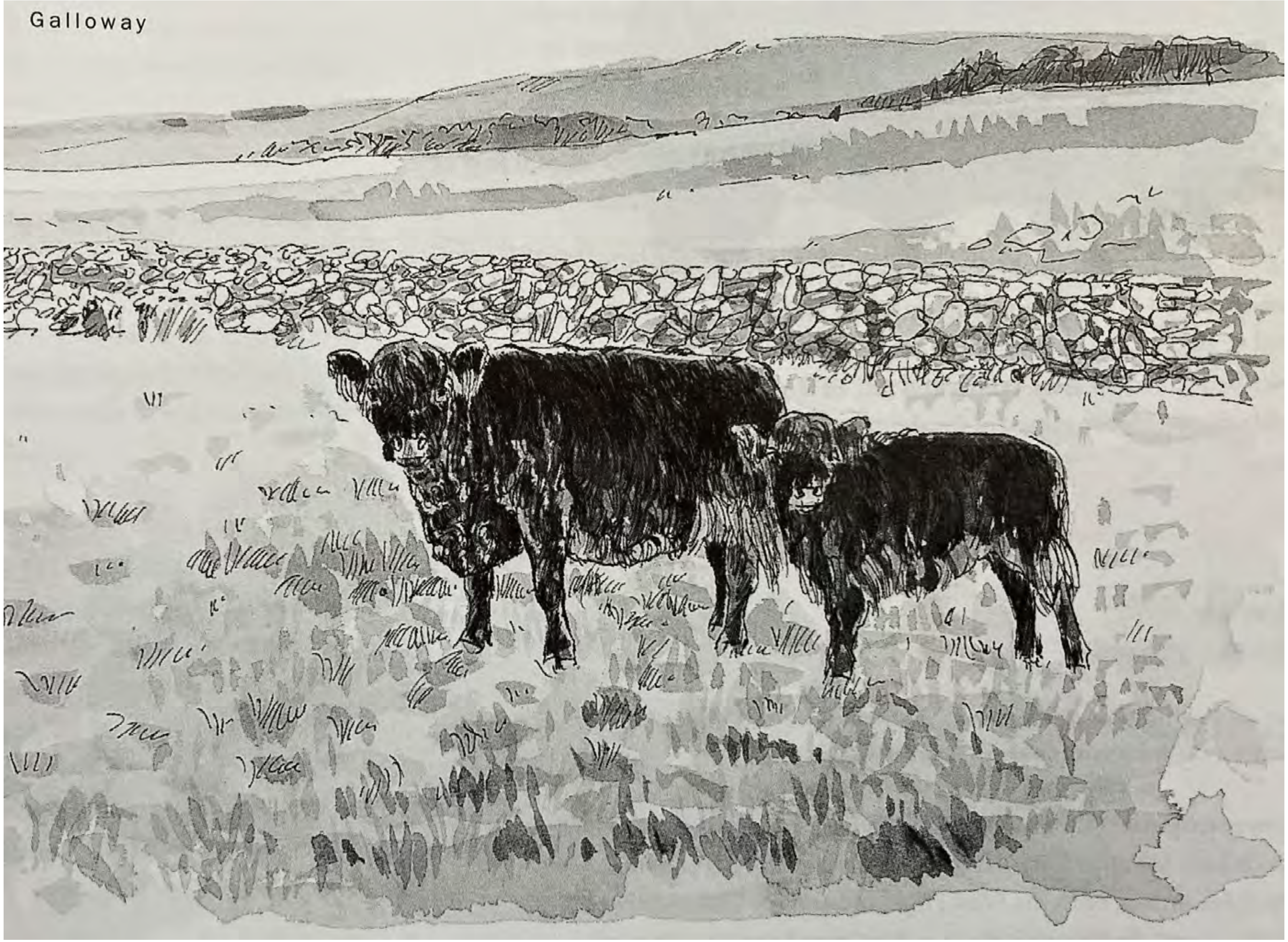

Marleen Felius, Cattle Breeds: An Encyclopedia. Trafalgar Square Publishing, 2007

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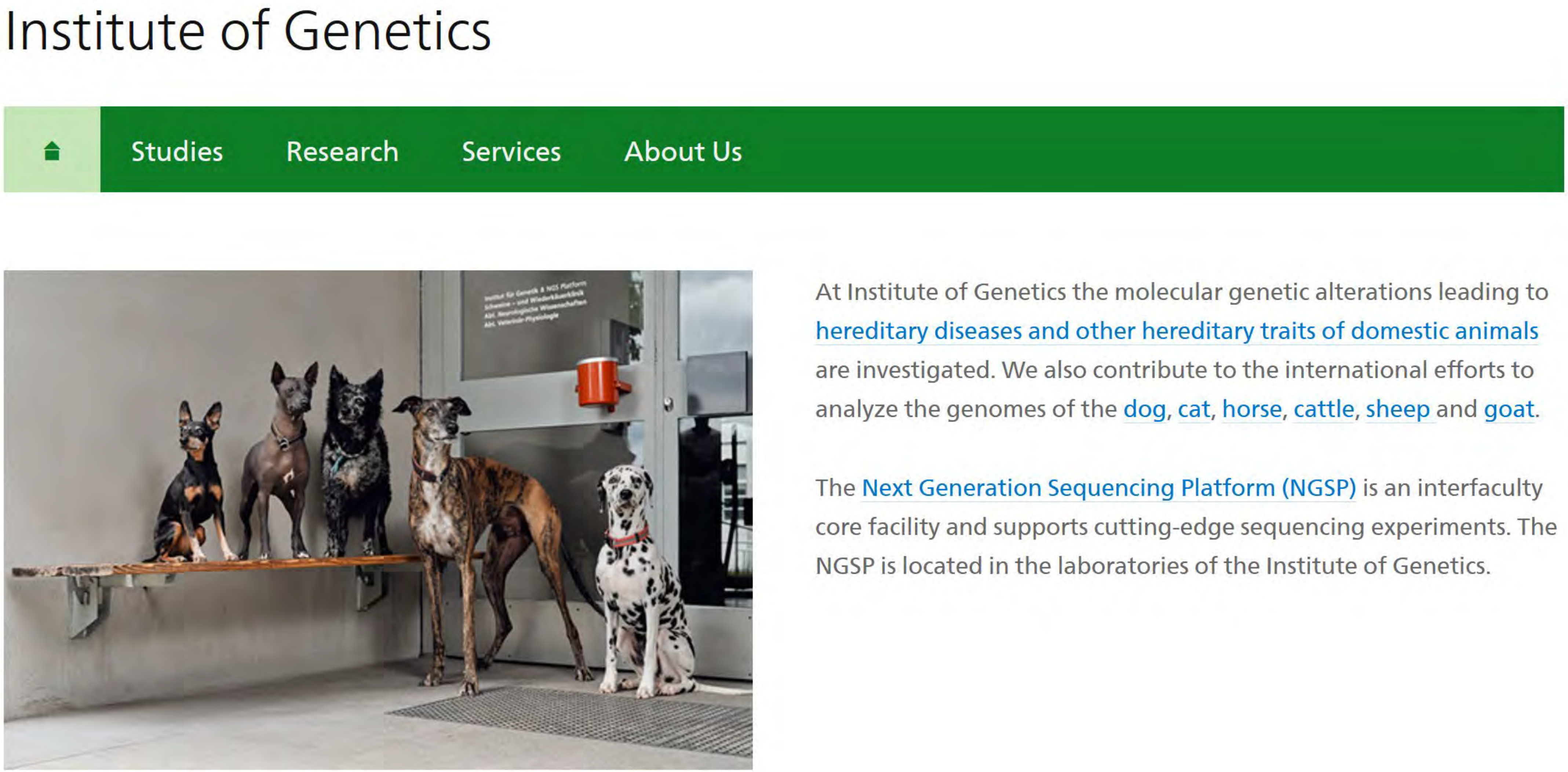
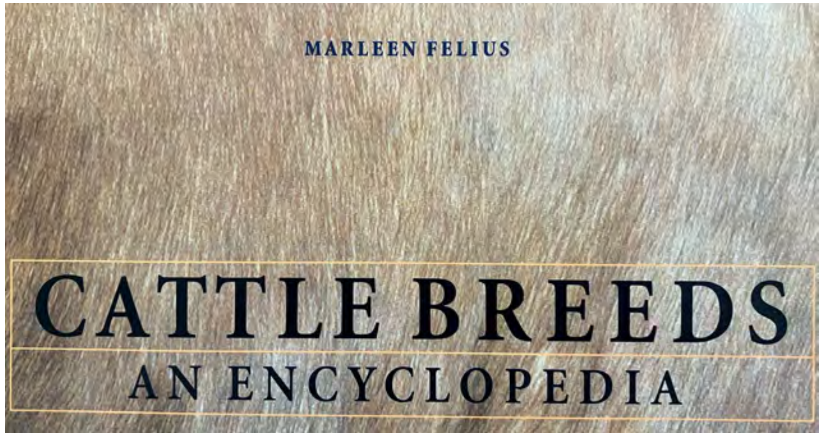


Institute of Genetics

At Institute of Genetics the molecular genetic alterations leading to hereditary diseases and other hereditary traits of domestic animals are investigated. We also contribute to the international efforts to analyze the genomes of the dog, cat, horse, cattle, sheep and goat.

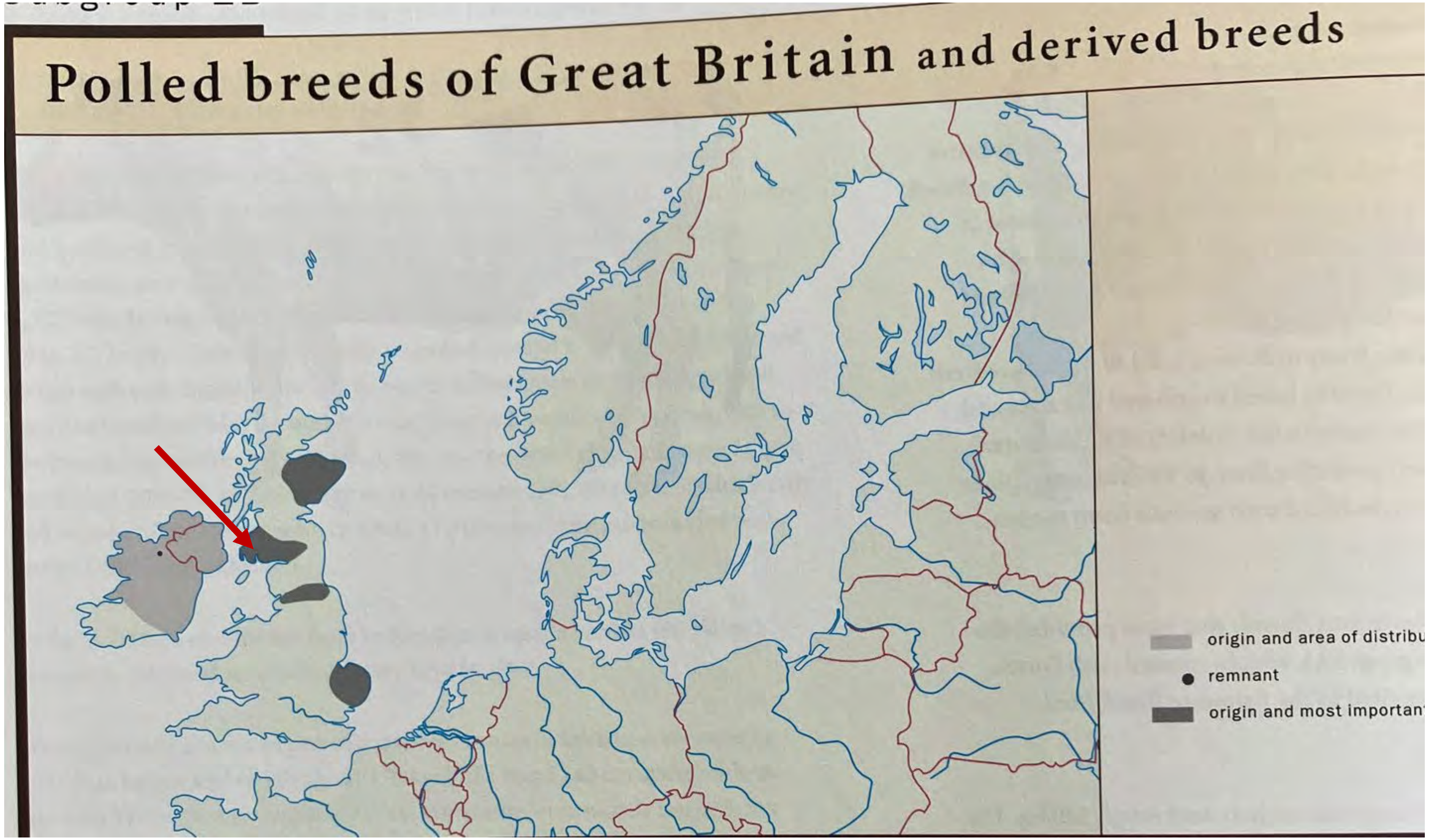
The Next Generation Sequencing Platform (NGSP) is an interfaculty core facility and supports cutting-edge sequencing experiments. The NGSP is located in the laboratories of the Institute of Genetics.

https://www.genetics.unibe.ch/index_eng.html



MARLEEN FELIUS

CATTLE BREEDS
AN ENCYCLOPEDIA

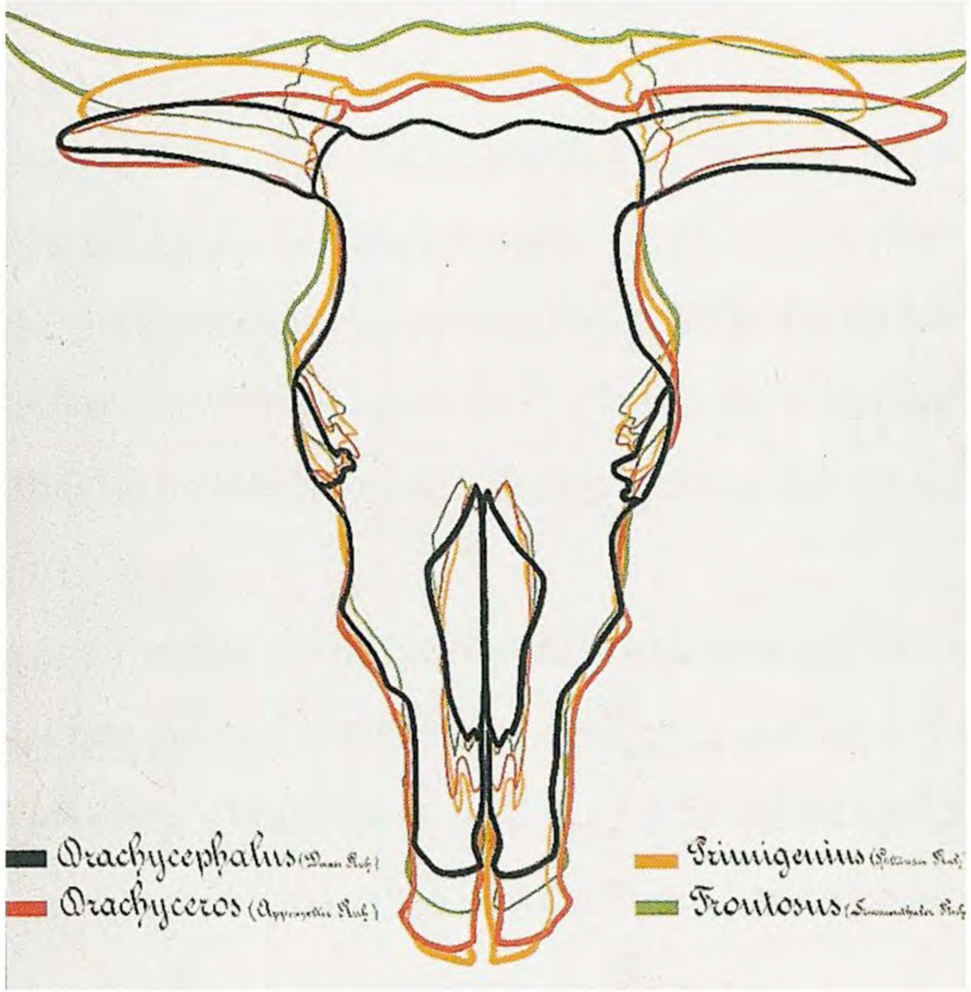


Polled breeds of Great Britain and derived breeds

Marleen Felius, Cattle Breeds: An Encyclopedia. Trafalgar Square Publishing, 2007

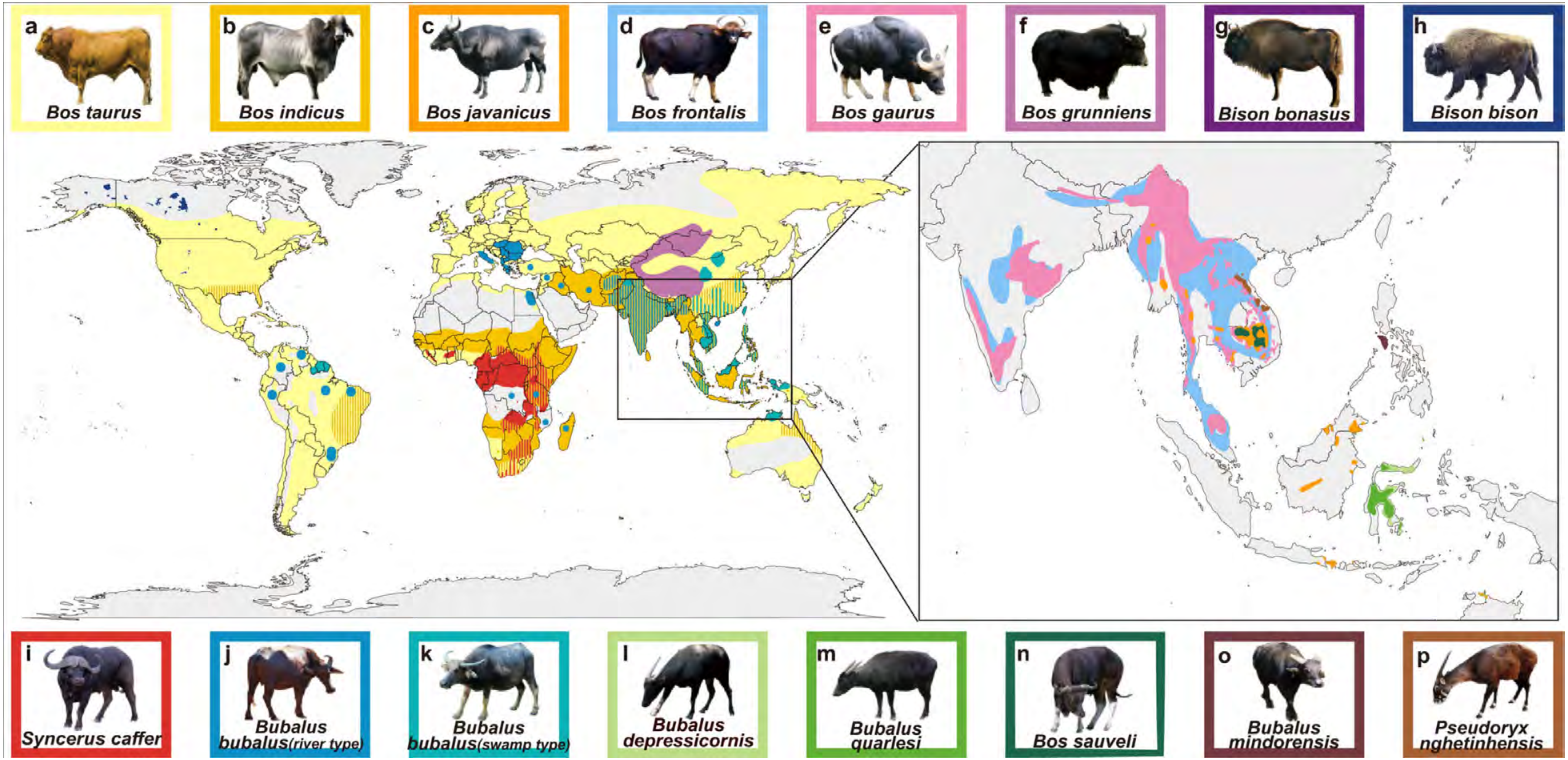
Primigeniusrind	***Bos taurus primigenius***	**aurochs type**	Podolian Grey Steppe cattle lowland dairy breeds **Galloway**

Figure 1. Basic types of cattle skulls, according to Wilckens [26]. Black, *brachycephalus*; orange, *primigenius*; red, *brachyceros*; green, *frontosus*.



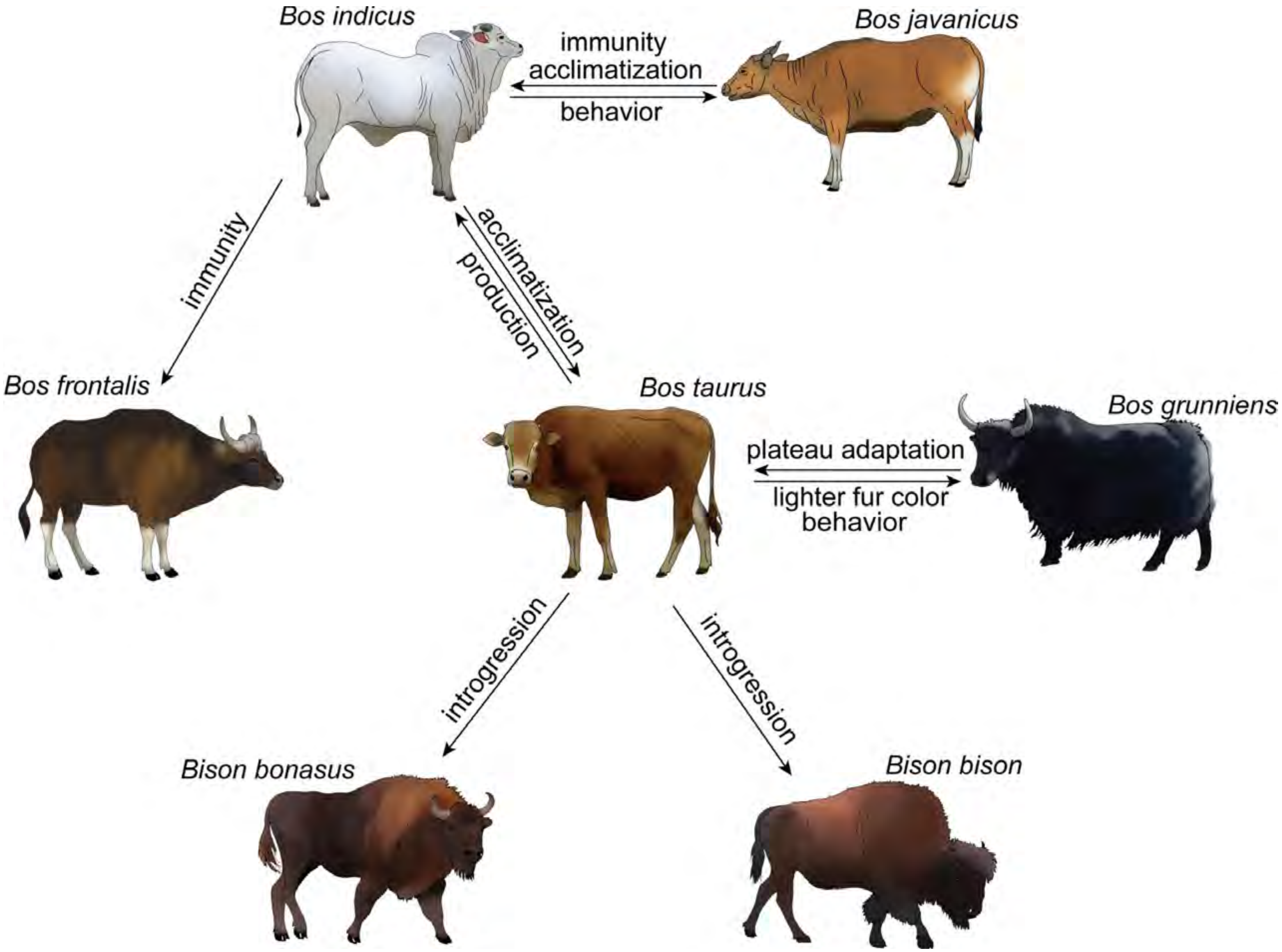
https://www.mdpi.com/1424-2818/3/4/660

16 species of cattle are found all over the world: cattle can be found everywhere except in the deserts and in the polar regions



https://onlinelibrary.wiley.com/doi/10.1111/age.12974

Gene flow and the likely adaptations of the introgressed genes between 7 bovine species



https://onlinelibrary.wiley.com/doi/10.1111/age.12974

Diversity **2011**, *3*, 660-692; doi:10.3390/d3040660

OPEN ACCESS

diversity

ISSN 1424-2818

www.mdpi.com/journal/diversity

Review

On the Breeds of Cattle—Historic and Current Classifications

Marleen Felius [1], Peter A. Koolmees [2], Bert Theunissen [2],
European Cattle Genetic Diversity Consortium [†] and Johannes A. Lenstra [2,*]

Figure 8. Classification of European breeds of Felius [2] (Table S33). Only breeds are shown that also have been classified by genetic analysis (Figure 9). In the three-letter code, the color of the first letter indicates the group according to the color key and the second and third letter the subgroup.

Groups	Subgroups
Northern Polled, Celtic	Nordic Polled / Longhorned Dairy / British Polled / Celtic
North-Western Lowland	Lowland Red / Lowland Pied Dairy / Lowland Pied Dual Purpose / British Shorthorn / English Lowland / Channel Island, NW France
Western-Central Highland	Vosges, Black Forest / Highland Red / Shortheaded Alpine / Central-European Yellow, Blonde / Broadheaded Spotted / Charolais
Highland Solid-colored	Middle France / SW French, Pyrenean Grey, Blonde / North-Italian Fawn-Brown / Central-European Brown, Gray / Illyric Shorthorn
Iberian	Isolated W Mediterranean / NW Iberian, Balearic Blond-Brown / NW Iberian Chestnut / Middle, SW Iberian Black / Middle, SW Iberian Red / SE Iberian
Podolian	Italian White / Italian, Croatian Podolian / E European / Balkan, Anatolian

https://www.mdpi.com/1424-2818/3/4/660

Modern classification of European cattle breeds on the basis of DNA (microsatellite) genotyping

Figure 9. Categorization of European cattle on the basis of microsatellite genotyping. (Table S34). The Eastern and Eastern crossbred categories from Russia are outside the range of this map. Breed codes are as in **Figure 8**. Colors indicate clusters or subclusters and for breeds ASV, GGB and VIL intermediate positions.

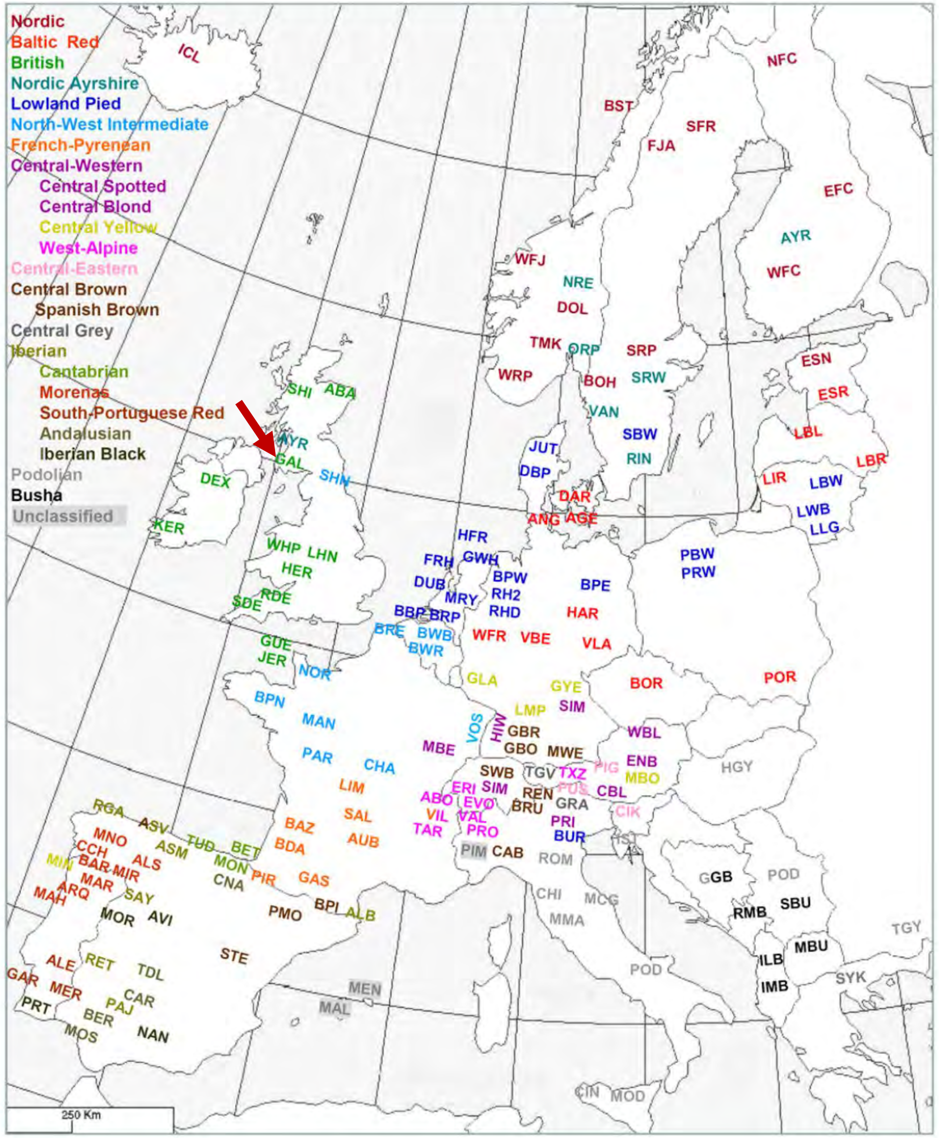
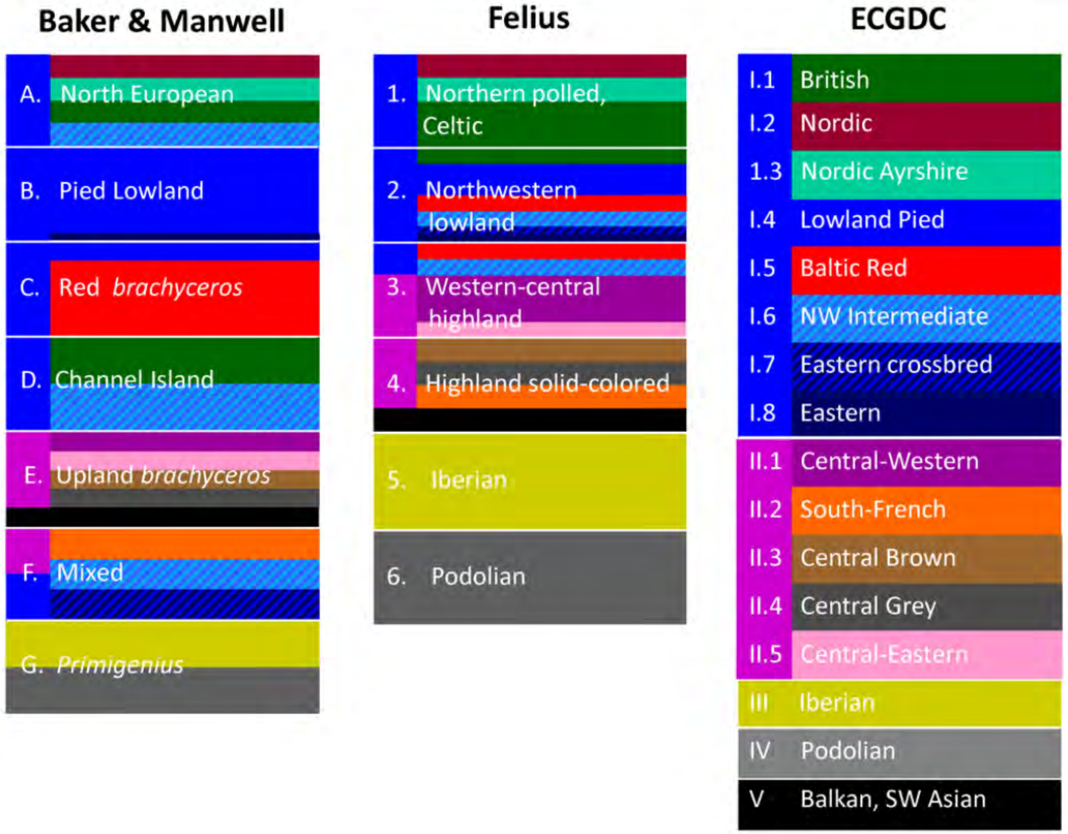


Figure 10. Comparison of the biochemical classification from Baker and Manwell [13], the integrated classification from Felius [2] and the microsatellite-based classification of the European Cattle Genetic Diversity Consortium (ECGDC). The horizontal color bars indicate the groups of the genetic classification. Even colors denote clusters of breeds that are more related to each other than to breeds of other clusters. Hatched colors denote groups of neighboring intermediate or crossbred breeds. The horizontal blocks at the left containing the numbering indicate the five main genetic types of cattle: northern European (blue); central European (violet); Iberian (ochre); Podolian (grey); and Balkan with Anatolian (black).



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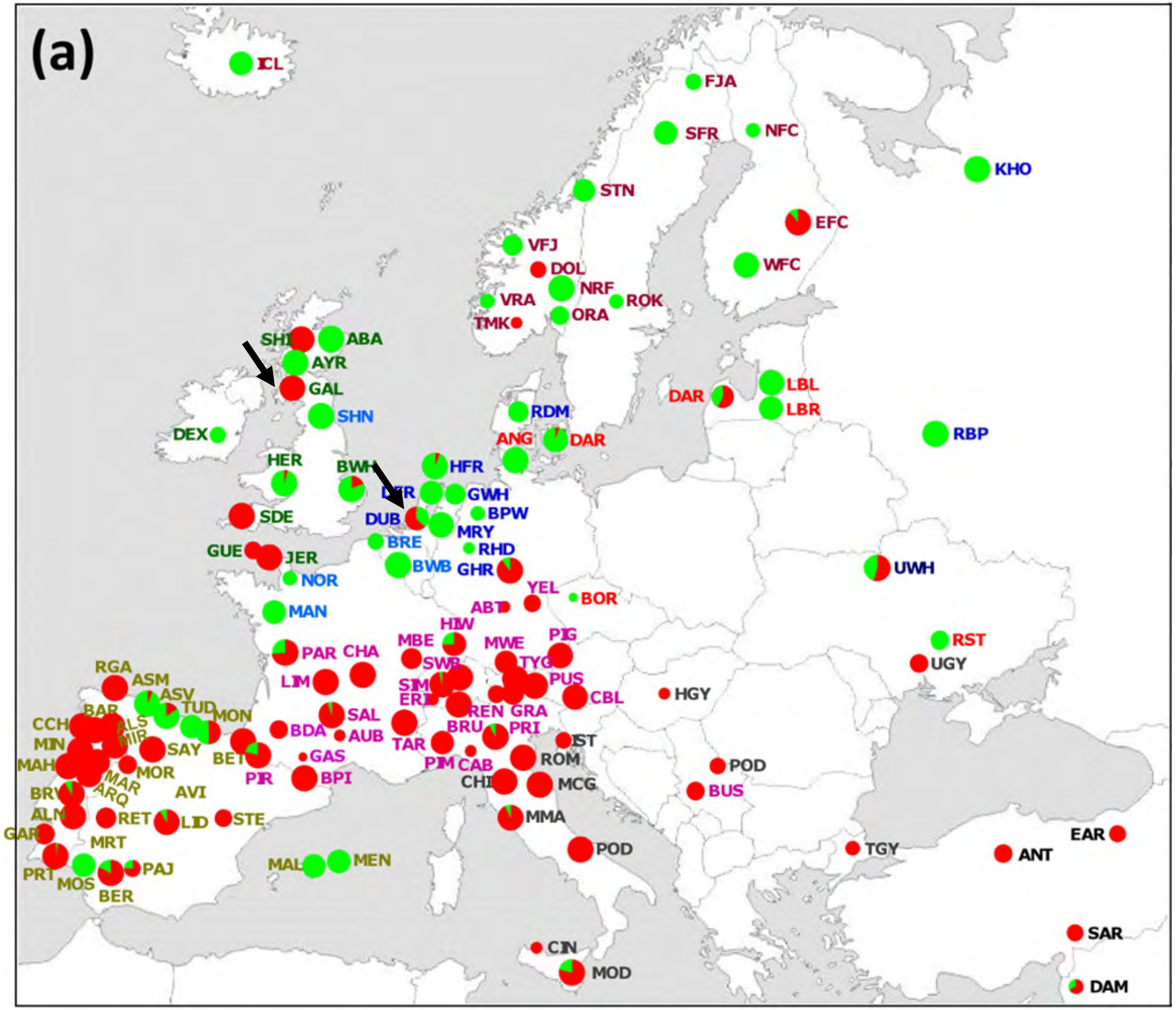
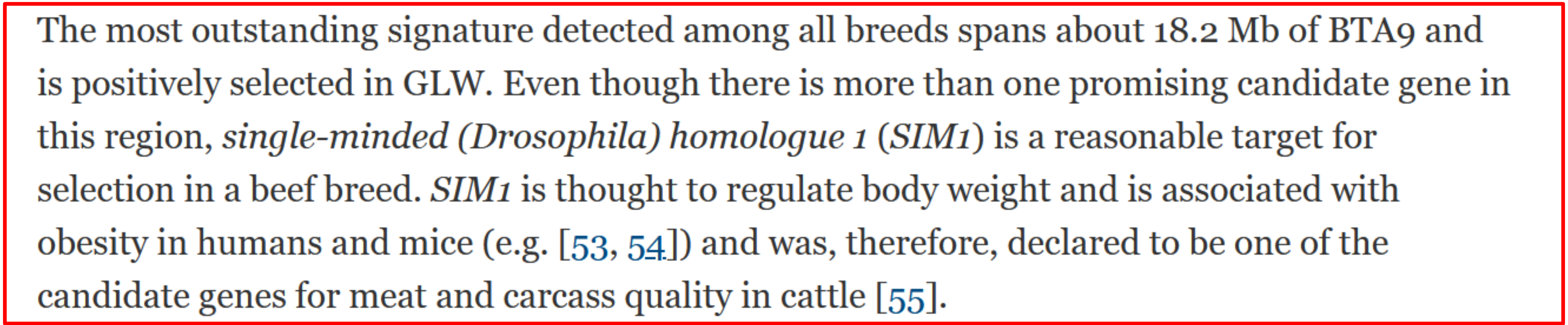
Modern classification of European cattle breeds on the basis of Y-chromosomal DNA markers

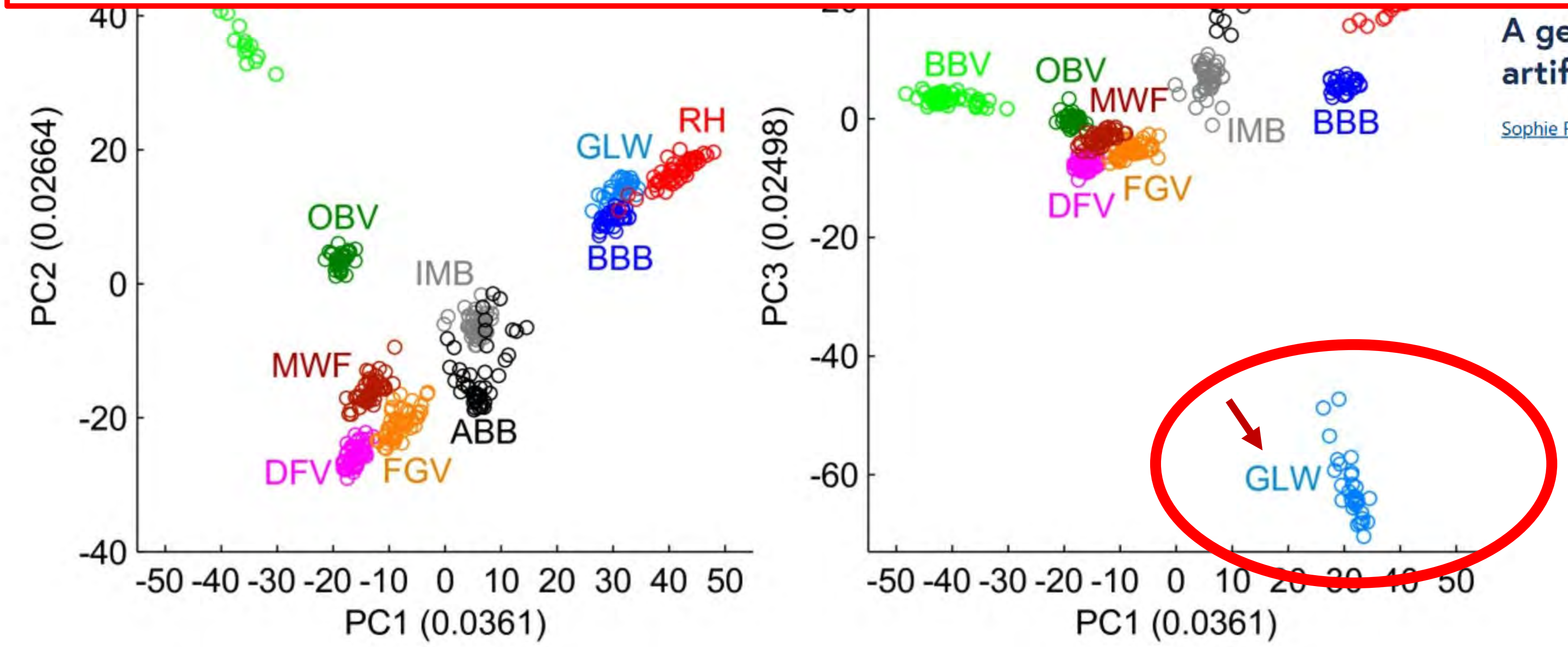


https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0015922

SNP genotyping data from cattle provide new insights like so-called "selection signature" detection



The most outstanding signature detected among all breeds spans about 18.2 Mb of BTA9 and is positively selected in GLW. Even though there is more than one promising candidate gene in this region, *single-minded (Drosophila) homologue 1* (*SIM1*) is a reasonable target for selection in a beef breed. *SIM1* is thought to regulate body weight and is associated with obesity in humans and mice (e.g. [53, 54]) and was, therefore, declared to be one of the candidate genes for meat and carcass quality in cattle [55].

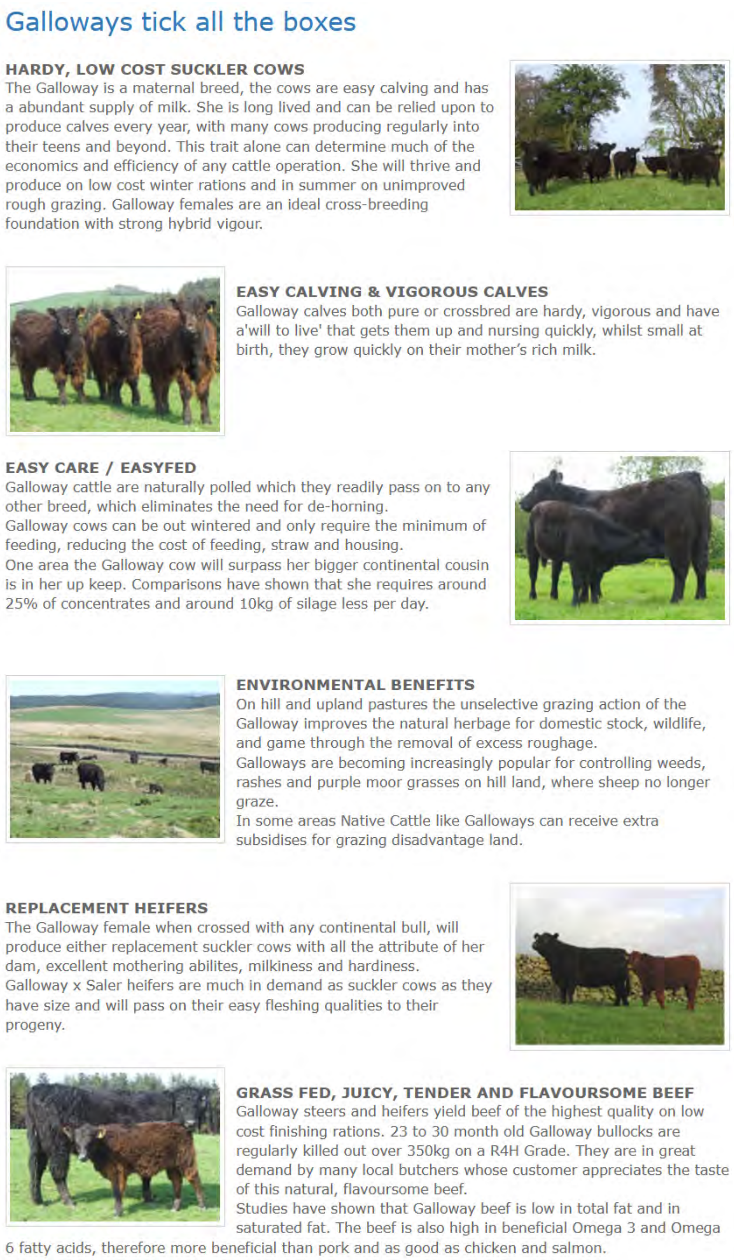


A genome-wide scan for signatures of differential artificial selection in ten cattle breeds

Sophie Rothammer, Doris Seichter, Martin Förster & Ivica Medugorac

https://bmcgenomics.biomedcentral.com/articles/10.1186/1471-2164-14-908

Whole-genome sequencing of Galloway cattle might provide new opportunities to find "the" genes behind



Galloways tick all the boxes

HARDY, LOW COST SUCKLER COWS
The Galloway is a maternal breed, the cows are easy calving and has a abundant supply of milk. She is long lived and can be relied upon to produce calves every year, with many cows producing regularly into their teens and beyond. This trait alone can determine much of the economics and efficiency of any cattle operation. She will thrive and produce on low cost winter rations and in summer on unimproved rough grazing. Galloway females are an ideal cross-breeding foundation with strong hybrid vigour.

EASY CALVING & VIGOROUS CALVES
Galloway calves both pure or crossbred are hardy, vigorous and have a'will to live' that gets them up and nursing quickly, whilst small at birth, they grow quickly on their mother's rich milk.

EASY CARE / EASYFED
Galloway cattle are naturally polled which they readily pass on to any other breed, which eliminates the need for de-horning.
Galloway cows can be out wintered and only require the minimum of feeding, reducing the cost of feeding, straw and housing.
One area the Galloway cow will surpass her bigger continental cousin is in her up keep. Comparisons have shown that she requires around 25% of concentrates and around 10kg of silage less per day.

ENVIRONMENTAL BENEFITS
On hill and upland pastures the unselective grazing action of the Galloway improves the natural herbage for domestic stock, wildlife, and game through the removal of excess roughage.
Galloways are becoming increasingly popular for controlling weeds, rashes and purple moor grasses on hill land, where sheep no longer graze.
In some areas Native Cattle like Galloways can receive extra subsidises for grazing disadvantage land.

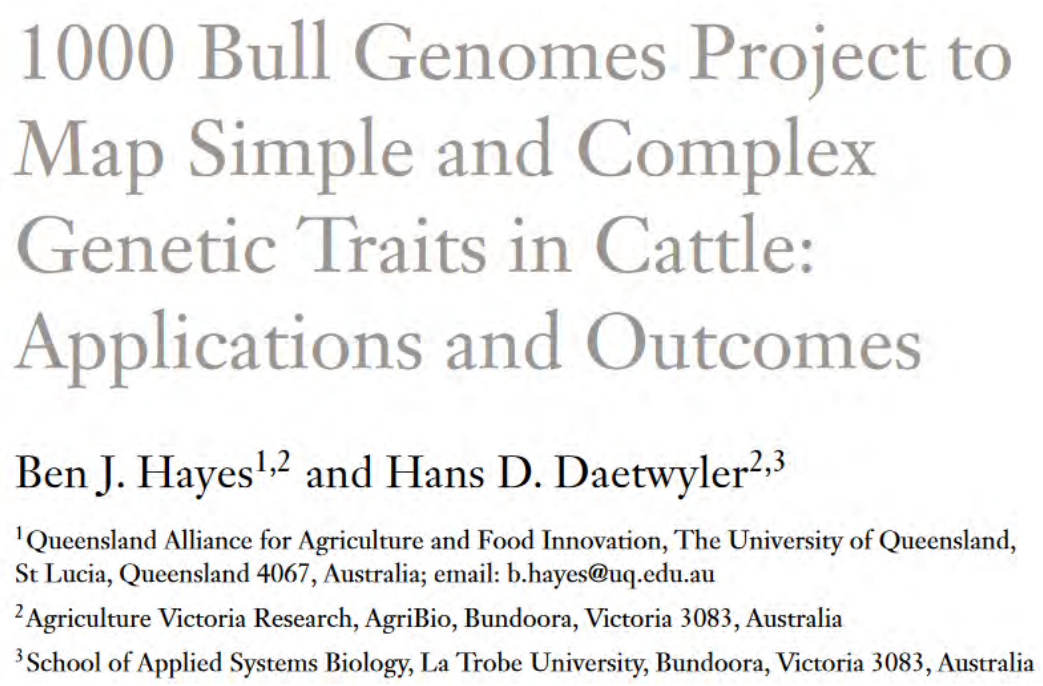
REPLACEMENT HEIFERS
The Galloway female when crossed with any continental bull, will produce either replacement suckler cows with all the attribute of her dam, excellent mothering abilites, milkiness and hardiness.
Galloway x Saler heifers are much in demand as suckler cows as they have size and will pass on their easy fleshing qualities to their progeny.

GRASS FED, JUICY, TENDER AND FLAVOURSOME BEEF
Galloway steers and heifers yield beef of the highest quality on low cost finishing rations. 23 to 30 month old Galloway bullocks are regularly killed out over 350kg on a R4H Grade. They are in great demand by many local butchers whose customer appreciates the taste of this natural, flavoursome beef.
Studies have shown that Galloway beef is low in total fat and in saturated fat. The beef is also high in beneficial Omega 3 and Omega 6 fatty acids, therefore more beneficial than pork and as good as chicken and salmon.

https://gallowaycattlesociety.co.uk/why-galloways.asp

Whole-genome sequencing of Galloway cattle almost not performed

only 4 Galloway among 5116 taurine cattle



1000 Bull Genomes Project to Map Simple and Complex Genetic Traits in Cattle: Applications and Outcomes

Ben J. Hayes[1,2] and Hans D. Daetwyler[2,3]

[1] Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, St Lucia, Queensland 4067, Australia; email: b.hayes@uq.edu.au

[2] Agriculture Victoria Research, AgriBio, Bundoora, Victoria 3083, Australia

[3] School of Applied Systems Biology, La Trobe University, Bundoora, Victoria 3083, Australia

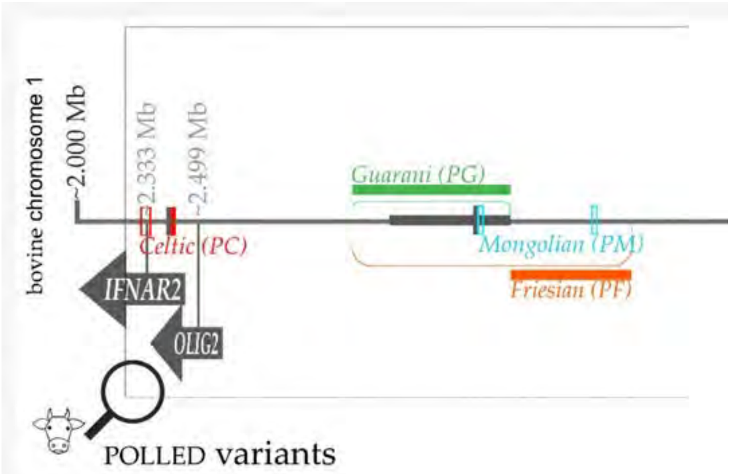
https://www.annualreviews.org/doi/abs/10.1146/annurev-animal-020518-115024

A first example to show what we can do today

Independent *Polled* Mutations Leading to Complex Gene Expression Differences in Cattle

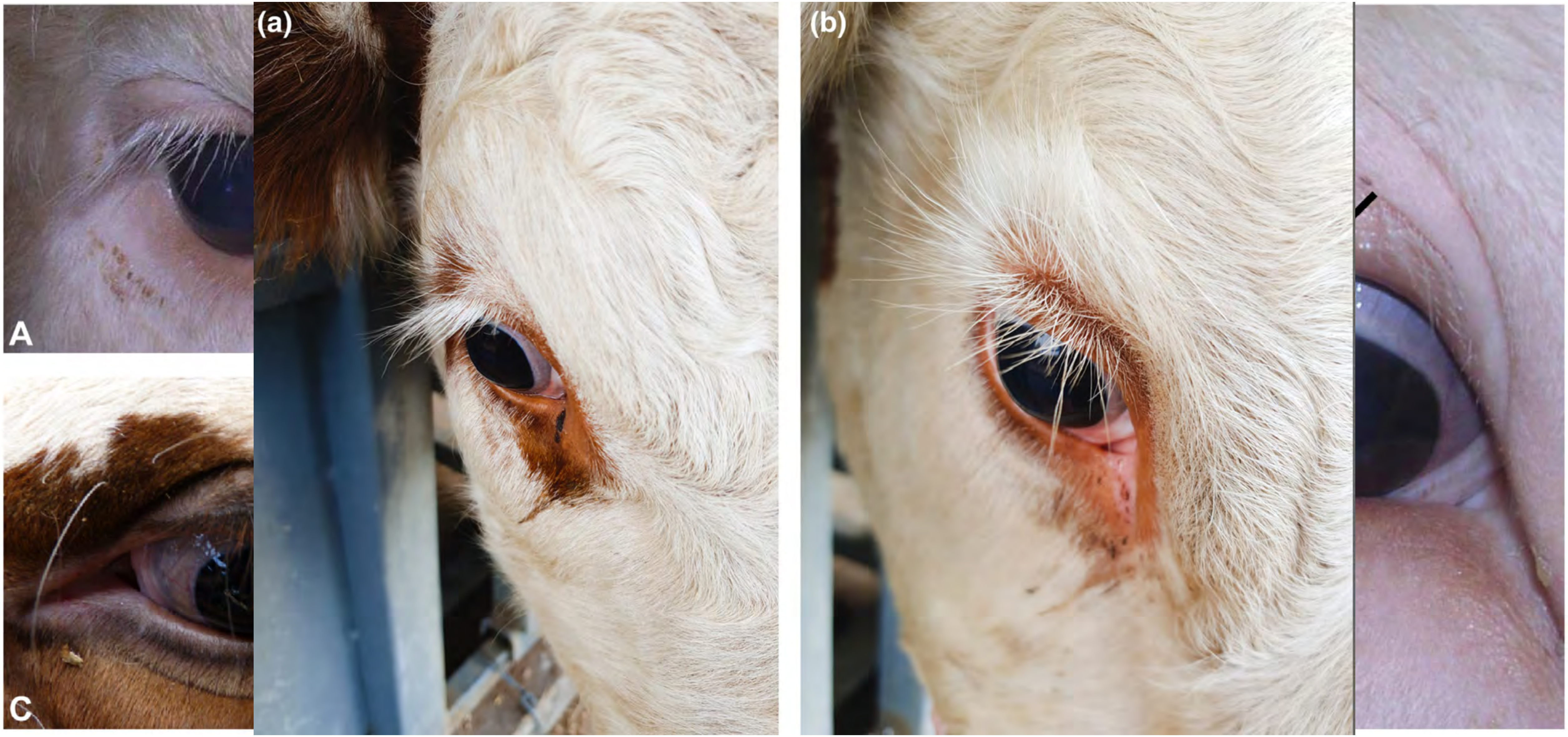
Natalie Wiedemar, Jens Tetens, Vidhya Jagannathan, Annie Menoud, Samuel Neuenschwander, Rémy Bruggmann, Georg Thaller, Cord Drögemüller

Published: March 26, 2014 • https://doi.org/10.1371/journal.pone.0093435



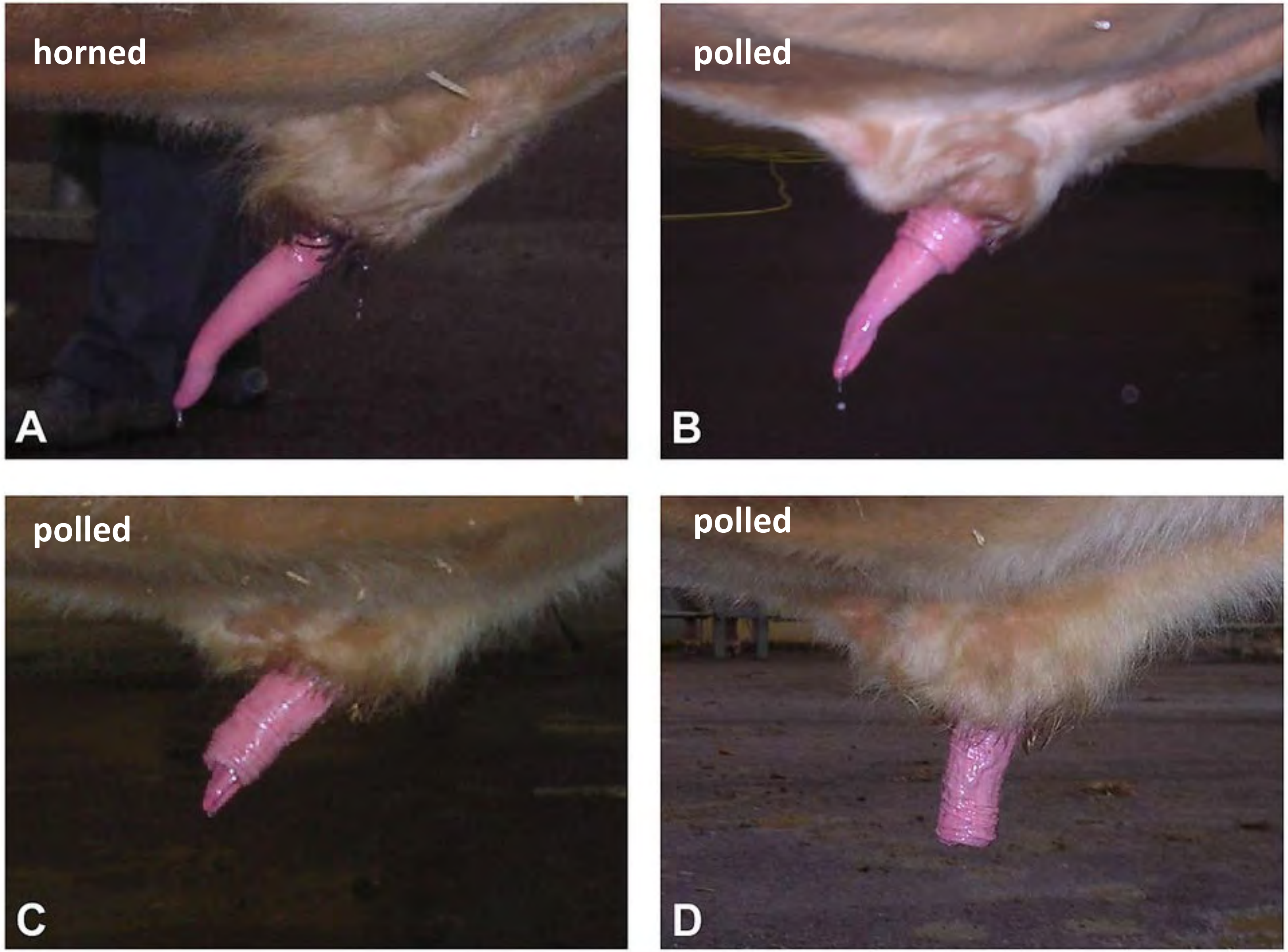
https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0039477

As is usually the case *"there is no free lunch"*: eyelash and eyelid phenotypes associated with polledness



https://onlinelibrary.wiley.com/doi/10.1111/age.12915

Details of the abnormal prepuce withdrawal phenotype displayed by some polled bulls



https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0063512

Genome editing in livestock? Proof of principle provided in 2016

Published: 06 May 2016

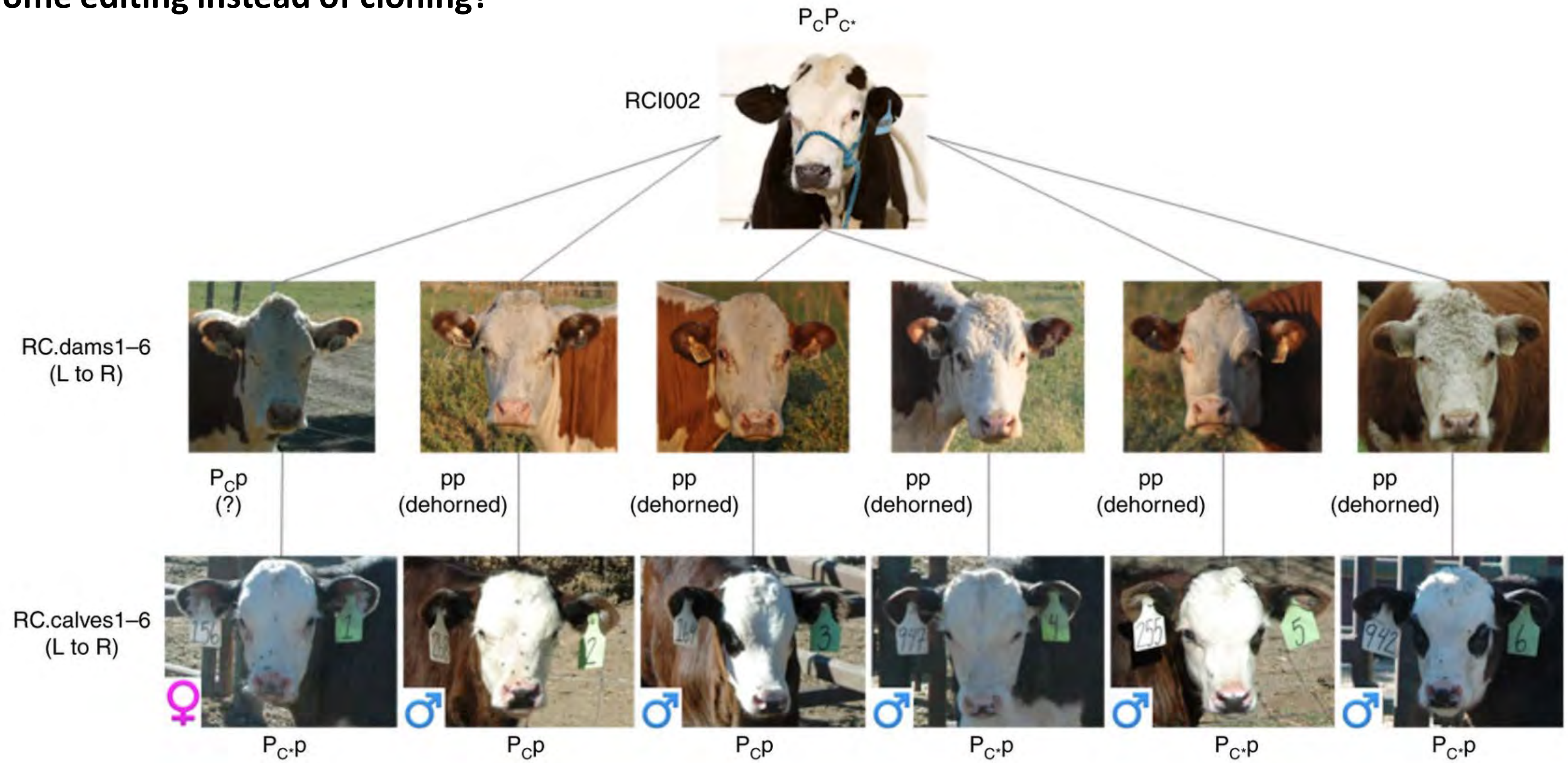
Production of hornless dairy cattle from genome-edited cell lines

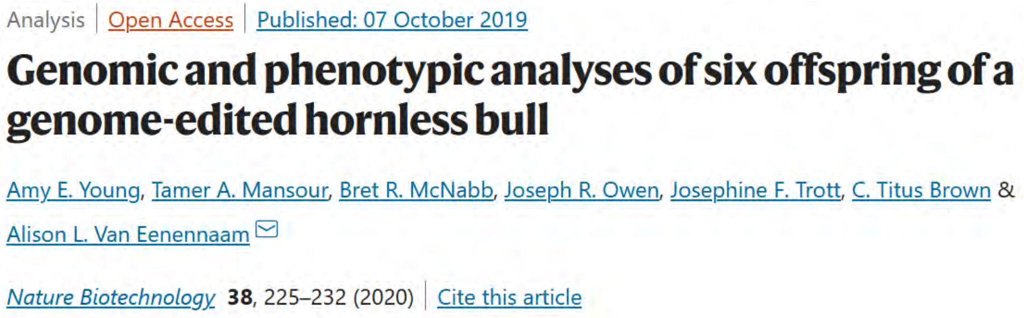
Daniel F Carlson, Cheryl A Lancto, Bin Zang, Eui-Soo Kim, Mark Walton, David Oldeschulte, Christopher Seabury, Tad S Sonstegard & Scott C Fahrenkrug

Nature Biotechnology **34**, 479–481 (2016) | Cite this article

https://www.nature.com/articles/nbt.3560

Genome editing instead of cloning?




Analysis | Open Access | Published: 07 October 2019

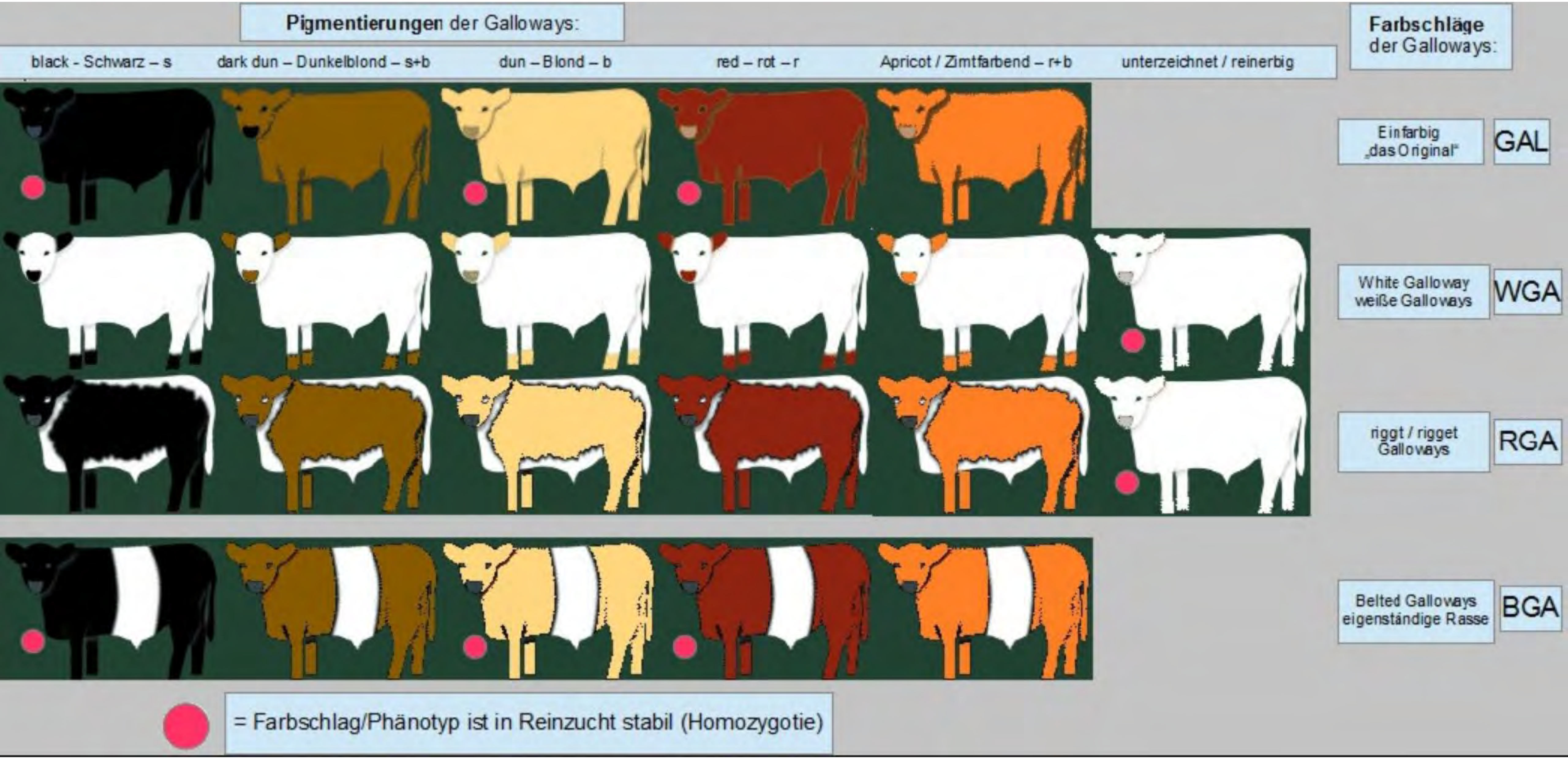
Genomic and phenotypic analyses of six offspring of a genome-edited hornless bull

Amy E. Young, Tamer A. Mansour, Bret R. McNabb, Joseph R. Owen, Josephine F. Trott, C. Titus Brown & Alison L. Van Eenennaam

Nature Biotechnology **38**, 225–232 (2020) | Cite this article

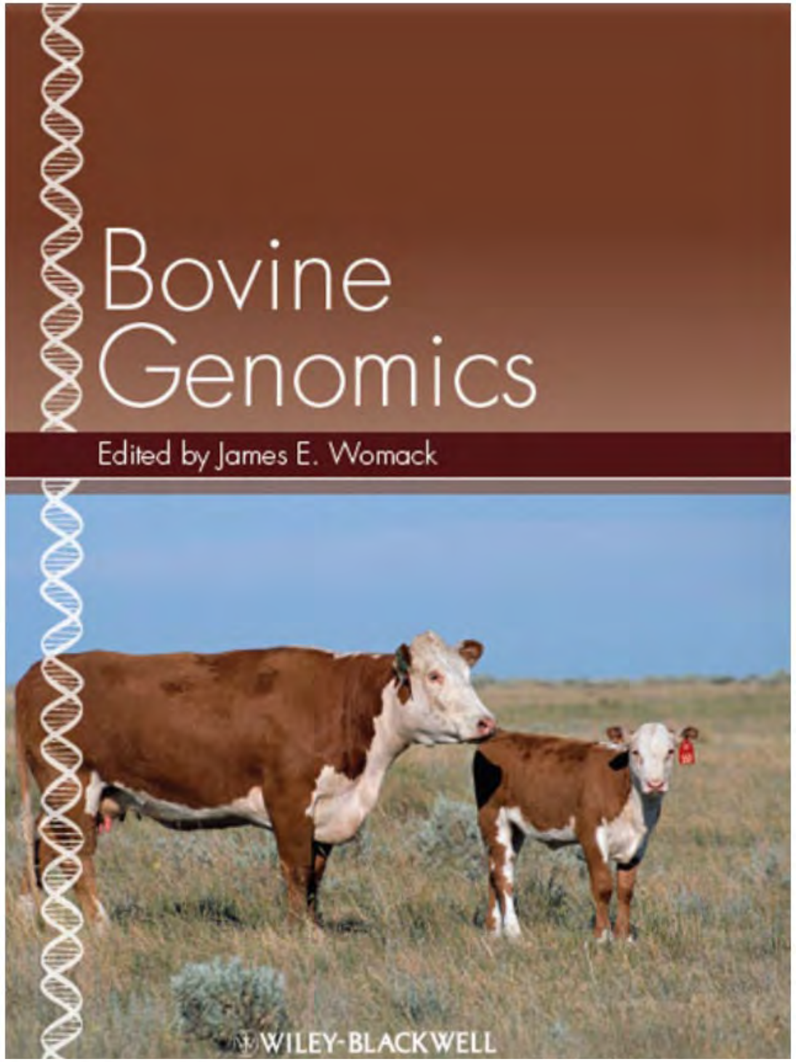
https://www.nature.com/articles/s41587-019-0266-0

Coat color genetics



http://www.miniature-cattle.com/graphics/Farbschl%C3%A4gePigmentierungenGALLOWAYS-free-share-wikimedia-commons.jpg

Coat color genetics



Chapter 3

Genetics of Coat Color in Cattle

Sheila M. Schmutz

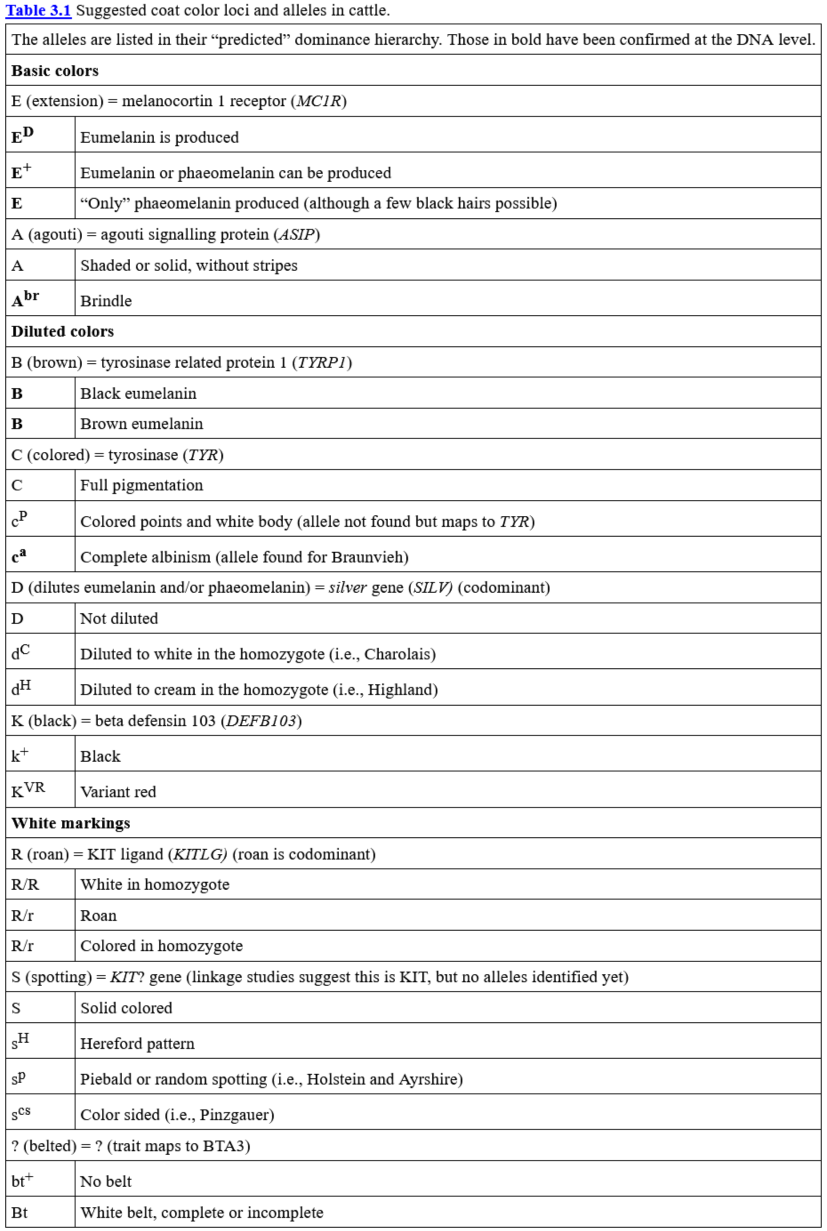
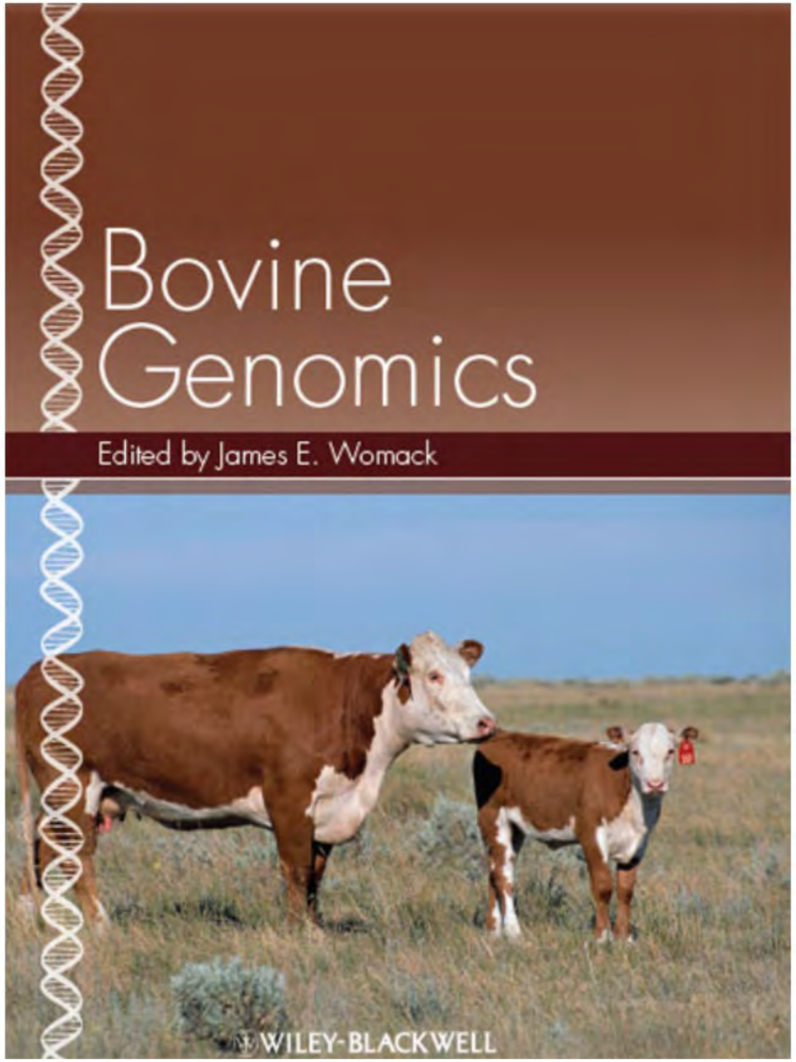


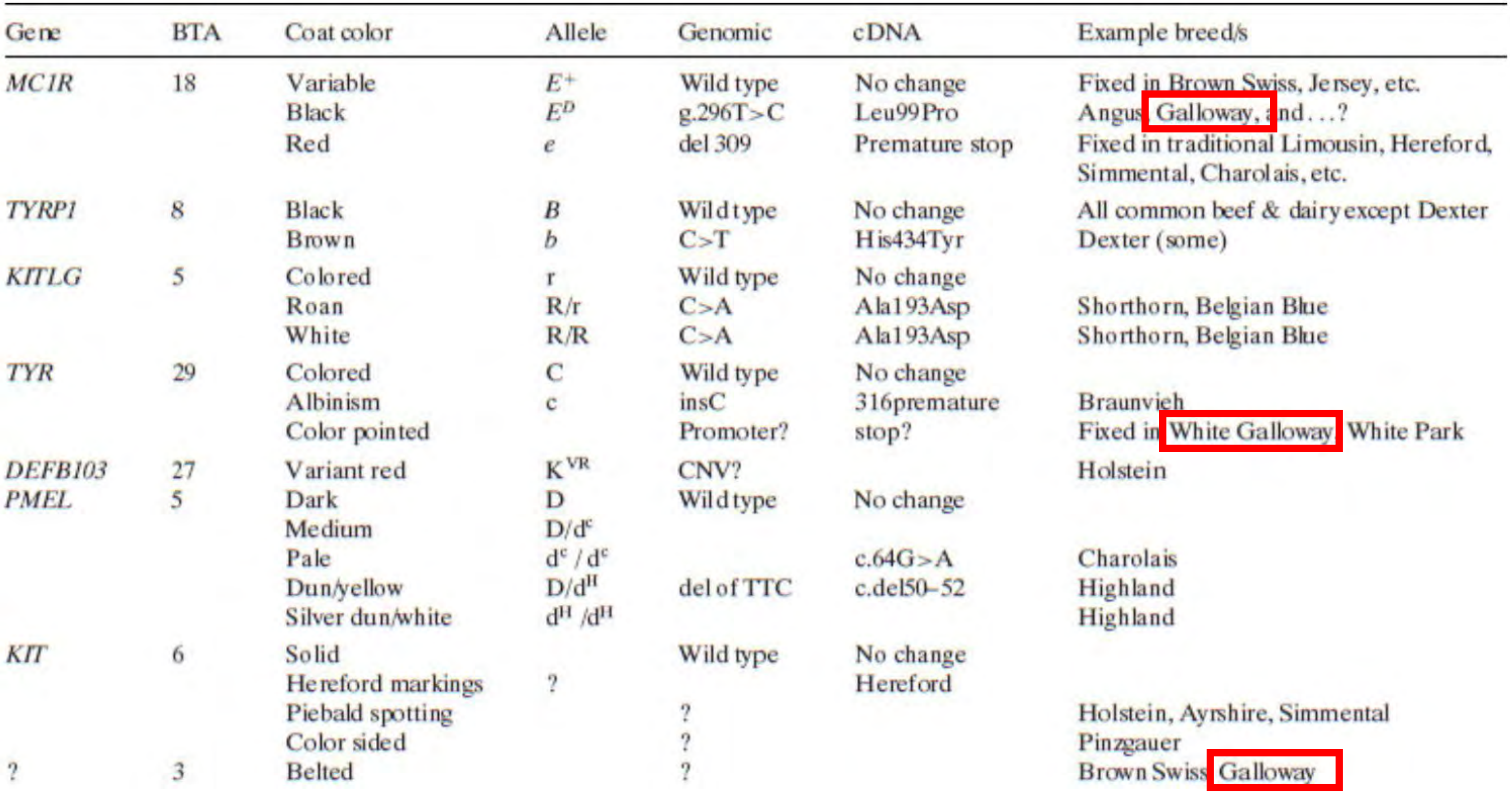
Table 3.1 Suggested coat color loci and alleles in cattle.

The alleles are listed in their "predicted" dominance hierarchy. Those in bold have been confirmed at the DNA level.	
Basic colors	
E (extension) = melanocortin 1 receptor (*MC1R*)	
E^{D}	Eumelanin is produced
E^{+}	Eumelanin or phaeomelanin can be produced
E	"Only" phaeomelanin produced (although a few black hairs possible)
A (agouti) = agouti signalling protein (*ASIP*)	
A	Shaded or solid, without stripes
A^{br}	Brindle
Diluted colors	
B (brown) = tyrosinase related protein 1 (*TYRP1*)	
B	Black eumelanin
B	Brown eumelanin
C (colored) = tyrosinase (*TYR*)	
C	Full pigmentation
c^{P}	Colored points and white body (allele not found but maps to *TYR*)
c^{a}	Complete albinism (allele found for Braunvieh)
D (dilutes eumelanin and/or phaeomelanin) = *silver* gene (*SILV*) (codominant)	
D	Not diluted
d^{C}	Diluted to white in the homozygote (i.e., Charolais)
d^{H}	Diluted to cream in the homozygote (i.e., Highland)
K (black) = beta defensin 103 (*DEFB103*)	
k^{+}	Black
K^{VR}	Variant red
White markings	
R (roan) = KIT ligand (*KITLG*) (roan is codominant)	
R/R	White in homozygote
R/r	Roan
R/r	Colored in homozygote
S (spotting) = *KIT*? gene (linkage studies suggest this is KIT, but no alleles identified yet)	
S	Solid colored
s^{H}	Hereford pattern
s^{P}	Piebald or random spotting (i.e., Holstein and Ayrshire)
s^{cs}	Color sided (i.e., Pinzgauer)
? (belted) = ? (trait maps to BTA3)	
bt^{+}	No belt
Bt	White belt, complete or incomplete

https://onlinelibrary.wiley.com/doi/pdf/10.1002/9781118301739#page=30

Coat color genetics





Gene	BTA	Coat color	Allele	Genomic	cDNA	Example breed/s
MC1R	18	Variable	E^+	Wild type	No change	Fixed in Brown Swiss, Jersey, etc.
		Black	E^D	g.296T>C	Leu99Pro	Angus, Galloway, and . . .?
		Red	e	del 309	Premature stop	Fixed in traditional Limousin, Hereford, Simmental, Charolais, etc.
TYRP1	8	Black	B	Wild type	No change	All common beef & dairy except Dexter
		Brown	b	C>T	His434Tyr	Dexter (some)
KITLG	5	Colored	r	Wild type	No change	
		Roan	R/r	C>A	Ala193Asp	Shorthorn, Belgian Blue
		White	R/R	C>A	Ala193Asp	Shorthorn, Belgian Blue
TYR	29	Colored	C	Wild type	No change	
		Albinism	c	insC	316premature	Braunvieh
		Color pointed		Promoter?	stop?	Fixed in White Galloway, White Park
DEFB103	27	Variant red	K^{VR}	CNV?		Holstein
PMEL	5	Dark	D	Wild type	No change	
		Medium	D/d^c			
		Pale	d^c/d^c		c.64G>A	Charolais
		Dun/yellow	D/d^H	del of TTC	c.del50–52	Highland
		Silver dun/white	d^H/d^H			Highland
KIT	6	Solid		Wild type	No change	
		Hereford markings	?		Hereford	
		Piebald spotting		?		Holstein, Ayrshire, Simmental
		Color sided		?		Pinzgauer
?	3	Belted		?		Brown Swiss, Galloway

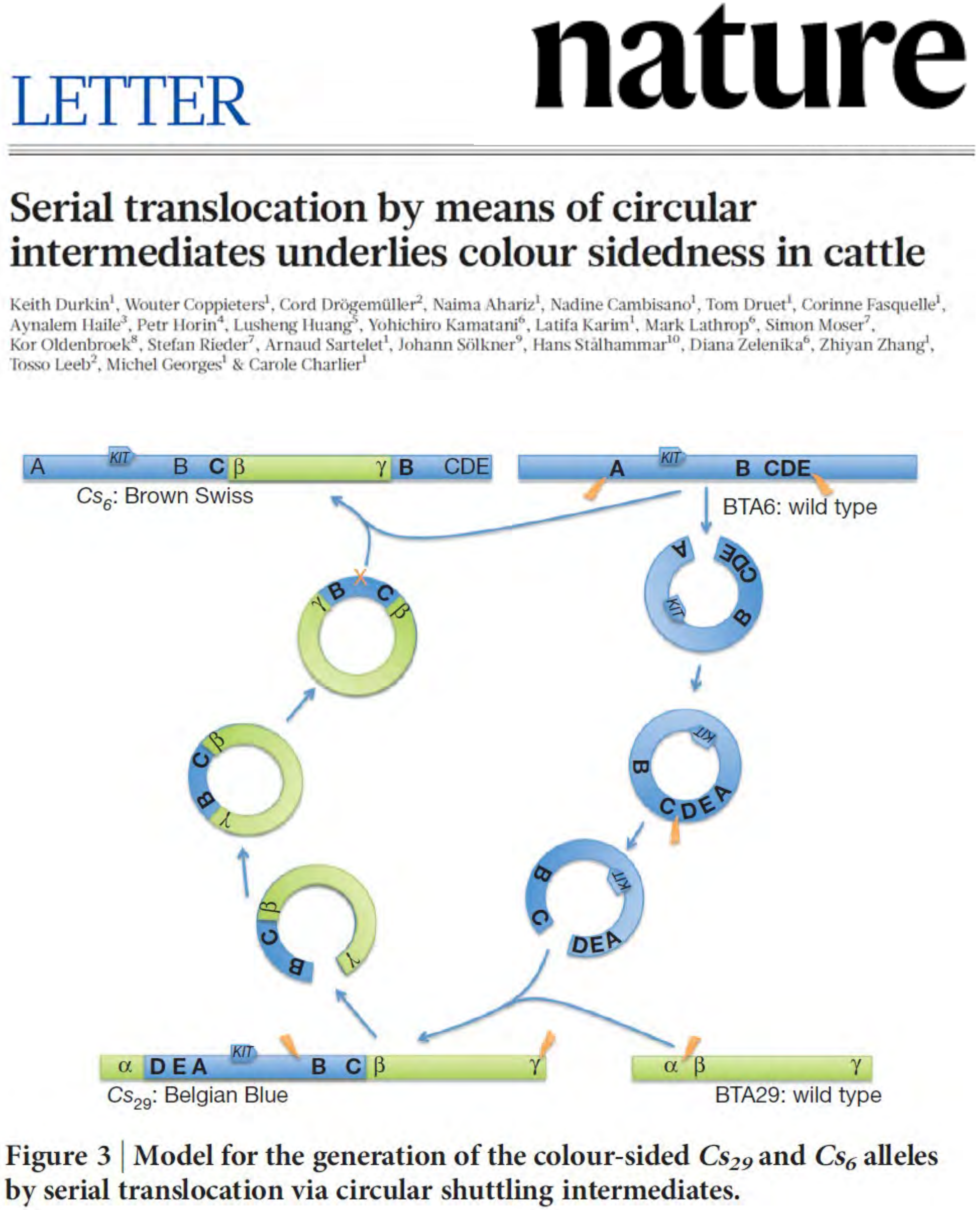
Chapter 3

Genetics of Coat Color in Cattle

Sheila M. Schmutz

https://onlinelibrary.wiley.com/doi/pdf/10.1002/9781118301739#page=30

KIT-associated colour sideness in cattle, a collaborative study of University of Bern and Université de Liège



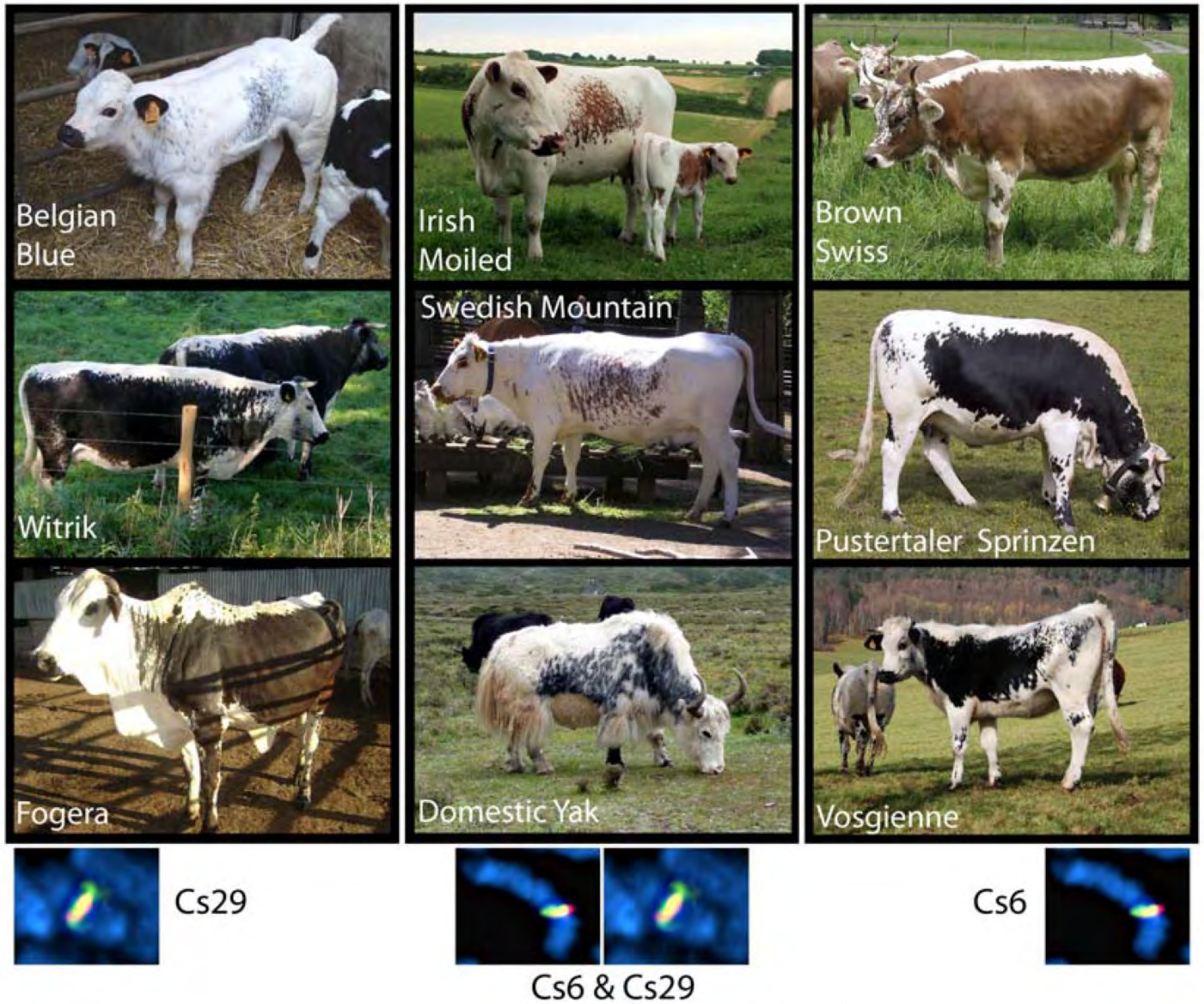
nature

LETTER

Serial translocation by means of circular intermediates underlies colour sidedness in cattle

Keith Durkin[1], Wouter Coppieters[1], Cord Drögemüller[2], Naima Ahariz[1], Nadine Cambisano[1], Tom Druet[1], Corinne Fasquelle[1], Aynalem Haile[3], Petr Horin[4], Lusheng Huang[5], Yohichiro Kamatani[6], Latifa Karim[1], Mark Lathrop[6], Simon Moser[7], Kor Oldenbroek[8], Stefan Rieder[7], Arnaud Sartelet[1], Johann Sölkner[9], Hans Stålhammar[10], Diana Zelenika[6], Zhiyan Zhang[1], Tosso Leeb[2], Michel Georges[1] & Carole Charlier[1]

Figure 3 | Model for the generation of the colour-sided Cs_{29} and Cs_6 alleles by serial translocation via circular shuttling intermediates.



https://www.nature.com/articles/nature10757

White Galloway carry the Colour sided *KIT*-allele (Cs_{29})

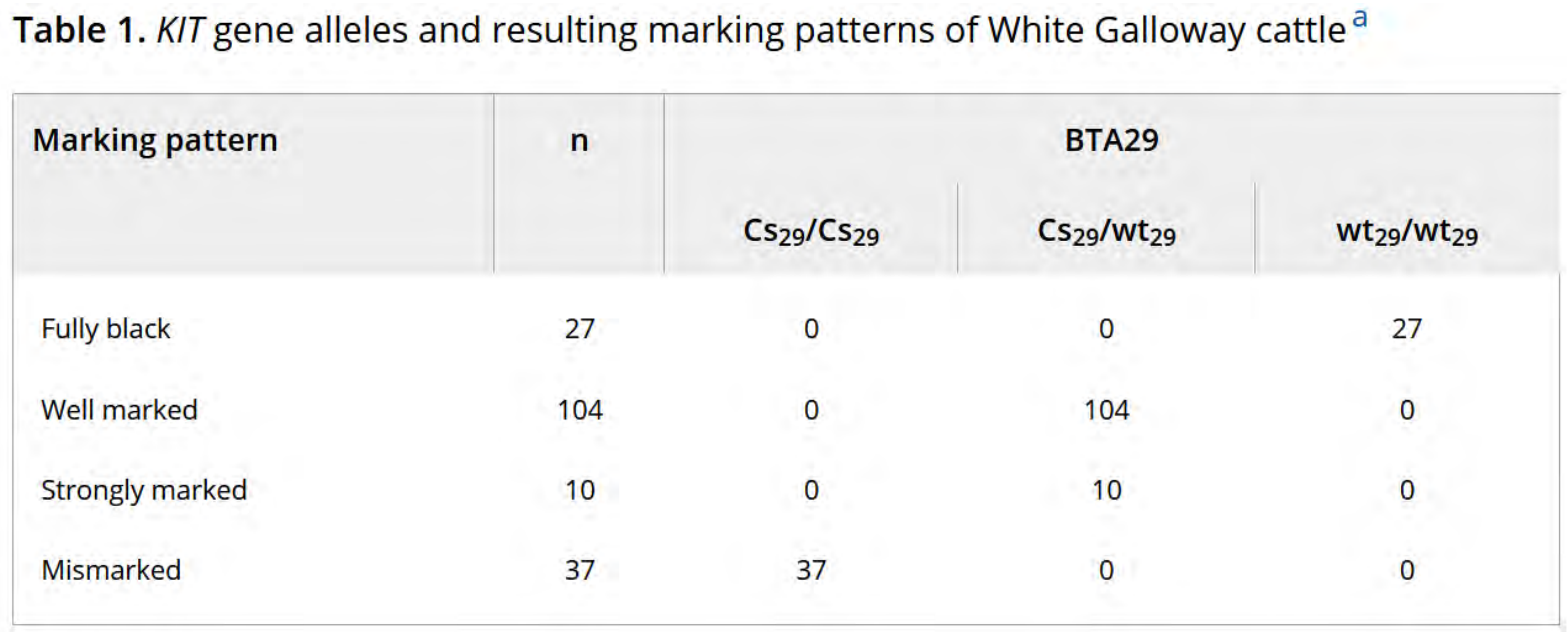
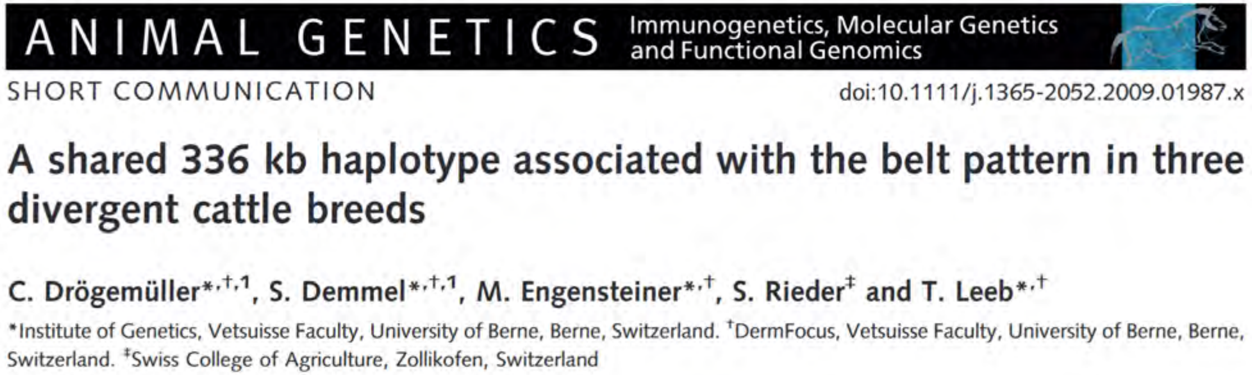


Table 1. *KIT* gene alleles and resulting marking patterns of White Galloway cattle[a]

Marking pattern	n	BTA29		
		Cs_{29}/Cs_{29}	Cs_{29}/wt_{29}	wt_{29}/wt_{29}
Fully black	27	0	0	27
Well marked	104	0	104	0
Strongly marked	10	0	10	0
Mismarked	37	37	0	0

https://onlinelibrary.wiley.com/doi/10.1111/age.12029

Original Braunvieh and **Belted Galloways** as well as **Dutch Belted (Lakenvelder) share the belt pattern**



ANIMAL GENETICS Immunogenetics, Molecular Genetics and Functional Genomics

SHORT COMMUNICATION

doi:10.1111/j.1365-2052.2009.01987.x

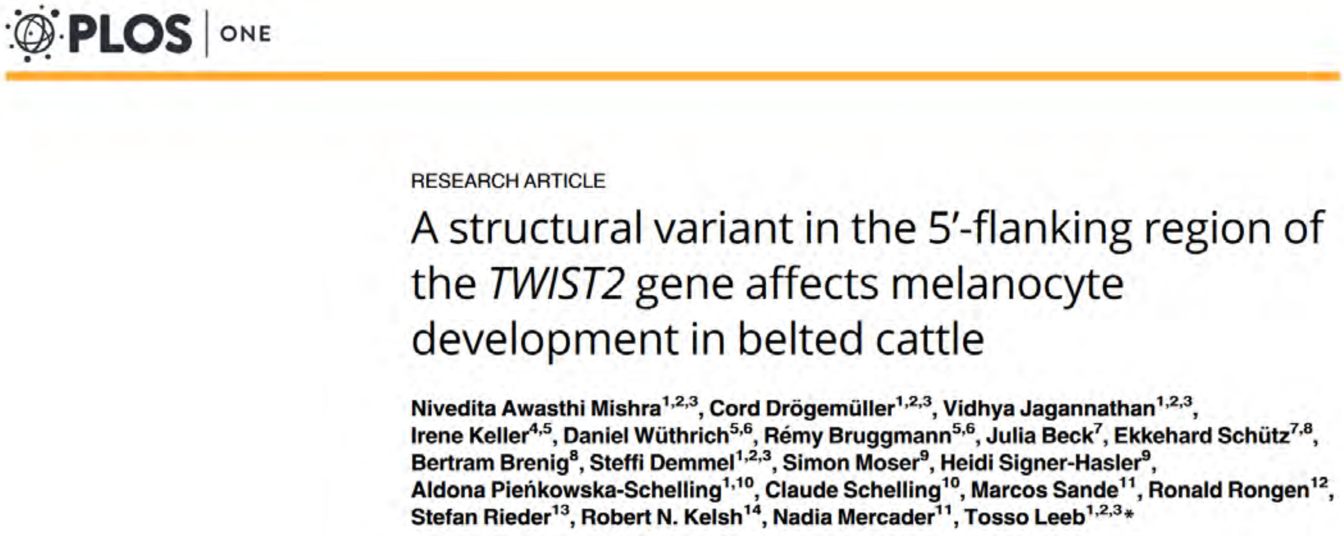
A shared 336 kb haplotype associated with the belt pattern in three divergent cattle breeds

C. Drögemüller[*,†,1], S. Demmel[*,†,1], M. Engensteiner[*,†], S. Rieder[‡] and T. Leeb[*,†]

[*] Institute of Genetics, Vetsuisse Faculty, University of Berne, Berne, Switzerland. [†] DermFocus, Vetsuisse Faculty, University of Berne, Berne, Switzerland. [‡] Swiss College of Agriculture, Zollikofen, Switzerland

https://onlinelibrary.wiley.com/doi/10.1111/j.1365-2052.2008.01826.x

Original Braunvieh and **Belted Galloways** as welle as **Dutch Belted (Lakenvelder) share a dominant *TWIST2* allele**


PLOS | ONE

RESEARCH ARTICLE

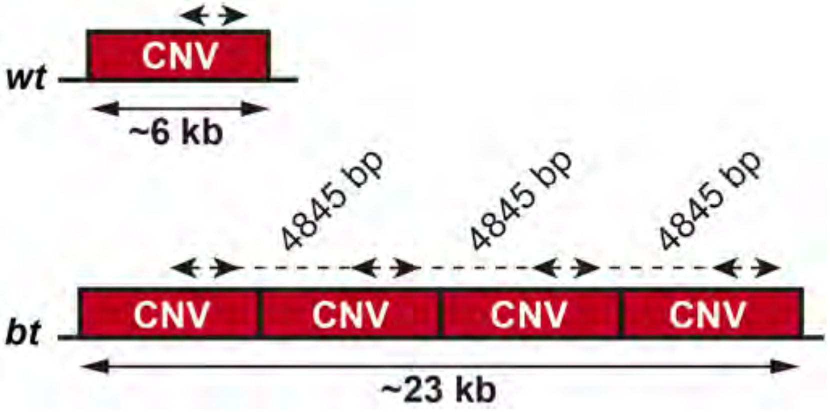
A structural variant in the 5′-flanking region of the *TWIST2* gene affects melanocyte development in belted cattle

Nivedita Awasthi Mishra[1,2,3], Cord Drögemüller[1,2,3], Vidhya Jagannathan[1,2,3], Irene Keller[4,5], Daniel Wüthrich[5,6], Rémy Bruggmann[5,6], Julia Beck[7], Ekkehard Schütz[7,8], Bertram Brenig[8], Steffi Demmel[1,2,3], Simon Moser[9], Heidi Signer-Hasler[9], Aldona Pieńkowska-Schelling[1,10], Claude Schelling[10], Marcos Sande[11], Ronald Rongen[12], Stefan Rieder[13], Robert N. Kelsh[14], Nadia Mercader[11], Tosso Leeb[1,2,3]*


Figure 3.3 Two belted Galloway cattle illustrating a complete belt on the left, and an incomplete belt on the right.

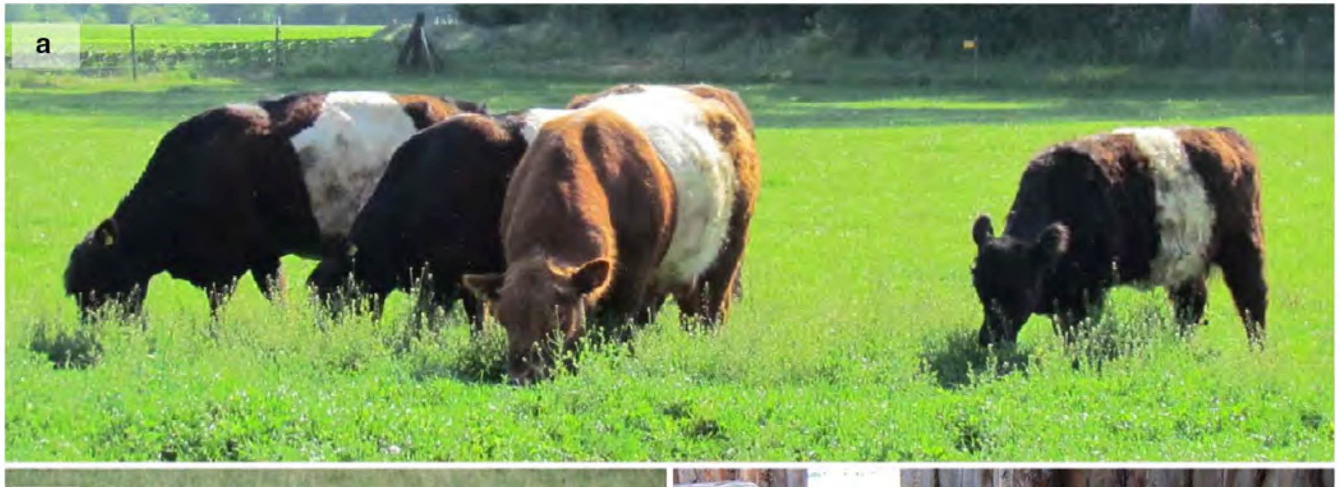
Sheila M. Schmutz

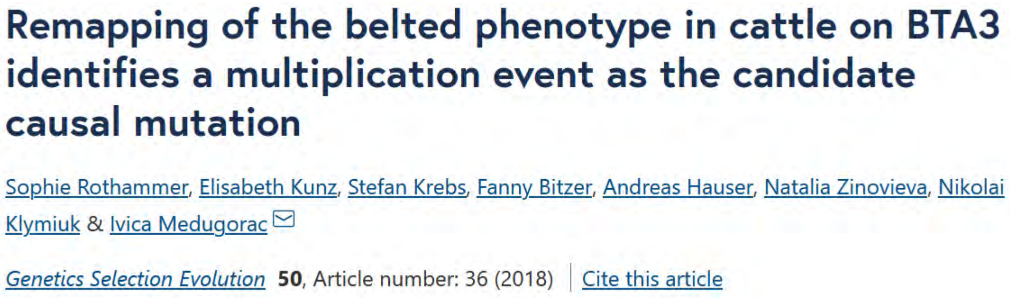
The belt-associated variant was a copy number variant (CNV) involving the quadruplication of a non-coding sequence located upstream of the *TWIST2* gene



https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0180170

What about the obvious differences in Belted Galloways?

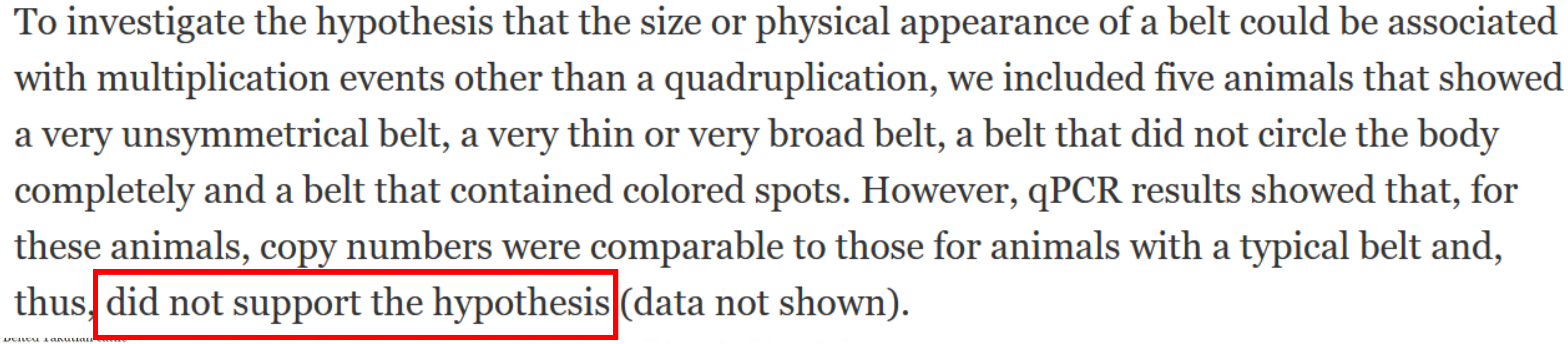




Remapping of the belted phenotype in cattle on BTA3 identifies a multiplication event as the candidate causal mutation

Sophie Rothammer, Elisabeth Kunz, Stefan Krebs, Fanny Bitzer, Andreas Hauser, Natalia Zinovieva, Nikolai Klymiuk & Ivica Medugorac

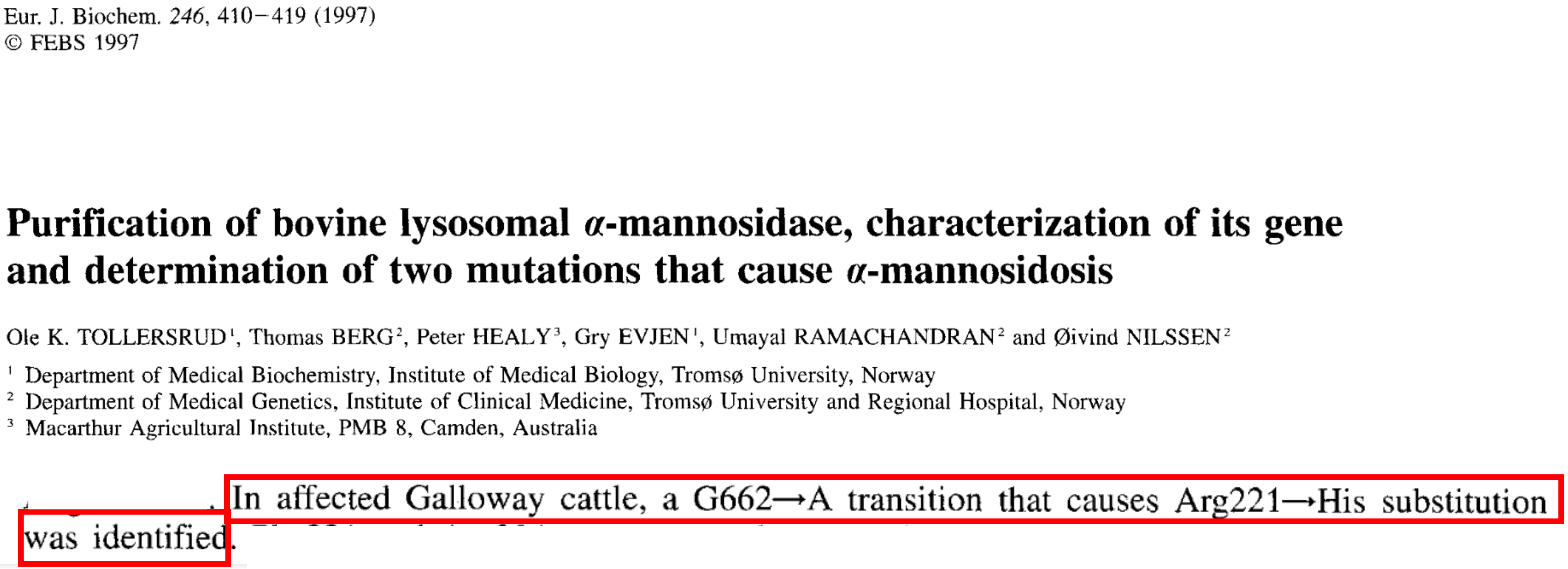
Genetics Selection Evolution **50**, Article number: 36 (2018) | Cite this article



To investigate the hypothesis that the size or physical appearance of a belt could be associated with multiplication events other than a quadruplication, we included five animals that showed a very unsymmetrical belt, a very thin or very broad belt, a belt that did not circle the body completely and a belt that contained colored spots. However, qPCR results showed that, for these animals, copy numbers were comparable to those for animals with a typical belt and, thus, did not support the hypothesis (data not shown).

https://doi.org/10.1186/s12711-018-0407-9

Genetic testing for inherited diseases: first Galloway causative mutation reported in 1997



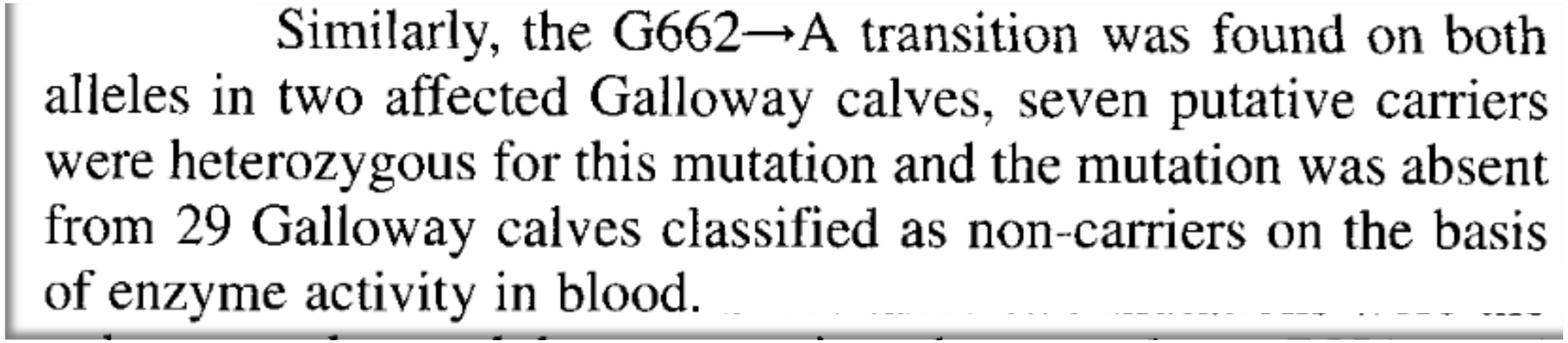
Eur. J. Biochem. *246*, 410–419 (1997)
© FEBS 1997

Purification of bovine lysosomal *α*-mannosidase, characterization of its gene and determination of two mutations that cause *α*-mannosidosis

Ole K. TOLLERSRUD[1], Thomas BERG[2], Peter HEALY[3], Gry EVJEN[1], Umayal RAMACHANDRAN[2] and Øivind NILSSEN[2]

[1] Department of Medical Biochemistry, Institute of Medical Biology, Tromsø University, Norway
[2] Department of Medical Genetics, Institute of Clinical Medicine, Tromsø University and Regional Hospital, Norway
[3] Macarthur Agricultural Institute, PMB 8, Camden, Australia

In affected Galloway cattle, a G662→A transition that causes Arg221→His substitution was identified.



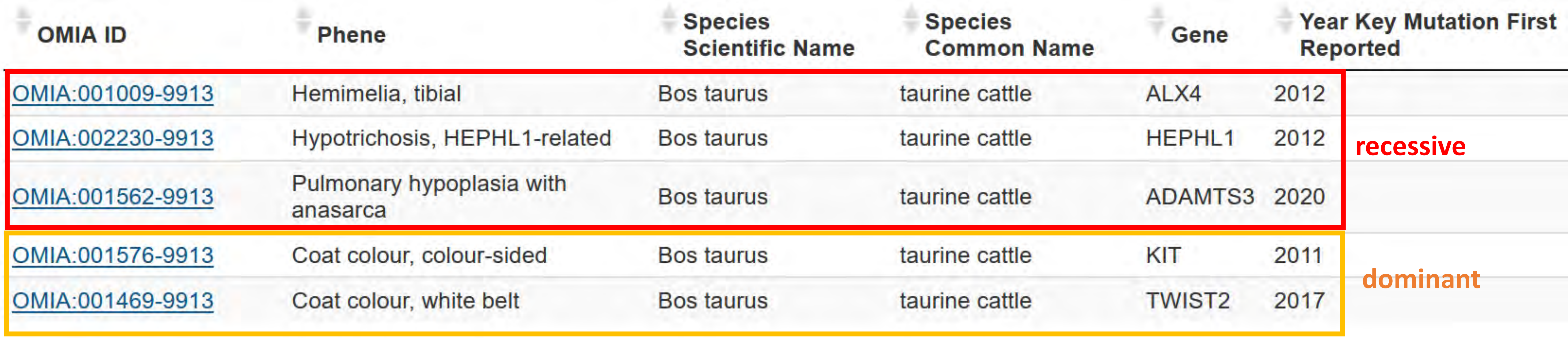
Similarly, the G662→A transition was found on both alleles in two affected Galloway calves, seven putative carriers were heterozygous for this mutation and the mutation was absent from 29 Galloway calves classified as non-carriers on the basis of enzyme activity in blood.

https://febs.onlinelibrary.wiley.com/doi/10.1111/j.1432-1033.1997.00410.x

Online Mendelian Inheritance in Animals (OMIA)

a catalogue of inherited disorders, other traits, and associated genes and variants in 480 animal species including cattle

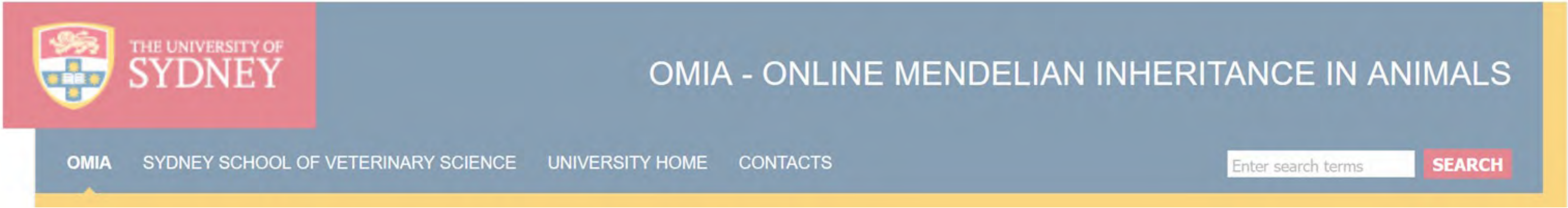
A search for "Galloway" results in this short list of 5 entries:



OMIA ID	Phene	Species Scientific Name	Species Common Name	Gene	Year Key Mutation First Reported
OMIA:001009-9913	Hemimelia, tibial	Bos taurus	taurine cattle	ALX4	2012
OMIA:002230-9913	Hypotrichosis, HEPHL1-related	Bos taurus	taurine cattle	HEPHL1	2012
OMIA:001562-9913	Pulmonary hypoplasia with anasarca	Bos taurus	taurine cattle	ADAMTS3	2020
OMIA:001576-9913	Coat colour, colour-sided	Bos taurus	taurine cattle	KIT	2011
OMIA:001469-9913	Coat colour, white belt	Bos taurus	taurine cattle	TWIST2	2017

recessive

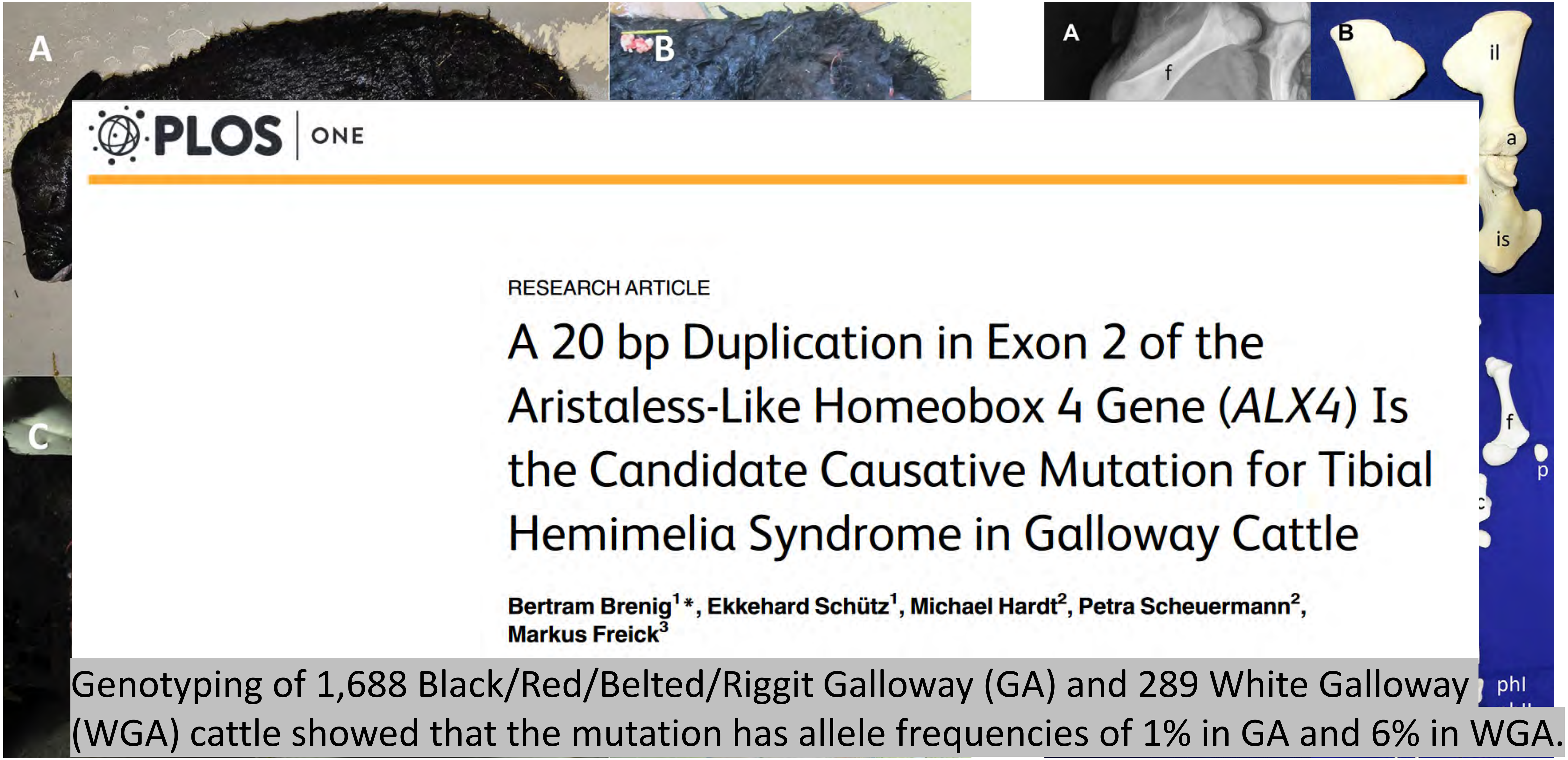
dominant



https://omia.org/home/

https://omia.org/home

Congenital anomalies and malformations in Black Galloway calves with tibial hemimelia syndrome



PLOS | ONE

RESEARCH ARTICLE

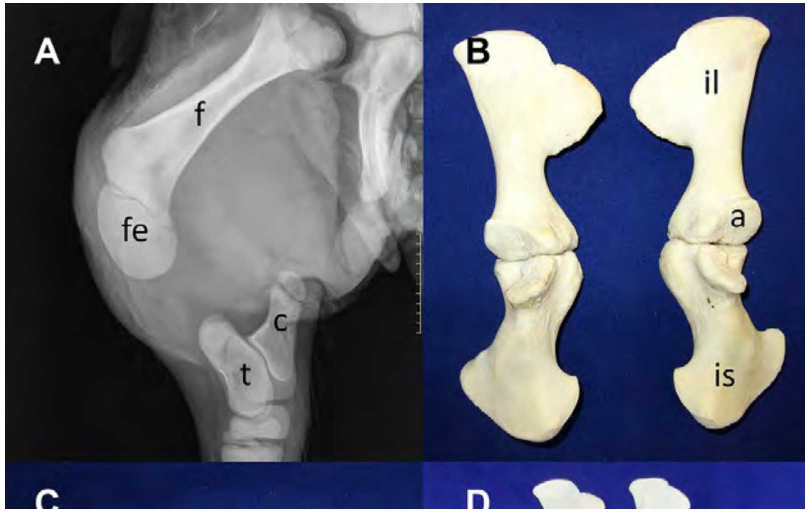
A 20 bp Duplication in Exon 2 of the Aristaless-Like Homeobox 4 Gene (*ALX4*) Is the Candidate Causative Mutation for Tibial Hemimelia Syndrome in Galloway Cattle

Bertram Brenig[1]*, Ekkehard Schütz[1], Michael Hardt[2], Petra Scheuermann[2], Markus Freick[3]

Genotyping of 1,688 Black/Red/Belted/Riggit Galloway (GA) and 289 White Galloway (WGA) cattle showed that the mutation has allele frequencies of 1% in GA and 6% in WGA.

https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0129208

Congenital anomalies and malformations in Black Galloway calves with tibial hemimelia syndrome




Received: 1 December 2022 | Accepted: 18 December 2022

DOI: 10.1111/age.13290

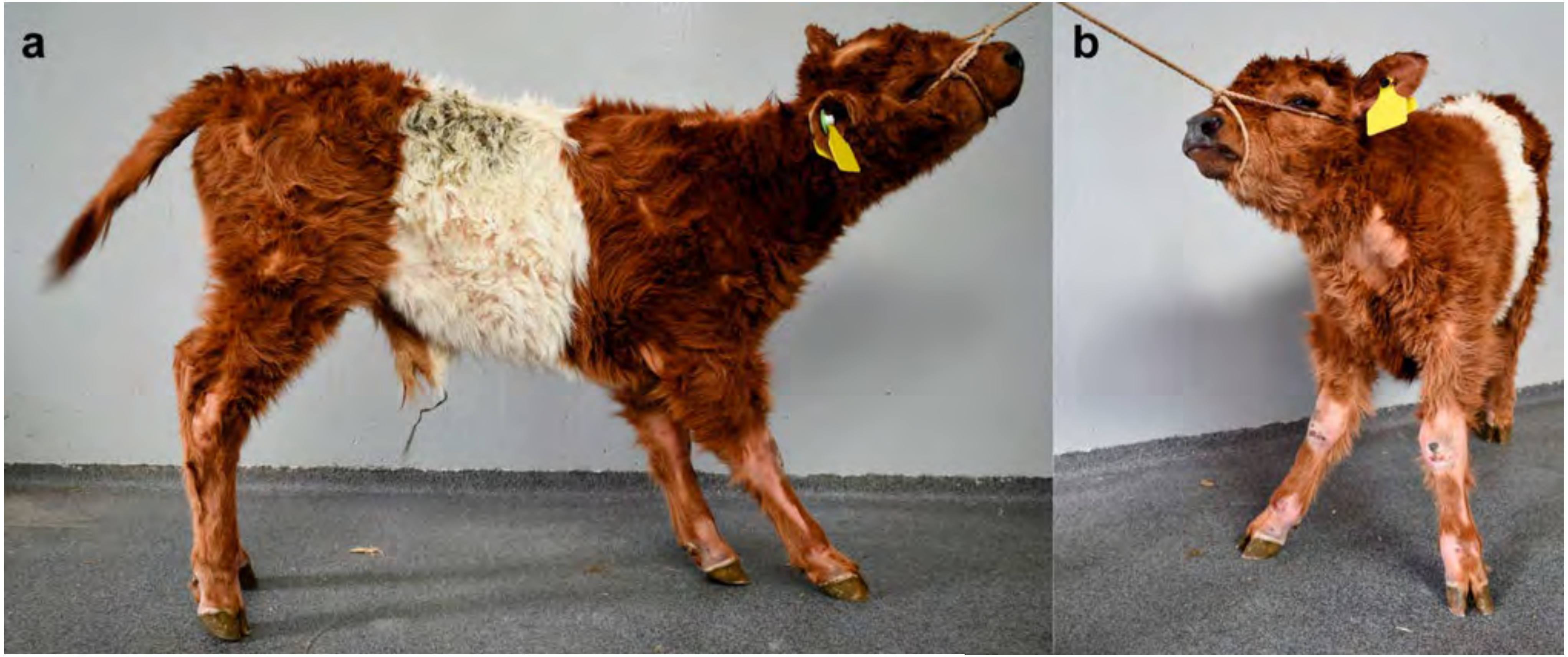
BRIEF REPORT

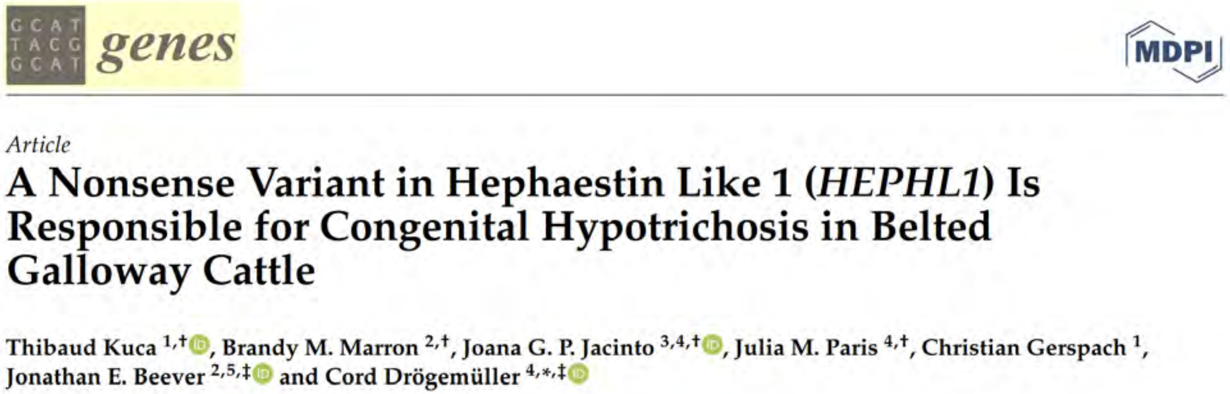
ANIMAL GENETICS WILEY

A case of tibial hemimelia in a German Galloway calf is associated with a novel mutation in the *ALX4* gene

https://omia.org/OMIA001009/9913/

Congenital hypotrichosis (HY) in a Swiss Belted Galloway cattle caused by a mutation in the *HEPHL1* gene





Article

A Nonsense Variant in Hephaestin Like 1 (*HEPHL1*) Is Responsible for Congenital Hypotrichosis in Belted Galloway Cattle

Thibaud Kuca [1,†], Brandy M. Marron [2,†], Joana G. P. Jacinto [3,4,†], Julia M. Paris [4,†], Christian Gerspach [1],
Jonathan E. Beever [2,5,‡] and Cord Drögemüller [4,*,‡]

https://www.mdpi.com/2073-4425/12/5/643

Congenital hypotrichosis (HY) in a Swiss Belted Galloway cattle caused by a mutation in the *HEPHL1* gene

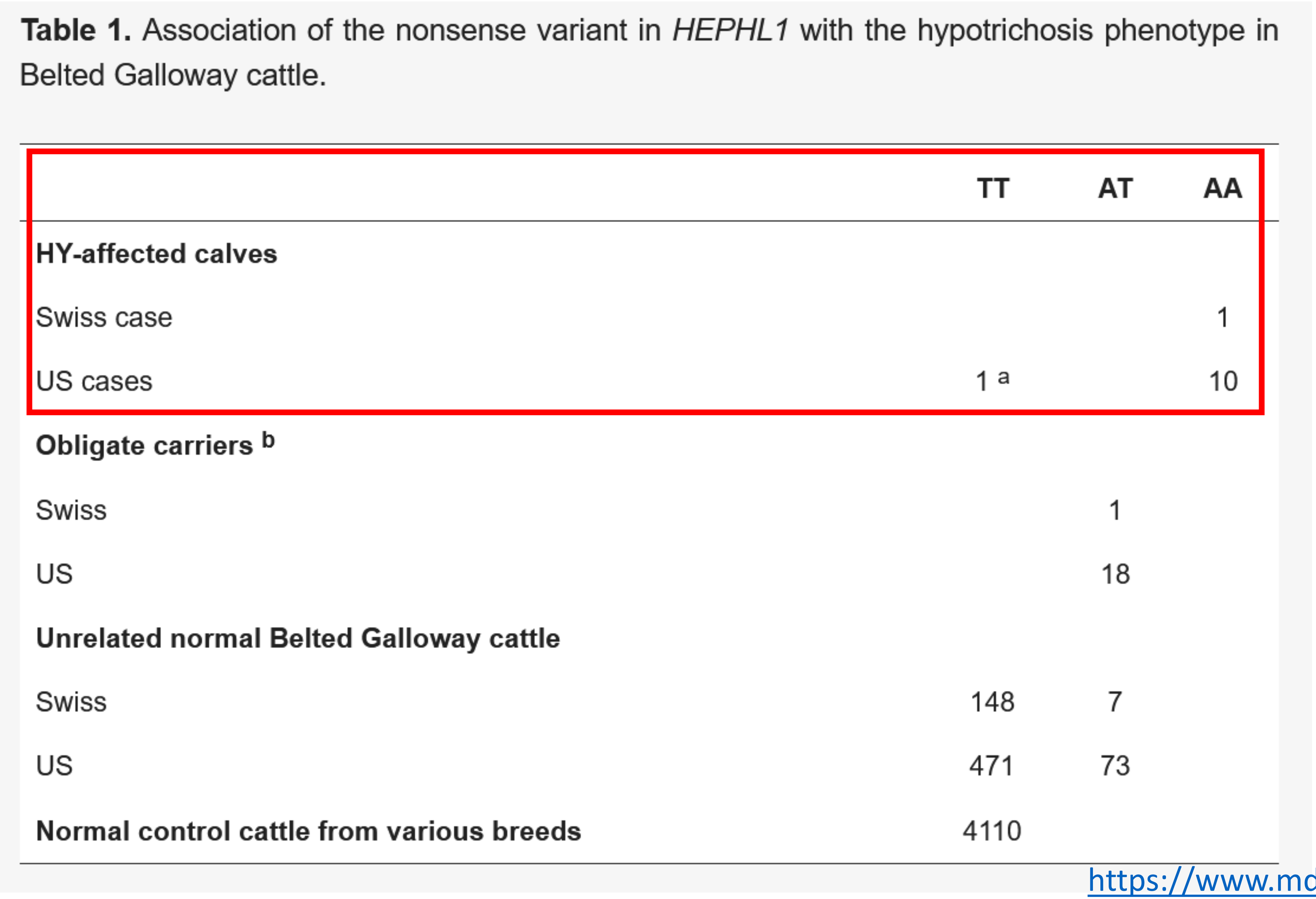
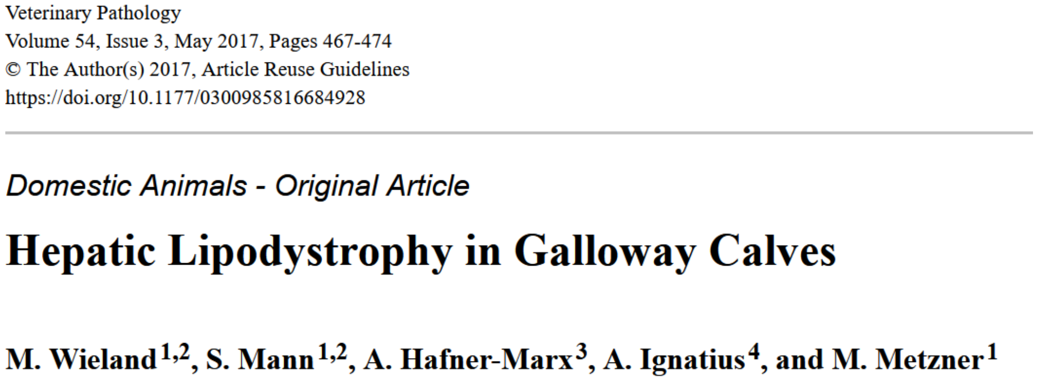


Table 1. Association of the nonsense variant in *HEPHL1* with the hypotrichosis phenotype in Belted Galloway cattle.

	TT	AT	AA
HY-affected calves			
Swiss case			1
US cases	1 [a]		10
Obligate carriers [b]			
Swiss		1	
US		18	
Unrelated normal Belted Galloway cattle			
Swiss	148	7	
US	471	73	
Normal control cattle from various breeds	4110		

https://www.mdpi.com/2073-4425/12/5/643

Hepatic lipodystrophy in Galloways: a possibly inherited fatal liver disease with unknown cause



Veterinary Pathology
Volume 54, Issue 3, May 2017, Pages 467-474
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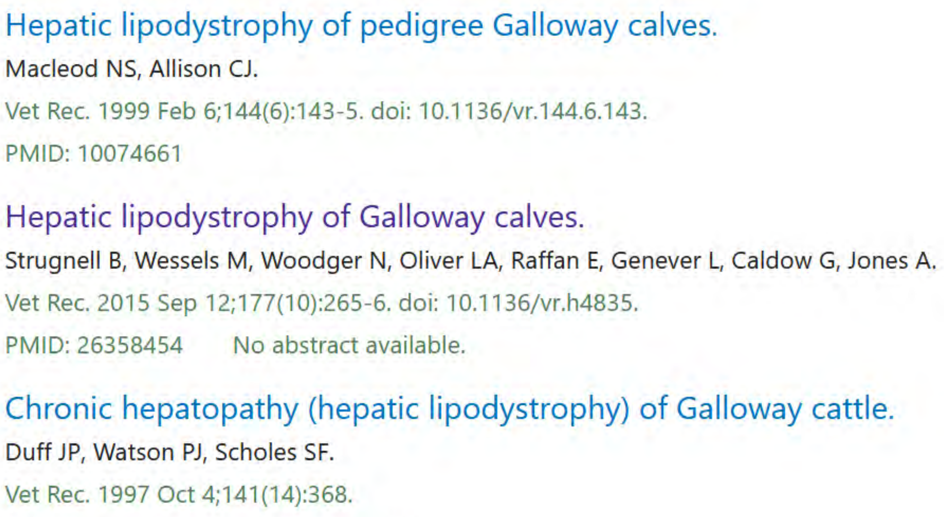
https://doi.org/10.1177/0300985816684928

Domestic Animals - Original Article

Hepatic Lipodystrophy in Galloway Calves

M. Wieland[1,2], S. Mann[1,2], A. Hafner-Marx[3], A. Ignatius[4], and M. Metzner[1]



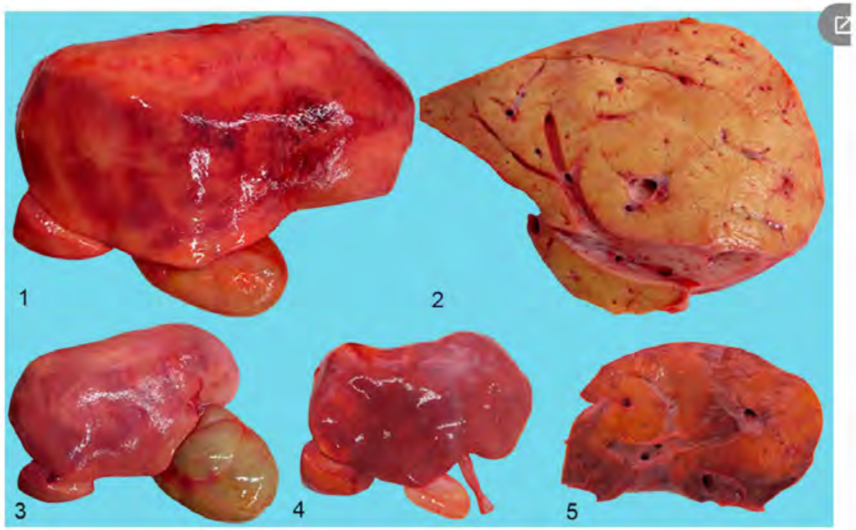
Hepatic lipodystrophy of pedigree Galloway calves.
Macleod NS, Allison CJ.
Vet Rec. 1999 Feb 6;144(6):143-5. doi: 10.1136/vr.144.6.143.
PMID: 10074661

Hepatic lipodystrophy of Galloway calves.
Strugnell B, Wessels M, Woodger N, Oliver LA, Raffan E, Genever L, Caldow G, Jones A.
Vet Rec. 2015 Sep 12;177(10):265-6. doi: 10.1136/vr.h4835.
PMID: 26358454 No abstract available.

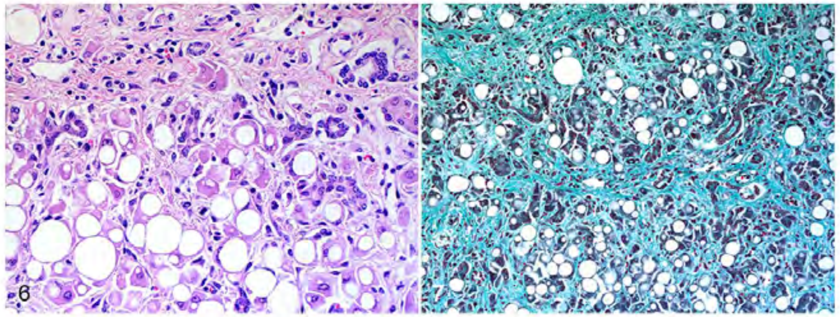
Chronic hepatopathy (hepatic lipodystrophy) of Galloway cattle.
Duff JP, Watson PJ, Scholes SF.
Vet Rec. 1997 Oct 4;141(14):368.

ailable.

it is thought to have a genetic origin, although this has not been proven



Figures 1–5. Hepatic lipodystrophy, liver and gallbladder; bovine. **Figures 1 and 2.** Calf No. 5, diffusely enlarged yellow liver with finely nodular surface and diffuse yellow cut face. **Figure 3.** Calf No. 6, finely granular surface of the liver and severely distended gallbladder. **Figures 4 and 5.** Calf No. 7, orange-brown discoloration and nodular cut surface.

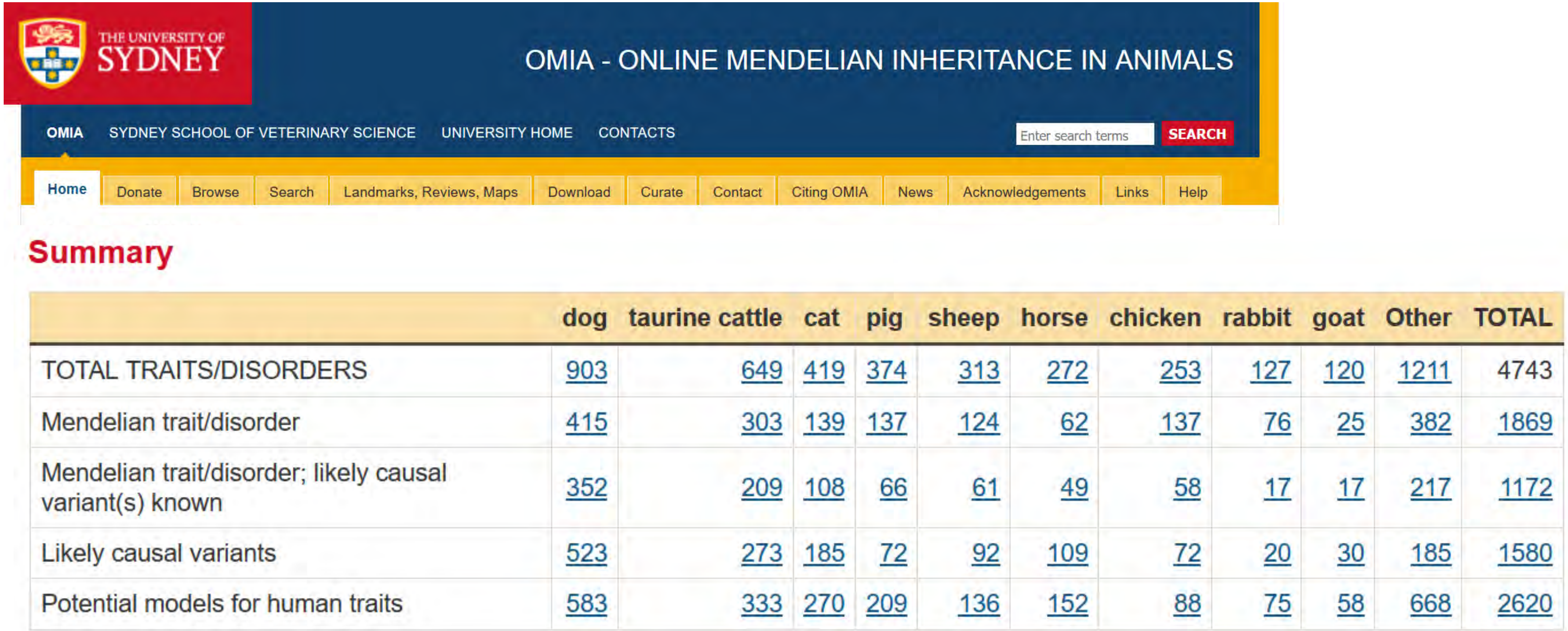


Figures 6 and 7. Hepatic lipodystrophy, liver; bovine. **Figure 6.** Loss of hepatocytes, hepatic lipidosis, and bile duct proliferation are prominent. Hematoxylin and eosin. **Figure 7.** There is extensive fibrosis. Goldner's trichrome.

https://journals.sagepub.com/doi/10.1177/0300985816684928

2023 in animals:

More than 1500 causal variants known



Summary

	dog	taurine cattle	cat	pig	sheep	horse	chicken	rabbit	goat	Other	TOTAL
TOTAL TRAITS/DISORDERS	903	649	419	374	313	272	253	127	120	1211	4743
Mendelian trait/disorder	415	303	139	137	124	62	137	76	25	382	1869
Mendelian trait/disorder; likely causal variant(s) known	352	209	108	66	61	49	58	17	17	217	1172
Likely causal variants	523	273	185	72	92	109	72	20	30	185	1580
Potential models for human traits	583	333	270	209	136	152	88	75	58	668	2620

https://omia.org/home/

If you have any questions: Please do not hesitate to contact us!

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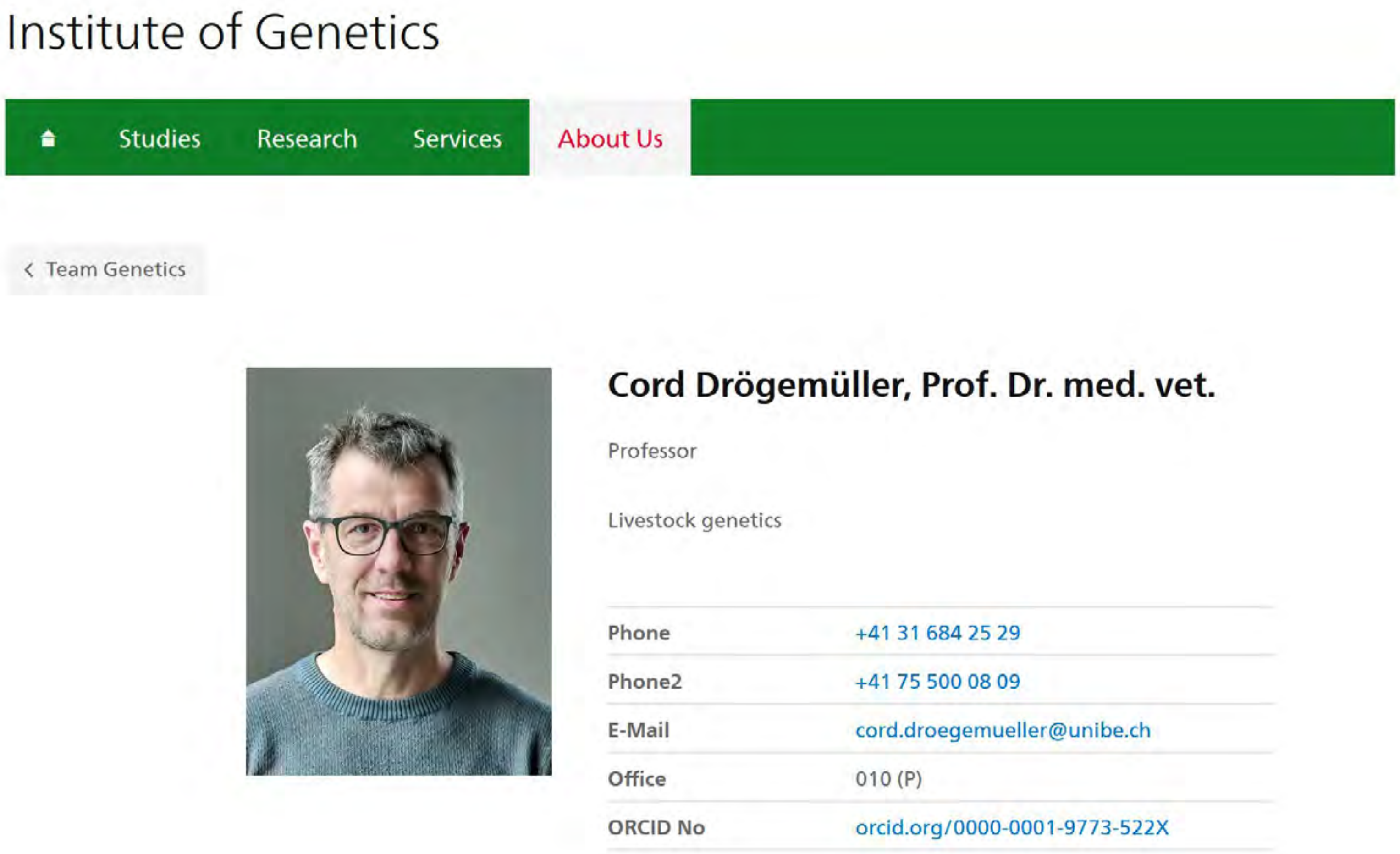

Institute of Genetics

Cord Drögemüller, Prof. Dr. med. vet.

Professor

Livestock genetics

Phone	+41 31 684 25 29
Phone2	+41 75 500 08 09
E-Mail	cord.droegemueller@unibe.ch
Office	010 (P)
ORCID No	orcid.org/0000-0001-9773-522X

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