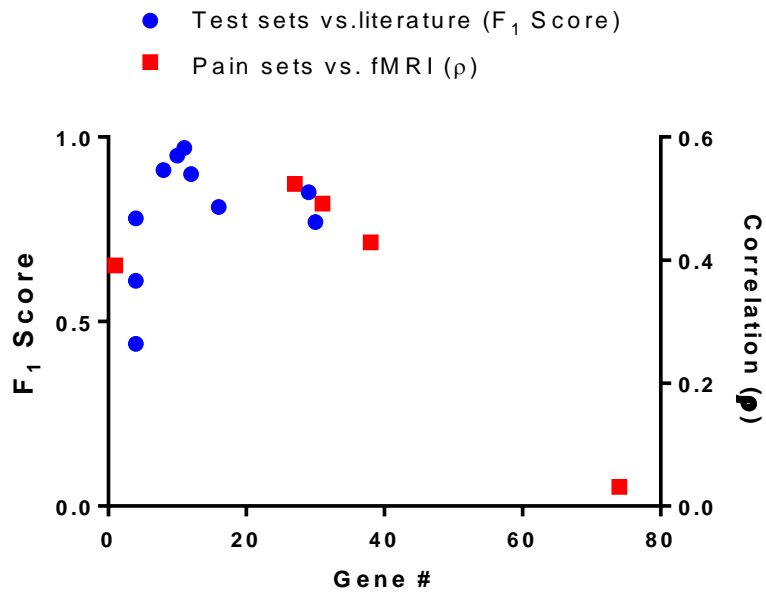


**Supplementary Figure 1. Principle predictions from genetic and connectomic brain data.** (A) Predicting functional brain maps from fusing genetic information (e. g., from genetic association studies) with genetic and connectomic brain data (this study). (B) Identifying genes underlying a specific behavioral trait from fusing functional brain maps (e. g., from literature, fMRI) with genetic and connectomic brain data. (C) Assigning a behavioral trait to a set of genes from fusing genetic and connectomic brain data with functional brain maps (e. g., from literature, fMRI).



**Supplementary Figure 2. Size of gene sets and prediction reliability.**

The reliability of the predictions (comparison of the functional maps predicted for 10 test sets vs. ground truth from literature (Fig. 2B, right bar) and of the functional maps predicted for pain sets vs. actual fMRI (Fig. 3C)) plotted against the gene set size in these comparisons. There is no significant correlation (Spearman correlations  $\rho(\text{F}_1 \text{ scores})=0.2638$ ,  $p=0.4627$ ,  $n=10$  and  $\rho(\rho)=-0.4000$ ,  $p=0.5167$ ,  $n=5$ ).