

Supplementary material. **Table S1.**
Percentage of reads showing homology to genes associated with KEGG pathways
(Full list).

KEGG pathway	% Green Mat ^a	% Red Mat ^a
10 Glycolysis / Gluconeogenesis [PATH:ko00010]	3.40	3.31
20 Citrate cycle (TCA cycle) [PATH:ko00020]	1.85 ± 0.017	1.58 ± 0.018
30 Pentose phosphate pathway [PATH:ko00030]	1.51 ± 0.015	1.24 ± 0.016
40 Pentose and glucuronate interconversions [PATH:ko00040]	0.64	0.55
51 Fructose and mannose metabolism [PATH:ko00051]	1.87 ± 0.017	1.72 ± 0.019
52 Galactose metabolism [PATH:ko00052]	0.64	0.61
53 Ascorbate and aldarate metabolism [PATH:ko00053]	0.15 ± 0.005	0.02 ± 0.002
61 Fatty acid biosynthesis [PATH:ko00061]	1.64 ± 0.016	1.11 ± 0.016
62 Fatty acid elongation in mitochondria [PATH:ko00062]	0.23 ± 0.006	0.06 ± 0.004
71 Fatty acid metabolism [PATH:ko00071]	2.07 ± 0.018	0.91 ± 0.014
72 Synthesis and degradation of ketone bodies [PATH:ko00072]	0.15	0.11
100 Steroid biosynthesis [PATH:ko00100]	0.04	0.09
120 Primary bile acid biosynthesis [PATH:ko00120]	0.09	0.01
130 Terpenoid-quinone biosynthesis [PATH:ko00130]	0.98 ± 0.013	0.66 ± 0.012
140 Steroid hormone biosynthesis [PATH:ko00140]	0.01 ± 0.001	0.12 ± 0.005
190 Oxidative phosphorylation [PATH:ko00190]	3.83	3.89
195 Photosynthesis [PATH:ko00195]	0.21 ± 0.006	0.44 ± 0.010
196 Photosynthesis - antenna proteins [PATH:ko00196]	0.09 ± 0.004	0.21 ± 0.007
230 Purine metabolism [PATH:ko00230]	6.43 ± 0.031	6.54 ± 0.036
232 Caffeine metabolism [PATH:ko00232]	0.01	NA
240 Pyrimidine metabolism [PATH:ko00240]	2.07 ± 0.018	2.26 ± 0.022
250 Alanine, aspartate and glutamate metabolism [PATH:ko00250]	2.30 ± 0.019	2.12 ± 0.021
260 Glycine, serine and threonine metabolism [PATH:ko00260]	2.75 ± 0.021	1.83 ± 0.020
270 Cysteine and methionine metabolism [PATH:ko00270]	1.97 ± 0.018	1.20 ± 0.016
280 Valine, leucine and isoleucine degradation [PATH:ko00280]	1.37 ± 0.015	1.03 ± 0.015
281 Geraniol degradation [PATH:ko00281]	0.50 ± 0.009	0.15 ± 0.006
290 Valine, leucine and isoleucine biosynthesis [PATH:ko00290]	1.52 ± 0.015	2.35 ± 0.022
300 Lysine biosynthesis [PATH:ko00300]	0.93	0.96
310 Lysine degradation [PATH:ko00310]	0.21	0.17
311 Penicillin and cephalosporin biosynthesis [PATH:ko00311]	0.20	0.13
330 Arginine and proline metabolism [PATH:ko00330]	2.29 ± 0.019	1.10 ± 0.016
340 Histidine metabolism [PATH:ko00340]	1.04	1.11
350 Tyrosine metabolism [PATH:ko00350]	0.67 ± 0.010	0.19 ± 0.006
351 1,1,1-Trichloro-2,2-bis(4-chlorophenyl)ethane (DDT) degradation [PATH:ko00351]	0.03	0.01
360 Phenylalanine metabolism [PATH:ko00360]	0.45 ± 0.008	0.21 ± 0.007
361 Chlorocyclohexane and chlorobenzene degradation [PATH:ko00361]	0.40 ± 0.008	0.10 ± 0.005

362	Benzoate degradation [PATH:ko00362]	0.43 ± 0.008	0.11 ± 0.005
363	Bisphenol degradation [PATH:ko00363]	0.01	0.06
380	Tryptophan metabolism [PATH:ko00380]	0.60 ± 0.010	0.31 ± 0.008
400	Phenylalanine, tyrosine and tryptophan biosynthesis [PATH:ko00400]	1.33 ± 0.014	1.22 ± 0.016
410	beta-Alanine metabolism [PATH:ko00410]	0.16	0.11
430	Taurine and hypotaurine metabolism [PATH:ko00430]	0.32 ± 0.007	0.22 ± 0.007
440	Phosphonate and phosphinate metabolism [PATH:ko00440]	0.14 ± 0.005	0.04 ± 0.003
450	Selenocompound metabolism [PATH:ko00450]	0.46	0.52
460	Cyanoamino acid metabolism [PATH:ko00460]	0.25	0.15
471	D-Glutamine and D-glutamate metabolism [PATH:ko00471]	0.29 ± 0.007	0.44 ± 0.010
473	D-Alanine metabolism [PATH:ko00473]	0.24 ± 0.006	0.37 ± 0.009
480	Glutathione metabolism [PATH:ko00480]	0.91 ± 0.012	0.48 ± 0.010
500	Starch and sucrose metabolism [PATH:ko00500]	1.39 ± 0.015	1.21 ± 0.016
510	N-Glycan biosynthesis [PATH:ko00510]	0.13 ± 0.005	0.30 ± 0.008
511	Other glycan degradation [PATH:ko00511]	0.20	0.14
512	Mucin type O-glycan biosynthesis [PATH:ko00512]	0.00	0.00
514	Other types of O-glycan biosynthesis [PATH:ko00514]	0.02	0.01
520	Amino sugar and nucleotide sugar metabolism [PATH:ko00520]	1.24	1.20
521	Streptomycin biosynthesis [PATH:ko00521]	0.93	0.89
531	Glycosaminoglycan degradation [PATH:ko00531]	0.07	0.04
540	Lipopolysaccharide biosynthesis [PATH:ko00540]	0.87 ± 0.012	1.03 ± 0.015
550	Peptidoglycan biosynthesis [PATH:ko00550]	1.17 ± 0.014	1.61 ± 0.019
561	Glycerolipid metabolism [PATH:ko00561]	0.55 ± 0.009	0.34 ± 0.009
562	Inositol phosphate metabolism [PATH:ko00562]	0.15 ± 0.005	0.05 ± 0.003
563	Glycosylphosphatidylinositol(GPI)-anchor biosynthesis [PATH:ko00563]	0.03	0.00
564	Glycerophospholipid metabolism [PATH:ko00564]	0.90 ± 0.012	0.43 ± 0.010
565	Ether lipid metabolism [PATH:ko00565]	0.04	0.01
590	Arachidonic acid metabolism [PATH:ko00590]	0.01	0.02
591	Linoleic acid metabolism [PATH:ko00591]	0.02	0.00
592	alpha-Linolenic acid metabolism [PATH:ko00592]	0.01	NA
600	Sphingolipid metabolism [PATH:ko00600]	0.05	0.04
620	Pyruvate metabolism [PATH:ko00620]	1.39 ± 0.015	1.03 ± 0.015
621	Dioxin degradation [PATH:ko00621]	0.00	0.00
623	Toluene degradation [PATH:ko00623]	0.15 ± 0.005	0.00 ± 0.001
625	Chloroalkane and chloroalkene degradation [PATH:ko00625]	0.02	0.04
627	Aminobenzoate degradation [PATH:ko00627]	0.00	0.09
630	Glyoxylate and dicarboxylate metabolism [PATH:ko00630]	1.23 ± 0.014	0.27 ± 0.008
633	Nitrotoluene degradation [PATH:ko00633]	0.09	0.06
640	Propanoate metabolism [PATH:ko00640]	0.27 ± 0.007	0.14 ± 0.006
643	Styrene degradation [PATH:ko00643]	0.01	0.01
650	Butanoate metabolism [PATH:ko00650]	0.25 ± 0.006	0.09 ± 0.004
660	C5-Branched dibasic acid metabolism [PATH:ko00660]	0.02	NA

670	One carbon pool by folate [PATH:ko00670]	0.27 ± 0.007	0.49 ± 0.010
680	Methane metabolism [PATH:ko00680]	0.28	0.27
710	Carbon fixation in photosynthetic organisms [PATH:ko00710]	0.08	0.05
730	Thiamine metabolism [PATH:ko00730]	0.94 ± 0.012	0.54 ± 0.011
740	Riboflavin metabolism [PATH:ko00740]	0.56	0.53
750	Vitamin B6 metabolism [PATH:ko00750]	0.38 ± 0.008	0.23 ± 0.007
760	Nicotinate and nicotinamide metabolism [PATH:ko00760]	1.00 ± 0.013	0.73 ± 0.013
770	Pantothenate and CoA biosynthesis [PATH:ko00770]	0.60 ± 0.010	0.46 ± 0.010
780	Biotin metabolism [PATH:ko00780]	0.33	0.34
785	Lipoic acid metabolism [PATH:ko00785]	0.16	0.18
790	Folate biosynthesis [PATH:ko00790]	0.63 ± 0.010	0.40 ± 0.009
791	Atrazine degradation [PATH:ko00791]	0.07	0.04
830	Retinol metabolism [PATH:ko00830]	0.03	0.03
860	Porphyrin and chlorophyll metabolism [PATH:ko00860]	2.59 ± 0.020	2.34 ± 0.022
900	Terpenoid backbone biosynthesis [PATH:ko00900]	0.69 ± 0.011	0.97 ± 0.015
903	Limonene and pinene degradation [PATH:ko00903]	0.00	0.02
904	Diterpenoid biosynthesis [PATH:ko00904]	0.00	0.00
906	Carotenoid biosynthesis [PATH:ko00906]	0.17	0.22
908	Zeatin biosynthesis [PATH:ko00908]	0.08	0.11
910	Nitrogen metabolism [PATH:ko00910]	1.03 ± 0.013	0.41 ± 0.010
920	Sulfur metabolism [PATH:ko00920]	0.11	0.10
930	Caprolactam degradation [PATH:ko00930]	0.07	NA
940	Phenylpropanoid biosynthesis [PATH:ko00940]	0.02	NA
941	Flavonoid biosynthesis [PATH:ko00941]	0.05	0.04
944	Flavone and flavonol biosynthesis [PATH:ko00944]	0.00	0.00
950	Isoquinoline alkaloid biosynthesis [PATH:ko00950]	0.01	0.00
960	Tropane, piperidine and pyridine alkaloid biosynthesis [PATH:ko00960]	0.04	0.04
970	Aminoacyl-tRNA biosynthesis [PATH:ko00970]	2.16 ± 0.018	4.34 ± 0.030
980	Metabolism of xenobiotics by cytochrome P450 [PATH:ko00980]	0.05	0.00
982	Drug metabolism - cytochrome P450 [PATH:ko00982]	0.01	NA
983	Drug metabolism - other enzymes [PATH:ko00983]	0.08	0.01
1040	Biosynthesis of unsaturated fatty acids [PATH:ko01040]	0.01	0.03
1053	Biosynthesis of siderophore group nonribosomal peptides [PATH:ko01053]	0.07	0.04
2010	ABC transporters [PATH:ko02010]	8.83 ± 0.036	5.12 ± 0.032
2020	Two-component system [PATH:ko02020]	4.59 ± 0.026	2.43 ± 0.023
2030	Bacterial chemotaxis [PATH:ko02030]	1.27 ± 0.014	0.08 ± 0.004
2040	Flagellar assembly [PATH:ko02040]	1.08 ± 0.013	0.31 ± 0.008
2060	Phosphotransferase system (PTS) [PATH:ko02060]	0.15	0.09
3008	Ribosome biogenesis in eukaryotes [PATH:ko03008]	0.00	0.09
3010	Ribosome [PATH:ko03010]	1.81 ± 0.017	1.95 ± 0.021
3013	RNA transport [PATH:ko03013]	0.00 ± 0.000	0.19 ± 0.006

3018	RNA degradation [PATH:ko03018]	1.03	1.10
3022	Basal transcription factors [PATH:ko03022]	0.02	0.01
3030	DNA replication [PATH:ko03030]	0.69 ± 0.011	1.01 ± 0.015
3040	Spliceosome [PATH:ko03040]	0.02	0.02
3050	Proteasome [PATH:ko03050]	0.02	0.01
3060	Protein export [PATH:ko03060]	1.26 ± 0.014	1.60 ± 0.019
3070	Bacterial secretion system [PATH:ko03070]	0.90 ± 0.012	0.55 ± 0.011
3320	PPAR signaling pathway [PATH:ko03320]	0.00	0.00
3410	Base excision repair [PATH:ko03410]	0.80	0.72
3420	Nucleotide excision repair [PATH:ko03420]	1.03 ± 0.013	2.43 ± 0.023
3430	Mismatch repair [PATH:ko03430]	0.42 ± 0.008	0.94 ± 0.014
3440	Homologous recombination [PATH:ko03440]	0.98 ± 0.013	1.50 ± 0.018
4010	MAPK signaling pathway [PATH:ko04010]	0.07	0.01

^a The given error is the standard error from False Discovery Rate analysis.

Table S2.**PCA analysis of SEED Subsystems level 1 (Meyer *et al.*, 2008).****Correlation of each variable with factor 1**

	Correlation	P-value
Cluster system	0.99922	2.95E-42
Cofactors and pigments	0.997675	2.18E-35
Miscellaneous	0.997555	4.52E-35
Amino acids	0.997344	1.50E-34
Carbohydrates	0.996973	9.97E-34
Protein metabolism	0.996624	4.83E-33
Cell division	0.995114	1.02E-30
Cell wall	0.995105	1.05E-30
Lipids	0.99492	1.79E-30
Nucleotides	0.994764	2.77E-30
DNA metabolism	0.994473	6.06E-30
RNA metabolism	0.994238	1.11E-29
Respiration	0.993927	2.37E-29
Stress response	0.993802	3.18E-29
Transport	0.993616	4.88E-29
Sulfur	0.992958	2.02E-28
Aromatic	0.992208	8.69E-28
Nitrogen	0.991532	2.89E-27
Secondary metabolism	0.990146	2.58E-26
Virulence	0.987861	5.24E-25
Cell signaling	0.987054	1.33E-24
Spore	0.980752	4.00E-22
Motility	0.97793	2.86E-21
Potassium	0.977141	4.73E-21
Phosphorus	0.97681	5.82E-21
Phages	0.969652	2.75E-19
Iron	0.969093	3.57E-19
Photosynthesis	0.927324	6.60E-14

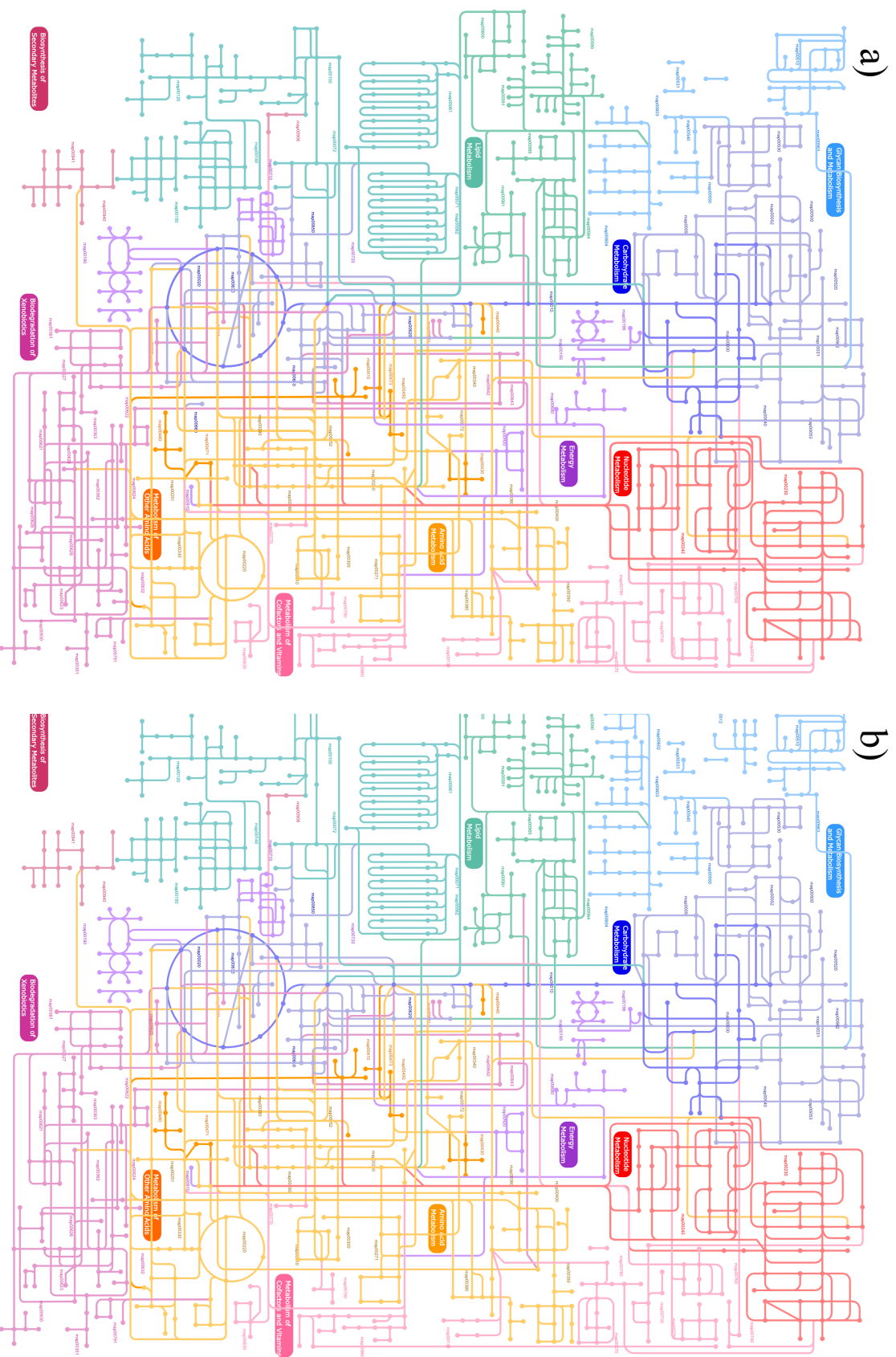


Figure S1. Graphic overview of the metabolism identified in the mats. Nodes represent compounds while edges represent enzymes. a) Pathways observed in Red mat; b) Pathways observed in Green mat. The underlying global pathways map is constructed using 123 KEGG pathways (Kanehisa 2008). This figure was made using iPath (Letunic 2008).