

Pedigree relationships to control inbreeding in optimum-contribution selection realise more genetic gain than genomic relationships

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Animal breeding

Maximises ΔG_{true} at acceptable ΔF_{true}



True breeding values



True inbreeding coefficients

Optimum-contribution selection

Maximises $\Delta G_{\text{predicted}}$ for given $\Delta F_{\text{predicted}}$

Optimum-contribution selection

$$\max (\underbrace{c' \hat{a}}_{\Delta G_{\text{predicted}}} - \lambda \underbrace{c' A c}_{\Delta F_{\text{predicted}}})$$

Optimum-contribution selection

$$\max (c' \hat{a} - \lambda c' A c)$$



PBLUP

GBLUP

Optimum-contribution selection

$$\max (c' \hat{a} - \lambda c' \mathbf{A} c)$$



G

POCS

vs

GOCS

$$\max (c' \hat{a} - \lambda c' \mathbf{A} c)$$

$$\underbrace{\hspace{10em}}_{\Delta F_{\text{pedigree}}}$$

$$\max (c' \hat{a} - \lambda c' \mathbf{G} c)$$

$$\underbrace{\hspace{10em}}_{\Delta F_{\text{genomic}}}$$

POCS vs GOCS

ΔG_{true} at same ΔF_{true}

ΔG_{true} at 0.01 ΔF_{true}

	PBLUP	GBLUP
POCS	100	100
GOCS	75-88	95-98

Liu et al.

GBLUP

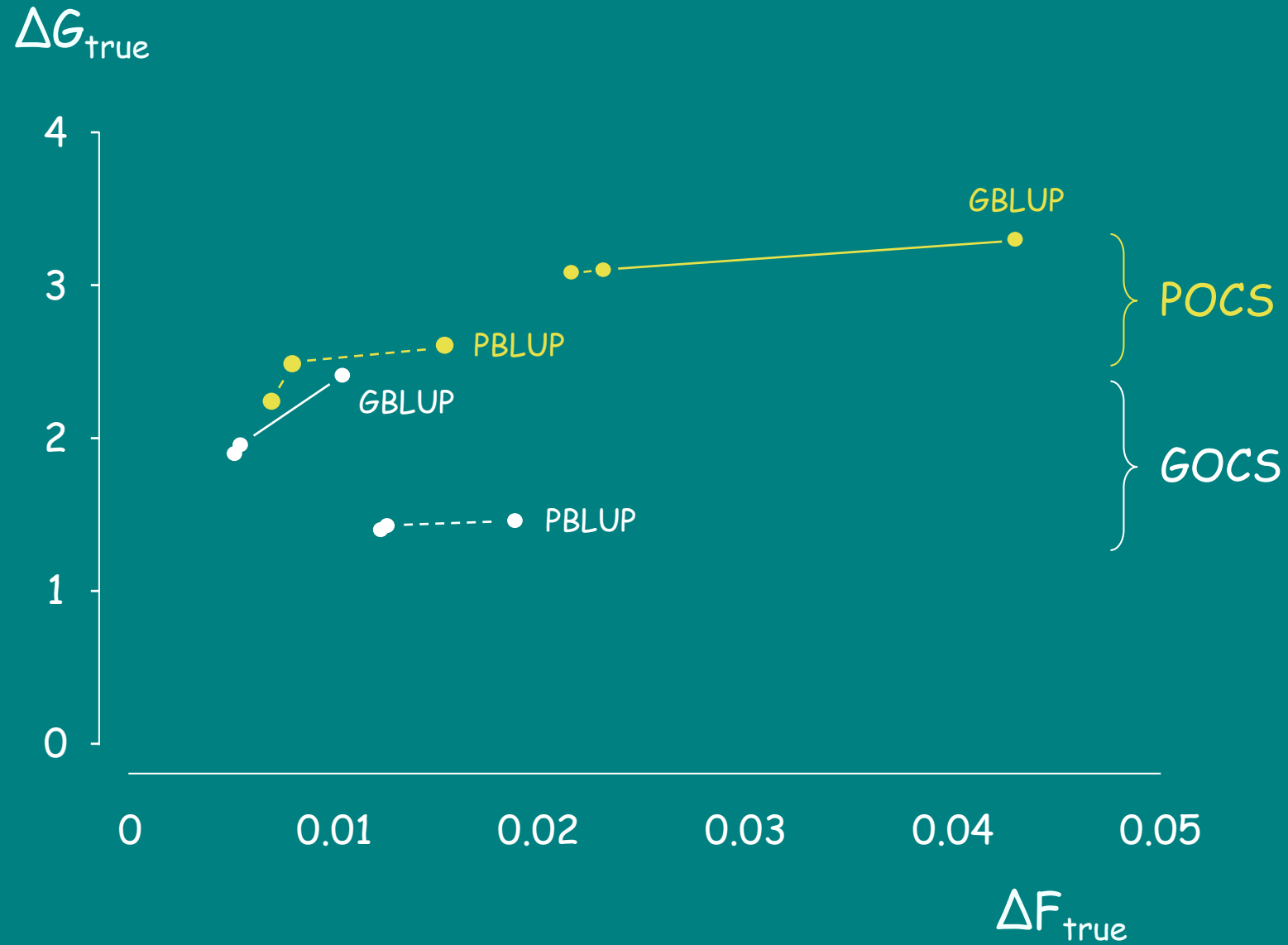
POCS

100

GOCS

84

Sonesson et al. 2012



POCS controls expected drift

Allows frequency of favourable-QTL alleles to increase

GOCS controls realised drift and selection

Penalises changes in marker-allele frequencies

Restricts changes in QTL-allele frequencies

GOCS controls realised drift and selection

$$\max (c' \hat{a} - \lambda c' G c)$$

$$G \sim ZZ'$$

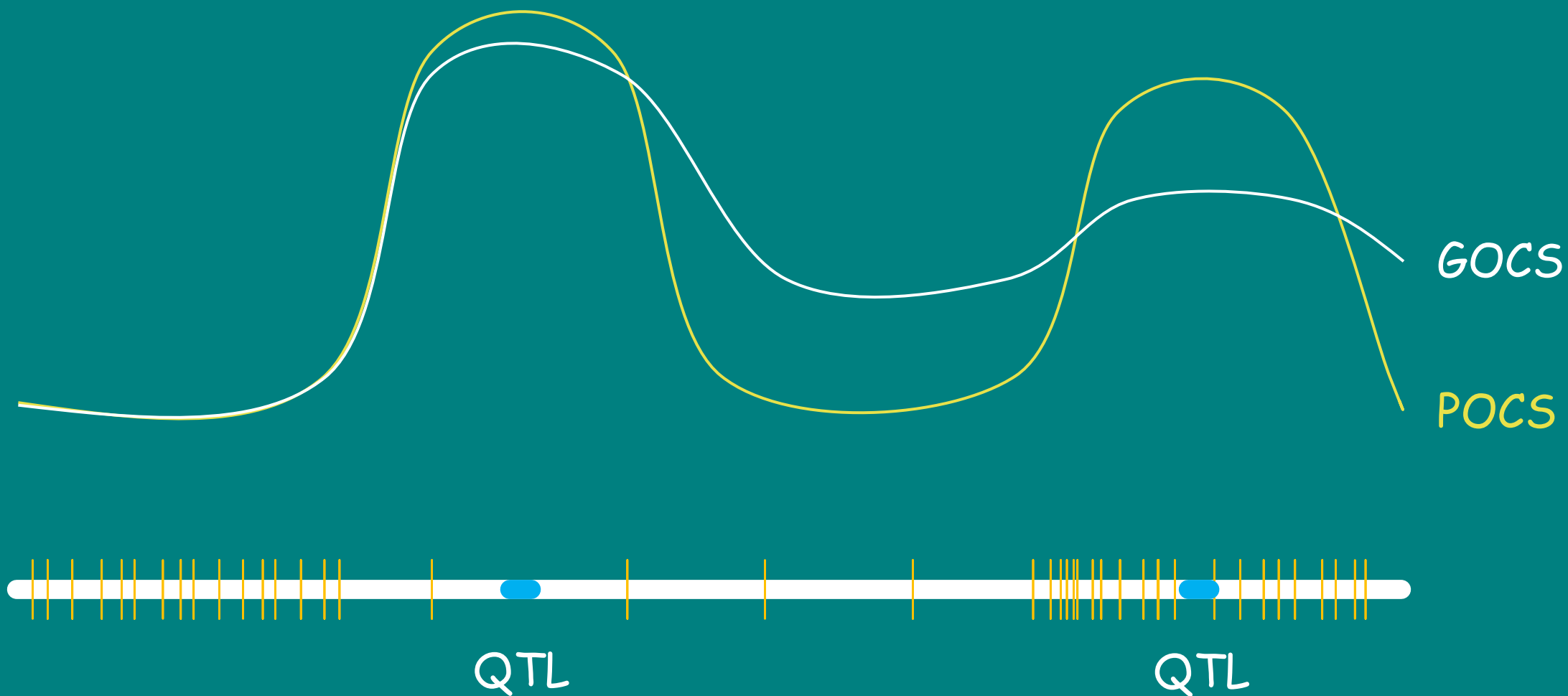
$$\sim c' ZZ' c$$

$Z'c/2$: Changes in marker-allele frequencies

POCS allows larger allele-frequency changes

	Favourable QTL	Marker
POCS	0.0046	0.049
GOCS	0.0044	0.047

POCS generates more IBD around QTL



So ...

POCS allows frequency of favourable QTL alleles to increase ...

... get more ΔG_{true} for IBD

POCS selects different animals

More candidates from more families

Higher-ranked candidates

POCS realises higher minimum ΔF_{true}

POCS 0.0012 - 0.0051

GOCS 0.0011 - 0.0047

So ...

GOCS more effective control of inbreeding ...

... too effective with selection for breeding value

Predicted inbreeding at 0.01 ΔF_{true}

	$\Delta F_{\text{pedigree}}$	$\Delta F_{\text{genomic}}$
POCS	0.0074 - 0.0088	
GOCS		0.0099 - 0.0127

Accurate predictors of ΔF_{true}

Manage risk

Maximise selection differential

So ...

POCS and GOCS proxies for ΔF_{true} ...

... don't know what we will get

Urgency to identify accurate predictors of ΔF_{true}

ΔG_{true} at 0.01 ΔF_{true}

	PBLUP	GBLUP
POCS	100	100
GOCS	75-88	95-98
IOCS	94-96	102-103

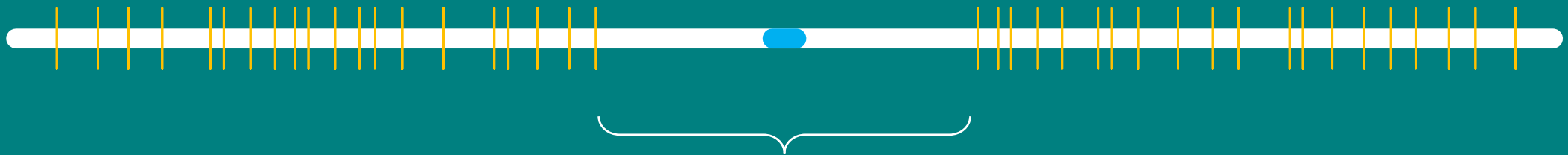
GOCS without "the brake"

QTL



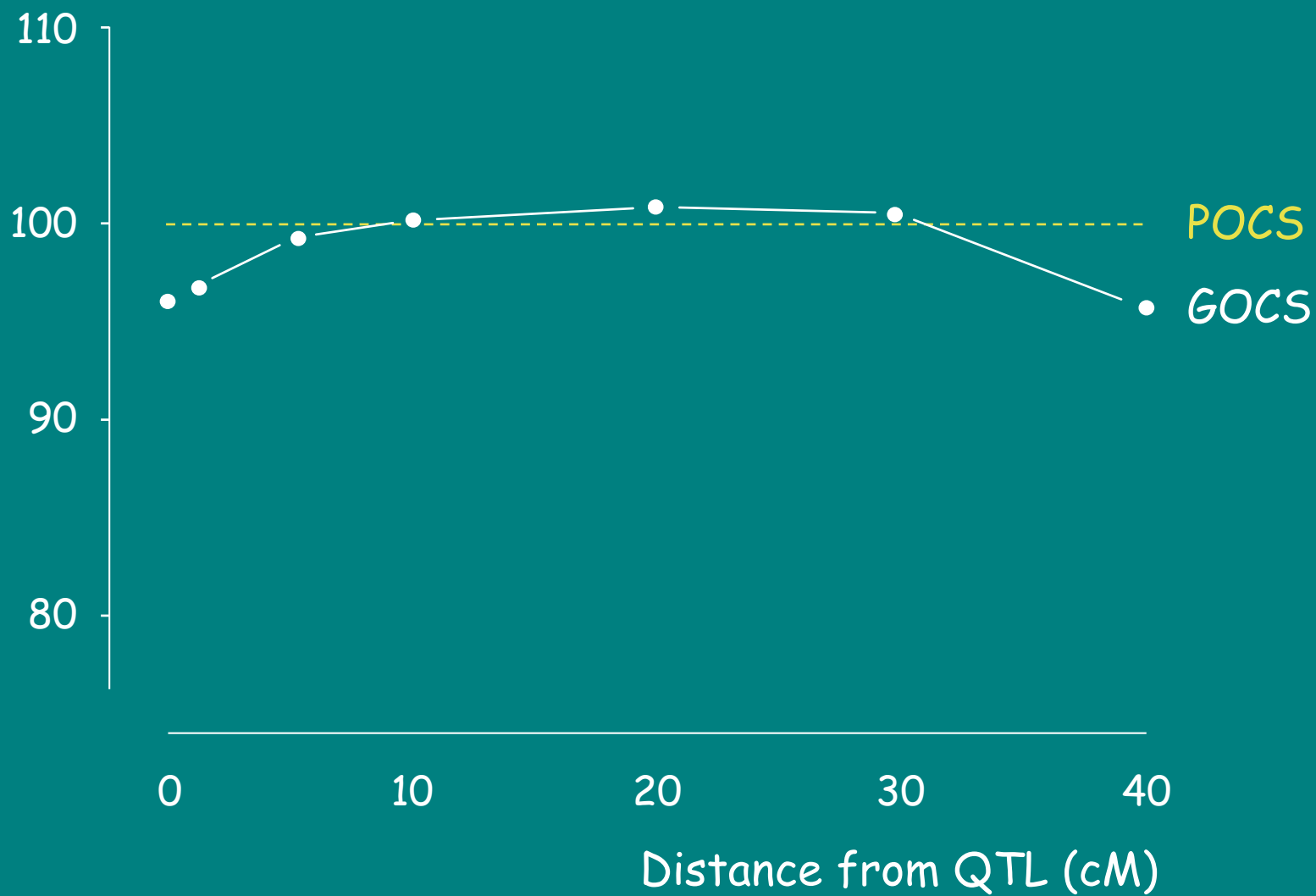
GOCS without "the brake"

QTL

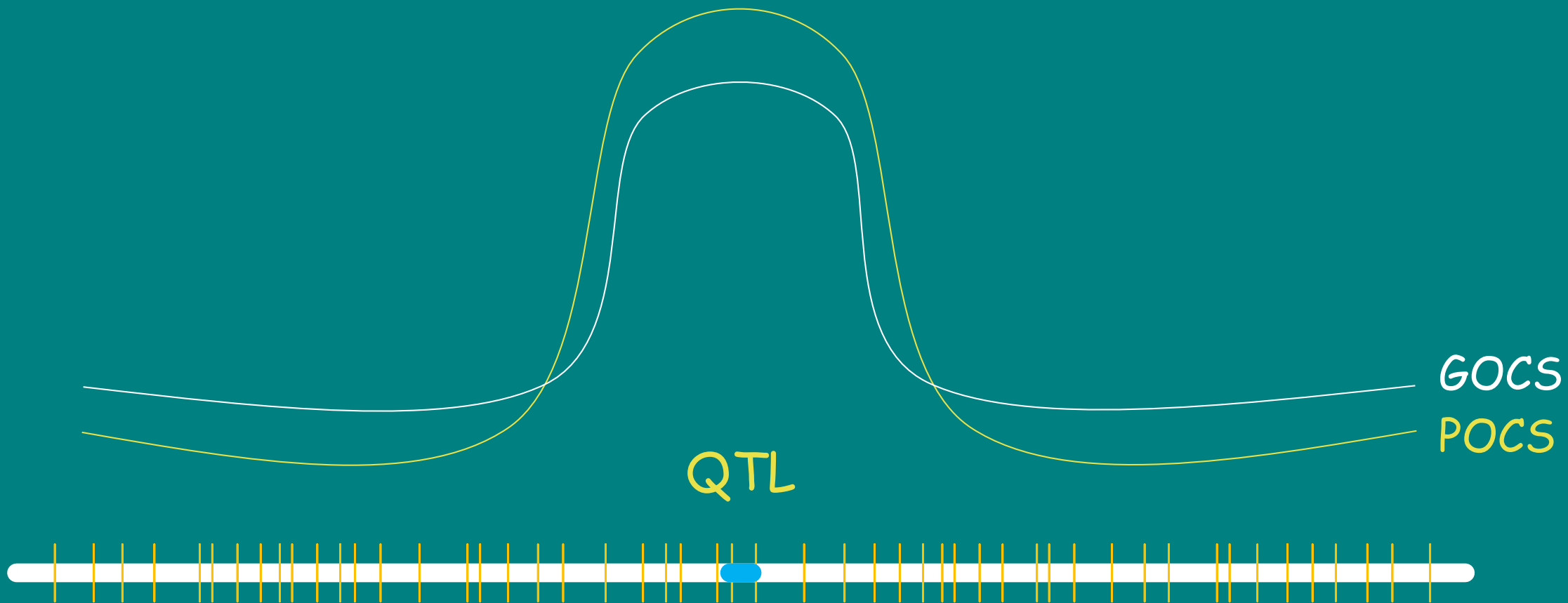


Relax inbreeding control

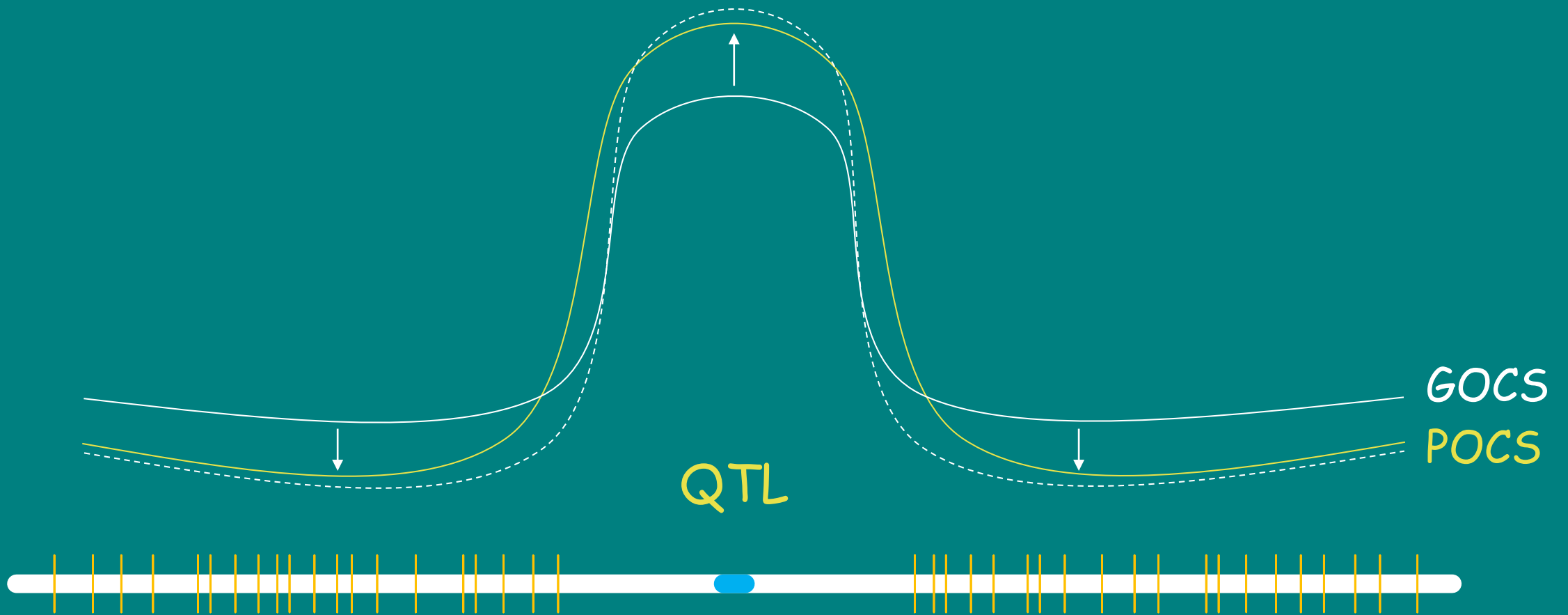
ΔG_{true} at $0.01 \Delta F_{\text{true}}$



IBD profiles



IBD profiles



Challenge

Don't know where QTL are located

So ...

POCS always realise more ΔG_{true} than GOCS

Implications

Inbreeding control is not prediction

Little incentive to use *GOCS*

Not learnt to control ΔF_{true} with genomic relationships

Conclusion

POCS is still a worthy method of OCS

Single trait

h^2 0.2

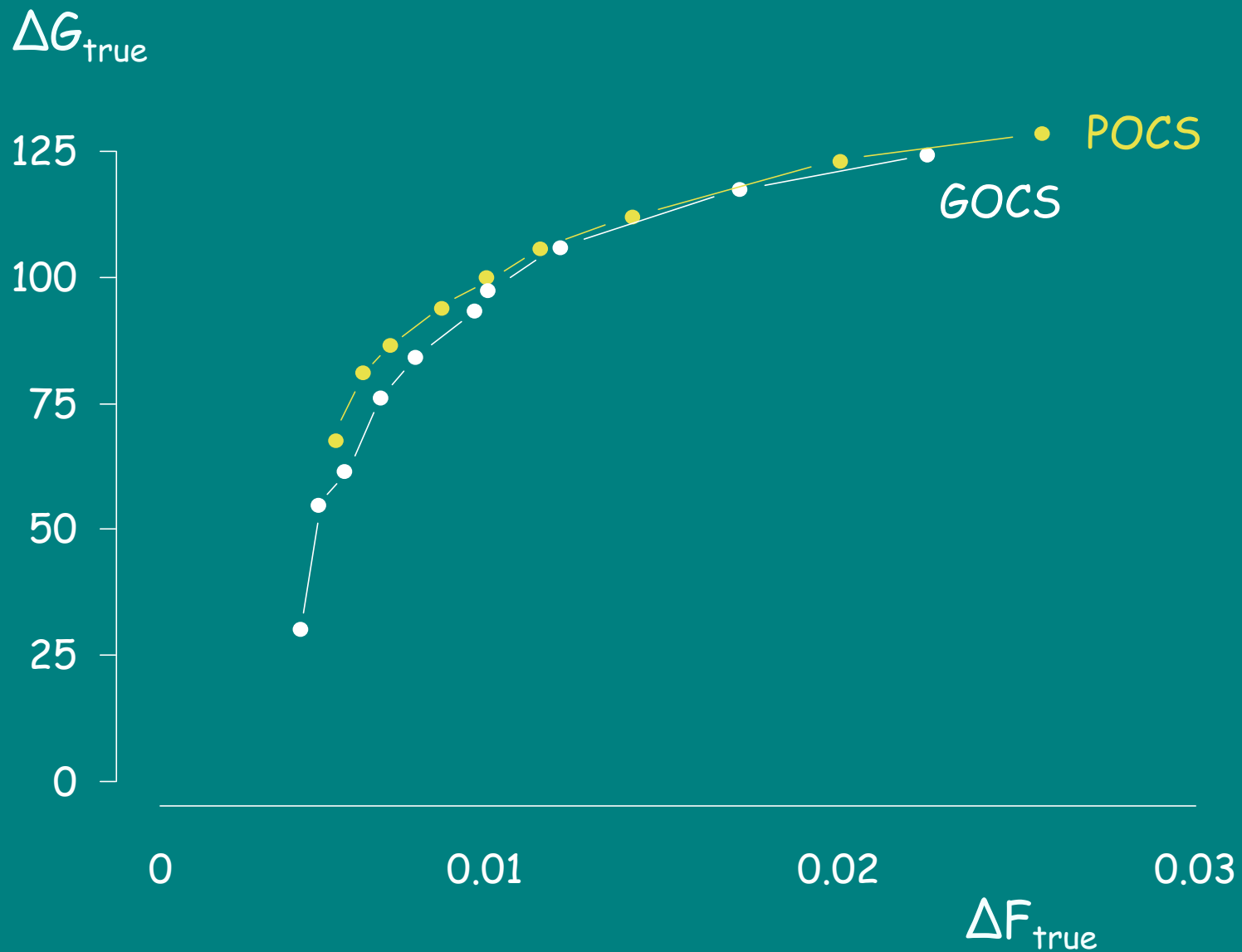
QTL 7702

Markers 54218

IBD-markers 6012

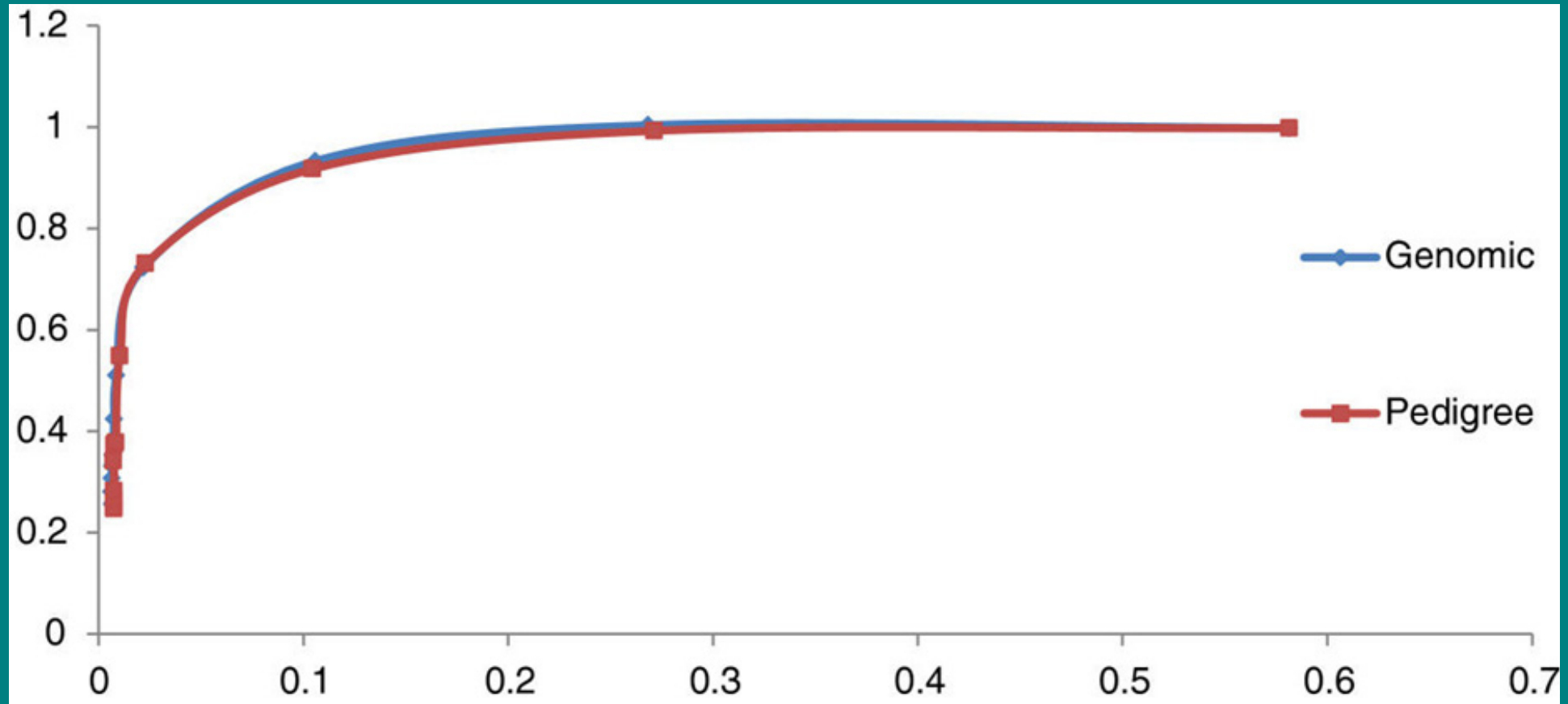
All animals phenotyped and genotyped

Response frontier with GBLUP



Clark et al. 2013

True breeding value



Genomic co-ancestry

POCS underestimates ΔF_{true}

Can't trace changes in IBD-allele frequencies

GOCS overestimates ΔF_{true}

Incomplete LD between marker and IBD alleles

Markers unevenly distributed across genome

IOCS controls realised drift and selection

$$\max (c' \hat{a} - \lambda c' \mathbf{B} c)$$

$$\mathbf{B} \sim \mathbf{D}\mathbf{D}'$$

$$\sim c' \mathbf{D}\mathbf{D}' c$$

$\mathbf{D}'c$: Numbers of each IBD allele at each locus