SI Appendix 1

Table 1. Number of singleton genes and duplicate genes in the different degree-defined bines

Degree (k)	*1*	*2*	*3*	*4*	*5*	*6*	*7*
singletons	329	257	234	171	149	106	84
duplicates	189	199	138	102	77	67	65

Degree (k)	*8*	*9*	*10*	*11*	*12*	*13*	*14*	*15*	*>15*
singletons	75	66	72	64	56	49	36	34	439
duplicates	42	44	35	28	24	29	23	19	347

Table 2. Regression analysis – phenotypes vs. degree (connectivity) in duplicates and singletons

	Logistic Regression* $log\left(\frac{P(k)}{1-P(k)}\right)=\alpha+\beta k$			Linear Regression* $P(k)=\alpha+\beta k$			
	α	β	P value	α	β	Error in β	r^2
Singletons	1.4933	-0.17	3.39e-098	0.8244	-0.036	0.005	0.91
Duplicates	2.6557	-0.1436	5.0e-5	0.9438	-0.019	0.006	0.67

* k – the degree (connectivity), P – the proportion of viable phenotypes with degree k.

Table 3. Dependencies of gene-deletion phenotypes on both the degree and paralogy* of the deleted gene (two-way ANOVA)

Source of phenotype* variability	Sum Sq.	d.f.	Mean Sq.	F	Prob>F
Degree (X1)	12.617	15	0.8411	7.88	0
Paralogy** (X2)	13.373	1	13.3725	125.26	0
Interaction (X1×X2)	3.807	15	0.2538	2.38	0.0021
Error	312.91	2931	0.1068		
Total	347.459	2962			

* Phenotypes were defined as Ph=1 if mutant was viable and Ph=0 otherwise.

** Paralogy was defined as X1=1 if a gene has a paralogous partner and X1=0 otherwise.

Table 4. Dependencies of gene-deletion phenotypes of duplicate genes on both degree and age of duplication (two-way ANOVA)

* Phenotypes were defined as Ph=1 if mutant was viable and Ph=0 otherwise.

Source of phenotype* variability	Sum Sq.	d.f.	Mean Sq.	F	Prob>F
Degree (X1)	3.475	3	1.15845	13.96	0
Duplication age** (X2)	0.619	1	0.61939	7.46	0.0064
Interaction (X1×X2)	0.576	3	0.19206	2.31	0.0743
Error	116.216	1400	0.08301		
Total	133.232	1407			

** Age was roughly defined as X2=0 for “early duplications” (Ks>1) and X2=1 for “late duplications” (Ks<1).

Table 5. Dependencies of gene-deletion phenotypes of duplicate genes on both degree and expression similarity (two-way ANOVA)

Source of phenotype* variability	Sum Sq.	d.f.	Mean Sq.	F	Prob>F
Degree (X1)	12.84	3	4.27996	51.55	0
m. exp. sim** (X2)	0.218	1	0.21792	2.62	0.1054

Source of phenotype* variability	Sum Sq.	d.f.	Mean Sq.	F	Prob>F
Interaction (X1×X2)	1.042	3	0.34727	4.18	0.0059
Error	116.242	1400	0.08303		
Total	133.232	1407			

* Phenotypes were defined as *Ph*=1 if mutant was viable and *Ph*=0 otherwise.

** Expression similarity was roughly defined as *X2*=1 if the mean expression similarity (Kafri, Bar-Even et al. 2005) of duplicates was greater than 0.3 and X2=0 otherwise.

Table 6. Dependencies of gene-deletion phenotypes of duplicate genes on degree, expression similarity and age of duplication (three-way ANOVA)

1. Phenotypes were defined as *Ph*=1 if mutant was viable and *Ph*=0 otherwise.

Source of phenotype[1] variability	Sum Sq.	d.f.	Mean Sq.	F	Prob>F
Degree[2] (X1)	9.391	1	9.39141	107.72	0
m. exp. Sim[3] (X2)	0.73	1	0.73038	8.38	0.0039
Duplication age[4] (X3)	0.412	1	0.41234	4.73	0.0298
Interaction (X1×X2×X3)	0.589	1	0.58907	6.76	0.0094
Error	122.323	1403	0.08719		
Total	133.232	1407			

2. Degree was roughly defined as X1=1 if degree was greater than 5 and X1=0 otherwise.

3. Expression similarity was roughly defined as *X2*=1 if the mean expression similarity (Kafri, Bar-Even et al. 2005) of duplicates was greater than 0.3 and X2=0 otherwise.

4. Age was roughly defined as X3=0 for “early duplications” (Ks>1) and X3=1 for “late duplications” (Ks<1).

References

Kafri R, *et al.* (2005) Transcription control reprogramming in genetic backup circuits. *Nat Genet* 37(3): 295-9.