**Correlation between SNP count and SNP P-value**

SNPs were assigned to genes through a window-based approach, in which SNPs were assigned to genes if they fell within a 10 kilobase (kb) window up- or downstream. We observe a correlation between the top SNP p-value and the number of captured SNPs per given gene. Therefore, genes scores were calculated as the most significant p-value of assigned SNPs normalized by number of captured SNPs. Given that there are approximately 20,000 protein-coding genes under analysis, we derive a gene score threshold of p = 0.05 / 20,000. Initial analysis shows that only 22 genes pass this threshold.

**Personalized PageRank Identifies New Novel Schizophrenia-Associated Genes**

Personalized PageRank was used to rescore the initial gene scores. Considering a personalization vector consisting of the initial gene node scores, the algorithm rescores the nodes according to visitation likelihood, as calculated from the input network topology as the probability of visiting each node according to a random walk of the graph either by an edge or a “teleportation” parameter *α*. Here, we set *α = 0.85*, the default setting in the networkx Python module.

The network used was the GIANT brain-tissue-specific genetic network. This network consists of 1,358,435 connections between 14,306 genes. We chose to use this network given its tissue specificity, given that the phenotype under study is a psychiatric disorder.

After transformation, the number of hits increases dramatically to 1,583 genes. As shown in **Figure[n]**, the network-based rescoring method clearly boosts a majority of the signals.