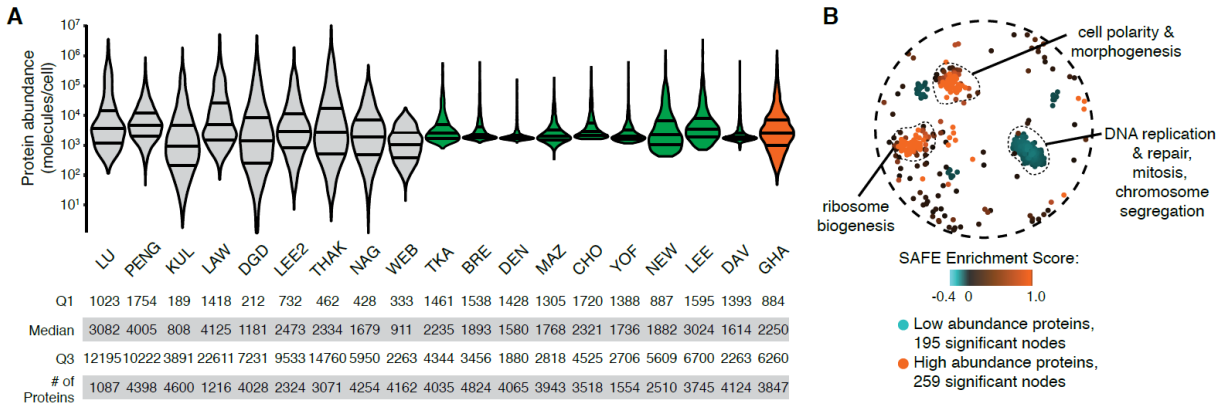

Figure 3. Distributions of protein abundance and functional enrichment. (A) The distribution of yeast protein abundance, as measured in each independent study in molecules per cell, is plotted, with the first quartile (Q1), median, and third quartile (Q3) indicated by horizontal bars. The areas of the violin plots are scaled proportionally to the number of observations. Mass spectrometry– , GFP–, and TAP immunblot–based studies are coloured in grey, green, and orange, respectively. The number of proteins detected and quantified by each study is also indicated. (B) SAFE annotation of the yeast genetic interaction similarity network (Costanzo et al. 2016) with protein abundance data. The protein abundance enrichment landscape is shown. Coloured nodes represent the centers of local neighborhoods enriched for high or low abundance proteins, shaded according to the log enrichment score. The outlines of the GO-based functional domains of the network where protein abundance enrichment is concentrated are shown.

Table 1. The nineteen protein abundance datasets considered

Abbreviation	Reference	Type of Study	Detection	Abundance measure	Media	Temp	Growth phase
LU	Lu et al. 2007 [32]	Mass spectrometry	label-free spectral counting	absolute	YPD	30°C	mid-log
PENG	Peng et al. 2012 [40]	Mass spectrometry	label-free spectral counting and ion volume based quantitation	absolute	Minimal		early log
KUL	Kulak et al. 2014 [25]	Mass spectrometry	label-free spectral counting	absolute	YPD	30°C	mid-log
LAW	Lawless et al. 2016 [27]	Mass spectrometry	stable-isotope labeled internal standards and selected reaction monitoring	absolute	Minimal		chemostat
DGD	de Godoy et al. 2008 [12]	Mass spectrometry	SILAC and ion chromatogram based quantification	relative	Minimal		mid-log
LEE2	Lee et al. 2011 [28]	Mass spectrometry	isobaric tagging and ion intensities	relative	YPD	30°C	mid-log
THAK	Thakur et al. 2011 [48]	Mass spectrometry	summed peptide intensity	relative	Minimal		mid-log
NAG	Nagaraj et al. 2012 [36]	Mass spectrometry	spike-in SILAC	relative	YPD	30°C	mid-log
WEB	Webb et al. 2013 [58]	Mass spectrometry	label-free spectral counting	relative	YPD	30°C	mid-log
TKA	Tkach et al. 2012 [50]	GFP-microscopy	live cells; confocal	relative	Minimal	30°C	mid-log
BRE	Breker et al. 2013 [5]	GFP-microscopy	live cells; confocal	relative	Minimal	30°C	mid-log
DEN	Denervaud et al. 2013 [13]	GFP-microscopy	live cells; wide field	relative	Minimal	30°C	steady-state
MAZ	Mazumder et al. 2013 [33]	GFP-microscopy	fixed cells; wide field	relative	Minimal	30°C	mid-log
CHO	Chong et al. 2015 [8]	GFP-microscopy	live cells; confocal	relative	Minimal	30°C	mid-log
YOF	Yofe et al. 2016 [61]	GFP-microscopy	N-teminal GFP; live cells; confocal	relative	Minimal	30°C	mid-log
NEW	Newman et al. 2006 [37]	GFP-flow cytometry	live cells	relative	YPD	30°C	mid-log
LEE	Lee et al. 2007 [29]	GFP-flow cytometry	live cells	relative	YPD	30°C	mid-log
DAV	Davidson et al. 2011 [11]	GFP-flow cytometry	live cells	relative	YPD	30°C	mid-log
GHA	Ghaemmaghami et al. 2003 [19]	TAP-immunoblot	SDS extract; immunoblot with internal standard	absolute	YPD	30°C	mid-log