

Table II. Expression ratios of *SNF1*-dependent genes involved in transport.

<u>GENE</u>	<u>Transport function and location</u>	<u>SNF1/Δsnf1</u>	<u>DR/R</u>	<u>CAT8/Δcat8</u>
	<u>Iron</u>			
<i>FIT1</i>	siderophore iron transport; mannoprotein	34.6	1.8	0.7
<i>FIT2</i>	siderophore iron transport; mannoprotein	82.2	3.6	1.6
<i>FIT3</i>	siderophore iron transport; mannoprotein	43.5	9.2	1.1
<i>ENB1</i>	Ferric-enterobactin/endosome	9.0	1.2	1.2
<i>ARN1</i>	siderochrome-iron transport; endosome	17.1	2.0	0.9
<i>TAF1/ARN2</i>	siderochrome iron transport	20.6	2.0	0.9
<i>FRE1</i>	Fe ³⁺ /Cu ²⁺ -reductase/plasma membrane	6.9	0.9	1.1
<i>FRE2</i>	Fe ³⁺ /Cu ²⁺ -reductase/plasma membrane	3.0	0.8	0.7
<i>FRE3</i>	Fe ³⁺ /Cu ²⁺ -reductase/plasma membrane	5.2	1.3	0.7
<i>FRE4</i>	Fe ³⁺ /Cu ²⁺ -reductase/plasma membrane	2.0	0.5	1.0
<i>FRE5</i>	Fe ³⁺ /Cu ²⁺ -reductase?	4.4	1.1	0.8
<i>FRE7</i>	Fe ³⁺ /Cu ²⁺ -reductase?	0.3	1.0	1.2
<i>SMF3</i>	iron transport/vacuolar membrane	4.2	1.2	1.2
<i>FET3</i>	high affinity iron transport	17.3	4.2	1.4
<i>FTR1</i>	high affinity iron transport	4.7	1.6	0.7
<i>SIT1</i>	siderophore iron transport; endosome	36.0	6.6	1.1
	<u>Zinc</u>			
<i>ZPS1</i>	Zn ²⁺ transport motif	13.0	1.0	0.6
<i>ZRT1</i>	high affinity Zn transport; plasma membrane	20.4	1.0	0.1
<i>ZRT3</i>	Zn ²⁺ transport/vacuolar membrane	3.5	0.6	0.8
<i>COT1</i>	H ⁺ /Zn ²⁺ antiport/vacuolar membrane	2.8	1.7	2.3
	<u>Copper</u>			
<i>CCC2</i>	Cu ²⁺ -exporting ATPase/Fe ²⁺ transport/Golgi	5.8	1.0	0.9
<i>ICS2</i>	increased copper sensitivity	4.1	6.7	0.8
<i>CTR1</i>	high-affinity uptake/plasma membrane	1.7	1.4	2.9
<i>CTR2</i>	copper uptake/transport/vacuolar membrane	3.5	0.7	1.0
<i>CTR3</i>	high-affinity uptake/plasma membrane	0.8	0.3	0.6
<i>CUP1-2</i>	copper binding/cytosol	1.2	3.0	1.0
	<u>Metabolites</u>			
<i>SFC1</i>	succinate transport; mitochondria	171.8	78.0	0.6
<i>JEN1</i>	lactate symporter; plasma membrane	28.1	98.4	2.1
<i>ODC1</i>	oxodicarboxylate/mito inner membrane	3.3	6.2	2.6
<i>YAT1</i>	carnitine acyl CoA/mito outer membrane	7.4	25.0	1.5
<i>CRC1</i>	carnitine acyl CoA/mito inner membrane	5.6	17.5	2.2
<i>YAT2</i>	carnitine acyl CoA/mitochondria	5.6	26.1	2.0

<i>AGP2</i>	carnitine transport/plasma membrane	4.1	2.1	1.8
<i>PXA1</i>	peroxisomal ABC transporter	5.2	18.2	1.0
<u>Amino acids</u>				
<i>PUT4</i>	neutral amino acid	13.9	14.5	1.7
<i>MMP1</i>	S-methylmethionine transporter	5.6	4.1	1.7
<i>AGP1</i>	aminoacid permease/broad range	4.3	0.7	4.1
<i>MHT1</i>	homocysteine-S-methylmethionine transferase	4.2	0.5	1.5
<i>ALP1</i>	basic amino acid permease	4.2	15.3	2.7
<i>GAPI</i>	general amino acid permease	3.2	0.8	9.1
<u>Ions</u>				
<i>PHO89</i>	Pi/Na symport	6.5	10.6	0.2
<i>ENA1</i>	Na ⁺ transport/ PM/P-type ATPase	3.7	1.7	0.3
<i>ENA2</i>	Na ⁺ transport/ PM/P-type ATPase	3.1	2.3	0.3
<i>ENA5</i>	Na ⁺ transport/ PM/P-type ATPase	4.8	2.9	0.3
<i>SMF2</i>	Mn ²⁺ transport-mitochondrial membrane	3.0	2.2	0.8
<i>KHA1</i>	K ⁺ /H ⁺ antiporter	3.8	1.2	0.7
<i>AAC1</i>	ATP/ADP exchange/mitochondrial inner membrane	3.5	4.6	0.7
<i>PMC1</i>	Ca ²⁺ transport/ATPase/vacuolar membrane	3.2	2.8	0.8
<u>Sugars</u>				
<i>HXT10</i>	hexose transporter	5.1	1.7	0.8
<i>HXT5</i>	hexose transporter	5.0	6.8	0.8
<i>GAL3</i>	galactose transport	4.2	1.0	1.7
<i>MAL11</i>	maltose transporter	3.6	4.4	0.9
<i>ITR1</i>	inositol transport/plasma membrane	2.4	0.5	1.9
<u>Miscellaneous membrane proteins</u>				
<i>PRM4</i>	integral membrane protein	12.5	5.1	2.8
<i>YNL194C</i>	endoplasmic reticulum	12.2	13.1	2.1
<i>OM45</i>	mitochondrial outer membrane	8.4	6.3	1.5
<i>PRY1</i>	endoplasmic reticulum/pathogen-related	7.3	1.0	1.7
<i>YDL222C</i>	integral membrane protein	4.9	12.2	0.5
<i>YTP1</i>	yeast putative transmembrane protein	4.0	2.1	1.0

Expression ratios in bold type indicate a significantly higher level of expression based on a λ statistic that is above the significance threshold.