

Gene expression changes in experimental evolutionary conditions.

Significant (Wilcoxon rank sum test; $P \leq 0.05$ shown in bold) functional categories involved in excess-nutrient adaptive evolutionary condition.

Bin	Functional annotation	No of Genes	MG/ MGAdp	No of Genes	DH/ DHAdp
1.2	Macromolecule degradation > GO:macromolecule catabolism ; GO:0009057	105	0.045	105	0.312
1.3	Energy metabolism (carbon) > GO:energy derivation by oxidation of organic compounds ; GO:0015980	299	0.012	299	0.920
2.1	DNA related > GO:DNA metabolism ; GO:0006259	163	0.006	163	0.004
4	Transport > GO:transporter activity ; GO:0005215 > GO:transport ; GO:0006810	1215	0.783	1215	0.028
5.1	Cell division > GO:cytokinesis ; GO:0000910	95	0.035	95	0.230
6.6	Ribosome > GO:cytosolic ribosome (sensu Bacteria) ; GO:0009281	68	0.098	68	0.018
8	extrachromosomal > GO:.	300	0.300	300	0.027
8.4	Colicin related > GO:.	9	0.165	9	0.034
1.1.2.2	3-phenylpropionate and 3-(3-hydroxyphenyl)propionate degradation > GO:3-phenylpropionate catabolism ; GO:0019380 > GO:3-(3-hydroxy)phenylpropionate catabolism ; GO:0019622	11	0.049	11	0.000
1.1.3	Amino acids > GO:amino acid catabolism ; GO:0009063	74	0.927	74	0.034
1.1.3.5	Glycine cleavage > GO:glycine decarboxylation via glycine cleavage system ; GO:0019464	7	0.611	7	0.010
1.1.5.2	Ethanol degradation > GO:ethanol catabolism ; GO:0006068	12	0.025	12	0.271
1.2.2	DNA > GO:DNA catabolism ; GO:0006308	26	0.043	26	0.068
1.3.9	Entner-Doudoroff pathway > GO:Entner-Doudoroff pathway ; GO:0009255	4	0.041	4	0.323
1.5.1.11	Serine > GO:serine biosynthesis ; GO:0006564	6	0.025	6	0.080
1.5.1.12	Cysteine > GO:cysteine biosynthesis ; GO:0019344	6	0.049	6	0.927
1.5.1.15	Tryptophan > GO:tryptophan biosynthesis ; GO:0000162	13	0.012	13	0.020
1.5.1.17	Alanine > GO:alanine biosynthesis ; GO:0006523	4	0.038	4	0.770
1.5.1.21	Homoserine > GO:homoserine biosynthesis ; GO:0009090	6	0.752	6	0.010
1.5.1.4	Proline > GO:proline biosynthesis ; GO:0006561	8	0.752	8	0.036
1.5.1.7	Lysine, diaminopimelate > GO:lysine biosynthesis via diaminopimelate ; GO:0009089	16	0.153	16	0.038
1.5.3.14	Enterochelin (enterobactin) > GO:enterobactin biosynthesis ; GO:0009239	6	0.589	6	0.011
1.5.3.4	Molybdenum (molybdopterin) > GO:Mo-molybdopterin cofactor biosynthesis ; GO:0006777	18	0.021	18	0.108
1.5.3.6	Pyridoxine (vitamin B6) > GO:pyridoxine biosynthesis ; GO:0008615	9	0.677	9	0.036
1.5.4	Fatty acid and phosphatidic acid > GO:fatty acid biosynthesis ; GO:0006633 ; GO:phosphatidic acid biosynthesis ; GO:0006654	26	0.005	26	0.215
1.6.12	Flagella > GO:flagella biogenesis ; GO:0009296	37	0.258	37	0.043

1.6.3.2	Core region > GO:lipopolysaccharide core region biosynthesis ; GO:0009244	17	0.952	17	0.029
1.6.6	Osmoregulated periplasmic glucan > GO:glucan biosynthesis ; GO:0009250	2	0.049	2	0.218
1.7.18	Betaine biosynthesis > GO:betaine biosynthesis ; GO:0006578	4	0.302	4	0.011
1.7.3	Pentose phosphate shunt, non-oxidative branch > GO:pentose-phosphate shunt, non-oxidative branch ; GO:0009052	8	0.036	8	0.019
2.1.5	DNA degradation > GO:DNA catabolism ; GO:0006308	27	0.049	27	0.069
2.2.3	RNA modification > GO:RNA modification ; GO:0009451	53	0.028	53	0.029
2.3.2	Translation > GO:protein biosynthesis ; GO:0006412	74	0.121	74	0.024
2.3.6	Turnover, degradation > GO:proteolysis and peptidolysis ; GO:0006508	10	0.527	10	0.002
2.3.8	Ribosomal proteins > GO:structural constituent of ribosome ; GO:0003735	57	0.190	57	0.017
3.1.1	DNA structure level > GO:.	14	0.010	14	0.002
3.1.1.2	Methylation > GO:DNA methylation ; GO:0006306	5	0.022	5	0.083
3.1.3.1	Translation attenuation and efficiency > GO:translational attenuation ; GO:0009386	10	0.024	10	0.101
3.1.3.4	Proteases, cleavage of compounds > GO:peptidase activity ; GO:0008233	9	0.268	9	0.036
4.10.119	methylgalactoside/galactose > GO:galactose transporter activity ; GO:0005354 > GO:galactose transporter activity ; GO:0005354 > GO:methylgalactoside transporter activity ; GO:0015592 > GO:methylgalactoside transport ; GO:0015765	4	0.660	4	0.049
4.10.155	phosphate > GO:phosphate transport ; GO:0006817 > GO:phosphate transporter activity ; GO:0015114	7	0.030	7	0.643
4.10.185	uracil > GO:uracil transport ; GO:0015857 > GO:uracil transporter activity ; GO:0015210	2	0.032	2	0.058
4.10.31	chloramphenicol > GO:chloramphenicol transport ; GO:0042892	2	0.023	2	0.022
4.10.5	alkanesulfonate > GO:alkanesulphonate transport ; GO:0042918 > GO:alkanesulphonate transporter activity ; GO:0042959	3	0.159	3	0.036
4.10.78	glycerol-3-P > GO:glycerol transport ; GO:0015793 > GO:glycerol-3-phosphate transporter activity ; GO:0015169	5	0.020	5	0.103
4.10.79	glycine betaine choline transport > GO:betaine transport ; GO:0015838 > choline transport ; GO:0015871	5	0.046	5	0.325
4.2.1	Porters (Uni-, Sym- and Antiporters) > GO:symporter activity ; GO:0015293 > GO:antiporter activity ; GO:0015297 > GO:uniporter activity ; GO:0015292	203	0.050	203	0.178
4.2.1.20	The Inorganic Phosphate Transporter (PiT) Family > GO:inorganic phosphate transporter ; GO:0005315	3	0.018	3	0.454
4.2.1.21	The Solute:Sodium Symporter (SSS) Family > GO:solute:sodium symporter ; GO:0015370	4	0.015	4	0.008
4.2.1.7	The Small Multidrug Resistance (SMR) Family > GO:multidrug transporter ; GO:0015239	6	0.050	6	0.190
4.3.1	Pyrophosphate Bond (ATP; GTP; P2) Hydrolysis-driven Active Transporters > GO:ATPase activity ; GO:0016887	262	0.046	262	0.603
4.3.1.1	The ATP-binding Cassette (ABC) Superfamily + ABC-type Uptake Permeases > GO:ATP-binding cassette (ABC) transporter activity ; GO:0004009	235	0.029	235	0.417
4.8.1.3	MPA1 Family auxillary transport protein> GO:.	2	0.083	2	0.035
4.9.1	Recognized transporters of unknown biochemical mechanism > GO:transporter activity ; GO:0005215 > GO:transport ; GO:0006810	4	0.243	4	0.034

Significant (Wilcoxon rank sum test; $P \leq 0.05$ shown in bold) functional categories involved in environmental shift evolutionary condition.

Bin	Functional annotation	No of Genes	MGal/ MGAdpGal	No of Genes	DHGal/ DHAdpGal
1.2	Macromolecule degradation > GO:macromolecule catabolism ; GO:0009057	104	0.801	104	0.022
6.3	Surface antigens (ECA, O antigen of LPS) > GO:cell surface antigen activity, host-interacting ; GO:0042280	63	0.184	63	0.002
8	extrachromosomal > GO:.	292	0.233	292	0.002
8.1	Prophage genes and phage related functions > GO:.	258	0.459	258	0.002
8.4	Colicin related > GO:.	9	0.028	9	0.660
1.2.2	DNA > GO:DNA catabolism ; GO:0006308	25	0.854	25	0.023
1.2.4	Polysaccharides > GO:polysaccharide catabolism ; GO:0000272	7	0.034	7	0.978
1.5.1.11	Serine > GO:serine biosynthesis ; GO:0006564	6	0.046	6	0.600
1.5.1.16	Histidine > GO:histidine biosynthesis ; GO:0000105	12	0.003	12	0.845
1.5.3.8	Thiamine (Vitamin B1) > GO:thiamin biosynthesis ; GO:0009228	15	0.666	15	0.013
1.6.3	Lipopolysaccharide > GO:lipopolysaccharide biosynthesis ; GO:0009103	47	0.081	47	0.001
1.6.3.1	O antigen > GO:O antigen biosynthesis ; GO:0009243	15	0.014	15	0.000
1.6.3.2	Core region > GO:lipopolysaccharide core region biosynthesis ; GO:0009244	17	0.829	17	0.004
1.6.4	Enterobacterial common antigen (surface glycolipid) > GO:enterobacterial common antigen biosynthesis ; GO:0009246	12	0.053	12	0.016
1.7.10	Sugar nucleotide biosynthesis, conversions > GO:nucleotide-sugar biosynthesis ; GO:0009226	15	0.341	15	0.008
1.7.13	Amino acid conversion > GO:amino acid metabolism ; GO:0006520	3	0.011	3	0.770
1.7.14	Polyamine biosynthesis > GO:polyamine biosynthesis ; GO:0006596	19	0.004	19	0.710
1.7.7	Galactose metabolism > GO:galactose metabolism ; GO:0006012	5	0.036	5	0.286
2.2.5	tRNA > GO:tRNA metabolism ; GO:0006399	2	0.036	2	0.401
3.1.2.3	Repressor > GO:transcriptional repressor activity ; GO:0016564	138	0.037	138	0.509
3.1.4	Regulation level unknown > GO:.	73	0.019	73	0.746
3.3.1	Operon (regulation of one operon) > GO:.	127	0.205	127	0.027
4.10.118	methionine > GO:methionine transport ; GO:0015821 > GO:methionine transporter activity ; GO:0015191	4	0.904	4	0.045
4.10.12	amino acid > GO:amino acid transporter activity ; GO:0015171 > GO:amino acid transport ; GO:0006865	12	0.628	12	0.047
4.10.173	sugar > GO:carbohydrate transport ; GO:0008643 > GO:carbohydrate transporter activity ; GO:0015144	33	0.006	33	0.674
4.10.177	thiamine > GO:thiamin transport ; GO:0015888 > GO:thiamin transporter activity ; GO:0015234	4	0.920	4	0.001
4.10.191	Zn > GO:zinc ion transport ; GO:0006829 > GO:zinc ion transporter activity ; GO:0005385	3	0.028	3	0.491
4.10.71	glucose > GO:glucose transport ; GO:0015758 > GO:glucose transporter activity ; GO:0005355	2	0.099	2	0.047
4.10.82	H+ > GO:proton transport ; GO:0015992 > GO:hydrogen ion transporter activity ; GO:0015078	14	0.530	14	0.007

4.2.1.38	The K ⁺ Transporter (Trk) Family > GO:potassium:hydrogen antiporter ; GO:0015386 > GO:potassium:hydrogen symporter ; GO:0015387	3	0.776	3	0.039
4.3.1.1.1	ATP binding component > GO:.	89	0.159	89	0.018
4.3.1.2	The H ⁺ /Na ⁺ -translocating F-, V- and A-type ATPase (F-ATPase) Superfamily > GO:hydrogen-translocating F-type ATPase complex (sensu Bacteria) ; GO:0045256 > GO:hydrogen-translocating V-type ATPase complex ; GO:0016471	8	0.640	8	0.012

Significant (Wilcoxon rank sum test; $P \leq 0.05$ shown in bold) functional categories involved in prolonged stationary phase evolutionary condition.

Bin	Functional annotation	No of Genes	MG/ MGStat	No of Genes	DH/ DHStat
1.6	Macromolecules (cellular constituent) biosynthesis > GO:macromolecule biosynthesis ; GO:0009059	272	0.001	272	0.335
5.2	Cell cycle physiology > GO:cell cycle ; GO:0007049	5	0.786	5	0.009
5.3	Motility (incl. chemotaxis, energytaxis, aerotaxis, redoxaxis) > GO:taxis ; GO:0042330	59	0.043	59	0.946
6.3	Surface antigens (ECA, O antigen of LPS) > GO:cell surface antigen activity, host-interacting ; GO:0042280	65	0.048	65	0.280
6.6	Ribosome > GO:cytosolic ribosome (sensu Bacteria) ; GO:0009281	66	0.514	66	0.031
8	extrachromosomal > GO:.	298	0.214	298	0.001
8.1	Prophage genes and phage related functions > GO:.	264	0.107	264	0.000
1.1.1.18	Trehalose degradation, low osmolarity > GO:trehalose catabolism ; GO:0005993	3	0.898	3	0.047
1.1.1.25	L-ascorbate degradation > GO:L-ascorbic acid catabolism ; GO:0019854	11	0.981	11	0.001
1.1.1.3	D-arabinose catabolism > GO:D-arabinose catabolism ; GO:0019571	3	0.077	3	0.011
1.1.2.2	3-phenylpropionate and 3-(3-hydroxyphenyl)propionate degradation > GO:3-phenylpropionate catabolism ; GO:0019380 > GO:3-(3-hydroxy)phenylpropionate catabolism ; GO:0019622	11	0.527	11	0.018
1.1.2.3	Propionate degradation > GO:propionate catabolism ; GO:0019543	9	0.968	9	0.010
1.1.3.7	Threonine catabolism > GO:threonine catabolism ; GO:0006567	12	0.050	12	0.023
1.1.4.3	Ornithine degradation > GO:ornithine catabolism ; GO:0006593	2	0.026	2	0.104
1.1.5	Others > GO:.	29	0.171	29	0.033
1.1.5.2	Ethanol degradation > GO:ethanol catabolism ; GO:0006068	10	0.347	10	0.018
1.5.1.17	Alanine > GO:alanine biosynthesis ; GO:0006523	4	0.962	4	0.004
1.5.1.21	Homoserine > GO:homoserine biosynthesis ; GO:0009090	6	0.271	6	0.024
1.5.1.6	Asparagine > GO:asparagine biosynthesis ; GO:0006529	4	0.038	4	0.191
1.5.3	Cofactor, small molecule carrier > GO:coenzymes and prosthetic group biosynthesis ; GO:0046138	168	0.009	168	0.300
1.5.3.12	Heme, porphyrine > GO:heme biosynthesis ; GO:0006783 > GO:porphyrin biosynthesis ; GO:0006779	16	0.971	16	0.041

1.5.3.2	Folic acid > GO:folic acid biosynthesis ; GO:0046656	10	0.035	10	0.061
1.5.3.5	Coenzyme A > GO:coenzyme A biosynthesis ; GO:0015937	11	0.038	11	0.467
1.5.3.7	Nicotinamide adenine dinucleotide (NAD) > GO:nicotinamide adenine dinucleotide biosynthesis ; GO:0009435	15	0.142	15	0.025
1.5.4	Fatty acid and phosphatidic acid > GO:fatty acid biosynthesis ; GO:0006633 ; GO:phosphatidic acid biosynthesis ; GO:0006654	27	0.319	27	0.020
1.6.1	Phospholipid > GO:phospholipid biosynthesis ; GO:0008654	21	0.000	21	0.142
1.7.26	Allantoin assimilation > GO:allantoin assimilation ; GO:0009442	8	0.722	8	0.018
1.7.8	Gluconeogenesis > GO:gluconeogenesis ; GO:0006094	17	0.056	17	0.050
2.3.2	Translation > GO:protein biosynthesis ; GO:0006412	73	0.543	73	0.021
2.3.8	Ribosomal proteins > GO:structural constituent of ribosome ; GO:0003735	56	0.241	56	0.028
3.1.2.1	Sigma factors, anti-sigmafactors > GO:sigma factor activity ; GO:0016987 > GO:sigma factor antagonist activity ; GO:0016989	17	0.004	17	0.132
4.1.2	Beta barrel porins (The Outer Membrane Porin (OMP) Functional Superfamily) > GO:porin ; GO:0015288	18	0.045	18	0.570
4.10.10	allose/ribose > GO:allose transport ; GO:0015754 > GO:ribose transport ; GO:0015752 > GO:allose transporter activity ; GO:0015593 > GO:ribose transporter activity ; GO:0015591	4	0.039	4	0.003
4.10.118	methionine > GO:methionine transport ; GO:0015821 > GO:methionine transporter activity ; GO:0015191	4	0.010	4	0.118
4.10.119	methylgalactoside/galactose > GO:galactose transporter activity ; GO:0005354 > GO:galactose transporter activity ; GO:0005354 > GO:methylgalactoside transporter activity ; GO:0015592 > GO:methylgalactoside transport ; GO:0015765	4	0.462	4	0.016
4.10.143	Ni ⁺⁺ > GO:nickel ion transport ; GO:0015675 > GO:nickel ion transporter activity ; GO:0015099	5	0.343	5	0.032
4.10.148	oligopeptide > GO:oligopeptide transport ; GO:0006857 > GO:oligopeptide transporter activity ; GO:0015198	12	0.557	12	0.001
4.10.152	peptide > GO:peptide transport ; GO:0015833 > GO:peptide transporter activity ; GO:0015197	12	0.025	12	0.060
4.10.155	phosphate > GO:phosphate transport ; GO:0006817 > GO:phosphate transporter activity ; GO:0015114	7	0.277	7	0.006
4.10.185	uracil > GO:uracil transport ; GO:0015857 > GO:uracil transporter activity ; GO:0015210	2	0.832	2	0.034
4.10.29	cellobiose/arbutin/salicin > GO:salicin transport ; GO:0042948 > GO:salicin transporter activity ; GO:0042950 > GO:cellobiose transport ; GO:0019533 > GO:cellobiose transporter activity ; GO:0019191 > GO:salicin transporter activity ; GO:0042950 > GO:salicin transporter activity ; GO:0042950	4	0.004	4	0.027
4.10.48	D-ribose > GO:ribose transport ; GO:0015752 > GO:D-ribose transporter activity ; GO:0015591	6	0.042	6	0.469
4.10.54	Fe ⁺⁺ > GO:ferric iron transport ; GO:0015682 > GO:ferric iron transporter activity ; GO:0015091	2	0.025	2	0.955
4.10.58	ferrichrome > GO:ferrichrome transport ; GO:0042928 > GO:ferrichrome transporter activity ; GO:0042929	5	0.581	5	0.017
4.10.75	glutamate/aspartate > GO:glutamate transport ; GO:0015813 > GO:aspartate transport ; GO:0015810 > GO:glutamate transporter activity ; GO:0005313 > GO:aspartate transporter activity ; GO:0015183	4	0.789	4	0.008
4.10.78	glycerol-3-P > GO:glycerol transport ; GO:0015793 > GO:glycerol-3-phosphate transporter activity ; GO:0015169	5	0.256	5	0.033
4.10.82	H ⁺ > GO:proton transport ; GO:0015992 > GO:hydrogen ion transporter activity ; GO:0015078	14	0.971	14	0.022
4.2.1.13	The C4-Dicarboxylate Uptake (Dcu) Family > GO:C4-dicarboxylate transporter ; GO:0015556	2	0.045	2	0.209
4.2.1.21	The Solute:Sodium Symporter (SSS) Family > GO:solute:sodium symporter ; GO:0015370	4	0.848	4	0.020
4.2.1.40	The Nucleobase:Cation Symporter-2 (NCS2) Family > GO:nucleobase:cation symporter ; GO:0015391	5	0.879	5	0.006

4.2.1.42	The Aromatic Amino Acid Permease (ArAAP) Family > GO:hydroxy/aromatic amino-acid permease ; GO:0015507	7	0.001	7	0.946
4.2.1.47	The Divalent Anion:Na+ Symporter (DASS) Family > GO:..	3	0.048	3	0.153
4.3.1.1.1	ATP binding component > GO:..	92	0.005	92	0.068
4.3.1.1.3	periplasmic binding component> GO:..	51	0.428	51	0.041
4.4.1.3	PTS Lactose-N,N'-Diacetylchitobiose-betaucoside (Lac) Family > GO:..	3	0.018	3	0.016
4.4.1.5	The PTS Galactitol (Gat) Family > GO:galactitol permease ; GO:0015588	5	0.021	5	0.710
4.8.1.3	MPA1 Family auxillary transport protein> GO:..	2	0.151	2	0.035
4.8.1.7	The Phosphotransferase System Enzyme I (EI) Family> GO:..	7	0.214	7	0.030
4.9.2.22	The Putative Permease (PerM) Family> GO:..	2	0.680	2	0.034
5.5.4	pH response > GO:response to pH ; GO:0009268	13	0.394	13	0.033
5.5.6	Other stresses (mechanical, nutritional, oxidative) > GO:response to mechanical stimulus ; GO:0009612 > GO:response to nutrients ; GO:0007584 > GO:response to oxidative stress ; GO:0006979	22	0.353	22	0.025

