Figure S3. Distributions of the positive and negative interacting protein pairs with various HRSS (MAX) values. HRSS was calculated for (A and B) yeast and (C and D) human protein-protein interactions in the gold standard positive and negative datasets for BP and CC ontologies (including IEA annotations). The [0,1] interval of HRSS values is equally divided into 11 categories, which are \(\{[0.1 \times i, 0.1 \times (i+1)), i = 0, 1, \ldots, 9\}\) plus HRSS = 1.