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EXCELLENCE IN MOUSE PHENOGENOMICS

TECHNICAL REPORT

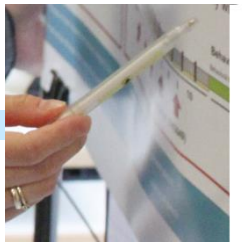
Humanization of mouse ApoE4 (expressing Rs429358 => TGC>CGC; C130R; missense variant) and its neighbors genes (TOMM40, and APOC1)/ KI

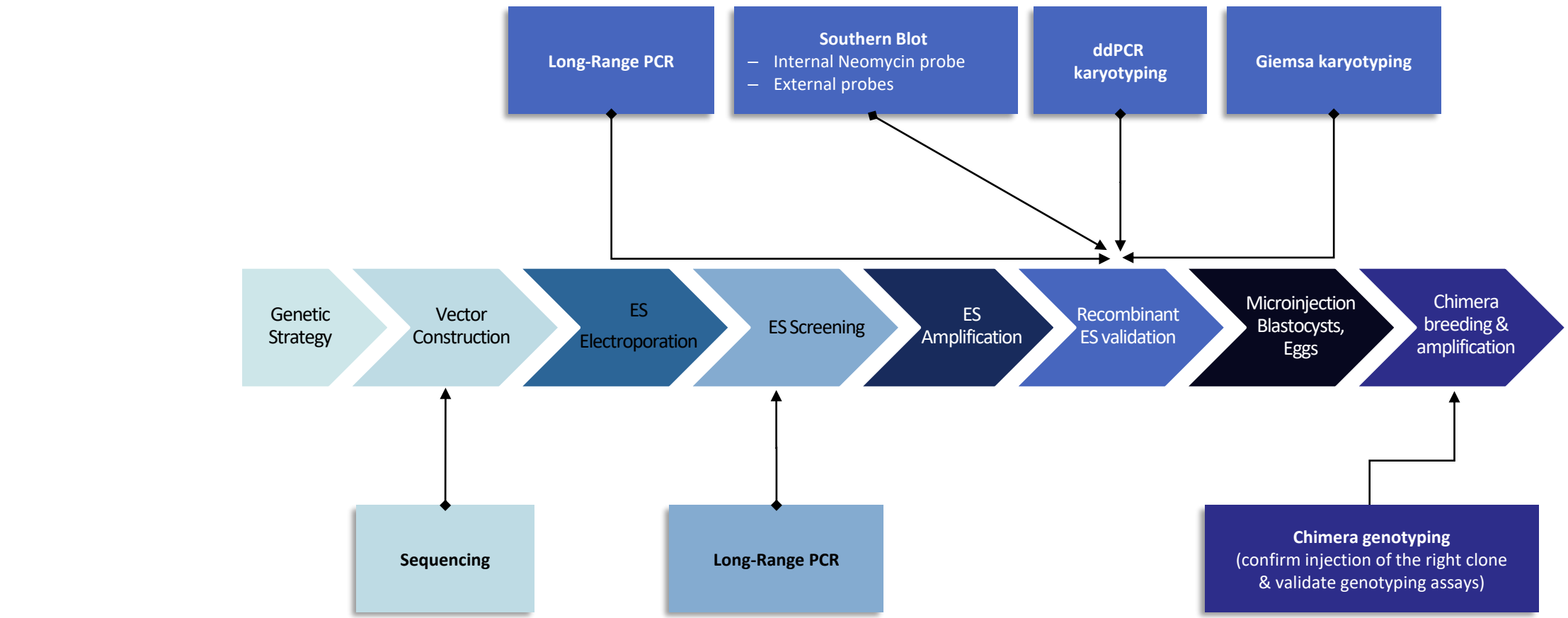
Project code: Kos6436

Report finalized the 6/02/2024

MODEL GENERATION TECHNICAL REPORT

Project process & quality controls





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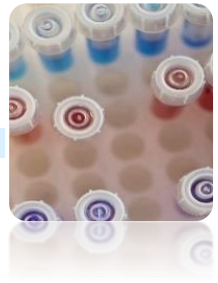
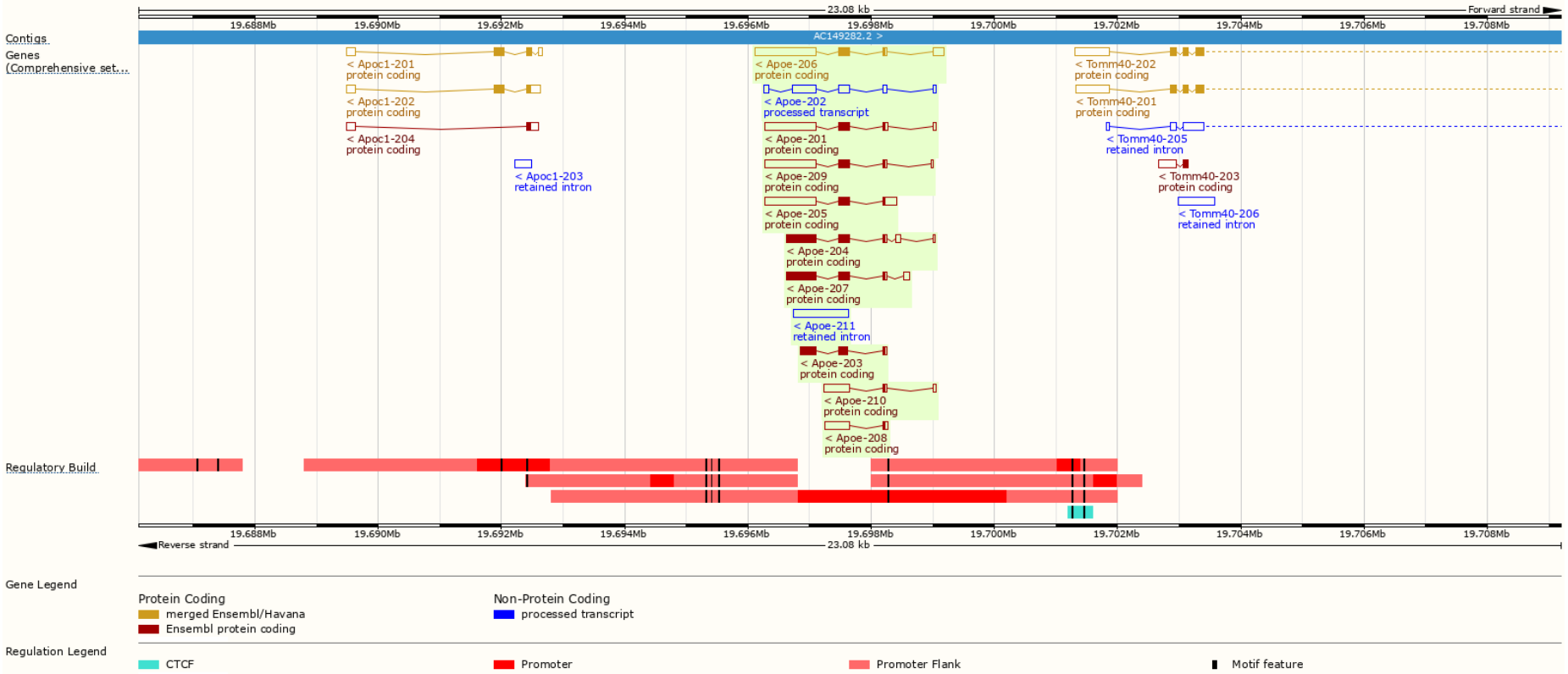
2 GENETIC STRATEGY

- Target locus structure
- Genetic strategy
- Sequence detail
- PRO & CONS evaluation of the strategy

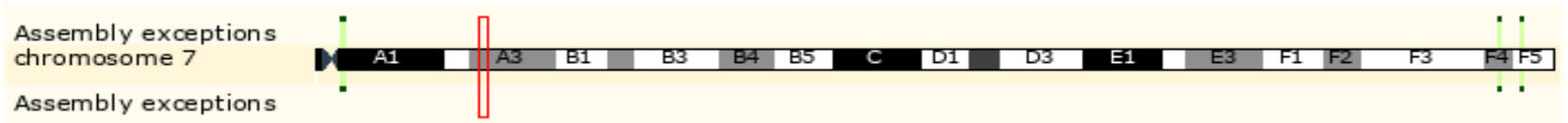
ApoE mouse genomic locus – structure



Gene: **ApoE ENSMUSG00000002985**



Chromosome 7: 19,696,109-19,699,188



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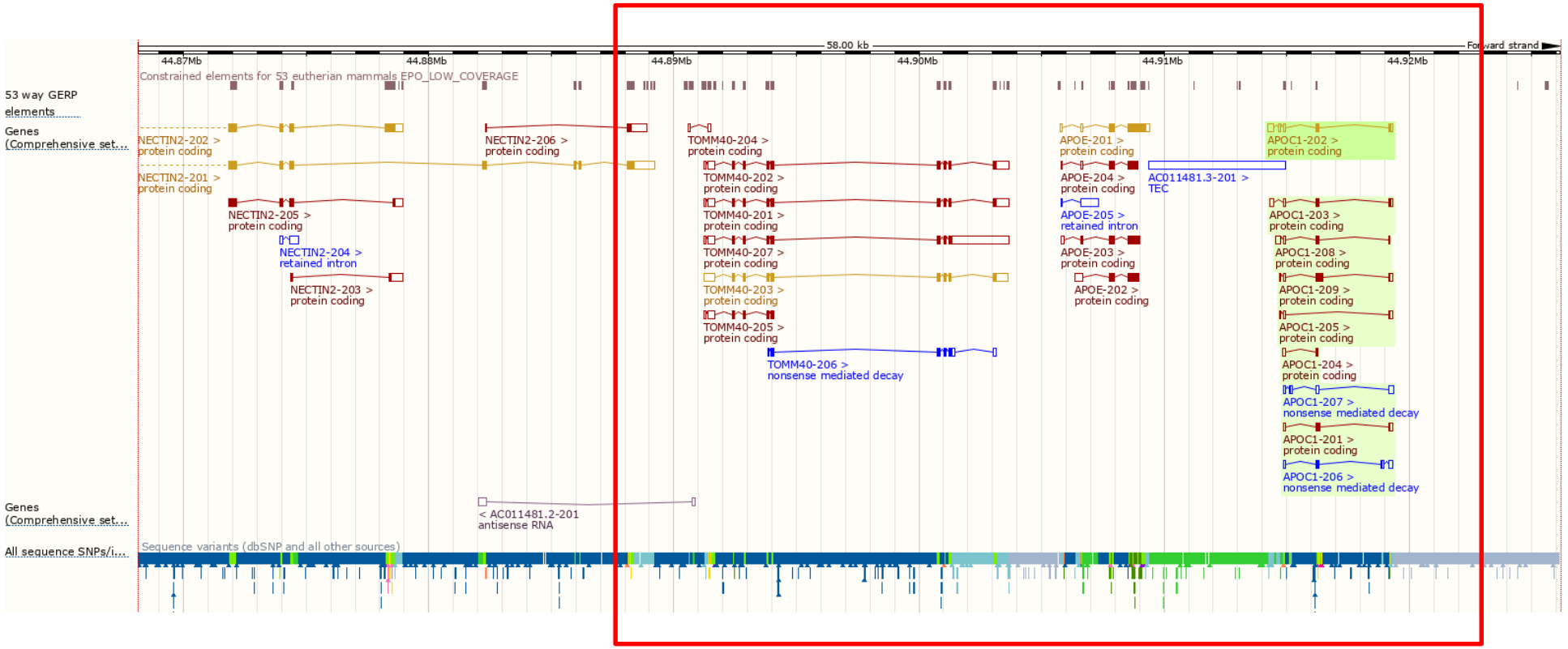
APOE human genomic locus – structure

Human region selected for humanization (34 kb)



Chromosome 19: 44,868,129-44,926,130

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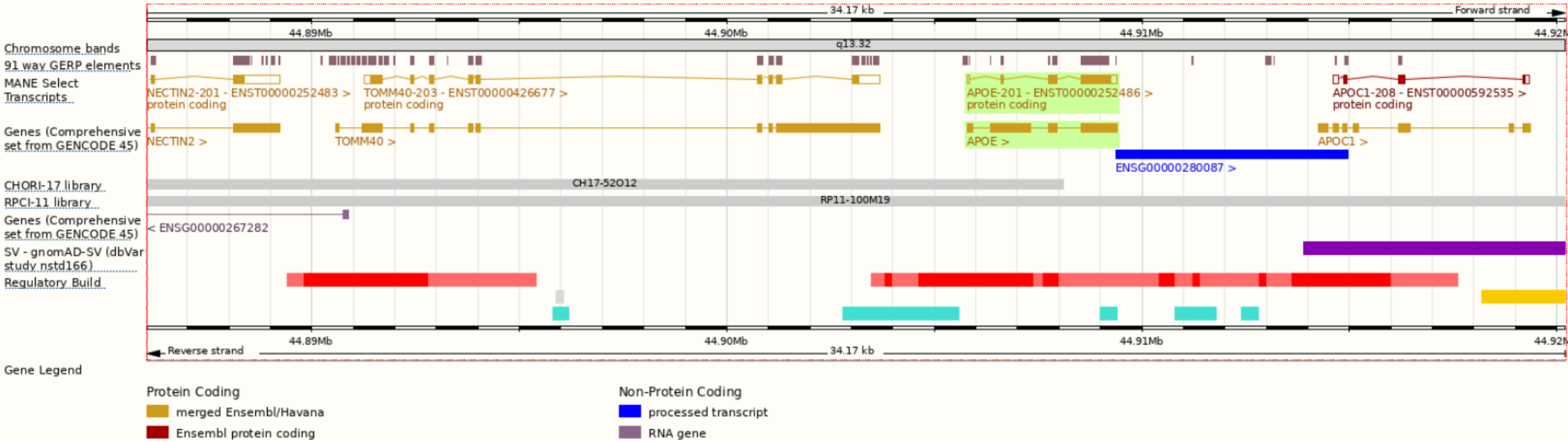
Sequence humanized (19:44886017-44920186; GRCh38.p14)

19:44886017-44920186



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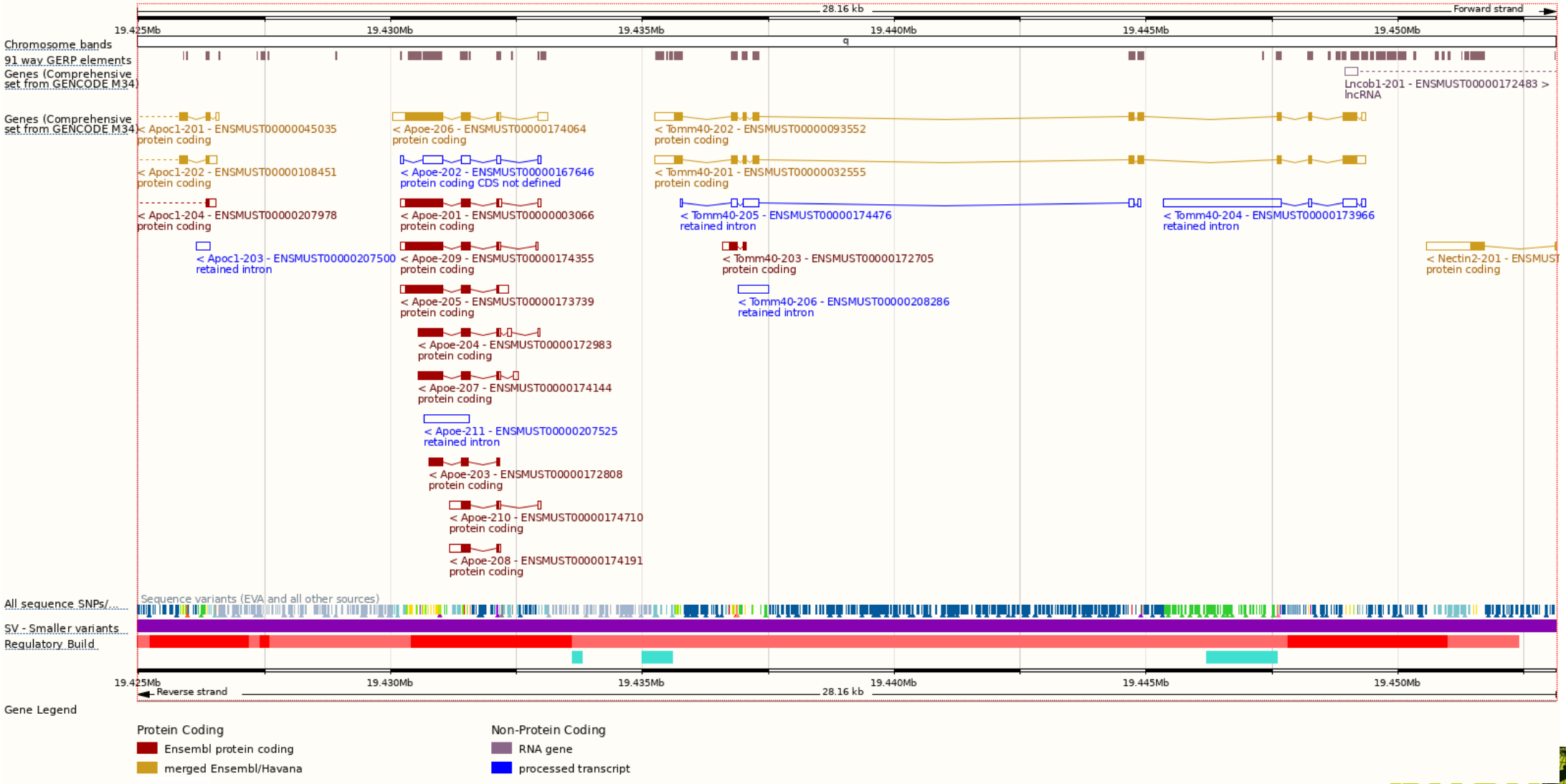
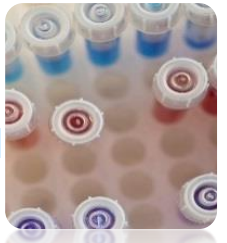
Murine sequence deleted and replaced by the human sequence

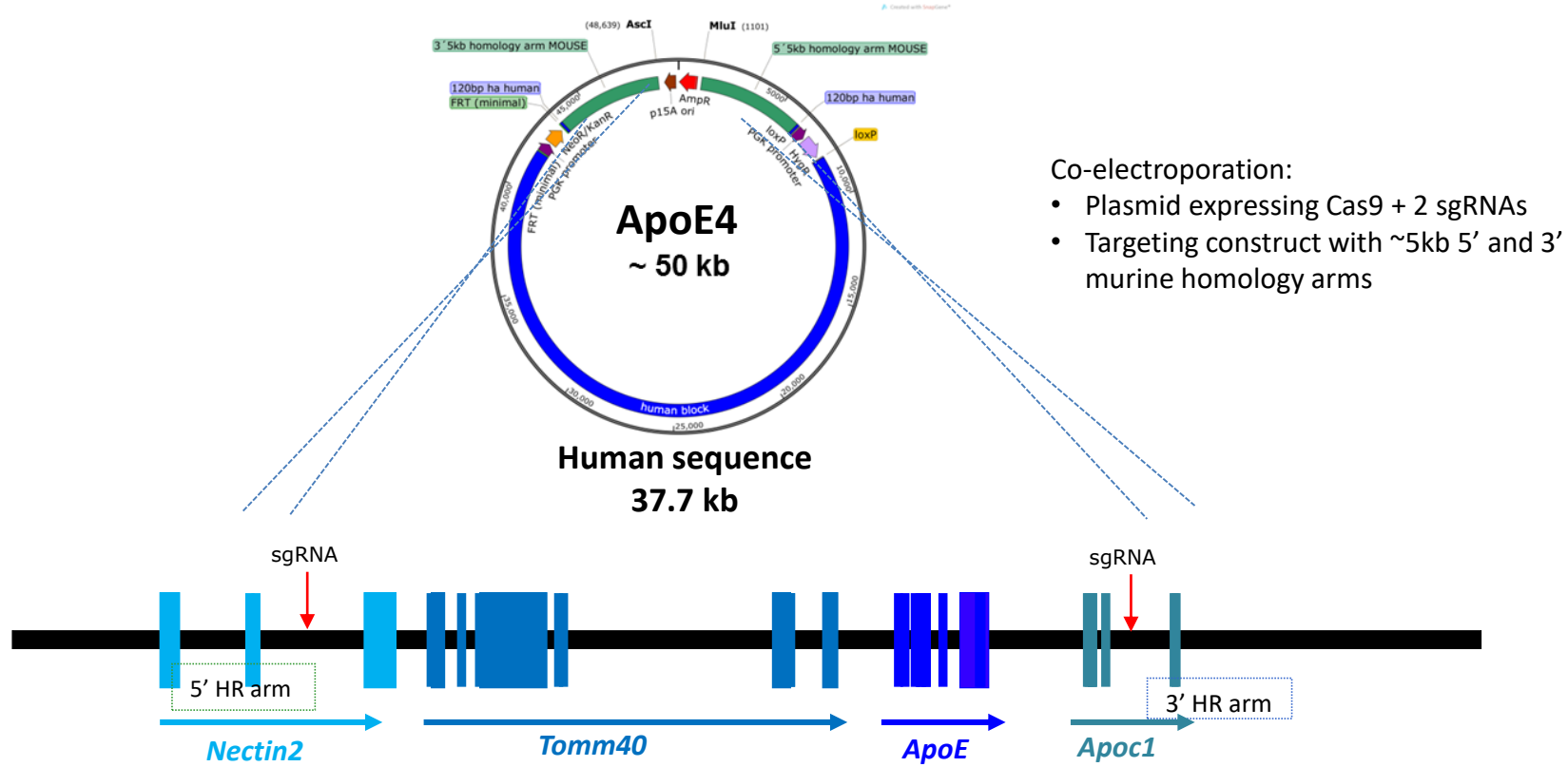
7:19424966-19453126 (GRCm39)



Approach selected; Humanization of a mouse locus with the help of CRISPR/Cas9



Aim: to generate APOE4 variant: Rs429358 => TGC>CGC; C130R; missense variant



Co-electroporation:

- Plasmid expressing Cas9 + 2 sgRNAs
- Targeting construct with ~5kb 5' and 3' murine homology arms

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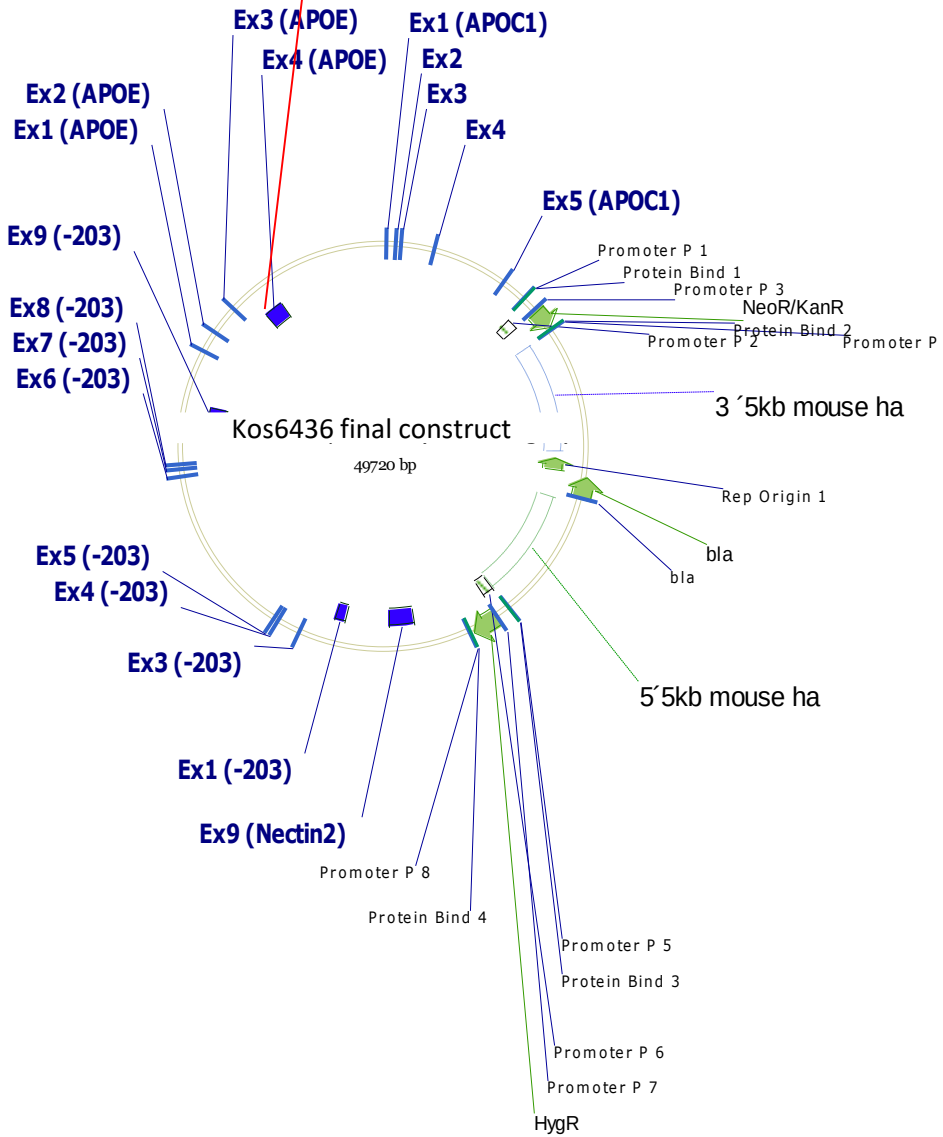
HOMOLOGOUS RECOMBINATION

Rs429358 => TGC>CGC; C130R; missense variant

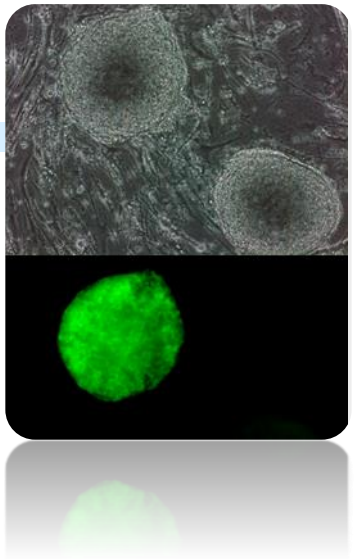
VECTOR MAP

Vector build by:



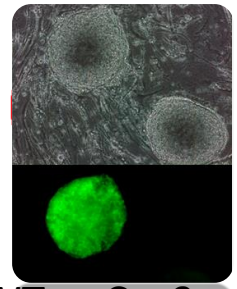
4 ES cell transfection &

Screening of recombinant clones



- Electroporation and screening process
- Long range PCR screening – strategy
- Long-Range 3’ PCR screening – results
- Recombinant ES validation by Long Range PCR
- Recombinant ES clones validation by Southern Blot – internal probe
- Aneuploidy screening in ES recombinant clones

Electroporation and screening process



The circular targeting vector was co-electroporated with a plasmid directed from pX330 that co-expresses the WT spCas9 and 2 guides RNA (gR83 –aagacgccatactttgatgc and gR92-gaatggccttctagactcgg directed against the mouse 5’ and 3’ extremity of the sequence to replace in the proprietary C57BL/6NCrl S3 cell line.

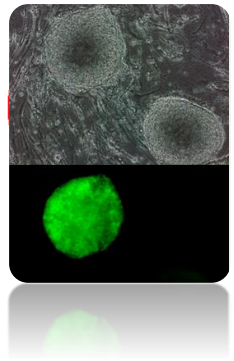
Transfected ES clones were submitted neomycin/hygromycin selection 186 resistant ES clones were isolated.
The clones were then submitted to the screening process allowing secured identification of those harbouring the expected recombination events at both ends of targeting vector (see Erbs et al., 2023*).

Screening process steps:

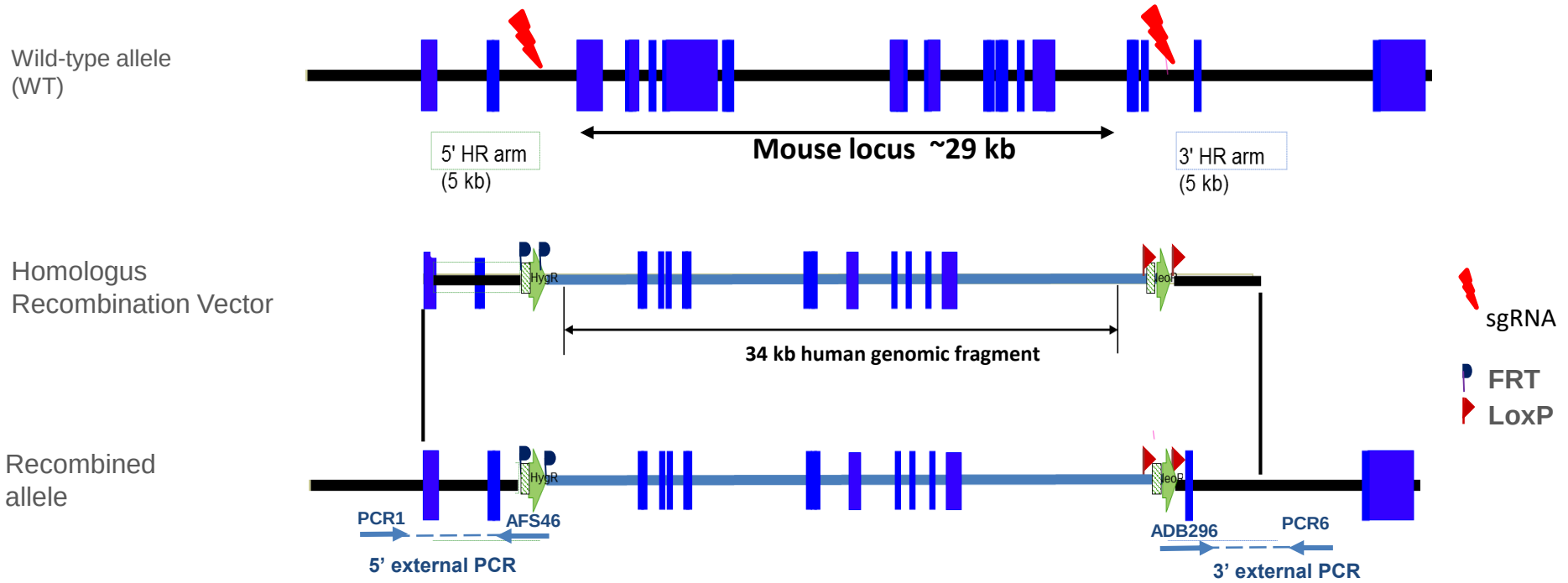
1. Identification of candidate recombinant clones by initial 3’ Long-Range PCR
2. 3’ LR-PCR positive clones are confirmed for 5’ recombination event by Long-Range PCR
3. Positive clones in step 2 are further validated by Southern blot analysis using internal and external probes
4. The karyotype of at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

*__Increased On-Target Rate and Risk of Concatemerization after CRISPR-Enhanced Targeting in ES Cells.__ Erbs V, Lorentz R, Eisenman B, Schaeffer L, Luppi L, Lindner L, Hérault Y, Pavlovic G, Wattenhofer-Donzé M, Birling MC. Genes (Basel). 2023 Feb 3;14(2):401. doi: 10.3390/genes14020401. PMID: 36833328

Long range PCR screening – strategy

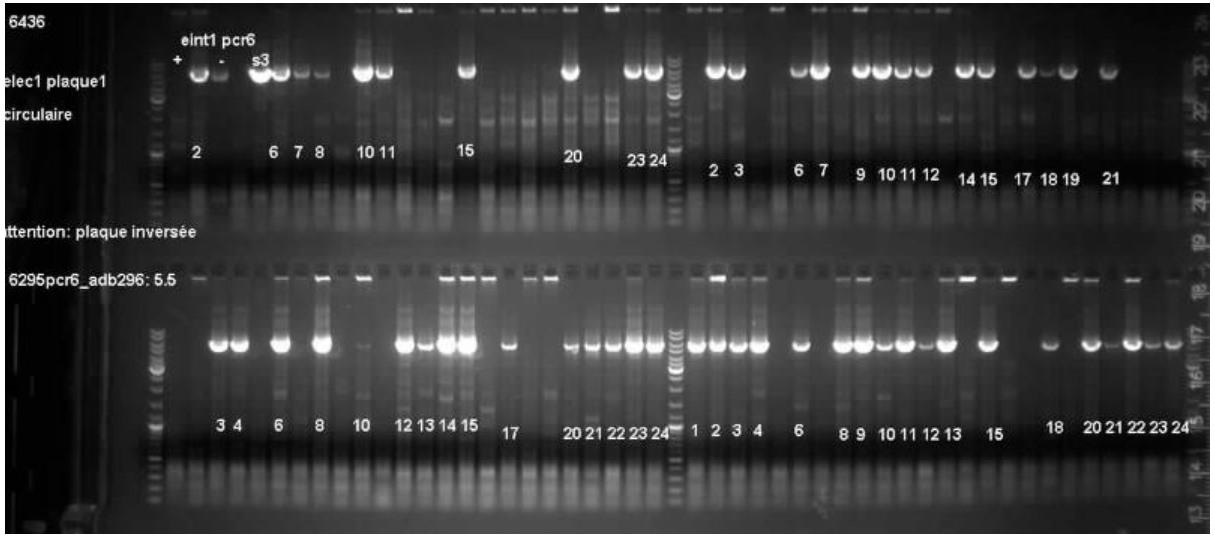


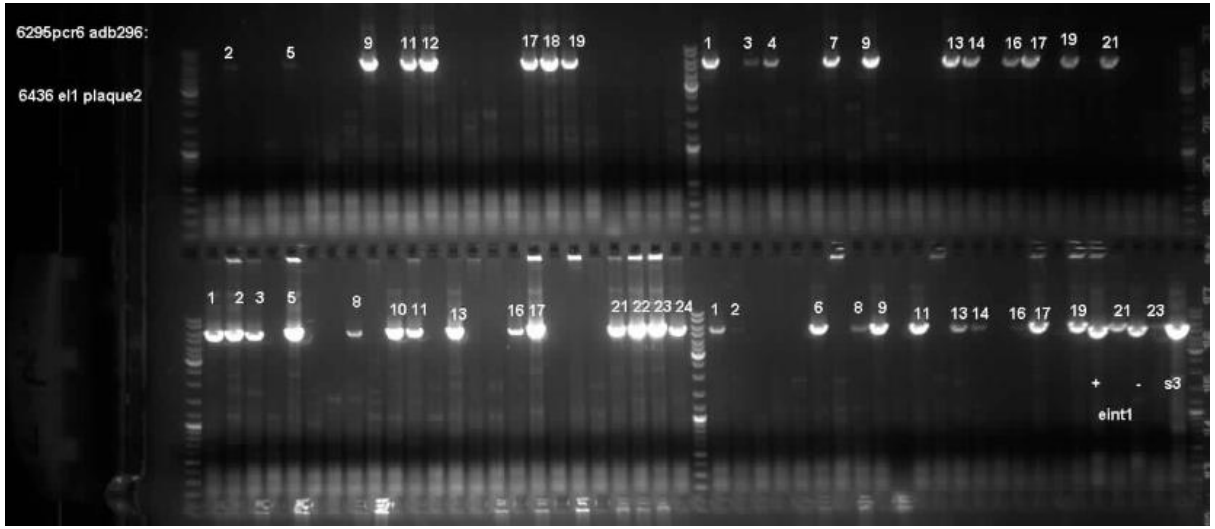
Schematic 5’ and 3’ PCR screening strategy

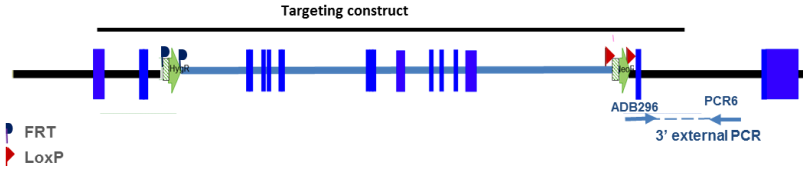


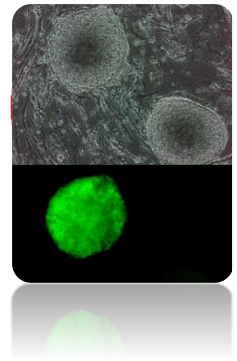
PCR	Primer Name	Primer sequences	PCR product size
5’PCR	AFS46	CTGCATCAGGTCGGAGACGCTGTCG	5,7 kb
	PCR1	CCCTACGATATAGACACTGGACACA	
3’ PCR	ADB296	AGGGGCTCGCGCCAGCCGAACTGTT	5,5 kb
	PCR6	GGCTGTTTGCTATTTGCTGCCTGCA	

Long-Range 3’ PCR screening - results









Eight candidate clones were amplified for Southern blot validation and confirmed by LR-PCR .

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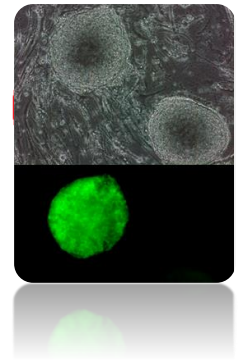
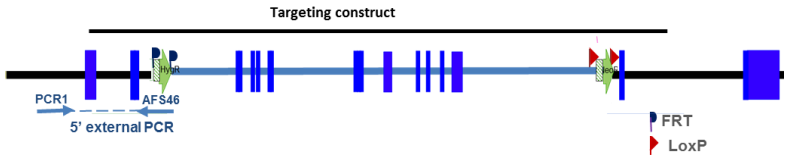
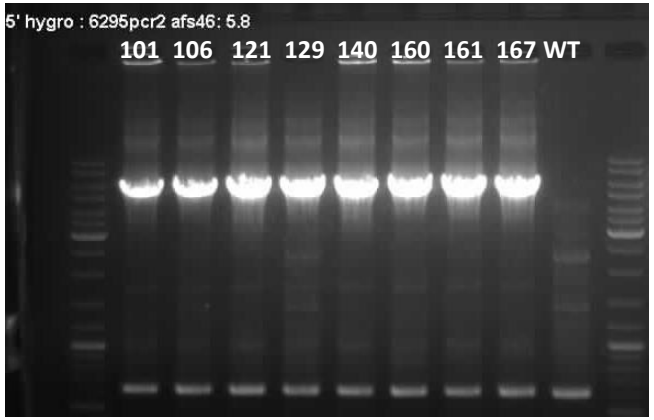
Recombinant ES validation by Long Range PCR

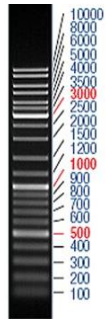


Validation of candidate recombinant ES clones by 5’ LR-PCR



Kos6295 – external 5’ PCR-hygro – 5,8 kb





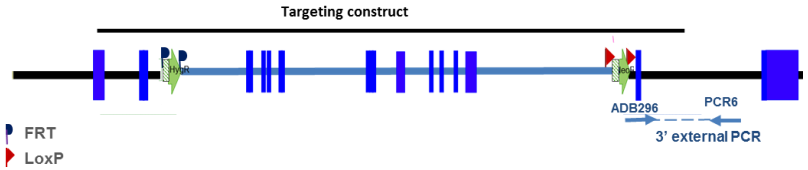
Ladder pattern

Backbone PCR

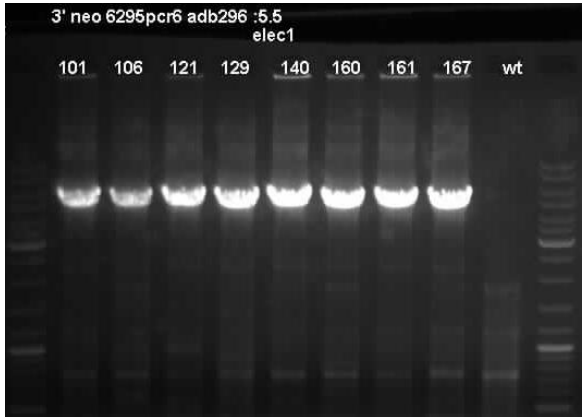
All negative

Confirmation of candidate by 3’ LR-PCR

Kos6295 – external 3’ PCR-Neo – 5,5 kb



Kos6295 – external 3’ PCR-Neo – 5,5 kb



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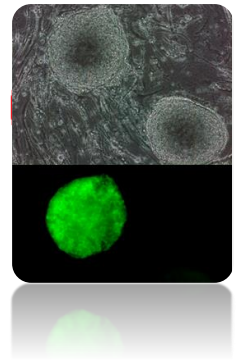
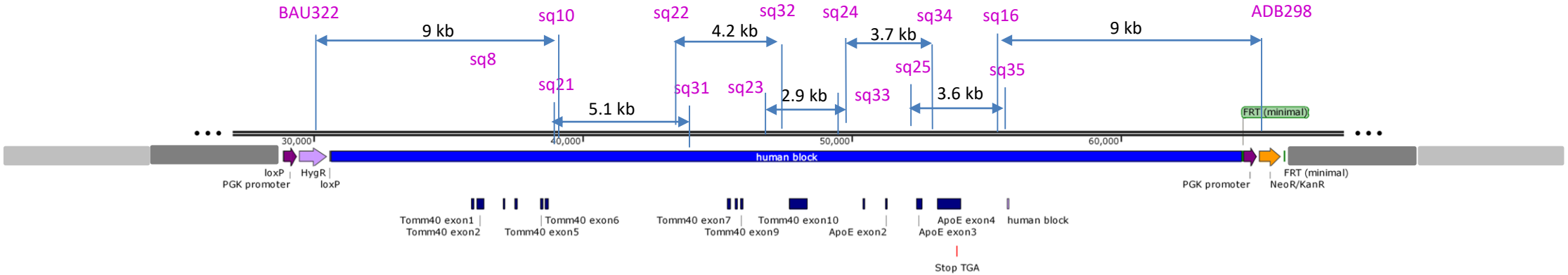
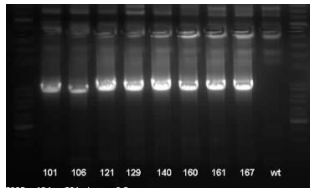
Recombinant ES validation by Long Range PCR



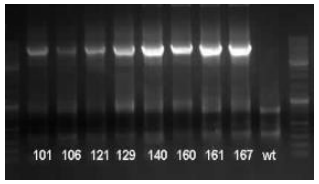
Validation of candidate recombinant ES clones by human specific PCR



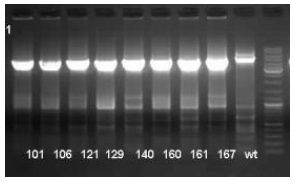
BAU322-sq10
Exp 9 kb



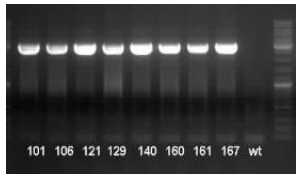
Sq21-sq31
Exp 5.1 kb



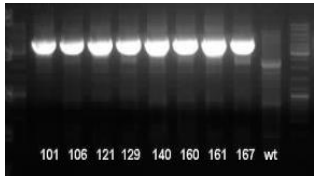
Sq22-sq32
Exp 4.2 kb



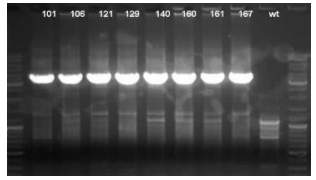
Sq23-sq33
Exp 2.9 kb



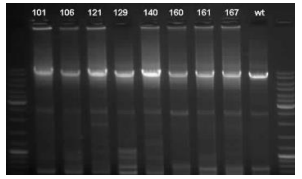
Sq24-sq34
Exp 3.7 kb

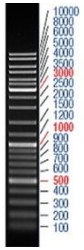


Sq25-sq35
Exp 3.6 kb



Sq16-ADB298
Exp 9 kb



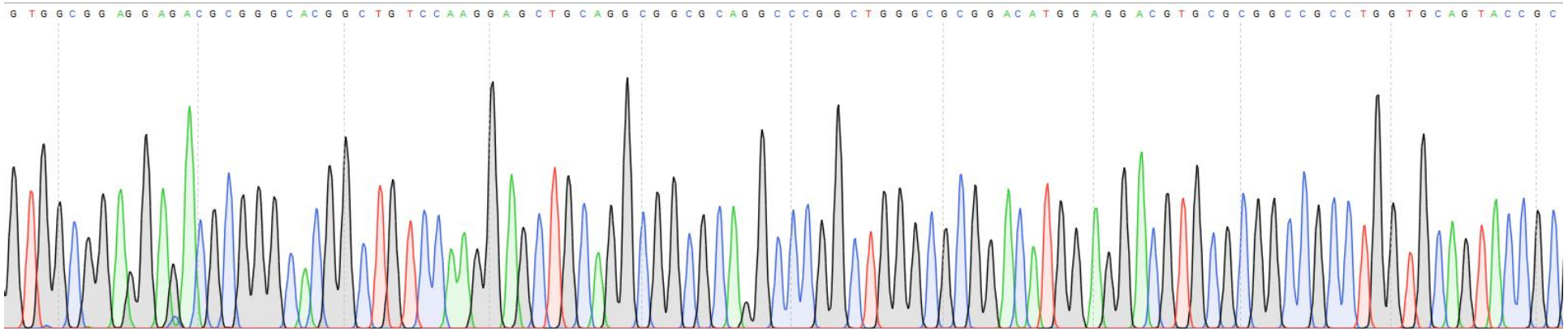


Ladder pattern

	101	106	121	129	140	160	161	167	WT ESC
PCR1-AFS46									
BAU322-sq10									
BAU322-sq5									
Sq21-sq31									
Sq22-sq32									
Sq23-sq33									
Sq24-sq34									
Sq25-sq35									
Sq16-ADB298									
ADB296-PCR6									

Ladder pattern

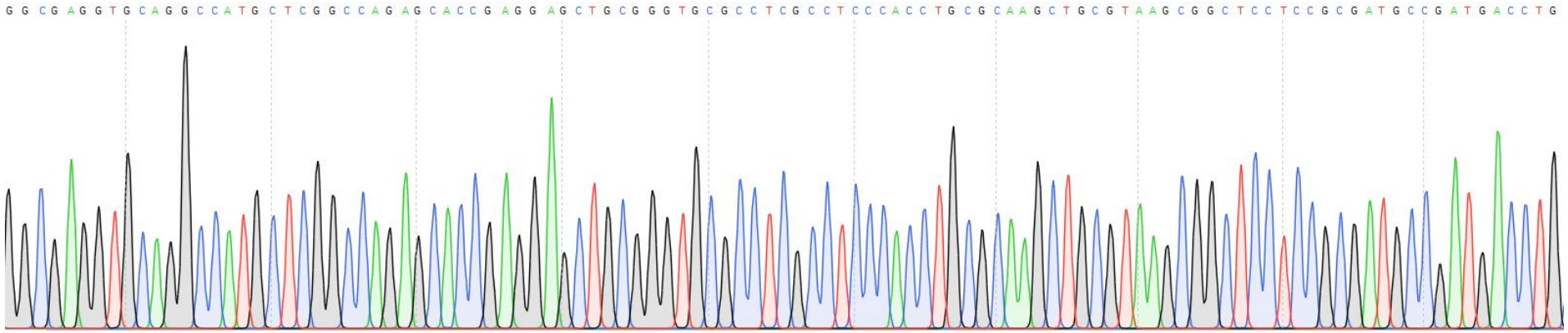
Confirmation of the presence of rs429358 variant by Sanger sequencing



GTGGCGGAGGAGACGCGGGCACGGCTGTCCAAGGAGCTGCAGGCGGCGCAGGCCCGGCTGGGCGCGGACATGGAGGACGTGCGCGGCCGCCTGGTGCAGTACCGC

V A E E T R A R L **S** K E L Q A A Q A R L G A D M E D V R G R L V Q Y R

S112 **R130**

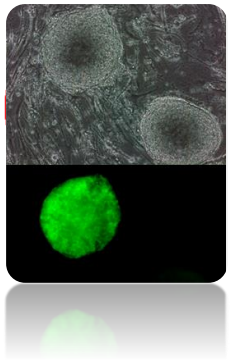


GGCGAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCCACCTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTG

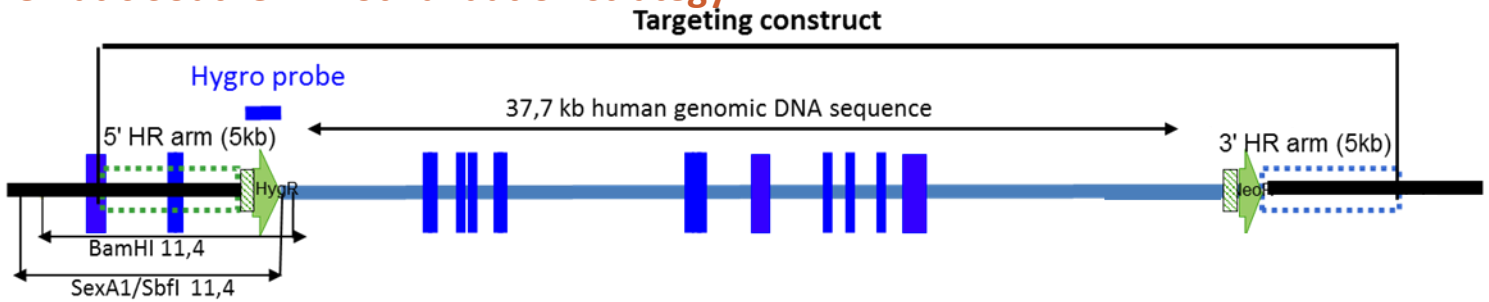
G E V Q A M L G Q S T E E L R V R L A S **H** L R K L R K R L L R D A D D L

H158

Recombinant ES clones validation by Southern Blot –Hygro internal probe



Schematic Southern Blot validation strategy



Internal probe : validation of the correct insertion of a single copy at the Apoe locus

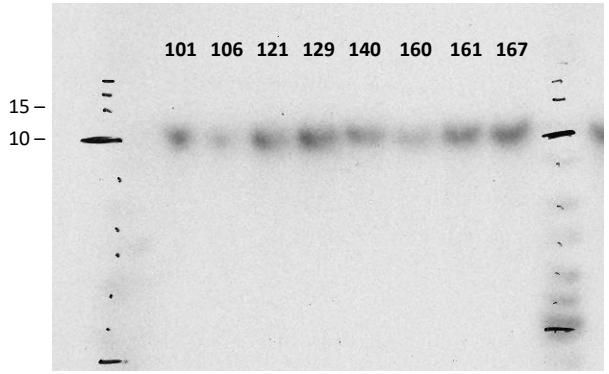
Digestions used to validate the 5'insertion

Probe	Name	Genomic DNA digest	WT allele (kb)	Targeted Allele (kb)
Hygro	5' first digest	BamH1	/	11,4
	5' second digest	SbfI/SexAI	/	11,4

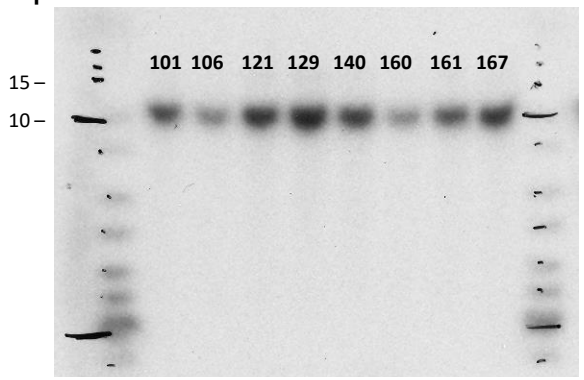
5' internal Hygro probe sequence

cctattgcatctcccgccgtgcacagggtgtcacgttgcaagacctgcctgaa
accgaactgcccgctgttctgcagccggtcgcggaggccatggatgcgatc
gctgcggccgatcttagccagacgagcgggttcggcccattcggaccgcaa
ggaatcggtcaatacactacatggcgtgatttcatatgcgcgattgctgatccc
catgtgtatcactggcaaactgtgatggacgacaccgtcagtgcgtccgtcgc
gcaggctctcgatgagctgatgctttgggccgaggactgccccgaagtccgg
cacctcgtgcacgcggatttcggctccaacaatgtcctgacggacaatggcc
gcataacagcggtcattgactggagcgaggcgatgttcggggattcccaata
cgaggtcgccaacatcttcttctggaggccgtggttggcttgtatggagcagca
gacgcgctacttcgagcggaggcatccggagcttgcaggatcgccgcggct
ccgggcgtatatgctccgcattggtc

Hygro probe



BamHI : 11.4



SexAI/SbfI : 11.4

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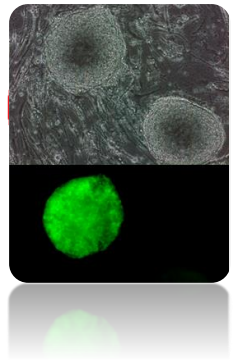
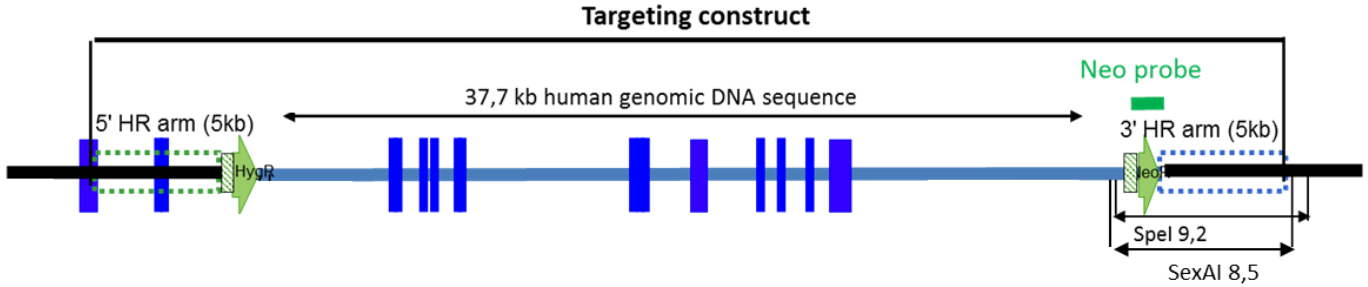
Recombinant ES clones validation by Southern Blot –Neo internal probe



Schematic Southern Blot validation strategy



Internal probe : validation of the correct insertion of a single copy at the ApoE locus

Digestions used to validate the 3'insertion

Probe	Name	Genomic DNA digest	WT allele (kb)	Targeted Allele (kb)
Neo	5' first digest	SpeI	/	9.2
	5' second digest	SexAI	/	8.5

3' internal Neo probe sequence

ctgcaggacgaggcagcgcggctatcgtggctggccacgacgggcgttcct
tgcgcagctgtgctcgacgttgtcactgaagcgggaagggactggctgctatt
gggcgaagtgccggggcaggatctcctgtcatctcaccttgctcctgccgag
aaagtatccatcatggctgatgcaatgcggcggctgcatacgcttgatccggc
tacctgcccattcgaccaccaagcgaaacatcgcatcgagcgagcacgtac
tcggatggaagccggtcttgtcgatcaggatgatctggacgaagagcatcag
gggctcgcgccagccgaactgttcgccaggctcaaggcgcgcatgcccga
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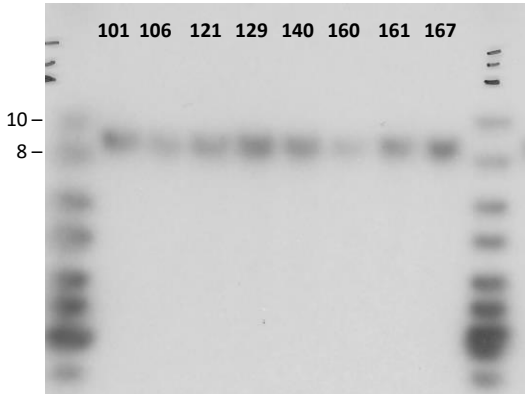
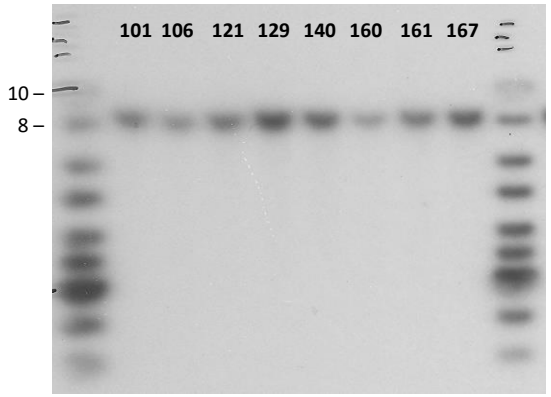
Neo probe



SpeI 9.2



SexAI 8.5

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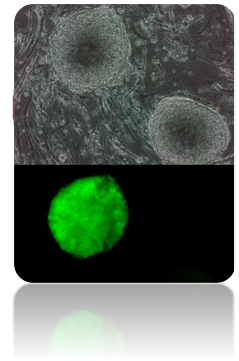
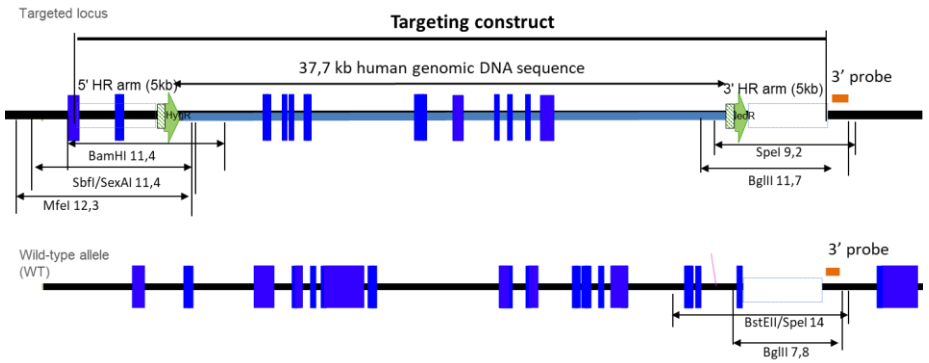
Recombinant ES clones validation by Southern Blot –External probe

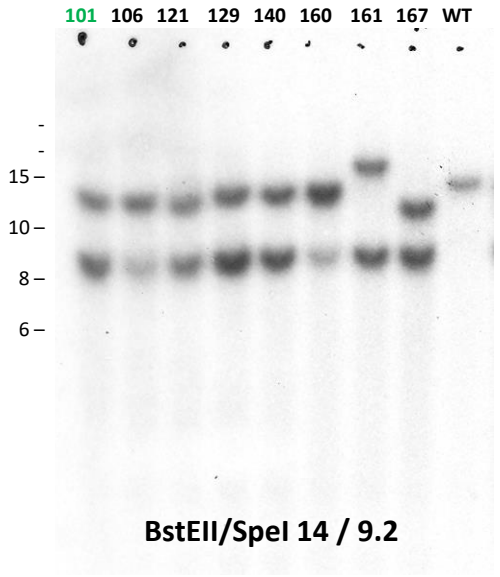


Schematic Southern Blot validation strategy

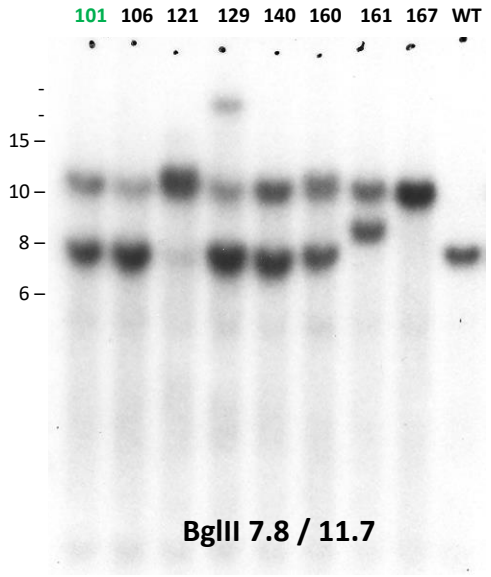


Digestions used to validate the 3' insertion

Probe	Name	Genomic DNA digest	WT allele (kb)	Targeted Allele (kb)
3'external probe	3' first digest	BstEII/SpeI	14	9.2
	3' second digest	BglII	7,8	11,7



BstEII/SpeI 14 / 9.2



BglII 7.8 / 11.7

3' external probe sequence

cctgagcgttatagtatggctgcacctcttctgatgctctgtcctgtctcaggccagcctacaagccaggtaatggtaagaca
gcaagtcacattttagtgtgagctaatcagcccgcagagactcagcaaccagcaacctgcacatagcctcaatgctgaaa
agagatggtgattggctataaacttcactccctcctgagtttctggggagtagggtcttcctaagtcacccaagcttaaactca
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aaccacagaacataacatttaccatttcagccagtttcgggtgtctaggtcagcagtgttgagacatttacatggttgtgcaac
agaacccaaaatctattcc

Note: As CRISPR/Cas9 was used to help to humanize the ES cells, the untargeted allele (previously wild type) could also be edited. This explains the differences in the sizes of the untargeted allele.

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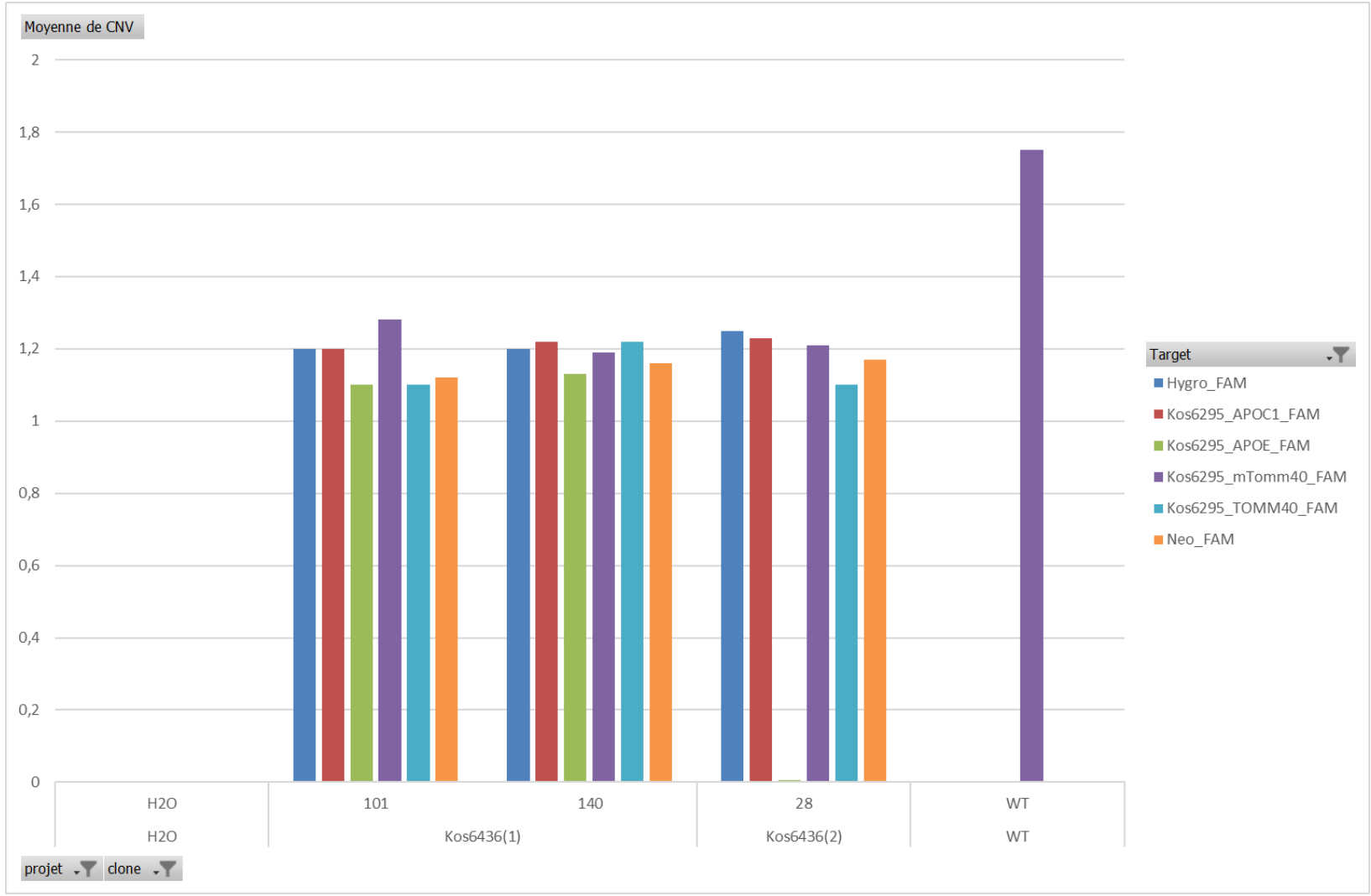
Recombinant ES clones validation by ddPCR



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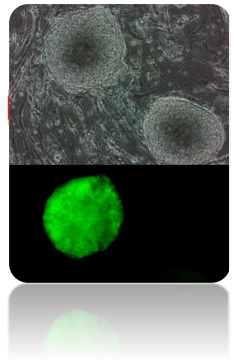
Aneuploidy screening in ES recombinant clones

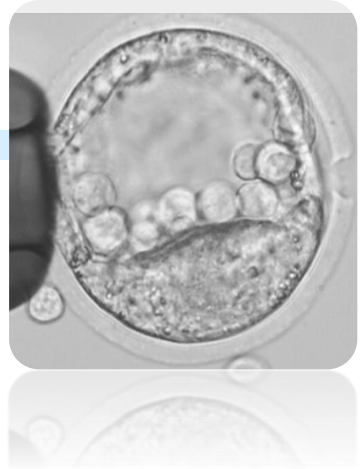


Selected recombinant ES cells clones were karyotyped by ddPCR as described in Codner *et al.* [1] and by Giemsa metaphase staining. Results of aneuploidy analysis are presented in the table below.

Clone ID	ddPCR	Giemsa
101	Pass	Pass
106	Pass	Not Done
121	Pass	Not Done
129	Pass	Not Done
140	Pass	Pass
160	Pass	Failed

[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., Hérault, 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.
- Recombinant ES clones #101 validated in previous project phase was 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			
	5%-40%	45% -55%	60% - 100%	Total
#101	1	0	17	18

Breeding to F1 generation

- Eight highly chimeric males derived from clone #101 generated in the previous phase by blastocyst injection of the ES clones were mated with Flp deleter females showing maternal contribution* to investigate whether the recombined ES cells have contributed to the germ layer.

- Black F1 pups were genotyped and F1 pups scored positive for the presence of the humanized knock-In (KI) allele by PCR and droplet digital PCR.

- Germ line transmission was obtained the week 49/2017

- F1 males were further bred with Cre deleter females showing maternal contribution* to obtain the final allele

***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.

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