# Introduction

Why we care about deleterious variants.  
Discuss results of Mezmouk 2014.  
We are extending this in three ways

* all deleterious SNPs not just coding
* genome-wide not just reduced representation
* using GS to test whether they improve prediction

# Methods

## Samples and Field Stuff

samples, diallel construction, field methods

## Phenotype analysis

heritability etc.

## Sequencing

sequence methods, alignment, snp calling comparison of our SNPs to GBS, 55K, HM2

### IBD analysis

### Gerp analysis

## Association tests

### GWAS

### GS

# Results

## Genotypes

SNPs, accuracy, IBD analysis

## Phenotypes

* percent heterosis, heritability
* main figure: boxplot of heterosis? per parent?

## GWAS

* Haplotype GWAS results = overdominance
* SNPs within show dominance
* enrichment for GERP??
* ≥1 main figure

## Cross-validation

* Gerp additive
* Gerp dominant
* ≥1 main figure

# Discussion

* how do results match with heritability and heterosis?
* do we support deleterious model of Mezmouk et al.?