

**Table S4.** Predicted KOs associated with multidrug or antibiotic resistance that were significantly different from the placebo in faecal samples after the use of antibiotics. Proportions of KOs in black significantly increased, while KOs in red – decreased after the exposure to the respective antibiotic.

Antibiotic	KO ID	Description	P value*
Clindamycin	K00012	<i>ugd</i> , M00671 Polycationic antibiotics resistance, <i>arn</i> lipopolysaccharide (LPS) modification operon	0.046
	K07552	<i>bcr</i> , MFS transporter, DHA1 family, bicyclomycin/chloramphenicol resistance protein	0.023
	K08641	<i>vanX</i> , M00651 Vancomycin resistance, VanB type	0.037
Ciprofloxacin	K03543	<i>emrA</i> , multidrug resistance protein A	0.027
	K00897	E2.7.1.95 kanamycin kinase, M00640 Aminoglycoside antibiotics resistance	0.03
	K03446	<i>emrB</i> , MFS transporter, DHA2 family, multidrug resistance protein B	0.009
	K05515	<i>mrdA</i> , penicillin-binding protein 2, ko00312 beta-Lactam resistance, M00626 beta-Lactam resistance, penicillin-binding protein variants	0.016
	K13888	<i>macA</i> , macrolide-specific efflux protein MacA	0.021
Minocycline	K03543	<i>emrA</i> , multidrug resistance protein A	0.047
	K08223	<i>fsr</i> , MFS transporter, FSR family, fosmidomycin resistance protein	0.043
	K12340	<i>tolC</i> , outer membrane channel protein, ko00312 beta-Lactam resistance, M00646 Multidrug resistance, efflux pump AcrAD-TolC, M00647 Multidrug resistance, efflux pump MexAB-OprM/SmeDEF/AcrAB-TolC	0.047
	K07576	metallo-beta-lactamase family protein	0.041
Amoxicillin	K00012	<i>ugd</i> , M00671 Polycationic antibiotics resistance, <i>arn</i> lipopolysaccharide (LPS) modification operon	0.01
	K03296	multidrug (acriflavin, doxorubicin, ethidium,	0.001

		rhodamine 6G, SDS, deoxycholate) efflux pump	
	K03327	<i>TC.MATE, SLC47A, norM, mdtK, dinF, multidrug resistance protein, MATE family</i>	0.039
	K03543	<i>emrA, multidrug resistance protein A</i>	0.025
	K03585	<i>acrA, mexA, adeI, smeD, membrane fusion protein, ko00312 beta-Lactam resistance, M00646 Multidrug resistance, efflux pump AcrAD-TolC, M00647 Multidrug resistance, efflux pump MexAB-OprM/SmeDEF/AcrAB-TolC</i>	0.015
	K05595	<i>marC, multiple antibiotic resistance protein</i>	0.012
	K08169	<i>yebQ, MFS transporter, DHA2 family, multidrug resistance protein</i>	0.036
	K08223	<i>fsr, MFS transporter, FSR family, fosmidomycin resistance protein</i>	0.013
	K12340	<i>tolC, outer membrane channel protein, ko00312 beta-Lactam resistance, M00646 Multidrug resistance, efflux pump AcrAD-TolC, M00647 Multidrug resistance, efflux pump MexAB-OprM/SmeDEF/AcrAB-TolC</i>	0.012
	K02547	<i>mecR1, methicillin resistance protein, ko00312 beta-Lactam resistance, M00625 Methicillin resistance</i>	0.002
	K03712	<i>marR, MarR family transcriptional regulator, multiple antibiotic resistance protein MarR</i>	0.002
	K07260	<i>vanY, D-alanyl-D-alanine carboxypeptidase [EC:3.4.16.4], ko00550 Peptidoglycan biosynthesis, M00651 Vancomycin resistance, VanB type, ko02020 Two-component system, M00652 Vancomycin resistance, VanE type</i>	0.038
	K10012	<i>arnC, pmrF, undecaprenyl-phosphate 4-deoxy-4-formamido-L-arabinose transferase [EC:2.4.2.53], ko00520 Amino sugar and nucleotide sugar metabolism, M00671 Polycationic antibiotics resistance, arn lipopolysaccharide (LPS) modification operon</i>	0.006

\* - P value after Storey FDR correction for multiple comparisons