

Figure S1. Positive prediction values (Sylvain Brohee, manuscript in preparation) for large-scale datasets using subcellular localization data from Huh et al., 2003 Nature 425, 671.

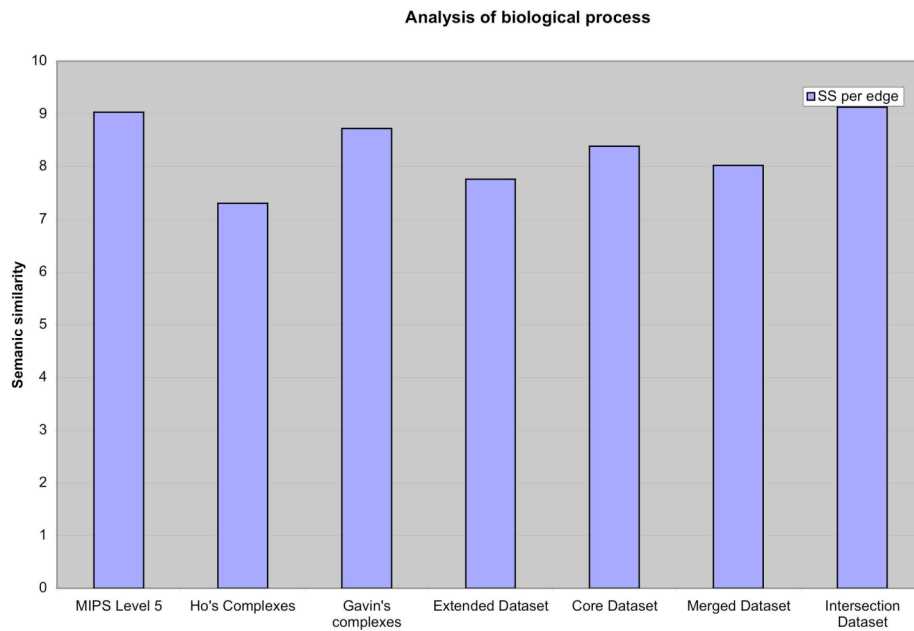


Figure S2. Semantic similarity scores (Lord et al. 2003 Bioinformatics 19, 1275) for large-scale datasets using GO biological process taxonomy (www.geneontology.org)

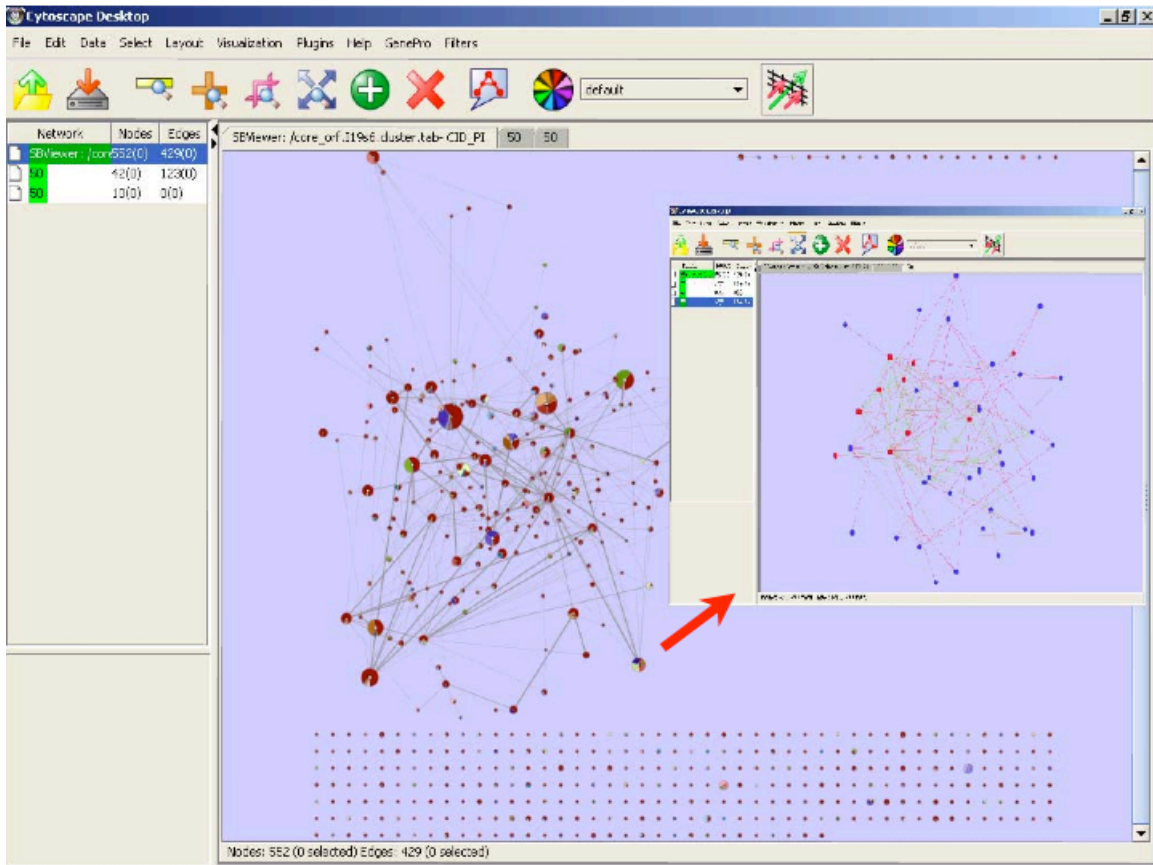


Figure S3. Screenshot of Cytoscape/GenePro representation of Core protein complex network. Each node represents an individual complex. An individual complex (Predicted complex #50) is enlarged in inset. Red indicates members of the complex while blue indicates neighbours of degree one.

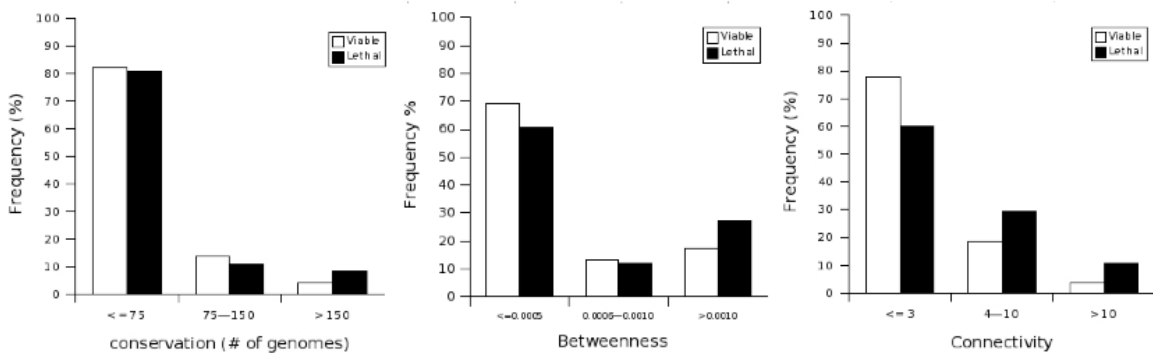


Figure S4. Essential genes are more conserved, connected and have more betweenness than non-essential genes

A.

| | Protein | ORF | Essential | Size (kDa) | Tagged subunits | | | | |
|-------------------|--------------|-----------|-----------|------------|-----------------|----------|----------|-----------|----------|
| | | | | | Rpb1-TAP | Rpb3-TAP | Rpb9-TAP | Rpb11-TAP | Iwr1-TAP |
| RNA Polymerase II | <i>Rpb1</i> | Ydl140c | Yes | 192 | + | + | + | + | + |
| | <i>Rpb2</i> | Yor151c | Yes | 139 | + | + | + | + | + |
| | <i>Rpb3</i> | Yil021w | Yes | 35 | + | + | + | + | + |
| | <i>Rpb4</i> | Yjl140w | No | 25 | + | + | + | + | + |
| | <i>Rpb5</i> | Ybr154c | Yes | 25 | + | + | + | + | + |
| | <i>Rpb6</i> | Ypr187w | Yes | 18 | + | + | + | + | + |
| | <i>Rpb7</i> | Ydr404c | Yes | 19 | + | + | + | + | + |
| | <i>Rpb8</i> | Yor224c | Yes | 17 | - | + | + | + | + |
| | <i>Rpb9</i> | Ygl070c | No | 14 | + | + | + | + | + |
| | <i>Rpb10</i> | Yor210w | Yes | 8 | + | + | + | + | + |
| | <i>Rpb11</i> | Yol005c | Yes | 14 | + | + | + | + | + |
| | <i>Rpb12</i> | Yhr143w-a | Yes | 8 | - | + | + | - | - |
| TFIIF | Tfg1 | Ygr186w | Yes | 82 | + | + | + | + | + |
| | Tfg2 | Ygr005c | Yes | 47 | + | + | + | + | + |
| | Tfg3 | Ypl129w | No | 27 | - | + | + | + | - |
| TFIIS | Spt5 | Yml010w | Yes | 116 | + | + | + | + | + |
| | Spt4 | Ygr063c | No | 11 | - | - | + | + | - |
| | Dst1 | Ygl043w | No | 35 | + | + | + | + | + |
| | Iwr1 | Ydl115c | No | 41 | + | + | + | + | + |
| | Pwr1 | Ycr079c | No | 49 | - | + | + | + | - |

B.

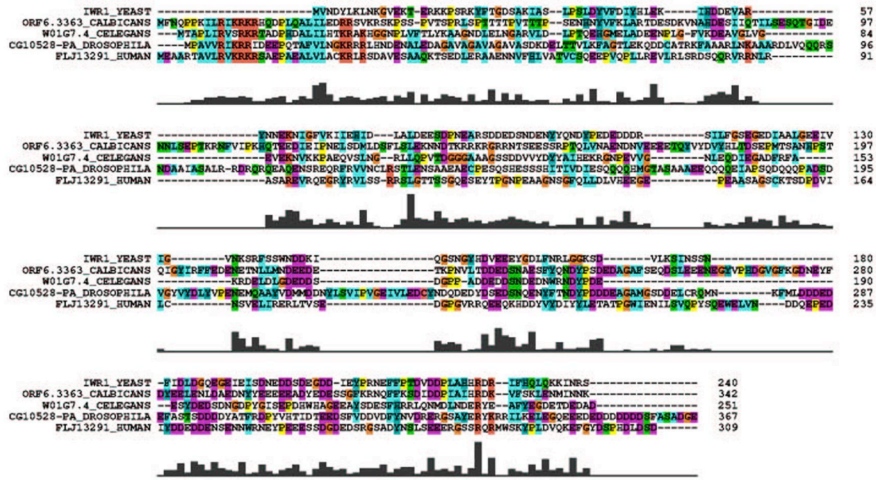


Figure S5. A. Summary of purifications using tagged Iwr1 and tagged unique subunits of RNA polymerase II. B. Amino acid alignment of Iwr1 (Ydl115c) sequence from various species.