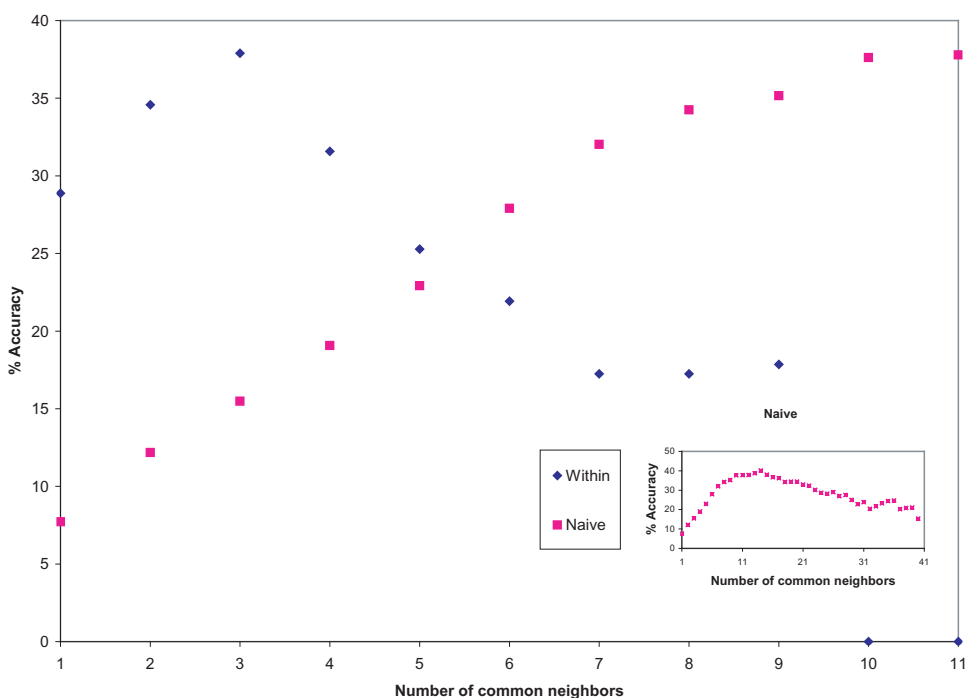


Supplementary Figure 3. Estimated prediction accuracy for naive and pathway-based within-pathway genetic predictions.

This graph displays the estimated accuracy of pathway-based and naive within-pathway genetic predictions. Within-pathway predictions were made by predicting genetic interactions between genes with common genetic interaction neighbors. The physical network was incorporated in the pathway-based predictions by restricting the proteins and neighbors to fall into a single within-pathway model. The number of common neighbors is therefore used as a measure of confidence in the implied genetic interactions. The maximum prediction accuracy obtained for within-pathway based predictions is $\approx 38\%$ using a prediction threshold of three common neighbors. The inset displays the estimated prediction accuracy over an expanded range for just the naive predictions.



Supplementary Figure 3: Estimated prediction accuracy for naive and pathway-based within-pathway predictions.