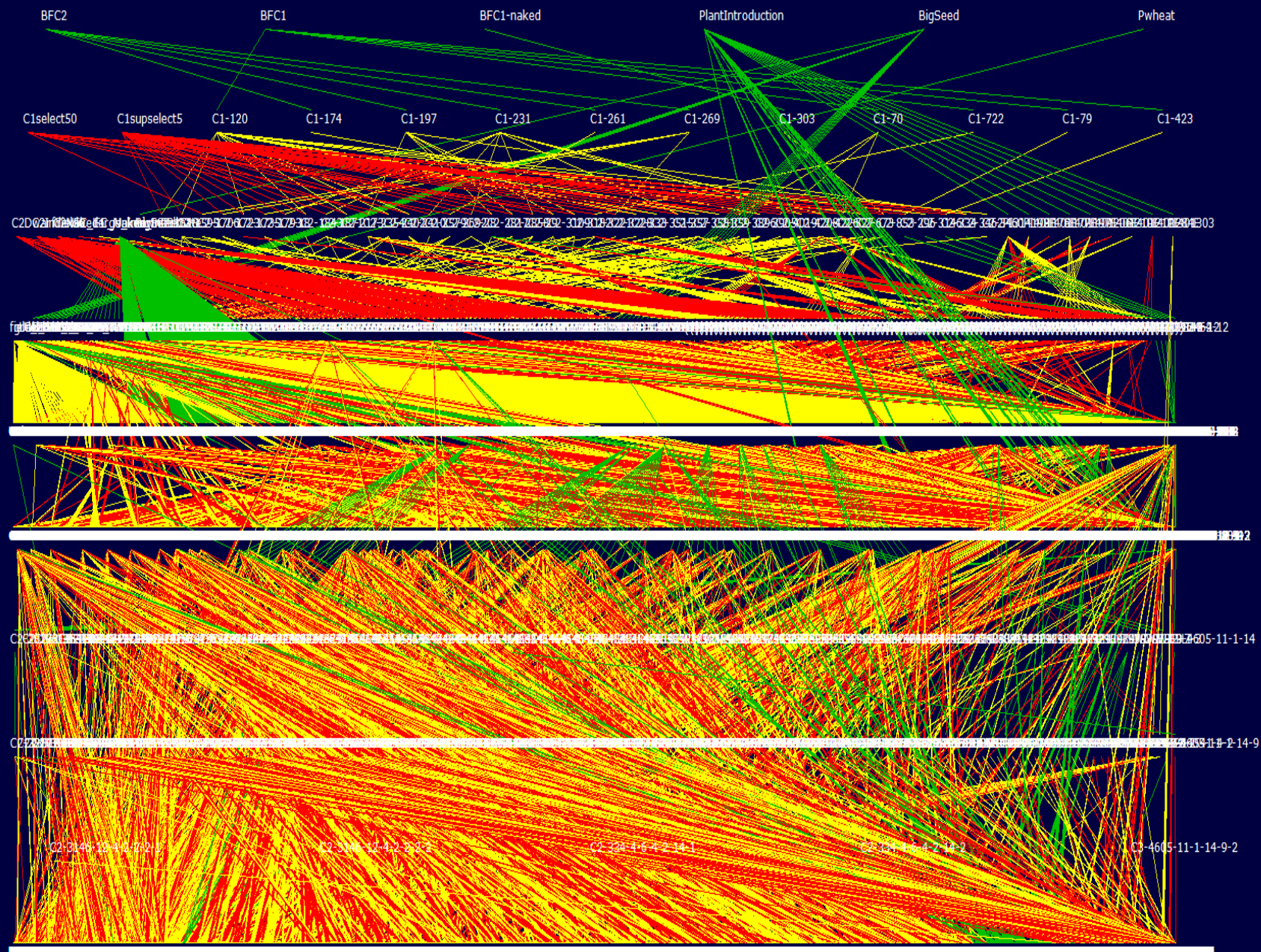
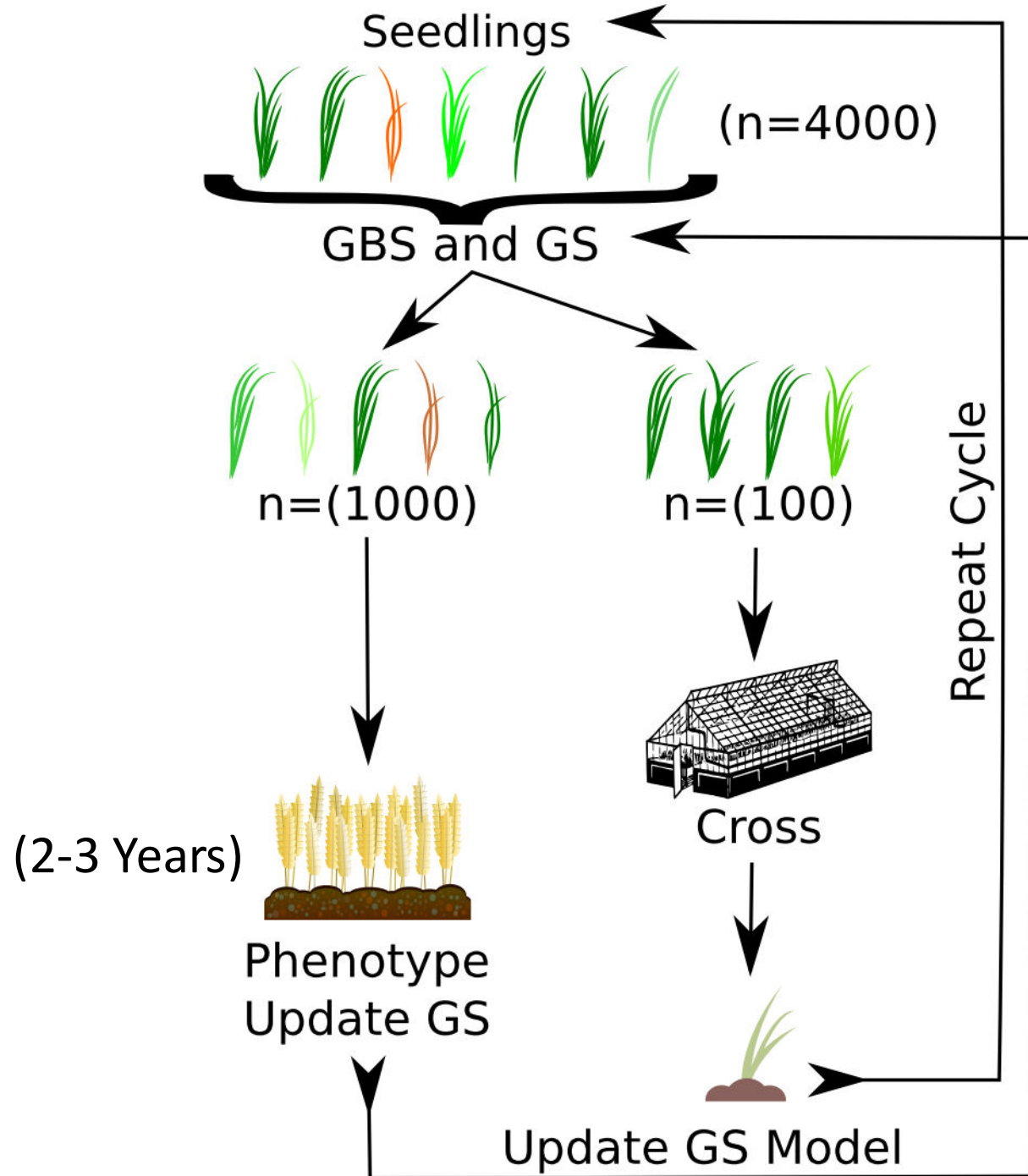






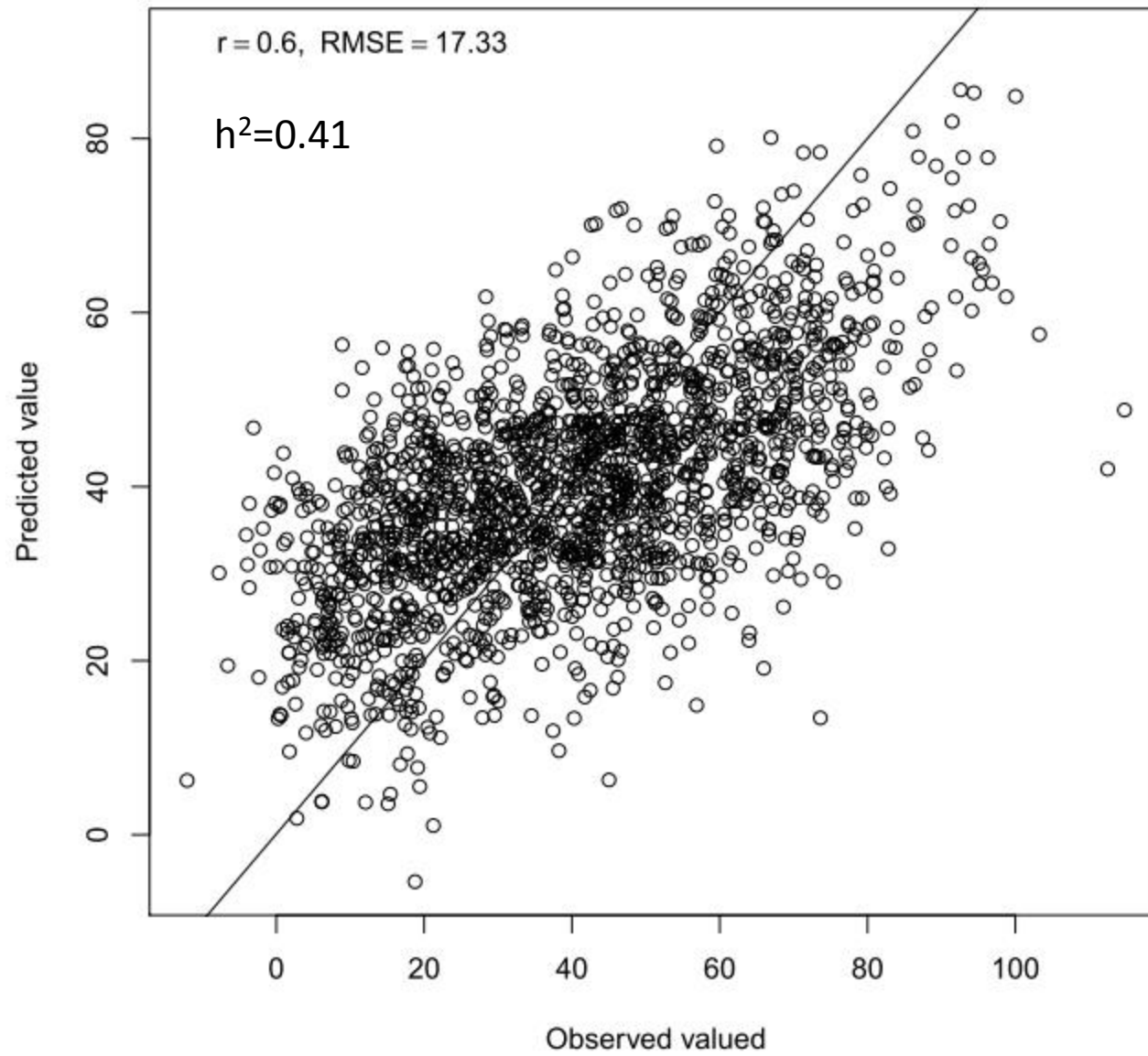




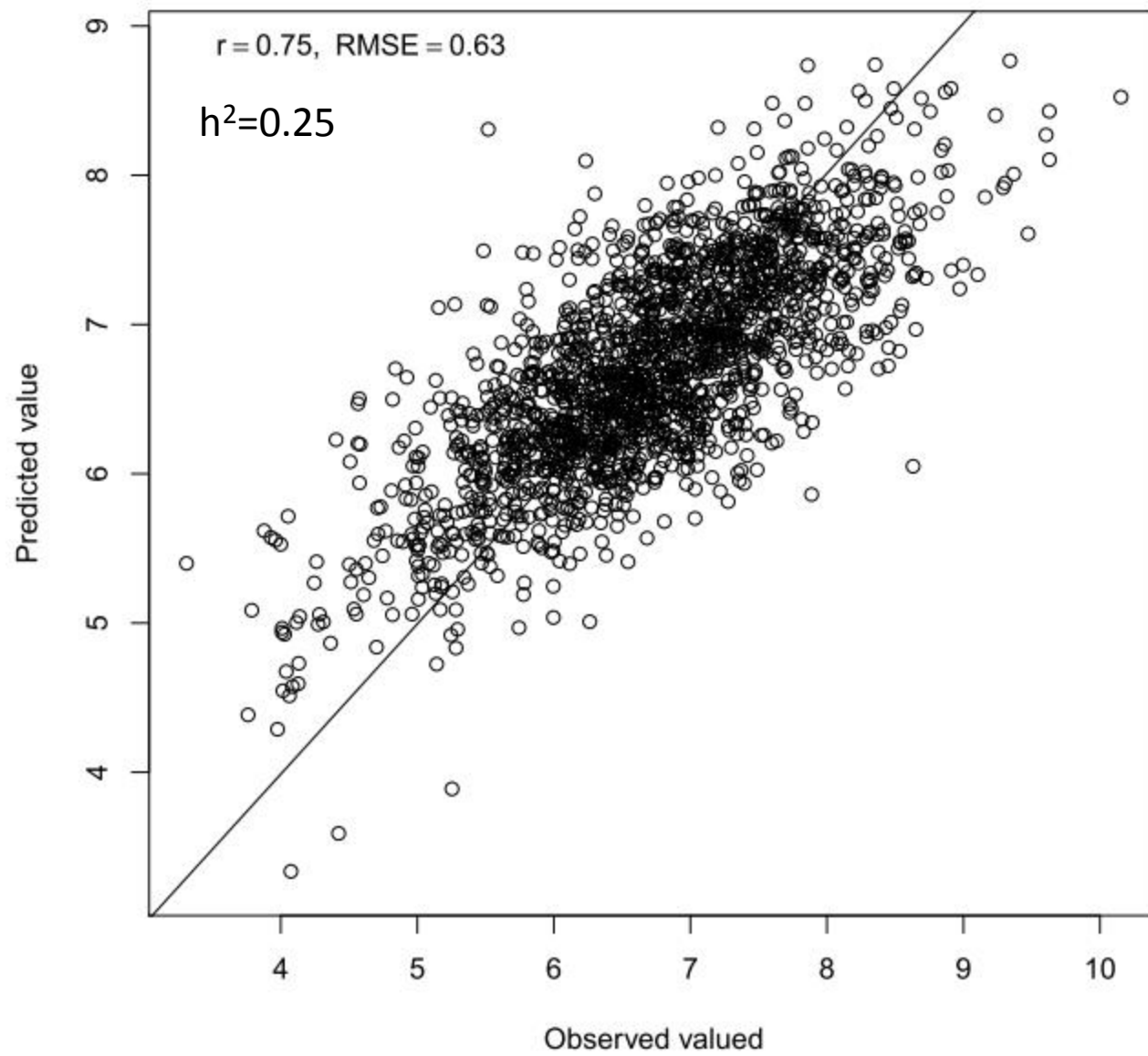
Genomic Selection Model Development and Validation

- 6364 SNP markers with less than 5% missing data used for model and minor allele frequency >0.05
- 2600 Plants genotyped
- Due to missing data, 1000 to 2600 data points per trait
- Validation by forming model with 90% of data to predict 10%, 10 resamplings without replacement

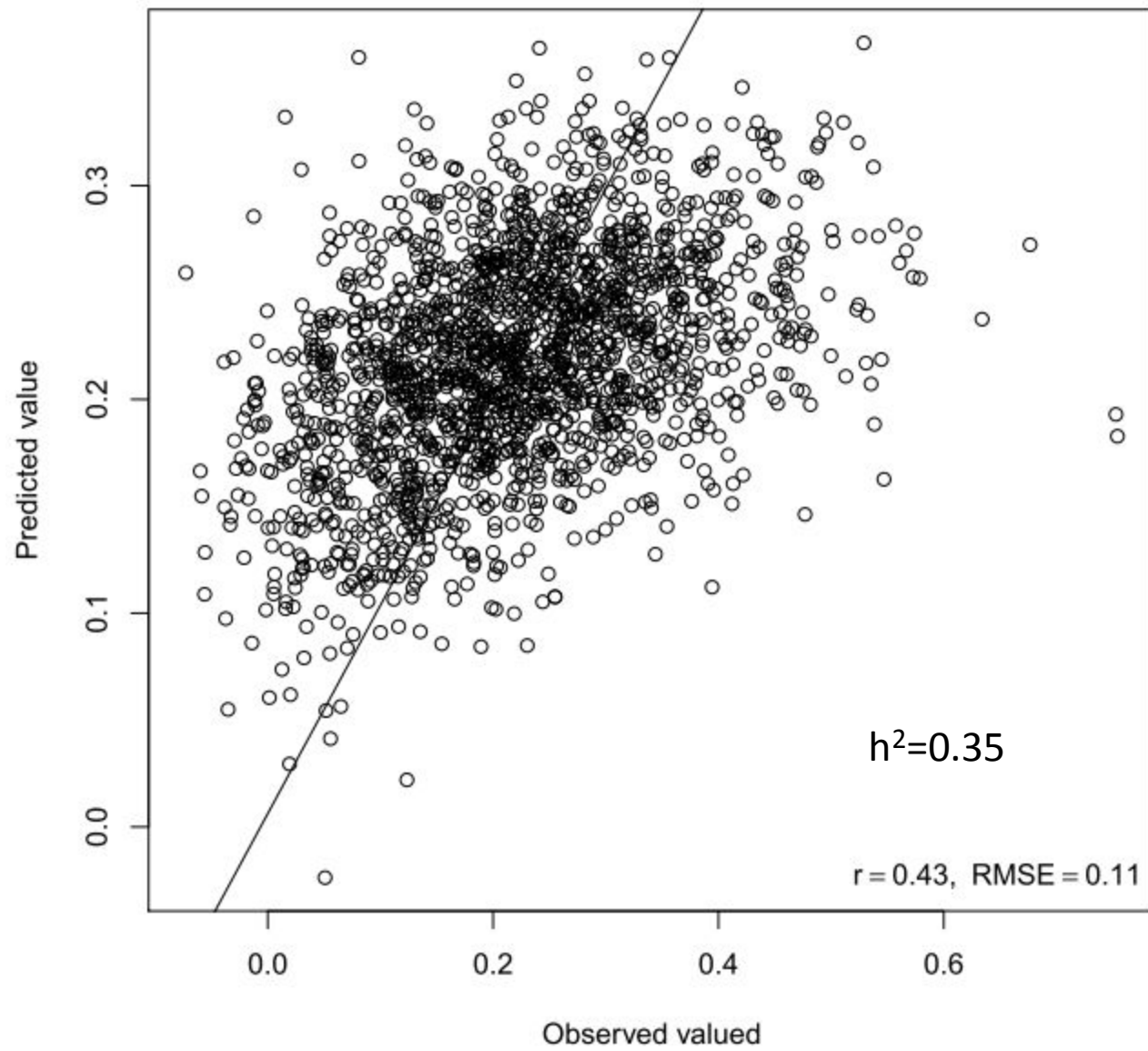
Free Threshing



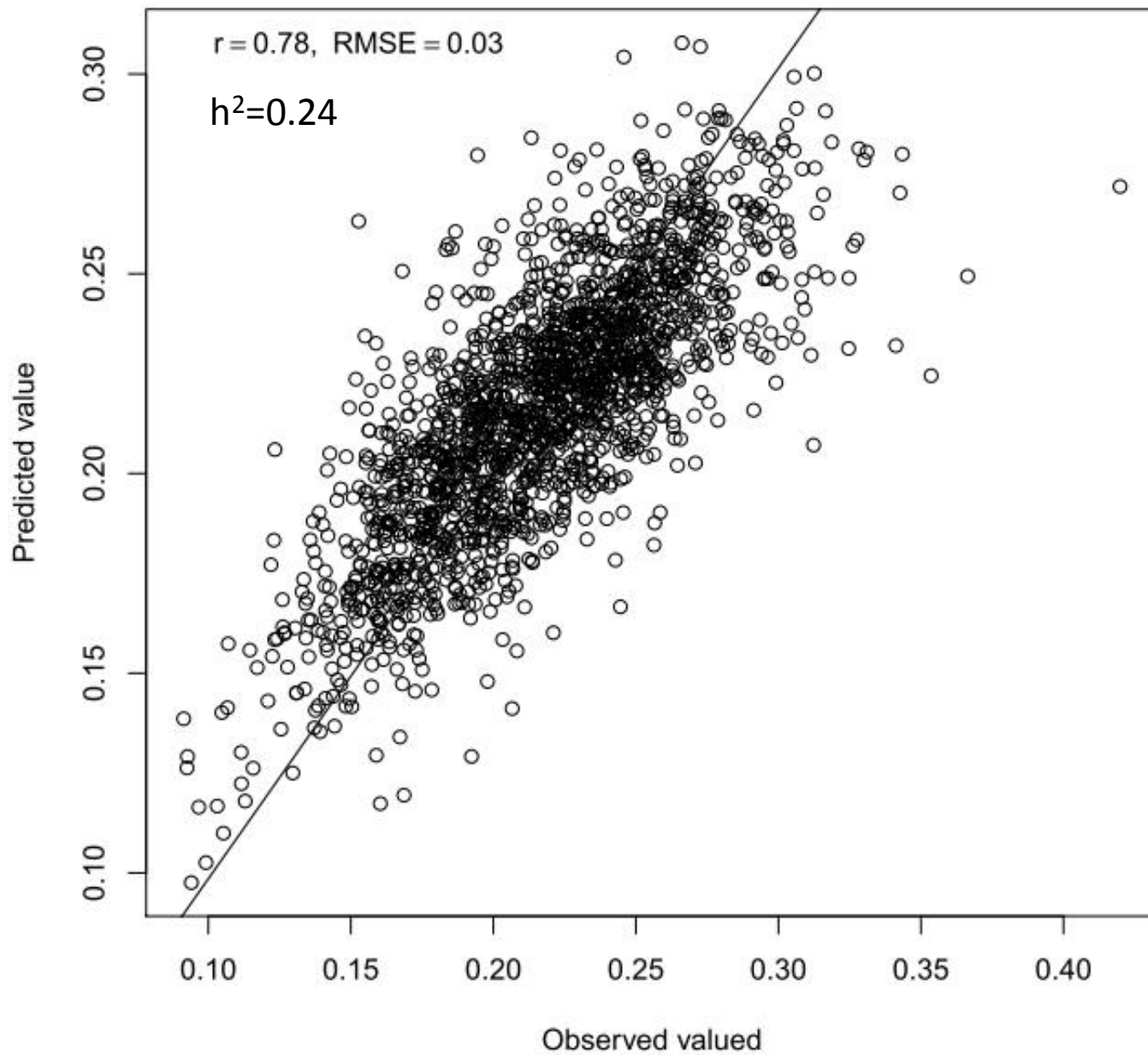
SDMG



Spike Yield



Percent Fertility

















Sydney Schiffner & Craig Sheaffer