

Additional file 1. Zap1 target genes from Lyons et al. not confirmed by E3.

ORF	Gene	Function	Fold induction				ZRE		sequence
			E1 ^a	E2 ^a	E3-1 ^b	E3-2 ^b	start ^c	score ^d	
YBL048W		function unknown	7.0	2.0	1.5	nd	-858	8.7	CCCTTGAGGGA
YBR066C	<i>NRG2</i>	transcription factor that mediates glucose repression	5.1	2.2	1.0	0.9	-920	7.8	AACCTTGAGGGT
YBR302C	<i>COS2</i>	vacuole protein, function unknown	2.1	2.0	nd	nd	-592	5.3	AACCTAGAGGT
							-314	8.9	ACCCTAAATGT
							-217	5.0	ACCGAAATGT
YDR285W	<i>ZIP1</i>	synaptonemal complex protein, meiotic recombination	4.5	2.1	1.1	1.1	-575	9.6	ACCTGAAAGGT
YFL062W	<i>COS4</i>	vacuole protein, function unknown	2.6	2.0	1.3	1.6	-865	5.0	AACCTAAATGT
							-584	5.6	AACCTAGAGGT
							-309	9.1	ACCTTAAATGT
YHL048W	<i>COS8</i>	ER protein, function unknown	2.2	2.1	1.4	1.4	-865	5.0	AACCTAAATGT
							-586	5.3	AACCTAGAGGT
							-314	9.1	ACCTTAAATGT
YKL113C	<i>RAD27</i>	nuclease, DNA replication and repair	2.2	4.7	1.3	1.2	-997	10.2	ACCCTCCGGGT
							-342	5.4	ACCAGCCGGGT
YKL174C	<i>TPO5</i>	putative polyamine transporter	3.2	2.0	0.9	1.1	-493	8.4	ACCATAAGGGT
YML132W	<i>COS3</i>	enhancer of Na ⁺ /H ⁺ antiporter function	2.7	2.2	1.3	nd	-592	5.3	AACCTAGAGGT
							-314	8.9	ACCCTAAATGT
YMR086W		ribosome-associated protein	1.9	2.4	1.5	1.4	-565	7.4	ACCTCGAGTGT
							-145	9.7	ACCTTAAAGGA
YNL234W		similar to globins, function unknown	2.6	2.1	1.2	0.9	-68	7.2	CCCTTGAGGGG
YOL151W	<i>GRE2</i>	methylglyoxal reductase	2.5	2.6	1.0	1.0	-920	9.8	GCCTTGAGGGT
YPL154C	<i>PEP4</i>	vacuolar proteinase A	2.6	2.1	1.0	1.1	-396	8.2	GCCTTCCGGGT

a) Expression ratios are the average of two independent microarray experiments (Lyons et. al. 2000).

b) Results from two independent microarray experiments (E3-1 and E3-2) are shown.

c) Numbers indicate the distance from the ATG initiation codon.

d) Score calculated for each sequence with a position-specific scoring matrix generated by RSAT.