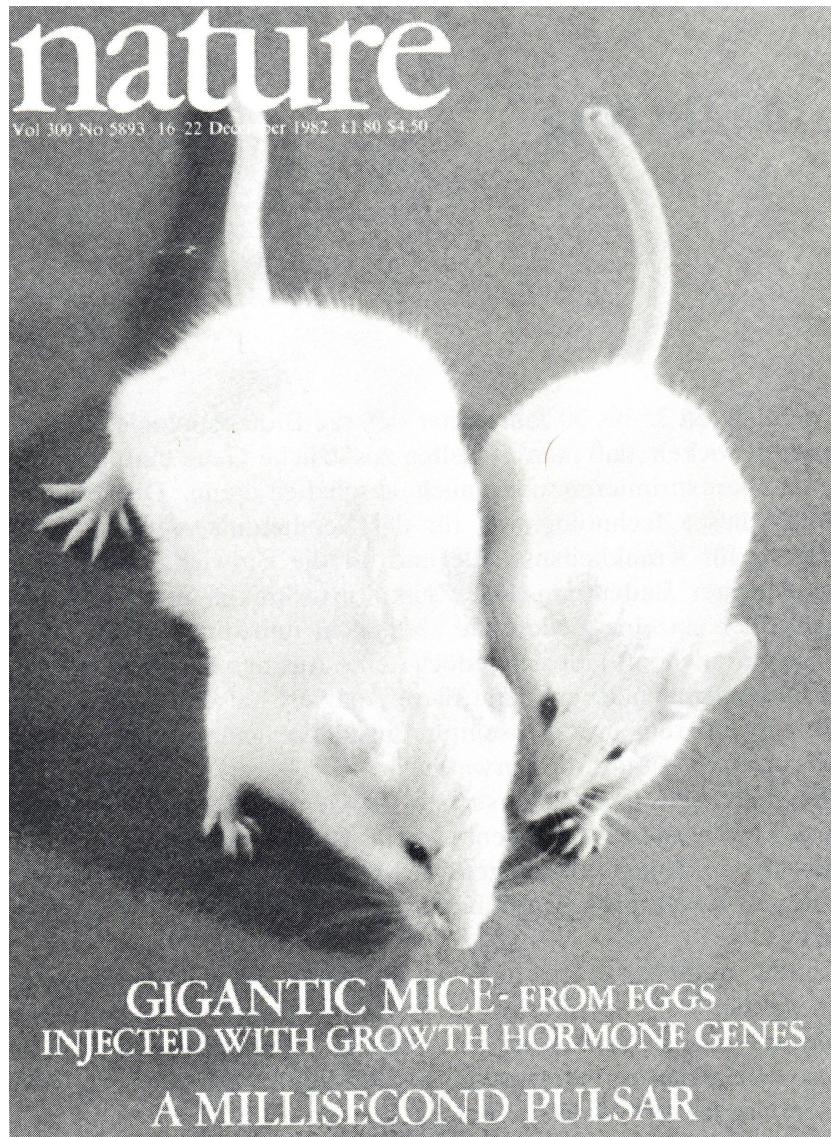
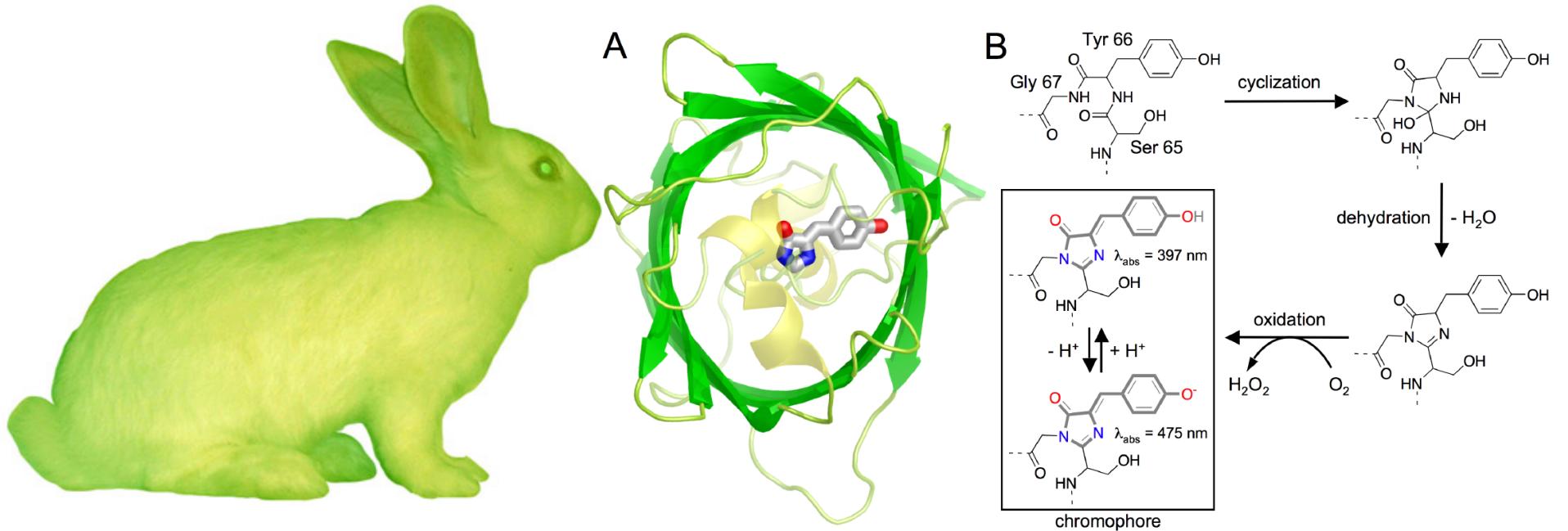


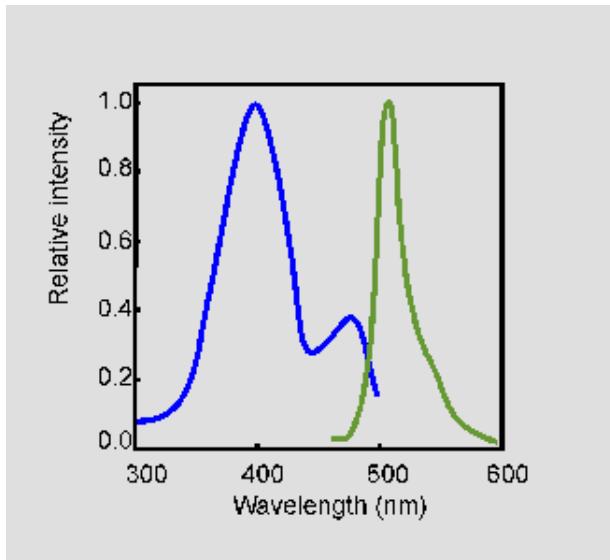
Genetische Modelle in der Immunologie

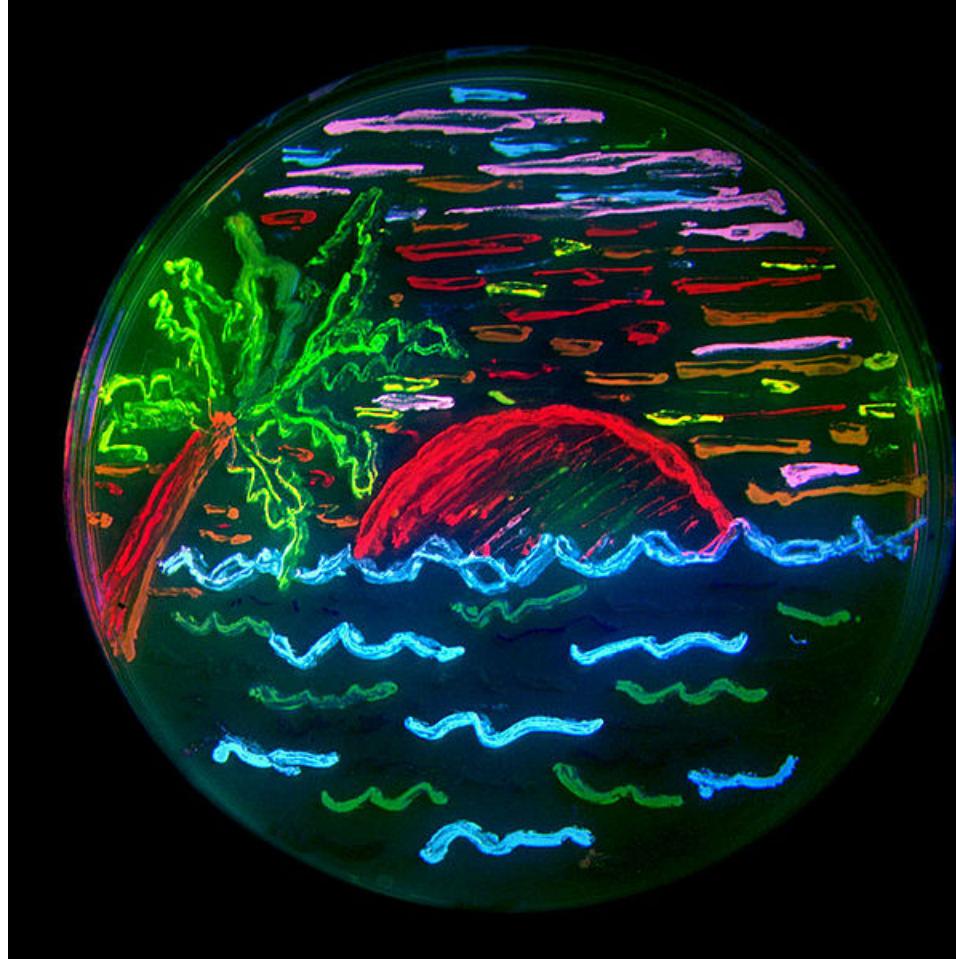


Priv.-Doz. Dr. Michael Stassen



(E)GFP: (Enhanced) Green Fluorescent Protein
238 aa Protein aus der Qualle *Aequorea victoria*





GFP-Mutanten und dsRed (Korallen-Spezies)

Reportergene

Vorlesungsinhalt

- Kongene, isogene und Inzuchtstämme der Maus
- Einschleusen von DNA in Zellen *in vitro* und in die Keimbahn *in vivo*
- Herstellung transgener Mäuse
- „Gene targeting“ klassisch: „Knock out“ und „Knock in“
- Konditionale Mutagenese: Das cre / loxP-System
- Gezielte Zell-Ablation: Diphterietoxin / Diphterietoxin-Rezeptor System
 - CRISPR gene-editing tested in a person for the first time**
The move by Chinese scientists could spark a biomedical duel between China and the United States.
- „Gene targeting 2.0“: Das CRISPR/Cas9-System **David Cyranoski**
15 November 2016

Maus: Zucht und Genetik

Mausgenom: 1650 cM, 20 Chromosomen (haploid), 20.210 Gene (Mensch: 19.042)

15.178 Gene bei Maus und Mensch haben gemeinsame Vorläufer (orthologe Gene)

(Trennung Nager / Primaten vor etwa 70 Millionen Jahren)

Dies sind rund 75% der Maus- und 80% der menschlichen Gene

Generationszeit etwa 3 Monate

Bis zu 8 Würfe mit bis zu 8 Jungen pro Jahr möglich

Geschlechts-/Zuchtreif mit 6/8 Wochen

Tragzeit 21 Tage

Inzuchtstämme

Mind. 20 Bruder x Schwester Paarungen mit zunehmender Homozygotie (!)
Problem: Zucht-Depression versus Heterosis

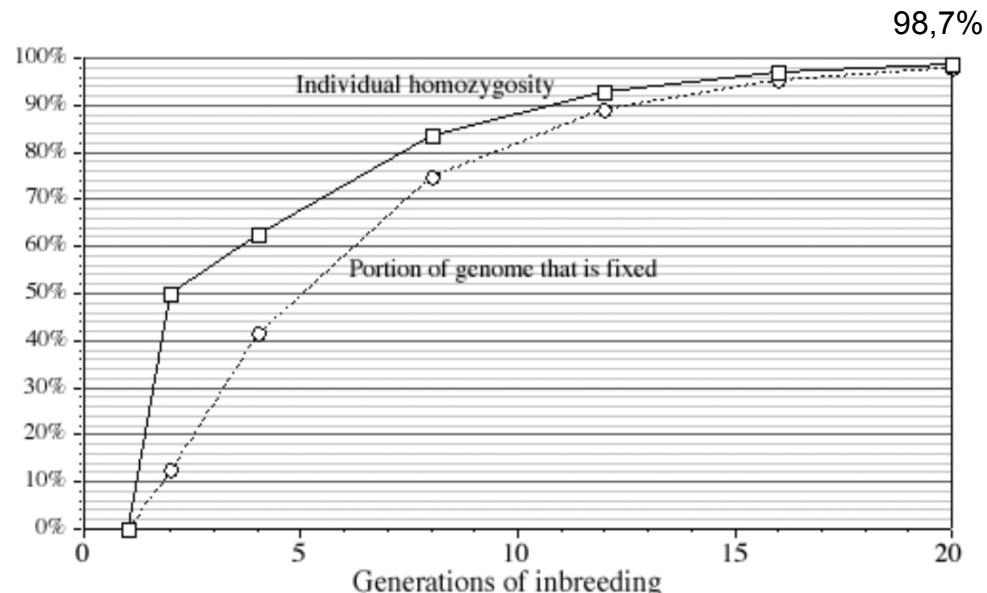
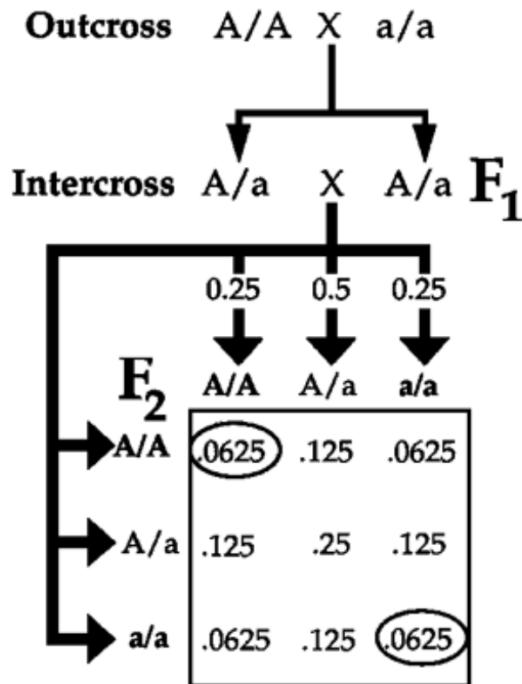


Figure 3.1 Consequences of inbreeding at the F₂ generation. The first cross illustrated is an outcross between animals homozygous for alternative alleles at the A locus. The F₁ offspring are all identically heterozygous A/a. An intercross between two F₁ animals will produce an F₂ generation with three possible genotypes having the probabilities shown. The final box indicates the different combinations of F₂ by F₂ matings that are possible and the probabilities associated with each one. The two mating combinations that cause fixation for one allele are circled. This illustration of the process of inbreeding is based on two simplifying assumptions: (1) genetic homogeneity in each of the original parents used for the outcross, and (2) contrasting alleles at every locus in these original parents. In actuality, inbreeding is often begun with parents that, on the one hand, are not homogeneous but, on the other hand, do share many alleles with each other.

Table 3.1 Some important inbred strains.
See also [Inbred Strains of Mice and Rats](#) at MGI.

Strain	Color	Major use	Other Characteristics	Origin	Generation ^a
129/Sv- <i>Sl</i> /+, <i>c⁺p⁺</i> (129)	Agouti	Source of most ES cell lines and genetic material used for homologous recombination. Used of studies of embryology and reproduction.	Relatively high testicular teratoma incidence. Relatively small size. Resistant to radiation.	~1930 (Dunn)	F79 (JAX)
BALB/c	Albino	Used in immunological studies and for the production of hybridomas. A new congenic strain BALB/cByJ-Rb(8.12)5Bnr available from JAX is most efficient for hybridoma production.	Docile females. Males of the J substrain only are extremely aggressive. Relatively poor breeders, but variation among sublines. Sensitive to radiation.	1913 (Bagg)	F105 (CR) F180 (JAX) F195 (Taconic)
C57BL/6 (B6)	Black	Standard strain for genetic studies; common backcross partner for congenic construction and mapping panels.	Relatively long lived and hearty. Excellent breeders. Resistant to radiation.	1921 (Little)	F160 (CR) F187 (JAX) F155 (Taconic)
C57BL/10 (B10)	Black	Commonly used in genetic studies performed outside of the US and for the construction of congenics at the H2 complex.	Common ancestry with B6.	1921 (Little)	F192 (JAX)
CAST/Ei	Agouti	Used in matings with traditional inbred strains to create F ₁ hybrids with high levels of heterozygosity for linkage studies. Better intercross reproductive performance than <i>M. spretus</i> strains.	Derived from wild animals of the subspecies <i>M. m. castaneus</i> . Male F ₁ hybrids formed with lab strains are fertile.	1971 (Marshall to Eicher)	F53 (JAX)
C3H	Agouti	Used commonly in genetic studies.	High mammary tumor incidence. Large adults.	1920 (Strong)	F167 (CR) F139 (JAX) F160 (Taconic)
DBA/2	Dilute	Used in crosses with B6		1909	F164 (CR)

Kennzeichnung von Inzuchtstämmen und Substämmen

Die Individuen eines Inzuchtstammes sind alle gleichen Ursprungs, aber die Zuchtkolonien verschiedener Anbieter sind teilweise seit Jahrzehnten voneinander getrennt, was eine langsame genetische Drift erlaubt (Kontamination, restl. Heterozygosität, Mutation).

Tiere sollten immer vom selben Anbieter stammen !

C57BL/6

C57BL/6J

C57BL/6NCrlBR

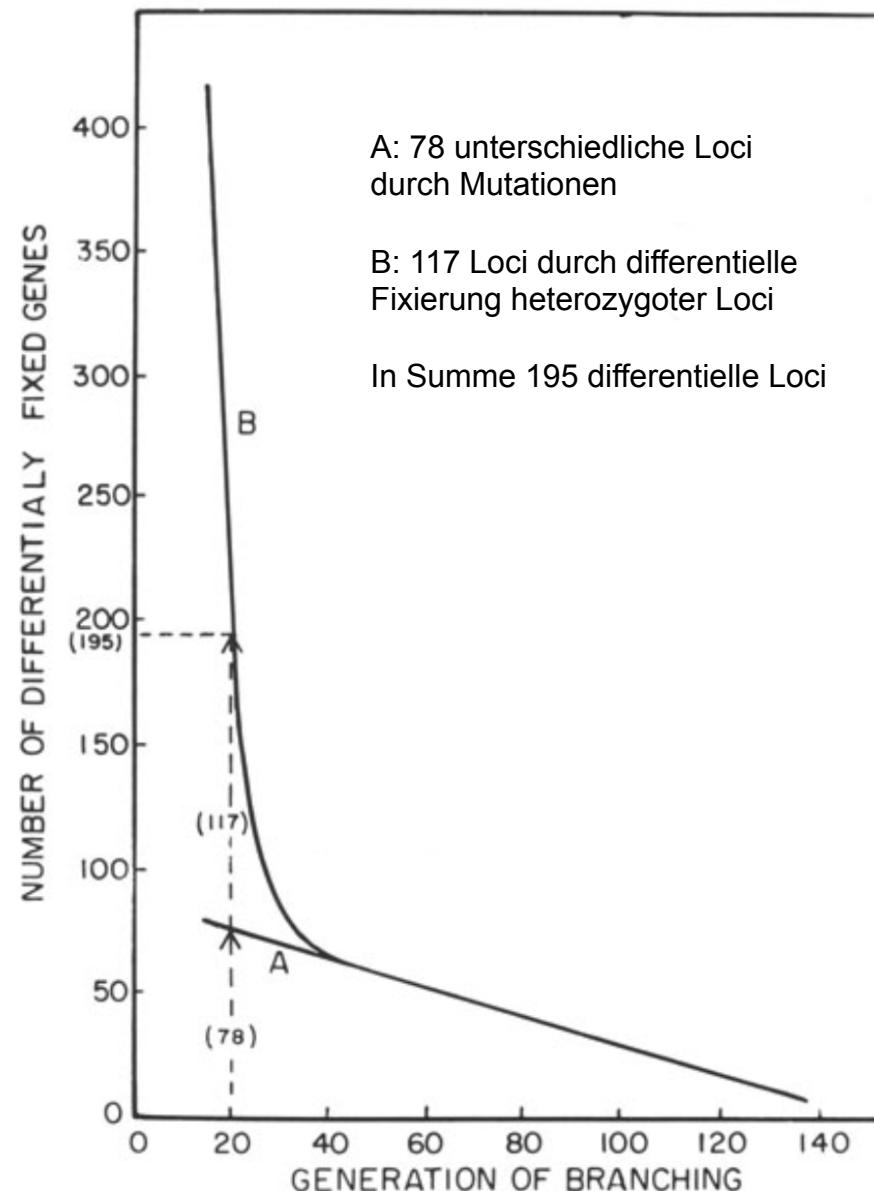
C57BL/6NTacfBR

JAX, Taconic Farms, Charles River Laboratories

N = Abstammung vom NIH

BR = Barrier Facility

Individuen eines Inzuchtstammes werden ab F₂₀ getrennt und für weitere 134 Generationen weiter gezüchtet (F₁₅₄)

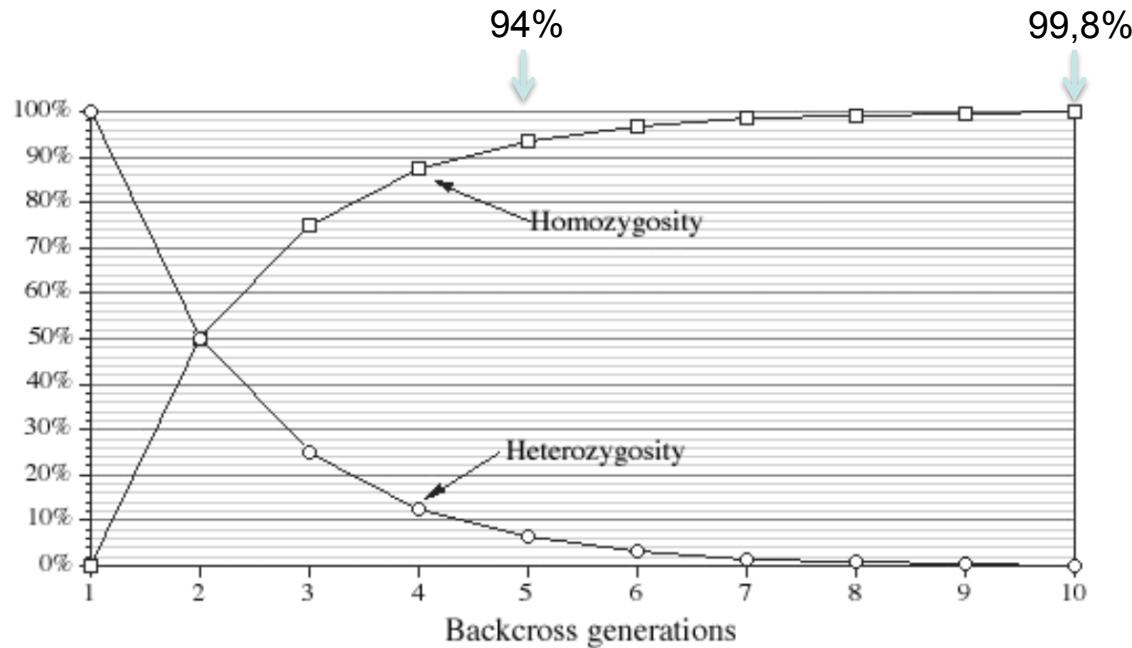
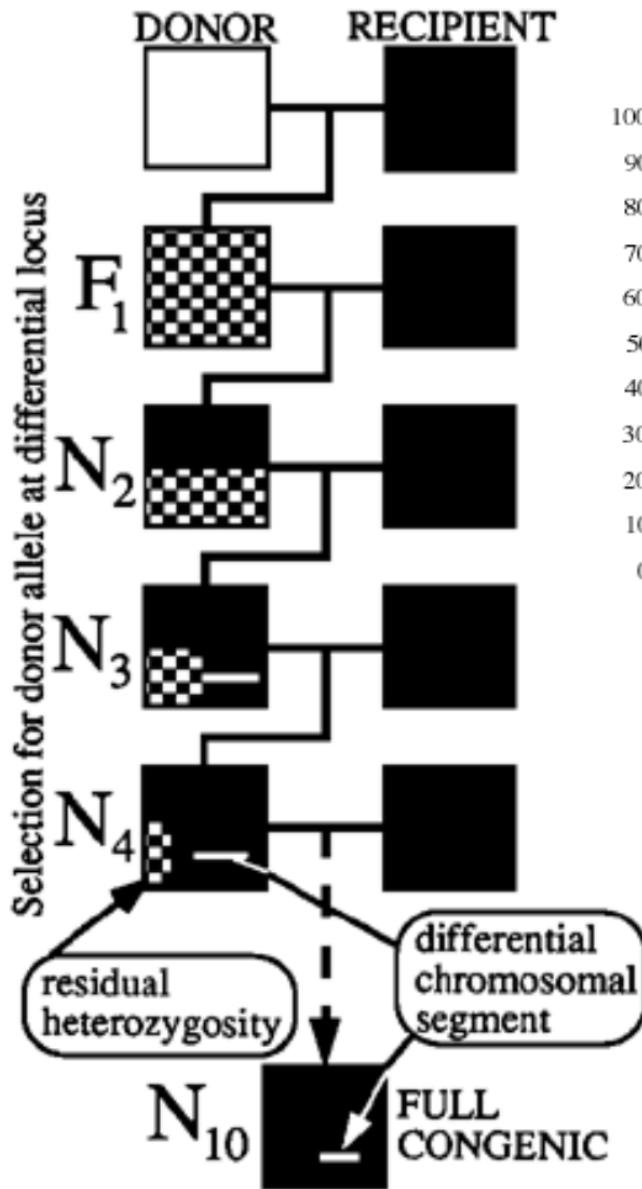


Koisogene und kongene Stämme

Koisogene Mäuse unterscheiden sich nur in einem genetischen Lokus (spontane Mutation, Transgen, knock in, knock out etc.) auf dem Hintergrund eines definierten Inzuchtstammes

Ein **kongener** Stamm wird erzeugt, indem ein spezifischer genetischer Lokus (Differentiallokus) von einem Donorstamm auf einen Rezipientenstamm übertragen wird

Zuchtschema zur Herstellung kongener Stämme



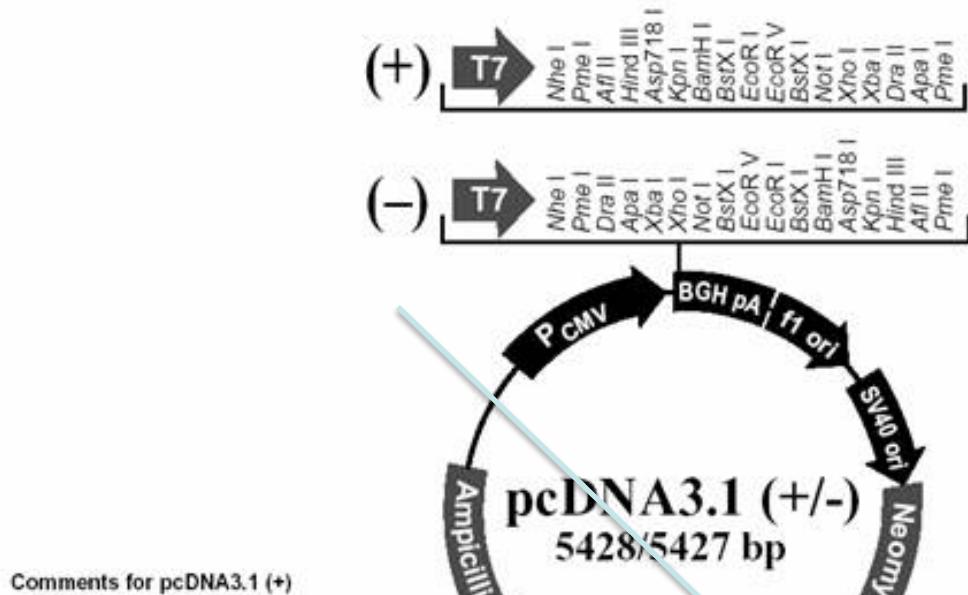
Cave: Den Differentiallokus flankierende Bereiche
Bilden ein differentielles chromosomales Segment
(Kopplungsgruppe) aus dem Donorstamm !

Für dessen Größe gilt:

$$\text{Ln (cM)} = 200/N \text{ (für } N > 5\text{)}$$

Für $N = 10$ ist $\text{Ln} = 20 \text{ cM}$
(ca. 20 – 40 MBp; 1% des Genoms!)

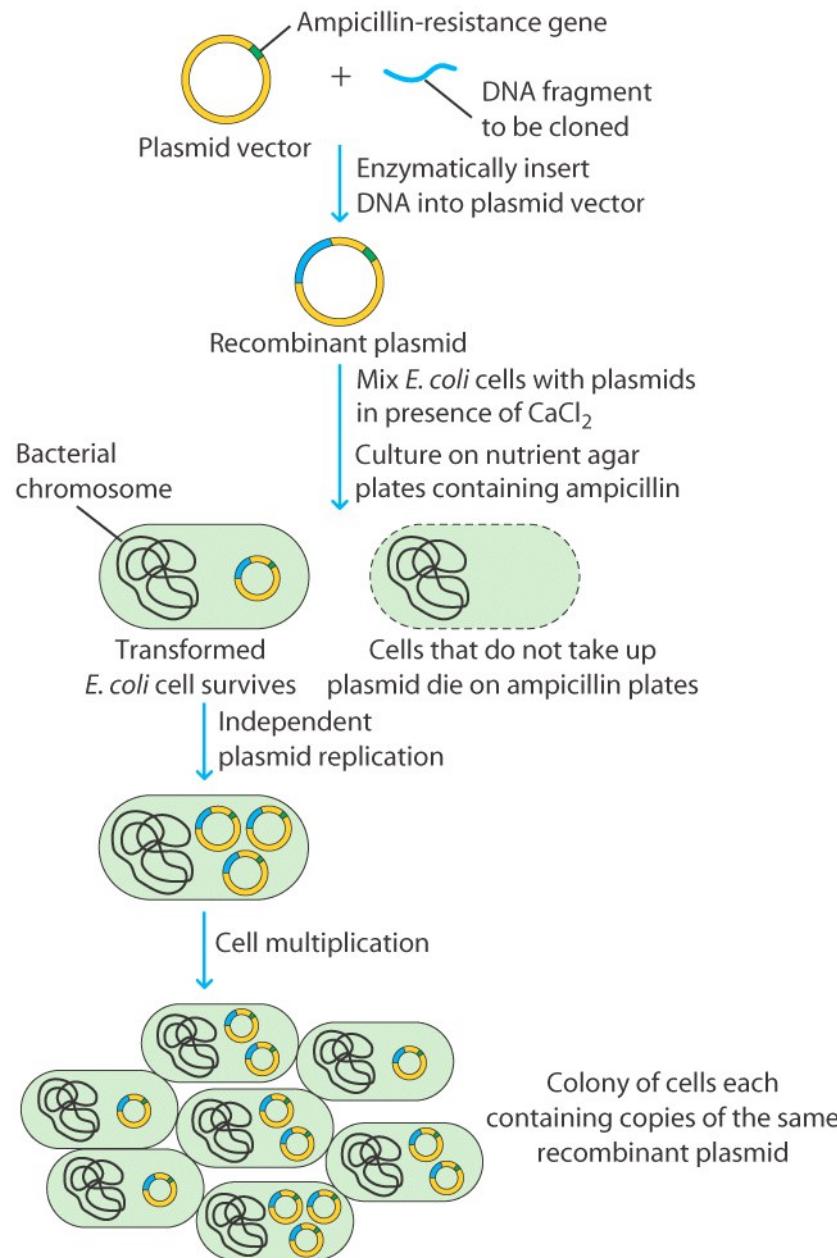
1. Klonierung in Expressionsvektor



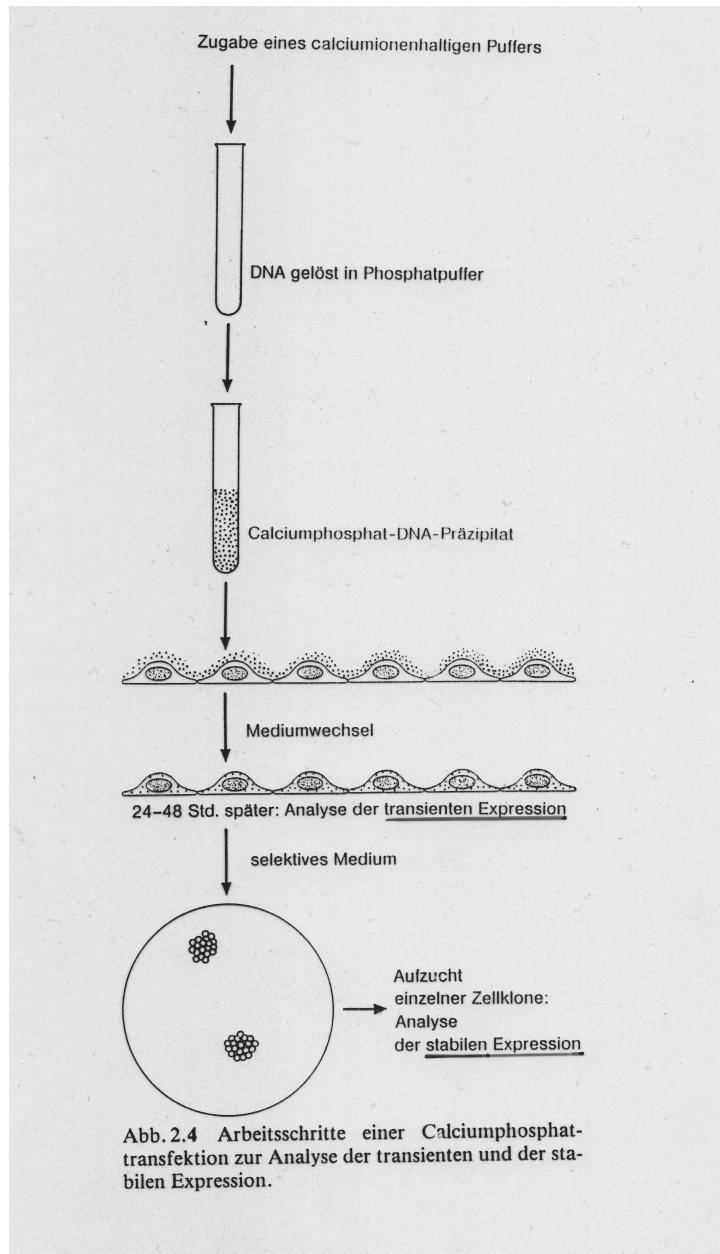
Comments for pcDNA3.1 (+)
5428 nucleotides

CMV promoter: bases 232-819
T7 promoter/priming site: bases 863-882
Multiple cloning site: bases 895-1010
pcDNA3.1/BGH reverse priming site: bases 1022-1039
BGH polyadenylation sequence: bases 1028-1252
f1 origin: bases 1298-1726
SV40 early promoter and origin: bases 1731-2074
Neomycin resistance gene (ORF): bases 2136-2930
SV40 early polyadenylation signal: bases 3104-3234
pUC origin: bases 3617-4287 (complementary strand)
Ampicillin resistance gene (*bla*): bases 4432-5428 (complementary strand)
ORF: bases 4432-5292 (complementary strand)
Ribosome binding site: bases 5300-5304 (complementary strand)
bla promoter (P3): bases 5327-5333 (complementary strand)

2. Vermehrung in Prokaryoten



3. Transfektion in eukaryotische Zellen



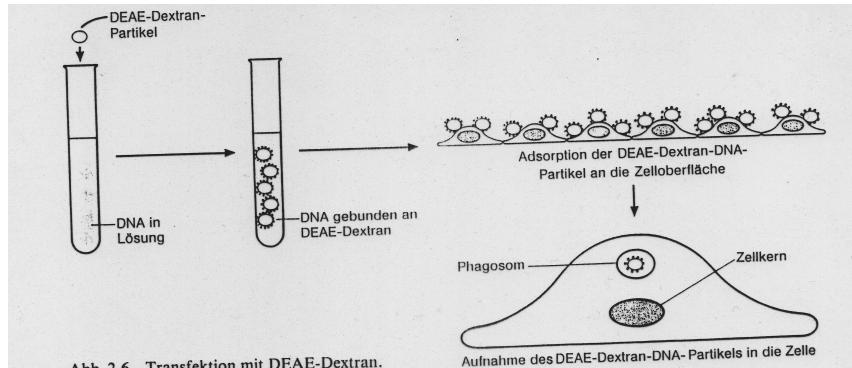


Abb. 2.6 Transfektion mit DEAE-Dextran.

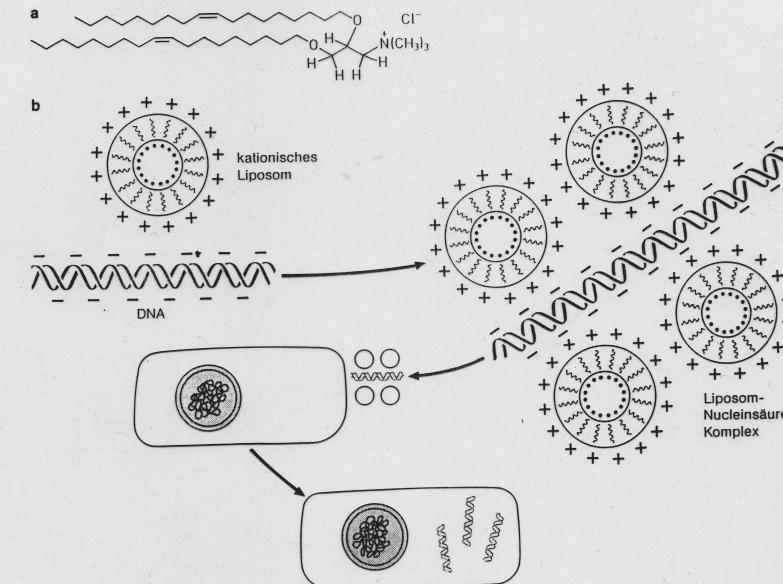


Abb. 2.8 Transfektion mit kationischen Liposomen. a Struktur des kationischen Lipids DOMTA.
b Schematische Darstellung der durch kationische Liposomen vermittelten Transfektion.

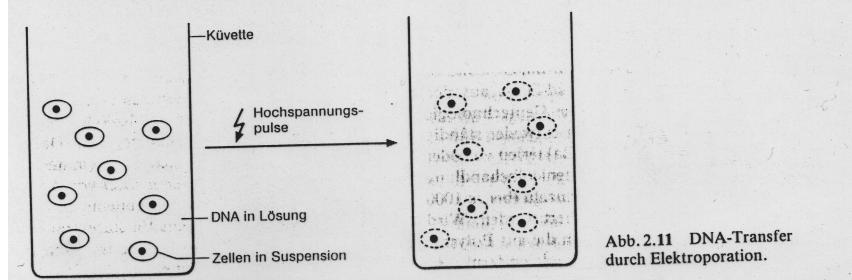


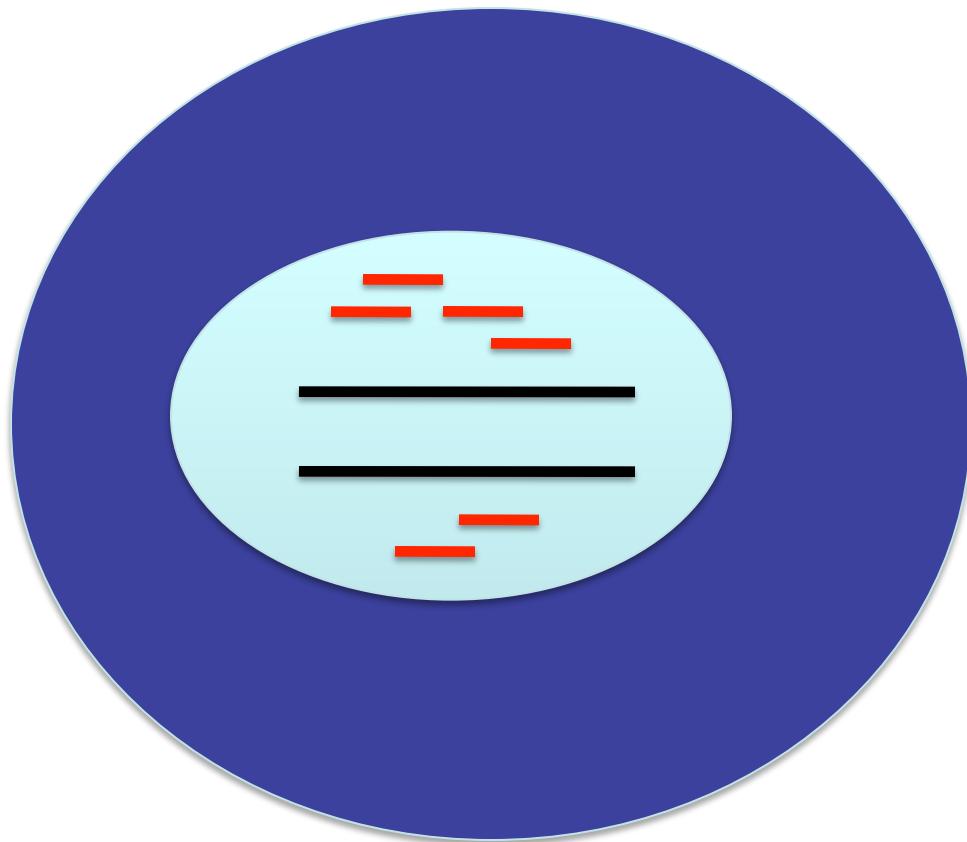
Abb. 2.11 DNA-Transfer durch Elektroporation.

Transiente Transfektion

Zelluläre DNA



Transfizierte DNA

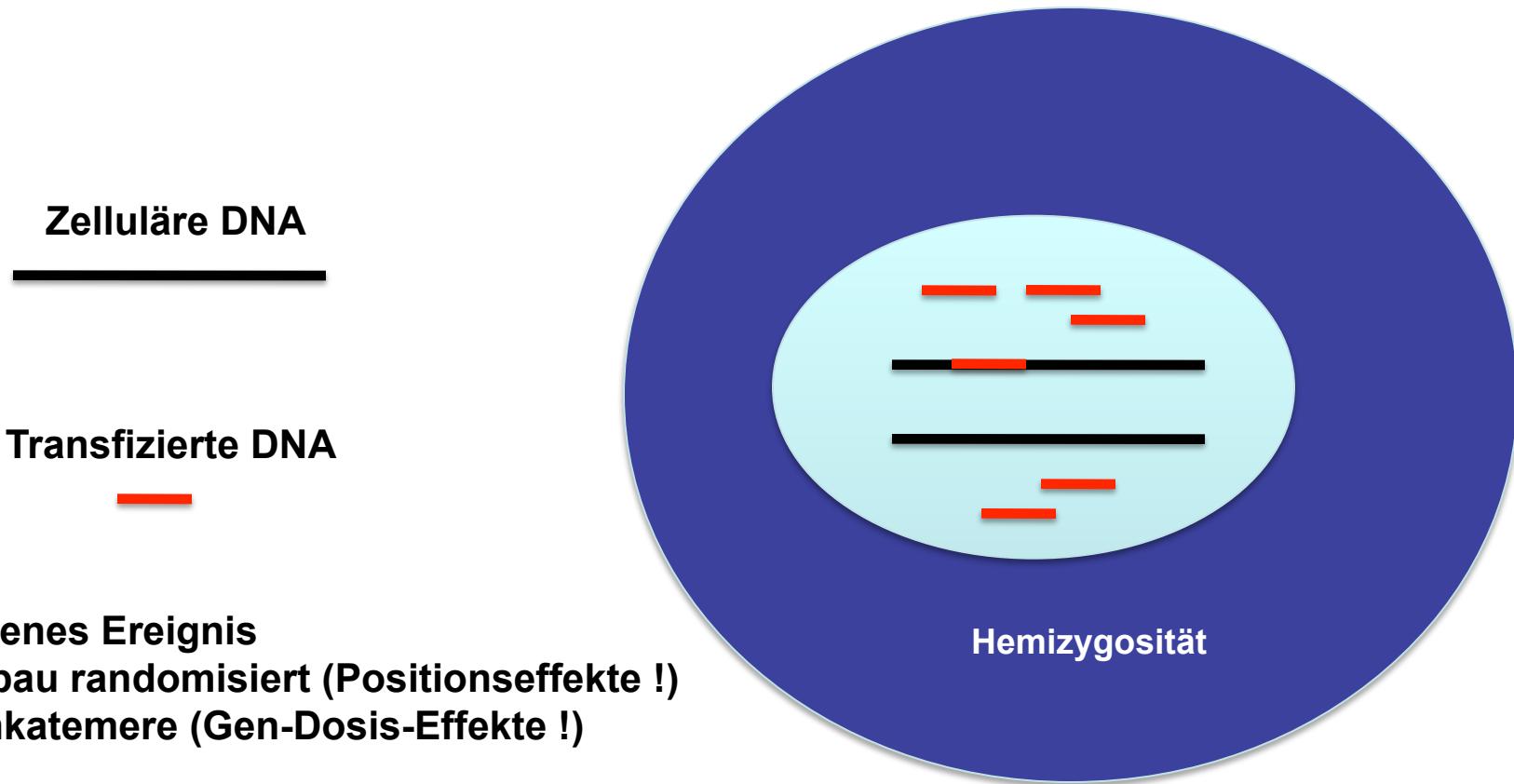


Hohe Effizienzen möglich

Nicht stabil

Abbau der transfizierten DNA

Stabile Transfektion durch Integration



Selektion durch Resistenzgen, Züchtung von Zellklonen

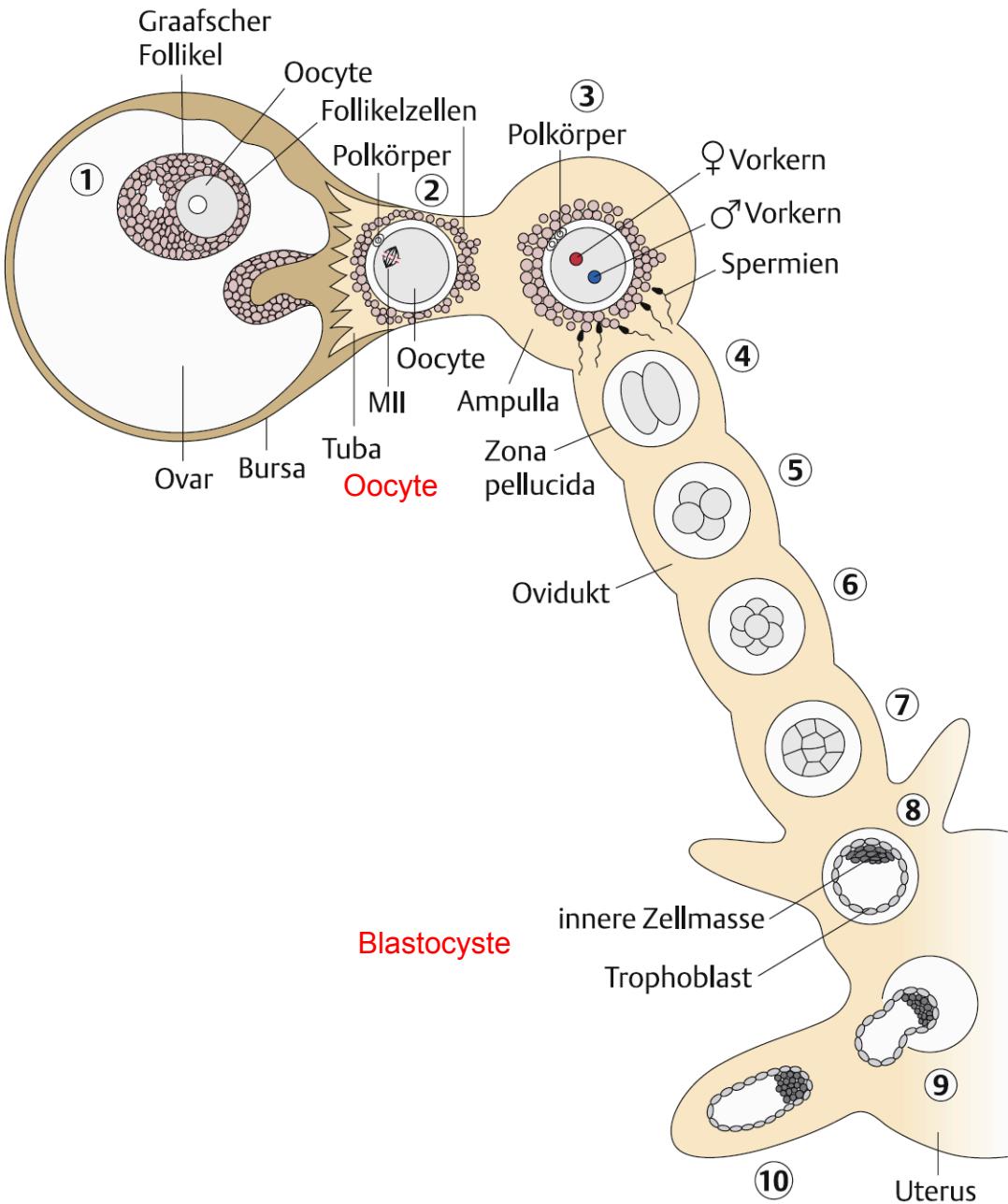
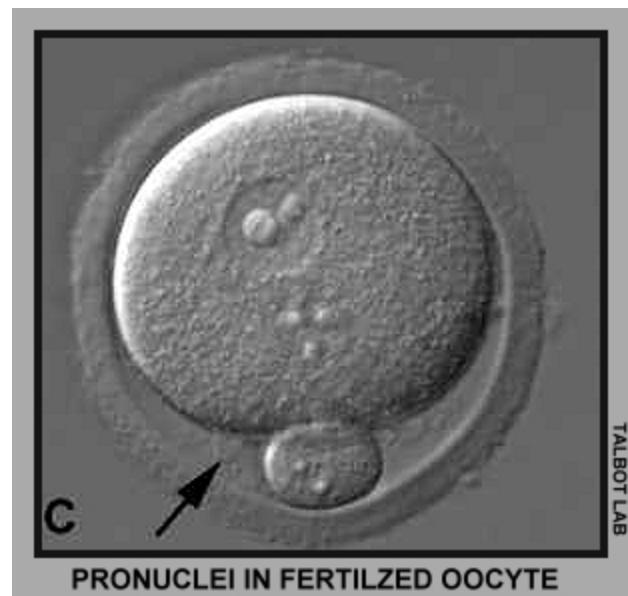
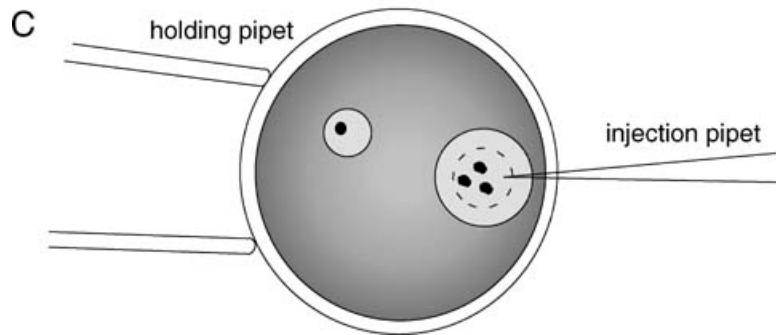
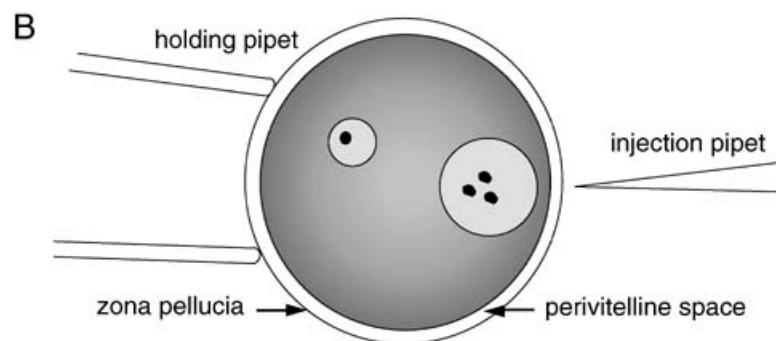
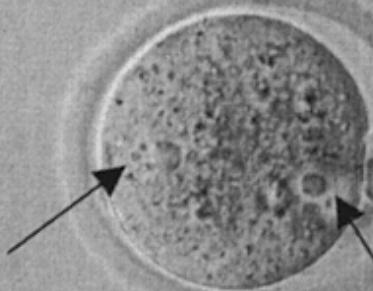
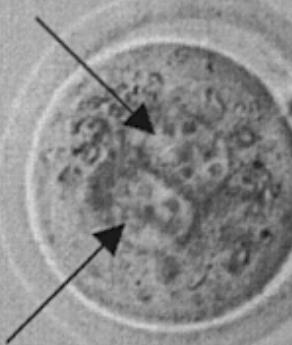
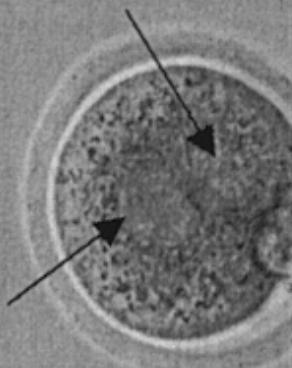


Abb. 3.17 Frühe Embryonalentwicklung der Maus bis zur Implantation. 1 Graaf'scher Follikel mit Oocyte. 2 Ovulation. 3 Befruchtung. 4 Furcung (2-Zeller). 5 4-Zellstadium. 6 Morula. 7 Kompaktion der Morula. 8 Blastocyste. 9 Schlüpfen. 10 Implantation.





A**B****C****D**

Transgenese der Maus durch Mikroinjektion

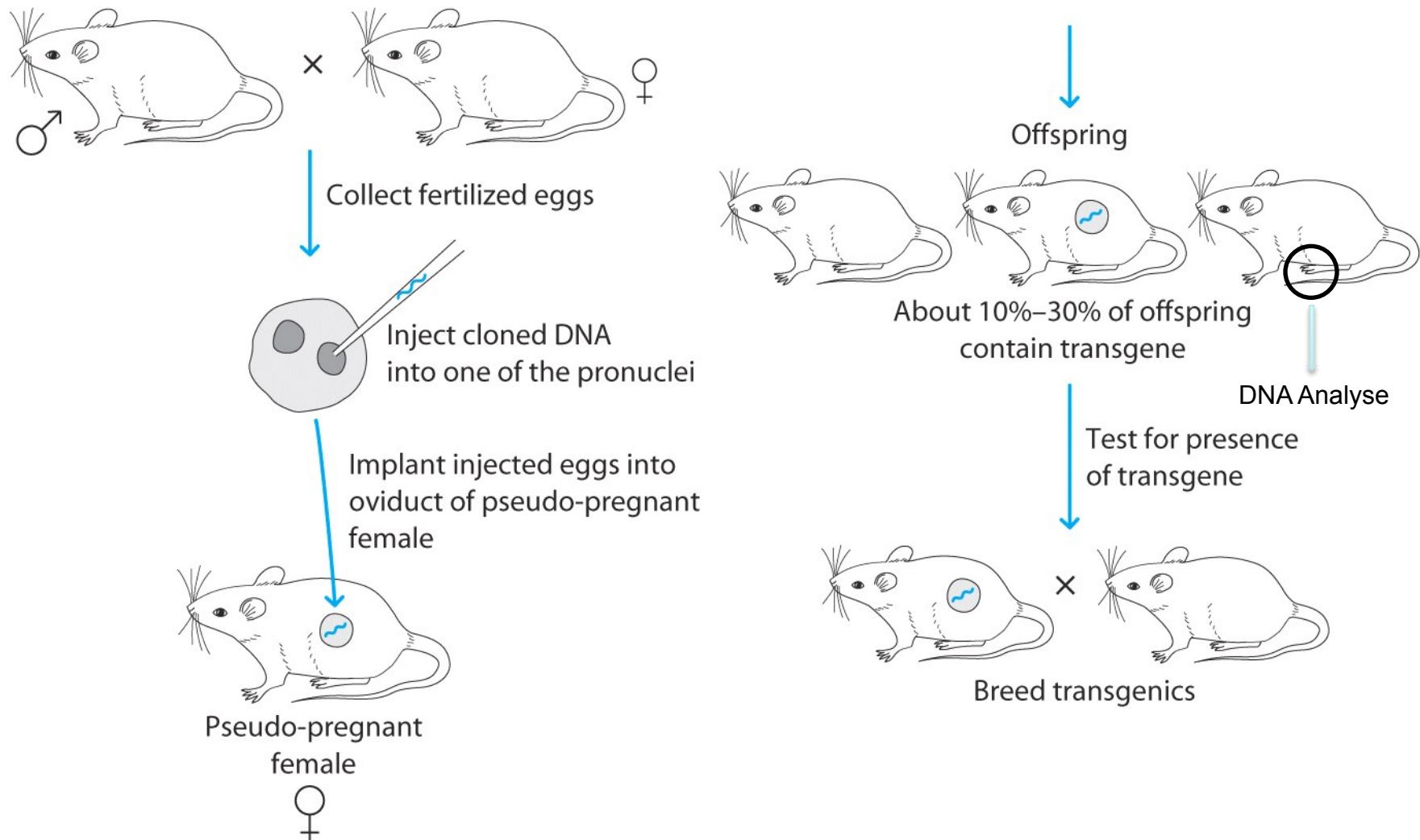


Tabelle 15.4: Ausbeuten bei der Herstellung transgener Rinder (nach [38])

Schritt	Gesamtzahl	Ausbeute
Eizellen	2 470	100%
reife Eizellen	2 297	93%
befruchtete Eizellen	1 358	55 %
injizierte Eizellen	1 154	47%
die Injektion überlebende Eizellen	981	40%
injizierte Zellen, die sich teilen	687	28%
transferierte Blastocysten	129	5%
Embryonen, aus denen eine Trächtigkeit resultierte	21	(0.85%)
erhaltene Tiere	16	0.65%
transgene Nachkommen	2	0.08%
Nachkommen, die das Transgen komplett integriert haben	1	0.04%

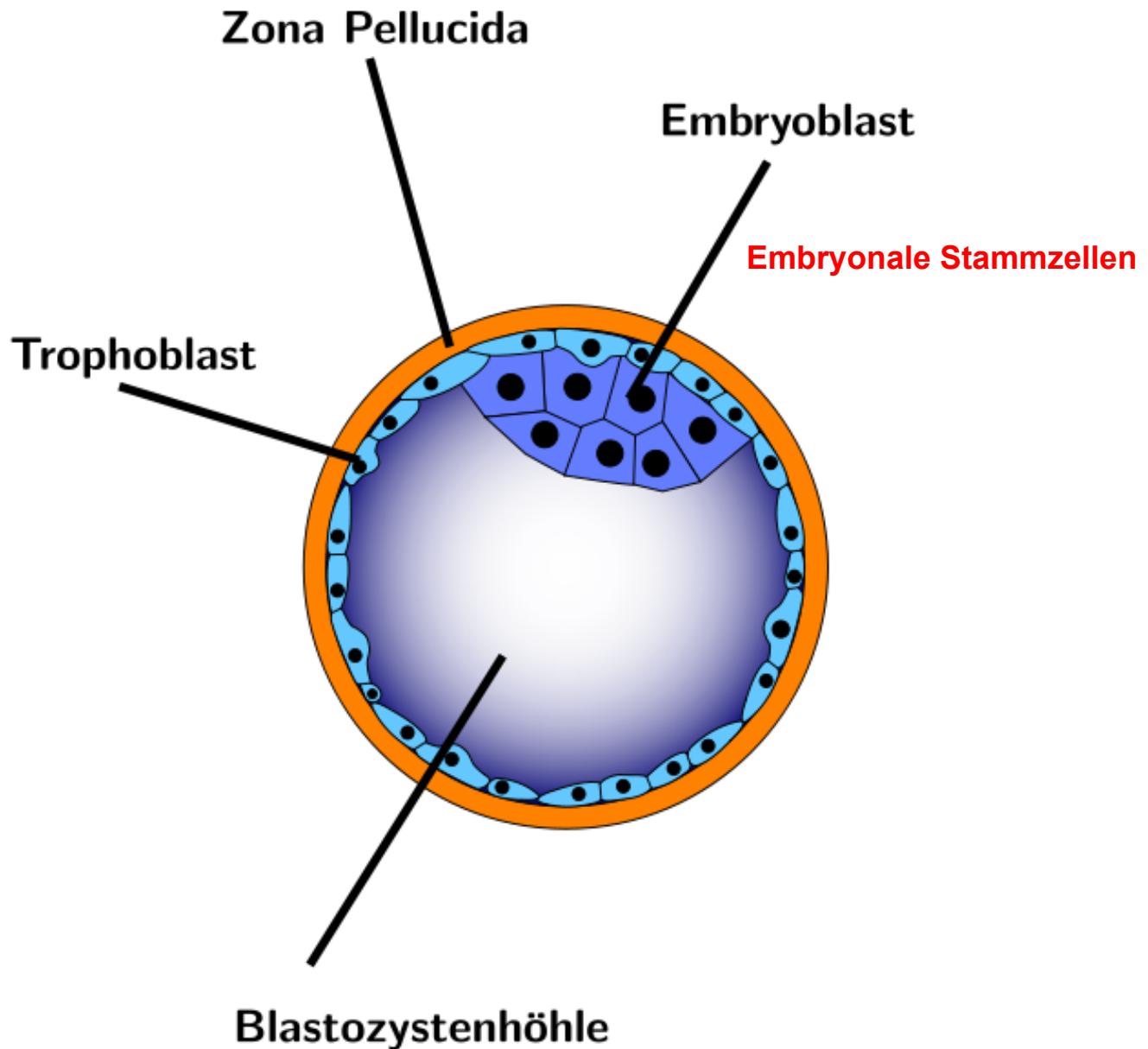
TABLE 23-7

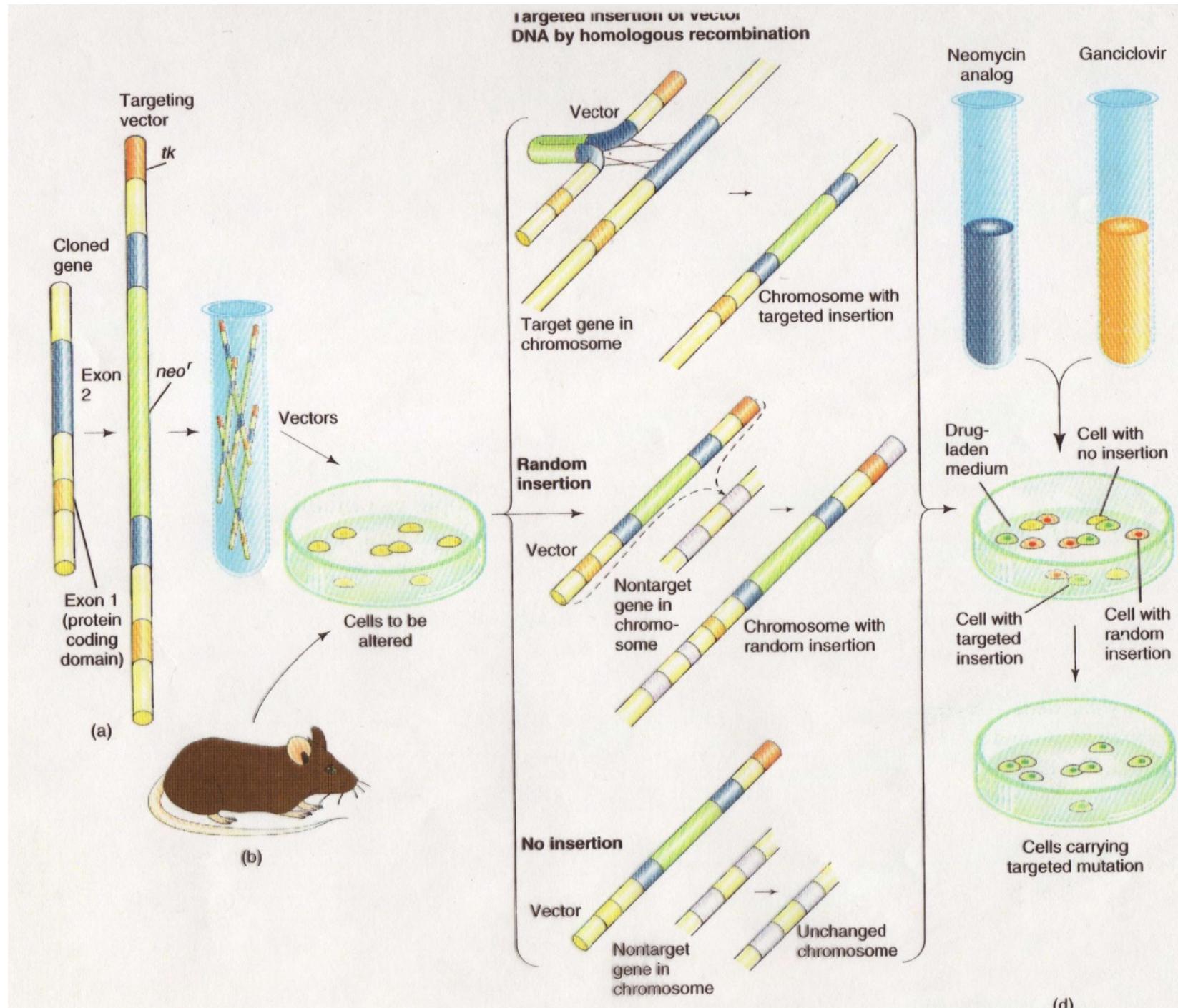
Comparison of transgenic and knockout mice

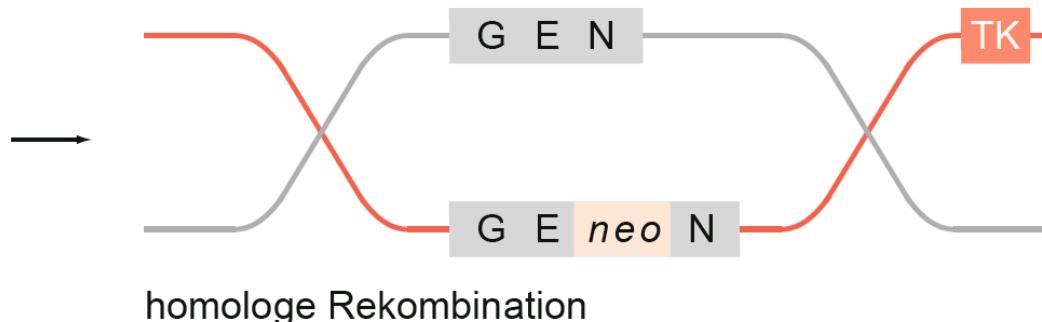
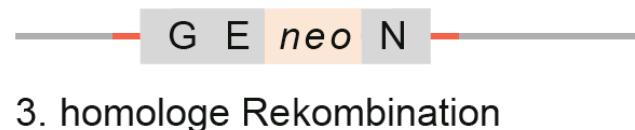
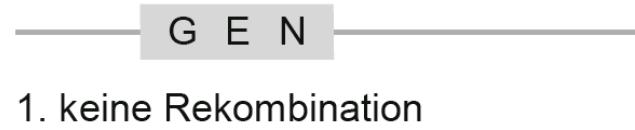
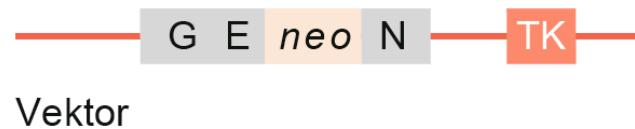
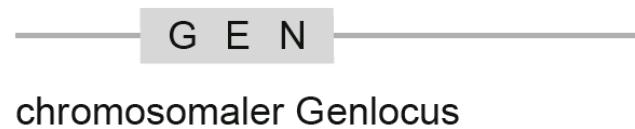
Characteristic	Transgenic mice	Knockout mice
Cells receiving DNA	Zygote	Embryonic stem (ES) cells
DNA constructs used	Natural gene or cDNA	Mutated gene
Means of delivery	Microinjection into zygote and implantation into foster mother	Transfer of ES cells to blastocyst and implantation into foster mother
Outcome	Gain of a gene	Loss of gene

→ Ungerichtete Integration des Transgens

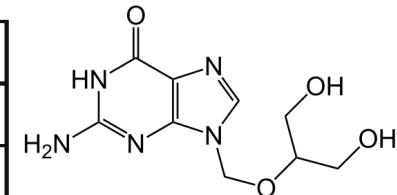
→ Gerichtete Integration durch Homologe Rekombination

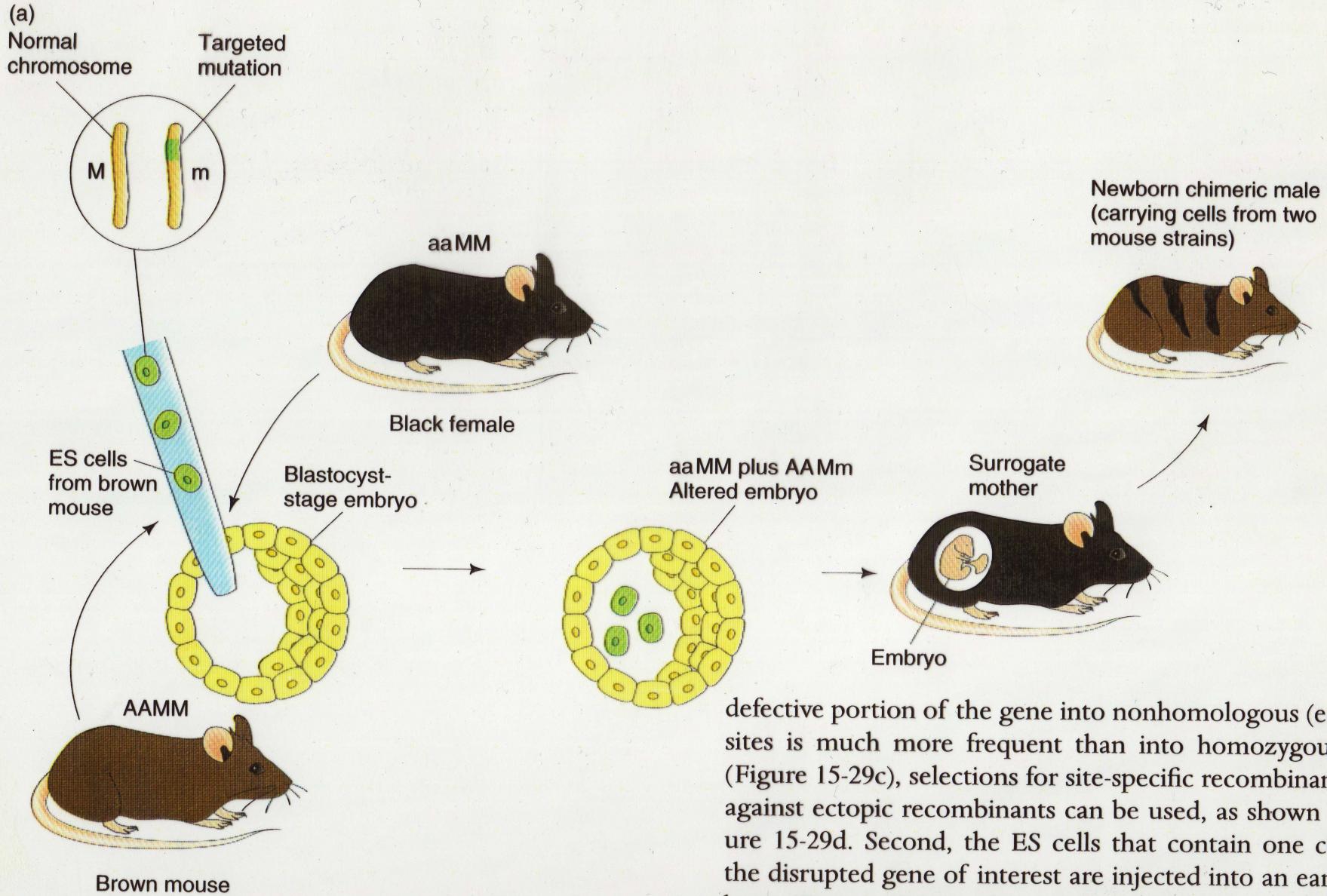




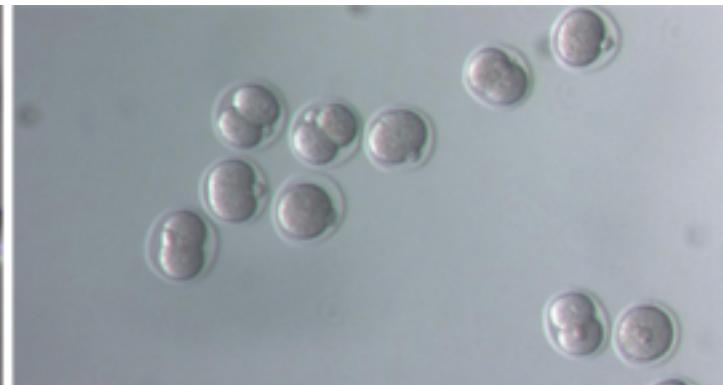


Selektion	
Neomycin	Ganciclovir
stirbt	
überlebt	stirbt
überlebt	überlebt

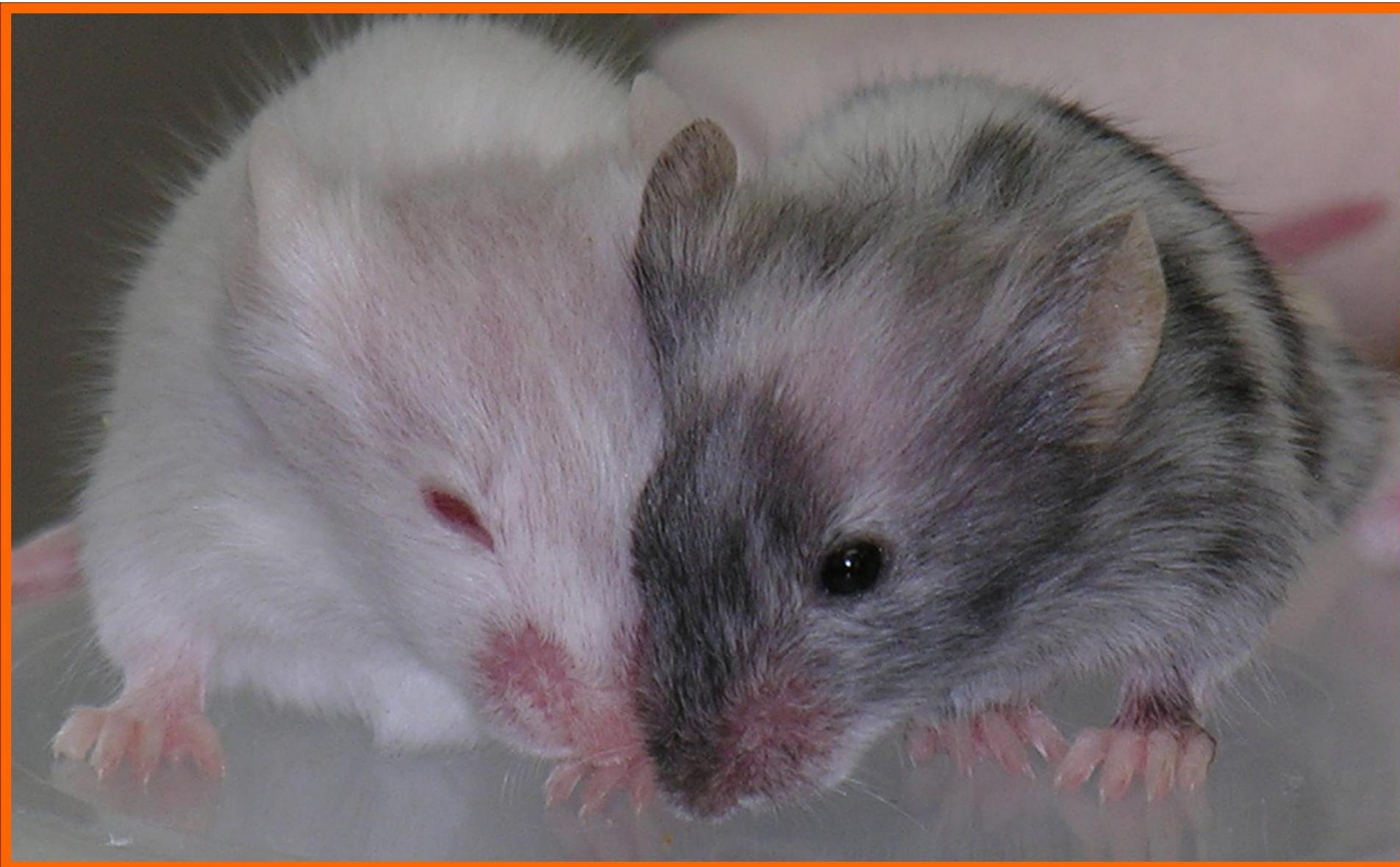




defective portion of the gene into nonhomologous (ectopic) sites is much more frequent than into homozygous (Figure 15-29c), selections for site-specific recombinants against ectopic recombinants can be used, as shown in Figure 15-29d. Second, the ES cells that contain one copy of the disrupted gene of interest are injected into an early embryo (Figure 15-30). The resulting chimeric







(b)

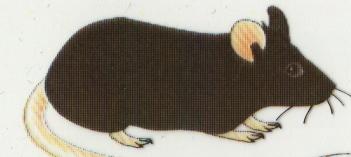
aa MM
plus
AA Mm



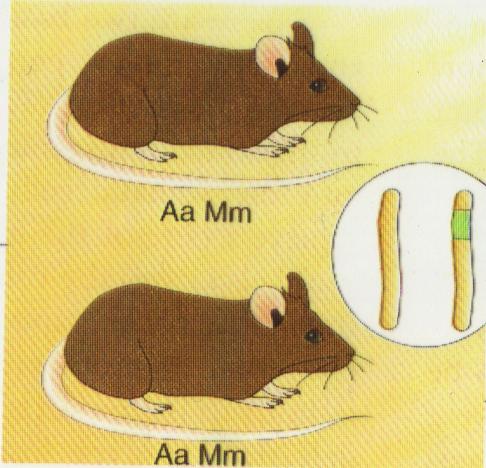
aa MM



aa MM



Aa Mm



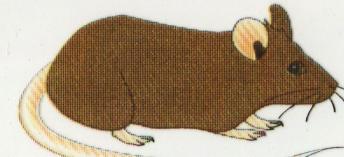
Aa MM



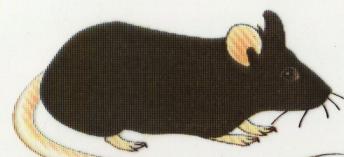
A- M-



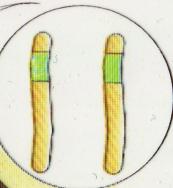
A- mm



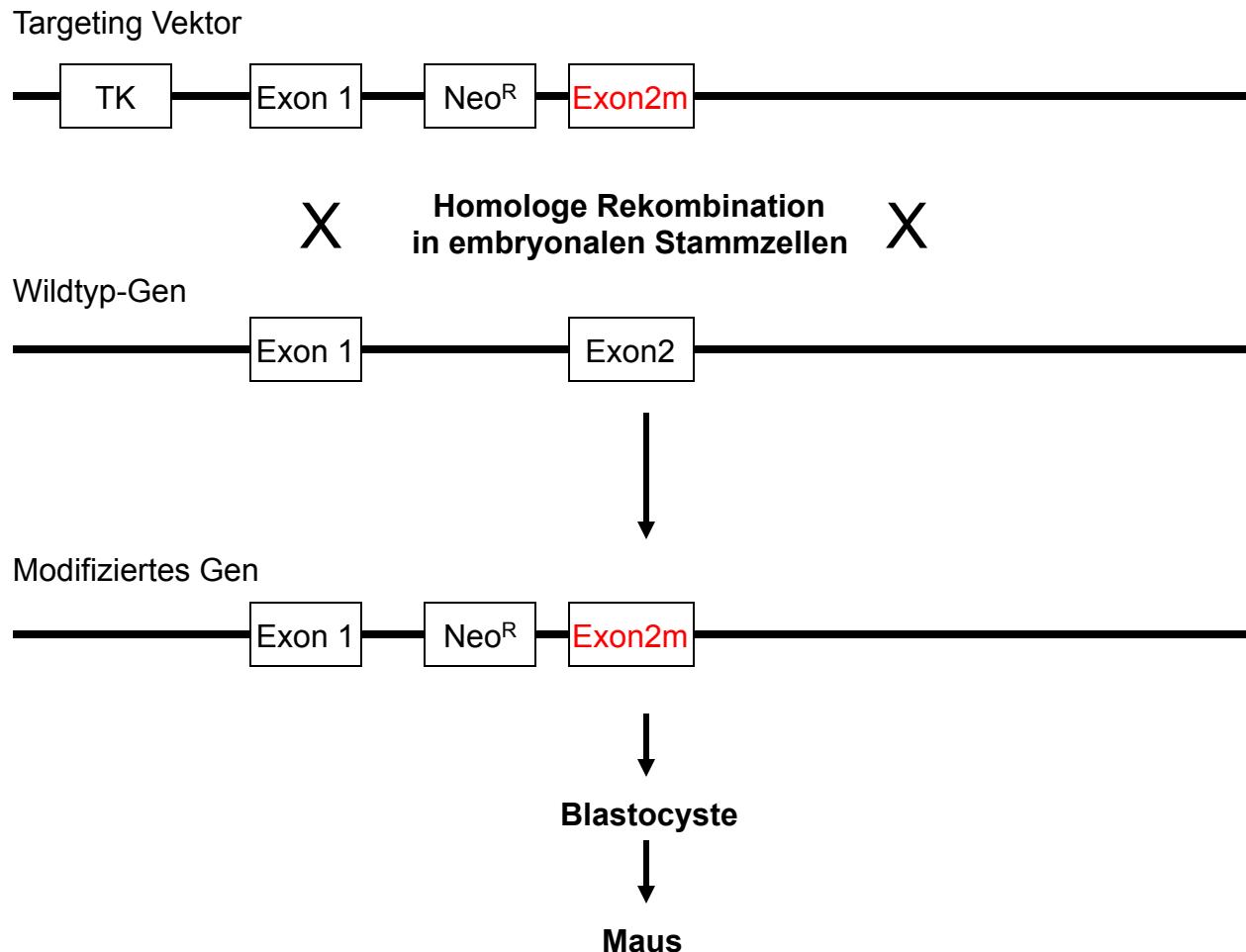
A- M-



aa M-



„Knock in“: Gezieltes Modifizieren von Genen durch homologe Rekombination



Cytokine	T-cell source	Effects on					Effect of gene knockout
		B cells	T cells	Macrophages	Hematopoietic cells	Other somatic cells	
Interleukin-2 (IL-2)	Naive, T _H 1, some CD8	Stimulates growth and J-chain synthesis	Growth	-	Stimulates NK cell growth	-	↓ T-cell responses IBD
Interferon-γ (IFN-γ)	T _H 1, CTL	Differentiation IgG2a synthesis (mouse)	Inhibits T _H 2 cell growth ↑ MHC class I and class II	Activation, induces NO production	Activates NK cells	Antiviral ↑ MHC class I and class II	Susceptible to mycobacteria, some viruses
Lymphotxin (LT, TNF-β)	T _H 1, some CTL	Inhibits	Kills	Activates, induces NO production	Activates neutrophils	Kills fibroblasts and tumor cells	Absence of lymph nodes Disorganized spleen
Interleukin-4 (IL-4)	T _H 2	Activation, growth IgG1, IgE ↑ MHC class II induction	Growth, survival	Inhibits macrophage activation	↑ Growth of mast cells	-	No T _H 2
Interleukin-5 (IL-5)	T _H 2	Mouse: Differentiation IgA synthesis	-	-	↑ Eosinophil growth and differentiation	-	Reduced eosinophilia
Interleukin-10 (IL-10)	T _H 2, (human: some T _H 1)	↑ MHC class II	Inhibits T _H 1	Inhibits cytokine release	Co-stimulates mast cell growth	-	IBD
Interleukin-3 (IL-3)	T _H 1, T _H 2, some CTL	-	-	-	Growth factor for progenitor hematopoietic cells (multi-CSF)	-	-
Tumor necrosis factor-α (TNF-α)	T _H 1, some T _H 2, some CTL	-	-	Activates, induces NO production	-	Activates microvascular endothelium	Resistance to Gram -ve sepsis
Granulocyte-macrophage colony-stimulating factor (GM-CSF)	T _H 1, some T _H 2, some CTL	Differentiation	Inhibits growth ?	Activation Differentiation to dendritic cells	↑ Production of granulocytes and macrophages (myelopoiesis) and dendritic cells	-	-
Transforming growth factor-β (TGF-β)	CD4 T cells	Inhibits growth IgA switch factor	Inhibits growth, promotes survival	Inhibits activation	Activates neutrophils	Inhibits/ stimulates cell growth	Death at ~10 weeks

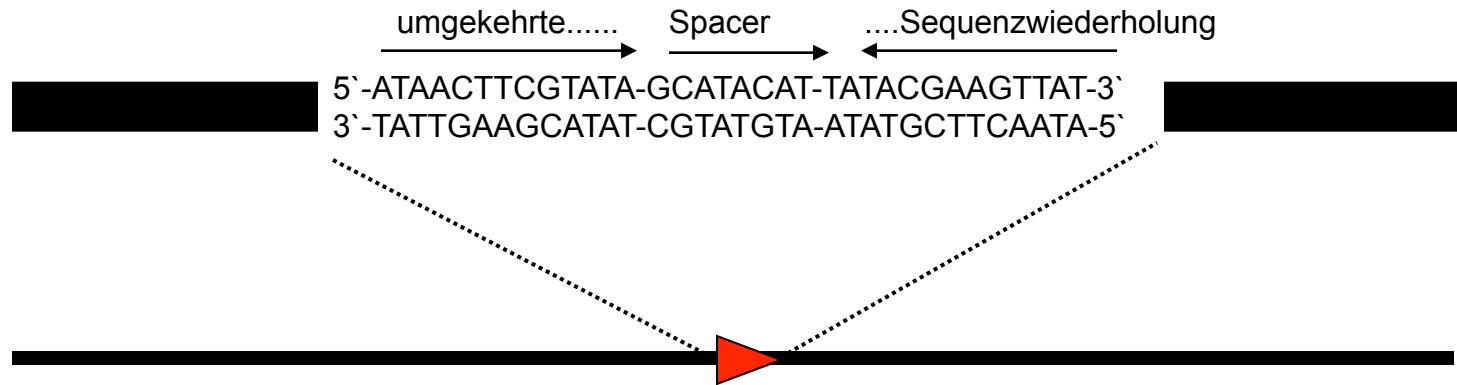
Figure 8-32 Immunobiology, 6/e. (© Garland Science 2005)

Cytokine	T-cell source	Effects on					Effect of gene knockout
		B cells	T cells	Macrophages	Hematopoietic cells	Other somatic cells	
Interleukin-2 (IL-2)	Naive, T _H 1, some CD8	Stimulates growth and J-chain synthesis	Growth	-	Stimulates NK cell growth	-	↓ T-cell responses IBD
Interferon-γ (IFN-γ)	T _H 1, CTL	Differentiation IgG2a synthesis (mouse)	Inhibits T _H 2 cell growth	Activation, ↑ MHC class I and class II	Activates NK cells	Antiviral ↑ MHC class I and class II	Susceptible to mycobacteria, some viruses
Lymphotxin (LT, TNF-β)	T _H 1, some CTL	Inhibits	Kills	Activates, induces NO production	Activates neutrophils	Kills fibroblasts and tumor cells	Absence of lymph nodes Disorganized spleen
Interleukin-4 (IL-4)	T _H 2	Activation, growth IgG1, IgE ↑ MHC class II induction	Growth, survival	Inhibits macrophage activation	↑ Growth of mast cells	-	No T _H 2
Interleukin-5 (IL-5)	T _H 2	Mouse: Differentiation IgA synthesis	-	-	↑ Eosinophil growth and differentiation	-	Reduced eosinophilia
Interleukin-10 (IL-10)	T _H 2, (human: some T _H 1)	↑ MHC class II	Inhibits T _H 1	Inhibits cytokine release	Co-stimulates mast cell growth	-	IBD
Interleukin-3 (IL-3)	T _H 1, T _H 2, some CTL	-	-	-	Growth factor for progenitor hematopoietic cells (multi-CSF)	-	-
Tumor necrosis factor-α (TNF-α)	T _H 1, some T _H 2, some CTL	-	-	Activates, induces NO production	-	Activates microvascular endothelium	Resistance to Gram -ve sepsis
Granulocyte-macrophage colony-stimulating factor (GM-CSF)	T _H 1, some T _H 2, some CTL	Differentiation	Inhibits growth ?	Activation Differentiation to dendritic cells	↑ Production of granulocytes and macrophages (myelopoiesis) and dendritic cells	-	
Transforming growth factor-β (TGF-β)	CD4 T cells	Inhibits growth IgA switch factor	Inhibits growth, promotes survival	Inhibits activation	Activates neutrophils	Inhibits stimulates cell growth	Death at ~10 weeks

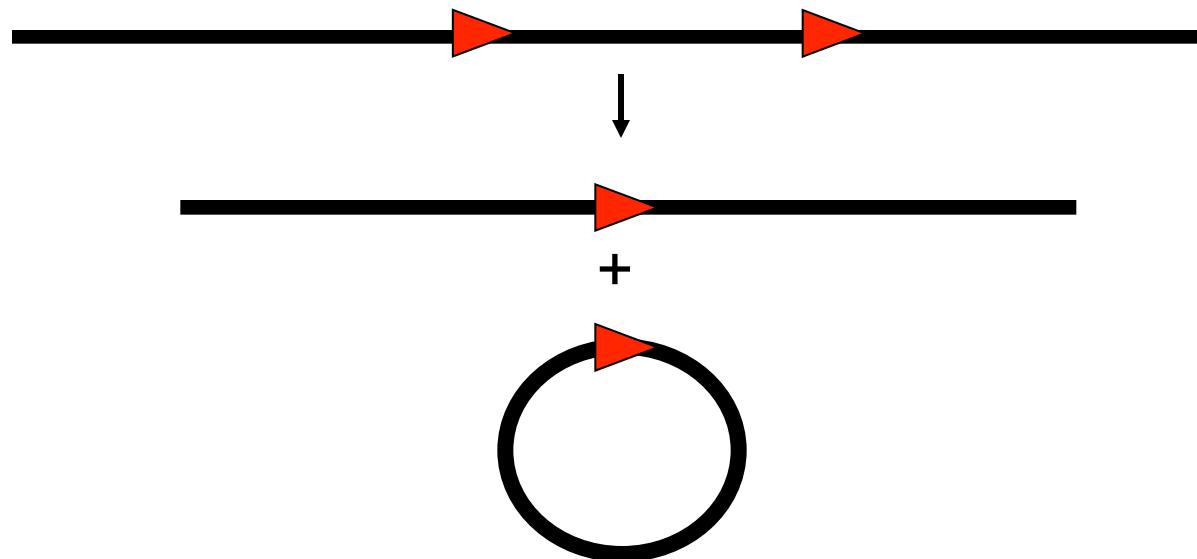
Figure 8-32 Immunobiology, 6/e. (© Garland Science 2005)

Konditionale Mutagenese: Das Cre-lox System

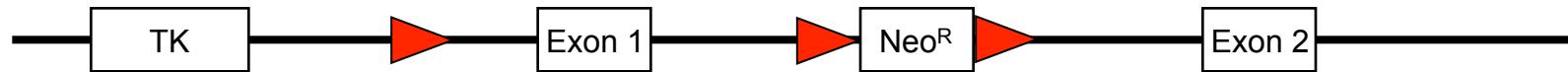
Struktur eines loxP-Elementes (locus of crossing over)



Cre-vermittelte Deletion (causes recombination)



Targeting-Vektor

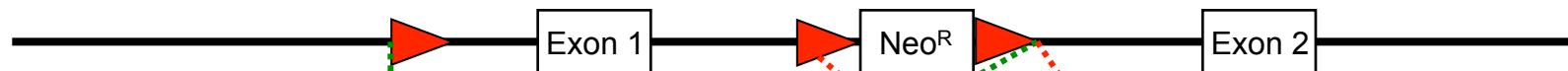


Wildtyp-Locus

X Homologe Rekombination in ES-Zellen



Targeted Allel



Transiente Expression von cre in ES-Zellen



Komplette Deletion

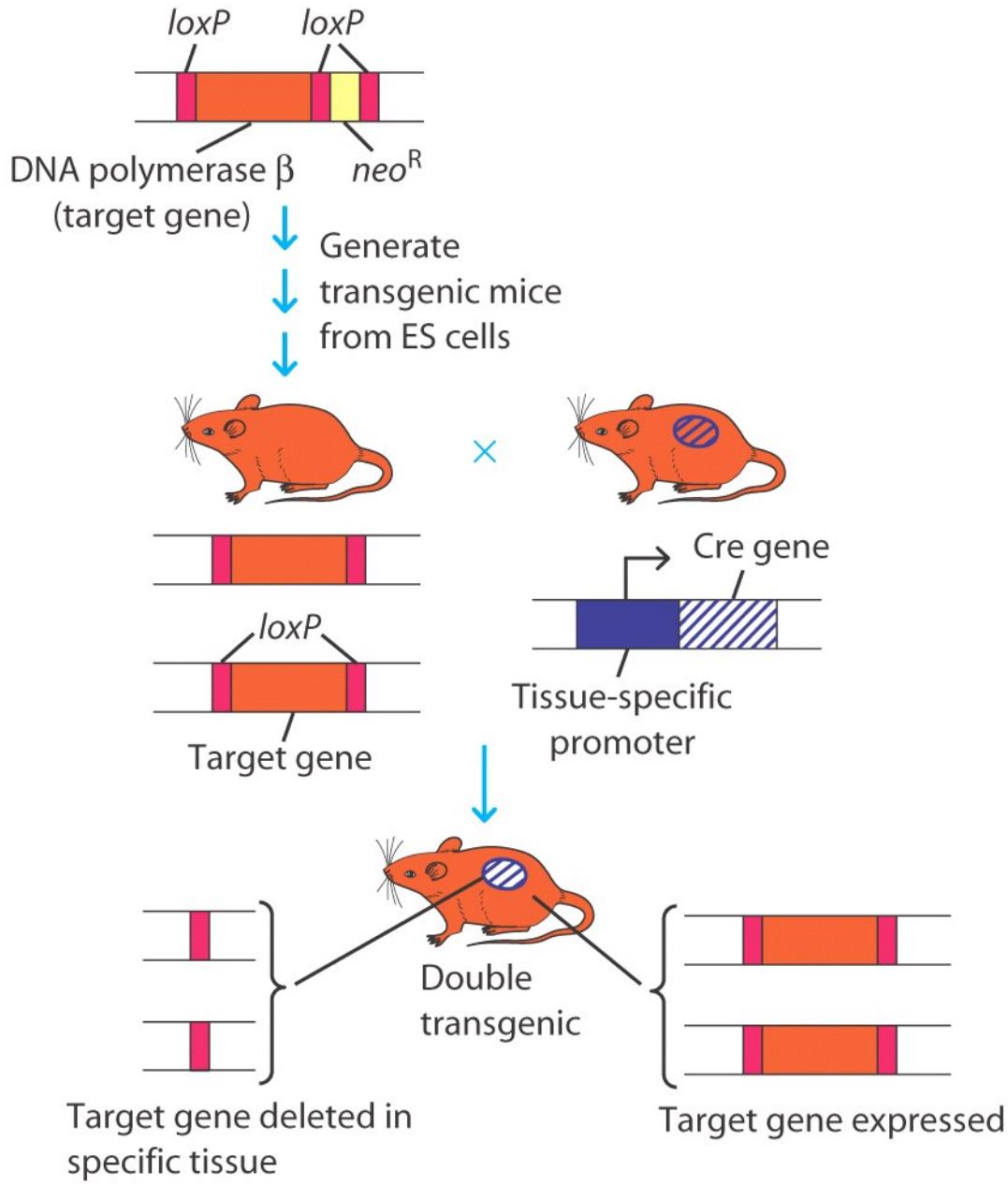


**Knock out Maus
("sauberer" KO)**

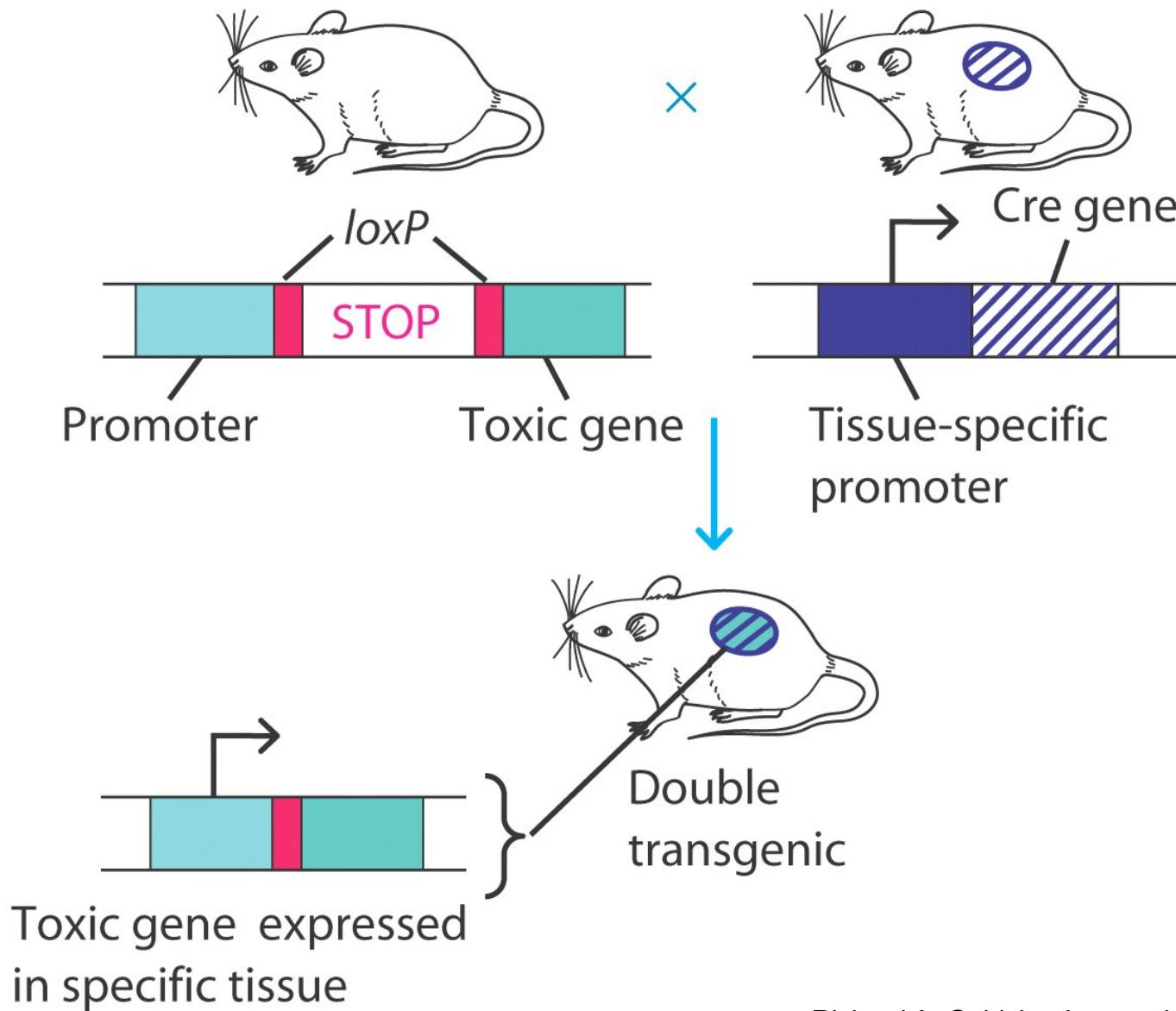
„Gefloxter“ Locus



„Geflochte“ Maus



Gezielte Ablation von Zellen durch das Cre-lox System: Expression des Diphtheria-Toxins



Gezielte Ablation von Zellen mit Hilfe des Diphtheria-Toxin Rezeptors

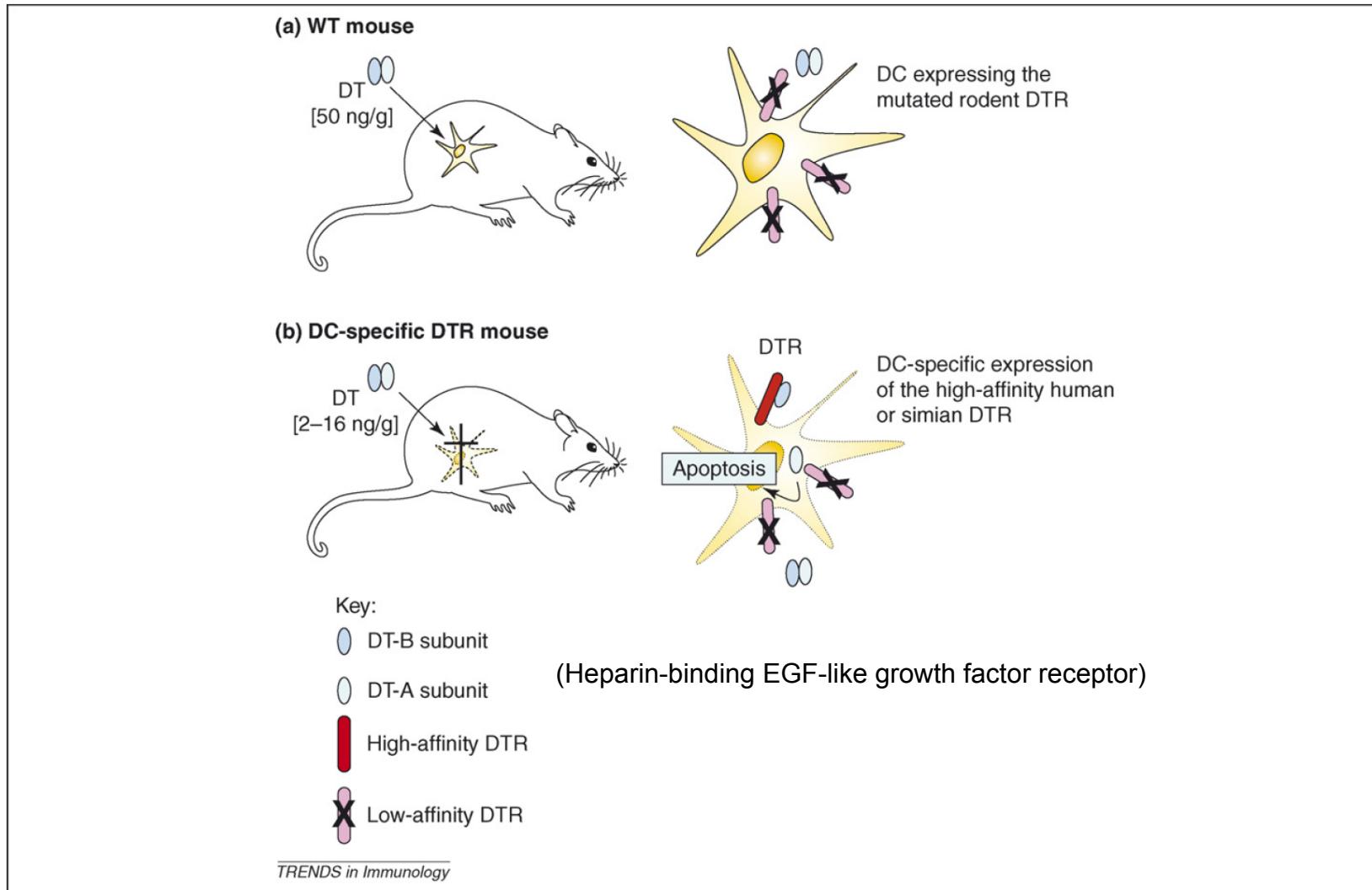


Figure 1. Depletion of DC from mice engineered to express a high-affinity DTR. **(a)** Mice are more than 1000 times more resistant to DT than humans or monkeys, principally owing to three amino acid changes in the DTR that prevent binding of the DT-B subunit to its receptor. **(b)** Expression of a high-affinity DTR by murine DC renders them uniquely sensitive to killing by low doses of DT. Binding of the B subunit to the DTR facilitates entry of the A subunit into the cell. Once internalised, the A subunit efficiently inhibits protein translation and induces apoptotic cell death.

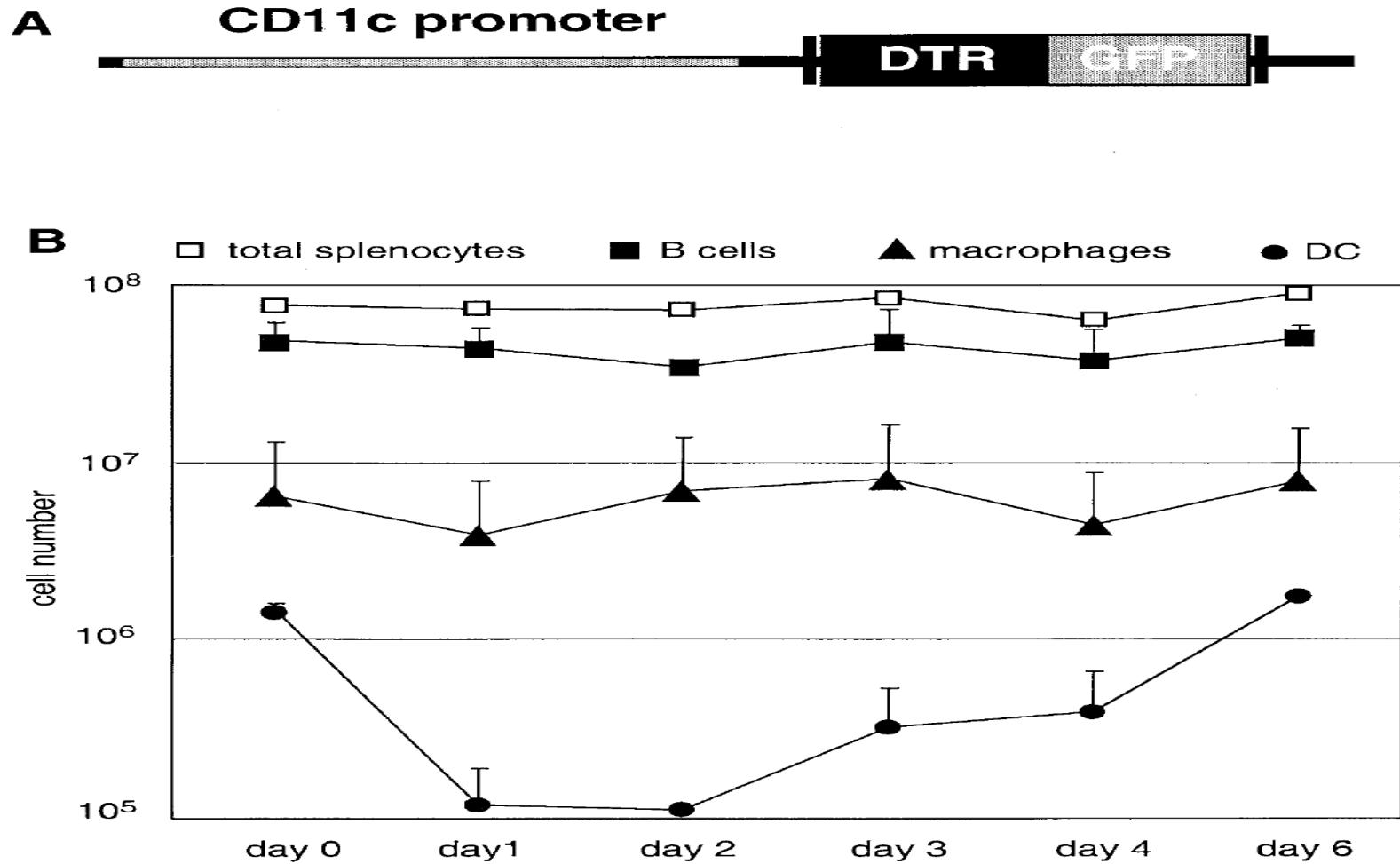
Bennett & Clausen, *Trends Immunol.* 2007



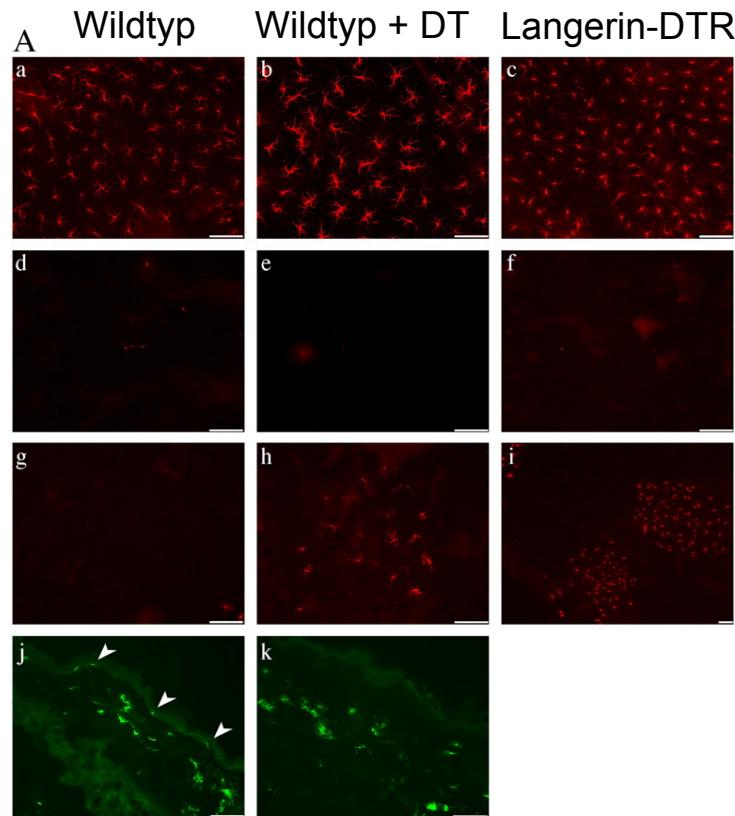
(E)GFP: (Enhanced) Green Fluorescent Protein
238 aa Protein aus der Qualle *Aequorea victoria*
als REPORTERGEN



Einbringen durch ungerichtete Transgenese oder gerichtetes „knock in“



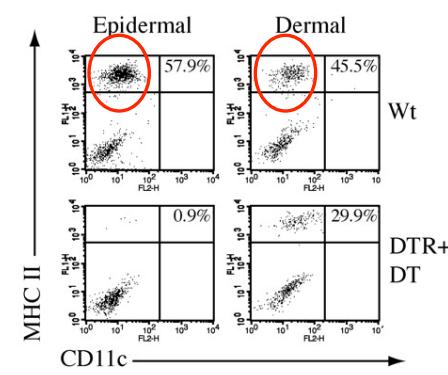
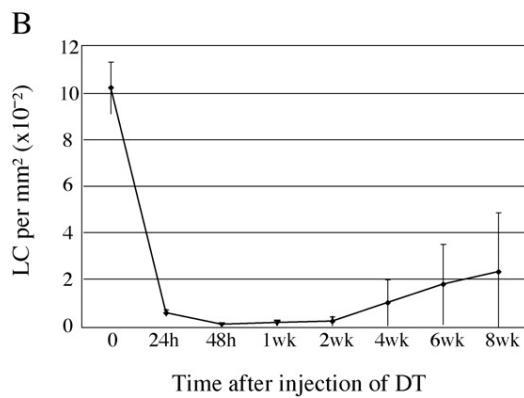
„Knock-in“ des Diphteria Toxin Rezeptors (DTR) in den Langerin-Locus (Langerin-DTR)

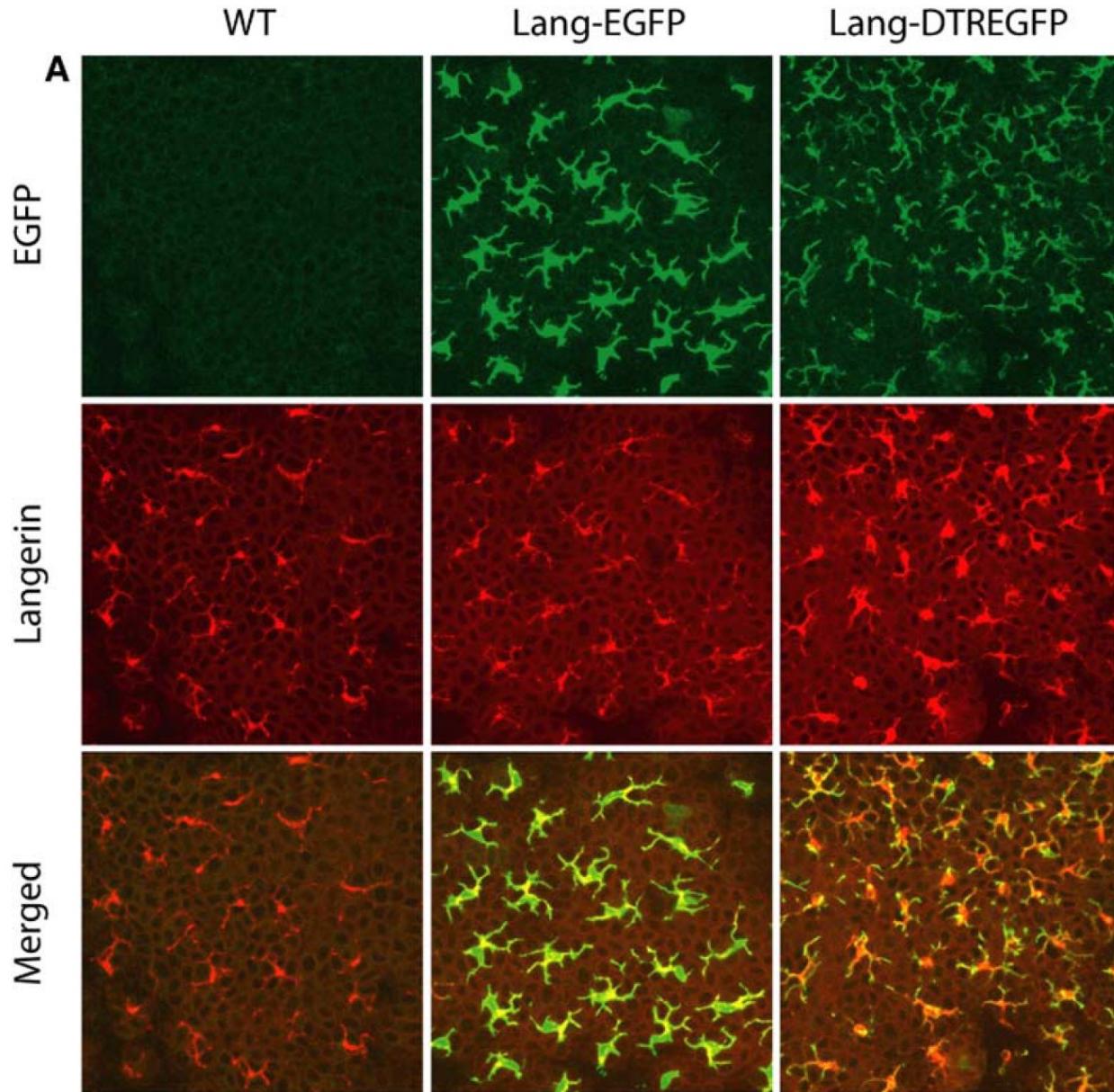


MHC II Färbung (a-c)

Langerin-DTR Mäuse nach DT Injektion:

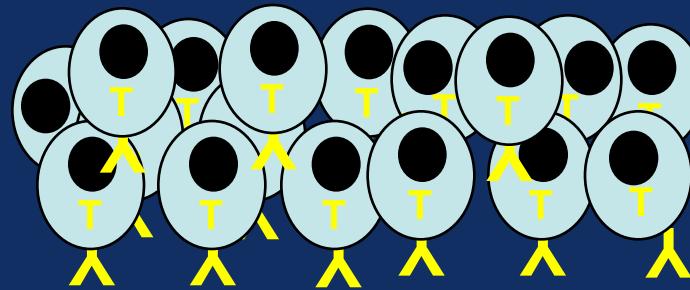
- d: nach 24 h
- e: nach 48 h
- f: nach 2 Wochen
- g-i: nach 4 Wochen



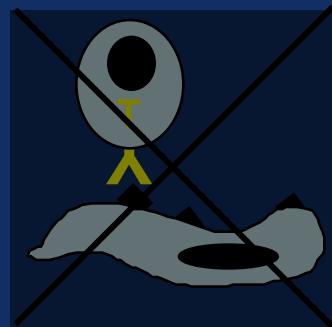


Thymic education: die young

Randomly generated
TCR repertoire
ensures diversity



Very high
avidity to
self



Harmful

Negatively
selected

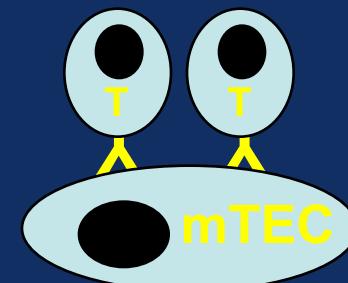
No
avidity to
self



Useless

Neglected

Intermediate
avidity to
self



Useful

Positively
selected

Is central tolerance sufficient ?

No, not all self-antigens are expressed in the thymus during development.

No, a single TCR may bind to a variety of different peptide/MHC complexes
("Promiscuity" of the TCR)



Many potentially auto-reactive T cells escape central tolerance

How can the immune system prevent the activation of these potentially self-reactive T cells in the periphery?

The “third function” of the thymus

- Negative selection of autoreactive T cells
- Positive selection of peripheral T effector cells
- Positive selection of $CD4^+CD25^+$ Tregs

FoxP3 ("scurfin")

- Transcription factor of the forkhead family
- Loss of function mutation gives rise to the scurfy phenotype:
 - X-linked recessive lymphoproliferative disease
 - Hyperresponsive CD4⁺ T cells
 - over-expression of various cytokines (IL-2, IL-4, etc.)
 - Autoimmune pathologies (diabetes, thyroiditis etc.)
 - Severe infections

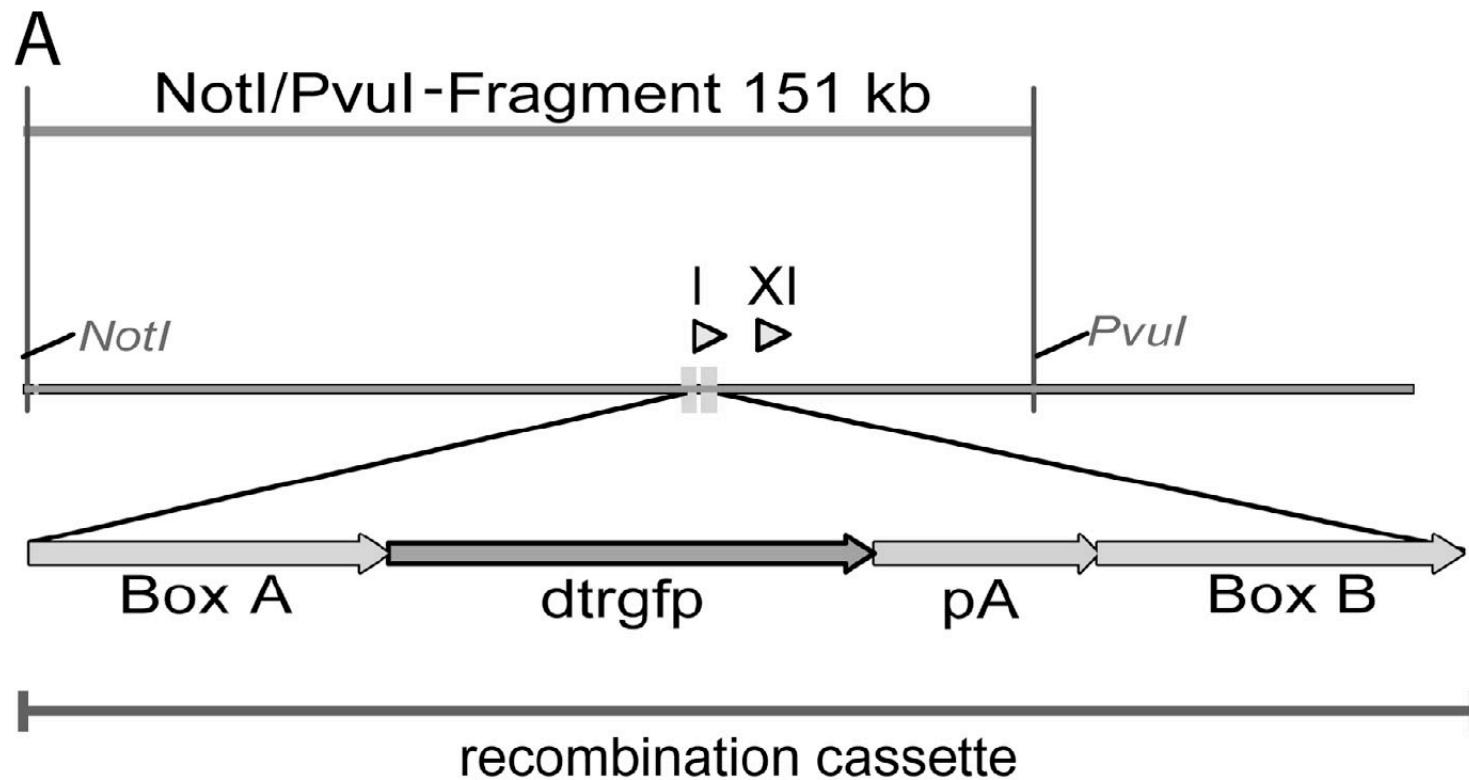


- Human equivalent: IPEX
(Immunodysregulation, polyendocrinopathy and enteropathy, X-linked)

DREG Mäuse: Depletion of regulatory T cells

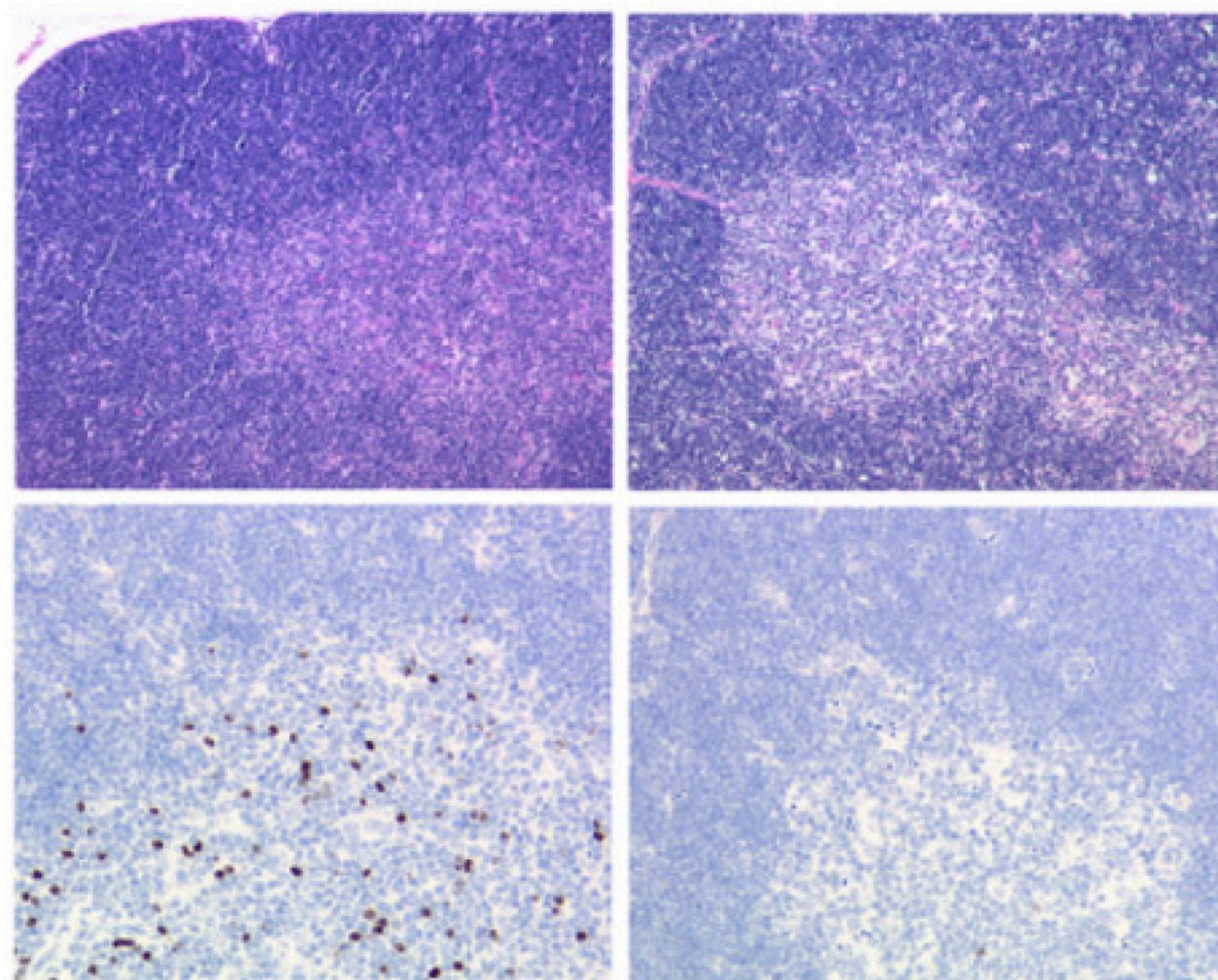
Exprimieren ein Diphteria Toxin Rezeptor-enhanced green fluorescent protein Fusionsprotein
Unter Kontrolle des *foxp3* Gens

Strategie: Generierung eines modifizierten „bacterial artificial chromosome“ und
Injektion des BAC in den Pronucleus als Transgen



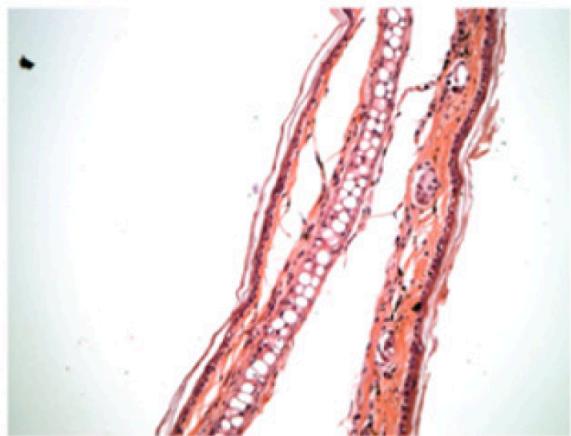
Box A, B: jeweils 1 kb homologer DNA

Depletion der regulatorischen T-Zellen durch Gabe des Diphteritoxins in Dereg-Mäuse..

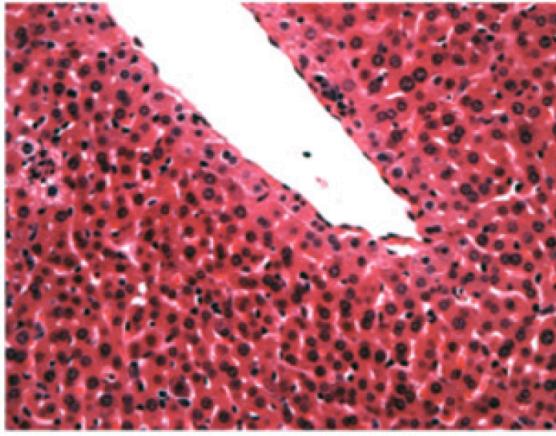


...führt zur Entwicklung autoaggressiver Phänomene

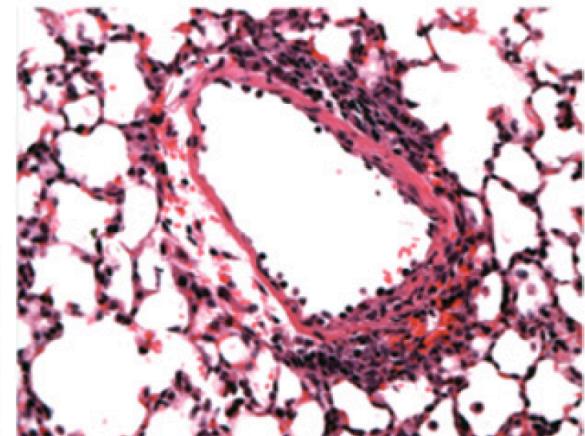
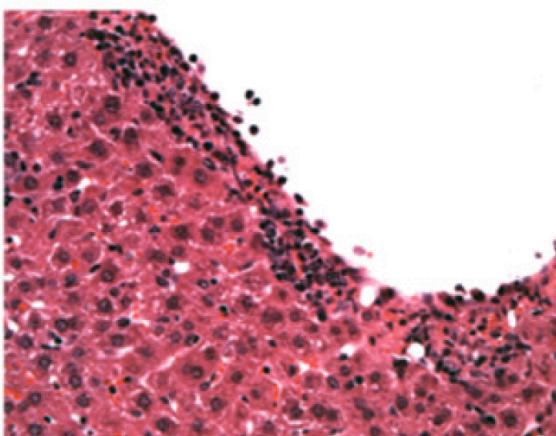
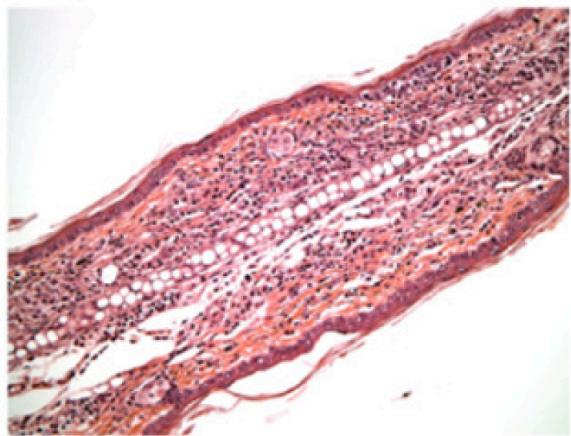
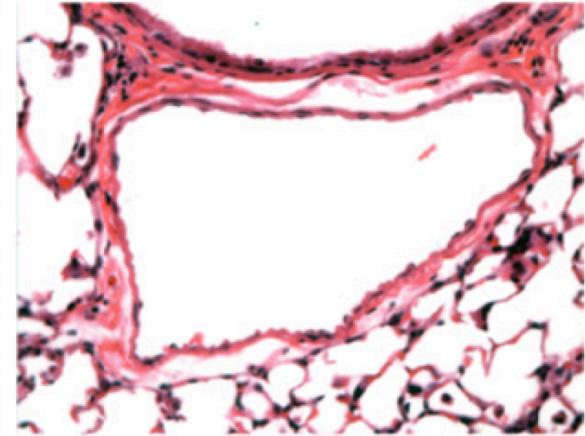
Skin



Liver



Lung



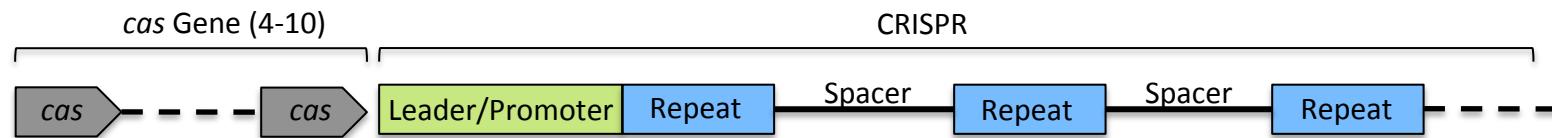
CRISPR/Cas: Immunität von Archaeen und Bakterien gegen fremde Nukleinsäuren

CRISPR: clustered regularly interspaced short palindromic repeats

Cas: CRISPR-associated (genes, proteins)

Finden sich in Archaeen (90%) und Bakterien (40%)

Entdeckt in E. coli (1987)



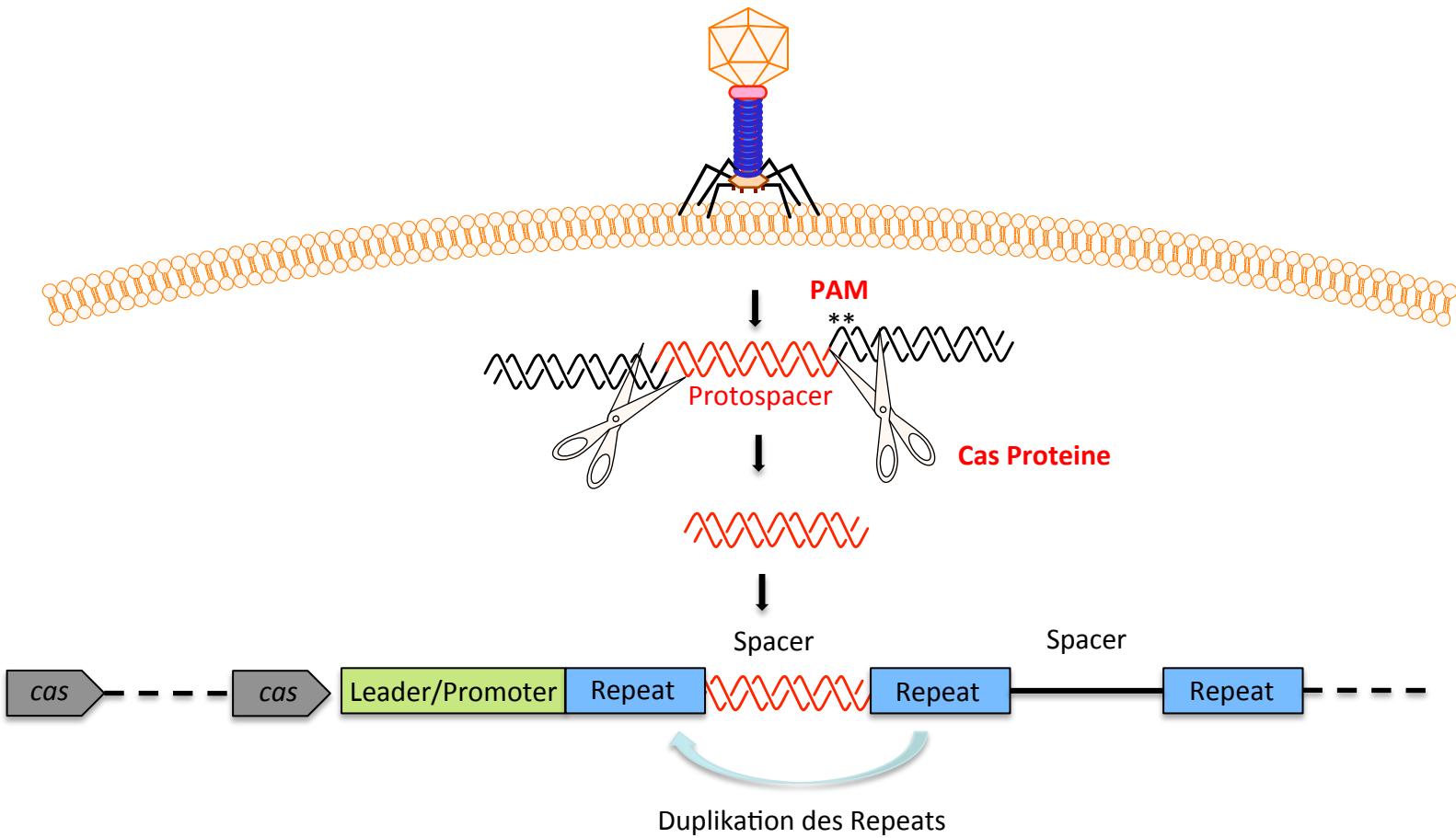
Cas: Große heterogene Gengruppe, deren Produkte Helikase u./o. Nuklease-Aktivität aufweisen

Repeats: 20-50 bp, innerhalb eines CRISPR-Locus konserviert, ansonsten heterogen

Spacer: Kurzes DNA-Fragment, das aus Viren oder Plasmiden stammt (Protospacer)

CRISPR/Cas-System verleiht Immunität gegen fremde Nukleinsäuren !

Einbau fremder DNA-Fragmente in den CRISPR-Locus



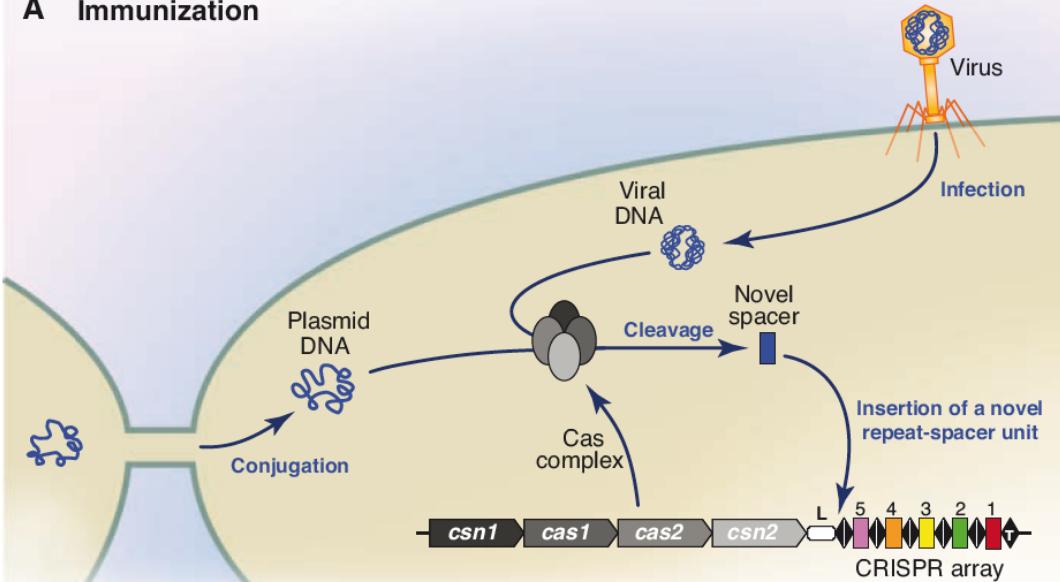
Protospacer werden nicht zufällig ausgewählt, sondern flankiert von PAM:

Protospacer adjacent motifs

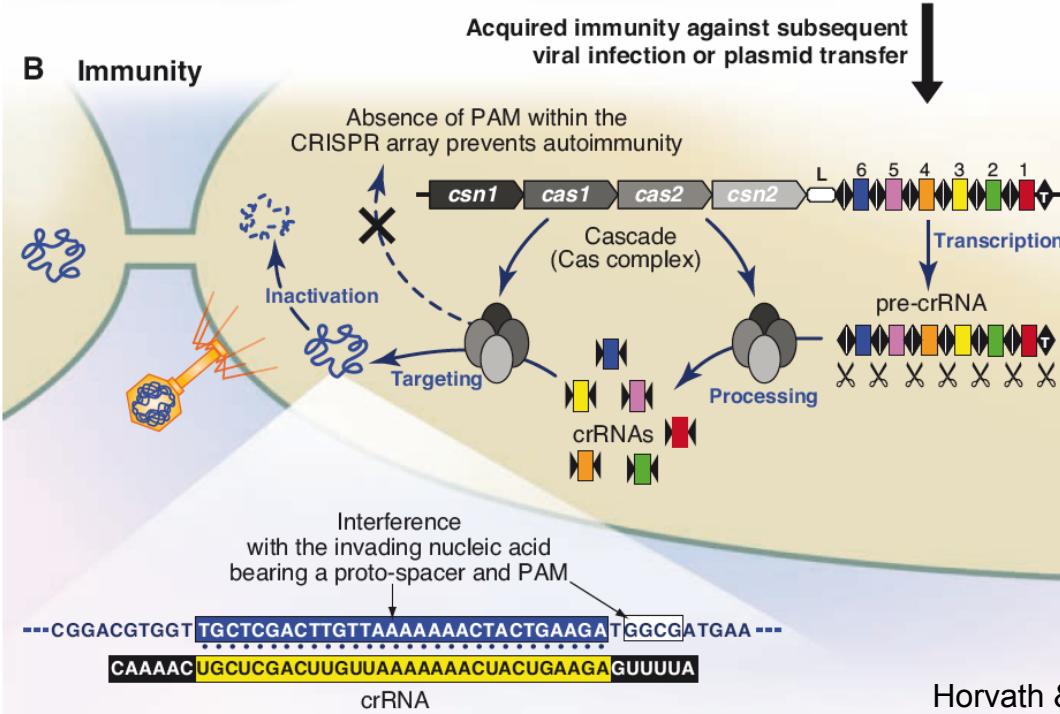
Table 2. CRISPR-Cas Systems Developed for Genome Editing and Their Cognate PAM Requirements

Species	PAM	References
<i>Streptococcus pyogenes</i>	NGG	Hsu et al., 2013
<i>Streptococcus mutans</i>	NGG	van der Ploeg, 2009
<i>Streptococcus thermophilus</i> (CRISPR3)	NGGNG	Deveau et al., 2008; Fonfara et al., 2014; Horvath et al., 2008
<i>Streptococcus thermophilus</i> (CRISPR1)	NNAAAAW	Fonfara et al., 2014
<i>Campylobacter jejuni</i>	NNNNACA	Fonfara et al., 2014
<i>Neisseria meningitidis</i>	NNNNGATT	Hou et al., 2013; Zhang et al., 2013
<i>Pasteurella multocida</i>	GNNNCNNA	Fonfara et al., 2014
<i>Francisella novicida</i>	NG	Fonfara et al., 2014
<i>Treponema denticola</i>	NAAAAN	Esvelt et al., 2013

A Immunization



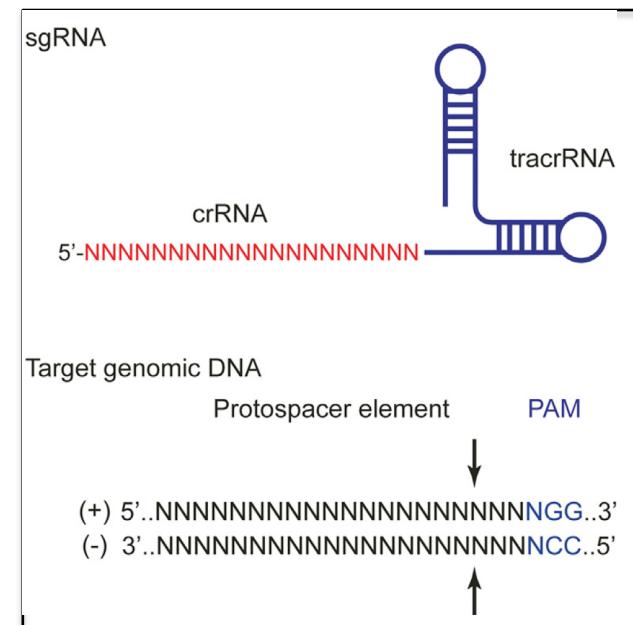
B Immunity



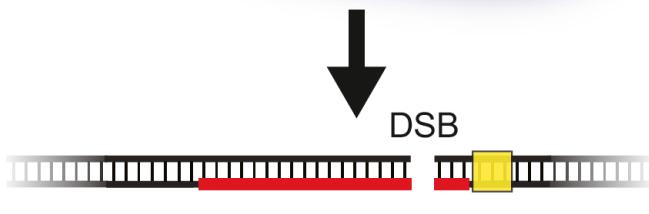
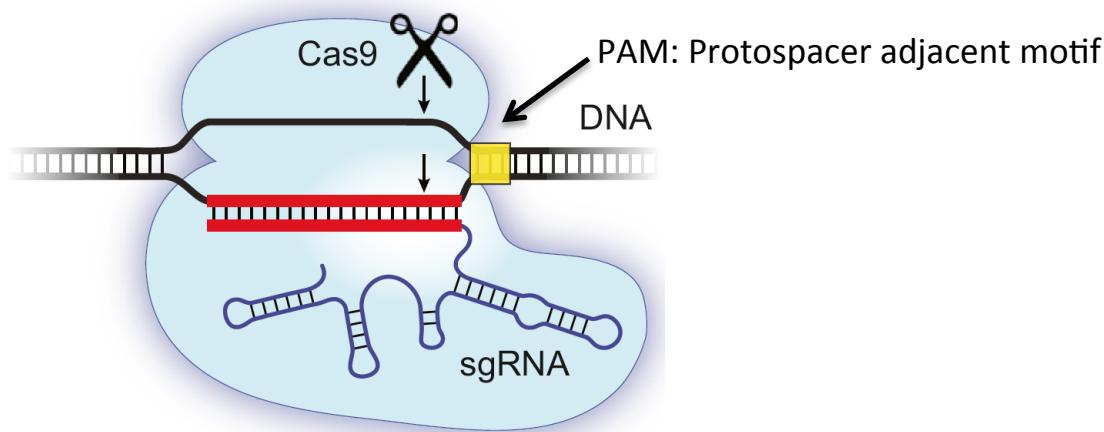
Genmanipulationen durch „RNA-guided DNA targeting“ mit Cas9

- Cas9 Endonuklease erzeugt Doppelstrangbrüche in DNA-Zielsequenzen
- Zielsequenzen werden durch einzelsträngige guide RNA (sgRNA) identifiziert
- sgRNA besteht aus crRNA und tracrRNA
- 5'-Ende der crRNA macht spez. Basenpaarungen mit DNA-Zielsequenz
- 3'-Ende der tracrRNA rekrutiert Cas9

Cas9 dient der Erkennung und Spaltung der Zielsequenz



Zelleigene Reparatsysteme werden zur Mutagenese benutzt



„Non-homologous end-joining“

In Abwesenheit geeigneter Matrizen
Fehleranfällig; oft kleine Insertionen oder Deletionen
(„Indels“)

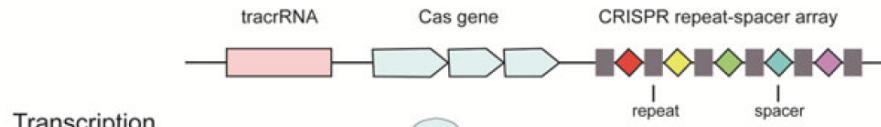
→ Einbau zufälliger Mutationen,
STOP-Codons

„homology-directed repair“

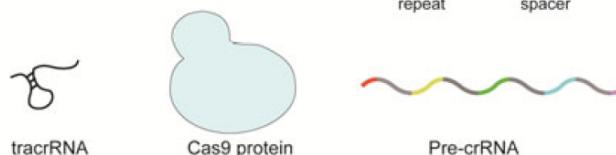
Einbau neuer Sequenzen mit
homologen Enden zur Zielsequenz

→ Punktmutationen, Deletionen,
Insertionen, konditionale Allele

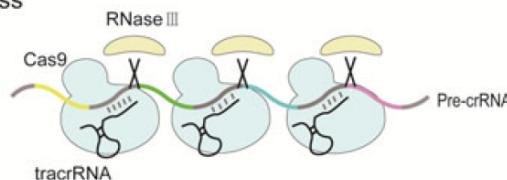
Genomic CRISPR locus



Transcription



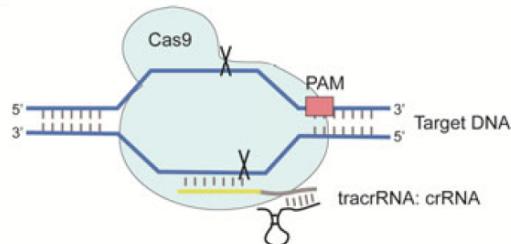
Post-transcription process



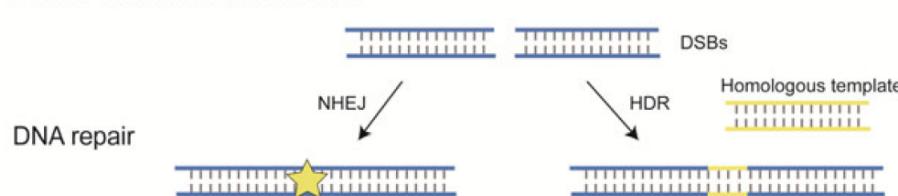
tracrRNA-crRNA-Cas9 complex formation



Cas9-mediated cleavage



Double strand breaks formation



PAM: protospacer adjacent motifs
 DSB: double strand break
 NHEJ: non-homologous end joining
 HDR: homology-directed repair

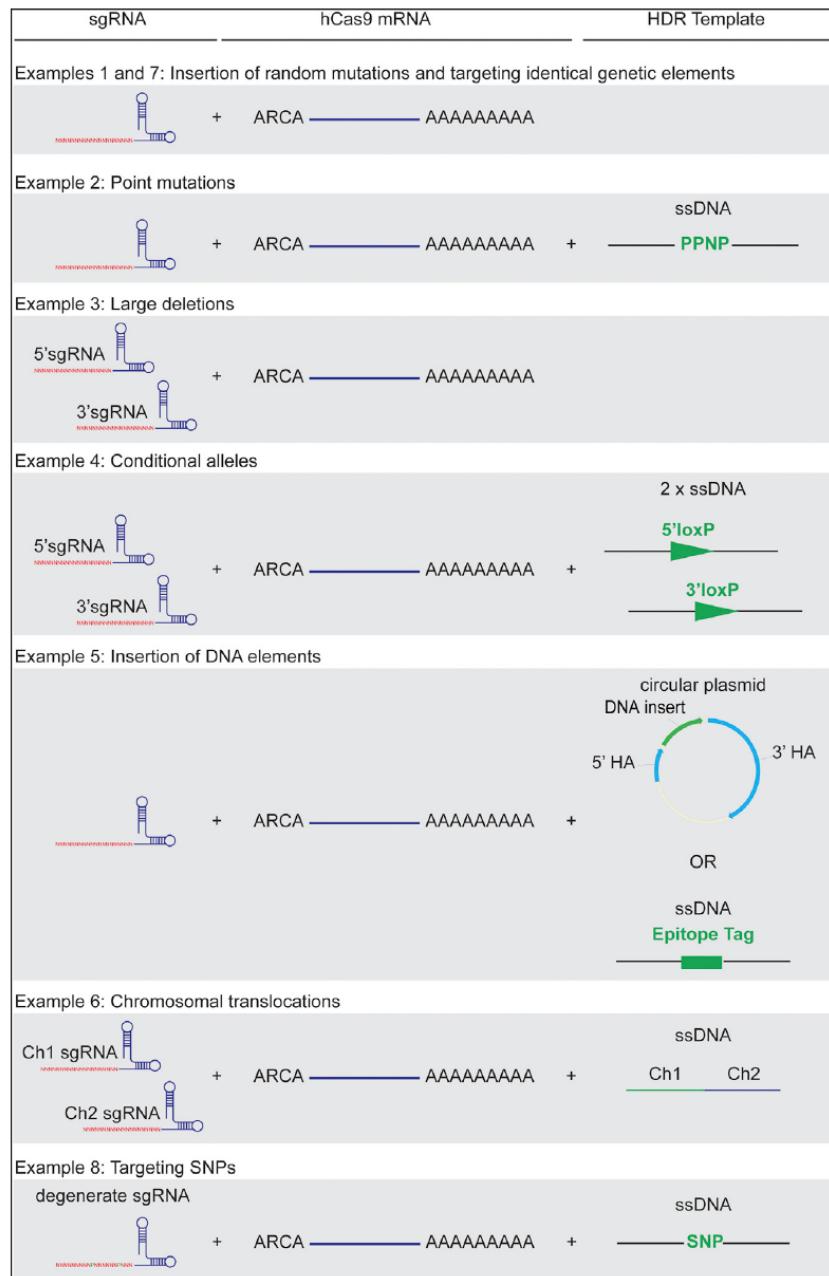


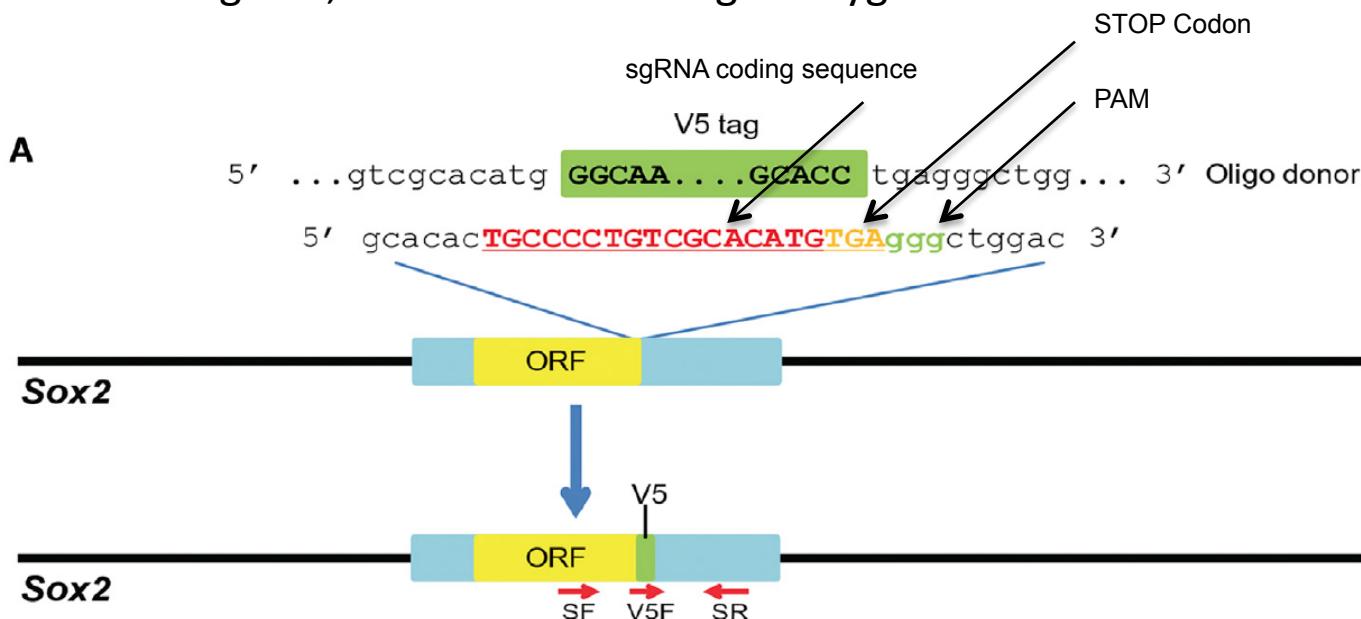
Figure 2. Targeting Strategies Used to Introduce Various Types of Mutations by CRISPR-Cas9 Technology

Examples 1 and 7 (insertion of random mutations and targeting identical genetic elements) make use of a single sgRNA together with Cas9 to target a single copy or multiple copy number genes. Resolution of the DSB(s) by NHEJ will result in the generation of several genetic modifications, including nonsense, missense, or various deletions. Example 2 (point mutations) makes use of a sgRNA together with Cas9 and an ssDNA oligonucleotide to facilitate HDR. Resolution of the DSB by HDR will result in the introduction of the desired mutation (P). Example 3 (large deletions) makes use of two sgRNAs flanking a region of interest. Resolution of the DSBs by NHEJ will result in the deletion of the region of interest. Example 4 (conditional alleles) also makes use of two sgRNAs flanking a region of interest, Cas9 and Cas2 ssDNA oligonucleotides, to facilitate HDR. Resolution of DSBs by HDR will introduce *loxP* sites at the desired locations. Example 5 (insertion of DNA elements) makes use of one sgRNA, Cas9, and a circular plasmid or ssDNA oligonucleotide. Resolution of DSBs by homologous recombination will introduce the DNA elements. Example 6 (chromosomal translocations) makes use of two sgRNAs designed to introduce DSBs on separate chromosomes (Ch1 and Ch2) together with Cas9 and a single ssDNA with sequence complementarity flanking the translocation break. Example 8 (targeting SNPs) makes use of a single degenerate sgRNA containing one or two mismatches with its target sequence. Resolution of the DSB by HDR will introduce a single-nucleotide mutation. The newly formed sites, now having an extra mismatch, might no longer be recognized by the degenerate sgRNA-Cas9 ribonucleoprotein complex and cleaved again, allowing the insertion of a SNP.

Anwendungen des CRISPR/Cas-Systems

Beispiel 1: Einbau eines synthetischen Epitops („tag“) in endogenes Gen

- sgRNA ist homolog zum Bereich des Stop-Codons des Zielgens
- ssDNA-Oligo mit 42b V5 tag und 60 homologen Basen auf jeder Seite fusioniert mit letztem Codon
- Injektion von sgRNA, Cas9mRNA und Oligo in Zygoten



Beispiel 2: Knock in eines Reportergens

