

# INCORPORATION OF CORRELATION BETWEEN SNPs INTO THE GENOMIC EVALUATION MODEL

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- **QTL MAS Workshop 2008**



- **Using information on SNP correlation in the model**
- **Recombination rate**
- **Disaster**



## MATERIAL

- Animals, markers, traits

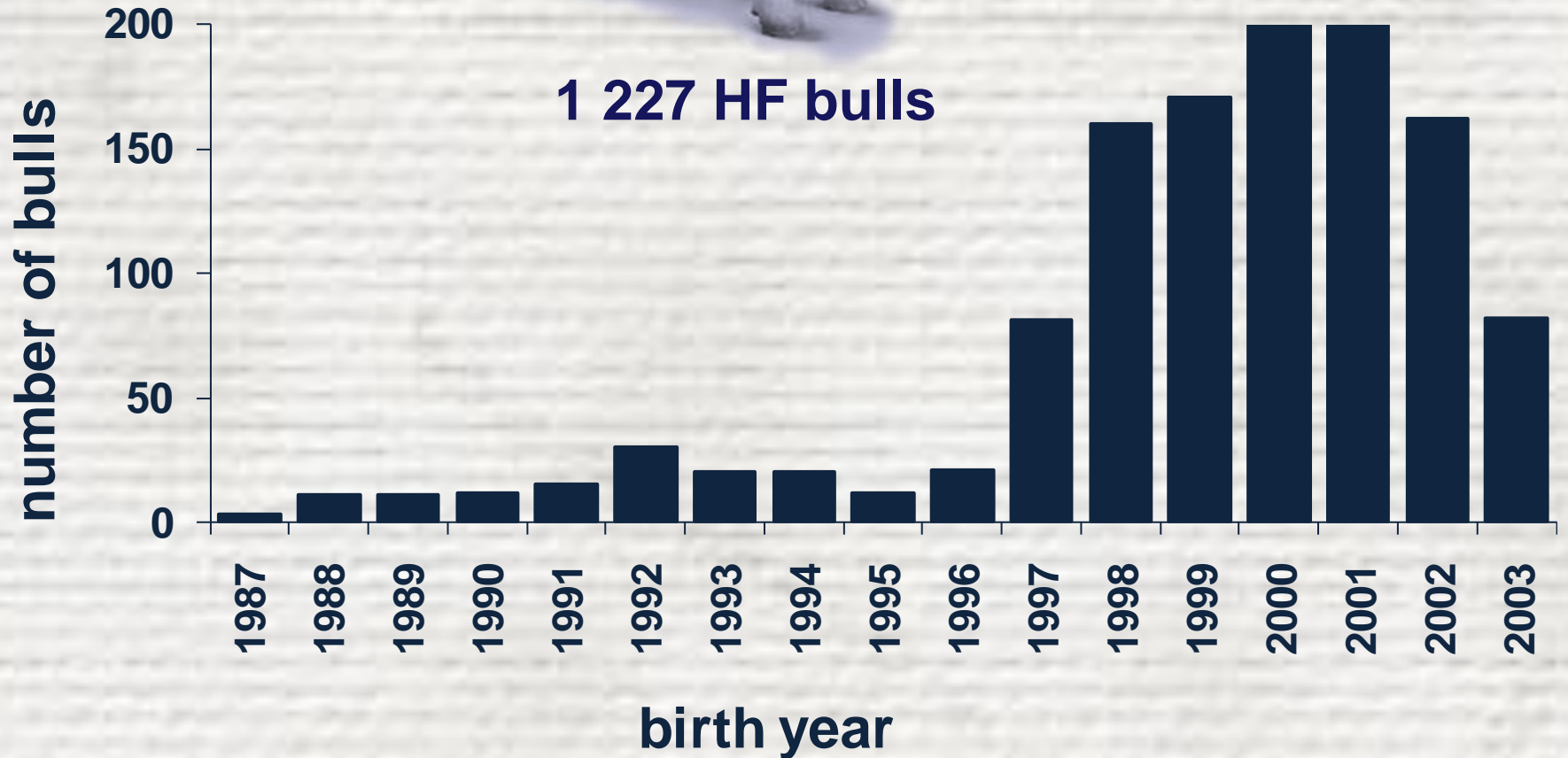
## METHODS

- LD calculation, DGV estimation

## RESULTS

- LD structure, SNP effects, DGV-EBV correlations

## CONCLUSIONS



## MARKERS

- Illumina bovine snp50 beadchip  
54 001 SNPs
- 46 267 tSNPs  
MAF  $\geq 0.01$ , call rate  $\geq 90\%$
- average call rate  
99.66% (all SNPs), 99.75% (tSNPs)
- average MAF  
0.23 (all SNPs), 0.26 (tSNPs)



## TRAITS

- Deregressed EBV (spring 2009)
- Milk yield



## LD ESTIMATION

- **PLINK** *Purcell et al. 2007*
- **Unphased genotypes**
- **Pairwise LD**
- **Correlation coefficients between allele counts**
- **Linked SNPs**



## SNP EFFECT ESTIMATION

$$\mathbf{y} = \boldsymbol{\mu} + \mathbf{Z}\mathbf{q} + \mathbf{e}$$

- $y$  deregressed EBV for MY
- $\mu$  general mean
- $q$  SNP
- $Z \in \{-1, 0, 1\}$
- $e$  residual

## COVARIANCE STRUCTURE

uncorrelated SNP 46 267x46 267

$$\begin{bmatrix} 1 & & \text{"0"} \\ & \dots & \\ \text{"0"} & & 1 \end{bmatrix} \frac{\sigma_a^2}{46267}$$

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## COVARIANCE STRUCTURE (chromosome diagonal)

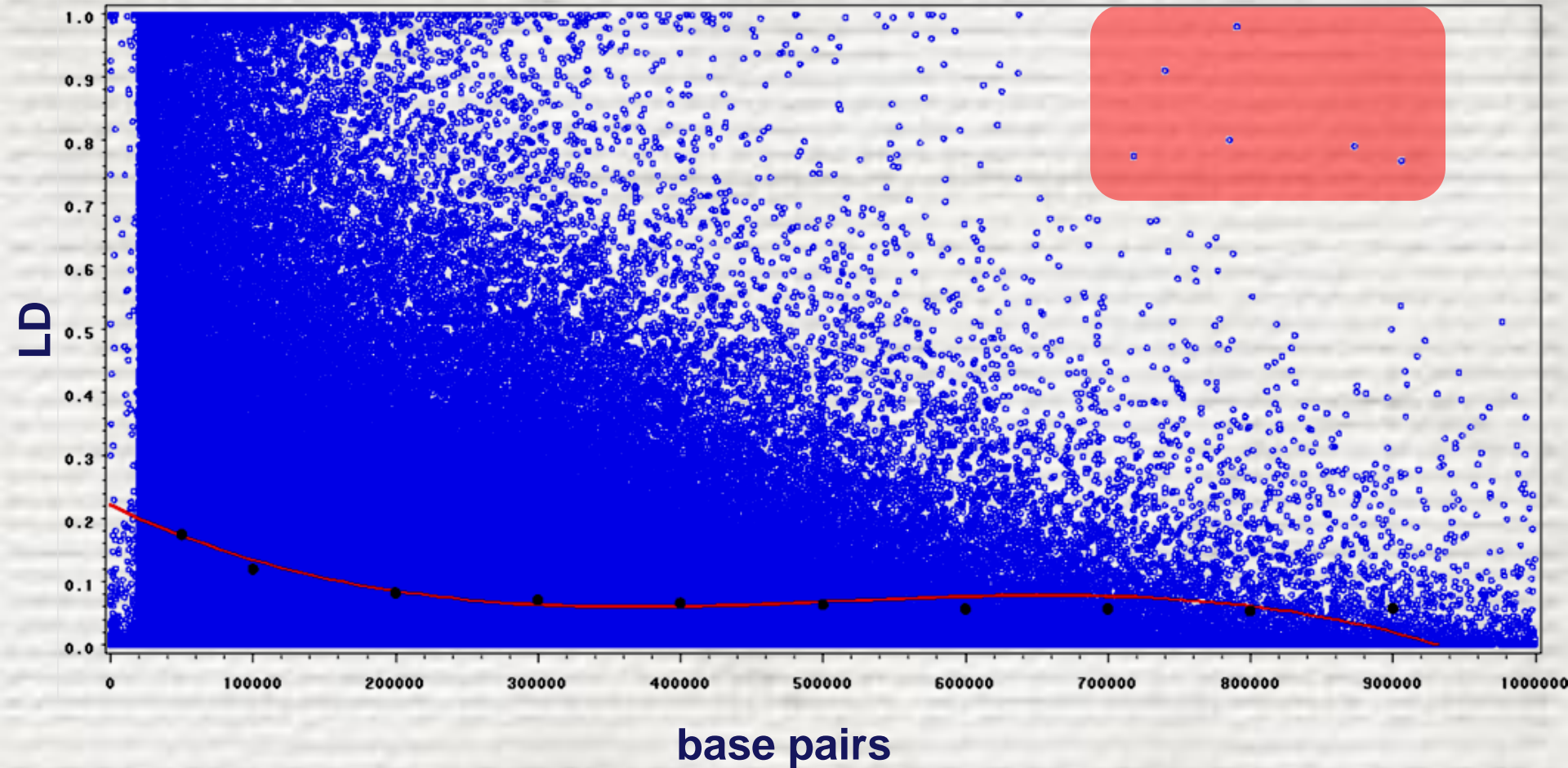
correlated SNP      46 267x46 267

**LD  $\geq 0.80$**

$$\begin{bmatrix} 1 & & \text{"LD"} \\ & \dots & \\ \text{"LD"} & & 1 \end{bmatrix} \frac{\sigma_a^2}{46267}$$

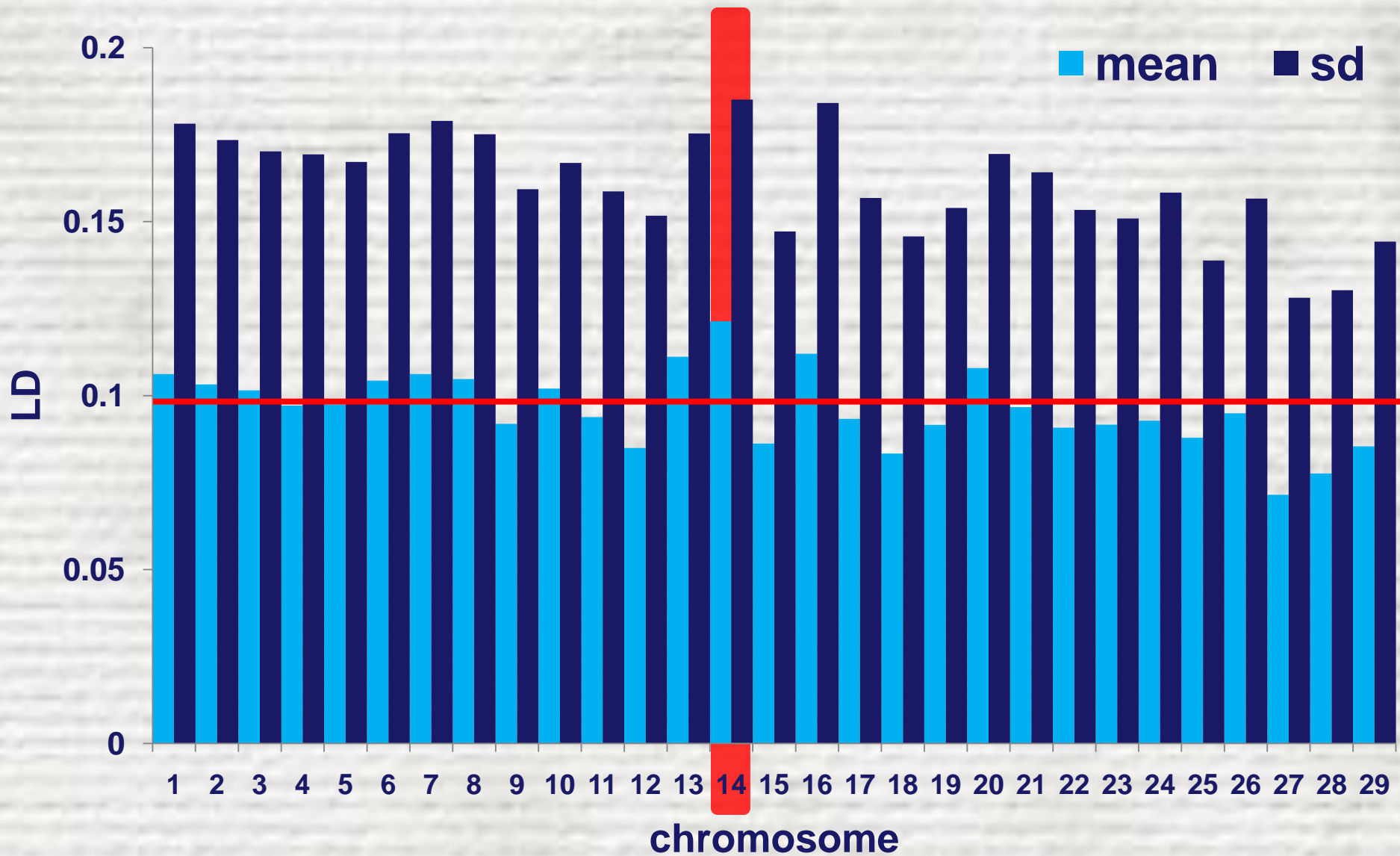
# RESULTS: *Linkage Disequilibrium structure*

## PAIRWISE GENOMEWISE LD



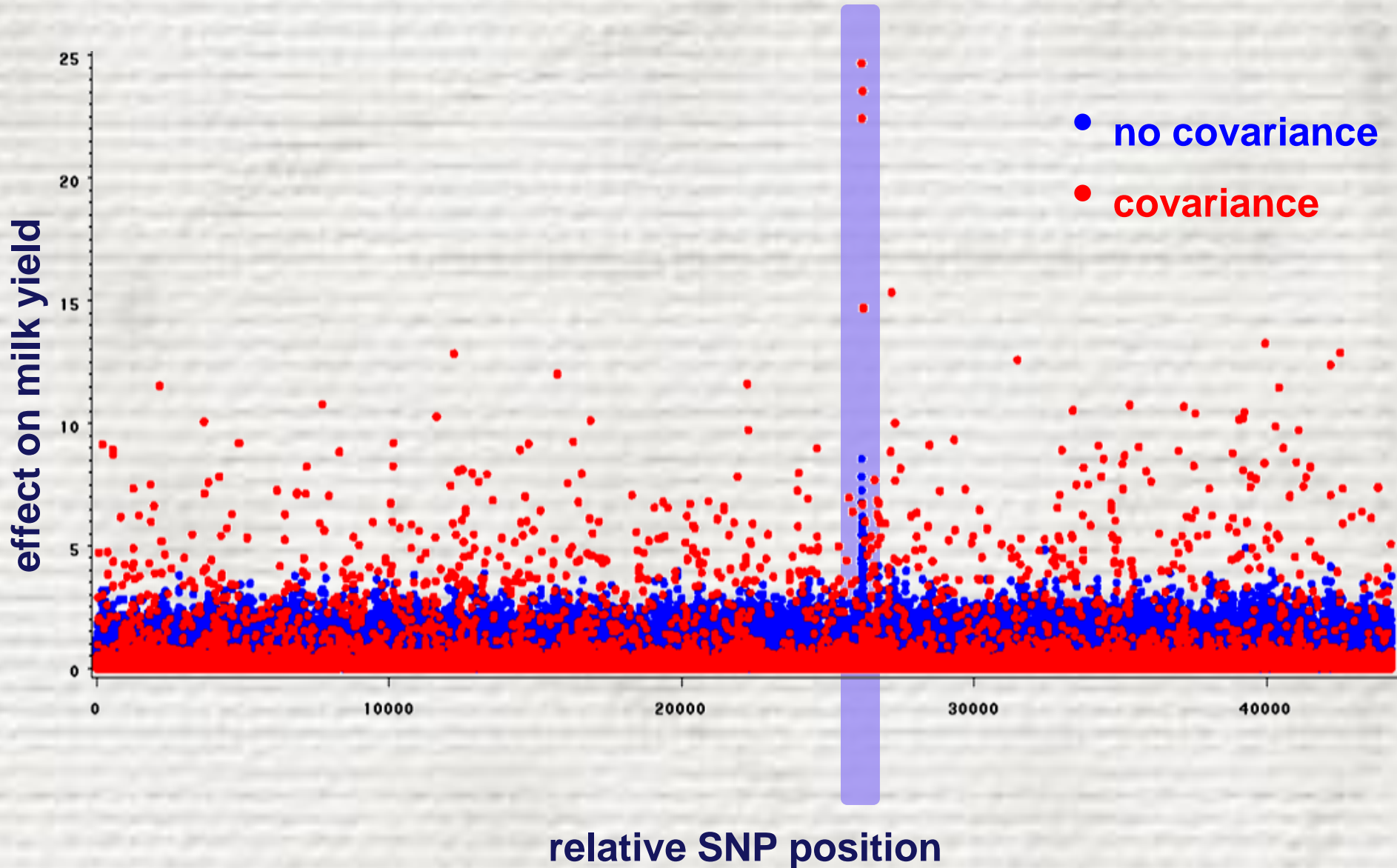
# RESULTS: *Linkage Disequilibrium structure*

## CHROMOSOMEWISE LD

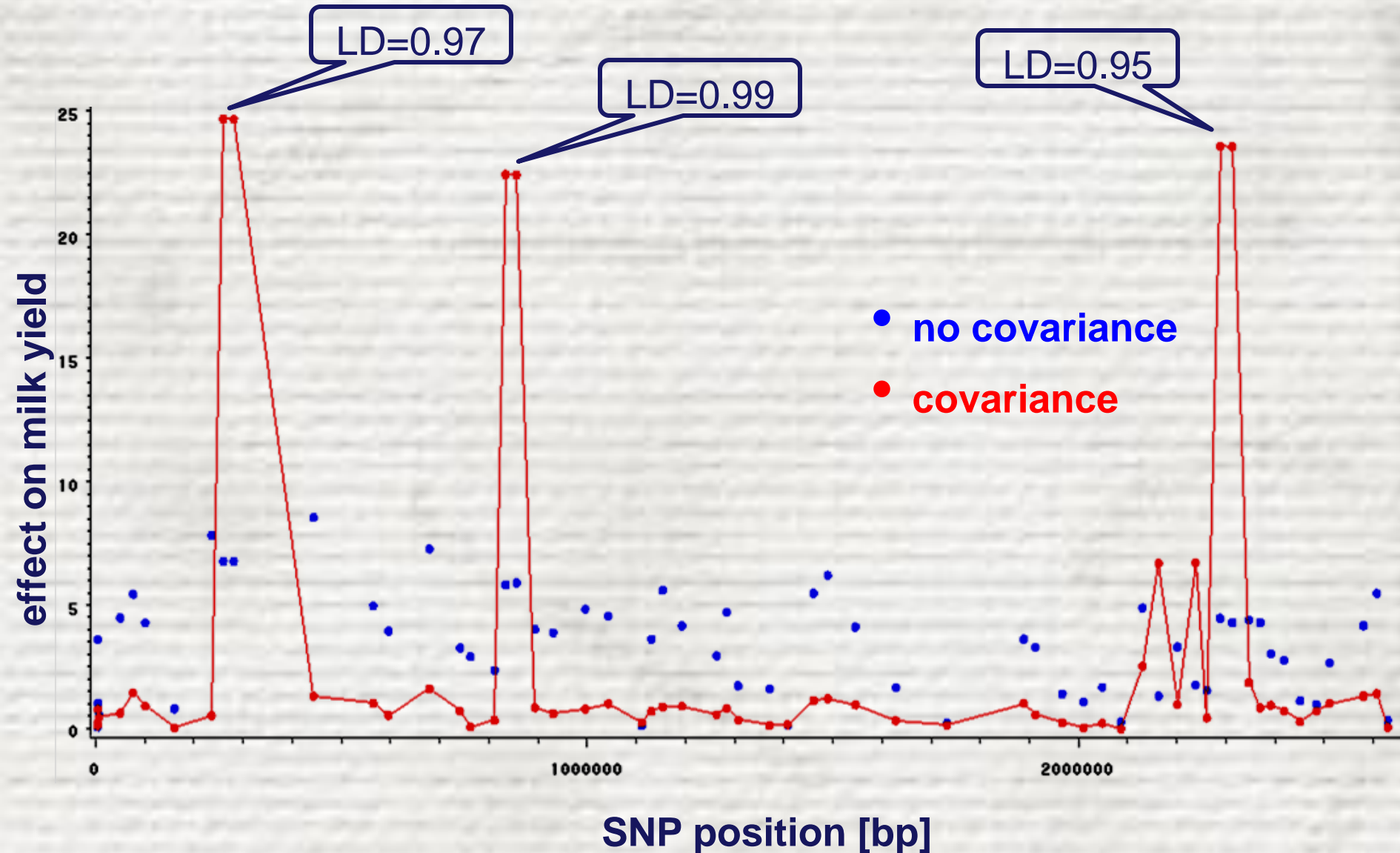


# RESULTS: SNP effect estimates

## ADDITIVE EFFECTS OF ALL SNPs

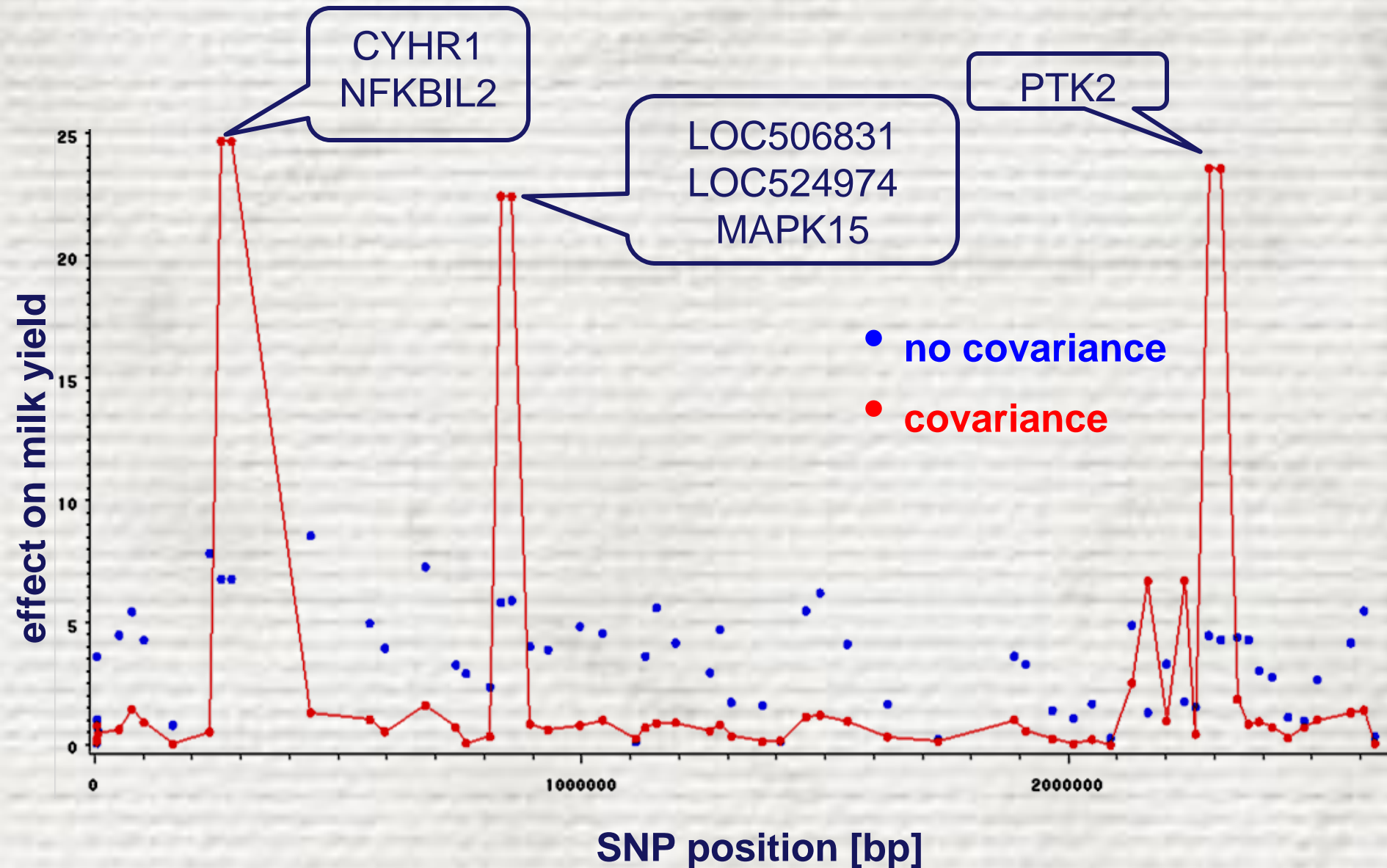


ADDITIVE EFFECTS OF SNPs ON BTA14 close to DGAT1



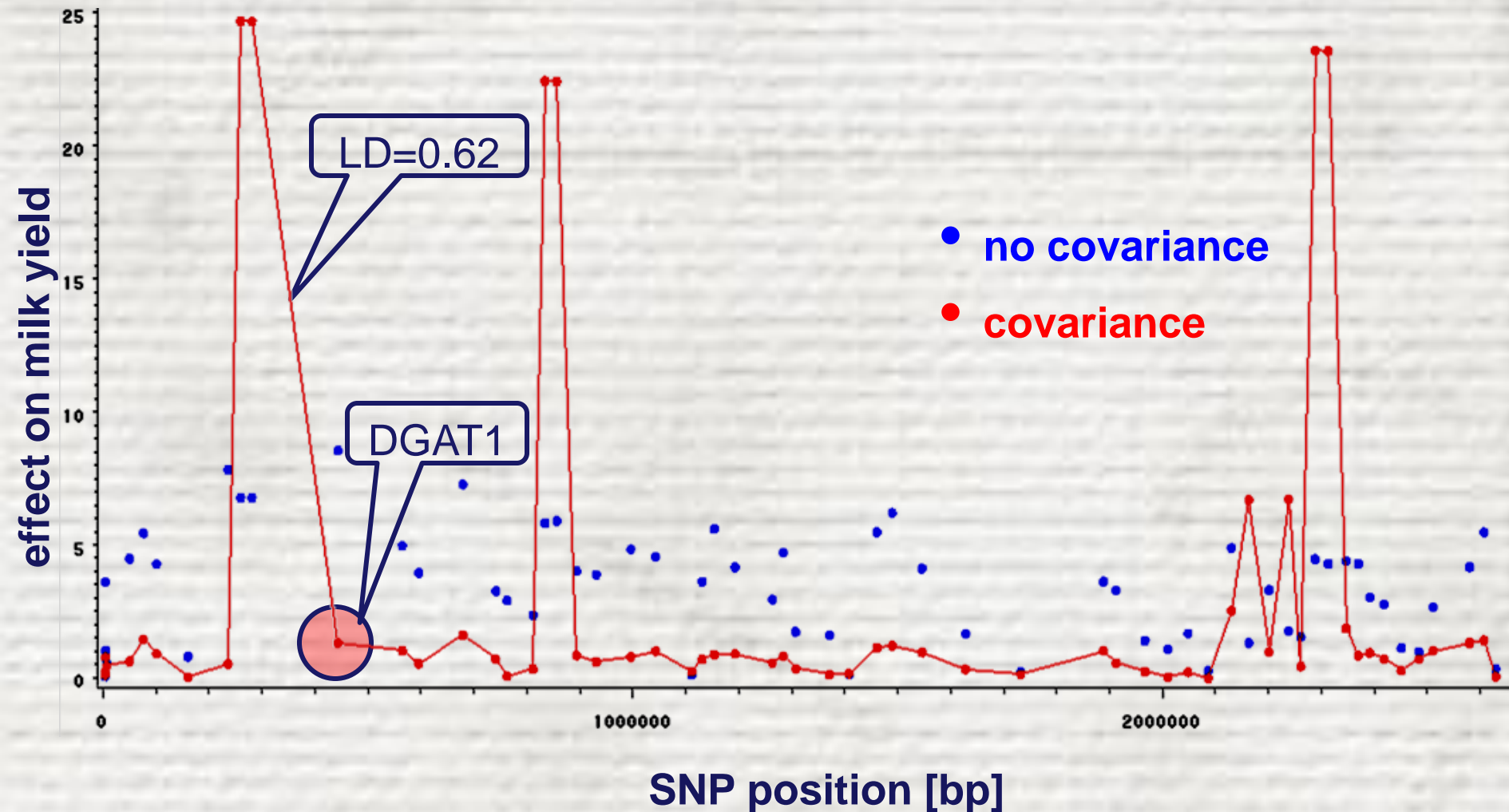
# RESULTS: SNP effect estimates

## ADDITIVE EFFECTS OF SNPs ON BTA14 close to DGAT1



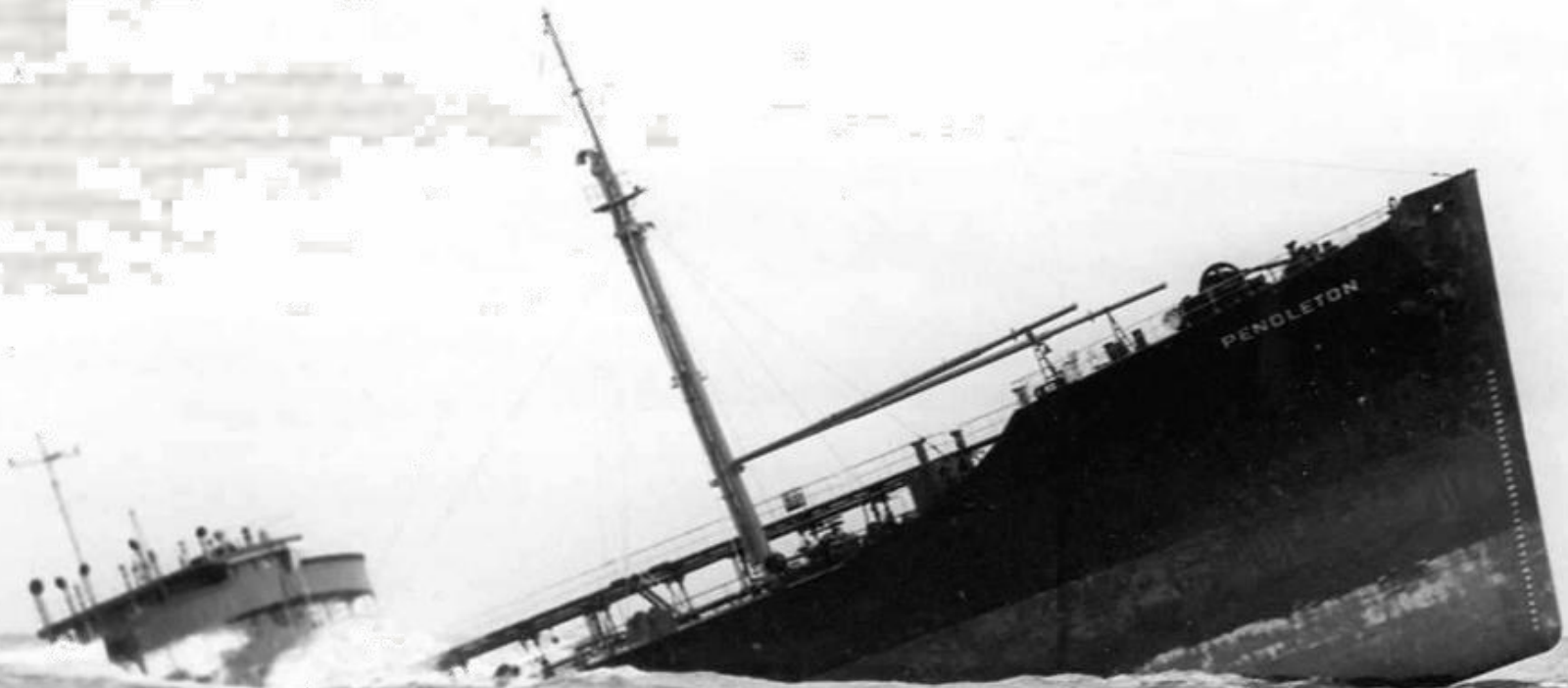
# RESULTS: SNP effect estimates

## ADDITIVE EFFECTS OF SNPs ON BTA14 close to DGAT1



CORRELATION DGV-EBV

- Without covariance between SNP: 0.98188
- With covariance between SNP: 0.58939



## COVARIANCE BETWEEN LD

- **Important for gene detection:**
  - **Statistically well defined approach**
  - **Identification of causal mutations**
  - **Design of a small chip**
  - **Between population comparison needed**
- **Disadvantageous for EBV prediction**
  - **Computationally difficult**
  - **Not suitable for routine evaluation**

**THANK YOU**

**FOR ATTENTION**

