

Table S2. Characterization of low-degree genes

2-1 Enrichment tests

Feature	DMA		TSA	
	Test result	p-value	Test result	p-value
Originated in Saccharomyces	Enrichment (x1.90)	6.29E-05		2.00E+00
Duplicated	Enrichment (x1.18)	2.55E-04		4.79E-01
SSD duplicate	Enrichment (x1.29)	2.79E-04		6.49E-02
WGD duplicate		1.38E-01		7.23E-02
Complex member	Depletion (x0.36)	0.00E+00		3.47E-01

2-2 Ranksum tests

Feature	DMA		TSA	
	Test result	p-value	Test result	p-value
Single mutant fitness defect	Lower	2.41E-92	Lower	5.60E-26
Curated phenotypes	Lower	2.42E-37	N/A	
Expression variance, genetic-B	Higher	3.01E-30		3.14E-01
Number of complexes	Lower (mean)	2.88E-21		1.28E-01
Copy number volatility	Higher	3.23E-17		8.92E-01
PPI degree, Tap MS	Lower	5.82E-17		4.56E-01
Chemical-genetic degree	Lower	1.15E-15		NaN
Yeast conservation	Lower	6.28E-11		5.69E-01
Multifunctionality	Lower	1.03E-10		7.98E-02
Expression variance, genetic-A	Higher	2.61E-10		2.45E-01
Protein disorder	Lower	8.10E-09		2.36E-01
Coexpression degree	Lower	1.81E-07		8.57E-01
Expression level	Lower	3.31E-07		3.93E-01
Expression variance, environ.	Higher	7.19E-07		3.02E-01
Phenotypic capacitance	Lower	8.48E-07	N/A	
Copy number	Higher (mean)	1.59E-06		3.38E-01
Broad conservation	Lower	6.26E-05		2.62E-01
dN/dS	Higher	6.65E-05	Higher	4.56E-02
Protein abundance in stress	Lower	1.06E-04		3.01E-01
Protein abundance	Lower	1.52E-04		3.31E-01
Effective number of codons	Higher	4.86E-03		4.41E-01
Deleterious SNP rate	Higher (mean)	7.91E-03		9.65E-01
CAI	Lower	1.72E-02		7.06E-01
Protein length	Lower	3.99E-02		2.14E-01
PPI degree, Y2H		1.11E-01		6.08E-01
Number of domains		1.56E-01		3.62E-01