

Supplementary Table 1Primers used for real-time PCR analysis of chromosome XV and sequencing of *TOR2*.

Name	Sequence
RT-PCR	
GLK1frt	5'-AGACCAGACCTCTCTAAACTCC-3'
GLK1rrt	5'-ACCCTGAGCGCTTAATTGC-3'
GPD1frt	5'-CCAGAAGTTTTCGCTCCAATAGTA-3'
GPD1rrt	5'-AGCAACCAAATTGTCGGGTAGA-3'
HSP30frt	5'-GCCTGGATATGCACATTACC-3'
HSP30rrt	5'-CGCAATGAAGAACATCACAAC-3'
IPP1frt	5'-ACAGCAAGGGTATTGATTTGACCA-3'
IPP1rrt	5'-AAGCTGGTGGGATGGCATCA-3'
ACS15	5'-CCCTCTGCCGTACAATCATC-3'
ACS13	5'-TAACAGGCGTTTAATTGGCC-3'
ALD65	5'-GCCATGACTAAGCTACACTTTGAC-3'
ALD63	5'-TCAACATCTTCAGTGGTGGC-3'
HSP265	5'-GCATGTCATTTAACAGTCCATTTT-3'
HSP263	5'-CAGATGGGAACAGGGACAAG-3'
YPL222wfrt	5'-GGACAATAATCAAAGCGCTG-3'
YPL222wrrt	5'-AATGCAAAATGAGCCCCCTG-3'
YPL071wfrt	5'-TTATCATCGGTGGTAGCCGT-3'
YPL071wrrt	5'-CAGATACTGCAGAACATGCG-3'
YAL061wfrt	5'-GAGAGCCTTAGCGTATTTTCG-3'
YAL061wrrt	5'-CCTGTGGCAATGGGTATGA-3'
YOR315wfrt	5'-GGGCTTGTAAATACCCAGTAC-3'
YOR315wrrt	5'-CCAGGACTGACAATATTCCG-3'
YOL159cfrt	5'-TATGTTGATATCACCAGCGG-3'
YOL159crrt	5'-ATCAAAGATTGCTGATCGCC-3'
GPP2FRT	5'-GGGATTGACTACTAAACCTC-3'
GPP2RRT	5'-TGGAGCGAACTTAGCAATGG-3'
ZMS1FRT	5'-ATGGAACCGTTCGCATTTGG-3'
ZMS1RRT	5'-GAGAGAGGCAATGTTTAACG-3'
PCR analysis of chromosome XV	
YOL164WF	5'-TCACTGTCTCACTACACAACCGGAT-3'
YOL164WR	5'-TCAAGTTTCTCGCCGATTTCTG-3'
Sth-YOL163W-5	5'-GACCATCTACTTTCCATCAC-3'
Sth-YOL163W-3	5'-TTCGGTTATCAGCAGTGTC-3'
160-W-5'	5'-GCACGATTCTATATGACAGTTTTG-3'
160-W-3'	5'-AAAGCACGCATCTATGTGATGG-3'
159-A-5'	5'-ACCAAACCAATACCATTTGTGG-3'
159-A-3'	5'-AACAGAGCTAGCATACGCATGAATC-3'
YOL159CF1000	5'-GCCCATGTCATTTTTGTGCA-3'
YOL159CR1000	5'-CATTGAACAGCTCAGGAGAA-3'
ENB1F	5'-AAGTGCTCGTGAATGTCTCTGAA-3'
ENB1R	5'-TTTGTATCGCTAGTACTCTCCAGC-3'
YOL157CF	5'-CATAAAGAAAAGAAAGCAACGTACA-3'
YOL157CR	5'-AATCTTGTGTCGTCACAATCATCA-3'
HXT11-5'	5'-GTTCTAAACGCTTTTTGTTACTC-3'
HXT11-3'	5'-CCAATTTACCGAAAAGTAGAAGA-3'
Sth-ZPS1-5	5'-GCTGATCATTGAGTGCCAAA-3'
Sth-ZPS1-3	5'-TTCTCCCCCAATGACAGTAA-3'
DCP1-5'	5'-TTTGCAACACATCACAAGAAAAGC-3'
DCP1-3'	5'-ATTCTCACTTGGGCATCTCACCT-3'
Sequencing of TOR2	
TOR25FULL	5'-TAACAAATACACCACGCCACC-3'
TOR2Rseq	5'-CGGGGTTGACAGAACTCAAT-3'
TOR2Fseq	5'-ATGAGGATTCGTCTGTCAGA-3'
TOR2A	5'-TATTAGGCCCCATGTCGAGA-3'
TOR2B	5'-CCAGAGCCTTAGATATCGAT-3'
TOR2C	5'-TGGGATGAAATAGCCCAGTA-3'
TOR2D	5'-GTAAGTAGAAGATCCCTTGATT-3'
TOR2E	5'-CGTCATCCAGACCCTCATCA-3'
TOR2FRBF	5'-CTCTCTCACGACAGAAAGCAGC-3'
TOR23FULL	5'-CAGAAATGGACACCAACCGATA-3'

Supplementary Table 2 Differential expression of genes up-regulated by sugar-induced osmotic stress in VIN7 and ST. Only genes with expression levels differing more than two-fold are listed.

Gene	ORF	Cellular process	SLR ^a	Fold difference ^b VIN7 vs ST
Genes expressed at higher levels in VIN7 than in ST				
<i>TRX3</i>	YCR083W	response to oxidative stress	1.290	2.4
<i>GRE1</i>	YPL223C	response to stress	2.053	4.2
<i>HSP26</i>	YBR072W	response to stress	1.630	3.1
<i>HSP30</i>	YCR021C	response to stress	2.693	6.5
<i>GCY1</i>	YOR120W	salinity response	1.273	2.4
<i>PDE1</i>	YGL248W	cAMP-mediated signaling	1.287	2.4
<i>PCL5</i>	YHR071W	cell cycle	1.110	2.2
<i>GSC2</i>	YGR032W	cell wall organization and biogenesis	1.120	2.2
<i>PIR3</i>	YKL163W	cell wall organization and biogenesis	1.783	3.4
<i>CYB2</i>	YML054C	electron transport	1.073	2.1
<i>CYC7</i>	YEL039C	electron transport	1.390	2.6
<i>PDC6</i>	YGR087C	ethanol metabolism	1.790	3.5
<i>GPH1</i>	YPR160W	glycogen catabolism	1.353	2.6
<i>HPA2</i>	YPR193C	histone acetylation	1.457	2.7
<i>FRE4</i>	YNR060W	iron-siderochrome transport	1.250	2.4
<i>SPO1</i>	YNL012W	meiosis	1.677	3.2
<i>YNL274C</i>	YNL274C	metabolism	0.993	2.0
<i>KTR2</i>	YKR061W	N-linked glycosylation	1.313	2.5
<i>YDR247W</i>	YDR247W	protein amino acid phosphorylation	1.783	3.4
<i>PEX18</i>	YHR160C	protein-peroxisome targeting	1.477	2.8
<i>YGL121C</i>	YGL121C	signal transduction	1.497	2.8
<i>BAG7</i>	YOR134W	small GTPase mediated signal transduction	2.020	4.1
<i>SMA1</i>	YPL027W	spore wall assembly (sensu <i>Saccharomyces</i>)	1.057	2.1
<i>SPS100</i>	YHR139C	spore wall assembly (sensu <i>Saccharomyces</i>)	1.073	2.1
<i>THI11</i>	YJR156C	thiamin biosynthesis	3.607	12.2
<i>DAL1</i>	YIR027C	allantoin catabolism	1.457	2.7
<i>COX5B</i>	YIL111W	anaerobic respiration	1.210	2.3
<i>YJR096W</i>	YJR096W	arabinose metabolism	1.157	2.2
<i>ARG3</i>	YJL088W	arginine biosynthesis	1.667	3.2
<i>DAN3</i>	YBR301W	biological process unknown	1.693	3.2
<i>FUN19</i>	YAL034C	biological process unknown	1.043	2.1
<i>PAU1</i>	YJL223C	biological process unknown	1.383	2.6
<i>PAU5</i>	YFL020C	biological process unknown	1.887	3.7
<i>PAU7</i>	YAR020C	biological process unknown	1.857	3.6
<i>PHM8</i>	YER037W	biological process unknown	1.553	2.9
<i>UGX2</i>	YDL169C	biological process unknown	1.220	2.3
<i>YAL061W</i>	YAL061W	biological process unknown	2.653	6.3
<i>YAL068C</i>	YAL068C	biological process unknown	1.430	2.7
<i>YBL049W</i>	YBL049W	biological process unknown	1.747	3.4
<i>YCL042W</i>	YCL042W	biological process unknown	1.337	2.5
<i>YDL124W</i>	YDL124W	biological process unknown	1.233	2.4
<i>YDR542W</i>	YDR542W	biological process unknown	1.413	2.7
<i>YFR017C</i>	YFR017C	biological process unknown	1.237	2.4
<i>YGL261C</i>	YGL261C	biological process unknown	1.423	2.7
<i>YGR043C</i>	YGR043C	biological process unknown	1.597	3.0
<i>YJL161W</i>	YJL161W	biological process unknown	1.960	3.9
<i>YKL071W</i>	YKL071W	biological process unknown	3.480	11.2
<i>YKL151C</i>	YKL151C	biological process unknown	1.093	2.1
<i>YMR090W</i>	YMR090W	biological process unknown	1.040	2.1
<i>YMR103C</i>	YMR103C	biological process unknown	1.760	3.4
<i>YMR181C</i>	YMR181C	biological process unknown	1.363	2.6
<i>YMR196W</i>	YMR196W	biological process unknown	1.287	2.4
<i>YMR322C</i>	YMR322C	biological process unknown	1.720	3.3
<i>YNL134C</i>	YNL134C	biological process unknown	1.357	2.6
<i>YOL047C</i>	YOL047C	biological process unknown	2.027	4.1
<i>YOR173W</i>	YOR173W	biological process unknown	1.613	3.1
<i>YOR338W</i>	YOR338W	biological process unknown	2.297	4.9
<i>YPL222W</i>	YPL222W	biological process unknown	2.810	7.0
<i>YPR093C</i>	YPR093C	biological process unknown	1.103	2.1
<i>YPR127W</i>	YPR127W	biological process unknown	1.320	2.5
Genes expressed at lower levels in VIN7 than in ST				
<i>YCR105W</i>	YCR105W	alcohol metabolism	-1.230	-2.3
<i>BAP2</i>	YBR068C	amino acid transport	-1.690	-3.2
<i>ARO9</i>	YHR137W	aromatic amino acid family metabolism	-1.650	-3.1
<i>ARO10</i>	YDR380W	leucine catabolism	-1.247	-2.4
<i>ADY2</i>	YCR010C	meiosis	-2.113	-4.3
<i>CHO2</i>	YGR157W	phosphatidylcholine biosynthesis	-1.153	-2.2
<i>GPX2</i>	YBR244W	response to oxidative stress	-1.630	-3.1
<i>FUI1</i>	YBL042C	uridine transport	-1.143	-2.2
<i>YDL218W</i>	YDL218W	biological process unknown	-2.043	-4.1
<i>YLR327C</i>	YLR327C	biological process unknown	-1.203	-2.3

^aSLR: signal log (base 2) ratio, average of three sets of data.

^bFold difference calculated from average SLR.

Supplementary Table 3 Differential expression of genes down-regulated by sugar-induced osmotic stress in VIN7 and ST. Only genes with expression levels differing more than two-fold are listed.

Gene	ORF	Cellular process	SLR ^a	Fold difference ^b VIN7 vs ST
Genes expressed at higher levels in VIN7 than in ST				
HXT3	YDR345C	hexose transport	1.460	2.8
HXT4	YHR092C	hexose transport	1.697	3.2
YNR065C	YNR065C	biological process unknown	1.360	2.6
Genes expressed at lower levels in VIN7 than in ST				
YGR280C	YGR280C	35S primary transcript processing	-1.697	-3.2
TYS1	YGR185C	amino acid activation	-1.033	-2.0
PCL9	YDL179W	cell cycle	-1.110	-2.2
YOL155C	YOL155C	cell wall organization and biogenesis	-1.697	-3.2
PLB2	YMR006C	glycerophospholipid metabolism	-2.277	-4.8
YOR108W	YOR108W	leucine biosynthesis	-1.703	-3.3
LYS12	YIL094C	lysine biosynthesis	-1.200	-2.3
LYS2	YBR115C	lysine biosynthesis, amino adipic pathway	-1.183	-2.3
LYS9	YNR050C	lysine biosynthesis, amino adipic pathway	-1.007	-2.0
ODC2	YOR222W	mitochondrial transport	-1.087	-2.1
CYC8	YBR112C	negative regulation of transcription	-1.010	-2.0
RKI1	YOR095C	pentose-phosphate shunt	-2.363	-5.1
CPT1	YNL130C	phosphatidylcholine biosynthesis	-1.047	-2.1
URA7	YBL039C	phospholipid biosynthesis	-2.060	-4.2
SRO9	YCL037C	protein biosynthesis	-1.313	-2.5
YNL246W	YNL246W	protein-vacuolar targeting	-1.073	-2.1
FUR1	YHR128W	pyrimidine salvage	-1.843	-3.6
MAE1	YKL029C	pyruvate metabolism	-1.483	-2.8
RRP13	YGR103W	ribosomal large subunit biogenesis	-1.427	-2.7
RRP5	YMR229C	rRNA processing	-1.190	-2.3
FEN1	YCR034W	sphingolipid biosynthesis	-1.073	-2.1
ATF2	YGR177C	steroid metabolism	-1.120	-2.2
PHO3	YBR092C	thiamin transport	-2.850	-7.2
RPA135	YPR010C	transcription from Pol I promoter	-1.127	-2.2
RPA190	YOR341W	transcription from Pol I promoter	-1.147	-2.2
RPC11	YDR045C	transcription from Pol III promoter	-1.110	-2.2
TEF4	YKL081W	translational elongation	-1.373	-2.6
TIF4631	YGR162W	translational initiation	-1.400	-2.6
YHM2	YMR241W	tricarboxylic acid transport	-1.170	-2.3
DBP2	YNL112W	biological process unknown	-1.683	-3.2
FLO9	YAL063C	biological process unknown	-1.587	-3.0
HAS1	YMR290C	biological process unknown	-1.327	-2.5
IMD4	YML056C	biological process unknown	-1.467	-2.8
NOP13	YNL175C	biological process unknown	-1.120	-2.2
RLI1	YDR091C	biological process unknown	-1.107	-2.2
YDR119W	YDR119W	biological process unknown	-1.267	-2.4
YDR133C	YDR133C	biological process unknown	-1.770	-3.4
YGL101W	YGL101W	biological process unknown	-1.227	-2.3
YHR149C	YHR149C	biological process unknown	-2.607	-6.1
YJL200C	YJL200C	biological process unknown	-1.653	-3.1
YJR070C	YJR070C	biological process unknown	-1.367	-2.6
YOR315W	YOR315W	biological process unknown	-4.473	-22.2
YPL183C	YPL183C	biological process unknown	-0.993	-2.0

^aSLR: signal log (base 2) ratio, average of three sets of data.

^bFold difference calculated from average SLR.

Supplementary Table 4 Genes regulated by Msn2/4p that are expressed at least two-fold differentially between VIN7 and ST.

Gene	ORF	Cellular process	SLR ^a	Fold difference ^b VIN7 vs ST
Genes expressed at higher levels in VIN7 than in ST				
<i>GPX1</i>	YKL026C	response to oxidative stress	1.423	2.7
<i>TRX3</i>	YCR083W	response to oxidative stress	1.290	2.4
<i>GRE1</i>	YPL223C	response to stress	2.053	4.2
<i>HSP26</i>	YBR072W	response to stress	1.630	3.1
<i>GCY1</i>	YOR120W	salinity response	1.273	2.4
<i>PIR3</i>	YKL163W	cell wall organization and biogenesis	1.783	3.4
<i>PRM8</i>	YGL053W	conjugation with cellular fusion	3.543	11.7
<i>CYC7</i>	YEL039C	electron transport	1.390	2.6
<i>GPH1</i>	YPR160W	glycogen catabolism	1.353	2.6
YNL274C	YNL274C	metabolism	0.993	2.0
<i>DIA3</i>	YDL024C	pseudohyphal growth	1.800	3.5
<i>TFS1</i>	YLR178C	regulation of proteolysis and peptidolysis	1.503	2.8
YGL121C	YGL121C	signal transduction	1.497	2.8
BAG7	YOR134W	small GTPase mediated signal transduction	2.020	4.1
<i>SPS100</i>	YHR139C	spore wall assembly (sensu <i>Saccharomyces</i>)	1.073	2.1
YJR096W	YJR096W	arabinose metabolism	1.157	2.2
YCL042W	YCL042W	biological process unknown	1.337	2.5
YDL124W	YDL124W	biological process unknown	1.233	2.4
YGR043C	YGR043C	biological process unknown	1.597	3.0
YJL017W	YJL017W	biological process unknown	1.563	3.0
YJL161W	YJL161W	biological process unknown	1.960	3.9
YKL151C	YKL151C	biological process unknown	1.093	2.1
YMR090W	YMR090W	biological process unknown	1.040	2.1
YMR181C	YMR181C	biological process unknown	1.363	2.6
YMR196W	YMR196W	biological process unknown	1.287	2.4
YNL134C	YNL134C	biological process unknown	1.357	2.6
YOR173W	YOR173W	biological process unknown	1.613	3.1
YOR338W	YOR338W	biological process unknown	2.297	4.9
YPR127W	YPR127W	biological process unknown	1.320	2.5
YPS5	YGL259W	biological process unknown	2.223	4.7
YPS6	YIR039C	biological process unknown	1.890	3.7
Gene expressed at lower level in VIN7 than in ST				
YLR327C	YLR327C	biological process unknown	-1.203	-2.3

^aSLR: signal log (base 2) ratio, average of three sets of data.^bFold difference calculated from average SLR.**Supplementary Table 5** Differential expression of *HOG1*-regulated genes. Only genes with expression levels differing at least two-fold in VIN7 and ST are listed.

Gene	ORF	Cellular process	SLR ^a	Fold difference ^b VIN7 vs ST
Genes expressed at higher levels in VIN7 than in ST				
<i>GRE1</i>	YPL223C	response to stress	2.053	4.2
<i>SPS100</i>	YHR139C	spore wall assembly (sensu <i>Saccharomyces</i>)	1.073	2.1
<i>TFS1</i>	YLR178C	regulation of proteolysis and peptidolysis	1.503	2.8
YAL061W	YAL061W	biological process unknown	2.653	6.3
YGR043C	YGR043C	biological process unknown	1.597	3.0
YKL151C	YKL151C	biological process unknown	1.093	2.1
YMR090W	YMR090W	biological process unknown	1.040	2.1
Gene expressed at lower level in VIN7 than in ST				
ARO9	YHR137W	aromatic amino acid family metabolism	-1.650	-3.1

^aSLR: signal log (base 2) ratio, average of three sets of data.^bFold difference calculated from average SLR.