



# Chromosomal partitioning of correlations between dairy and beef traits in dual purpose Fleckvieh

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# Introduction



- Fleckvieh breeding goal  
(improve dairy and maintain beef characteristics)
- Genetic correlations
  - Slightly positive or close to zero
  - Studies mainly carried out before 1980's
  - Small scale experiments
- Aim
  - Estimate overall genetic correlations
  - Partition correlations by chromosomes

# Material



- 4105 progeny tested bulls
- Progeny phenotype deviations
  - dairy traits
    - milk yield, **MY**
    - fat yield, **FY**
  - beef traits
    - net gain, **NG**
    - carcass grading, **CG**
- 50K Illumina SNP genotypes



# Methods - overview

- Bivariate marker model
    - Monte Carlo Markov Chain method
- Allele substitution effects



Breeding values



Co-variance components



Correlations

# Methods - nitty gritty details

- Bivariate marker model

$$\begin{pmatrix} \mathbf{y}_1 \\ \mathbf{y}_2 \end{pmatrix} = \begin{pmatrix} \mathbf{X}_1 & \mathbf{0} \\ \mathbf{0} & \mathbf{X}_2 \end{pmatrix} \begin{pmatrix} \mathbf{b}_1 \\ \mathbf{b}_2 \end{pmatrix} + \begin{pmatrix} \mathbf{Z}_1 & \mathbf{0} \\ \mathbf{0} & \mathbf{Z}_2 \end{pmatrix} \mathbf{W} \begin{pmatrix} \boldsymbol{\alpha}_1 \\ \boldsymbol{\alpha}_2 \end{pmatrix} + \begin{pmatrix} \mathbf{e}_1 \\ \mathbf{e}_2 \end{pmatrix}$$

$$\begin{pmatrix} \boldsymbol{\alpha}_1 \\ \boldsymbol{\alpha}_2 \end{pmatrix} \sim N \left( \begin{pmatrix} \mathbf{0} \\ \mathbf{0} \end{pmatrix}, \begin{pmatrix} \sigma_{\alpha_1, \alpha_1} & \sigma_{\alpha_1, \alpha_2} \\ sym. & \sigma_{\alpha_2, \alpha_2} \end{pmatrix} \otimes \mathbf{I} \right)$$

- Breeding values

$$\mathbf{a}_1^i = \mathbf{W} \boldsymbol{\alpha}_1^i$$

$$\mathbf{a}_2^i = \mathbf{W} \boldsymbol{\alpha}_2^i$$

- Co-variance components

$$\sigma_{a,1}^{2,i} = Var(\mathbf{a}_1^i)$$

$$\sigma_{a,2}^{2,i} = Var(\mathbf{a}_2^i)$$

- Correlation

$$\rho_{a,1,2}^i = \frac{\sigma_{a,1,2}^i}{\sigma_{a,1}^i \sigma_{a,2}^i}$$

$$\sigma_{a,1,2}^i = Cov(\mathbf{a}_1^i, \mathbf{a}_2^i)$$

# Partition by chromosomes

- Calculate chromosomal breeding values
- Co-variances between traits & chrom.

$$\begin{pmatrix} \sigma_{a_1,a_1} & \sigma_{a_1,a_2} \\ \text{sym.} & \sigma_{a_2,a_2} \end{pmatrix} = \begin{pmatrix} \begin{matrix} \sigma_{a_{1,1},a_{1,1}} & \sigma_{a_{1,1},a_{1,2}} & \cdots & \sigma_{a_{1,1},a_{1,29}} \\ & \sigma_{a_{1,2},a_{1,2}} & & \sigma_{a_{1,2},a_{1,29}} \\ & & \ddots & \vdots \\ \text{Trait1} & & & \sigma_{a_{1,29},a_{1,29}} \end{matrix} & \begin{matrix} \sigma_{a_{1,1},a_{2,1}} & \sigma_{a_{1,1},a_{2,2}} & \cdots & \sigma_{a_{1,1},a_{2,29}} \\ \sigma_{a_{1,2},a_{2,1}} & \sigma_{a_{1,2},a_{2,2}} & & \sigma_{a_{1,2},a_{2,29}} \\ \vdots & \vdots & & \vdots \\ \sigma_{a_{1,29},a_{2,1}} & \sigma_{a_{1,29},a_{2,2}} & \cdots & \sigma_{a_{1,29},a_{2,29}} \end{matrix} \\ \text{sym.} & \begin{matrix} \sigma_{a_{2,1},a_{2,1}} & \sigma_{a_{2,1},a_{2,2}} & \cdots & \sigma_{a_{2,1},a_{2,29}} \\ & \sigma_{a_{2,2},a_{2,2}} & & \sigma_{a_{2,2},a_{2,29}} \\ & & \ddots & \vdots \\ \text{Trait2} & & & \sigma_{a_{2,29},a_{2,29}} \end{matrix} \end{pmatrix}$$

# Results

# Allele substitution effects correlation

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	FY	NG	CG
MY	0.30 <sub>0.02</sub>	0.17 <sub>0.02</sub>	0.15 <sub>0.02</sub>
FY		0.17 <sub>0.02</sub>	0.15 <sub>0.02</sub>
NG			0.28 <sub>0.02</sub>

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# Breeding value (overall) correlations

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	FY	NG	CG
MY	0.76 <sub>0.002</sub>	0.16 <sub>0.004</sub>	-0.06 <sub>0.004</sub>
FY		0.17 <sub>0.004</sub>	-0.10 <sub>0.004</sub>
NG			0.46 <sub>0.004</sub>

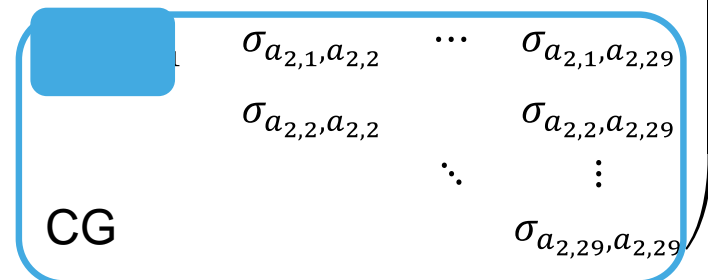
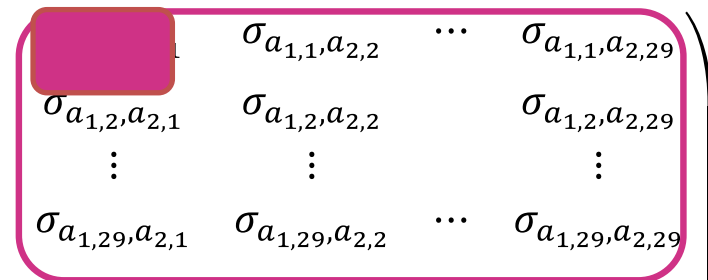
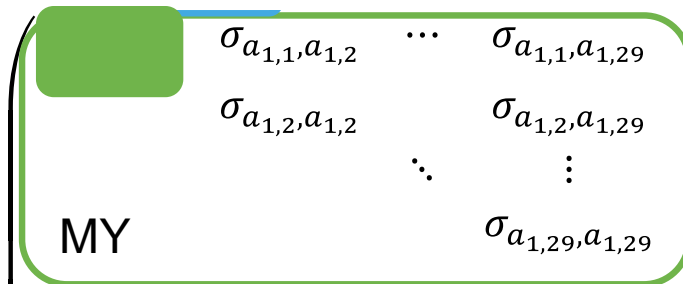
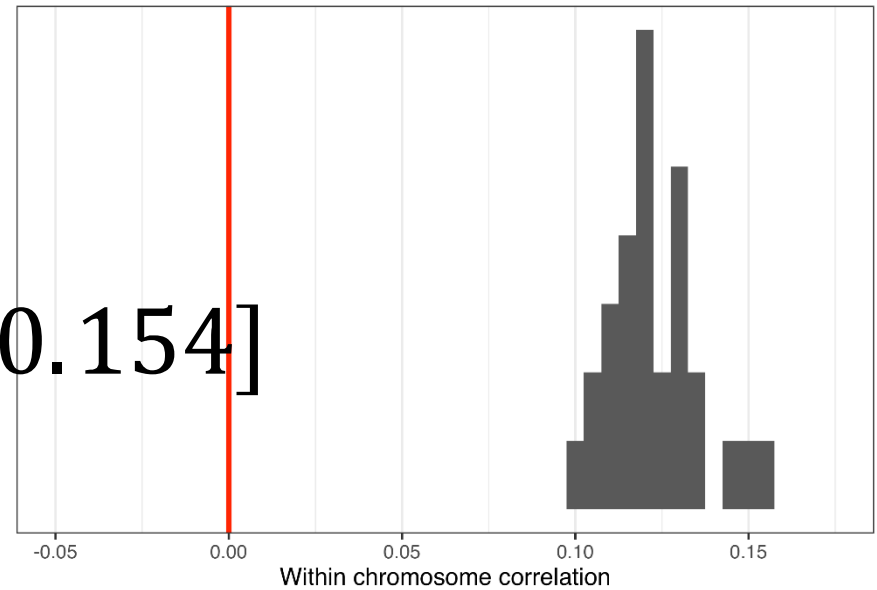
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Let's drill into  
MY:CG  
by chromosomes

# Individual chromosomes (n=29)

$$\rho_{a_{MY,c}, a_{CG,c}} = 0.12$$

$$[0.099, 0.154]$$

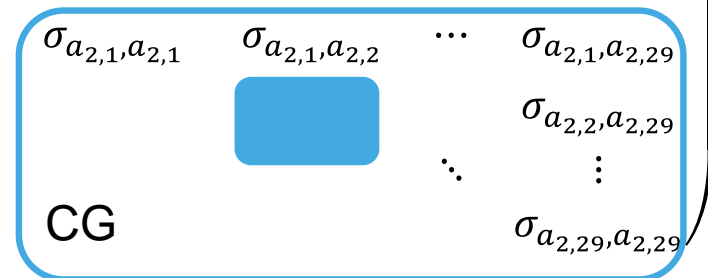
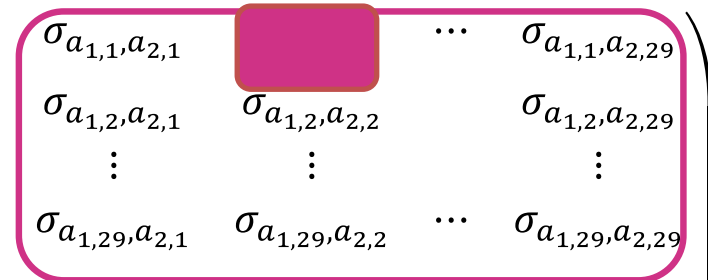
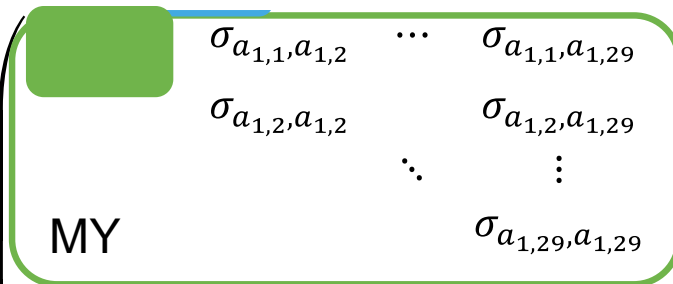
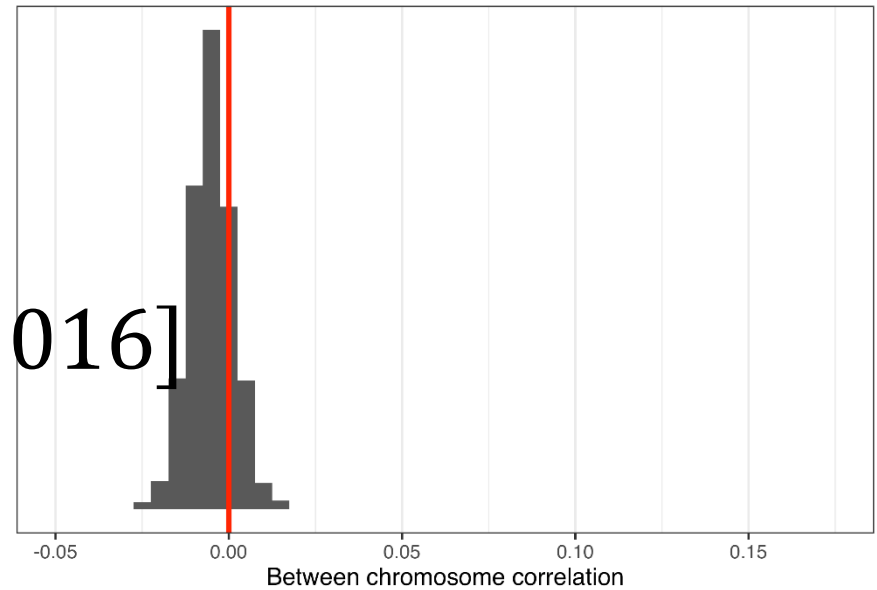


sym.

# Chromosome pairs (n=812)

$$\rho_{a_{MY,c1}, a_{CG,c2}} = -0.005$$

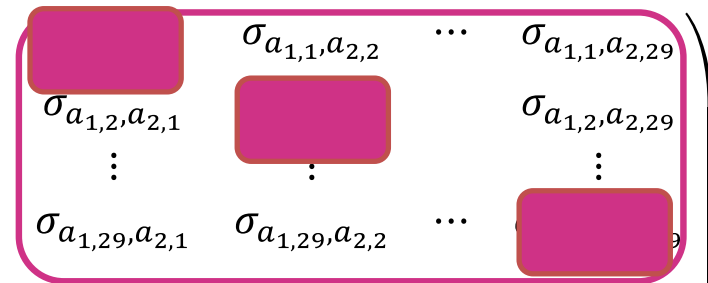
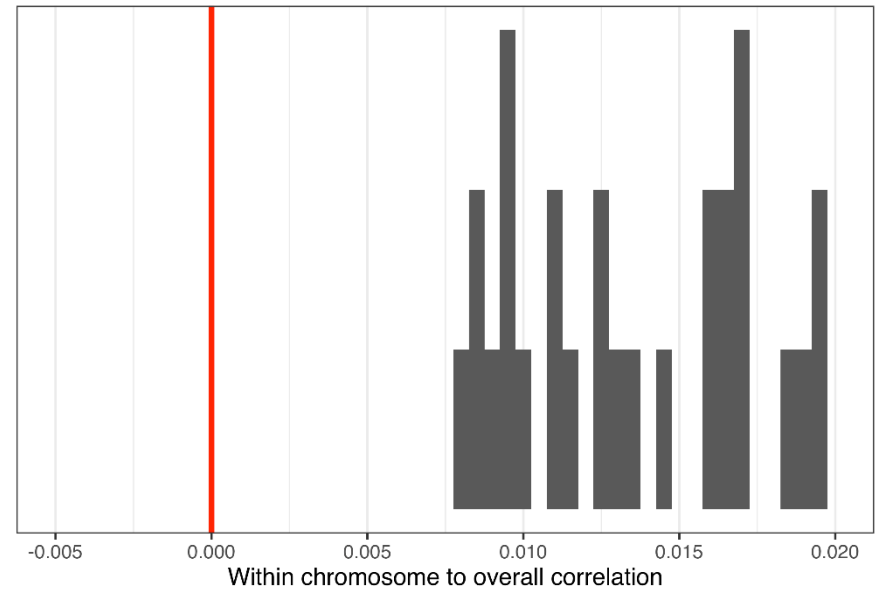
$$[-0.024, 0.016]$$



sym.

# Individual chrom. to overall (n=29)

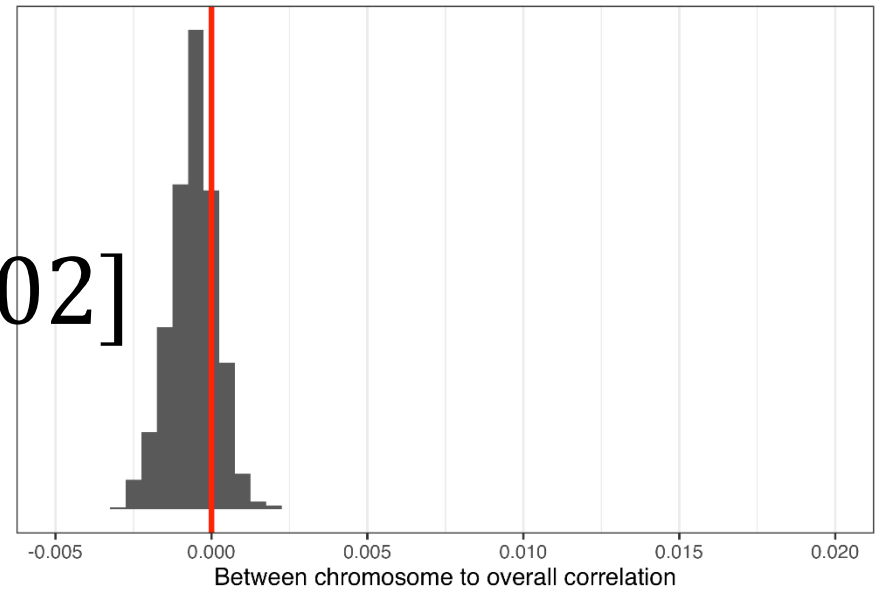
$$\rho_{a_{MY}, a_{CG}} = \begin{matrix} 0.014 \\ [0.008, 0.024] \\ 0.41 \end{matrix}$$



*sym.*

# Chrom. pairs to overall (n=812)

$$\rho_{a_{MY}, a_{CG}} = \begin{matrix} -0.0006 \\ [-0.003, 0.002] \\ -0.47 \end{matrix}$$



*sym.*

CG

# The many correlations for MY:CG

- Allele substitution effects 0.15
- Breeding values
  - Whole-genome -0.06
  - Chromosomes
    - Individual chromosomes
      - average correlation 0.12
      - contribution to overall 0.41
    - Chromosome pairs
      - average correlation -0.005
      - contribution to overall -0.47

# All trait combinations

	Loci	IndChr	ChrPair	Genome	IndChrG	ChrPairG
MY:FY	0.30	0.34 [0.186, 0.415]	-0.003 [-0.024, 0.023]	0.76	1.07 [0.02, 0.06]	-0.31 [-0.003, 0.003]
MY:NG	0.17	0.16 [0.062, 0.201]	-0.004 [-0.026, 0.021]	0.16	0.54 [0.008, 0.032]	-0.38 [-0.004, 0.003]
MY:CG	0.15	0.12 [0.099, 0.154]	-0.005 [-0.024, 0.016]	-0.06	0.41 [0.008, 0.024]	-0.47 [-0.003, 0.002]
FY:NG	0.17	0.15 [0.126, 0.176]	-0.004 [-0.024, 0.019]	0.11	0.49 [0.009, 0.027]	-0.38 [-0.003, 0.003]
FY:CG	0.15	0.12 [0.073, 0.144]	-0.005 [-0.022, 0.016]	-0.10	0.39 [0.005, 0.021]	-0.49 [-0.003, 0.002]
NG:CG	0.28	0.31 [0.283, 0.354]	-0.006 [-0.028, 0.017]	0.46	1.11 [0.022, 0.066]	-0.65 [-0.004, 0.002]

# Conclusions

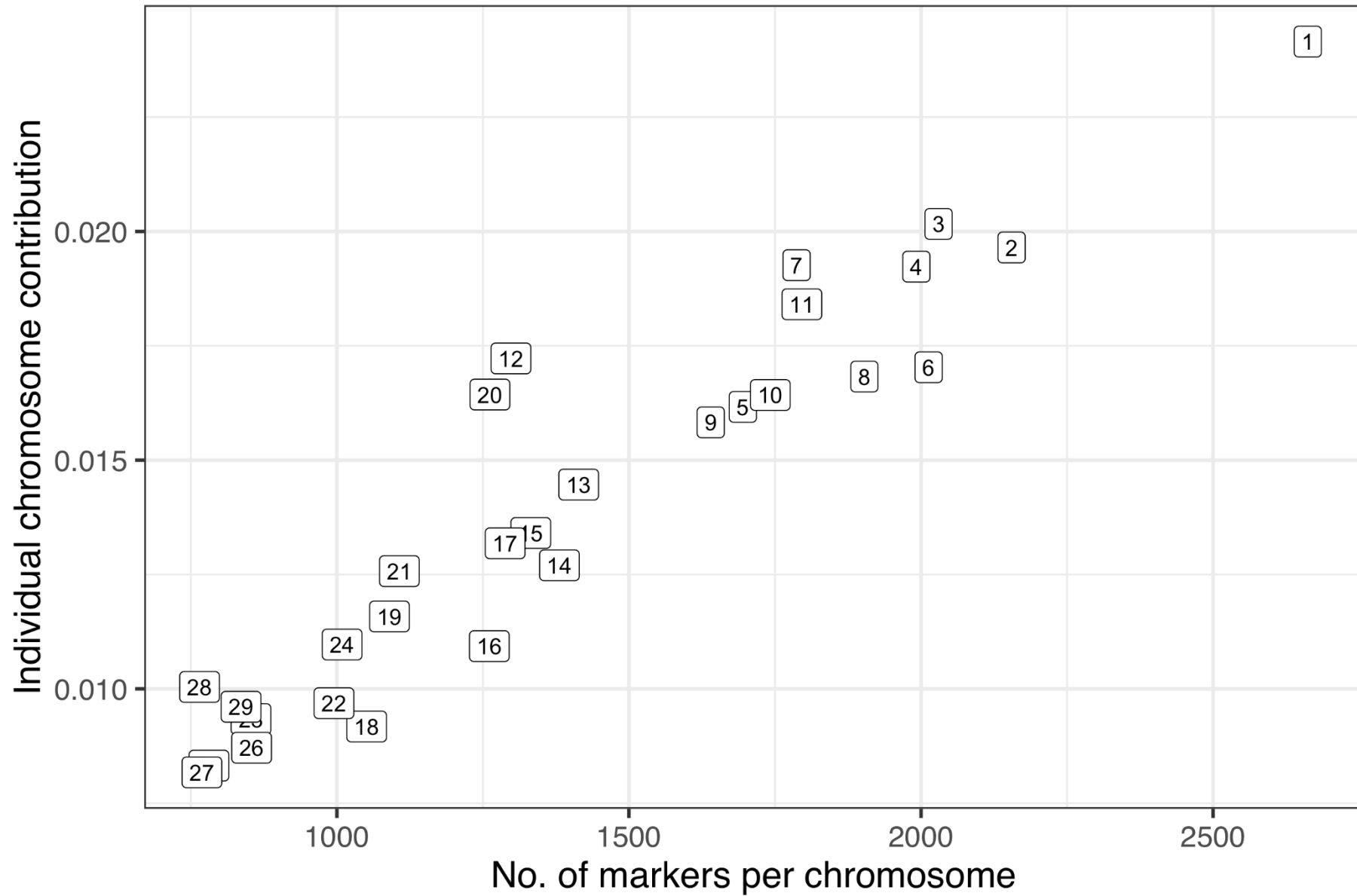
- Genetic correlations from posterior samples of allele substitution effects and genotypes
- The many correlations
  - Allele subst. effects **PLEIOTROPY**
  - Breeding values
    - Whole-genome
    - Chromosomes
      - Individual chromosomes
      - Chromosome pairs
- Future: chromosome region correlations



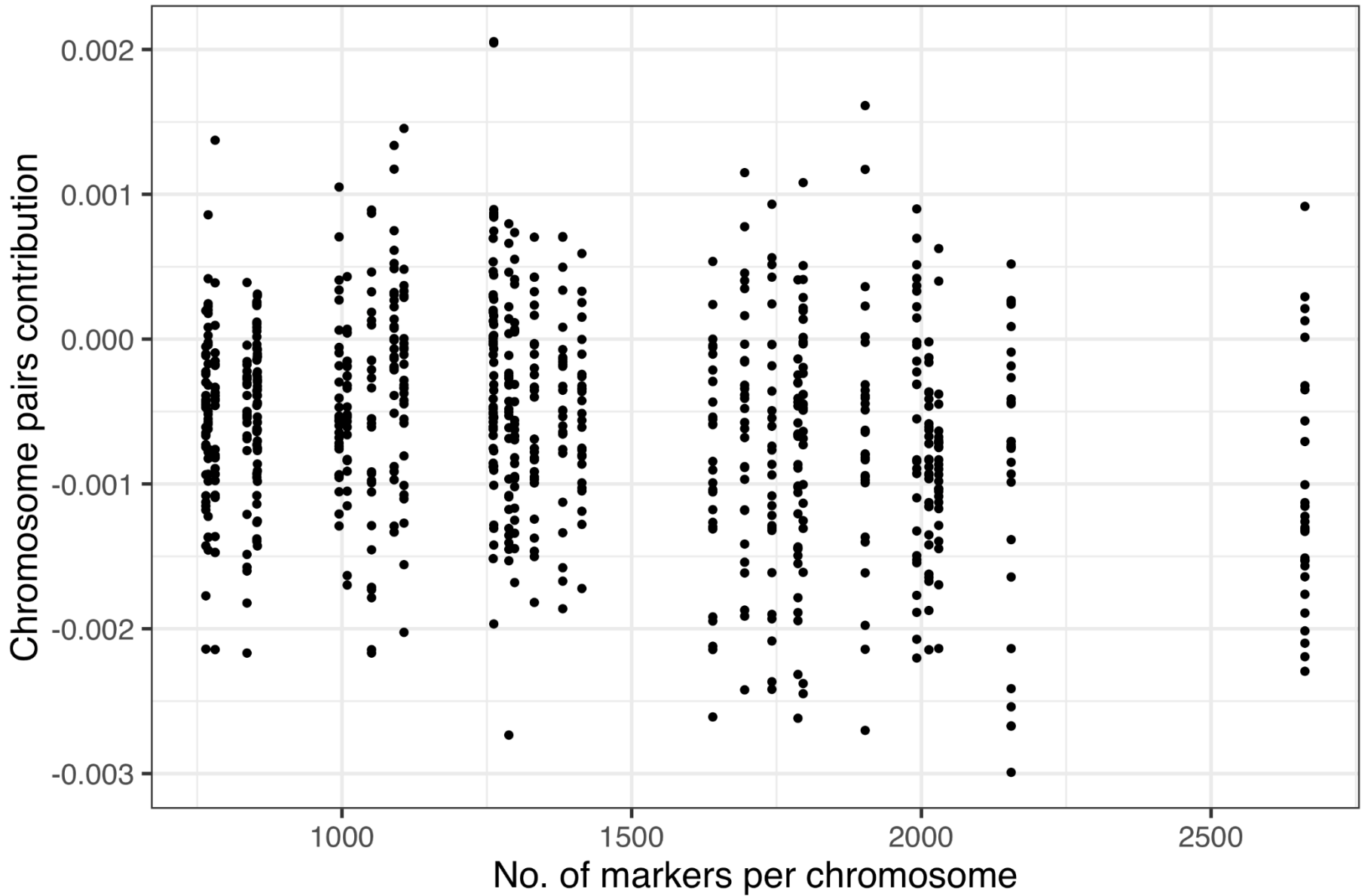
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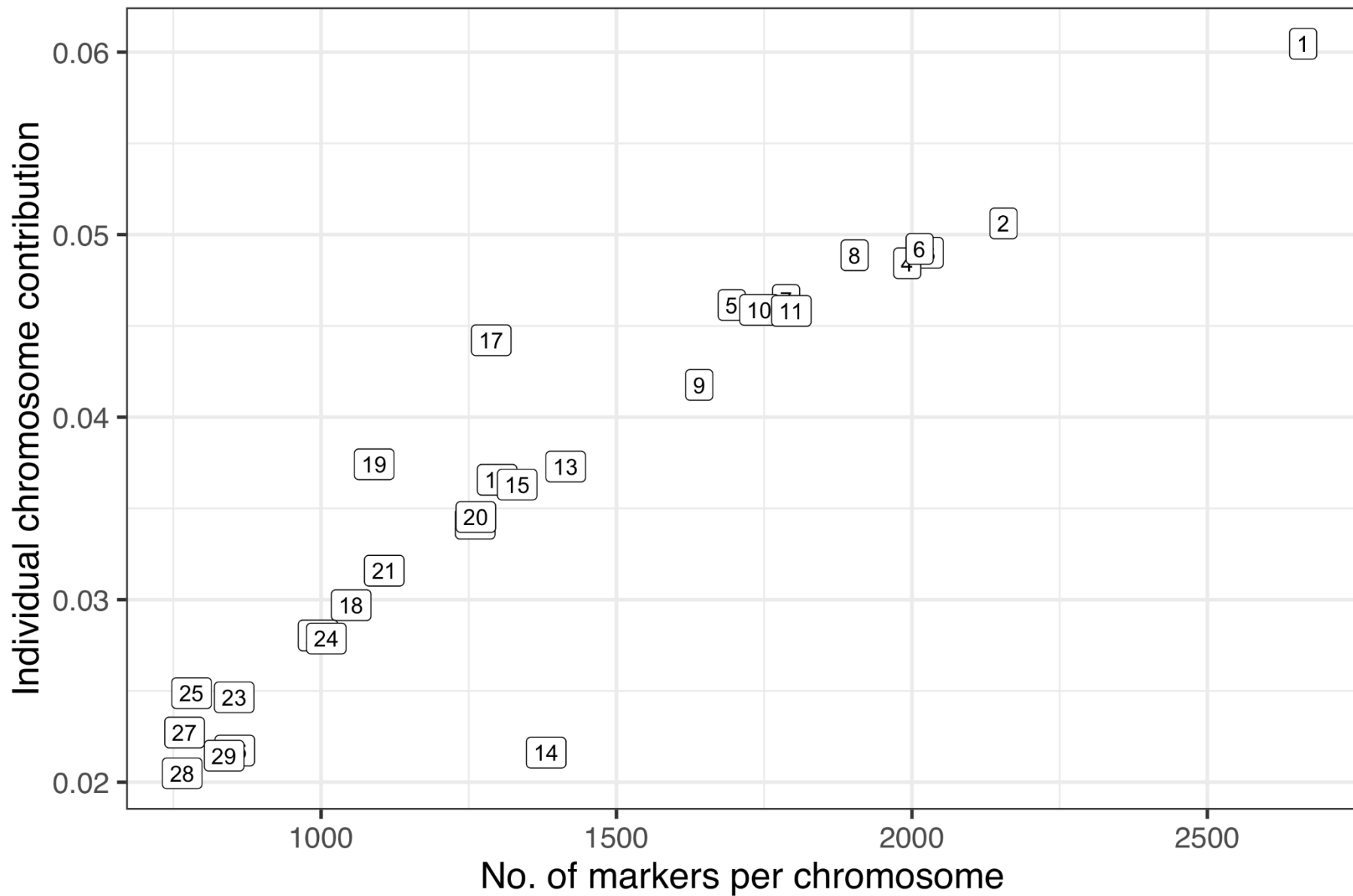
# MY:CG



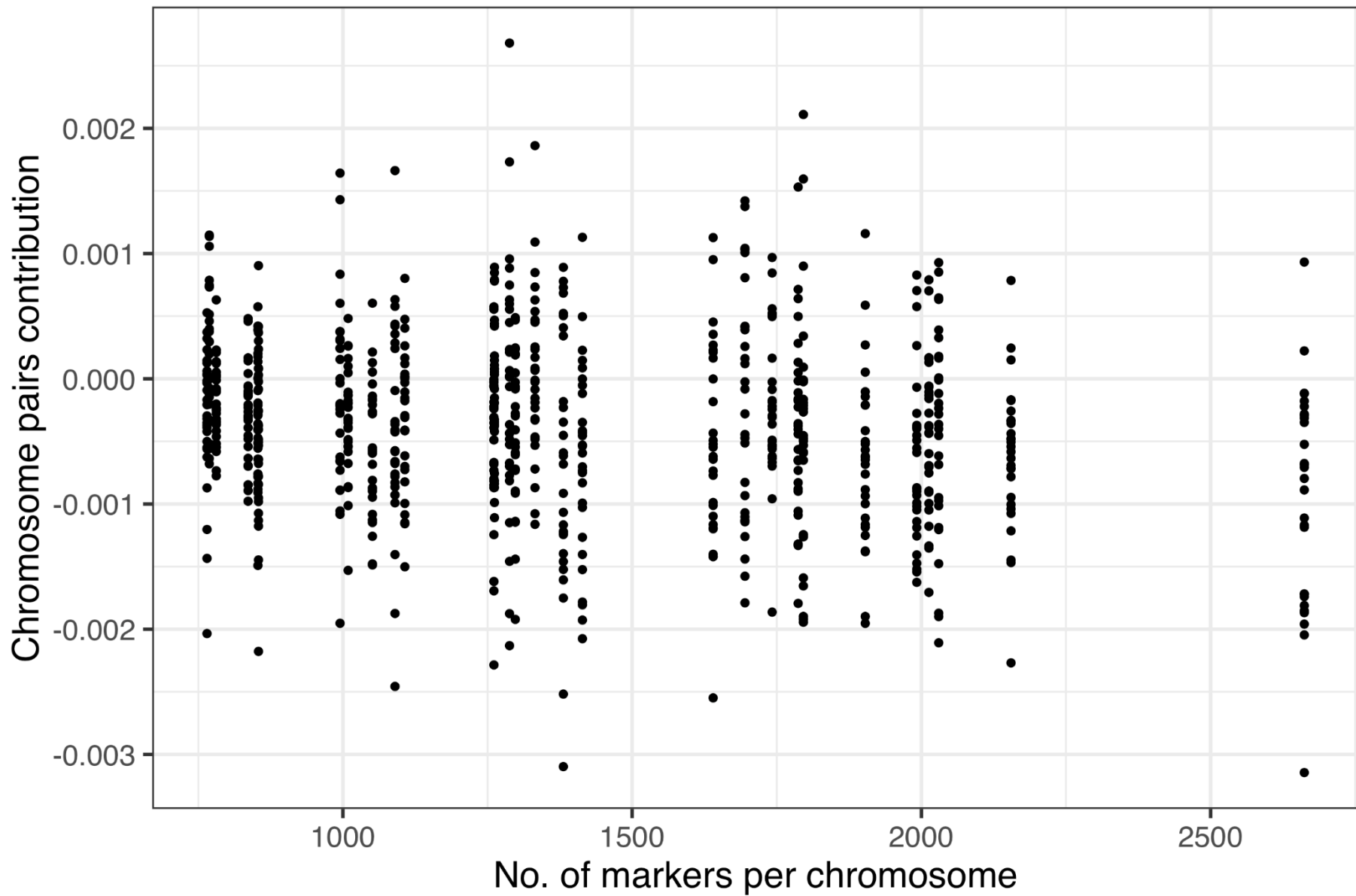
# MY:CG



# MY:FY



# MY:FY



# Comparison with pedigree model

	Pedigree	Genomic
$\sigma_{a_{MY}, a_{MY}} =$	0.72	1.02
$\sigma_{a_{CG}, a_{CG}} =$	1.03	1.01
$\sigma_{a_{MY}, a_{CG}} =$	-0.05	-0.06
$\rho_{a_{MY}, a_{CG}} =$	-0.06	-0.06

- Pedigree → pedigree base population!
- Genomic → genotyped animals,  
%var explained by markers