**Supplementary Figure 1**

VisANT graph similar to that in the main Fig 1A, except that the low-throughput data in Johnson et al (2010) is assigned its own node, which has the effect if skewing the gold standard data because it is ‘pulled’ towards the Johnson et al (2010) node.

**Supplementary Figure 2 Characterisation of antibodies that recognize specific phosphorylated residues on DBNL, SMAUG2 and KLC2**

The indicated amounts (0.05 to 1 μg) of synthetic phosphorylated peptides (P) and their non-phosphorylated counterparts (N) were spotted onto nitrocellulose. The peptides were immunoblotted with 1 μg/ml affinity purified antibody preincubated in the presence or absence of phosphorylated immunogen or unphosphorylated peptide. The phosphopeptides and antibodies for SMAUG2 were VMGKVC(pT484)QLLVSR (antibody S395C, 3\textsuperscript{rd} bleed; this antibody did not perform), SVQRTH(pS642)LPVHSS (antibody S391C, 1\textsuperscript{st} bleed). For KLC2 phosphopeptides and antibodies were CLRRSG(pS545)FGKLRD (antibody S099B, 2\textsuperscript{nd} bleed (1\textsuperscript{st} and 3\textsuperscript{rd} bleeds gave similar results) and RMKRAS(pS582)LNFLNK (antibody S136B, 2\textsuperscript{nd} bleed, 1\textsuperscript{st} and 3\textsuperscript{rd} bleeds gave similar results). For DBNL, phosphopeptides and antibodies were CQKERAM(pS269)TTSISS (antibody S906B, 3\textsuperscript{rd} bleed) and CFLQKQL(pT291)QPETHF (antibody S907B, 1\textsuperscript{st}, 2\textsuperscript{nd} and 3\textsuperscript{rd} bleeds mixed).

**Supplementary Table 1 The 14-3-3 interactome**

For the articles under analysis (Experiment), the table lists the UniProt accession number (UniProt\_id), the UniProt name (UniProt\_name) and the UniProt description (UniProt\_description) of the proteins identified as 14-3-3 binding partners. The “in\_GD” column contains the tag “yes” or “no” according the presence of the protein in the Gold Standard list published in Johnson et al (2010) and the “Degree” column reports how many articles describe the protein as a 14-3-3 binder.

**Supplementary Table 2 The 14-3-3 interactome with Gold Standard**

The table joins the proteins in Supplementary Table 1 and the proteins listed in Johnson et al (2010) with the format described in Supplementary Table 1. This table was used to create the VisANT graph in Supplementary Figure 1.

**Supplementary Table 3 Clustering analysis**

The table lists the UniProt accession number (UniProt\_id), the UniProt name (UniProt\_name) and the UniProt description (UniProt\_description) for the 284 proteins discovered in more than 2 studies (Experiment). The “Nucleolar proteins” and “Mitochondrial proteins” columns contain the tags “yes” or “not” according the presence of the protein in MitoMiner and Nucleolar Protein databases respectively. The “Cytoplasmic proteins” and “mRNA processing” columns contain the tag “yes” or “no” according the presence of the protein in the clusters identified by David analysis. The “in\_GD” column contains the tags “yes” or “no” according the presence of the protein in the Gold Standard list published in Johnson et al. (2010) and the “Degree” column reports how many articles describe the protein as 14-3-3 binder.