

Supplemental Table 1

Plate	Well	Int.	ORF	Gene	Aliases	Description
Known VPS Genes						
380	E3	S	YKR001C	VPS1	GRD1, LAM1, SPO15, VPL1, VPT26	Dynamin-like GTPase
346	C5	S	YDR495C	VPS3	PEP6, VPL3, VPT17	Low abundance, hydrophilic protein
323	E9	S	YPR173C	VPS4	CSC1, DID6, END13, GRD13, VPL4, VPT10	AAA ATPase; homologous to mouse SKD1 and human hVPS4; interacts with Vps32p
306	D7	S	YOR069W	VPS5	GRD2, PEP10, VPT5	Component of Vps5p-Vps17p-Vps26p-Vps29p-Vps35p retromer complex; homologous to mammalian sorting nexins
306	B5	S	YOR036W	VPS6	PEP12, VPL6, VPT13	t-SNARE
301	E2	S	YAL002W	VPS8	FUN15, VPT8	Membrane-associated hydrophilic protein containing a C-terminal cysteine-rich region (RING-H2 finger)
330	G7	S	YML097C	VPS9	VPL31, VPT9	GEF for Vps21p
324	F2	S	YBL017C	VPS10	PEP1, VPT1	Sorting receptor for CPY and proteinase A; homologous to human sortilin
301	H9	S	YLL040C	VPS13	SOI1, VPT2	Involved in Golgi to endosome trafficking; homologous to mammalian chorein
372	C12	S	YPL045W	VPS16	SVL6, VAM9, VPT16	Component of Vps11p-Vps18p-Vps16p-Vps33p-Vps39p-Vps41p complex
318	B3	S	YOR132W	VPS17	PEP21	Component of Vps5p-Vps17p-Vps26p-Vps29p-Vps35p retromer complex; has PX domain
372	A5	S	YLR148W	VPS18	PEP3, VAM8, VPS18, VPT18	Component of Vps11p-Vps18p-Vps16p-Vps33p-Vps39p-Vps41p complex
327	E1	S	YDR323C	VPS19	PEP7, VAC1, VPL21, VPT19	Involved in vacuolar sorting and inheritance; binds phosphatidylinositol 3-phosphate via FYVE domain
329	C10	M	YMR077C	VPS20		Class E factor; small coiled coil protein; component of Vps2p-Vps20p-Vps24p-Vps32p complex
306	E11	S	YOR089C	VPS21	VPS12, VPT12, YPT21, YPT51	Rab5-like GTPase
323	A6	M	YPL002C	VPS22	SNF8	Class E factor; Component of Vps22p-Vps25p-Vps36p complex
315	B9	M	YCL008C	VPS23	STP22	Component of Vps23p-Vps28p-Vps37p ESCRT-I complex; has UBC domain; binds ubiquitin; homologous to mammalian TSG101
316	G2	M	YKL041W	VPS24	DID3	Class E factor; Component of Vps2p-Vps20p-Vps24p-Vps32p complex; small coiled coil protein
333	B1	M	YJR102C	VPS25		Class E factor; Component of Vps22p-Vps25p-Vps36p complex
332	E3	S	YJL053W	VPS26	GRD6, PEP8, VPS26, VPT4	Component of Vps5p-Vps17p-Vps26p-Vps29p-Vps35p retromer complex
339	C2	S	YNR006W	VPS27	GRD11, DID7, SSV17, VPL23, VPL27, VPT27	Controls traffic through prevacuolar compartment; binds PI3P via FYVE domain; homologous to mammalian Hrs
322	E12	M	YPL065W	VPS28	VPT28	Component of Vps23p-Vps28p-Vps37p ESCRT-I complex
313	H10	S	YHR012W	VPS29	PEP11	Component of Vps5p-Vps17p-Vps26p-Vps29p-Vps35p retromer complex
309	C10	S	YPL120W	VPS30	APG6, VPT30	Involved in endosome to Golgi transport and autophagy; homologous to human beclin 1
302	C10	M	YLR025W	VPS32	SNF7, DID1	Class E factor; small coiled coil protein; component of Vps2p-Vps20p-Vps24p-Vps32p complex
372	D8	S	YLR396C	VPS33	CLS14, MET27, PEP14, SLP1, VAM5, VPL25, VPT33	Component of Vps11p-Vps18p-Vps16p-Vps33p-Vps39p-Vps41p complex
372	B8	S	YLR240W	VPS34	END12, PEP15, VPL7, VPT29	Phosphatidylinositol 3-kinase
319	D10	S	YJL154C	VPS35	GRD9, VPT7	Component of Vps5p-Vps17p-Vps26p-Vps29p-Vps35p retromer complex
320	C11	M	YLR417W	VPS36	GRD12, VAC3, VPL11	Class E factor; Component of Vps22p-Vps25p-Vps36p ESCRT-II complex
302	H6	S	YLR119W	VPS37	SRN2	Component of Vps23p-Vps28p-Vps37p ESCRT-I complex
319	H4	S	YLR360W	VPS38	VPL17	439 aa
345	F10	S	YDL077C	VPS39	CVT4, VAM6, VPL18, VPL22	Component of Vps11p-Vps18p-Vps16p-Vps33p-Vps39p-Vps41p complex
310	D8	S	YDR080W	VPS41	CVT8, FET2, SVL2, VAM2, VPL20	Component of Vps11p-Vps18p-Vps16p-Vps33p-Vps39p-Vps41p complex
346	A5	S	YDR456W	VPS44	NHX1	Monovalent inorganic cation transporter
372	C3	S	YGL095C	VPS45	STT10, VPL28	Sec1p-like protein
348	B11	S	YDR484W	VPS52	SAC2	Suppressor of actin mutations; Component of Vps52p-Vps53p-Vps54p complex involved in endosome to Golgi transport
336	B12	S	YJL029C	VPS53		Component of Vps52p-Vps53p-Vps54p complex involved in endosome to Golgi transport
335	D4	S	YDR027C	VPS54	LUV1, RKI1, TCS3	Component of Vps52p-Vps53p-Vps54p complex involved in endosome to Golgi transport
347	H7	S	YJR044C	VPS55		Transmembrane protein homologous to human OB-RGRP protein
348	B12	W	YDR486C	VPS60	MOS10	Class E factor; small coiled coil protein
Other genes implicated in Vacuole Biogenesis or Function						
342	E10	M	YBR131W	CCZ1		Calcium, caffeine, zinc sensitivity; sporulation defect
316	E4	M	YKL002W	DID4		Class E factor; small coiled coil protein; interacts with many proteins including Apg17p and Ypt31p
380	B1	S	YHL031C	GOS1		v-SNARE
331	H5	M	YPR079W	MRL1		Mannose 6-phosphate receptor homolog involved in vacuolar protein sorting

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331	B1	M	YMR004W	<i>MVP1</i>		Suppressor of <i>vps1</i> mutants
345	C5	M	YDL006W	<i>PTC1</i>	<i>CWH47, KCS2, TPD1</i>	Protein phosphatase type 2C
380	D4	W	YDR137W	<i>RGP1</i>		Reduced growth phenotype; component of Ric1p-Rgp1p complex that functions as Ypt6p GEF
330	D3	M	YLR039C	<i>RIC1</i>		Forms a complex with Rgp1p with GEF activity towards Ypt6p
336	B1	M	YJL004C	<i>SYS1</i>		Multicopy suppressor of <i>ypt6</i> and <i>ric1</i> mutants; related to mammalian synptogyrin
307	E4	S	YOL018C	<i>TLG2</i>		t-SNARE
321	G7	S	YGL212W	<i>VAM7</i>		v-SNARE; has PX domain
320	E12	M	YLR262C	<i>YPT6</i>		Rab6-like GTP-binding protein
303	E9	M	YML001W	<i>YPT7</i>	<i>AST4, VAM4</i>	Rab7-like GTP-binding protein
Vacuolar ATPase						
337	C9	M	YDL185W	<i>VMA1</i>	<i>CLS8, TFP1</i>	Subunit of vacuolar ATPase, V1 subcomplex
343	H11	M	YBR127C	<i>VMA2</i>	<i>ATPVS, VAT2</i>	Subunit of vacuolar ATPase, V1 subcomplex
306	H10	S	YOR332W	<i>VMA4</i>		Subunit of vacuolar ATPase, V1 subcomplex; YOR331C on opposite strand also positive
333	F8	M	YLR447C	<i>VMA6</i>		Subunit of vacuolar ATPase, V0 subcomplex
312	A9	M	YEL051W	<i>VMA8</i>		Subunit of vacuolar ATPase, V1 subcomplex
328	G5	M	YHR039C-B	<i>VMA10</i>	<i>YHR039C-B</i>	Subunit of vacuolar ATPase, V1 subcomplex
308	D6	M	YPL234C	<i>VMA11</i>	<i>CLS9, TFP3</i>	Subunit of vacuolar ATPase, V0 subcomplex
317	D2	M	YKL119C	<i>VMA12</i>	<i>CLS10, VPH2</i>	Involved in assembly of vacuolar ATPase
331	E10	M	YPR036W	<i>VMA13</i>	<i>CLS11</i>	Subunit of vacuolar ATPase, V1 subcomplex
337	F6	M	YGR105W	<i>VMA21</i>		Assembly factor for vacuolar ATPase localized to ER
314	C1	M	YHR060W	<i>VMA22</i>	<i>CEV1, VPH6</i>	Assembly factor for vacuolar ATPase localized to ER
343	F6	M	YOR270C	<i>VPH1</i>		Subunit of vacuolar ATPase, V0 subcomplex
Glycosylation						
380	E6	M	YLR342W	<i>FKS1</i>	<i>CND1, CWH53, ETG1, GSC1, PBR1</i>	1,3 beta glucan synthase involved in cell wall assembly
323	E2	M	YPR159W	<i>KRE6</i>	<i>CWH48</i>	Putative beta-glucan synthase involved in cell wall assembly
339	G5	M	YBR015c	<i>MNN2</i>	<i>TTP1</i>	Alpha-1,2-mannosyltransferase
372	B10	M	YPL050C	<i>MNN9</i>		Alpha 1,6-mannosyltransferase
319	C5	M	YJL183W	<i>MNN11</i>		Alpha-1,3-mannosyltransferase; member of a complex with Mnn10p, Hoc1p, Anp1p, Mnn9p
372	C5	M	YGL038C	<i>OCH1</i>	<i>NGD29</i>	Alpha-1,6-mannosyltransferase
306	E7	M	YOR085W	<i>OST3</i>		Dolichyl-diphosphooligosaccharide-protein glycosyltransferase
345	H2	M	YDL095W	<i>PMT1</i>		Dolichyl-phosphodolichyl phosphate-D-mannose:protein O-D-mannosyltransferase; acts in a complex with Pmt2p
343	E3	M	YML115C	<i>VAN1</i>	<i>VRG7, VRG8</i>	Vanadate resistance protein; mannosyltransferase
AP-3 Subunits						
308	F9	M	YPL195W	<i>APL5</i>		Delta subunit of AP-3 complex
328	E11	M	YGR261C	<i>APL6</i>		Beta subunit of AP-3 complex
342	F8	M	YBR288C	<i>APM3</i>		Mu3 subunit of AP-3 complex
336	B9	M	YJL024C	<i>APS3</i>		Sigma3 subunit of AP-3 complex
ARF and ARF-Related						
334	G7	M	YDL192W	<i>ARF1</i>		ADP-ribosylation factor 1; small GTP-binding protein of the Ras superfamily
345	B12	S	YBR164C	<i>ARL1</i>		ARF-like protein 1; small GTP-binding protein
322	G1	M	YPL051W	<i>ARL3</i>		ARF-like protein 3; small GTP-binding protein; cold sensitive growth
Monensin and Brefeldin A Hypersensitive						
346	F9	M	YGL124C	<i>MON1</i>		Monensin and brefeldin A sensitivity; homologs in all eukaryotes
372	B1	M	YNL297C	<i>MON2</i>		Monensin and brefeldin A sensitivity; limited homology to Sec7p

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Actin-related

372	A3	M	YEL036C	<i>ANP1</i>	<i>CAX1, GEM3, MCD2, MNN8</i>	Actin organization; protein glycosylation; retention of glycosyltransferases in Golgi complex
310	A1	M	YBR231C	<i>AOR1</i>		Actin-overexpression resistant; mutant sensitive to NaCl and NaF
348	G5	S	YNL059C	<i>ARP5</i>		Actin-related protein 5
302	F7	M	YLR085C	<i>ARP6</i>		Actin-related protein 6
337	D9	S	YGR036C	<i>CAX4</i>		Actin organization; genetic interactions with calmodulin; contains stretches of amino acids that are characteristic of phosphatases
303	G11	M	YMR032W	<i>HOF1</i>	<i>CYK2</i>	SH3 domain containing-protein required for cytokinesis
372	A1	M	YOL076W	<i>MDM20</i>	<i>DEC1</i>	Regulates actin assembly; involved in mitochondrial inheritance
310	G6	M	YDR126W	<i>PSL10</i>		Profilin synthetic lethal; interacts with <i>bre5</i> , mutant sensitive to BFA
321	B6	M	YDR159W	<i>SAC3</i>		Suppressor of actin mutations; involved in processes affecting the actin cytoskeleton and mitosis
341	E1	W-M	YNL079C	<i>TPM1</i>		Tropomyosin I; actin filament organization; suppressor of <i>mdm20</i>

Ribosomal Proteins

342	H7	M	YBR191W	<i>RPL21A</i>		Component of large ribosome subunit
313	H9	M	YHR010W	<i>RPL27A</i>		Component of large ribosome subunit
334	G6	M	YDL191W	<i>RPL35A</i>	<i>SOS1</i>	Component of large ribosome subunit
345	G2	M	YDL081C	<i>RPP1A</i>		Component of large ribosome subunit
322	D5	M	YPL090C	<i>RPS6A</i>		Component of small ribosome subunit

Miscellaneous

329	E6	S	YOL086C	<i>ADH1</i>	<i>ADC1</i>	Alcohol dehydrogenase
346	E11	M	YGL105W	<i>ARC1</i>		Associated with tRNA and amino acyl-tRNA synthetases; opposite 3' YGL104C (<i>VPS73</i>)
372	A10	M	YLR399C	<i>BDF1</i>		Transcription factor regulating sporulation; has two bromodomains
322	D10	M	YPL084W	<i>BRO1</i>	<i>LPF2</i>	BCK1-like resistance to osmotic shock; Temperature-sensitive growth defect; sensitive to caffeine; rhophilin homology; interacts with Vps4p and Vps32p
301	E5	M	YAR014C	<i>BUD14</i>		Random budding in diploid null mutants; has SH3 domain
372	D5	M	YGR262C	<i>BUD32</i>		Diploid mutants exhibit random budding; has protein kinase domain
325	C10	M	YGL019W	<i>CKB1</i>		Casein kinase II beta subunit
339	B4	S	YNL041C	<i>COD2</i>		COmplexed with Dor1p 2
380	D9	S	YGL223C	<i>COD3</i>		COmplexed with Dor1p 3
341	C11	S	YNL051W	<i>COD4</i>		COmplexed with Dor1p 4
325	B12	M	YGL005C	<i>COD5</i>		COmplexed with Dor1p 5
337	B1	M	YDL160C	<i>DHH1</i>		Putative RNA helicase of DEAD box family; interacts with Rsp5, ubiquitin ligase
330	F12	M	YML071C	<i>DOR1</i>		Dependent On Ric1
310	F4	M	YDR108W	<i>GSG1</i>	<i>TRS85</i>	Probably has role late in meiosis following DNA replication; cannot sporulate
325	F4	M	YGL084C	<i>GUP1</i>		Putative glycerol transporter
306	D8	M	YOR070C	<i>GYP1</i>		GAP for Ypt1p
312	A3	M	YEL044W	<i>IES6</i>		Ino Eighty Subunit 6 ; chromatin remodelling
342	D1	S	YKR019C	<i>IRS4</i>		Increased rDNA silencing; has EH domain
372	A6	M	YNL296W	<i>KRE25</i>		Killer toxin resistant, opposite <i>MON2</i>
331	F7	M	YPR051W	<i>MAK3</i>		N-acetyltransferase; YPR050C on opposite strand also tested positive; interacts with Mak10p ad Mak31p
312	A11	M	YEL053C	<i>MAK10</i>		Glucose-repressible protein
380	E11	M	YMR091C	<i>NPL6</i>		Nuclear protein targeting
316	G12	M	YKL055C	<i>OAR1</i>		3-oxoacyl-[acyl-carrier-protein] reductase; phospholipid remodelling
372	C1	M	YCR044C	<i>PER1</i>		Protein processing in the ER
331	C11	M	YMR123W	<i>PKR1</i>		Confers resistance to SMK toxin when overexpressed
347	A7	S	YGL167C	<i>PMR1</i>	<i>BSD1</i>	Golgi Ca2+ ATPase; YGL168W on opposite strand also positive
322	A6	M	YGL246C	<i>RAI1</i>	<i>NRE387, G0580</i>	RNA processing/modification
323	H5	M	YDR525W-	<i>SNA2</i>		Homology to PMP3/SNA1 (Sensitivity to Na+)

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319	H3	M	YLR357W	<i>RSC2</i>		Member of RSC complex, which remodels the structure of chromatin; YLR358C on opposite strand also positive
341	C6	M	YDL194W	<i>SNF3</i>		Glucose permease or sensor
311	H5	M	YEL031W	<i>SPF1</i>	<i>COD1</i>	P-type ATPase; sensitivity to SMKT killer toxin; glycosylation defects
345	E4	M	YDL048C	<i>STP4</i>		Involved in pre-tRNA splicing and in uptake of branched-chain amino acids
308	A2	M	YOL072W	<i>THP1</i>		Null mutant is viable and shows transcription-associated hyper-recombination and transcription elongation impairment
333	G10	M	YMR060C	<i>TOM37</i>	<i>MAS37, PET3027</i>	Mitochondria outer membrane translocase protein transporter; 3' of FET3
341	F5	M	YNL107W	<i>YAF9</i>		Yeast homolog of human leukemogenic protein AF9; member of a large protein complex
Hypothetical ORFs						
310	H4	S	YDR136C	<i>VPS61</i>		Hypothetical ORF; 190 aa; interacts with <i>SPO21</i>
313	A2	M	YGR141W	<i>VPS62</i>		Hypothetical ORF; 467 aa; closely homologous to YPR157W; interacts with Ste2p;
320	E11	M	YLR261C	<i>VPS63</i>		Hypothetical ORF; 108 aa
321	D6	M	YDR200C	<i>VPS64</i>		Hypothetical ORF; 604aa; has FHA domain; closely homologous to YLR238W
321	A6	M	YLR322W	<i>VPS65</i>		Hypothetical ORF; 104 aa; opposite <i>SFH1</i> (systematic deletion of <i>SFH1</i> is inviable)
323	C11	M	YPR139C	<i>VPS66</i>		Hypothetical ORF; 300 aa
326	E7	S	YKR020W	<i>VPS67</i>		Hypothetical ORF; 164 aa; interacts with Luv1p and Vps52p
329	H6	M	YOL129W	<i>VPS68</i>		Hypothetical ORF; 184 aa; interacts with Gcs1p (Arf GAP)
331	H7	M	YPR087W	<i>VPS69</i>		Hypothetical ORF; 106 aa; opposite SRP54 (3'end); systematic deletion of SRP54 = inviable
334	E7	M	YJR126C	<i>VPS70</i>		Hypothetical ORF; 811 aa; peptidase and transferrin receptor 2 homology
343	B4	M	YML041C	<i>VPS71</i>		Hypothetical ORF; 280 aa; interacts with Bud7p
346	B11	M	YDR485C	<i>VPS72</i>		Hypothetical ORF; 810 aa
346	E10	M	YGL104C	<i>VPS73</i>		Hypothetical ORF; 486 aa; glucose transporter; interacts with Vam7p
372	B3	M	YDR372C	<i>VPS74</i>		Hypothetical ORF; 345 aa; limited homology to Lte1 GDP/GTP exchange factor; homology to rat GMX33; interacts with Vps26p
372	A7	M	YNL246W	<i>VPS75</i>		Hypothetical ORF; 264 aa; opposite YNL245c; 179aa; homologous to SET protein; interacts with Bud7p