Table A2. Cycling antisense transcripts

overlapping sense feature	gene name	peak	chr	strand	start	end	length	function of the sense counterpart
YJR146W, YJR147W	HMS2	0	10	-	703349	705149	1801	Protein with similarity to heat shock transcription factors; overexpression suppresses the pseudohyphal filamentation
		-						defect of a diploid mep1 mep2 homozygous null mutant
YEL041W	YEF1	8	5	-	76101	77413	1313	ATP-NADH kinase; phosophorylates both NAD and NADH; homooctameric structure consisting of 60-kDa subunits;
YIL166C		8	9	+	31185	32561	1377	sequence similarity to Utr1p and Pos5p; overexpression complements certain pos5 phenotypes Putative protein with similarity to the allantoate permease (Dal5p) subfamily of the major facilitator superfamily; mRNA
								expression is elevated by sulfur limitation; YIL166C is a non-essential gene
	1/0//4					233909	1041	Vacuolar H+/Ca2+ exchanger involved in control of cytosolic Ca2+ concentration; has similarity to sodium/calcium
YDL128W	VCX1	11	4	-	232869			exchangers, including the bovine Na+/Ca2+,K+ antiporter
YOR026W	BUB3	14	15	_	380333			Kinetochore checkpoint WD40 repeat protein that localizes to kinetochores during prophase and metaphase, delays
	0000							anaphase in the presence of unattached kinetochores; forms complexes with Mad1p-Bub1p and with Cdc20p, binds
YLR030W, YLR031W		15	12	-	203261	204717	1457	Putative protein of unknown function
YLR050C		15	12	+	245577	246177	601	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the endoplasmic reticulum; YLR050C is not an essential gene
YHR177W		16	8		456343	458487	2145	Putative protein of unknown function
YKL221W	MCH2	16	11	-	6205	7749	1545	Protein with similarity to mammalian monocarboxylate permeases, which are involved in transport of monocarboxylic
								acids across the plasma membrane; mutant is not deficient in monocarboxylate transport
YPR134W	MSS18	17	16	-	798015	799023	1009	Nuclear encoded protein needed for efficient splicing of mitochondrial COX1 al5beta intron; mss18 mutations block
								cleavage of 5' exon - intron junction; phenotype of intronless strain suggests additional functions
YLR341W	SPO77	18	12	-	807211	808699 619429	1489 1041	Meiosis-specific protein of unknown function, required for spore wall formation during sporulation; dispensable for both
								nuclear divisions during meiosis
YMR178W		21	13	-	618389			Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to both the cytoplasm and
						244217 1		nucleus and is induced in response to the DNA-damaging agent MMS; YMR178W is not an essential gene Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the membrane of
YPL162C		21	16	+	243193		1025	vacuole with cell cycle-correlated morphology
		1	1.					Vacuolar glutathione S-conjugate transporter of the ATP-binding cassette family, has a role in detoxifying metals such
YDR135C	YCF1	23	4	+	722298	723026	729	as cadmium, mercury, and arsenite; also transports unconjugated bilirubin; similar to human cystic fibrosis protein CFTR
YKL101W	HSL1	23	11	-	251040	251384		Nim1p-related protein kinase that regulates the morphogenesis and septin checkpoints; associates with the assembled
								septin filament; required along with HsI7p for bud neck recruitment, phosphorylation, and degradation of Swe1p
YMR253C	GTB1	23 25	13 4	+	775985 908055	776769 909407	1353	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a
111112000								punctate pattern; YMR253C is not an essential gene
YDR221W								Glucosidase II beta subunit, forms a complex with alpha subunit Rot2p, involved in removal of two glucose residues
YHR142W	CHS7	29	8	-	383677	384573	897	from N-linked glycans during glycoprotein biogenesis in the ER Protein of unknown function, involved in chitin biosynthesis by regulating Chs3p export from the ER
			Ŭ				557	Putative transcription factor containing a C2H2 zinc finger; mutation affects transcriptional regulation of genes involved
YPL230W	USV1	31	16	-	114485	116357		in protein folding, ATP binding, and cell wall biosynthesis
YIL063C	YRB2	34	9	+	243633	243929		Protein of unknown function involved in nuclear processes of the Ran-GTPase cycle; involved in nuclear protein export;
								contains Ran Binding Domain and FxFG repeats; interacts with Srm1p, GTP-Gsp1p, Rna1p and Crm1p; is not essential

	1			-	-			
YPL249C	GYP5	38	16	+	76705	78609		GTPase-activating protein (GAP) for yeast Rab family members, involved in ER to Golgi trafficking; exhibits GAP activity
								toward Ypt1p that is stimulated by Gyl1p, also acts on Sec4p; interacts with Gyl1p, Rvs161p and Rvs167p
YCR042C	TAF2	43	3	+	202729	204209	1481	TFIID subunit (150 kDa), involved in RNA polymerase II transcription initiation
YJL157C	FAR1	43	10	+	123737	125449	1713	Cyclin-dependent kinase inhibitor that mediates cell cycle arrest in response to pheromone; also forms a complex with
								Cdc24p, Ste4p, and Ste18p that may specify the direction of polarized growth during mating; potential Cdc28p substrate
YML087C		49	13	+	94457	95585		Putative protein of unknown function
YNL134C		51	14	1	372473	374273	1801	Putative protein of unknown function with similarity to dehydrogenases from other model organisms; green fluorescent
TNL 1340		51	14	Ŧ	512415	514215	1001	protein (GFP)-fusion protein localizes to both the cytoplasm and nucleus and is induced by the DNA-damaging agent
YHR139C	SPS100	53	8	+	378137	380073	1937	Protein required for spore wall maturation; expressed during sporulation; may be a component of the spore wall
YOR097C		57	15	+	506945	507817	873	Putative protein of unknown function; identified as interacting with Hsp82p in a high-throughput two-hybrid screen;
								YOR097C is not an essential gene
YBR067C	TIP1	58	2	+	372119	372543	425	Major cell wall mannoprotein with possible lipase activity; transcription is induced by heat- and cold-shock; member of
								the Srp1p/Tip1p family of serine-alanine-rich proteins
YKL127W	PGM1	66	11	-	203832	204600	769	Phosphoglucomutase, minor isoform; catalyzes the conversion from glucose-1-phosphate to glucose-6-phosphate,
								which is a key step in hexose metabolism
YGL021W	ALK1	68	7	-	454935	455087		Protein kinase; accumulation and phosphorylation are periodic during the cell cycle; phosphorylated in response to DNA
								damage; contains characteristic motifs for degradation via the APC pathway; similar to Alk2p and to mammalian haspins
YPR135W	CTF4	74	16	-	799783	800391	609	Chromatin-associated protein, required for sister chromatid cohesion; interacts with DNA polymerase alpha (Pol1p) and
								may link DNA synthesis to sister chromatid cohesion
YBR180W	DTR1	75	2	-	590100	591348	1249	Multidrug resistance dityrosine transporter of the major facilitator superfamily, essential for spore wall synthesis,
TBICTOOW								facilitates the translocation of bisformyl dityrosine through the prospore membrane
YPR194C, YPR195C	OPT2 excluded	78	16	+	924291	928339	4049	Oligopeptide transporter; member of the OPT family, with potential orthologs in S. pombe and C. albicans
YJL078C	PRY3	80	10	+	291913	293537	1625	Protein of unknown function, has similarity to Pry1p and Pry2p and to the plant PR-1 class of pathogen related proteins
YMR181C		82	13	+	623585	625281		Protein of unknown function; mRNA transcribed as part of a bicistronic transcript with a predicted transcriptional repressor RGM1/YMR182C; mRNA is destroyed by nonsense-mediated decay (NMD); YMR181C is not an essential
YNL300W			1			 		Glycosylphosphatidylinositol-dependent cell wall protein, expression is periodic and decreases in respone to ergosterol
		82	14	-	65757	66037	281	perturbation or upon entry into stationary phase; depletion increases resistance to lactic acid
YAR035W	YAT1		1	-	189427	191819	2393	Outer mitochondrial carnitine acetyltransferase, minor ethanol-inducible enzyme involved in transport of activated acyl
								groups from the cytoplasm into the mitochondrial matrix; phosphorylated
	1	1	1					
for which opposite ORF		1	1					
cycles				1				
yelee								