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Supplementary Table 1. Metagenomic sequencing statistics.

Sample ID	Sample type	Mouse	Timepoint	Cage	Fut2 genotype	Barcode	Filtered reads	% CDS
JOE.2	16S-Seq	34294	Pre-LPS	2	+/-	CCGAATTGACAA	923,243	NA
JOE.4	16S-Seq	34294	Post-LPS	2	+/-	GGACAGTGTATT	292,328	NA
JOE.8	16S-Seq	34364	Pre-LPS	1	+/-	GTTTGCTCGAGA	514,844	NA
JOE.9	16S-Seq	34364	Post-LPS	1	+/-	AATCCTCGGAGT	306,466	NA
JOE.6	16S-Seq	34366	Pre-LPS	1	+/-	GTTCCGGATTAG	1,329,669	NA
JOE.3	16S-Seq	34366	Post-LPS	1	+/-	ACGCTTAACGAC	293,339	NA
JOE.10	16S-Seq	34295	Pre-LPS	2	-/-	CAAACGCACTAA	262,914	NA
JOE.7	16S-Seq	34295	Post-LPS	2	-/-	TGTGGAAACTCC	1,134,642	NA
JOE.11	16S-Seq	34362	Pre-LPS	1	-/-	GGTGGTCGTTCT	339,389	NA
JOE.14	16S-Seq	34362	Post-LPS	1	-/-	CTGGACGCATTA	297,799	NA
JOE.5	16S-Seq	34363	Pre-LPS	1	-/-	TGAAAGCGGCGA	317,693	NA
JOE.1	16S-Seq	34363	Post-LPS	1	-/-	TAACGGCGCTCT	284,785	NA
JOE.12	16S-Seq	34365	Pre-LPS	1	-/-	AGGGCTATAGTT	309,283	NA
JOE.13	16S-Seq	34365	Post-LPS	1	-/-	GTGTAGGTGCTT	302,140	NA
RNA5.1	RNA-seq	34294	Pre-LPS	2	+/-	GATCAG	10,480,286	23.2

RNA5.2	RNA-seq	34294	Post-LPS	2	+/-	TAGCTT	15,373,517	37.6
RNA3.1	RNA-seq	34364	Pre-LPS	1	+/-	ACAGTG	10,716,116	21.4
RNA3.2	RNA-seq	34364	Post-LPS	1	+/-	GCCAAT	18,755,463	22.7
RNA4.1	RNA-seq	34366	Pre-LPS	1	+/-	CAGATC	13,141,153	17.9
RNA4.2	RNA-seq	34366	Post-LPS	1	+/-	ACTTGA	14,337,984	29.6
RNA6.1	RNA-seq	34295	Pre-LPS	2	-/-	GGCTAC	13,207,703	30.1
RNA6.2	RNA-seq	34295	Post-LPS	2	-/-	CTTGTA	12,066,305	25.6
RNA1.1	RNA-seq	34362	Pre-LPS	1	-/-	ATCACG	8,568,384	29.1
RNA1.2	RNA-seq	34362	Post-LPS	1	-/-	CGATGT	14,033,216	16.5
RNA2.1	RNA-seq	34363	Pre-LPS	1	-/-	TTAGGC	11,122,562	36.5
RNA2.2	RNA-seq	34363	Post-LPS	1	-/-	TGACCA	13,978,674	29.1
DNA5.1	DNA-seq	34294	Pre-LPS	2	+/-	GATCAG	4,597,540	98.6
DNA5.2	DNA-seq	34294	Post-LPS	2	+/-	TAGCTT	7,182,937	98.8
DNA3.1	DNA-seq	34364	Pre-LPS	1	+/-	ACAGTG	5,002,390	98.7
DNA3.2	DNA-seq	34364	Post-LPS	1	+/-	GCCAAT	7,784,501	98.8
DNA4.1	DNA-seq	34365	Pre-LPS	1	+/-	CAGATC	6,039,760	98.9
DNA4.2	DNA-seq	34366	Post-LPS	1	+/-	ACTTGA	5,808,287	98.9

DNA6.1	DNA-seq	34295	Pre-LPS	2	-/-	GGCTAC	7,871,043	98.8
DNA6.2	DNA-seq	34295	Post-LPS	2	-/-	CTTGTA	7,143,713	98.8
DNA1.1	DNA-seq	34362	Pre-LPS	1	-/-	ATCACG	6,941,277	98.7
DNA1.2	DNA-seq	34362	Post-LPS	1	-/-	CGATGT	6,388,491	98.8
DNA2.1	DNA-seq	34363	Pre-LPS	1	-/-	TTAGGC	6,970,171	98.7
DNA2.2	DNA-seq	34363	Post-LPS	1	-/-	TGACCA	6,400,245	98.9

Supplementary Table 2. Differentially expressed Kyoto Encyclopedia of Genes and Genomes (KEGG) orthologous groups (KOs) between LPS-treated and control samples (n=3/group; paired test using edgeR; *q*<0.05, >2-fold change; NS-not significant, UD-undefined).

KO	Fut2+/- fold-change	Fut2-/- fold-change	Annotation	Pathway(s)
K01615	2.67	NS	glutaconyl-CoA decarboxylase	Benzoate degradation via CoA ligation;Butanoate metabolism
K00241	2.68	NS	succinate dehydrogenase cytochrome b-556 subunit	Benzoate degradation via CoA ligation;Reductive carboxylate cycle (CO2 fixation);Citrate cycle (TCA cycle);Oxidative phosphorylation;Butanoate metabolism
K09891	3.65	NS	hypothetical protein	Function unknown
K11938	4.90	NS	HMP-PP phosphatase	General function prediction only
K07214	2.27	NS	enterochelin esterase and related enzymes	Inorganic ion transport and metabolism
K01627	2.64	NS	2-dehydro-3-deoxyphosphooctonate aldolase (KDO 8-P synthase)	Lipopolysaccharide biosynthesis
K03832	2.25	NS	periplasmic protein TonB	Membrane and intracellular structural molecules
K12234	5.61	NS	F420-0:gamma-glutamyl ligase	Metabolism of other cofactors and vitamins

K01302	2.95	NS	UD	Other amino acid metabolism
K00346	2.96	NS	Na+-transporting NADH:ubiquinone oxidoreductase subunit A	Other energy metabolism
K00350	2.93	NS	Na+-transporting NADH:ubiquinone oxidoreductase subunit E	Other energy metabolism
K00351	2.88	NS	Na+-transporting NADH:ubiquinone oxidoreductase subunit F	Other energy metabolism
K00347	2.64	NS	Na+-transporting NADH:ubiquinone oxidoreductase subunit B	Other energy metabolism
K00349	2.49	NS	Na+-transporting NADH:ubiquinone oxidoreductase subunit D	Other energy metabolism
K08773	50.42	NS	RalA-binding protein 1	Pancreatic cancer;Pathways in cancer
K03287	2.19	NS	outer membrane factor, OMF family	Pores ion channels
K01603	2.55	NS	methylmalonyl-CoA decarboxylase	Propanoate metabolism
K07394	12.30	NS	SM-20-related protein	Protein folding and associated processing

K02890	2.27	NS	large subunit ribosomal protein L22	Ribosome
K02429	2.70	NS	MFS transporter, FHS family, L-fucose permease	Transporters
K11068	NS	2.06	hemolysin III	Bacterial toxins
K05973	NS	4.43	poly(3-hydroxybutyrate) depolymerase	Butanoate metabolism
K07341	NS	3.00	death on curing protein	Cell motility and secretion
K00478	NS	2.37	UD	Diterpenoid biosynthesis
K09160	NS	2.58	hypothetical protein	Function unknown
K07286	NS	2.18	uncharacterized lipoprotein	Membrane and intracellular structural molecules
K01001	NS	101.60	UDP-N-acetylglucosamine--dolichyl-phosphate	N-Glycan biosynthesis;Glycosyltransferases
K12061	NS	2.65	conjugal transfer pilus assembly protein TraW	Secretion system
K08253	NS	2.65	non-specific protein-tyrosine kinase	Signal transduction mechanisms
K00903	NS	2.38	protein-tyrosine kinase	Signal transduction mechanisms

K10972	NS	13.18	LysR family transcriptional regulator, transcriptional activator of	Transcription factors
K06714	NS	2.53	arginine utilization regulatory protein	Transcription factors
K02077	NS	2.06	zinc/manganese transport system substrate-binding protein	Transporters
K07705	NS	3.00	two-component system, LytT family, response regulator LytT	Two-component system
K10953	NS	2.40	RTX toxin RtxA	Vibrio cholerae infection;Bacterial toxins
K01173	NS	0.50	endonuclease	Apoptosis
K02394	NS	0.48	flagellar P-ring protein precursor FlgI	Bacterial motility proteins;Flagellar assembly
K02656	NS	0.42	type IV pilus assembly protein PilF	Bacterial motility proteins;Secretion system
K08358	NS	0.38	tetrathionate reductase subunit B	Electron transfer carriers
K03744	NS	0.36	LemA protein	Function unknown
K09763	NS	0.05	hypothetical protein	Function unknown

K06929	NS	0.46	UD	General function prediction only
K06866	NS	0.40	autonomous glycyl radical cofactor	General function prediction only
K11939	NS	0.36	inner membrane transporter RhtA	General function prediction only
K06883	NS	0.27	UD	General function prediction only
K06908	NS	0.23	UD	General function prediction only
K07055	NS	0.06	UD	General function prediction only
K00113	NS	0.35	glycerol-3-phosphate dehydrogenase subunit C	Glycerophospholipid metabolism
K01096	NS	0.33	phosphatidylglycerophosphatase B	Glycerophospholipid metabolism
K11179	NS	0.48	tRNA 2-thiouridine synthesizing protein E	Inorganic ion transport and metabolism
K01083	NS	0.21	3-phytase	Inositol phosphate metabolism
K00324	NS	0.41	NAD(P) transhydrogenase subunit alpha	Nicotinate and nicotinamide metabolism
K00952	NS	0.38	nicotinamide-nucleotide adenylyltransferase	Nicotinate and nicotinamide metabolism

K03385	NS	0.37	formate-dependent nitrite reductase, periplasmic cytochrome c552	Nitrogen metabolism
K01668	NS	0.44	tyrosine phenol-lyase	Nitrogen metabolism;Tyrosine metabolism
K03465	NS	0.49	thymidylate synthase (FAD)	One carbon pool by folate;Pyrimidine metabolism
K06606	NS	0.23	inosose isomerase	Other carbohydrate metabolism
K04755	NS	0.19	ferredoxin, 2Fe-2S	Other energy metabolism
K01146	NS	0.37	UD	Other replication, recombination and repair proteins
K01147	NS	0.43	exoribonuclease II	Other translation proteins
K00329	NS	0.40	NADH dehydrogenase	Oxidative phosphorylation
K05581	NS	0.10	NADH dehydrogenase I subunit J	Oxidative phosphorylation
K04034	NS	0.48	anaerobic magnesium-protoporphyrin IX monomethyl ester cyclase	Porphyrin and chlorophyll metabolism
K02494	NS	0.40	outer membrane lipoprotein LolB	Porphyrin and chlorophyll metabolism
K00932	NS	0.34	propionate kinase	Propanoate metabolism
K00958	NS	0.31	sulfate adenylyltransferase	Purine metabolism;Selenoamino acid metabolism;Sulfur metabolism

K01679	NS	0.43	fumarate hydratase, class II	Reductive carboxylate cycle (CO2 fixation);Pathways in cancer;Citrate cycle (TCA cycle);Renal cell carcinoma
K02221	NS	0.49	YggT family protein	Secretion system
K00394	NS	0.14	adenylylsulfate reductase, subunit A	Selenoamino acid metabolism;Sulfur metabolism
K00395	NS	0.12	adenylylsulfate reductase, subunit B	Selenoamino acid metabolism;Sulfur metabolism
K03851	NS	0.20	taurine-pyruvate aminotransferase	Taurine and hypotaurine metabolism
K03486	NS	0.32	GntR family transcriptional regulator, trehalose operon	Transcription factors
K05819	NS	0.36	MFS transporter, AAHS family, 3-hydroxyphenylpropionic acid	Transporters
K11181	NS	0.31	sulfite reductase, dissimilatory-type beta subunit	Trinitrotoluene degradation
K11180	NS	0.30	sulfite reductase, dissimilatory-type alpha subunit	Trinitrotoluene degradation

K01826	NS	0.38	5-carboxymethyl-2-hydroxymuconate isomerase	Tyrosine metabolism;Benzoate degradation via hydroxylation
K10012	0.27	NS	undecaprenyl-phosphate 4-deoxy-4-formamido-L-arabinose transferase	Amino sugar and nucleotide sugar metabolism
K01470	0.31	NS	creatinine amidohydrolase	Arginine and proline metabolism
K02655	0.23	NS	type IV pilus assembly protein PilE	Bacterial motility proteins;Secretion system
K01034	0.26	NS	acetate CoA-transferase alpha subunit	Benzoate degradation via CoA ligation;Propanoate metabolism;Two-component system;Butanoate metabolism
K03562	0.29	NS	biopolymer transport protein TolQ	Cell motility and secretion
K03645	0.10	NS	negative modulator of initiation of replication	Chromosome;DNA replication proteins
K05982	0.32	NS	deoxyribonuclease V	DNA repair and recombination proteins
K03690	0.32	NS	hypothetical protein	Function unknown
K09861	0.30	NS	hypothetical protein	Function unknown
K09929	0.23	NS	hypothetical protein	Function unknown
K09805	0.19	NS	hypothetical protein	Function unknown

K07006	0.36	NS	UD	General function prediction only
K07127	0.27	NS	UD	General function prediction only
K03918	0.26	NS	L-lysine 6-transaminase	Lysine biosynthesis
K06605	0.40	NS	myo-inositol catabolism protein IolH	Other carbohydrate metabolism
K05926	0.07	NS	UD	Other enzymes
K03316	0.47	NS	monovalent cation:H+ antiporter, CPA1 family	Other ion-coupled transporters
K03757	0.34	NS	cadaverine:lysine antiporter	Other ion-coupled transporters
K02274	0.39	NS	cytochrome c oxidase subunit I	Oxidative phosphorylation
K05351 *	0.25	NS	D-xylulose reductase	Pentose and glucuronate interconversions
K01657	0.49	NS	anthranilate synthase component I	Phenylalanine, tyrosine and tryptophan biosynthesis;Two-component system
K05517	0.38	NS	nucleoside-specific channel-forming protein	Pores ion channels
K03286	0.18	NS	OmpA-OmpF porin, OOP family	Pores ion channels
K09883	0.39	NS	cobaltochelatase CobT	Porphyrin and chlorophyll metabolism

K12294	0.37	NS	two-component system, AgrA family, sensor histidine kinase ComD	Protein kinases;Two-component system;Secretion system
K01486	0.39	NS	adenine deaminase	Purine metabolism
K11902	0.32	NS	type VI secretion system protein ImpA	Secretion system
K02461	0.34	NS	general secretion pathway protein L	Secretion system;Bacterial secretion system
K00390	0.34	NS	phosphoadenosine phosphosulfate reductase	Sulfur metabolism
K06284	0.39	NS	transcriptional pleiotropic regulator of transition state genes	Transcription factors
K03765	0.17	NS	transcriptional activator of cad operon	Transcription factors
K08218	0.47	NS	MFS transporter, PAT family, beta-lactamase induction signal	Transporters
K02069	0.34	NS	putative ABC transport system permease protein	Transporters

K05820	0.22	NS	MFS transporter, PPP family, 3-phenylpropionic acid transporter	Transporters
K05772	0.31	NS	putative tungstate transport system substrate-binding protein	Transporters;ABC transporters
K09694	0.14	NS	lipooligosaccharide transport system permease protein	Transporters;ABC transporters
K10234	0.01	NS	alpha-glucoside transport system permease protein	Transporters;ABC transporters
K11382	0.36	NS	MFS transporter, OPA family, phosphoglycerate transporter protein	Transporters;Two-component system
K11444	0.24	NS	two-component system, PleD family, response regulator WspR	Two-component system
K07666	0.24	NS	two-component system, OmpR family, response regulator QseB	Two-component system
K00275	0.27	NS	pyridoxamine 5'-phosphate oxidase	Vitamin B6 metabolism

K00523	0.16	0.22	CDP-4-dehydro-6-deoxyglucose reductase	Amino sugar and nucleotide sugar metabolism
K06975	0.36	0.33	UD	General function prediction only
K08313	0.32	0.46	fructose-6-phosphate aldolase 1	Other carbohydrate metabolism
K07734	0.32	0.31	transcriptional regulator	Transcription factors
K10243	0.37	0.41	cellobiose transport system ATP-binding protein	Transporters;ABC transporters

*This KO was also found at significantly decreased abundance in DNA shotgun sequencing data from heterozygous mice (paired test using edgeR; $q<0.05$, >2-fold change).