

Supplementary table 3 - 313 significantly differentially represented metagenomic pathways between Mg2800 and Mg500 FMT recipients*.

ID number	Pathway description	Source	p-value	Mg2800_abundance	Mg500_abundance	fold_difference
Increased abundance in recipients from Mg2800 FMT						
K03519	coxM, cutM; aerobic carbon-monoxide dehydrogenase medium subunit [EC:1.2.5.3]	KO	0.002052	1140.857	16.889	67.551
K08323	rspA, manD; mannonate dehydratase [EC:4.2.1.8]	KO	0.002178	2196.714	43.333	50.693
K08322	rspB; L-gulonate 5-dehydrogenase [EC:1.1.1.380]	KO	0.000978	1663.000	42.333	39.283
EC:2.5.1.26	Alkylglycerone-phosphate synthase	EC	0.000832	21.500	0.611	35.182
K00803	AGPS, agpS; alkyldihydroxyacetonephosphate synthase [EC:2.5.1.26]	KO	0.000832	21.500	0.611	35.182
K05780	phnL; alpha-D-ribose 1-methylphosphonate 5-triphosphate synthase subunit PhnL [EC:2.7.8.37]	KO	0.000954	21.500	0.611	35.182
K05781	phnK; putative phosphonate transport system ATP-binding protein	KO	0.000954	21.500	0.611	35.182
K06162	phnM; alpha-D-ribose 1-methylphosphonate 5-triphosphate diphosphatase [EC:3.6.1.63]	KO	0.000954	21.500	0.611	35.182
K06163	phnJ; alpha-D-ribose 1-methylphosphonate 5-phosphate C-P lyase [EC:4.7.1.1]	KO	0.000954	21.500	0.611	35.182
K06164	phnI; alpha-D-ribose 1-methylphosphonate 5-triphosphate synthase subunit PhnI [EC:2.7.8.37]	KO	0.000954	21.500	0.611	35.182
K06165	phnH; alpha-D-ribose 1-methylphosphonate 5-triphosphate synthase subunit PhnH [EC:2.7.8.37]	KO	0.000954	21.500	0.611	35.182
K06166	phnG; alpha-D-ribose 1-methylphosphonate 5-triphosphate synthase subunit PhnG [EC:2.7.8.37]	KO	0.000954	21.500	0.611	35.182
EC:1.1.1.28†	D-arabinitol dehydrogenase (NADP+)	EC	0.000959	41.857	1.222	34.247
EC:2.7.1.16†	Glycerate 2-kinase	EC	0.000959	20.929	0.611	34.247
EC:3.6.3.36	Taurine-transporting ATPase	EC	0.000959	20.929	0.611	34.247
EC:4.1.1.46	o-pyrocatechuate decarboxylase	EC	0.000959	20.929	0.611	34.247
K01820	rhaA; L-rhamnose isomerase / sugar isomerase [EC:5.3.1.14 5.3.1.-]	KO	0.000959	20.929	0.611	34.247
K06121	dhbC; glycerol dehydratase medium subunit [EC:4.2.1.30]	KO	0.000959	20.929	0.611	34.247
K10831	tauB; taurine transport system ATP-binding protein [EC:3.6.3.36]	KO	0.000959	20.929	0.611	34.247
K11529	gck, gckA, GLYCK; glycerate 2-kinase [EC:2.7.1.165]	KO	0.000959	20.929	0.611	34.247
K11922	mngR, farR; GntR family transcriptional regulator, mannosyl-D-glycerate transport/metabolism system repress	KO	0.000959	20.929	0.611	34.247
K12997	rgpB; rhamnosyltransferase [EC:2.4.1.-]	KO	0.000959	20.929	0.611	34.247
K14333	DHBD; 2,3-dihydroxybenzoate decarboxylase [EC:4.1.1.46]	KO	0.000959	20.929	0.611	34.247
K14988	salK; two-component system, NarL family, secretion system sensor histidine kinase SalK	KO	0.000959	20.929	0.611	34.247
K14989	salR; two-component system, NarL family, secretion system response regulator SalR	KO	0.000959	20.929	0.611	34.247
K15654	surFA, IchAA; surfactin family lipopeptide synthetase A	KO	0.000959	20.929	0.611	34.247
K17331	dasC; N,N'-diacetylchitobiose transport system permease protein	KO	0.000959	20.929	0.611	34.247
K17818	ARD1; D-arabinitol dehydrogenase (NADP+) [EC:1.1.1.287]	KO	0.000959	41.857	1.222	34.247
K18282	cynD; cyanide dihydratase [EC:3.5.5.-]	KO	0.000959	20.929	0.611	34.247
K18427	hpdB; 4-hydroxyphenylacetate decarboxylase large subunit [EC:4.1.1.83]	KO	0.000959	83.714	2.444	34.247
K18428	hpdC; 4-hydroxyphenylacetate decarboxylase small subunit [EC:4.1.1.83]	KO	0.000959	41.857	1.222	34.247
K19076	cmr2, cas10; CRISPR-associated protein Cmr2	KO	0.000959	20.929	0.611	34.247
K19141	cmr5; CRISPR-associated protein Cmr5	KO	0.000959	20.929	0.611	34.247
EC:4.1.1.83	4-hydroxyphenylacetate decarboxylase	EC	0.000959	125.571	3.667	34.247
K16951	asrB; anaerobic sulfite reductase subunit B	KO	0.001309	1273.071	39.028	32.620
EC:1.2.1.27	Methylmalonate-semialdehyde dehydrogenase (CoA acylating)	EC	0.000833	588.571	24.333	24.188
K00140	mmsA, iolA, ALDH6A1; malonate-semialdehyde dehydrogenase (acylating) / methylmalonate-semialdehyde	KO	0.000833	588.571	24.333	24.188
K00385	asrC; anaerobic sulfite reductase subunit C	KO	0.001052	744.500	32.694	22.771
K16950	asrA; anaerobic sulfite reductase subunit A	KO	0.001052	744.500	32.694	22.771
K19333	kdgR; iclR family transcriptional regulator, KDG regulon repressor	KO	0.000465	621.500	27.611	22.509
K03476	ulaG; L-ascorbate 6-phosphate lactonase [EC:3.1.1.-]	KO	0.000825	1771.643	81.100	21.845
K05396	dcyD; D-cysteine desulfhydrase [EC:4.4.1.15]	KO	0.000731	710.571	38.111	18.645
K10537	araF; L-arabinose transport system substrate-binding protein	KO	0.000783	25.214	1.389	18.154
K03338	iolC; 5-dehydro-2-deoxygluconokinase [EC:2.7.1.92]	KO	0.000517	822.786	56.333	14.606
K00073	aID; ureidoglycolate dehydrogenase (NAD+) [EC:1.1.1.350]	KO	0.002182	680.714	51.444	13.232
K01436	KO1436; amidohydrolase [EC:3.5.1.-]	KO	0.001916	885.094	68.306	12.958
EC:1.1.1.12†	2-deoxy-D-gluconate 3-dehydrogenase	EC	0.000804	1464.786	133.944	10.936
K00065	kduD; 2-dehydro-3-deoxy-D-gluconate 5-dehydrogenase [EC:1.1.1.127]	KO	0.000804	1464.786	133.944	10.936
K01060	cah; cephalosporin-C deacetylase [EC:3.1.1.41]	KO	0.000760	1249.286	114.889	10.874
K03300	TC.CITMHS; citrate-Mg2+-H+ or citrate-Ca2+-H+ symporter, CitMHS family	KO	0.000711	143.000	14.222	10.055
K13016	wbpB; UDP-N-acetyl-2-amino-2-deoxyglucuronate dehydrogenase [EC:1.1.1.335]	KO	0.000016	425.951	49.222	8.654
EC:2.7.1.29	Glycerone kinase	EC	0.000255	791.571	107.417	7.369
K00863	DAK, TKFC; triose/dihydroxyacetone kinase / FAD-AMP lyase (cyclizing) [EC:2.7.1.28 2.7.1.29 4.6.1.15]	KO	0.000255	791.571	107.417	7.369
K03388	hdrA2; heterodisulfide reductase subunit A2 [EC:1.8.7.3 1.8.98.4 1.8.98.5 1.8.98.6]	KO	0.000388	2809.951	453.889	6.191
EC:2.7.1.16	Ribulokinase	EC	0.000244	1601.857	279.667	5.728
K00853	araB; L-ribulokinase [EC:2.7.1.16]	KO	0.000244	1601.857	279.667	5.728
K01644	citE; citrate lyase subunit beta / citryl-CoA lyase [EC:4.1.3.34]	KO	0.001825	2176.143	389.889	5.581
K15922	yihQ; sulfoquinovosidase [EC:3.2.1.199]	KO	0.001560	97.286	18.000	5.405
EC:1.8.98.1	CoB-CoM heterodisulfide reductase	EC	0.000104	6844.140	1342.667	5.097
K03389	hdrB2; heterodisulfide reductase subunit B2 [EC:1.8.7.3 1.8.98.4 1.8.98.5 1.8.98.6]	KO	0.000104	2281.380	447.556	5.097
K13953	adhP; alcohol dehydrogenase, propanol-preferring [EC:1.1.1.1]	KO	0.001333	1304.143	273.222	4.773
K02747	PTS-Aga-EIID, agaE; PTS system, N-acetylgalactosamine-specific IID component	KO	0.002003	296.857	65.028	4.565
K01730	ogl; oligogalacturonide lyase [EC:4.2.2.6]	KO	0.001923	4610.286	1044.667	4.413
K13002	wbyL; glycosyltransferase [EC:2.4.1.-]	KO	0.001923	4610.286	1044.667	4.413
K13581	ccrM; modification methylase [EC:2.1.1.72]	KO	0.001923	4610.286	1044.667	4.413
K01643	citF; citrate lyase subunit alpha / citrate CoA-transferase [EC:2.8.3.10]	KO	0.001530	1647.571	376.556	4.375
K18148	rtcB; release factor H-coupled RctB family protein	KO	0.001378	105.143	25.000	4.206
K02022	ABC.MR.TX; HlyD family secretion protein	KO	0.001829	4837.771	1162.267	4.162
EC:6.2.1.22	[Citrate (pro-3S)-lyase] ligase	EC	0.001685	1562.857	376.556	4.150
K01910	citC; [citrate (pro-3S)-lyase] ligase [EC:6.2.1.22]	KO	0.001685	1562.857	376.556	4.150
K08676	tri; tricorn protease [EC:3.4.21.-]	KO	0.000744	5025.923	1216.922	4.130
K14977	yIbA, UGHY; (S)-ureidoglycine aminohydrolase [EC:3.5.3.26]	KO	0.000309	104.429	25.444	4.104
K13927	citXG; holo-ACP synthase / triphosphoribosyl-dephospho-CoA synthase [EC:2.7.7.61 2.4.2.52]	KO	0.001564	973.429	243.111	4.004
K03390	hdrC2; heterodisulfide reductase subunit C2 [EC:1.8.7.3 1.8.98.4 1.8.98.5 1.8.98.6]	KO	0.000014	1752.809	441.222	3.973
EC:4.2.2.23	Rhamnogalacturonan endolyase	EC	0.001934	10086.714	2573.111	3.920
K18197	yesW; rhamnogalacturonan endolyase [EC:4.2.2.23]	KO	0.001934	10086.714	2573.111	3.920
K03931	ygjK; putative isomerase	KO	0.001928	10093.571	2593.156	3.892
PWY-7003	glycerol degradation to butanol	pathways	0.000196	2296.391	599.602	3.830
K01706	gudD; glucarate dehydratase [EC:4.2.1.40]	KO	0.001528	99.429	26.000	3.824
K06971	K06971; uncharacterized protein	KO	0.000549	485.643	127.389	3.812
K04032	eutT; ethanolamine utilization cobalamin adenosyltransferase [EC:2.5.1.17]	KO	0.002480	1043.714	278.556	3.747
K07795	tctC; putative tricarboxylic transport membrane protein	KO	0.002470	67.286	18.000	3.738
K13918	gudX; glucarate dehydratase-related protein	KO	0.002468	66.714	18.000	3.706
K04019	eutA; ethanolamine utilization protein EutA	KO	0.001588	1987.571	541.778	3.669
K02688	prpR; transcriptional regulator, propionate catabolism operon regulatory protein	KO	0.001048	85.143	23.333	3.649

PWY0-41	allantoin degradation IV (anaerobic)	pathways	0.000485	187.615	51.798	3.622
K03444	MFS.SP; MFS transporter, SP family, sugar porter, other	KO	0.002201	5480.000	1528.444	3.585
K01183	E3.2.1.14; chitinase [EC:3.2.1.14]	KO	0.002207	5552.257	1567.644	3.542
K07334	higB-1; toxin HigB-1	KO	0.002207	5544.357	1612.500	3.438
EC:2.3.1.20:	UDP-2-acetamido-3-amino-2,3-dideoxy-glucuronate N-acetyltransferase	EC	0.000004	680.637	198.256	3.433
K13018	wbpD, wibB; UDP-2-acetamido-3-amino-2,3-dideoxy-glucuronate N-acetyltransferase [EC:2.3.1.20]	KO	0.000004	680.637	198.256	3.433
EC:4.2.1.42	Galactarate dehydratase	EC	0.001981	59.429	18.000	3.302
K01708	garD; galactarate dehydratase [EC:4.2.1.42]	KO	0.001981	59.429	18.000	3.302
EC:4.1.2.53	2-keto-3-deoxy-L-rhamnonate aldolase	EC	0.001979	58.857	18.000	3.270
K02854	rhaR; AraC family transcriptional regulator, L-rhamnose operon transcriptional activator RhaR	KO	0.001979	58.857	18.000	3.270
K12660	rhmA; 2-dehydro-3-deoxy-L-rhamnonate aldolase [EC:4.1.2.53]	KO	0.001979	58.857	18.000	3.270
PWY-6629	superpathway of L-tryptophan biosynthesis	pathways	0.002291	588.030	181.666	3.237
K01746	E4.3.1.4; formiminotetrahydrofolate cyclodeaminase [EC:4.3.1.4]	KO	0.001538	967.714	301.444	3.210
K10709	frtC; fructoselysine 3-epimerase [EC:5.1.3.41]	KO	0.001708	1412.571	441.500	3.199
K07075	K07075; uncharacterized protein	KO	0.001145	5540.343	1745.544	3.174
K01608	gcl; tartronate-semialdehyde synthase [EC:4.1.1.47]	KO	0.000733	64.714	20.667	3.131
K07221	oprO_P; phosphate-selective porin OprO and OprP	KO	0.000612	8111.664	2600.037	3.120
K00483	hpaB; 4-hydroxyphenylacetate 3-monoxygenase [EC:1.14.14.9]	KO	0.000733	64.143	20.667	3.104
GLUCARDEC	D-glucarate degradation I	pathways	0.000855	150.875	48.853	3.088
K09684	pucR; purine catabolism regulatory protein	KO	0.002055	853.571	277.222	3.079
K15527	K15527; cysteate synthase [EC:2.5.1.76]	KO	0.000114	1045.451	340.222	3.073
K07109	K07109; uncharacterized protein	KO	0.000929	960.094	313.889	3.059
K01646	citD; citrate lyase subunit gamma (acyl carrier protein)	KO	0.002111	1119.000	370.222	3.023
EC:2.4.1.11	Glycogen(starch) synthase	EC	0.000124	1069.023	354.000	3.020
K16153	K16153; glycogen phosphorylase/synthase [EC:2.4.1.1 2.4.1.11]	KO	0.000124	1069.023	354.000	3.020
EC:2.1.1.34	tRNA (guanosine(18)-2'-O)-methyltransferase	EC	0.001135	1122.594	376.333	2.983
K00556	trmH; tRNA (guanosine-2'-O)-methyltransferase [EC:2.1.1.34]	KO	0.001135	1122.594	376.333	2.983
EC:1.3.5.3	Protoporphyrinogen IX dehydrogenase (menaquinone)	EC	0.002399	1012.000	340.778	2.970
K00230	hemG; menaquinone-dependent protoporphyrinogen oxidase [EC:1.3.5.3]	KO	0.002399	1012.000	340.778	2.970
EC:1.3.1.34	2,4-dienoyl-CoA reductase (NADPH)	EC	0.001390	1051.429	354.222	2.968
K00219	fadhI; 2,4-dienoyl-CoA reductase (NADPH2) [EC:1.3.1.34]	KO	0.001390	1051.429	354.222	2.968
GALACTARC	D-galactarate degradation I	pathways	0.000879	102.454	34.799	2.944
GLUCARGAI	superpathway of D-glucarate and D-galactarate degradation	pathways	0.000879	102.454	34.799	2.944
K01843	kamA; lysine 2,3-aminomutase [EC:5.4.3.2]	KO	0.001160	8119.256	2761.987	2.940
EC:2.4.2.52	Triphosphoribosyl-dephospho-CoA synthase	EC	0.002313	1081.143	370.222	2.920
EC:2.7.7.61	Citrate lyase holo-[acyl-carrier protein] synthase	EC	0.002341	1086.429	384.600	2.825
K01966	PCCB, pccB; propionyl-CoA carboxylase beta chain [EC:6.4.1.3 2.1.3.15]	KO	0.001069	8813.799	3149.770	2.798
EC:6.4.1.3	Propionyl-CoA carboxylase	EC	0.002333	8815.941	3169.992	2.781
K16849	uxaA1; altronate dehydratase small subunit [EC:4.2.1.7]	KO	0.001473	335.429	122.111	2.747
K04026	eutL; ethanolamine utilization protein EutL	KO	0.001687	1459.000	535.444	2.725
ENTBACSYN	enterobactin biosynthesis	pathways	0.002125	217.318	79.840	2.722
PWY-7090	UDP-2,3-diacetamido-2,3-dideoxy- α -D-mannuronate biosynthesis	pathways	0.000443	184.031	67.612	2.722
K09979	K09979; uncharacterized protein	KO	0.000883	849.500	313.333	2.711
K16850	uxaA2; altronate dehydratase large subunit [EC:4.2.1.7]	KO	0.001639	322.286	119.444	2.698
K03298	TC.DME; drug/metabolite transporter, DME family	KO	0.000126	898.714	336.389	2.672
K03446	emrB; MFS transporter, DHA2 family, multidrug resistance protein	KO	0.001665	853.643	320.333	2.665
K00662	aacC; aminoglycoside 3-N-acetyltransferase [EC:2.3.1.81]	KO	0.000536	471.643	177.333	2.660
K14205	mprF, fmtC; phosphatidylglycerol lysyltransferase [EC:2.3.2.3]	KO	0.001367	537.429	203.417	2.642
K02454	gspE; general secretion pathway protein E	KO	0.000004	1331.427	513.870	2.591
K06726	rbsD; D-ribose pyranase [EC:5.4.99.62]	KO	0.002072	1279.929	507.461	2.522
K03741	ARSC2, arsC; arsenate reductase [EC:1.20.4.1]	KO	0.000033	6425.714	2582.222	2.488
K03303	lctP; lactate permease	KO	0.000511	6360.716	2569.778	2.475
K02598	nirC; nitrite transporter	KO	0.000119	980.000	405.750	2.415
K00680	ytml; uncharacterized N-acetyltransferase [EC:2.3.1.-]	KO	0.000713	3070.686	1298.256	2.365
K13641	iclR; IclR family transcriptional regulator, acetate operon repressor	KO	0.001591	58.857	25.000	2.354
PWY-7456	mannan degradation	pathways	0.000110	13612.667	5866.519	2.320
EC:1.21.98.:	Cyclic dehydropantoinyl futasolase synthase	EC	0.001133	1399.643	614.167	2.279
EC:2.5.1.12	Aminodeoxyfutasolase synthase	EC	0.001133	1399.643	614.167	2.279
K11782	mqnA; chorismate dehydratase [EC:4.2.1.151]	KO	0.001133	1399.643	614.167	2.279
K11784	mqnC; cyclic dehydropantoinyl futasolase synthase [EC:1.21.98.1]	KO	0.001133	1399.643	614.167	2.279
K11785	mqnD; 1,4-dihydroxy-6-naphthoate synthase [EC:1.14.-.-]	KO	0.001133	1399.643	614.167	2.279
K18285	mqnE; aminodeoxyfutasolase synthase [EC:2.5.1.120]	KO	0.001133	1399.643	614.167	2.279
PWY-7371	1,4-dihydroxy-6-naphthoate biosynthesis II	pathways	0.001133	1399.643	614.167	2.279
PWY-7374	1,4-dihydroxy-6-naphthoate biosynthesis I	pathways	0.001123	1395.256	613.944	2.273
K11783	mqnB; futasolase hydrolase [EC:3.2.2.26]	KO	0.001109	1388.929	613.611	2.264
K09949	K09949; uncharacterized protein	KO	0.000325	1070.472	478.426	2.237
K02584	nifA; Nif-specific regulatory protein	KO	0.000326	1070.047	491.648	2.176
K16841	hpxA; allantoin racemase [EC:5.1.99.3]	KO	0.001990	147.000	67.556	2.176
EC:3.1.3.90	Maltose 6'-phosphate phosphatase	EC	0.000007	226.571	104.333	2.172
K06896	mapP; maltose 6'-phosphate phosphatase [EC:3.1.3.90]	KO	0.000007	226.571	104.333	2.172
K05995	pepE; dipeptidase E [EC:3.4.13.21]	KO	0.000948	1901.880	880.667	2.160
K03760	eptA, pmrC; lipid A ethanolaminephosphotransferase [EC:2.7.8.43]	KO	0.000590	963.571	454.444	2.120
K01667	tnaA; tryptophanase [EC:4.1.99.1]	KO	0.000435	2503.023	1191.111	2.101
K03713	glnR; MerR family transcriptional regulator, glutamine synthetase repressor	KO	0.002364	216.000	103.556	2.086
PWY-6263	superpathway of menaquinol-8 biosynthesis II	pathways	0.000847	3523.433	1696.657	2.077
K04030	eutQ; ethanolamine utilization protein EutQ	KO	0.001083	1418.143	683.000	2.076
K09778	K09778; uncharacterized protein	KO	0.000304	1122.119	545.370	2.058
K09994	phnO; aminoalkylphosphonate N-acetyltransferase [EC:2.3.1.-]	KO	0.002298	89.714	43.667	2.055
K16926	htsT; energy-coupling factor transport system substrate-specific component	KO	0.000541	2432.429	1226.167	1.984
K17213	K17213; inositol transport system substrate-binding protein	KO	0.001801	1089.857	562.556	1.937
K10974	codB; cytosine permease	KO	0.001508	767.071	398.572	1.925
K00924	E2.7.1.-; kinase [EC:2.7.1.-]	KO	0.001491	190.429	99.556	1.913
K08177	oxIT; MFS transporter, OFA family, oxalate/formate antiporter	KO	0.001674	4433.786	2334.417	1.899
K13041	ttrR; two-component system, LuxR family, response regulator TtrR	KO	0.002068	1219.000	646.556	1.885
K01305	iadA; beta-aspartyl-dipeptidase (metallo-type) [EC:3.4.19.-]	KO	0.000533	1272.071	687.822	1.849
K03299	TC.GNTP; gluconate:H+ symporter, GntP family	KO	0.001732	8862.616	4834.006	1.833
K04023	eutH; ethanolamine transporter	KO	0.001022	2590.786	1436.667	1.803
EC:2.7.7.43	N-acylneuraminate cytidyllyltransferase	EC	0.001733	9133.351	5129.200	1.781
K00983	neuA; N-acylneuraminate cytidyllyltransferase [EC:2.7.7.43]	KO	0.001733	9133.351	5129.200	1.781
EC:2.4.1.18:	mannosaminyltransferase	EC	0.001285	17687.477	10158.914	1.741

K05946	tagA, tarA; N-acetylglucosaminylidiphosphoundecaprenol N-acetyl-beta-D-mannosaminyltransferase [EC:2.4.1.10]	KO	0.001285	17687.477	10158.914	1.741
EC:2.7.8.20	Phosphatidylglycerol--membrane-oligosaccharide glycerophosphotransferase	EC	0.002502	2697.857	1570.750	1.718
K14260	alaA; alanine-synthesizing transaminase [EC:2.6.1.66 2.6.1.2]	KO	0.001848	999.929	583.500	1.714
K04029	eutP; ethanolamine utilization protein EutP	KO	0.000961	2679.286	1569.500	1.707
K09707	K09707; uncharacterized protein	KO	0.001743	2469.000	1448.056	1.705
K00042	garR, glxR; 2-hydroxy-3-oxopropionate reductase [EC:1.1.1.60]	KO	0.000597	3761.001	2210.611	1.701
K02453	gspD; general secretion pathway protein D	KO	0.000536	2587.094	1528.018	1.693
K02477	K02477; two-component system, LytTR family, response regulator	KO	0.001216	16925.430	10089.694	1.677
K10254	ohyA, sph; oleate hydratase [EC:4.2.1.53]	KO	0.001960	2972.286	1775.517	1.674
K10824	nikE; nickel transport system ATP-binding protein [EC:3.6.3.24]	KO	0.001976	443.429	267.333	1.659
K02009	cbiN; cobalt/nickel transport protein	KO	0.002498	2289.214	1394.472	1.642
K01295	cpg; glutamate carboxypeptidase [EC:3.4.17.11]	KO	0.000066	1344.857	833.000	1.614
K12507	fadK; acyl-CoA synthetase [EC:6.2.1.-]	KO	0.000744	121.571	75.833	1.603
EC:1.2.1.21	Glycolaldehyde dehydrogenase	EC	0.001117	142.543	89.144	1.599
EC:1.2.1.22	Lactaldehyde dehydrogenase	EC	0.001117	142.543	89.144	1.599
K02626	pdaD; arginine decarboxylase [EC:4.1.1.19]	KO	0.001117	142.543	89.144	1.599
K07248	aldA; lactaldehyde dehydrogenase / glycolaldehyde dehydrogenase [EC:1.2.1.22 1.2.1.21]	KO	0.001117	142.543	89.144	1.599
K00968	PCYT1; choline-phosphate cytidyltransferase [EC:2.7.7.15]	KO	0.001154	142.543	89.144	1.599
K01247	alkA; DNA-3-methyladenine glycosylase II [EC:3.2.2.21]	KO	0.000344	540.143	344.667	1.567
K18331	hndC; NADP-reducing hydrogenase subunit HndC [EC:1.12.1.3]	KO	0.000121	5046.994	3220.867	1.567
K01760	metC; cystathionine beta-lyase [EC:4.4.1.8]	KO	0.001958	1016.857	658.667	1.544
K03326	TC.DCUC, dcuC, dcuD; C4-dicarboxylate transporter, DcuC family	KO	0.001173	4893.857	3173.444	1.542
EC:4.3.1.18	D-serine ammonia-lyase	EC	0.002041	561.000	368.222	1.524
K01753	dsdA; D-serine dehydratase [EC:4.3.1.18]	KO	0.002041	561.000	368.222	1.524
K09928	K09928; uncharacterized protein	KO	0.000596	2099.333	1386.537	1.514
EC:1.1.3.15	(S)-2-hydroxy-acid oxidase	EC	0.000160	2181.834	1441.842	1.513
K00104	glcD; glycolate oxidase [EC:1.1.3.15]	KO	0.000160	2181.834	1441.842	1.513
K07315	rsbU_P; phosphoserine phosphatase RsbU/P [EC:3.1.3.3]	KO	0.000368	2205.850	1499.792	1.471
GLYCOL-GU	superpathway of glycol metabolism and degradation	pathways	0.000291	235.238	160.769	1.463
PWY-5705	allantoin degradation to glyoxylate III	pathways	0.000804	325.928	224.224	1.454
K00563	rImA1; 23S rRNA (guanine745-N1)-methyltransferase [EC:2.1.1.187]	KO	0.002503	3306.714	2287.583	1.446
K02666	piIQ; type IV pilus assembly protein PiIQ	KO	0.001040	1891.666	1317.944	1.435
K01589	purK; 5-(carboxyamino)imidazole ribonucleotide synthase [EC:6.3.4.18]	KO	0.002045	3238.714	2256.778	1.435
EC:2.8.1.1	Thiosulfate sulfurtransferase	EC	0.002077	583.714	407.389	1.433
K02200	ccmH; cytochrome c-type biogenesis protein CcmH	KO	0.002291	914.429	639.556	1.430
K18332	hndD; NADP-reducing hydrogenase subunit HndD [EC:1.12.1.3]	KO	0.000892	4467.780	3128.144	1.428
EC:1.7.2.3	Trimethylamine-N-oxide reductase (cytochrome c)	EC	0.002305	913.286	639.556	1.428
EC:1.12.1.3	Hydrogen dehydrogenase (NADP+)	EC	0.001083	16404.906	11515.189	1.425
K01480	speB; agmatinase [EC:3.5.3.11]	KO	0.001278	4997.809	3510.250	1.424
K02526	kdgT; 2-keto-3-deoxygluconate permease	KO	0.001000	147.714	105.778	1.396
K02794	PTS-Man-EIIB, manX; PTS system, mannose-specific IIB component [EC:2.7.1.191]	KO	0.001442	4628.500	3348.906	1.382
K15725	czcC; outer membrane protein, cobalt-zinc-cadmium efflux system	KO	0.000460	2116.800	1534.011	1.380
K01011	TST, MPST, sseA; thiosulfate/3-mercaptopropionate sulfurtransferase [EC:2.8.1.1 2.8.1.2]	KO	0.000290	529.571	385.056	1.375
K02440	GLPF; glycerol uptake facilitator protein	KO	0.000416	1119.494	819.839	1.366
K00332	nuoC; NADH-quinone oxidoreductase subunit C [EC:1.6.5.3]	KO	0.000039	1398.333	1025.537	1.364
K01466	allB; allantoinase [EC:3.5.2.5]	KO	0.001250	344.929	255.667	1.349
K04024	eutI; ethanolamine utilization protein EutI	KO	0.001362	978.429	727.778	1.344
ARGORNPR	arginine, ornithine and proline interconversion	pathways	0.000600	1757.222	1323.235	1.328
K02445	glpT; MFS transporter, OPA family, glycerol-3-phosphate transporter	KO	0.001495	7261.309	5490.611	1.322
K016379	E4.1.3.3, nanA, NPL; N-acetylneuraminase lyase [EC:4.1.3.3]	KO	0.001319	19287.839	14726.142	1.310
EC:3.5.3.9	Allantoate deiminase	EC	0.000996	422.500	324.111	1.304
K02083	allC; allantoate deiminase [EC:3.5.3.9]	KO	0.000996	422.500	324.111	1.304
K02483	K02483; two-component system, OmpR family, response regulator	KO	0.002121	2465.714	1893.111	1.302
K02031	ABC.PE.A; peptide/nickel transport system ATP-binding protein	KO	0.000709	18858.049	14496.192	1.301
K03556	malT; LuxR family transcriptional regulator, maltose regulon positive regulatory protein	KO	0.002502	109.786	84.944	1.292
K00184	K00184; prokaryotic molybdopterin-containing oxidoreductase family, iron-sulfur binding subunit	KO	0.001601	2073.690	1616.814	1.283
K00333	nuoD; NADH-quinone oxidoreductase subunit D [EC:1.6.5.3]	KO	0.000033	1416.476	1106.648	1.280
K01154	hdsS; type I restriction enzyme, S subunit [EC:3.1.21.3]	KO	0.001198	64701.709	50912.000	1.271
K00185	K00185; prokaryotic molybdopterin-containing oxidoreductase family, membrane subunit	KO	0.000004	1538.619	1212.092	1.269
K02474	wbpO; UDP-N-acetyl-D-galactosamine dehydrogenase [EC:1.1.1.1-]	KO	0.000787	7242.989	5716.233	1.267
K03581	recD; exodeoxyribonuclease V alpha subunit [EC:3.1.11.5]	KO	0.001297	17022.931	13568.656	1.255
K10823	oppF; oligopeptide transport system ATP-binding protein	KO	0.001164	18539.737	14884.201	1.246
K08223	fsr; MFS transporter, FSR family, fosmidomycin resistance protein	KO	0.000073	7217.757	5824.533	1.239
K00294	E1.2.1.88; 1-pyrroline-5-carboxylate dehydrogenase [EC:1.2.1.88]	KO	0.000913	1278.494	1034.311	1.236
K03319	TC.DASS; divalent anion:Na+ symporter, DASS family	KO	0.001313	913.286	743.000	1.229
K13954	yaI; alcohol dehydrogenase [EC:1.1.1.1]	KO	0.000617	788.643	647.472	1.218
K01464	DPYS, dht, hydA; dihydropyrimidinase [EC:3.5.2.2]	KO	0.001820	6338.929	5214.639	1.216
K03772	fkpA; FKBP-type peptidyl-prolyl cis-trans isomerase FkpA [EC:5.2.1.8]	KO	0.000348	7266.161	5992.570	1.213
K15583	oppD; oligopeptide transport system ATP-binding protein	KO	0.000396	14895.261	12371.703	1.204
K02759	PTS-Cel-EIIA, celC, chbA; PTS system, cellobiose-specific IIA component [EC:2.7.1.196 2.7.1.205]	KO	0.000207	1540.286	1283.906	1.200
EC:5.1.3.14	UDP-N-acetylglucosamine 2-epimerase (non-hydrolyzing)	EC	0.002392	29604.099	24805.039	1.193
K01791	wecB; UDP-N-acetylglucosamine 2-epimerase (non-hydrolyzing) [EC:5.1.3.14]	KO	0.002392	29604.099	24805.039	1.193
K11741	sugE; quaternary ammonium compound-resistance protein SugE	KO	0.002461	8330.947	7060.737	1.180
K07150	K07150; uncharacterized protein	KO	0.000646	8602.714	7329.139	1.174
K14652	ribBA; 3,4-dihydroxy 2-butanone 4-phosphate synthase / GTP cyclohydrolase II [EC:4.1.99.12 3.5.4.25]	KO	0.000894	26900.271	22932.831	1.173
K01439	dapE; succinyl-diaminopimelate desuccinylase [EC:3.5.1.18]	KO	0.001176	14139.857	12085.778	1.170
EC:1.1.5.3	Glycerol-3-phosphate dehydrogenase	EC	0.000157	17327.636	15543.506	1.115
EC:3.2.1.86	6-phospho-beta-glucosidase	EC	0.000224	18308.144	16605.522	1.103
K00318	PRODH; proline dehydrogenase [EC:1.5.-.-]	KO	0.000793	1008.543	916.867	1.100
K02035	ABC.PE.S; peptide/nickel transport system substrate-binding protein	KO	0.002087	31683.574	28921.261	1.096
K00111	glpA, glpD; glycerol-3-phosphate dehydrogenase [EC:1.1.5.3]	KO	0.000028	16721.447	15372.839	1.088
P161-PWY	acetylene degradation	pathways	0.001368	11740.449	10842.758	1.083
K09792	K09792; uncharacterized protein	KO	0.000495	1880.429	1747.722	1.076
K00852	rbsK, RBKS; ribokinase [EC:2.7.1.15]	KO	0.001228	14842.614	13846.161	1.072
EC:1.16.3.1	Ferroxidase	EC	0.000191	9140.280	8534.478	1.071
K03594	bfr; bacterioferritin [EC:1.16.3.1]	KO	0.000191	9140.280	8534.478	1.071
EC:1.2.1.10	Acetaldehyde dehydrogenase (acetylating)	EC	0.001271	7466.286	7069.628	1.056
HOMOSER-I	L-methionine biosynthesis I	pathways	0.001751	1377.439	1304.585	1.056
K07404	pgl; 6-phosphogluconolactonase [EC:3.1.1.31]	KO	0.002196	10515.073	10003.944	1.051
K04072	adhE; acetaldehyde dehydrogenase / alcohol dehydrogenase [EC:1.2.1.10 1.1.1.1]	KO	0.001993	6119.714	5836.961	1.048

MET-SAM-P	superpathway of S-adenosyl-L-methionine biosynthesis	pathways	0.001583	2072.658	1985.722	1.044
K08234	yaer; glyoxylase I family protein	KO	0.000682	949.300	913.428	1.039
K01478	arcA; arginine deiminase [EC:3.5.3.6]	KO	0.002518	1221.594	1182.667	1.033
PWY-5347	superpathway of L-methionine biosynthesis (transsulfuration)	pathways	0.001521	2973.714	2886.478	1.030
K07152	SCO1_2; protein SCO1/2	KO	0.000354	1885.429	1831.278	1.030
K01271	pepQ; Xaa-Pro dipeptidase [EC:3.4.13.9]	KO	0.000041	1691.071	1663.194	1.017
Decreased abundance in recipients from Mg2800 FMT						
K00507	SCD, desC; stearoyl-CoA desaturase (Delta-9 desaturase) [EC:1.14.19.1]	KO	0.001063	13.714	81.667	-5.955
EC:1.14.19.1	Stearoyl-[acyl-carrier-protein] 9-desaturase	EC	0.000999	13.714	81.111	-5.914
K01555	FAH, fahA; fumarylacetoacetase [EC:3.7.1.2]	KO	0.000999	13.714	81.111	-5.914
K03921	FAB2, SSI2, desA1; acyl-[acyl-carrier-protein] desaturase [EC:1.14.19.2 1.14.19.11 1.14.19.26]	KO	0.000999	13.714	81.111	-5.914
K09992	K09992; uncharacterized protein	KO	0.000999	13.714	81.111	-5.914
K06443	lycB, crtL1, crtY; lycopene beta-cyclase [EC:5.5.1.19]	KO	0.001017	13.714	81.111	-5.914
EC:1.2.1.4	Aldehyde dehydrogenase (NADP(+))	EC	0.001091	14.286	81.111	-5.678
K03405	chlI, bchI; magnesium chelatase subunit I [EC:6.6.1.1]	KO	0.001091	14.286	81.111	-5.678
K14519	aldH; NADP-dependent aldehyde dehydrogenase [EC:1.2.1.4]	KO	0.001091	14.286	81.111	-5.678
EC:6.6.1.1	Magnesium chelatase	EC	0.001131	14.286	81.111	-5.678
K08976	K08976; putative membrane protein	KO	0.002175	15.714	83.556	-5.317
K16961	yxex; putative amino-acid transport system substrate-binding protein	KO	0.000503	68.571	188.000	-2.742
K16962	yxexN; putative amino-acid transport system permease protein	KO	0.000503	68.571	188.000	-2.742
K01630	garI; 2-dehydro-3-deoxyglucarate aldolase [EC:4.1.2.20]	KO	0.002060	408.571	776.889	-1.901
K02347	polX, dpx; DNA polymerase (family X)	KO	0.001017	81.286	141.222	-1.737
TYRFUMCA	L-tyrosine degradation I	pathways	0.000802	205.673	334.248	-1.625
K08097	comA; phosphosulfolactate synthase [EC:4.4.1.19]	KO	0.002343	83.286	132.667	-1.593
K02839	prfH; peptide chain release factor	KO	0.001445	111.714	172.556	-1.545
K02761	PTS-Cel-EIIC, celB, chbC; PTS system, cellobiose-specific IIC component	KO	0.001415	2280.714	3276.728	-1.437
K09680	coaW; type II pantothenate kinase [EC:2.7.1.33]	KO	0.000908	7363.629	9041.144	-1.228
EC:4.1.2.52	4-hydroxy-2-oxoheptanedioate aldolase	EC	0.002084	841.857	1023.444	-1.216
K02510	hpaI, hpcH; 4-hydroxy-2-oxoheptanedioate aldolase [EC:4.1.2.52]	KO	0.002084	841.857	1023.444	-1.216
K01684	dgoD; galactonate dehydratase [EC:4.2.1.6]	KO	0.002476	141.429	170.889	-1.208
PWY-5920	superpathway of heme biosynthesis from glycine	pathways	0.000213	2303.938	2707.644	-1.175
K02276	coxC, ctaE; cytochrome c oxidase subunit III [EC:1.9.3.1]	KO	0.000178	1290.714	1508.111	-1.168
P4-PWY	superpathway of L-lysine, L-threonine and L-methionine biosynthesis I	pathways	0.001783	4131.509	4676.903	-1.132
K02274	coxA, ctaD; cytochrome c oxidase subunit I [EC:1.9.3.1]	KO	0.000316	1279.000	1429.444	-1.118
K02275	coxB, ctaC; cytochrome c oxidase subunit II [EC:1.9.3.1]	KO	0.000317	1279.571	1429.444	-1.117
K01724	PCBD, phhB; 4a-hydroxytetrahydrobiopterin dehydratase [EC:4.2.1.96]	KO	0.000312	1276.714	1425.667	-1.117
K10764	metZ; O-succinylhomoserine sulphydrylase [EC:2.5.1.-]	KO	0.000310	1276.714	1425.111	-1.116
K08973	K08973; putative membrane protein	KO	0.000323	1287.429	1425.111	-1.107
K00406	ccoP; cytochrome c oxidase cbb3-type subunit III	KO	0.000322	1288.000	1425.111	-1.106
K03325	ACR3, arsB; arsenite transporter	KO	0.001860	990.714	1094.278	-1.105
PWY-3781	aerobic respiration I (cytochrome c)	pathways	0.000092	10241.562	11248.524	-1.098
EC:4.1.2.40	Tagatose-bisphosphate aldolase	EC	0.001796	1322.429	1438.917	-1.088
ARG+POLYA	superpathway of arginine and polyamine biosynthesis	pathways	0.002147	2165.215	2257.813	-1.043
K02779	PTS-Glc-EIIC, ptsG; PTS system, glucose-specific IIC component	KO	0.000125	517.714	539.111	-1.041
K19055	prdX, proX; Ala-tRNA(Pro) deacylase [EC:3.1.1.-]	KO	0.001012	7346.451	7623.028	-1.038
K08998	K08998; uncharacterized protein	KO	0.002414	21691.627	22397.764	-1.033
K03786	aroQ, qutE; 3-dehydroquinate dehydratase II [EC:4.2.1.10]	KO	0.002581	22422.080	22856.867	-1.019
K01817	trpF; phosphoribosylanthranilate isomerase [EC:5.3.1.24]	KO	0.000874	24430.943	24864.659	-1.018
K02760	PTS-Cel-EIIB, celA, chbB; PTS system, cellobiose-specific IIB component [EC:2.7.1.196 2.7.1.205]	KO	0.000331	1756.571	1781.350	-1.014

* day 12 post FMT; ordered according to fold-difference; p-values based on ANOVA; grey highlights pathways and processes mentioned in the manuscript.