

Table S1. Characterization of high-degree genes

1-1 Enrichment tests

Feature	DMA		TSA	
	Test result	p-value	Test result	p-value
Complex member	Enrichment (x2.14)	0.00E+00		2.47E-01
Duplicated	Depletion (x0.72)	2.27E-10		1.77E+00
WGD duplicate	Depletion (x0.70)	3.25E-07		1.19E+00
SSD duplicate	Depletion (x0.72)	8.61E-05		1.74E+00
Originated in Saccharomyces	Depletion (x0.36)	2.22E-04		2.00E+00

1-2 Ranksum tests

Feature	DMA		TSA	
	Test result	p-value	Test result	p-value
Single mutant fitness defect	Higher	3.67E-279	Higher	5.70E-32
Curated phenotypes	Higher	3.09E-172	N/A	
Number of complexes	Higher (mean)	1.13E-72		1.18E-01
Chemical-genetic degree	Higher	2.45E-48	N/A	
Expression variance, genetic-B	Lower	1.91E-42		1.16E-01
Phenotypic capacitance	Higher	1.53E-36	N/A	
PPI degree, Tap MS	Higher	3.20E-36		4.34E-01
Copy number volatility	Lower	5.46E-26		9.77E-01
Multifunctionality	Higher	8.17E-24		2.62E-01
Copy number	Lower (mean)	1.31E-17		6.10E-01
Expression variance, genetic-A	Lower	1.28E-13	Lower	4.07E-02
Yeast conservation	Higher	2.54E-13		2.93E-01
Broad conservation	Higher	3.07E-13		2.11E-01
Expression variance, environ.	Lower	1.84E-10		9.04E-02
Expression level	Higher	2.14E-09		1.00E-01
dN/dS	Lower	5.27E-07		7.82E-02
Coexpression degree	Higher	5.60E-07		1.58E-01
Protein abundance	Higher	3.77E-06		1.02E-01
Protein abundance in stress	Higher	8.42E-06		1.55E-01
Protein disorder	Higher	9.08E-06		8.79E-01
CAI	Higher	2.23E-05		6.69E-01
Deleterious SNP rate	Lower (mean)	2.83E-05		3.23E-01
Effective number of codons	Lower	3.53E-05		8.71E-01
PPI degree, Y2H	Higher (mean)	1.43E-03		8.11E-01
Protein length		4.21E-01		4.65E-01
Number of domains		9.71E-01		6.71E-01