



Supplementary Figure 2. Prediction of functional links by “scaled epsilon”. Comparison of the ability to predict functional links of: ϵ values (“epsilon”), the combined metric described in **Fig. 2c** (“combined”), and a recently described scale for epistasis¹⁹ (“scaled epsilon”). For each predictor, the plot shows the true positive rate (or sensitivity, defined here as the fraction of gene pairs correctly predicted to have functional links) and false-positive rate (or 1-specificity, defined here as the fraction of non-functionally-linked gene pairs incorrectly predicted to have functional links) at a series of score thresholds. Functional links are defined if a gene pair shares a common biological process Gene Ontology (GO) term that has been annotated to fewer than 30 yeast genes. There are 35 functionally linked gene pairs in this dataset.

¹⁹ Segre, D., Deluna, A., Church, G.M. & Kishony, R. Modular epistasis in yeast metabolism. *Nat Genet* **37**, 77-83 (2005).