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# The *LCORL* locus is under selection in large-sized Pakistani goat breeds

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## Genetics of depigmentation phenotypes (SNSF 31003A 172964 / 1)

01.04.2017 – 31.03.2021

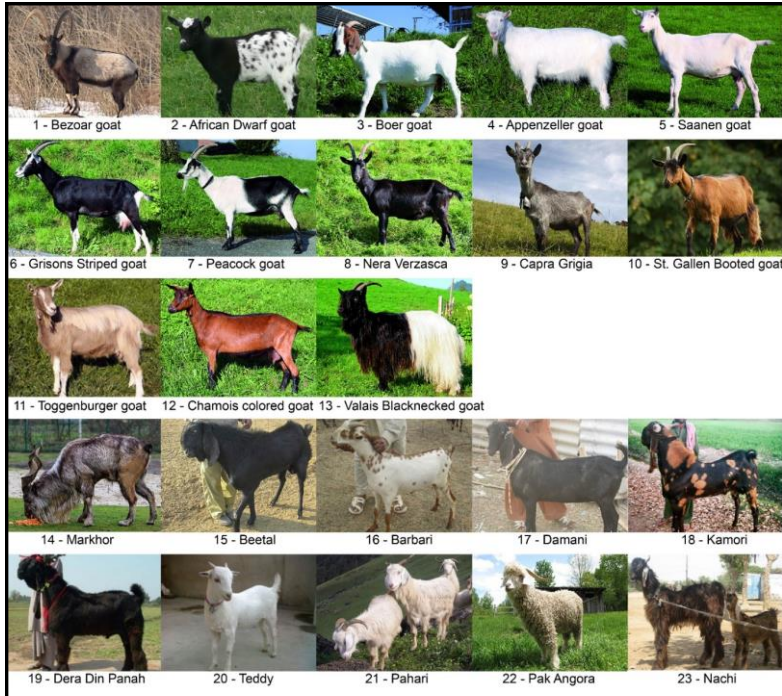


Jan Henkel



Rashid Saif





Vol 464 | 25 March 2010 | doi:10.1038/nature08832 **nature** Nature 464:587-591 (2010)

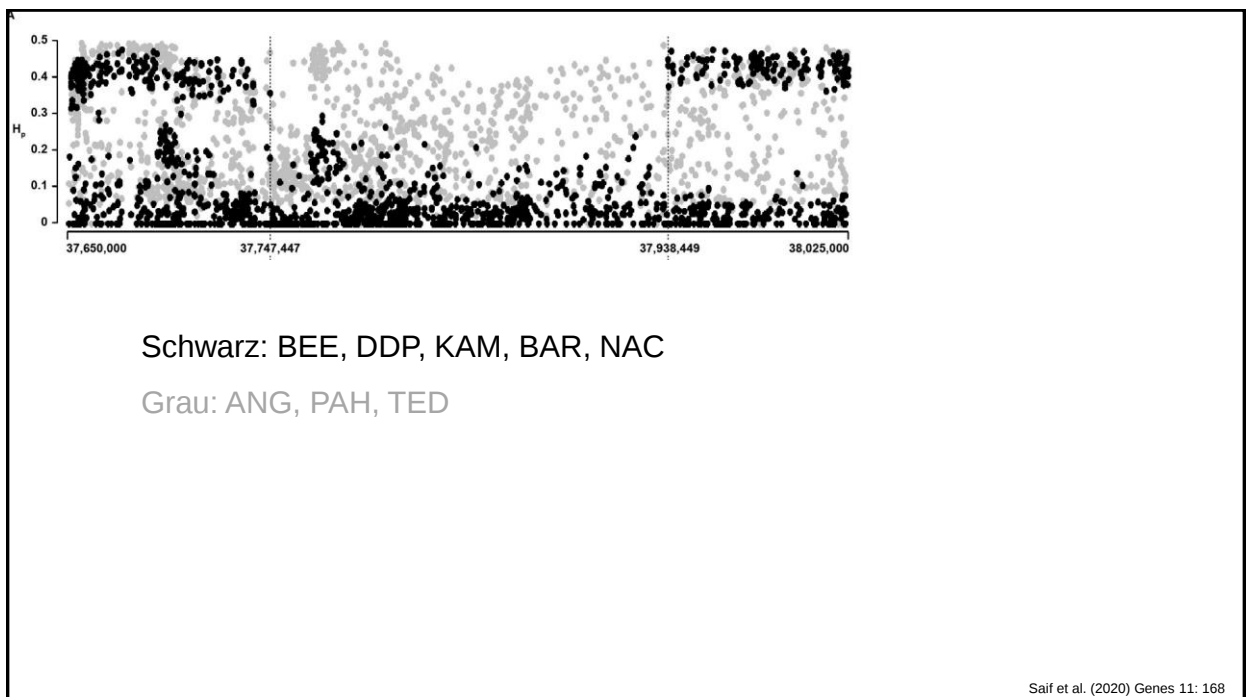
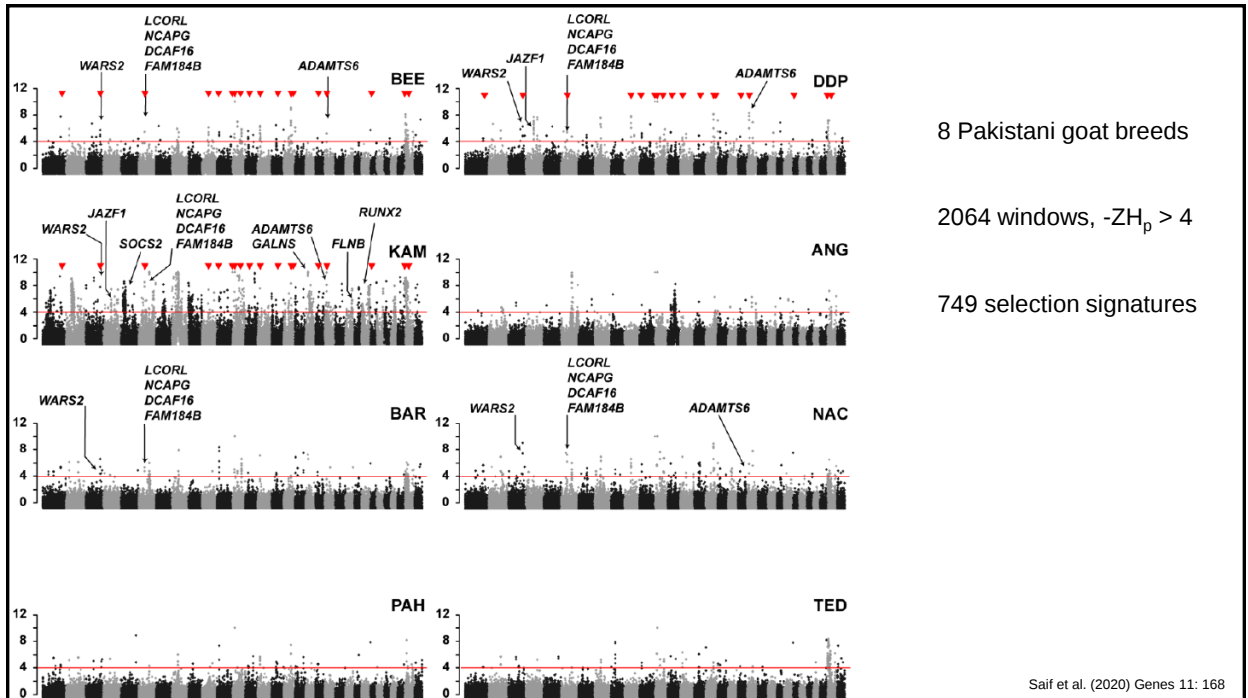
## LETTERS

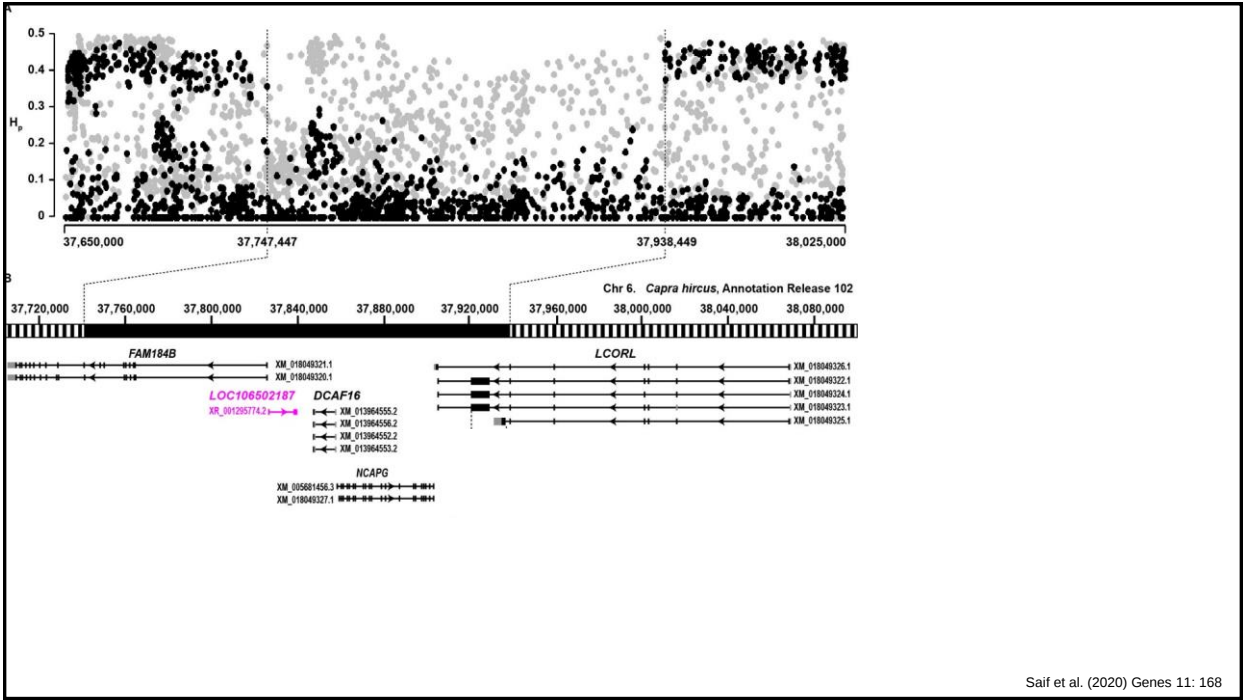
### Whole-genome resequencing reveals loci under selection during chicken domestication

Carl-Johan Rubin<sup>1\*</sup>, Michael C. Zody<sup>1,2\*</sup>, Jonas Eriksson<sup>1</sup>, Jennifer R. S. Meadows<sup>1</sup>, Ellen Sherwood<sup>3</sup>, Matthew T. Webster<sup>1</sup>, Lin Jiang<sup>4</sup>, Max Ingman<sup>5</sup>, Ted Sharpe<sup>6</sup>, Sojeong Ka<sup>3</sup>, Finn Hallböök<sup>3</sup>, Francois Besnier<sup>6</sup>, Örjan Carlborg<sup>6</sup>, Bertrand Bed'hom<sup>7</sup>, Michèle Tixier-Boichard<sup>7</sup>, Per Jensen<sup>8</sup>, Paul Siegel<sup>9</sup>, Kerstin Lindblad-Toh<sup>1,2</sup> & Leif Andersson<sup>1,6</sup>

**Methodology for the detection of selection signatures**

- regions of reduced heterozygosity
- whole genome sequence data from pools of animals (pool-seq)





Saif et al. (2020) Genes 11: 168

**nature COMMUNICATIONS**

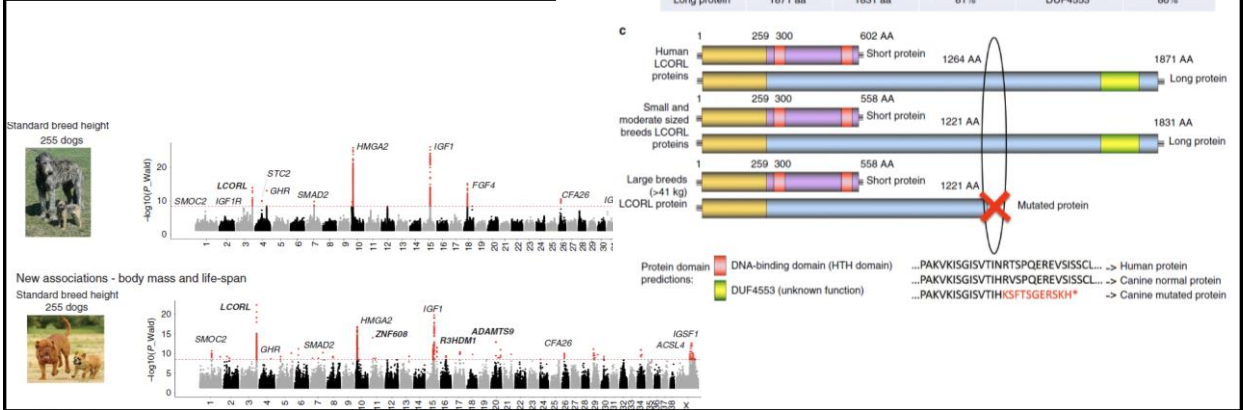
ARTICLE

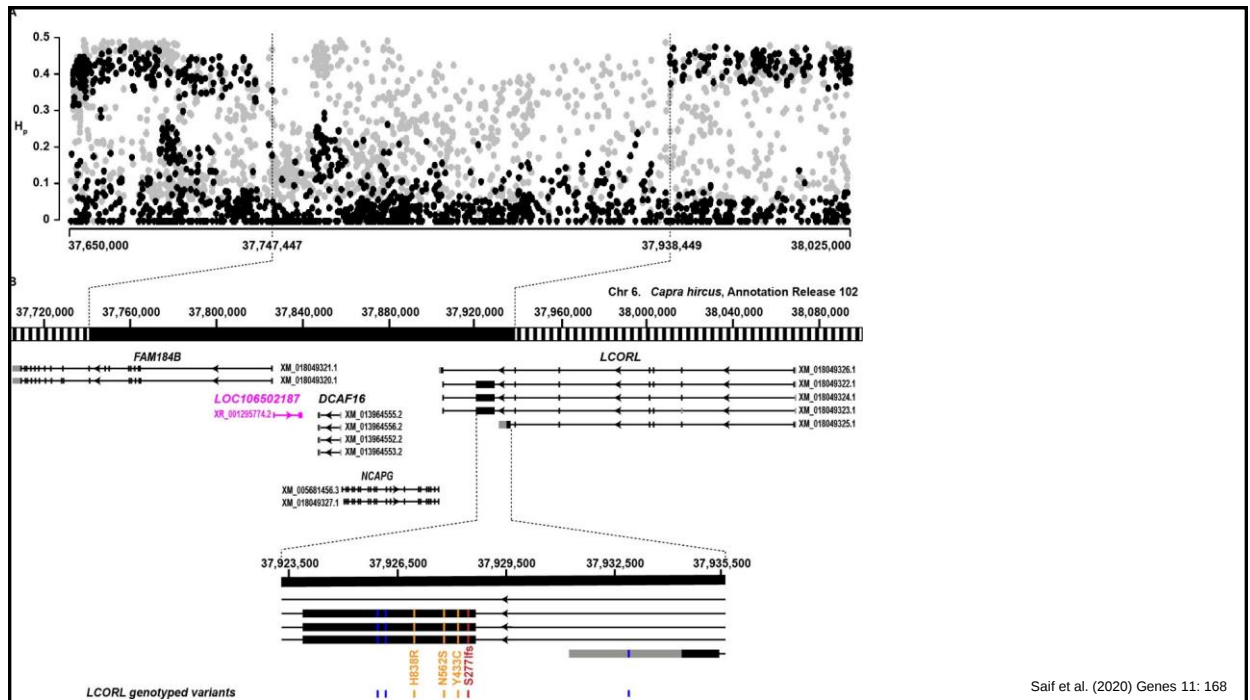
<https://doi.org/10.1038/s41467-019-09371-9> OPEN

### Whole genome sequencing of canids reveals genomic regions under selection and variants influencing morphology

Jocelyn Plassais<sup>1</sup>, Jaemin Kim<sup>1</sup>, Brian W. Davis<sup>1,2</sup>, Danielle M. Karyadi<sup>1,3</sup>, Andrew N. Hogan<sup>1</sup>, Alex C. Harris<sup>1</sup>, Brennan Decker<sup>1,4</sup>, Heidi G. Parker<sup>2</sup> & Elaine A. Ostrander<sup>1</sup>

Plassais et al. (2019) Nat Comm 10: 1489





Saif et al. (2020) Genes 11: 168

**Table 4.** Genotype phenotype association of selected SNVs in the *LCORL* gene.

| Position   | cDNA Variant<br>XM_018049322.1 | Protein Variant<br>XP_017904811.1   | Alternative<br>Allele Frequency<br>in Breeds with<br>the Selection<br>Signature <sup>a</sup> | Alternative<br>Allele Frequency<br>in Breeds without<br>the Selection<br>Signature <sup>b</sup> | <i>p</i> -Value       |
|------------|--------------------------------|-------------------------------------|----------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------|-----------------------|
| 37,925,990 | c.3480C>T                      | p.=                                 | 0.05                                                                                         | 0.26                                                                                            | $3.0 \times 10^{-04}$ |
| 37,926,110 | c.3360G>A                      | p.=                                 | 0.93                                                                                         | 0.35                                                                                            | $2.1 \times 10^{-13}$ |
| 37,926,957 | c.2513A>G                      | p.His838Arg                         | 1.00                                                                                         | 1.00                                                                                            | NA                    |
| 37,927,785 | c.1685A>G                      | p.Asn562Ser                         | 0.01                                                                                         | 0.26                                                                                            | $1.8 \times 10^{-07}$ |
| 37,928,172 | c.1298A>G                      | p.Tyr433Cys                         | 0.96                                                                                         | 0.53                                                                                            | $3.9 \times 10^{-10}$ |
| 37,928,645 | c.828_829insA                  | p.Ser277Ilefs*38                    | 0.95                                                                                         | 0.35                                                                                            | $8.0 \times 10^{-15}$ |
| 37,932,928 | c.777-4235T>C                  | intronic/3'-UTR of<br>short isoform | 0.01                                                                                         | 0.09                                                                                            | $1.0 \times 10^{-02}$ |

<sup>a</sup> BAR, BEE, DDP, KAM; NAC, <sup>b</sup> ANG, PAH, TED.

Saif et al. (2020) Genes 11: 168

# The *LCORL* Locus Is under Selection in Large-Sized Pakistani Goat Breeds

Rashid Saif <sup>1,2</sup>, Jan Henkel <sup>1</sup>, Vidhya Jagannathan <sup>1</sup>, Cord Drögemüller <sup>1</sup>, Christine Flury <sup>3</sup> and Tosso Leeb <sup>1,\*</sup>

## Summary

- 749 selection signatures in 8 Pakistani goat breeds
- *LCORL* selection signature in 3 large and 2 medium-sized breeds
- candidate causative variant identified (XM\_018049322.1:c.828\_829insA)
- mutant allele increases size

Saif et al. (2020) Genes 11: 168

## Dank

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