# Permuted Phenotypes

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I did two sets of permuted phenotype analyses for the nine panicle trait * environment combinations.

In the first, I resampled each phenotype separately. This broke up the correlation structure *within* PLANT_ID and removed the genetic signal.

In the second, I kept the correlation structure *within* PLANT_ID. That is, I resampled which PLANT_ID was assigned each set of nine panicle trait * environment phenotypes. This removed the genetic signal but not the correlation structure of traits for each PLANT_ID.

I ran my typical GWAS & then mash on these sets of permuted phenotypes. I ran mash including both the BLUPs (so there was some real signal) and two sets of permuted phenotypes, permuted as above.

When the correlation structure in the data was removed, here was what the covariance matrix loadings looked like:
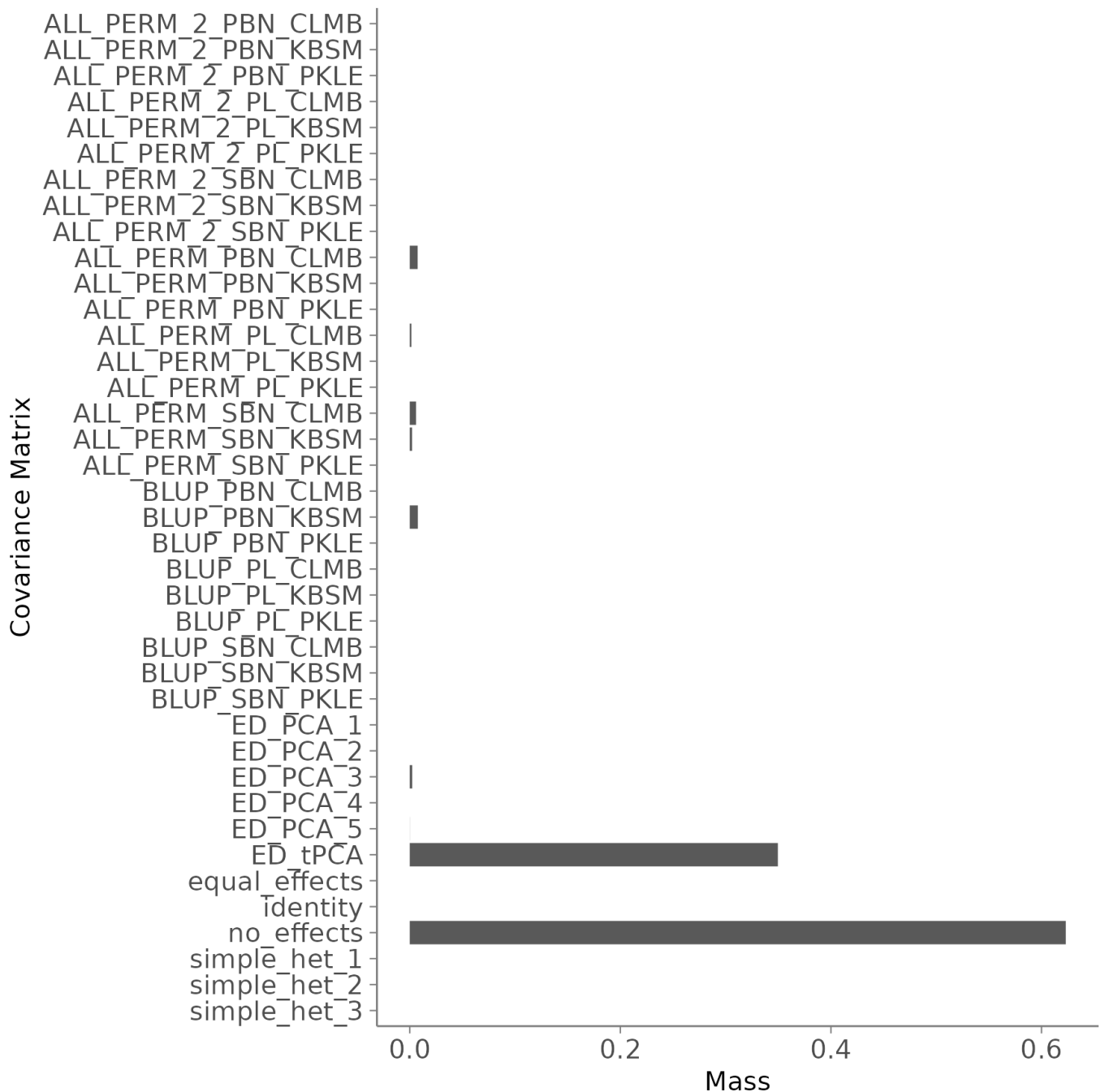
Lots of weight on the tPCA matrix, and none on the equal effects matrix.

When the data was permuted but the correlation structure in the data was kept, here was what the covariance matrix loadings looked like:
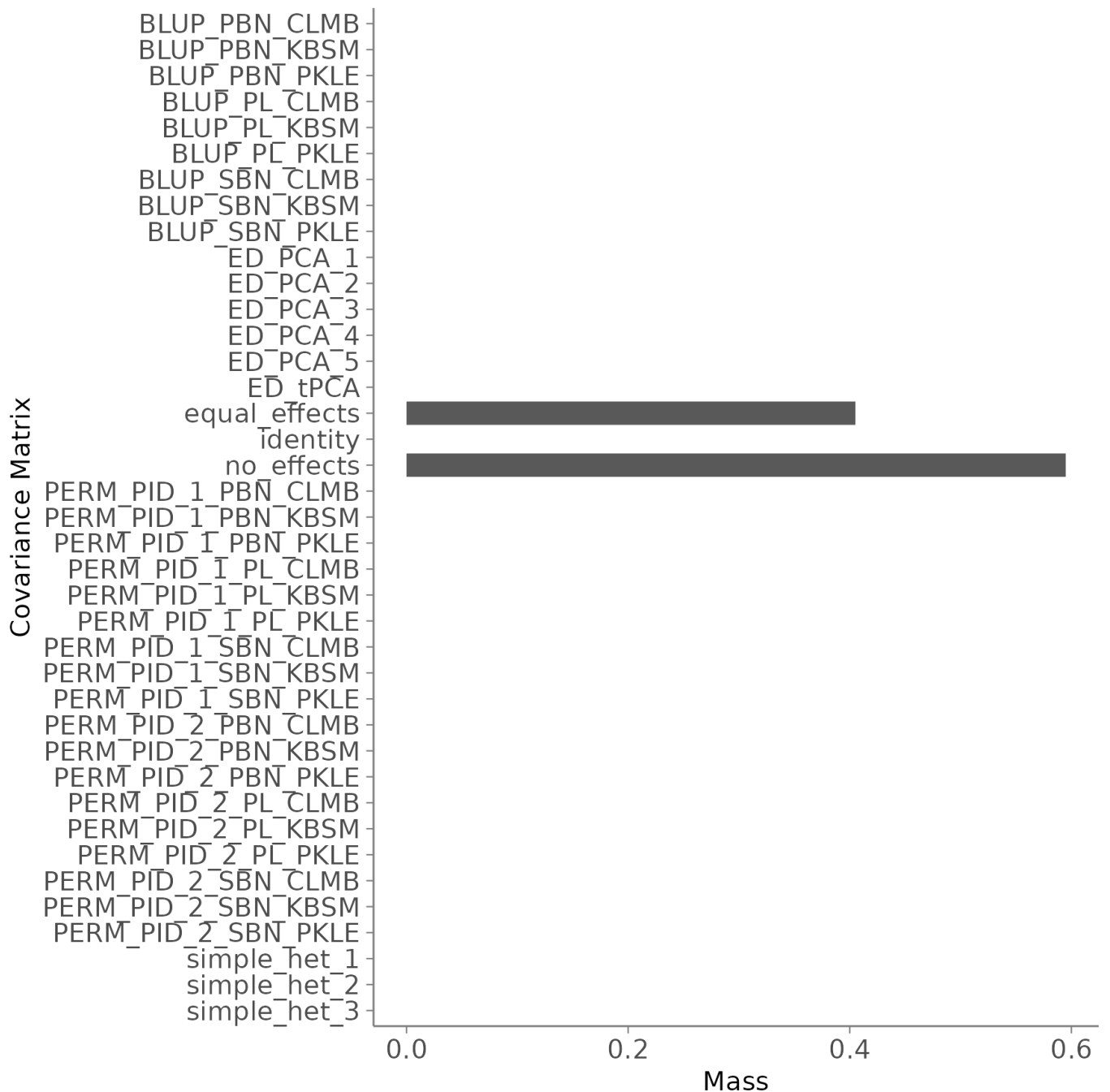
These are extremely similar to what we got for the panicle paper. Lots of weight on teh equal effects matrix.

tl;dr This seems unequivocal to me that it is the correlation structure of the phenotypes within PLANT_ID itself that is putting lots of weight on the equal effects matrix.

I don't think this should be a cause for concern unless you think that phenotypes for the same PLANT_ID should be uncorrelated.

Here are the effects for the top SNP estimated for the permutation that breaks up within-individual correlation:

Chr03K_57804124
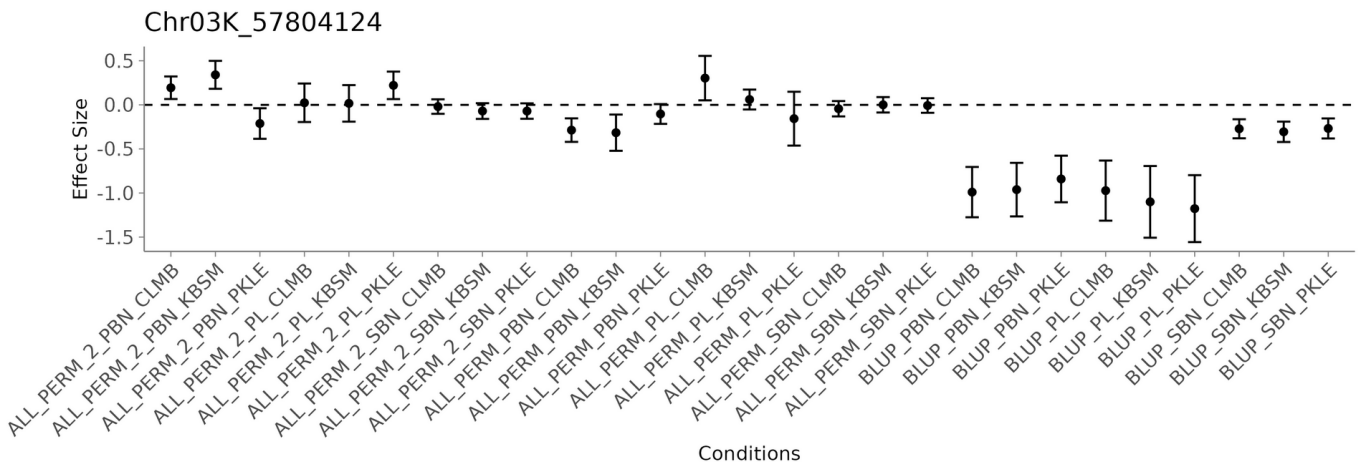
Very few PERM phenotypes are significant, but the BLUP phenotypes follow the pattern that we saw in the panicle paper for the phenotypes, aka larger effects for PBN & PL and smaller effects of the same sign for SBN.

Here is the correlation structure for the ED_tPCA that has high loadings for the no within-individual correlation permutation:

ED_tPCA
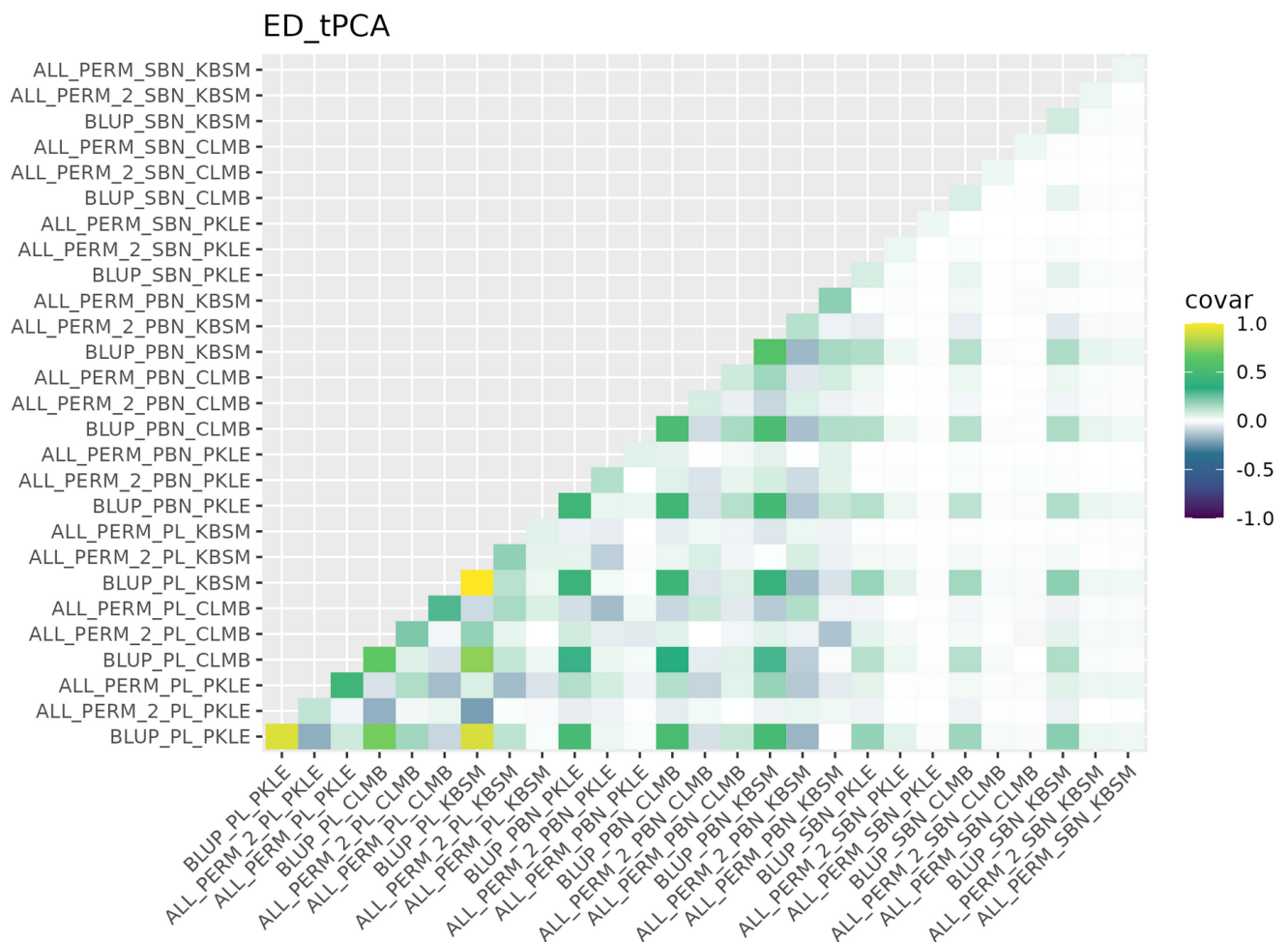
It may be hard to see, but the BLUP phenotypes are the only ones that are highly correlated here.

And, this shouldn't surprise you, but here are the effects for the top SNP estimated for the permutation that does not break up within-individual correlation:

Chr02K_66063954
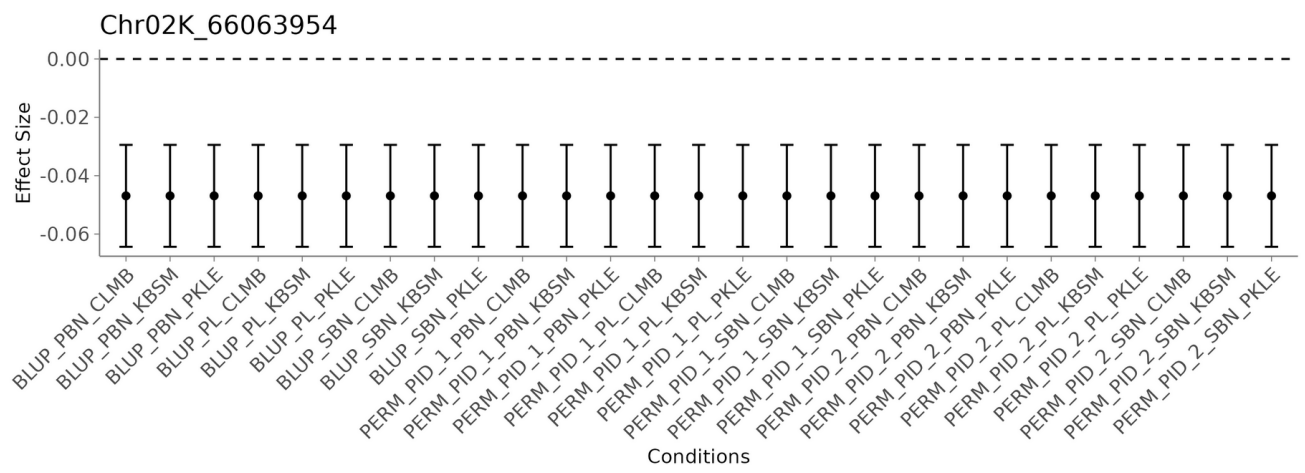
All the BLUPs and the permuted phenotypes have the same estimated effects.