

Table 1. Overlaps among autophagy, cytoplasm to vacuole targeting and pexophagy genes in yeast.

<b>Gene</b>			<b>Protein characteristics</b>
S.c.	P.p.	H.p.	
<u>APG1</u> AUT3 CVT10	GSA10 PAZ1	PDD7	Serine/threonine protein kinase
<u>APG2</u> AUT8	GSA11 PAZ7		Peripheral membrane protein
<u>APG5</u>			Component of Apg12-Apg5-Apg16 complex
<u>APG7</u> CVT2	GSA7 PAZ12		E1-like enzyme that activates the ubiquitin-like proteins Apg12 and Aut7
<u>APG9</u> AUT9 CVT7	GSA14 PAZ9		Transmembrane protein
<u>APG10</u>			E2 ortholog that conjugates Apg12 to Apg5
<u>APG12</u>			Ubiquitin-like protein conjugated to Apg5
<u>APG13</u>			Phosphoprotein that interacts with Apg1
<u>APG14</u> CVT12			Component of Vps34 PtdIns 3-kinase complex I
<u>APG16</u>	PAZ3		Coiled-coil protein that binds Apg5
<u>APG17</u>			Autophagy-specific protein that binds Apg1
<u>AUT1</u> APG3	GSA20		E2 ortholog conjugates Aut7 to phosphatidylethanolamine
<u>AUT2</u> APG4	PAZ8		Cysteine protease that removes C-terminal arginine from nascent Aut7
<u>AUT7</u> APG8 CVT5	PAZ2		Ubiquitin-like protein associated with autophagosomes and Cvt vesicles

<u>AUT10</u> <u>CVT18</u>	GSA12		WD40 protein
<u>CVT9</u>	GSA9 PAZ6	PDD18	Coiled-coil protein specific for the Cvt pathway and pexophagy, binds Apg1 and Cvt19
<u>CVT19</u>			Receptor for prApe1 and Ams1
<u>CVT20</u> <u>SNX42</u>			PX domain protein that binds Cvt13 and Apg17
<u>GCN1</u>	PAZ10		Starvation-induced activation of Gcn2
<u>GCN2</u>	PAZ11		eIF2 kinase
<u>GCN3</u>	PAZ5		subunit of eIF2B
<u>GCN4</u>	PAZ19		Transcriptional activator of amino acid biosynthetic genes
	GSA13		
	GSA17		
	GSA18		
<u>MAI1</u> <u>CVT21</u>			CVT18 homologue
<u>PFK1</u>	GSA1		Phosphofructokinase
<u>SNX4</u> <u>CVT13</u>	PAZ16		PX domain protein that binds Cvt20 and Apg17
<u>UGT1</u>	PAZ4		UDP-glucose:sterol glucosyltransferase
<u>VAC8</u>	GSA21 PpVAC8		Armadillo repeat protein that binds Apg13
<u>VPS15</u>	GSA19 PAZ13 PpVPS15	PDD19	Serine/threonine protein kinase in complex with Vps34
<u>VPS30</u> <u>APG6</u>			Component of Vps34 PtdIns 3-kinase complex

VPS34

PDD1

Phosphatidylinositol 3-kinase

VPS51

CVT22

Component of VFT complex involved  
in recycling from early endosome

The genes are listed alphabetically by the standard name (underlined) based on the *Saccharomyces* Genome Database. *S.c.*, *Saccharomyces cerevisiae*; *P.p.*, *Pichia pastoris*; *H.p.*, *Hansenula polymorpha*.