

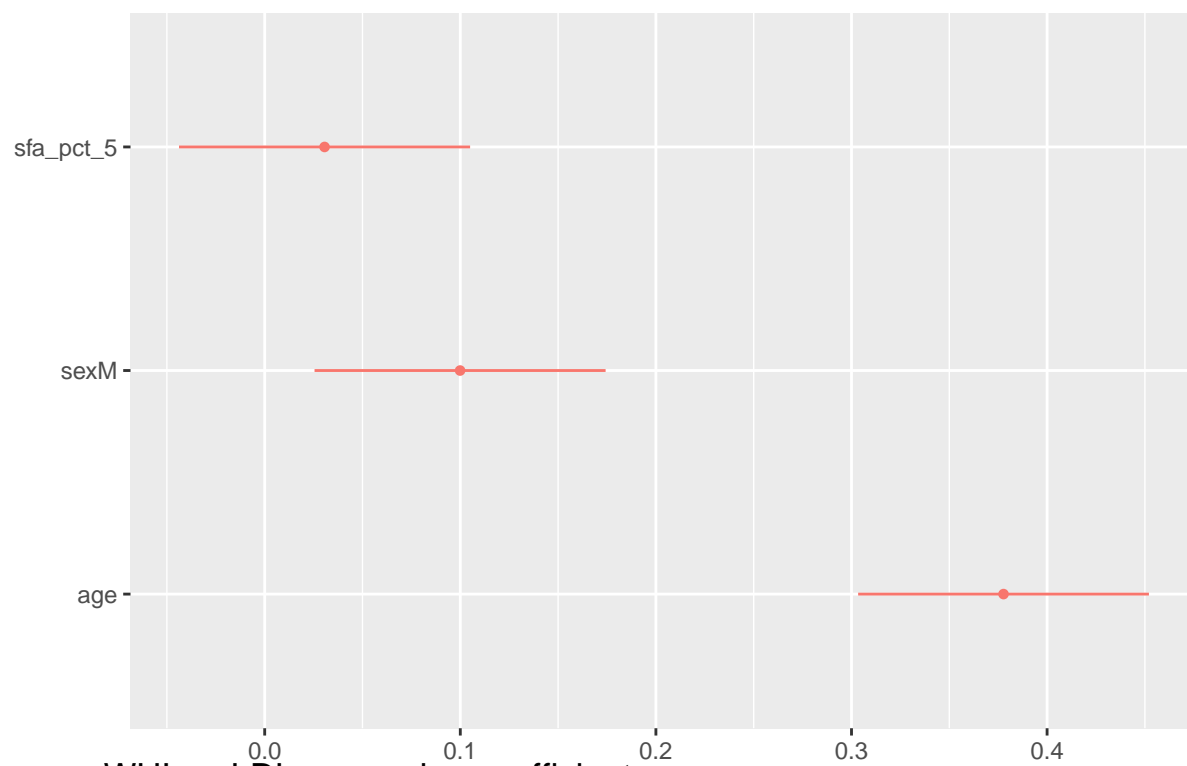
GWIS w/ SFA for LDL-C

Diet-phenotype investigation

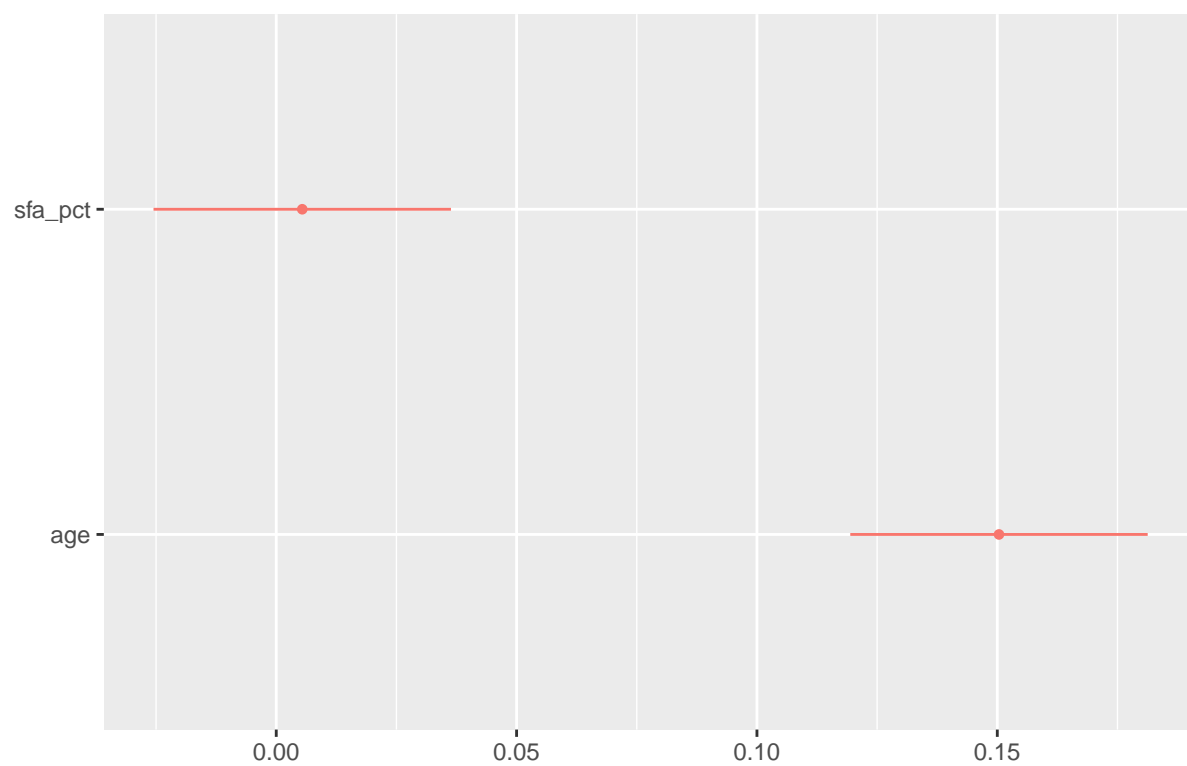
	FHS	WHI
N	3219.0	2.98e+04
% female	53.2	1.00e+02
% white	1.0	5.83e-01
% taking statins	7.0	1.22e+01
Median SFA intake (grams)	NA	1.81e+01
Median LDL (mg/dL)	125.0	1.46e+02

First, check out the basic behavior of SFA (specifically, % energy from SFA) with respect to LDL cholesterol levels with only basic confounder adjustment (statin users have been removed).

FHS -- LDL regression coefficients



WHI -- LDL regression coefficients



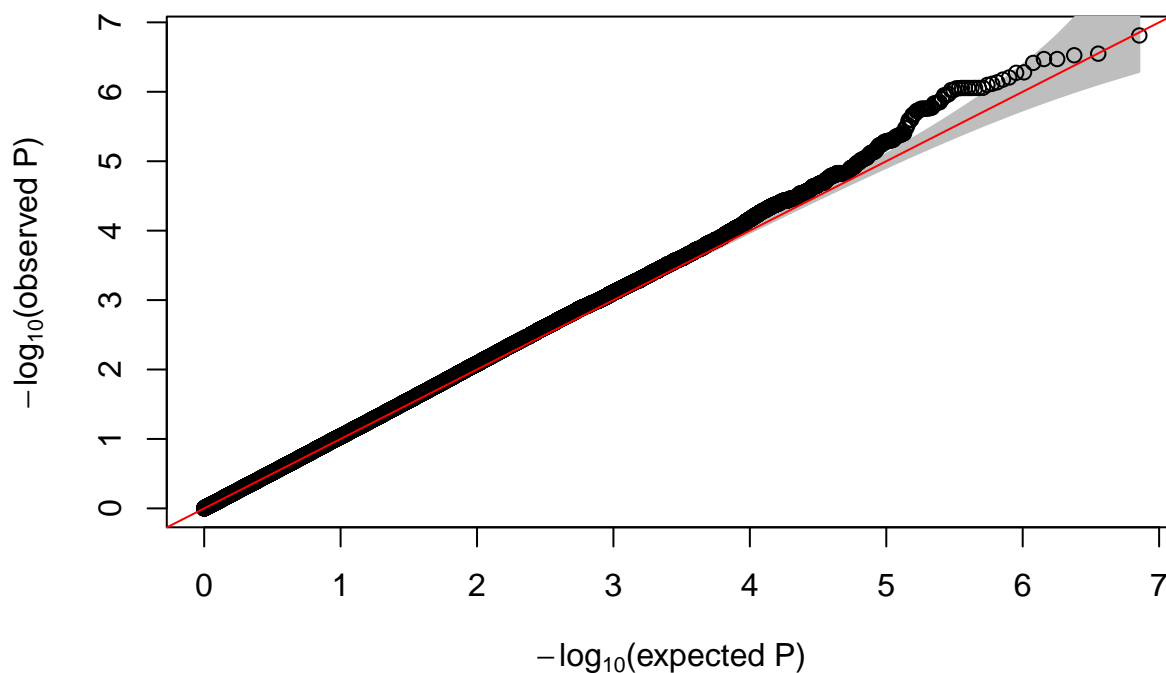
Genome-wide interaction study

The intent of the preliminary analysis is to discover specific SNPs that modify the relationship between SFA intake and LDL-C levels. A meta-analysis of FHS Offspring and WHI will be performed to serve as the discovery set.

```
## Warning in rbind(names(probs), probs_f): number of columns of result is not
## a multiple of vector length (arg 1)

## Warning: 84 parsing failures.
## row # A tibble: 5 x 5 col      row    col    expected actual      file expected    <int> <chr>
## ... .....
## See problems(...) for more details.
```

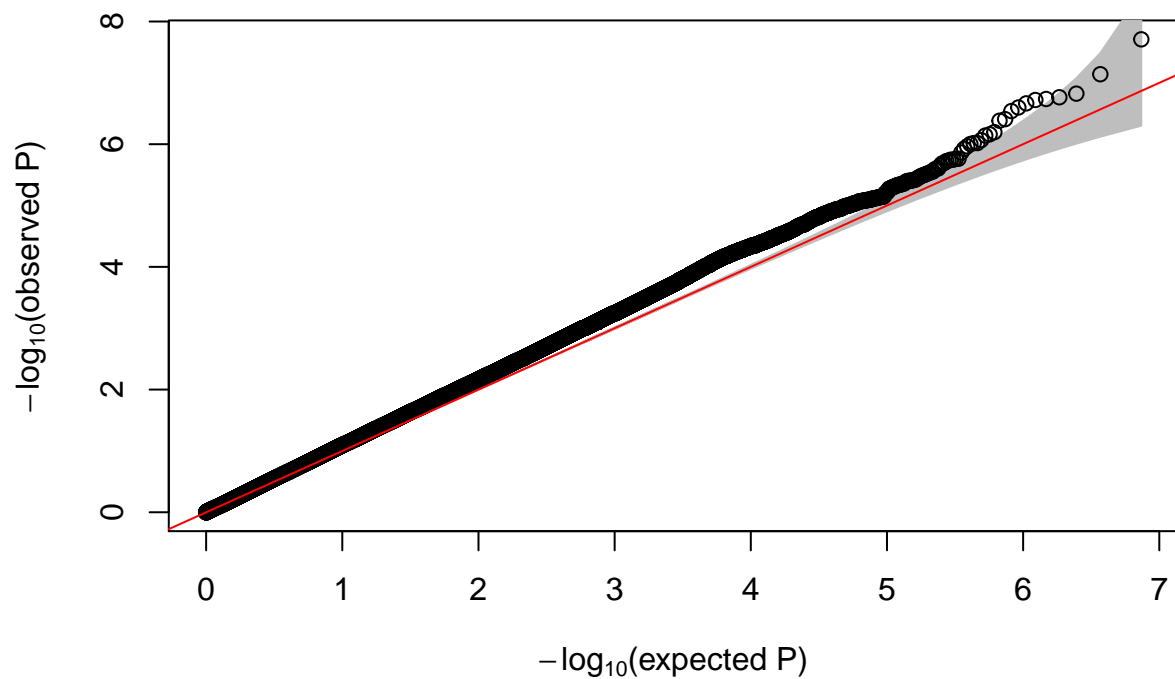
QQ-plot for interaction p-values (lambda =1.06)



```
## Warning in rbind(names(probs), probs_f): number of columns of result is not
## a multiple of vector length (arg 1)

## Warning: 84 parsing failures.
## row # A tibble: 5 x 5 col      row    col    expected actual      file expected    <int> <chr>
## ... .....
## See problems(...) for more details.
```

QQ-plot for interaction p-values (lambda =1.14581071802655)



##

For example usage please run: vignette('qqman')

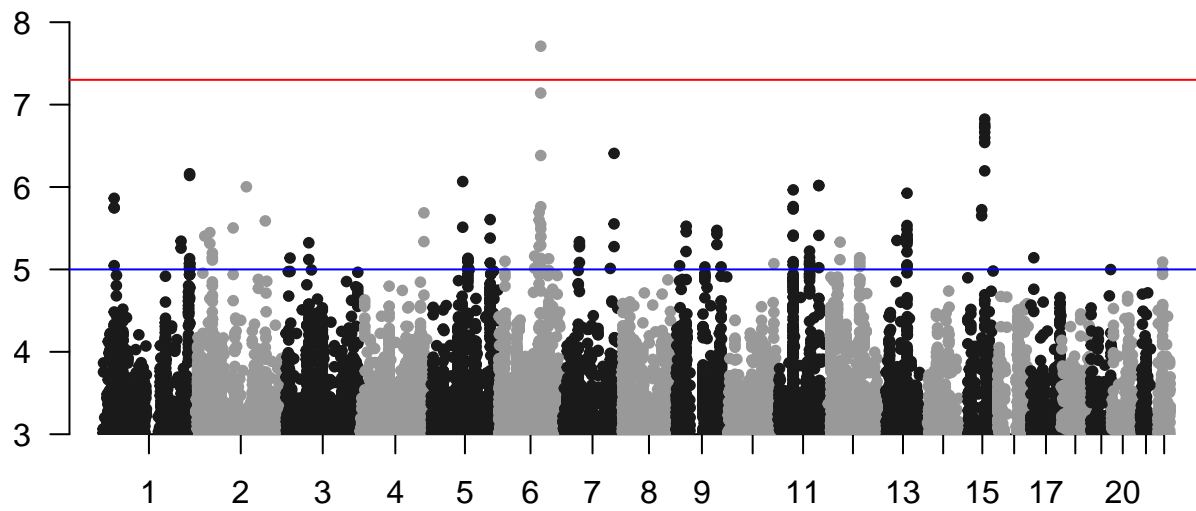
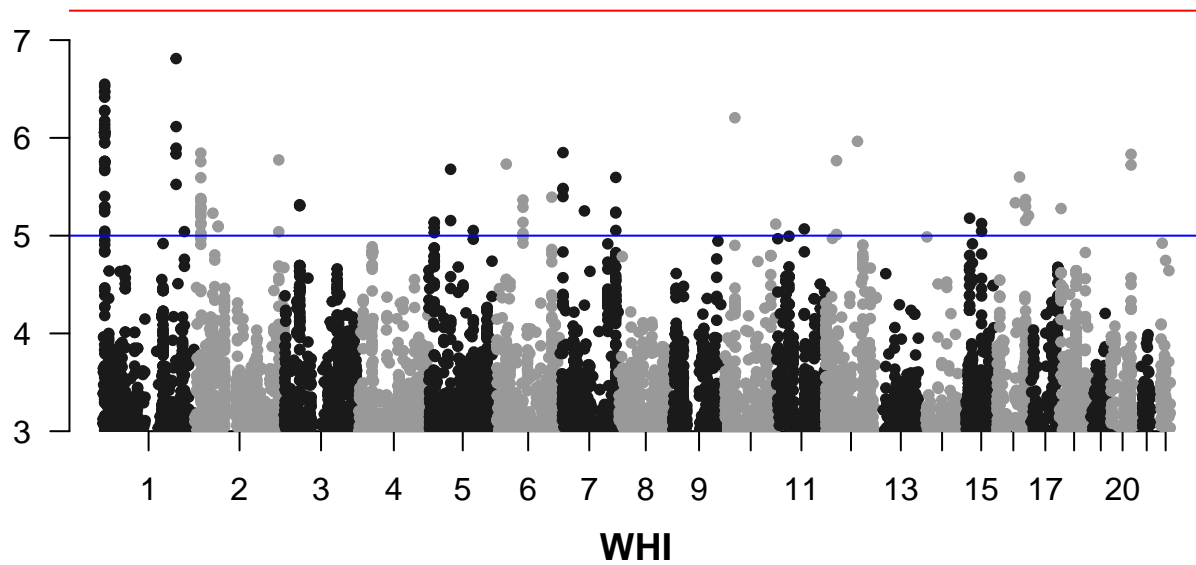
##

Citation appreciated but not required:

Turner, S.D. qqman: an R package for visualizing GWAS results using Q-Q and manhattan plots. *bioRxiv*

##

FHS



```
## Parsed with column specification:
## cols(
##   CHR = col_integer(),
##   BP = col_integer(),
##   SNP = col_character(),
##   A1 = col_character(),
##   P = col_double(),
##   BETA = col_double(),
##   I = col_double()
## )
```

Manhattan plot for meta-analysis

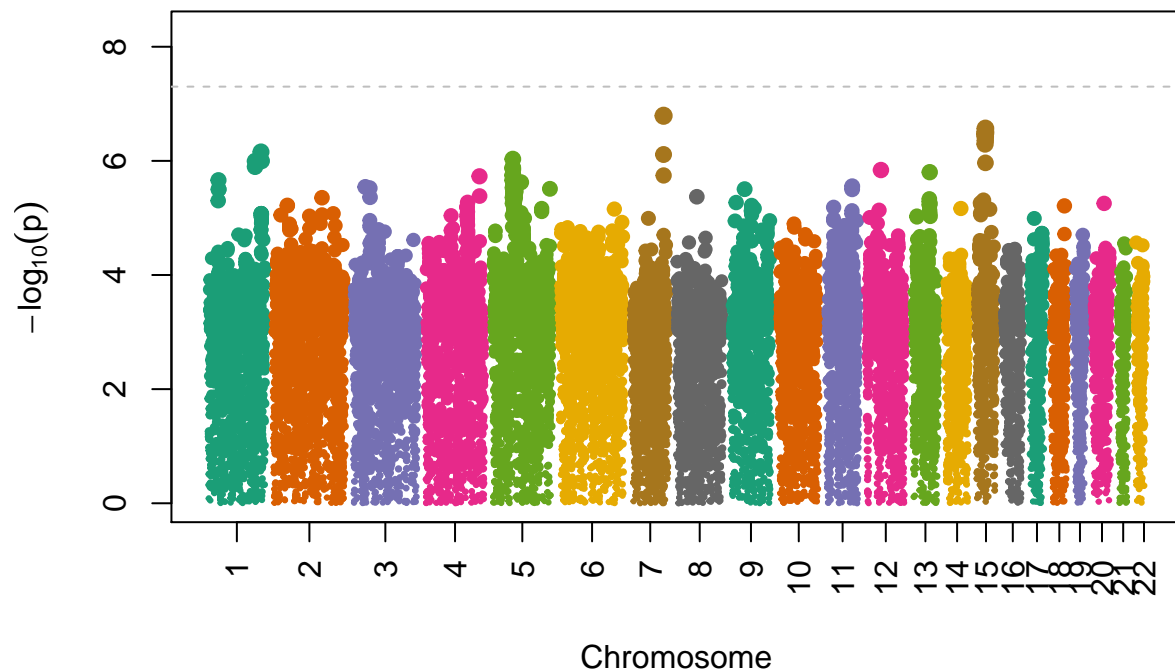


Table 2: Testing the APOA2 SNP as a positive control

CHR	BP	SNP	A1	P	BETA	I
1	1.61e+08	rs5082	G	0.04	27	0