

# ACMG-ClinVar Penetrance RMarkdown

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**Working Directory:** /Users/jamesdiao/Documents/Kohane\_Lab/2017-ACMG-penetrance/ACMG\_Penetrance

# 1 Download, Transform, and Load Data

## 1.1 Collect ACMG Gene Panel

<http://www.ncbi.nlm.nih.gov/clinvar/docs/acmg/>

## Table from ACMG SF v2.0 Paper 60 x 8 (selected rows):

	Phenotype	MIM_disorder	PMID_Gene_Reviews_entry
<b>N1</b>	Hereditary breast and ovarian cancer	604370 612555	20301425
<b>N2</b>	Hereditary breast and ovarian cancer	604370 612555	20301425
<b>N3</b>	Li-Fraumeni syndrome	151623	20301488
<b>N4</b>	Peutz-Jeghers syndrome	175200	20301443
<b>N5</b>	Lynch syndrome	120435	20301390

Table continues below

	Typical_age_of_onset	Gene	MIM_gene	Inheritance	Variants_to_report
<b>N1</b>	Adult	BRCA1	113705	AD	KP&EP
<b>N2</b>	Adult	BRCA2	600185	AD	KP&EP
<b>N3</b>	Child/Adult	TP53	191170	AD	KP&EP
<b>N4</b>	Child/Adult	STK11	602216	AD	KP&EP
<b>N5</b>	Adult	MLH1	120436	AD	KP&EP

## ACMG-59 Genes:

```
## [1] BRCA1 BRCA2 TP53 STK11 MLH1 MSH2 MSH6 PMS2
## [9] APC MUTYH BMPR1A SMAD4 VHL MEN1 RET PTEN
## [17] RB1 SDHD SDHAF2 SDHC SDHB TSC1 TSC2 WT1
## [25] NF2 COL3A1 FBN1 TGFBR1 TGFBR2 SMAD3 ACTA2 MYH11
## [33] MYBPC3 MYH7 TNNT2 TNNI3 TPM1 MYL3 ACTC1 PRKAG2
## [41] GLA MYL2 LMNA RYR2 PKP2 DSP DSC2 TMEM43
## [49] DSG2 KCNQ1 KCNH2 SCN5A LDLR APOB PCSK9 ATP7B
## [57] OTC RYR1 CACNA1S
```

## 1.2 Download ClinVar VCF

`ftp://ftp.ncbi.nlm.nih.gov/pub/clinvar/vcf_GRCh37/clinvar.vcf.gz`

ClinVar is the central repository for variant interpretations. Relevant information from the VCF includes:

(a) CLNSIG = “Variant Clinical Significance, 0 - Uncertain, 1 - Not provided, 2 - Benign, 3 - Likely benign, 4 - Likely pathogenic, 5 - Pathogenic, 6 - Drug response, 7 - Histocompatibility, 255 - Other”

(b) CLNDBN = “Variant disease name”

(c) CLNDSDBID = “Variant disease database ID”

(d) CLNREVSTAT = “Review Status, no\_assertion, no\_criteria, single - criterion provided single submitter, mult - criteria provided multiple submitters no conflicts, conf - criteria provided conflicting interpretations, exp - Reviewed by expert panel, guideline - Practice guideline”

(e) INTERP = Pathogenicity (likely pathogenic or pathogenic; CLNSIG = 4 or 5)

## Processed ClinVar data frame 204730 x 15 (selected rows/columns):

VAR_ID	CHROM	POS	ID	REF	ALT	CLNSIG
1_957568_A_G	1	957568	rs115704555	A	G	2
1_957605_G_A	1	957605	rs756623659	G	A	5
1_957640_C_T	1	957640	rs6657048	C	T	255
1_957693_A_T	1	957693	rs879253787	A	T	5

Table continues below

CLNDBN	CLNREVSTAT	CLNDSDBID	INTERP
not_specified	single	CN169374	FALSE
Congenital_myasthenic_syndrome	no_criteria	C0751882:ORPHA590	TRUE
not_specified	conf	CN169374	FALSE
Congenital_myasthenic_syndrome	no_criteria	C0751882:ORPHA590	TRUE

## 1.3 Download 1000 Genomes VCFs

`ftp://ftp.1000genomes.ebi.ac.uk/vol1/ftp/release/20130502/ALL.[chrom].phase3_[version].20130502.genotypes.vcf.gz`

Downloaded 1000 Genomes VCFs are saved in: `/Users/jamesdiao/Documents/Kohane_Lab/2017-ACMG-penetrance/1000G/`

## Download report: region and successes: 59 x 6 (selected rows):

gene	name	chrom	start	end	downloaded
BRCA1	NM_007294	17	41196311	41277500	TRUE
BRCA2	NM_000059	13	32889616	32973809	TRUE
TP53	NM_000546	17	7571719	7590868	TRUE
STK11	NM_000455	19	1205797	1228434	TRUE
MLH1	NM_000249	3	37034840	37092337	TRUE

## File saved as `download_output.txt` in `Supplementary_Files`

## 1.4 Import and Process 1000 Genomes VCFs

- Unnest the data frames to 1 row per variant\_ID key (CHROM\_POSITION\_REF\_ALT).
- Remove all insertions, deletions, CNV, etc, and keep only missense variants (1 REF, 1 ALT)
- For 1000 Genomes: convert genomes to allele counts. For example: (0|1) becomes 1, (1|1) becomes 2. Multiple alleles are unnested into multiple counts. For example: (0|2) becomes 0 for the first allele (no 1s) and 1 for the second allele (one 2).

## Processed 1000 Genomes VCFs: 141467 x 2516 (selected rows/columns):

GENE	AF_1000G	VAR_ID	CHROM	POS	ID	REF	ALT
BRCA1	0.004193290	17_41196363_C_T	17	41196363	rs8176320	C	T
BRCA1	0.008386580	17_41196368_C_T	17	41196368	rs184237074	C	T
BRCA1	0.000998403	17_41196372_T_C	17	41196372	rs189382442	T	C
BRCA1	0.342252000	17_41196408_G_A	17	41196408	rs12516	G	A
BRCA1	0.000399361	17_41196409_G_C	17	41196409	rs548275991	G	C

Table continues below

HG00096	HG00097	HG00099	HG00100	HG00101	HG00102
0	0	0	0	0	0
0	0	0	0	0	0
0	0	0	0	0	0
1	0	1	1	0	2
0	0	0	0	0	0

## 1.5 Import and Process gnomAD/ExAC VCFs

- Unnest the data frames to 1 row per variant\_ID key (CHROM\_POSITION\_REF\_ALT).
- Remove all insertions, deletions, CNV, etc, and keep only missense variants (1 REF, 1 ALT)
- Collect superpopulation-level allele frequencies: African = AFR, Latino = AMR, European (Finnish + Non-Finnish) = EUR, East.Asian = EAS, South.Asian = SAS.

## Processed gnomAD VCFs: 96742 x 48 (selected rows/columns):

	GENE	AF_GNOMAD	VAR_ID
<b>472103</b>	PCSK9	0.00013400	1_55518036_C_T
<b>52449</b>	TPM1	0.00000406	15_63336199_T_C
<b>68085</b>	DSC2	0.00000397	18_28667746_A_G
<b>14034</b>	APC	0.00000397	5_112128222_C_G
<b>56259</b>	MYL2	0.00000792	12_111351103_G_A

## Processed ExAC VCFs: 59883 x 45 (selected rows/columns):

	GENE	AF_EXAC	VAR_ID
<b>2878</b>	BRCA2	0.000009726	13_32937713_A_C
<b>12049</b>	BMPRI1A	0.000041180	10_88683210_G_C
<b>39013</b>	RYS2	0.000029260	1_237955399_A_C
<b>62711</b>	LDLR	0.000008320	19_11226923_G_A
<b>82612</b>	APOB	0.000008243	2_21230362_T_C

## 1.6 Collect 1000 Genomes Phase 3 Populations Map

This will allow us to assign genotypes from the 1000 Genomes VCF to ancestral groups.

From: [ftp://ftp.1000genomes.ebi.ac.uk/vol1/ftp/release/20130502/integrated\\_call\\_samples\\_v3.20130502.ALL.panel](ftp://ftp.1000genomes.ebi.ac.uk/vol1/ftp/release/20130502/integrated_call_samples_v3.20130502.ALL.panel)

## Phase 3 Populations Map Table: 2504 x 4 (selected rows)

sample	pop	super_pop	gender
NA18881	YRI	AFR	female
HG02840	GWD	AFR	female
HG02012	ACB	AFR	female
HG01187	PUR	AMR	male
HG02345	PEL	AMR	female
NA20542	TSI	EUR	female

## 1.7 Merge ClinVar with gnomAD, ExAC, and 1000 Genomes

## Breakdown of ClinVar Variants

Subset_ClinVar	Number_of_Variants
Total ClinVar	204730
LP/P	33774
ACMG LP/P	6729
ACMG LP/P in gnomAD	1130
ACMG LP/P in ExAC	797
ACMG LP/P in 1000 Genomes	99

## Breakdown of ACMG-gnomAD Variants

Subset_gnomAD	Number_of_Variants
ACMG in gnomAD	96742
ClinVar-ACMG in gnomAD	13897
LP/P-ACMG in gnomAD	1130

## Breakdown of ACMG-ExAC Variants

Subset_gnomAD	Number_of_Variants
ACMG in ExAC	59883
ClinVar-ACMG in ExAC	10778
LP/P-ACMG in ExAC	797

## Breakdown of ACMG-1000G Variants

Subset_gnomAD	Number_of_Variants
ACMG in 1000G	141466
ClinVar-ACMG in 1000G	6012
LP/P-ACMG in 1000G	99

## 1.8 Comparison with ClinVar Browser Query Results

clinvar\_query.txt contains all results matched by the search query: “(APC[GENE] OR MYH11[GENE]... OR WT1[GENE]) AND (clinsig\_pathogenic[prop] OR clinsig\_likely\_pathogenic[prop])” from the ClinVar website. The exact query is saved in /Supplementary\_Files/query\_input.txt

This presents another way of collecting data from ClinVar.

Intermediate step: convert hg38 locations to hg19 using the Batch Coordinate Conversion tool (liftOver) from UCSC Genome Browser Utilities.

## ClinVar Query Results Table (substitutions only): 6445 x 13 (selected rows/columns)

VAR_ID	Gene(s)	Condition(s)	Frequency
1_17350520_G_C	SDHB	Paragangliomas 4	NA
1_45798631_T_A	MUTYH	Hereditary cancer-predisposing syndrome	NA
1_201334766_A_T	TNNT2	Familial hypertrophic cardiomyopathy 2	NA
3_38646328_G_C	SCN5A	Atrial fibrillation, familial, 10	NA
3_38647447_G_C	SCN5A	Atrial fibrillation, familial, 10	NA

Table continues below

Clinical significance (Last reviewed)	Review status
Pathogenic/Likely pathogenic, not provided (Last reviewed: Feb 2, 2015)	criteria provided, single submitter
Pathogenic (Last reviewed: Sep 17, 2015)	criteria provided, single submitter
Pathogenic/Likely pathogenic (Last reviewed: Feb 27, 2016)	criteria provided, multiple submitters, no conflicts
Pathogenic (Last reviewed: Apr 15, 2008)	no assertion criteria provided
Pathogenic (Last reviewed: Apr 15, 2008)	no assertion criteria provided

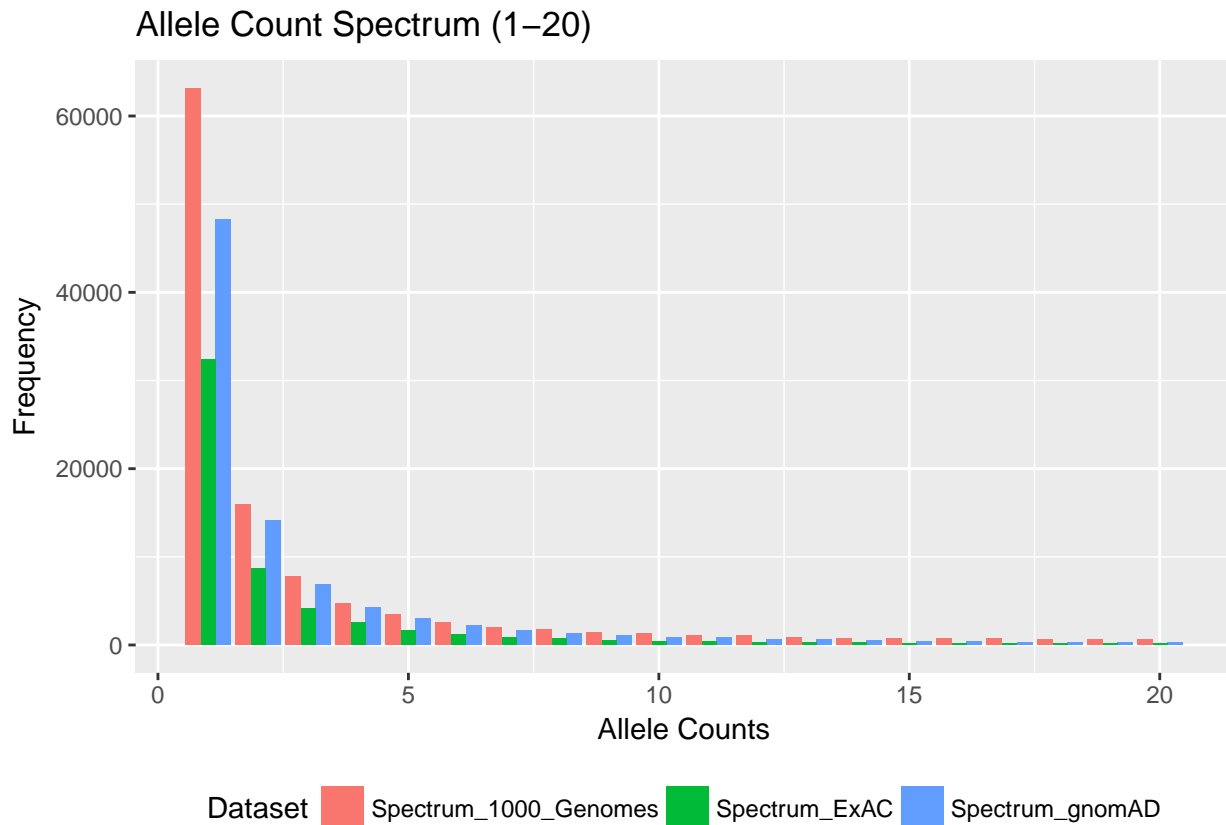
## Breakdown of ClinVar Query Results Table:

Subset	Number_of_Variants
Initial Count	14097
Filter Substitutions (N>N')	7039
Filter Coupling/Bad-Locations	6445
In ClinVar VCF	494
In LP/P-ClinVar	493
In LP/P-ACMG & gnomAD	45
In LP/P-ACMG & ExAC	33
In LP/P-ACMG & 1000G	1

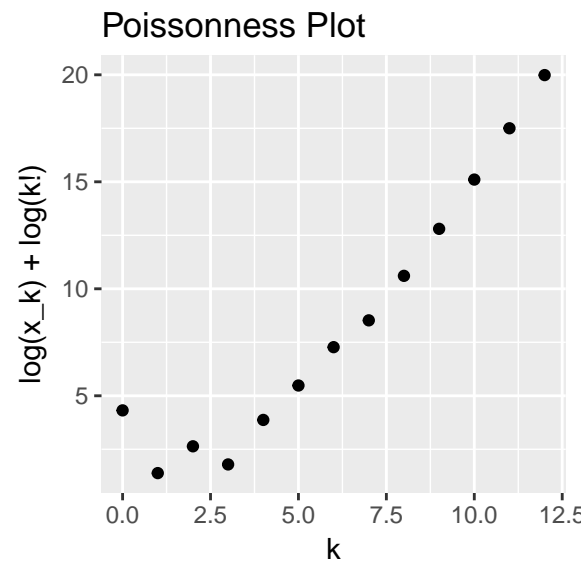
## Note the large reduction after merging the online query results with the VCF.

## 2 Plot Summary Statistics Across Populations

### 2.1 Distribution of Allele Frequencies



We can model this as a Poisson binomial- the summed occurrence of variants with different allele frequencies. If we assume that the allele frequencies are approximately the same and that variants are independent, (may not be good assumptions), then the distribution follows  $\text{Binom}(n, p)$ ,  $n = \#$  samples and  $p =$  allele frequency. Because  $n$  is large and  $p$  is small, we can then use a Poisson approximation to the binomial. The fit of this approximation may be tested by the Poissonness plot (Hoaglin 1980), or  $\log(x_k) + \log(k!)$  vs.  $k$ . If  $x_k = n \Pr(X = k) = n \left( \frac{\lambda^k e^{-\lambda}}{k!} \right)$ , then  $\ln x_k + \ln k! = \ln n + k \ln \lambda - \lambda =$  linear function of  $k$ . Despite some upward concavity, the plot demonstrates reasonable Poissonness, with correlation = 0.95.





## 2.2 Overall Non-Reference Sites

### 2.2.0.1 For 1000 Genomes

Each individual has  $n$  non-reference sites, which can be found by counting. The mean number is computed for each population.

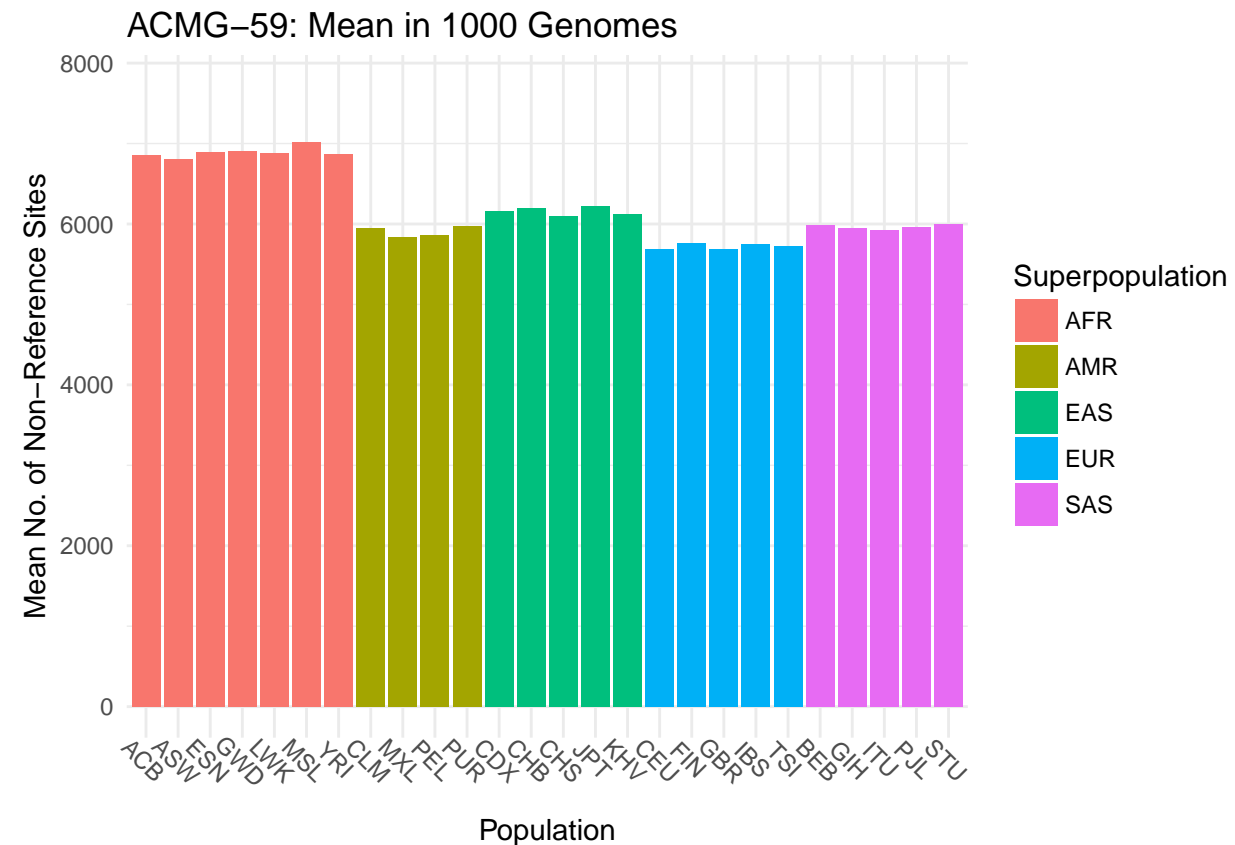
Ex: the genotype of 3 variants in 3 people looks like this:

	HG00366	HG00367	HG00368
<b>Variant 1</b>	2	1	1
<b>Variant 2</b>	2	1	1
<b>Variant 3</b>	1	0	0

Count the number of non-reference sites per individual:

HG00366	HG00367	HG00368
3	2	2

## Mean = 2.33



Note: the error bars denote standard deviation, not standard error.

### 2.2.0.2 For gnomAD/ExAC

The mean number of non-reference sites is  $E(V)$ , where  $V = \sum_{i=1}^n v_i$  is the number of non-reference sites at all variant positions  $v_1$  through  $v_n$ .

At each variant site, the probability of having at least 1 non-reference allele is  $P(v_i) = P(v_{i,a} \cup v_{i,b})$ , where  $a$  and  $b$  indicate the 1st and 2nd allele at each site.

If the two alleles are independent,  $P(v_{i,a} \cup v_{i,b}) = 1 - (1 - P(v_{i,a}))(1 - P(v_{i,b})) = 1 - (1 - AF(v_i))^2$

If all variants are independent,  $E(V) = \sum_{i=1}^n 1 - (1 - AF(v_i))^2$  for any set of allele frequencies.

Ex: the allele frequencies of 3 variants across the 5 superpopulations looks like this:

	AFR	AMR	EAS	EUR	SAS
<b>Variant 1</b>	0.1	0.2	0	0	0.3
<b>Variant 2</b>	0.2	0	0.3	0	0.1

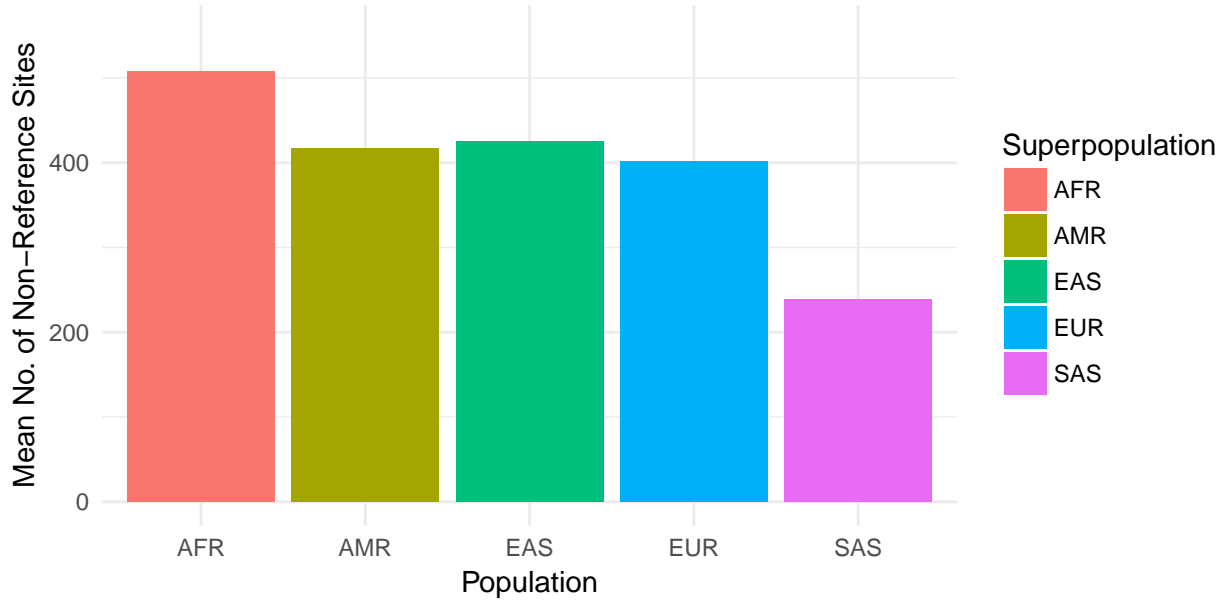
The probability of having at least 1 non-reference site at each variant - (0|1) (1|0) or (1|1) is given by  $1 - (1 - AF)^2$ . Note that this is approximately  $2 * AF$  when  $AF$  is small:

	AFR	AMR	EAS	EUR	SAS
<b>Variant 1</b>	0.19	0.36	0	0	0.51
<b>Variant 2</b>	0.36	0	0.51	0	0.19

By linearity of expectation, the expected (mean) number of non-reference sites is  $\sum E(V_i) = \sum (columns)$ .

AFR	AMR	EAS	EUR	SAS
0.55	0.36	0.51	0	0.7

ACMG-59: Mean in gnomAD





## 2.4 Fraction of Individuals with Pathogenic Sites

### 2.4.0.1 For 1000 Genomes

We can count up the fraction of individuals with 1+ non-reference site(s) in each population. This is the fraction of individuals who would receive a positive genetic test result in at least 1 of the ACMG-59 genes.

Ex: the genotype of 3 variants in 3 people looks like this:

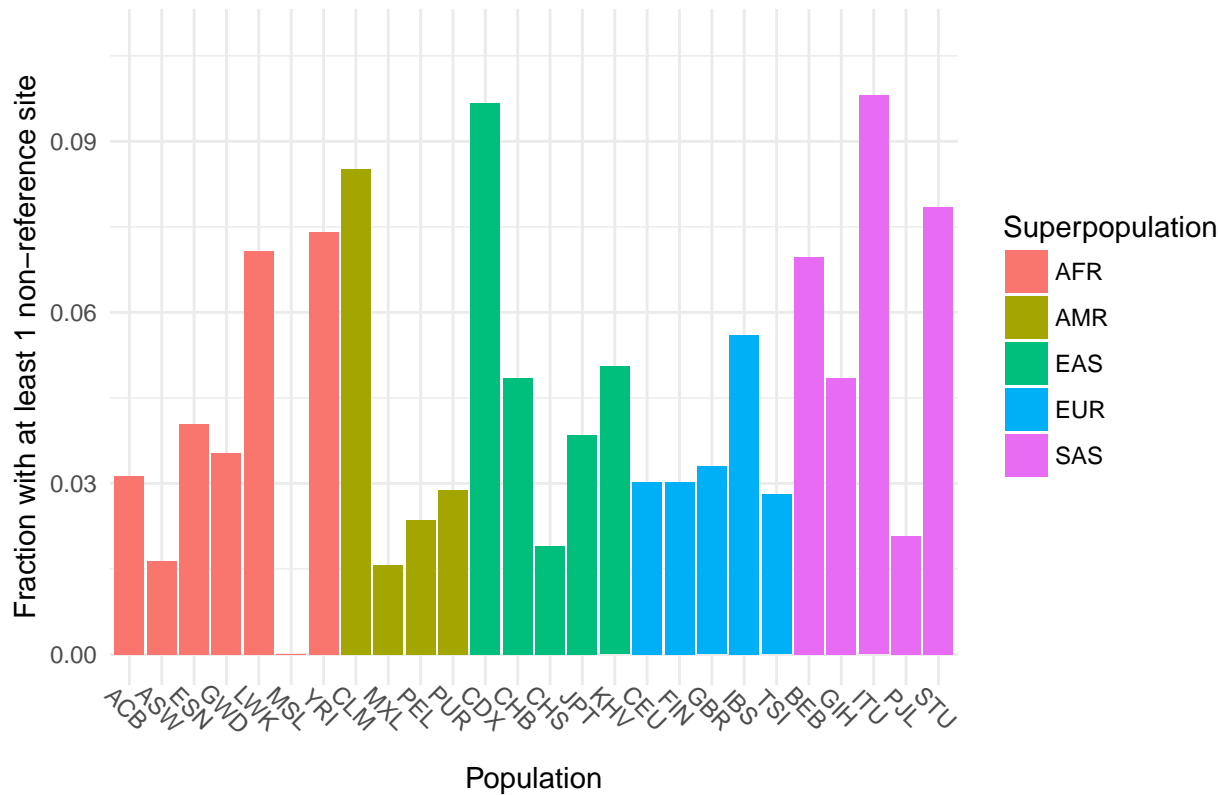
	HG00366	HG00367	HG00368
<b>Variant 1</b>	2	1	1
<b>Variant 2</b>	2	1	1
<b>Variant 3</b>	1	0	0

Count each individual as having a non-reference site (1) or having only reference sites (0):

HG00366	HG00367	HG00368
1	1	1

## Mean = 1

### ACMG-59 Pathogenic: Fraction in 1000 Genomes



### 2.4.0.2 For gnomAD/ExAC

The probability of having at least 1 non-reference site is  $P(X)$ , where  $X$  indicates a non-reference site at any variant position  $v_1$  through  $v_n$ .

Recall that  $P(v_i) = P(v_{i,a} \cup v_{i,b}) = 1 - (1 - AF(v))^2$  when alleles are independent.

If all alleles are independent,  $P(X) = P(\bigcup_{i=1}^n v_i) = 1 - \prod_{i=1}^n (1 - AF(v_i))^2$

Ex: the allele frequencies of 3 variants across the 5 superpopulations looks like this:

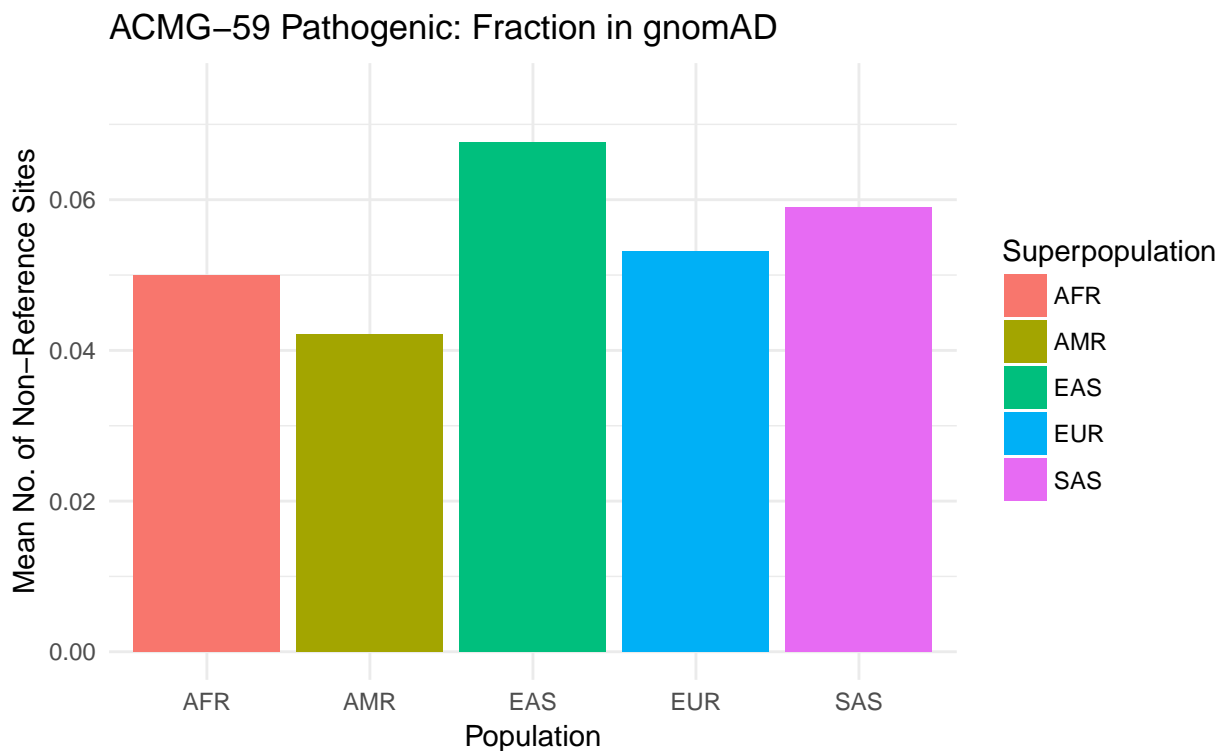
	AFR	AMR	EAS	EUR	SAS
<b>Variant 1</b>	0.1	0.2	0	0	0.3
<b>Variant 2</b>	0.2	0	0.3	0	0.1

The probability of having at least 1 non-reference site at each variant - (0|1) (1|0) or (1|1) is given by  $1 - (1 - AF)^2$ . Note that this is approximately  $2 * AF$  when  $AF$  is small:

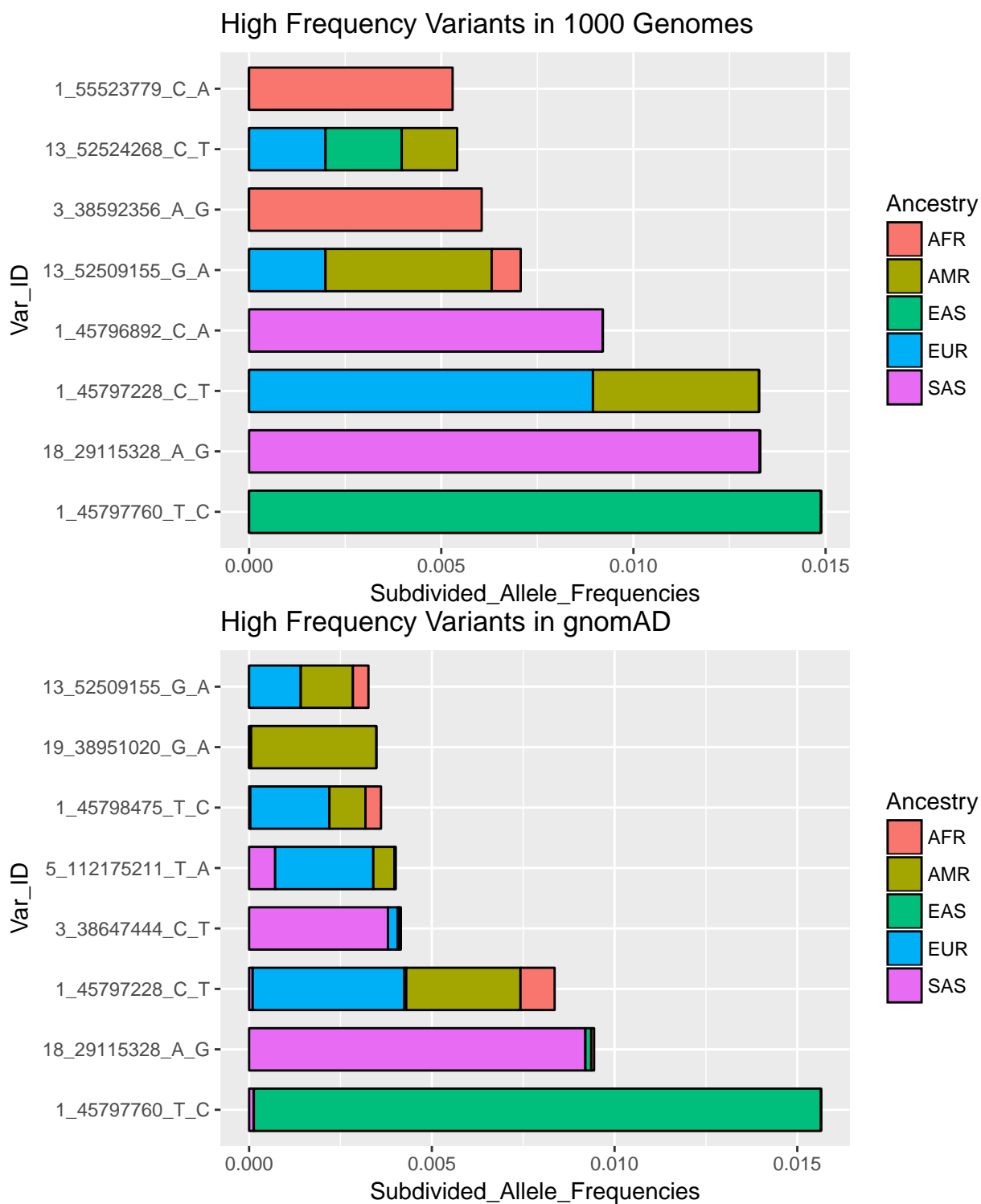
	AFR	AMR	EAS	EUR	SAS
<b>Variant 1</b>	0.19	0.36	0	0	0.51
<b>Variant 2</b>	0.36	0	0.51	0	0.19

The expected (mean) number of non-reference sites is given by  $1 - \prod (1 - AF)^2$ .

AFR	AMR	EAS	EUR	SAS
0.4816	0.36	0.51	0	0.6031



## 2.5 Common Pathogenic Variants by Ancestry



### 3 Penetrance Estimates

#### 3.1 Bayes' Rule as a Model for Estimating Penetrance

Let  $V_x$  be the event that an individual has 1 or more variant related to disease  $x$ , and  $D_x$  be the event that the individual is later diagnosed with disease  $x$ .

In this case, we can define the following probabilities:

1. Prevalence =  $P(D_x)$
2. Population Allele Frequency (PAF) =  $P(V_x)$
3. Case Allele Frequency (CAF) =  $P(V_x|D_x)$
4. Penetrance =  $P(D_x|V_x)$

By Bayes' Rule, the penetrance of a variant related to disease  $x$  may be defined as:

$$P(D_x|V_x) = \frac{P(D_x) * P(V_x|D_x)}{P(V_x)} = \frac{(Prevalence)(Population\ Allele\ Frequency)}{Case\ Allele\ Frequency}$$

To compute penetrance estimates for each of the diseases related to the ACMG-59 genes, we will use the prevalence data we collected into `Literature_Prevalence_Estimates.csv`, allele frequency data from 1000 Genomes/ExAC/gnomAD, and a broad range of values for case allele frequency.

#### 3.2 Import Literature-Based Disease Prevalence Data

Data Collection:

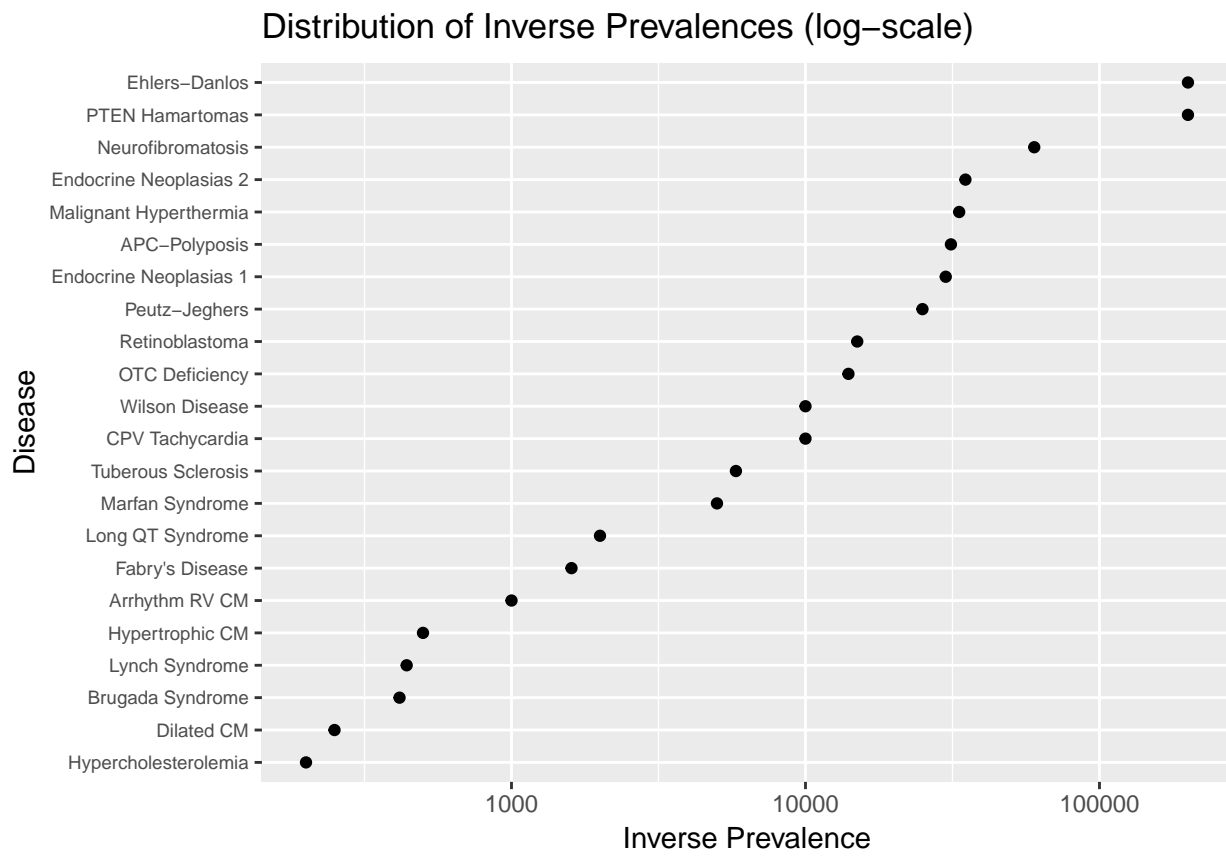
1. Similar disease subtypes were grouped together (e.g., the 8 different types of familial hypertrophic cardiomyopathy), resulting in 30 disease categories across 59 genes.
2. The search query “[disease name] prevalence” was used to find articles using Google Scholar.
3. Prevalence estimates were recorded along with URL, journal, region, publication year, sample size, first author, population subset (if applicable), date accessed, and potential issues. Preference was given to studies with PubMed IDs, more citations, and larger sample sizes.

Prevalence was recorded as reported: either a point estimate or a range. Values of varying quality were collected across all diseases.

**## Table of Literature-Based Estimates 22 x 18 (selected rows/columns):**

Gene	Phenotype	Inverse_Prevalence	Case_Allele_Frequency
STK11	Peutz-Jeghers syndrome	25000	0.96
RB1	Retinoblastoma	15000	0.97
FBN1 TGFB1	Marfan syndrome	5000	0.9
SCN5A	Brugada syndrome	416	0.3

### 3.3 Distribution of Prevalences





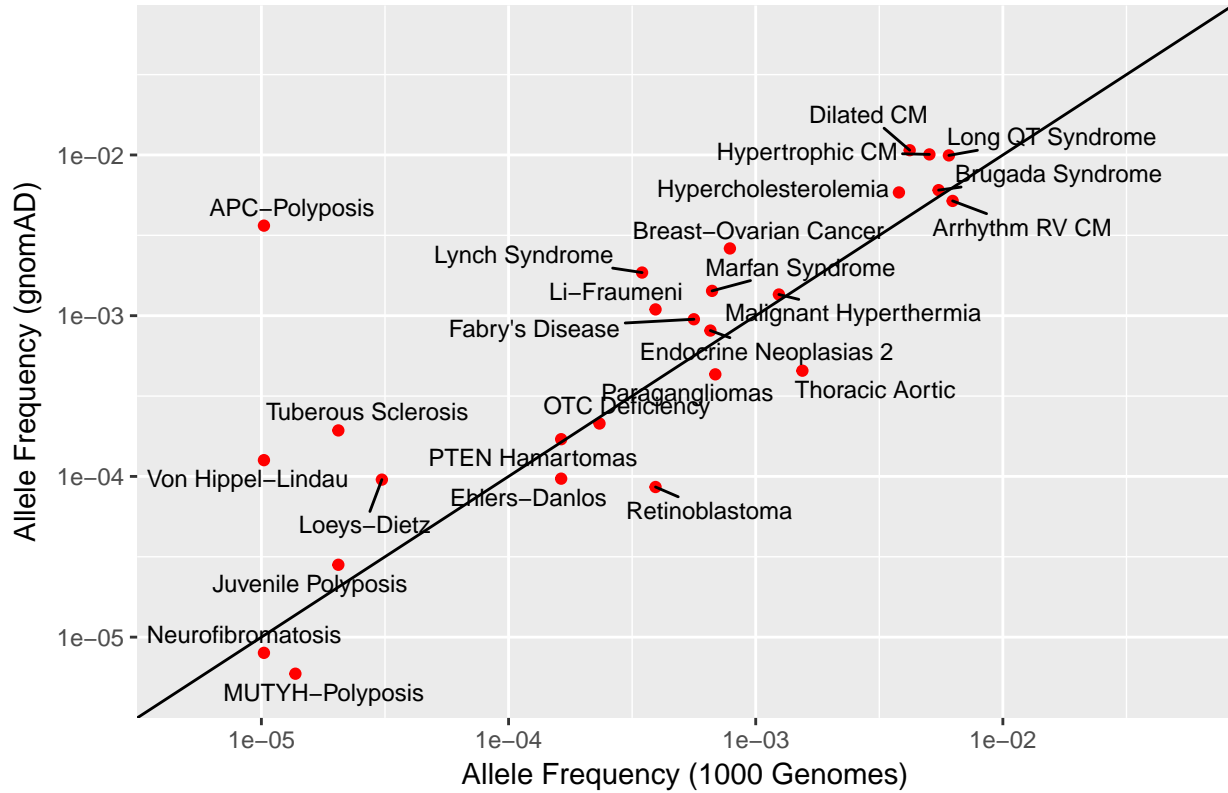
### 3.4 Collect and Aggregate Allele Frequencies at the Disease-Level

We define  $AF(\text{disease})$  as the probability of having at least 1 variant associated with the disease.

The frequencies across the relevant variants can be aggregated in two ways:

- (1) By direct counting, from genotype data in 1000 Genomes.
- (2)  $AF(\text{disease}) = 1 - \prod_{\text{variant}} (1 - AF_{\text{variant}})$ , from population data in ExAC (assumes independence).

Scatterplot: gnomAD v. 1000 Genomes

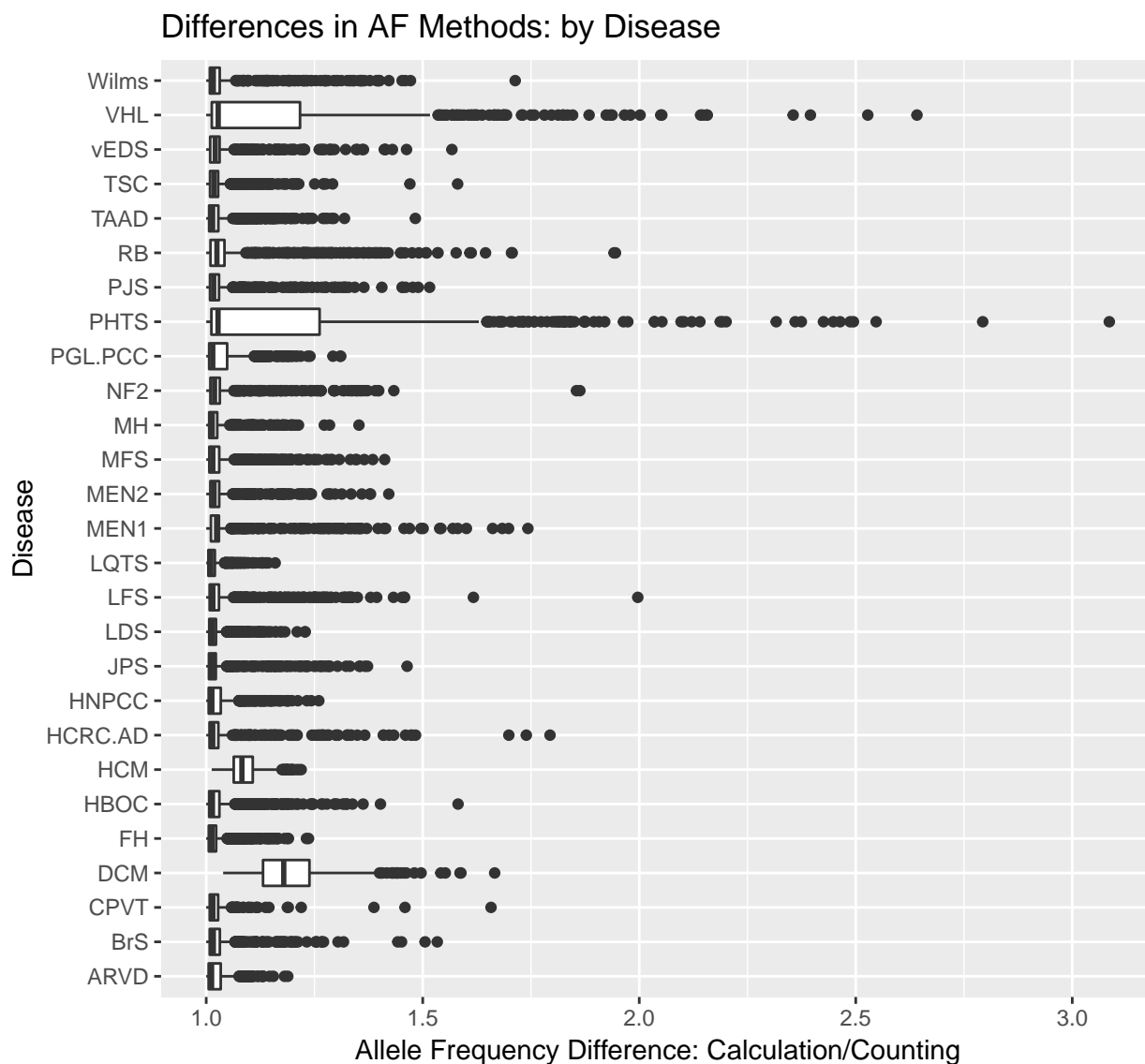


Ratio\_1000G (red, top) computes  $AF(\text{calculation in 1000 Genomes}) / AF(\text{counting in 1000 Genomes})$ .  
Ratio\_gnomAD (blue, bottom) computes  $AF(\text{calculation in gnomAD}) / AF(\text{calculation in 1000 Genomes})$ .

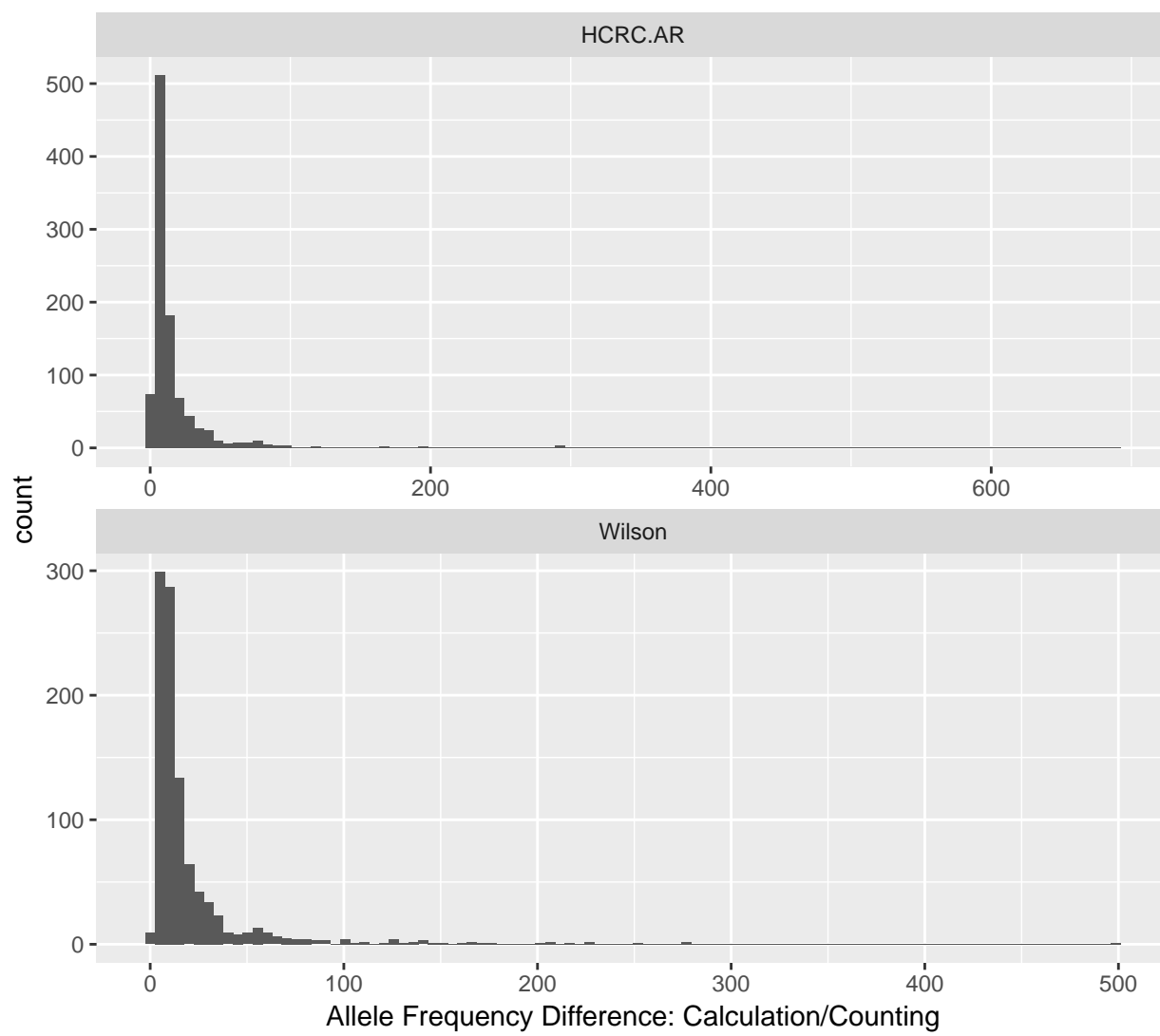
### Ratios of Allele Frequencies from Different Methods



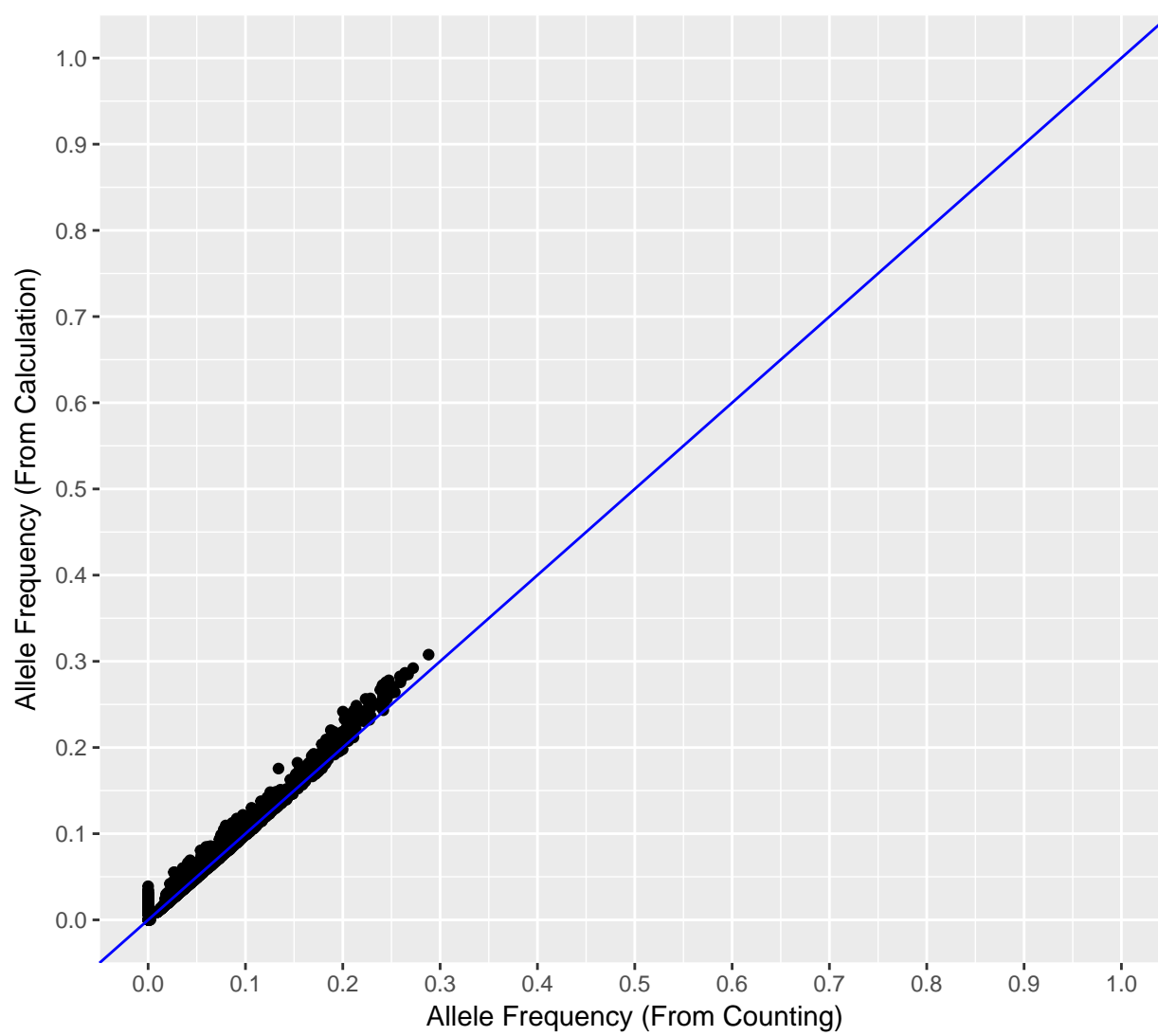
Sampling 1000 variants from all variants in 1000 Genomes to test deviations from independence assumptions. Repeat for 1000 trials and plot the distribution of disease-level allele frequencies (1000 points per disease). Only variants with allele frequency  $> 0.01$  are evaluated. Since we look at 17 variants per disease, the maximum is approximately  $1 - (1 - 0.01)^{34} \approx 0.29$



## Differences in AF Methods: by Disease (Outliers)



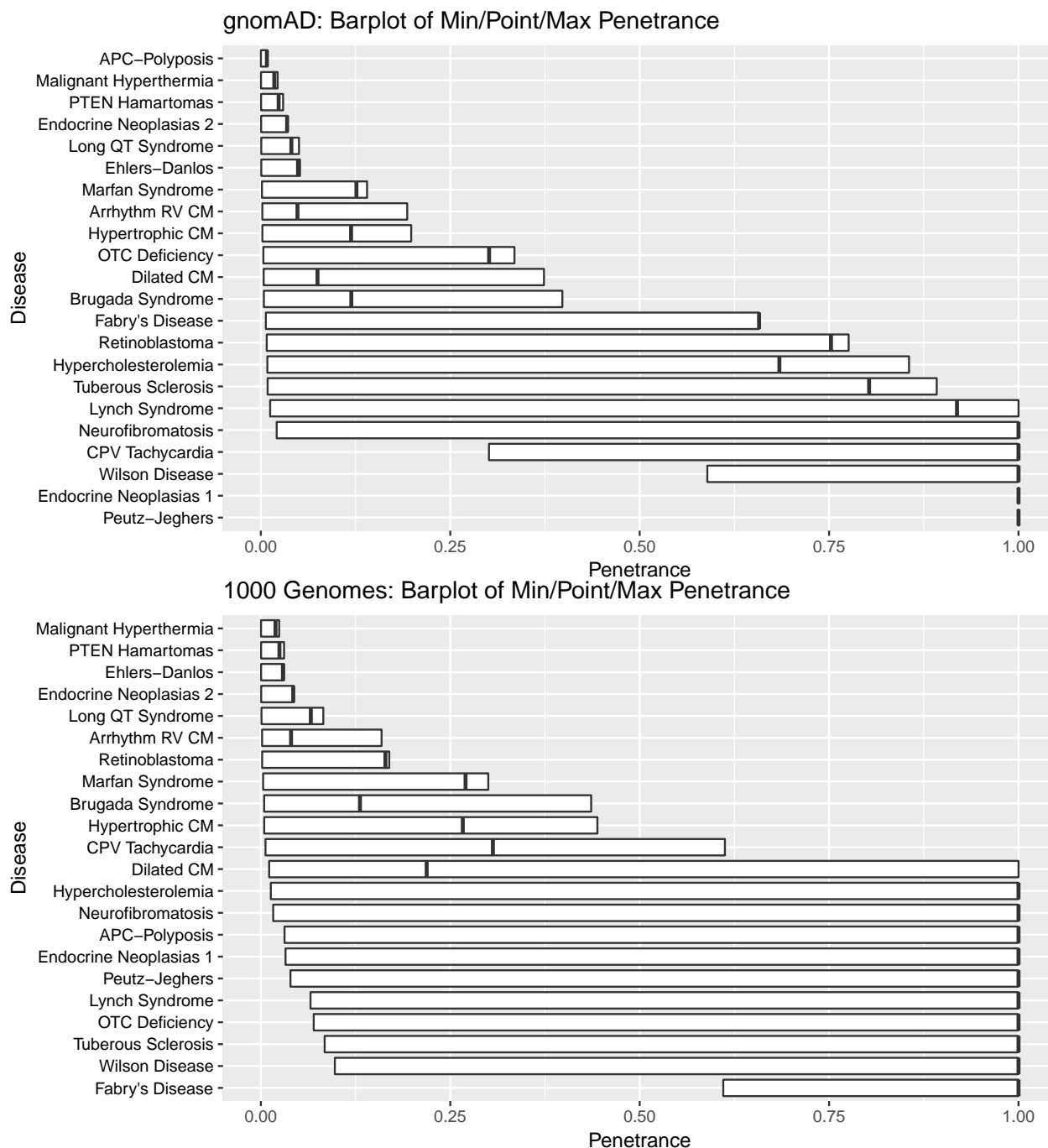
## Testing Independence with Random Sampling



```
## 30 diseases x 1000 points = 30,000 points.  
## This plot has been downsampled 10x and contains 3,000 points.  
## Pearson correlation: 0.995  
## Mean ratio (Calculation/Counting): 0.971
```

### 3.5 Penetrance as a Function of $P(V|D)$

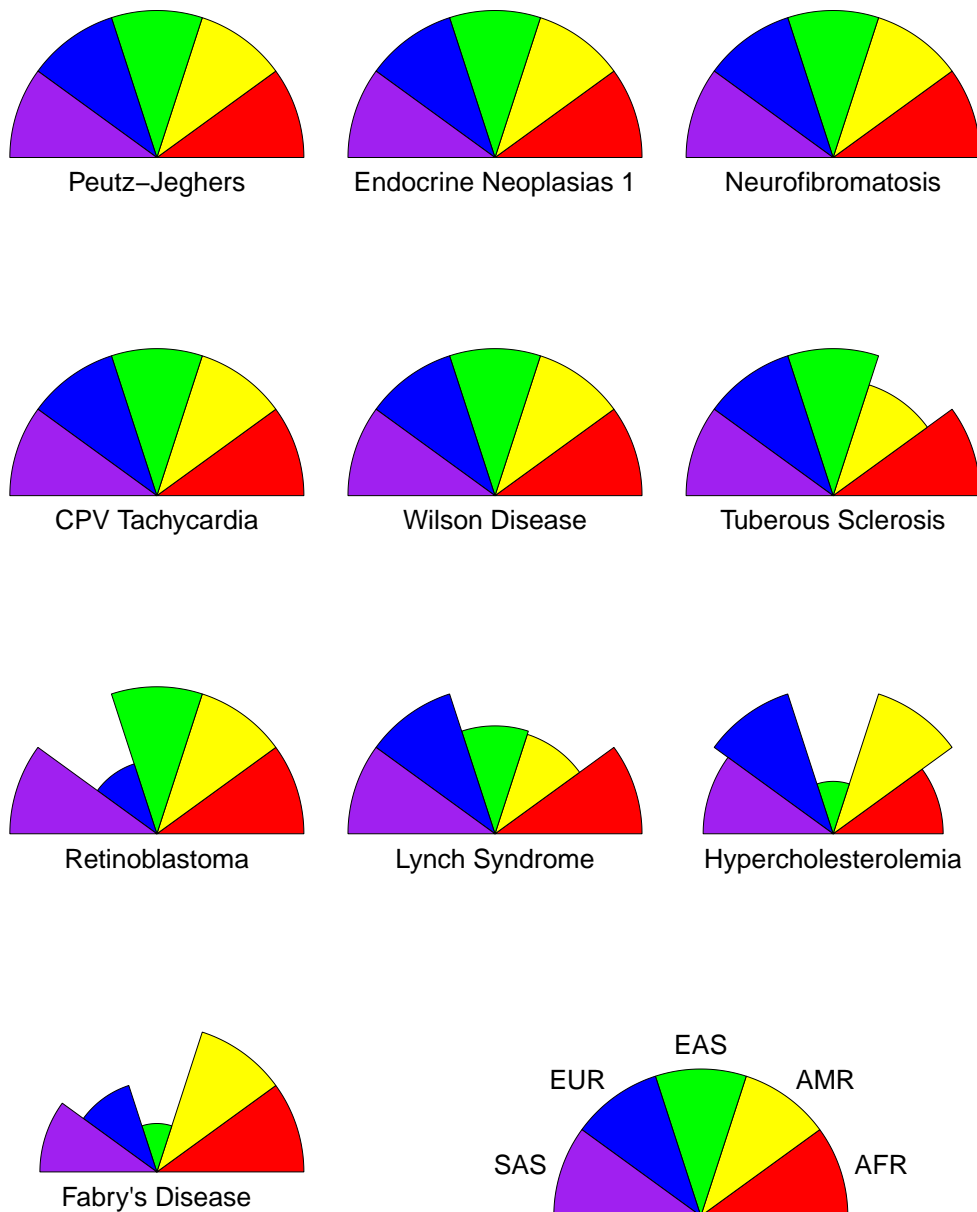
The left end of the boxplot indicates  $P(V|D) = 0.01$ ,  
the bold line in the middle indicates  $P(V|D) = \text{point value}$ ,  
the right end of the boxplot indicates  $P(V|D) = 1$ .



Note: Some diseases have mean theoretical penetrance = 1 because the assumed allelic heterogeneity is greater than is possible, given the observed prevalence and allele frequencies.

### 3.6 Penetrance Estimates by Ancestry

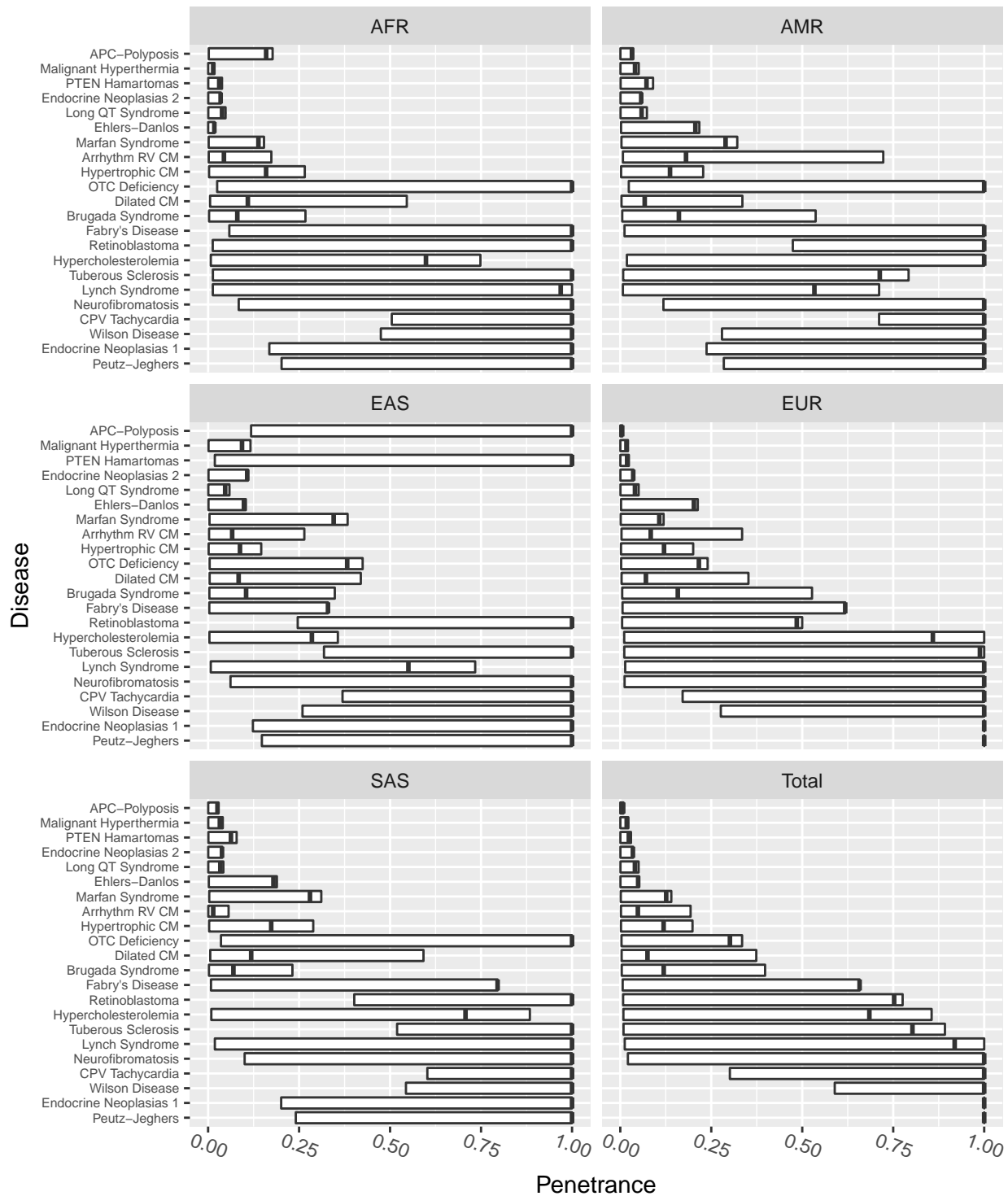
#### Radar Plot: Max Penetrance by Ancestry (gnomAD)



## [1] These are the top 10 diseases by summed allele frequencies. NULL values are not plotted.

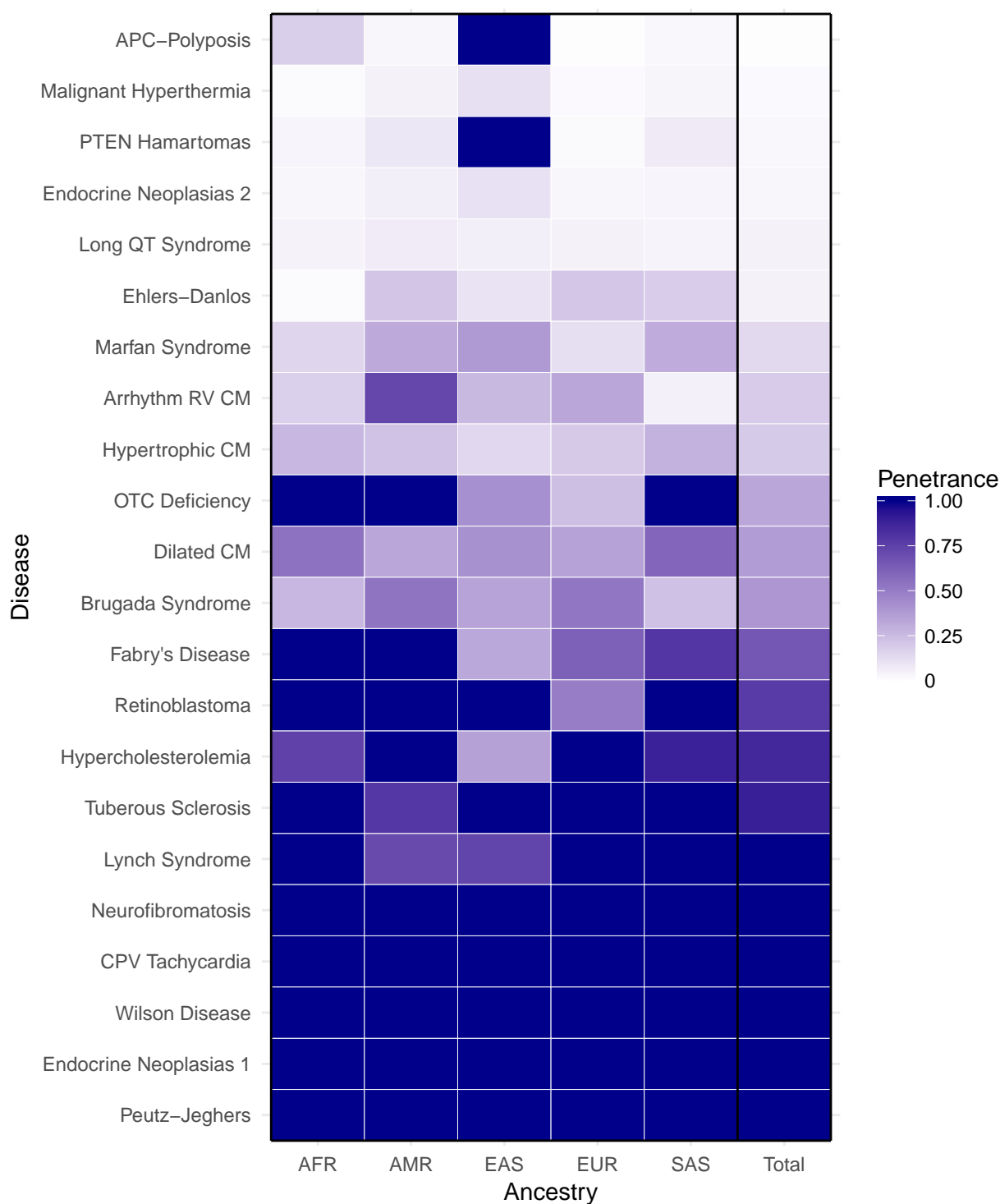
## [1] Each radius is proportional to the penetrance of the disease in the given population.

Barplot: Penetrance by Ancestry (gnomAD)





Heatmap: Max Penetrance by Ancestry (gnomAD)



## Dark gray boxes are NA: no associated variants discovered in that ancestral population.