

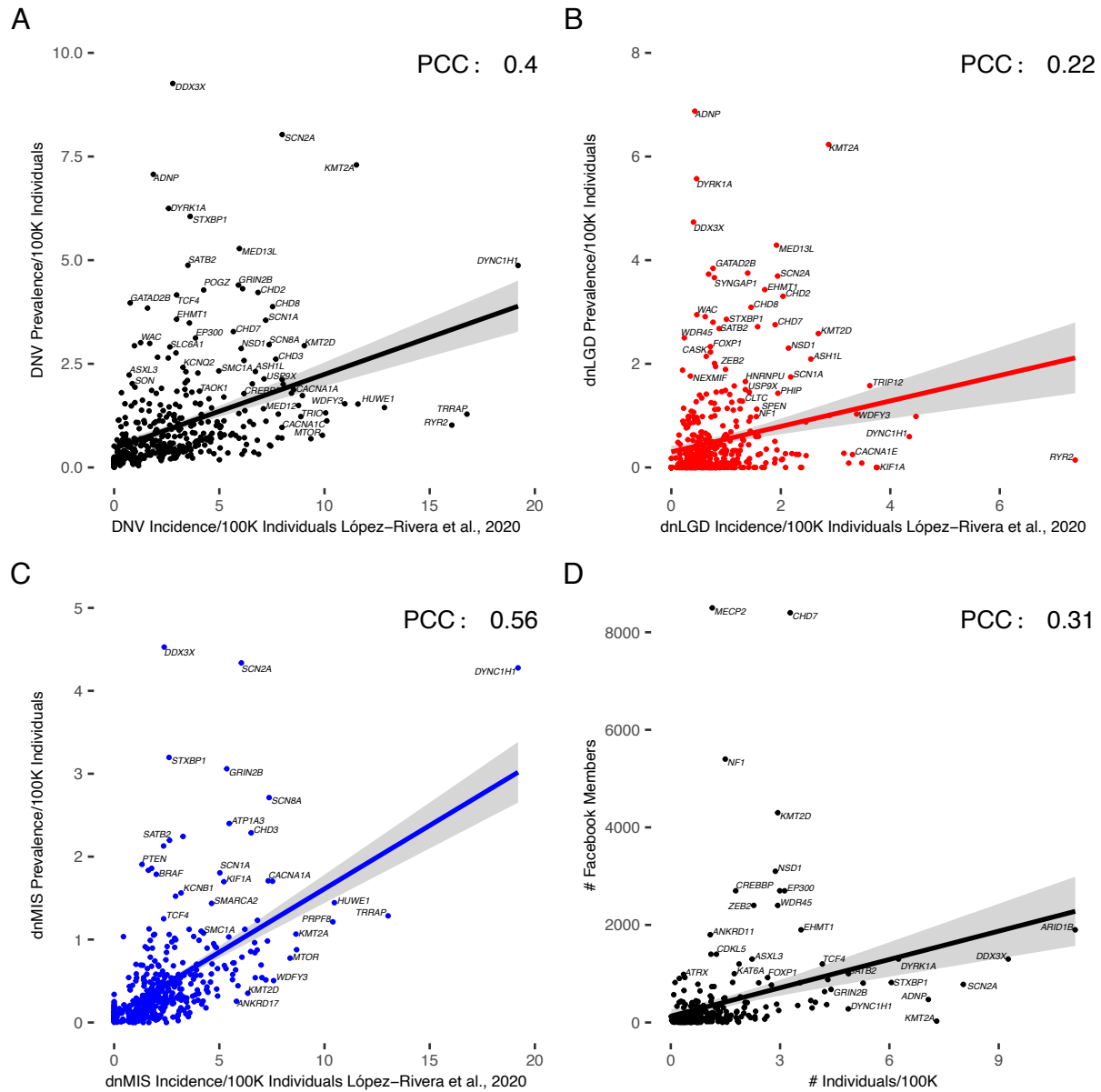


Figure S1. Prevalence of DNVs in candidate NDD genes versus incidence estimates from [14], along with comparison to social media estimates. Confidence intervals are shown in grey. (A) NDD DNV cases ($p > 0.0001$ with Bonferroni correction), (B) NDD dnLGD cases (not significant), and (C) NDD dnMIS cases ($p > 0.0001$ with Bonferroni correction). All mutation types had a positive correlation with previous incidence estimates, shown with Pearson's correlation coefficients (PCC). (D) Correlation of prevalence with number of members in gene-focused Facebook groups (not significant). Genes were searched on Facebook if they were in the top 500 of all NDD genes and/or had a named syndrome in OMIM as of July 2022 ($n = 293$).

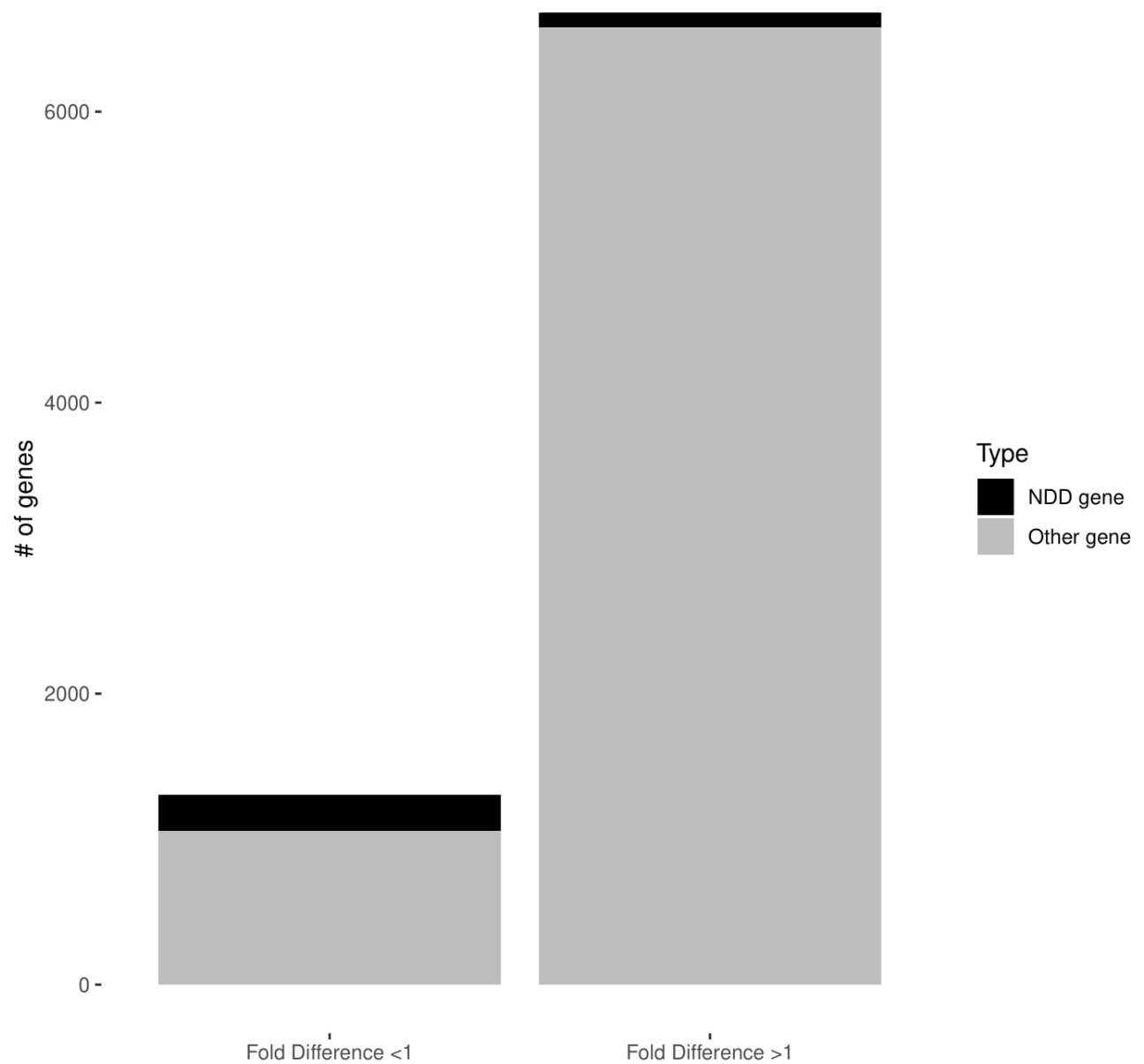


Figure S2. Fold difference between our prevalence estimates and López-Rivera et al.'s incidence estimates. Most genes had a higher prevalence than incidence, as expected. Of the 19% of genes that had lower prevalence than incidence, 1.5% were NDD candidate genes (Chi squared test, $p = 0.0005$).