Using genomic selection to improve calf health

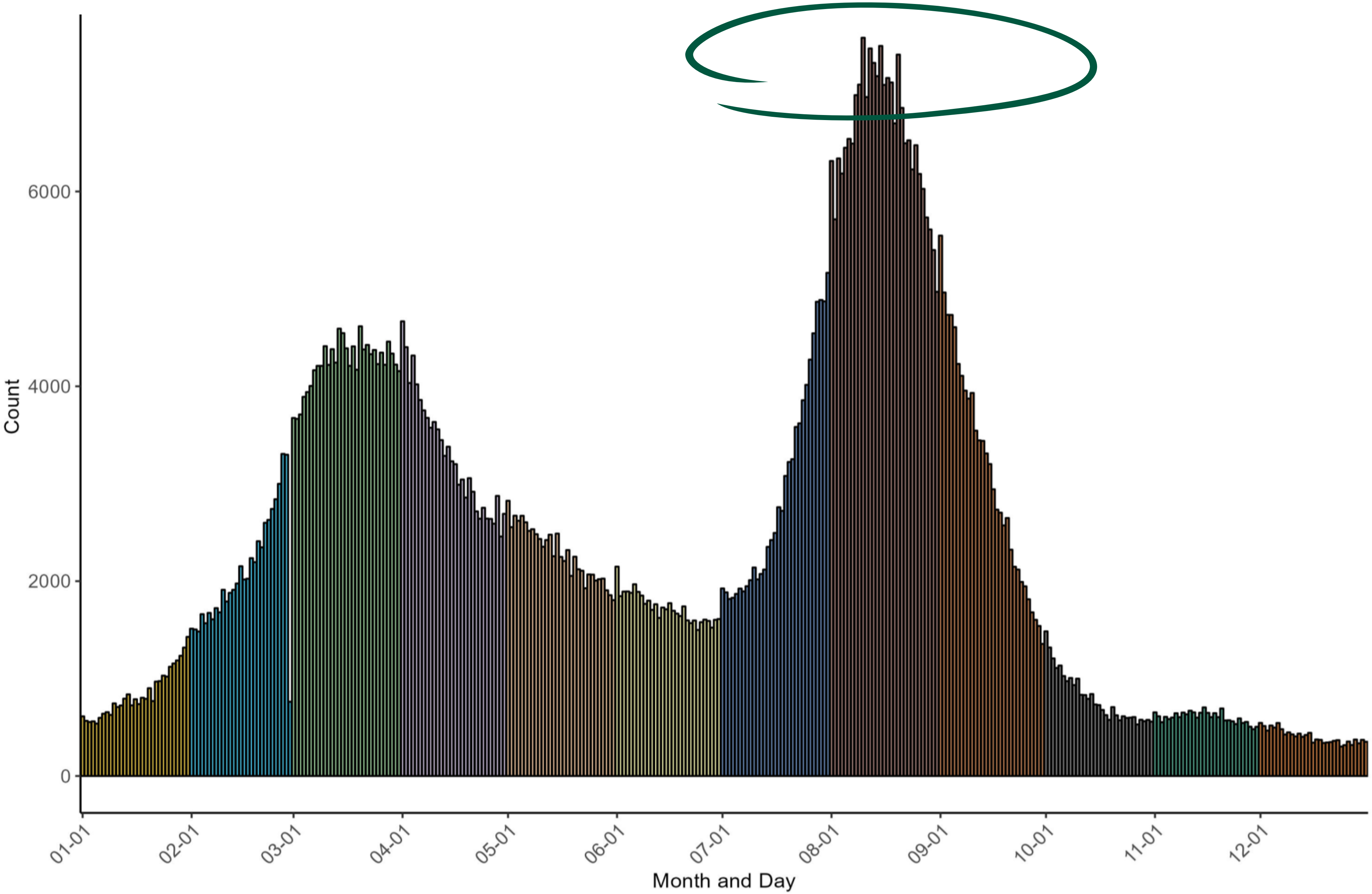
Michelle Axford

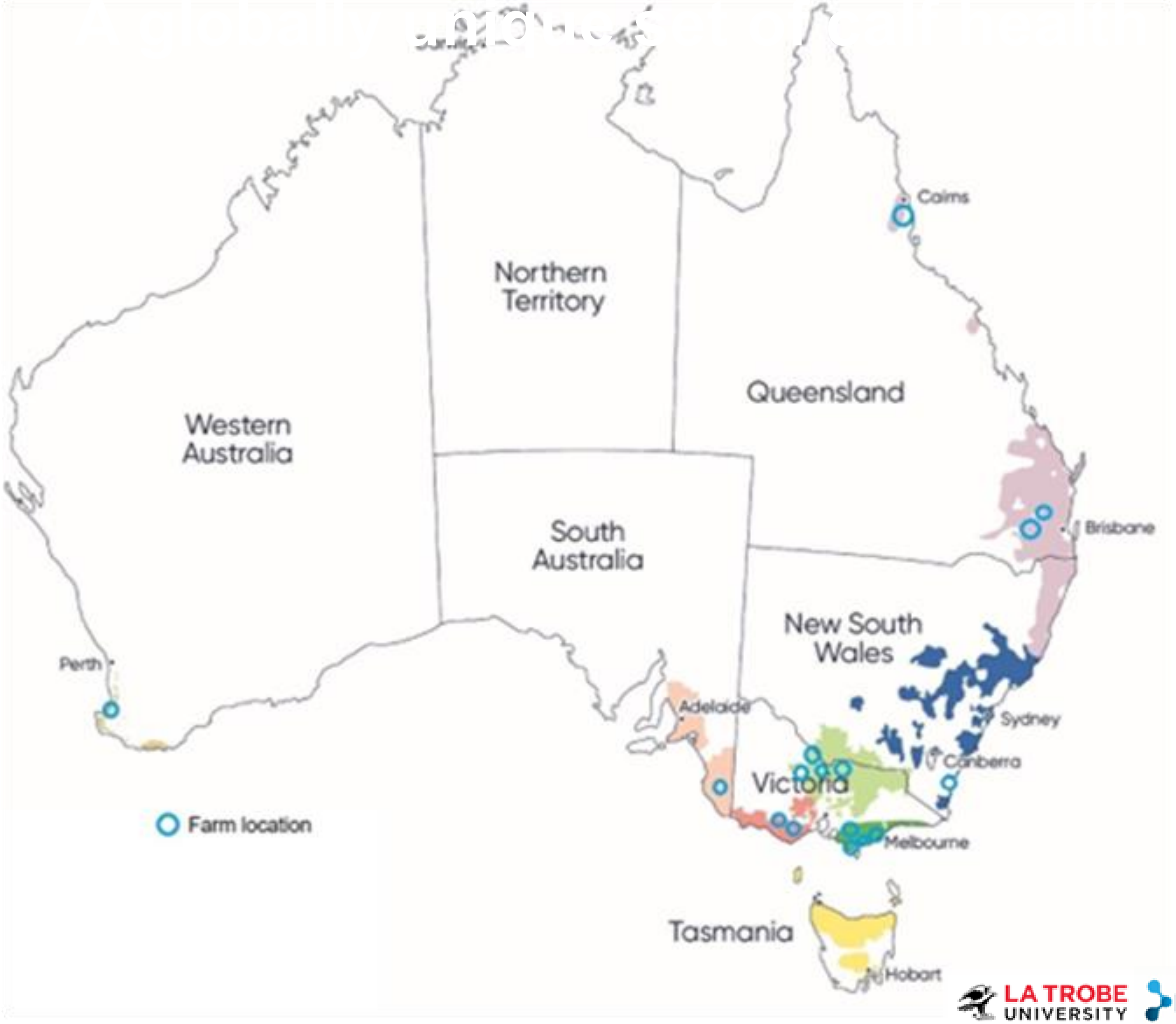
Prof Jennie Pryce, Dr Amanda Chamberlain, Dr Majid Khansefid, Prof Mike Goddard, Dr Mekonnen Haile-Mariam, Dr Iona MacLeod, Dr Tuan Nguyen, Dr Irene Van den Berg

AGRICULTURE VICTORIA

Distribution of calving dates

DataGene CDR 2014-2023




Cairns
Northern Territory
Queensland
Western Australia
South Australia
Brisbane
New South Wales
Perth
Adelaide
Sydney
Canberra
Victoria
Farm location
Melbourne
Tasmania
Hobart

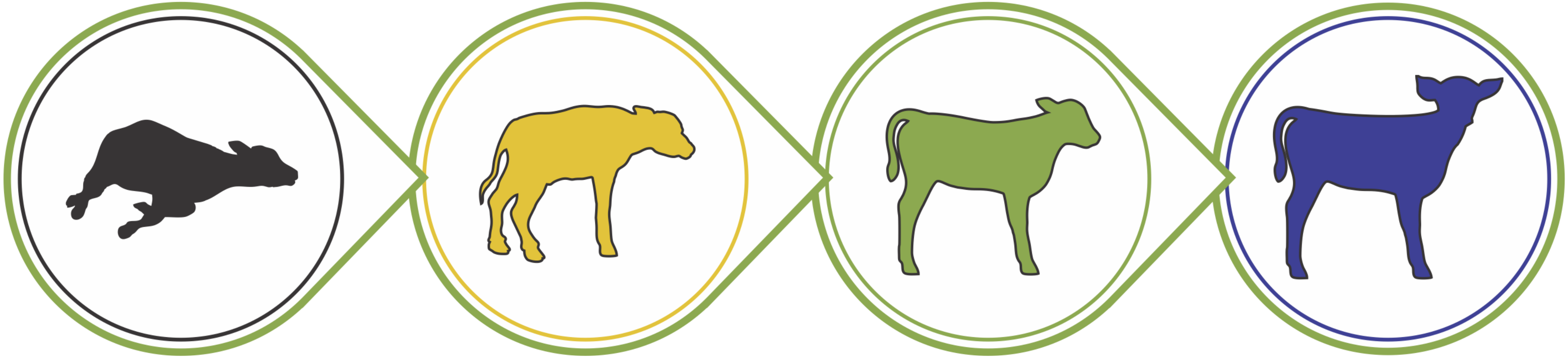
53 herds

20,000 calves

Calf phenotypes

- Fate
  - Dead
  - Alive
- Calf Size
  - Tiny
  - Small
  - Average
  - Big
  - Huge
- Calving Ease
  - No difficulty
  - Slight difficulty
  - Moderate difficulty
  - High difficulty
- Wean
  - Dead
  - Survived to day 84
- Health
  - Health
  - Scours
  - Respiratory Disease
  - Pestivirus
- Calf vitality
  - Scored

Calf vitality



Dead

Dud

OK

Ripper

basic model

$$y = Xb + Zu + e$$

Random residual effect

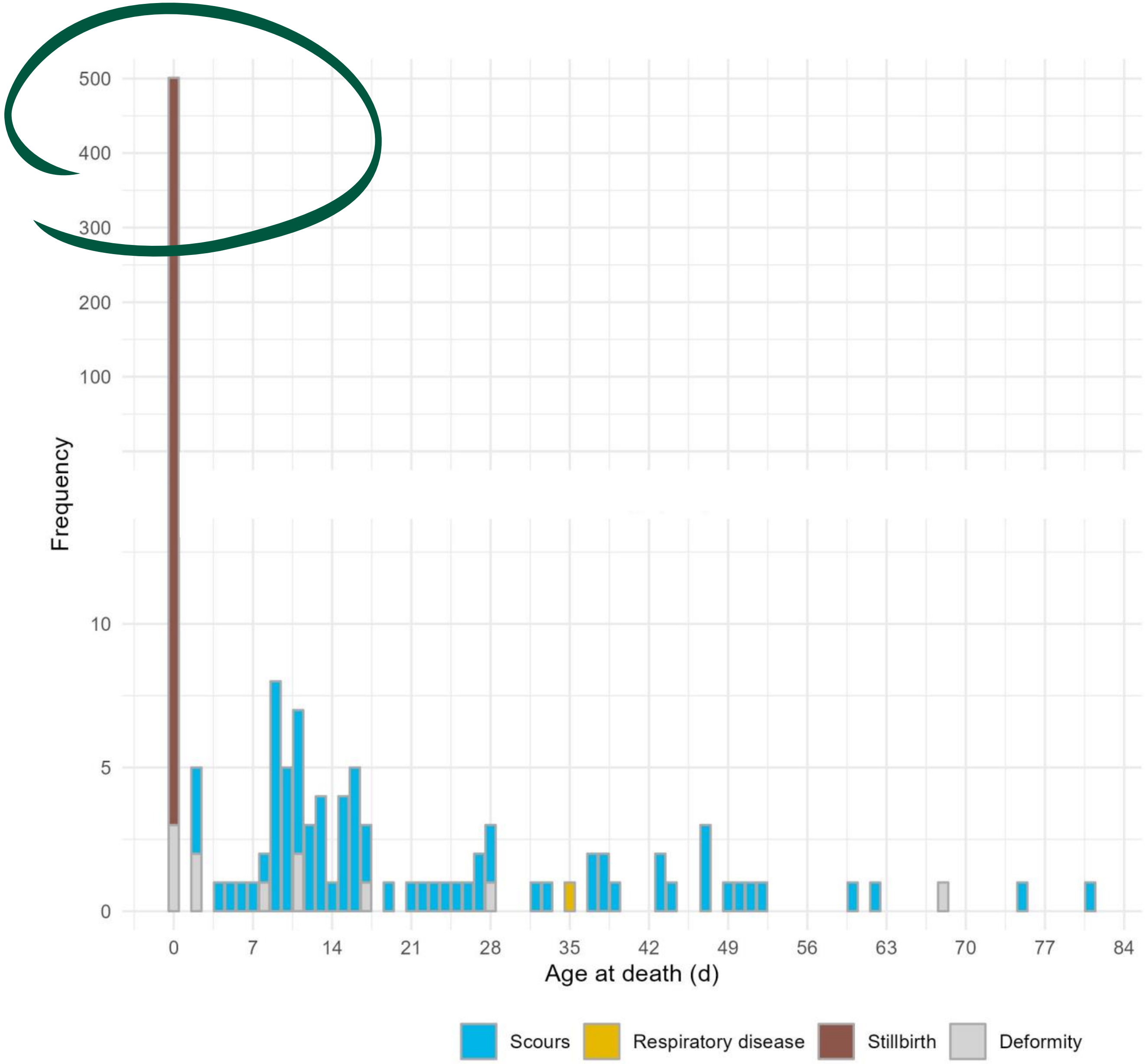
phenotypic record
Stillbirth
Pre-wean mortality
Scours
Respiratory disease
Health
Calf vitality
BVD

b fixed effects
Herd Year Season
Parity group
Calving ease
Sex

u random additive effect
Genomic relationship matrix

Age at death

Frequency of age at death by reason



Disease prevalence

	Historical dataset		Calf dataset			
	Holstein (n=778,002)	Jersey (n=115,898)	Holstein (n=11,182)		Jersey (n=949)	
	Overall mean	Overall mean	Overall mean (SE)	Herd max (SE)	Overall mean (SE)	Herd max (SE)
Scours (lived and died)			0.059 (0.002)	0.458 (0.065)	0.048 (0.007)	0.184 (0.045)
Scours (died)			0.010 (0.001)	0.136 (0.045)	0.015 (0.004)	0.026 (0.018)
Respiratory disease (lived and died)			0.004 (0.001)	0.039 (0.017)	0.001 (0.001)	0.000 (0.000)
Respiratory disease (died)			0.001 (0.000)	0.018 (0.008)	0.000 (0.000)	0.000 (0.000)
Pre-Weaning Mortality	0.019	0.041	0.020 (0.001)	0.153 (0.047)	0.027 (0.005)	0.079 (0.031)
Stillbirth	.064	0.082	0.041 (0.002)	0.180 (0.050)	0.048 (0.007)	0.160 (0.034)
Deformity			0.002 (0.000)	0.033 (0.023)	0.005 (0.002)	0.013 (0.013)

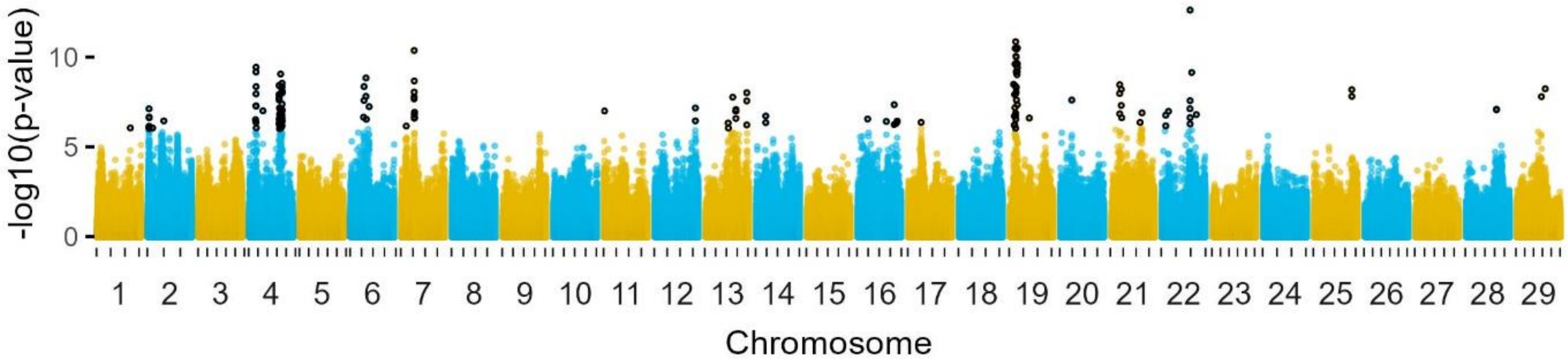
Heritability estimates

based on univariate normal animal model with GRM

Trait	Holstein
	$h^2 \pm SE$
Stillbirth Direct	0.025 ± 0.009
Pre-weaning mortality	0.006 ± 0.005
Health	0.040 ± 0.010
Scours	0.045 ± 0.010
Respiratory Disease **Pestivirus**	-
Vitality	0.114 ± 0.038

Deeper look using GWAS (Holstein Stillbirth direct)

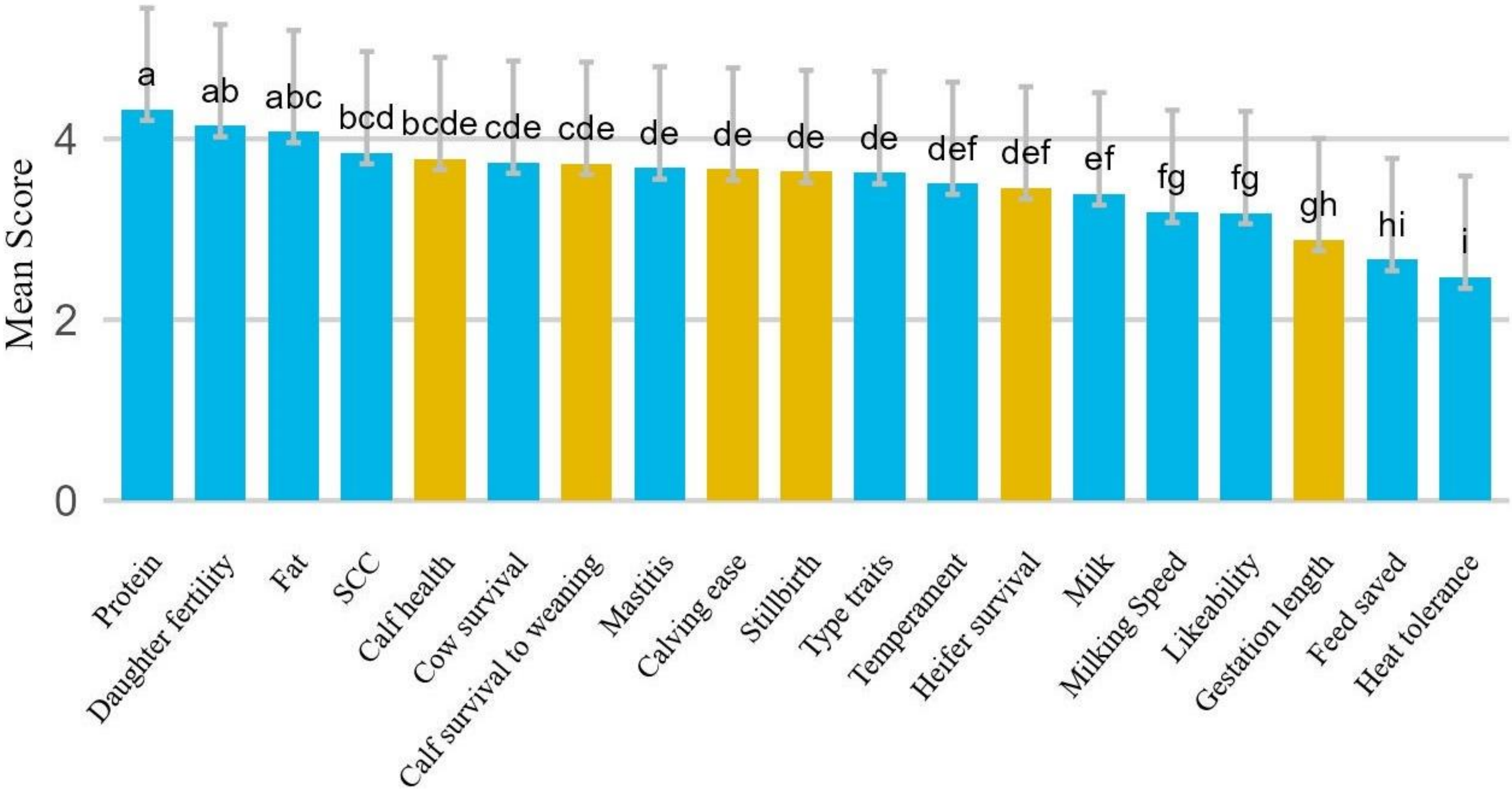
- Polygenic - 162 significant variants ($p<10^{-6}$) with an effect size of ~7% ±3 more stillborn calves
- Peaks on BTA 4,6,7,19,22 involving many genes
- Variant on BTA19 – in the region covered by BH2 in Brown Swiss, MKS1 linked to lethal malformation in humans
- Some variants in common with Cole *et al*., 2011



Do farmers care?

Industry survey trait preferences

Weighted mean scores for trait preferences n=109



Summary

- Calves are vital to profitability and sustainability
- Farmers value calf health traits
- The main problem to address is stillbirth, followed by scours.
- Heritability ranges from 1-11% depending on the trait and breed.
- There is scope to use genomic selection to improve calf health

Thank you

Participating farmers, their herd recording centres and genomic service providers, advisors, media, industry organisations

Supervisors: Jennie Pryce, Amanda Chamberlain, Majid Khansefid and committee chair, Tony Gendall

Co-authors: Mekonnen Haile-Mariam, Mike Goddard, Irene Van den Berg, Iona MacLeod, Tuan Nguyen, Erica Jewell

Genomics & cellular sciences team

La Trobe's Graduate Research School and Kendra Whiteman

DataGene colleagues: Erica Jewell, Gert Nieuwhof, Mary Abdelsayed, Matthew Shaffer, Lee Monks, Pete Williams, Pete Thurn, Connie Smee, Laura Calder, Nora Veljanovski

Fellow PhD students: Beth Scott, Ee Cheng Ooi, Boris Sepulveda, Fazel Almasi, Mohammad Ghoreishifar, Anastasiia Kudriashova, Laura Jensen

Zoetis