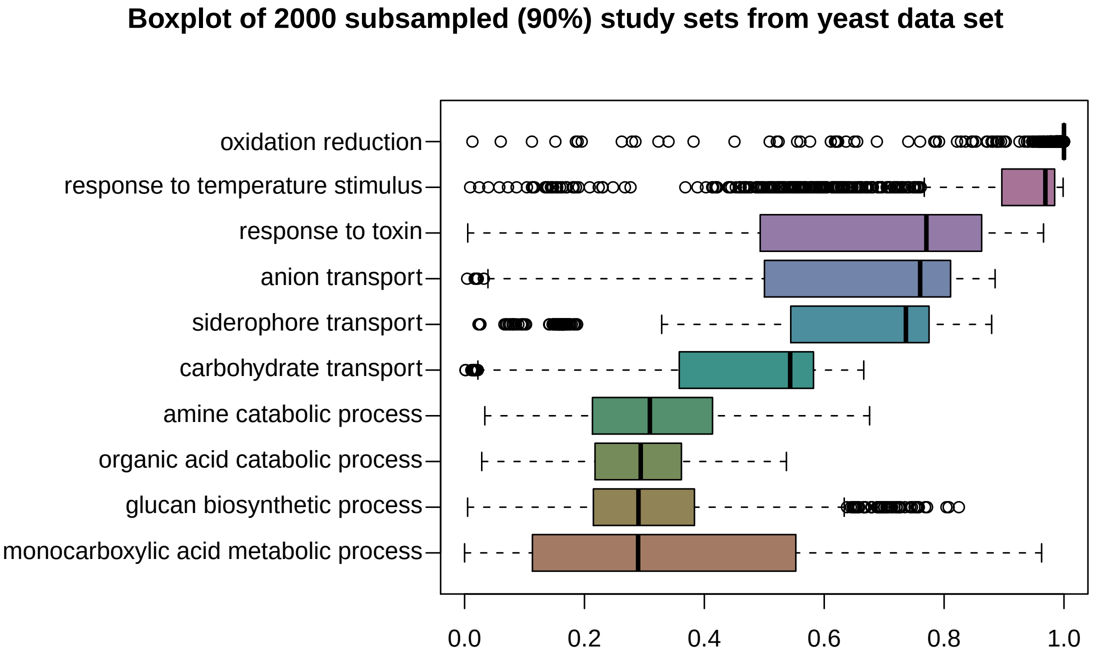
1 Figure S1

We performed a further simulation study by subsampling 2,000 study sets at random each of which was chosen to have 90% of the genes of the yeast set that has been used in the Results section. We present the results in form of boxplots of the marginal probabilities reported for each term. The figure shows the ten terms that had the largest median. All terms identified by the orginal analysis were consistently identified also in the subsamples.



2 Table S1

GO ID	Name	Pop	Study	MGSA	TfT	PCu
GO:0055114	oxidation reduction	314	113	1.000/1.000/1.000	1.80×10^{-41} (2.16×10^{-38})	3.15×10^{-42} (3.67×10^{-39})
GO:0009266	response to temperature stimulus	207	59	0.976/0.983/0.987	7.04×10^{-16} (6.04×10^{-14})	1.32×10^{-7} (6.71×10^{-6})
GO:0009636	response to toxin	22	8	0.832/0.846/0.870	(0.006)	0.002 (0.027)
GO:0015891	siderophore transport	6	4	0.814/0.826/0.840	(0.010)	0.001 (0.020)
GO:0006820	anion transport	31	10	0.771/0.789/0.813	(0.004)	0.568 (1.000)
GO:0008643	carbohydrate transport	27	8	0.553/0.571/0.593	0.003 (0.021)	0.003 (0.039)
GO:0032787	monocarboxylic acid metabolic process	143	40	0.410/0.462/0.502	8.44×10^{-11} (3.07×10^{-9})	0.016 (0.145)
GO:0009250	glucan biosynthetic process	27	9	0.353/0.381/0.431	(0.006)	0.012 (0.123)
GO:0009310	amine catabolic process	42	17	0.358/0.372/0.396	7.01×10^{-8} (1.96×10^{-6})	(0.004)
GO:0034637	cellular carbohydrate biosynthetic process	83	20	0.301/0.343/0.381	5.53×10^{-5} ()	7.47×10^{-5} (0.002)
GO:0051099	positive regulation of binding	3	2	0.315/0.326/0.337	0.025 (0.137)	0.014 (0.129)
GO:0019794	nonprotein amino acid metabolic process	10	5	0.279/0.291/0.304	0.001 (0.011)	0.020 (0.170)
GO:0009084	glutamine family amino acid biosynthetic process	28	14	0.279/0.288/0.302	3.94×10^{-8} (1.13×10^{-6})	(0.013)
GO:0046395	carboxylic acid catabolic process	51	25	0.257/0.283/0.309	2.70×10^{-13} (1.08×10^{-11})	2.69×10^{-6} ()
GO:0016054	organic acid catabolic process	51	25	0.257/0.269/0.296	2.70×10^{-13} (1.08×10^{-11})	2.89×10^{-10} (1.98×10^{-8})
GO:0031670	cellular response to nutrient	14	4	0.236/0.251/0.261	0.036 (0.186)	0.049 (0.313)
GO:0045990	regulation of transcription by carbon catabolites	14	4	0.237/0.249/0.263	0.036 (0.186)	0.003 (0.039)
GO:0016052	carbohydrate catabolic process	83	22	0.197/0.220/0.252	4.50×10^{-6} (8.71×10^{-5})	(0.013)

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Table 1 – Continued

GO ID	Name	Pop	Study	MGSA	TfT	PCu
GO:0008645	hexose transport	15	6	0.202/0.218/0.231	0.002 (0.014)	1.000 (1.000)
GO:0015749	monosaccharide transport	15	6	0.202/0.218/0.238	0.002 (0.014)	0.186 (0.668)
GO:0015711	organic anion transport	9	5	0.185/0.208/0.223	(0.007)	0.090 (0.465)
GO:0046898	response to cycloheximide	4	2	0.182/0.194/0.200	0.046 (0.221)	1.000 (1.000)
GO:0014071	response to cycloalkane	4	2	0.175/0.189/0.197	0.046 (0.221)	0.600 (1.000)
GO:0032048	cardiolipin metabolic process	5	2	0.179/0.189/0.205	0.072 (0.308)	0.476 (0.973)
GO:0006857	oligopeptide transport	5	2	0.168/0.180/0.188	0.072 (0.308)	0.357 (0.902)
GO:0000097	sulfur amino acid biosynthetic process	35	6	0.166/0.177/0.182	0.104 (0.337)	0.712 (1.000)
GO:0019751	polyol metabolic process	25	7	0.146/0.159/0.169	0.007 (0.048)	0.178 (0.654)
GO:0006577	betaine metabolic process	3	3	0.142/0.153/0.168	(0.008)	0.010 (0.101)
GO:0009437	carnitine metabolic process	3	3	0.139/0.152/0.162	(0.008)	0.014 (0.132)
GO:0014070	response to organic cyclic substance	5	2	0.132/0.137/0.142	0.072 (0.308)	0.031 (0.226)
GO:0009086	methionine biosynthetic process	30	5	0.132/0.136/0.143	0.144 (0.434)	0.500 (0.973)
GO:0009313	oligosaccharide catabolic process	5	2	0.125/0.131/0.140	0.072 (0.308)	0.329 (0.881)
GO:0045333	cellular respiration	100	50	0.114/0.128/0.134	4.76×10^{-26} (1.43×10^{-23})	(0.017)
GO:0009070	serine family amino acid biosynthetic process	22	5	0.115/0.119/0.126	0.049 (0.231)	0.549 (1.000)
GO:0046471	phosphatidylglycerol metabolic process	7	2	0.105/0.110/0.115	0.134 (0.410)	0.061 (0.363)
GO:0006526	arginine biosynthetic process	10	4	0.102/0.109/0.118	0.010 (0.068)	0.818 (1.000)
GO:0006109	regulation of carbohydrate metabolic process	38	11	0.100/0.107/0.114	(0.005)	(0.004)
GO:0007584	response to nutrient	17	4	0.100/0.106/0.111	0.068 (0.304)	0.115 (0.531)
GO:0019541	propionate metabolic process	5	5	0.089/0.103/0.112	7.10×10^{-6} ()	0.001 (0.026)
GO:0000429	regulation of transcription from RNA polymerase II promoter by carbon catabolites	8	3	0.092/0.100/0.103	0.032 (0.173)	0.009 (0.097)
GO:0006084	acetyl-CoA metabolic process	34	24	0.090/0.098/0.108	6.71×10^{-18} (1.01×10^{-15})	3.25×10^{-9} (1.80×10^{-7})
GO:0046337	phosphatidylethanolamine metabolic process	6	2	0.092/0.096/0.102	0.102 (0.332)	0.232 (0.745)
GO:0051187	cofactor catabolic process	35	23	0.087/0.092/0.100	3.97×10^{-16} (3.67×10^{-14})	3.17×10^{-13} (3.00×10^{-11})
GO:0009063	cellular amino acid catabolic process	38	16	0.078/0.090/0.104	8.84×10^{-8} (2.31×10^{-6})	0.001 (0.023)
GO:0015806	S-methylmethionine transport	1	1	0.085/0.089/0.096	0.094 (0.319)	0.167 (0.642)
GO:0019400	alditol metabolic process	14	5	0.074/0.083/0.091	0.007 (0.050)	0.141 (0.591)
GO:0006071	glycerol metabolic process	14	5	0.072/0.082/0.091	0.007 (0.050)	1.000 (1.000)
GO:0006817	phosphate transport	11	4	0.073/0.081/0.095	0.015 (0.092)	0.221 (0.726)
GO:0010107	potassium ion import	1	1	0.077/0.081/0.086	0.094 (0.319)	0.125 (0.564)
GO:0044275	cellular carbohydrate catabolic process	60	17	0.073/0.079/0.084	2.14×10^{-5} ()	(0.007)
GO:0005984	disaccharide metabolic process	16	3	0.071/0.078/0.081	0.184 (0.478)	0.690 (1.000)
GO:0006113	fermentation	15	5	0.070/0.078/0.091	0.010 (0.065)	0.804 (1.000)
GO:0006855	multidrug transport	10	3	0.071/0.077/0.080	0.060 (0.275)	0.264 (0.787)
GO:0006564	L-serine biosynthetic process	4	2	0.073/0.076/0.080	0.046 (0.221)	0.179 (0.656)
GO:0006878	cellular copper ion homeostasis	10	2	0.072/0.074/0.078	0.240 (0.594)	0.481 (0.973)
GO:0055070	copper ion homeostasis	10	2	0.070/0.073/0.079	0.240 (0.594)	0.481 (0.973)
GO:0046677	response to antibiotic	8	2	0.066/0.071/0.075	0.168 (0.469)	0.230 (0.745)
GO:0000040	low-affinity iron ion transport	1	1	0.065/0.070/0.074	0.094 (0.319)	0.400 (0.939)
GO:0009061	anaerobic respiration	2	2	0.065/0.070/0.073	0.009 (0.060)	0.247 (0.764)
GO:0046173	polyol biosynthetic process	9	3	0.061/0.070/0.075	0.045 (0.221)	0.245 (0.757)
GO:0006072	glycerol-3-phosphate metabolic process	4	3	0.063/0.067/0.074	0.003 (0.025)	0.011 (0.109)
GO:0006433	prolyl-tRNA aminoacylation	2	1	0.062/0.067/0.071	0.179 (0.469)	0.054 (0.338)
GO:0015833	peptide transport	8	2	0.063/0.067/0.071	0.168 (0.469)	0.174 (0.654)
GO:0042149	cellular response to glucose starvation	4	1	0.063/0.065/0.068	0.326 (0.655)	0.418 (0.953)

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Table 1 – Continued

GO ID	Name	Pop	Study	MGSA	TfT	PCu
GO:0060962	regulation of ribosomal protein gene transcription from RNA polymerase II promoter	2	1	0.059/0.064/0.067	0.179 (0.469)	0.080 (0.421)
GO:0010688	negative regulation of ribosomal protein gene transcription from RNA polymerase II promoter	2	1	0.060/0.063/0.067	0.179 (0.469)	0.182 (0.659)
GO:0032092	positive regulation of protein binding	1	1	0.059/0.062/0.067	0.094 (0.319)	0.500 (0.973)
GO:0034440	lipid oxidation	11	6	0.056/0.062/0.068	(0.002)	0.015 (0.134)
GO:0006591	ornithine metabolic process	7	4	0.058/0.061/0.067	0.002 (0.018)	0.500 (0.973)
GO:0043388	positive regulation of DNA binding	2	1	0.057/0.061/0.064	0.179 (0.469)	0.533 (0.996)
GO:0000413	protein peptidyl-prolyl isomerization	1	1	0.055/0.060/0.064	0.094 (0.319)	0.028 (0.213)
GO:0019395	fatty acid oxidation	11	6	0.055/0.060/0.064	(0.002)	0.010 (0.109)
GO:0034397	telomere localization	2	1	0.055/0.060/0.063	0.179 (0.469)	0.052 (0.329)
GO:0042407	cristae formation	4	4	0.056/0.060/0.065	7.64×10^{-5} (0.001)	(0.016)
GO:0045141	meiotic telomere clustering	2	1	0.056/0.060/0.064	0.179 (0.469)	0.035 (0.246)
GO:0051101	regulation of DNA binding	9	2	0.056/0.060/0.063	0.204 (0.515)	0.345 (0.893)
GO:0000414	regulation of histone H3-K36 methylation	1	1	0.056/0.059/0.062	0.094 (0.319)	0.333 (0.883)
GO:0000415	negative regulation of histone H3-K36 methylation	1	1	0.056/0.059/0.062	0.094 (0.319)	1.000 (1.000)
GO:0031061	negative regulation of histone methylation	1	1	0.056/0.059/0.065	0.094 (0.319)	0.043 (0.289)
GO:0006114	glycerol biosynthetic process	3	2	0.054/0.058/0.063	0.025 (0.137)	0.215 (0.723)
GO:0010452	histone H3-K36 methylation	1	1	0.056/0.058/0.063	0.094 (0.319)	0.067 (0.377)
GO:0031057	negative regulation of histone modification	1	1	0.055/0.058/0.061	0.094 (0.319)	0.028 (0.213)
GO:0033015	tetrapyrrole catabolic process	1	1	0.051/0.058/0.060	0.094 (0.319)	0.269 (0.793)
GO:0042167	heme catabolic process	1	1	0.055/0.058/0.060	0.094 (0.319)	0.235 (0.746)
GO:0000412	histone peptidyl-prolyl isomerization	1	1	0.054/0.057/0.060	0.094 (0.319)	0.030 (0.223)
GO:0006787	porphyrin catabolic process	1	1	0.054/0.057/0.060	0.094 (0.319)	0.510 (0.976)
GO:0006788	heme oxidation	1	1	0.055/0.057/0.061	0.094 (0.319)	0.235 (0.746)
GO:0006829	zinc ion transport	9	2	0.054/0.057/0.061	0.204 (0.515)	0.492 (0.973)
GO:0019401	alditol biosynthetic process	3	2	0.052/0.057/0.064	0.025 (0.137)	0.142 (0.592)
GO:0033692	cellular polysaccharide biosynthetic process	43	10	0.054/0.057/0.064	0.005 (0.040)	0.002 (0.027)
GO:0046149	pigment catabolic process	1	1	0.053/0.057/0.060	0.094 (0.319)	0.129 (0.567)
GO:0015695	organic cation transport	8	3	0.051/0.056/0.063	0.032 (0.173)	0.308 (0.848)
GO:0046365	monosaccharide catabolic process	66	16	0.052/0.056/0.060	(0.003)	0.406 (0.950)
GO:0006825	copper ion transport	14	3	0.050/0.054/0.058	0.137 (0.415)	0.457 (0.967)
GO:0005998	xylulose catabolic process	1	1	0.047/0.053/0.057	0.094 (0.319)	0.500 (0.973)
GO:0006000	fructose metabolic process	6	3	0.048/0.053/0.058	0.013 (0.083)	0.148 (0.604)
GO:0006003	fructose 2,6-bisphosphate metabolic process	4	3	0.047/0.053/0.057	0.003 (0.025)	0.200 (0.699)
GO:0019323	pentose catabolic process	5	2	0.049/0.053/0.057	0.072 (0.308)	0.323 (0.873)
GO:0046164	alcohol catabolic process	70	17	0.049/0.053/0.056	(0.002)	0.007 (0.081)
GO:0006007	glucose catabolic process	53	13	0.049/0.052/0.056	(0.009)	0.564 (1.000)
GO:0009311	oligosaccharide metabolic process	23	4	0.049/0.052/0.057	0.163 (0.469)	0.726 (1.000)
GO:0042732	D-xylose metabolic process	6	3	0.047/0.052/0.057	0.013 (0.083)	0.176 (0.654)
GO:0042762	regulation of sulfur metabolic process	1	1	0.047/0.052/0.055	0.094 (0.319)	0.060 (0.360)
GO:0043392	negative regulation of DNA binding	3	1	0.050/0.052/0.055	0.256 (0.594)	0.533 (0.996)
GO:0043433	negative regulation of transcription factor activity	3	1	0.050/0.052/0.055	0.256 (0.594)	0.375 (0.917)
GO:0090048	negative regulation of transcription regulator activity	3	1	0.048/0.052/0.056	0.256 (0.594)	0.371 (0.917)

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Table 1 – Continued

GO ID	Name	Pop	Study	MGSA	TfT	PCu
GO:0005997	xylulose metabolic process	2	2	0.048/0.051/0.055	0.009 (0.060)	0.065 (0.374)
GO:0010906	regulation of glucose metabolic process	21	7	0.044/0.051/0.057	0.002 (0.019)	0.225 (0.733)
GO:0015677	copper ion import	6	2	0.047/0.051/0.055	0.102 (0.332)	0.743 (1.000)
GO:0006826	iron ion transport	29	7	0.045/0.050/0.057	0.015 (0.095)	0.065 (0.374)
GO:0006560	proline metabolic process	8	4	0.045/0.049/0.052	0.004 (0.031)	0.051 (0.323)
GO:0015718	monocarboxylic acid transport	15	4	0.046/0.049/0.054	0.045 (0.221)	0.219 (0.723)
GO:0006561	proline biosynthetic process	5	2	0.045/0.048/0.051	0.072 (0.308)	0.460 (0.967)
GO:0009069	serine family amino acid metabolic process	34	6	0.044/0.048/0.050	0.093 (0.319)	0.622 (1.000)
GO:0016036	cellular response to phosphate starvation	3	1	0.044/0.048/0.051	0.256 (0.594)	0.330 (0.881)
GO:0051274	beta-glucan biosynthetic process	10	3	0.043/0.048/0.054	0.060 (0.275)	0.722 (1.000)
GO:0000023	maltose metabolic process	4	1	0.045/0.047/0.052	0.326 (0.655)	0.607 (1.000)
GO:0015879	carnitine transport	1	1	0.041/0.047/0.050	0.094 (0.319)	0.051 (0.325)
GO:0015698	inorganic anion transport	20	5	0.042/0.046/0.051	0.034 (0.180)	0.940 (1.000)
GO:0006006	glucose metabolic process	87	22	0.039/0.045/0.048	1.03×10^{-5} ()	0.371 (0.917)
GO:0006598	polyamine catabolic process	4	1	0.041/0.045/0.047	0.326 (0.655)	0.637 (1.000)
GO:0006824	cobalt ion transport	3	1	0.041/0.045/0.049	0.256 (0.594)	0.397 (0.938)
GO:0042402	biogenic amine catabolic process	11	3	0.041/0.045/0.048	0.076 (0.314)	0.688 (1.000)
GO:0043393	regulation of protein binding	2	1	0.043/0.045/0.049	0.179 (0.469)	0.253 (0.767)
GO:0050983	spermidine catabolic process to deoxyhypusine, using deoxyhypusine synthase	1	1	0.040/0.045/0.049	0.094 (0.319)	1.000 (1.000)
GO:0006099	tricarboxylic acid cycle	30	22	0.038/0.044/0.047	4.44×10^{-17} (5.34×10^{-15})	(0.006)
GO:0009051	pentose-phosphate shunt, oxidative branch	4	2	0.040/0.044/0.049	0.046 (0.221)	0.269 (0.793)
GO:0046203	spermidine catabolic process	1	1	0.040/0.044/0.047	0.094 (0.319)	0.167 (0.642)
GO:0006097	glyoxylate cycle	8	5	0.037/0.043/0.049	(0.004)	0.012 (0.123)
GO:0015980	energy derivation by oxidation of organic compounds	156	63	0.036/0.043/0.052	4.32×10^{-26} (1.43×10^{-23})	0.053 (0.332)
GO:0046356	acetyl-CoA catabolic process	30	22	0.040/0.043/0.052	4.44×10^{-17} (5.34×10^{-15})	0.019 (0.161)
GO:0046487	glyoxylate metabolic process	9	6	0.037/0.043/0.050	4.32×10^{-5} ()	0.012 (0.119)
GO:0000271	polysaccharide biosynthetic process	44	10	0.035/0.042/0.048	0.006 (0.047)	0.002 (0.033)
GO:0009092	homoserine metabolic process	10	2	0.041/0.042/0.047	0.240 (0.594)	0.584 (1.000)
GO:0010675	regulation of cellular carbohydrate metabolic process	31	9	0.035/0.042/0.045	0.002 (0.014)	(0.013)
GO:0019343	cysteine biosynthetic process via cystathionine	2	1	0.039/0.042/0.045	0.179 (0.469)	0.318 (0.867)
GO:0031400	negative regulation of protein modification process	2	1	0.040/0.042/0.044	0.179 (0.469)	0.066 (0.374)
GO:0015908	fatty acid transport	4	1	0.038/0.041/0.043	0.326 (0.655)	0.347 (0.893)
GO:0019344	cysteine biosynthetic process	12	2	0.039/0.041/0.044	0.312 (0.655)	0.782 (1.000)
GO:0031167	rRNA methylation	10	2	0.039/0.041/0.044	0.240 (0.594)	0.130 (0.567)
GO:0046838	phosphorylated carbohydrate dephosphorylation	3	1	0.039/0.041/0.044	0.256 (0.594)	0.459 (0.967)
GO:0046855	inositol phosphate dephosphorylation	3	1	0.038/0.041/0.043	0.256 (0.594)	0.491 (0.973)
GO:0015893	drug transport	17	4	0.037/0.040/0.044	0.068 (0.304)	0.071 (0.393)
GO:0051100	negative regulation of binding	4	1	0.036/0.039/0.041	0.326 (0.655)	0.464 (0.967)
GO:0005978	glycogen biosynthetic process	18	6	0.035/0.038/0.044	0.005 (0.035)	0.231 (0.745)
GO:0019654	acetate fermentation	1	1	0.035/0.038/0.041	0.094 (0.319)	0.350 (0.893)
GO:0006094	gluconeogenesis	31	8	0.033/0.037/0.042	0.006 (0.047)	0.497 (0.973)
GO:0046835	carbohydrate phosphorylation	2	1	0.034/0.037/0.040	0.179 (0.469)	0.351 (0.893)

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Table 1 – Continued

GO ID	Name	Pop	Study	MGSA	TfT	PCu
GO:0006110	regulation of glycolysis	6	3	0.033/0.036/0.038	0.013 (0.083)	0.125 (0.564)
GO:0043471	regulation of cellular carbohydrate catabolic process	8	4	0.034/0.036/0.038	0.004 (0.031)	(0.017)
GO:0051273	beta-glucan metabolic process	11	3	0.031/0.036/0.038	0.076 (0.314)	0.504 (0.974)
GO:0000296	spermine transport	4	1	0.033/0.035/0.038	0.326 (0.655)	0.576 (1.000)
GO:0005993	trehalose catabolic process	3	1	0.032/0.035/0.038	0.256 (0.594)	0.455 (0.967)
GO:0030259	lipid glycosylation	3	1	0.031/0.035/0.037	0.256 (0.594)	0.621 (1.000)
GO:0043470	regulation of carbohydrate catabolic process	8	4	0.033/0.035/0.037	0.004 (0.031)	0.057 (0.348)
GO:0000052	citrulline metabolic process	1	1	0.032/0.034/0.037	0.094 (0.319)	0.213 (0.723)
GO:0000053	argininosuccinate metabolic process	1	1	0.032/0.034/0.038	0.094 (0.319)	0.500 (0.973)
GO:0000461	endonucleolytic cleavage to generate mature 3'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	4	1	0.034/0.034/0.038	0.326 (0.655)	0.108 (0.517)
GO:0006098	pentose-phosphate shunt	14	4	0.031/0.034/0.036	0.036 (0.186)	0.590 (1.000)
GO:0009098	leucine biosynthetic process	5	1	0.030/0.034/0.035	0.389 (0.747)	0.872 (1.000)
GO:0015697	quaternary ammonium group transport	2	1	0.030/0.034/0.038	0.179 (0.469)	0.255 (0.768)
GO:0016559	peroxisome fission	2	1	0.030/0.034/0.037	0.179 (0.469)	0.064 (0.373)
GO:0046513	ceramide biosynthetic process	4	1	0.032/0.034/0.036	0.326 (0.655)	0.308 (0.848)
GO:0046520	sphingoid biosynthetic process	4	1	0.031/0.034/0.036	0.326 (0.655)	0.154 (0.618)
GO:0006551	leucine metabolic process	8	3	0.032/0.033/0.037	0.032 (0.173)	0.334 (0.883)
GO:0010921	regulation of phosphatase activity	4	1	0.031/0.033/0.036	0.326 (0.655)	0.399 (0.938)
GO:0015793	glycerol transport	4	1	0.030/0.033/0.035	0.326 (0.655)	0.748 (1.000)
GO:0015838	betaine transport	2	1	0.032/0.033/0.035	0.179 (0.469)	1.000 (1.000)
GO:0016337	cell-cell adhesion	4	1	0.029/0.033/0.035	0.326 (0.655)	0.786 (1.000)
GO:0019318	hexose metabolic process	104	25	0.026/0.033/0.037	6.88×10^{-6} ()	0.165 (0.642)
GO:0033214	iron assimilation by chelation and transport	4	2	0.029/0.033/0.036	0.046 (0.221)	0.800 (1.000)
GO:0035303	regulation of dephosphorylation	4	1	0.031/0.033/0.035	0.326 (0.655)	0.129 (0.567)
GO:0043666	regulation of phosphoprotein phosphatase activity	4	1	0.031/0.033/0.035	0.326 (0.655)	1.000 (1.000)
GO:0000752	agglutination involved in conjugation with cellular fusion	4	1	0.031/0.032/0.035	0.326 (0.655)	0.239 (0.748)
GO:0000771	agglutination involved in conjugation	4	1	0.030/0.032/0.035	0.326 (0.655)	0.140 (0.586)
GO:0006525	arginine metabolic process	16	6	0.031/0.032/0.038	0.002 (0.020)	0.522 (0.986)
GO:0006646	phosphatidylethanolamine biosynthetic process	4	1	0.029/0.032/0.034	0.326 (0.655)	0.276 (0.804)
GO:0007157	heterophilic cell adhesion	4	1	0.030/0.032/0.034	0.326 (0.655)	1.000 (1.000)
GO:0008612	peptidyl-lysine modification to hypusine	3	1	0.030/0.032/0.035	0.256 (0.594)	0.300 (0.839)
GO:0015892	siderophore-iron transport	4	2	0.028/0.032/0.035	0.046 (0.221)	0.238 (0.748)
GO:0045014	negative regulation of transcription by glucose	6	2	0.029/0.032/0.033	0.102 (0.332)	0.417 (0.953)
GO:0046516	hypusine metabolic process	3	1	0.030/0.032/0.035	0.256 (0.594)	0.447 (0.967)
GO:0000433	negative regulation of transcription from RNA polymerase II promoter by glucose	6	2	0.029/0.031/0.033	0.102 (0.332)	0.714 (1.000)
GO:0000436	positive regulation of transcription from RNA polymerase II promoter by carbon catabolites	2	1	0.028/0.031/0.033	0.179 (0.469)	0.146 (0.600)
GO:0000437	negative regulation of transcription from RNA polymerase II promoter by carbon catabolites	6	2	0.029/0.031/0.033	0.102 (0.332)	0.070 (0.389)
GO:0006081	cellular aldehyde metabolic process	22	8	0.027/0.031/0.036	(0.006)	(0.013)

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Table 1 – Continued

GO ID	Name	Pop	Study	MGSA	TfT	PCu
GO:0010520	regulation of reciprocal meiotic recombination	4	1	0.029/0.031/0.033	0.326 (0.655)	0.217 (0.723)
GO:0019320	hexose catabolic process	59	14	0.028/0.031/0.033	(0.008)	0.648 (1.000)
GO:0045013	negative regulation of transcription by carbon catabolites	7	2	0.029/0.031/0.034	0.134 (0.410)	0.030 (0.223)
GO:0046335	ethanolamine biosynthetic process	4	1	0.029/0.031/0.034	0.326 (0.655)	0.286 (0.813)
GO:0060631	regulation of meiosis I	4	1	0.029/0.031/0.032	0.326 (0.655)	0.138 (0.581)
GO:0005991	trehalose metabolic process	11	2	0.028/0.030/0.032	0.276 (0.628)	0.786 (1.000)
GO:0031060	regulation of histone methylation	3	1	0.029/0.030/0.032	0.256 (0.594)	0.115 (0.531)
GO:0032973	amino acid export	4	1	0.028/0.030/0.033	0.326 (0.655)	0.387 (0.932)
GO:0051131	chaperone-mediated protein complex assembly	5	1	0.027/0.029/0.032	0.389 (0.747)	0.215 (0.723)
GO:0006083	acetate metabolic process	6	3	0.026/0.028/0.030	0.013 (0.083)	0.215 (0.723)
GO:0006498	N-terminal protein lipidation	5	1	0.026/0.028/0.031	0.389 (0.747)	0.158 (0.630)
GO:0006499	N-terminal protein myristoylation	5	1	0.026/0.028/0.031	0.389 (0.747)	1.000 (1.000)
GO:0006778	porphyrin metabolic process	17	4	0.027/0.028/0.031	0.068 (0.304)	0.766 (1.000)
GO:0016139	glycoside catabolic process	4	1	0.026/0.028/0.029	0.326 (0.655)	0.717 (1.000)
GO:0018319	protein amino acid myristoylation	5	1	0.026/0.028/0.031	0.389 (0.747)	1.000 (1.000)
GO:0018377	protein myristoylation	5	1	0.026/0.028/0.030	0.389 (0.747)	0.178 (0.654)
GO:0019346	transsulfuration	4	1	0.025/0.028/0.029	0.326 (0.655)	0.453 (0.967)
GO:0019509	methionine salvage	5	1	0.026/0.028/0.029	0.389 (0.747)	0.577 (1.000)
GO:0033013	tetrapyrrole metabolic process	17	4	0.025/0.028/0.030	0.068 (0.304)	0.042 (0.284)
GO:0034605	cellular response to heat	173	51	0.023/0.028/0.037	1.73×10^{-14} (1.04×10^{-12})	6.19×10^{-19} (1.44×10^{-16})
GO:0042168	heme metabolic process	17	4	0.027/0.028/0.030	0.068 (0.304)	0.159 (0.630)
GO:0043102	amino acid salvage	5	1	0.026/0.028/0.031	0.389 (0.747)	0.570 (1.000)
GO:0046352	disaccharide catabolic process	4	1	0.026/0.028/0.030	0.326 (0.655)	0.731 (1.000)
GO:0006563	L-serine metabolic process	9	2	0.026/0.027/0.030	0.204 (0.515)	0.513 (0.976)
GO:0006631	fatty acid metabolic process	58	13	0.024/0.027/0.031	0.002 (0.019)	0.068 (0.381)
GO:0015680	intracellular copper ion transport	4	1	0.025/0.027/0.029	0.326 (0.655)	0.142 (0.592)
GO:0034755	iron ion transmembrane transport	5	2	0.025/0.027/0.030	0.072 (0.308)	0.578 (1.000)
GO:0000430	regulation of transcription from RNA polymerase II promoter by glucose	7	2	0.024/0.026/0.028	0.134 (0.410)	0.917 (1.000)
GO:0006020	inositol metabolic process	11	2	0.025/0.026/0.028	0.276 (0.628)	0.924 (1.000)
GO:0006835	dicarboxylic acid transport	3	2	0.024/0.026/0.030	0.025 (0.137)	0.072 (0.394)
GO:0008655	pyrimidine salvage	5	1	0.023/0.026/0.027	0.389 (0.747)	0.199 (0.699)
GO:0015696	ammonium transport	6	2	0.025/0.026/0.027	0.102 (0.332)	0.893 (1.000)
GO:0015729	oxaloacetate transport	1	1	0.023/0.026/0.028	0.094 (0.319)	0.667 (1.000)
GO:0034207	steroid acetylation	1	1	0.024/0.026/0.028	0.094 (0.319)	0.130 (0.567)
GO:0034209	sterol acetylation	1	1	0.024/0.026/0.028	0.094 (0.319)	0.064 (0.373)
GO:0034659	isopropylmalate transport	1	1	0.024/0.026/0.029	0.094 (0.319)	0.667 (1.000)
GO:0043467	regulation of generation of precursor metabolites and energy	14	4	0.023/0.026/0.028	0.036 (0.186)	0.065 (0.374)
GO:0046015	regulation of transcription by glucose	8	2	0.025/0.026/0.028	0.168 (0.469)	0.825 (1.000)
GO:0006627	mitochondrial protein processing during import	5	1	0.023/0.025/0.027	0.389 (0.747)	0.188 (0.670)
GO:0010992	ubiquitin homeostasis	5	1	0.023/0.025/0.027	0.389 (0.747)	0.462 (0.967)
GO:0010993	regulation of ubiquitin homeostasis	5	1	0.024/0.025/0.026	0.389 (0.747)	0.242 (0.756)
GO:0015780	nucleotide-sugar transport	4	1	0.023/0.025/0.027	0.326 (0.655)	0.779 (1.000)
GO:0034982	mitochondrial protein processing	5	1	0.023/0.025/0.027	0.389 (0.747)	0.345 (0.893)
GO:0000409	regulation of transcription by galactose	4	1	0.023/0.024/0.026	0.326 (0.655)	0.790 (1.000)
GO:0000411	positive regulation of transcription by galactose	4	1	0.023/0.024/0.027	0.326 (0.655)	0.800 (1.000)

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Table 1 – Continued

GO ID	Name	Pop	Study	MGSA	TfT	PCu
GO:0006013	mannose metabolic process	7	2	0.022/0.024/0.026	0.134 (0.410)	0.536 (1.000)
GO:0006090	pyruvate metabolic process	42	10	0.021/0.024/0.027	0.004 (0.034)	0.821 (1.000)
GO:0009109	coenzyme catabolic process	34	22	0.020/0.024/0.026	2.91×10^{-15} (1.94×10^{-13})	5.72×10^{-7} (2.56×10^{-5})
GO:0033212	iron assimilation	6	3	0.021/0.024/0.027	0.013 (0.083)	0.014 (0.132)
GO:0006037	cell wall chitin metabolic process	15	1	0.021/0.023/0.026	0.772 (1.000)	0.889 (1.000)
GO:0006580	ethanolamine metabolic process	5	1	0.022/0.023/0.025	0.389 (0.747)	0.604 (1.000)
GO:0006592	ornithine biosynthetic process	4	2	0.021/0.023/0.024	0.046 (0.221)	0.643 (1.000)
GO:0006740	NADPH regeneration	19	6	0.021/0.023/0.025	0.006 (0.046)	0.648 (1.000)
GO:0016137	glycoside metabolic process	12	2	0.021/0.023/0.026	0.312 (0.655)	0.758 (1.000)
GO:0050667	homocysteine metabolic process	6	1	0.022/0.023/0.024	0.446 (0.821)	0.643 (1.000)
GO:0008216	spermidine metabolic process	3	1	0.020/0.022/0.024	0.256 (0.594)	0.375 (0.917)
GO:0009065	glutamine family amino acid catabolic process	10	8	0.020/0.022/0.025	2.15×10^{-7} (5.37×10^{-6})	0.002 (0.029)
GO:0019795	nonprotein amino acid biosynthetic process	6	2	0.021/0.022/0.024	0.102 (0.332)	0.436 (0.963)
GO:0031647	regulation of protein stability	9	2	0.019/0.022/0.023	0.204 (0.515)	0.123 (0.562)
GO:0045722	positive regulation of gluconeogenesis	5	2	0.020/0.022/0.026	0.072 (0.308)	0.033 (0.238)
GO:0045991	positive regulation of transcription by carbon catabolites	5	1	0.020/0.022/0.023	0.389 (0.747)	0.274 (0.801)
GO:0006075	1,3-beta-glucan biosynthetic process	2	1	0.019/0.021/0.022	0.179 (0.469)	0.533 (0.996)
GO:0006078	1,6-beta-glucan biosynthetic process	8	2	0.020/0.021/0.023	0.168 (0.469)	0.848 (1.000)
GO:0006085	acetyl-CoA biosynthetic process	3	1	0.019/0.021/0.023	0.256 (0.594)	0.620 (1.000)
GO:0006096	glycolysis	34	8	0.020/0.021/0.023	0.011 (0.075)	0.966 (1.000)
GO:0006800	oxygen and reactive oxygen species metabolic process	14	4	0.019/0.021/0.023	0.036 (0.186)	0.036 (0.250)
GO:0019321	pentose metabolic process	18	5	0.019/0.021/0.023	0.022 (0.132)	0.339 (0.892)
GO:0019543	propionate catabolic process	2	2	0.019/0.021/0.022	0.009 (0.060)	0.255 (0.768)
GO:0006074	1,3-beta-glucan metabolic process	2	1	0.019/0.020/0.022	0.179 (0.469)	0.491 (0.973)
GO:0006616	SRP-dependent cotranslational protein targeting to membrane, translocation	10	4	0.018/0.020/0.022	0.010 (0.068)	5.58×10^{-5} (0.002)
GO:0009083	branched chain family amino acid catabolic process	10	5	0.017/0.020/0.023	0.001 (0.011)	0.204 (0.711)
GO:0019629	propionate catabolic process, 2-methylcitrate cycle	2	2	0.018/0.020/0.022	0.009 (0.060)	1.000 (1.000)
GO:0051469	vesicle fusion with vacuole	1	1	0.017/0.020/0.021	0.094 (0.319)	0.039 (0.267)
GO:0006091	generation of precursor metabolites and energy	242	88	0.015/0.019/0.022	2.39×10^{-32} (1.43×10^{-29})	1.21×10^{-33} (7.06×10^{-31})
GO:0006111	regulation of gluconeogenesis	15	4	0.017/0.019/0.020	0.045 (0.221)	0.007 (0.085)
GO:0006534	cysteine metabolic process	15	2	0.017/0.019/0.020	0.417 (0.788)	0.781 (1.000)
GO:0006576	biogenic amine metabolic process	37	8	0.016/0.019/0.022	0.019 (0.116)	0.316 (0.867)
GO:0008272	sulfate transport	4	1	0.018/0.019/0.020	0.326 (0.655)	0.718 (1.000)
GO:0016051	carbohydrate biosynthetic process	94	21	0.015/0.019/0.023	(0.002)	(0.004)
GO:0005980	glycogen catabolic process	4	3	0.016/0.018/0.018	0.003 (0.025)	0.023 (0.184)
GO:0006101	citrate metabolic process	4	4	0.016/0.018/0.019	7.64×10^{-5} (0.001)	0.002 (0.034)
GO:0006279	premeiotic DNA synthesis	6	1	0.017/0.018/0.020	0.446 (0.821)	0.077 (0.411)
GO:0007039	vacuolar protein catabolic process	107	29	0.015/0.018/0.020	7.87×10^{-8} (2.15×10^{-6})	3.35×10^{-13} (3.00×10^{-11})
GO:0009408	response to heat	193	54	0.017/0.018/0.021	3.16×10^{-14} (1.72×10^{-12})	2.13×10^{-14} (2.48×10^{-12})

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Table 1 – Continued

GO ID	Name	Pop	Study	MGSA	TfT	PCu
GO:0010676	positive regulation of cellular carbohydrate metabolic process	8	2	0.016/0.018/0.019	0.168 (0.469)	0.302 (0.842)
GO:0010907	positive regulation of glucose metabolic process	8	2	0.015/0.018/0.019	0.168 (0.469)	0.652 (1.000)
GO:0019933	cAMP-mediated signaling	7	1	0.018/0.018/0.019	0.498 (0.882)	1.000 (1.000)
GO:0019935	cyclic-nucleotide-mediated signaling	7	1	0.016/0.018/0.020	0.498 (0.882)	0.269 (0.793)
GO:0031118	rRNA pseudouridine synthesis	6	1	0.017/0.018/0.019	0.446 (0.821)	0.464 (0.967)
GO:0032950	regulation of beta-glucan metabolic process	2	1	0.016/0.018/0.019	0.179 (0.469)	0.479 (0.973)
GO:0034201	response to oleic acid	3	1	0.016/0.018/0.019	0.256 (0.594)	1.000 (1.000)
GO:0045913	positive regulation of carbohydrate metabolic process	8	2	0.015/0.018/0.020	0.168 (0.469)	0.304 (0.842)
GO:0070542	response to fatty acid	3	1	0.017/0.018/0.020	0.256 (0.594)	1.000 (1.000)
GO:0000101	sulfur amino acid transport	6	1	0.016/0.017/0.018	0.446 (0.821)	0.529 (0.993)
GO:0006021	inositol biosynthetic process	6	1	0.016/0.017/0.018	0.446 (0.821)	0.930 (1.000)
GO:0006022	aminoglycan metabolic process	21	2	0.015/0.017/0.019	0.599 (1.000)	0.929 (1.000)
GO:0006030	chitin metabolic process	21	2	0.016/0.017/0.019	0.599 (1.000)	0.830 (1.000)
GO:0006635	fatty acid beta-oxidation	10	5	0.016/0.017/0.019	0.001 (0.011)	1.000 (1.000)
GO:0007155	cell adhesion	8	2	0.015/0.017/0.019	0.168 (0.469)	0.147 (0.603)
GO:0009062	fatty acid catabolic process	11	6	0.016/0.017/0.018	(0.002)	0.056 (0.344)
GO:0015758	glucose transport	8	3	0.016/0.017/0.019	0.032 (0.173)	0.769 (1.000)
GO:0015791	polyol transport	6	1	0.016/0.017/0.018	0.446 (0.821)	0.750 (1.000)
GO:0022610	biological adhesion	8	2	0.015/0.017/0.018	0.168 (0.469)	0.168 (0.646)
GO:0032951	regulation of beta-glucan biosynthetic process	2	1	0.016/0.017/0.019	0.179 (0.469)	0.426 (0.963)
GO:0033993	response to lipid	3	1	0.016/0.017/0.019	0.256 (0.594)	0.175 (0.654)
GO:0044270	nitrogen compound catabolic process	58	18	0.012/0.017/0.021	2.93×10^{-6} (5.87×10^{-5})	(0.006)
GO:0055072	iron ion homeostasis	36	6	0.016/0.017/0.018	0.115 (0.370)	0.514 (0.976)
GO:0060917	regulation of 1,6-beta-glucan biosynthetic process	2	1	0.016/0.017/0.019	0.179 (0.469)	0.464 (0.967)
GO:0001407	glycerophosphodiester transport	1	1	0.015/0.016/0.018	0.094 (0.319)	1.000 (1.000)
GO:0006008	glucose 1-phosphate utilization	2	1	0.015/0.016/0.017	0.179 (0.469)	1.000 (1.000)
GO:0006010	glucose 6-phosphate utilization	2	1	0.015/0.016/0.016	0.179 (0.469)	1.000 (1.000)
GO:0006107	oxaloacetate metabolic process	1	1	0.014/0.016/0.017	0.094 (0.319)	0.348 (0.893)
GO:0006527	arginine catabolic process	2	2	0.014/0.016/0.017	0.009 (0.060)	0.239 (0.748)
GO:0006533	aspartate catabolic process	1	1	0.014/0.016/0.017	0.094 (0.319)	0.571 (1.000)
GO:0006538	glutamate catabolic process	3	2	0.014/0.016/0.017	0.025 (0.137)	0.773 (1.000)
GO:0006562	proline catabolic process	4	3	0.014/0.016/0.016	0.003 (0.025)	0.073 (0.396)
GO:0006572	tyrosine catabolic process	2	2	0.015/0.016/0.017	0.009 (0.060)	0.036 (0.250)
GO:0006637	acyl-CoA metabolic process	1	1	0.014/0.016/0.016	0.094 (0.319)	0.265 (0.790)
GO:0006843	mitochondrial citrate transport	1	1	0.015/0.016/0.017	0.094 (0.319)	0.104 (0.511)
GO:0006846	acetate transport	2	1	0.014/0.016/0.017	0.179 (0.469)	0.589 (1.000)
GO:0006879	cellular iron ion homeostasis	36	6	0.015/0.016/0.018	0.115 (0.370)	0.514 (0.976)
GO:0009068	aspartate family amino acid catabolic process	6	4	0.014/0.016/0.018	(0.010)	0.026 (0.203)
GO:0015727	lactate transport	1	1	0.015/0.016/0.017	0.094 (0.319)	0.350 (0.893)
GO:0015740	C4-dicarboxylate transport	1	1	0.014/0.016/0.017	0.094 (0.319)	0.667 (1.000)
GO:0015741	fumarate transport	1	1	0.015/0.016/0.017	0.094 (0.319)	0.545 (1.000)
GO:0015744	succinate transport	1	1	0.015/0.016/0.017	0.094 (0.319)	0.556 (1.000)
GO:0015746	citrate transport	2	1	0.015/0.016/0.017	0.179 (0.469)	0.778 (1.000)
GO:0015748	organophosphate ester transport	1	1	0.015/0.016/0.017	0.094 (0.319)	0.556 (1.000)
GO:0015761	mannose transport	2	1	0.014/0.016/0.017	0.179 (0.469)	0.657 (1.000)
GO:0019255	glucose 1-phosphate metabolic process	2	1	0.014/0.016/0.017	0.179 (0.469)	0.444 (0.967)

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Table 1 – Continued

GO ID	Name	Pop	Study	MGSA	TfT	PCu
GO:0043649	dicarboxylic acid catabolic process	1	1	0.014/0.016/0.017	0.094 (0.319)	0.435 (0.963)
GO:0051156	glucose 6-phosphate metabolic process	2	1	0.015/0.016/0.017	0.179 (0.469)	0.444 (0.967)
GO:0000098	sulfur amino acid catabolic process	2	1	0.014/0.015/0.016	0.179 (0.469)	0.435 (0.963)
GO:0000947	amino acid catabolic process to alcohol via Ehrlich pathway	11	2	0.014/0.015/0.017	0.276 (0.628)	0.650 (1.000)
GO:0000949	aromatic amino acid family catabolic process to alcohol via Ehrlich pathway	4	1	0.014/0.015/0.017	0.326 (0.655)	0.670 (1.000)
GO:0000950	branched chain family amino acid catabolic process to alcohol via Ehrlich pathway	2	1	0.014/0.015/0.016	0.179 (0.469)	0.625 (1.000)
GO:0000951	methionine catabolic process to 3-methylthiopropanol	1	1	0.014/0.015/0.016	0.094 (0.319)	0.182 (0.659)
GO:0000955	amino acid catabolic process via Ehrlich pathway	11	2	0.014/0.015/0.016	0.276 (0.628)	0.991 (1.000)
GO:0001315	age-dependent response to reactive oxygen species	3	1	0.014/0.015/0.016	0.256 (0.594)	0.547 (1.000)
GO:0005981	regulation of glycogen catabolic process	2	1	0.014/0.015/0.017	0.179 (0.469)	0.657 (1.000)
GO:0005999	xylulose biosynthetic process	1	1	0.013/0.015/0.017	0.094 (0.319)	0.286 (0.813)
GO:0006011	UDP-glucose metabolic process	3	1	0.014/0.015/0.017	0.256 (0.594)	0.569 (1.000)
GO:0006040	amino sugar metabolic process	23	2	0.013/0.015/0.016	0.649 (1.000)	0.981 (1.000)
GO:0006044	N-acetylglucosamine metabolic process	23	2	0.013/0.015/0.016	0.649 (1.000)	1.000 (1.000)
GO:0006077	1,6-beta-glucan metabolic process	9	2	0.013/0.015/0.017	0.204 (0.515)	0.945 (1.000)
GO:0006089	lactate metabolic process	6	3	0.014/0.015/0.017	0.013 (0.083)	0.215 (0.723)
GO:0006102	isocitrate metabolic process	5	4	0.014/0.015/0.016	(0.004)	0.009 (0.096)
GO:0006103	2-oxoglutarate metabolic process	4	4	0.014/0.015/0.017	7.64×10^{-5} (0.001)	0.008 (0.088)
GO:0006104	succinyl-CoA metabolic process	2	1	0.014/0.015/0.016	0.179 (0.469)	0.490 (0.973)
GO:0006106	fumarate metabolic process	2	2	0.014/0.015/0.016	0.009 (0.060)	0.111 (0.522)
GO:0006108	malate metabolic process	4	2	0.014/0.015/0.016	0.046 (0.221)	0.435 (0.963)
GO:0006116	NADH oxidation	10	5	0.014/0.015/0.017	0.001 (0.011)	0.318 (0.867)
GO:0006120	mitochondrial electron transport, NADH to ubiquinone	1	1	0.014/0.015/0.016	0.094 (0.319)	0.818 (1.000)
GO:0006121	mitochondrial electron transport, succinate to ubiquinone	5	4	0.014/0.015/0.016	(0.004)	0.790 (1.000)
GO:0006122	mitochondrial electron transport, ubiquinol to cytochrome c	10	8	0.014/0.015/0.016	2.15×10^{-7} (5.37×10^{-6})	0.774 (1.000)
GO:0006123	mitochondrial electron transport, cytochrome c to oxygen	7	6	0.014/0.015/0.016	4.25×10^{-6} (8.37×10^{-5})	0.622 (1.000)
GO:0006467	protein thiol-disulfide exchange	2	1	0.013/0.015/0.016	0.179 (0.469)	0.056 (0.344)
GO:0006530	asparagine catabolic process	1	1	0.014/0.015/0.016	0.094 (0.319)	0.611 (1.000)
GO:0006545	glycine biosynthetic process	2	1	0.015/0.015/0.016	0.179 (0.469)	0.367 (0.915)
GO:0006546	glycine catabolic process	3	1	0.014/0.015/0.016	0.256 (0.594)	0.643 (1.000)
GO:0006550	isoleucine catabolic process	1	1	0.014/0.015/0.016	0.094 (0.319)	0.357 (0.902)
GO:0006552	leucine catabolic process	3	2	0.014/0.015/0.017	0.025 (0.137)	0.341 (0.893)
GO:0006559	L-phenylalanine catabolic process	5	2	0.014/0.015/0.017	0.072 (0.308)	0.357 (0.902)
GO:0006567	threonine catabolic process	3	1	0.014/0.015/0.016	0.256 (0.594)	0.745 (1.000)

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Table 1 – Continued

GO ID	Name	Pop	Study	MGSA	TfT	PCu
GO:0006569	tryptophan catabolic process	7	2	0.014/0.015/0.016	0.134 (0.410)	0.318 (0.867)
GO:0006570	tyrosine metabolic process	3	2	0.014/0.015/0.017	0.025 (0.137)	0.041 (0.280)
GO:0006573	valine metabolic process	1	1	0.013/0.015/0.016	0.094 (0.319)	0.261 (0.784)
GO:0006574	valine catabolic process	1	1	0.014/0.015/0.016	0.094 (0.319)	0.500 (0.973)
GO:0009071	serine family amino acid catabolic process	4	1	0.014/0.015/0.016	0.326 (0.655)	0.781 (1.000)
GO:0009074	aromatic amino acid family catabolic process	7	2	0.014/0.015/0.016	0.134 (0.410)	0.719 (1.000)
GO:0009087	methionine catabolic process	1	1	0.014/0.015/0.016	0.094 (0.319)	0.196 (0.688)
GO:0009409	response to cold	7	1	0.014/0.015/0.016	0.498 (0.882)	0.578 (1.000)
GO:0009414	response to water deprivation	1	1	0.014/0.015/0.017	0.094 (0.319)	0.111 (0.522)
GO:0009436	glyoxylate catabolic process	1	1	0.014/0.015/0.016	0.094 (0.319)	0.492 (0.973)
GO:0009438	methylglyoxal metabolic process	3	1	0.014/0.015/0.016	0.256 (0.594)	0.764 (1.000)
GO:0010133	proline catabolic process to glutamate	2	2	0.013/0.015/0.016	0.009 (0.060)	0.386 (0.932)
GO:0010962	regulation of glucan biosynthetic process	9	2	0.013/0.015/0.017	0.204 (0.515)	0.091 (0.466)
GO:0019243	methylglyoxal catabolic process to D-lactate	3	1	0.014/0.015/0.016	0.256 (0.594)	0.950 (1.000)
GO:0019265	glycine biosynthetic process, by transamination of glyoxylate	1	1	0.014/0.015/0.016	0.094 (0.319)	0.500 (0.973)
GO:0019266	asparagine biosynthetic process from oxaloacetate	1	1	0.014/0.015/0.017	0.094 (0.319)	0.250 (0.766)
GO:0019319	hexose biosynthetic process	34	8	0.013/0.015/0.017	0.011 (0.075)	0.428 (0.963)
GO:0019405	alditol catabolic process	4	1	0.013/0.015/0.015	0.326 (0.655)	0.769 (1.000)
GO:0019413	acetate biosynthetic process	3	1	0.014/0.015/0.017	0.256 (0.594)	0.479 (0.973)
GO:0019547	arginine catabolic process to ornithine	1	1	0.014/0.015/0.017	0.094 (0.319)	0.625 (1.000)
GO:0019551	glutamate catabolic process to 2-oxoglutarate	1	1	0.014/0.015/0.017	0.094 (0.319)	0.857 (1.000)
GO:0019563	glycerol catabolic process	4	1	0.014/0.015/0.015	0.326 (0.655)	0.874 (1.000)
GO:0019566	arabinose metabolic process	4	1	0.013/0.015/0.016	0.326 (0.655)	0.766 (1.000)
GO:0019568	arabinose catabolic process	4	1	0.014/0.015/0.016	0.326 (0.655)	1.000 (1.000)
GO:0022900	electron transport chain	55	26	0.013/0.015/0.016	2.64×10^{-13} (1.08×10^{-11})	0.008 (0.087)
GO:0022904	respiratory electron transport chain	22	18	0.014/0.015/0.016	1.20×10^{-15} (8.45×10^{-14})	5.14×10^{-5} (0.002)
GO:0032881	regulation of polysaccharide metabolic process	9	2	0.014/0.015/0.017	0.204 (0.515)	0.091 (0.466)
GO:0032885	regulation of polysaccharide biosynthetic process	9	2	0.014/0.015/0.017	0.204 (0.515)	0.083 (0.435)
GO:0042436	indole derivative catabolic process	7	2	0.014/0.015/0.016	0.134 (0.410)	0.231 (0.745)
GO:0042631	cellular response to water deprivation	1	1	0.014/0.015/0.017	0.094 (0.319)	0.113 (0.528)
GO:0042743	hydrogen peroxide metabolic process	4	3	0.014/0.015/0.016	0.003 (0.025)	0.041 (0.279)
GO:0042744	hydrogen peroxide catabolic process	3	2	0.014/0.015/0.016	0.025 (0.137)	0.047 (0.306)
GO:0042773	ATP synthesis coupled electron transport	22	18	0.013/0.015/0.016	1.20×10^{-15} (8.45×10^{-14})	0.035 (0.247)
GO:0042775	mitochondrial ATP synthesis coupled electron transport	22	18	0.014/0.015/0.016	1.20×10^{-15} (8.45×10^{-14})	1.000 (1.000)
GO:0042843	D-xylose catabolic process	4	1	0.014/0.015/0.017	0.326 (0.655)	1.000 (1.000)
GO:0043255	regulation of carbohydrate biosynthetic process	25	6	0.013/0.015/0.016	0.025 (0.137)	0.003 (0.046)
GO:0045721	negative regulation of gluconeogenesis	9	2	0.014/0.015/0.016	0.204 (0.515)	0.080 (0.421)
GO:0046168	glycerol-3-phosphate catabolic process	2	1	0.014/0.015/0.016	0.179 (0.469)	0.800 (1.000)
GO:0046185	aldehyde catabolic process	6	2	0.014/0.015/0.016	0.102 (0.332)	0.178 (0.654)
GO:0046218	indolalkylamine catabolic process	7	2	0.013/0.015/0.016	0.134 (0.410)	0.369 (0.915)

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Table 1 – Continued

GO ID	Name	Pop	Study	MGSA	TfT	PCu
GO:0046323	glucose import	3	1	0.014/0.015/0.016	0.256 (0.594)	0.821 (1.000)
GO:0051090	regulation of transcription factor activity	8	1	0.013/0.015/0.015	0.545 (0.939)	0.270 (0.794)
GO:0051596	methylglyoxal catabolic process	3	1	0.014/0.015/0.016	0.256 (0.594)	0.800 (1.000)
GO:0070484	dehydro-D-arabinono-1,4-lactone metabolic process	2	1	0.014/0.015/0.016	0.179 (0.469)	0.287 (0.813)
GO:0070485	dehydro-D-arabinono-1,4-lactone biosynthetic process	2	1	0.014/0.015/0.017	0.179 (0.469)	0.331 (0.881)
GO:0090046	regulation of transcription regulator activity	8	1	0.014/0.015/0.016	0.545 (0.939)	0.373 (0.917)
GO:0005979	regulation of glycogen biosynthetic process	7	1	0.013/0.014/0.015	0.498 (0.882)	0.978 (1.000)
GO:0006041	glucosamine metabolic process	23	2	0.013/0.014/0.016	0.649 (1.000)	1.000 (1.000)
GO:0006537	glutamate biosynthetic process	13	9	0.013/0.014/0.016	2.64×10^{-7} (6.48×10^{-6})	0.099 (0.497)
GO:0006814	sodium ion transport	7	2	0.013/0.014/0.016	0.134 (0.410)	0.555 (1.000)
GO:0009251	glucan catabolic process	5	3	0.013/0.014/0.015	0.007 (0.051)	0.057 (0.348)
GO:0010677	negative regulation of cellular carbohydrate metabolic process	12	2	0.013/0.014/0.015	0.312 (0.655)	0.459 (0.967)
GO:0033617	mitochondrial respiratory chain complex IV assembly	11	3	0.012/0.014/0.014	0.076 (0.314)	0.415 (0.950)
GO:0045912	negative regulation of carbohydrate metabolic process	12	2	0.013/0.014/0.015	0.312 (0.655)	0.433 (0.963)
GO:0046174	polyol catabolic process	4	1	0.013/0.014/0.016	0.326 (0.655)	0.695 (1.000)
GO:0070873	regulation of glycogen metabolic process	7	1	0.013/0.014/0.016	0.498 (0.882)	0.908 (1.000)
GO:0005992	trehalose biosynthetic process	7	1	0.012/0.013/0.014	0.498 (0.882)	0.891 (1.000)
GO:0006012	galactose metabolic process	11	2	0.012/0.013/0.014	0.276 (0.628)	0.798 (1.000)
GO:0009312	oligosaccharide biosynthetic process	7	1	0.012/0.013/0.014	0.498 (0.882)	0.831 (1.000)
GO:0010043	response to zinc ion	2	1	0.011/0.013/0.014	0.179 (0.469)	0.368 (0.915)
GO:0016138	glycoside biosynthetic process	7	1	0.012/0.013/0.014	0.498 (0.882)	0.863 (1.000)
GO:0019655	glucose catabolic process to ethanol	7	1	0.012/0.013/0.014	0.498 (0.882)	0.893 (1.000)
GO:0019660	glycolytic fermentation	7	1	0.013/0.013/0.014	0.498 (0.882)	0.902 (1.000)
GO:0042219	cellular amino acid derivative catabolic process	19	3	0.012/0.013/0.015	0.261 (0.605)	0.468 (0.970)
GO:0046351	disaccharide biosynthetic process	7	1	0.012/0.013/0.015	0.498 (0.882)	0.863 (1.000)
GO:0006555	methionine metabolic process	40	6	0.012/0.012/0.013	0.167 (0.469)	0.744 (1.000)
GO:0006595	polyamine metabolic process	8	1	0.011/0.012/0.012	0.545 (0.939)	0.889 (1.000)
GO:0010383	cell wall polysaccharide metabolic process	17	1	0.011/0.012/0.013	0.813 (1.000)	0.970 (1.000)
GO:0031668	cellular response to extracellular stimulus	58	10	0.011/0.012/0.013	0.041 (0.210)	0.028 (0.213)
GO:0031669	cellular response to nutrient levels	56	9	0.010/0.012/0.013	0.074 (0.314)	0.635 (1.000)
GO:0000060	protein import into nucleus, translocation	2	1	0.010/0.011/0.012	0.179 (0.469)	0.073 (0.396)
GO:0000096	sulfur amino acid metabolic process	47	7	0.010/0.011/0.012	0.146 (0.439)	0.763 (1.000)
GO:0001682	tRNA 5'-leader removal	2	1	0.010/0.011/0.012	0.179 (0.469)	0.038 (0.264)
GO:0005996	monosaccharide metabolic process	139	30	0.009/0.011/0.013	8.83×10^{-6} ()	0.152 (0.612)
GO:0006177	GMP biosynthetic process	3	1	0.010/0.011/0.012	0.256 (0.594)	0.158 (0.629)
GO:0006531	aspartate metabolic process	2	1	0.010/0.011/0.012	0.179 (0.469)	0.303 (0.842)
GO:0006532	aspartate biosynthetic process	2	1	0.010/0.011/0.012	0.179 (0.469)	0.268 (0.793)
GO:0006558	L-phenylalanine metabolic process	6	2	0.010/0.011/0.013	0.102 (0.332)	0.184 (0.665)

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Table 1 – Continued

GO ID	Name	Pop	Study	MGSA	TfT	PCu
GO:0006734	NADH metabolic process	12	5	0.010/0.011/0.012	0.003 (0.026)	0.095 (0.483)
GO:0006842	tricarboxylic acid transport	3	1	0.011/0.011/0.012	0.256 (0.594)	0.432 (0.963)
GO:0010942	positive regulation of cell death	3	2	0.010/0.011/0.012	0.025 (0.137)	0.048 (0.311)
GO:0015824	proline transport	2	1	0.011/0.011/0.013	0.179 (0.469)	0.667 (1.000)
GO:0015846	polyamine transport	12	2	0.009/0.011/0.012	0.312 (0.655)	0.412 (0.950)
GO:0015866	ADP transport	2	1	0.010/0.011/0.012	0.179 (0.469)	0.500 (0.973)
GO:0015867	ATP transport	4	1	0.010/0.011/0.012	0.326 (0.655)	1.000 (1.000)
GO:0015868	purine ribonucleotide transport	4	1	0.010/0.011/0.011	0.326 (0.655)	0.800 (1.000)
GO:0015976	carbon utilization	4	1	0.010/0.011/0.012	0.326 (0.655)	0.333 (0.883)
GO:0017062	respiratory chain complex III assembly	3	2	0.010/0.011/0.012	0.025 (0.137)	0.143 (0.592)
GO:0019388	galactose catabolic process	6	1	0.010/0.011/0.012	0.446 (0.821)	0.813 (1.000)
GO:0019676	ammonia assimilation cycle	5	2	0.010/0.011/0.012	0.072 (0.308)	0.549 (1.000)
GO:0031056	regulation of histone modification	6	1	0.010/0.011/0.012	0.446 (0.821)	0.135 (0.572)
GO:0032780	negative regulation of ATPase activity	3	2	0.010/0.011/0.012	0.025 (0.137)	0.500 (0.973)
GO:0033215	iron assimilation by reduction and transport	2	1	0.011/0.011/0.012	0.179 (0.469)	0.800 (1.000)
GO:0034354	de novo NAD biosynthetic process from tryptophan	4	1	0.010/0.011/0.012	0.326 (0.655)	1.000 (1.000)
GO:0034551	mitochondrial respiratory chain complex III assembly	3	2	0.010/0.011/0.012	0.025 (0.137)	0.117 (0.536)
GO:0034614	cellular response to reactive oxygen species	4	2	0.010/0.011/0.012	0.046 (0.221)	0.108 (0.517)
GO:0034627	de novo NAD biosynthetic process	4	1	0.010/0.011/0.012	0.326 (0.655)	0.364 (0.912)
GO:0042439	ethanolamine and derivative metabolic process	14	2	0.010/0.011/0.012	0.383 (0.747)	0.786 (1.000)
GO:0043065	positive regulation of apoptosis	3	2	0.010/0.011/0.012	0.025 (0.137)	0.107 (0.517)
GO:0043068	positive regulation of programmed cell death	3	2	0.010/0.011/0.012	0.025 (0.137)	0.091 (0.466)
GO:0043462	regulation of ATPase activity	4	3	0.010/0.011/0.013	0.003 (0.025)	0.002 (0.036)
GO:0044247	cellular polysaccharide catabolic process	6	3	0.010/0.011/0.012	0.013 (0.083)	0.016 (0.147)
GO:0046688	response to copper ion	2	1	0.010/0.011/0.012	0.179 (0.469)	0.368 (0.915)
GO:0051503	adenine nucleotide transport	4	1	0.010/0.011/0.012	0.326 (0.655)	0.800 (1.000)
GO:0070301	cellular response to hydrogen peroxide	4	2	0.010/0.011/0.012	0.046 (0.221)	0.214 (0.723)
GO:0000105	histidine biosynthetic process	11	3	0.009/0.010/0.011	0.076 (0.314)	0.308 (0.848)
GO:0006067	ethanol metabolic process	12	3	0.009/0.010/0.010	0.095 (0.321)	1.000 (1.000)
GO:0006536	glutamate metabolic process	18	12	0.009/0.010/0.012	4.45×10^{-9} (1.40×10^{-7})	0.001 (0.021)
GO:0006547	histidine metabolic process	11	3	0.009/0.010/0.011	0.076 (0.314)	0.234 (0.746)
GO:0006749	glutathione metabolic process	14	3	0.009/0.010/0.011	0.137 (0.415)	0.624 (1.000)
GO:0006882	cellular zinc ion homeostasis	10	2	0.009/0.010/0.011	0.240 (0.594)	0.481 (0.973)
GO:0008360	regulation of cell shape	11	3	0.009/0.010/0.010	0.076 (0.314)	0.025 (0.194)
GO:0009075	histidine family amino acid metabolic process	11	3	0.008/0.010/0.010	0.076 (0.314)	0.325 (0.876)
GO:0009076	histidine family amino acid biosynthetic process	11	3	0.009/0.010/0.011	0.076 (0.314)	0.488 (0.973)
GO:0009082	branched chain family amino acid biosynthetic process	14	3	0.009/0.010/0.010	0.137 (0.415)	0.682 (1.000)
GO:0034308	monohydric alcohol metabolic process	12	3	0.008/0.010/0.010	0.095 (0.321)	0.413 (0.950)
GO:0045454	cell redox homeostasis	29	5	0.009/0.010/0.011	0.129 (0.409)	0.021 (0.170)
GO:0046655	folic acid metabolic process	4	1	0.009/0.010/0.011	0.326 (0.655)	0.563 (1.000)

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Table 1 – Continued

GO ID	Name	Pop	Study	MGSA	TfT	PCu
GO:0046656	folic acid biosynthetic process	4	1	0.009/0.010/0.011	0.326 (0.655)	0.540 (1.000)
GO:0055069	zinc ion homeostasis	10	2	0.009/0.010/0.011	0.240 (0.594)	0.481 (0.973)
GO:0000290	deadenylation-dependent decapping of nuclear-transcribed mRNA	8	1	0.008/0.009/0.010	0.545 (0.939)	0.462 (0.967)
GO:0006119	oxidative phosphorylation	50	33	0.008/0.009/0.010	9.35×10^{-23} (2.24×10^{-20})	2.27×10^{-12} (1.89×10^{-10})
GO:0006544	glycine metabolic process	7	2	0.008/0.009/0.010	0.134 (0.410)	0.360 (0.906)
GO:0006739	NADP metabolic process	23	7	0.008/0.009/0.010	0.004 (0.031)	0.464 (0.967)
GO:0009081	branched chain family amino acid metabolic process	23	6	0.007/0.009/0.010	0.017 (0.103)	0.225 (0.733)
GO:0015802	basic amino acid transport	8	1	0.009/0.009/0.010	0.545 (0.939)	0.643 (1.000)
GO:0015850	organic alcohol transport	8	1	0.008/0.009/0.009	0.545 (0.939)	0.555 (1.000)
GO:0000304	response to singlet oxygen	4	1	0.007/0.008/0.009	0.326 (0.655)	0.670 (1.000)
GO:0006023	aminoglycan biosynthetic process	16	1	0.007/0.008/0.009	0.793 (1.000)	0.993 (1.000)
GO:0006031	chitin biosynthetic process	16	1	0.007/0.008/0.009	0.793 (1.000)	0.992 (1.000)
GO:0006073	cellular glucan metabolic process	43	10	0.006/0.008/0.009	0.005 (0.040)	0.112 (0.525)
GO:0006206	pyrimidine base metabolic process	16	2	0.008/0.008/0.009	0.451 (0.827)	0.171 (0.649)
GO:0006549	isoleucine metabolic process	5	1	0.008/0.008/0.009	0.389 (0.747)	0.816 (1.000)
GO:0006656	phosphatidylcholine biosynthetic process	9	1	0.007/0.008/0.009	0.588 (1.000)	0.435 (0.963)
GO:0006760	folic acid and derivative metabolic process	12	1	0.006/0.008/0.008	0.693 (1.000)	0.932 (1.000)
GO:0006779	porphyrin biosynthetic process	16	3	0.007/0.008/0.009	0.184 (0.478)	0.104 (0.509)
GO:0006783	heme biosynthetic process	16	3	0.007/0.008/0.009	0.184 (0.478)	0.496 (0.973)
GO:0006813	potassium ion transport	8	1	0.007/0.008/0.009	0.545 (0.939)	0.906 (1.000)
GO:0008535	respiratory chain complex IV assembly	13	3	0.008/0.008/0.009	0.115 (0.370)	0.014 (0.129)
GO:0009060	aerobic respiration	87	40	0.007/0.008/0.010	2.62×10^{-19} (5.24×10^{-17})	0.993 (1.000)
GO:0009396	folic acid and derivative biosynthetic process	11	1	0.007/0.008/0.008	0.662 (1.000)	0.509 (0.976)
GO:0015804	neutral amino acid transport	3	1	0.007/0.008/0.009	0.256 (0.594)	0.304 (0.842)
GO:0015812	gamma-aminobutyric acid transport	3	1	0.007/0.008/0.008	0.256 (0.594)	0.750 (1.000)
GO:0015865	purine nucleotide transport	5	1	0.007/0.008/0.009	0.389 (0.747)	0.455 (0.967)
GO:0019439	aromatic compound catabolic process	9	2	0.007/0.008/0.008	0.204 (0.515)	0.327 (0.880)
GO:0033014	tetrapyrrole biosynthetic process	16	3	0.007/0.008/0.009	0.184 (0.478)	0.617 (1.000)
GO:0044042	glucan metabolic process	43	10	0.007/0.008/0.010	0.005 (0.040)	0.129 (0.567)
GO:0045980	negative regulation of nucleotide metabolic process	4	2	0.007/0.008/0.009	0.046 (0.221)	0.101 (0.499)
GO:0000272	polysaccharide catabolic process	9	3	0.007/0.007/0.008	0.045 (0.221)	0.057 (0.348)
GO:0000289	nuclear-transcribed mRNA poly(A) tail shortening	9	1	0.006/0.007/0.007	0.588 (1.000)	0.397 (0.938)
GO:0006042	glucosamine biosynthetic process	18	1	0.006/0.007/0.008	0.830 (1.000)	0.960 (1.000)
GO:0006045	N-acetylglucosamine biosynthetic process	18	1	0.006/0.007/0.008	0.830 (1.000)	0.960 (1.000)
GO:0006827	high-affinity iron ion transport	4	1	0.006/0.007/0.007	0.326 (0.655)	1.000 (1.000)
GO:0009651	response to salt stress	17	2	0.006/0.007/0.008	0.483 (0.878)	0.282 (0.809)
GO:0010565	regulation of cellular ketone metabolic process	19	4	0.007/0.007/0.008	0.095 (0.321)	0.107 (0.517)
GO:0015674	di-, tri-valent inorganic cation transport	43	8	0.005/0.007/0.008	0.044 (0.221)	0.914 (1.000)
GO:0016973	poly(A)+ mRNA export from nucleus	9	1	0.006/0.007/0.007	0.588 (1.000)	0.130 (0.567)
GO:0046349	amino sugar biosynthetic process	18	1	0.006/0.007/0.008	0.830 (1.000)	0.994 (1.000)
GO:0000041	transition metal ion transport	52	9	0.005/0.006/0.008	0.050 (0.236)	0.611 (1.000)
GO:0006140	regulation of nucleotide metabolic process	5	2	0.005/0.006/0.006	0.072 (0.308)	0.067 (0.377)

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Table 1 – Continued

GO ID	Name	Pop	Study	MGSA	TfT	PCu
GO:0006528	asparagine metabolic process	5	2	0.006/0.006/0.007	0.072 (0.308)	0.185 (0.665)
GO:0006529	asparagine biosynthetic process	4	1	0.005/0.006/0.006	0.326 (0.655)	0.514 (0.976)
GO:0006741	NADP biosynthetic process	4	1	0.005/0.006/0.007	0.326 (0.655)	0.678 (1.000)
GO:0009225	nucleotide-sugar metabolic process	7	1	0.006/0.006/0.007	0.498 (0.882)	0.363 (0.912)
GO:0010941	regulation of cell death	6	2	0.005/0.006/0.006	0.102 (0.332)	0.060 (0.358)
GO:0015807	L-amino acid transport	4	1	0.005/0.006/0.007	0.326 (0.655)	0.387 (0.932)
GO:0030162	regulation of proteolysis	7	2	0.006/0.006/0.007	0.134 (0.410)	0.055 (0.340)
GO:0042542	response to hydrogen peroxide	8	2	0.005/0.006/0.006	0.168 (0.469)	0.615 (1.000)
GO:0042723	thiamin and derivative metabolic process	13	1	0.006/0.006/0.007	0.722 (1.000)	0.924 (1.000)
GO:0042981	regulation of apoptosis	6	2	0.005/0.006/0.007	0.102 (0.332)	0.392 (0.934)
GO:0043067	regulation of programmed cell death	6	2	0.005/0.006/0.007	0.102 (0.332)	0.343 (0.893)
GO:0044273	sulfur compound catabolic process	8	1	0.006/0.006/0.007	0.545 (0.939)	0.674 (1.000)
GO:0046037	GMP metabolic process	5	1	0.005/0.006/0.006	0.389 (0.747)	0.250 (0.766)
GO:0051346	negative regulation of hydrolase activity	5	2	0.005/0.006/0.006	0.072 (0.308)	0.072 (0.394)
GO:0070086	ubiquitin-dependent endocytosis	10	1	0.005/0.006/0.006	0.627 (1.000)	0.281 (0.809)
GO:0006566	threonine metabolic process	9	1	0.004/0.005/0.005	0.588 (1.000)	0.825 (1.000)
GO:0017004	cytochrome complex assembly	7	2	0.005/0.005/0.006	0.134 (0.410)	0.034 (0.245)
GO:0042558	pteridine and derivative metabolic process	7	1	0.004/0.005/0.005	0.498 (0.882)	0.445 (0.967)
GO:0042559	pteridine and derivative biosynthetic process	7	1	0.004/0.005/0.005	0.498 (0.882)	0.768 (1.000)
GO:0044092	negative regulation of molecular function	24	4	0.004/0.005/0.005	0.182 (0.477)	0.114 (0.531)
GO:0044272	sulfur compound biosynthetic process	58	6	0.004/0.005/0.006	0.464 (0.850)	0.431 (0.963)
GO:0000032	cell wall mannoprotein biosynthetic process	12	1	0.004/0.004/0.005	0.693 (1.000)	1.000 (1.000)
GO:0000154	rRNA modification	24	3	0.003/0.004/0.004	0.394 (0.752)	0.020 (0.170)
GO:0000266	mitochondrial fission	5	1	0.004/0.004/0.005	0.389 (0.747)	0.092 (0.466)
GO:0006057	mannoprotein biosynthetic process	12	1	0.004/0.004/0.004	0.693 (1.000)	0.515 (0.977)
GO:0006672	ceramide metabolic process	13	1	0.003/0.004/0.004	0.722 (1.000)	0.867 (1.000)
GO:0007129	synapsis	10	1	0.004/0.004/0.005	0.627 (1.000)	0.380 (0.924)
GO:0009072	aromatic amino acid family metabolic process	21	3	0.003/0.004/0.005	0.314 (0.655)	0.680 (1.000)
GO:0019322	pentose biosynthetic process	6	1	0.003/0.004/0.004	0.446 (0.821)	0.752 (1.000)
GO:0030476	ascospore wall assembly	28	4	0.003/0.004/0.004	0.265 (0.609)	1.000 (1.000)
GO:0031506	cell wall glycoprotein biosynthetic process	12	1	0.004/0.004/0.005	0.693 (1.000)	0.458 (0.967)
GO:0034599	cellular response to oxidative stress	9	2	0.004/0.004/0.005	0.204 (0.515)	0.294 (0.827)
GO:0042244	spore wall assembly	28	4	0.003/0.004/0.004	0.265 (0.609)	0.216 (0.723)
GO:0046470	phosphatidylcholine metabolic process	11	1	0.004/0.004/0.005	0.662 (1.000)	0.543 (1.000)
GO:0070192	chromosome organization involved in meiosis	10	1	0.003/0.004/0.005	0.627 (1.000)	0.172 (0.651)
GO:0070590	spore wall biogenesis	28	4	0.003/0.004/0.004	0.265 (0.609)	0.319 (0.868)
GO:0070591	ascospore wall biogenesis	28	4	0.003/0.004/0.004	0.265 (0.609)	0.243 (0.756)
GO:0070726	cell wall assembly	29	5	0.003/0.004/0.004	0.129 (0.409)	0.005 (0.064)
GO:0000302	response to reactive oxygen species	14	3	0.003/0.003/0.003	0.137 (0.415)	0.596 (1.000)
GO:0006553	lysine metabolic process	10	1	0.003/0.003/0.003	0.627 (1.000)	0.858 (1.000)
GO:0006568	tryptophan metabolic process	12	2	0.003/0.003/0.004	0.312 (0.655)	0.612 (1.000)
GO:0006586	indolalkylamine metabolic process	12	2	0.003/0.003/0.004	0.312 (0.655)	0.823 (1.000)
GO:0006790	sulfur metabolic process	89	12	0.002/0.003/0.004	0.126 (0.400)	0.126 (0.564)
GO:0007007	inner mitochondrial membrane organization	15	4	0.003/0.003/0.004	0.045 (0.221)	0.038 (0.263)

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Table 1 – Continued

GO ID	Name	Pop	Study	MGSA	TfT	PCu
GO:0008219	cell death	51	28	0.003/0.003/0.003	1.99×10^{-16} (2.00×10^{-14})	1.90×10^{-17} (3.69×10^{-15})
GO:0008652	cellular amino acid biosynthetic process	130	30	0.002/0.003/0.004	2.06×10^{-6} (4.35×10^{-5})	0.002 (0.036)
GO:0009085	lysine biosynthetic process	10	1	0.003/0.003/0.003	0.627 (1.000)	0.821 (1.000)
GO:0010553	negative regulation of gene-specific transcription from RNA polymerase II promoter	11	1	0.003/0.003/0.004	0.662 (1.000)	0.483 (0.973)
GO:0016265	death	51	28	0.003/0.003/0.004	1.99×10^{-16} (2.00×10^{-14})	1.99×10^{-16} (3.32×10^{-14})
GO:0018130	heterocycle biosynthetic process	50	9	0.002/0.003/0.003	0.040 (0.208)	0.031 (0.227)
GO:0018205	peptidyl-lysine modification	10	1	0.003/0.003/0.003	0.627 (1.000)	0.460 (0.967)
GO:0019878	lysine biosynthetic process via aminoadipic acid	8	1	0.003/0.003/0.003	0.545 (0.939)	0.800 (1.000)
GO:0032582	negative regulation of gene-specific transcription	11	1	0.003/0.003/0.004	0.662 (1.000)	0.295 (0.827)
GO:0042430	indole and derivative metabolic process	12	2	0.003/0.003/0.004	0.312 (0.655)	0.251 (0.767)
GO:0042434	indole derivative metabolic process	12	2	0.003/0.003/0.004	0.312 (0.655)	1.000 (1.000)
GO:0042440	pigment metabolic process	26	4	0.003/0.003/0.003	0.223 (0.560)	0.237 (0.748)
GO:0042790	transcription of nuclear rRNA large RNA polymerase I transcript	11	1	0.003/0.003/0.004	0.662 (1.000)	0.212 (0.723)
GO:0044036	cell wall macromolecule metabolic process	29	2	0.003/0.003/0.004	0.770 (1.000)	0.603 (1.000)
GO:0046686	response to cadmium ion	9	1	0.003/0.003/0.004	0.588 (1.000)	0.932 (1.000)
GO:0051180	vitamin transport	10	1	0.002/0.003/0.003	0.627 (1.000)	0.636 (1.000)
GO:0051259	protein oligomerization	7	2	0.003/0.003/0.003	0.134 (0.410)	0.075 (0.405)
GO:0000045	autophagic vacuole formation	9	1	0.001/0.002/0.002	0.588 (1.000)	0.288 (0.814)
GO:0005976	polysaccharide metabolic process	66	12	0.001/0.002/0.002	0.018 (0.111)	0.002 (0.035)
GO:0005977	glycogen metabolic process	31	7	0.002/0.002/0.003	0.022 (0.132)	0.487 (0.973)
GO:0006797	polyphosphate metabolic process	9	1	0.002/0.002/0.002	0.588 (1.000)	0.803 (1.000)
GO:0009067	aspartate family amino acid biosynthetic process	49	7	0.002/0.002/0.003	0.171 (0.469)	0.987 (1.000)
GO:0009309	amine biosynthetic process	138	31	0.002/0.002/0.003	2.57×10^{-6} (5.32×10^{-5})	0.013 (0.124)
GO:0009435	NAD biosynthetic process	11	1	0.001/0.002/0.002	0.662 (1.000)	0.987 (1.000)
GO:0009605	response to external stimulus	64	10	0.002/0.002/0.002	0.072 (0.308)	0.133 (0.572)
GO:0009991	response to extracellular stimulus	64	10	0.002/0.002/0.003	0.072 (0.308)	1.000 (1.000)
GO:0015985	energy coupled proton transport, down electrochemical gradient	27	14	0.002/0.002/0.002	2.15×10^{-8} (6.46×10^{-7})	0.017 (0.155)
GO:0015986	ATP synthesis coupled proton transport	27	14	0.001/0.002/0.002	2.15×10^{-8} (6.46×10^{-7})	0.673 (1.000)
GO:0030005	cellular di-, tri-valent inorganic cation homeostasis	65	10	0.001/0.002/0.002	0.079 (0.319)	0.008 (0.093)
GO:0030258	lipid modification	30	8	0.001/0.002/0.002	0.005 (0.039)	0.004 (0.047)
GO:0031365	N-terminal protein amino acid modification	14	1	0.001/0.002/0.002	0.748 (1.000)	0.586 (1.000)
GO:0031399	regulation of protein modification process	11	1	0.002/0.002/0.003	0.662 (1.000)	0.412 (0.950)
GO:0031667	response to nutrient levels	62	9	0.002/0.002/0.002	0.122 (0.390)	0.978 (1.000)
GO:0032844	regulation of homeostatic process	12	1	0.002/0.002/0.003	0.693 (1.000)	0.499 (0.973)
GO:0042401	biogenic amine biosynthetic process	13	1	0.002/0.002/0.003	0.722 (1.000)	0.968 (1.000)
GO:0043086	negative regulation of catalytic activity	20	3	0.002/0.002/0.002	0.287 (0.651)	0.161 (0.631)
GO:0044038	cell wall macromolecule biosynthetic process	24	1	0.002/0.002/0.002	0.906 (1.000)	0.968 (1.000)
GO:0046165	alcohol biosynthetic process	81	15	0.001/0.002/0.002	0.007 (0.053)	0.008 (0.086)
GO:0046519	sphingoid metabolic process	15	1	0.002/0.002/0.003	0.772 (1.000)	0.455 (0.967)
GO:0051098	regulation of binding	30	4	0.002/0.002/0.003	0.308 (0.655)	0.219 (0.723)

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Table 1 – Continued

GO ID	Name	Pop	Study	MGSA	TfT	PCu
GO:0055066	di-, tri-valent inorganic cation homeostasis	65	10	0.001/0.002/0.002	0.079 (0.319)	0.006 (0.067)
GO:0070589	cellular component macromolecule biosynthetic process	24	1	0.002/0.002/0.002	0.906 (1.000)	0.810 (1.000)
GO:0001522	pseudouridine synthesis	16	1	0.000/0.001/0.001	0.793 (1.000)	0.337 (0.889)
GO:0006056	mannoprotein metabolic process	16	1	0.001/0.001/0.001	0.793 (1.000)	0.626 (1.000)
GO:0006066	alcohol metabolic process	245	47	0.000/0.001/0.001	9.57×10^{-7} (2.09×10^{-5})	1.52×10^{-6} (6.09×10^{-5})
GO:0006112	energy reserve metabolic process	41	8	0.001/0.001/0.002	0.034 (0.180)	1.000 (1.000)
GO:0006518	peptide metabolic process	24	3	0.001/0.001/0.001	0.394 (0.752)	0.396 (0.938)
GO:0006575	cellular amino acid derivative metabolic process	68	12	0.000/0.001/0.001	0.023 (0.135)	0.622 (1.000)
GO:0006613	cotranslational protein targeting to membrane	21	4	0.000/0.001/0.001	0.127 (0.405)	0.019 (0.162)
GO:0006614	SRP-dependent cotranslational protein targeting to membrane	19	4	0.001/0.001/0.001	0.095 (0.321)	0.163 (0.637)
GO:0006769	nicotinamide metabolic process	47	13	0.000/0.001/0.001	(0.003)	0.011 (0.109)
GO:0006862	nucleotide transport	11	1	0.001/0.001/0.002	0.662 (1.000)	0.348 (0.893)
GO:0006915	apoptosis	23	5	0.001/0.001/0.001	0.058 (0.269)	0.633 (1.000)
GO:0006972	hyperosmotic response	12	1	0.001/0.001/0.002	0.693 (1.000)	0.557 (1.000)
GO:0009064	glutamine family amino acid metabolic process	57	20	0.001/0.001/0.002	8.38×10^{-8} (2.24×10^{-6})	(0.008)
GO:0009267	cellular response to starvation	41	5	0.001/0.001/0.002	0.339 (0.680)	0.524 (0.986)
GO:0009303	rRNA transcription	14	1	0.001/0.001/0.002	0.748 (1.000)	0.410 (0.950)
GO:0009415	response to water	32	4	0.001/0.001/0.001	0.352 (0.703)	0.731 (1.000)
GO:0009820	alkaloid metabolic process	47	13	0.000/0.001/0.001	(0.003)	4.45×10^{-5} (0.002)
GO:0012501	programmed cell death	25	5	0.001/0.001/0.001	0.078 (0.319)	1.000 (1.000)
GO:0015918	sterol transport	15	1	0.001/0.001/0.001	0.772 (1.000)	0.615 (1.000)
GO:0016053	organic acid biosynthetic process	167	31	0.000/0.001/0.001	(0.002)	(0.009)
GO:0016236	macroautophagy	24	2	0.000/0.001/0.001	0.673 (1.000)	0.775 (1.000)
GO:0018409	peptide or protein amino-terminal blocking	14	1	0.001/0.001/0.002	0.748 (1.000)	1.000 (1.000)
GO:0019359	nicotinamide nucleotide biosynthetic process	15	2	0.000/0.001/0.001	0.417 (0.788)	0.969 (1.000)
GO:0019674	NAD metabolic process	23	6	0.001/0.001/0.001	0.017 (0.103)	0.712 (1.000)
GO:0019740	nitrogen utilization	19	2	0.001/0.001/0.001	0.543 (0.939)	0.461 (0.967)
GO:0022603	regulation of anatomical structure morphogenesis	21	3	0.000/0.001/0.001	0.314 (0.655)	0.170 (0.647)
GO:0022604	regulation of cell morphogenesis	18	3	0.001/0.001/0.002	0.235 (0.590)	0.060 (0.358)
GO:0030001	metal ion transport	76	13	0.001/0.001/0.002	0.023 (0.137)	0.996 (1.000)
GO:0032258	CVT pathway	20	2	0.000/0.001/0.001	0.572 (0.983)	0.585 (1.000)
GO:0032990	cell part morphogenesis	12	1	0.000/0.001/0.001	0.693 (1.000)	0.275 (0.802)
GO:0033108	mitochondrial respiratory chain complex assembly	22	5	0.001/0.001/0.001	0.049 (0.231)	0.003 (0.046)
GO:0034220	ion transmembrane transport	40	17	0.001/0.001/0.001	2.92×10^{-8} (8.56×10^{-7})	0.001 (0.027)
GO:0034968	histone lysine methylation	15	1	0.000/0.001/0.001	0.772 (1.000)	0.652 (1.000)
GO:0042026	protein refolding	16	1	0.001/0.001/0.001	0.793 (1.000)	0.552 (1.000)
GO:0042594	response to starvation	44	5	0.000/0.001/0.001	0.397 (0.754)	0.579 (1.000)
GO:0043648	dicarboxylic acid metabolic process	23	8	0.001/0.001/0.001	(0.008)	0.100 (0.499)
GO:0044093	positive regulation of molecular function	24	2	0.001/0.001/0.001	0.673 (1.000)	0.632 (1.000)
GO:0044264	cellular polysaccharide metabolic process	60	11	0.001/0.001/0.001	0.022 (0.132)	0.003 (0.042)
GO:0046148	pigment biosynthetic process	25	3	0.001/0.001/0.001	0.420 (0.791)	0.388 (0.932)
GO:0046364	monosaccharide biosynthetic process	58	10	0.001/0.001/0.002	0.041 (0.210)	0.916 (1.000)
GO:0046394	carboxylic acid biosynthetic process	167	31	0.000/0.001/0.001	(0.002)	0.931 (1.000)
GO:0046496	nicotinamide nucleotide metabolic process	46	13	0.001/0.001/0.001	(0.003)	0.388 (0.932)
GO:0070584	mitochondrion morphogenesis	12	1	0.000/0.001/0.001	0.693 (1.000)	0.584 (1.000)
GO:0070925	organelle assembly	13	1	0.000/0.001/0.001	0.722 (1.000)	0.378 (0.922)

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Table 1 – Continued

GO ID	Name	Pop	Study	MGSA	TfT	PCu
GO:0000001	mitochondrion inheritance	29	1	0.000/0.000/0.000	0.943 (1.000)	0.460 (0.967)
GO:0000002	mitochondrial genome maintenance	38	2	0.000/0.000/0.000	0.884 (1.000)	0.771 (1.000)
GO:0000003	reproduction	337	14	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0000018	regulation of DNA recombination	17	1	0.000/0.000/0.001	0.813 (1.000)	0.383 (0.930)
GO:0000027	ribosomal large subunit assembly	42	1	0.000/0.000/0.000	0.984 (1.000)	0.462 (0.967)
GO:0000070	mitotic sister chromatid segregation	73	1	0.000/0.000/0.000	0.999 (1.000)	0.617 (1.000)
GO:0000075	cell cycle checkpoint	59	1	0.000/0.000/0.000	0.997 (1.000)	0.831 (1.000)
GO:0000079	regulation of cyclin-dependent protein kinase activity	20	1	0.000/0.000/0.000	0.861 (1.000)	0.384 (0.930)
GO:0000087	M phase of mitotic cell cycle	204	3	0.000/0.000/0.000	1.000 (1.000)	0.878 (1.000)
GO:0000122	negative regulation of transcription from RNA polymerase II promoter	73	5	0.000/0.000/0.000	0.828 (1.000)	0.079 (0.421)
GO:0000183	chromatin silencing at rDNA	20	1	0.000/0.000/0.000	0.861 (1.000)	0.185 (0.665)
GO:0000184	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	32	2	0.000/0.000/0.000	0.816 (1.000)	0.745 (1.000)
GO:0000209	protein polyubiquitination	20	3	0.000/0.000/0.000	0.287 (0.651)	0.012 (0.120)
GO:0000278	mitotic cell cycle	324	3	0.000/0.000/0.000	1.000 (1.000)	0.978 (1.000)
GO:0000279	M phase	343	9	0.000/0.000/0.000	1.000 (1.000)	0.165 (0.642)
GO:0000280	nuclear division	198	2	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0000282	cellular bud site selection	63	1	0.000/0.000/0.000	0.998 (1.000)	0.594 (1.000)
GO:0000288	nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	43	3	0.000/0.000/0.000	0.782 (1.000)	0.685 (1.000)
GO:0000375	RNA splicing, via transesterification reactions	106	2	0.000/0.000/0.000	1.000 (1.000)	0.664 (1.000)
GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	101	2	0.000/0.000/0.000	0.999 (1.000)	0.907 (1.000)
GO:0000398	nuclear mRNA splicing, via spliceosome	99	2	0.000/0.000/0.000	0.999 (1.000)	0.701 (1.000)
GO:0000422	mitochondrion degradation	36	2	0.000/0.000/0.000	0.864 (1.000)	0.932 (1.000)
GO:0000447	endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	39	1	0.000/0.000/0.000	0.979 (1.000)	0.696 (1.000)
GO:0000460	maturation of 5.8S rRNA	70	1	0.000/0.000/0.000	0.999 (1.000)	0.952 (1.000)
GO:0000462	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	89	3	0.000/0.000/0.000	0.992 (1.000)	0.967 (1.000)
GO:0000466	maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	70	1	0.000/0.000/0.000	0.999 (1.000)	1.000 (1.000)
GO:0000469	cleavages during rRNA processing	60	1	0.000/0.000/0.000	0.997 (1.000)	0.920 (1.000)
GO:0000478	endonucleolytic cleavages during rRNA processing	41	1	0.000/0.000/0.000	0.983 (1.000)	0.683 (1.000)
GO:0000479	endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	41	1	0.000/0.000/0.000	0.983 (1.000)	1.000 (1.000)
GO:0000746	conjugation	110	4	0.000/0.000/0.000	0.994 (1.000)	0.541 (1.000)
GO:0000747	conjugation with cellular fusion	106	3	0.000/0.000/0.000	0.998 (1.000)	0.986 (1.000)
GO:0000749	response to pheromone during conjugation with cellular fusion	47	3	0.000/0.000/0.000	0.831 (1.000)	0.146 (0.600)

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Table 1 – Continued

GO ID	Name	Pop	Study	MGSA	TfT	PCu
GO:0000750	pheromone-dependent signal transduction involved in conjugation with cellular fusion	26	1	0.000/0.000/0.000	0.923 (1.000)	0.875 (1.000)
GO:0000753	cellular morphogenesis during conjugation with cellular fusion	17	1	0.000/0.000/0.000	0.813 (1.000)	0.740 (1.000)
GO:0000767	cell morphogenesis during conjugation	18	1	0.000/0.000/0.000	0.830 (1.000)	0.330 (0.881)
GO:0000819	sister chromatid segregation	78	1	0.000/0.000/0.000	1.000 (1.000)	0.781 (1.000)
GO:0000902	cell morphogenesis	145	3	0.000/0.000/0.000	1.000 (1.000)	0.970 (1.000)
GO:0000910	cytokinesis	113	1	0.000/0.000/0.000	1.000 (1.000)	0.842 (1.000)
GO:0000956	nuclear-transcribed mRNA catabolic process	84	6	0.000/0.000/0.000	0.813 (1.000)	0.929 (1.000)
GO:0001300	chronological cell aging	23	4	0.000/0.000/0.000	0.163 (0.469)	0.235 (0.746)
GO:0001302	replicative cell aging	44	5	0.000/0.000/0.000	0.397 (0.754)	0.701 (1.000)
GO:0001403	invasive growth in response to glucose limitation	48	3	0.000/0.000/0.000	0.841 (1.000)	0.219 (0.723)
GO:0001510	RNA methylation	29	2	0.000/0.000/0.000	0.770 (1.000)	0.154 (0.618)
GO:0005975	carbohydrate metabolic process	320	65	0.000/0.000/0.000	5.33×10^{-10} (1.88×10^{-8})	2.76×10^{-11} (2.14×10^{-9})
GO:0006082	organic acid metabolic process	390	84	0.000/0.000/0.000	2.97×10^{-14} (1.70×10^{-12})	5.95×10^{-15} (7.69×10^{-13})
GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	1655	103	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0006163	purine nucleotide metabolic process	71	16	0.000/0.000/0.000	(0.007)	0.516 (0.977)
GO:0006164	purine nucleotide biosynthetic process	67	16	0.000/0.000/0.000	(0.004)	0.003 (0.046)
GO:0006259	DNA metabolic process	389	6	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0006260	DNA replication	154	2	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0006281	DNA repair	240	1	0.000/0.000/0.000	1.000 (1.000)	0.996 (1.000)
GO:0006310	DNA recombination	115	4	0.000/0.000/0.000	0.996 (1.000)	0.066 (0.374)
GO:0006312	mitotic recombination	37	1	0.000/0.000/0.000	0.974 (1.000)	0.794 (1.000)
GO:0006323	DNA packaging	67	1	0.000/0.000/0.000	0.999 (1.000)	0.998 (1.000)
GO:0006325	chromatin organization	229	4	0.000/0.000/0.000	1.000 (1.000)	0.720 (1.000)
GO:0006333	chromatin assembly or disassembly	79	2	0.000/0.000/0.000	0.996 (1.000)	0.428 (0.963)
GO:0006334	nucleosome assembly	27	1	0.000/0.000/0.000	0.930 (1.000)	0.235 (0.746)
GO:0006342	chromatin silencing	108	1	0.000/0.000/0.000	1.000 (1.000)	0.996 (1.000)
GO:0006350	transcription	686	25	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0006351	transcription, DNA-dependent	574	21	0.000/0.000/0.000	1.000 (1.000)	0.612 (1.000)
GO:0006352	transcription initiation	67	2	0.000/0.000/0.000	0.989 (1.000)	0.725 (1.000)
GO:0006355	regulation of transcription, DNA-dependent	425	20	0.000/0.000/0.000	1.000 (1.000)	0.020 (0.170)
GO:0006357	regulation of transcription from RNA polymerase II promoter	236	14	0.000/0.000/0.000	0.981 (1.000)	0.019 (0.161)
GO:0006360	transcription from RNA polymerase I promoter	49	1	0.000/0.000/0.000	0.992 (1.000)	0.852 (1.000)
GO:0006364	rRNA processing	249	9	0.000/0.000/0.000	1.000 (1.000)	0.021 (0.170)
GO:0006366	transcription from RNA polymerase II promoter	356	15	0.000/0.000/0.000	1.000 (1.000)	0.253 (0.767)
GO:0006367	transcription initiation from RNA polymerase II promoter	47	1	0.000/0.000/0.000	0.990 (1.000)	0.875 (1.000)
GO:0006396	RNA processing	512	11	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0006397	mRNA processing	194	4	0.000/0.000/0.000	1.000 (1.000)	0.830 (1.000)
GO:0006399	tRNA metabolic process	167	3	0.000/0.000/0.000	1.000 (1.000)	0.957 (1.000)
GO:0006401	RNA catabolic process	99	6	0.000/0.000/0.000	0.913 (1.000)	0.322 (0.872)
GO:0006402	mRNA catabolic process	85	6	0.000/0.000/0.000	0.821 (1.000)	0.029 (0.216)
GO:0006403	RNA localization	133	3	0.000/0.000/0.000	1.000 (1.000)	0.853 (1.000)
GO:0006405	RNA export from nucleus	96	3	0.000/0.000/0.000	0.996 (1.000)	0.287 (0.813)
GO:0006406	mRNA export from nucleus	69	1	0.000/0.000/0.000	0.999 (1.000)	0.948 (1.000)
GO:0006409	tRNA export from nucleus	32	2	0.000/0.000/0.000	0.816 (1.000)	0.243 (0.756)
GO:0006412	translation	705	80	0.000/0.000/0.000	0.033 (0.180)	8.17×10^{-9} (4.32×10^{-7})
GO:0006413	translational initiation	49	2	0.000/0.000/0.000	0.952 (1.000)	0.933 (1.000)
GO:0006414	translational elongation	314	46	0.000/0.000/0.000	0.001 (0.011)	9.77×10^{-7} (4.21×10^{-5})

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Table 1 – Continued

GO ID	Name	Pop	Study	MGSA	TfT	PCu
GO:0006415	translational termination	30	2	0.000/0.000/0.000	0.787 (1.000)	0.857 (1.000)
GO:0006417	regulation of translation	183	14	0.000/0.000/0.000	0.827 (1.000)	0.603 (1.000)
GO:0006418	tRNA aminoacylation for protein translation	37	1	0.000/0.000/0.000	0.974 (1.000)	0.990 (1.000)
GO:0006457	protein folding	110	5	0.000/0.000/0.000	0.982 (1.000)	0.955 (1.000)
GO:0006461	protein complex assembly	190	13	0.000/0.000/0.000	0.916 (1.000)	0.005 (0.060)
GO:0006464	protein modification process	611	21	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0006468	protein amino acid phosphorylation	134	5	0.000/0.000/0.000	0.997 (1.000)	0.998 (1.000)
GO:0006473	protein amino acid acetylation	53	2	0.000/0.000/0.000	0.965 (1.000)	0.892 (1.000)
GO:0006479	protein amino acid methylation	35	1	0.000/0.000/0.000	0.968 (1.000)	0.918 (1.000)
GO:0006486	protein amino acid glycosylation	69	3	0.000/0.000/0.000	0.964 (1.000)	0.968 (1.000)
GO:0006487	protein amino acid N-linked glycosylation	46	3	0.000/0.000/0.000	0.819 (1.000)	0.290 (0.817)
GO:0006497	protein amino acid lipidation	53	2	0.000/0.000/0.000	0.965 (1.000)	0.559 (1.000)
GO:0006505	GPI anchor metabolic process	30	1	0.000/0.000/0.000	0.948 (1.000)	0.612 (1.000)
GO:0006506	GPI anchor biosynthetic process	29	1	0.000/0.000/0.000	0.943 (1.000)	0.763 (1.000)
GO:0006508	proteolysis	332	15	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0006511	ubiquitin-dependent protein catabolic process	185	3	0.000/0.000/0.000	1.000 (1.000)	0.979 (1.000)
GO:0006513	protein monoubiquitination	19	2	0.000/0.000/0.000	0.543 (0.939)	0.127 (0.564)
GO:0006519	cellular amino acid and derivative metabolic process	301	55	0.000/0.000/0.000	5.64×10^{-7} (1.26×10^{-5})	2.97×10^{-7} (1.44×10^{-5})
GO:0006520	cellular amino acid metabolic process	235	43	0.000/0.000/0.000	1.02×10^{-5} ()	0.938 (1.000)
GO:0006541	glutamine metabolic process	23	2	0.000/0.000/0.000	0.649 (1.000)	1.000 (1.000)
GO:0006605	protein targeting	238	11	0.000/0.000/0.000	0.998 (1.000)	0.127 (0.564)
GO:0006606	protein import into nucleus	60	1	0.000/0.000/0.000	0.997 (1.000)	0.961 (1.000)
GO:0006612	protein targeting to membrane	54	4	0.000/0.000/0.000	0.759 (1.000)	0.221 (0.726)
GO:0006623	protein targeting to vacuole	65	4	0.000/0.000/0.000	0.871 (1.000)	0.215 (0.723)
GO:0006625	protein targeting to peroxisome	22	2	0.000/0.000/0.000	0.625 (1.000)	0.372 (0.917)
GO:0006626	protein targeting to mitochondrion	51	2	0.000/0.000/0.000	0.959 (1.000)	0.892 (1.000)
GO:0006629	lipid metabolic process	275	26	0.000/0.000/0.000	0.513 (0.905)	0.423 (0.961)
GO:0006643	membrane lipid metabolic process	33	1	0.000/0.000/0.000	0.962 (1.000)	0.972 (1.000)
GO:0006644	phospholipid metabolic process	112	8	0.000/0.000/0.000	0.837 (1.000)	0.963 (1.000)
GO:0006650	glycerophospholipid metabolic process	78	5	0.000/0.000/0.000	0.868 (1.000)	0.748 (1.000)
GO:0006665	sphingolipid metabolic process	33	1	0.000/0.000/0.000	0.962 (1.000)	1.000 (1.000)
GO:0006725	cellular aromatic compound metabolic process	140	16	0.000/0.000/0.000	0.236 (0.593)	0.238 (0.748)
GO:0006730	one-carbon metabolic process	86	4	0.000/0.000/0.000	0.967 (1.000)	0.968 (1.000)
GO:0006732	coenzyme metabolic process	144	41	0.000/0.000/0.000	2.60×10^{-11} (9.76×10^{-10})	0.552 (1.000)
GO:0006733	oxidoreduction coenzyme metabolic process	60	13	0.000/0.000/0.000	0.003 (0.025)	0.958 (1.000)
GO:0006752	group transfer coenzyme metabolic process	30	1	0.000/0.000/0.000	0.948 (1.000)	1.000 (1.000)
GO:0006753	nucleoside phosphate metabolic process	196	53	0.000/0.000/0.000	2.57×10^{-13} (1.08×10^{-11})	0.021 (0.170)
GO:0006754	ATP biosynthetic process	39	14	0.000/0.000/0.000	5.59×10^{-6} ()	0.428 (0.963)
GO:0006766	vitamin metabolic process	89	19	0.000/0.000/0.000	(0.005)	(0.011)
GO:0006767	water-soluble vitamin metabolic process	86	18	0.000/0.000/0.000	(0.008)	0.886 (1.000)

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Table 1 – Continued

GO ID	Name	Pop	Study	MGSA	TfT	PCu
GO:0006793	phosphorus metabolic process	300	53	0.000/0.000/0.000	2.71×10^{-6} (5.51×10^{-5})	1.88×10^{-6} (7.30×10^{-5})
GO:0006796	phosphate metabolic process	295	48	0.000/0.000/0.000	7.66×10^{-5} (0.001)	1.000 (1.000)
GO:0006807	nitrogen compound metabolic process	1910	154	0.000/0.000/0.000	0.994 (1.000)	1.000 (1.000)
GO:0006810	transport	1241	119	0.000/0.000/0.000	0.401 (0.762)	0.132 (0.571)
GO:0006811	ion transport	187	60	0.000/0.000/0.000	6.58×10^{-19} (1.13×10^{-16})	2.68×10^{-22} (7.80×10^{-20})
GO:0006812	cation transport	122	30	0.000/0.000/0.000	4.86×10^{-7} (1.14×10^{-5})	0.999 (1.000)
GO:0006818	hydrogen transport	33	14	0.000/0.000/0.001	5.16×10^{-7} (1.17×10^{-5})	4.52×10^{-7} (2.11×10^{-5})
GO:0006839	mitochondrial transport	66	7	0.000/0.000/0.000	0.425 (0.799)	0.005 (0.057)
GO:0006865	amino acid transport	45	5	0.000/0.000/0.000	0.416 (0.788)	0.953 (1.000)
GO:0006869	lipid transport	40	2	0.000/0.000/0.000	0.901 (1.000)	0.910 (1.000)
GO:0006873	cellular ion homeostasis	116	11	0.000/0.000/0.000	0.531 (0.931)	0.045 (0.300)
GO:0006886	intracellular protein transport	324	12	0.000/0.000/0.000	1.000 (1.000)	0.529 (0.993)
GO:0006888	ER to Golgi vesicle-mediated transport	87	1	0.000/0.000/0.000	1.000 (1.000)	0.483 (0.973)
GO:0006897	endocytosis	97	3	0.000/0.000/0.000	0.996 (1.000)	0.229 (0.745)
GO:0006906	vesicle fusion	35	1	0.000/0.000/0.000	0.968 (1.000)	0.506 (0.974)
GO:0006913	nucleocytoplasmic transport	154	5	0.000/0.000/0.000	0.999 (1.000)	1.000 (1.000)
GO:0006914	autophagy	135	14	0.000/0.000/0.000	0.386 (0.747)	0.886 (1.000)
GO:0006944	membrane fusion	71	4	0.000/0.000/0.000	0.911 (1.000)	0.423 (0.961)
GO:0006950	response to stress	765	86	0.000/0.000/0.000	0.034 (0.181)	0.191 (0.674)
GO:0006970	response to osmotic stress	97	6	0.000/0.000/0.000	0.903 (1.000)	0.976 (1.000)
GO:0006974	response to DNA damage stimulus	282	2	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0006979	response to oxidative stress	82	17	0.000/0.000/0.000	0.001 (0.012)	0.003 (0.046)
GO:0006984	ER-nuclear signaling pathway	84	3	0.000/0.000/0.000	0.988 (1.000)	0.480 (0.973)
GO:0006986	response to unfolded protein	31	2	0.000/0.000/0.000	0.802 (1.000)	0.881 (1.000)
GO:0006996	organelle organization	1103	38	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0006997	nucleus organization	69	1	0.000/0.000/0.000	0.999 (1.000)	0.918 (1.000)
GO:0007005	mitochondrion organization	275	19	0.000/0.000/0.000	0.944 (1.000)	(0.013)
GO:0007006	mitochondrial membrane organization	32	4	0.000/0.000/0.000	0.352 (0.703)	0.088 (0.459)
GO:0007010	cytoskeleton organization	223	1	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0007031	peroxisome organization	47	6	0.000/0.000/0.000	0.275 (0.628)	0.004 (0.054)
GO:0007033	vacuole organization	46	3	0.000/0.000/0.000	0.819 (1.000)	0.208 (0.723)
GO:0007034	vacuolar transport	118	4	0.000/0.000/0.000	0.997 (1.000)	0.616 (1.000)
GO:0007047	cell wall organization	216	18	0.000/0.000/0.000	0.738 (1.000)	0.569 (1.000)
GO:0007049	cell cycle	620	11	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0007059	chromosome segregation	157	2	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0007062	sister chromatid cohesion	35	1	0.000/0.000/0.000	0.968 (1.000)	0.483 (0.973)
GO:0007064	mitotic sister chromatid cohesion	28	1	0.000/0.000/0.000	0.937 (1.000)	0.350 (0.893)
GO:0007067	mitosis	188	2	0.000/0.000/0.000	1.000 (1.000)	0.962 (1.000)
GO:0007088	regulation of mitosis	32	1	0.000/0.000/0.000	0.958 (1.000)	0.438 (0.966)
GO:0007091	mitotic metaphase/anaphase transition	33	1	0.000/0.000/0.000	0.962 (1.000)	0.451 (0.967)
GO:0007093	mitotic cell cycle checkpoint	31	1	0.000/0.000/0.000	0.953 (1.000)	0.501 (0.973)
GO:0007094	mitotic cell cycle spindle assembly checkpoint	20	1	0.000/0.000/0.000	0.861 (1.000)	0.606 (1.000)
GO:0007096	regulation of exit from mitosis	27	1	0.000/0.000/0.000	0.930 (1.000)	0.586 (1.000)
GO:0007105	cytokinesis, site selection	63	1	0.000/0.000/0.000	0.998 (1.000)	0.685 (1.000)
GO:0007114	cell budding	85	1	0.000/0.000/0.000	1.000 (1.000)	0.998 (1.000)
GO:0007120	axial cellular bud site selection	19	1	0.000/0.000/0.000	0.846 (1.000)	0.181 (0.659)
GO:0007126	meiosis	166	8	0.000/0.000/0.000	0.991 (1.000)	0.003 (0.046)
GO:0007127	meiosis I	69	3	0.000/0.000/0.000	0.964 (1.000)	0.173 (0.652)
GO:0007131	reciprocal meiotic recombination	41	3	0.000/0.000/0.000	0.753 (1.000)	0.030 (0.223)
GO:0007154	cell communication	434	24	0.000/0.000/0.000	0.999 (1.000)	0.996 (1.000)
GO:0007163	establishment or maintenance of cell polarity	115	1	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0007165	signal transduction	371	15	0.000/0.000/0.000	1.000 (1.000)	0.955 (1.000)

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Table 1 – Continued

GO ID	Name	Pop	Study	MGSA	TfT	PCu
GO:0007166	cell surface receptor linked signal transduction	50	1	0.000/0.000/0.000	0.993 (1.000)	0.891 (1.000)
GO:0007186	G-protein coupled receptor protein signaling pathway	32	1	0.000/0.000/0.000	0.958 (1.000)	0.640 (1.000)
GO:0007242	intracellular signaling cascade	269	8	0.000/0.000/0.000	1.000 (1.000)	0.972 (1.000)
GO:0007264	small GTPase mediated signal transduction	106	4	0.000/0.000/0.000	0.992 (1.000)	0.391 (0.934)
GO:0007265	Ras protein signal transduction	63	3	0.000/0.000/0.000	0.943 (1.000)	0.464 (0.967)
GO:0007266	Rho protein signal transduction	22	2	0.000/0.000/0.000	0.625 (1.000)	0.277 (0.805)
GO:0007346	regulation of mitotic cell cycle	79	2	0.000/0.000/0.000	0.996 (1.000)	0.282 (0.809)
GO:0007568	aging	71	8	0.000/0.000/0.000	0.347 (0.694)	0.126 (0.564)
GO:0007569	cell aging	61	7	0.000/0.000/0.000	0.346 (0.693)	0.271 (0.795)
GO:0008033	tRNA processing	104	2	0.000/0.000/0.000	1.000 (1.000)	0.840 (1.000)
GO:0008104	protein localization	589	18	0.000/0.000/0.000	1.000 (1.000)	0.895 (1.000)
GO:0008150	biological_process	5206	488	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0008152	metabolic process	3572	344	0.000/0.000/0.000	0.188 (0.485)	0.188 (0.670)
GO:0008202	steroid metabolic process	50	3	0.000/0.000/0.000	0.861 (1.000)	0.852 (1.000)
GO:0008213	protein amino acid alkylation	35	1	0.000/0.000/0.000	0.968 (1.000)	0.648 (1.000)
GO:0008361	regulation of cell size	108	1	0.000/0.000/0.000	1.000 (1.000)	0.915 (1.000)
GO:0008380	RNA splicing	130	2	0.000/0.000/0.000	1.000 (1.000)	0.814 (1.000)
GO:0008610	lipid biosynthetic process	152	7	0.000/0.000/0.000	0.991 (1.000)	0.991 (1.000)
GO:0008654	phospholipid biosynthetic process	69	6	0.000/0.000/0.000	0.638 (1.000)	0.576 (1.000)
GO:0009056	catabolic process	857	111	0.000/0.000/0.000	9.57×10^{-5} (0.001)	(0.004)
GO:0009057	macromolecule catabolic process	603	59	0.000/0.000/0.000	0.379 (0.747)	0.025 (0.197)
GO:0009058	biosynthetic process	2017	179	0.000/0.000/0.000	0.849 (1.000)	0.964 (1.000)
GO:0009059	macromolecule biosynthetic process	1598	119	0.000/0.000/0.000	0.999 (1.000)	0.728 (1.000)
GO:0009066	aspartate family amino acid metabolic process	61	10	0.000/0.000/0.001	0.055 (0.260)	0.735 (1.000)
GO:0009100	glycoprotein metabolic process	75	4	0.000/0.000/0.000	0.931 (1.000)	0.758 (1.000)
GO:0009101	glycoprotein biosynthetic process	74	4	0.000/0.000/0.000	0.926 (1.000)	0.818 (1.000)
GO:0009108	coenzyme biosynthetic process	68	4	0.000/0.000/0.000	0.893 (1.000)	1.000 (1.000)
GO:0009110	vitamin biosynthetic process	49	3	0.000/0.000/0.000	0.851 (1.000)	0.851 (1.000)
GO:0009112	nucleobase metabolic process	38	2	0.000/0.000/0.000	0.884 (1.000)	0.999 (1.000)
GO:0009117	nucleotide metabolic process	196	53	0.000/0.000/0.000	2.57×10^{-13} (1.08×10^{-11})	1.000 (1.000)
GO:0009123	nucleoside monophosphate metabolic process	36	1	0.000/0.000/0.000	0.971 (1.000)	1.000 (1.000)
GO:0009124	nucleoside monophosphate biosynthetic process	31	1	0.000/0.000/0.000	0.953 (1.000)	0.998 (1.000)
GO:0009126	purine nucleoside monophosphate metabolic process	21	1	0.000/0.000/0.000	0.874 (1.000)	0.996 (1.000)
GO:0009127	purine nucleoside monophosphate biosynthetic process	18	1	0.000/0.000/0.000	0.830 (1.000)	0.991 (1.000)
GO:0009141	nucleoside triphosphate metabolic process	48	14	0.000/0.000/0.000	8.08×10^{-5} (0.001)	0.417 (0.953)
GO:0009142	nucleoside triphosphate biosynthetic process	44	14	0.000/0.000/0.000	2.74×10^{-5} ()	(0.008)
GO:0009144	purine nucleoside triphosphate metabolic process	41	14	0.000/0.000/0.000	1.09×10^{-5} ()	0.002 (0.027)
GO:0009145	purine nucleoside triphosphate biosynthetic process	40	14	0.000/0.000/0.000	7.88×10^{-6} ()	0.003 (0.044)
GO:0009150	purine ribonucleotide metabolic process	61	15	0.000/0.000/0.000	(0.004)	0.048 (0.311)
GO:0009152	purine ribonucleotide biosynthetic process	57	15	0.000/0.000/0.000	(0.002)	0.021 (0.170)
GO:0009156	ribonucleoside monophosphate biosynthetic process	25	1	0.000/0.000/0.000	0.915 (1.000)	0.999 (1.000)

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Table 1 – Continued

GO ID	Name	Pop	Study	MGSA	TfT	PCu
GO:0009161	ribonucleoside monophosphate metabolic process	28	1	0.000/0.000/0.000	0.937 (1.000)	0.999 (1.000)
GO:0009165	nucleotide biosynthetic process	110	18	0.000/0.000/0.000	0.013 (0.083)	0.021 (0.172)
GO:0009167	purine ribonucleoside monophosphate metabolic process	20	1	0.000/0.000/0.000	0.861 (1.000)	0.997 (1.000)
GO:0009168	purine ribonucleoside monophosphate biosynthetic process	17	1	0.000/0.000/0.000	0.813 (1.000)	0.992 (1.000)
GO:0009199	ribonucleoside triphosphate metabolic process	43	14	0.000/0.000/0.000	2.04×10^{-5} ()	(0.019)
GO:0009201	ribonucleoside triphosphate biosynthetic process	42	14	0.000/0.000/0.000	1.50×10^{-5} ()	0.002 (0.034)
GO:0009205	purine ribonucleoside triphosphate metabolic process	41	14	0.000/0.000/0.000	1.09×10^{-5} ()	0.007 (0.081)
GO:0009206	purine ribonucleoside triphosphate biosynthetic process	40	14	0.000/0.000/0.000	7.88×10^{-6} ()	0.009 (0.101)
GO:0009259	ribonucleotide metabolic process	71	15	0.000/0.000/0.000	0.002 (0.018)	0.944 (1.000)
GO:0009260	ribonucleotide biosynthetic process	67	15	0.000/0.000/0.000	0.001 (0.010)	0.019 (0.166)
GO:0009272	fungal-type cell wall biogenesis	38	4	0.000/0.000/0.000	0.483 (0.878)	0.633 (1.000)
GO:0009308	amine metabolic process	289	52	0.000/0.000/0.000	1.92×10^{-6} (4.12×10^{-5})	1.15×10^{-9} (6.67×10^{-8})
GO:0009451	RNA modification	126	3	0.000/0.000/0.000	1.000 (1.000)	0.842 (1.000)
GO:0009607	response to biotic stimulus	37	2	0.000/0.000/0.000	0.874 (1.000)	0.920 (1.000)
GO:0009628	response to abiotic stimulus	328	66	0.000/0.000/0.000	5.87×10^{-10} (2.02×10^{-8})	1.25×10^{-10} (9.13×10^{-9})
GO:0009653	anatomical structure morphogenesis	329	23	0.000/0.000/0.000	0.953 (1.000)	0.779 (1.000)
GO:0009889	regulation of biosynthetic process	847	41	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0009890	negative regulation of biosynthetic process	237	8	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0009891	positive regulation of biosynthetic process	180	7	0.000/0.000/0.000	0.999 (1.000)	0.998 (1.000)
GO:0009892	negative regulation of metabolic process	283	10	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0009893	positive regulation of metabolic process	197	7	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0009894	regulation of catabolic process	60	9	0.000/0.000/0.000	0.105 (0.339)	0.079 (0.420)
GO:0009966	regulation of signal transduction	121	1	0.000/0.000/0.000	1.000 (1.000)	0.998 (1.000)
GO:0009987	cellular process	4323	373	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0010033	response to organic substance	146	9	0.000/0.000/0.000	0.940 (1.000)	0.997 (1.000)
GO:0010035	response to inorganic substance	30	4	0.000/0.000/0.000	0.308 (0.655)	0.458 (0.967)
GO:0010038	response to metal ion	20	4	0.000/0.000/0.001	0.111 (0.358)	0.177 (0.654)
GO:0010324	membrane invagination	136	5	0.000/0.000/0.000	0.997 (1.000)	0.853 (1.000)
GO:0010458	exit from mitosis	28	1	0.000/0.000/0.000	0.937 (1.000)	0.397 (0.938)
GO:0010467	gene expression	1750	114	0.000/0.000/0.000	1.000 (1.000)	0.756 (1.000)
GO:0010468	regulation of gene expression	815	38	0.000/0.000/0.000	1.000 (1.000)	0.999 (1.000)
GO:0010498	proteasomal protein catabolic process	79	2	0.000/0.000/0.000	0.996 (1.000)	0.630 (1.000)
GO:0010551	regulation of gene-specific transcription from RNA polymerase II promoter	25	1	0.000/0.000/0.000	0.915 (1.000)	0.788 (1.000)
GO:0010556	regulation of macromolecule biosynthetic process	830	39	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0010557	positive regulation of macromolecule biosynthetic process	176	6	0.000/0.000/0.000	0.999 (1.000)	0.994 (1.000)
GO:0010558	negative regulation of macromolecule biosynthetic process	224	6	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)

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Table 1 – Continued

GO ID	Name	Pop	Study	MGSA	TfT	PCu
GO:0010564	regulation of cell cycle process	90	3	0.000/0.000/0.000	0.993 (1.000)	0.216 (0.723)
GO:0010604	positive regulation of macromolecule metabolic process	192	6	0.000/0.000/0.000	1.000 (1.000)	0.992 (1.000)
GO:0010605	negative regulation of macromolecule metabolic process	266	6	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0010608	posttranscriptional regulation of gene expression	195	16	0.000/0.000/0.000	0.752 (1.000)	0.009 (0.095)
GO:0010628	positive regulation of gene expression	159	6	0.000/0.000/0.000	0.998 (1.000)	0.957 (1.000)
GO:0010629	negative regulation of gene expression	201	6	0.000/0.000/0.000	1.000 (1.000)	0.992 (1.000)
GO:0010639	negative regulation of organelle organization	45	2	0.000/0.000/0.000	0.933 (1.000)	0.466 (0.969)
GO:0010646	regulation of cell communication	122	1	0.000/0.000/0.000	1.000 (1.000)	0.999 (1.000)
GO:0010876	lipid localization	42	2	0.000/0.000/0.000	0.915 (1.000)	0.415 (0.950)
GO:0010926	anatomical structure formation	617	36	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0010948	negative regulation of cell cycle process	37	1	0.000/0.000/0.000	0.974 (1.000)	0.595 (1.000)
GO:0015031	protein transport	492	16	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0015672	monovalent inorganic cation transport	46	17	0.000/0.000/0.001	3.37×10^{-7} (8.10×10^{-6})	0.013 (0.124)
GO:0015837	amine transport	53	6	0.000/0.000/0.000	0.378 (0.747)	0.399 (0.938)
GO:0015849	organic acid transport	78	14	0.000/0.000/0.000	0.012 (0.082)	0.013 (0.124)
GO:0015931	nucleobase, nucleoside, nucleotide and nucleic acid transport	136	5	0.000/0.000/0.000	0.997 (1.000)	0.998 (1.000)
GO:0015992	proton transport	33	14	0.000/0.000/0.001	5.16×10^{-7} (1.17×10^{-5})	0.189 (0.671)
GO:0016042	lipid catabolic process	38	7	0.000/0.000/0.000	0.060 (0.275)	0.161 (0.631)
GO:0016043	cellular component organization	1652	68	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0016044	membrane organization	260	12	0.000/0.000/0.000	0.999 (1.000)	0.996 (1.000)
GO:0016050	vesicle organization	67	2	0.000/0.000/0.000	0.989 (1.000)	0.686 (1.000)
GO:0016070	RNA metabolic process	1126	37	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0016071	mRNA metabolic process	259	9	0.000/0.000/0.000	1.000 (1.000)	0.488 (0.973)
GO:0016072	rRNA metabolic process	258	9	0.000/0.000/0.000	1.000 (1.000)	0.479 (0.973)
GO:0016073	snRNA metabolic process	30	2	0.000/0.000/0.000	0.787 (1.000)	0.253 (0.767)
GO:0016125	sterol metabolic process	47	3	0.000/0.000/0.000	0.831 (1.000)	0.998 (1.000)
GO:0016192	vesicle-mediated transport	370	6	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0016237	microautophagy	41	2	0.000/0.000/0.000	0.908 (1.000)	0.823 (1.000)
GO:0016310	phosphorylation	227	40	0.000/0.000/0.000	5.16×10^{-5} ()	0.169 (0.646)
GO:0016311	dephosphorylation	53	2	0.000/0.000/0.000	0.965 (1.000)	1.000 (1.000)
GO:0016458	gene silencing	112	1	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0016481	negative regulation of transcription	200	6	0.000/0.000/0.000	1.000 (1.000)	0.856 (1.000)
GO:0016485	protein processing	39	3	0.000/0.000/0.000	0.722 (1.000)	0.857 (1.000)
GO:0016558	protein import into peroxisome matrix	20	2	0.000/0.000/0.000	0.572 (0.983)	0.109 (0.519)
GO:0016567	protein ubiquitination	84	3	0.000/0.000/0.000	0.988 (1.000)	0.432 (0.963)
GO:0016568	chromatin modification	195	3	0.000/0.000/0.000	1.000 (1.000)	0.894 (1.000)
GO:0016569	covalent chromatin modification	100	3	0.000/0.000/0.000	0.997 (1.000)	0.133 (0.572)
GO:0016570	histone modification	100	3	0.000/0.000/0.000	0.997 (1.000)	0.563 (1.000)
GO:0016571	histone methylation	23	1	0.000/0.000/0.000	0.897 (1.000)	0.502 (0.973)
GO:0016573	histone acetylation	43	2	0.000/0.000/0.000	0.922 (1.000)	0.348 (0.893)
GO:0016579	protein deubiquitination	21	1	0.000/0.000/0.000	0.874 (1.000)	0.459 (0.967)
GO:0017038	protein import	131	4	0.000/0.000/0.000	0.999 (1.000)	0.655 (1.000)
GO:0018193	peptidyl-amino acid modification	105	6	0.000/0.000/0.000	0.938 (1.000)	0.134 (0.572)
GO:0019219	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	676	26	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0019220	regulation of phosphate metabolic process	47	2	0.000/0.000/0.000	0.943 (1.000)	0.999 (1.000)
GO:0019222	regulation of metabolic process	1015	53	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0019236	response to pheromone	90	4	0.000/0.000/0.000	0.975 (1.000)	0.924 (1.000)

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Table 1 – Continued

GO ID	Name	Pop	Study	MGSA	TfT	PCu
GO:0019362	pyridine nucleotide metabolic process	49	13	0.000/0.000/0.001	(0.005)	0.373 (0.917)
GO:0019363	pyridine nucleotide biosynthetic process	17	2	0.000/0.000/0.001	0.483 (0.878)	0.731 (1.000)
GO:0019438	aromatic compound biosynthetic process	18	1	0.000/0.000/0.000	0.830 (1.000)	0.819 (1.000)
GO:0019538	protein metabolic process	1684	136	0.000/0.000/0.000	0.989 (1.000)	0.974 (1.000)
GO:0019637	organophosphate metabolic process	116	11	0.000/0.000/0.000	0.531 (0.931)	0.570 (1.000)
GO:0019725	cellular homeostasis	148	17	0.000/0.000/0.000	0.221 (0.558)	0.134 (0.572)
GO:0019748	secondary metabolic process	56	13	0.000/0.000/0.000	0.002 (0.014)	0.002 (0.033)
GO:0019752	carboxylic acid metabolic process	372	81	0.000/0.000/0.000	4.93×10^{-14} (2.47×10^{-12})	1.000 (1.000)
GO:0019932	second-messenger-mediated signaling	26	1	0.000/0.000/0.000	0.923 (1.000)	0.562 (1.000)
GO:0019941	modification-dependent protein catabolic process	236	6	0.000/0.000/0.000	1.000 (1.000)	0.519 (0.980)
GO:0019953	sexual reproduction	235	14	0.000/0.000/0.000	0.980 (1.000)	0.006 (0.068)
GO:0019954	asexual reproduction	85	1	0.000/0.000/0.000	1.000 (1.000)	0.984 (1.000)
GO:0022402	cell cycle process	516	9	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0022403	cell cycle phase	418	9	0.000/0.000/0.000	1.000 (1.000)	0.148 (0.603)
GO:0022411	cellular component disassembly	94	2	0.000/0.000/0.000	0.999 (1.000)	0.910 (1.000)
GO:0022413	reproductive process in single-celled organism	143	9	0.000/0.000/0.000	0.930 (1.000)	0.261 (0.784)
GO:0022414	reproductive process	149	9	0.000/0.000/0.000	0.948 (1.000)	0.948 (1.000)
GO:0022607	cellular component assembly	480	20	0.000/0.000/0.000	1.000 (1.000)	0.691 (1.000)
GO:0022613	ribonucleoprotein complex biogenesis	406	10	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0022618	ribonucleoprotein complex assembly	117	1	0.000/0.000/0.000	1.000 (1.000)	0.977 (1.000)
GO:0030003	cellular cation homeostasis	102	10	0.000/0.000/0.000	0.490 (0.882)	0.484 (0.973)
GO:0030010	establishment of cell polarity	99	1	0.000/0.000/0.000	1.000 (1.000)	0.861 (1.000)
GO:0030029	actin filament-based process	110	1	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0030036	actin cytoskeleton organization	104	1	0.000/0.000/0.000	1.000 (1.000)	0.458 (0.967)
GO:0030071	regulation of mitotic metaphase/anaphase transition	26	1	0.000/0.000/0.000	0.923 (1.000)	0.667 (1.000)
GO:0030148	sphingolipid biosynthetic process	20	1	0.000/0.000/0.001	0.861 (1.000)	0.606 (1.000)
GO:0030154	cell differentiation	209	20	0.000/0.000/0.000	0.497 (0.882)	0.004 (0.054)
GO:0030163	protein catabolic process	428	41	0.000/0.000/0.000	0.466 (0.851)	0.080 (0.421)
GO:0030384	phosphoinositide metabolic process	49	1	0.000/0.000/0.000	0.992 (1.000)	0.994 (1.000)
GO:0030435	sporulation resulting in formation of a cellular spore	190	20	0.000/0.000/0.000	0.325 (0.655)	0.135 (0.572)
GO:0030437	ascospore formation	88	9	0.000/0.000/0.000	0.444 (0.821)	0.011 (0.109)
GO:0030447	filamentous growth	105	5	0.000/0.000/0.000	0.974 (1.000)	0.216 (0.723)
GO:0030490	maturation of SSU-rRNA	90	3	0.000/0.000/0.000	0.993 (1.000)	0.693 (1.000)
GO:0031123	RNA 3'-end processing	75	2	0.000/0.000/0.000	0.995 (1.000)	0.496 (0.973)
GO:0031124	mRNA 3'-end processing	41	1	0.000/0.000/0.000	0.983 (1.000)	0.634 (1.000)
GO:0031125	rRNA 3'-end processing	22	1	0.000/0.000/0.000	0.886 (1.000)	0.558 (1.000)
GO:0031137	regulation of conjugation with cellular fusion	30	1	0.000/0.000/0.000	0.948 (1.000)	0.636 (1.000)
GO:0031323	regulation of cellular metabolic process	952	51	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0031324	negative regulation of cellular metabolic process	257	10	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0031325	positive regulation of cellular metabolic process	196	7	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0031326	regulation of cellular biosynthetic process	843	41	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0031327	negative regulation of cellular biosynthetic process	235	8	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0031328	positive regulation of cellular biosynthetic process	180	7	0.000/0.000/0.000	0.999 (1.000)	0.998 (1.000)

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Table 1 – Continued

GO ID	Name	Pop	Study	MGSA	TfT	PCu
GO:0031329	regulation of cellular catabolic process	38	6	0.000/0.000/0.000	0.140 (0.423)	0.115 (0.531)
GO:0031497	chromatin assembly	49	1	0.000/0.000/0.000	0.992 (1.000)	0.876 (1.000)
GO:0031505	fungal-type cell wall organization	21	1	0.000/0.000/0.000	0.874 (1.000)	0.854 (1.000)
GO:0031577	spindle checkpoint	27	1	0.000/0.000/0.000	0.930 (1.000)	0.458 (0.967)
GO:0032005	signal transduction involved in conjugation with cellular fusion	26	1	0.000/0.000/0.000	0.923 (1.000)	0.669 (1.000)
GO:0032259	methylation	64	3	0.000/0.000/0.000	0.947 (1.000)	0.731 (1.000)
GO:0032268	regulation of cellular protein metabolic process	216	17	0.000/0.000/0.000	0.813 (1.000)	0.401 (0.940)
GO:0032269	negative regulation of cellular protein metabolic process	23	1	0.000/0.000/0.000	0.897 (1.000)	0.842 (1.000)
GO:0032446	protein modification by small protein conjugation	106	3	0.000/0.000/0.000	0.998 (1.000)	0.503 (0.974)
GO:0032502	developmental process	410	30	0.000/0.000/0.000	0.946 (1.000)	0.946 (1.000)
GO:0032505	reproduction of a single-celled organism	188	10	0.000/0.000/0.000	0.986 (1.000)	0.177 (0.654)
GO:0032506	cytokinetic process	92	1	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0032535	regulation of cellular component size	118	1	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0032569	gene-specific transcription from RNA polymerase II promoter	31	1	0.000/0.000/0.000	0.953 (1.000)	0.752 (1.000)
GO:0032583	regulation of gene-specific transcription	31	1	0.000/0.000/0.000	0.953 (1.000)	0.788 (1.000)
GO:0032774	RNA biosynthetic process	576	21	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0032879	regulation of localization	135	6	0.000/0.000/0.000	0.990 (1.000)	0.949 (1.000)
GO:0032984	macromolecular complex disassembly	91	2	0.000/0.000/0.000	0.999 (1.000)	0.855 (1.000)
GO:0032989	cellular component morphogenesis	157	4	0.000/0.000/0.000	1.000 (1.000)	0.939 (1.000)
GO:0033036	macromolecule localization	690	23	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0033043	regulation of organelle organization	106	2	0.000/0.000/0.000	1.000 (1.000)	0.975 (1.000)
GO:0033044	regulation of chromosome organization	31	1	0.000/0.000/0.000	0.953 (1.000)	0.447 (0.967)
GO:0033205	cytokinesis during cell cycle	71	1	0.000/0.000/0.000	0.999 (1.000)	0.716 (1.000)
GO:0033365	protein localization in organelle	151	5	0.000/0.000/0.000	0.999 (1.000)	0.622 (1.000)
GO:0033554	cellular response to stress	511	57	0.000/0.000/0.000	0.087 (0.319)	0.589 (1.000)
GO:0034293	sexual sporulation	88	9	0.000/0.000/0.000	0.444 (0.821)	0.110 (0.521)
GO:0034470	ncRNA processing	343	10	0.000/0.000/0.000	1.000 (1.000)	0.076 (0.410)
GO:0034504	protein localization in nucleus	62	1	0.000/0.000/0.000	0.998 (1.000)	0.932 (1.000)
GO:0034613	cellular protein localization	359	12	0.000/0.000/0.000	1.000 (1.000)	0.366 (0.915)
GO:0034621	cellular macromolecular complex subunit organization	438	10	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0034622	cellular macromolecular complex assembly	313	8	0.000/0.000/0.000	1.000 (1.000)	0.958 (1.000)
GO:0034623	cellular macromolecular complex disassembly	91	2	0.000/0.000/0.000	0.999 (1.000)	0.650 (1.000)
GO:0034641	cellular nitrogen compound metabolic process	271	58	0.000/0.000/0.000	6.20×10^{-10} (2.07×10^{-8})	3.68×10^{-10} (2.26×10^{-8})
GO:0034645	cellular macromolecule biosynthetic process	1595	119	0.000/0.000/0.000	0.999 (1.000)	0.707 (1.000)
GO:0034660	ncRNA metabolic process	401	13	0.000/0.000/0.000	1.000 (1.000)	0.587 (1.000)
GO:0034727	piecemeal microautophagy of nucleus	33	2	0.000/0.000/0.000	0.829 (1.000)	0.558 (1.000)
GO:0034728	nucleosome organization	60	1	0.000/0.000/0.000	0.997 (1.000)	0.756 (1.000)
GO:0034960	cellular biopolymer metabolic process	2661	170	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0034961	cellular biopolymer biosynthetic process	1482	114	0.000/0.000/0.000	0.997 (1.000)	0.002 (0.027)
GO:0034962	cellular biopolymer catabolic process	462	38	0.000/0.000/0.000	0.834 (1.000)	0.103 (0.508)

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Table 1 – Continued

GO ID	Name	Pop	Study	MGSA	TfT	PCu
GO:0034984	cellular response to DNA damage stimulus	251	1	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0040007	growth	142	5	0.000/0.000/0.000	0.998 (1.000)	0.998 (1.000)
GO:0040020	regulation of meiosis	23	1	0.000/0.000/0.000	0.897 (1.000)	0.633 (1.000)
GO:0040029	regulation of gene expression, epigenetic	109	1	0.000/0.000/0.000	1.000 (1.000)	0.996 (1.000)
GO:0042144	vacuole fusion, non-autophagic	28	2	0.000/0.000/0.000	0.753 (1.000)	0.393 (0.936)
GO:0042157	lipoprotein metabolic process	54	3	0.000/0.000/0.000	0.894 (1.000)	0.715 (1.000)
GO:0042158	lipoprotein biosynthetic process	53	2	0.000/0.000/0.000	0.965 (1.000)	0.919 (1.000)
GO:0042176	regulation of protein catabolic process	26	3	0.000/0.000/0.000	0.446 (0.821)	0.409 (0.950)
GO:0042180	cellular ketone metabolic process	383	81	0.000/0.000/0.000	2.71×10^{-13} (1.08×10^{-11})	6.46×10^{-14} (6.84×10^{-12})
GO:0042221	response to chemical stimulus	428	49	0.000/0.000/0.000	0.076 (0.314)	0.280 (0.809)
GO:0042254	ribosome biogenesis	363	10	0.000/0.000/0.000	1.000 (1.000)	0.322 (0.872)
GO:0042255	ribosome assembly	72	1	0.000/0.000/0.000	0.999 (1.000)	0.861 (1.000)
GO:0042257	ribosomal subunit assembly	58	1	0.000/0.000/0.000	0.997 (1.000)	0.806 (1.000)
GO:0042273	ribosomal large subunit biogenesis	75	1	0.000/0.000/0.000	0.999 (1.000)	0.874 (1.000)
GO:0042274	ribosomal small subunit biogenesis	53	1	0.000/0.000/0.000	0.995 (1.000)	0.757 (1.000)
GO:0042325	regulation of phosphorylation	41	1	0.000/0.000/0.000	0.983 (1.000)	1.000 (1.000)
GO:0042364	water-soluble vitamin biosynthetic process	49	3	0.000/0.000/0.000	0.851 (1.000)	1.000 (1.000)
GO:0042398	cellular amino acid derivative biosynthetic process	26	1	0.000/0.000/0.000	0.923 (1.000)	0.919 (1.000)
GO:0042493	response to drug	116	11	0.000/0.000/0.000	0.531 (0.931)	0.828 (1.000)
GO:0042546	cell wall biogenesis	68	7	0.000/0.000/0.000	0.457 (0.838)	0.031 (0.227)
GO:0042592	homeostatic process	192	17	0.000/0.000/0.000	0.637 (1.000)	0.024 (0.189)
GO:0042787	protein ubiquitination during ubiquitin-dependent protein catabolic process	19	1	0.000/0.000/0.000	0.846 (1.000)	0.355 (0.902)
GO:0043038	amino acid activation	41	1	0.000/0.000/0.000	0.983 (1.000)	1.000 (1.000)
GO:0043039	tRNA aminoacylation	41	1	0.000/0.000/0.000	0.983 (1.000)	0.573 (1.000)
GO:0043094	cellular metabolic compound salvage	61	2	0.000/0.000/0.000	0.982 (1.000)	0.983 (1.000)
GO:0043161	proteasomal ubiquitin-dependent protein catabolic process	79	2	0.000/0.000/0.000	0.996 (1.000)	0.391 (0.934)
GO:0043170	macromolecule metabolic process	2790	188	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0043241	protein complex disassembly	68	2	0.000/0.000/0.000	0.990 (1.000)	0.556 (1.000)
GO:0043254	regulation of protein complex assembly	19	1	0.000/0.000/0.000	0.846 (1.000)	0.678 (1.000)
GO:0043283	biopolymer metabolic process	2749	178	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0043284	biopolymer biosynthetic process	1483	114	0.000/0.000/0.000	0.997 (1.000)	0.003 (0.043)
GO:0043285	biopolymer catabolic process	554	47	0.000/0.000/0.000	0.797 (1.000)	0.046 (0.303)
GO:0043412	biopolymer modification	716	24	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0043413	biopolymer glycosylation	69	3	0.000/0.000/0.000	0.964 (1.000)	0.412 (0.950)
GO:0043414	biopolymer methylation	63	3	0.000/0.000/0.000	0.943 (1.000)	0.778 (1.000)
GO:0043436	oxoacid metabolic process	372	81	0.000/0.000/0.000	4.93×10^{-14} (2.47×10^{-12})	0.106 (0.517)
GO:0043543	protein amino acid acylation	67	3	0.000/0.000/0.000	0.958 (1.000)	0.410 (0.950)
GO:0043549	regulation of kinase activity	34	1	0.000/0.000/0.000	0.965 (1.000)	0.791 (1.000)
GO:0043574	peroxisomal transport	22	2	0.000/0.000/0.000	0.625 (1.000)	0.176 (0.654)
GO:0043603	cellular amide metabolic process	62	13	0.000/0.000/0.000	0.004 (0.032)	0.600 (1.000)
GO:0043623	cellular protein complex assembly	129	6	0.000/0.000/0.000	0.986 (1.000)	0.443 (0.967)
GO:0043624	cellular protein complex disassembly	68	2	0.000/0.000/0.000	0.990 (1.000)	0.556 (1.000)
GO:0043628	ncRNA 3’-end processing	36	1	0.000/0.000/0.000	0.971 (1.000)	0.673 (1.000)

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Table 1 – Continued

GO ID	Name	Pop	Study	MGSA	TfT	PCu
GO:0043632	modification-dependent macromolecule catabolic process	254	6	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0043687	post-translational protein modification	426	12	0.000/0.000/0.000	1.000 (1.000)	0.932 (1.000)
GO:0043900	regulation of multi-organism process	30	1	0.000/0.000/0.000	0.948 (1.000)	0.812 (1.000)
GO:0043933	macromolecular complex subunit organization	488	17	0.000/0.000/0.000	1.000 (1.000)	0.835 (1.000)
GO:0043934	sporulation	190	20	0.000/0.000/0.000	0.325 (0.655)	0.016 (0.147)
GO:0043935	sexual sporulation resulting in formation of a cellular spore	88	9	0.000/0.000/0.000	0.444 (0.821)	0.639 (1.000)
GO:0044085	cellular component biogenesis	796	31	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0044087	regulation of cellular component biogenesis	43	1	0.000/0.000/0.000	0.986 (1.000)	0.903 (1.000)
GO:0044106	cellular amine metabolic process	235	43	0.000/0.000/0.000	1.02×10^{-5} ()	0.477 (0.973)
GO:0044182	filamentous growth of a population of unicellular organisms	79	3	0.000/0.000/0.000	0.983 (1.000)	0.904 (1.000)
GO:0044237	cellular metabolic process	3405	320	0.000/0.000/0.000	0.489 (0.882)	0.004 (0.049)
GO:0044238	primary metabolic process	3281	295	0.000/0.000/0.000	0.900 (1.000)	1.000 (1.000)
GO:0044242	cellular lipid catabolic process	25	6	0.000/0.000/0.000	0.025 (0.137)	0.069 (0.384)
GO:0044248	cellular catabolic process	746	98	0.000/0.000/0.000	(0.002)	8.75×10^{-5} (0.003)
GO:0044249	cellular biosynthetic process	1999	177	0.000/0.000/0.000	0.856 (1.000)	0.904 (1.000)
GO:0044255	cellular lipid metabolic process	269	26	0.000/0.000/0.000	0.465 (0.851)	0.468 (0.970)
GO:0044257	cellular protein catabolic process	339	32	0.000/0.000/0.000	0.512 (0.905)	0.152 (0.612)
GO:0044260	cellular macromolecule metabolic process	2695	181	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0044262	cellular carbohydrate metabolic process	286	60	0.000/0.000/0.000	7.04×10^{-10} (2.29×10^{-8})	3.64×10^{-10} (2.26×10^{-8})
GO:0044265	cellular macromolecule catabolic process	511	50	0.000/0.000/0.000	0.393 (0.752)	0.043 (0.287)
GO:0044267	cellular protein metabolic process	1588	129	0.000/0.000/0.000	0.983 (1.000)	1.41×10^{-5} ()
GO:0044271	nitrogen compound biosynthetic process	183	34	0.000/0.000/0.000	6.43×10^{-5} ()	4.19×10^{-5} (0.001)
GO:0045017	glycerolipid biosynthetic process	53	3	0.000/0.000/0.000	0.886 (1.000)	0.861 (1.000)
GO:0045047	protein targeting to ER	27	4	0.000/0.000/0.000	0.243 (0.594)	0.025 (0.196)
GO:0045132	meiotic chromosome segregation	23	1	0.000/0.000/0.000	0.897 (1.000)	0.505 (0.974)
GO:0045184	establishment of protein localization	530	18	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0045229	external encapsulating structure organization	216	18	0.000/0.000/0.000	0.738 (1.000)	0.599 (1.000)
GO:0045449	regulation of transcription	624	23	0.000/0.000/0.000	1.000 (1.000)	0.995 (1.000)
GO:0045786	negative regulation of cell cycle	22	1	0.000/0.000/0.000	0.886 (1.000)	0.412 (0.950)
GO:0045814	negative regulation of gene expression, epigenetic	108	1	0.000/0.000/0.000	1.000 (1.000)	0.991 (1.000)
GO:0045839	negative regulation of mitosis	20	1	0.000/0.000/0.000	0.861 (1.000)	0.190 (0.671)
GO:0045841	negative regulation of mitotic metaphase/anaphase transition	20	1	0.000/0.000/0.000	0.861 (1.000)	0.606 (1.000)
GO:0045859	regulation of protein kinase activity	33	1	0.000/0.000/0.000	0.962 (1.000)	0.971 (1.000)
GO:0045892	negative regulation of transcription, DNA-dependent	180	6	0.000/0.000/0.000	1.000 (1.000)	0.660 (1.000)
GO:0045893	positive regulation of transcription, DNA-dependent	123	6	0.000/0.000/0.000	0.979 (1.000)	0.263 (0.786)
GO:0045934	negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	224	8	0.000/0.000/0.000	1.000 (1.000)	0.979 (1.000)

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Table 1 – Continued

GO ID	Name	Pop	Study	MGSA	TfT	PCu
GO:0045935	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	167	6	0.000/0.000/0.000	0.999 (1.000)	0.957 (1.000)
GO:0045941	positive regulation of transcription	158	6	0.000/0.000/0.000	0.998 (1.000)	0.500 (0.973)
GO:0045944	positive regulation of transcription from RNA polymerase II promoter	87	5	0.000/0.000/0.000	0.921 (1.000)	0.278 (0.806)
GO:0046034	ATP metabolic process	40	14	0.000/0.000/0.000	7.88×10^{-6} ()	0.659 (1.000)
GO:0046467	membrane lipid biosynthetic process	20	1	0.000/0.000/0.001	0.861 (1.000)	0.843 (1.000)
GO:0046474	glycerophospholipid biosynthetic process	51	3	0.000/0.000/0.000	0.870 (1.000)	0.897 (1.000)
GO:0046483	heterocycle metabolic process	219	34	0.000/0.000/0.000	0.002 (0.018)	0.002 (0.031)
GO:0046486	glycerolipid metabolic process	83	5	0.000/0.000/0.000	0.900 (1.000)	0.947 (1.000)
GO:0046489	phosphoinositide biosynthetic process	32	1	0.000/0.000/0.000	0.958 (1.000)	0.858 (1.000)
GO:0046578	regulation of Ras protein signal transduction	35	1	0.000/0.000/0.000	0.968 (1.000)	0.891 (1.000)
GO:0046700	heterocycle catabolic process	30	6	0.000/0.000/0.001	0.056 (0.262)	0.210 (0.723)
GO:0046907	intracellular transport	602	21	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0046942	carboxylic acid transport	65	11	0.000/0.000/0.000	0.037 (0.194)	0.825 (1.000)
GO:0046999	regulation of conjugation	30	1	0.000/0.000/0.000	0.948 (1.000)	0.726 (1.000)
GO:0048193	Golgi vesicle transport	180	1	0.000/0.000/0.000	1.000 (1.000)	0.999 (1.000)
GO:0048284	organelle fusion	66	1	0.000/0.000/0.000	0.999 (1.000)	0.908 (1.000)
GO:0048285	organelle fission	205	4	0.000/0.000/0.000	1.000 (1.000)	0.944 (1.000)
GO:0048308	organelle inheritance	63	1	0.000/0.000/0.000	0.998 (1.000)	0.897 (1.000)
GO:0048311	mitochondrion distribution	29	1	0.000/0.000/0.000	0.943 (1.000)	0.887 (1.000)
GO:0048468	cell development	88	9	0.000/0.000/0.000	0.444 (0.821)	0.096 (0.485)
GO:0048518	positive regulation of biological process	224	9	0.000/0.000/0.000	0.999 (1.000)	0.999 (1.000)
GO:0048519	negative regulation of biological process	386	10	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0048522	positive regulation of cellular process	214	9	0.000/0.000/0.000	0.999 (1.000)	0.997 (1.000)
GO:0048523	negative regulation of cellular process	351	10	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0048610	reproductive cellular process	143	9	0.000/0.000/0.000	0.930 (1.000)	0.881 (1.000)
GO:0048646	anatomical structure formation involved in morphogenesis	190	20	0.000/0.000/0.000	0.325 (0.655)	0.001 (0.021)
GO:0048856	anatomical structure development	329	23	0.000/0.000/0.000	0.953 (1.000)	0.779 (1.000)
GO:0048869	cellular developmental process	347	23	0.000/0.000/0.000	0.976 (1.000)	0.935 (1.000)
GO:0048878	chemical homeostasis	153	11	0.000/0.000/0.000	0.862 (1.000)	0.966 (1.000)
GO:0050657	nucleic acid transport	115	3	0.000/0.000/0.000	0.999 (1.000)	0.974 (1.000)
GO:0050658	RNA transport	115	3	0.000/0.000/0.000	0.999 (1.000)	1.000 (1.000)
GO:0050789	regulation of biological process	1476	80	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0050790	regulation of catalytic activity	106	7	0.000/0.000/0.000	0.881 (1.000)	0.960 (1.000)
GO:0050793	regulation of developmental process	24	3	0.000/0.000/0.000	0.394 (0.752)	0.155 (0.619)
GO:0050794	regulation of cellular process	1355	73	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0050801	ion homeostasis	152	11	0.000/0.000/0.000	0.857 (1.000)	0.928 (1.000)
GO:0050896	response to stimulus	1050	112	0.000/0.000/0.000	0.062 (0.285)	0.062 (0.367)
GO:0051028	mRNA transport	84	1	0.000/0.000/0.000	1.000 (1.000)	0.982 (1.000)
GO:0051031	tRNA transport	35	2	0.000/0.000/0.000	0.853 (1.000)	0.219 (0.723)
GO:0051049	regulation of transport	126	6	0.000/0.000/0.000	0.983 (1.000)	0.988 (1.000)
GO:0051052	regulation of DNA metabolic process	60	1	0.000/0.000/0.000	0.997 (1.000)	0.951 (1.000)
GO:0051056	regulation of small GTPase mediated signal transduction	41	1	0.000/0.000/0.000	0.983 (1.000)	0.665 (1.000)

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Table 1 – Continued

GO ID	Name	Pop	Study	MGSA	TfT	PCu
GO:0051128	regulation of cellular component organization	168	6	0.000/0.000/0.000	0.999 (1.000)	0.893 (1.000)
GO:0051129	negative regulation of cellular component organization	66	2	0.000/0.000/0.000	0.989 (1.000)	0.767 (1.000)
GO:0051168	nuclear export	127	3	0.000/0.000/0.000	1.000 (1.000)	0.962 (1.000)
GO:0051169	nuclear transport	154	5	0.000/0.000/0.000	0.999 (1.000)	0.659 (1.000)
GO:0051170	nuclear import	60	1	0.000/0.000/0.000	0.997 (1.000)	0.919 (1.000)
GO:0051171	regulation of nitrogen compound metabolic process	681	26	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0051172	negative regulation of nitrogen compound metabolic process	224	8	0.000/0.000/0.000	1.000 (1.000)	0.998 (1.000)
GO:0051173	positive regulation of nitrogen compound metabolic process	167	6	0.000/0.000/0.000	0.999 (1.000)	0.995 (1.000)
GO:0051174	regulation of phosphorus metabolic process	47	2	0.000/0.000/0.000	0.943 (1.000)	0.921 (1.000)
GO:0051179	localization	1352	122	0.000/0.000/0.000	0.713 (1.000)	0.713 (1.000)
GO:0051181	cofactor transport	49	1	0.000/0.000/0.000	0.992 (1.000)	0.994 (1.000)
GO:0051186	cofactor metabolic process	194	55	0.000/0.000/0.000	9.59×10^{-15} (6.06×10^{-13})	4.24×10^{-15} (6.17×10^{-13})
GO:0051188	cofactor biosynthetic process	103	7	0.000/0.000/0.000	0.862 (1.000)	0.917 (1.000)
GO:0051234	establishment of localization	1277	120	0.000/0.000/0.000	0.506 (0.895)	0.506 (0.974)
GO:0051236	establishment of RNA localization	115	3	0.000/0.000/0.000	0.999 (1.000)	0.999 (1.000)
GO:0051246	regulation of protein metabolic process	272	20	0.000/0.000/0.000	0.903 (1.000)	0.557 (1.000)
GO:0051248	negative regulation of protein metabolic process	46	1	0.000/0.000/0.000	0.989 (1.000)	0.975 (1.000)
GO:0051252	regulation of RNA metabolic process	433	20	0.000/0.000/0.000	1.000 (1.000)	0.433 (0.963)
GO:0051253	negative regulation of RNA metabolic process	181	6	0.000/0.000/0.000	1.000 (1.000)	0.546 (1.000)
GO:0051254	positive regulation of RNA metabolic process	127	6	0.000/0.000/0.000	0.984 (1.000)	0.211 (0.723)
GO:0051276	chromosome organization	379	7	0.000/0.000/0.000	1.000 (1.000)	0.992 (1.000)
GO:0051301	cell division	307	4	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0051321	meiotic cell cycle	171	8	0.000/0.000/0.000	0.993 (1.000)	0.002 (0.034)
GO:0051327	M phase of meiotic cell cycle	166	8	0.000/0.000/0.000	0.991 (1.000)	0.013 (0.129)
GO:0051336	regulation of hydrolase activity	35	4	0.000/0.000/0.000	0.419 (0.789)	0.161 (0.631)
GO:0051338	regulation of transferase activity	36	1	0.000/0.000/0.000	0.971 (1.000)	0.951 (1.000)
GO:0051445	regulation of meiotic cell cycle	24	1	0.000/0.000/0.000	0.906 (1.000)	0.584 (1.000)
GO:0051603	proteolysis involved in cellular protein catabolic process	245	6	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0051604	protein maturation	41	3	0.000/0.000/0.000	0.753 (1.000)	0.512 (0.976)
GO:0051640	organelle localization	112	1	0.000/0.000/0.000	1.000 (1.000)	0.979 (1.000)
GO:0051641	cellular localization	733	23	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0051646	mitochondrion localization	32	1	0.000/0.000/0.000	0.958 (1.000)	0.286 (0.813)
GO:0051649	establishment of localization in cell	650	21	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0051704	multi-organism process	128	4	0.000/0.000/0.000	0.999 (1.000)	0.999 (1.000)
GO:0051716	cellular response to stimulus	541	61	0.000/0.000/0.000	0.066 (0.302)	0.019 (0.161)
GO:0051726	regulation of cell cycle	166	4	0.000/0.000/0.000	1.000 (1.000)	0.968 (1.000)
GO:0051783	regulation of nuclear division	32	1	0.000/0.000/0.000	0.958 (1.000)	0.338 (0.890)
GO:0051784	negative regulation of nuclear division	20	1	0.000/0.000/0.000	0.861 (1.000)	0.250 (0.766)
GO:0051789	response to protein stimulus	32	2	0.000/0.000/0.000	0.816 (1.000)	0.627 (1.000)
GO:0055080	cation homeostasis	106	10	0.000/0.000/0.000	0.541 (0.939)	0.101 (0.499)
GO:0055082	cellular chemical homeostasis	116	11	0.000/0.000/0.000	0.531 (0.931)	0.541 (1.000)
GO:0055085	transmembrane transport	237	43	0.000/0.000/0.000	1.27×10^{-5} ()	1.32×10^{-6} (5.49×10^{-5})

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Table 1 – Continued

GO ID	Name	Pop	Study	MGSA	TfT	PCu
GO:0055086	nucleobase, nucleoside and nucleotide metabolic process	222	55	0.000/0.000/0.000	4.36×10^{-12} (1.69×10^{-10})	5.54×10^{-24} (2.15×10^{-21})
GO:0060255	regulation of macromolecule metabolic process	942	48	0.000/0.000/0.000	1.000 (1.000)	0.995 (1.000)
GO:0065002	intracellular protein transmembrane transport	91	4	0.000/0.000/0.000	0.977 (1.000)	0.996 (1.000)
GO:0065003	macromolecular complex assembly	366	15	0.000/0.000/0.000	1.000 (1.000)	0.346 (0.893)
GO:0065004	protein-DNA complex assembly	69	1	0.000/0.000/0.000	0.999 (1.000)	0.867 (1.000)
GO:0065007	biological regulation	1669	95	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0065008	regulation of biological quality	369	23	0.000/0.000/0.000	0.990 (1.000)	0.345 (0.893)
GO:0065009	regulation of molecular function	132	11	0.000/0.000/0.000	0.705 (1.000)	0.124 (0.562)
GO:0070085	glycosylation	69	3	0.000/0.000/0.000	0.964 (1.000)	1.000 (1.000)
GO:0070271	protein complex biogenesis	190	13	0.000/0.000/0.000	0.916 (1.000)	0.018 (0.158)
GO:0070585	protein localization in mitochondrion	51	2	0.000/0.000/0.000	0.959 (1.000)	0.550 (1.000)
GO:0070646	protein modification by small protein removal	28	1	0.000/0.000/0.000	0.937 (1.000)	0.511 (0.976)
GO:0070647	protein modification by small protein conjugation or removal	133	3	0.000/0.000/0.000	1.000 (1.000)	0.871 (1.000)
GO:0070727	cellular macromolecule localization	371	12	0.000/0.000/0.000	1.000 (1.000)	0.752 (1.000)
GO:0070783	growth of unicellular organism as a thread of attached cells	79	3	0.000/0.000/0.000	0.983 (1.000)	1.000 (1.000)
GO:0070882	cell wall organization or biogenesis	245	20	0.000/0.000/0.000	0.779 (1.000)	0.640 (1.000)
GO:0070887	cellular response to chemical stimulus	54	6	0.000/0.000/0.000	0.395 (0.754)	0.549 (1.000)
GO:0070972	protein localization in endoplasmic reticulum	27	4	0.000/0.000/0.000	0.243 (0.594)	0.004 (0.048)
GO:0080090	regulation of primary metabolic process	954	51	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)
GO:0090066	regulation of anatomical structure size	118	1	0.000/0.000/0.000	1.000 (1.000)	1.000 (1.000)

Table **S1**: Analysis of expression data from fermentative and respiratory respiration in yeast. A study set consisting of 488 differentially regulated and annotated genes from a population of 5206 annotated yeast genes was analyzed. The columns **GO ID** and **Name** identify the GO term being analyzed. The column **Pop** shows that number of genes in the population annotated to the term, and the column **Study** shows the number of genes in the study set. The column **MGSA** shows the 5th percentile, the median, and the 95th percentile of the posterior probability value for the term in question being active (calculated in 20 independent MCMC runs). The column **TfT** shows the corresponding Term-for-Term (exact Fischer test) P-value (The corresponding False Discovery Rate [FDR] is shown in parentheses). The column **PCu** shows the parent-child-union P-value (the corresponding FDR is shown in parentheses).