



Figure 4. Comparison of the predictions based on three different sets of candidate genes: all 6094 candidate genes, 1514 hypothetical genes and 1514 randomly selected known non-metabolic genes. There is about 40-50% increase in terms of predictive power when only the hypothetical genes were used. But the increment is mainly due to the smaller number of candidate set, as we observed almost identical performance in the randomly selected 1514 gene set.