



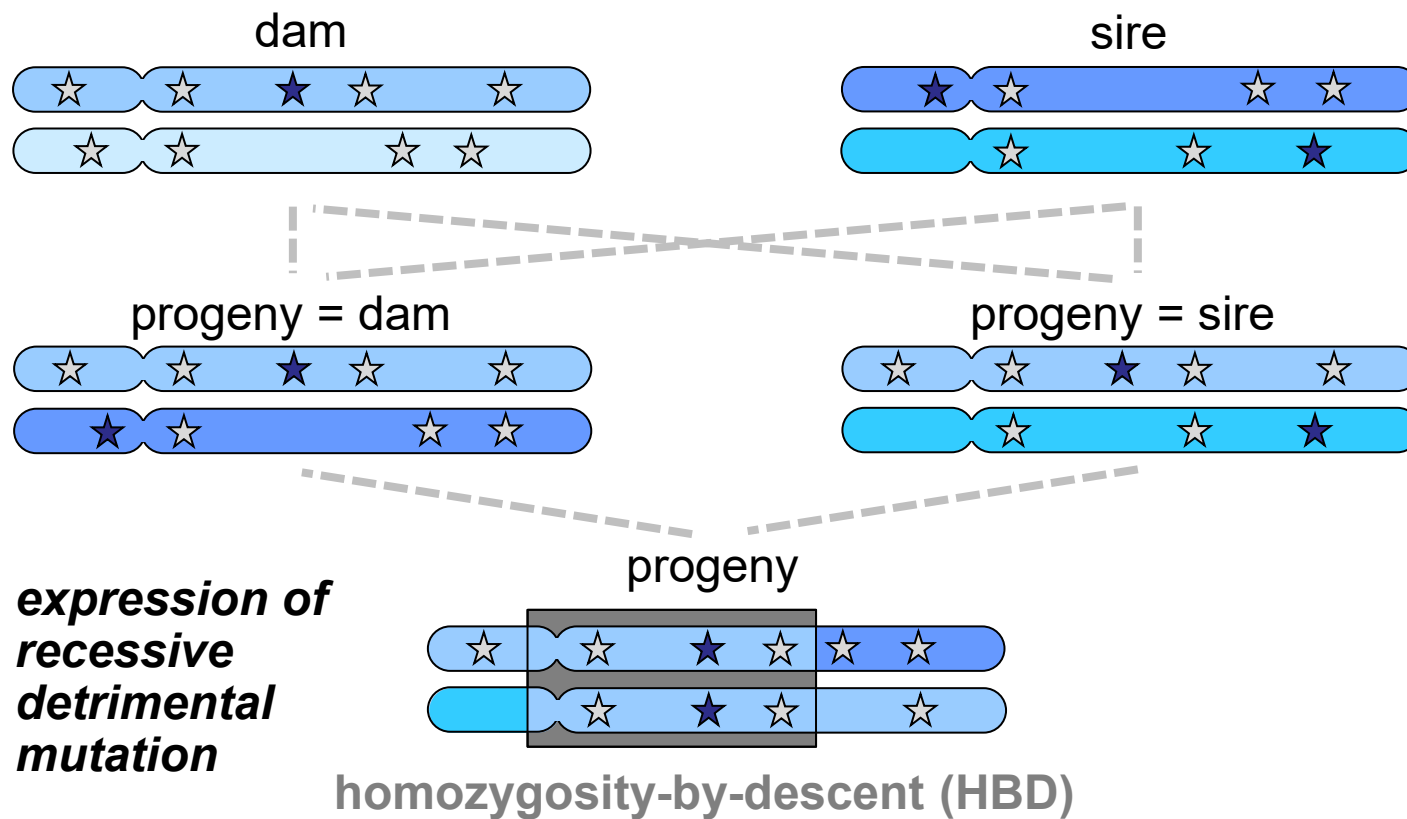
Assessing genome complementarity in beef-on-dairy crosses through selection scans, runs of homozygosity and genomic variation

**Dorothea Lindtke, Sylvain Lerch, Isabelle Morel &
Markus Neuditschko**

September 1, 2024

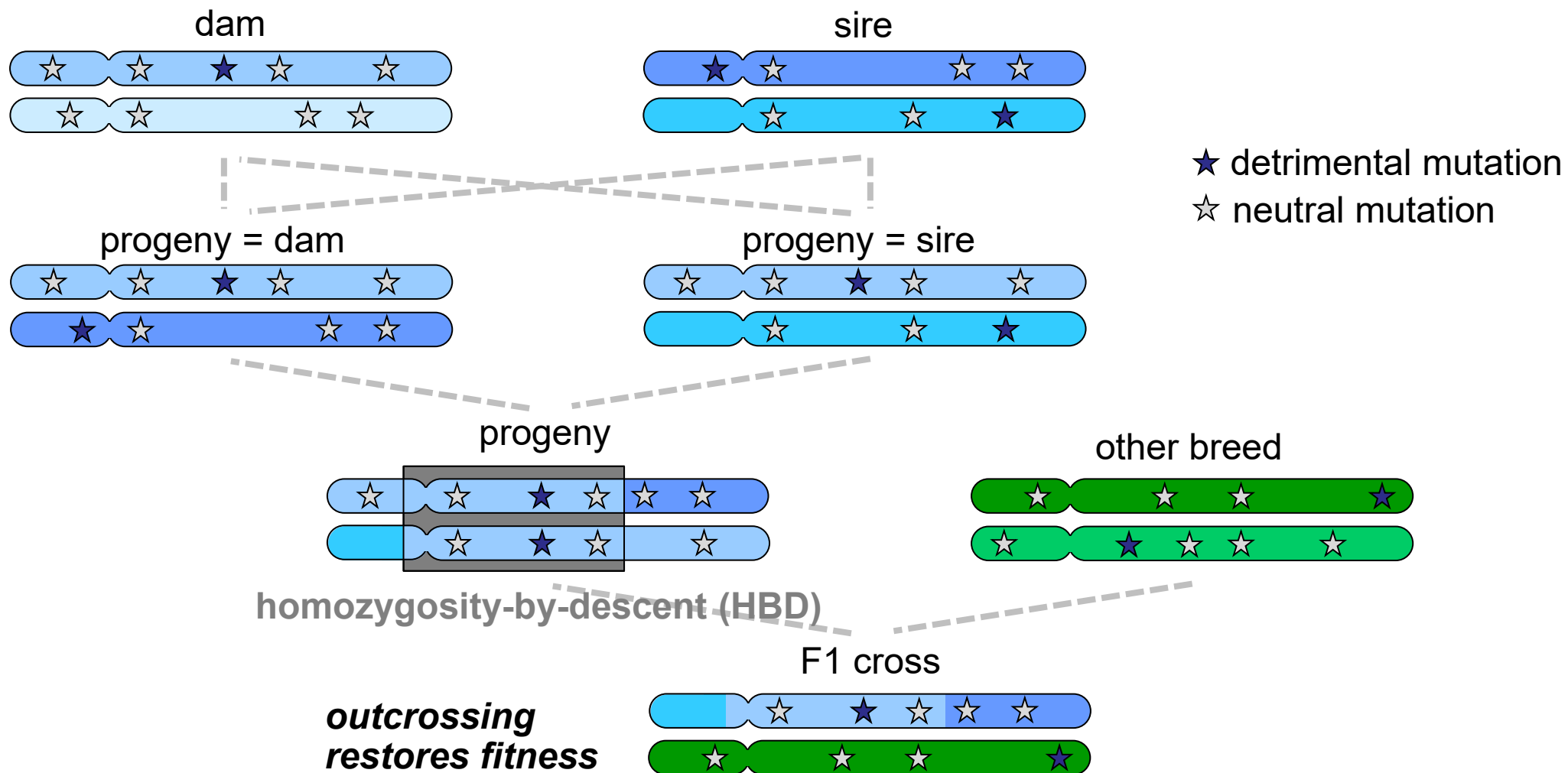


Inbreeding



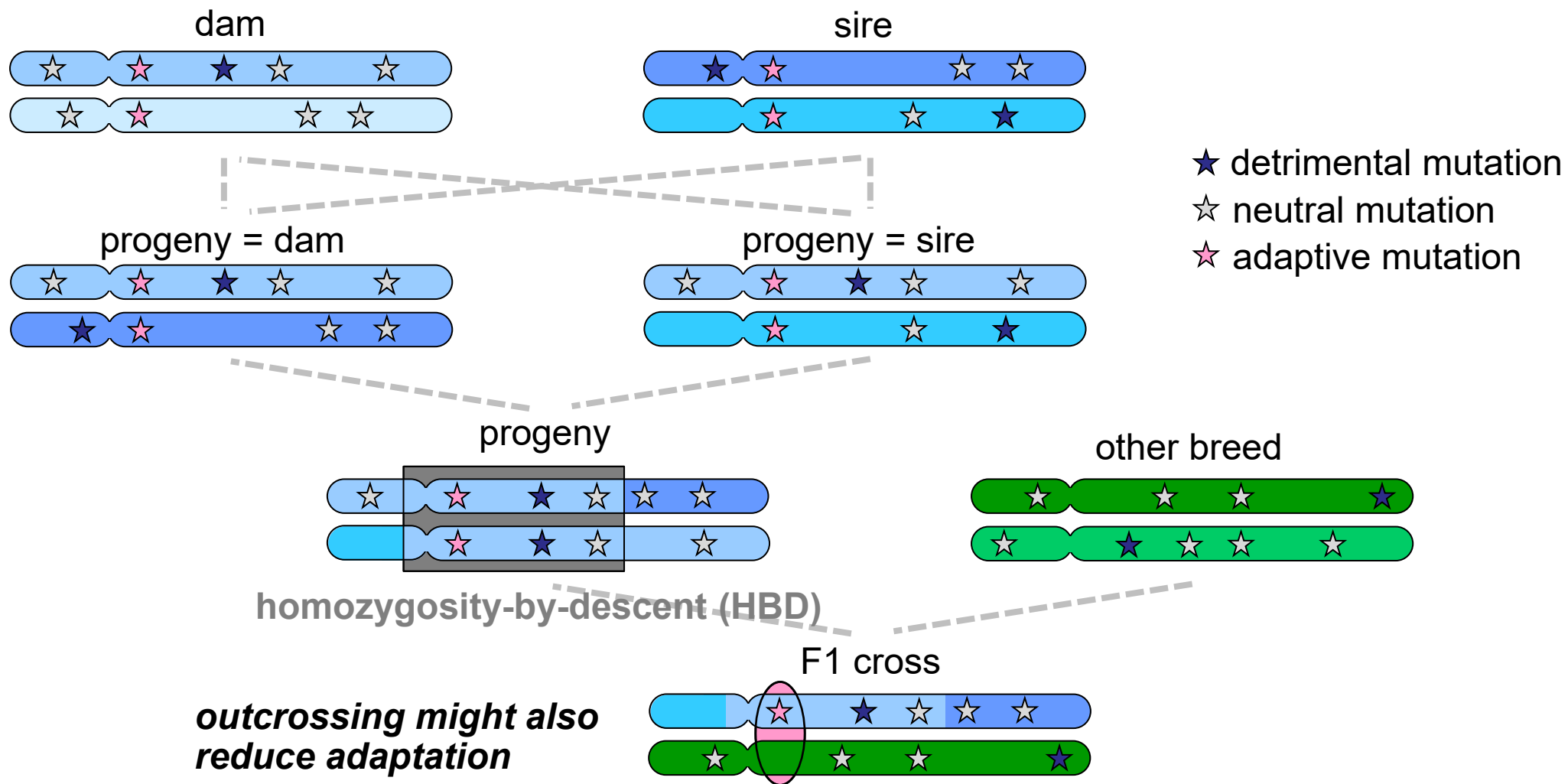


Inbreeding and outcrossing





Inbreeding and outcrossing





Beef-on-dairy for improved economic gain



Picture: brown-swiss.org

Beef-on-dairy

- inbreeding reduction with potential positive effects on calf health
- increased meat yield from surplus calves improves economic gain

Brown Swiss (BSW)

- breed founded at the end of 19th century from about 170 Original Braunvieh ancestors
- intense artificial selection for milk production
- high levels of genomic inbreeding

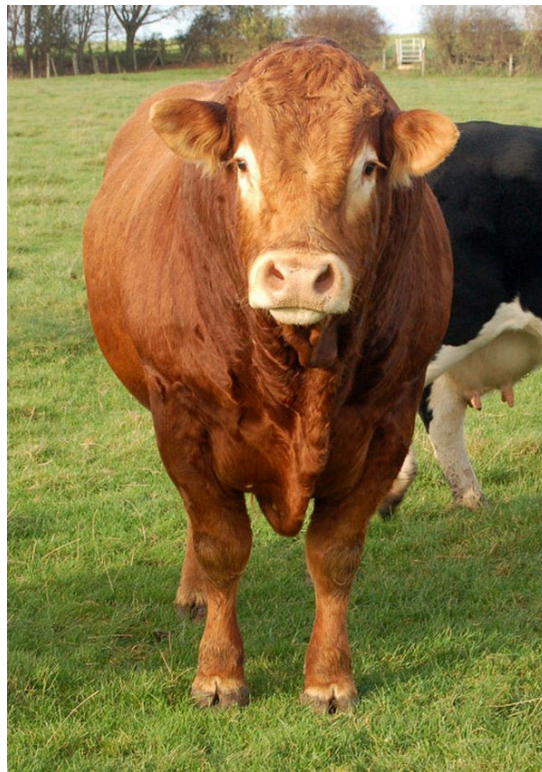


Breeds of beef bulls used for crossing to BSW

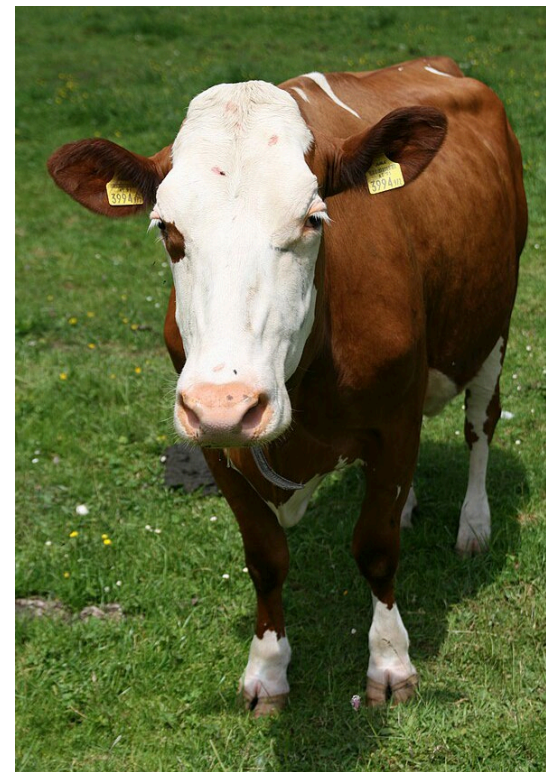
Angus (AAN)



Limousin (LIM)



Simmental (SIM)



Pictures: <https://commons.wikimedia.org/> ; Evelyn Simak; Andy F.; Richard Bartz



Experimental setup

- F1 crosses: 89 AAN×BSW, 121 LIM×BSW, and 91 SIM×BSW
- DNA from parents: 8 AAN, 18 LIM, 8 SIM, 181 BSW
- low-pass sequencing data with 8,296,799 autosomal SNPs after filtering
- phenotypic measurements for 248 F1 crosses (slaughtered at pre-defined body weight, median 524 kg):
 - weight at arrival
 - age at slaughter
 - hot carcass weight
 - hot carcass protein and lipid masses and proportions
 - *Longissimus thoracis* intramuscular fat content



Methods

- i. amount of inbreeding reduction through crossbreeding was assessed by computing homozygosity-by-descent (HBD) segments^[1] in BSW and F1s
- ii. genes possibly under selection in BSW were identified by using the integrated haplotype score (iHS)^[2], the haplotype homozygosity score (H12)^[3], and a composite likelihood ratio test (CLR)^[4]
- iii. among the detected genes, the ones divergent from the beef breeds were identified (neighbor-joining trees of p-distances^[5] followed by clustering)
- iv. association tests between SNPs located in candidate genes and phenotypes were performed using linear mixed-effects models

[1] R package RZooRoH; Bertrand et al. 2019 Methods Ecol Evol

[2] R package rehh; Gautier et al. 2017 Mol Ecol Resour

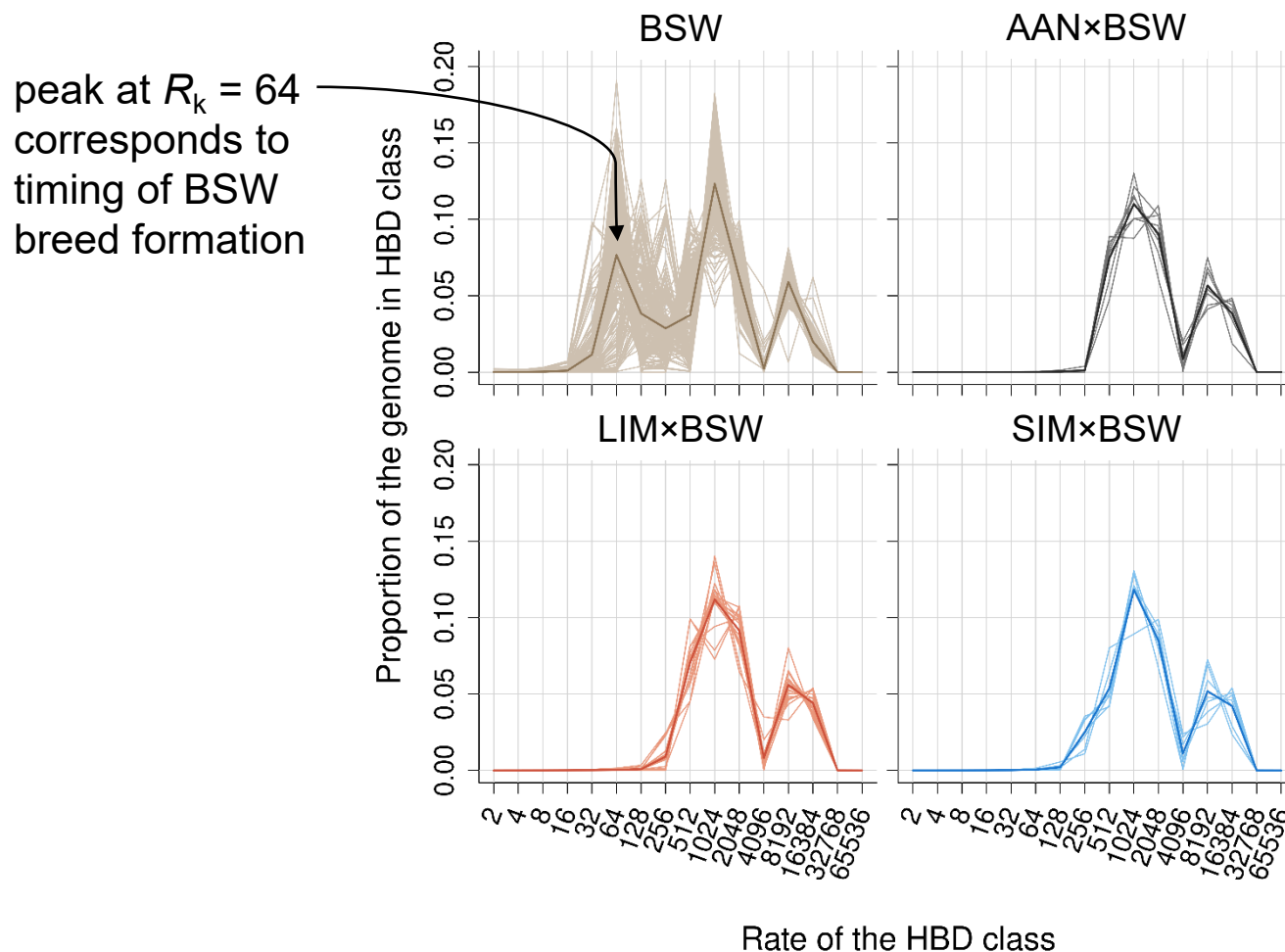
[3] Garud et al. 2015 Plos Genet

[4] SweepFinder2; DeGiorgio et al. 2016 Bioinformatics

[5] ngsDist; Vieira et al. 2016 Biol J Linn Soc



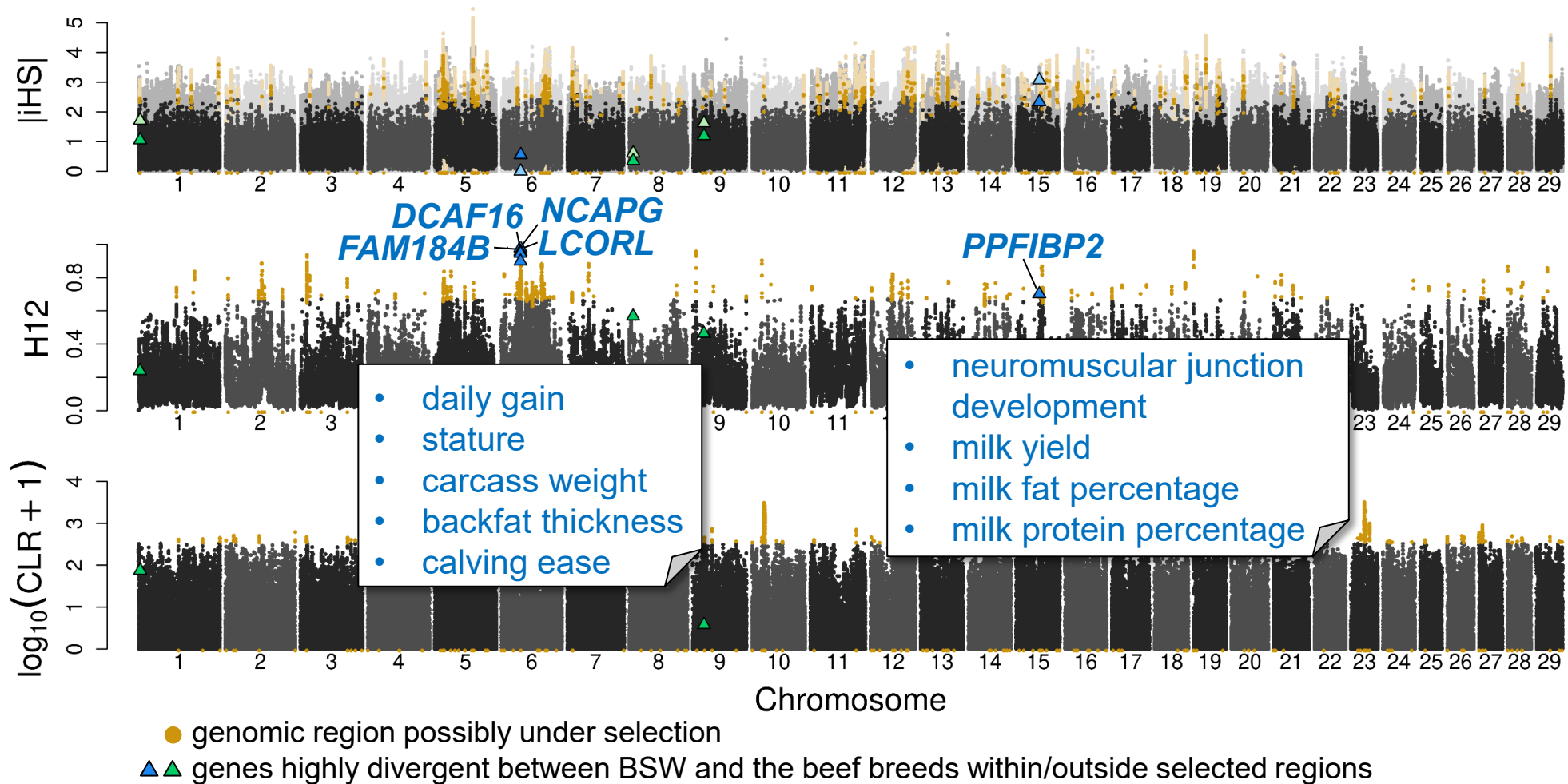
Long HBD segments from more recent inbreeding are effectively removed by crossbreeding



Rate R_k corresponds to roughly twice the number of generations back to the common ancestor

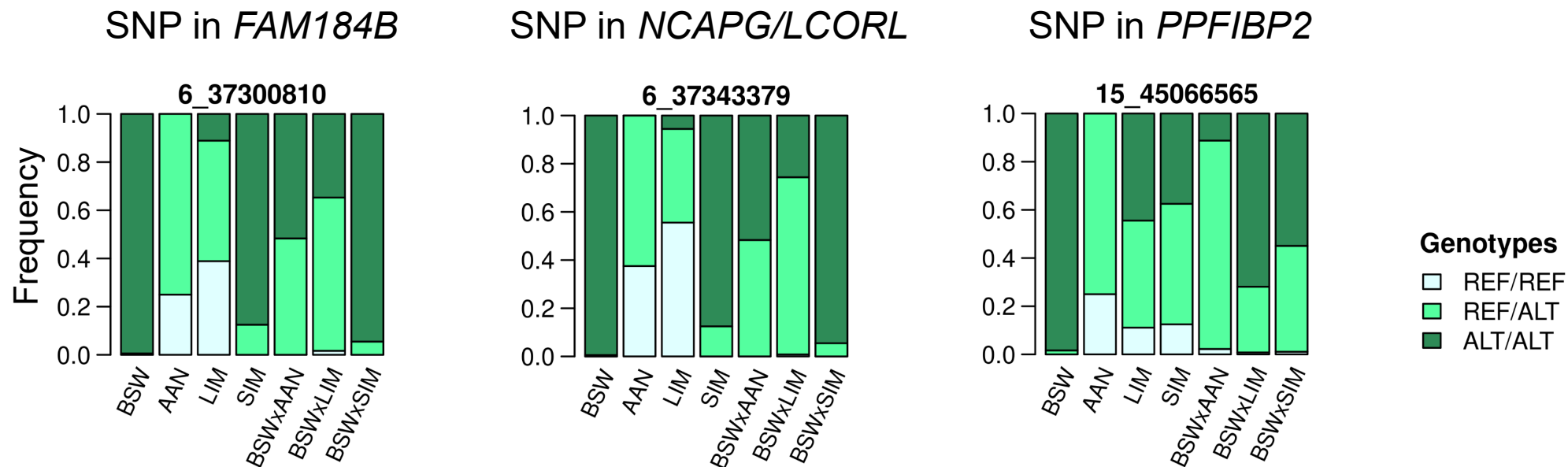


Selection scans identify regions possibly under selection across the whole BSW genome



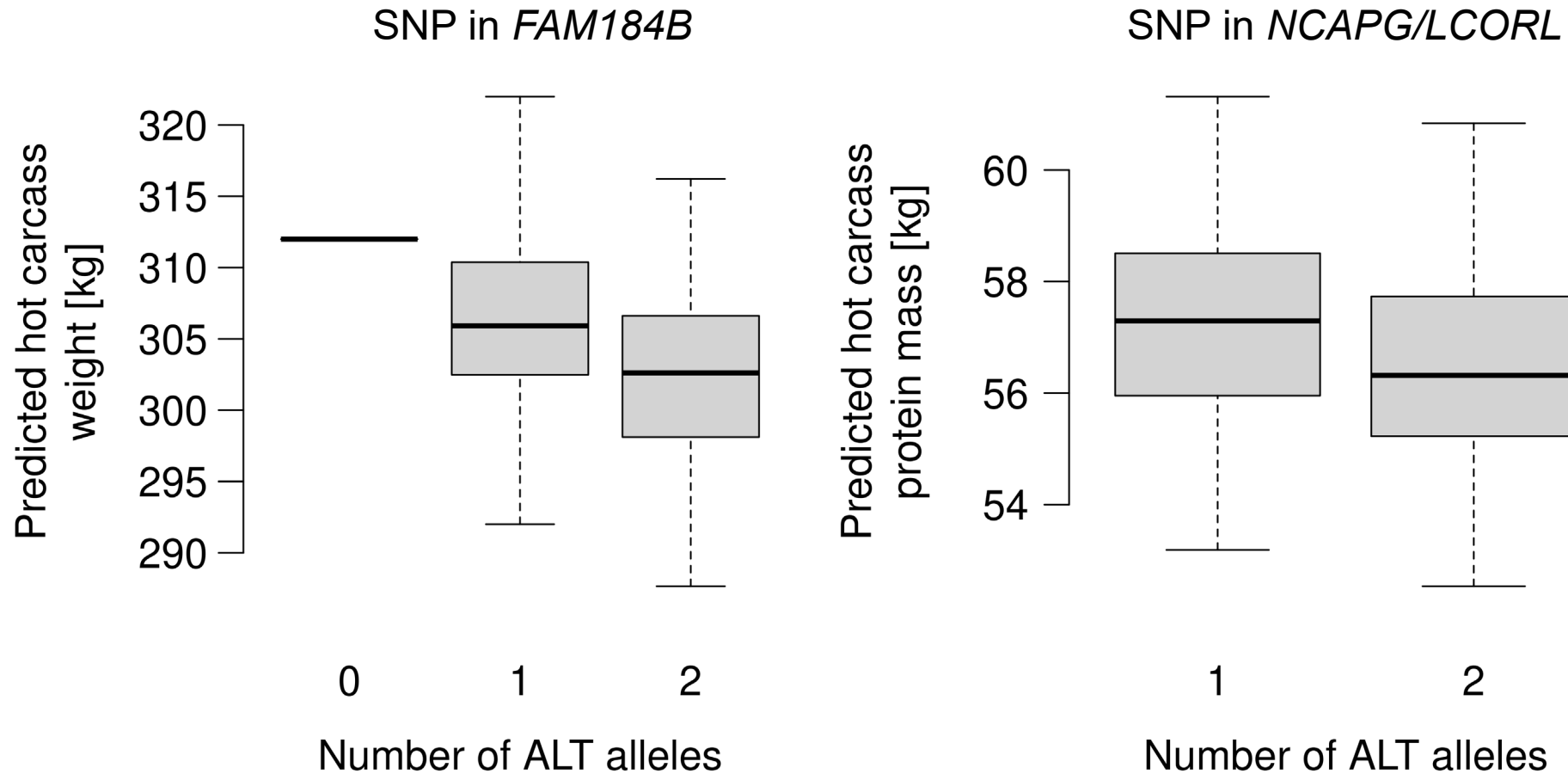


In candidate genes, BSW-like alleles segregate in the beef breeds





SNPs within the *FAM184B* – *LCORL* complex show associations with carcass weight and protein mass





Conclusions

- Mating AAN, LIM, or SIM bulls to BSW females result in similar amounts of recent inbreeding reduction
- Few genes under selection in BSW are simultaneously divergent from beef breeds and are thus of specific interest
- *FAM184B – LCORL* region of particular importance, where bulls segregate for divergent haplotypes, which show associations to carcass traits
- Absence of completely fixed differences between BSW and beef breeds allows for selection of the best possible bull given the genotype of the female



Acknowledgements

Agroscope

Raphaël Siegenthaler
Caroline Xavier
Guy Maikoff
The Barn Team
The Slaughterhouse Team

u^b

b
UNIVERSITÄT
BERN

Cord Drögemüller

Qualitas

Franz Seefried

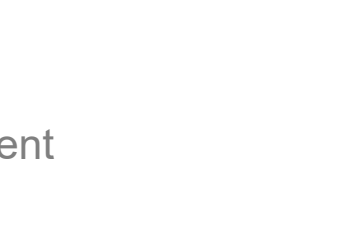
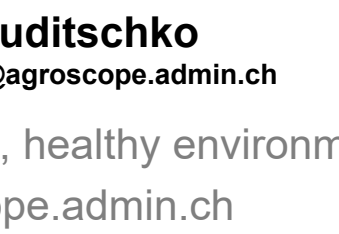
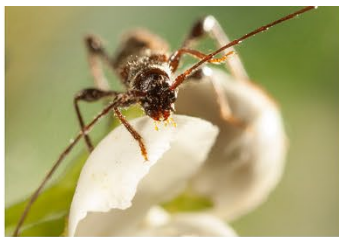
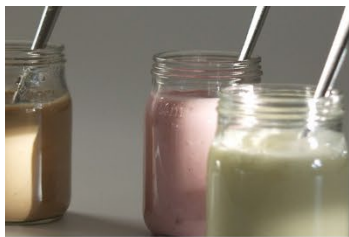
BRAUNVIEH 

 MUTTERKUH SCHWEIZ
VACHE MÈRE SUISSE
VACCA MADRE SVIZZERA
VATGA MAMMA SVIZRA

swissgenetics 

 **PROVIANDE**

SWISS 
herdbook



Thank you for your attention

Dorothea Lindtke

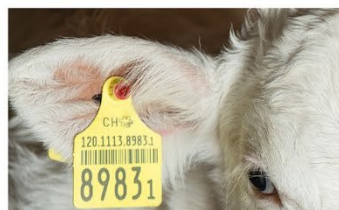
dorothea.lindtke@agroscope.admin.ch

Markus Neuditschko

markus.neuditschko@agroscope.admin.ch

Agroscope good food, healthy environment

www.agroscope.admin.ch





Genetic divergence between BSW and the beef breeds is increased within and near genes

Outlier SNPs: at most three non-homozygous BSW samples and at most three bulls across two beef breeds homozygous for the major BSW allele

class	outlier	non-outlier
exonic	52	58818
• nonsynonymous	19	24402
• synonymous	33	34225
intronic	1880	2677366
UTR5	18	10432
UTR3	25	29067
upstream	74	84185
downstream	54	81445
intergenic	1708	5315074

15 nonsynonymous SNPs are within regions possibly under selection in BSW

overrepresented
underrepresented



Five candidate genes possibly under selection in BSW with high divergence from beef breeds

