



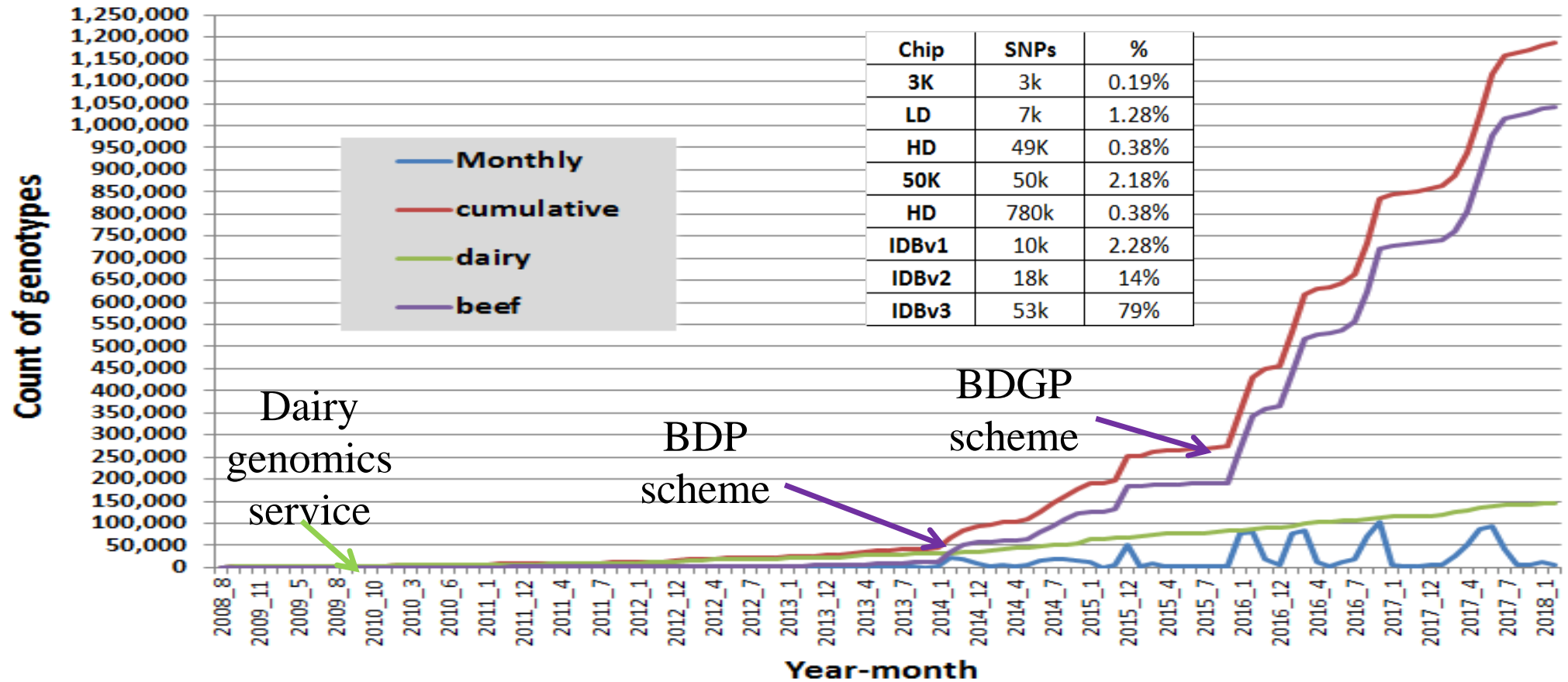
**IRISH CATTLE BREEDING FEDERATION**

## Experiences with large scale implementation of genomic selection in a predominantly crossbred beef population

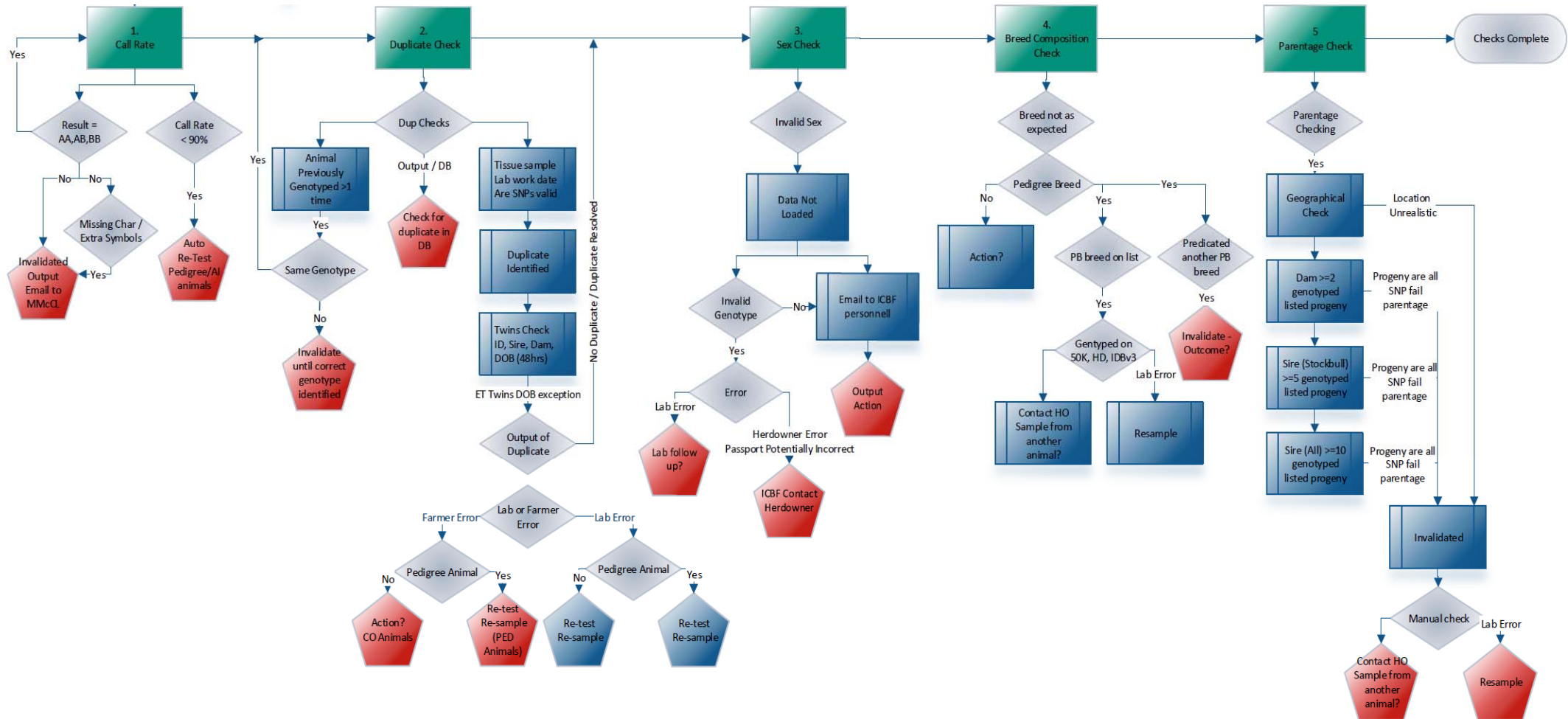
Evans, R.D., Cromie A., McCarthy J., Kearney J.F., Pabiou, T., and Berry D.P.



# Genotyping history at ICBF



# Evolving genotype quality control process



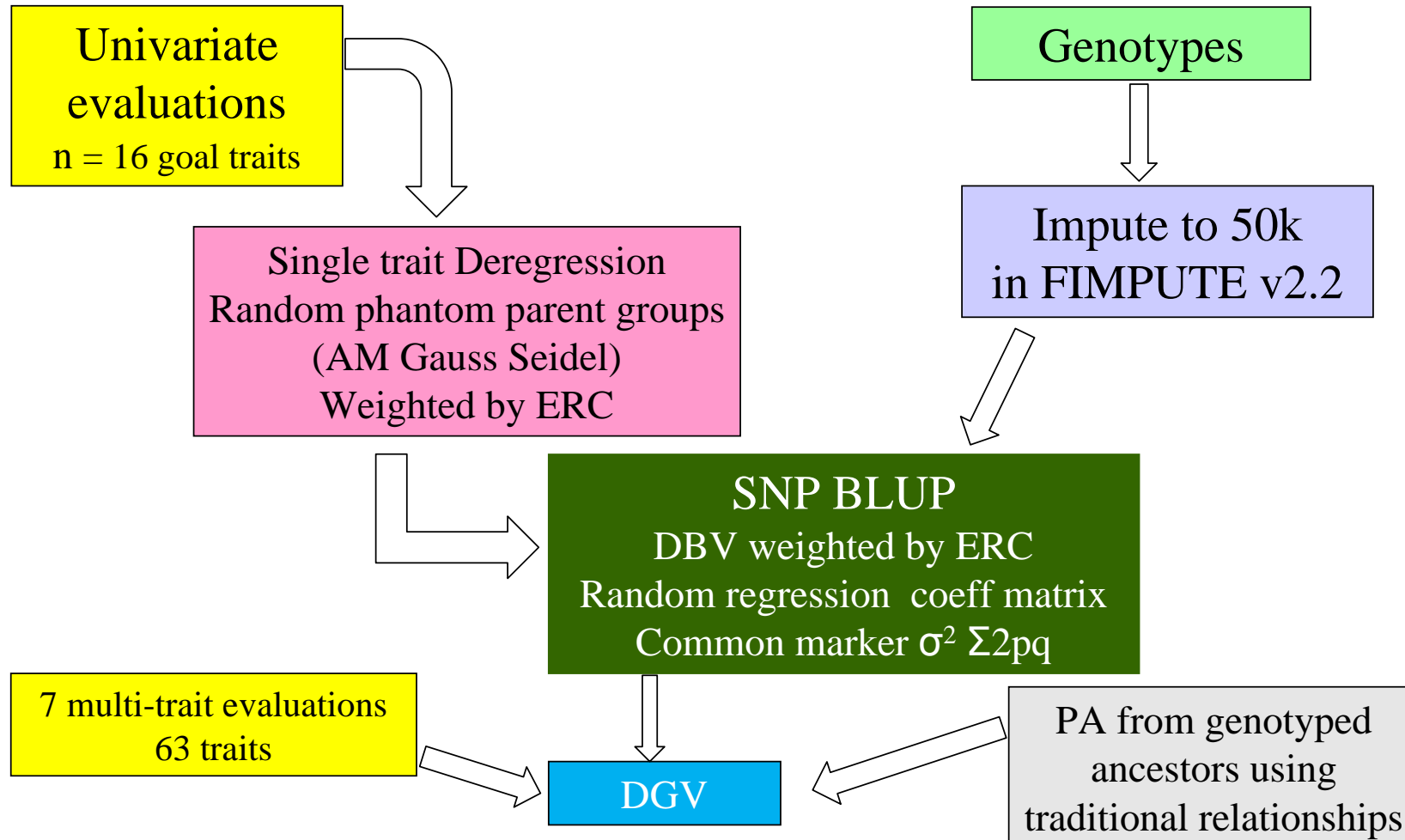
# Sire error rates and parentage prediction

- Parentage prediction based on 800 SNPs
- 200 ISAG (minus 5, clustering and low MAF)
- 605 additional based on high MAF >45% across 50 breeds in reference population
- Sire error rate 9.5%, 5% in pedigree animals
- Twins
  - 6,076 twin sets genotyped 4.7% identical
  - 4,902 sets also sire genotyped,
  - 0.98% heteropaternal superfecundation (twins with different sires)
- 525,916 animals put through prediction process if either no sire or sire not genotyped
- 201,742 predicted (38%) based on SNP mismatch rate <1%

# Characteristics of genotyped animals (n = 1.16m)

<i>Primary Breed</i>	<i>Total</i>	<i>animals with multiple breeds</i>	<i>AI sires</i>	<i>Animals Sired by AI</i>	<i>Natural service sires</i>	<i>Cows</i>	<i>Sire also genotyped</i>
Limousin	377,366	301,097	423	103,610	16,245	204,662	245,043
Charolais	257,624	195,910	470	57,622	16,888	112,869	172,322
Holstein	121,122	97,442	2,437	87,176	8,719	50,865	90,006
Angus	113,054	85,639	260	34,753	6,493	59,054	61,463
Simmental	90,389	68,386	294	24,894	2,797	62,487	50,843
Hereford	63,249	47,062	188	13,630	3,573	37,190	28,032
Belgian Blue	43,324	39,760	269	27,974	1,124	27,354	33,388
Saler	20,571	15,410	52	5,935	527	12,916	11,813
Shorthorn	19,749	13,598	77	6,908	493	13,946	9,567

# 2-Step Genomic Evaluation (Mix99)



Blending using selection index methodology

(Van Raden et al. 2009)

# Informative animals by trait

<i>Trait</i>	<i>Genotyped animal phenotypes</i>	<i>Genotyped animal phenotypes individual cows</i>	<i>SNP training animals</i>	<i>h<sup>2</sup></i>	<i>Mean ERC</i>	<i>Std ERC</i>
<b>calving difficulty</b>	818,122		106,470	0.09	22.6	231.18
<b>gestation</b>	179,107		125,659	0.35	7.0	112.40
<b>mortality</b>	921,050		100,629	0.04	17.9	203.68
<b>docility</b>	218,130		209,560	0.35	1.6	10.77
<b>feed intake</b>	2,147		3,892	0.44	0.7	0.58
<b>carcass weight</b>	134,371		227,943	0.38	4.1	58.89
<b>carcass conformation</b>	134,371		246,365	0.33	4.1	60.71
<b>carcass fat</b>	134,371		260,385	0.30	4.0	61.55
<b>Age 1st calving</b>	498,695		252,161	0.31	1.1	4.30
<b>maternal calving diff</b>	2,215,972	594,727	383,670	0.04	10.0	160.29
<b>Maternal wean wt</b>	310,014		164,805	0.25	4.0	6.24
<b>cow milkability score</b>	1,373,592	508,912	266,703	0.20	5.1	6.93
<b>cow calving interval</b>	1,919,463	474,696	247,384	0.02	6.5	31.73
<b>cow survival</b>	2,025,018	489,280	241,567	0.02	6.7	41.38
<b>cow liveweight</b>	101,038	76,270	78,055	0.32	6.6	42.05
<b>cull cow weight</b>	103,653		95,645	0.29	3.6	65.30

# Validation dataset

- Date at which 66% of animals with genotypes and phenotypes were born.
- Reason for 33% was to have reasonable dataset size to validate
  - Small CGs
  - Single sire CGs
  - Downside
  - (r SNPeffects = avg 0.69
  - range 0.49 to 0.83)

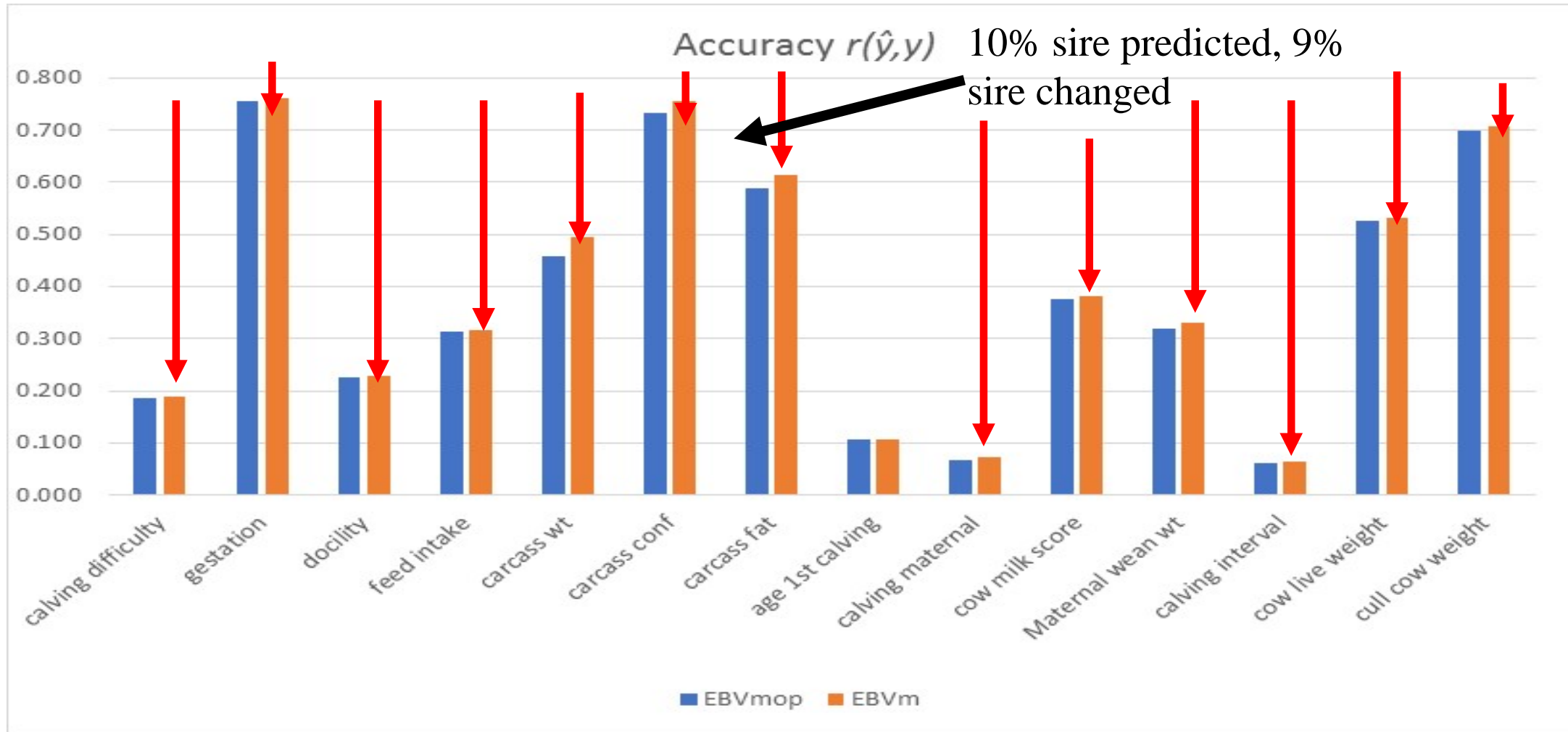
Trait	Training pop full	valid dob cutoff	Training pop validation	validation	loss %	<i>Validation candidates</i>
calving difficulty	106,470	31/12/2014	49,320	49,320	-54%	109,174
gestation	125,659	31/12/2014	71,903	71,903	-43%	38,060
dolcility	209,560	27/01/2016	135,584	135,584	-35%	45,139
feed intake	3,892	30/08/2013	1,532	1,532	-61%	910
carcass wt	227,943	12/04/2015	72,581	72,581	-68%	31,731
carcass conf	246,365	12/04/2015	84,261	84,261	-66%	31,731
carcass fat	260,385	12/04/2015	90,929	90,929	-65%	31,731
age 1st calving	252,161	26/07/2012	165,995	165,995	-34%	77,747
calving maternal	383,670	31/12/2014	199,709	199,709	-48%	13,244
cow milk score	266,703	18/03/2012	219,940	219,940	-18%	127,303
Maternal wean wt	164,805	18/03/2012	46,760	46,760	-72%	27,518
calving interval	247,384	26/07/2012	232,141	232,141	-6%	59,352
cow live weight	78,055	23/04/2011	27,667	27,667	-65%	13,601
cull cow weight	95,645	08/05/2010	33,233	33,233	-65%	19,973



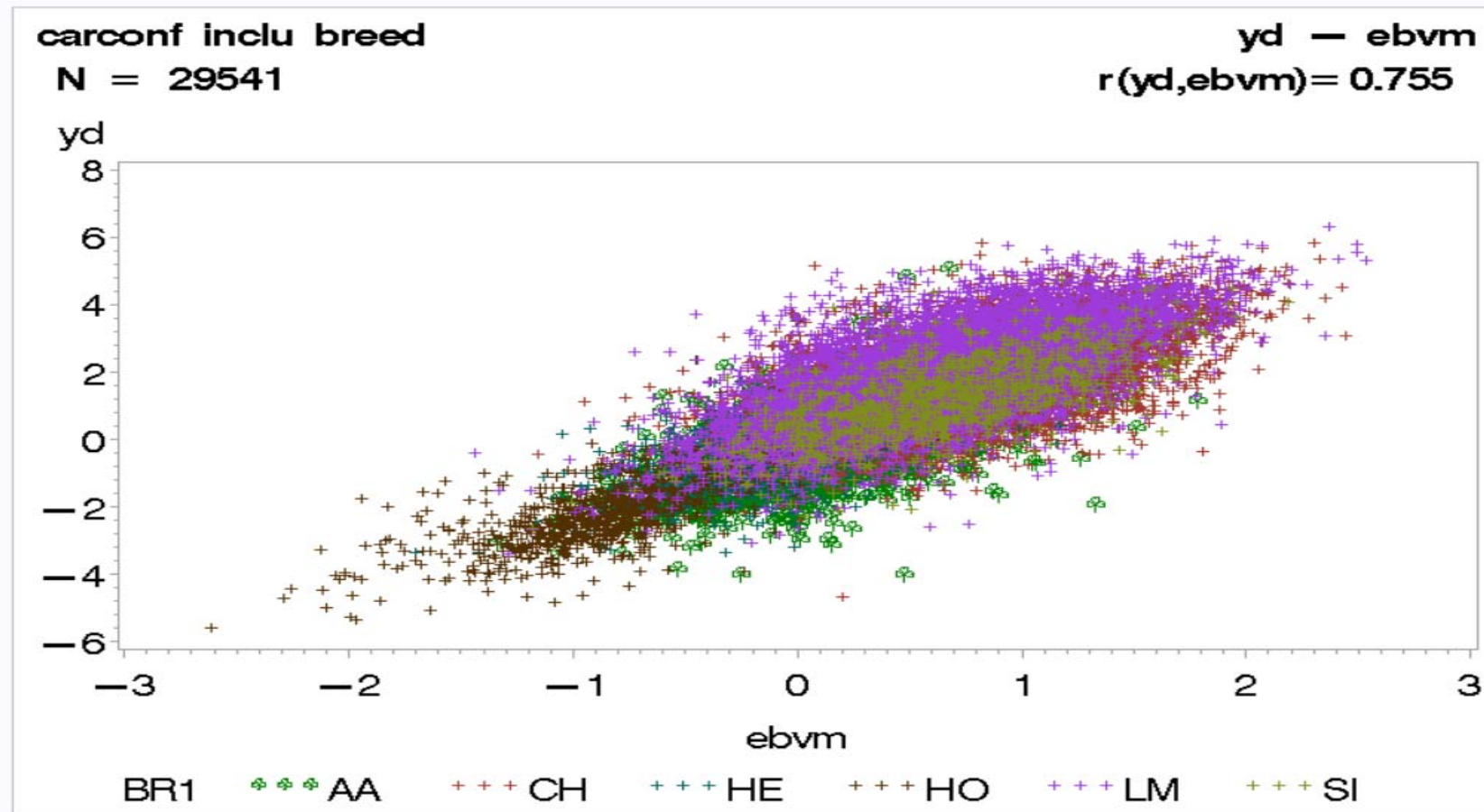
# Validation

- Yield deviations from Mix99 as validation phenotype
- $YD = Y - (CG + \text{fixed effects})$ . Genetic effect inclusive of breed effect through pedigree groups
- Maternal traits: YD of their progeny, direct genetic effect corrected
- Validation questions:
  - (1) Impact of ancestry change/updates based on genotype data
  - (2) Accuracy of prediction using single v multi trait EBV
  - (3) Accuracy of prediction of EBV, DGV and GEBV
  - (4) Accuracy of prediction in (3) but adjusting for breed

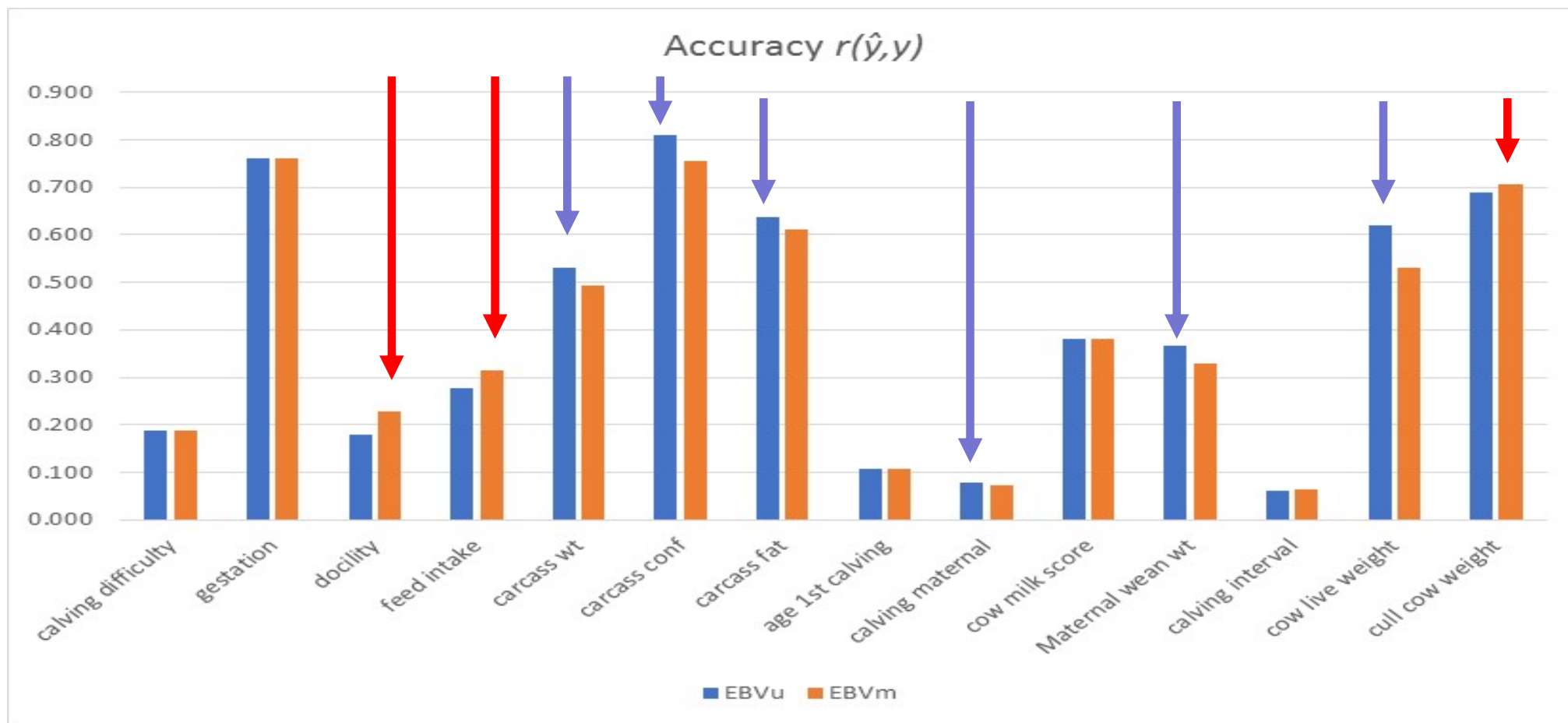
# Impact of ancestry changes (160k) on EBVs



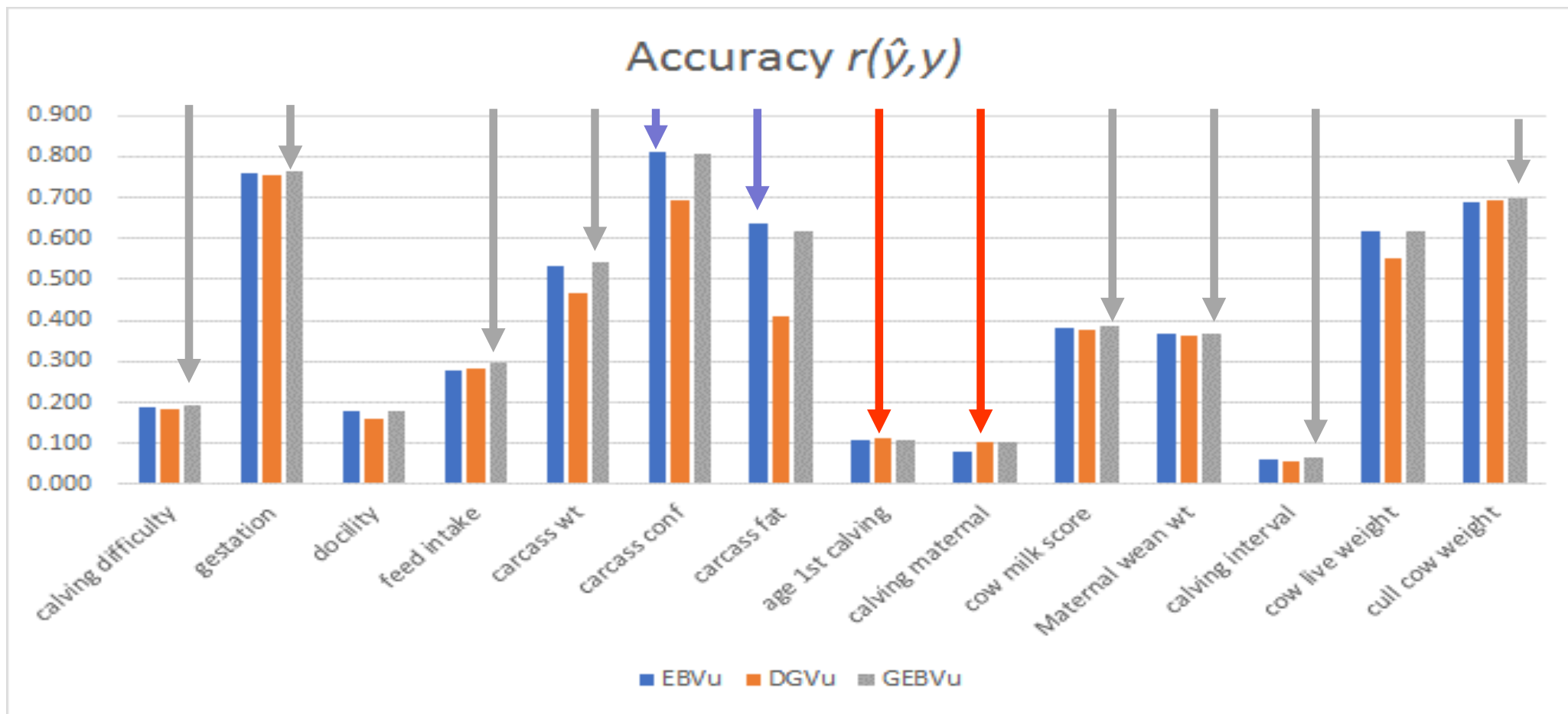
# Inflation of correlation due to large breed effects



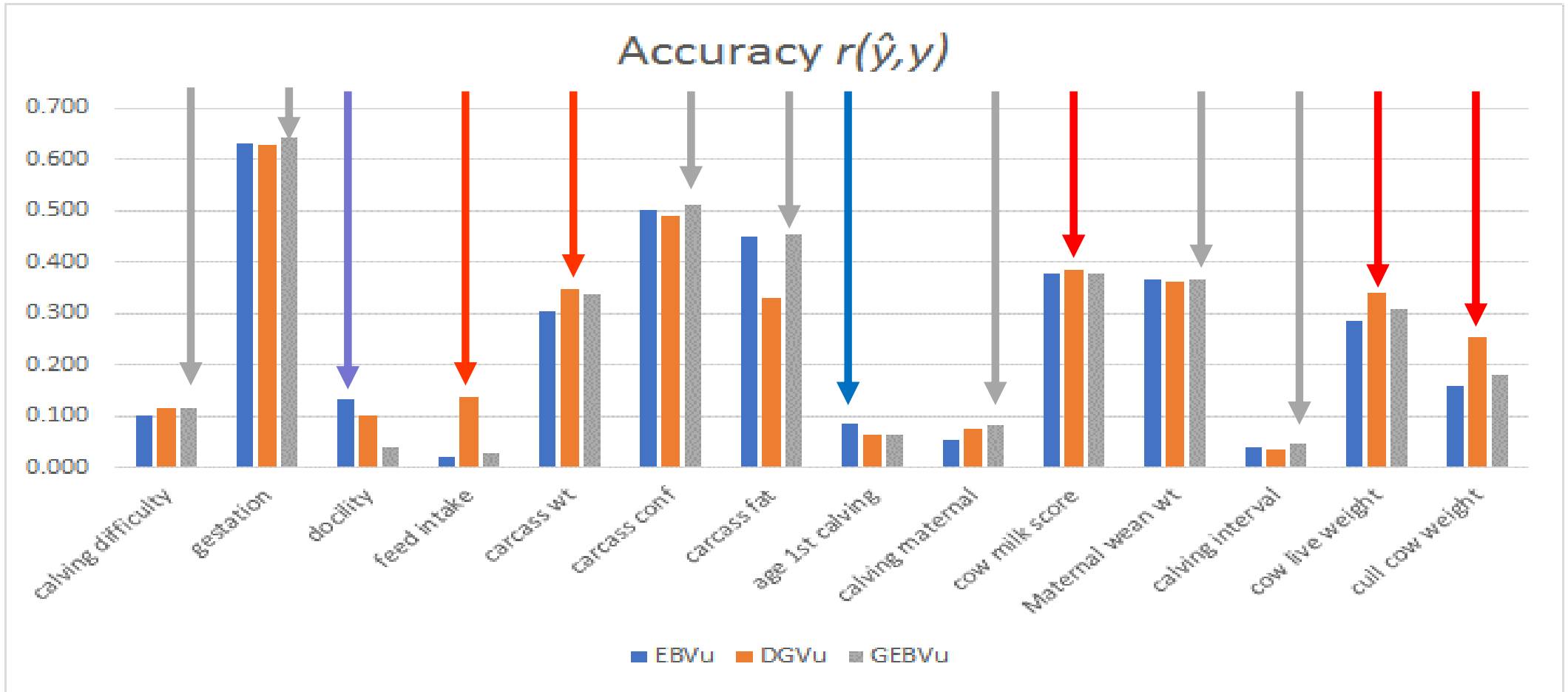
# Choice of EBV for SNP BLUP



# Validation Accuracy for EBV, DGV & GEBV



# Breed corrected Accuracy



# Summary

- Genomic GEBVs are now published routinely in Ireland
- Validation indicating:
  - Benefit from genotype in correcting and adding ancestry
  - Choice of candidate ebv for SNP BLUP also important
  - Benefit from genomic proofs but more modest than ancestry change
  - Some traits (docility, afc) need more focus
- Working with Scientific advisory committee
  - Defining workable validation procedures
  - Re-run with less severe impact on training population
  - Single step solutions



**Thanks for listening!**

