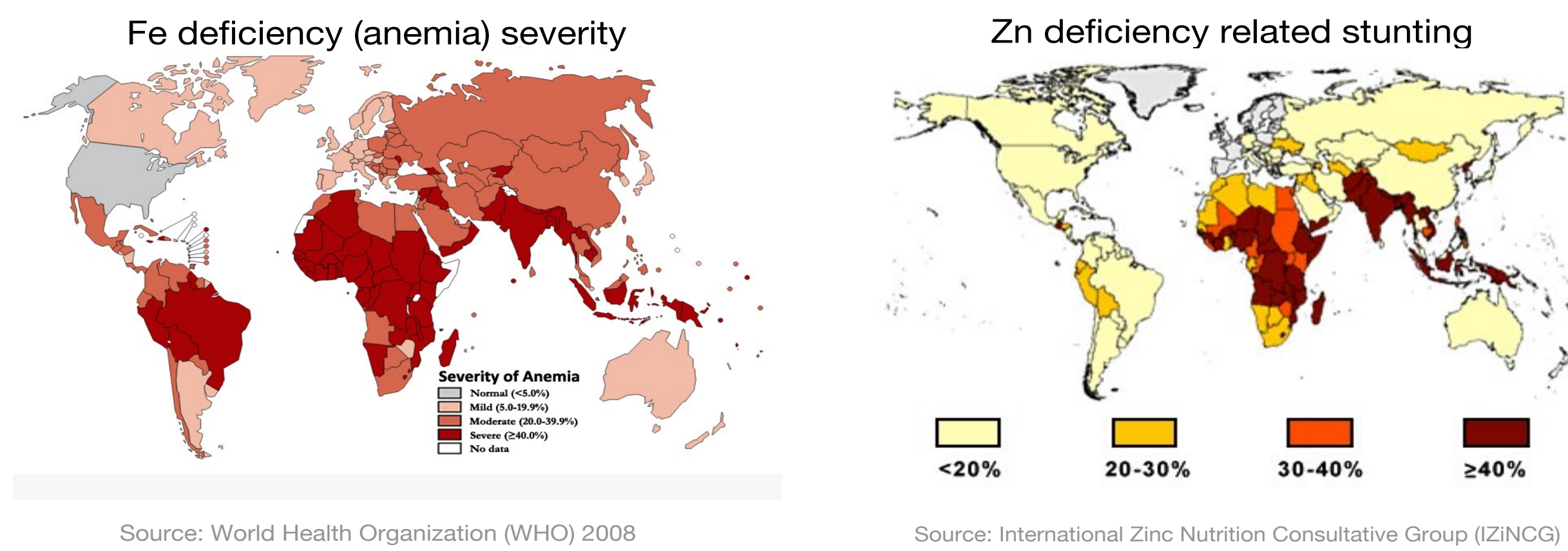


Philip Kear¹, Greg Zeigler², Owen Hoekenga¹, Margaret E. Smith¹ and Ivan Baxter²

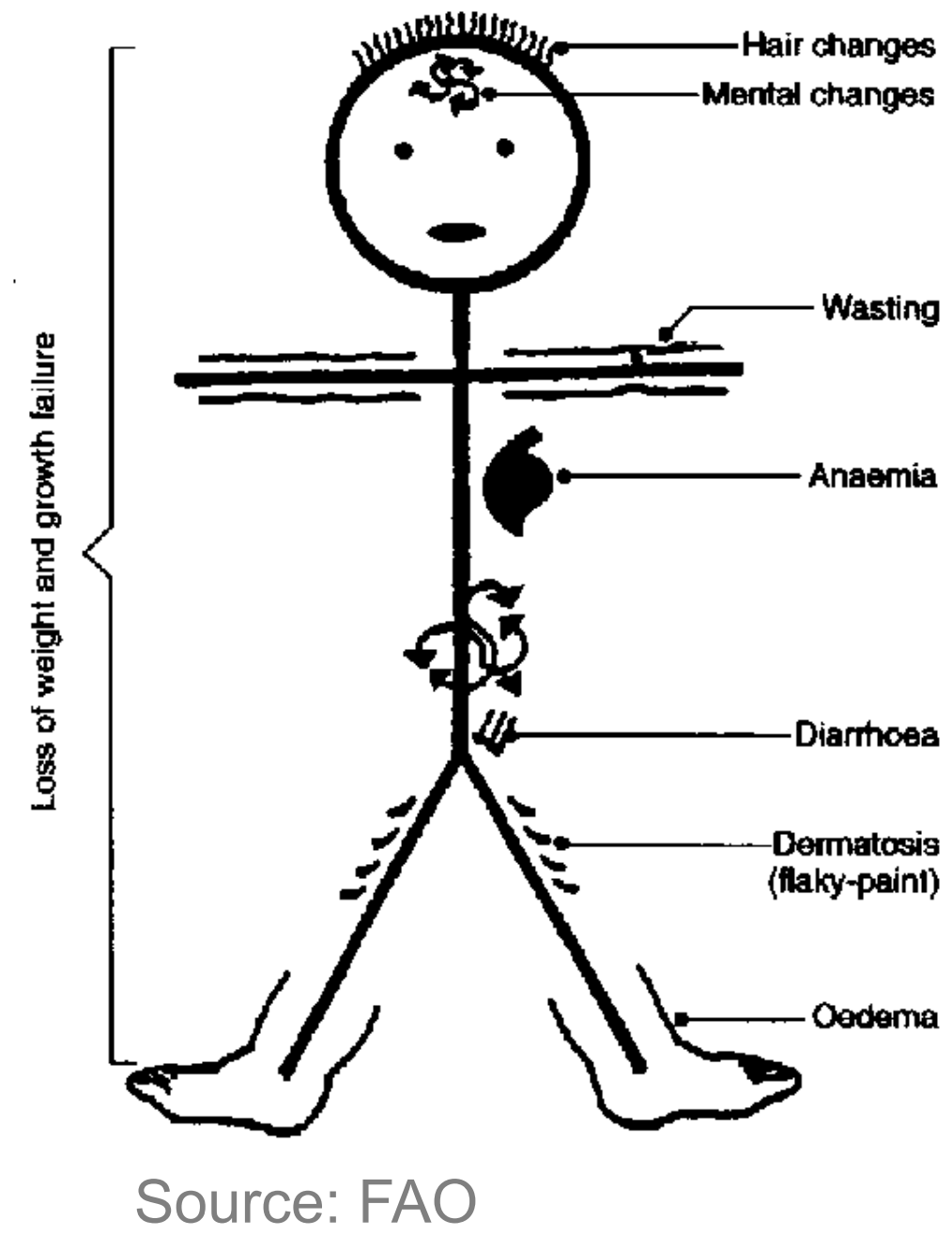
¹ Cornell University, Ithaca

² USDA/Danforth Plant Science Center, St Louis

The Prevalence of Fe and Zn Deficiency around the World



Approximately 2 billion of the world's population does not receive adequate nutrition from the food they consume. Maize grain is used as staple food in many undernourished communities around the world. Fe and Zn deficiencies remains one of the most prevalent causes of global death, disease, Zn deficiency causes late sexual maturation, and reduced cognitive ability directly correlating with poverty and food insecurity.

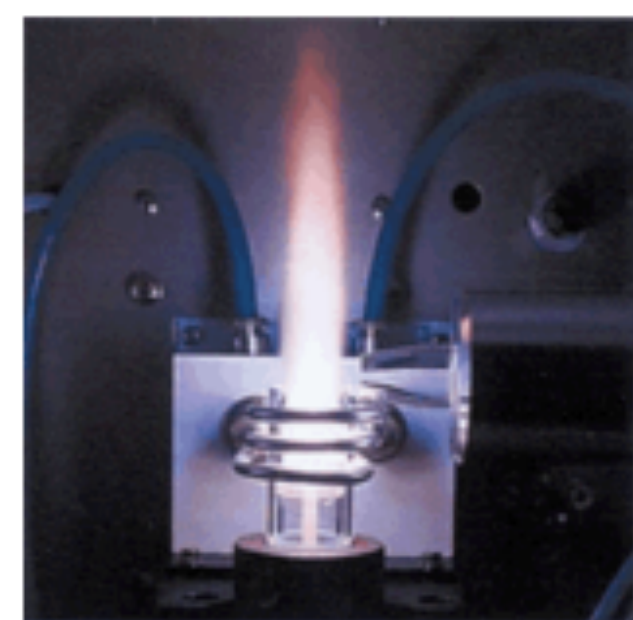


Risk factor	Ratio (%)
Underweight	14.9
Unsafe sex	10.2
Unsafe water	5.5
Indoor smoke	3.7
Zinc deficiency	3.2
Iron deficiency	3.1
Vitamin A deficiency	3.0
Blood pressure	2.5
Tobacco	2.0
Cholesterol	1.9

Experimental Design

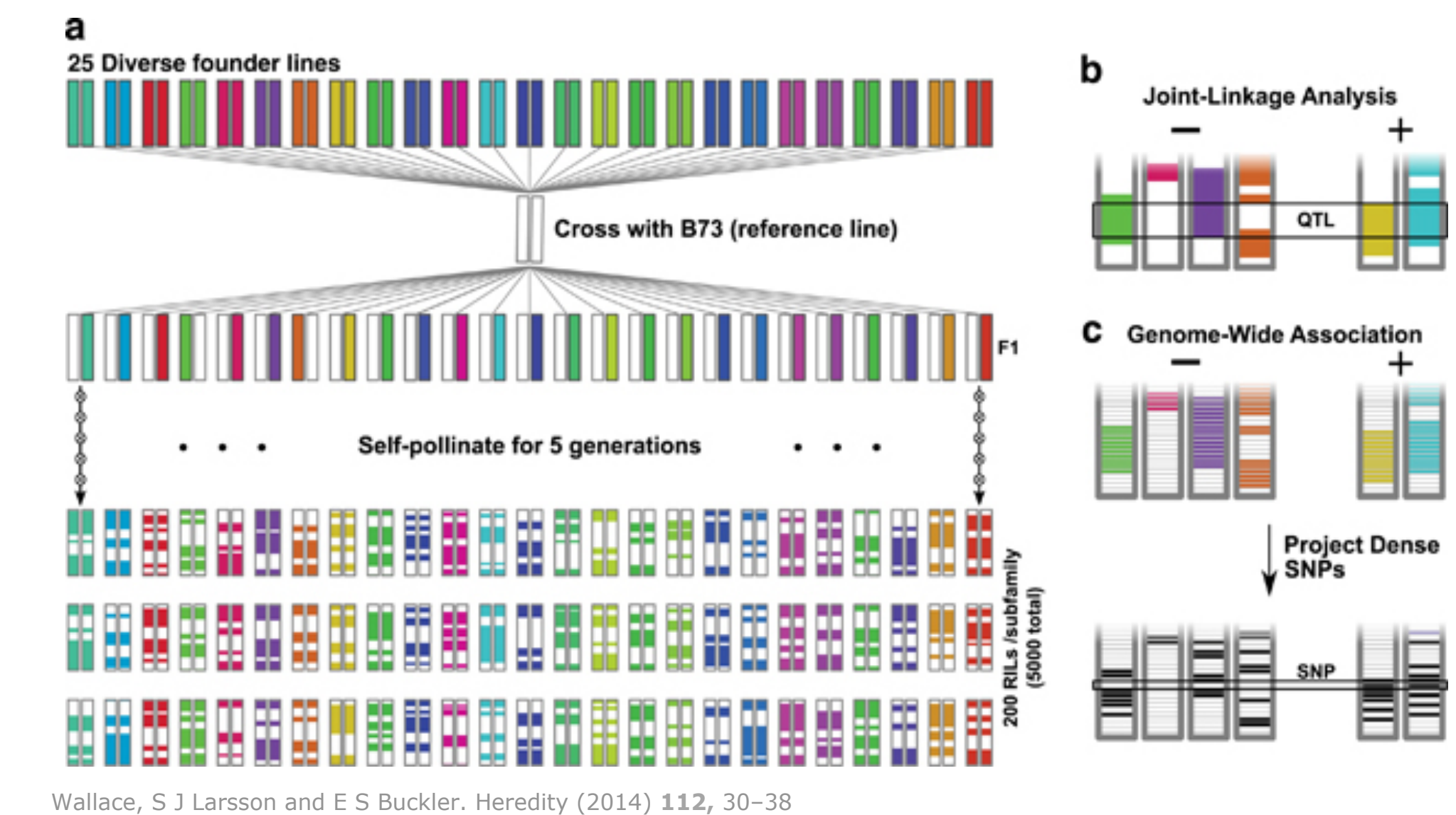
Use of novel bioinformatics to screen for significant QTL associated with Fe and Zn

1. Estimate the ionome



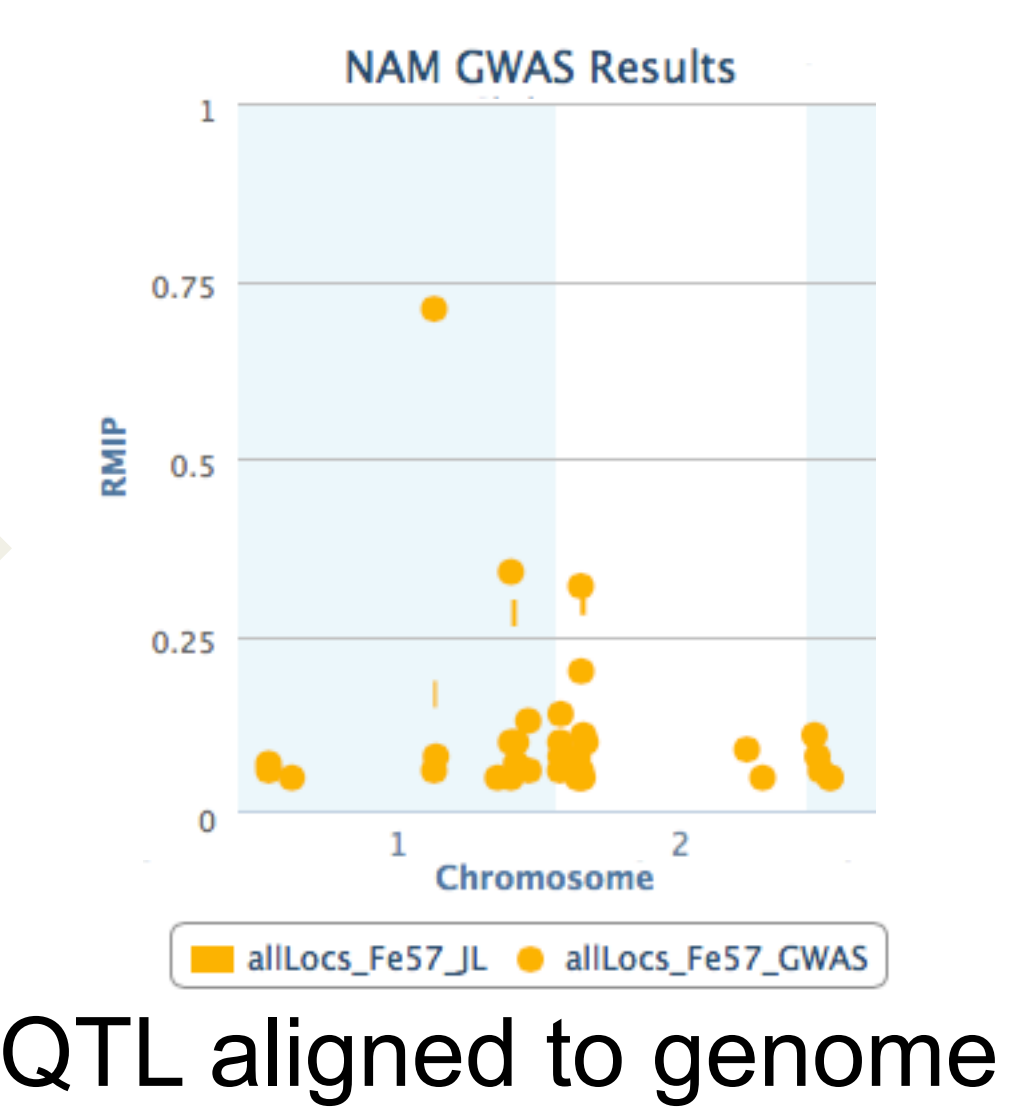
ICP for Fe & Zn Concentrations estimated

2. Discover quantitative trait loci (QTL)

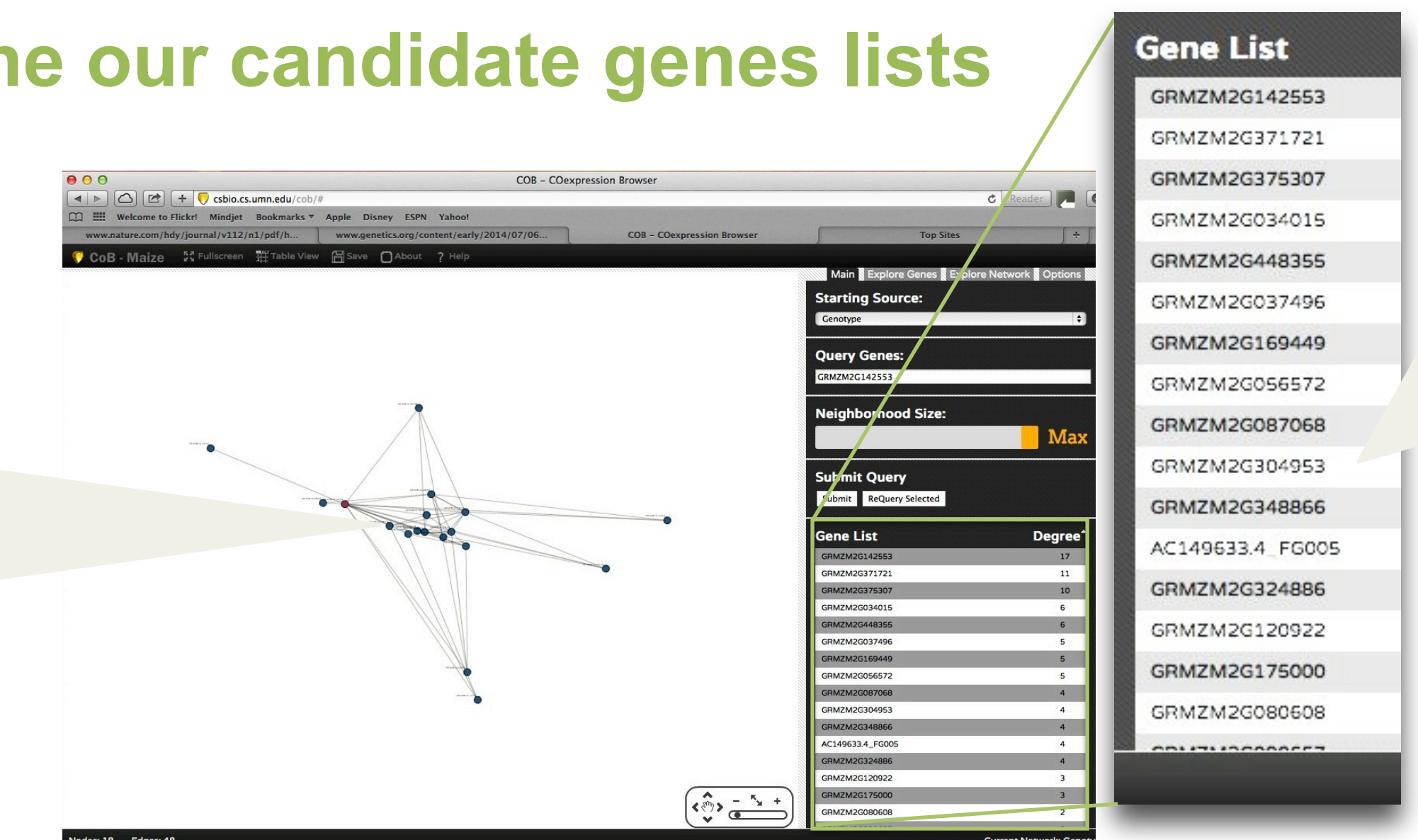
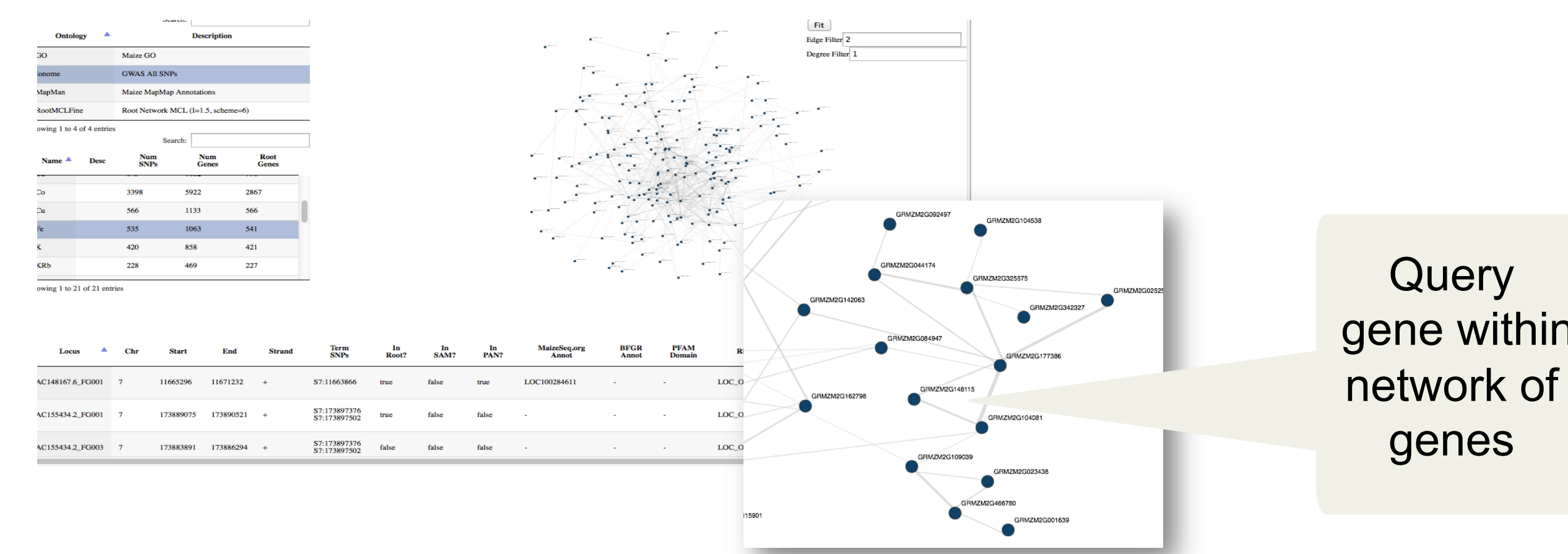


3. Candidate gene discovery

QTL from JL or GWAS



4. Use the transcriptome to refine our candidate genes lists



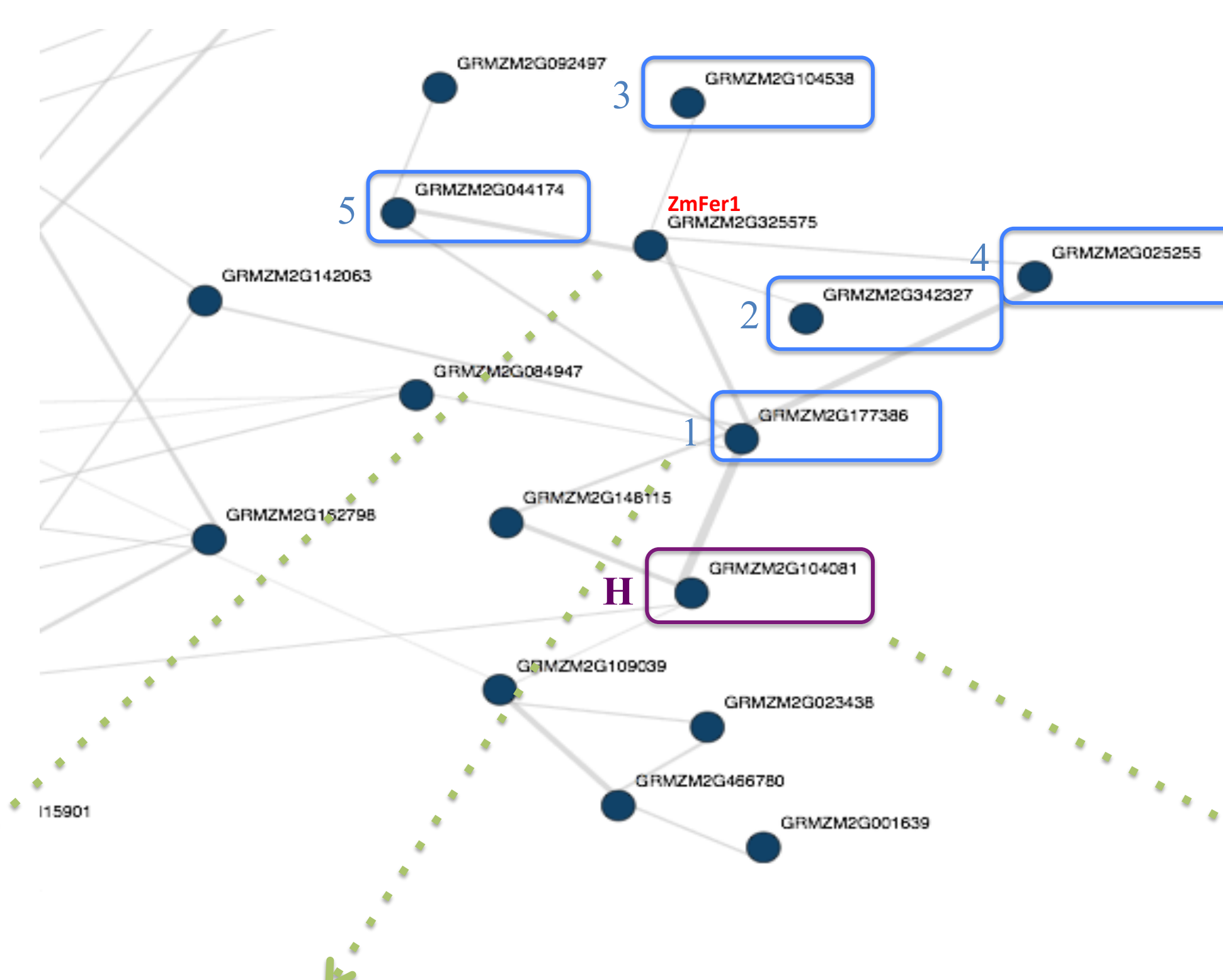
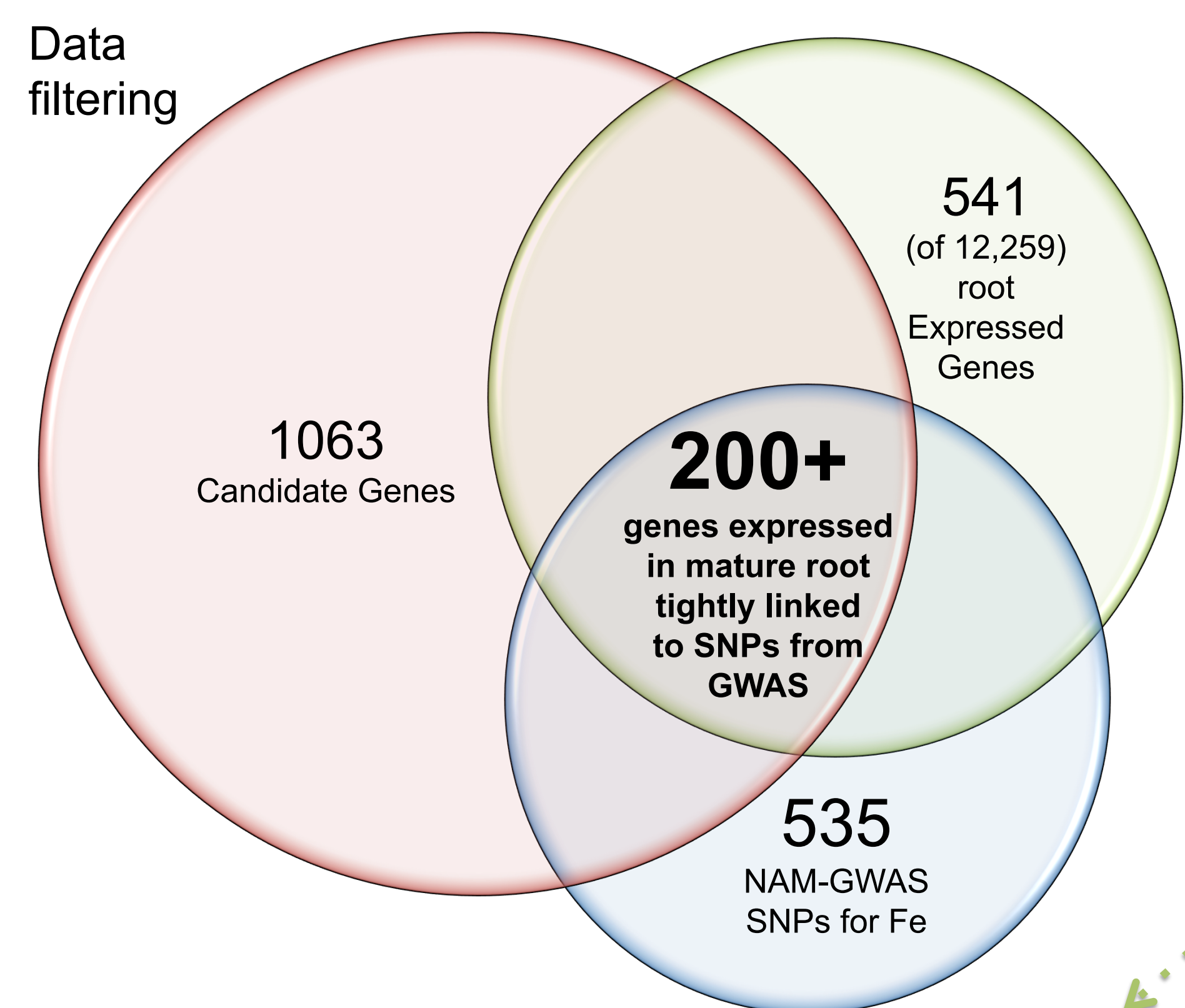
Creates list of genes in network. Allows assumptions to be made about gene's function.

(a). Defining the root transcriptome from 48 inbred maize varieties

(b). Filters returned QTL results by association with co-expressed gene pathways

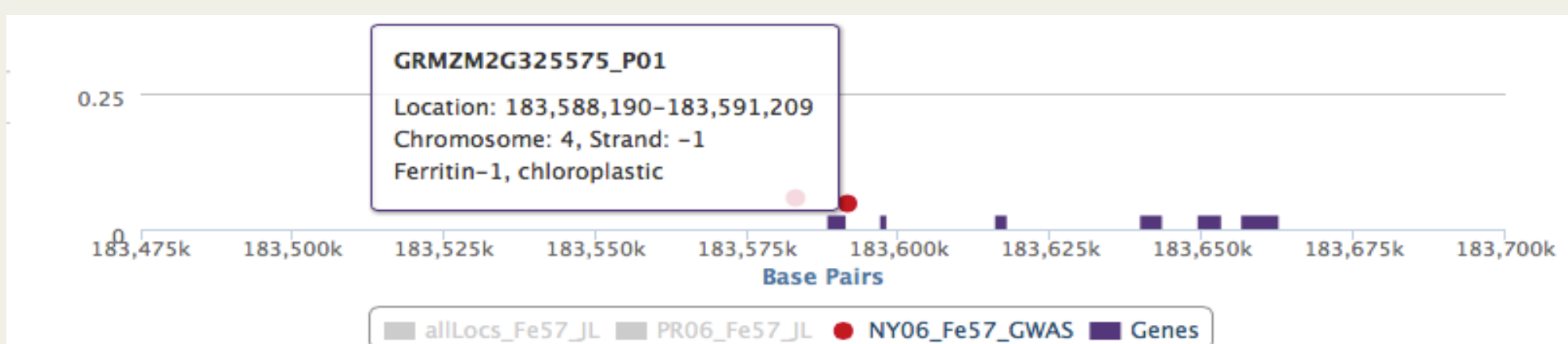
Preliminary Results

Results suggest regulation of expressed genes shaped by location
Discovery of predicted and novel genes

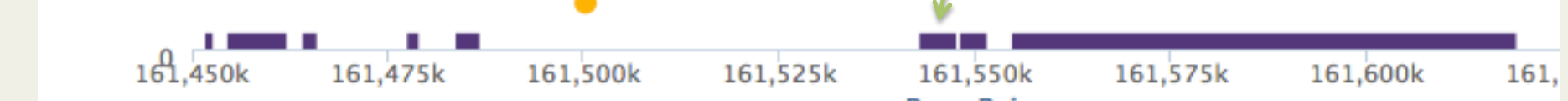


Ferritin (*ZmFer1*) and its five nearest neighbors from the root gene expression network. Hexokinase1 (*H*) is nearby.

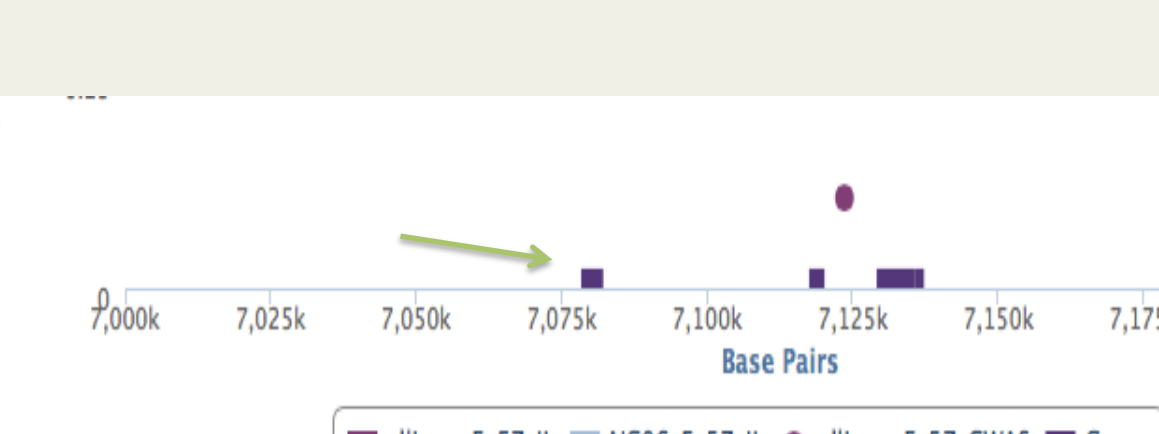
ZmFer1 is consistent with a GWAS result for NY'06



1 is a protein phosphatase, nearest neighbor to *ZmFer1* and consistent with GWAS results for the All Locations seed Fe BLUP



H: All Locations seed Fe

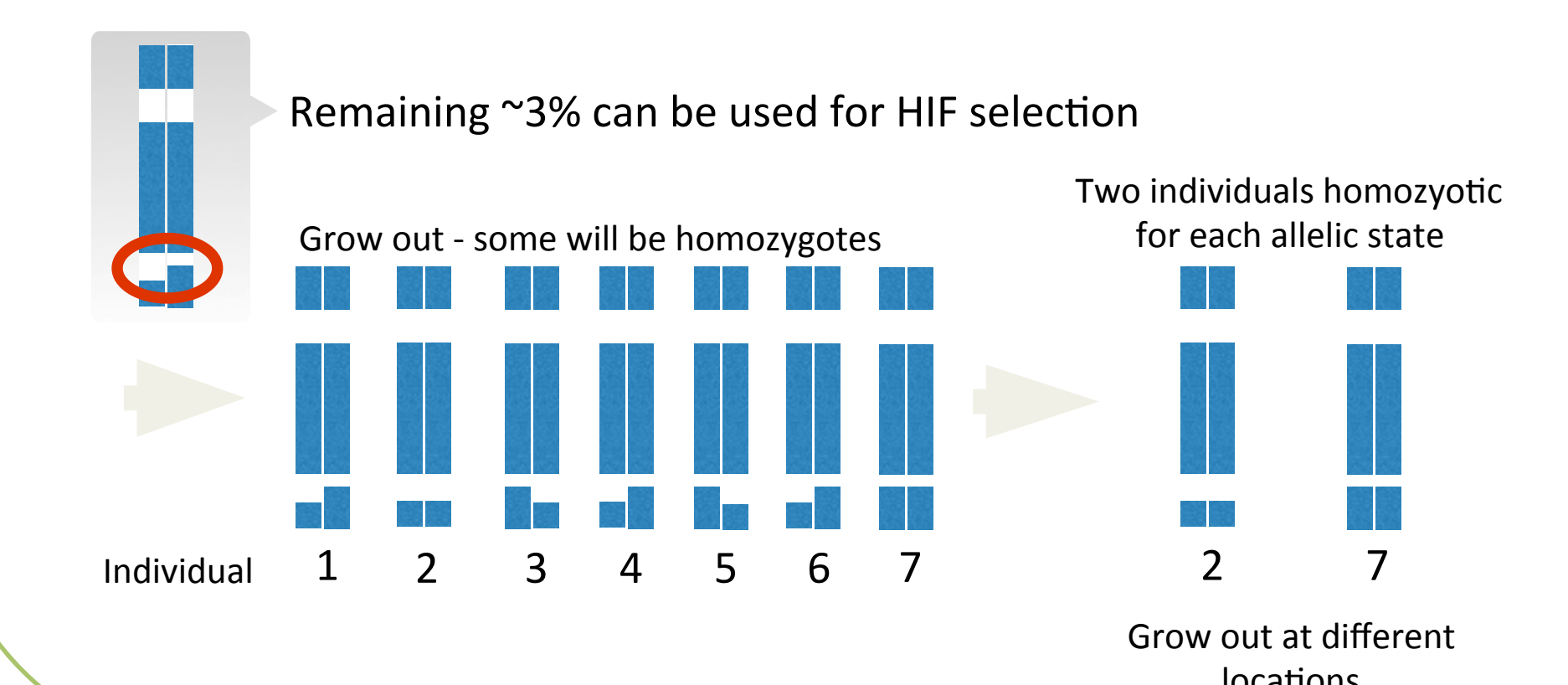


Next Steps

5. Derived lines help confirm allelic G x E interaction

a. Chromosome segment substitution lines

b. Heterogeneous inbred families



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