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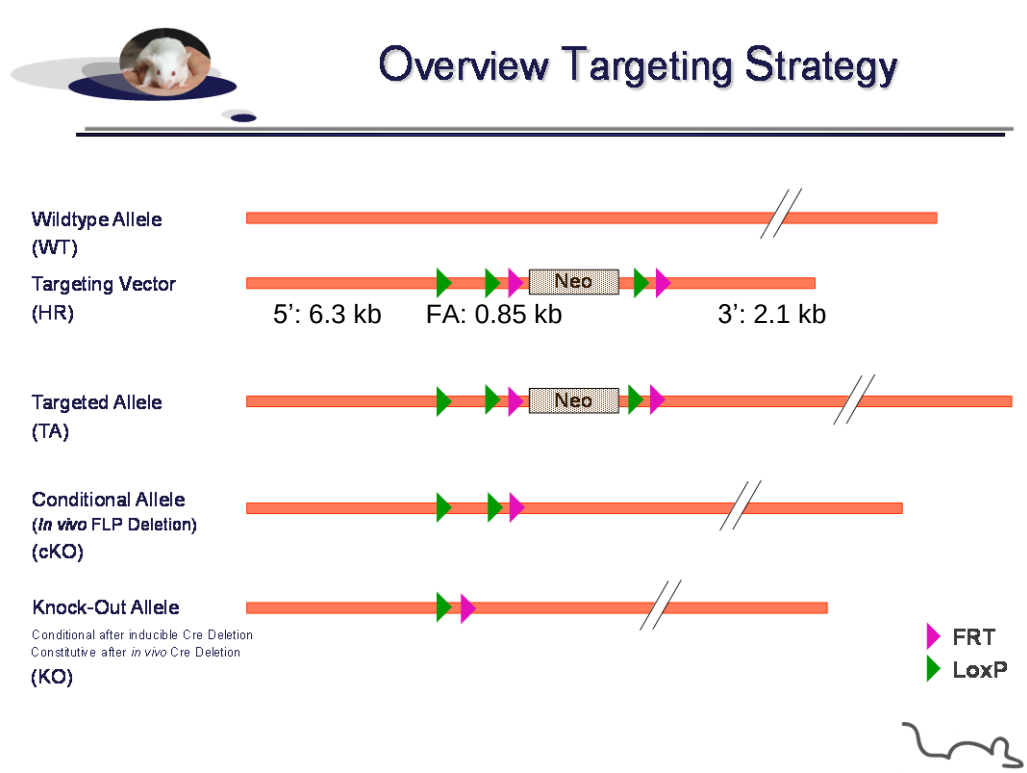
Web site: http://www.phenomin.fr/en-us/

This protocol has been prepared by Claudia Caradec, Engineer
This protocol has been validated by Sylvie Jacquot, Ph.D., Project Manager

1. Schematic representation of the locus

1.1. Overview

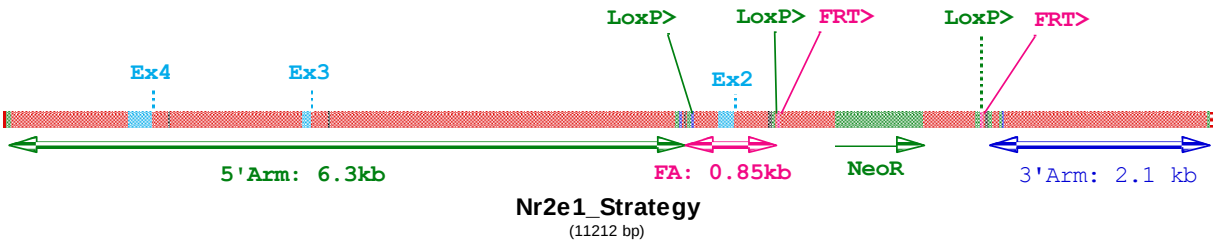


Legend:
5': 5' homology arm; FA: floxed fragment; 3': 3' homology arm
This schematic representation is not on scale

1.2. Strategy chosen: flox of exon 2

Nr2e1 gene (also named Tlx) is a member of the nuclear receptor family. Additional information on this gene can be accessed at:
http://www.informatics.jax.org/javawi2/servlet/WIFetch?page=markerDetail&key=34591

Strategy used to generate the conditional knock out model



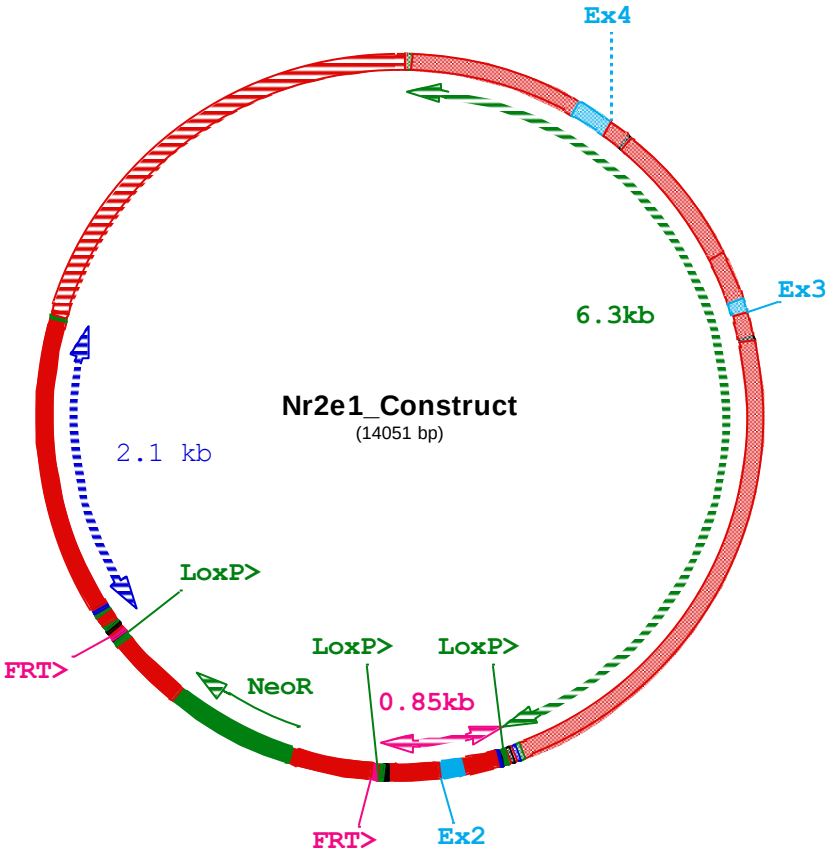
Nr2e1_Strategy
(11212 bp)

2. Construct used for homologous recombination in ES cells: Nr2e1 project

2.1. Legend

loxP sites are indicated in green ; FRT sites are indicated in purple; *Mus musculus* sequences are indicated in uppercase ; exogenous sequences are marked in lowercase.
The targeting vector was generated in 129Sv/Pas and was not fully sequenced. Regions sequenced are indicated in bolds.

2.2. Map of targeting vector plasmid



2.3. 5' homology arm (6.3 kb)

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2.5. PGK-Neo region

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2.6. 3' homology arm (2.4 kb)

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2.7. Vector backbone sequence

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3. ES cell lines targeted and validation data:

3.1. ES cell lines targeted

The targeting vector was electroporated in P1 ES cells [MCI-129Sv/Pas background]

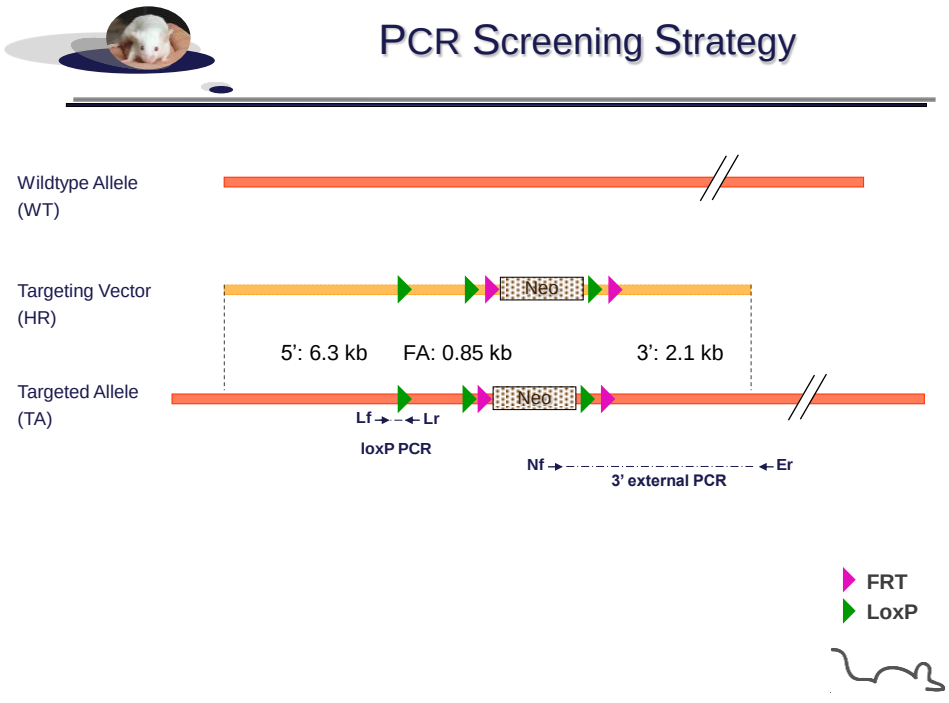
Number of clones screened: 465
Number of positive: 3

Reference of clone used to generate the mouse line:

- clone **K185-79**

3.2. PCR data on positive clone

3.2.1.PCR screening strategy

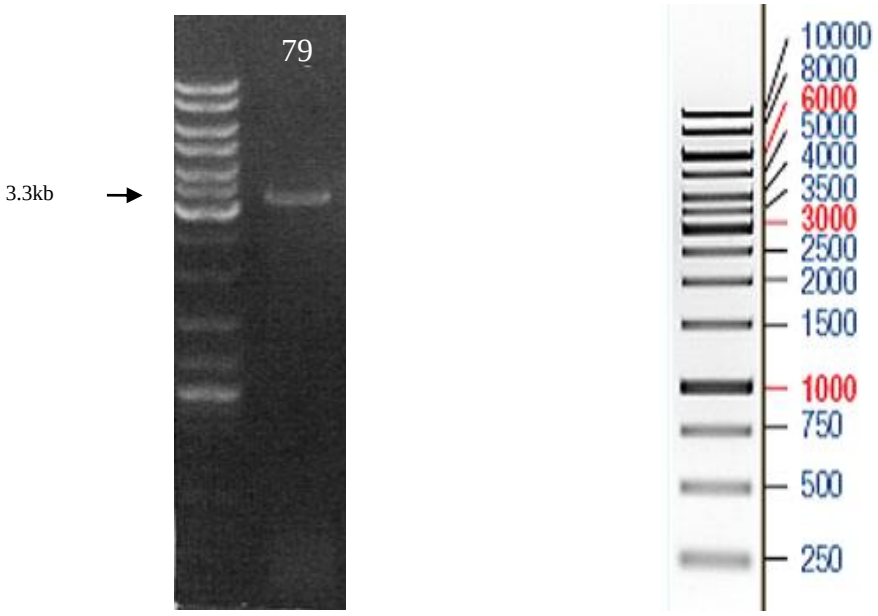


Primers used for PCR validation of ES clone

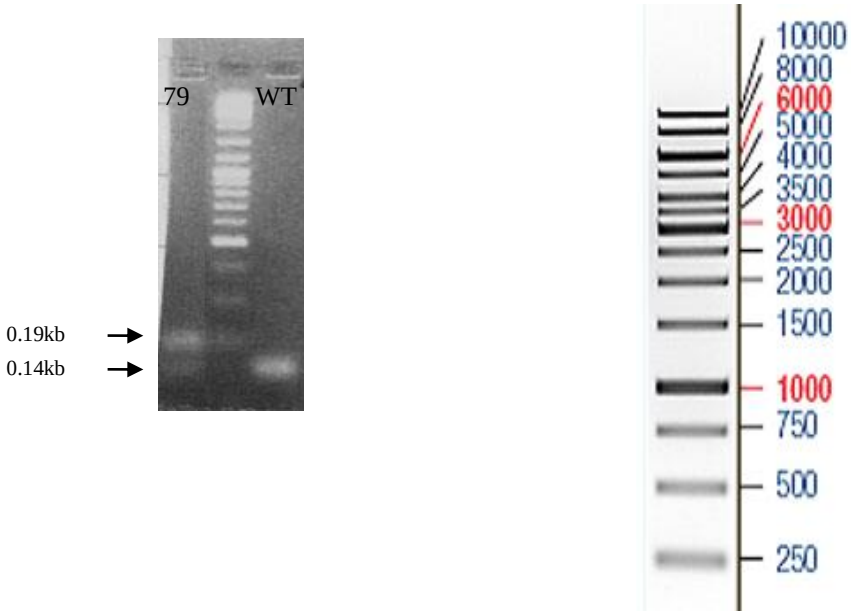
PCR	Primer Name	Primer sequences	PCR product size
loxP	Lf	CTCAGTGGTCGAAGACTGAGCTTGG	0.14 kb WT 0.19 kb TA
	Lr	CACTGAACAAGGCCCACACCTAGTC	
3' external	Nf	AGGGGCTCGCGCCAGCCGAACTGTT	3.3kb
	Er	CCTTGAAGGCCTGGAGACTCCAGTC	

3.2.2.Picture of PCR on positive clone

3' external PCR ladder

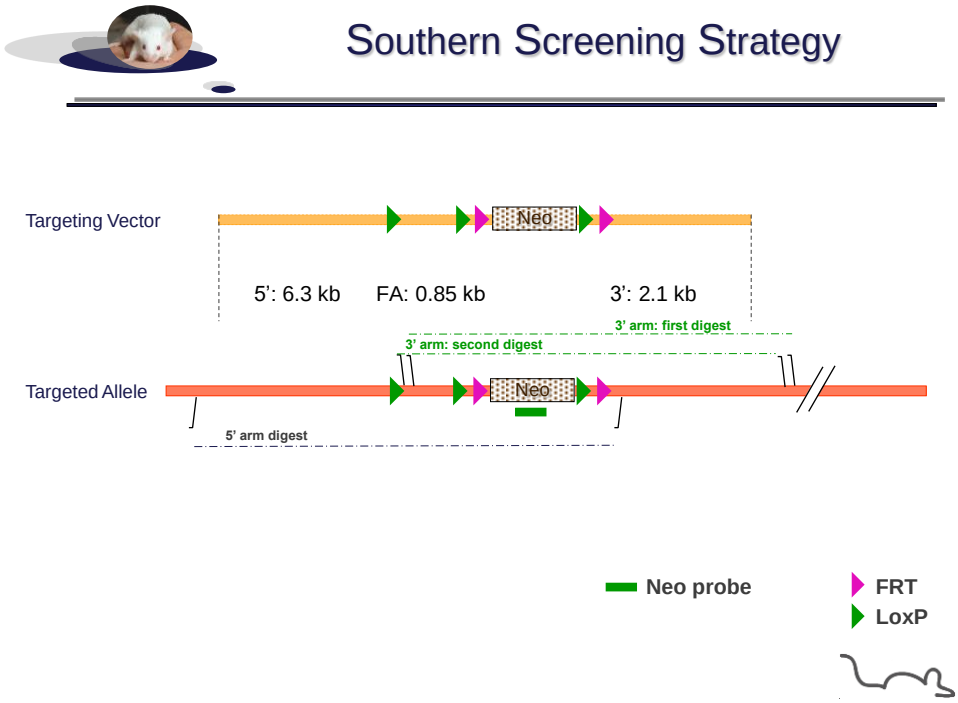


LoxP PCR ladder



3.3. Southern data on positive clone

3.3.1.Neo Southern strategy



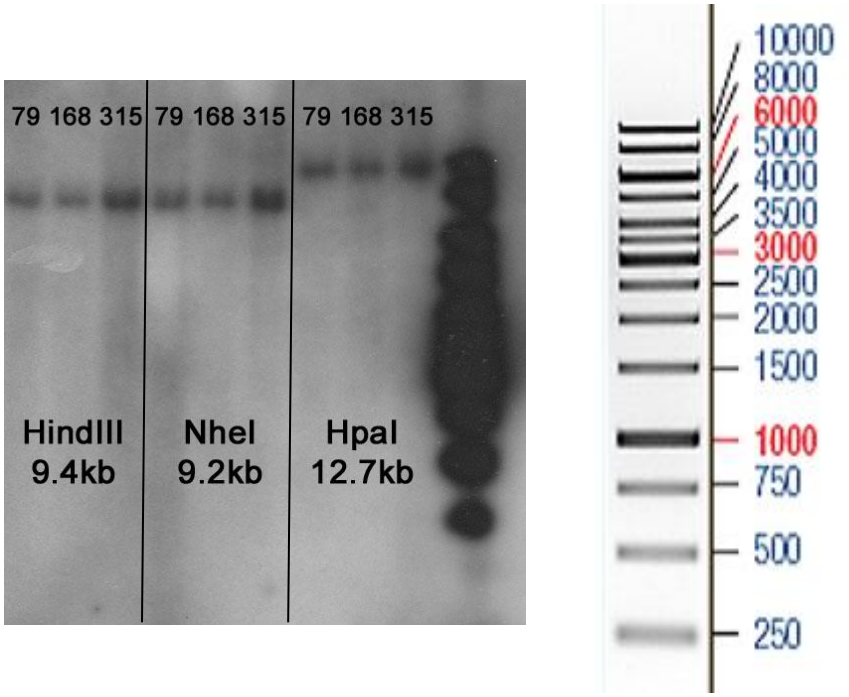
Digestions used to validate the 5' and 3' insertion

Probe	Name	Genomic DNA digest	WT allele (kb)	Targeted Allele (kb)
Neo	5' arm digest	HpaI	/	12.7
	3' arm first digest	HindIII	/	9.4
	3' arm second digest	NheI	/	9.2

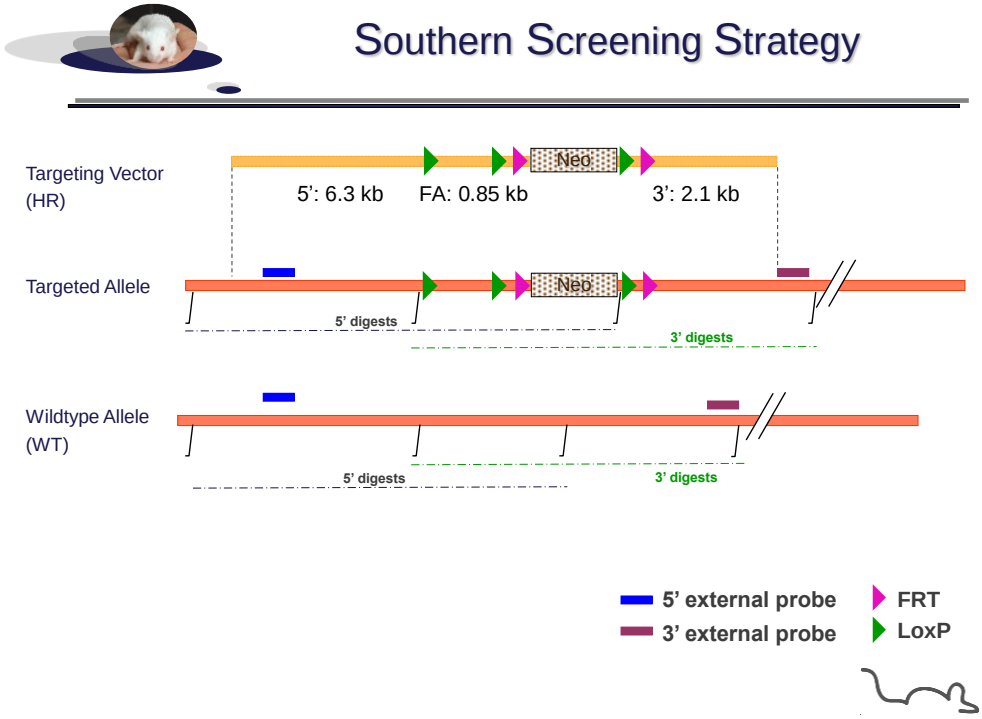
Three different digests are used to validate correct HR event. One digest validates the 5' insertion, 2 other digests validate the 3' insertion

3.3.2.Picture of Neo Southern

Neo southern blot: 5' and 3'arm validation ladder



3.3.3.External probes Southern strategy



Digestions used to validate with 5' and 3' probes

Probe	Name	Genomic DNA digest	WT allele (kb)	Targeted Allele (kb)
5' external	first digest	XbaI	16.9	7.6
	second digest	HpaI	10.7	12.7
3' external	first digest	NheI	7.1	9.2
	second digest	HindIII	7.3	9.4

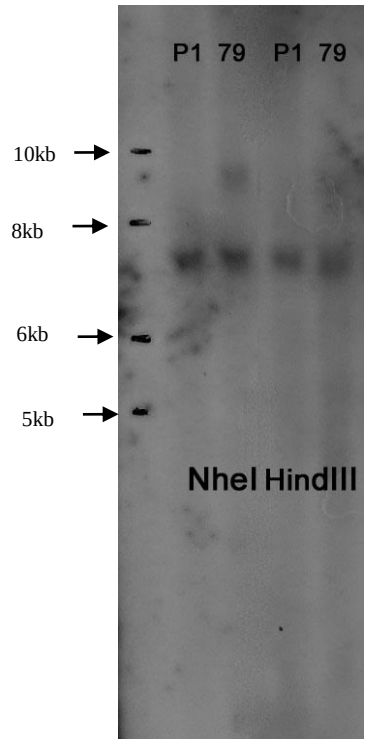
Primers for probe synthesis:

5' probe:
TTCACCGATGCATTGAAATGTCAGC
GATAAGTGGCTTCCTTGTGGTTCCG

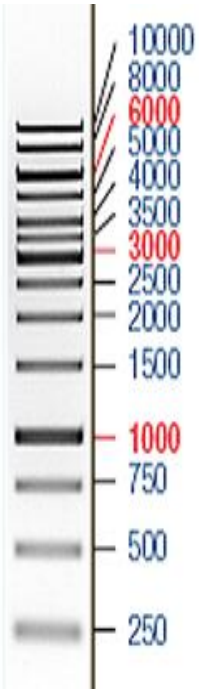
3' probe:
AGTGGGTCCTCGGAGAAGAGGGAAG
GCCTCGAGACTGGCCCCACTGCTCTC

3.3.4.Picture of Southern with external 5’ and 3’ probes

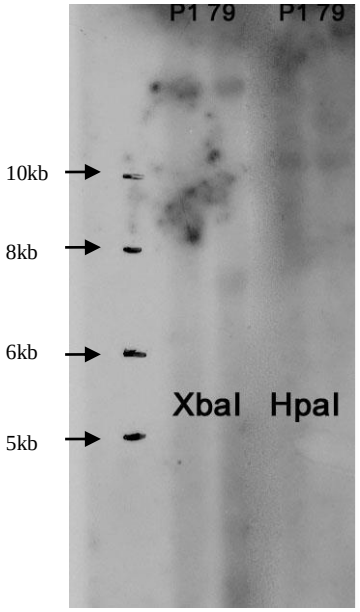
5’ external probe validation



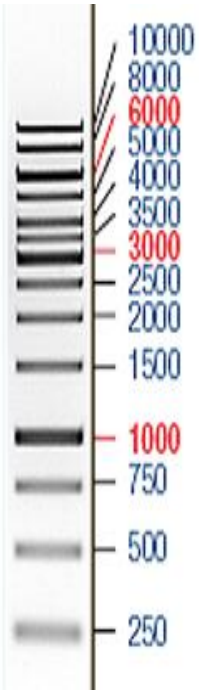
Ladder



3' external probe validation



Ladder



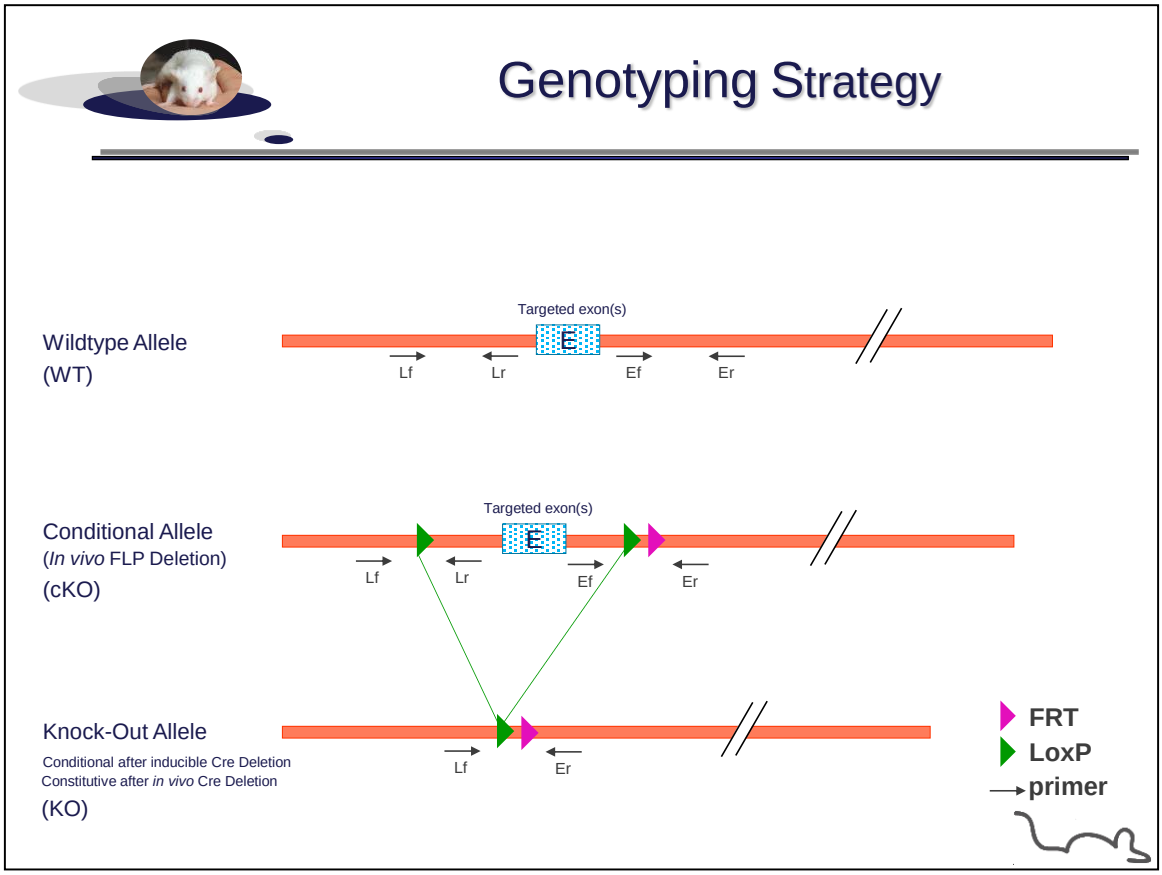
4. Data on conditional and knock-out animals

Both conditional and knock-out mouse models were backcrossed in C57BL/6J background.

4.1. Genotyping protocol and data

4.1.1. 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	2363	GTCTCCTCTAATCGCCGAGACC
Er	2364	GCTATCTCTGCTCTTGCTCACACC
Lf	2360	CTCAGTGGTCGAAGACTGAGCTTGG
Lr	2362	CCTTGCAAAGTGTGTGGTGACCG

PCR fragments expected size (bp):

Region analyzed	**Primers used**	Position on the primer (see the map above)	Conditional allele (cKO)	Knock-Out allele (KO)	WT allele (WT)
Presence of the distal loxP	2360-2362	Lf / Lr	543	---	493
Excision of the selection marker(Neo excision)	2363-2364	Ef / Er	592	---	461
Excision of the floxed exon(s), i.e. knock out	2360-2364	Lf / Er	1388*	601	1208*

* This PCR product will not be observed using our PCR genotyping conditions (see description below)
--- No Amplicon should be obtained

4.2. PCR protocol

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

Reagents:	Volume:
-10x Buffer (Roche)	2.5µl
-dNTPs 10mM (Amersham Biosciences)	0.5µl
-Taq DNA Polymerase (Roche)	0.2µl
-DNA (50ng/µl)	3µl
-5' primer (100 µM)	0.125µl
-3' primer (100 µM)	0.125µl
-Sterile H2O	up to 25 µl

Cycling conditions:

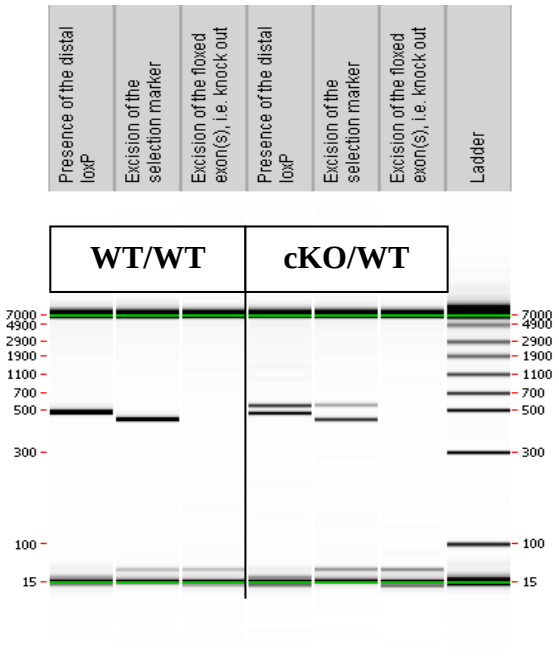
Temp	Time	#Cycles
94°C	3min	1
94°C	1min	
62°C	1min	2
72°C	1min	
94°C	30s	
62°C	30s	30
72°C	30s	
72°C	3min	1
4°C	∞	

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

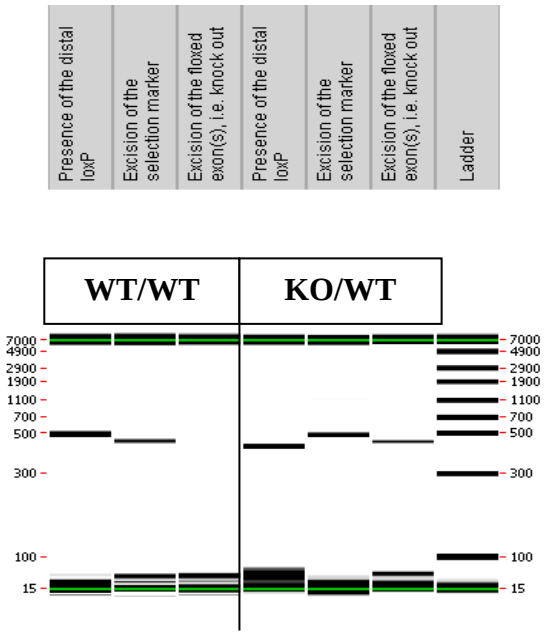
4.3. Picture of genotyping with various alleles

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.

- Picture of genotyping with conditional knock-out (cKO) allele



- Picture of genotyping with knock-out (KO) allele



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