

Supplementary Material

Tissue specificity and the human protein interaction network

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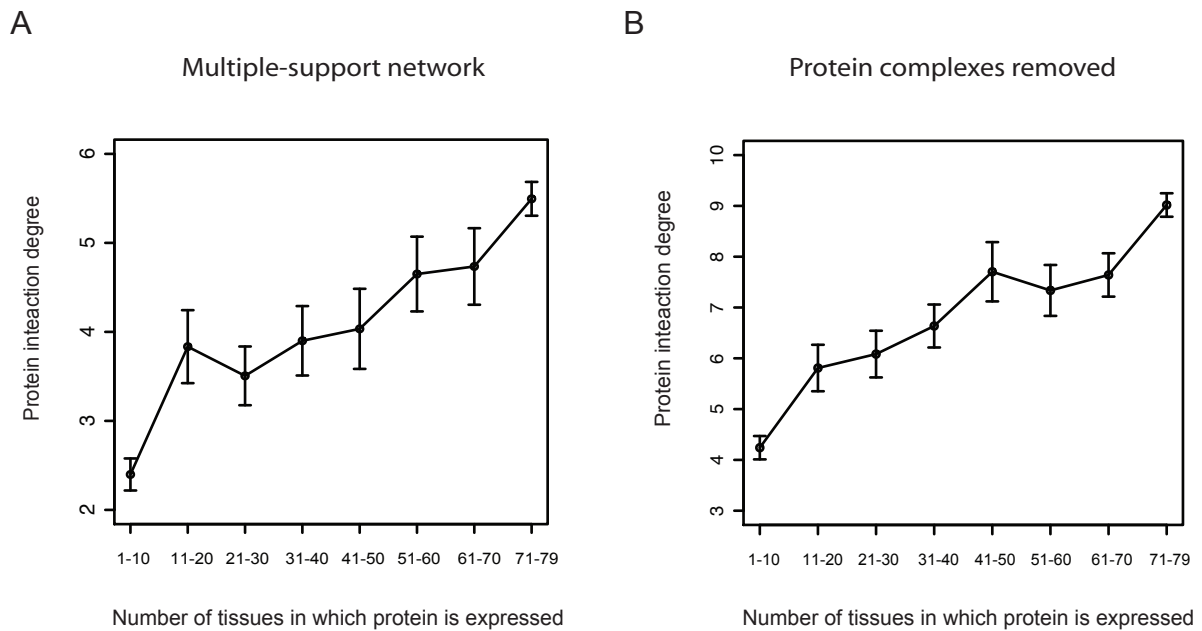
3 supplementary figures (this file).

1 supplementary table (available as an additional data file).

Supplementary table 1 (additional data file).

The integrated human protein interaction network (CRG-all) analyzed in this study. Interacting proteins, the experimental and computational evidence supporting each interaction, the primary publications in which the interaction is reported (PMIDs), and the databases that contain each interaction are listed (see table 1 for the references for each dataset). For interactions for which both proteins have expression data, the tissues in which the interaction can occur are indicated using the standard stringency (200) for expression.

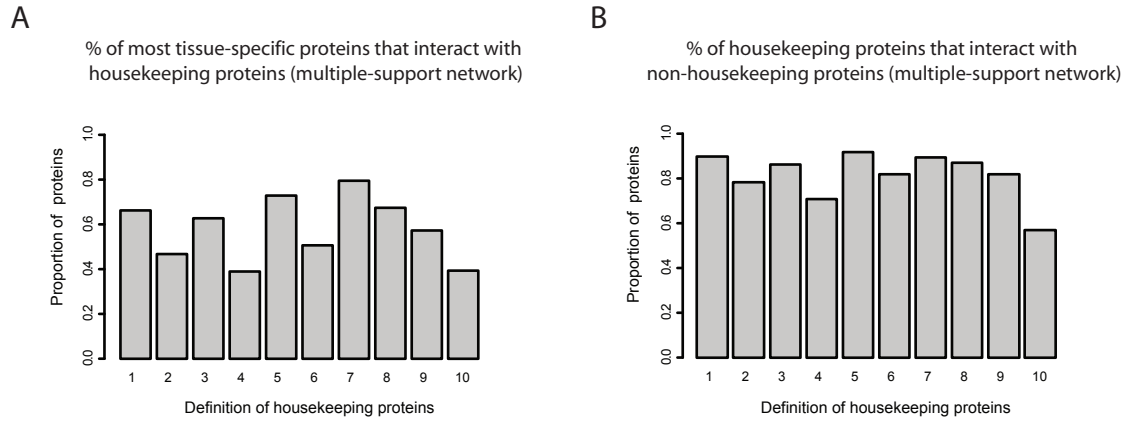
Supplementary figure 1



Supplementary figure 1. Tissue-specific proteins make fewer protein interactions than widely expressed proteins.

The relationship between protein interaction degree and protein expression breadth (the number of tissues in which a protein is expressed) is shown for (A) a filtered multiple-support high confidence human protein interactome, (B) excluding all interactions derived from literature-curated or affinity-purified protein complexes.

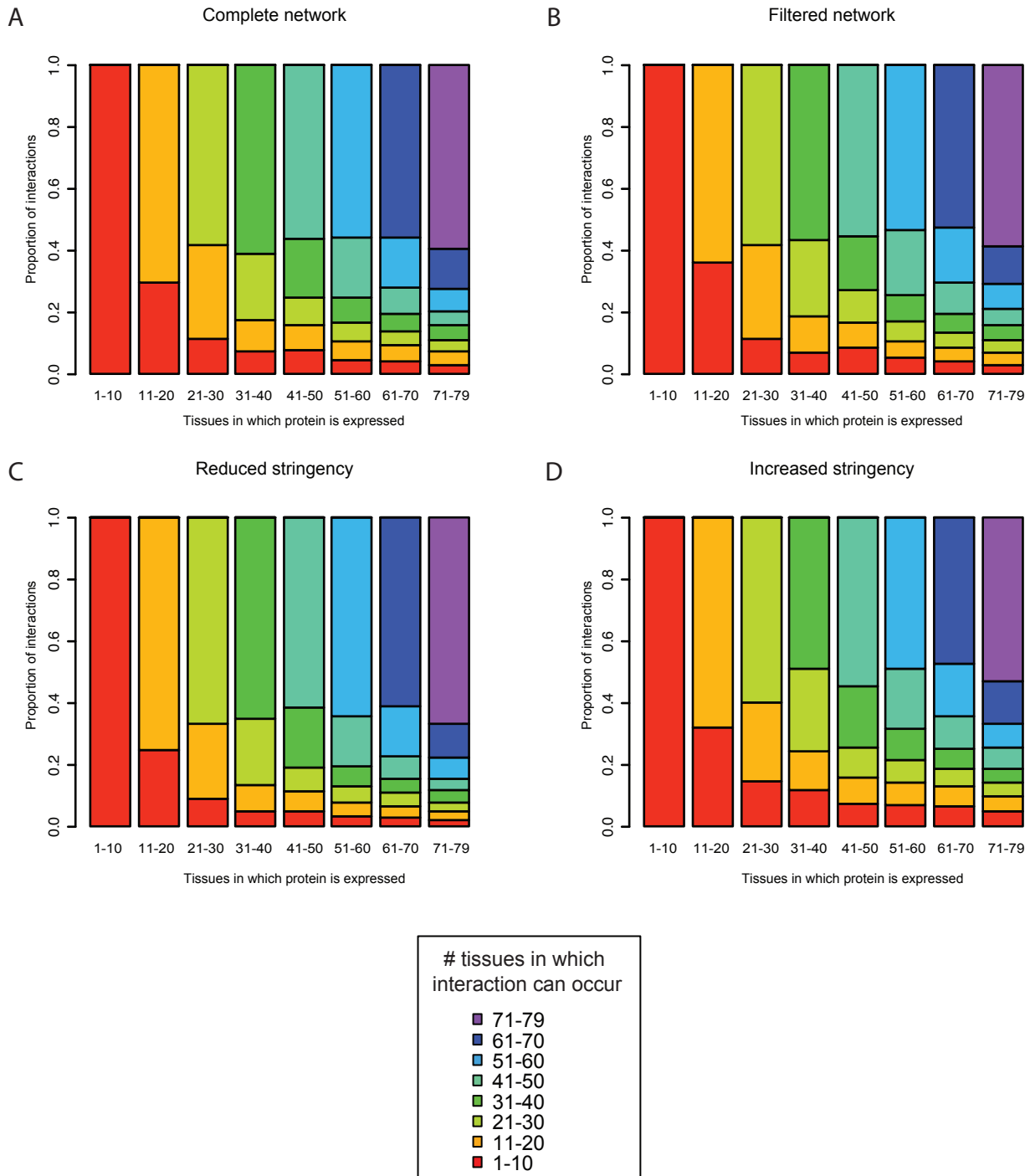
Supplementary figure 2



Supplementary figure 2. Most tissue-specific proteins interact with core cellular components, and most housekeeping proteins have tissue-specific interactions.

(A) The proportion of the most tissue-specific proteins (proteins expressed in only 1-10/79 tissues) that interact with universally expressed housekeeping proteins. (B) The percentage of housekeeping proteins that interact with non-housekeeping proteins. These data are the same analysis as shown in figure 2, but for the high-confidence multiple-support network only. Housekeeping proteins are defined by ten criteria: 1 – this study 79/79 tissues, 2 – this study 71-79 tissues, 3 – this study 79/79 tissues with reduced stringency, 4 – this study 71-79 tissues with reduced stringency, 5 – this study 79/79 tissues with increased stringency, 6 – this study 71-79 tissues with increased stringency, 7 – Zhu et al. microarray data 18/18 tissues, 8 – Zhu et al. microarray data 16-18 tissues, 9 – Zhu et al. EST data 18/18 tissues, 10 – Zhu et al. EST data 16-18 tissues (Zhu et al, 2008).

Supplementary figure 3



Supplementary figure 3. Many proteins make interactions that can only occur in a subset of the tissues in which they are expressed.

The number of tissues in which the interactions of a protein can occur are compared to the number of tissues in which a protein is expressed for proteins falling into each of eight bins of tissue-specificity. Data are shown for (A) the complete network, (B) the filtered multiple-support network, (C) using a reduced stringency threshold at which a protein is considered expressed in a sample (150), (D) using an increased stringency threshold (250).