

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 <i>mep1 mep2</i> homozygous null mutant
YEL041W	YEF1	8	5	-	76101	77413	1313	ATP-NADH kinase; phosphorylates both NAD and NADH; homooctameric structure consisting of 60-kDa subunits; sequence similarity to <i>Utr1p</i> and <i>Pos5p</i> ; overexpression complements certain <i>pos5</i> phenotypes
YIL166C		8	9	+	31185	32561	1377	Putative protein with similarity to the allantoate permease (<i>Dal5p</i>) subfamily of the major facilitator superfamily; mRNA expression is elevated by sulfur limitation; YIL166C is a non-essential gene
YDL128W	VCX1	11	4	-	232869	233909	1041	Vacuolar H ⁺ /Ca ²⁺ exchanger involved in control of cytosolic Ca ²⁺ concentration; has similarity to sodium/calcium exchangers, including the bovine Na ⁺ /Ca ²⁺ ,K ⁺ antiporter
YOR026W	BUB3	14	15	-	380333	380469		Kinetochore checkpoint WD40 repeat protein that localizes to kinetochores during prophase and metaphase, delays anaphase in the presence of unattached kinetochores; forms complexes with <i>Mad1p-Bub1p</i> and with <i>Cdc20p</i> , 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 α 5beta intron; <i>mss18</i> mutations block cleavage of 5' exon - intron junction; phenotype of intronless strain suggests additional functions
YLR341W	SPO77	18	12	-	807211	808699	1489	Meiosis-specific protein of unknown function, required for spore wall formation during sporulation; dispensable for both nuclear divisions during meiosis
YMR178W		21	13	-	618389	619429	1041	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to both the cytoplasm and nucleus and is induced in response to the DNA-damaging agent MMS; YMR178W is not an essential gene
YPL162C		21	16	+	243193	244217	1025	Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the membrane of vacuole with cell cycle-correlated morphology
YDR135C	YCF1	23	4	+	722298	723026	729	Vacuolar glutathione S-conjugate transporter of the ATP-binding cassette family, has a role in detoxifying metals such as cadmium, mercury, and arsenite; also transports unconjugated bilirubin; similar to human cystic fibrosis protein CFTR
YKL101W	HSL1	23	11	-	251040	251384	345	<i>Nim1p</i> -related protein kinase that regulates the morphogenesis and septin checkpoints; associates with the assembled septin filament; required along with <i>Hsl7p</i> for bud neck recruitment, phosphorylation, and degradation of <i>Swe1p</i>
YMR253C		23	13	+	775985	776769		Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm in a punctate pattern; YMR253C is not an essential gene
YDR221W	GTB1	25	4	-	908055	909407	1353	Glucosidase II beta subunit, forms a complex with alpha subunit <i>Rot2p</i> , involved in removal of two glucose residues from N-linked glycans during glycoprotein biogenesis in the ER
YHR142W	CHS7	29	8	-	383677	384573	897	Protein of unknown function, involved in chitin biosynthesis by regulating <i>Chs3p</i> export from the ER
YPL230W	USV1	31	16	-	114485	116357		Putative transcription factor containing a C2H2 zinc finger; mutation affects transcriptional regulation of genes involved 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 <i>Srm1p</i> , <i>GTP-Gsp1p</i> , <i>Rna1p</i> and <i>Crm1p</i> ; is not essential

