

Table S2 related to Figure 6 and Figure S5
Top 171 genes showing 30% growth defect in the presence of 0.6 mg/ml AZC compared to wild-type.

Systematic Name	Gene/TS Allele	Average Score	Name Description
1 YBR067C	TIP1	-0.805455	Temperature shock-Inducible Protein
2 YBR082C	UBC4	-0.711185	UBiquitin-Conjugating
3 YBR082C	UBC4	-0.676755	UBiquitin-Conjugating
4 YPL144W	POC4	-0.666215	PrOteasome Chaperone
5 YML111W	BUL2	-0.623745	Binds UBiquitin Ligase
6 YML099C	ARG81	-0.605765	ARGinine requiring
7 YCR053W	THR4	-0.60126	THReonine requiring
8 YOR035C	SHE4	-0.592995	Swi5p-dependent HO Expression
9 YML100W-A		-0.587035	
10 YEL062W	NPR2	-0.585935	Nitrogen Permease Regulator
11 YOR014W	RTS1	-0.520575	Rox Three Suppressor
12 YJR139C	HOM6	-0.51992	HOMoserine requiring
13 YHL025W	SNF6	-0.518725	Sucrose NonFermenting
14 YHR025W	THR1	-0.516405	THReonine requiring
15 YDR216W	ADR1	-0.49421	Alcohol Dehydrogenase II synthesis Regulator
16 YPR051W	MAK3	-0.476835	MAintenance of Killer
17 YPL157W	TGS1	-0.47618	TrimethylGuanosine Synthase
18 YLR438W	CAR2	-0.46403	Catabolism of ARGinine
19 YOR027W	STI1	-0.453735	STress Inducible
20 YMR202W	ERG2	-0.448985	ERGosterol biosynthesis
21 YNL323W	LEM3	-0.44173	Ligand-Effect Modulator
22 YFL023W	BUD27	-0.439285	BUD site selection
23 YNR051C	BRE5	-0.42672	BREfeldin A sensitivity
24 YOR026W	BUB3	-0.423785	Budding Uninhibited by Benzimidazole
25 YFR010W	UBP6	-0.417845	UBiquitin-specific Protease
26 YMR294W	JNM1	-0.41727	Just Nuclear Migration
27 YDL001W	RMD1	-0.416315	Required for Meiotic nuclear Division
28 YJL175W		-0.413185	
29 YDL192W	ARF1	-0.404275	ADP-Ribosylation Factor
30 YDR049W	VMS1	-0.402475	VCP/Cdc48-associated Mitochondrial Stress-responsive
31 YOL087C	DUF1	-0.40126	DUB-associated Factor 1
32 YLR065C	SND2	-0.396995	SRP-INDependent targeting
33 YDR048C		-0.392555	
34 YNL215W	IES2	-0.390735	Ino Eighty Subunit
35 YLR021W	IRC25	-0.390425	Increased Recombination Centers
36 YLR199C	PBA1	-0.385935	Proteasome Biogenesis-Associated
37 YDR108W	TRS85	-0.38476	TRapp Subunit
38 YLR056W	ERG3	-0.370365	ERGosterol biosynthesis
39 YBR289W	SNF5	-0.369755	Sucrose NonFermenting
40 YPL052W	OAZ1	-0.368495	Ornithine decarboxylase AntiZyme
41 YOL115W	PAP2	-0.36712	Poly(A) Polymerase
42 YBR272C	HSM3	-0.364905	enHanced Spontaneous Mutability
43 YPL174C	NIP100	-0.36426	Nuclear ImPort
44 YLR386W	VAC14	-0.362385	VACuole morphology and inheritance mutant
45 YGR184C	UBR1	-0.360765	
46 YLR370C	ARC18	-0.359755	Arp2/3 Complex subunit
47 YMR042W	ARG80	-0.35804	ARGinine requiring
48 YDR241W	BUD26	-0.3575	BUD site selection
49 YDR293C	SSD1	-0.35511	Suppressor of SIT4 Deletion
50 YPL111W	CAR1	-0.35364	Catabolism of ARGinine
51 YOR124C	UBP2	-0.353375	UBiquitin-specific Protease
52 YPL181W	CTI6	-0.350165	Cyc8-Tup1 Interacting protein
53 YGR135W	PRE9	-0.346515	PRoteinase yscE
54 YER151C	UBP3	-0.343515	UBiquitin-specific Protease
55 YHL023C	NPR3	-0.342885	Nitrogen Permease Regulator
56 YLR444C		-0.341315	
57 YNL242W	ATG2	-0.33593	AuTophagy related
58 YBL094C		-0.33563	
59 YOL001W	PHO80	-0.334455	PHOSphate metabolism
60 YLR398C	SKI2	-0.332145	SuperKiller
61 YOL071W	SDH5	-0.33206	Succinate DeHydrogenase
62 YNL238W	KEX2	-0.33111	Killer EXpression defective
63 YPL047W	SGF11	-0.328355	SaGa associated Factor 11kDa
64 YBR098W	MMS4	-0.321545	Methyl MethaneSulfonate sensitivity
65 YGL066W	SGF73	-0.32044	SaGa associated Factor. 73 kDa
66 YCR009C	RVS161	-0.318465	Reduced Viability on Starvation
67 YMR299C	DYN3	-0.31443	DYNein
68 YKR084C	HBS1	-0.31392	Hsp70 subfamily B Suppressor
69 YLL029W	FRA1	-0.311025	Fe Repressor of Activation
70 YKL109W	HAP4	-0.3103	Heme Activator Protein
71 YBR048W	RPS11B	-0.307865	Ribosomal Protein of the Small subunit
72 YHR129C	ARP1	-0.307125	Actin-Related Protein
73 YJL103C	GSM1	-0.30655	Glucose Starvation Modulator
74 YMR099C		-0.306205	
75 YBR078W	ECM33	-0.30532	ExtraCellular Mutant
76 YNL319W		-0.304255	
77 YOR243C	PUS7	-0.30323	PseudoUridine Synthase
78 YML017W	PSP2	-0.303025	Polymerase SuPpressor
79 YCL010C	SGF29	-0.301545	SaGa associated Factor
80 YGR178C	PBP1	-0.300395	Pab1p-Binding Protein
81 YKL145W	rpt1-1	-0.79946	Regulatory Particle Triple-A protein. or Regulatory Particle Triphosphatase
82 YOR259C	rpt4-150	-0.75261	Regulatory Particle Triple-A protein. or Regulatory Particle Triphosphatase
83 YOR181W	las17-1	-0.72392	
84 YOR259C	rpt4-145	-0.72274	Regulatory Particle Triple-A protein. or Regulatory Particle Triphosphatase
85 YHR027C	rpn1-821	-0.72224	Regulatory Particle Non-ATPase
86 YOR157C	pup1-1	-0.71925	PUTative Proteasome subunit
87 YKL210W	uba1-1	-0.69896	UBiquitin Activating

88	YGL048C	rpt6-20	-0.68112	Regulatory Particle Triple-A protein. or Regulatory Particle Triphosphatase
89	YER012W	pre1-1	-0.68082	Proteinase yscE
90	YDL028C	mps1-1	-0.67534	MonoPolar Spindle
91	YFR004W	rpn11-14	-0.66412	Regulatory Particle Non-ATPase
92	YOR259C	rpt4-145	-0.64914	Regulatory Particle Triple-A protein. or Regulatory Particle Triphosphatase
93	YGL048C	rpt6-25	-0.6186	Regulatory Particle Triple-A protein. or Regulatory Particle Triphosphatase
94	YER013W	prp22-1	-0.61843	Pre-mRNA Processing
95	YLL036C	prp19-1	-0.61785	Pre-RNA Processing
96	YFR004W	rpn11-8	-0.61697	Regulatory Particle Non-ATPase
97	YDL097C	rpn6-1	-0.61475	Regulatory Particle Non-ATPase
98	YOR259C	rpt4-150	-0.6103	Regulatory Particle Triple-A protein. or Regulatory Particle Triphosphatase
99	YPL094C	sec62-ts	-0.60522	SECretoary
100	YNL118C	dcp2-7A	-0.60487	mRNA DeCaPping
101	YHR052W	cic1-2	-0.60383	Core Interacting Component
102	YDR356W	spc110-221	-0.59962	Spindle Pole Component
103	YGR113W	dam1-19	-0.59487	Duo1 And Mps1 interacting
104	YGL073W	hsf1-848	-0.59179	Heat Shock transcription Factor
105	YFR052W	rpn12-1	-0.58521	Regulatory Particle Non-ATPase
106	YGR158C	mtr3-ts	-0.57913	MRNA TRansport
107	YHR007C	erg11-td	-0.5702	ERGosterol biosynthesis
108	YHR027C	rpn1-821	-0.56878	Regulatory Particle Non-ATPase
109	YOR257W	cdc31-2	-0.56553	Cell Division Cycle
110	YPR108W	rpn7-3	-0.56501	Regulatory Particle Non-ATPase
111	YER012W	pre1-1	-0.54708	Proteinase yscE
112	YDR394W	rpt3-1	-0.53756	Regulatory Particle Triple-A protein. or Regulatory Particle Triphosphatase
113	YER013W	prp22-1	-0.53374	Pre-mRNA Processing
114	YBR160W	cdc28-1	-0.52693	Cell Division Cycle
115	YBR160W	cdc28-1	-0.52659	Cell Division Cycle
116	YOR157C	pup1-1	-0.51747	PUTative Proteasome subunit
117	YGL048C	rpt6-1	-0.51416	Regulatory Particle Triple-A protein. or Regulatory Particle Triphosphatase
118	YLR045C	stu2-10	-0.50558	Suppressor of TUBulin
119	YDR021W	fal1-1	-0.50408	eukaryotic translation initiation factor Four A Like
120	YJL091C	gwt1-20	-0.49441	GPI-anchored Wall protein Transfer
121	YOL139C	cdc33-E72G	-0.48909	Cell Division Cycle
122	YLR298C	yhc1-7	-0.48802	Yeast Homolog of human U1C
123	YDR373W	frq1-1	-0.48729	FReQuenin homolog
124	YGL048C	rpt6-25	-0.48137	Regulatory Particle Triple-A protein. or Regulatory Particle Triphosphatase
125	YDR356W	spc110-221	-0.46963	Spindle Pole Component
126	YOR257W	cdc31-2	-0.46954	Cell Division Cycle
127	YDR087C	rrp1-1	-0.46365	Ribosomal RNA Processing
128	YDL028C	mps1-1	-0.46314	MonoPolar Spindle
129	YMR236W	taf9-ts2	-0.45798	TATA binding protein-Associated Factor
130	YGR099W	tel2-7	-0.44898	TELOmere maintenance
131	YLR045C	stu2-11	-0.44382	Suppressor of TUBulin
132	YGR140W	cbf2-1	-0.44184	Centromere-Binding Factor
133	YKR086W	prp16-2	-0.42997	Pre-mRNA Processing
134	YOL139C	cdc33-E72G	-0.42853	Cell Division Cycle
135	YDL105W	nse4-ts3	-0.42348	Non-SMC Element
136	YNL262W	pol2-12	-0.41355	POLymerase
137	YDR189W	sly1-ts	-0.4119	Suppressor of Loss of Ypt1
138	YCR093W	cdc39-1	-0.41185	Cell Division Cycle
139	YNL163C	ria1-ts	-0.41104	Ribosome Assembly
140	YPL124W	spc29-20	-0.4106	Spindle Pole Component
141	YDR311W	tfb1-6	-0.39358	Transcription Factor B
142	YPR178W	prp4-1	-0.39338	Pre-mRNA Processing
143	YDR182W	cdc1-4	-0.38955	Cell Division Cycle
144	YNR011C	prp2-1	-0.38738	Pre-mRNA Processing
145	YGR113W	dam1-19	-0.38377	Duo1 And Mps1 interacting
146	YPL209C	ipl1-1	-0.38304	Increase in PLoidy
147	YHR191C	ctf8-162	-0.38212	Chromosome Transmission Fidelity
148	YMR079W	sec14-3	-0.38163	SECretoary
149	YJL194W	cdc6-1	-0.37697	Cell Division Cycle
150	YLL036C	prp19-1	-0.37668	Pre-RNA Processing
151	YLR310C	cdc25-1	-0.3753	Cell Division Cycle
152	YER147C	scc4-4	-0.36757	Sister Chromatid Cohesion
153	YKL145W	rpt1-1	-0.36652	Regulatory Particle Triple-A protein. or Regulatory Particle Triphosphatase
154	YFL039C	act1-155	-0.36637	ACTin
155	YDR087C	rrp1-1	-0.35873	Ribosomal RNA Processing
156	YCL059C	krr1-17	-0.35825	contains KRR-R motif
157	YMR240C	cus1-3	-0.35472	Cold sensitive U2 snRNA Suppressor
158	YFL039C	act1-112	-0.35052	ACTin
159	YPL217C	bms1-1	-0.35051	BMh Sensitive
160	YGL001C	erg26-1	-0.34735	ERGosterol biosynthesis
161	YCL059C	krr1-18	-0.33005	contains KRR-R motif
162	YDL064W	ubc9-2	-0.32575	UBiquitin-Conjugating
163	YFL009W	cdc4-3	-0.32124	Cell Division Cycle
164	YLR459W	gab1-1	-0.31691	GPI and Actin Bar
165	YGR245C	sda1-2	-0.31231	Severe Depolymerization of Actin
166	YLL031C	gpi13-5	-0.30741	GlycosylPhosphatidylinositol anchor biosynthesis
167	YJR046W	tah11-ts	-0.30406	Topo-A Hypersensitive
168	YDR325W	ycg1-2	-0.3012	Yeast Cap G
169	YPL209C	ipl1-1	-0.30094	Increase in PLoidy
170	YBR080C	sec18-1	-0.30062	SECretoary
171	YBR247C	enp1-1	-0.3002	Essential Nuclear Protein