



Genotyping protocol

Mmp9

IR00004166 / P4166

(ICS internal reference)

This report has been prepared by: **Pauline Cayrou**
33 (0)3 88 65 56 55
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: 19 Apr 2013

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 contents	2
1. Genotyping protocol and data	2
1.1. Genotyping strategy	2
1.2. PCR protocol	4
1.3. Picture of genotyping with various alleles	5
2. Cre and Flp genotyping method	6
2.1. Cre and Flp genotyping	6
2.2. PCR Protocol	7

1. Genotyping protocol and data

This section describes the condition used at the Mouse Clinical Institute (ICS) to genotype your **Mmp9** 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.

imgstrat

Sequence of primers used for genotyping:

Position	Primers	Sequence
Ef	6806	GTGGATAGCTGAGAAGGGCTG
Er	6554	ACATCTCTGGGCACTGAGCGC
Er2	1936	GTGGATGTGGAATGTGTGCGAGG
Er3	6809	CTGCGCCATGTCACAACCCCTT
Kr	3209	CCAACAGCTTCCCCACAACGG
L3f	6807	GATGTGGCTCAGCTGTAGGAAGAG
L3r	6808	GCTGACCCTTCTTGCTGAGGAG
Lxf	6295	TTATGTTTAAACGGCGCGCCC
Lxf2	6013	TCATGTCTGGATCCGGAATAACTTCGTA
Lxr	3255	ACTGATGGCGAGCTCAGACCATAAC
Ri1f	5966	GCACATGGCTGAATATCGACGGT

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)
Lox interne K7Eur (with DMSO)	6295-6554 (with 5% DMSO)	Lxf / Er	119	---	---	---
Lox interne K7Eur (with DMSO)	6013-1936 (with 5% DMSO)	Lxf2 / Er2	199	---	---	---
5' part of the selection marker	6806-3209	Ef / Kr	332	---	---	---
Presence of the distal loxP	6807-6808	L3f / L3r	254	254	---	220
Distal loxP specific PCR	6807-3255	L3f / Lxr	164	164	---	---
Excision of the selection marker	6806-6809	Ef / Er3	7282*	378	---	205
Cre total excision	5966-3255	Ri1f / Lxr	---*	---	---	---

*: 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.

1.3. Picture of genotyping with various alleles

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

_ADD_THE_PHOTO_

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

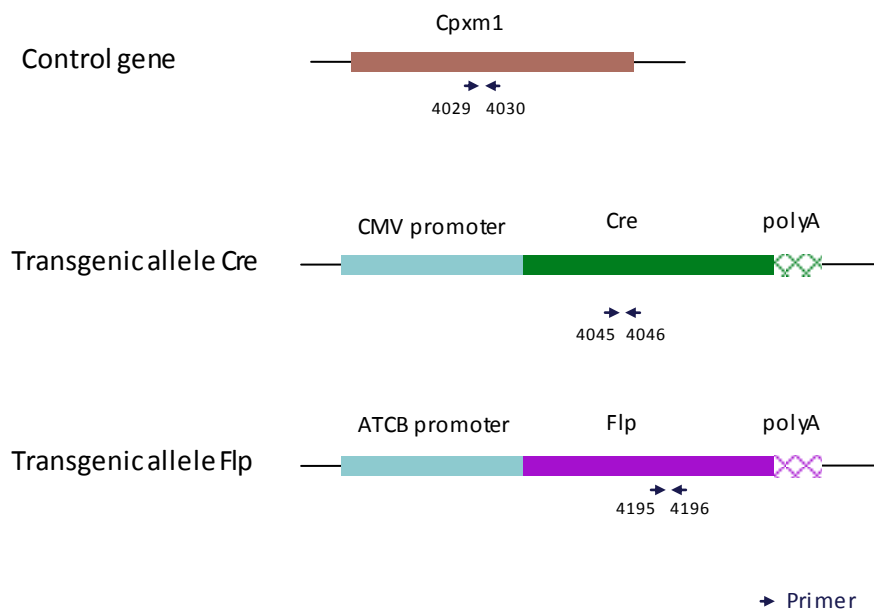
2. Cre and Flp genotyping method

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	TCGCCATCTCCAGCAGG
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)	7.5 μ l
DNA (50ng/ μ l)	1.5 μ l
5' primer (100 μ M)	0.05 μ l
3' primer (100 μ M)	0.05 μ l
Sterile H ₂ O	up to 15 μ l

Cycling conditions are identical to those described in chapter 1.2