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DEPARTMENT OF
ANIMAL
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CGIL

Genome-wide association study and functional analysis of infectious and horn type hoof lesions in Canadian Holstein cattle

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Hoof Lesions

- Lameness considered the number one health issue by Canadian dairy producers
- Prevalence of 30 to 70% of cows with at least one hoof lesion – North America and Europe

Classification of Hoof Lesions

- Hoof lesions traditionally classified according to their etiology and pathogenesis:
  - **Infectious or partly infectious lesions:** Mostly related to environmental hygiene
    - e.g., Digital and interdigital dermatitis, foot rot, and heel erosion
  - **Horn lesions:** Mostly caused by metabolic or mechanical factors
    - e.g., Sole and toe ulcer, sole hemorrhage, and white line disease

Infectious and Horn Lesions

- Weak genetic correlations reported between infectious and horn lesions
- Defining candidate genes harboring important regions will allow a more comprehensive understanding of the mechanisms involved in these different groups of lesions
  - Potentially contribute to a more accurate genetic selection for these traits

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Objective

- To perform a genome-wide association study and a functional analysis for infectious and horn lesions in Canadian Holstein cattle

Data

- 249,709 records from 105,450 cows
- 1,080 Canadian herds between 2009 and 2016
- 51 hoof trimmers
- Hoof supervisor® system
  (KS Dairy Consulting, Dresser, Wisconsin)
- Pedigree file 331,587 animals

Data

- Lesions classified according to their etiology and pathogenesis
    - **Infectious/partly infectious lesions**: digital and interdigital dermatitis, foot rot, and heel erosion
    - **Horn lesions**: sole and toe ulcer, sole haemorrhage, and white line disease
- Hoof lesions considered as binary variables
    - 0: no lesion
    - 1: presence of a lesion

Data Analysis - Model

- Linear animal model DMU *(Madsen and Jensen, 2008)*:

$$Y = \mu + HERD + TRIMMER + PARITY + STAGE + a + pe + e$$

HERD: herd-date of hoof trimming

TRIMMER: hoof trimmer

PARITY: parity at trimming

STAGE: stage of lactation at trimming

a: random additive genetic animal effect

pe: random permanent environmental effect

e: random error term

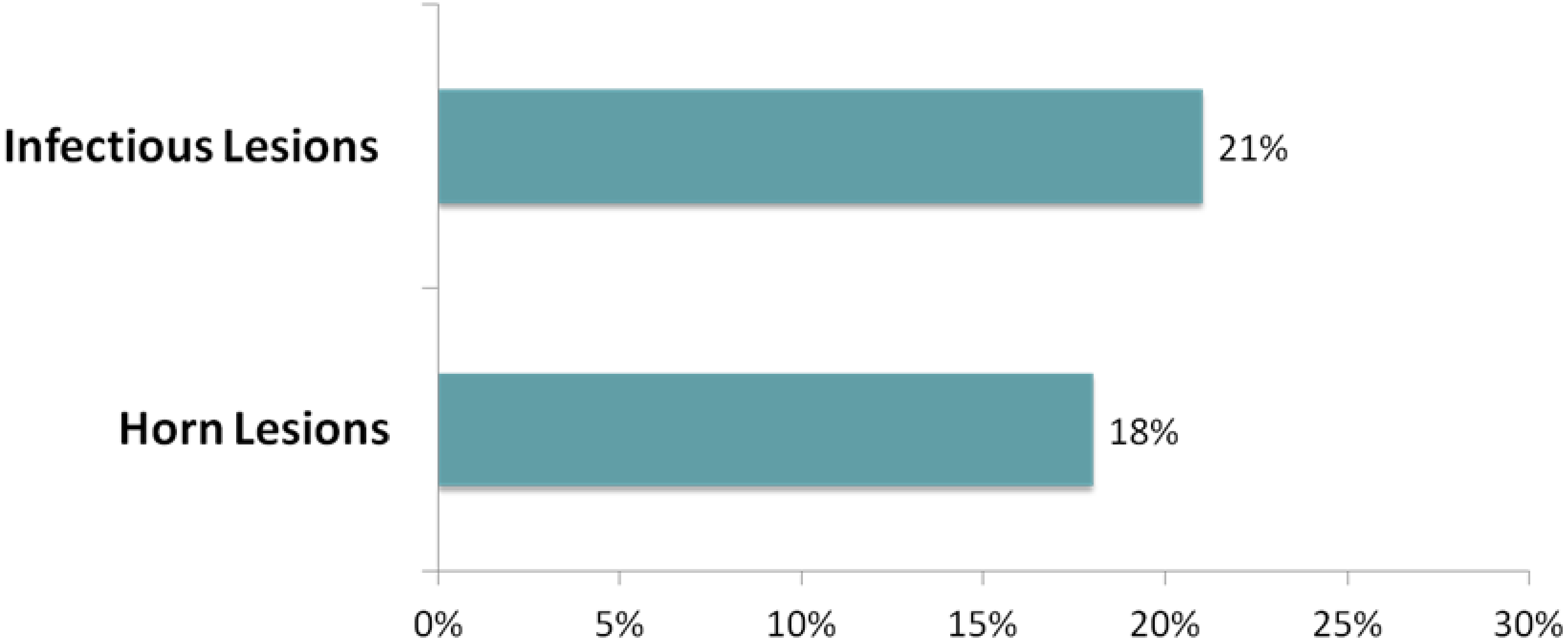
Data Analysis - GWAS

- De-regressed EBV *(VanRaden et al., 2009)*
- EBV reliability greater than 0.10 and genotyped
  - 13,657 for Horn Lesions
  - 13,834 for Infectious Lesions
- Animals genotyped (or imputed) 50K

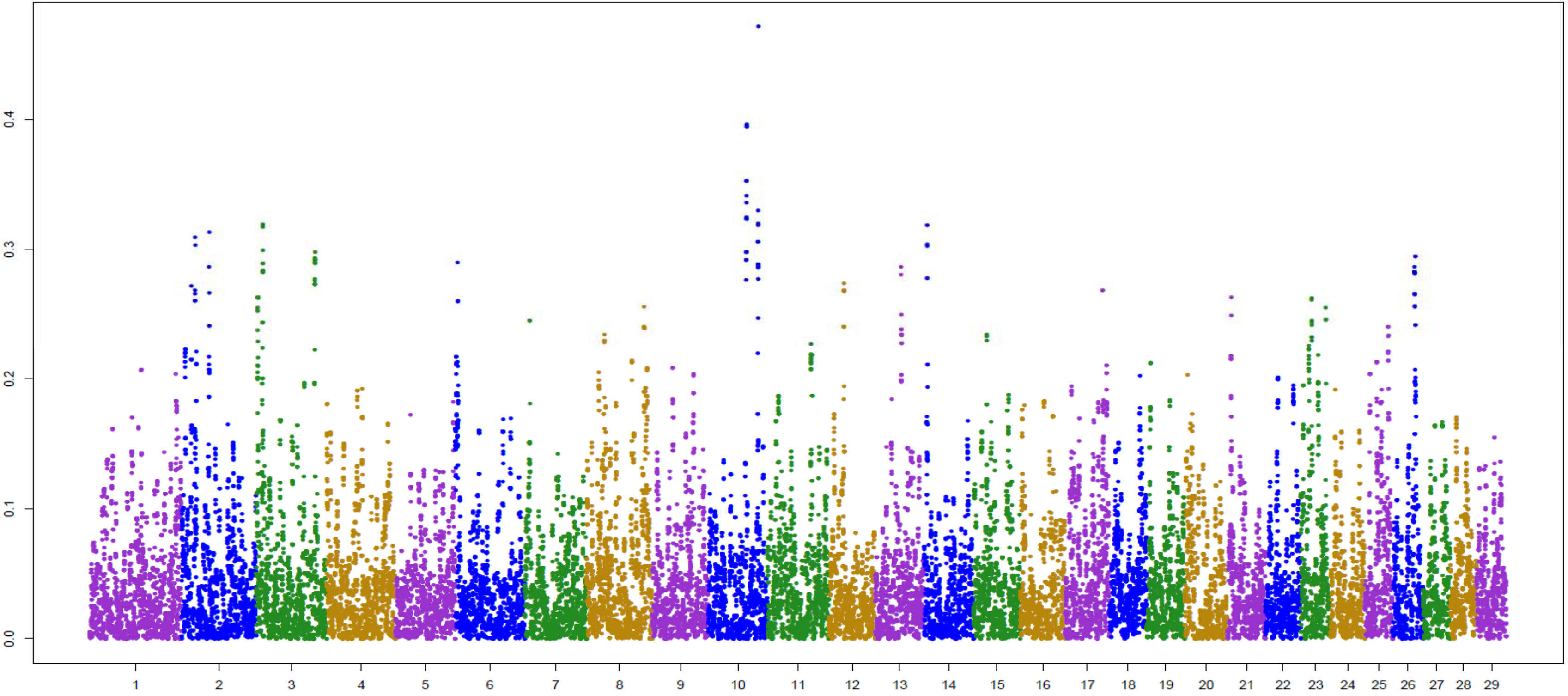
Data Analysis - GWAS

- Direct genomic values for each animal and trait predicted based on the GBLUP method *(VanRaden, 2008)*
  - De-regressed EBV as pseudo-phenotypes
- SNP effects obtained using POSTGSF90
- 20-adjacent-SNP moving windows explaining more than 0.30% of genetic variance

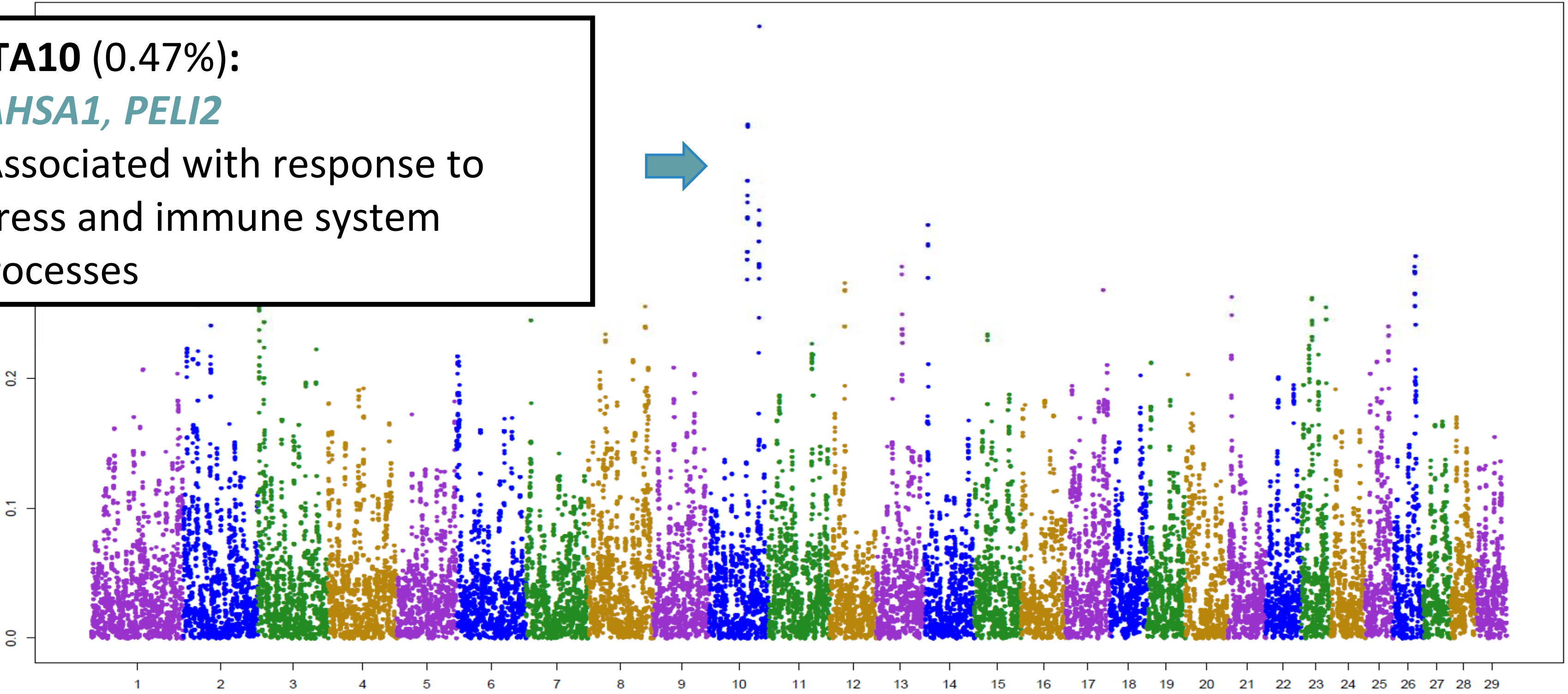
Infectious and Horn Lesions - Prevalence



Infectious Lesions



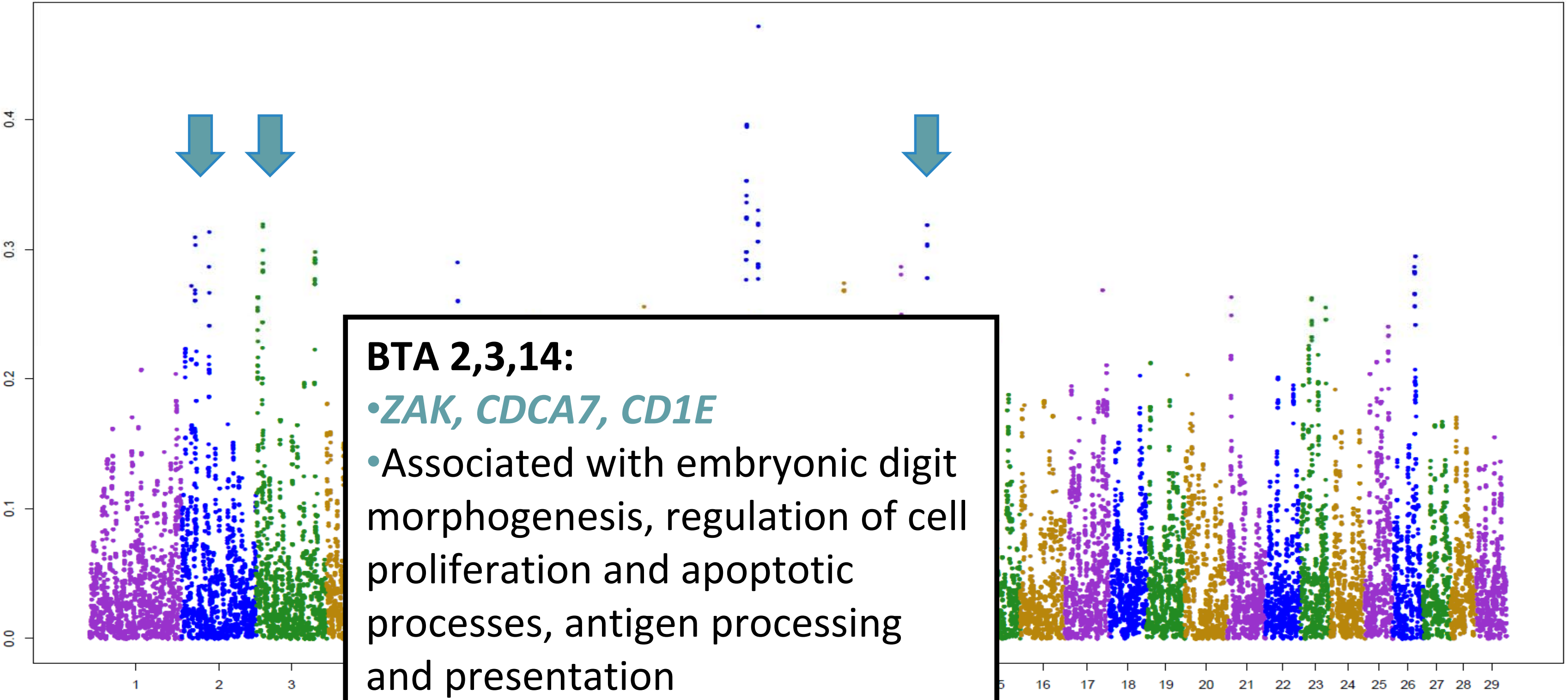
Infectious Lesions



BTA10 (0.47%):

- *AHSA1, PELI2*
- Associated with response to stress and immune system processes

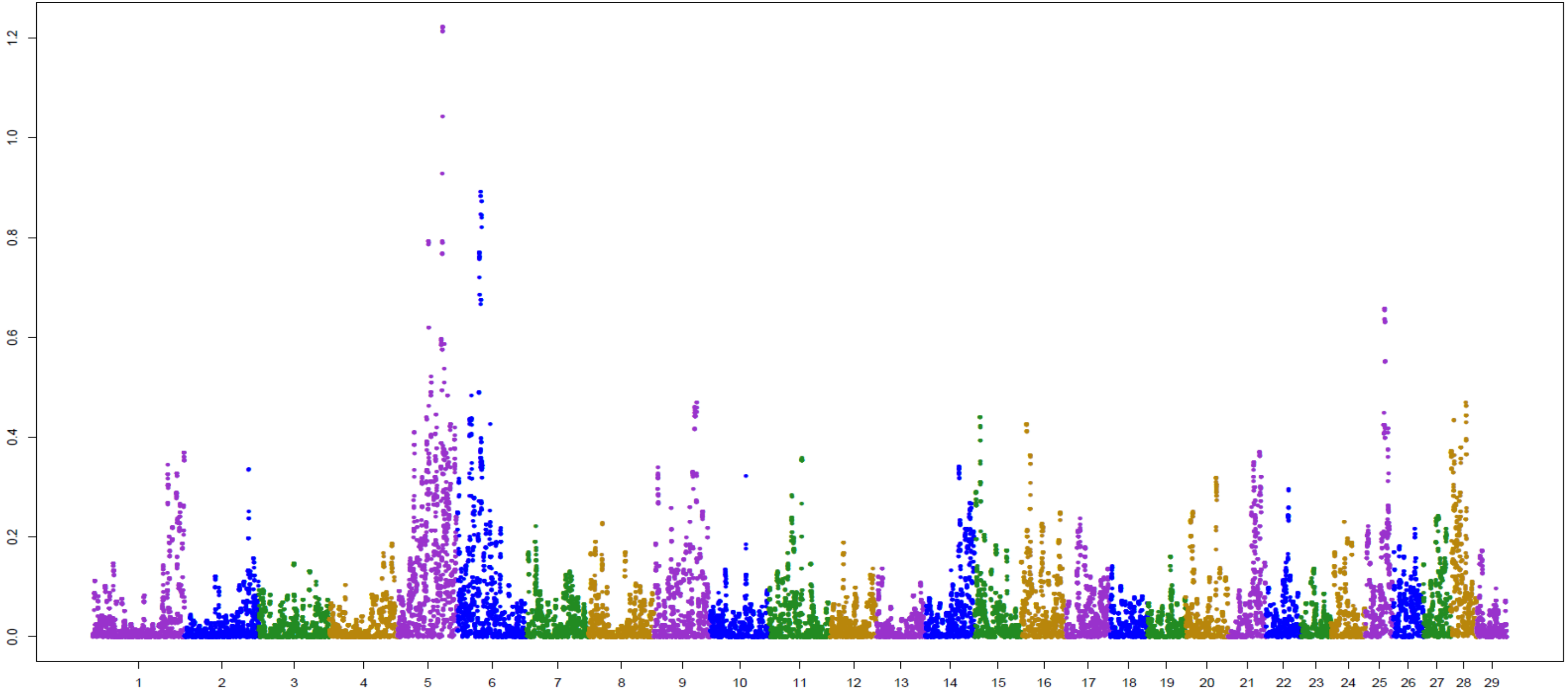
Infectious Lesions



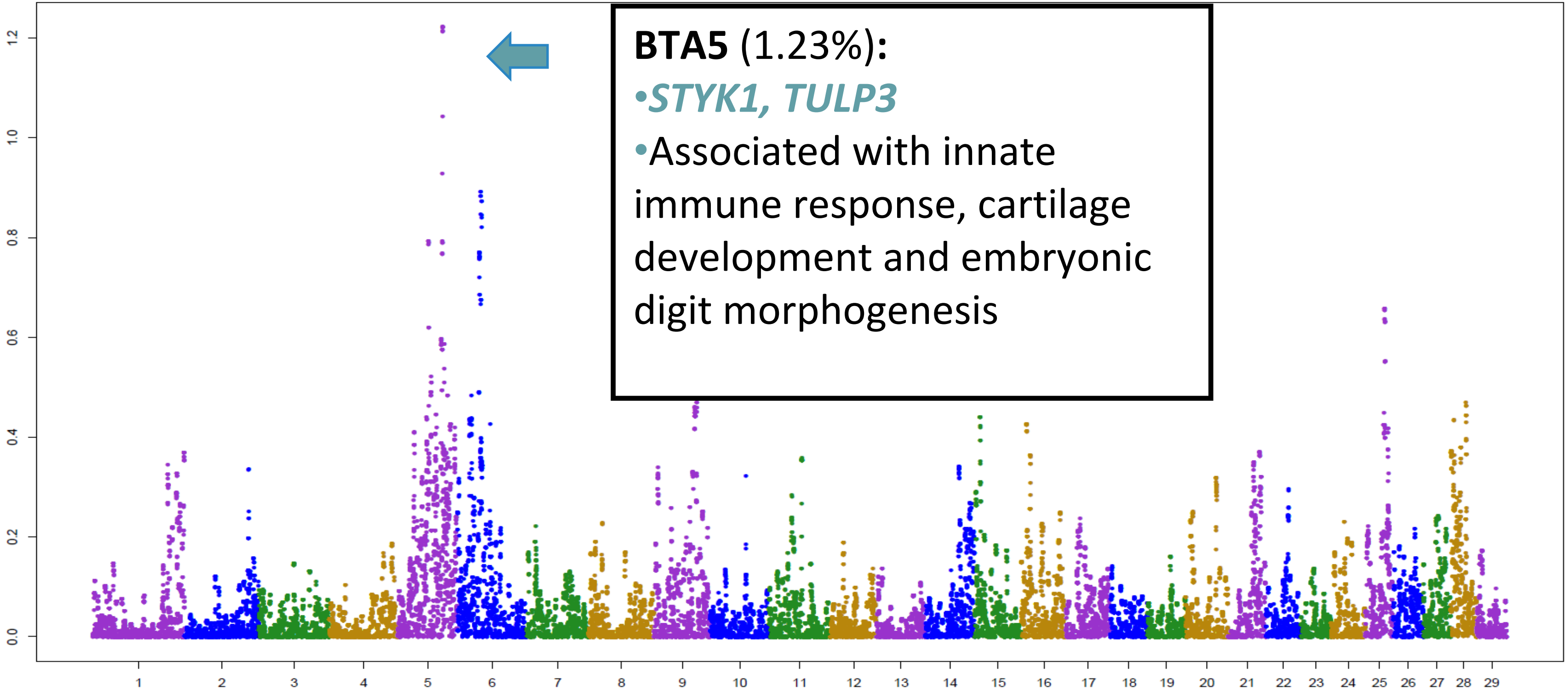
BTA 2,3,14:

- *ZAK, CDCA7, CD1E*
- Associated with embryonic digit morphogenesis, regulation of cell proliferation and apoptotic processes, antigen processing and presentation

Horn Lesions



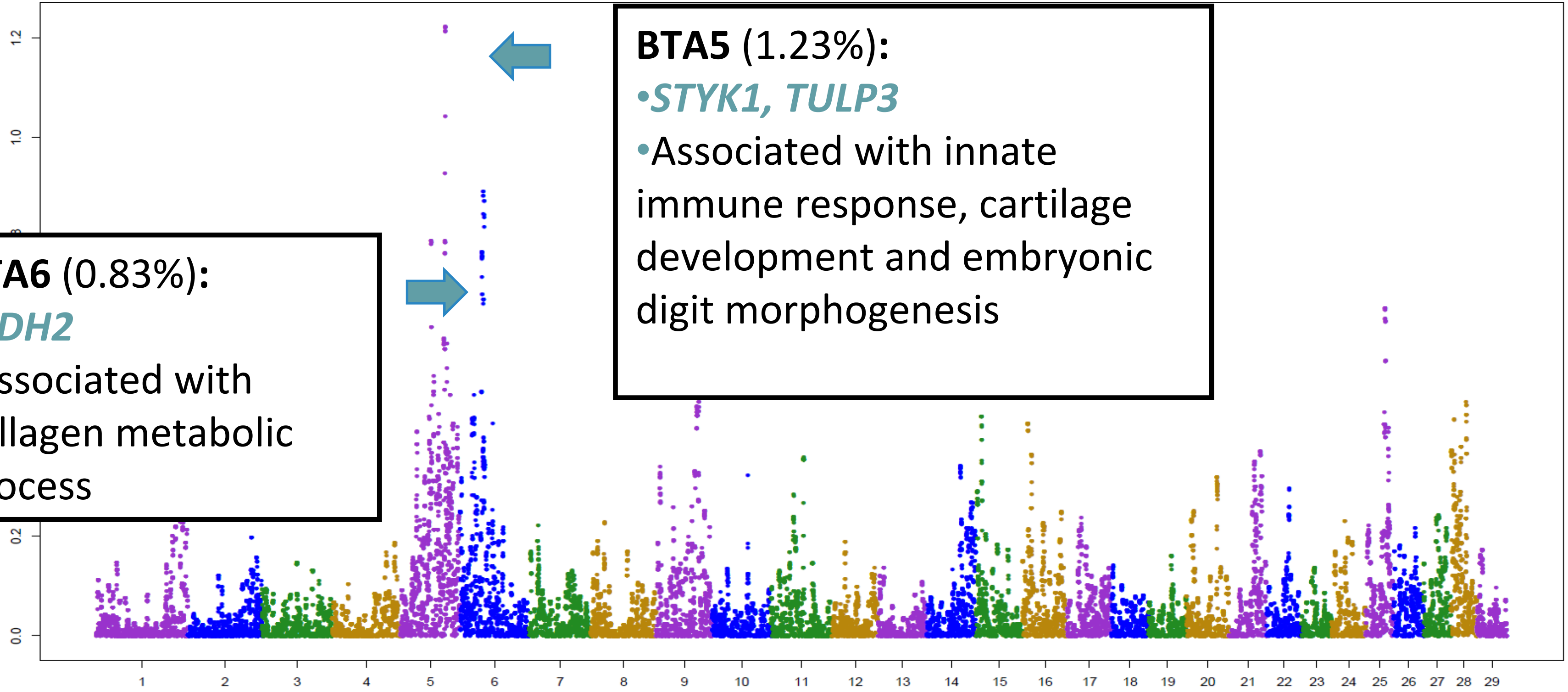
Horn Lesions



BTA5 (1.23%)**:**

- ***STYK1, TULP3***
- Associated with innate immune response, cartilage development and embryonic digit morphogenesis

Horn Lesions



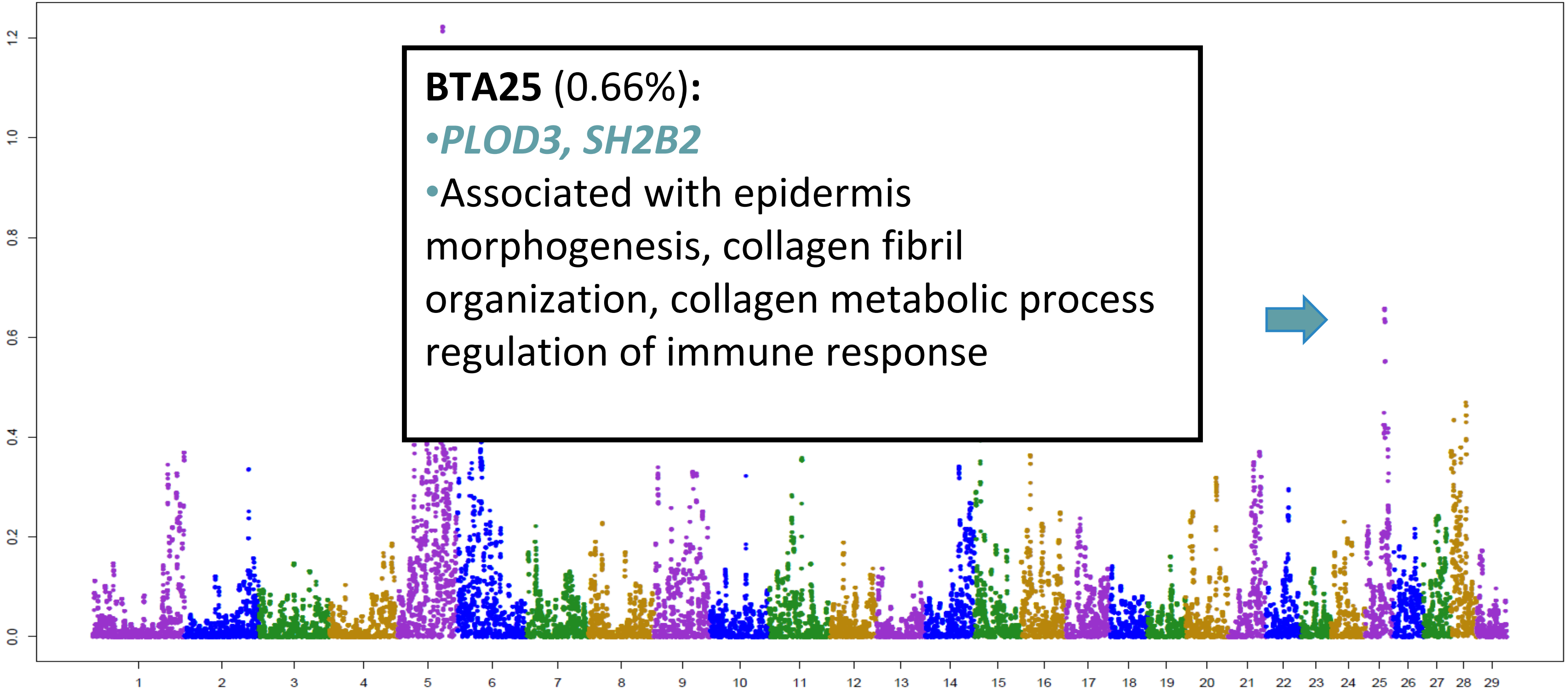
BTA6 (0.83%)**:**

- ***BDH2***
- Associated with collagen metabolic process

BTA5 (1.23%)**:**

- ***STYK1, TULP3***
- Associated with innate immune response, cartilage development and embryonic digit morphogenesis

Horn Lesions



BTA25 (0.66%):

- *PLOD3, SH2B2*
- Associated with epidermis morphogenesis, collagen fibril organization, collagen metabolic process regulation of immune response

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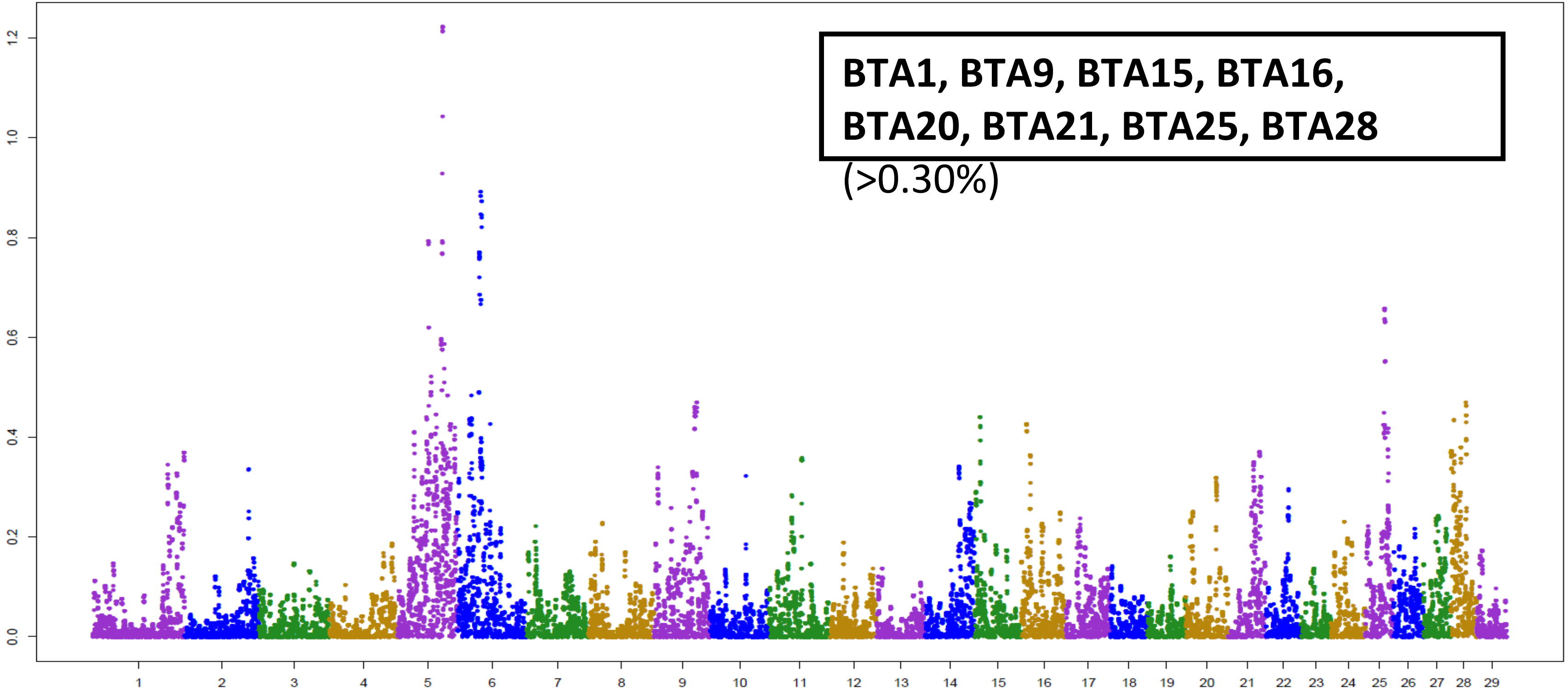
Horn Lesions



BTA1, BTA9, BTA15, BTA16, BTA20, BTA21, BTA25, BTA28

(>0.30%)

Summary

- Important genomic regions associated with infectious and horn lesions were identified
- List of functional candidate genes within or next to these regions was created
- The next step is to perform analyses for individual hoof health traits

Acknowledgements

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LES PRODUCTEURS LAITIERS DU CANADA

Réseau laitier canadien
CDN
Canadian Dairy Network

Agriculture and Agri-Food Canada
Agriculture et Agroalimentaire Canada

Canadian Dairy Commission
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Dairy Research Cluster
Dairy Research for a Healthy World.

Ontario Genomics

Alberta milk

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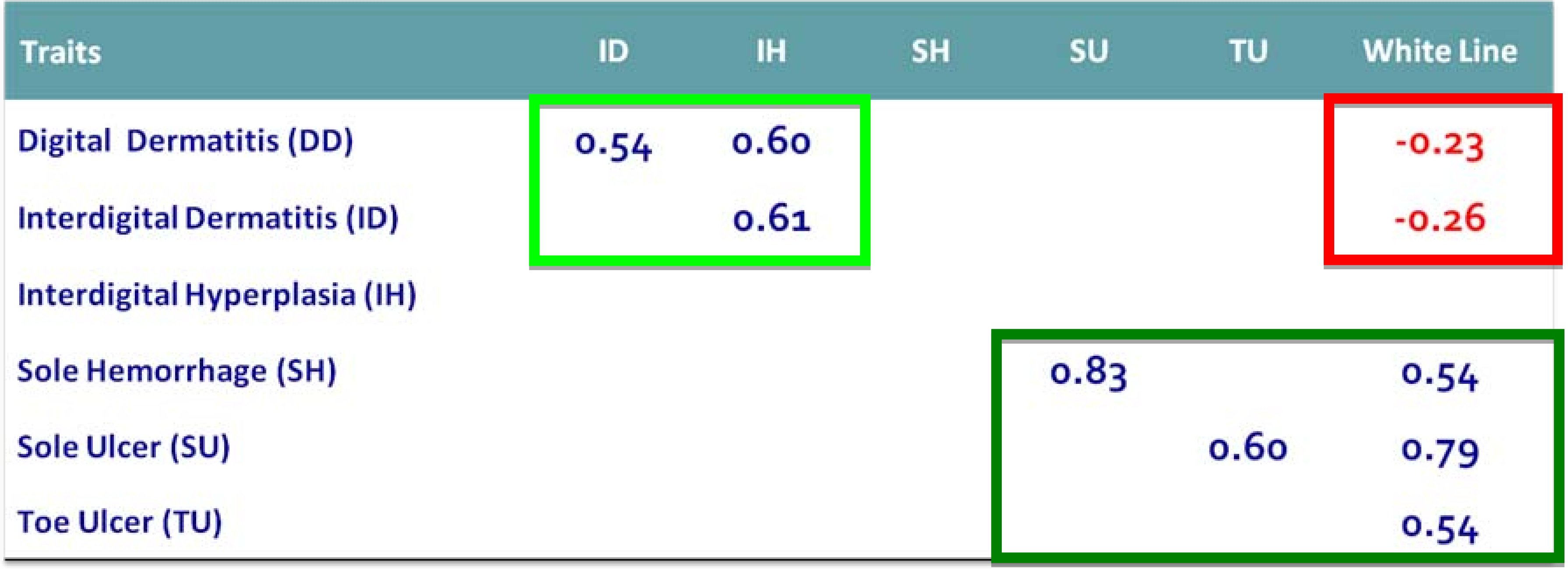
valacta

Genetic correlations between hoof lesions



Traits	ID	IH	SH	SU	TU	White Line
Digital Dermatitis (DD)	0.54	0.60				-0.23
Interdigital Dermatitis (ID)		0.61				-0.26
Interdigital Hyperplasia (IH)						
Sole Hemorrhage (SH)				0.83		0.54
Sole Ulcer (SU)					0.60	0.79
Toe Ulcer (TU)						0.54

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