

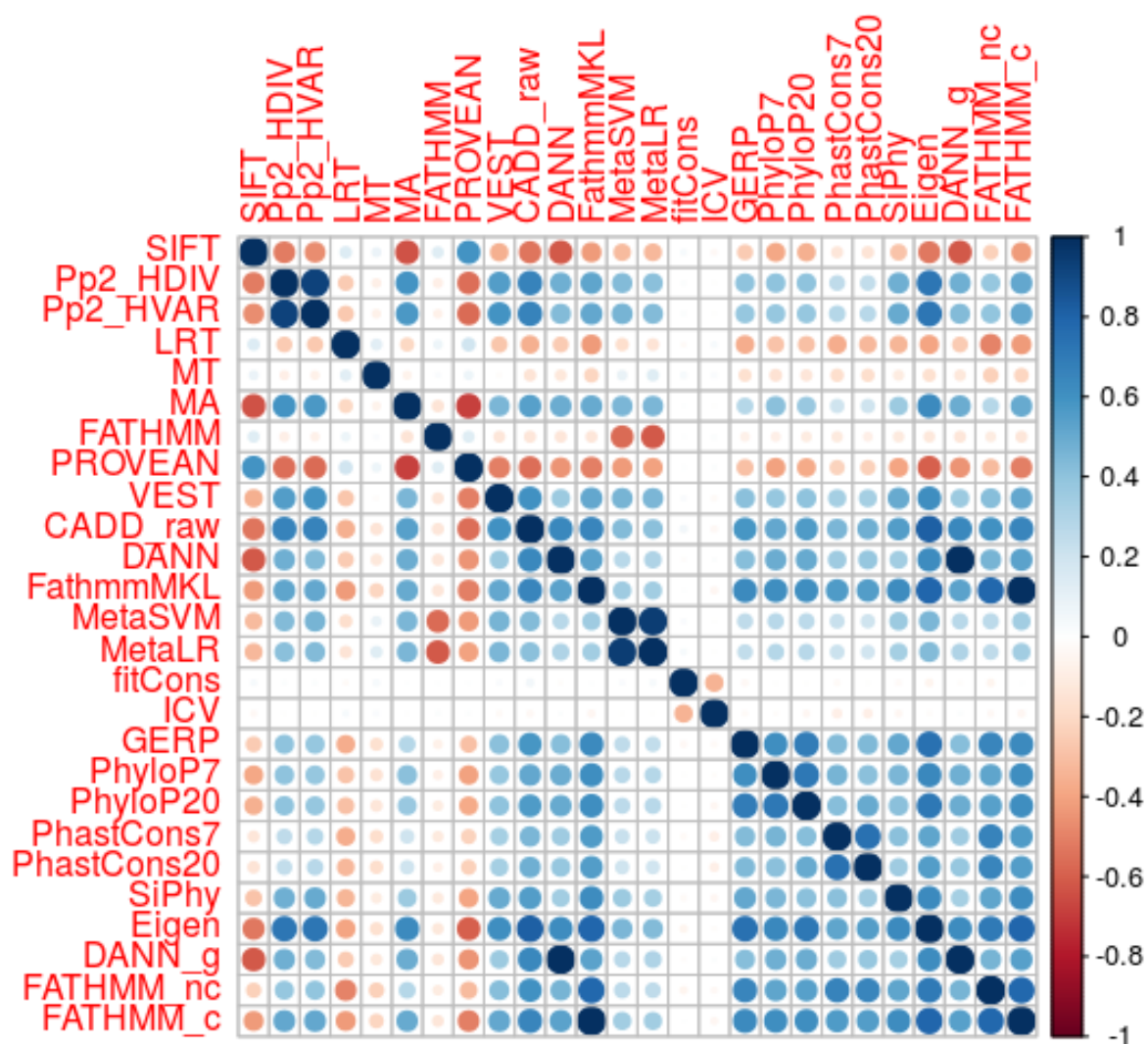


FIGURE S2. Correlation between prediction and conservation scores. We plotted the correlation matrix of 26 mutation scoring algorithm outputs for the pathogenic variants identified in this study using variant scores obtained from tNGS data. **metaLR** and **metaSVM** were well-correlated and were used to predict the deleteriousness of sequence variants. See Figure S3 for comparison of 17 different scores for each of the deleterious variants.