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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

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

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

- Breeding values

$$\boldsymbol{a}_1^i = \boldsymbol{W}\boldsymbol{\alpha}_1^i$$
$$\boldsymbol{a}_2^i = \boldsymbol{W}\boldsymbol{\alpha}_2^i$$

- Co-variance components

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

- Correlation

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

Partition by chromosomes

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

$$\begin{pmatrix} \boxed{\sigma_{a_1,a_1}} & \boxed{\sigma_{a_1,a_2}} \\ sym. & \boxed{\sigma_{a_2,a_2}} \end{pmatrix} =$$

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

Results

Allele substution effects correlation

	FY	NG	CG
MY	$0.30_{0.02}$	$0.17_{0.02}$	$0.15_{0.02}$
FY		$0.17_{0.02}$	$0.15_{0.02}$
NG			$0.28_{0.02}$

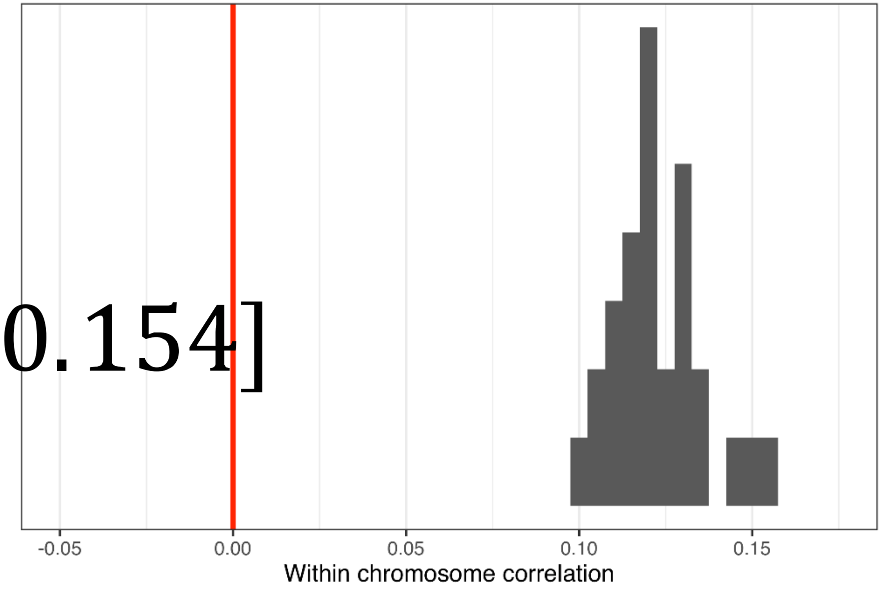
Breeding value (overall) correlations

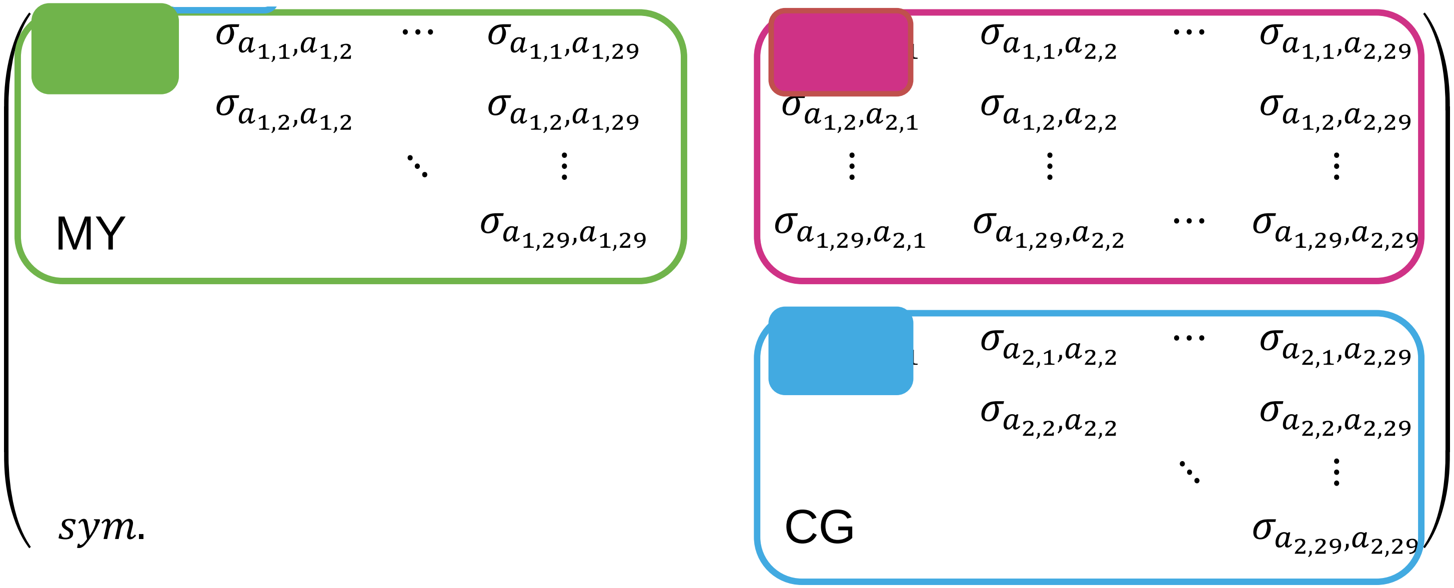
	FY	NG	CG
MY	$0.76_{0.002}$	$0.16_{0.004}$	$-0.06_{0.004}$
FY		$0.17_{0.004}$	$-0.10_{0.004}$
NG			$0.46_{0.004}$

Let’s drill into
MY:CG
by chromosomes

Individual chromosomes (n=29)

$$\rho_{a_{MY,c},a_{CG,c}} = \begin{matrix} 0.12 \\ [0.099,0.154] \end{matrix}$$

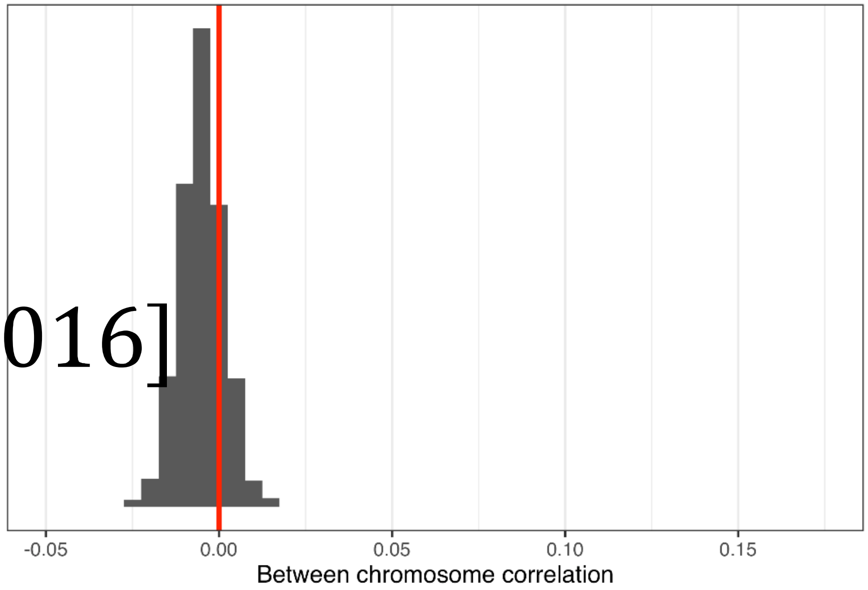




$$\left(\begin{array}{cccc|cccc}
 & \sigma_{a_{1,1},a_{1,2}} & \cdots & \sigma_{a_{1,1},a_{1,29}} & & \sigma_{a_{1,1},a_{2,2}} & \cdots & \sigma_{a_{1,1},a_{2,29}} \\
 & \sigma_{a_{1,2},a_{1,2}} & & \sigma_{a_{1,2},a_{1,29}} & \sigma_{a_{1,2},a_{2,1}} & \sigma_{a_{1,2},a_{2,2}} & & \sigma_{a_{1,2},a_{2,29}} \\
 & & \ddots & \vdots & \vdots & \vdots & & \vdots \\
\text{MY} & & & \sigma_{a_{1,29},a_{1,29}} & \sigma_{a_{1,29},a_{2,1}} & \sigma_{a_{1,29},a_{2,2}} & \cdots & \sigma_{a_{1,29},a_{2,29}} \\
 & & & & & \sigma_{a_{2,1},a_{2,2}} & \cdots & \sigma_{a_{2,1},a_{2,29}} \\
 & & & & & \sigma_{a_{2,2},a_{2,2}} & & \sigma_{a_{2,2},a_{2,29}} \\
 & & & & & & \ddots & \vdots \\
sym. & & & & \text{CG} & & & \sigma_{a_{2,29},a_{2,29}}
\end{array}\right)$$

Chromosome pairs (n=812)

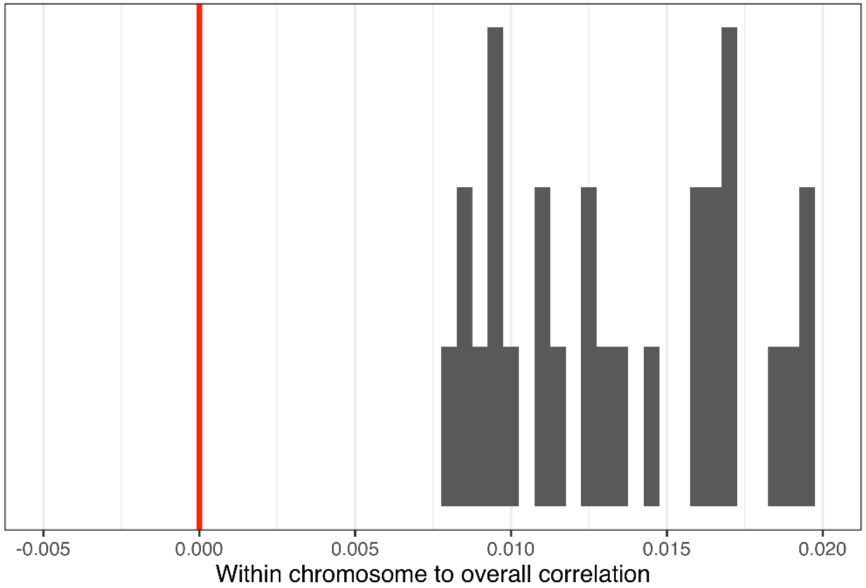
$$\rho_{a_{MY,c1},a_{CG,c2}} = \begin{matrix} \text{-0.005} \\ [-0.024, 0.016] \end{matrix}$$

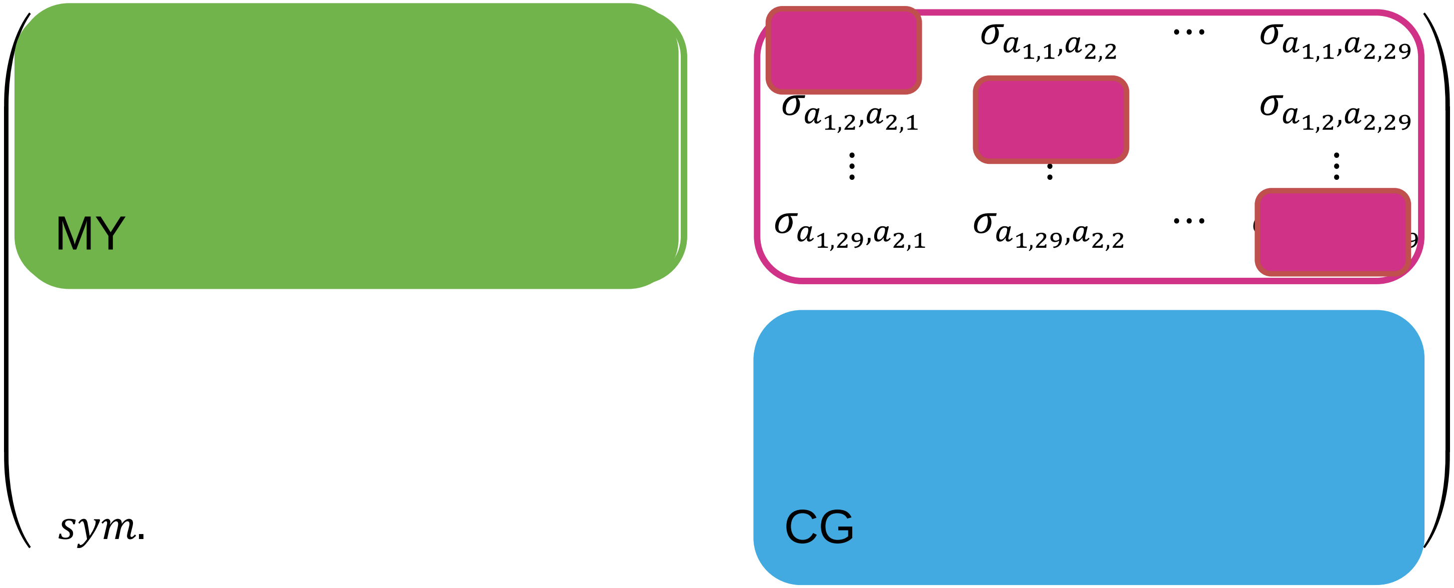


$$\left(\begin{array}{cccc|cccc}
\blacksquare & \sigma_{a_{1,1},a_{1,2}} & \cdots & \sigma_{a_{1,1},a_{1,29}} & \sigma_{a_{1,1},a_{2,1}} & \blacksquare & \cdots & \sigma_{a_{1,1},a_{2,29}} \\
 & \sigma_{a_{1,2},a_{1,2}} & & \sigma_{a_{1,2},a_{1,29}} & \sigma_{a_{1,2},a_{2,1}} & \sigma_{a_{1,2},a_{2,2}} & & \sigma_{a_{1,2},a_{2,29}} \\
 & & \ddots & \vdots & \vdots & \vdots & & \vdots \\
\text{MY} & & & \sigma_{a_{1,29},a_{1,29}} & \sigma_{a_{1,29},a_{2,1}} & \sigma_{a_{1,29},a_{2,2}} & \cdots & \sigma_{a_{1,29},a_{2,29}} \\
 & & & & \sigma_{a_{2,1},a_{2,1}} & \sigma_{a_{2,1},a_{2,2}} & \cdots & \sigma_{a_{2,1},a_{2,29}} \\
 & & & & & \blacksquare & & \sigma_{a_{2,2},a_{2,29}} \\
 & & & & & & \ddots & \vdots \\
sym. & & & & \text{CG} & & & \sigma_{a_{2,29},a_{2,29}}
\end{array}\right)$$

Individual chrom. to overall (n=29)

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





MY

$\sigma_{a_{1,1},a_{2,2}}$ $\cdots$ $\sigma_{a_{1,1},a_{2,29}}$

$\sigma_{a_{1,2},a_{2,1}}$ $\sigma_{a_{1,2},a_{2,29}}$

$\vdots$ $\vdots$ $\vdots$

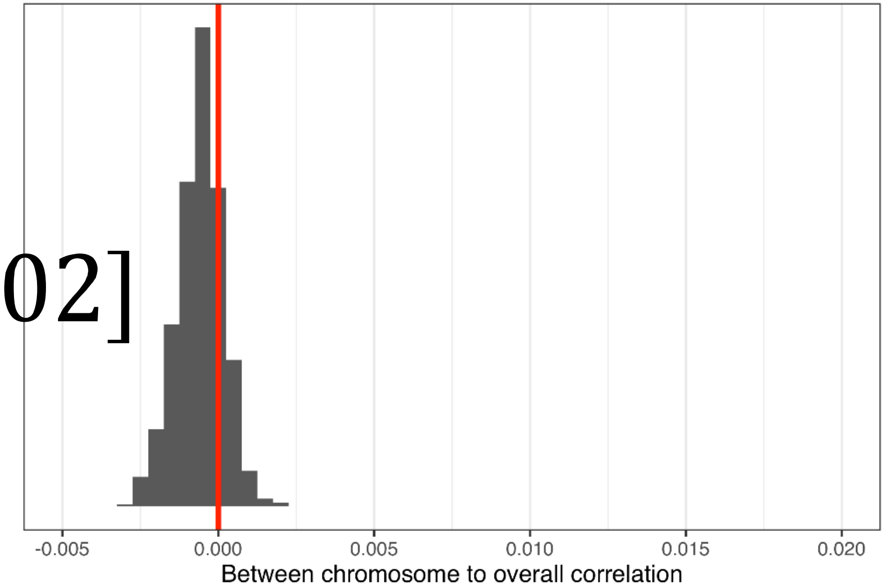
$\sigma_{a_{1,29},a_{2,1}}$ $\sigma_{a_{1,29},a_{2,2}}$ $\cdots$

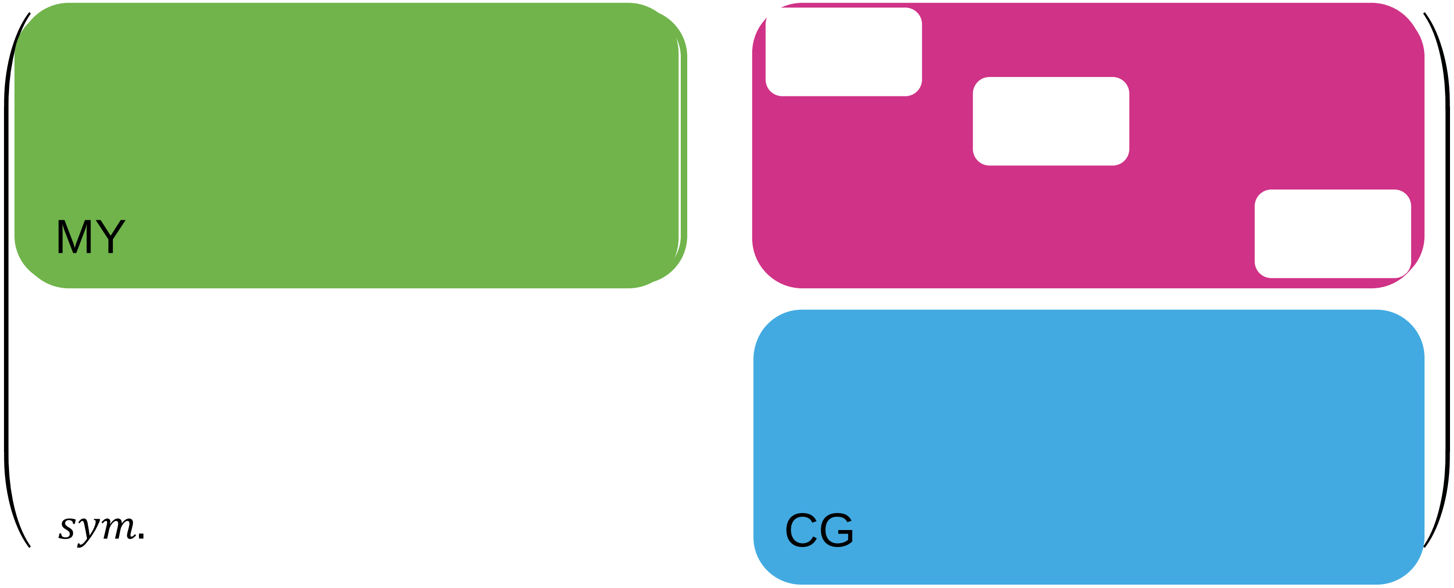
sym.

CG

Chrom. pairs to overall (n=812)

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





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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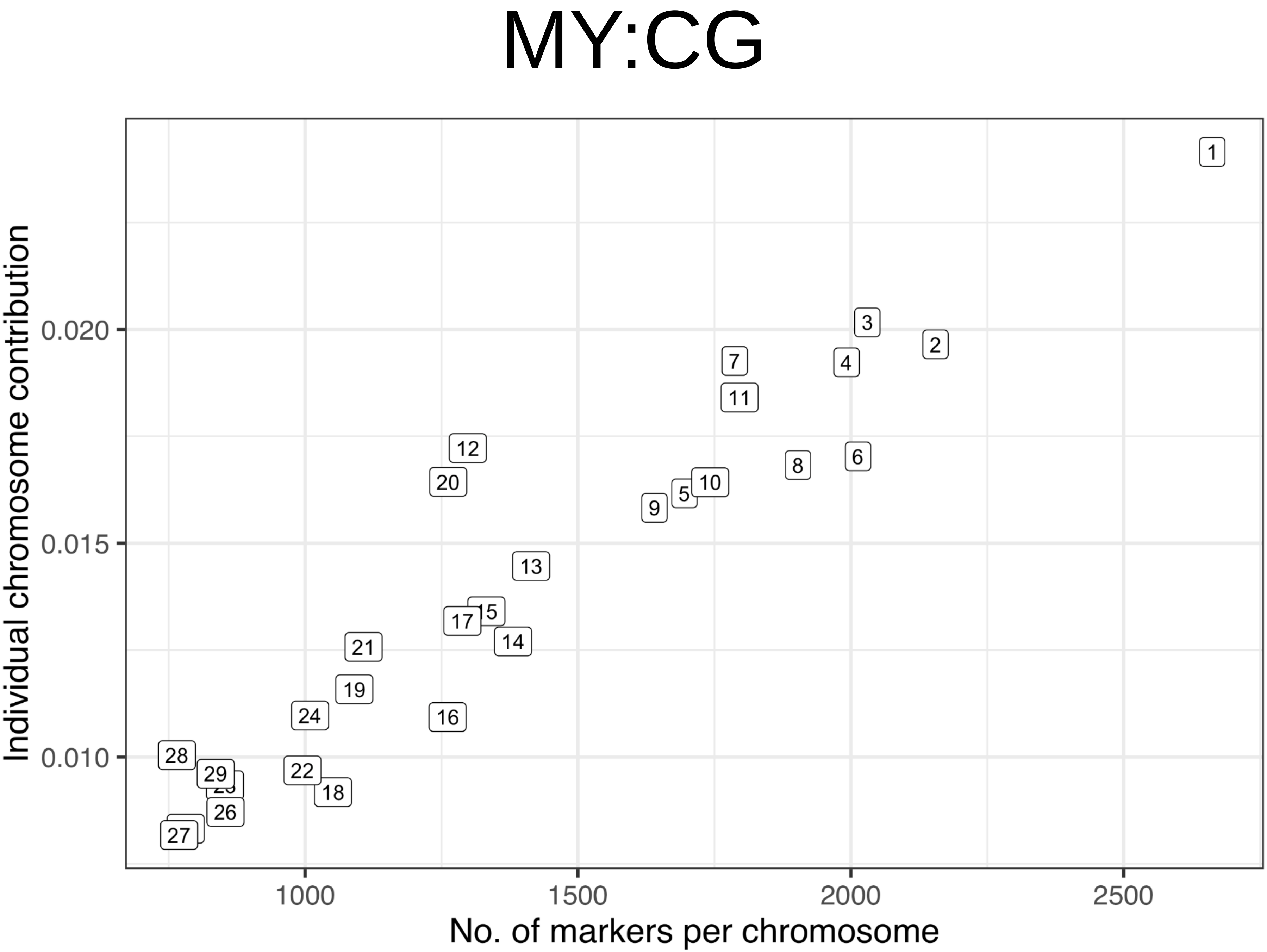
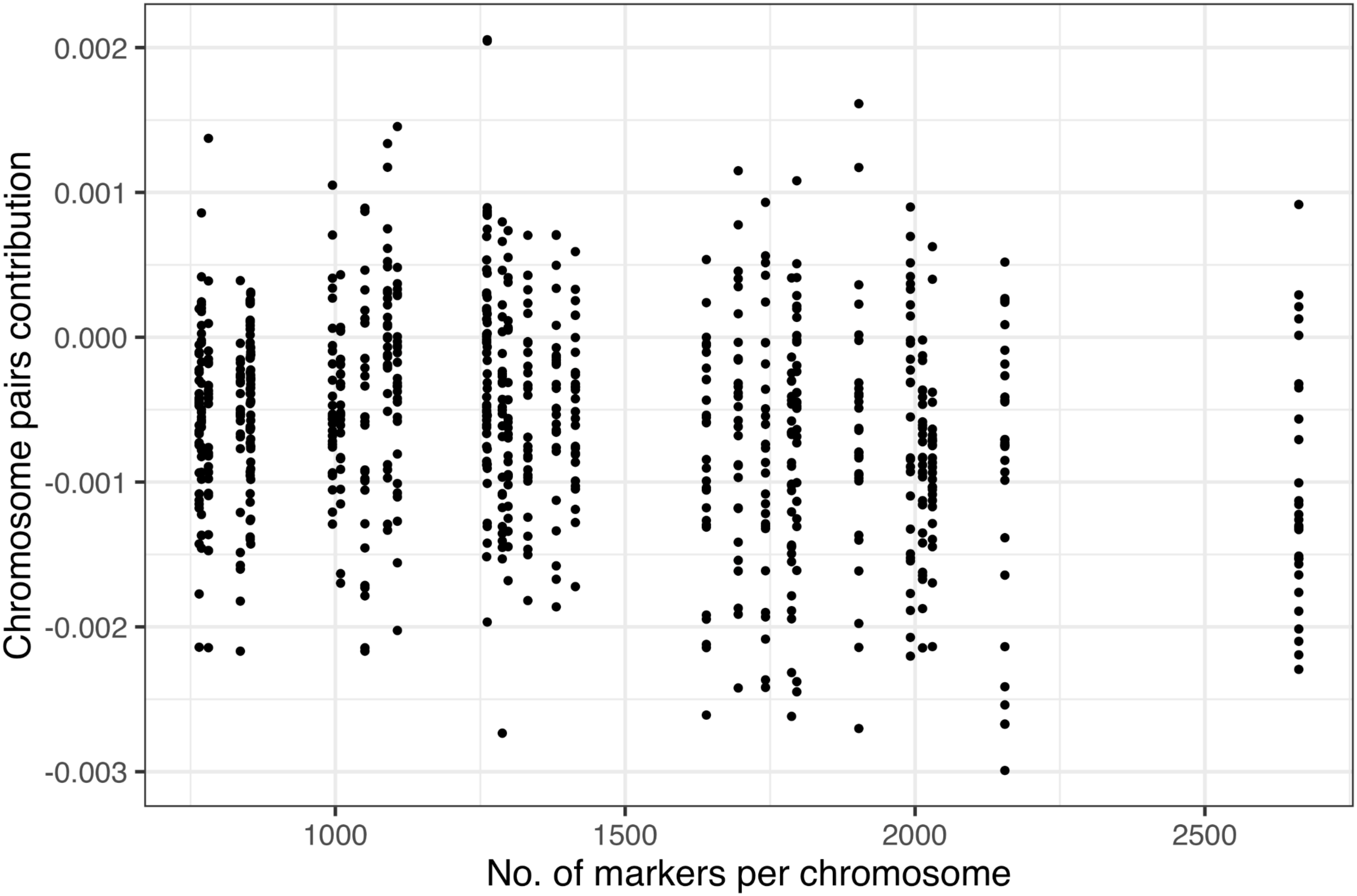
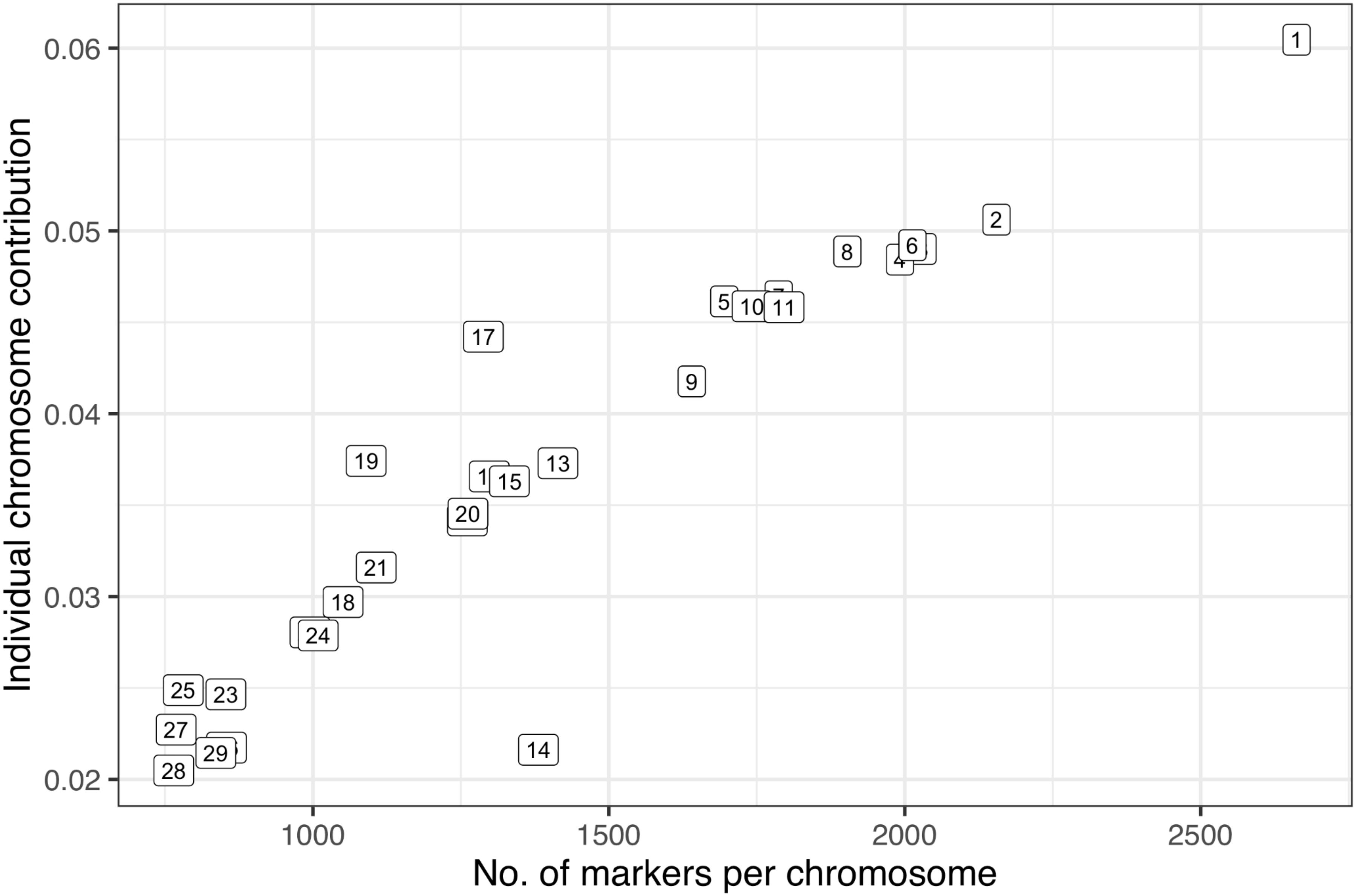

MY:CG
Individual chromosome contribution
0.020
0.015
0.010
No. of markers per chromosome
1000
1500
2000
2500
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
24
26
27
28
29

MY:CG

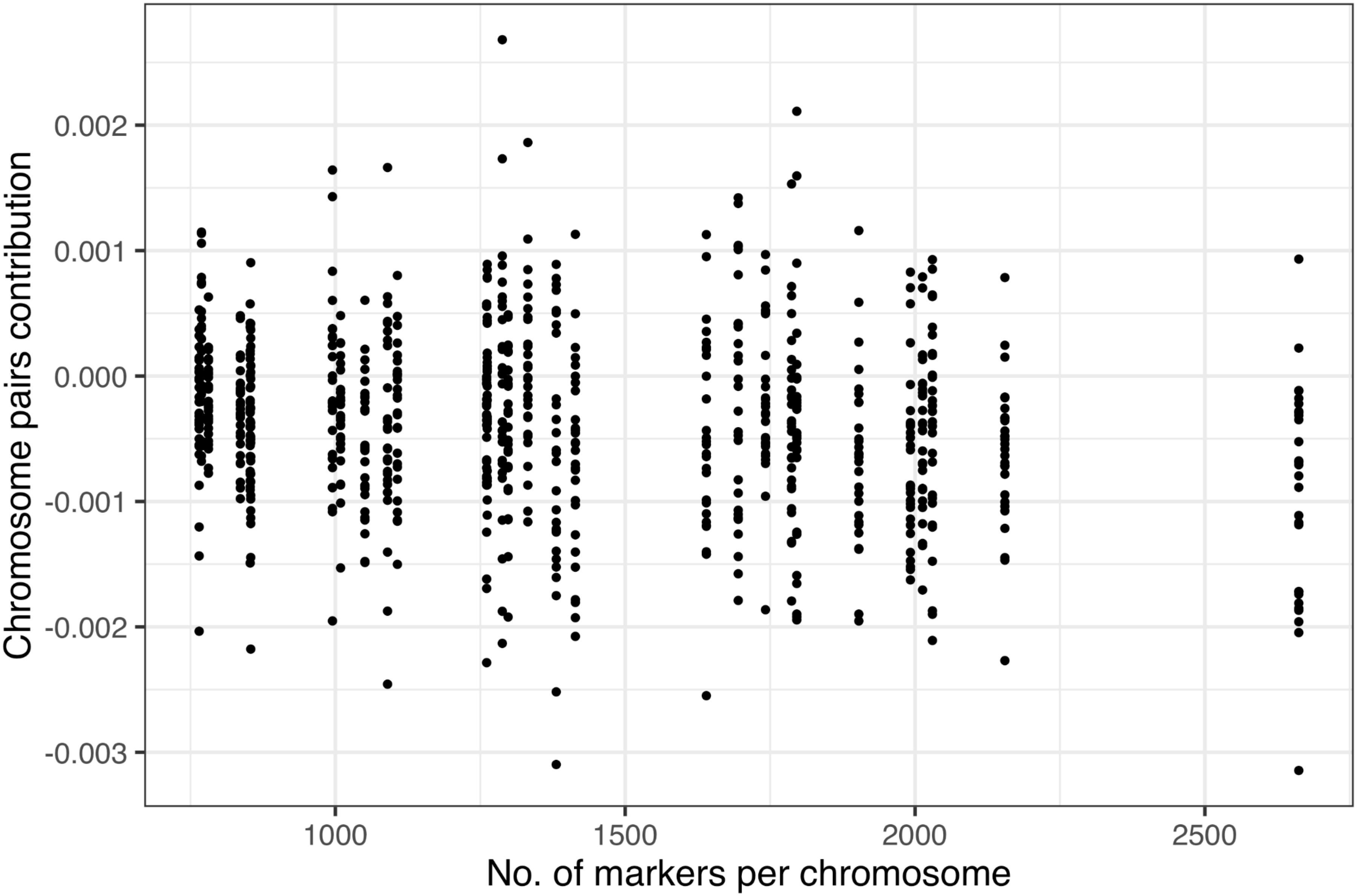


Chromosome pairs contribution
0.002
0.001
0.000
-0.001
-0.002
-0.003
1000
1500
2000
2500
No. of markers per chromosome

MY:FY


Individual chromosome contribution
0.06
0.05
0.04
0.03
0.02
No. of markers per chromosome
1000
1500
2000
2500
1
2
8
6
4
5
10
11
17
9
19
13
15
20
21
18
24
25
23
27
29
28
14

MY:FY


Chromosome pairs contribution
0.002
0.001
0.000
-0.001
-0.002
-0.003
1000
1500
2000
2500
No. of markers per chromosome

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