

# Genetic Architecture of Transcriptome Regulation

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## 1 Abstract

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## 2 Introduction

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## 3 Methods

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### 3.1 Equations

The deterministic part of the model is defined by this **in-line equation** as  $\mu_i = \beta_0 + \beta_1 x$ , and the stochastic part by the **centered equation**:

$$\frac{1}{\sqrt{2\pi}\sigma} e^{-(x-\mu_i)^2/(2\sigma^2)}$$

## 3.2 Tables

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	0.11	0.11	0.99	0.32
x	2.02	0.11	18.64	0.00

Table 1: This is a GLM summary table.

## 3.3 Plots

## 3.4 Citations

The relationship was first described by Halpern et al. (2006). However, there are also opinions that the relationship is spurious (Keil *et al.* 2012). We used R for our calculations (R Core Team 2015), and we used package `knitcitations` (Boettiger 2014) to make the bibliography.

# 4 Results and discussion

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## References

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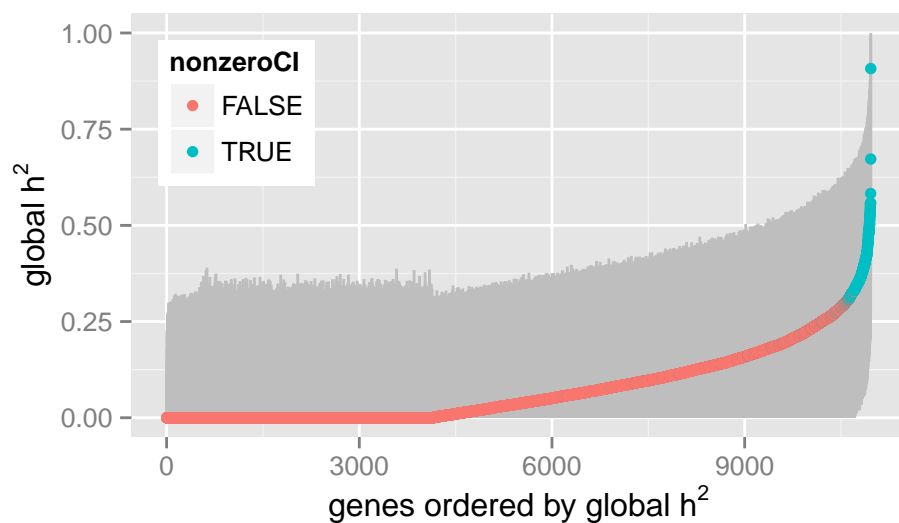
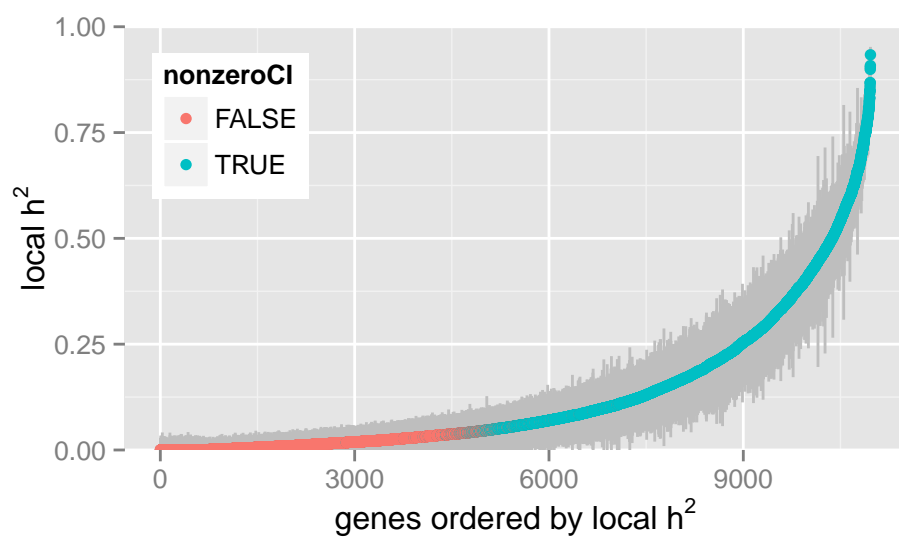
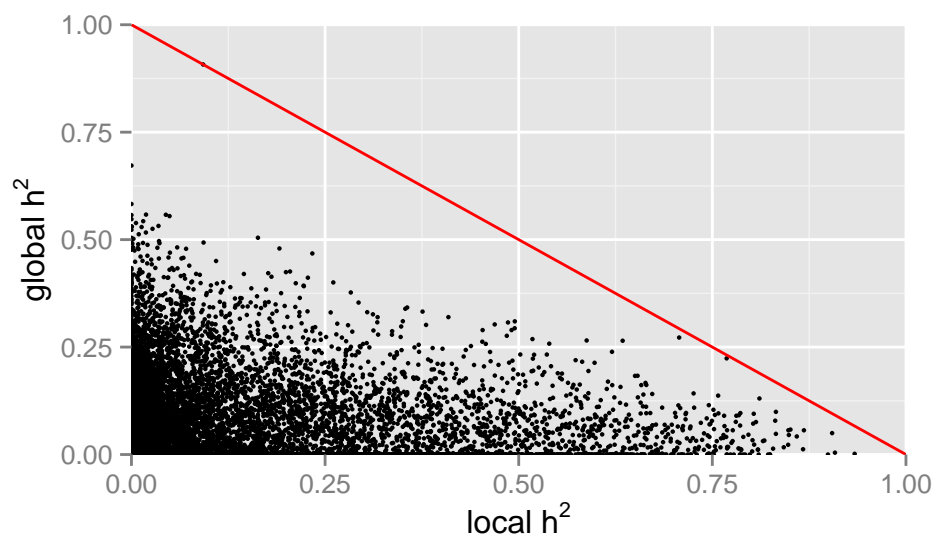


Figure 1: DGN-WB joint heritability. Local  $h^2$  is estimated with SNPs within 1 Mb of each gene. Global  $h^2$  is estimated with SNPs that are eQTLs in the Framingham Heart Study on other chromosomes (FDR < 0.05).

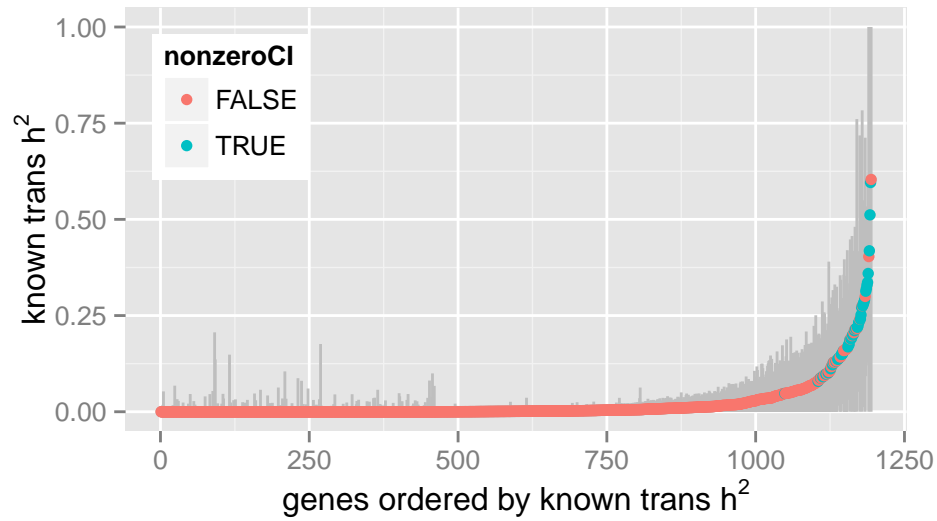
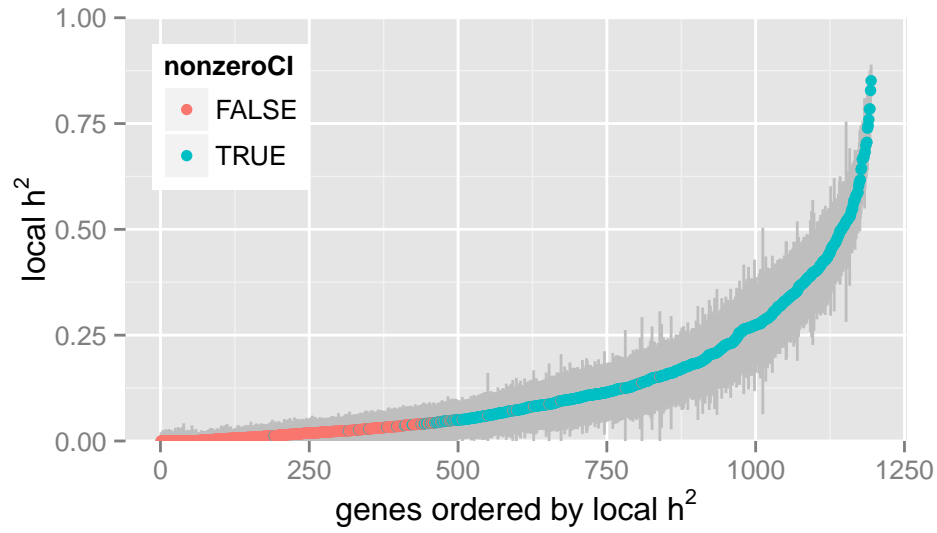
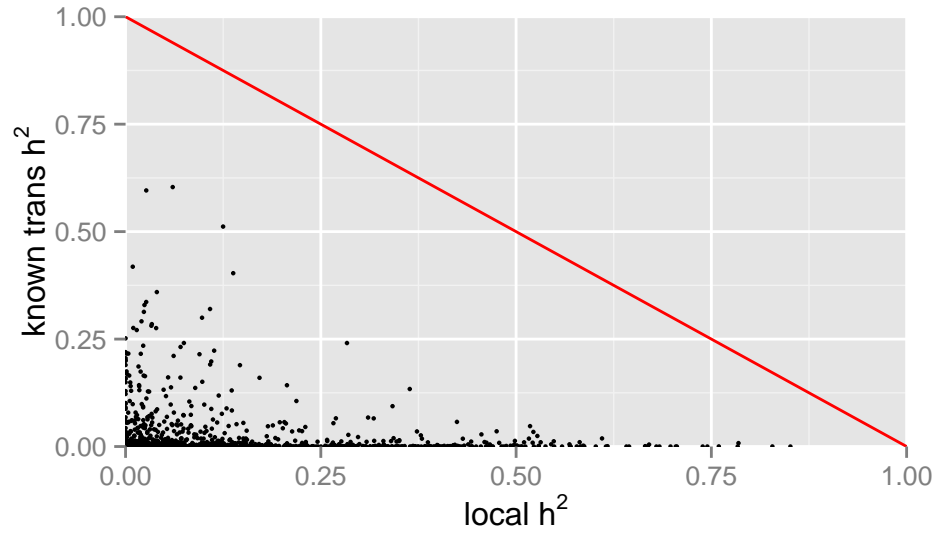


Figure 2: DGN-WB joint heritability with known trans-eQTLs. Local  $h^2$  is estimated with SNPs within 1 Mb of each gene. Known trans  $h^2$  is estimated with SNPs that are trans-eQTLs in the Framingham Heart Study for each gene (FDR < 0.05).