

Table III. *SNF1*-dependent regulatory genes

<u>Gene/ORF</u>	<u>Function</u>	<u><i>SNF1/Δsnf1</i></u>	<u><i>CAT8/Δcat8</i></u>	<u>DRXR</u>
<u>Transcription factors</u>				
<i>YGR067C</i>	C2H2 zinc fingers-ADR1-like	39.3	7.1	32.7
<i>HAC1</i>	Transcription factor/UPR	4.7	0.9	0.8
<i>CAT8</i>	Transcription factor/CSRE	2.5	nd	1.5
<i>IME1</i>	Transcription factor/meiosis	3.4	2.9	13.7
<i>SIP4</i>	Transcription factor/CAT8 homolog	7.5	4.9	6.2
<i>YOX1</i>	Homeodomain-protein	4.5	1.4	0.5
<i>XBPI</i>	Transcription factor/stress response	6.1	0.9	4.3
<i>ZAP1</i>	Transcription factor/zinc-regulated	4.2	0.6	0.6
<i>CUP9</i>	Transcription factor/Cu ⁺⁺ -regulated	3.8	0.9	1.3
<i>CUP2</i>	Transcription factor/Cu ⁺⁺ -regulated	2.1	0.6	nd
<u>Protein kinase regulatory subunits</u>				
<i>CLB1</i>	B-type cyclin	3.6	1.6	nd
<i>CLB2</i>	B-type cyclin	3.1	2.5	nd
<i>SIP2</i>	<i>SNF1</i> -subunit	5.3	1.9	2.9
<u>Protein phosphatase regulatory subunits</u>				
<i>REG2</i>	<i>GLC7</i> -regulatory subunit/cell growth	42.1	5.0	20.9
<i>GAC1</i>	<i>GLC7</i> -regulatory subunit/glycogen	3.8	1.9	5.7
<u>Ras GEP</u>				
<i>SDC25</i>	Ras guanine-nucleotide exchange factor	3.6	0.8	2.5

nd - not determined because no data was obtained for this gene from the microarray analysis. Expression ratios in bold type indicate a significantly higher level of expression based on a λ statistic that is above the significance threshold.