

Table S1. List CTBT sensitive mutant strains. +, growth; sl, slow growth; -, no growth.

ORF	Gene name	CTBT		Description
		2 ug/ml	4 ug/ml	
YOL086C	<i>ADH1</i>	-	-	Alcohol dehydrogenase
YER017C	<i>AFG3</i>	+	-	Component of the mitochondrial inner membrane m-AAA protease
YDR264C	<i>AKR1</i>	sl	-	Palmitoyl transferase involved in protein palmitoylation required for endocytosis
YEL036C	<i>ANP1</i>	sl	-	Subunit of the alpha-1,6 mannosyltransferase complex
YHR013C	<i>ARD1</i>	sl	-	Subunit of the N-terminal acetyltransferase NatA (Nat1p, Ard1p, Nat5p)
YDR173C	<i>ARG82</i>	+	sl	Inositol polyphosphate multikinase (IPMK)
YNL059C	<i>ARP5</i>	-	-	Nuclear actin-related protein involved in chromatin remodeling
YMR116C	<i>ASC1</i>	sl	-	G-protein beta subunit and guanine nucleotide dissociation inhibitor for Gpa2p
YBL099W	<i>ATP1</i>	sl	sl	Alpha subunit of the F1 sector of mitochondrial F1F0 ATP synthase
YNL315C	<i>ATP11</i>	-	-	Molecular chaperone, required for the assembly of alpha and beta subunits into the F1 sector of mitochondrial F1F0 ATP synthase
YJL180C	<i>ATP12</i>	-	-	Protein required for assembly of alpha and beta subunits into the F1 sector of mitochondrial F1F0 ATP synthase
YML081C-A	<i>ATP18</i>	+	sl	Subunit of the mitochondrial F1F0 ATP synthase
YNL101W	<i>AVT4</i>	+	sl	Vacuolar transporter, exports large neutral amino acids from the vacuole
YJL095W	<i>BCK1</i>	+	-	Mitogen-activated protein (MAP) kinase kinase kinase
YBR200W	<i>BEM1</i>	sl	sl	Protein containing SH3-domains, scaffold protein for complexes that include Cdc24p, Ste5p, Ste20p, and Rsr1p
YER016W	<i>BIM1</i>	sl	sl	Microtubule-binding protein
YOR026W	<i>BUB3</i>	sl	sl	Kinetochore checkpoint WD40 repeat protein
YER014C-A	<i>BUD25</i>	sl	-	Protein involved in bud-site selection
YFL023W	<i>BUD27</i>	+	sl	Protein involved in bud-site selection, nutrient signaling, and gene expression controlled by TOR kinase
YLR226W	<i>BUR2</i>	sl	-	Cyclin for the Sgv1p (Bur1p) protein kinase
YMR038C	<i>CCS1</i>	-	-	Copper chaperone for superoxide dismutase Sod1p
YCR094W	<i>CDC50</i>	sl	-	Endosomal protein that regulates cell polarity
YLR418C	<i>CDC73</i>	sl	-	Constituent of Paf1 complex with RNA polymerase II, Paf1p, Hpr1p, Ctr9, Leo1, Rtf1 and Ccr4p
YER026C	<i>CHO1</i>	-	-	Phosphatidylserine synthase, functions in phospholipid biosynthesis
YGR157W	<i>CHO2</i>	+	-	Phosphatidylethanolamine methyltransferase (PEMT)
YMR198W	<i>CIK1</i>	sl	-	Kinesin-associated protein
YNR001C	<i>CIT1</i>	sl	-	Citrate synthase

YCR086W	<i>CSM1</i>	sl	-	Nucleolar protein that binds Mam1p at kinetochores during meiosis I to mediate accurate chromosome segregation
YMR078C	<i>CTF18</i>	+	-	Subunit of a complex with Ctf8p, required for sister chromatin cohesion
YKL139W	<i>CTK1</i>	sl	-	Catalytic (alpha) subunit of C-terminal domain kinase I (CTDK-I) involved in phosphorylation of RNA polymerase II
YPR124W	<i>CTR1</i>	-	-	High-affinity copper transporter of the plasma membrane
YCL007C	<i>CWH36</i>	sl	-	Dubious ORF, overlapping YCL005W-A encoding subunit e of the V-ATPase V0 subcomplex
YAL012W	<i>CYS3</i>	-	-	Cystathionine gamma-lyase
YOR065W	<i>CYT1</i>	sl	-	Cytochrome c1, component of the mitochondrial respiratory chain
YPL170W	<i>DAP1</i>	-	-	Heme-binding protein involved in regulation of cytochrome P450 protein Erg11p
YOR080W	<i>DIA2</i>	+	-	Origin-binding F-box protein that forms an SCF ubiquitin ligase complex
YHR011W	<i>DIA4</i>	sl	-	Probable mitochondrial seryl-tRNA synthetase
YEL059W	<i>ENV6</i>	sl	sl	Involved at the late endosome and vacuole interface
YMR202W	<i>ERG2</i>	+	-	C-8 sterol isomerase
YNL280C	<i>ERG24</i>	sl	-	C-14 sterol reductase, acts in ergosterol biosynthesis
YLR056W	<i>ERG3</i>	sl	-	C-5 sterol desaturase
YML008C	<i>ERG6</i>	+	-	Delta(24)-sterol C-methyltransferase
YIL097W	<i>FYV10</i>	+	sl	Protein of unknown function, involved in proteasomal ubiquitin dependent protein catabolic process
YHR100C	<i>GEP4</i>	sl	-	Protein of unknown function, required for respiratory growth
YER083C	<i>GET2</i>	sl	sl	Subunit of the GET complex
YHR183W	<i>GND1</i>	-	-	6-phosphogluconate dehydrogenase (decarboxylating)
YGL194C	<i>HOS2</i>	+	-	Histone deacetylase
YDR138W	<i>HPR1</i>	sl	-	Subunit of THO/TREX complexes that couple transcription elongation with mitotic recombination and with mRNA metabolism and export
YOL012C	<i>HTZ1</i>	sl	-	Histone variant H2AZ
YEL044W	<i>IES6</i>	sl	-	Protein that associates with the INO80 chromatin remodeling complex under low-salt conditions
YER086W	<i>ILV1</i>	sl	-	Threonine deaminase, catalyzes the first step in isoleucine biosynthesis
YMR150C	<i>IMP1</i>	+	sl	Catalytic subunit of the mitochondrial inner membrane peptidase complex
YLL027W	<i>ISA1</i>	-	-	Mitochondrial matrix protein involved in biogenesis of the iron-sulfur (Fe/S) cluster of Fe/S proteins
YPR067W	<i>ISA2</i>	sl	-	Protein required for maturation of mitochondrial and cytosolic Fe/S proteins
YDR017C	<i>KCS1</i>	+	-	Inositol hexakisphosphate (IP6) and inositol

				heptakisphosphate (IP7) kinase
YDR532C	<i>KRE28</i>	sl	-	Protein of unknown function
YLR244C	<i>MAP1</i>	-	-	Methionine aminopeptidase
YMR060C	<i>MAS37</i>	sl	-	Component of the Sorting and Assembly Machinery (SAM or TOB complex) of the mitochondrial outer membrane
YOR147W	<i>MDM32</i>	-	-	Mitochondrial inner membrane protein with similarity to Mdm31p
YOL027C	<i>MDM38</i>	sl	-	Mitochondrial inner membrane protein
YDL005C	<i>MED2</i>	-	-	Subunit of the RNA polymerase II mediator complex
YIL128W	<i>MET18</i>	sl	-	DNA repair and TFIIH regulator
YIR033W	<i>MGA2</i>	-	-	ER membrane protein involved in regulation of <i>OLE1</i> transcription
YOR211C	<i>MGM1</i>	sl	-	Mitochondrial GTPase related to dynamin
YOR330C	<i>MIP1</i>	sl	-	Catalytic subunit of the mitochondrial DNA polymerase
YPR164W	<i>MMS1</i>	sl	-	Protein that acts with Mms22p in a DNA repair pathway
YBR098W	<i>MMS4</i>	-	-	Subunit of the structure-specific Mms4p-Mus81p endonuclease
YMR224C	<i>MRE11</i>	-	-	Subunit of a complex with Rad50p and Xrs2p (MRX complex)
YJL096W	<i>MRPL49</i>	+	sl	Mitochondrial ribosomal protein of the large subunit
YGR165W	<i>MRPS35</i>	sl	-	Mitochondrial ribosomal protein of the small subunit
YIR021W	<i>MRS1</i>	+	sl	Protein required for the splicing of two mitochondrial group I introns (BI3 in COB and AI5beta in COX1)
YPL097W	<i>MSY1</i>	-	-	Mitochondrial tyrosyl-tRNA synthetase
YDR128W	<i>MTC5</i>	sl	-	Protein of unknown function, involved in maintenance of telomere capping
YMR097C	<i>MTG1</i>	sl	-	Peripheral GTPase of the mitochondrial inner membrane
YGR055W	<i>MUP1</i>	-	-	High affinity methionine permease
YDL040C	<i>NAT1</i>	sl	-	Subunit of the N-terminal acetyltransferase NatA (Nat1p, Ard1p, Nat5p)
YPR131C	<i>NAT3</i>	-	-	Catalytic subunit of the NatB N-terminal acetyltransferase
YDR162C	<i>NBP2</i>	+	sl	Protein involved in the HOG (high osmolarity glycerol) pathway
YJL206C-A	<i>NCE101</i>	-	-	Protein of unknown function, involved in protein secretion+E121
YOR209C	<i>NPT1</i>	-	-	Nicotinate phosphoribosyltransferase
YDL167C	<i>NRP1</i>	sl	-	Putative RNA binding protein of unknown function
YKR082W	<i>NUP133</i>	sl	sl	Subunit of the Nup84p subcomplex of the nuclear pore complex (NPC)
YGL038C	<i>OCH1</i>	sl	-	Mannosyltransferase of the cis-Golgi apparatus
YKL134C	<i>OCT1</i>	sl	-	Mitochondrial intermediate peptidase
YHL020C	<i>OPI1</i>	+	-	Transcriptional regulator of a variety of genes involved in lipid metabolism

YLR350W	<i>ORM2</i>	sl	-	Evolutionarily conserved protein with similarity to Orm1p, involved in response to unfolded proteins
YGR101W	<i>PCP1</i>	sl	-	Mitochondrial serine protease
YLR044C	<i>PDC1</i>	+	-	Major of three pyruvate decarboxylase isozymes
YGL025C	<i>PGD1</i>	sl	-	Subunit of the RNA polymerase II mediator complex
YGR132C	<i>PHB1</i>	sl	-	Subunit of the prohibitin complex (Phb1p-Phb2p), inner mitochondrial membrane chaperone
YPL031C	<i>PHO85</i>	sl	-	Cyclin-dependent kinase
YGR135W	<i>PRE9</i>	sl	-	Alpha 3 subunit of the 20S proteasome, the only nonessential 20S subunit
YOR323C	<i>PRO2</i>	+	-	Gamma-glutamyl phosphate reductase
YCR066W	<i>RAD18</i>	sl	-	Protein involved in postreplication repair
YNL250W	<i>RAD50</i>	+	-	Subunit of MRX complex, with Mre11p and Xrs2p
YER095W	<i>RAD51</i>	-	-	Strand exchange protein, forms a helical filament with DNA that searches for homology
YGL163C	<i>RAD54</i>	sl	-	DNA-dependent ATPase
YDR004W	<i>RAD57</i>	sl	-	Protein that stimulates strand exchange by stabilizing the binding of Rad51p to single-stranded DNA
YGL058W	<i>RAD6</i>	sl	-	Ubiquitin-conjugating enzyme (E2)
YGL246C	<i>RAI1</i>	sl	-	Nuclear protein that binds to and stabilizes the exoribonuclease Rat1p
YJL204C	<i>RCY1</i>	-	-	F-box protein involved in recycling plasma membrane proteins
YDR195W	<i>REF2</i>	sl	-	RNA-binding protein involved in the cleavage step of mRNA 3'-end formation prior to polyadenylation
YDR028C	<i>REG1</i>	-	-	Regulatory subunit of type 1 protein phosphatase Glc7p
YER067W	<i>RG11</i>	sl	sl	Putative protein of unknown function
YGR044C	<i>RME1</i>	+	sl	Zinc finger protein involved in control of meiosis
YEL050C	<i>RML2</i>	sl	-	Mitochondrial ribosomal protein of the large subunit
YGR180C	<i>RNR4</i>	+	-	Ribonucleotide-diphosphate reductase (RNR), small subunit
YBL093C	<i>ROX3</i>	+	-	Subunit of the RNA polymerase II mediator complex
YJL121C	<i>RPE1</i>	+	-	D-ribulose-5-phosphate 3-epimerase
YGL135W	<i>RPL1B</i>	sl	-	N-terminally acetylated protein component of the large (60S) ribosomal subunit
YFR031C-A	<i>RPL2A</i>	+	sl	Protein component of the large (60S) ribosomal subunit
YHR141C	<i>RPL42B</i>	-	-	Protein component of the large (60S) ribosomal subunit
YBL025W	<i>RRN10</i>	sl	-	Protein involved in promoting high level transcription of rDNA
YGR056W	<i>RSC1</i>	sl	sl	Component of the RSC chromatin remodeling complex
YNR037C	<i>RSM19</i>	sl	-	Mitochondrial ribosomal protein of the small subunit
YOL138C	<i>RTC1</i>	sl	sl	Protein of unknown function
YGL244W	<i>RTF1</i>	sl	-	Subunit of the RNA polymerase II-associated Paf1 complex
YLL002W	<i>RTT109</i>	sl	-	Histone acetyltransferase

YER087C-A	<i>SBH1</i>	+	sl	Beta subunit of the Sec61p ER translocation complex (Sec61p-Sss1p-Sbh1p)
YGL066W	<i>SGF73</i>	sl	sl	Subunit of SAGA histone acetyltransferase complex
YHR206W	<i>SKN7</i>	+	sl	Nuclear response regulator and transcription factor
YDR477W	<i>SNF1</i>	sl	-	AMP-activated serine/threonine protein kinase
YOR290C	<i>SNF2</i>	sl	-	Catalytic subunit of the SWI/SNF chromatin remodeling complex
YJR104C	<i>SOD1</i>	-	-	Cytosolic superoxide dismutase
YHR008C	<i>SOD2</i>	-	-	Mitochondrial superoxide dismutase
YOL148C	<i>SPT20</i>	-	-	Subunit of the SAGA transcriptional regulatory complex
YGR063C	<i>SPT4</i>	sl	-	Protein involved in the regulating Pol I and Pol II transcription
YGR104C	<i>SRB5</i>	sl	-	Subunit of the RNA polymerase II mediator complex
YDR463W	<i>STP1</i>	sl	sl	Transcription factor, activates transcription of amino acid permease genes
YJL176C	<i>SWI3</i>	sl	-	Subunit of the SWI/SNF chromatin remodeling complex
YER111C	<i>SWI4</i>	+	-	DNA binding component of the SBF complex (Swi4p-Swi6p)
YPL129W	<i>TAF14</i>	-	-	Subunit of TFIID, TFIIF, INO80, SWI/SNF, and NuA3 complexes
YBR069C	<i>TAT1</i>	+	-	Amino acid transport protein for valine, leucine, isoleucine, and tyrosine
YDL185W	<i>TFP1</i>	sl	-	Vacuolar ATPase V1 domain subunit A
YPL234C	<i>TFP3</i>	sl	-	Vacuolar ATPase V0 domain subunit c'
YNL139C	<i>THO2</i>	+	sl	Subunit of the THO complex which is required for efficient transcription elongation
YER090W	<i>TRP2</i>	-	-	Anthranilate synthase, catalyzes the initial step of tryptophan biosynthesis
YKL211C	<i>TRP3</i>	+	-	Bifunctional enzyme exhibiting both indole-3-glycerol-phosphate synthase and anthranilate synthase activities
YGL026C	<i>TRP5</i>	sl	-	Tryptophan synthase involved in tryptophan biosynthesis
YOR187W	<i>TUF1</i>	sl	sl	Mitochondrial translation elongation factor Tu
YDR207C	<i>UME6</i>	sl	-	Key transcriptional regulator of early meiotic genes
YGR105W	<i>VMA21</i>	+	sl	Integral membrane protein that is required for vacuolar H ⁺ -ATPase (V-ATPase) function
YHR060W	<i>VMA22</i>	sl	-	Peripheral membrane protein that is required for vacuolar H ⁺ -ATPase (V-ATPase) function
YOR332W	<i>VMA4</i>	sl	-	Subunit E of the eight-subunit V1 peripheral membrane domain of the vacuolar H ⁺ -ATPase (V-ATPase)
YBR097W	<i>VPS15</i>	sl	-	Myristoylated serine/threonine protein kinase
YMR077C	<i>VPS20</i>	+	-	Myristoylated subunit of ESCRTIII, the endosomal sorting complex
YLR240W	<i>VPS34</i>	sl	-	Phosphatidylinositol 3-kinase
YDR369C	<i>XRS2</i>	sl	-	Protein required for DNA repair
YNL107W	<i>YAF9</i>	sl	-	Subunit of both the NuA4 histone H4 acetyltransferase complex and the SWR1 complex
YML007W	<i>YAP1</i>	+	-	Basic leucine zipper (bZIP) transcription factor

YOL028C	<i>YAP7</i>	sl	-	Putative basic leucine zipper (bZIP) transcription factor
YMR151W	<i>YIM2</i>	+	-	Dubious open reading frame, overlapping the <i>IMP1</i> promoter
YBL100C		sl	sl	Dubious open reading frame, overlapping the <i>ATP1</i> gene
YDR008C		sl	-	Dubious open reading frame, overlapping the <i>TRP1</i> gene
YDR049W		sl	-	Zinc finger protein
YDR114C		+	sl	Putative protein of unknown function, overlapping YDR115w
YDR115W		+	sl	Putative mitochondrial ribosomal protein of the large subunit
YGL024W		sl	-	Dubious open reading frame, overlapping the <i>PGD1</i> gene involved in RNA polymerase II mediator complex
YGL085W		sl	sl	Putative mitochondrial protein of unknown function, induced in response to MMS
YGR064W		sl	-	Dubious open reading frame, overlapping the <i>SPT4</i> gene
YHR045W		-	-	Putative protein of unknown function, synthetically lethal with <i>ERG11</i>
YJL120W		+	-	Dubious open reading frame, overlapping the <i>RPE1</i> promoter
YJL175W		sl	-	Dubious open reading frame, overlapping the <i>SWI3</i> gene
YJL182C		-	-	Dubious open reading frame, overlapping the YJL181w promoter
YJR018W		+	-	Dubious open reading frame, overlapping the <i>ESS1</i> gene involved in regulation of the RNA polymerase II phosphorylation
YMR031W-A		sl	-	Dubious open reading frame
YNR065C		sl	sl	Protein of unknown function
YOR305W		+	sl	Protein of unknown function, putative mitochondrial protein
YOR331C		sl	-	Dubious open reading frame, overlapping the <i>VMA4</i> gene encoding subunit of the V-ATPase V1 subcomplex
