

Supplemental Table 2

Plate	Well	Int.	ORF	Gene	Aliases	Description
Vacuole Biogenesis or Function						
333	E1	W	YLR423C	<i>APG17</i>		Involved in autophagy; required for activation of Apg1 protein kinase
338	F10	W	YCL038C	<i>AUT4</i>		Autophagy gene essential for breakdown of autophagic vesicles in the vacuole
342	G3	W	YCR032W	<i>BPH1</i>		Beige protein homolog 1
307	B4	W	YOR357C	<i>GRD19</i>	<i>SNX3</i>	Functions in Golgi retention; contains PX domain found in human SNX1 (Sorting Nexin-1)
320	H10	W	YLR309C	<i>IMH1</i>	<i>SYS3</i>	Synthetic interactions with <i>RIC1</i> and <i>YPT6</i>
332	F2	W	YJL036W	<i>SNX4</i>		Sorting NeXin
327	D11	W	YDR320C	<i>SWA2</i>		Auxilin-like protein
320	A10	W	YLR386W	<i>VAC14</i>		Involved in vacuole inheritance
317	H9	W	YOR106W	<i>VAM3</i>	<i>PTH1</i>	t-SNARE; Golgi to vacuole transport
311	B1	W	YDR359C	<i>VID21</i>		Vacuolar import and degradation
320	A1	W	YLR373C	<i>VID22</i>		Vacuole import and degradation
316	G11	W	YKL054	<i>VID31</i>		Vacuole import and degradation
Vacuolar ATPase						
336	D9	W	YJR033C	<i>RAV1</i>		Regulator of vacuolar ATPase
341	G6	W	YDR202C	<i>RAV2</i>		Regulator of vacuolar ATPase
311	G12	W	YEL027W	<i>VMA3</i>	<i>CUP5, CLS7, GEF2</i>	Subunit of vacuolar ATPase, V0 sector
370	E3	W	YKL080W	<i>VMA5</i>	<i>CSL5, VAT3</i>	Subunit of vacuolar ATPase, V1 sector
322	C12	W	YGR020C	<i>VMA7</i>		Subunit of vacuolar ATPase, V1 sector
Glycosylation or Cell Wall Assembly						
308	D10	W	YPL227C	<i>ALG5</i>		UDP-glucose:dolichyl-phosphate glucosyltransferase
315	B8	W	YCL007C	<i>CWH36</i>		Cell wall assembly; calcofluor hypersensitivity
333	A6	W	YJR075W	<i>HOC1</i>		Alpha-1,6-mannosyltransferase
305	C12	W	YNL322C	<i>KRE1</i>		Cell wall assembly
313	B9	W	YGR166W	<i>KRE11</i>	<i>TRS65</i>	Cell wall assembly
323	E2	W	YPR159W	<i>KRE6</i>	<i>CWH48</i>	Cell wall assembly; beta-glucan synthase (putative)
301	C9	W	YAL023C	<i>PMT2</i>	<i>FUN25</i>	Dolichyl-phosphate-mannose-protein mannosyltransferase
325	B1	W	YBL082C	<i>RHK1</i>	<i>ALG3</i>	Resistance to Hansenula killer 1; Dol-P-Man dependent alpha(1-3) mannosyltransferase
324	C10	W	YGR229C	<i>SMI1</i>	<i>KNR4</i>	Cell wall assembly; involved in (1,3)-beta-glucan synthesis
342	A11	W	YJL139C	<i>YUR1</i>		Cell wall assembly; mannosyltransferase
312	G6	W	YER083C			Protein involved in cell wall function

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ARF GAPs						
327	G9	W	YIL044C	<i>AGE2</i>	<i>SAT2</i>	Arf GAP
335	A4	W	YDL226C	<i>GCS1</i>		Arf GAP
347	C9	W	YER122C	<i>GLO3</i>		Arf GAP
Actin-related						
305	F5	W	YNL271C	<i>BNI1</i>	<i>PPF3</i>	Protein involved in actin filament organization; has FH domain; interacts with Rho1p
326	C11	W	YKL212W	<i>SAC1</i>	<i>RSD1</i>	Suppressor of actin mutations; integral membrane protein localizing to the ER and Golgi
311	C10	W	YDR389W	<i>SAC7</i>		Suppressor of actin mutations; Rho GTPase activator
Brefeldin A Hypersensitive						
318	E4	W	YOR198C	<i>BFR1</i>		Multicopy suppressor of brefeldin A-induced lethality; secretion and nuclear segregation
333	H7	W	YNR051C	<i>BRE5</i>		Brefeldin A sensitivity; has NTF2 domain; limited Ras GAP homology
324	C5	W	YGL012W	<i>ERG4</i>		Brefeldin A sensitivity; sterol C-24(28) reductase
Protein Trafficking						
340	B8	W	YBR059C	<i>AKL1</i>		Ark-family kinase-like protein
327	A7	W	YDR264C	<i>AKRI</i>		Ankyrin repeat-containing protein involved in endocytosis and signal transduction
328	B1	W	YFL025C	<i>BST1</i>		Negatively regulates COPII vesicle formation
301	A10	W	YAL058W	<i>CNE1</i>	<i>FUN48</i>	Calnexin and calreticulin homolog; functions in endoplasmic reticulum quality control
311	D11	W	YDR414C	<i>ERD1</i>		Protein required for retention of luminal ER proteins
334	F11	W	YML067C	<i>ERV41</i>		ER vesicle protein
317	A4	W	YKL073W	<i>LHS1</i>	<i>CER1, SSI1</i>	Required for efficient translocation of proteins across the ER membrane
318	E12	W	YOR216C	<i>RUD3</i>	<i>GRP1</i>	Relieves uso1-1 transport defect; golgin-160 related protein
316	C8	W	YLR208W	<i>SEC13</i>		COPII subunit
320	F6	W	YLR268W	<i>SEC22</i>	<i>SLY2, TSL26</i>	Synaptobrevin (v-SNARE) homolog present on ER to Golgi vesicles
372	E12	W	YBR171W	<i>SEC66</i>	<i>HSS1, SEC71</i>	Signal recognition particle receptor
335	F3	W	YBR283C	<i>SSH1</i>		Sec61p homolog involved in co-translational pathway of protein transport
332	F5	W	YER031C	<i>YPT31</i>	<i>YPT8</i>	Rab-like GTP binding proteins; intra-Golgi transport
Ribosomal Proteins						
320	C7	W	YGR085C	<i>RPL11B</i>		Component of large ribosome subunit
312	B1	W	YEL054C	<i>RPL12A</i>		Component of large ribosome subunit
330	D8	W	YMR142C	<i>RPL13B</i>		Component of large ribosome subunit
348	G6	W	YNL069C	<i>RPL16B</i>	<i>RP23</i>	Component of large ribosome subunit
342	B9	W	YJL177W	<i>RPL17B</i>		Component of large ribosome subunit
328	E7	W	YFR031C-A	<i>RPL2A</i>	<i>RPL5B</i>	Component of large ribosome subunit
304	D2	W	YMR194W	<i>RPL36A</i>	<i>RPL39B</i>	Component of large ribosome subunit

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316	B10	W	YLR185W	<i>RPL37A</i>		Component of large ribosome subunit
342	B11	W	YJL189W	<i>RPL39</i>	<i>PUB2, RPL46, SPB2</i>	Component of large ribosome subunit
340	F9	W	YIL148W	<i>RPL40A</i>	<i>UBI1</i>	Component of large ribosome subunit
348	F12	W	YML073C	<i>RPL6A</i>	<i>YL16A</i>	Component of large ribosome subunit
338	C8	W	YGL076C	<i>RPL7A</i>		Component of large ribosome subunit
336	H7	W	YDL130W	<i>RPP1B</i>	<i>RPL44', RPLA3</i>	Component of large ribosome subunit
342	A9	W	YJL136C	<i>RPS21B</i>		Component of small ribosome subunit
320	A12	W	YLR388W	<i>RPS29A</i>		Component of small ribosome subunit
341	F12	W	YBR189W	<i>RPS9B</i>	<i>RPS13A, SUP46</i>	Component of small ribosome subunit

Miscellaneous

380	F3	W	YGR204W	<i>ADE3</i>		C1-tetrahydrofolate synthase required for the biosynthesis of purines
333	B3	W	YJR105W	<i>ADOI</i>		Adenosine kinase
317	C10	W	YKL114C	<i>APN1</i>		Major apurinic/aprimidinic endonuclease/3'-repair diesterase
346	H3	W	YGL148W	<i>ARO2</i>		Chorismate synthase
348	H4	W	YNL315C	<i>ATP11</i>		Mitochondrial chaperone
333	D5	W	YKR099W	<i>BAS1</i>		Transcription factor
380	F11	W	YER016W	<i>BIM1</i>	<i>YEB1</i>	Structural protein of cytoskeleton (microtubules)
335	F7	W	YBR290W	<i>BSD2</i>		Putative metal transport protein
322	E8	W	YPL069C	<i>BTS1</i>		Geranylgeranyl diphosphate synthase required for membrane attachment of Ypt1p and Sec4p
335	H10	W	YCR063W	<i>BUD31</i>		Diploid mutants exhibit random budding
380	C9	W	YCR002C	<i>CDC10</i>		Structural protein of cytoskeleton (septin)
323	A3	W	YPL008W	<i>CHL1</i>	<i>CTF1, LPA9</i>	DEAD box protein involved in mitotic chromosome segregation
322	H11	W	YPL018W	<i>CTF19</i>	<i>MCM18</i>	Kinetochore protein important for chromosome segregation
323	C9	W	YPR135W	<i>CTF4</i>	<i>CHL15, POB1</i>	DNA polymerase alpha binding protein
342	C7	W	YKL139W	<i>CTK1</i>		Putative kinase subunit of complex that phosphorylates the RPO21 CTD
330	H11	W	YML112W	<i>CTK3</i>		RNA polymerase II C-terminal domain kinase gamma subunit
335	F8	W	YBR291C	<i>CTP1</i>		Citrate transport protein; in 3' of BSD2
336	G9	W	YDL117W	<i>CYK3</i>		involved in CYtoKinesis
328	H5	W	YIR027C	<i>DAL1</i>		Allantoinase
326	E9	W	YKR024C	<i>DBP7</i>		ATP dependent RNA helicase
338	E1	W	YIL010W	<i>DOT5</i>		Derepression Of Telomeric silencing
327	B9	W	YDR284C	<i>DPP1</i>	<i>ZRG1</i>	Diacylglycerol pyrophosphate phosphatase involved in phospholipid metabolism
319	C1	W	YOR144C	<i>EFD1</i>		Enhanced frequency of direct-repeat recombination
316	G7	W	YKL048C	<i>ELM1</i>		Protein kinase involved in cytokinesis, axial budding, and osmotic response
372	B2	W	YNL280C	<i>ERG24</i>		Sterol C-14 reductase involved in ergosterol biosynthesis
312	D12	W	YER044C	<i>ERG28</i>		Ergosterol biosynthesis
311	B3	W	YDR363W	<i>ESC2</i>		Establishes Silent Chromatin

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305	B8	W	YMR307W	<i>GAS1</i>	<i>CWH52, GGP1</i>	GPI-anchored surface protein (115-120 kDa)
348	E7	W	YGR252W	<i>GCN5</i>	<i>ADA4, SWI9</i>	Functions in the Ada, SAGA complexes to acetylate nucleosome histones
312	A1	W	YEL042W	<i>GDA1</i>		Guanosine diphosphatase of Golgi membrane
336	E2	W	YJR040W	<i>GEF1</i>		Transport protein involved in intracellular iron metabolism (putative)
328	H2	W	YIR024C	<i>GIF1</i>		G1 Factor needed for normal G1 phase
335	H11	W	YCR065W	<i>HCM1</i>		Dosage-dependent suppressor of cmd1-1 mutation; homology to forkhead family
339	H10	W	YBR034C	<i>HMT1</i>	<i>HCP1, ODP1, RMT1</i>	hnRNP methyltransferase
318	H7	W	YOR258W	<i>HNT3</i>		Histidine triad superfamily, third branch
310	H5	W	YDR138W	<i>HPR1</i>		Hyperrecombination protein that suppresses intrachromosomal excision recombination
321	E11	W	YDR225W	<i>HTA1</i>	<i>H2A1, SPT11</i>	Histone H2A
335	G5	W	YCR020W-B	<i>HTL1</i>		High-temperature lethal
307	D11	W	YOL012C	<i>HTZI</i>	<i>HTA3</i>	Chromatin binding, histone-related protein that can suppress histone H4 point mutation
302	G2	W	YLR095C	<i>IOC2</i>		Iswi One Complex involved in chromatin remodelling
312	C11	W	YER019W	<i>ISC1</i>		Phospholipase C
310	A9	W	YBR245C	<i>ISWI</i>	<i>SGN2</i>	ATPase component of a four subunit chromatin remodeling complex
323	E4	W	YPR164W	<i>KIM3</i>		Killed in mutagen; sensitive to diepoxybutane and/or mitomycin C
334	A11	W	YAL058C-A	<i>KRE20</i>		Killer toxin REsistant 20
372	F2	W	YDR532C	<i>KRE28</i>		Killer toxin REsistant 28
332	D8	W	YJL062W	<i>LAS21</i>	<i>GPI7</i>	Local Anesthetics Sensitive; involved in the attachment of GPI anchors to proteins.
328	D1	W	YFR001W	<i>LOC1</i>		Localization of mRNA
346	C9	W	YDR503C	<i>LPP1</i>		Lipid phosphate phosphatase
311	B12	W	YDR378C	<i>LSM6</i>		Like Sm-F protein; snRNP protein
348	H2	W	YNL268W	<i>LYP1</i>		Lysine permease
342	D5	W	YKL029C	<i>MAE1</i>		Mitochondrial malic enzyme
348	F3	W	YGR289C	<i>MAL11</i>	<i>AGT1</i>	General alpha-glucoside:hydrogen symporter; part of MAL1 complex locus
303	H2	W	YMR036C	<i>MIHI</i>		Protein tyrosine phosphatase that induces M-phase
328	H3	W	YIR025W	<i>MND2</i>		Meiotic recombination; opposite YIR024C
316	E8	W	YKL009W	<i>MRT4</i>		mRNA turnover 4
331	A11	W	YML128C	<i>MSC1</i>		Meiotic Sister-Chromatid recombination
340	H11	W	YIR009W	<i>MSL1</i>		U2 snRNP component involved in splicing
323	C8	W	YPR134W	<i>MSS18</i>		Protein involved in splicing intron a15beta of COX1
317	A5	W	YKL074C	<i>MUD2</i>		Involved in early pre-mRNA splicing
332	G3	W	YHR004C	<i>NEM1</i>		Nuclear Envelope Morphology
305	A4	W	YMR285C	<i>NGL2</i>		Putative RNase/DNase; homologous to Drosophila Angelgene
308	G12	W	YPL174C	<i>NIP100</i>	<i>PAC13</i>	Nuclear import protein; large subunit of dynactin complex

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316	H3	W	YKL057C	<i>NUP120</i>	<i>RAT2</i>	Nucleoporin; mRNA-nucleus export
336	G8	W	YDL116W	<i>NUP84</i>		Component of nuclear pores
336	E8	W	YJR051W	<i>OSM1</i>		Fumarate reductase (NADH); osmotic growth protein; sensitive to hypertonic medium
319	C8	W	YJL179W	<i>PFD1</i>		Prefoldin subunit 1; chaperone
380	C5	W	YOR104W	<i>PIN2</i>		[PSI ⁺] prion induction; may also disrupt YOR105W; hypothetical ORF 108 aa
372	F4	W	YPL268W	<i>PLC1</i>		1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase
325	C2	W	YGL006W	<i>PMC1</i>		Ca ²⁺ ATPase (putative)
380	B4	W	YPL188W	<i>POS5</i>		Involved in oxidative stress
327	C8	W	YDR300C	<i>PRO1</i>		Gamma-glutamyl kinase; catalyzes first step in proline biosynthesis
335	C5	W	YDR014W	<i>RAD61</i>		Affects radiation sensitivity.
345	G9	W	YDL090C	<i>RAM1</i>	<i>DPR1, FUS8, SCG2, SGP2, STE16</i>	Farnesyltransferase beta subunit involved in Ras processing
321	D3	W	YDR195W	<i>REF2</i>		RNA-binding protein involved in cleavage step of mRNA 3'-end formation
341	A8	W	YNL139C	<i>RLR1</i>	<i>THO2, ZRG13</i>	Involved in transcription
337	E10	W	YGR056W	<i>RSC1</i>		Rsc1p is a component of the RSC complex, which remodels the structure of chromatin
313	F6	W	YHL034C	<i>SBP1</i>	<i>SSBR1</i>	RNA processing; single stranded nucleic acid binding protein
304	C12	W	YMR190C	<i>SGS1</i>		DNA helicase signature motifs; involved in maintaining genome stability
324	H6	W	YBL058W	<i>SHP1</i>		Suppressor of the overexpression of the phosphoprotein phosphatase 1 Glc7p
302	F1	W	YLR079W	<i>SIC1</i>	<i>SDB25</i>	P40 inhibitor of Cdc28p-Clb5 protein kinase complex
315	A12	W	YHR206W	<i>SKN7</i>	<i>BRY1, POS9</i>	Protein with similarity to DNA-binding region of heat shock transcription factors
339	C9	W	YNR015w	<i>SMM1</i>		tRNA dihydrouridine synthase; Suppressor of Mitochondrial Mutation in the tRNA ^{asp} gene
348	B9	W	YDR477W	<i>SNF1</i>	<i>CAT1, CCR1, GLC2, HAF3, PAS14</i>	Serine/threonine kinase required for release from glucose repression
342	F9	W	YBR289W	<i>SNF5</i>	<i>HAF4, SWI10, TYE4</i>	Non-specific RNA polymerase II transcription factor; opposite APM3, not overlapping
301	D9	W	YAL009W	<i>SPO7</i>		Required for recombination, meiosis, glycogen degradation and sporulation
331	D1	W	YMR125W	<i>STO1</i>	<i>CBC1, GCR3, CBP80</i>	Large subunit of the nuclear cap-binding protein complex
327	D2	W	YDR310C	<i>SUM1</i>		Involved in chromatin silencing
327	E5	W	YDR334W	<i>SWR1</i>		Sick With RSC; involved in chromatin remodeling; putative ATPase
311	D2	W	YDR395W	<i>SXM1</i>	<i>KAP108</i>	Importin-beta like gene product; karyopherin beta family member
321	B7	W	YDR161W	<i>TCI1</i>		Protein phosphatase Two C-Interacting protein
332	E4	W	YJL052W	<i>TDH1</i>	<i>GLD3</i>	Glyceraldehyde-3-phosphate dehydrogenase 1
380	F10	W	YPR163C	<i>TIF3</i>	<i>RBL3, STM1</i>	Translation initiation factor eIF-4B
321	D9	W	YDR207C	<i>UME6</i>	<i>CAR80, NIM2, RIM16</i>	Regulation of both repression and induction of early meiotic genes
305	G6	W	YGR072W	<i>UPF3</i>	<i>SUA6</i>	Factor stimulating decay of mRNAs containing premature stop codons
338	D11	W	YIL008W	<i>URM1</i>		Ubiquitin-like protein
342	B1	W	YJL141C	<i>YAK1</i>		Serine-threonine protein kinase
328	F4	W	YGR270W	<i>YTA7</i>		Member of Cdc48p/Pas1p/Sec18p family of ATPases
328	H4	W	YIR026C	<i>YVH1</i>		Protein tyrosine phosphatase induced by nitrogen starvation
333	B8	W	YJR127C	<i>ZMS1</i>		Transcription factor

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Hypothetical ORFs					
345	D10	W	YDL033C		tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase
341	E2	W	YNL080C		Deletion causes slight growth defect, similar to <i>U. maydis</i> Myp1 protein
341	E12	W	YNL099C		Protein phosphatase involved in cell cycle control and stress
301	D12	W	YAL004W		Hypothetical ORF; 215 aa; opposite <i>SSA1</i> , ATPase/chaperone
301	D7	W	YAL011W		Hypothetical ORF; 638 aa
301	D5	W	YAL014C		Hypothetical ORF; 205 aa
310	A11	W	YBR246W		Hypothetical ORF; 387 aa
310	B11	W	YBR266C		Hypothetical ORF; 150 aa
310	B12	W	YBR267W		Hypothetical ORF; 393 aa
342	G4	W	YCR033W	<i>SNT1</i>	Hypothetical ORF; 1226 aa
335	H6	W	YCR050C		Hypothetical ORF; 102 aa
336	F8	W	YDL096C		Hypothetical ORF; 108 aa; opposite 5' PMT1 dolichyl-phosphateprotein mannosyl-transferase
380	D2	W	YDL119C		Hypothetical ORF; 307 aa; mitochondrial transporter; opposite YDL118W
310	F2	W	YDR105C		Hypothetical ORF; 473 aa
321	C11	W	YDR186C		Hypothetical ORF; 877 aa
321	D7	W	YDR203W		Hypothetical ORF; 105 aa; opposite YDR200C
311	E7	W	YDR425W		Hypothetical ORF; 625 aa; opposite YDR426c
311	E8	W	YDR426C		Hypothetical ORF; 125 aa; opposite YDR425w
312	A2	W	YEL043W		Hypothetical ORF; 956 aa
338	B7	W	YGL020C		Hypothetical ORF; 235 aa
325	E10	W	YGL072C		Hypothetical ORF; 119 aa
321	F9	W	YGL198W		Hypothetical ORF; 452aa; putative oxidoreductase
337	F2	W	YGR064W		Hypothetical ORF; 122 aa; opposite <i>SPT4</i> encoding transription regulator
313	D11	W	YGR206W		Hypothetical ORF; 101aa
313	F10	W	YHL029C		Hypothetical ORF; 679aa
332	G6	W	YHR009C		Hypothetical ORF; 518 aa
314	E5	W	YHR111W		Hypothetical ORF; 440aa; protein conjugation factor
315	A7	W	YHR199C		Hypothetical ORF; 310aa
338	F1	W	YIL067C		Hypothetical ORF; 678aa
340	D8	W	YIL110W		Hypothetical ORF; 377 aa; 3' of <i>SEC24</i>
372	D6	W	YJL075C		Hypothetical ORF; 138aa; opposite <i>NET1</i> (nucleolus)
336	C11	W	YJR018W		Hypothetical ORF; 120 aa; opposite <i>ESS1</i> (mRNA processing)
333	A8	W	YJR079W		Hypothetical ORF; 109aa
334	D9	W	YJR100C		Hypothetical ORF; 327 aa
326	F3	W	YKR035C		Hypothetical ORF; 213 aa; opposite <i>DID2</i>
302	G12	W	YLR111W		Hypothetical ORF; 110 aa

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316	B7	W	YLR181C			Hypothetical ORF; 330aa
316	D12	W	YLR225C			Hypothetical ORF; 407aa
372	C11	W	YLR350W			Hypothetical ORF; 216 aa
320	A2	W	YLR374C			Hypothetical ORF; 129 aa; in 5'UTR of <i>VID22</i>
320	A7	W	YLR381W			Hypothetical ORF; 733 aa
333	E3	W	YLR426W			Hypothetical ORF; 326aa; oxidoreductase
333	E11	W	YLR435W			Hypothetical ORF; 249aa
303	D9	W	YML013C-A			Hypothetical ORF; 125 aa; opposite YML014W
305	B1	W	YMR299C			Hypothetical ORF; 312 aa
341	B3	W	YNL127W			Hypothetical ORF; 953 aa
341	A9	W	YNL136W			Hypothetical ORF; 425aa
318	B7	W	YOR135C			Hypothetical ORF; 113aa
306	F8	W	YOR292C			Hypothetical ORF; 309 aa
308	G4	W	YPL184C			Hypothetical ORF; 612 aa