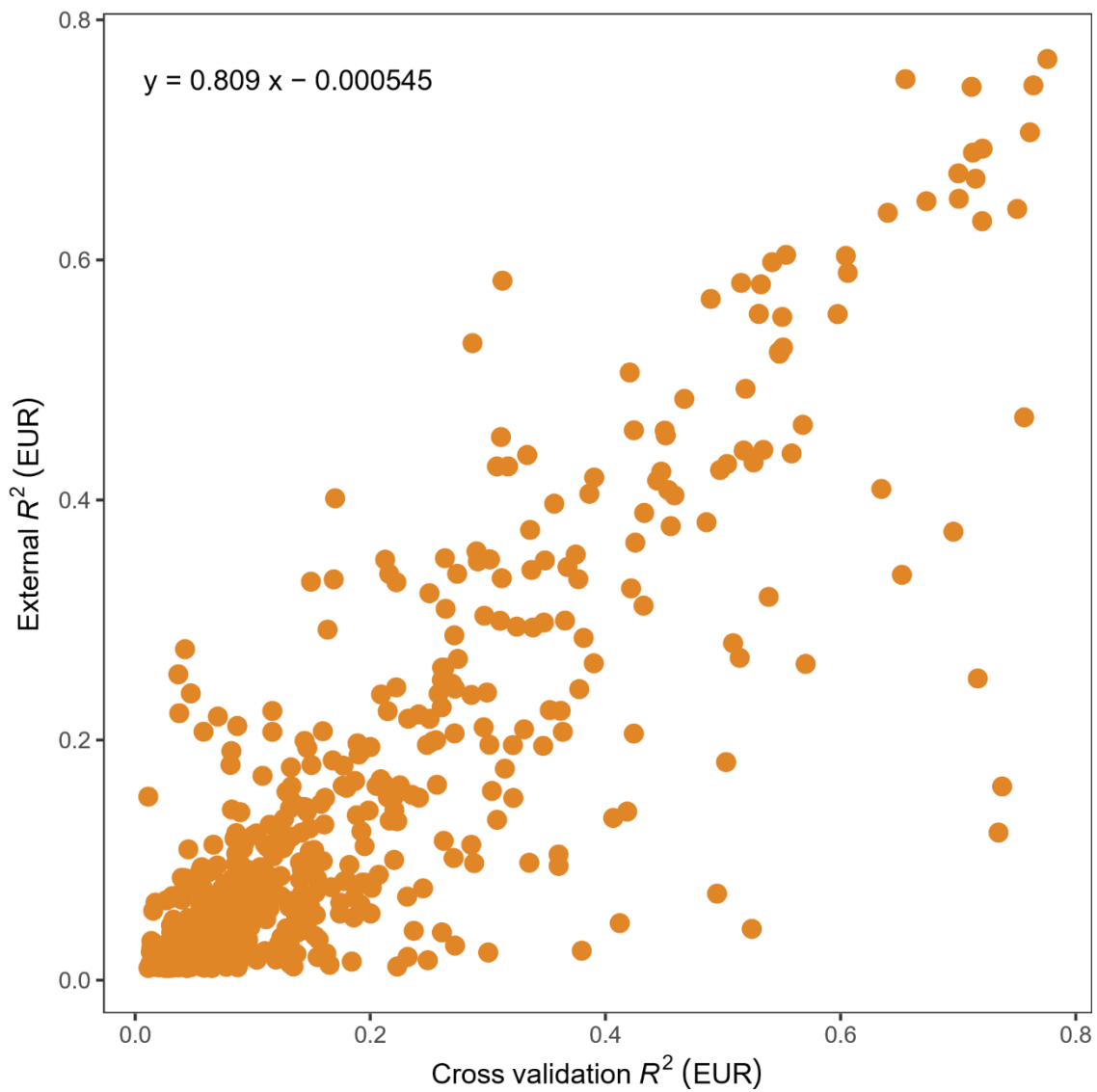


Proteome-wide association study of prostate cancer risk across populations

Supplementary figures



Supplementary Figure 1. Performance of protein genetic prediction models in European ancestry with cross-validation R^2 and external R^2 . Sample sizes for Cross validation and External validation are 785 and 1,685, respectively. Source data are provided as a Source Data file.