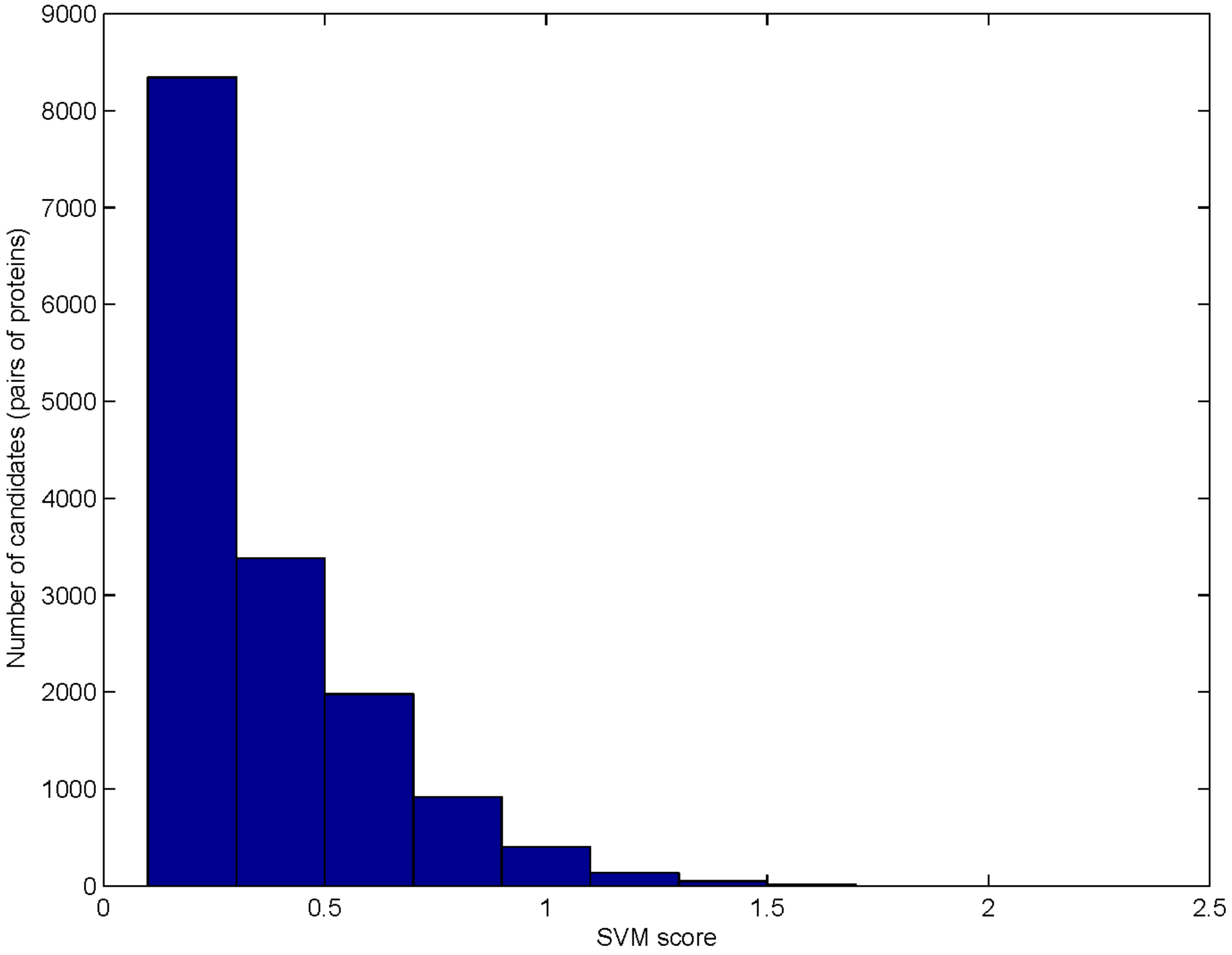
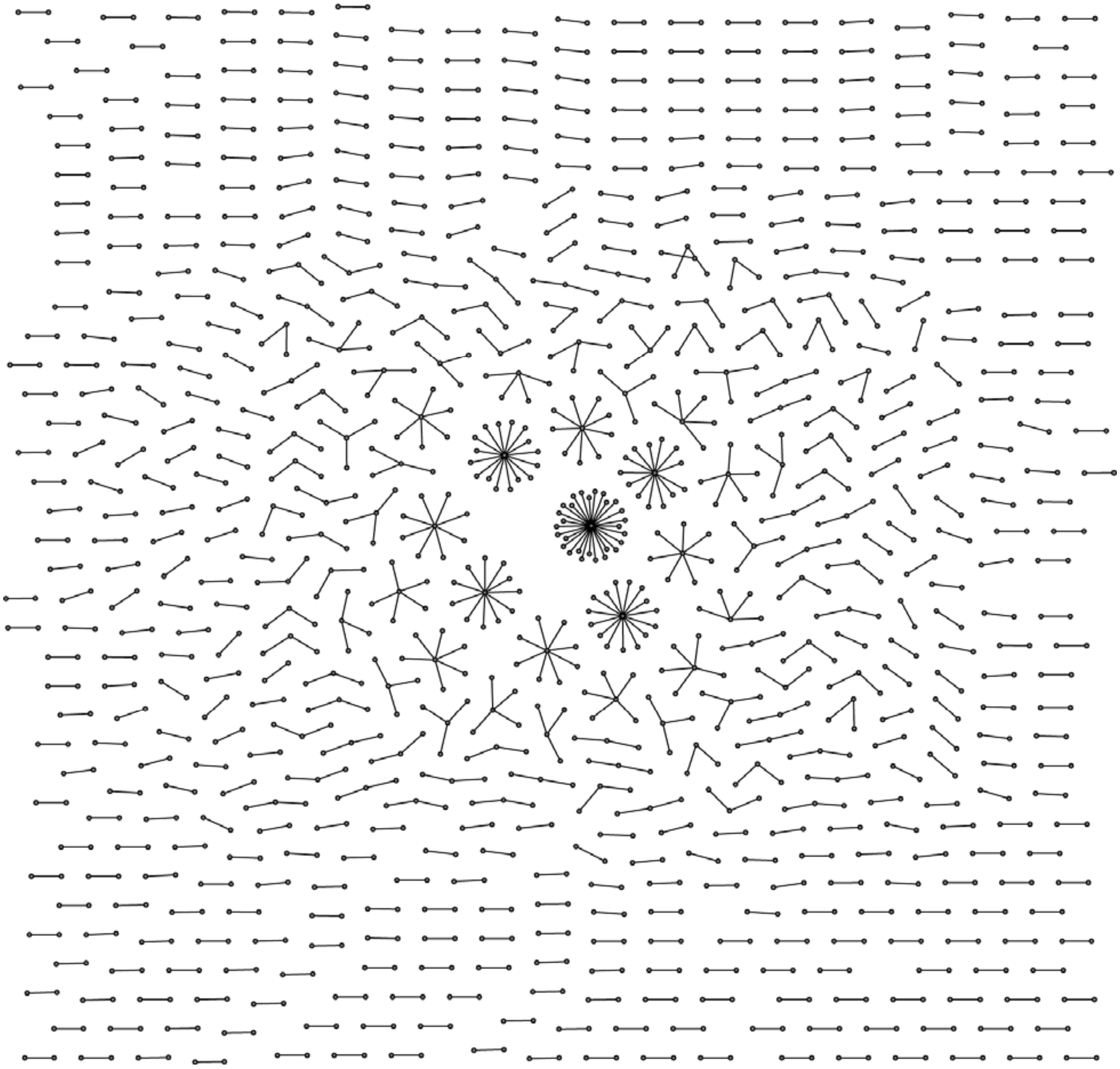
Supplementary Table 1. Supporting abstracts provided by human-curated databases.

No. of distinct interactions	HPRD	BIND	DIP	MINT	IntAct
with 1 supporting abstract	253	287	295	280	278
with 2 supporting abstracts	38	11	5	14	18
with >3 supporting abstracts	9	2	0	6	4

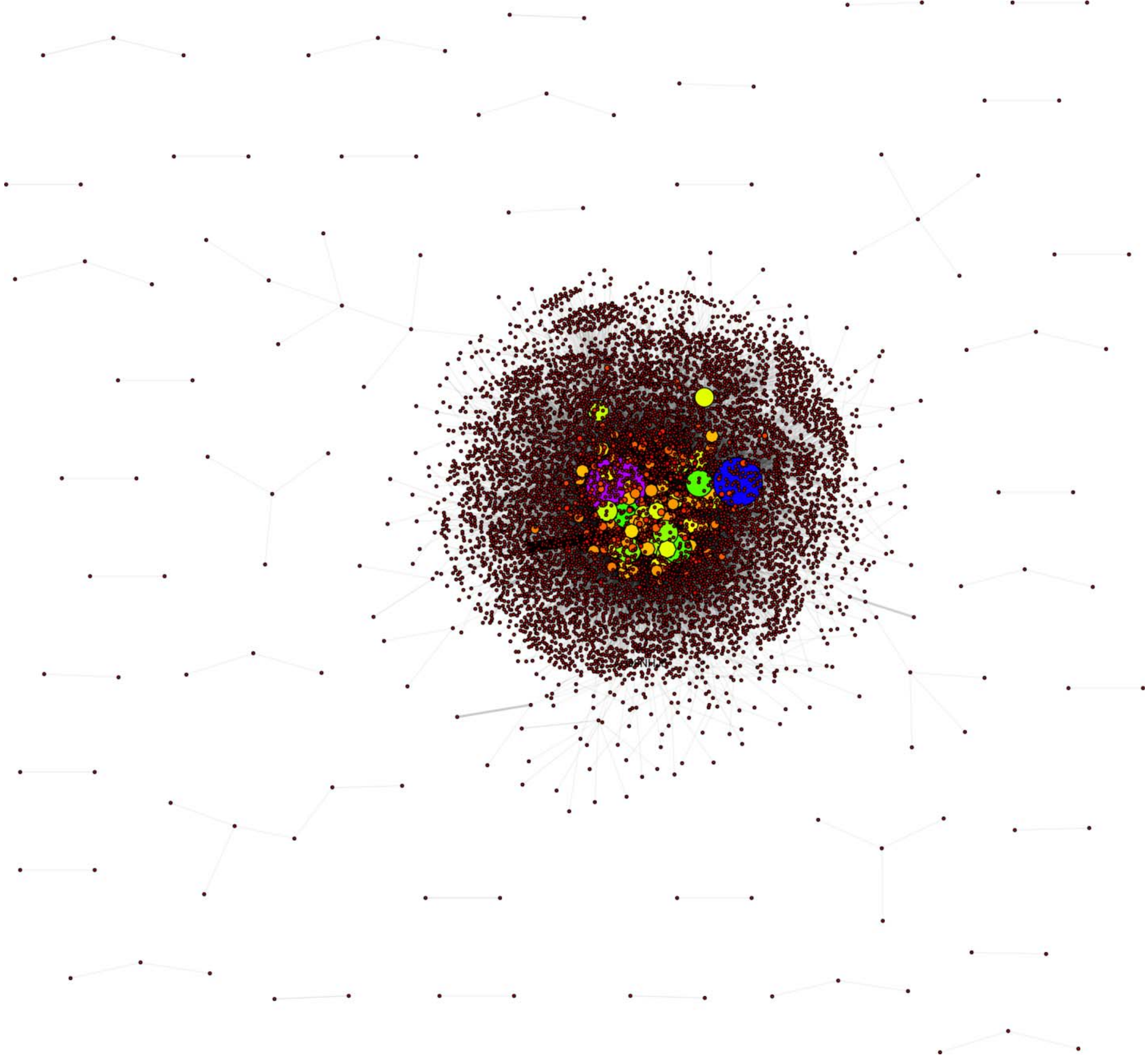
Supplementary Figure 1. The distribution of the SVM scores of all positive pairs of proteins.



Supplementary Figure 2. Protein-protein interactions with new evidence from automatic text mining. New evidence connects 206 protein with 110 interactions.



Supplementary Figure 3. Protein-protein interactions with new evidence from automatic text mining. Expanding the original set of 1,433 proteins and 845 interactions by including interactions from I2D results in a network with 8,250 proteins and 21,652 interactions. Node color and size is according to node degree in the network.



Supplementary Figure 4. Protein-protein interactions with new evidence from automatic text mining. Expanding the original set of 1,433 proteins and 845 interactions by including interactions from I2D results in a network with 8,250 proteins and 21,652 interactions. Subgraph from Supplementary Figure 3, showing only the largest connected component and highlighting new evidence, new evidence for human curated PPIs, predicted PPIs and PPIs from high-throughput experiments. Combined network comprises 392 interactions on 322 proteins. Node color is according to GeneOntology, as shown in the legend. Node size is based on node degree in the network. For simplicity, only protein names of high degree nodes are shown. Edge color is according to the PPI source, as described in the legend.