

Supplemental Figure Descriptions

Figure S1- Concordance maps for predictions made by 3 yeast models against experimentally determined essentiality

Concordance maps were constructed displaying the accuracy of predictions made by the (A) iFF708, (B) iLL672 and (C) iND750 models. The columns of each map represents the 16 conditions under which deletion viabilities were determined and the rows are deletion mutants for which there was at least one discordant prediction. Because each model had different predictions, and therefore different discordances with the experimental data, each model's concordance map has a different set of genes. Concordance patterns for predictions made using both FBA and MOMA are incorporated into the maps. Different colors indicate different combinations of experimental, FBA and MOMA predictions. White and gray boxes represent experimental viabilities and essentialities that were correctly predicted using both FBA and MOMA. Light and dark blue boxes represent experimental viabilities and essentialities that were incorrectly predicted using both FBA and MOMA. Dark red boxes represent experimentally viable genes correctly predicted by FBA, and not MOMA. Light red boxes represent experimentally essential genes correctly predicted by MOMA, and not by FBA.

Figure S2 – Comparison of experimental phenotypes to previously published data sets

Comparisons of the phenotype data generated in the current study were performed with previously published data sets from (A) Steinmetz et al., Nature Genetics, 2002 and (B) Kuepfer et al., Genome Research, 2005. (A) The data from Steinmetz et al. was generated using the commonly applied competitive batch assay. There were four conditions which overlapped between the Steinmetz data and the current data set (YPD, YPGly, YPEtOH and YPLac). While there is a strong correlation between our data and the Steinmetz data based on the illustrated boxplots, there are some outliers. A potentially interesting question is whether these differences are because of experimental artefacts of one of the two assays, or if they represent a set of genes which have differential importance in a competitive vs. non-competitive environment. (B) The data generated by Kuepfer et al. was done using a plate assay. Therefore the strong similarity between the two data sets is not surprising. It was difficult to do a comprehensive comparison between the two methods, as there was only an overlap in a single condition (minimal glucose media) between the two data sets.

Figure S1A

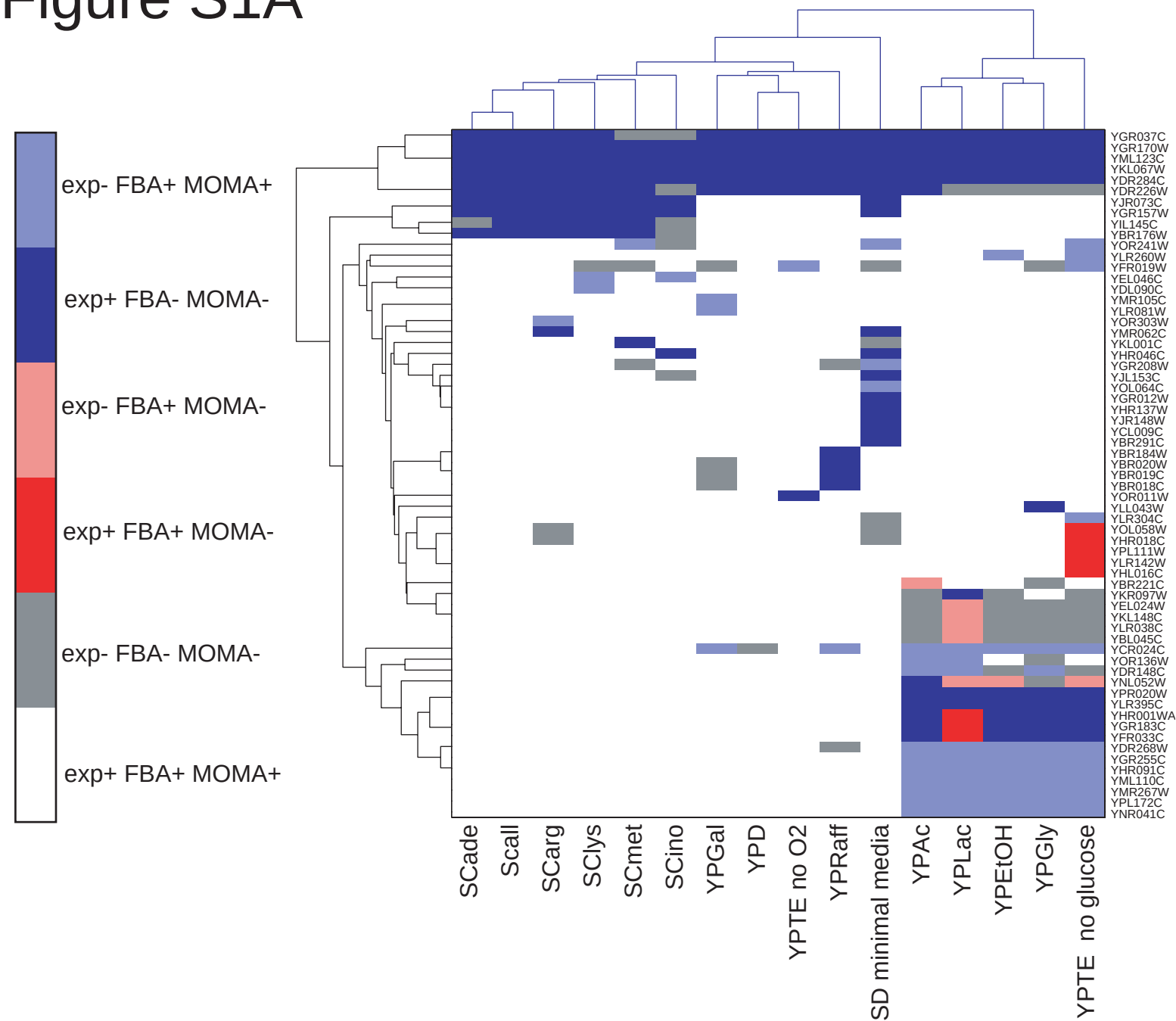


Figure S1B

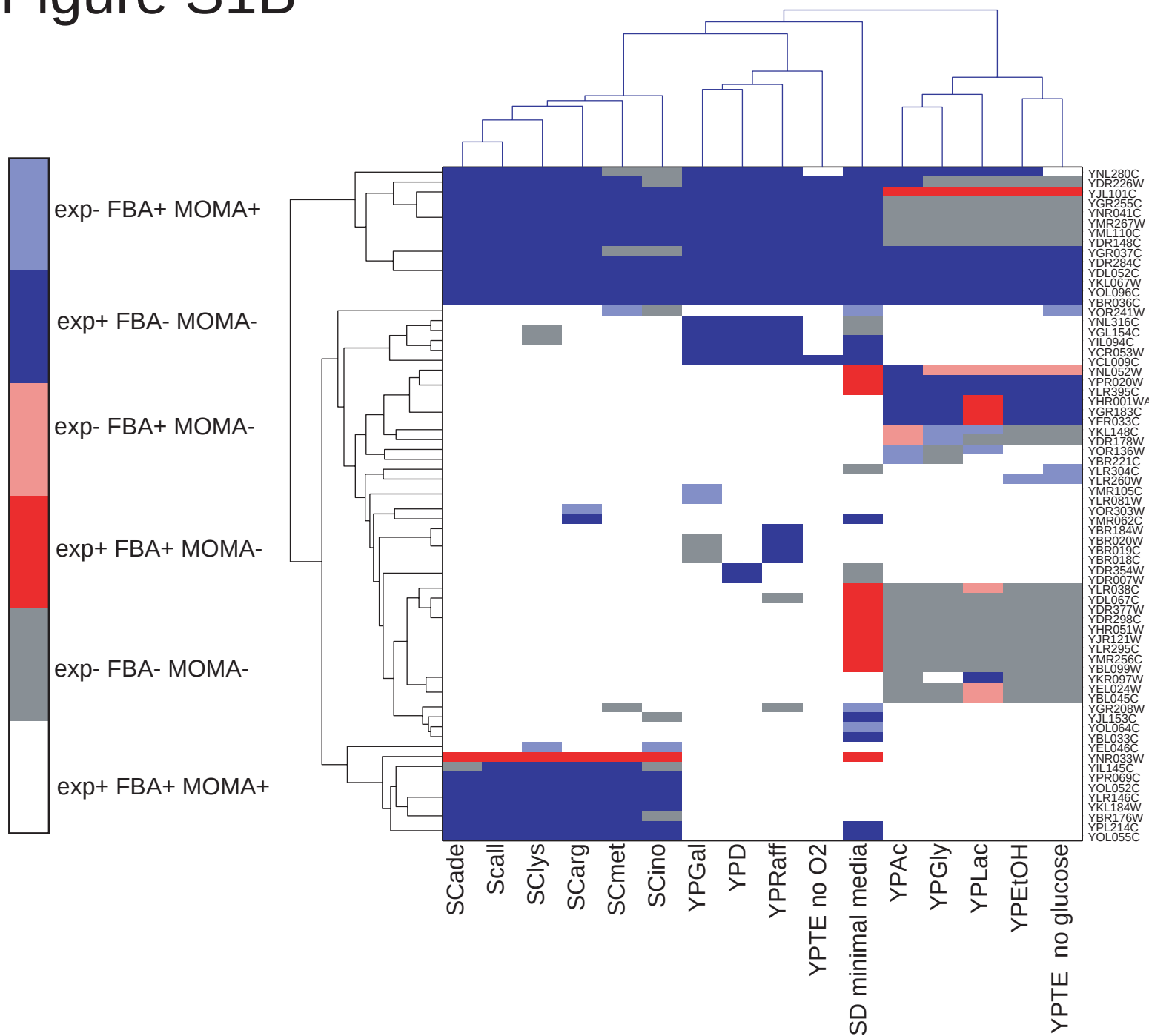


Figure S1C

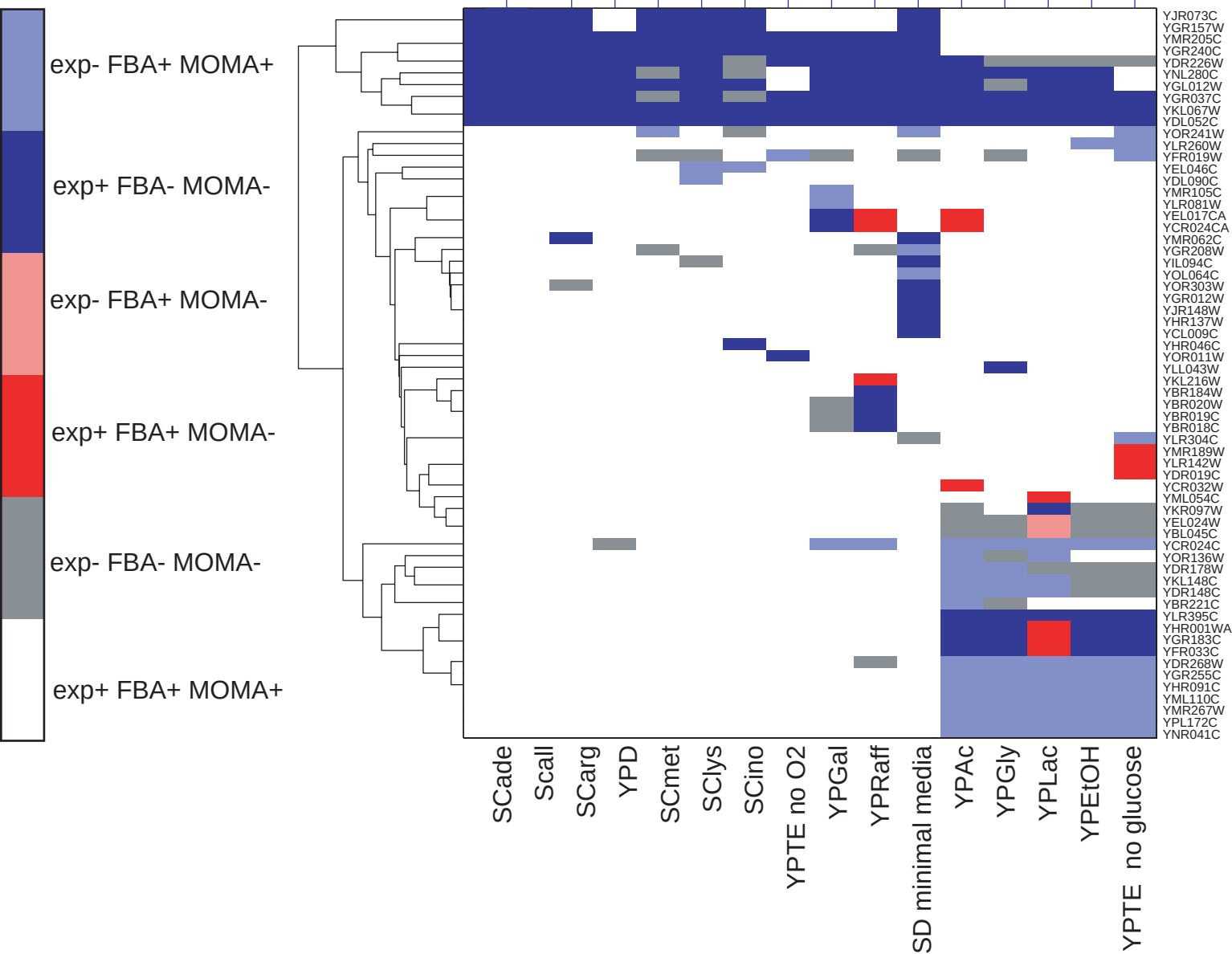


Figure S2A

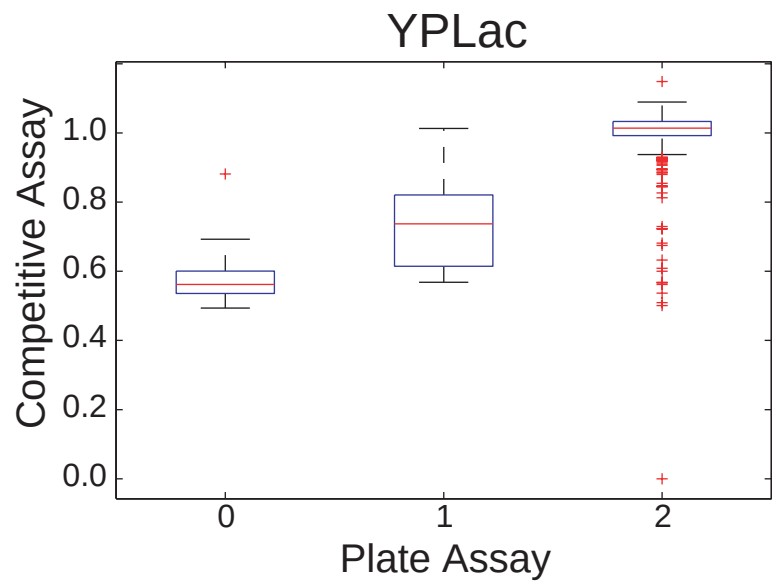
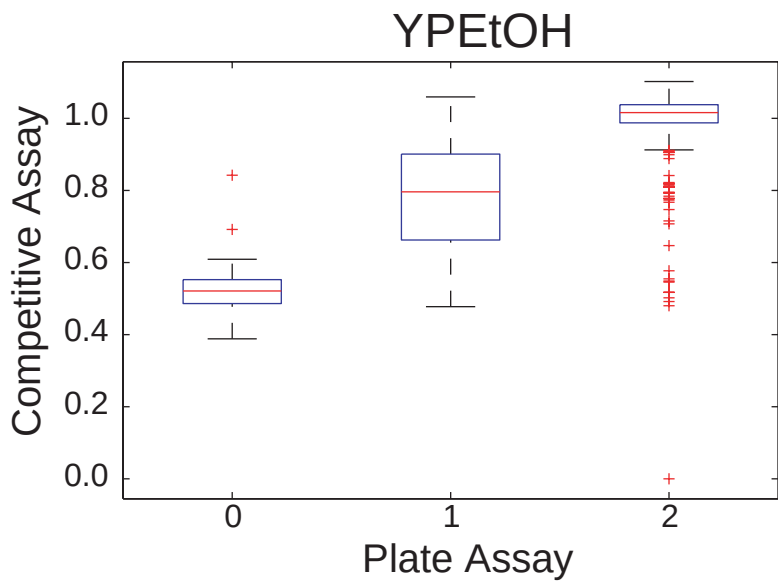
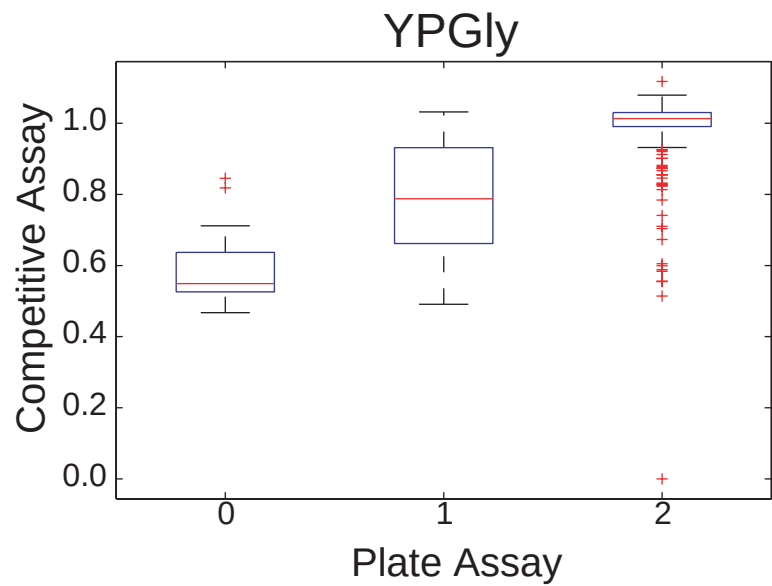
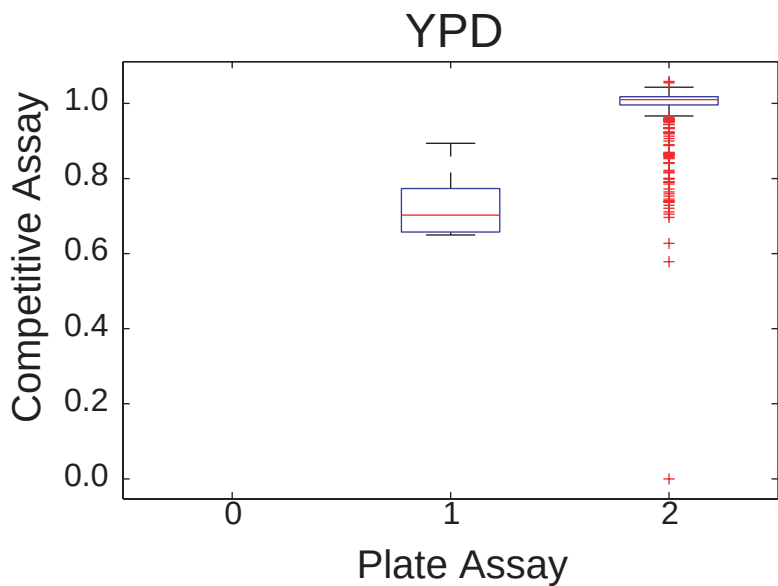


Figure S2B

