



MODEL GENERATION TECHNICAL REPORT

Generation of mouse model : Med23 cKO

Project code: G4622 / IR4622

Report finalized: 06/10/2023

1 PROJECT PROCESS & QUALITY CONTROLS

2 GENETIC STRATEGY

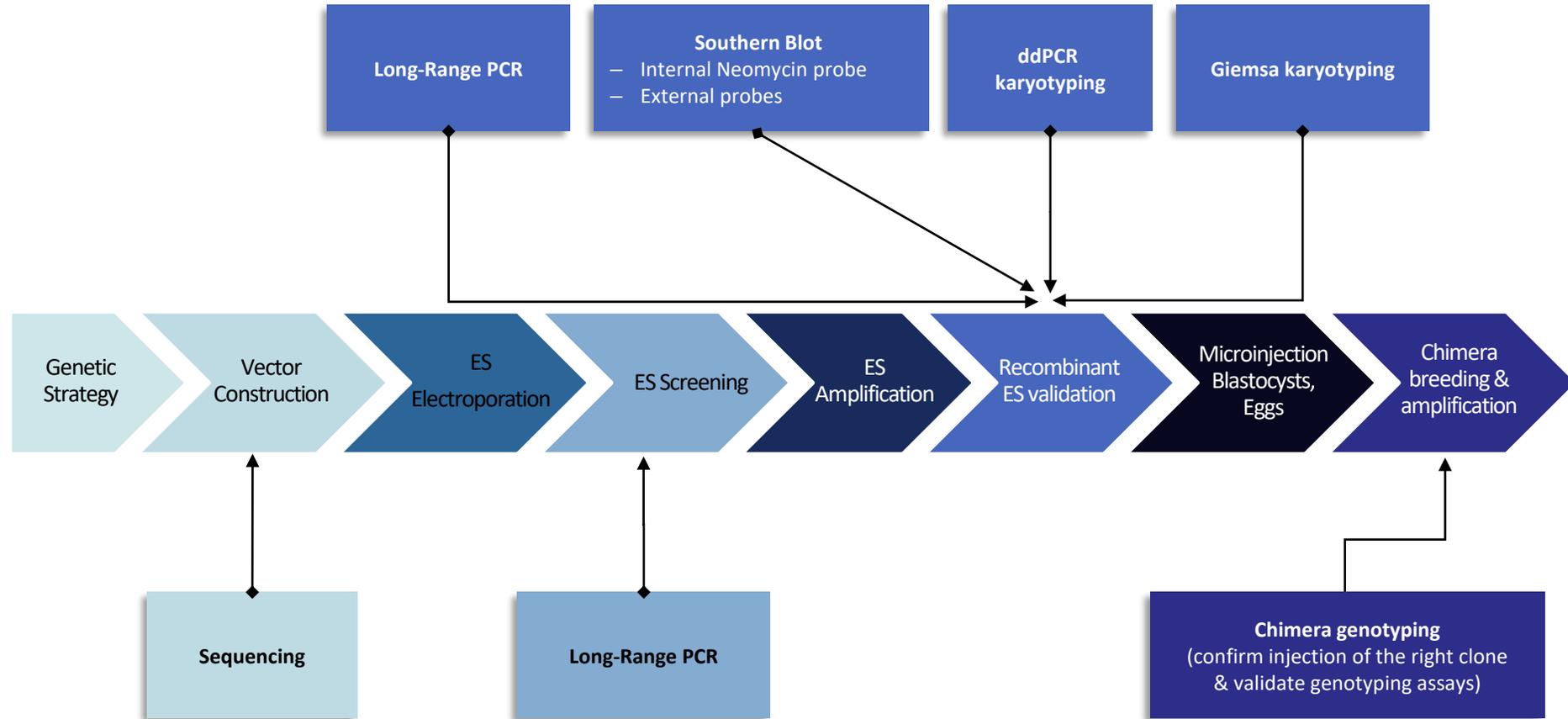
3 HOMOLOGOUS RECOMBINATION VECTOR CONSTRUCTION

4 ES ELECTROPORATION & SCREENING OF RECOMBINANT CLONES

5 MICROINJECTION & BREEDING

6 SEQUENCE OF THE DELIVERED ALLELE

PROJECT PROCESS & QUALITY CONTROLS



2 GENETIC STRATEGY

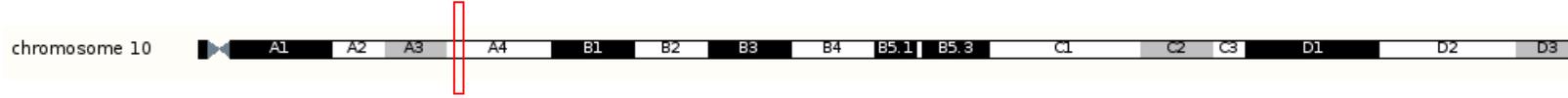


- Target locus structure
- mRNA(s) and protein(s)
- Genetic strategy
- PRO & CONS evaluation of the strategy

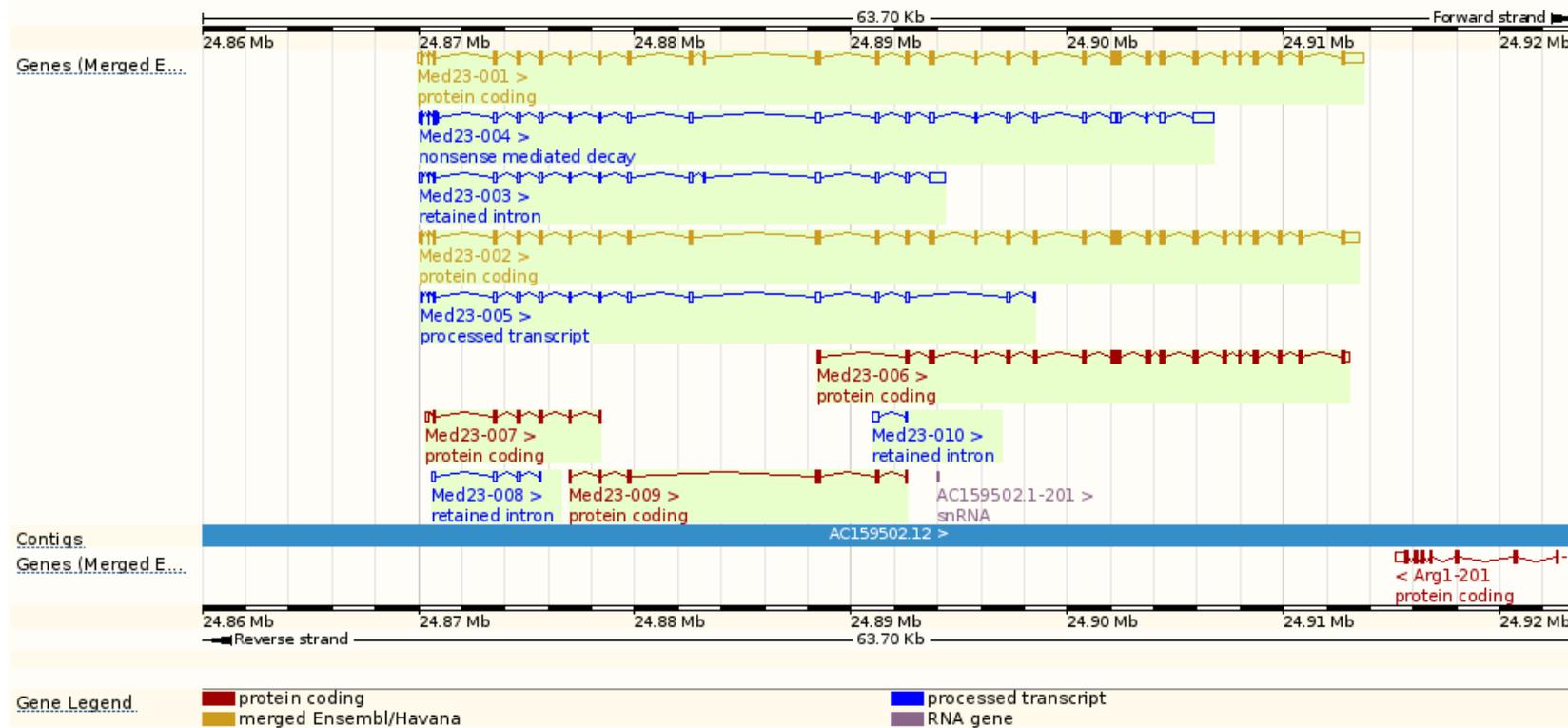
Med23 mouse genomic locus – structure



Location



Ensembl Gene ID: Med23 ENSMUSG00000019984

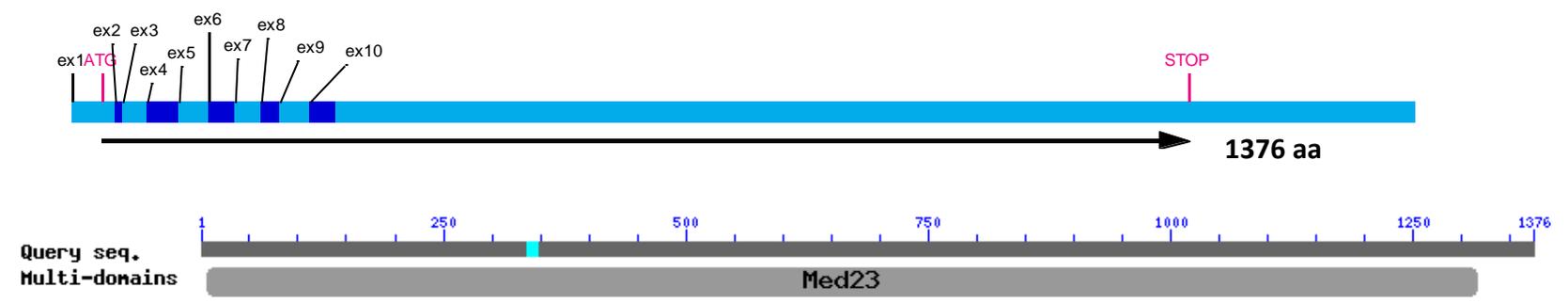


■ Med23 mRNA(s) and protein(s)



Name	Transcript ID	Length (bp)	Protein ID	Length (aa)	Biotype	CDS incomplete	CCDS
Med23-001	ENSMUST00000092646	5098	ENSMUSP00000090316	1376	Protein coding	-	CCDS48522
Med23-002	ENSMUST00000020159	4798	ENSMUSP00000020159	1370	Protein coding	-	CCDS35871
Med23-006	ENSMUST00000176285	3226	ENSMUSP00000135232	1010	Protein coding	5'	-
Med23-007	ENSMUST00000176313	770	ENSMUSP00000135751	197	Protein coding	3'	-
Med23-009	ENSMUST00000176502	704	ENSMUSP00000134836	234	Protein coding	5' and 3'	-
Med23-004	ENSMUST00000177232	3953	ENSMUSP00000134866	58	Nonsense mediated decay	-	-
Med23-005	ENSMUST00000176827	1635	No protein product	-	Processed transcript	-	-
Med23-003	ENSMUST00000177522	2192	No protein product	-	Retained intron	-	-
Med23-008	ENSMUST00000177175	419	No protein product	-	Retained intron	-	-
Med23-010	ENSMUST00000175786	368	No protein product	-	Retained intron	-	-

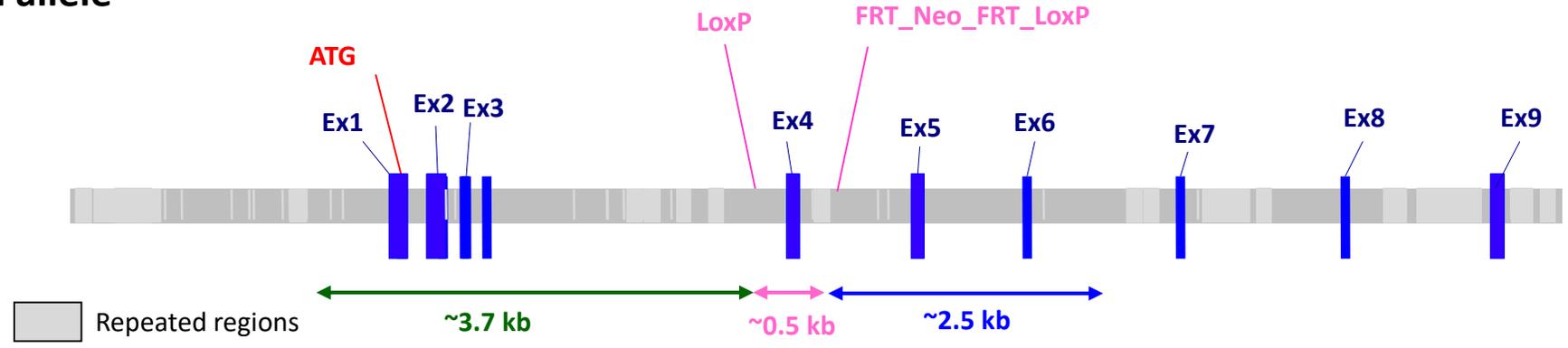
Med23-001 ENSMUST00000092646



■ Approach selected: flox exon 4



Targeted allele



Ex4: ENSMUSE00001034764

mRNA and protein obtained after Cre mediated excision (-001)



■ PROs& CONs evaluation of the strategy



■ Pros

- Appropriate size of the floxed fragment

■ Cons

- A protein of 50 aa might be expressed after Cre mediated excision if RNA decay does not occur
- Presence of repeated regions (in light grey) in both homology arms (green and blue arrows) might render PCR amplification and/or homologous recombination at the locus difficult

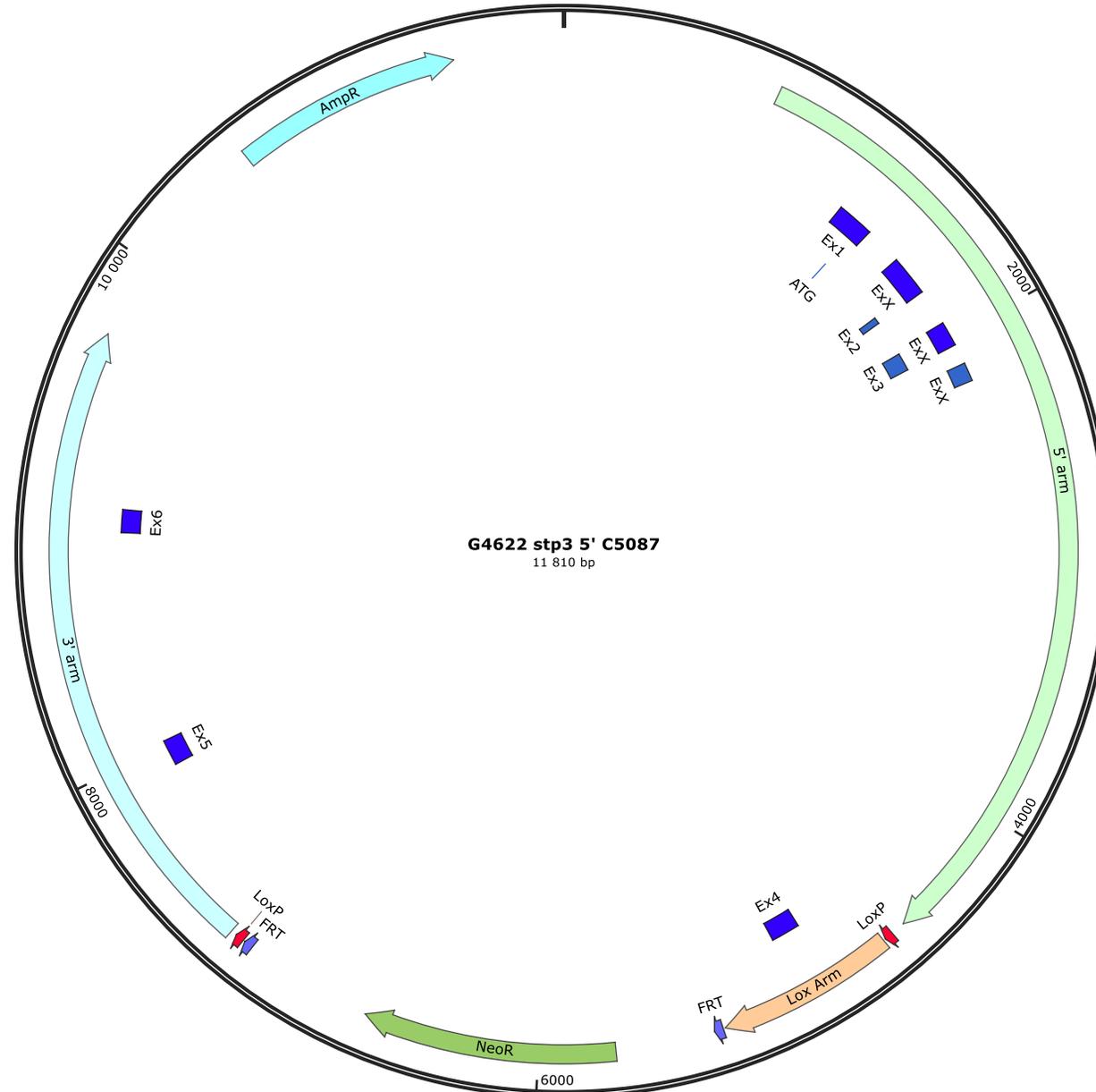
The selection cassette (FRT-Neo-FRT) will be removed by breeding male chimera with a flp deleter line which shows maternal contribution (*Birling et al.*, 2012)

Highly-efficient, fluorescent, locus directed cre and FlpO deleter mice on a pure C57BL/6N genetic background.

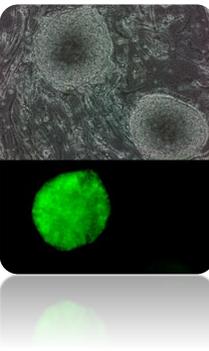
Birling MC, Dierich A, Jacquot S, Hérault Y, Pavlovic G. *Genesis*. 2012 Jun;50(6):482-9. doi: 10.1002/dvg.20826.

3 HOMOLOGOUS RECOMBINATION - VECTOR CONSTRUCTION

Created by SnapGene

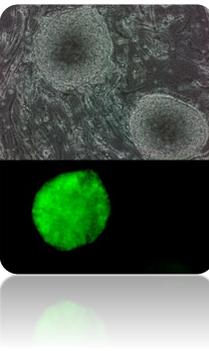


4 ES cell electroporation & Screening of recombinant clones



- Electroporation and screening process
- Long range PCR screening – strategy
- Long-Range 5' PCR screening – results
- Recombinant ES validation by Long Range PCR
- Recombinant ES clones validation by Southern Blot – internal probe
- Recombinant ES clones validation by Southern Blot – External probe
- Aneuploidy screening in ES recombinant clones

■ Electroporation and screening process



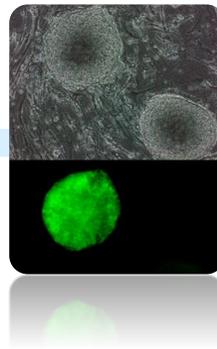
The targeting vector was electroporated in the proprietary C57BL/6N TB1 cell line.

Transfected ES clones were submitted to neomycin selection (G418) and 93 resistant ES clones were isolated. The clones were then submitted to the screening process allowing secured identification of those harbouring the expected recombination events at both ends of targeting vector.

Screening process steps:

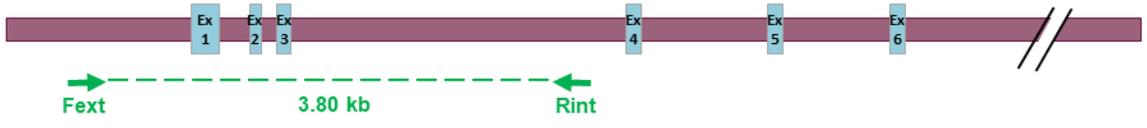
1. Identification of candidate recombinant clones by initial 5' Long-Range PCR
2. Six of 5' PCR positive clones are confirmed for 3' recombination event by Long-Range PCR
3. Positive clones in step2 are further validated by Southern blot analysis using internal and external probes
4. The karyotype of at least 2 validated clones is verified Giemsa staining

Long range PCR screening – strategy

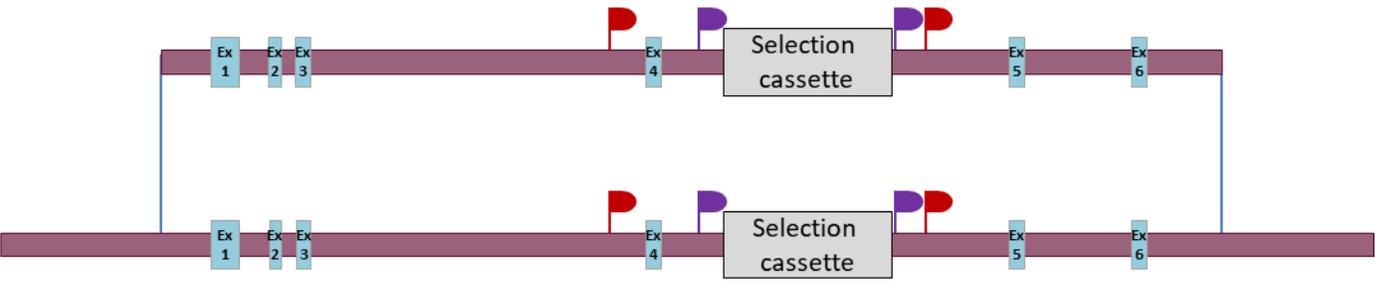


Schematic 5' and 3' PCR screening strategy

Wild type Allele (WT)

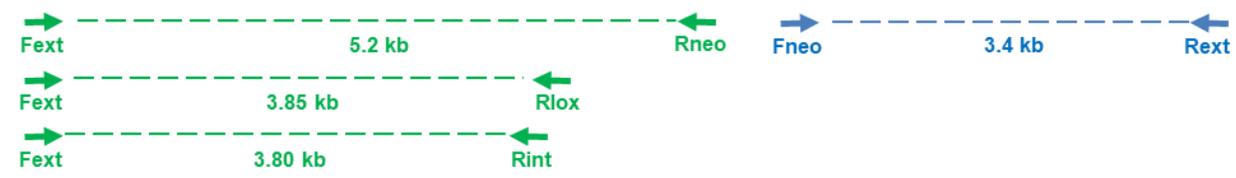


Targeting Vector



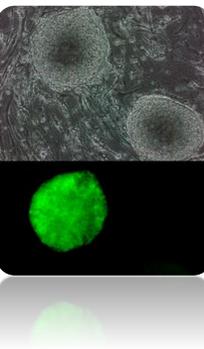
LoxP
FRT

Targeted Allele (HR)

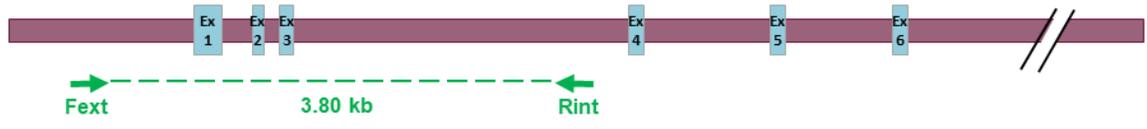


PCR	Primer Name	Primer sequences	PCR product size
5' PCR	Fext	AAGTTTCTGGAAGAAAACATTGACG	5.2 kb
	Rneo	GCGGCCGAGAACCTGCGTGCAATC	
5' PCR	Fext	AAGTTTCTGGAAGAAAACATTGACG	3.85 kb
	Rlox	GTTATCTGCAGGTCGACCTTAAGCT	
5' PCR	Fext	AAGTTTCTGGAAGAAAACATTGACG	3.80 kb
	Rint	CTTCCAGAGCATCCTGGGAGGATCT	
3' PCR	Fneo	AGGGGCTCGGCCAGCCGAAGTGT	3.4 kb
	Rext	CCACAAGGTATATGCACACATATGT	

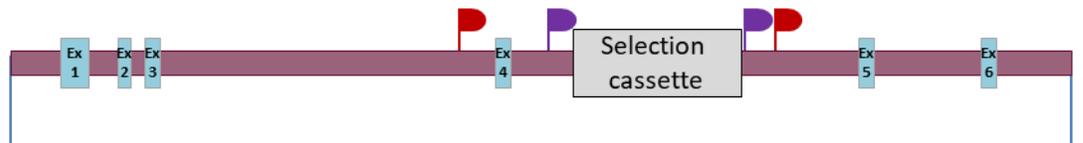
Long-Range 5' PCR screening – results



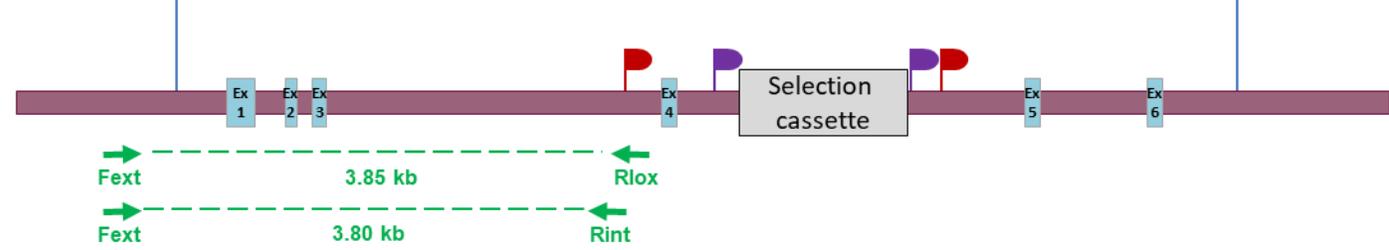
Wildtype Allele (WT)



Targeting Vector

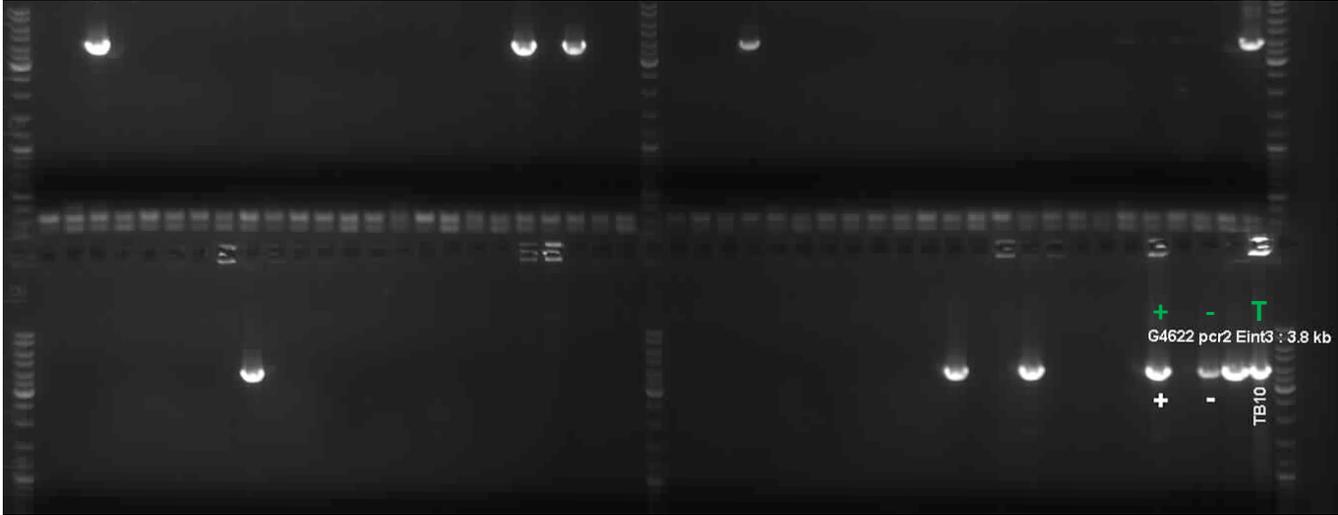


Targeted Allele (HR)

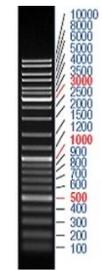


LoxP
FRT

PCR Fext – Rlox : 3.85 kb



G4622 pcr2 Eint3 : 3.8 kb



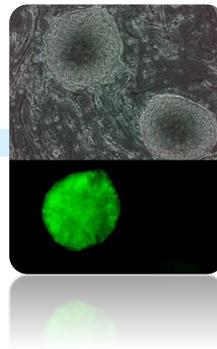
Ladder pattern

+ / - / T : Controls DNAs

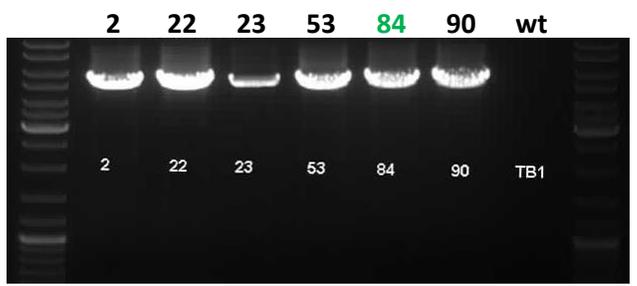
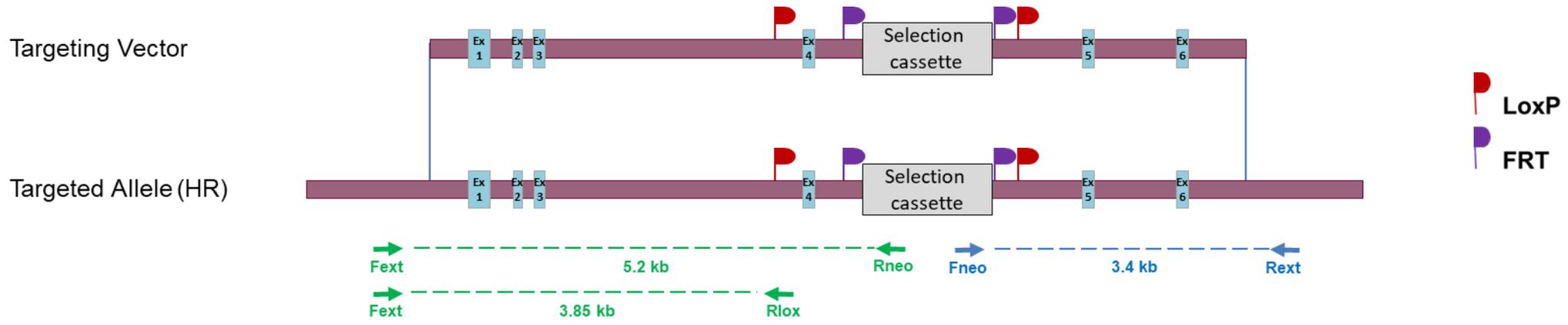
PCR Fext – Rint : 3.80 kb

Six candidate clones out of the nine positive clones were selected for 3' Long-Range PCR and Southern blot validation.

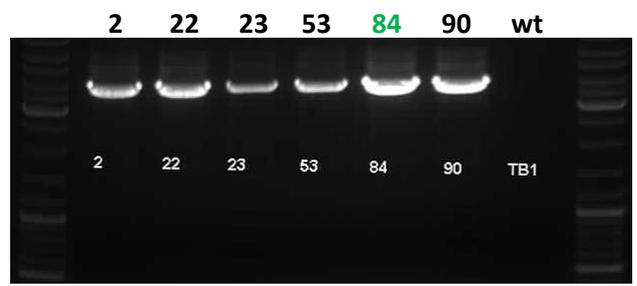
Recombinant ES validation by Long Range PCR



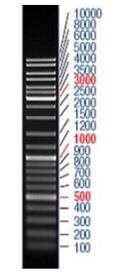
Confirmation and Validation of candidate recombinant ES clones by 5' and 3' PCRs



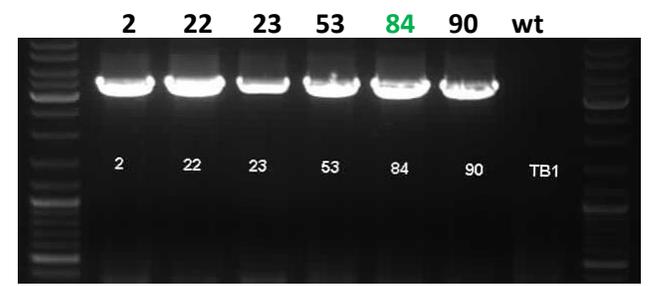
PCR Fext – Rneo : 5.2kb



PCR Fext – Rlox : 3.85 kb



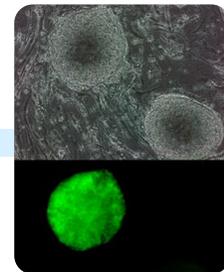
Ladder pattern



PCR Fneo – Rext : 3.4 kb

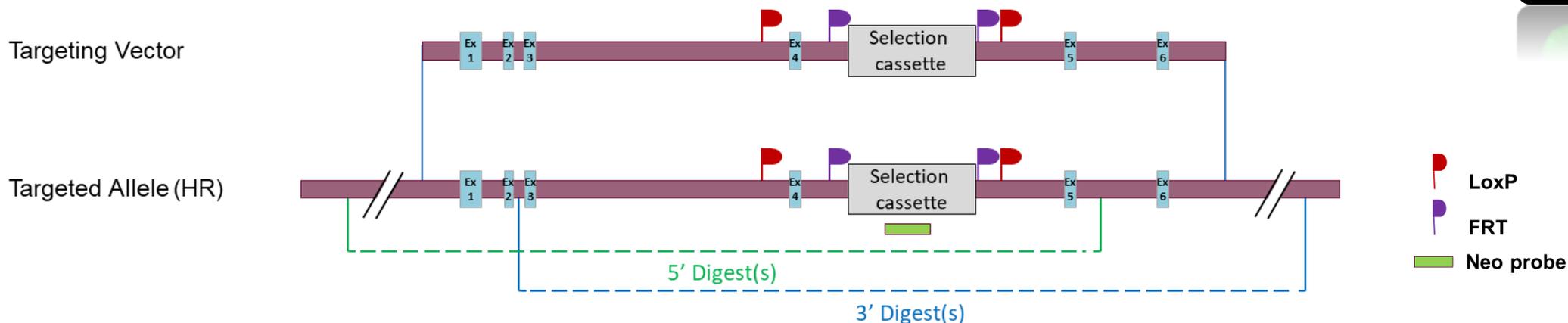
Six candidate clones identified by 5' PCR screening were further analysed by 3' PCR screening. Six clones (clones #2, #22, #23, #53, #84 and #90) were confirmed.

Recombinant ES clones validation by Southern Blot – Internal probe



Schematic Southern Blot validation strategy

Digests on the scheme illustrate the position of the chosen restriction sites relative to the probe. They don't show the exact position of the restriction sites.



Digestions used to validate the 5' and 3' insertion

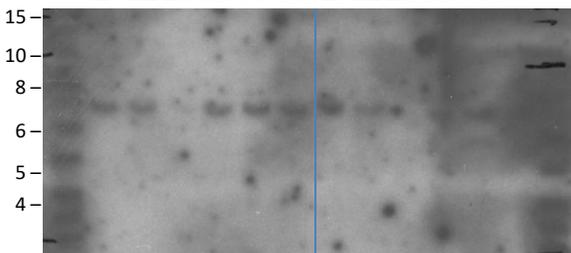
Probe		Genomic DNA digest	Targeted Allele (kb)
Neo	5' digest	EcoRV	7.1
		XcmI	7.5
	3' digest	AfIII	6.9
		BglI	5

Neo probe sequence

```
CTGCAGGACGAGGCAGCGGGCTATCGTGGCTGGCCACGACGGGCGTTTCTTGCAGCTGTGCTCGACGTTGTC
ACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCT
GCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCATTCGAC
CACCAAGCGAAACATCGCATCGAGCGAGCAGTACTCGGATGGAAGCCGGTCTTGTGATCAGGATGATCTGGAC
GAAGAGCATCAGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATGCCGACGGCGAGGATCTC
GTCGTGACCCATGGCGATGCTGCTTGGCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTTCGACTGT
GGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGC
GAATGGGCTGACCGCTTCTCGTGCTTTACGGTATCGCCGCTCCCGATTGCGAGCGCATCGCCTTCTATCGCCTT
CTTGACGAGTTCTTCTGAGGGGATCCGCTGTAAGTCT
```

Southern blot - Neo 5'

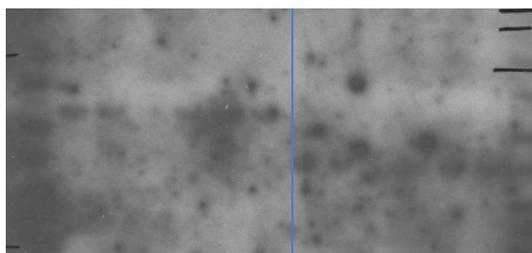
2 22 23 53 84 90 2 22 23 53 84 90



EcoRV XcmI

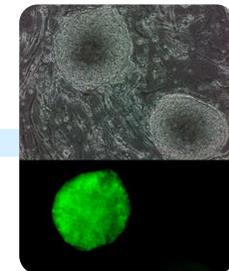
Southern blot - Neo 3'

2 22 23 53 84 90 2 22 23 53 84 90



AfIII BglI

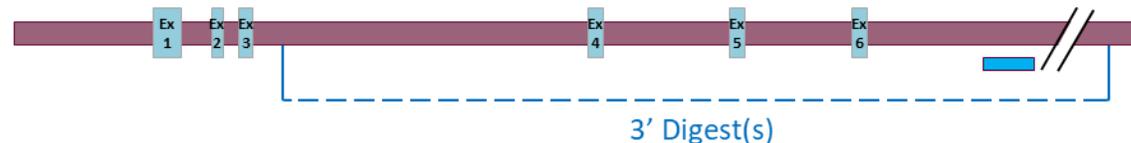
Recombinant ES clones validation by Southern Blot – External probe



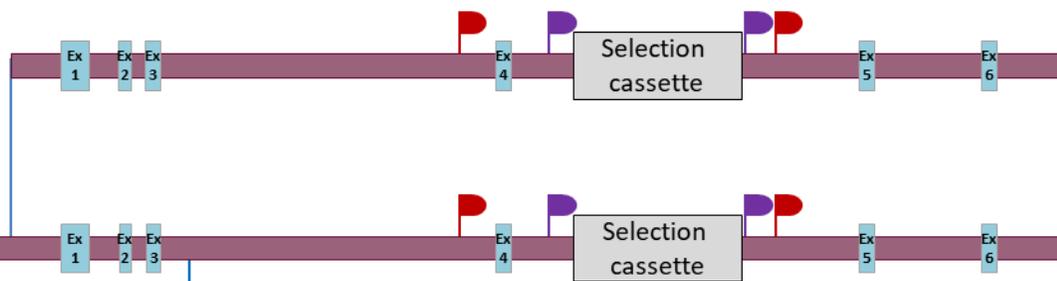
Schematic Southern Blot validation strategy

Digests on the scheme illustrate the position of the chosen restriction sites relative to the probe. They don't show the exact position of the restriction sites.

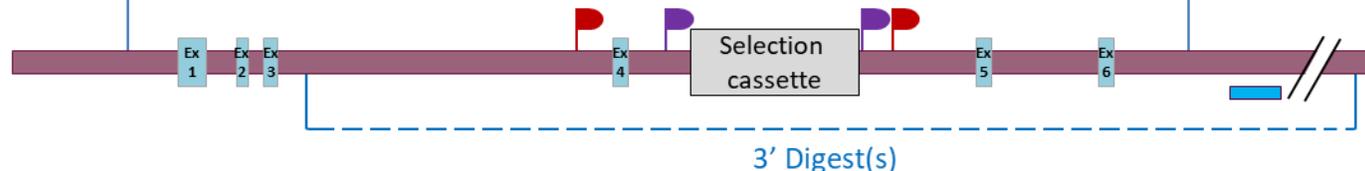
Wild type Allele (WT)



Targeting Vector

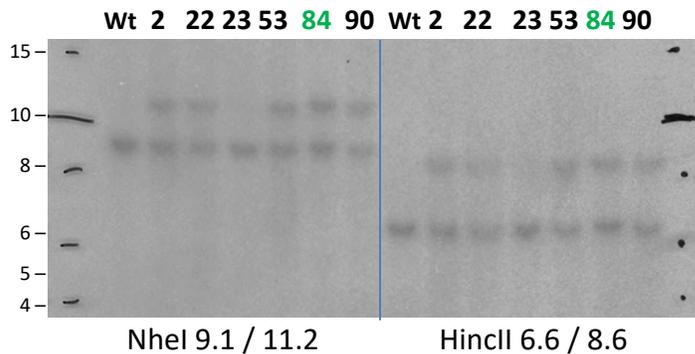


Targeted Allele (HR)



- LoxP
- FRT
- 3' external probe

Southern blot – 3' probe



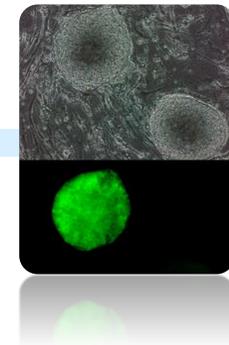
3' probe sequence

```
GCTCCCTCCCACACAGATACAAGCACACTTTGCCA
ACTAAGCTATTGTCCCAGCCCCATTTAGTCATTTG
TAAATATACTTTTTTGTGTGGCGTCGTTGTATT
TATAGGTTGTTTGTGTGAGCCTAGTCAAGAATAAT
GCTTTTTGCTTGTTTTAGGTTATAGCTTATATCTT
AGAACGAAATGCCTGCCTATTGCCGGCCTACTTTG
CAGTCACAGAGATCAGAAAATATATCCTGAGGGA
AAACTTCCACACTGGG
```

Digestions used to validate the 5' and 3' insertion

Probe	Name	Genomic DNA digest	WT allele (kb)	Targeted Allele (kb)
3' external probe	3' first digest	NheI	9.1	11.2
	3' second digest	HincII	6.6	8.6

■ Aneuploidy screening in ES recombinant clones



Selected recombinant ES cells clones were karyotyped by Giemsa metaphase staining. Results of aneuploidy analysis are presented in the table below.

Clone ID	qPCR	Giemsa
#2	Pass	Pass
#22	Pass	Not done
#53	Pass	Failed
#84	Pass	Pass
#90	Pass	Not done

¹ Codner, G.F., Lindner, L., Caulder, A., Wattenhofer-Donzé, M., Radage, A., Mertz, A., Eisenmann, B., Mianné, J., Evans, E.P., Beechey, C.V., Fray, M.D., Birling, M.-C., Héroult, Y., Pavlovic, G., Teboul, L
Aneuploidy screening of embryonic stem cell clones by metaphase karyotyping and droplet digital polymerase chain reaction.
BMC Cell Biology 2016 doi:10.1186/s12860-016-0108-6

5 MICROINJECTION & BREEDING



- Microinjection
- Breeding to F1 generation

■ Microinjection



- The ES cells used in the injection experiment were originally derived from a C57BL/6N mouse strain (which have black coat colour). These cells were injected into blastocysts derived from an BALB/cN strain, which have a white coat colour. The resulting offspring are thus chimeras of two different cell types (ES cell-derived cells and host blastocyst-derived cells) and the degree of chimerism was monitored by the percentage of light and dark patches on these animals.
- Recipient blastocysts were isolated from mated BALB/cN females (Health status SPF Specific Pathogens Free).
- Recombinant ES clones #2 and #84 validated in previous project phase were injected into blastocysts to generate chimeric males. The results are presented in the table below.

Clone ID	Number of chimeric males identified according to chimerism rate (Number of chimeric males bred to F1 generation)			
	5 - 40%	45% - 55%	60-100%	Total
#2	5	0	3	8
#84	2	0	3	5

■ Breeding to F1 generation

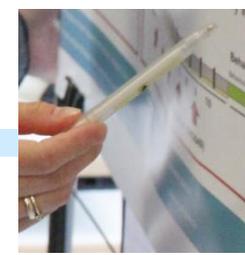


- Three highly chimeric males generated in the previous phase by blastocyst injection of the ES clones were mated with Flp deleted C57BL/6N females that show maternal contribution* (health status SPF – Specific Pathogen Free) to investigate whether the recombined ES cells have contributed to the germ layer.
- Germ line transmission was obtained the : 18/06/2014
- Allele nomenclature (following MGI guidelines) : **Med23^{tm1.1lcs}**

*Highly-efficient, fluorescent, locus directed cre and FlpO deleter mice on a pure C57BL/6N genetic background.

Birling MC, Dierich A, Jacquot S, Hérault Y, Pavlovic G. Genesis. 2012 Jun;50(6):482-9. doi: 10.1002/dvg.20826.

6 SEQUENCE OF THE ALLELE



CAACCAATATAATTTCTCTGAAGGCATATAATAAAATAGTAATACTTTCTTATCCTTGTGTATCAAGCACTGGGAAATTTATCTTGGTAAAATTTACTTTTTATCTTTCAATATTTAGCACATTT
TATGCATTTTTAATTTTAAAATATTTGTTGGTCTTTTTATTTTAACTTTGTGTGTGTGTATGTGTGTTGTGTGTGTGTATGTGTGTGACAGTACTTGTGTACAGGTCAGAGGACAACCTTA
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CTCAATGTTTGAGCTTTCTTCTAAGTAAGAATTAGGAAGTATTTTCATATACCTGGAATACTTTAACAGTATAG

LoxP

FRT

Exon 4



REPORT REDACTION & VALIDATION

Protocol finalized on 2023/10/06

Prepared by Romain LORENTZ, IE

Verified and finalized by Marie-Christine BIRLING, PhD

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