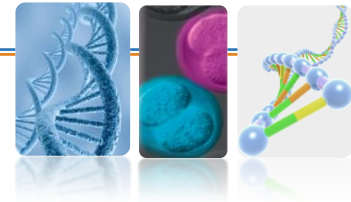


IMG: From gene function to understanding gene mutation

**functional genomics
based on mouse and rat models**

Radislav Sedláček



IMG

basic facts

Director: Václav Hořejší

- ❑ construction costs – over 35 mil. €
- ❑ opened in January 2007
- ❑ modern animal facility (for 30.000 mice)
- ❑ conference hall for 300 people
- ❑ total - cca 350 people including 140 PhD and MSc students



BIOCEV

basic facts

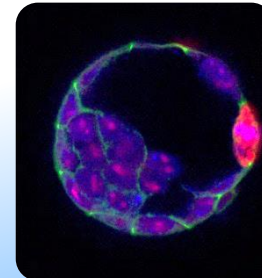
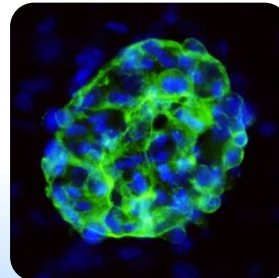


- ❑ **project: IMG & 6 partners incl. Charles University, Prague**
- ❑ **400 researchers & 200 students**
- ❑ **55 research teams in 5 programmes**
- ❑ **integration into European Research Area**
- ❑ **estimated total cost: 120 mil. €**
- ❑ **completion: May 2015**
- ❑ **5 state-of-the-art core facilities/infrastructures**
 - **Czech center for Phenogenomics**

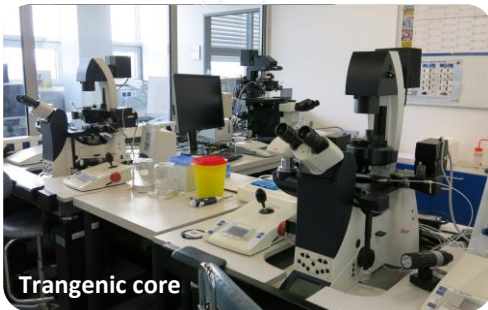
Czech Centre for Phenogenomics (CCP)

basic facts

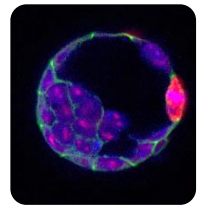
- ❑ unique in the Czech Republic, large national infrastructure
- ❑ 7200 m², 24 mil. €, 30 000 cages
- ❑ one of 5 in Europe, and of 12 in the world
- ❑ International centre, open acces



Czech Centre for Phenogenomics (CCP) activities



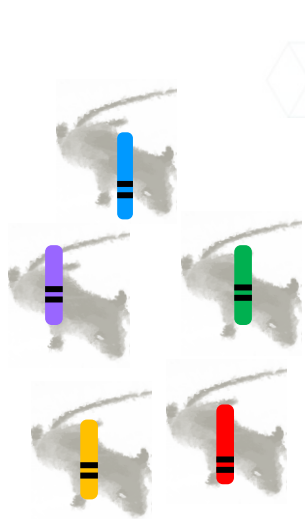
- ❑ new genetically modified (transgenic) models
- ❑ examination of the role of informative mutation in all main physiological systems
- ❑ standardized primary (410 parameters) and secondary phenotyping
- ❑ cryo-archiving and distribution of transgenic models



Phenogenomics:

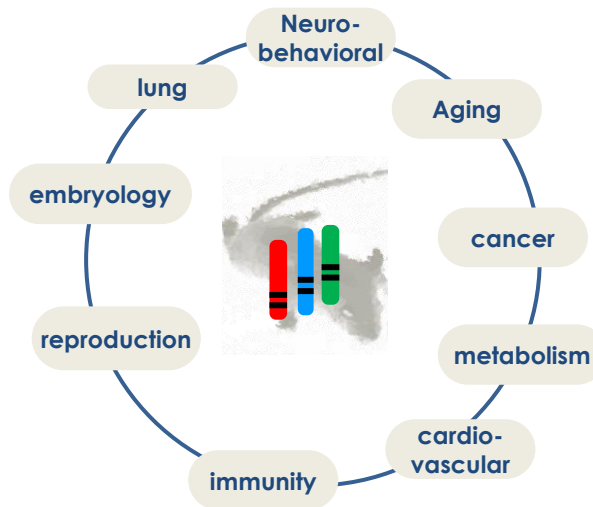
Systematic phenotypic analysis of animal models for annotation of gene function

genes to knock-out
(informative mutation)



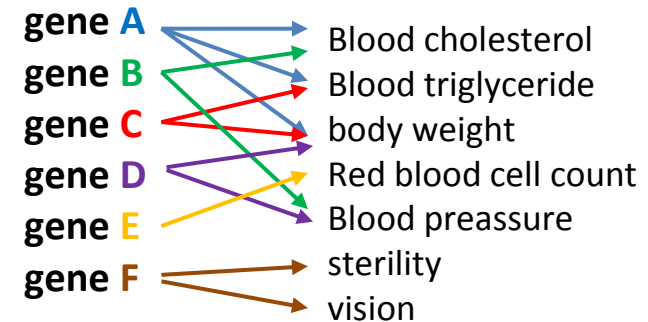
potential relevance to
human diseases

comprehensive & large-scale
phenotyping



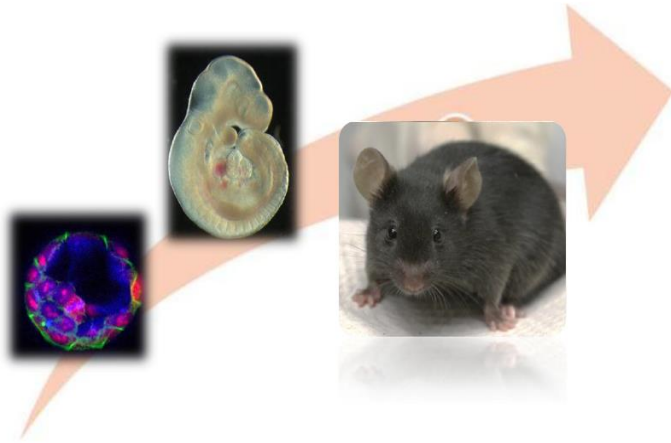
more than 400
standardized parameters

Phenotype:
deciphering functions of
individual genes



Encyclopaedic database
on gene function

research projects



Systemic standardized phenotyping (functions of individual genes)

410 parameters

new technologies of genetic manipulation
aging, epigenetics, embryogenesis

Genetically modified mouse models to study human diseases:

Reproduction

mouse strains with chromosomal substitutions
(consomic strains),
epigenetics, genetically controlled sterility, gene
duplication



research projects

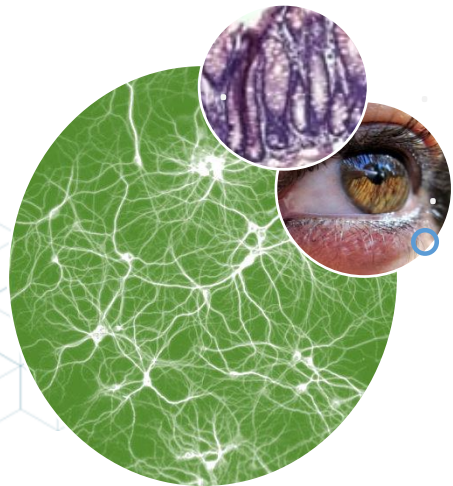
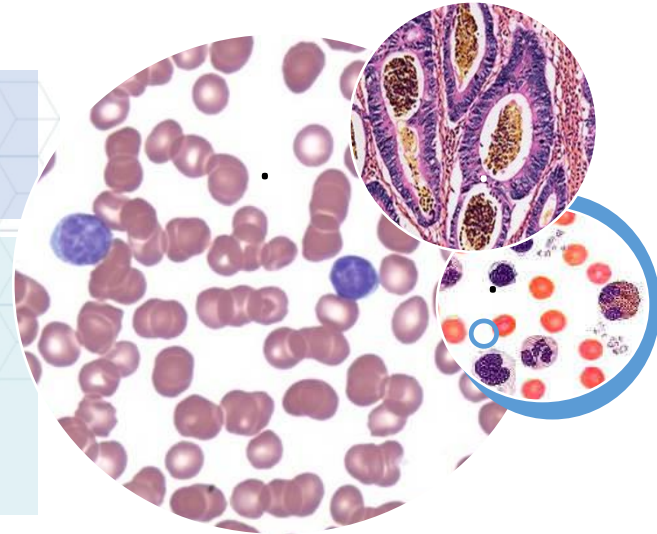
cancer:

colorectal carcinoma

Inflammatory bowel diseases

Patho-physiology of gut epithelia

Metabolic and cardiovascular diseases



Hematologic disorders:

chronic lymphatic leukaemia, non-Hodgkin lymphoma
remodeling of chromatin structures

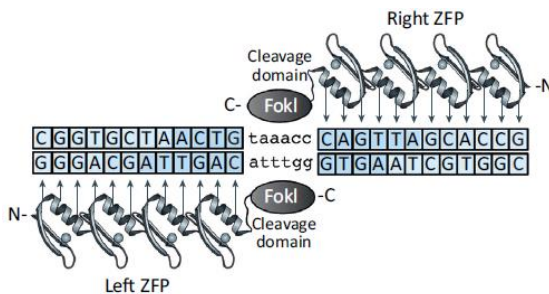
Neurobehavioral studies, auditory and visual functions
genetic disorders of eye, hearing impairment

programmable nucleases

-mediated gene modifications

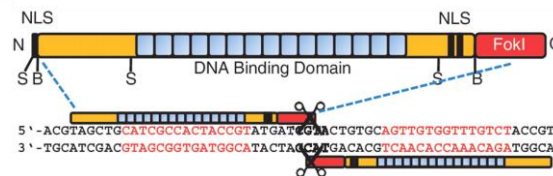
Zinc Finger Nucleases

- Cys2-His2 zinc finger domain
- Artificial arrays of 3-6 Zinc Fingers (9 – 18 bp)
- C-terminal fusion with endonuclease (FokI) – ZFN



Transcription Activator-Like Effectors nucleases (TALENs)

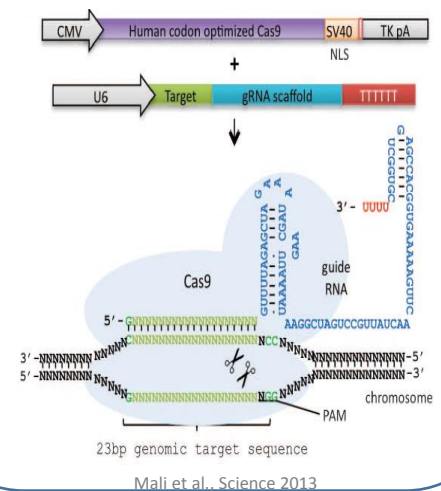
- Central Repeat Domain (CRD) responsible for DNA binding
- CRD consisting of 34aa highly homologous repeat modules
- DNA specificity determined by aminoacids 12 and 13 of each repeat – repeat variable diresidues (RVDs)



Modular assembly allows efficient and low-cost generation of TALEN vectors

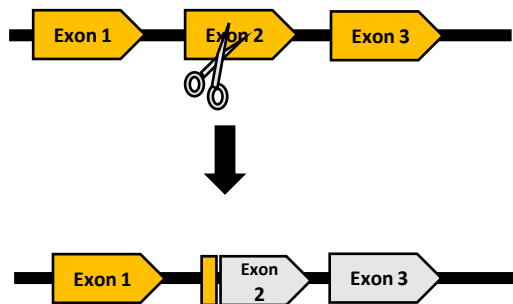
CRISPR/Cas9 system

- interspaced short palindromic repeats (CRISPR) systems
- CRISPR RNAs (crRNAs) in complex with CRISPR-associated (Cas) proteins

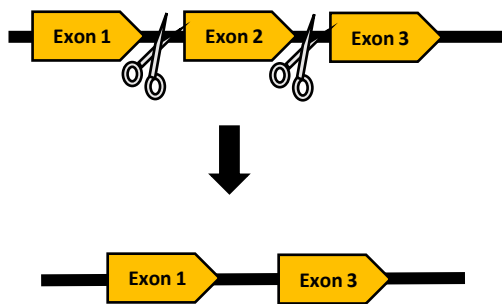


possibilities using programmable nucleases

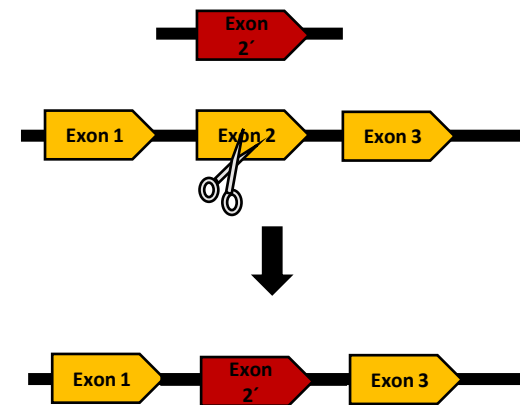
Generation of indel mutation
=> KO mouse



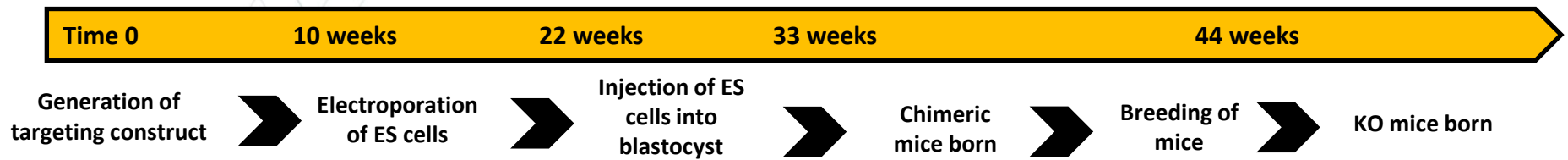
Excision of DNA fragment



Site-specific integration
of DNA fragment



KO mouse generation by homologous recombination in ES cells vs TALEN technology





programmable nucleases

Transcription Activator-Like Effectors (TALEN) technology



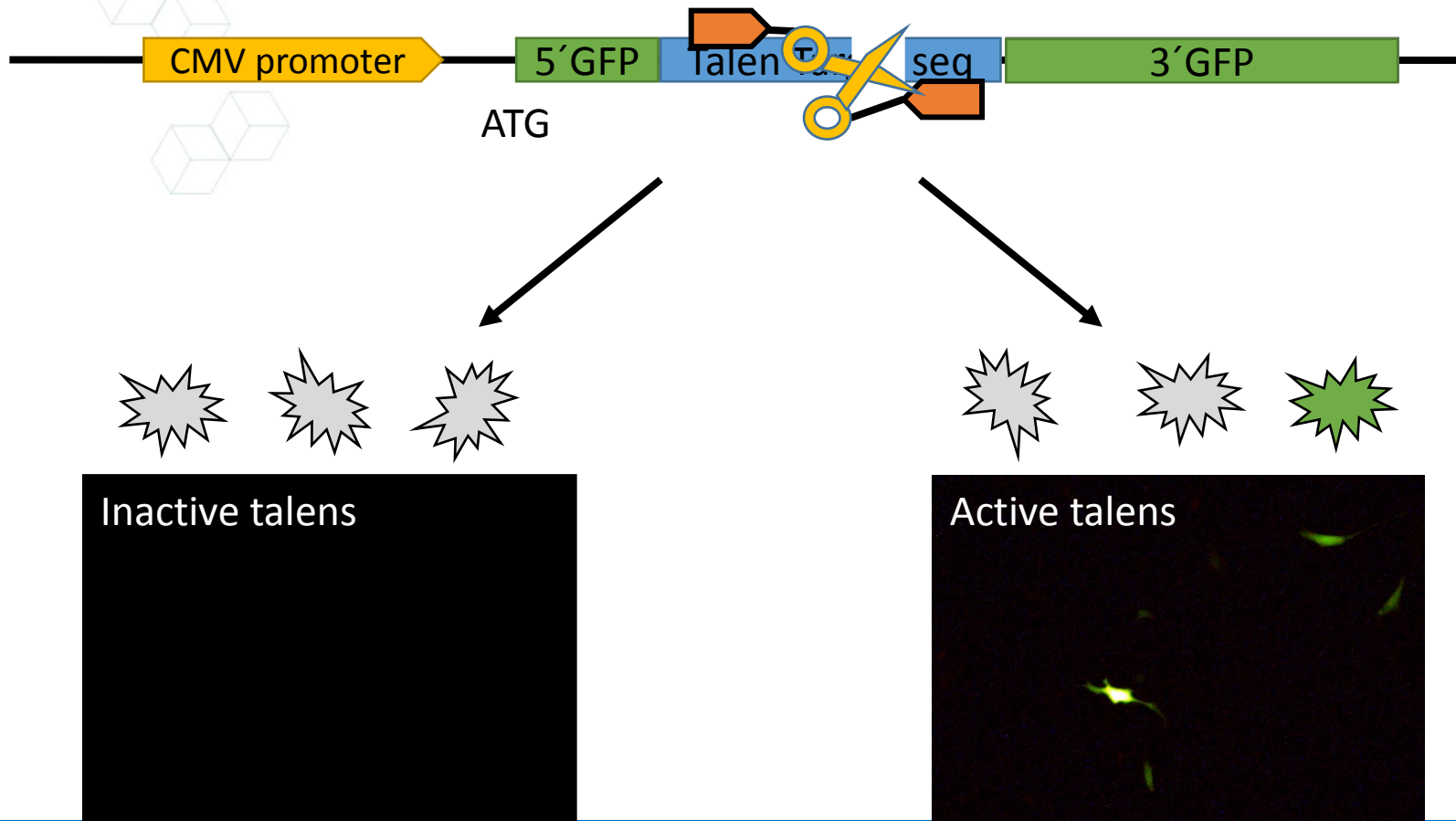
application examples

From gene function to understanding gene mutation

Enrichment of TALEN-targeted cells

- **Reporter plasmid**

- re-constitution of GFP activity





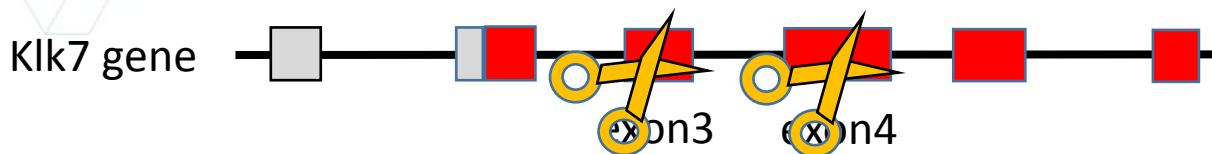
programmable nucleases

TALEN technology

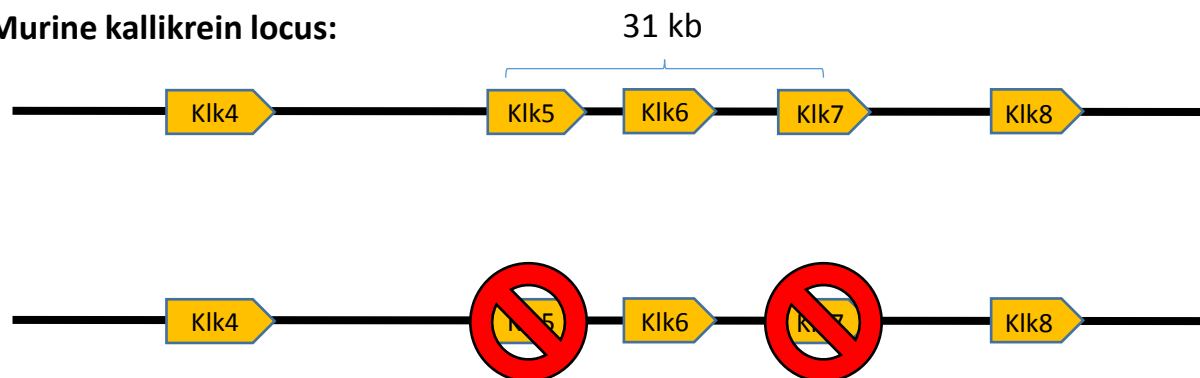
deletion mutants/knockouts

Generation of Kallikrein 7 KO mouse & double KLK5/7 KO mouse

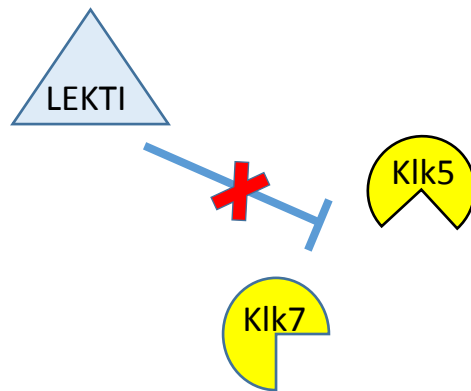
Generation of Klk5 KO mice



Murine kallikrein locus:



Generation of Kallikrein 7 KO mouse & double KLK5/7 KO mouse & triple Spink/KLK5/7 KO mouse



Netherton syndrome

Model:
Spink5 (LEKTI)-deficient mouse

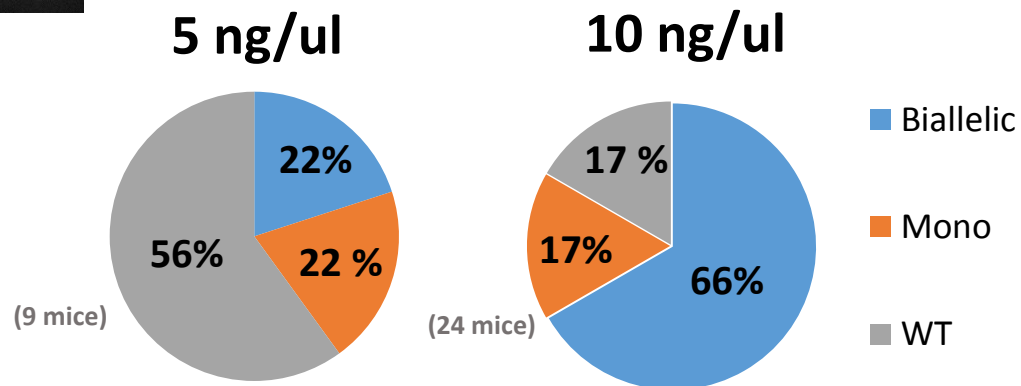
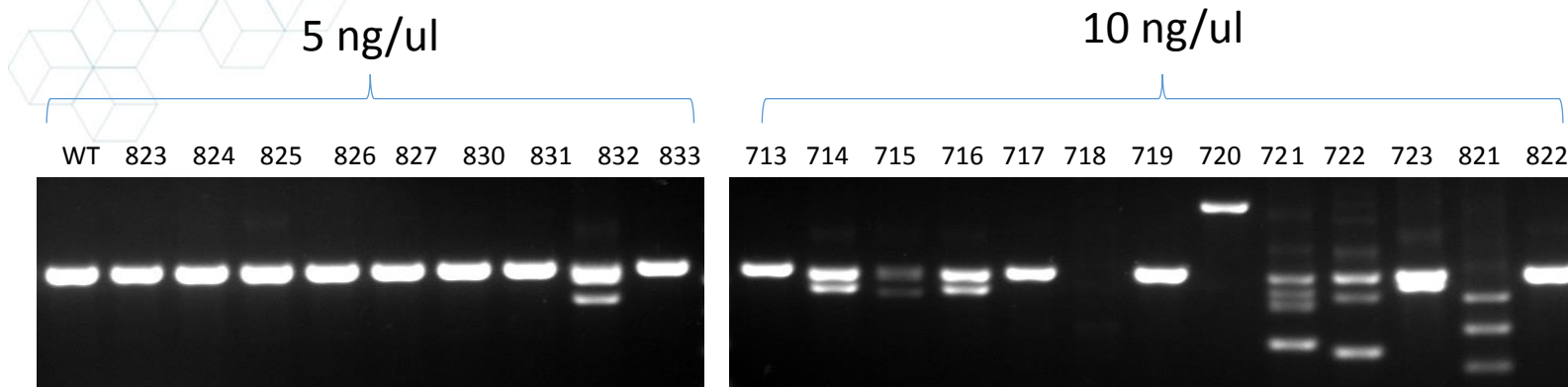
Patient



Descargues P. et al., Nature Genetics, 2005

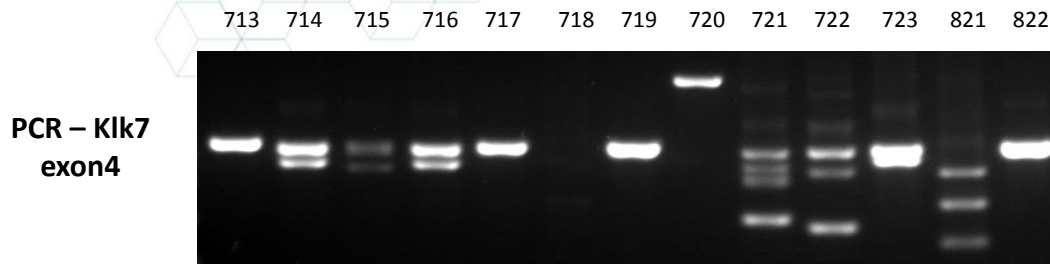
Generation of Klk7 KO mouse

Efficient targeting of Klk7 locus by TALE nucleases



Generation of Klk7 KO mouse

Klk7 KO - Sequencing of indel mutations



WT

AGTGGAGGCAGTCCAGCTTCCT**GAACACTGTGAACCC**CCAGGGACGTCATGTAC**CGTCTCTGGATGGGGC**ACCACAACCAGCCCAGACG

AGTGGAGGCAGTCCAGCTTCCT**GAACACTGTGAACCC**CCAGGG-----GTAC**CGTCTCTGGATGGGGC**ACCACAACCAGCCCAGACG -7 bp

AGTGGAGGCAGTCCAGCTTCCT**GAACACTGTGAACCC**CCAGGGACGT**TACT**CATGTAC**CGTCTCTGGATGGGGC**ACCACAACCAGCCCAGACG +4 bp

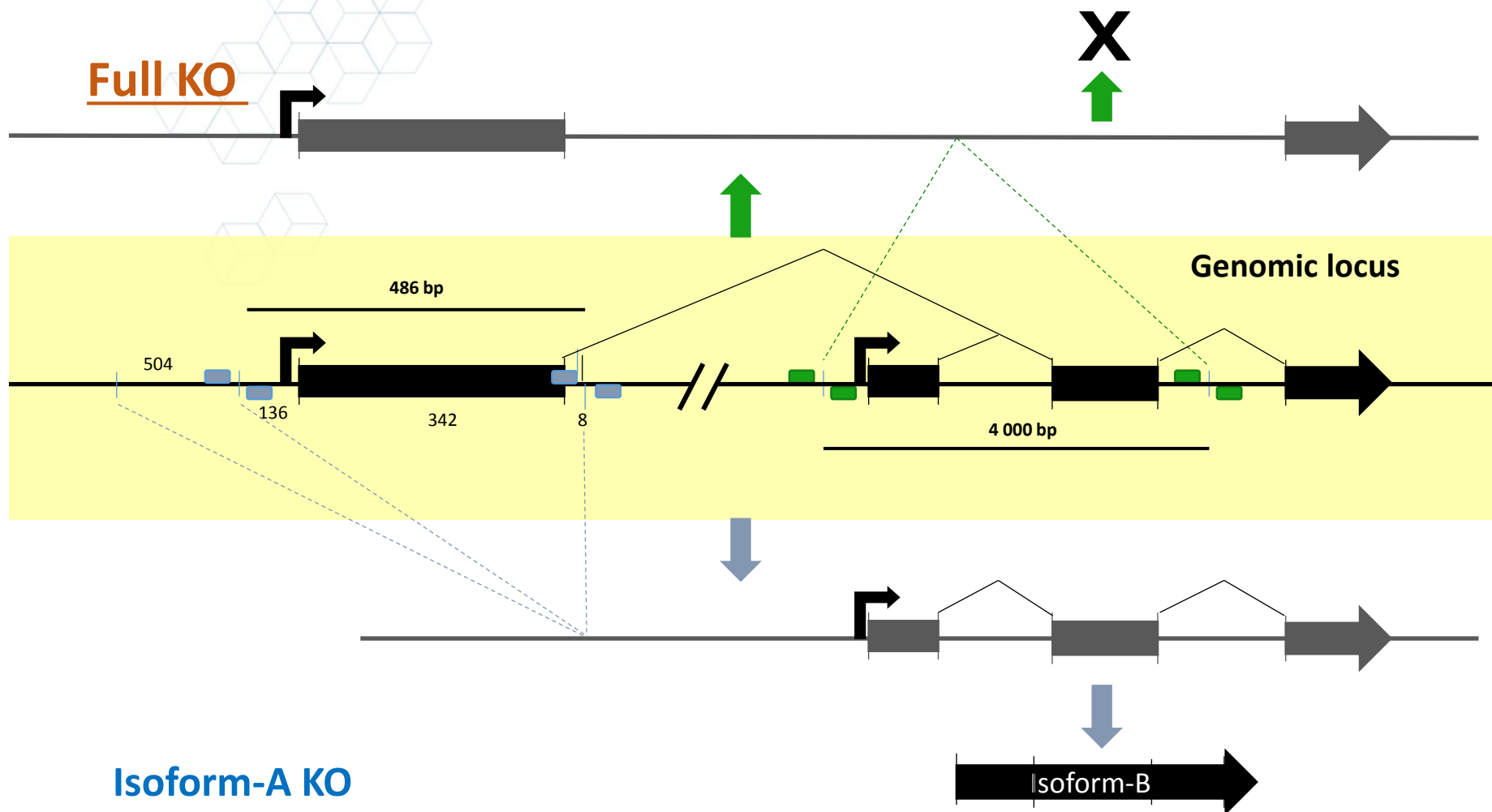
AGTGGAGGCAGTCCAGCTTCCT**GAACACTGTGAACCC**CCAGG---GTCATGTAC**CGTCTCTGGATGGGGC**ACCACAACCAGCCCAGACG -3 bp

AGTGGAGGCAGTCCAGCTTCCT**GAACACTGTGAACCC**CCA**cGTCTGGGCTGGTTGtGgTGCCCaTCCagAGACgtG**ACAACCAGCCCAGACG - 33 bp, + 37 bp

AGTGGAGG-----TTCATGTAC**CGTCTCTGGATGGGGC**ACCACAACCAGCCCAGACG - 38 bp, + 1 bp

AGTGGAGGCAGTCCAGCTTCCT**GAACACTGTGAACCC**CCAGG-----**AACGTCTCTGGATGGGGC**ACCACAACCAGCCCAGACG - 12 bp, + 2 bp

Isoform-specific KO of a microtubule associated protein: full KO vs. isoform-A KO



TALEN-mediated deletion of the MT-C element in Dicer intron 6

A Retrotransposon-Driven Dicer Isoform Directs Endogenous Small Interfering RNA Production in Mouse Oocytes

Matyas Flemr,¹ Radek Malik,¹ Vedran Franke,² Jana Nejeplinska,¹ Radislav Sedlacek,¹ Kristian Vlahovicek,^{2,3} and Petr Svoboda^{1,*}

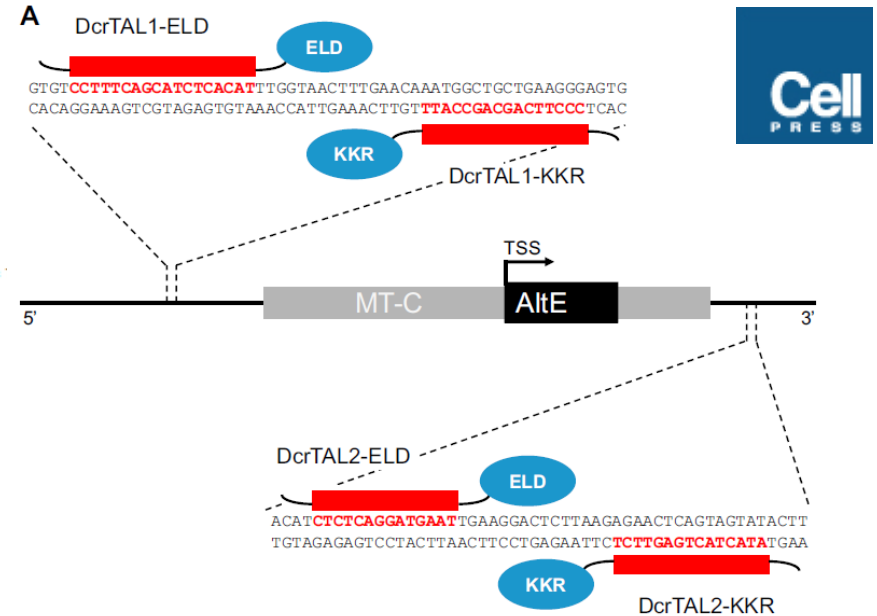
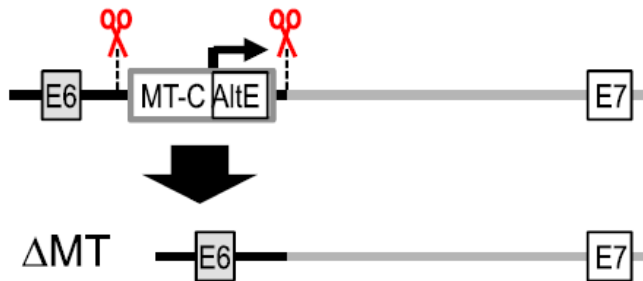
¹Institute of Molecular Genetics, Academy of Sciences of the Czech Republic, Videnska 1083, 142 20 Prague 4, Czech Republic

²Bioinformatics Group, Department of Molecular Biology, Division of Biology, Faculty of Science, University of Zagreb, Horvatovac 10000 Zagreb, Croatia

³Department of Informatics, University of Oslo, P.O. Box 1080 Blindern, NO-0316 Oslo, Norway

*Correspondence: svobodap@img.cas.cz

<http://dx.doi.org/10.1016/j.cell.2013.10.001>



B

animal	sex	genotype	allele	deletion position (m38/mm10)
28Y-06162	M	delMT ^{684/710}	684	chr12:104,727,100-104,727,783
			710	chr12:104,727,089-104,727,798
28Y-06163	M	delMT ⁴⁶³ / wt	463	chr12:104,727,100-104,727,562
28Y-06170	M	delMT ⁶⁷² / wt	672	chr12:104,727,110-104,727,781
28Y-06171	M	delMT ⁶⁶³ / wt	663	chr12:104,727,114-104,727,776
28Y-06172	M	delMT ⁶⁶⁹ / wt	669	chr12:104,727,109-104,727,777
28Y-06180	M	delMT ⁶⁷⁴ / wt	674	chr12:104,727,106-104,727,779
28Y-06188	M	delMT ⁶⁶⁷ / wt	667	chr12:104,727,110-104,727,776
28Y-06194	F	delMT ⁶⁴³ / wt	643	chr12:104,727,104-104,727,746
28Y-06203	F	delMT ⁷¹⁴ / wt	714	chr12:104,727,086-104,727,799

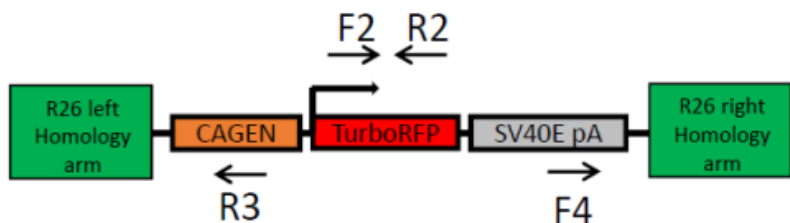
programmable nucleases

TALEN technology

insertional mutants

- point mutations
- reporter proteins/mouse
- fusion proteins

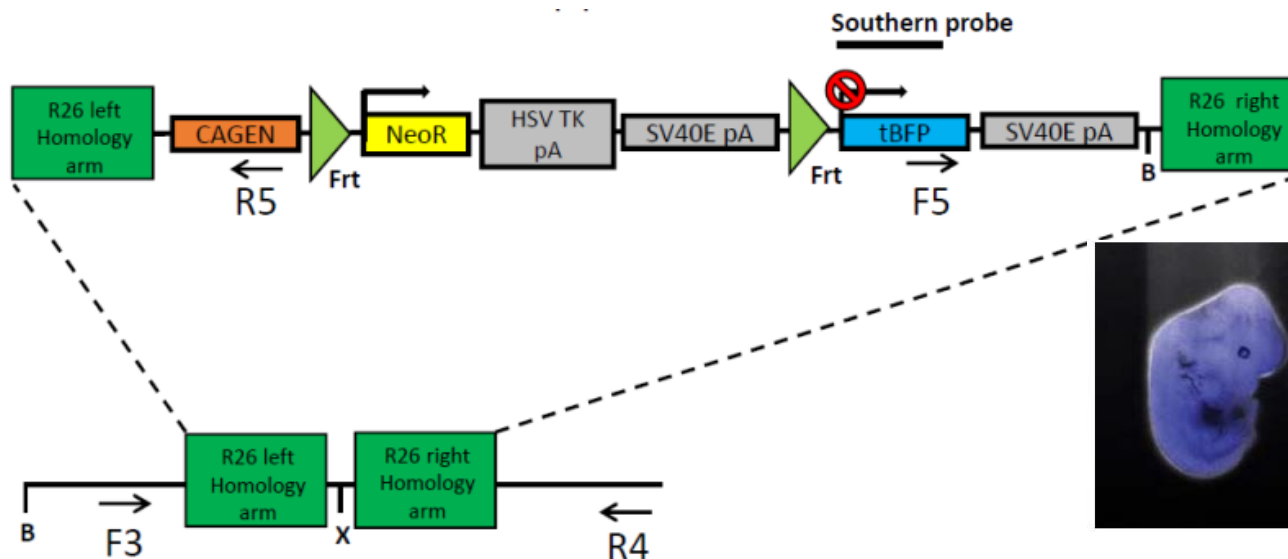
TALEN-mediated targeting into *ROSA* locus



turboRFP targeting vector



P. Kaspárek

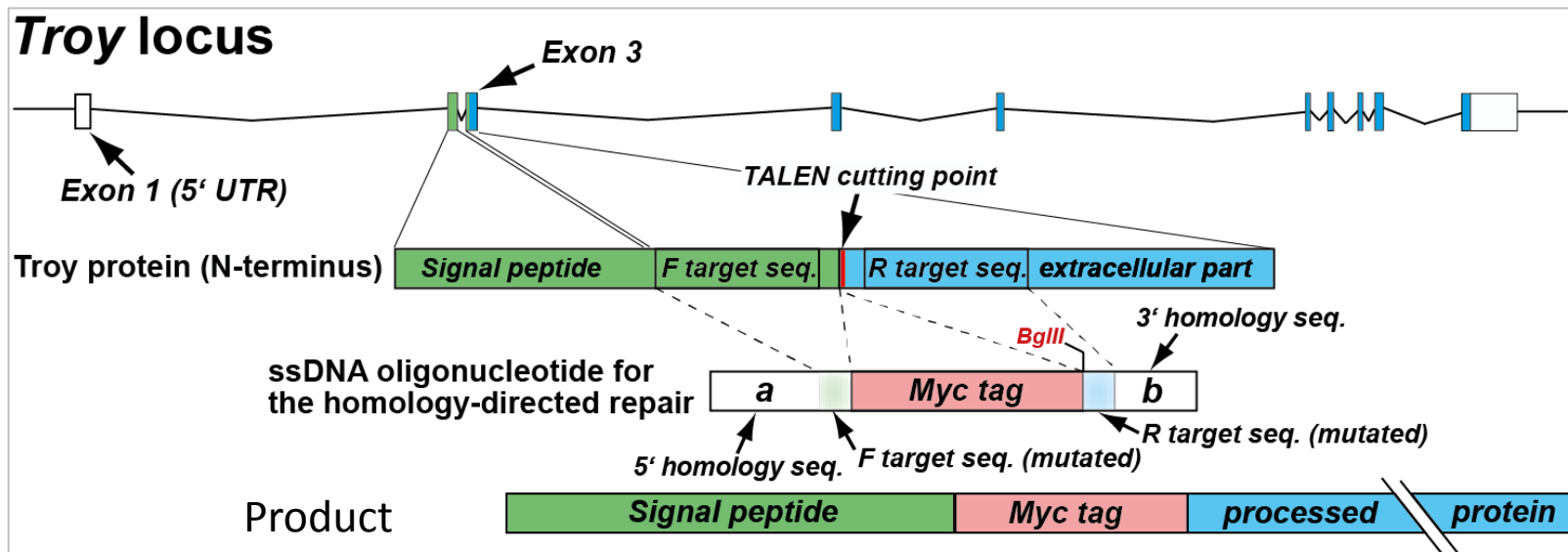
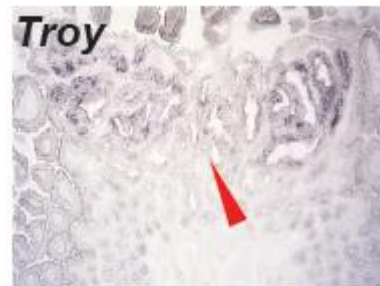
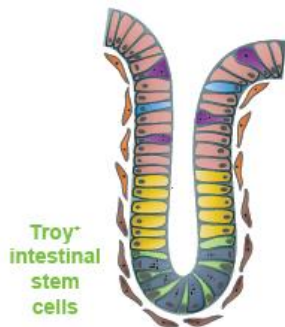


Blueflirt targeting vector



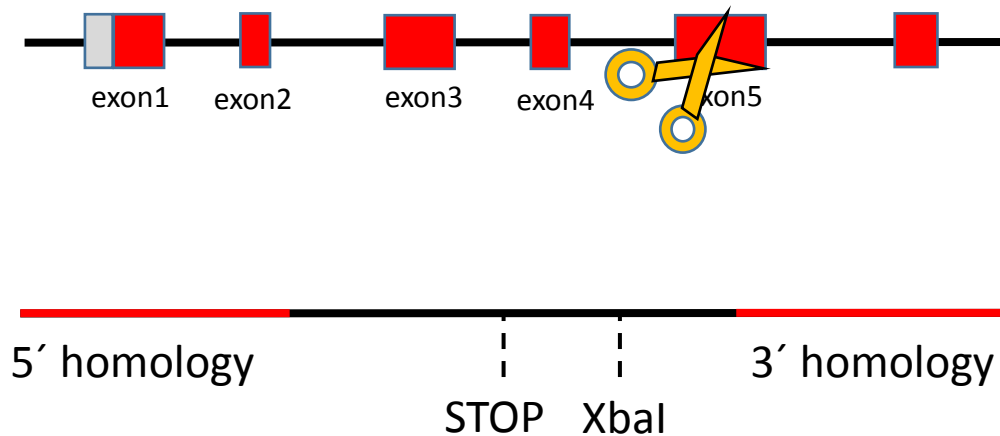
Reporter protein/mouse:

N-Myc TROY mouse

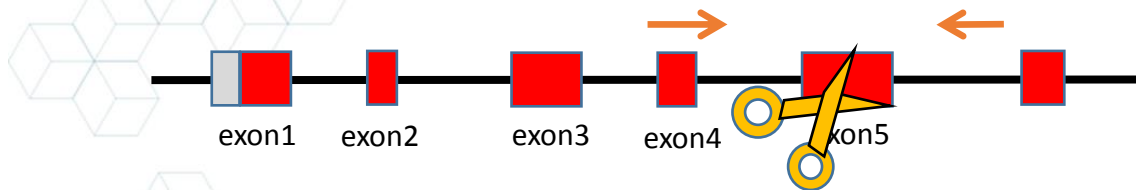


mouse model for Netherton syndrome

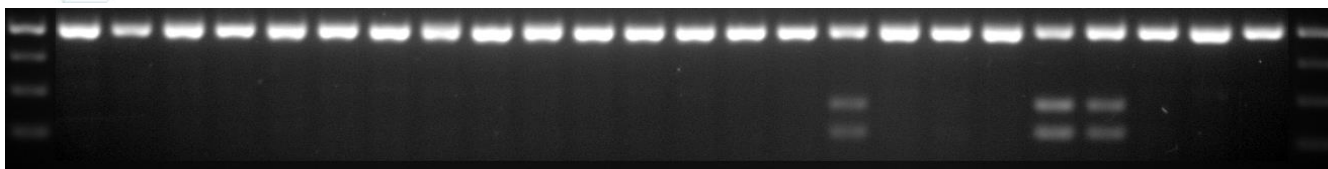
- Autosomal recessive skin disorder
- Point mutation in exon5 of Spink5 (-> STOP codon)



mouse model for Netherton syndrome



Spink5 PCR
- XbaI



STOP XbaI

GGCACAGATGGGAAAACATACCGCAGTAGATGTGAACTGTGCTGATCTAGAAATGCGTGAGTACCCTATAAAGCAGATATAGTGTTTATGCA

WT AGTTTGTGGCACAGATGGGAAAACATACCGCAGTAGATGTGAACTGTGTGCTGAGAAATGCGTGAGTACCCTATAAAGCAGATATAGTGTTTATGCAAATC

AGTTTGTGGCACAGATGGGAAAACATACCGCAGTAGATGTGAACTGTGCTGATCTAGAAATGCGTGAGGTACACCCTATAAAGCAGATATAGTGTTTATGCAAATC

STOP XbaI

mouse model for Netherton syndrome

AGTTTGTGGCACAGATGGGAAAACATACCGCAGTAGATGTGAACTGTGCTGATCTAGAAATGCGTGAGGTACACCCTATAAAGCAGATATAGTGTTTATGCAAATC

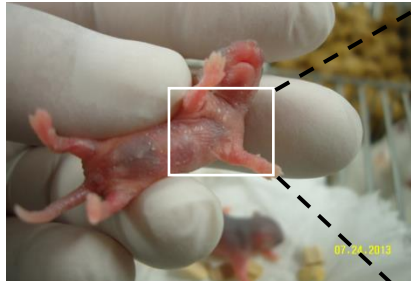
STOP XbaI

WT

MKTATVPMLLTLAFYLTQDAAGEKGNQDPCMFKFAQMKNGLTLCPKGNSSQSLNDIIFQSECI LCKRALEQGAPT KIMNVKLSRANRATDPAKLNCE SFKQRRKDGDFI CPSDTSSVCGTDGKTYRSRCELCAENA KSNHVDVKSEGE CGSSHLETDMCSDFRAY
VQDGR LGCTRES DPILGPDGRTHGNRCAMCAELFLKEAKENATRNRRESRIRRD AEKELKEFENQVRNGLFTRES DPIRGPDGMHGNKCALCAE I FMRQFT EEKGA EKND AEERAKAKMEIQKRCSEFQDRARNGTLFCTRENDPIRGLDGKTHGNLCSMCQAF
FKTEAEKKAEAGSRNRGSESESYAKLCD EYRKARKNGLYCTRENAPIRGPDGKIHGNTCSMCQAFFIQEDKARAKVKREAAKEMCSEFRNQARNGMLMCTRENDPVVGPDPGKRHSNKCAMCASVFLLEEEKKKDDTKVDAGKAKKEAVQELCRKYHTQLRNG
FLRCTRRNPIEGLDGKMYKNACFMCWAF FQQA KKS GAGFRPKVKREVKVDCSEYLALSKRGEIFCTRENDPVRGPDGKTHGNKCAMCKAVFKKENEERKRKEGENQRITSGESSGGNPKAKDECAQYRESMKHGQLSCTRESDFVRGVDGEHYNNKCVMKELLQ
KEMEETNKNSASRSNGTGSATGKDVCDDQFRSQMKNG

mut

MKTATVPMLLTLAFYLTQDAAGEKGNQDPCMFKFAQMKNGLTLCPKGNSSQSLNDIIFQSECI LCKRALEQGAPT KIMNVKLSRANRATDPAKLNCE SFKQRRKDGDFI CPSDTSSVCGTDGKTYRSRCELX





Czech Centre for Phenogenomics

HOME ABOUT US NEWS PHENOTYPING MODEL GENERATION RESEARCH & PROJECTS EDUCATION PARTNERS



Our research is

enhancing the understanding of the genetic bases for human diseases

Phenotyping

CCP: model generation services

Research

Thank you for your attention

Show all news →



G3 2014



Seminar - Genome editing using programmable nucleases



Second call for mouse production service