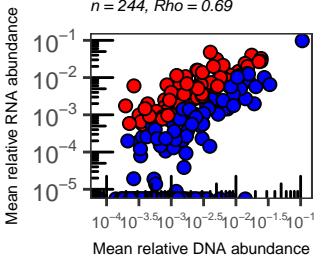
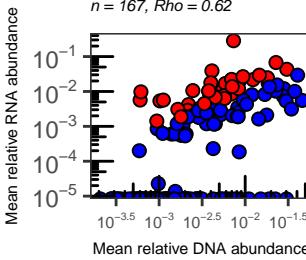




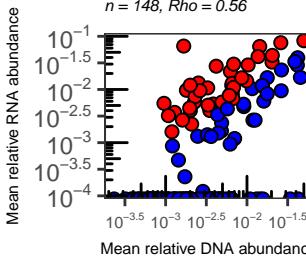
*PWY-7219*  
adenosine  
ribonucleotides de novo biosynth  
*n* = 244, *Rho* = 0.69



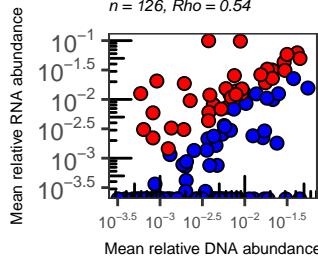
*PWY-6277*  
superpathway  
of 5-aminoimidazole ribonucleoti  
*n* = 167, *Rho* = 0.62



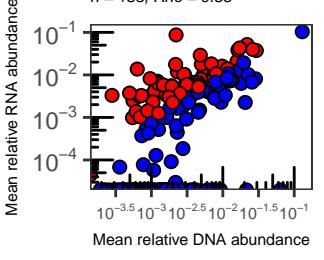
*PWY-6387*  
UDP-N-acetylglucosamyl-penta  
biosynthesis I (meso-diaminopi  
*n* = 148, *Rho* = 0.56



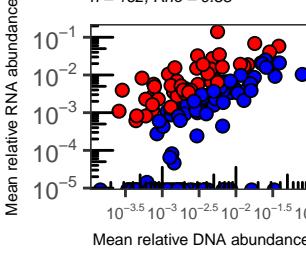
*PWY-5667*  
CDP-diacylglycerol  
biosynthesis I  
*n* = 126, *Rho* = 0.54



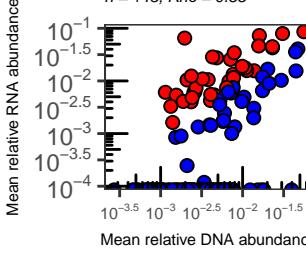
*PWY-7221*  
guanosine  
ribonucleotides de novo biosynth  
*n* = 183, *Rho* = 0.58



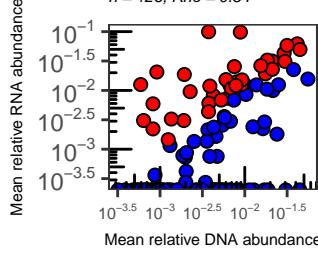
*VALSYN-PWY*  
*L*-valine  
biosynthesis  
*n* = 162, *Rho* = 0.58



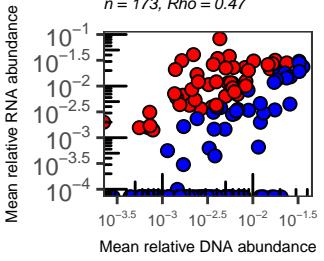
*PWY-6386*  
UDP-N-acetylglucosamyl-penta  
biosynthesis II (lysine-containin  
*n* = 143, *Rho* = 0.55



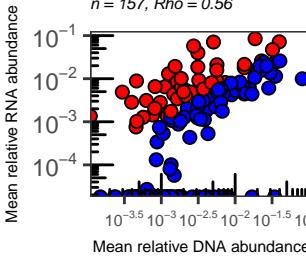
*PWY-0-1319*  
CDP-diacylglycerol  
biosynthesis II  
*n* = 126, *Rho* = 0.54



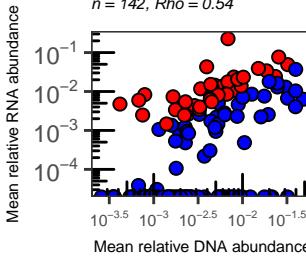
*COA-PWY-1*  
coenzyme  
*A* biosynthesis II (mammalian)  
*n* = 173, *Rho* = 0.47



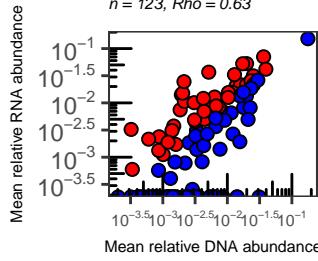
*PWY-7111*  
pyruvate  
fermentation to isobutanol (engine  
*n* = 157, *Rho* = 0.56



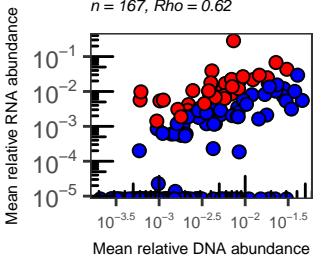
*PWY-6121*  
5-aminoimidazole  
ribonucleotide biosynthesis I  
*n* = 142, *Rho* = 0.54



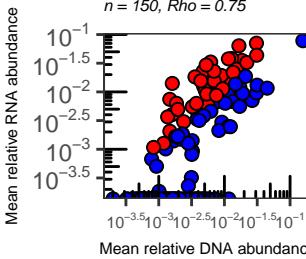
*PWY-2942*  
*L*-lysine  
biosynthesis III  
*n* = 123, *Rho* = 0.63



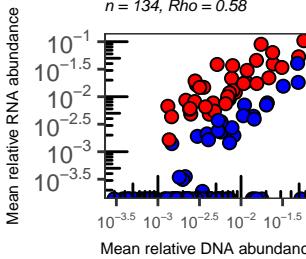
*PWY-6122*  
5-aminoimidazole  
ribonucleotide biosynthesis II  
*n* = 167, *Rho* = 0.62



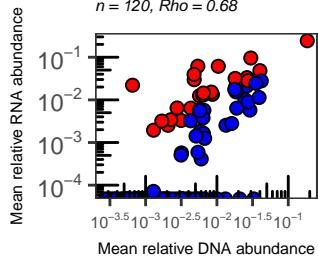
*PWY-5686*  
UMP  
biosynthesis  
*n* = 150, *Rho* = 0.75



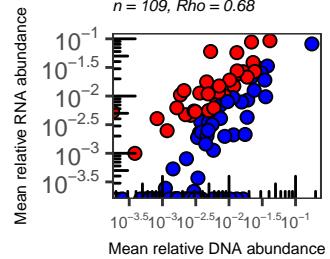
*PEPTIDOGLYCANSYN-PWY*  
peptidoglycan  
biosynthesis I (meso-diaminopi  
*n* = 134, *Rho* = 0.58



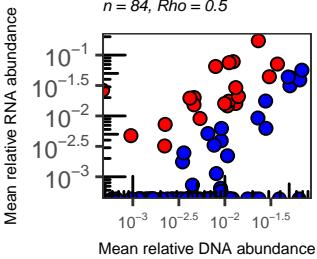
*PWY-6151*  
*S*-adenosyl-*L*-methionine  
cycle I  
*n* = 120, *Rho* = 0.68



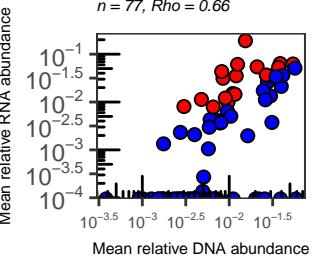
*PWY-5097*  
*L-lysine*  
*biosynthesis VI*  
*n* = 109, *Rho* = 0.68



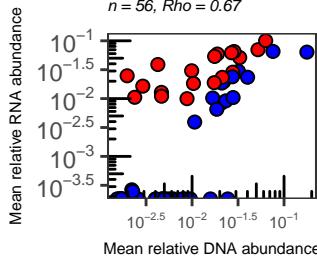
*NONMEVIPP-PWY*  
*methylerythritol*  
*phosphate pathway I*  
*n* = 84, *Rho* = 0.5



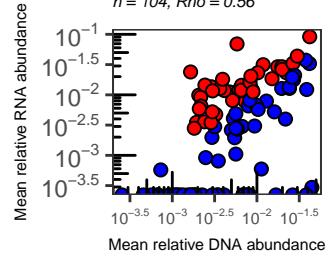
*PWY-6703*  
*preQ0*  
*biosynthesis*  
*n* = 77, *Rho* = 0.66



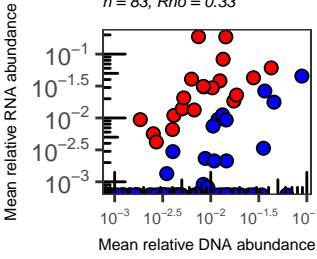
*PWY-1042*  
*glycolysis*  
*IV (plant cytosol)*  
*n* = 56, *Rho* = 0.67



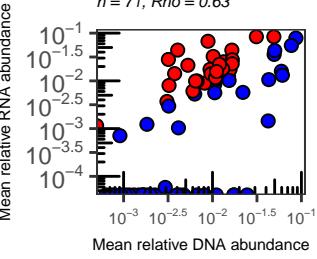
*PANTO-PWY*  
*phosphopantetheate*  
*biosynthesis I*  
*n* = 104, *Rho* = 0.56



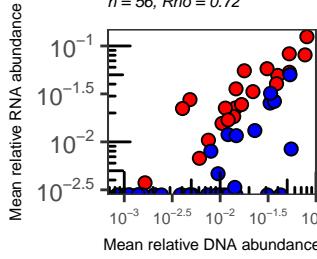
*PWY-6163*  
*chorismate*  
*biosynthesis from 3-dehydroqu*  
*n* = 83, *Rho* = 0.33



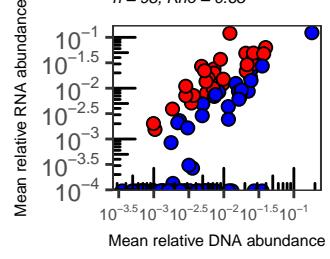
*PWY-5695*  
*urate*  
*biosynthesis/inosine 5'-phosph*  
*n* = 71, *Rho* = 0.63



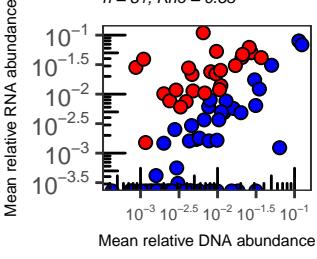
*PWY-3841*  
*folate*  
*transformations II*  
*n* = 56, *Rho* = 0.72



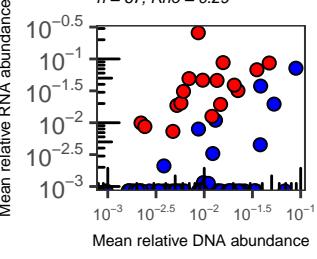
*PWY-6700*  
*queuosine*  
*biosynthesis*  
*n* = 98, *Rho* = 0.65



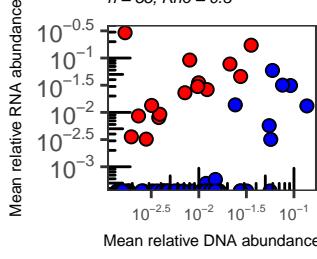
*PWY-6737*  
*starch*  
*degradation V*  
*n* = 81, *Rho* = 0.53



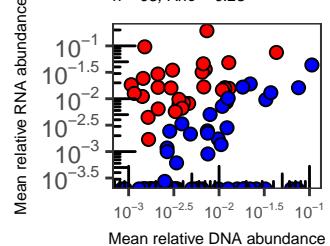
*ARO-PWY*  
*chorismate*  
*biosynthesis I*  
*n* = 67, *Rho* = 0.29



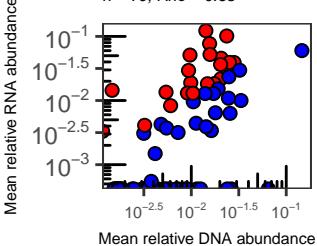
*PWY-5188*  
*tetrapyrrole*  
*biosynthesis I (from glutamate)*  
*n* = 55, *Rho* = 0.3



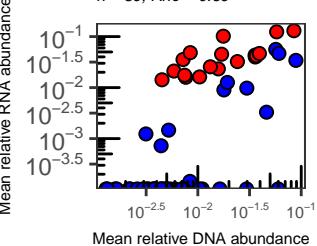
*PWY-1296*  
*purine*  
*ribonucleosides degradation*  
*n* = 98, *Rho* = 0.25



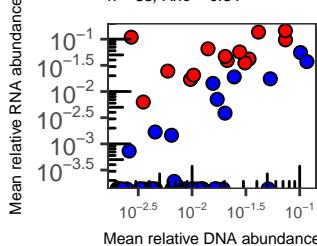
*PWY-6609*  
*adenine*  
*and adenosine salvage III*  
*n* = 79, *Rho* = 0.63



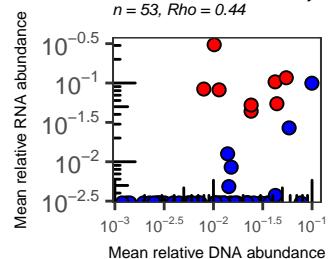
*PWY-7228*  
*superpathway*  
*of guanosine nucleotides de no*  
*n* = 59, *Rho* = 0.69



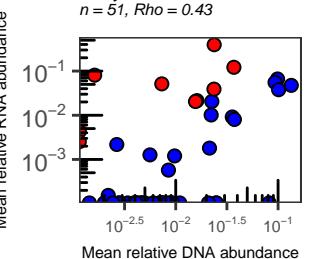
*COA-PWY*  
*coenzyme*  
*A biosynthesis I*  
*n* = 53, *Rho* = 0.54



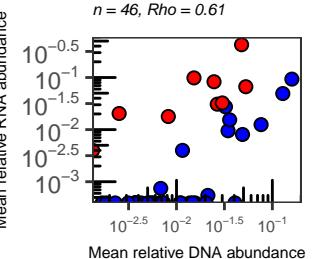
**COMPLETE-ARO-PWY**  
superpathway  
of aromatic amino acid biosynth:  
 $n = 53$ ,  $\text{Rho} = 0.44$



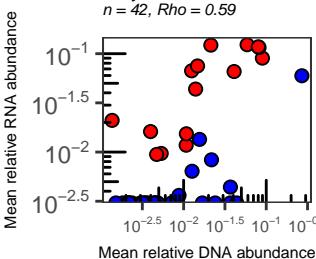
**PWY-7222**  
guanosine  
deoxyribonucleotides de novo bio  
 $n = 51$ ,  $\text{Rho} = 0.43$



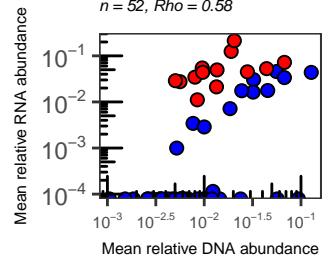
**PWY-5100**  
pyruvate  
fermentation to acetate and lact  
 $n = 46$ ,  $\text{Rho} = 0.61$



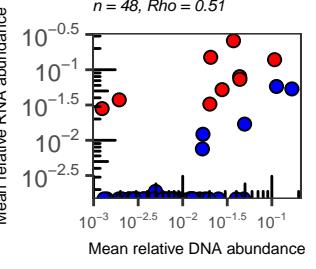
**PWY-5103**  
*L*-isoleucine  
biosynthesis III  
 $n = 42$ ,  $\text{Rho} = 0.59$



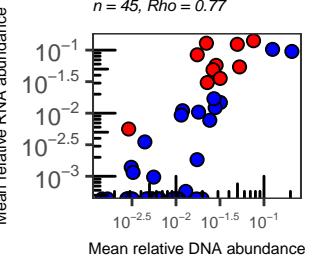
**PWY-7208**  
superpathway  
of pyrimidine nucleobases salvag  
 $n = 52$ ,  $\text{Rho} = 0.58$



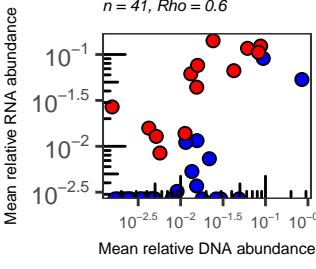
**THRESYN-PWY**  
superpathway  
of *L*-threonine biosynthesis  
 $n = 48$ ,  $\text{Rho} = 0.51$



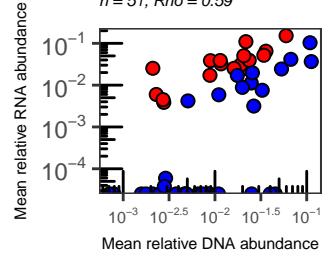
**DTDPRHAMSIN-PWY**  
*d*TDP-L-rhamnose  
biosynthesis I  
 $n = 45$ ,  $\text{Rho} = 0.77$



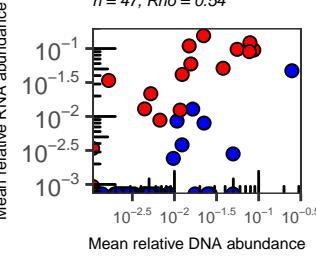
**BRANCHED-CHAIN-AA-SYN**  
superpathway  
of branched amino acid biosyn  
 $n = 41$ ,  $\text{Rho} = 0.6$



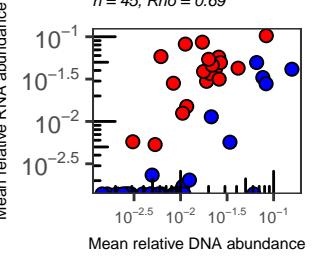
**NONOXIPENT-PWY**  
pentose  
phosphate pathway (non-oxidativ  
 $n = 51$ ,  $\text{Rho} = 0.59$



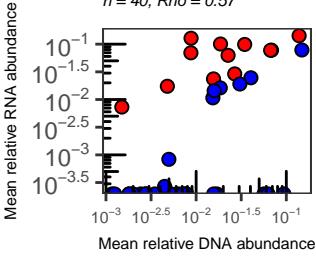
**ILEUSYN-PWY**  
*L*-isoleucine  
biosynthesis I (from threonine)  
 $n = 47$ ,  $\text{Rho} = 0.54$



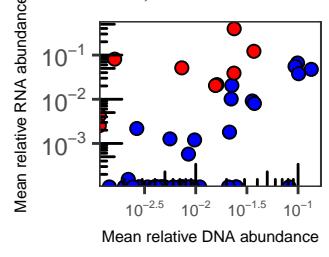
**PWY-6124**  
inosine-5'-phosphate  
biosynthesis II  
 $n = 45$ ,  $\text{Rho} = 0.69$



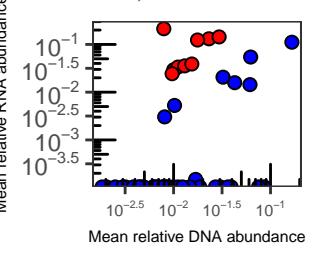
**PWY66-422**  
*D*-galactose  
degradation V (Leloir pathway)  
 $n = 40$ ,  $\text{Rho} = 0.57$



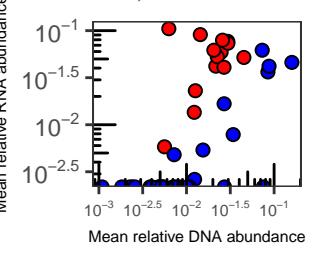
**PWY-7220**  
adenosine  
deoxyribonucleotides de novo bio  
 $n = 51$ ,  $\text{Rho} = 0.43$



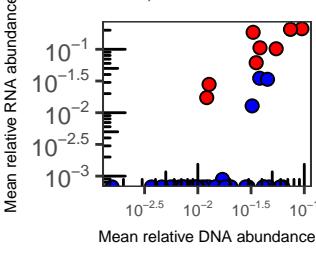
**PWY-7197**  
pyrimidine  
deoxyribonucleotide phosphory  
 $n = 47$ ,  $\text{Rho} = 0.45$



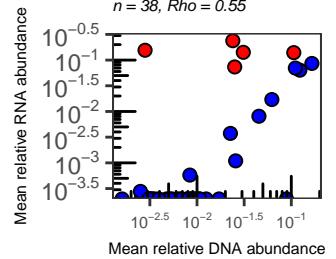
**PWY-6123**  
inosine-5'-phosphate  
biosynthesis I  
 $n = 43$ ,  $\text{Rho} = 0.65$



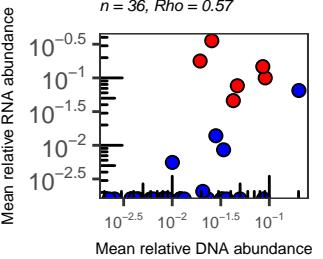
**HISTSYN-PWY**  
*L*-histidine  
biosynthesis  
 $n = 39$ ,  $\text{Rho} = 0.53$



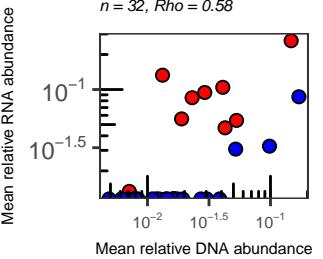
*PWY-6126*  
superpathway  
of adenosine nucleotides de novo  
 $n = 38$ ,  $\text{Rho} = 0.55$



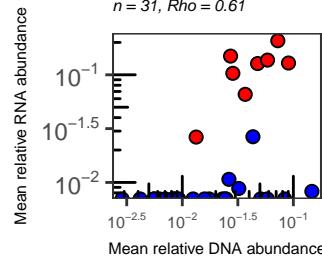
*PWY-7357*  
*thiamin*  
formation from pyridoxamine and  
 $n = 36$ ,  $\text{Rho} = 0.57$



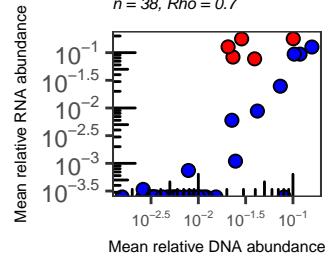
*PWY-4242*  
*pantothenate*  
and coenzyme A biosynthesis I  
 $n = 32$ ,  $\text{Rho} = 0.58$



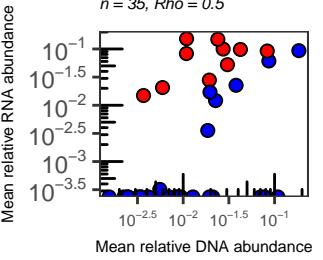
*RHAMCAT-PWY*  
*L-rhamnose*  
degradation I  
 $n = 31$ ,  $\text{Rho} = 0.61$



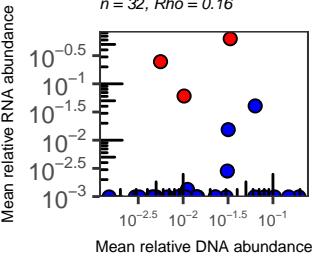
*PWY-7229*  
superpathway  
of adenosine nucleotides de novo  
 $n = 38$ ,  $\text{Rho} = 0.7$



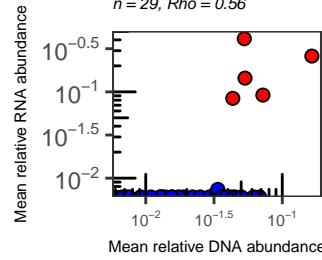
*PWY-6317*  
*galactose*  
degradation I (*Leloir pathway*)  
 $n = 35$ ,  $\text{Rho} = 0.5$



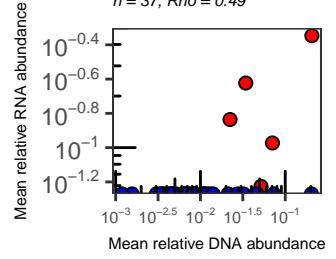
*PWY-6936*  
*seleno-amino*  
acid biosynthesis  
 $n = 32$ ,  $\text{Rho} = 0.16$



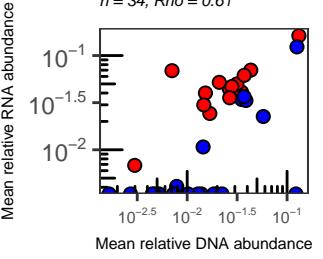
*PWY-4981*  
*L-proline*  
biosynthesis II (from arginine)  
 $n = 29$ ,  $\text{Rho} = 0.56$



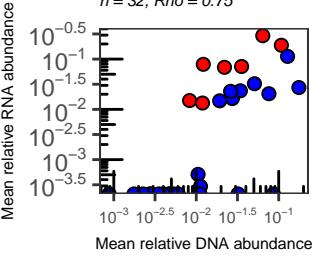
*UDPNAGSYN-PWY*  
*UDP-N-acetyl-D-glucosamine*  
biosynthesis I  
 $n = 37$ ,  $\text{Rho} = 0.49$



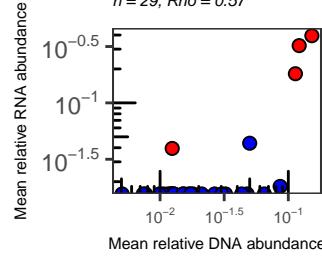
*PWY-7663*  
*gondotetra*  
biosynthesis (anaerobic)  
 $n = 34$ ,  $\text{Rho} = 0.61$



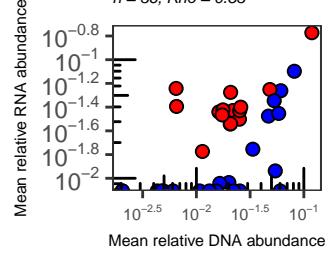
*SER-GLYSYN-PWY*  
superpathway  
of L-serine and glycine biosynthesis  
 $n = 32$ ,  $\text{Rho} = 0.75$



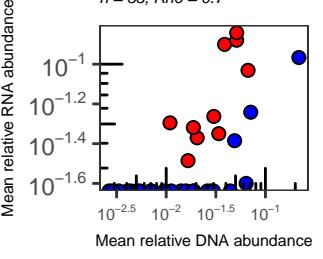
*PWY-1297*  
superpathway  
of purine deoxyribonucleosides  
 $n = 29$ ,  $\text{Rho} = 0.57$



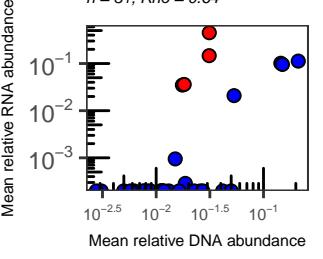
*1CMET2-PWY*  
*N10-formyl-tetrahydrofolate*  
biosynthesis  
 $n = 36$ ,  $\text{Rho} = 0.53$



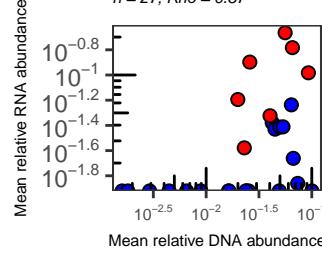
*PWY-6385*  
*peptidoglycan*  
biosynthesis III (mycobacteria)  
 $n = 33$ ,  $\text{Rho} = 0.7$



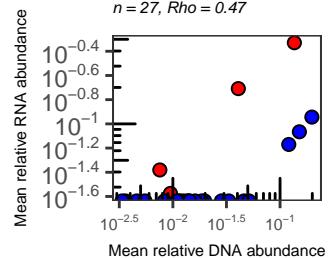
*PWY-6125*  
superpathway  
of guanosine nucleotides de novo  
 $n = 31$ ,  $\text{Rho} = 0.64$



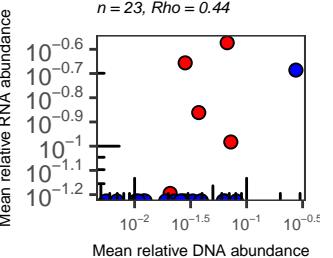
*PWY-1269*  
*CMP-3-deoxy-D-manno-octulic*  
biosynthesis I  
 $n = 27$ ,  $\text{Rho} = 0.57$



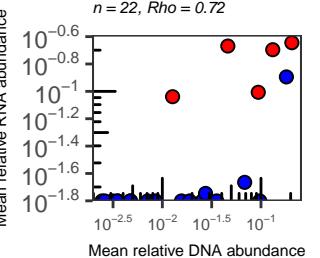
PWY-0-1586  
peptidoglycan  
maturation (meso-diaminopimine)  
 $n = 27$ ,  $\text{Rho} = 0.47$



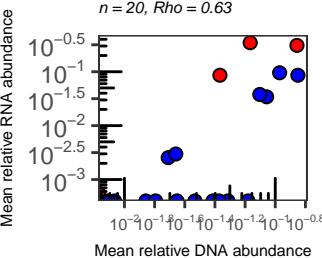
GLUTORN-PWY  
L-ornithine  
biosynthesis  
 $n = 23$ ,  $\text{Rho} = 0.44$



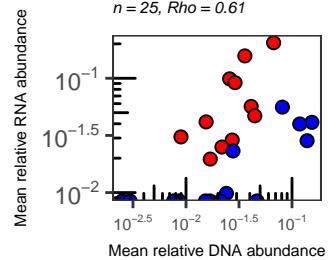
PWY-6527  
stachyose  
degradation  
 $n = 22$ ,  $\text{Rho} = 0.72$



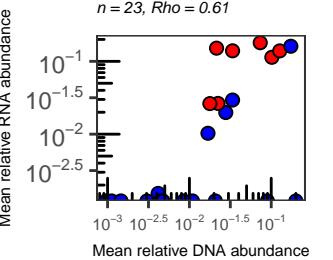
ANAGLYCOLYSIS-PWY  
glycolysis  
III (from glucose)  
 $n = 20$ ,  $\text{Rho} = 0.63$



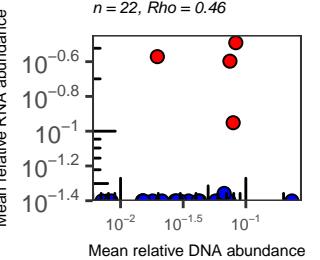
PWY-5659  
GDP-mannose  
biosynthesis  
 $n = 25$ ,  $\text{Rho} = 0.61$



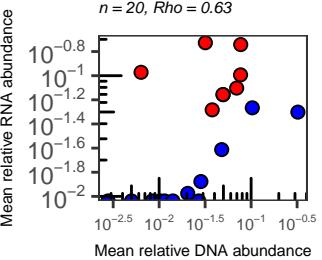
GLYCOGENSYNTH-PWY  
glycogen  
biosynthesis I (from ADP-D-GI)  
 $n = 23$ ,  $\text{Rho} = 0.61$



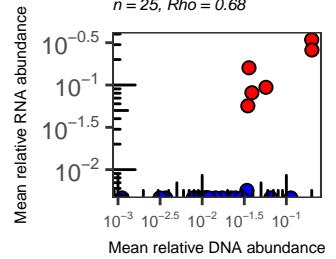
PWY-7199  
pyrimidine  
deoxyribonucleosides salvage  
 $n = 22$ ,  $\text{Rho} = 0.46$



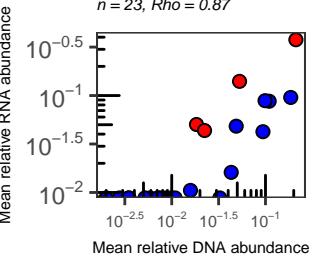
ASPASN-PWY  
superpathway  
of L-aspartate and L-asparagine  
 $n = 20$ ,  $\text{Rho} = 0.63$



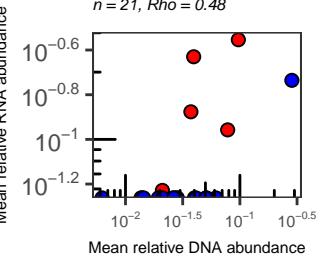
TRPSYN-PWY  
L-tryptophan  
biosynthesis  
 $n = 25$ ,  $\text{Rho} = 0.68$



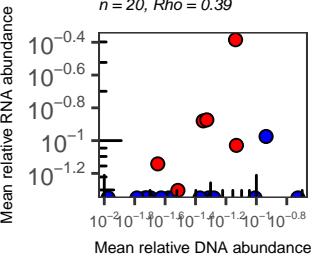
PWY-621  
sucrose  
degradation III (sucrose invertase)  
 $n = 23$ ,  $\text{Rho} = 0.87$



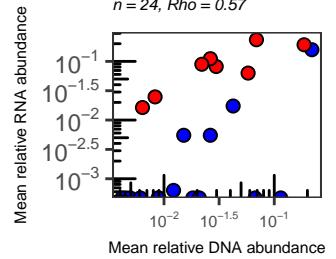
ARGSYN-PWY  
L-arginine  
biosynthesis I (via L-ornithine)  
 $n = 21$ ,  $\text{Rho} = 0.48$



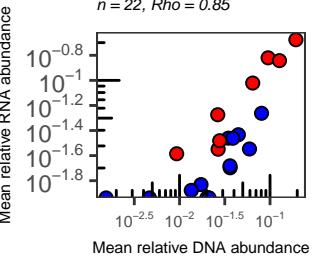
LACTOSECAT-PWY  
lactose  
and galactose degradation I  
 $n = 20$ ,  $\text{Rho} = 0.39$



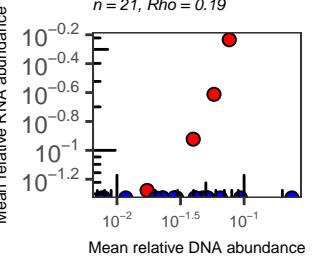
CALVIN-PWY  
Calvin-Benson-Bassham  
cycle  
 $n = 24$ ,  $\text{Rho} = 0.57$



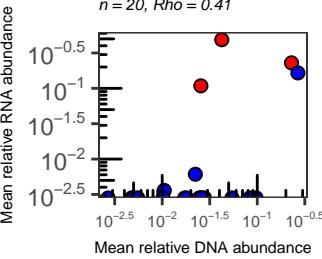
ARGININE-SYN4-PWY  
L-ornithine  
de novo biosynthesis  
 $n = 22$ ,  $\text{Rho} = 0.85$



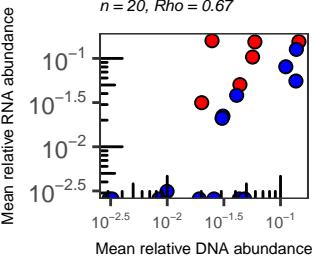
PWY-2941  
L-lysine  
biosynthesis II  
 $n = 21$ ,  $\text{Rho} = 0.19$



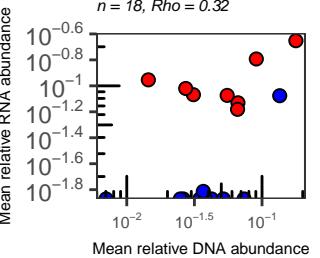
PWY-724  
superpathway  
of L-lysine, L-threonine and L-  
 $n = 20$ ,  $\text{Rho} = 0.41$



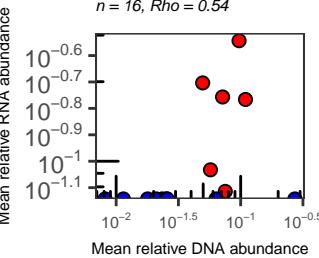
**PYRIDNUCSYN-PWY**  
NAD  
biosynthesis I (from aspartate)  
 $n = 20$ ,  $\text{Rho} = 0.67$



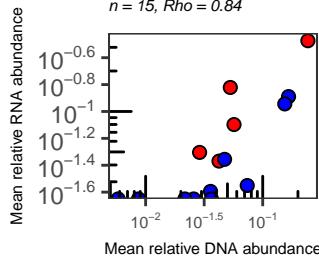
**PANTOSYN-PWY**  
pantothenate  
and coenzyme A biosynthesis I  
 $n = 18$ ,  $\text{Rho} = 0.32$



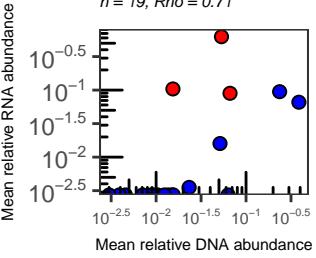
**PWY-6147**  
6-hydroxymethyl-dihydropterin  
diphosphate biosynthesis I  
 $n = 16$ ,  $\text{Rho} = 0.54$



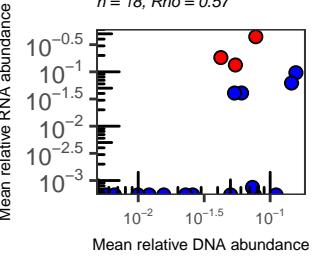
**PYRIDOXSYN-PWY**  
pyridoxal  
5'-phosphate biosynthesis I  
 $n = 15$ ,  $\text{Rho} = 0.84$



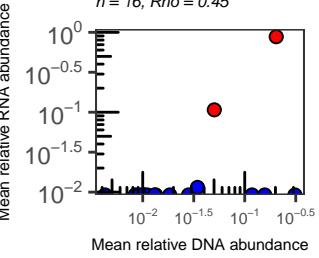
**HISDEG-PWY**  
*L*-histidine  
degradation I  
 $n = 19$ ,  $\text{Rho} = 0.71$



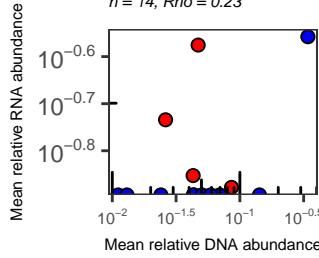
**PWY-6305**  
putrescine  
biosynthesis IV  
 $n = 18$ ,  $\text{Rho} = 0.57$



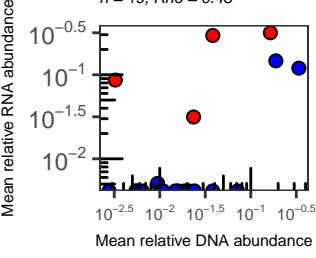
**SO4ASSIM-PWY**  
sulfate  
reduction I (assimilatory)  
 $n = 16$ ,  $\text{Rho} = 0.45$



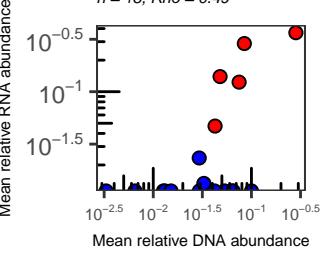
**ARGSYNBSUB-PWY**  
*L*-arginine  
biosynthesis II (acetyl cycle)  
 $n = 14$ ,  $\text{Rho} = 0.23$



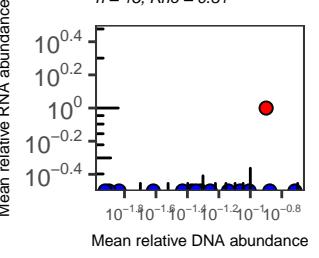
**PWY-3001**  
superpathway  
of *L*-isoleucine biosynthesis I  
 $n = 19$ ,  $\text{Rho} = 0.48$



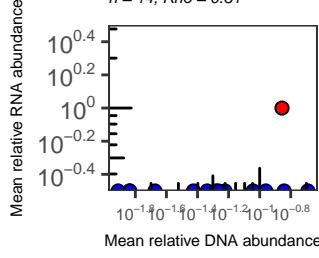
**THISYNARA-PWY**  
superpathway  
of thiamin diphosphate biosynth.  
 $n = 18$ ,  $\text{Rho} = 0.49$



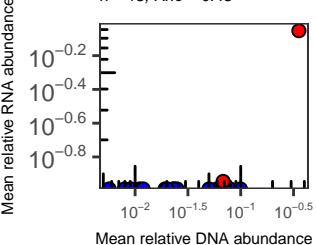
**METSYN-PWY**  
*L*-homoserine  
and *L*-methionine biosynthesis  
 $n = 15$ ,  $\text{Rho} = 0.31$



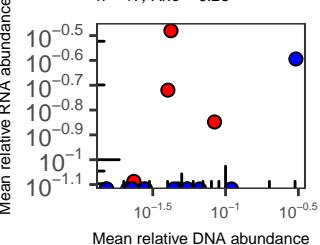
**MET-SAM-PWY**  
superpathway  
of *S*-adenosyl-*L*-methionine b...  
 $n = 14$ ,  $\text{Rho} = 0.31$



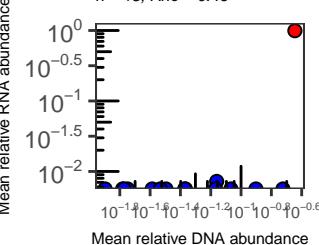
**HOMOSER-METSYN-PWY**  
*L*-methionine  
biosynthesis I  
 $n = 18$ ,  $\text{Rho} = 0.45$



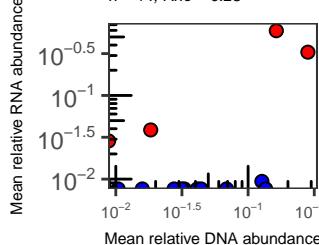
**PWY-7400**  
*L*-arginine  
biosynthesis IV (archaeabacteria)  
 $n = 17$ ,  $\text{Rho} = 0.26$



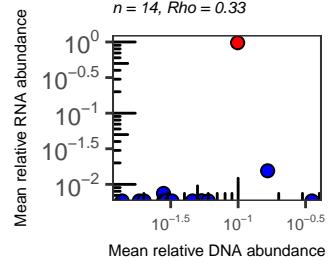
**PWY0-1061**  
superpathway  
of *L*-alanine biosynthesis  
 $n = 15$ ,  $\text{Rho} = 0.46$



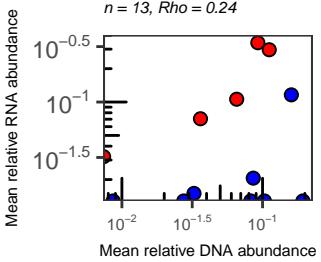
**PWY-5189**  
tetrapyrrole  
biosynthesis II (from glycine)  
 $n = 14$ ,  $\text{Rho} = 0.28$



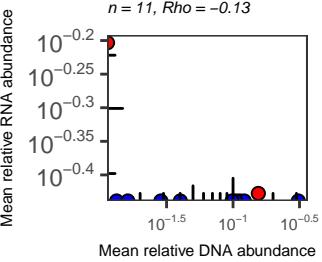
PWY-7234  
inosine-5'-phosphate  
biosynthesis III  
 $n = 14$ ,  $Rho = 0.33$



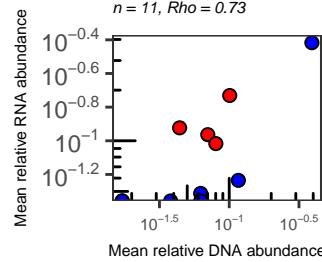
PWY-6608  
guanosine  
nucleotides degradation III  
 $n = 13$ ,  $Rho = 0.24$



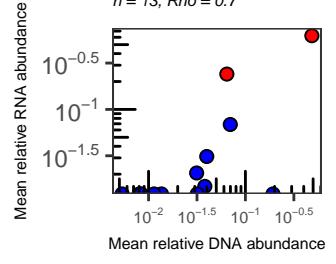
DAPLYSINESYN-PWY  
L-lysine  
biosynthesis I  
 $n = 11$ ,  $Rho = -0.13$



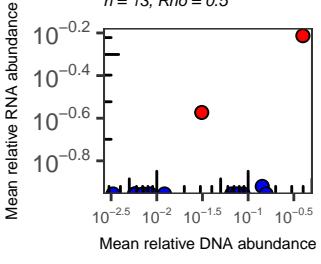
PWY0-845  
superpathway  
of pyridoxal 5'-phosphate biosy  
 $n = 11$ ,  $Rho = 0.73$



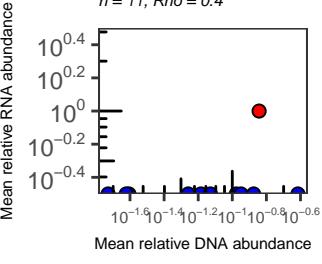
GLCMANNANAUT-PWY  
superpathway  
of N-acetylglucosamine, N-ace  
 $n = 13$ ,  $Rho = 0.7$



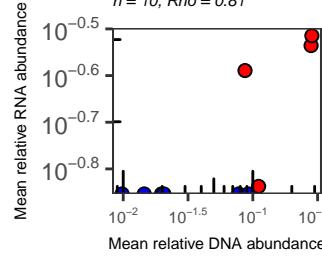
PWY-7237  
myo-,  
chiro- and scillo-inositol degra  
 $n = 13$ ,  $Rho = 0.5$



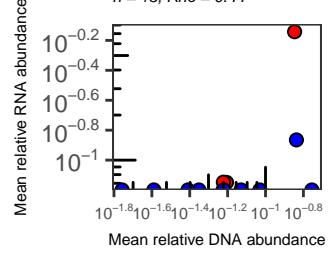
PWY-5347  
superpathway  
of L-methionine biosynthesis (t)  
 $n = 11$ ,  $Rho = 0.4$



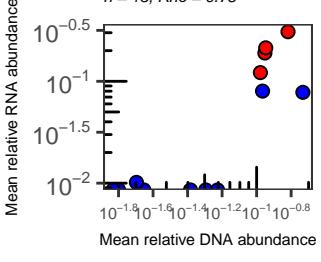
COBALSYN-PWY  
adenosylcobalamin  
salvage from cobinamide I  
 $n = 10$ ,  $Rho = 0.81$



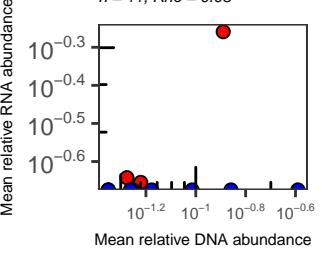
NAGLIPASYN-PWY  
lipid  
IVA biosynthesis  
 $n = 13$ ,  $Rho = 0.44$



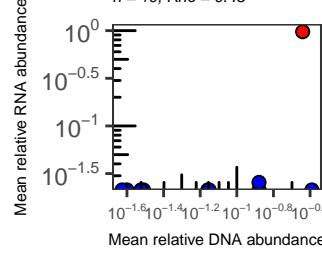
PWY66-400  
glycolysis  
VI (metazoan)  
 $n = 13$ ,  $Rho = 0.78$



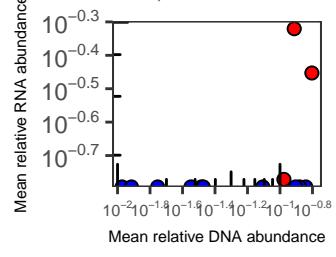
PWY-7184  
pyrimidine  
deoxyribonucleotides de novo b  
 $n = 11$ ,  $Rho = 0.03$



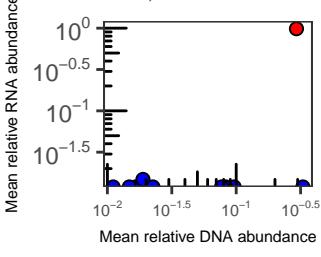
FASYN-INITIAL-PWY  
superpathway  
of fatty acid biosynthesis initiat  
 $n = 10$ ,  $Rho = 0.45$



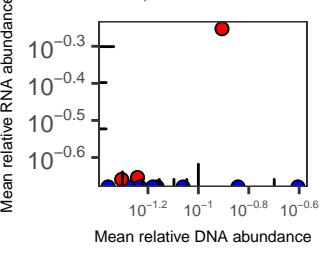
P461-PWY  
hexitol  
fermentation to lactate, formate,  
 $n = 13$ ,  $Rho = 0.44$



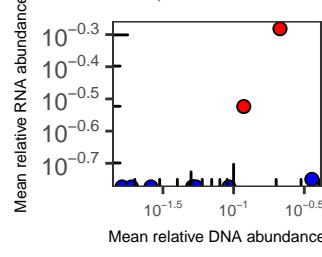
NAD-BIOSYNTHESIS-II  
NAD  
salvage pathway II  
 $n = 12$ ,  $Rho = 0.28$



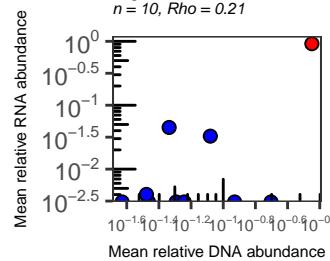
PWY0-166  
superpathway  
of pyrimidine deoxyribonucleot  
 $n = 11$ ,  $Rho = -0.11$



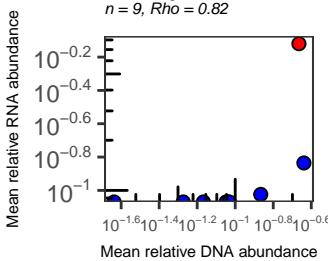
HEMESYN2-PWY  
heme  
biosynthesis II (anaerobic)  
 $n = 10$ ,  $Rho = 0.77$



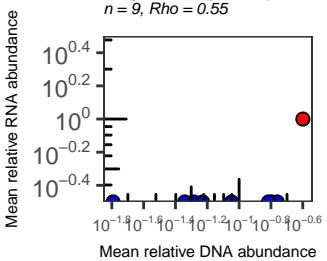
*P161-PWY*  
acetylene  
degradation  
 $n = 10$ ,  $Rho = 0.21$



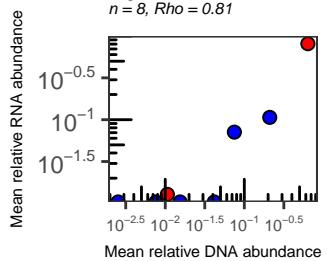
*FASYN-ELONG-PWY*  
fatty  
acid elongation -- saturated  
 $n = 9$ ,  $Rho = 0.82$



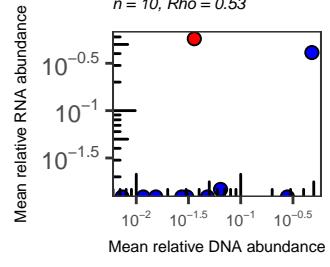
*PWY4FS-7*  
phosphatidylglycerol  
biosynthesis I (plastidic)  
 $n = 9$ ,  $Rho = 0.55$



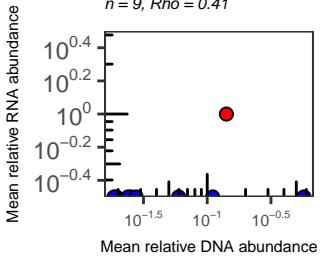
*PWY-7242*  
*D-fructuronate*  
degradation  
 $n = 8$ ,  $Rho = 0.81$



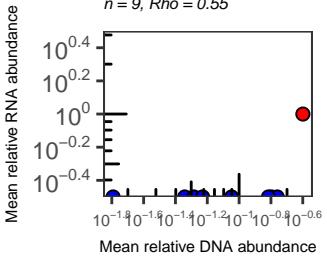
*PWY-5973*  
*cis-vaccenate*  
biosynthesis  
 $n = 10$ ,  $Rho = 0.53$



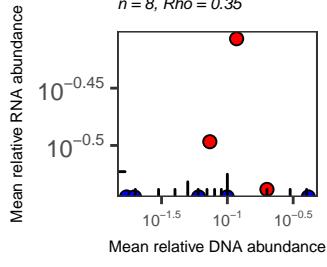
*PENTOSE-P-PWY*  
pentose  
phosphate pathway  
 $n = 9$ ,  $Rho = 0.41$



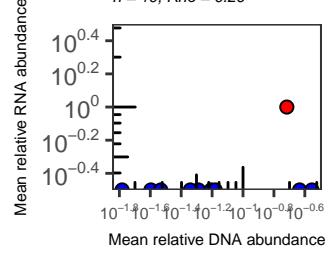
*PWY4FS-8*  
phosphatidylglycerol  
biosynthesis II (non-plastidic)  
 $n = 9$ ,  $Rho = 0.55$



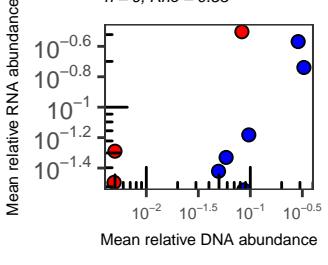
*PWY-7371*  
*1,4-dihydroxy-6-naphthoate*  
biosynthesis II  
 $n = 8$ ,  $Rho = 0.35$



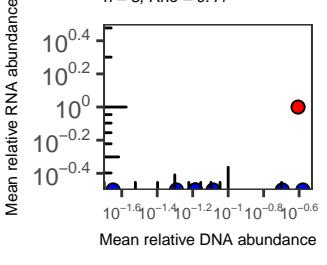
*PWY-6897*  
*thiamin*  
salvage II  
 $n = 10$ ,  $Rho = 0.29$



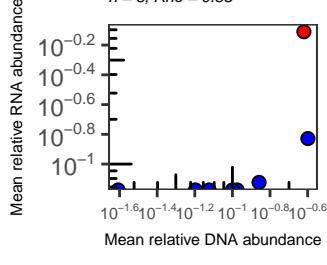
*PWY-5104*  
*L-isoleucine*  
biosynthesis IV  
 $n = 9$ ,  $Rho = 0.53$



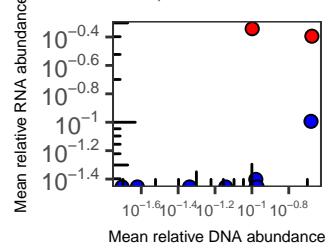
*PHOSLIPSYN-PWY*  
superpathway  
of phospholipid biosynthesis I (I  
 $n = 8$ ,  $Rho = 0.41$



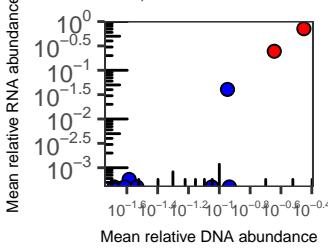
*PWY-7664*  
*oleate*  
biosynthesis IV (anaerobic)  
 $n = 8$ ,  $Rho = 0.85$



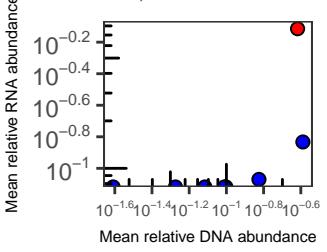
*PWY0-862*  
*(5Z)-dodec-5-enote*  
biosynthesis  
 $n = 10$ ,  $Rho = 0.53$



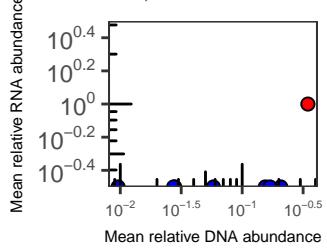
*PWY-5173*  
superpathway  
of acetyl-CoA biosynthesis  
 $n = 9$ ,  $Rho = 0.68$



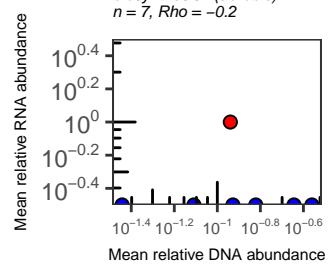
*PWY-6282*  
*palmoleate*  
biosynthesis I (from (5Z)-dodec  
 $n = 8$ ,  $Rho = 0.85$



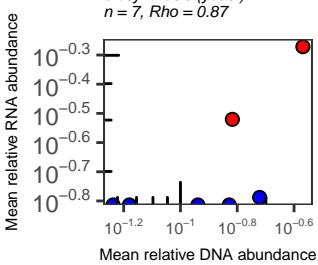
*PWY0-162*  
superpathway  
of pyrimidine ribonucleotides de  
 $n = 8$ ,  $Rho = 0.58$



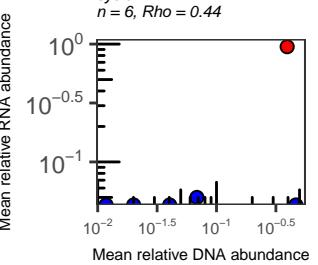
*HEME-BIOSYNTHESIS-II*  
*heme*  
*biosynthesis I (aerobic)*  
*n = 7, Rho = -0.2*



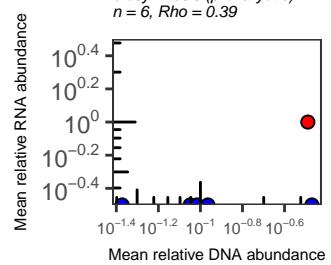
*PWY-7282*  
4-amino-2-methyl-5-phospho  
biosynthesis (yeast)  
*n = 7, Rho = 0.87*



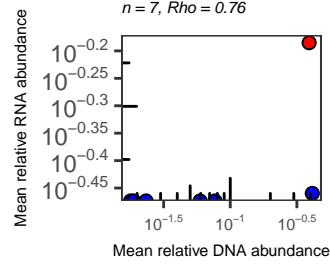
*GLYOXYLATE-BYPASS*  
*glyoxylate*  
*cycle*  
*n = 6, Rho = 0.44*



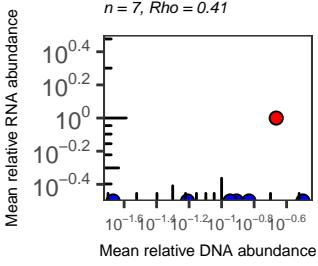
*PWY-5855*  
*ubiquinol-7*  
*biosynthesis (prokaryotic)*  
*n = 6, Rho = 0.39*



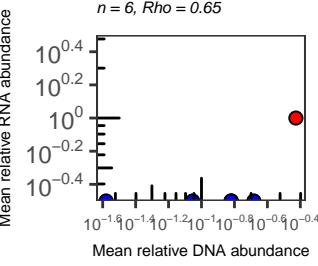
*PWY-4041*  
&gamma;-glutamyl  
cycle  
*n = 7, Rho = 0.76*



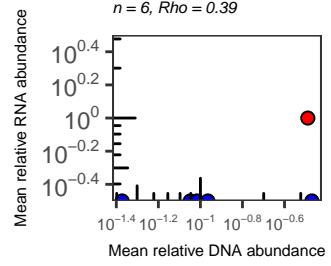
*PWY-7388*  
octanoyl-[acyl-carrier  
protein] biosynthesis (mitochon  
*n = 7, Rho = 0.41*



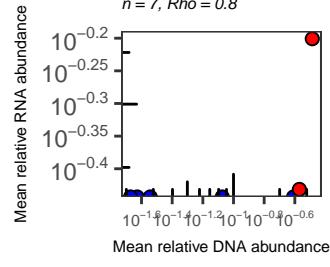
*PWY-5484*  
glycolysis  
*II (from fructose 6-phosphate)*  
*n = 6, Rho = 0.65*



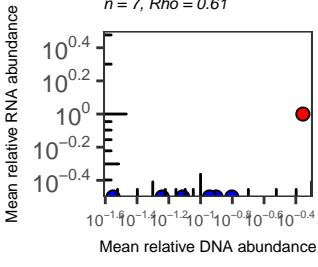
*PWY-5856*  
*ubiquinol-9*  
*biosynthesis (prokaryotic)*  
*n = 6, Rho = 0.39*



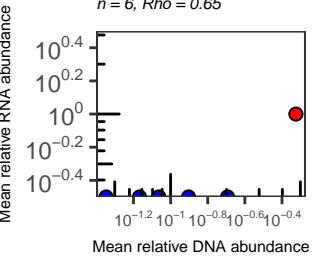
*PWY-5083*  
NAD/NADH  
phosphorylation and dephosp  
*n = 7, Rho = 0.8*



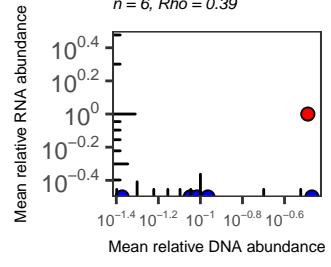
*PWY0-1241*  
ADP-L-glycero-&beta;,-D-mai  
biosynthesis  
*n = 7, Rho = 0.61*



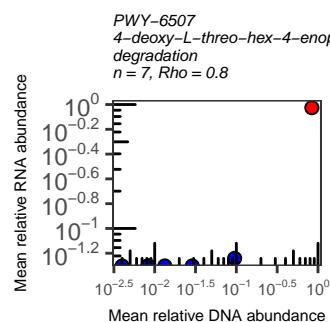
*PWY-5791*  
1,4-dihydroxy-2-naphthoate  
biosynthesis II (plants)  
*n = 6, Rho = 0.65*



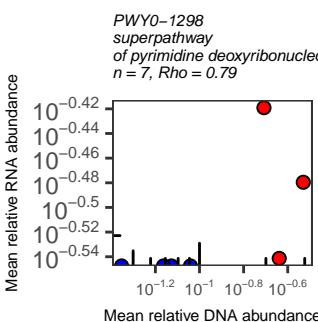
*PWY-5857*  
*ubiquinol-10*  
*biosynthesis (prokaryotic)*  
*n = 6, Rho = 0.39*



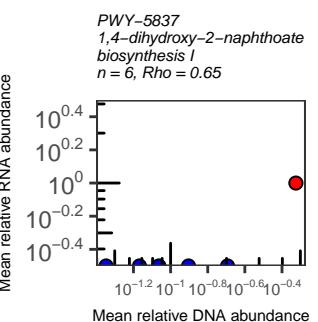
*PWY-6507*  
4-deoxy-L-threo-hex-4-enop  
degradation  
*n = 7, Rho = 0.8*



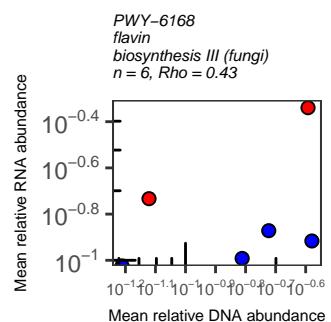
*PWY0-1298*  
superpathway  
of pyrimidine deoxyribonucleos  
*n = 7, Rho = 0.79*



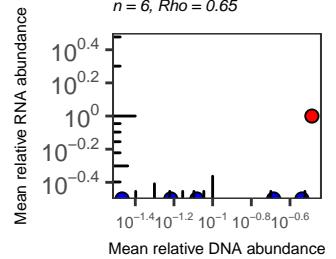
*PWY-5837*  
1,4-dihydroxy-2-naphthoate  
biosynthesis I  
*n = 6, Rho = 0.65*



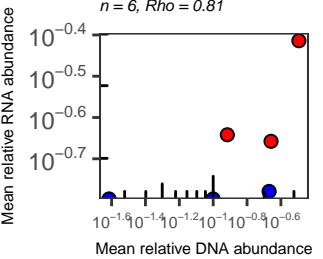
*PWY-6168*  
*flavin*  
*biosynthesis III (fungi)*  
*n = 6, Rho = 0.43*



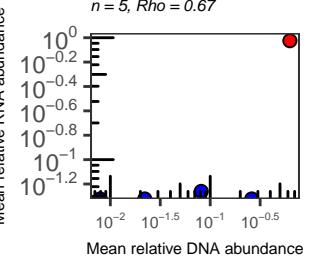
PWY-6519  
8-amino-7-oxononanoate  
biosynthesis I  
 $n = 6$ ,  $Rho = 0.65$



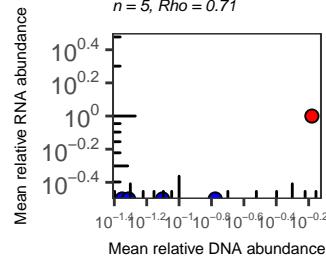
PWY-7539  
6-hydroxymethyl-dihydropterin  
diphosphate biosynthesis III (Cl)  
 $n = 6$ ,  $Rho = 0.81$



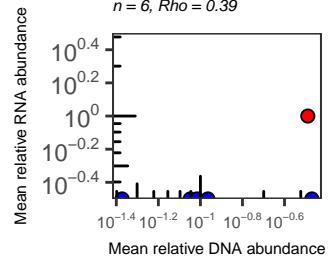
PWY-5367  
petroselinate  
biosynthesis  
 $n = 5$ ,  $Rho = 0.67$



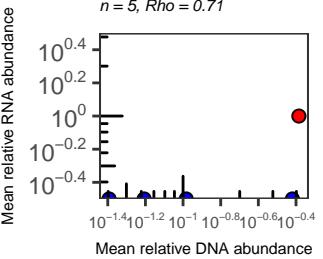
PWY-6859  
all-trans-farnesol  
biosynthesis  
 $n = 5$ ,  $Rho = 0.71$



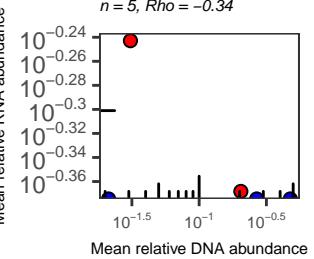
PWY-6708  
ubiquinol-8  
biosynthesis (prokaryotic)  
 $n = 6$ ,  $Rho = 0.39$



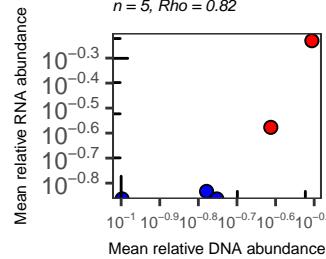
BIOTIN-BIOSYNTHESIS-PWY  
biotin  
biosynthesis I  
 $n = 5$ ,  $Rho = 0.71$



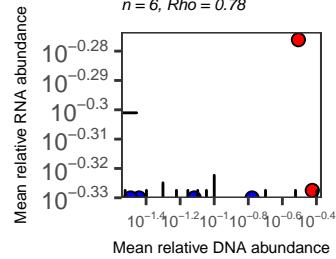
PWY-5690  
TCA  
cycle II (plants and fungi)  
 $n = 5$ ,  $Rho = -0.34$



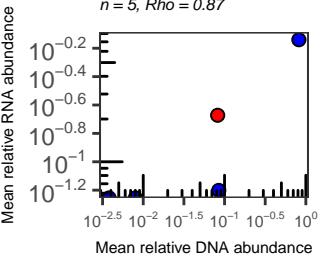
PWY-7323  
superpathway  
of GDP-mannose-derived O-a  
 $n = 5$ ,  $Rho = 0.82$



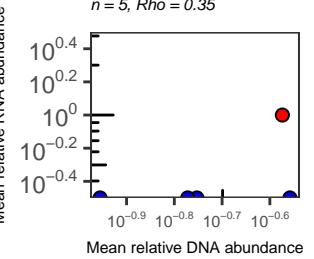
PWY-6803  
phosphatidylcholine  
acyl editing  
 $n = 6$ ,  $Rho = 0.78$



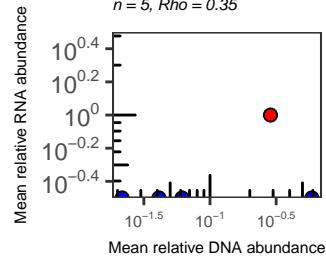
GALACTUROCAT-PWY  
D-galacturonate  
degradation I  
 $n = 5$ ,  $Rho = 0.87$



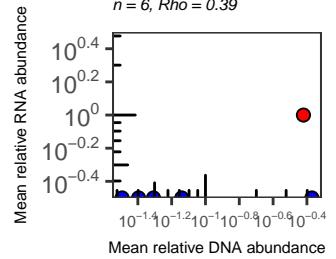
PWY-5989  
stearate  
biosynthesis II (bacteria and pla  
 $n = 5$ ,  $Rho = 0.35$



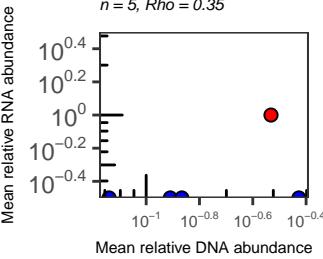
TCA  
TCA  
cycle I (prokaryotic)  
 $n = 5$ ,  $Rho = 0.35$



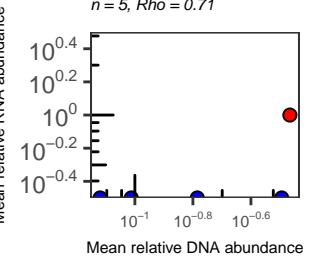
PWY-7013  
L-1,2-propanediol  
degradation  
 $n = 6$ ,  $Rho = 0.39$



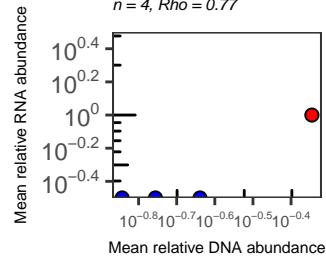
PWY-5154  
L-arginine  
biosynthesis III (via N-acetyl-L  
 $n = 5$ ,  $Rho = 0.35$



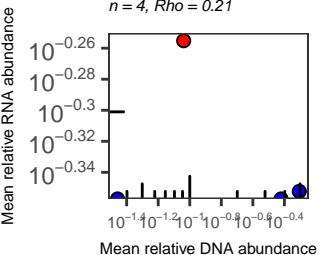
PWY-6628  
superpathway  
of L-phenylalanine biosynthesis  
 $n = 5$ ,  $Rho = 0.71$



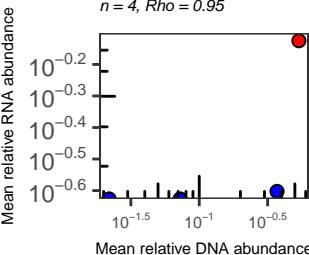
FAO-PWY  
fatty  
acid &beta;-oxidation I  
 $n = 4$ ,  $Rho = 0.77$



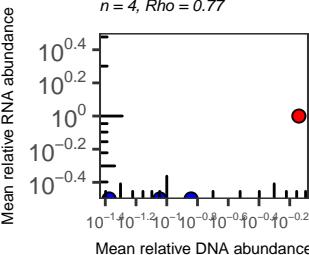
FUCCAT-PWY  
fucose  
degradation  
 $n = 4$ ,  $Rho = 0.21$



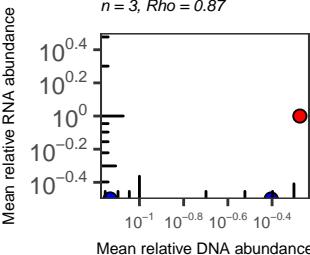
PWY-5384  
sucrose  
degradation IV (sucrose phospho)  
 $n = 4$ ,  $Rho = 0.95$



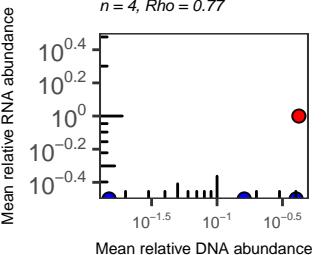
TCA-GLYOX-BYPASS  
superpathway  
of glyoxylate bypass and TCA  
 $n = 4$ ,  $Rho = 0.77$



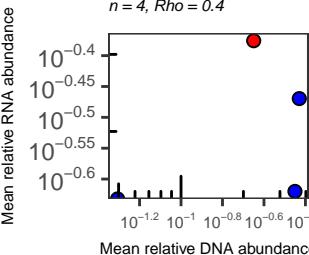
PWY-6270  
isoprene  
biosynthesis I  
 $n = 3$ ,  $Rho = 0.87$



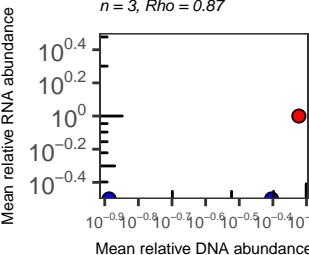
GLUCOSE1PMETAB-PWY  
glucose  
and glucose-1-phosphate deg  
 $n = 4$ ,  $Rho = 0.77$



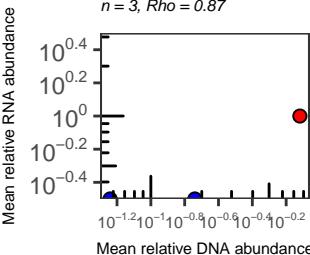
PWY-7456  
mannan  
degradation  
 $n = 4$ ,  $Rho = 0.4$



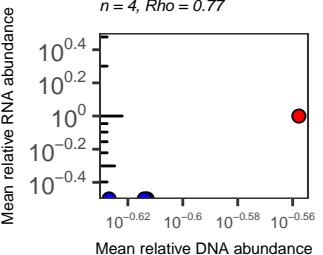
HCAMPHPDEG-PWY  
3-phenylpropanoate  
and 3-(3-hydroxyphenyl)propa  
 $n = 3$ ,  $Rho = 0.87$



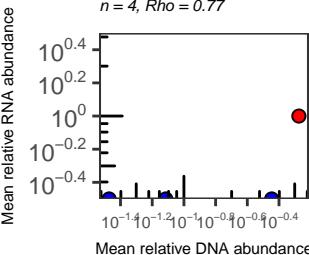
PWY-6612  
superpathway  
of tetrahydrofolate biosynthesis  
 $n = 3$ ,  $Rho = 0.87$



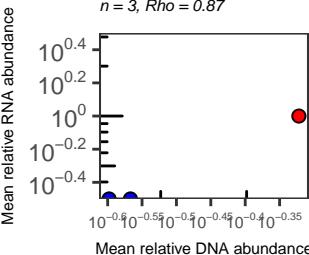
PWY-4984  
urea  
cycle  
 $n = 4$ ,  $Rho = 0.77$



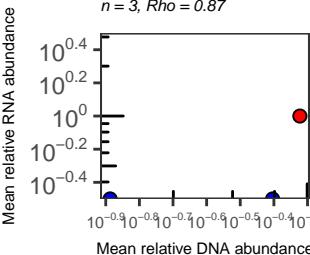
PWY-7560  
methylerithritol  
phosphate pathway II  
 $n = 4$ ,  $Rho = 0.77$



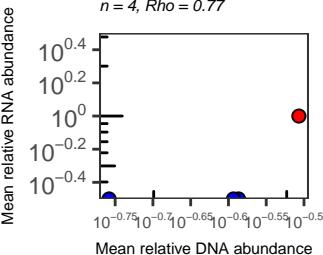
PWY-3781  
aerobic  
respiration I (cytochrome c)  
 $n = 3$ ,  $Rho = 0.87$



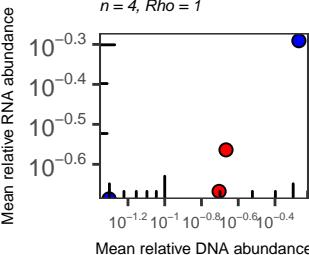
PWY-6690  
cinnamate  
and 3-hydroxycinnamate degra  
 $n = 3$ ,  $Rho = 0.87$



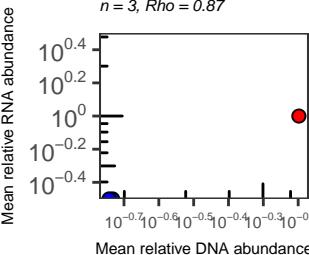
PWY-5138  
unsaturated,  
even numbered fatty acid & beta  
 $n = 4$ ,  $Rho = 0.77$



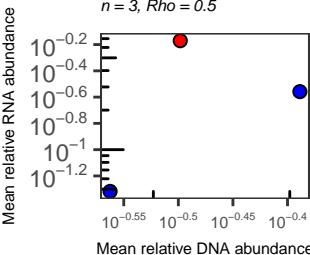
PWY-1479  
tRNA  
processing  
 $n = 4$ ,  $Rho = 1$



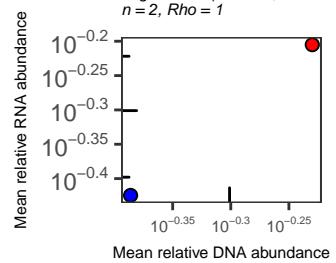
PWY-5136  
fatty  
acid & beta;-oxidation II (peroxis  
 $n = 3$ ,  $Rho = 0.87$



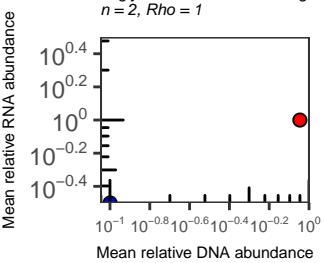
SALVADEHYPOX-PWY  
adenosine  
nucleotides degradation II  
 $n = 3$ ,  $Rho = 0.5$



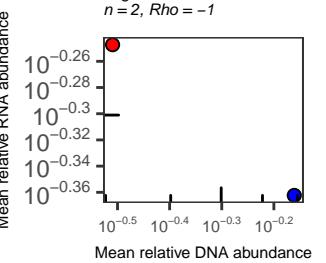
TALPHADEHYDROX-PWY  
cholate  
degradation (bacteria, anaerob)  
 $n = 2$ ,  $Rho = 1$



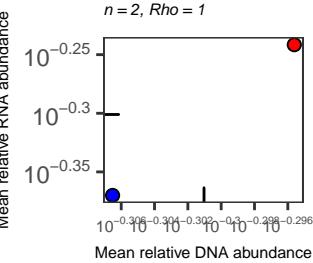
GLYCOL-GLYCOXDEG-PWY  
superpathway  
of glycol metabolism and degra  
 $n = 2$ ,  $Rho = 1$



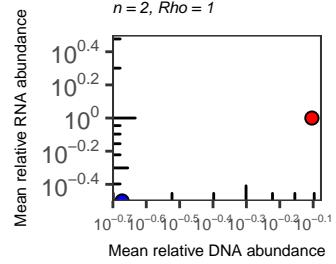
PWY-4702  
phytate  
degradation I  
 $n = 2$ ,  $Rho = -1$



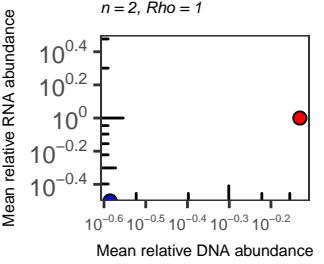
PWY-6588  
pyruvate  
fermentation to acetone  
 $n = 2$ ,  $Rho = 1$



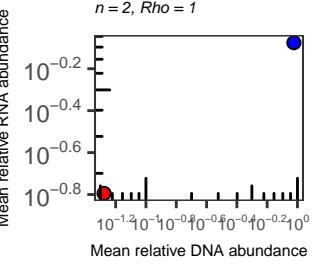
FOLSYN-PWY  
superpathway  
of tetrahydrofolate biosynthesis  
 $n = 2$ ,  $Rho = 1$



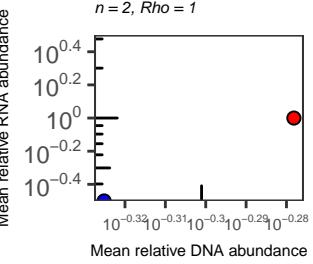
GLYCOLYSIS  
glycolysis  
I (from glucose 6-phosphate)  
 $n = 2$ ,  $Rho = 1$



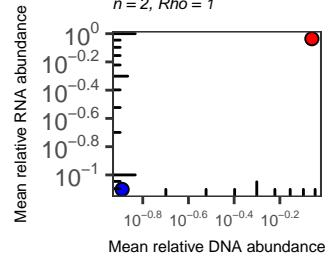
PWY-5101  
L-isoleucine  
biosynthesis II  
 $n = 2$ ,  $Rho = 1$



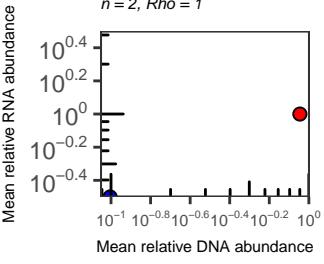
PWY-6630  
superpathway  
of L-tyrosine biosynthesis  
 $n = 2$ ,  $Rho = 1$



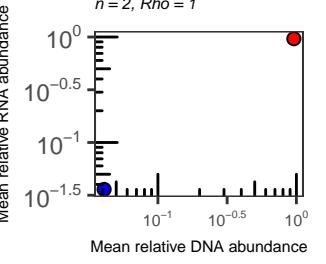
GALACT-GLUCUROCAT-PWY  
superpathway  
of hexuronide and hexuronate c  
 $n = 2$ ,  $Rho = 1$



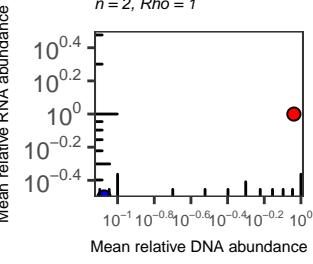
METHANOGENESIS-PWY  
methanogenesis  
from H2 and CO2  
 $n = 2$ ,  $Rho = 1$



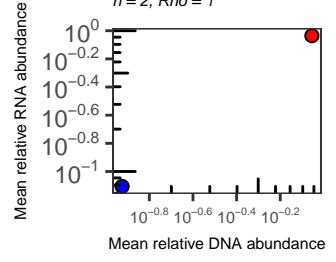
PWY-5177  
glutaryl-CoA  
degradation  
 $n = 2$ ,  $Rho = 1$



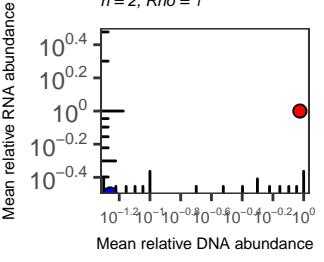
PWY-7269  
NAD/NADP-NADH/NADPH  
mitochondrial interconversion (y  
 $n = 2$ ,  $Rho = 1$



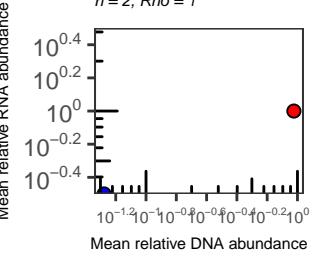
GLUCUROCAT-PWY  
superpathway  
of &beta;-D-glucuronide and D  
 $n = 2$ ,  $Rho = 1$



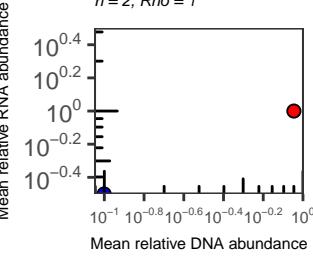
PWY-2723  
trehalose  
degradation V  
 $n = 2$ ,  $Rho = 1$



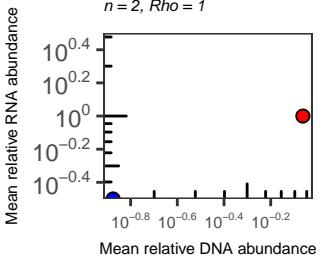
PWY-5198  
factor  
420 biosynthesis  
 $n = 2$ ,  $Rho = 1$



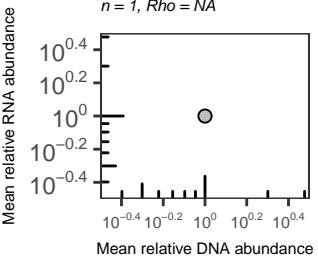
PWY-7315  
dTDP-N-acetylthiomosamine  
biosynthesis  
 $n = 2$ ,  $Rho = 1$



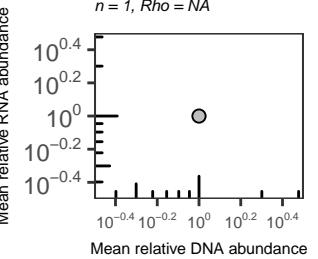
*PWY-0-1261*  
anhydromuropeptides  
recycling  
 $n = 2$ ,  $Rho = 1$



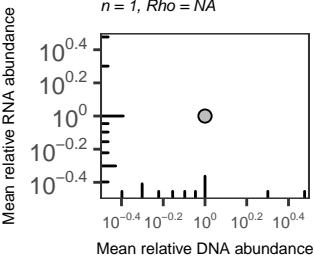
*ENTBACSYN-PWY*  
enterobactin  
biosynthesis  
 $n = 1$ ,  $Rho = NA$



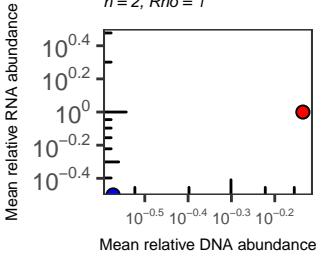
*LPSSYN-PWY*  
superpathway  
of lipopolysaccharide biosynthe  
 $n = 1$ ,  $Rho = NA$



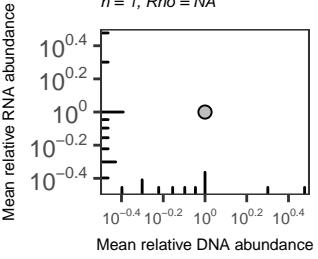
*PWY-5840*  
superpathway  
of menaquinol-7 biosynthesis  
 $n = 1$ ,  $Rho = NA$



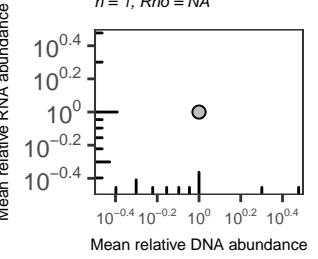
*PWY66-409*  
superpathway  
of purine nucleotide salvage  
 $n = 2$ ,  $Rho = 1$



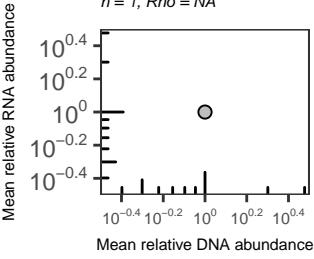
*GLYCOLYSIS-E-D*  
superpathway  
of glycolysis and Entner-Doudc  
 $n = 1$ ,  $Rho = NA$



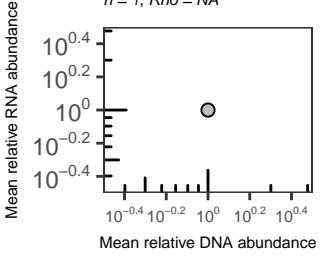
*P261-PWY*  
coenzyme  
M biosynthesis I  
 $n = 1$ ,  $Rho = NA$



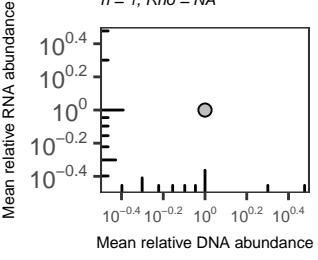
*PWY-5845*  
superpathway  
of menaquinol-9 biosynthesis  
 $n = 1$ ,  $Rho = NA$



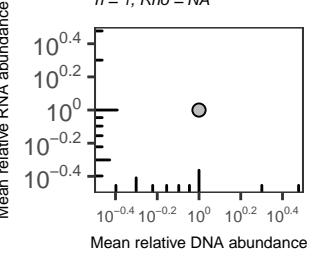
*AEROBACTINSYN-PWY*  
aerobactin  
biosynthesis  
 $n = 1$ ,  $Rho = NA$



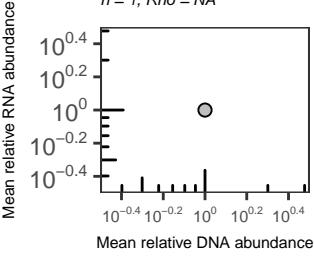
*HSMERMETANA-PWY*  
L-methionine  
biosynthesis III  
 $n = 1$ ,  $Rho = NA$



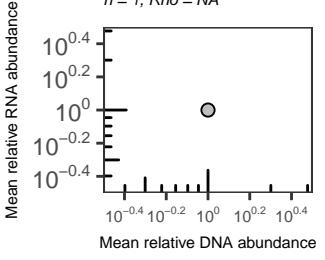
*POLYISOPRENSYN-PWY*  
polyisoprenoid  
biosynthesis (*E. coli*)  
 $n = 1$ ,  $Rho = NA$



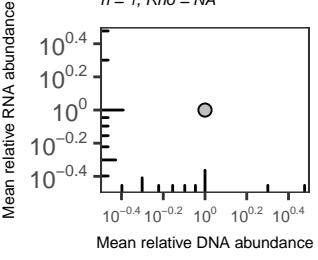
*PWY-5850*  
superpathway  
of menaquinol-6 biosynthesis I  
 $n = 1$ ,  $Rho = NA$



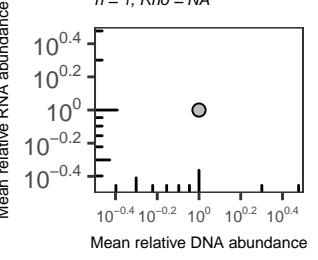
*ECASYN-PWY*  
enterobacterial  
common antigen biosynthesis  
 $n = 1$ ,  $Rho = NA$



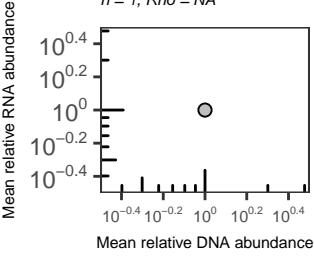
*KDO-NAGLIPASYN-PWY*  
superpathway  
of (Kdo)2-lipid A biosynthesis  
 $n = 1$ ,  $Rho = NA$



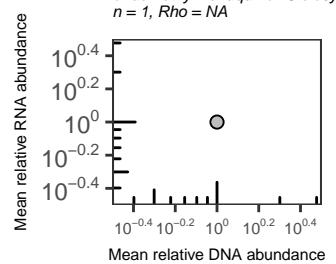
*PWY-5838*  
superpathway  
of menaquinol-8 biosynthesis I  
 $n = 1$ ,  $Rho = NA$



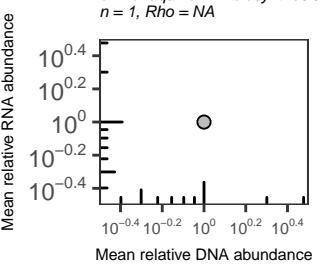
*PWY-5860*  
superpathway  
of demethylmenaquinol-6 biosy  
 $n = 1$ ,  $Rho = NA$



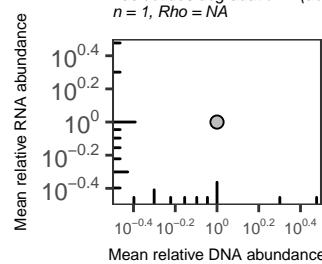
*PWY-5861*  
superpathway  
of demethylmenaquinol-8 biosy  
 $n = 1$ ,  $Rho = NA$



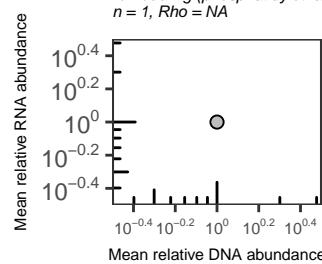
*PWY-5897*  
superpathway  
of menaquinol-11 biosynthesis  
 $n = 1$ ,  $Rho = NA$



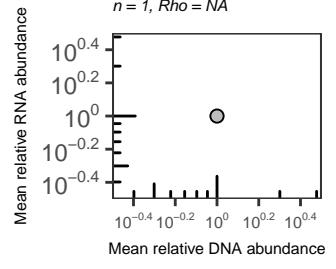
*PWY-6353*  
purine  
nucleotides degradation II (aero  
 $n = 1$ ,  $Rho = NA$



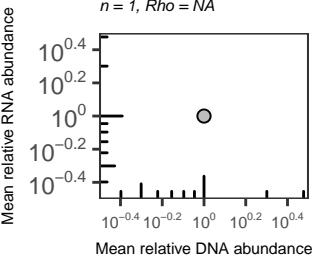
*PWY-7409*  
phospholipid  
remodeling (phosphatidylethanolam  
 $n = 1$ ,  $Rho = NA$



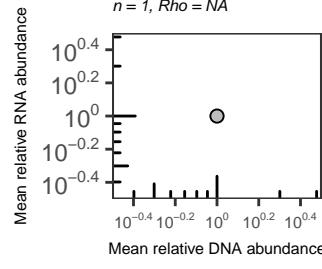
*PWY-5862*  
superpathway  
of demethylmenaquinol-9 biosy  
 $n = 1$ ,  $Rho = NA$



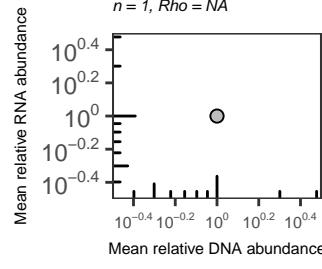
*PWY-5898*  
superpathway  
of menaquinol-12 biosynthesis  
 $n = 1$ ,  $Rho = NA$



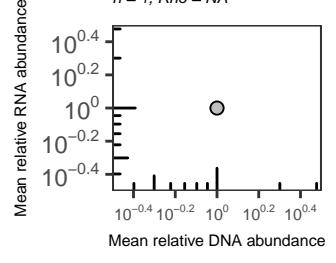
*PWY-6467*  
*Kdo*  
transfer to lipid IVA III (Chlamyd  
 $n = 1$ ,  $Rho = NA$



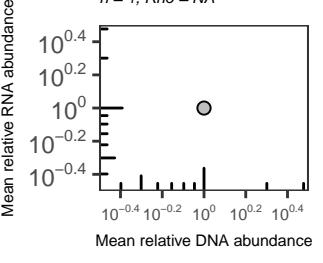
*PWY-1533*  
methylphosphonate  
degradation I  
 $n = 1$ ,  $Rho = NA$



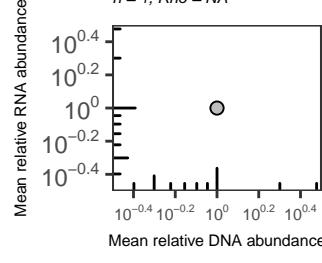
*PWY-5863*  
superpathway  
of phylloquinol biosynthesis  
 $n = 1$ ,  $Rho = NA$



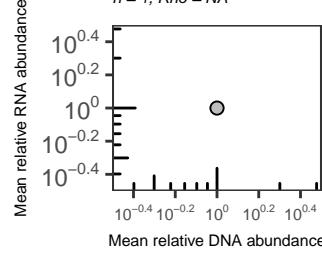
*PWY-5899*  
superpathway  
of menaquinol-13 biosynthesis  
 $n = 1$ ,  $Rho = NA$



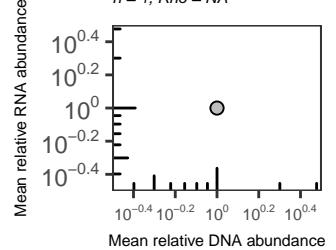
*PWY-6823*  
molybdenum  
cofactor biosynthesis  
 $n = 1$ ,  $Rho = NA$



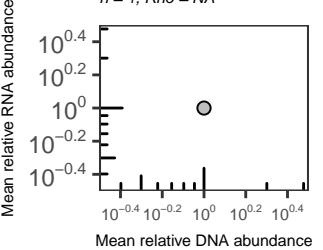
*RIBOSYN2-PWY*  
flavin  
biosynthesis I (bacteria and pla  
 $n = 1$ ,  $Rho = NA$



*PWY-5896*  
superpathway  
of menaquinol-10 biosynthesis  
 $n = 1$ ,  $Rho = NA$



*PWY-6167*  
flavin  
biosynthesis II (archaea)  
 $n = 1$ ,  $Rho = NA$



*PWY-7279*  
aerobic  
respiration II (cytochrome c) (yeast)  
 $n = 1$ ,  $Rho = NA$

