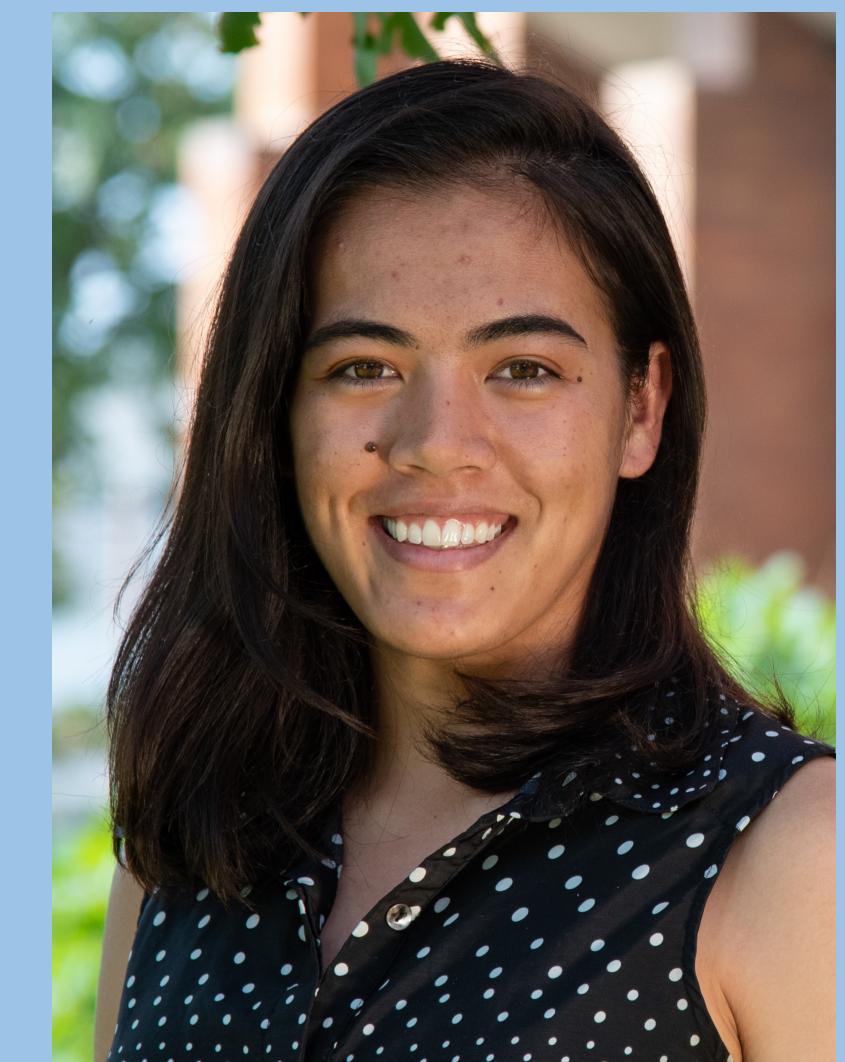


Elucidating the extent of pleiotropy in maize and its functional relevance towards trait prediction



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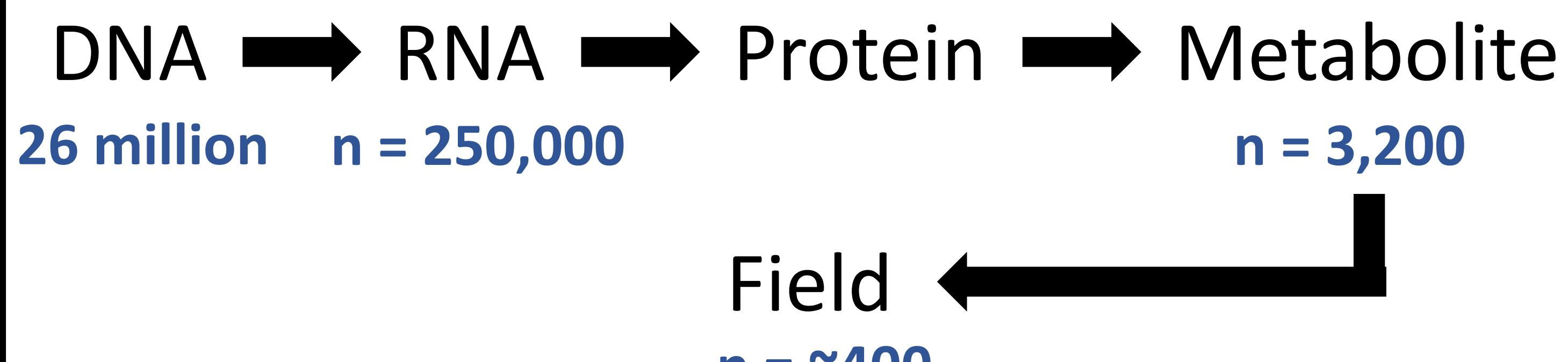
Watch the video: <https://www.maizegenetics.net/merrittkhaipho-burch>

Hypothesis: Due to the shared genetic architecture of traits across maize populations, pleiotropy is common & widespread among quantitative traits

Methods

Phenotypes

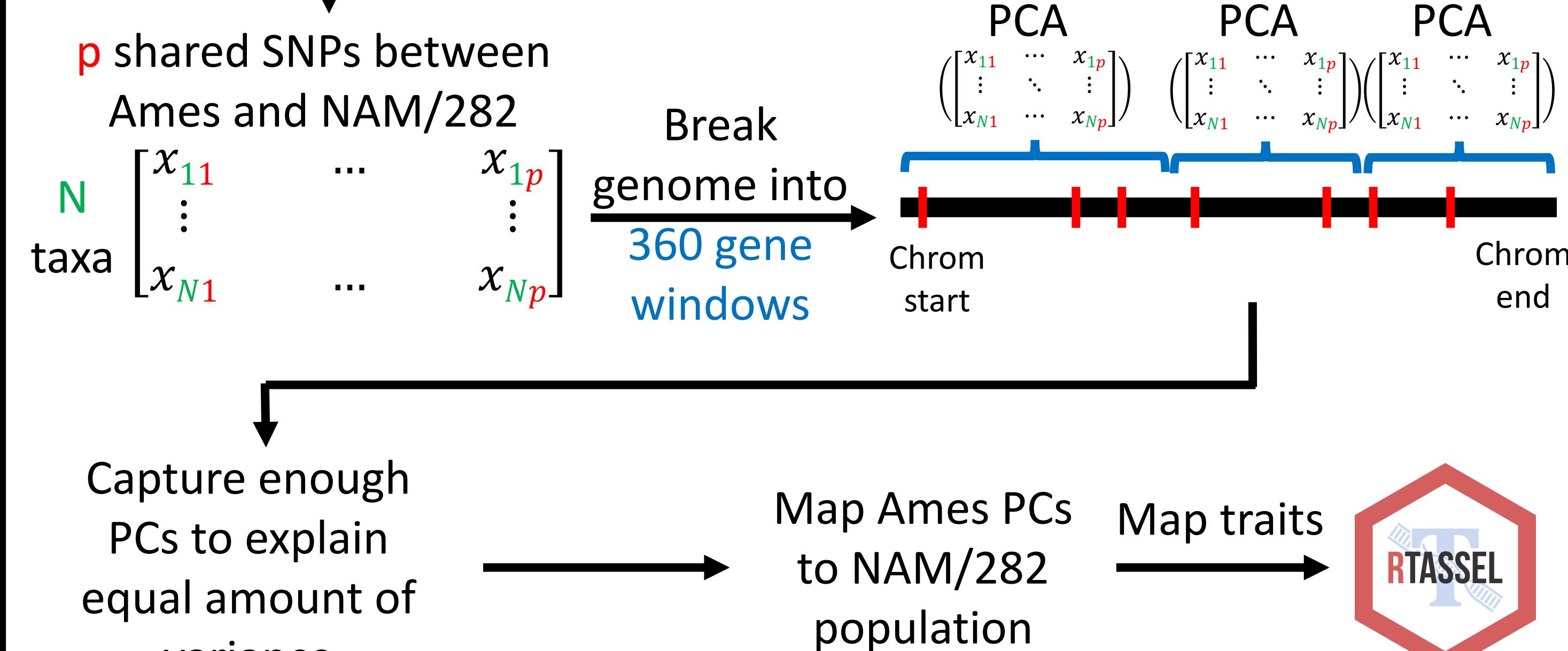
Counts of previously published phenotypes in NAM and the Goodman Association Panel



Association Mapping

Model:

$$y = X\beta_1 + 3 \text{ global PC} \pm \text{window PCs} + e$$

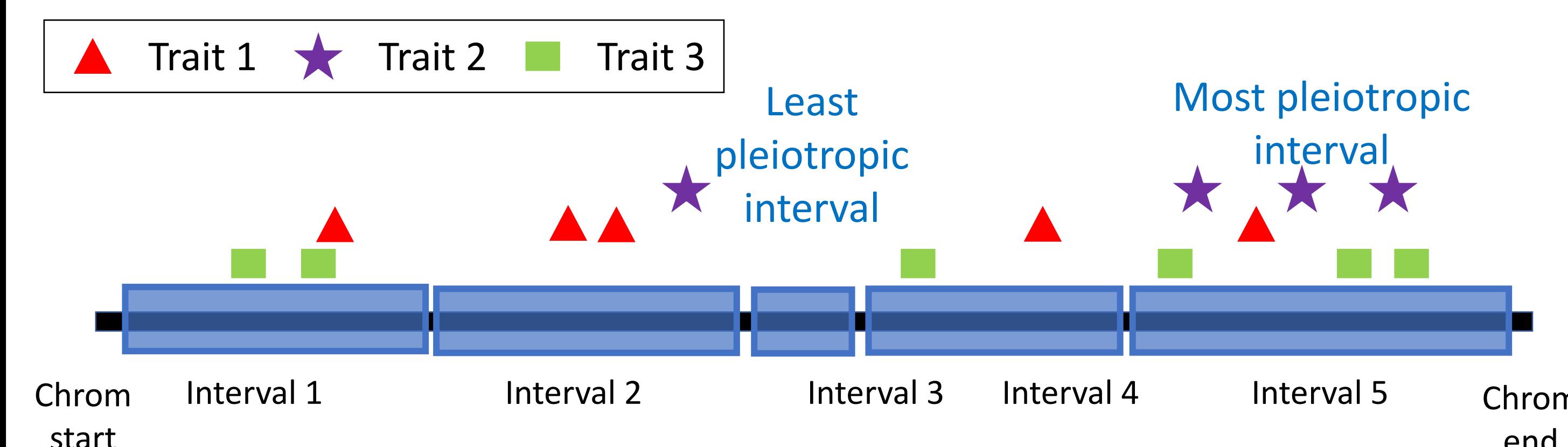


Pleiotropy Estimation

Pleiotropy Formula:

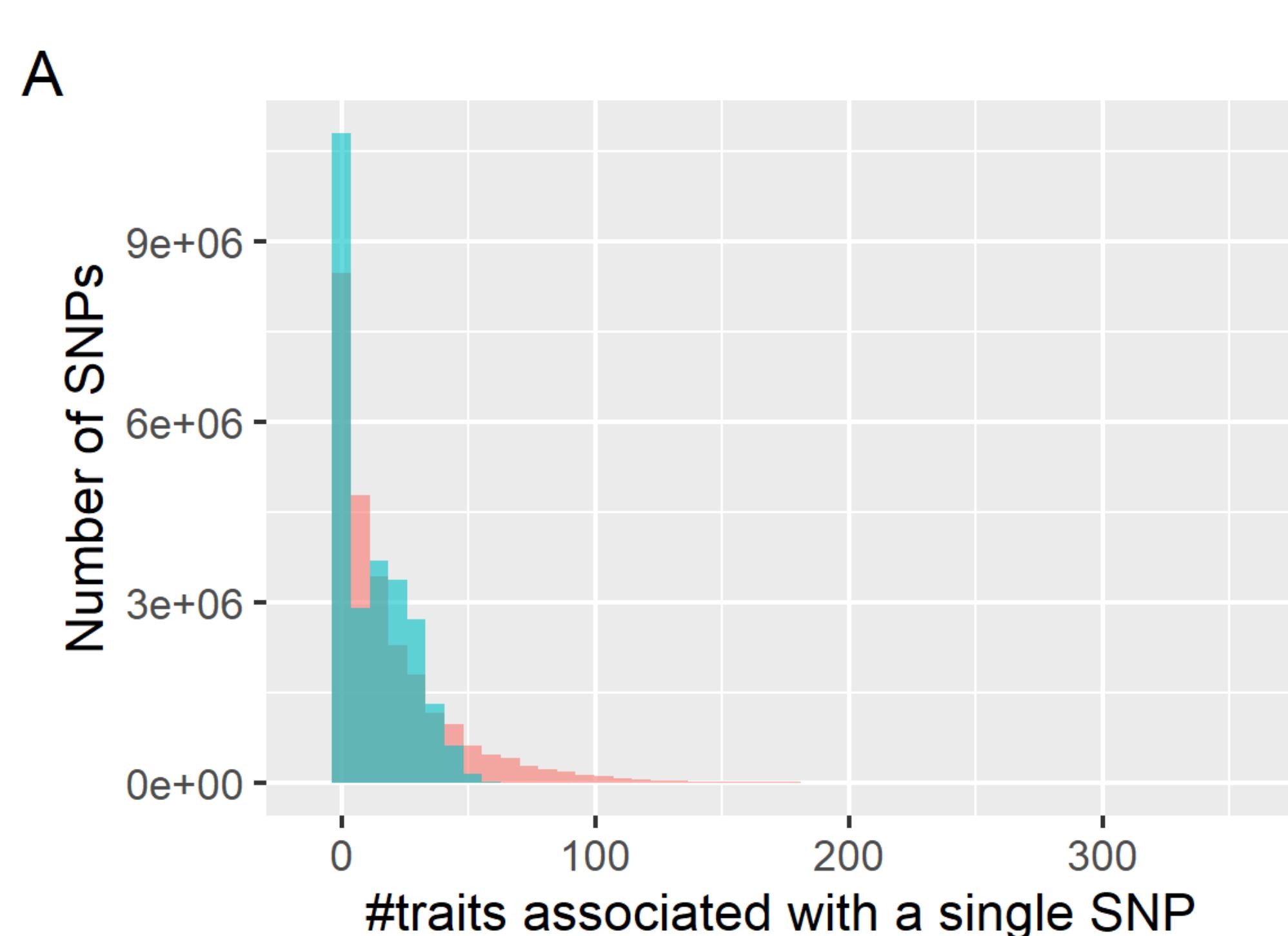
Number of traits within an interval scaled by the number of traits and GWAS hits genome wide.

$$\frac{\# \text{ of unique traits within interval}}{\text{total number of mapped traits}} \times \frac{\# \text{ of GWAS hits within interval}}{\text{total # of GWAS hits genome wide}}$$

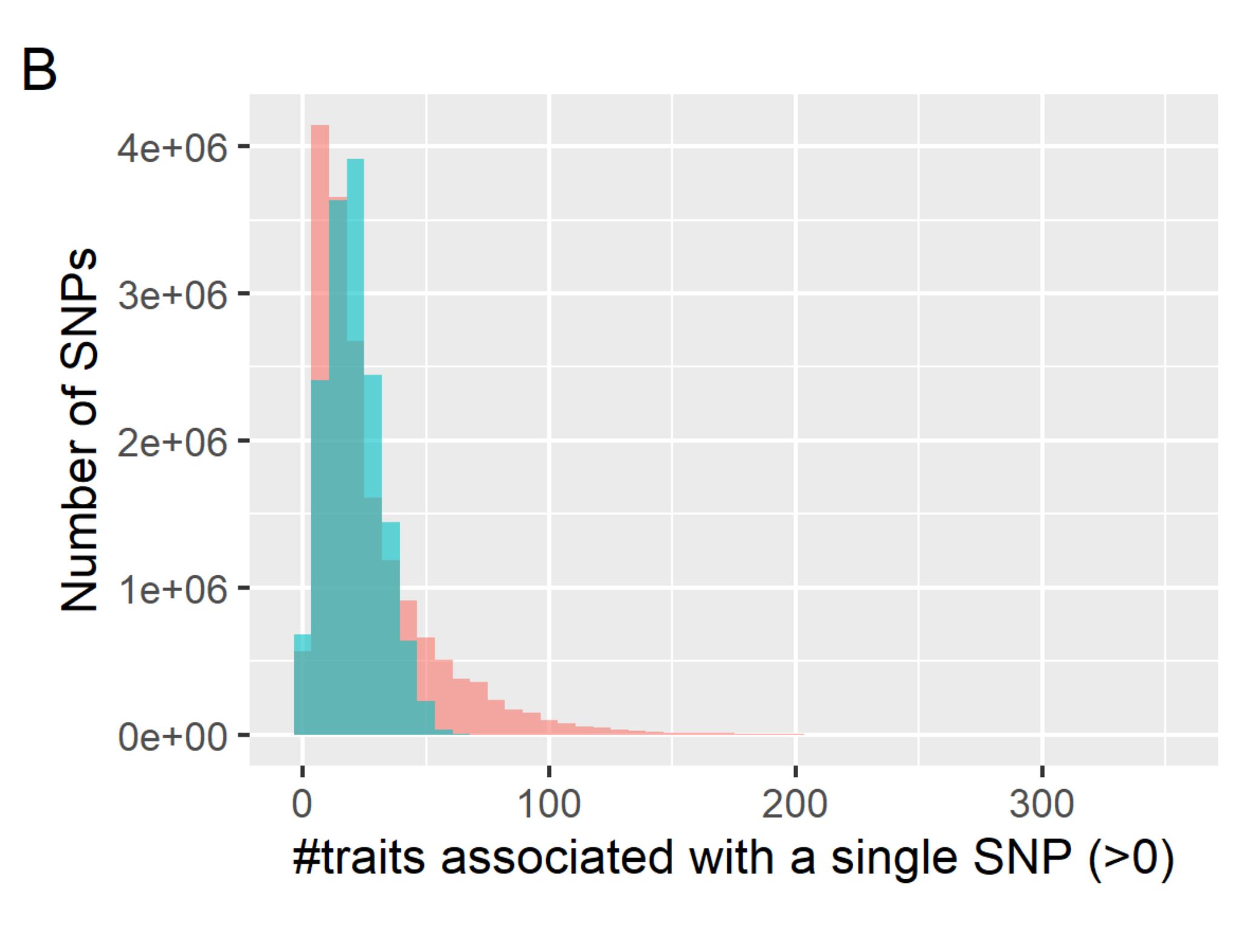


Results

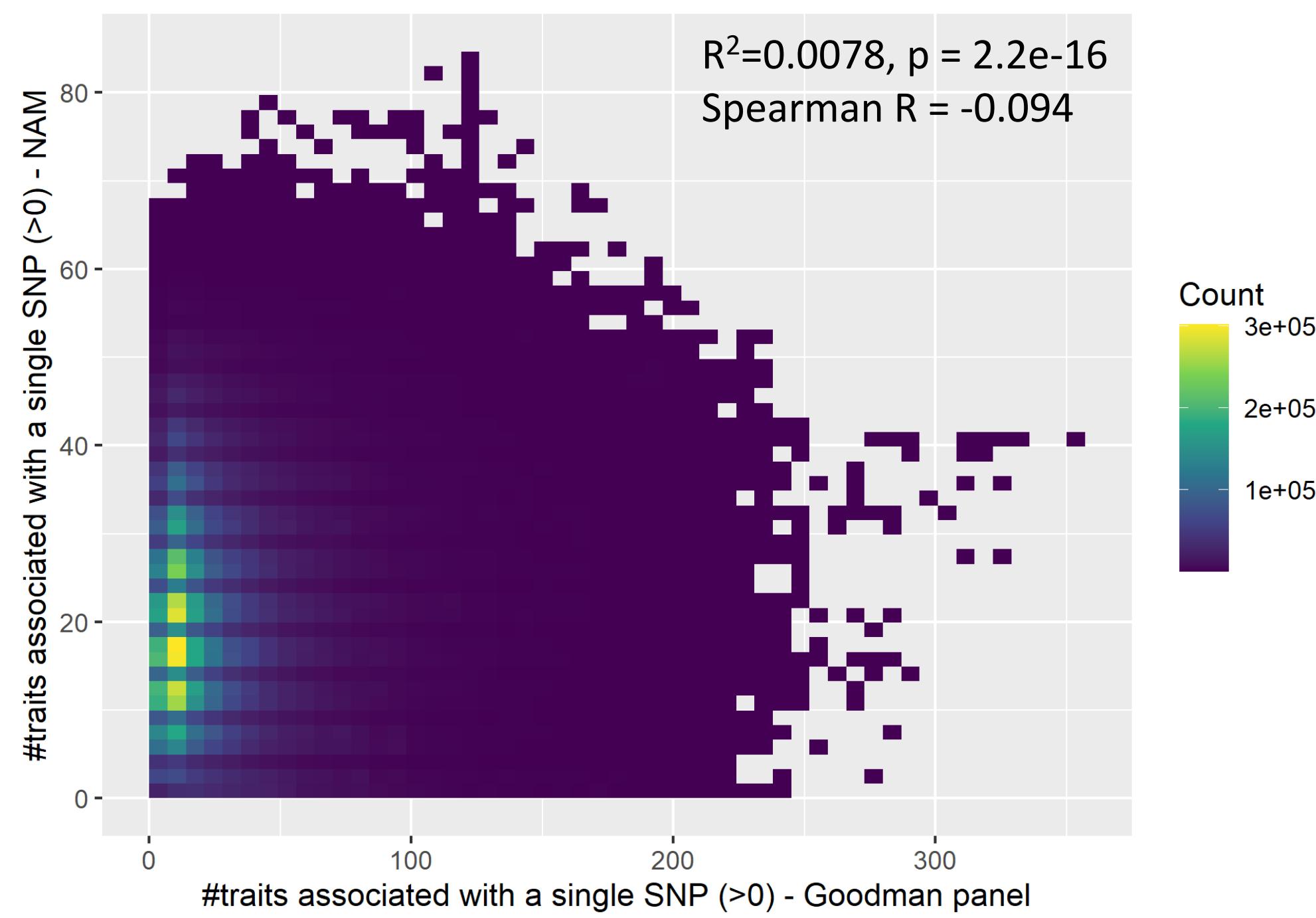
30-40% SNPs have no trait associations



~19 traits associate with a single SNP



No correlation between NAM and Goodman Panel trait-SNP associations



Watch the video & learn more



Discussion & Future Directions

- Inferring pleiotropy & causal relationships at the SNP level is confounded by linkage disequilibrium
- Pleiotropy resolution at the haplotype level may be more plausible