# ClinVar Report

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## Contents



**Sourcing ClinVar input from**: clinvar_2016-11-06.vcf
**Sending output to**: Report_2016-11-06.pdf

# 1 Collect and Merge ClinVar Data

## 1.1 Import ClinVar VCF

```
## Processed ClinVar data frame 126349 x 14 (selected rows/columns):
```

## 1.2 Merge ClinVar with 1000 Genomes and ExAC

```
## Breakdown of ClinVar Variants
```

| Subset_ClinVar | Number_of_Variants |
|---|---|
| Total ClinVar | 126349 |
| LP/P-ClinVar | 33033 |
| LP/P-ClinVar & ACMG | 6252 |
| LP/P-ClinVar & ACMG & ExAC | 826 |
| LP/P-ClinVar & ACMG & 1000 Genomes | 122 |

```
## Breakdown of ACMG-1000 Genomes Variants
```

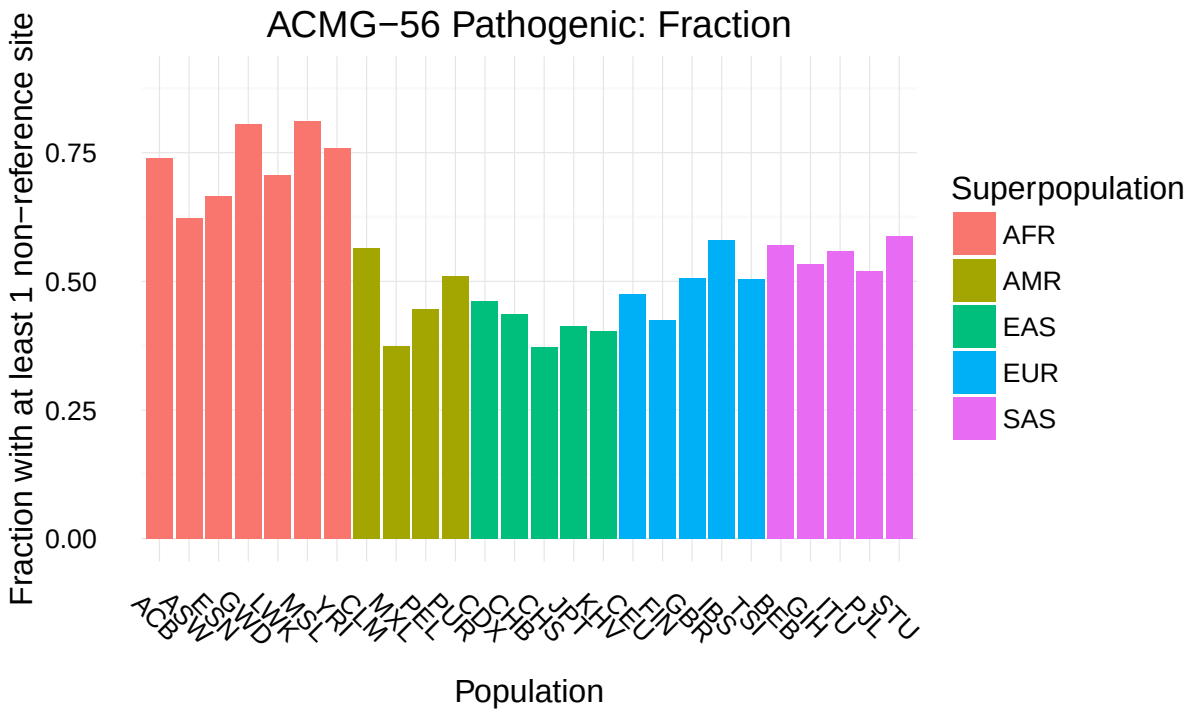
| Subset_1000_Genomes | Number_of_Variants |
|---|---|
| Total 1000_Genomes & ACMG | 139335 |
| 1000_Genomes & ACMG & ClinVar | 4891 |
| 1000_Genomes & ACMG & LP/P-ClinVar | 122 |

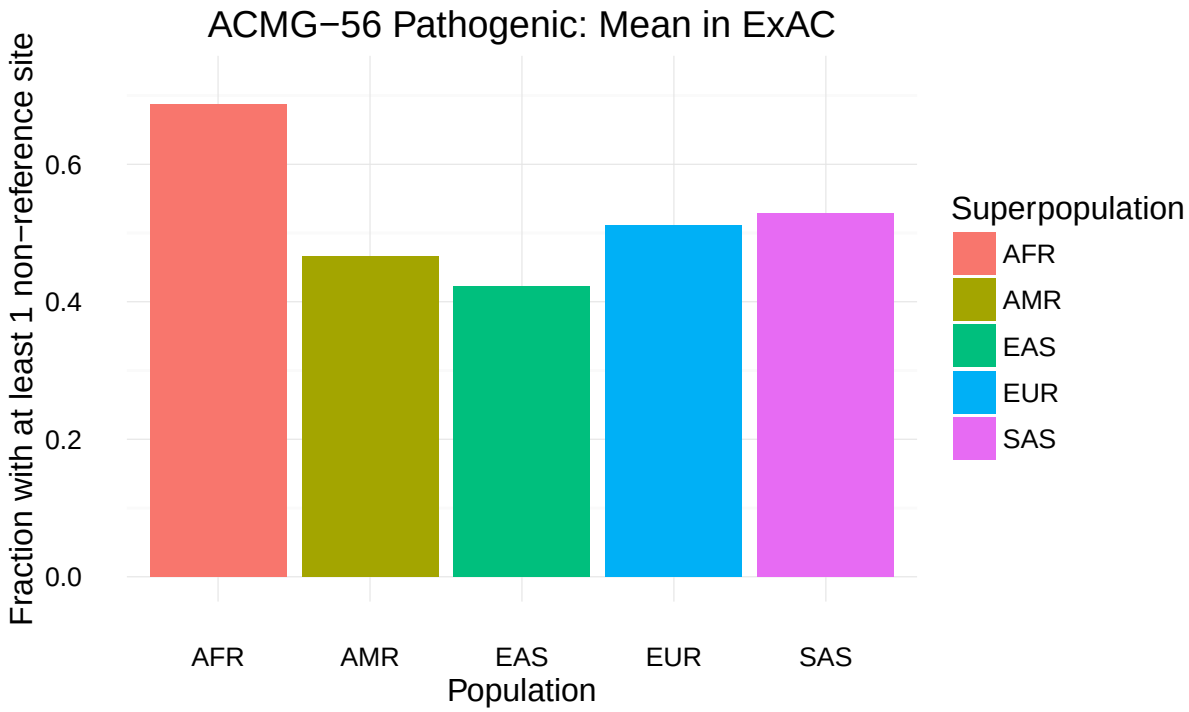
```
## Breakdown of ACMG-ExAC Variants
```

| Subset_ExAC | Number_of_Variants |
|---|---|
| Total ExAC & ACMG | 58873 |
| ExAC & ACMG & ClinVar | 10043 |
| ExAC & ACMG & LP/P-ClinVar | 826 |

## 2 Summary Statistics

### 2.1 Fraction of Individuals with Pathogenic Non-Reference Sites

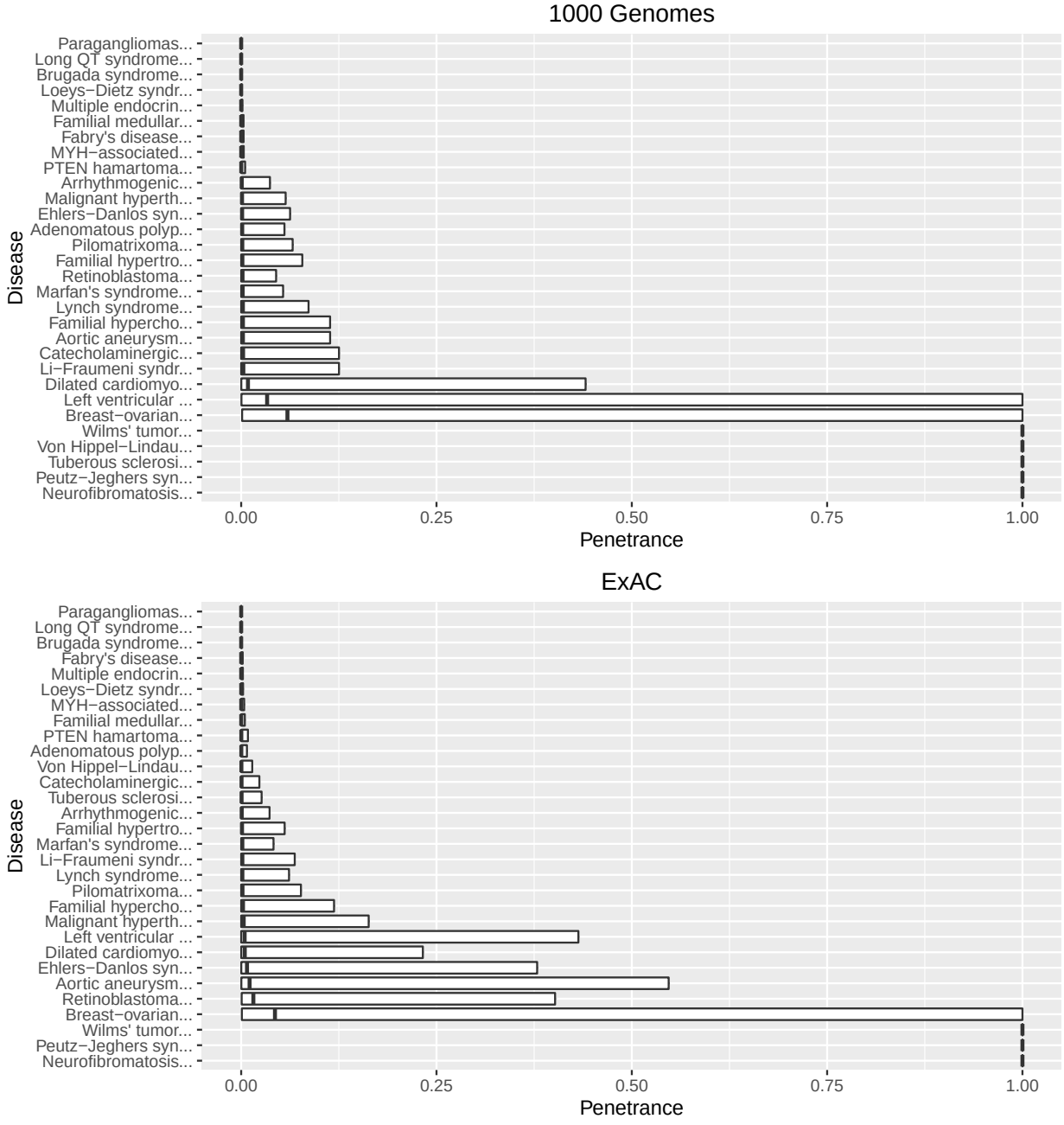


# 3 Penetrance Estimates

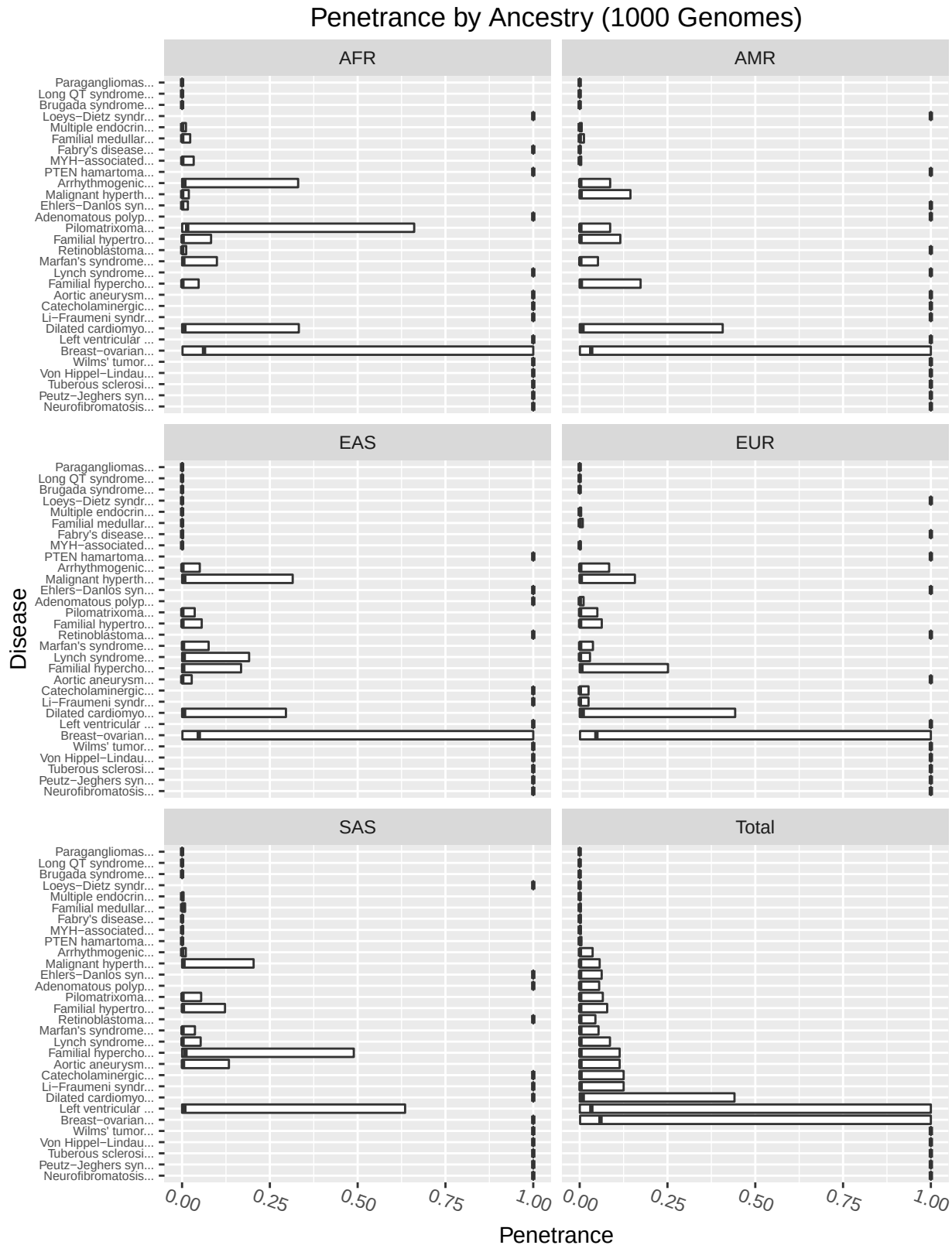
## 3.1 Max/Min Penetrance as a Function of P(D) and P(V|D)

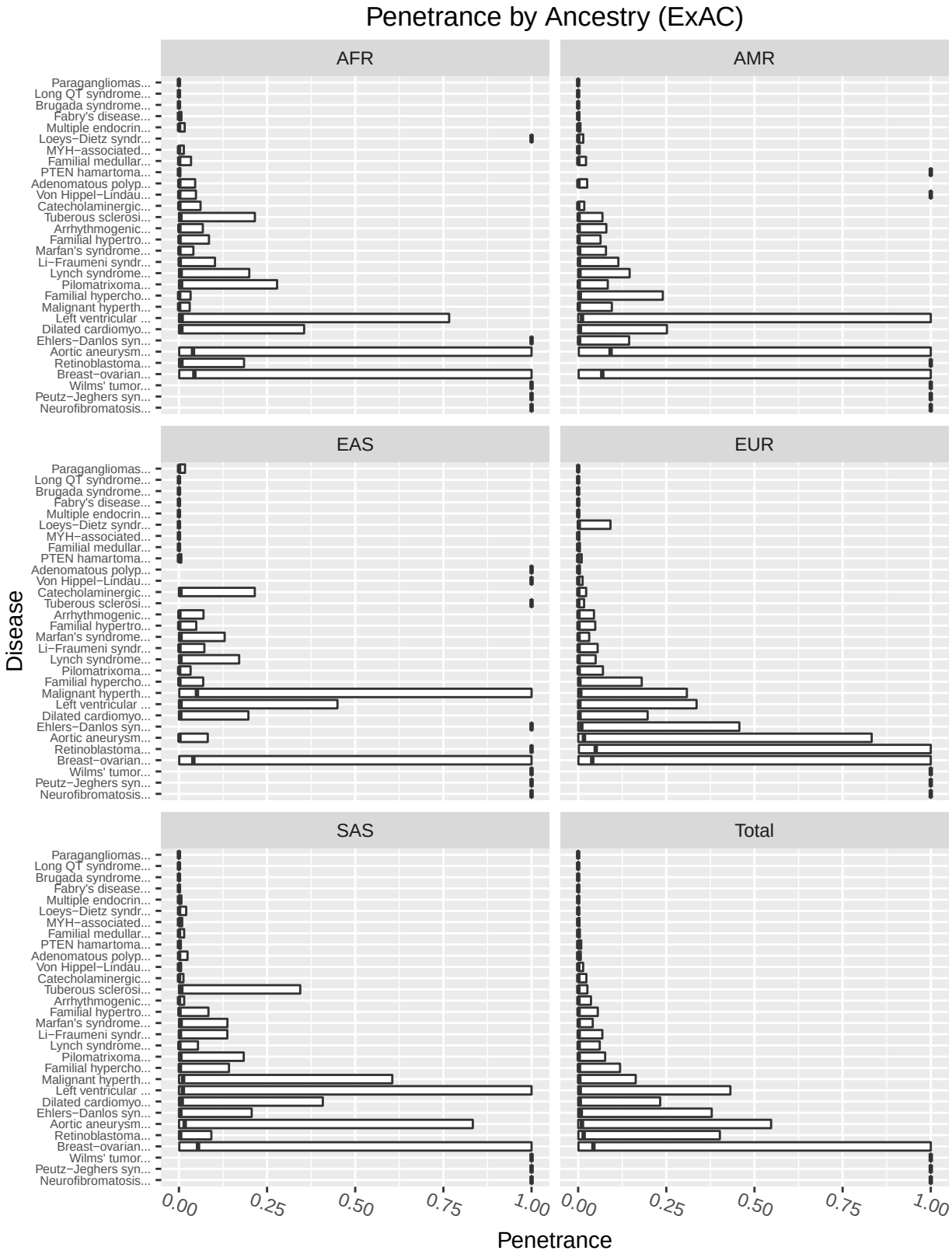
The left end of the boxplot indicates P(D) AND P(V|D) = lower value,
the bold line in the middle indicates P(D) AND P(V|D) = geometric_mean(values),
the right end of the boxplot indicates P(D) AND P(V|D) = upper value.



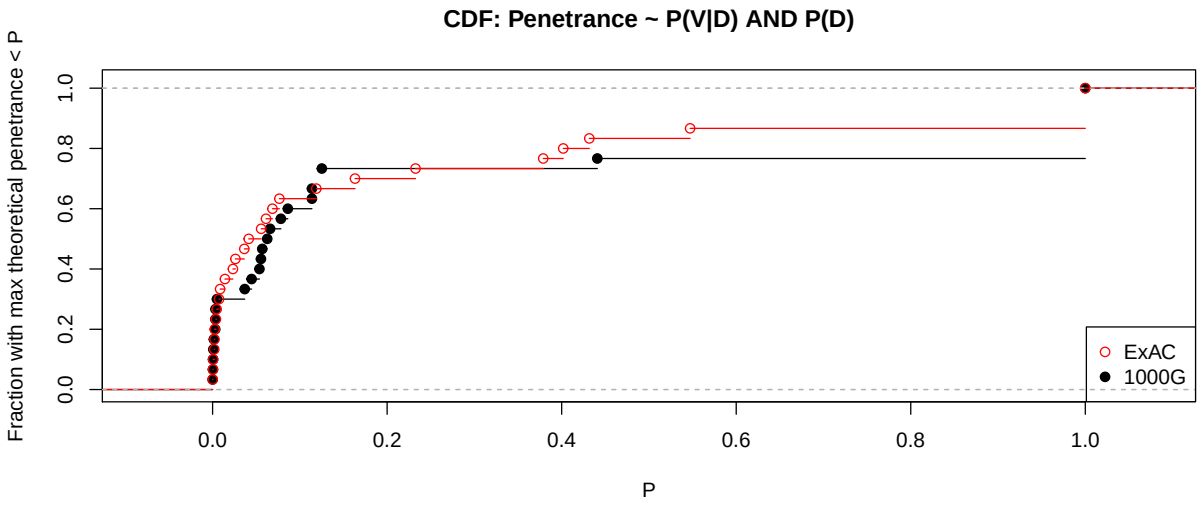

Note: Prevalence ranges of 5x were assumed for all point estimates of prevalence.
For example: a point estimate of 0.022 would be given the range 0.01-0.05.

### 3.2 Penetrance Estimates by Ancestry

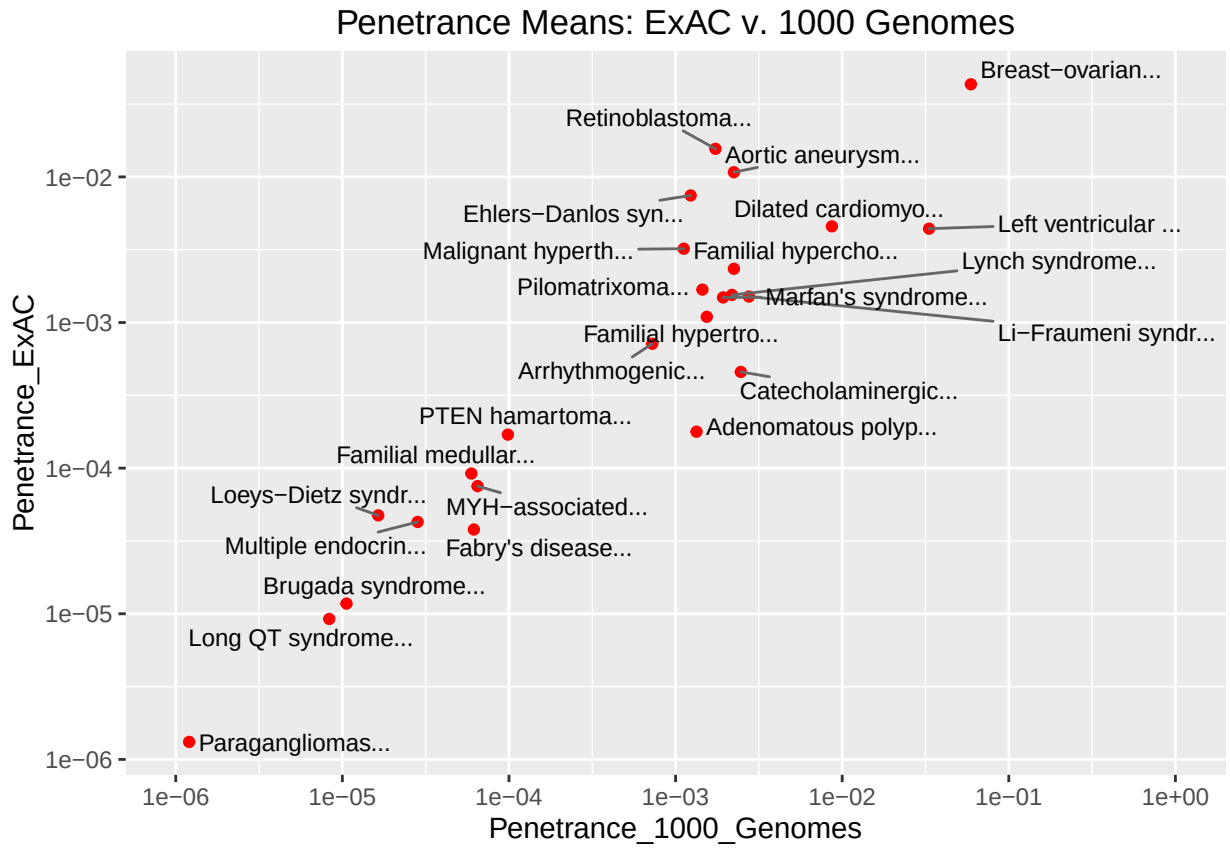



Penetrance by Ancestry (ExAC)
AFR
AMR
EAS
EUR
SAS
Total
Disease
Paragangliomas...
Long QT syndrome...
Brugada syndrome...
Fabry's disease...
Multiple endocrin...
Loeys−Dietz syndr...
MYH−associated...
Familial medullar...
PTEN hamartoma...
Adenomatous polyp...
Von Hippel−Lindau...
Catecholaminergic...
Tuberous sclerosi...
Arrhythmogenic...
Familial hypertro...
Marfan's syndrome...
Li−Fraumeni syndr...
Lynch syndrome...
Pilomatrixoma...
Familial hypercho...
Malignant hyperth...
Left ventricular ...
Dilated cardiomyo...
Ehlers−Danlos syn...
Aortic aneurysm...
Retinoblastoma...
Breast−ovarian...
Wilms' tumor...
Peutz−Jeghers syn...
Neurofibromatosis...
0.00
0.25
0.50
0.75
1.00
Penetrance

### 3.3 Empirical CDFs for All Penetrance Plots




### 3.4 Comparing Mean Penetrance between ExAC and 1000 Genomes




The Pearson correlation is 0.82.
Max penetrance values computed using 1000 Genomes are 1.2-fold larger than those computed using ExAC.