

## Supplementary Information

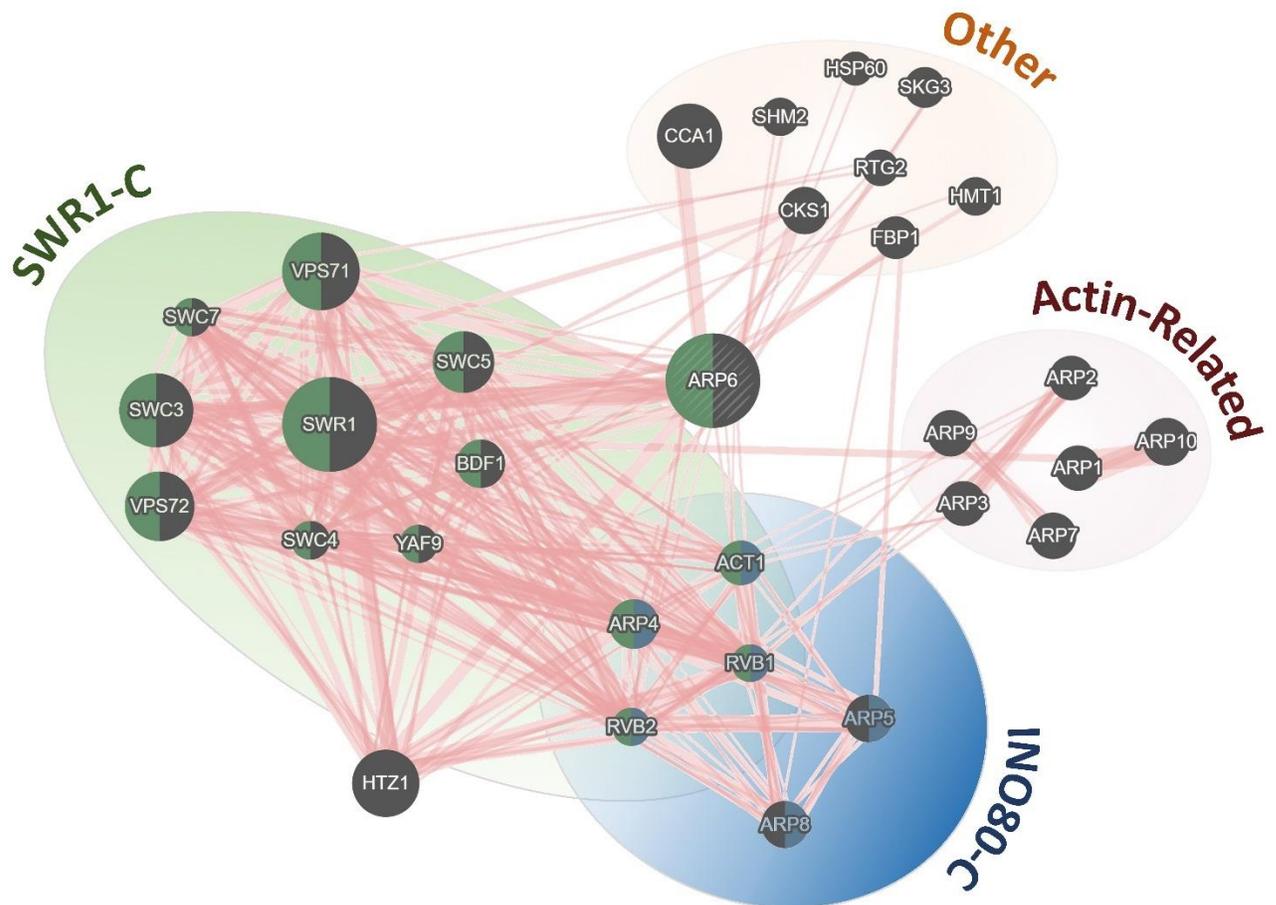


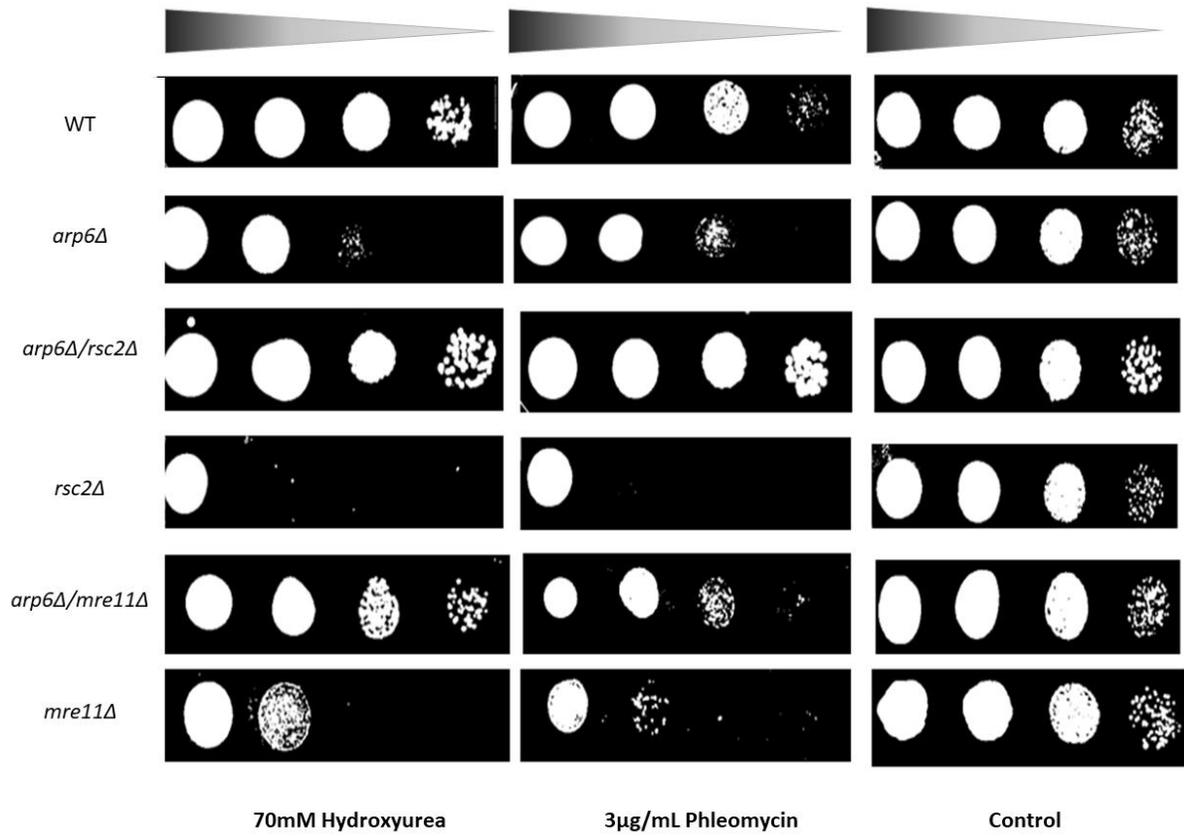
Figure S1: Protein-protein interaction network of Arp6 and associated proteins suggests functional associations with members of the SWR1-C and INO80-related chromatin remodeling complexes. Network produced using GeneMania ([www.genemania.org](http://www.genemania.org)). Nodes labelled with green are functionally-associated with the SWR1 complex and blue nodes indicate association with INO80-type complex (blue/green nodes are associated with both). Other genes are grouped into actin-related proteins (light red background) and other (light orange background).

Table S1: Functional gene ontology (GO) analysis of proteins within the Arp6 physical interaction network displayed in Figure S1. Q-values from a FDR-corrected hypergeometric test for GO term enrichment are reported.

Function	FDR	Genes in network	Genes in genome
Swr1 complex	6.82E-31	14	14
INO80-type complex	4.46E-30	16	25
SWI/SNF superfamily-type complex	3.13E-27	18	58
Chromatin remodeling	3.71E-24	18	83
Chromatin modification	7.81E-21	20	191
Histone exchange	1.19E-19	11	18
ATP-dependent chromatin remodeling	1.19E-19	13	37

Table S2: Overexpression of *ARP6* compensates (rescues) sensitivity of *MMS22*, *MRE11*, *RSC2*, and *NUP84* mutants under DNA damaging conditions.

Gene name	Fitness under DNA damaging conditions relative to WT	
	Single mutant	Single mutant +ARP6 overexpression
<i>mms22Δ</i>	43%	81%
<i>mre11Δ</i>	26%	64%
<i>nup84Δ</i>	38%	62%
<i>rsc2Δ</i>	31%	76%



**Figure S2: Conditional chemical-genetic analysis indicates a functional relationship between *ARP6* and *MRE11/RSC2*.** Relative mutants are serially-diluted and spotted on control medium (YPD) or conditional medium (YPD+Drug) 70mM HU and 3μg/ml PHLM. Note: Some spots in this figure are the same as Figure 1A and are included as a reference.