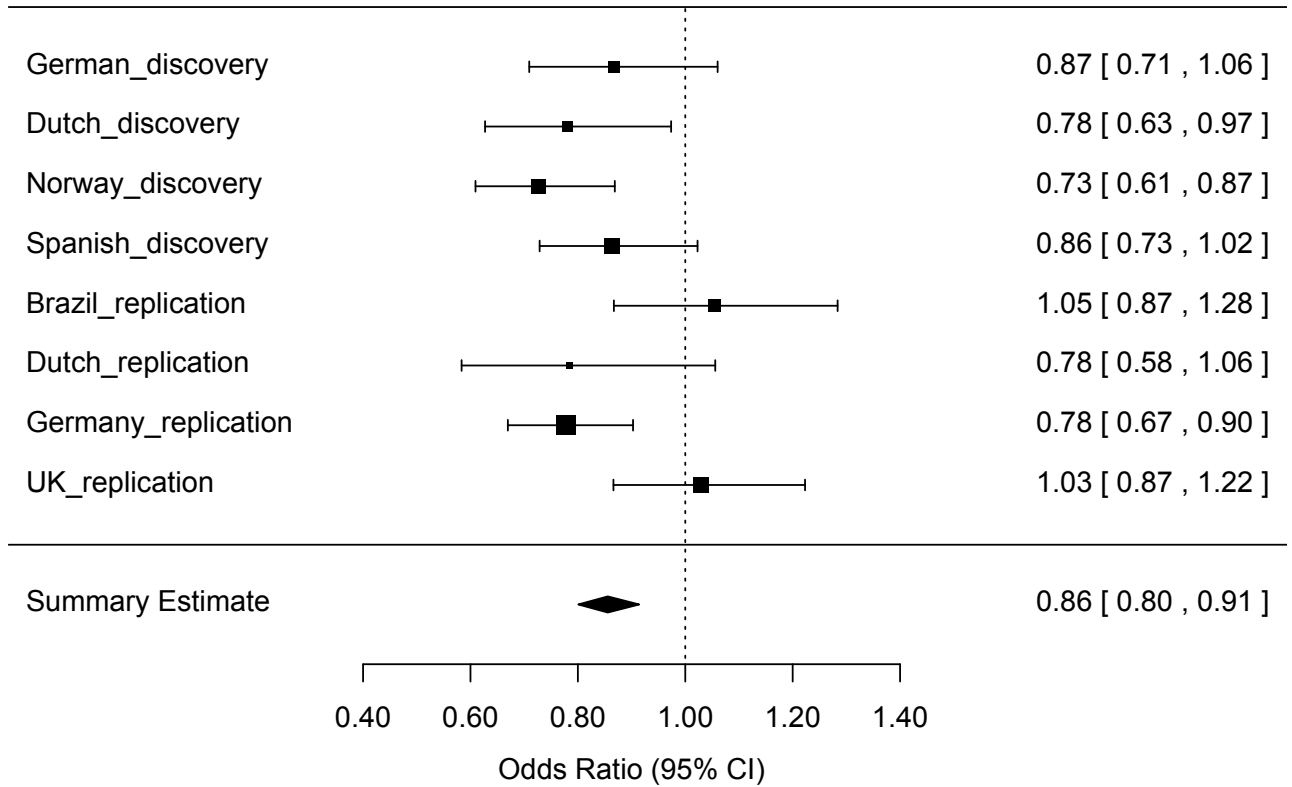


Supplementary Figure 2. Forest plots reflecting the overall meta-analysis (discovery and replication datasets together) for the most significant top three common SNVs observed in this study.

A) rs9325032 (*PPP2R2B* gene)

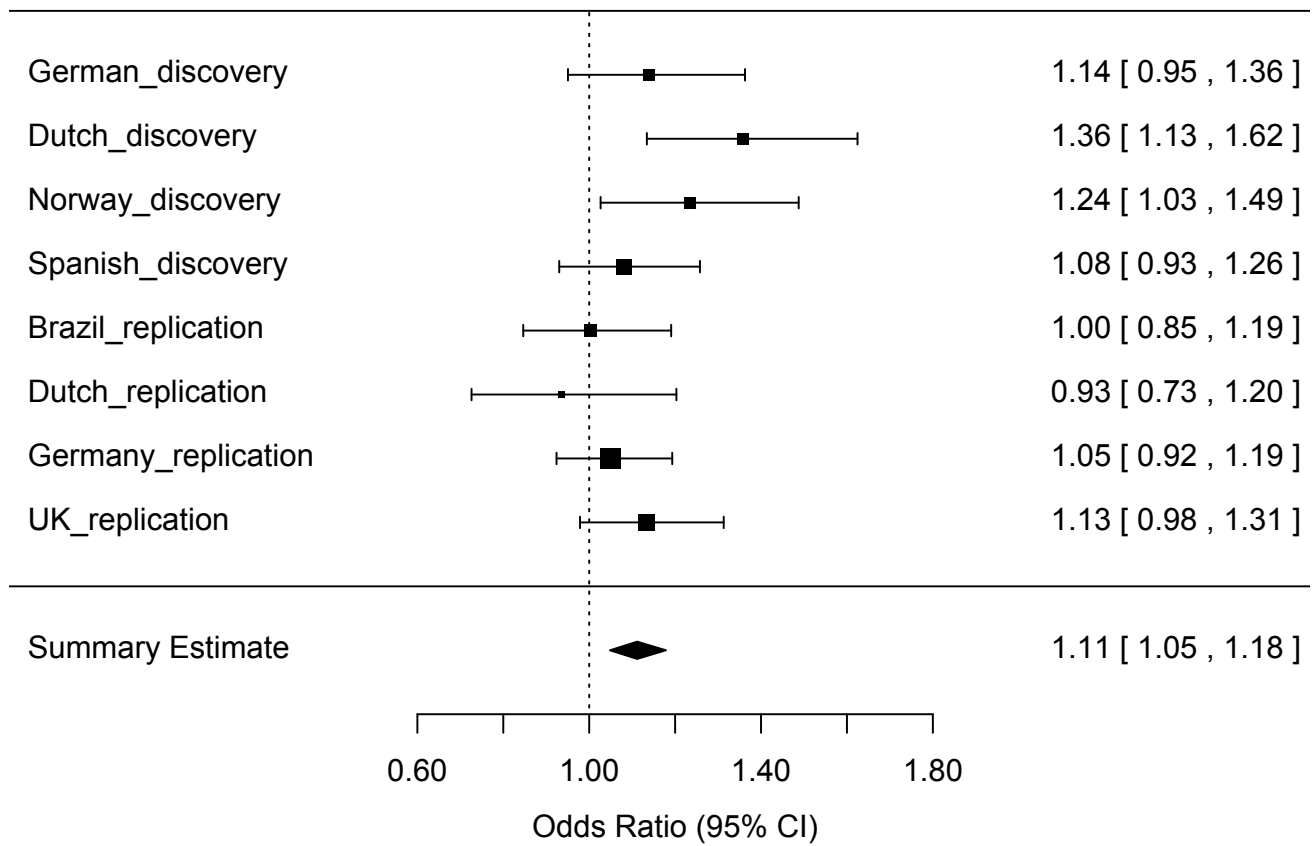
Association p-value= 3.97225588935779e-06
Heterogeneity p-value= 0.0417366770248054



B) rs3095150 (intergenic)

Association p-value= 0.000392603313280398

Heterogeneity p-value= 0.177227509705407



C) rs117611723 (*SYNRG* gene)

Association p-value= 7.98034831517963e-05

Heterogeneity p-value= 0.757078085736703

