**Supplemental data S1: Gene ontology enrichment of the expression class genes**

Here we report the ontology enrichments for each of the three expression classes compared against the set of all genes for which we have expression data. A more detailed analysis on the function of these classes can be found in Meysman et al. (2013).

**Gene ontology enrichments of the E. coli stress expression class genes**

- organic substance catabolic process: $2.11 \times 10^{-7}$ (110 of 394)
- cellular catabolic process: $4.78 \times 10^{-8}$ (103 of 353)
- oxidation-reduction process: $7.82 \times 10^{-8}$ (130 of 479)
- carbohydrate catabolic process: $4.64 \times 10^{-7}$ (41 of 107)
- lipid modification: $7.20538195616898 \times 10^{-5}$ (9 of 13)
- response to heat: $6.05566537641835 \times 10^{-8}$ (20 of 33)
- response to reactive oxygen species: $7.156 \times 10^{-5}$ (13 of 24)
- carboxylic acid catabolic process: $3.533 \times 10^{-11}$ (57 of 136)
- fatty acid catabolic process: $6.12 \times 10^{-6}$ (10 of 13)
- organic acid catabolic process: $3.53 \times 10^{-11}$ (57 of 136)
- lipid catabolic process: $1.17 \times 10^{-5}$ (11 of 16)
- response to oxidative stress: $1.01 \times 10^{-6}$ (25 of 53)
- single-organism carbohydrate catabolic process: $2.47 \times 10^{-7}$ (38 of 94)
- small molecule catabolic process: $2.19 \times 10^{-12}$ (69 of 171)
- succinate metabolic process: $3.50 \times 10^{-5}$ (6 of 6)
- response to stress: $1.08 \times 10^{-13}$ (89 of 236)
- fatty acid beta-oxidation: $6.30 \times 10^{-6}$ (7 of 7)
- catabolic process: $3.63 \times 10^{-8}$ (115 of 405)
- monooxidase catabolic process: $3.95 \times 10^{-7}$ (29 of 64)
- cellular carbohydrate catabolic process: $4.25 \times 10^{-6}$ (19 of 37)
- lipid catabolic process: $1.91 \times 10^{-6}$ (13 of 19)
- response to stimulus: $2.23 \times 10^{-6}$ (110 of 411)
- single-organism catabolic process: $2.19 \times 10^{-12}$ (69 of 171)

**Gene ontology enrichments of the E. coli general metabolism expression class genes**

- transport: $8.40 \times 10^{-12}$ (435 of 694)
- signal transduction: $2.74 \times 10^{-5}$ (72 of 101)
- biological adhesion: $1.74 \times 10^{-9}$ (44 of 48)
- cell adhesion: $5.94 \times 10^{-6}$ (38 of 42)
- single-organism transport: $1.53 \times 10^{-7}$ (271 of 431)
- anion transport: $2.84 \times 10^{-6}$ (47 of 61)
- single-organism process: $1.12 \times 10^{-6}$ (460 of 783)
- regulation of transcription, DNA-dependent: $2.80 \times 10^{-5}$ (224 of 365)
- transmembrane transport: $3.52 \times 10^{-5}$ (160 of 252)

**Gene ontology enrichments of the E. coli growth expression class genes**

- cellular lipid metabolic process: $5.55 \times 10^{-8}$ (81 of 161)
- RNA modification: $1.34 \times 10^{-11}$ (40 of 53)
- pyridine-containing compound biosynthetic process: $1.75 \times 10^{-5}$ (15 of 19)
- carbohydrate derivative biosynthetic process: $3.48 \times 10^{-16}$ (104 of 175)
- alpha-amino acid biosynthetic process: $3.31 \times 10^{-8}$ (60 of 108)
- ribose phosphate metabolic process: $4.04 \times 10^{-14}$ (37 of 43)
- RNA processing: $2.28 \times 10^{-10}$ (43 of 62)
purine ribonucleoside monophosphate biosynthetic process: $4.98 \cdot 10^{-9}$ (20 of 22)
ribonucleoside monophosphate metabolic process: $1.74 \cdot 10^{-15}$ (32 of 37)
ribonucleotide metabolic process: $6.52 \cdot 10^{-6}$ (82 of 164)
heterocycle metabolic process: $7.44 \cdot 10^{-15}$ (215 of 465)
nucleobase-containing compound metabolic process: $4.27 \cdot 10^{-20}$ (240 of 495)
single-organism biosynthetic process: $1.42 \cdot 10^{-18}$ (140 of 249)
oligosaccharide biosynthetic process: $5.03 \cdot 10^{-6}$ (28 of 44)
purine nucleotide metabolic process: $1.24 \cdot 10^{-5}$ (71 of 152)
macromolecule modification: $9.56 \cdot 10^{-6}$ (66 of 138)
phosphate-containing compound metabolic process: $6.67 \cdot 10^{-6}$ (203 of 524)
cellular amino acid metabolic process: $1.10 \cdot 10^{-6}$ (128 of 279)
lipid metabolic process: $2.52 \cdot 10^{-7}$ (82 of 168)
ncRNA processing: $2.01 \cdot 10^{-10}$ (36 of 48)
tRNA aminoacylation: $1.08 \cdot 10^{-9}$ (23 of 26)
intracellular protein transport: $1.87 \cdot 10^{-7}$ (13 of 13)
Gram-negative-bacterium-type cell outer membrane assembly: $6.75 \cdot 10^{-6}$ (10 of 10)
pteridine-containing compound metabolic process: $5.04 \cdot 10^{-5}$ (15 of 20)
hydrogen transport: $2.41 \cdot 10^{-7}$ (24 of 32)
cellular biosynthetic process: $5.59 \cdot 10^{-30}$ (284 of 552)
cellular macromolecule biosynthetic process: $8.96 \cdot 10^{-6}$ (54 of 107)
cellular nitrogen compound biosynthetic process: $1.06 \cdot 10^{-22}$ (157 of 271)
purine ribonucleotide biosynthetic process: $5.68 \cdot 10^{-11}$ (24 of 26)
glycosyl compound biosynthetic process: $9.49 \cdot 10^{-6}$ (28 of 45)
ncRNA metabolic process: $1.29 \cdot 10^{-17}$ (59 of 76)
nucleoside biosynthetic process: $9.49 \cdot 10^{-6}$ (28 of 45)
sulfur compound biosynthetic process: $6.01 \cdot 10^{-6}$ (35 of 60)
ribose phosphate biosynthetic process: $4.04 \cdot 10^{-14}$ (37 of 43)
macromolecule metabolic process: $1.11 \cdot 10^{-18}$ (212 of 430)
heterocycle biosynthetic process: $1.97 \cdot 10^{-19}$ (145 of 257)
tetrahydrofolate metabolic process: $1.02 \cdot 10^{-5}$ (13 of 15)
lipopolysaccharide core region biosynthetic process: $2.73 \cdot 10^{-8}$ (20 of 23)
organophosphate biosynthetic process: $7.52 \cdot 10^{-16}$ (112 of 195)
purine nucleoside monophosphate metabolic process: $4.98 \cdot 10^{-6}$ (20 of 22)
O antigen biosynthetic process: $2.23 \cdot 10^{-5}$ (9 of 9)
thiamine diphosphate metabolic process: $5.37 \cdot 10^{-5}$ (10 of 11)
pyrimidine ribonucleotide metabolic process: $2.92 \cdot 10^{-5}$ (12 of 14)
membrane assembly: $6.75 \cdot 10^{-6}$ (10 of 10)
nucleobase-containing compound biosynthetic process: $4.08 \cdot 10^{-14}$ (92 of 156)
apha-amino acid metabolic process: $4.13 \cdot 10^{-8}$ (83 of 189)
phosphorus metabolic process: $1.91 \cdot 10^{-5}$ (206 of 540)
membrane organization: $2.04 \cdot 10^{-6}$ (11 of 11)
monovalent inorganic cation transport: $6.30 \cdot 10^{-7}$ (24 of 33)
vitamin biosynthetic process: $5.11 \cdot 10^{-10}$ (43 of 63)
nucleotide metabolic process: $1.07 \cdot 10^{-10}$ (127 of 261)
translation: $6.59 \cdot 10^{-43}$ (95 of 101)
fatty acid biosynthetic process: $2.94 \cdot 10^{-6}$ (18 of 23)
cofactor metabolic process: $5.64 \cdot 10^{-11}$ (71 of 121)
purine-containing compound biosynthetic process: $2.65 \cdot 10^{-7}$ (27 of 38)
lipopolysaccharide core region metabolic process: $2.73 \cdot 10^{-8}$ (20 of 23)
carbohydrate biosynthetic process: $7.43 \cdot 10^{-6}$ (64 of 132)
cellular aromatic compound metabolic process: $1.01 \cdot 10^{-9}$ (187 of 432)
poly saccharide biosynthetic process: $2.23 \cdot 10^{-5}$ (51 of 102)
tRNA modification: $1.60 \cdot 10^{-10}$ (34 of 44)
purine nucleoside monophosphate biosynthetic process: $4.98 \cdot 10^{-9}$ (20 of 22)
lipopolysaccharide biosynthetic process: $4.11 \cdot 10^{-6}$ (43 of 78)
purine ribonucleotide metabolic process: $1.78 \cdot 10^{-5}$ (69 of 148)
pteridine-containing compound biosynthetic process: $2.92 \cdot 10^{-5}$ (12 of 14)
energy coupled proton transmembrane transport, against electrochemical gradient: $2.23 \cdot 10^{-5}$ (9 of 9)
lipid biosynthetic process: $8.61 \cdot 10^{-10}$ (70 of 124)
guanosine-containing compound metabolic process: $1.50 \cdot 10^{-6}$ (22 of 30)
coenzyme biosynthetic process: $1.10 \cdot 10^{-11}$ (55 of 83)
tRNA aminoacylation for protein translation: $3.19 \cdot 10^{-9}$ (22 of 25)
tRNA methylation: $6.75 \cdot 10^{-6}$ (10 of 10)
tRNA processing: $5.07 \cdot 10^{-10}$ (35 of 47)
ATP synthesis coupled proton transport: $2.23 \cdot 10^{-5}$ (9 of 9)
cellular macromolecule metabolic process: $2.78 \cdot 10^{-28}$ (185 of 351)
pyrimidine nucleotide biosynthetic process: $2.44 \cdot 10^{-6}$ (17 of 21)
pyrimidine ribonucleotide biosynthetic process: $2.93 \cdot 10^{-5}$ (12 of 14)
water-soluble vitamin metabolic process: $9.88 \cdot 10^{-8}$ (44 of 73)
nucleoside phosphate biosynthetic process: $8.11 \cdot 10^{-15}$ (71 of 107)
protein peptidyl-prolyl isomerization: $5.38 \cdot 10^{-5}$ (10 of 11)
organic substance biosynthetic process: $5.20 \cdot 10^{-32}$ (282 of 536)
'de novo' IMP biosynthetic process: $6.18 \cdot 10^{-7}$ (12 of 12)
macromolecule methylation: $1.50 \cdot 10^{-11}$ (34 of 42)
ribonucleotide biosynthetic process: $4.04 \cdot 10^{-15}$ (36 of 40)
small molecule biosynthetic process: $2.82 \cdot 10^{-18}$ (139 of 248)
organophosphate metabolic process: $6.51 \cdot 10^{-12}$ (170 of 366)
cofactor biosynthetic process: $4.71 \cdot 10^{-9}$ (60 of 104)
pyrimidine ribonucleoside biosynthetic process: $2.93 \cdot 10^{-5}$ (12 of 14)
organic acid biosynthetic process: $1.32 \cdot 10^{-11}$ (100 of 187)
biosynthetic process: $1.17 \cdot 10^{-29}$ (300 of 596)
r ibonucleoside monophosphate biosynthetic process: $9.89 \cdot 10^{-13}$ (31 of 35)
methylation: $3.98 \cdot 10^{-11}$ (46 of 66)
O antigen metabolic process: $2.23 \cdot 10^{-5}$ (9 of 9)
water-soluble vitamin biosynthetic process: $5.11 \cdot 10^{-10}$ (43 of 63)
rRNA base methylation: $1.75 \cdot 10^{-5}$ (15 of 19)
rRNA methylation: $2.11 \cdot 10^{-5}$ (17 of 23)
energy coupled proton transport, down electrochemical gradient: $2.22 \cdot 10^{-5}$ (9 of 9)
cellular polysaccharide biosynthetic process: $2.68 \cdot 10^{-5}$ (50 of 100)
lipopolysaccharide metabolic process: $6.42 \cdot 10^{-6}$ (43 of 79)
carboxylic acid biosynthetic process: $1.32 \cdot 10^{-11}$ (100 of 187)
RNA methylation: $1.72 \cdot 10^{-9}$ (28 of 35)
nucleotide biosynthetic process: $8.11 \cdot 10^{-15}$ (71 of 107)
organonitrogen compound biosynthetic process: $6.66 \cdot 10^{-22}$ (173 of 313)
organic substance metabolic process: $1.87 \cdot 10^{-5}$ (405 of 1156)
pyrimidine-containing compound biosynthetic process: $1.10 \cdot 10^{-7}$ (28 of 39)
cellular nitrogen compound metabolic process: $1.39 \cdot 10^{-13}$ (239 of 542)
m acromolecule biosynthetic process: $4.79 \cdot 10^{-6}$ (76 of 148)
nucleoside monophosphate biosynthetic process: $2.77 \cdot 10^{-12}$ (33 of 39)
proton transport: $2.41 \cdot 10^{-7}$ (24 of 32)
tRNA metabolic process: $3.43 \cdot 10^{-17}$ (58 of 75)
rRNA processing: $4.09 \cdot 10^{-8}$ (27 of 36)
small molecule metabolic process: $2.39 \cdot 10^{-5}$ (297 of 819)
coenzyme metabolic process: $5.39 \cdot 10^{-9}$ (65 of 116)
purine nucleotide biosynthetic process: $4.08 \cdot 10^{-11}$ (26 of 29)
organic cyclic compound biosynthetic process: $1.19 \cdot 10^{-19}$ (145 of 256)
thiamine diphosphate biosynthetic process: $5.38 \cdot 10^{-5}$ (10 of 11)
avromatic compound biosynthetic process: $1.03 \cdot 10^{-18}$ (125 of 213)
carbohydrate derivative metabolic process: $4.91 \cdot 10^{-11}$ (160 of 346)
cellular amino acid biosynthetic process: $1.53 \cdot 10^{-9}$ (82 of 160)
cellular membrane organization: $2.04 \cdot 10^{-6}$ (11 of 11)
folic acid-containing compound biosynthetic process: $2.92 \cdot 10^{-5}$ (12 of 14)
r ibonucleoside biosynthetic process: $2.57 \cdot 10^{-6}$ (28 of 43)
pyrimidine nucleotide metabolic process: $2.44 \cdot 10^{-6}$ (17 of 21)
amino acid activation: $5.20 \cdot 10^{-9}$ (23 of 27)
nucleoside monophosphate metabolic process: $4.03 \cdot 10^{-12}$ (34 of 41)
organonitrogen compound metabolic process: \(1.36 \cdot 10^{-11}\) (244 of 575)

purine ribonucleoside monophosphate metabolic process: \(4.98 \cdot 10^{-9}\) (20 of 22)

IMP metabolic process: \(1.70 \cdot 10^{-8}\) (15 of 15)

nucleoside phosphate metabolic process: \(1.48 \cdot 10^{-10}\) (127 of 262)

organic cyclic compound metabolic process: \(4.88 \cdot 10^{-11}\) (215 of 498)

RNA metabolic process: \(7.11 \cdot 10^{-17}\) (83 of 126)

dicarboxylic acid biosynthetic process: \(6.15 \cdot 10^{-7}\) (27 of 39)

nucleic acid metabolic process: \(3.04 \cdot 10^{-15}\) (101 of 172)

IMP biosynthetic process: \(1.70 \cdot 10^{-8}\) (15 of 15)

vitamin metabolic process: \(9.88 \cdot 10^{-8}\) (44 of 73)

nucleobase-containing small molecule metabolic process: \(1.73 \cdot 10^{-7}\) (139 of 320)

nitrogen compound metabolic process: \(1.05 \cdot 10^{-11}\) (295 of 722)

peptidyl-proline modification: \(5.38 \cdot 10^{-5}\) (10 of 11)