Supplementary Table 1. The detailed sources of each individual feature.

Feature Name	Source	Feature Name	Source	Feature Name	Source
5'UTR length	Nagalakshmi [2]	3'UTR length	Nagalakshmi [2]	Transcription level	Nagalakshmi [2]
Transcriptional frequency	Holstege [1]	mRNA expression level	Holstege [1]	mRNA half-life	Holstege [1]
Transcriptional plasticity	Lin [3]	Translational efficiency	Csárdi [6]	# of mRNA isoforms	Pelechano [4]
Protein half-life	Christiano [5]	Protein abundance in normal/stress conditions	Ho [7]	# of interactors in the (PI, GI) networks	BioGRID [11]
CDS length	SGD [10]	Amino acid composition	SGD [10]	Atomic composition	SGD [10]
Protein physical details (length, molecular weight, pI, aliphatic index, instability index)	SGD [10]	Coding region translation calculation (codon bias, codon adaptation index, frequency of optimal codons, hydropathicity of protein, aromaticity score)	SGD [10]	# of fungal homologs # of non-fungal and S. cerevisiae homologs	YeastMine [13]
# of interactors in the (CC, CX, DC, GN, GT, HT, LC, PG, TS) networks	YeastNet [8]	# of GO terms # of GO slim terms # of pathways # of domains # of publications # of mutant phenotypes	SGD [10]	# of PTMs # of transcriptional regulators	YeastMine [13]
# of interactors in the (EPA, FAA, GIA, LEA, MPA, PIA, TFBA, TFRA) networks	YAGM [9]	Extinction coefficients at 280nm (all Cys residues appear as half cystines, no Cys residues appear as half cystines)	SGD [10]	# of interactors in the EPA network	SPELL [12]

CDS: coding sequence

UTR: untranslated region

GO: gene ontology

PTM: post-translational modification,

pI: isoelectric point,

PI: physical interaction,

GI: genetic interaction,

CC: inferred links by co-citation of two genes across 46,111 pubmed Medline article abstracts for yeast biology from YeastNet,

CX: inferred links by co-expression pattern of two genes (based on high-dimensional gene expression data) from YeastNet,

DC: inferred links by co-occurrence of protein domains between two coding genes from YeastNet

GN: inferred links by similar genomic context of bacterial orthologs of two yeast genes from YeastNet

GT: inferred links by similar profiles of genetic interaction partners from YeastNet

HT: links by high-throughput protein-protein interactions

LC: links by small/medium-scale protein-protein interactions (collected from protein-protein interaction data bases)

PG: Inferred links by similar phylogenetic profiles between two yeast genes from YeastNet

TS: inferred links by 3-D protein structure of interacting orthologous proteins between two yeast proteins from YeastNet

EPA: expression profile association

FAA: functional annotation association

GIA: genetic interaction association

LEA: literature evidence association,

MPA: mutant phenotype association

PIA: physical interaction association

TFBA: transcription factor binding association

TFRA: transcription factor regulation association

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