

Aldh3a2 (IR00002472 / E38 ICS internal reference) mouse line genotyping protocol

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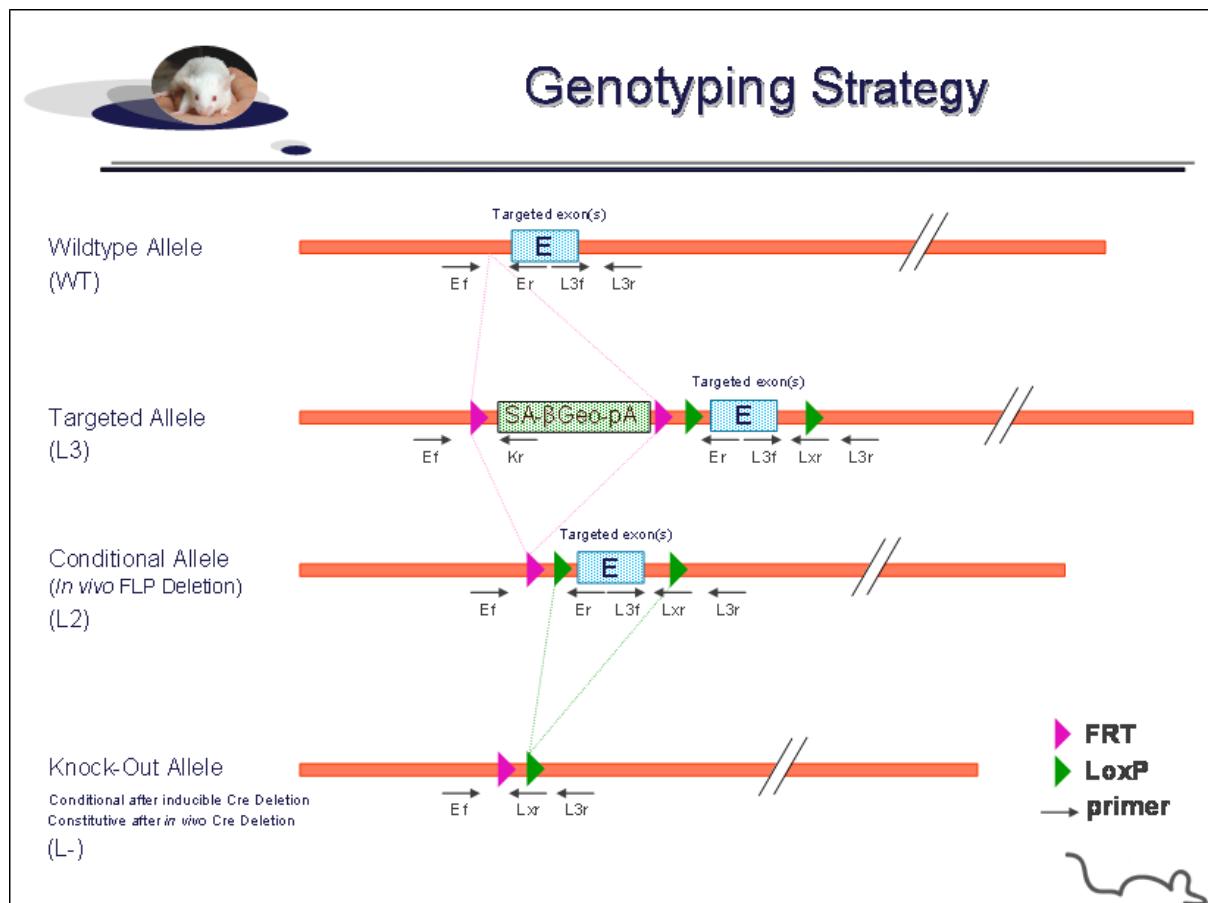
This protocol has been validated by Valérie Rousseau.

1. Genotyping protocol and data

This section describes the condition used at the Mouse Clinical Institute (ICS) to genotype your **Aldh3a2** 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	3936	GGAGGGTAGTGCATGTACCGGG
Er	3939	ACGAGGGCGGATGCTCTAAGGG
Kr	3277	CTCCTACA TAG TTGGCAGTGTGGGG
L3f	3938	GTGCTCAGGAATACTGGAGCCTCTCG
L3f	3940	GGCCTGCCAGCATGGCA TTTTCC
L3r	3937	CGCTGGTTGAAGAGGTGGGGC
Lxr	3254	TTATCATTAA TTGCGTTGCCATC



Genotyping protocol Aldh3a2 (IR00002472 / E38 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	3936-3277	Ef / Kr	333	---	---	---
Presence of the distal loxP	3940-3937	L3f / L3r	379	379**	---	412
Distal loxP specific PCR	3938-3254	L3f / Lxr	153	153**	---	---
Excision of the selection marker	3936-3939	Ef / Er	5840*	440**	---	399
Excision of the floxed exon(s), i.e. knock out	3936-3937	Ef / L3r	6931*	1531*	563**	1523**

* 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	
62°C	30s	34
72°C	1min	
72°C	7min	1
20°C	5 min	1

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

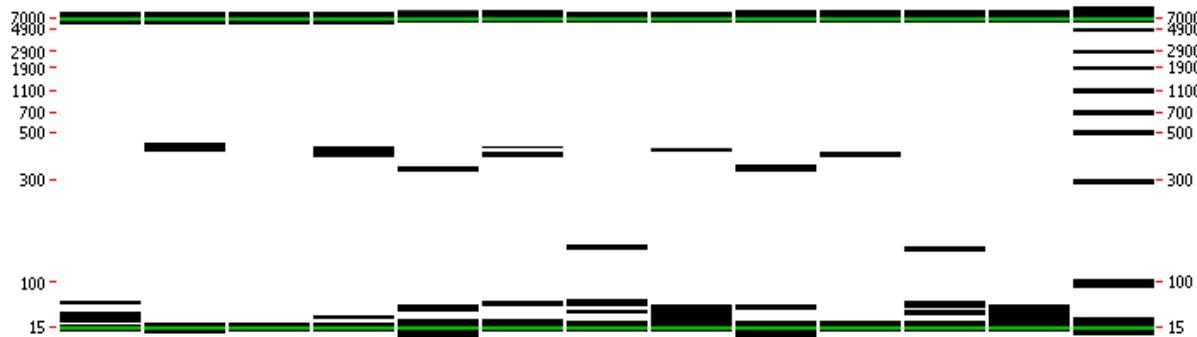
1.3. Picture of genotyping with various alleles

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

5' part of the selection marker	Presence of the distal loxP	Distal LoxP specific PCR	Excision of the selection marker	5' part of the selection marker	Presence of the distal loxP	Distal LoxP specific PCR	Excision of the selection marker	5' part of the selection marker	Presence of the distal loxP	Distal LoxP specific PCR	Excision of the selection marker	Ladder B
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WT/WT	L3/WT	L3/L3
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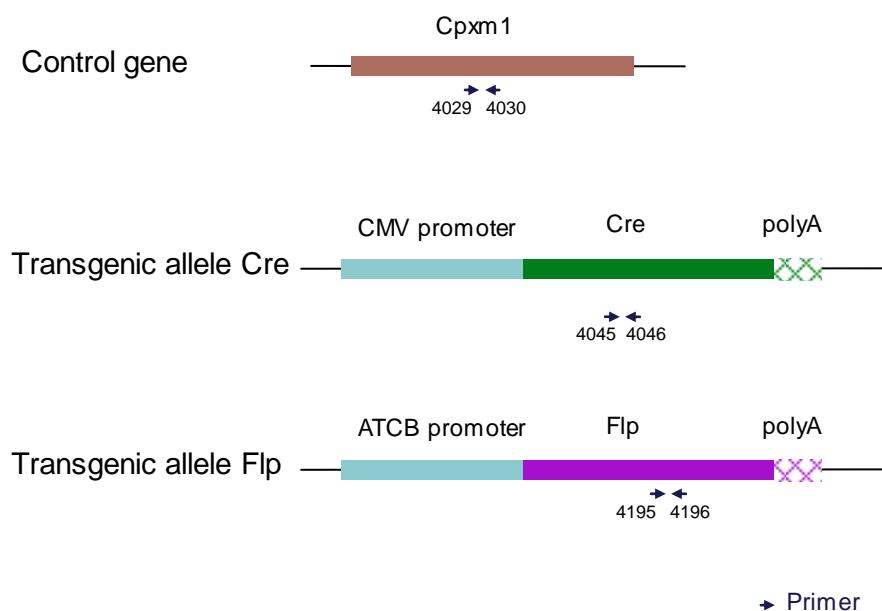
Note that as this technology is more sensitive than gel analysis, non specific signals and/or primer dimers may be visible on the picture.

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 an Flp genotyping

Schematic representation of the genotyping strategy



Sequence of primers used for genotyping:

Primers	Sequence
4029	ACTGGGATCTTCGAACCTTTGGAC
4030	GATGTTGGGCCACTGCTCATTCA
4045	CCATCTGCCACCAGCCAG
4046	TCGCCATCTTCCAGCAGG
4195	TCTTAGCGCAAGGGTAGGATCG
4196	GTCCTGGCACGGCAGAAC

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	/	/	446
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

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