Genetic architecture of transcriptome regulation and orthogonal tissue decompositon to improve transcriptome prediction

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# Abstract

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# Introduction

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# Results

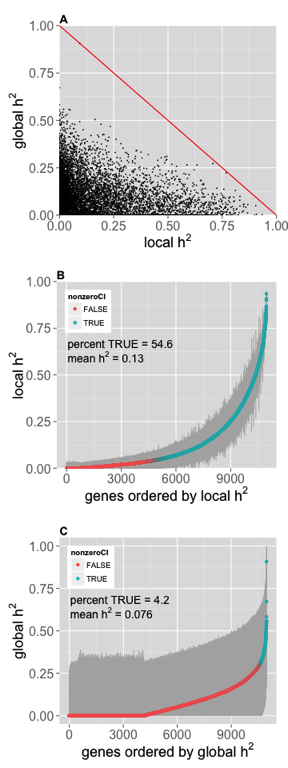
## Local genetic variation explains a large proportion of gene expression variance

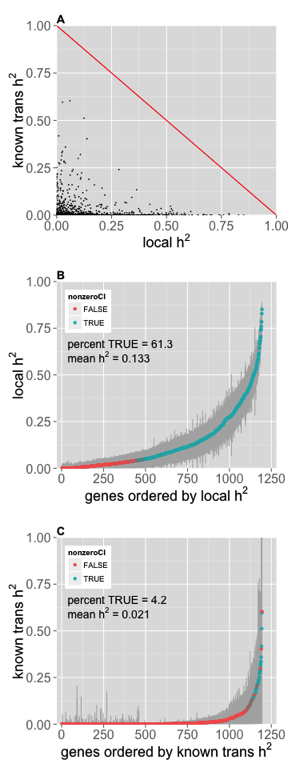
We estimated the heritability of gene expression in whole blood from the Depression Genes and Networks (DGN) cohort (n=922) using a mixed-effects model (see Materials and Methods) and calculated variances using restricted maximum likelihood as implemented in GCTA [1]. We fit a joint model with a local GRM (SNPs within 1 Mb of gene) and a global GRM (SNPs that ar)

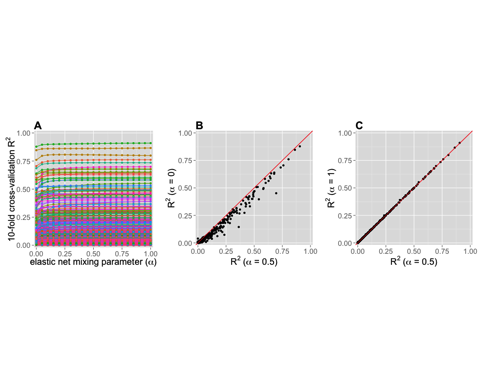
## The effect of local genetic variation on gene expression is sparse rather than polygenic

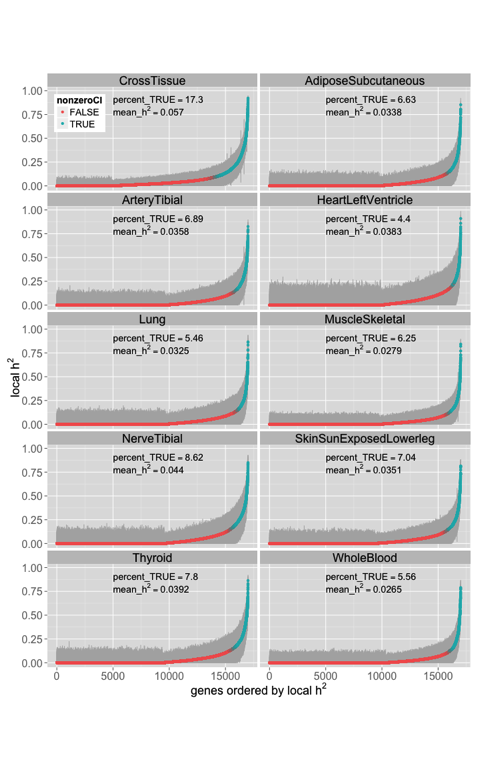
## Cross-tissue and tissue-specific gene expression by orthogonal tissue decomposition

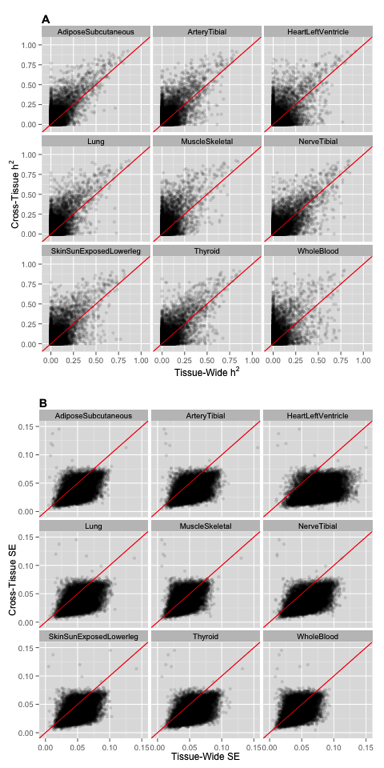
## Plots

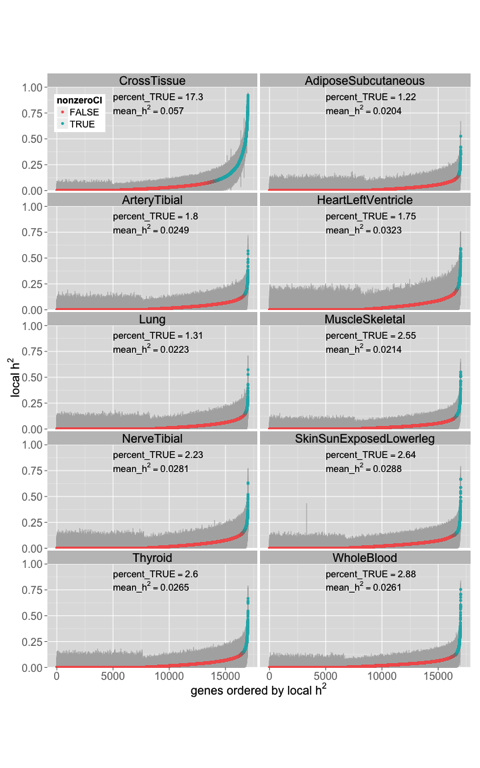


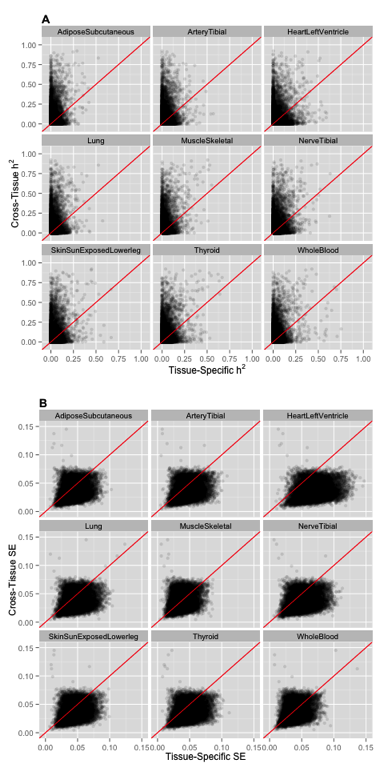












## Citations

The relationship was first described by Reference 2. However, there are also opinions that the relationship is spurious [3]. We used R for our calculations [4], and we used package knitcitations [5] to make the bibliography.

# Discussion

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# Methods

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## Equations

The deterministic part of the model is defined by this **in-line equation** as , and the stochastic part by the **centered equation**:

## Tables

## Warning: package 'knitr' was built under R version 3.1.3

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Estimate | Std. Error | t value | Pr(>|t|) |
| (Intercept) | -0.05 | 0.1 | -0.49 | 0.63 |
| x | 2.02 | 0.1 | 20.09 | 0.00 |

This is a GLM summary table.

# References

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3. Keil P, Belmaker J, Wilson AM, Unitt P, Jetz W. Downscaling of species distribution models: a hierarchical approach. Freckleton R, editor. Methods Ecol Evol. Wiley-Blackwell; 2012;4: 82–94. doi:[10.1111/j.2041-210x.2012.00264.x](http://dx.doi.org/10.1111/j.2041-210x.2012.00264.x)

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