

ClinVar Report

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January 8, 2017

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Sourcing ClinVar input from: clinvar_2016-10-03.vcf

Sending output to: Report_2016-10-03.pdf

1 Collect and Merge ClinVar Data

1.1 Import ClinVar VCF

1.2 Merge ClinVar with 1000 Genomes and ExAC

Breakdown of ClinVar Variants

Subset_ClinVar	Number_of_Variants
Total ClinVar	117355
LP/P	33615
ACMG LP/P	7390
ACMG LP/P in gnomAD	1425
ACMG LP/P in ExAC	1012
ACMG LP/P in 1000 Genomes	159

Breakdown of ACMG-gnomAD Variants

Subset_gnomAD	Number_of_Variants
ACMG in gnomAD	96742
ClinVar-ACMG in gnomAD	11836
LP/P-ACMG in gnomAD	1425

Breakdown of ACMG-ExAC Variants

Subset_gnomAD	Number_of_Variants
ACMG in ExAC	59883
ClinVar-ACMG in ExAC	9506
LP/P-ACMG in ExAC	1012

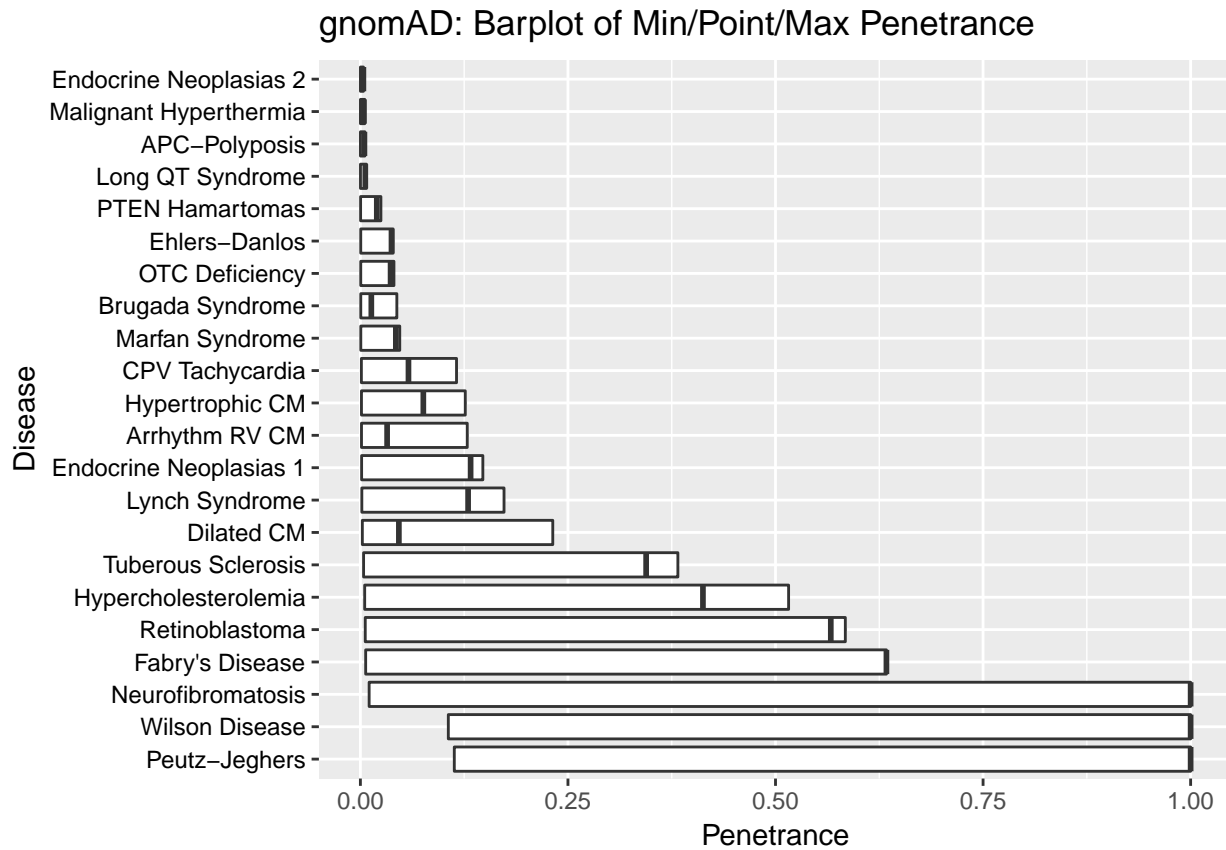
Breakdown of ACMG-1000G Variants

Subset_gnomAD	Number_of_Variants
ACMG in 1000G	141466
ClinVar-ACMG in 1000G	4416
LP/P-ACMG in 1000G	159

3 Penetrance Estimates

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

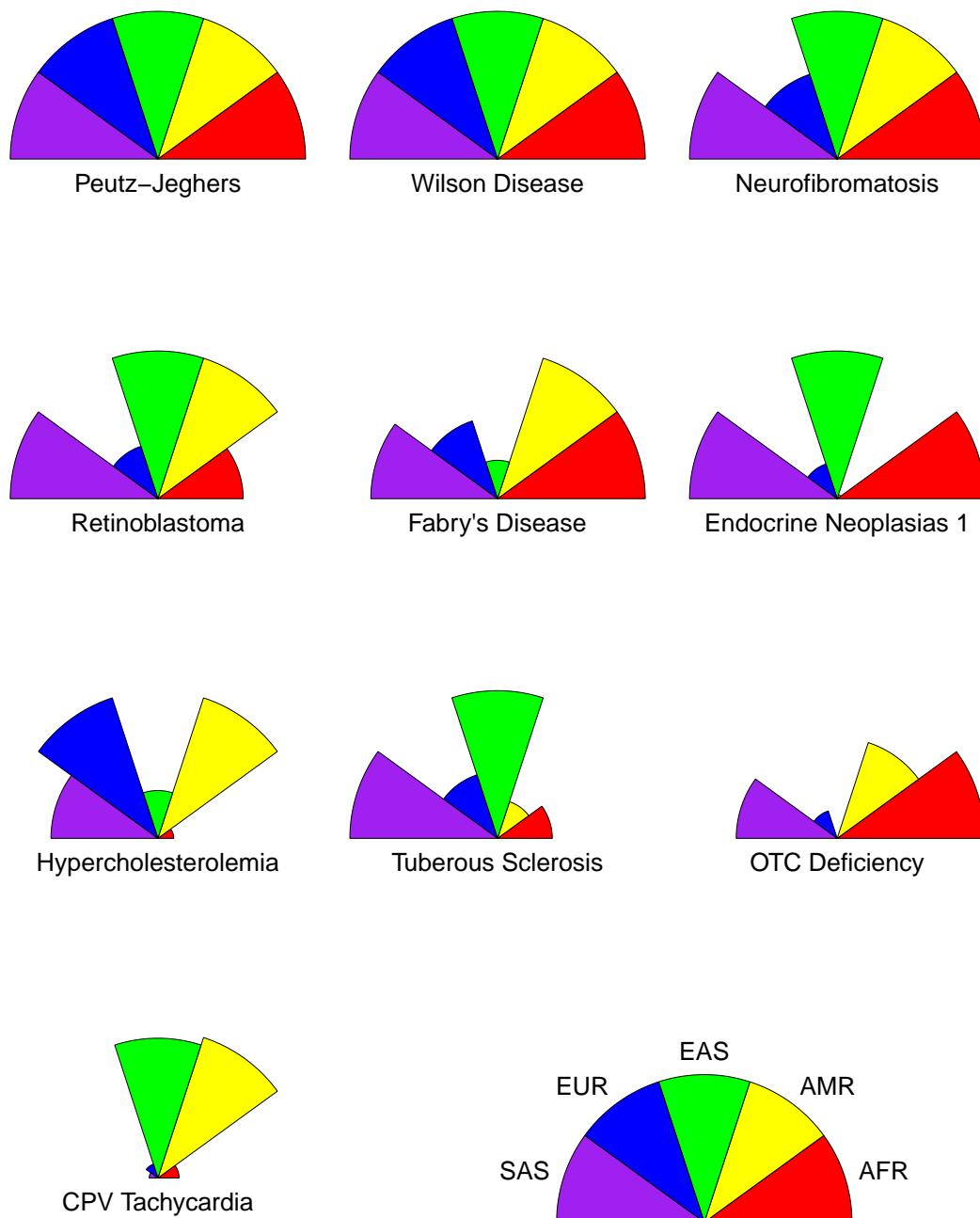
The left end of the boxplot indicates $P(V|D) = 0.01$,
the bold line in the middle indicates $P(V|D) = \text{point value}$,
the right end of the boxplot indicates $P(V|D) = 1$.



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.

3.2 Penetrance Estimates by Ancestry

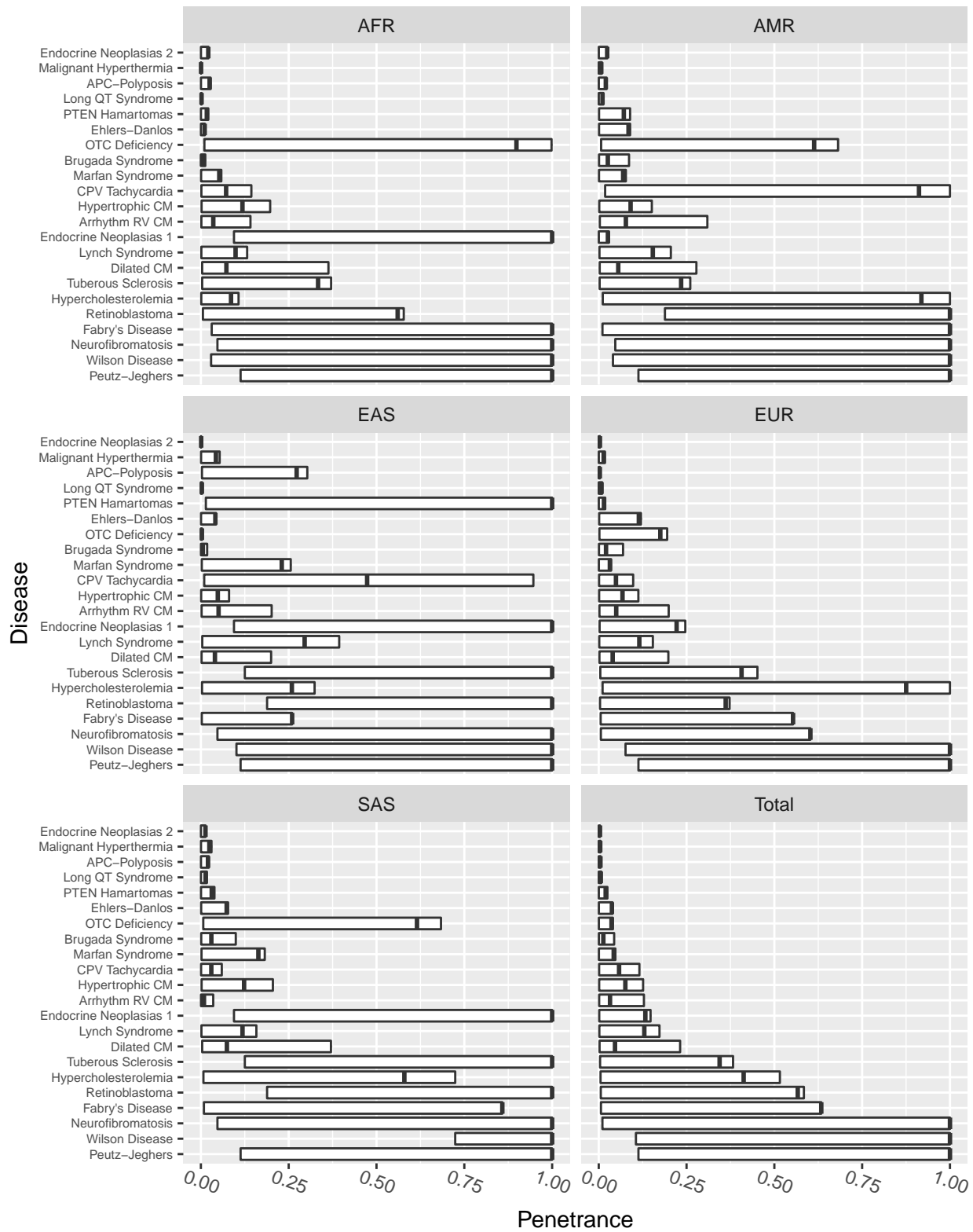
Radar Plot: Max Penetrance by Ancestry (gnomAD)



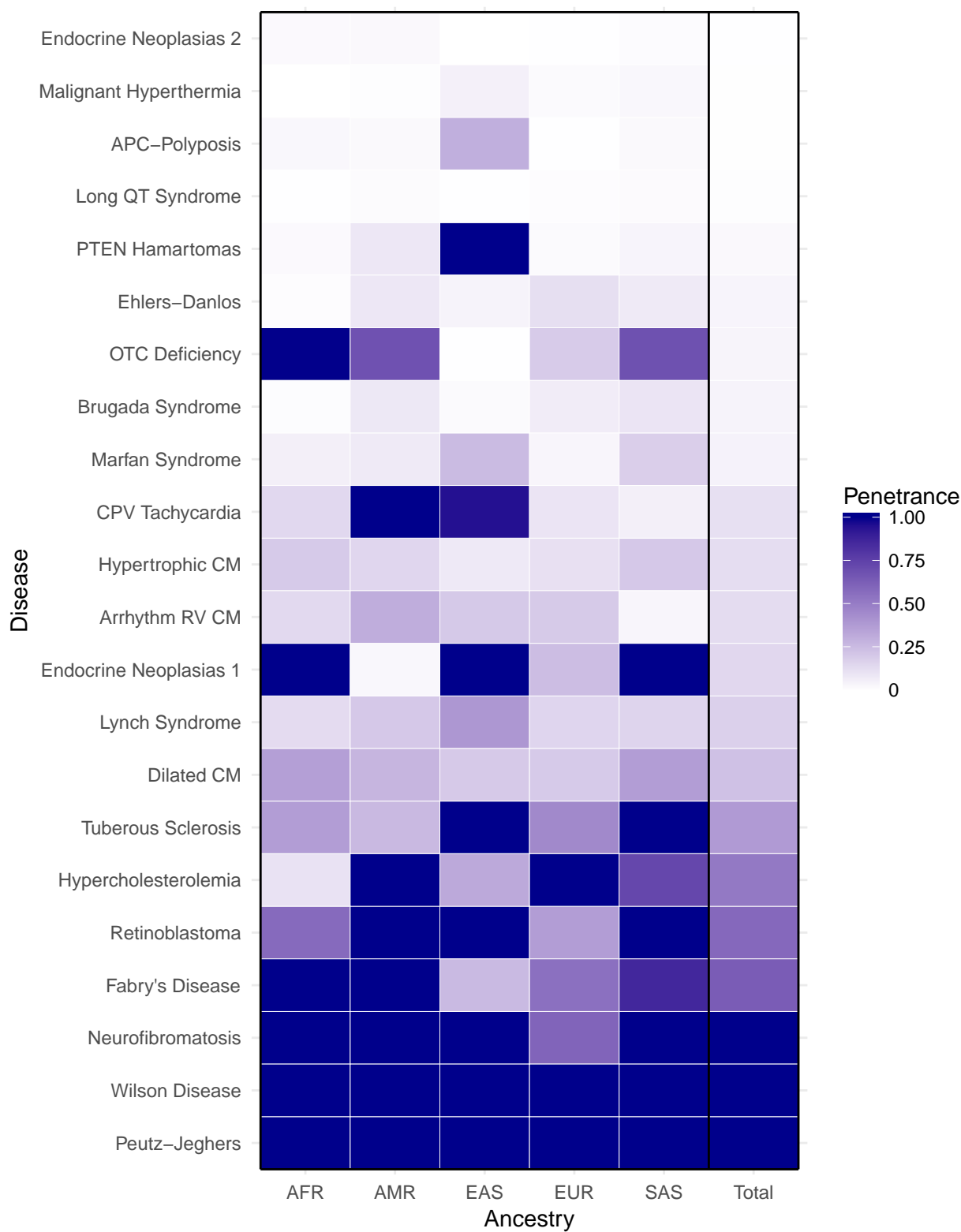
[1] These are the top 10 diseases by summed allele frequencies. NULL values are not plotted.

[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.