

Supplementary Materials

Supplemental Table S1. Gene information. All data were mainly provided by Alliance of Genome Resources, Nov 2021 and support data were obtained from additional references.

Gene	Location	Other Expression	Additional Reference
<i>PGM1</i>	cytosol		
<i>PGM2</i>	cytosol	<i>GAL5</i>	
<i>PRM15</i>	cytosol; nucleus	<i>PGM3</i>	
<i>PGI1</i>	mitochondrion	<i>CDC30</i>	(1)
<i>HXK</i>	cytosol; mitochondrion		
<i>HXK1</i>	mitochondrion		(2)
<i>HXK2</i>	cytosol; mitochondrial membrane; nucleus	<i>HEX1, HKB, SCI2</i>	
<i>GLK1</i>	cytosol; plasma membrane	<i>HOR3</i>	
<i>GAL10</i>	cytosol		
<i>PFK1</i>	mitochondrion		(3)
<i>FBP1</i>	cytosol; periplasmic space	<i>ACN8</i>	
<i>FBA1</i>	cytosol; mitochondrion	<i>LOT1</i>	
<i>TPI1</i>	mitochondrion		(4)
<i>TDH1</i>	cell wall; lipid droplet; mitochondrion	<i>GLD3</i>	(2)
<i>TDH2</i>	cell wall; lipid droplet; mitochondrion	<i>GLD2</i>	(2)
<i>TDH3</i>	cell wall; lipid droplet; mitochondrion	<i>GLD1, HSP35, HSP36, SSS2.</i>	(2)
<i>PGK1</i>	mitochondrion		
<i>TDA10</i>	cytosol; nucleus		
<i>ALD2</i>	cytosol		(5),(6)
<i>ALD3</i>	cytosol		(7)
<i>ALD4</i>	mitochondrion; cytosol		(5),(8)
<i>ALD5</i>	mitochondrion; cytosol		(5),(6)
<i>ALD6</i>	mitochondrion; cytosol		(5)
<i>HFD1</i>	lipid droplet		
<i>GCY1</i>	cytosol; nucleus		
<i>DAK1</i>	cytosol		
<i>DAK2</i>	cytosol		
<i>GUT1</i>	mitochondrion; cytosol		(9)
<i>GPP1</i>	cytosol		
<i>GPP2</i>	cytosol; nucleus	<i>HOR2</i>	
<i>GPT2</i>	endoplasmic reticulum; lipid droplet	<i>GAT1</i>	
<i>SCT1</i>	endoplasmic reticulum; lipid droplet	<i>GAT2</i>	
<i>PHM8</i>	cytosol; nucleus		
<i>GPM2</i>	cytosol		

<i>ENO1</i>	fungal-type vacuole; mitochondrion; cytosol	<i>HSP48</i>	(10)
<i>CDC19</i>	cytosol	<i>PYK1</i>	
<i>PCK1</i>	cytosol	<i>JPM2, PPC1</i>	
<i>PDA1</i>	mitochondrial nucleoid		
<i>PDB1</i>	mitochondrial nucleoid		
<i>THI3</i>	nucleus	<i>KID1</i>	
<i>PDC1</i>	cytosol; nucleus; replication compartment		
<i>PDC5</i>	nucleus		
<i>PDC6</i>	cytoplasm	<i>RHR2</i>	
<i>LPD1</i>	mitochondrion	<i>HPD1</i>	
<i>LAT1</i>	mitochondrion	<i>ODP2, PDA2</i>	
<i>ACS1</i>	cytosol	<i>FUN44</i>	
<i>ACS2</i>	cytosol; nucleolus		
<i>HFD1</i>	lipid droplet		
<i>ADH1</i>	cytoplasm; replication compartment; cytosol	<i>ADC1</i>	
<i>ADH2</i>	cytosol	<i>ADR2</i>	
<i>ADH3</i>	mitochondrial matrix; cytosol		
<i>ADH4</i>	mitochondrion; cytosol	<i>NRC465, ZRG5</i>	
<i>ADH5</i>	cytoplasm; nucleus		
<i>ADH6</i>	cytosol		
<i>ADH7</i>	cytosol		
<i>SFA1</i>	mitochondrion	<i>ADH5</i>	
<i>CIT1</i>	mitochondrion	<i>LYS6</i>	
<i>CIT2</i>	peroxisome		
<i>CIT3</i>	mitochondrion		
<i>ACO1</i>	cytosol; mitochondrion	<i>GLU1</i>	
<i>IDP1</i>	mitochondrion		
<i>IDP2</i>	cytosol		
<i>IDP3</i>	peroxisome		
<i>IDH1</i>	mitochondrion		
<i>IDH2</i>	mitochondrion		
<i>KGD1</i>	mitochondrion	<i>OGD1</i>	
<i>LPD1</i>	mitochondrion	<i>HPD1</i>	
<i>KGD2</i>	mitochondrion		
<i>LSC1</i>	mitochondrion		
<i>LSC2</i>	mitochondrion		

<i>SDH1</i>	mitochondrion	
<i>SDH2</i>	mitochondrion	<i>ACN17</i>
<i>SDH3</i>	mitochondrion	<i>CYB3, YKL4</i>
<i>SDH4</i>	mitochondrion	<i>ACN18</i>
<i>SDH9</i>	mitochondrion	
<i>SHH3</i>	mitochondrion	
<i>SHH4</i>	fungal-type vacuole	
<i>FUM1</i>	cytosol; mitochondrion; nucleus.	
<i>MDH1</i>	mitochondrion	
<i>MDH2</i>	cytosol; nuclear periphery	
<i>MDH3</i>	peroxisome	
<i>PCK1</i>	cytosol	<i>JPM2, PPC1</i>

Supplemental References

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- (2) Thakur SS, Geiger T, Chatterjee B, Bandilla P, Fröhlich F, Cox J, Mann M. Deep and highly sensitive proteome coverage by LC-MS/MS without prefractionation. 2011. Mol Cell Proteomics 10:M110.003699.
- (3) Petelenz-Kurdziel E, Kuehn C, Nordlander B, Klein D, Hong K-K, Jacobson T, Dahl P, Schaber J, Nielsen J, Hohmann S, Klipp E. Quantitative analysis of glycerol accumulation, glycolysis and growth under hyper osmotic stress. 2013. PLoS Comput. Biol. 9:e1003084.
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- (5) Daran-Lapujade P, Jansen MLA, Daran JM, van Gulik W, de Winde JH, Pronk JT. Role of transcriptional regulation in controlling fluxes in central carbon metabolism of *Saccharomyces cerevisiae*. A chemostat culture study. 2004. J Biol Chem 279:9125-9138.
- (6) Yu M, Juwono N.K.P, Foo J.L, Leong S.S, Chang M.W, Metabolic engineering of *Saccharomyces cerevisiae* for the overproduction of short branched-chain fatty acids. 2016. Meta. Eng 34:36-43.
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- (8) Hoang P.T.N, Ko ja K, Gong G, Um Y, Lee S.M. Genomic and phenotypic characterization of a refactored xylose-utilizing *Saccharomyces cerevisiae* strain for lignocellulosic biofuel production. 2018. Biotechnol Biofuel Bioproducts 11:268.
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- Norbeck J, Blomberg A. Metabolic and regulatory changes associated with growth of *Saccharomyces cerevisiae* in 1.4 M NaCl. Evidence for osmotic induction of glycerol dissimilation via the dihydroxyacetone pathway. 1997. *J Biol Chem* 272:5544-5554.

Supplemental Table S2. Primer-pairs of each enzyme gene were prepared for qPCR.

Gene		Primer Sequences (5'→3')
TDH2	F	cggtagatacgctggtgaagttc
	R	tgaaagatggaggcagtgataacaac
TDH3	F	tttcccacgatgacaaggcac
	R	gaagcccatggcaagtttagc
RDN18	F	aactcaccagggtccagacacaataagg
	R	aagggtcggtcggtatcgcaattaagc
KRE11	F	aactggttctgttacccaaatcaactcaac
	R	aacgcttaatgtgacttctgtttccc
SGA1	F	tccaaacggatattctgggtggtactgag
	R	gcatgatctattgtgttacattagcggtag
PGM1	F	tgatcctgccaaggcatacg
	R	ttgcgcgttgcgttaagaa
PGM2	F	gcctggtacctctggttgc
	R	ccatcaccaccgacaacaag
PRM15	F	aagaggtcaccgctctgc
	R	accagcagtgc当地actgaa
PGI1	F	acttcacccaaaccccatg
	R	tcgaatggagcaaccaaatg
HXK	F	aggggaggttagttgcaatgg
	R	tccgtgaaaggaagattgg
HXK1	F	attccaatgattcccggttg
	R	ccgctcaacttgaccaacac
HXK2	F	aaatttgcgttggccttg
	R	tgtccatgacgaaaggcttg
GLK1	F	gccggtcatcgatgtattt
	R	gaccccccattcgacattgtat
GAL10	F	tgaaatggcagaccgagttg
	R	gcctcgacaccccttaactg
PFK1	F	actcccggtgcctttgttgg
	R	atcgccaccggtagcaataac
FBP1	F	cgcctcaaaaggccatctac
	R	tgtctgctgggttgtttg
FBA1	F	ggctttgcaccaatctctc
	R	aaagcgatgtcaccagcgta
TPI1	F	ggtaccggttggctgctac
	R	gctaccgttagcggaccac

	F	atggtccatcccacaaggac
<i>TDH1</i>	R	ggcaagaccttaccgacagc
	F	attggtgtggtagactgc
<i>PGK1</i>	R	agcaacacctggcaattcct
	F	gcgcaacccagaaatcaaat
<i>TDA10</i>	R	gcacttgtcgtcggtcatc
	F	tcattcccccaaccatcttc
<i>ALD2</i>	R	gcgagccgttagcaagtatc
	F	tcattcccccaaccatcttc
<i>ALD3</i>	R	gcgagccgttagcaagtatc
	F	aaccaacggggttgcgttc
<i>ALD4</i>	R	gcctttccacatgcgtcctc
	F	aaggtcgtgccgatactgt
<i>ALD5</i>	R	cgcagcaaacttcaccagag
	F	tgaatggctacccaagacc
<i>ALD6</i>	R	gtaacatccccacgggctaa
	F	gcccacaaaaggaaaagctc
<i>HFD1</i>	R	ggcgtaaccccccacttgta
	F	tggcagtcgaaagagaacga
<i>GCY1</i>	R	ttgatggcttgaccgacttg
	F	aggcgtaaaagctgcagag
<i>DAK1</i>	R	tgaatcgccgacatacgaag
	F	ctgatcgatgctctgcaacc
<i>DAK2</i>	R	ttcggcaccatcataagcag
	F	atggcgcactgacgactcta
<i>GUT1</i>	R	tagccattggaccacagcac
	F	catcgaagttccagggtgctg
<i>GPP1</i>	R	tgtcacgggtaccagagggt
	F	cattgaagtcccagggtcag
<i>GPP2</i>	R	atcacgggtaccggaagttg
	F	accacccggaaatcatcaag
<i>GPT2</i>	R	tccgggatttccttgatttg
	F	tatggctcttgggtgcattgg
<i>SCT1</i>	R	atggggtcaccgaattcaac
	F	ttgcaaagtgggtgtcgag
<i>PHM8</i>	R	atggataacatggccatcc
	F	gcaagcacaccatcaatgt
<i>GPM2</i>	R	gcgtcaatccaaccacagaa

	F	tgacgaagggtggtgtgctc
<i>ENO1</i>	R	cttaccgtcgtaaccagcag
	F	cgatttgcagctttgtctg
<i>CDC19</i>	R	aaaacatcggtggcggtct
	F	cagaatcaaagtccgcgttg
<i>PCK1</i>	R	ctgaccagcggtccagacag
	F	cttcattcaaacgccaacca
<i>PDA1</i>	R	tgtcctcaggggccttcta
	F	ccgcttgaagggttgaag
<i>PDB1</i>	R	tttgcagcggaaattgacaac
	F	gcaagctttgggatctg
<i>THI3</i>	R	ttgcgggaatttatccttg
	F	catgatcagatgggcttga
<i>PDC1</i>	R	gagccttggaccgtgaatc
	F	gatcagaaacgccacccctcc
<i>PDC5</i>	R	ctggcacagcaacaggtttgc
	F	gcctcacgcagactacaacg
<i>PDC6</i>	R	tggcgatcttgcattttcg
	F	gccacgggctctgaagttac
<i>LPD1</i>	R	aaccttccaatccgatg
	F	ggctaagagggtgccagatg
<i>LAT1</i>	R	gtggcaacagcgactgagac
	F	ttttatgtcgcccaactgc
<i>ACS1</i>	R	acccaagcaacgcaagattt
	F	ccttgggtaccgcctcaata
<i>ACS2</i>	R	tgggtagccttgcacgttg
	F	gcmcacaaaaggaaaagctc
<i>HFD1</i>	R	ggcgtaacccccacttgtta
	F	cgttaaggctggaaagatcg
<i>ADH1</i>	R	ccagacaagtcagcgtgagg
	F	cgttaaggctggaaagatcg
<i>ADH2</i>	R	ccagacaagtcagcgtgagg
	F	aagccgc当地attcaacag
<i>ADH3</i>	R	accagagatggcaacccagt
	F	gctgttgcgtcaacgatcc
<i>ADH4</i>	R	gaggcggtggaaacataagc
	F	tcgatggtaatgccaag
<i>ADH5</i>	R	actccatgagaaccgcatt

	F	tccatcacattggctgctc
<i>ADH6</i>	R	tttttacctggaccgcAACCC
	F	ggcgatcatgacgttgatgt
<i>ADH7</i>	R	tgggactggaccccaattac
	F	aatgactgatggggctgg
<i>SFA1</i>	R	ggcagccacaccaatgataa
	F	acccatggccaaatgttgat
<i>CIT1</i>	R	ggagcaccaacagccctatc
	F	attcgatcacgaagggtgg
<i>CIT2</i>	R	caaacctgatgcaagggaca
	F	tgcgttgagtgaccctgtatc
<i>CIT3</i>	R	cttgtgtcttaaccatgc
	F	tgcctatcaagagacccattg
<i>ACO1</i>	R	tccagcgttccacattctg
	F	atgtgccaccatcactctg
<i>IDP1</i>	R	cggcgagaatgttctgatg
	F	tccggccaaatattggaaagc
<i>IDP2</i>	R	tagattccaccgcgtcaatg
	F	ataggccgtcatgctttgg
<i>IDP3</i>	R	gcgatcccaccacttttagg
	F	atccgtccctggtagtgg
<i>IDH1</i>	R	ggcgaagtcaaaggcaaatc
	F	aagggtggcaccaacccatc
<i>IDH2</i>	R	taaagaaccggcgctaaac
	F	acccattcccatggctcag
<i>KGD1</i>	R	tctgttatgcccacgaaacc
	F	gccacgggctctgaagttac
<i>LPD1</i>	R	aaccatttccaatccgatg
	F	tattccagccgtcaatggtg
<i>KGD2</i>	R	ttacgaacgacggggtaac
	F	atgggtggtagtgcatttcc
<i>LSC1</i>	R	ttcgattcggcattaccac
	F	ggattttccagcggtcactcc
<i>LSC2</i>	R	cctctaccccggtcaatgc
	F	attcccacgaagtggaaatgg
<i>SDH1</i>	R	ttggcaccatggacagaaac
	F	ggaaggcattttgtttggtg
<i>SDH2</i>	R	tagcacttggctcgatggaa

	F	ctccgcctttcaagagcag
<i>SDH3</i>	R	ccgcttggtgttcattca
	F	caggtggtgttagggcact
<i>SDH4</i>	R	acgacggacaaggcaaagat
	F	gggtctggctgcctaattcac
<i>SDH9</i>	R	ttccatggtgattgctctgg
	F	ccccgagcatctgtattcgt
<i>SHH3</i>	R	cggccattgtggaattcttt
	F	aaagcagagctcagggttcg
<i>SHH4</i>	R	accaagggaaactgcgatcag
	F	aagaatgccattgccttgg
<i>FUM1</i>	R	ggcctgttgaatagccttgg
	F	tccgtggtaagggtttac
<i>MDH1</i>	R	atggcgaacaagtcatcacg
	F	acatggaacgcaaccaaatg
<i>MDH2</i>	R	tcatgtcaacgaaattccaag
	F	tggaaagttcgcaccaaatg
<i>MDH3</i>	R	ctgcacgtaccaggtaagg
	F	cagaatcaaagtccgcgttg
<i>PCK1</i>	R	ctgaccagcgttccagacag