ClinVar Report

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Contents

Sourcing ClinVar input from: clinvar_2013-01-14.vcf
Sending output to: Report_2013-01-14.pdf

1 Collect and Merge ClinVar Data

1.1 Import ClinVar VCF

```
## Processed ClinVar data frame 67257 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	67257
LP/P-ClinVar	12607
LP/P-ClinVar & ACMG	915
LP/P-ClinVar & ACMG & ExAC	206
LP/P-ClinVar & ACMG & 1000 Genomes	65

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

Subset__1000__Genomes	Number__of__Variants
Total 1000_Genomes & ACMG	139335
1000_Genomes & ACMG & ClinVar	1214
1000_Genomes & ACMG & LP/P-ClinVar	65

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

Subset__ExAC	Number__of__Variants
Total ExAC & ACMG	58873
ExAC & ACMG & ClinVar	2256
ExAC & ACMG & LP/P-ClinVar	206

2 Summary Statistics

2.1 Fraction of Individuals with Pathogenic Non-Reference Sites

ACMG−56 Pathogenic: Fraction

### ACMG−56 Pathogenic: Mean in ExAC
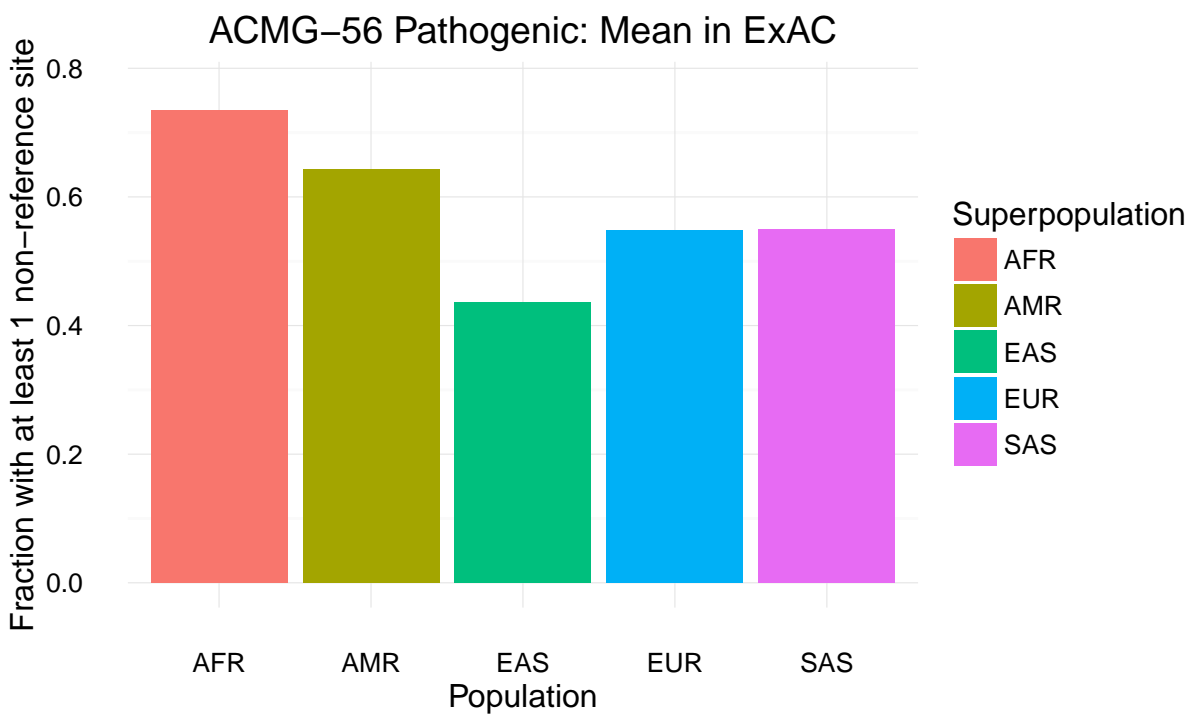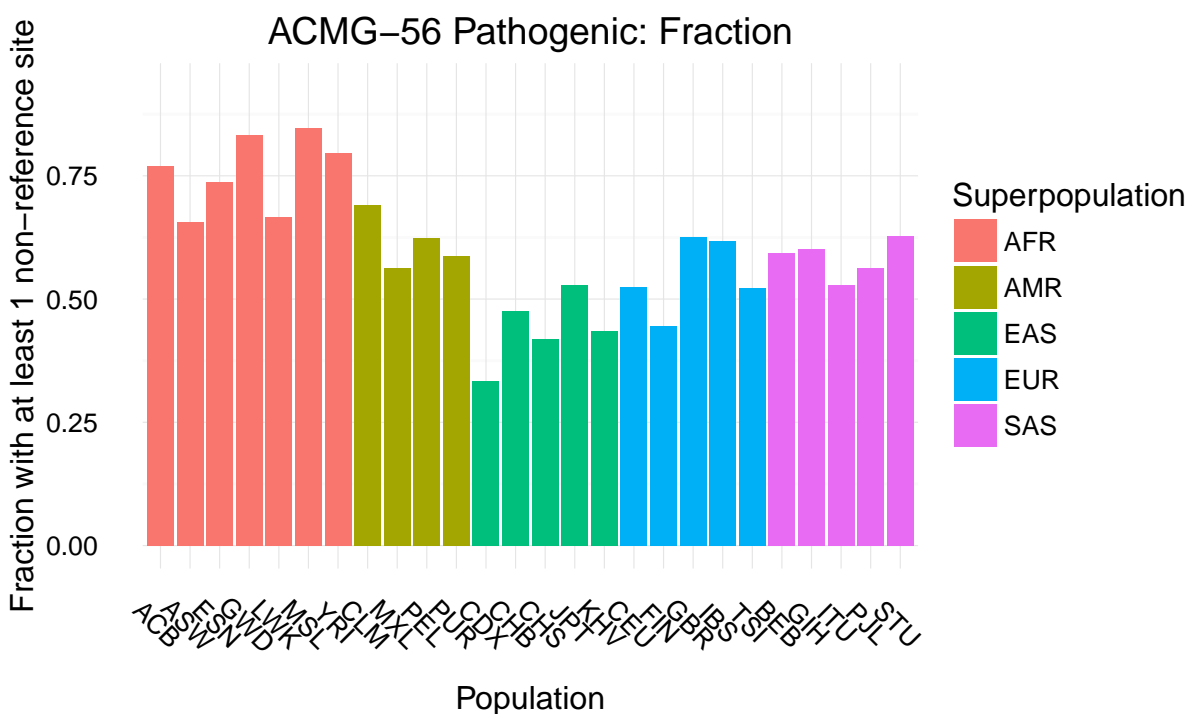
3 Penetrance Estimates

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),
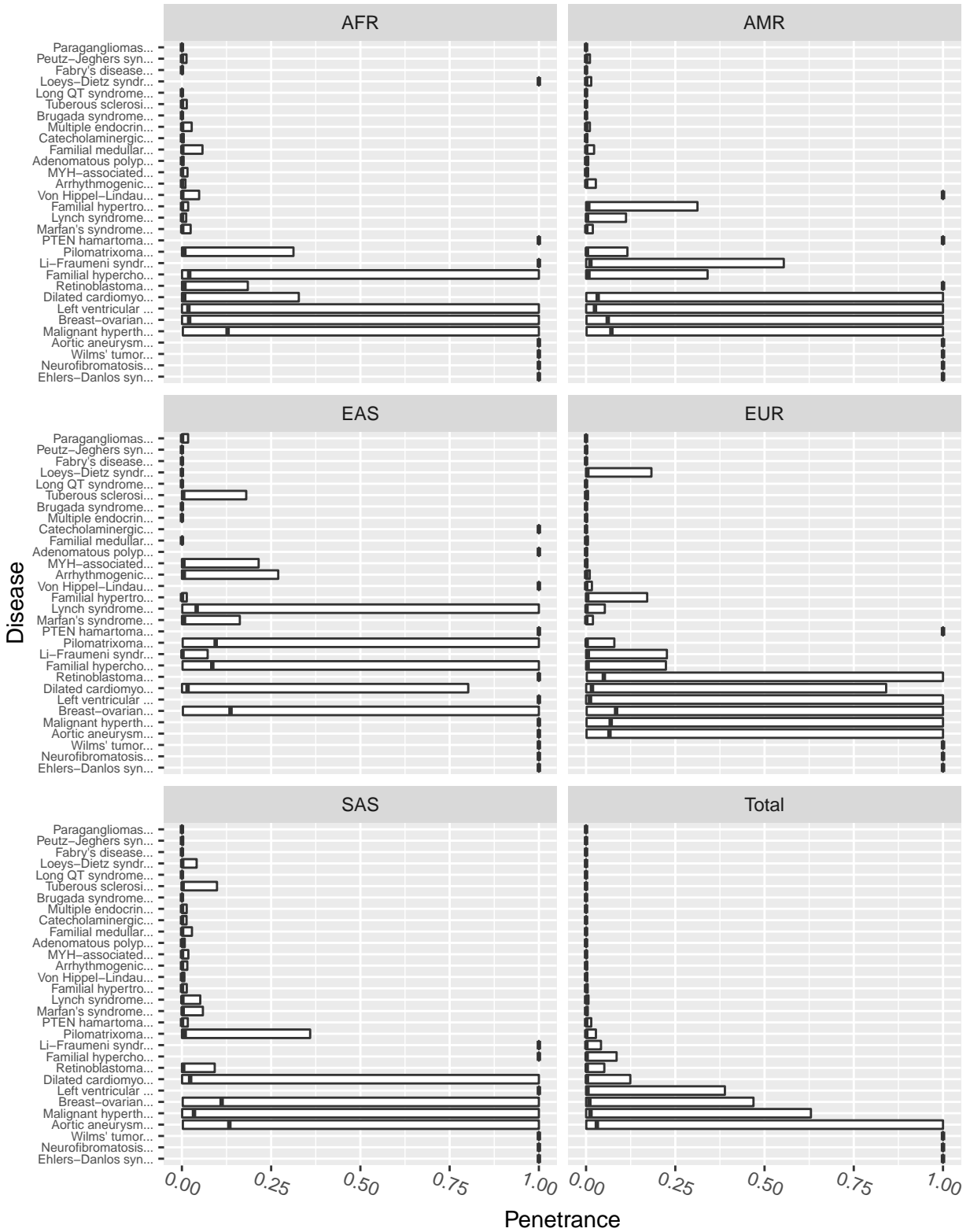the right end of the boxplot indicates P(D) AND P(V|D) = upper value.
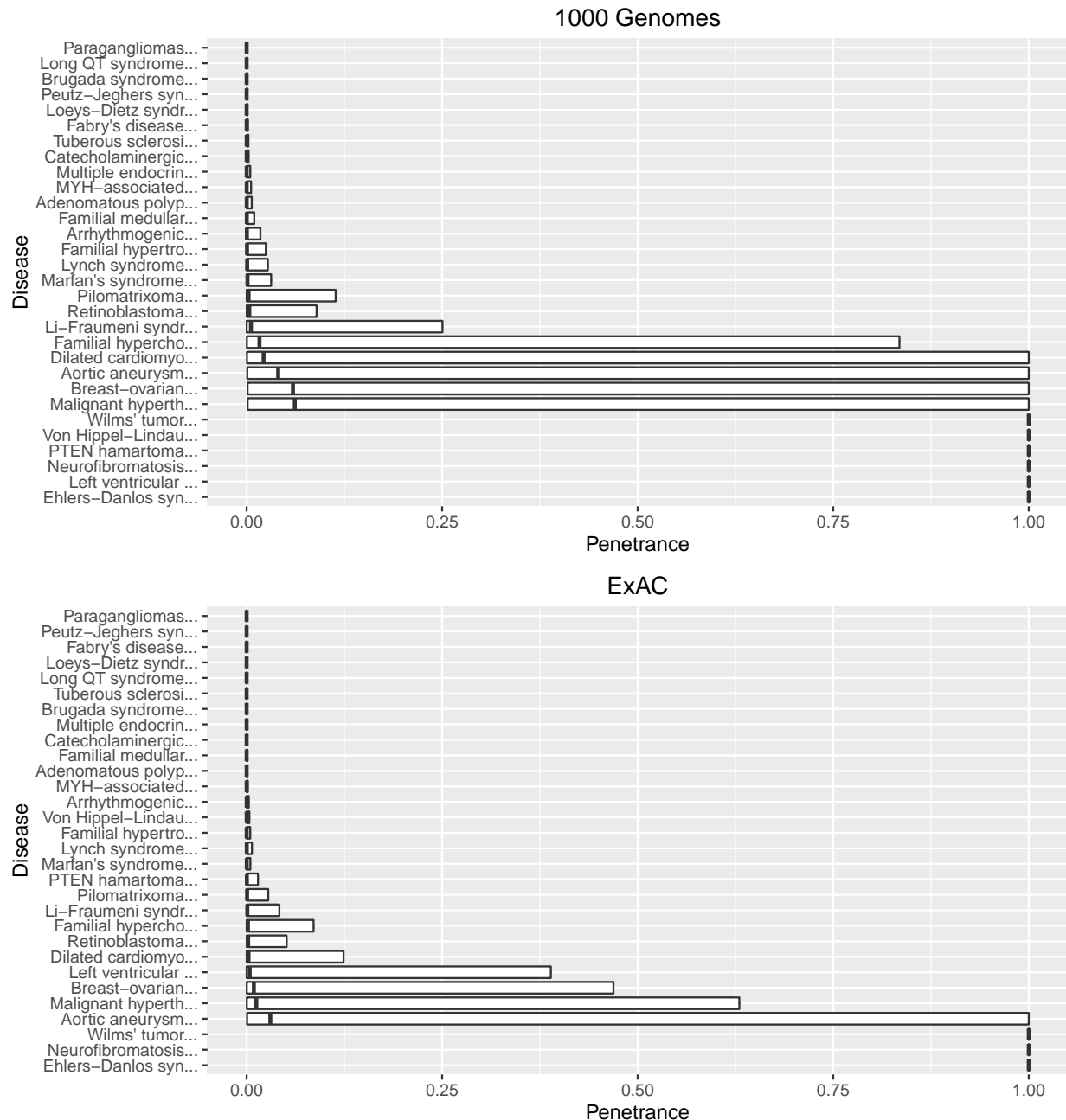
Note: Prevalence ranges of 5x were assumed for all point estimates of prevalence.
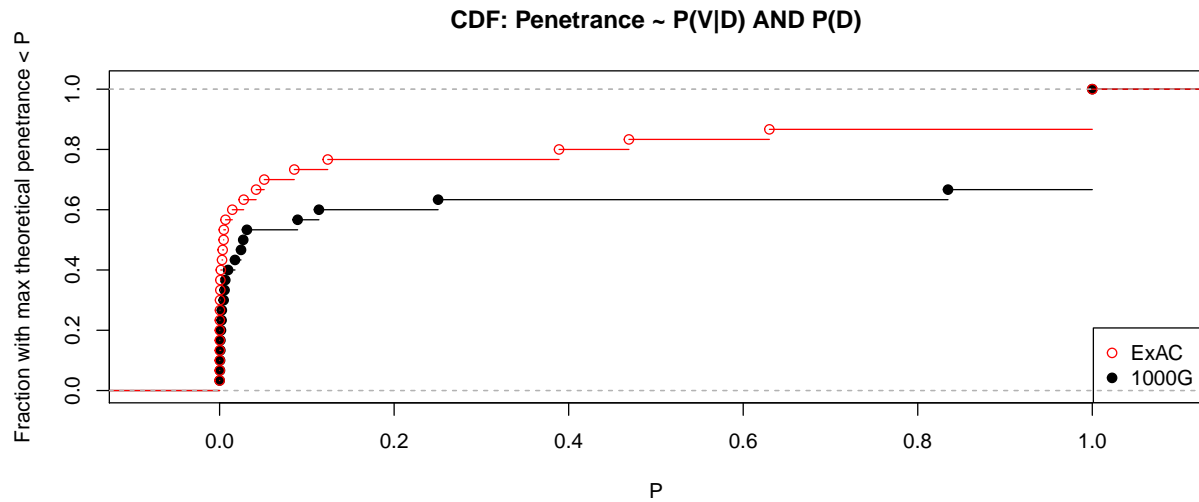For example: a point estimate of 0.022 would be given the range 0.01-0.05.
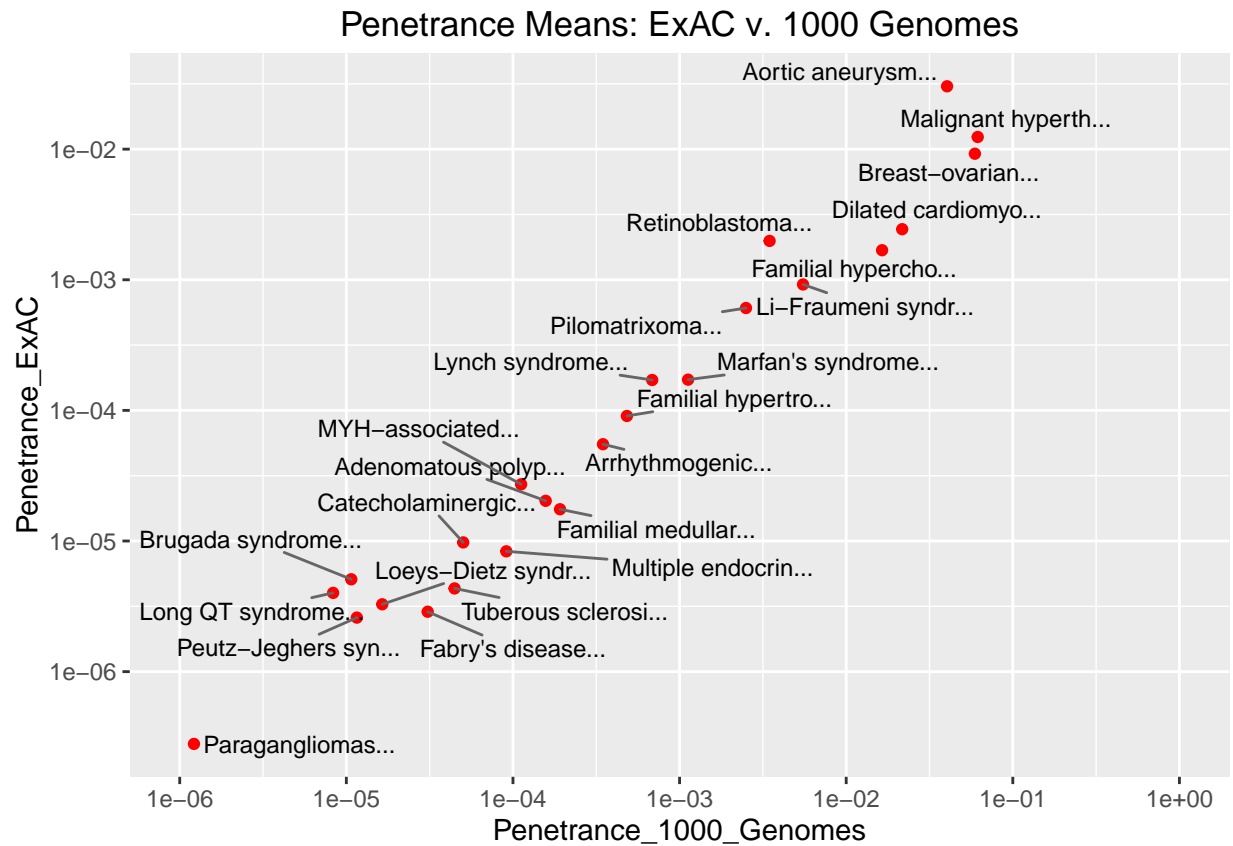
3.2 Penetrance Estimates by Ancestry

Penetrance by Ancestry (1000 Genomes)
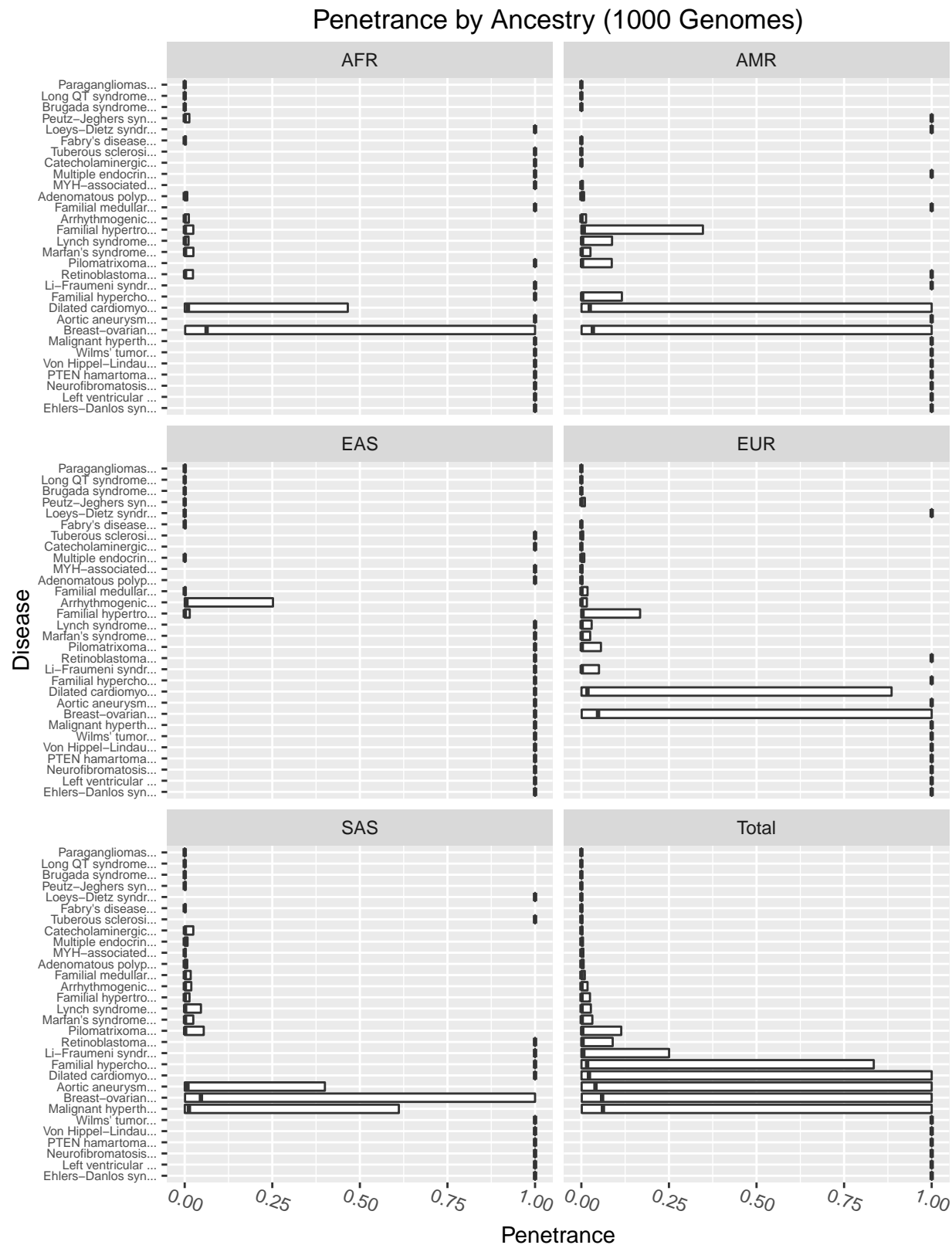
Penetrance by Ancestry (ExAC)

3.3 Empirical CDFs for All Penetrance Plots

CDF: Penetrance ~ P(V|D) AND P(D)

3.4 Comparing Mean Penetrance between ExAC and 1000 Genomes

Penetrance Means: ExAC v. 1000 Genomes

The Pearson correlation is 0.74.

Max penetrance values computed using 1000 Genomes are 2-fold larger than those computed using ExAC.