# ClinVar Report

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# November 4, 2016

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		ng ClinVar input from: clinvar_2016-04-05.vcf ng output to: Report_2016-04-05.pdf		

# 1 Collect and Merge ClinVar Data

# 1.1 Import ClinVar VCF

## Processed ClinVar data frame 100642 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	100642
LP/P-ClinVar	31042
LP/P-ClinVar & ACMG	6289
LP/P-ClinVar & ACMG & ExAC	955
LP/P-ClinVar & ACMG & 1000	168
Genomes	

#### ## Breakdown of ACMG-1000 Genomes Variants

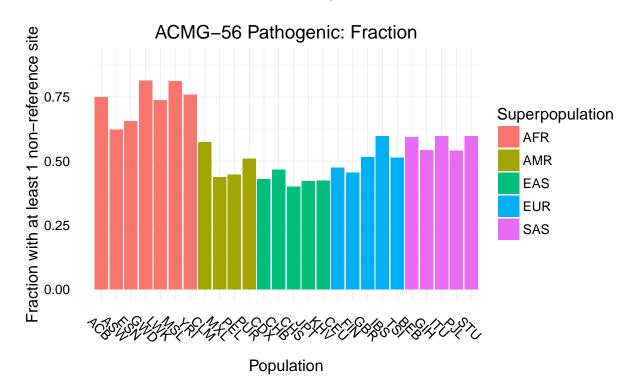
Subset_1000_Genomes	Number_of_Variants
Total 1000_Genomes & ACMG	139335
$1000\_Genomes \ \& \ ACMG \ \& \ ClinVar$	4050
1000_Genomes & ACMG &	168
LP/P-ClinVar	

#### ## Breakdown of ACMG-ExAC Variants

Subset_ExAC	Number_of_Variants
Total ExAC & ACMG	58873
ExAC & ACMG & ClinVar	8091
ExAC & ACMG & LP/P-ClinVar	955

# 2 Summary Statistics

# 2.1 Fraction of Individuals with Pathogenic Non-Reference Sites



ACMG-56 Pathogenic: Mean in ExAC

Superpopulation

AFR

AMR

EAS

Population

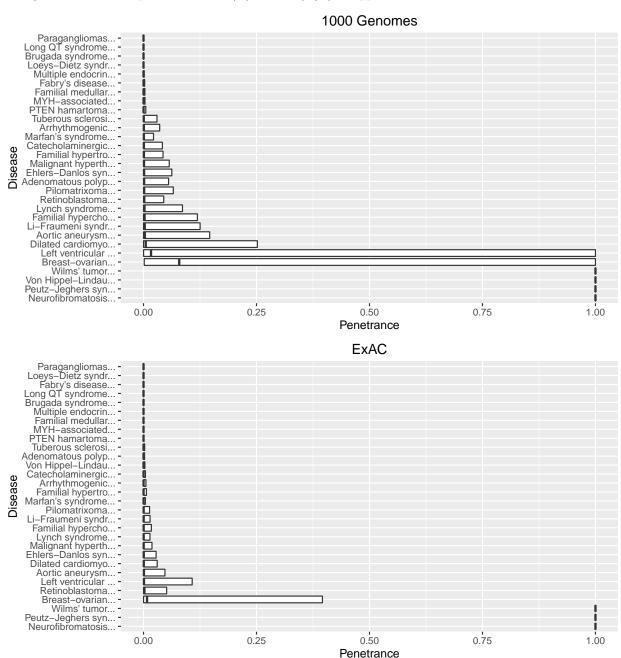
AFR

SAS

#### 3 Penetrance Estimates

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

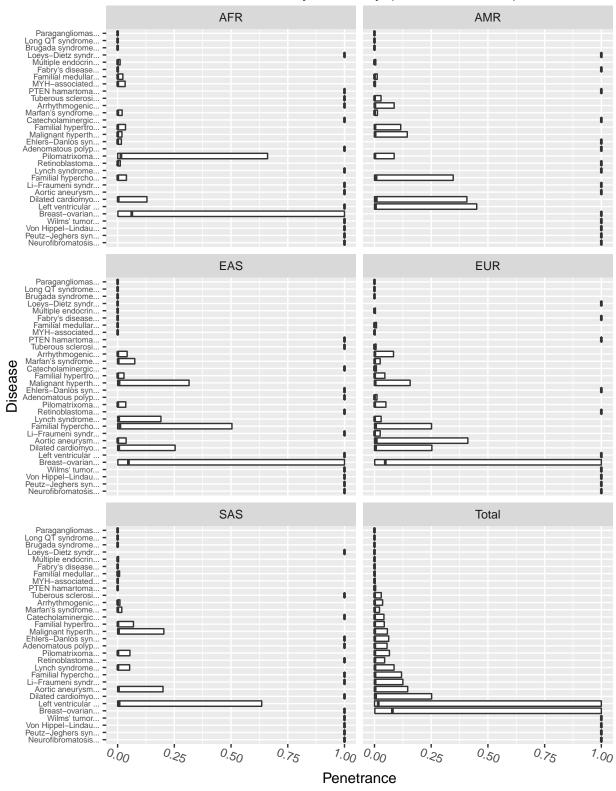
The left end of the boxplot indicates P(D) AND P(V|D) = lower value, the bold line in the middle indicates P(D) AND  $P(V|D) = geometric\_mean(values)$ , the right end of the boxplot indicates P(D) AND P(V|D) = upper value.



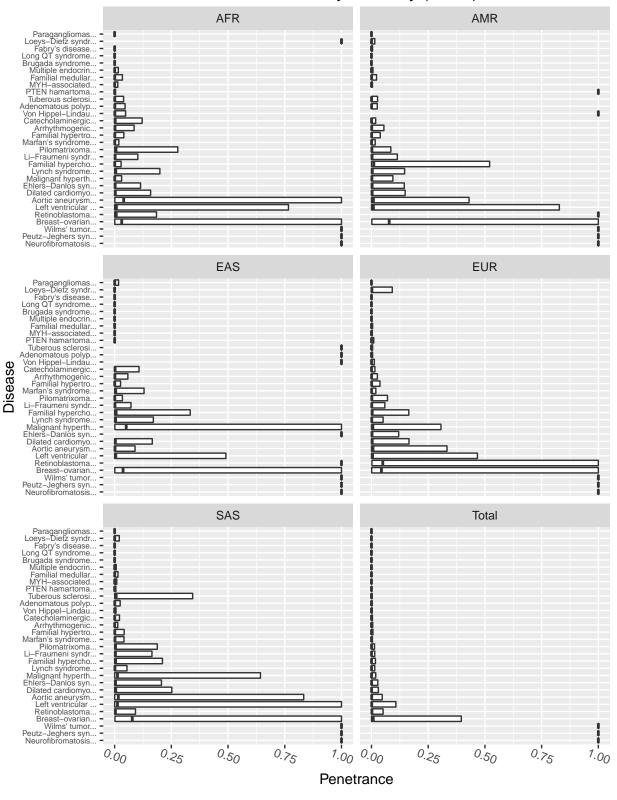
Note: Prevalence ranges of 5x were assumed for all point estimates of prevalence. For example: a point estimate of 0.022 would be given the range 0.01-0.05.

#### 3.2 Penetrance Estimates by Ancestry

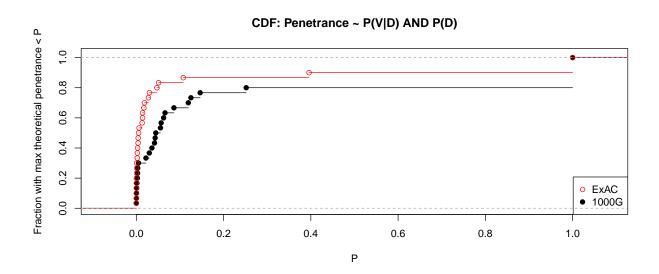




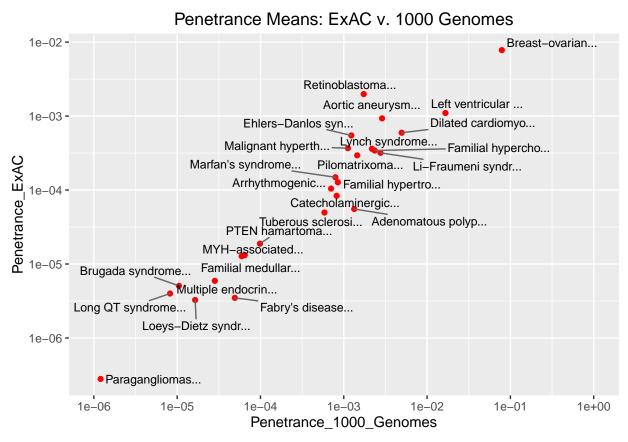
### Penetrance by Ancestry (ExAC)



#### 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 9.7-fold larger than those computed using ExAC.