Sheep Ireland update

Eamon Wall

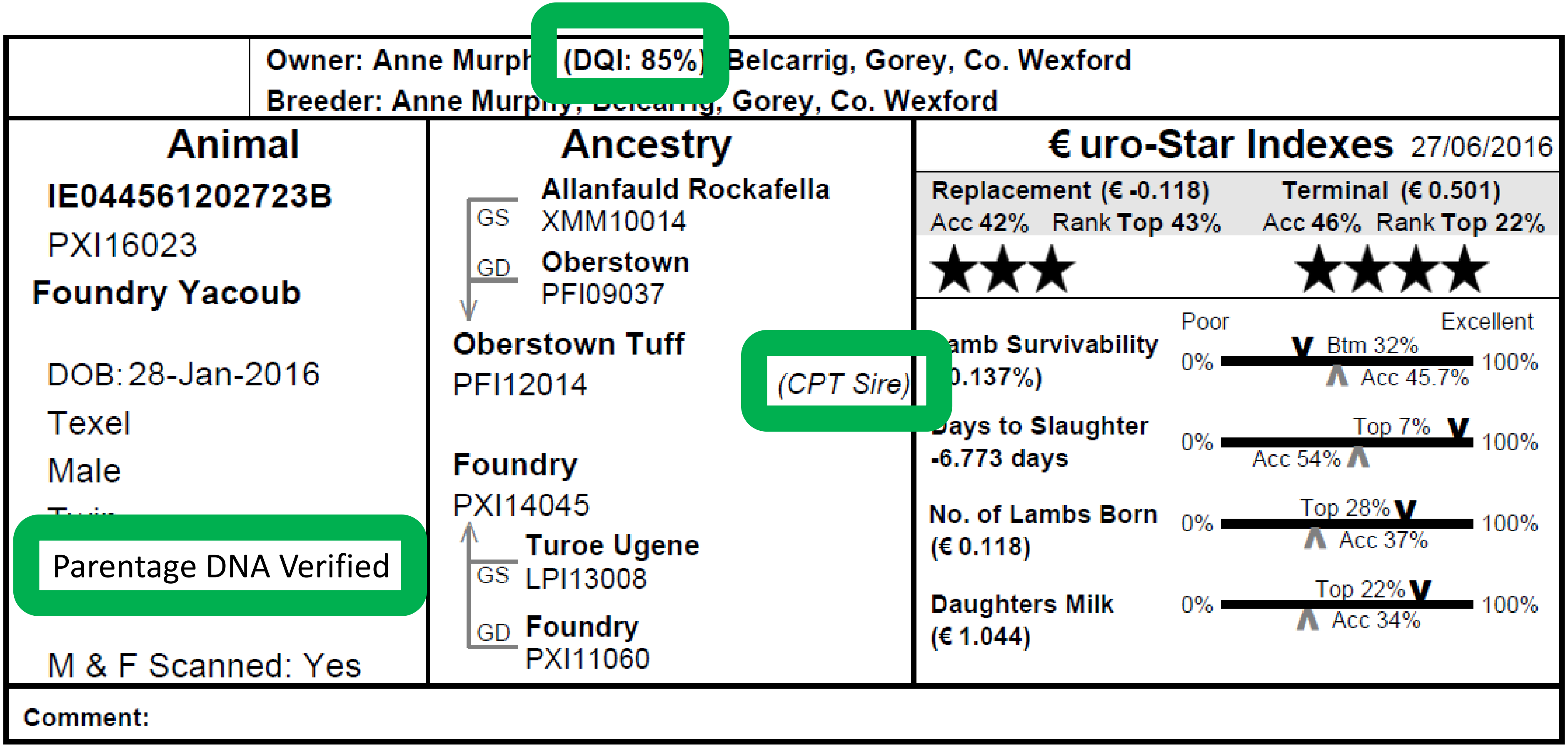
Sheep Ireland Update

- Breeder number slightly up again
- Very successful CPT season this year
    - Growing number of traits being recorded on these farms
    - Carcase data now flowing from factories
- Genomics Pilot project
- CPT semen pilot project planned for Autumn
- LambPlus Sale – August 27th

Ram Breeder Workshops

- Two workshops complete – three to go
  - Anne Murphy (South East)
  - Arthur O'Keeffe (South)
- Remaining Workshops
  - Eamonn Duffy Fri 8th (North East)
  - James McKane Mon 11th (Donegal)
  - Michael Murphy Fri 15th (West)

Catalogue Updates



Owner: Anne Murph (DQI: 85%) Belcarrig, Gorey, Co. Wexford
Breeder: Anne Murp Gorey, Co. Wexford

Animal

IE044561202723B
PXI16023
Foundry Yacoub

DOB: 28-Jan-2016
Texel
Male

Parentage DNA Verified

M & F Scanned: Yes

Ancestry

GS **Allanfauld Rockafella**
XMM10014
GD **Oberstown**
PFI09037

Oberstown Tuff
PFI12014 *(CPT Sire)*

Foundry
PXI14045
GS **Turoe Ugene**
LPI13008
GD **Foundry**
PXI11060

€uro-Star Indexes 27/06/2016

Replacement (€ -0.118)	**Terminal (€ 0.501)**
Acc 42% Rank Top 43%	Acc 46% Rank Top 22%
★★★	★★★★

	Poor		Excellent
amb Survivability **0.137%)**	0%	Btm 32% Acc 45.7%	100%
ays to Slaughter **-6.773 days**	0%	Top 7% Acc 54%	100%
No. of Lambs Born **(€ 0.118)**	0%	Top 28% Acc 37%	100%
Daughters Milk **(€ 1.044)**	0%	Top 22% Acc 34%	100%

Comment:

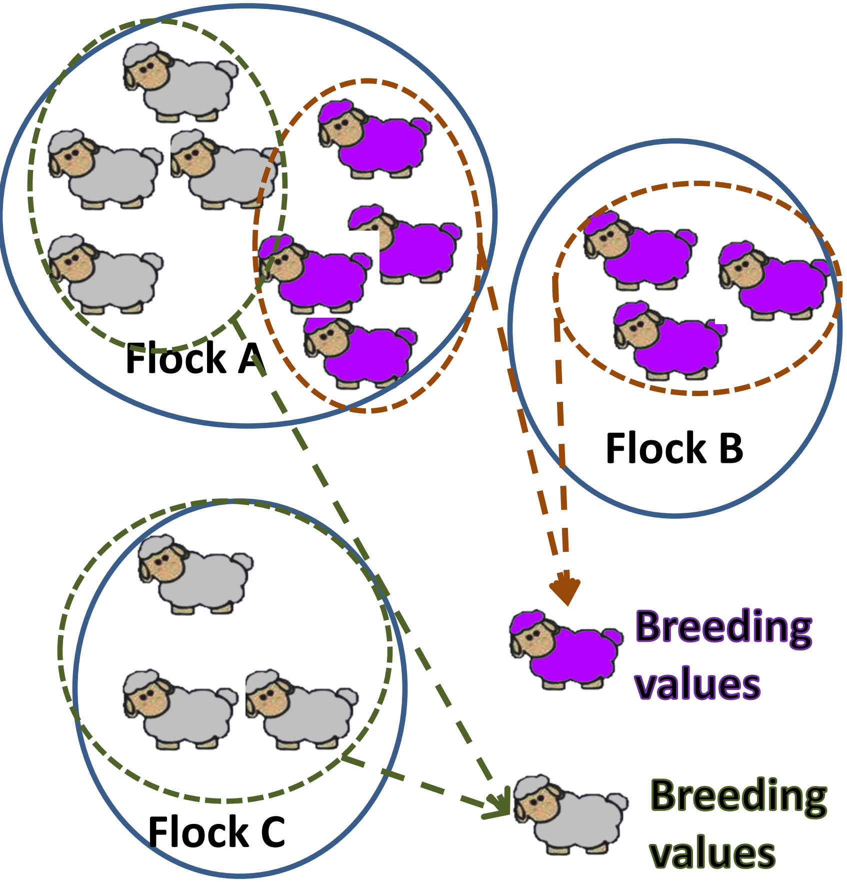
Sheep Ireland
www.sheep.ie

Across Breed Evaluations

Thierry Pabiou

Across-Breed Evaluation

Within breed



Flock A

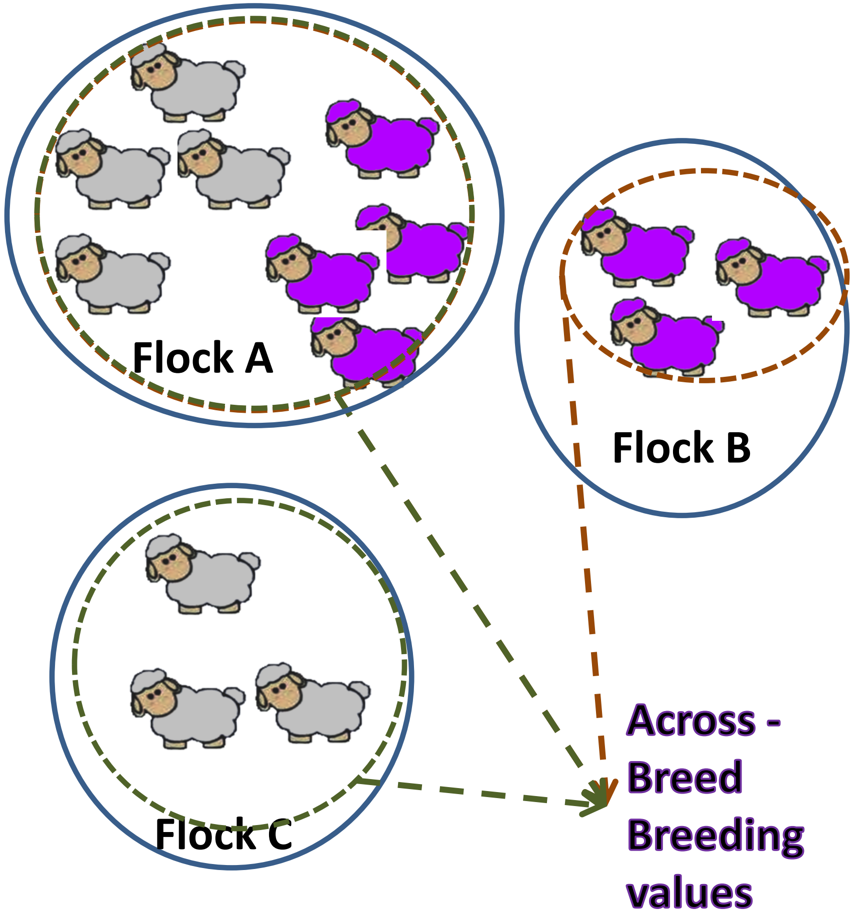
Flock B

Flock C

Breeding values

Breeding values

Across breed



Flock A

Flock B

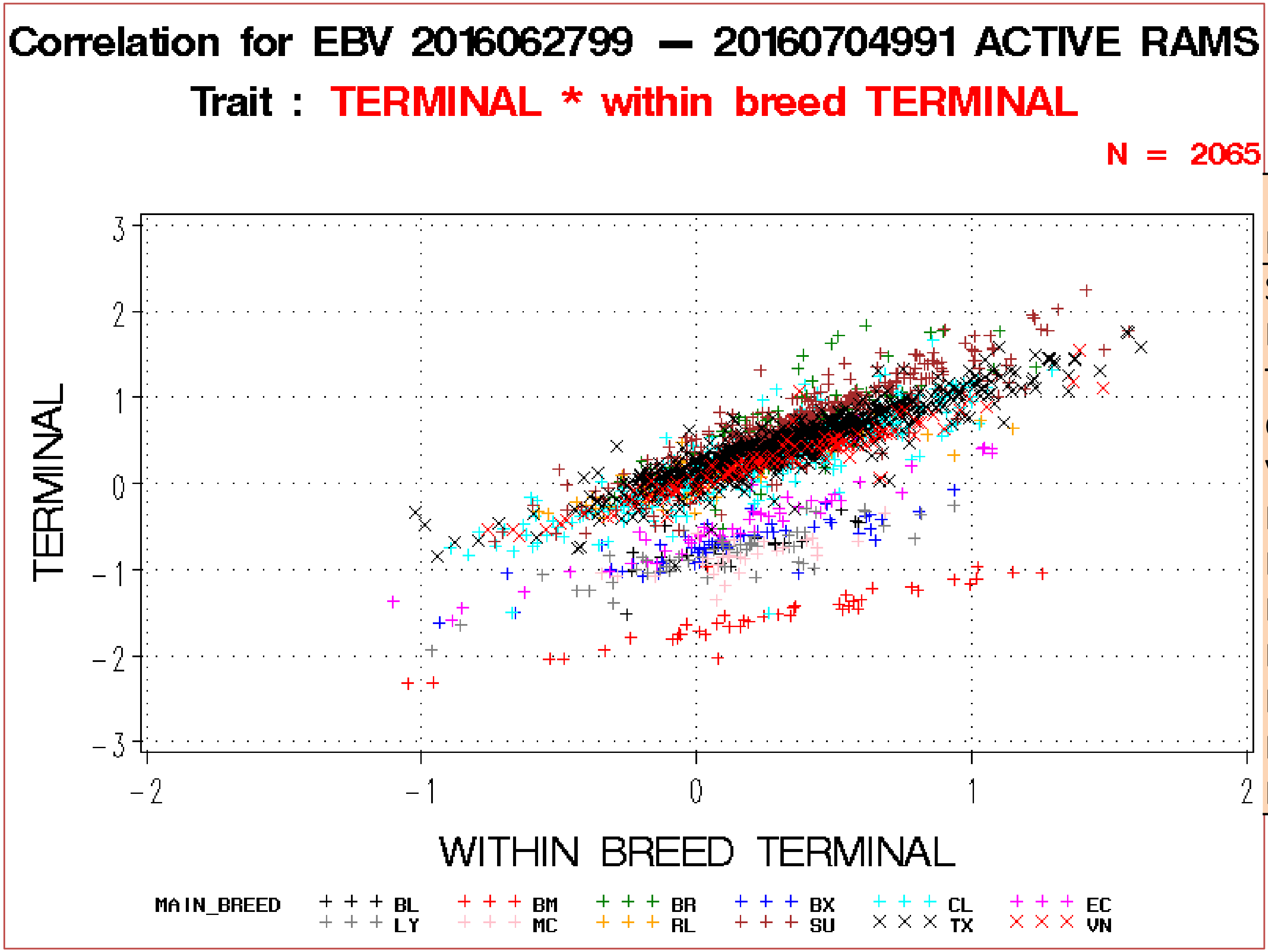
Flock C

Across - Breed Breeding values

Requirements

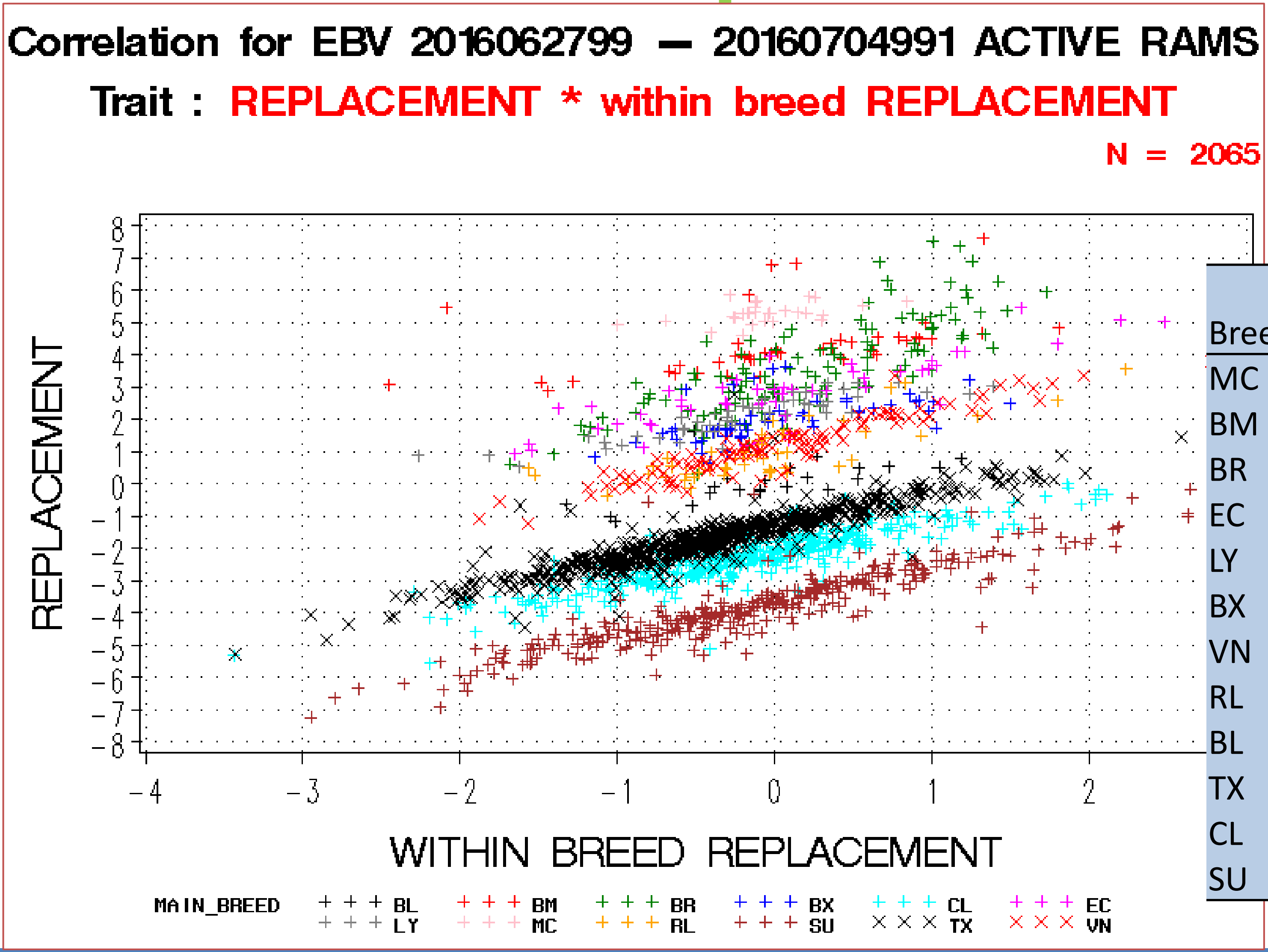
- Crossbred records
- Correction for breed composition in the model
  - 14 Animal breeds + other hill / lowland breeds
- Breed composition solution are added back up to the breeding values

Results : Terminal Index



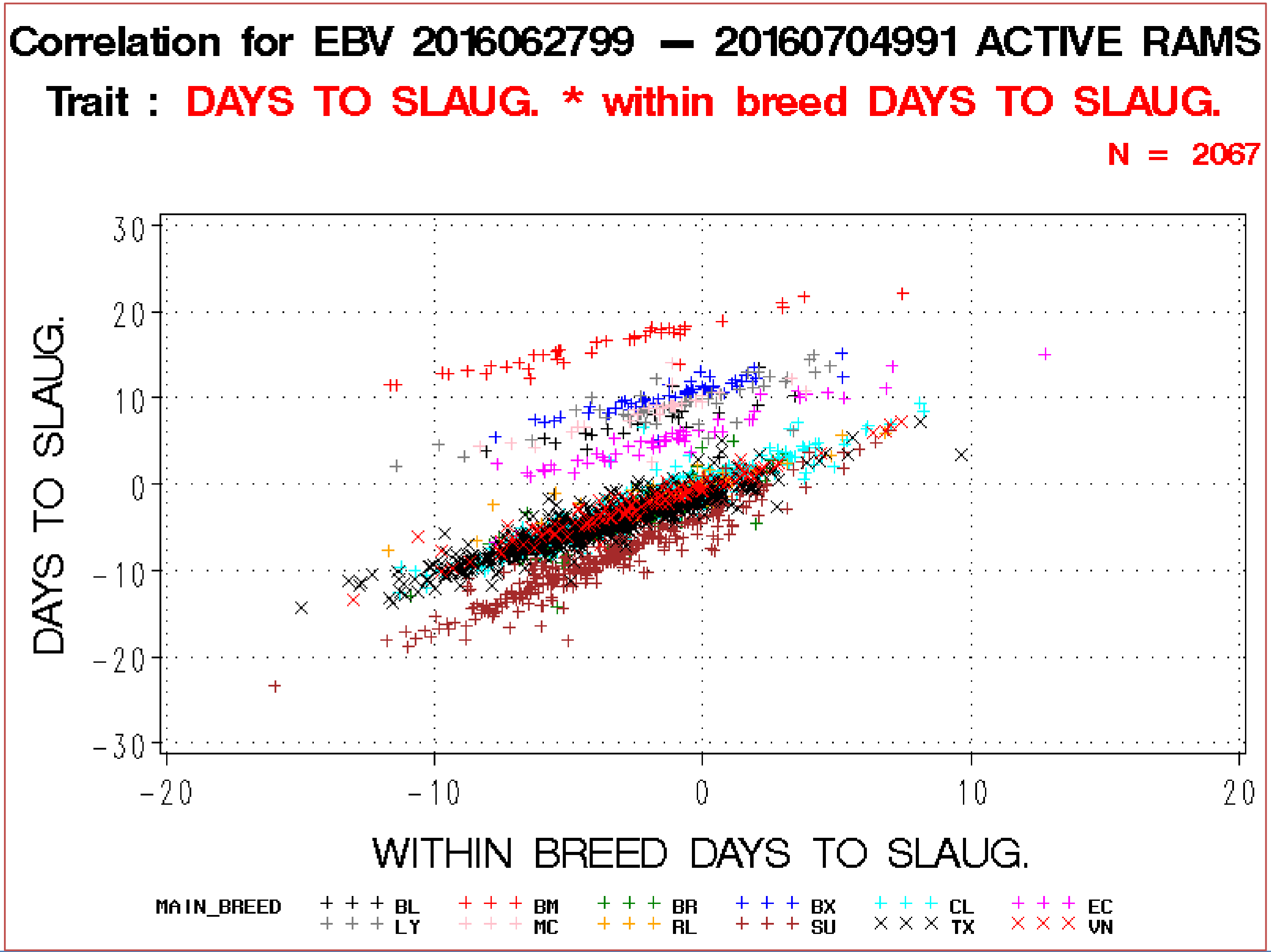
Breed	N	Average Terminal
SU	352	0.71
BR	119	0.62
TX	737	0.44
CL	448	0.27
VN	110	0.27
RL	52	0.07
EC	53	-0.44
BX	56	-0.70
BL	22	-0.71
LY	58	-0.81
MC	38	-0.85
BM	43	-1.54

Results : Replacement Index



Breed	N	Average Replacement
MC	38	5.28
BM	43	4.28
BR	119	3.63
EC	53	2.73
LY	58	2.04
BX	56	2.00
VN	110	1.19
RL	52	0.97
BL	22	0.05
TX	737	-1.68
CL	448	-2.30
SU	352	-3.80

Results : Growth to Slaughter



Correlation for EBV 2016062799 – 20160704991 ACTIVE RAMS

Trait : DAYS TO SLAUG. * within breed DAYS TO SLAUG.

N = 2067

Breed	N	Average Growth
SU	352	-8.19
TX	737	-4.55
BR	119	-3.35
VN	110	-2.31
CL	448	-2.29
RL	52	-0.70
EC	53	5.16
BL	22	6.84
MC	38	8.58
LY	58	9.27
BX	56	10.28
BM	43	16.23

Weaning Weights 2016

Nb 2016 weaning weight = 12,706

% Crossbred records = 21%

	Dam breed																				
Sire breed	**BL**	**BM**	**BN**	**BO**	**BR**	**BX**	**CL**	**CV**	**EC**	**GL**	**HD**	**HL**	**LY**	**MC**	**PR**	**RL**	**SH**	**SU**	**TX**	**VN**	**ZB**
BL																			13		
BM																					
BN			35																		
BO																					
BR	12			3	1045		62				3		8			2		222	315	39	
BX						142										13					
CL	6			7	111	3	2818				2		19			12		132	166	76	
CV								70											5		
EC																					
GL										142											
HD											28										
HL																					
LY				1	30	2	15						493					9	14	12	
MC																					
PR																					
RL																272					
SH																	91				
SU	16	17			254	5	37			8			13			2		1919	174	34	
TX	21			4	380	3	32	10					6	7		13		127	2630	66	
VN					26		11									5		28	33	358	
ZB																					17

Weaning Weights 2015-2016

Nb 2015-16 wean. weight = 29,033
% Crossbred records = 20%

	Dam breed																								
Sire breed	**BL**	**BM**	**BN**	**BO**	**BR**	**BX**	**CL**	**CV**	**DT**	**EC**	**GL**	**HD**	**HL**	**IF**	**LK**	**LY**	**MC**	**PR**	**RL**	**SH**	**SU**	**TX**	**VN**	**WS**	**ZB**
BL	29	16					3									5	1					14			
BM		32														2	3					2			
BN			64																						
BO	0	0														0	0								
BR	13			3	2346	8	116			28		3				8	10		58		443	482	111	6	
BX						315													13			0			
CL	6	3		7	289	7	5993	1				2			5	55	0		15		243	300	133		3
CV								91														5			
DT							2		17					4								6			
EC					1					552			0				105	0						69	
GL											290														
HD												93													
HL													23			0									
IF					8									0		3					1	0		6	
LK															1		6								
LY				1	40	2	15									1760					86	16	16		
MC		0															440								
PR																0		42							
RL					2		1										9		467			18			
SH																				159					
SU	47	29		0	626	6	64		2	73	8			12	2	82	4		3		4055	344	85		
TX	103			4	647	3	90	16	2	17					2	6	57		22		225	5455	127	2	
VN	8				86	2	31		1	22						1	0		14		42	49	907	0	
WS					26					1						18						6	4	9	
ZB																7									26

Summary

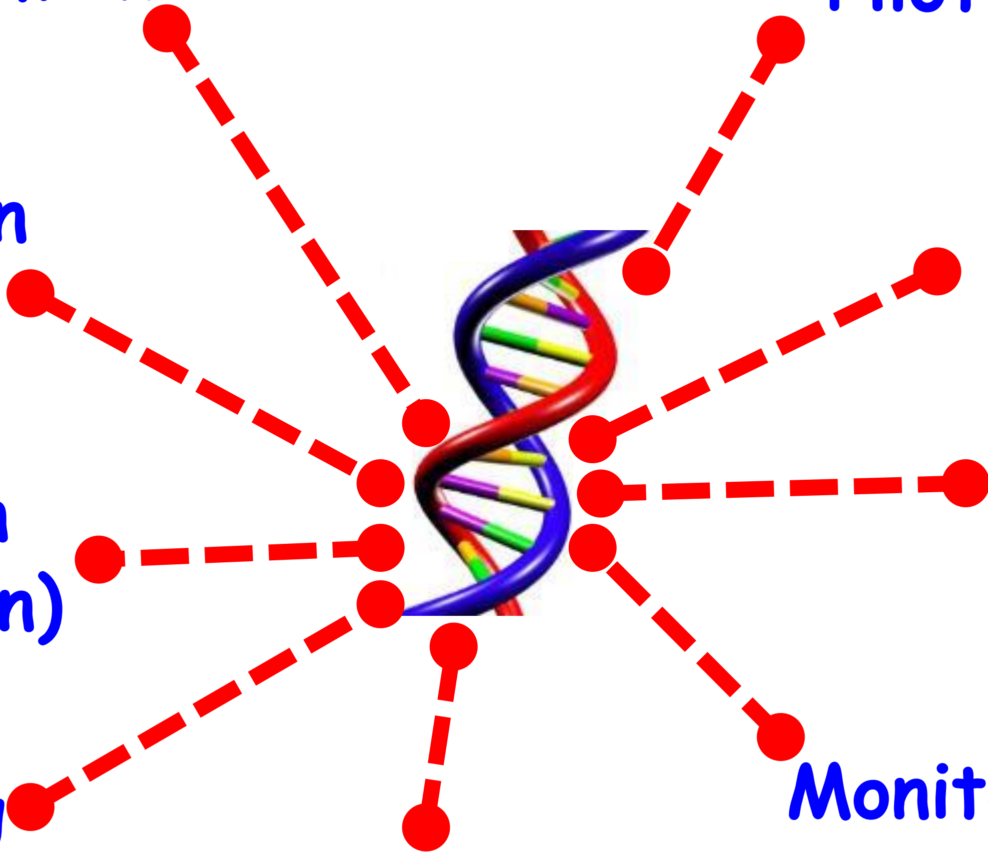
- Across-breed => breed stratification
  - Terminal breeds separates from Maternal breeds
  - More Xbred records needed in some breeds
- Some positive impact on accuracy
- Breeding values are comparable across breed
  - Easier ram choice for commercial farmers
- Ovigen Task 2: feasibility of across breed evaluation
  - Definition of across breed base for main breeds
  - Definition of within breed base for other breeds
    - ≥ Map the process for getting access to across breed evaluation

OviGen

Multi-breed sheep genetic and genomic evaluations

Sheep Industry Meeting, 7th July 2016

Áine O' Brien, Deirdre Purfield,
Nóirín McHugh, Donagh Berry



Parentage assignment

Pilot study

Gender determination

Genomic evaluations

Imputation (up and down)

Scrapie

Inbreeding

Monitoring major genes

Monitoring lethal genes

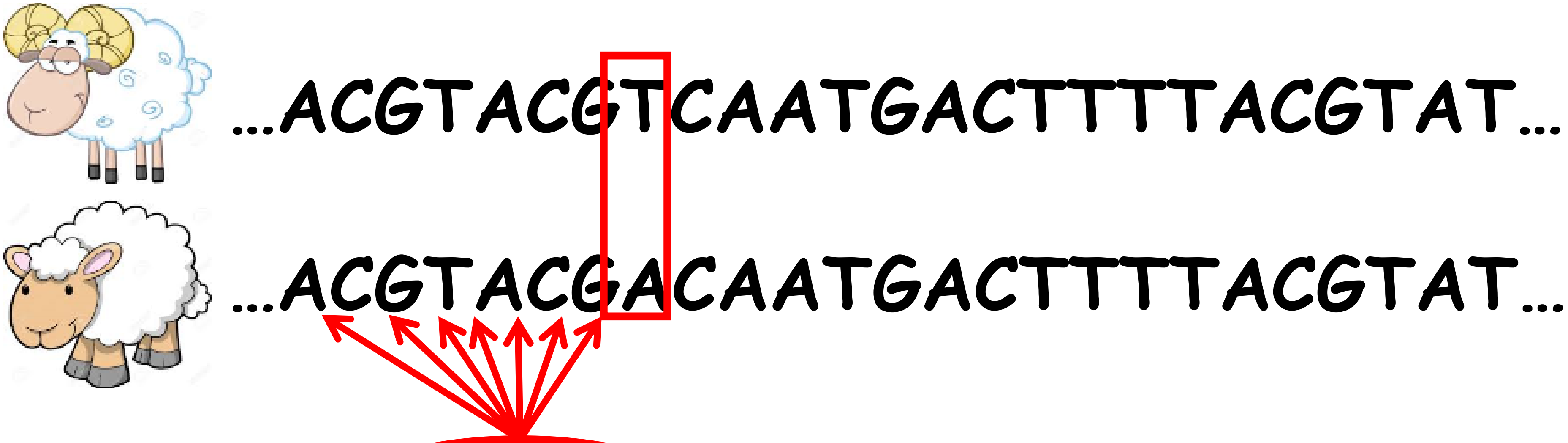
Genotyping Status

DNA - From the tip of your nose to the tops of your toes!!

DNA is the same in every cell of your body and doesn't change throughout your life

What is a SNP?

- 99.9% of our DNA is identical – most of the differences are in the form of SNPs

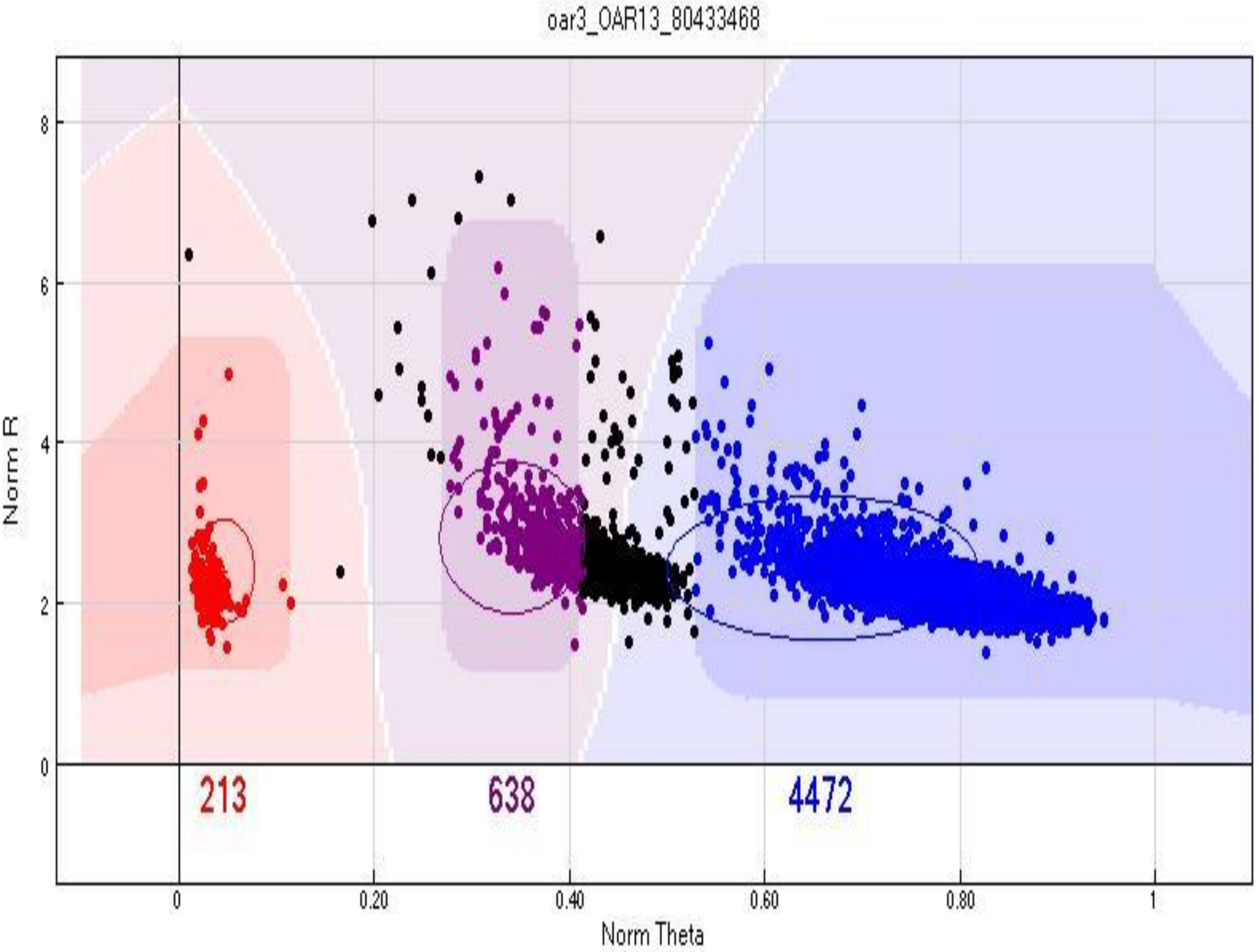


...ACGTACGTCAATGACTTTTTACGTAT...

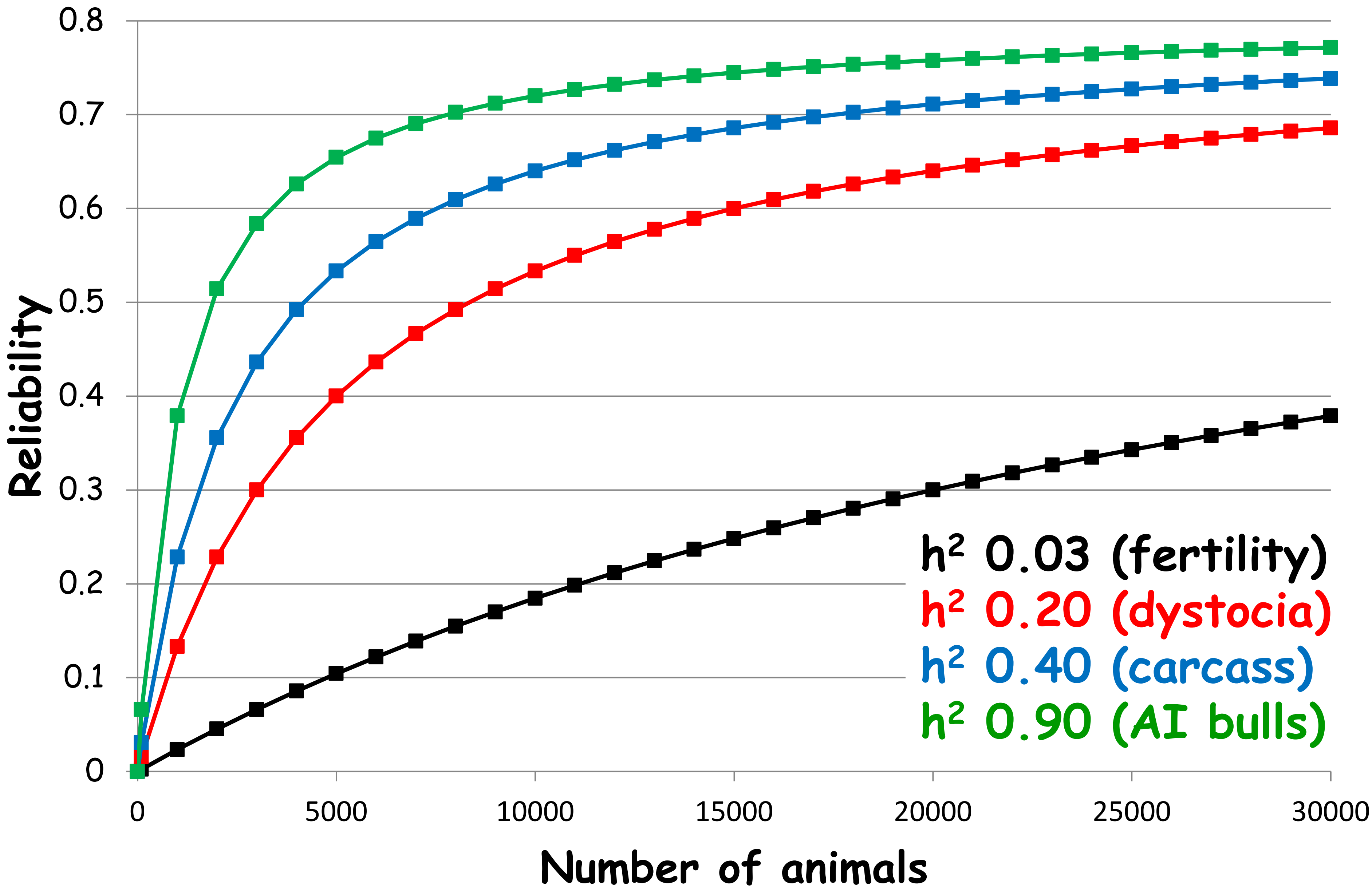
...ACGTACGACAATGACTTTTTACGTAT...

- Single Nucleotide Polymorphism

Change


oar3_OAR13_80433468
Norm R
0
2
4
6
8
213
638
4472
0
0.20
0.40
0.60
0.80
1
Norm Theta

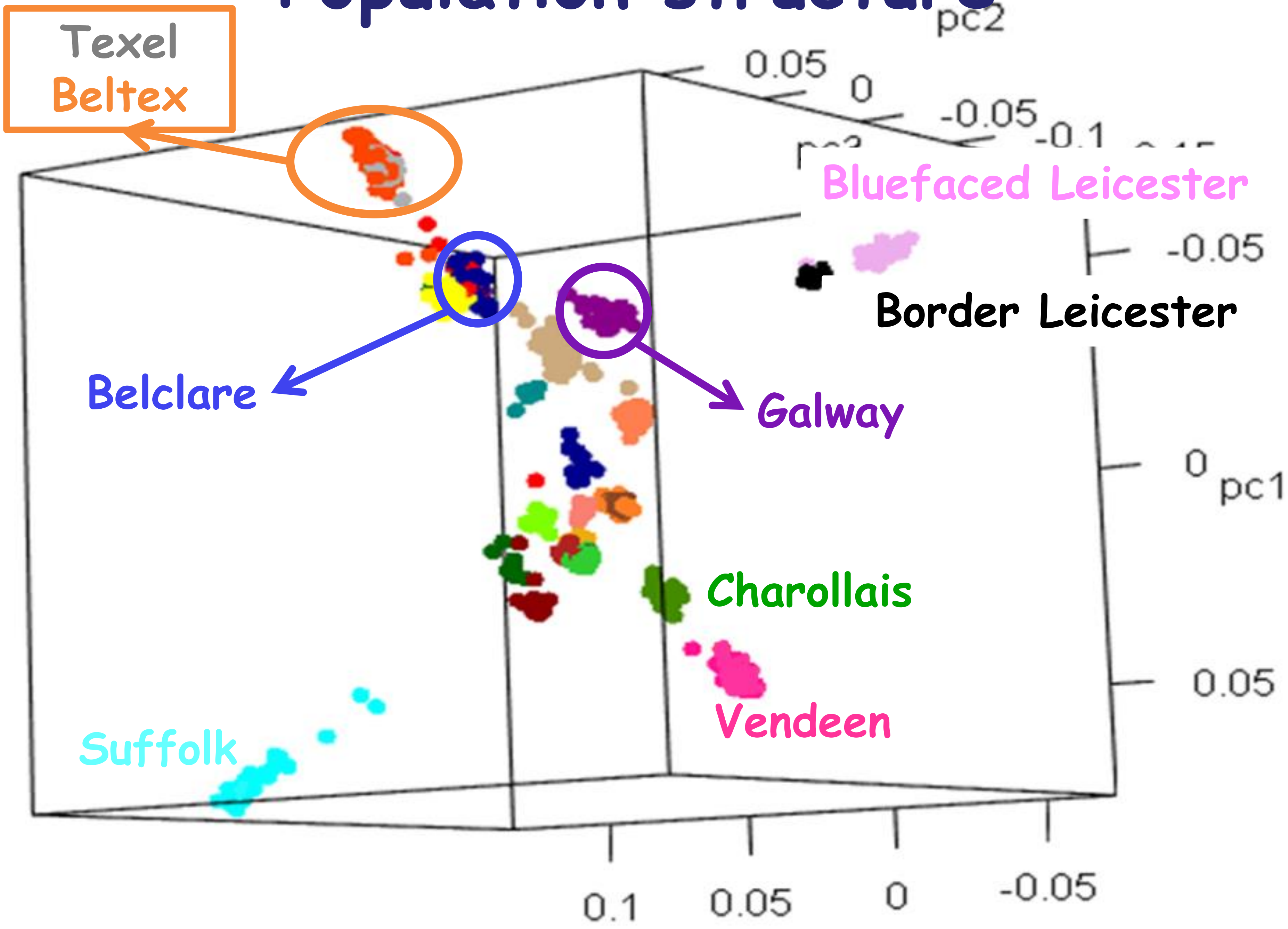
Need a large population per breed



Original plan

- Genotype the largest 5 breeds in the national breeding programme
  - Belclare, Charollais, Suffolk, Texel, Vendeen
- But what about the other breeds?
  - Population structure
  - Genotyped 19 other 'minor/rare' breeds

Population structure



Original plan

- Genotype the largest 5 breeds in the national breeding programme
    - Belclare
    - Charollais
    - Suffolk
    - Texel
    - Vendeen
    - Beltex

Breeds genotyped

Belclare	Lleyn
Beltex	Mayo Connemara
Bluefaced Leicester	Primera
Border Leicester	Rouge de l'Quest
Charollais	Scottish Blackface
Donegal Cheviot	Shropshire
Easy Care	Suffolk
Finn	Swaledale
Galway	Texel
Hampshire Down	Vendeen
Highlander	Waterford Blackface
Kerry Blackface	Wicklow Cheviot

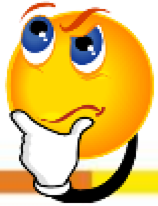
Genotyping panels

50K

- 51,135 SNPs
- Parentage ✓
- Major genes ✗
- Genomic Selection ✓
- €62

15K

- 15,000 SNPs
- Parentage ✓
- Major genes ✓
- Genomic Selection ✗
- €28.50



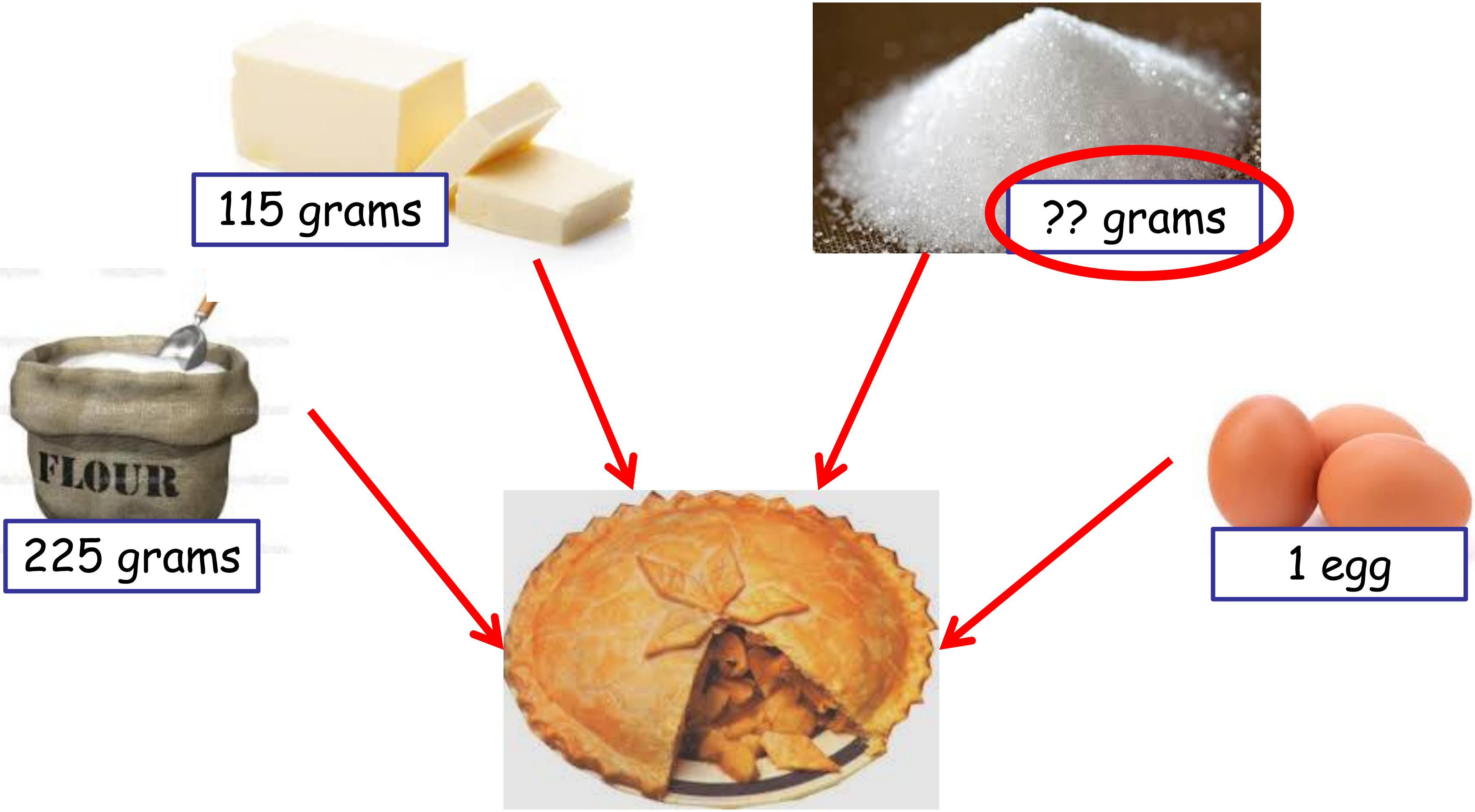
Genotyping to date

- Only animals that lambed down in 2016
- 50K (51,135 SNPs)
  - "Big 6" and minor breeds
  - 3756 completed
  - For imputation – discussed later
- 15K (15,000 SNPs)
  - "Big 6" only
  - 9825 completed
  - Pilot project animals

Genotyping by breed

	50K (51,135 SNPs)	15K (15,000 SNPs)	Total
Belclare	650	602	1252
Beltex	64	90	154
Charollais	674	2328	3056
Suffolk	784	1329	2113
Texel	494	3023	3023
Vendeen	640	132	772

Incomplete data



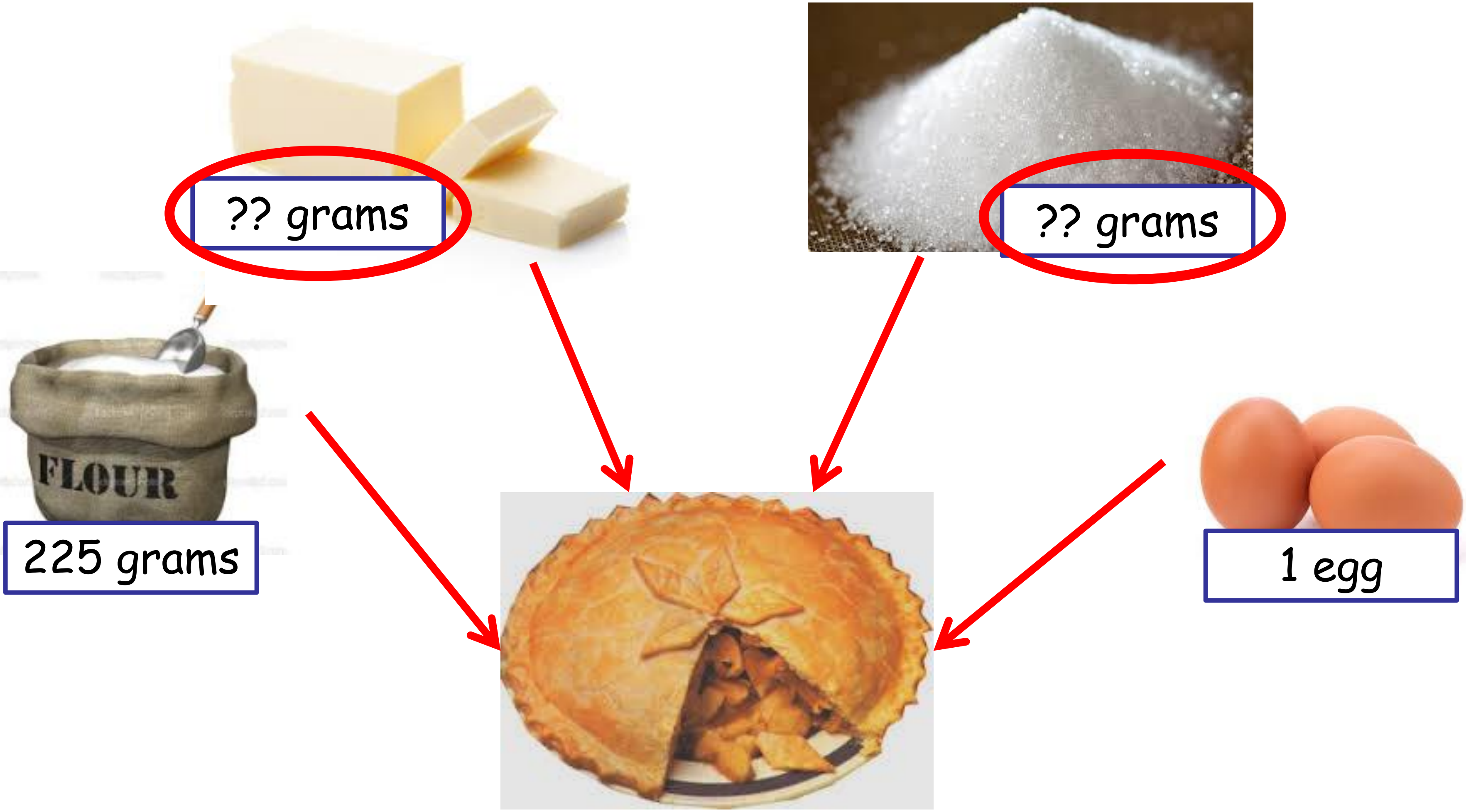
115 grams

?? grams

225 grams

1 egg

Incomplete data



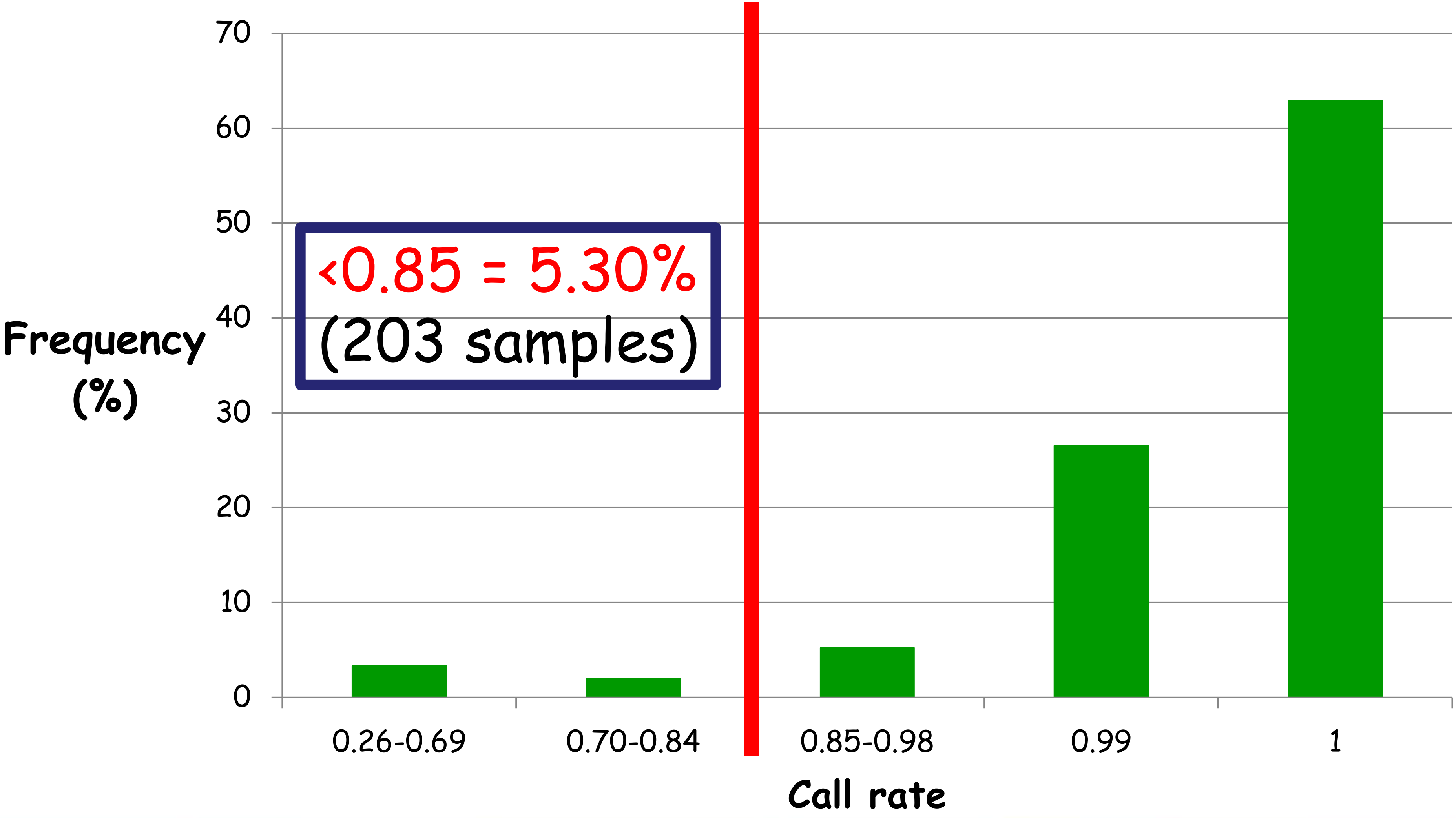
?? grams

?? grams

225 grams

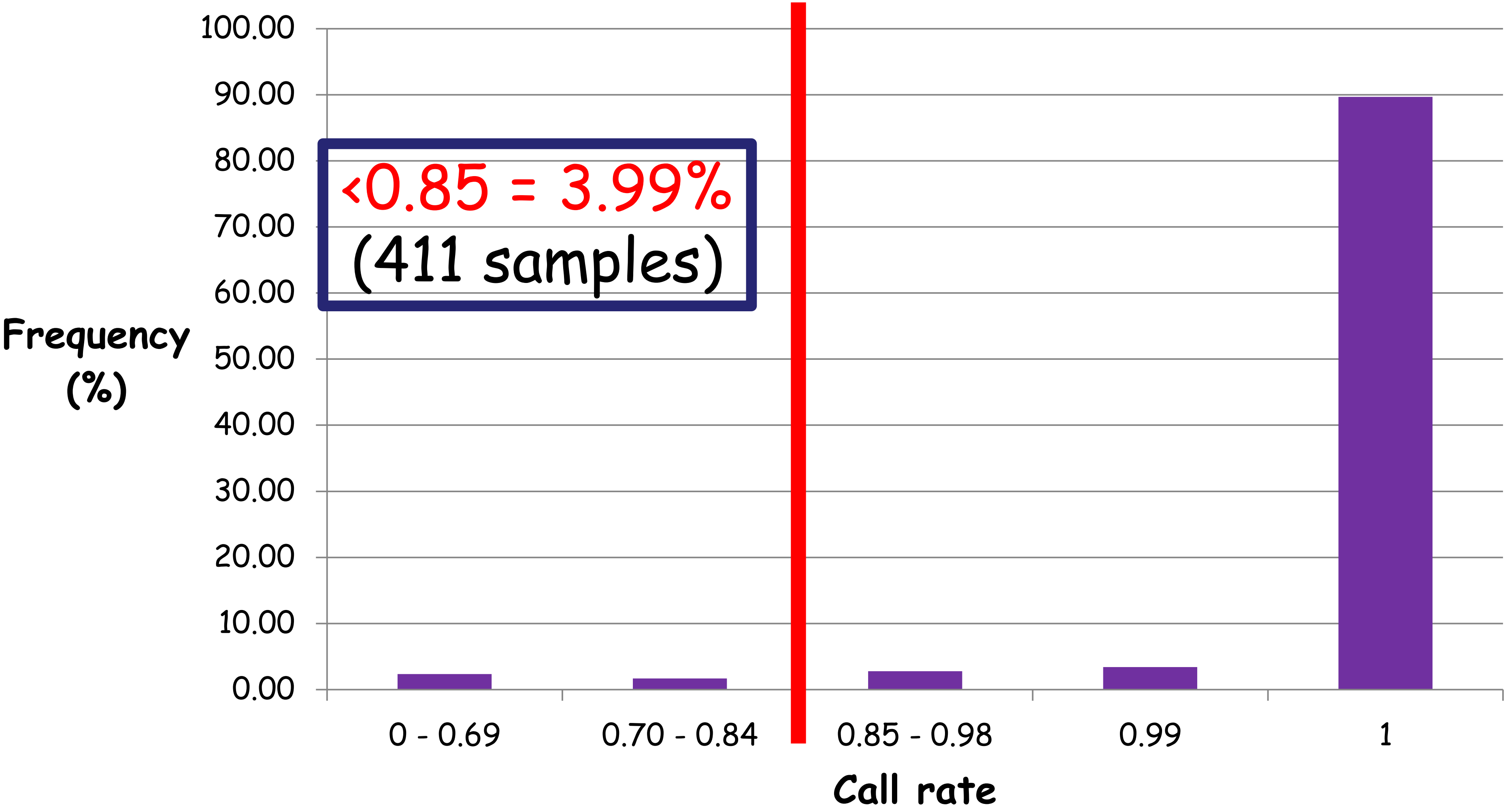
1 egg

Call rates – 50K



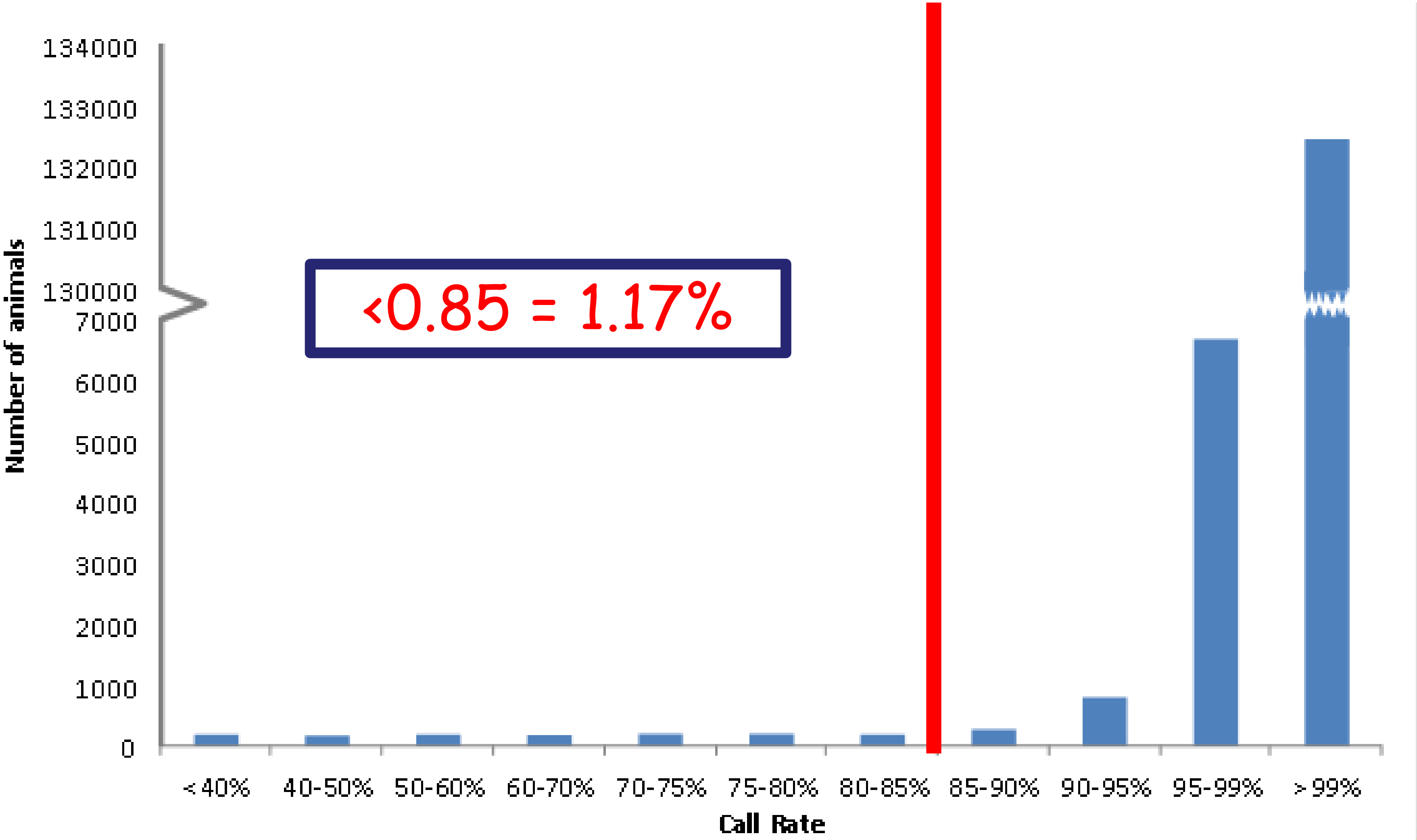
<0.85 = 5.30%
(203 samples)

Call rates - LD (15K)



<0.85 = 3.99%
(411 samples)

Compared to cattle



<0.85 = 1.17%

D. Purfield

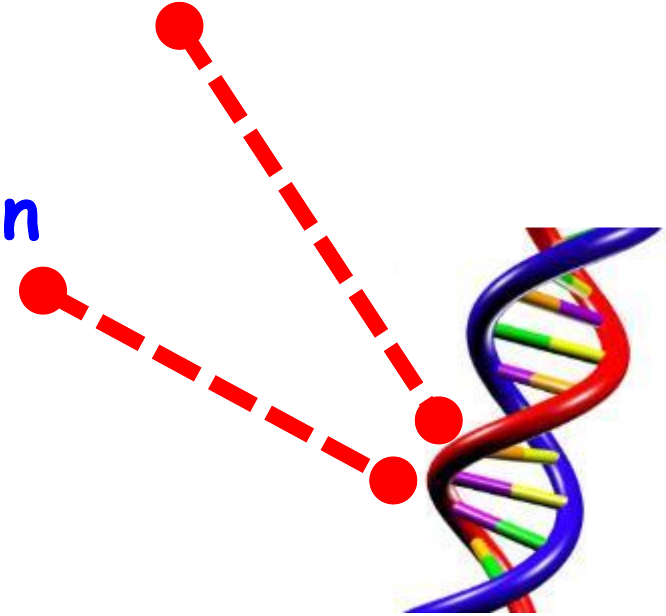
Why low call rates?

- Error at sampling
  - Lack of biological material
  - Conta
- Handling
  - Inapp
  - Issue
  - “Punge
- Lab erro
  - DNA extraction
  - Errors here are minimal


Main cause

Improving call rates over time

- Initial call rates – very poor
- Tag identified as main issue
  - Preservative
- Type of tag changed
  - Double the volume of preservative
- Notable improvement in call rate



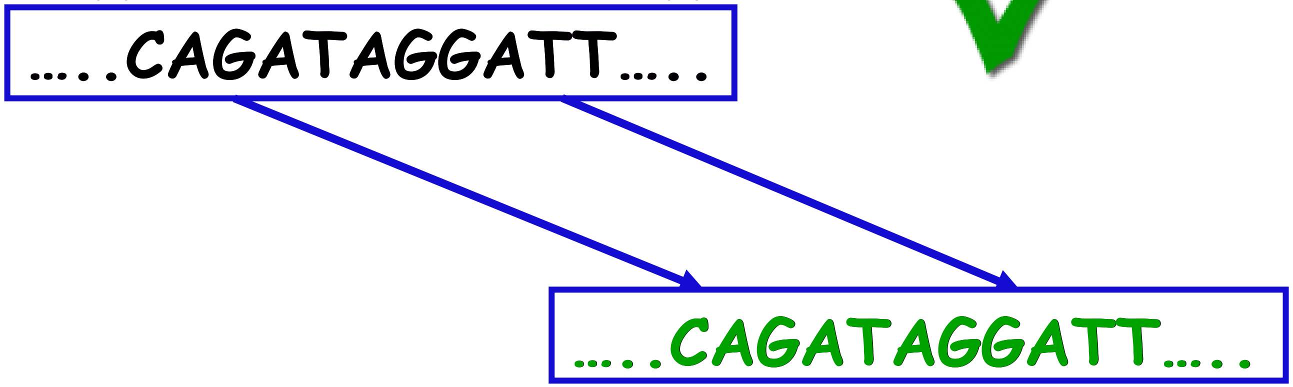
Parentage assignment

Gender determination

Determining Parentage

Sire

…..TCACCGCTGAG…..



…..CAGATAGGATT…..

✓

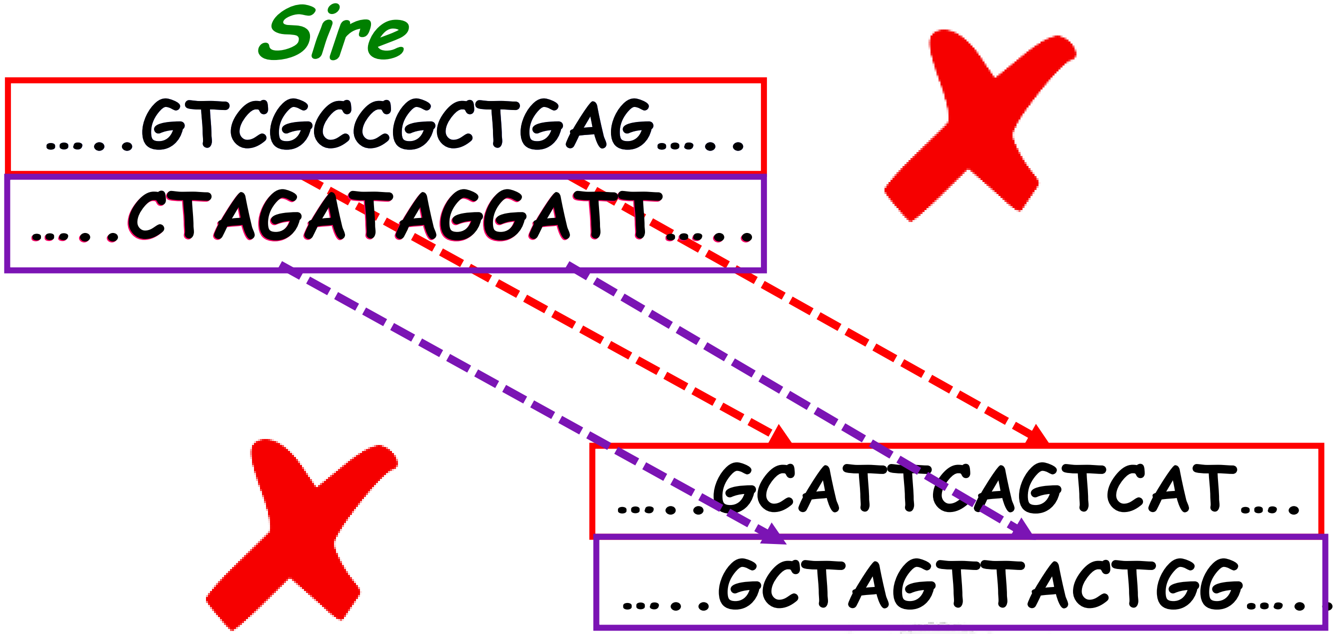
…..CAGATAGGATT…..

…..GTTAGCCTGTCA …..

Offspring

Determining Parentage

Sire



…..GTCGCCGCTGAG…..

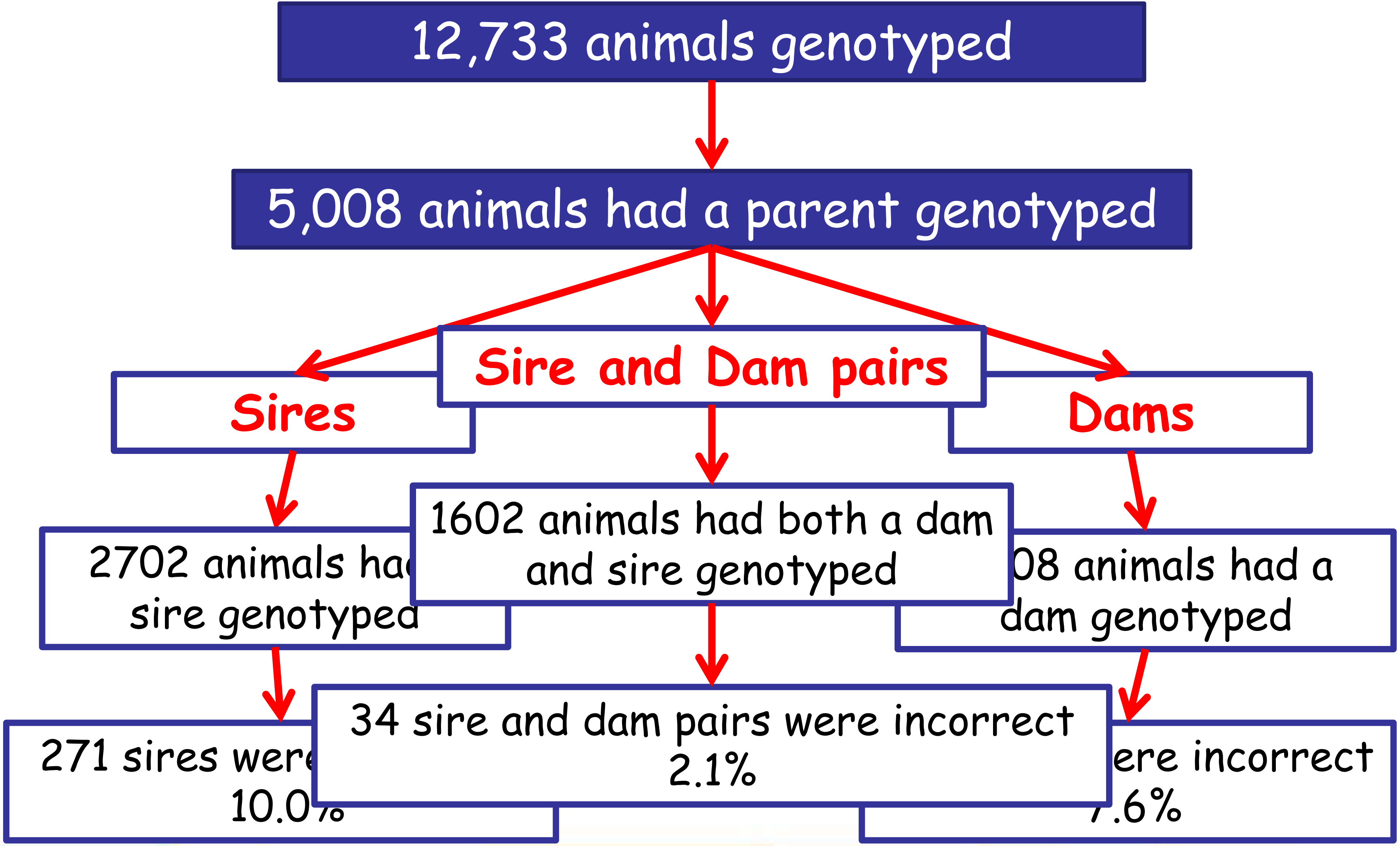
…..CTAGATAGGATT…..

…..GCATTCAGTCAT….

…..GCTAGTTACTGG…..

Offspring

Parentage



12,733 animals genotyped

5,008 animals had a parent genotyped

Sires

Sire and Dam pairs

Dams

2702 animals ha
sire genotyped

1602 animals had both a dam
and sire genotyped

08 animals had a
dam genotyped

271 sires were
10.0

34 sire and dam pairs were incorrect
2.1%

ere incorrect
.6%

Compared to Irish beef cattle

Parentage errors

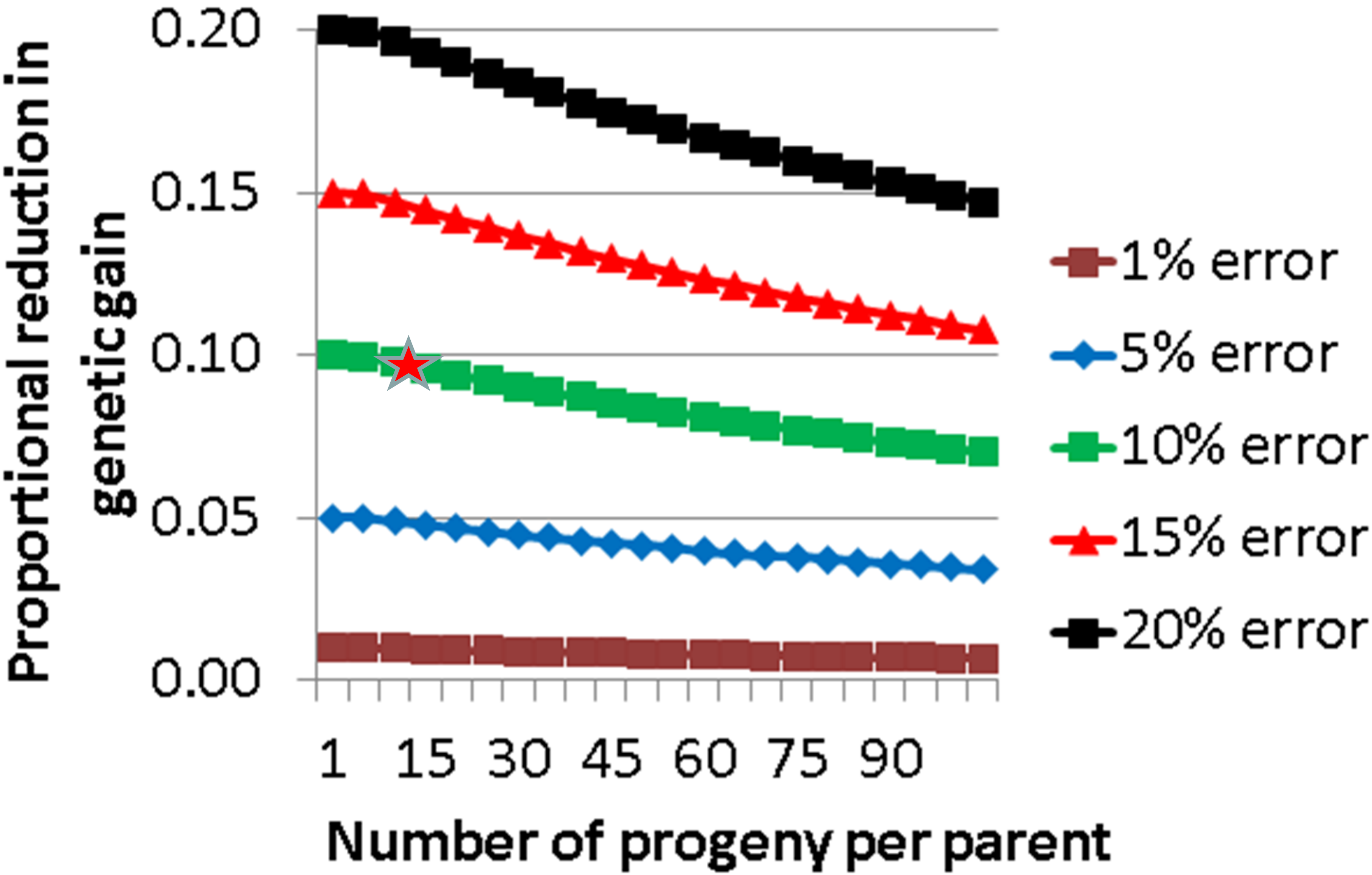
- **Sires**
  - 44,491 sires were incorrect 13.28%
- **Sire and Dam pairs**
  - 5,424 sire and dam pairs were incorrect 3.13%
- **Dams**
  - 13,529 dams were incorrect 10.18%

D Purfield

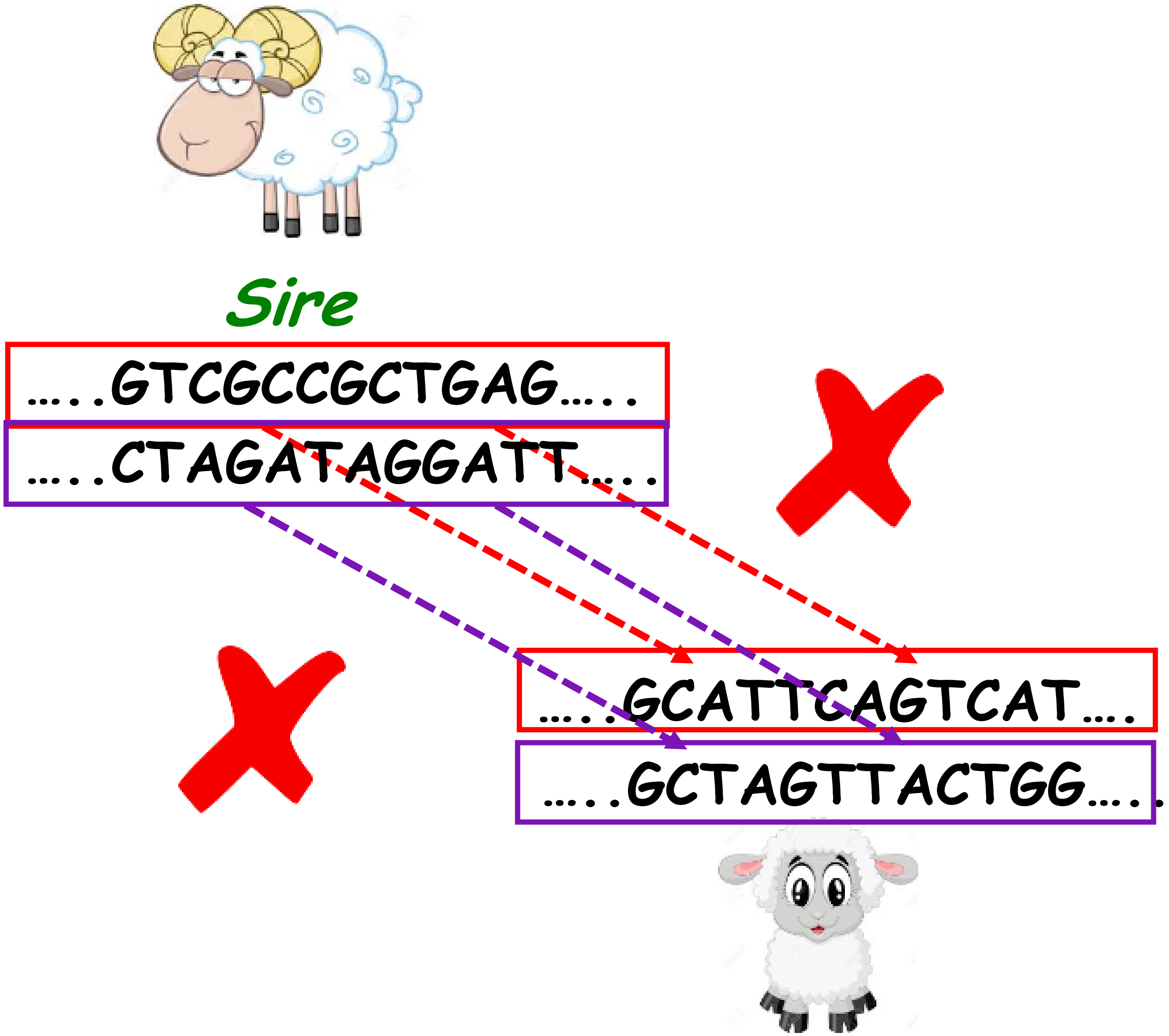
How could these be wrong?

- Sampling error
  - Wrong animal sampled
  - Incorrect assignment of DNA ID
- Escapees at mating
- Lamb mismatch at birth
- Different parents recorded in flockbook and Sheep Ireland database

Impact on genetic gain



Parentage resolution



Sire

…..GTCGCCGCTGAG…..

…..CTAGATAGGATT…..

…..GCATTCAGTCAT….

…..GCTAGTTACTGG…..

Offspring

Parentage resolution

Database

"Sire 1" …..ATTCGGGCTGTG…..

"Sire 2" …..CAGATAGGATTC…..

"Sire 3" …..GTCACCGCTGAG…

"Sire 4" …..GCATTCAGTCAT…..

…..GCATTCAGTCAT….

…..GCTAGTTACTGG…..

Offspring

Parentage resolution

Database

"Sire 1" …...ATTCGGGCTGTG…...

"Sire 2" …...CAGATAGGATTC…...

"Sire 3" …...GTCACCGCTGAG…

"Sire 4" …...GCATTCAGTCAT…...

✗

…...GCATTCAGTCAT…..

…...GCTAGTTACTGG…...

Offspring

Parentage resolution

Database

“Sire 1” …..ATTCGGGCTGTG…..

“Sire 2” …..CAGATAGGATTC…..

"Sire 3" …..GTCACCGCTGAG…

“Sire 4” …..GCATTCAGTCAT…..

…..GCATTCAGTCAT….

…..GCTAGTTACTGG…..

Offspring

Parentage resolution

Database

"Sire 1" .....ATTCGGGCTGTG.....

"Sire 2" .....CAGATAGGATTC.....

"Sire 3" .....GTCACCGCTGAG...

"Sire 4" .....GCATTCAGTCAT.....

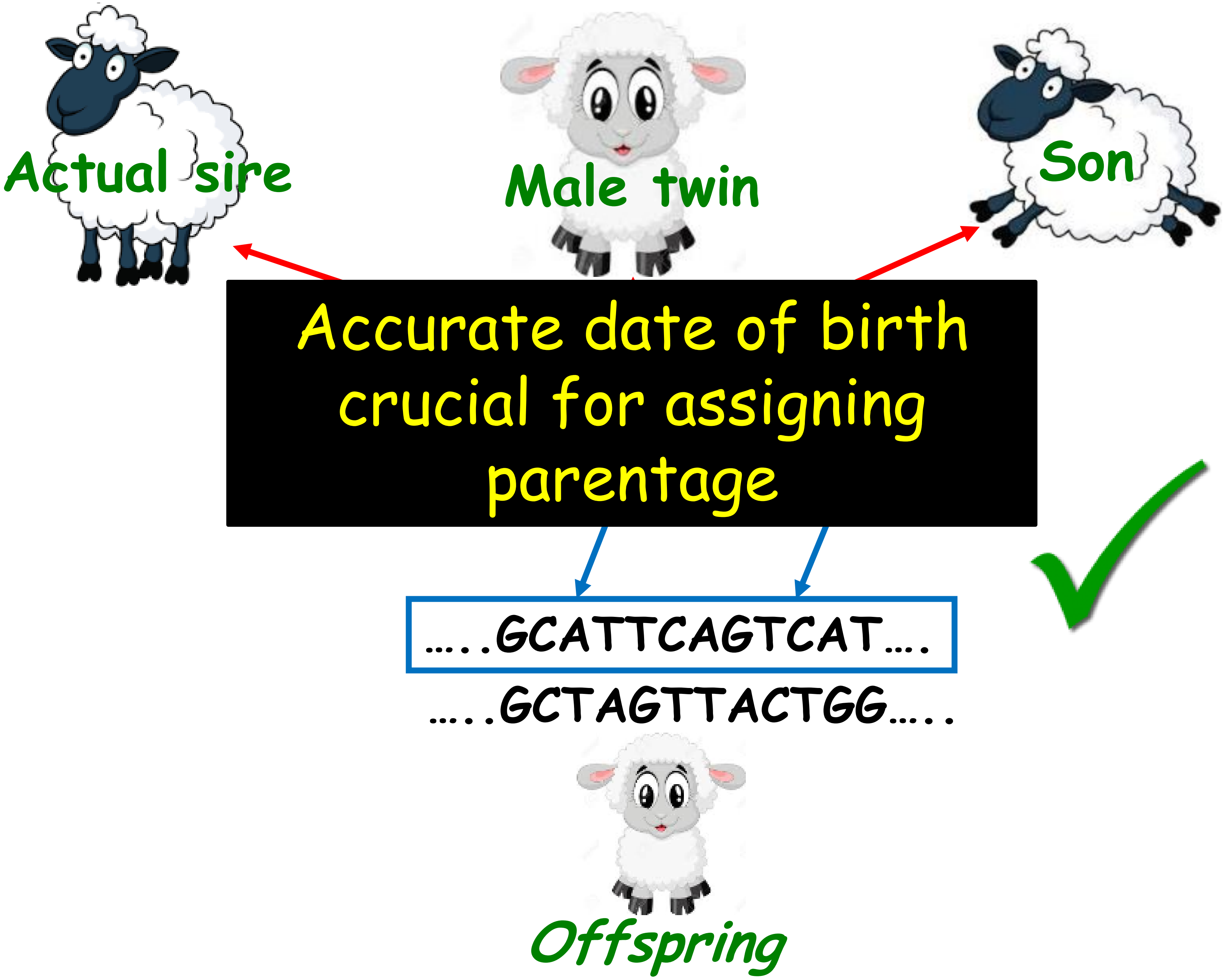
.....GCATTCAGTCAT.....

.....GCTAGTTACTGG.....

✓

Offspring

But…



Actual sire

Male twin

Son

Accurate date of birth crucial for assigning parentage

…..GCATTCAGTCAT….

…..GCTAGTTACTGG…..

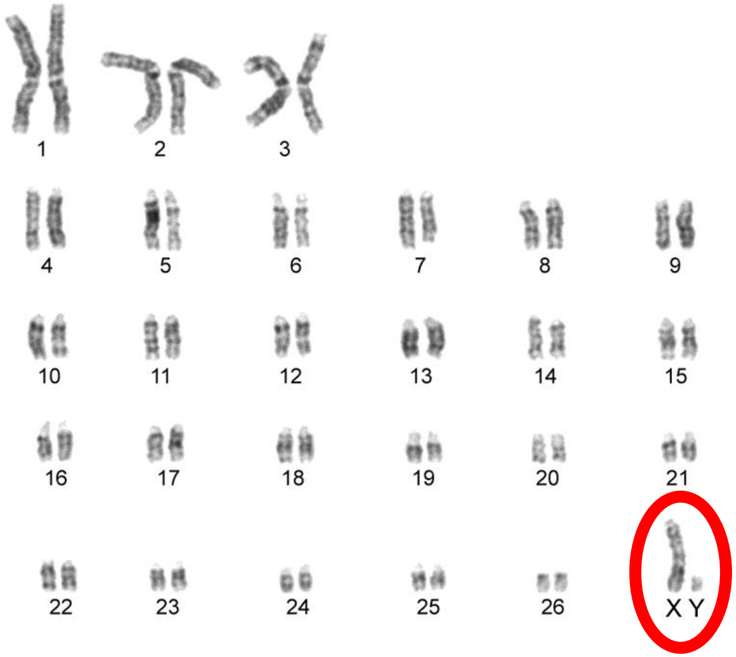
✓

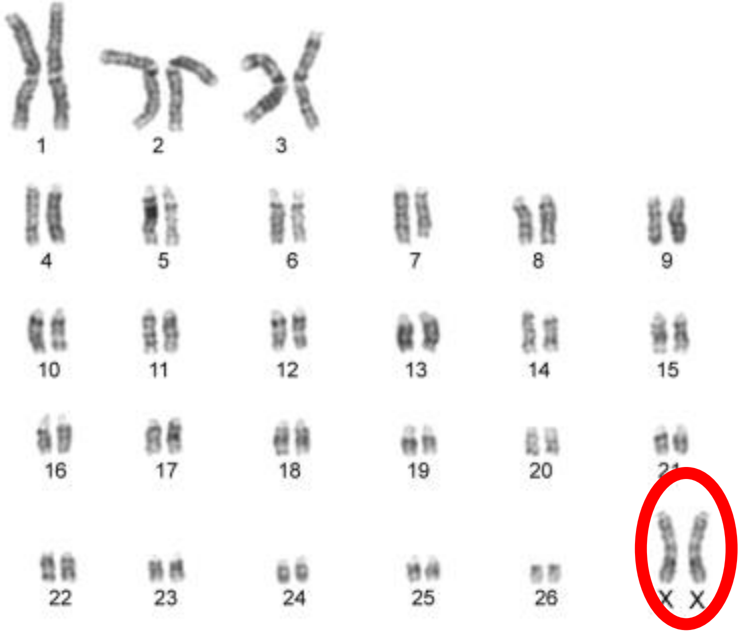
Offspring

Parentage resolution

- Correcting pedigree in flockbooks
  - Option – resampling
  - Breed societies – changing pedigree
    - Issuing of new pedigree certificates?
- Needs to be discussed
  - Clear approach

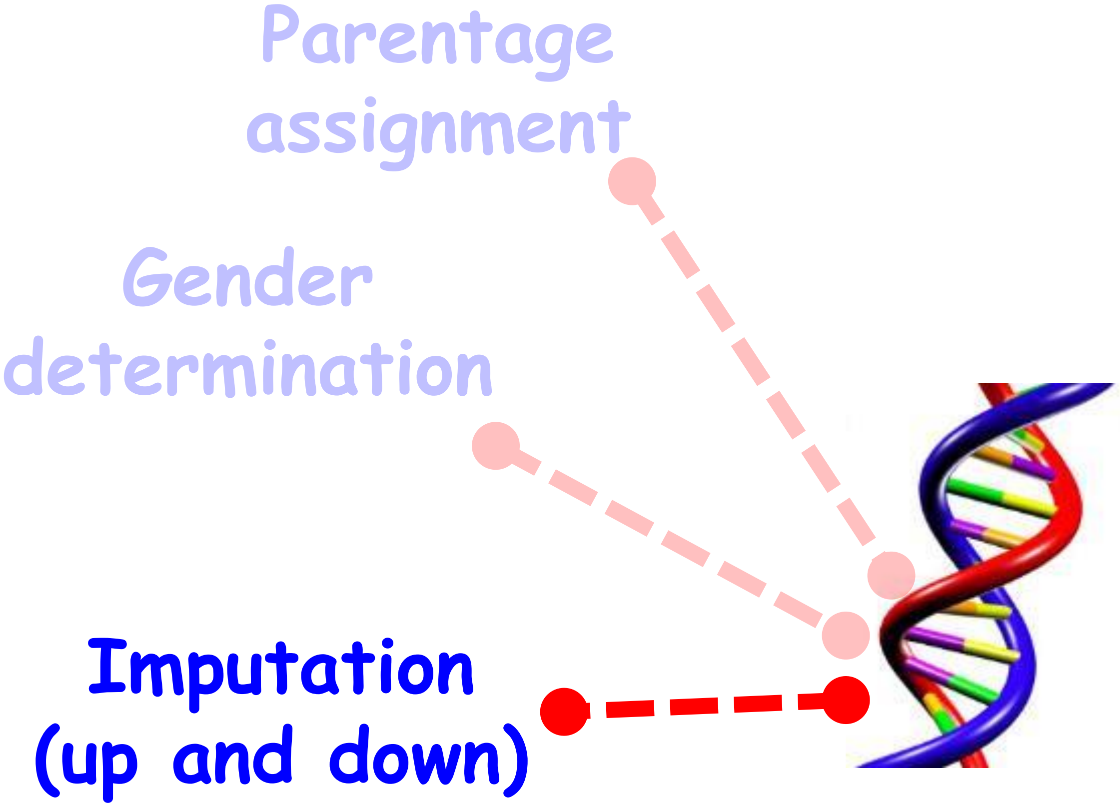
Gender differentiation





1938 males & 9076 females

All correct



Parentage assignment

Gender determination

Imputation (up and down)

Filling in the blanks

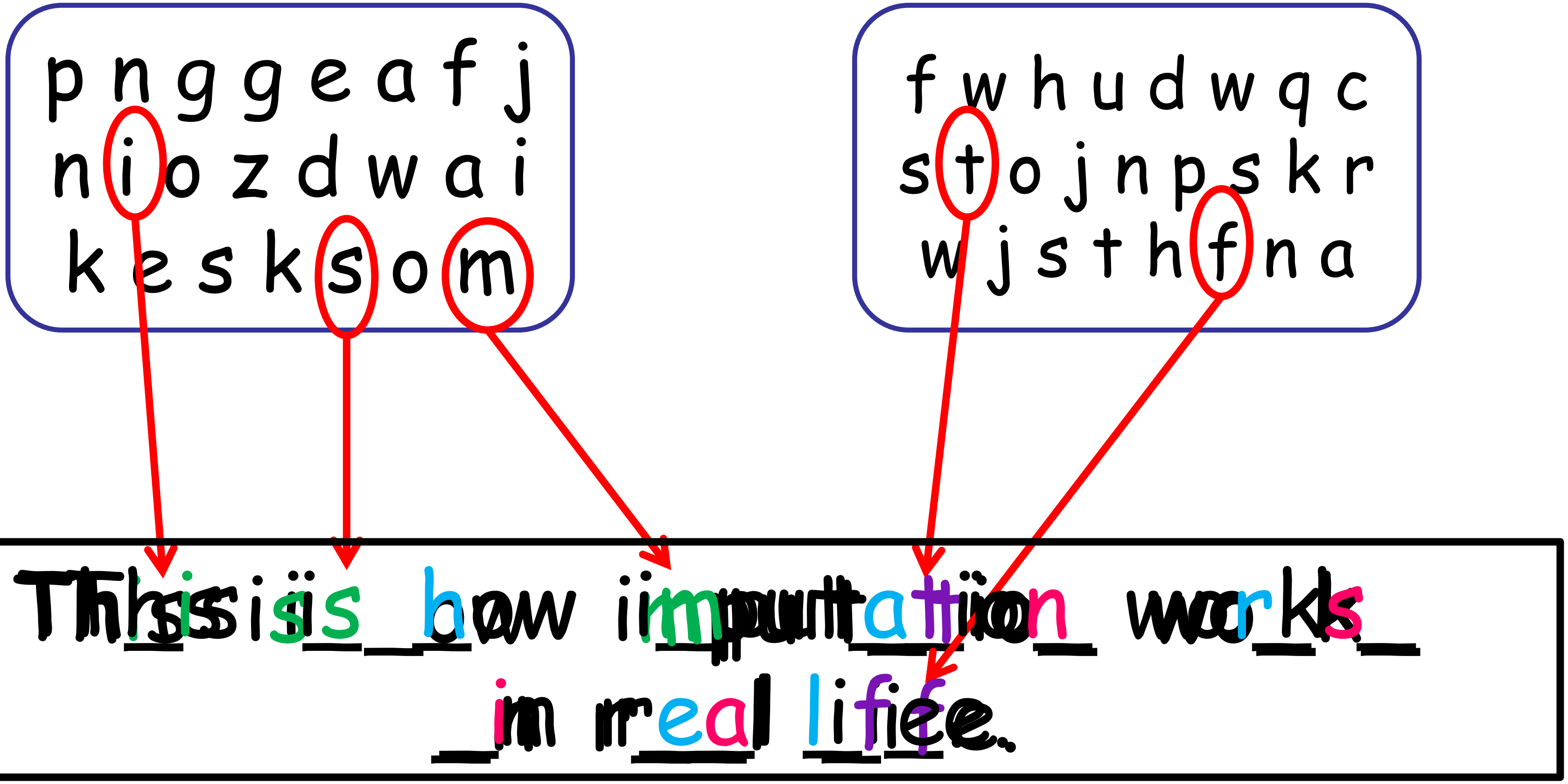
p n g g i e a f i
n i o z d w a i
k e s k s o m

Th_s _ _ow i_put_ro_ wo_k_
_n r__l _i_e

f i w h u d w q k c
i s t o j n p s k r
w j s t h f n a

The Irish Agriculture and Food Development Authority

Filling in the blanks

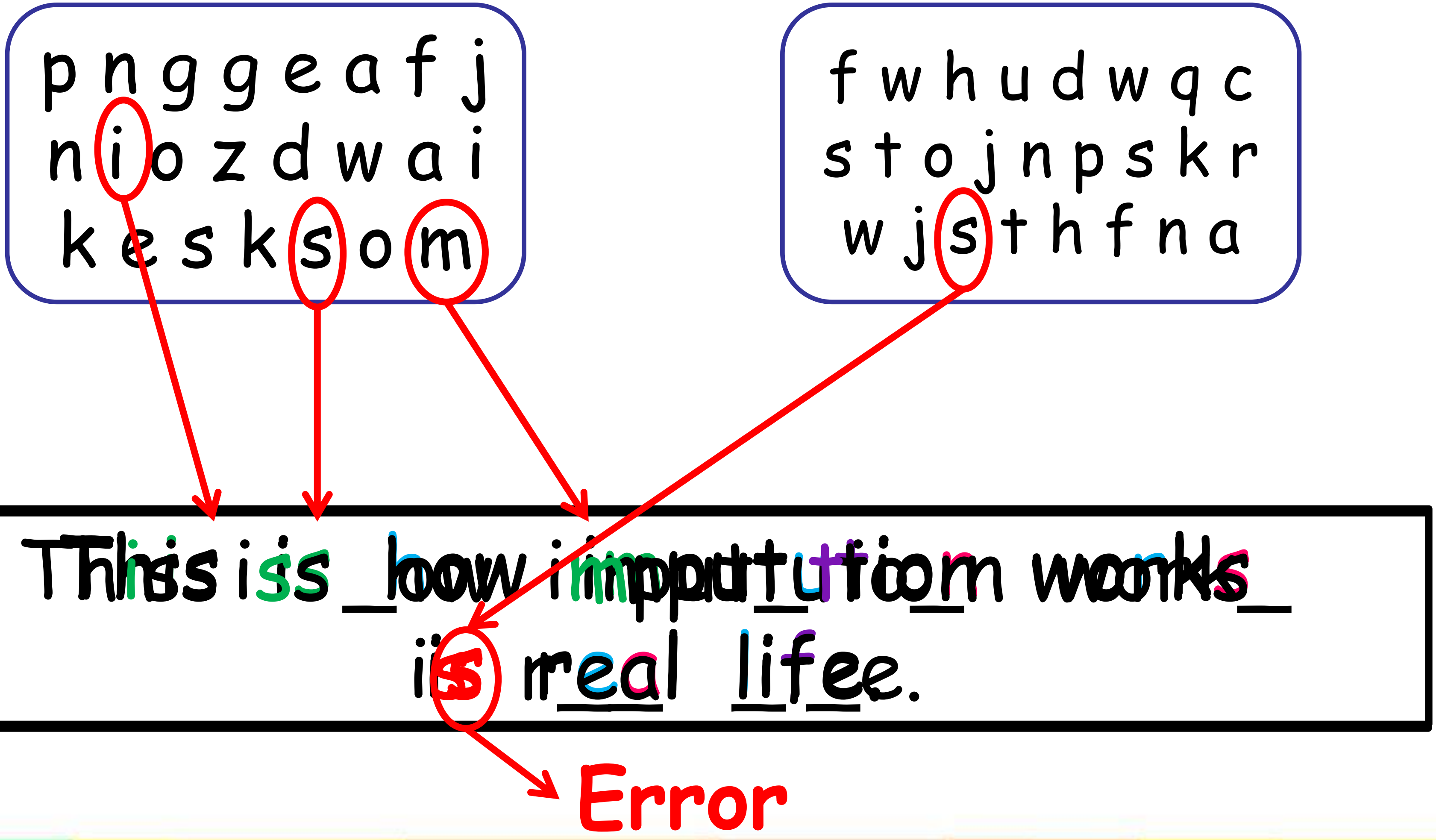


p n g g e a f j
n i o z d w a i
k e s k s o m

f w h u d w q c
s t o j n p s k r
w j s t h f n a

This is how imputation works in real life.

Filling in the blanks



p n g g e a f j
n i o z d w a i
k e s k s o m

f w h u d w q c
s t o j n p s k r
w j s t h f n a

This is how imputation works is real life.

Error

Imputation

Sire

…..TCACCGCTGAG…..

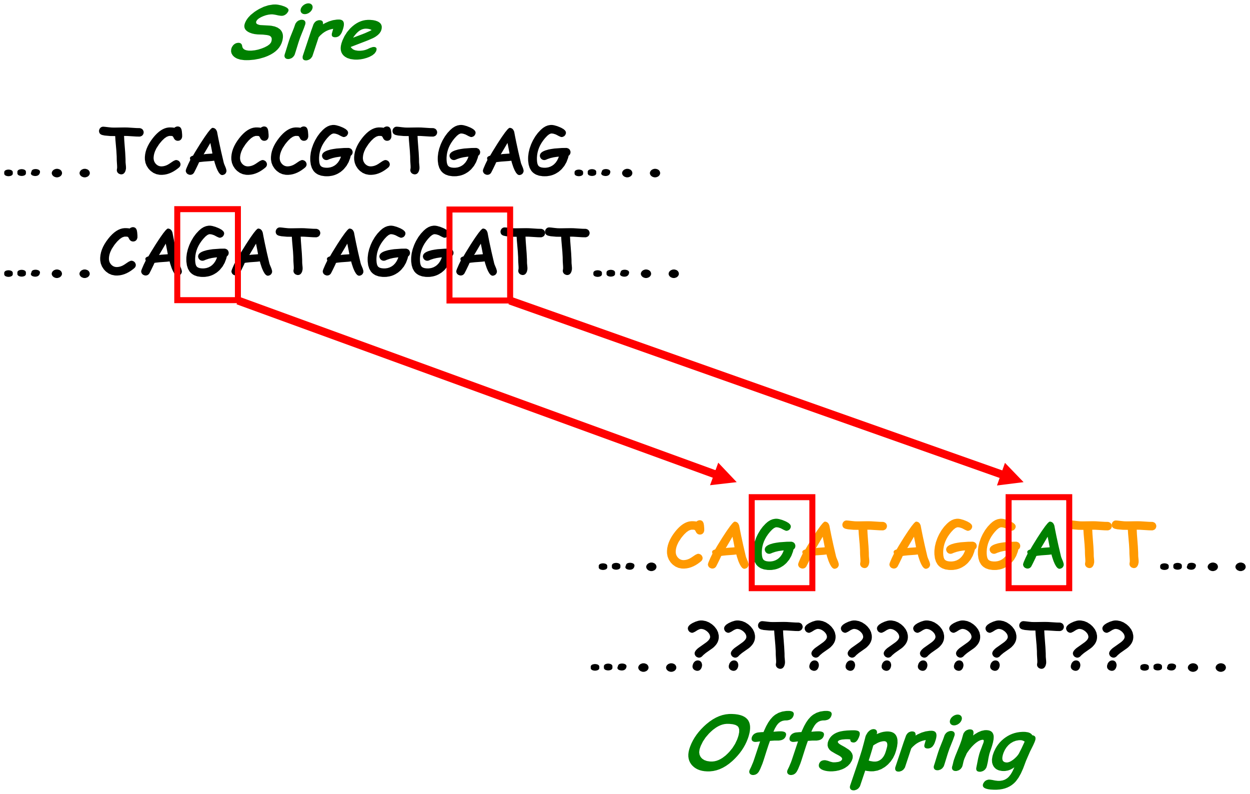
…..CAGATAGGATT…..

…..??G??????A??….

…..??T??????T??…..

Offspring

Imputation



Sire

…..TCACCGCTGAG…..

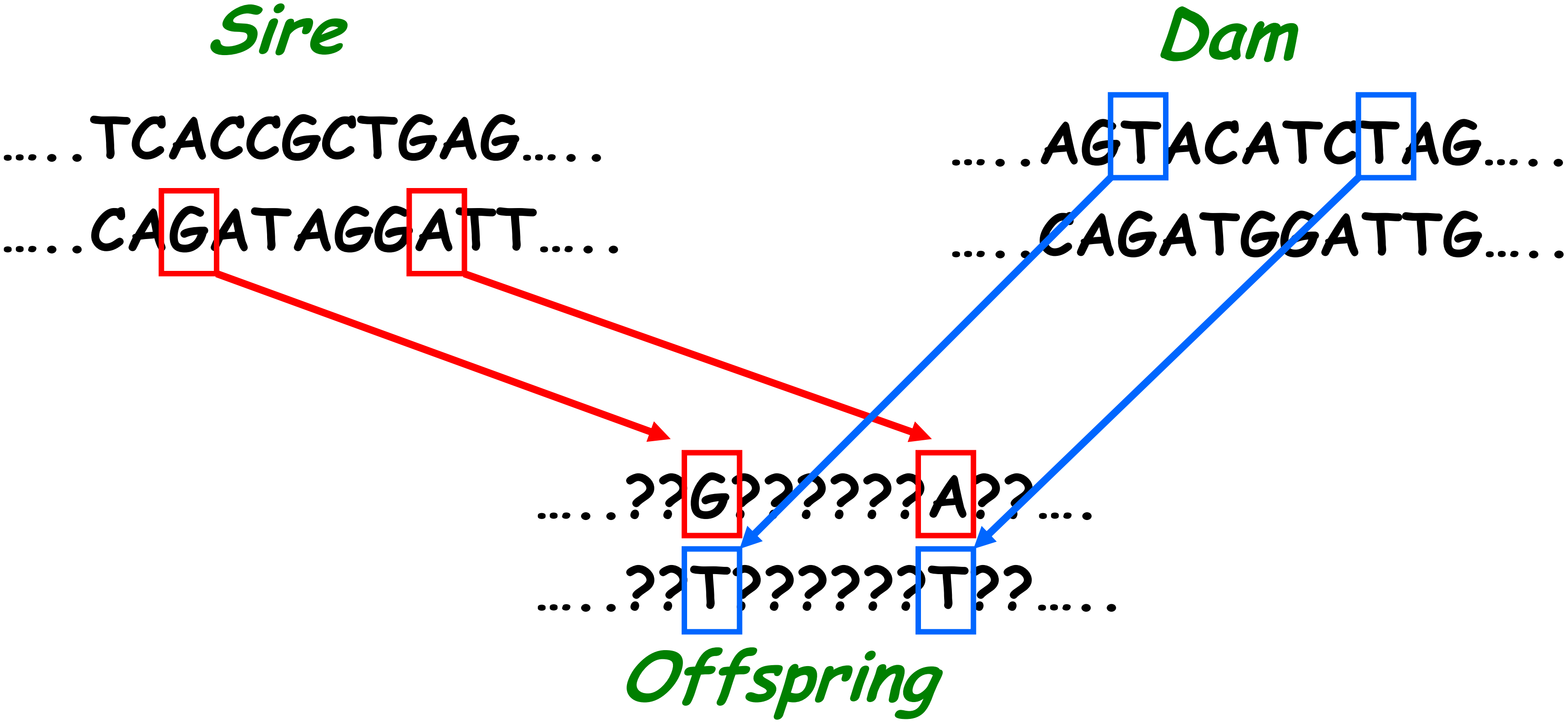
…..CAGATAGGATT…..

….CAGATAGGATT…..

…..??T??????T??…..

Offspring

Imputation



Sire

.....TCACCGCTGAG.....

.....CAGATAGGATT.....

Dam

.....AGTACATCTAG.....

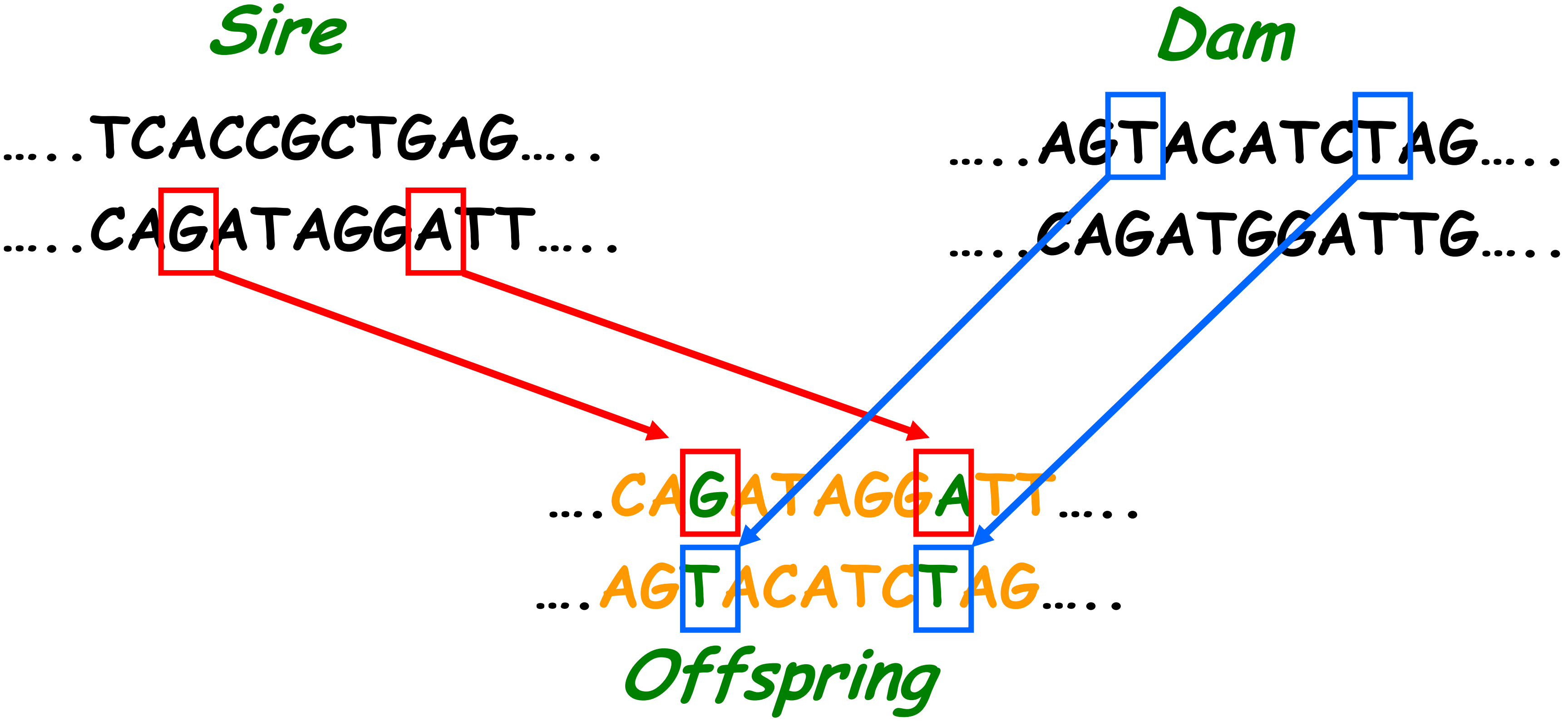
.....CAGATGGATTG.....

.....??G??????A??....

.....??T??????T??.....

Offspring

Imputation



Sire

.....TCACCGCTGAG.....
.....CAGATAGGATT.....

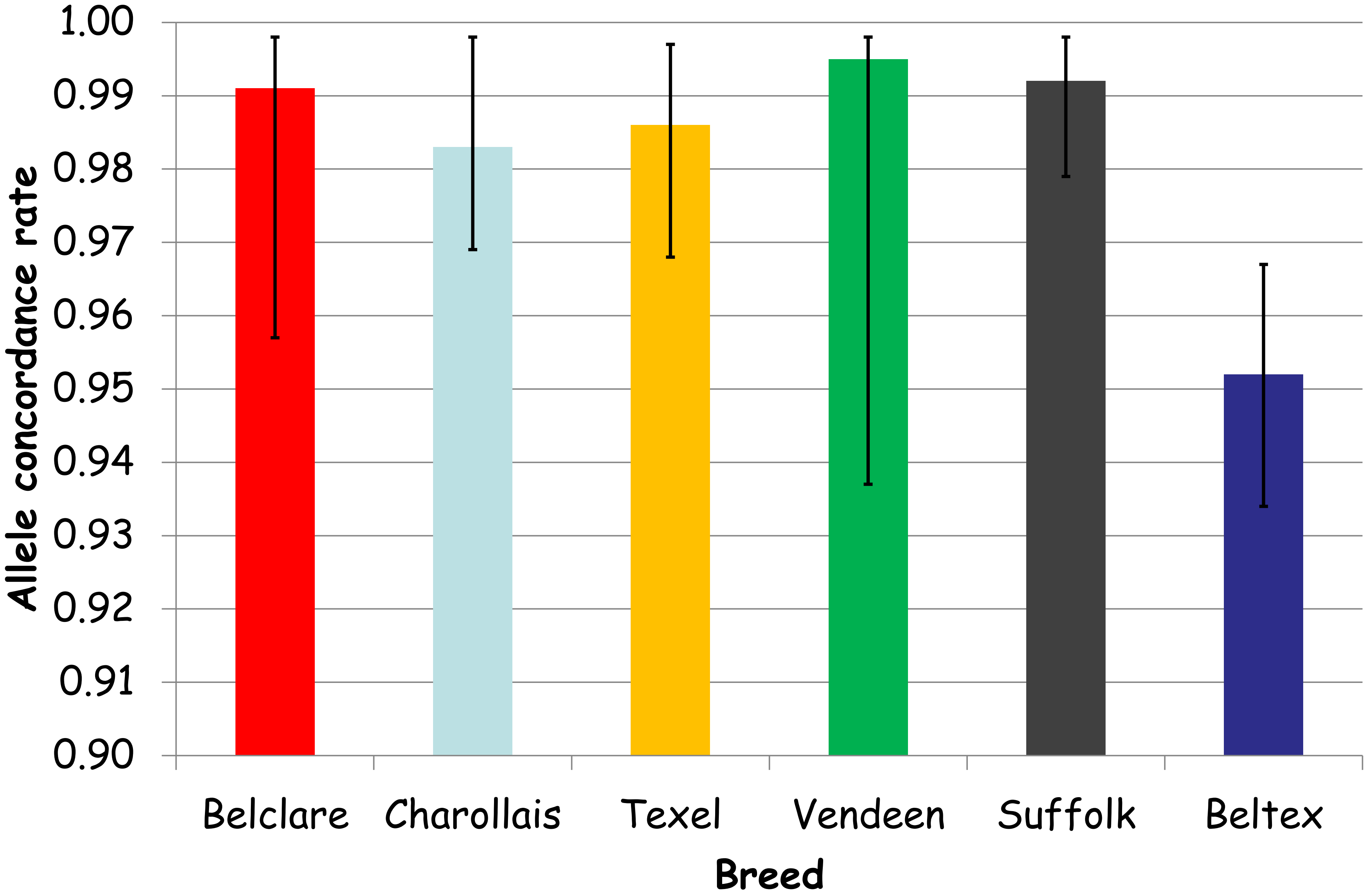
Dam

.....AGTACATCTAG.....
.....CAGATGGATTG.....

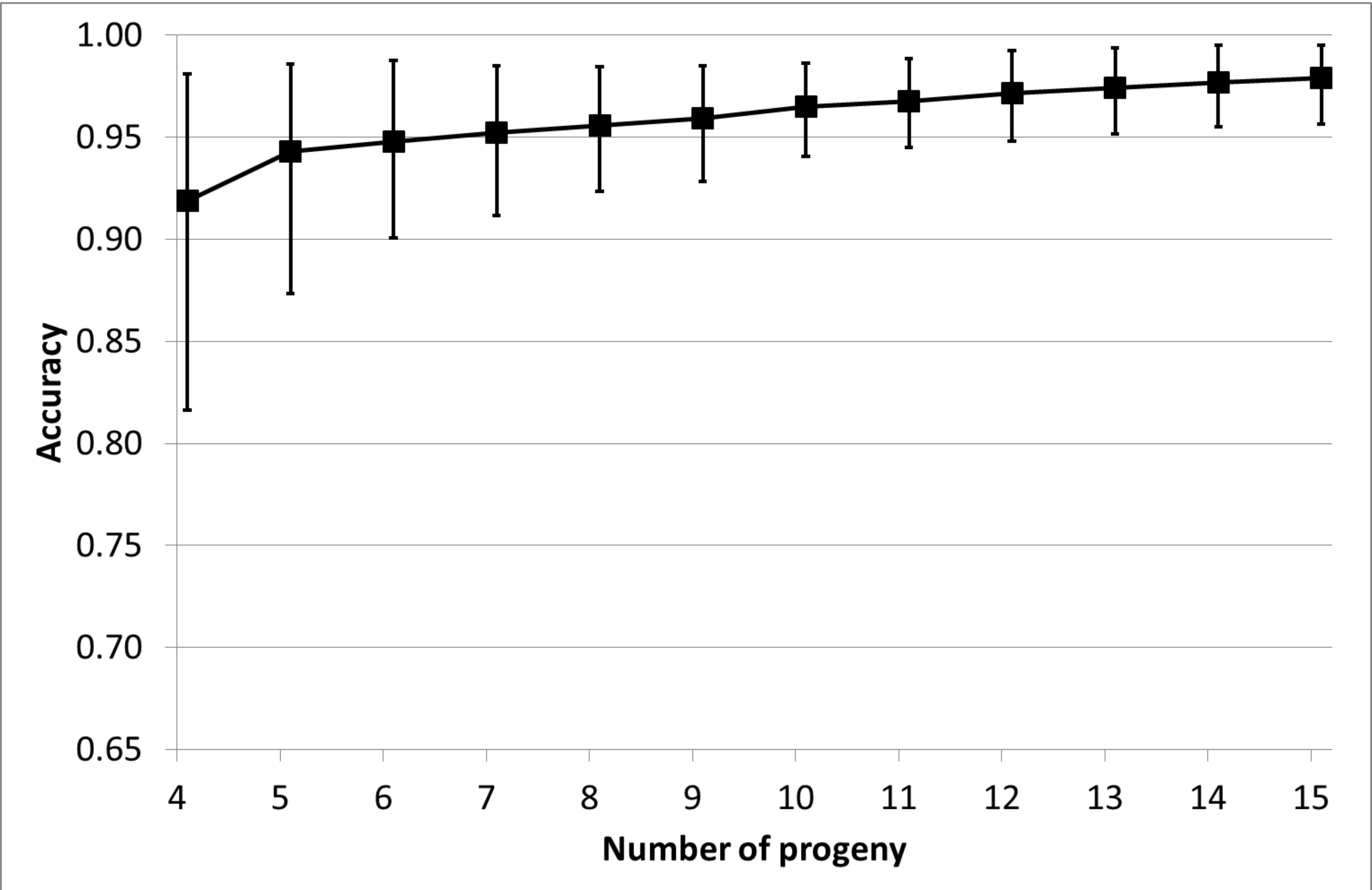
....CAGATAGGATT.....
....AGTACATCTAG.....

Offspring

Imputation accuracy

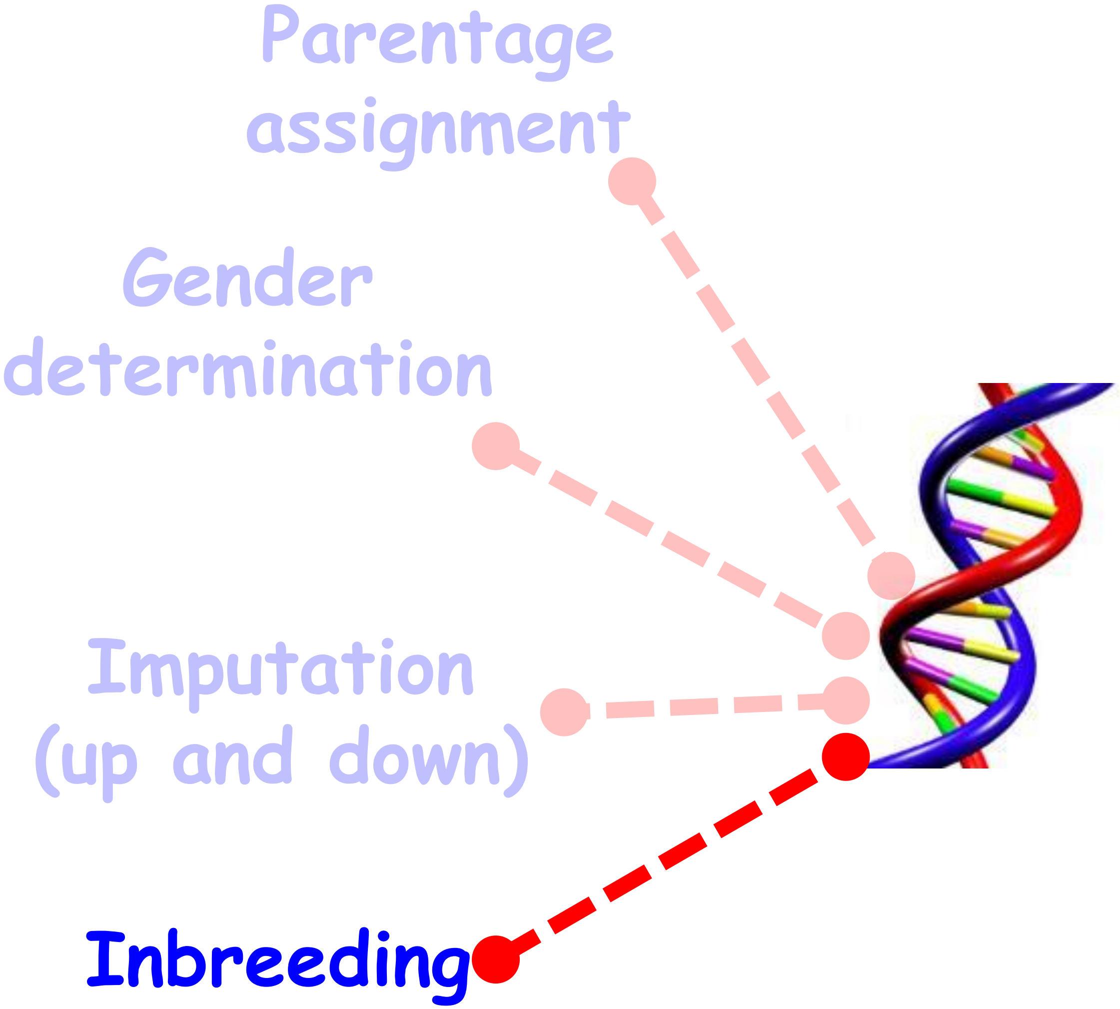


Back imputation



Reducing the cost of genotyping

- Fewer SNPs = reduced cost
- Develop lower density panels
  - 384 SNPs, 1 000, 2 000, 3 000, 6 000
- Using SNPs common between 50K and 15K platform - 11,322 SNPs
- Select SNPs – using various methods
- Impute to a higher density



Parentage assignment

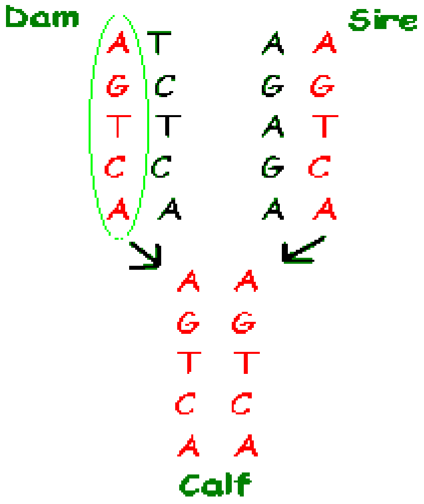
Gender determination

Imputation (up and down)

Inbreeding

Genomic Inbreeding

Using DNA to tell you how **inbred** an animal is



How?

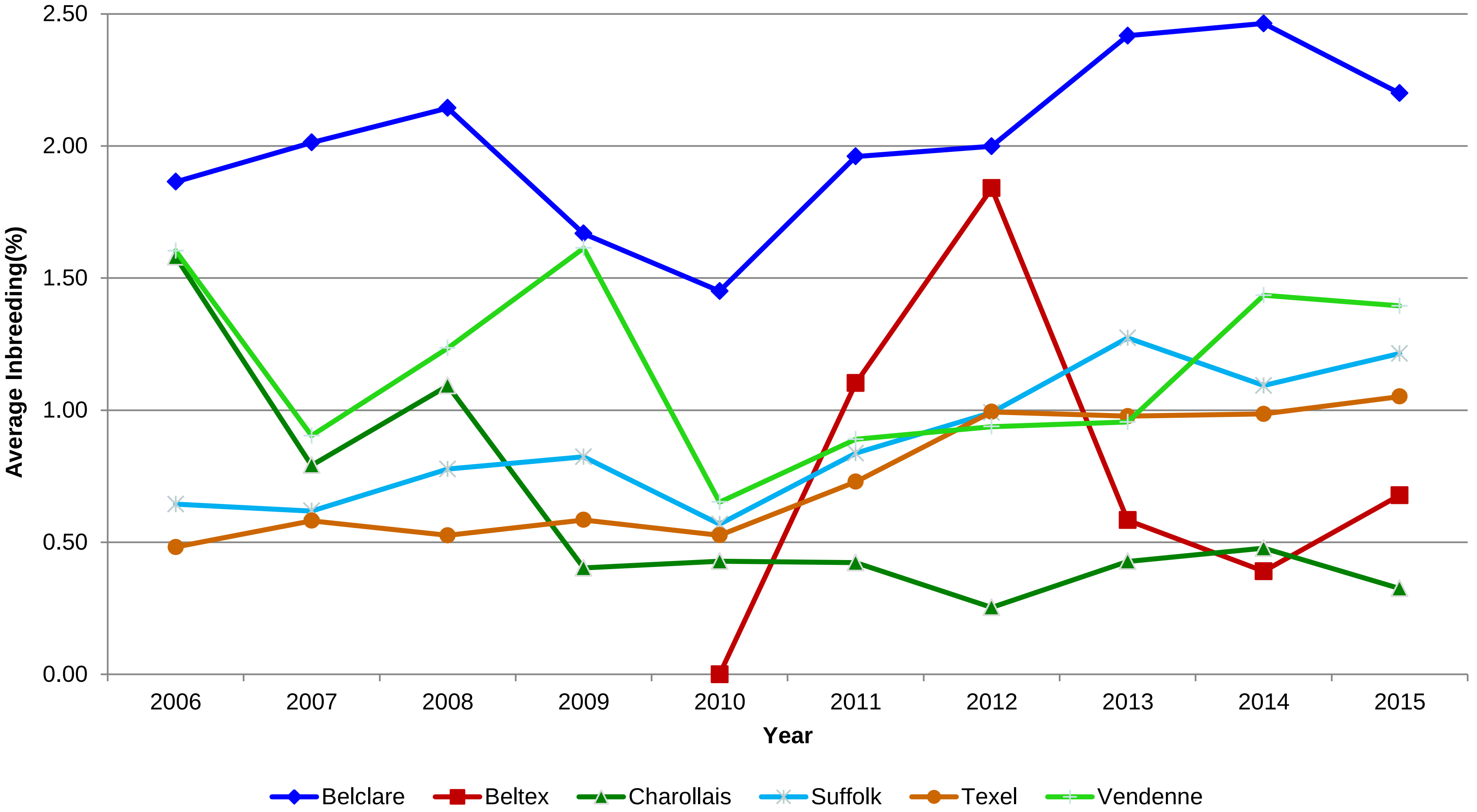
- Measure of double copy genotypes in an animal

Why genomic over pedigree?

- More accurate than pedigree recording
- Mendelian sampling-not always the same chunks of DNA inherited from parents
- Can be used to inform on future mating decision

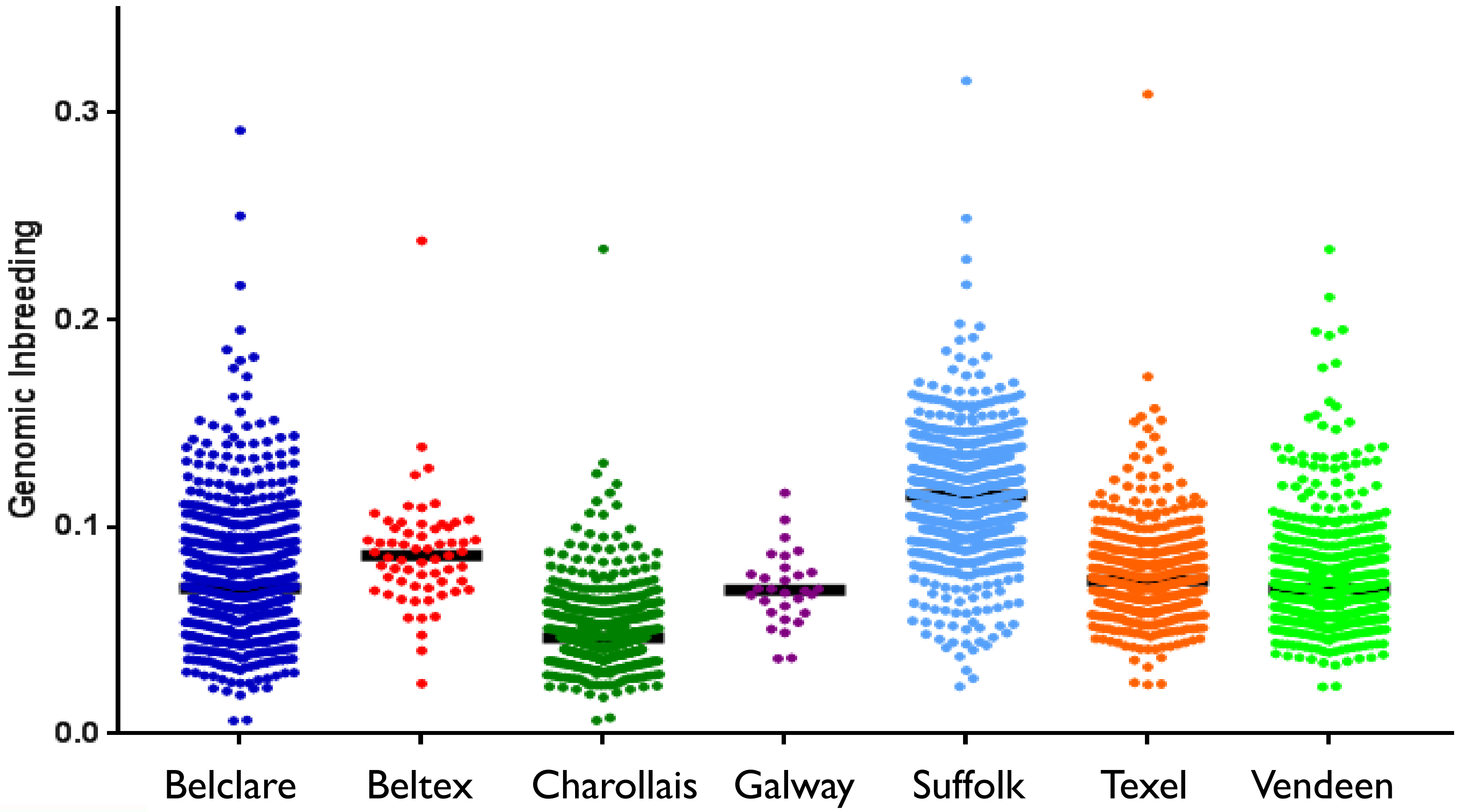
Pedigree Inbreeding Trends

Complete generation equivalents >=3



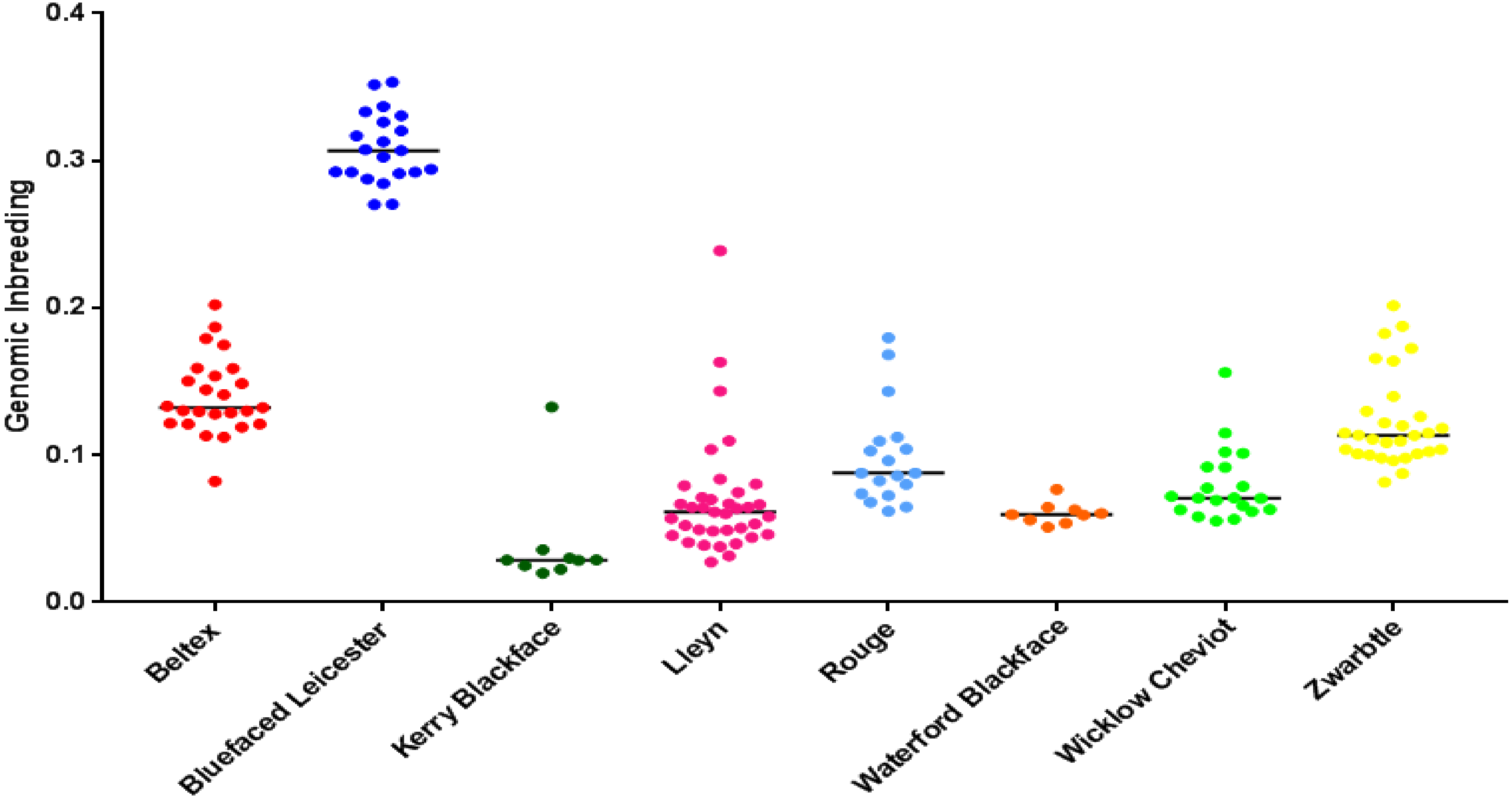
Genomic Inbreeding

OvineSNP50 panel

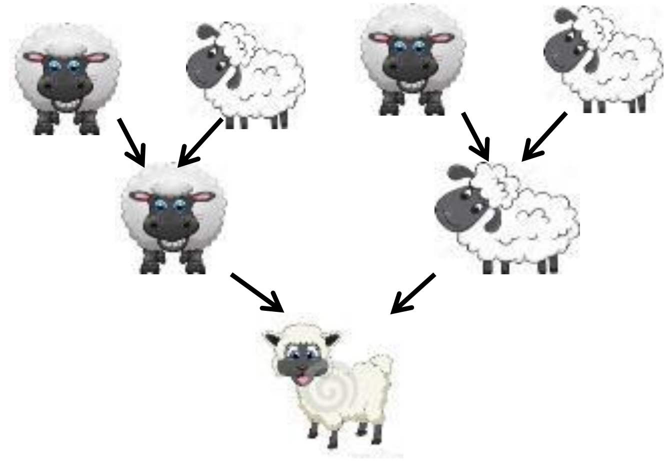


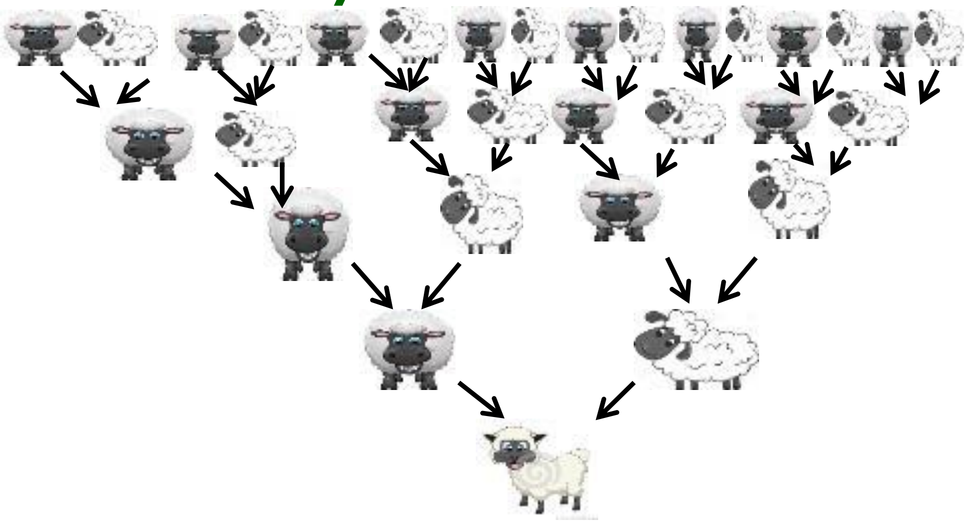
Genomic Inbreeding

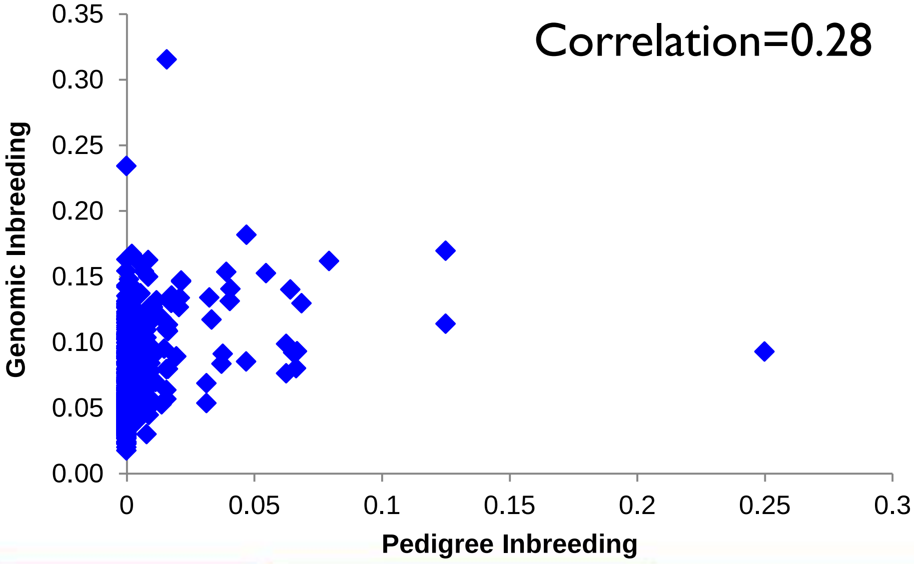
HD genotyping panel



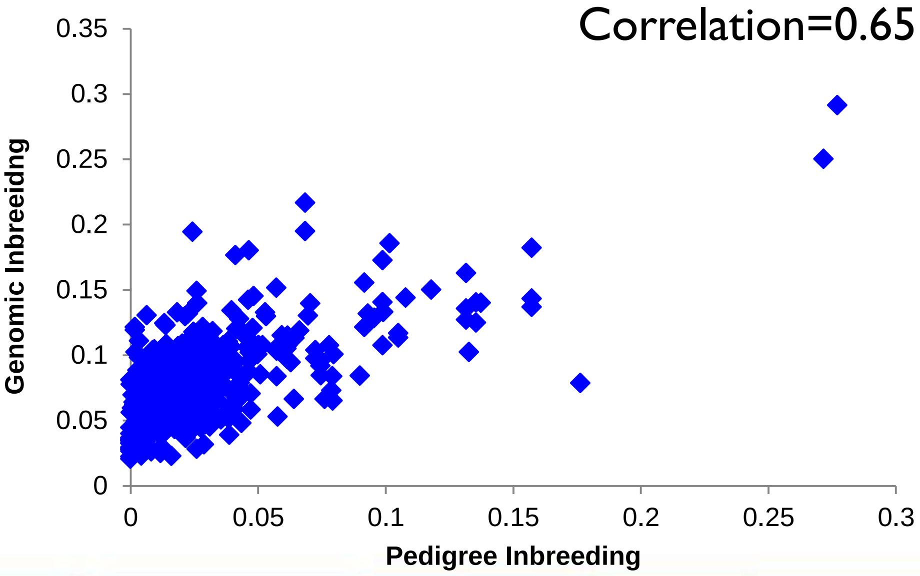
Importance of back ancestry data







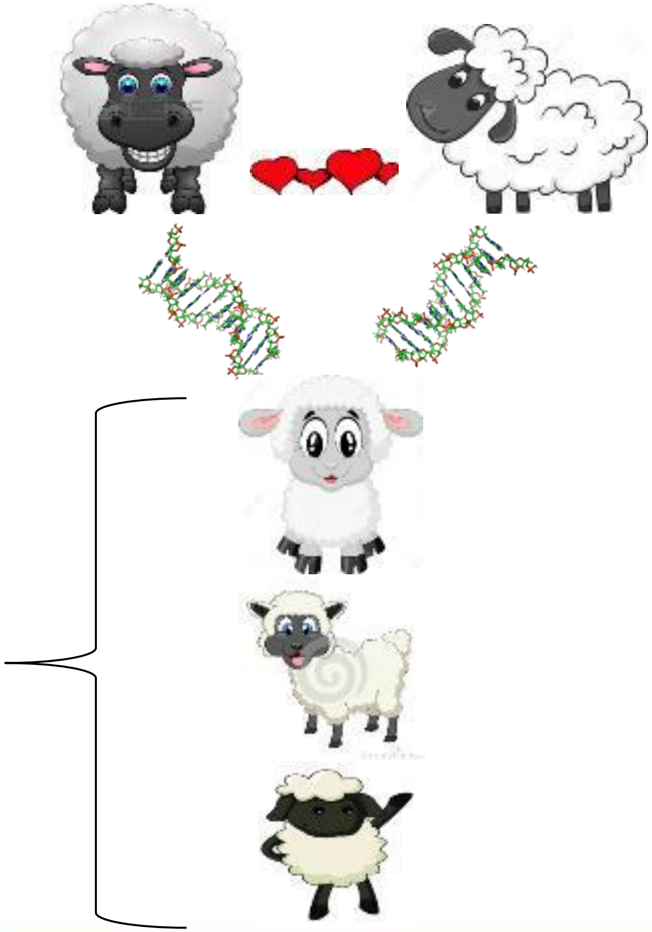
Correlation=0.28



Correlation=0.65

Mendelian Sampling + Inbreeding

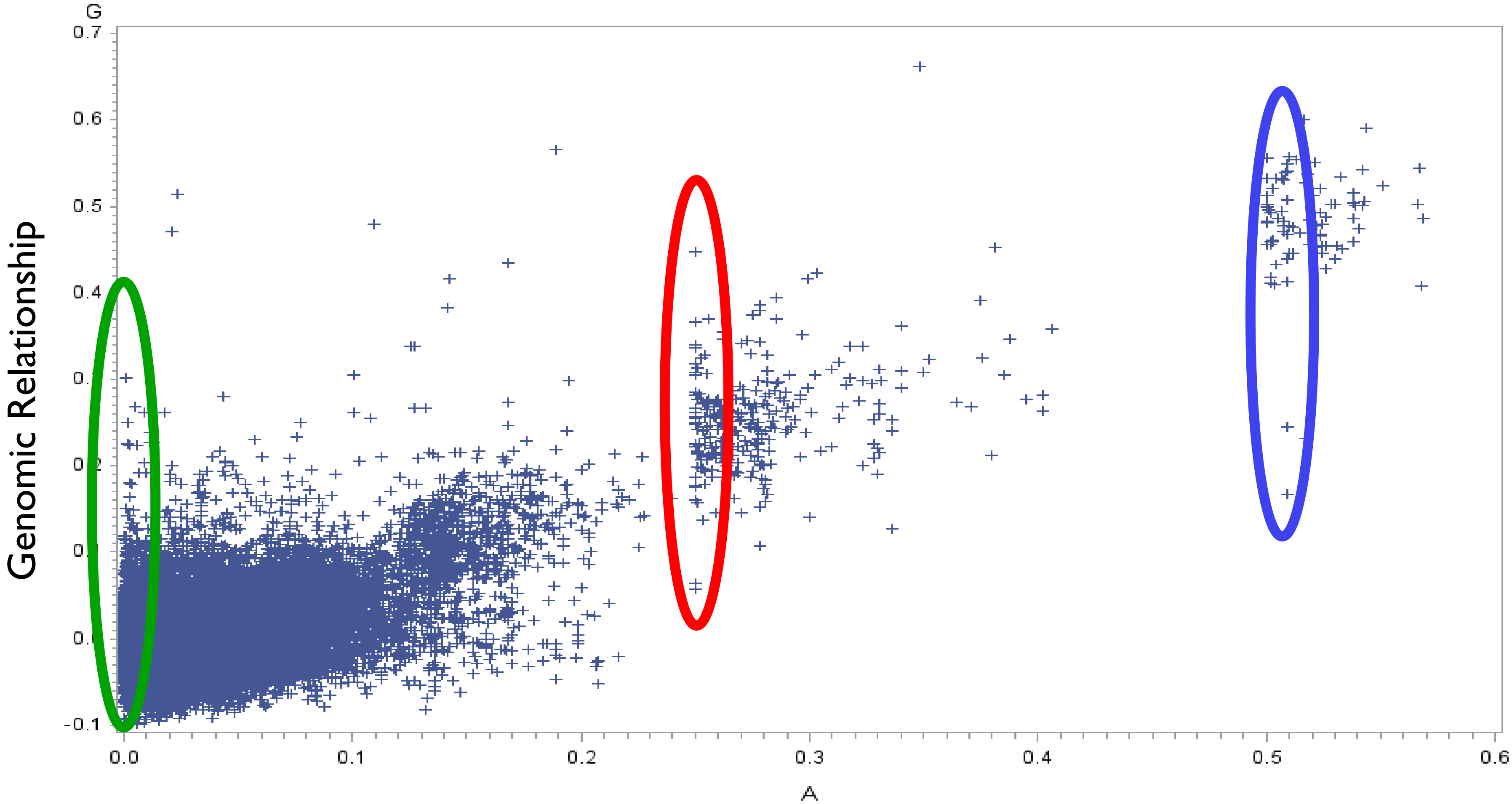
Mendelian Sampling:not always the same DNA inherited from parents



Full Sibs

Pedigree Inbreeding	Genomic Inbreeding
0.17%	5.48%
0.17%	6.46%
0.17%	12.15%

Genomic versus Pedigree Relationship



Pedigree Relationship

Parentage assignment

Gender determination

Imputation (up and down)

Inbreeding

Monitoring major genes

Monitoring lethal genes

Major genes

- Prolificacy genes
- BMP15 Xb → associated with Belclare breed
- 1 copy increased ovulation rate
- 2 copies sterile

Genotyped	1 copy
All population	0.07%
Belclare	9.78%

+0.53 lambs born

Major genes - GDF8

2 copy

Major genes - GDF8

Population	2 copy	1 copy	0 copy
All breeds	43%	12%	45%
Beltex	0%	2%	98%
Vendeen	100%	0%	0%

Muscle Scan (mm)	0.00	0.71	1.18

Major genes

- **Known Diseases**
- Spider Lamb
- McArdle disease
- Batten disease

Absent

- **Others**
- Yellow fat
- Superior milk production
- Meat tenderness

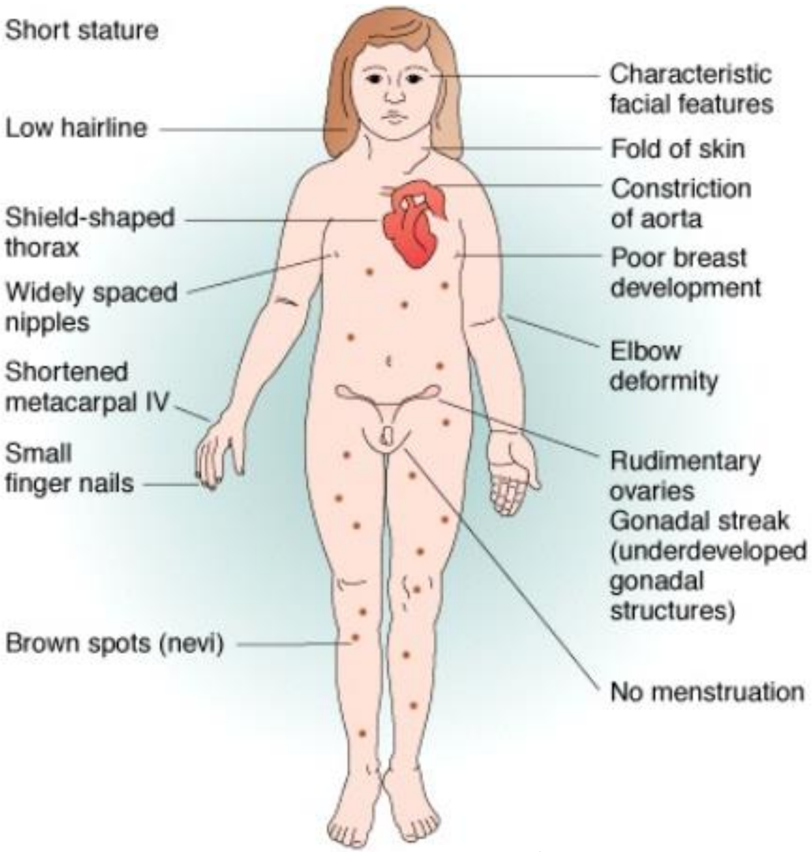
Others???

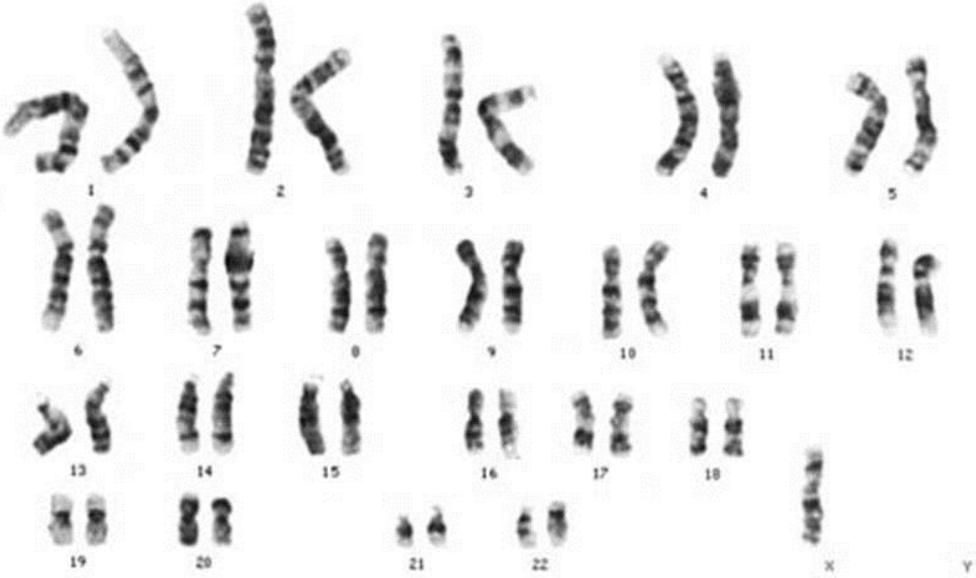
Over or undershot jaw

Blue Texels

Entropion – inverted eyelids

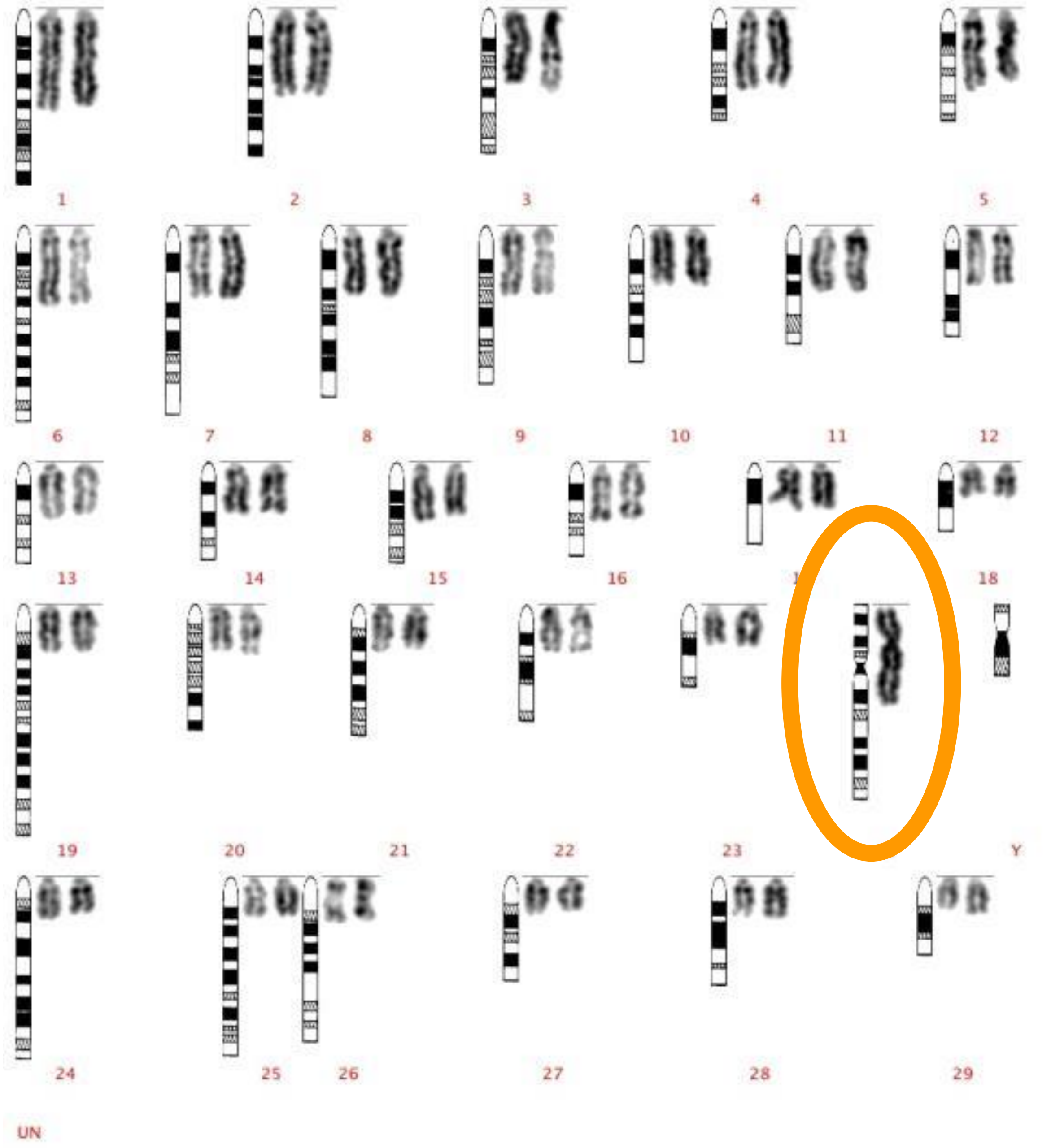
Turner female

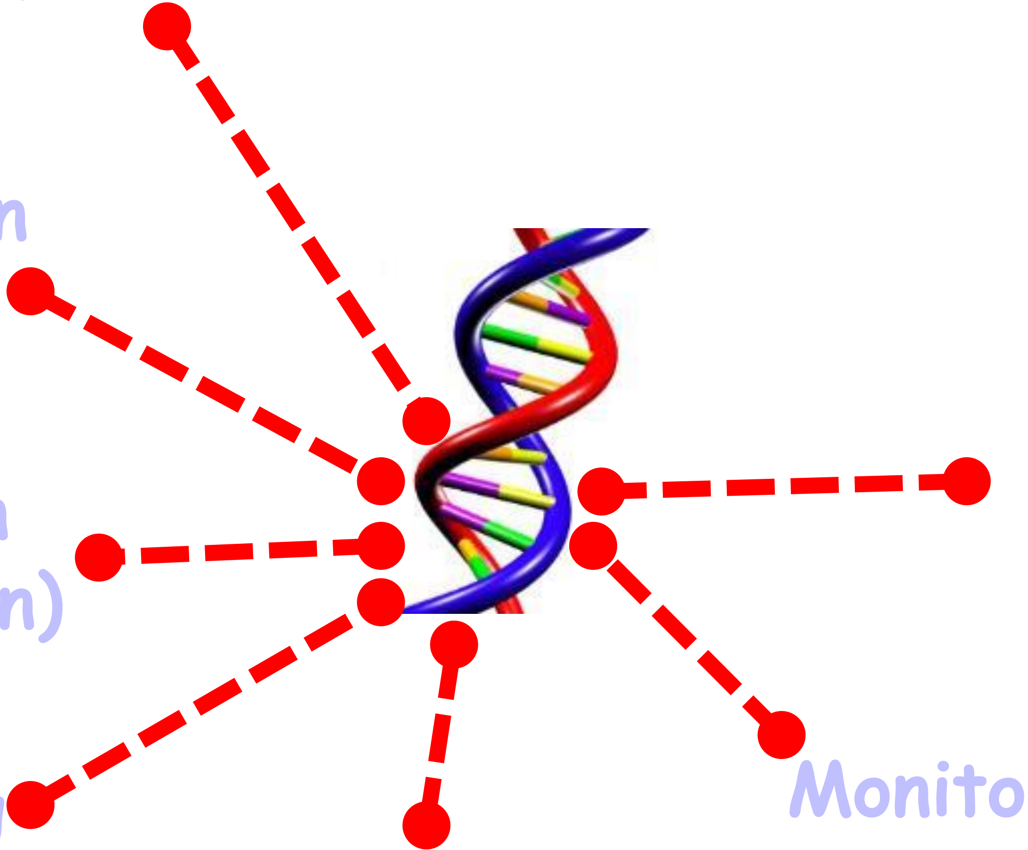




1 in 2500 in humans

Turner syndrome in the cow





Parentage assignment

Gender determination

Imputation (up and down)

Inbreeding

Monitoring major genes

Monitoring lethal genes

Scrapie

Scrapie

- 5 nucleotides in PrP gene
  - 3 amino acid changes
  - • Codon 136: alanine (A) or valine (V)
  - • Codon 154: arginine (R) or histidine (H)
  - • Codon 171: glutamine (Q), arginine (R) or histidine (H)

Scrapie on 50K

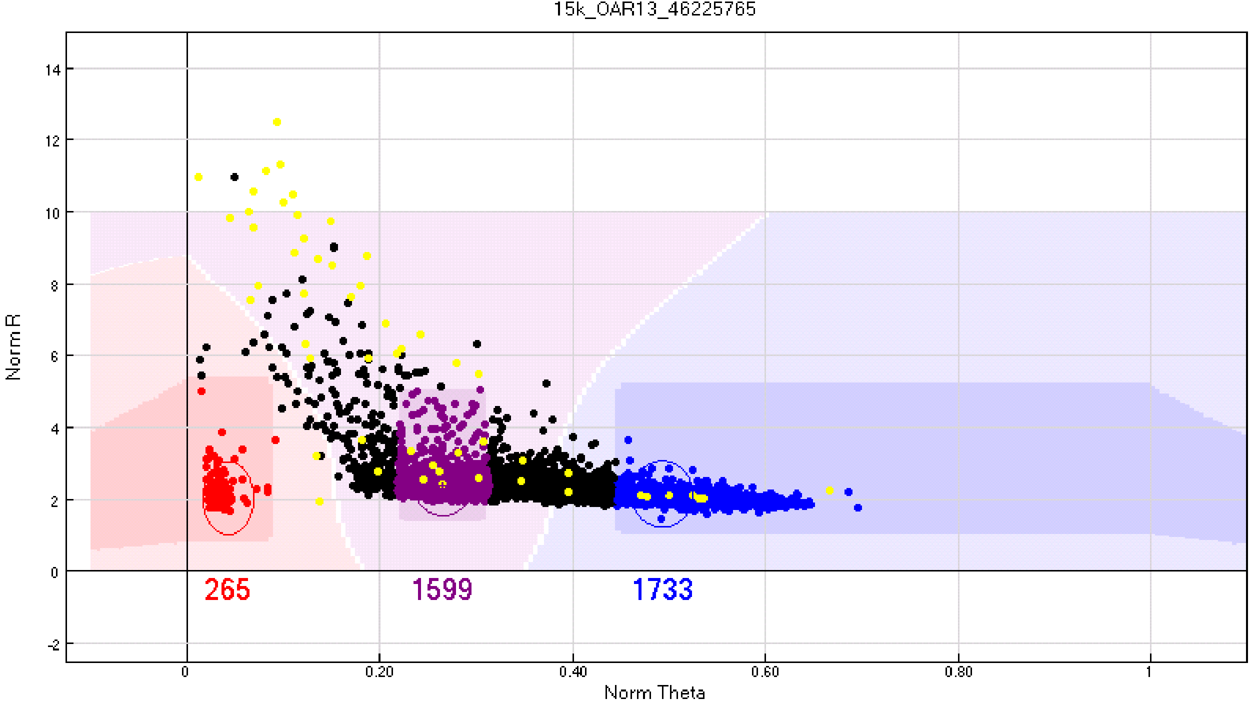
- 7 SNPs representing the 5 nucleotides
  - 2 duplicated
  -

Name	Chr	Position	SNP	Orientation
15k_OAR13_46225660	13	46225660	[T/C]	Forward
oar3_OAR13_46225660	13	46225660	[T/C]	Forward
15k_OAR13_46225714[a]	13	46225714	[A/G]	Forward
oar3_OAR13_46225714[a]	13	46225714	[A/G]	Forward
15k_OAR13_46225764	13	46225764	[A/C]	Forward
15k_OAR13_46225765	13	46225765	[A/G]	Forward
15k_OAR13_46225766	13	46225766	[T/G]	Forward

[a] Failed clustering

Success rate

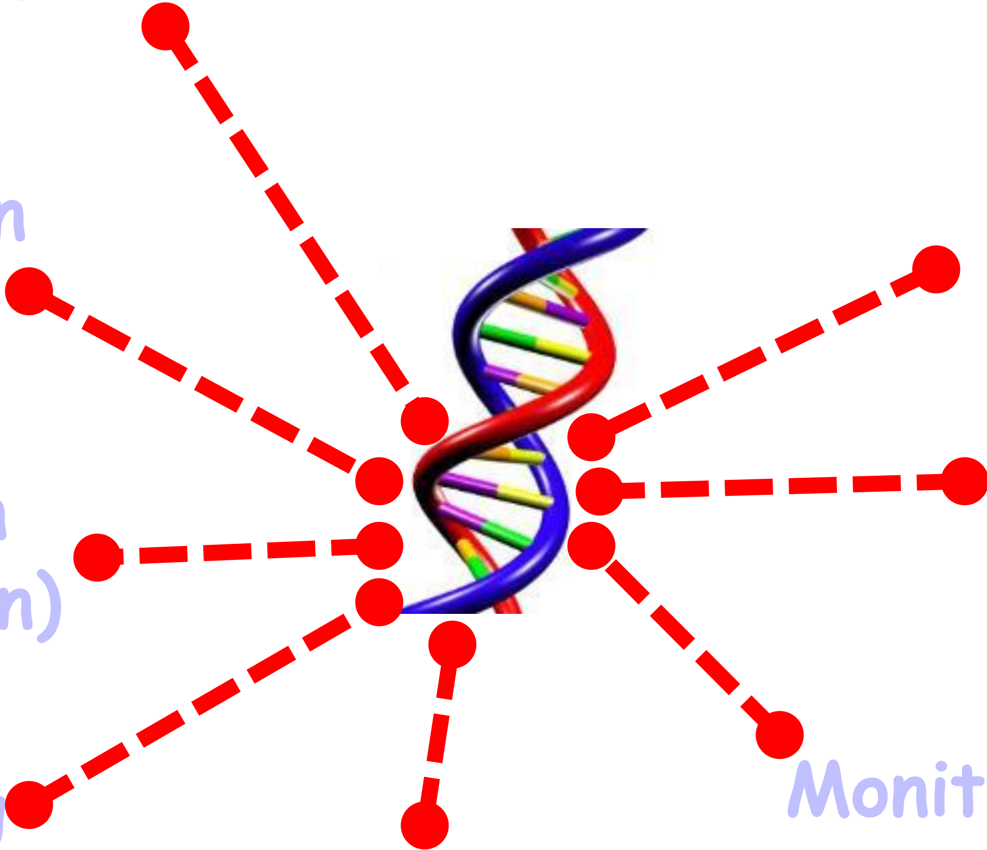
- Not all SNPs worked to our satisfaction making it difficult to determine scrapie genotype with complete certainty
- Still work in progress



Scrapie genotypes

Genotype	All breeds	Belclare	Charollais	Suffolk	Texel	Vendeen
1	73%	74%	72%	93%	54%	79%
2	25%	23%	27%	7%	43%	20%
3	1.7%	3%	1%		2%	1%
4						
5	0.3%				1%	

Genotype result	Type	Degree of resistance/susceptibility
ARR/ARR	1	Sheep that are genetically most resistant to scrapie.
ARR/AHQ ARR/ARH ARR/ARQ	2	Sheep that are genetically resistant to scrapie, but will need careful selection when used for further breeding.
AHQ/AHQ AHQ/ARH AHQ/ARQ ARH/ARH ARH/ARQ ARQ/ARQ	3	Sheep that genetically have little resistance to scrapie and will need careful selection when used for further breeding.
ARR/VRQ	4	Sheep that are genetically susceptible to scrapie and should not be used for breeding unless in the context of a controlled breeding programme approved by NSPAC.
AHQ/VRQ ARH/VRQ ARQ/VRQ VRQ/VRQ	5	Sheep that are highly susceptible to scrapie and should not be used for breeding.



Parentage assignment

Gender determination

Genomic evaluations

Scrapie

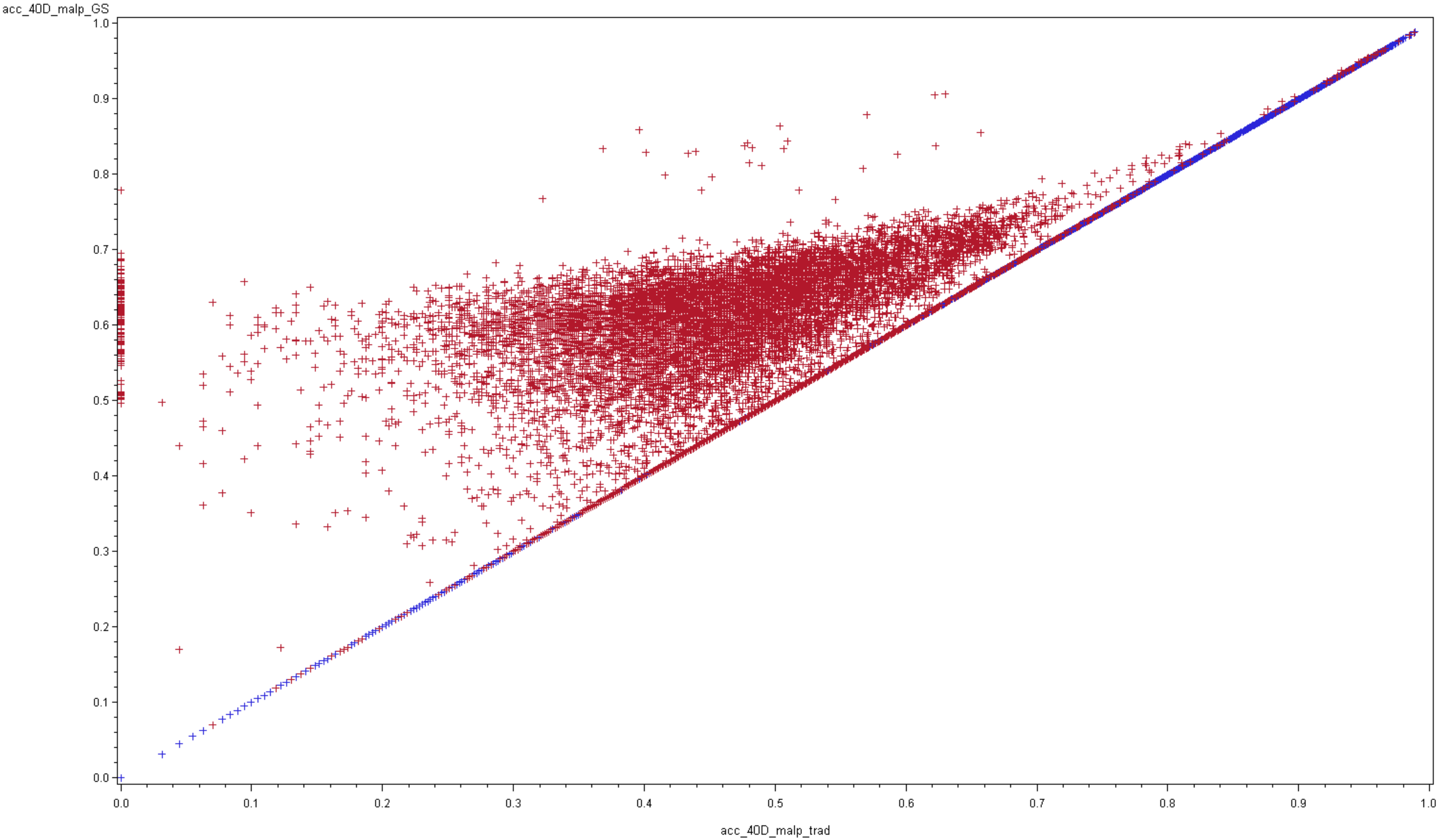
Imputation (up and down)

Inbreeding

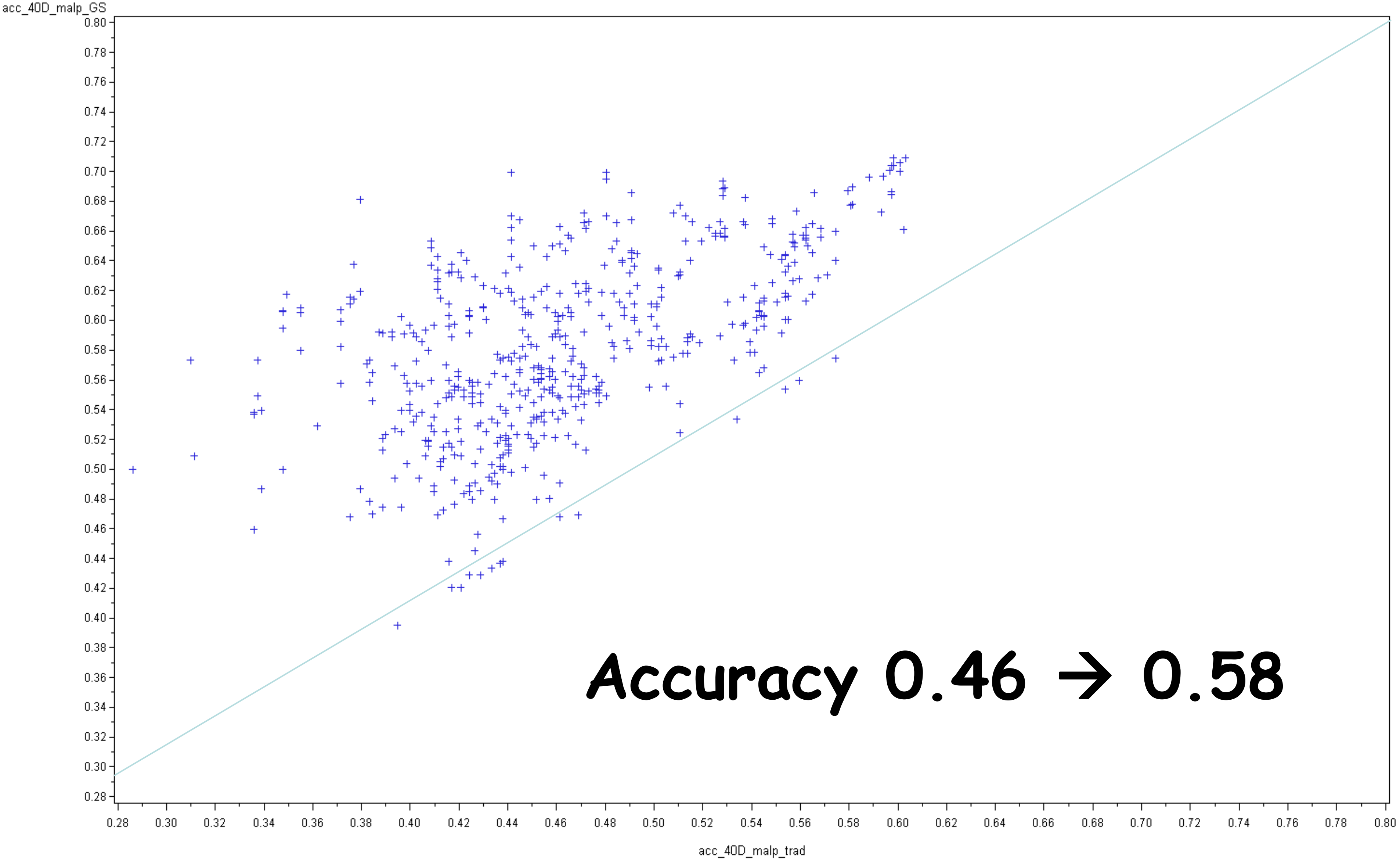
Monitoring major genes

Monitoring lethal genes

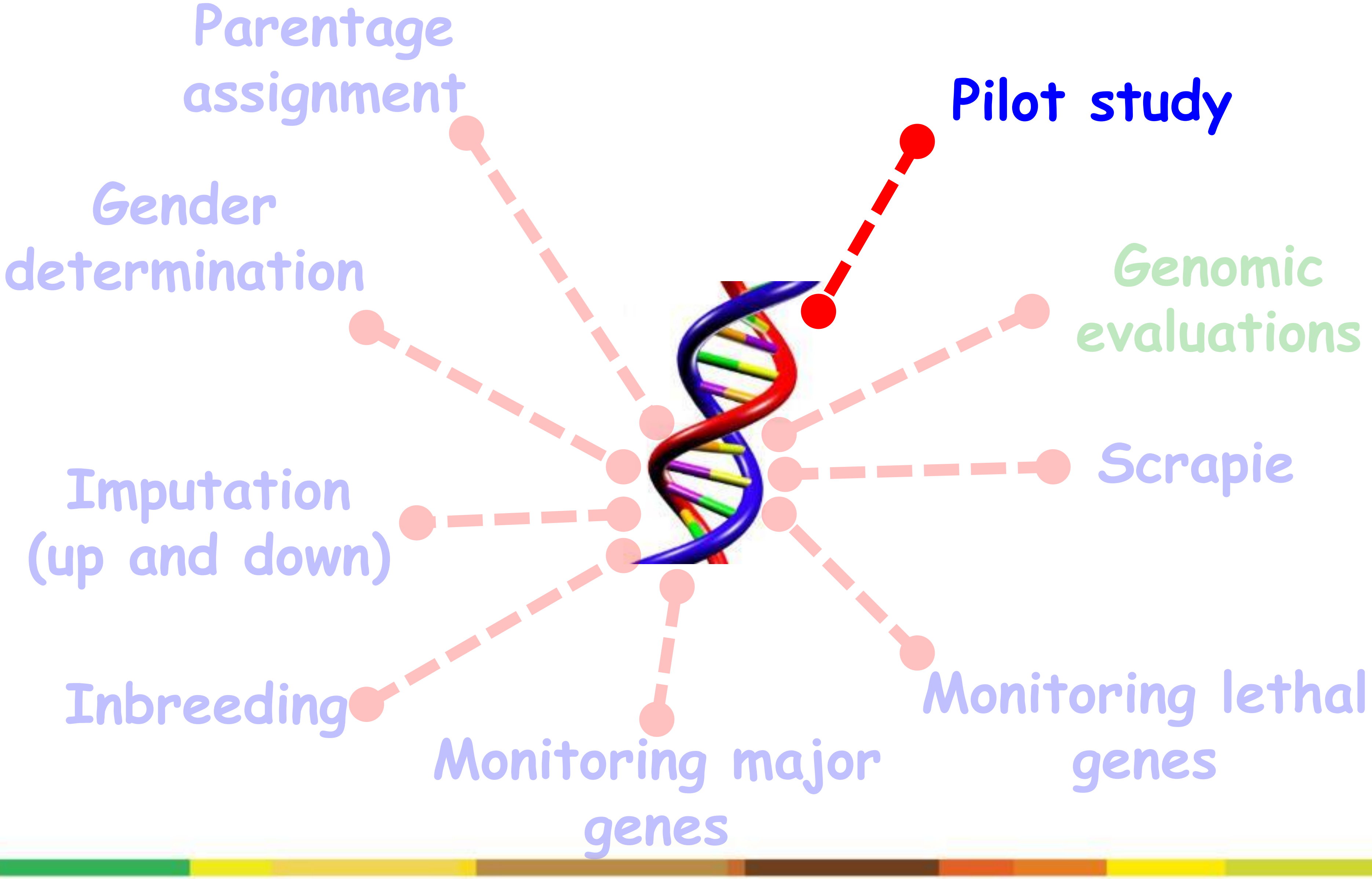
Genomic evaluations



Genomic evaluations



Accuracy 0.46 → 0.58



Parentage assignment

Pilot study

Gender determination

Genomic evaluations

Scrapie

Imputation (up and down)

Inbreeding

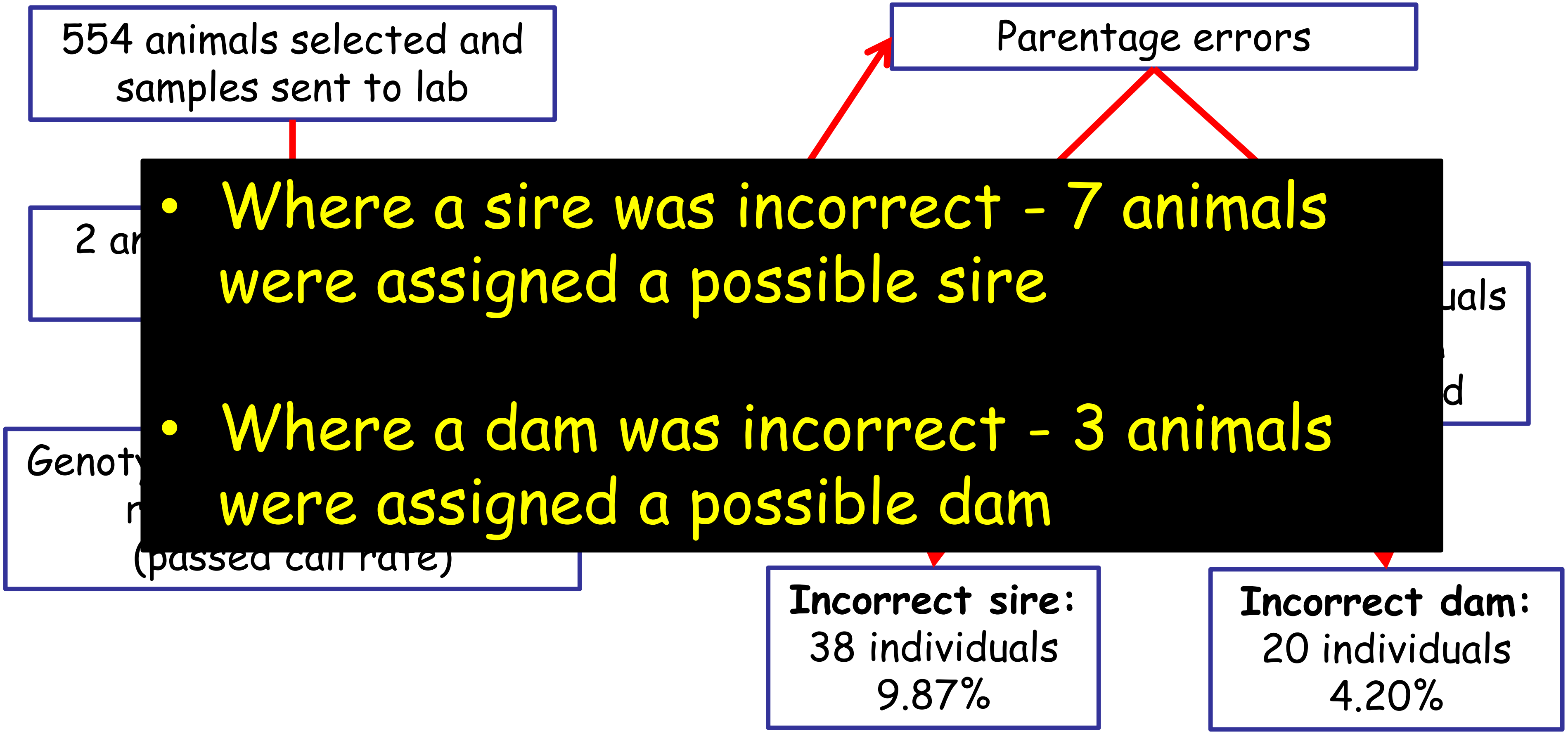
Monitoring major genes

Monitoring lethal genes

Pilot Project

- Purpose
  - Trial run of the genotyping and reporting process – time scales etc.
  - Before rolling out across all animals
- Flock selection
  - 5 breeds X 10 flocks
  - Highest DQI per breed
- 50% of 2016 born males genotyped
- All animals genotyped on the 15K panel

Pilot Project



554 animals selected and samples sent to lab

2 ar

Genoty
n
(passed call rate)

Parentage errors

uals
d

Incorrect sire:
38 individuals
9.87%

Incorrect dam:
20 individuals
4.20%

- Where a sire was incorrect - 7 animals were assigned a possible sire
- Where a dam was incorrect - 3 animals were assigned a possible dam

Future Plans

Genotyping 2017 options

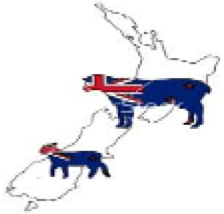
1. Genotype replacements lambing in 2017 from OVIGEN flocks
   - Funding available for 1 year only
2. Subsidise genotyping replacements lambing in 2017
   - Breeder pays €10 + tag (some samples already taken)
   - Potential funding for 2 years
3. Genotype all rams for the next 3 years

INZAC Flock

Nóirín McHugh & Fiona McGovern

7th July 2016, Sheep Ireland industry meeting

New Zealand vs. Ireland



- Similar production systems
  - Se
- Simil
  - Sa

(num r....)

Response to selection

Dual_{NZ} €1.16
Dual_{IRE} €0.27

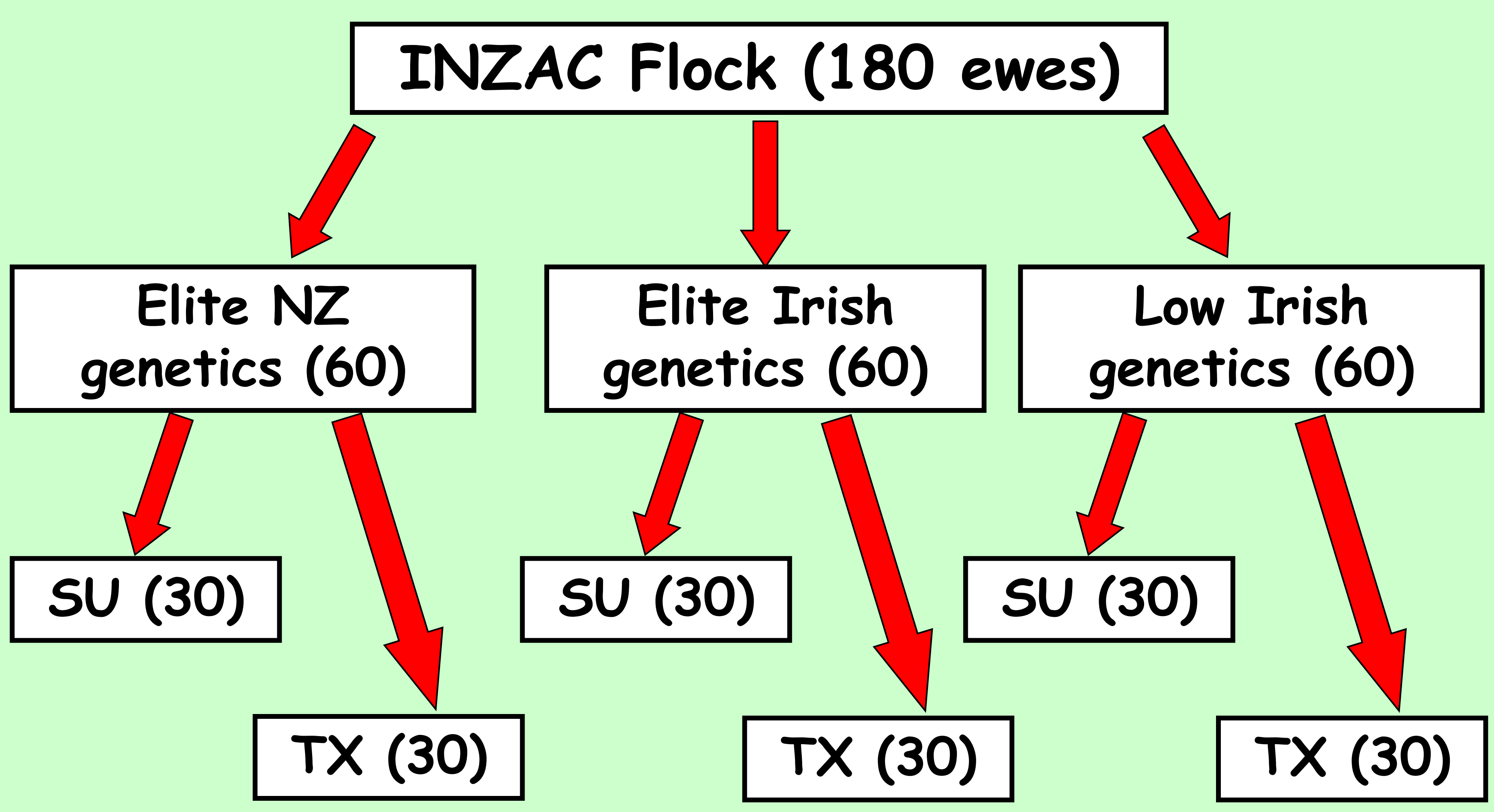
Term_{NZ} €1.07
Term_{IRE} €0.28

  - Are genetic elite NZ animals suitable for Ireland???

Research Objectives

1. Compare NZ versus Irish genetic elite animals
2. Establish a nucleus flock for the Suffolk and Texel flocks → superior genetics available to the industry
3. Generate genetic linkage between NZ and Ireland
   - Useful for:
     - across country evaluations
     - Genomic selection

Validation of indexes



INZAC Flock (180 ewes)

Elite NZ genetics (60)

Elite Irish genetics (60)

Low Irish genetics (60)

SU (30)

TX (30)

SU (30)

TX (30)

SU (30)

TX (30)

Management

- Three independent farmlets:
  - NZ
  - Elite Irish
  - Low Irish

  - Stocking rate: 12ewes / ha
  - 150kg N per ha per year

Animal Performance

- **Fertility** – barren, scanning rates
- **Lambing data** - lambing ease, survival, birth weights, vigour, mothering ability
- **Milk yield** – weigh suckle weigh
- **Feed intake** – ewes at pasture
- **Lamb performance** – weights, GR, back fat & muscle scan, quality and dagg scores
- **Health data** – lameness, mastitis, lamb FEC
- **Ewe Longevity** – replacement rates

Lambing 2016

- **Lambing commenced on February 27th**
- **82% of ewes lambed within three weeks**

	NZ	**Irish High**	**Irish Low**
Lambing Date	8th March	10th March	4th March
NLB	1.92	1.71	1.70
Birth weight	4.87	5.09	4.83
Lambing difficulty	49%	73%	76%
Lamb Mortality	7.14%	7.76%	5.17%

Flock Health

Ewes:

- Mastitis
- Sore teats

Lambs:

- Dosed 6 weeks for nematodirus
- Individual spot treatments for Coccidia
- FEC fortnightly from Week 10
  - Dosed Week 11, Week 16
- Cobalt drench fortnightly from Week 12

Lamb Performance

	NZ	Irish High	Irish Low
40 day wt	18.5	18.1	17.9
Weaning wt	32.6	31.2	30.6
ADG (g/kg)	289	287	274

Timeline

Ewes imported

Lamb (autumn)

Second Importation

2014 2015 2016 2017 2018 2019

Identify Irish elite and national average animals

Ewes mated

1st crop lambs born

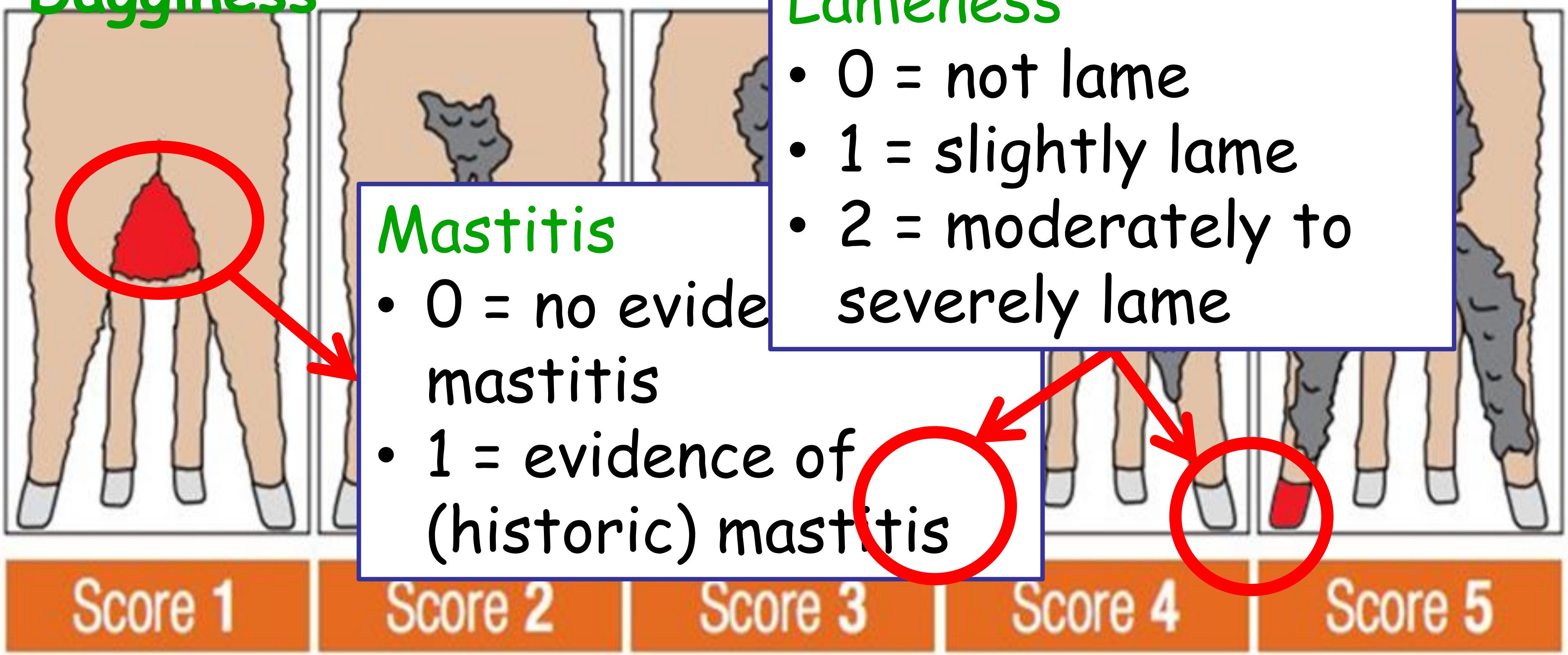
2nd crop lambs

3rd Crop lambs

4th Crop lambs

Genetic parameters for health traits

The traits



Dagginess

Mastitis

- 0 = no evide
  mastitis
- 1 = evidence of (historic) mastitis

Lameness

- 0 = not lame
- 1 = slightly lame
- 2 = moderately to severely lame

Prevalence

Dagginess

Total records

Ewes 6,831

Lambs 23,179

Score	Ewes	Lambs
1	49.55	52.07
2	29.25	25.00
3	13.63	17.11
4	6.98	4.62
5	0.59	1.21

Prevalence

Lameness

Total records

Ewes 7,862

Lambs 21,847

Score	Ewes	Lambs
0	89.86	83.91
1	9.63	13.70
2	0.51	2.39

Prevalence

Mastitis

Total records

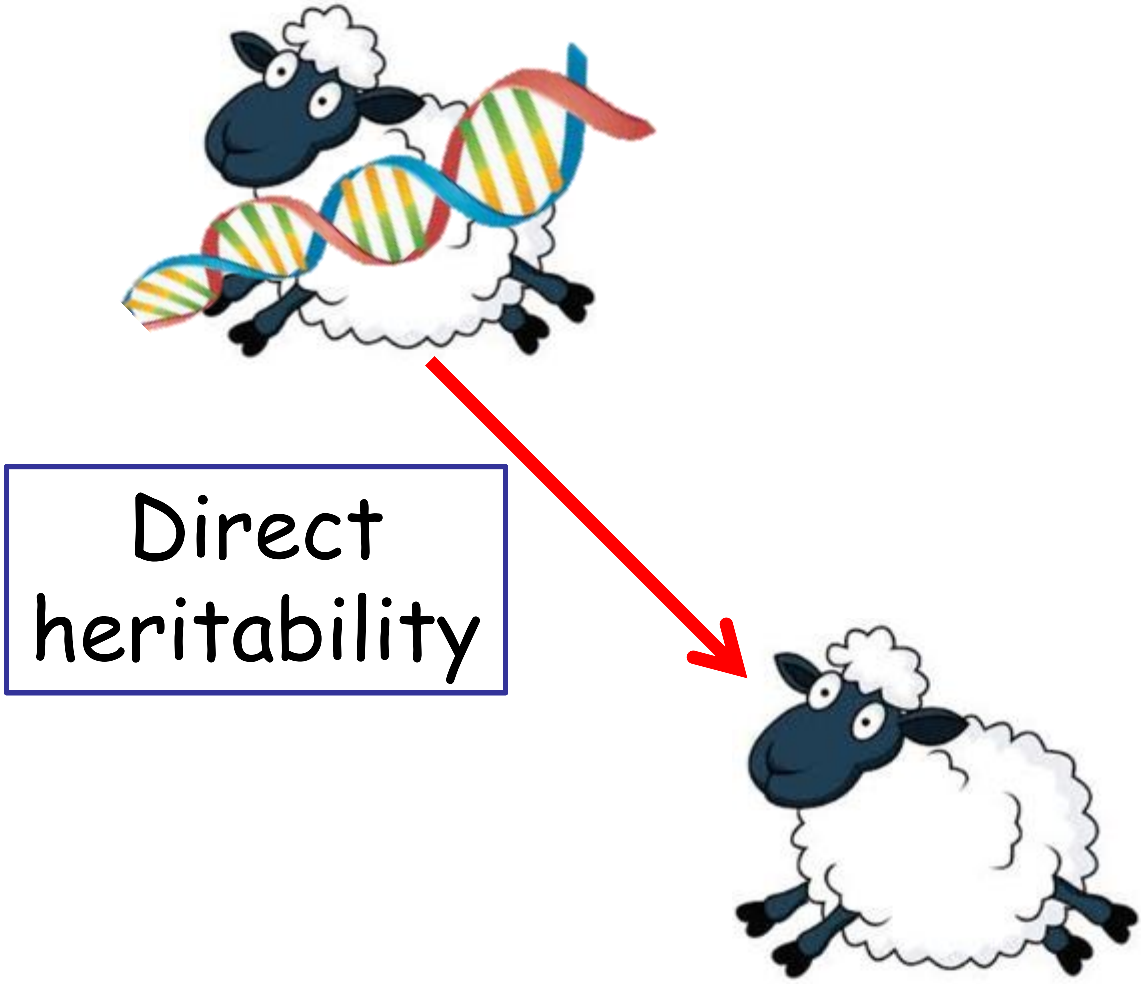
↓

Ewes

3,378

Score	Ewes
0	97.45
1	2.55

Heritability



Direct heritability

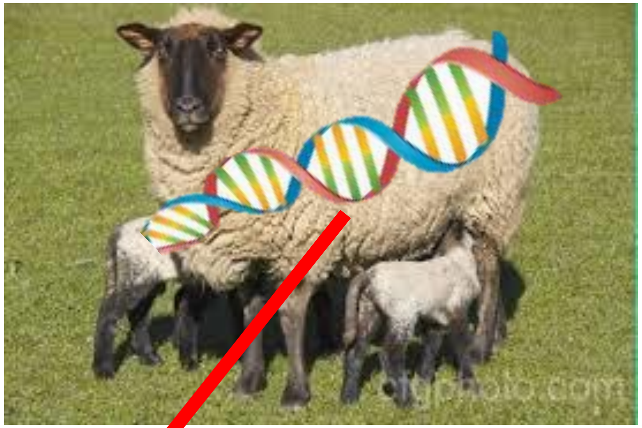
Genetic parameters

Direct Heritability	Lamb h^2	Ewe h^2
Dagginess	0.14 (0.02)	0.15 (0.03)
Lameness	0.12 (0.02)	0.06 (0.02)
Mastitis		0.04 (0.03)

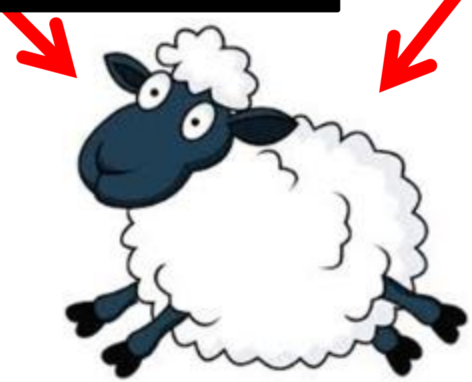
Heritability

Dagginess had a maternal heritability of 0.05 (0.02)

heritability



Maternal heritability



Going forward

- Dagginess, lameness and mastitis will be included in the national breeding goal
- Creation of a health index
- Generation of breeding values for all animals