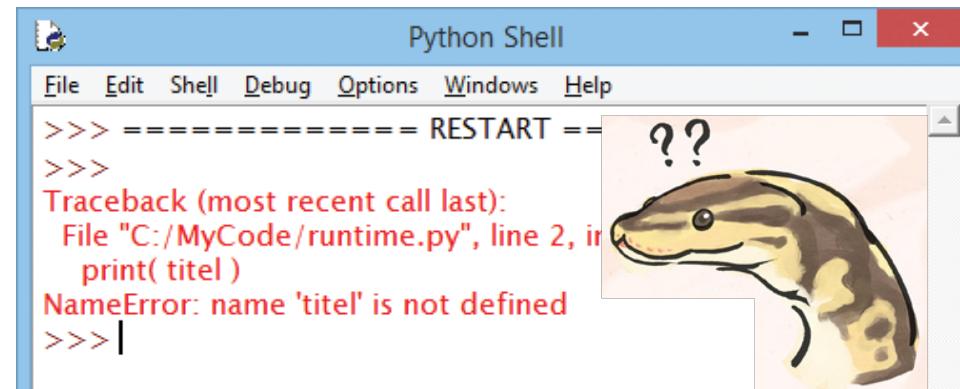


# Association Mapping across Numerous Traits Reveals Patterns of Functional Variation in Maize

Wallace et al.

Replicated by "Perplexed Pythons"

- Zihao Zheng
- Zainab Riaz
- Timothy Nessel



(william-snekspeare.tumblr.com)

# Question Being Investigated

- To identify genetic loci governing phenotypic variation in maize.
  - The intent was to uncover genetic patterns behind function variation.
- Using
  - Maize Nested Association Mapping (NAM)
  - Genome-wide association Studies (GWAS)



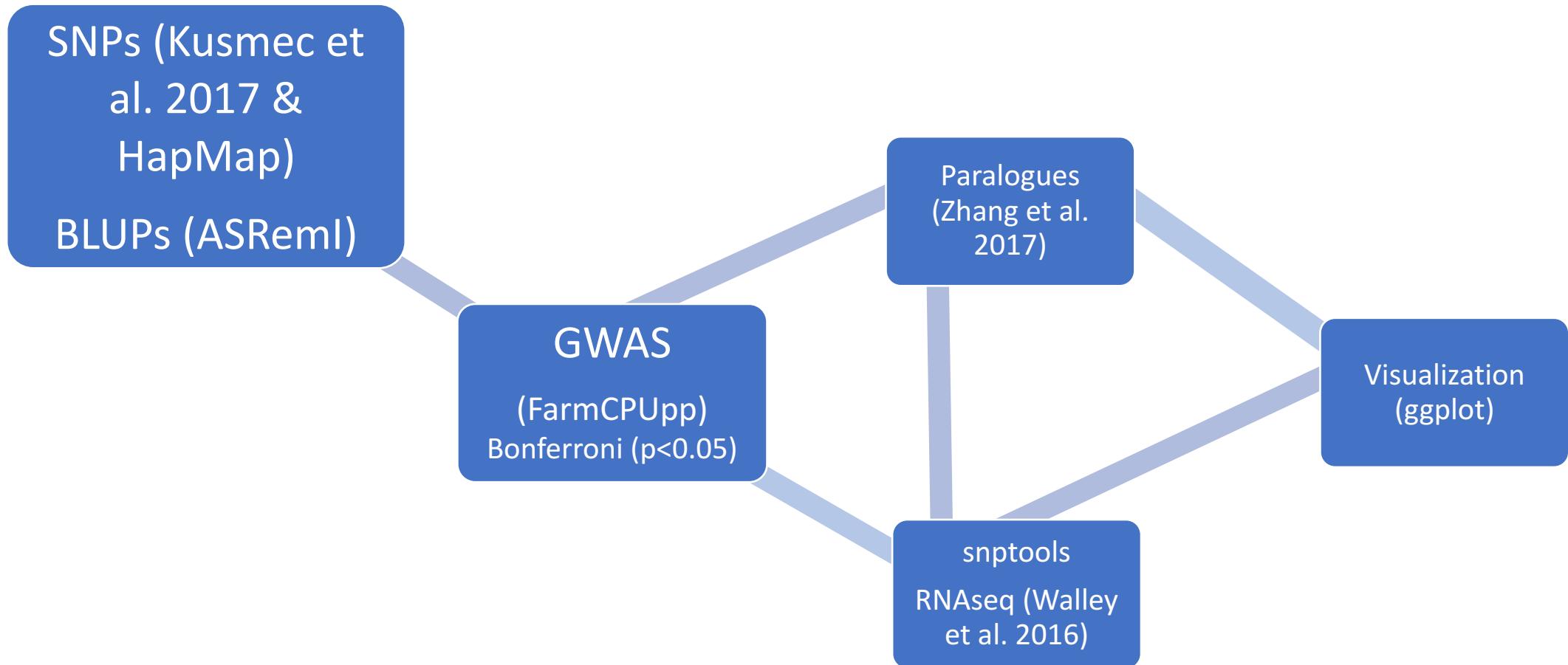
# Will it Replicate?

- Dataset available?
- Possible with available resources?
- Satisfactory documentation?



Pacific Standard Magazine

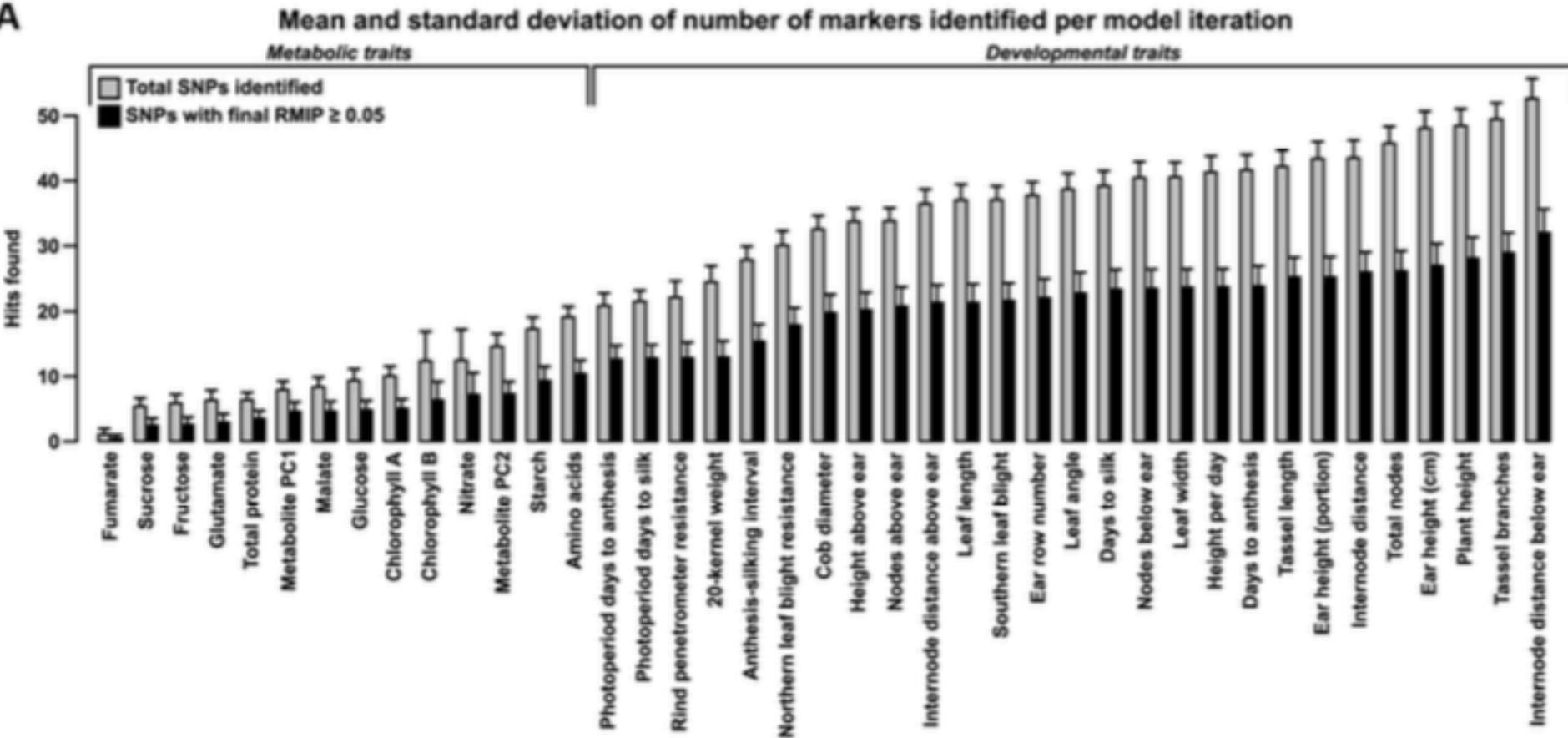
# Workflow



# Variance Explained per Trait

- In general, more complex traits are more heavily enriched

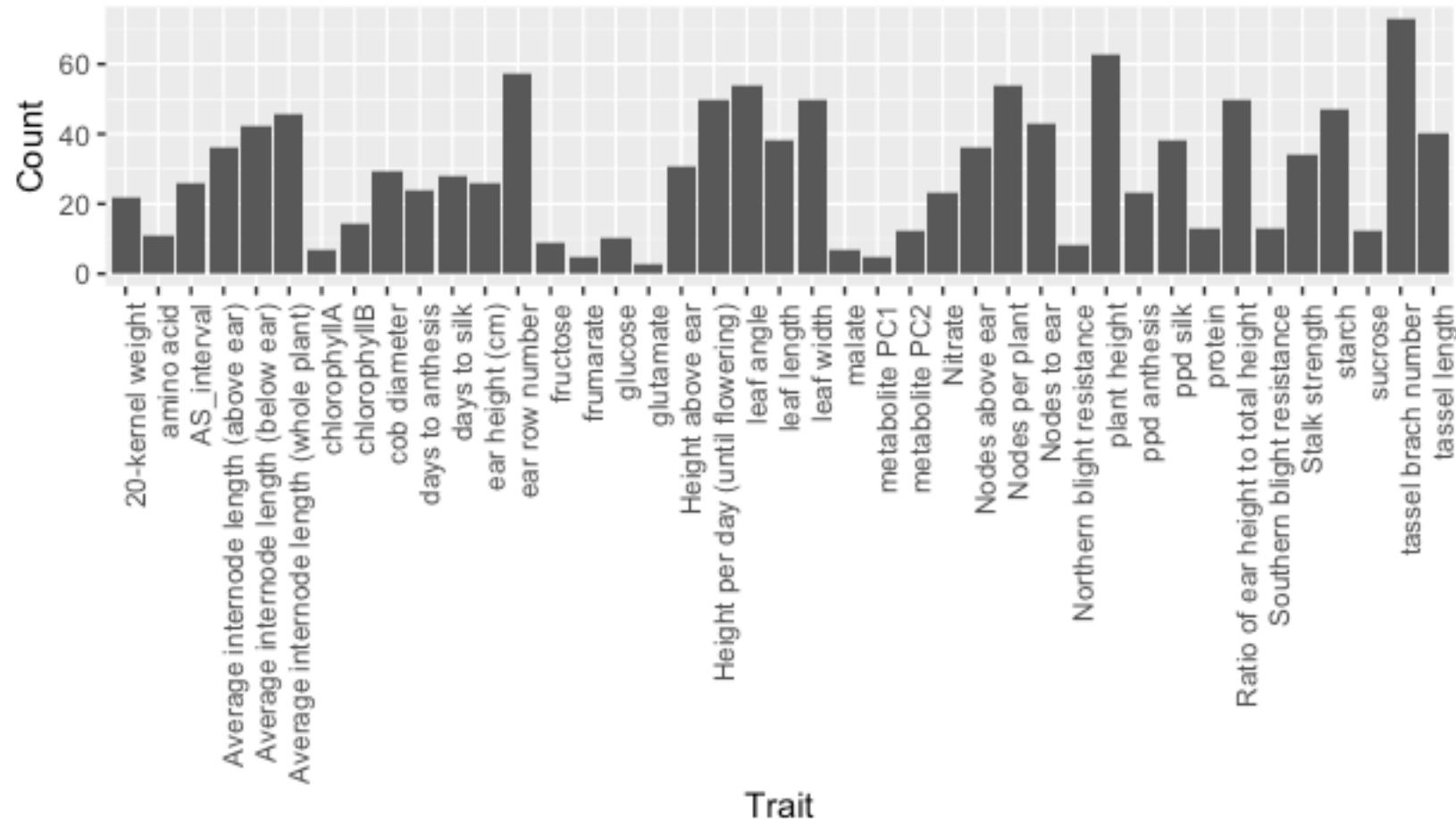
A



# Variance Explained per Trait

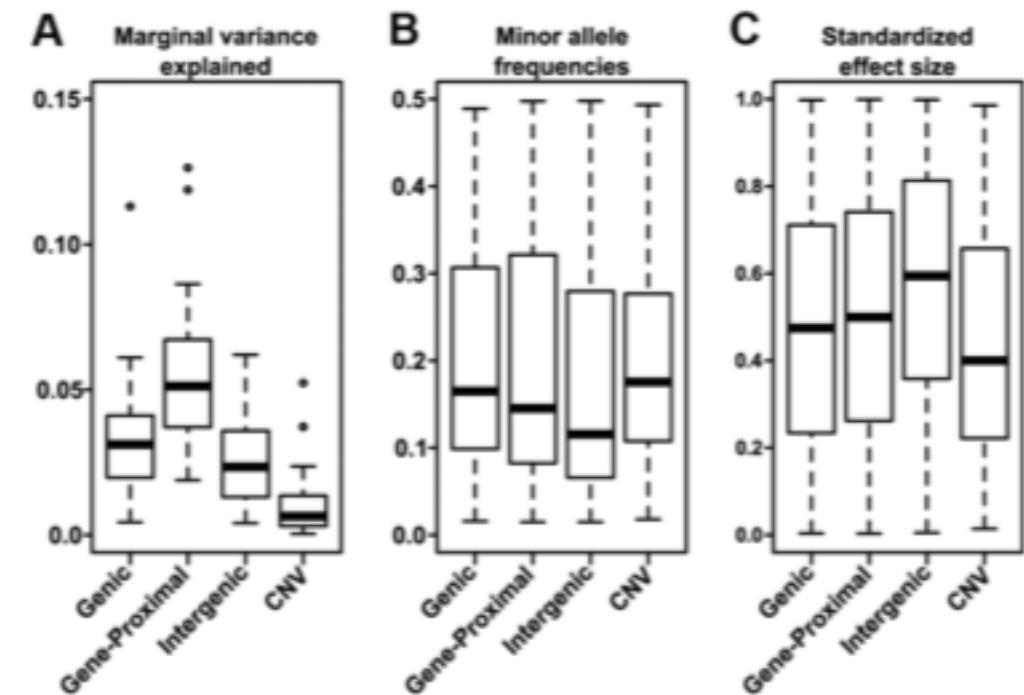
- In general, more complex traits are more heavily enriched

Proportion Variance Explained Replication



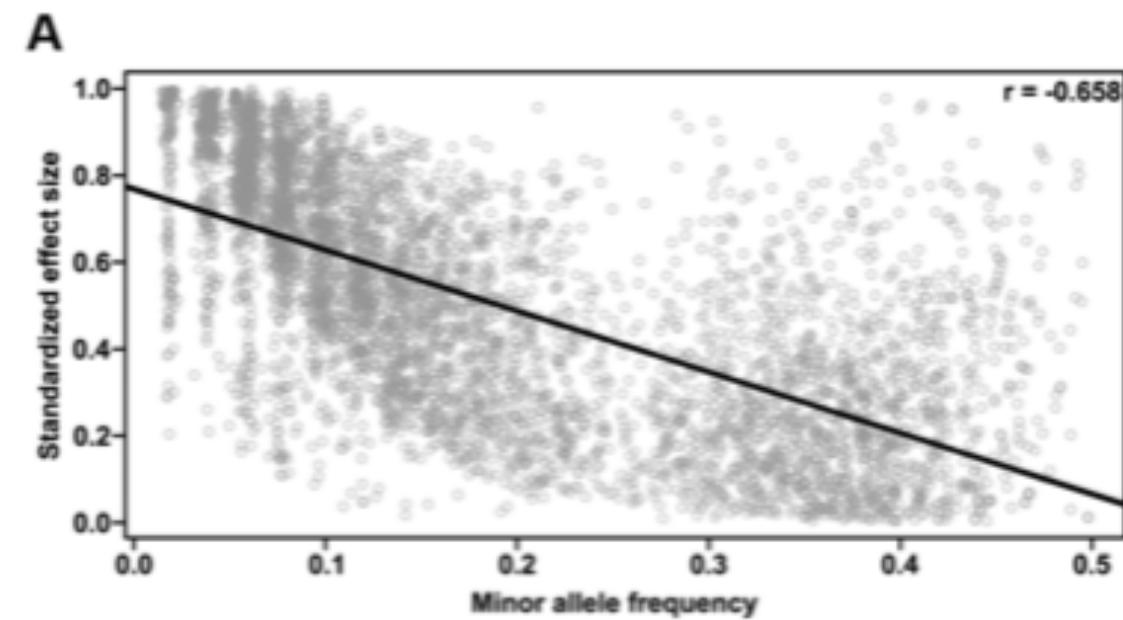
# Minor Allele Frequency and Effect Size

- Both minor allele frequency and effect size have an significant effect on variation explained

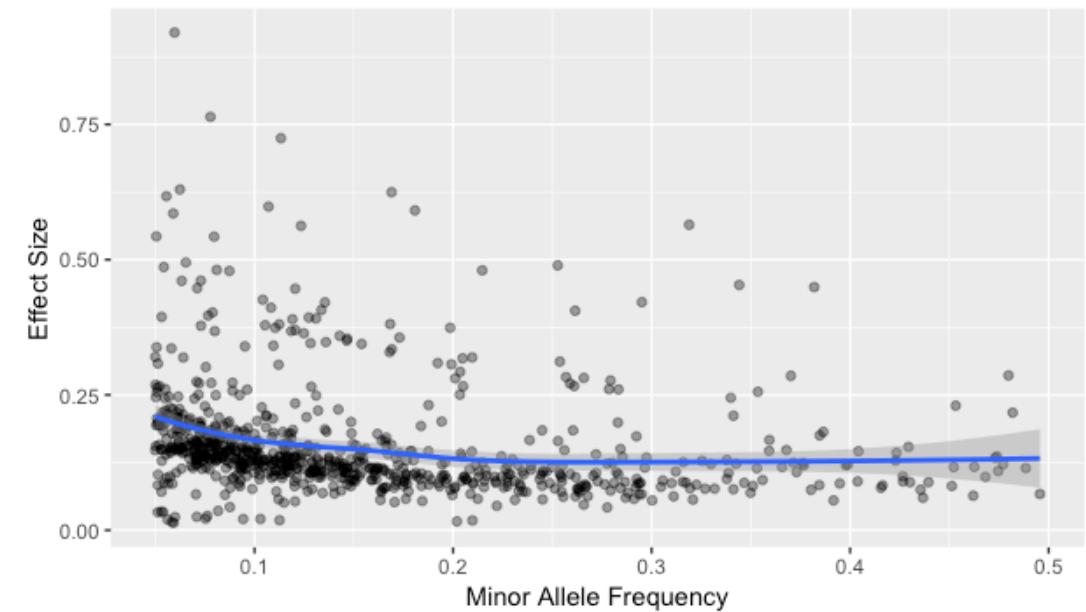


# Minor Allele Frequency and Effect Size

- Polymorphism effect sizes is negatively correlated with allele frequency

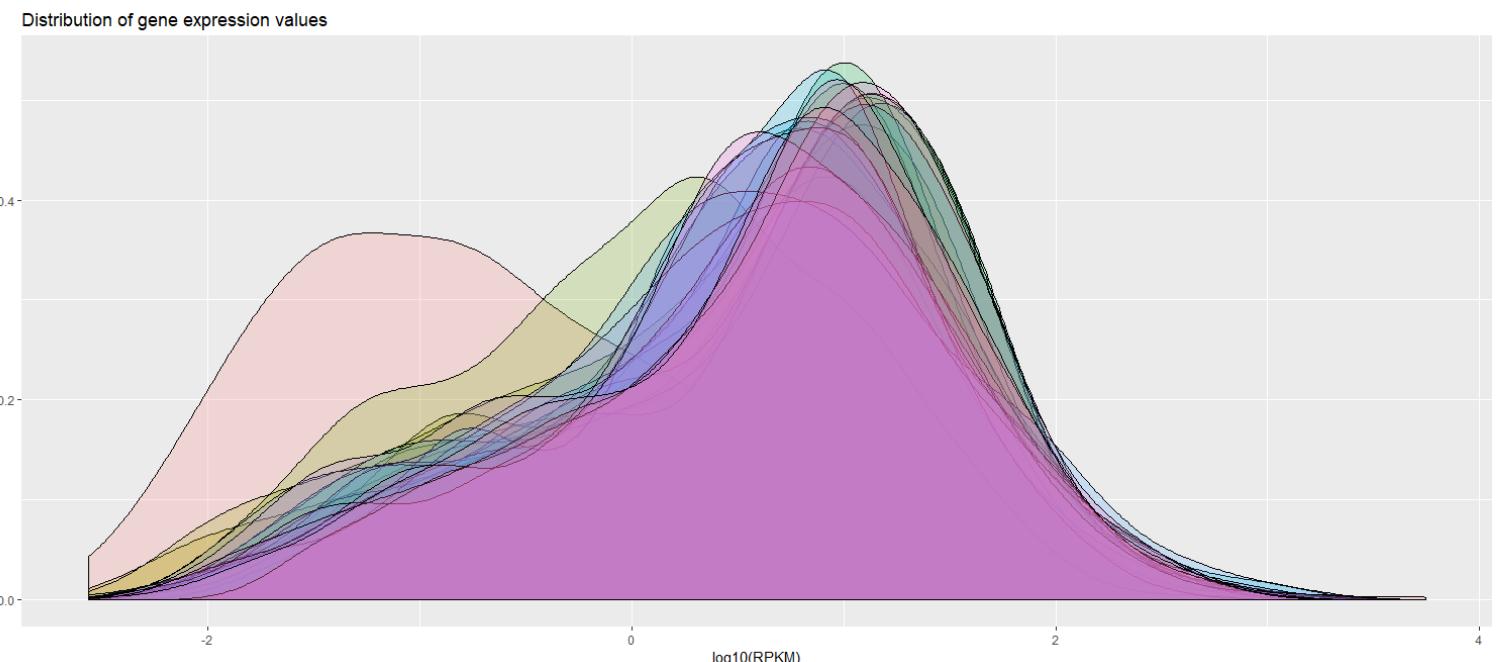
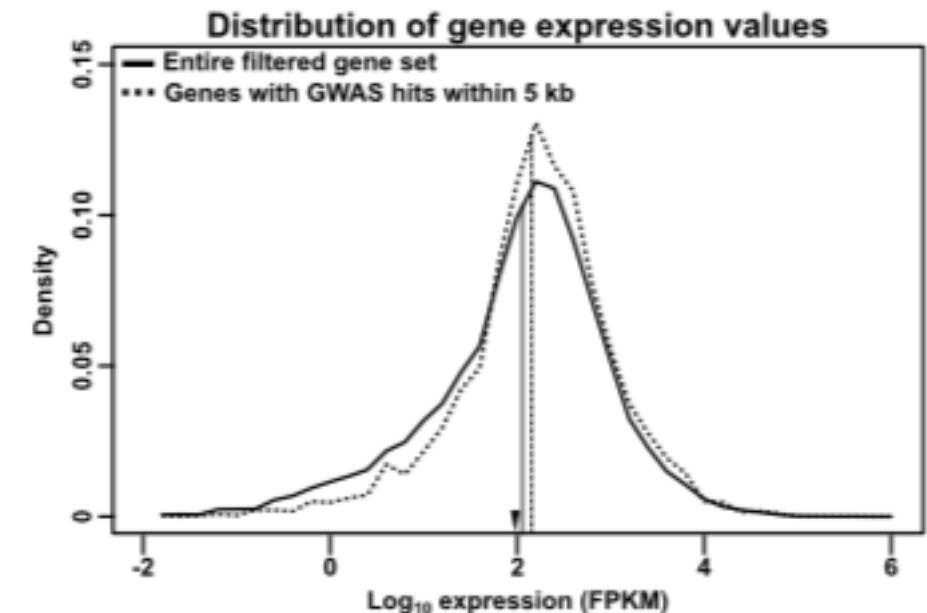


Minor allele frequency vs effect size: Replication



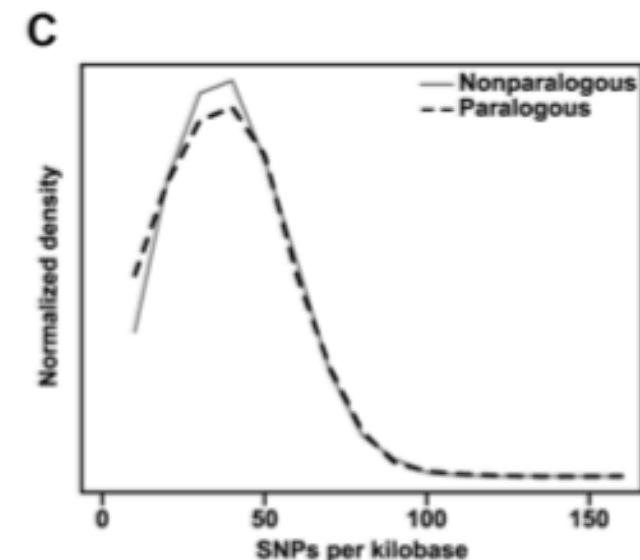
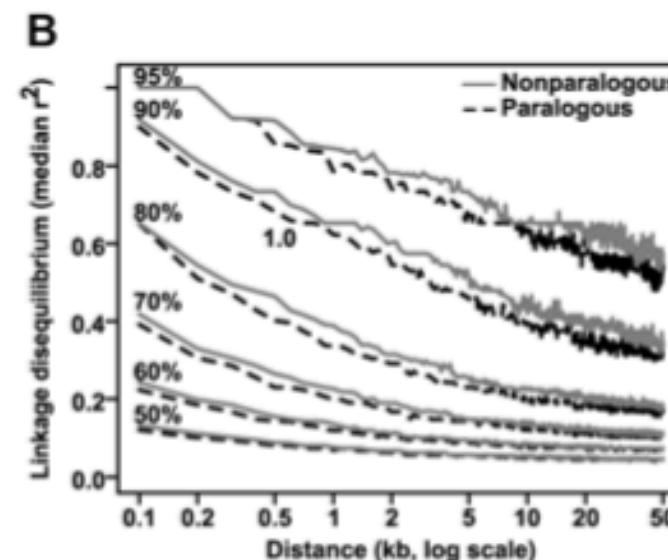
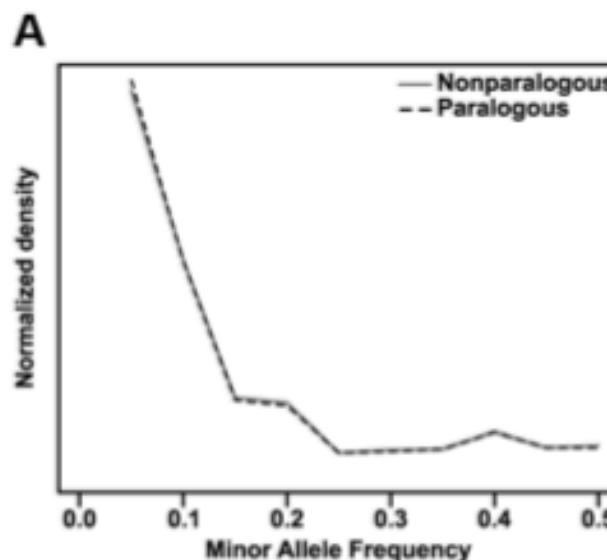
# Expression Pattern

- Low-expressed genes are less likely to explain variation, and are under-enriched in GWAS analysis



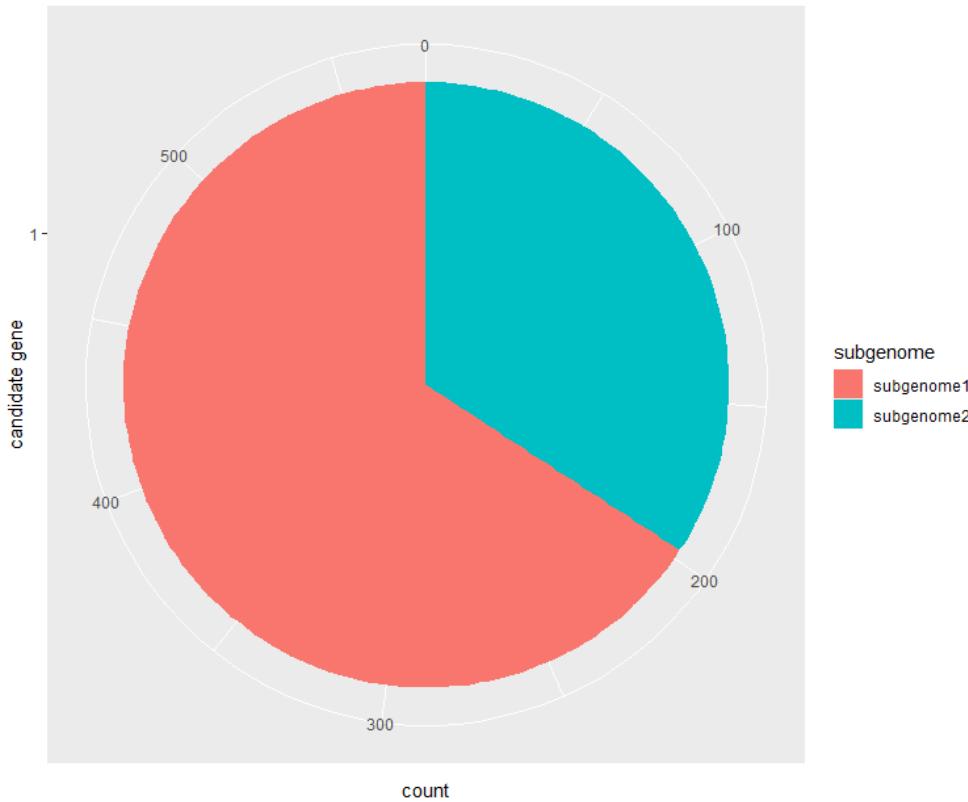
# Paralogous to Nonparalogous Genes

- “Genes with GWAS hits in their primary transcripts are 50% more likely to have a paralog than expected by chance” and this is not explained by confounding effects:

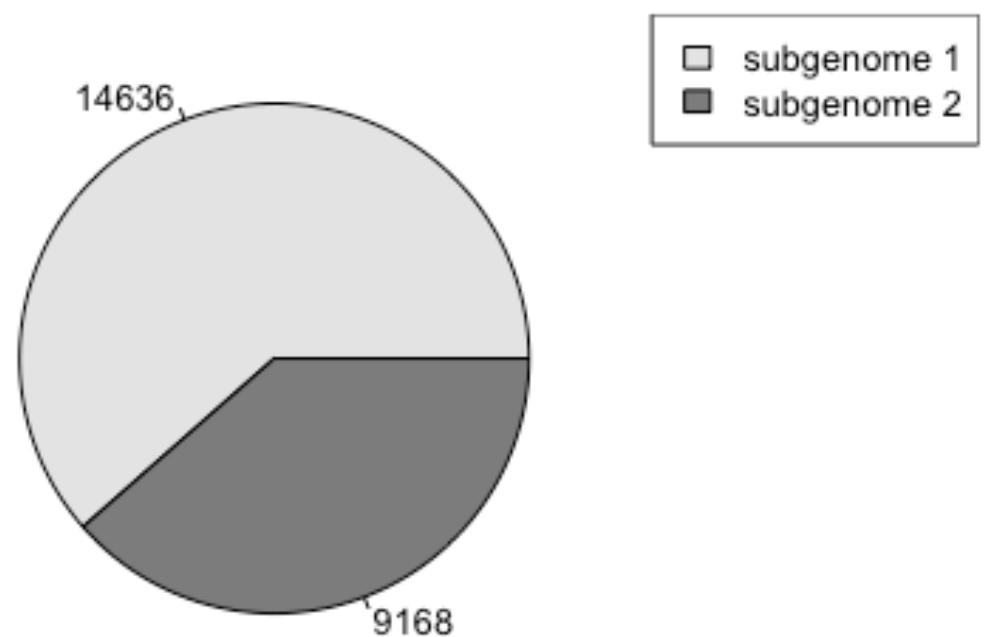


# Paralogous to Nonparalogous Genes

Candidate Genes in Subgenomes 1 and 2



Total genes in subgenomes 1 and 2

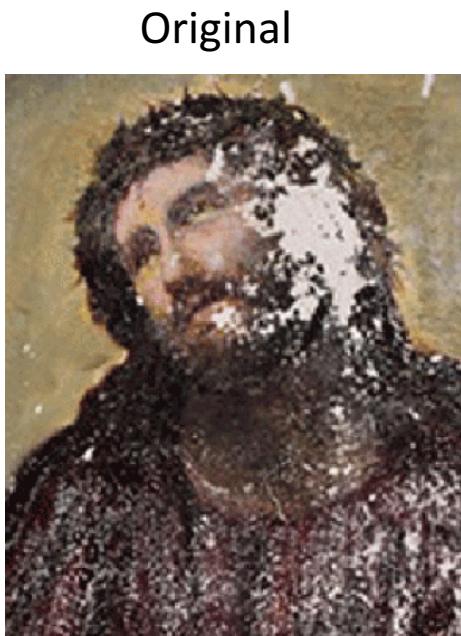


# Conclusion: Results

- More complex phenotypes are generally more enriched
- Polymorphism effect size is negatively correlated with allele frequency
- Genes with lower expression levels are less likely to explain phenotypic variation
- Genes with paralogues are more likely to explain phenotypic variation

# Conclusion: Replication

- Generally successful, but not close enough for validation
- Smaller / Different Sample Size
- Slight differences in analysis



Original



Replication

Thank you!



Questions?