

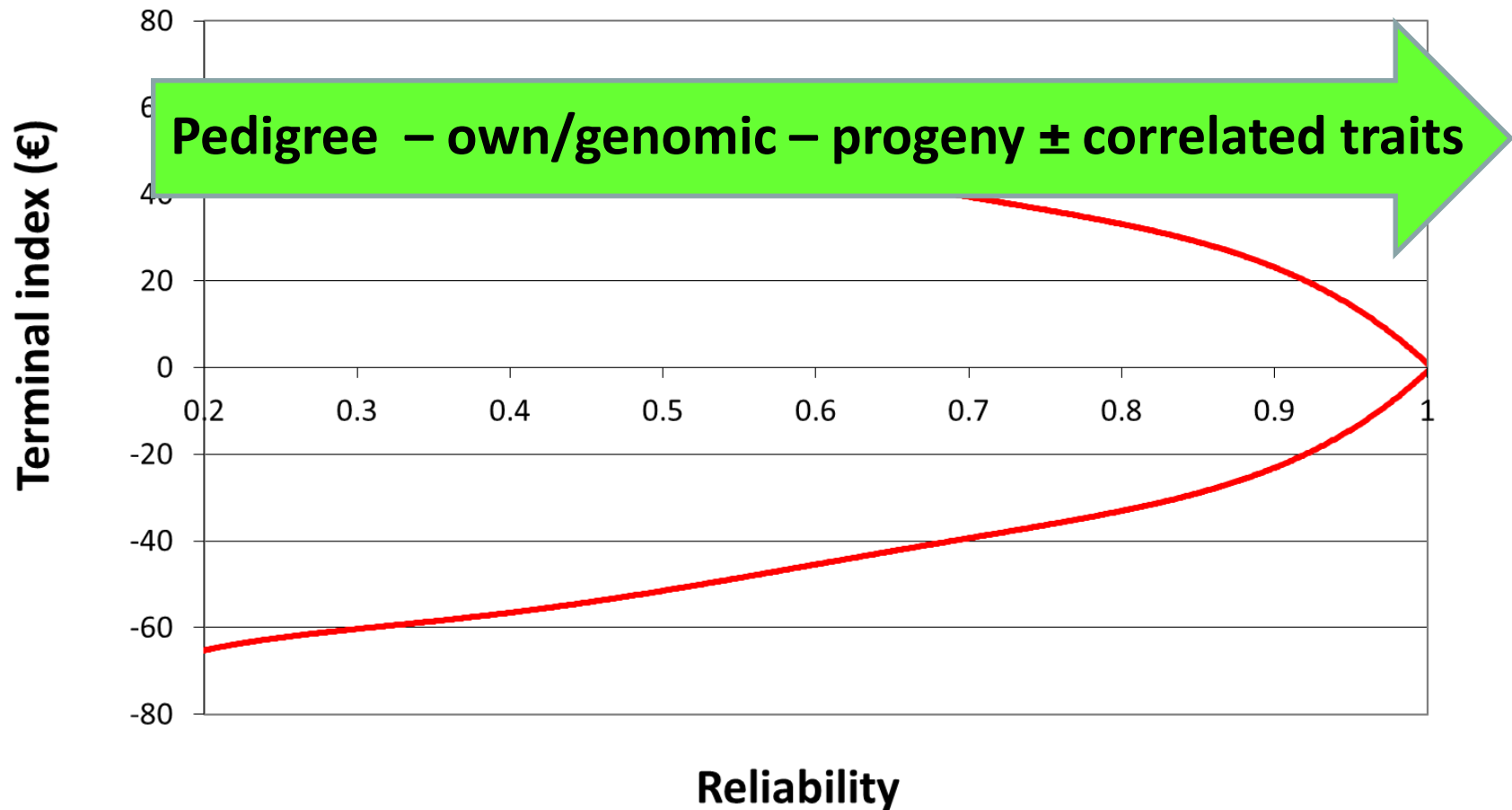
Reliability

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Reliability

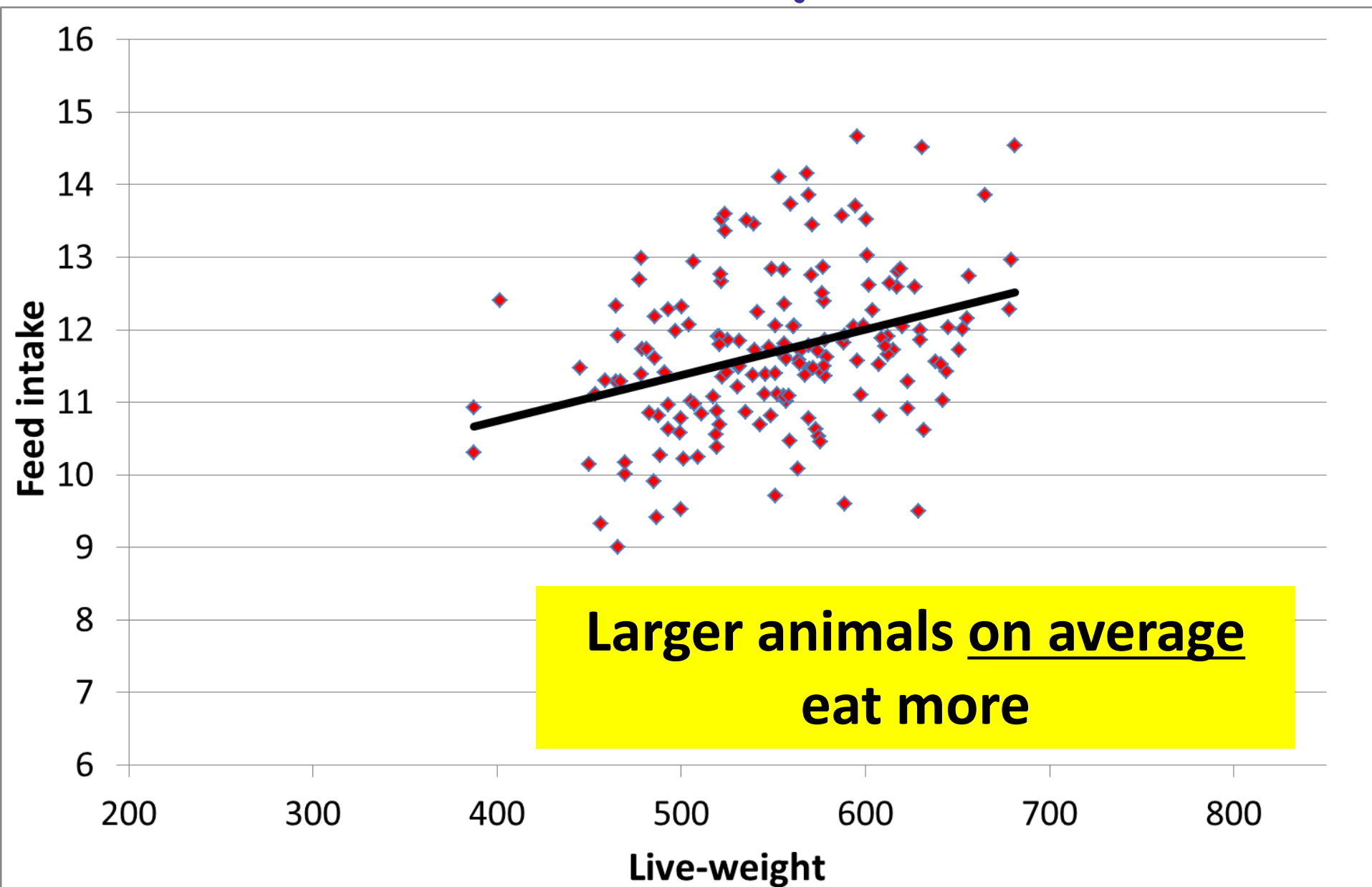
- How confident are we that the published index will not change as more information accumulates



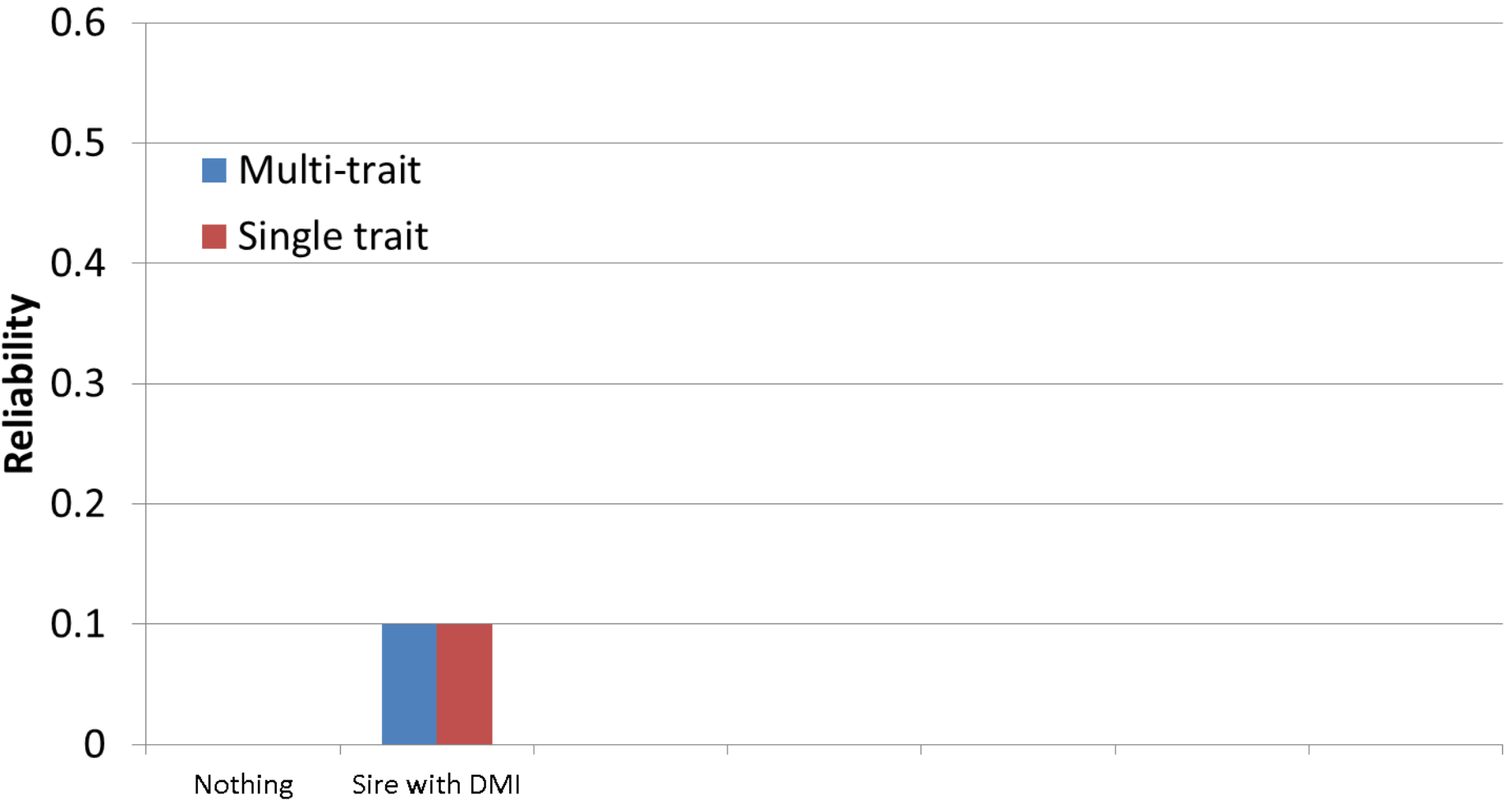
Who eats more??



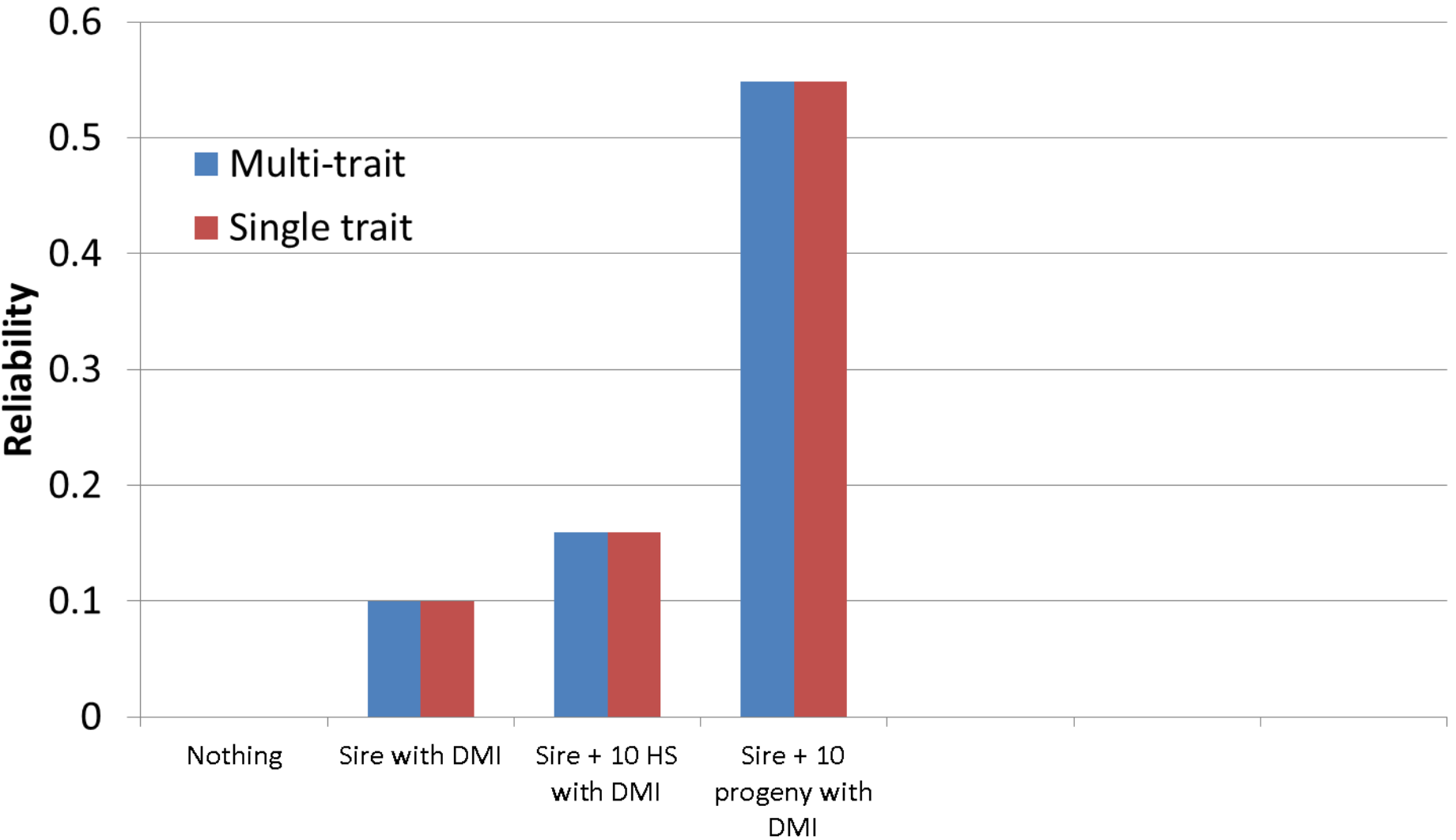
Recent Tully data



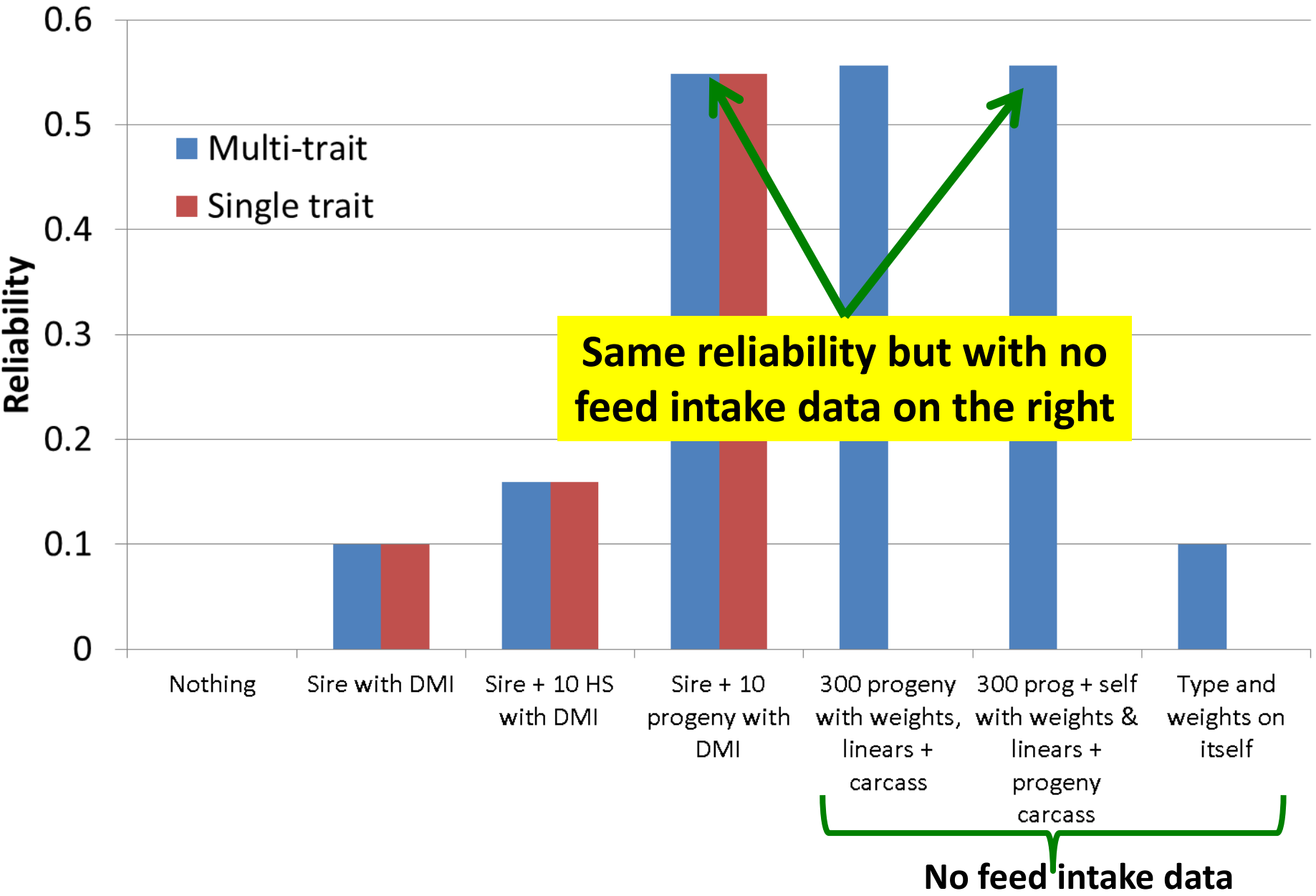
Multi-trait genetic evaluations



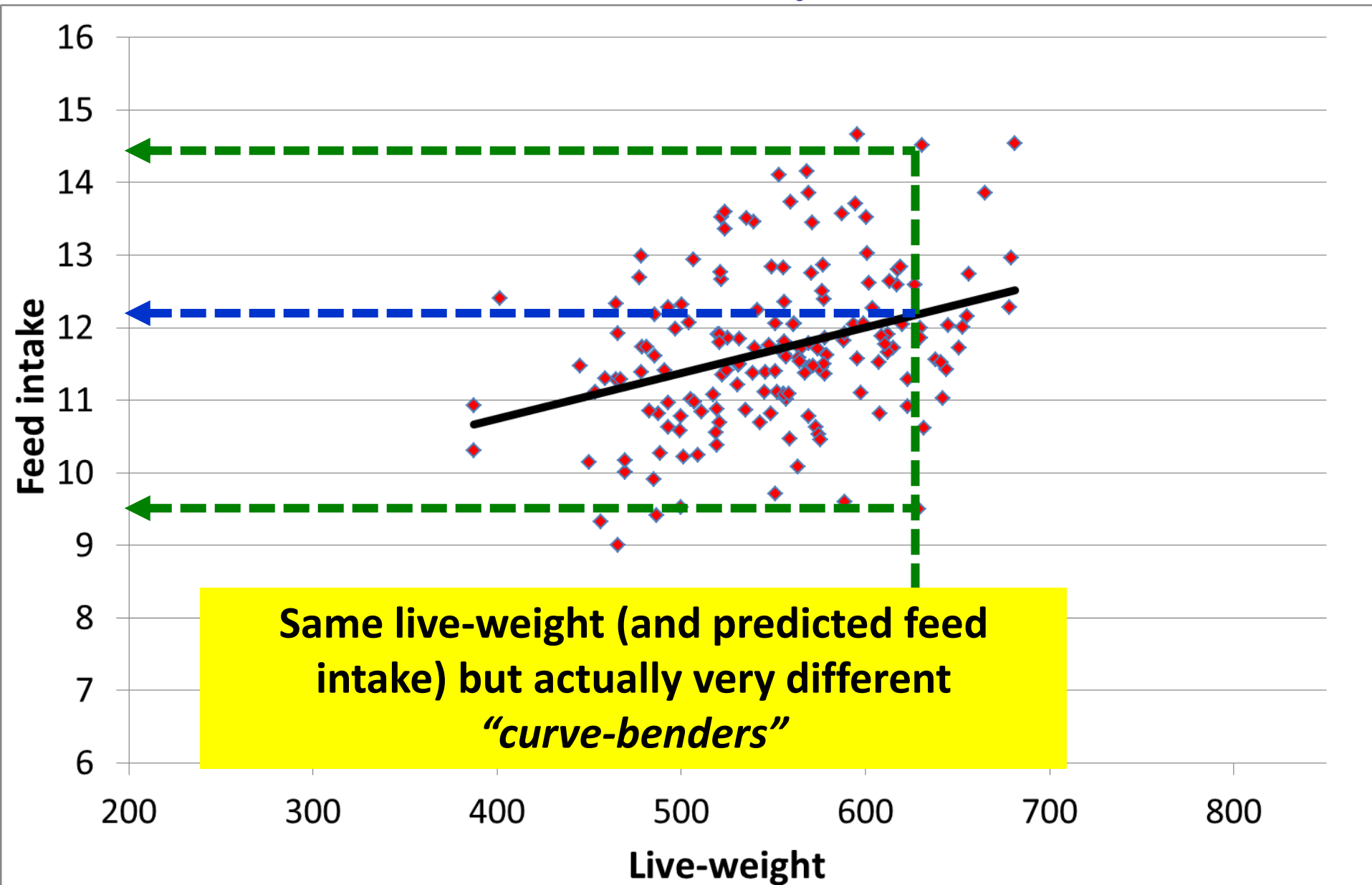
Multi-trait genetic evaluations



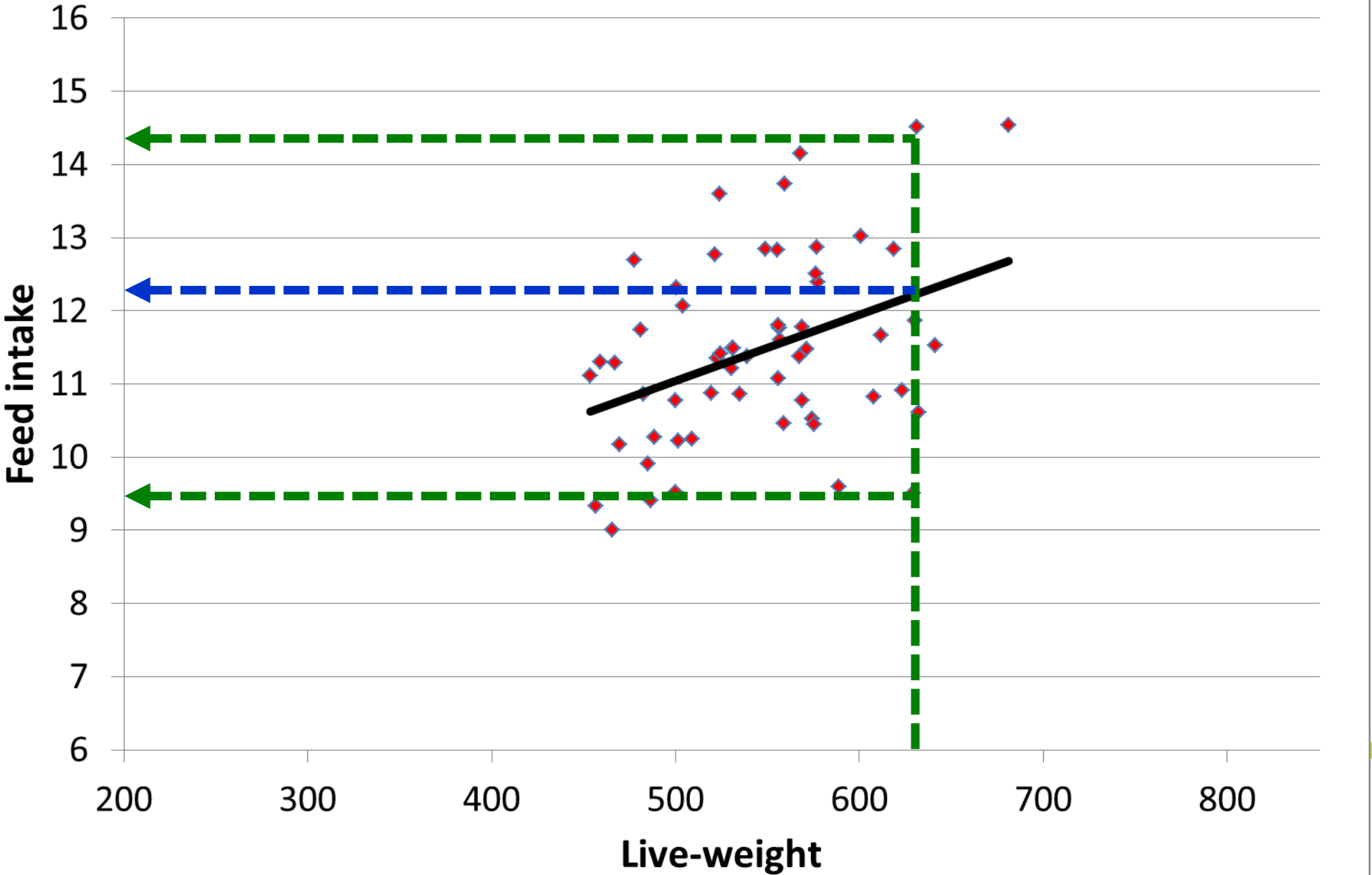
Multi-trait genetic evaluations



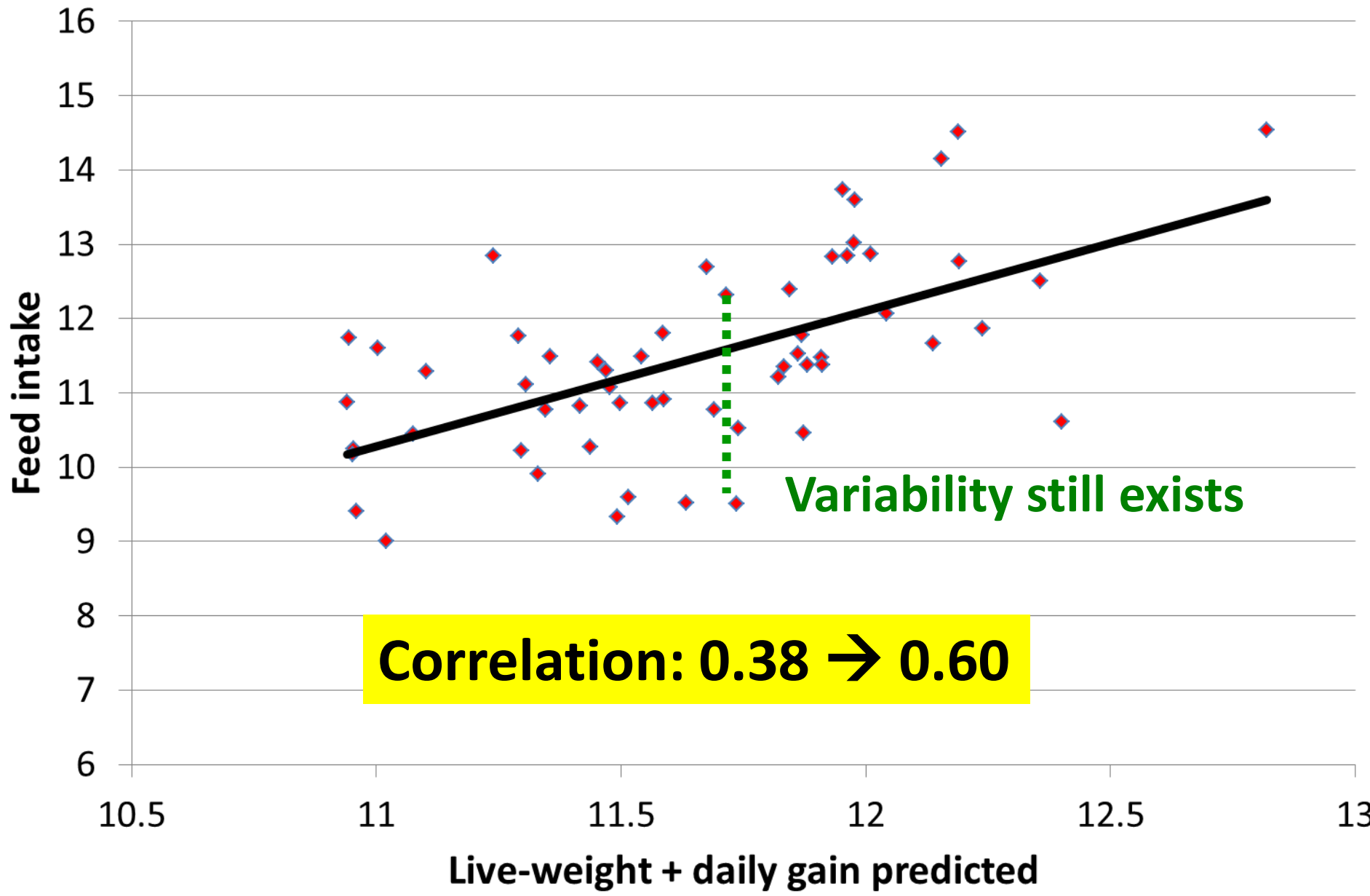
Recent Tully data



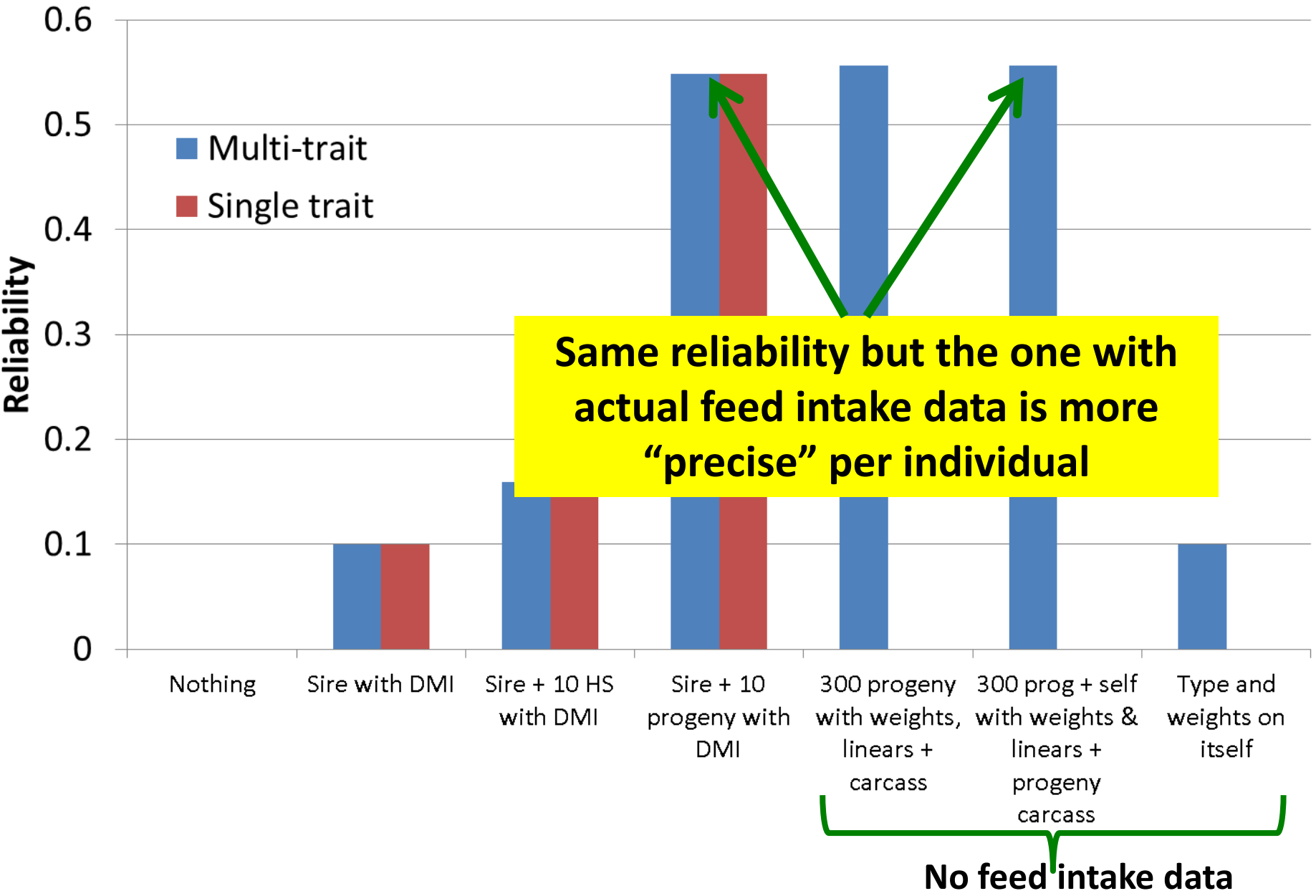
Recent Tully data (Lims)



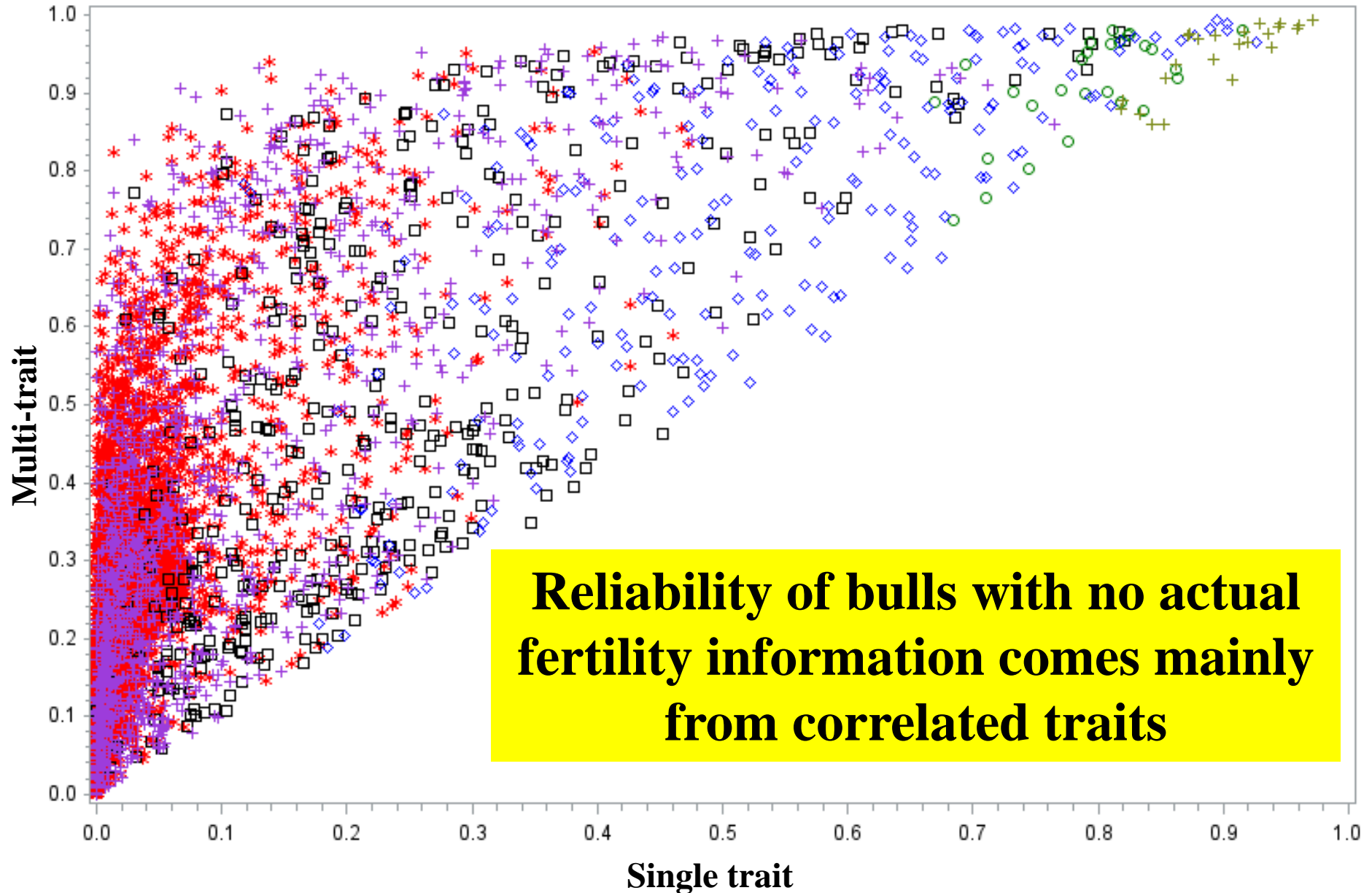
Recent Tully data (Lims)



Multi-trait genetic evaluations



Fertility multi- v single trait reliability

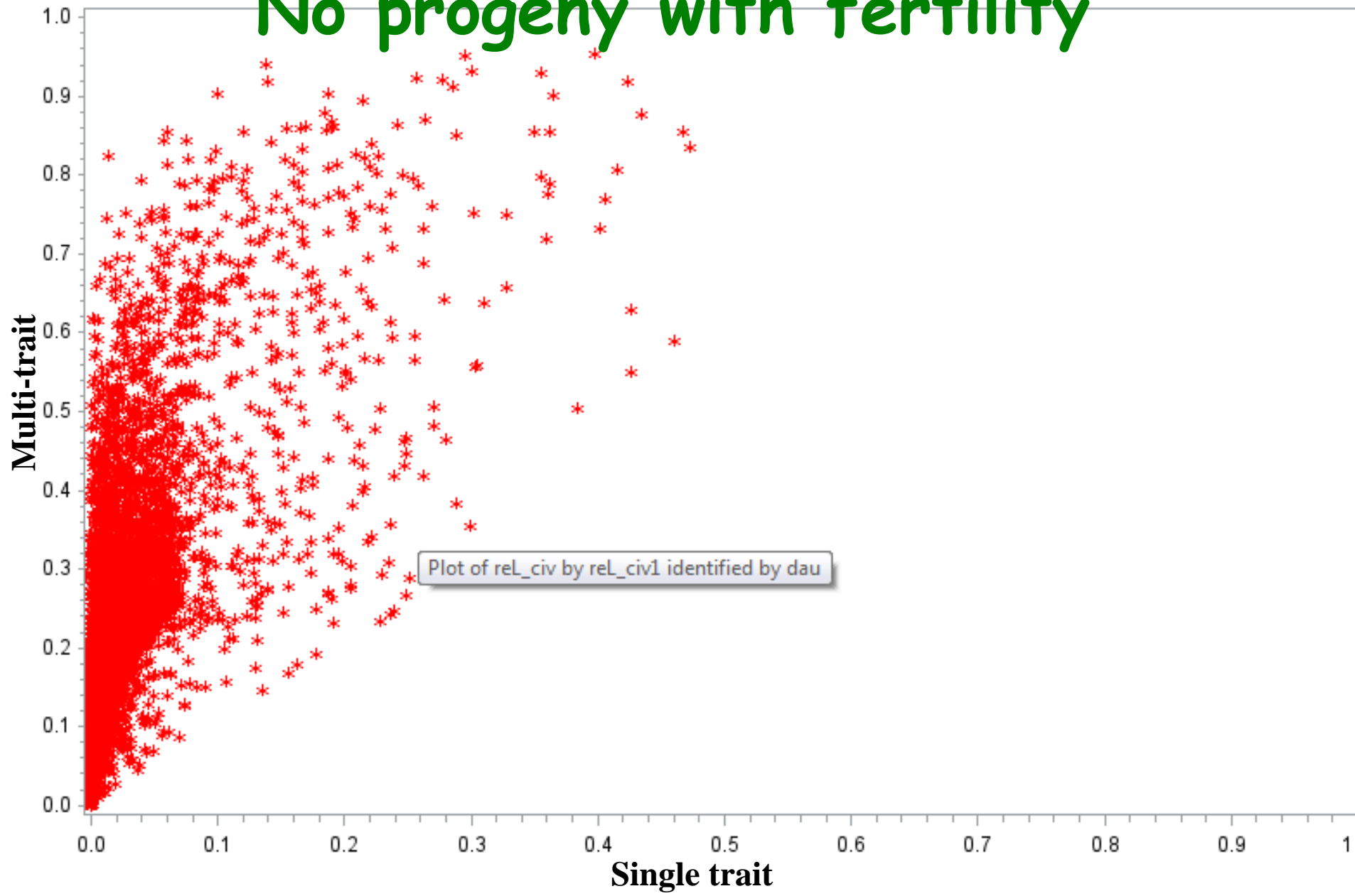


Reliability of bulls with no actual fertility information comes mainly from correlated traits

dau * * * 0 □ □ □ 11-50 ○ ○ ○ 501-1000 ◇ ◇ ◇ 51-500 + + + <10 + + + >1000

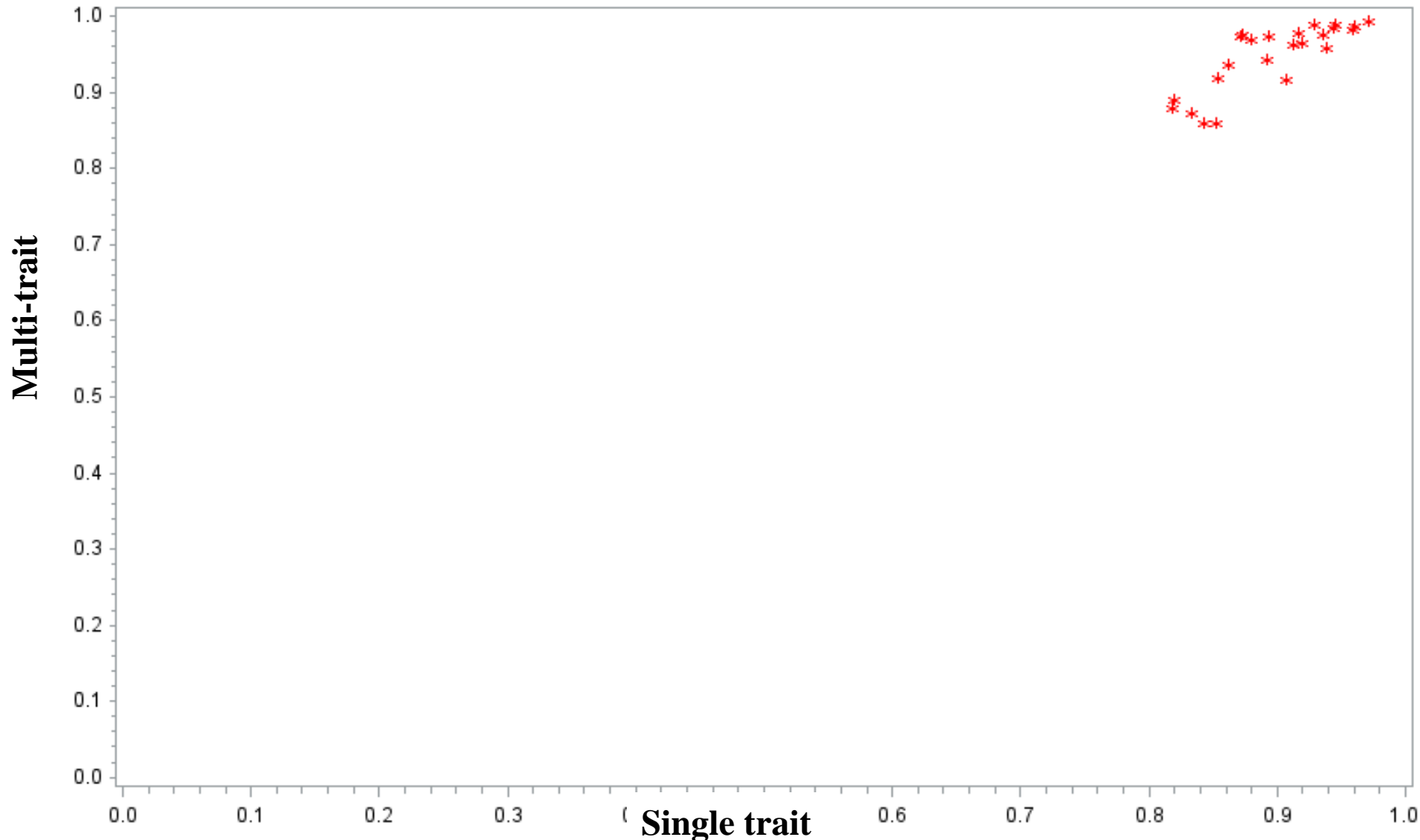
Fertility multi- v single trait reliability

No progeny with fertility



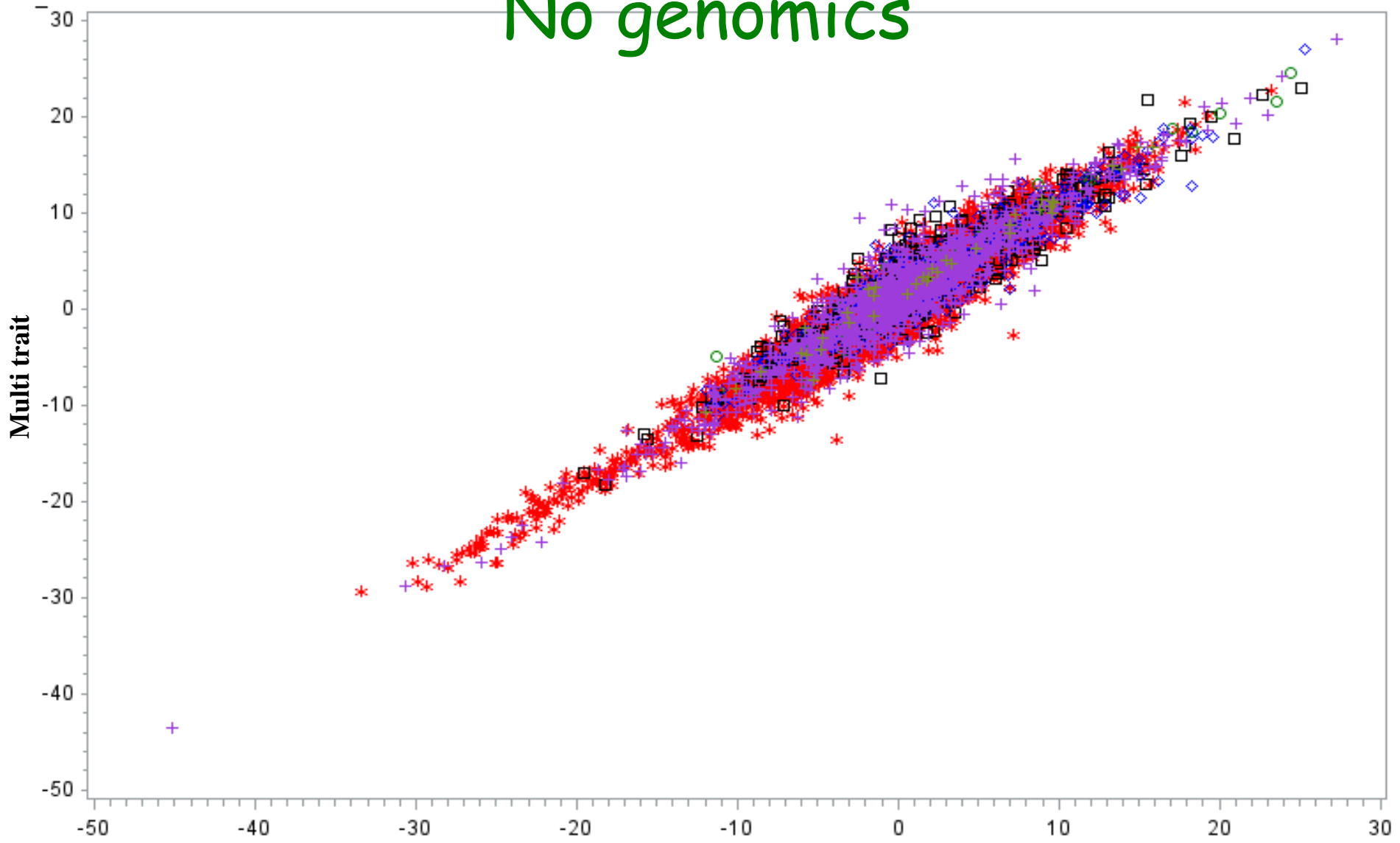
Fertility multi- v single trait reliability

Several thousand progeny with fertility



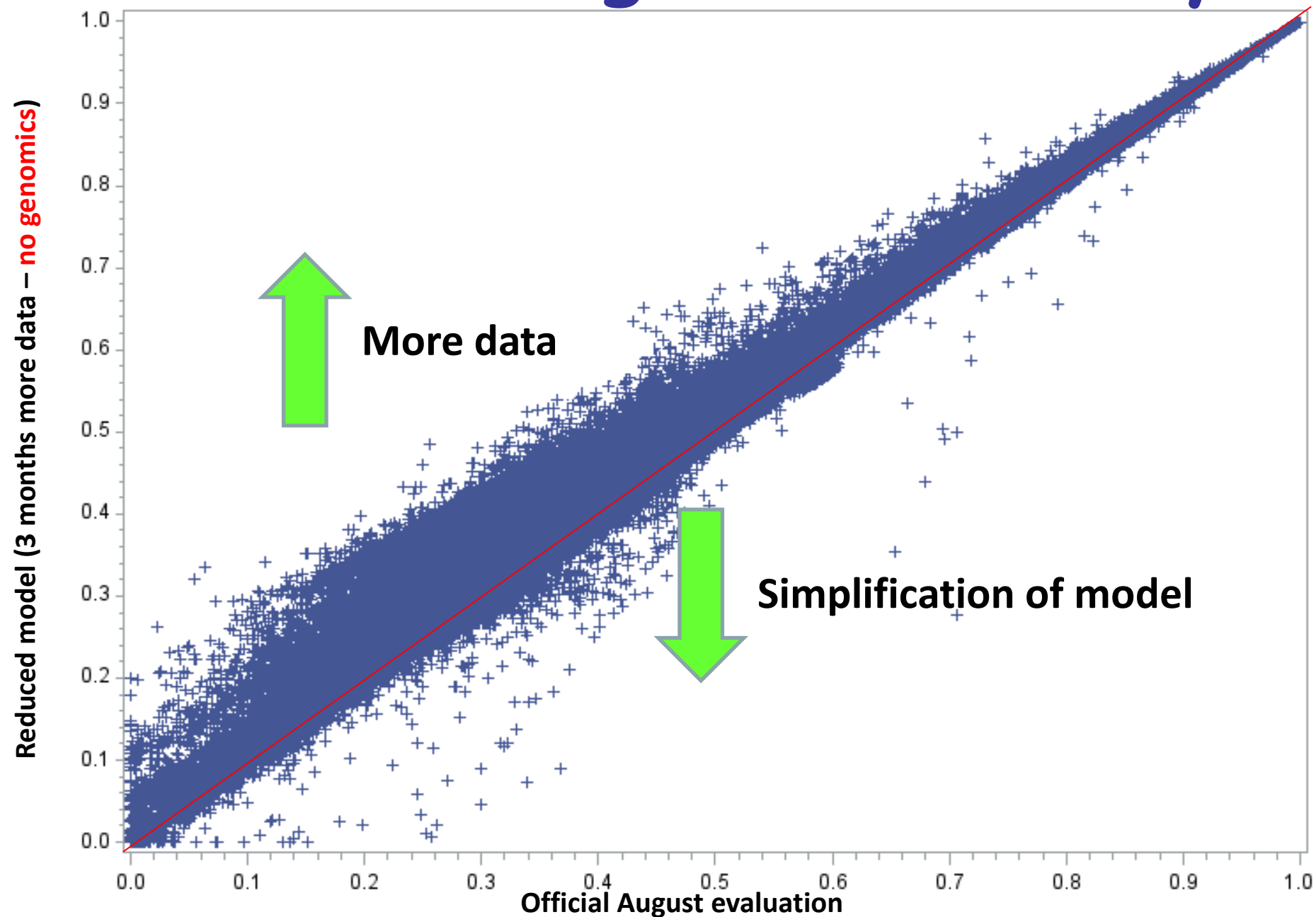
Fertility multi- v single trait EBVs

No genomics

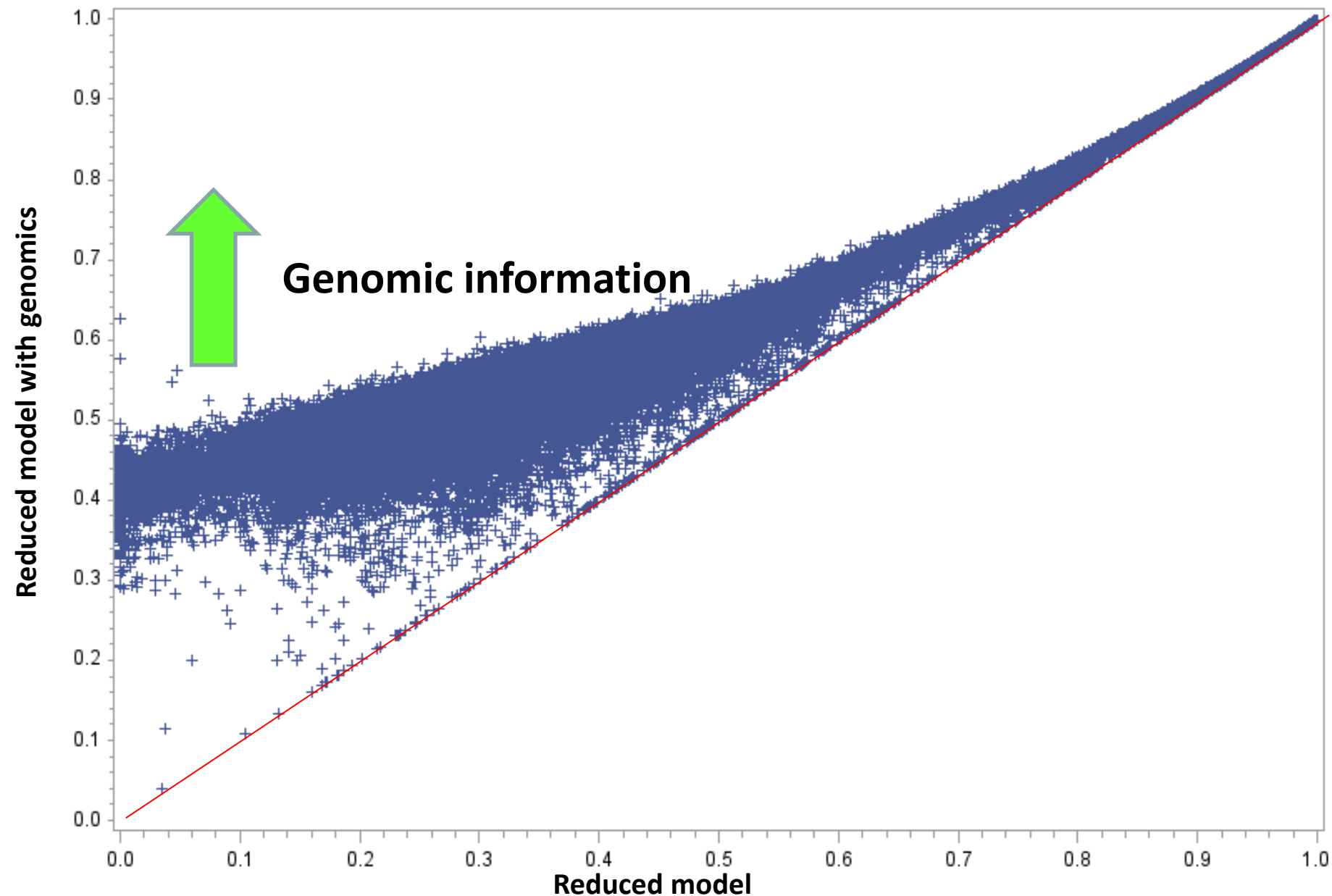


dau * * * 0 □ □ □ 11-50 ○ ○ ○ 501-1000 ◇ ◇ ◇ 51-500 + + + <10 + + + >1000

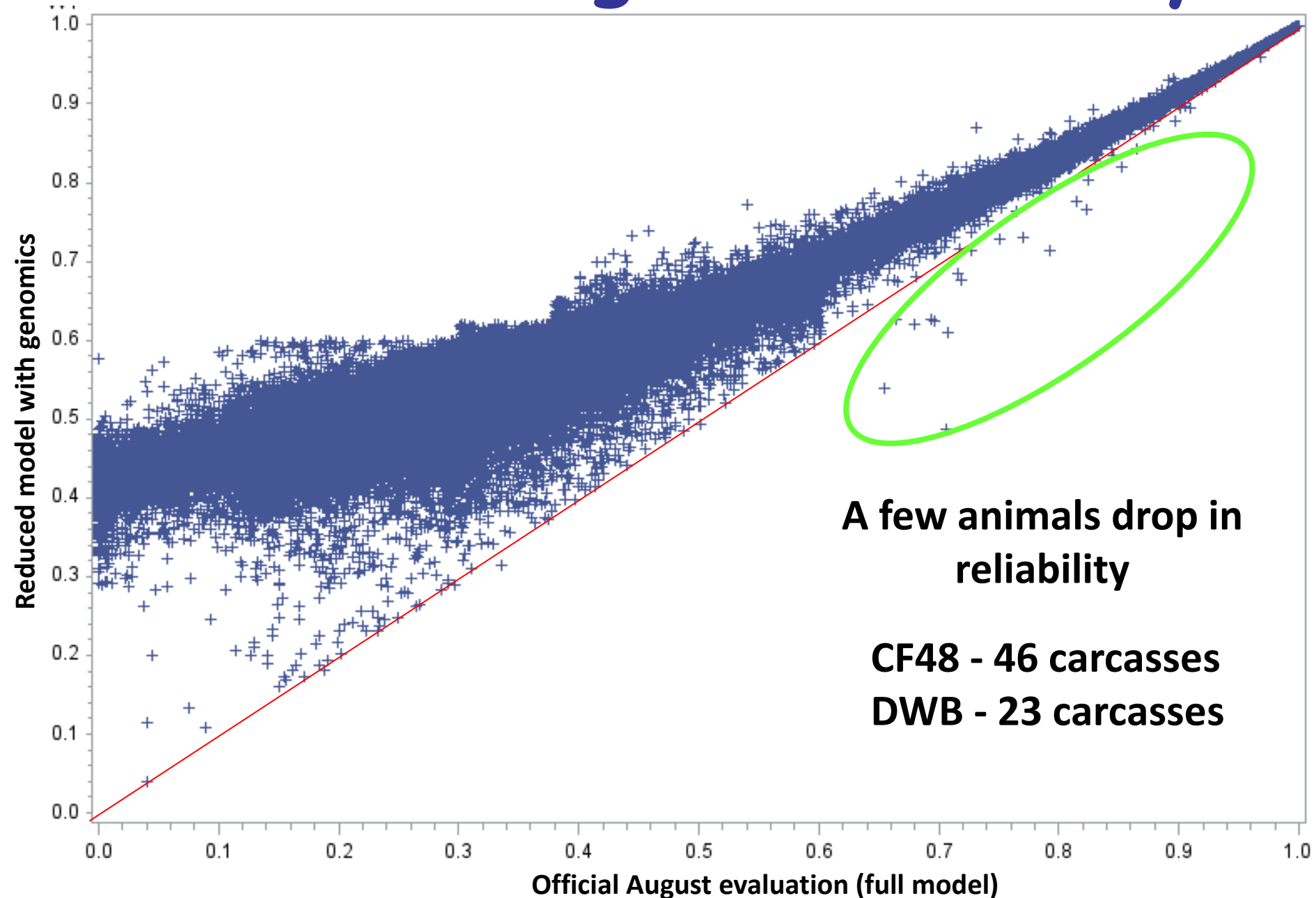
Carcass weight - reliability



Carcass weight - reliability



Carcass weight - reliability



Why simpler models?

- Best reflection of genetic merit for a trait is data on the trait itself
 - Feed intake or live-weight??
- Complicated models are more difficult to run and take considerably longer
 - Computing power becomes an issue
 - Carcass eval:
 - 45 million \rightarrow 13 million equations
 - 15 days \rightarrow 8 days
- Helps identify “curve benders”

Future

- **Computing**
- **Memory efficiency**
 - 16,000 Gb (traditional) → 800 Gb (APY)
 - 2000 laptops to 100 laptops
- **Speed of evaluations**
 - 28 days → 8 days with doubling of genotypes
- **Increased efficiency is not synonymous with increased speed**

Conclusions

- Models changed to be more efficient with minimal loss in information
- Without genomics: drop in reliability and some movement in proofs
- More precise evaluations with genomics



IRISH CATTLE BREEDING FEDERATION

Genomic evaluations research update



Current evaluations

- 6 evaluations for suckler herd
- Beef performance (29 traits: 6 goal traits)
- Calving performance (15 traits: 4 goal traits)
- maternal weaning wt (15 traits: 1 goal)
- fertility (14 traits: 3 goal traits)
- docility (3 traits: 1 goal trait),
- linear (13 traits)

Beef performance evaluation

Beef performance evaluation

150-250 day lwt

250-350 day lwt

350-450 day lwt

450-550 day lwt

550-650 day lwt

Cow liveweight

calf quality

mart calf price

mart weanling price

mart yearling price

Tully feed intake

Tully ultrasound muscle

Skeletal

Muscle

Carcass weight

Carcass conformation

Carcass fat

Cull cow weight

Cull cow conformation

Cull cow fat

Foreign ebv weaning

Foreign ebv muscle

Foreign ebv skeletal

Foreign ebv carcass

Foreign ebv conformation

Evaluation new 1

150-250 day lwt

250-350 day lwt

350-450 day lwt

450-550 day lwt

550-650 day lwt

Cow liveweight

Skeletal

Carcass wt

Cull cow weight

Foreign ebv weaning

Foreign ebv skeletal

Foreign ebv carcass

Evaluation new 2

calf quality

mart calf price

mart weanling price

mart yearling price

Carcass conformation

Cull cow conformation

Muscle

Foreign ebv muscle

Foreign ebv conformation

Evaluation new 3

350-450 day lwt

450-550 day lwt

550-650 day lwt

Skeletal

Tully feed intake

Tully ultrasound muscle

Carcass weight

Carcass conformation

Carcass fat

Foreign ebv weaning

Foreign ebv carcass

Foreign ebv conformation

Current test run

- August 2015 evaluation files
- 105,000 genotypes included
- 6 evaluations completed
 - Carcass wt (12 trt), conformation (9 trt), feed intake and fat (12 trt), fertility (6 trt), docility (3 trt) evaluations completed
- Run with 150,000 genotypes and December evaluation files not completed yet

Proportion of Replacement index with genomics

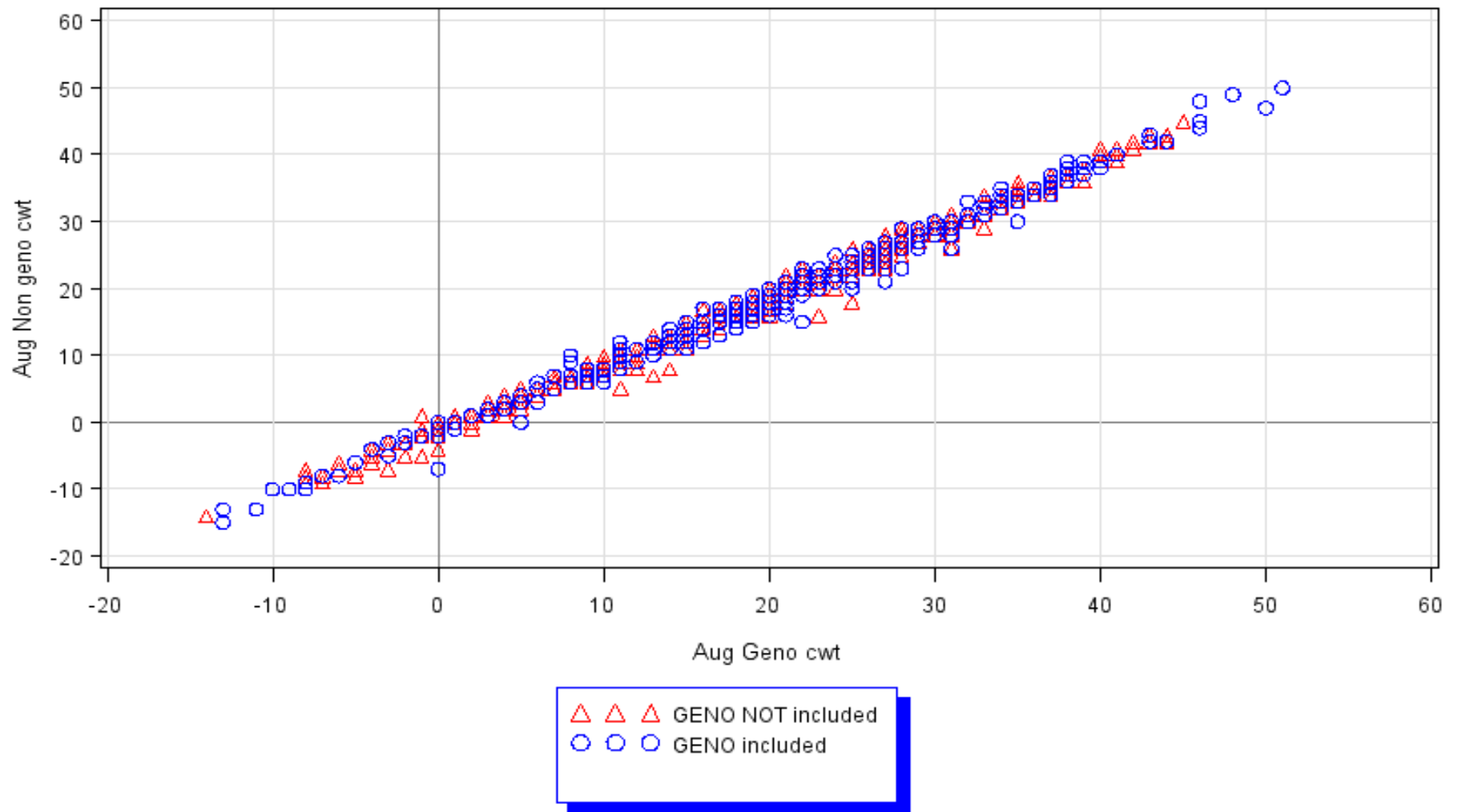
Trait	Relative emphasis in Replacement Index	% currently with genomics
Age 1st Calving	6%	6%
Maternal calving difficulty	6%	
Maternal weaning weight	18%	
Calving interval	9%	9%
Survival	8%	8%
Heifer feed intake/cow livewt	8%	8%
Cow feed intake/cow livewt	6%	6%
Cow docility	4%	4%
Cull cow weight	7%	7%
Calving difficulty	7%	
Gestation	2%	
Mortality	1%	
docility	1%	1%
Feed intake	4%	4%
Carcass weight	10%	10%
Carcass conformation	3%	3%
	100%	65%

AI sires > 90% rel previous cwt rel

No of bulls 898 correlation $r = 0.996$

Aug Non Geno cwt = 19.2 {stdev = 12.3}

Aug Geno cwt = 20.68 {stdev = 12.21}

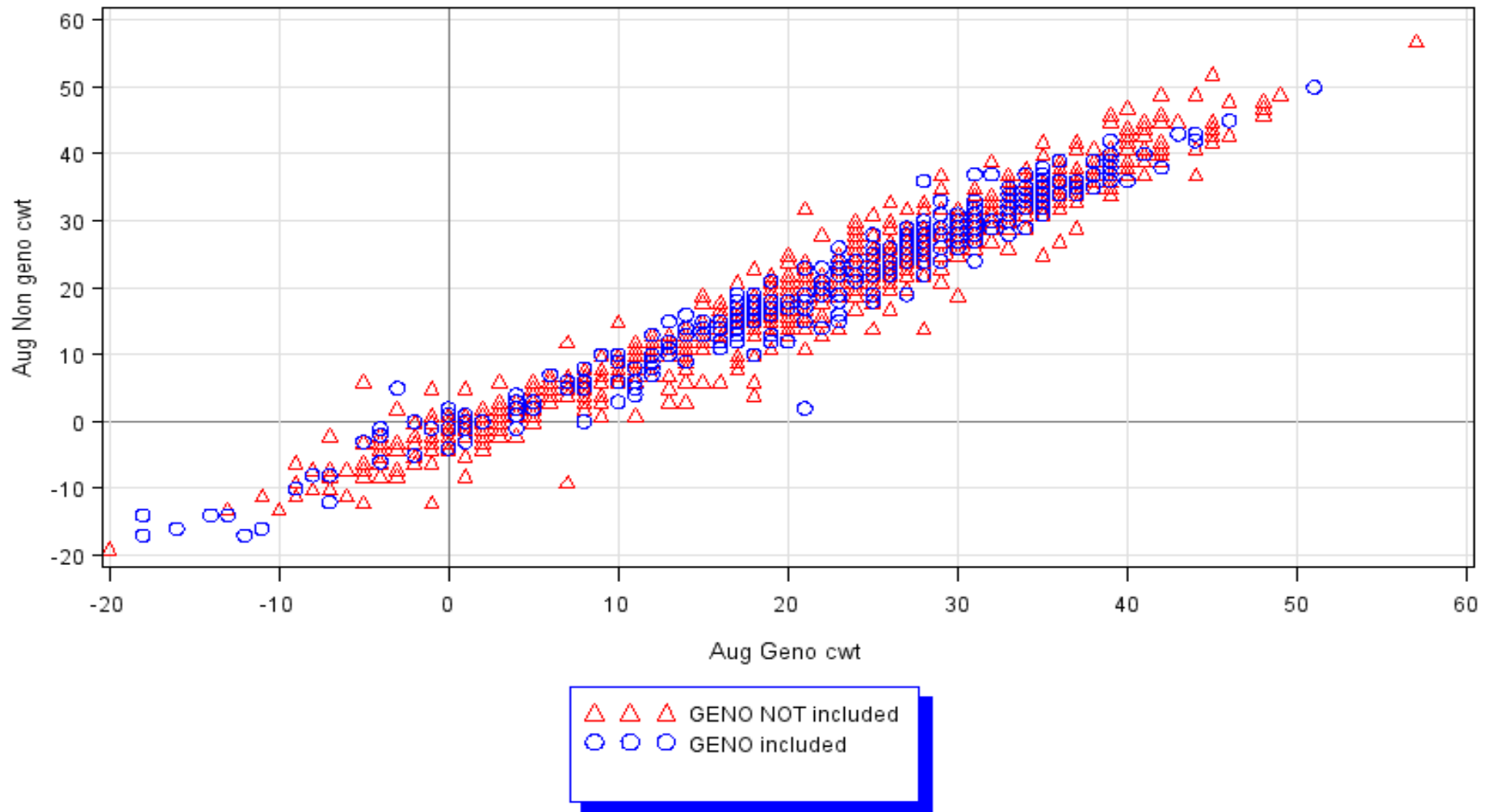


AI sires 50 to 90% rel previous cwt rel

No of bulls 1278 correlation $r = 0.978$

Aug Non Geno cwt = 19.15 {stdev = 13.57}

Aug Geno cwt = 20.65 {stdev = 12.98}

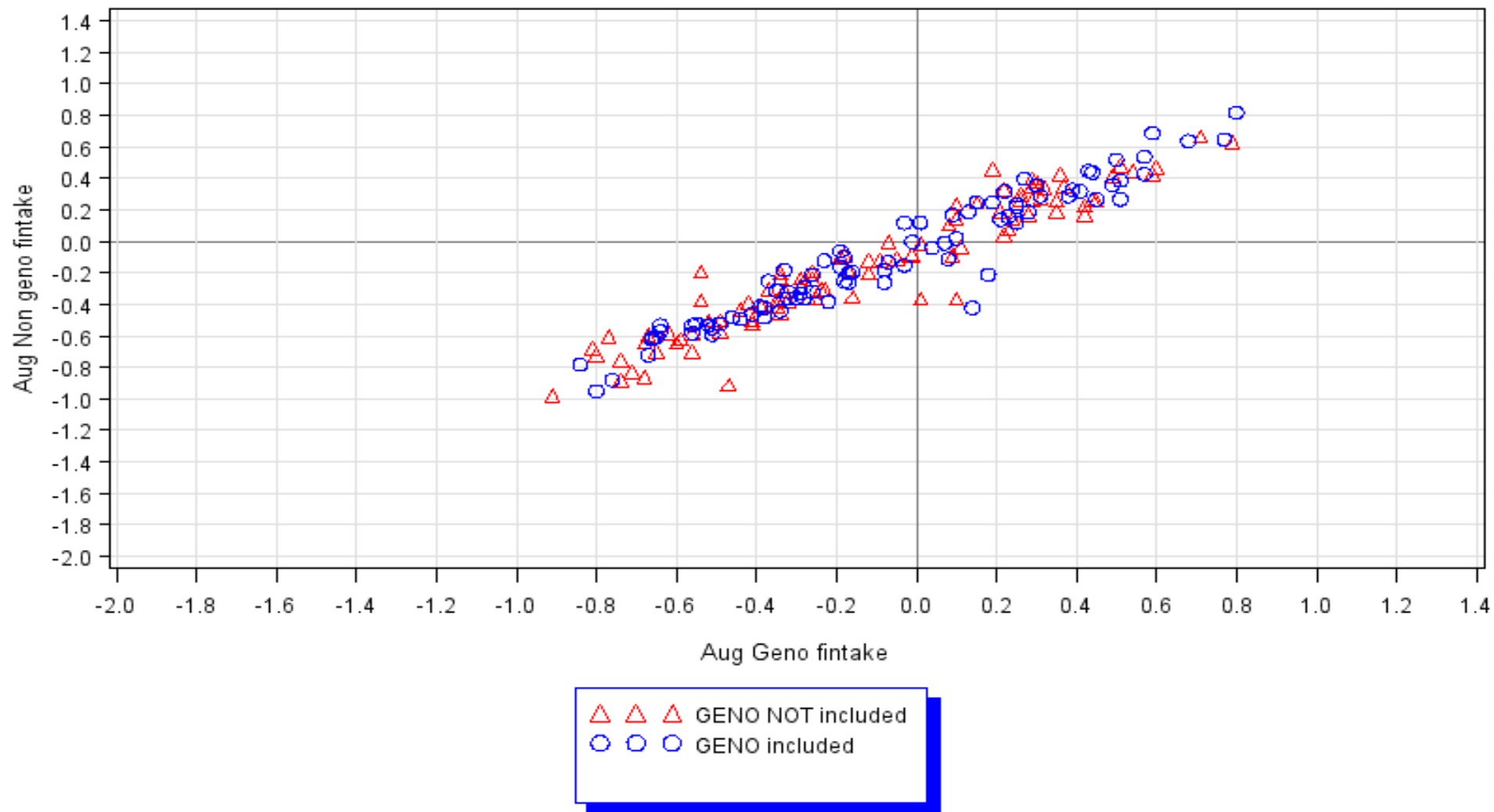


AI sires > 70% rel previous fint rel

No of bulls 181 correlation $r = 0.958$

Aug Non Geno fintake = -0.13 {stdev = 0.4}

Aug Geno fintake = -0.09 {stdev = 0.4}

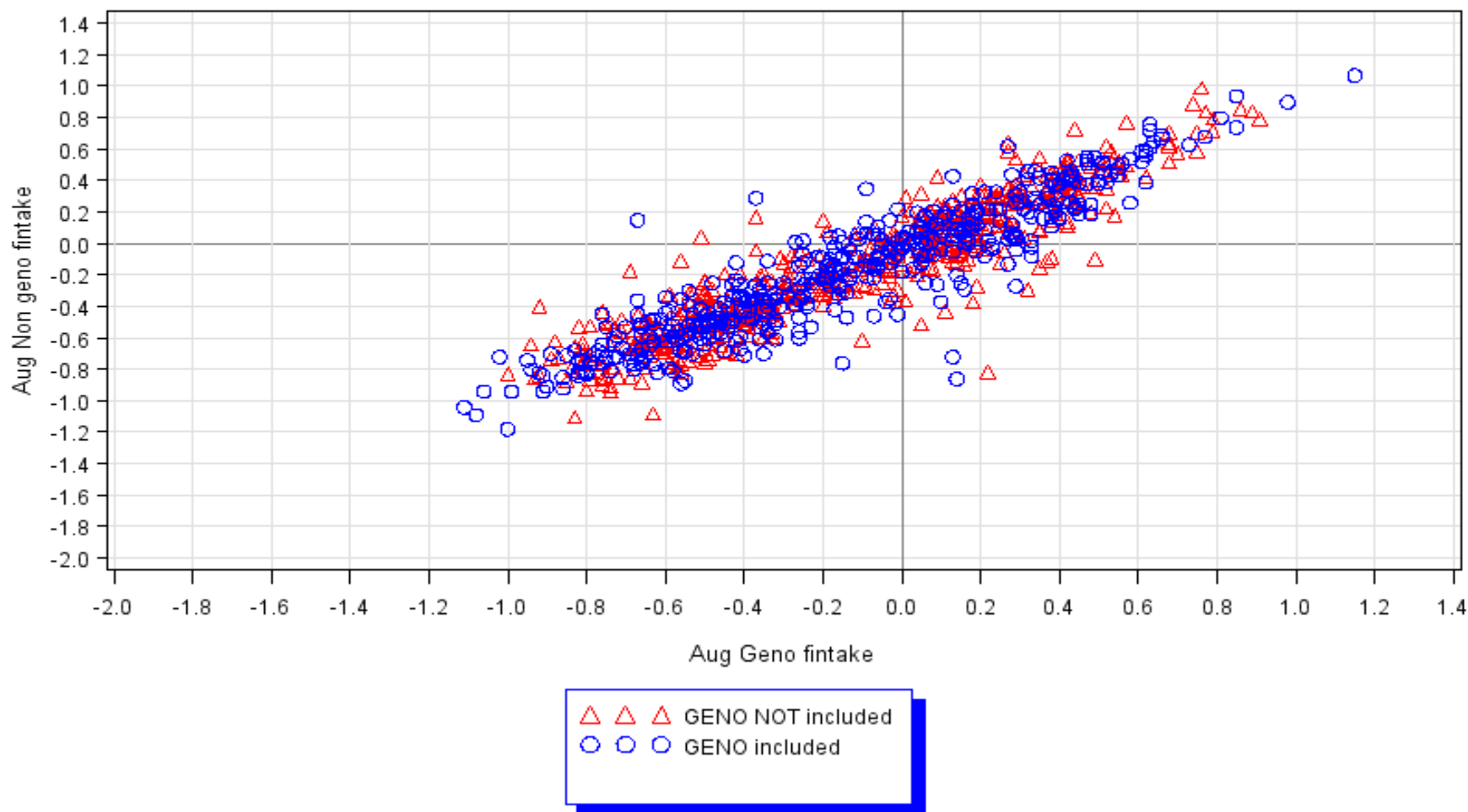


AI sires 40 to 70% rel previous feed int rel

No of bulls 981 correlation $r = 0.958$

Aug Non Geno fintake = -0.15 {stdev = 0.42}

Aug Geno fintake = -0.12 {stdev = 0.42}



AI Code: GUX
 Animal Name: GENEREUX
 National ID: 1991009241
 International ID: LIMFRAM001991009241

Breed: LM (100%)
 Owner: NATIONAL CATTLE BREEDING CNTR
 Date of Birth: 21-APR-1991
 Date of Evaluation: Dec 2015

- Euro-star Index
- Replacement Graphics
- Terminal Graphics
- Linear Type
- Pedigree
- Prev Eval

« Back Compare Evaluations

Calving Interval (Days)

Ranking information

Date of Evaluation	Percentile Rank within breed	Star rating within Breed	PTA	Reliability	Percentile Rank across Breed	Star rating across all Breeds
Dec 2015	3	★☆☆☆☆	5.11	94	2	★☆☆☆☆

Sire Progeny and Progeny Herdmate Information

Date of Evaluation	No. of Progeny	No. of Herdmates	Calving Interval (Days)	
			Average Daughter	Average Herdmate
Dec 2015	914	4407	431	423

Information on Dams of Progeny (Cows mated to the sire)

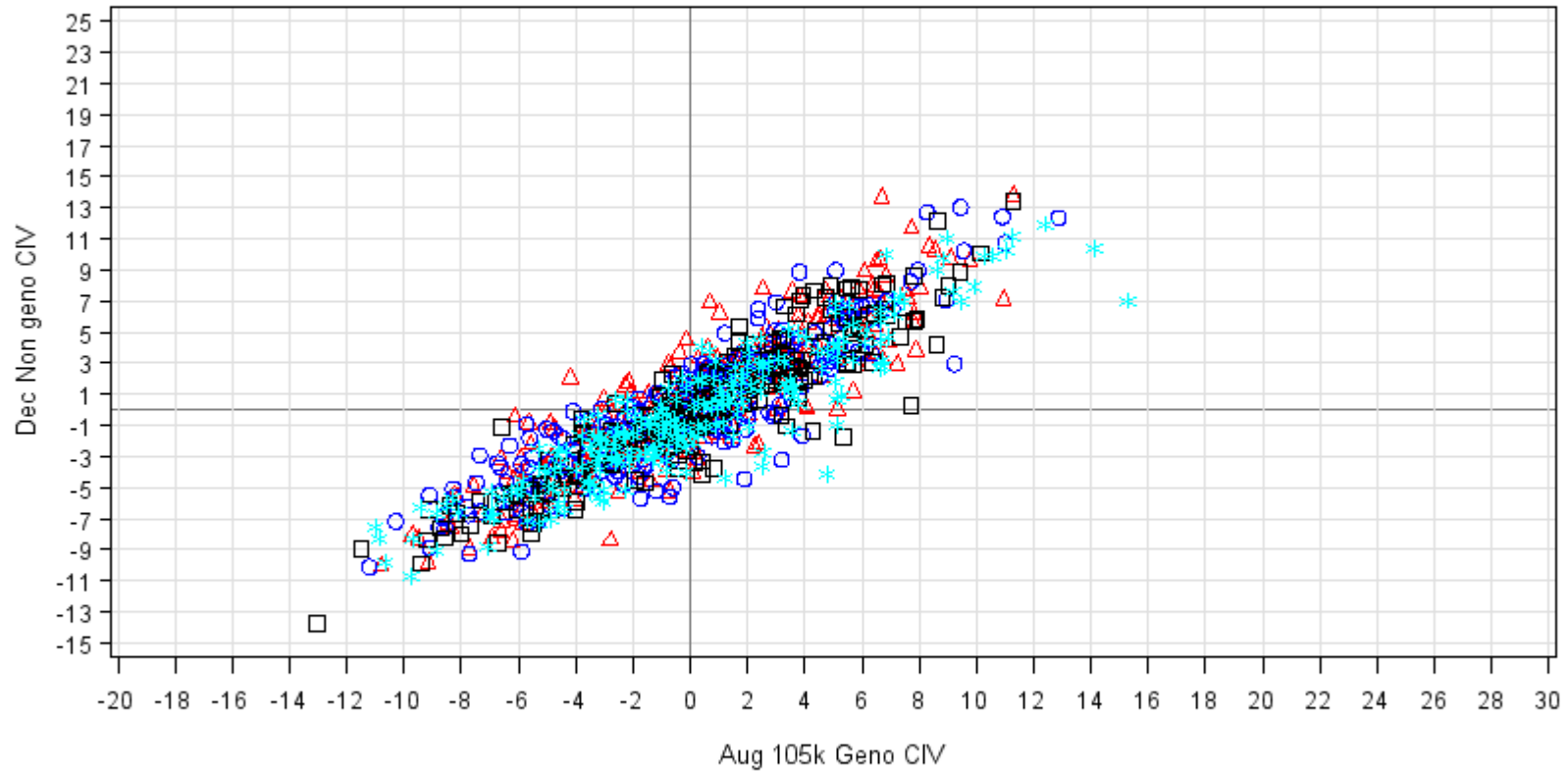
Date of Evaluation	Avg PTA Calving Interval	Average % in Dams By Breed									
		AA	BA	BB	CH	FR	HE	HO	LM	SI	
Dec 2015	-1	0%	0%	0%	0%	0%	0%	1%	95%	1%	

AI sires 50 to 90% rel previous CIV

No of bulls 1018 correlation $r = 0.895$

Dec Non Geno CIV = 0.19 {stdev = 4.38}

Aug 105k Geno CIV = 0.14 {stdev = 4.43}



△ △ △ 50to60 ○ ○ ○ 60to70 □ □ □ 70to80 * * * 80to90

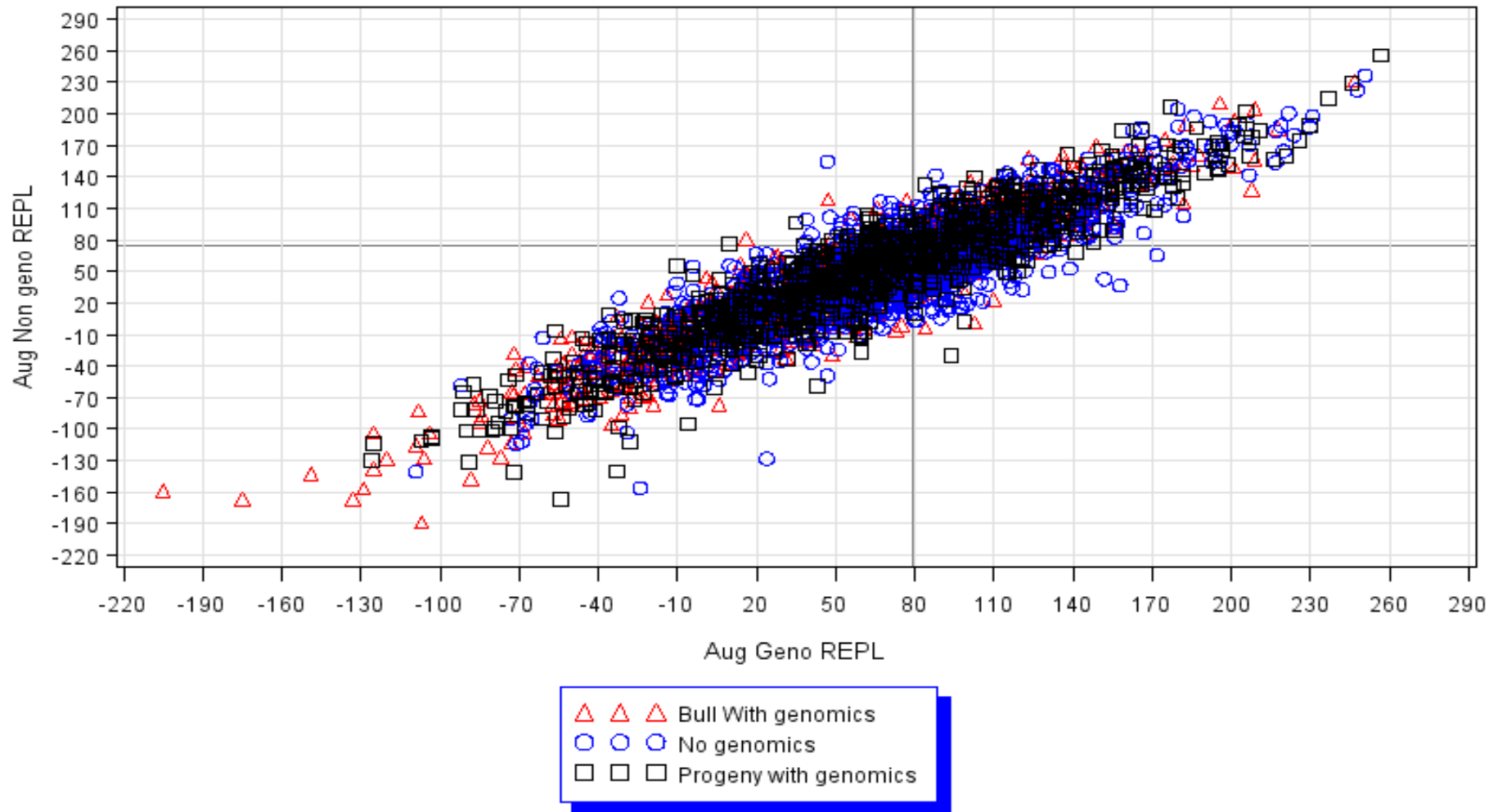
CATEGORY	Bull With genomics	Progeny with genomics	No genomics
Count of Bulls	850	1,137	1,885
Replacement - Aug 15	€40 (63%)	€52 (59%)	€55 (24%)
Replacement - Genomic	€51 (68%)	€66 (59%)	€80 (25%)
Terminal - Aug 15	€91 (73%)	€88 (69%)	€69 (31%)
Terminal - Genomic	€98 (76%)	€95 (69%)	€77 (32%)
Carcass wt - Aug 15	21 kg (81%)	19 kg (76%)	12 kg (37%)
Carcass wt - Genomic	22 kg (85%)	20 kg (78%)	14 kg (38%)
Carcass conf - Aug 15	1.6 (78%)	1.5 (74%)	1.2 (34%)
Carcass conf - Genomic	1.8 (83%)	1.7 (75%)	1.4 (34%)
Feed intake - Aug 15	-0.12 (45%)	-0.11 (40%)	-0.12 (15%)
Feed intake - Genomic	-0.1 (46%)	-0.09 (33%)	-0.09 (13%)
Docility - Aug 15	0.03 (69%)	0.02 (65%)	0.01 (19%)
Docility - Genomic	0.03 (77%)	0.02 (67%)	0.02 (21%)
Age 1st calving- Aug 15	-10 (66%)	-10 (62%)	-4 (23%)
Age 1st calving - Genomic	-10 (70%)	-8 (60%)	0 (22%)
Calving interval- Aug 15	0.7 (56%)	0.2 (50%)	-0.7 (16%)
Calving interval - Genomic	0.5 (59%)	-0.5 (46%)	-2.1 (17%)

AI sires compare Replacement index by genotype status

No of bulls 3580 correlation $r = 0.905$

Aug Non Geno REPL = 47.79 {stdev = 56.49}

Aug Geno REPL = 65.41 {stdev = 58.41}

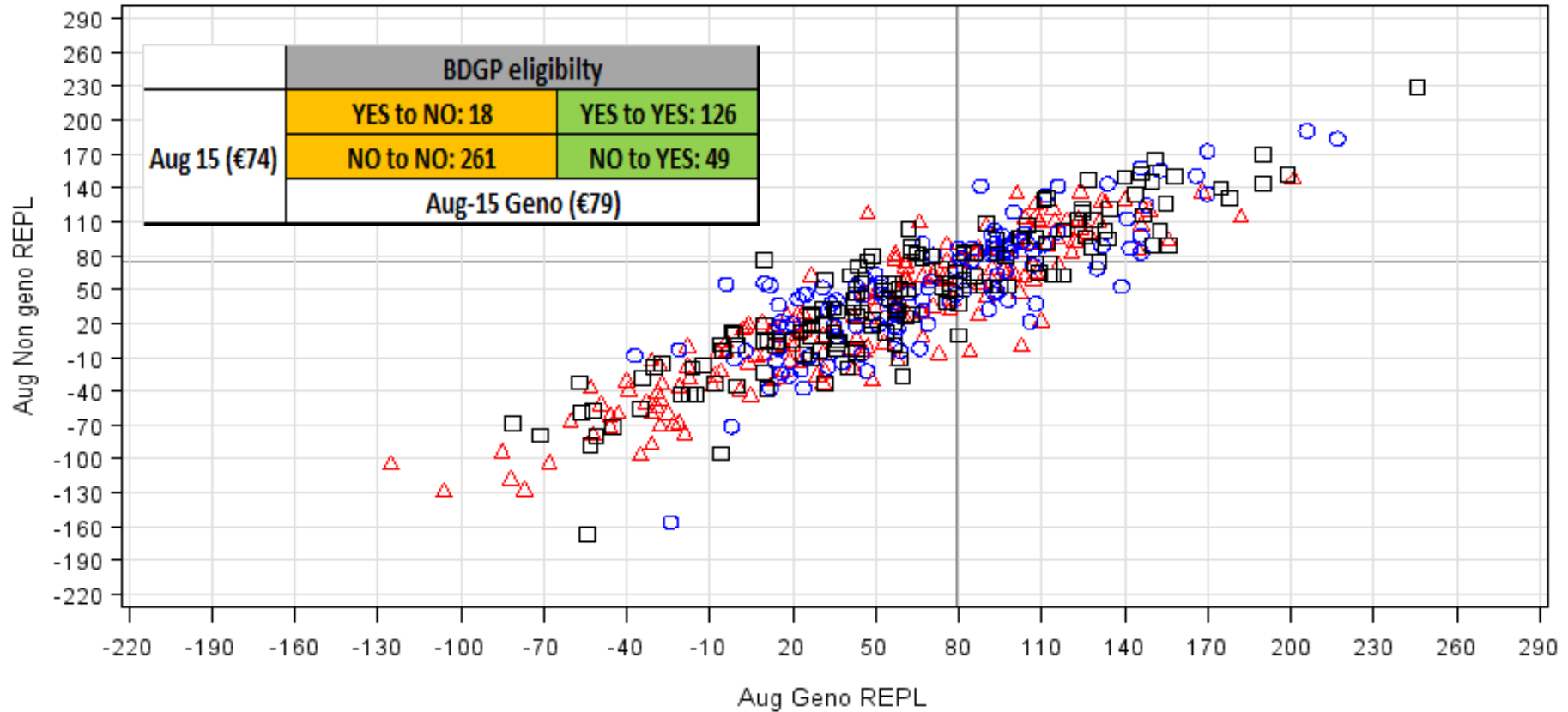


Active AI sires Replacement index by genotype status

No of bulls 454 correlation $r = 0.896$

Aug Non Geno REPL = 40.54 {stdev = 62.82}

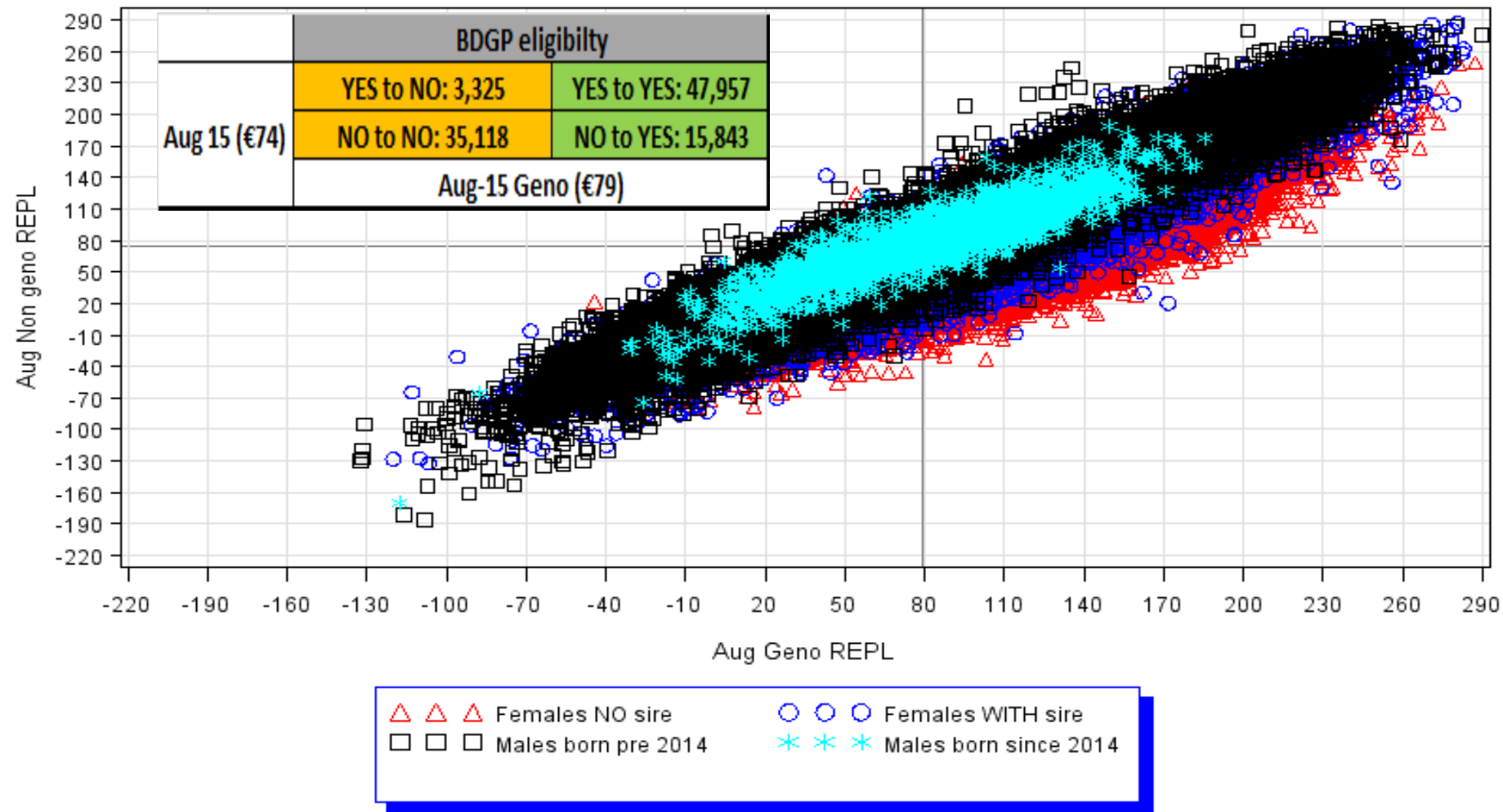
Aug Geno REPL = 59.47 {stdev = 59.53}



- △ △ △ Bull With genomics
- ○ ○ No genomics
- □ □ Progeny with genomics

Non AI Genotyped animals compare Replacement index

No of animals 101522 correlation $r = 0.883$
 Aug Non Geno REPL = 77.37 {stdev = 54.79}
 Aug Geno REPL = 96.38 {stdev = 56.82}



Genotyped non AI animals

CATEGORY	Animals	Aug-15 official Repl index	Aug-15 genomic Repl index	Aug-15 rel %	Aug-15 genomic rel %
Females NO sire	36,300	€79	€118	19	39
Females WITH sire	26,417	€82	€101	32	45
Males born pre 2014	37,499	€73	€73	34	44
Males born since 2014	2,027	€81	€83	21	36

Workplan

- Commencing new round of evaluations next week
- Update phenotypic and pedigree data
- Update genotype file
- More test results when that run is finished in late February/ Early March