

**Table S1. Genes identified via high-throughput genetic screening.**

	Gene name	Systematic name	Not targeted to vacuole under starvation conditions	Targeted to vacuole under nutrient-rich conditions	Description
<b>Trafficking</b>	<i>DID2</i>	YKR035W-A	+		Class E protein of the vacuolar protein sorting (Vps) pathway
	<i>DID4</i>	YKL002W	+		Class E Vps protein of the ESCRT-III complex
	<i>DOA4</i>	YDR069C	+		Ubiquitin isopeptidase
	<i>ERV46</i>	YAL042W	+		Protein localized to COPII-coated vesicles
	<i>HSE1</i>	YHL002W	+		Component of the ESCRT-0 complex
	<i>MVB12</i>	YGR206W	+		Component of the ESCRT-I complex
	<i>SAR1</i>	YPL218W	+		Arf family GTPase involved in ER-Golgi transport
	<i>SHR3</i>	YDL212W		±	Endoplasmic reticulum packaging chaperone (DAmP collection)
	<i>SMY2</i>	YBR172C	+		Protein of unknown function involved in COPII vesicle formation
	<i>SNF8</i>	YPL002C	+		Component of the ESCRT-II complex
	<i>SWA2</i>	YDR320C	±		Auxilin-like protein involved in vesicular transport
	<i>VAM3</i>	YOR106W	+		Syntaxin-like vacuolar t-SNARE
	<i>VAM6</i>	YDL077C	+		Vacuolar protein that plays a critical role in the tethering steps of vacuolar membrane
	<i>VPS20</i>	YMR077C	+		Myristoylated subunit of ESCRTIII
	<i>VPS23</i>	YCL008C	+		Component of the ESCRT-I complex
	<i>VPS24</i>	YKL041W	+		Component of the ESCRT-III complex
	<i>VPS25</i>	YJR102C	+		Component of the ESCRT-II complex
	<i>VPS27</i>	YNR006W	+		Component of the ESCRT-0 complex
	<i>VPS28</i>	YPL065W	+		Component of the ESCRT-I complex
	<i>VPS4</i>	YPR173C	+		AAA-ATPase involved in MVB protein sorting

	<i>VPS41</i>	YDR080W	+		Vacuolar membrane protein that is a subunit of the HOPS complex
	<i>VPS52</i>	YDR484W		±	Component of the GARP complex
	<i>VPS60</i>	YDR486C	+		Cytoplasmic and vacuolar membrane protein involved in late endosome to vacuole transport
	<i>VPS8</i>	YAL002W	+		Membrane-binding component of the CORVET complex
	<i>VTI1</i>	YLR181C	+		MVB protein involved in endosomal protein sorting
	<i>YPT7</i>	YML001W	+		Rab family GTPase involved in endosomal protein sorting
<b>Ubiquitination</b>	<i>DOA1</i>	YKL213C	+		WD repeat protein required for ubiquitin-mediated protein degradation
	<i>TUL1</i>	YKL034W	+		Golgi-localized RING-finger ubiquitin ligase (E3)
	<i>UBC4</i>	YBR082C	+		Ubiquitin-conjugating enzyme (E2)
	<i>UBX3</i>	YDL091C	+		UBX (ubiquitin regulatory X) domain-containing protein that interacts with Cdc48
	<i>DSC3</i>	YOR223W	+		Subunit of the DSC ubiquitin ligase complex
	<i>UBP15</i>	YMR304W		±	Ubiquitin-specific protease involved in protein de-ubiquitination
<b>Starvation response</b>	<i>ADE2</i>	YOR128C		+	Phosphoribosylaminoimidazole carboxylase
	<i>ARO2</i>	YGL148W	+		Bifunctional chorismate synthase and flavin reductase
	<i>CYS4</i>	YGR155W		+	Cystathionine beta-synthase
	<i>FPR1</i>	YNL135C	+		Peptidyl-prolyl cis-trans isomerase (PPIase), binds to FK506 and rapamycin
	<i>LYS14</i>	YDR034C		+	Transcriptional activator involved in regulation of genes of the lysine biosynthesis pathway
	<i>ODC2</i>	YOR222W	+		Mitochondrial inner membrane transporter
	<i>PHO80</i>	YOL001W	±		Cyclin
	<i>SIT4</i>	YDL047W	±		Type 2A-related serine-threonine phosphatase
	<i>URA4</i>	YLR420W	+		Dihydroorotase, converts carbamoyl-L-aspartate into dihydroorotate
<b>Proteasome</b>	<i>RPN4</i>	YDL020C	±		Transcription factor that stimulates expression of proteasome genes
	<i>GCR1</i>	YPL075W	+		Transcriptional activator of genes involved in glycolysis (DAmP collection)
	<i>MCP1</i>	YOR228C	+		Mitochondrial protein of unknown function involved in lipid homeostasis
	<i>NDC1</i>	YML031W	+		Subunit of the transmembrane ring of the nuclear pore complex (DAmP collection)
	<i>SPF1</i>	YEL031W	+		P-type ATPase, ion transporter of the ER membrane