



S2 Fig. R^2 of gene models. (a) R^2 estimated by correlating the predicted and measured expression levels in ROSMAP. CEWAS attained lower R^2 as expected, since CEWAS is designed to extract a specific component of gene expression, namely the epigenomic component that is driven by genetic effects. In contrast, MetaXcan and EpiXcan are optimized for predicting gene expression. (b) R^2 estimated by applying ROSMAP models to CMC genotype data and correlating the predicted expression levels with that measured in CMC. R^2 appears similar across methods, but CEWAS actually attained slightly lower R^2 if we zoom into the results (see Fig S3).