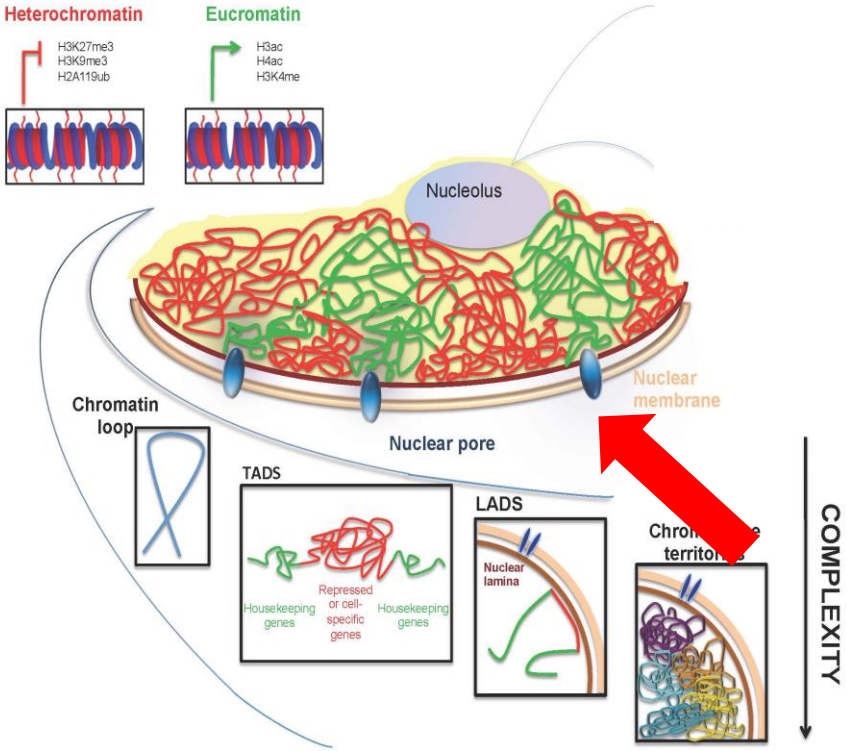
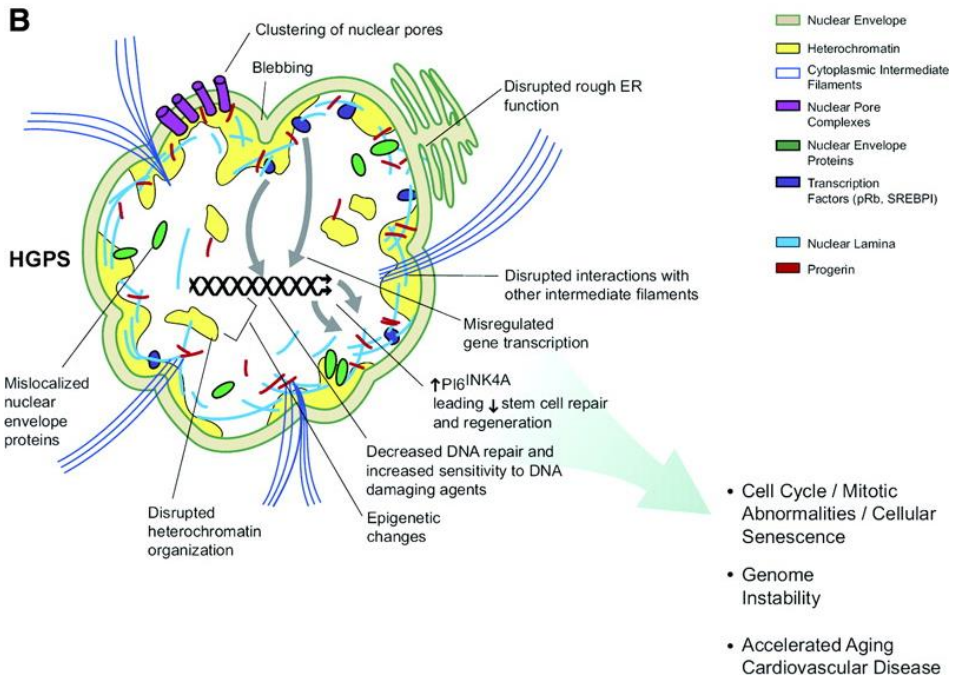
SINGLE NUCLEOTIDE VARIATIONS ASSOCIATED WITH PROTEIN IMPORTANT IN CHROMATIN ORGANIZATION, LAMININ, INDUCES LAMINOPATHIES





Lamins: Nuclear Intermediate Filament Proteins with Fundamental Functions in Nuclear Mechanics and Genome Regulation

Yosef Gruenbaum[1] and Roland Foisner[2]

Annu. Rev. Biochem. 2015. 84:131–64

- **Lamins** are intermediate filament proteins that **form a scaffold, termed nuclear lamina, at the nuclear periphery**. A small fraction of lamins also localize throughout the nucleoplasm.

- **Lamins bind to a growing number of nuclear protein complexes**

- **Lamins** are implicated in both **nuclear and cytoskeletal organization, mechanical stability, chromatin organization, gene regulation, genome stability, differentiation, and tissue-specific functions**.

- Mutation in lamins are involved in human **laminopathies**, ranging from muscular dystrophy to accelerated aging, as observed in Hutchinson–Gilford progeria and atypical Werner syndromes.

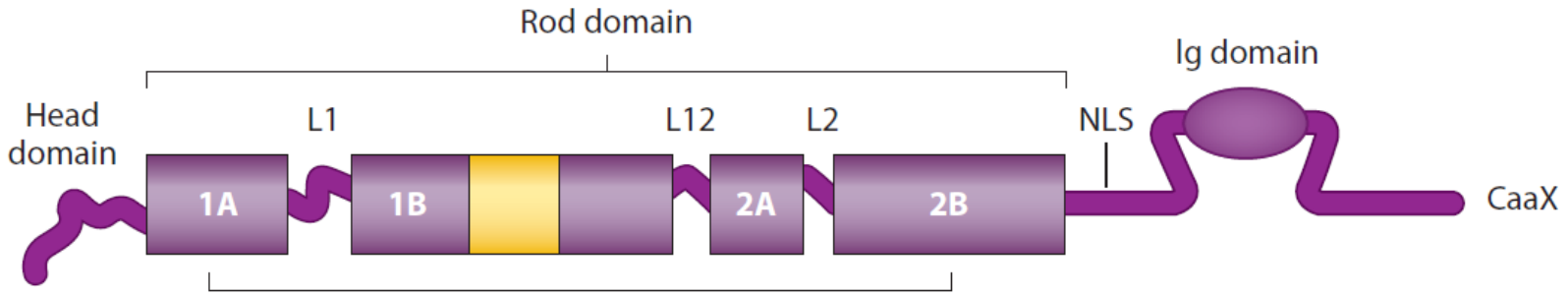
The domain organization of a lamin monomer

the **N-terminal (head)** domain;

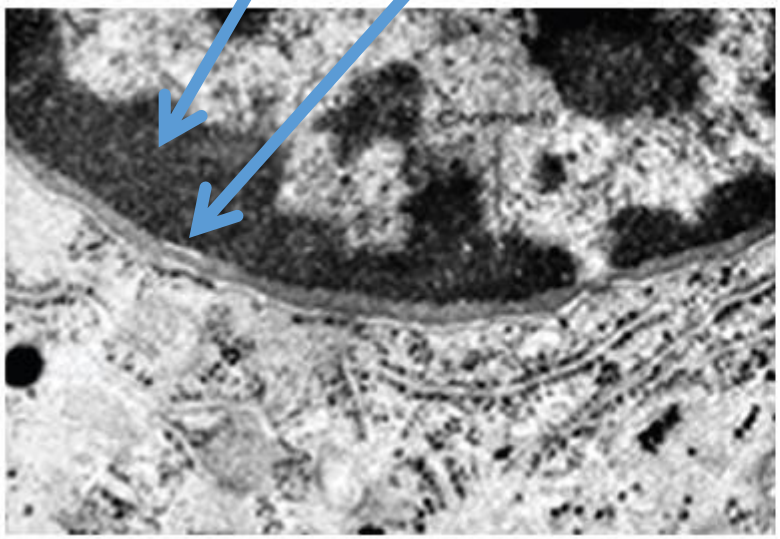
the **central rod domain**, which is composed of four α-helices (1A, 1B, 2A, 2B); three linker regions (L1, L12, L2);

C-terminal (tail) domain, which includes the nuclear localization signal (NLS), immunoglobulin (Ig) domain, and a CaaX motif (C, cysteine; a, aliphatic amino acid; X, any amino acid).

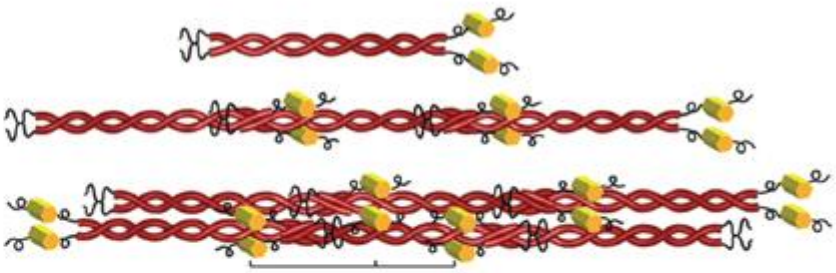
Six heptads present in lamins and absent in mammalian cytoplasmic intermediate filaments.



Peripheral heterochromatin (*black layer) that is underneath a thick nuclear lamina (gray layer).*

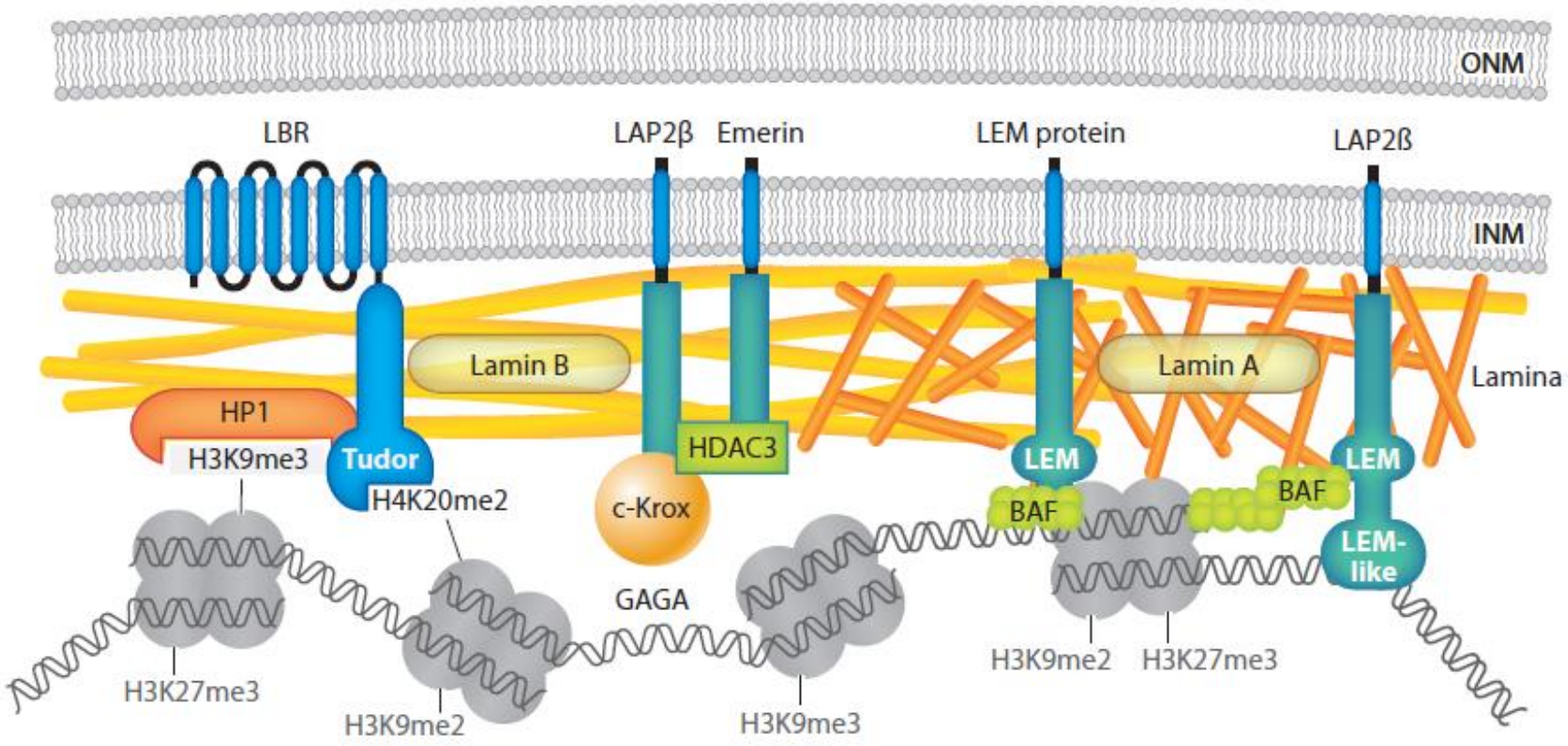


A transmission electron micrograph of nuclei from old rat liver



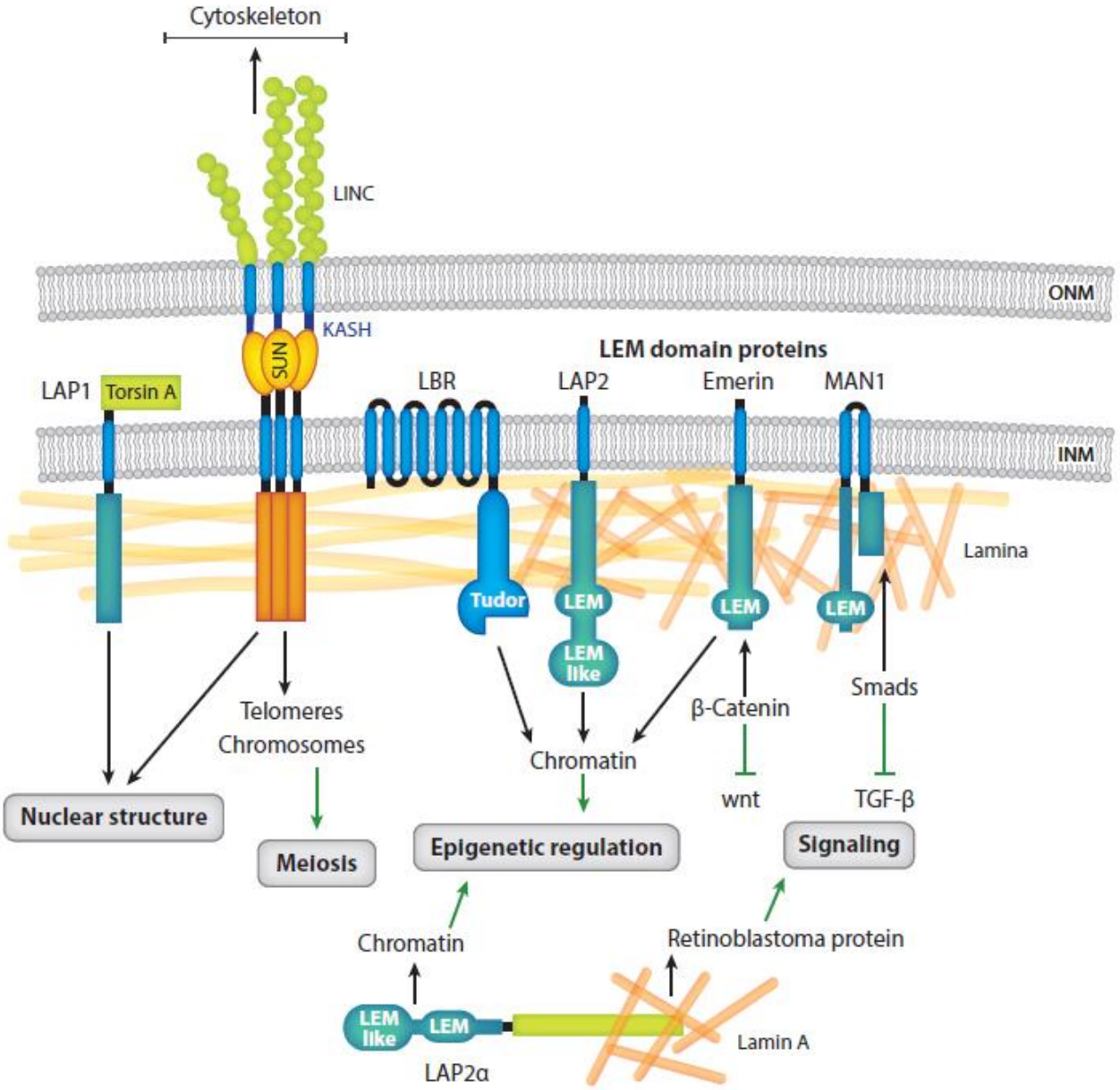
Lamin polypeptides assemble first into parallel dimers, and the dimers associate longitudinally to form polar head-to-tail polymer structures. Two head-to-tail polymers interact laterally in an antiparallel fashion to form protofilaments.

Lamina-associated domains (LADs) in the genome **are enriched in transcriptionally inactive genes and heterochromatic histone marks**

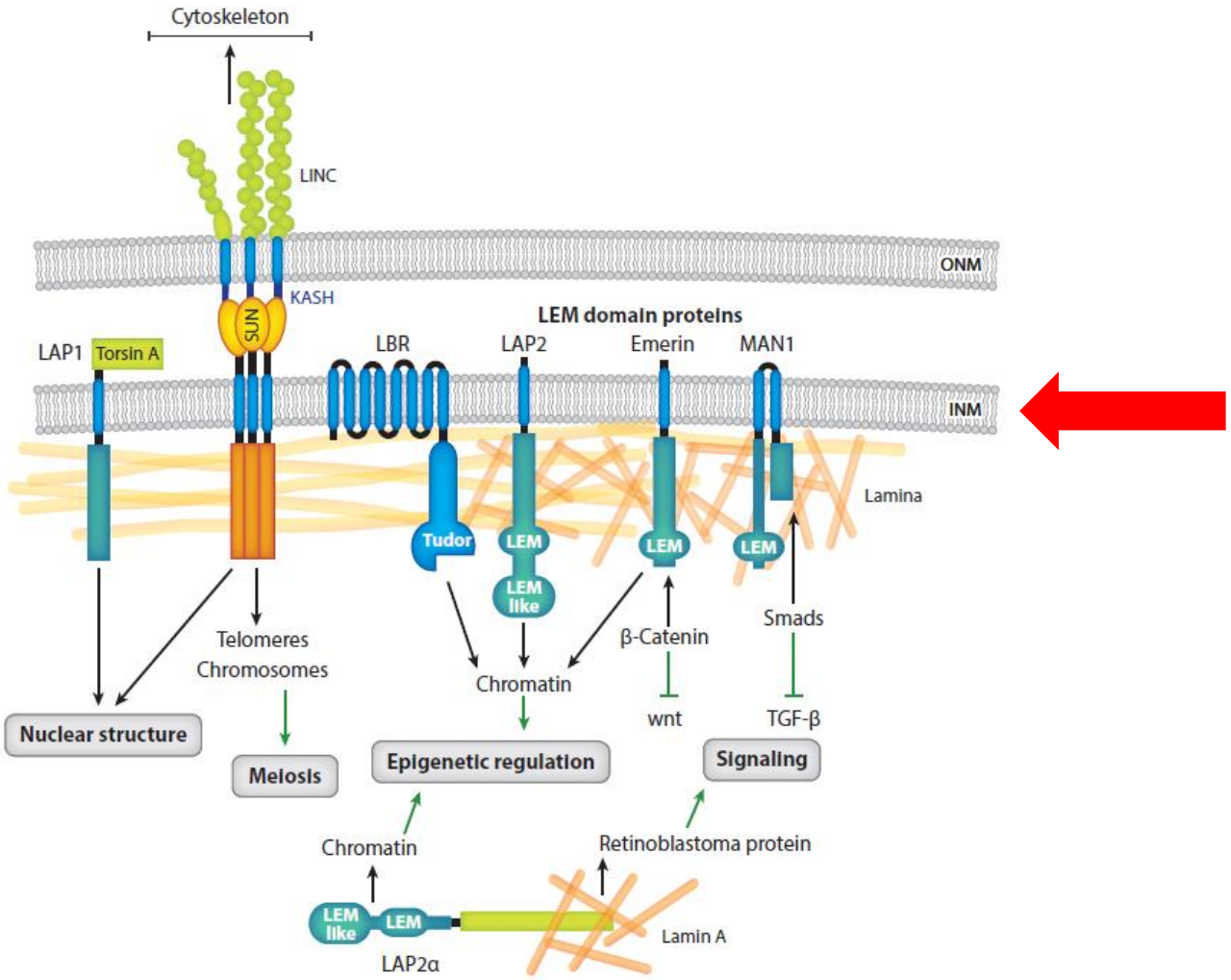


Silence epigenetic marks **Lamina-associated domain**

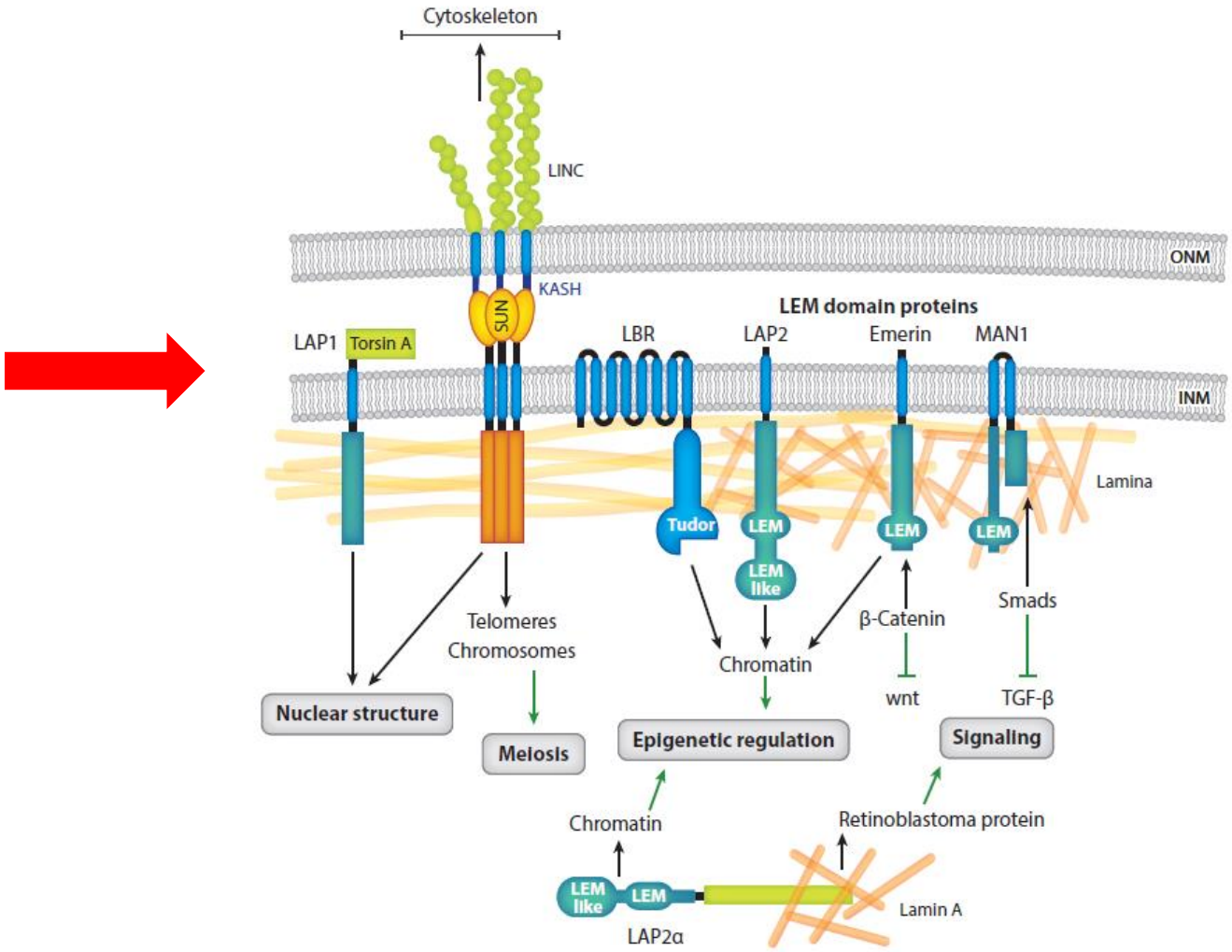
Characterized lamin-binding proteins and their functions.



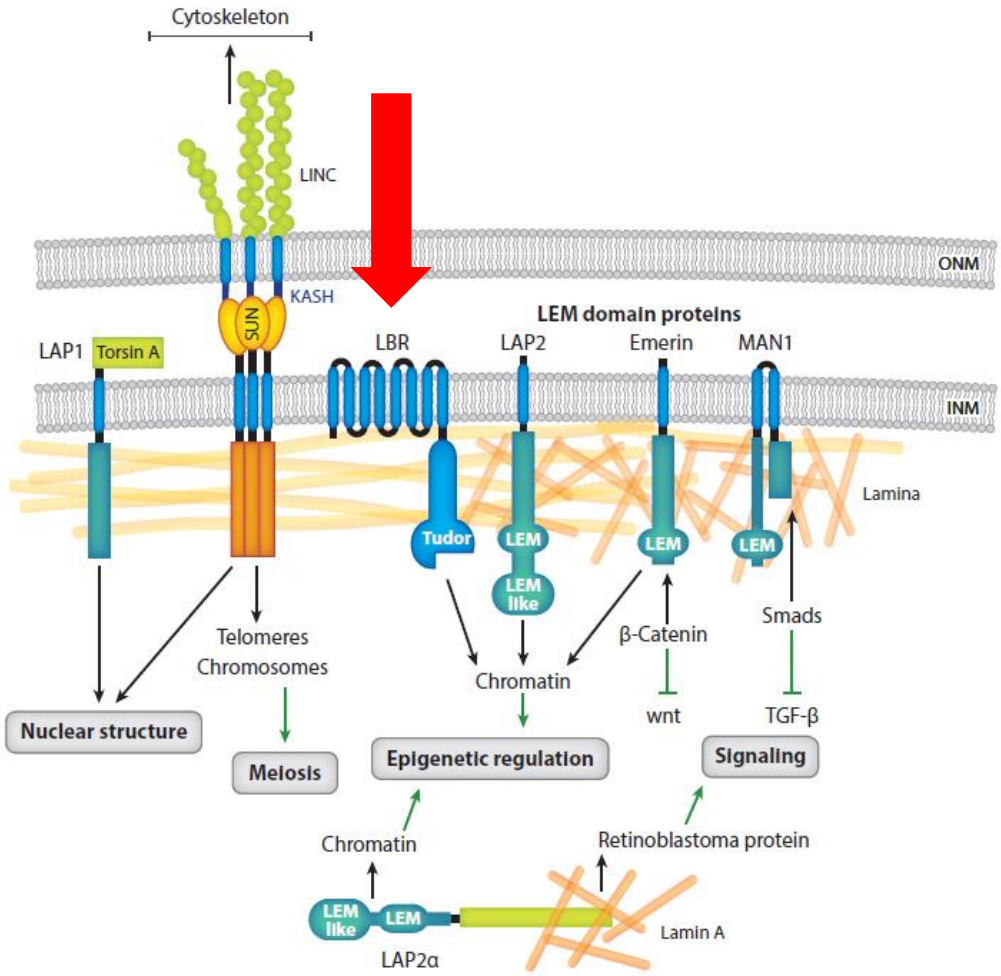
Complexes of tissue-specific nuclear envelope transmembrane proteins (NETs) with abundantly expressed lamins **may define the tissue-specific functions of lamin,** giving rise to tissue-specific phenotypes seen in lamin-linked diseases



Lamina-associated polypeptide 1 (LAP1), which also binds AAA+ ATPase torsin A in the perinuclear lumen and the LEM protein emerin in the INM. **LAP1 regulates torsin A ATPase activity** , and this interaction seems to be particularly important in neuronal cells because a torsin A mutant that exhibits stronger binding to LAP1 causes DYT1 dystonia, a disease of the central nervous system.



LBR is an INM protein with eight transmembrane domains and has sterol reductase activity. Mutations in this gene cause a Pelger-Huet anomaly, most likely linked to nuclear defects, and Greenberg skeletal dysplasia, linked to a deficiency in sterol reductase activity. Recent studies have revealed an essential **role of LBR in tethering chromatin to the lamina and in epigenetic gene silencing.**

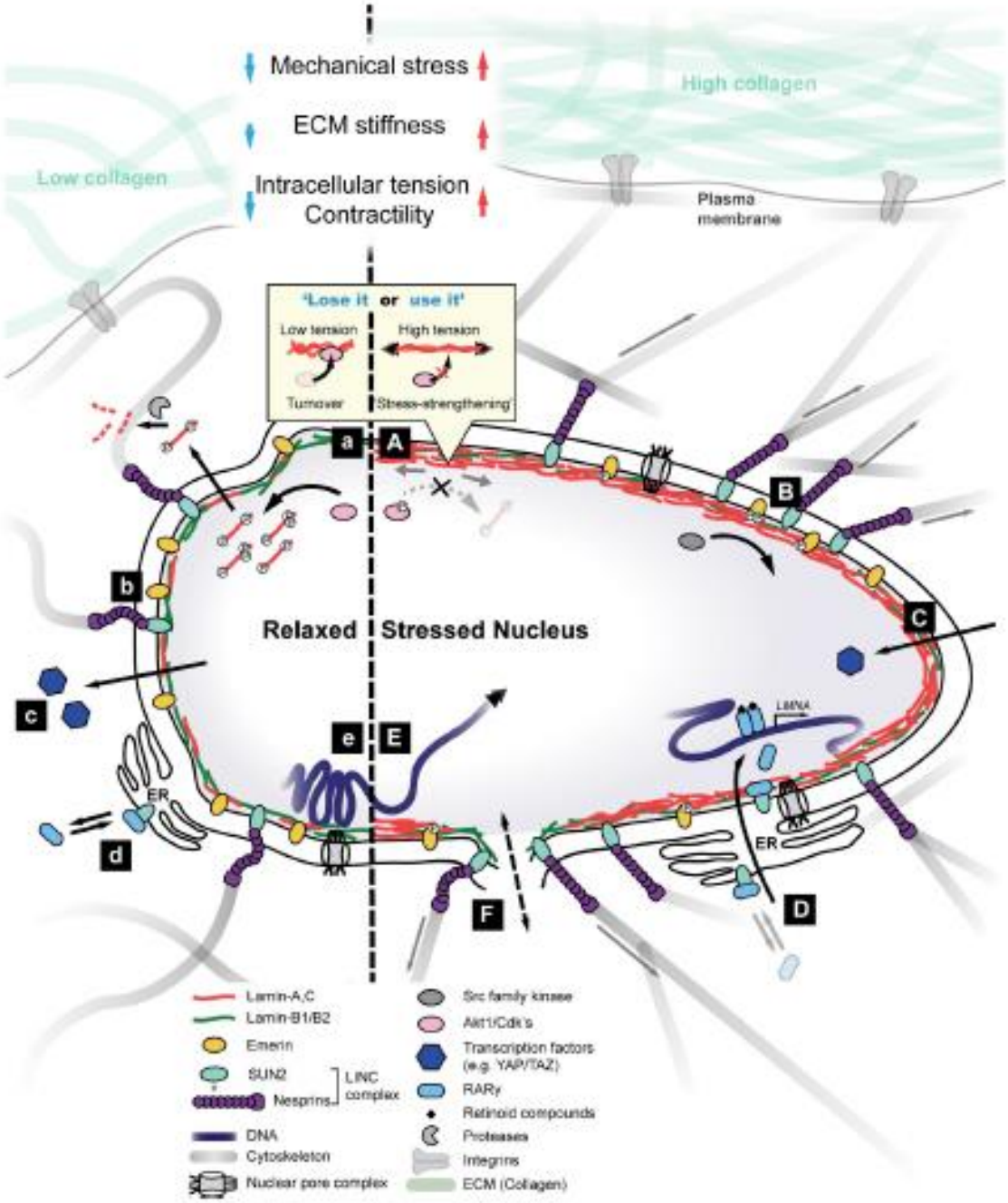


Mechanosensing by the nucleus: From pathways to scaling relationships

Sangkyun Cho, Jerome Irianto, and Dennis E. Discher

Nucleocytoskeletal coupling of the lamina with the cytoskeleton via proteins **allows force transmission** from the extracellular matrix (ECM) through cell adhesion complexes and the cytoskeleton into the nucleus and contributes to **mechanosignal transduction**

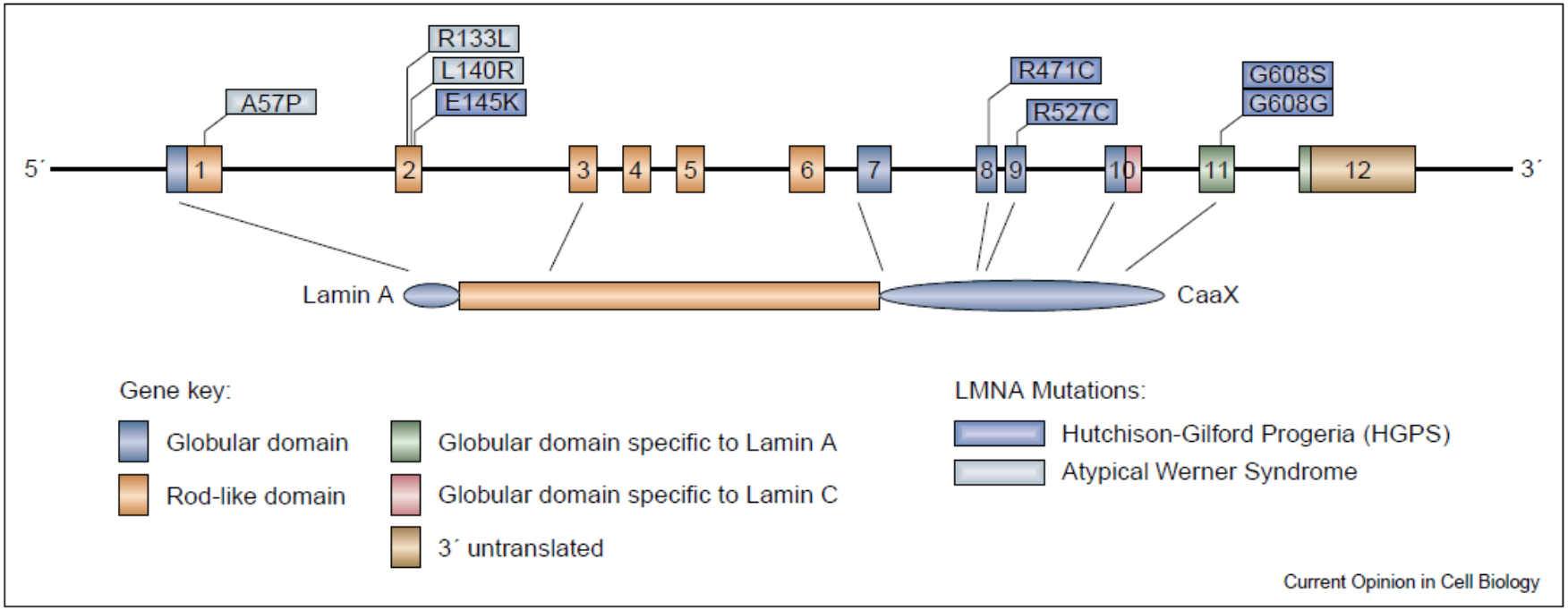
J. Cell Biol. Vol. 216 No. 2 305–315
https://doi.org/10.1083/jcb.201610042


Mechanical stress
ECM stiffness
Intracellular tension
Contractility
Low collagen
High collagen
Plasma membrane
'Lose it or use it'
Low tension
High tension
Turnover
Stress-strengthening
Relaxed
Stressed Nucleus
a
A
B
b
C
c
e
E
ER
d
F
D
LMNA
Lamin-A,C
Lamin-B1/B2
Emerin
SUN2
Nesprins
LINC complex
DNA
Cytoskeleton
Nuclear pore complex
Src family kinase
Akt1/Cdk's
Transcription factors (e.g. YAP/TAZ)
RARγ
Retinoid compounds
Proteases
Integrins
ECM (Collagen)

Aging and nuclear organization: lamins and progeria

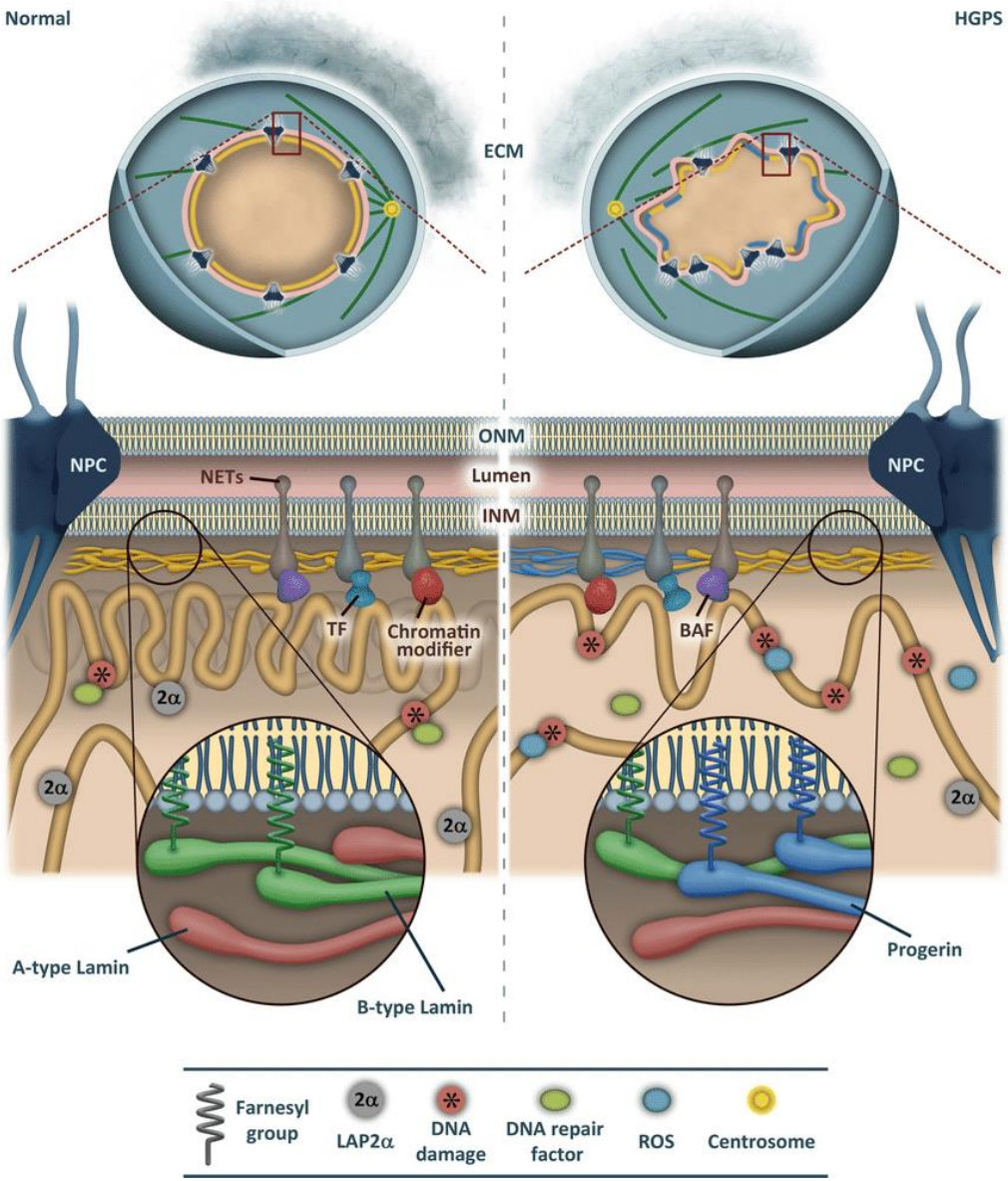
Leslie C Mounkes and Colin L Stewart[1]

Figure 1



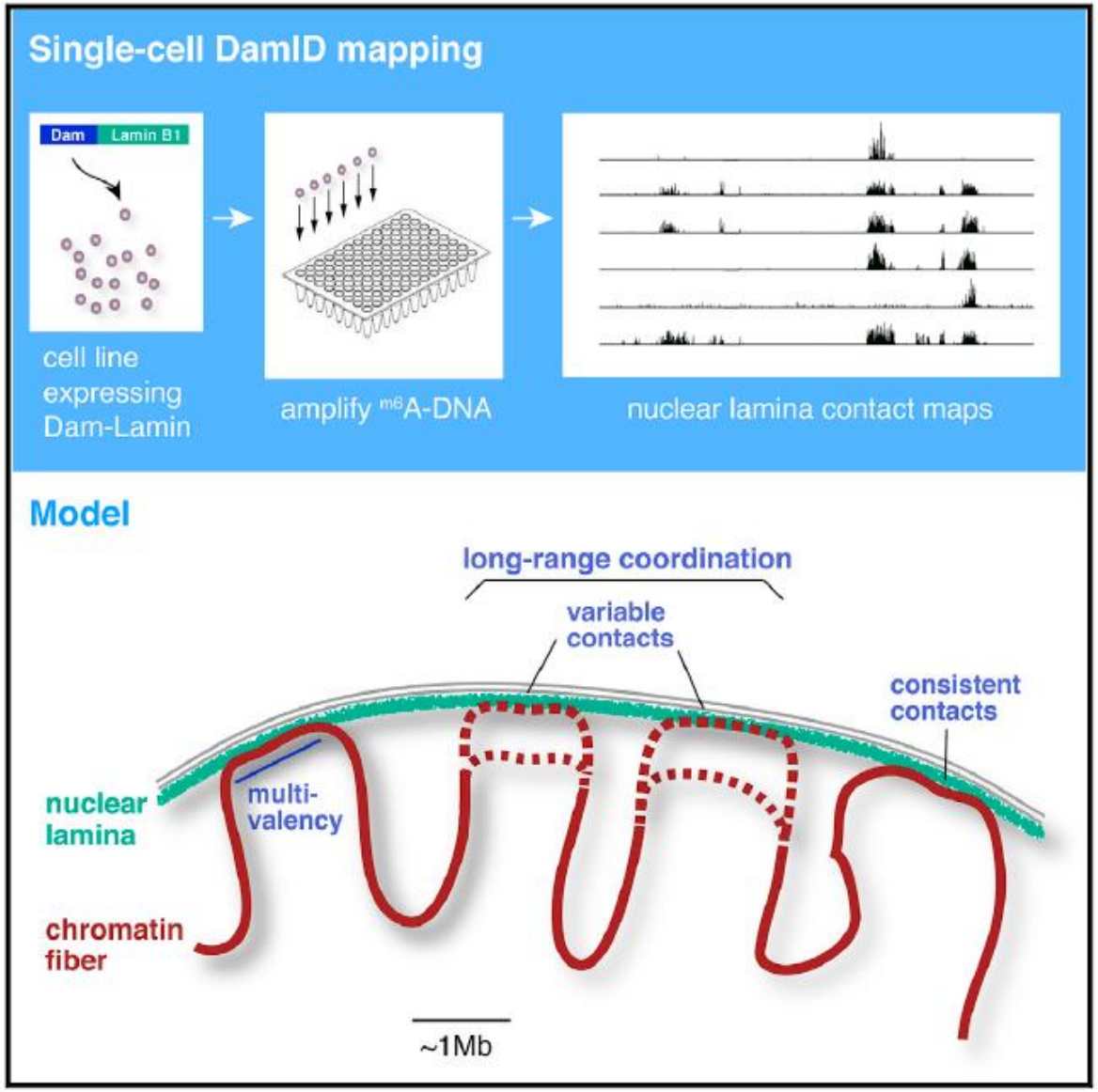
The distribution of mutations in the *LMNA* gene that result in HGPS and atypical Werner's syndrome are shown in relation to the gene and protein structure. The most common HGPS-causing mutation is the splicing mutation at G608 in exon 11.

Progerin creates a disorganization in the nucleus structure and changes in the protein association that control biological function



DamID : DNA adenine methyltransferase identification

Graphical Abstract

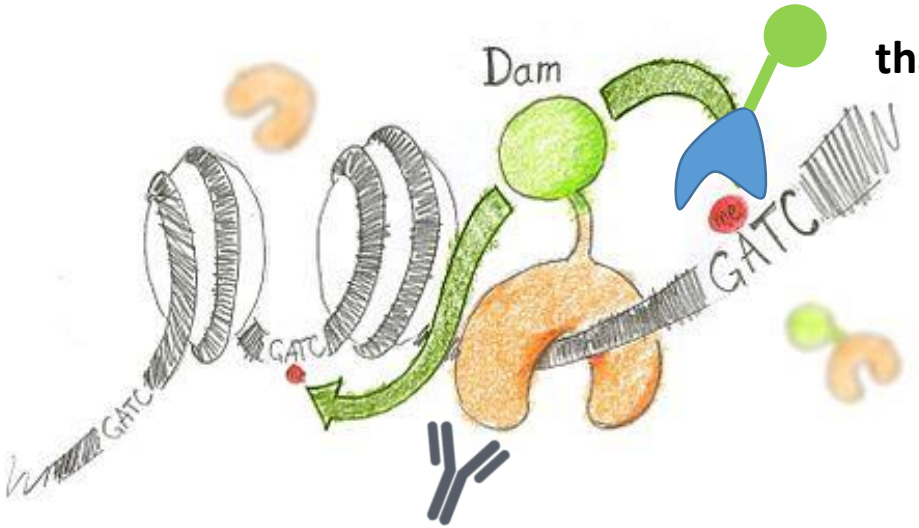


A modified DamID method enables the mapping of genome-wide nuclear lamina interactions in single human cells, providing insight into the cell-to-cell variation in the interphase chromosome architecture and suggesting extensive intra-chromosomal coordination of nuclear lamina contacts.

Kind et al., 2015, Cell *163*, 134–147

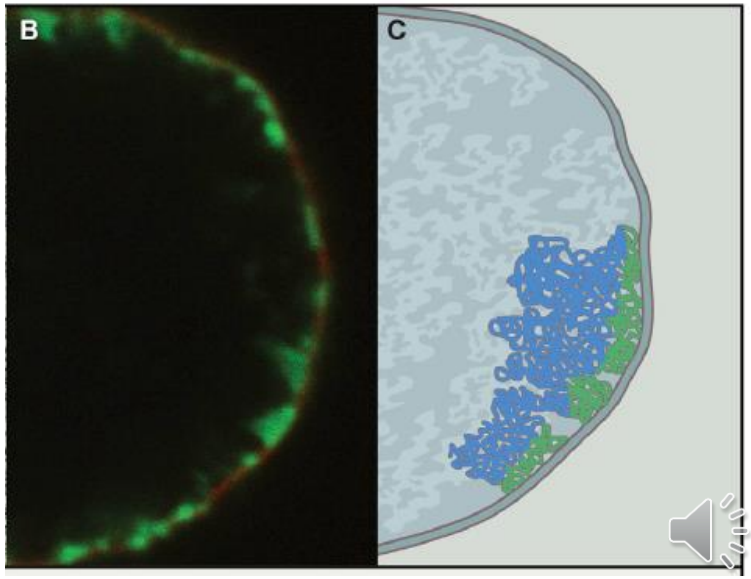
DamID (DNA adenine methyltransferase identification)

DamID identifies binding sites by expressing the proposed DNA-binding protein as a fusion protein with DNA methyltransferase. Binding of the protein of interest to DNA localizes the methyltransferase in the region of the binding site

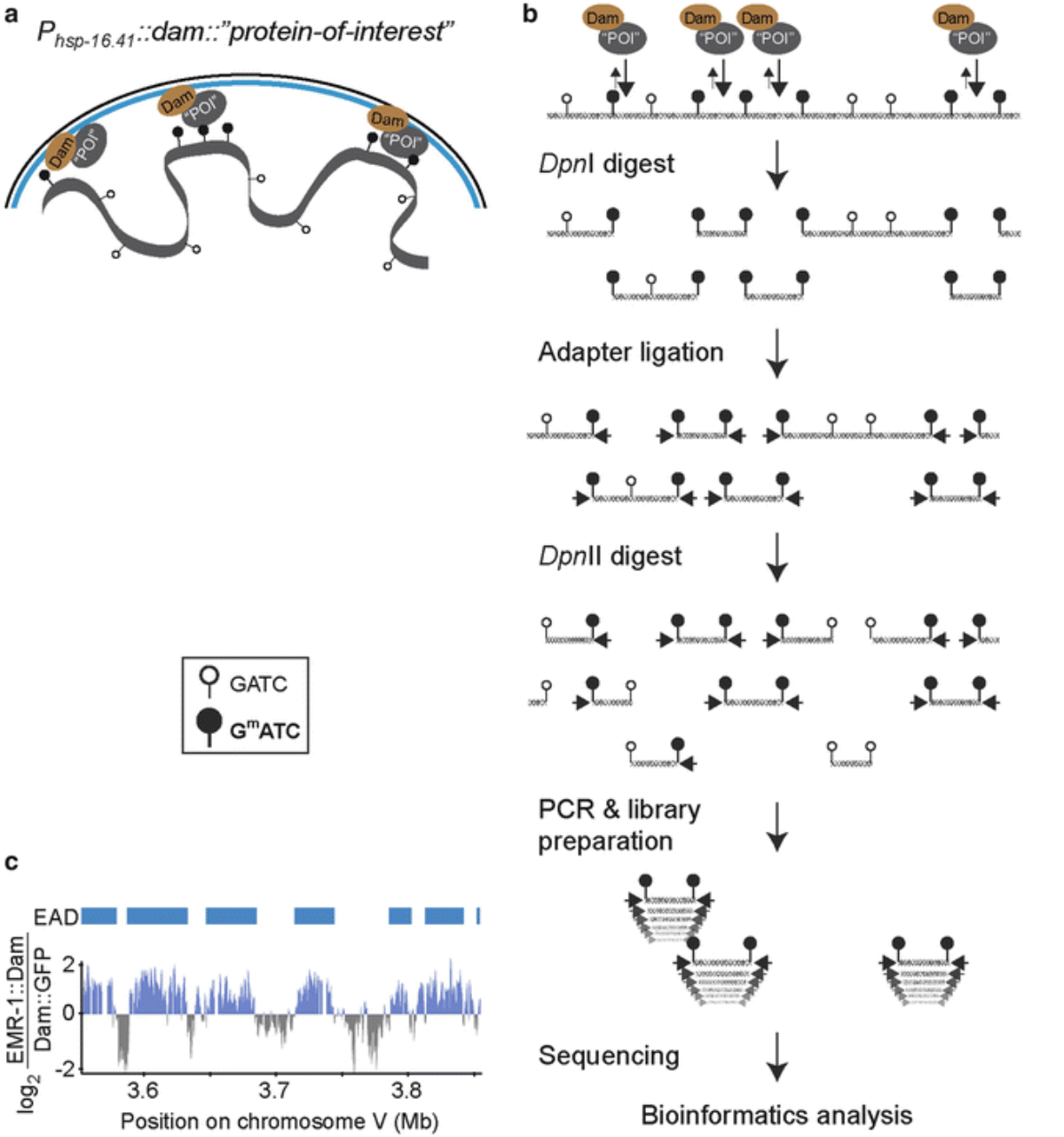


GFP-tagged m6A -tracer protein that binds to adenine-methylated DNA (green)

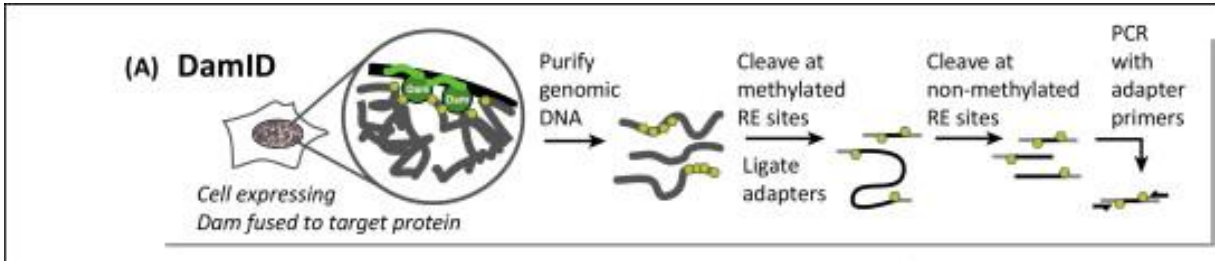
Antibodies against laminB1 red

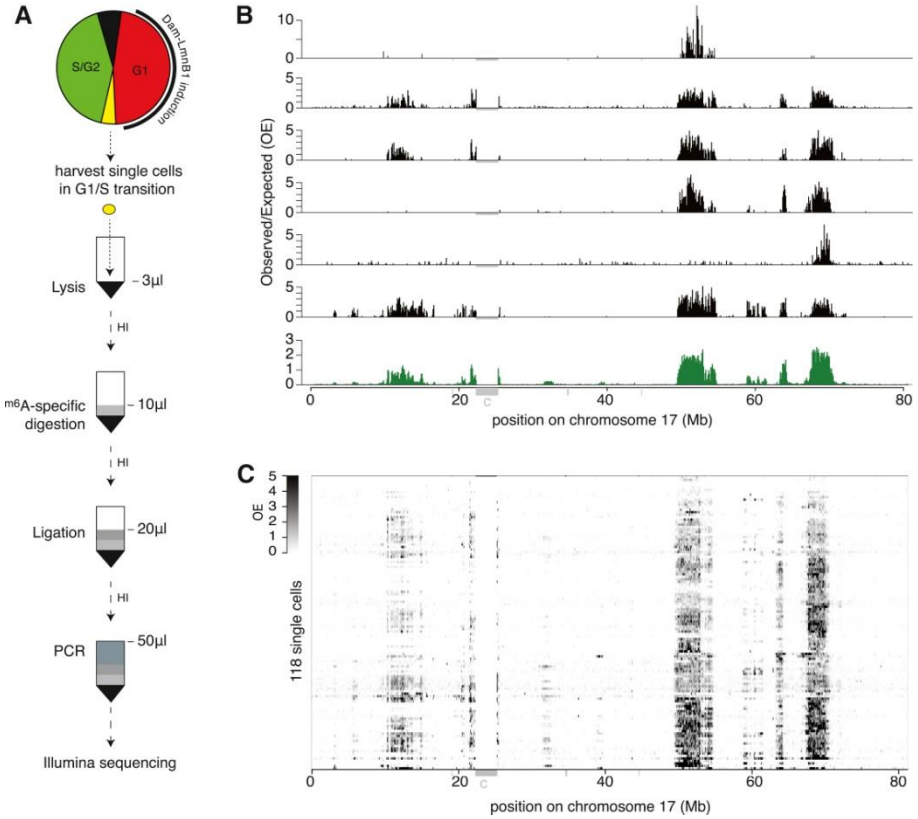


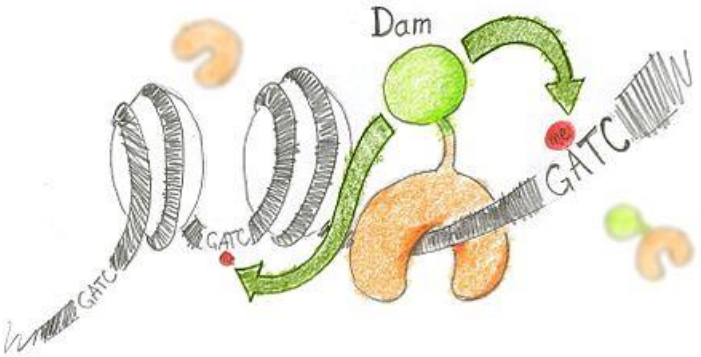
DamID : DNA adenine methyltransferase identification



DamID : DNA adenine methyltransferase identification

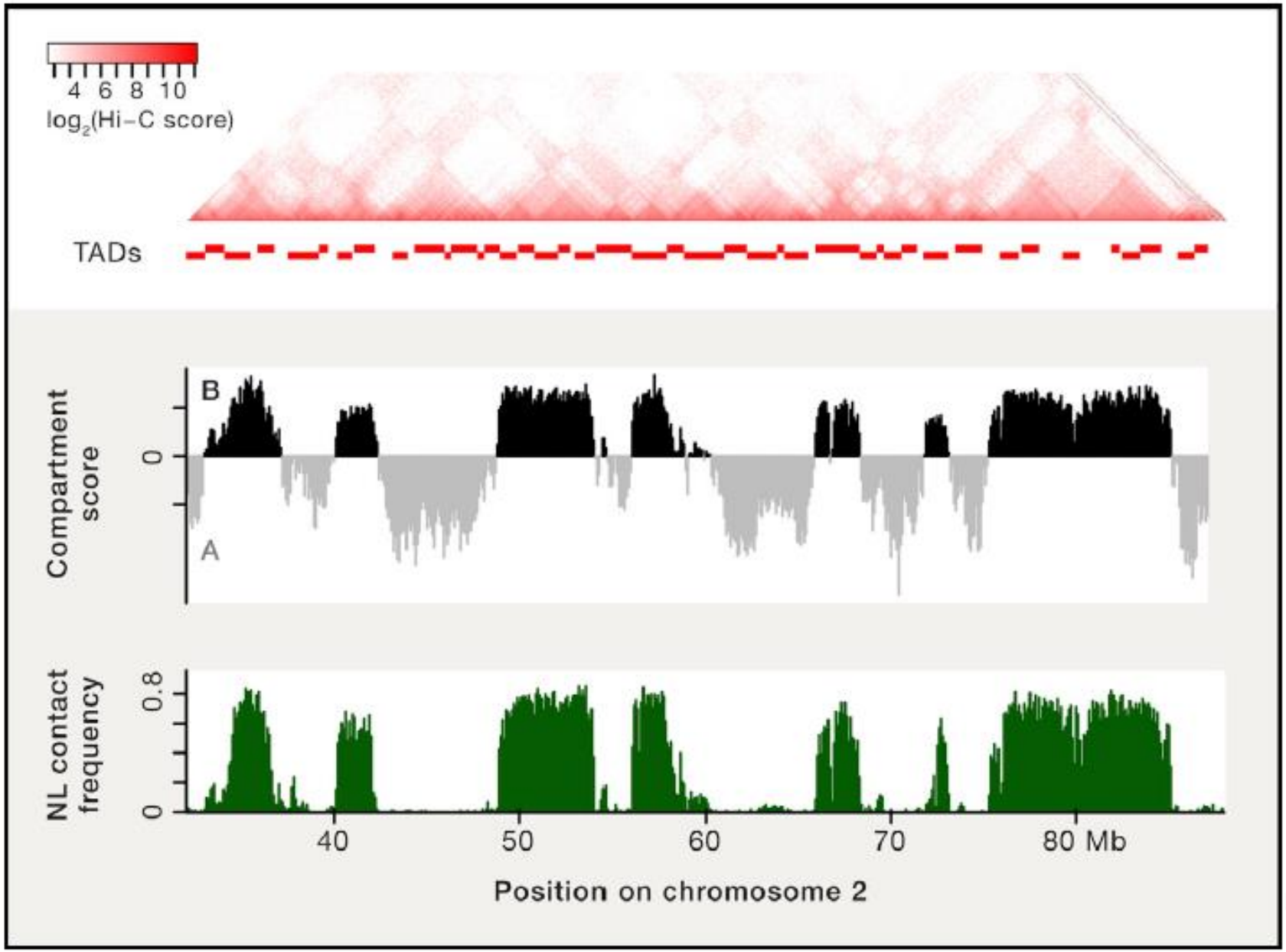




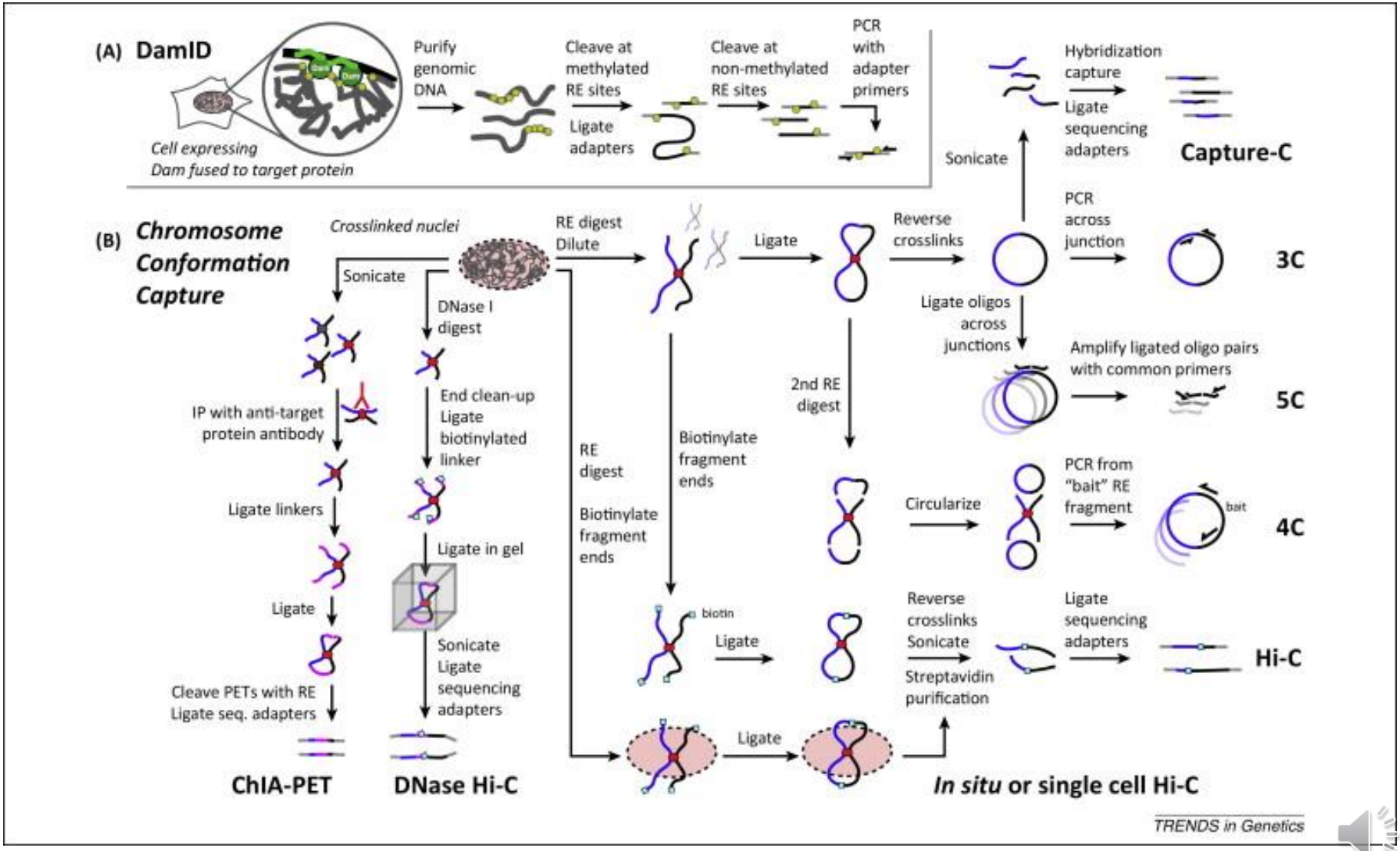


DamID is a molecular biology protocol used to map the binding sites of DNA- and chromatin-binding proteins in eukaryotes. DamID identifies binding sites by expressing the proposed DNA-binding protein as a fusion protein with DNA methyltransferase. Binding of the protein of interest to DNA localizes the methyltransferase in the region of the binding site.

Model derived from comparation of signals between Hi-C and DamID assays



CHROMATIN ORGANIZATION IN THE NUCLEUS USING CHROMATIN LOOPING TECHNIQUES



Hutchinson-Gilford progeria syndrome (HGPS)
PROGERIA

is caused by a **point mutation in the LMNA gene** that activates a cryptic donor splice site and yields a truncated form of prelamin A called progerin

LAMINA ALTERATIONS INDUCE DISEASE

Progeria, or Hutchinson–Gilford progeria syndrome (HGPS), is a rare, fatal genetic disease characterized by an **appearance of accelerated aging in children**.

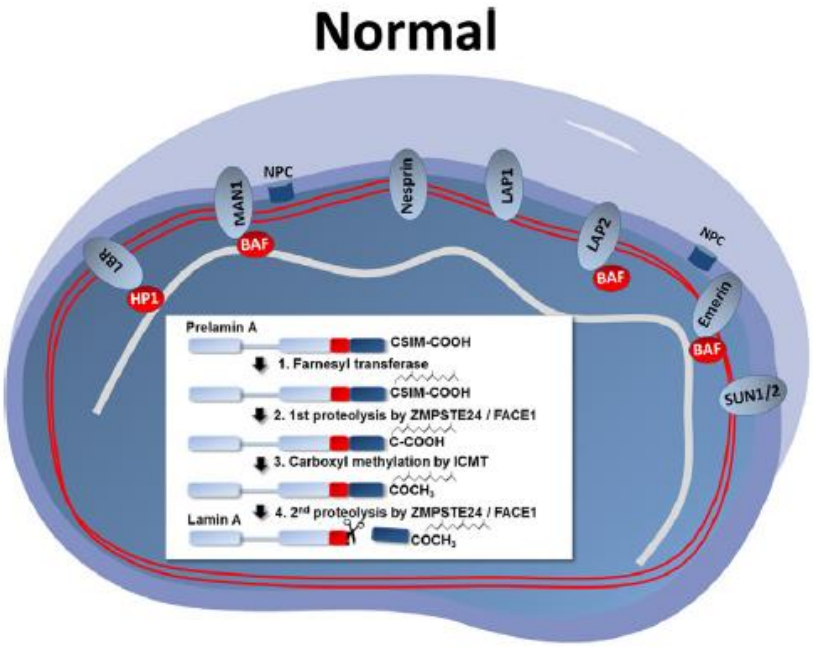
This syndrome is typically caused by mutations **in codon 1824, cryptic splincing site (p.G608G, no change aminoacid)** of the LMNA, leading to the production of a mutated form of lamin A precursor called **progerin**.

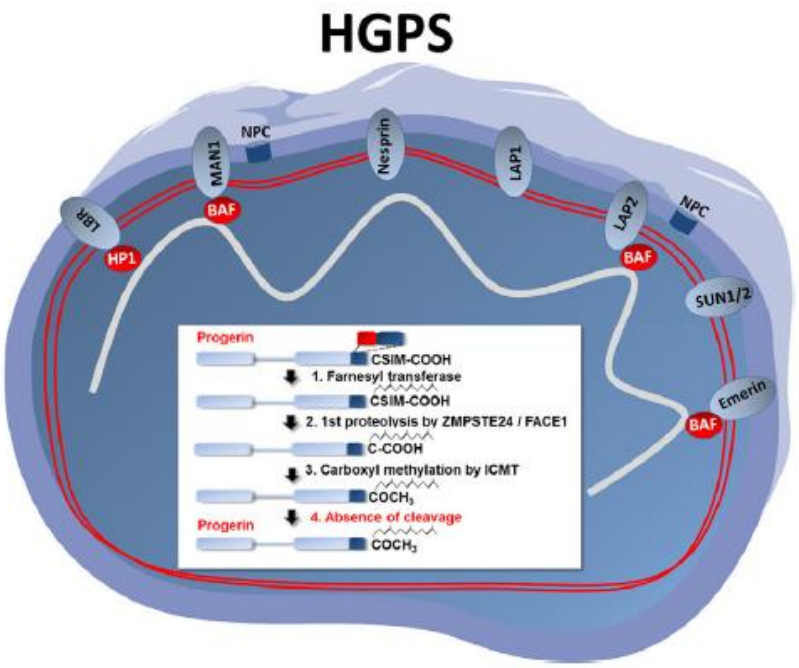
Progerin accumulates in cells causing progressive molecular defects, including nuclear shape abnormalities, chromatin disorganization, damage to DNA and delays in cell proliferation.

LAMINA ALTERATIONS INDUCE DISEASE

Progeria, or Hutchinson–Gilford progeria syndrome (HGPS)

Aminoacid 608 (p.G608G) of the LMNA: mutated form of lamin A precursor called **progerin**.



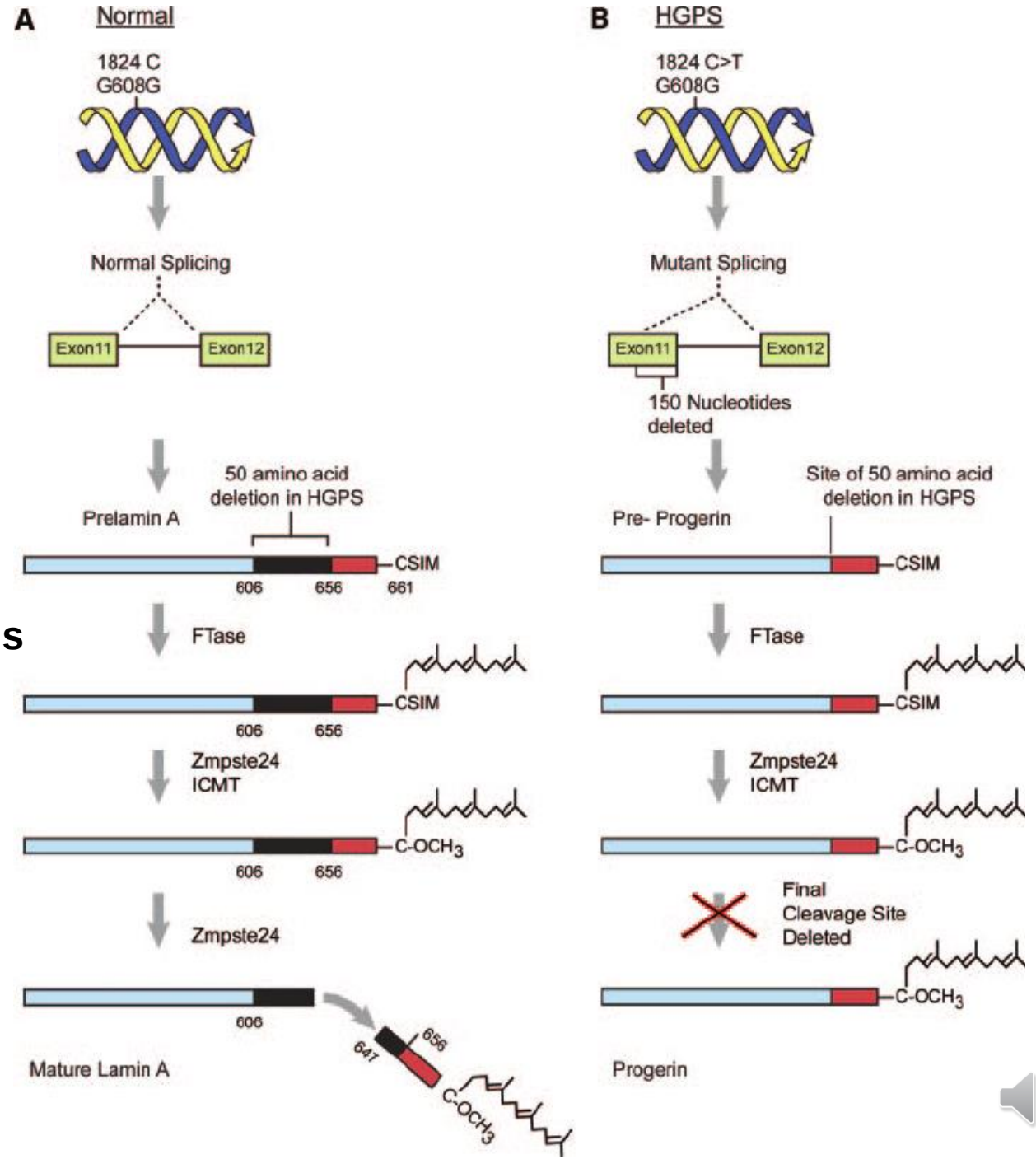


PRELAMININ A

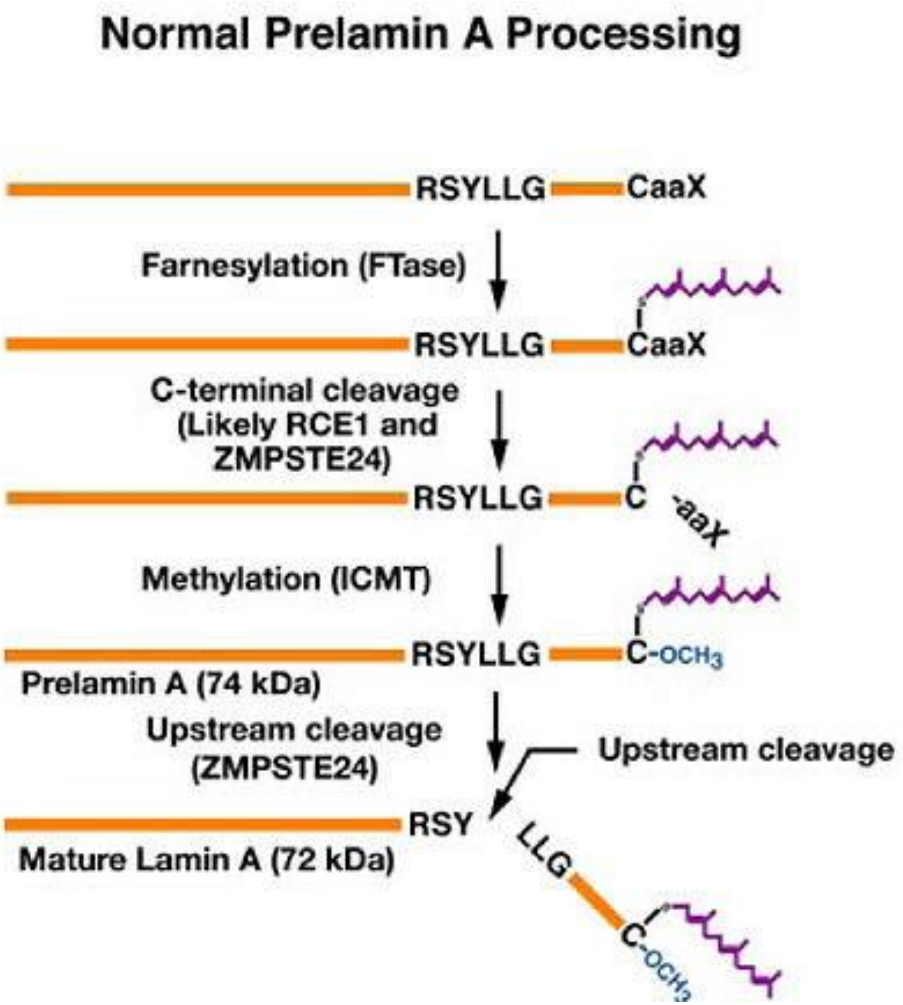
farnesylated C-terminus

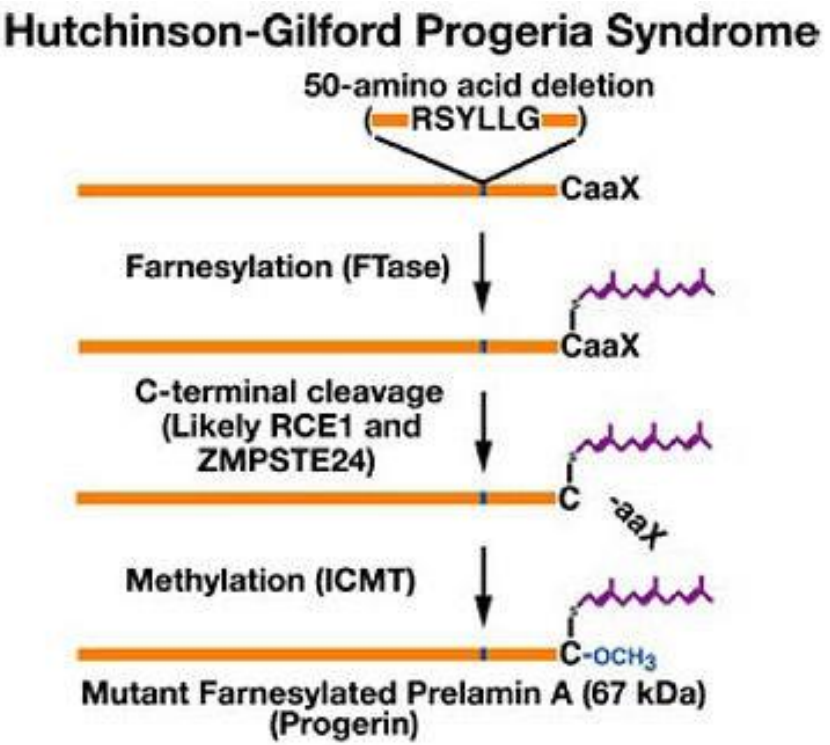
ZMPSTE24 enzyme cleave the farnesylated C-terminus

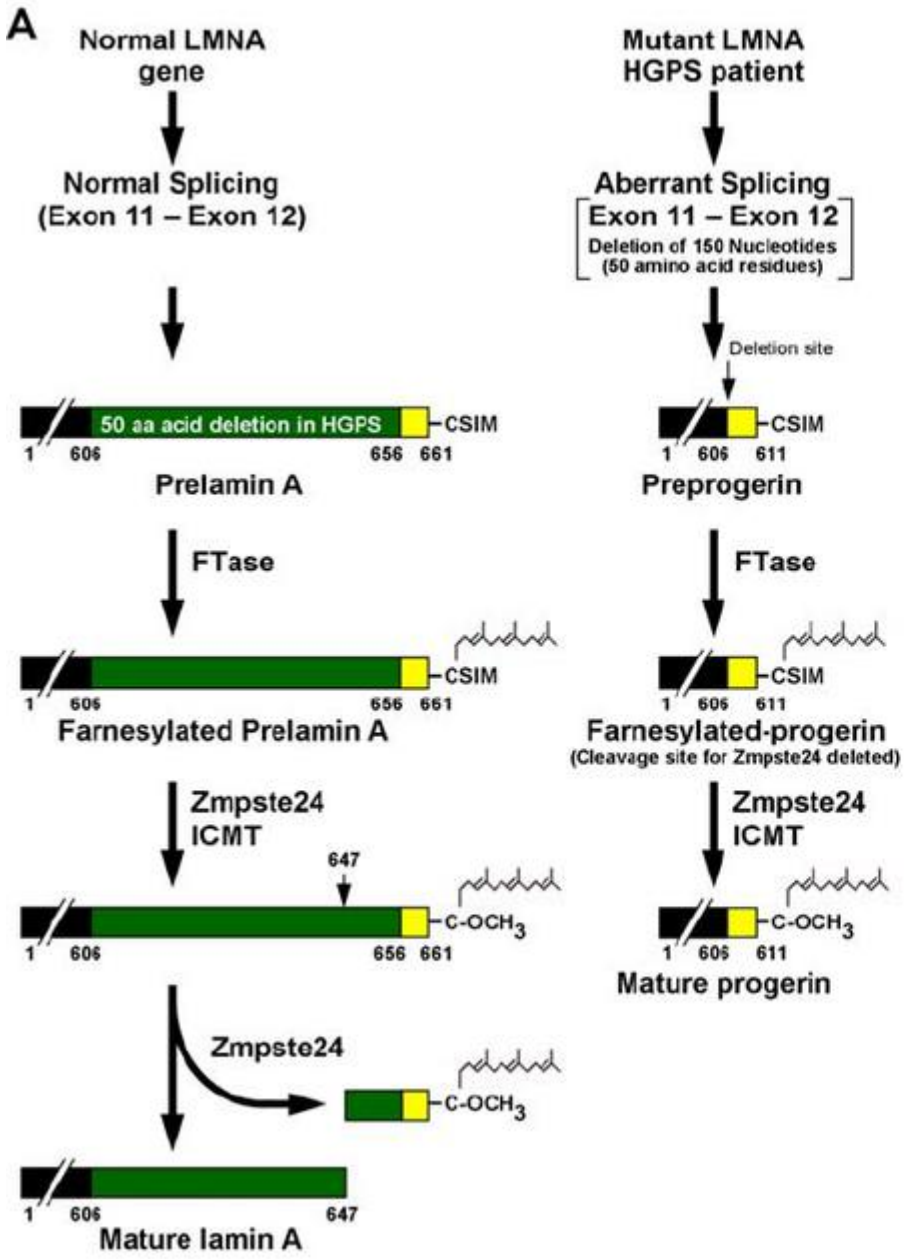
LAMININ A

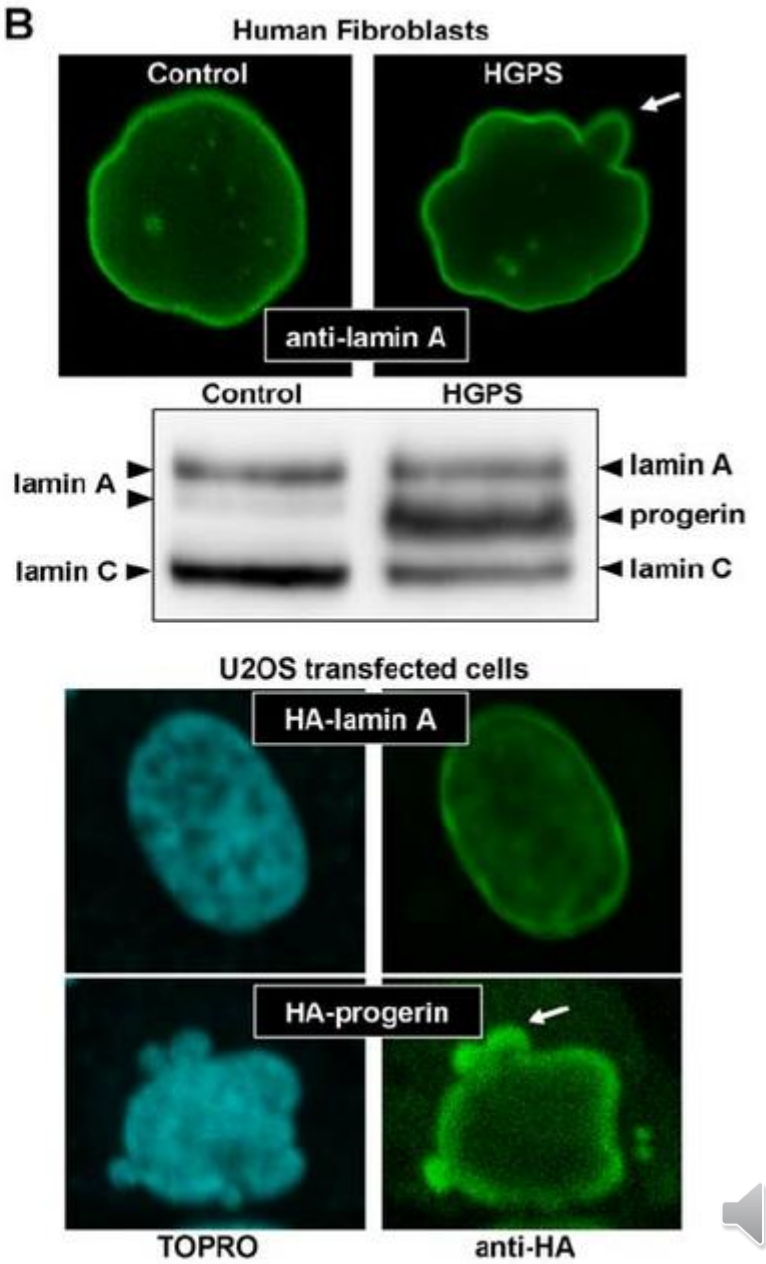


Loss of splicing site induce a deletion of aminoacid sequence that is recognized by ZMPSTE24 enzyme

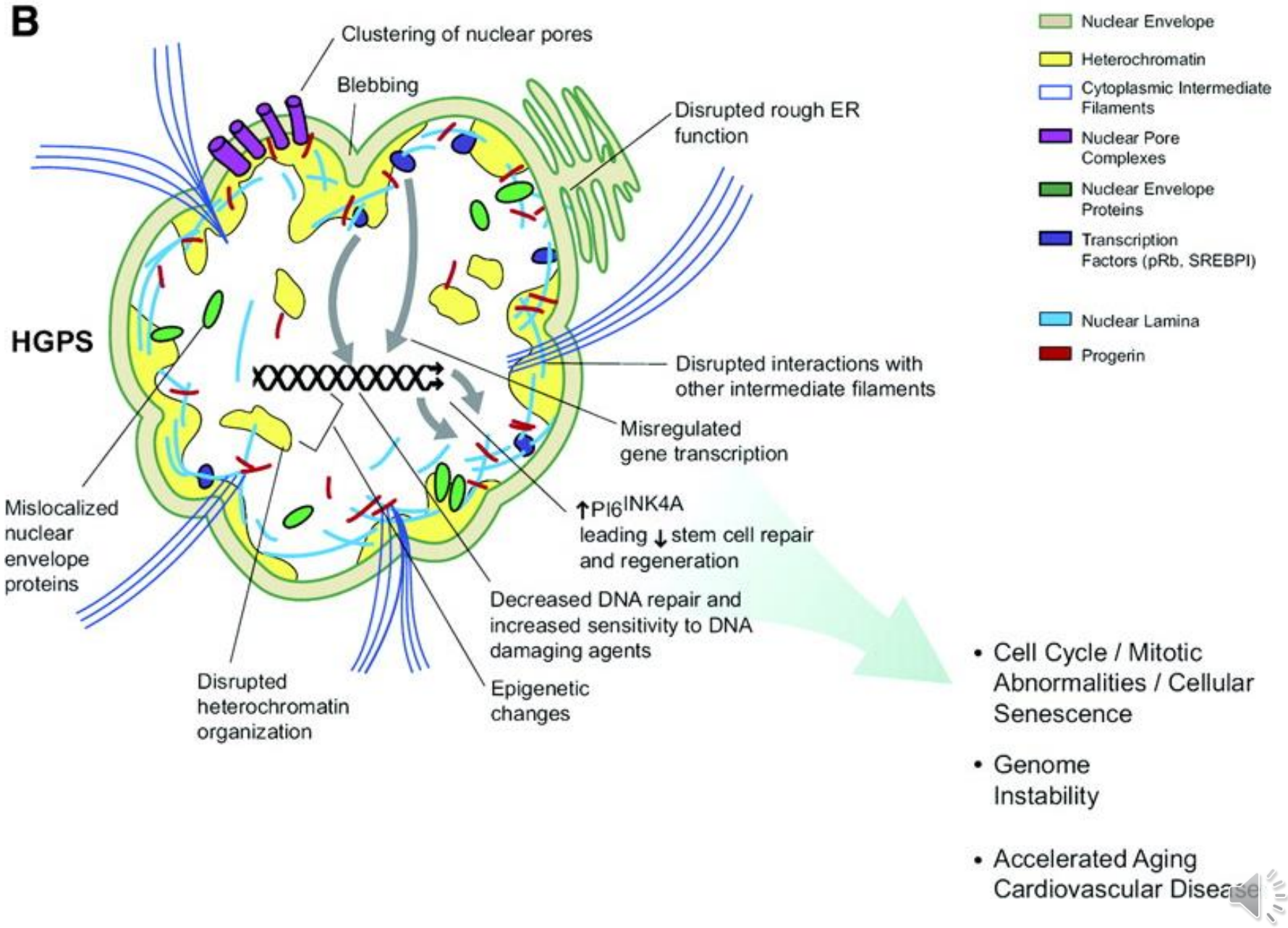




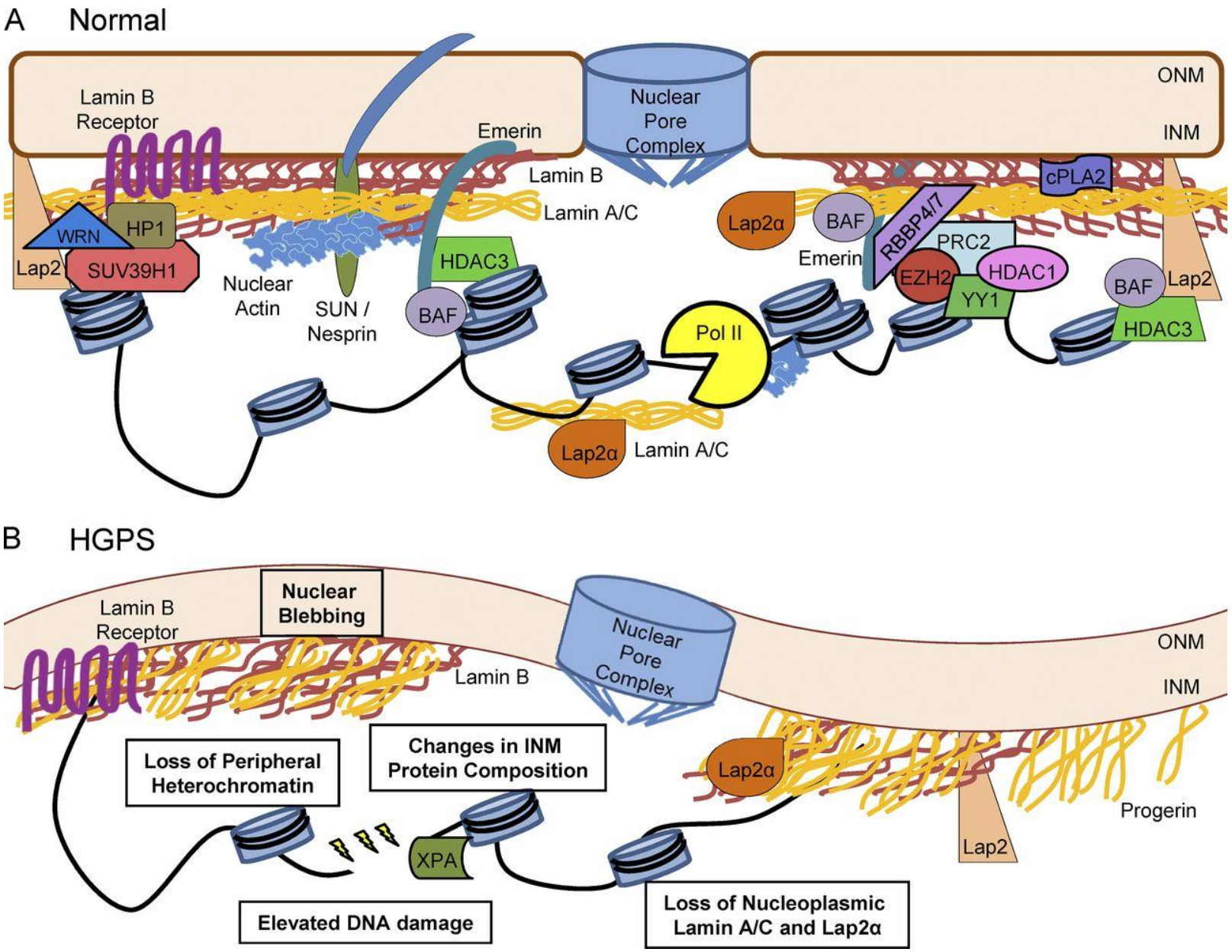

A
Normal LMNA gene
Normal Splicing (Exon 11 – Exon 12)
50 aa acid deletion in HGPS
CSIM
1 606 656 661
Prelamin A
FTase
CSIM
1 606 656 661
Farnesylated Prelamin A
Zmpste24 ICMT
647
C-OCH3
1 606 656 661
Zmpste24
C-OCH3
1 606 647
Mature lamin A
Mutant LMNA HGPS patient
Aberrant Splicing
Exon 11 – Exon 12
Deletion of 150 Nucleotides (50 amino acid residues)
Deletion site
CSIM
1 606 611
Preprogerin
FTase
CSIM
1 606 611
Farnesylated-progerin
(Cleavage site for Zmpste24 deleted)
Zmpste24 ICMT
C-OCH3
1 606 611
Mature progerin


B
Human Fibroblasts
Control
HGPS
anti-lamin A
Control
HGPS
lamin A
lamin C
lamin A
progerin
lamin C
U2OS transfected cells
HA-lamin A
HA-progerin
TOPRO
anti-HA

PROGERIA EFFECTS ON THE BIOLOGICAL FUNCTIONS



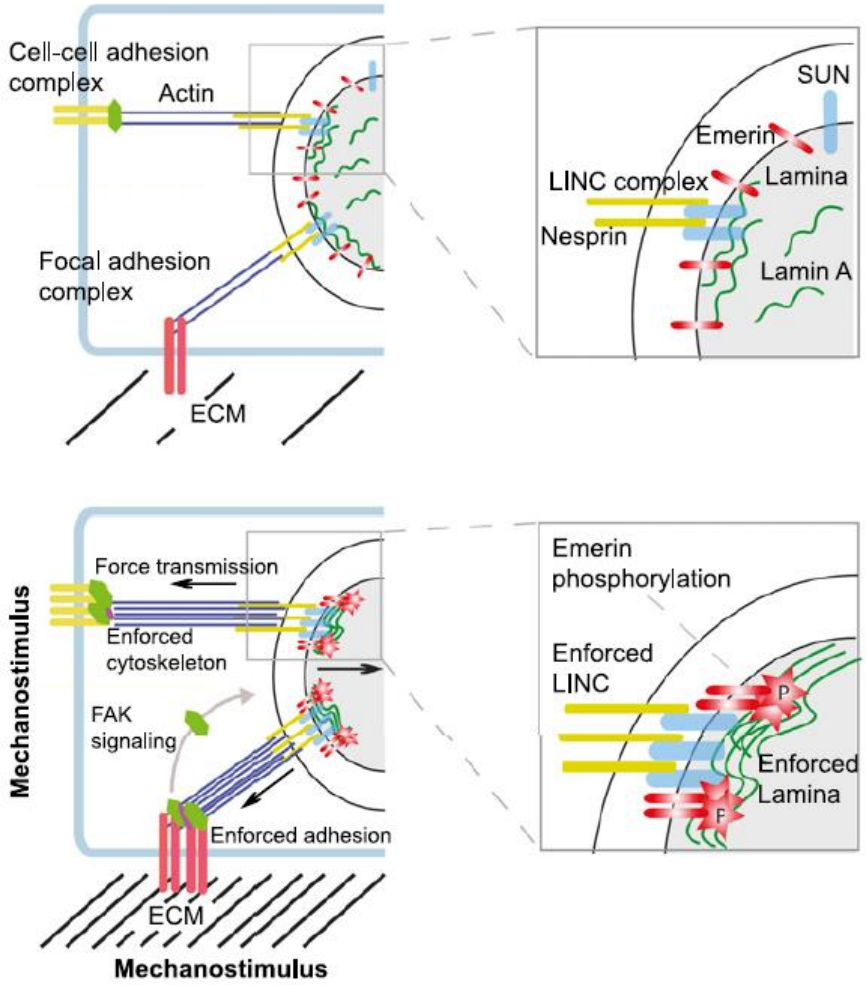
Loss of protein complexes organization in HGPS



Lamins at the crossroads of mechanosignaling

Selma Osmanagic-Myers, Thomas Dechat, and Roland Foisner

Max F. Perutz Laboratories, Department of Medical Biochemistry, Medical University Vienna, A-1030 Vienna, Austria

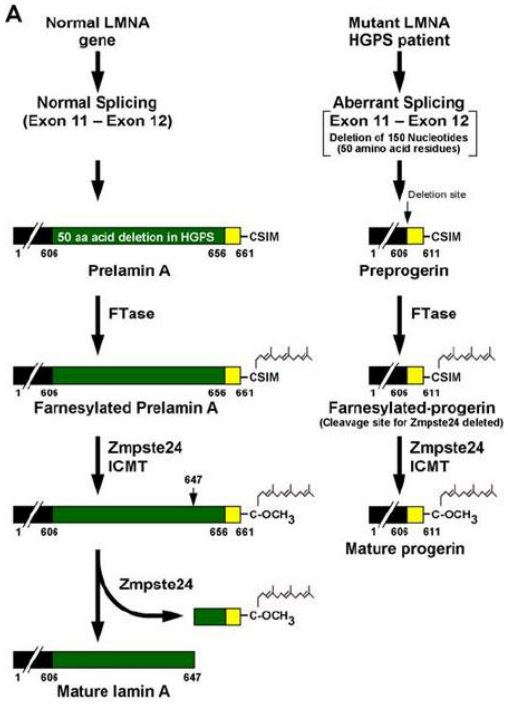


In summary

In HGPS:

- the mutation leads to alternative splicing in exon 11 and to the loss of 50 amino acids in prelamin A
- ZMPSTE24 enzyme not cleave the farnesylated C-terminus of this protein.
- This mutant protein, called progerin, remains permanently farnesylated
- Alteration of lamin A processing induce nuclear shape and protein complexes dysorganization.

THERAPHY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Normal LMNA gene
Normal Splicing (Exon 11 – Exon 12)
50 aa acid deletion in HGPS
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Prelamin A
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Farnesylated Prelamin A
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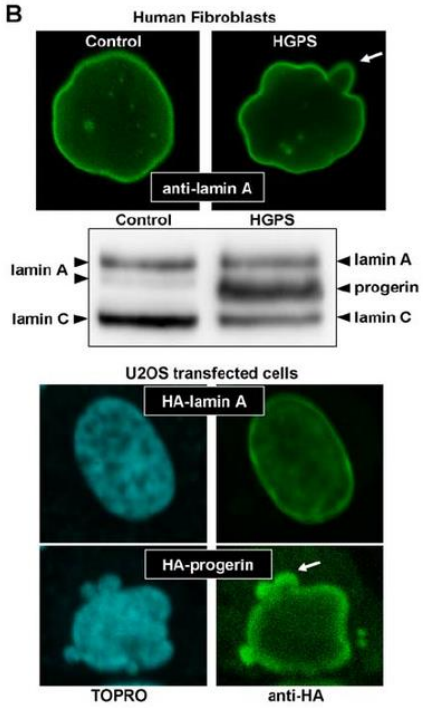
C-OCH3
Mature lamin A
Mutant LMNA HGPS patient
Aberrant Splicing Exon 11 – Exon 12
Deletion of 150 Nucleotides (50 amino acid residues)
Deletion site
1 606 611
Preprogerin
Farnesylated-progerin
(Cleavage site for Zmpste24 deleted)
Mature progerin


B
Human Fibroblasts
Control
HGPS
anti-lamin A
lamin A
lamin C
progerin
U2OS transfected cells
HA-lamin A
HA-progerin
TOPRO
anti-HA

Splicing-Directed Therapy in a New Mouse Model of Human Accelerated Aging

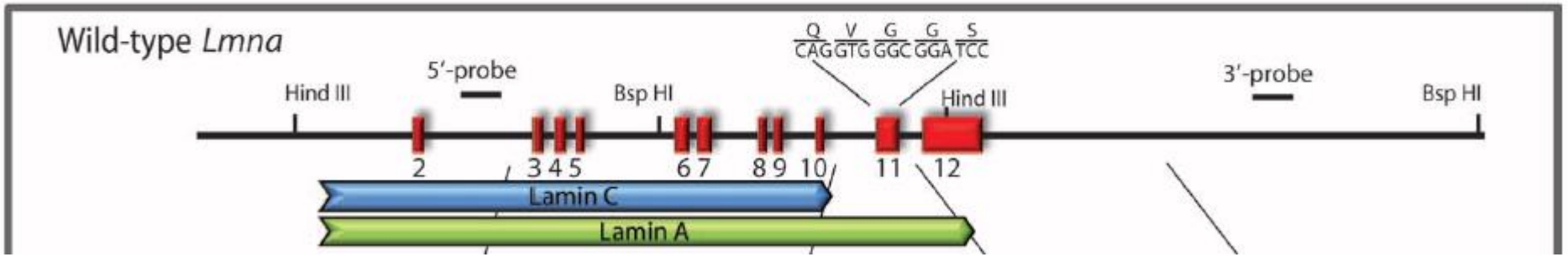
Fernando G. Osorio,[1] Claire L. Navarro,[2] Juan Cadiñanos,[1]* Isabel C. López-Mejía,[3] Pedro M. Quirós,[1] Catherine Bartoli,[2] José Rivera,[4] Jamal Tazi,[3] Gabriela Guzmán,[5] Ignacio Varela,[1] Danielle Depetris,[2] Félix de Carlos,[6] Juan Cobo,[6] Vicente Andrés,[4] Annachiara De Sandre-Giovannoli,[2,7] José M. P. Freije,[1] Nicolas Lévy,[2,7] Carlos López-Otín[1†]

Hutchinson-Gilford progeria syndrome (HGPS) is caused by a point mutation in the *LMNA* gene that activates a cryptic donor splice site and yields a truncated form of prelamin A called progerin. Small amounts of progerin are also produced during normal aging. Studies with mouse models of HGPS have allowed the recent development of the first therapeutic approaches for this disease. However, none of these earlier works have addressed the aberrant and pathogenic *LMNA* splicing observed in HGPS patients because of the lack of an appropriate mouse model. Here, we report a genetically modified mouse strain that carries the HGPS mutation. These mice accumulate progerin, present histological and transcriptional alterations characteristic of progeroid models, and phenocopy the main clinical manifestations of human HGPS, including shortened life span and bone and cardiovascular aberrations. Using this animal model, we have developed an antisense morpholino–based therapy that prevents the pathogenic *Lmna* splicing, markedly reducing the accumulation of progerin and its associated nuclear defects. Treatment of mutant mice with these morpholinos led to a marked amelioration of their progeroid phenotype and substantially extended their life span, supporting the effectiveness of antisense oligonucleotide–based therapies for treating human diseases of accelerated aging.

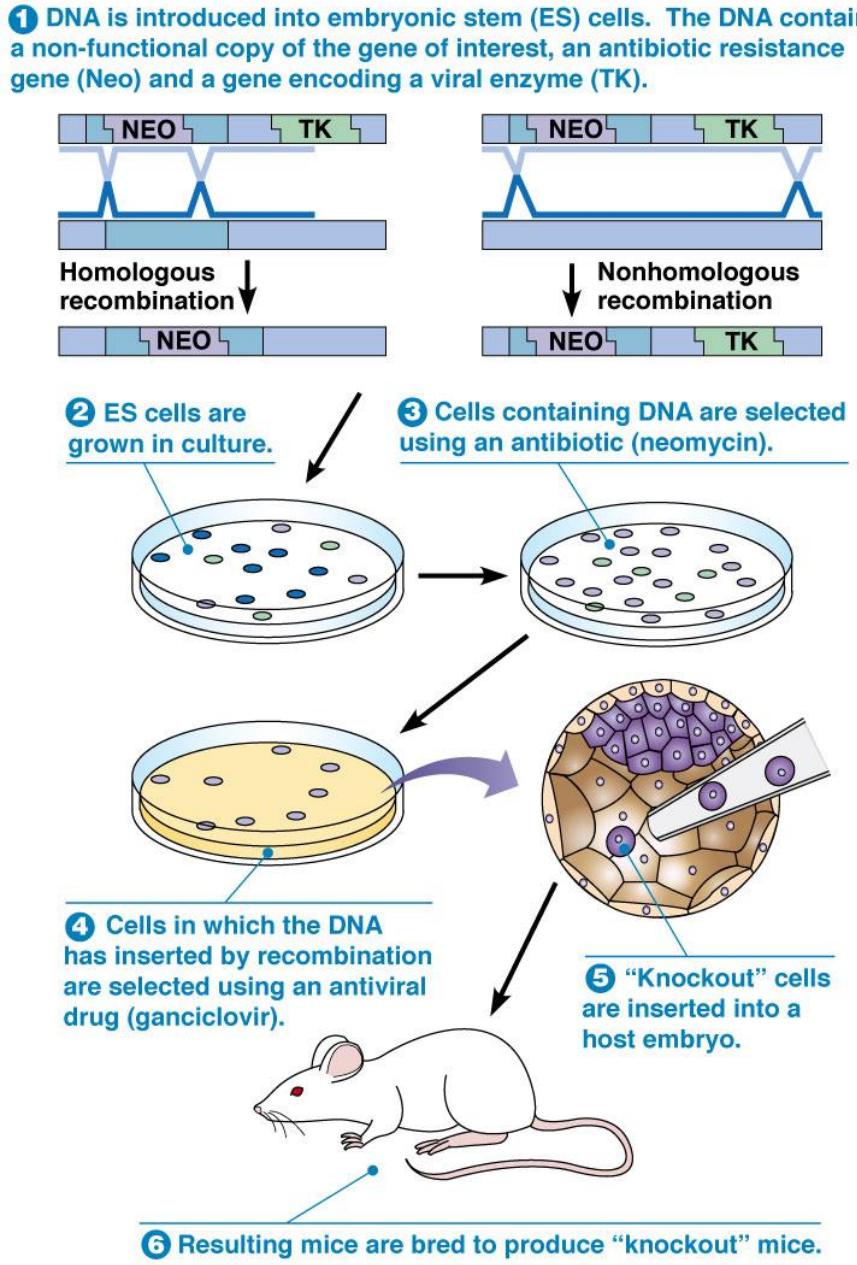
CONDITIONAL TRANSGENIC MICE

PROGERIN MODEL

Wild type locus Lmna that encodes for lamin C and lamin A



Enrichment for homologous recombinants



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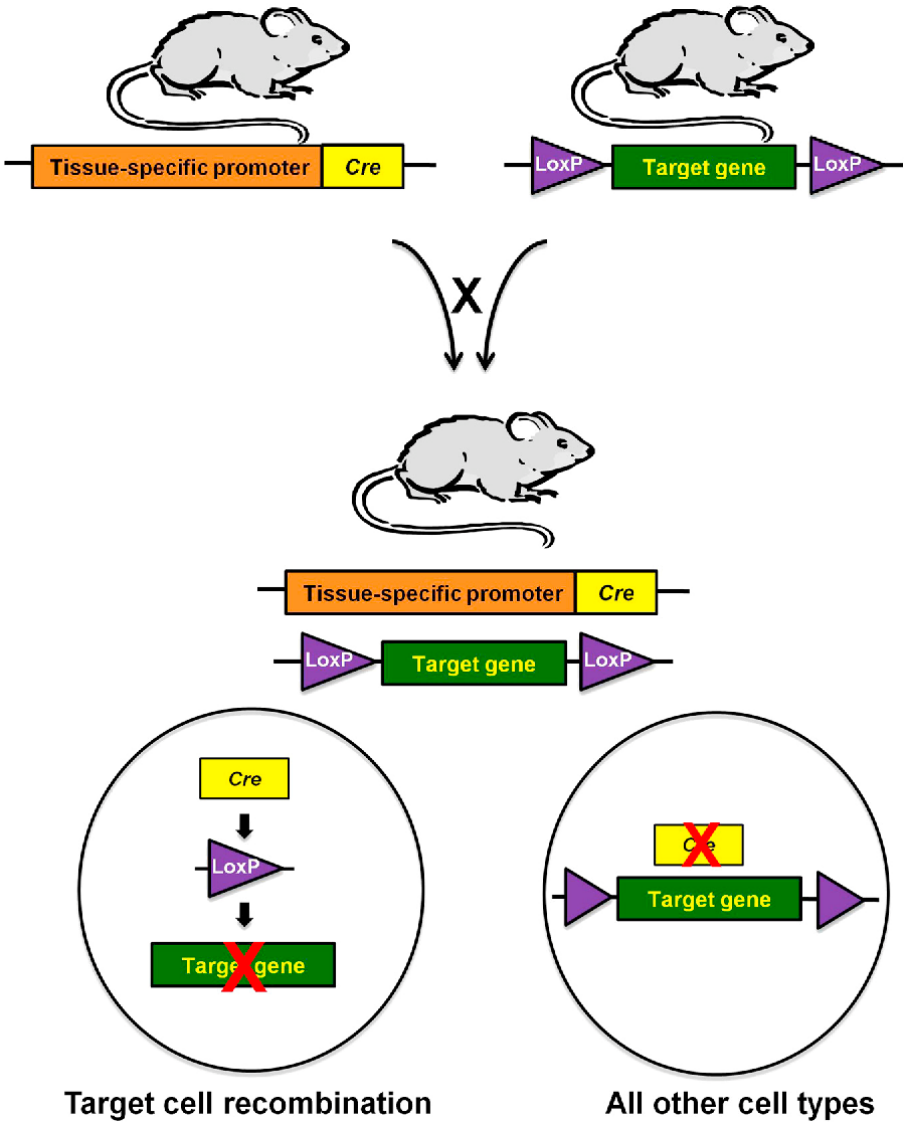
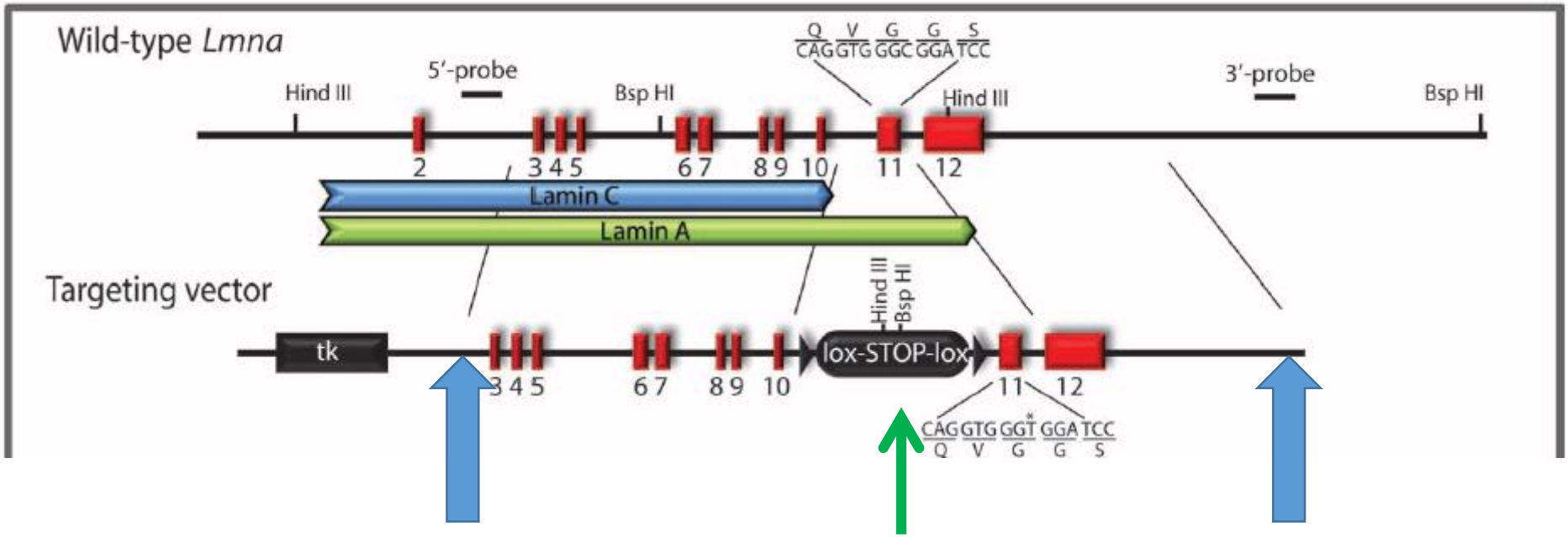
TK: thymidine kinase
Converts ganciclovir in a toxic product

Cre/LoxP system

1. mouse with a targeted "floxed" allele
2. mouse with a cre recombinase enzyme expressed under the control of a transgenic promoter

- Breed together to generate a line that carries both
- Tissue specific deletion of floxed allele in tissues where cre recombinase is expressed

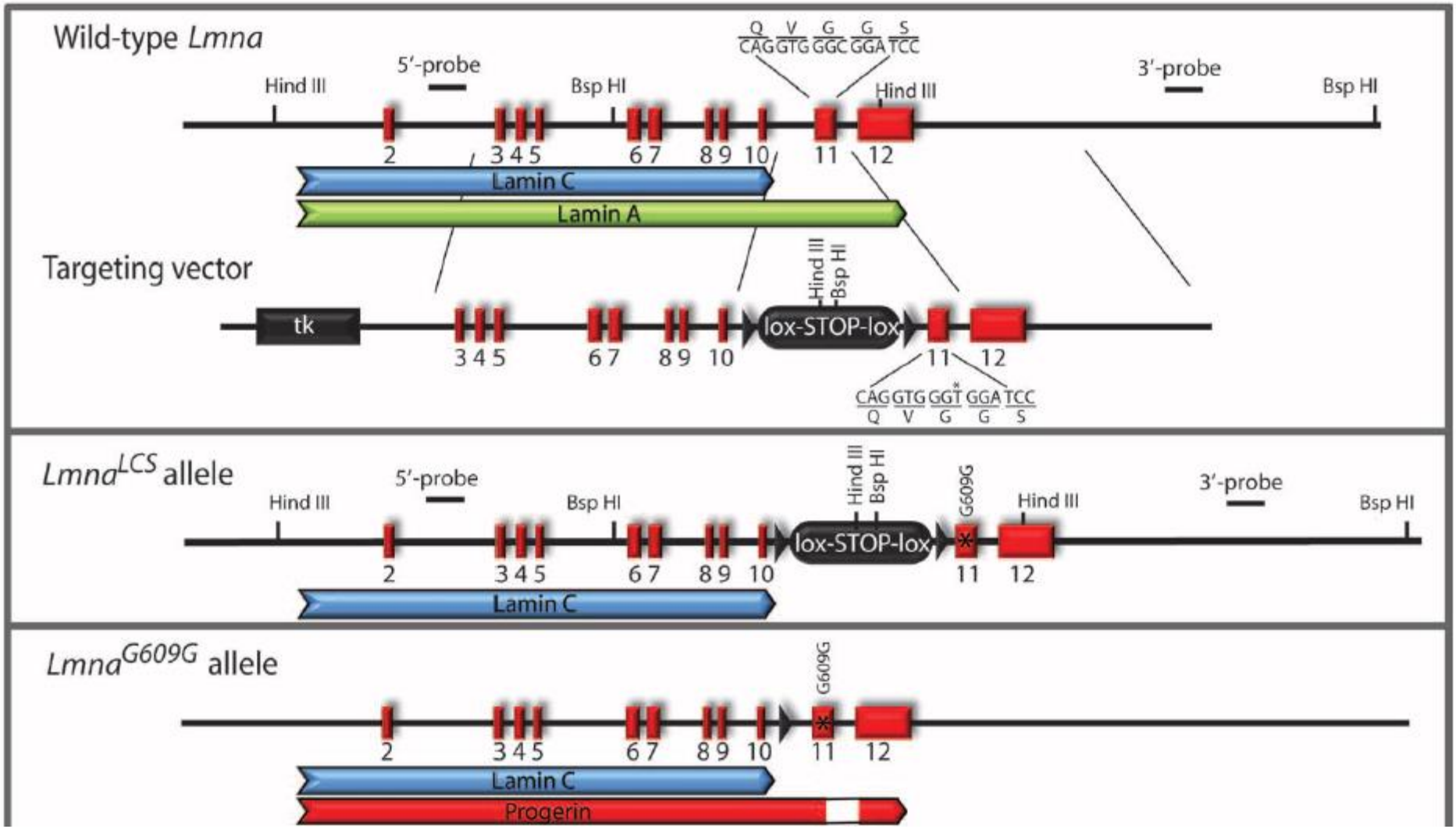




Sites for homologous recombination

neomycin

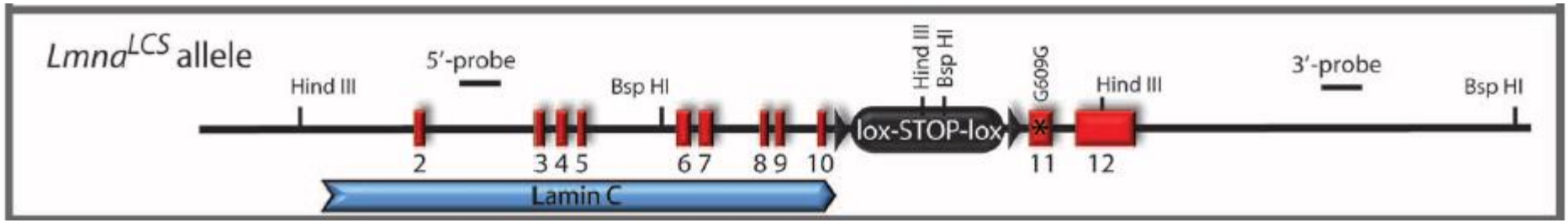
A conditional mutant allele with a neomycin resistance gene flanked by two loxP sites close to Lmna intron 10. This cassette was able to prevent the formation of prelamin A transcripts by blocking lamin A–specific splicing and is obtained the transcript for lamin C.



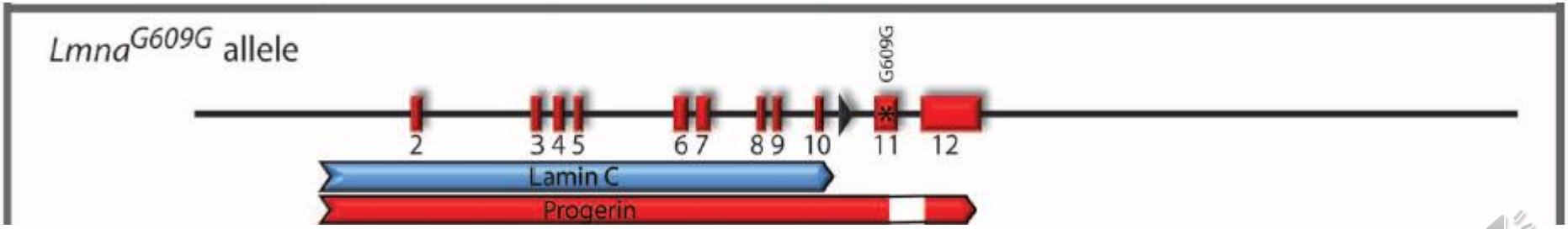
LmnaLCS/+mice and crossed them with a **Cre-deleter mouse strain** to obtain germline removal of the neomycin resistance cassette. LmnaG609G knock-in allele, which expressed lamin C, lamin A, and progerin.

Plan to create Progerin model:

- LmnaLCS (Lamin C–Stop), directs only the expression of lamin C and allows study of the potential effects of lamin A deficiency.

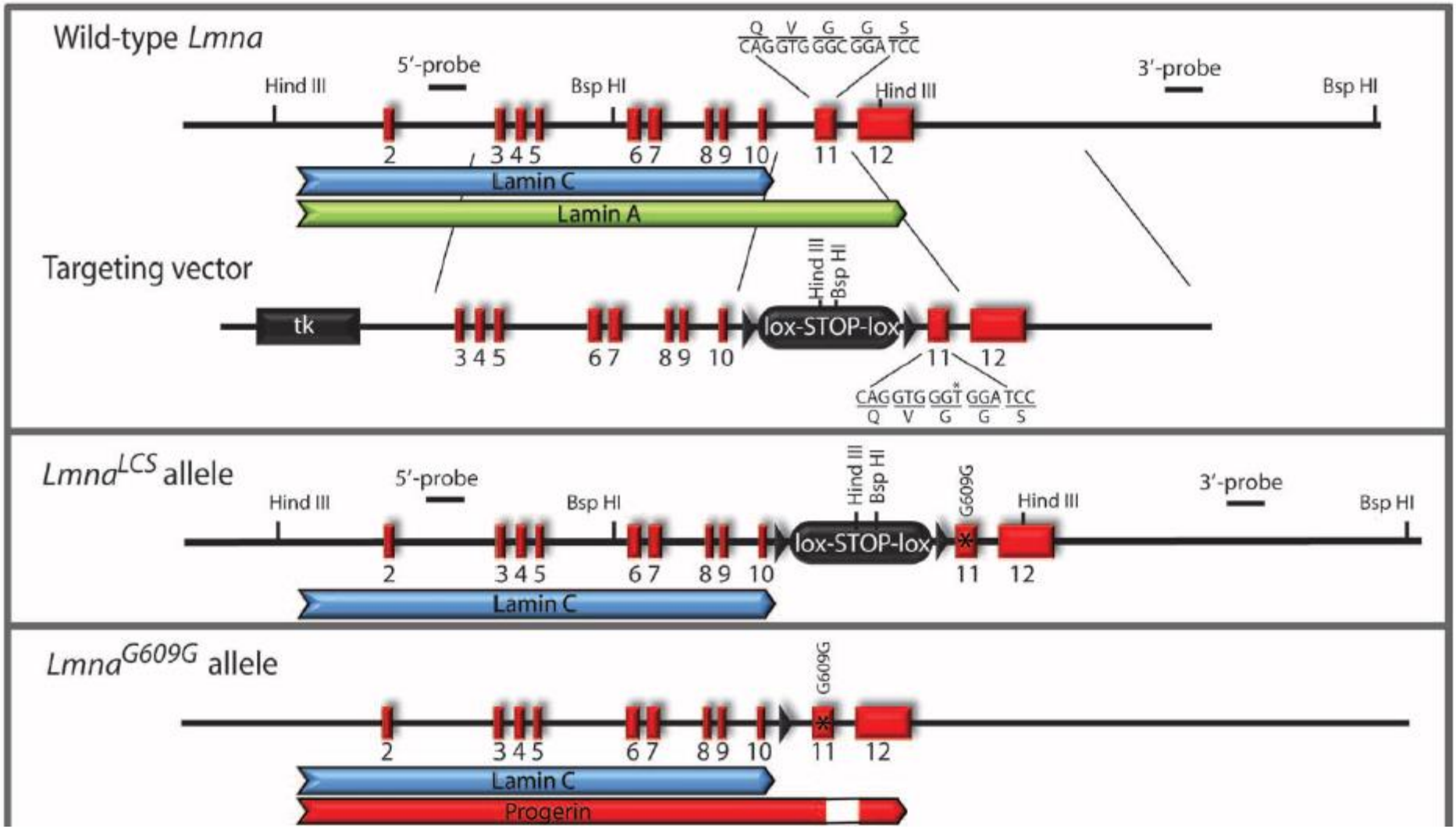


- LmnaG609G knock-in allele, which expressed lamin C, lamin A, and progerin

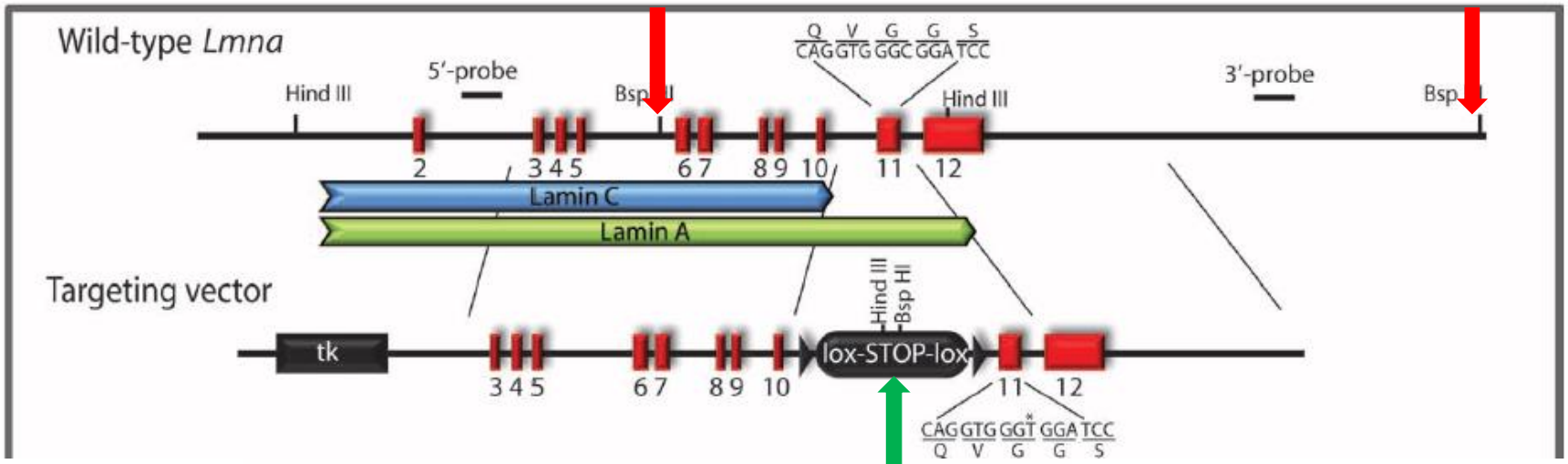


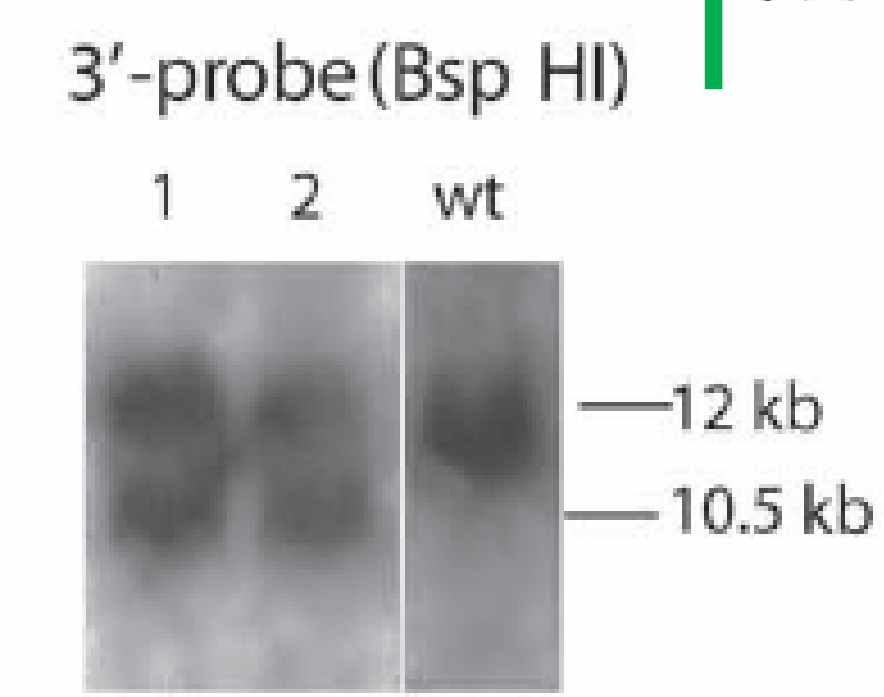
CONDITIONAL TRANSGENIC MICE

GENOTYPING
AND
CHARACTERIZATION



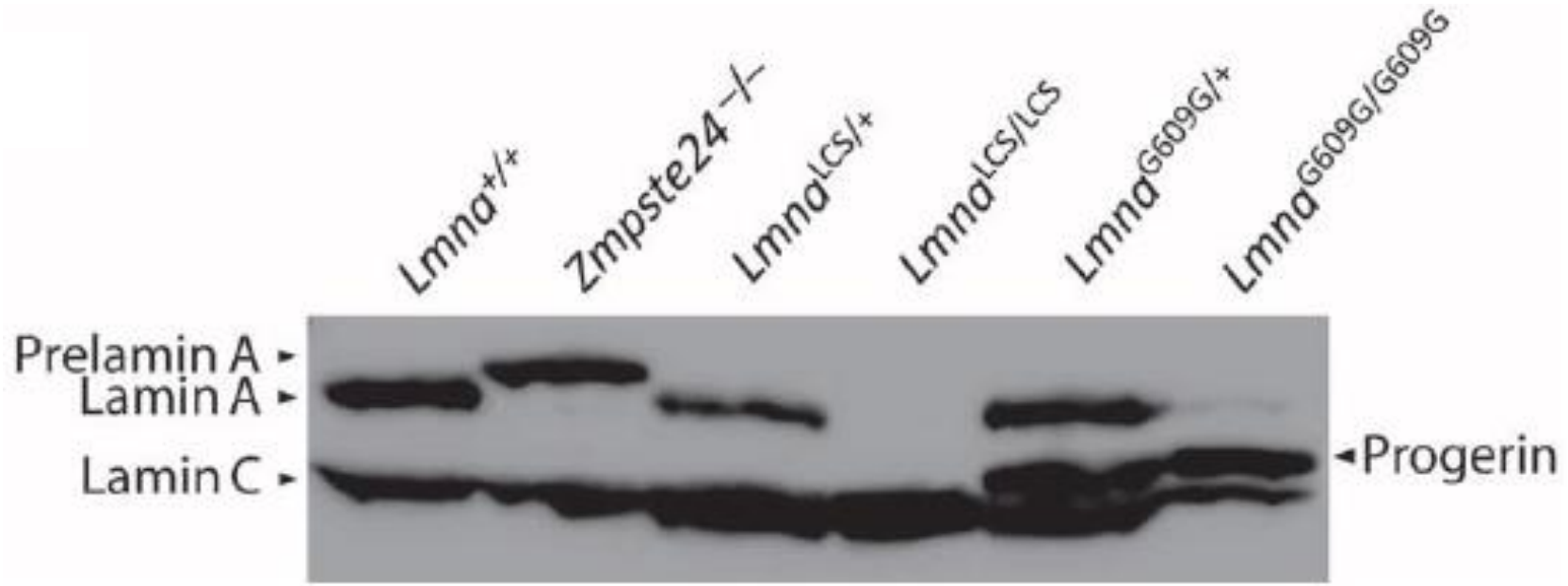
LmnaLCS/+mice and crossed them with a **Cre-deleter mouse strain** to obtain germline removal of the neomycin resistance cassette. LmnaG609G knock-in allele, which expressed lamin C, lamin A, and progerin.





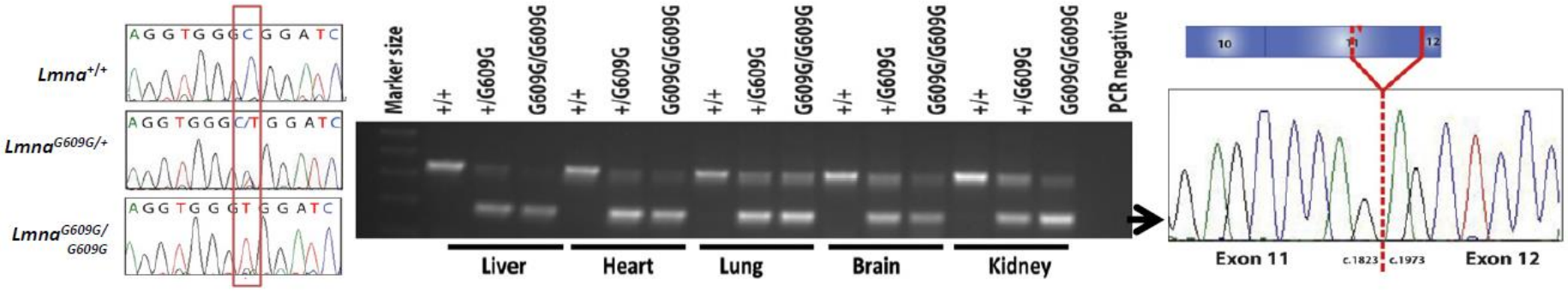
In the southern blot, 12 kbp corrispondes with wt sample because there are two restriction sites in this locus. 10.5 kbp derived from an additional site in the lox sites that is used to obtain transgenic mice.

PROGERIN AND LAMININ TYPES PROTEIN EXPRESSION

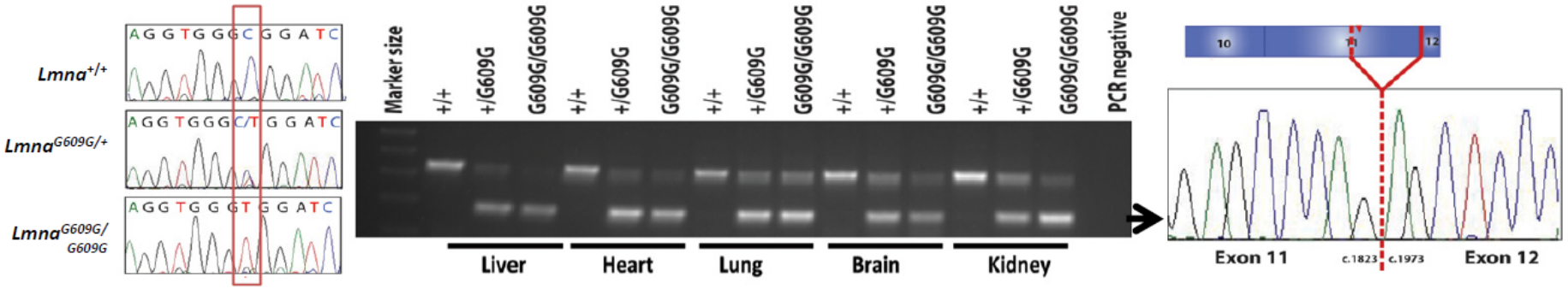


Western (immuno) blot analysis of mouse adult fibroblasts obtained from the mice with the various genotypes used in the study. Lamin A, lamin C, prelamin A, and progerin were detected with a monoclonal antibody against lamin A/C (Manlac-1).

GENOTYPING OF SEVERAL MICE TISSUES



GENOTYPING OF SEVERAL MICE TISSUES

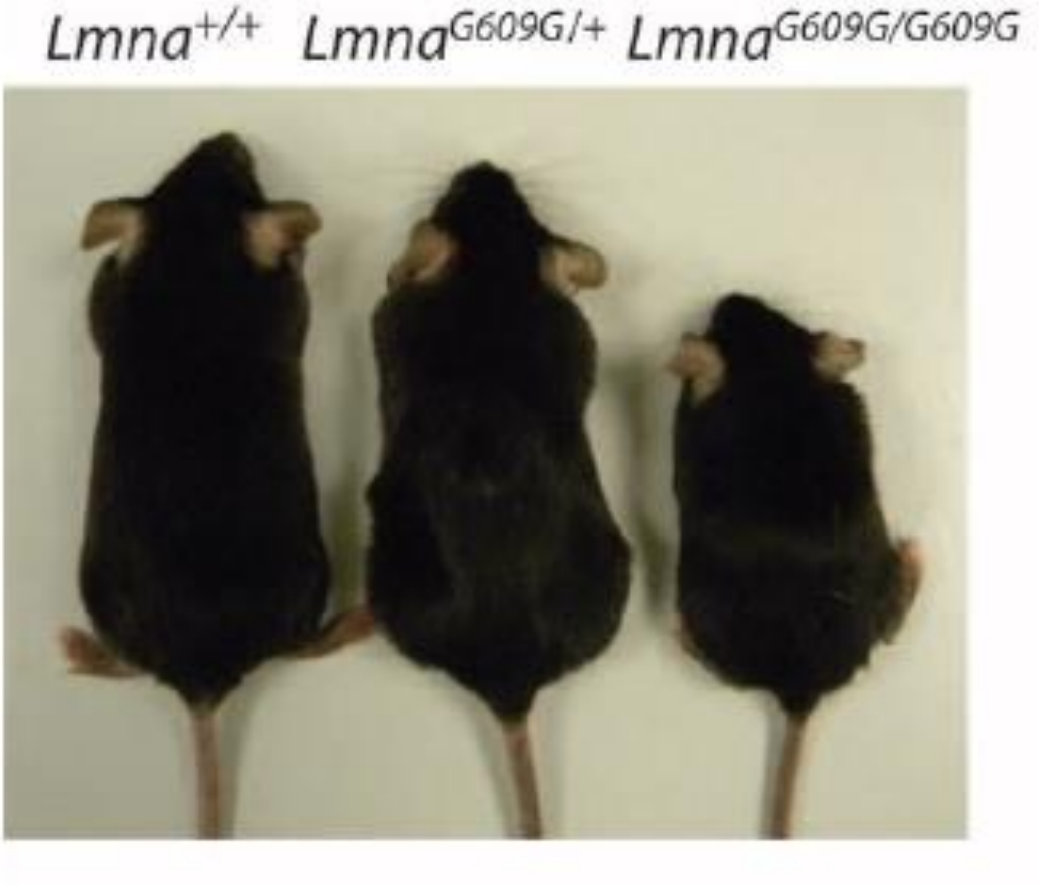


Genomic sequencing of *Lmna* exon 11 showing the wild-type sequence or heterozygous/homozygous mutations respectively in $Lmna^{+/+}$, $Lmna^{G609G/+}$and $Lmna^{G609G/G609G}$ mice (left panel). Semi-quantitative RT-PCR transcriptional analysis of mouse tissues. Primers were located in exons 10 (Fw) and 12 (Rv), yielding 334 bp fragments for wild-type lamin A-encoding transcripts and 184 bp fragments for progerin-encoding transcripts (middle panel). The smaller transcript from liver was sequenced, confirming the internal 150 nt deletion and the aberrant junction between exons 11 and 12 (right panel), as indicated on the representation of the terminal part of the lamin A transcript.

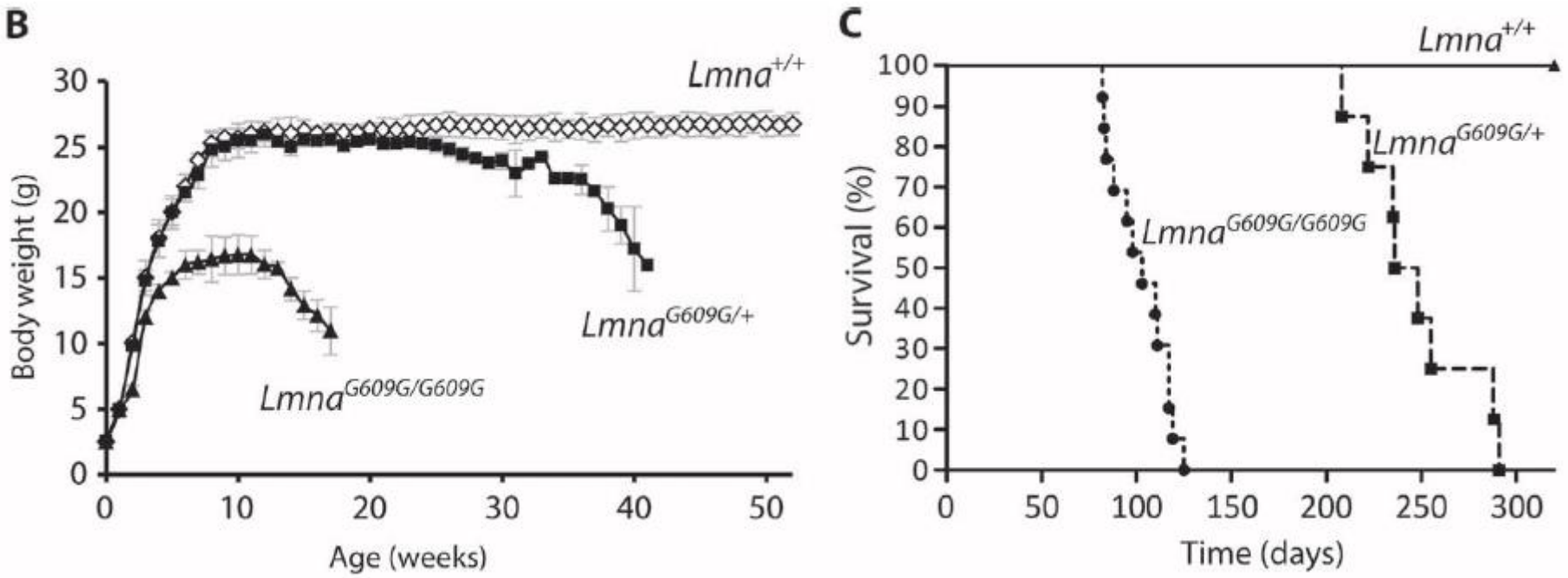
CONDITIONAL TRANSGENIC MICE
PROGERIN MODEL

PHENOTYPE

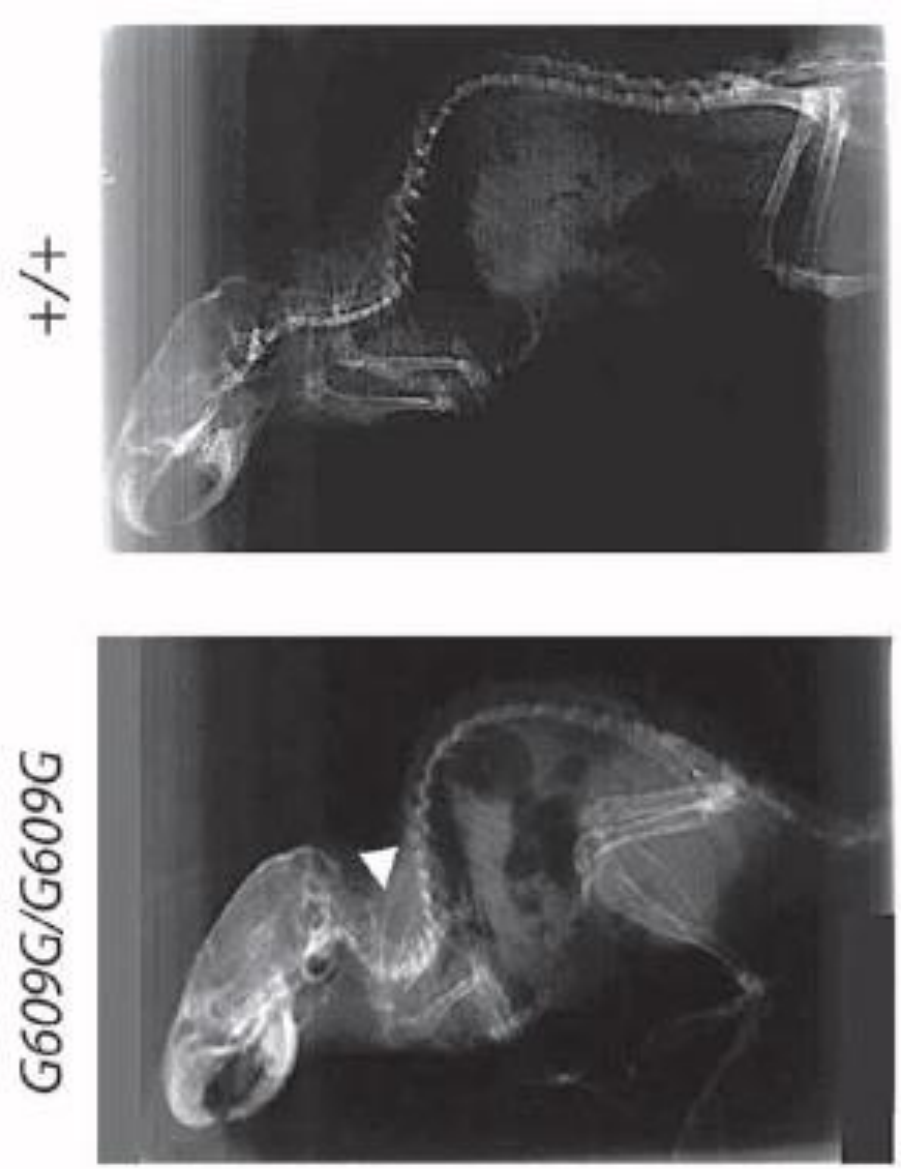
Lmna G609G has reduction in growth rates



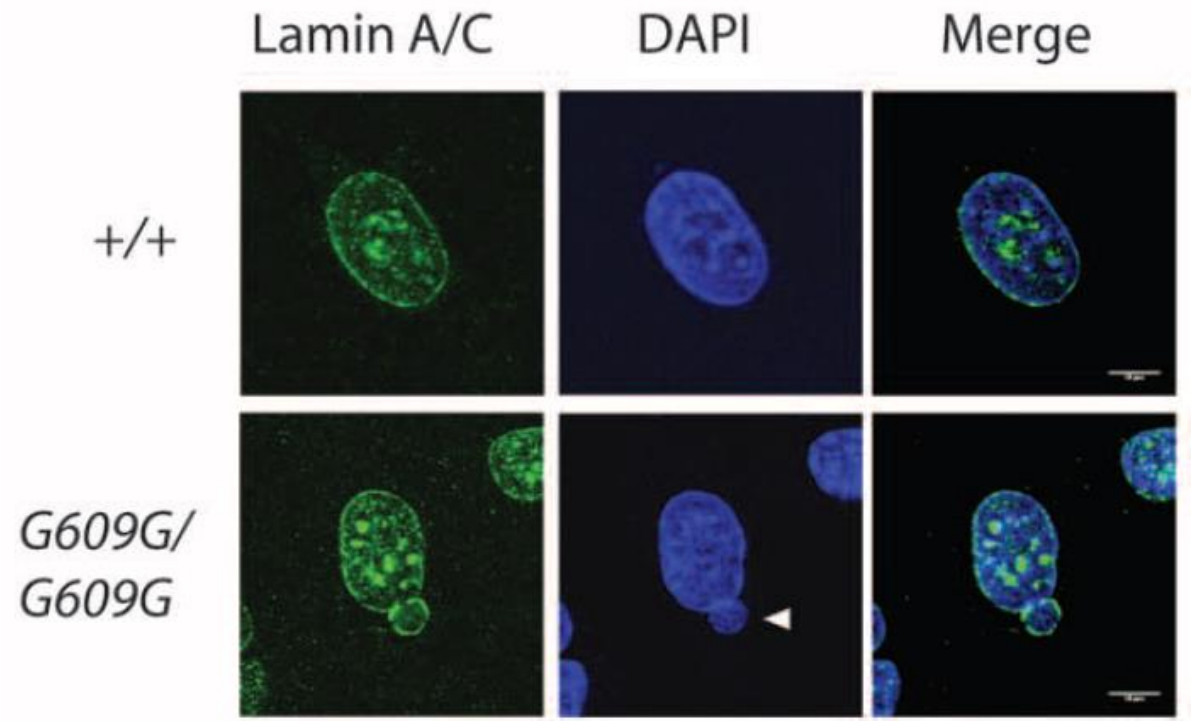
Lmna G609G has loss of weight and short life

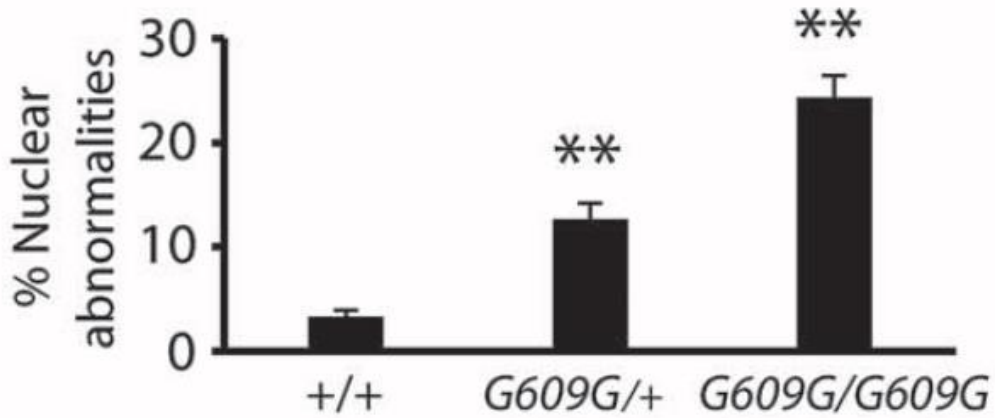


Lmna G609G has a marked curvature of the spine (cervicothoracic lordokyphosis)

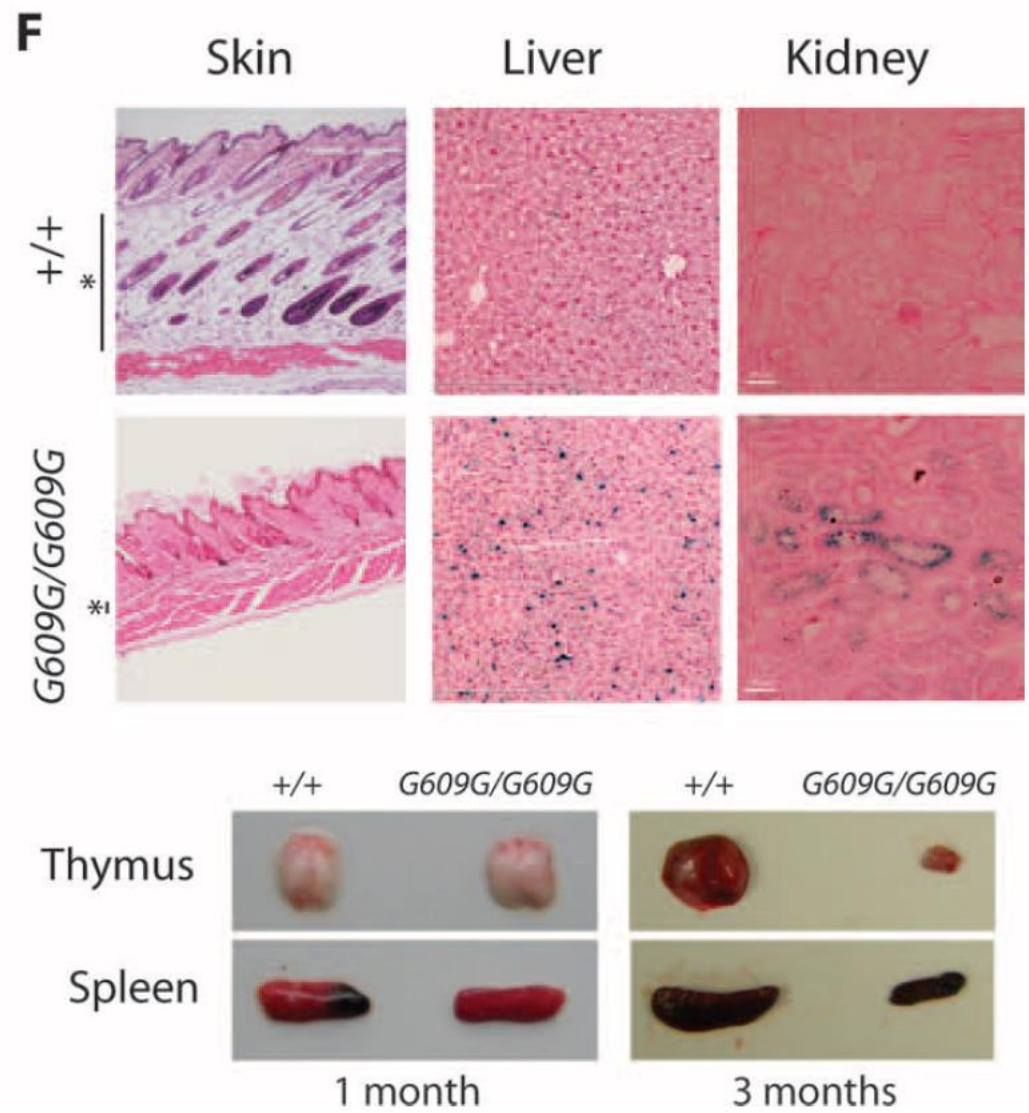


Progerin distribution is altered in mutant mice
Using immunofluorescence assay by confocal microscopy

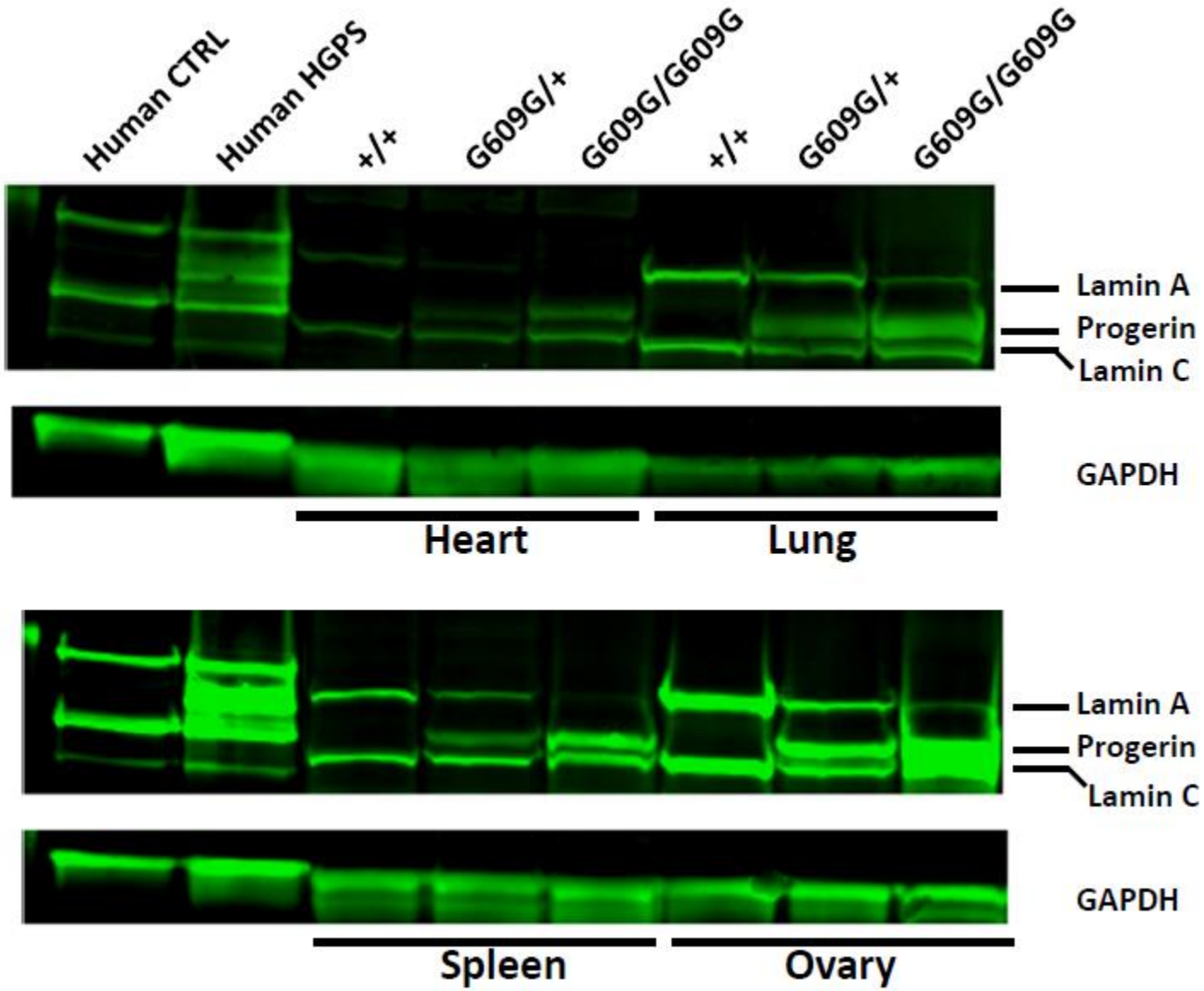




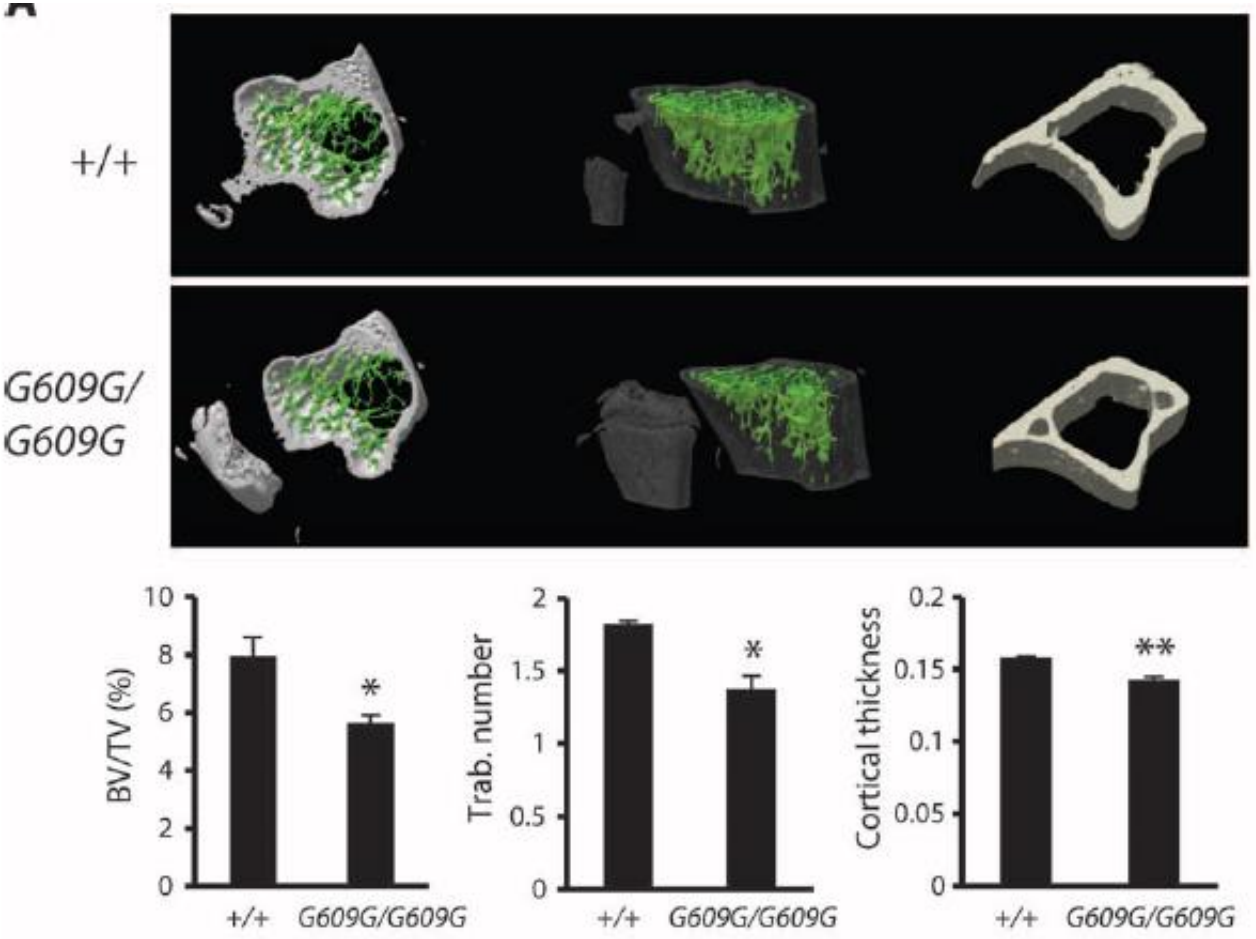
Tissue Senescence are tested using b-galattosidase



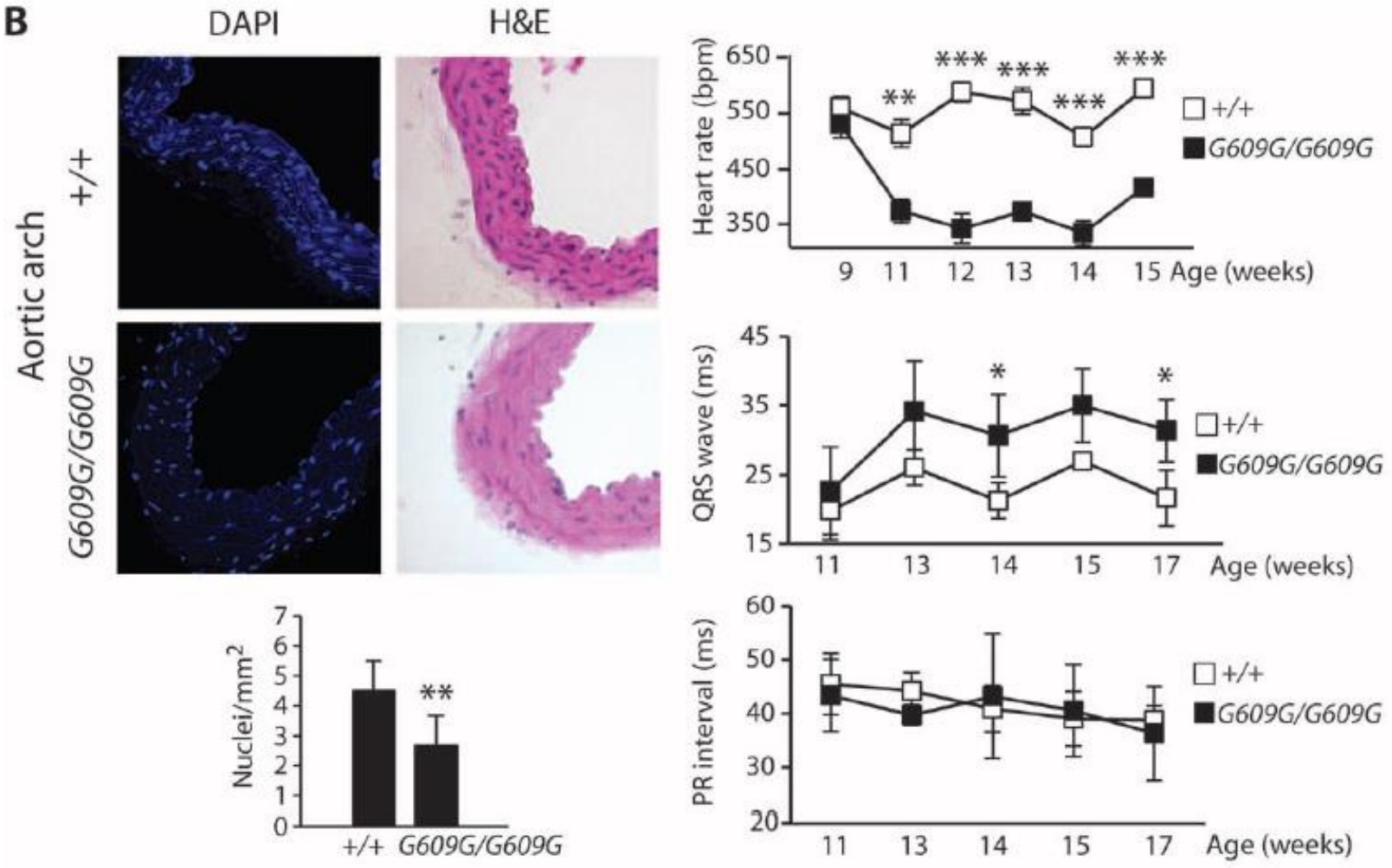
Progerin and laminin types are tested in several mice tissues



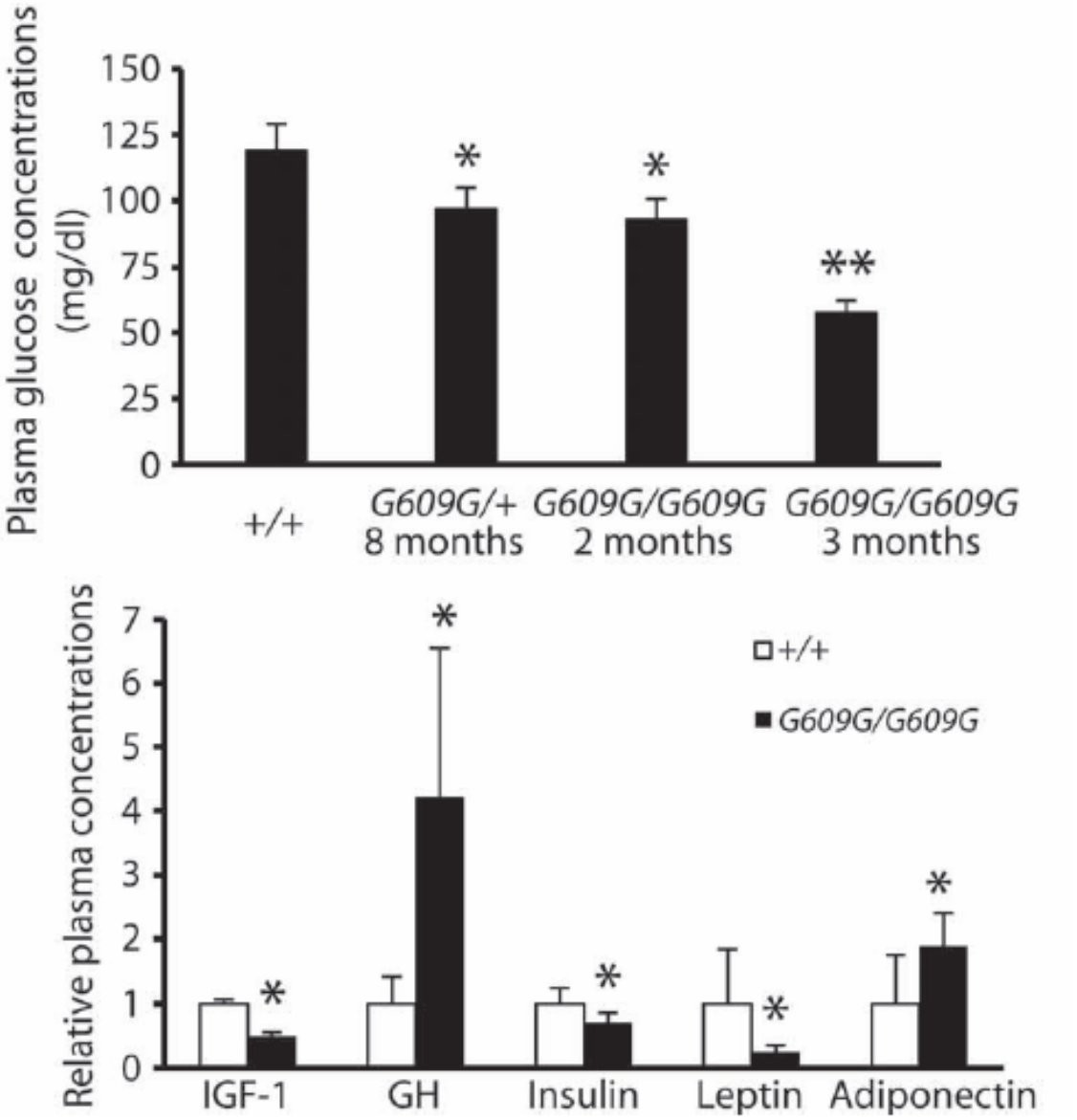
Tibias of mutant mice showed a reduction in bone density and cortical thickness as well as an increased porosity



Alteration of heat parameters functionality

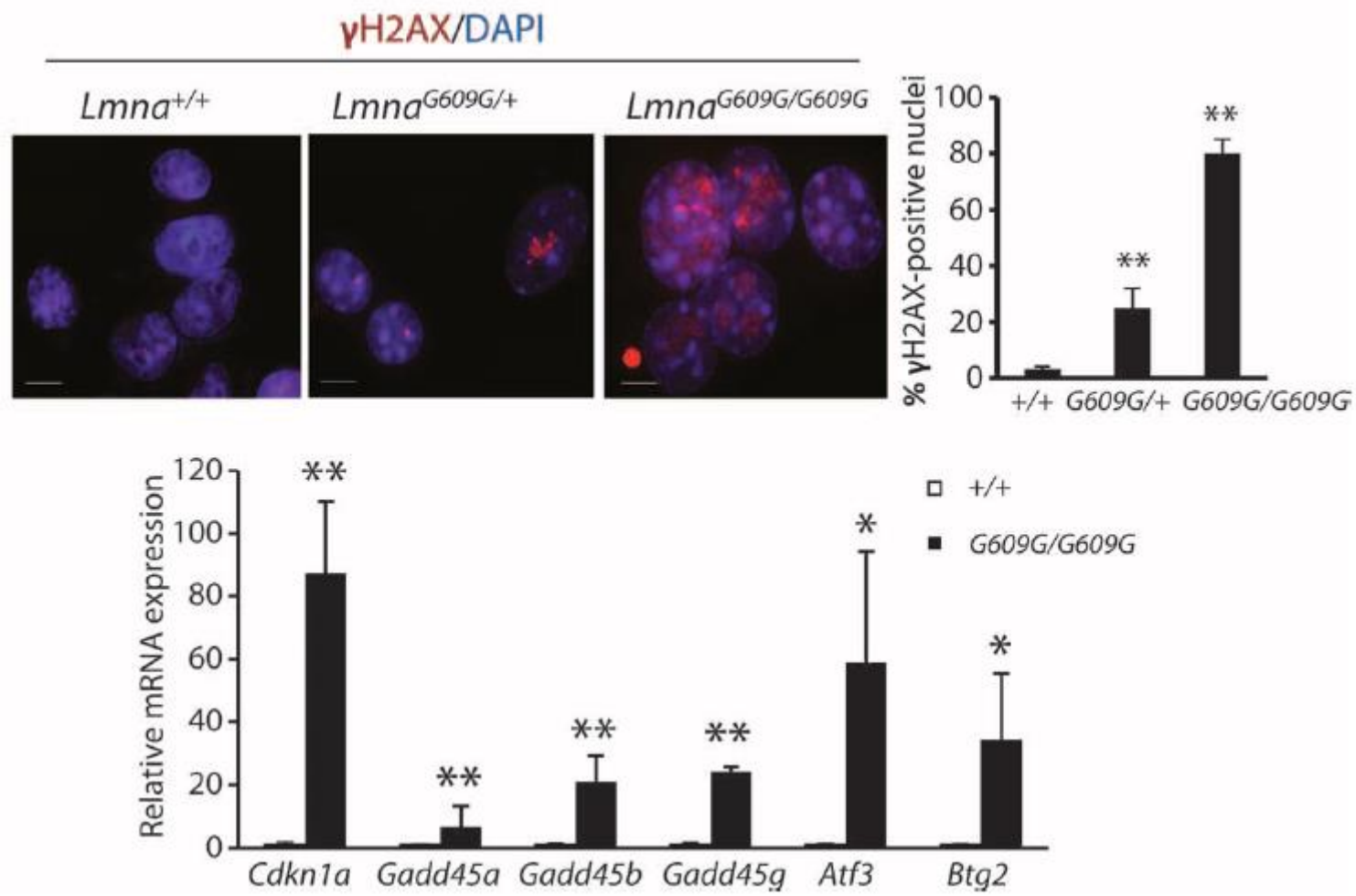


Alteration of glucose concentration and hormones associated with metabolism



DNA damage and gene validation of microarray

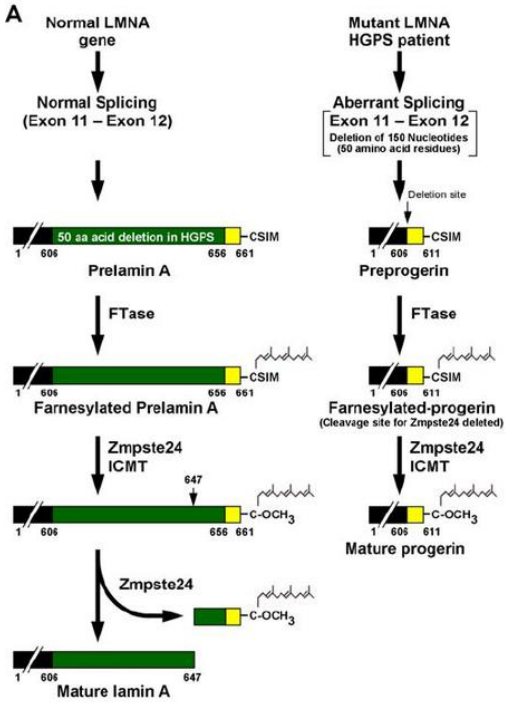
H2AX, marker for the amount of nuclear DNA double-strand breaks

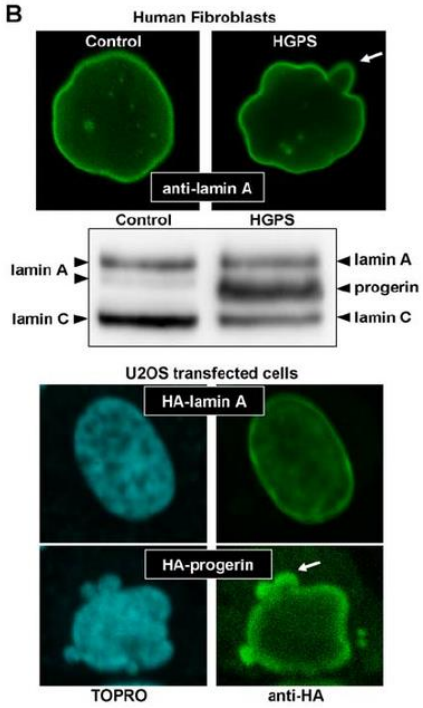


PROGERIA MODEL
CONDITIONAL TRANSGENIC MICE

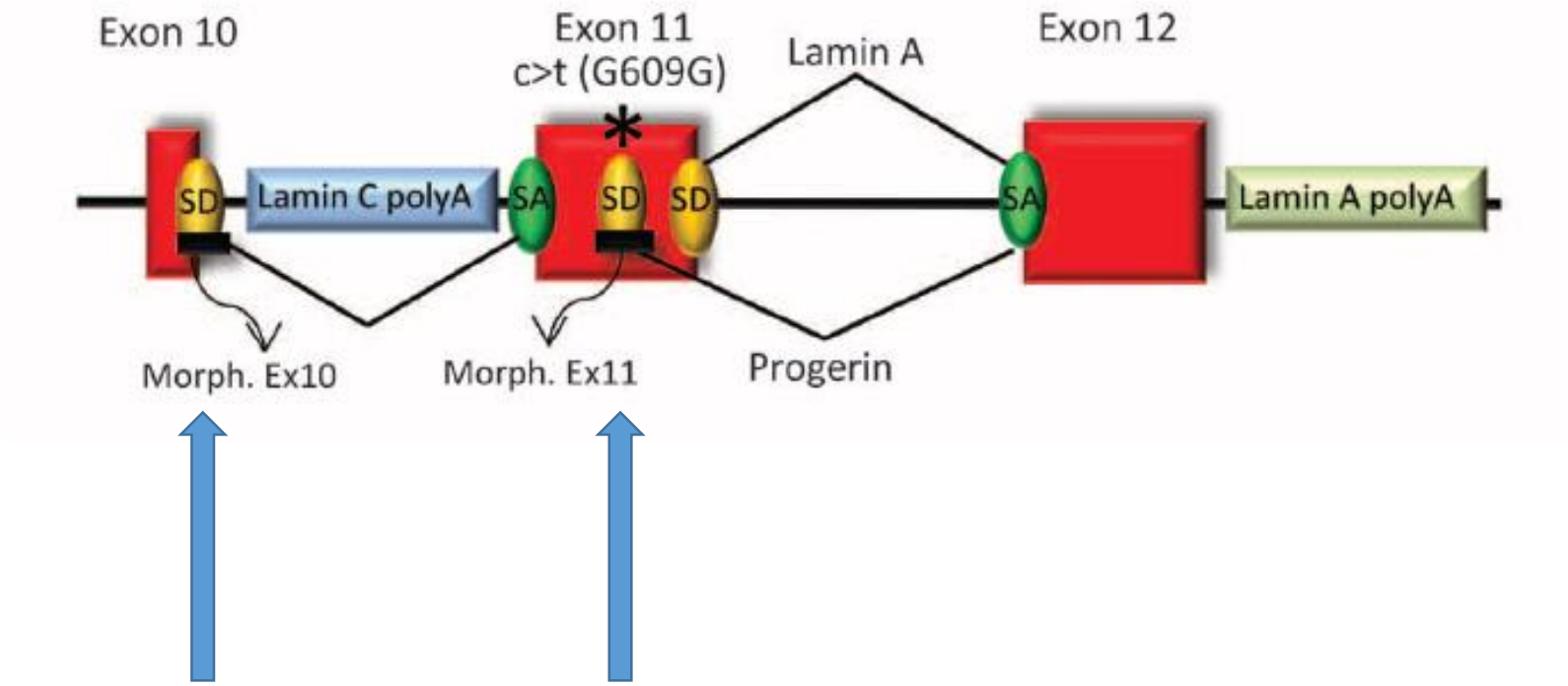
- Lmna G609G has reduction in growth rates and body weight
- Lmna G609G changes in cytoskeleton structure
- Lmna G609G is associated with blebbing membrane (bleb is a protrusion of cell membrane) and DNA damage
- Lmna G609G has tissues senescence and changes in organs size

THERAPHY


A
Normal LMNA gene
Normal Splicing (Exon 11 – Exon 12)
50 aa acid deletion in HGPS
CSIM
1 606 656 661
Prelamin A
FTase
Farnesylated Prelamin A
Zmpste24
ICMT
647
C-OCH3
Mature lamin A
Mutant LMNA HGPS patient
Aberrant Splicing Exon 11 – Exon 12
Deletion of 150 Nucleotides (50 amino acid residues)
Deletion site
1 606 611
Preprogerin
Farnesylated-progerin
(Cleavage site for Zmpste24 deleted)
Mature progerin


B
Human Fibroblasts
Control
HGPS
anti-lamin A
lamin A
lamin C
progerin
U2OS transfected cells
HA-lamin A
HA-progerin
TOPRO
anti-HA

Schematic representation of the morpholino-based strategy for Lmna splicing modulation



Morpholino target regions

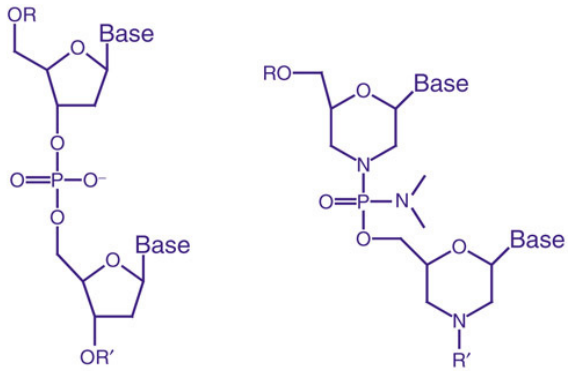
MORFOLINO

Morfolino are molecules similar to **RNA or DNA** with nitrogenous bases,

morpholine rings are linked through **uncharged phosphorodiamidate groups,**

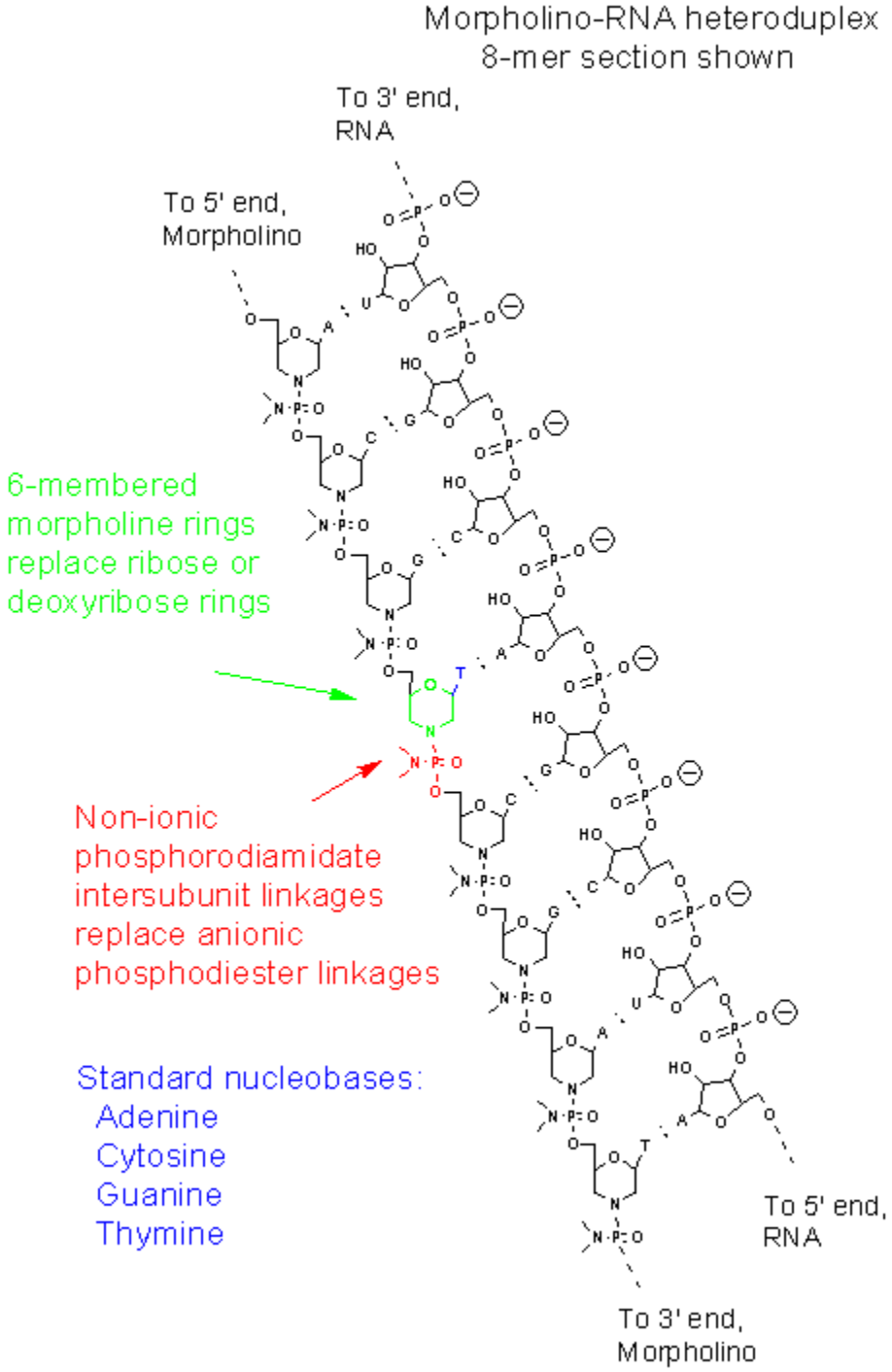
Morfolinos are 18–30 bases in length and **bind to targeted RNA sequences by base pairing**,

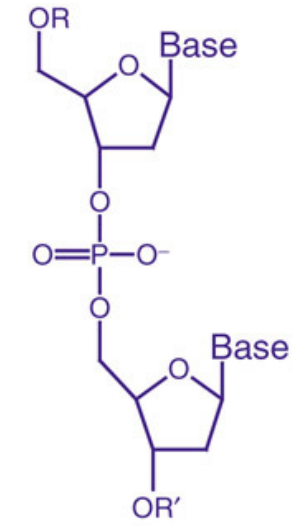
phosphorodiamidate morpholino oligomers (PMOs or Morpholinos) do not result in degradation of their target RNA: not recognized by cellular nucleases.



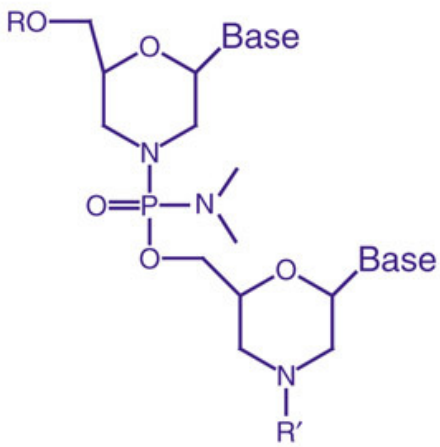
Phosphodiester DNA

Morpholino





Phosphodiester
DNA



Morpholino

Phosphorodiamidate group

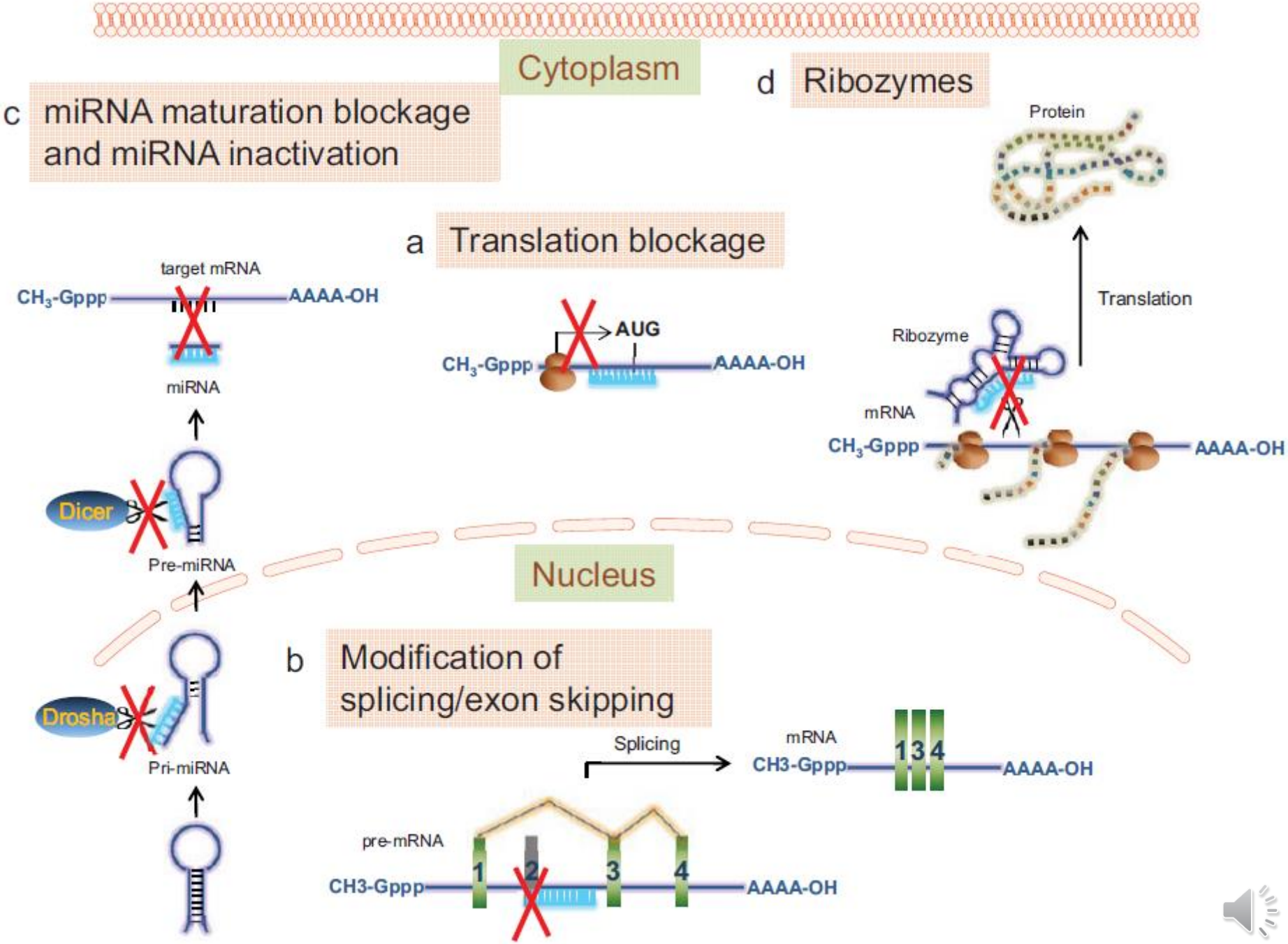
Mechanisms of action of antisense morpholino oligomers.

(a) **Translational blockage**. PMOs block the translation initiation complex binding sites on mRNA and prevent translation from occurring.

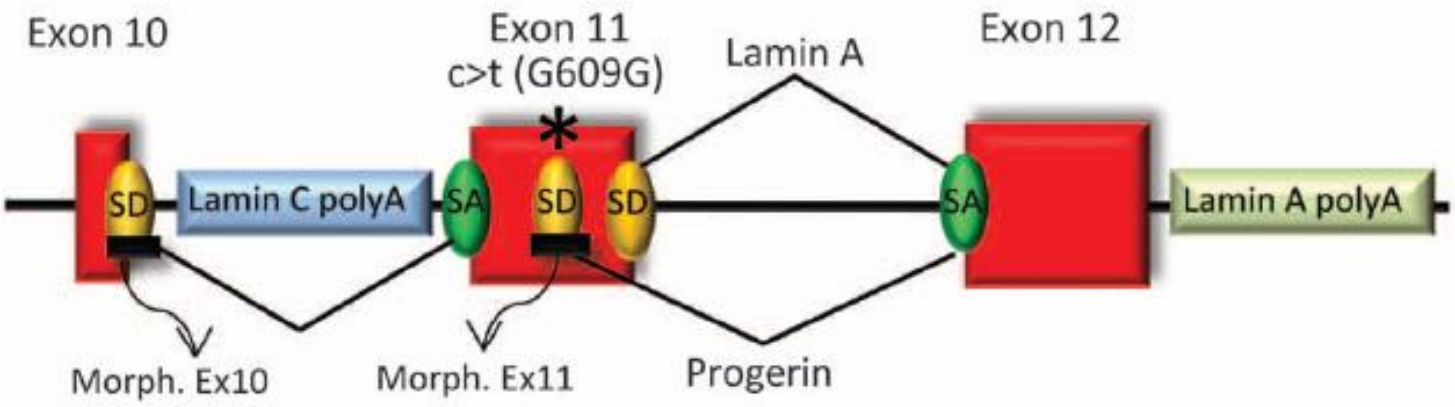
(b) **Modification of splicing/exon skipping**. PMOs block splice sites on pre-mRNA, prevent recognition of these sites by the spliceosome that in turn causes exon skipping.

(c) **miRNA maturation blockage and miRNA inactivation**. PMOs may block maturation enzyme cleavage sites (i.e., Drosha, Dicer) on pri- or pre-miRNA to prevent its maturation. PMOs may complementarily bind to mature miRNA and prevent it from binding to target mRNA.

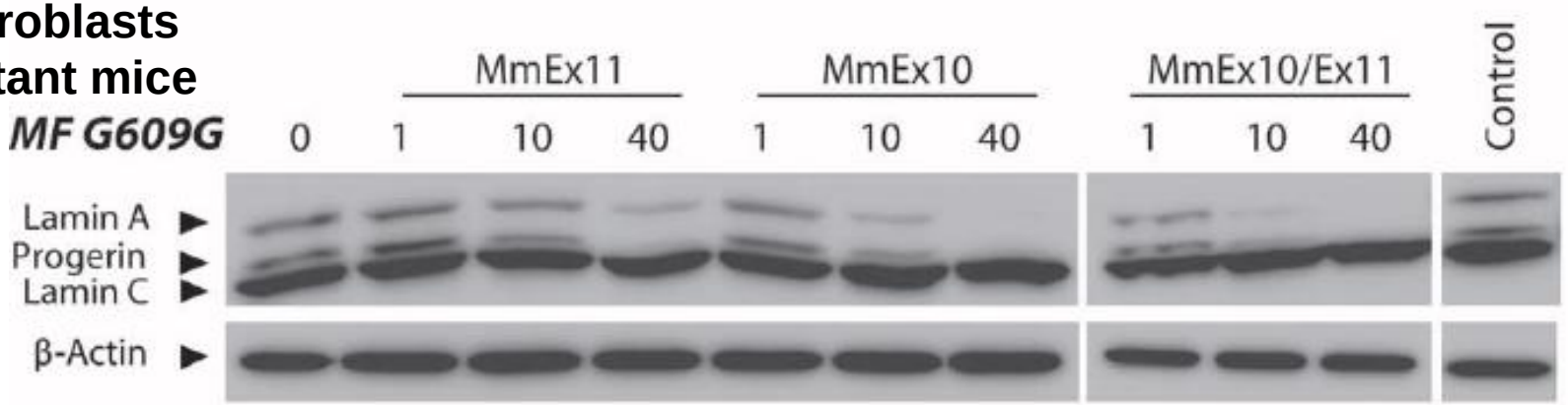
(d) **Ribozymes.** PMOs may bind to enzymatically active RNAs (ribozymes), blocking their active sites and preventing them from cleaving their target mRNAs.


Cytoplasm
c miRNA maturation blockage and miRNA inactivation
d Ribozymes
Protein
a Translation blockage
target mRNA
CH3-Gppp
AAAA-OH
AUG
Translation
Ribozyme
mRNA
miRNA
Dicer
Pre-miRNA
Nucleus
b Modification of splicing/exon skipping
Drosha
Pri-miRNA
Splicing
mRNA
CH3-Gppp
1 3 4
AAAA-OH
pre-mRNA
1 2 3 4

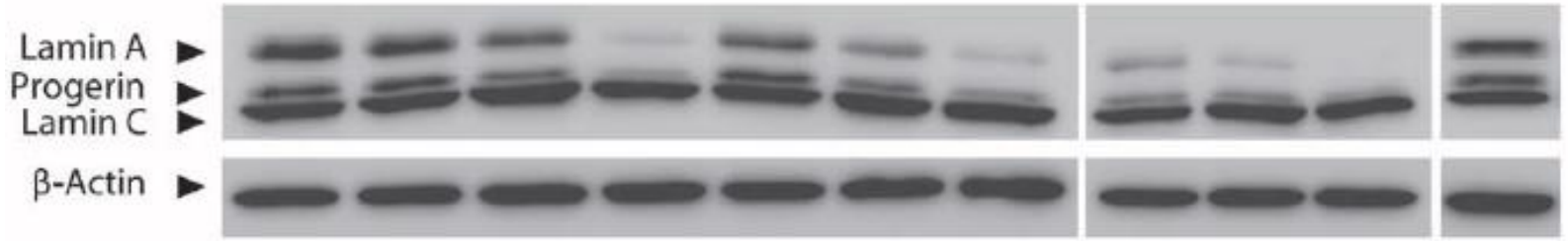
Both MmEx10 and MmEx11 morpholinos each reduced progerin amount in a dose-dependent manner



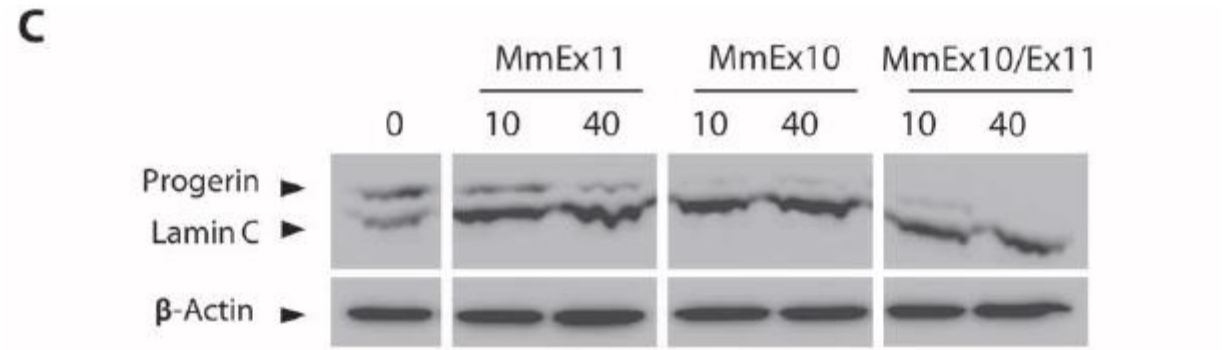
Fibroblasts mutant mice

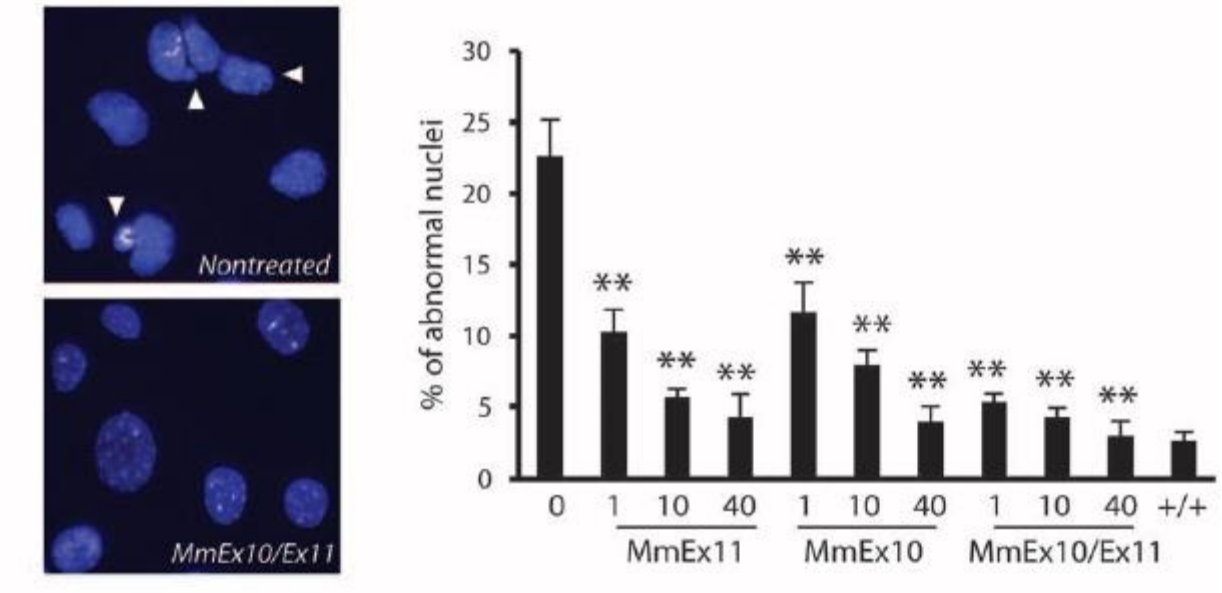


HF G608G **Fibroblasts from patients**



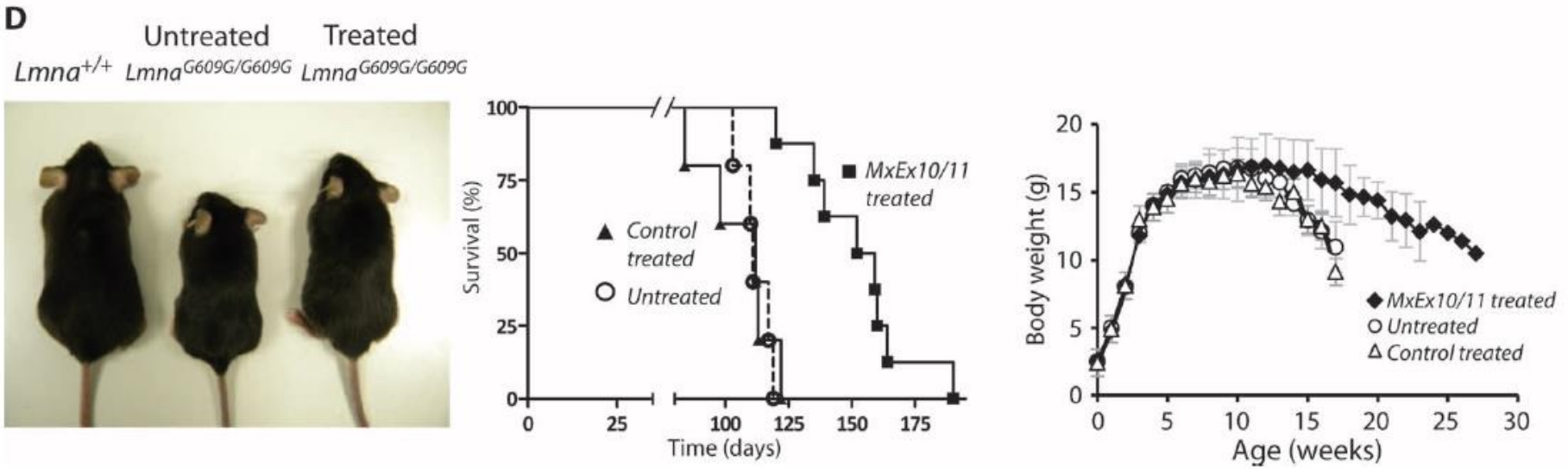
MmEx10 and MmEx11 inhibited progerin production



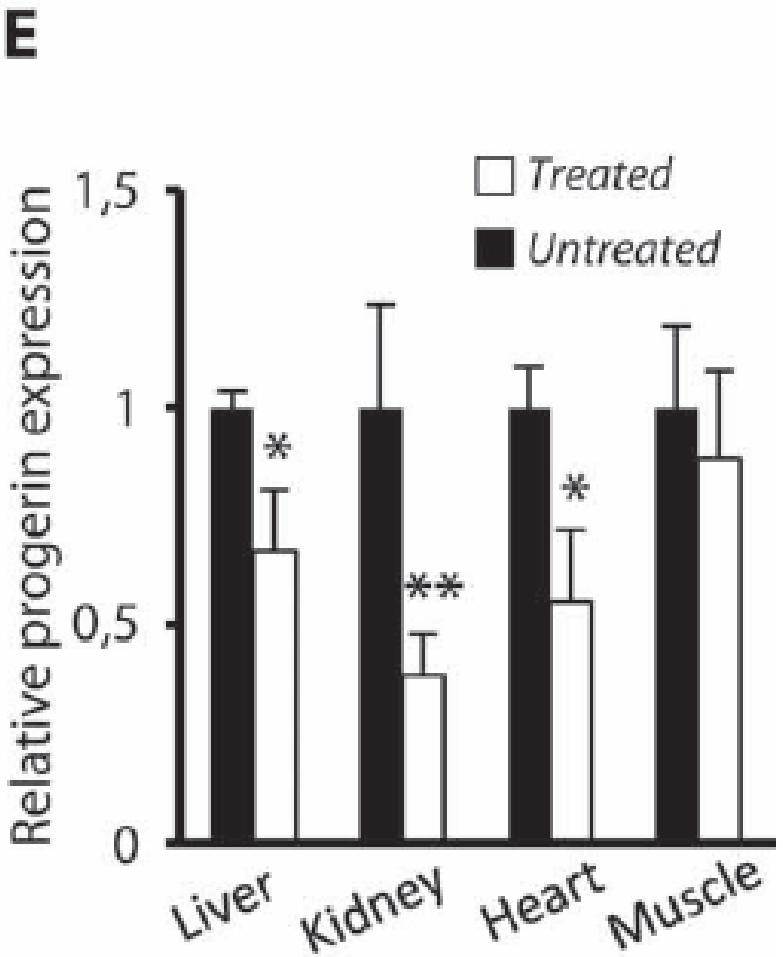


MmEx10 and MmEx11 induced reduction of nucleus abnormalities

MmEx10 and MmEx11 increased survival and restored normal body weight



MmEx10 and MmEx11 inhibited progerin production in several tissues



nature medicine

BRIEF COMMUNICATION

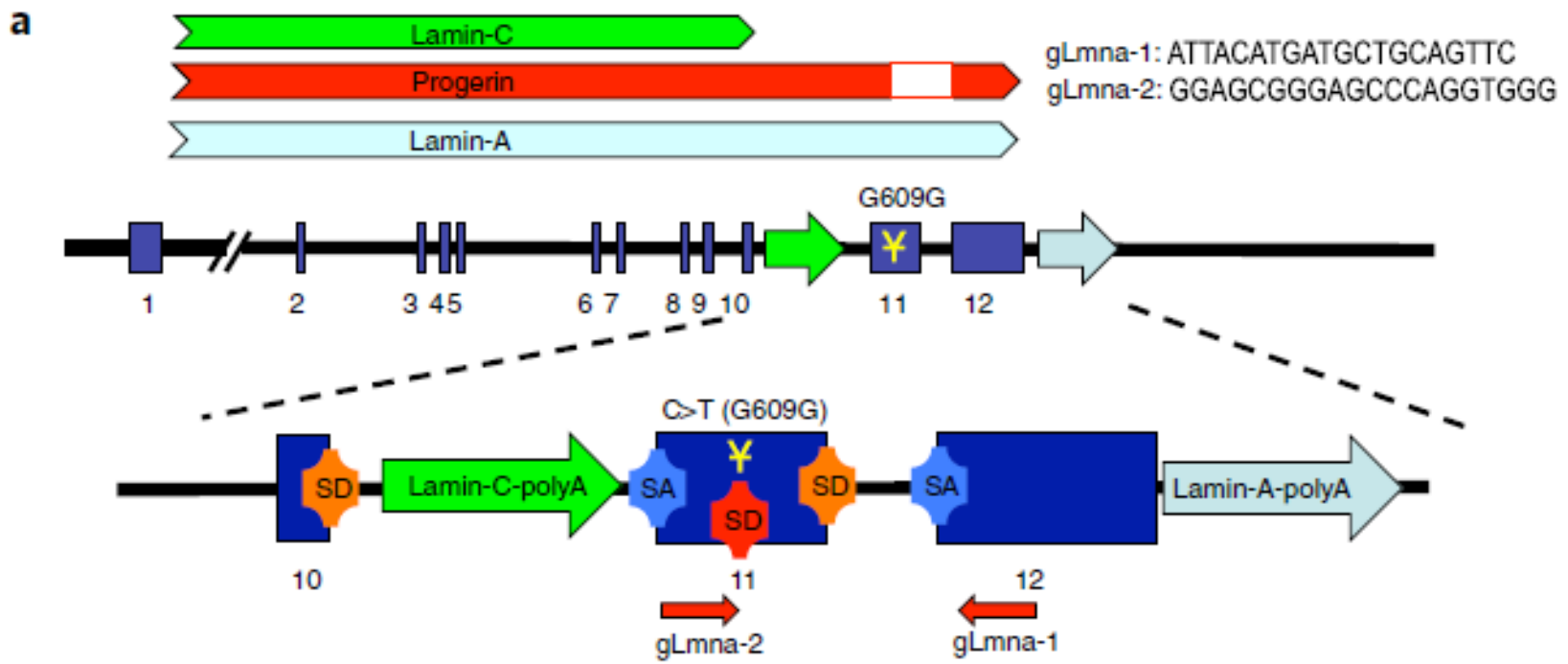
https://doi.org/10.1038/s41591-019-0343-4

Single-dose CRISPR–Cas9 therapy extends lifespan of mice with Hutchinson–Gilford progeria syndrome

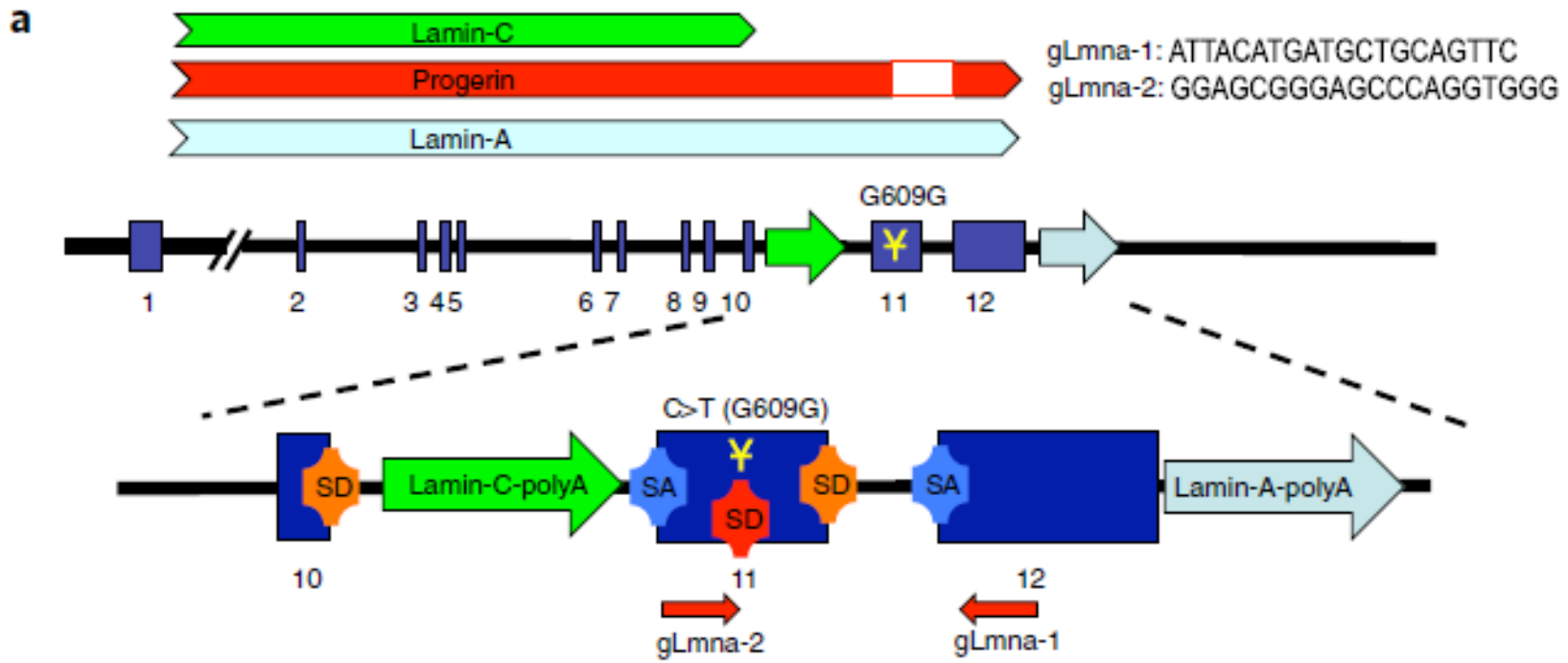
Ergin Beyret[1,3], Hsin-Kai Liao[1,3], Mako Yamamoto[1,2], Reyna Hernandez-Benitez[1], Yunpeng Fu[1], Galina Erikson[1], Pradeep Reddy[1] and Juan Carlos Izpisua Belmonte[1*]

NATURE MEDICINE | VOL 25 | MARCH 2019 | 419–422 |

Induction of the corresponding **mutation in the mouse (Gly609Gly)** induces phenotypes similar to those in human patients. On the other hand, lamin A appears to be dispensable, possibly due to compensation from its shorter isoform, lamin C14,15, and mice without lamin A live longer than wild-type (WT) mice, indicating that HGPS results not from lack of lamin A but from the accumulation of progerin. Therefore, **HGPS can be treated by CRISPR–Cas9-targeted disruption of lamin A/progerin.**

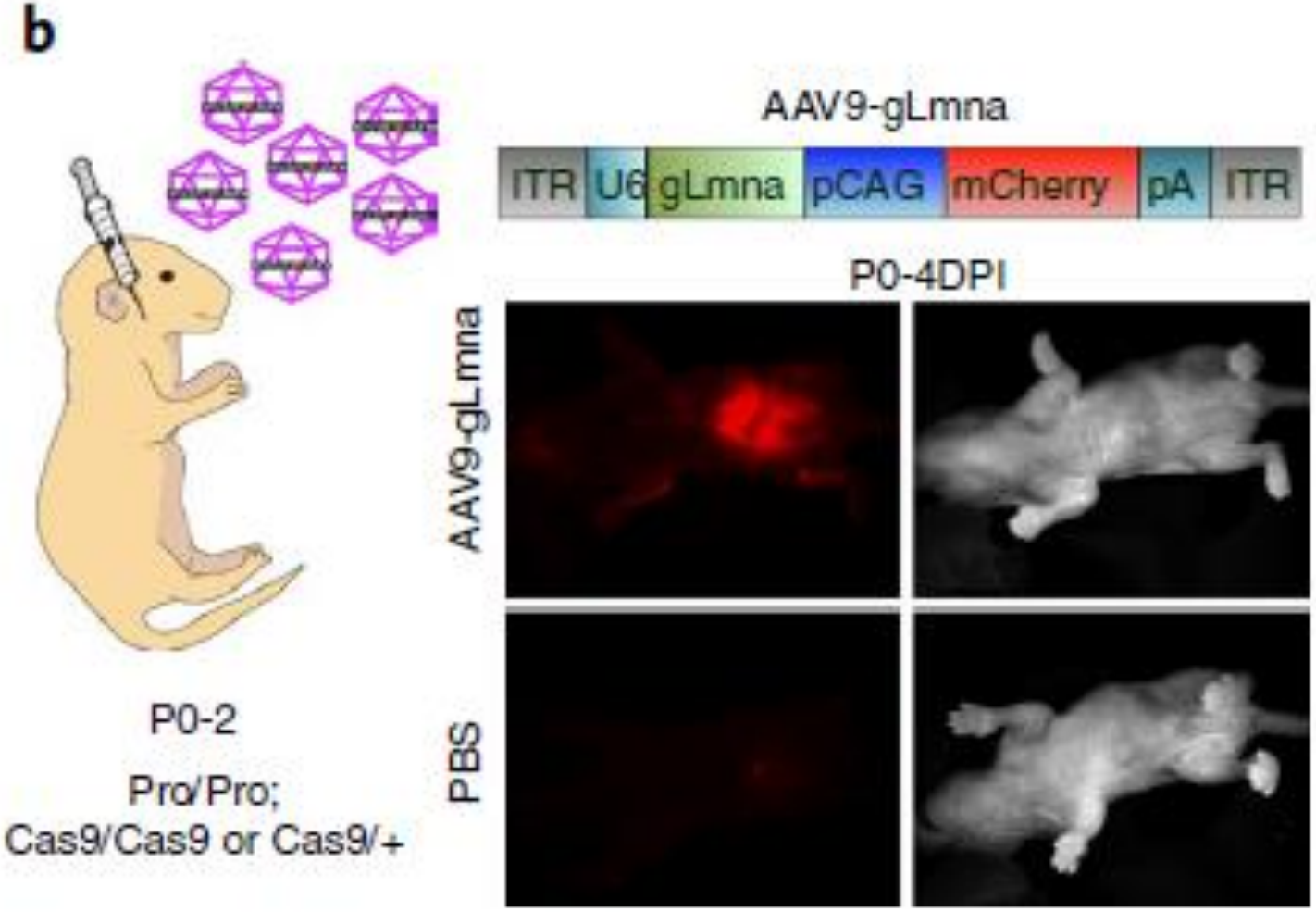


Two guide RNAs (gRNAs; gLmna-1 and gLmna-2) for *Streptococcus pyogenes* Cas9 targeting lamin A downstream of lamin C were designed to reduce lamin A/progerin without perturbing lamin C

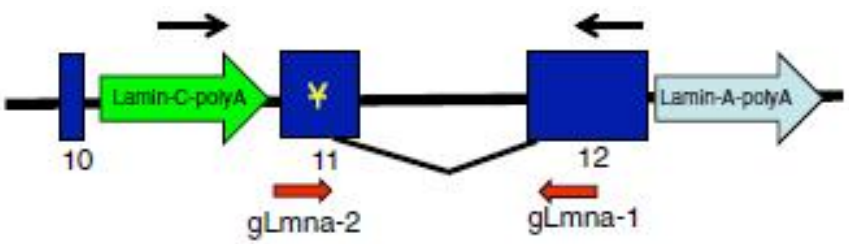


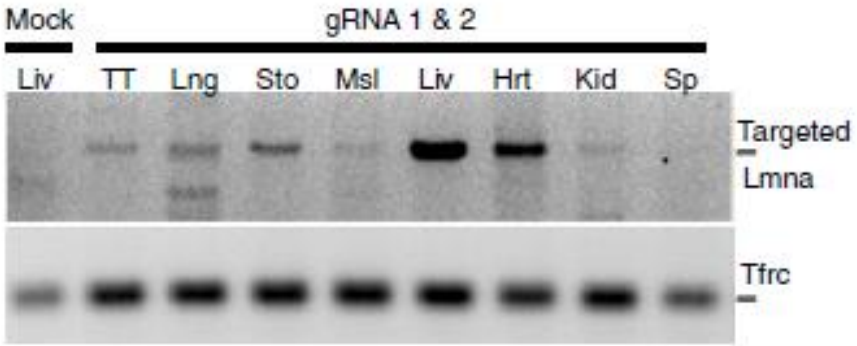
The in vivo gene therapy scheme.

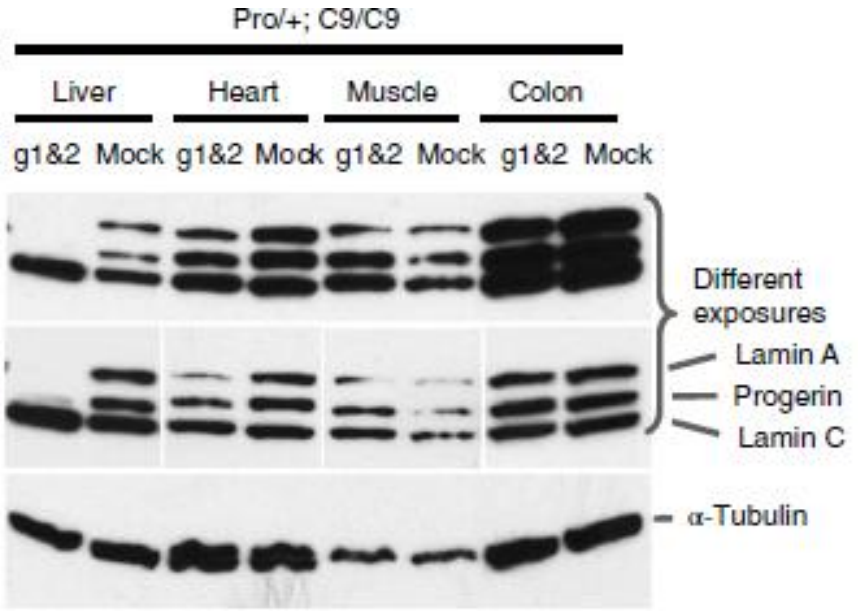
AAV9-mCherry-gLmna was injected into 0- to 2-day-old mice (P0-2). Upper panels show the mCherry signal 4 days post-injection (DPI) of a P0 mouse (P0-4DPI) versus the PBS-injected control (lower panels).



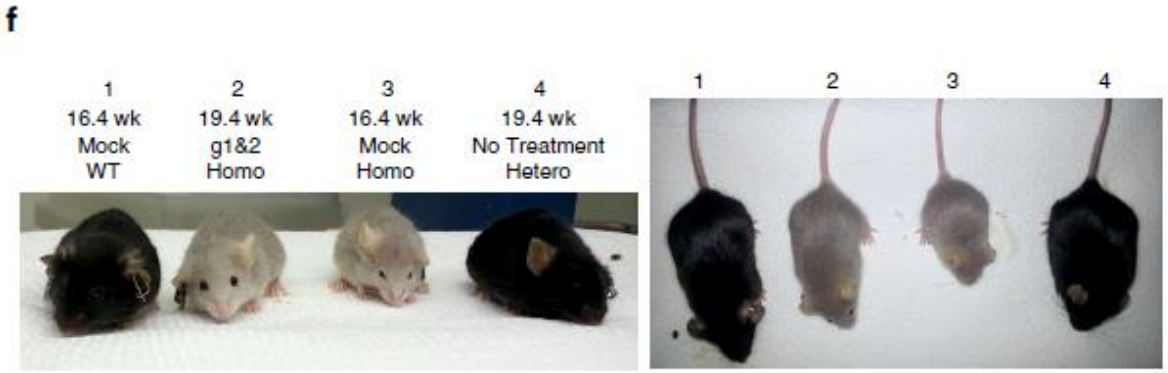
Effect of RNA guides versus splincing sites at exon 11-12 on proteins expression in different tissues

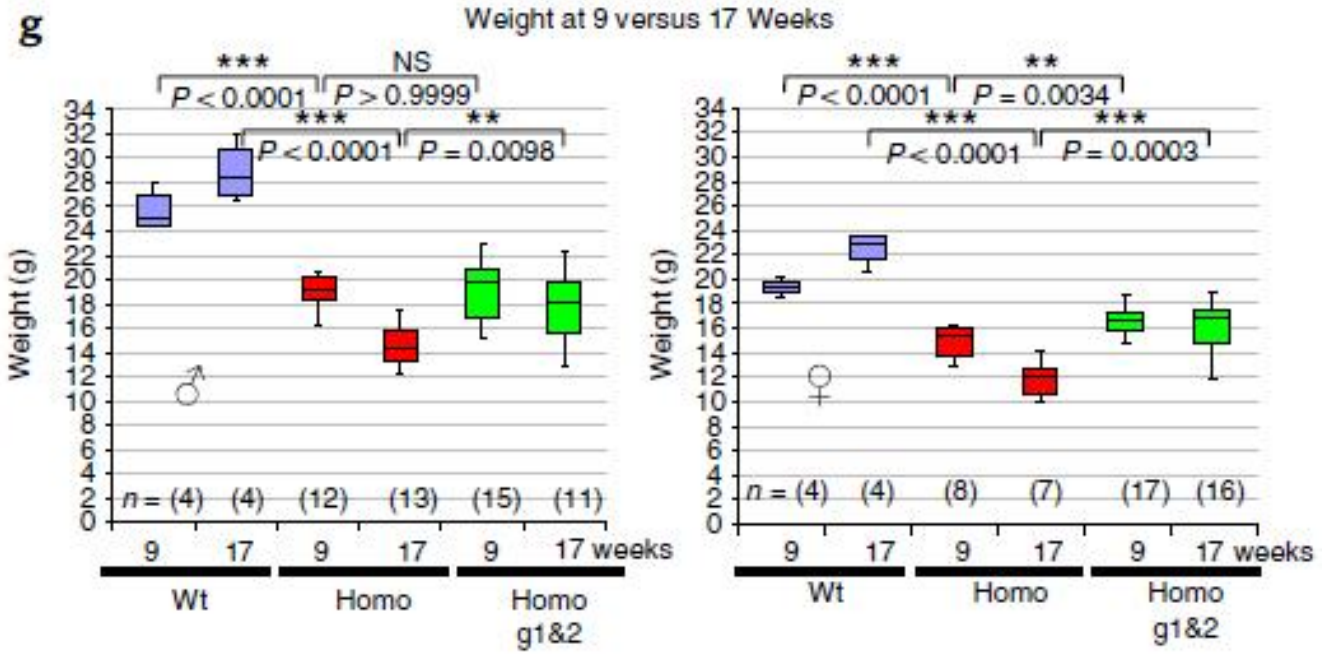






Effect of RNA guides versus splincing sites at exon 11-12 on weight





nature medicine

BRIEF COMMUNICATION

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Development of a CRISPR/Cas9-based therapy for Hutchinson–Gilford progeria syndrome

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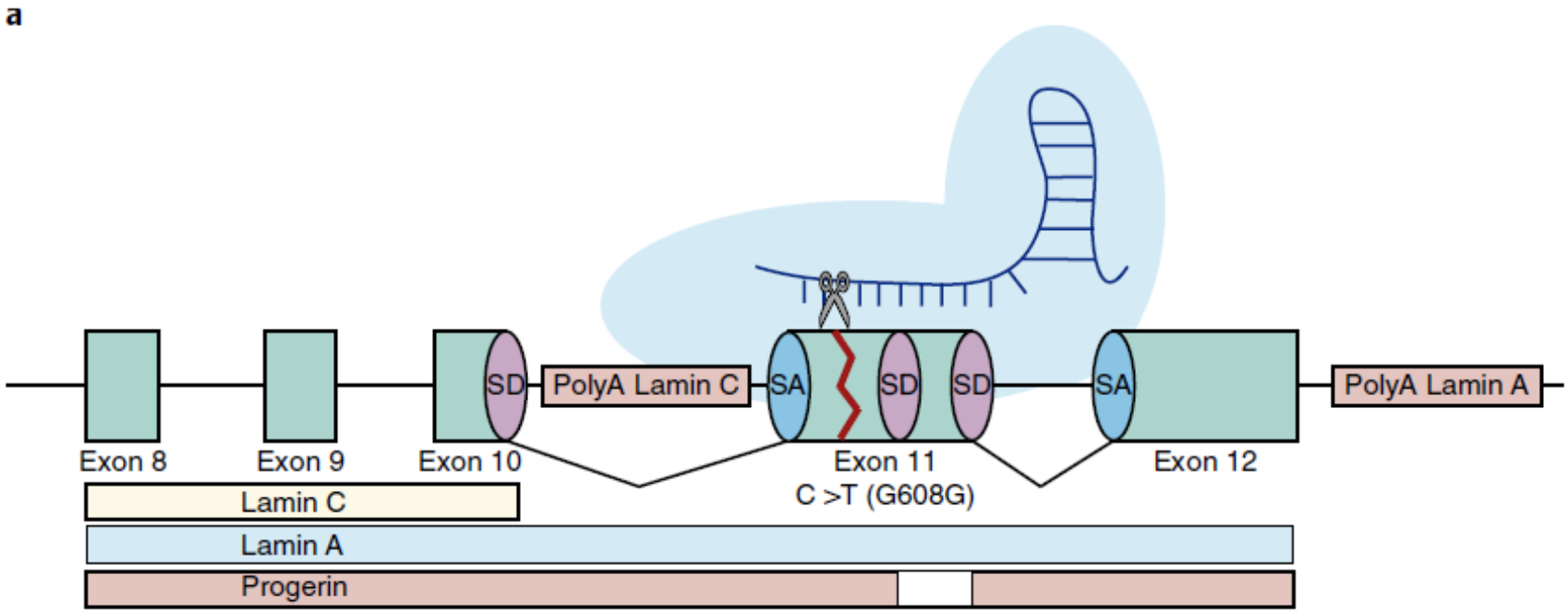
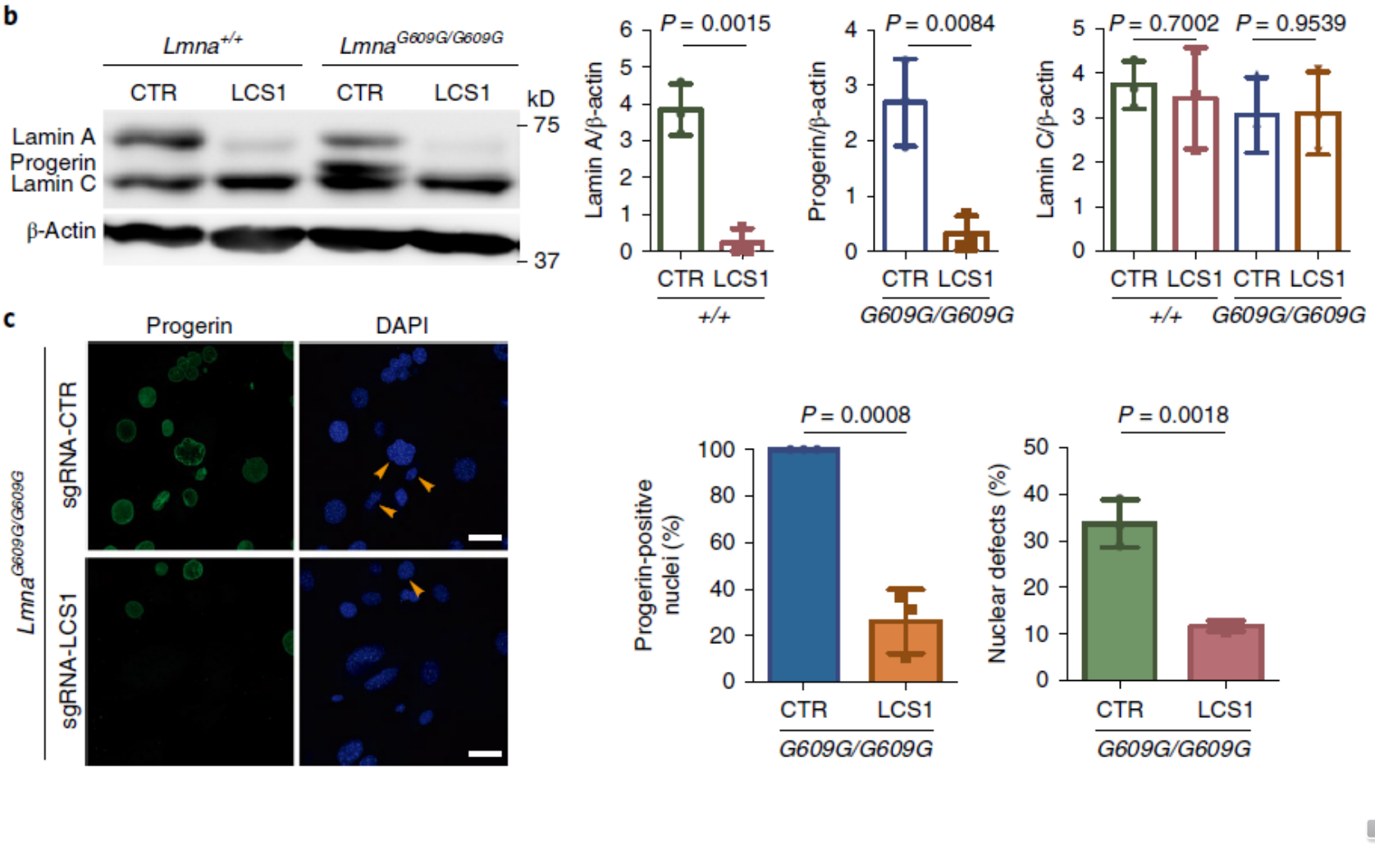
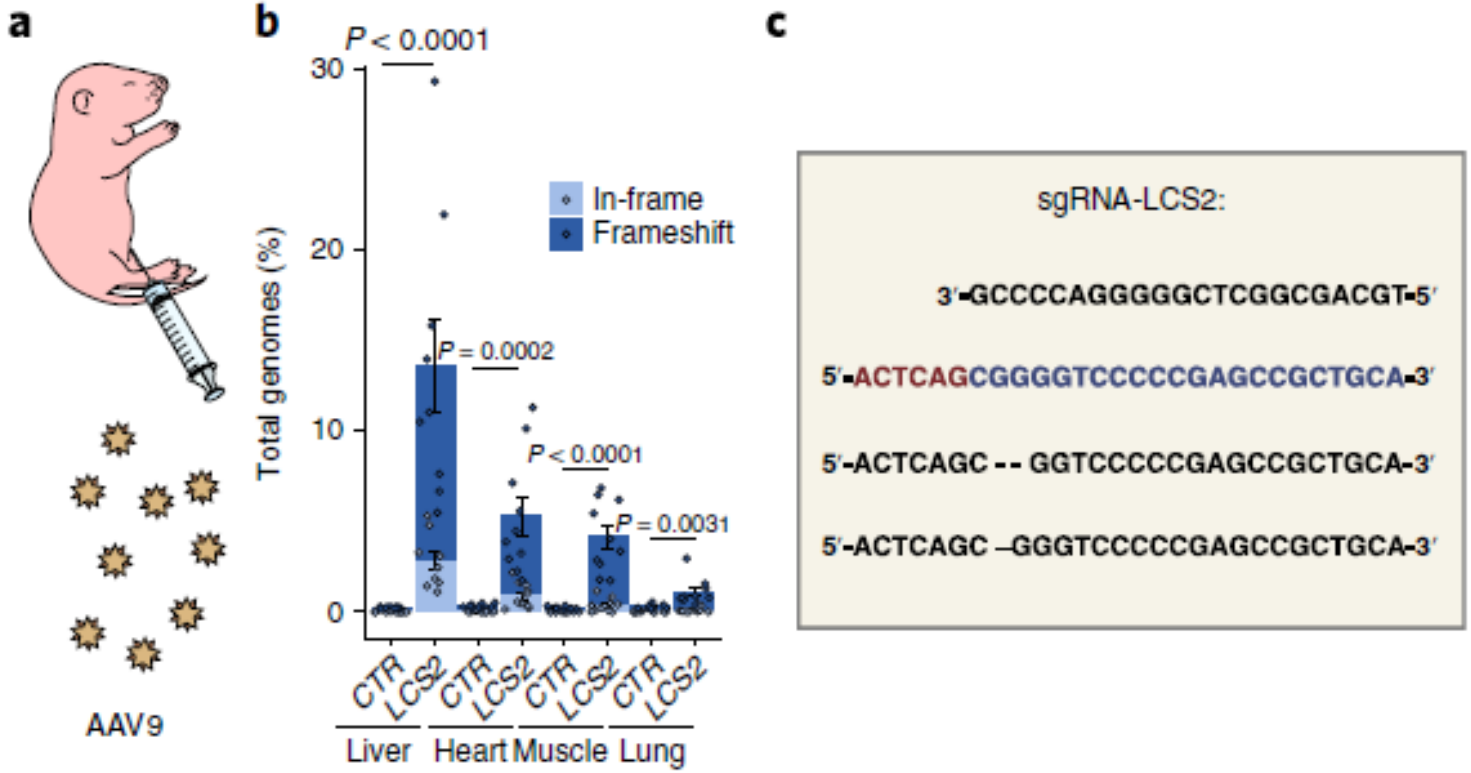
CRISPR/Cas9-based therapies hold considerable promise for the treatment of genetic diseases. Among these, Hutchinson-Gilford progeria syndrome, caused by a point mutation in the *LMNA* gene, stands out as a potential candidate. Here, we explore the efficacy of a CRISPR/Cas9-based approach that reverts several alterations in Hutchinson-Gilford progeria syndrome cells and mice by introducing frameshift mutations in the *LMNA* gene.


a
SD
PolyA Lamin C
SA
SD
SD
SA
PolyA Lamin A
Exon 8
Exon 9
Exon 10
Exon 11
C >T (G608G)
Exon 12
Lamin C
Lamin A
Progerin

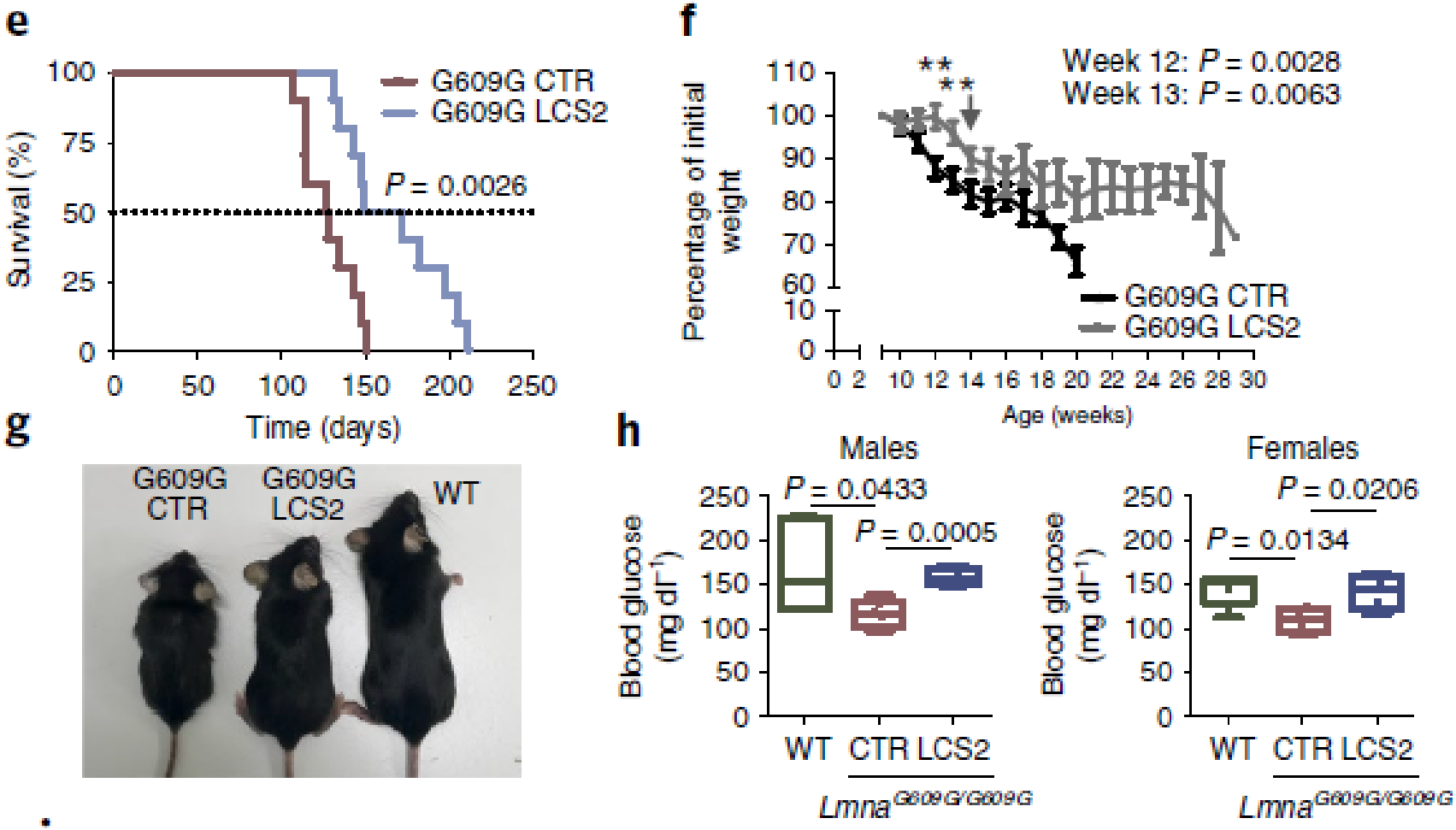
LCS1 reduced Lamin A and progerin, no changed LaminC, and nuclear blebbing



LCS2 effect on genome in several tissues



Progerin reduction in AAV9-sgRNA-LCS2- transduced mice was translated into an increase in their survival, growth and blood glucose level



IN SUMMARY:

- **High order of chromatin structure is a component for TRANSCRIPTION REGULATION**
- **Alteration of LAMININ A, important in chromatin organization, induces PROGERIA**
- **MICE MODEL IS USED TO STUDY MOLECULAR MECHANISM IN DISEASE PROGRESSION**