

Table S1

Gene Pair	Type	Publications	Published Quantitative GI Scores	Published Non-Quantitative GIs
<i>arp6Δsin3Δ</i>	Negative	4	$\epsilon = -0.4711^1$ $s = -9.0381^2$	Synthetic Lethal ³ Synthetic Growth Defect ⁴
<i>sin3Δsnt1Δ</i>	Negative	3	$\epsilon = -0.3606^1$ $s = -7.4923^2$ $s = -3.8016^5$	
<i>arp6Δdep1Δ</i>	Negative	3	$\epsilon = -0.3964^1$ $s = -9.2601^2$	Synthetic Lethality ⁶
<i>arp6Δsap30Δ</i>	Negative	5	$\epsilon = -0.4597^1$ $s = -12.3508^2$	Synthetic Lethality ⁶ Synthetic Growth Defect ^{3,4}
<i>arp6Δsds3Δ</i>	Negative	3	$\epsilon = -0.367^1$ $s = -10.7073^2$	Synthetic Growth Defect ⁴
<i>arp6Δrpd3Δ</i>	Negative	4	$\epsilon = -0.412^1$ $s = -6.631^2$	Synthetic Lethal ³ Synthetic Growth Defect ⁴
<i>arp6Δpho23Δ</i>	Negative	5	$\epsilon = -0.4046^1$ $s = -11.7012^2$	Synthetic Growth Defect ^{3,4,6}
<i>dep1Δsnt1Δ</i>	Negative	3	$\epsilon = -0.3668^1$ $s = -12.3968^2$	Synthetic Lethality ⁶
<i>arp6Δsnt1Δ</i>	Negative	2	$\epsilon = -0.3884^1$	Synthetic Growth Defect ⁴
<i>snt1Δsds3Δ</i>	Negative	3	$\epsilon = -0.2734^1$ $s = -8.2462^2$ $s = -8.389^5$	
<i>snt1Δdgk1Δ</i>	Negative	1	$\epsilon = -0.3551^1$	
<i>snt1Δpho23Δ</i>	Negative	3	$\epsilon = -0.3436^1$ $s = -3.947^2$ $s = -3.5671^5$	
<i>snt1Δrpd3Δ</i>	Negative	2	$\epsilon = -0.3372^1$	Phenotypic Enhancement ⁷
<i>sap30Δsnt1Δ</i>	Negative	2	$\epsilon = -0.1983^1$ $s = -6.7316^2$	
<i>sin3Δsds3Δ</i>	Positive	1	$\epsilon = 0.1777^1$	

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Gene Pair	Type	Publications	Published Quantitative GI Scores	Published Non-Quantitative GIs
<i>dgk1Δsin3Δ</i>	Positive	1		Phenotypic Suppression ⁷
<i>sin3Δpho23Δ</i>	Positive	3	$s = 2.9662^5$ $s = 2.0226^8$	Positive Genetic ⁹
<i>sin3Δrpd3Δ</i>	Positive	2	$s = 4.6737^2$	Positive Genetic ⁹
<i>sin3Δsap30Δ</i>	Positive	3	$\epsilon = 0.1894^1$ $s = 2.1593^{10}$	Positive Genetic ⁹
<i>dep1Δrpd3Δ</i>	Positive	1	$s = 3.0745^2$	
<i>rpd3Δpho23Δ</i>	Positive	1		Positive Genetic ⁹
<i>dgk1Δsds3Δ</i>	Positive	1	$\epsilon = 0.2087^1$	
<i>sap30Δsds3Δ</i>	Positive	2	$\epsilon = 0.1995^1$ $s = 2.7149^5$	
<i>dep1Δpho23Δ</i>	Positive	1	$\epsilon = 0.1659^1$	
<i>sds3Δpho23Δ</i>	Positive	2	$\epsilon = 0.3153^1$ $s = 2.8751^5$	
<i>dep1Δsds3Δ</i>	Positive	1	$\epsilon = 0.4403^1$	
<i>sds3Δrpd3Δ</i>	Positive	2	$\epsilon = 0.3473^1$	Phenotypic Suppression ¹¹
<i>sap30Δpho23Δ</i>	Positive	2	$s = 2.532^5$	Positive Genetic ⁹
<i>rpd3Δsap30Δ</i>	Positive	1		Positive Genetic ⁹
<i>sin3Δdep1Δ</i>	None			
<i>dep1Δsap30Δ</i>	None			
<i>dgk1Δdep1Δ</i>	None			
<i>dgk1Δarp6Δ</i>	None			
<i>dgk1Δpho23Δ</i>	None			
<i>dgk1Δsap30Δ</i>	None			
<i>dgk1Δrpd3Δ</i>	None			

Source Publications:

1. Costanzo, M. *et al.* The genetic landscape of a cell. *Science* **327**, 425–431 (2010).

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2. Collins, S. R. *et al.* Functional dissection of protein complexes involved in yeast chromosome biology using a genetic interaction map. *Nature* **446**, 806–810 (2007).
3. Lin, Y.-Y. *et al.* A comprehensive synthetic genetic interaction network governing yeast histone acetylation and deacetylation. *Genes Dev.* **22**, 2062–2074 (2008).
4. Krogan, N. J. *et al.* A Snf2 family ATPase complex required for recruitment of the histone H2A variant Htz1. *Mol. Cell* **12**, 1565–1576 (2003).
5. Zheng, J. *et al.* Epistatic relationships reveal the functional organization of yeast transcription factors. *Mol. Syst. Biol.* **6**, 420 (2010).
6. Tong, A. H. Y. *et al.* Global mapping of the yeast genetic interaction network. *Science* **303**, 808–813 (2004).
7. Beltrao, P. *et al.* Evolution of phosphoregulation: comparison of phosphorylation patterns across yeast species. *PLoS Biol.* **7**, e1000134 (2009).
8. Bandyopadhyay, S. *et al.* Rewiring of genetic networks in response to DNA damage. *Science* **330**, 1385–1389 (2010).
9. Breslow, D. K. *et al.* A comprehensive strategy enabling high-resolution functional analysis of the yeast genome. *Nat. Methods* **5**, 711–718 (2008).
10. Wilmes, G. M. *et al.* A genetic interaction map of RNA-processing factors reveals links between Sem1/Dss1-containing complexes and mRNA export and splicing. *Mol. Cell* **32**, 735–746 (2008).
11. Torres-Machorro, A. L. & Pillus, L. Bypassing the requirement for an essential MYST acetyltransferase. *Genetics* **197**, 851–863 (2014).