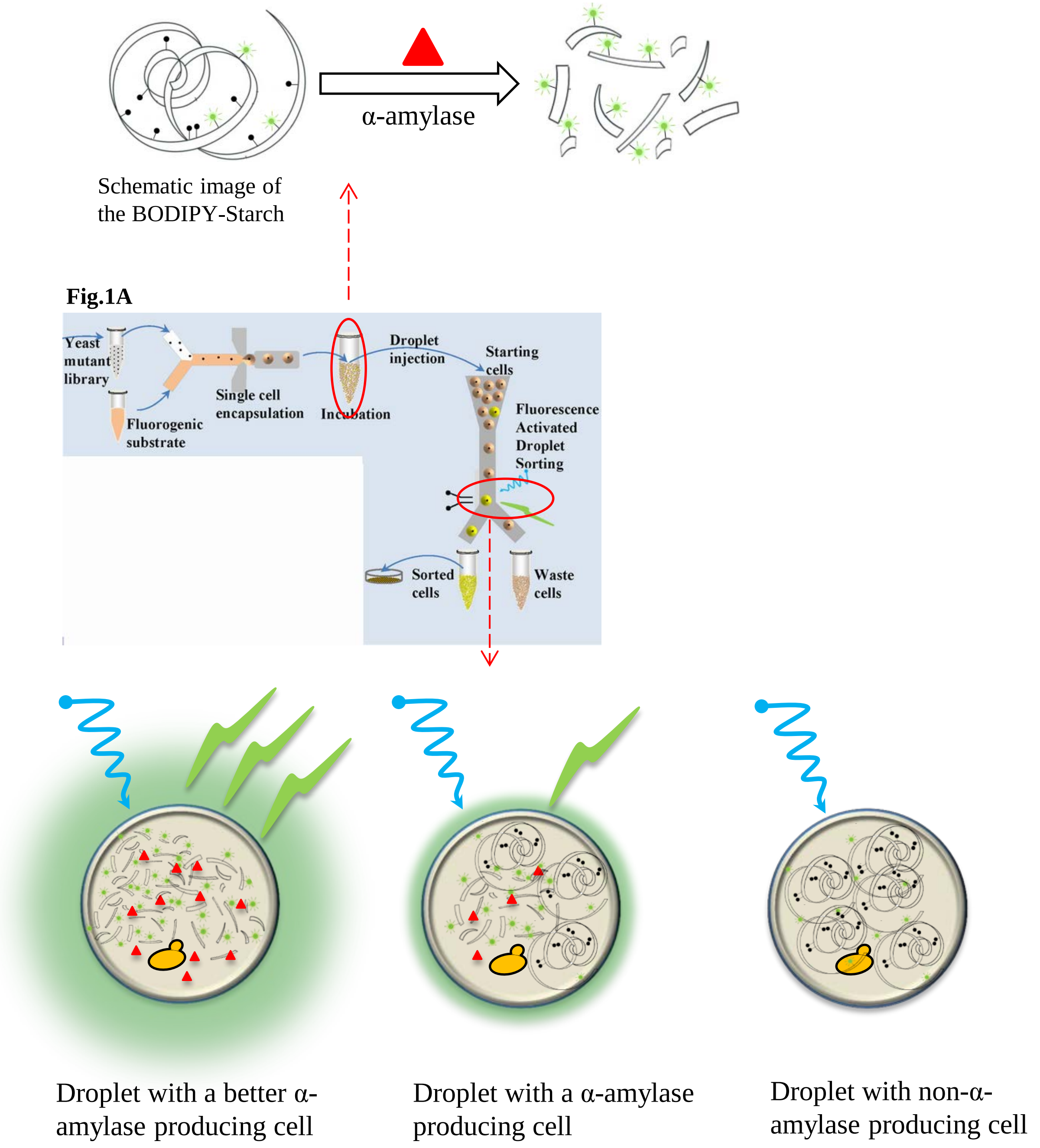
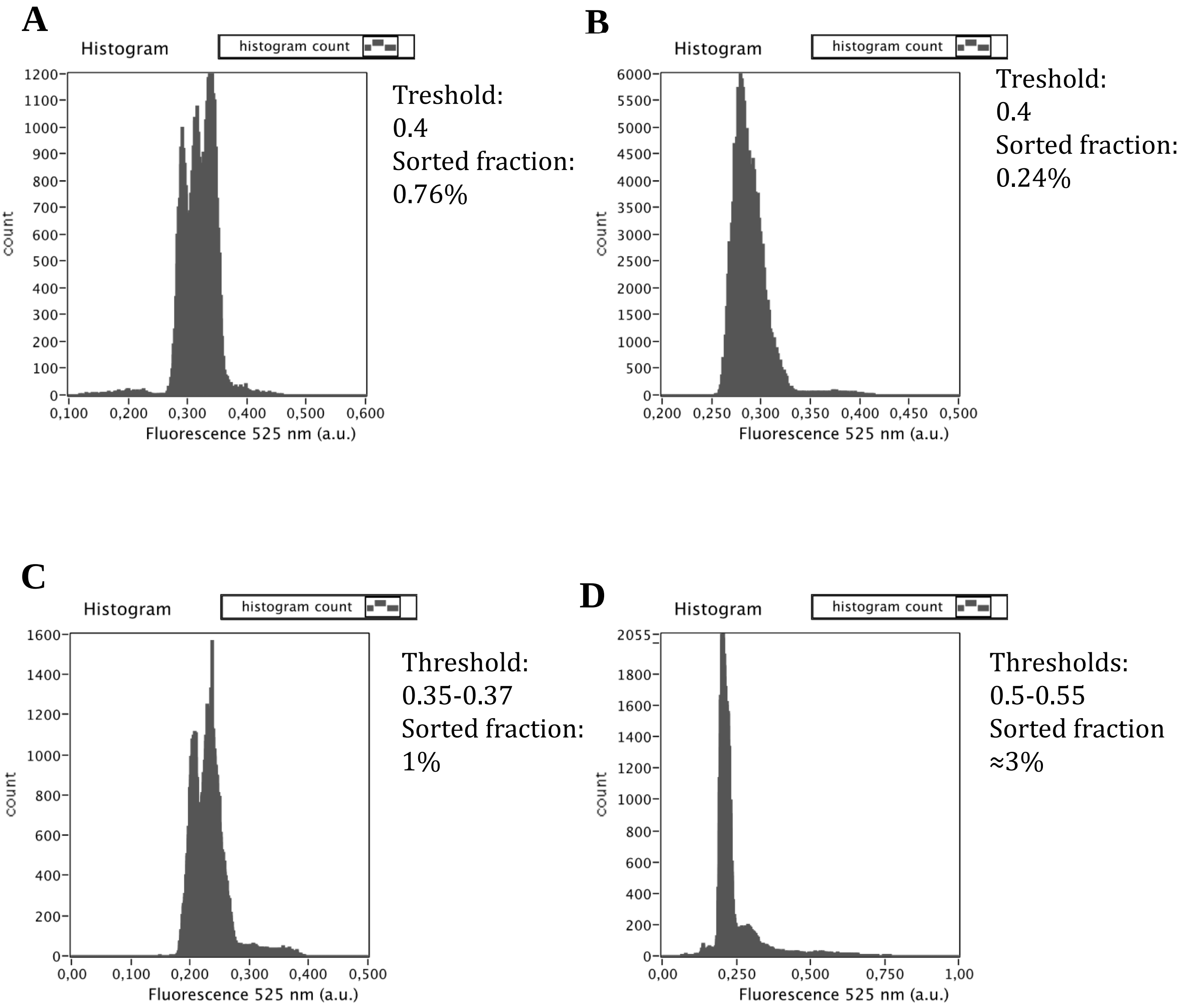


Supplementary Figure S1 Fluorescent substrate digestion in the droplet. Droplet with a better α-amylase producing cell will have higher α-amylase concentration inside the droplet and thus more BODIPY-starch can be degraded in the same unit of time. This will give rise to a stronger fluorescent signal that will be emitted upon excitation.



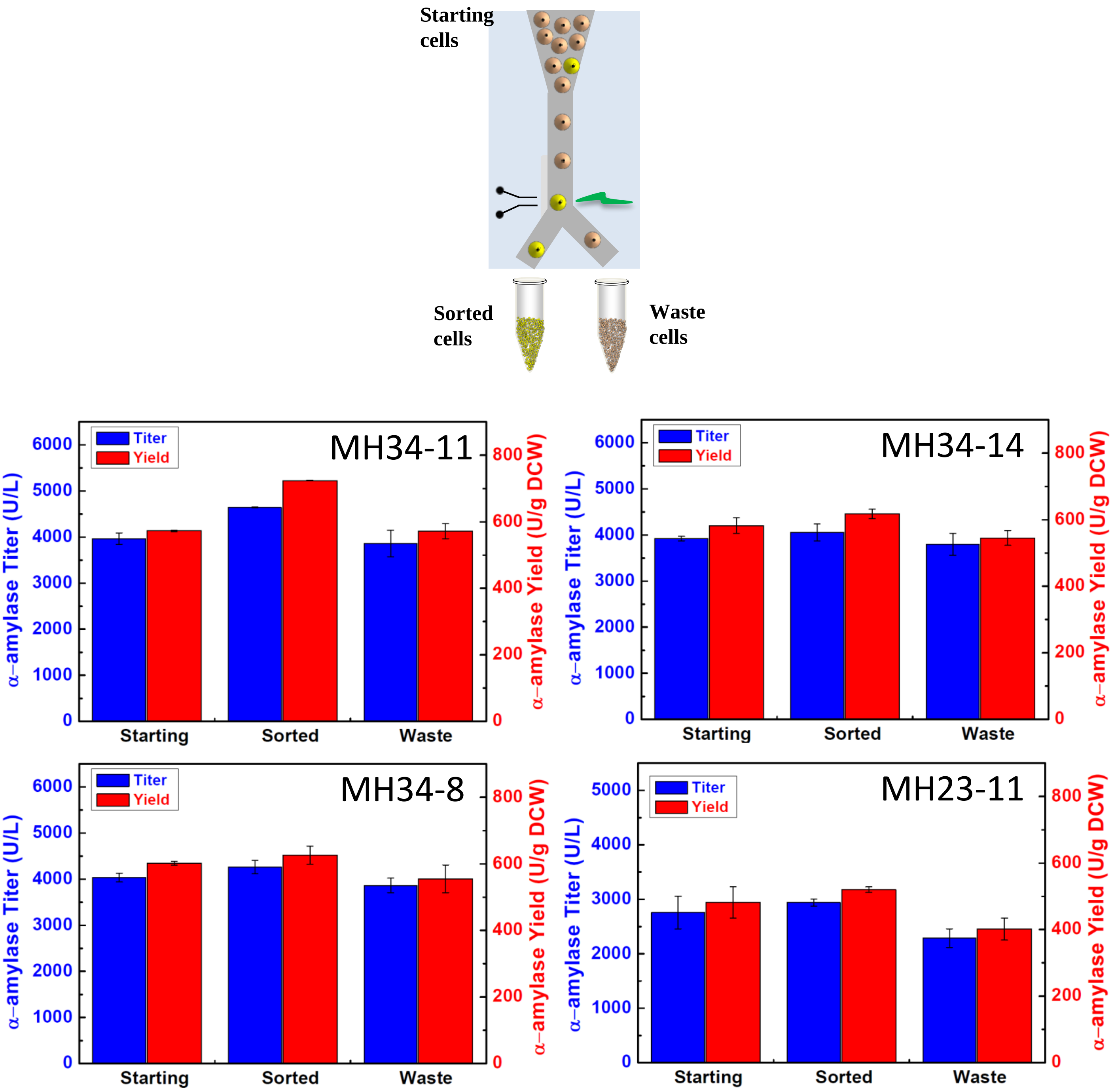
Treshold:
0.4
Sorted fraction:
0.76%

Treshold:
0.4
Sorted fraction:
0.24%

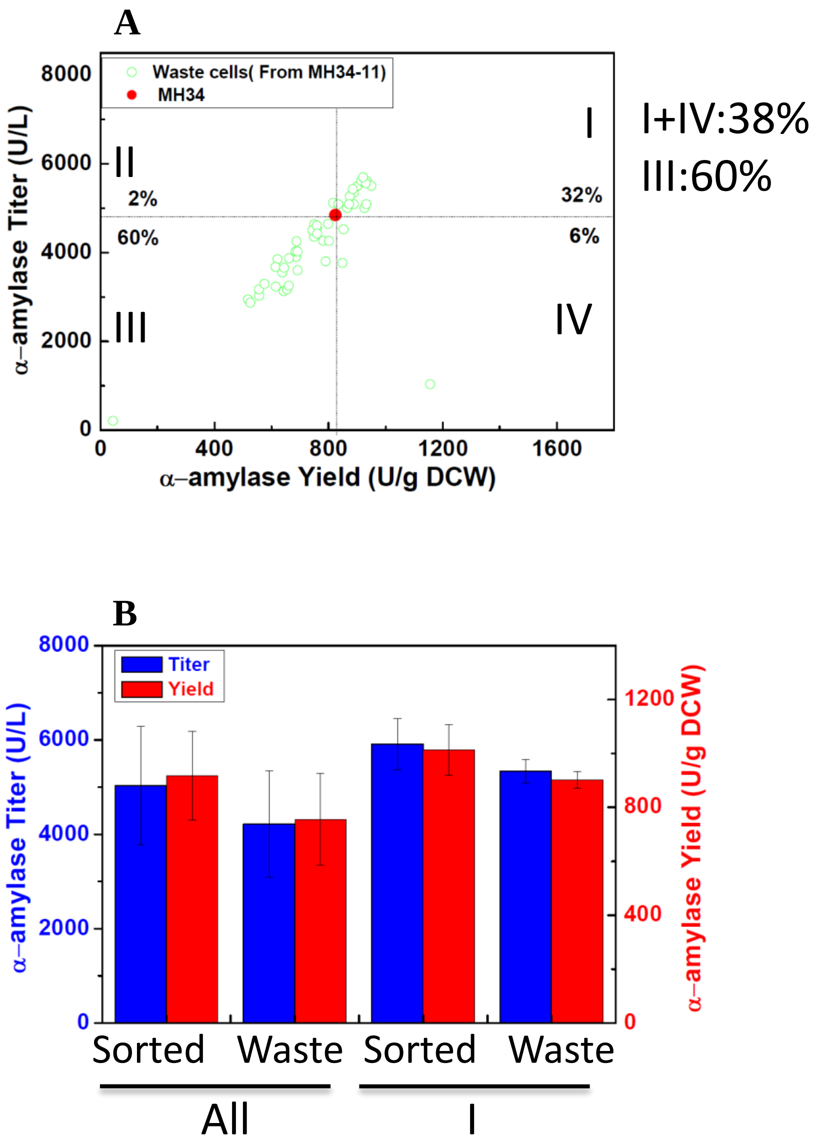
Threshold:
0.35-0.37
Sorted fraction:
1%

Thresholds:
0.5-0.55
Sorted fraction
≈3%

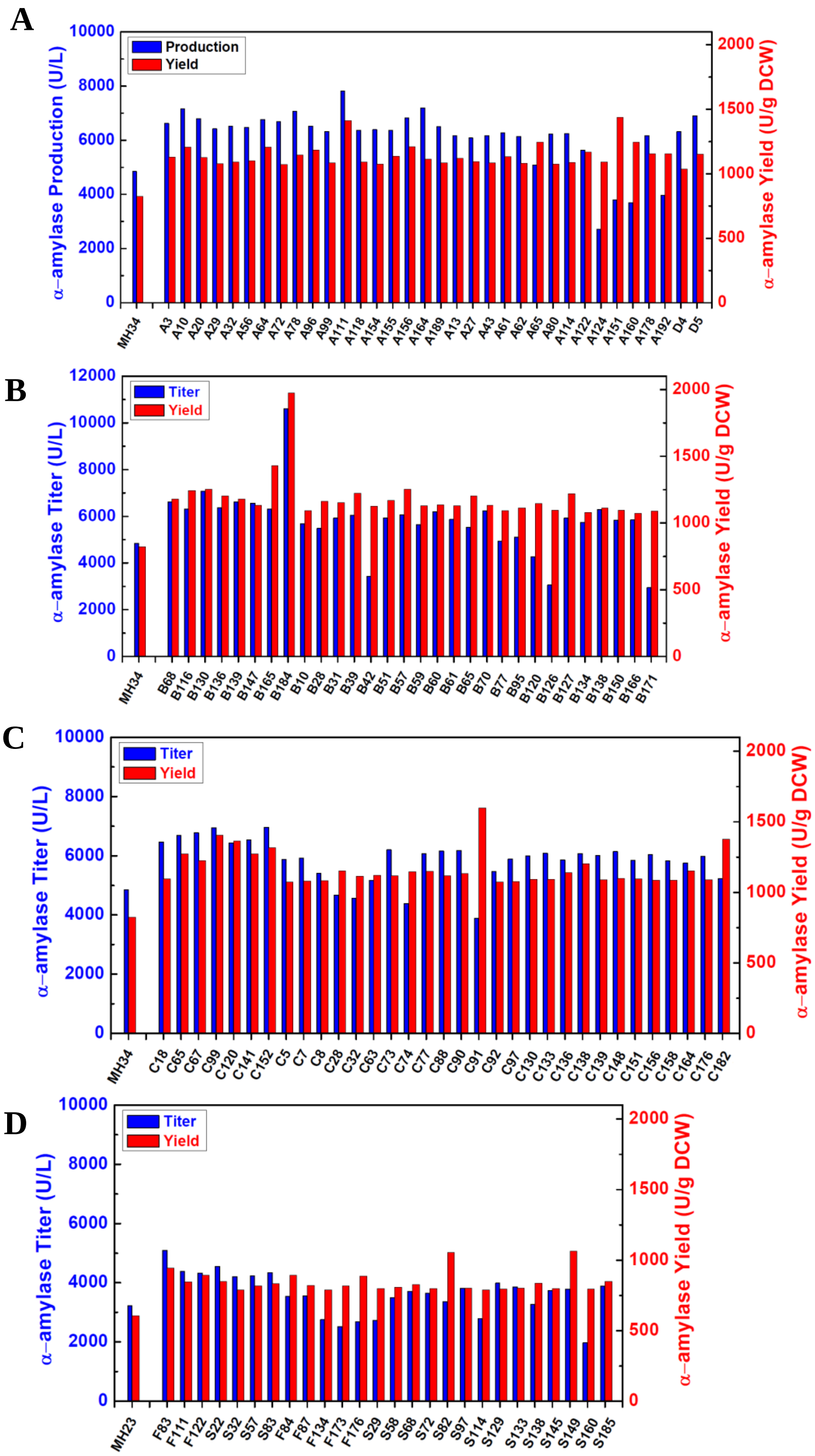
Supplementary Figure S2 Histogram showing droplet fluorescence of yeast libraries in the second round of screening. (**A**) The Library MH34-11. (**B**) The Library MH34-14. (**C**) The Library MH34-8. (**D**) The Library MH23-11.



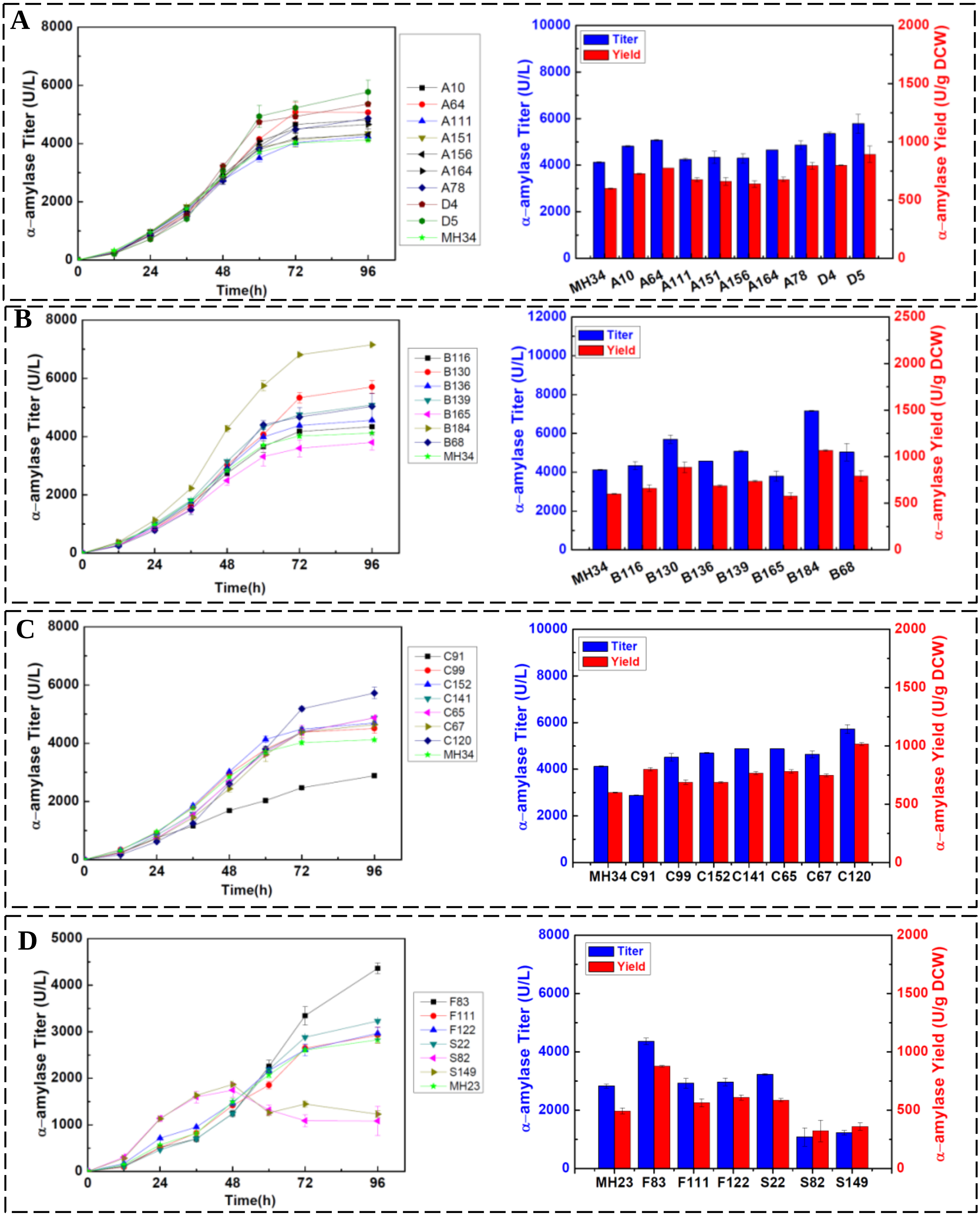
Supplementary Figure S3 Fermentation of mixed colonies for evaluation of the titer and yield of α-amylase produced by different yeast populations before and after sorting. 50 colonies were randomly picked up from different populations of the library and mixed together for fermentation.



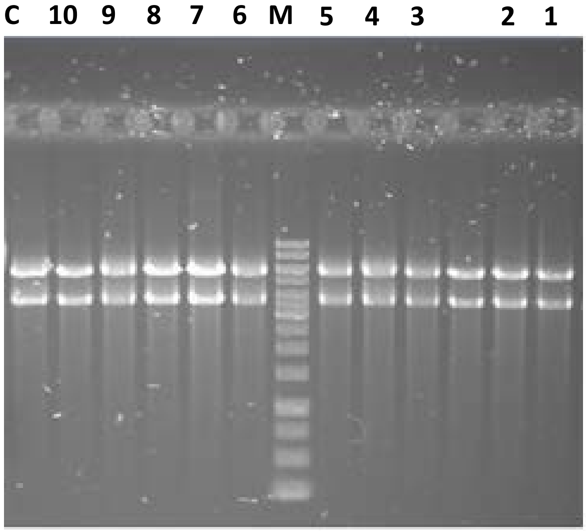
Supplementary Figure S4 (**A**) 50 waste colonies from the library MH34-11 were tested in tube fermentation. (**B**) Average α-amylase titer and yield of sorted cells and waste cells from the library MH34-11.



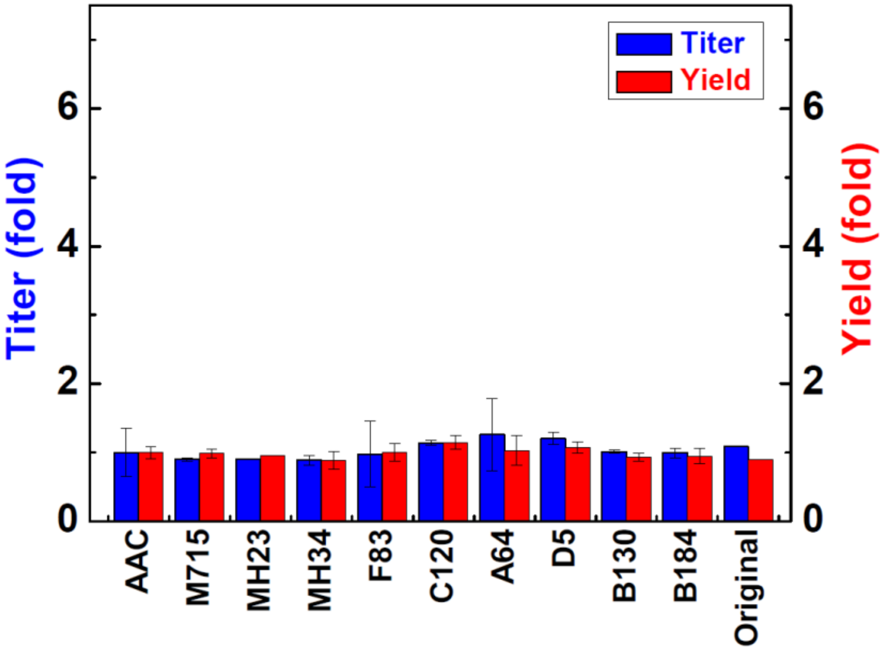
Supplementary Figure S5 Strains achieve at least 30% α-amylase yield increase in tube fermentation. From the sorted population of the library (**A**) MH34-11. (**B**) MH34-14. (**C**) MH34-8. (**D**) MH23-11.



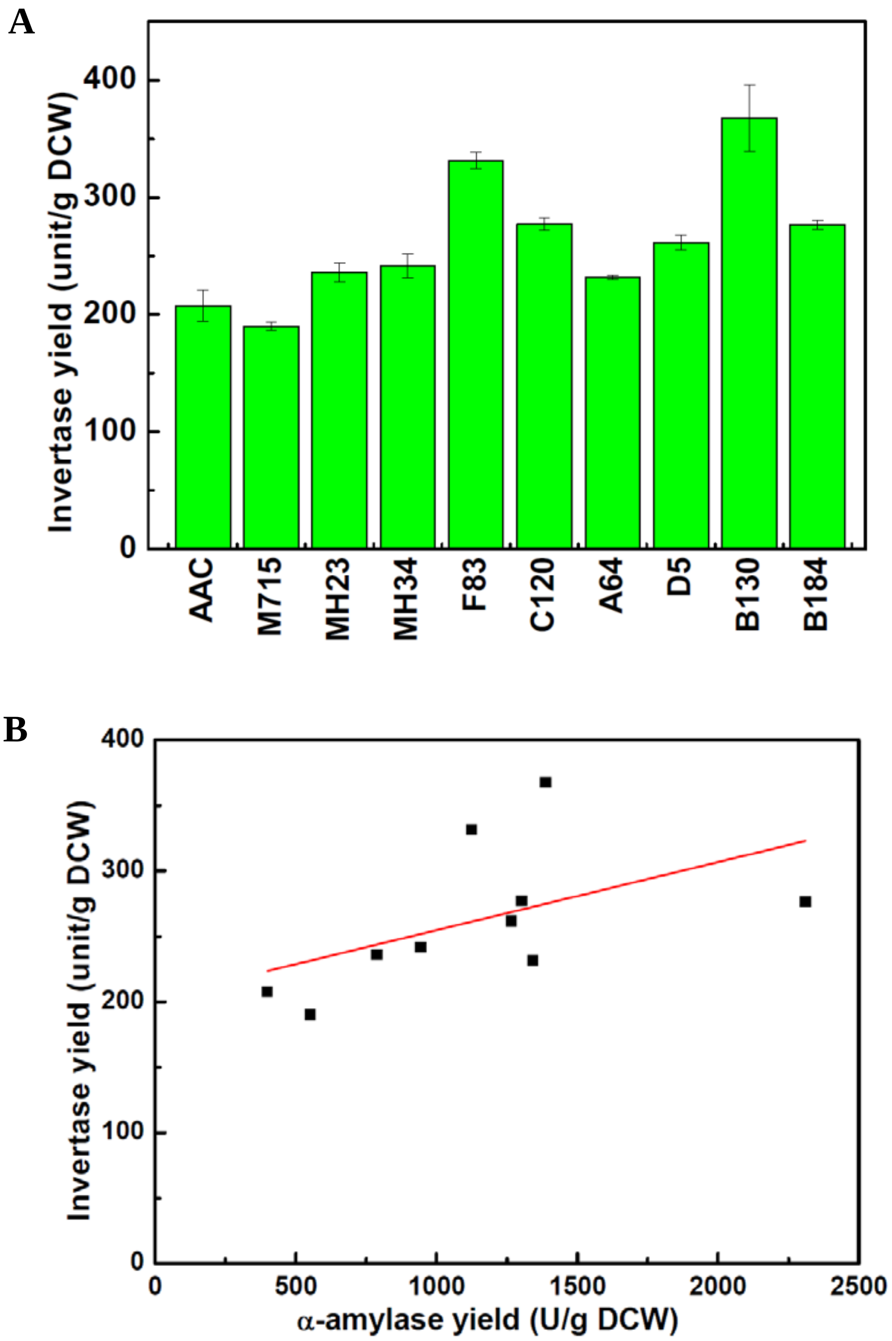
Supplementary Figure S6 Shake flask fermentation of selected strains based on tube fermentations. Left panel: α-amylase production over time; Right panel: the final α-amylase titer and yield (at 96 h). (**A**) Selected strains from the library MH34-11. (**B**) Selected strains from the library MH34-14. (**C**) Selected strains from the library MH34-8. (**D**) Selected strains from the library MH23-11.



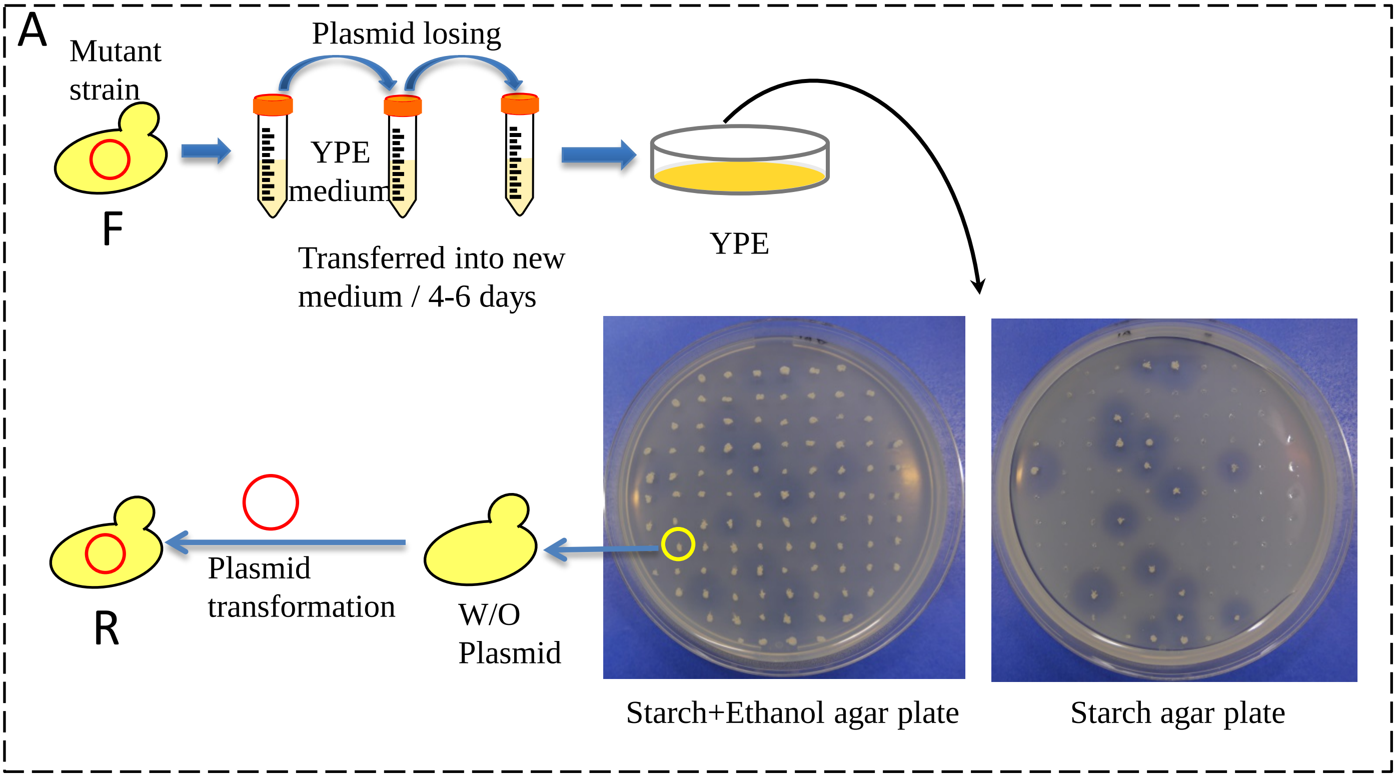
Supplementary Figure S7 Restriction analysis of plasmids from selected mutant strains showed that all plasmids were structural stable. Plasmids from: 1.AAC, 2.M715, 3.MH23, 4.MH34, 5.A64, 6.B130, 7.B184, 8.C120, 9.D5 and 10.F83. C: Control; M: DNA Ladder.

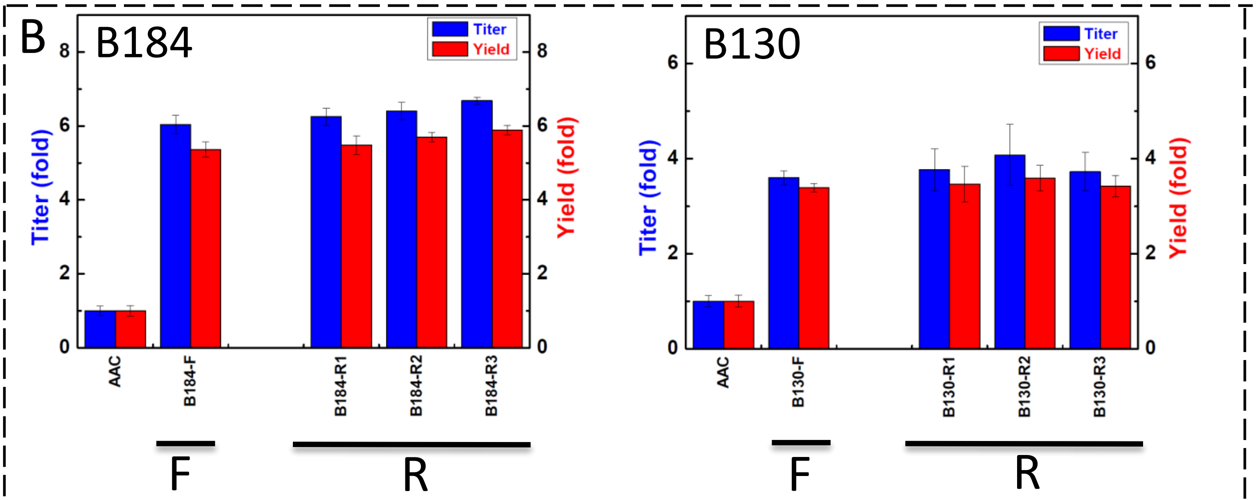


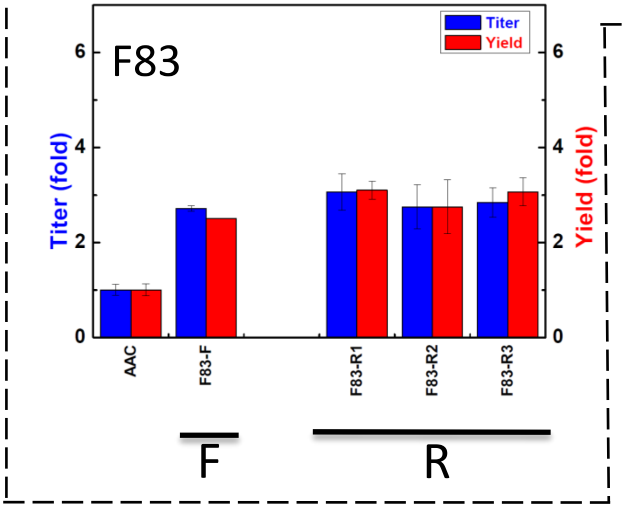
Supplementary Figure S8 α-amylase production capacity of wild type strain harboring different isolated plasmids from the wild type and selected mutant strains. The production capacity of α-amylase was found to be almost identical for all strains.



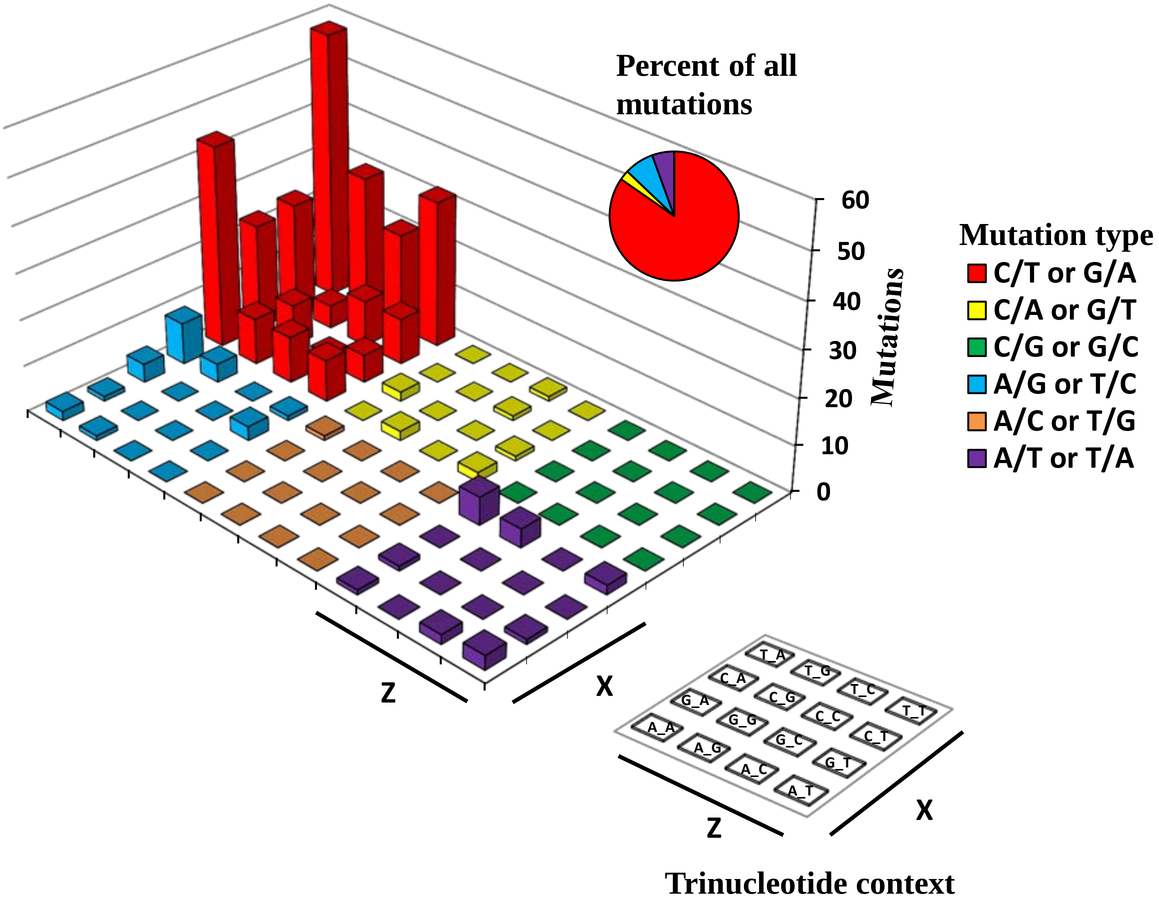
Supplementary Figure S9 (**A**) Invertase activity of selected mutant strains. (**B**) A scatter plotting shows the positive correlation between invertase yield and α-amylase yield.



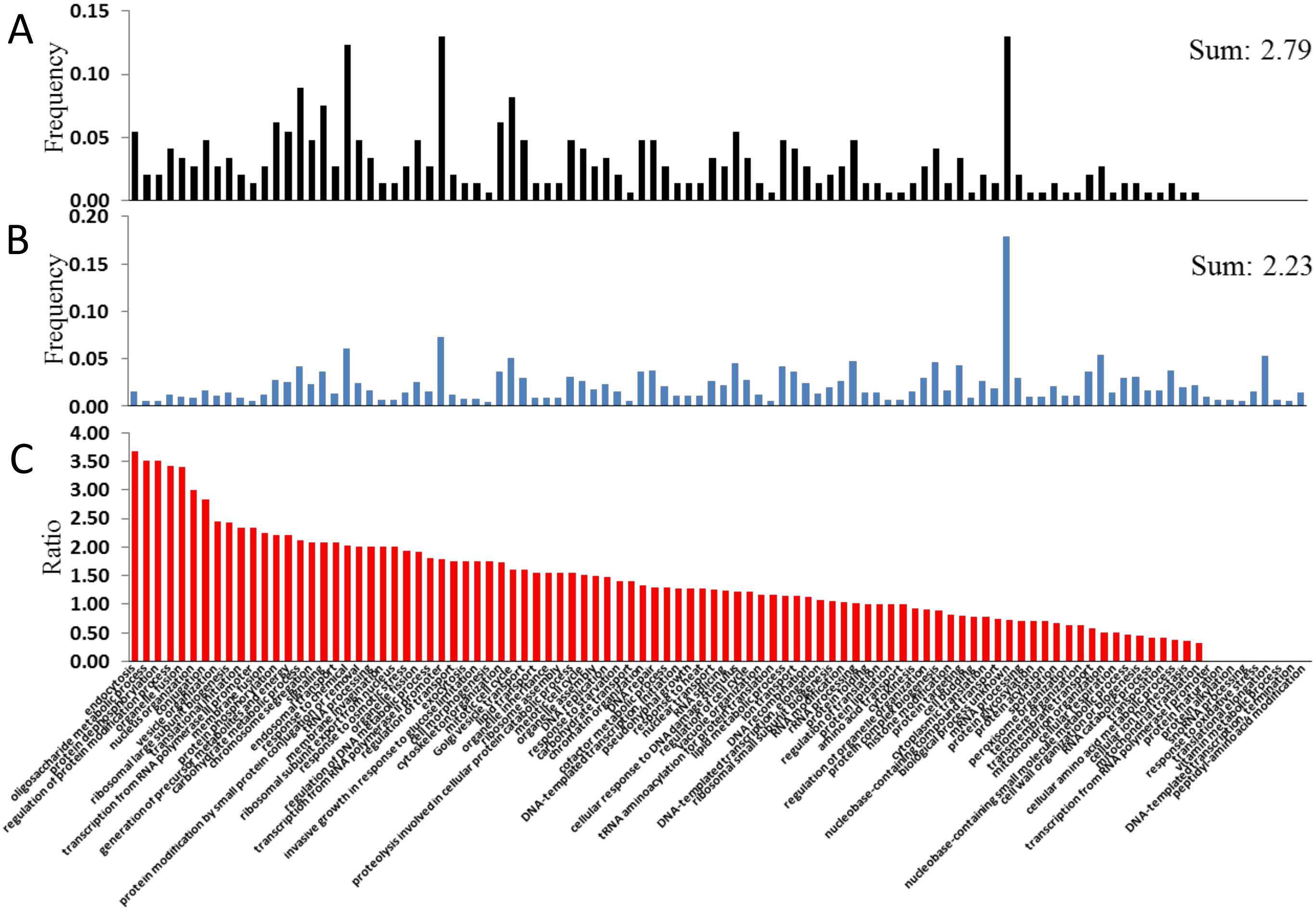




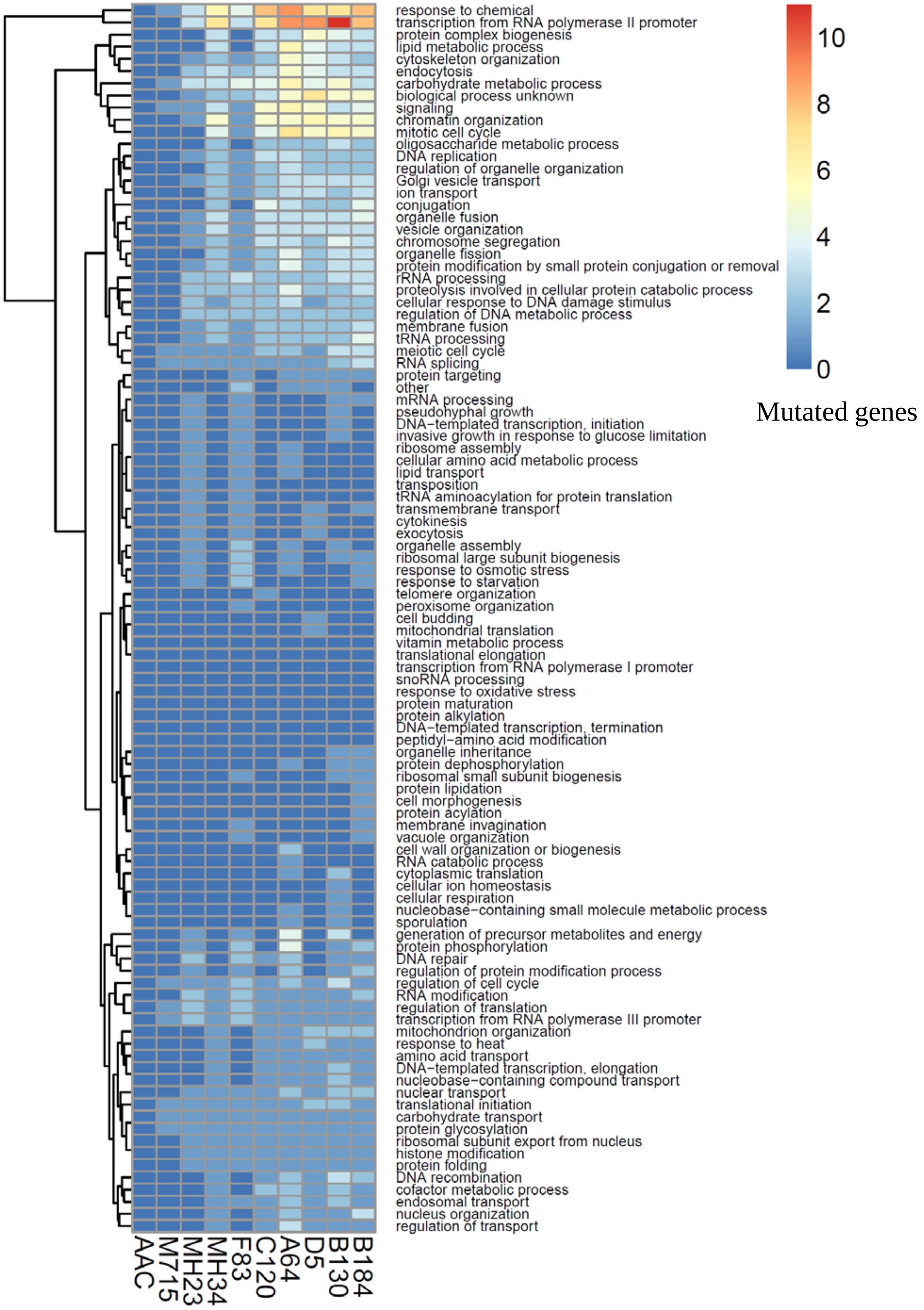
Supplementary Figure S10 α-amylase secretion capacity of mutant strains is genetically stable. (**A**) A series of selective transfers in YPE medium for elimination of plasmid from the mutant strain; then plasmid was re-transformed to the mutant strain. (**B**) α-amylase production of mutant strains with former plasmid (F) or with retransformation plasmid(R). For each mutant strain, three independent plasmid elimination clones were randomly picked and made component for transformation (R1, R2 and R3). Then 3 or 4 transformants were picked from each transformation for testing α-amylase secretion capacity.



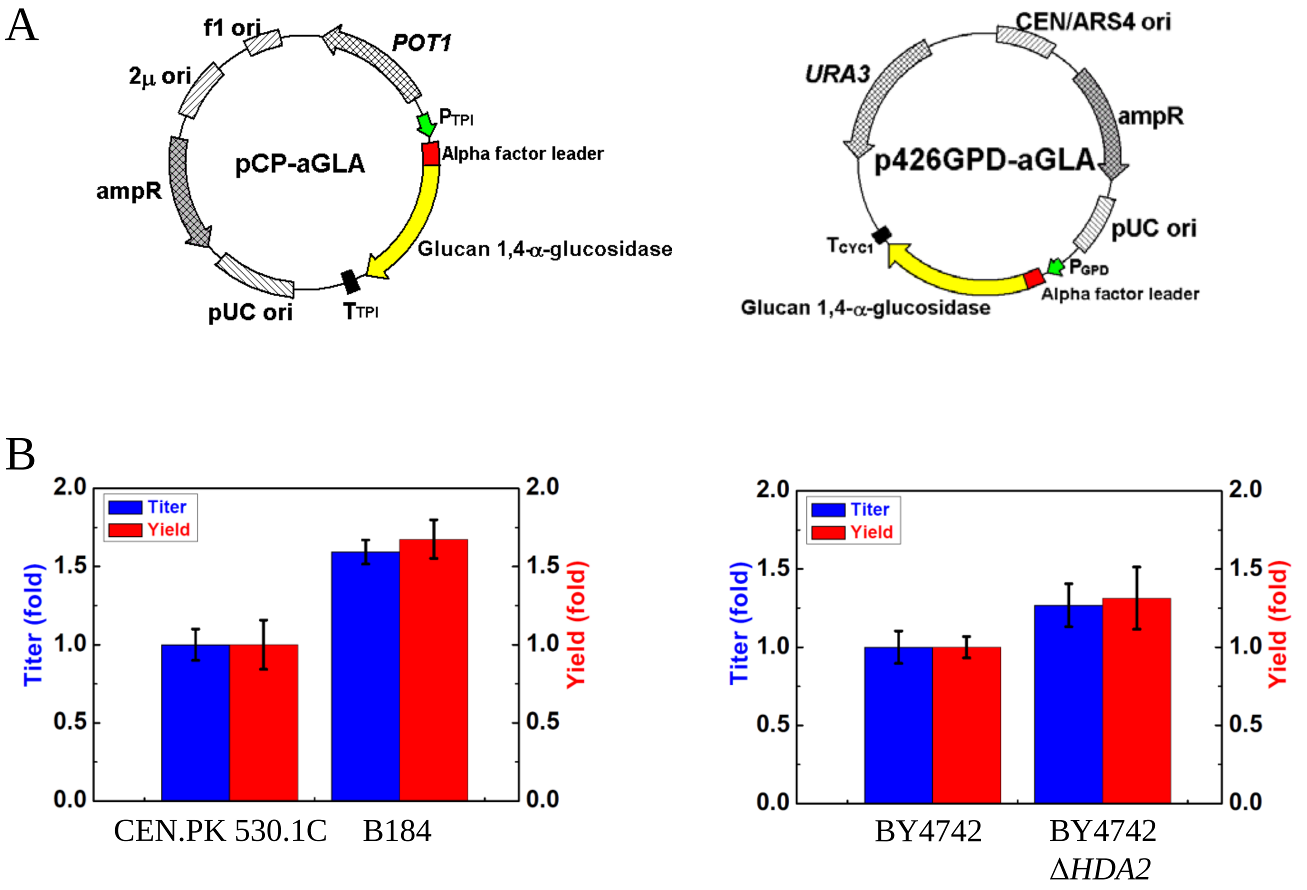
Supplementary Figure S11 Classification of all single nucleotide substitutions of mutant strains. The C to T substitution and the G to A substitution are dominant.



Supplementary Figure S12 GO Slim Process category analysis. (**A**) 146 mutated genes that give rise to altered proteins. (**B**) all 6334 genes of *S. cerevisiae*. (**C**) The ratio of the frequency of mutated genes in process category to the frequency of all genes in process category.



Supplementary Figure S13 Mutation genes of mutant strains in GO Slim Process categories.



Supplementary Figure S14 Secretion of glucan 1,4-α-glucosidase by different *S. cerevisiae* strains. (**A**) Glucan 1,4-α-glucosidase gene derived from *Rhizopus oryza*e is cloned in plasmid CPOTud and p426GPD and named pCP-aGLA and p426GPD-aGLA respectively, which are used for secretory expression in CEN.PK and BY4742 background. Alpha factor leader is used as the secretory signal peptide. (**B**) Glucan 1,4-α-glucosidase secretion increases in mutant strains compared with wildtype strains.

Table S1. Chromosome structural variations of strains.

Whole/partial chromosome duplications			
chromosome	position	samples	type
chr11	160000-320000	all strains	duplication
chr3	whole chr	MH34 and strains derived from MH34	duplication

Smaller deletions					
chromosome	position	samples	type	gene id	gene
chr4	554701-555600	all strains	deletion	YDR050C	*TPI1*
chr4	1155000-1159000	MH34 and strains derived from MH34	deletion	no gene	

Table S2. List of Genes on the chromosome III of CEN.PK 113.7D.

Systematic gene name	Standard gene name	Gene description
YCL001W	RER1	Protein involved in retention of membrane proteins
YCL001W-A		Putative protein of unknown function
YCL001W-B		Putative protein of unknown function
YCL002C		Putative protein of unknown function
YCL004W	PGS1	Phosphatidylglycerolphosphate synthase
YCL005W	LDB16	Protein of unknown function
YCL008C	STP22	Component of the ESCRT-I complex
YCL009C	ILV6	Regulatory subunit of acetolactate synthase
YCL010C	SGF29	Component of the HAT/Core module of the SAGA, SLIK, and ADA complexes
YCL011C	GBP2	Poly(A+) RNA-binding protein
YCL012C		Putative protein of unknown function
YCL014W	BUD3	Protein involved in bud-site selection
YCL016C	DCC1	Subunit of a complex with Ctf8p and Ctf18p
YCL017C	NFS1	Cysteine desulfurase
YCL018W	LEU2	Beta-isopropylmalate dehydrogenase (IMDH)
YCL021W-A		Putative protein of unknown function
YCL024W	KCC4	Protein kinase of the bud neck involved in the septin checkpoint
YCL025C	AGP1	Low-affinity amino acid permease with broad substrate range
YCL026C-A	FRM2	Type II nitroreductase, using NADH as reductant
YCL026C-B	HBN1	Protein of unknown function
YCL027W	FUS1	Membrane protein localized to the shmoo tip
YCL028W	RNQ1	[PIN(+)] prion
YCL029C	BIK1	Microtubule-associated protein
YCL030C	HIS4	Multifunctional enzyme containing phosphoribosyl-ATP pyrophosphatase
YCL031C	RRP7	Essential protein involved in rRNA processing and ribosome biogenesis
YCL032W	STE50	Adaptor protein for various signaling pathways
YCL033C	MXR2	Methionine-R-sulfoxide reductase
YCL034W	LSB5	Protein of unknown function
YCL035C	GRX1	Glutathione-dependent disulfide oxidoreductase
YCL036W	GFD2	Protein of unknown function
YCL037C	SRO9	Cytoplasmic RNA-binding protein
YCL038C	ATG22	Vacuolar integral membrane protein required for efflux of amino acids
YCL039W	GID7	Subunit of GID Complex that binds directly to central component Vid30p
YCL040W	GLK1	Glucokinase
YCL043C	PDI1	Protein disulfide isomerase
YCL044C	MGR1	Subunit of the mitochondrial (mt) i-AAA protease supercomplex
YCL045C	EMC1	Member of conserved endoplasmic reticulum membrane complex
YCL047C	POF1	Nicotinamide mononucleotide-specific adenylyltransferase (NMNAT)
YCL048W	SPS22	Protein of unknown function
YCL048W-A		Putative protein of unknown function
YCL049C		Protein of unknown function
YCL050C	APA1	AP4A phosphorylase
YCL051W	LRE1	Protein involved in control of cell wall structure and stress response
YCL052C	PBN1	Component of glycosylphosphatidylinositol-mannosyltransferase I
YCL054W	SPB1	AdoMet-dependent methyltransferase

Systematic gene name	Standard gene name	Gene description
YCL055W	KAR4	Transcription factor required for response to pheromones
YCL056C	PEX34	Protein that regulates peroxisome populations
YCL057C-A	MIC10	Conserved component of the MICOS complex
YCL057W	PRD1	Zinc metalloendopeptidase
YCL058W-A	ADF1	Transcriptional repressor encoded by the FYV5 antisense strand
YCL059C	KRR1	Nucleolar protein required for rRNA synthesis and ribosomal assembly
YCL061C	MRC1	S-phase checkpoint protein required for DNA replication
YCL063W	VAC17	Phosphoprotein involved in vacuole inheritance
YCL064C	CHA1	Catabolic L-serine (L-threonine) deaminase
YCL067C	HMLALPHA2	Silenced copy of ALPHA2 at HML
YCL073C	GEX1	Proton:glutathione antiporter
YCR002C	CDC10	Component of the septin ring, required for cytokinesis
YCR003W	MRPL32	Mitochondrial ribosomal protein of the large subunit
YCR004C	YCP4	Protein of unknown function
YCR005C	CIT2	Citrate synthase
YCR007C		Putative integral membrane protein
YCR008W	SAT4	Ser/Thr protein kinase involved in salt tolerance
YCR009C	RVS161	Amphiphysin-like lipid raft protein
YCR010C	ADY2	Acetate transporter required for normal sporulation
YCR011C	ADP1	Putative ATP-dependent permease of the ABC transporter family
YCR012W	PGK1	3-phosphoglycerate kinase
YCR014C	POL4	DNA polymerase IV
YCR015C	CTO1 (Reserved)	Putative protein of unknown function
YCR016W		Putative protein of unknown function
YCR017C	CWH43	Putative sensor/transporter protein involved in cell wall biogenesis
YCR019W	MAK32	Protein necessary for stability of L-A dsRNA-containing particles
YCR020C	PET18	Protein of unknown function
YCR020C-A	MAK31	Non-catalytic subunit of N-terminal acetyltransferase of the NatC type
YCR020W-B	HTL1	Component of the RSC chromatin remodeling complex
YCR021C	HSP30	Negative regulator of the H(+)-ATPase Pma1p
YCR023C		Vacuolar membrane protein of unknown function
YCR024C	SLM5	Mitochondrial asparaginyl-tRNA synthetase
YCR024C-A	PMP1	Regulatory subunit for the plasma membrane H(+)-ATPase Pma1p
YCR026C	NPP1	Nucleotide pyrophosphatase/phosphodiesterase
YCR027C	RHB1	Putative Rheb-related GTPase
YCR028C	FEN2	Plasma membrane H+-pantothenate symporter
YCR028C-A	RIM1	ssDNA-binding protein essential for mitochondrial genome maintenance
YCR030C	SYP1	Negative regulator of WASP-Arp23 complex
YCR031C	RPS14A	Protein component of the small (40S) ribosomal subunit
YCR032W	BPH1	Protein homologous to Chediak-Higashi syndrome and Beige proteins
YCR033W	SNT1	Subunit of the Set3C deacetylase complex
YCR034W	ELO2	Fatty acid elongase, involved in sphingolipid biosynthesis
YCR035C	RRP43	Exosome non-catalytic core component
YCR036W	RBK1	Putative ribokinase
YCR037C	PHO87	Low-affinity inorganic phosphate (Pi) transporter
YCR038C	BUD5	GTP/GDP exchange factor for Rsr1p (Bud1p)
YCR042C	TAF2	TFIID subunit (150 kDa)
YCR043C		Putative protein of unknown function

Systematic gene name	Standard gene name	Gene description
YCR044C	PER1	Protein of the endoplasmic reticulum
YCR045C	RRT12	Probable subtilisin-family protease
YCR046C	IMG1	Mitochondrial ribosomal protein of the large subunit
YCR047C	BUD23	Methyltransferase
YCR048W	ARE1	Acyl-CoA:sterol acyltransferase
YCR051W		Putative protein of unknown function
YCR052W	RSC6	Component of the RSC chromatin remodeling complex
YCR053W	THR4	Threonine synthase
YCR054C	CTR86	Essential protein of unknown function
YCR057C	PWP2	Conserved 90S pre-ribosomal component
YCR059C	YIH1	Negative regulator of eIF2 kinase Gcn2p
YCR060W	TAH1	Component of conserved R2TP complex (Rvb1-Rvb2-Tah1-Pih1)
YCR061W		Protein of unknown function
YCR063W	BUD31	Component of the SF3b subcomplex of the U2 snRNP
YCR065W	HCM1	Forkhead transcription factor
YCR066W	RAD18	E3 ubiquitin ligase
YCR067C	SED4	Integral ER membrane protein that stimulates Sar1p GTPase activity
YCR068W	ATG15	Lipase required for intravacuolar lysis of autophagic and Cvt bodies
YCR069W	CPR4	Peptidyl-prolyl cis-trans isomerase (cyclophilin)
YCR071C	IMG2	Mitochondrial ribosomal protein of the large subunit
YCR072C	RSA4	WD-repeat protein involved in ribosome biogenesis
YCR073C	SSK22	MAP kinase kinase kinase of HOG1 mitogen-activated signaling pathway
YCR073W-A	SOL2	Protein with a possible role in tRNA export
YCR075C	ERS1	Protein with similarity to human cystinosin
YCR075W-A		Putative protein of unknown function
YCR076C	FUB1	Proteasome-binding protein
YCR079W	PTC6	Mitochondrial type 2C protein phosphatase (PP2C)
YCR081W	SRB8	Subunit of the RNA polymerase II mediator complex
YCR082W	AHC2	Component of the ADA histone acetyltransferase complex
YCR083W	TRX3	Mitochondrial thioredoxin
YCR084C	TUP1	General repressor of transcription
YCR086W	CSM1	Nucleolar protein that mediates homolog segregation during meiosis I
YCR087C-A		Putative protein of unknown function
YCR088W	ABP1	Actin-binding protein of the cortical actin cytoskeleton
YCR090C		Putative protein of unknown function
YCR091W	KIN82	Putative serine/threonine protein kinase
YCR092C	MSH3	Mismatch repair protein
YCR093W	CDC39	Component of the CCR4-NOT1 core complex
YCR094W	CDC50	Endosomal protein that interacts with phospholipid flippase Drs2p
YCR095C	OCA4	Cytoplasmic protein required for replication of Brome mosaic virus
YCR098C	GIT1	Plasma membrane permease
YCR099C		Putative protein of unknown function
YCR100C		Putative protein of unknown function

Table S3. Single nucleotide variations.

Location	**Strains**										**Nucleotide change ori/mut**	**Effect**	**Systematic gene name**	**Codon change**	**Amino acid change**	**Five nucleotides context**	**trinucleotide context**
	AAC	**M715**	**MH23**	**MH34**	**A64**	**B130**	**B184**	**C120**	**D5**	**F83**							
chr0:12756		SNV	SNV	SNV	SNV	SNV	SNV	SNV	SNV	SNV	G/A	INTERGENIC				atGaa	tGa
chr1:49928				SNV	SNV	SNV	SNV	SNV	SNV		C/T	NON_SYNONYMOUS_CODING	YAL051W	Cca/Tca	P/S	atCca	tCc
chr1:83437									SNV		G/A	SYNONYMOUS_CODING	YAL032C	aaC/aaT	N/N	taGtt	aGt
chr1:121091					SNV						C/T	NON_SYNONYMOUS_CODING	YAL017W	Cca/Tca	P/S	ccCca	cCc
chr2:32778									SNV		C/T	SYNONYMOUS_CODING	YBL099W	tcC/tcT	S/S	tcCat	cCa
chr2:123579				SNV	SNV	SNV	SNV	SNV	SNV		C/T	NON_SYNONYMOUS_CODING	YBL047C	Gaa/Aaa	E/K	ttCcc	tCc
chr2:162938		SNV									C/A	UPSTREAM: 387 bases, DOWNSTREAM: 961 bases, UPSTREAM: 492 bases	YBL028C, YBL029W, YBR084C-A			taCgt	aCg
chr2:182401									SNV		C/T	NON_SYNONYMOUS_CODING	YBL017C	aGa/aAa	R/K	ttCtt	tCt
chr2:251844										SNV	G/A	UPSTREAM: 196 bases	YBR007C			taGaa	aGa
chr2:332214							SNV				C/T	SYNONYMOUS_CODING	YBR050C	gcG/gcA	A/A	ctCgc	tCg
chr2:460650							SNV				C/T	SYNONYMOUS_CODING	YBR114W	ttC/ttT	F/F	ttCca	tCc
chr2:645838								SNV			G/A	NON_SYNONYMOUS_CODING	YBR213W	Gaa/Aaa	E/K	gaGaa	aGa
chr2:707966										SNV	G/A	NON_SYNONYMOUS_CODING	YBR247C	Cgt/Tgt	R/C	acGaa	cGa
chr2:762058								SNV			G/A	SYNONYMOUS_CODING	YBR281C	ttC/ttT	F/F	gaGaa	aGa
chr3:19164			SNV							SNV	C/T	SYNONYMOUS_CODING	YCL061C	gaG/gaA	E/E	tcCtc	cCt
chr3:44524			SNV							SNV	A/T	NON_SYNONYMOUS_CODING	YCL045C	tTc/tAc	F/Y	tgAaa	gAa
chr3:68490				SNV	SNV	SNV	SNV	SNV	SNV		G/A	NON_SYNONYMOUS_CODING	YCL029C	tCg/tTg	S/L	ccGat	cGa
chr3:180425				SNV	SNV	SNV	SNV	SNV	SNV		C/T	UPSTREAM: 943 bases	YCR032W			atCga	tCg
chr4:85150							SNV				G/A	NON_SYNONYMOUS_CODING	YDL209C	cCa/cTa	P/L	ctGga	tGg
chr4:85151							SNV				G/A	NON_SYNONYMOUS_CODING	YDL209C	Cca/Tca	P/S	tgGaa	gGa
chr4:110630		SNV	SNV	SNV	SNV	SNV	SNV	SNV	SNV	SNV	C/T	NON_SYNONYMOUS_CODING	YDL194W	tCt/tTt	S/F	gtCta	tCt
chr4:192829					SNV						G/A	SYNONYMOUS_CODING	YDL146W	ttG/ttA	L/L	ttGgc	tGg
chr4:192830					SNV						G/A	NON_SYNONYMOUS_CODING	YDL146W	Gct/Act	A/T	tgGct	gGc
chr4:199553					SNV						C/T	SYNONYMOUS_CODING	YDL143W	atC/atT	I/I	atCtg	tCt
chr4:231957								SNV			C/T	SYNONYMOUS_CODING	YDL128W	gtC/gtT	V/V	gtCca	tCc
chr4:266882								SNV			C/T	SYNONYMOUS_CODING	YDL108W	Ctg/Ttg	L/L	ttCtg	tCt
chr4:277803						SNV					G/A	SYNONYMOUS_CODING	YDL102W	ctG/ctA	L/L	ctGag	tGa
chr4:305061			SNV							SNV	C/T	SYNONYMOUS_CODING	YDL084W	ttC/ttT	F/F	ttCaa	tCa
chr4:340416					SNV						C/T	UPSTREAM: 107 bases, UPSTREAM: 714 bases	YDL060W, YDL061C			ctCat	tCa
chr4:346549				SNV	SNV	SNV	SNV	SNV	SNV		C/T	NON_SYNONYMOUS_CODING	YDL058W	tCt/tTt	S/F	ttCtc	tCt
chr4:352412				SNV	SNV	SNV	SNV	SNV	SNV		C/T	NON_SYNONYMOUS_CODING	YDL056W	cCc/cTc	P/L	tcCct	cCc
chr4:414634			SNV							SNV	G/A	NON_SYNONYMOUS_CODING	YDL020C	Cca/Tca	P/S	tgGaa	gGa
chr4:439286							SNV				A/T	NON_SYNONYMOUS_CODING	YDL006W	tAt/tTt	Y/F	atAta	tAt
chr4:483697									SNV		G/A	SYNONYMOUS_CODING	YDR019C	ctC/ctT	L/L	aaGag	aGa
chr4:585289				SNV	SNV	SNV	SNV	SNV	SNV		G/A	NON_SYNONYMOUS_CODING	YDR069C	tCa/tTa	S/L	ttGat	tGa

Location	**Strains**										**Nucleotide change ori/mut**	**Effect**	**Systematic gene name**	**Codon change**	**Amino acid change**	**Five nucleotides context**	**trinucleotide context**
	AAC	**M715**	**MH23**	**MH34**	**A64**	**B130**	**B184**	**C120**	**D5**	**F83**							
chr4:585398				SNV	SNV	SNV	SNV	SNV	SNV		G/A	NON_SYNONYMOUS_CODING	YDR069C	Ctt/Ttt	L/F	aaGat	aGa
chr4:595180				SNV	SNV	SNV	SNV	SNV	SNV		C/T	NON_SYNONYMOUS_CODING	YDR074W	Cgt/Tgt	R/C	ttCgt	tCg
chr4:642292							SNV				G/A	NON_SYNONYMOUS_CODING	YDR097C	tCt/tTt	S/F	aaGag	aGa
chr4:669439						SNV					C/T	SYNONYMOUS_CODING	YDR110W	ttC/ttT	F/F	ttCgt	tCg
chr4:711836					SNV						A/G	SYNONYMOUS_CODING	YDR132C	ttT/ttC	F/F	aaAaa	aAa
chr4:966359				SNV	SNV	SNV	SNV	SNV	SNV		G/A	SYNONYMOUS_CODING	YDR255C	agC/agT	S/S	aaGct	aGc
chr4:1052323				SNV	SNV	SNV	SNV	SNV	SNV		G/A	STOP_GAINED	YDR295C	Caa/Taa	Q/*	ttGag	tGa
chr4:1121403										SNV	G/A	NON_SYNONYMOUS_CODING	YDR326C	tCc/tTc	S/F	tgGaa	gGa
chr4:1136687								SNV			C/T	UPSTREAM: 741 bases	YDR334W			ttCat	tCa
chr4:1138124									SNV		G/A	NON_SYNONYMOUS_CODING	YDR334W	Gat/Aat	D/N	aaGat	aGa
chr4:1200718									SNV		C/T	UPSTREAM: 440 bases, UPSTREAM: 62 bases	YDR363W-A , tRNA			atCtt	tCt
chr4:1219453						SNV					G/A	NON_SYNONYMOUS_CODING	YDR371W	aGa/aAa	R/K	taGaa	aGa
chr4:1223310						SNV					G/T	NON_SYNONYMOUS_CODING	YDR374C	tCc/tAc	S/Y	agGaa	gGa
chr4:1223393						INS					*/+A	FRAME_SHIFT, 1 bp insert	YDR374C			aaGta	aGt
chr4:1223394						SNV					T/C	NON_SYNONYMOUS_CODING	YDR374C	tAc/tGc	Y/C	agTaa	gTa
chr4:1248040							SNV				C/T	NON_SYNONYMOUS_CODING	YDR387C	Gaa/Aaa	E/K	ttCgt	tCg
chr4:1275639					SNV						G/A	DOWNSTREAM: 404 bases, DOWNSTREAM: 38 bases	YDR403W, YDR404C			aaGgc	aGg
chr4:1284344					SNV						A/G	NON_SYNONYMOUS_CODING	YDR407C	Ttt/Ctt	F/L	aaAat	aAa
chr4:1343273									SNV		G/A	DOWNSTREAM: 1 bases, DOWNSTREAM: 275 bases	YDR440W, YDR441C			gaGgc	aGg
chr4:1343274									SNV		G/A	DOWNSTREAM: 2 bases, DOWNSTREAM: 274 bases	YDR440W, YDR441C			agGca	gGc
chr4:1343864									SNV		G/A	NON_SYNONYMOUS_CODING	YDR441C	tCc/tTc	S/F	ggGat	gGa
chr4:1344340									SNV		G/A	DOWNSTREAM: 365 bases UPSTREAM: 247 bases	YDR443C, YDR441C			acGaa	cGa
chr4:1378469							SNV				C/T	NON_SYNONYMOUS_CODING	YDR457W	tCc/tTc	S/F	ttCca	tCc
chr4:1380160							SNV				C/T	NON_SYNONYMOUS_CODING	YDR458C	aGa/aAa	R/K	ctCtt	tCt
chr4:1381362							SNV				C/A	NON_SYNONYMOUS_CODING	YDR459C	aGt/aTt	S/I	caCta	aCt
chr4:1381372							SNV				C/T	NON_SYNONYMOUS_CODING	YDR459C	Ggt/Agt	G/S	acCag	cCa
chr4:1411478			SNV							SNV	C/T	SYNONYMOUS_CODING	YDR477W	caC/caT	H/H	caCca	aCc
chr4:1411479			SNV							SNV	C/T	NON_SYNONYMOUS_CODING	YDR477W	Cac/Tac	H/Y	acCac	cCa
chr4:1481916							SNV				G/A	SYNONYMOUS_CODING	YDR520C	caC/caT	H/H	tgGtg	gGt
chr4:1517541							SNV				G/A	DOWNSTREAM: 756 bases	YDR541C			taGaa	aGa
chr5:35587						SNV					G/A	NON_SYNONYMOUS_CODING	YEL061C	Ctt/Ttt	L/F	aaGag	aGa
chr5:75858					SNV						G/A	UPSTREAM: 279 bases DOWNSTREAM: 343 bases	YEL040W, YEL041W			agGga	gGg
chr5:75859					SNV						G/A	UPSTREAM: 278 bases DOWNSTREAM: 344 bases	YEL040W, YEL041W			ggGaa	gGa
chr5:75979					SNV						G/A	UPSTREAM: 158 bases DOWNSTREAM: 464 bases	YEL040W, YEL041W			gtGga	tGg

Location	Strains										Nucleotide change ori/mut	Effect	Systematic gene name	Codon change	Amino acid change	Five nucleotides context	trinucleotide context
	AAC	M715	MH23	MH34	A64	B130	B184	C120	D5	F83							
chr5:96599			SNV							SNV	G/A	UPSTREAM: 713 bases	YEL029C			atGaa	tGa
chr5:135270									SNV		C/T	INTERGENIC				ttCtt	tCt
chr5:181139				SNV	SNV	SNV	SNV	SNV	SNV		C/T	SYNONYMOUS_CODING	YER014W	ttC/ttT	F/F	ttCag	tCa
chr5:198811			SNV							SNV	G/A	SYNONYMOUS_CODING	YER022W	ttG/ttA	L/L	ttGaa	tGa
chr5:218967									SNV		G/A	SYNONYMOUS_CODING	YER033C	Ctg/Ttg	L/L	caGag	aGa
chr5:239830					SNV						C/T	SYNONYMOUS_CODING	YER045C	aaG/aaA	K/K	tcCtt	cCt
chr5:278493										SNV	C/T	NON_SYNONYMOUS_CODING	YER062C	Gaa/Aaa	E/K	ttCaa	tCa
chr5:292430							SNV				G/A	SYNONYMOUS_CODING	YER068W	caG/caA	Q/Q	caGaa	aGa
chr5:307408					SNV						C/T	NON_SYNONYMOUS_CODING	YER075C	Gat/Aat	D/N	atCat	tCa
chr5:308186			SNV							SNV	G/A	SYNONYMOUS_CODING	YER075C	ttC/ttT	F/F	ggGaa	gGa
chr5:409300				SNV	SNV	SNV	SNV	SNV	SNV		C/T	NON_SYNONYMOUS_CODING	YER125W	Cca/Tca	P/S	ctCca	tCc
chr5:420847								SNV			G/A	UPSTREAM: 361 bases	YER130C			ttGaa	tGa
chr5:422289						SNV					C/T	NON_SYNONYMOUS_CODING	YER131W	Cca/Tca	P/S	gaCca	aCc
chr5:422290						SNV					C/T	NON_SYNONYMOUS_CODING	YER131W	cCa/cTa	P/L	acCaa	cCa
chr5:434293				SNV	SNV	SNV	SNV	SNV	SNV		C/T	UPSTREAM: 377 bases	tRNA			atCtt	tCt
chr5:452458					SNV						C/T	SYNONYMOUS_CODING	YER141W	ttC/ttT	F/F	ttCct	tCc
chr5:452877					SNV						T/C	NON_SYNONYMOUS_CODING	YER141W	tTg/tCg	L/S	ttTgg	tTg
chr6:159482								SNV			C/T	STOP_GAINED	YFR008W	Caa/Taa	Q/*	ctCaa	tCa
chr6:181966							SNV				C/T	UPSTREAM: 131 bases	YFR017C			ctCag	tCa
chr6:190455					SNV						G/A	DOWNSTREAM: 166 bases, DOWNSTREAM: 6 bases	YFR019W, tRNA			gaGaa	aGa
chr7:10508						SNV					T/C	UPSTREAM: 237 bases	YGL258W			ccTac	cTa
chr7:14391					SNV						C/T	UPSTREAM: 411 bases, UPSTREAM: 591 bases	YGL256W, YGL257C			ctCca	tCc
chr7:14809					SNV						C/T	NON_SYNONYMOUS_CODING	YGL256W	tCc/tTc	S/F	ttCcg	tCc
chr7:56921						SNV					G/A	SYNONYMOUS_CODING	YGL234W	caG/caA	Q/Q	caGat	aGa
chr7:62380				INS	INS	INS	INS	INS	INS		*/+GA	FRAME_SHIFT, 2 bp insert	YGL232W			gtTaa	tTa
chr7:118523					SNV						C/T	NON_SYNONYMOUS_CODING	YGL201C	Gag/Aag	E/K	ctCta	tCt
chr7:118585					SNV						C/T	NON_SYNONYMOUS_CODING	YGL201C	aGg/aAg	R/K	gcCtt	cCt
chr7:213242				SNV	SNV	SNV	SNV	SNV	SNV		G/A	NON_SYNONYMOUS_CODING	YGL156W	Gaa/Aaa	E/K	atGaa	tGa
chr7:260149				SNV	SNV	SNV	SNV	SNV	SNV		C/T	STOP_GAINED	YGL133W	Cga/Tga	R/*	gtCga	tCg
chr7:289240				SNV	SNV	SNV	SNV	SNV	SNV		A/T	SYNONYMOUS_CODING	YGL117W	atA/atT	I/I	atAga	tAg
chr7:306189						SNV					G/A	NON_SYNONYMOUS_CODING	YGL107C	Ctt/Ttt	L/F	aaGaa	aGa
chr7:328295					SNV						C/T	UPSTREAM: 465 bases, DOWNSTREAM: 756 bases	tRNA, YGL095C			ttCca	tCc
chr7:344703								SNV			C/T	NON_SYNONYMOUS_CODING	YGL090W	tCc/tTc	S/F	atCcg	tCc
chr7:344704								SNV			C/T	SYNONYMOUS_CODING	YGL090W	tcC/tcT	S/S	tcCgg	cCg
chr7:368737									SNV		C/T	UPSTREAM: 193 bases, UPSTREAM: 472 bases	YGL073W, YGL075C			ttCac	tCa
chr7:369204									SNV		T/C	NON_SYNONYMOUS_CODING	YGL073W	tTa/tCa	L/S	ttTag	tTa
chr7:369279									SNV		C/T	NON_SYNONYMOUS_CODING	YGL073W	cCt/cTt	P/L	tcCta	cCt

Location	**Strains**										**Nucleotide change ori/mut**	**Effect**	**Systematic gene name**	**Codon change**	**Amino acid change**	**Five nucleotides context**	**trinucleotide context**
	AAC	**M715**	**MH23**	**MH34**	**A64**	**B130**	**B184**	**C120**	**D5**	**F83**							
chr7:416666			SNV							SNV	C/T	NON_SYNONYMOUS_CODING	YGL044C	Gat/Aat	D/N	atCtc	tCt
chr7:588482		SNV	SNV	SNV	SNV	SNV	SNV	SNV	SNV	SNV	G/A	NON_SYNONYMOUS_CODING	YGR047C	Ctt/Ttt	L/F	aaGaa	aGa
chr7:594130						SNV					C/T	SYNONYMOUS_CODING	YGR052W	ttC/ttT	F/F	ttCga	tCg
chr7:646593		SNV									G/T	NON_SYNONYMOUS_CODING	YGR083C	agC/agA	S/R	tcGct	cGc
chr7:703922					INS						*/+A	FRAME_SHIFT, 1 bp insert	YGR108W			aaAgg	aAg
chr7:732569				SNV	SNV	SNV	SNV	SNV	SNV		C/T	NON_SYNONYMOUS_CODING	YGR121C	Ggt/Agt	G/S	acCga	cCg
chr7:859863					SNV						C/T	NON_SYNONYMOUS_CODING	YGR184C	Gat/Aat	D/N	atCgc	tCg
chr7:867105			SNV							SNV	G/A	NON_SYNONYMOUS_CODING	YGR185C	Ctt/Ttt	L/F	aaGaa	aGa
chr7:867888						SNV					C/T	NON_SYNONYMOUS_CODING	YGR186W	cCc/cTc	P/L	tcCct	cCc
chr7:903295				SNV	SNV	SNV	SNV	SNV	SNV		G/A	NON_SYNONYMOUS_CODING	YGR202C	tCa/tTa	S/L	ctGat	tGa
chr7:976412						SNV					G/A	UPSTREAM: 690 bases, UPSTREAM: 65 bases	YGR243W, YGR241C			ttGat	tGa
chr7:983701			SNV							SNV	G/A	NON_SYNONYMOUS_CODING	YGR246C	gCt/gTt	A/V	taGcc	aGc
chr7:985625					SNV						G/A	DOWNSTREAM: 372 bases, UPSTREAM: 114 bases	YGR247W, YGR248W			gcGaa	cGa
chr7:1001853			SNV							SNV	G/A	SYNONYMOUS_CODING	YGR254W	ttG/ttA	L/L	ttGgt	tGg
chr7:1008542					SNV						A/T	NON_SYNONYMOUS_CODING	YGR258C	gTt/gAt	V/D	aaAct	aAc
chr7:1060822							SNV				A/G	NON_SYNONYMOUS_CODING	YGR284C	tTa/tCa	L/S	ttAat	tAa
chr8:17521		SNV	SNV	SNV	SNV	SNV	SNV	SNV	SNV	SNV	A/G	NON_SYNONYMOUS_CODING	YHL038C	aTg/aCg	M/T	tcAtg	cAt
chr8:32631				SNV	SNV	SNV	SNV	SNV	SNV		G/A	NON_SYNONYMOUS_CODING	YHL031C	tCt/tTt	S/F	aaGac	aGa
chr8:46429					SNV						G/A	STOP_GAINED	YHL026C	Caa/Taa	Q/*	ttGat	tGa
chr8:58567									SNV		G/A	SYNONYMOUS_CODING	YHL021C	Ctg/Ttg	L/L	caGga	aGg
chr8:58626									SNV		G/A	NON_SYNONYMOUS_CODING	YHL021C	tCg/tTg	S/L	gcGaa	cGa
chr8:58744									SNV		G/A	NON_SYNONYMOUS_CODING	YHL021C	Cct/Tct	P/S	agGag	gGa
chr8:77374						SNV					G/A	NON_SYNONYMOUS_CODING	YHL009C	Ctt/Ttt	L/F	aaGat	aGa
chr8:102923					SNV						T/C	SYNONYMOUS_CODING	YHR002W	ttT/ttC	F/F	ttTaa	tTa
chr8:114325									SNV		G/A	NON_SYNONYMOUS_CODING	YHR007C	cCa/cTa	P/L	gtGga	tGg
chr8:117651										SNV	T/A	NON_SYNONYMOUS_CODING	YHR009C	gAt/gTt	D/V	caTct	aTc
chr8:170565				SNV	SNV	SNV	SNV	SNV	SNV		G/A	NON_SYNONYMOUS_CODING	YHR034C	tCc/tTc	S/F	cgGag	gGa
chr8:170665				SNV	SNV	SNV	SNV	SNV	SNV		G/A	NON_SYNONYMOUS_CODING	YHR034C	Ccg/Tcg	P/S	cgGgt	gGg
chr8:170666				SNV	SNV	SNV	SNV	SNV	SNV		G/A	SYNONYMOUS_CODING	YHR034C	gaC/gaT	D/D	ggGtc	gGt
chr8:193820			SNV							SNV	G/A	NON_SYNONYMOUS_CODING	YHR047C	Cca/Tca	P/S	tgGat	gGa
chr8:272959							SNV				G/A	DOWNSTREAM: 82 bases	YHR086W			ttGta	tGt
chr8:443915								SNV			T/C	SYNONYMOUS_CODING	YHR172W	ctT/ctC	L/L	ctTta	tTt
chr8:487581			SNV							SNV	C/T	NON_SYNONYMOUS_CODING	YHR197W	aCt/aTt	T/I	caCta	aCt
chr8:515330				SNV	SNV	SNV	SNV	SNV	SNV		C/T	UPSTREAM: 343 bases	YHR210C			taCcc	aCc
chr9:96486										SNV	C/T	UPSTREAM: 114 bases, UPSTREAM: 842 bases	YIL135C, YIL134W			taCtg	aCt
chr9:109175				SNV	SNV	SNV	SNV	SNV	SNV		G/A	SYNONYMOUS_CODING	YIL129C	atC/atT	I/I	acGat	cGa

Location	Strains										Nucleotide change ori/mut	Effect	Systematic gene name	Codon change	Amino acid change	Five nucleotides context	trinucleotide context
	AAC	M715	MH23	MH34	A64	B130	B184	C120	D5	F83							
chr9:142457			SNV							SNV	G/A	UPSTREAM: 455 bases, UPSTREAM: 904 bases	YIL116W, YIL117C			ttGag	tGa
chr9:175291					INS						*/+A	DOWNSTREAM: 17 bases, UPSTREAM: 403 bases, DOWNSTREAM: 187 bases	YIL101C, YIL102C, tRNA			aaAtg	aAt
chr9:183945					SNV						C/T	NON_SYNONYMOUS_CODING	YIL095W	cCa/cTa	P/L	tcCac	cCa
chr9:329312					SNV						C/T	SYNONYMOUS_CODING	YIL013C	aaG/aaA	K/K	gcCtt	cCt
chr9:334662				SNV	SNV	SNV	SNV	SNV	SNV		C/T	NON_SYNONYMOUS_CODING	YIL011W	tCt/tTt	S/F	ttCtt	tCt
chr9:367955									SNV		G/A	NON_SYNONYMOUS_CODING	YIR006C	tCa/tTa	S/L	ttGaa	tGa
chr9:370759				SNV	SNV	SNV	SNV	SNV	SNV		C/T	UPSTREAM: 56 bases, UPSTREAM: 343 bases, UPSTREAM: 451 bases	tRNA, YIR007W, YIR006C			ccCaa	cCa
chr9:387383					SNV						G/A	INTERGENIC				agGag	gGa
chr9:387394					SNV						G/A	INTERGENIC				aaGaa	aGa
chr9:436222										SNV	G/A	UPSTREAM: 236 bases, DOWNSTREAM: 824 bases	YIR042C,YHL048W			atGat	tGa
chr10:97965										SNV	G/A	STOP_GAINED	YJL162C	Caa/Taa	Q/*	ttGat	tGa
chr10:117718								SNV			G/A	NON_SYNONYMOUS_CODING	YJL153C	Ctt/Ttt	L/F	aaGgg	aGg
chr10:117719								SNV			G/A	SYNONYMOUS_CODING	YJL153C	gcC/gcT	A/A	agGgc	gGg
chr10:211469						SNV					G/A	DOWNSTREAM: 104 bases	YJL103C			aaGaa	aGa
chr10:250095					SNV						C/T	SYNONYMOUS_CODING	YJL089W	tcC/tcT	S/S	tcCct	cCc
chr10:255973									SNV		C/T	NON_SYNONYMOUS_CODING	YJL085W	tCt/tTt	S/F	ttCta	tCt
chr10:270895								SNV			C/T	NON_SYNONYMOUS_CODING	YJL080C	Ggt/Agt	G/S	acCcg	cCc
chr10:284492								SNV			C/T	SYNONYMOUS_CODING	YJL074C	caG/caA	Q/Q	ttCtg	tCt
chr10:310014					SNV						C/A	NON_SYNONYMOUS_CODING	YJL058C	Gca/Tca	A/S	tgCat	gCa
chr10:310636					SNV						G/A	DOWNSTREAM: 46 bases, UPSTREAM: 199 bases	YJL057C, YJL058C			aaGta	aGt
chr10:310644					SNV						A/T	DOWNSTREAM: 38 bases, UPSTREAM: 207 bases	YJL057C, YJL058C			atAaa	tAa
chr10:350162									SNV		C/T	DOWNSTREAM: 870 bases, UPSTREAM: 76 bases	YJL039C, YJL041W			acCaa	cCa
chr10:350766									SNV		T/A	DOWNSTREAM: 266 bases, DOWNSTREAM: 109 bases	YJL039C, YJL041W			aaTta	aTt
chr10:350772									SNV		T/C	DOWNSTREAM: 260 bases, DOWNSTREAM: 115 bases	YJL039C, YJL041W			ttTaa	tTa
chr10:373924			SNV							SNV	C/T	UPSTREAM: 297 bases, UPSTREAM: 992 bases, UPSTREAM: 559 bases	tRNA, YJL026W YJL029C			atCtt	tCt
chr10:420954								SNV			C/T	SYNONYMOUS_CODING	YJR001W	Ctg/Ttg	L/L	ttCtg	tCt
chr10:427541					SNV						G/A	UPSTREAM: 169 bases, UPSTREAM: 893 bases	YJR004C, YJR005W			taGaa	aGa
chr10:515880										SNV	C/T	SYNONYMOUS_CODING	YJR052W	ttC/ttT	F/F	ttCat	tCa
chr10:519489								SNV			T/C	SYNONYMOUS_CODING	YJR054W	acT/acC	T/T	acTtt	cTt
chr10:592960										SNV	G/A	NON_SYNONYMOUS_CODING	YJR095W	Ggt/Agt	G/S	cgGgt	gGg

Location	Strains										Nucleotide change ori/mut	Effect	Systematic gene name	Codon change	Amino acid change	Five nucleotides context	trinucleotide context
	AAC	M715	MH23	MH34	A64	B130	B184	C120	D5	F83							
chr10:594264			SNV							SNV	C/T	SYNONYMOUS_CODING	YJR096W	taC/taT	Y/Y	taCtg	aCt
chr10:632913				SNV	SNV	SNV	SNV	SNV	SNV		C/T	SYNONYMOUS_CODING	YJR122W	ttC/ttT	F/F	ttCga	tCg
chr10:649540				SNV	SNV	SNV	SNV	SNV	SNV		G/A	SYNONYMOUS_CODING	YJR130C	ttC/ttT	F/F	atGaa	tGa
chr10:701173				SNV	SNV	SNV	SNV	SNV	SNV		G/A	INTERGENIC				caGaa	aGa
chr11:20308							SNV				G/A	INTERGENIC				caGag	aGa
chr11:50065			SNV							SNV	C/T	SYNONYMOUS_CODING	YKL205W	atC/atT	I/I	atCga	tCg
chr11:102903					SNV						T/C	NON_SYNONYMOUS_CODING	YKL182W	tTa/tCa	L/S	gtTac	tTa
chr11:314683				SNV	SNV	SNV	SNV	SNV	SNV		C/T	UPSTREAM: 107 bases	YKL067W			ttCgt	tCg
chr11:421395						SNV					T/C	DOWNSTREAM: 23 bases, UPSTREAM: 185 bases	YKL010C, YKL011C			ctTaa	tTa
chr11:509760			SNV							SNV	G/A	SYNONYMOUS_CODING	YKR036C	acC/acT	T/T	gcGgt	cGg
chr11:632200							SNV				C/T	SYNONYMOUS_CODING	YKR097W	atC/atT	I/I	atCct	tCc
chr11:654652									SNV		G/A	NON_SYNONYMOUS_CODING	YKR103W	Gaa/Aaa	E/K	gaGaa	aGa
chr11:654754									SNV		G/A	NON_SYNONYMOUS_CODING	YKR103W	Gga/Aga	G/R	atGga	tGg
chr11:654755									SNV		G/A	NON_SYNONYMOUS_CODING	YKR103W	gGa/gAa	G/E	tgGag	gGa
chr11:654970									SNV		G/A	NON_SYNONYMOUS_CODING	YKR103W	Gac/Aac	D/N	ctGac	tGa
chr12:3811				SNV	SNV	SNV	SNV	SNV	SNV		G/A	NON_SYNONYMOUS_CODING	YLL061W	Ggt/Agt	G/S	aaGgt	aGg
chr12:3812				SNV	SNV	SNV	SNV	SNV	SNV		G/A	NON_SYNONYMOUS_CODING	YLL061W	gGt/gAt	G/D	agGta	gGt
chr12:4208				SNV	SNV	SNV	SNV	SNV	SNV		G/A	STOP_GAINED	YLL061W	tGg/tAg	W/*	atGgt	tGg
chr12:86013			SNV							SNV	C/T	SYNONYMOUS_CODING	YLL021W	gtC/gtT	V/V	gtCtc	tCt
chr12:101816							SNV				C/T	STOP_GAINED	YLL015W	Caa/Taa	Q/*	ctCaa	tCa
chr12:115820							SNV				G/A	UPSTREAM: 148 bases, UPSTREAM: 967 bases, DOWNSTREAM: 443 bases	YLL010C, YLL008W, YLL009C			gcGat	cGa
chr12:116116							SNV				G/T	UPSTREAM: 444 bases, UPSTREAM: 671 bases, DOWNSTREAM: 147 bases	YLL010C, YLL008W, YLL009C			gaGga	aGg
chr12:116117							SNV				G/A	UPSTREAM: 445 bases, UPSTREAM: 670 bases, DOWNSTREAM: 146 bases	YLL010C, YLL008W, YLL009C			agGac	gGa
chr12:121186									SNV		C/T	NON_SYNONYMOUS_CODING	YLL007C	Gaa/Aaa	E/K	ttCat	tCa
chr12:121505									SNV		C/T	UPSTREAM: 126 bases, UPSTREAM: 160 bases	YLL006W, YLL007C			ttCaa	tCa
chr12:132817				SNV	SNV	SNV	SNV	SNV	SNV		G/A	UPSTREAM: 98 bases, DOWNSTREAM: 191 bases	YLL001W, YLL002W			atGaa	tGa
chr12:233314					SNV						C/T	SYNONYMOUS_CODING	YLR056W	ttC/ttT	F/F	ttCct	tCc
chr12:237324			SNV							SNV	G/A	SYNONYMOUS_CODING	YLR058C	ttC/ttT	F/F	ttGaa	tGa
chr12:322125			SNV							SNV	G/A	NON_SYNONYMOUS_CODING	YLR097C	Cat/Tat	H/Y	atGga	tGg
chr12:355123						SNV					G/A	DOWNSTREAM: 807 bases, UPSTREAM: 21 bases	YLR109W, YLR110C			gcGaa	cGa
chr12:375613								SNV			G/A	UPSTREAM: 337 bases	YLR121C			acGag	cGa
chr12:378341					SNV						G/A	UPSTREAM: 149 bases	YLR125W			ggGat	gGa

Location	**Strains**										**Nucleotide change ori/mut**	**Effect**	**Systematic gene name**	**Codon change**	**Amino acid change**	**Five nucleotides context**	**trinucleotide context**
	AAC	**M715**	**MH23**	**MH34**	**A64**	**B130**	**B184**	**C120**	**D5**	**F83**							
chr12:379714									SNV		C/T	DOWNSTREAM: 814 bases DOWNSTREAM: 57 bases	YLR125W, YLR126C			acCtt	cCt
chr12:483636					SNV						G/A	UPSTREAM: 587 bases, DOWNSTREAM: 942 bases, UPSTREAM: 311 bases	YLR166C, YLR168C, YLR167W			ctGgg	tGg
chr12:483884								SNV			G/A	UPSTREAM: 835 bases, DOWNSTREAM: 694 bases, UPSTREAM: 63 bases	YLR166C, YLR168C, YLR167W			aaGaa	aGa
chr12:504134				SNV	SNV	SNV	SNV	SNV	SNV		C/T	SYNONYMOUS_CODING	YLR182W	gtC/gtT	V/V	gtCaa	tCa
chr12:660821						SNV					G/A	NON_SYNONYMOUS_CODING	YLR266C	aCt/aTt	T/I	aaGtt	aGt
chr12:674166					SNV						T/C	NON_SYNONYMOUS_CODING	YLR273C	Aat/Gat	N/D	atTag	tTa
chr12:686228						SNV					T/A	NON_SYNONYMOUS_CODING	YLR278C	Aat/Tat	N/Y	atTat	tTa
chr12:752156								SNV			A/T	NON_SYNONYMOUS_CODING	YLR318W	Agc/Tgc	S/C	atAgc	tAg
chr12:805637					SNV						A/T	STOP_GAINED	YLR345W	Aaa/Taa	K/*	atAaa	tAa
chr12:856143					SNV						G/A	NON_SYNONYMOUS_CODING	YLR373C	cCg/cTg	P/L	tcGgg	cGg
chr12:856144					SNV						G/A	NON_SYNONYMOUS_CODING	YLR373C	Ccg/Tcg	P/S	cgGgt	gGg
chr12:899027										SNV	G/T	NON_SYNONYMOUS_CODING	YLR397C	gaC/gaA	D/E	gaGtc	aGt
chr12:923315						SNV					G/A	SYNONYMOUS_CODING	YLR410W	aaG/aaA	K/K	aaGat	aGa
chr12:973542				SNV	SNV	SNV	SNV	SNV	SNV		C/T	NON_SYNONYMOUS_CODING	YLR427W	tCa/tTa	S/L	ttCaa	tCa
chr12:1013307				SNV	SNV	SNV	SNV	SNV	SNV		G/A	UPSTREAM: 546 bases, UPSTREAM: 415 bases	YLR448W, YLR447C			ttGat	tGa
chr12:1020872								SNV			C/T	DOWNSTREAM: 110 bases	YLR450W			ctCtt	tCt
chr12:1032728									SNV		T/A	STOP_GAINED	YLR454W	tTa/tAa	L/*	ttTaa	tTa
chr13:86691					SNV						G/T	UPSTREAM: 265 bases	YML088W			atGct	tGc
chr13:118427					SNV						A/G	SYNONYMOUS_CODING	YML073C	tcT/tcC	S/S	ttAga	tAg
chr13:118428					SNV						G/A	NON_SYNONYMOUS_CODING	YML073C	tCt/tTt	S/F	taGag	aGa
chr13:147095			SNV							SNV	C/T	NON_SYNONYMOUS_CODING	YML060W	Cct/Tct	P/S	ttCct	tCc
chr13:183767					SNV						G/A	SYNONYMOUS_CODING	YML049C	ttC/ttT	F/F	ttGaa	tGa
chr13:223300				SNV	SNV	SNV	SNV	SNV	SNV		G/A	DOWNSTREAM: 956 bases, UPSTREAM: 114 bases, UPSTREAM: 159 bases	YML021C, YML023C, YML022W			gtGgg	tGg
chr13:223301				SNV	SNV	SNV	SNV	SNV	SNV		G/A	DOWNSTREAM: 955 bases, UPSTREAM: 115 bases, UPSTREAM: 158 bases	YML021C, YML023C, YML022W			tgGga	gGg
chr13:251534						SNV					G/A	SYNONYMOUS_CODING	YML006C	ttC/ttT	F/F	ttGaa	tGa
chr13:274080					SNV						C/T	NON_SYNONYMOUS_CODING	YMR006C	gGt/gAt	G/D	caCca	aCc
chr13:288113					SNV						T/C	SYNONYMOUS_CODING	YMR012W	atT/atC	I/I	atTga	tTg
chr13:318074				SNV	SNV	SNV	SNV	SNV	SNV		G/A	NON_SYNONYMOUS_CODING	YMR025W	Gag/Aag	E/K	acGag	cGa
chr13:470350						SNV					G/A	STOP_GAINED	YMR105C	Caa/Taa	Q/*	ttGat	tGa
chr13:486426				SNV	SNV	SNV	SNV	SNV	SNV		G/A	SYNONYMOUS_CODING	YMR110C	ttC/ttT	F/F	aaGaa	aGa
chr13:487185				SNV	SNV	SNV	SNV	SNV	SNV		G/A	SYNONYMOUS_CODING	YMR111C	aaC/aaT	N/N	tgGtt	gGt
chr13:556291					SNV						C/T	SYNONYMOUS_CODING	YMR149W	tcC/tcT	S/S	tcCtc	cCt
chr13:613022						SNV					C/T	SYNONYMOUS_CODING	YMR178W	atC/atT	I/I	atCat	tCa

Location	**Strains**										**Nucleotide change ori/mut**	**Effect**	**Systematic gene name**	**Codon change**	**Amino acid change**	**Five nucleotides context**	**trinucleotide context**
	AAC	**M715**	**MH23**	**MH34**	**A64**	**B130**	**B184**	**C120**	**D5**	**F83**							
chr13:658634						SNV					C/T	NON_SYNONYMOUS_CODING	YMR199W	tCa/tTa	S/L	ttCat	tCa
chr13:680767							SNV				C/T	NON_SYNONYMOUS_CODING	YMR209C	Gat/Aat	D/N	atCtc	tCt
chr13:722740						SNV					A/T	NON_SYNONYMOUS_CODING	YMR229C	cTa/cAa	L/Q	ctAgt	tAg
chr13:726463		SNV	SNV	SNV	SNV	SNV	SNV	SNV	SNV	SNV	G/A	UPSTREAM: 626 bases, UPSTREAM: 665 bases	YMR229C, YMR230W			aaGaa	aGa
chr13:731688							SNV				G/A	NON_SYNONYMOUS_CODING	YMR232W	Gat/Aat	D/N	atGat	tGa
chr13:779011					SNV						G/A	SYNONYMOUS_CODING	YMR259C	ttC/ttT	F/F	caGaa	aGa
chr13:810872						SNV					G/A	NON_SYNONYMOUS_CODING	YMR275C	cCa/cTa	P/L	ttGgg	tGg
chr13:810873						SNV					G/A	NON_SYNONYMOUS_CODING	YMR275C	Cca/Tca	P/S	tgGga	gGg
chr13:819980									SNV		G/A	NON_SYNONYMOUS_CODING	YMR279C	Ctt/Ttt	L/F	aaGaa	aGa
chr13:821772									SNV		G/A	STOP_GAINED	YMR280C	Caa/Taa	Q/*	ttGag	tGa
chr13:898767										SNV	C/T	UPSTREAM: 589 bases, DOWNSTREAM: 387 bases	YMR316W, YMR315W			ttCga	tCg
chr14:58165						SNV					A/G	SYNONYMOUS_CODING	YNL301C	tcT/tcC	S/S	gaAga	aAg
chr14:58173						SNV					G/A	NON_SYNONYMOUS_CODING	YNL301C	Ctt/Ttt	L/F	aaGat	aGa
chr14:59303										SNV	C/T	UPSTREAM: 752 bases, UPSTREAM: 430 bases	YNL301C, YNL300W			gtCac	tCa
chr14:162701									SNV		G/A	NON_SYNONYMOUS_CODING	YNL254C	tCt/tTt	S/F	taGaa	aGa
chr14:187347										SNV	A/G	NON_SYNONYMOUS_CODING	YNL242W	cAa/cGa	Q/R	tcAaa	cAa
chr14:272286						SNV					C/T	SYNONYMOUS_CODING	YNL192W	atC/atT	I/I	atCgt	tCg
chr14:275202						SNV					G/A	SYNONYMOUS_CODING	YNL191W	ttG/ttA	L/L	ttGga	tGg
chr14:309348					SNV						G/A	NON_SYNONYMOUS_CODING	YNL172W	aGa/aAa	R/K	aaGag	aGa
chr14:373248				SNV	SNV	SNV	SNV	SNV	SNV		A/T	DOWNSTREAM: 767 bases, DOWNSTREAM: 300 bases, DOWNSTREAM: 33 bases	YNL132W, YNL130C, YNL131W			ttAga	tAg
chr14:381866						SNV					G/A	SYNONYMOUS_CODING	YNL126W	gaG/gaA	E/E	gaGag	aGa
chr14:393947			SNV							SNV	G/A	SYNONYMOUS_CODING	YNL121C	Cta/Tta	L/L	taGag	aGa
chr14:404160						SNV					T/C	NON_SYNONYMOUS_CODING	YNL115C	cAa/cGa	Q/R	ctTga	tTg
chr14:461297				SNV	SNV	SNV	SNV	SNV	SNV		A/T	SYNONYMOUS_CODING	YNL085W	atA/atT	I/I	atAtt	tAt
chr14:461298				SNV	SNV	SNV	SNV	SNV	SNV		T/A	NON_SYNONYMOUS_CODING	YNL085W	Ttc/Atc	F/I	taTtc	aTt
chr14:527549						SNV					C/T	NON_SYNONYMOUS_CODING	YNL051W	tCc/tTc	S/F	ttCct	tCc
chr14:566084			SNV							SNV	C/T	INTERGENIC				aaCca	aCc
chr14:566085			SNV							SNV	C/T	INTERGENIC				acCat	cCa
chr14:585613			SNV							SNV	C/T	NON_SYNONYMOUS_CODING	YNL022C	aGa/aAa	R/K	ctCta	tCt
chr14:650938					SNV						G/A	NON_SYNONYMOUS_CODING	YNR016C	cCt/cTt	P/L	caGgg	aGg
chr15:9510										SNV	C/T	UPSTREAM: 25 bases	YOL163W			tcCct	cCc
chr15:60408					SNV						G/A	SYNONYMOUS_CODING	YOL139C	gcC/gcT	A/A	aaGgc	aGg
chr15:61254					SNV						G/A	SYNONYMOUS_CODING	YOL138C	ctC/ctT	L/L	tcGag	cGa
chr15:167264							SNV				C/T	DOWNSTREAM: 411 bases	YOL083W			tcCaa	cCa
chr15:275588			SNV							SNV	C/T	NON_SYNONYMOUS_CODING	YOL025W	cCc/cTc	P/L	ccCca	cCc
chr15:279919									SNV		C/T	NON_SYNONYMOUS_CODING	YOL023W	cCt/cTt	P/L	tcCtc	cCt

Location	Strains										Nucleotide change ori/mut	Effect	Systematic gene name	Codon change	Amino acid change	Five nucleotides context	trinucleotide context
	AAC	M715	MH23	MH34	A64	B130	B184	C120	D5	F83							
chr15:315162				SNV	SNV	SNV	SNV	SNV	SNV		G/A	NON_SYNONYMOUS_CODING	YOL006C	tCt/tTt	S/F	caGag	aGa
chr15:353053			SNV							SNV	C/T	NON_SYNONYMOUS_CODING	YOR011W	Ctt/Ttt	L/F	ttCtt	tCt
chr15:361167						SNV					G/A	UPSTREAM: 57 bases, UPSTREAM: 271 bases	YOR016C, YOR017W			gtGaa	tGa
chr15:375446			SNV							SNV	G/A	NON_SYNONYMOUS_CODING	YOR022C	Cct/Tct	P/S	agGag	gGa
chr15:455418						SNV					G/A	NON_SYNONYMOUS_CODING	YOR069W	Gaa/Aaa	E/K	taGaa	aGa
chr15:455718						SNV					G/A	NON_SYNONYMOUS_CODING	YOR069W	Gaa/Aaa	E/K	agGaa	gGa
chr15:455790						SNV					G/A	NON_SYNONYMOUS_CODING	YOR069W	Gat/Aat	D/N	aaGat	aGa
chr15:496253							SNV				C/T	NON_SYNONYMOUS_CODING	YOR092W	tCc/tTc	S/F	ttCca	tCc
chr15:535728					SNV						C/T	NON_SYNONYMOUS_CODING	YOR113W	tCt/tTt	S/F	ttCta	tCt
chr15:606212				SNV	SNV	SNV	SNV	SNV	SNV		C/T	UPSTREAM: 205 bases, UPSTREAM: 138 bases	YOR147W, YOR145C			ttCcc	tCc
chr15:617684					SNV						G/A	NON_SYNONYMOUS_CODING	YOR152C	Cca/Tca	P/S	tgGaa	gGa
chr15:667488					SNV						T/A	DOWNSTREAM: 275 bases, UPSTREAM: 408 bases	YOR178C, YOR177C			taTaa	aTa
chr15:679700					SNV						C/T	SYNONYMOUS_CODING	YOR184W	tcC/tcT	S/S	tcCct	cCc
chr15:680961			SNV							SNV	G/A	DOWNSTREAM: 380 bases, DOWNSTREAM: 520 bases	YOR185C, YOR184W			aaGag	aGa
chr15:685862										SNV	C/T	NON_SYNONYMOUS_CODING	YOR188W	Cat/Tat	H/Y	tcCat	cCa
chr15:765016						SNV					T/A	STOP_GAINED	YOR227W	tTa/tAa	L/*	ttTaa	tTa
chr15:776687										SNV	C/T	NON_SYNONYMOUS_CODING	YOR233W	Cat/Tat	H/Y	ctCat	tCa
chr15:817509					SNV						C/T	NON_SYNONYMOUS_CODING	YOR262W	cCg/cTg	P/L	tcCgg	cCg
chr15:918128		SNV									G/A	NON_SYNONYMOUS_CODING	YOR321W	Gcg/Acg	A/T	acGcg	cGc
chr15:930648			SNV							SNV	G/A	NON_SYNONYMOUS_CODING	YOR327C	cCt/cTt	P/L	taGga	aGg
chr15:977525						SNV					C/T	NON_SYNONYMOUS_CODING	YOR344C	Gaa/Aaa	E/K	ttCat	tCa
chr15:1025167			SNV							SNV	G/A	SYNONYMOUS_CODING	YOR365C	ctC/ctT	L/L	ttGag	tGa
chr15:1039743					SNV						C/T	UPSTREAM: 70 bases, DOWNSTREAM: 381 bases	YOR374W, YOR373W			ttCtt	tCt
chr15:1040094					SNV						C/T	SYNONYMOUS_CODING	YOR374W	gcC/gcT	A/A	gcCtt	cCt
chr16:64912										SNV	G/A	DOWNSTREAM: 3 bases	YPL256C			agGaa	gGa
chr16:72809				SNV	SNV	SNV	SNV	SNV	SNV		G/A	NON_SYNONYMOUS_CODING	YPL253C	Cct/Tct	P/S	agGtc	gGt
chr16:91710			SNV							SNV	C/T	NON_SYNONYMOUS_CODING	YPL242C	aGa/aAa	R/K	atCta	tCt
chr16:91711			SNV							SNV	T/C	NON_SYNONYMOUS_CODING	YPL242C	Aga/Gga	R/G	tcTat	cTa
chr16:146402					SNV						G/A	STOP_GAINED	YPL216W	tgG/tgA	W/*	tgGgc	gGg
chr16:180376						SNV					G/A	NON_SYNONYMOUS_CODING	YPL194W	gGa/gAa	G/E	agGaa	gGa
chr16:224253						SNV					G/A	NON_SYNONYMOUS_CODING	YPL172C	Cct/Tct	P/S	agGat	gGa
chr16:251141			SNV							SNV	G/A	SYNONYMOUS_CODING	YPL159C	atC/atT	I/I	ttGat	tGa
chr16:274950					SNV						C/T	STOP_GAINED	YPL147W	Caa/Taa	Q/*	ttCaa	tCa
chr16:360804							SNV				C/T	NON_SYNONYMOUS_CODING	YPL101W	Ccg/Tcg	P/S	ctCcg	tCc
chr16:385753			SNV							SNV	G/A	NON_SYNONYMOUS_CODING	YPL086C	tCg/tTg	S/L	gcGaa	cGa

Location	**Strains**										**Nucleotide change ori/mut**	**Effect**	**Systematic gene name**	**Codon change**	**Amino acid change**	**Five nucleotides context**	**trinucleotide context**
	AAC	**M715**	**MH23**	**MH34**	**A64**	**B130**	**B184**	**C120**	**D5**	**F83**							
chr16:388199			SNV							SNV	C/T	UPSTREAM: 285 bases	YPL085W			caCtg	aCt
chr16:463605						SNV					C/T	NON_SYNONYMOUS_CODING	YPL049C	Gag/Aag	E/K	ctCta	tCt
chr16:464746				SNV	SNV	SNV	SNV	SNV	SNV		G/A	NON_SYNONYMOUS_CODING	YPL048W	Gac/Aac	D/N	ttGac	tGa
chr16:476452			SNV							SNV	T/A	SYNONYMOUS_CODING	YPL040C	ctA/ctT	L/L	ttTag	tTa
chr16:489492			SNV							SNV	G/A	NON_SYNONYMOUS_CODING	YPL032C	cCt/cTt	P/L	aaGga	aGg
chr16:489493			SNV							SNV	G/A	NON_SYNONYMOUS_CODING	YPL032C	Cct/Tct	P/S	agGag	gGa
chr16:552265									SNV		G/A	SYNONYMOUS_CODING	YPL003W	caG/caA	Q/Q	caGta	aGt
chr16:570898						SNV					C/T	NON_SYNONYMOUS_CODING	YPR007C	gGa/gAa	G/E	ttCct	tCc
chr16:571076						SNV					T/C	NON_SYNONYMOUS_CODING	YPR007C	Aga/Gga	R/G	tcTaa	cTa
chr16:571094							SNV				C/T	NON_SYNONYMOUS_CODING	YPR007C	Gaa/Aaa	E/K	ttCga	tCg
chr16:595155				SNV	SNV	SNV	SNV	SNV	SNV		G/A	NON_SYNONYMOUS_CODING	YPR018W	Gaa/Aaa	E/K	atGaa	tGa
chr16:610328					SNV						C/T	UPSTREAM: 369 bases, UPSTREAM: 81 bases	YPR023C, YPR024W			agCtt	gCt
chr16:651647					SNV						G/A	NON_SYNONYMOUS_CODING	YPR042C	tCa/tTa	S/L	ctGaa	tGa
chr16:665315						SNV					T/C	SYNONYMOUS_CODING	YPR051W	Ttg/Ctg	L/L	acTtg	cTt
chr16:696881									SNV		C/T	UPSTREAM: 145 bases, DOWNSTREAM: 183 bases	YPR075C, YPR078C			ttCtg	tCt
chr16:711195								SNV			G/A	DOWNSTREAM: 123 bases, DOWNSTREAM: 141 bases	YPR086W, YPR088C			taGaa	aGa
chr16:714202								SNV			T/C	NON_SYNONYMOUS_CODING	YPR089W	tTa/tCa	L/S	ctTat	tTa
chr16:885517				SNV	SNV	SNV	SNV	SNV	SNV		C/T	SYNONYMOUS_CODING	YPR171W	caC/caT	H/H	caCcc	aCc
chr16:893015						SNV					G/A	NON_SYNONYMOUS_CODING	YPR178W	Gat/Aat	D/N	taGat	aGa
chr16:895637			SNV							SNV	G/A	STOP_GAINED	YPR179C	Caa/Taa	Q/*	ttGat	tGa
chr16:907673							SNV				C/T	NON_SYNONYMOUS_CODING	YPR185W	Ctc/Ttc	L/F	ttCtc	tCt
chr16:935323					SNV						C/T	SYNONYMOUS_CODING	YPR198W	gaC/gaT	D/D	gaCtt	aCt

Table S4. Protein altering genes.

Location	Strains										Nuc change	Effect	Systematic gene name	Cdn change	Amino acid change	Standard gene name	Gene description	Link to SGD
	AAC	M715	MH23	MH34	A64	B130	B184	C120	D5	F83								
chr4:110630		SNV	SNV	SNV	SNV	SNV	SNV	SNV	SNV	SNV	C/T	Nonsynonymous	YDL194W	tCt/tTt	S97F	SNF3	Plasma membrane low glucose sensor, regulates glucose transport; contains 12 predicted transmembrane segments and a long C-terminal tail required for induction of hexose transporters; also senses fructose and mannose; SNF3 has a paralog, RGT2, that arose from the whole genome duplication	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=SNF3
chr7:588482		SNV	SNV	SNV	SNV	SNV	SNV	SNV	SNV	SNV	G/A	Nonsynonymous	YGR047C	Ctt/Ttt	L273F	TFC4	Subunit of RNA polymerase III transcription initiation factor complex; one of six subunits of RNA polymerase III transcription initiation factor complex (TFIIIC); part of the TauA domain of TFIIIC that binds BoxA DNA promoter sites of tRNA and similar genes; has TPR motifs; human homolog is TFIIIC-102	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=TFC4
chr8:17521		SNV	SNV	SNV	SNV	SNV	SNV	SNV	SNV	SNV	A/G	Nonsynonymous	YHL038C	aTg/aCg	M385T	CBP2	Required for splicing of the group I intron bI5 of the COB pre-mRNA; nuclear-encoded mitochondrial protein that binds to the RNA to promote splicing; also involved in but not essential for splicing of the COB bI2 intron and the intron in the 21S rRNA gene	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=CBP2
chr3:44524			SNV							SNV	A/T	Nonsynonymous	YCL045C	tTc/tAc	F671Y	EMC1	Member of conserved endoplasmic reticulum membrane complex; involved in efficient folding of proteins in the ER; null mutant displays induction of the unfolded protein response; interacts with Gal80p; homologous to worm H17B01.4/EMC-1, fly CG2943, and human KIAA0090	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=EMC1
chr4:414634			SNV							SNV	G/A	Nonsynonymous	YDL020C	Cca/Tca	P340S	RPN4	Transcription factor that stimulates expression of proteasome genes; Rpn4p levels are in turn regulated by the 26S proteasome in a negative feedback control mechanism; RPN4 is transcriptionally regulated by various stress responses; relative distribution to the nucleus increases upon DNA replication stress	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=RPN4
chr4:1411479			SNV							SNV	C/T	Nonsynonymous	YDR477W	Cac/Tac	H20Y	SNF1	AMP-activated serine/threonine protein kinase; found in a complex containing Snf4p and members of the Sip1p/Sip2p/Gal83p family; required for transcription of glucose-repressed genes, thermotolerance, sporulation, and peroxisome biogenesis; involved in regulation of the nucleocytoplasmic shuttling of Hxk2p; regulates filamentous growth in response to starvation	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=SNF1
chr7:416666			SNV							SNV	C/T	Nonsynonymous	YGL044C	Gat/Aat	D68N	RNA15	Component of the cleavage and polyadenylation factor I (CF I); CF 1, composed of the CF 1A complex (Rna14p, Rna15p, Clp1p, Pcf11p) and Hrp1, is involved in cleavage and polyadenylation of mRNA 3' ends; interacts with the A-rich polyadenylation signal in complex with Rna14p and Hrp1p; mutant displays reduced transcription elongation in the G-less-based run-on (GLRO) assay; required for gene looping	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=RNA15
chr7:867105			SNV							SNV	G/A	Nonsynonymous	YGR185C	Ctt/Ttt	L76F	TYS1	Cytoplasmic tyrosyl-tRNA synthetase; required for cytoplasmic protein synthesis; interacts with positions 34 and 35 of the tRNATyr anticodon; mutations in human ortholog YARS are associated with Charcot-Marie-Tooth (CMT) neuropathies; protein abundance increases in response to DNA replication stress	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=TYS1
chr7:983701			SNV							SNV	G/A	Nonsynonymous	YGR246C	gCt/gTt	A113V	BRF1	TFIIIB B-related factor; one of three subunits of RNA polymerase III transcription initiation factor TFIIIB, binds TFIIIC and TBP and recruits RNA pol III to promoters, amino-terminal half is homologous to TFIIB	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=BRF1
chr8:193820			SNV							SNV	G/A	Nonsynonymous	YHR047C	Cca/Tca	P249S	AAP1	Arginine/alanine amino peptidase; overproduction stimulates glycogen accumulation; AAP1 has a paralog, APE2, that arose from the whole genome duplication	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=AAP1

Location	Strains										Nuc change	Effect	Systematic gene name	Cdn change	Amino acid change	Standard gene name	Gene description	Link to SGD
	AAC	M715	MH23	MH34	A64	B130	B184	C120	D5	F83								
chr8:487581			SNV							SNV	C/T	Nonsynonymous	YHR197W	aCt/aTt	T176I	RIX1	Component of the Rix1 complex and possibly pre-replicative complexes; required for processing of ITS2 sequences from 35S pre-rRNA; component of the pre-60S ribosomal particle with the dynein-related AAA-type ATPase Mdn1p; required for pre-replicative complex (pre-RC) formation and maintenance during DNA replication licensing; relocalizes to the cytosol in response to hypoxia;	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=RIX1
chr12:322125			SNV							SNV	G/A	Nonsynonymous	YLR097C	Cat/Tat	H44Y	HRT3	Putative SCF-ubiquitin ligase F-box protein; based on both genetic and physical interactions and sequence similarity; identified in association with Cdc53p, Skp1p and Ubi4 in large and small-scale studies	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=HRT3
chr13:147095			SNV							SNV	C/T	Nonsynonymous	YML060W	Cct/Tct	P167S	OGG1	Nuclear and mitochondrial glycosylase/lyase; specifically excises 7,8-dihydro-8-oxoguanine residues located opposite cytosine or thymine residues in DNA, repairs oxidative damage to mitochondrial DNA, contributes to UVA resistance	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=OGG1
chr14:585613			SNV							SNV	C/T	Nonsynonymous	YNL022C	aGa/aAa	R425K	RCM1	rRNA m5C methyltransferase; methylates cytosine at position 2278 of 25S rRNA while Nop2p methylates cytosine at position 2870; contains seven beta-strand methyltransferase motif; localized to the nucleolus; interacts with Trm112p; homolog of NSUN5A, a human gene which is deleted in Williams-Beuren Syndrome	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=RCM1
chr15:275588			SNV							SNV	C/T	Nonsynonymous	YOL025W	cCc/cTc	P262L	LAG2	Protein that negatively regulates the SCF E3-ubiquitin ligase; regulates by interacting with and preventing neddyation of the cullin subunit, Cdc53p; longevity determinant that is preferentially expressed in young cells; similar to mammalian Cand1	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=LAG2
chr15:353053			SNV							SNV	C/T	Nonsynonymous	YOR011W	Ctt/Ttt	L1158F	AUS1	Plasma membrane sterol transporter of the ATP-binding cassette family; required, along with Pdr11p, for uptake of exogenous sterols and their incorporation into the plasma membrane; activity is stimulated by phosphatidylserine; sterol uptake is required for anaerobic growth because sterol biosynthesis requires oxygen; AUS1 has a paralog, PDR11, that arose from the whole genome duplication	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=AUS1
chr15:375446			SNV							SNV	G/A	Nonsynonymous	YOR022C	Cct/Tct	P148S		Putative carboxylic ester hydrolase; similar to bovine phospholipase A1; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=YOR02
chr15:930648			SNV							SNV	G/A	Nonsynonymous	YOR327C	cCt/cTt	P109L	SNC2	Vesicle membrane receptor protein (v-SNARE); involved in the fusion between Golgi-derived secretory vesicles with the plasma membrane; member of the synaptobrevin/VAMP family of R-type v-SNARE proteins; SNC2 has a paralog, SNC1, that arose from the whole genome duplication	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=SNC2
chr16:91710			SNV							SNV	C/T	Nonsynonymous	YPL242C	AGa/GAa	R1112E	IQG1	Essential protein required for determination of budding pattern; promotes localization of axial markers Bud4p and Cdc12p and functionally interacts with Sec3p, localizes to the contractile ring during anaphase, member of the IQGAP family; relocalizes from bud neck to cytoplasm upon DNA replication stress	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=IQG1
chr16:91711			SNV							SNV	T/C	Nonsynonymous						
chr16:385753			SNV							SNV	G/A	Nonsynonymous	YPL086C	tCg/tTg	S217L	ELP3	Subunit of Elongator complex; Elongator is required for modification of wobble nucleosides in tRNA; exhibits histone acetyltransferase activity that is directed to histones H3 and H4; disruption confers resistance to K. lactis zymotoxin	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=ELP3
chr16:489492			SNV							SNV	G/A	Nonsynonymous	YPL032C	Cct/TTt	P601F	SVL3	Protein of unknown function; mutant phenotype suggests a potential role in vacuolar function; green fluorescent protein (GFP)-fusion protein localizes to the cell periphery, cytoplasm, bud, and bud neck; relocalizes from bud neck to cytoplasm upon DNA replication stress; SVL3 has a paralog, PAM1, that arose from the whole genome duplication	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=SVL3
chr16:489493			SNV							SNV	G/A	Nonsynonymous						

Location	Strains										Nuc change	Effect	Systematic gene name	Cdn change	Amino acid change	Standard gene name	Gene description	Link to SGD
	AAC	M715	MH23	MH34	A64	B130	B184	C120	D5	F83								
chr16:895637			SNV							SNV	G/A	Stop gained	YPR179C	Caa/Taa	Q47*	HDA3	Subunit of the HDA1 histone deacetylase complex; possibly tetrameric trichostatin A-sensitive class II histone deacetylase complex contains Hda1p homodimer and an Hda2p-Hda3p heterodimer; required for the activity of the complex; relocalizes to the cytosol in response to hypoxia; similar to Hda2p	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=HDA3
chr2:707966										SNV	G/A	Nonsynonymous	YBR247C	Cgt/Tgt	R445C	ENP1	Protein associated with U3 and U14 snoRNAs; required for pre-rRNA processing and 40S ribosomal subunit synthesis; localized in the nucleus and concentrated in the nucleolus	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=ENP1
chr4:1121403										SNV	G/A	Nonsynonymous	YDR326C	tCc/tTc	S849F	YSP2	Protein involved in programmed cell death; mutant shows resistance to cell death induced by amiodarone or intracellular acidification; YSP2 has a paralog, YHR080C, that arose from the whole genome	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=YSP2
chr5:278493										SNV	C/T	Nonsynonymous	YER062C	Gaa/Aaa	E92K	HOR2	DL-glycerol-3-phosphate phosphatase involved in glycerol biosynthesis; also known as glycerol-1-phosphatase; induced in response to hyperosmotic or oxidative stress, and during diauxic shift; GPP2 has a paralog, GPP1, that arose from the whole genome duplication	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=HOR2
chr8:117651										SNV	T/A	Nonsynonymous	YHR009C	gAt/gTt	D397V	TDA3	Putative oxidoreductase involved in late endosome to Golgi transport; physical and genetical interactions with Btn2p; null mutant is viable, has extended S phase, and sensitive to expression of top1-T722A allele; similar to human FOXRED1	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=TDA3
chr10:97965										SNV	G/A	Stop gained	YJL162C	Caa/Taa	Q69*	JJJ2	Protein of unknown function; contains a J-domain, which is a region with homology to the E. coli DnaJ protein	http://www.yeastgenome.org/cgi-
chr10:592960										SNV	G/A	Nonsynonymous	YJR095W	Ggt/Agt	G225S	SFC1	Mitochondrial succinate-fumarate transporter; transports succinate into and fumarate out of the mitochondrion; required for ethanol and acetate utilization	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=SFC1
chr12:899027										SNV	G/T	Nonsynonymous	YLR397C	gaC/gaA	D358E	AFG2	ATPase of the CDC48/PAS1/SEC18 (AAA) family, forms a hexameric complex; is essential for pre-60S maturation and release of several preribosome maturation factors; releases Rlp24p from purified pre-60S particles in vitro; may be involved in degradation of aberrant	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=AFG2
chr14:187347										SNV	A/G	Nonsynonymous	YNL242W	cAa/cGa	Q686R	ATG2	Peripheral membrane protein required for autophagic vesicle formation; also required for vesicle formation during pexophagy and the cytoplasm-to-vaucole targeting (Cvt) pathway; involved in Atg9p cycling between the phagophore assembly site and mitochondria; essential for cell cycle progression from G2/M to G1 under nitrogen starvation; forms cytoplasmic foci upon DNA replication stress	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=ATG2
chr15:685862										SNV	C/T	Nonsynonymous	YOR188W	Cat/Tat	H64Y	MSB1	Protein of unknown function; may be involved in positive regulation of 1,3-beta-glucan synthesis and the Pkc1p-MAPK pathway; multicopy suppressor of temperature-sensitive mutations in CDC24 and CDC42, and of mutations in BEM4; potential Cdc28p substrate; relocalizes from bud neck to cytoplasm upon DNA replication stress	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=MSB1
chr15:776687										SNV	C/T	Nonsynonymous	YOR233W	Cat/Tat	H316Y	KIN4	Serine/threonine protein kinase; inhibits the mitotic exit network (MEN) when the spindle position checkpoint is activated; localized asymmetrically to mother cell cortex, spindle pole body and bud neck; KIN4 has a paralog, FRK1, that arose from the whole genome duplication	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=KIN4
chr1:49928				SNV	SNV	SNV	SNV	SNV	SNV		C/T	Nonsynonymous	YAL051W	Cca/Tca	P437S	OAF1	Oleate-activated transcription factor; acts alone and as a heterodimer with Pip2p; activates genes involved in beta-oxidation of fatty acids and peroxisome organization and biogenesis; involved in diauxic shift; OAF1 has a paralog, PIP2, that arose from the whole genome duplication	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=OAF1

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	AAC	M715	MH23	MH34	A64	B130	B184	C120	D5	F83								
chr2:123579				SNV	SNV	SNV	SNV	SNV	SNV		C/T	Nonsynonymous	YBL047C	Gaa/Aaa	E1057K	EDE1	Endocytic protein; involved in a network of interactions with other endocytic proteins, binds membranes in a ubiquitin-dependent manner, may also bind ubiquitinated membrane-associated proteins; interacts with Cmk2 and functions upstream of CMK2 in regulating non-apoptotic cell death	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=EDE1
chr3:68490				SNV	SNV	SNV	SNV	SNV	SNV		G/A	Nonsynonymous	YCL029C	tCg/tTg	S365L	BIK1	Microtubule-associated protein; component of the interface between microtubules and kinetochore, involved in sister chromatid separation; essential in polyploid cells but not in haploid or diploid cells; ortholog of mammalian CLIP-170	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=BIK1
chr4:346549				SNV	SNV	SNV	SNV	SNV	SNV		C/T	Nonsynonymous	YDL058W	tCt/tTt	S660F	USO1	Essential protein involved in vesicle-mediated ER to Golgi transport; binds membranes and functions during vesicle docking to the Golgi; required for assembly of the ER-to-Golgi SNARE complex	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=USO1
chr4:352412				SNV	SNV	SNV	SNV	SNV	SNV		C/T	Nonsynonymous	YDL056W	cCc/cTc	P211L	MBP1	Transcription factor; involved in regulation of cell cycle progression from G1 to S phase, forms a complex with Swi6p that binds to MluI cell cycle box regulatory element in promoters of DNA synthesis genes	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=MBP1
chr4:585289				SNV	SNV	SNV	SNV	SNV	SNV		G/A	Nonsynonymous	YDR069C	tCa/tTa	S498L	DOA4	Ubiquitin hydrolase that deubiquitinates ILV cargo proteins; required for recycling ubiquitin from proteasome-bound ubiquitinated intermediates, acts at the late endosome/prevacuolar compartment to recover ubiquitin from ubiquitinated membrane proteins en route to the vacuole; DOA4 has a paralog, UBP5, that arose from the whole genome duplication	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=DOA4
chr4:585398				SNV	SNV	SNV	SNV	SNV	SNV		G/A	Nonsynonymous		Ctt/Ttt	L462F			
chr4:595180				SNV	SNV	SNV	SNV	SNV	SNV		C/T	Nonsynonymous	YDR074W	Cgt/Tgt	R735C	TPS2	Phosphatase subunit of the trehalose-6-P synthase/phosphatase complex; involved in synthesis of the storage carbohydrate trehalose; expression is induced by stress conditions and repressed by the Ras-cAMP pathway; protein abundance increases in response to DNA replication stress	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=TPS2
chr4:1052323				SNV	SNV	SNV	SNV	SNV	SNV		G/A	Stop gained	YDR295C	Caa/Taa	Q452*	HDA2	Subunit of the HDA1 histone deacetylase complex; possibly tetrameric trichostatin A-sensitive class II histone deacetylase complex contains Hda1p homodimer and an Hda2p-Hda3p heterodimer; involved in telomere maintenance; relocalizes to the cytosol in response to hypoxia	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=HDA2
chr5:409300				SNV	SNV	SNV	SNV	SNV	SNV		C/T	Nonsynonymous	YER125W	Cca/Tca	P343S	RSP5	E3 ubiquitin ligase of the NEDD4 family; involved in regulating many cellular processes including MVB sorting, heat shock response, transcription, endocytosis, and ribosome stability; human homolog is involved in Liddle syndrome; mutant tolerates aneuploidy; deubiquitinated by Ubp2p; autoubiquitinates and ubiquitinates Sec23p and Sna3p	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=RSP5
chr7:62380				INS	INS	INS	INS	INS	INS		*/+GA	Frame shift, 2 bp insert	YGL232W			TAN1	Putative tRNA acetyltransferase; RNA-binding protein required for the formation of the modified nucleoside N(4)-acetylcytidine in serine and leucine tRNAs but not required for the same modification in 18S rRNA; protein abundance increases in response to DNA replication stress	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=TAN1
chr7:213242				SNV	SNV	SNV	SNV	SNV	SNV		G/A	Nonsynonymous	YGL156W	Gaa/Aaa	E859K	AMS1	Vacuolar alpha mannosidase; involved in free oligosaccharide (fOS) degradation; delivered to the vacuole in a novel pathway separate from the secretory pathway	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=AMS1

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	AAC	M715	MH23	MH34	A64	B130	B184	C120	D5	F83								
chr7:260149				SNV	SNV	SNV	SNV	SNV	SNV		C/T	Stop gained	YGL133W	Cga/Tga	R732*	ITC1	Subunit of ATP-dependent Isw2p-Itc1p chromatin remodeling complex; required for repression of a-specific genes, repression of early meiotic genes during mitotic growth, and repression of INO1; similar to mammalian Acf1p, the regulatory subunit of the mammalian ATP-utilizing chromatin assembly and modifying factor (ACF) complex; ITC1 has a paralog, YPL216W, that arose from the whole genome duplication	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=ITC1
chr7:732569				SNV	SNV	SNV	SNV	SNV	SNV		C/T	Nonsynonymous	YGR121C	Ggt/Agt	G63S	MEP1	Ammonium permease; belongs to a ubiquitous family of cytoplasmic membrane proteins that transport only ammonium (NH4+); expression is under the nitrogen catabolite repression regulation; MEP1 has a paralog, MEP3, that arose from the whole genome duplication	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=MEP1
chr7:903295				SNV	SNV	SNV	SNV	SNV	SNV		G/A	Nonsynonymous	YGR202C	tCa/tTa	S422L	PCT1	Cholinephosphate cytidylyltransferase; a rate-determining enzyme of the CDP-choline pathway for phosphatidylcholine synthesis, inhibited by Sec14p, activated upon lipid-binding; contains an element within the regulatory domain involved in both silencing and activation of enzymatic activity	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=PCT1
chr8:32631				SNV	SNV	SNV	SNV	SNV	SNV		G/A	Nonsynonymous	YHL031C	tCt/tTt	S6F	GOS1	v-SNARE protein involved in Golgi transport; homolog of the mammalian protein GOS-28/GS28	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=GOS1
chr8:170565				SNV	SNV	SNV	SNV	SNV	SNV		G/A	Nonsynonymous	YHR034C	tCc/tTc	S230F	PIH1	Component of the conserved R2TP complex (Rvb1-Rvb2-Tah1-Pih1); R2TP complex interacts with Hsp90 (Hsp82p and Hsc82p) to mediate assembly large protein complexes such as box C/D snoRNPs and RNA polymerase II	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=PIH1
chr8:170665				SNV	SNV	SNV	SNV	SNV	SNV		G/A	Nonsynonymous		Ccg/Tcg	P197S			
chr9:334662				SNV	SNV	SNV	SNV	SNV	SNV		C/T	Nonsynonymous	YIL011W	tCt/tTt	S212F	TIR3	Cell wall mannoprotein; member of Srp1p/Tip1p family of serine-alanine-rich proteins; expressed under anaerobic conditions and required for anaerobic growth; TIR3 has a paralog, TIR2, that arose from the whole genome duplication	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=TIR3
chr12:3811				SNV	SNV	SNV	SNV	SNV	SNV		G/A	Nonsynonymous	YLL061W	Ggt/AAt	G103N	MMP1	High-affinity S-methylmethionine permease; required for utilization of S-methylmethionine as a sulfur source; has similarity to S-adenosylmethionine permease Sam3p	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=MMP1
chr12:3812				SNV	SNV	SNV	SNV	SNV	SNV		G/A	Nonsynonymous						
chr12:4208				SNV	SNV	SNV	SNV	SNV	SNV		G/A	Stop gained		tGg/tAg	W235*			
chr12:973542				SNV	SNV	SNV	SNV	SNV	SNV		C/T	Nonsynonymous	YLR427W	tCa/tTa	S34L	MAG2	Cytoplasmic protein of unknown function; induced in response to mycotoxin patulin; ubiquitinated protein similar to the human ring finger motif protein RNF10; predicted to be involved in repair of alkylated DNA due to interaction with MAG1	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=MAG2
chr13:318074				SNV	SNV	SNV	SNV	SNV	SNV		G/A	Nonsynonymous	YMR025W	Gag/Aag	E19K	CSI1	Subunit of the Cop9 signalosome; which is required for deneddylation, or removal of the ubiquitin-like protein Rub1p from Cdc53p (cullin); involved in adaptation to pheromone signaling; functional equivalent of canonical Csn6 subunit of the COP9 signalosome	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=CSI1
chr14:461298				SNV	SNV	SNV	SNV	SNV	SNV		T/A	Nonsynonymous	YNL085W	Ttc/Atc	F70I	MKT1	Protein that forms a complex with Pbp1p; complex may mediate posttranscriptional regulation of HO; involved in propagation of M2 dsRNA satellite of L-A virus; allelic variation affects mitochondrial genome stability, drug resistance, and more; forms cytoplasmic foci upon DNA replication stress	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=MKT1
chr15:315162				SNV	SNV	SNV	SNV	SNV	SNV		G/A	Nonsynonymous	YOL006C	tCt/tTt	S37F	TOP1	Topoisomerase I; nuclear enzyme that relieves torsional strain in DNA by cleaving and re-sealing the phosphodiester backbone; relaxes both positively and negatively supercoiled DNA; functions in replication, transcription, and recombination	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=TOP1

Location	Strains										Nuc change	Effect	Systematic gene name	Cdn change	Amino acid change	Standard gene name	Gene description	Link to SGD
	AAC	M715	MH23	MH34	A64	B130	B184	C120	D5	F83								
chr16:72809				SNV	SNV	SNV	SNV	SNV	SNV		G/A	Nonsynonymous	YPL253C	Cct/Tct	P46S	VIK1	Protein that forms a kinesin-14 heterodimeric motor with Kar3p; localizes Kar3p at mitotic spindle poles; has a structure similar to a kinesin motor domain but lacks an ATP-binding site and is catalytically inactive; binds microtubules; required for sister chromatid cohesion; VIK1 has a paralog, CIK1, that arose from the whole genome duplication	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=VIK1
chr16:464746				SNV	SNV	SNV	SNV	SNV	SNV		G/A	Nonsynonymous	YPL048W	Gac/Aac	D137N	CAM1	Nuclear protein required for transcription of MXR1; binds the MXR1 promoter in the presence of other nuclear factors; binds calcium and phospholipids; has similarity to translational cofactor EF-1 gamma	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=CAM1
chr16:595155				SNV	SNV	SNV	SNV	SNV	SNV		G/A	Nonsynonymous	YPR018W	Gaa/Aaa	E251K	RLF2	Largest subunit (p90) of the Chromatin Assembly Complex (CAF-1); chromatin assembly by CAF-1 is important for multiple processes including silencing at telomeres, mating type loci, and rDNA; maintenance of kinetochore structure; deactivation of the DNA damage checkpoint after DNA repair; and chromatin dynamics during transcription	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=RLF2
chr2:182401									SNV		C/T	Nonsynonymous	YBL017C	aGa/aAa	R1299K	PEP1(VPS10)	Type I transmembrane sorting receptor for multiple vacuolar hydrolases; cycles between the late-Golgi and prevacuolar endosome-like compartments	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=PEP1
chr4:1138124									SNV		G/A	Nonsynonymous	YDR334W	Gat/Aat	D233N	SWR1	Swi2/Snf2-related ATPase; structural component of the SWR1 complex, which exchanges histone variant H2AZ (Htz1p) for chromatin-bound histone H2A; relocalizes to the cytosol in response to hypoxia	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=SWR1
chr4:1343864									SNV		G/A	Nonsynonymous	YDR441C	tCc/tTc	S77F	APT2	Potential adenine phosphoribosyltransferase; encodes a protein with similarity to adenine phosphoribosyltransferase, but artificially expressed protein exhibits no enzymatic activity; APT2 has a paralog, APT1, that arose from the whole genome duplication	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=APT2
chr7:369204									SNV		T/C	Nonsynonymous	YGL073W	tTa/tCa	L92S	HSF1	Trimeric heat shock transcription factor; activates multiple genes in response to highly diverse stresses, including hyperthermia; recognizes variable heat shock elements (HSEs) consisting of inverted NGAAN repeats; monitors translational status of cell at the ribosome through an RQC (Ribosomal Quality Control)-mediated translation-stress signal; involved in diauxic shift; posttranslationally regulated	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=HSF1
chr7:369279									SNV		C/T	Nonsynonymous		cCt/cTt	P117L			
chr8:58626									SNV		G/A	Nonsynonymous	YHL021C	tCg/tTg	S132L	AIM17	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies; null mutant displays reduced frequency of mitochondrial genome loss	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=AIM17
chr8:58744									SNV		G/A	Nonsynonymous		Cct/Tct	P93S			
chr8:114325									SNV		G/A	Nonsynonymous	YHR007C	cCa/cTa	P56L	ERG11	Lanosterol 14-alpha-demethylase; catalyzes the C-14 demethylation of lanosterol to form 4,4"-dimethyl cholesta-8,14,24-triene-3-beta-ol in the ergosterol biosynthesis pathway; member of the cytochrome P450 family; associated and coordinately regulated with the P450 reductase Ncp1p	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=ERG11
chr9:367955									SNV		G/A	Nonsynonymous	YIR006C	tCa/tTa	S785L	PAN1	Part of actin cytoskeleton-regulatory complex Pan1p-Sla1p-End3p; associates with actin patches on cell cortex; promotes protein-protein interactions essential for endocytosis; binds to and activates Arp2/3 complex in vitro; phosphorylation of Thr-1225 is regulated by MAPK Hog1p in response to osmotic stress; previously thought to be a subunit of poly(A) ribonuclease	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=PAN1

Location	Strains										Nuc change	Effect	Systematic gene name	Cdn change	Amino acid change	Standard gene name	Gene description	Link to SGD
	AAC	M715	MH23	MH34	A64	B130	B184	C120	D5	F83								
chr10:255973									SNV		C/T	Nonsynonymous	YJL085W	tCt/tTt	S196F	EXO70	Subunit of the exocyst complex; the exocyst mediates polarized targeting and tethering of post-Golgi secretory vesicles to active sites of exocytosis prior to SNARE-mediated fusion; PtdIns[4,5]P2-binding protein that localizes to exocytic sites in an actin-independent manner, targeting and anchoring the exocyst with Sec3p; involved in exocyst assembly; direct downstream effector of Rho3p and Cdc42p; relocalizes from bud neck to cytoplasm upon DNA replication stress	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=EXO70
chr11:654652									SNV		G/A	Nonsynonymous	YKR103W	Gaa/Aaa	E754K	NFT1	Putative transporter of the MRP subfamily; adjacent ORFs YKR103W and YKR104W are merged in different strain backgrounds; MRP stands for multidrug resistance-associated protein	http://www.yeastgenome.org/cgi-bin/locus.fpl?dbid=S000001811
chr11:654754									SNV		G/A	Nonsynonymous		GGa/AAa	G788K			
chr11:654755									SNV		G/A	Nonsynonymous						
chr11:654970									SNV		G/A	Nonsynonymous		Gac/Aac	D860N			
chr12:121186									SNV		C/T	Nonsynonymous	YLL007C	Gaa/Aaa	E54K		Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YLL007C is not an essential gene	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=YLL007
chr12:1032728									SNV		T/A	Stop gained	YLR454W	tTa/tAa	L1237*	FMP27	Putative protein of unknown function; the authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=FMP27
chr13:819980									SNV		G/A	Nonsynonymous	YMR279C	Ctt/Ttt	L301F		Putative boron transporter involved in boron efflux and resistance; overexpression mutant but not null mutant displays boron tolerance phenotype; identified as a heat-induced gene in a high-throughput screen; YMR279C is not an essential gene; YMR279C has a paralog, ATR1, that arose from the whole genome duplication	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=YMR279C
chr13:821772									SNV		G/A	Stop gained	YMR280C	Caa/Taa	Q1359*	CAT8	Zinc cluster transcriptional activator; necessary for derepression of a variety of genes under non-fermentative growth conditions, active after diauxic shift, binds carbon source responsive elements; relative distribution to the nucleus increases upon DNA replication stress	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=CAT8
chr14:162701									SNV		G/A	Nonsynonymous	YNL254C	tCt/tTt	S173F	RTC4	Protein of unknown function; null mutation suppresses cdc13-1 temperature sensitivity; (GFP)-fusion protein localizes to both the cytoplasm and the nucleus	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=RTC4
chr15:279919									SNV		C/T	Nonsynonymous	YOL023W	cCt/cTt	P673L	IFM1	Mitochondrial translation initiation factor 2	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=IFM1
chr2:645838								SNV			G/A	Nonsynonymous	YBR213W	Gaa/Aaa	E265K	MET8	Bifunctional dehydrogenase and ferrochelatase; involved in the biosynthesis of siroheme, a prosthetic group used by sulfite reductase; required for sulfate assimilation and methionine biosynthesis	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=MET8
chr6:159482								SNV			C/T	Stop gained	YFR008W	Caa/Taa	Q27*	FAR7	Protein involved in recovery from pheromone-induced cell cycle arrest; acts in a Far1p-independent pathway; interacts with Far3p, Far8p, Far9p, Far10p, and Far11p; protein abundance increases in response to DNA replication stress	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=FAR7
chr7:344703								SNV			C/T	Nonsynonymous	YGL090W	tCc/tTc	S403F	LIF1	Component of the DNA ligase IV complex; this complex mediates nonhomologous end joining in DNA double-strand break repair; physically interacts with Dnl4p and Nej1p; homologous to mammalian XRCC4 protein	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=LIF1

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	AAC	M715	MH23	MH34	A64	B130	B184	C120	D5	F83								
chr10:117718								SNV			G/A	Nonsynonymous	YJL153C	Ctt/Ttt	L236F	INO1	Inositol-3-phosphate synthase; involved in synthesis of inositol phosphates and inositol-containing phospholipids; transcription is coregulated with other phospholipid biosynthetic genes by Ino2p and Ino4p, which bind the UASINO DNA element	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=INO1
chr10:270895								SNV			C/T	Nonsynonymous	YJL080C	Ggt/Agt	G298S	SCP160	Essential RNA-binding G protein effector of mating response pathway; mainly associated with nuclear envelope and ER, interacts in mRNA-dependent manner with translating ribosomes via multiple KH domains, similar to vertebrate vigilins	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=SCP160
chr12:752156								SNV			A/T	Nonsynonymous	YLR318W	Agc/Tgc	S202C	EST2	Reverse transcriptase subunit of the telomerase holoenzyme; essential for telomerase core catalytic activity, involved in other aspects of telomerase assembly and function; mutations in human homolog are associated with aplastic anemia; Also known as: TERT	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=EST2
chr16:714202								SNV			T/C	Nonsynonymous	YPR089W	tTa/tCa	L332S		Protein of unknown function; exhibits genetic interaction with ERG11 and protein-protein interaction with Hsp82p	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=YPR08
chr4:85150							SNV				G/A	Nonsynonymous	YDL209C	CCa/TTa	P278L	CWC2	Member of the NineTeen Complex (NTC); this complex contains Prp19p and stabilizes U6 snRNA in catalytic forms of the spliceosome containing U2, U5, and U6 snRNAs; binds directly to U6 snRNA; similar to S. pombe Cwf2	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=CWC2
chr4:85151							SNV				G/A	Nonsynonymous						
chr4:439286							SNV				A/T	Nonsynonymous	YDL006W	tAt/tTt	Y144F	PTC1	Type 2C protein phosphatase (PP2C); dephosphorylates Hog1p, inactivating osmosensing MAPK cascade; involved in Fus3p activation during pheromone response; deletion affects precursor tRNA splicing, mitochondrial inheritance, and sporulation	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=PTC1
chr4:642292							SNV				G/A	Nonsynonymous	YDR097C	tCt/tTt	S209F	MSH6	Protein required for mismatch repair in mitosis and meiosis; forms a complex with Msh2p to repair both single-base & insertion-deletion mispairs; also involved in interstrand cross-link repair; potentially phosphorylated by Cdc28p	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=MSH6
chr4:1248040							SNV				C/T	Nonsynonymous	YDR387C	Gaa/Aaa	E270K		Putative transporter; member of the sugar porter family; YDR387C is not an essential gene	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=YDR38
chr4:1378469							SNV				C/T	Nonsynonymous	YDR457W	tCc/tTc	S3218F	TOM1	E3 ubiquitin ligase of the hect-domain class; has a role in mRNA export from the nucleus and may regulate transcriptional coactivators; involved in degradation of excess histones; interacts with Dia2p and is required for Dia2p degradation; required to target Cdc6p for ubiquitin-mediated destruction during G1 phase	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=TOM1
chr4:1380160							SNV				C/T	Nonsynonymous	YDR458C	aGa/aAa	R305K	HEH2	Inner nuclear membrane (INM) protein; contains helix-extension-helix (HEH) motif, nuclear localization signal sequence; targeting to the INM requires the Srp1p-Kap95p karyopherins and the Ran cycle; HEH2 has a paralog, SRC1, that arose from the whole genome duplication	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=HEH2
chr4:1381362							SNV				C/A	Nonsynonymous	YDR459C	aGt/aTt	S370I	PFA5	Palmitoyltransferase with autoacylation activity; likely functions in pathway(s) outside Ras; member of a family of putative palmitoyltransferases containing an Asp-His-His-Cys-cysteine rich (DHHC-CRD) domain	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=PFA5
chr4:1381372							SNV				C/T	Nonsynonymous		Ggt/Agt	G367S			
chr7:1060822							SNV				A/G	Nonsynonymous	YGR284C	tTa/tCa	L193S	ERV29	Protein localized to COPII-coated vesicles; involved in vesicle formation and incorporation of specific secretory cargo; protein abundance increases in response to DNA replication stress	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=ERV29

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	AAC	M715	MH23	MH34	A64	B130	B184	C120	D5	F83								
chr12:101816							SNV				C/T	Stop gained	YLL015W	Caa/Taa	Q128*	BPT1	ABC type transmembrane transporter of MRP/CFTR family; found in vacuolar membrane, involved in the transport of unconjugated bilirubin and in heavy metal detoxification via glutathione conjugates, along with Ycf1p	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=BPT1
chr13:680767							SNV				C/T	Nonsynonymous	YMR209C	Gat/Aat	D405N		Putative S-adenosylmethionine-dependent methyltransferase; YMR209C is not an essential gene	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=YMR209C
chr13:731688							SNV				G/A	Nonsynonymous	YMR232W	Gat/Aat	D17N	FUS2	Cytoplasmic protein localized to the shmoo tip; required for the alignment of parental nuclei before nuclear fusion during mating	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=FUS2
chr15:496253							SNV				C/T	Nonsynonymous	YOR092W	tCc/tTc	S312F	ECM3	Non-essential protein of unknown function; involved in signal transduction and the genotoxic response; induced rapidly in response to treatment with 8-methoxypsoralen and UVA irradiation; relocalizes from ER to cytoplasm upon DNA replication stress; ECM3 has a paralog, YNL095C, that arose from the whole genome duplication	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=ECM3
chr16:360804							SNV				C/T	Nonsynonymous	YPL101W	Ccg/Tcg	P223S	ELP4	Subunit of hexameric RecA-like ATPase Elp456 Elongator subcomplex; which is required for modification of wobble nucleosides in tRNA; required for Elongator structural integrity	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=ELP4
chr16:571094							SNV				C/T	Nonsynonymous	YPR007C	Gaa/Aaa	E74K	REC8	Meiosis-specific component of sister chromatid cohesion complex; maintains cohesion between sister chromatids during meiosis I; maintains cohesion between centromeres of sister chromatids until meiosis II; independent of its role in sister chromatid cohesion, Rec8p promotes allelic collisions and prevents nonspecific chromosome interactions; homolog of S. pombe Rec8p	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=REC8
chr16:907673							SNV				C/T	Nonsynonymous	YPR185W	Ctc/Ttc	L152F	ATG13	Regulatory subunit of the Atg1p signaling complex; stimulates Atg1p kinase activity; required for vesicle formation during autophagy and the cytoplasm-to-vacuole targeting (Cvt) pathway; contains a HORMA domain required for autophagy and for recruitment of the phosphatidylinositol 3-kinase complex subunit Atg14p to the pre-autophagosomal structure	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=ATG13
chr4:1219453						SNV					G/A	Nonsynonymous	YDR371W	aGa/aAa	R335K	CTS2	Putative chitinase; functionally complements A. gossypii cts2 mutant sporulation defect	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=CTS2
chr4:1223310						SNV					G/T	Nonsynonymous	YDR374C	tCc/tAc	S41Y	PHO92	Posttranscriptional regulator of phosphate metabolism; regulates PHO4 mRNA stability by binding to PHO4's 3'UTR in phosphate-dependent manner; contains YTH (YT521-B Homology) domain and is a homolog of human YTHDF2	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=YDR374C
chr4:1223393						INS					*/+A	Frame shift, 1 bp insert						
chr4:1223394						SNV					T/C	Nonsynonymous		tAc/tGc	Y/C			
chr5:35587						SNV					G/A	Nonsynonymous	YEL061C	Ctt/Ttt	L675F	CIN8	Kinesin motor protein; involved in mitotic spindle assembly and chromosome segregation	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=CIN8
chr5:422289						SNV					C/T	Nonsynonymous	YER131W	CCa/TTa	P101L	RPS26B	Protein component of the small (40S) ribosomal subunit; homologous to mammalian ribosomal protein S26, no bacterial homolog; RPS26B has a paralog, RPS26A, that arose from the whole genome duplication	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=RPS26B
chr5:422290						SNV					C/T	Nonsynonymous						
chr7:306189						SNV					G/A	Nonsynonymous	YGL107C	Ctt/Ttt	L88F	RMD9	Mitochondrial protein required for respiratory growth; mutant phenotype and genetic interactions suggest a role in delivering mt mRNAs to ribosomes; located on matrix face of the inner membrane and loosely associated with mitoribosomes; RMD9 has a paralog, YBR238C, that arose from the whole genome duplication	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=RMD9

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	AAC	M715	MH23	MH34	A64	B130	B184	C120	D5	F83								
chr7:867888						SNV					C/T	Nonsynonymous	YGR186W	cCc/cTc	P102L	TFG1	TFIIF (Transcription Factor II) largest subunit; involved in both transcription initiation and elongation of RNA polymerase II; homologous to human RAP74	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=TFG1
chr8:77374						SNV					G/A	Nonsynonymous	YHL009C	Ctt/Ttt	L283F	YAP3	Basic leucine zipper (bZIP) transcription factor	http://www.yeastgenome.org/cgi-bin/locus.fpl?dbid=S000001001
chr12:660821						SNV					G/A	Nonsynonymous	YLR266C	aCt/aTt	T627I	PDR8	Transcription factor; targets include ATP-binding cassette (ABC) transporters, major facilitator superfamily transporters, and other genes involved in the pleiotropic drug resistance (PDR) phenomenon; PDR8 has a paralog, YRR1, that arose from the whole genome duplication	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=PDR8
chr12:686228						SNV					T/A	Nonsynonymous	YLR278C	Aat/Tat	N935Y		Zinc-cluster protein; GFP-fusion protein localizes to the nucleus; mutant shows moderate growth defect on caffeine; has a prion-domain like fragment that increases frequency of [URE3]	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=YLR278C
chr13:470350						SNV					G/A	Stop gained	YMR105C	Caa/Taa	Q453*	PGM2	Phosphoglucomutase; catalyzes the conversion from glucose-1-phosphate to glucose-6-phosphate, which is a key step in hexose metabolism; functions as the acceptor for a Glc-phosphotransferase; protein abundance increases in response to DNA replication stress; PGM2 has a paralog, PGM1, that arose from the whole genome duplication	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=PGM2
chr13:658634						SNV					C/T	Nonsynonymous	YMR199W	tCa/tTa	S444L	CLN1	G1 cyclin involved in regulation of the cell cycle; activates Cdc28p kinase to promote the G1 to S phase transition; late G1 specific expression depends on transcription factor complexes, MBF (Swi6p-Mbp1p) and SBF (Swi6p-Swi4p); CLN1 has a paralog, CLN2, that arose from the whole genome duplication	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=CLN1
chr13:722740						SNV					A/T	Nonsynonymous	YMR229C	cTa/cAa	L1033Q	RRP5	RNA binding protein involved in synthesis of both 18S and 5.8S rRNAs; component of both the ribosomal small subunit (SSU) processosome and the 90S preribosome; has binding preference for single stranded tracts of U's; relocalizes from nucleolus to nucleus upon DNA replication stress	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=RRP5
chr13:810872						SNV					G/A	Nonsynonymous	YMR275C	CCa/TTa	P752L	BUL1	Ubiquitin-binding component of the Rsp5p E3-ubiquitin ligase complex; disruption causes temperature-sensitive growth, overexpression causes missorting of amino acid permeases; BUL1 has a paralog, BUL2, that arose from the whole genome duplication	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=BUL1
chr13:810873						SNV					G/A							
chr14:58173						SNV					G/A	Nonsynonymous	YNL301C	Ctt/Ttt	L127F	RPL18B	Ribosomal 60S subunit protein L18B; homologous to mammalian ribosomal protein L18, no bacterial homolog; RPL18B has a paralog, RPL18A, that arose from the whole genome duplication	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=RPL18B
chr14:404160						SNV					T/C	Nonsynonymous	YNL115C	cAa/cGa	Q628R		Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to mitochondria; YNL115C is not an essential gene	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=YNL115C
chr14:527549						SNV					C/T	Nonsynonymous	YNL051W	tCc/tTc	S302F	COG5	Component of the conserved oligomeric Golgi complex; a cytosolic tethering complex (Cog1p through Cog8p) that functions in protein trafficking to mediate fusion of transport vesicles to Golgi compartments	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=COG5

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	AAC	M715	MH23	MH34	A64	B130	B184	C120	D5	F83								
chr15:455418						SNV					G/A	Nonsynonymous	YOR069W	Gaa/Aaa	E508K	VPS5	Nexin-1 homolog; required for localizing membrane proteins from a prevacuolar/late endosomal compartment back to late Golgi; structural component of retromer membrane coat complex; forms a retromer subcomplex with Vps17p; required for recruiting the retromer complex to the endosome membranes; VPS5 has a paralog, YKR078W, that arose from the whole genome duplication;Also known as: YOR29-20	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=VPS5
chr15:455718						SNV					G/A	Nonsynonymous		Gaa/Aaa	E608K			
chr15:455790						SNV					G/A	Nonsynonymous		Gat/Aat	D632N			
chr15:765016						SNV					T/A	Stop gained	YOR227W	tTa/tAa	L764*	HER1	Protein of unknown function; required for proliferation or remodeling of the ER that is caused by overexpression of Hmg2p; may interact with ribosomes, based on co-purification experiments; HER1 has a paralog, GIP3, that arose from the whole genome duplication	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=HER1
chr15:977525						SNV					C/T	Nonsynonymous	YOR344C	Gaa/Aaa	E151K	TYE7	Serine-rich protein that contains a bHLH DNA binding motif; binds E-boxes of glycolytic genes and contributes to their activation; may function as a transcriptional activator in Ty1-mediated gene expression; bHLH stands for basic-helix-loop-helix	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=TYE7
chr16:180376						SNV					G/A	Nonsynonymous	YPL194W	gGa/gAa	G388E	DDC1	DNA damage checkpoint protein; part of a PCNA-like complex required for DNA damage response, required for pachytene checkpoint to inhibit cell cycle in response to unrepaired recombination intermediates; potential Cdc28p substrate; forms nuclear foci upon DNA replication stress	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=DDC1
chr16:224253						SNV					G/A	Nonsynonymous	YPL172C	Cct/Tct	P441S	COX10	Heme A:farnesyltransferase; catalyzes the first step in the conversion of protoheme to the heme A prosthetic group required for cytochrome c oxidase activity; human ortholog is associated with mitochondrial disorders	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=COX10
chr16:463605						SNV					C/T	Nonsynonymous	YPL049C	Gag/Aag	E58K	DIG1	MAP kinase-responsive inhibitor of the Ste12p transcription factor; involved in the regulation of mating-specific genes and the invasive growth pathway; related regulators Dig1p and Dig2p bind to Ste12p; DIG1 has a paralog, DIG2, that arose from the whole genome duplication	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=DIG1
chr16:570898						SNV					C/T	Nonsynonymous	YPR007C	gGa/gAa	G139E	REC8	Meiosis-specific component of sister chromatid cohesion complex; maintains cohesion between sister chromatids during meiosis I; maintains cohesion between centromeres of sister chromatids until meiosis II; independent of its role in sister chromatid cohesion, Rec8p promotes allelic collisions and prevents nonspecific chromosome interactions; homolog of S. pombe Rec8p	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=REC8
chr16:571076						SNV					T/C	Nonsynonymous		Aga/Gga	R80G			
chr16:893015						SNV					G/A	Nonsynonymous	YPR178W	Gat/Aat	D225N	PRP4	Splicing factor; component of the U4/U6-U5 snRNP complex	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=PRP4
chr1:121091					SNV						C/T	Nonsynonymous	YAL017W	Cca/Tca	P237S	PSK1	PAS domain-containing serine/threonine protein kinase; coordinately regulates protein synthesis and carbohydrate metabolism and storage in response to a unknown metabolite that reflects nutritional status; PSK1 has a paralog, PSK2, that arose from the whole genome duplication	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=PSK1
chr4:192830					SNV						G/A	Nonsynonymous	YDL146W	Gct/Act	A449T	LDB17	Protein involved in the regulation of endocytosis; transiently recruited to actin cortical patches in a SLA1-dependent manner after late coat component assembly; GFP-fusion protein localizes to the periphery, cytoplasm, bud, and bud neck	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=LDB17

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	AAC	M715	MH23	MH34	A64	B130	B184	C120	D5	F83								
chr4:1284344					SNV						A/G	Nonsynonymous	YDR407C	Ttt/Ctt	F873L	TRS120	One of 10 subunits of the transport protein particle (TRAPP) complex; the TRAPP complex is of the cis-Golgi and mediates vesicle docking and fusion; involved in endoplasmic reticulum (ER) to Golgi membrane traffic	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=TRS120
chr5:307408					SNV						C/T	Nonsynonymous	YER075C	Gat/Aat	D634N	PTP3	Phosphotyrosine-specific protein phosphatase; involved in the inactivation of mitogen-activated protein kinase (MAPK) during osmolarity sensing; dephosporylates Hog1p MAPK and regulates its localization; localized to the cytoplasm	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=PTP3
chr5:452877					SNV						T/C	Nonsynonymous	YER141W	tTg/tCg	L443S	COX15	Protein required for the hydroxylation of heme O to form heme A; heme A is an essential prosthetic group for cytochrome c oxidase	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=COX15
chr7:14809					SNV						C/T	Nonsynonymous	YGL256W	tCc/tTc	S3F	ADH4	Alcohol dehydrogenase isoenzyme type IV; dimeric enzyme demonstrated to be zinc-dependent despite sequence similarity to iron-activated alcohol dehydrogenases; transcription is induced in response to zinc deficiency	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=ADH4
chr7:118523					SNV						C/T	Nonsynonymous	YGL201C	Gag/Aag	E853K	MCM6	Protein involved in DNA replication; component of the Mcm2-7 hexameric helicase complex that binds chromatin as a part of the pre-replicative complex; forms a subcomplex with Mcm4p and Mcm7p	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=MCM6
chr7:118585					SNV						C/T	Nonsynonymous		aGg/aAg	R832K			
chr7:703922					INS						*/+A	Frame shift, 1 bp insert	YGR108W		161	CLB1	B-type cyclin involved in cell cycle progression; activates Cdc28p to promote the transition from G2 to M phase; accumulates during G2 and M, then targeted via a destruction box motif for ubiquitin-mediated degradation by the proteasome; CLB1 has a paralog, CLB2, that arose from the whole genome duplication	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=CLB1
chr7:859863					SNV						C/T	Nonsynonymous	YGR184C	Gat/Aat	D1901N	UBR1	E3 ubiquitin ligase (N-recognin); heterodimerizes with Rad6p to ubiquitinate substrates in the N-end rule pathway; role in endoplasmic reticulum-associated protein degradation (ERAD) in the absence of canonical ER membrane ligases or after stress; major role in targeting misfolded cytosolic proteins for degradation; regulates peptide transport via Cup9p ubiquitination; mutation in human UBR1 causes Johansson-Blizzard Syndrome (JBS)	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=UBR1
chr7:1008542					SNV						A/T	Nonsynonymous	YGR258C	gTt/gAt	V664D	RAD2	Single-stranded DNA endonuclease; cleaves single-stranded DNA during nucleotide excision repair to excise damaged DNA; subunit of Nucleotide Excision Repair Factor 3 (NEF3); homolog of human XPG protein	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=RAD2
chr8:46429					SNV						G/A	Stop gained	YHL026C	Caa/Taa	Q301*		Putative protein of unknown function; transcriptionally regulated by Upc2p via an upstream sterol response element; YHL026C is not an essential gene; in 2005 the start site was moved 141 nt upstream	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=YHL026
chr9:183945					SNV						C/T	Nonsynonymous	YIL095W	cCa/cTa	P4L	PRK1	Protein serine/threonine kinase; regulates the organization and function of the actin cytoskeleton and reduces endocytic ability of cell through the phosphorylation of the Pan1p-Sla1p-End3p protein complex; PRK1 has a paralog, ARK1, that arose from the whole genome duplication	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=PRK1
chr10:310014					SNV						C/A	Nonsynonymous	YJL058C	Gca/Tca	A142S	BIT61	Subunit of TORC2 membrane-associated complex; involved in regulation of cell cycle-dependent actin cytoskeletal dynamics during polarized growth and cell wall integrity; BIT61 has a paralog, BIT2, that arose from the whole genome duplication	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=BIT61

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	AAC	M715	MH23	MH34	A64	B130	B184	C120	D5	F83								
chr11:102903					SNV						T/C	Nonsynonymous	YKL182W	tTa/tCa	L751S	FAS1	Beta subunit of fatty acid synthetase; complex catalyzes the synthesis of long-chain saturated fatty acids; contains acetyltransacylase, dehydratase, enoyl reductase, malonyl transacylase, and palmitoyl transacylase activities	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=FAS1
chr12:674166					SNV						T/C	Nonsynonymous	YLR273C	Aat/Gat	N633D	PIG1	Putative targeting subunit for type-1 protein phosphatase Glc7p; tethers Glc7p to Gsy2p glycogen synthase; PIG1 has a paralog, GAC1, that arose from the whole genome duplication	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=PIG1
chr12:805637					SNV						A/T	Stop gained	YLR345W	Aaa/Taa	K39*		Similar to 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase enzymes responsible for the metabolism of fructoso-2,6-bisphosphate; mRNA expression is repressed by the Rfx1p-Tup1p-	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=YLR345
chr12:856143					SNV						G/A	Nonsynonymous	YLR373C	CCg/TTg	P17L	VID22	Glycosylated integral membrane protein localized to plasma membrane; plays a role in fructose-1,6-bisphosphatase (FBPase) degradation; involved in FBPase transport from the cytosol to Vid (vacuole import and degradation) vesicles; VID22 has a paralog, ENV11, that arose from the whole genome duplication	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=VID22
chr12:856144					SNV						G/A							
chr13:118428					SNV						G/A	Nonsynonymous	YML073C	tCt/tTt	S156F	RPL6A	Ribosomal 60S subunit protein L6A; N-terminally acetylated; binds 5.8S rRNA; homologous to mammalian ribosomal protein L6, no bacterial homolog; RPL6A has a paralog, RPL6B, that arose from the whole genome duplication	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=RPL6A
chr13:274080					SNV						C/T	Nonsynonymous	YMR006C	gGt/gAt	G108D	PLB2	Phospholipase B (lysophospholipase) involved in lipid metabolism; displays transacylase activity in vitro; overproduction confers resistance to lysophosphatidylcholine	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=PLB2
chr14:309348					SNV						G/A	Nonsynonymous	YNL172W	aGa/aAa	R1584K	APC1	Largest subunit of the Anaphase-Promoting Complex/Cyclosome; APC/C is a ubiquitin-protein ligase required for degradation of anaphase inhibitors, including mitotic cyclins, during the metaphase/anaphase transition; component of the platform domain of the APC/C, based on structural analysis; localizes to nuclear foci that become diffuse upon DNA replication stress	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=APC1
chr14:650938					SNV						G/A	Nonsynonymous	YNR016C	cCt/cTt	P1488L	ACC1	Acetyl-CoA carboxylase, biotin containing enzyme; catalyzes carboxylation of cytosolic acetyl-CoA to form malonyl-CoA and regulates histone acetylation by regulating the availablity of acetyl-CoA; required for de novo biosynthesis of long-chain fatty acids; ACC1 has a paralog, HFA1, that arose from the whole genome duplication	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=ACC1
chr15:535728					SNV						C/T	Nonsynonymous	YOR113W	tCt/tTt	S476F	AZF1	Zinc-finger transcription factor; involved in diauxic shift; in the presence of glucose, activates transcription of genes involved in growth and carbon metabolism; in nonfermentable carbon sources, activates transcription of genes involved in maintenance of cell wall integrity; relocalizes to the cytosol in response to hypoxia	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=AZF1
chr15:617684					SNV						G/A	Nonsynonymous	YOR152C	Cca/Tca	P170S		Putative protein of unknown function; YOR152C is not an essential gene	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=YOR15
chr15:817509					SNV						C/T	Nonsynonymous	YOR262W	cCg/cTg	P108L	GPN2	Putative GTPase with a role in biogenesis of RNA pol II and polIII; may be involved in assembly of RNA polymerases II and III and in their transport into the nucleus; contains a Gly-Pro-Asn motif in the G domain; similar to Npa3p and Gpn3p; highly conserved across species and homologous to human gene GPN2/ATPBD1B; required for establishment of sister chromatid cohesion	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=GPN2
chr16:146402					SNV						G/A	Stop gained	YPL216W	tgG/tgA	W882*		Putative protein of unknown function; not an essential gene; YPL216W has a paralog, ITC1, that arose from the whole genome duplication	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=YPL216

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	AAC	**M715**	**MH23**	**MH34**	**A64**	**B130**	**B184**	**C120**	**D5**	**F83**								
chr16:274950					SNV						C/T	Stop gained	YPL147W	Caa/Taa	Q605*	PXA1	Subunit of a heterodimeric peroxisomal ABC transport complex; required for import of long-chain fatty acids into peroxisomes; similarity to human adrenoleukodystrophy transporter ABCD1 and ABCD2 and ALD-related proteins; mutations in ABCD1 cause X-linked adrenoleukodystrophy (X-ALD), a peroxisomal disorder; complex also includes Pxa2p	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=PXA1
chr16:651647					SNV						G/A	Nonsynonymous	YPR042C	tCa/tTa	S648L	PUF2	mRNA-binding protein; member of the PUF protein family, which is defined by the presence of Pumilio homology domains that confer RNA binding activity; preferentially binds mRNAs encoding membrane-associated proteins; PUF2 has a paralog, JSN1, that arose from the whole genome duplication	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=PUF2
chr7:646593		SNV									G/T	Nonsynonymous	YGR083C	agC/agA	S2R	GCD2	Delta subunit of the translation initiation factor eIF2B; the guanine-nucleotide exchange factor for eIF2; activity subsequently regulated by phosphorylated eIF2; first identified as a negative regulator of GCN4 expression	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=GCD2
chr15:918128		SNV									G/A	Nonsynonymous	YOR321W	Gcg/Acg	A736T	PMT3	Protein O-mannosyltransferase; transfers mannose residues from dolichyl phosphate-D-mannose to protein serine/threonine residues; acts in a complex with Pmt5p, can instead interact with Pmt1p in some conditions; antifungal drug target; PMT3 has a paralog, PMT2, that arose from the whole genome duplication	http://www.yeastgenome.org/cgi-bin/locus.fpl?locus=PMT3