

SUPPLEMENTARY FIGURES

Supplementary Figure 1. Subjects and single SNP exclusion schema for the GWAS

Supplementary Figure 2. Principal component plot for the genotyped IFM cohort and 3 HapMap phase III reference populations. The first two components are plotted, each sample is represented by a colored circle. Magenta: IFM samples; Red : IFM outliers; Pink: Utah residents with Northern and Western European ancestry from the CEPH collection (CEU); Green: Han Chinese in Beijing, China (CHB); Blue: Yoruba in Ibadan, Nigeria (YRI).

Supplementary Figure 3. OR for 6 SNPs associated with BiPN discovery study ; for each allele, OR and CI is drawn (left: 0 risk-allele, middle :1 risk-allele, right: 2 risk-allele).

Supplementary Figure 4. Manhattan plots for association analyses. Genome-wide association test results are shown as $-\text{Log}_{10}$ transformed P-values . Chromosomal location of SNPs is indicated on the x-axis. The five candidate gene SNPs are indicated.

Supplementary Figure 1

French exploration study

Samples removed:
n= 2 Contrast QC < 0.4
n= 8 Call rate < 97%
n= 3 Heterozygosity rate > mean het+3SD
Samples remaining: 469
155 cases/ 314 controls

482 subjects
IFM MM cases (BiPN grade ≥ 2)
n = 160
IFM MM controls (no BiPN and grade 1 BiPN)
n = 322
Human SNP 6.0: 909,622 SNPs

SNP removed:
n= 130 Affymetrix unannotated
n= 37,326 mitochondrial and sex chromosomes
n=16,743 genotype undetermined (> 5% in subjects)
n= 483,984 minor allele homozygous genotype (< 5% in subjects)
n= 834 failed HW (< 10^{-5} in subjects)
SNPs remaining: n= 370,605

6 SNPs with P-value < 10^{-5} to replication



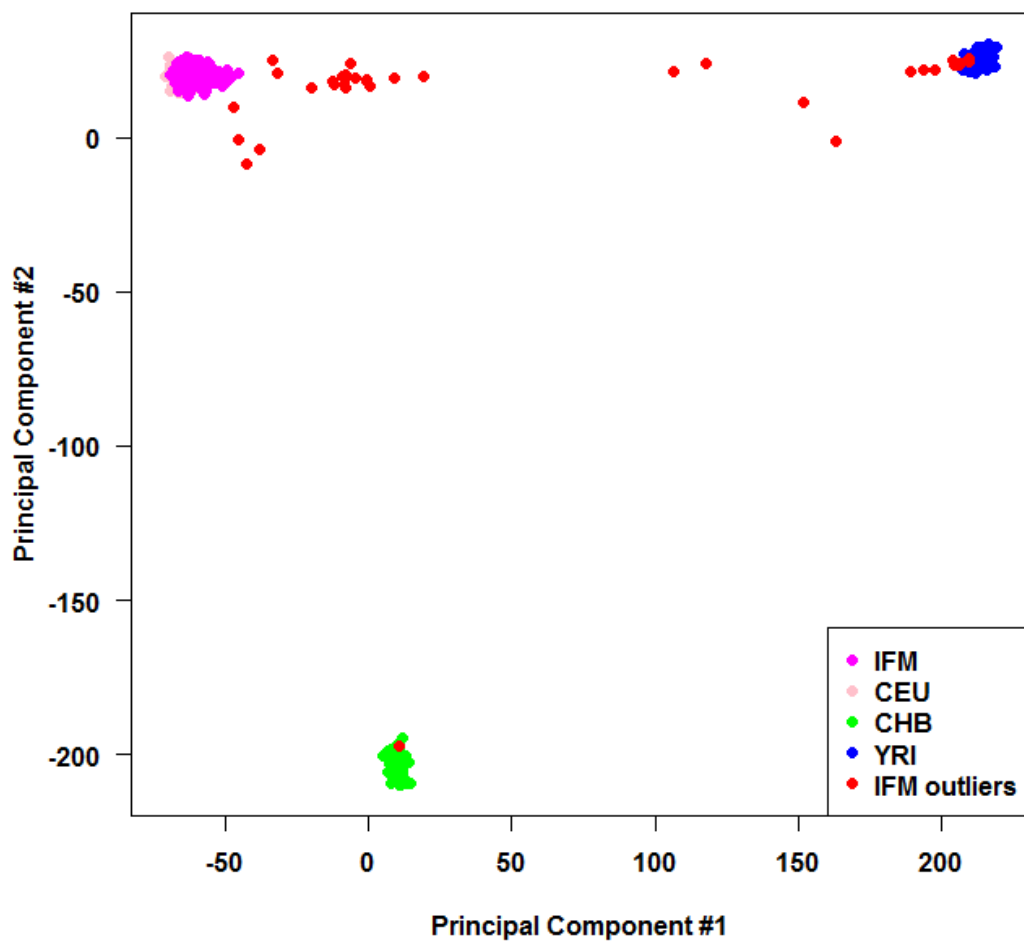
Dutch/ German replication study

1 SNP with P-value < 10^{-2}

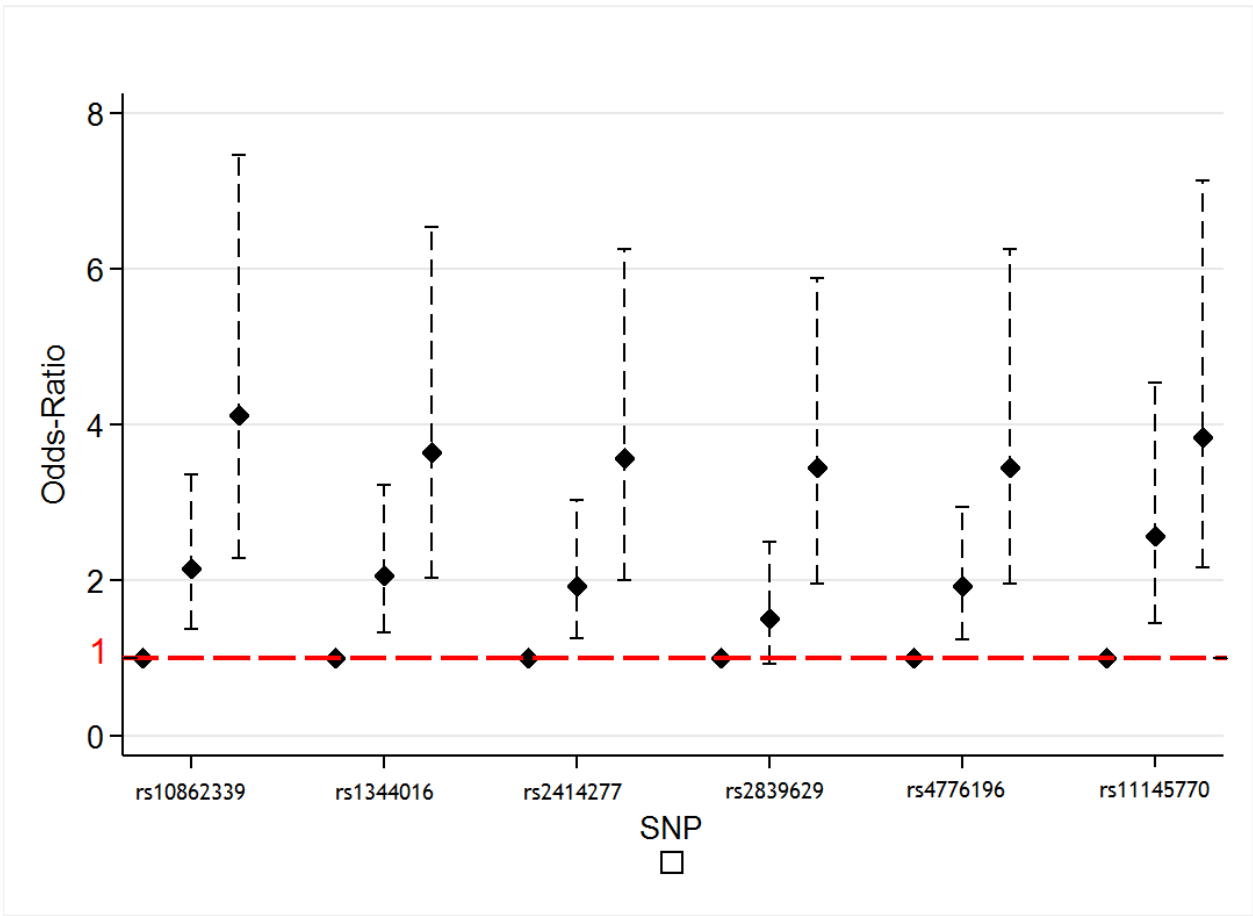
Samples removed:
n = 2 genotype failed
Samples remaining : 114
40 cases/ 74 controls

116 subjects
Hovon MM cases (BiPN grade ≥ 2)
n = 41
IFM MM controls (BiPN grade < 2)
n = 75
Human SNP 6.0: 909,622 SNPs

Supplementary Figure 2



Supplementary Figure 3



Supplementary Figure 4

