

Additional data file 2

A list of all three-node interconnection patterns examined

Motif ID	Interconnection pattern	p value	N _{real}	N _{rand}	Fraction involving essential genes (%)
A1	-R-R	<0.0002	468	(2.6 ± 0.5) × 10 ²	N/A
A2	R-R-X	<0.0002	30	5.4 ± 3.2	N/A
B1	R- -P	<0.0002	131	3.3 ± 3.7	N/A
B2	R- -H	<0.0002	613	(8.0 ± 2.3) × 10 ¹	N/A
C1	-R-P	<0.0002	5,925	(5.4 ± 0.5) × 10 ²	N/A
C2	-R-X	<0.0002	3,471	(2.7 ± 0.3) × 10 ²	N/A
C3	-R-H	<0.0002	1,857	(5.3 ± 0.5) × 10 ²	N/A
D1	P-P-P	<0.0002	571,461	(1.1 ± 0.0) × 10 ⁵	N/A
D2	P-P-X	<0.0002	90,725	(8.2 ± 0.3) × 10 ³	N/A
D3	P-X-X	<0.0002	67,044	(5.2 ± 0.2) × 10 ³	N/A
D4	X-X-X	<0.0002	1,237,201	(2.7 ± 0.1) × 10 ⁴	N/A
E1	S-S-S	<0.0002	2,670	(1.7 ± 0.1) × 10 ³	12.5%
E2	H-S-S	<0.0002	980	(3.8 ± 0.4) × 10 ²	8.1%
E3	H-H-S	<0.0002	3,160	(1.3 ± 0.1) × 10 ³	10.5%
E4	H-H-H	<0.0002	563,498	(1.0 ± 0.2) × 10 ⁵	N/A
F1	P-P-S	<0.0002	1,207	(7.6 ± 0.7) × 10 ²	36.4%
F2	X-X-S	<0.0002	272	(1.5 ± 0.3) × 10 ²	1.5%
F3	P-X-S	<0.0002	275	(1.3 ± 0.2) × 10 ²	24.4%
F4	P-P-H	<0.0002	41,488	(1.1 ± 0.0) × 10 ⁴	N/A
F5	P-X-H	<0.0002	10,609	(2.0 ± 0.1) × 10 ³	N/A
F6	X-X-H	<0.0002	43,688	(2.4 ± 0.1) × 10 ³	N/A
G1	P-S-S	<0.0002	2,046	(2.4 ± 0.3) × 10 ²	8.8%
G2	P-H-S	<0.0002	720	(3.5 ± 0.3) × 10 ²	24.3%
G3	P-H-H	<0.0002	29,619	(1.2 ± 0.1) × 10 ⁴	N/A
G4	X-S-S	<0.0002	280	(7.0 ± 1.5) × 10 ¹	8.6%
G5	X-H-S	<0.0002	251	(1.2 ± 0.2) × 10 ²	8.8%
G6	X-H-H	<0.0002	42,648	(4.0 ± 0.2) × 10 ³	N/A
H1	R-P-P	<0.0002	776	(5.4 ± 0.5) × 10 ²	N/A
H2	R-H-H	<0.0002	3,173	(2.5 ± 0.2) × 10 ³	N/A
H3	R-H-X	<0.0002	308	(6.2 ± 1.3) × 10 ¹	N/A
H4	R-X-H	<0.0002	268	(1.9 ± 0.2) × 10 ²	N/A
H5	R-X-X	<0.0002	3,273	(2.6 ± 0.4) × 10 ²	N/A
	R-X-P	0.043	76	(5.6 ± 1.1) × 10 ¹	N/A
	R-P-X	0.432	91	(8.9 ± 1.6) × 10 ¹	N/A
	R-P-H	0.963	381	(4.5 ± 0.4) × 10 ²	N/A
	R- -X	<0.0002	101	(2.3 ± 1.1) × 10 ¹	N/A
	R-S-X	<0.0002	58	(1.8 ± 0.6) × 10 ¹	N/A
	R-S-H	0.0046	54	(3.1 ± 0.8) × 10 ¹	N/A
	R-S-S	0.0058	49	(2.5 ± 0.8) × 10 ¹	N/A
	R-H-P	0.0166	132	(9.3 ± 1.6) × 10 ¹	N/A
	-R-S	0.0094	43	(2.3 ± 0.7) × 10 ¹	N/A
	R-R-H	0.212	41	(3.3 ± 0.9) × 10 ¹	N/A
	R-X-S	0.006	15	4.5 ± 3.1	N/A
	R-H-S	0.0098	32	(1.5 ± 0.6) × 10 ¹	N/A
	R-R-P	0.385	8	6.9 ± 3.3	N/A
	R-S-P	0.065	10	5.0 ± 2.7	N/A
	R-P-S	0.199	15	(1.1 ± 0.4) × 10 ¹	N/A
	R-R-R	0.388	1	0.5 ± 0.8	N/A
	R-R-S	0.440	1	0.6 ± 0.9	N/A
	R- -S	1	0	0.0 ± 0.0	N/A

For each interconnection pattern, N_{real} is the number of corresponding subgraphs in the real network, and N_{rand} describes the number of corresponding subgraphs in a randomized network, represented by the average and the standard deviation. For a significantly enriched pattern, its Motif ID corresponds to the motif identifier in Figure 1. For each motif containing an SSL link, the column 'Fraction Involving Essential Genes (%)' records the fraction of matching subgraphs with at least one SSL link involving an essential gene. Each three-node interconnection pattern (with nodes *a*, *b* and *c*) is described by three letters, representing the edge from node *a* to *b*, the edge from node *b* to *c*, and the edge from node *c* to *a*, respectively. 'S' represents synthetic sickness or lethality; 'H' represents sequence homology; 'X' represents correlated expression; 'P' represents stable physical interaction; and 'R' represents transcriptional regulation. Because transcriptional regulation link is directed, we used ' ' to represent reversed transcriptional regulation. For example, ' -R-X' represents a gene triad composed of transcriptional regulation links from node *b* to *a* and from node *b* to *c* and a link of correlated expression between node *a* and *c*. Note that such representation is not unique since there exist multiple ways of labeling the nodes.