

Table 1.

GO_term	Frequency	Genome frequency	Probability	Gene(s)
Carbohydrate metabolism	17/69, 24.6%	211/7,264, 2.9%	1.05E-11	GAL1 GAL7 GAL10 GAL2 HXK1 HOR2 PGM2 SDH1 PYC1 GAL80 GAL3 GSY1 GLK1 GSY1 GAC1 SDH4 GPH1
Galactose metabolism	6/69, 8.6%	7/7,264, 0.0%	9.11E-11	GAL1 GAL7 GAL10 GAL2 GAL80 GAL3
Alcohol metabolism	13/69, 18.8%	147/7,264, 2.0%	1.27E-09	GAL1 GAL7 GAL10 GAL2 ADH6 HXK1 RHR2 HOR2 PGM2 PYC1 GAL80 GAL3 GSY1
Monosaccharide metabolism	10/69, 14.4%	86/7,264, 1.1%	9.73E-09	GAL1 GAL7 GAL10 GAL2 HXK1 PGM2 PYC1 GAL80 GAL3 GSY1
Hexose metabolism	9/69, 13.0%	79/7,264, 1.0%	6.69E-08	GAL1 GAL7 GAL10 GAL2 HXK1 PGM2 PYC1 GAL80 GAL3
Carbohydrate transport	5/69, 7.2%	31/7,264, 0.4%	1.26E-05	GAL2 HXT6 HXT4 HXT3 HXT7
Energy derivation by oxidation of organic compounds	9/69, 13.0%	186/7,264, 2.5%	6.69E-05	RHR2 HOR2 SDH1 BDH1 PYC1 GSY1 GAC1 SDH4 GPH1
Energy pathways	9/69, 13.0%	186/7,264, 2.5%	6.69E-05	RHR2 HOR2 SDH1 BDH1 PYC1 GSY1 GAC1 SDH4 GPH1
Hexose transport	4/69, 5.7%	23/7,264, 0.3%	7.37E-05	HXT6 HXT4 HXT3 HXT7
Monosaccharide transport	4/69, 5.7%	23/7,264, 0.3%	7.37E-05	HXT6 HXT4 HXT3 HXT7
Response to abiotic stimulus	9/69, 13.0%	201/7,264, 2.7%	0.00012	RHR2 HOR2 AHP1 FAR1 GCY1 LAP3 HBT1 GAC1 AGP2
Polyol biosynthesis	2/69, 2.8%	2/7,264, 0.0%	0.00017	RHR2 HOR2
Glycerol biosynthesis	2/69, 2.8%	2/7,264, 0.0%	0.00017	RHR2 HOR2
Fermentation	3/69, 4.3%	15/7,264, 0.2%	0.00041	RHR2 HOR2 BDH1
Mitochondrial electron transport, succinate to ubiquinone	2/69, 2.8%	4/7,264, 0.0%	0.00069	SDH1 SDH4
Carboxylic acid metabolism	9/69, 13.0%	257/7,264, 3.5%	0.00072	ACH1 HIS4 KRS1 AGX1 HIS1 FDH1 LEU2 AGP2
Organic acid metabolism	9/69, 13.0%	257/7,264, 3.5%	0.00072	ACH1 HIS4 KRS1 AGX1 HIS1 FDH1 LEU2 AGP2
Response to external stimulus	9/69, 13.0%	259/7,264, 3.5%	0.00076	RHR2 HOR2 AHP1 FAR1 GCY1 LAP3 HBT1 GAC1 AGP2
Electron transport	3/69, 4.3%	20/7,264, 0.2%	0.00095	CYB2 SDH1 SDH4
Glycogen metabolism	3/69, 4.3%	25/7,264, 0.3%	0.0018	GSY1 GAC1 GPH1
Response to osmotic stress	4/69, 5.7%	58/7,264, 0.7%	0.00232	RHR2 HOR2 GCY1 AGP2
Polyol metabolism	2/69, 2.8%	8/7,264, 0.1%	0.0027	RHR2 HOR2
Glycerol metabolism	2/69, 2.8%	8/7,264, 0.1%	0.0027	RHR2 HOR2
Energy reserve metabolism	3/69, 4.3%	30/7,264, 0.4%	0.00301	GSY1 GAC1 GPH1 GAL1 GAL7 GAL10 GAL2 CYB2 ADH6 HXK1 RHR2 HOR2 PGM2 SDH1 ADE2 ACH1 BDH1 PYC1 HIS4 KRS1 NSR1 RPL34B GAL80 GAL3 HSP30 AGX1 GCY1 GLK1 HIS1 DDR48 SSE1 SHM1 FUN34 FDH1 LEU2 RPA49 GSY1 GAC1 RPL13A ECM2 RPL31A RPA34 PRC1 AGP2 SDH4 GPH1
Metabolism	44/69, 63.7%	3,391/7,264, 46.6%	0.00318	
Acylglycerol metabolism	2/69, 2.8%	10/7,264, 0.1%	0.00418	RHR2 HOR2
Glycerol ether metabolism	2/69, 2.8%	10/7,264, 0.1%	0.00418	RHR2 HOR2
Neutral lipid metabolism	2/69, 2.8%	10/7,264, 0.1%	0.00418	RHR2 HOR2
Triacylglycerol metabolism	2/69, 2.8%	10/7,264, 0.1%	0.00418	RHR2 HOR2
Glycerolipid metabolism	2/69, 2.8%	10/7,264, 0.1%	0.00418	RHR2 HOR2
Alcohol biosynthesis	3/69, 4.3%	34/7,264, 0.4%	0.00426	RHR2 HOR2 PYC1
One-carbon compound metabolism	2/69, 2.8%	11/7,264, 0.1%	0.00502	SHM1 FDH1
Glucan metabolism	3/69, 4.3%	37/7,264, 0.5%	0.00538	GSY1 GAC1 GPH1
Response to stimulus	11/69, 15.9%	489/7,264, 6.7%	0.00619	RHR2 HOR2 AHP1 HSP30 FAR1 GCY1 DDR48 LAP3 HBT1 GAC1 AGP2
Amino acid metabolism	6/69, 8.6%	175/7,264, 2.4%	0.00641	HIS4 KRS1 AGX1 HIS1 LEU2
Histidine family amino acid metabolism	2/69, 2.8%	14/7,264, 0.1%	0.00799	HIS4 HIS1
Protein-disulfide reduction	2/69, 2.8%	14/7,264, 0.1%	0.00799	SDH1 SDH4
ATP synthesis coupled electron transport (sensu Eukarya)	2/69, 2.8%	14/7,264, 0.1%	0.00799	SDH1 SDH4
Histidine biosynthesis	2/69, 2.8%	14/7,264, 0.1%	0.00799	HIS4 HIS1
Histidine family amino acid biosynthesis	2/69, 2.8%	14/7,264, 0.1%	0.00799	HIS4 HIS1
Histidine metabolism	2/69, 2.8%	14/7,264, 0.1%	0.00799	HIS4 HIS1
ATP synthesis coupled electron transport	2/69, 2.8%	14/7,264, 0.1%	0.00799	SDH1 SDH4
Amino acid and derivative metabolism	6/69, 8.6%	187/7,264, 2.5%	0.00875	HIS4 KRS1 AGX1 HIS1 LEU2
Tricarboxylic acid cycle	2/69, 2.8%	15/7,264, 0.2%	0.00912	SDH1 SDH4
Branched chain family amino acid metabolism	2/69, 2.8%	16/7,264, 0.2%	0.01032	LEU2
Amine metabolism	6/69, 8.6%	198/7,264, 2.7%	0.01137	HIS4 KRS1 AGX1 HIS1 LEU2
Polysaccharide metabolism	3/69, 4.3%	50/7,264, 0.6%	0.01219	GSY1 GAC1 GPH1
Serine family amino acid metabolism	2/69, 2.8%	20/7,264, 0.2%	0.01573	AGX1
Amino acid biosynthesis	4/69, 5.7%	101/7,264, 1.3%	0.01579	HIS4 AGX1 HIS1 LEU2
Amine biosynthesis	4/69, 5.7%	108/7,264, 1.4%	0.01966	HIS4 AGX1 HIS1 LEU2

Anion transport	2/69, 2.8%	26/7,264, 0.3%	0.02565	PHO84 JEN1
Response to chemical substance	4/69, 5.7%	118/7,264, 1.6%	0.02613	AHP1 FAR1 LAP3 HBT1
Main pathways of carbohydrate metabolism	3/69, 4.3%	67/7,264, 0.9%	0.02618	SDH1 PYC1 SDH4
Transcription from Pol I promoter	2/69, 2.8%	28/7,264, 0.3%	0.02939	RPA49 RPA34
Nicotinamide metabolism	2/69, 2.8%	29/7,264, 0.3%	0.03133	PYC1 FDH1
Pyridine nucleotide metabolism	2/69, 2.8%	31/7,264, 0.4%	0.03538	PYC1 FDH1
Oxidative phosphorylation	2/69, 2.8%	34/7,264, 0.4%	0.0418	SDH1 SDH4
Nucleotide metabolism	3/69, 4.3%	85/7,264, 1.1%	0.04746	ADE2 PYC1 FDH1
Response to stress	7/69, 10.1%	365/7,264, 5.0%	0.05787	RHR2 HOR2 HSP30 GCY1 DDR48 GAC1 AGP2
Oxidoreduction coenzyme metabolism	2/69, 2.8%	41/7,264, 0.5%	0.05828	PYC1 FDH1
Protein folding	2/69, 2.8%	43/7,264, 0.5%	0.06335	HSP30 SSE1
Carboxylic acid transport	2/69, 2.8%	44/7,264, 0.6%	0.06593	DIP5 JEN1
Organic acid transport	2/69, 2.8%	45/7,264, 0.6%	0.06856	DIP5 JEN1
Response to pheromone during conjugation with cellular fusion	2/69, 2.8%	48/7,264, 0.6%	0.07662	FAR1 HBT1
Coenzyme metabolism	3/69, 4.3%	108/7,264, 1.4%	0.08373	ACH1 PYC1 FDH1
Transport	12/69, 17.3%	831/7,264, 11.4%	0.09126	GAL2 HXT6 HXT4 HXT3 DIP5 FIT2 HXT7 FIT3 PHO84 FUN34 AGP2 JEN1
Glucose metabolism	2/69, 2.8%	56/7,264, 0.7%	0.09946	PGM2 PYC1