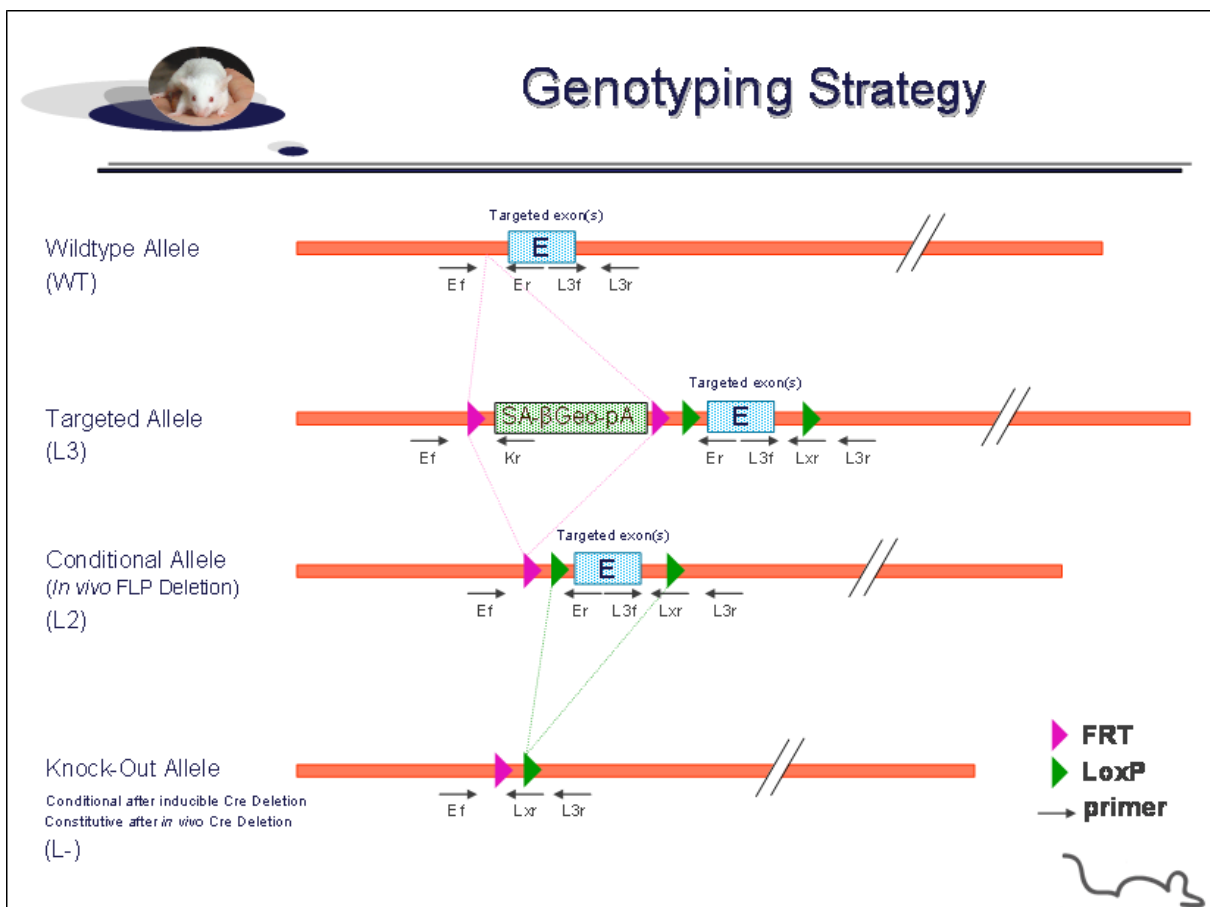
 2.2. PCR Protocol6

1. Genotyping protocol and data

This section describes the condition used at the Mouse Clinical Institute (ICS) to genotype your **Slc1a7** Constitutive Knockout / Conditional Knockout (KO-cKO) project.

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:

Position	Primers	Sequence
Ef	5460	CATCCTTCAGCGGTATGCCTGC
Ef ²	5459	CTACCTAGACGGCCATAAGCTACCTGG
Er	5464	CATCACACCCGGTGCAGCTTTC
Kr	3209	CCAACAGCTTCCCCACAACGG
L3f	5461	TCTGTACCACCTGCTCTGACCCAGC
L3f ²	5462	CAGTTCCTGGAGAACTCTTGATGCG
L3r	5463	CATCGGGAACAGAATTCCTTTGG
Lxr	3255	ACTGATGGCGAGCTCAGACCATAAC
Mq1f	4981	GGGATCTCATGCTGGAGTTCTTCG

PCR fragments expected size (bp):

Region analyzed	Primers used	Position on the primer (see the map above)	Targeted allele (KO allele) (L3)	cKO allele (L2)	KO allele (L-)	WildType allele (WT)
5' part of the selection marker	5460-3209	Ef / Kr	365	---	---	---
Presence of the distal loxP	5461-5463	L3f / L3r	597	597	---	597
Distal loxP specific PCR	5462-3255	L3f ² / Lxr	410	410	---	---
Excision of the selection marker	5460-5464	Ef / Er	6473*	461	---	312
Excision of the floxed exon(s), i.e. knock out	5459-5463	Ef ² / L3r	7389*	1377*	512**	1228**

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

** : this PCR is only verified if mice are generated

---: 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.

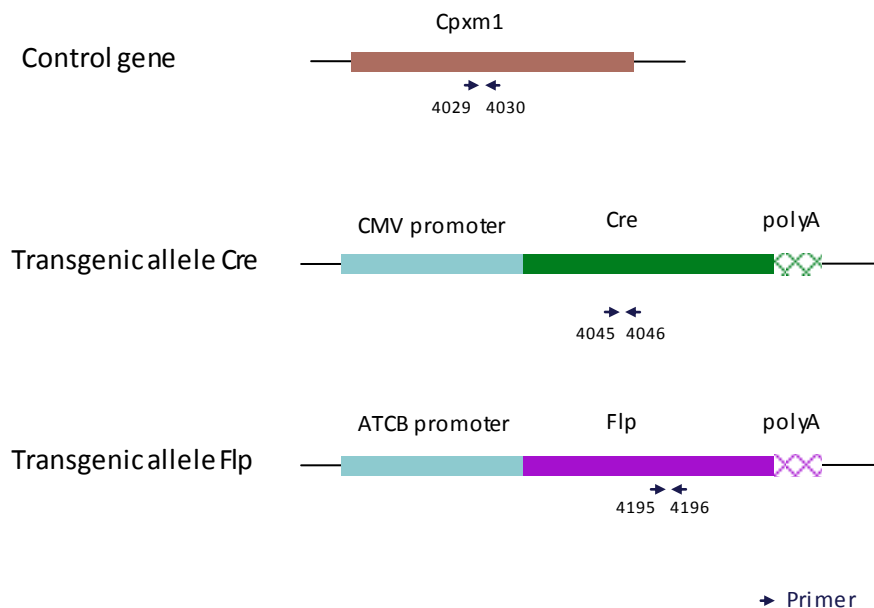
2. Cre and Flp genotyping method

The protocol used to segregate the cre and/or flp transgene is indicated below.

Detection of cre transgene and flp transgene is done using a multiplex assay: primer pairs were designed for each gene and for a positive control (Cpxm1 gene).

2.1. Cre and Flp genotyping

Schematic representation of the genotyping strategy



Sequence of primers used for genotyping:

Primers	Sequence
4029	ACTGGGATCTTCGAACTCTTTGGAC
4030	GATGTTGGGGCACTGCTCATTACC
4045	CCATCTGCCACCAGCCAG
4046	TCGCCATCTTCCAGCAGG
4195	TCTTTAGCGCAAGGGGTAGGATCG
4196	GTCCTGGCCACGGCAGAAGC

PCR fragments expected size (bp):

Primer pair	4045-4046	4195-4196	4029-4030
Region analyzed	Middle part of Cre transgene	Middle part of Flp transgene	Cpxm1 control gene
Control gene	/	/	397
Tg allele	281	328	/

2.2. 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)	0.05µl
3' primer (100 µM)	0.05µl
Sterile H ₂ O	up to 15 µl

Cycling conditions are identical to those described in chapter 1.2