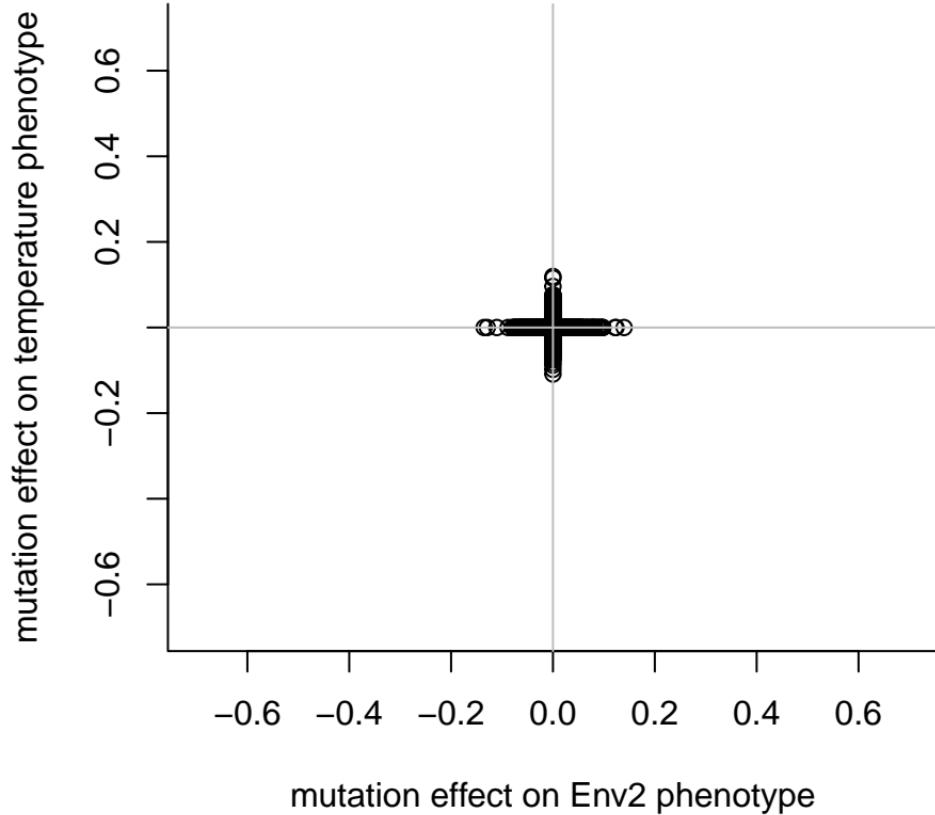
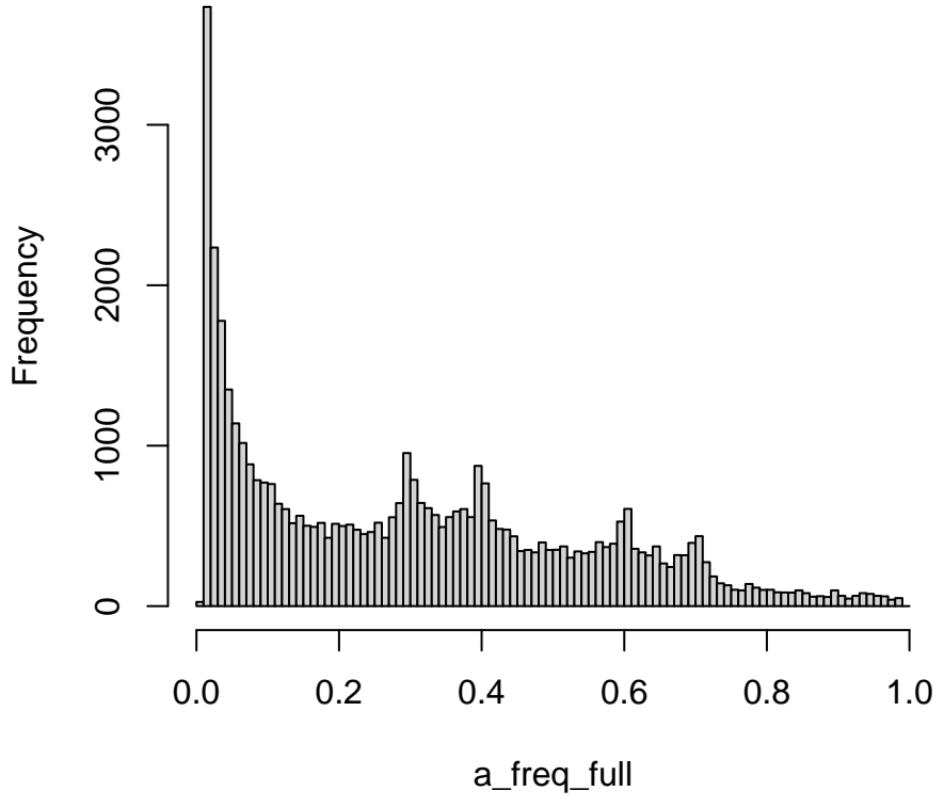


highly-polygenic\_2-trait-no-pleiotropy-equal-S\_SS-Clines\_N-equal\_m\_breaks  
1231116



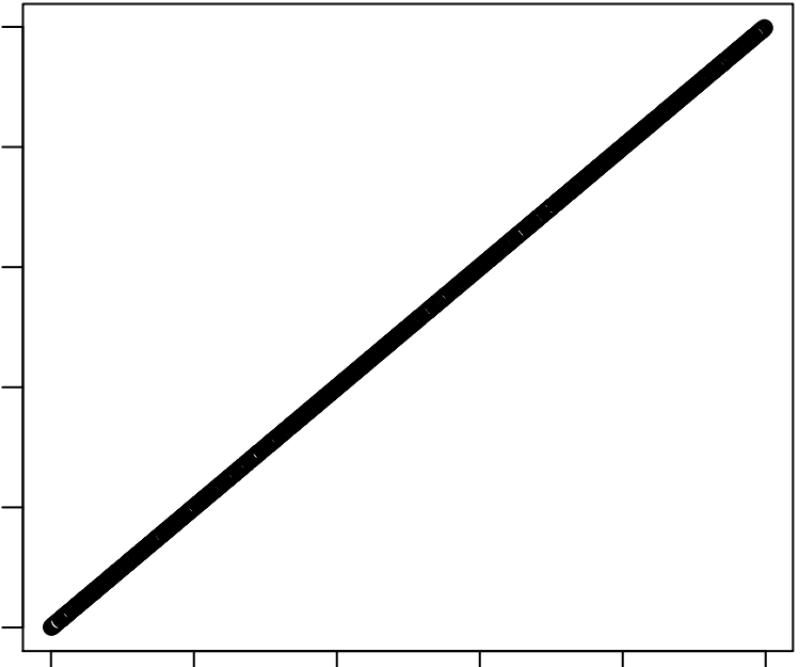
## Histogram of a\_freq\_full

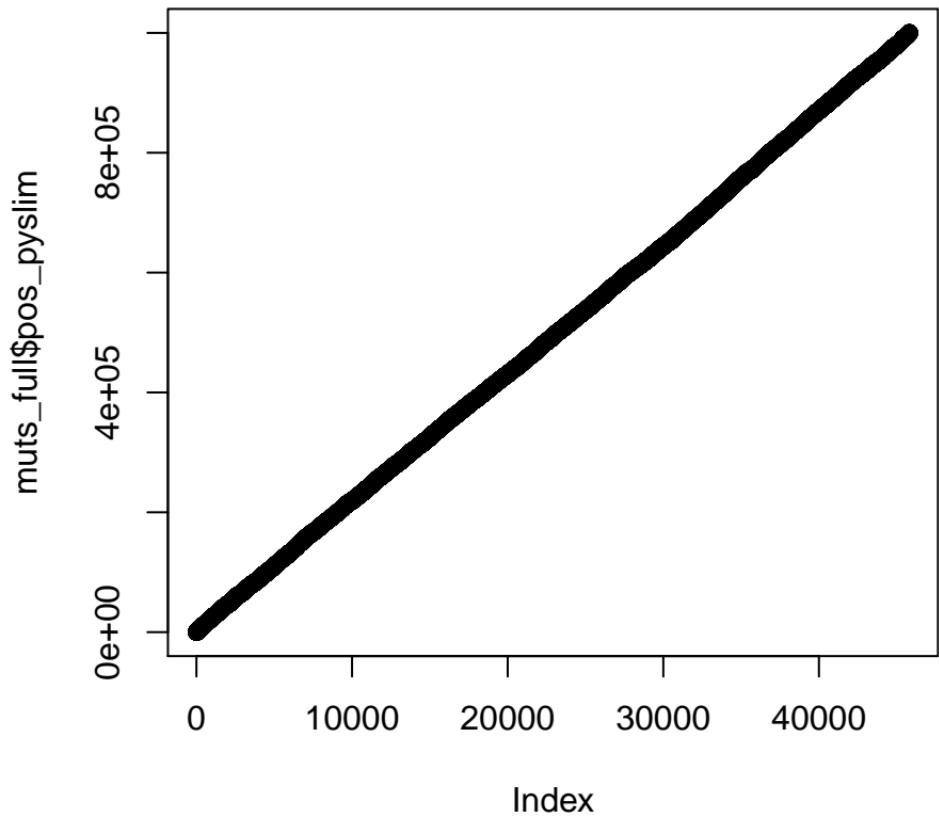


indPhen\_df\$indID[which(indPhen\_df\$subset)]

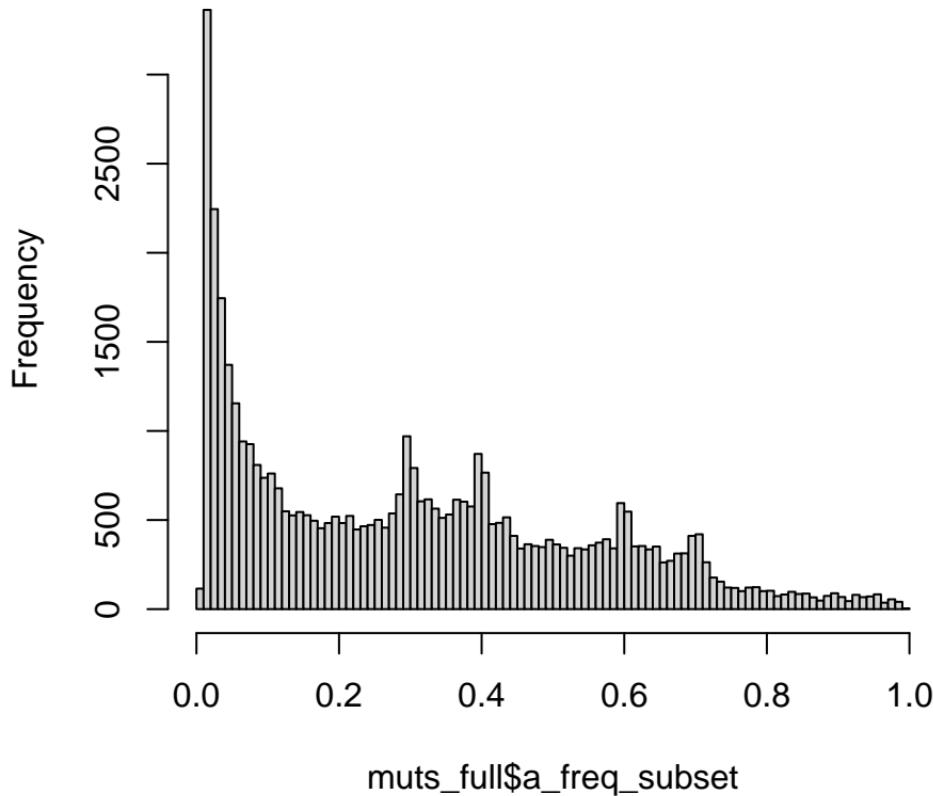
0 2000 4000 6000 8000 10000

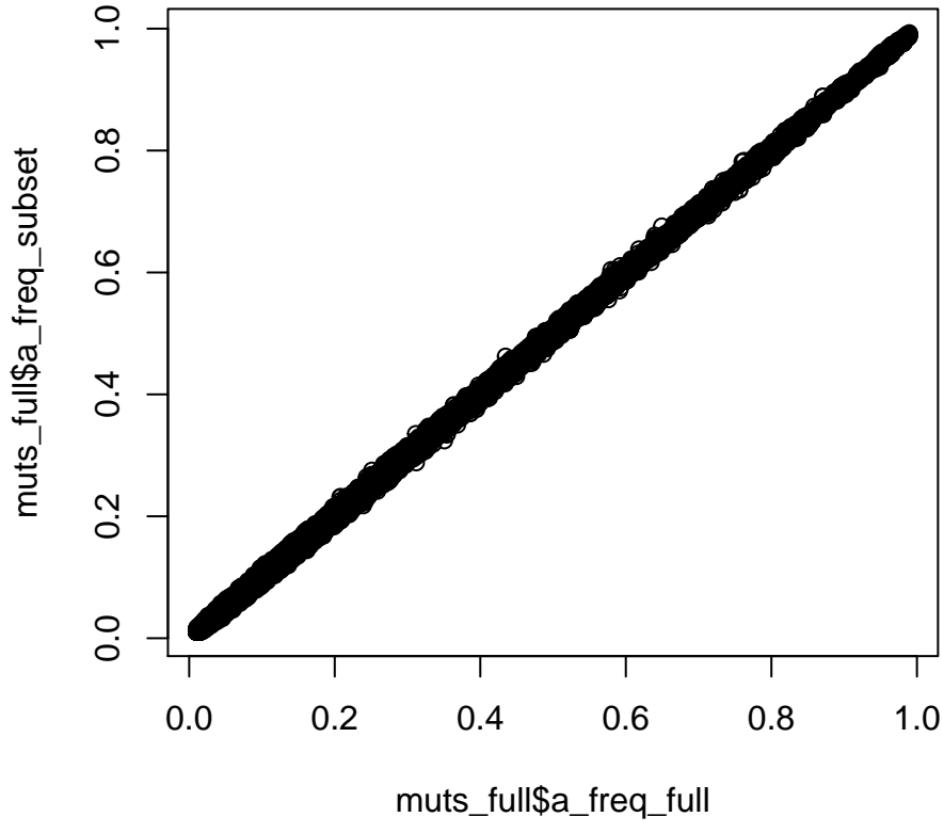
colnames(G\_full\_subset)



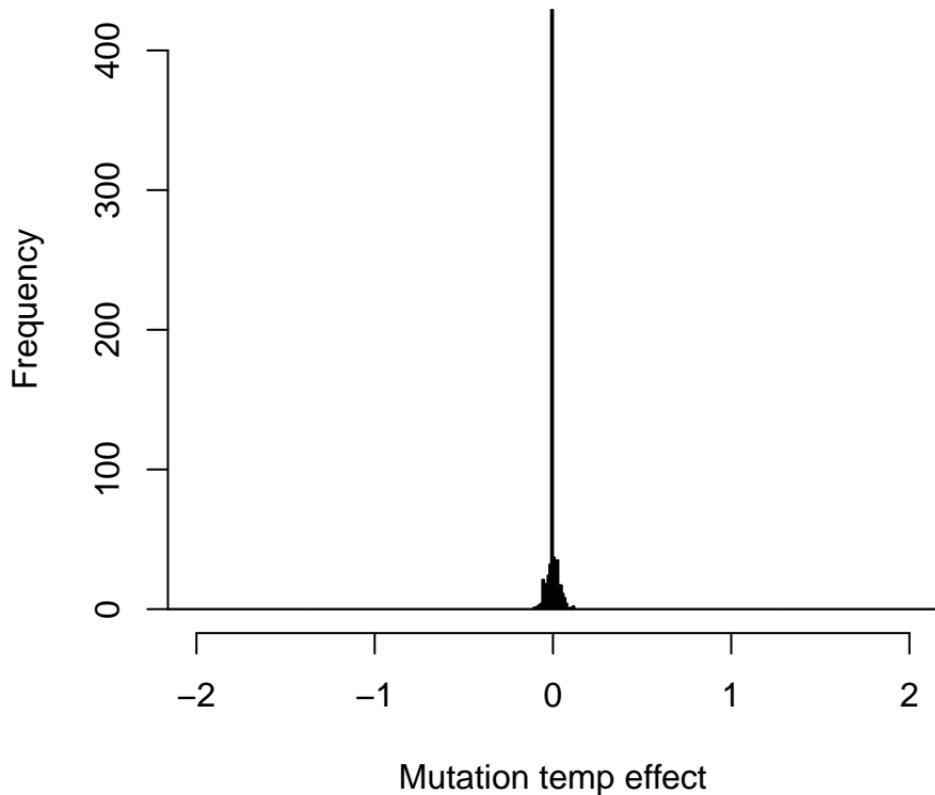


## Histogram of muts\_full\$a\_freq\_subset

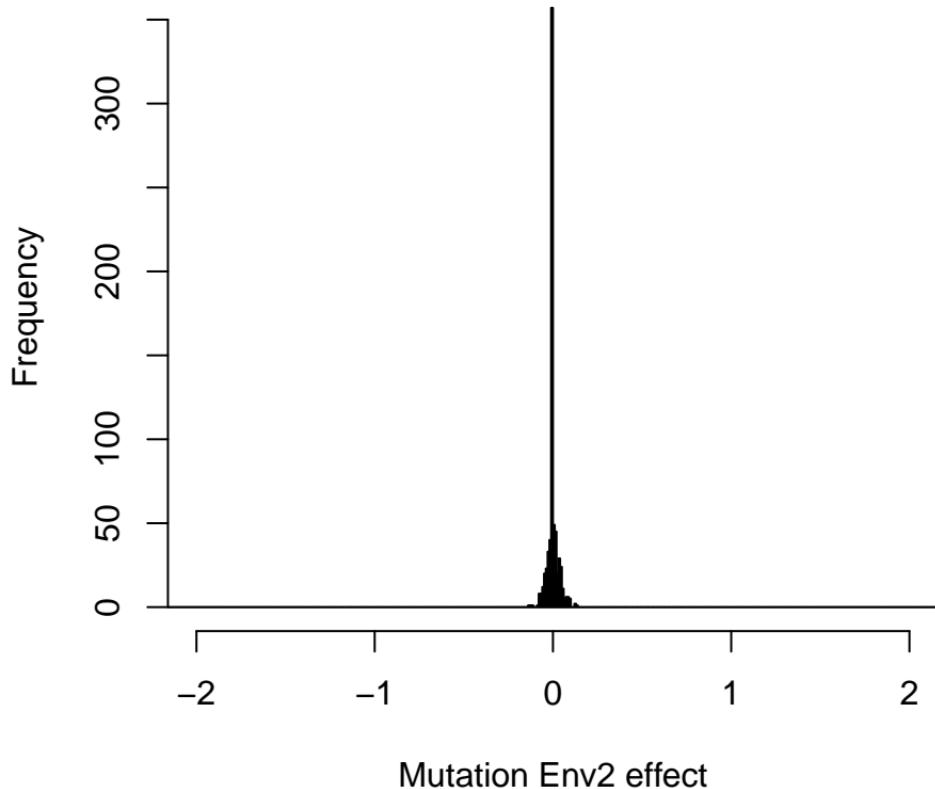




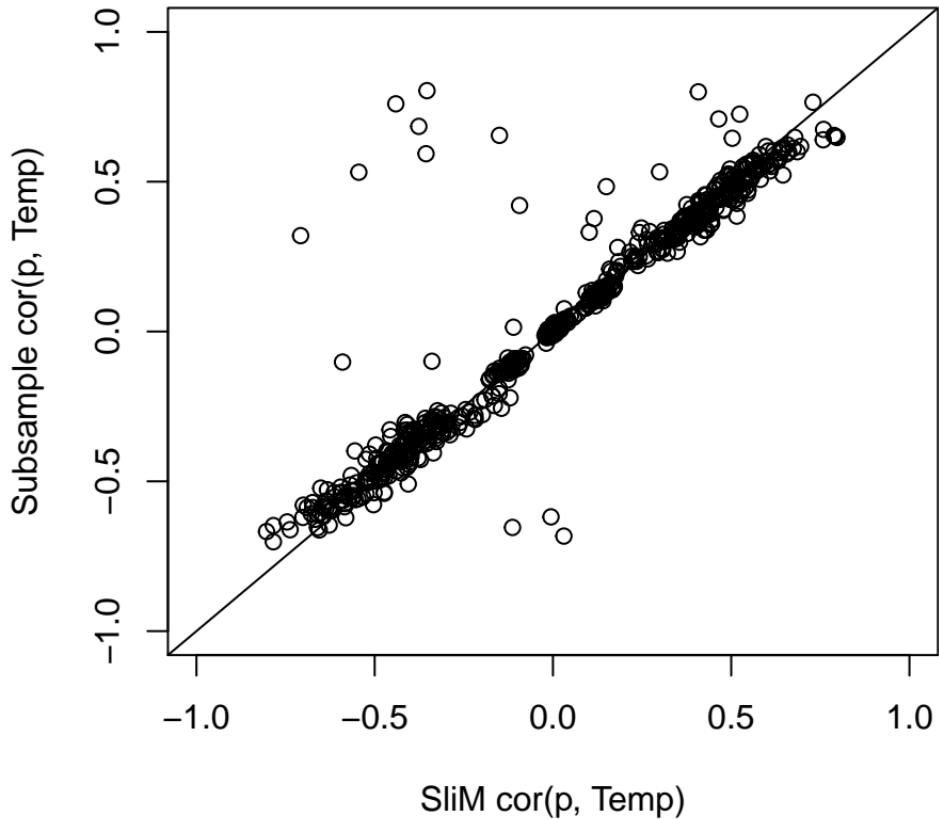
highly-polygenic\_2-trait-no-pleiotropy-equal-S\_SS-Clines\_N-equal\_m\_breaks  
1231116



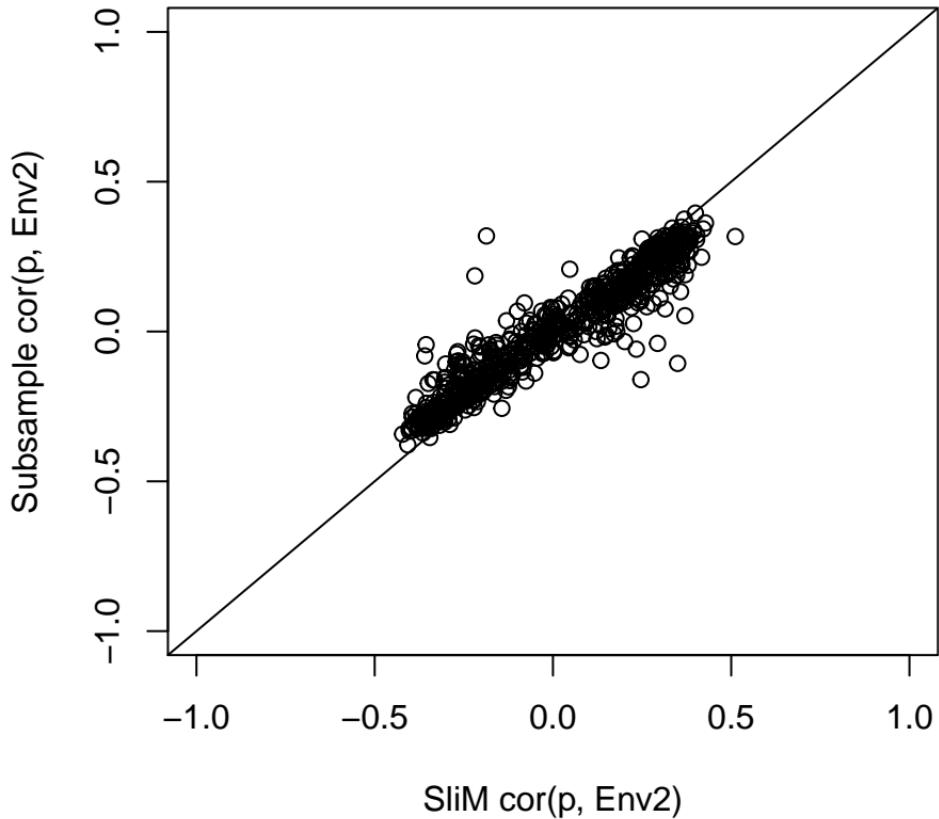
highly-polygenic\_2-trait-no-pleiotropy-equal-S\_SS-Clines\_N-equal\_m\_breaks  
1231116



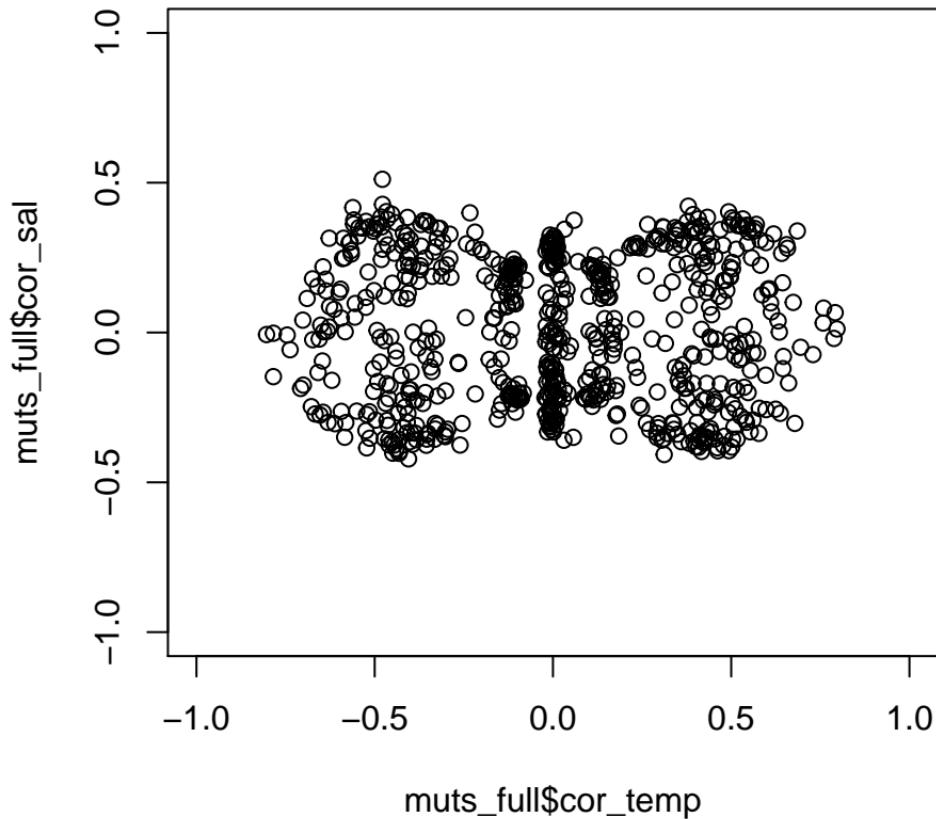
genic\_2-trait-no-pleiotropy-equal-S\_SS-Clines\_N-  
1231116



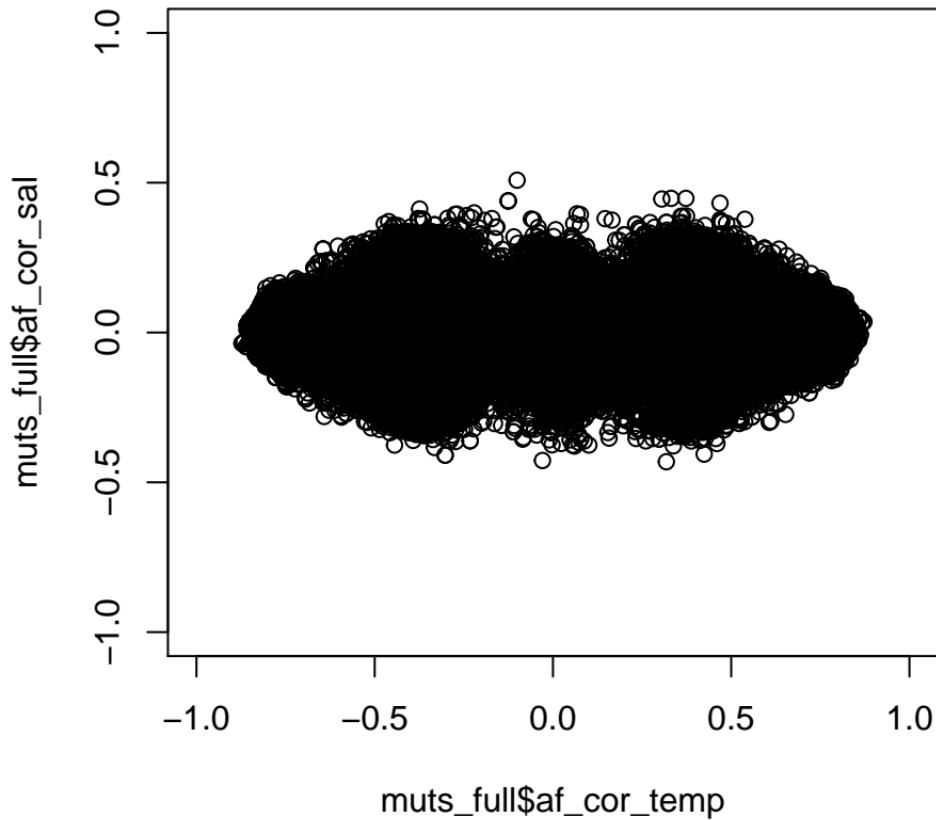
genic\_2-trait-no-pleiotropy-equal-S\_SS-Clines\_N-  
1231116



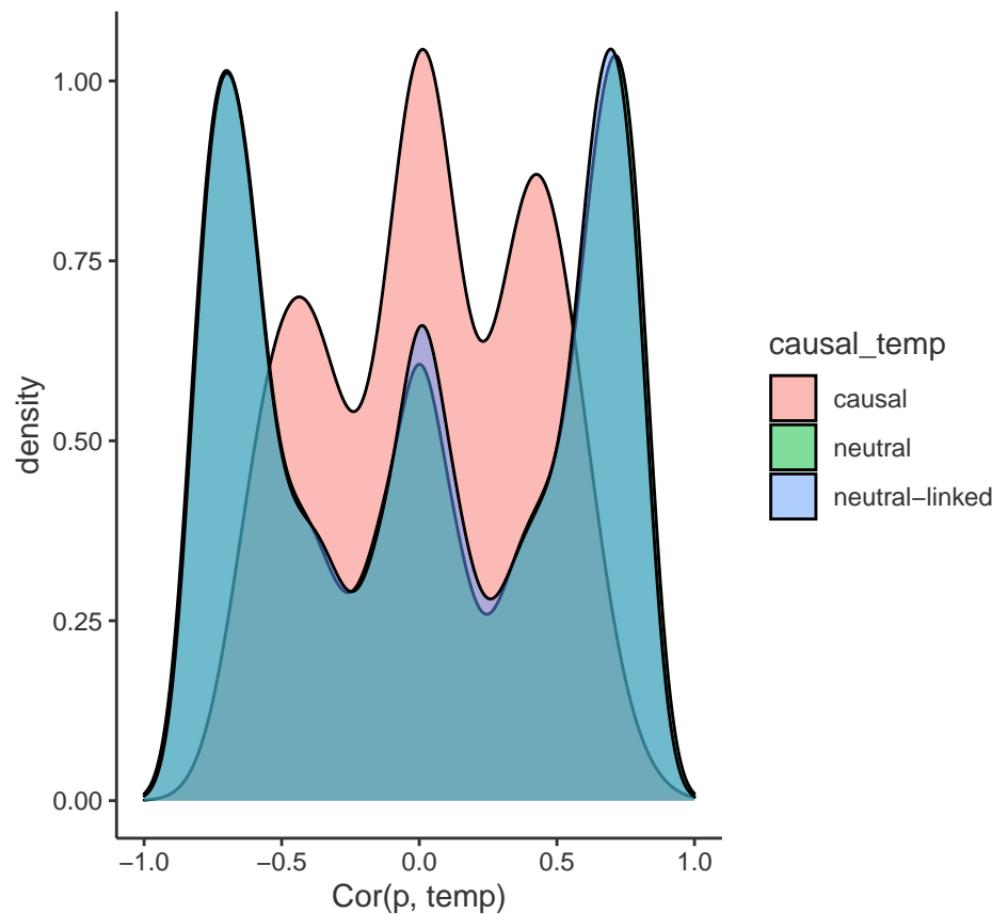
## SiM Correlation (AF, ENV) all samples



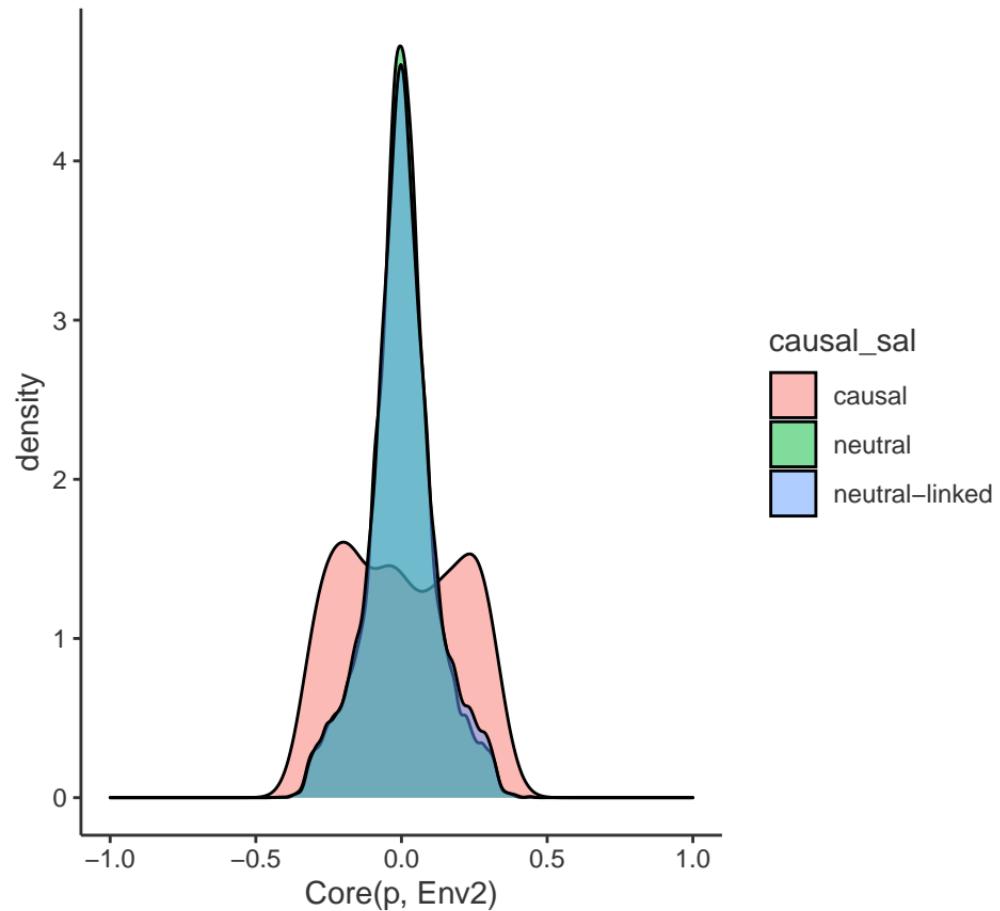
## Subsample Correlation (AF, ENV) all samples



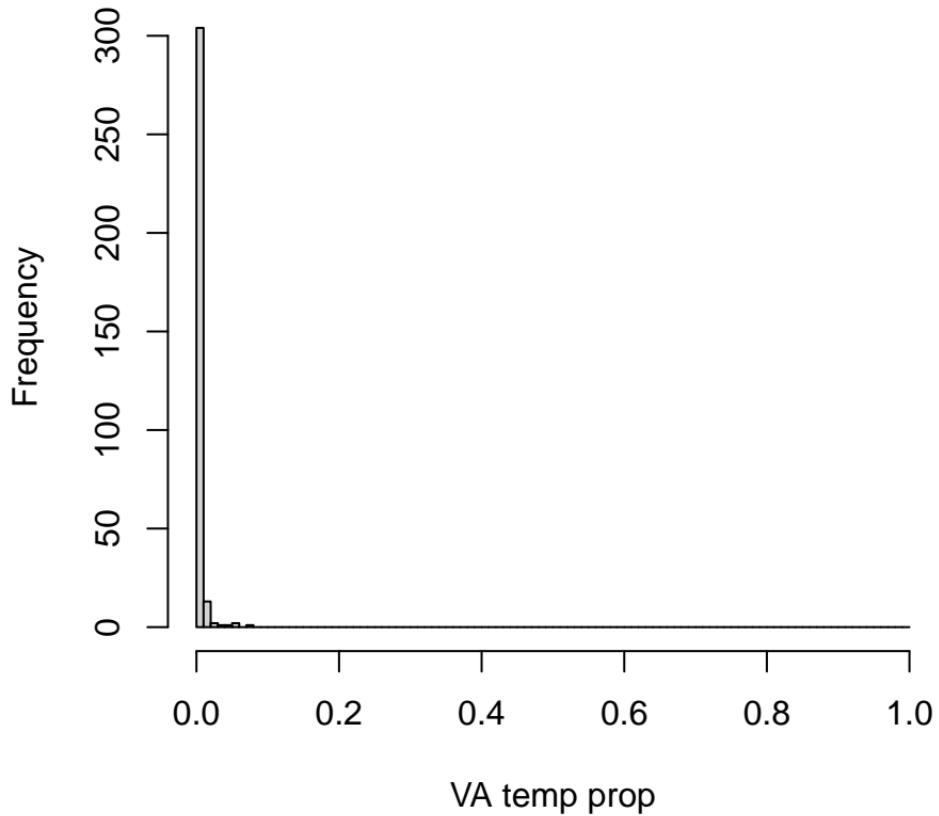
highly-polygenic\_2-trait-no-pleiotropy-equal-S\_SS-  
1231116



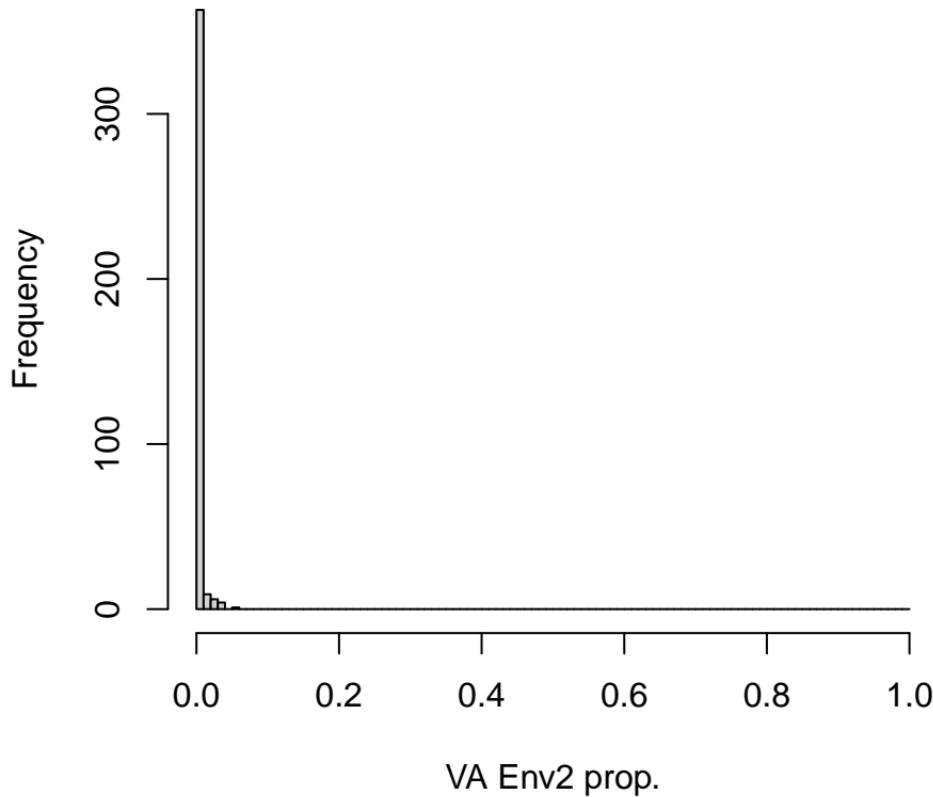
highly-polygenic\_2-trait-no-pleiotropy-equal-S\_SS-C  
1231116



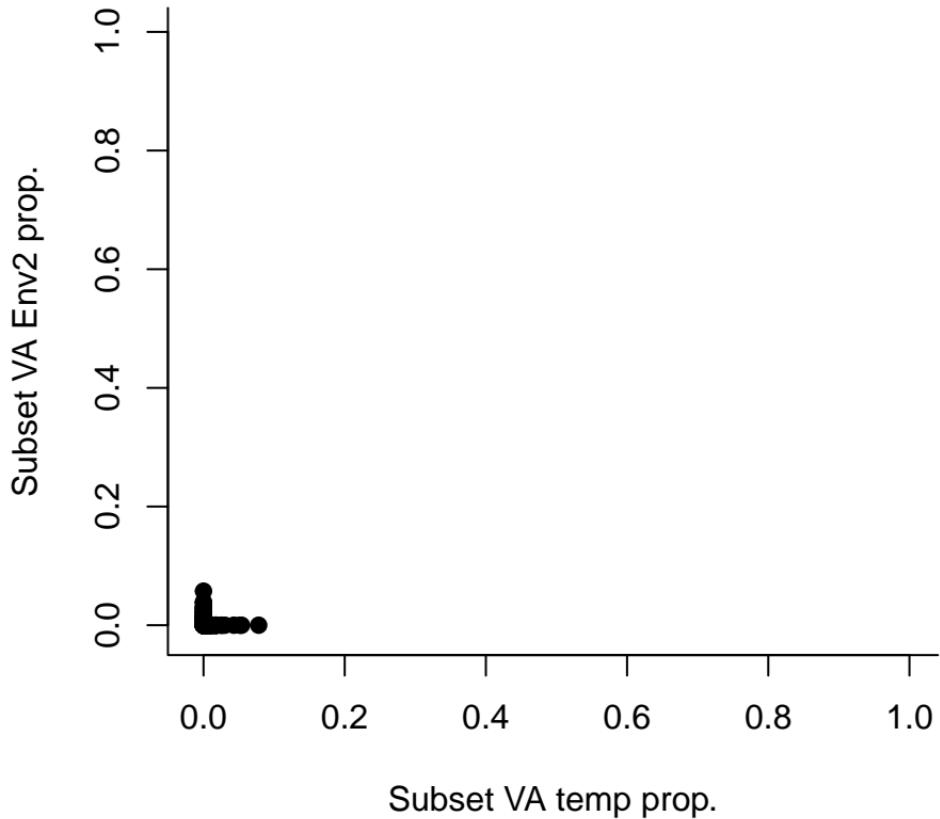
genic\_2-trait-no-pleiotropy-equal-S\_SS-Clines\_N-  
1231116



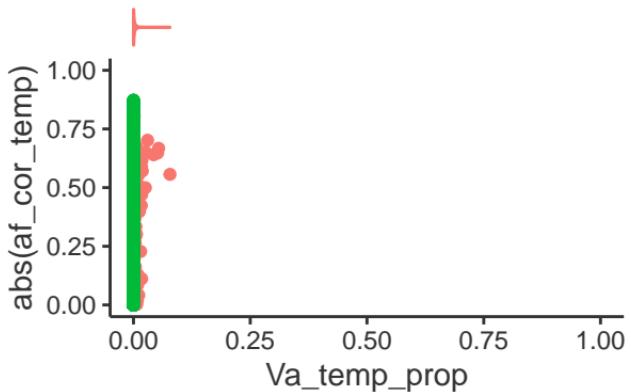
genic\_2-trait-no-pleiotropy-equal-S\_SS-Clines\_N-  
1231116



genic\_2-trait-no-pleiotropy-equal-S\_SS-Clines\_N-  
1231116



highly-polygenic\_2-trait-no-pl  
1231116

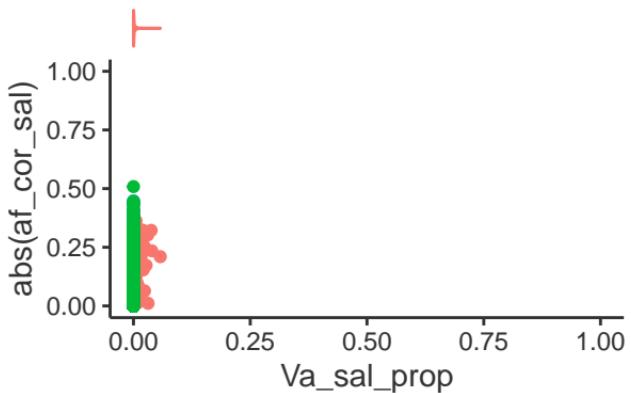


causal\_temp

- causal
- neutral
- neutral-linked



highly-polygenic\_2-trait-no-pl  
1231116



causal\_sal

- causal
- neutral
- neutral-linked

