

# ClinVar Report

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*November 4, 2016*

## Contents

<b>1</b>	<b>Collect and Merge ClinVar Data</b>	<b>2</b>
1.1	Import ClinVar VCF . . . . .	2
1.2	Merge ClinVar with 1000 Genomes and ExAC . . . . .	2
<b>2</b>	<b>Summary Statistics</b>	<b>3</b>
2.1	Fraction of Individuals with Pathogenic Non-Reference Sites . . . . .	3
<b>3</b>	<b>Penetrance Estimates</b>	<b>4</b>
3.1	Max/Min Penetrance as a Function of $P(D)$ and $P(V D)$ . . . . .	4
3.2	Penetrance Estimates by Ancestry . . . . .	5
3.3	Empirical CDFs for All Penetrance Plots . . . . .	7
3.4	Comparing Mean Penetrance between ExAC and 1000 Genomes . . . . .	7

**Sourcing ClinVar input from:** clinvar\_2014-04-01.vcf

**Sending output to:** Report\_2014-04-01.pdf

# 1 Collect and Merge ClinVar Data

## 1.1 Import ClinVar VCF

## Processed ClinVar data frame 69779 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	69779
LP/P-ClinVar	16381
LP/P-ClinVar & ACMG	1986
LP/P-ClinVar & ACMG & ExAC	312
LP/P-ClinVar & ACMG & 1000 Genomes	75

## Breakdown of ACMG-1000 Genomes Variants

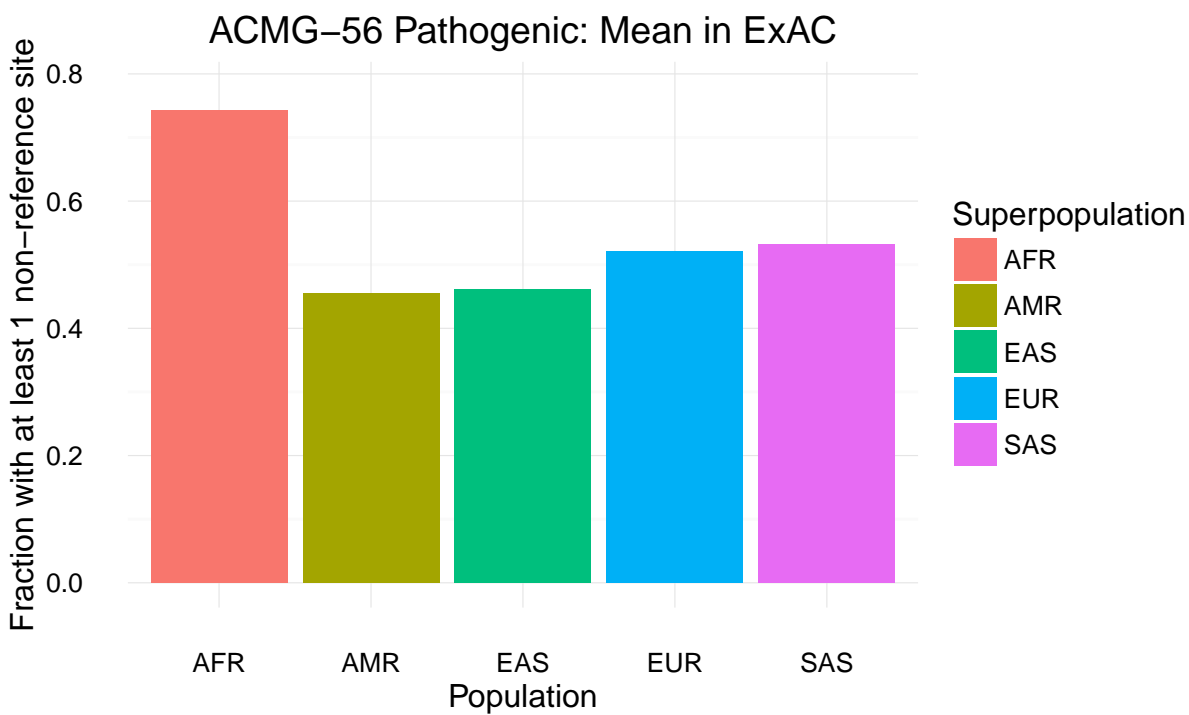
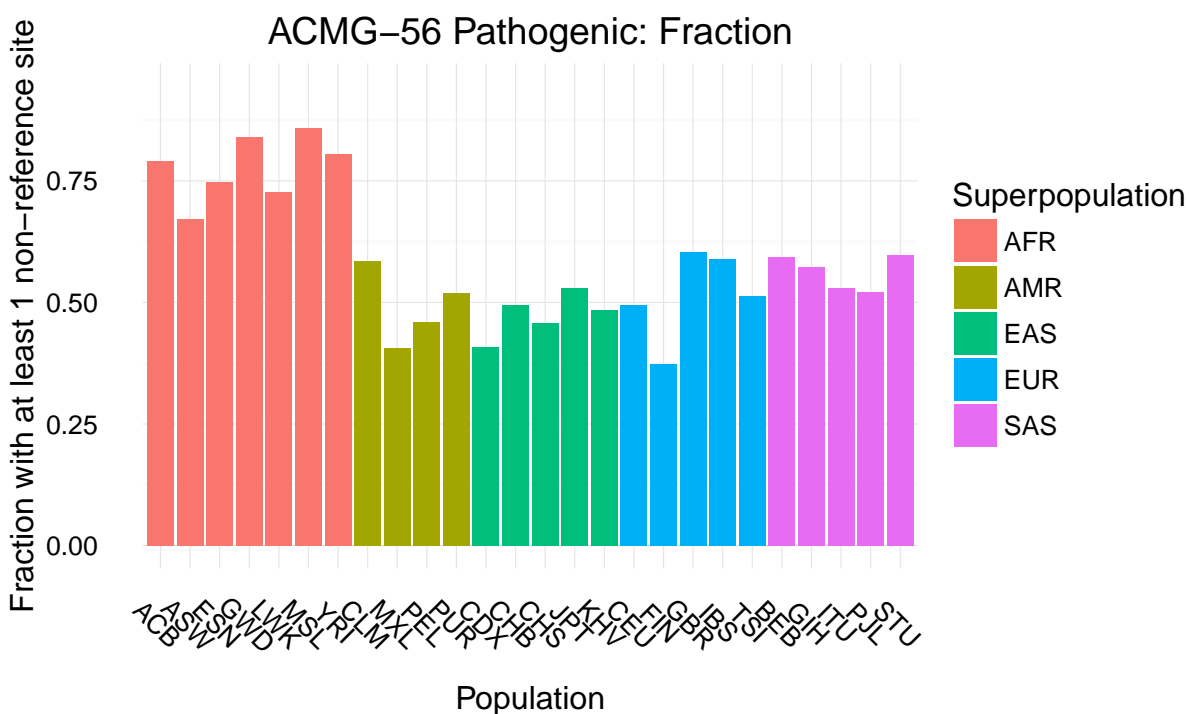
Subset_1000_Genomes	Number_of_Variants
Total 1000_Genomes & ACMG	139335
1000_Genomes & ACMG & ClinVar	1625
1000_Genomes & ACMG & LP/P-ClinVar	75

## Breakdown of ACMG-ExAC Variants

Subset_ExAC	Number_of_Variants
Total ExAC & ACMG	58873
ExAC & ACMG & ClinVar	3368
ExAC & ACMG & LP/P-ClinVar	312

## 2 Summary Statistics

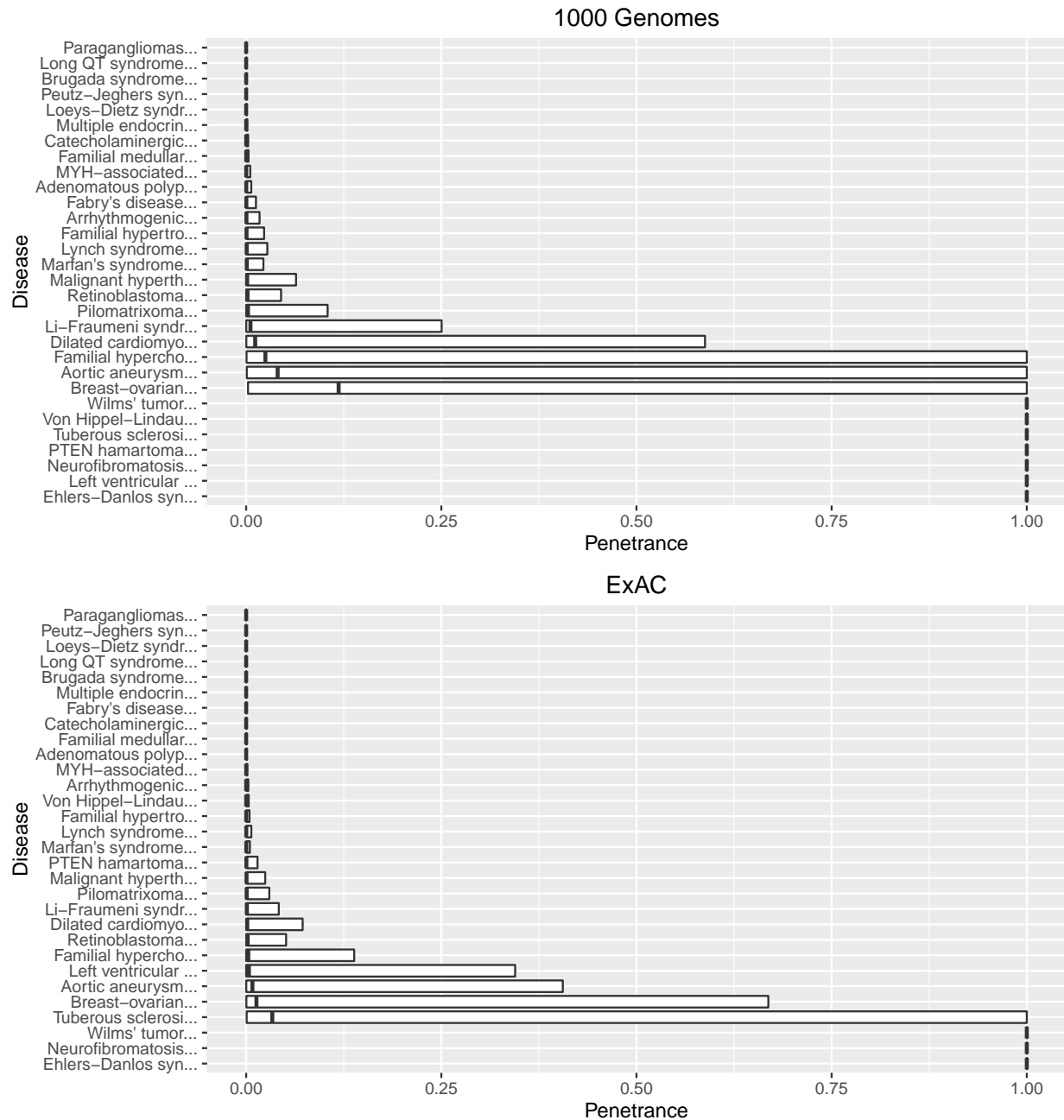
### 2.1 Fraction of Individuals with Pathogenic Non-Reference Sites



### 3 Penetrance Estimates

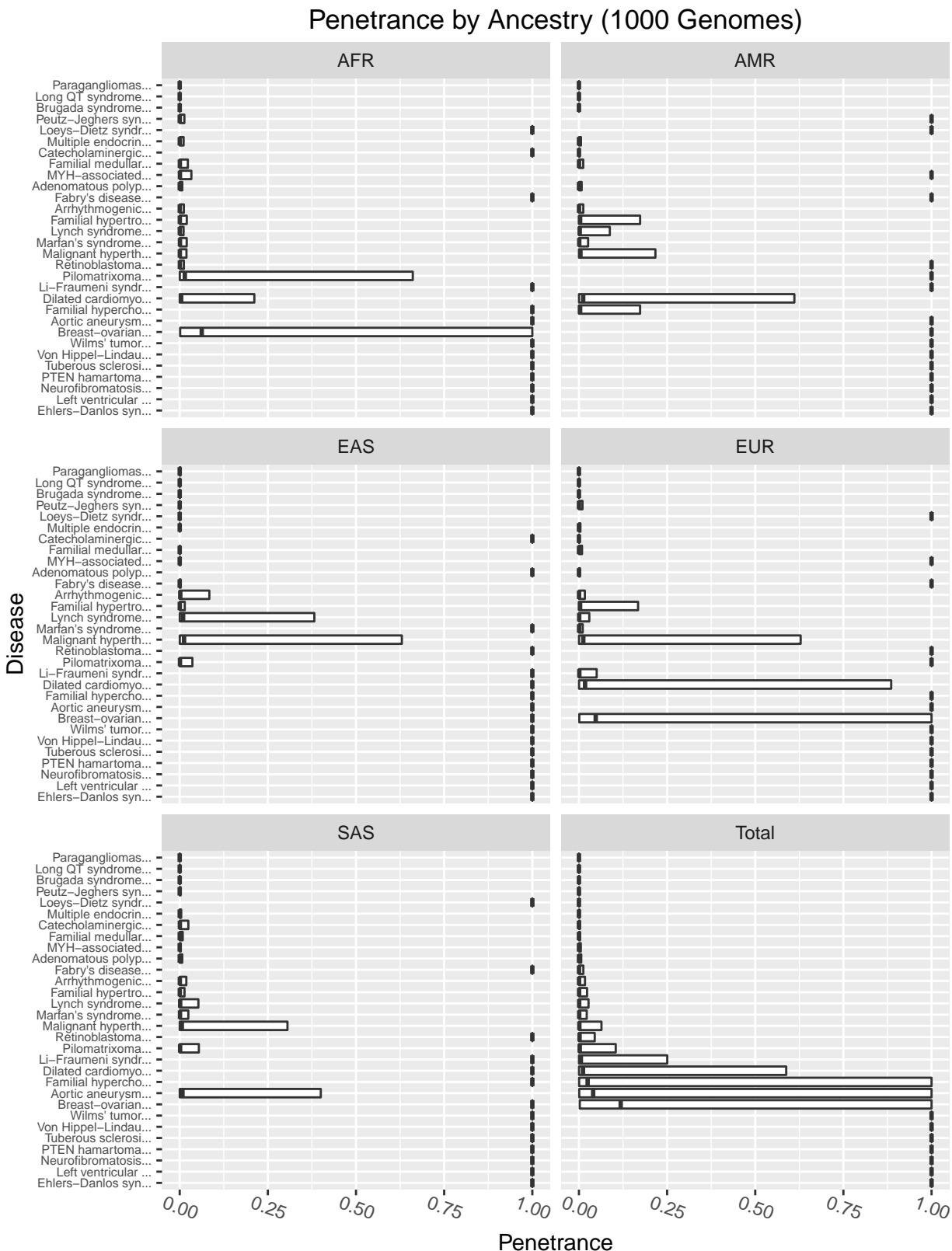
#### 3.1 Max/Min Penetrance as a Function of $P(D)$ and $P(V|D)$

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.

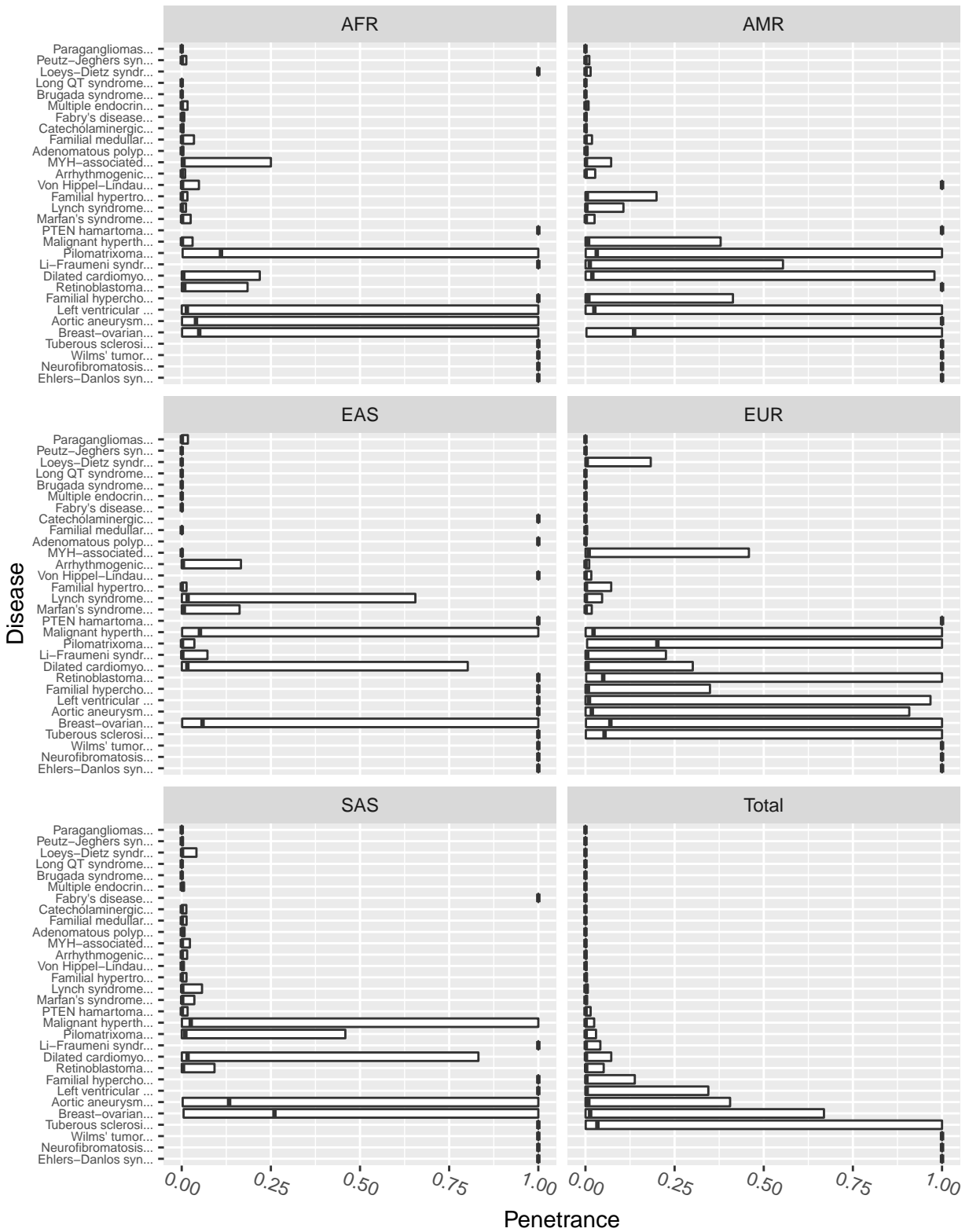


Note: Prevalence ranges of 5x were assumed for all point estimates of prevalence.  
For example: a point estimate of 0.022 would be given the range 0.01-0.05.

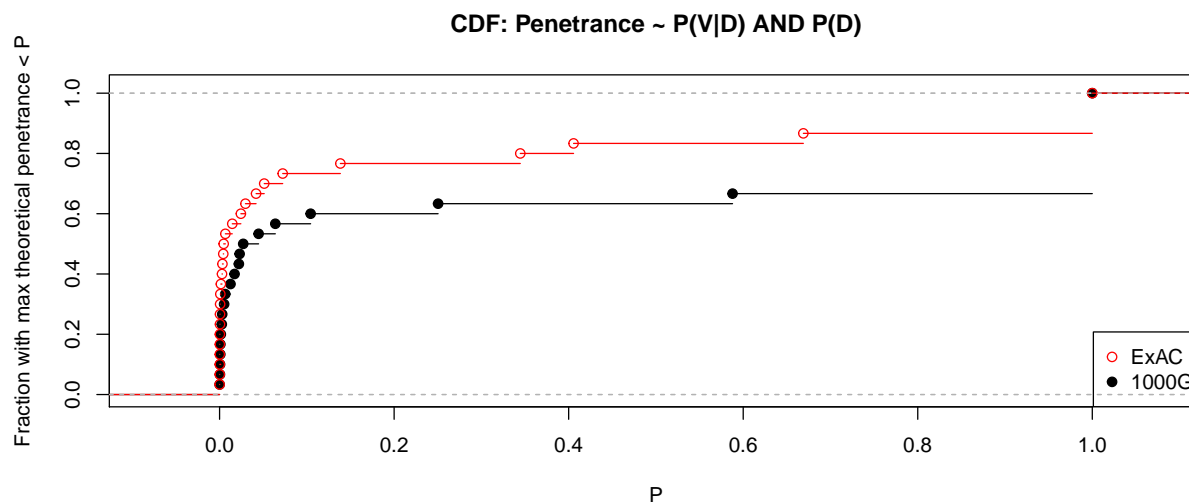
### 3.2 Penetrance Estimates by Ancestry



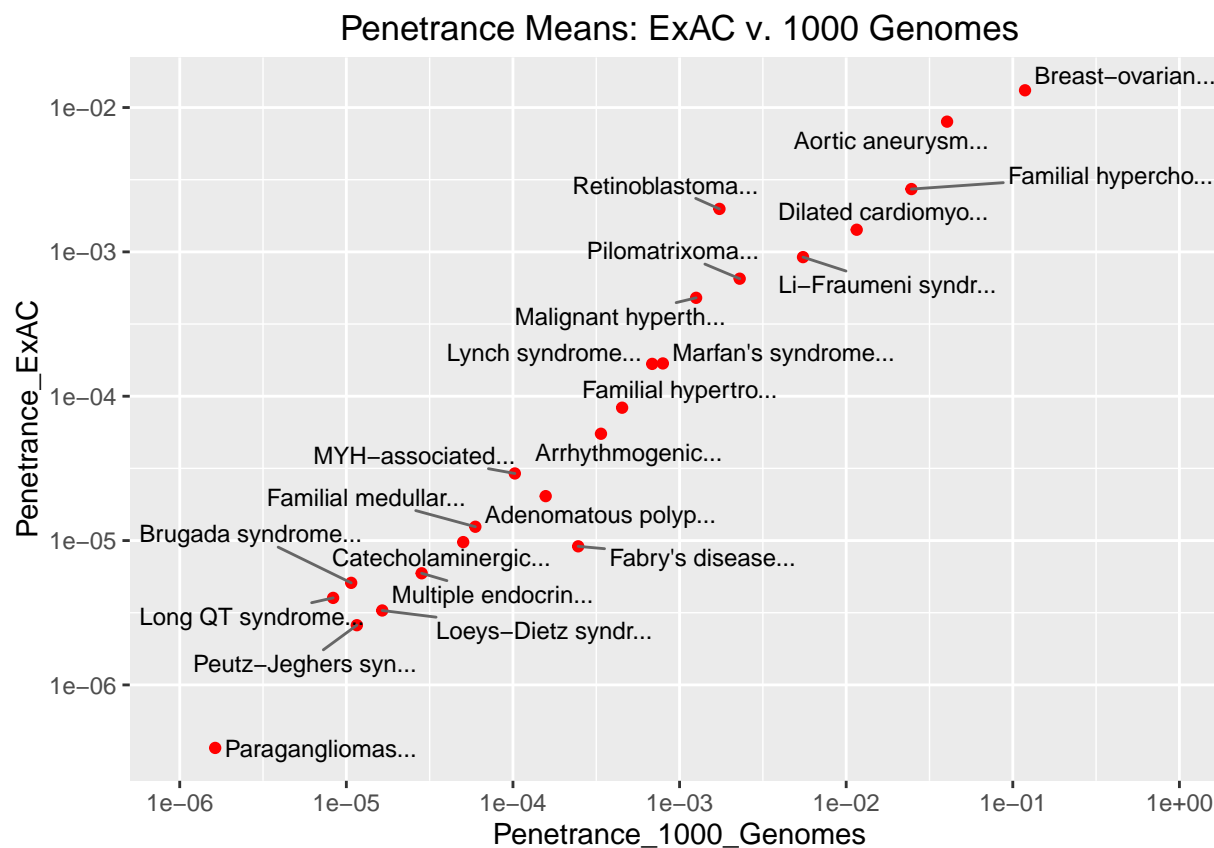
## Penetrance by Ancestry (ExAC)



### 3.3 Empirical CDFs for All Penetrance Plots



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



The Pearson correlation is 0.97.

Max penetrance values computed using 1000 Genomes are 8-fold larger than those computed using ExAC.