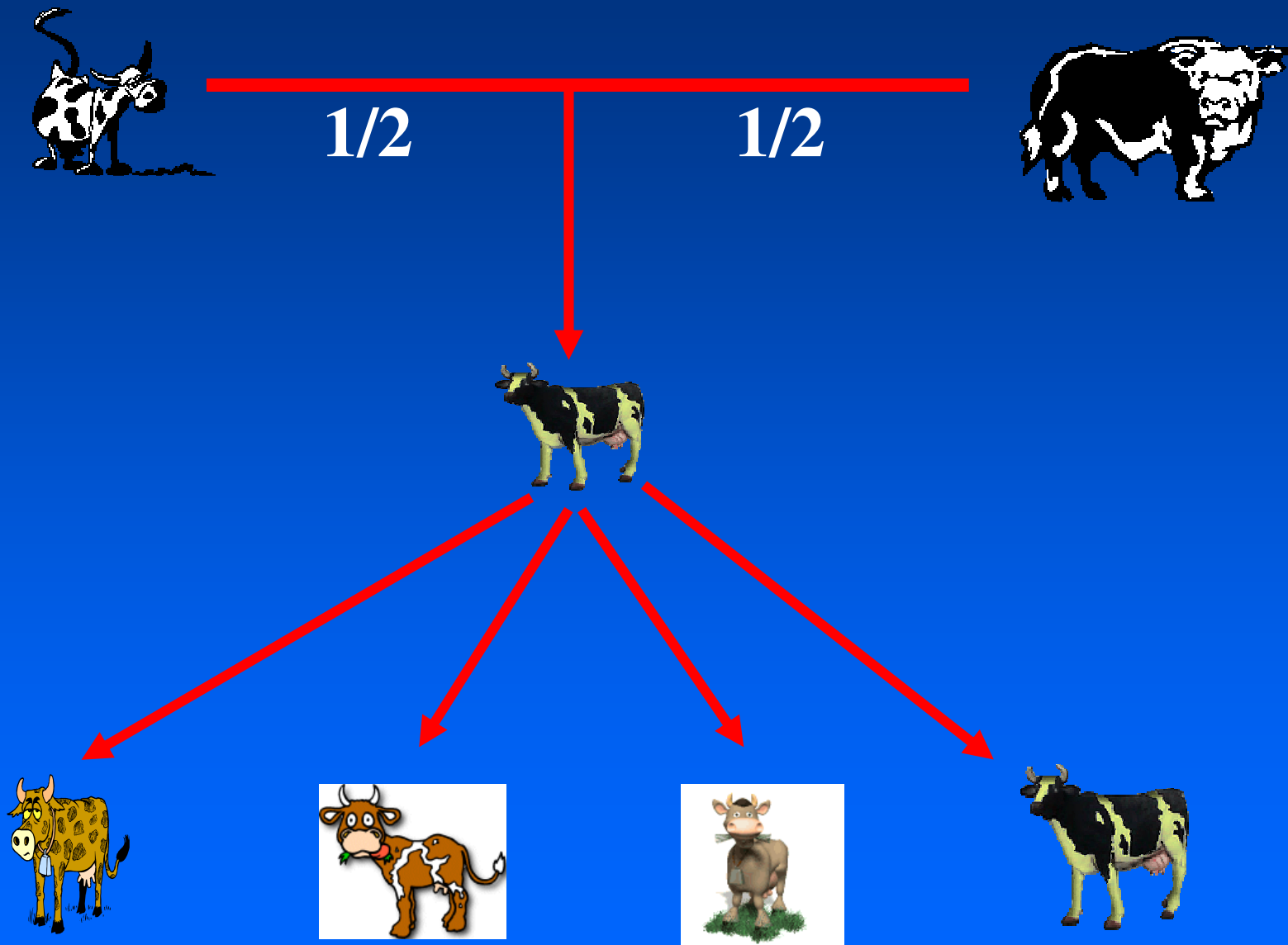


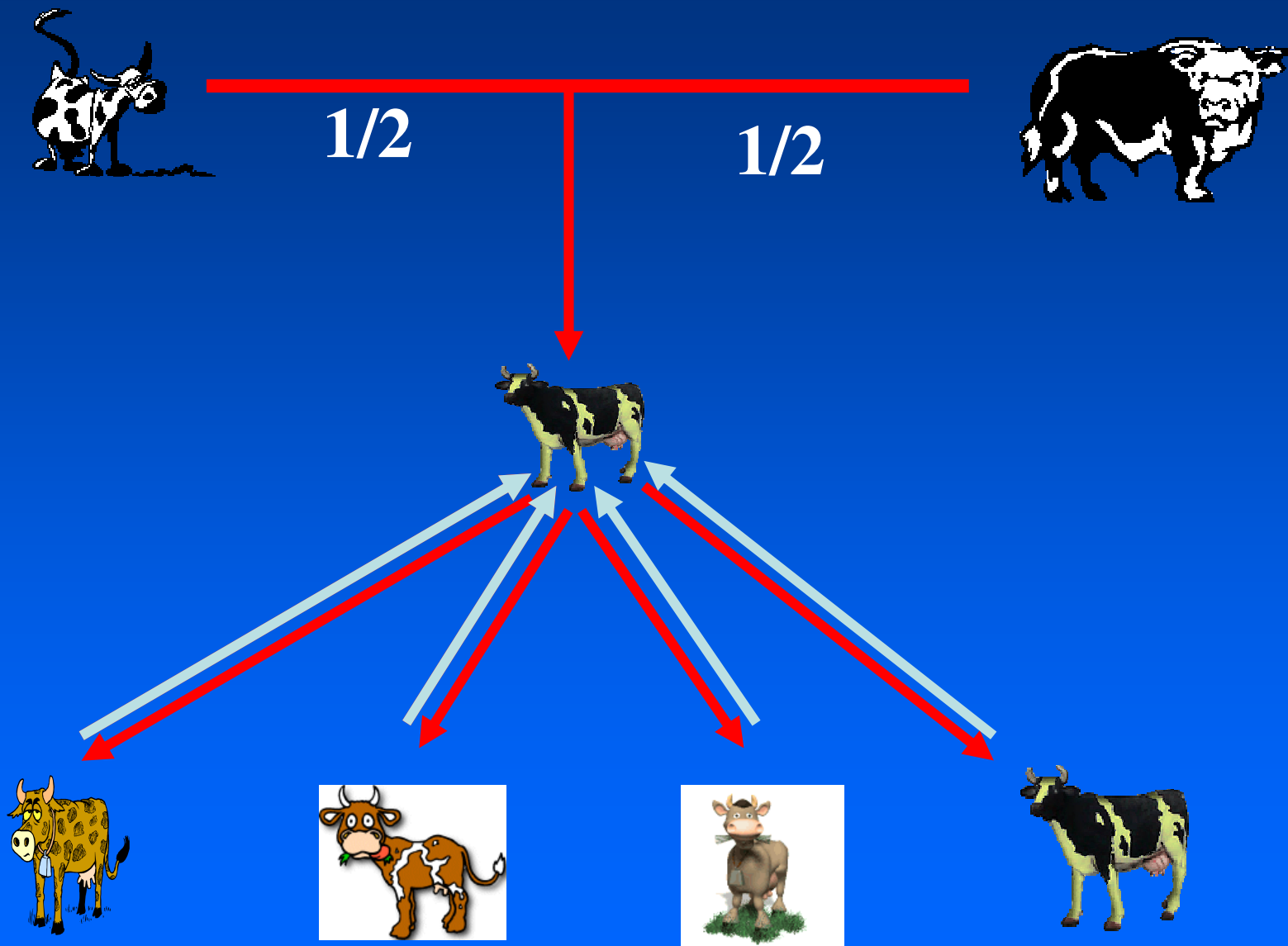
Genomic selection

Donagh Berry
21st January 2009

Present approach



Present approach



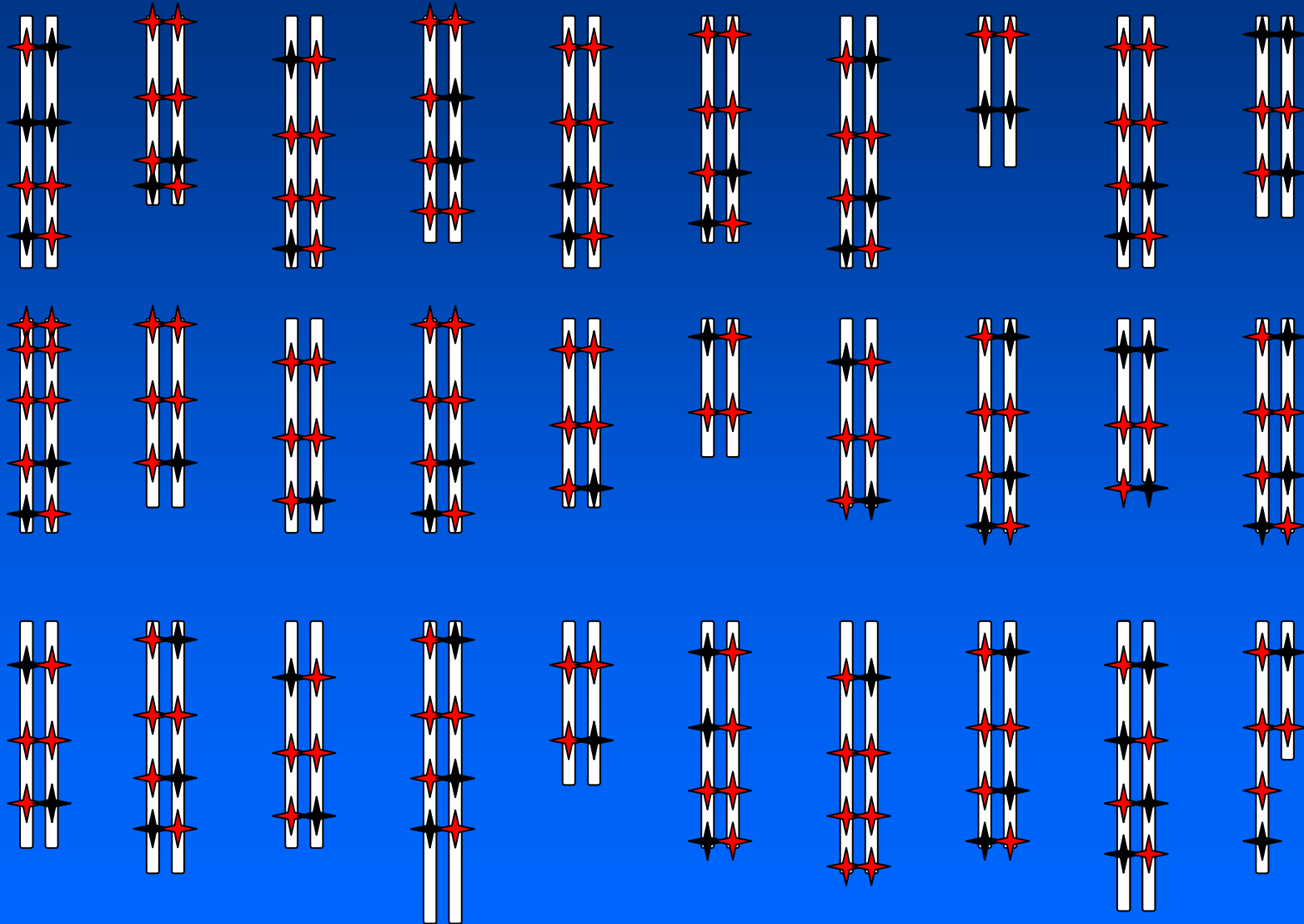
Slogan v Addison

Trait	ESZ	EZA
EBI	€80	€35
Milk kg	64	754
Fat kg	5	8
Protein kg	5	20
Calv. Int.	-2.7	4.42
Survival	0.96	-1.75

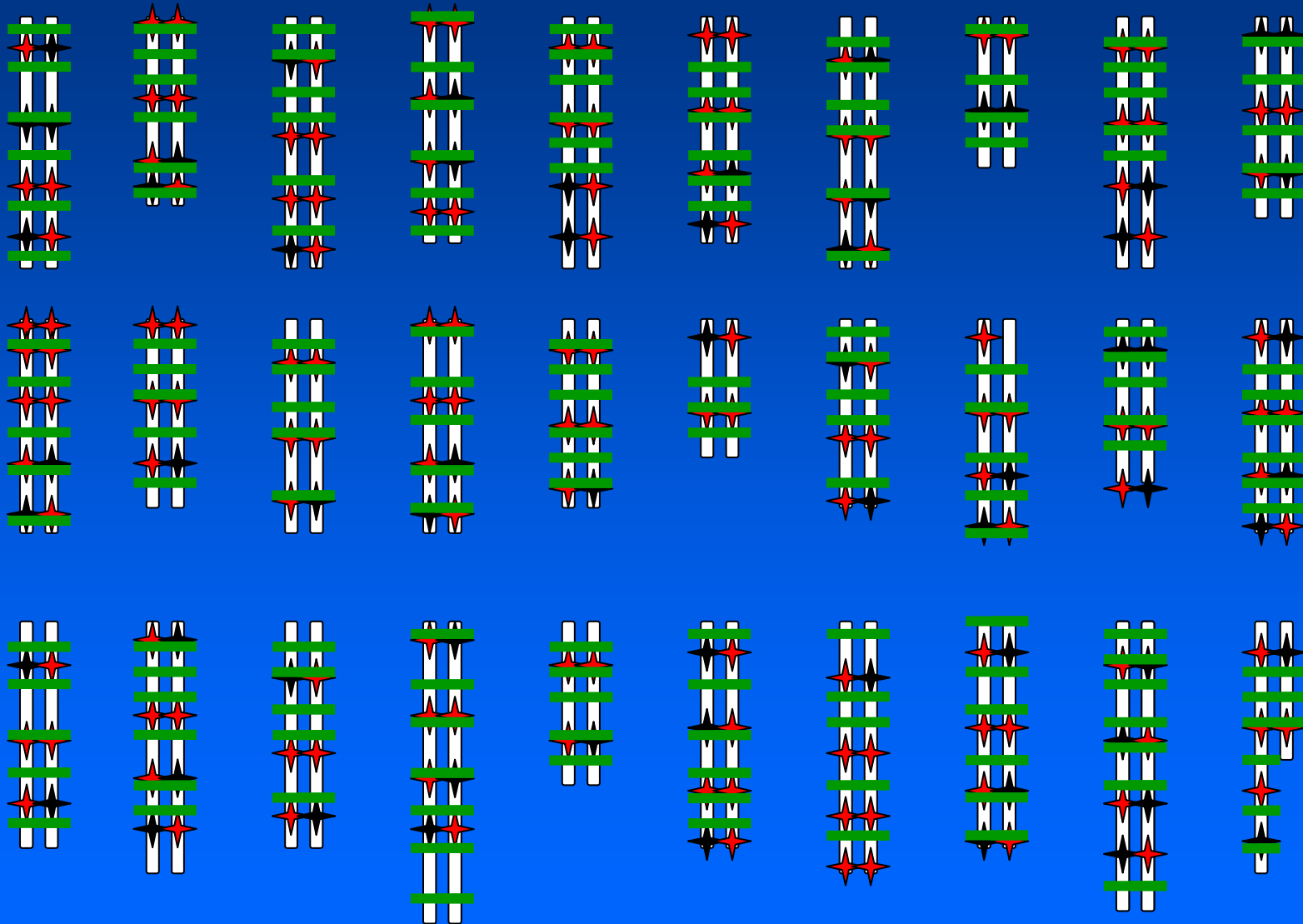
Background

- Idea written down in 2001 – Theo Meuwissen and colleagues
- Really became possible in late 2007

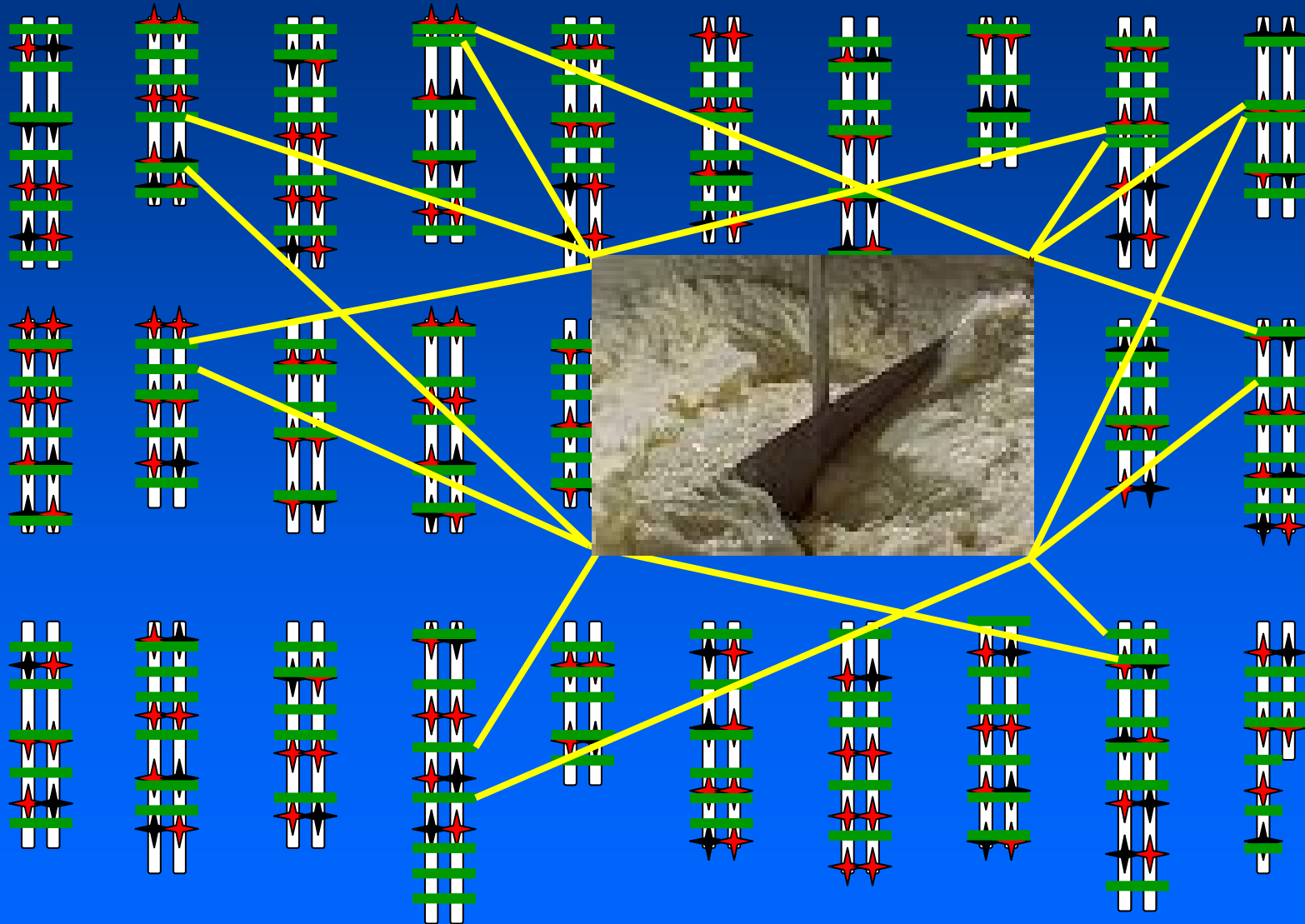
Genomic selection



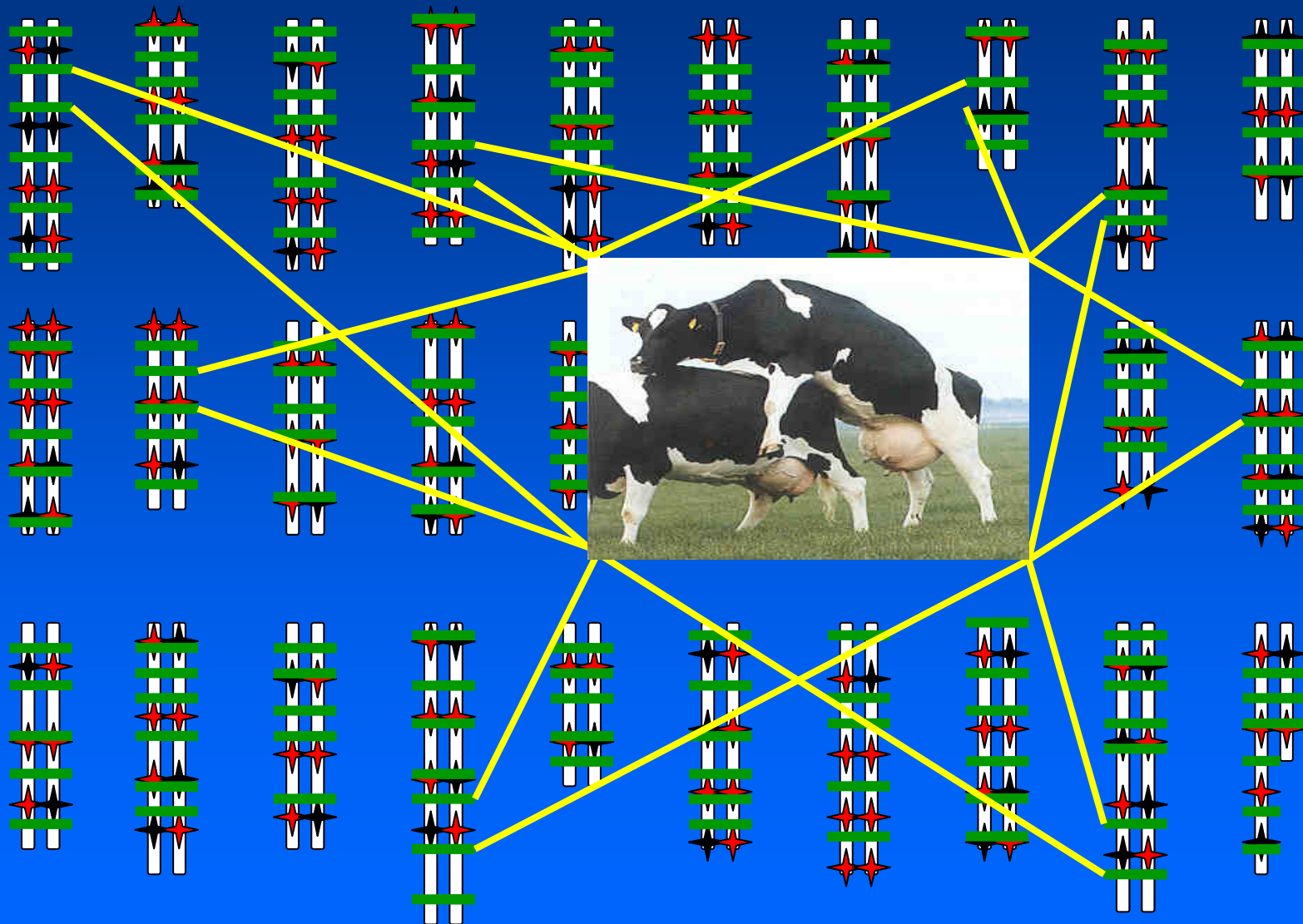
Genomic selection



Genomic selection



Genomic selection



Requirements

- **Big training population of animals proven in Ireland**
- **Procedures to get access to data quickly**
- **Software to undertake the analysis**
- **Knowledge on the optimal breeding program**

Procedures

- Get proofs from National Genetic evaluation
- Calculate parental averages and reliabilities
- Gather SNP data and clean
- Make pedigree file
- “Deregress” or remove pedigree effects
- Undertake genomic selection
- Blend genomic selection and parental average

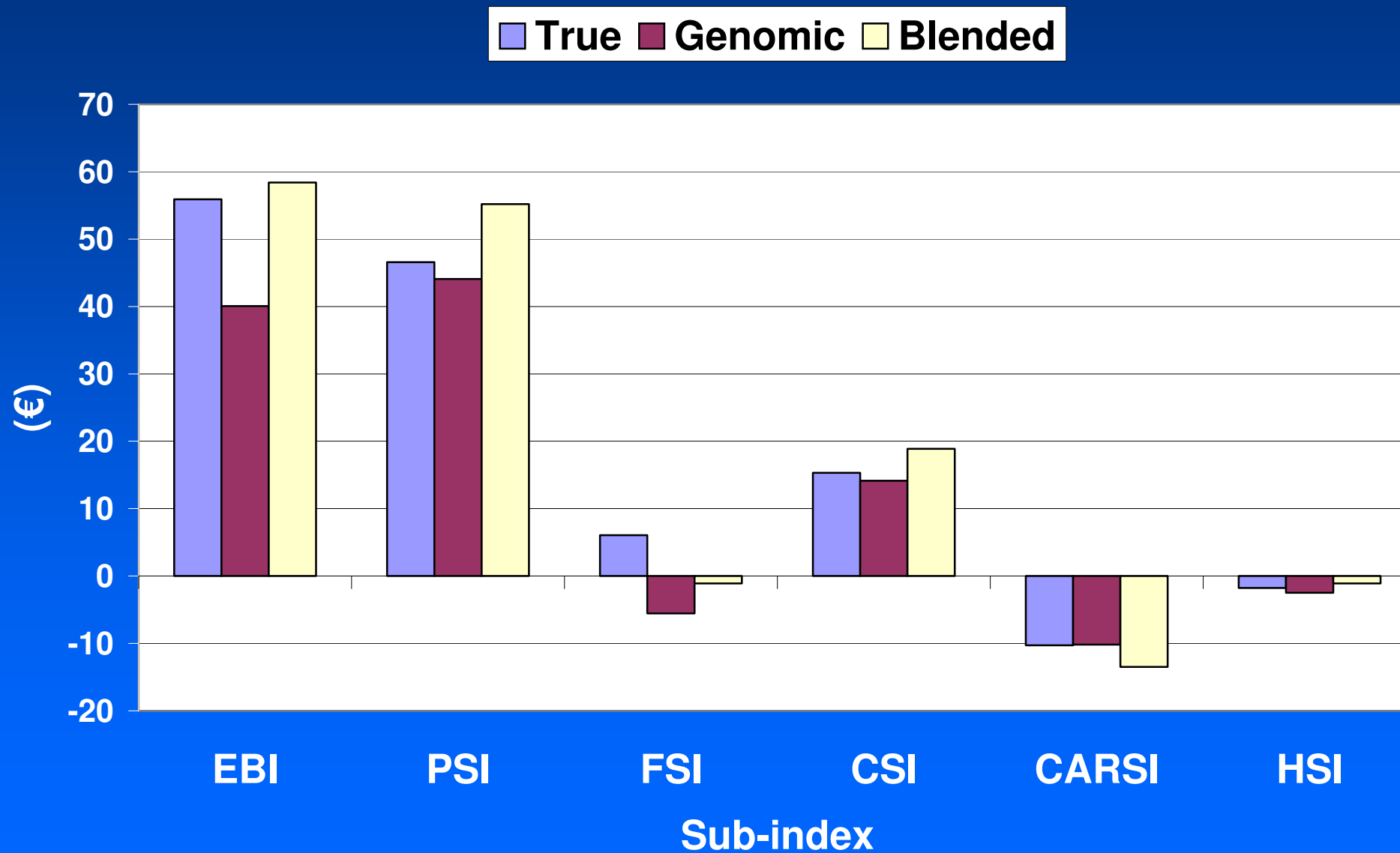
Research

- Testing the procedures
- Applying the procedures

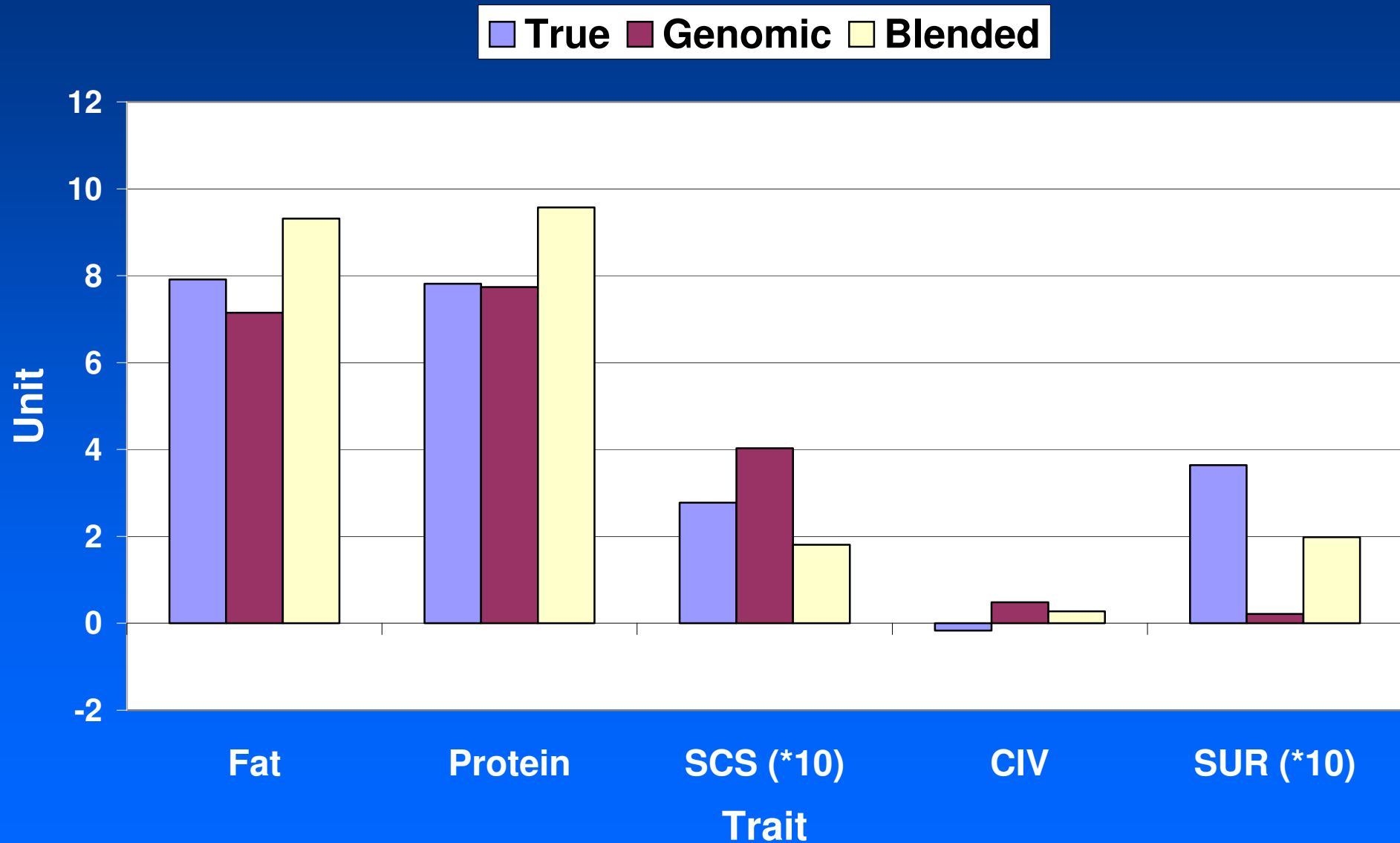
Testing the procedures

- Split team of proven bulls ($n=803$) into 2 groups
 - Training (born <1997 ; $n=596$)
 - validation (born ≥ 1997 ; $n=207$)
- Estimate SNP effects in training dataset
- Apply SNP effects on validation dataset
 - We know the answers
- Test the accuracy

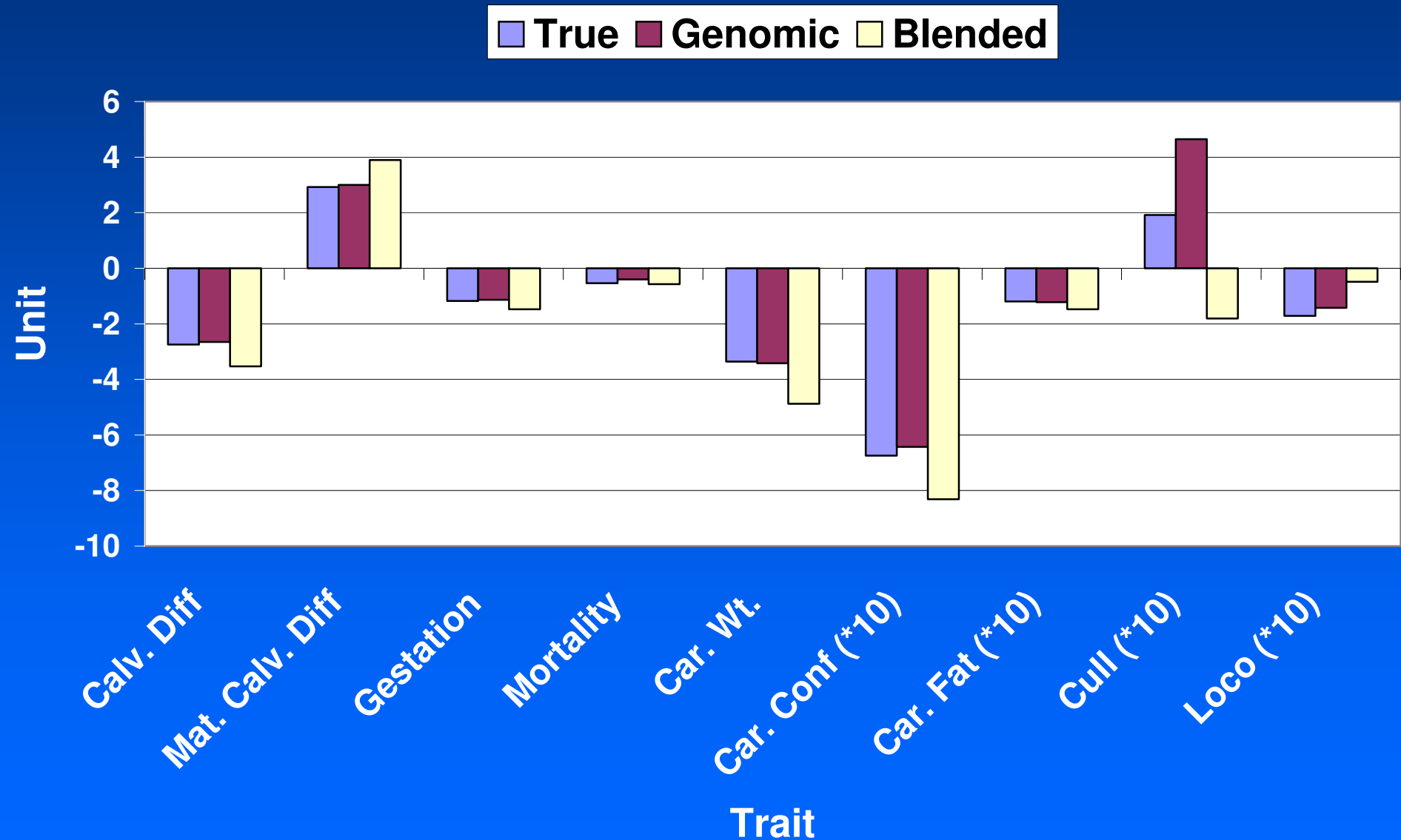
Means - Indexes



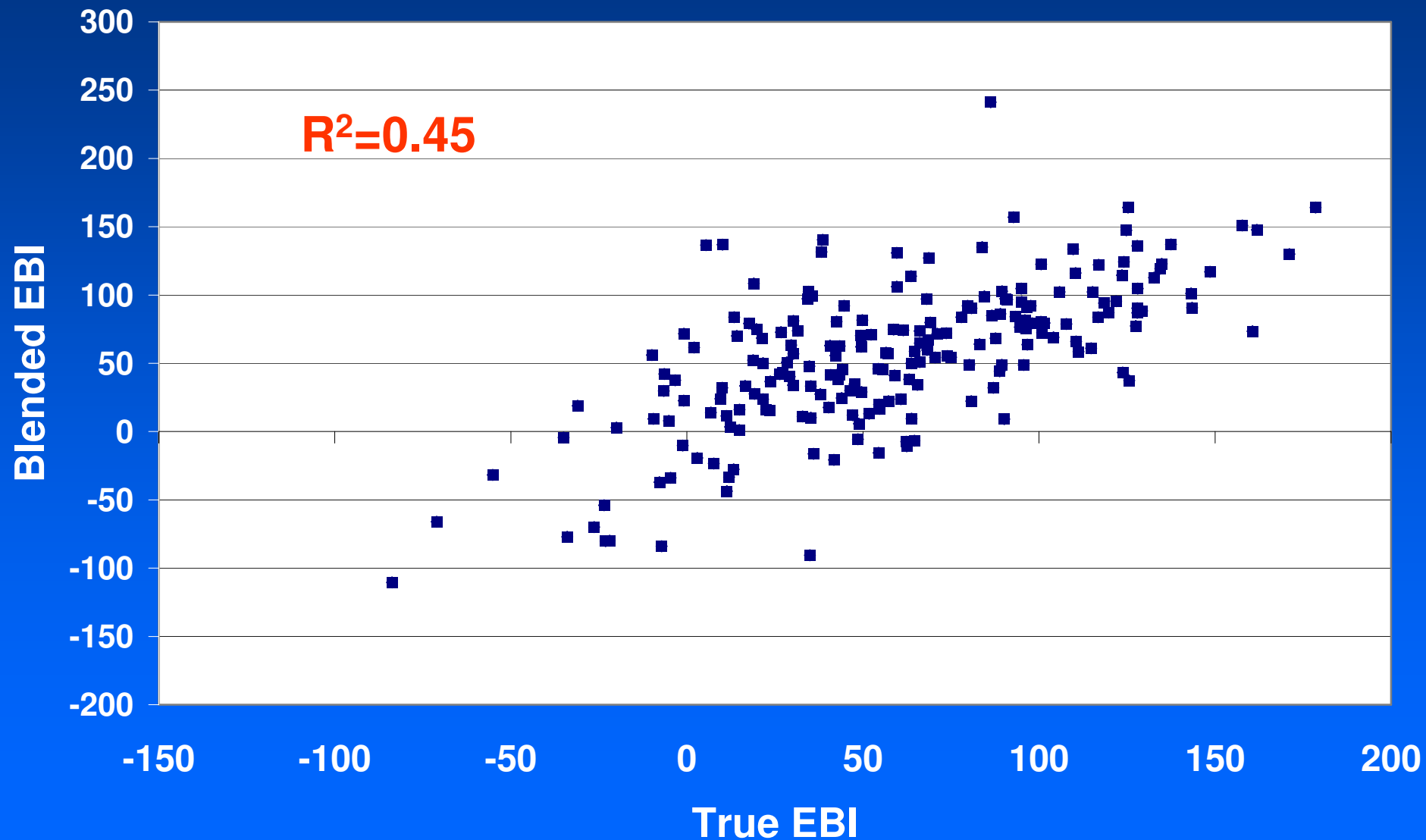
Means – production/fertility



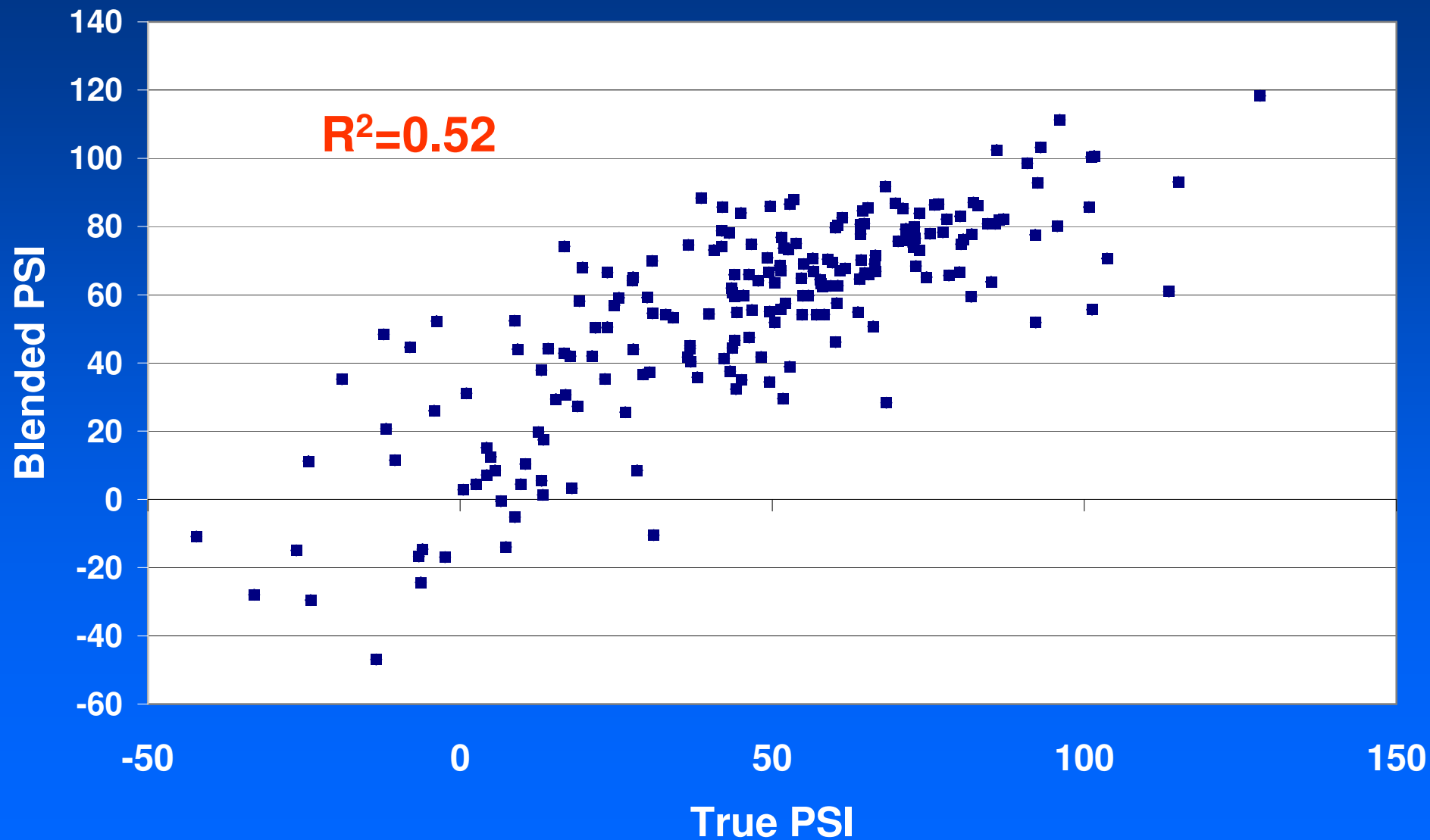
Means – Calving/beef



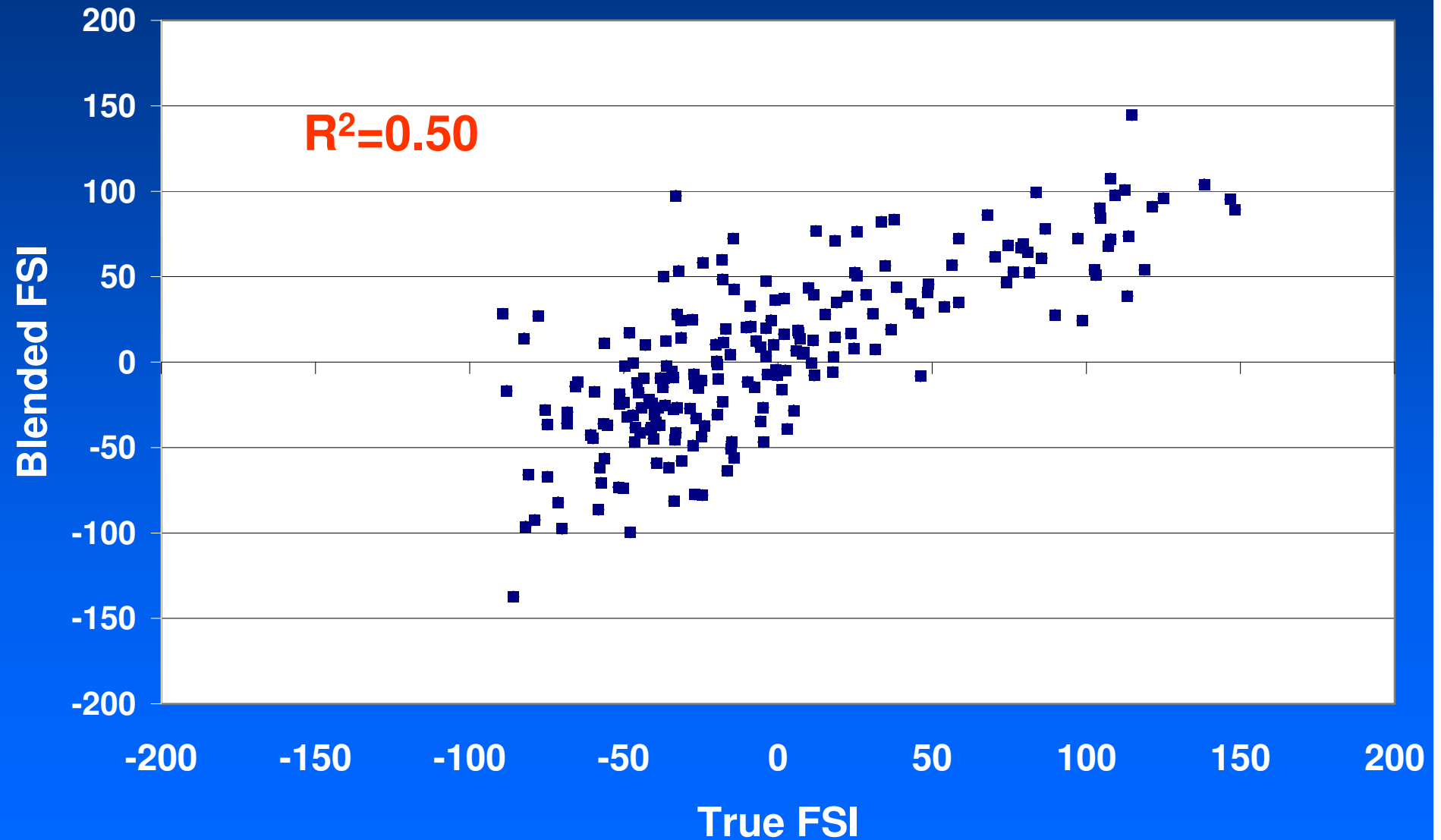
Blended versus Actual EBI



Blended versus Actual PSI



Blended versus Actual FSI

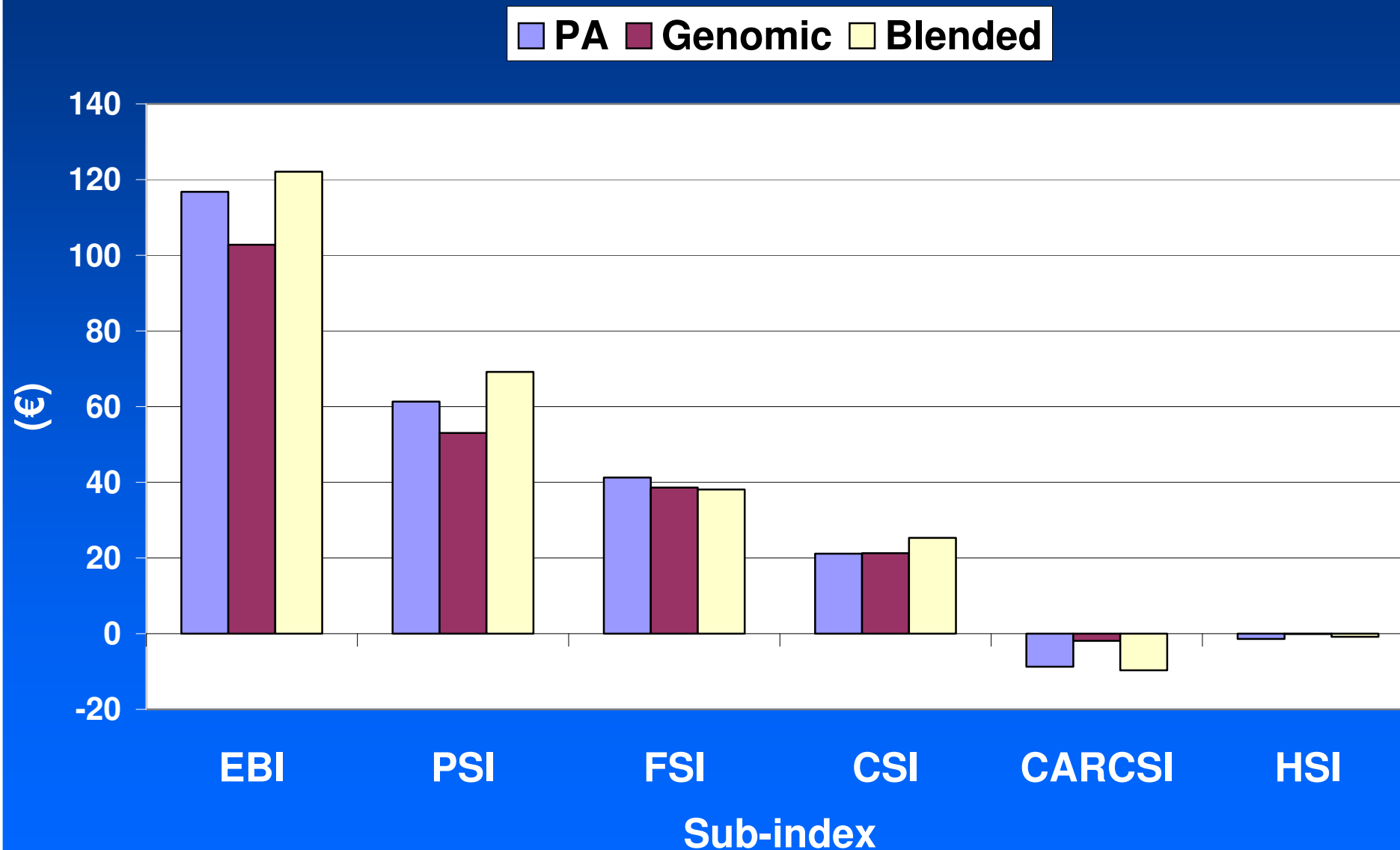


Young Bulls

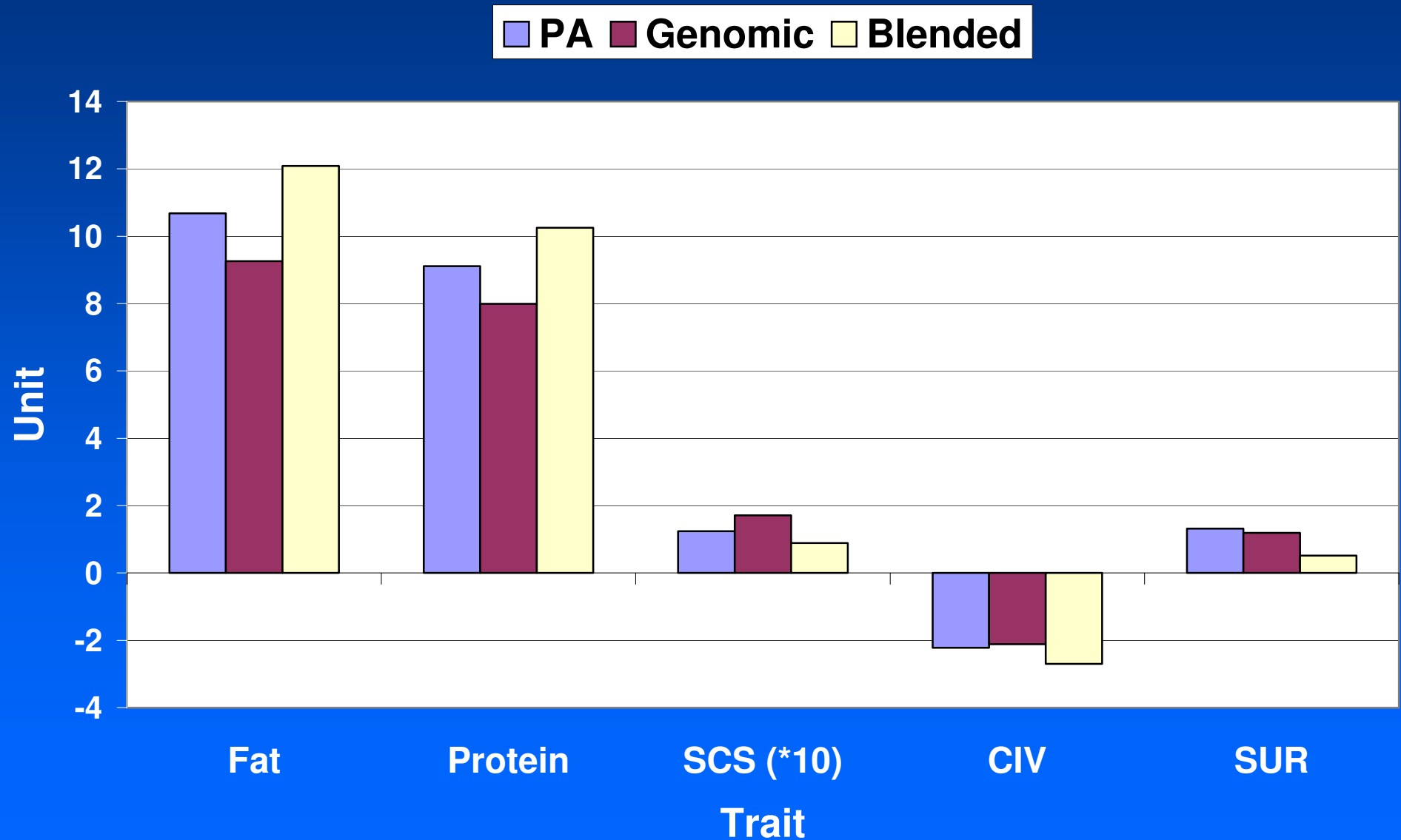
Applying the procedures

- Split genotyped bulls ($n=1,209$) into 2 groups
 - Training ($n=945$)
 - Young bulls ($n=264$)
- Estimate SNP effects in training dataset
- Apply SNP effects on young bulls

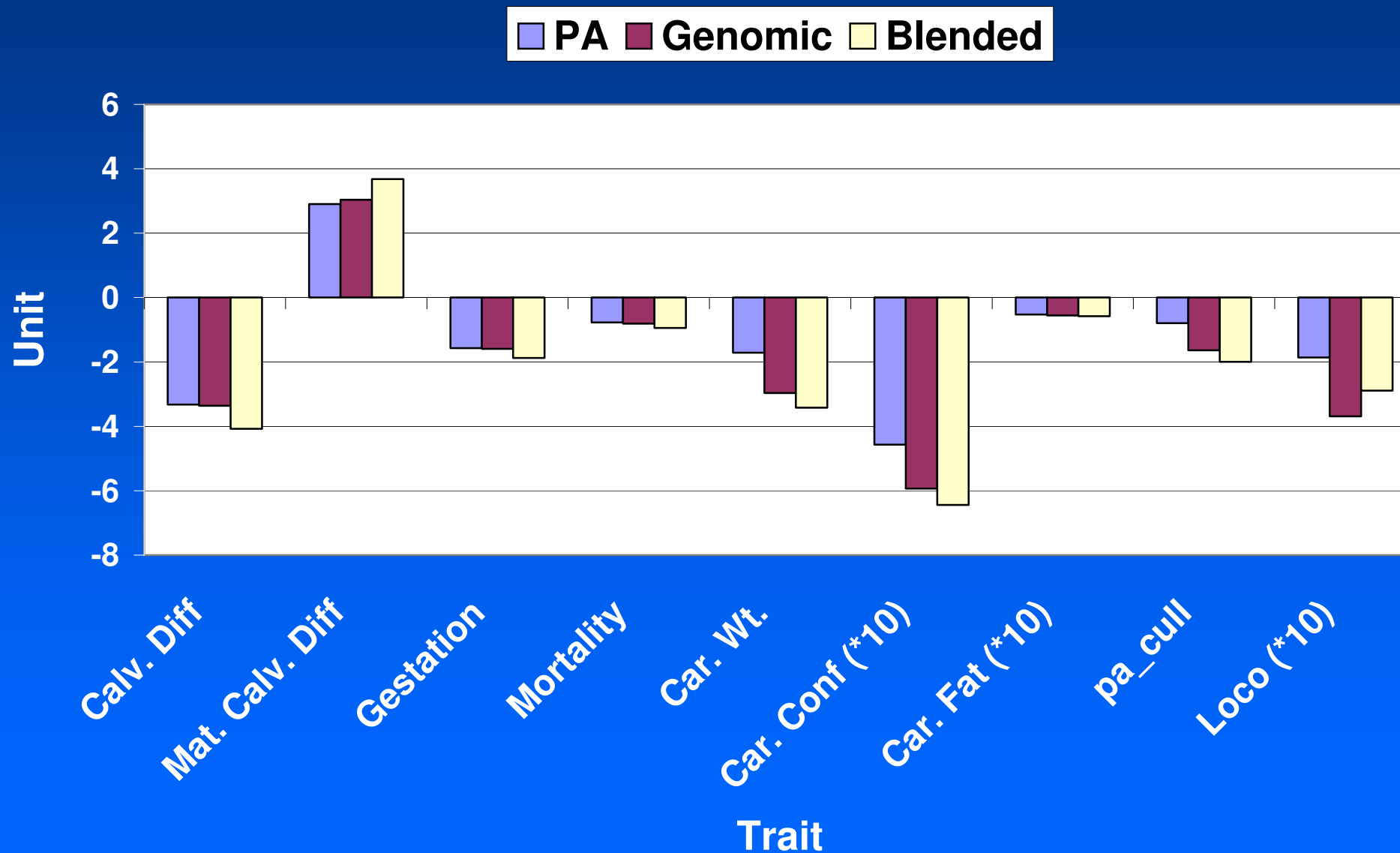
Means - Indexes



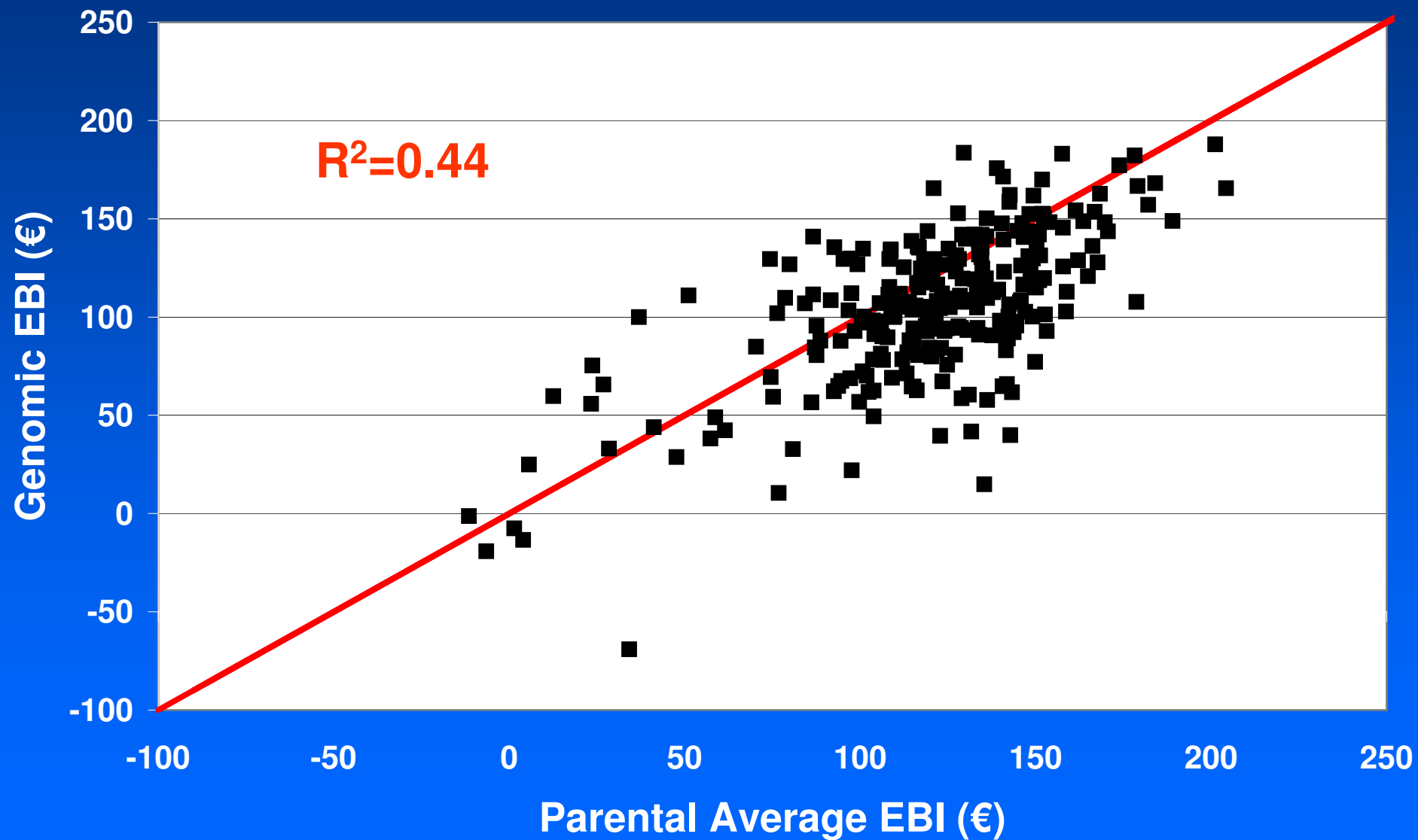
Means – Production/fertility



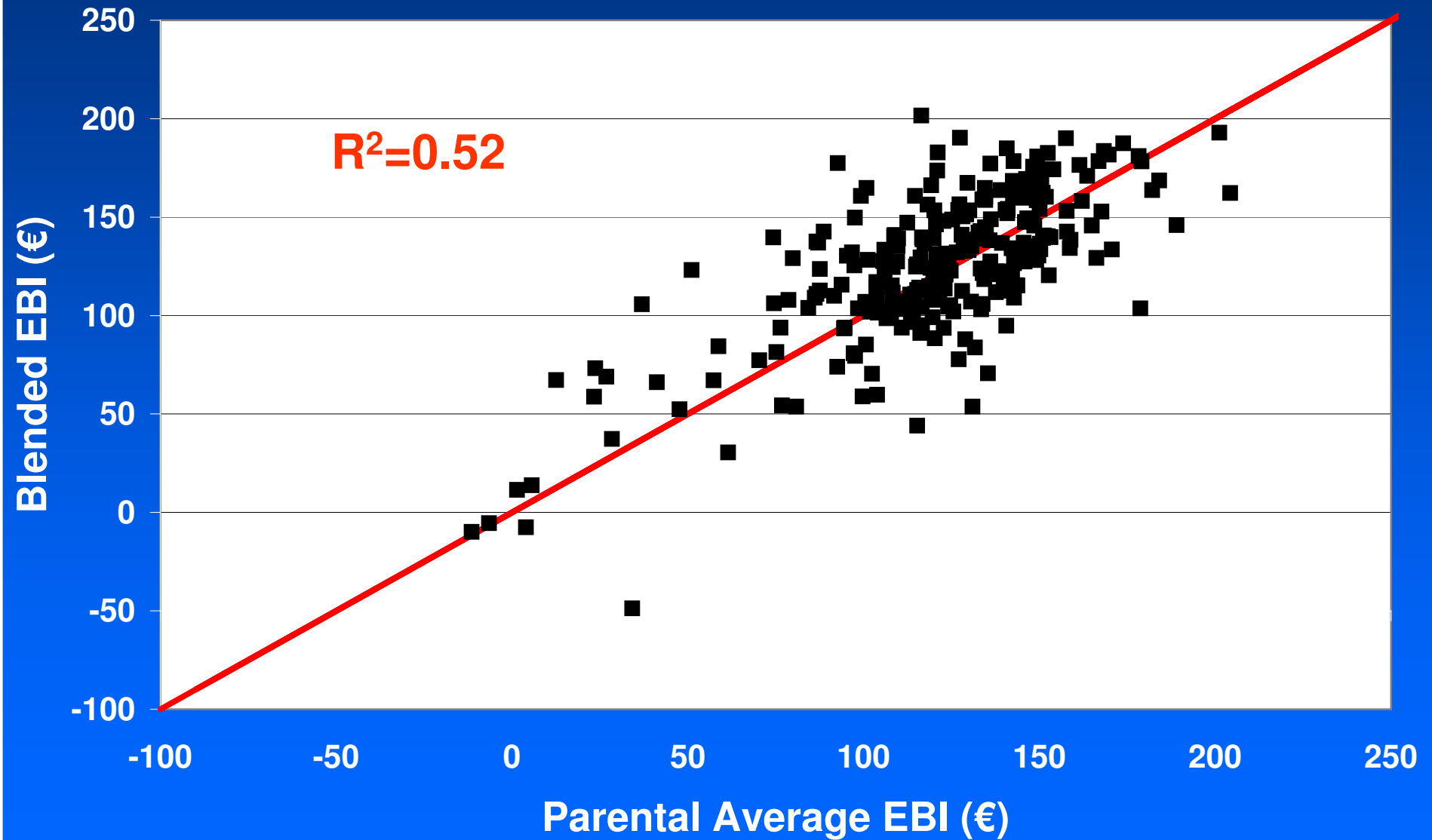
Means – Calving/carcass



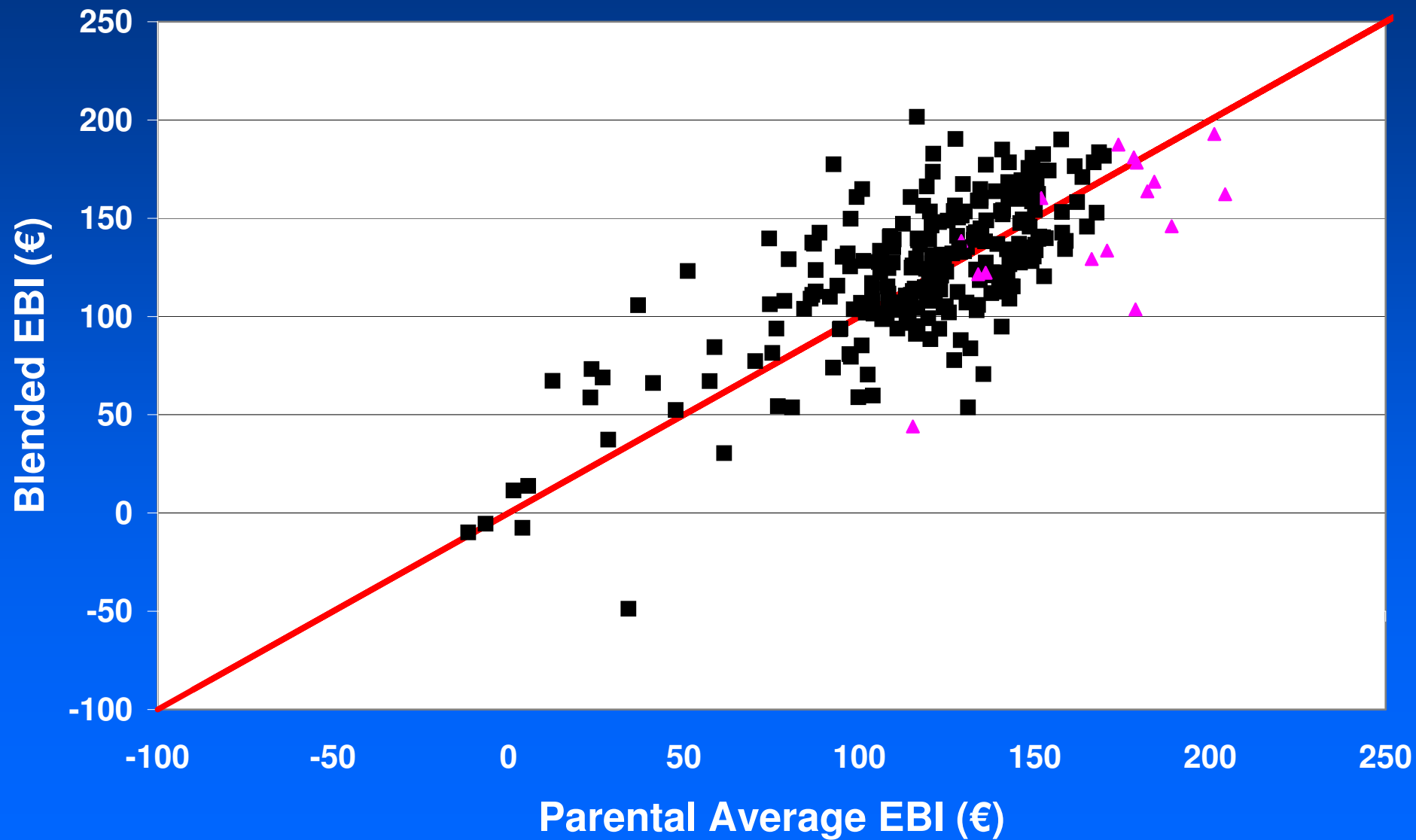
Genomic & PA - EBI



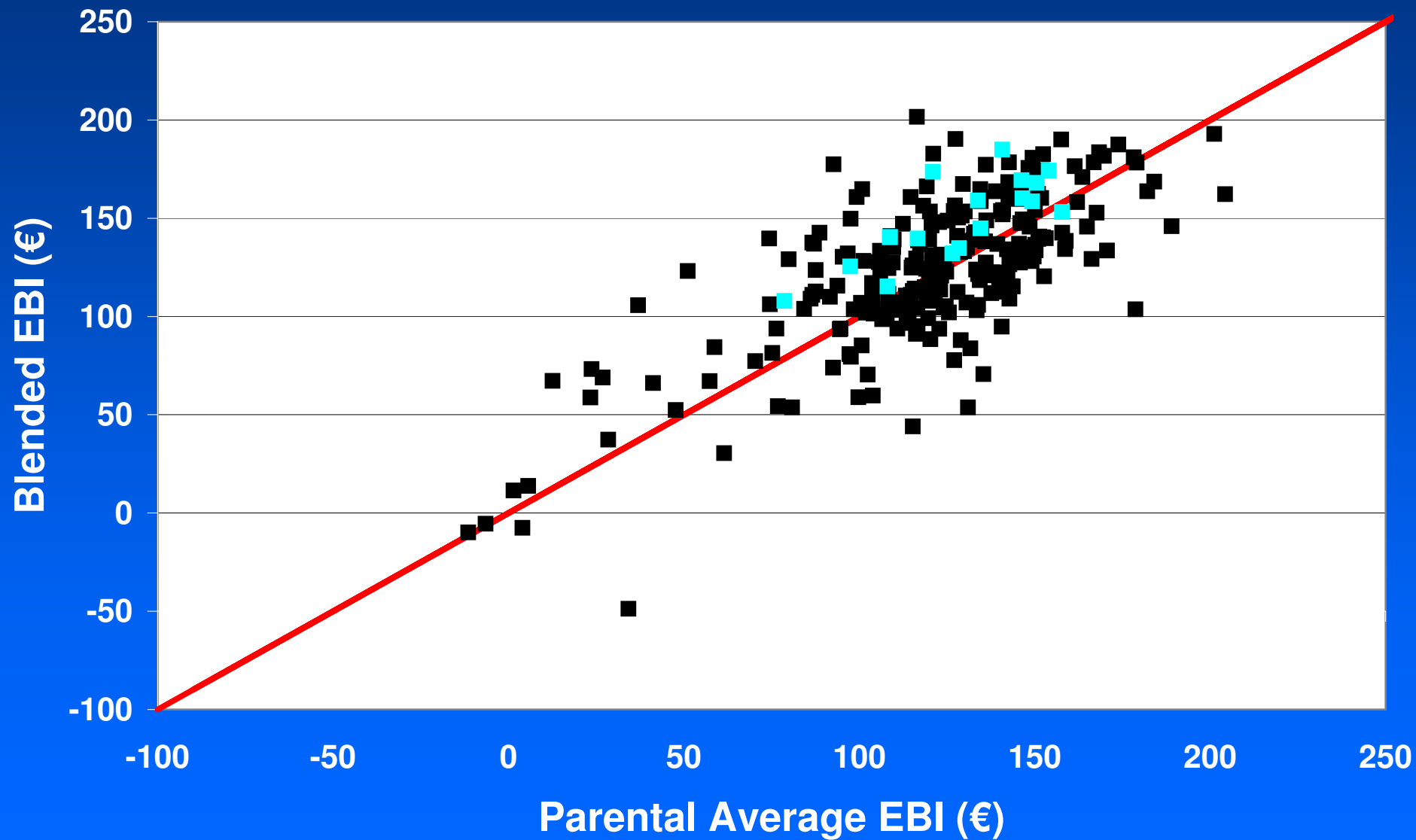
Blend & PA - EBI



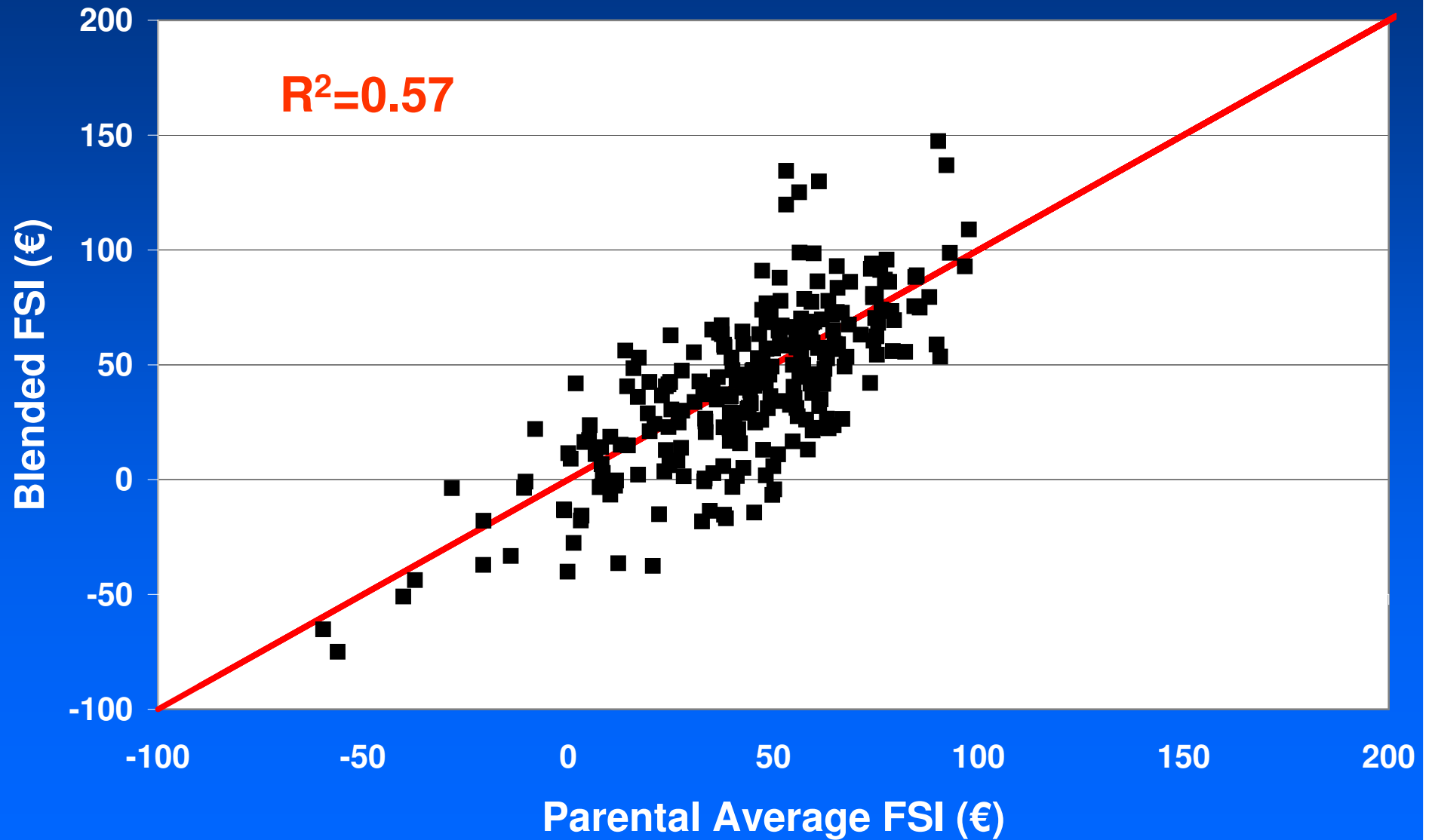
Blend & PA – EBI - OJI



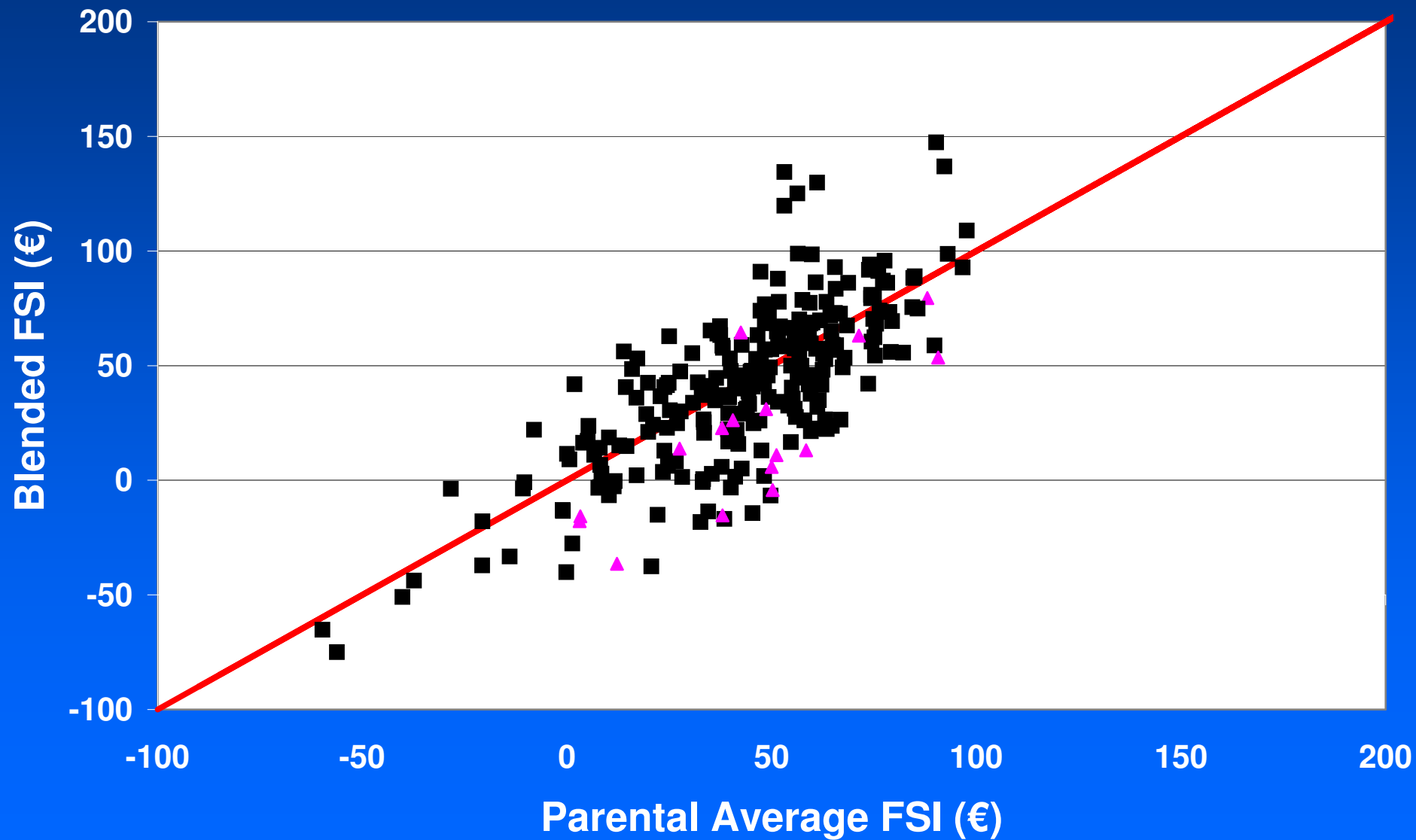
Blend & PA – EBI - NZ



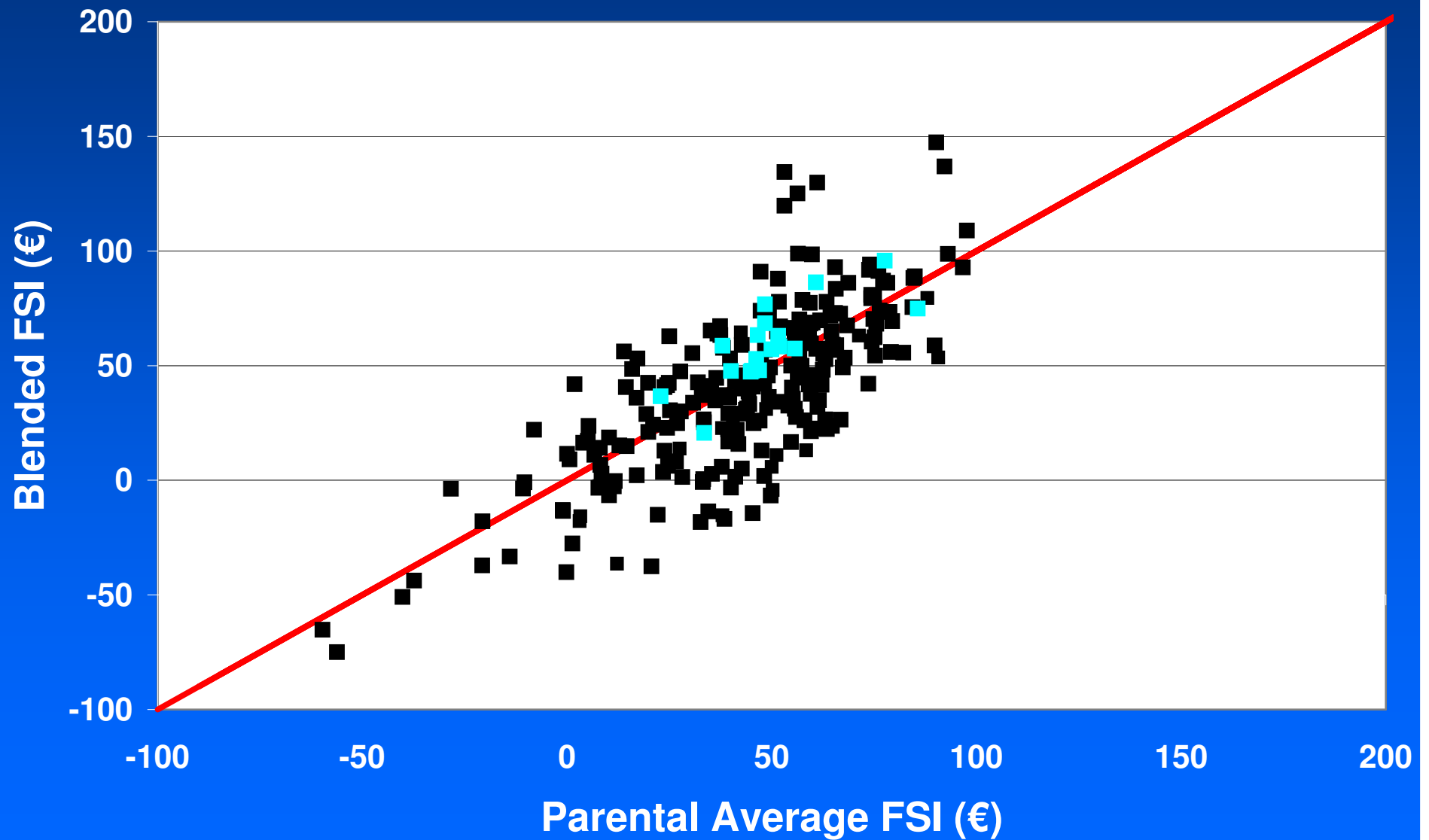
Blend & PA – FSI



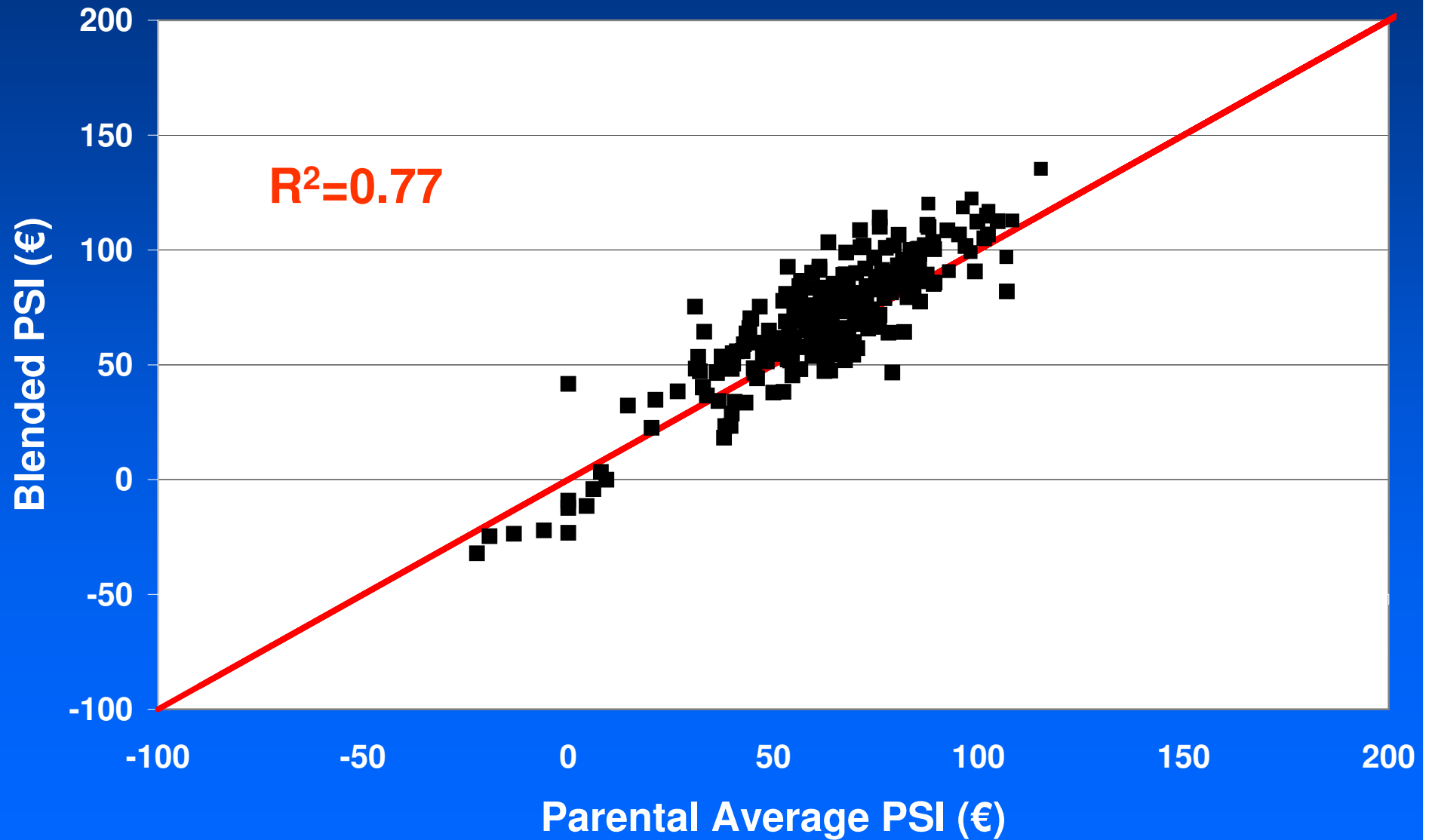
Blend & PA – FSI - OJI



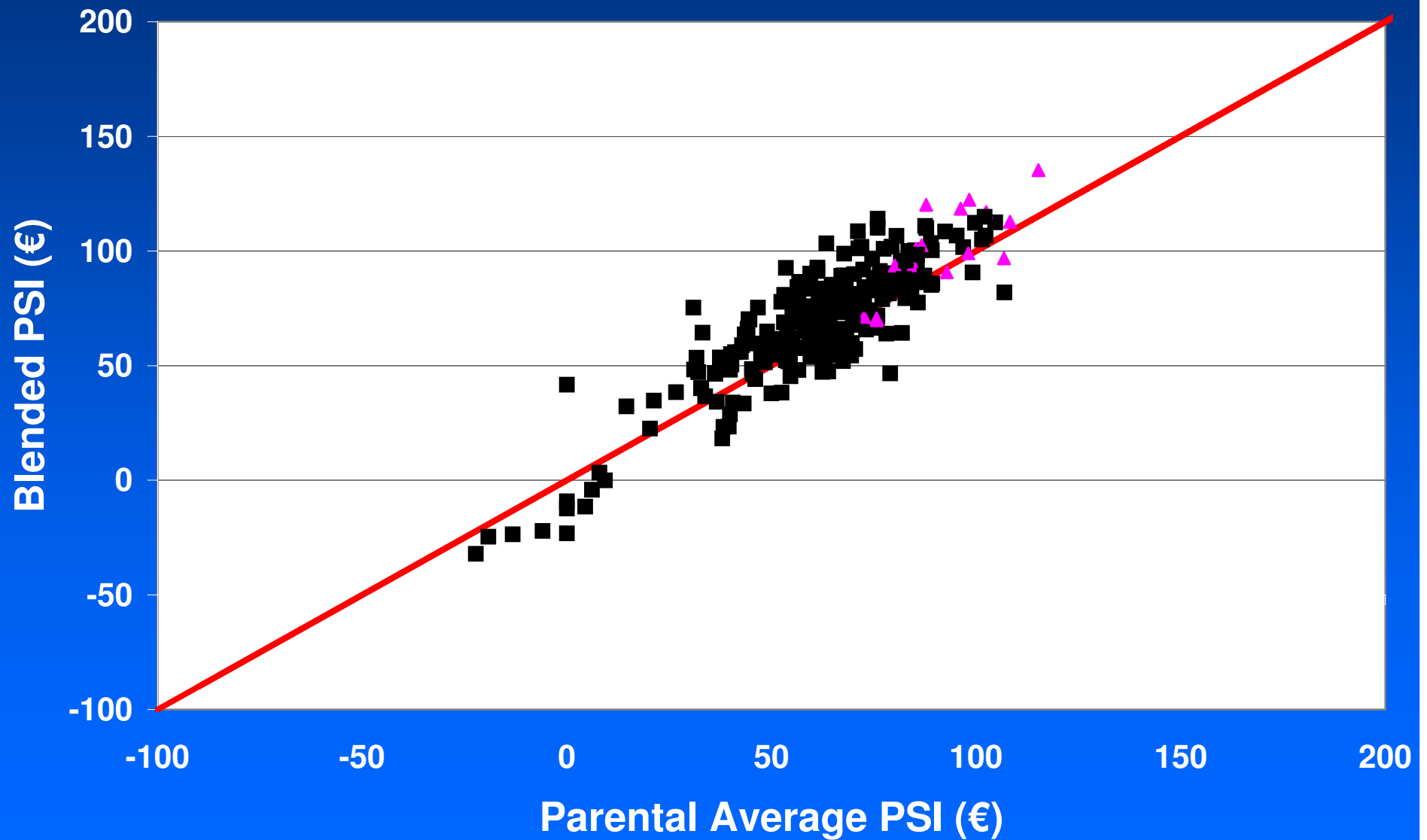
Blend & PA – FSI - NZ



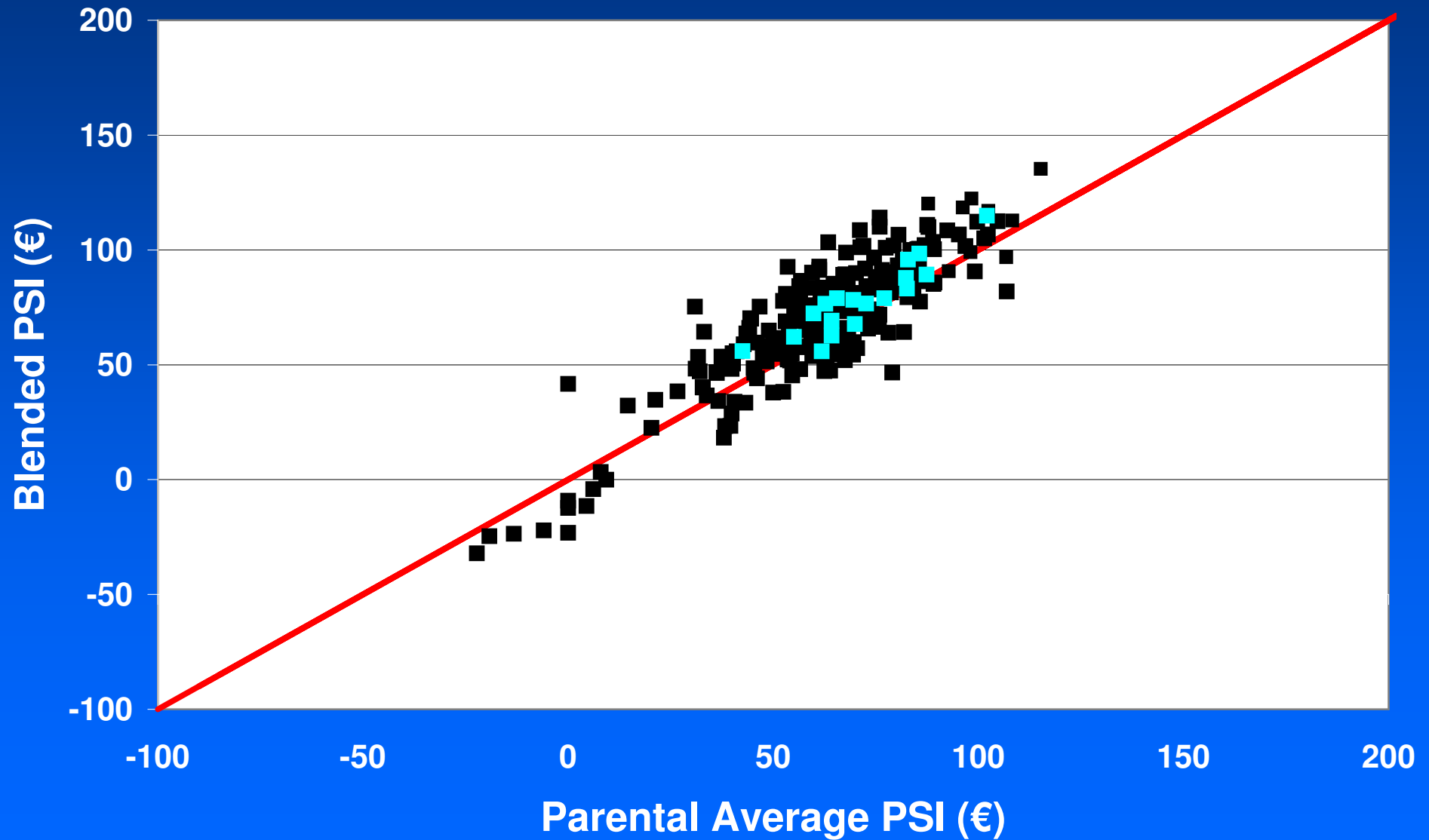
Blend & PA – PSI



Blend & PA – PSI - OJI

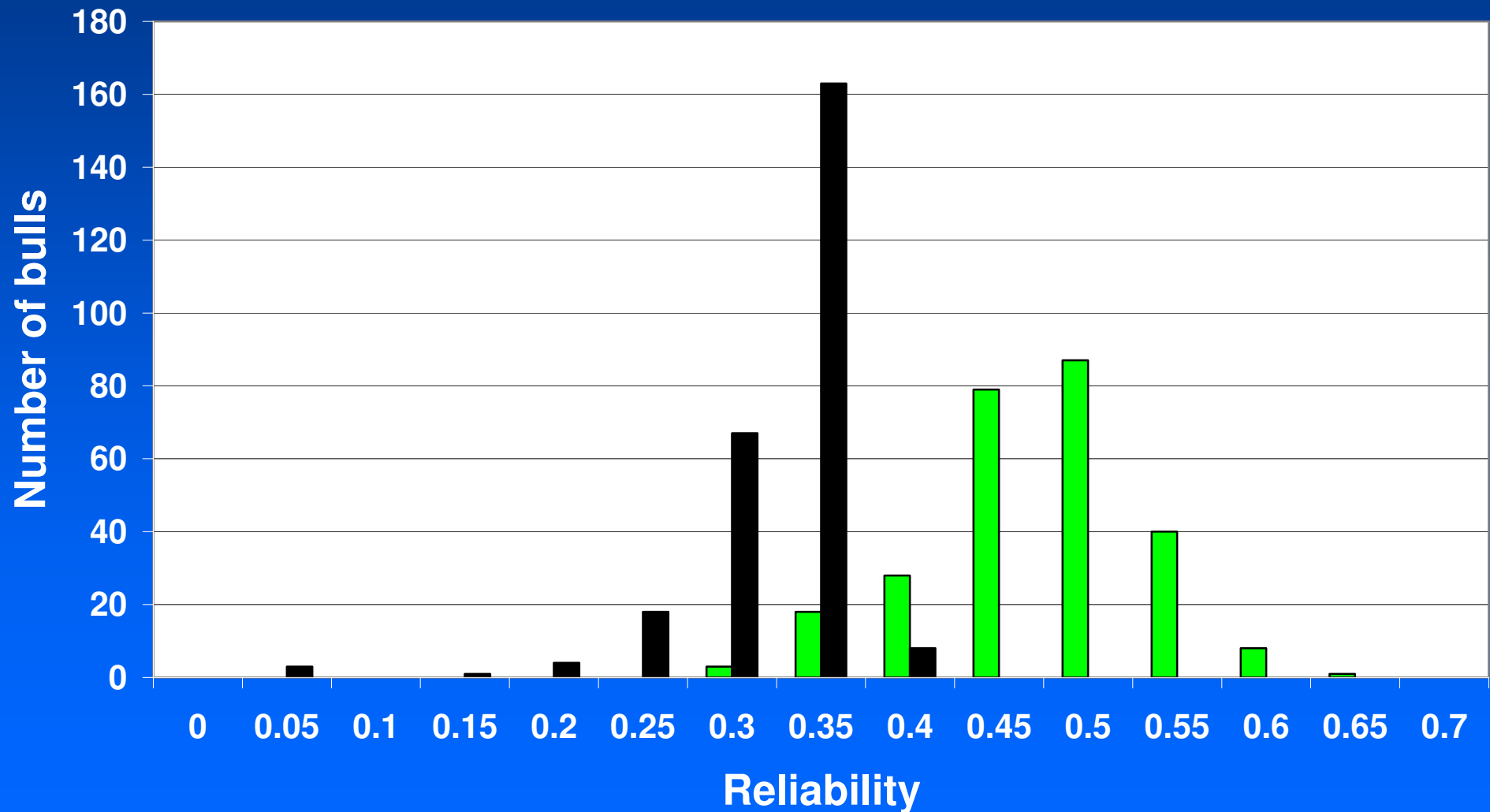


Blend & PA – PSI - NZ



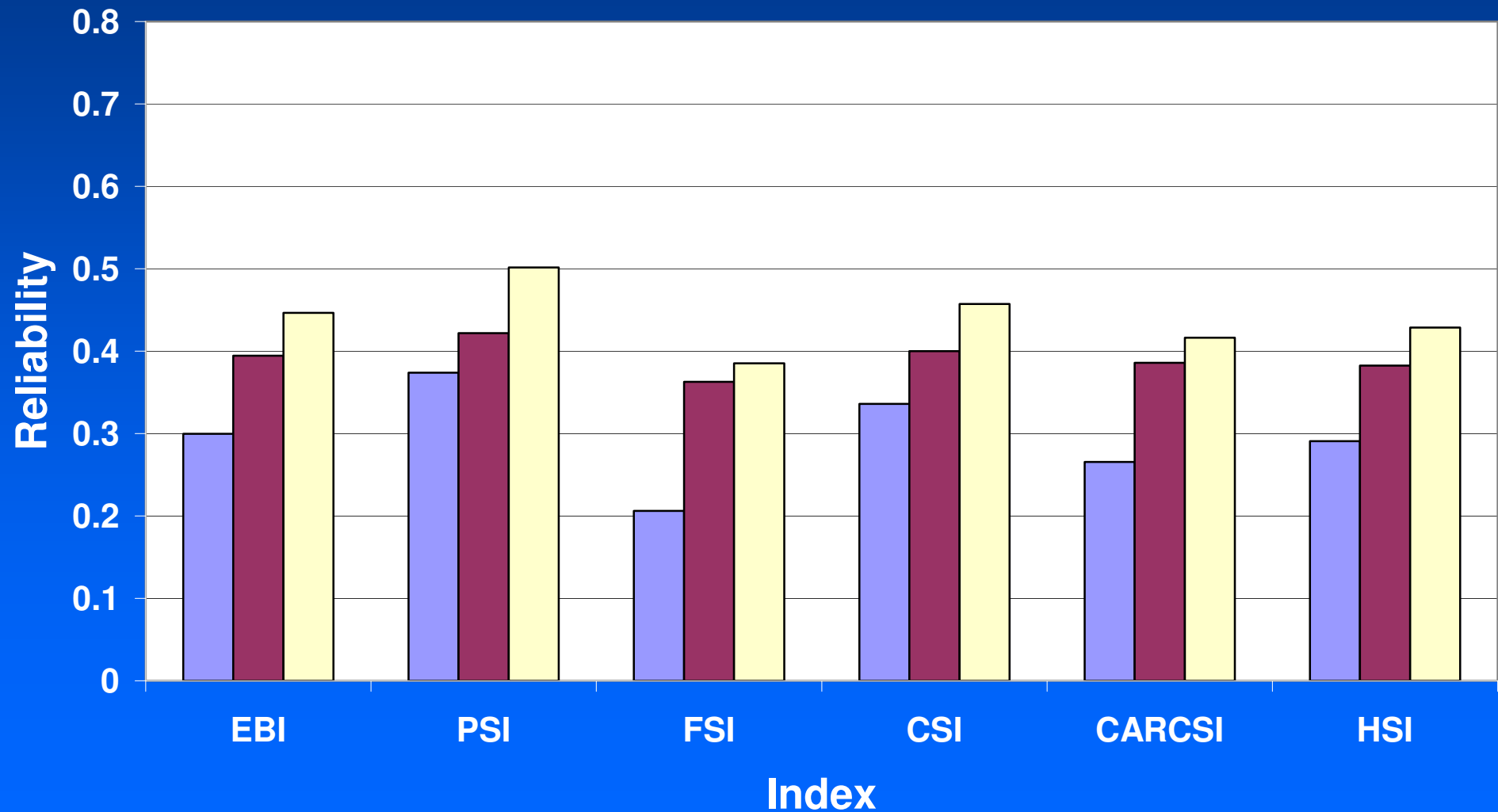
Reliability - EBI

■ Blended ■ Parent Average

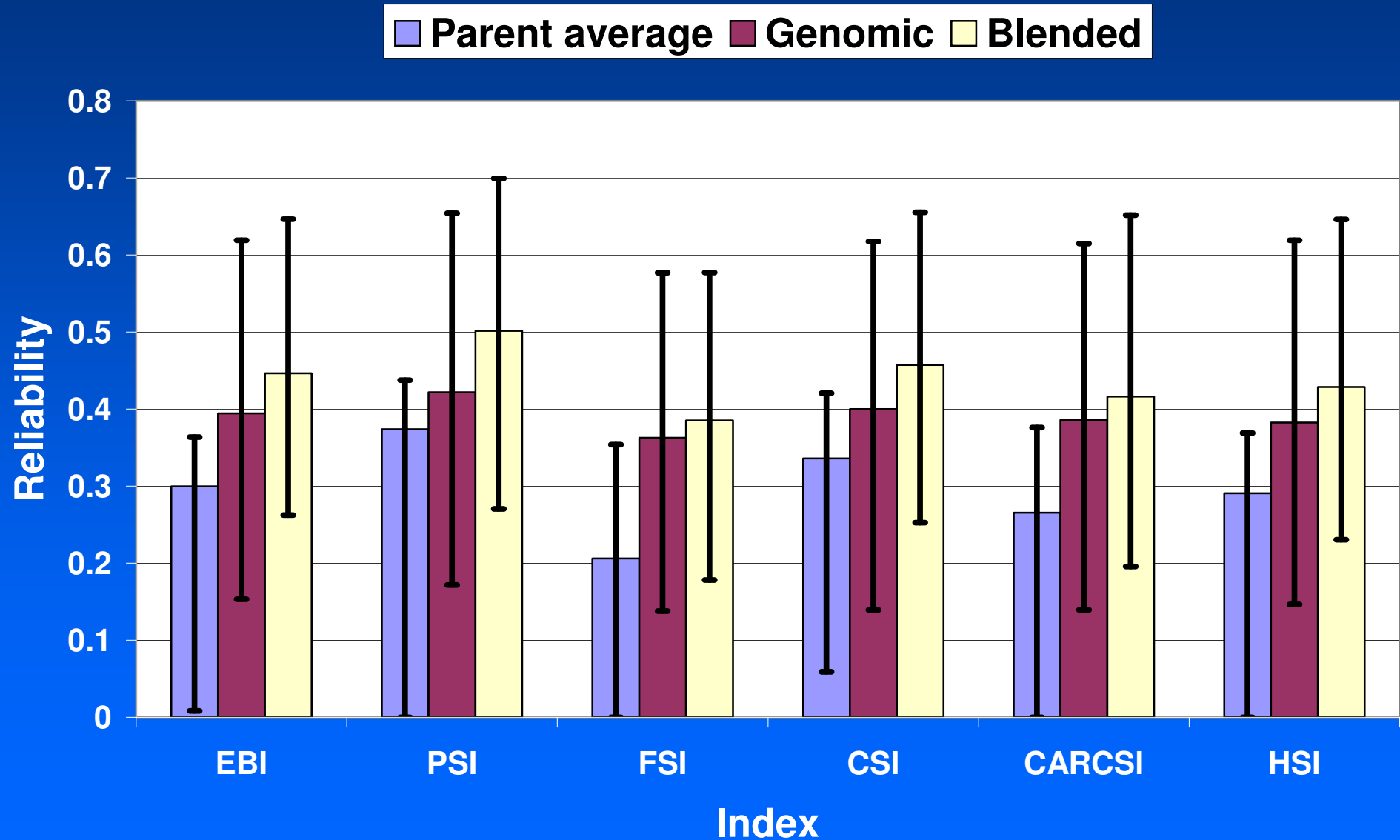


Reliability - EBI

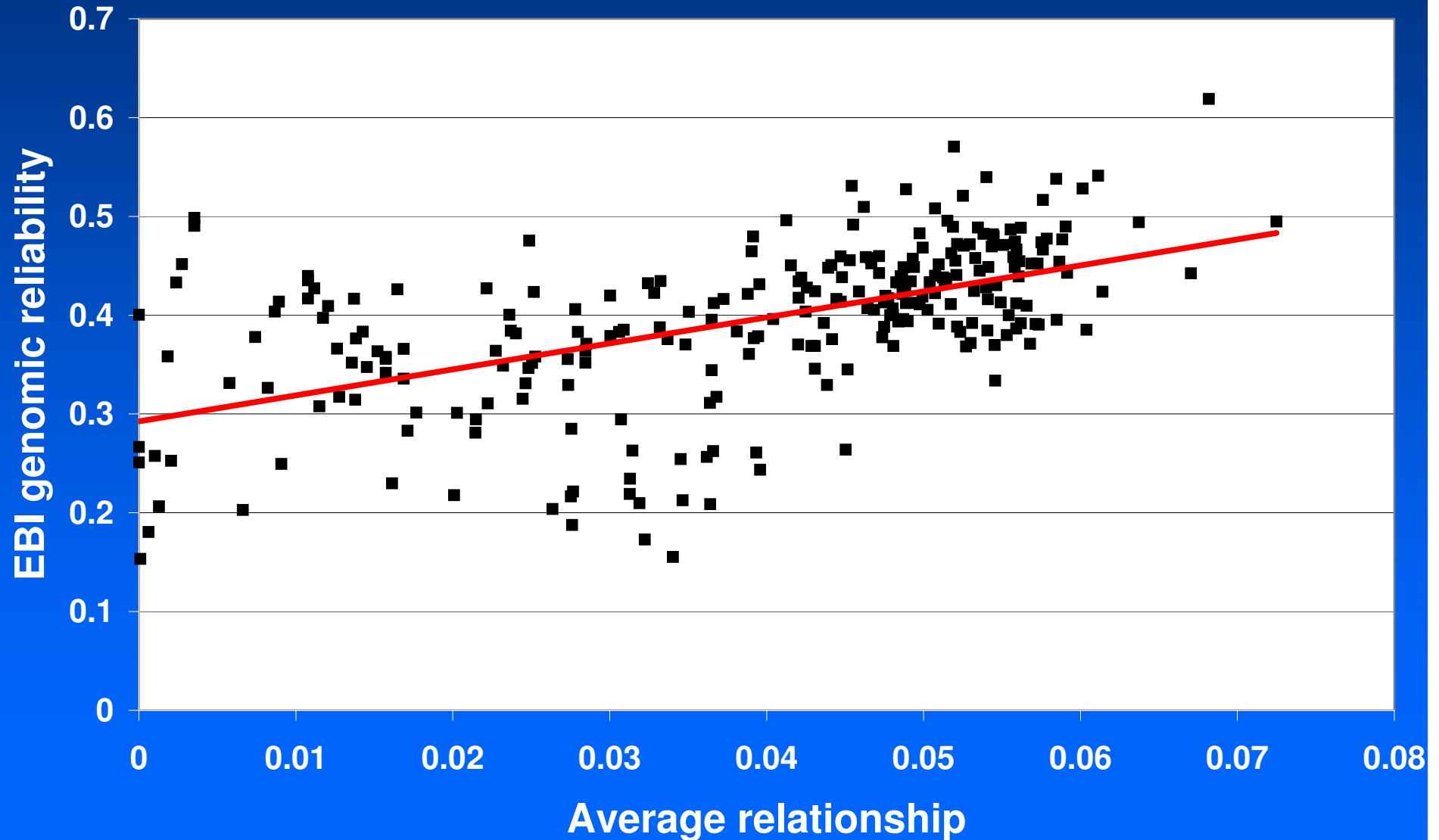
Parent average Genomic Blended



Reliability - EBI



Why we need genotypes!!!



Short to medium term research

- Logistics
- Including more data in training population
- Smaller, less expensive chip
- Handle more data
- Accounting for admixture of breeds

Conclusions

- Results to date look very promising
- Genomic selection has lots to offer but must not be oversold
- Reliability is improved, BUT still low
- Collaboration is vital
- **WE NEED MORE GENOTYPES!!!**