



lft122 (IR00002579 / E66 ICS internal reference) mouse line genotyping protocol

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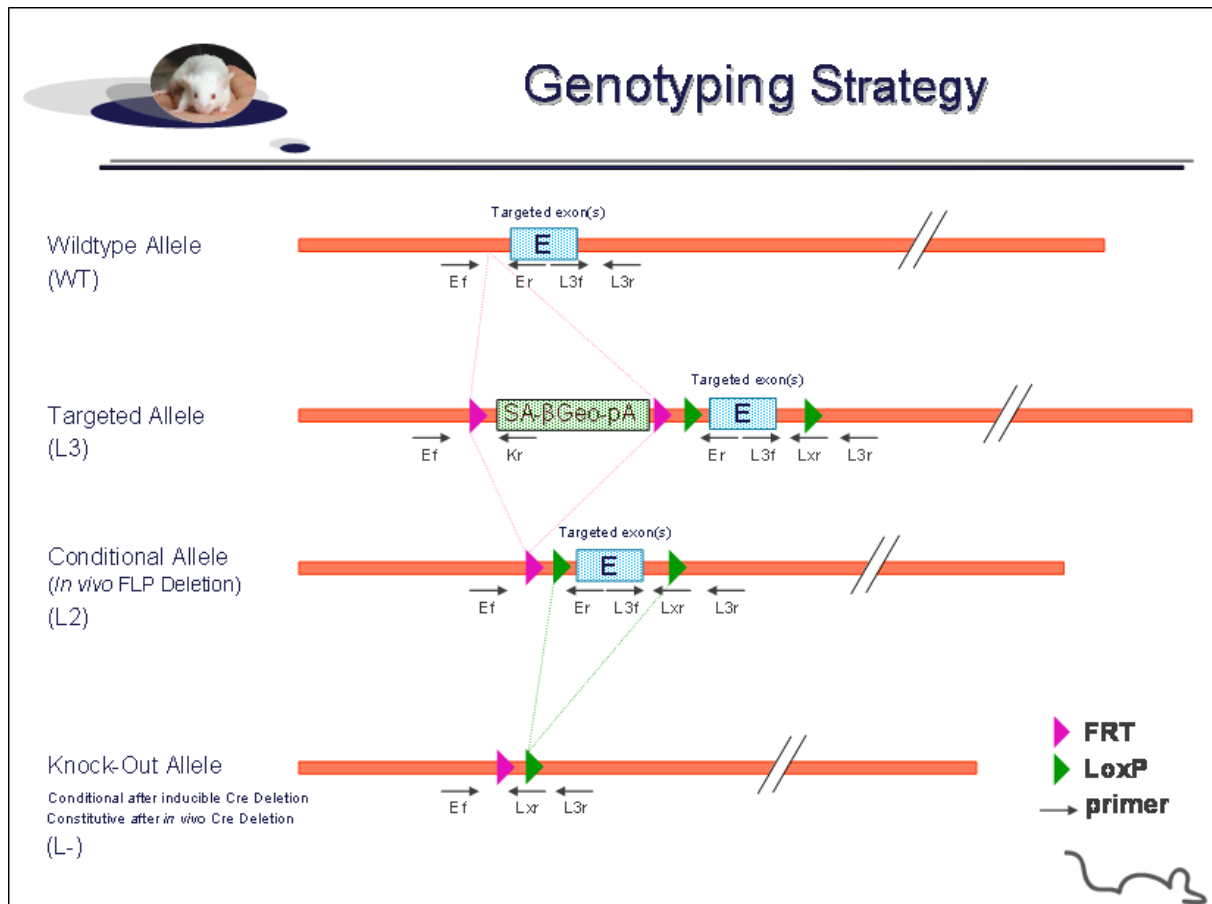
This protocol has been validated by Christelle Roth.

1. Genotyping protocol and data

This section describes the condition used at the Mouse Clinical Institute (ICS) to genotype your **Ift122** 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	4517	CCTGCCTTGATGGGTCAATTCATTCAAG
Er	4519	GCACTGTACAATGCCAGACAAGCC
Kr	4518	GGCAAGAACATAAAGTGACCCTCC
L3f	4520	GCCTTGTA GCTGCTCAGCTTTC
L3r	4521	CCTCATCGAGCTTCCCAACAAGG
Lxr	4522	CGAAGTTATCA TTAATTGCGTTGCGC



Genotyping protocol

Ift122 (IR00002579/ E66 ICS internal reference)

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	4517-4518	Ef / Kr	353	---	---	---
Presence of the distal loxP	4520-4521	L3f / L3r	273	273	---	290
Distal loxP specific PCR	4520-4522	L3f / Lxr	165	165	---	---
Excision of the selection marker	4517-4519	Ef / Er	7277*	373	---	258
Excision(s) of the floxed exon(s), i.e. knock out	4517-4521	Ef / L3r	8010*	1106*	348**	1008**

* 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:

-10x Buffer (Roche)
 -dNTPs 10mM (Amersham Biosciences)
 -Taq DNA Polymerase (Roche)
 -DNA (50ng/μl)
 -5' primer (100 μM)
 -3' primer (100 μM)
 -Sterile H2O

Volume:

2.5μl
 0.5μl
 0.2μl
 3μl
 0.125μl
 0.125μl
 up to 25 μl

Cycling conditions:

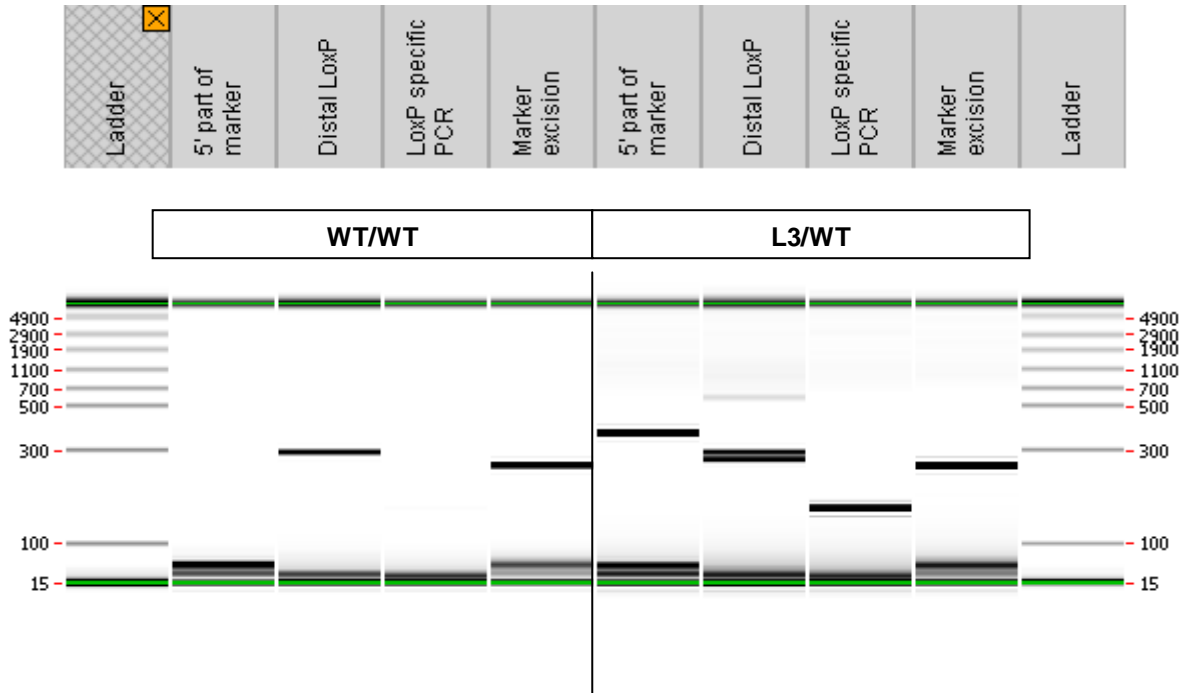
Temp	Time	#Cycles
94°C	3min	1
94°C	1min	2
62°C	1min	
72°C	1min	
94°C	30s	30
62°C	30s	
72°C	30s	
72°C	3min	1
4°C	∞	

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

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



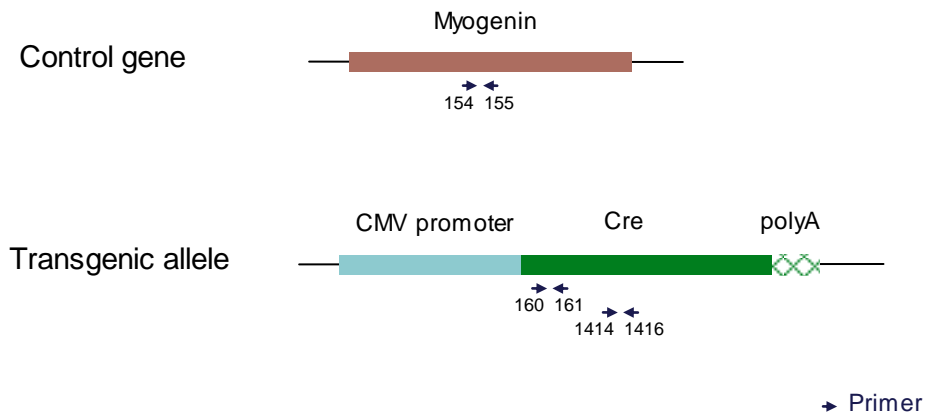
Note that as this technology is more sensitive than gel analysis, non specific signals and/or primer dimers may be visible on the picture.

2. Cre and Flp genotyping method

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

2.1. Cre genotyping

Schematic representation of the genotyping strategy



Sequence of primers used for genotyping

Primers	Sequence
154	ACTCCCTTACGTCCATCGTG
155	ACCCAGCCTGACAGACAATC
160	GAACCTGATGGACATGTTCAAG
161	AGTGCGTTCGAACGCTAGAGCCTGT
1414	CGTACTGACGGTGGGAGAA T
1416	CCCGGCAAAACAGGTAGTTA

PCR fragments expected size (bp):

Primer pair	160-161	1414-1416	154-155
Region analyzed	5' part of Cre transgene	Middle of Cre transgene	Myogenin control gene
Control gene	/	/	99
Tg allele	345	165	/

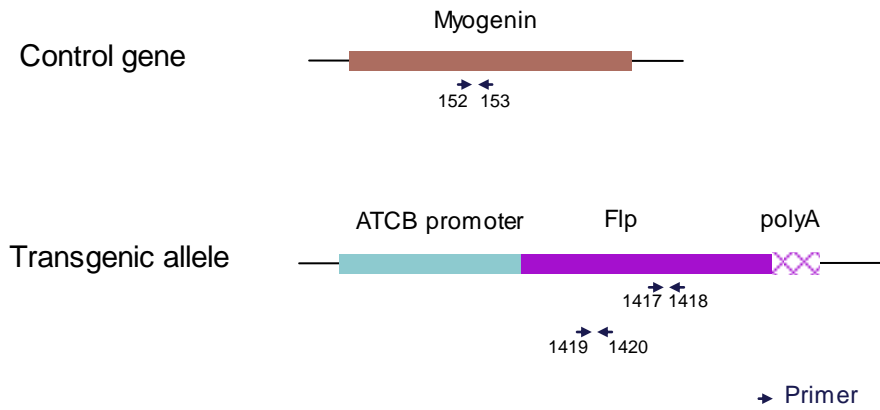
Cycling conditions:

Temp	Time	#Cycles
95°C	3min	1
95°C	10s	35
62°C	20s	
72°C	20s	
95°C	5s	1 (melting curve generation)
62°C	30s	
72°C	72s	
37°C	30s	1
4°C	∞	

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

2.2. Flp genotyping

Schematic representation of the genotyping strategy



Sequence of primers used for genotyping

Primers	Sequence
152	TTACGTCCATCGTGACAGC
153	TGGGCTGGGTGTTAGCCTTA
1417	TTCTTTAGCGCAAGGGGTAG
1418	GCTCCAATTTCCCACAACAT
1419	TGGGAAATTGGAGCGATAAG
1420	CTGCCACTCCTCAATTGGAT

PCR fragments expected size (bp):

Primer pair	1417-1418	1419-1420	152-153
Region analyzed	Middle part of Flp transgene	5' of Flp transgene	Myogenin control gene
Control gene	/	/	245
Tg allele	299	175	/

PCR protocol and cycling conditions are identical to those described in chapter 1.2