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This protocol has been prepared by Loic Lindner, Engineer

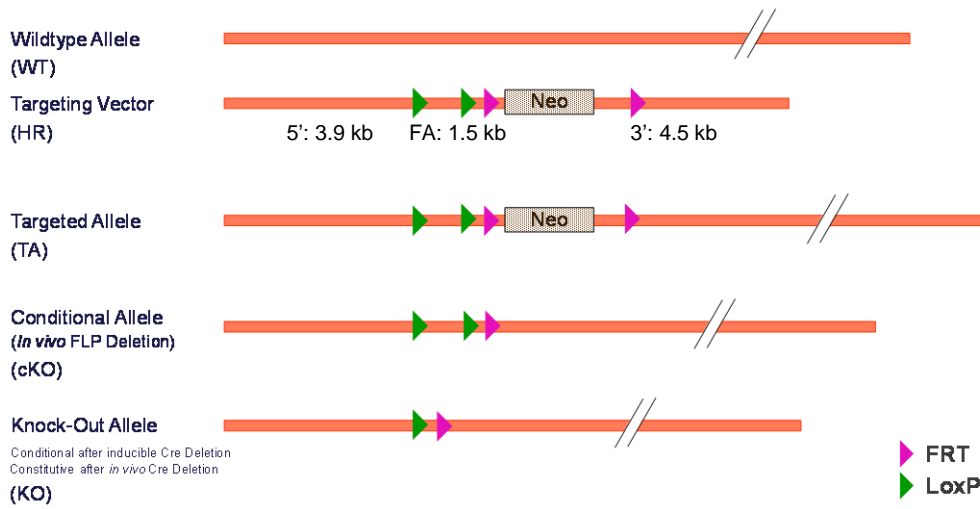
This protocol has been validated by Sylvie Jacquot, Ph.D., Project Manager

1. Schematic representation of the locus

1.1. Overview



Overview Targeting Strategy



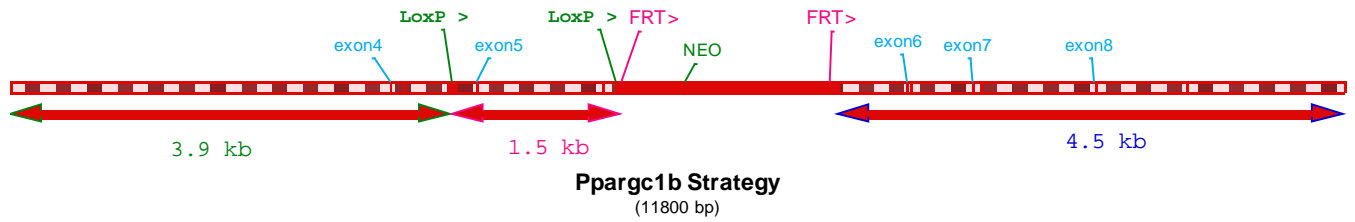
Legend:

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 5

Ppargc1b gene (also named PGC-1 β) 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=85796>

Strategy used to generate the conditional knock out model



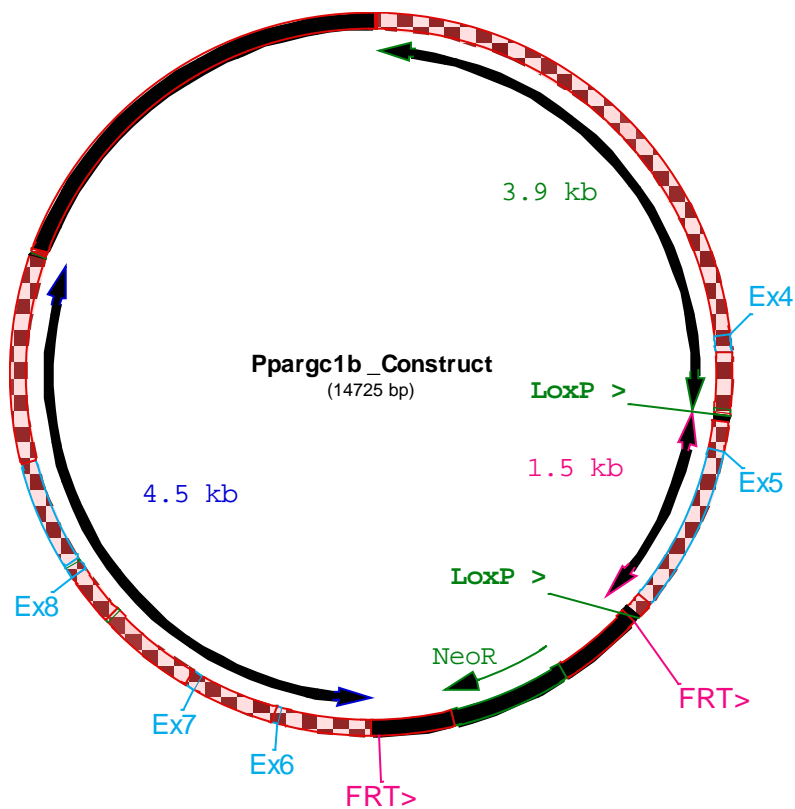
2. Construct used for homologous recombination in ES cells: Ppargc1b project

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. Sequenced regions are indicated in bold.

2.2. Map of targeting vector plasmid





TCTGGCGTATTTCTTCTCCAGGTGGATGGCACCCAGGATAAGAAGACCCCCACACTGCGGGCTCAGAGCCGGCC
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 GCCAATCCCCCAGGCCTGCAGCAGCCTCTCCAGGCAGGTTCAACCCCGATCCCGGCATCCCCCAAAGCCTTCTG
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 ttat

2.5. PGK-Neo region

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 acttcattctcagatattgttttgccaagttctaattccatcagaagctcgataaccgtcgaggaagtctctattct
 ctagaaagtataggaacttcgagggatccatcgacccccgag

2.6. 3' homology arm (4.5 kb)

CCGTATAACTTGGCAGACCTTCAAGAAAATACTTGGTCTTCTTCAAGATTTTCATCATGCATATCAAAGCACTGC
 TTAATGAACAGAGAACAAGAGGCCTTATCCATGCCTGGATAAAGGACAAGGGATGGTAAAAAATAATAATAATA
 ATAAAGTTAGGCACAATACTTAGGAAGCAGAGACAGGAGGATAGAATTTGATAGAGGATAGAATATGTAGTCTGG
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 GGGCCCGTCACTAGAACCATGTAGAATCACAGCTTGGGCTTGGAGCCTTGGCCTCAGTGCATGGCTACCGTGCTG
 CACTGTTTGGCCAGCAAGGGTTGCCTGGCCCATCTGCTATTTCTGCAAAGTGAGGAGATCTGCTGGCTGAGCCCC
 AGCCATGCAAGATGGATTTGAATTGCACCCGATCCTTCCCTTAGATGGCCATATGTCACCTTAAAGGGCATCTGT
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2.7. Vector backbone sequence

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ggaaacagctatgacctgattacgccaagcgcgcaattaaccctcactaaagggaaacaaaagctggagctcgcg
gccgcggcgcgc

3. ES cell lines targeted and validation data:

3.1. ES cell lines targeted

The targeting vector was electroporated in BD10 ES cells [MCI-C57BL/6NTac background]

Number of clones screened: 372

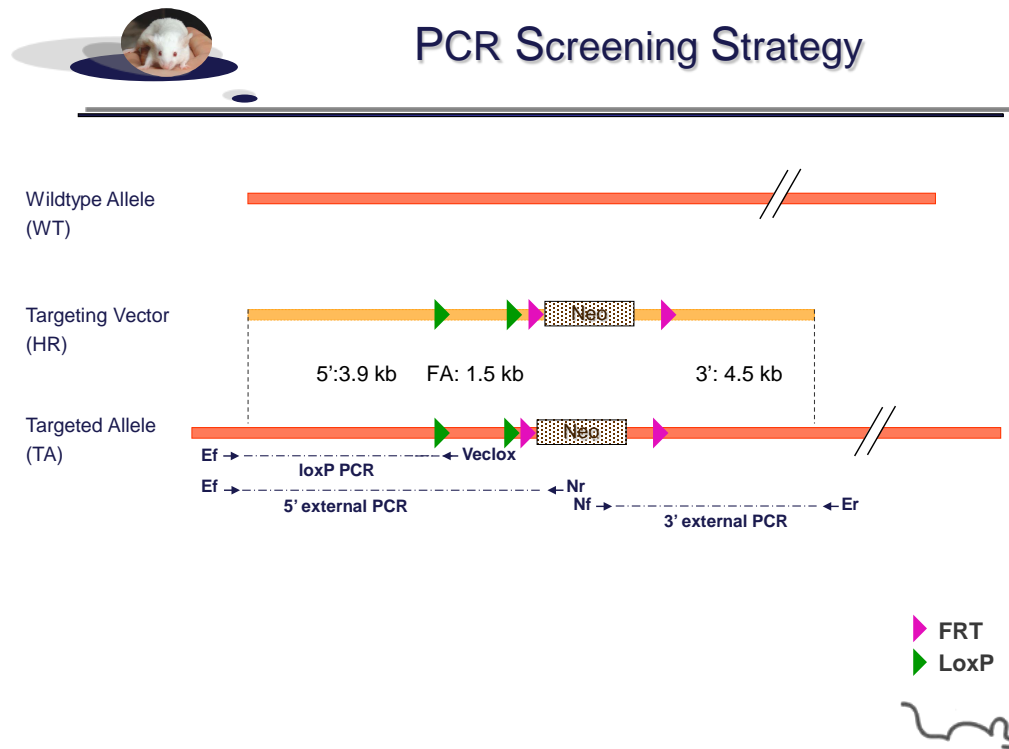
Number of positives: 5

Reference of clone used to generate the mouse line:

- clone **K189BD10-271**

3.2. PCR data on positive clone

3.2.1. PCR screening strategy



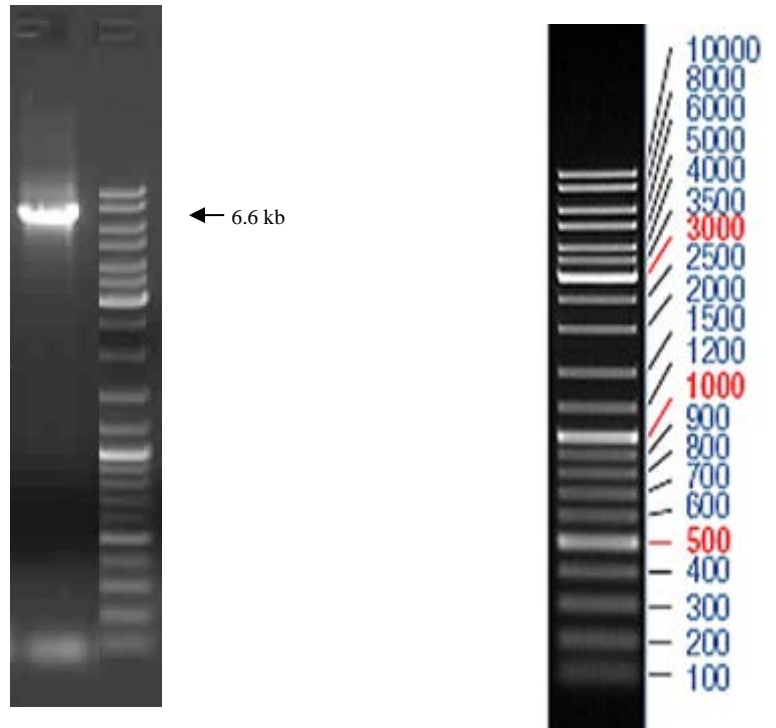
Primers used for PCR validation of ES clone

PCR	Primer Name	Primer sequences	PCR product size
5' external	Ef	ATCTCTAAATAGGCTACCTTCTGCC	6.6 kb
	Nr	GCGGCCGAGAACCTGCGTGCAATC	
3' external	Nf	AGGGGCTCGCGCCAGCCGAAGTGT	5.7 kb
	Er	CTCGTGACTTGCTAACTTTCAACGC	
LoxP	Ef	ATCTCTAAATAGGCTACCTTCTGCC	4.5 kb
	Veclox	GGCCAGCCATATTCCATAACTTCGT	

3.2.2. Picture of PCR on positive clone

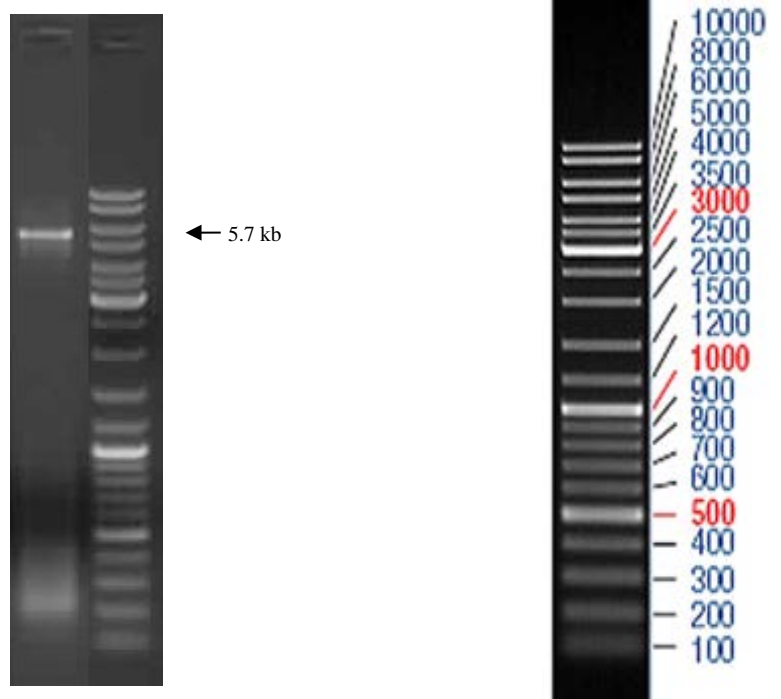
5' external PCR

ladder



3' external PCR

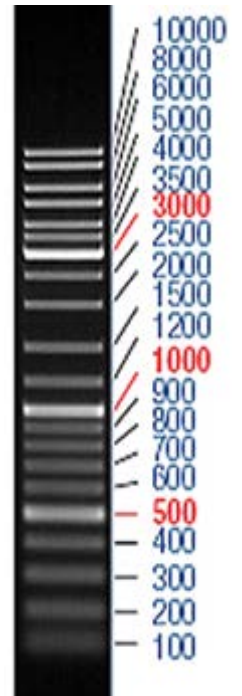
ladder





LoxP PCR

ladder

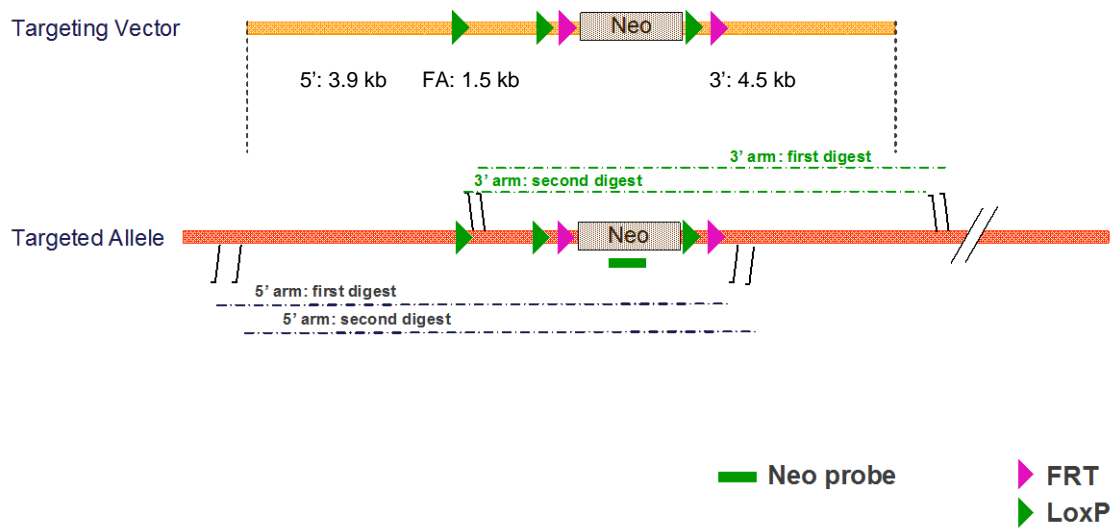


3.3. Southern data on positive clone

3.3.1. Neo Southern strategy



Southern Screening Strategy



Digestions used to validate the 5' and 3' insertion

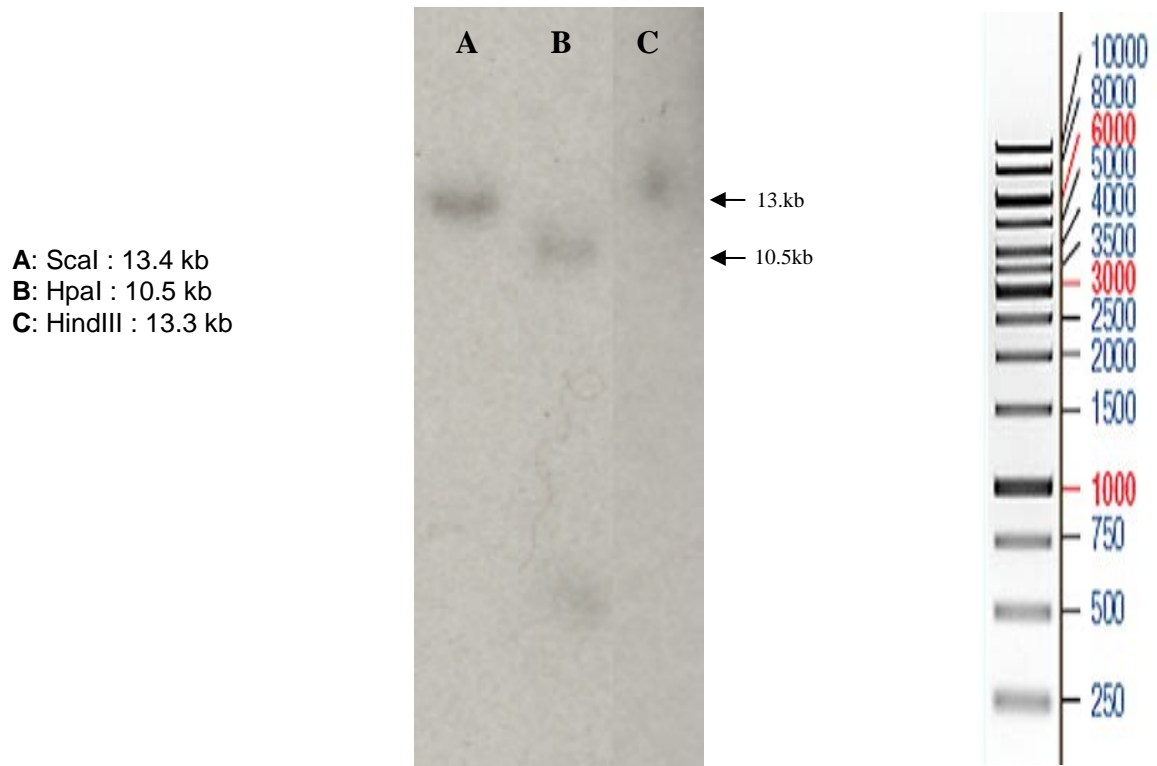
Probe	Name	Genomic DNA digest	WT allele (kb)	Targeted Allele (kb)
Neo	5' arm first digest	Scal	/	13.4
	3' arm first digest	HpaI	/	10.5
	3' arm second digest	HindIII	/	13.3

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

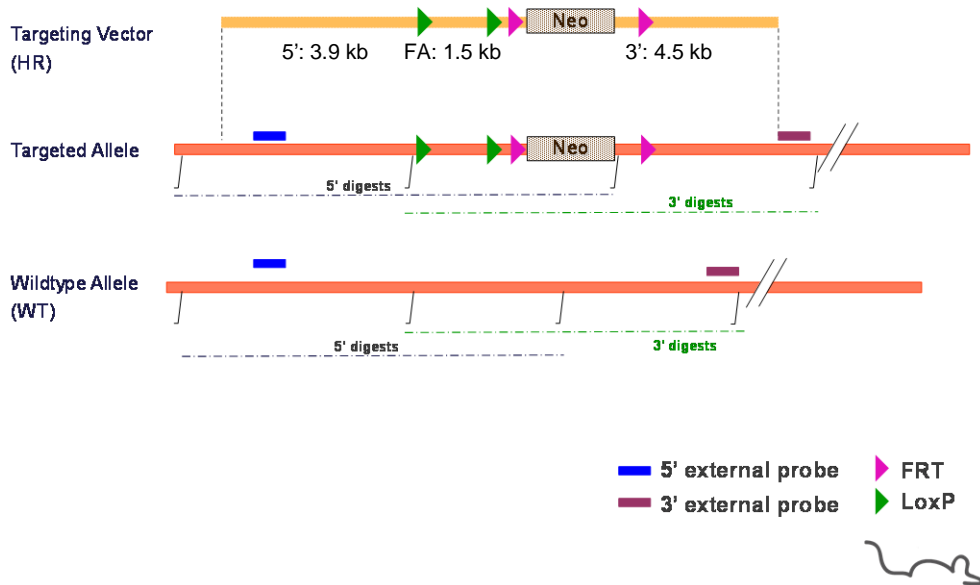
ladder



3.3.3.External probes Southern strategy



Southern Screening 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	NheI/Scal	15.9	10.0
	second digest	HindIII	6.9	13.3
3' external	first digest	NheI/Scal	14.9	8.3
	second digest	HindIII	6.9	13.3

Primers for probe synthesis:

5' probe:

CACCCTTGGATGTGCCCGGCTTGC
 CTGAACCTACTACACAAGGTGAGGG

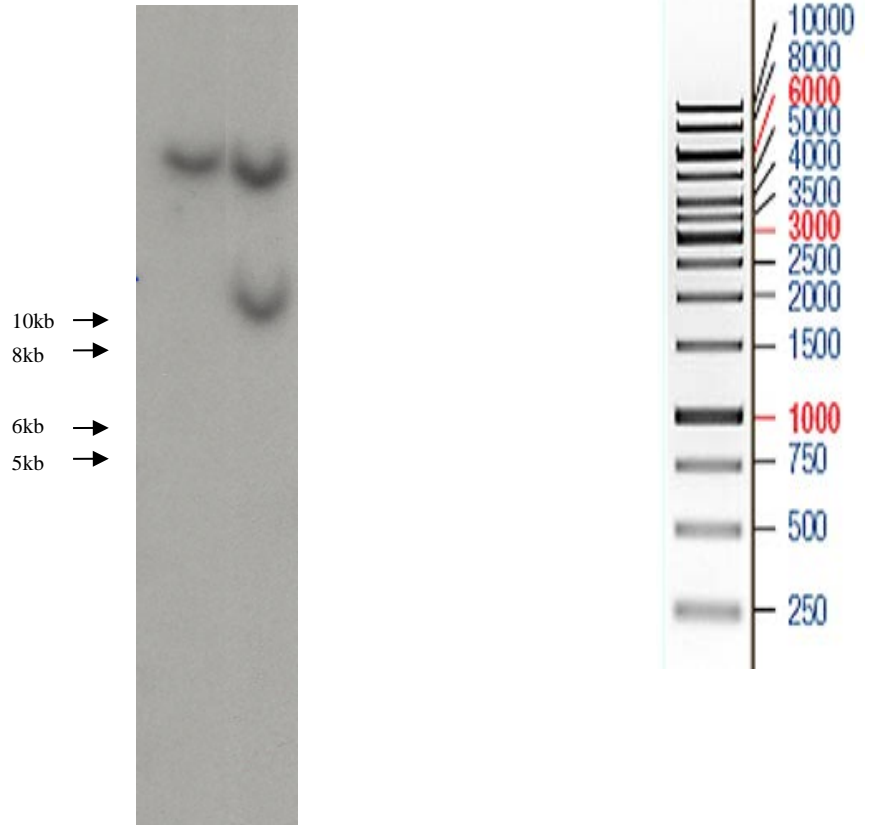
3' probe:

GGGTTTAAGTTCAACCCGTGGAGCT
 TCTTCATGTTAGGGGTAGATAGCCC

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

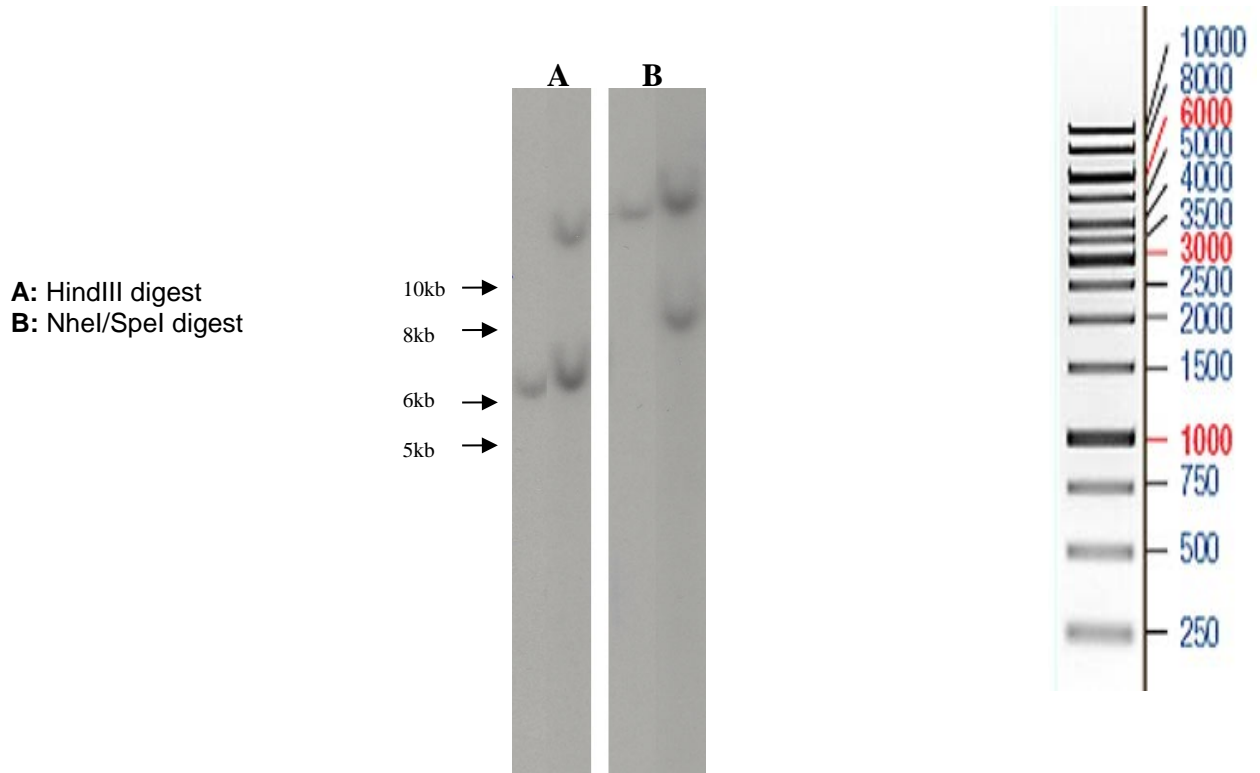
5' external probe validation

Ladder



3' external probe validation

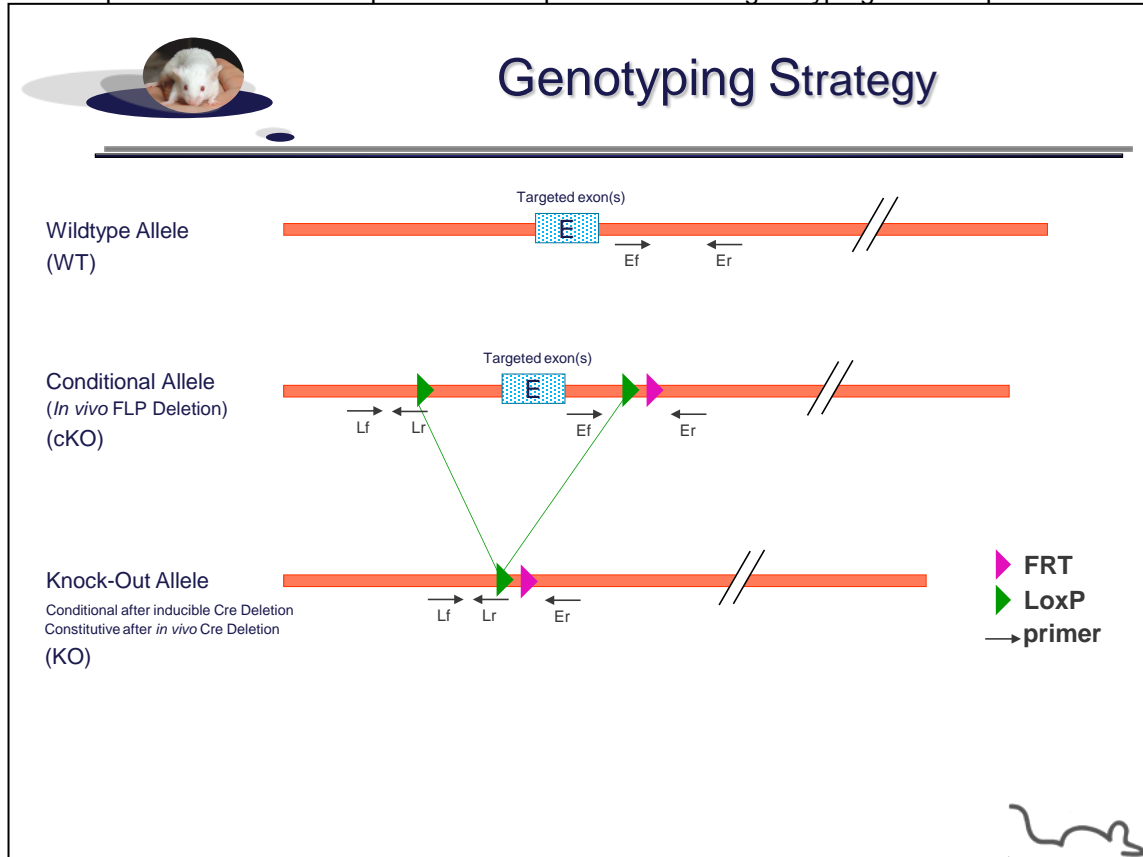
Ladder



4. Genotyping protocol and data on conditional and knock-out animals

4.1. **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	Primer	Sequence
Ef	3039	GTGAGGTTGGATCTGCTTATCCACTG
Er	3041	CCTGTCTCTGCTTCCTAAGTATTGTGC
Lf	3038	CTCTGGGGCCTCATGAGCTAATG
Lr	3037	ACGAAGTTATGGAATATGGCTGGCC



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	3038-3037	Lf / Lr	164	164	---
Excision of the selection marker	3039-3041	Ef / Er	329	---	219
Excision of the floxed exon(s), i.e. knock out	3038-3041	Lf / Er	1898*	442	1781*

*: 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:

- FastStart PCR Master (Roche)
- DNA (50ng/μl)
- 5' primer (100 μM)
- 3' primer (100 μM)
- Sterile H₂O

Volume:

- 7.5μl
- 1.5μl
- 0.06μl
- 0.06μl
- up to 15 μl

Cycling conditions:

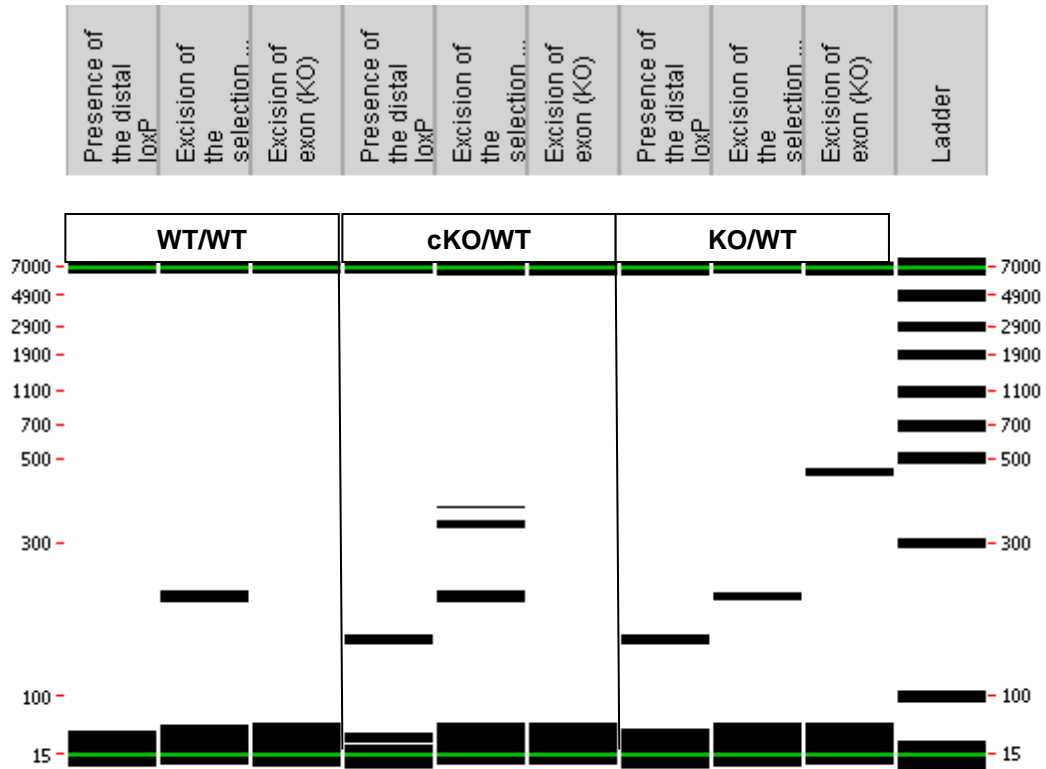
Temp	Time	#Cycles
95°C	4min	1
94°C	30s	34
62°C	30s	
72°C	1min	
72°C	7min	1
20°C	5 min	1

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 done by 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.