ACMG-ClinVar Penetrance RMarkdown

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February 1, 2017

Contents

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
N1	Hereditary breast and ovarian cancer	604370|612555	20301425
N2	Hereditary breast and ovarian cancer	604370|612555	20301425
N3	Li-Fraumeni syndrome	151623	20301488
N4	Peutz-Jeghers syndrome	175200	20301443
N5	Lynch syndrome	120435	20301390

Table continues below

	Typical_age_of_onset	Gene	MIM_gene	Inheritance	Variants_to_report
N1	Adult	BRCA1	113705	AD	KP&EP
N2	Adult	BRCA2	600185	AD	KP&EP
N3	Child/Adult	TP53	191170	AD	KP&EP
N4	Child/Adult	STK11	602216	AD	KP&EP
N5	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 16 (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

(a) Unnest the data frames to 1 row per variant_ID key (CHROM_POSITION_REF_ALT).
(b) Remove all insertions, deletions, CNV, etc, and keep only missense variants (1 REF, 1 ALT)
(c) 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

(a) Unnest the data frames to 1 row per variant_ID key (CHROM_POSITION_REF_ALT).
(b) Remove all insertions, deletions, CNV, etc, and keep only missense variants (1 REF, 1 ALT)
(c) 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
44181	MYH11	0.00003310	16_15812604_A_C
378104	ATP7B	0.00000396	13_52511504_C_G
51933	TNNI3	0.00000398	19_55666227_G_C
37564	FBN1	0.00003300	15_48741051_T_C
246311	APOB	0.00005750	2_21235042_G_A

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

	GENE	AF_EXAC	VAR_ID
1020	BRCA1	0.001469000	17_41249263_G_A
13707	RET	0.000008289	10_43595990_G_A
15856	SDHD	0.000030640	11_111957535_G_A
17708	TSC1	0.000008257	9_135801142_A_T
23000	COL3A1	0.013690000	2_189864023_G_A

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

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

sample	pop	super_pop	gender
HG03193	ESN	AFR	male
NA18582	CHB	EAS	female
NA19011	JPT	EAS	female
HG01871	KHV	EAS	female
NA20882	GIH	SAS	female
HG04076	ITU	SAS	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
```

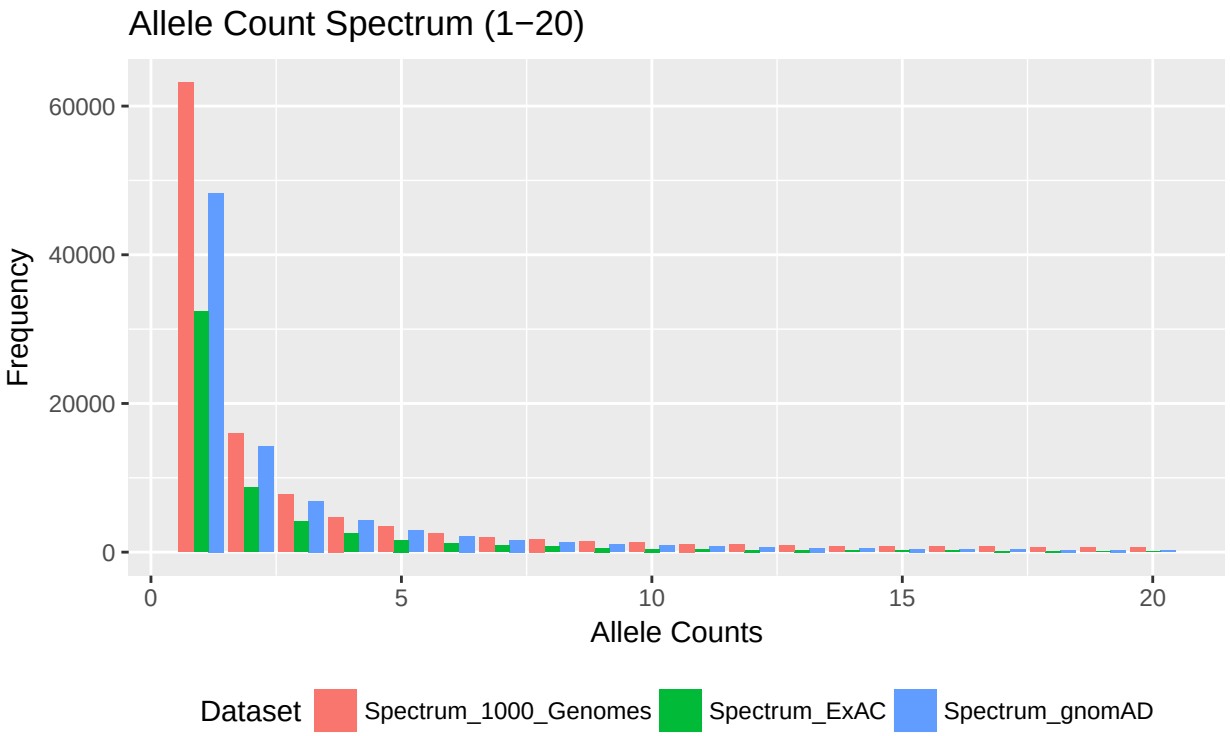
Subset_gnomAD	Number_of_Variants
ACMG in ExAC	59883
ClinVar-ACMG in ExAC	10778
LP/P-ACMG in ExAC	797

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

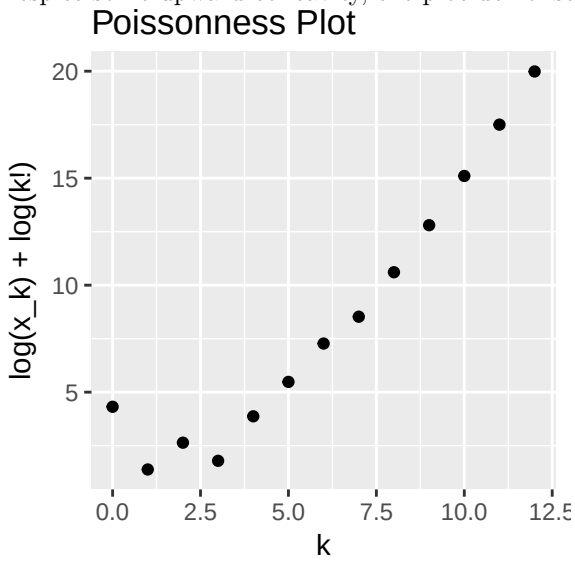
Subset_gnomAD	Number_of_Variants
ACMG in 1000G	141466
ClinVar-ACMG in 1000G	6012
LP/P-ACMG in 1000G	99

2 Plot Summary Statistics Across Populations

2.1 Distribution of Allele Counts



We can model this as a Poisson binomial- the summed occurance 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 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 $x_k = n \Pr(X = k) = n \left(\frac{\lambda^k e^{-k}}{k!} \right)$, 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.

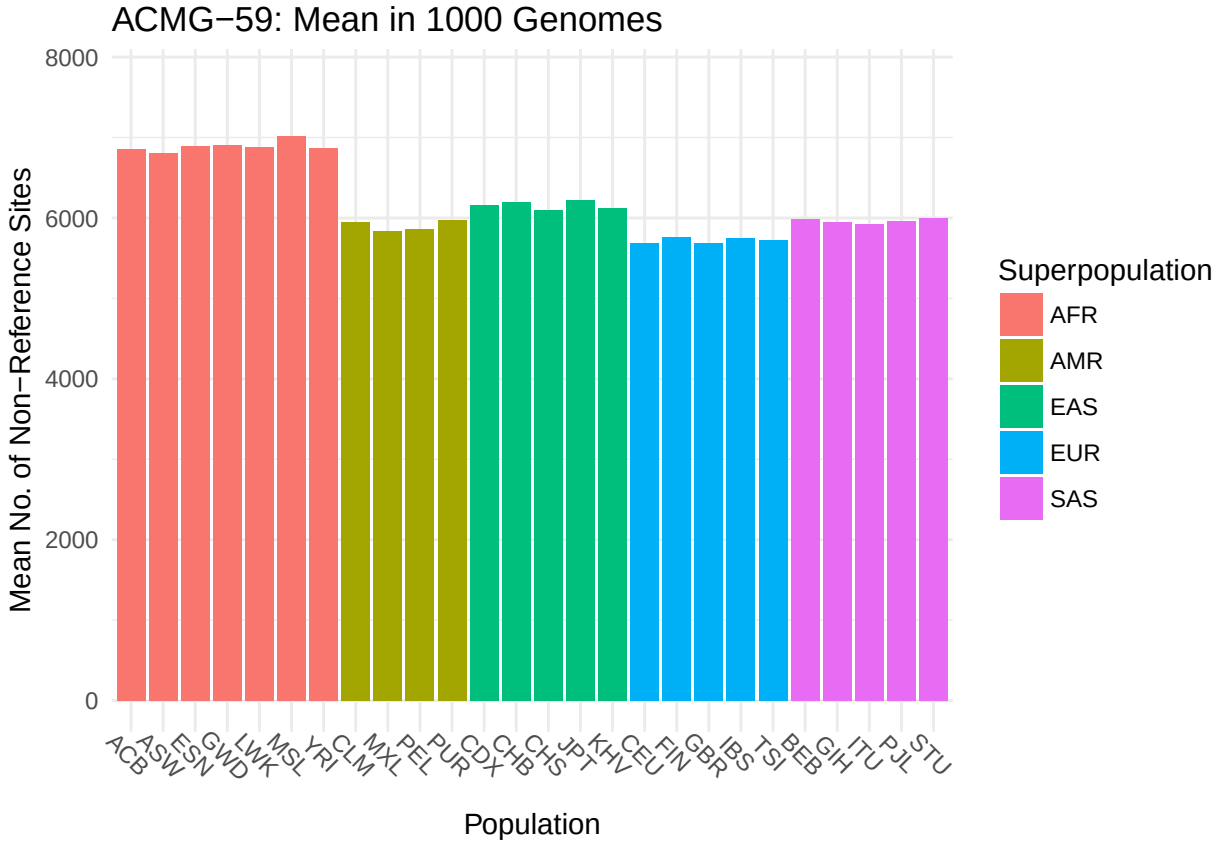
Ex: the genotype of 3 variants in 3 people looks like this:

	HG00366	HG00367	HG00368
Variant 1	2	1	1
Variant 2	2	1	1
Variant 3	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:

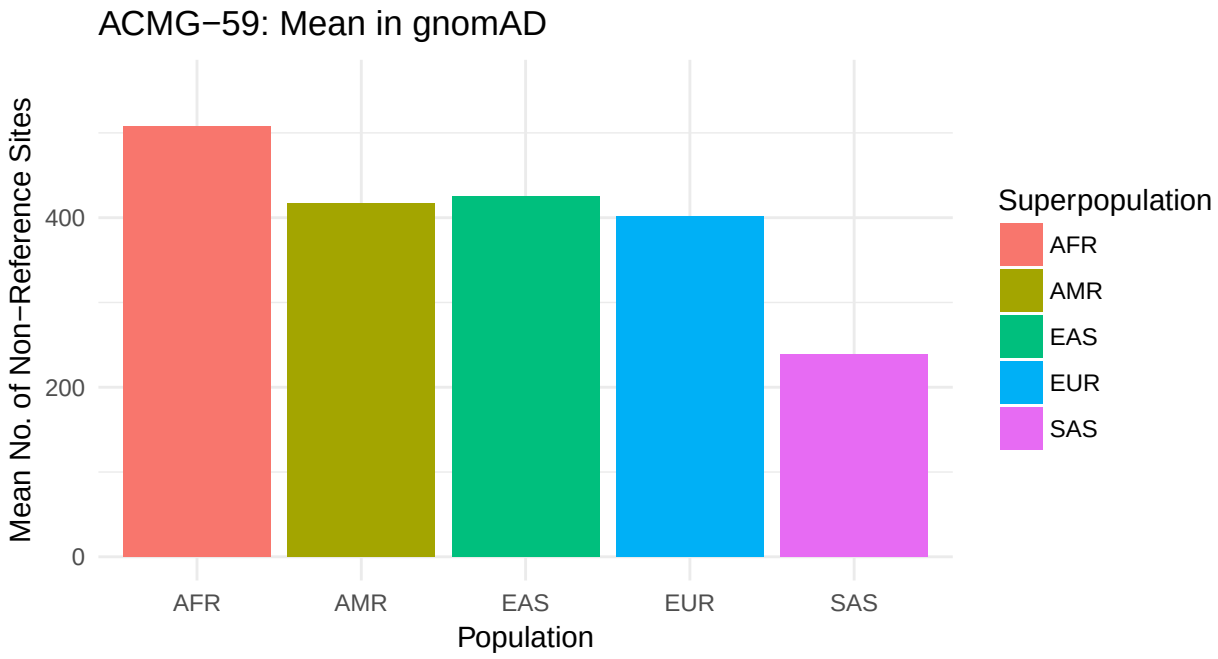
	AFR	AMR	EAS	EUR	SAS
Variant 1	0.1	0.2	0	0	0.3
Variant 2	0.2	0	0.3	0	0.1

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
Variant 1	0.19	0.36	0	0	0.51
Variant 2	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



2.3 Fraction of Individuals with Pathogenic Sites

2.3.0.1 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.

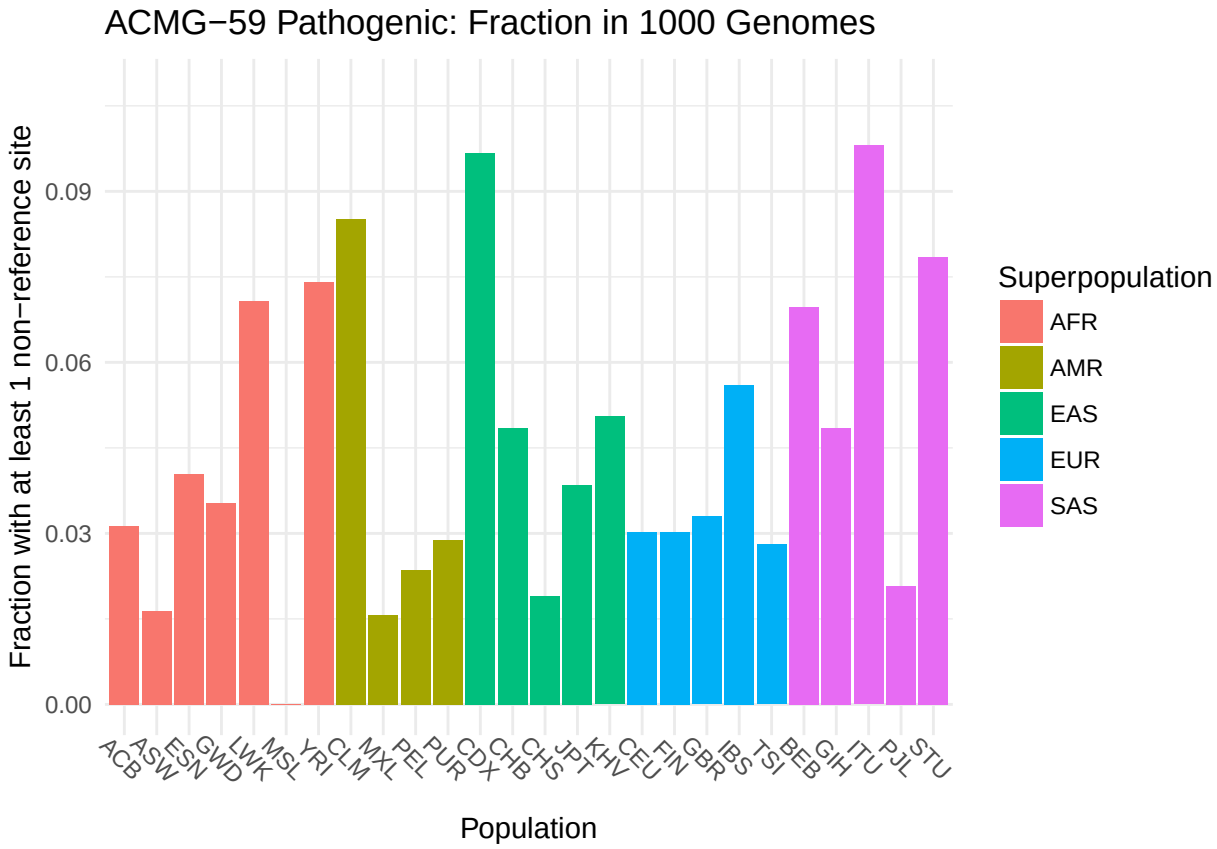
Ex: the genotype of 3 variants in 3 people looks like this:

	HG00366	HG00367	HG00368
Variant 1	2	1	1
Variant 2	2	1	1
Variant 3	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
```



2.3.0.2 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:

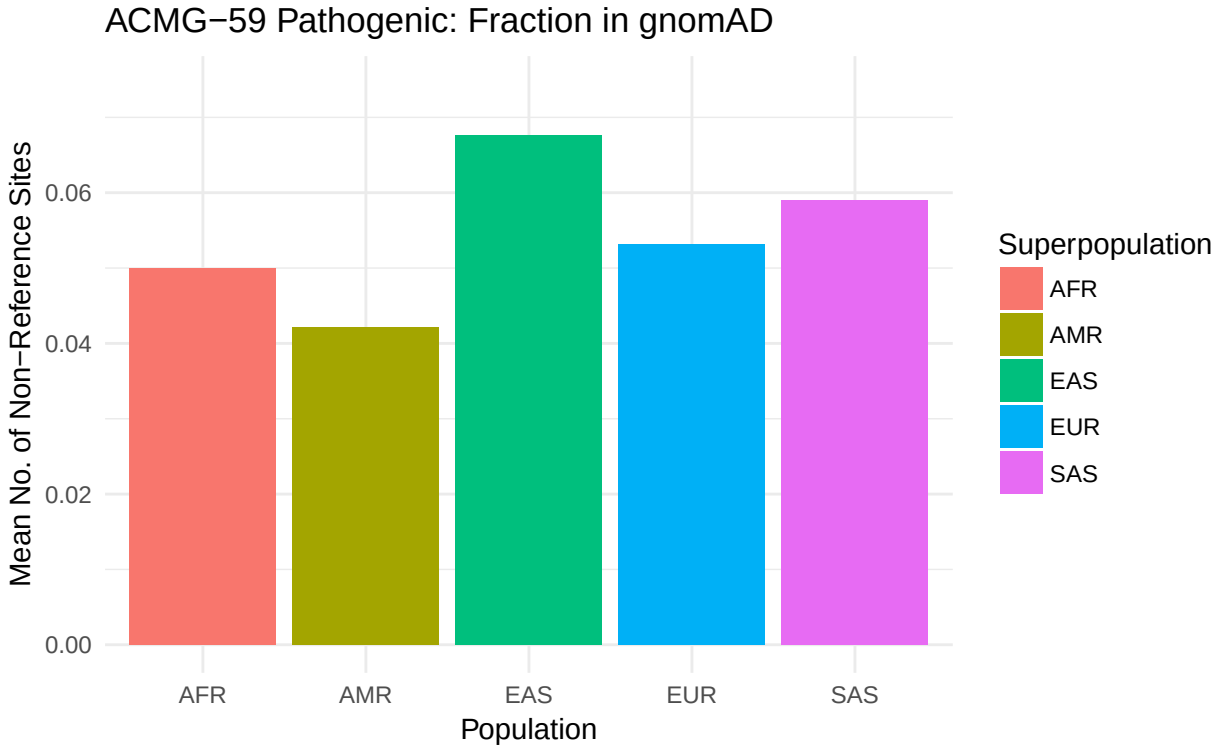
	AFR	AMR	EAS	EUR	SAS
Variant 1	0.1	0.2	0	0	0.3
Variant 2	0.2	0	0.3	0	0.1

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:

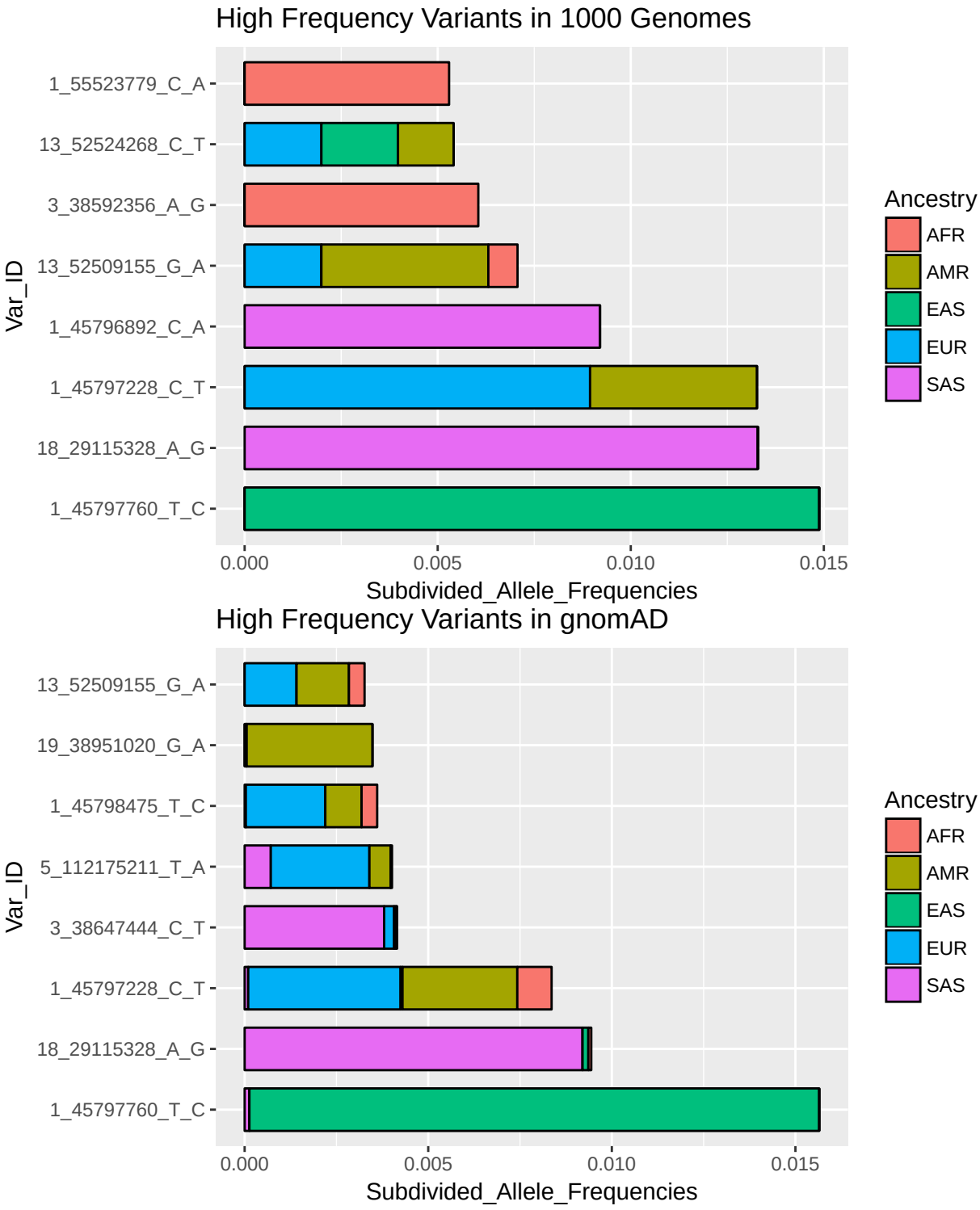
	AFR	AMR	EAS	EUR	SAS
Variant 1	0.19	0.36	0	0	0.51
Variant 2	0.36	0	0.51	0	0.19

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



2.4 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.

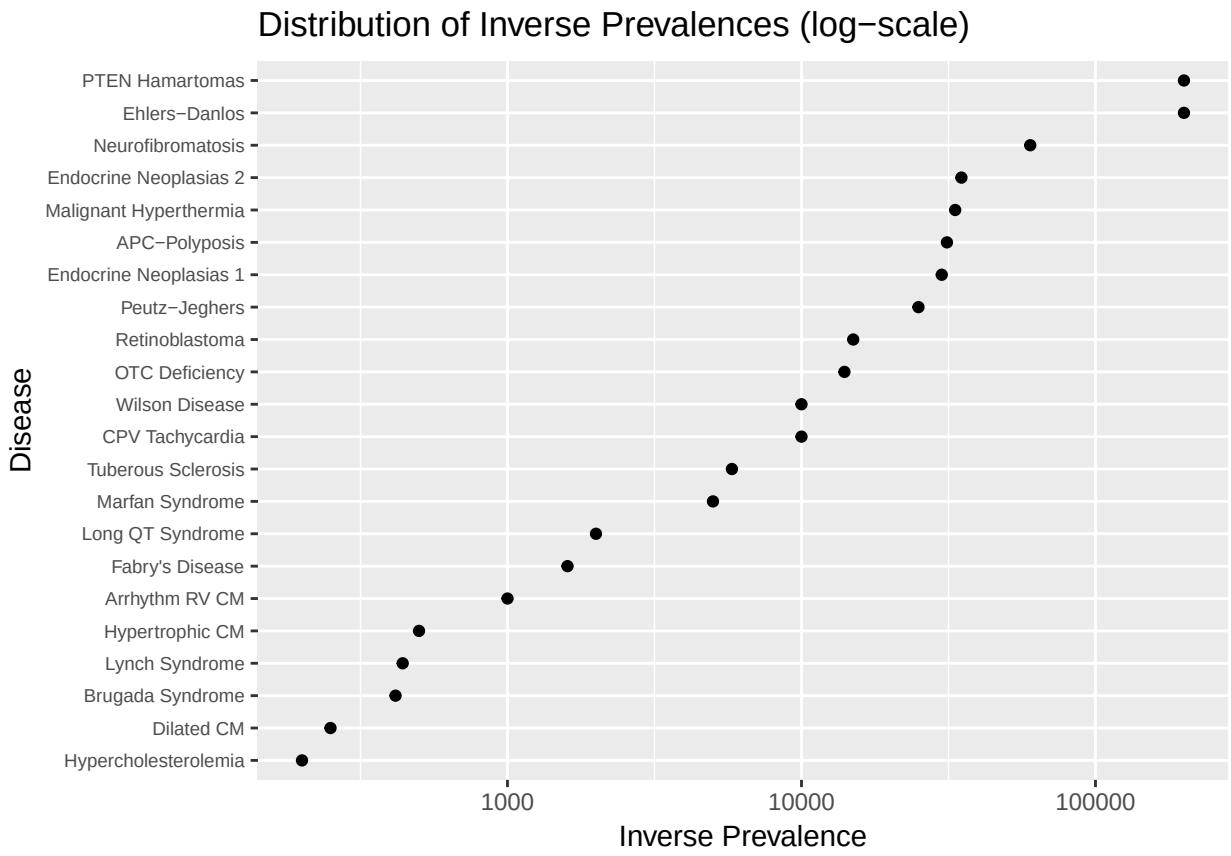
```
## Table of Literature-Based Estimates 22 x 20 (selected rows/columns):
```

Gene	Phenotype
APC	Familial adenomatous polyposis
MEN1	Multiple endocrine neoplasia type 1
MYH7|TPM1|MYBPC3|PRKAG2|TNNI3|MYL3|MYL2|ACTC1	Hypertrophic cardiomyopathy
STK11	Peutz-Jeghers syndrome

Table continues below

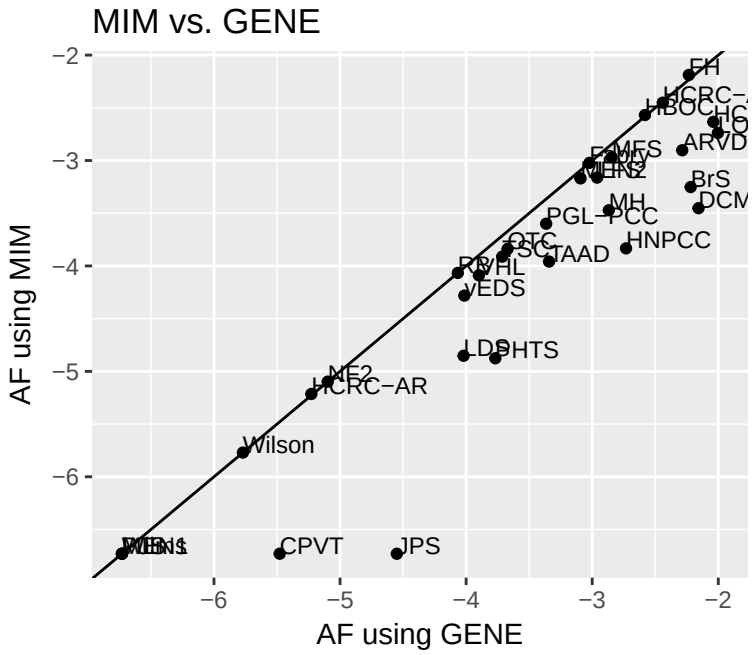
Inverse_Prevalence	Case_Allele_Frequency
31250	0.9
30000	0.9
500	0.6
25000	0.96

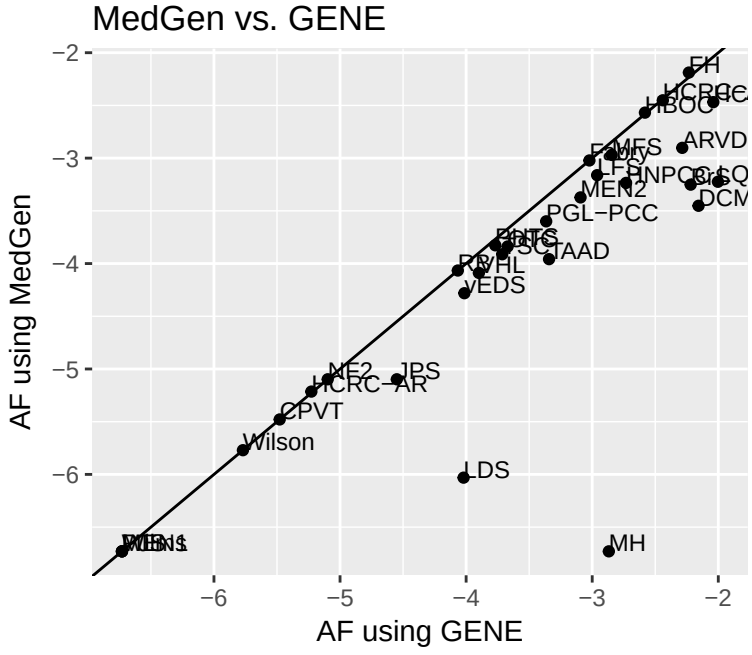
3.3 Distribution of Prevalences



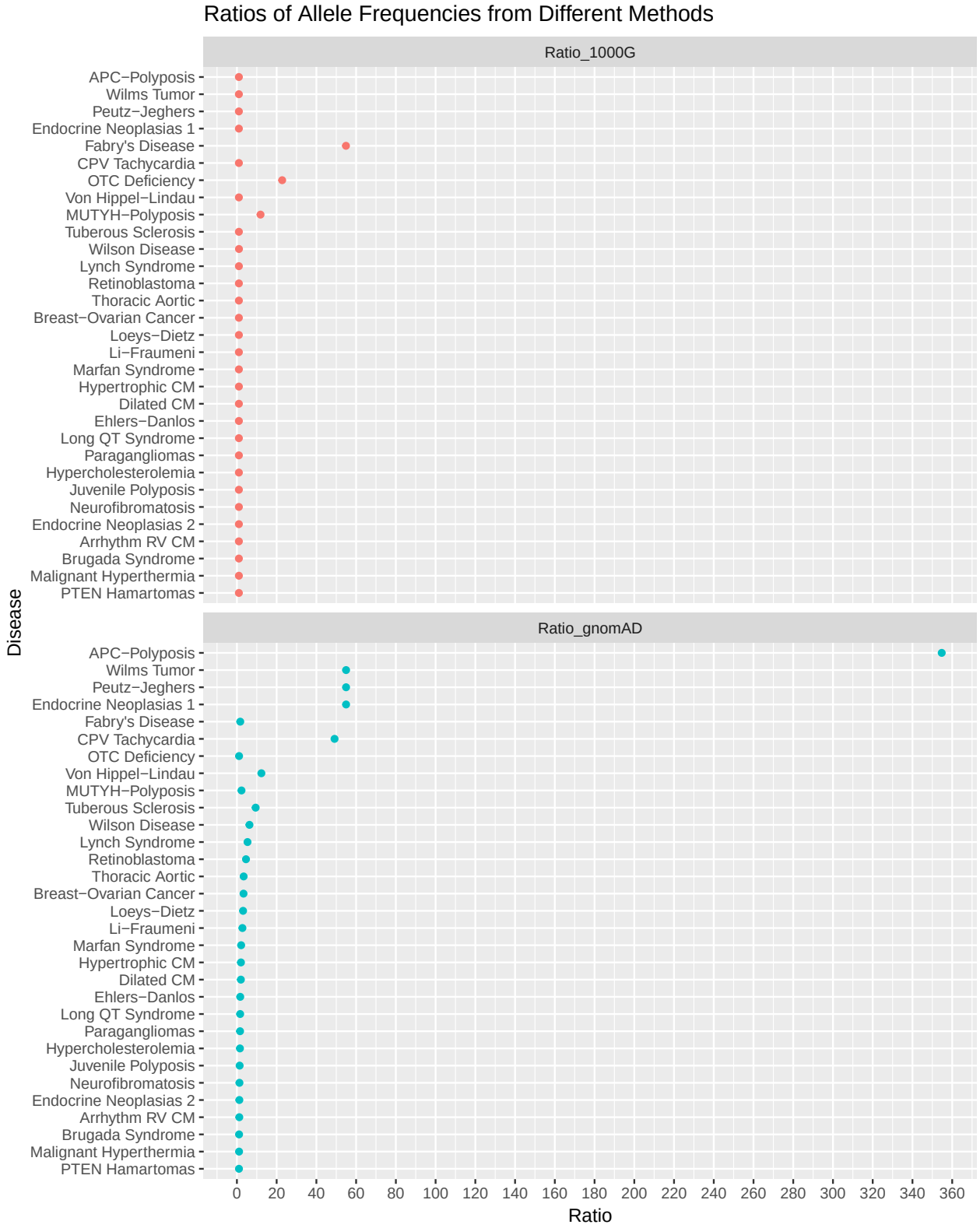
3.4 Collect and Aggregate Allele Frequencies at the Disease-Level

We define AF(disease) as the probability of having at least 1 variant associated with the disease. The variants can be assigned to diseases in two ways:
(1) By associating it by MIM. An MIM code is assigned for around 31% of assertions in each dataset.
(1) By associating it by MedGen. An MIM code is assigned for around 22% of assertions in each dataset.
(2) By associating it by gene. All variants are associated with genes, but some variants may be designated as pathogenic for non-ACMG conditions.
The frequencies across the relevant variants can be aggregated in two ways:
(1) By direct counting, from genotype data in 1000 Genomes.
(2) AF(disease) $= 1 - \prod_{variant}(1 - AF_{variant})$, from population data in 1000 Genomes, ExAC, or gnomAD (assumes independence).

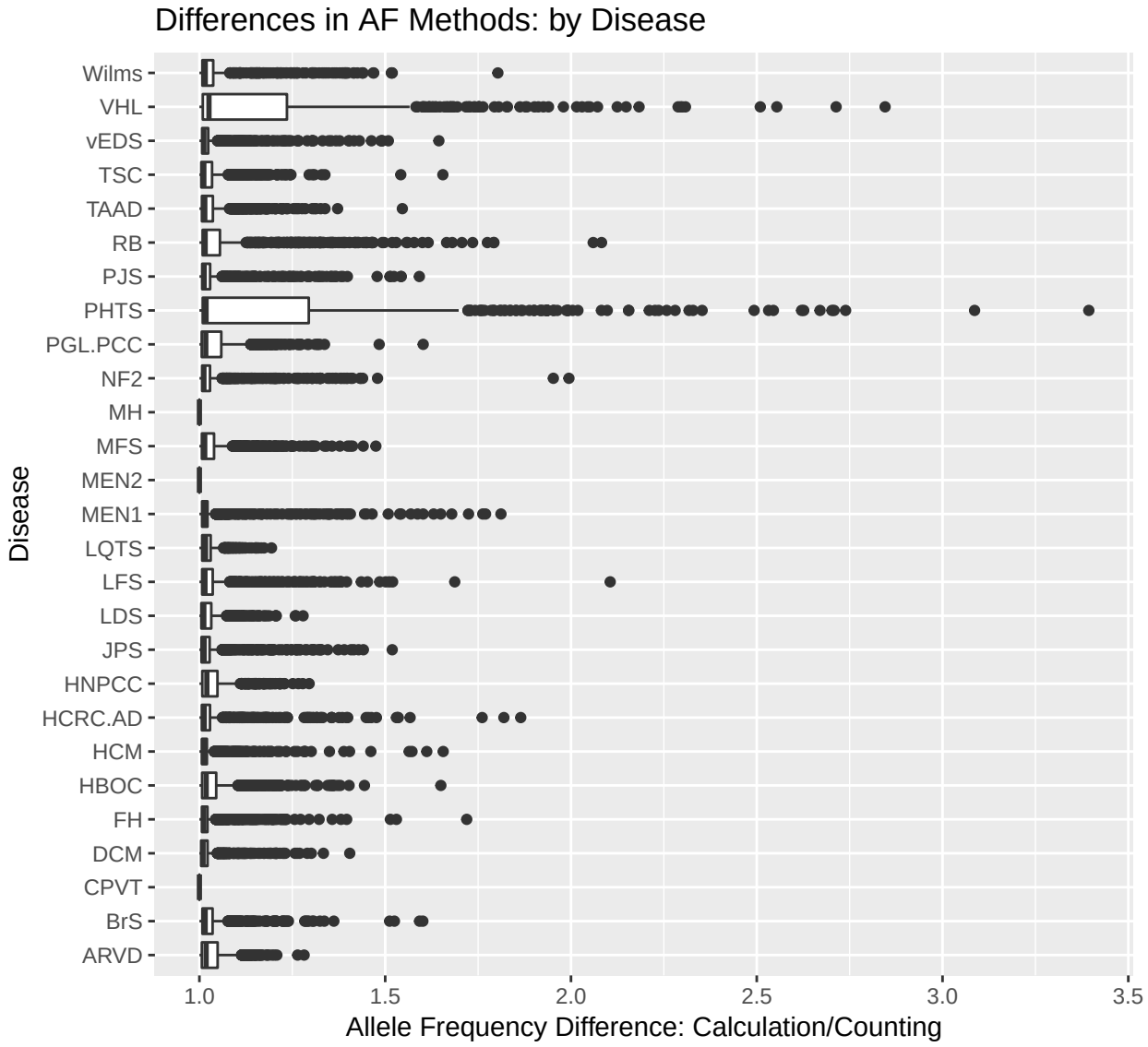


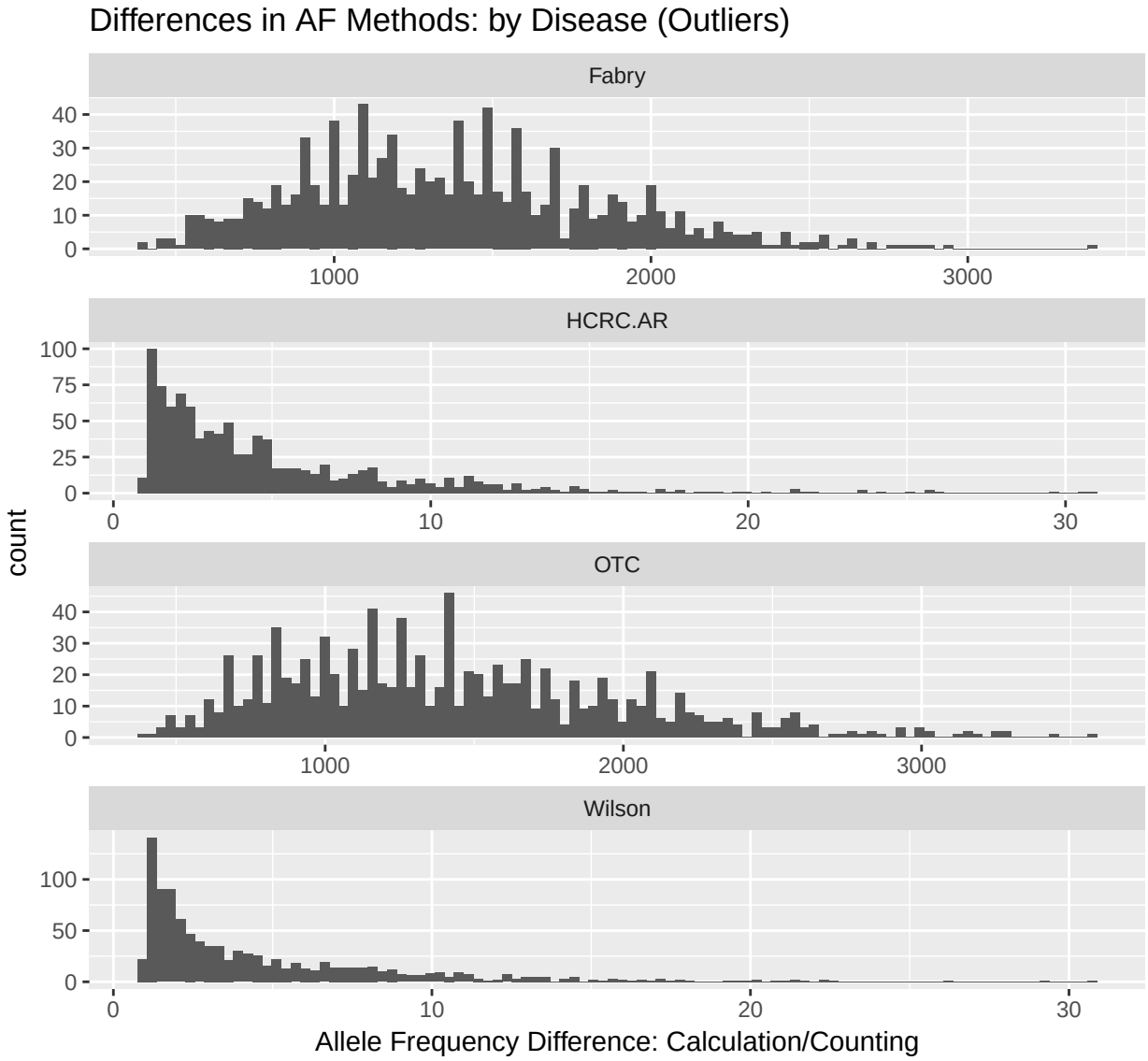


Ratio_1000G (red, top) computes AF(calculation in 1000 Genomes) / AF(counting in 1000 Genomes).
Ratio_gnomAD (blue, bottom) computes AF(calculation in gnomAD) / AF(calculation in 1000 Genomes).



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 $< 1\%$ are evaluated. Since we look at 17 variants per disease, the maximum is approximately $1 - (1 - 0.01)^{34} \approx 0.29$



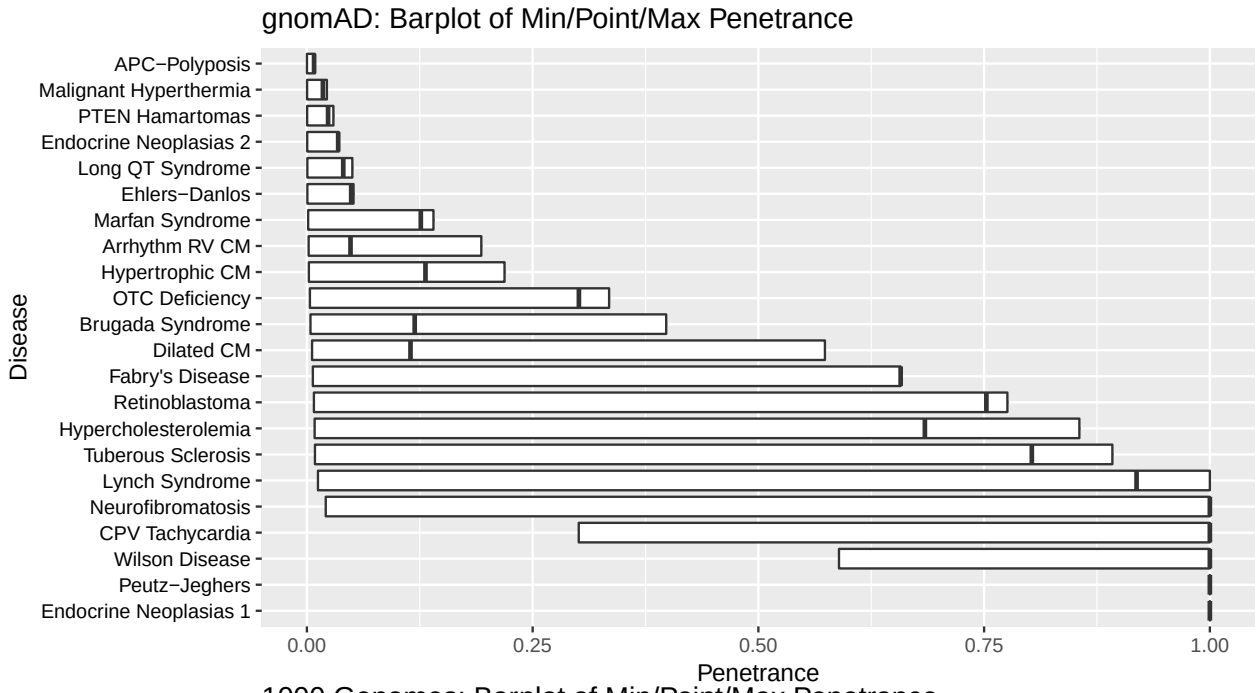

Differences in AF Methods: by Disease (Outliers)
Fabry
HCRC.AR
OTC
Wilson
count
Allele Frequency Difference: Calculation/Counting

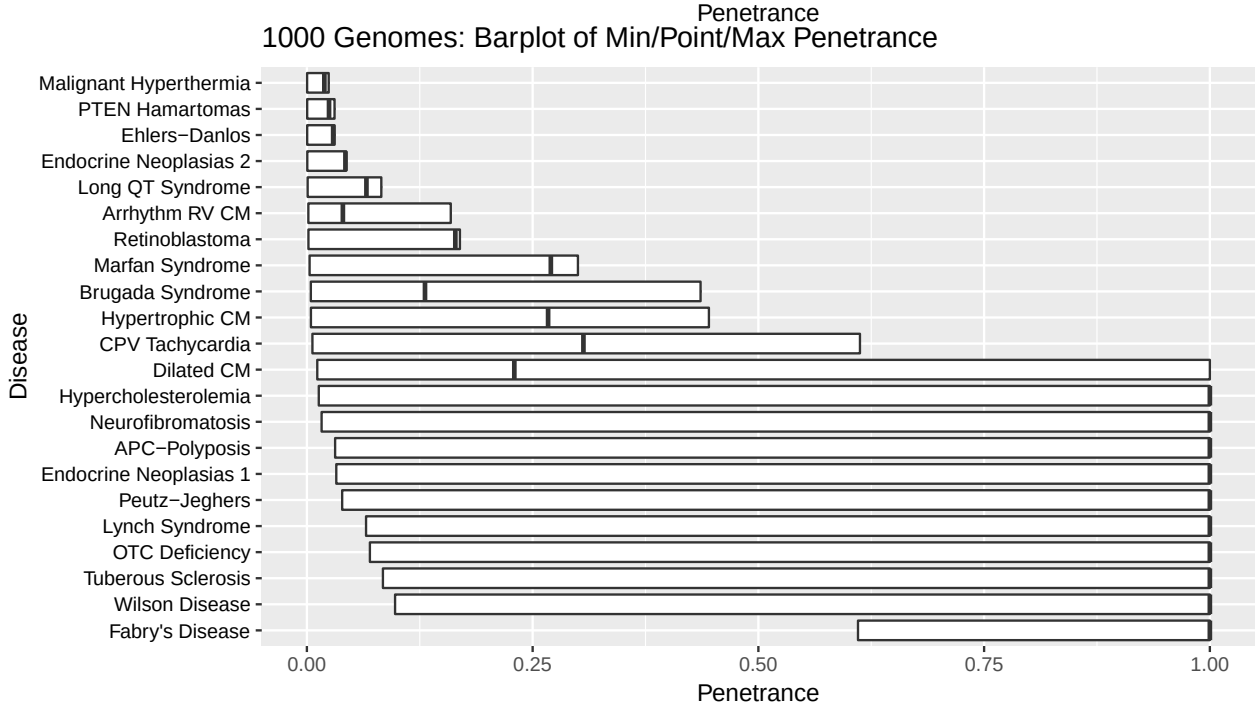

```
## 31 diseases x 1000 points = 31,000 points.
## This plot has been downsampled 100x and contains 310 points.
## AR (autosomal recessive) and XL (X-linked) diseases are colored in red.
```

```
## Pearson correlation: 0.989
```

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

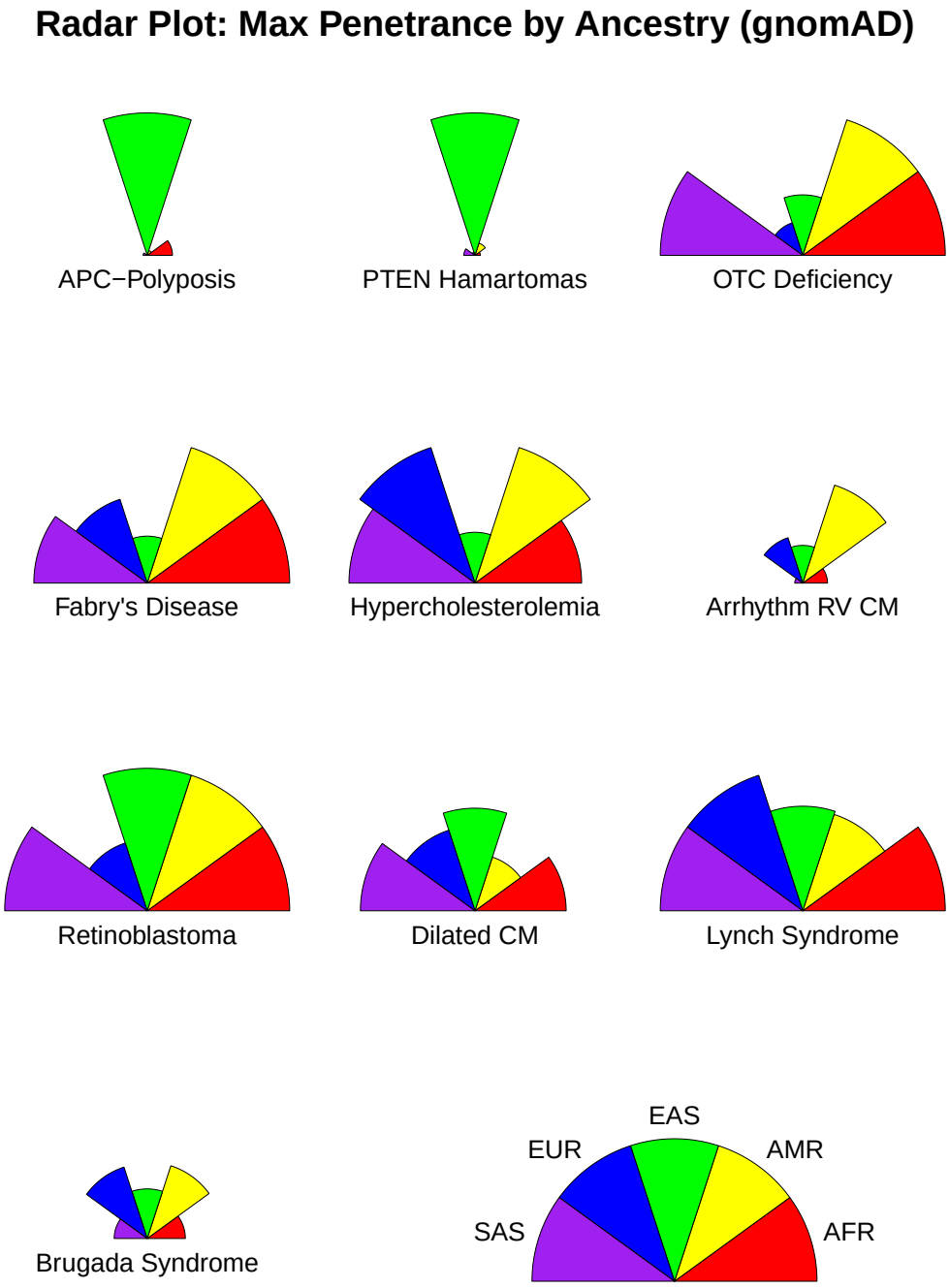
The left end of the boxplot indicates P(V|D) = 0.01,
the bold line in the middle indicates P(V|D) = point value,
the right end of the boxplot indicates P(V|D) = 1.



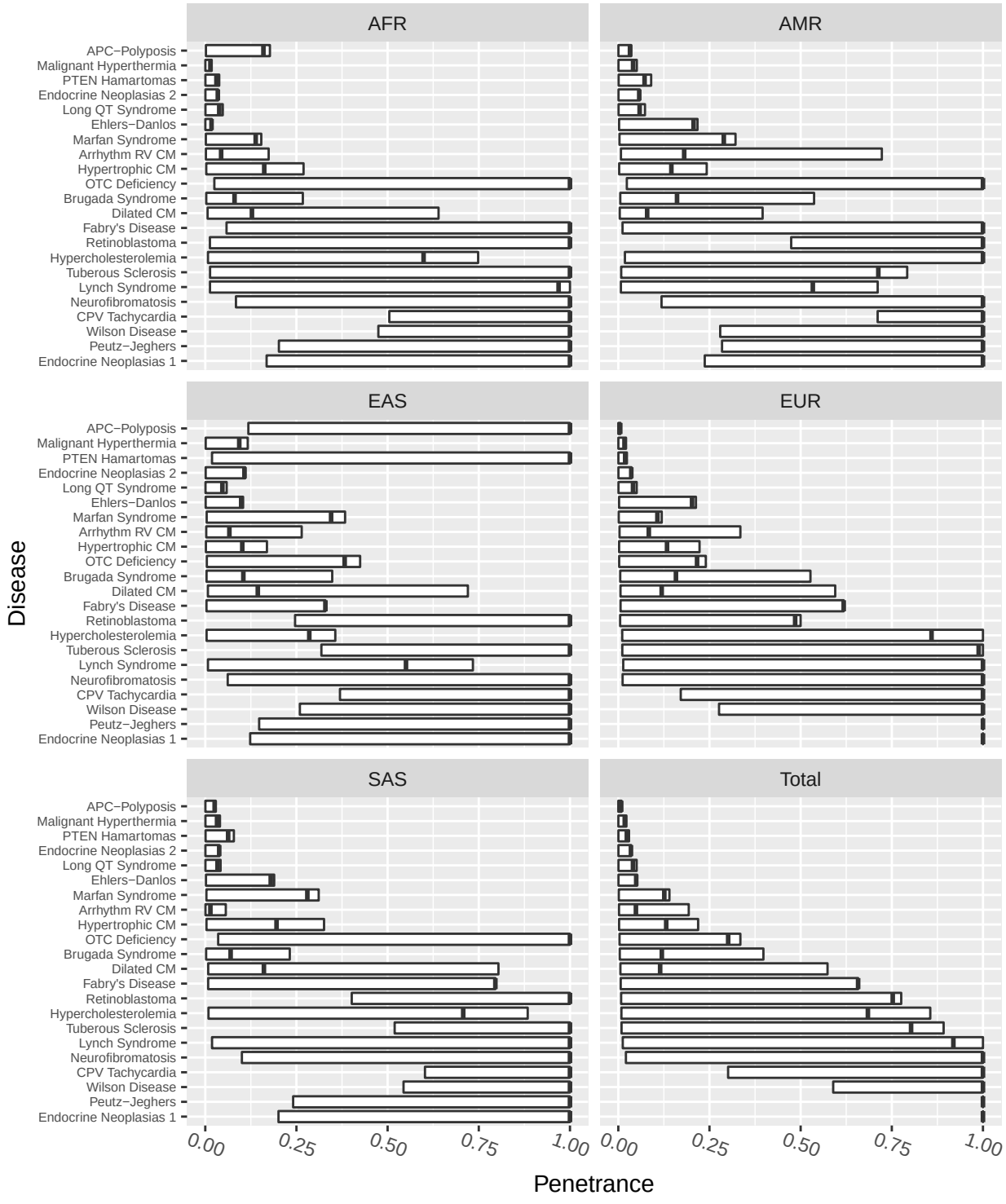


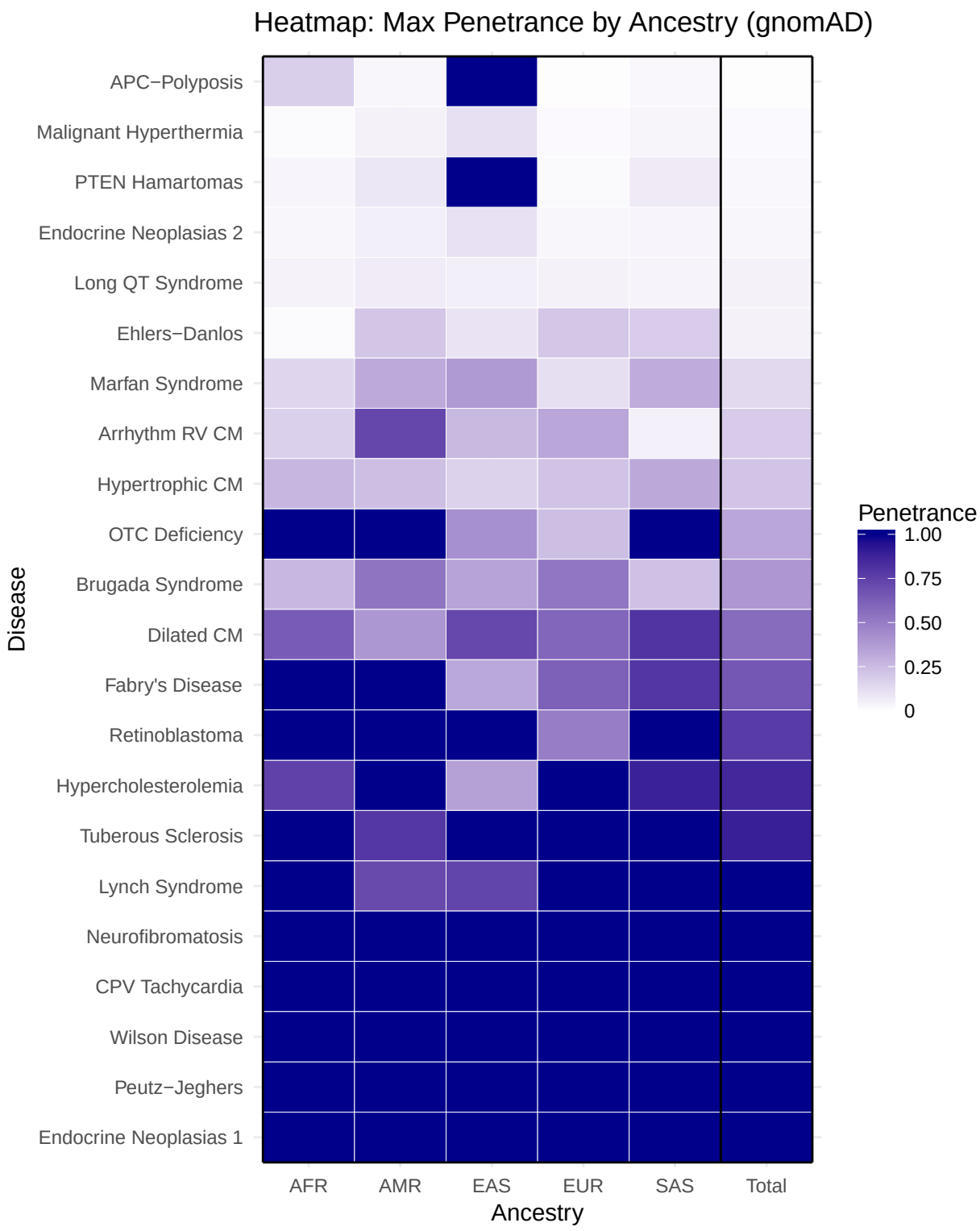
Note: Some diseases have mean theoretical penetrance = 1 because the assumed allelic heterogeneity is greater than is possible, given the observed prevalence and allele frequencies.

3.6 Penetrance Estimates by Ancestry




```
## [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)
AFR
AMR
EAS
EUR
SAS
Total
Disease
APC−Polyposis
Malignant Hyperthermia
PTEN Hamartomas
Endocrine Neoplasias 2
Long QT Syndrome
Ehlers−Danlos
Marfan Syndrome
Arrhythm RV CM
Hypertrophic CM
OTC Deficiency
Brugada Syndrome
Dilated CM
Fabry's Disease
Retinoblastoma
Hypercholesterolemia
Tuberous Sclerosis
Lynch Syndrome
Neurofibromatosis
CPV Tachycardia
Wilson Disease
Peutz−Jeghers
Endocrine Neoplasias 1
0.00
0.25
0.50
0.75
1.00
Penetrance


Heatmap: Max Penetrance by Ancestry (gnomAD)
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Malignant Hyperthermia
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