Applying different genomic selection approaches on QTLMAS2010 data

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Genomic Selection

- Selection based on genomic information or **G**enomic **EBV**
- GEBV can be calculated in different ways including different methods within Bayesian framework and GBLUP
- **P**olygenic effect can also be added to the model

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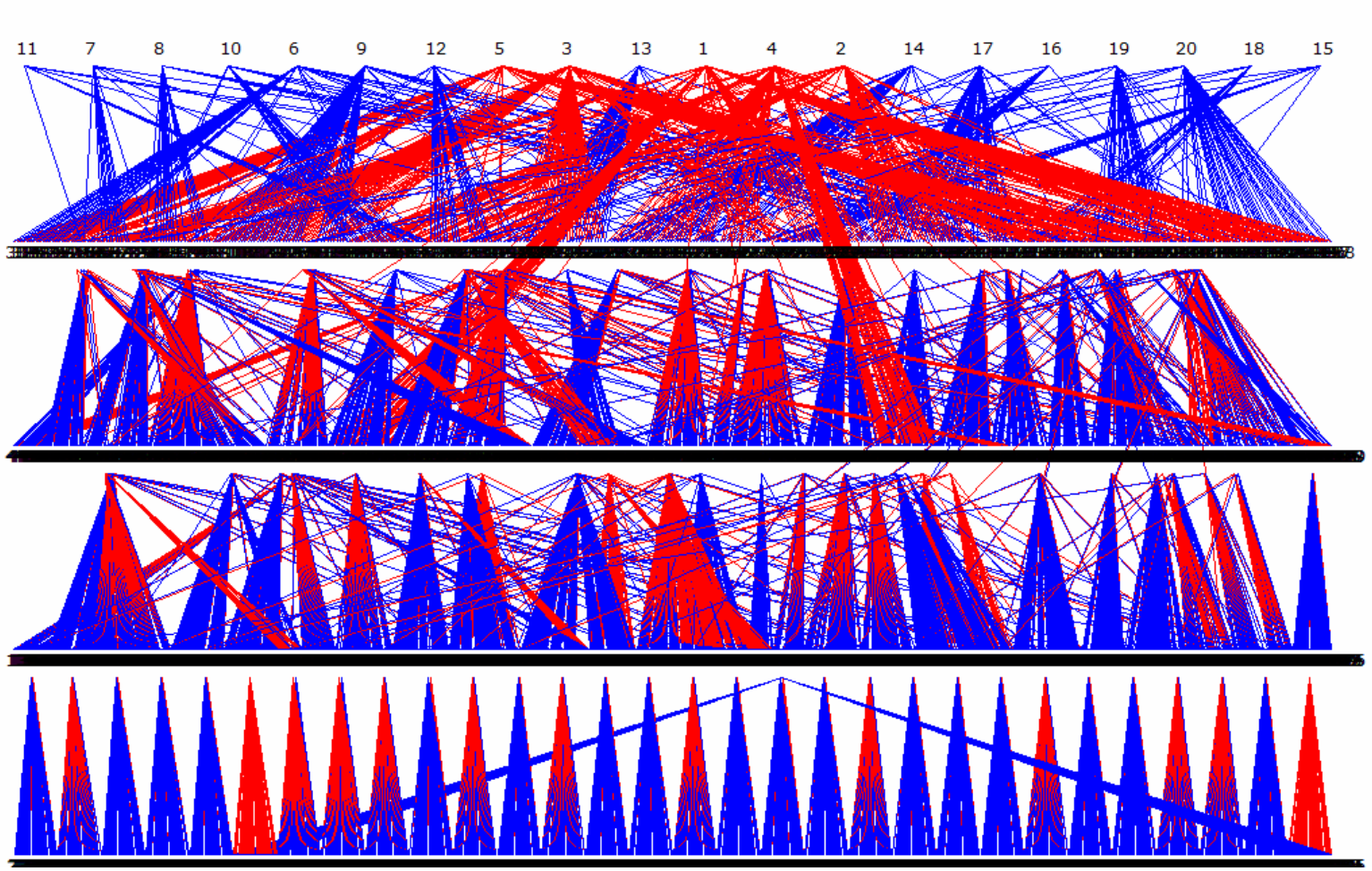
20 Founders

5 Generations

2326+900 individuals



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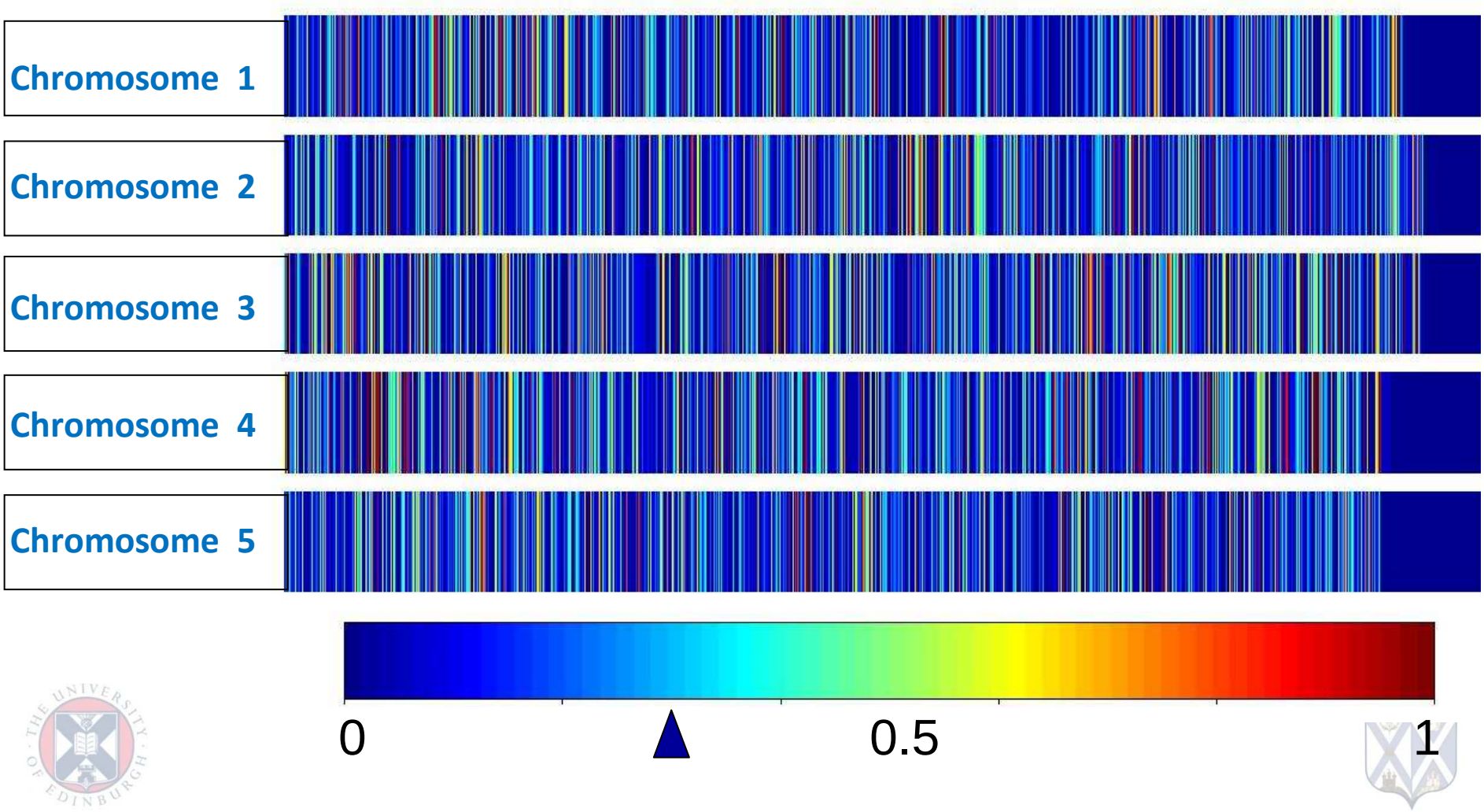
Overall mean r^2 of adjacent SNP pairs



Approaches used for estimation of GEBV

In the model:	**B**ayes **B** type	**BLUP** type
Genomic (SNP)	**GBB**	**GBLUP**
Genomic & **P**olygenic	**GPBB**	**GPBLUP**

Approaches used for estimation of GEBV

- Bayes B type :
  - **G**BB $y = \mu + \sum z_i \beta_i + e$
  - **GP**BB $y = \mu + \sum z_i \beta_i$ + **P**olygenic +e
    - β_i ~N(0,σ^2_{snp}) with prob **Π**
    - β_i 0 with prob (1- **Π**)
    - **P**olygenic ~N(0,**A**σ^2_{pol}) **A** Calculated using pedigree information

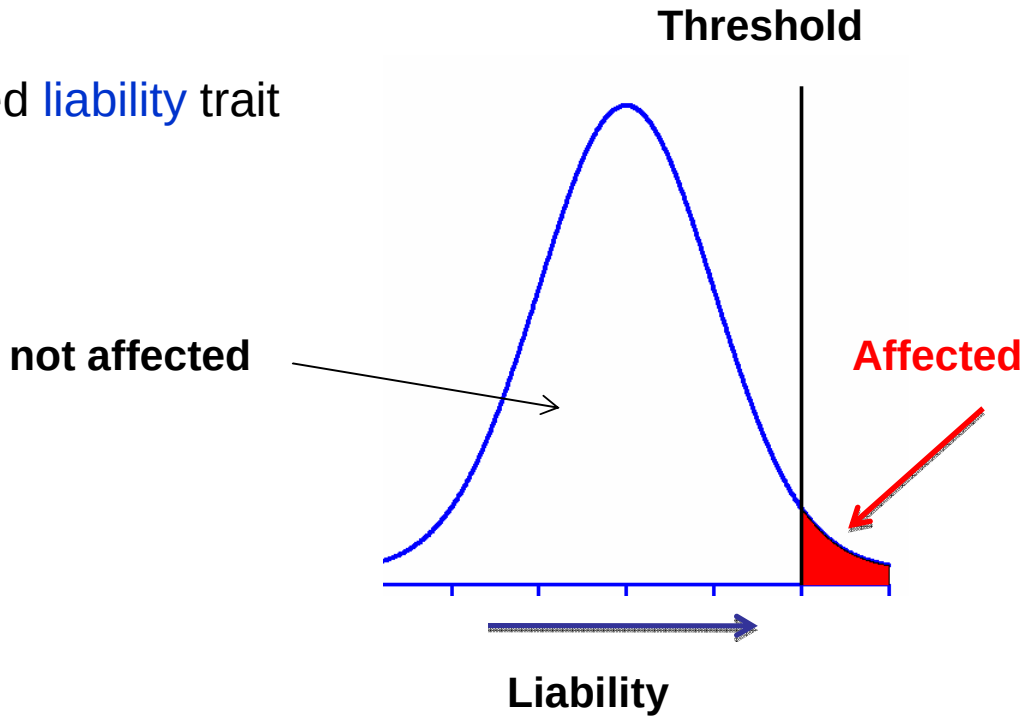
Π and σ_{snp}^2 were estimated from **data**

Approaches used for estimation of GEBV

- BLUP type:
  - **G**BLUP $Y = \mu + \mathbf{g} + e$
  - **GP**BLUP $Y = \mu + \mathbf{g} + \mathbf{P}\text{olygenic} + e$
    - **g** ~N $(0, \mathbf{G}\sigma_g^2)$, **G**: Calculate using marker information (IBS relationship)
    - **P**olygenic ~N $(0, \mathbf{A}\sigma_{pol}^2)$ **A** Calculated using pedigree information
  - **ASReml** (Gilmour *et al. 2000)*

Models for the Binary trait

- Bayes B type
  - Underlying normally distributed liability trait



- BLUP type
  - Logit as the link function.

Care needed when comparing between BB and BLUP type

Supplementary QTL and association analyses

- Linkage analysis
  - Variance components (Quantitative trait):
    - IBD matrix at QTL positions
    - Variance components estimation using REML
  - Regression approach, Half-sib analysis (Binary trait)
    - GridQTL

- Association analysis
  - GRAMMAR
    - Phenotypes corrected for polygenic effects were used and SNP additive effects were fitted using **GenABLE** *(Aulchenko YS et al 2007)*

Genetic variance explained by SNP in BB analyses

- Calculated using approximation from infinitesimal model theory

$$\text{Var (EBV)} = r^2 \sigma^2_g$$

$$\text{PEV} = (1-r^2) \sigma^2_g$$

$$\sigma^2_g = \text{Var(EBV)} + \text{mean (PEV)}$$

Heritability estimates: 1- Quantitative trait

		polygenic	SNP (genomic)	Total
BB	**GP**BB	16	40	56
	GBB	-	47	47
	Polygenic only	55	-	55
BLUP	**GP**BLUP	15	36	51
	GBLUP	-	42	42
	Polygenic only	54	-	54

Polygenic component ~30% of total genetic variance when fitting both components (**P** & **G**)

Model comparison for the Quantitative trait

		Bayes Factor (BF)
BB	**GP**BB	51
	GBB	0
		LRT
BLUP	**GP**BLUP	12
	GBLUP	0

Better fit when adding polygenic component

Heritability estimates: 2- Binary trait

		Polygenic	SNP	Total
BB	**GP**BB	5	45	50
	GBB	-	46	46
	Polygenic only	43	-	43
BLUP	**GP**BLUP	~0	65	65
	GBLUP	-	65	65
	Polygenic only	44	-	44

Liability model

Logit link function

Polygenic components were not important

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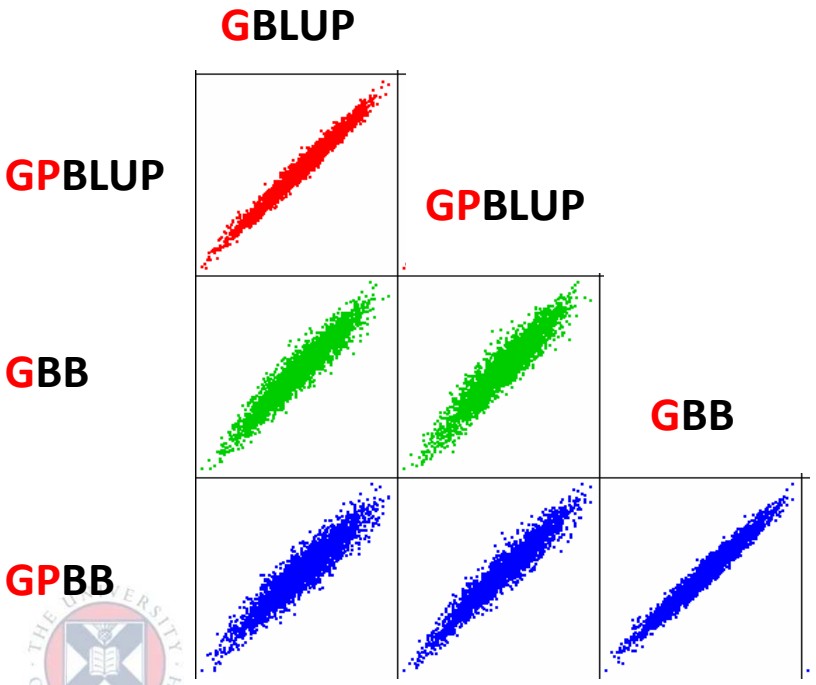
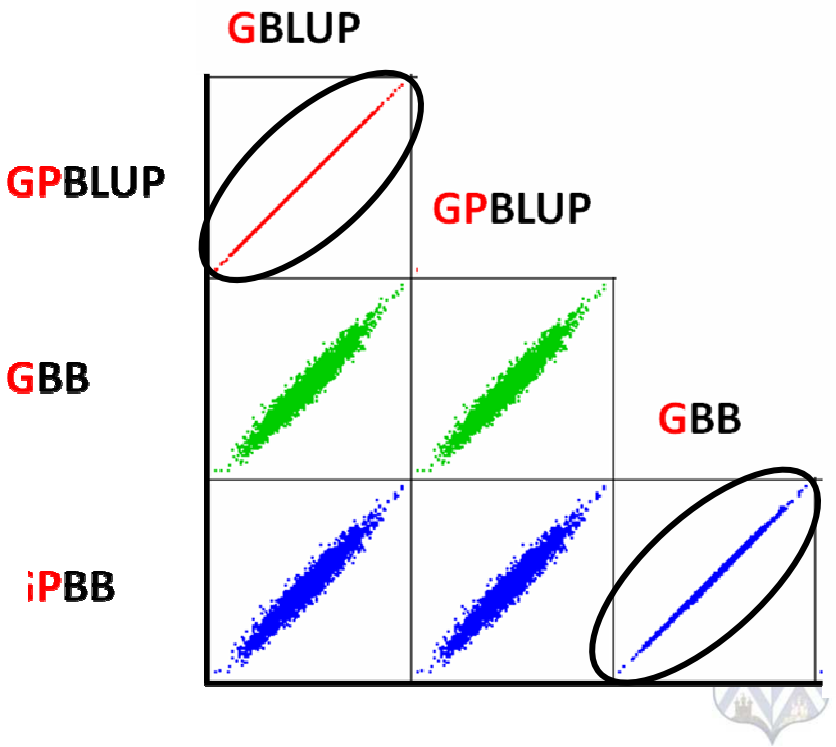
Correlation between EBVs obtained by different methods

Quantitative Trait



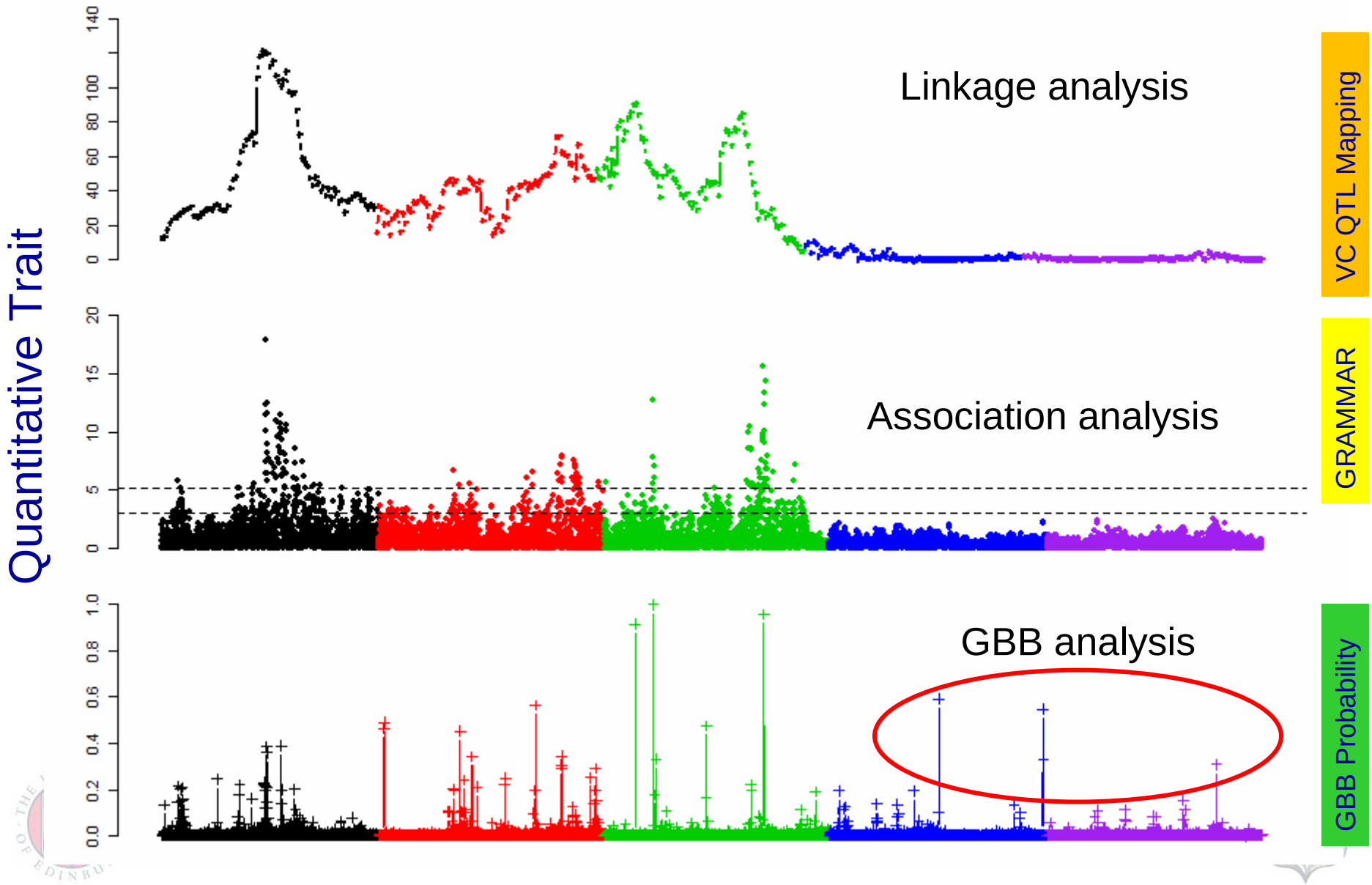
Binary Trait



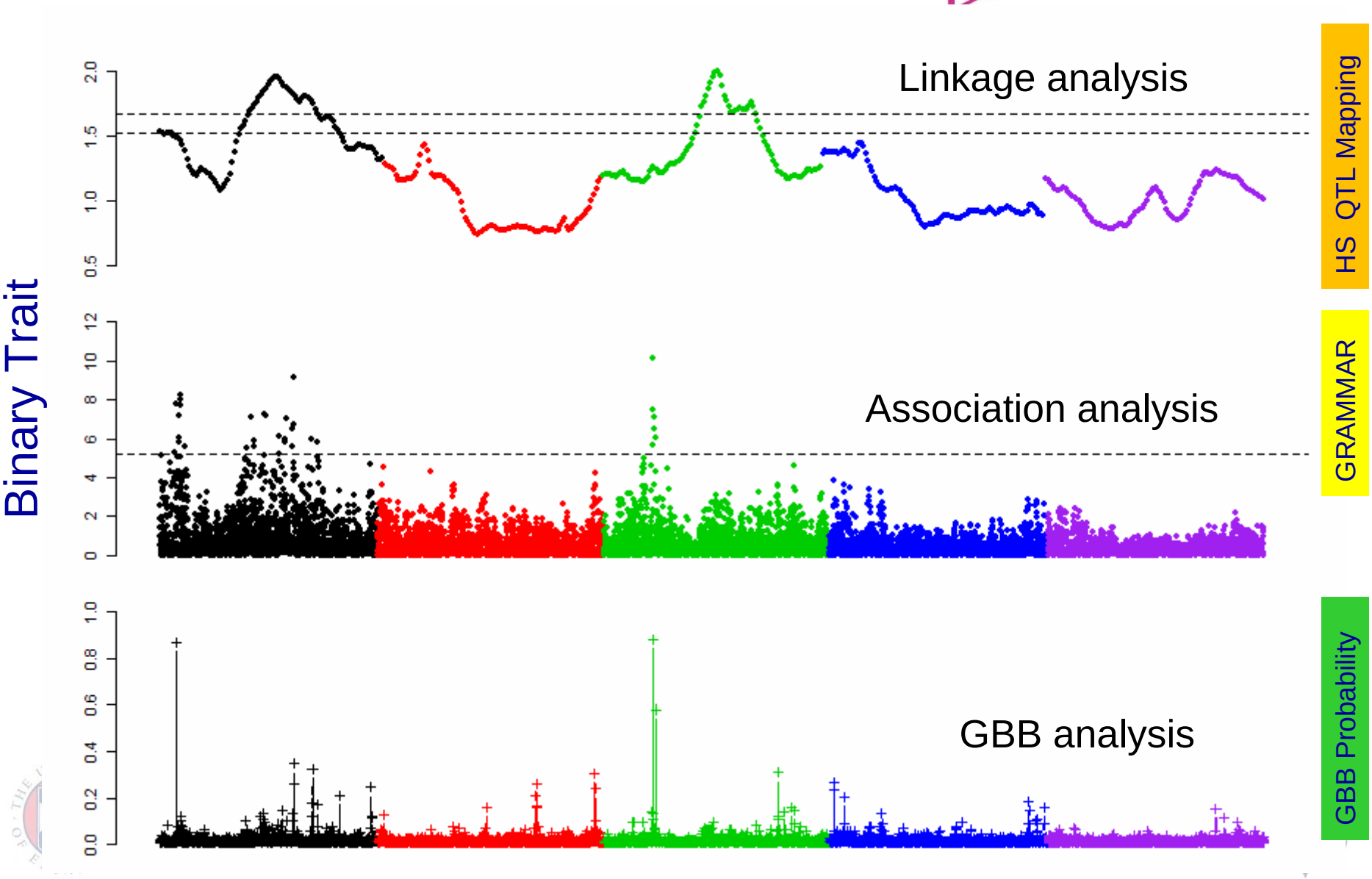
Estimation of the Π (SNP with effects)

Quantitative Trait	Binary Trait
5%	10%

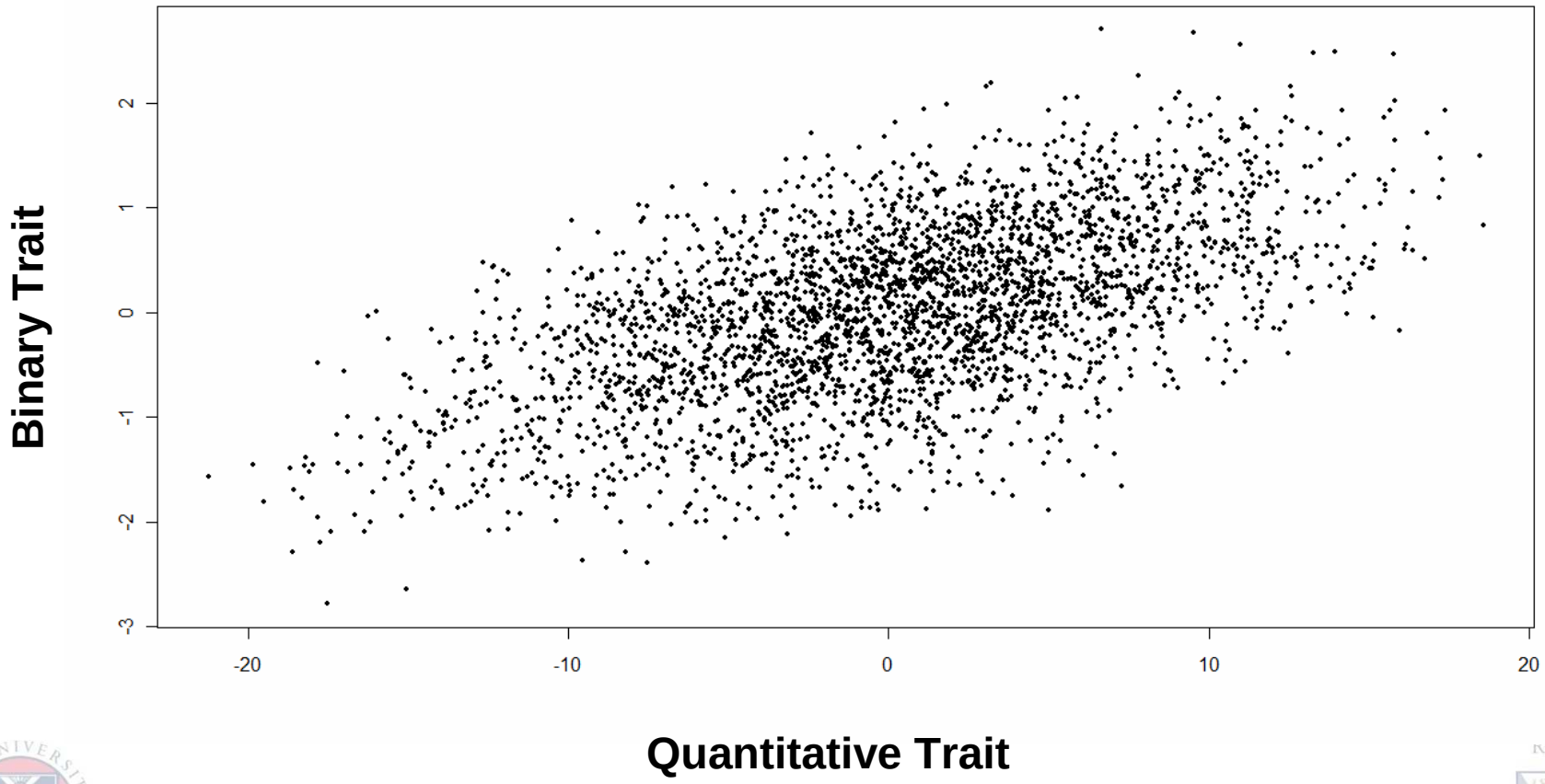
QTL mapping: signals from different approaches (Quantitative trait)



QTL mapping: signals from different approaches (Binary trait)



Relationship between univariate EBVs of the two traits (r^2=0.58)



Traits are correlated: Might benefit from a multivariate analysis

Conclusions

- Adding polygenic effect
  - Quantitative trait: improve model fitting
  - Binary trait: not important

- Consistent results were obtained using all 4 approaches (r^2 grater than 0.94)

Conclusions

- Percentage SNP as QTL
  - Quantitative trait: 5%
  - Binary trait: 10%

- Greatest evidence with all methods for QTLs on chr 1&3 for both traits

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CUTTING EDGE GENOMICS FOR SUSTAINABLE ANIMAL BREEDING

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