

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.

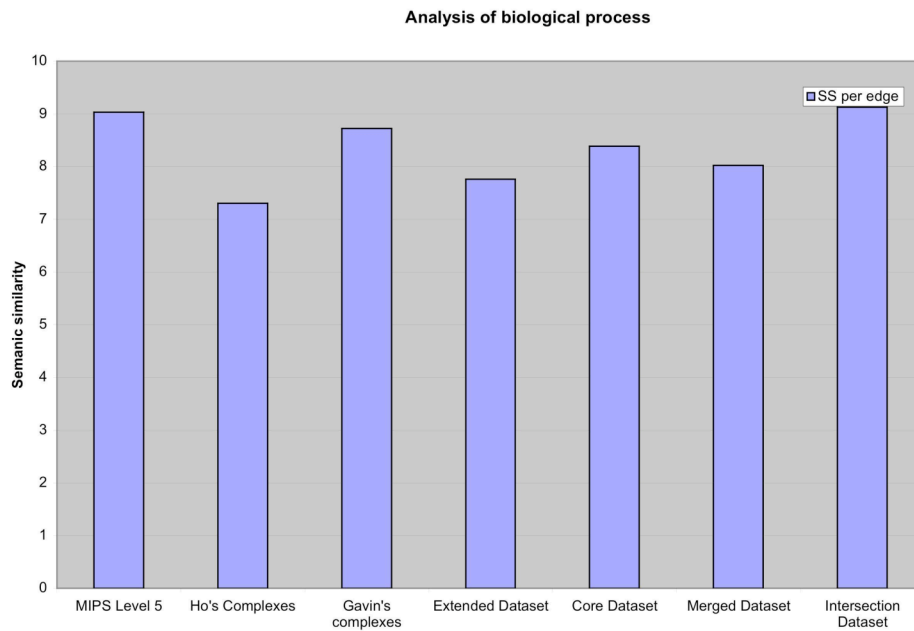


Figure S2. Semantic similarity scores (Lord et al. 2003 Bioinformatics 19, 1275) for large-scale datasets using GO biological process taxonomy (www.geneontology.org)

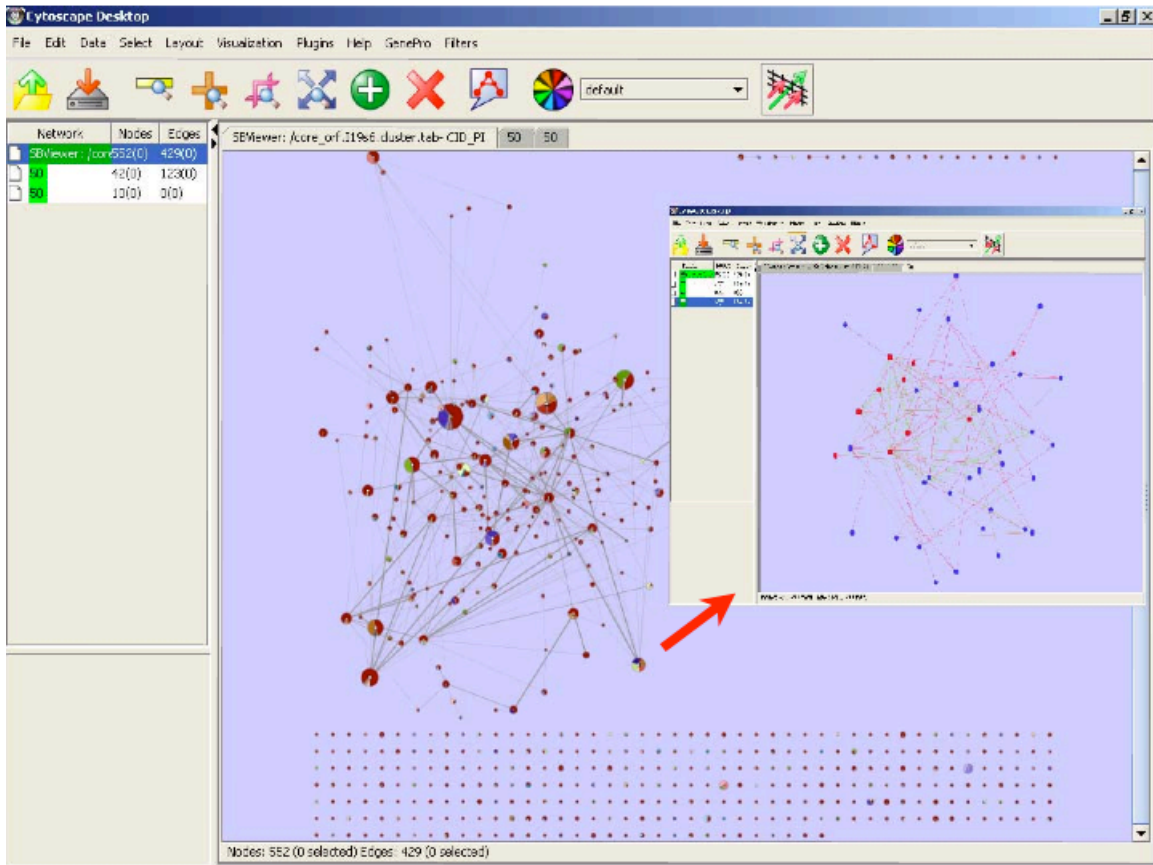


Figure S3. Screenshot of Cytoscape/GenePro representation of Core protein complex network. Each node represents an individual complex. An individual complex (Predicted complex #50) is enlarged in inset. Red indicates members of the complex while blue indicates neighbours of degree one.

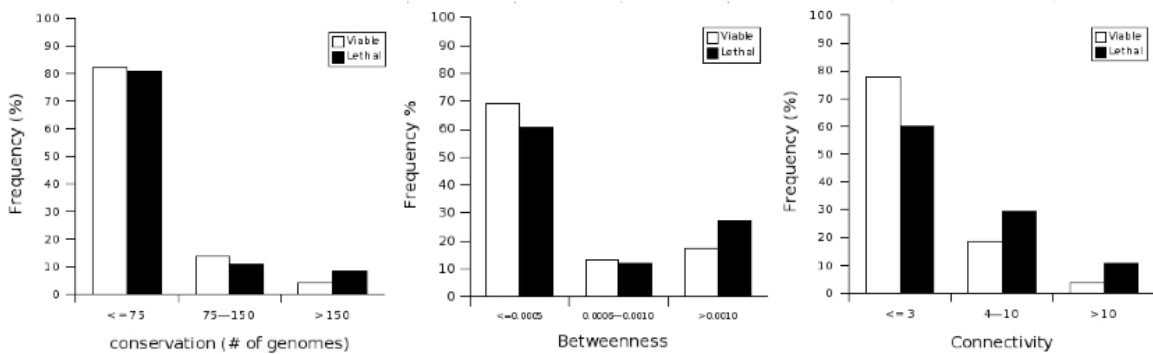


Figure S4. Essential genes are more conserved, connected and have more betweenness than non-essential genes

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.

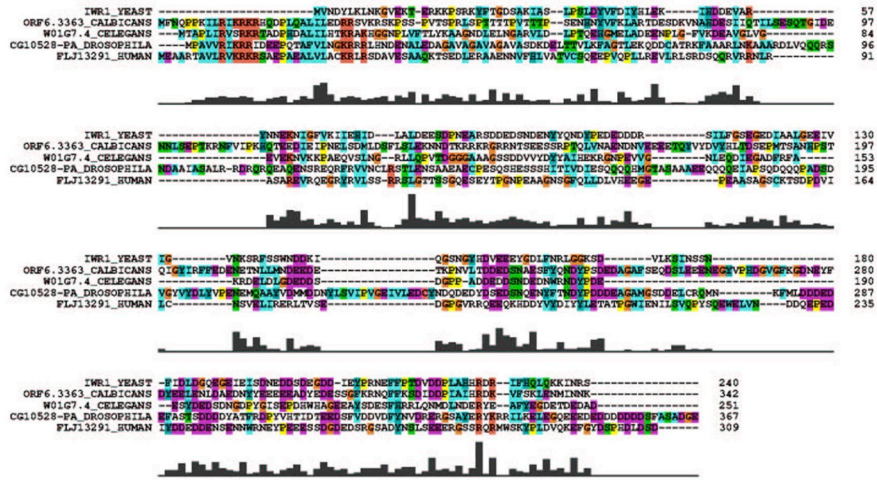


Figure S5. A. Summary of purifications using tagged Iwr1 and tagged unique subunits of RNA polymerase II. B. Amino acid alignment of Iwr1 (Ydl115c) sequence from various species.