

simple and multiple regression of the phenotype

Model specification

```
basic.model <- ANC ~ 1  
full.model <- ANC ~ sex + site + dose
```

PGRNseq GWAS

Simple Regression

```
seq.reg.results <- mlreg(basic.model, seq.geno, trait="gaussian")  
qqunif(seq.reg.results[, "P1df"])  
title('PGRNseq Simple Linear Regression GWAS')
```

Multiple Regression

```
seq.reg.results <- mlreg(full.model, seq.geno, trait="gaussian")  
qqunif(seq.reg.results[, "P1df"])  
title('PGRNseq Multiple Linear Regression GWAS')
```

Exome chip GWAS

Simple Regression

```
exome.reg.results <- mlreg(basic.model, exome.geno, trait="gaussian")  
qqunif(exome.reg.results[, "P1df"])  
title('Exome chip Simple Linear Regression GWAS')
```

Multiple Regression

```
exome.reg.results <- mlreg(full.model, exome.geno, trait="gaussian")  
qqunif(seq.reg.results[, "P1df"])  
title('Exome Chip Multiple Linear Regression')
```

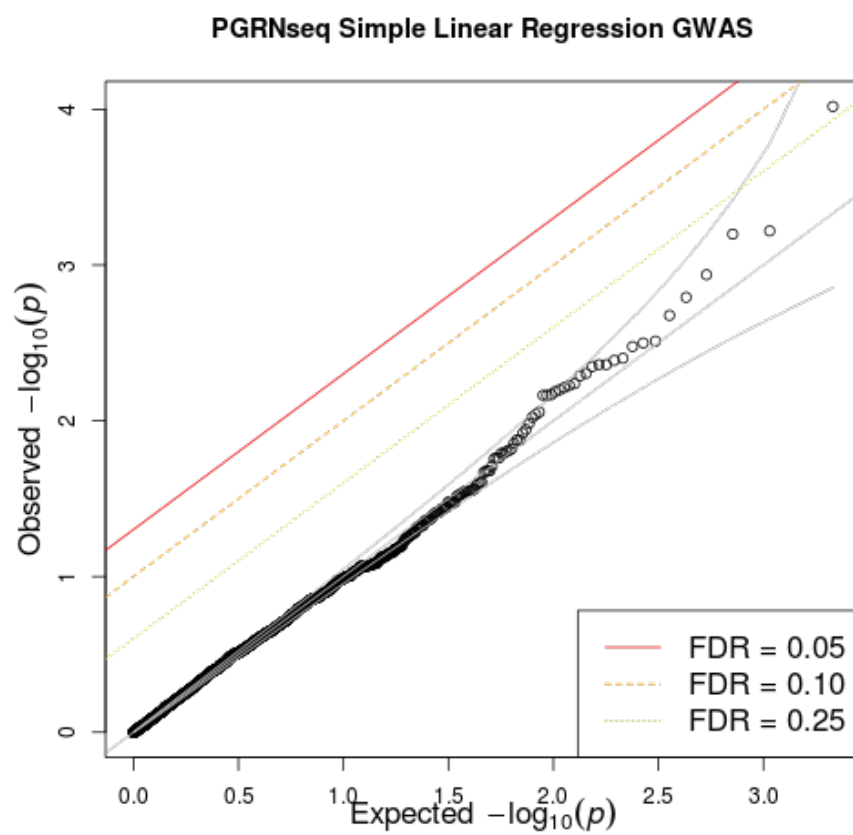


Figure 1: plot of chunk seq_simple_regression

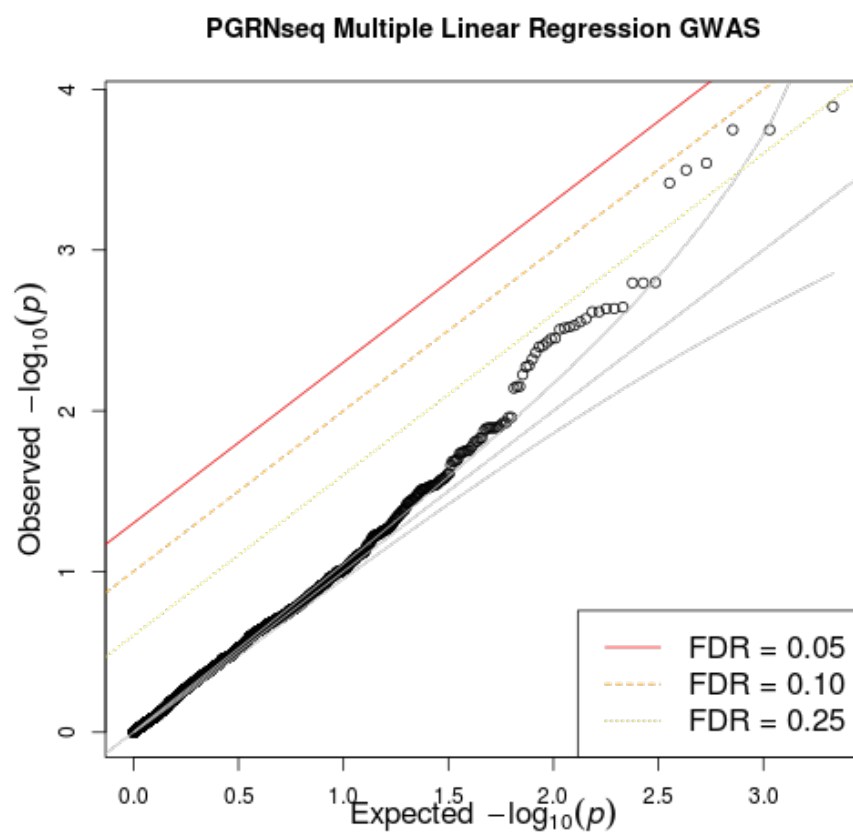


Figure 2: plot of chunk seq_multiple_regression

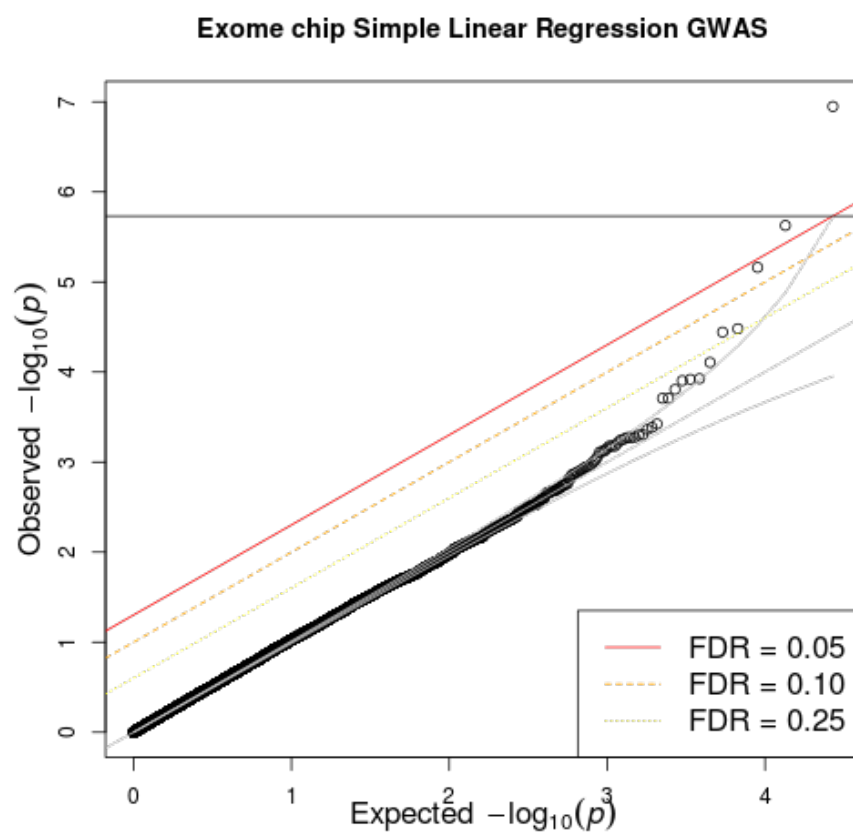


Figure 3: plot of chunk exome_simple_regression

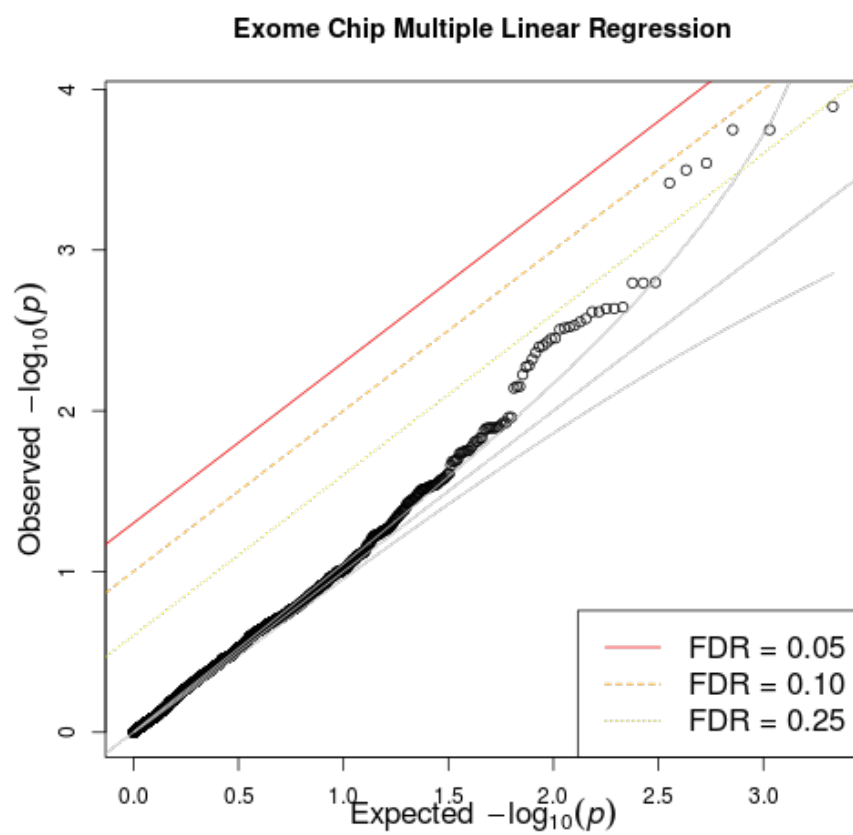


Figure 4: plot of chunk exome_multiple_regression

Known signals

UGT1A1*93: rs10929302
hg19 chr2:234,665,782 G/A
1000 Genomes allele frequencies:
A: 27%
G: 73%

```
rs10929302.res <- results(seq.reg.results)['chr2:234665782:G:A',]  
kable( rs10929302.res[,c('A1', 'A2', 'N', 'effB', 'se_effB', 'P1df')] )
```

	A1	A2	N	effB	se_effB	P1df	
chr2:234665782:G:A	T	G	163	-0.2356	0.1786	0.1871	