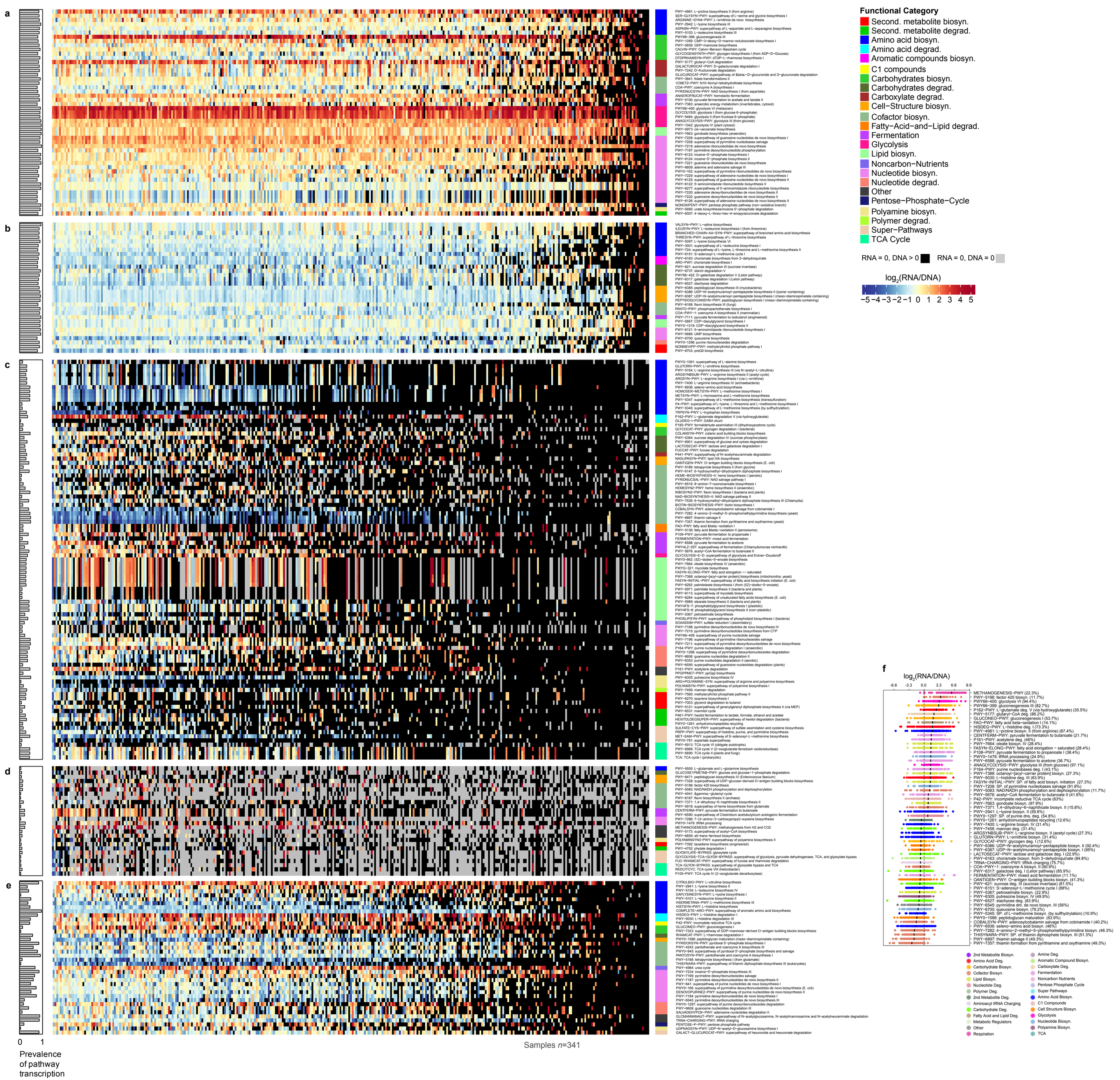
a
PWY−4981: L−proline biosynthesis II (from arginine)
SER−GLYSYN−PWY: superpathway of L−serine and glycine biosynthesis I
ARGININE−SYN4−PWY: L−ornithine de novo biosynthesis
PWY−2942: L−lysine biosynthesis III
ASPASN−PWY: superpathway of L−aspartate and L−asparagine biosynthesis
PWY−5103: L−isoleucine biosynthesis III
PWY66−399: gluconeogenesis III
PWY−1269: CMP−3−deoxy−D−manno−octulosonate biosynthesis I
PWY−5659: GDP−mannose biosynthesis
CALVIN−PWY: Calvin−Benson−Bassham cycle
GLYCOGENSYNTH−PWY: glycogen biosynthesis I (from ADP−D−Glucose)
DTDPRHAMSYN−PWY: dTDP−L−rhamnose biosynthesis I
PWY−5177: glutaryl−CoA degradation
GALACTUROCAT−PWY: D−galacturonate degradation I
PWY−7242: D−fructuronate degradation
GLUCUROCAT−PWY: superpathway of β−D−glucuronide and D−glucuronate degradation
PWY−3841: folate transformations II
1CMET2−PWY: N10−formyl−tetrahydrofolate biosynthesis
COA−PWY: coenzyme A biosynthesis I
PYRIDNUCSYN−PWY: NAD biosynthesis I (from aspartate)
ANAEROFRUCAT−PWY: homolactic fermentation
PWY−5100: pyruvate fermentation to acetate and lactate II
PWY−7383: anaerobic energy metabolism (invertebrates, cytosol)
PWY66−400: glycolysis VI (metazoan)
GLYCOLYSIS: glycolysis I (from glucose 6−phosphate)
PWY−5484: glycolysis II (from fructose 6−phosphate)
ANAGLYCOLYSIS−PWY: glycolysis III (from glucose)
PWY−1042: glycolysis IV (plant cytosol)
PWY−5973: cis−vaccenate biosynthesis
PWY−7663: gondoate biosynthesis (anaerobic)
PWY−7228: superpathway of guanosine nucleotides de novo biosynthesis I
PWY−7208: superpathway of pyrimidine nucleobases salvage
PWY−7219: adenosine ribonucleotides de novo biosynthesis
PWY−7197: pyrimidine deoxyribonucleotide phosphorylation
PWY−6123: inosine−5'−phosphate biosynthesis I
PWY−6124: inosine−5'−phosphate biosynthesis II
PWY−7221: guanosine ribonucleotides de novo biosynthesis
PWY−6609: adenine and adenosine salvage III
PWY0−162: superpathway of pyrimidine ribonucleotides de novo biosynthesis
PWY−7229: superpathway of adenosine nucleotides de novo biosynthesis I
PWY−6125: superpathway of guanosine nucleotides de novo biosynthesis II
PWY−6122: 5−aminoimidazole ribonucleotide biosynthesis II
PWY−6277: superpathway of 5−aminoimidazole ribonucleotide biosynthesis
PWY−7220: adenosine deoxyribonucleotides de novo biosynthesis II
PWY−7222: guanosine deoxyribonucleotides de novo biosynthesis II
PWY−6126: superpathway of adenosine nucleotides de novo biosynthesis II
NONOXIPENT−PWY: pentose phosphate pathway (non−oxidative branch)
PWY−5695: urate biosynthesis/inosine 5'−phosphate degradation
PWY−6507: 4−deoxy−L−threo−hex−4−enopyranuronate degradation
b
VALSYN−PWY: L−valine biosynthesis
ILEUSYN−PWY: L−isoleucine biosynthesis I (from threonine)
BRANCHED−CHAIN−AA−SYN−PWY: superpathway of branched amino acid biosynthesis
THREONINE−SYN−PWY: superpathway of L−threonine biosynthesis
PWY−5097: L−lysine biosynthesis VI
PWY−3001: superpathway of L−isoleucine biosynthesis I
PWY−724: superpathway of L−lysine, L−threonine and L−methionine biosynthesis II
PWY−6151: S−adenosyl−L−methionine cycle I
PWY−6163: chorismate biosynthesis from 3−dehydroquinate
ARO−PWY: chorismate biosynthesis I
PWY−621: sucrose degradation III (sucrose invertase)
PWY−6737: starch degradation V
PWY66−422: D−galactose degradation V (Leloir pathway)
PWY−6317: galactose degradation I (Leloir pathway)
PWY−6527: stachyose degradation
PWY−6385: peptidoglycan biosynthesis III (mycobacteria)
PWY−6386: UDP−N−acetylmuramoyl−pentapeptide biosynthesis II (lysine−containing)
PWY−6387: UDP−N−acetylmuramoyl−pentapeptide biosynthesis I (meso−diaminopimelate containing)
PEPTIDOGLYCANSYN−PWY: peptidoglycan biosynthesis I (meso−diaminopimelate containing)
PWY−6168: flavin biosynthesis III (fungi)
PANTO−PWY: phosphopantothenate biosynthesis I
COA−PWY−1: coenzyme A biosynthesis II (mammalian)
PWY−7111: pyruvate fermentation to isobutanol (engineered)
PWY−5667: CDP−diacylglycerol biosynthesis I
PWY0−1319: CDP−diacylglycerol biosynthesis II
PWY−6121: 5−aminoimidazole ribonucleotide biosynthesis I
PWY−5686: UMP biosynthesis
PWY−6700: queuosine biosynthesis
PWY0−1296: purine ribonucleosides degradation
NONMEVIPP−PWY: methylerythritol phosphate pathway I
PWY−6703: preQ0 biosynthesis
c
PWY0−1061: superpathway of L−alanine biosynthesis
GLUTORN−PWY: L−ornithine biosynthesis
PWY−5154: L−arginine biosynthesis III (via N−acetyl−L−citrulline)
ARGSYNBSUB−PWY: L−arginine biosynthesis II (acetyl cycle)
ARGSYN−PWY: L−arginine biosynthesis I (via L−ornithine)
PWY−7400: L−arginine biosynthesis IV (archaebacteria)
PWY−6936: seleno−amino acid biosynthesis
HOMOSER−METSYN−PWY: L−methionine biosynthesis I
METSYN−PWY: L−homoserine and L−methionine biosynthesis
PWY−5347: superpathway of L−methionine biosynthesis (transsulfuration)
P4−PWY: superpathway of L−lysine, L−threonine and L−methionine biosynthesis I
PWY−5345: superpathway of L−methionine biosynthesis (by sulfhydrylation)
TRPSYN−PWY: L−tryptophan biosynthesis
P162−PWY: L−glutamate degradation V (via hydroxyglutarate)
GLUDEG−I−PWY: GABA shunt
P185−PWY: formaldehyde assimilation III (dihydroxyacetone cycle)
GLYCOCAT−PWY: glycogen degradation I (bacterial)
COLANSYN−PWY: colanic acid building blocks biosynthesis
PWY−5384: sucrose degradation IV (sucrose phosphorylase)
PWY−6901: superpathway of glucose and xylose degradation
LACTOSECAT−PWY: lactose and galactose degradation I
FUCCAT−PWY: fucose degradation
P441−PWY: superpathway of N−acetylneuraminate degradation
NAGLIPASYN−PWY: lipid IVA biosynthesis
OANTIGEN−PWY: O−antigen building blocks biosynthesis (E. coli)
PWY−5189: tetrapyrrole biosynthesis II (from glycine)
PWY−6147: 6−hydroxymethyl−dihydropterin diphosphate biosynthesis I
HEME−BIOSYNTHESIS−II: heme biosynthesis I (aerobic)
PYRIDNUCSAL−PWY: NAD salvage pathway I
PWY−6519: 8−amino−7−oxononanoate biosynthesis I
HEMESYN2−PWY: heme biosynthesis II (anaerobic)
RIBOSYN2−PWY: flavin biosynthesis I (bacteria and plants)
NAD−BIOSYNTHESIS−II: NAD salvage pathway II
PWY−7539: 6−hydroxymethyl−dihydropterin diphosphate biosynthesis III (Chlamydia)
BIOTIN−BIOSYNTHESIS−PWY: biotin biosynthesis I
COBALSYN−PWY: adenosylcobalamin salvage from cobinamide I
PWY−7282: 4−amino−2−methyl−5−phosphomethylpyrimidine biosynthesis (yeast)
PWY−6897: thiamin salvage II
PWY−7357: thiamin formation from pyrithiamine and oxythiamine (yeast)
FAO−PWY: fatty acid β−oxidation I
PWY−5136: fatty acid β−oxidation II (peroxisome)
P108−PWY: pyruvate fermentation to propanoate I
FERMENTATION−PWY: mixed acid fermentation
PWY−6588: pyruvate fermentation to acetone
PWY4LZ−257: superpathway of fermentation (Chlamydomonas reinhardtii)
PWY−5676: acetyl−CoA fermentation to butanoate II
GLYCOLYSIS−E−D: superpathway of glycolysis and Entner−Doudoroff
PWY0−862: (5Z)−dodec−5−enoate biosynthesis
PWY−7664: oleate biosynthesis IV (anaerobic)
PWY0−1081: septumbiosynthesis
FASYN−ELONG−PWY: fatty acid elongation −− saturated
PWY−7388: octanoyl−[acyl−carrier protein] biosynthesis (mitochondria, yeast)
FASYN−INITIAL−PWY: superpathway of fatty acid biosynthesis initiation (E. coli)
PWY−6282: palmitoleate biosynthesis I (from (5Z)−dodec−5−enoate)
PWY−5971: palmitate biosynthesis II (bacteria and plants)
PWY−6113: superpathway of mycolate biosynthesis
PWY−6284: superpathway of unsaturated fatty acids biosynthesis (E. coli)
PWY−5989: stearate biosynthesis II (bacteria and plants)
PWY4FS−7: phosphatidylglycerol biosynthesis I (plastidic)
PWY4FS−8: phosphatidylglycerol biosynthesis II (non−plastidic)
PWY−5367: petroselinate biosynthesis
PHOSLIPSYN−PWY: superpathway of phospholipid biosynthesis I (bacteria)
SOASSIM−PWY: sulfate reduction I (assimilatory)
PWY−7198: pyrimidine deoxyribonucleotides de novo biosynthesis IV
PWY−7210: pyrimidine deoxyribonucleotides biosynthesis from CTP
PWY66−409: superpathway of purine nucleotide salvage
PWY−7196: superpathway of pyrimidine ribonucleosides salvage
PWY−7211: superpathway of pyrimidine deoxyribonucleotides de novo biosynthesis
P164−PWY: purine nucleobases degradation I (anaerobic)
PWY0−1298: superpathway of pyrimidine deoxyribonucleosides degradation
PWY−6606: guanosine nucleotides degradation II
PWY−6353: purine nucleotides degradation II (aerobic)
PWY−6595: superpathway of guanosine nucleotides degradation (plants)
P161−PWY: acetylene degradation
PPGPPMET−PWY: ppGpp biosynthesis
PWY−6305: putrescine biosynthesis IV
ARG+POLYAMINE−SYN: superpathway of arginine and polyamine biosynthesis
POLYAMSYN−PWY: superpathway of polyamine biosynthesis I
PWY−7456: mannan degradation
PWY−7560: methylerythritol phosphate pathway II
PWY−6270: isoprene biosynthesis I
PWY−7003: glycerol degradation to butanol
PWY−5121: superpathway of geranylgeranyl diphosphate biosynthesis II (via MEP)
PWY−6531: mannitol cycle
P461−PWY: hexitol fermentation to lactate, formate, ethanol and acetate
HEXITOLDEGSUPER−PWY: superpathway of hexitol degradation (bacteria)
PWY0−1261: anhydromuropeptides recycling
SULFATE−CYS−PWY: superpathway of sulfate assimilation and cysteine biosynthesis
PRPP−PWY: superpathway of histidine, purine, and pyrimidine biosynthesis
MET−SAM−PWY: superpathway of S−adenosyl−L−methionine biosynthesis
PWY0−781: aspartate superpathway
PWY−5913: TCA cycle VI (obligate autotrophs)
PWY−6969: TCA cycle V (2−oxoglutarate ferredoxin oxidoreductase)
PWY−5690: TCA cycle II (plants and fungi)
TCA: TCA cycle I (prokaryotic)
d
PWY−5505: L−glutamate and L−glutamine biosynthesis
GLUCOSE1PMETAB−PWY: glucose and glucose−1−phosphate degradation
PWY−6471: peptidoglycan biosynthesis IV (Enterococcus faecium)
PWY−7328: superpathway of UDP−glucose−derived O−antigen building blocks biosynthesis
PWY−5198: factor 420 biosynthesis
PWY−5083: NAD/NADH phosphorylation and dephosphorylation
PWY−4041: γ−glutamyl cycle
PWY−6167: flavin biosynthesis II (archaea)
PWY−7371: 1,4−dihydroxy−6−naphthoate biosynthesis II
PWY−5918: superpathway of heme biosynthesis from glutamate
CENTFERM−PWY: pyruvate fermentation to butanoate
PWY−6590: superpathway of Clostridium acetobutylicum acidogenic fermentation
PWY−7286: 7−(3−amino−3−carboxypropyl)−wyosine biosynthesis
PWY0−1479: tRNA processing
METHANOGENESIS−PWY: methanogenesis from H2 and CO2
PWY−5173: superpathway of acetyl−CoA biosynthesis
PWY−6859: all−trans−farnesol biosynthesis
POLYAMINSYN3−PWY: superpathway of polyamine biosynthesis II
PWY−7392: taxadiene biosynthesis (engineered)
PWY−4702: phytate degradation I
GLYOXYLATE−BYPASS: glyoxylate cycle
GLYCOLYSIS−TCA−GLYOX−BYPASS: superpathway of glycolysis, pyruvate dehydrogenase, TCA, and glyoxylate bypass
FUC−RHAMCAT−PWY: superpathway of fucose and rhamnose degradation
TCA−GLYOX−BYPASS: superpathway of glyoxylate bypass and TCA
REDCITCYC: TCA cycle VIII (helicobacter)
P105−PWY: TCA cycle IV (2−oxoglutarate decarboxylase)
e
CITRULBIO−PWY: L−citrulline biosynthesis
PWY−2941: L−lysine biosynthesis II
PWY−5104: L−isoleucine biosynthesis IV
DAPLYSINESYN−PWY: L−lysine biosynthesis I
PWY−5101: L−isoleucine biosynthesis II
HSERMETANA−PWY: L−methionine biosynthesis III
HISTSYN−PWY: L−histidine biosynthesis
COMPLETE−ARO−PWY: superpathway of aromatic amino acid biosynthesis
HISDEG−PWY: L−histidine degradation I
PWY−5030: L−histidine degradation III
P42−PWY: incomplete reductive TCA cycle
GLUCONEO−PWY: gluconeogenesis I
PWY−7323: superpathway of GDP−mannose−derived O−antigen building blocks biosynthesis
RHAMCAT−PWY: L−rhamnose degradation I
PWY0−1586: peptidoglycan maturation (meso−diaminopimelate containing)
PYRIDOXSYN−PWY: pyridoxal 5'−phosphate biosynthesis I
PWY−4242: pantothenate and coenzyme A biosynthesis III
PWY0−845: superpathway of pyridoxal 5'−phosphate biosynthesis and salvage
PANTOSYN−PWY: pantothenate and coenzyme A biosynthesis I
PWY−5188: tetrapyrrole biosynthesis I (from glutamate)
THISYNARA−PWY: superpathway of thiamin diphosphate biosynthesis III (eukaryotes)
PWY−4984: urea cycle
PWY−7234: inosine−5'−phosphate biosynthesis III
PWY−7199: pyrimidine deoxyribonucleosides salvage
PWY−7187: pyrimidine deoxyribonucleotides de novo biosynthesis II
PWY−841: superpathway of purine nucleotides de novo biosynthesis I
PWY0−166: superpathway of pyrimidine deoxyribonucleotides de novo biosynthesis (E. coli)
DENOVOPURINE2−PWY: superpathway of purine nucleotides de novo biosynthesis II
PWY−7184: pyrimidine deoxyribonucleotides de novo biosynthesis I
PWY−6545: pyrimidine deoxyribonucleotides de novo biosynthesis III
PWY0−1297: superpathway of purine deoxyribonucleosides degradation
PWY−6608: guanosine nucleotides degradation III
SALVADEHYPOX−PWY: adenosine nucleotides degradation II
GLCMANNANAUT−PWY: superpathway of N−acetylglucosamine, N−acetylmannosamine and N−acetylneuraminate degradation
TRNA−CHARGING−PWY: tRNA charging
PENTOSE−P−PWY: pentose phosphate pathway
UDPNAGSYN−PWY: UDP−N−acetyl−D−glucosamine biosynthesis I
GALACT−GLUCUROCAT−PWY: superpathway of hexuronide and hexuronate degradation
0
1
Prevalence of pathway transcription
Samples n=341
Functional Category
Second. metabolite biosyn.
Second. metabolite degrad.
Amino acid biosyn.
Amino acid degrad.
Aromatic compounds biosyn.
C1 compounds
Carbohydrates biosyn.
Carbohydrates degrad.
Carboxylate degrad.
Cell−Structure biosyn.
Cofactor biosyn.
Fatty−Acid−and−Lipid degrad.
Fermentation
Glycolysis
Lipid biosyn.
Noncarbon−Nutrients
Nucleotide biosyn.
Nucleotide degrad.
Other
Pentose−Phosphate−Cycle
Polyamine biosyn.
Polymer degrad.
Super−Pathways
TCA Cycle
RNA = 0, DNA > 0
RNA = 0, DNA = 0
log2(RNA/DNA)
−5 −4 −3 −2 −1 0 1 2 3 4 5
f
log2(RNA/DNA)
-6.6 -3.3 0.0 3.3 6.6 9.9
METHANOGENESIS−PWY (22.3%)
PWY−5198: factor 420 biosyn. (11.7%)
PWY66−400: glycolysis VI (94.4%)
PWY66−399: gluconeogenesis III (82.7%)
P162−PWY: L−glutamate deg. V (via hydroxyglutarate) (35.5%)
PWY−5177: glutaryl−CoA deg. (86.2%)
GLUCONEO−PWY: gluconeogenesis I (53.7%)
FAO−PWY: fatty acid beta−oxidation I (14.1%)
HISDEG−PWY: L−histidine deg. I (73.3%)
PWY−4981: L−proline biosyn. II (from arginine) (87.4%)
CENTFERM−PWY: pyruvate fermentation to butanoate (21.7%)
P161−PWY: acetylene deg. (46%)
PWY−7664: oleate biosyn. IV (28.4%)
FASYN−ELONG−PWY: fatty acid elongation − saturated (28.4%)
P108−PWY: pyruvate fermentation to propanoate I (38.4%)
PWY0−1479: tRNA processing (24.9%)
PWY−6588: pyruvate fermentation to acetone (36.7%)
ANAGLYCOLYSIS−PWY: glycolysis III (from glucose) (97.1%)
P164−PWY: purine nucleobases deg. I (43.1%)
PWY−7388: octanoyl−[acyl−carrier protein] biosyn. (27.3%)
PWY−5030: L−histidine deg. III (63.9%)
FASYN−INITIAL−PWY: SP. of fatty acid biosyn. initiation (27.3%)
PWY−7208: SP. of pyrimidine nucleobases salvage (91.8%)
PWY−5083: NAD/NADH phosphorylation and dephosphorylation (11.7%)
PWY−5676: acetyl−CoA fermentation to butanoate II (41.6%)
P42−PWY: incomplete reductive TCA cycle (63%)
PWY−7663: gondoate biosyn. (97.9%)
PWY−7371: 1,4−dihydroxy−6−naphthoate biosyn. II (15.8%)
PWY−2941: L−lysine biosyn. II (69.8%)
PWY0−1297: SP. of purine dns. deg. (54.8%)
PWY0−1261: anhydromuropeptides recycling (12.6%)
PWY−7400: L−arginine biosyn. IV (31.4%)
PWY−7456: mannan deg. (31.4%)
ARGSYNBSUB−PWY: L−arginine biosyn. II (acetyl cycle) (27.3%)
GLUTORN−PWY: L−ornithine biosyn. (31.4%)
GLYCOCAT−PWY: glycogen deg. I (12.6%)
PWY−6386: UDP−N−acetylmuramoyl−pentapeptide biosyn. II (92.4%)
PWY−6387: UDP−N−acetylmuramoyl−pentapeptide biosyn. I (95%)
LACTOSECAT−PWY: lactose and galactose deg. I (22.9%)
PWY−6163: chorismate biosyn. from 3−dehydroquinate (84.8%)
TRNA−CHARGING−PWY: tRNA charging (75.7%)
COA−PWY−1: coenzyme A biosyn. II (90.9%)
PWY−6317: galactose deg. I (Leloir pathway) (85.9%)
FERMENTATION−PWY: mixed acid fermentation (11.1%)
OANTIGEN−PWY: O−antigen building blocks biosyn. (41.3%)
PWY−621: sucrose deg. III (sucrose invertase) (81.5%)
PWY−6151: S−adenosyl−L−methionine cycle I (88%)
PWY−5367: petroselinate biosyn. (22.9%)
PWY−6305: putrescine biosyn. IV (49.9%)
PWY−6527: stachyose deg. (83.9%)
PWY−6545: pyrimidine dnt. de novo biosyn. III (56%)
PWY−6700: queuosine biosyn. (79.2%)
PWY−5345: SP. of L−methionine biosyn. (by sulfhydrylation) (10.9%)
PWY0−1586: peptidoglycan maturation (63.9%)
COBALSYN−PWY: adenosylcobalamin salvage from cobinamide I (40.2%)
PWY−6936: seleno−amino acid biosyn. (46%)
PWY−7282: 4−amino−2−methyl−5−phosphomethylpyrimidine biosyn. (46.3%)
THISYNARA−PWY: SP. of thiamin diphosphate biosyn. III (51.3%)
PWY−6897: thiamin salvage II (49.3%)
PWY−7357: thiamin formation from pyrithiamine and oxythiamine (49.3%)
2nd Metabolite Biosyn.
Amino Acid Deg.
Carbohydrate Biosyn.
Cofactor Biosyn.
Lipid Biosyn.
Nucleotide Deg.
Polymer Deg.
2nd Metabolite Deg.
Aminoacyl tRNA Charging
Carbohydrate Deg.
Fatty Acid and Lipid Deg.
Metabolic Regulators
Other
Respiration
Amine Deg.
Aromatic Compound Biosyn.
Carboxylate Deg.
Fermentation
Noncarbon Nutrients
Pentose Phosphate Cycle
Super Pathways
Amino Acid Biosyn.
C1 Compounds
Cell Structure Biosyn.
Glycolysis
Nucleotide Biosyn.
Polyamine Biosyn.
TCA