

Fig. S1

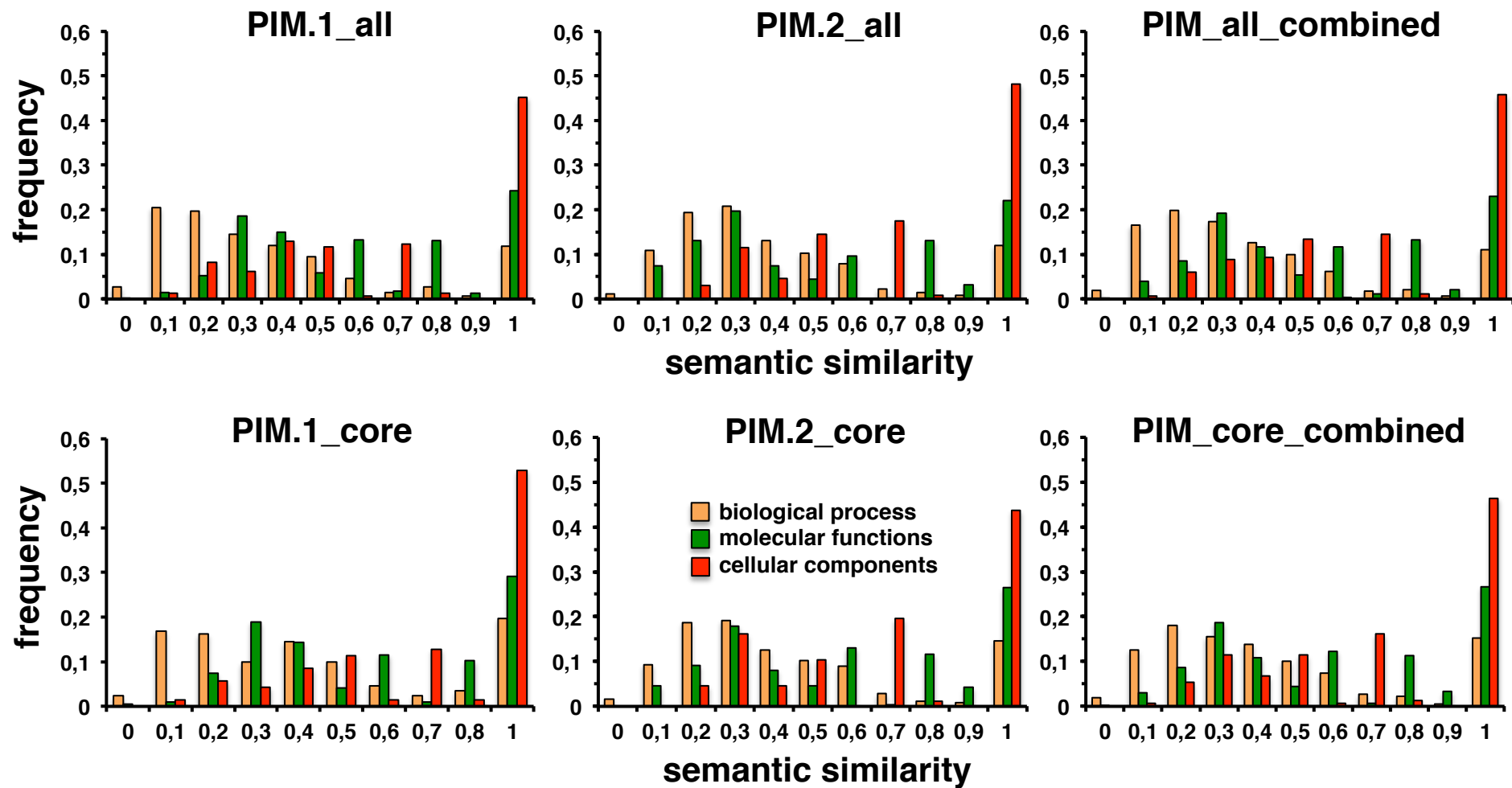
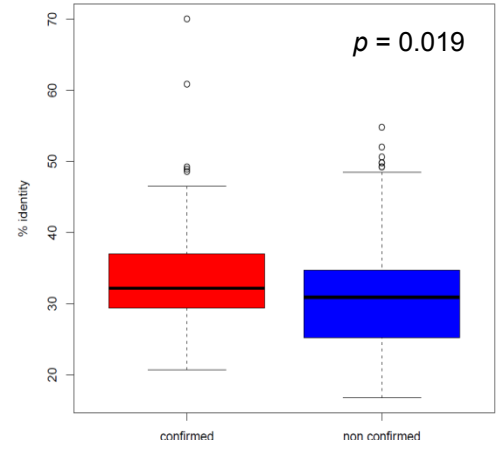
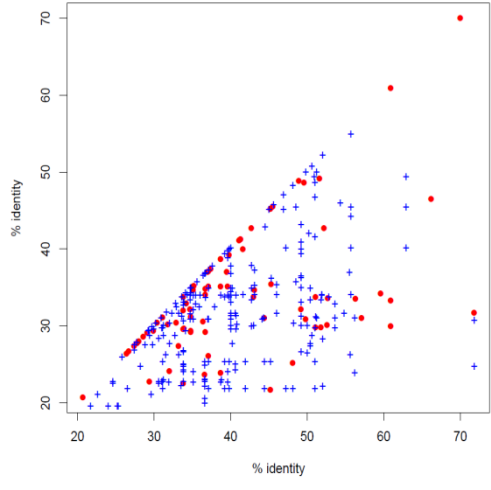
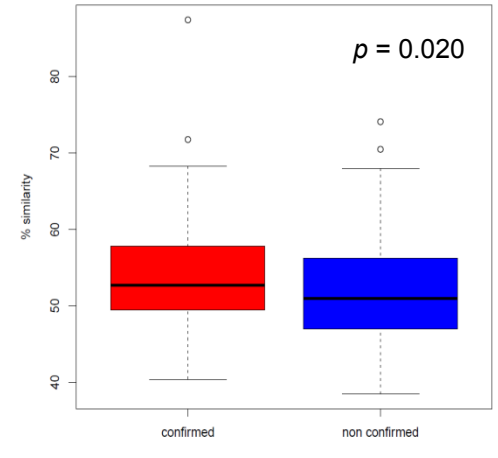
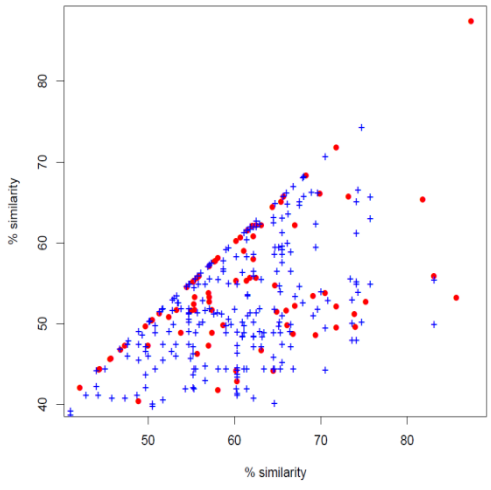


Fig. S2

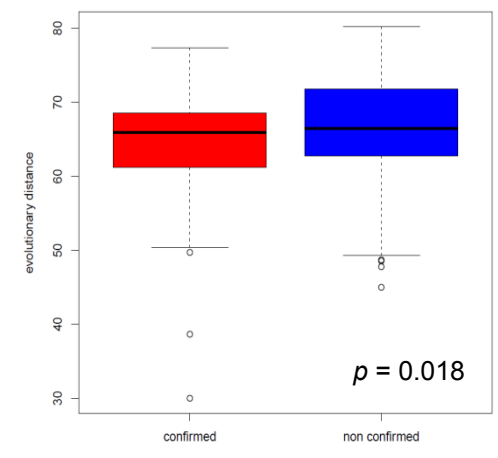
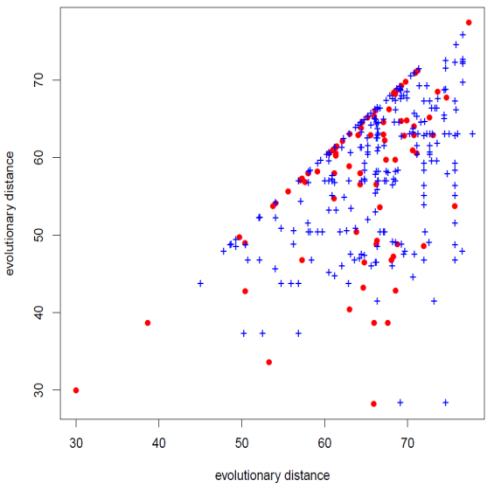
A



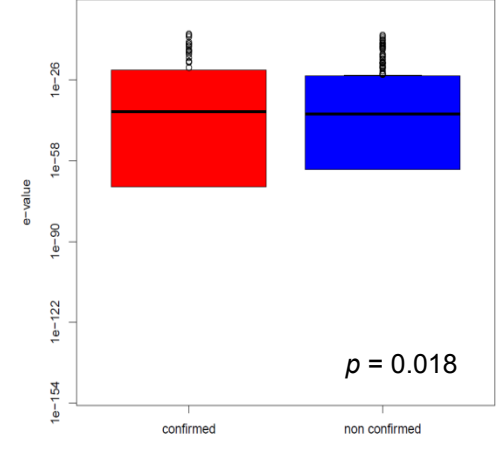
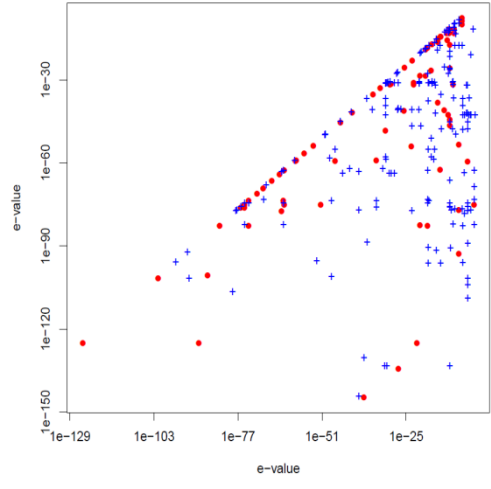
B



C



D



Supplemental figure legends

Figure S1. Semantic similarity between GO terms of interacting proteins of the *H. pylori* networks. GO terms focused on: biological processes, molecular function and cellular components. The different *H. pylori* PIM subsets are compared.

Figure S2. Conservation properties of interologs. Protein pairs of the experimentally tested interactions from our pairwise *E. coli* Y2H tests are plotted against the percental sequence identities **A**, similarities **B**, blast *e*-values **C**, and evolutionary distance **D** with their ortholog. Scatter plots on the left: each dot represents an interolog in *E. coli*: the x-axis represent the selected measure (percental sequence identity or similarity, blast *e*-value, evolutionary distance) between the first *H. pylori* protein in the interaction and its ortholog in *E. coli*, while the value between the second *H. pylori* protein and its ortholog in *E. coli* is indicated on the y-axis. The first protein is always chosen as the one with the highest value. Red dots show positively verified interactions, blue crosses non-confirmed ones. The box plots (right panel) compare the distribution of each property in the confirmed network and in the non-confirmed network. In case of “identity” and “similarity” we considered the partner of a protein pair that exhibits the lowest value, in case of “*e*-value” and “evolutionary distance” the partner that exhibits the highest value. The significance of the difference between the distribution of conserved and non-conserved interactions is indicated by the *p*-value in the box plot.