

# ClinVar Report

*James Diao*

*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\_2013-12-03.vcf

**Sending output to:** Report\_2013-12-03.pdf

# 1 Collect and Merge ClinVar Data

## 1.1 Import ClinVar VCF

## Processed ClinVar data frame 41580 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	41580
LP/P-ClinVar	16274
LP/P-ClinVar & ACMG	1468
LP/P-ClinVar & ACMG & ExAC	284
LP/P-ClinVar & ACMG & 1000 Genomes	82

## Breakdown of ACMG-1000 Genomes Variants

Subset_1000_Genomes	Number_of_Variants
Total 1000_Genomes & ACMG	139335
1000_Genomes & ACMG & ClinVar	1106
1000_Genomes & ACMG & LP/P-ClinVar	82

## Breakdown of ACMG-ExAC Variants

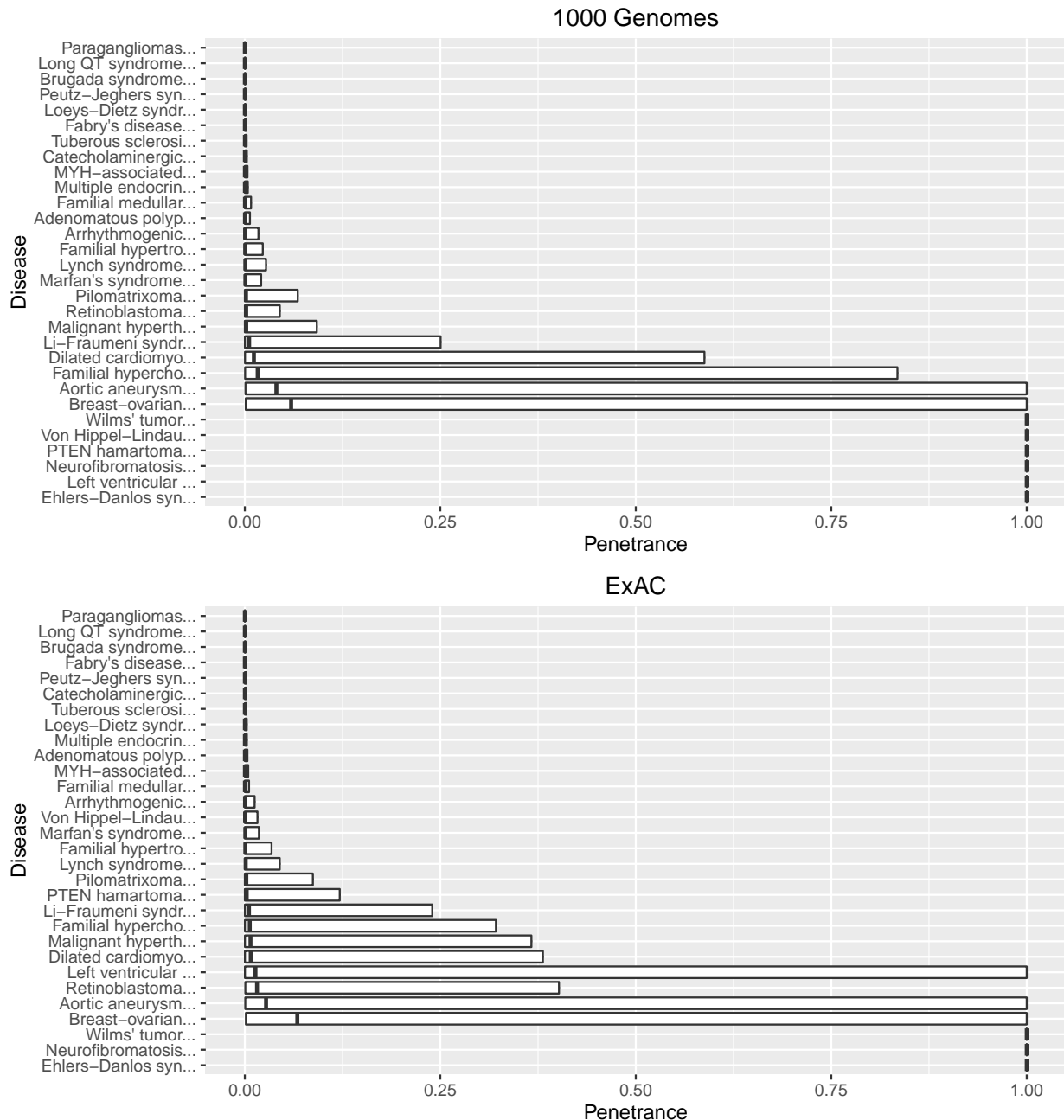
Subset_ExAC	Number_of_Variants
Total ExAC & ACMG	58873
ExAC & ACMG & ClinVar	2194
ExAC & ACMG & LP/P-ClinVar	284



### 3 Penetrance Estimates

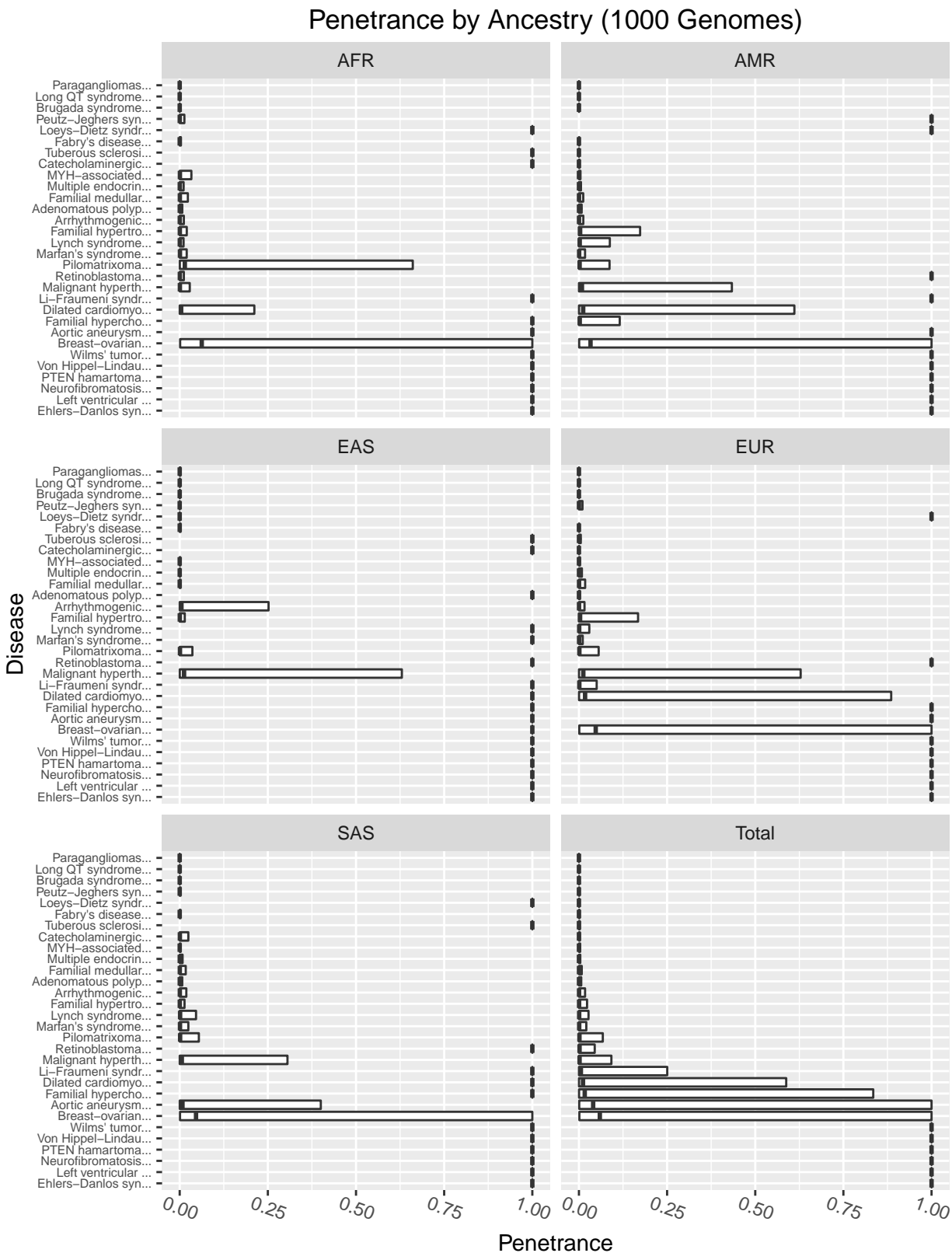
#### 3.1 Max/Min Penetrance as a Function of $P(D)$ and $P(V|D)$

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.

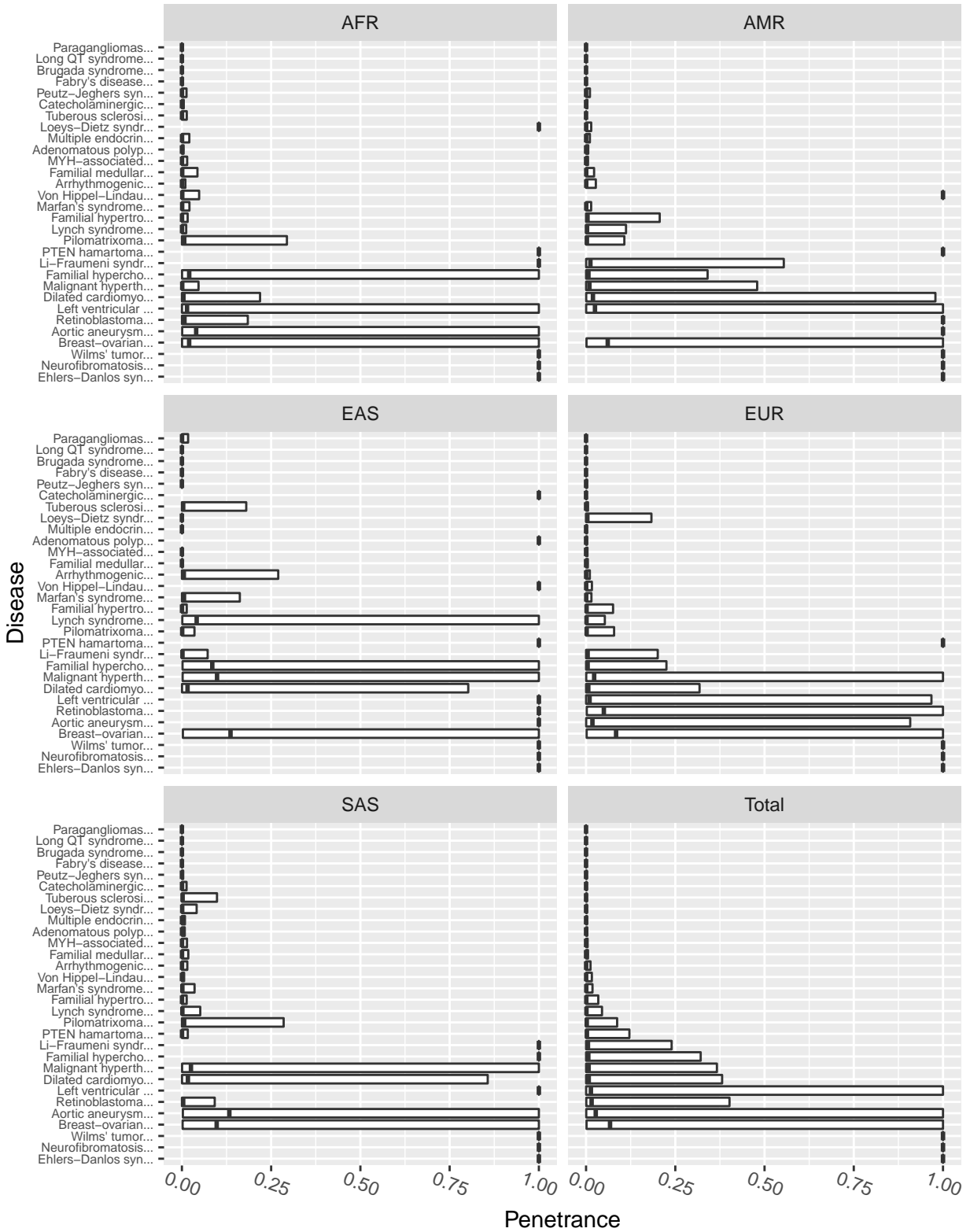


Note: Prevalence ranges of 5x were assumed for all point estimates of prevalence.  
For example: a point estimate of 0.022 would be given the range 0.01-0.05.

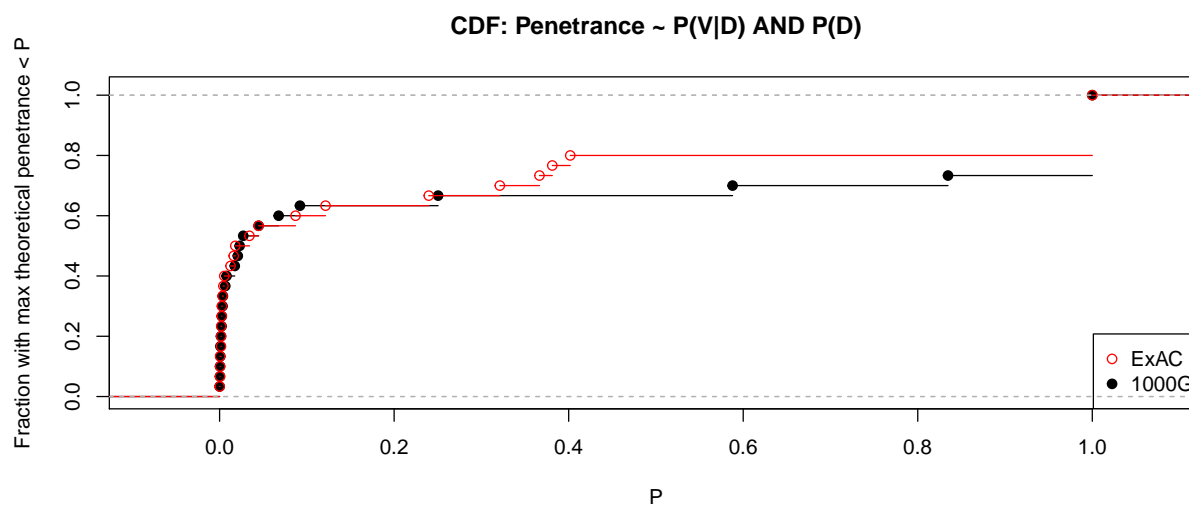
### 3.2 Penetrance Estimates by Ancestry



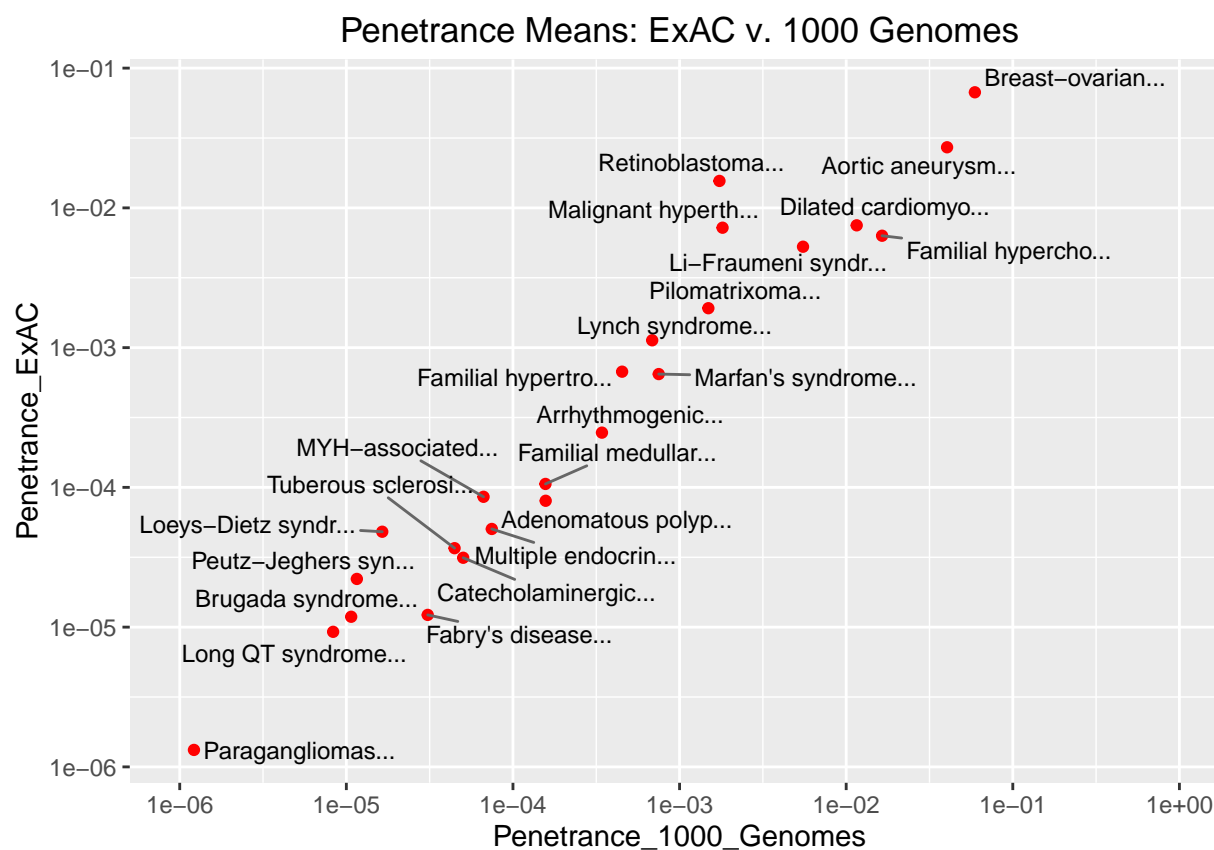
## Penetrance by Ancestry (ExAC)



### 3.3 Empirical CDFs for All Penetrance Plots



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



The Pearson correlation is 0.94.

Max penetrance values computed using 1000 Genomes are 0.93-fold larger than those computed using ExAC.