

SUPPLEMENTARY TABLE 2. Significant GO Process Terms of Relevant Clusters

(p values < 10⁻⁴)

Cluster no	Gene Ontology term	Cluster frequency	Background frequency	p-value	Genes annotated to the term
0	generation of precursor metabolites and energy	17 / 34 50.0%	336 / 7288 4.6%	3.40e-12	<i>AAC1, ATP1, CIT1, COX1, FUM1, GLK1, GND2, IDP1, KGD1, PGII, PGK1, PGM2, RIP1, SDH3, TDH2, TKL1, ZWF1</i>
0	energy derivation by oxidation of organic compounds	16 / 34 47.1%	298 / 7288 4.1%	1.07e-11	<i>AAC1, CIT1, COX1, FUM1, GLK1, GND2, IDP1, KGD1, PGII, PGK1, PGM2, RIP1, SDH3, TDH2, TKL1, ZWF1</i>
0	cellular carbohydrate metabolic process	13 / 34 38.2%	209 / 7288 2.9%	7.71e-10	<i>CIT1, FUM1, GLK1, GND2, IDP1, KGD1, PGII, PGK1, PGM2, SDH3, TDH2, TKL1, ZWF1</i>
0	carbohydrate metabolic process	13 / 34 38.2%	229 / 7288 3.1%	2.47e-09	<i>CIT1, FUM1, GLK1, GND2, IDP1, KGD1, PGII, PGK1, PGM2, SDH3, TDH2, TKL1, ZWF1</i>
0	carbohydrate metabolic	13 / 34	229 / 7288	2.47e-09	<i>CIT1, FUM1, GLK1,</i>

	process	38.2%	3.1%		<i>GND2, IDP1, KGD1, PGII, PGK1, PGM2, SDH3, TDH2, TKL1, ZWF1</i>
0	glucose catabolic process	7 / 34 20.6%	34 / 7288 0.5%	2.83e-08	<i>GLK1, GND2, PGII, PGK1, TDH2, TKL1, ZWF1</i>
0	hexose catabolic process	7 / 34 20.6%	37 / 7288 0.5%	5.37e-08	<i>GLK1, GND2, PGII, PGK1, TDH2, TKL1, ZWF1</i>
0	glucose metabolic process	8 / 34 23.5%	64 / 7288 0.9%	7.89e-08	<i>GLK1, GND2, PGII, PGK1, PGM2, TDH2, TKL1, ZWF1</i>
0	monosaccharide catabolic process	7 / 34 20.6%	42 / 7288 0.6%	1.38e-07	<i>GLK1, GND2, PGII, PGK1, TDH2, TKL1, ZWF1</i>
0	alcohol catabolic process	7 / 34 20.6%	45 / 7288 0.6%	2.30e-07	<i>GLK1, GND2, PGII, PGK1, TDH2, TKL1, ZWF1</i>
0	hexose metabolic process	8 / 34 23.5%	85 / 7288 1.2%	8.02e-07	<i>GLK1, GND2, PGII, PGK1, PGM2, TDH2, TKL1, ZWF1</i>
0	monosaccharide metabolic process	8 / 34 23.5%	92 / 7288 1.3%	1.51e-06	<i>GLK1, GND2, PGII, PGK1, PGM2, TDH2, TKL1, ZWF1</i>
0	coenzyme metabolic process	9 / 34 26.5%	135 / 7288 1.9%	1.60e-06	<i>ATP1, CIT1, FUM1, GND2, KGD1, PGII, SDH3, TKL1, ZWF1</i>
0	nucleotide metabolic process	8 / 34 genes, 23.5%	109 / 7288 1.5%	5.86e-06	<i>ADK1, ATP1, GND2, PGII, PRS2, TKL1, YNK1, ZWF1</i>
0	cofactor metabolic	9 / 34	168 / 7288	1.09e-05	<i>ATP1, CIT1, FUM1, GND2,</i>

	process	26.5%	2.3%		<i>KGDI, PGII, SDH3, TKL1, ZWF1</i>
0	carbohydrate catabolic process	7 / 34 20.6%	78 / 7288 1.1%	1.20e-05	<i>GLK1, GND2, PGII, PGK1, TDH2, TKL1, ZWF1</i>
0	aerobic respiration	7 / 34 20.6%	80 / 7288 1.1%	1.44e-05	<i>AAC1, CIT1, COX1, FUM1, KGDI, RIP1, SDH3</i>
0	cellular respiration	7 / 34 20.6%	86 / 7288 1.2%	2.38e-05	<i>AAC1, CIT1, COX1, FUM1, KGDI, RIP1, SDH3</i>
0	pentose-phosphate shunt	4 / 34 11.8%	11 / 7288 0.2%	2.94e-05	<i>GND2, PGII, TKL1, ZWF1</i>
0	amino acid biosynthetic process	7 / 34 20.6%	103 / 7288 1.4%	8.33e-05	<i>CIT1, GDH3, IDP1, PRS2, SER1, SER2, SER3</i>
0	NADPH regeneration	4 / 34 11.8%	14 / 7288 0.2%	8.83e-05	<i>GND2, PGII, TKL1, ZWF1</i>
2	carboxylic acid metabolic process	23 / 30 76.7%	307 / 7288 4.2%	3.04e-24	<i>AAT2, ACS1, ARG1, ARG3, ARG4, CARI, CAT2, CIT2, CPA2, CRC1, FBA1, GCV1, GLN1, GLT1, HOM2, HOM3, HOM6, MAE1, PGII, PYC1, THR1, THR4, YAT1</i>
2	amino acid and derivative metabolic	18 / 30 60.0%	199 / 7288 2.7%	4.06e-19	<i>AAT2, ARG1, ARG3, ARG4, CARI, CAT2, CIT2, CPA2,</i>

	process				<i>GCV1, GLN1, GLT1, HOM2, HOM3, HOM6, MAE1, THR1, THR4, YAT1</i>
2	amine metabolic process	18 / 30 60.0%	222 / 7288 3.0%	3.05e-18	<i>AAT2, ARG1, ARG3, ARG4, CAR1, CAT2, CIT2, CPA2, GCV1, GLN1, GLT1, HOM2, HOM3, HOM6, MAE1, THR1, THR4, YAT1</i>
2	nitrogen compound metabolic process	18 / 30 60.0%	243 / 7288 3.3%	1.59e-17	<i>AAT2, ARG1, ARG3, ARG4, CAR1, CAT2, CIT2, CPA2, GCV1, GLN1, GLT1, HOM2, HOM3, HOM6, MAE1, THR1, THR4, YAT1</i>
2	amino acid metabolic process	16 / 30 53.3%	184 / 7288 2.5%	2.87e-16	<i>AAT2, ARG1, ARG3, ARG4, CAR1, CIT2, CPA2, GCV1, GLN1, GLT1, HOM2, HOM3, HOM6, MAE1, THR1, THR4</i>
2	glutamine family amino acid metabolic process	9 / 30 30.0%	43 / 7288 0.6%	8.82e-12	<i>AAT2, ARG1, ARG3, ARG4, CAR1, CIT2, CPA2, GLN1, GLT1</i>
2	amino acid biosynthetic process	11 / 30 36.7%	103 / 7288 1.4%	2.16e-11	<i>AAT2, ARG1, ARG3, ARG4, CIT2, CPA2, GLN1, GLT1,</i>

					<i>HOM2, HOM3, HOM6</i>
2	nitrogen compound biosynthetic process	11 / 30 36.7%	111 / 7288 1.5%	5.03e-11	<i>AAT2, ARG1, ARG3, ARG4, CIT2, CPA2, GLN1, GLT1, HOM2, HOM3, HOM6</i>
2	glutamine family amino acid biosynthetic process	7 / 30 23.3%	27 / 7288 0.4%	1.50e-09	<i>ARG1, ARG3, ARG4, CIT2, CPA2, GLN1, GLT1</i>
2	threonine metabolic process	5 / 30 16.7%	8 / 7288 0.1%	8.78e-09	<i>HOM2, HOM3, HOM6, THR1, THR4</i>
2	monocarboxylic acid metabolic process	9 / 30 30.0%	121 / 7288 1.7%	1.44e-07	<i>ACSI, CAT2, CIT2, CRC1, FBA1, MAE1, PGII, PYC1, YATI</i>
2	urea cycle intermediate metabolic process	5 / 30 16.7%	15 / 7288 0.2%	4.61e-07	<i>ARG1, ARG3, ARG4, CAR1, CPA2</i>
2	arginine metabolic process	5 / 30 16.7%	15 / 7288 0.2%	4.61e-07	<i>ARG1, ARG3, ARG4, CAR1, CPA2</i>
2	homoserine metabolic process	4 / 30 13.3%	7 / 7288 0.1%	1.53e-06	<i>HOM2, HOM3, HOM6, THR1</i>
2	aspartate family amino acid metabolic process	6 / 30 20.0%	45 / 7288 0.6%	3.96e-06	<i>AAT2, HOM2, HOM3, HOM6, THR1, THR4</i>
2	glycolysis	5 / 30 16.7%	24 / 7288 0.3%	6.36e-06	<i>FBA1, HXK2, PFK2, PGII, TPII</i>
2	serine family amino	5 / 30	24 / 7288	6.36e-06	<i>GCV1, HOM2, HOM3,</i>

	acid metabolic process	16.7%	0.3%		<i>HOM6, THR1</i>
2	metabolic process	28 / 30 93.3%	3510 / 7288 48.2%	2.94e-05	<i>AAT2, ACS1, ARG1, ARG3, ARG4, CAR1, CAT2, CIT2, CPA2, CRC1, FBA1, GCV1, GLN1, GLT1, HOM2, HOM3, HOM6, HXK2, IPP1, MAE1, PDC6, PFK2, PGII, PYC1, THR1, THR4, TPII, YAT1</i>
2	glucose metabolic process	6 / 30 20.0%	64 / 7288 0.9%	3.45e-05	<i>FBA1, HXK2, PFK2, PGII, PYC1, TPII</i>
2	alcohol metabolic process	8 / 30 26.7%	163 / 7288 2.2%	3.85e-05	<i>FBA1, HXK2, PDC6, PFK2, PGII, PYC1, TPII, YAT1</i>
4	cellular biosynthetic process	10 out of 12 genes, 83.3%	1152 out of 7288 background genes, 15.8%	7.40e-05	<i>DPM1, GSC2, GSY1, IDP2, ILV2, ILV3, ILV5, PMT2, PSA1, RKII</i>
8	cellular carbohydrate metabolic process	10 / 18 55.6%	209 / 7288 2.9%	2.13e-09	<i>ATH1, ENO1, FUM1, GPM1, LSC2, MDH3, PGMI, PMI40, TDH1, TPS2</i>
8	energy derivation by	11 / 18	298 / 7288	2.15e-09	<i>ADH5, ATH1, ENO1,</i>

	oxidation of organic compounds	61.1%	4.1%		<i>FUM1, GPM1, LSC2, MDH3, PGM1, PMI40, TDH1, TPS2</i>
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