Metabolic Network-based Analysis of Yeast Gene-Nutrient Interactions: Supplemental material

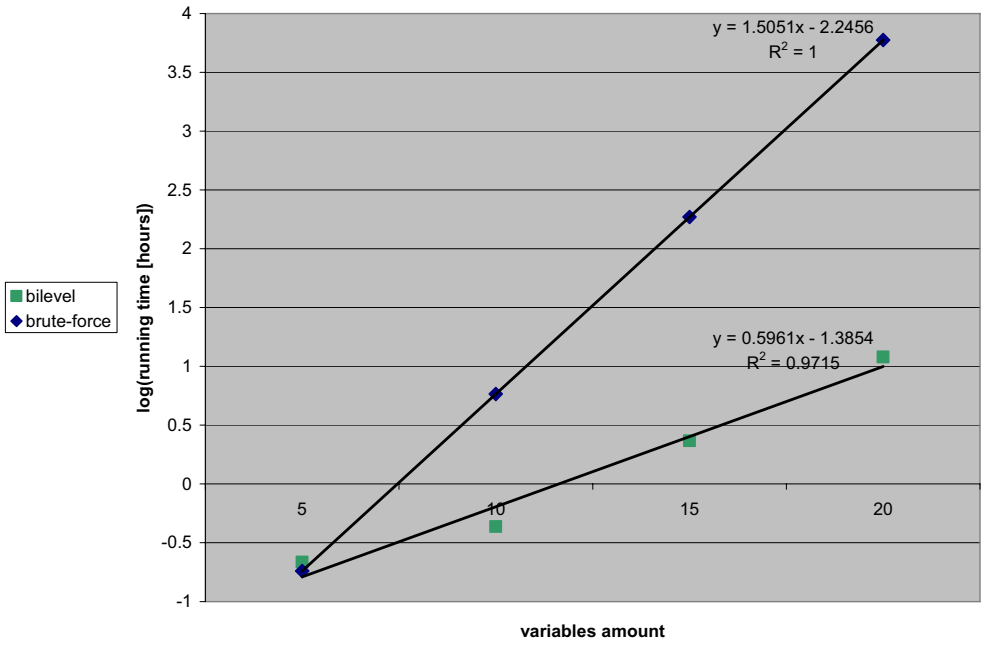

Fig. S1: A comparison of run times between the MILP optimization method presented (green) and a brute-force enumeration of all possible growth media (blue), in predicting strong GNIs between yeast genes and amino-acids. The improvement in running time obtained by our method is exponentially dependent on the number of nutrients analyzed.

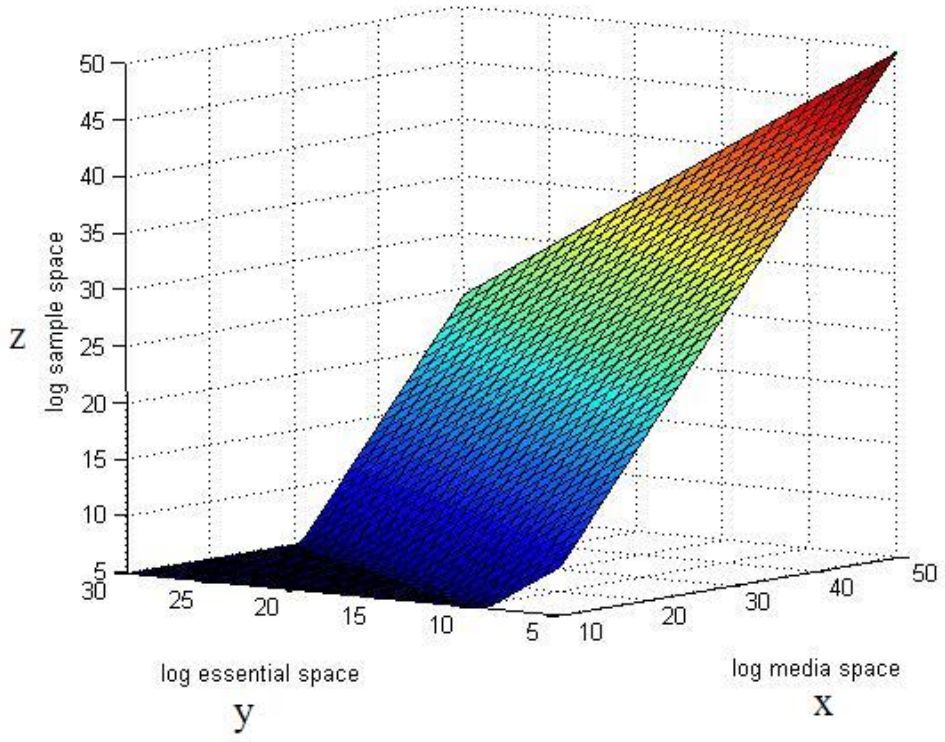

Fig. S2: Although the strong GNIs were identified in this study via an optimization method, theoretically they can also be identified with high probability via sampling of random growth media and analyzing the essentiality of genes under each medium. The figure shows the number of random growth media samples (denoted *z*) required to predict a strong GNI between a gene and nutrient of interest with high probability (as specified below), as a function of two parameters: (i) The total size of *the media space* (i.e. 2 to the power of the number of nutrients), denoted x, and (ii) the size of the media space in which the gene is essential (*the essential media space*), denoted y. The ratio between *y* and *x*, reflects the probability of identifying a medium in which the gene is essential when choosing a random medium. Hence, sampling *z* random growth media results in an expected set of *z*(y/x)* media under which the gene is essential (termed *the sampled essential media space*). A strong GNI is predicted if the nutrient is consistently present or absent across the entire sampled essential media space. However, this space should be large enough such that the observed pattern of consistent presence/absence would be unlikely to occur by chance. Therefore, *z* is assigned a minimal value such that the

probability that a random nutrient would be consistently present/absent across the entire sampled essential media space is lower than 0.05 (assuming a geometric distribution with probability 0.5 for the presence of a nutrient in each random medium; correcting for multiple testing for all pairs of possible GNIs via Bonferroni).

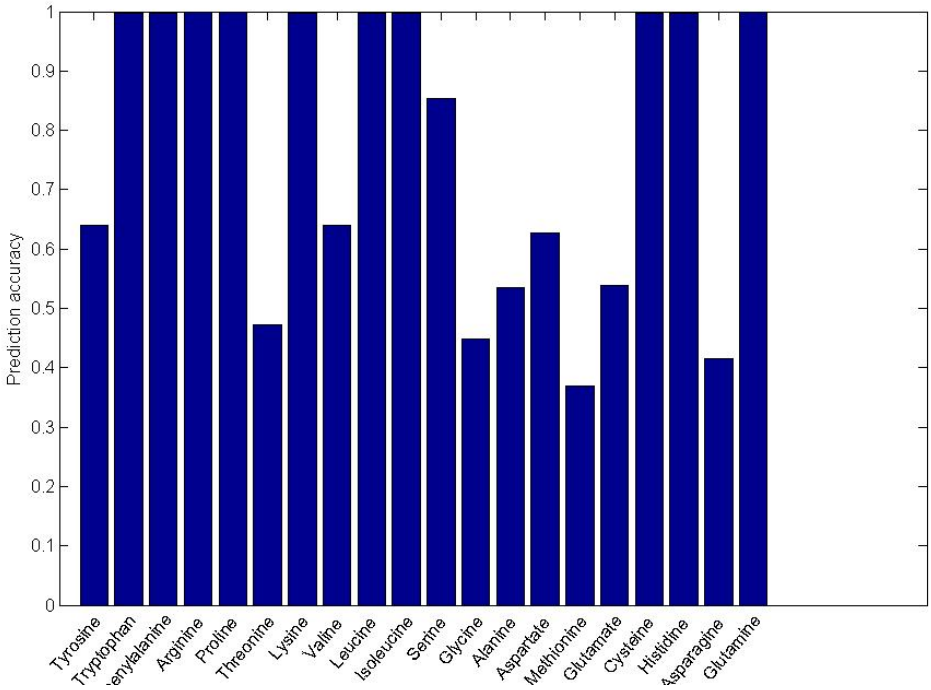

Fig. S3: The optimal possible prediction accuracy of amino-acid presence in the growth media for the different amino acids, based on the observed GNIs.