

Supplementary Data

Supplementary figure legend

Figure S1 The predicted “quiet” and “noisy” genes have different properties.

(A) The predicted “quiet” genes contain more haploinsufficient genes. (B) The predicted “quiet” genes contain more essential genes. (C) Protein interaction hubs (degree > 10) are highly enriched among the predicted “quiet” genes. Error bars represent 95th percentile confidence intervals from bootstrap re-sampling.

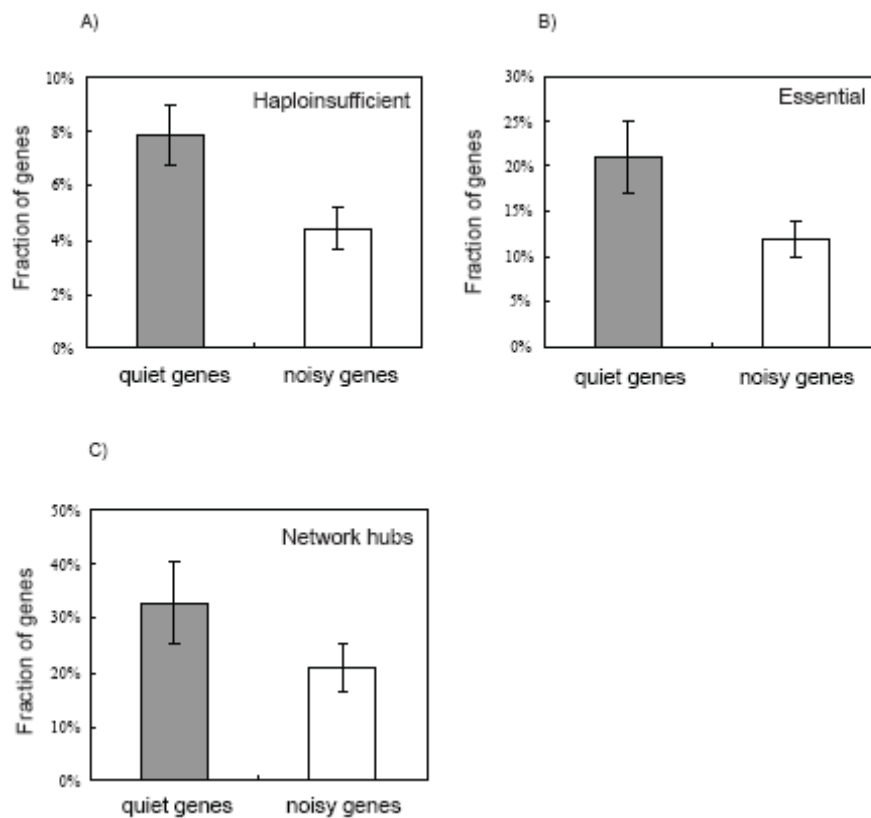


Table S1 Enriched GO categories in ‘noisy’ and ‘quiet’ genes in the measured and modeled datasets

	GO ID	GO term	FDR	# of genes	
BP	GO:0008152	metabolic process	3.84E-08	85	
	GO:0008652	cellular amino acid biosynthetic process	4.47E-06	32	
	GO:0015986	ATP synthesis coupled proton transport	1.23E-05	17	
	GO:0006096	glycolysis	3.73E-05	16	
	GO:0042309	homeiothermy	1.47E-04	14	
	GO:0006811	ion transport	2.68E-04	29	
	GO:0050826	response to freezing	3.10E-04	14	
	GO:0015992	proton transport	1.12E-03	14	
	GO:0001302	replicative cell aging	1.30E-02	10	
	GO:0006970	response to osmotic stress	1.55E-02	12	
	GO:0006979	response to oxidative stress	1.68E-02	15	
	GO:0005975	carbohydrate metabolic process	2.02E-02	24	
	GO:0009058	biosynthetic process	2.69E-02	12	
	GO:0006950	response to stress	3.61E-02	30	
	noisy' genes	GO:0016491	oxidoreductase activity	8.45E-11	90
GO:0003824		catalytic activity	2.22E-06	107	
GO:0050825		ice binding	5.14E-04	14	
GO:0046933		hydrogen ion transporting ATP synthase activity, rotational mechanism	7.39E-04	14	
MF		GO:0015078	hydrogen ion transmembrane transporter activity	1.04E-03	14
GO:0005506		iron ion binding	7.50E-03	30	
GO:0030170		pyridoxal phosphate binding	1.87E-02	13	
GO:0003779		actin binding	2.80E-02	10	
GO:0046961		proton-transporting ATPase activity, rotational mechanism	3.47E-02	10	
CC		GO:0005886	plasma membrane	8.47E-03	40
	GO:0016469	proton-transporting two-sector ATPase complex	1.44E-02	10	
	GO:0030479	actin cortical patch	1.85E-02	12	
	GO:0009277	fungal-type cell wall	2.36E-03	22	
	GO:0005739	mitochondrion	1.12E-07	197	
	GO:0005759	mitochondrial matrix	4.71E-07	25	
	GO:0005762	mitochondrial large ribosomal subunit	4.06E-03	14	

		GO:0006412	translation	1.34E-14	183
		GO:0042254	ribosome biogenesis	2.50E-12	126
		GO:0006364	rRNA processing	1.07E-06	86
		GO:0015031	protein transport	1.34E-06	153
		GO:0006888	ER to Golgi vesicle-mediated transport	2.33E-06	45
		GO:0006402	mRNA catabolic process	1.42E-05	23
		GO:0006368	RNA elongation from RNA polymerase II promoter	1.90E-04	28
		GO:0000027	ribosomal large subunit assembly	3.39E-04	22
	BP	GO:0000723	telomere maintenance	4.43E-04	101
		GO:0006897	endocytosis	9.19E-04	37
		GO:0006886	intracellular protein transport	1.46E-03	49
		GO:0007121	bipolar cellular bud site selection	1.85E-03	18
		GO:0008610	lipid biosynthetic process	2.53E-03	23
		GO:0006887	exocytosis	4.52E-03	20
		GO:0051028	mRNA transport	6.55E-03	25
		GO:0016192	vesicle-mediated transport	7.07E-03	61
		GO:0065002	intracellular protein transmembrane transport	7.77E-03	30
		GO:0006417	regulation of translation	9.93E-03	16
		GO:0003735	structural constituent of ribosome	8.62E-09	121
	MF	GO:0003743	translation initiation factor activity	1.97E-03	22
		GO:0008565	protein transporter activity	5.92E-03	40
		GO:0004175	endopeptidase activity	8.50E-03	17
		GO:0005840	ribosome	1.43E-11	132
		GO:0005935	cellular bud neck	8.36E-03	39
		GO:0005794	Golgi apparatus	1.55E-05	85
		GO:0030529	ribonucleoprotein complex	5.68E-14	154
	CC	GO:0005622	intracellular	9.25E-05	174
		GO:0043234	protein complex	1.02E-04	25
		GO:0005643	nuclear pore	3.56E-02	25
		GO:0005730	nucleolus	3.04E-05	79
		GO:0005737	cytoplasm	5.45E-08	627
		GO:0005829	cytosol	4.69E-03	72
		GO:0005975	carbohydrate metabolic process	1.9E-05	26
		GO:0030435	sporulation resulting in formation of a cellular spore	4.7E-04	21
	BP	GO:0008643	carbohydrate transport	4.0E-03	10
		GO:0030476	ascospore wall assembly	1.0E-02	10
		GO:0008152	metabolic process	1.8E-02	46

	GO:0005215	transporter activity	9.1E-05	28
	GO:0005351	sugar:hydrogen symporter activity	9.2E-03	10
MF	GO:0003700	transcription factor activity	1.3E-02	27
	GO:0043565	sequence-specific DNA binding	3.7E-02	14
	GO:0050660	FAD binding	4.2E-02	8
CC	GO:0005618	cell wall	1.4E-02	14
	GO:0009277	fungal-type cell wall	4.1E-05	21
	GO:0006281	DNA repair	6.0E-07	97
	GO:0006974	response to DNA damage stimulus	1.3E-05	94
	GO:0000398	nuclear mRNA splicing, via spliceosome	8.3E-04	40
	GO:0006355	regulation of transcription, DNA-dependent	1.1E-03	210
	GO:0000070	mitotic sister chromatid segregation	3.2E-03	22
	GO:0008380	RNA splicing	4.5E-03	51
	GO:0006397	mRNA processing	5.0E-03	74
	GO:0007126	meiosis	6.6E-03	64
	GO:0006289	nucleotide-excision repair	6.6E-03	18
BP	GO:0007131	reciprocal meiotic recombination	7.1E-03	23
	GO:0006914	autophagy	8.3E-03	21
	GO:0007049	cell cycle	8.4E-03	132
	GO:0007067	mitosis	1.5E-02	57
	GO:0006260	DNA replication	2.5E-02	40
	GO:0006623	protein targeting to vacuole	3.2E-02	30
	GO:0006350	transcription	3.4E-02	200
	GO:0006367	transcription initiation from RNA polymerase II promoter	4.1E-02	22
	GO:0051301	cell division	4.2E-02	77
MF	GO:0016251	general RNA polymerase II transcription factor activity	4.4E-02	23
	GO:0000778	condensed nuclear chromosome kinetochore	3.9E-02	18
CC	GO:0000781	chromosome, telomeric region	5.7E-03	25
	GO:0005681	spliceosomal complex	3.2E-05	37

Table S2 Enriched GO categories in noise diverged genes and noise conserved genes.

	GO ID	GO term	FDR	# of genes
Noise conserved genes	GO:0006807	nitrogen compound metabolic process	4.6E-02	15
	GO:0006890	retrograde vesicle-mediated transport, Golgi to ER	1.5E-02	21
	GO:0006166	purine ribonucleoside salvage	1.3E-02	9
	GO:0007118	budding cell apical bud growth	1.7E-02	12
	BP GO:0006511	ubiquitin-dependent protein catabolic process	3.0E-02	58
	GO:0009116	nucleoside metabolic process	4.0E-02	10
	GO:0009165	nucleotide biosynthetic process	1.3E-02	9
	GO:0046686	response to cadmium ion	2.1E-02	8
	GO:0000162	tryptophan biosynthetic process	8.2E-03	10
	MF	GO:0004175	endopeptidase activity	7.9E-03
	GO:0004298	threonine-type endopeptidase activity	6.1E-03	14
Noise diverged genes	GO:0019773	proteasome core complex, alpha-subunit complex	4.9E-02	7
	GO:0019774	proteasome core complex, beta-subunit complex	4.9E-02	7
	CC GO:0032045	guanyl-nucleotide exchange factor complex	4.9E-02	7
	GO:0043234	protein complex	2.4E-02	33
	GO:0005839	proteasome core complex	1.4E-02	14
	GO:0007243	protein kinase cascade	1.7E-02	3
	GO:0045721	negative regulation of gluconeogenesis	1.1E-02	6
	GO:0006102	isocitrate metabolic process	1.7E-02	4
	BP GO:0016126	sterol biosynthetic process	4.6E-02	12
	GO:0006528	asparagine metabolic process	1.7E-02	4
GO:0005993	trehalose catabolic process	1.7E-02	3	
GO:0006995	cellular response to nitrogen starvation	1.7E-02	4	
GO:0015293	symporter activity	9.0E-03	6	
GO:0016616	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	7.7E-03	13	
MF	GO:0004338	glucan 1,3-beta-glucosidase activity	6.8E-03	4
	GO:0004555	alpha,alpha-trehalase activity	2.4E-02	3
	GO:0004067	asparaginase activity	2.6E-02	4
	GO:0004450	isocitrate dehydrogenase (NADP+) activity	2.4E-02	3
	GO:0008023	transcription elongation factor complex	2.0E-02	9
	GO:0000145	exocyst	3.7E-02	5