SUPPLEMENTAL MATERIAL

Table S1. ***Lactobacillus*** **species (N=134).**

Ace–Dex	Dio–Kim	Kim–Pla	Pob–Xia
L. acetotolerans	*L. diolivorans*	*L. kimchiensis*	*L. pobuzihii*
L. acidifarinae	*L. equi*	*L. koreensis*	*L. pontis*
L. acidipiscis	*L. equicursoris*	*L. kullabergensis*	*L. psittaci*
L. acidophilus	*L. equigenerosi*	*L. kunkeei*	*L. rapi*
L. agilis	*L. fabifermentans*	*L. lindneri*	*L. rennini*
L. algidus	*L. farciminis*	*L. lindneri**	*L. reuteri*
L. alimentarius	*L. farraginis*	*L. malefermentans*	*L. rhamnosus*
L. amylolyticus	*L. fermentum*	*L. manihotivorans*	*L. rossiae*
L. amylotrophicus	*L. floricola*	*L. mellifer*	*L. ruminis*
L. amylovorus	*L. florum*	*L. mellifer**	*L. saerimneri*
*L. amylovorus**	*L. fructivorans*	*L. mellis*	*L. sakei*
L. animalis	*L. frumenti*	*L. mindensis*	*L. salivarius*
L. antri	*L. fuchuensis*	*L. mucosae*	*L. salivarius**
L. apinorum	*L. gasseri*	*L. mucosae**	*L. sanfranciscensis*
L. apis	*L. gastricus*	*L. nagelii*	*L. sanfranciscensis**
*L. apis**	*L. ghanensis*	*L. nasuensis*	*L. saniviri*
L. aquaticus	*L. gigeriorum*	*L. nodensis*	*L. satsumensis*
L. aviarius	*L. ginsenosidimutans*	*L. odoratitofui*	*L. secaliphilus*
L. bifermentans	*L. graminis*	*L. oeni*	*L. selangorensis*
L. brantae	*L. hamsteri*	*L. oligofermentans*	*L. senioris*
L. brevis	*L. harbinensis*	*L. oryzae*	*L. sharpeae*
*L. brevis**	*L. hayakitensis*	*L. ozensis*	*L. shenzhenensis*
L. buchneri	*L. heilongjiangensis*	*L. panis*	*L. siliginis*
*L. buchneri**	*L. helveticus*	*L. pantheris*	*L. similis*
L. cacaonum	*L. herbarum*	*L. parabrevis*	*L. spicheri*
L. camelliae	*L. hilgardii*	*L. parabuchneri*	*L. sucicola*
L. capillatus	*L. hokkaidonensis*	*L. parabuchneri**	*L. suebicus*
L. ceti	*L. hokkaidonensis**	*L. paracasei*	*L. thailandensis*
L. coleohominis	*L. hominis*	*L. paracasei**	*L. tucceti*
L. composti	*L. hordei*	*L. paracollinoides*	*L. uvarum*
L. concavus	*L. iners*	*L. paracollinoides**	*L. vaccinostercus*
L. coryniformis	*L. ingluviei*	*L. parafarraginis*	*L. vaginalis*
L. crispatus	*L. intestinalis*	*L. paralimentarius*	*L. versmoldensis*
L. crustorum	*L. jensenii*	*L. pasteurii*	*L. vini*
*L. crustorum**	*L. kalixensis*	*L. paucivorans*	*L. wasatchensis*
L. curieae	*L. kefiranofaciens*	*L. perolens*	*L. xiangfangensis*
L. delbrueckii	*L. kefiranofaciens**	*L. plantarum*	
L. dextrinicus	*L. kimchicus*	*L. plantarum**	

Bacterial plasmids are denoted with an asterisk.

Table S2. Common microbial genera (N=91, prevalence ≥1%, abundance ≥0.1%).

Ace–Dia	Die–Lac	Mar–Vei
Acetivibrio	*Dielma*	*Marvinbryantia*
Acidaminococcus	*Dorea*	*Megamonas*
Actinomyces	*Eggerthella*	*Megasphaera*
Adlercreutzia	*Eisenbergiella*	*Methanobrevibacter*
Akkermansia	*Enorma*	*Methanomassiliicoccus*
Alistipes	*Enterobacter*	*Mitsuokella*
Alloprevotella	*Enterococcus*	*Odoribacter*
Anaerostipes	*Erysipelatoclostridium*	*Oscillibacter*
Anaerotruncus	*Escherichia*	*Parabacteroides*
Bacteroides	*Escherichia**	*Paraprevotella*
*Bacteroides**	*Eubacterium*	*Parasutterella*
Barnesiella	*Eubacterium**	*Phascolarctobacterium*
Bifidobacterium	*Faecalibacterium*	*Phocea*
Bilophila	*Faecalicatena*	*Porphyromonas*
Bittarella	*Faecalicoccus*	*Prevotella*
Blautia	*Faecalitalea*	*Roseburia*
Butyricicoccus	*Fournierella*	*Ruminiclostridium*
Butyricimonas	*Gordonibacter*	*Ruminococcus*
Butyrivibrio	*Haemophilus*	*Ruthenibacterium*
Catenibacterium	*Halapricum*	*Sanguibacteroides*
Caudovirales	*Holdemanella*	*Sellimonas*
Cellulomonas	*Holdemania*	*Senegalimassilia*
Citrobacter	*Hungatella*	*Shigella*
Clostridioides	*Intestinibacter*	*Solobacterium*
Clostridium	*Johnsonella*	*Streptococcus*
Collinsella	*Klebsiella*	*Subdoligranulum*
Coprobacillus	*Klebsiella**	*Sutterella*
Coprobacter	*Kluyvera*	*Tannerella*
Coprococcus	*Lachnoanaerobaculum*	*Turicibacter*
Dakarella	*Lachnoclostridium*	*Tyzzerella*
Desulfovibrio	*Lactobacillus*	*Veillonella*
Dialister	*Lactococcus*	

Bacterial plasmids are denoted with an asterisk.

Table S3. Associations between blood pressure indices and microbial alpha diversity.

	Age- and sex-adjusted model		Multivariable-adjusted model	
	β (95%-CI)	p	β (95%-CI)	p
Systolic BP	-0.54 (-0.96 to -0.12)	0.012	-0.20 (-0.62 to 0.21)	0.334
Diastolic BP	-0.31 (-0.56 to -0.06)	0.016	-0.10 (-0.35 to 0.14)	0.404
Mean arterial pressure	-0.39 (-0.66 to -0.12)	0.005	-0.14 (-0.40 to 0.12)	0.304
Pulse pressure	-0.23 (-0.59 to 0.13)	0.203	-0.10 (-0.46 to 0.26)	0.580
Hypertension	0.91 (0.86 to 0.96)	<0.001	0.98 (0.92 to 1.04)	0.498

Multivariable-adjusted model is adjusted for age, sex, BMI, smoking, exercise, diuretics, beta blockers, calcium channel blockers, and renin–angiotensin system blockers. BP, blood pressure.

Table S4. Associations between blood pressure indices and microbial beta diversity.

	Age- and sex adjusted model		Multivariable adjusted model	
	R^2	p	R^2	p
Systolic BP	0.046%	0.001	0.018%	0.195
Diastolic BP	0.053%	0.001	0.024%	0.032
Mean arterial pressure	0.058%	0.001	0.020%	0.126
Pulse pressure	0.024%	0.038	0.020%	0.086
Hypertension	0.046%	0.002	0.015%	0.376

Analysis of variance for beta diversity was calculated using 999 permutations. Multivariable-adjusted model is adjusted for age, sex, BMI, smoking, exercise, diuretics, beta blockers, calcium channel blockers, and renin–angiotensin system blockers. BP, blood pressure.

Table S5. Associations between gut microbial genera and blood pressure indices.

	Systolic BP		Diastolic BP		Pulse pressure		Mean arterial pressure		Hypertension	
	Log2FC±SE	p	Log2FC±SE	p	Log2FC±SE	p	Log2FC±SE	p	Log2FC±SE	p
Acidaminococcus			0.32±0.04	<0.001	-0.29±0.04	<0.001	0.20±0.04	<0.001		
Actinomyces			0.04±0.01	0.011	-0.03±0.01	0.045			0.10±0.03	0.008
Adlercreutzia	-0.07±0.02	0.008	-0.06±0.02	0.042			-0.07±0.02	0.006		
Alloprevotella									-0.12±0.04	0.006
Anaerostipes	0.06±0.02	0.015							0.16±0.04	<0.001
Anaerotruncus	-0.05±0.01	<0.001			-0.05±0.01	<0.001	-0.03±0.01	0.010	-0.06±0.02	0.037
Bacteroides			0.05±0.02	0.027			0.05±0.02	0.022		
*Bacteroides**			0.17±0.04	<0.001			0.16±0.04	<0.001		
Blautia	0.04±0.01	0.015	0.03±0.01	0.038			0.04±0.01	0.008	0.11±0.03	<0.001
Cellulomonas	0.10±0.03	0.016			0.15±0.03	<0.001				
Citrobacter			-0.43±0.04	<0.001	0.17±0.04	<0.001	-0.33±0.04	<0.001	0.35±0.10	0.002
Clostridioides			0.13±0.02	<0.001	-0.12±0.02	<0.001	0.09±0.02	<0.001		
Collinsella			0.13±0.02	<0.001			0.12±0.02	<0.001	0.19±0.05	0.002
Coprobacillus	-0.12±0.02	<0.001	-0.06±0.02	0.006	-0.10±0.02	<0.001	-0.10±0.02	<0.001	-0.20±0.04	<0.001
Coprococcus	0.05±0.01	0.004			0.05±0.01	0.004			0.10±0.03	0.012
Desulfovibrio	0.13±0.03	<0.001	0.16±0.03	<0.001			0.17±0.03	<0.001		
Dialister	0.10±0.04	0.039			0.13±0.04	0.002				
Dielma	0.23±0.03	<0.001	0.14±0.03	<0.001	0.15±0.03	<0.001	0.22±0.03	<0.001	0.28±0.07	0.001
Dorea									0.08±0.03	0.030
Eisenbergiella			0.16±0.03	<0.001			0.13±0.03	<0.001	0.17±0.06	0.018
Enorma									0.11±0.04	0.050
Enterobacter	0.25±0.04	<0.001	-0.15±0.04	<0.001	0.32±0.04	<0.001			0.89±0.09	<0.001
Erysipelatoclostridium			0.06±0.02	0.006			0.05±0.02	0.031	0.13±0.04	0.011
Faecalicoccus	-0.05±0.02	0.041			-0.06±0.02	0.003				
Faecalitalea									0.08±0.03	0.047

	Systolic BP		Diastolic BP		Pulse pressure		Mean arterial pressure		Hypertension	
	Log2FC±SE	p	Log2FC±SE	p	Log2FC±SE	p	Log2FC±SE	p	Log2FC±SE	p
Fournierella	-0.02±0.01	0.022					-0.03±0.01	0.015	-0.07±0.02	0.002
Holdemania	0.10±0.02	<0.001	0.10±0.02	<0.001			0.12±0.02	<0.001	0.20±0.04	<0.001
Hungatella	-0.09±0.02	<0.001			-0.09±0.02	<0.001	-0.06±0.02	0.006		
Intestinibacter									0.17±0.06	0.030
Kluyvera			-0.26±0.04	<0.001	0.24±0.04	<0.001	-0.11±0.04	0.047	0.55±0.09	<0.001
Lachnoclostridium			0.04±0.01	0.008	-0.04±0.01	0.005				
Lactococcus									0.18±0.07	0.047
Megasphaera	0.19±0.03	<0.001			0.19±0.03	<0.001	0.14±0.03	<0.001	0.23±0.07	0.008
Mitsuokella	0.15±0.04	0.001	-0.14±0.04	0.001	0.25±0.04	<0.001				
Paraprevotella	0.09±0.03	0.017			0.10±0.03	0.005				
Parasutterella			-0.10±0.04	0.030						
Phascolarctobacterium	0.10±0.03	0.011			0.08±0.03	0.042	0.08±0.03	0.038	0.22±0.07	0.007
Prevotella			-0.09±0.03	0.048						
Ruthenibacterium	0.07±0.02	0.004			0.08±0.02	0.001			0.12±0.05	0.034
Sanguibacteroides			0.08±0.02	0.005			0.08±0.02	0.006		
Sellimonas			-0.15±0.02	<0.001	0.09±0.02	<0.001	-0.10±0.02	<0.001		
Senegalimassilia									-0.18±0.05	0.003
Solobacterium	-0.08±0.02	0.001			-0.07±0.02	0.005	-0.06±0.02	0.014		
Sutterella	0.11±0.04	0.010	0.11±0.03	0.008			0.13±0.04	0.002		
Turicibacter	0.16±0.04	<0.001	0.13±0.03	<0.001	0.09±0.03	0.030	0.17±0.04	<0.001		
Tyzzerella			-0.04±0.01	0.033						

Models are adjusted for age, sex, BMI, smoking, exercise, diuretics, beta blockers, calcium channel blockers, and renin–angiotensin system blockers. Association with bacterial plasmid is denoted using asterisk. BP, blood pressure. Log2FC, base 2 log of fold change.

Table S6. Associations between *Lactobacillus* species and blood pressure indices.

	Systolic BP		Diastolic BP		Pulse pressure		Mean arterial pressure		Hypertension	
	Log2FC±SE	p	Log2FC±SE	p	Log2FC±SE	p	Log2FC±SE	p	Log2FC±SE	p
L. agilis			-0.19±0.06	0.017			-0.20±0.06	0.013		
L. algidus									0.30±0.09	0.010
L. amylotrophicus			-0.22±0.06	0.003						
L. aviarius	-0.13±0.03	0.001			-0.09±0.03	0.043	-0.12±0.03	0.003		
L. equicursoris									-0.25±0.07	0.003
L. farciminis	-0.33±0.05	<0.001	-0.19±0.04	<0.001	-0.27±0.04	<0.001	-0.30±0.05	<0.001	-0.60±0.10	<0.001
L. hominis	-0.26±0.04	<0.001			-0.27±0.04	<0.001	-0.16±0.04	0.003	-0.42±0.09	<0.001
L. iners	-0.18±0.05	0.013	0.44±0.05	<0.001	-0.43±0.05	<0.001	0.17±0.05	0.02	-0.45±0.11	0.001
L. jensenii					-0.16±0.05	0.011				
L. kalixensis	0.23±0.07	0.013					0.22±0.06	0.013		
L. kefiranofaciens	0.20±0.06	0.025								
L. kimchicus					-0.61±0.19	0.025	0.65±0.20	0.023		
L. parabuchneri									0.50±0.15	0.017
L. paracasei	-0.15±0.04	0.020	-0.23±0.04	<0.001			-0.23±0.04	<0.001		
L. pasteurii					-0.12±0.03	<0.001			-0.29±0.06	<0.001
L. rhamnosus									0.65±0.12	<0.001
L. ruminis			-0.32±0.04	<0.001			-0.26±0.04	<0.001	-0.49±0.08	<0.001
L. sakei	0.15±0.04	0.009					0.13±0.04	0.038		
*L. salivarius**					0.52±0.11	<0.001				

Models are adjusted for age, sex, BMI, smoking, exercise, diuretics, beta blockers, calcium channel blockers, and renin–angiotensin system blockers. Association with bacterial plasmid is denoted using asterisk. BP, blood pressure. Log2FC, base 2 log of fold change.

Table S7. Associations between KO groups and systolic BP.

KO-group	Definition	β (95%-CI)	*P*
K00169	pyruvate ferredoxin oxidoreductase alpha subunit	-0.04 (-0.06 to -0.02)	0.029
K00170	pyruvate ferredoxin oxidoreductase beta subunit	-0.04 (-0.06 to -0.02)	0.029
K00171	pyruvate ferredoxin oxidoreductase delta subunit	-0.04 (-0.06 to -0.02)	0.029
K00172	pyruvate ferredoxin oxidoreductase gamma subunit	-0.04 (-0.06 to -0.02)	0.029
K00402	methyl-coenzyme M reductase gamma subunit	-0.04 (-0.06 to -0.02)	0.029
K00581	tetrahydromethanopterin S-methyltransferase subunit E	-0.04 (-0.06 to -0.02)	0.029
K01854	UDP-galactopyranose mutase	-0.04 (-0.06 to -0.02)	0.029
K02201	pantetheine-phosphate adenylyltransferase	-0.04 (-0.06 to -0.02)	0.029
K02910	large subunit ribosomal protein L31e	-0.04 (-0.06 to -0.02)	0.029
K02944	large subunit ribosomal protein LX	-0.04 (-0.06 to -0.02)	0.029
K03049	DNA-directed RNA polymerase subunit E'	-0.04 (-0.06 to -0.02)	0.029
K03105	signal recognition particle subunit SRP19	-0.04 (-0.06 to -0.02)	0.029
K03136	transcription initiation factor TFIIE subunit alpha	-0.05 (-0.07 to -0.03)	0.029
K03538	ribonuclease P protein subunit POP4	-0.04 (-0.06 to -0.02)	0.029
K04801	replication factor C small subunit	-0.04 (-0.06 to -0.02)	0.029
K07060	endoribonuclease Nob1	-0.04 (-0.06 to -0.02)	0.029
K07133	uncharacterized protein	-0.04 (-0.06 to -0.02)	0.029
K07143	UPF0148 protein	-0.04 (-0.06 to -0.02)	0.029
K07333	archaeal flagellar protein FlaJ	-0.04 (-0.06 to -0.02)	0.029
K07722	CopG family transcriptional regulator, nickel-responsive regulator	-0.04 (-0.06 to -0.02)	0.029
K07730	putative transcriptional regulator	-0.04 (-0.06 to -0.02)	0.029
K07991	archaeal preflagellin peptidase FlaK	-0.04 (-0.06 to -0.02)	0.029
K09713	uncharacterized protein	-0.05 (-0.07 to -0.02)	0.029
K09738	uncharacterized protein	-0.04 (-0.06 to -0.02)	0.029
K12960	5-methylthioadenosine/S-adenosylhomocysteine deaminase	-0.04 (-0.06 to -0.02)	0.029
K13787	geranylgeranyl diphosphate synthase, type I	-0.04 (-0.06 to -0.02)	0.029
K14100	energy-converting hydrogenase A subunit I	-0.04 (-0.06 to -0.02)	0.029
K14104	energy-converting hydrogenase A subunit M	-0.04 (-0.06 to -0.02)	0.029
K14561	U3 small nucleolar ribonucleoprotein protein IMP4	-0.05 (-0.07 to -0.03)	0.029
K14654	2,5-diamino-6-(ribosylamino)-4(3H)-pyrimidinone 5'-phosphate reductase	-0.05 (-0.07 to -0.02)	0.029
K17104	phosphoglycerol geranylgeranyltransferase	-0.04 (-0.06 to -0.02)	0.029
K18237	ribose 1,5-bisphosphate isomerase	-0.04 (-0.06 to -0.02)	0.029
K04800	replication factor C large subunit	-0.04 (-0.06 to -0.02)	0.029
K07739	elongator complex protein 3	-0.04 (-0.06 to -0.02)	0.029
K07142	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase	-0.04 (-0.06 to -0.02)	0.030
K00180	indolepyruvate ferredoxin oxidoreductase, beta subunit	-0.04 (-0.06 to -0.02)	0.030
K01251	adenosylhomocysteinase	-0.04 (-0.06 to -0.02)	0.030
K02908	large subunit ribosomal protein L30e	-0.04 (-0.06 to -0.02)	0.030
K03234	elongation factor 2	-0.04 (-0.06 to -0.02)	0.030

K06875	programmed cell death protein 5	-0.04 (-0.06 to -0.02)	0.030
K08981	putative membrane protein	-0.04 (-0.06 to -0.02)	0.030
K17884	archaetidylinositol phosphate synthase	-0.04 (-0.06 to -0.02)	0.030
K00651	homoserine O-succinyltransferase/O-acetyltransferase	-0.04 (-0.06 to -0.02)	0.030
K02885	large subunit ribosomal protein L19e	-0.04 (-0.06 to -0.02)	0.030
K04518	prephenate dehydratase	-0.04 (-0.06 to -0.02)	0.030
K06218	mRNA interferase RelE/StbE	-0.04 (-0.06 to -0.02)	0.030
K06898	pyridinium-3,5-biscarboxylic acid mononucleotide synthase	-0.04 (-0.06 to -0.02)	0.030
K07166	ACT domain-containing protein	-0.04 (-0.06 to -0.02)	0.030
K18882	DNA primase large subunit	-0.04 (-0.06 to -0.02)	0.030
K03047	DNA-directed RNA polymerase subunit D	-0.04 (-0.06 to -0.02)	0.032
K16306	fructose-bisphosphate aldolase / 2-amino-3,7-dideoxy-D-threo-hept-6-ulosonate synthase	-0.04 (-0.06 to -0.02)	0.032
K00611	ornithine carbamoyltransferase	-0.04 (-0.06 to -0.02)	0.033
K09157	uncharacterized protein	-0.04 (-0.06 to -0.02)	0.033
K00262	glutamate dehydrogenase (NADP+)	-0.04 (-0.06 to -0.02)	0.034
K00319	methylenetetrahydromethanopterin dehydrogenase	-0.04 (-0.06 to -0.02)	0.034
K01912	phenylacetate-CoA ligase	-0.04 (-0.06 to -0.02)	0.034
K07727	putative transcriptional regulator	-0.04 (-0.06 to -0.02)	0.034
K00058	D-3-phosphoglycerate dehydrogenase / 2-oxoglutarate reductase	-0.04 (-0.06 to -0.02)	0.034
K00177	2-oxoglutarate ferredoxin oxidoreductase subunit gamma	-0.04 (-0.06 to -0.02)	0.034
K00179	indolepyruvate ferredoxin oxidoreductase, alpha subunit	-0.04 (-0.06 to -0.02)	0.034
K00184	dimethyl sulfoxide reductase iron-sulfur subunit	-0.04 (-0.06 to -0.02)	0.034
K00185	dimethyl sulfoxide reductase membrane subunit	-0.04 (-0.06 to -0.02)	0.034
K00582	tetrahydromethanopterin S-methyltransferase subunit F	-0.04 (-0.06 to -0.02)	0.034
K00818	acetylornithine aminotransferase	-0.04 (-0.06 to -0.02)	0.034
K00930	acetylglutamate kinase	-0.04 (-0.06 to -0.02)	0.034
K00940	nucleoside-diphosphate kinase	-0.04 (-0.06 to -0.02)	0.034
K01012	biotin synthase	-0.04 (-0.06 to -0.02)	0.034
K01091	phosphoglycolate phosphatase	-0.04 (-0.06 to -0.02)	0.034
K01151	deoxyribonuclease IV	-0.04 (-0.06 to -0.02)	0.034
K01421	putative membrane protein	-0.04 (-0.06 to -0.02)	0.034
K01439	succinyl-diaminopimelate desuccinylase	-0.04 (-0.06 to -0.02)	0.034
K01478	arginine deiminase	-0.04 (-0.06 to -0.02)	0.034
K01482	dimethylargininase	-0.04 (-0.06 to -0.02)	0.034
K01523	phosphoribosyl-ATP pyrophosphohydrolase	-0.04 (-0.06 to -0.02)	0.034
K01693	imidazoleglycerol-phosphate dehydratase	-0.04 (-0.06 to -0.02)	0.034
K01885	glutamyl-tRNA synthetase	-0.04 (-0.06 to -0.02)	0.034
K02195	heme exporter protein C	-0.04 (-0.06 to -0.02)	0.034
K02198	cytochrome c-type biogenesis protein CcmF	-0.04 (-0.06 to -0.02)	0.034
K02203	phosphoserine / homoserine phosphotransferase	-0.04 (-0.06 to -0.02)	0.034
K02282	pilus assembly protein CpaE	-0.04 (-0.06 to -0.02)	0.034
K02319	DNA polymerase, archaea type	-0.04 (-0.06 to -0.02)	0.034

K02434	aspartyl-tRNA(Asn)/glutamyl-tRNA(Gln) amidotransferase subunit B	-0.04 (-0.06 to -0.02)	0.034
K02573	ferredoxin-type protein NapG	-0.04 (-0.06 to -0.02)	0.034
K02574	ferredoxin-type protein NapH	-0.04 (-0.06 to -0.02)	0.034
K02912	large subunit ribosomal protein L32e	-0.04 (-0.06 to -0.02)	0.034
K02929	large subunit ribosomal protein L44e	-0.04 (-0.06 to -0.02)	0.034
K02930	large subunit ribosomal protein L4e	-0.04 (-0.06 to -0.02)	0.034
K03205	type IV secretion system protein VirD4	-0.04 (-0.06 to -0.02)	0.034
K03385	nitrite reductase (cytochrome c-552)	-0.04 (-0.06 to -0.02)	0.034
K03465	thymidylate synthase (FAD)	-0.04 (-0.06 to -0.02)	0.034
K03498	trk system potassium uptake protein	-0.04 (-0.06 to -0.02)	0.034
K03499	trk system potassium uptake protein	-0.04 (-0.06 to -0.02)	0.034
K03540	ribonuclease P protein subunit RPR2	-0.04 (-0.06 to -0.02)	0.034
K03655	ATP-dependent DNA helicase RecG	-0.04 (-0.06 to -0.02)	0.034
K03758	arginine:ornithine antiporter / lysine permease	-0.04 (-0.06 to -0.02)	0.034
K04041	fructose-1,6-bisphosphatase III	-0.04 (-0.06 to -0.02)	0.034
K04655	hydrogenase expression/formation protein HypE	-0.04 (-0.06 to -0.02)	0.034
K04656	hydrogenase maturation protein HypF	-0.04 (-0.06 to -0.02)	0.034
K05780	alpha-D-ribose 1-methylphosphonate 5-triphosphate synthase subunit PhnL	-0.04 (-0.06 to -0.02)	0.034
K05781	putative phosphonate transport system ATP-binding protein	-0.04 (-0.06 to -0.02)	0.034
K06163	alpha-D-ribose 1-methylphosphonate 5-phosphate C-P lyase	-0.04 (-0.06 to -0.02)	0.034
K06914	tyramine---L-glutamate ligase	-0.04 (-0.06 to -0.02)	0.034
K06915	uncharacterized protein	-0.04 (-0.06 to -0.02)	0.034
K06963	tRNA acetyltransferase TAN1	-0.04 (-0.06 to -0.02)	0.034
K07079	uncharacterized protein	-0.04 (-0.06 to -0.02)	0.034
K07154	serine/threonine-protein kinase HipA	-0.04 (-0.06 to -0.02)	0.034
K07307	anaerobic dimethyl sulfoxide reductase subunit B	-0.04 (-0.06 to -0.02)	0.034
K07308	anaerobic dimethyl sulfoxide reductase subunit C	-0.04 (-0.06 to -0.02)	0.034
K07309	Tat-targeted selenate reductase subunit YnfE	-0.04 (-0.06 to -0.02)	0.034
K07580	Zn-ribbon RNA-binding protein	-0.04 (-0.06 to -0.02)	0.034
K07776	two-component system, OmpR family, response regulator RegX3	-0.04 (-0.06 to -0.02)	0.034
K07979	GntR family transcriptional regulator	-0.04 (-0.06 to -0.02)	0.034
K08372	putative serine protease PepD	-0.04 (-0.06 to -0.02)	0.034
K08600	sortase B	-0.04 (-0.06 to -0.02)	0.034
K08979	putative membrane protein	-0.04 (-0.06 to -0.02)	0.034
K09121	pyridinium-3,5-bisthiocarboxylic acid mononucleotide nickel chelatase	-0.04 (-0.06 to -0.02)	0.034
K10040	aspartate/glutamate/glutamine transport system permease protein	-0.04 (-0.06 to -0.02)	0.034
K10206	LL-diaminopimelate aminotransferase	-0.04 (-0.06 to -0.02)	0.034
K11176	IMP cyclohydrolase	-0.04 (-0.06 to -0.02)	0.034
K11755	phosphoribosyl-AMP cyclohydrolase / phosphoribosyl-ATP pyrophosphohydrolase	-0.04 (-0.06 to -0.02)	0.034
K11913	type VI secretion system protein	-0.04 (-0.06 to -0.02)	0.034

K12257	SecD/SecF fusion protein	-0.04 (-0.06 to -0.02)	0.034
K13252	putrescine carbamoyltransferase	-0.04 (-0.06 to -0.02)	0.034
K13640	MerR family transcriptional regulator, heat shock protein HspR	-0.04 (-0.06 to -0.02)	0.034
K13812	bifunctional enzyme Fae/Hps	-0.04 (-0.06 to -0.02)	0.034
K14088	ech hydrogenase subunit C	-0.04 (-0.06 to -0.02)	0.034
K14188	D-alanine--poly(phosphoribitol) ligase subunit 2	-0.04 (-0.06 to -0.02)	0.034
K15429	tRNA (guanine37-N1)-methyltransferase	-0.04 (-0.06 to -0.02)	0.034
K16214	UDP-N-acetylglucosamine kinase	-0.04 (-0.06 to -0.02)	0.034
K16793	methanogen homoaconitase small subunit	-0.04 (-0.06 to -0.02)	0.034
K20265	glutamate:GABA antiporter	-0.04 (-0.06 to -0.02)	0.034
K00145	N-acetyl-gamma-glutamyl-phosphate reductase	-0.04 (-0.06 to -0.01)	0.034
K00176	2-oxoglutarate ferredoxin oxidoreductase subunit delta	-0.04 (-0.06 to -0.01)	0.034
K00399	methyl-coenzyme M reductase alpha subunit	-0.04 (-0.06 to -0.01)	0.034
K00613	glycine amidinotransferase	-0.04 (-0.06 to -0.01)	0.034
K00666	fatty-acyl-CoA synthase	-0.04 (-0.06 to -0.01)	0.034
K00846	ketohexokinase	-0.04 (-0.06 to -0.01)	0.034
K01372	bleomycin hydrolase	-0.04 (-0.06 to -0.01)	0.034
K01470	creatinine amidohydrolase	-0.04 (-0.06 to -0.01)	0.034
K01661	naphthoate synthase	-0.04 (-0.06 to -0.01)	0.034
K02069	putative ABC transport system permease protein	-0.04 (-0.06 to -0.01)	0.034
K02435	aspartyl-tRNA(Asn)/glutamyl-tRNA(Gln) amidotransferase subunit C	-0.04 (-0.06 to -0.01)	0.034
K03521	electron transfer flavoprotein beta subunit	-0.04 (-0.06 to -0.01)	0.034
K03552	holliday junction resolvase Hjr	-0.04 (-0.06 to -0.01)	0.034
K03739	membrane protein involved in D-alanine export	-0.04 (-0.06 to -0.02)	0.034
K04653	hydrogenase expression/formation protein HypC	-0.04 (-0.06 to -0.01)	0.034
K05516	curved DNA-binding protein	-0.04 (-0.06 to -0.01)	0.034
K06162	alpha-D-ribose 1-methylphosphonate 5-triphosphate diphosphatase	-0.04 (-0.06 to -0.01)	0.034
K07171	mRNA interferase MazF	-0.04 (-0.06 to -0.01)	0.034
K07306	anaerobic dimethyl sulfoxide reductase subunit A	-0.04 (-0.06 to -0.02)	0.034
K07402	xanthine dehydrogenase accessory factor	-0.04 (-0.06 to -0.01)	0.034
K07562	nonsense-mediated mRNA decay protein 3	-0.04 (-0.06 to -0.01)	0.034
K07581	RNA-binding protein	-0.04 (-0.06 to -0.02)	0.034
K08177	MFS transporter, OFA family, oxalate/formate antiporter	-0.04 (-0.06 to -0.02)	0.034
K08999	uncharacterized protein	-0.04 (-0.06 to -0.01)	0.034
K09013	Fe-S cluster assembly ATP-binding protein	-0.04 (-0.06 to -0.01)	0.034
K09167	uncharacterized protein	-0.04 (-0.06 to -0.01)	0.034
K10536	agmatine deiminase	-0.04 (-0.06 to -0.01)	0.034
K11358	aspartate aminotransferase	-0.04 (-0.06 to -0.02)	0.034
K11912	serine/threonine-protein kinase PpkA	-0.04 (-0.06 to -0.01)	0.034
K12136	hydrogenase-4 component A	-0.04 (-0.06 to -0.02)	0.034
K12143	hydrogenase-4 component H	-0.04 (-0.06 to -0.02)	0.034
K18926	MFS transporter, DHA2 family, lincomycin resistance protein	-0.04 (-0.06 to -0.01)	0.034

K08744	cardiolipin synthase (CMP-forming)	-0.04 (-0.06 to -0.01)	0.034
K09790	uncharacterized protein	-0.04 (-0.06 to -0.01)	0.034
K14086	ech hydrogenase subunit A	-0.04 (-0.06 to -0.01)	0.034
K02322	DNA polymerase II large subunit	-0.04 (-0.06 to -0.01)	0.035
K00123	formate dehydrogenase major subunit	-0.03 (-0.06 to -0.01)	0.035
K01895	acetyl-CoA synthetase	-0.03 (-0.06 to -0.01)	0.035
K01959	pyruvate carboxylase subunit A	-0.03 (-0.06 to -0.01)	0.035
K02279	pilus assembly protein CpaB	-0.03 (-0.06 to -0.01)	0.035
K02927	ubiquitin-large subunit ribosomal protein L40e	-0.04 (-0.06 to -0.01)	0.035
K03231	elongation factor 1-alpha	-0.04 (-0.06 to -0.01)	0.035
K03522	electron transfer flavoprotein alpha subunit	-0.03 (-0.06 to -0.01)	0.035
K03783	purine-nucleoside phosphorylase	-0.03 (-0.06 to -0.01)	0.035
K06982	pantoate kinase	-0.03 (-0.06 to -0.01)	0.035
K07558	tRNA nucleotidyltransferase (CCA-adding enzyme)	-0.04 (-0.06 to -0.01)	0.035
K09730	uncharacterized protein	-0.04 (-0.06 to -0.01)	0.035
K11741	quaternary ammonium compound-resistance protein SugE	-0.03 (-0.06 to -0.01)	0.035
K01814	phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase	-0.03 (-0.06 to -0.01)	0.035
K00053	ketol-acid reductoisomerase	-0.03 (-0.06 to -0.01)	0.035
K00931	glutamate 5-kinase	-0.03 (-0.06 to -0.01)	0.035
K02433	aspartyl-tRNA(Asn)/glutamyl-tRNA(Gln) amidotransferase subunit A	-0.03 (-0.06 to -0.01)	0.035
K02614	acyl-CoA thioesterase	-0.03 (-0.06 to -0.01)	0.035
K02683	DNA primase small subunit	-0.03 (-0.06 to -0.01)	0.035
K03151	tRNA uracil 4-sulfurtransferase	-0.03 (-0.06 to -0.01)	0.035
K03622	archaea-specific DNA-binding protein	-0.03 (-0.06 to -0.01)	0.035
K06206	sugar fermentation stimulation protein A	-0.03 (-0.06 to -0.01)	0.035
K06921	uncharacterized protein	-0.03 (-0.06 to -0.01)	0.035
K07164	uncharacterized protein	-0.03 (-0.06 to -0.01)	0.035
K07452	5-methylcytosine-specific restriction enzyme B	-0.03 (-0.06 to -0.01)	0.035
K09693	teichoic acid transport system ATP-binding protein	-0.03 (-0.06 to -0.01)	0.035
K02922	large subunit ribosomal protein L37e	-0.03 (-0.06 to -0.01)	0.035
K00052	3-isopropylmalate dehydrogenase	-0.03 (-0.05 to -0.01)	0.035
K00286	pyrroline-5-carboxylate reductase	-0.03 (-0.05 to -0.01)	0.035
K00817	histidinol-phosphate aminotransferase	-0.03 (-0.05 to -0.01)	0.035
K00926	carbamate kinase	-0.03 (-0.05 to -0.01)	0.035
K01129	dGTPase	-0.03 (-0.05 to -0.01)	0.035
K01704	3-isopropylmalate/(R)-2-methylmalate dehydratase small subunit	-0.03 (-0.05 to -0.01)	0.035
K02042	phosphonate transport system permease protein	-0.03 (-0.05 to -0.01)	0.035
K02068	putative ABC transport system ATP-binding protein	-0.03 (-0.05 to -0.01)	0.035
K02653	type IV pilus assembly protein PilC	-0.03 (-0.05 to -0.01)	0.035
K03313	Na+:H+ antiporter, NhaA family	-0.03 (-0.05 to -0.01)	0.035
K03502	DNA polymerase V	-0.03 (-0.05 to -0.01)	0.035
K03688	ubiquinone biosynthesis protein	-0.03 (-0.05 to -0.01)	0.035

K05919	superoxide reductase	-0.03 (-0.05 to -0.01)	0.035
K06164	alpha-D-ribose 1-methylphosphonate 5-triphosphate synthase subunit PhnI	-0.03 (-0.05 to -0.01)	0.035
K06165	alpha-D-ribose 1-methylphosphonate 5-triphosphate synthase subunit PhnH	-0.03 (-0.05 to -0.01)	0.035
K06166	alpha-D-ribose 1-methylphosphonate 5-triphosphate synthase subunit PhnG	-0.03 (-0.06 to -0.01)	0.035
K06196	cytochrome c-type biogenesis protein	-0.03 (-0.05 to -0.01)	0.035
K06972	presequence protease	-0.03 (-0.05 to -0.01)	0.035
K07045	uncharacterized protein	-0.03 (-0.05 to -0.01)	0.035
K07126	uncharacterized protein	-0.03 (-0.05 to -0.01)	0.035
K07405	alpha-amylase	-0.03 (-0.05 to -0.01)	0.035
K08659	dipeptidase	-0.03 (-0.05 to -0.01)	0.035
K09773	[pyruvate, water dikinase]-phosphate phosphotransferase /	-0.03 (-0.06 to -0.01)	0.035
K11928	sodium/proline symporter	-0.03 (-0.05 to -0.01)	0.035
K12410	NAD-dependent deacetylase	-0.03 (-0.05 to -0.01)	0.035
K14564	nucleolar protein 56	-0.03 (-0.06 to -0.01)	0.035
K17828	dihydroorotate dehydrogenase (NAD+) catalytic subunit	-0.03 (-0.05 to -0.01)	0.035
K17870	NADH oxidase (H2O2-forming)	-0.03 (-0.06 to -0.01)	0.035
K03116	sec-independent protein translocase protein TatA	-0.03 (-0.05 to -0.01)	0.036
K07220	uncharacterized protein	-0.03 (-0.05 to -0.01)	0.036
K16153	glycogen phosphorylase/synthase	-0.03 (-0.05 to -0.01)	0.036
K19067	cyclohexane-1-carbonyl-CoA dehydrogenase	-0.03 (-0.05 to -0.01)	0.036
K01733	threonine synthase	-0.03 (-0.05 to -0.01)	0.036
K02654	leader peptidase (prepilin peptidase) / N-methyltransferase	-0.03 (-0.05 to -0.01)	0.036
K03183	demethylmenaquinone methyltransferase / 2-methoxy-6-polyprenyl-1,4-benzoquinol methylase	-0.03 (-0.05 to -0.01)	0.036
K03307	solute:Na+ symporter, SSS family	-0.03 (-0.05 to -0.01)	0.036
K03340	diaminopimelate dehydrogenase	-0.03 (-0.05 to -0.01)	0.036
K06943	nucleolar GTP-binding protein	-0.03 (-0.05 to -0.01)	0.036
K06962	uncharacterized protein	-0.03 (-0.05 to -0.01)	0.036
K07446	tRNA (guanine10-N2)-dimethyltransferase	-0.03 (-0.05 to -0.01)	0.036
K12511	tight adherence protein C	-0.03 (-0.05 to -0.01)	0.036
K16792	methanogen homoaconitase large subunit	-0.03 (-0.05 to -0.01)	0.036
K19955	alcohol dehydrogenase	-0.03 (-0.05 to -0.01)	0.036
K07144	5-(aminomethyl)-3-furanmethanol phosphate kinase	-0.03 (-0.05 to -0.01)	0.036
K01426	amidase	-0.03 (-0.05 to -0.01)	0.037
K00174	2-oxoglutarate/2-oxoacid ferredoxin oxidoreductase subunit alpha	-0.03 (-0.05 to -0.01)	0.037
K00794	6,7-dimethyl-8-ribityllumazine synthase	-0.03 (-0.05 to -0.01)	0.037
K01649	2-isopropylmalate synthase	-0.03 (-0.05 to -0.01)	0.037
K01687	dihydroxy-acid dehydratase	-0.03 (-0.05 to -0.01)	0.037
K02875	large subunit ribosomal protein L14e	-0.03 (-0.05 to -0.01)	0.037
K03316	monovalent cation:H+ antiporter, CPA1 family	-0.03 (-0.05 to -0.01)	0.037
K08963	methylthioribose-1-phosphate isomerase	-0.03 (-0.05 to -0.01)	0.037
K03243	translation initiation factor 5B	-0.03 (-0.05 to -0.01)	0.037

K00147	glutamate-5-semialdehyde dehydrogenase	-0.03 (-0.05 to -0.01)	0.037
K03722	ATP-dependent DNA helicase DinG	-0.03 (-0.05 to -0.01)	0.037
K16926	energy-coupling factor transport system substrate-specific component	-0.03 (-0.05 to -0.01)	0.037
K02197	cytochrome c-type biogenesis protein CcmE	-0.03 (-0.05 to -0.01)	0.037
K03242	translation initiation factor 2 subunit 3	-0.03 (-0.05 to -0.01)	0.037
K08096	GTP cyclohydrolase IIa	-0.03 (-0.05 to -0.01)	0.037
K18828	tRNA(fMet)-specific endonuclease VapC	-0.03 (-0.05 to -0.01)	0.037
K03306	inorganic phosphate transporter, PiT family	-0.03 (-0.05 to -0.01)	0.038
K15449	tRNA wybutosine-synthesizing protein 1	-0.03 (-0.05 to -0.01)	0.038
K08352	thiosulfate reductase / polysulfide reductase chain A	-0.03 (-0.05 to -0.01)	0.038
K10254	oleate hydratase	-0.03 (-0.05 to -0.01)	0.038
K00313	electron transfer flavoprotein-quinone oxidoreductase	-0.03 (-0.05 to -0.01)	0.039
K00442	coenzyme F420 hydrogenase subunit delta	-0.03 (-0.05 to -0.01)	0.039
K00868	pyridoxine kinase	-0.03 (-0.05 to -0.01)	0.039
K01710	dTDP-glucose 4,6-dehydratase	-0.03 (-0.05 to -0.01)	0.039
K02564	glucosamine-6-phosphate deaminase	-0.03 (-0.05 to -0.01)	0.039
K02669	twitching motility protein PilT	-0.03 (-0.05 to -0.01)	0.039
K03639	GTP 3',8-cyclase	-0.03 (-0.05 to -0.01)	0.039
K04751	nitrogen regulatory protein P-II 1	-0.03 (-0.05 to -0.01)	0.039
K09138	uncharacterized protein	-0.03 (-0.05 to -0.01)	0.039
K12589	exosome complex component RRP42	-0.03 (-0.05 to -0.01)	0.039
K15888	tritrans,polycis-undecaprenyl-diphosphate synthase	-0.03 (-0.05 to -0.01)	0.039
K16785	energy-coupling factor transport system permease protein	-0.03 (-0.05 to -0.01)	0.039
K00548	5-methyltetrahydrofolate--homocysteine methyltransferase	-0.03 (-0.05 to -0.01)	0.039
K00764	amidophosphoribosyltransferase	-0.03 (-0.05 to -0.01)	0.039
K01524	exopolyphosphatase / guanosine-5'-triphosphate,3'-diphosphate pyrophosphatase	-0.03 (-0.05 to -0.01)	0.039
K01571	oxaloacetate decarboxylase (Na+ extruding) subunit alpha	-0.03 (-0.05 to -0.01)	0.039
K02019	molybdate transport system regulatory protein	-0.03 (-0.05 to -0.01)	0.039
K02283	pilus assembly protein CpaF	-0.03 (-0.05 to -0.01)	0.039
K03427	type I restriction enzyme M protein	-0.03 (-0.05 to -0.01)	0.039
K03620	Ni/Fe-hydrogenase 1 B-type cytochrome subunit	-0.03 (-0.05 to -0.01)	0.039
K05837	rod shape determining protein RodA	-0.03 (-0.05 to -0.01)	0.039
K06935	uncharacterized protein	-0.03 (-0.05 to -0.01)	0.039
K06953	uncharacterized protein	-0.03 (-0.05 to -0.01)	0.039
K08681	5'-phosphate synthase pdxT subunit	-0.03 (-0.05 to -0.01)	0.039
K11041	exfoliative toxin A/B	-0.03 (-0.05 to -0.01)	0.039
K11927	ATP-dependent RNA helicase RhlE	-0.03 (-0.05 to -0.01)	0.039
K00762	orotate phosphoribosyltransferase	-0.03 (-0.05 to -0.01)	0.039
K01006	pyruvate, orthophosphate dikinase	-0.03 (-0.05 to -0.01)	0.039
K01499	methenyltetrahydromethanopterin cyclohydrolase	-0.03 (-0.05 to -0.01)	0.039
K01653	acetolactate synthase I/III small subunit	-0.03 (-0.05 to -0.01)	0.039
K01681	aconitate hydratase	-0.03 (-0.05 to -0.01)	0.039

K02823	dihydroorotate dehydrogenase electron transfer subunit	-0.03 (-0.05 to -0.01)	0.039
K03051	DNA-directed RNA polymerase subunit F	-0.03 (-0.05 to -0.01)	0.039
K05715	2-phosphoglycerate kinase	-0.03 (-0.05 to -0.01)	0.039
K07533	foldase protein PrsA	-0.03 (-0.05 to -0.01)	0.039
K15830	formate hydrogenlyase subunit 5	-0.03 (-0.05 to -0.01)	0.039
K15669	D-glycero-alpha-D-manno-heptose 1-phosphate guanylyltransferase	-0.03 (-0.05 to -0.01)	0.040
K00789	S-adenosylmethionine synthetase	-0.03 (-0.05 to -0.01)	0.040
K02217	ferritin	-0.03 (-0.05 to -0.01)	0.040
K00555	tRNA (guanine26-N2/guanine27-N2)-dimethyltransferase	-0.03 (-0.05 to -0.01)	0.040
K02017	molybdate transport system ATP-binding protein	-0.03 (-0.05 to -0.01)	0.040
K06610	MFS transporter, SP family, inositol transporter	-0.03 (-0.05 to -0.01)	0.040
K09153	small membrane protein	-0.03 (-0.05 to -0.01)	0.040
K00003	homoserine dehydrogenase	-0.03 (-0.05 to -0.01)	0.041
K00175	2-oxoglutarate/2-oxoacid ferredoxin oxidoreductase subunit beta	-0.03 (-0.05 to -0.01)	0.041
K00848	rhamnulokinase	-0.03 (-0.05 to -0.01)	0.041
K01737	6-pyruvoyltetrahydropterin/6-carboxytetrahydropterin synthase	-0.03 (-0.05 to -0.01)	0.041
K01915	glutamine synthetase	-0.03 (-0.05 to -0.01)	0.041
K01937	CTP synthase	-0.03 (-0.05 to -0.01)	0.041
K02977	ubiquitin-small subunit ribosomal protein S27Ae	-0.03 (-0.05 to -0.01)	0.041
K03106	signal recognition particle subunit SRP54	-0.03 (-0.05 to -0.01)	0.041
K03150	2-iminoacetate synthase	-0.03 (-0.05 to -0.01)	0.041
K03696	ATP-dependent Clp protease ATP-binding subunit ClpC	-0.03 (-0.05 to -0.01)	0.041
K04773	protease IV	-0.03 (-0.05 to -0.01)	0.041
K07569	RNA-binding protein	-0.03 (-0.05 to -0.01)	0.041
K07704	two-component system, LytTR family, sensor histidine kinase LytS	-0.03 (-0.05 to -0.01)	0.041
K10117	raffinose/stachyose/melibiose transport system substrate-binding protein	-0.03 (-0.05 to -0.01)	0.041
K14652	3,4-dihydroxy 2-butanone 4-phosphate synthase / GTP cyclohydrolase II	-0.03 (-0.05 to -0.01)	0.041
K18350	two-component system, OmpR family, sensor histidine kinase VanS	-0.03 (-0.05 to -0.01)	0.041
K18704	CDP-ribitol ribitolphosphotransferase / teichoic acid ribitol-phosphate polymerase	-0.03 (-0.05 to -0.01)	0.041
K01493	dCMP deaminase	-0.03 (-0.05 to -0.01)	0.041
K03856	3-deoxy-7-phosphoheptulonate synthase	-0.03 (-0.05 to -0.01)	0.041
K07738	transcriptional repressor NrdR	-0.03 (-0.05 to -0.01)	0.041
K09735	uncharacterized protein	-0.03 (-0.05 to -0.01)	0.041
K12240	pyochelin synthetase	-0.03 (-0.05 to -0.01)	0.041
K14656	FAD synthetase	-0.03 (-0.05 to -0.01)	0.041
K20859	phosphoribosyl 1,2-cyclic phosphate 1,2-diphosphodiesterase	-0.03 (-0.05 to -0.01)	0.041
K09767	cyclic-di-GMP-binding protein	-0.03 (-0.05 to -0.01)	0.041
K02567	nitrate reductase (cytochrome)	-0.03 (-0.05 to -0.01)	0.041
K03627	putative transcription factor	-0.03 (-0.05 to -0.01)	0.041

K03646	colicin import membrane protein	-0.03 (-0.05 to -0.01)	0.041
K19137	CRISPR-associated protein Csn2	-0.03 (-0.05 to -0.01)	0.041
K01873	valyl-tRNA synthetase	-0.03 (-0.05 to -0.01)	0.041
K01874	methionyl-tRNA synthetase	-0.03 (-0.05 to -0.01)	0.041
K01939	adenylosuccinate synthase	-0.03 (-0.05 to -0.01)	0.041
K03237	translation initiation factor 2 subunit 1	-0.03 (-0.05 to -0.01)	0.041
K03602	exodeoxyribonuclease VII small subunit	-0.03 (-0.05 to -0.01)	0.041
K07572	putative nucleotide binding protein	-0.03 (-0.05 to -0.01)	0.041
K07334	toxin HigB-1	-0.03 (-0.05 to -0.01)	0.042
K01938	formate--tetrahydrofolate ligase	-0.03 (-0.05 to -0.01)	0.042
K04654	hydrogenase expression/formation protein HypD	-0.03 (-0.05 to -0.01)	0.042
K00031	isocitrate dehydrogenase	-0.03 (-0.05 to -0.01)	0.042
K06937	7,8-dihydro-6-hydroxymethylpterin dimethyltransferase	-0.03 (-0.05 to -0.01)	0.042
K00125	formate dehydrogenase (coenzyme F420) beta subunit	-0.03 (-0.05 to -0.01)	0.042
K00891	shikimate kinase	-0.03 (-0.05 to -0.01)	0.042
K01740	O-acetylhomoserine (thiol)-lyase	-0.03 (-0.05 to -0.01)	0.042
K01868	threonyl-tRNA synthetase	-0.03 (-0.05 to -0.01)	0.042
K02551	2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase	-0.03 (-0.05 to -0.01)	0.042
K03282	large conductance mechanosensitive channel	-0.03 (-0.05 to -0.01)	0.042
K04517	prephenate dehydrogenase	-0.03 (-0.05 to -0.01)	0.042
K07076	uncharacterized protein	-0.03 (-0.05 to -0.01)	0.042
K18918	RHH-type transcriptional regulator, rel operon repressor / antitoxin RelB	-0.03 (-0.05 to -0.01)	0.042
K00991	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	-0.03 (-0.05 to -0.01)	0.042
K01170	tRNA-intron endonuclease, archaea type	-0.03 (-0.05 to -0.01)	0.042
K04652	hydrogenase nickel incorporation protein HypB	-0.03 (-0.05 to -0.01)	0.043
K03057	transcription factor S	-0.03 (-0.05 to -0.01)	0.043
K07134	uncharacterized protein	-0.03 (-0.05 to -0.01)	0.043
K01883	cysteinyl-tRNA synthetase	-0.03 (-0.05 to -0.01)	0.044
K00077	2-dehydropantoate 2-reductase	-0.03 (-0.05 to -0.01)	0.044
K00443	coenzyme F420 hydrogenase subunit gamma	-0.03 (-0.05 to -0.01)	0.044
K01579	aspartate 1-decarboxylase	-0.03 (-0.05 to -0.01)	0.044
K01755	argininosuccinate lyase	-0.03 (-0.05 to -0.01)	0.044
K02323	DNA polymerase II small subunit	-0.03 (-0.05 to -0.01)	0.044
K05934	precorrin-3B C17-methyltransferase	-0.03 (-0.05 to -0.01)	0.044
K09141	uncharacterized protein	-0.03 (-0.05 to -0.01)	0.044
K11717	cysteine desulfurase / selenocysteine lyase	-0.03 (-0.05 to -0.01)	0.044
K09724	uncharacterized protein	-0.03 (-0.05 to -0.01)	0.044
K01104	protein-tyrosine phosphatase	-0.03 (-0.05 to -0.01)	0.044
K03055	DNA-directed RNA polymerase subunit K	-0.03 (-0.05 to -0.01)	0.044
K03687	molecular chaperone GrpE	-0.03 (-0.05 to -0.01)	0.044
K01155	type II restriction enzyme	-0.03 (-0.05 to -0.01)	0.044
K03421	methyl-coenzyme M reductase subunit C	-0.03 (-0.05 to -0.01)	0.044

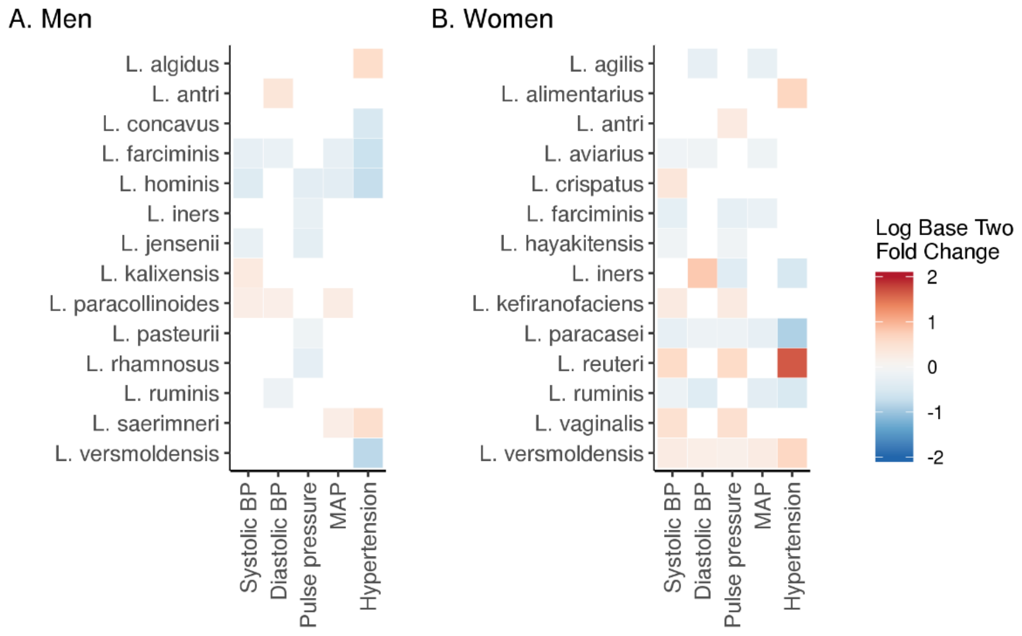
K19545	lincosamide nucleotidyltransferase A/C/D/E	-0.03 (-0.05 to -0.01)	0.044
K00793	riboflavin synthase	-0.03 (-0.05 to -0.01)	0.045
K04766	acetoin utilization protein AcuA	-0.03 (-0.05 to -0.01)	0.045
K08972	putative membrane protein	-0.03 (-0.05 to -0.01)	0.045
K04043	molecular chaperone DnaK	-0.03 (-0.05 to -0.01)	0.045
K11131	H/ACA ribonucleoprotein complex subunit 4	-0.03 (-0.05 to -0.01)	0.045
K01265	methionyl aminopeptidase	-0.03 (-0.05 to -0.01)	0.045
K02492	glutamyl-tRNA reductase	-0.03 (-0.05 to -0.01)	0.045
K02988	small subunit ribosomal protein S5	-0.03 (-0.05 to -0.01)	0.045
K03310	alanine or glycine:cation symporter, AGCS family	-0.03 (-0.05 to -0.01)	0.045
K03534	L-rhamnose mutarotase	-0.03 (-0.05 to -0.01)	0.045
K03686	molecular chaperone DnaJ	-0.03 (-0.05 to -0.01)	0.045
K06147	ATP-binding cassette, subfamily B, bacterial	-0.03 (-0.05 to -0.01)	0.045
K06862	energy-converting hydrogenase B subunit Q	-0.03 (-0.05 to -0.01)	0.045
K08316	16S rRNA (guanine966-N2)-methyltransferase	-0.03 (-0.05 to -0.01)	0.045
K07271	lipopolysaccharide cholinephosphotransferase	-0.03 (-0.05 to -0.01)	0.045
K09726	uncharacterized protein	-0.03 (-0.05 to -0.01)	0.045
K14128	F420-non-reducing hydrogenase small subunit	-0.03 (-0.05 to -0.01)	0.045
K00600	glycine hydroxymethyltransferase	-0.03 (-0.05 to -0.01)	0.046
K09714	uncharacterized protein	-0.03 (-0.05 to -0.01)	0.046
K00590	site-specific DNA-methyltransferase (cytosine-N4-specific)	-0.03 (-0.05 to -0.01)	0.046
K01866	tyrosyl-tRNA synthetase	-0.03 (-0.05 to -0.01)	0.046
K03637	cyclic pyranopterin monophosphate synthase	-0.03 (-0.05 to -0.01)	0.046
K05896	segregation and condensation protein A	-0.03 (-0.05 to -0.01)	0.046
K07310	Tat-targeted selenate reductase subunit YnfF	-0.03 (-0.05 to -0.01)	0.046
K14113	energy-converting hydrogenase B subunit D	-0.03 (-0.05 to -0.01)	0.046
K14125	energy-converting hydrogenase B subunit P	-0.03 (-0.05 to -0.01)	0.046
K19147	5-methylcytosine-specific restriction enzyme subunit McrC	-0.03 (-0.05 to -0.01)	0.046
K01179	endoglucanase	-0.03 (-0.05 to -0.01)	0.046
K01872	alanyl-tRNA synthetase	-0.03 (-0.05 to -0.01)	0.046
K03976	Cys-tRNA(Pro)/Cys-tRNA(Cys) deacylase	-0.03 (-0.05 to -0.01)	0.046
K06200	carbon starvation protein	-0.03 (-0.05 to -0.01)	0.046
K07030	uncharacterized protein	-0.03 (-0.05 to -0.01)	0.046
K14111	energy-converting hydrogenase B subunit B	-0.03 (-0.05 to -0.01)	0.046
K14116	energy-converting hydrogenase B subunit G	-0.03 (-0.05 to -0.01)	0.046
K14119	energy-converting hydrogenase B subunit J	-0.03 (-0.05 to -0.01)	0.046
K14120	energy-converting hydrogenase B subunit K	-0.03 (-0.05 to -0.01)	0.046
K14122	energy-converting hydrogenase B subunit M	-0.03 (-0.05 to -0.01)	0.046
K14123	energy-converting hydrogenase B subunit N	-0.03 (-0.05 to -0.01)	0.046
K00440	coenzyme F420 hydrogenase subunit alpha	-0.03 (-0.05 to -0.01)	0.046
K02035	peptide/nickel transport system substrate-binding protein	-0.03 (-0.05 to -0.01)	0.046
K02189	cobalt-precorrin 5A hydrolase	-0.03 (-0.05 to -0.01)	0.046
K02866	large subunit ribosomal protein L10e	-0.03 (-0.05 to -0.01)	0.046

K07111	uncharacterized protein	-0.03 (-0.05 to -0.01)	0.046
K20021	L-cysteine desulfidase	-0.03 (-0.05 to -0.01)	0.046
K00244	fumarate reductase flavoprotein subunit	-0.03 (-0.05 to -0.01)	0.046
K03042	DNA-directed RNA polymerase subunit A"	-0.03 (-0.05 to -0.01)	0.047
K06920	7-cyano-7-deazaguanine synthase	-0.03 (-0.05 to -0.01)	0.047
K12297	23S rRNA (guanine2445-N2)-methyltransferase / 23S rRNA (guanine2069-N7)-methyltransferase	-0.03 (-0.05 to -0.01)	0.047
K00219	2,4-dienoyl-CoA reductase (NADPH2)	-0.03 (-0.05 to -0.01)	0.047
K00239	succinate dehydrogenase / fumarate reductase, flavoprotein subunit	-0.03 (-0.05 to -0.01)	0.047
K01425	glutaminase	-0.03 (-0.05 to -0.01)	0.047
K01738	cysteine synthase	-0.03 (-0.05 to -0.01)	0.047
K02906	large subunit ribosomal protein L3	-0.03 (-0.05 to -0.01)	0.047
K04651	hydrogenase nickel incorporation protein HypA/HybF	-0.03 (-0.05 to -0.01)	0.047
K07068	uncharacterized protein	-0.03 (-0.05 to -0.01)	0.047
K09721	uncharacterized protein	-0.03 (-0.05 to -0.01)	0.047
K09732	uncharacterized protein	-0.03 (-0.05 to -0.01)	0.047
K09742	uncharacterized protein	-0.03 (-0.05 to -0.01)	0.047
K10553	fructose transport system permease protein	-0.03 (-0.05 to -0.01)	0.047
K14110	energy-converting hydrogenase B subunit A	-0.03 (-0.05 to -0.01)	0.047
K14112	energy-converting hydrogenase B subunit C	-0.03 (-0.05 to -0.01)	0.047
K14114	energy-converting hydrogenase B subunit E	-0.03 (-0.05 to -0.01)	0.047
K14115	energy-converting hydrogenase B subunit F	-0.03 (-0.05 to -0.01)	0.047
K14121	energy-converting hydrogenase B subunit L	-0.03 (-0.05 to -0.01)	0.047
K14124	energy-converting hydrogenase B subunit O	-0.03 (-0.05 to -0.01)	0.047
K15773	HTH-type transcriptional regulator / antitoxin HipB	-0.03 (-0.05 to -0.01)	0.047
K00558	DNA (cytosine-5)-methyltransferase 1	-0.03 (-0.05 to -0.01)	0.047
K02548	1,4-dihydroxy-2-naphthoate polyprenyltransferase	-0.03 (-0.05 to -0.01)	0.047
K02570	periplasmic nitrate reductase NapD	-0.03 (-0.05 to -0.01)	0.047
K02881	large subunit ribosomal protein L18	-0.03 (-0.05 to -0.01)	0.048
K02907	large subunit ribosomal protein L30	-0.03 (-0.05 to -0.01)	0.048
K03969	phage shock protein A	-0.03 (-0.05 to -0.01)	0.048
K08357	tetrathionate reductase subunit A	-0.03 (-0.05 to -0.01)	0.048
K01520	dUTP pyrophosphatase	-0.03 (-0.05 to -0.01)	0.048
K01547	potassium-transporting ATPase ATP-binding subunit	-0.03 (-0.05 to -0.01)	0.048
K00609	aspartate carbamoyltransferase catalytic subunit	-0.03 (-0.05 to -0.01)	0.048
K01588	5-(carboxyamino)imidazole ribonucleotide mutase	-0.03 (-0.05 to -0.01)	0.048
K03168	DNA topoisomerase I	-0.03 (-0.05 to -0.01)	0.048
K11175	phosphoribosylglycinamide formyltransferase 1	-0.03 (-0.05 to -0.01)	0.048
K03330	glutamyl-tRNA(Gln) amidotransferase subunit E	-0.03 (-0.05 to -0.01)	0.048
K03529	chromosome segregation protein	-0.03 (-0.05 to -0.01)	0.048
K03750	molybdopterin molybdotransferase	-0.03 (-0.05 to -0.01)	0.048
K07812	trimethylamine-N-oxide reductase (cytochrome c)	-0.03 (-0.05 to -0.01)	0.048
K18209	fumarate reductase (CoM/CoB) subunit A	-0.03 (-0.05 to -0.01)	0.048

K07458	DNA mismatch endonuclease, patch repair protein	-0.03 (-0.05 to -0.01)	0.048
K00567	methylated-DNA-[protein]-cysteine S-methyltransferase	-0.03 (-0.05 to -0.01)	0.049
K01011	thiosulfate/3-mercaptopyruvate sulfurtransferase	-0.03 (-0.05 to -0.01)	0.049
K14392	sodium/pantothenate symporter	-0.03 (-0.05 to -0.01)	0.049
K01153	type I restriction enzyme, R subunit	-0.03 (-0.05 to -0.01)	0.049
K01756	adenylosuccinate lyase	-0.03 (-0.05 to -0.01)	0.049
K02982	small subunit ribosomal protein S3	-0.03 (-0.05 to -0.01)	0.049
K03166	DNA topoisomerase VI subunit A	-0.03 (-0.05 to -0.01)	0.049
K07096	uncharacterized protein	-0.03 (-0.05 to -0.01)	0.049
K08298	L-carnitine CoA-transferase	-0.03 (-0.05 to -0.01)	0.049
K09482	glutamyl-tRNA(Gln) amidotransferase subunit D	-0.03 (-0.05 to -0.01)	0.049
K10896	fanconi anemia group M protein	-0.03 (-0.05 to -0.01)	0.049
K11212	LPPG:FO 2-phospho-L-lactate transferase	-0.03 (-0.05 to -0.01)	0.049
K14982	two-component system, OmpR family, sensor histidine kinase CiaH	-0.03 (-0.05 to -0.01)	0.049
K15731	carboxy-terminal domain RNA polymerase II polypeptide A small phosphatase	-0.03 (-0.05 to -0.01)	0.049
K18830	HTH-type transcriptional regulator / antitoxin PezA	-0.03 (-0.05 to -0.01)	0.049
K00763	nicotinate phosphoribosyltransferase	-0.03 (-0.05 to -0.01)	0.049
K12141	hydrogenase-4 component F	-0.03 (-0.05 to -0.01)	0.049
K01546	potassium-transporting ATPase potassium-binding subunit	-0.03 (-0.05 to -0.01)	0.049
K02933	large subunit ribosomal protein L6	-0.03 (-0.05 to -0.01)	0.049
K07442	tRNA (adenine57-N1/adenine58-N1)-methyltransferase catalytic subunit	-0.03 (-0.05 to -0.01)	0.049
K02904	large subunit ribosomal protein L29	-0.03 (-0.05 to -0.01)	0.049
K06913	uncharacterized protein	-0.03 (-0.05 to -0.01)	0.049
K01975	RNA 2',3'-cyclic 3'-phosphodiesterase	-0.03 (-0.05 to -0.01)	0.049
K02994	small subunit ribosomal protein S8	-0.03 (-0.05 to -0.01)	0.049
K06019	pyrophosphatase PpaX	-0.03 (-0.05 to -0.01)	0.050
K07114	Ca-activated chloride channel homolog	-0.03 (-0.05 to -0.01)	0.050

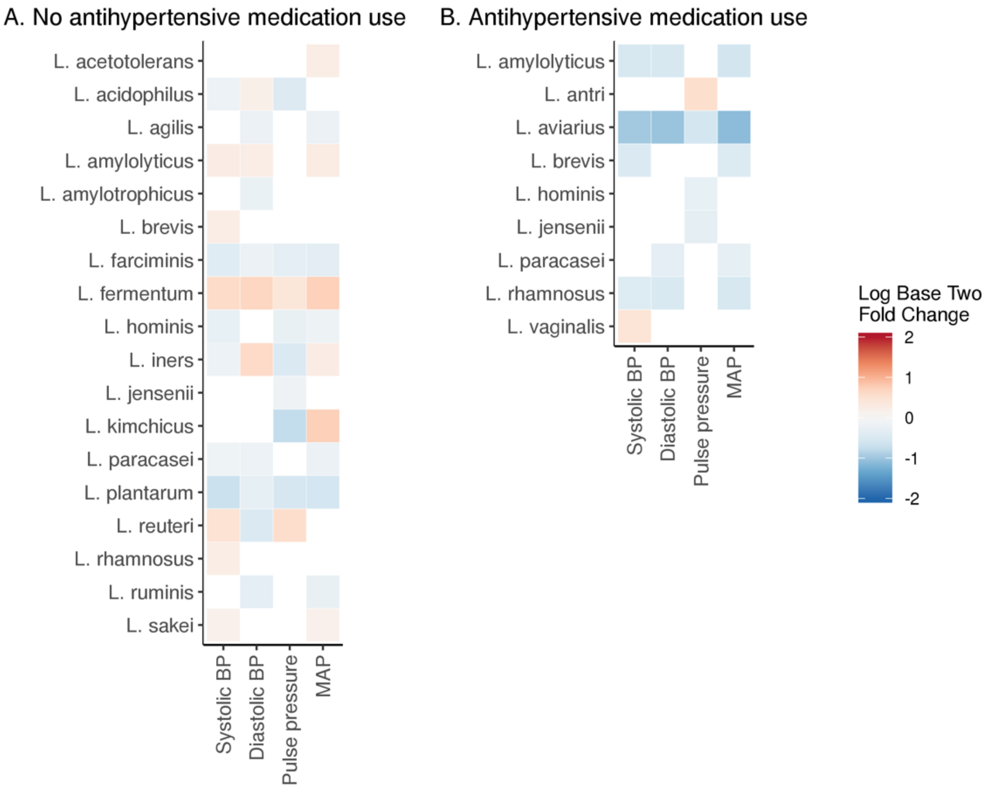
P values are adjusted for multiple testing using FDR correction.

Figure S1. Associations between *Lactobacilli* and blood pressure by sex.



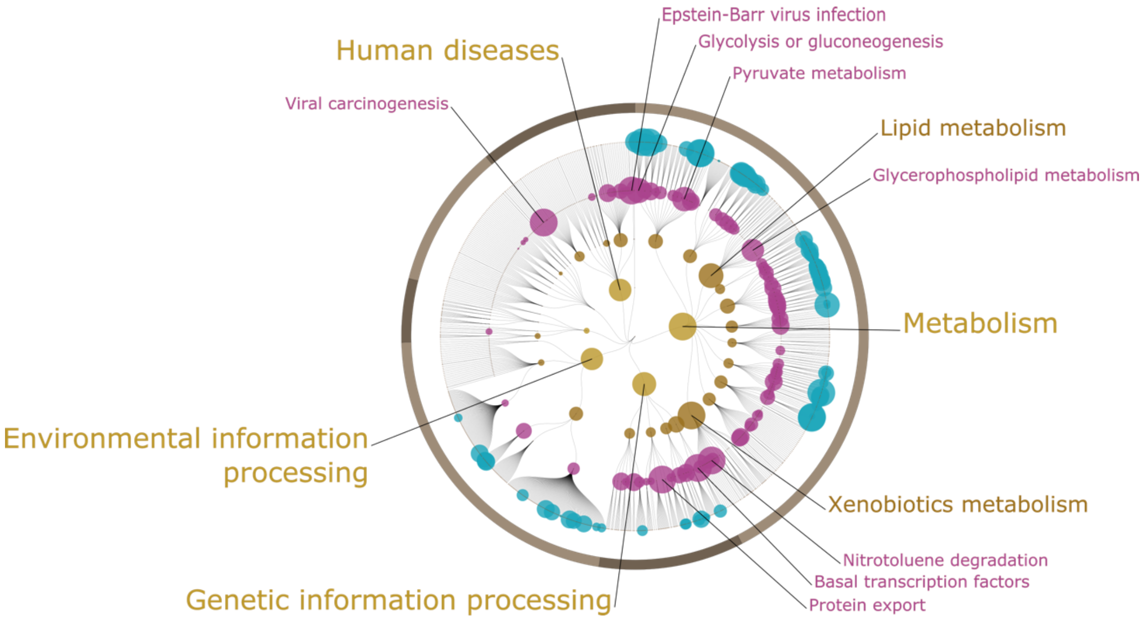
The models are adjusted for age, BMI, smoking, exercise, diuretics, beta blockers, calcium channel blockers, and renin–angiotensin system blockers. N=3 819 for women and N=3 134 for men. BP, Blood pressure; MAP, Mean arterial pressure.

Figure S2. Associations between *Lactobacilli* and blood pressure by antihypertensive medication use.



The models are adjusted for age, sex, BMI, smoking, exercise, diuretics, beta blockers, calcium channel blockers, and renin–angiotensin system blockers. Association with bacterial plasmid is denoted using asterisk. N=1 253 for antihypertensive medication users and N=5 700 for non-users. BP, Blood pressure; MAP, Mean arterial pressure.

Figure S3. Functional pathways associated with systolic BP.



For the module (cyan), pathway (purple), biological process (dark brown), and biological category (light brown) functional layers, node size corresponds to the average inverse P value of the KO group assigned to that node. Only KO groups that were negatively associated with systolic BP were included. Node titles are shown for nodes in the three highest layers with a size > 200.