

**Table S1.** Genes Identified through Mutants that Affect the Physical Interaction Between *NHP6A::F[1,2]*; *HTB2::F[3]*

Systematic Name	Standard Name	Description
<b>Chromatin remodeling</b>		
<i>YOL012C</i>	<i>HTZ1</i>	Histone variant H2AZ, exchanged for histone H2A in nucleosomes by the SWR1 complex; involved in transcriptional regulation through prevention of the spread of silent heterochromatin
<i>YDR334W</i>	<i>SWR1</i>	Swi2/Snf2-related ATPase that is the structural component of the SWR1 complex, which exchanges histone variant H2AZ (Htz1p) for chromatin-bound histone H2A
<i>YGR270W</i>	<i>YTA7</i>	Protein that localizes to chromatin and has a role in regulation of histone gene expression; has a bromodomain-like region that interacts with the N-terminal tail of histone H3, and an ATPase domain; potentially phosphorylated by Cdc28p
<b>Protein biosynthesis and modification</b>		
<i>YDL132W</i>	<i>CDC53</i>	Cullin, structural protein of SCF complexes (which also contain Skp1p, Cdc34p, Hrt1p and an F-box protein) involved in ubiquitination; SCF promotes the G1-S transition by targeting G1 cyclins and the Cln-CDK inhibitor Sic1p for degradation
<i>YML092C</i>	<i>PRE8</i>	Alpha 2 subunit of the 20S proteasome
<i>YDR434W</i>	<i>GPII7</i>	Transmembrane protein subunit of the glycosylphosphatidylinositol transamidase complex that adds GPIs to newly synthesized proteins
<b>Transcription and RNA processing</b>		
<i>YGR006W</i>	<i>PRP18</i>	Splicing factor involved in the positioning of the 3' splice site during the second catalytic step of splicing, part of snRNP U5, interacts with Slu7p
<i>YPR178W</i>	<i>PRP4</i>	Splicing factor, component of the U4/U6-U5 snRNP complex
<i>YHR085W</i>	<i>IPI1</i>	Essential component of the Rix1 complex (with Rix1p and Ipi3p) that is required for processing of ITS2 sequences from 35S pre-rRNA; Rix1 complex associates with Mdn1p in pre-60S ribosomal particles
<i>YDL098C</i>	<i>SNU23</i>	Component of U4/U6.U5 snRNP involved in mRNA splicing via spliceosome
<i>YOR194C</i>	<i>TOA1</i>	TFIIA large subunit; involved in transcriptional activation, acts as antirepressor or as coactivator; homologous to largest and second largest subunits of human and Drosophila TFIIA
<b>DNA replication</b>		
<i>YOR060C</i>	<i>SLD7</i>	Protein with a role in chromosomal DNA replication; interacts with Sld3p and reduces its affinity for Cdc45p; deletion mutant has aberrant mitochondria
<b>Transport and secretion</b>		
<i>YOL130W</i>	<i>ALR1</i>	Plasma membrane Mg(2+) transporter, expression and turnover are regulated by Mg(2+) concentration; overexpression confers increased tolerance to Al(3+) and Ga(3+) ions
<i>YGR257C</i>	<i>MTM1</i>	Mitochondrial protein of the mitochondrial carrier family, involved in activating mitochondrial Sod2p probably by facilitating insertion of an essential manganese cofactor
<i>YDR246W</i>	<i>TRS23</i>	One of 10 subunits of the transport protein particle (TRAPP) complex of the cis-Golgi which mediates vesicle docking and fusion; involved in endoplasmic reticulum (ER) to Golgi membrane traffic
<i>YGR120C</i>	<i>COG2</i>	Essential component of the conserved oligomeric Golgi complex (Cog1p through Cog8p), a cytosolic tethering complex that functions in protein trafficking to mediate fusion of transport vesicles to Golgi compartments
<i>YDL145C</i>	<i>COP1</i>	Alpha subunit of COPI vesicle coatamer complex, which surrounds transport vesicles in the early secretory pathway
<i>YNL272C</i>	<i>SEC2</i>	Guanyl-nucleotide exchange factor for the small G-protein Sec4p; essential for post-Golgi vesicle transport and for autophagy; associates with the exocyst, via exocyst subunit Sec15p, on secretory vesicles

<i>YPR055W</i>	<i>SEC8</i>	Essential 121 kDa subunit of the exocyst complex; the exocyst complex (Sec3p, Sec5p, Sec6p, Sec8p, Sec10p, Sec15p, Exo70p, and Exo84p) has the essential function of mediating polarized targeting of secretory vesicles to active sites of exocytosis; relocalizes away from bud neck upon DNA replication stress
<i>YNR026C</i>	<i>SEC12</i>	Guanine nucleotide exchange factor (GEF), activates Sar1p by catalyzing the exchange of GDP for GTP; required for the initiation of COPII vesicle formation in ER to Golgi transport; glycosylated integral membrane protein of the ER
<i>YNL287W</i>	<i>SEC21</i>	Gamma subunit of coatomer, a heptameric protein complex that together with Arf1p forms the COPI coat; involved in ER to Golgi transport of selective cargo
<i>YGL137W</i>	<i>SEC27</i>	Essential beta'-coat protein of the COPI coatomer, involved in ER-to-Golgi and Golgi-to-ER transport
<i>YLR440C</i>	<i>SEC39</i>	Component of the Dsl1p tethering complex that interacts with ER SNAREs Sec20p and Use1p; proposed to be involved in protein secretion; localizes to the ER and nuclear envelope
<b>Unknown</b>		
<i>YMR134W</i>	<i>ERG29</i>	Protein of unknown function that may be involved in iron metabolism; mutant bm-8 has a growth defect on iron-limited medium that is complemented by overexpression of Yfh1p; shows localization to the ER; highly conserved in ascomycetes

Biologically relevant proteins with a score between 0.1 and 0.2

<b>Chromatin remodeling</b>		
<i>YML041C</i>	<i>VPS71</i>	Nucleosome-binding component of the SWR1 complex, which exchanges histone variant H2AZ (Htz1p) for chromatin-bound histone H2A; required for vacuolar protein sorting
<i>YDR485C</i>	<i>VPS72</i>	Htz1p-binding component of the SWR1 complex; exchanges histone variant H2AZ (Htz1p) for chromatin-bound histone H2A
<i>YFR037C</i>	<i>RSC8</i>	Component of the RSC chromatin remodeling complex; essential for viability and mitotic growth; homolog of SWI/SNF subunit Swi3p
<i>YML127W</i>	<i>RSC9</i>	Component of the RSC chromatin remodeling complex; DNA-binding protein involved in the synthesis of rRNA and in transcriptional repression and activation of genes regulated by the Target of Rapamycin (TOR) pathway
<i>YLR182W</i>	<i>SWI6</i>	Transcription cofactor; forms complexes with Swi4p and Mbp1p to regulate transcription at the G1/S transition; involved in meiotic gene expression
<i>YPR034W</i>	<i>ARP7</i>	Component of both the SWI/SNF and RSC chromatin remodeling complexes; actin-related protein involved in transcriptional regulation
<b>Transcription and RNA processing</b>		
<i>YBR193C</i>	<i>MED8</i>	Subunit of the RNA polymerase II mediator complex; associates with core polymerase subunits to form the RNA polymerase II holoenzyme; essential for transcriptional regulation
<i>YER022W</i>	<i>SRB4</i>	Subunit of the RNA polymerase II mediator complex; associates with core polymerase subunits to form the RNA polymerase II holoenzyme; essential for transcriptional regulation