IRISH CATTLE BREEDING FEDERATION

Beef Genomic Evaluations.

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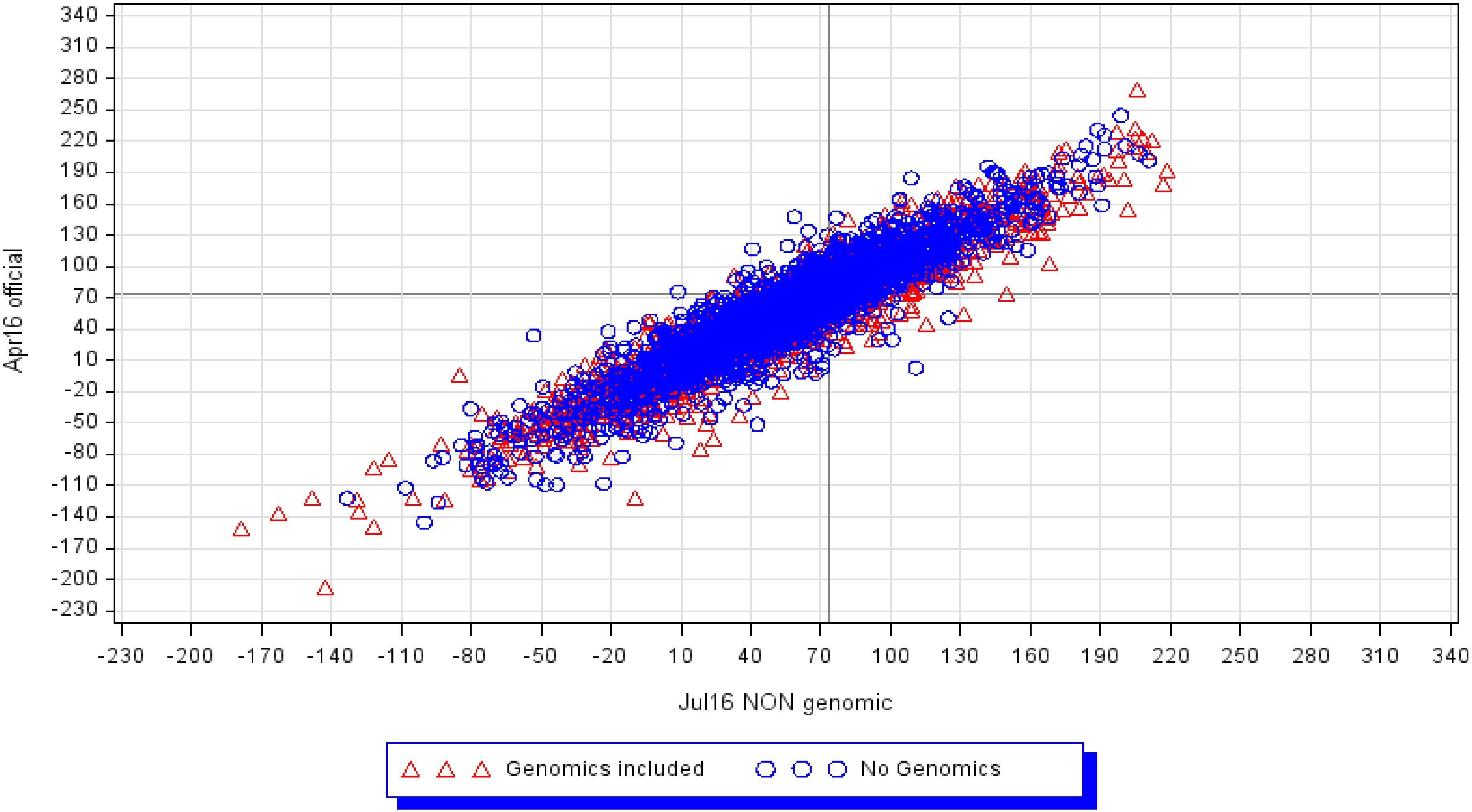
Replacement index Apr16 official v Jul16 NON genomic new milk

No of bulls 3795 correlation r = 0.931

Apr16 official = 56.96 {stdev = 56.75}

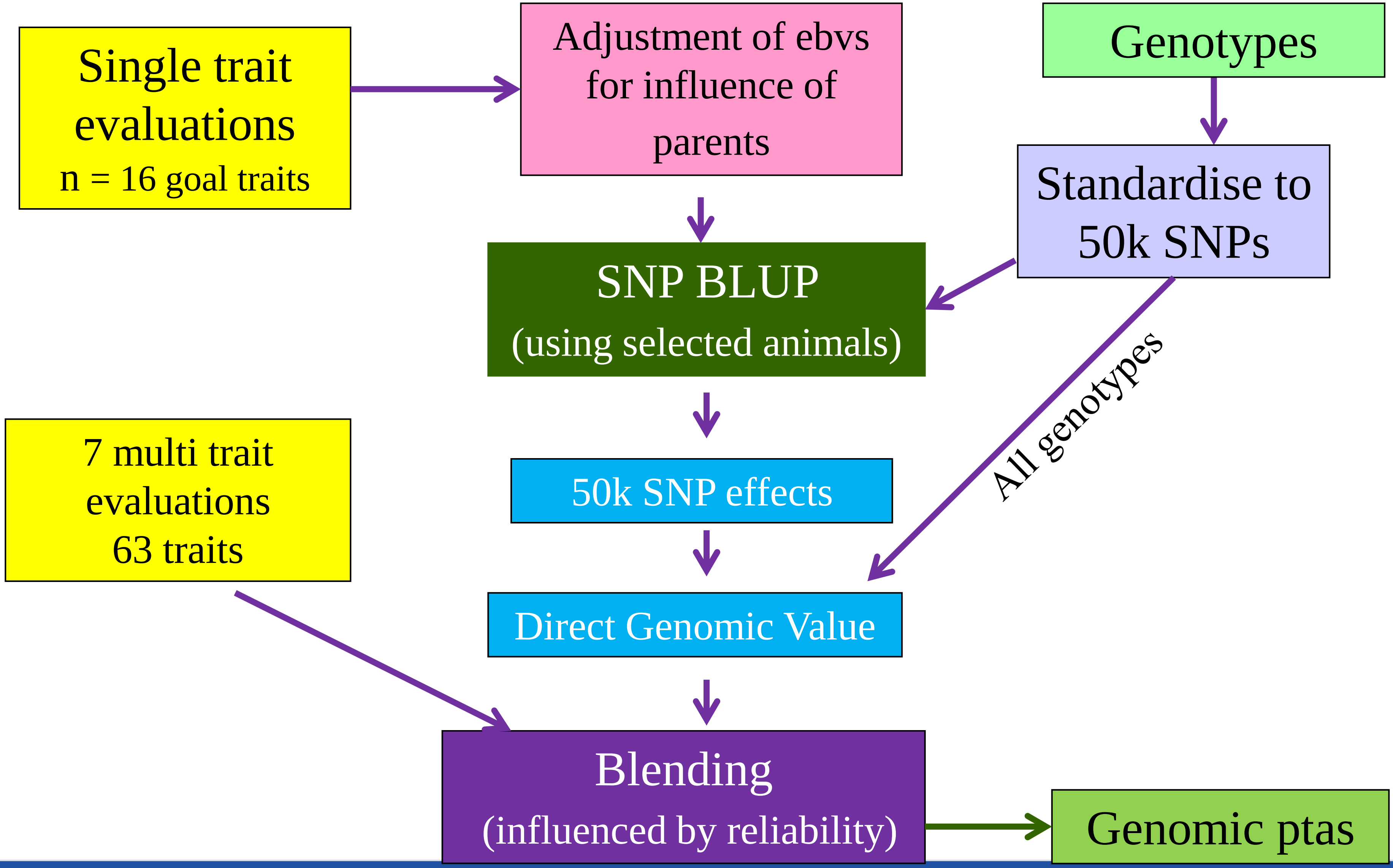
Jul16 NON genomic = 55.7 {stdev = 50.8}



Update since last meeting

- New blending method
- New data, pedigree and genotypes
- Combining of maternal wwt and cow milk score

Genomic evaluation steps



Single trait evaluations
n = 16 goal traits

Adjustment of ebvs for influence of parents

Genotypes

Standardise to 50k SNPs

SNP BLUP
(using selected animals)

All genotypes

7 multi trait evaluations
63 traits

50k SNP effects

Direct Genomic Value

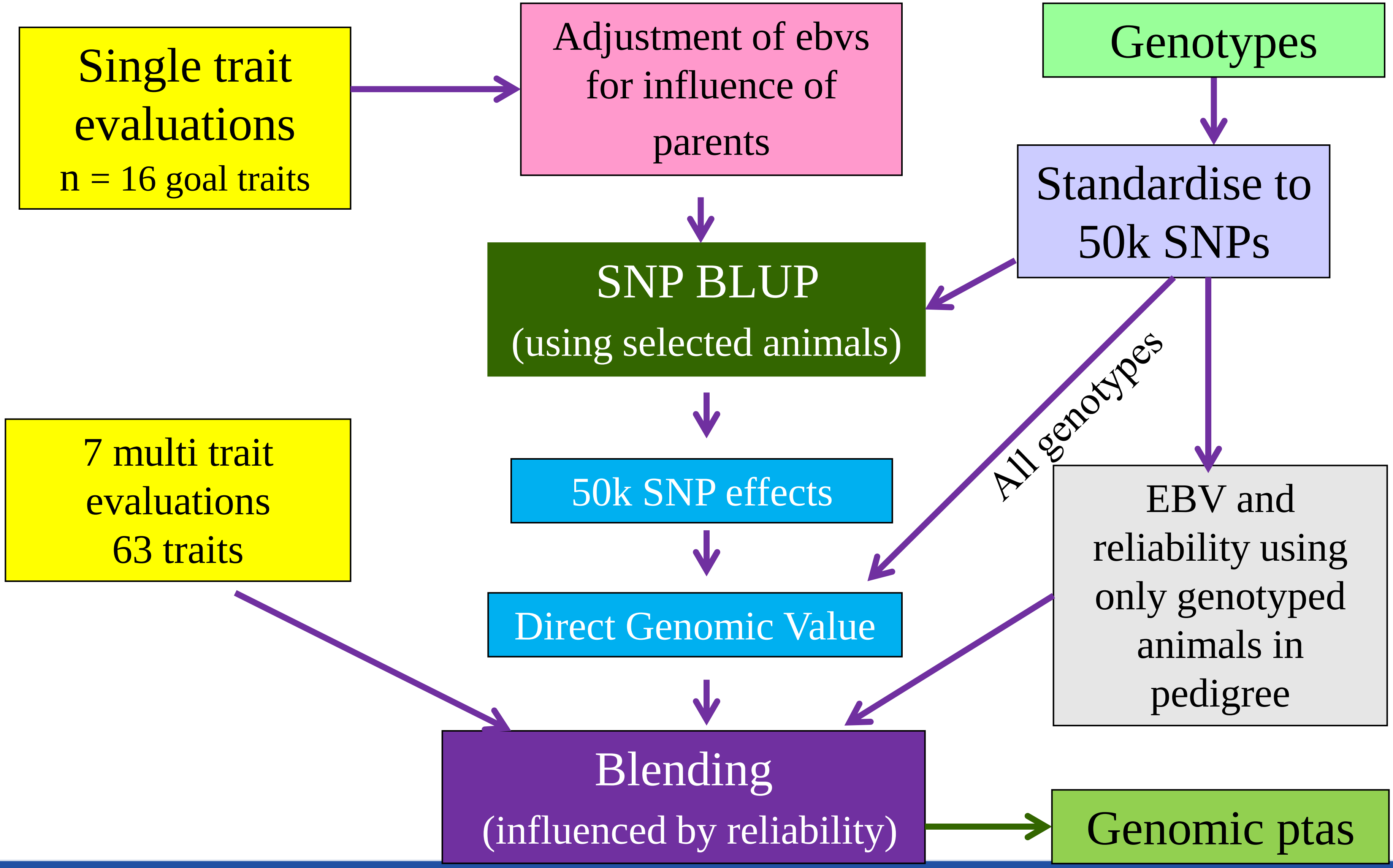
Blending
(influenced by reliability)

Genomic ptas

Blending method

- June method: Combined 2 sources of info: Traditional EBV and DGV
- Works okay where most of ancestry is also genotyped and where traits have a lot of data in traditional evaluations
- But: Many genotyped animals have no sire, dam or mgs genotyped
- Also traits like feed intake and cow live weight do not have a huge level of data
- Additional step needed

Genomic evaluation steps



Single trait evaluations
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EBV and reliability using only genotyped animals in pedigree

Direct Genomic Value

Blending
(influenced by reliability)

Genomic ptas

Sire file circulated

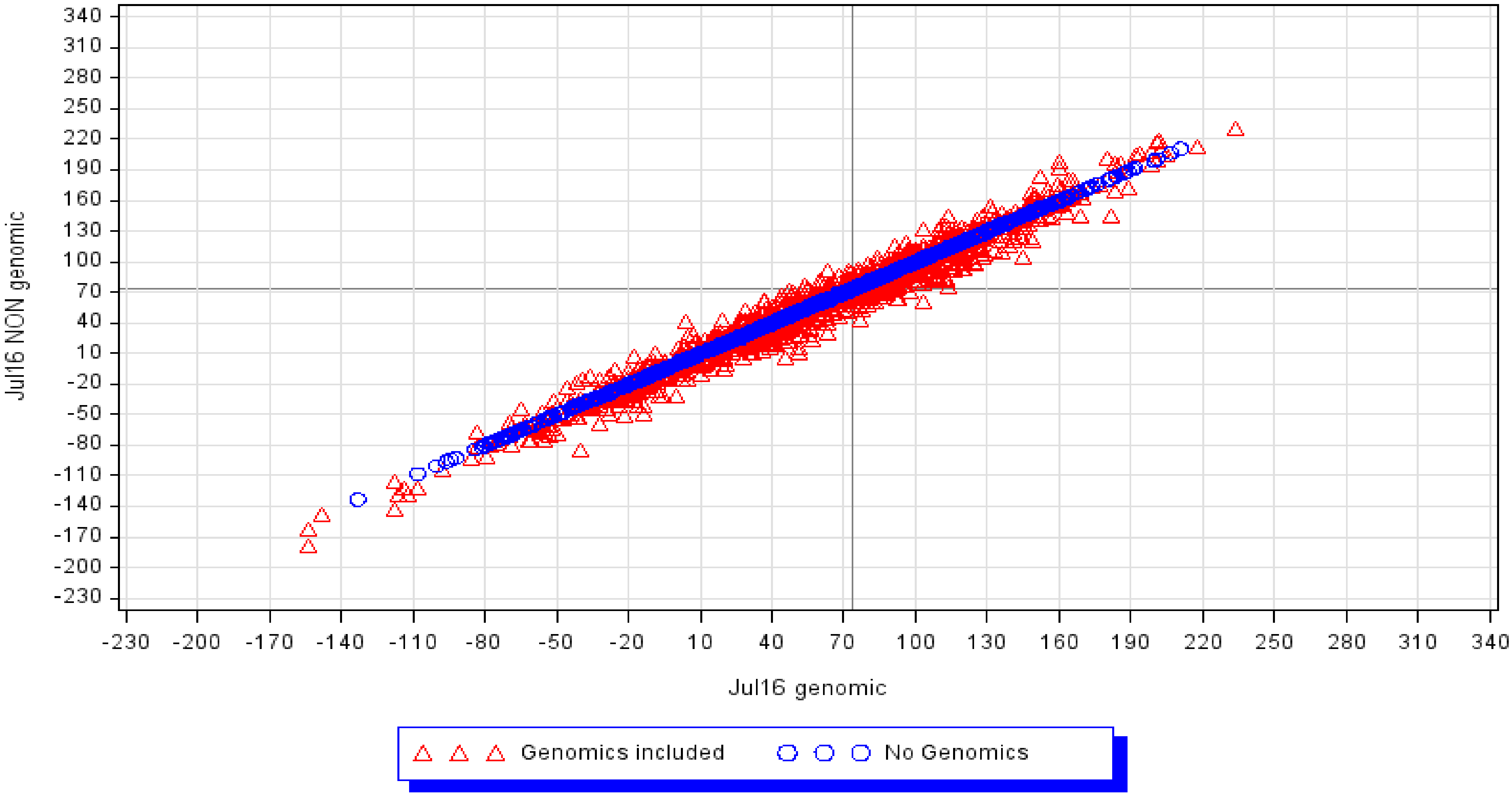
- 3,795 beef AI sires
- 1,505 with a genotype and genomics
- 439 with a sire genotyped with genomics
- 2,290 sires with no genotype
- 86 sires requested but no sample back
- 51 with DNA received, awaiting genotypes
- 38 with poor DNA, DNA mis-match or other genotype problem

Replacement index Jul16 NON genomic v Jul16 with genomics new milk

No of bulls 3795 correlation r = 0.992

Jul16 NON genomic = 55.7 {stdev = 50.8}

Jul16 genomic = 56.62 {stdev = 50.16}

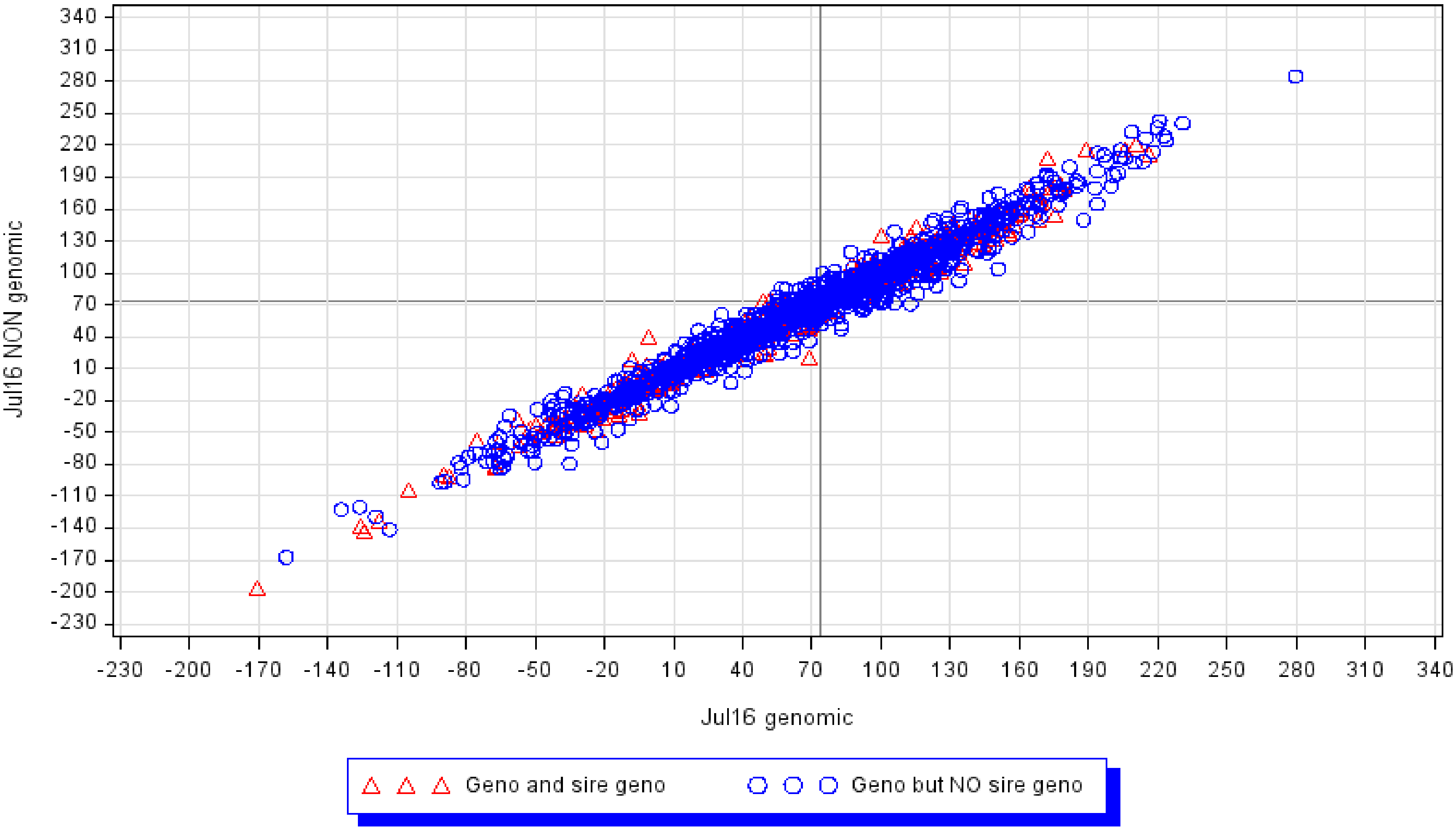


Replacement index Jul16 NON genomic v Jul16 with genomics: genotypes sires

No of bulls 1505 correlation r = 0.984

Jul16 NON genomic = 61.31 {stdev = 62.39}

Jul16 genomic = 63.12 {stdev = 60.79}



Combining maternal weaning weight and cow milk score

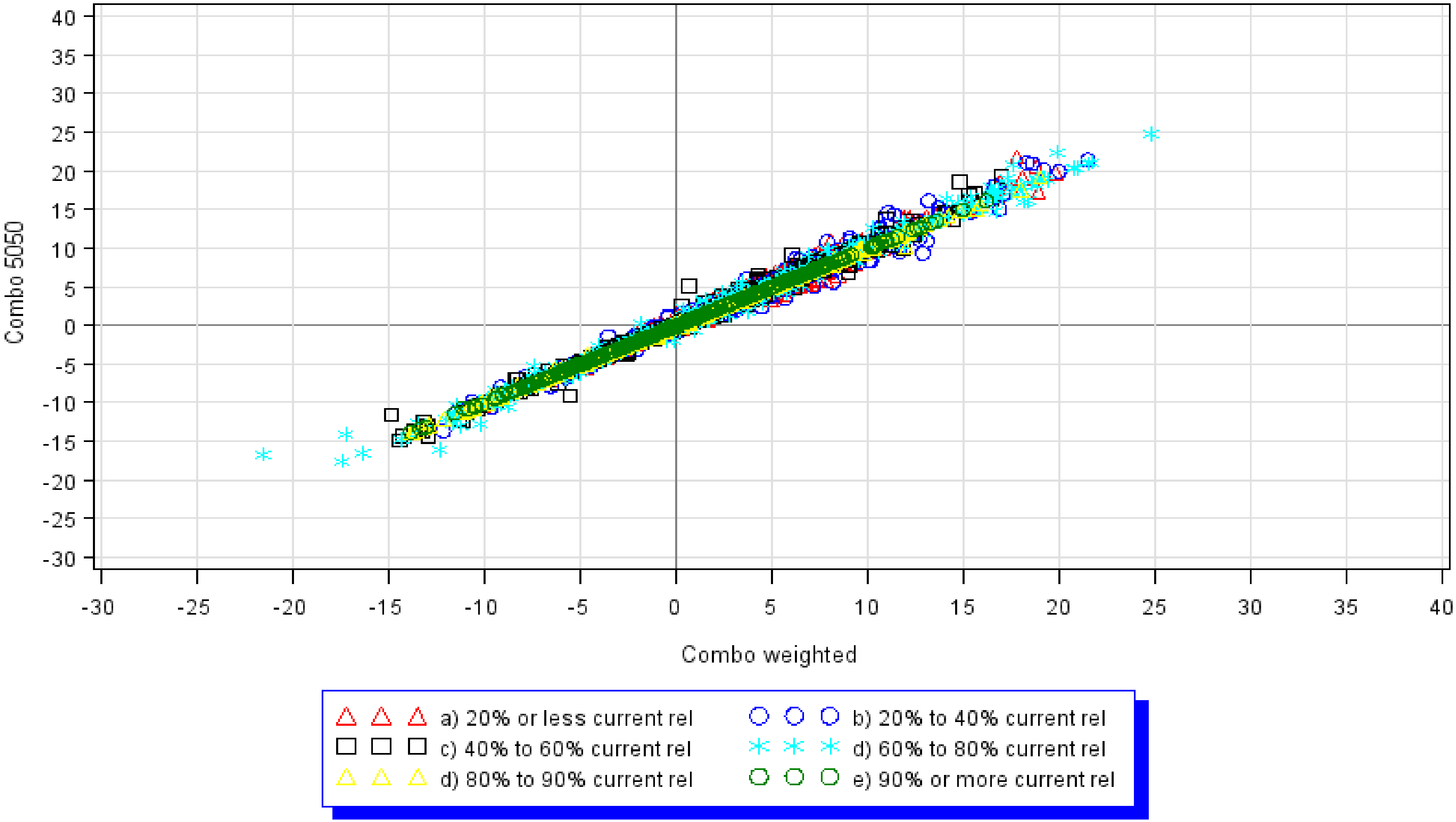
- Simple average of the two
- Weight according to single trait reliability
- If higher reliability for any one trait then more influence from that trait
- Not a huge difference as multi-trait evaluation will drive both in the same direction with correlation of 0.8

Milk combo5050 v Combo wtd : AI sires

No of animals 3696 correlation r = 0.996

Combo 5050 = 2.23 {stdev = 5.75}

Combo wtd = 2.15 {stdev = 5.68}

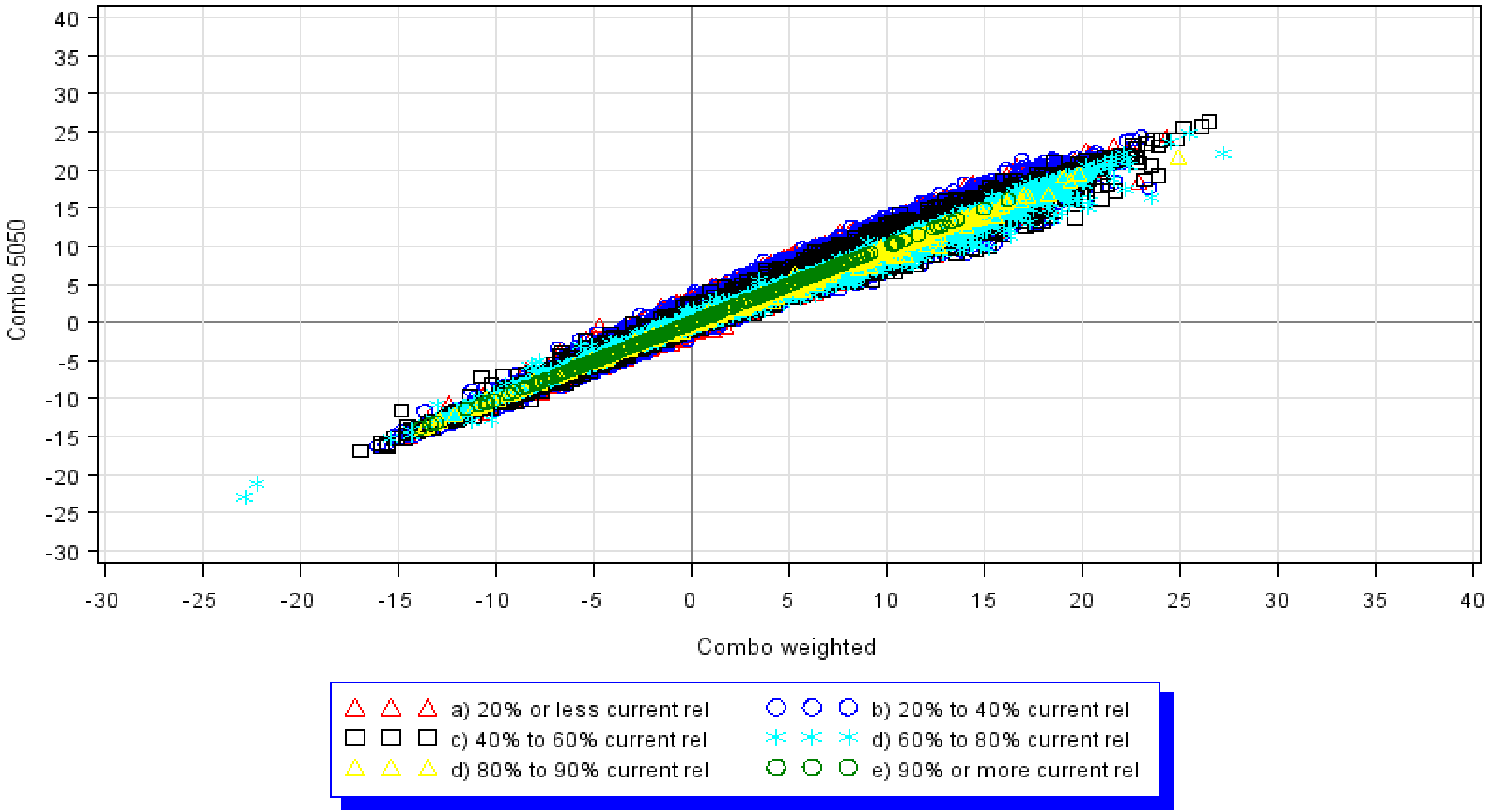


Milk combo5050 v Combo wtd : All geno animals

No of animals 336139 correlation r = 0.993

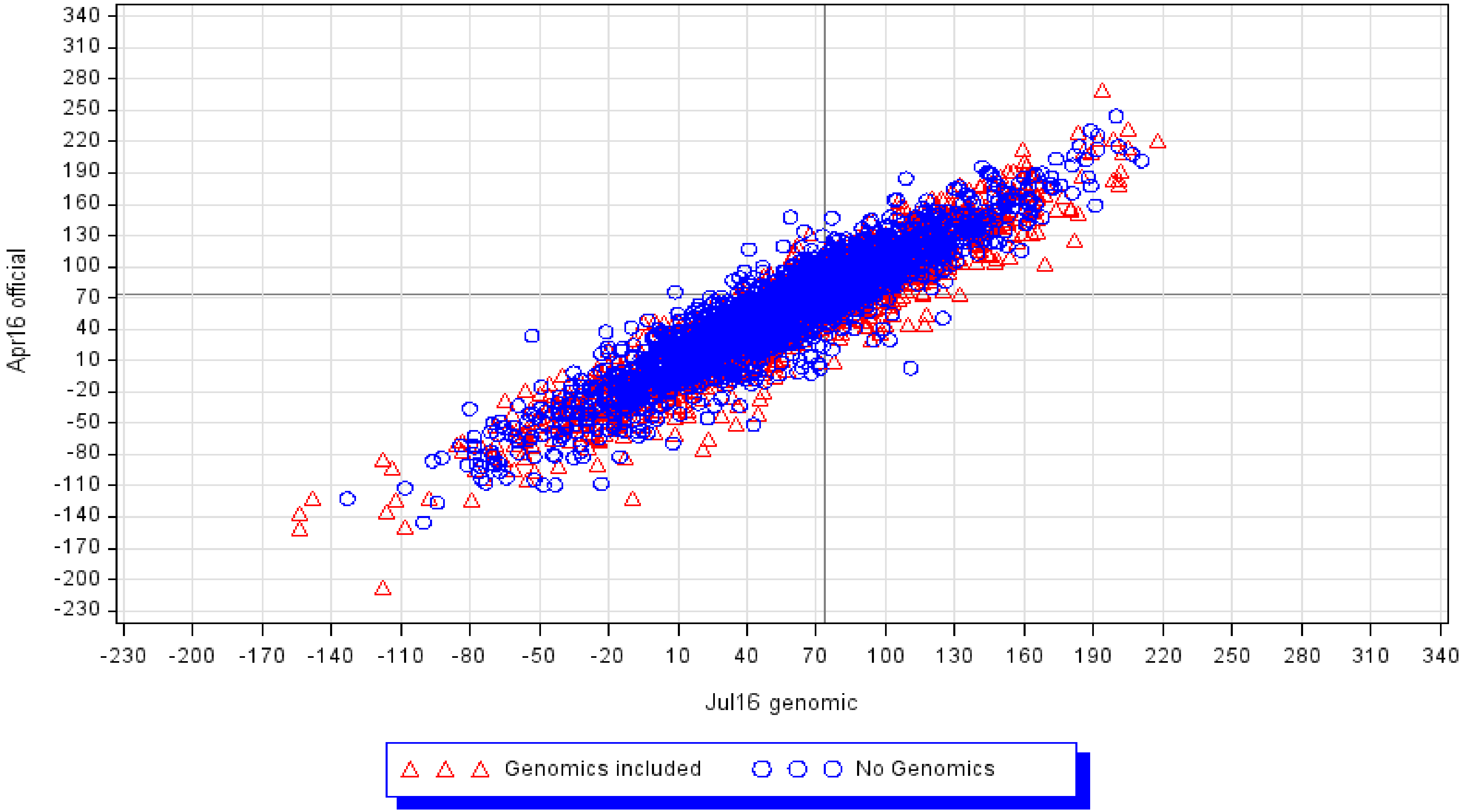
Combo 5050 = 3.6 {stdev = 5.17}

Combo wtd = 3.3 {stdev = 5}



Replacement index Apr16 official v Jul16 with genomics new milk

No of bulls 3795 correlation r = 0.927
Apr16 official = 56.96 {stdev = 56.75}
Jul16 genomic = 56.62 {stdev = 50.16}



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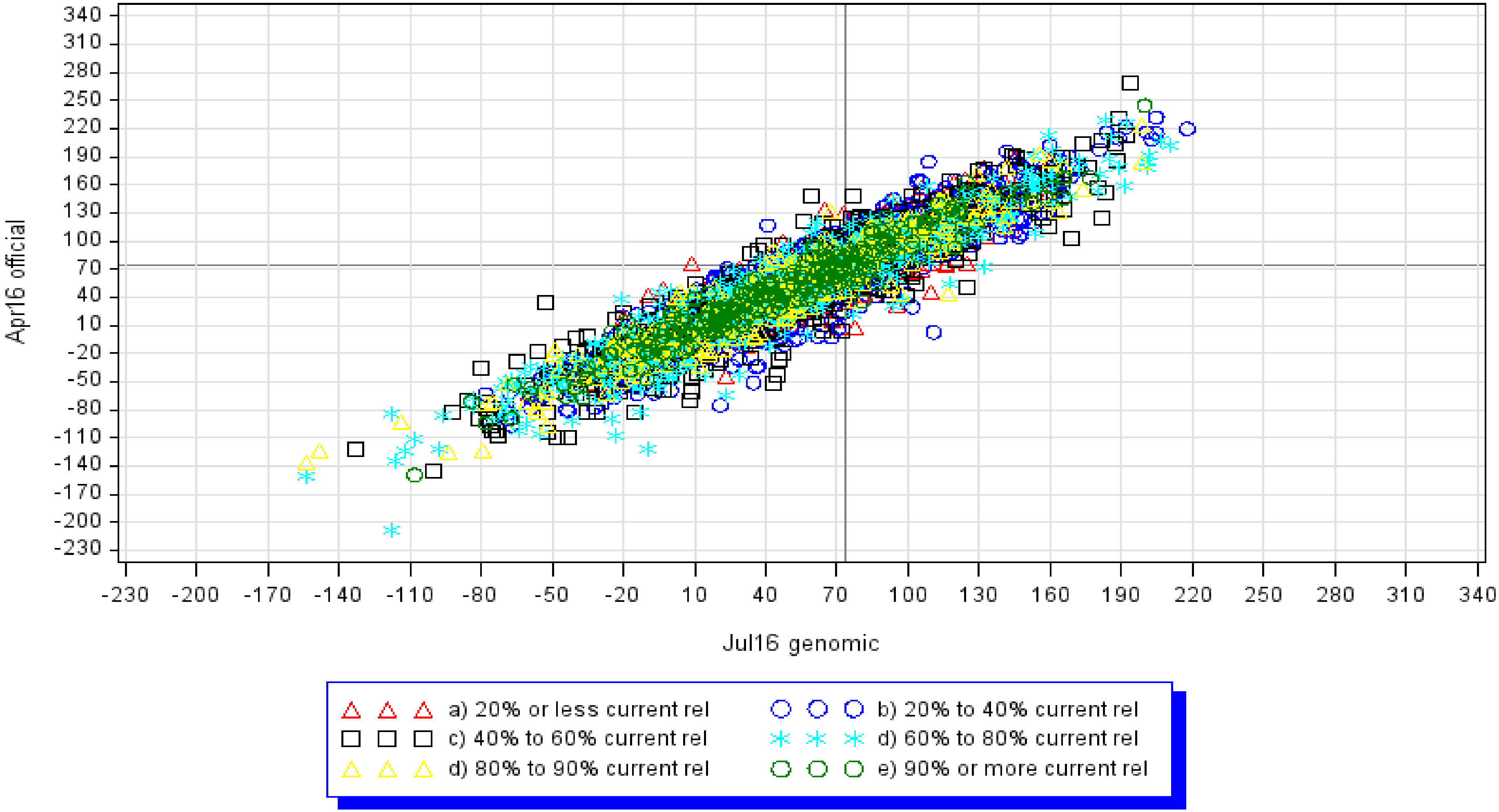
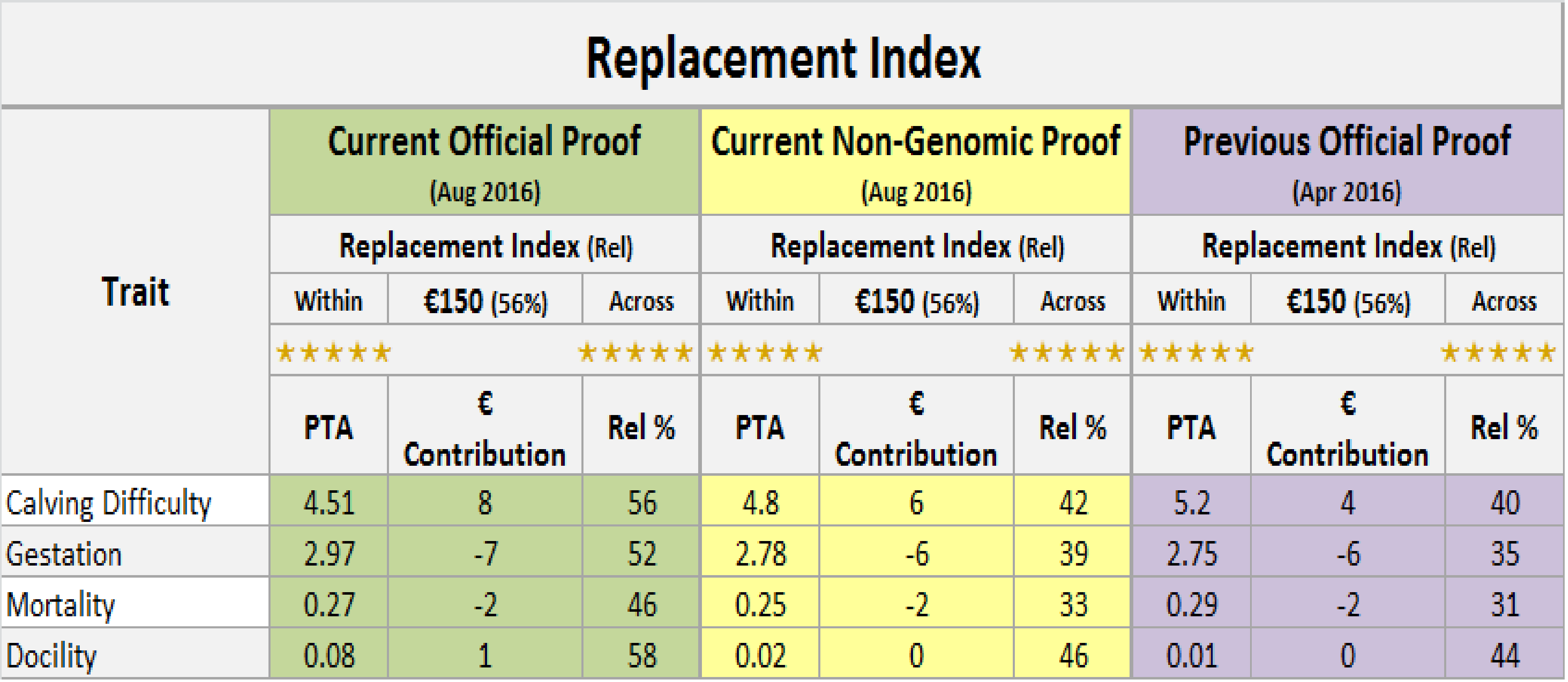


Next Steps

- Updated calving run will be included
- Loading of files to the database
- Calculation of indexes for all animals
- New bull search facility to view impact of genomics on proofs
- Automation of evaluations (currently 197 different steps in process)

New bull search tab



Replacement Index

Trait	Current Official Proof (Aug 2016)			Current Non-Genomic Proof (Aug 2016)			Previous Official Proof (Apr 2016)		
	Replacement Index (Rel)			Replacement Index (Rel)			Replacement Index (Rel)		
	Within	€150 (56%)	Across	Within	€150 (56%)	Across	Within	€150 (56%)	Across
	★★★★★		★★★★★	★★★★★		★★★★★	★★★★★		★★★★★
	PTA	€ Contribution	Rel %	PTA	€ Contribution	Rel %	PTA	€ Contribution	Rel %
Calving Difficulty	4.51	8	56	4.8	6	42	5.2	4	40
Gestation	2.97	-7	52	2.78	-6	39	2.75	-6	35
Mortality	0.27	-2	46	0.25	-2	33	0.29	-2	31
Docility	0.08	1	58	0.02	0	46	0.01	0	44

Ability to see impact of genomics versus new data