

# Numerous monogenic recessive disorders segregate in Swiss dairy populations

---

**Irene M. Häfliger**

**Institute of Genetics, Vetsuisse Faculty**

SABRE-TP

10. November 2021, Zürich

# Forward genetics approach



phenotype

whole-  
genome  
sequencing

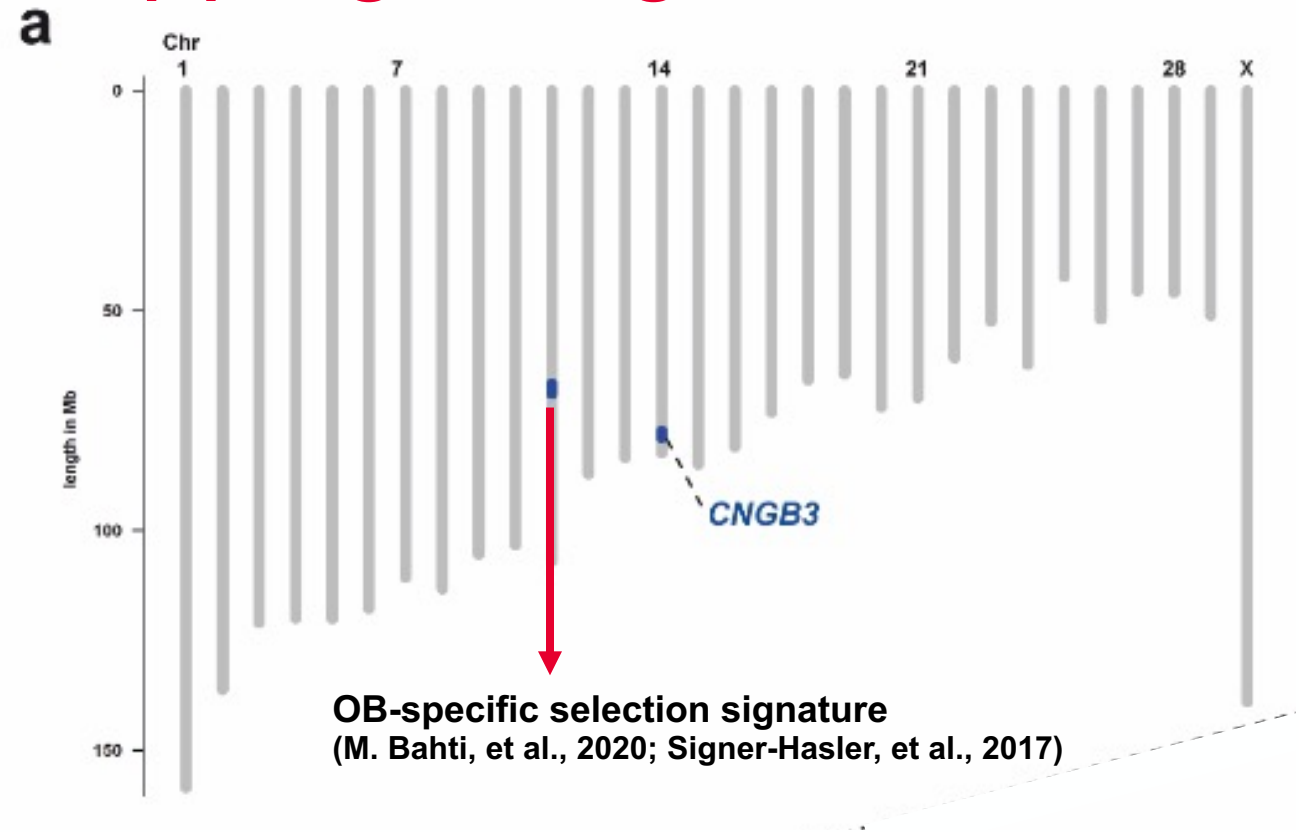
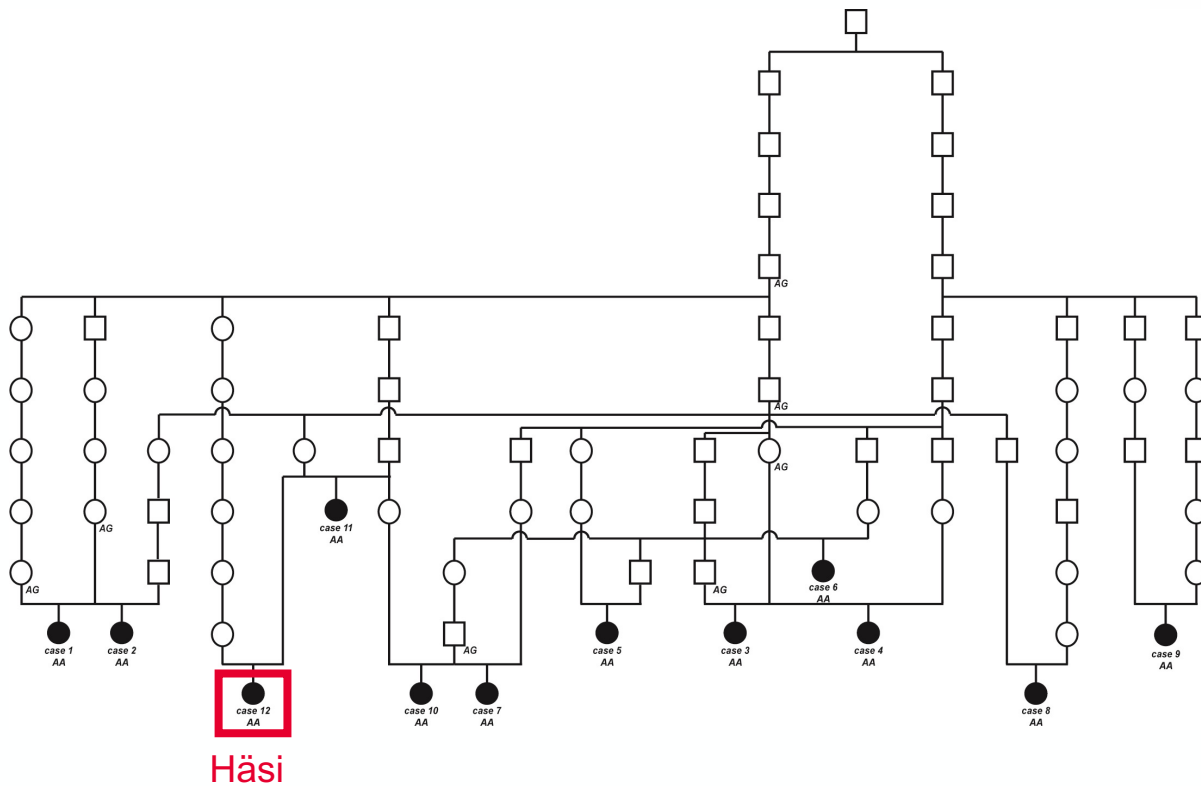
find the  
cause

# *CNGB3*-associated achromatopsia in Original Braunvieh



 **impaired vision similar to day-blindness in human (and dogs)**

# Genetic analysis: IBD mapping using 12 cases

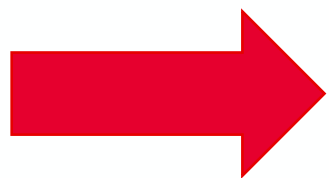


**~2.5 Mb run of homozygosity on chromosome 14**

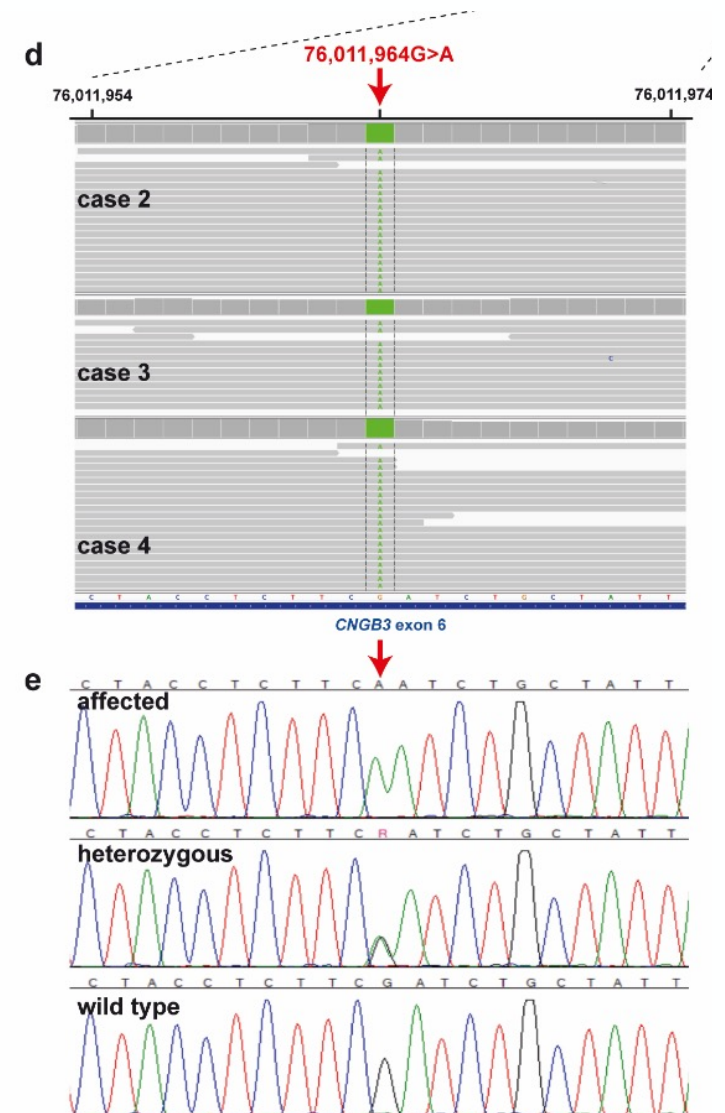


# Candidate variant identification

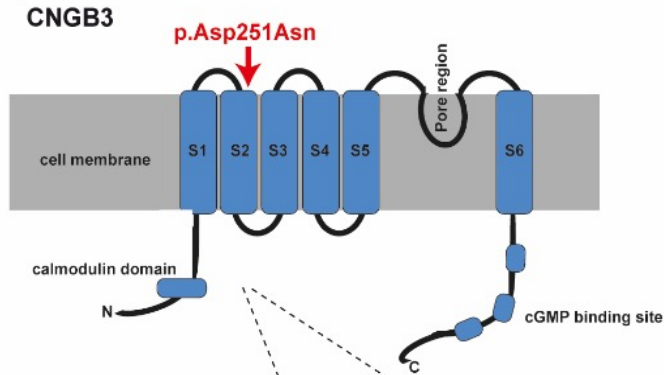
- WGS data
  - 3 cases, their 3 dams and 2 sires
  - 567 control genomes
- Variant filtering:
  - 1/1 in the cases
  - 0/1 in all parents
  - 0/1 or 0/0 in all other animals



**Chr 14:76011964 G>A**  
**CNGB3:p.Asp262Asn**

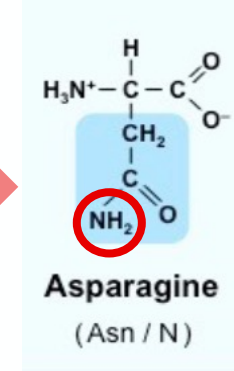
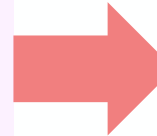
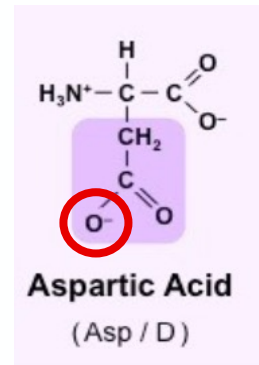


# Validity of the *CNGB3* variant



impairing channel bio-genesis Asp/Asn mutations affect the electrostaticity within the S1-S4 (N. Tanaka, et al., 2014)

	CNGB3	
cattle	XP_015330040.2	ITD L I C D T I Y L F D L L L I Q P R L Q F M R
human	NP_061971.3	. A . I . . . . . I . . . . . M . F . . . . . V .
mouse	NP_038955.1	. . . I V . . . . . I . . . . . C . I . . . . . V .
dog	NP_001003030.1	. . . I T . . . . . I . . . . . C . M . . . . . I K
rat	NP_001258167.1	. . . I . . . . . I . G . I . . . . . V .
chicken	XP_425928.4	A I . I . . . . . I C . . . . . C . . . . . F V . . . . . L .
zebrafish	XP_691142.4	L F . F A . . . . . L V N V I . I T M F . . . . . V K



- **Allele frequency**

- **0.099 in >2'950 Original Braunvieh**
- **0.0015 in >15'000 Brown Swiss**

submitted

Article

*CNGB3* missense variant causes recessive achromatopsia in Original Braunvieh cattle

Irene M. Häfliger<sup>1\*</sup>, Emma Marchionatti<sup>2\*</sup>, Michele Stengård<sup>3\*</sup>, Sonja Wolf-Hofstetter<sup>1</sup>, Julia M. Paris<sup>1</sup>, Joana G. P. Jacinto<sup>4</sup>, Christine Watté<sup>5</sup>, Katrin Voelter<sup>6</sup>, Laurence M. Occelli<sup>6</sup>, András M Komáromy<sup>6</sup>, Anna Oevermann<sup>7</sup>, Christine Goepfert<sup>8</sup>, Angelica Borgo<sup>9</sup>, Raphaël Roduit<sup>9</sup>, Mirjam Spengeler<sup>10</sup>, Franz R. Seefried<sup>10</sup> and Cord Drögemüller<sup>1\*</sup>

# *APOB*-associated cholesterol deficiency (CD) in Holstein

- 1.3kb ERV insertion in *APOB* linked to CDH
- Biologically incapable of digesting cholesterol in the intestine
- Clinical signs: asymptomatic diarrhea
- Calves mostly “starve” to death
- Allele frequency in Swiss Holstein population (2021) at **0.0612**

ANIMAL GENETICS

Immunogenetics, Molecular Genetics  
and Functional Genomics



SHORT COMMUNICATION

doi: 10.1111/age.12801

## *APOB*-associated cholesterol deficiency in Holstein cattle is not a simple recessive disease

Irene Monika Häfliger\*, Sonja Hofstetter\*, Thomas Mock<sup>†</sup>, Manuela Hanna Stettler<sup>†</sup>, Mireille Meylan<sup>†</sup>, Kemal Mehinagic<sup>‡</sup>, Nadine Stokar-Regenscheit<sup>‡</sup> and Cord Drögemüller\* 

\*Institute of Genetics, Vetsuisse Faculty, University of Bern, Bern, 3001, Switzerland . <sup>†</sup>Clinic for Ruminants, Vetsuisse Faculty, University of Bern, Bern, 3001, Switzerland . <sup>‡</sup>Institute of Animal Pathology, Vetsuisse Faculty, University of Bern, Bern, 3001, Switzerland .

# *APOB*-associated cholesterol deficiency (CD) in Holstein

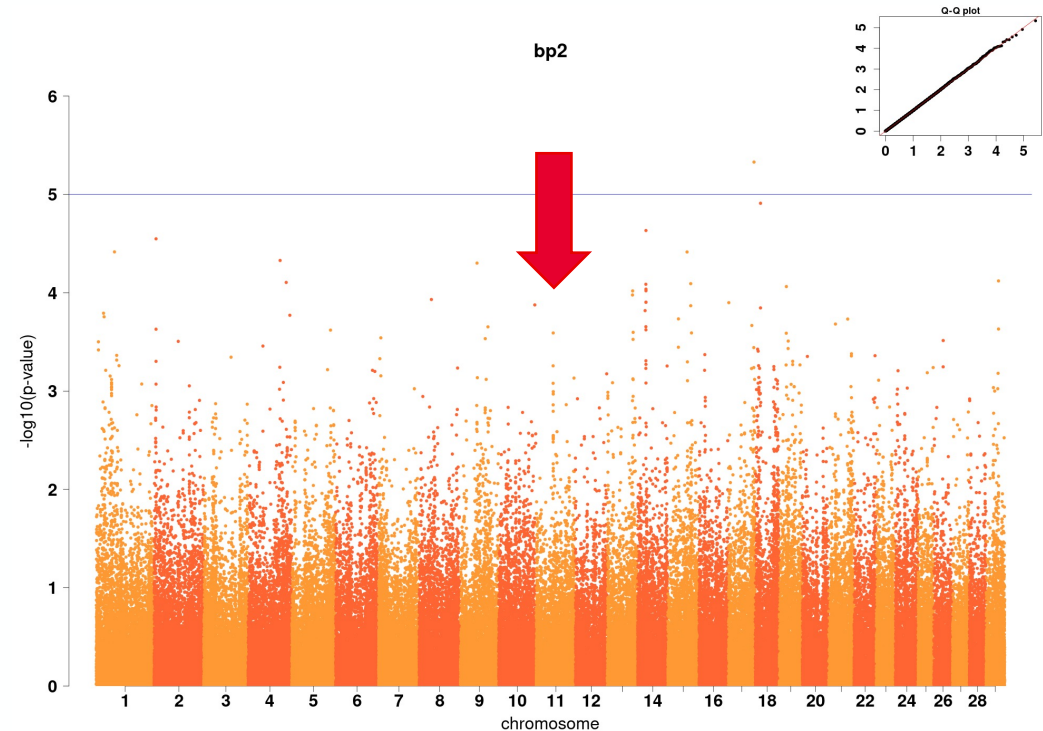
- **Problem:** Co-dominant effect
- Sample calculation

Assumption	# animals
Herdebooks (Population size)	250'000 healthy cows
Homozous wt HWE	220'360
Homozous carrier HWE	935 🦠
Heterozygous carrier HWE	28'705

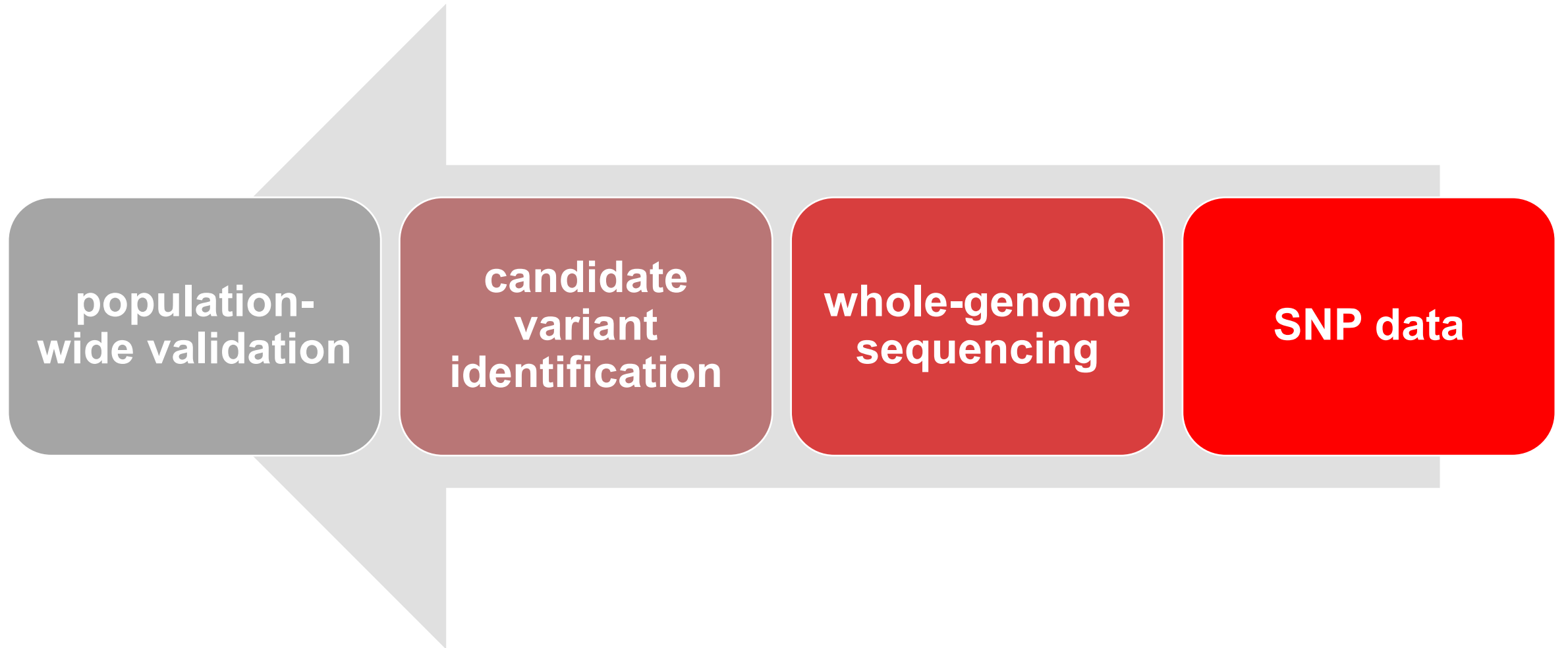
Every 3<sup>rd</sup> heterozygous carrier shows symptoms 9'568

Every 10<sup>th</sup> heterozygous carrier dies due to the symptoms 2'871 🦠

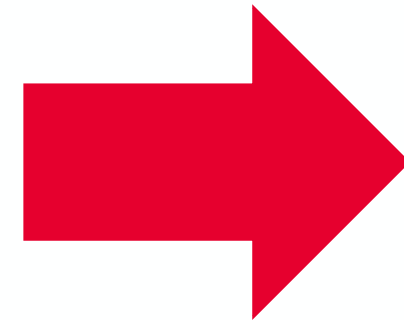
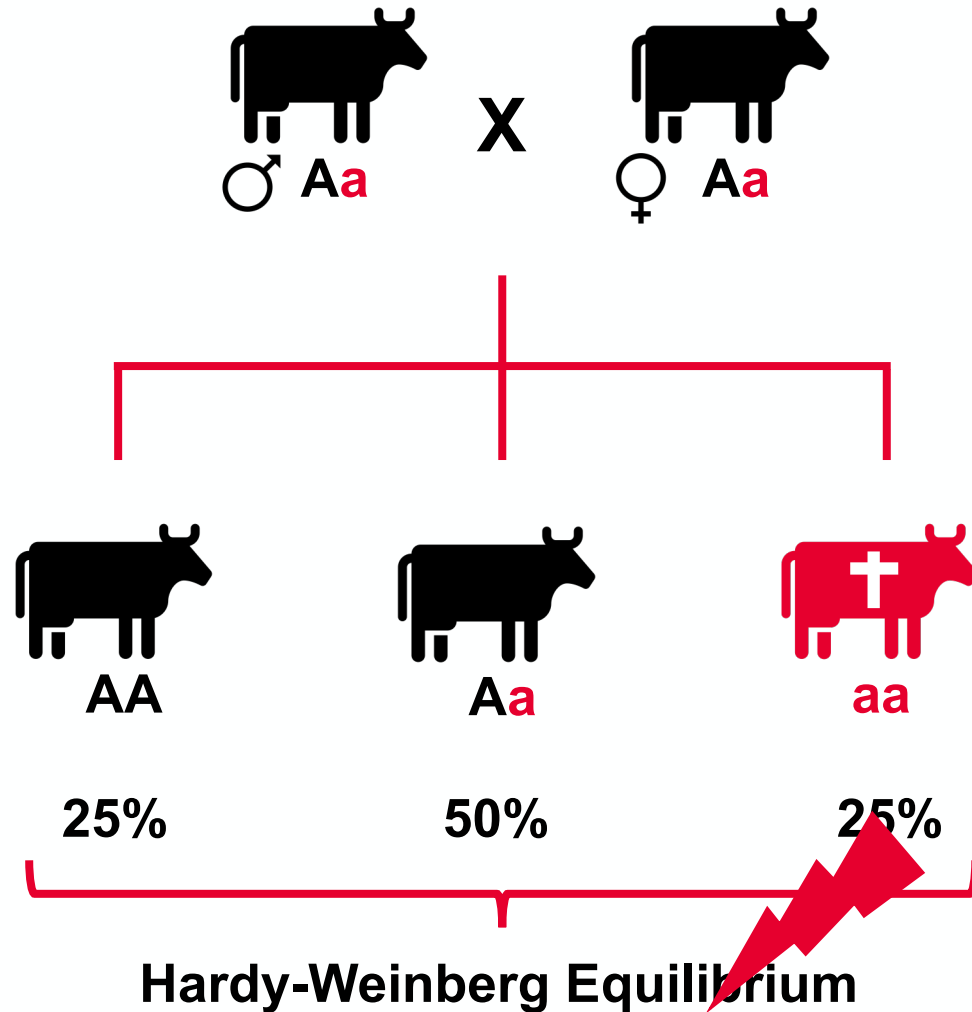
sum 🦠 3'806 🦠



# Reverse genetics approach



# Mendelian Inheritance Theory of Recessive Variants

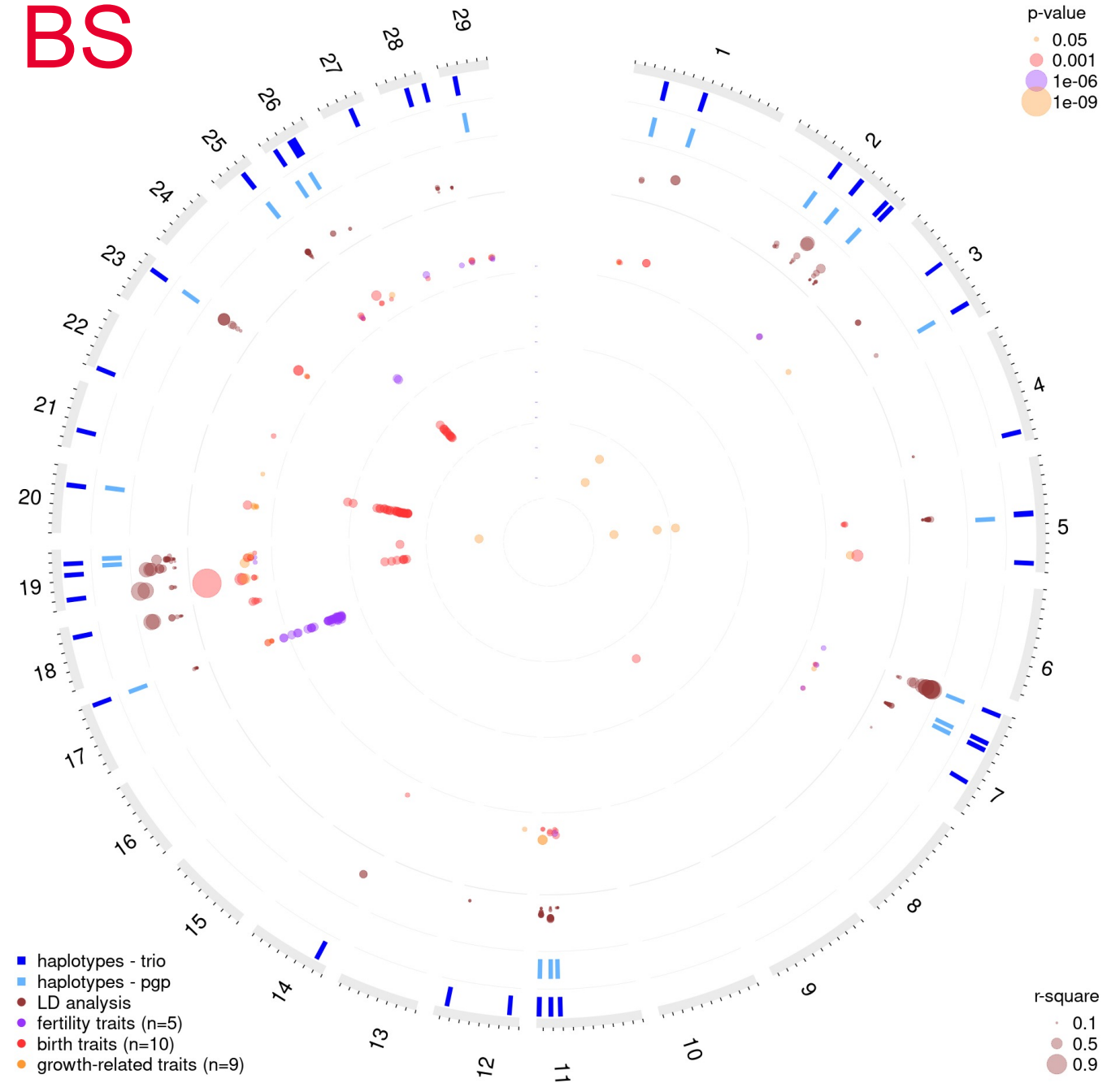


**Missing of  
homozygous  
animals**

# Results – Overview BS

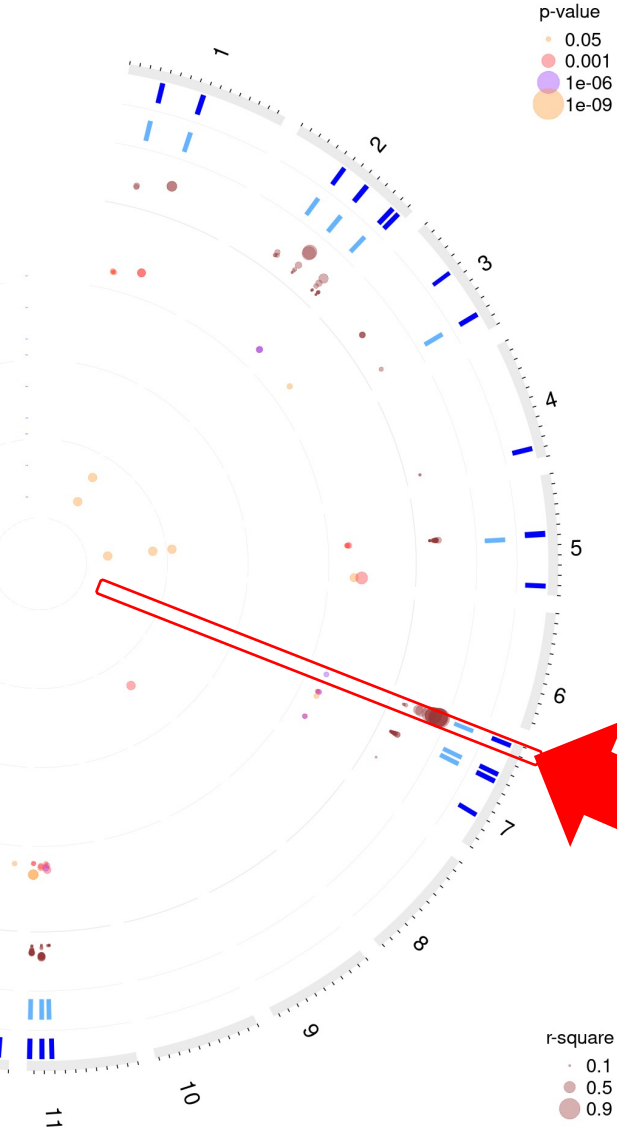


Häfliger I.M., Seefried F.R., Spengeler M. & Drögemüller C. 2021. Mining massive genomic data of two Swiss Braunvieh cattle populations reveals six novel candidate variants impairing reproductive success. *Genetics Selection Evolution*, submitted.





# BH14 in the spotlight



- **Haplotype:**

- 0 of 45 expected homozygous animals
- Allele frequency: 0.03
- Associations:
  - interval first to last insemination, cows
  - interval calving to first service
  - fat cover
  - **heifer survival rate up to 458d**

- **Candidate causal variant:** Chr7 2996436 C>T  
**MRPL55:** p.Arg57\* (nonsense variant)

- High LD with haplotype
- NO homozygous animal in > 4'500 WGS
- NO homozygous animal in > 13'000 custom array



# BH14-associated *MRPL55* variant

- **Gene:** *MRPL55*
  - mitochondrial ribosomal protein L55
- Gen function:
  - Essential role in the mitochondrial ribosomal complex
  - Protein binding enzyme
- Associated disorder:
  - **Early embryonic death in homozygous knock-out mice** (Cheong et al. 2021)

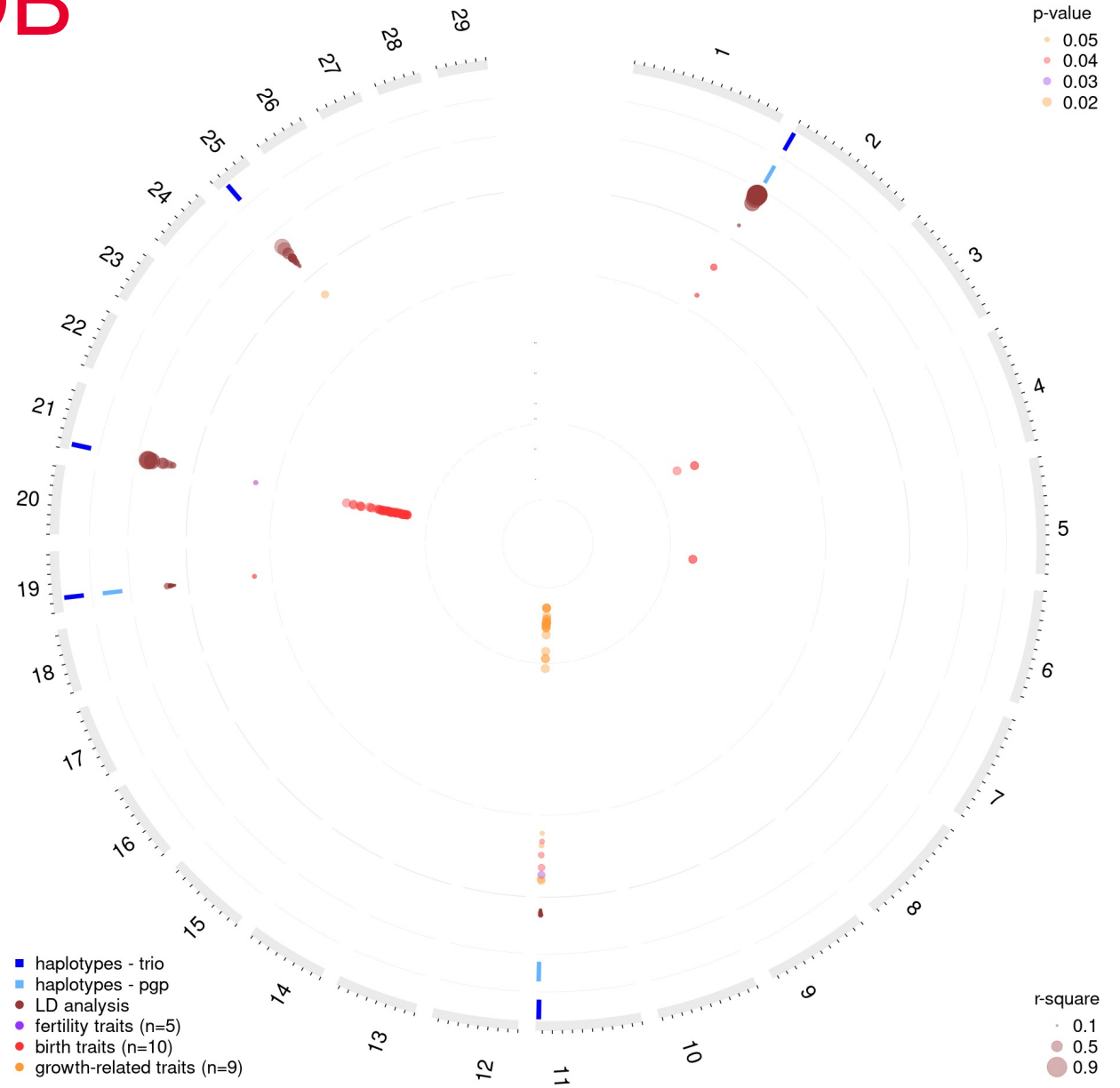


**Hypothesis:** homozygous embryos are non-viable and are aborted during early embryogenesis

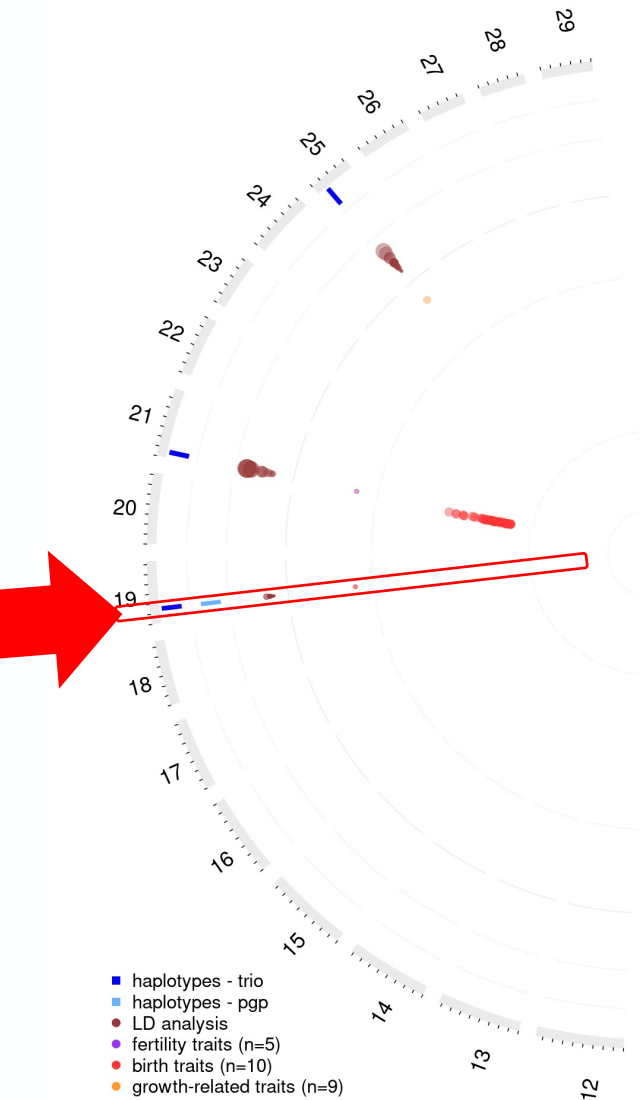
# Results – Overview OB



Häfliger I.M., Seefried F.R., Spengeler M. & Drögemüller C. 2021. **Mining massive genomic data of two Swiss Braunvieh cattle populations reveals six novel candidate variants impairing reproductive success.** *Genetics Selection Evolution*, submitted.



# OH6 in the spotlight



- **Haplotype:**

- 0 of 15 expected homozygous animals
- Allele frequency: 0.039
- Association:
  - — percentage live birth, maternal

- **Candidate causal variant:**

- Chr19:15080335 GGCACCT>G  
**LIG3**: p.Lys828fs (frame-shift variant; splice site)
- perfect LD with haplotype
- NO homozygous animal in > 4'500 WGS

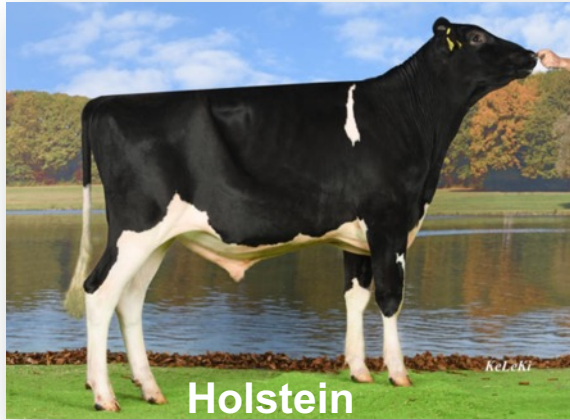
# OH6-associated *LIG3* variant

- **Gene:** *LIG3*
  - DNA ligase 3
  - Gene function:
    - Repair of DNA strand breaks
    - Essential for repair of mitochondrial DNA
  - Associated disorders:
    - **Homozygous lethal in knock-out mice** (Shokolenko et al., 2013)

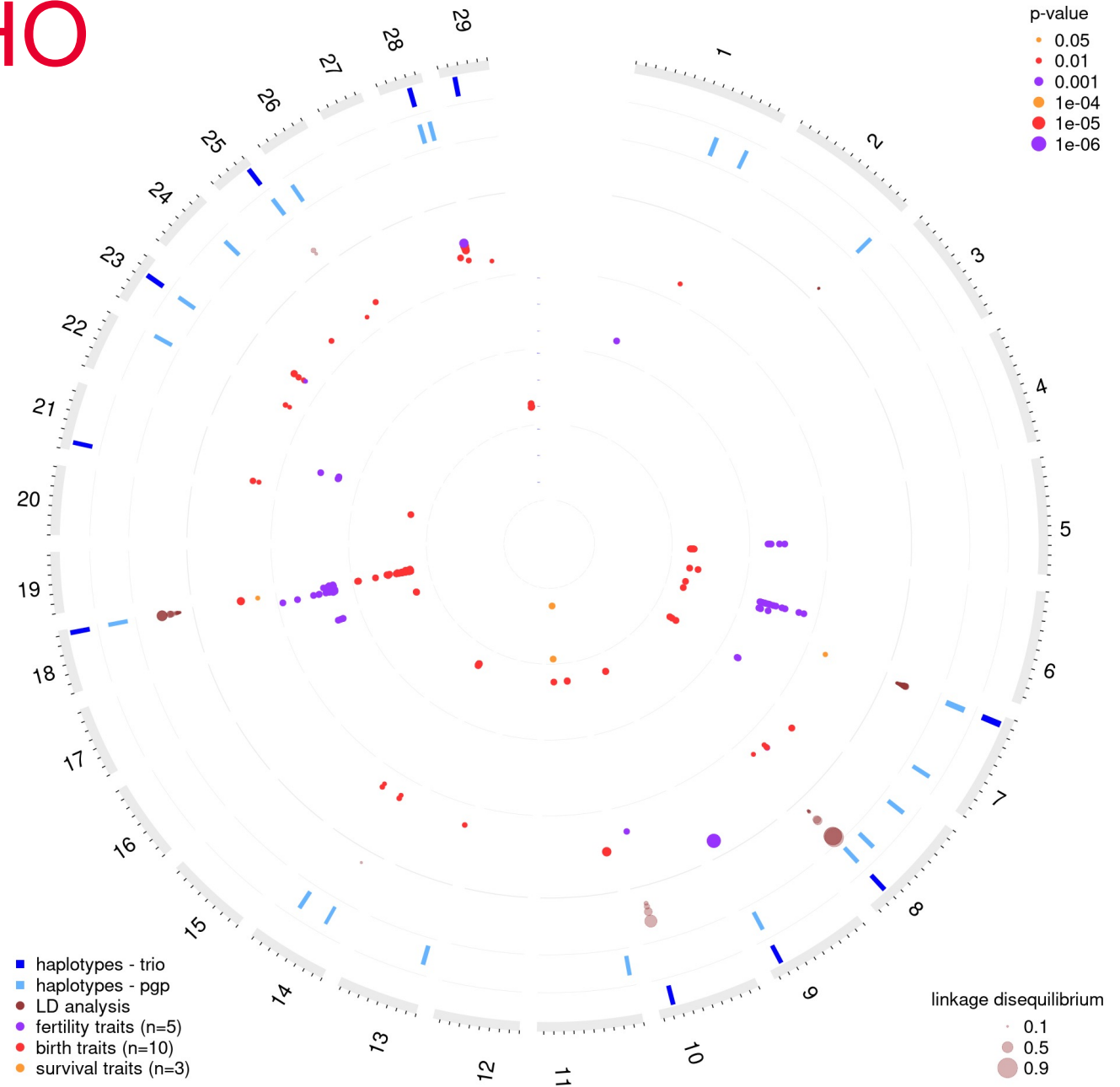


**Hypothesis:** homozygous embryos are non-viable and are aborted during early embryogenesis

# Results – Overview HO



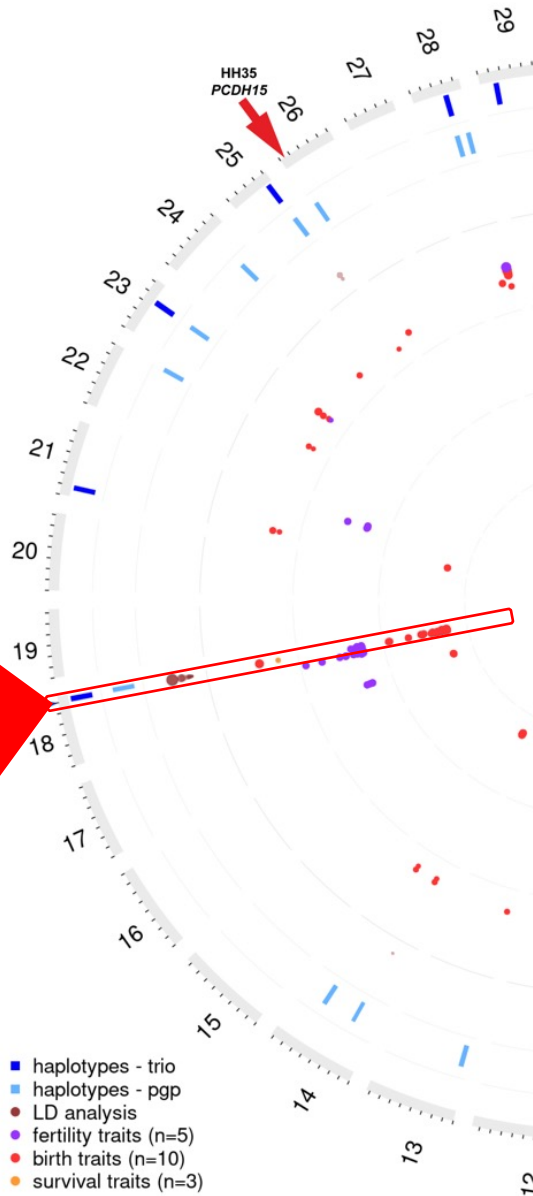
Häfliger I.M., Spengeler M., Seefried F.R. & Drögemüller C. 2021. **Four novel candidate causal variants for deficient homozygous haplotypes in Holstein cattle.** *Scientific Reports*, submitted.



# HH13 in the spotlight

- **Haplotype:**

- 1 of 17 expected homozygous animals
- Allele frequency: 0.018
- Associations: (including GWAS)
  - ⊕ Non-return rate
  - ⊕ Interval first to last insemination
  - ⊕ Birth weight, direct



2013

OPEN ACCESS Freely available online

PLOS ONE

## Detection of Haplotypes Associated with Prenatal Death in Dairy Cattle and Identification of Deleterious Mutations in GART, SHBG and SLC37A2

Sébastien Fritz<sup>1,2</sup>, Aurelien Capitan<sup>1,2</sup>, Anis Djari<sup>3</sup>, Sabrina C. Rodriguez<sup>2,3</sup>, Anne Barbat<sup>2</sup>, Aurélie Baur<sup>1,2</sup>, Cécile Grohs<sup>2</sup>, Bernard Weiss<sup>2</sup>, Mekki Boussaha<sup>2</sup>, Diane Esquerré<sup>4</sup>, Christophe Klopp<sup>3</sup>, Dominique Rocha<sup>2</sup>, Didier Boichard<sup>2\*</sup>

1 UNCEIA, Genetics Team, Paris, France, 2 INRA, UMR1313 Animal Genetics and Integrative Biology, Jouy-en-Josas, France, 3 INRA, Sigenae, UR875 Biométrie et Intelligence Artificielle, Castanet-Tolosan, France, 4 INRA, GeT Genomics Facility, UMR444 Laboratoire de Génétique Cellulaire, Castanet-Tolosan, France

# HH13 in the spotlight

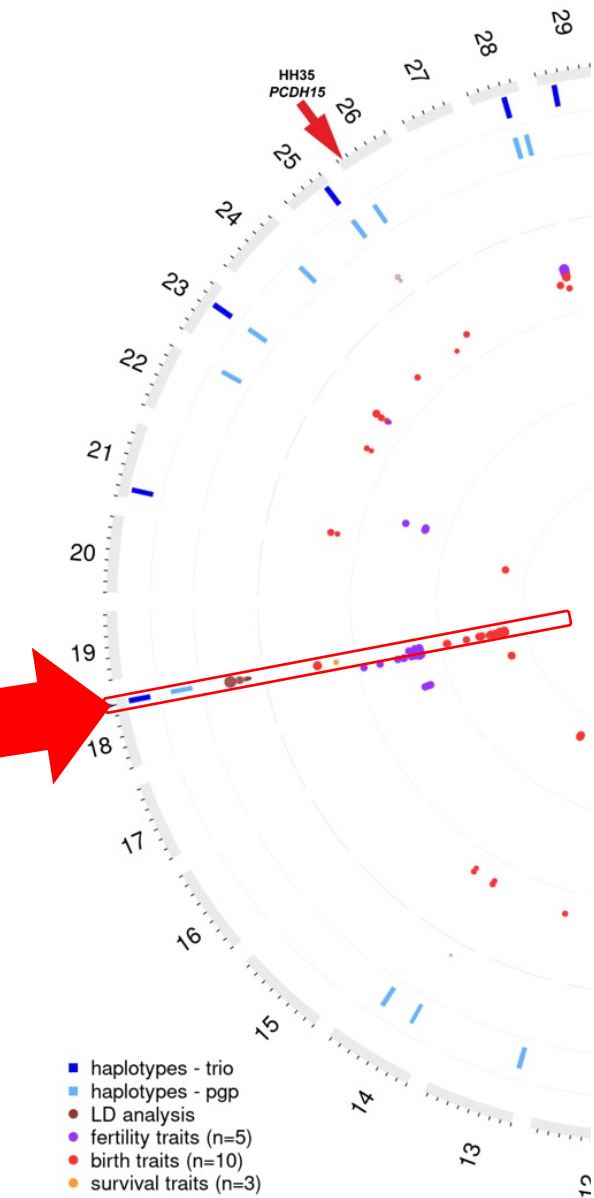
- **Haplotype:**

- 1 of 17 expected homozygous animals
- Allele frequency: 0.018
- Associations: (including GWAS)
  - ⊕ Non-return rate
  - ⊕ Interval first to last insemination
  - ⊕ Birth weight, direct

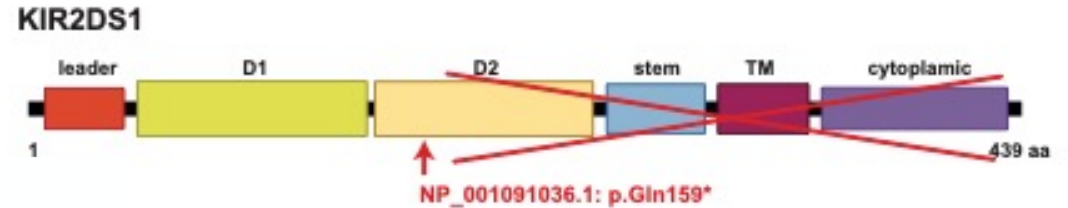
- **Candidate causal variant: Chr18 62758881 G>A**

- ***KIR2DS1*: p.Gln159\*** (nonsense variant)

- average LD with Haplotype
- NO homozygous animals in > 4'200 WGS
- NO homozygous animals in > 13'000 SWISScow



# HH13-associated *KIR2DS1* variant



- **Gene:** *KIR2DS1*

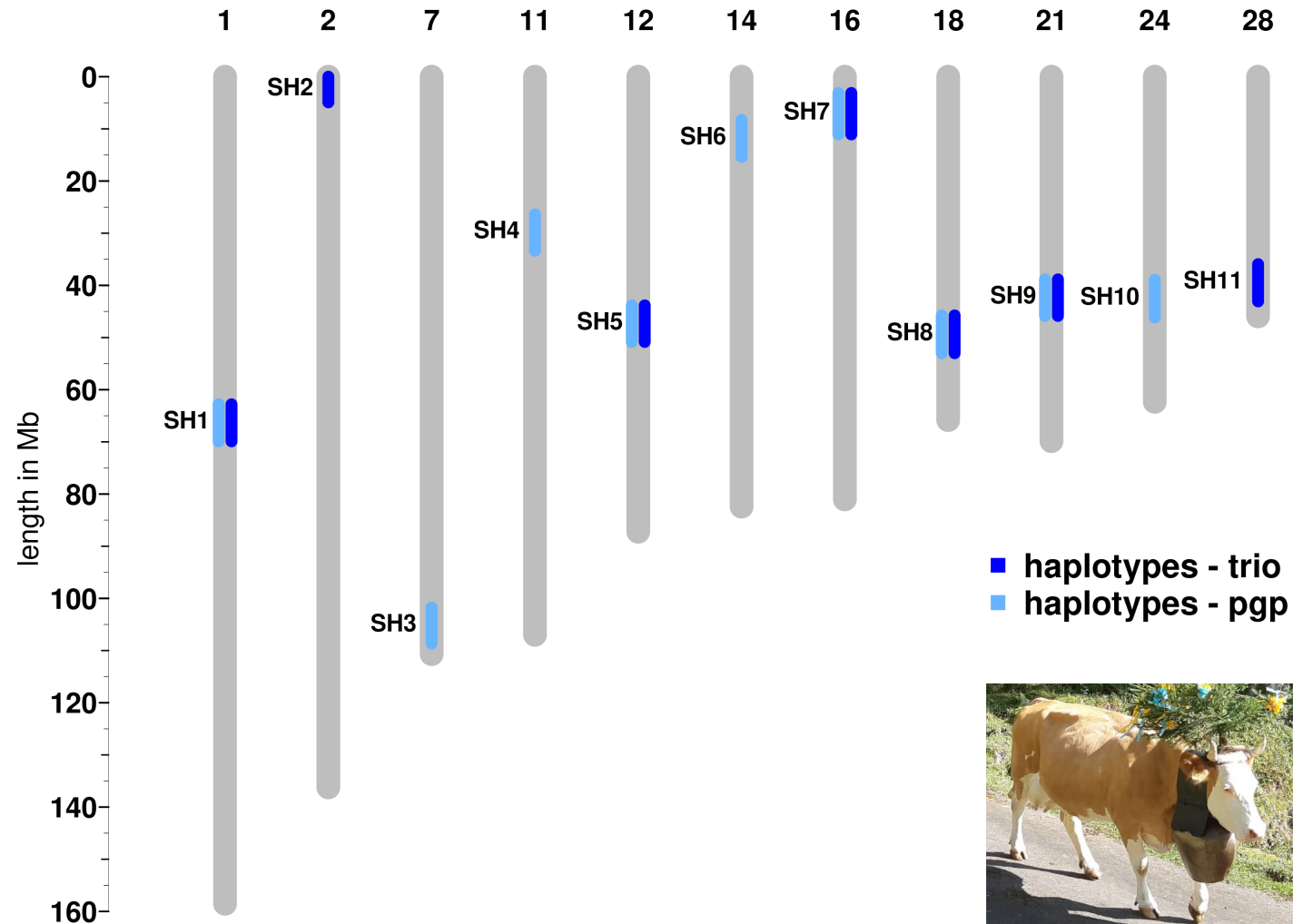
- killer cell immunoglobulin like receptor, two Ig domains and short cytoplasmic tail 1
- Gene function:
  - Placentation success; embryonic growth
  - Immune system
- Associated disorders:
  - **Pregnancy loss**
  - **Infections during pregnancy**



**Hypothesis:** homozygous embryos fuse not in the placenta and/or are aborted during early embryogenesis

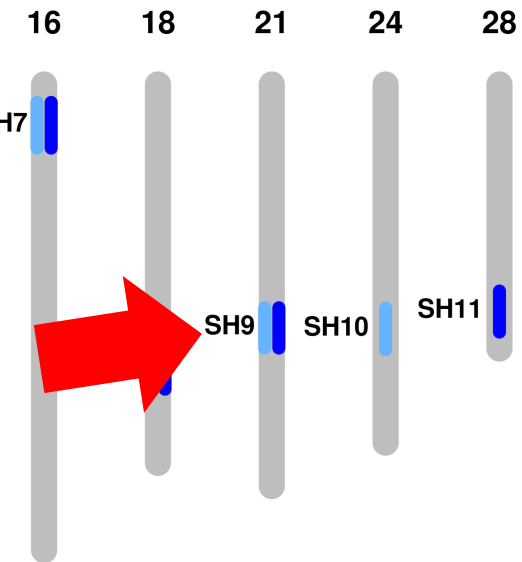


# Results – Overview SI



Häfliger I.M., Seefried F.R. & Drögemüller C. 2021. **Reverse genetic screen for deleterious recessive variants in the local Simmental cattle population of Switzerland.** *Animals*, submitted.

# SH9 in the spotlight



- haplotypes - trio
- haplotypes - ppg



- **Haplotype:**
  - 2 of 19 expected homozygous animals
  - Allele frequency: 0.0433
- **Candidate causal variant:** Chr21 42154344 C>A
- ***NUBPL*:** p.Ser143Tyr (missense variant)
  - perfect LD with Haplotype
  - Highly conserved base and residue
  - NO homozygous animals in > 4'200 WGS

# SH9-associated *NUBPL* variant

- **Gene:** *NUBPL*

- nucleotide binding protein like

- Gene function:

- Assembly of the respiratory complex I
- Immune system

- Associated disorders:

- **Mitochondrial complex I deficiency disorder (OMIM: 613621,618242)**
  - Ataxia, spasticity, etc.
- **Homozygous lethal in knock-out mice (MGI:1924076)**

**NUBPL**

**p.Ser143Tyr**



cattle	MRPLLNYGIACMSMGFLVEETAPLV	NP_001179971.1
human	.....SE.V.	NP_0794288.2
mouse	.....	NP_084036.2
dog	.....I.....V.	XP_001006653.1
rat	.....	NP_001171954.1



**Hypothesis:** homozygous embryos are non-viable and are aborted during early embryogenesis

# Summary of selected causal variants

Phenotype / Haplotype	Breed	Associated gene	Allele / haplotype frequency
Cholesterol deficiency	Holstein	<i>APOB</i>	0.061
Ichthyosis	Scottish Highland	<i>DSP</i>	0.012
Achromatopsia (OH1)	Original Braunvieh	<i>CNGB3</i>	0.099
BH14	Brown Swiss	<i>MRPL55</i>	0.032
OH6	Original Braunvieh	<i>LIG3</i>	0.039
HH13	Holstein	<i>KIR2DS1</i>	0.049
SH9	Simmental	<i>NUBPL</i>	0.043

# Outlook

- Unsolved homozygous deficient haplotypes → need solving
- Phenotype validation:
  - Monitoring of risk-matings
  - non-embryonic lethal variants/haplotypes
- Inclusion in daily breeding practice → avoid further risk-matings
- Similar reverse genetics screens can be performed in other (beef, local) populations with increasing SNP data availability

# Thank you very much!

**Qualitas** 

 **Schweizerischer  
Nationalfonds**



**u<sup>b</sup>**

**UNIVERSITÄT  
BERN**

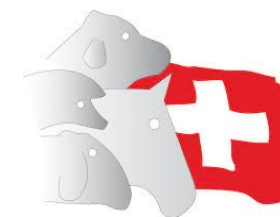
**gcb**

Graduate School  
for Cellular and  
Biomedical Sciences

*swissgenetics* 

**ASR**

Arbeitsgemeinschaft Schweizerischer Rinderzüchter  
Communauté de travail des éleveurs bovins suisses



**SWISS**   
**herdbook**  
S I N C E 1 8 9 0

**BRAUNVIEH** 

**Thank you for your attention!**

**Questions?**

