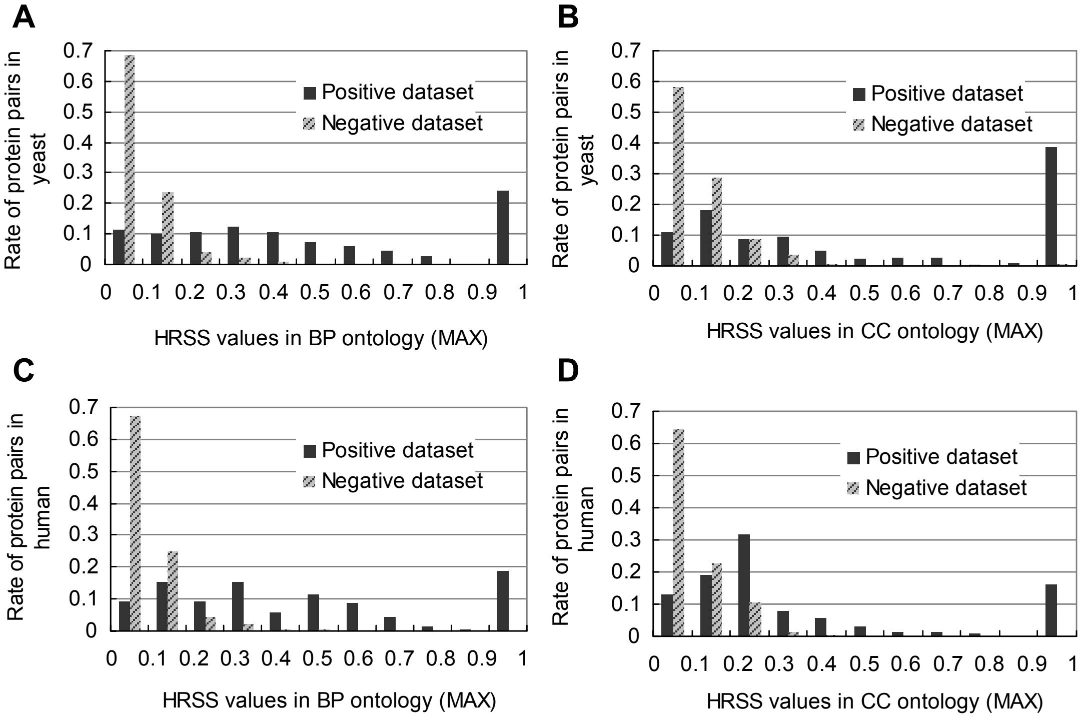

Figure S3. Distributions of the positive and negative interacting protein pairs with various HRSS (MAX) values. HRSS was calculated for (**A** and **B**) yeast and (**C** and **D**) human protein-protein interactions in the gold standard positive and negative datasets for BP and CC ontologies (including 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.