

Viral metagenomics reveals diverse viruses and antibiotic resistance genes in fecal samples of swine from farms in Shandong province

Running title: Viral metagenomics reveals diverse viruses

Section: Original Research

Supplementary material

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Table S1. Statistical Table of Fresh Pig Manure Sampling Information in Shandong Province

Sampling time	Location	Farm size	Old(Days)	Temperature	Sample number
2019.10.22	Yantai	90 reproductive sows	140	18°C	YT1-1, YT1-2, YT1-3
		4000	70	19°C	YT2-1, YT2-2, YT2-3
		10000	180	18°C	YT3-1, YT3-2, YT3-3
		500 reproductive sows	140	18°C	YT4-1, YT4-2, YT4-3
		500 reproductive sows	140	19°C	YT5-1, YT5-2, YT5-3
2019.5.17	Linyi	300	138	27°C	LY1-1, LY1-2, LY1-3
		600	150	27°C	LY2-1, LY2-2, LY2-3
		2500	100-110	27°C	LY3-1, LY3-2, LY3-3
2019.11.8	Binzhou	NA	NA	12°C	BZ1-1, BZ1-2, BZ1-3
		NA	NA	13°C	BZ2-1, BZ2-2, BZ2-3
		NA	NA	14°C	BZ3-1, BZ3-2, BZ3-3
2020.1.13	Jinan	40 reproductive sows	100	10°C	J1-1, J1-2, J1-3
		40 reproductive sows	80	20°C	J2-1, J2-2, J2-3
		300	110	10°C	J3-1, J3-2, J3-3
2020.6.13	Tai'an	3000	150	23°C	TA1-1, TA1-2, TA1-3
		4000 reproductive sows	200	25°C	TA2-1, TA2-2, TA2-3
		12000	180	26°C	TA3-1, TA3-2, TA3-3
2020.6.13	Jining	800	120	23°C	JN1-1, JN1-2, JN1-3
		1000	140-150	23°C	JN2-1, JN2-2, JN2-3
		600	130	23°C	JN3-1, JN3-2, JN3-3
2020.6.27	Weihai	7000	85	21°C	WH1-1, WH1-2, WH1-3
		2000	500	28°C	WH2-1, WH2-2, WH2-3
		840	68	26°C	WH3-1, WH3-2, WH3-3

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Sampling time	Location	Farm size	Old(Days)	Temperature	Sample number
			215		
		55	160	25°C	LC1-1, LC1-2, LC1-3
2020.7.5	Liaocheng		145		
		67	150	26°C	LC2-1, LC2-2, LC2-3
		60 reproductive sows	150	26°C	LC3-1, LC3-2, LC3-3
		3000 reproductive sows	240	30°C	QD1-1, QD1-2, QD1-3
2020.7.13	Qingdao	5000 reproductive sows	240	30°C	QD2-1, QD2-2, QD2-3
		1500	200	30°C	QD3-1, QD3-2, QD3-3
		3000	140	28°C	DY1-1, DY1-2, DY1-3
2020.7.16	Dongying	2000	150	32°C	DY2-1, DY2-2, DY2-3
		15000	90	33°C	DY3-1, DY3-2, DY3-3
		40-50	150	29°C	ZZ1-1, ZZ1-2, ZZ1-3
2020.7.20	Zaozhuang	50-60	90	29°C	ZZ2-1, ZZ2-2, ZZ2-3
		100	120	29°C	ZZ3-1, ZZ3-2, ZZ3-3
		1000	210	19°C	DZ1-1, DZ1-2, DZ1-3
2020.7.23	Dezhou	500	120	19°C	DZ2-1, DZ2-2, DZ2-3
		1500	150	19°C	DZ3-1, DZ3-2, DZ3-3
		4000	198	27°C	HZ1-1, HZ1-2, HZ1-3
2020.7.24	Heze	200	180	27°C	HZ2-1, HZ2-2, HZ2-3
		25000	140	27°C	HZ3-1, HZ3-2, HZ3-3
		3500	120	32°C	WF1-1, WF1-2, WF1-3
		600	150-180	32°C	WF2-1, WF2-2, WF2-3
2020.7.25	Weifang	3000	130	32°C	WF3-1, WF3-2, WF3-3
		3000	180	32°C	WF4-1, WF4-2, WF4-3
		500	250	23°C	ZB1-1, ZB1-2, ZB1-3
2020.7.26	Zibo	800	240	22°C	ZB2-1, ZB2-2, ZB2-3

Table S1. Statistical Table of Fresh Pig Manure Sampling Information in Shandong Province

Sampling time	Location	Farm size	Old(Days)	Temperature	Sample number
2020.7.27	Rizhao	700	100	23℃	ZB3-1, ZB3-2, ZB3-3
		600	90	28℃	RZ1-1, RZ1-2, RZ1-3
		490	120	28℃	RZ2-1, RZ2-2, RZ2-3
		500	70	28℃	RZ3-1, RZ3-2, RZ3-3

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
HZ_3_1.2 0610_6	k__Bacteria; p__Actinobacteria; c__Actinomycetia; o__Corynebacteriales; f__Corynebacteriaceae; g__Corynebacterium	tetracycline	tetracycline_resistance_protein	0.010828	0.447309	0.662083	0.531466	0.012865	0.059307	0.093312	0.06948	0.21216	0.111617	0.480419	0.17861	0.252634	0.009856	0.045275	0.328084
ZZ_1_1.45 7364_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae; g__Escherichia	multidrug	emrD	0	0	0	0	0	0	0.102224	0	0	0	0	0	0	0	0.064919	0.228174
QD_2_1.1 90721_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	adeJ	0	0	0.010478	0.016989	0	0	0.00779	0.00899	0.134932	0	0	0	0.009092	0	0	0
TA_1_1.1 31259_1	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae; g__Staphylococcus	multidrug	norA	0	0	0.025776	0	0	0	0	0	0	0.027227	0.276141	0	0	0	0	0
WF_3_1.3 112_1	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus; s__Enterococcus aquimarinus	multidrug	EmrB-QacA_family_major_facilitator_transporter	0	0	0.304787	0.516374	0	0	0	0.229424	0	0	0	0.238286	0	0	0	0
DZ_1_1.1 8912_2	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales	aminoglycoside	ant9-I	48.79631	26.72057	27.67252	21.95848	33.79735	29.55551	32.31361	43.26759	23.05823	24.26255	22.0225	35.26166	23.12261	56.67754	21.85388	31.43164
ZZ_3_1.11 2994_3	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria	aminoglycoside	aac6-II	0.022901	1.394344	0.442583	0.652196	0.086444	0.028827	0.109697	0.157889	0.073079	0.406017	0.103189	0.11217	0.32335	0.013439	0.018887	0.480675
LY_1_1.86 886_1	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales; f__Oscillospiraceae; g__Flavonifractor; s__uncultured Flavonifractor sp.*	tetracycline	tet40	58.25709	67.75259	57.02928	60.36372	76.8832	71.8527	66.51308	48.10799	60.94305	35.49544	34.36285	60.08951	46.3493	47.71757	75.80431	77.37516

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
DZ_3_1.9 0371_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	adeJ	0	0	0.175272	0	0	0	0	0	0	0	0	0	0	0	0	0
ZZ_3_1.43 9226_1	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales; f__Clostridiaceae; g__Clostridium; s__uncultured Clostridium sp.	bacitracin	bacA	0	0	0	0	0	0.409392	0	0	0	0	0	0	0	0	0	0
ZZ_3_1.12 5637_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Pseudomonadales; f__Pseudomonadaceae; g__Oblitimonas; s__Oblitimonas alkaliphila*	multidrug	mexB	0	0	0.060212	0.013248	0	0	0.012125	0.027352	0.014086	0.05564	0	0	0	0	0	0.163599
WF_1_1.9 3743_1	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales	tetracycline	tetQ	11.58081	4.469549	5.127002	5.557448	7.975444	5.158333	4.687897	10.48368	6.25029	5.481232	3.310239	4.888999	3.2313	12.70084	3.727686	11.0881
WH_2_1.5 8031_7	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Enterobacterales	unclassified	bacterial_ regulatory _protein_ LuxR	0.439838	0.548684	0.428657	6.045778	0.211436	0.2264	4.091351	0.238933	0.173106	3.135325	6.578906	0.2217	4.285047	2.601769	0.061625	1.271336
WH_2_1.5 8031_8	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Enterobacterales; f__Enterobacteriaceae	multidrug	emrK	0.394381	0.406518	0.220137	4.101375	0.105993	0.215449	3.307827	0.207146	0.225286	2.325989	4.60878	0.186808	3.074974	1.716017	0.031378	0.886418
LY_3_1.52 5562_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	adeJ	0	0	0	0	0	0	0	0.117671	0	0	0	0	0.04916	0	0	0
WF_3_1.3 25272_2	k__Bacteria; p__Firmicutes; c__Bacilli	aminoglycosi de	aph2-le	0.006582	0.030039	0.694059	0.12372	0.007329	0.017025	0.041764	0	0.026199	0.187165	0.059925	0.154219	0.007692	0	0.073441	0.009327
WH_2_1.1 7294_5	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Enterobacterales; f__Enterobacteriaceae	multidrug	ToIC	0.227008	0.350468	0.264043	3.782488	0.11529	0.214775	3.087385	0.142643	0.114686	1.772573	3.788082	0.22963	2.693745	1.371076	0.063993	0.720313

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
HZ_1_1.1 71883_3	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ;o__Enterobacterales; f__Enterobacteriaceae	unclassified	sdiA	0.275409	0.405641	0.245279	3.112311	0.107721	0.258928	2.76497	0.162805	0.069684	1.985387	3.38752	0.150544	2.615677	1.234999	0.030972	1.019914
DY_3_1.2 59888_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ;o__Enterobacterales; f__Enterobacteriaceae	unclassified	DNA- binding_p rotein_H- NS	0.599942	0.981695	0.436967	6.199987	0.111663	0.331997	5.377526	0.126137	0.241701	3.571499	9.731864	0.4354	4.829257	2.551011	0	1.335621
RZ_2_1.44 1359_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ;o__Aeromonadales; f__Aeromonadaceae; g__Aeromonas; s__Aeromonas hydrophila	beta-lactam	AER-1	0	0	0	0	0	0	0	0	0.008345	0.271246	0	0	0	0	0	0
ZZ_3_1.39 7568_2	k__Bacteria; p__Firmicutes	vancomycin	vanR	0.136814	0.225737	0.076255	0.075067	0	0.185598	0	0.131072	0	0.15384	0	0.075605	0	0	0	0.161086
WH_2_1.5 6747_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ;o__Enterobacterales; f__Enterobacteriaceae	multidrug	acrA	0.010461	0.027173	0.015365	0.117259	0	0	0.076922	0	0.006729	0.027108	0.02692	0	0.166447	0.114555	0	0.020172
TA_2_1.4 90820_1	k__Bacteria; p__Firmicutes; c__Bacilli n	macrolide- lincosamide- streptogrami n	lsa	0	0	0.185947	0	0	0	0.049874	0	0.113957	0.05821	0.125101	0.05416	0.119704	0	0	0
TA_3_1.1 81660_11	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ;o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia; s__Escherichia fergusonii	multidrug	mdtH	0.008823	0.040225	0	0.028064	0.009343	0	0.004994	0	0.005815	0	0.203925	0.016547	0	0	0	0.018873
QD_2_1.9 4232_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ;o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia	kasugamycin	kasugamy cin_resista nce_prot ein_ksgA	0.101041	0.099557	0.05363	1.081692	0.055224	0.031717	0.718412	0.136909	0.082003	0.606707	1.381477	0.166214	0.759518	0.391222	0.020766	0.199941

[illegible]

[illegible]

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
WH_2_1.1 83948_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria	trimethoprim	dfrA19	0	0	0.040475	0	0	0	0	0	0	0	0	0	0.317056	0	0	0
DZ_3_1.1 24870_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	adeJ	0	0	0.253129	0	0	0	0	0	0	0	0	0	0	0	0	0
YT_2_1.25 291_3	k__Bacteria; p__Bacteroidetes; c__Bacteroidia	macrolide- lincosamide- streptogramin	ermF	2.285135	4.178245	2.046106	2.732105	5.553532	1.677918	1.959247	9.522315	0.826847	4.595441	3.239351	4.023058	1.839813	4.213909	3.126227	7.668481
LC_3_1.64 94_2	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales	aminoglycoside	ant9-I	7.563495	4.983177	3.702654	2.794938	6.227345	5.866828	6.163227	6.322072	4.300466	4.386613	3.771422	4.381582	4.03869	11.37977	3.76581	7.814974
BZ_2_1.13 8551_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Enterobacterales; f__Enterobacteriaceae	multidrug	mdtA	0.241647	0.317933	0.154948	2.891713	0.076165	0.155013	2.231609	0.137786	0.107054	1.431505	3.100331	0.109613	1.975586	1.064274	0.036092	0.664864
TA_3_1.9 8109_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia	multidrug	mdtG	0.030152	0	0.014469	0.247632	0	0	0.045285	0	0	0.051941	0.277455	0.013288	0	0.072543	0	0.025645
LC_2_1.19 5956_1	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales	tetracycline	tetQ	2.504449	0.568192	0.779063	0.517771	1.16225	1.490172	1.01894	2.197287	1.582671	0.952627	0.81783	0.863336	0.41888	1.879854	0.660381	1.85644
QD_1_1.7 2288_3	k__Bacteria; p__Firmicutes	vancomycin	vanR	0	0	0	0	0	0	0	0	0.57381	0	0	0	0	0	0	0
ZZ_3_1.18 6933_2	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales	tetracycline	tetQ	0	0	0	0	0	0	0	0	0	0	0	0.137393	0	0	0	0.726666
HZ_3_1.3 40437_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria	trimethoprim	dfrA14	0.064551	0.237505	0.088897	2.024054	0.071404	0.138208	2.004059	0.097229	0.12726	0.081268	0.230106	0	0.353583	0.211948	0.032844	0.189016
WH_1_1.3 11742_4	k__Bacteria; p__Firmicutes	vancomycin	vanG	0.084807	0.006824	0.006611	0	0.202759	0	0	0.017683	0.027634	0	0	0	0.207985	0.025968	0.007023	0.084005

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
HZ_3_1.5 613_4	k__Bacteria; p__Firmicutes; c__Bacilli	macrolide- lincosamide- streptogrami n	ermA	0.062181	0.387032	1.155384	1.187984	0.093728	0.069539	0.106921	0.256931	0.535899	0.992143	0.679726	0.959776	0.806476	0.068589	0.701293	0.072689
LY_1_1.64 745_2	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales; f__Clostridiaceae; g__Butyrivibrio; s__Butyrivibrio sp. AM42-5AC	vancomycin	vanU	0.684829	0.50314	0	0	0.892212	0	0.175817	0.50559	0.205368	0	0.205416	0	0.966335	0	0	0
BZ_1_1.20 5165_19	k__Bacteria; p__Firmicutes	vancomycin	vanG	0.588986	0.064931	0.012509	0.033196	0.354372	0.033249	0.051408	0.056852	0.043402	0	0.079224	0.024632	0.442168	0.063593	0	0.03648
BZ_1_1.20 5165_17	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Streptococcus; s__Streptococcus agalactiae	vancomycin	vanW	0.54144	0.02283	0.011534	0	0.243635	0	0.080292	0.01952	0.047267	0	0	0.021254	0.223402	0.035366	0.009878	0.021532
HZ_3_1.2 75921_2	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Weeksellaceae; g__Elizabethkingia; s__Elizabethkingia anophelis	chlorampheni col	catB	0	0	0	0.29183	0	0	0	0.135701	0	0	0	0	0	0	0	0
DZ_2_1.1 58066_1	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales; f__Thermohalobacteracea e; g__Clostridiisalibacter; s__Clostridiisalibacter paucivorans*	macrolide- lincosamide- streptogrami n	mefA	0.009606	0	0.331179	0.143714	0.005095	0	0.02345	0.042981	0.093882	0.034369	0.055748	0.022325	0.016563	0.005635	0.045719	0

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
BZ_1_1.46 0775_4	k__Bacteria; p__Proteobacteria; c__Epsilonproteobacteria; o__Campylobacteriales; f__Campylobacteraceae; g__Campylobacter; s__Campylobacter jejuni	aminoglycoside	bifunctional_aminoglycoside_N-acetyltransferase_and_aminoglycoside_phosphotransferase	0.106583	0.876833	0.764561	0.735493	0	0.289988	0.220095	1.066949	0.220796	0	0.078959	0.029365	0.052162	0.560756	0.031448	0.234454
QD_2_1.4 82039_1	k__Bacteria; p__Firmicutes	tetracycline	tetW	3.730885	4.081366	3.637034	3.49999	4.651236	1.796978	1.682101	1.865704	2.775249	0.880346	1.869477	0.87497	1.462043	2.820425	2.166298	4.526184
WH_2_1.4 46329_3	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pasteurellales; f__Pasteurellaceae; g__Pasteurella; s__Pasteurella multocida	aminoglycoside	aadA	0	0	0	0.174583	0	0	0.036305	0.090425	0	0	0	0.01766	0.134274	0.016954	0	0
ZB_3_1.28 5632_1	k__Bacteria; p__Firmicutes	macrolide-lincosamide-streptogramin	vatB	0.037254	0.090709	0	0.227561	0.219834	0.048285	0	0	0	0	0	0.04596	0.186811	0.045896	0.154722	0.046186
TA_3_1.2 79274_2	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Oceanobacillus; s__Oceanobacillus rezensis	quinolone	norB	0	0	0	0	0	0	0	0	0	0	0.447497	0	0	0	0	0
QD_2_1.7 9131_1	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus	vancomycin	vanS	0.363195	2.354117	16.89968	5.043879	0.190002	0	0.491537	0.205429	6.394074	2.247432	2.514899	8.203478	1.503151	0	0.33422	0
WH_2_1.5 5199_1	k__Bacteria; p__NA; c__NA; o__NA; f__NA; g__NA; s__uncultured bacterium T3 7 42578	tetracycline	tetL	2.274427	13.40659	23.04917	11.76748	11.27948	9.276091	18.11823	2.968619	5.620874	3.35442	11.09068	19.26592	1.497891	2.976159	13.63701	2.040454

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
TA_3_1.2 12391_6	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia; s__Escherichia fergusonii	unclassified	sdiA	0	0.011294	0.058381	0	0.009513	0	0.019863	0	0	0	0.31573	0.021902	0	0.010421	0.013833	0.023648
WH_2_1.4 84385_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Enterobacterales; f__Enterobacteriaceae	multidrug	mdtM	0.038669	0.047459	0.006651	0.413626	0.004933	0.006015	0.275155	0.020612	0.017598	0.251223	0.282815	0.016932	0.403949	0.106908	0	0.057253
TA_2_1.3 38264_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Alteromonadales; f__Pseudoalteromonadaceae; g__Pseudoalteromonas; s__Pseudoalteromonas sp. 58	tetracycline	tet31	0.012895	0.134488	0.061007	0.0648	0.004415	0	0.023827	0.077802	0.005704	0.061699	0.163776	0.037873	0.005857	0	0.027489	0.035789
RZ_3_1.28 994_2	k__Bacteria; p__Firmicutes; c__Tissierellia; o__Tissierellales; f__Peptoniphilaceae; g__Anaerococcus	bacitracin	bacA	0	0	0	0	0	0	0.008803	0	0	0.426153	0	0	0	0	0.036603	0
JN_3_1.31 7635_1	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae	aminoglycoside	aadD	0.137487	12.20002	5.444046	5.710762	0.782837	0.30179	2.62256	1.278419	7.759663	14.52766	2.924076	3.505299	2.878032	0.502663	13.08687	0.535379
TA_2_1.2 4828_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	adeJ	0.03295	0.016105	0.008506	0.092024	0.019622	0.01456	0	0.002512	0.010052	0.007536	0.236554	0	0.205333	0	0	0
JN_1_1.57 102_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Enterobacterales; f__Morganellaceae; g__Proteus; s__Proteus mirabilis	chloramphenicol	floR	0.813638	0.783505	0.979858	0.403251	0.04139	0.229803	1.806294	0.089392	0.023175	0.267808	0.143869	0.429985	0.105379	0.519007	0.050075	0.29193

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
DZ_2_1.1 39474_2	k__Bacteria; p__Firmicutes	tetracycline	tetT	0.009772	0.404485	2.770943	1.201553	0.010338	0.167923	0.798651	0.317275	1.039614	8.522841	1.103571	0.703751	0.114409	0.029651	4.113304	0.122215
DZ_2_1.2 22497_1	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales; f__Oscillospiraceae; g__Oscillibacter; s__Oscillibacter ruminantium	macrolide- lincosamide- streptogrami n	vatB	0	0.019426	0.167605	0.030803	0	0	0	0	0	0.029351	0	0	0	0	0	0
HZ_3_1.8 8878_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter; s__Acinetobacter sichuanensis	multidrug	adeJ	0	0	0	0.095016	0	0	0.002851	0.00249	0.035937	0.005041	0	0	0.007128	0	0	0
TA_3_1.8 0448_4	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae; g__Escherichia	macrolide- lincosamide- streptogrami n	macB	0.014738	0.017308	0.009704	0.018473	0.005157	0	0.009989	0.002415	0	0	0.218115	0.019241	0	0.019529	0.012283	0.010188
JN_2_1.14 75_1	k__Bacteria; p__Firmicutes	tetracycline	tetW	3.23581	6.482934	3.009746	6.851803	1.899787	2.411202	4.026019	2.678224	4.062912	1.758937	2.795902	5.387471	6.423642	2.16916	3.739928	4.506955
HZ_3_1.5 5841_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria	aminoglycosi de	aac6-31	0	0	0.313378	0.155394	0	0	0	0	0	0	0	0	0	0	0	0
YT_3_1.14 6309_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria	aminoglycosi de	aph6-l	0.368777	2.119701	3.378952	7.995748	0.388308	0.494358	1.913146	0.914622	1.277092	2.64023	3.740538	1.127666	4.870616	0.98256	0.190119	1.710936
TA_3_1.1 81702_1	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus; s__Enterococcus asini	multidrug	multidrug _transport er	0	0	0.051778	0.152236	0	0	0	0	0	0	0.108925	0	0	0	0	0
JN_2_1.42 0506_1	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Limosilactobacillus; s__Limosilactobacillus fermentum	macrolide- lincosamide- streptogrami n	ermT	3.34414	35.69691	6.166497	2.103146	16.69533	14.73081	37.53319	10.95505	4.118893	2.72977	7.177812	23.10313	5.917522	40.5549	4.271331	1.268402

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
DZ_2_1.9 3493_2	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales	tetracycline	tetP	0.255564	0.681332	3.089809	1.140664	0.33129	0.70734	1.085092	0.49171	0.98955	0.89218	2.735796	1.407207	0.747361	0.343217	2.10176	1.199757
DZ_2_1.9 3493_3	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales; f__Lachnospiraceae; g__Anaerobium; s__Anaerobium acetethylicum*	tetracycline	tetP	0.030635	0.070718	3.565332	0.631421	0	0	0.062528	0	0.07271	0.18046	0.03649	0.034495	0.121083	0	0	0.111023
WH_2_1.2 09095_1	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales; f__Clostridiaceae; g__Butyricicoccus; s__Butyricicoccus sp. AM05-1	chloramphenicol	catD	0.435685	0.146572	0.222233	0.082592	0.190944	0.188618	0.327677	0.11428	0.110785	0.079632	0.210074	0.339613	0.250248	0.328952	0.038443	0.031383
WF_1_1.5 06424_1	k__Bacteria; p__Firmicutes	vancomycin	vanG	0	0	0.067654	0.030495	0	0.047428	0	0.012384	0	0.056053	0	0.08063	0	0	0	0.015833
HZ_2_1.1 43391_2	k__Bacteria; p__Actinobacteria; c__Actinomycetia	macrolide-lincosamide-streptogramin	ermX	0.006611	0.58607	0.96583	1.945074	0.113217	0.390864	0.331605	0.222356	0.351072	0.447517	1.350073	1.646397	0.510064	0.062431	0.317149	0.770593
WF_3_1.4 22234_4	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	mexT	0	0	0.026387	1.801064	0	0	0.008443	0.051978	1.285497	0.38983	0.037835	0.07984	1.510149	0.008479	0	0.016383
BZ_1_1.27 8992_1	k__Bacteria; p__Firmicutes	macrolide-lincosamide-streptogramin	vatB	0.117648	0.073138	0.033132	0	0	0	0	0	0.070085	0	0.142253	0.038736	0	0	0	0
HZ_1_1.4 11672_2	k__Bacteria; p__NA; c__NA; o__NA; f__NA; g__NA; s__uncultured bacterium	aminoglycoside	rmtF	0.133717	0	0.159775	0.42432	0.236193	0.558291	0.535588	0.646397	0.776301	0.72062	0.519678	0.156681	0.398154	0.285863	0.125377	0.159978
DZ_2_1.1 58246_1	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales	macrolide-lincosamide-streptogramin	mefA	0	0	0.340128	0.025885	0	0	0	0.027018	0.027777	0.027647	0.028047	0	0.075524	0	0	0
WH_1_1.1 45467_2	k__Bacteria; p__Firmicutes	vancomycin	vanG	0.010752	0	0	0	0.011028	0	0	0	0	0	0.013872	0	0.153273	0.006353	0	0

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
DY_2_1.4 3163_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Xanthomonadales; f__Xanthomonadaceae; g__Luteimonas; s__Luteimonas sp. YGD11-2	multidrug	multidrug_transporter	0	0.436268	0.017014	0	0.011546	0	0	0.007392	0	0.006371	0	0	0	0	0	0.008006
ZZ_3_1.42 846_2	k__Bacteria; p__Firmicutes	macrolide-lincosamide-streptogramin	lsa	0.581666	1.096721	1.152953	0.634658	1.087721	1.285601	0.908675	0.415742	0.301921	0.325678	0.248719	0.836819	1.060738	0.524668	1.210286	1.517012
TA_3_1.6 797_5	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia; s__Escherichia fergusonii	multidrug	mdtP	0.03345	0.052337	0.032677	0.01309	0	0	0.011861	0	0.00838	0	0.216047	0.029774	0	0.022556	0.011108	0.037425
DZ_3_1.2 9502_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter; s__Acinetobacter baumannii	chloramphenicol	catB	0	0.10676	0.184837	0.183591	0.063499	0	0.029127	0	0.014905	0.044177	0.191689	0.113102	0.098013	0	0.017803	0.030412
WH_1_1.6 36_12	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales	chloramphenicol	catA	0	0.778972	0	0	0	0.08408	0.015904	0	0	0.051622	0	0.029307	0.422285	0	0	0
DY_3_1.1 4898_1	k__Bacteria; p__Synergistetes; c__Synergistia; o__Synergistales; f__Synergistaceae; g__Cloacibacillus; s__Cloacibacillus porcorum	tetracycline	tetracycline_resistance_protein	5.359661	8.314199	4.841504	6.141532	7.03765	5.643716	6.352847	5.131607	5.767015	3.448628	3.556788	5.822844	5.128809	3.816342	4.91379	7.938004
LY_3_1.63 2918_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	adeJ	0	0	0	0	0	0	0	0.213035	0.0193	0	0	0	0	0	0	0

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
HZ_1_1.1 7900_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacterales; f__Enterobacteriaceae	multidrug	mdtN	0	0	0	0.116713	0	0.052713	0	0	0	0	0	0.053027	0.121336	0	0.111794	0
HZ_3_1.2 00051_1	k__Bacteria; p__Firmicutes	macrolide- lincosamide- streptogramin	mefA	0.313456	0.109188	1.053379	0.494031	0.053201	0.112871	0.122684	0.332169	0.361315	0.170398	0.245356	0.224739	0.24424	0.13594	0.102419	0.118121
RZ_2_1.82 188_7	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacterales; f__Enterobacteriaceae	bacitracin	bacA	0.327421	0.411775	0.248856	3.799952	0.133191	0.216449	3.118101	0.265592	0.138967	2.129754	3.794586	0.156337	2.88164	1.291666	0.049679	0.683583
DZ_2_1.3 03189_1	k__Bacteria; p__Firmicutes	tetracycline	tetM	0	0.032381	0.418043	0.027174	0	0.029447	0.087755	0.028305	0.05502	0.376468	0.088047	0	0	0	0.171893	0
RZ_2_1.24 7533_4	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	mexT	0	0.009548	0.437228	0.029056	0	0	0.082992	0	0.023054	0.196676	0.00772	0.029157	0.171862	0	0.02048	0.065893
RZ_1_1.31 2182_1	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales	beta-lactam	CfxA2	5.272913	1.279647	0.652388	0.997587	2.419063	1.854292	0.785472	5.408616	1.28738	2.457216	0.821716	1.357837	0.771562	2.943471	1.001393	3.580136
DY_2_1.5 3130_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	adeJ	0	0.132487	0	0	0	0	0.059999	0	0	0.022226	0.047958	0	0	0	0	0
YT_3_1.28 9789_1	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales; f__Lachnospiraceae; g__NA; s__Lachnospiraceae bacterium	tetracycline	tet40	0	0	0	0	0.10669	0	0	0	0	0	0	0	0	0.133814	0	0
WF_3_1.1 5537_2	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Weissella; s__Weissella thailandensis	bacitracin	bacA	0	0	0.068443	0.028055	0	0.019403	0	0	0.009584	0	0.019574	0.77628	0	0	0.088207	0

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
BZ_2_1.492354_1	k__Bacteria; p__Actinobacteria; c__Actinomycetia; o__Bifidobacteriales; f__Bifidobacteriaceae; g__Bifidobacterium; s__Bifidobacterium thermonphilum	tetracycline	tetracycline_resistance_protein	0.197853	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ZZ_1_1.78476_4	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacterales; f__Enterobacteriaceae	multidrug	mdtO	0.271232	0.309294	0.213012	3.231019	0.127048	0.160223	2.692252	0.151026	0.131321	1.605675	3.307868	0.158312	2.178557	1.149948	0.027798	0.68362
HZ_3_1.459449_1	k__Bacteria; p__Firmicutes; c__Bacilli	macrolide-lincosamide-streptogramin	lsa	0.020843	0.043463	0.038602	0.07249	0	0.006755	0.005986	0	0.090579	0.027425	0.067356	0	0.063338	0	0.033539	0
BZ_2_1.30205_24	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacterales; f__Enterobacteriaceae	multidrug	mdtK	0.182745	0.297742	0.133718	2.666204	0.059347	0.16834	2.109378	0.092623	0.076164	1.402578	2.771916	0.167783	1.885533	1.125029	0.042333	0.583099
HZ_2_1.187828_2	k__Bacteria; p__Actinobacteria; c__Coriobacteriia; o__Coriobacteriales; f__Coriobacteriaceae; g__Collinsella; s__Collinsella sp. AM17-1	aminoglycoside	aph2-le	0.060818	0.008862	0.131563	0.207604	0.055739	0.040069	0.021775	0.024587	0.040969	0.014415	0.074651	0.0259	0.022289	0.05611	0	0.079154
WH_1_1.338076_1	k__Bacteria; p__Firmicutes	vancomycin	vanX	0	0.13695	0.070102	0	0	0	0	0.066401	0	0	0.067972	0	0.635783	0	0	0
BZ_1_1.518850_1	k__Bacteria; p__Proteobacteria	sulfonamide	sul1	0.155442	3.186828	3.751001	3.385985	0.105209	0.290904	0.947857	0.394094	0.867637	1.660952	3.018536	1.51996	2.028536	0.372236	0.391597	1.985947
QD_1_1.246718_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia; s__Escherichia coli	multidrug	acrB	0	0	0	0	0	0	0	0	0.065448	0	0.293433	0	0.349556	0	0	0.138178
J_3_1.166216_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Psychrobacter	bacitracin	bacA	0	0	0	0	0.608105	0	0	0	0	0	0.379793	0	0.135414	0	0	0

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
WH_3_1.3 0470_1	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales	beta-lactam	OXA-209	0.054994	0.020631	0.019092	0	0	0	0	0	0	0	0	0	0.382849	0	0	0
LY_2_1.43 4330_3	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides; s__Bacteroides oropionicifaciens	tetracycline	tet36	0.117832	0.169256	2.755913	2.82955	0.030614	0.22175	0.203677	0.819068	0.269326	0.464323	0.978861	0.209637	0.583877	0.061934	0.868165	0.283944
TA_3_1.2 15856_4	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia	multidrug	ToIC	0.017181	0.019268	0.027951	0.004734	0.007246	0	0.023361	0.006763	0	0	0.268568	0.008603	0	0.014135	0.01094	0.013794
RZ_2_1.25 4673_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria	multidrug	mexD	0	0.451096	0	0.127166	0	0	0	0	0	0.157728	0.136124	0	0	0	0	0
HZ_3_1.3 82995_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	mexT	0	0	0	0.119997	0	0	0.010763	0	0.029344	0.009638	0	0	0	0	0	0
HZ_3_1.6 1018_3	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia; s__Escherichia coli	multidrug	emrE	0.199626	0.156339	0.051943	1.295871	0.046542	0.075326	1.454659	0.065905	0.04656	1.283163	1.785972	0.24482	1.105565	0.45572	0	0.275133
TA_2_1.2 75528_6	k__Bacteria; p__Firmicutes	chloramphenicol	chloramphenicol_and_florfenicol_resistance_gene	0.015024	0.022967	1.336093	0.62729	0.01621	0.038607	0.151737	0.077228	0.281717	1.672456	0.255813	0.19195	0.099662	0.00595	0.420367	0.099909
YT_1_1.11 4569_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Enterobacterales; f__Enterobacteriaceae	unclassified	DNA-binding_transcriptional_regulator_gadX	0.47466	0.664341	0.415675	5.478135	0.215948	0.411528	5.224587	0.383648	0.187771	3.524242	6.781379	0.369502	4.270384	2.167382	0.07364	1.210357

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
TA_3_1.1 17420_3	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia; s__Escherichia fergusonii	polymyxin	arnA	0.002404	0.019605	0.016645	0.015369	0.007568	0.003106	0.008179	0.002363	0	0.00312	0.229831	0.015819	0	0.012742	0.003836	0.00657
RZ_3_1.88 093_2	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales	macrolide- lincosamide- streptogrami n	ermG	0.009252	0.459724	0.083057	0.068305	0	0	0.092085	0.042108	0.12862	0.097501	0.805959	0.076449	0.057586	0.043677	0.275105	0.011788
J_1_1.262 845_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Moraxellales; f__Moraxellaceae; g__Psychrobacter	bacitracin	bacA	0.009622	0	0	0	0.21147	0	0	0	0	0	0.054848	0	0.130391	0	0	0
ZB_2_1.41 6404_1	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales; f__Clostridiaceae; g__Clostridium	bacitracin	bacA	0.030028	0	0.020643	0	0	0	0.053455	0.052638	0.055648	0.017199	0.057616	0.021668	0.019816	0	0.112145	0
DZ_3_1.1 47792_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	adeJ	0	0	0.118901	0	0	0	0	0	0	0	0	0	0	0	0	0
LC_3_1.18 0941_4	k__Bacteria; p__Firmicutes; c__Tissierellia; o__Tissierellales; f__Peptoniphilaceae; g__Anaerococcus; s__Anaerococcus lactolyticus	bacitracin	bacA	0	0.222939	2.650401	0.271172	0	0.296625	0.335491	0.017911	0.858338	0.831638	1.386602	0.623847	0.081435	0.049768	1.384931	0
QD_2_1.5 7677_11	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Weeksellaceae; g__Empedobacter; s__Empedobacter falsenii	beta-lactam	metallo- beta- lactamase	0	0.015642	0.014266	1.230603	0	0	0.014208	0.075528	0.31116	0.059876	0	0.086082	0.675589	0	0.032255	0.027444

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
RZ_2_1.42 9200_3	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales; f__Clostridiaceae; g__Clostridium	bacitracin	bacA	0.349005	0.012011	0.213627	0.160737	0.02399	0.114467	0.178308	0.197219	0.141619	0.252042	0.519566	0.29204	0.125416	0.113647	0.816777	0.411306
DZ_2_1.4 4059_10	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Bacillus; s__Bacillus oleivorans	macrolide- lincosamide- streptogrami n	lsa	0	0.010528	0.913123	0.111449	0.013926	0	0.025637	0.008777	0.027027	0.01181	0.008614	0.004291	0.027815	0	0	0.014673
J_3_1.491 207_9	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides; s__Bacteroides xylanisolvens	beta-lactam	CfxA2	8.588081	2.239867	2.662852	2.114151	3.281055	3.504498	1.465275	4.63188	2.412097	2.394635	2.301363	1.897927	1.743162	3.403176	1.425832	4.116375
WH_2_1.2 34989_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	adeC	0	0	0.029635	0.073264	0	0	0	0	0.078557	0	0.027405	0	0.094823	0	0	0
HZ_2_1.2 16882_3	k__Bacteria; p__Firmicutes; c__Tissierellia; o__Tissierellales; f__Peptoniphilaceae; g__Anaerococcus; s__Anaerococcus prevotii	bacitracin	bacA	0	0.008773	0	0.204138	0	0.017608	0.109611	0	0.026247	6.873712	0.088284	0.042241	0	0.008135	0.397882	0
WH_2_1.2 34614_1	k__Bacteria; p__Firmicutes	macrolide- lincosamide- streptogrami n	mphB	0.08924	0	0.623506	0.189232	0	0	0.104987	0	0.083873	0.103671	0.10617	0	0.189944	0	0.404639	0
QD_2_1.2 44209_2	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus; s__Enterococcus gallinarum	vancomycin	vanD	0	0	0	0	0	0	0	0	0.510344	0	0	0	0	0	0	0

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
QD_3_1.5 60176_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Enterobacterales; f__Enterobacteriaceae	multidrug	emrK	0	0	0.012817	0	0	0.065648	0	0	0.06805	0.01957	0	0.022674	0.009949	0	0	0
WF_3_1.1 15822_2	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales	aminoglycosi de	aad9	0	0	0	0	0	0	0	0	0	0	0	1.891299	0.009696	0	0	0
TA_1_1.3 07845_2	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae; g__Staphylococcus	multidrug	norA	0	0	0.026465	0.02335	0	0	0	0	0.017338	0.006074	0.096695	0.029289	0.005385	0.005537	0.007437	0.020094
YT_1_1.75 739_14	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Enterobacterales; f__Enterobacteriaceae	multidrug	acrB	0.196672	0.345408	0.185881	2.951991	0.063999	0.184702	2.42253	0.160002	0.131496	1.424801	3.049202	0.1847	2.151729	1.121659	0.023332	0.652489
DZ_3_1.3 37161_1	k__Bacteria; p__Firmicutes	macrolide- lincosamide- streptogrami n	lsa	2.422602	5.314496	2.840562	4.74699	2.182759	4.005219	4.901096	2.634849	2.72873	1.295767	3.040462	2.568326	3.479371	2.036631	5.471464	4.732298
WH_2_1.2 34358_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Vibrionales; f__Vibrionaceae; g__Vibrio; s__Vibrio vulnificus	rifamycin	ADP- ribosylatin g_transfer ase_arr	0.053056	0.108029	0.122187	0.593986	0.057072	0.049784	0.437119	0.079141	0.015914	0.134735	0.085759	0.048454	0.414709	0.056155	0	0.066327
WF_3_1.5 6933_2	k__Bacteria; p__Firmicutes; c__Bacilli	tetracycline	tetS	0.023614	0.003134	0.342653	0.105982	0.005128	0.086291	0.014591	0.025696	0.026298	0.036359	0.229235	0.891622	0.228136	0.002937	0.020526	0.02891
WH_1_1.2 56155_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Moraxellales; f__Moraxellaceae; g__Psychrobacter	multidrug	mexT	0.020653	0	0	0	0.117917	0.007505	0	0.007678	0	0	0.037099	0	0.158175	0.008515	0	0
YT_1_1.11 4569_5	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Enterobacterales; f__Enterobacteriaceae	multidrug	mdtF	0.257252	0.393072	0.225692	3.43144	0.10697	0.172459	2.714316	0.135584	0.121163	1.81484	3.299198	0.195738	2.29124	1.351626	0.044625	0.66295

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
LY_3_1.13 1126_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	adeJ	0	0	0	0	0	0	0	0.152068	0	0	0	0	0	0	0	0
WH_1_1.2 13635_2	k__Bacteria; p__Firmicutes	vancomycin	vanW	0.025248	0.061615	0	0	0.026397	0	0.026257	0	0.030524	0	0	0.028951	0.096375	0	0.035948	0
WH_1_1.2 13635_1	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus	vancomycin	vanY	0.221751	0	0	0.19933	0	0	0	0.16427	0	0	0.202793	0	0.376026	0	0	0
RZ_1_1.14 0794_1	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales; f__Clostridiaceae; g__Clostridium; s__Clostridium beijerinckii	tetracycline	tetP	0.027237	0.086774	2.173744	0.147774	0.02571	0.053654	0.091443	0.063883	0.44671	0.24121	0.241472	0.137333	0.085207	0.02452	0.194631	0.135132
DZ_3_1.3 97169_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	mexT	0	0.019096	0.277705	0.058111	0	0	0.105655	0.014915	0.08453	0.166419	0.045419	0.029157	0.028421	0	0.01024	0.148154
QD_2_1.4 16875_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	adeJ	0	0	0.061052	0.021517	0	0	0	0	0.10957	0.006538	0.007322	0	0.033992	0	0	0
ZZ_1_1.45 2208_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae; g__Escherichia	multidrug	mdfA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.592693
TA_3_1.2 3256_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria	aminoglycoside	aac3-VI	0	0.010916	0	0.04936	0	0	0.018002	0	0	0	0.09462	0	0	0	0	0

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
QD_2_1.4 7153_29	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter; s__Acinetobacter sp. B51(2017)	multidrug	adeJ	0	0	0.040085	0.429835	0	0.003643	0.128792	0.001859	0.247733	0.096063	0.3862	0	1.089096	0	0	0.002019
WF_3_1.8 0771_3	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Enterobacterales; f__Enterobacteriaceae	multidrug	mdtD	0.186005	0.271749	0.180587	2.577404	0.073108	0.127938	2.209428	0.135513	0.084497	1.343785	2.516037	0.164943	1.829545	0.868668	0.030238	0.480875
WF_3_1.4 49841_1	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae	tetracycline	tetQ	3.462363	1.147275	1.812073	1.057463	2.782511	1.741769	1.946228	2.847448	1.398118	1.172106	1.031461	2.229009	0.896278	2.137996	0.862546	2.611718
TA_3_1.1 43551_3	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia	multidrug	mdtH	0	0	0.006544	0.00554	0	0	0.005027	0	0	0.023024	0.137937	0	0	0.006496	0	0.028577
QD_2_1.2 16771_15	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Cytobacillus; s__Cytobacillus eiseniae	tetracycline	tetL	0	0	0.08426	0.084371	0	0.004836	0	0	0.45521	0.209149	0.037761	0.004694	0.145306	0	0	0.010656
DZ_2_1.1 03394_1	k__Bacteria; p__Firmicutes	vancomycin	vanG	0	0.012073	0.155674	0.018499	0	0	0	0.00983	0	0.069664	0	0.051483	0	0	0	0.01059
WF_3_1.1 91191_4	k__Bacteria; p__Proteobacteria	aminoglycoside	aph3-l	0.192213	0.49289	0.626103	21.63615	0.18265	0.02145	0.154198	0.331029	0.197635	0.085239	0.420768	0.267819	0.306479	0.039584	0.068178	0.28527
RZ_2_1.47 7775_7	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Enterobacterales; f__Enterobacteriaceae	polymyxin	arnA	0.23453	0.270731	0.14877	2.918479	0.076023	0.210365	2.440529	0.158868	0.104254	1.485261	3.167238	0.168088	2.136673	1.231162	0.03211	0.613987
WF_2_1.8 9612_1	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales	bacitracin	bacA	0	0	0	0	0	0	0	0.494207	0	0	0	0.246576	0	0.22963	0	0
QD_2_1.1 96415_2	k__Bacteria; p__Firmicutes	vancomycin	vanD	0	0	0.014266	0.012204	0	0.025293	0	0	0.088971	0	0	0	0	0	0	0

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
HZ_3_1.4 47557_1	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus	vancomycin	vanE	0	0	0.019353	0.126867	0	0	0.011376	0.010042	0	0	0.020297	0.019627	0	0	0	0
HZ_3_1.9 5347_2	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus; s__Enterococcus hirae	multidrug	EmrB- QacA_fam ily_major_ facilitator _transport er	0	0	0.071899	0.065475	0	0	0	0	0.06962	0.143739	0	0	0	0	0	0
J_1_1.273 587_3	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia; s__Escherichia coli	multidrug	emrE	0.066958	0.079518	0.086304	0.238676	0.080544	0.161608	0.548669	0.085045	0.070534	0.259893	0.510453	0.239382	0.798196	0	0	0.082196
LY_3_1.14 0957_1	k__Bacteria; p__Firmicutes	macrolide- lincosamide- streptogrami n	ermA	1.801975	3.016002	3.723975	3.075375	5.89321	5.272411	1.639644	10.78753	2.149581	5.050859	5.114134	6.218697	1.239973	2.703336	3.789784	12.97526
TA_3_1.2 19154_3	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria	aminoglycosi de	ant3-lh- aac6-Ild	0.026533	0.187448	0.389773	0.658703	0	0.061706	0.06115	0.317402	0.058645	0.105883	0.292668	0.082129	0.299688	0	0.055409	0.14108
ZZ_2_1.18 5395_1	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales	tetracycline	tetQ	5.039636	1.274083	1.1091	1.793316	2.26751	2.808383	1.717236	3.247477	2.550443	1.787605	1.753389	1.84489	1.077551	3.342453	1.341585	4.399446
RZ_2_1.11 1624_1	k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Burkholderiales; f__Oxalobacteraceae; g__Oxalobacter; s__Oxalobacter formigenes	bacitracin	bacA	0.007574	0.102549	0.011407	0.067705	0.023562	0	0.04992	0.019591	0.038697	0.088197	0.009699	0.050505	0.052806	0.053697	0.013072	0.074011
LC_1_1.31 9667_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Enterobacterales; f__Enterobacteriaceae	multidrug	mdtC	0.178568	0.250687	0.13747	2.120944	0.050406	0.110282	1.804102	0.087938	0.086311	1.071815	2.21644	0.125988	1.475454	0.870794	0.021652	0.479487
ZZ_2_1.35 272_1	k__Bacteria; p__Firmicutes	tetracycline	tetM	3.947195	4.803473	5.432264	4.2691	7.660073	4.596734	3.988518	4.578514	5.543604	4.182062	3.283242	4.661203	5.652252	4.287226	7.556257	5.607282

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
QD_2_1.2 58713_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia; s__Escherichia coli	aminoglycoside	aac3-II	0.099929	0.09037	0.379786	3.729082	0.112667	0.04542	0.599376	0.14895	0.277139	0.234446	2.221597	0.147598	1.862066	0.125538	0.009321	0.28258
ZB_1_1.26 404_2	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae	bacitracin	bacA	0	0	0	0	0.033038	0	0	0	0	0	0	0	0	0	0.206167	0
HZ_2_1.2 07077_19	k__Bacteria; p__Firmicutes; c__Tissierellia; o__Tissierellales; f__Peptoniphilaceae; g__Anaerococcus	bacitracin	bacA	0	0	0.062593	0.496748	0	0.026548	0.010008	0	0.008792	0	0.017658	0.093187	0	0.008177	0.008956	0
ZZ_1_1.27 799_6	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Enterobacterales; f__Enterobacteriaceae	multidrug	mdtB	0.158297	0.245774	0.159414	2.368403	0.067911	0.102025	1.831904	0.097172	0.084622	1.130643	2.556192	0.140664	1.646385	0.884078	0.029692	0.403378
WH_3_1.6 9620_1	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales	vancomycin	vanR	0.098685	0.110354	0.026214	0.012118	0.212903	0.074288	0.038619	0.09397	0.141829	0.045366	0.064638	0.037426	0.731767	0.107319	0.050103	0.054958
WH_1_1.2 33240_1	k__Bacteria; p__Firmicutes	vancomycin	vanU	1.648838	0	0	0	0.535632	0	0.363172	0	0	0	0	0	0.991507	0	0.29949	0
LC_2_1.69 006_1	k__Bacteria; p__Firmicutes	tetracycline	tetP	1.310909	1.812103	3.615587	3.53021	1.142647	2.334427	2.936871	2.432827	3.128921	3.188757	8.640869	5.729088	1.947086	1.540641	6.407478	3.540461
HZ_3_1.4 68774_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Pasteurellales; f__Pasteurellaceae; g__Pasteurella; s__Pasteurella multocida	aminoglycoside	aadA	0	0	0.049035	0.28311	0	0	0	0.0893	0	0	0	0	0.159859	0	0	0
DY_2_1.3 72958_2	k__Bacteria; p__Proteobacteria	chloramphenicol	floR	0	0.103088	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DZ_1_1.2 75248_1	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae; g__Staphylococcus	bacitracin	bcrA	0	0	0.222705	0.018591	0	0	0	0	0	0	0.050359	0	0.018286	0	0.018884	0

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
LY_3_1.43 2261_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	major_facilitator_superfamily_transporter	0	0	0	0	0	0	0	0.206414	0	0	0	0	0.023944	0	0	0
QD_2_1.2 50378_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	adeC	0.00726	0	0.021623	1.438395	0	0.004681	0.015913	0.065323	1.398402	0.267073	0.046757	0.095405	1.155038	0	0.006496	0.041273
QD_2_1.2 50378_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	adeJ	0.009799	0	0.037768	1.283589	0	0	0.012412	0.037908	1.363287	0.241557	0.038264	0.066215	1.011424	0.003732	0.00257	0.044403
QD_2_1.5 0462_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	emrB	0	0	0.014521	0.059739	0	0	0	0	0.139586	0	0.012531	0	0.057004	0	0	0
DZ_3_1.4 79598_2	k__Bacteria; p__Proteobacteria; c__Epsilonproteobacteria; o__Campylobacteriales; f__Campylobacteraceae; g__Campylobacter; s__Campylobacter coli	multidrug	cmeA	0	0	0.656437	0.006902	0	0	0	0	0	0.013002	0	0	0	0	0	0.007161
DZ_3_1.4 79598_1	k__Bacteria; p__Proteobacteria; c__Epsilonproteobacteria; o__Campylobacteriales; f__Campylobacteraceae; g__Campylobacter; s__Campylobacter coli	multidrug	cmeB	0.004054	0.00222	0.52335	0.002164	0.003156	0	0	0	0	0.001747	0	0.002465	0.002121	0	0	0
ZB_3_1.12 2684_7	k__Bacteria; p__Firmicutes; c__Bacilli	macrolide-lincosamide-streptogramin	mphB	0.053538	0.372694	1.106417	0.516561	0.236595	0.059222	0.608461	0.259166	1.336608	0.927222	1.833932	0.492767	0.393017	0.023349	9.334184	0.098291
RZ_1_1.32 1054_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Aeromonadales; f__Succinivibrionaceae	unclassified	cAMP-regulatory_protein	0	0	0.017452	0	0	0.044367	0	0	0	0.285793	0	0	0	0	0	0

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
QD_2_1.4 02813_4	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria	sulfonamide	sul2	0.42388	4.441012	2.895511	18.2564	0.471248	0.406702	2.447825	1.815006	2.169821	2.725178	2.959229	0.93109	8.208699	0.725879	0.328743	1.117811
RZ_2_1.41 4425_1	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides	beta-lactam	class_A_beta-lactamase	0	0	0	0	0	0	0.008897	0	0.009954	0.13257	0.050828	0	0.037135	0.009303	0	0
RZ_3_1.86 426_1	k__Bacteria; p__Firmicutes; c__Tissierellia; o__Tissierellales; f__Peptoniphilaceae; g__Anaerococcus	bacitracin	bacA	0	0	0	0.023839	0	0	0	0	0	0.227624	0	0	0	0	0	0.013439
WH_2_1.3 41013_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	adeC	0	0.008533	0.39952	0.02586	0	0.013353	0.04278	0	0.020518	0.154119	0.006867	0.006483	0.103922	0	0	0.02199
WH_1_1.4 12251_4	k__Bacteria; p__Proteobacteria	multidrug	mexT	0.046498	0.028645	0.015736	0.196126	0.006224	0.030021	0.006603	0	0.023054	0	0.528475	0.014579	0.380099	0	0	0.007501
TA_1_1.2 25618_7	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae; g__Escherichia; s__Escherichia coli	multidrug	mdtM	0.173229	0.261752	0.230072	2.578588	0.066104	0.109799	2.504645	0.161903	0.097797	1.463783	2.891027	0.118025	2.00002	1.02575	0.011313	0.547159
RZ_2_1.73 245_3	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae	chloramphenicol	catB	0	0.037992	0.080569	0.108406	0.040936	0.010098	0.011376	0.020084	0	0.468119	0.051826	0.009813	0.046419	0	0	0.152674
ZZ_3_1.14 5207_1	k__Bacteria; p__Firmicutes; c__Tissierellia; o__Tissierellales; f__Peptoniphilaceae; g__Helcococcus; s__Helcococcus kunzii	tetracycline	tetT	0.030953	1.052206	5.868101	3.30711	0.036943	0.359116	1.821109	0.430152	2.99751	20.12357	2.232643	1.755141	0.173239	0.107699	10.80808	0.255985

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
DY_2_1.2 63954_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Xanthomonadales; f__Xanthomonadaceae; g__Luteimonas; s__Luteimonas sp. YGD11-2	multidrug	multidrug_transporter	0	0.174912	0.021277	0	0	0	0	0	0	0.006247	0	0	0	0	0	0
HZ_3_1.3 16502_10	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter; s__Acinetobacter larvae	multidrug	mexT	0	0	0	3.924061	0	0	0	0	0	0	0	0	0	0	0	0
DZ_3_1.1 57167_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	adeJ	0	0	0.126426	0	0	0	0	0	0	0	0	0	0.017514	0	0	0
LY_1_1.27 5318_1	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales	tetracycline	tetQ	7.966421	3.112123	3.30421	3.460107	4.00788	4.793743	3.377986	6.791239	4.544553	3.57424	2.528274	3.82895	2.46437	6.975636	3.174234	6.306852
DZ_2_1.4 57742_1	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Streptococcus; s__Streptococcus suis	aminoglycoside	aadE	0	0	0.304787	0.27069	0	0	0	0.229424	0.531087	1.123623	0	0	0.243256	0	0.311244	0
WF_2_1.2 20514_3	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae; g__Staphylococcus; s__Staphylococcus aureus	aminoglycoside	streptomycin_resistance_protein	0.071613	0.451435	1.530157	0.98264	0.084456	0.075089	0.248107	0.116877	0.601358	0.330929	1.893409	7.993423	0.482105	0.034376	1.551274	0.430564
WF_1_1.3 07223_1	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales; f__Lachnospiraceae; g__Lacrimispora; s__Lacrimispora celerecrescens	chloramphenicol	chloramphenicol_and_florfenicol_resistance_gene	0.034401	0.051247	0.820501	0.410483	0	0.021722	0.058889	0	0.225887	0.204068	0.125937	0.080866	0.128173	0	0.052962	0.056916

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
TA_3_1.8 0448_3	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia	macrolide- lincosamide- streptogrami n	macA	0.009877	0.060488	0.007323	0.006206	0.005287	0	0.005635	0.004909	0	0	0.190827	0.020154	0	0.007276	0.015794	0.014078
WH_2_1.3 18180_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	mexB	0	0	0	0	0	0	0	0	0	0	0	0	0.073407	0	0	0
TA_2_1.4 99240_1	k__Bacteria; p__Bacteroidetes	macrolide- lincosamide- streptogrami n	erm35	0	0.012874	0.851761	0.41892	0	0	0.292798	0.141091	0.121454	0.195523	0.195767	0.142074	0.084275	0	0.593458	0.022403
JN_1_1.18 3884_1	k__Bacteria; p__Bacteroidetes	tetracycline	tet36	0.142625	0.386175	4.382955	3.062156	0	0.486369	0.488244	1.386964	0.423717	1.09972	1.225599	0.36837	1.284754	0.189726	0.687755	0.445054
HZ_2_1.4 13653_2	k__Bacteria; p__Actinobacteria	tetracycline	tetracyclin e_resistan ce_protei n	2.257196	2.598835	3.284101	3.421961	2.392566	2.534675	3.046151	1.496638	2.979017	1.675595	1.9441	2.595618	3.252681	1.632162	2.294764	2.752338
YT_1_1.11 7428_4	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacterales; f__Enterobacteriaceae	fosmidomyci n	rosB	0.204134	0.348981	0.182241	2.993982	0.087816	0.113291	2.202709	0.132789	0.079946	1.39047	3.067596	0.205334	2.01672	1.158043	0.010373	0.641341
LY_3_1.69 0132_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	oprM	0	0	0	0	0	0	0	0.293661	0	0	0	0	0	0	0	0
WH_2_1.2 0871_1	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Niallia; s__Niallia nealsonii	chlorampheni col	cat_chloramphenicol _acetyltran sferase	0	0	0	0	0	0	0	0	0.104337	0.029451	0	0	0.120662	0	0	0
DZ_2_1.1 64749_1	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales	vancomycin	vanR	0	0	0.170986	0.048949	0	0.026769	0	0.11265	0	0.024358	0	0.058661	0	0	0	0.027355

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
DY_3_1.1 50334_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacterales; f__Enterobacteriaceae; g__Klebsiella; s__Klebsiella pneumoniae	aminoglycoside	aadA	0.67349	4.944686	3.284499	11.34762	0.414038	0.456743	5.543718	0.261626	0.826502	4.391699	5.484561	1.13564	5.910743	1.464936	0.195429	1.585433
TA_1_1.7 725_6	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Streptococcus	tetracycline	tetM	0.438156	2.216828	7.670143	4.514289	0.492496	0.822825	3.417356	1.766991	4.142951	2.429033	4.023669	8.224911	3.20514	1.44133	6.678652	1.714264
RZ_2_1.43 8444_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	adeJ	0	0.016736	0.35779	0.024739	0	0.00182	0.112326	0	0.02569	0.151583	0.008994	0.015886	0.142362	0	0.00257	0.060339
YT_1_1.36 9237_1	k__Bacteria; p__Proteobacteria; c__Epsilonproteobacteria; o__Campylobacteriales; f__Campylobacteraceae; g__Campylobacter	beta-lactam	OXA-61	0.099965	0.128555	0.591082	0.034231	0.045113	0.177707	0.037717	0.191222	0.097776	0.177761	0.043023	0.034819	0.019392	0.450977	0.105631	0.152306
TA_2_1.4 95585_1	k__Bacteria; p__Proteobacteria	trimethoprim	dfrA16	0.023939	0.51809	0.645344	2.249291	0.076573	0.086005	0.062598	0.141527	0.432732	0.666994	2.113338	0.19798	0.882828	0	0.03447	0.446435
ZB_3_1.85 806_3	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales	macrolide-lincosamide-streptogramin	lsa	0.030605	0.171683	0.406728	1.491706	0	0.035136	0.074044	0.022198	0.821049	0.293079	0.673843	0.163869	1.183835	0.028257	0.271876	0.013256
TA_3_1.1 85941_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia	multidrug	emrD	0.009472	0.012594	0.018624	0.030137	0	0	0.005409	0	0.00624	0	0.234316	0.023676	0	0.012518	0	0.013468
LC_2_1.26 1073_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	adeJ	0	0.005003	0.072746	0.01736	0	0	0.064674	0.003195	0	0.051936	0.025992	0	0.017692	0	0.008555	0.008724

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
WF_1_1.3 77144_2	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae; g__Staphylococcus; s__Staphylococcus aureus	macrolide- lincosamide- streptogrami n	vgaE	0.037519	0.50171	0.8109	0.815442	0.043807	0.031847	0.299628	0.078384	0.610999	0.494527	0.721625	0.902641	0.24427	0.049888	7.873738	0.043104
HZ_3_1.2 84296_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter; s__Acinetobacter defluvii	multidrug	adeC	0	0	0	0.097301	0	0	0	0	0.045886	0	0.011316	0.010881	0.011856	0	0	0
J_3_1.653 45_1	k__Bacteria; p__Firmicutes	tetracycline	tet32	0.339527	0.752282	0.556497	0.547152	0.304476	0.415434	0.563017	0.373764	0.241339	0.208978	0.274927	0.320993	0.275724	0.436598	0.535648	0.609878
DZ_2_1.4 3713_4	k__Bacteria; p__Firmicutes	macrolide- lincosamide- streptogrami n	ermTR	0	0.065297	0.747726	0.332385	0.020741	0.023865	0.087823	0.106352	0.128862	0.385189	0.160589	0.069276	0.0328	0	0.136198	0
ZB_3_1.36 171_4	k__Bacteria; p__Firmicutes; c__Tissierellia; o__Tissierellales; f__Peptoniphilaceae; g__Anaerococcus; s__Anaerococcus lactolyticus	bacitracin	bacA	0	0.008959	0.868533	1.589987	0	0.058555	0.390796	0	0.267658	2.77868	0.008971	0.457668	0	0.008305	0.636689	0
BZ_3_1.32 2292_1	k__Bacteria; p__Firmicutes	tetracycline	tetW	0.065148	0.428457	0.522446	0.08773	0.660561	0	0	0.315767	0.163129	0	0.088813	0	0.162613	0.087826	0.091556	0.247416
QD_3_1.5 71453_1	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae; g__Staphylococcus; s__Staphylococcus aureus	macrolide- lincosamide- streptogrami n	ermC	0.008813	0.039969	0.383172	0.25005	0.029427	0.022626	0.022998	0.011544	0.461934	0.021634	2.783162	0.483362	0.312162	0.010412	0.058521	0.097611
WH_1_1.5 3551_2	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales; f__Oscillospiraceae; g__Flavonifractor; s__Flavonifractor sp. An306	vancomycin	vanR	0	0	0	0	0.157952	0	0	0	0	0	0	0	0.339019	0	0	0

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
TA_1_1.2 19618_7	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae; g__Staphylococcus	unclassified	truncated _putative _response _regulator _ArlR	0	0	0.063284	0.013564	0	0	0	0	0.013634	0	0.186008	0.054731	0	0	0	0
HZ_3_1.4 61332_1	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus; s__Enterococcus hirae	aminoglycoside	aac6-II	0	0	0	0.241985	0	0	0	0	0	0.066274	0	0	0	0	0	0
WH_3_1.5 6181_2	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales	tetracycline	tetQ	11.18214	4.29727	3.049734	6.993445	7.99776	6.330408	3.64488	8.246638	3.458877	9.189557	3.009571	2.651865	3.50887	9.725675	2.038869	11.12637
WF_3_1.4 25636_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria	beta-lactam	PSE-1	0.006547	0.157284	0.223277	0.961442	0.028723	0.016809	0.007398	0.108403	0.128582	0.261741	1.358914	0.146957	0.257176	0	0.010342	0.138025
YT_3_1.57 1624_7	k__Bacteria; p__Bacteroidetes	beta-lactam	CfxA3	5.724177	3.583499	2.074971	1.939274	2.728016	2.559756	2.510263	5.625289	1.344555	1.434776	1.074454	2.116468	1.763164	4.997634	1.899193	4.418479
DY_2_1.1 30686_3	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides; s__Bacteroides xylanisolvens	beta-lactam	CfxA2	39.92554	10.72764	6.650927	8.917503	19.98437	16.88822	4.961066	42.91056	9.626253	24.40367	8.112148	10.57991	7.830673	22.20535	7.2331	24.50977
DZ_3_1.4 98710_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia; s__Escherichia coli	multidrug	mdtP	0.114865	0.149869	0.107052	1.448446	0.092452	0.075446	1.472591	0.039437	0.078551	0.846275	1.426189	0.105067	0.789113	0.732743	0.004802	0.366459
DZ_1_1.4 12213_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria	trimethoprim	dfrA20	0.019745	0.02776	0.147617	0.228044	0	0	0.052795	0.071983	0.06344	0.145579	0.303888	0.192533	0.265846	0	0.11707	0.049009

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
DY_2_1.3 72958_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacterales; f__Enterobacteriaceae; g__Enterobacter; s__Enterobacter sp. MGH 10	sulfonamide	sul1	0	0.356427	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ZZ_3_1.36 2065_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	adeJ	0	0.015207	0.084885	0.05303	0	0.003891	0.023921	0	0.017499	0.099929	0.016017	0.009331	0.028031	0	0	0.080577
LY_2_1.33 4528_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria	beta-lactam	PSE-1	0	0.07338	0.140952	0.850118	0.38235	0	0.149117	0.323804	0	0.07187	0.967944	0.198762	0.249291	0	0	0
LC_2_1.19 5679_3	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__NA; g__Exiguobacterium; s__Exiguobacterium sp. S3-2	macrolide-lincosamide-streptogramin	mphB	0.431975	0.281983	0.609868	0.971587	0.414801	0.545898	1.252657	0.339418	1.341598	0.307161	0.53054	0.444351	0.581609	1.02183	0.942167	0.358921
QD_3_1.5 33368_1	k__Bacteria; p__Actinobacteria	tetracycline	tetW	4.103932	5.332287	4.763373	5.776961	5.409859	4.058061	4.813632	2.8232	4.423204	2.609391	3.562482	4.765422	4.451441	3.981481	4.533044	6.319307
DZ_1_1.7 4387_1	k__Bacteria; p__Bacteroidetes	beta-lactam	CfxA2	37.55086	22.06402	17.52349	15.83235	15.2425	18.87745	15.51384	17.63504	12.76243	5.543461	15.13518	14.29022	14.15253	24.32573	9.426402	9.728105
TA_1_1.3 78630_6	k__Bacteria; p__Firmicutes; c__Tissierellia; o__Tissierellales; f__Peptoniphilaceae; g__Helcococcus; s__Helcococcus kunzii	tetracycline	tetT	0.014993	1.118132	7.941825	3.501602	0.073695	0.482479	2.393168	0.845399	3.73985	25.18511	3.447053	2.236365	0.273441	0.139509	12.34146	0.281631
LY_3_1.26 4828_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Psychrobacter; s__Psychrobacter pasteurii	multidrug	mexT	0.044975	0.076675	0.231589	0.1609	0	0	0.065334	0.088491	0.007399	0.048761	0.228325	0.068145	0.039776	0.006605	0.063279	0.065706
TA_3_1.2 92611_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia	multidrug	mdtK	0.007522	0.025294	0.019451	0.014101	0	0	0.017042	0	0	0	0.229316	0.004707	0	0.009953	0.023929	0.005395

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
ZZ_2_1.24 6493_2	k__NA; p__NA; c__NA; o__NA; f__NA; g__NA; s__uncultured organism	tetracycline	tetW	0	0	0	0	0	0	0	0	0	0	0	0	0	0.165482	0.139739	0
QD_2_1.3 95528_3	k__Bacteria; p__Actinobacteria; c__Actinomycetia; o__Corynebacteriales; f__Corynebacteriaceae; g__Corynebacterium; s__Corynebacterium glutamicum	tetracycline	tetZ	0.008491	0.429875	1.329203	1.728659	0.038967	0.081362	0.330708	0.133698	0.479078	0.365854	1.640508	1.04621	0.667369	0.024993	0.182754	0.449009
DZ_2_1.1 01208_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	adeJ	0	0	0.065305	0.018194	0	0	0	0.018869	0.019425	0	0	0	0.08762	0	0	0
J_2_1.303 614_8	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales; f__Clostridiaceae; g__Clostridium; s__Clostridium sp. SN20	macrolide- lincosamide- streptogrami n	vatB	0.04194	0.112728	0.034314	0.014717	0.15375	0.03042	0.074879	0.042406	0.028507	0.01399	0	0.030656	0.245985	0.057115	0.045373	0.016508
TA_3_1.2 74882_1	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Fredinandcohnia; s__Fredinandcohnia aciditolerans	macrolide- lincosamide- streptogrami n	ermG	0	0	0	0	0	0	0	0	0	0	0.039401	0	0	0	0	0
ZB_2_1.10 4482_2	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales	bacitracin	bacA	0	0.011828	0.060124	0	0	0.018073	0.021184	0.134093	0.019248	0.117092	0	0.011224	0.02552	0.025943	0.312427	0.020518
WH_1_1.4 27849_1	k__Bacteria; p__Firmicutes	vancomycin	vanB	0.010549	0	0	0	0.00711	0.008804	0.023488	0.006797	0.009041	0	0.036029	0.009198	0.159444	0	0	0.019401
WH_1_1.4 27849_2	k__Bacteria; p__Firmicutes	vancomycin	vanH	0.038179	0.022587	0	0	0.015708	0	0.02188	0	0	0.0098	0.069921	0	0.128196	0	0	0
QD_2_1.3 25012_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	mexT	0	0	0	0.20744	0	0	0	0	0.146689	0	0	0	0.277179	0	0	0

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
DY_2_1.8 2798_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales; f__Cellvibrionaceae; g__Cellvibrio; s__Cellvibrio mixtus	multidrug	mexD	0	0.150365	0	0	0	0	0	0	0	0	0	0	0	0	0	0
WH_2_1.9 0264_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	mexB	0	0	0	0	0	0	0	0	0	0	0	0	0.148957	0	0	0
ZB_1_1.38 3066_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia; s__Escherichia coli	macrolide- lincosamide- streptogrami n	ermB	0.129121	2.791925	0.929329	1.351609	1.658996	1.67902	1.628047	2.270782	3.575923	0.647028	3.947657	1.699199	4.52607	2.36388	2.642659	0.823777
QD_2_1.4 49153_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	adeJ	0	0	0.042589	0	0	0	0	0	0.226568	0	0	0	0.069062	0	0	0
TA_2_1.4 97377_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacterales; f__Enterobacteriaceae	trimethoprim	dfrA17	0.076865	0.45839	0.2309	1.158014	0.042263	0.04886	0.285005	0.130827	0.165154	0.360294	0.672958	0.221907	1.961494	0.119125	0.103202	0.248927
DZ_3_1.1 4281_1	k__Bacteria; p__Bacteroidetes	macrolide- lincosamide- streptogrami n	ermF	0	0	0.691575	0	0	0	0	0	0	0	0	0	0	0	0	0
ZB_1_1.31 3233_3	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales	macrolide- lincosamide- streptogrami n	vatE	2.141857	50.79241	3.104766	9.193367	6.2832	24.62106	36.02201	11.2067	4.802293	3.774016	22.75901	60.09503	25.7663	23.78243	10.03533	2.125309
WH_2_1.2 3994_2	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Weeksellaceae; g__Empedobacter; s__Empedobacter falsenii	beta-lactam	metallo- beta- lactamase	0	0	0	0.066398	0	0	0	0	0	0	0	0	0.097721	0	0	0

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
RZ_3_1.32 435_4	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria	multidrug	qacEdelta 1	0.303299	9.220467	11.96156	11.86268	0.947	0.863615	3.046945	1.992744	2.532668	5.758015	9.297946	4.207206	8.819809	1.464588	0.83456	6.160072
HZ_3_1.2 43725_1	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Myroides	beta-lactam	MUS-1	0	0	0	0.102017	0	0	0	0	0	0.013381	0	0	0	0	0	0
HZ_3_1.3 81468_2	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus; s__Enterococcus asini	multidrug	multidrug _transport er	0	0	0	0.205558	0	0	0	0	0	0.0315	0	0.02993	0	0	0	0
DZ_1_1.2 31770_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia; s__Escherichia coli	aminoglycosi de	aadA	0.016023	0.24461	0.256996	0.550434	0.008636	0.133582	0.107153	0.030657	0.209346	0.308659	0.217347	0.089877	1.100124	0.030619	0.050537	0.249381
TA_1_1.1 06179_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; s__Pseudomonas aeruginosa	aminoglycosi de	aadA	0	0.119763	0.155248	0.017545	0	0.008583	0.009716	0.025676	0.017085	0.129099	0.224926	0.03346	0.04058	0	0.043453	0.018932
RZ_2_1.49 161_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria	aminoglycosi de	aac6-l	0.024845	0.491496	0.449538	0.872597	0.058977	0.014314	0.081162	0.139864	0.142864	0.392472	0.144108	0.306233	0.421025	0.030823	0.054567	0.313528
ZB_3_1.40 5409_1	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae	tetracycline	tetS	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.626904	0
HZ_3_1.1 76079_2	k__Bacteria; p__Firmicutes	tetracycline	tetP	0.016464	0	0.459711	0.120018	0	0	0	0.010694	0.027554	0.041925	0.016045	0.010455	0.147841	0.004937	0.094578	0.005927
TA_1_1.1 10627_3	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae; g__Staphylococcus	bacitracin	bacA	0	0	0.020375	0.043305	0	0	0	0	0.008878	0	0.207763	0.069662	0	0	0	0.029591

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
RZ_2_1.49 2009_1	k__Bacteria; p__Firmicutes; c__Erysipelotrichia; o__Erysipelotrichales; f__Coprobacillaceae; g__Coprobacillus	tetracycline	tet32	0.252692	0.054228	0.310063	0.213956	0	0.116618	0.225372	0.023845	0.3512	0.542589	0.168756	0	0.046408	0.068961	0.028911	0
WH_1_1.3 11742_3	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Streptococcus; s__Streptococcus agalactiae	vancomycin	vanW	0.015284	0	0	0.009487	0.172142	0.009463	0.045822	0.017334	0.029061	0.029731	0	0.011715	0.338567	0.02018	0.012065	0.010709
WH_3_1.4 20078_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae	aminoglycoside	ant2-I	0.078768	0.510278	0.71178	0.608973	0.03524	0.113887	0.063617	0.107238	0.130078	0.100553	0.420694	0.432287	0.518288	0.013176	0.053359	0.426988
ZZ_1_1.11 8488_6	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Limosilactobacillus; s__Limosilactobacillus mucosae	bacitracin	bacA	0	0.039469	0.010927	0.009952	0.023326	0.120321	0	0.089909	0.02791	0.017653	0.084293	0.009032	0.105454	0.031602	0.012549	0.193659
BZ_1_1.20 5165_18	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Streptococcus; s__Streptococcus agalactiae	vancomycin	vanG	0.336613	0.025108	0.022891	0.014087	0.182276	0.027453	0.042567	0.022766	0.006912	0.006086	0.028442	0	0.156571	0	0.008516	0.00791
LY_3_1.62 0973_1	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales; f__Clostridiaceae; g__Clostridium	bacitracin	bacA	0	0	0	0	0	0	0	0.391457	0	0	0	0	0	0	0	0
TA_3_1.6 797_3	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae; g__Escherichia	multidrug	mdtN	0.011015	0.035612	0.006772	0.028857	0.005861	0	0.006229	0	0	0	0.269173	0	0	0.008036	0.034887	0.037613

[illegible]

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
WH_3_1.2 30898_1	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales; f__Oscillospiraceae; g__Ruminococcus; s__Ruminococcus bromii	vancomycin	vanW	0.063398	0.168746	0.081866	0	0.146326	0.078298	0	0	0	0	0	0.164124	0.316695	0.16425	0.070084	0
TA_2_1.3 60012_1	k__Bacteria; p__Firmicutes; c__Bacilli	macrolide- lincosamide- streptogramin	lsa	0	0	0.473076	0	0	0	0	0	0	0.225331	0.223786	0	0.210317	0	0	0
WH_2_1.2 66091_7	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	mexT	0	0	0.017113	0.457597	0	0.007505	0.165087	0	0.361175	0.128596	0.439736	0	1.425432	0	0	0
ZB_3_1.57 831_2	k__Bacteria; p__Firmicutes	macrolide- lincosamide- streptogramin	ermTR	0	0	0	0	0	0	0	0	0.05443	0	0.098004	0.057942	0.048604	0.028181	0.081172	0.053254
TA_1_1.2 32481_1	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae; g__Staphylococcus	macrolide- lincosamide- streptogramin	msrA	0	0.00578	0.035869	0.03031	0	0	0.003923	0.007841	0.013592	0.004491	0.179039	0.034677	0	0.005077	0	0.034249
WF_2_1.3 40290_1	k__Bacteria; p__Firmicutes	macrolide- lincosamide- streptogramin	mphB	0.528525	0.049291	0.719097	0.832109	0.113258	0.892854	0.590958	0.516323	0.47415	0.220526	0.560317	0.229864	0.575009	0.650253	0.332526	0.754067
TA_3_1.1 81660_21	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia	multidrug	mdtG	0.008709	0.035321	0.011779	0.022858	0.004755	0	0	0.010023	0	0	0.178512	0.016335	0	0.005144	0.013832	0
WF_3_1.1 79423_5	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae; g__Staphylococcus	macrolide- lincosamide- streptogramin	vgaA	0	0.007997	0.379702	0.048411	0.010121	0	0.020095	0.007179	0.008279	0	0.089843	0.16677	0.045859	0	0.035998	0.052305

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
QD_2_1.2 05788_4	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter; s__Acinetobacter cumulans	tetracycline	tetY	0.010177	0.010212	0.023365	0.484539	0	0	0.035665	0.065436	0.481154	0.242876	0.233752	0.014952	1.058431	0	0	0.033127
RZ_2_1.35 4360_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia; s__Escherichia coli	multidrug	mdtC	0.03875	0.067031	0.038714	0.77148	0	0.10895	0.389348	0.067956	0.059979	0.303333	0.790088	0	0.639478	0.17515	0.020262	0.09578
LC_1_1.30 351_1	k__Bacteria; p__Actinobacteria; c__Actinomycetia; o__Bifidobacteriales; f__Bifidobacteriaceae; g__Bifidobacterium; s__Bifidobacterium longum	tetracycline	tetQ	80.23123	46.98675	44.01149	35.29867	55.04067	46.75414	48.13937	75.36013	36.3991	38.88741	28.05353	42.69718	29.97071	63.11381	28.11853	106.5932
TA_3_1.1 35351_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia	multidrug	multidrug _transport er	0.010202	0.013803	0.012503	0	0	0	0	0	0	0	0.134088	0	0	0	0.01597	0.014119
HZ_3_1.3 01483_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria	beta-lactam	OXA-1	0.152856	0.231729	0.394743	1.483973	0.067285	0.017926	0.613037	0.486021	0.200151	0.214699	0.244211	0.132628	0.64247	0.133354	0.023148	0.197628
YT_3_1.13 2151_4	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales	macrolide- lincosamide- streptogrami n	ermG	47.28344	32.42256	23.03868	36.17528	40.63301	43.62054	40.23453	54.83907	40.68686	26.25994	28.38466	26.89245	35.32144	64.15509	25.48478	59.80415
DY_1_1.1 39418_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia; s__Escherichia coli	beta-lactam	class_C_b eta- lactamase	0.325018	0.452509	0.173972	3.627784	0.10322	0.140554	2.806823	0.201172	0.159662	1.985676	3.544657	0.229675	2.556311	1.410356	0.069655	0.723958

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
WH_2_1.2 13790_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	mexT	0	0	0	0	0	0	0	0	0	0	0	0	0.188243	0	0	0
YT_3_1.27 4490_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Aeromonadales; f__Succinivibrionaceae	unclassified	cAMP- regulatory _protein	0	0	0	0.11552	0	0	0	0.198278	0.106969	0	0	0	0.103553	0.101844	0	0.577794
TA_3_1.3 8069_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria ; o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia; s__Escherichia albertii	multidrug	mdtG	0	0	0.034559	0	0	0	0.028279	0	0	0.065245	0.360361	0	0	0	0	0
TA_1_1.2 17258_1	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae; g__Staphylococcus	multidrug	multidrug _ABC_tran sporter	0	0	0.005972	0	0	0	0	0	0	0	0.112701	0.012134	0	0	0	0.006934
WF_2_1.1 14998_1	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Limosilactobacillus; s__Limosilactobacillus reuteri	aminoglycosi de	aad9	0.338328	5.992998	7.135702	6.592649	0.996642	0.27932	3.096758	1.023891	4.246897	10.24906	3.327284	5.985538	4.325394	0.239727	18.92395	0.429002
DZ_2_1.2 3274_1	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales; f__Peptococcaceae; g__Candidatus Formimonas; s__Candidatus Formimonas warabiya*	macrolide- lincosamide- streptogrami n	mefA	0	0	0.175427	0.053525	0	0	0	0.034512	0.023177	0.02338	0	0	0.010642	0	0.014195	0.012573

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
QD_3_1.1 875_1	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus; s__Enterococcus faecium	unclassified	antibiotic_ resistance_ rRNA_ad enine_me thyltransf erase	2.568128	1.674083	3.015741	2.146851	0.534153	0.205484	1.577747	0.11026	0.932204	3.470473	1.260826	2.835835	0.725513	0.299721	0.385255	0.631354
ZZ_3_1.93 473_1	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales; f__Oscillospiraceae; g__Faecalibacterium; s__Faecalibacterium sp. OF04-11AC	macrolide- lincosamide- streptogrami n	vatB	0.170972	0	0	0	0	0.550432	0.166689	0	0	0.171087	0.189558	0	0	0	0	0.62785
DZ_2_1.5 203_3	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales	vancomycin	vanR	0	0	0.197047	0	0	0	0	0	0	0	0	0	0.011886	0	0	0
HZ_2_1.2 32612_1	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales	macrolide- lincosamide- streptogrami n	ermF	96.18705	80.12985	98.65978	62.72627	100.9282	87.48521	92.29438	118.149	57.56572	67.6866	52.18685	92.3598	70.33656	118.7855	41.07386	145.6502
QD_3_1.7 2454_1	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales; f__Clostridiaceae; g__Clostridium	bacitracin	bacA	0	0	0	0	0.015004	0	0	0	0.101755	0	0	0	0.018994	0	0.052318	0
WH_1_1.4 09118_1	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae; g__Staphylococcus	multidrug	norA	0	0	0.009217	0.023494	0.013463	0	0	0	0.008048	0	0.040687	0.007862	0.093898	0	0	0.016178
TA_2_1.1 26198_5	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Planococcaceae; g__Metalysinibacillus; s__Metalysinibacillus jejuensis	bacitracin	bacA	0.01516	0	1.74309	0.03774	0	0	0.030657	0.026942	0.978871	0.077687	0.185441	0.110017	0.188161	0.045042	0.383962	0.053255
HZ_3_1.8 0883_1	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus; s__Enterococcus hirae	multidrug	EmrB- QacA_fam ily_major_ facilitator _transport er	0	0	0.009965	0.100466	0	0	0	0	0.010653	0.021005	0.010424	0	0	0	0	0.020781

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
J_1_1.383 363_1	k__Bacteria; p__Firmicutes	vancomycin	vanW	0	0	0	0	0.107357	0	0	0	0	0	0	0	0.076206	0	0	0
DY_2_1.3 46591_1	k__Bacteria; p__Proteobacteria	chloramphenicol	floR	0	0.141157	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DY_1_1.1 33438_6	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacterales; f__Enterobacteriaceae	multidrug	emrD	0.304863	0.324693	0.144659	3.428739	0.096186	0.151715	2.751132	0.158262	0.136243	1.750992	3.208995	0.184444	2.51318	1.000193	0.057957	0.678658
QD_3_1.5 53759_2	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales	bacitracin	bacA	0.011451	0.015216	0	0	0.098018	0	0.032323	0.01479	0.069746	0.039395	0	0.017021	0.013341	0	0.057176	0
BZ_1_1.20 5165_14	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales; f__Oscillospiraceae; g__NA; s__[Eubacterium] siraeum	vancomycin	vanR	0.554639	0.012742	0.014832	0.03653	0.241138	0	0.133879	0.019634	0	0.011372	0.05168	0	0.106338	0.011734	0	0
DY_2_1.2 60109_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria	chloramphenicol	floR	0.040697	0.170619	0.053829	0	0	0	0	0	0	0.074822	0	0	0	0	0	0
YT_1_1.19 0058_7	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia; s__Escherichia coli	aminoglycoside	aph3-l	0.449905	1.507634	2.687206	6.076765	0.37674	0.284464	1.434572	0.577749	0.931604	2.068696	2.79554	0.785743	3.699336	0.554988	0.173686	1.120726
WH_2_1.2 15386_1	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales	bacitracin	bacA	0	0	0	0.059829	0	0	0	0	0	0.030382	0.102615	0	0.238327	0	0	0
HZ_3_1.4 02263_2	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae; g__Staphylococcus	unclassified	truncated _putative _response _regulator _ArlR	0	0	0.078027	0.034459	0.034386	0	0	0	0	0	0.038274	0	0.078102	0	0	0
TA_3_1.3 7400_6	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia	multidrug	multidrug _transport er	0.010029	0.03735	0.018215	0.009194	0.004512	0	0.01684	0.00424	0.007249	0.003738	0.266315	0.01733	0	0.008914	0.013816	0.00787

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
TA_3_1.1 44733_8	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia	multidrug	mdtF	0.014393	0.0208	0.009621	0.007411	0.006112	0	0.003268	0.001413	0.001904	0	0.198821	0.017174	0	0.018672	0.004605	0.01738
HZ_3_1.2 3077_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria	beta-lactam	VEB-6	0	0	0.039842	0.216544	0	0	0.019432	0.094146	0.008819	0	0	0.025095	0.197407	0	0	0.037767
ZB_2_1.38 010_4	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Streptococcus; s__Streptococcus suis	macrolide- lincosamide- streptogrami n	ermT	2.824255	34.34481	6.017352	2.078741	17.60644	14.10732	36.75902	5.544286	3.435873	2.746582	2.192679	20.45507	2.536072	35.32643	4.477402	0.703915
ZB_1_1.22 9090_1	k__Bacteria	macrolide- lincosamide- streptogrami n	mefA	0	0.111907	0.238995	0	0	0.162748	0	0.145826	0.154549	0	0	0	0	0	0	0
ZB_1_1.31 6188_1	k__Bacteria	tetracycline	tetracyclin e_resistan ce_protei n	0.149622	0.134757	0.13517	0.082439	0.197072	0.139234	0.099218	0.171111	0.088231	0.038304	0.21919	0.103822	0.042981	0.086791	0.078189	0.073841
YT_1_1.27 0548_2	k__Bacteria	chlorampheni col	cat_chloram phenicol_ acetyltra nsferase	0.091545	0.41306	1.568938	1.554768	0.477635	0.459605	0.636089	0.464891	0.594415	0.413883	0.414917	2.468101	0.344598	1.432139	1.463854	0.212167
YT_1_1.35 3064_6	k__Bacteria	multidrug	emrA	0.309208	0.296308	0.178399	3.177676	0.098036	0.106622	2.472271	0.174433	0.14315	1.665589	3.277933	0.182807	2.194301	0.92381	0.016392	0.657593
YT_3_1.41 9007_1	k__Bacteria	beta-lactam	ROB-1	0.150007	0.05946	0.015821	0.08751	0.082286	0	0.012419	0.099835	0.028059	0.02559	0	0.016625	0	0.107437	0.01847	0.095989
YT_2_1.46 6938_4	k__Bacteria	tetracycline	tetX2	0	0.426405	0.261941	0.711034	1.82342	0.262812	0.278485	1.220037	0	0.669602	0.12825	0.190594	0.210821	1.652438	0.277503	1.05763
TA_2_1.2 17316_1	k__Bacteria	chlorampheni col	cat_chloram phenicol_ acetyltra nsferase	0	0.114455	0.805697	0.267426	0.847253	0	0	0.08246	0.100932	0.026804	0.55572	0.190496	0.118597	0	0.175473	0.182419
TA_2_1.2 58516_1	k__Bacteria	beta-lactam	OXA-10	0	0.010587	0.148955	0.154806	0	0	0.040632	0.069206	0	0.051761	0.04303	0.011	0.166974	0.033739	0	0.044833
TA_2_1.2 77408_1	k__Bacteria	tetracycline	tetX2	5.703887	6.472079	5.897838	8.062233	4.933484	4.019274	4.089035	8.323804	4.11681	3.536593	3.030723	3.055082	4.4063	5.746115	2.414126	5.844484

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
TA_2_1.3 27749_1	k__Bacteria	aminoglycoside	aadE	0	0	0.04113	0.032053	0	0	0	0	0	0	0.0417	0	0	0	0.027857	0
ZB_3_1.25 5882_2	k__Bacteria	vancomycin	vanS	0.083475	0.380481	2.852027	1.055589	0	0	0.226627	0.026219	1.126802	0.348336	0.631888	0.869254	0.354201	0	0.384151	0.055507
ZB_3_1.37 8667_1	k__Bacteria	aminoglycoside	aadA	0.034401	0.086719	0.317501	0.149414	0.015064	0.066338	0.013941	0.360143	0.054727	0.0295	0.086924	0	1.491831	0	0.186531	0.201878
ZB_3_1.38 9856_5	k__Bacteria	macrolide-lincosamide-streptogramin	lnuB	2.8153	3.478649	18.84589	7.076736	2.002672	5.56301	5.777255	2.286407	10.89518	6.61821	14.54387	5.590946	4.728312	3.602075	9.234782	5.377434
LC_1_1.26 6010_3	k__Bacteria	tetracycline	tet44	9.728405	15.68336	9.213858	17.7469	17.65909	18.60671	17.6508	12.72837	19.45698	9.399143	15.74586	16.9526	23.60503	17.90306	15.48441	11.98155
LC_1_1.31 4362_2	k__Bacteria	multidrug	emrB	0.208066	0.309552	0.14504	2.59904	0.093104	0.150436	2.245141	0.170938	0.131435	1.358324	2.91391	0.184747	1.972988	1.121995	0.042667	0.550626
LC_1_1.44 6053_12	k__Bacteria	multidrug	mdtH	0.194956	0.164369	0.077447	2.304771	0.075115	0.102009	2.01354	0.127024	0.089682	1.235103	2.329119	0.122576	1.876649	1.005466	0.036925	0.401289
LC_1_1.44 6752_2	k__Bacteria	aminoglycoside	aac6-I	1.40703	2.296422	2.012119	0.870412	3.453595	0.390098	1.136528	0.790518	0.593053	0.431016	0.508266	1.074617	1.015213	0.587326	0.536717	0.625416
LC_1_1.46 5964_3	k__Bacteria	tetracycline	tetH	0.200758	0.161085	0.535471	0	0.2333	0	0	0	0	0.104308	0.489332	0.104909	0.088403	0.12341	0.339499	0
LC_3_1.41 7820_2	k__Bacteria	aminoglycoside	bifunctional_aminoglycoside_N-acetyltransferase_and_aminoglycoside_phosphotransferase	0.917251	2.169807	3.316169	0.760371	3.872089	0.911107	1.248535	0.812007	0.864997	0.609109	0.273791	0.949443	4.566445	0.856382	0.818917	1.78253
LC_3_1.50 4636_1	k__Bacteria	aminoglycoside	aad9	0.008865	0.014124	0.316519	0.819084	0.048189	0	0.214581	0.067681	0.05609	2.074078	0.173307	0.158814	0.063861	0.020979	0.306288	0
WF_1_1.4 06733_2	k__Bacteria	bacitracin	bacA	0	0	0.052376	0.058415	0	0.08367	0	0	0.007872	0.08395	0	0.199665	0	0.007245	1.069579	0
WF_1_1.5 00520_1	k__Bacteria	tetracycline	tetL	4.465391	22.23777	33.19539	17.69275	16.75838	18.73088	25.95615	7.386306	13.68126	6.827083	3.731206	29.3015	2.524821	8.530718	34.93315	5.606245
TA_2_1.4 56829_1	k__Bacteria	chloramphenicol	catB	0	0	0.131668	0	0	0.072905	0	0	0	0.068866	0.217626	0	0	0	0	0.066851
ZB_3_1.15 4163_1	k__Bacteria	tetracycline	tetW	6.860528	9.460511	7.390777	9.791767	7.167162	9.873163	8.78231	5.143348	6.467193	5.57666	4.212148	8.350494	7.422156	5.352471	7.384762	12.5521

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
TA_1_1.3 41581_1	k__Bacteria	multidrug	multidrug_ABC_transporter	0.005441	0	0.031938	0.047413	0	0	0	0	0.012951	0	0.14048	0.020386	0	0	0.009575	0.015507
TA_1_1.3 61418_3	k__Bacteria	multidrug	mdfA	0.263426	0.255114	0.207359	3.031678	0.050337	0.12736	2.471463	0.13612	0.14182	1.468929	2.975387	0.175724	2.285196	1.118562	0.028309	0.641184
DY_1_1.5 06095_3	k__Bacteria	multidrug	acrA	0.28391	0.330812	0.264125	3.462746	0.091367	0.191671	2.8518	0.15308	0.160375	1.802262	3.834639	0.170601	2.577324	1.215452	0.022347	0.706192
RZ_2_1.27 0447_9	k__Bacteria	tetracycline	tetB	0.159978	0.071455	0.079848	1.017412	0.157751	0.078544	0.50816	0.062243	0.099162	1.312954	0.848139	0.021851	0.417433	0.327368	0.041628	0.308778
RZ_2_1.28 3885_1	k__Bacteria	chloramphenicol	floR	0.077339	0.371228	0.090365	0.046692	0.126	0.064547	0.018061	0.028699	0.014602	0.098231	0	0.018981	0.104153	0.045275	0	0.085034
RZ_2_1.28 9863_1	k__Bacteria	beta-lactam	NPS-1	0	0.017793	0	0.014017	0	0	0	0	0	0.094867	0	0	0.053767	0	0	0
BZ_1_1.33 0760_1	k__Bacteria	tetracycline	tetX1	1.391455	0.30436	0.741552	0.642723	1.747488	0.775589	1.038555	0.655234	1.959735	0.48484	0.19577	1.789603	0.597825	1.10173	0.197875	1.056246
DZ_3_1.2 33882_2	k__Bacteria	beta-lactam	OXA-2	0.104237	0.13664	0.7676	0.196823	0.015993	0.037837	0	0.007363	0.018053	0.077108	0.125464	0.039898	0.061422	0.067668	0.02461	0.202187
DZ_3_1.3 29151_1	k__Bacteria	multidrug	norA	0	0	0.099187	0	0	0.017771	0	0	0	0	0	0	0	0	0	0
DZ_3_1.3 68523_1	k__Bacteria	aminoglycoside	aph3-I	0	0.012394	0.430738	0.028622	0	0	0	0	0	0.039866	0	0.019184	0.020871	0	0	0.032306
QD_2_1.4 95585_3	k__Bacteria	aminoglycoside	aadE	17.86524	28.71731	23.11219	24.35055	27.43674	15.98935	30.61474	14.52813	16.06177	13.22984	12.9633	22.1701	25.76915	14.09496	14.14506	16.94309
YT_1_1.21 412_2	k__Bacteria	tetracycline	tetW	0	0	0	0.08926	0	0	0	0	0	0	0	0	0	0.106417	0	0
YT_1_1.54 671_4	k__Bacteria	unclassified	transcriptional_regulatory_protein_CpxR_cpxR	0.392296	0.493978	0.210581	4.966603	0.129849	0.192227	3.984587	0.253686	0.196921	2.312526	5.208242	0.249557	3.114237	1.776097	0.031477	1.059836
YT_1_1.11 4569_6	k__Bacteria	multidrug	mdtE	0.261198	0.429	0.18124	3.682164	0.074688	0.180895	2.790403	0.204274	0.118504	1.852007	3.357623	0.233067	2.482163	1.245941	0.023258	0.789886
WH_2_1.3 16074_7	k__Bacteria	beta-lactam	OXA-360	0	0	0	0.356924	0.150089	0	0	0	0	0	2.657295	0	1.355205	0	0	0
WH_2_1.4 08065_3	k__Bacteria	macrolide-lincosamide-streptogramin	mphB	0.013161	0.010737	0.200336	0.073875	0.020716	0.008486	0	0	0.024682	0.025677	0.025225	0.032974	0.905774	0.009622	0	0.027848
WH_2_1.4 62308_2	k__Bacteria	aminoglycoside	rmtB	0	0	0	0	0	0	0	0	0	0	0	0	0.093299	0	0	0.011258
QD_2_1.3 27714_1	k__Bacteria	tetracycline	tetM	0	0.195022	0	0.109297	0	0	0.644043	4.06062	0.274125	0.507692	0.615398	3.601791	3.28629	4.776215	0	0

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
DY_2_1.2 22001_3	k__Bacteria	tetracycline	tetA	0.027638	0.263533	0.011147	0.059955	0.019499	0.039878	0.052282	0.13431	0.071768	0.026882	0.005998	0.142217	0.047324	0.018561	0.079098	0.177334
DY_2_1.2 79453_4	k__Bacteria	macrolide- lincosamide- streptogrami n	ermC	0.043215	0.501473	4.122328	1.377321	0.118133	0.24817	0.716962	0.183423	1.127745	0.801119	18.63555	2.246776	1.037421	0.212795	1.117949	0.54565
DY_2_1.2 86448_1	k__Bacteria	aminoglycosi de	aadA	0.007883	0.164634	0	0	0	0	0	0	0	0	0	0	0.009284	0	0	0
DY_2_1.4 05890_1	k__Bacteria	chlorampheni col	floR	0	0.293145	0.011316	0.012645	0	0	0	0	0	0	0	0	0.010859	0	0	0
DY_2_1.4 31058_1	k__Bacteria	tetracycline	tetD	0.006582	0.129441	0	0.008248	0	0	0	0	0.008462	0.017202	0	0	0	0	0.020983	0.084138
HZ_1_1.3 56127_1	k__Bacteria	tetracycline	tetW	0.228022	0.348913	0.189362	0.221613	0.107854	0.299445	0.156426	0.461521	1.041937	0.042314	0.388003	0.968548	1.243603	0.563875	0	0.157318
HZ_1_1.4 31301_2	k__Bacteria	kasugamycin	kasugamy cin_resista nce_prote in_ksgA	0.300366	0.300778	0.143906	3.0526	0.081877	0.08898	2.704094	0.125761	0.156493	1.44896	3.132129	0.19006	2.237447	1.074366	0.037546	0.573746
WF_1_1.2 0017_1	k__Bacteria	tetracycline	tetW	4.985398	23.66733	31.06665	17.49127	21.17717	17.16063	28.41429	4.49911	10.49712	4.661301	1.513416	30.74524	2.557585	6.975401	28.34137	6.272913
YT_2_1.38 052_1	k__Bacteria	tetracycline	tetQ	20.09212	18.96147	13.26779	14.39707	16.46171	15.09455	13.59052	22.3174	13.90886	9.145905	9.488632	15.38137	10.71806	20.59952	12.46636	25.40776
HZ_3_1.1 92412_2	k__Bacteria	chlorampheni col	catA	0.011125	0	0.016614	0.232432	0	0	0.112679	0	0	0.043094	0.029087	0	0.196173	0.032039	0	0.043854
HZ_3_1.1 95409_2	k__Bacteria	multidrug	qacG	0	0.081803	0.797639	0.33823	0.081314	0.094612	0	0.167745	0.430397	0	0.966708	0.573917	0.612393	0	0	0.185758
HZ_3_1.1 98611_1	k__Bacteria	multidrug	acrB	0	0.005383	0.008878	0.063331	0	0.004394	0.035773	0	0	0.017078	0.012836	0	0.072555	0.046797	0	0.003285
HZ_3_1.2 12865_2	k__Bacteria	aminoglycosi de	aph6-l	0	0.099064	0	0.234837	0	0	0.080577	0	0.155152	0	0.093425	0	0	0	0	0.061927
HZ_3_1.2 53421_2	k__Bacteria	chlorampheni col	catQ	0.072383	0	2.631266	0.48163	0.024292	0.028657	0.157348	0.039284	0.594725	0.172148	0.043499	0.138797	0.211487	0.081936	0.062898	0.076701
HZ_3_1.2 74915_1	k__Bacteria	aminoglycosi de	aph2-III	0.035919	0.164224	0.500881	0.195812	0.061379	0.173226	0.115392	0.032016	0.664586	0.289421	0.226515	0.124317	0.528951	0.410538	0.093255	0.054055
HZ_3_1.2 99343_1	k__Bacteria	multidrug	multidrug _transport er	0	0	0.029809	0.096481	0	0	0	0	0.014662	0	0.014724	0	0	0	0	0.028571
HZ_3_1.3 04962_2	k__Bacteria	tetracycline	tetC	0.238554	0.118712	0.141155	1.918921	0.178944	0.069355	0.979913	0.146446	0.054163	1.986576	1.674169	0.041246	0.663858	0.635587	0.069107	0.404734
HZ_3_1.3 53829_1	k__Bacteria	aminoglycosi de	aadE	0	0	0	0.07488	0	0	0	0	0	0.03709	0.053755	0.022115	0	0	0.064156	0

[illegible]

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
WF_3_1.2 16767_2	k__Bacteria	tetracycline	tetP	0.369532	0.403422	1.014855	0.798717	0.043113	0.259213	0.469053	0.615822	0.645948	0.476255	2.299026	0.913698	0.329708	0.253313	1.033675	0.970308
WF_3_1.2 25747_1	k__Bacteria	aminoglycoside	aadA	0	0.25312	0.081866	0.245946	0.07115	0	0.068528	0.077562	0	0	0.082971	0.379262	0.154568	0	0	0.161086
WF_3_1.2 46216_1	k__Bacteria	multidrug	multidrug_ABC_transporter	0	0.012466	0.013243	0.011284	0	0	0.020664	0	0.01147	0.010443	0.023745	0.105048	0	0	0	0.012737
HZ_2_1.2 67577_1	k__Bacteria	tetracycline	tetW	10.11249	10.39114	9.546645	14.50526	12.39168	15.16027	11.37746	10.24978	12.16055	8.628472	11.6025	11.80486	13.75846	8.891382	10.04667	10.23423
ZZ_1_1.38 8420_1	k__Bacteria	multidrug	acrB	0	0	0	0	0	0	0.091176	0	0	0.035087	0	0	0	0	0	0.102243
LC_1_1.48 9392_1	k__Bacteria	trimethoprim	dfrA15	0	0.413771	0.428598	0.393362	0	0	0.187793	0.107583	0.319999	0.55059	0.030739	0.386255	0.133242	0	0.137697	0.261646
QD_3_1.2 91453_1	k__Bacteria	chloramphenicol	catD	0	0.019107	0	0	0.054206	0.015704	0.03146	0.16288	0.105811	0.129544	0	0.079614	0.194268	0.014625	0.031021	0.170167
QD_3_1.3 10732_1	k__Bacteria	tetracycline	tetW	0	1.11609	1.087411	0.6232	0	0.50649	1.264216	0	0.538689	0	0	1.387916	0	0.062508	0.163532	0
WH_1_1.2 78758_3	k__Bacteria	tetracycline	tetX5	0.169261	0.14514	1.141243	2.126494	0.019151	0.038369	0.760197	0.156949	2.673737	1.267346	1.389078	0.26384	5.624791	0.013091	0.028992	0.256207
WH_1_1.3 47555_1	k__Bacteria	vancomycin	vanS	0	0.04045	0	0.018963	0	0.006179	0.00574	0.012967	0.006682	0	0.060417	0.006338	0.123645	0	0.017917	0
WH_1_1.3 47555_2	k__Bacteria	vancomycin	vanR	0.011035	0	0	0.013564	0.023687	0.056234	0.024887	0	0.014426	0.012795	0.028974	0	0.237347	0	0.036939	0
WH_1_1.4 14632_2	k__Bacteria	beta-lactam	mecl	0	0	0	0.063763	0	0	0	0	0.067862	0	0	0	0.211928	0	0	0
JN_1_1.32 7467_5	k__Bacteria	aminoglycoside	aadE	16.57173	35.23771	24.64026	32.14651	25.40986	38.39918	39.96664	29.88353	43.86237	16.1207	28.78266	39.222	43.34825	33.48498	41.83927	20.9386
JN_1_1.33 1757_1	k__Bacteria	tetracycline	tet44	0.019129	0.053337	0.096462	0	0	0.024087	0	0.019154	0.022925	0	0	0	0.023225	0	0.029947	0
JN_1_1.36 6419_1	k__Bacteria	macrolide-lincosamide-streptogramin	ermG	0	0.221198	0.869299	0.403457	0.357209	0.82065	0.857168	0.784045	0.880984	0.399532	0.205292	1.117399	0.798626	0.83973	0	0.439038
ZZ_1_1.47 32_1	k__Bacteria	aminoglycoside	aadE	0.072146	0.299074	0.235497	0.29039	0.263166	0.240147	0.340564	0.138852	0.417958	0.41787	0.379132	0.44567	0.257804	0.122482	0.322538	0.190799
ZZ_1_1.34 043_5	k__Bacteria	trimethoprim	dfrA12	0.402316	0.938121	0.328346	5.120638	0.068502	0.377868	4.467783	0.242033	0.228014	2.92534	6.148623	0.594762	5.228556	2.486857	0.091676	1.235474
WH_3_1.7 135_5	k__Bacteria	aminoglycoside	aph4-I	0.022211	0.172315	1.11546	0.570037	0.040525	0.064623	0.456425	0.081876	0.19376	0.178922	0.76753	0.154165	0.855369	0.019686	0.036138	0.262582
WH_3_1.7 135_7	k__Bacteria	aminoglycoside	aac3-IV	0.023928	0.189967	1.144651	0.788218	0.059731	0.102192	0.541156	0.071116	0.177906	0.113492	0.995694	0.122759	1.050632	0.021005	0.012554	0.300514
JN_2_1.36 5238_1	k__Bacteria	aminoglycoside	aph3-I	0.23772	1.429001	2.343999	5.253844	0.183279	0.388645	2.960972	0.876383	1.556026	1.921676	2.667648	0.769708	4.999972	1.484582	0.16078	1.37319

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
JN_2_1.420103_2	k__Bacteria	multidrug	mdtP	0.159918	0.205003	0.09105	1.909169	0.074948	0.151344	1.502114	0.096852	0.104908	0.993552	2.12435	0.111582	1.649426	0.614661	0.022046	0.382305
QD_1_1.34437_1	k__Bacteria	bleomycin	bleomycin_resistance_protein	0.371732	4.558848	3.378808	5.871635	0.751859	0.305952	2.774405	0.561472	5.502563	15.55285	2.194535	1.721789	3.249157	2.664546	9.764434	1.528167
QD_1_1.65089_1	k__Bacteria	tetracycline	tet32	0.015771	0.007348	0.013284	0.029275	0	0	0.005076	0.052441	0.085123	0.051804	0.005605	0.011543	0	0	0.02367	0.022862
JN_2_1.500035_3	k__Bacteria	multidrug	mdtG	0.186924	0.258875	0.114496	2.765181	0.054467	0.128936	2.303932	0.150637	0.119654	1.414087	2.797807	0.127557	1.968888	1.0096	0.028488	0.536124
HZ_3_1.4764_1	k__Bacteria	beta-lactam	NPS-1	0	0.019426	0.017914	0.154007	0	0	0	0	0	0.056163	0	0	0.044263	0	0	0
HZ_3_1.47187_1	k__Bacteria	tetracycline	tetT	0	0.19268	2.195749	0.910876	0.015343	0.242291	1.176879	0.018178	0.899997	7.084138	1.070316	0.782154	0.104216	0.074787	3.237544	0.115407
HZ_3_1.55841_1	k__Bacteria	beta-lactam	OXA-10	0.02407	0.102994	0	0.385897	0	0.010276	0.141155	0.0248	0	0.040506	0.045207	0.039945	0	0	0.041376	0.09462
HZ_3_1.89108_34	k__Bacteria	tetracycline	tetH	0.076308	0.068724	0.375601	1.388483	0.028725	0.005698	0.070213	0.572115	0.32336	0.076895	0.279534	0.177256	0.738414	0.010849	0.118612	0.171487
ZB_2_1.119174_2	k__Bacteria	tetracycline	tetO	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.172431	0
LY_1_1.412505_1	k__Bacteria	chloramphenicol	catD	0.269992	0.54278	0.161378	0.18665	0.067298	0.078596	0.160411	0.142673	0.134245	0.099078	0.242525	0.106339	0.106565	0.161332	0.055226	0.14785
DZ_2_1.103798_7	k__Bacteria	aminoglycoside	bifunctional_aminoglycoside_N-acetyltransferase_and_aminoglycoside_phosphotransferase	1.234059	4.140255	22.13024	7.754547	3.73733	3.616021	4.665716	1.634071	7.463118	50.56513	7.483707	5.522831	4.80948	3.061825	16.71451	3.012499
DZ_2_1.128704_3	k__Bacteria	aminoglycoside	aph2-II	1.380958	3.044604	2.09086	0.920524	3.134257	0.341582	1.256844	0.667413	0.662019	0.456597	0.658728	1.260559	1.19043	0.657399	0.33994	0.529688
DZ_2_1.144665_3	k__Bacteria	macrolide-lincosamide-streptogramin	ermF	0	0	0.470625	0	0	0.201991	0	0	0	0.175607	0	0.199388	0	0.227272	0	0
DZ_2_1.196269_1	k__Bacteria	aminoglycoside	aadE	0	0	0.186931	0.069094	0	0	0.020054	0.017899	0	0.018239	0	0	0	0	0	0.01928
DZ_2_1.278765_2	k__Bacteria	aminoglycoside	aad9	0	0	0.198922	0.030589	0	0.010603	0	0	0	0.149321	0.010622	0.09492	0	0	0.390148	0

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
QD_3_1.33080_1	k__Bacteria	tetracycline	tetracycline_resistance_protein	1.631862	1.850066	1.564456	2.640512	1.286994	1.909049	2.643075	1.048342	2.11779	1.330491	1.105811	1.795016	1.525944	1.444081	1.811774	2.222059
QD_3_1.142953_1	k__Bacteria	tetracycline	tet32	0.789276	0.650092	0.499514	0.736461	0.249481	1.428167	0.982658	0.458633	1.309037	0.379497	0.854408	0.656055	1.646638	0.696322	0.537823	0.543287
QD_3_1.148531_2	k__Bacteria	tetracycline	tetO	11.79597	11.41495	11.5928	11.5822	22.53441	14.95967	12.66856	13.48493	11.89518	9.632162	9.497037	13.49855	12.70925	12.67677	17.20301	13.59316
QD_3_1.160146_1	k__Bacteria	bacitracin	bacA	0.072397	0	0.093889	0.025646	0.412176	0.105738	0	0.349154	0.132508	0.97641	0	0.208284	0.048091	0.057146	0.931788	0.514402
LC_3_1.178463_3	k__Bacteria	macrolide-lincosamide-streptogramin	mefA	33.21277	15.42737	9.64102	9.959645	13.21082	17.39833	13.57496	21.50336	12.56341	13.43108	10.74098	14.10804	11.38183	23.62244	6.714787	22.59962
LC_3_1.191714_2	k__Bacteria	aminoglycoside	aadE	2.345457	5.518703	21.38023	8.692516	1.370529	4.377548	6.428285	2.611222	10.8207	22.18884	14.29847	9.383348	5.302322	3.788639	19.62844	4.472453
TA_2_1.96665_2	k__Bacteria	aminoglycoside	rmtF	0.090252	0.111015	0.075169	0.145066	0.030088	0.106328	0.096579	0.033542	0.158151	0.068883	0.21765	0.070722	0.031374	0.069203	0	0
WH_3_1.450889_1	k__Bacteria	trimethoprim	dfrA1	0.01372	0.06301	0.301519	0.624194	0.014678	0.017418	0.151684	0.192064	0.088156	0.106134	0.090109	0.33259	0.344424	0.016264	0.038406	0.358812
WH_2_1.6289_6	k__Bacteria	aminoglycoside	ant9-I	2.322102	5.836068	18.93531	7.985745	1.346891	4.301502	5.791126	2.492156	9.564651	22.25755	13.08553	6.284168	6.243271	2.790218	14.98017	3.868134
WH_2_1.42612_4	k__Bacteria	macrolide-lincosamide-streptogramin	ermC	0	0	1.921721	0.683363	0	0	0.126439	0	0.215956	0.470913	1.33507	0.112111	0.961392	0.253536	0.15274	0
WH_2_1.54063_11	k__Bacteria	aminoglycoside	aadA	0.043787	0.125162	0.164221	0.327964	0.015452	0.009395	0.069507	0.093405	0.03816	0	0.12185	0.193795	0.569747	0	0.012676	0.029144
WH_2_1.71813_1	k__Bacteria	multidrug	mdtK	0	0	0	0	0	0	0	0	0.066947	0	0	0	0.161226	0	0	0
WH_2_1.84160_4	k__Bacteria	chloramphenicol	chloramphenicol_exporter	0	0.013865	0.048189	0.2922	0	0.01077	0	0.005347	0.038576	0.04335	0.01054	0.010455	0.518351	0	0.007441	0.005927
WH_2_1.126969_3	k__Bacteria	trimethoprim	dfrA1	0.273511	1.190906	2.50083	15.2594	0.492235	0.056489	1.142266	1.235071	1.207424	1.362792	2.395699	0.530362	8.796038	0.239887	0.378164	1.000731
WH_2_1.167430_2	k__Bacteria	chloramphenicol	cmlA	0.155442	0.414344	0.314671	3.061119	0.043809	0.165716	2.085689	0.117709	0.187507	1.744513	3.157104	0.189766	2.418299	0.997717	0.059789	0.497116
LC_1_1.191335_1	k__Bacteria	tetracycline	tetQ	1.274518	0.478731	0.479588	1.044074	1.596474	0.635058	0.365334	1.385978	0.490441	0.563831	0.663219	0.563751	0.294595	1.189228	0.265347	0.276848
TA_1_1.36884_6	k__Bacteria	multidrug	mdtL	0.326233	0.42559	0.29559	3.547914	0.074314	0.230428	3.06056	0.242688	0.147121	1.933294	3.706048	0.302636	2.353697	1.418286	0.022793	0.690387

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TA_1_1.3 7010_3	k__Bacteria	macrolide-lincosamide-streptogramin	mefA	35.5081	16.07234	11.00761	10.02627	13.19358	16.59517	13.56428	20.80168	13.29634	13.07235	11.23601	15.73863	12.32192	25.21801	7.572542	22.48947
TA_1_1.6 8055_1	k__Bacteria	macrolide-lincosamide-streptogramin	lsa	0	0	0	0	0	0	0	0	0	0	0.186439	0	0	0	0	0
TA_1_1.1 68754_1	k__Bacteria	multidrug	multidrug_ABC_transporter	0	0.016804	0.035827	0.046205	0	0	0.014131	0	0.029828	0	0.146497	0.046681	0	0.018043	0	0.069553
TA_1_1.1 90872_1	k__Bacteria	aminoglycoside	ant9-I	0.058304	0.292734	1.652248	0.797373	0.107947	0.109391	0.153116	0.196137	0.329434	1.556527	0.927179	0.589212	0.556832	0.02249	0.98062	0.176652
QD_2_1.7 3865_12	k__Bacteria	tetracycline	tet39	0.01355	0.067629	0.384043	4.95413	0.023211	0.023352	0.136051	0.151786	3.28538	0.388972	0.986264	0.10229	3.133566	0.005369	0.022094	0.135207
LC_2_1.13 6158_3	k__Bacteria	beta-lactam	CTX-M-55	0.006987	0.019224	0.010187	0.043337	0	0.017926	0.687922	0	0.017756	0.018087	0	0.026123	0.049396	0	0	0
LC_2_1.15 9899_1	k__Bacteria	beta-lactam	CTX-M-14	0.0208	0.019224	0.010187	0.086674	0.029157	0.053777	0.173621	0	0.007735	0.179787	0.009222	0.008708	0.164655	0.024785	0	0
LC_2_1.19 6754_1	k__Bacteria	aminoglycoside	aac6-I	0.010202	0.026305	0.057689	0	0.022137	0	0.363203	0.043047	0.014726	0.07014	0.045954	0.015067	0.072924	0.10334	0	0
LC_2_1.21 0076_3	k__Bacteria	multidrug	mdtN	0.258612	0.351534	0.19833	2.809116	0.100683	0.162668	2.668712	0.175157	0.130612	1.625771	3.135446	0.20151	2.189409	1.126375	0	0.584424
DZ_3_1.4 107_3	k__Bacteria	tetracycline	tetA	0.23609	0.694503	0.422823	3.658255	0.04746	0.185517	3.574874	0.160062	0.141968	1.325933	3.047251	0.280004	2.809894	1.041942	0.087575	0.644321
DZ_3_1.5 006_2	k__Bacteria	multidrug	mexT	0	0	0.071654	0	0	0	0	0	0	0	0.032949	0	0.051146	0	0	0
DZ_3_1.8 4682_1	k__Bacteria	chloramphenicol	cat_chloramphenicol_acetyltransferase	0	0	0.127522	0.033999	0.016977	0.052142	0.038193	0.02298	0.035018	0.01734	0.190747	0.072058	0	0	0.039808	0.018591
DY_2_1.7 95_1	k__Bacteria	sulfonamide	sul1	0	0.366322	0.033921	0.055931	0	0	0.025982	0	0.030033	0.089838	0	0	0.028649	0	0	0.030778
DY_2_1.2 7721_1	k__Bacteria	tetracycline	tetO	19.54712	20.09701	20.9234	16.60832	33.72969	24.53551	20.24002	23.83481	21.73047	15.83991	14.22594	22.03634	20.2197	20.82524	26.70305	21.58155
DY_2_1.2 9007_1	k__Bacteria	tetracycline	tetM	3.001494	4.232336	3.395922	2.98421	5.09113	3.882798	2.759886	3.074751	2.684694	1.525006	2.997879	2.390064	3.306183	2.203763	4.535035	3.064398
DY_2_1.3 4088_3	k__Bacteria	tetracycline	tetG	0.064278	1.141168	0.236949	0.291993	0.03917	0.035531	0.054516	0.070513	0.04226	0.449939	0.052379	0.075763	0.456518	0.032453	0.043909	0.245892

gene_id	Taxonomy	ARG_ Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
DY_2_1.1 25027_1	k__Bacteria	macrolide- lincosamide- streptogrami n	ereA	0	0.061359	0	0	0	0	0	0	0.027363	0	0	0	0.024792	0	0	0
DY_2_1.1 30463_1	k__Bacteria	beta-lactam	GES-5	0	0.369865	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DY_2_1.1 39949_2	k__Bacteria	chlorampheni col	floR	0.020727	0.515326	0.156013	0.137011	0.009343	0.033122	0.077421	0.027079	0.01163	0.144998	0.011137	0.045213	0.114312	0	0.007837	0.042722
DY_2_1.1 53879_3	k__Bacteria	aminoglycosi de	bifunction al_aminog lycoside_ N- acetyltran sferase_a nd_amino glycoside_ phosphotr ansferase	0	0.374329	0	0	0	0	0	0	0.28667	0	0	0	0.479621	0	0	0
DY_2_1.1 56429_2	k__Bacteria	chlorampheni col	floR	0.038143	0.425727	0.042149	0.094066	0	0	0	0.044804	0.044396	0.044839	0	0	0	0	0	0.044964
DY_2_1.1 71467_2	k__Bacteria	aminoglycosi de	aadA	0	0.349537	0.011715	0	0	0	0	0	0	0	0.010359	0.010045	0	0	0	0
DY_2_1.1 93521_1	k__Bacteria	chlorampheni col	floR	0	0.196696	0.013782	0	0	0	0	0	0	0.012347	0	0	0	0	0	0
JN_1_1.17 5047_3	k__Bacteria	chlorampheni col	chloramp henicol_e xporter	6.989591	28.25536	28.74678	9.003731	26.90739	25.7326	34.95045	5.68931	6.585289	3.181599	9.690393	82.64516	26.95209	9.72158	2.823889	2.09978
JN_1_1.19 0355_3	k__Bacteria	chlorampheni col	cat_chlora mphenicol _acetyltra nsferase	16.45725	58.38479	31.22023	41.15366	26.70451	22.60976	41.58333	18.64283	35.74546	13.14419	28.74119	48.83326	35.66881	18.01712	25.13806	27.22074
WH_1_1.2 6536_2	k__Bacteria	aminoglycosi de	aadA	0.284739	2.37674	2.469172	5.669248	0.194192	0.438065	4.67849	0.399749	0.806156	3.568977	5.873693	0.918124	7.340775	1.602093	0.210716	1.769402
DZ_1_1.2 05547_1	k__Bacteria	macrolide- lincosamide- streptogrami n	ermB	0.274903	0.165025	0.1116	0	0.034667	0.041959	0.11009	0.069412	0.034014	0.037727	0.039401	0.037387	0.079719	0.150361	0	0.038219
DZ_1_1.2 33906_2	k__Bacteria	beta-lactam	CARB-8	0.074056	0.143766	0.445857	0.242715	0.187679	0	0.205034	0.190501	0.017725	0.056338	0.516432	0.310431	0.22915	0.007973	0.088408	0.124526
TA_3_1.6 6814_1	k__Bacteria	bacitracin	bcrA	0	0.012329	0.049154	0	0	0	0	0.00976	0	0	0.115214	0	0	0	0	0

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
TA_3_1.1 27815_2	k__Bacteria	chloramphenicol	cat_chloramphenicol_acetyltransferase	2.746011	8.302047	2.610464	6.672835	8.996083	3.730455	7.506466	4.6549	4.969842	4.38115	8.260951	5.577184	7.886527	2.153651	0	9.874799
TA_3_1.1 43492_1	k__Bacteria	multidrug	bicyclomycin-multidrug_efflux_protein_bcr	0.314594	0.349512	0.190034	3.08957	0.089201	0.12565	2.681674	0.14469	0.099716	1.834661	3.244282	0.174318	2.22005	1.251409	0.029038	0.688333
TA_3_1.1 71468_2	k__Bacteria	aminoglycoside	ant9-l	0.008476	0.287609	0.371532	0.116046	0.035943	0.075957	0.034039	0.019178	0.075067	0.020548	0.47592	2.03782	0.282484	0.012281	0.081132	0.16431
TA_3_1.1 96563_1	k__Bacteria	beta-lactam	TEM-1	0.535711	0.760125	0.527686	8.784975	0.424603	0.420495	6.016057	0.201007	0.362354	1.529175	3.475647	0.429539	4.581821	2.837867	0.033934	0.879751
JN_3_1.14 756_9	k__Bacteria	tetracycline	tetW	25.69794	52.80163	44.22244	48.43957	39.43481	43.54824	51.73255	23.88358	36.62597	18.63708	24.69805	53.8226	33.41547	27.45662	45.63072	31.09893
JN_3_1.32 912_1	k__Bacteria	tetracycline	tetracycline_resistance_protein	36.87175	48.4895	38.24133	47.5361	34.8376	41.3653	46.33167	31.45991	40.2929	22.00635	31.91112	43.31512	41.60713	28.09708	38.13811	44.27694
HZ_1_1.8 8083_2	k__Bacteria	unclassified	16S_rRNA_methylase	0.055754	0.154501	0.047835	0.386315	0.061854	0.014013	0.028424	0.01412	0	0	0.102232	0	12.15982	0.01602	0.017376	0
DY_3_1.2 294_1	k__Bacteria	tetracycline	tetW	0.176444	0.836598	0	0.660672	0.366812	0.432572	0.621385	0.607258	0.218133	0.193318	0.447572	0.47144	0.415251	0.210849	0.322192	1.26729
DY_3_1.6 9798_2	k__Bacteria	vancomycin	vanY	0.021204	0.171771	0	0.02609	0.022329	0.013524	0.015179	0	0	0	0.027536	0	0.08432	0.012579	0.017813	0
DY_3_1.8 2104_2	k__Bacteria	sulfonamide	sul3	0.377061	0.661913	0.530683	6.606125	0.195064	0.515197	5.756681	0.368814	0.333151	4.124455	8.048964	0.450991	5.502527	3.960613	0.115659	1.730963
HZ_3_1.4 08157_11	k__Bacteria	multidrug	adeJ	0.001409	0	0	3.025532	0	0	0.0016	0	0	0	0	0	0	0	0.002575	0.00204
HZ_3_1.4 10400_1	k__Bacteria	chloramphenicol	cat_chloramphenicol_acetyltransferase	0	0.029744	0.120146	0.155195	0	0	0.012941	0	0.099176	0	0.19445	0.120182	0.029116	0.013626	0.037127	0.045306
WF_3_1.8 6991_3	k__Bacteria	tetracycline	tetK	0	0.034388	0.430608	0.192461	0.04801	0.004763	0.02796	0.024216	0.086876	0.042835	2.362462	0.927851	0.18633	0.008835	0.026009	0.500203
ZZ_1_1.19 6949_1	k__Bacteria	tetracycline	tetW	0	0.201298	0.174417	0	0	0	0	0	0	0	0	0	0	0	0	0
DY_3_1.3 75115_2	k__Bacteria	tetracycline	tetW	33.74964	55.02554	31.36878	46.77191	34.06328	36.3795	36.41647	32.55071	31.82335	21.06233	24.50441	44.26098	33.44816	20.36794	25.02479	49.37622
HZ_2_1.4 6274_2	k__Bacteria	tetracycline	tetW	4.125184	5.011848	3.450509	4.887466	2.929456	4.592435	4.937409	2.27908	3.669624	2.509244	3.223687	3.900373	3.912106	2.910624	3.598597	4.600117

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
HZ_2_1.78082_1	k__Bacteria	tetracycline	tetW	3.526869	3.416389	1.396909	1.044297	2.702372	2.12601	5.609318	0.634049	4.712873	1.216545	3.353408	3.022318	1.720138	1.255003	3.039067	3.850701
DZ_1_1.47489_1	k__Bacteria	macrolide-lincosamide-streptogramin	ermC	0.146471	0.347479	3.689881	1.335441	0.218757	0.158888	0.390424	0.162386	0.380584	0.254773	12.62427	4.625372	1.996285	0.087826	0.183112	1.014717
ZZ_3_1.330421_14	k__Bacteria	bacitracin	bacA	0	0.011422	0	0	0	0	0	0	0.01855	0.032196	0	0.043309	0	0	0.785632	0.361791
WF_2_1.103862_1	k__Bacteria	tetracycline	tetA	0.078342	0.250048	0.118913	1.918939	0.04448	0.040143	1.821938	0.038308	0.120127	0.686296	1.737988	0.286528	1.343441	0.567838	0	0.247293
WF_2_1.260382_1	k__Bacteria	beta-lactam	class_A_beta-lactamase	0	0.010116	0.010725	0.036527	0.007907	0	0.008319	0.009391	0.025691	0	0.048396	0.107508	0.028639	0	0	0.031157
WF_2_1.267156_4	k__Bacteria	aminoglycoside	aph3-III	114.2488	296.0905	180.5675	141.2191	261.1703	124.8116	267.5832	95.45343	118.9442	81.871	84.13864	244.2229	233.074	134.1789	59.55052	135.9011
QD_1_1.226235_1	k__Bacteria	aminoglycoside	bifunctional_aminoglycoside_N-acetyltransferase_and_aminoglycoside_phosphotransferase	0	0	0	0	0	0	0	0	0.060891	0	0	0	0.035763	0	0	0
LY_3_1.463041_1	k__Bacteria	aminoglycoside	aadE	0.160514	0	0.449064	0.475575	0.041381	3.245948	0	0.076627	0.008157	0.191738	2.773084	0.10562	0.014928	0	1.485893	0.041013
WH_3_1.120153_1	k__Bacteria	aminoglycoside	aac6-I	8.141378	16.32096	27.71356	21.17368	24.60996	17.3012	12.05719	7.751109	6.562237	2.460522	6.076521	7.905066	20.16803	6.169152	5.803116	12.6423
J_3_1.35171_2	k__Bacteria	chloramphenicol	chloramphenicol_exporter	2.516466	8.051947	11.2209	18.95156	8.267357	3.970133	10.75654	3.443782	4.46083	4.93226	3.739411	12.41907	10.99747	3.571581	0.584145	3.621778
J_3_1.36000_1	k__Bacteria	tetracycline	tetX2	5.026321	3.053008	3.293665	4.589451	4.471594	3.178321	3.532948	5.716474	3.995675	2.536127	1.5717	2.751771	2.486368	5.46347	1.733202	3.607348
DY_3_1.107443_11	k__Bacteria	beta-lactam	OXA-85	4.314398	2.799393	0.35554	0.179434	0.243285	0.873803	0.151907	0.52825	1.270666	0.051033	0.276998	0.28292	1.489873	1.653374	0.115821	0.058033
DY_3_1.172650_2	k__Bacteria	chloramphenicol	cat_chloramphenicol_acetyltransferase	0.1194	0.335031	0.215112	0.781764	0.100091	0.130806	0.145822	0.041215	0.083747	0.042699	0.13545	0.265752	0.442211	0.151777	0.017803	0

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
LY_2_1.149988_1	k__Bacteria	tetracycline	tetM	0.737349	3.856237	10.83167	7.932688	0.779411	1.074	3.860537	1.833473	6.764941	3.651321	7.653554	21.20139	4.900512	1.377019	15.67777	2.016152
LY_2_1.238523_1	k__Bacteria	aminoglycoside	aadE	0.021353	0.074154	0.754467	0.581883	0.097668	0.03653	0.081824	0.264331	0.222719	0.194691	0.497526	0.073169	0.152119	0.01037	0.218437	0.087409
LY_2_1.254322_4	k__Bacteria	polymyxin	mcr-1	0.008915	0.044478	0.0408	0.003816	0.018547	0.038039	0.024763	0.132781	0.003984	0	0.007854	0.009524	0.011733	0.003564	0	0
LY_3_1.160787_3	k__Bacteria	tetracycline	tet44	0.412917	0.645879	0.380459	0.168462	0.064636	0.547084	0.316203	0.6903	0.352602	0.032549	0.279976	0.075378	0.281329	0.286953	2.052316	0.297081
J_2_1.222358_8	k__Bacteria	bacitracin	bacA	0.133361	0.011422	0.093841	0.019388	1.783192	0.008693	0.010213	0.201866	0.035865	0.320369	0	0.145493	0.130991	0.025045	0.118758	0.029995
J_2_1.250776_1	k__Bacteria	unclassified	sdiA	0.045495	0.100161	0.082701	1.667272	0.142905	0.076308	1.075118	0.094659	0.24688	0.805044	1.609823	0.121395	1.250126	0.705648	0.03495	0.229571
J_2_1.374715_3	k__Bacteria	aminoglycoside	aph2-II	3.760192	18.32266	8.30359	6.225894	9.212289	4.05245	5.867255	4.975595	7.217204	1.252402	3.50175	6.95447	10.23867	5.418097	4.125264	6.296078
YT_1_1.386301_2	k__Bacteria	multidrug	acrB	0.006281	0.017256	0.011198	0.077308	0.002134	0	0.025861	0	0.002782	0.012071	0.022563	0	0.084006	0.10149	0.003377	0.023305
ZZ_3_1.156972_1	k__Bacteria	tetracycline	tet44	2.265666	4.02946	2.9763	5.903555	0.844365	4.270591	3.744929	3.676246	5.115276	2.145618	4.825279	2.819139	3.112542	4.67607	6.300732	1.407095
RZ_2_1.7423_5	k__Bacteria	unclassified	cAMP-regulatory_protein	0.535474	0.769478	0.333337	5.605316	0.249675	0.336848	4.836873	0.234004	0.349615	3.177162	5.305988	0.324532	3.80015	2.115982	0.058604	1.239204
RZ_2_1.35456_4	k__Bacteria	macrolide-lincosamide-streptogramin	mphA	0.052905	0.065035	0.067905	0.058614	0.021515	0	1.107865	0	0.008733	0.162377	0.017244	0.092331	0.321023	0.53779	0.010492	0.036503
RZ_2_1.49161_4	k__Bacteria	chloramphenicol	catB	0.084477	0.839266	0.572363	0.813853	0.052659	0.030586	0.385524	0.274674	0.15401	0.474842	0.345398	0.134816	0.22869	0.048823	0.01994	0.741475
RZ_2_1.182431_1	k__Bacteria	trimethoprim	dfrA5	0	0.104359	0.033455	0.029365	0	0.030663	0.027318	0	0	0.189002	0.065595	0	0.086057	0.102935	0	0
BZ_2_1.637647_3	k__Bacteria	aminoglycoside	aadE	81.55349	67.24263	54.70319	59.60913	58.75821	50.86942	60.26821	42.45687	47.1715	29.11465	39.44662	60.09959	70.66497	57.18514	40.79201	46.0383
LC_2_1.49152_2	k__Bacteria	tetracycline	tetY	0	0.331646	0.045174	0.826529	0.009414	0	0.159684	0.018391	0.141791	0.099997	0.188534	0.011517	0.070732	0.016327	0	0.05344
LY_1_1.172199_1	k__Bacteria	tetracycline	tet32	0.250484	0.283635	0.278384	0.29082	0.208353	0.344395	0.24675	0.213874	0.329797	0.070835	0.203721	0.207562	0.17531	0.267793	0.158167	0.204909
JN_2_1.120405_1	k__Bacteria	chloramphenicol	catD	6.0763	16.19704	6.775164	9.638185	9.577639	6.674361	14.22527	4.216583	5.62295	2.647113	6.896165	15.25786	11.4517	6.76779	4.627447	3.688326
ZZ_2_1.4442_3	k__Bacteria	aminoglycoside	aadE	11.57176	31.29717	30.50721	18.01814	23.49217	16.32324	27.53731	10.4357	12.49247	13.08669	14.41936	22.83521	13.95735	15.40898	23.30128	13.24574
ZZ_2_1.10930_3	k__Bacteria	aminoglycoside	aph2-II	0.331342	0.669983	0.76854	0.13628	0.802497	0.168237	0.214522	0.222057	0.209056	0.495598	0.22212	0.132764	0.229914	0.114929	0.353388	0.353715
ZZ_2_1.156849_1	k__Bacteria	beta-lactam	ROB-1	0.045032	0.054866	0	0.07308	0.020361	0	0.046861	0.102728	0.024102	0.023269	0	0	0	0.06626	0	0.217051

gene_id	Taxonomy	ARG_Category	ARG	BZ	DY	DZ	HZ	J	JN	LC	LY	QD	RZ	TA	WF	WH	YT	ZB	ZZ
ZZ_2_1.23 1411_1	k__Bacteria	tetracycline	tetW	24.77823	32.03121	25.54041	31.71477	21.51968	25.53984	33.56557	21.6881	28.57008	15.62551	22.20012	26.16097	25.8944	18.96692	24.85112	33.53494
BZ_2_1.42 1826_4	k__Bacteria	tetracycline	tetD	0.205708	0	0.12444	2.378823	0.03618	0	1.090657	0.039892	0.076134	2.577326	2.79583	0.078572	0.599681	0.365283	0.181755	0.666176

gene_id	Taxonomy	ARG_Catego ry	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
HZ_3_1.20610_6	k__Bacteria; p__Actinobacteria; c__Actinomycetia; o__Corynebacteriales; f__Corynebacteriaceae; g__Corynebacterium	tetracycline	tetracycline_resistance_protein	0.012617	0.019867	0	1.278083	0	0.063844	0.153262	0.540523	1.292463	1.429177	0.086855	0.078365	0.038596	0	0	0	0.097529
ZZ_1_1.457364_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia	multidrug	emrD	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
QD_2_1.190721_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	adeJ	0	0	0	0	0	0	0.031434	0	0	0.050968	0	0	0	0	0	0	0
TA_1_1.131259_1	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae; g__Staphylococcus	multidrug	norA	0	0	0	0	0	0	0	0	0.077329	0	0	0	0	0	0	0	0
WF_3_1.3112_1	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus; s__Enterococcus aquimarinus	multidrug	EmrB-QacA_family_major_facilitator_transporter	0	0	0	0	0	0	0.91436	0	0	1.549123	0	0	0	0	0	0	0
DZ_1_1.18912_2	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales	aminoglycoside	ant9-I	47.69589	49.70566	48.98737	21.2279	35.12088	23.81293	20.60267	24.09253	38.32238	9.964439	39.57242	16.3386	37.5487	30.6403	33.20305	37.13524	37.85474
ZZ_3_1.112994_3	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria	aminoglycoside	aac6-II	0	0	0.068704	4.183031	0	0	0.273387	0.680378	0.373985	1.817354	0.139234	0	0.107589	0.037079	0.114665	0	0.08648
LY_1_1.8686_1	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales; f__Oscillospiraceae; g__Flavonifractor; s__uncultured Flavonifractor sp.*	tetracycline	tet40	64.81542	61.33574	48.62012	59.52648	91.81865	51.91265	56.08277	51.19124	63.81382	48.09066	55.72966	77.27084	73.92578	81.12825	75.59557	68.17757	82.49424

gene_id	JN_3_1	LC_2_1	LC_3_1	LC_1_1	LY_3_1	LY_2_1	LY_1_1	QD_2_1	QD_3_1	QD_1_1	RZ_1_1	RZ_2_1	RZ_3_1	TA_2_1	TA_3_1	TA_1_1	WF_3_1	WF_2_1	WF_1_1	WH_2_1	WH_1_1
HZ_3_1.20 610_6	0.080393	0.11429	0	0.165646	0.083063	0.125376	0	0.548923	0.032703	0.054854	0	0.293851	0.041	0.38185	0.083566	0.975842	0.394454	0.102174	0.039203	0.253129	0.273271
ZZ_1_1.457 364_2	0	0.306672	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
QD_2_1.19 0721_1	0	0	0.023371	0	0.02697	0	0	0.404795	0	0	0	0	0	0	0	0	0	0	0	0.027277	0
TA_1_1.131 259_1	0	0	0	0	0	0	0	0	0	0	0	0.08168	0	0	0	0.828424	0	0	0	0	0
WF_3_1.31 12_1	0	0	0	0	0	0.688271	0	0	0	0	0	0	0	0	0	0	0.714859	0	0	0	0
DZ_1_1.18 912_2	13.67655	47.45726	19.03002	30.45355	27.53209	45.83893	56.43174	18.14005	23.28016	27.7545	40.75986	31.77181	0.255977	42.39393	18.87454	4.79904	43.97114	47.22398	14.58986	15.38773	13.69788
ZZ_3_1.112 994_3	0	0.038182	0	0.290908	0	0.473666	0	0.177389	0.041848	0	0.039395	1.139099	0.039557	0.221065	0.044536	0.043965	0.336509	0	0	0.717957	0.092006
LY_1_1.868 86_1	64.8863	55.74338	70.92936	72.8665	62.43173	44.02492	37.86731	58.51081	55.22389	69.09443	42.33008	60.47125	3.685005	46.49405	37.21089	19.38362	34.35248	72.66217	73.25387	43.82586	45.97578

gene_id	WH_3_1	YT_1_1	YT_3_1	YT_2_1	ZB_1_1	ZB_2_1	ZB_3_1	ZZ_2_1	ZZ_3_1	ZZ_1_1
HZ_3_1.20 610_6	0.231501	0	0	0.029567	0.022457	0.033185	0.080182	0.615334	0.12523	0.243689
ZZ_1_1.457 364_2	0	0	0	0	0.194756	0	0	0	0	0.684523
QD_2_1.19 0721_1	0	0	0	0	0	0	0	0	0	0
TA_1_1.131 259_1	0	0	0	0	0	0	0	0	0	0
WF_3_1.31 12_1	0	0	0	0	0	0	0	0	0	0
DZ_1_1.18 912_2	40.28223	37.12966	90.19694	42.70603	23.81577	13.90546	27.84041	32.14826	29.60528	32.54137
ZZ_3_1.112 994_3	0.160086	0	0	0.040316	0.056662	0	0	0.283775	1.028626	0.129623
LY_1_1.868 86_1	49.24625	42.16867	49.76282	51.22121	91.26087	85.16301	50.98906	83.82246	81.62033	66.68268

gene_id	Taxonomy	ARG_Catego ry	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
DZ_3_1.90 371_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	adeJ	0	0	0	0	0	0	0	0.525816	0	0	0	0	0	0	0	0	0
ZZ_3_1.439 226_1	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales; f__Clostridiaceae; g__Clostridium; s__uncultured Clostridium sp.	bacitracin	bacA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ZZ_3_1.125 637_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Pseudomonadales; f__Pseudomonadaceae; g__Oblitimonas; s__Oblitimonas alkaliphila*	multidrug	mexB	0	0	0	0	0	0	0.048295	0.092758	0.039584	0.039743	0	0	0	0	0	0	0
WF_1_1.93 743_1	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales	tetracycline	tetQ	11.42453	11.86292	11.45499	2.202737	5.736191	5.469719	6.135058	5.049847	4.1961	2.434143	12.42496	1.813245	8.435767	6.96869	8.521876	8.218311	6.255026
WH_2_1.58 031_7	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Enterobacterales	unclassified	bacterial_r egulatory_ protein_Lu xR	1.16436	0	0.155154	0.176308	0.864519	0.605225	0	1.192818	0.093153	17.66929	0.468046	0	0.040521	0.334914	0.258872	0.048381	0.532516
WH_2_1.58 031_8	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Enterobacterales; f__Enterobacteriaceae	multidrug	emrK	1.064879	0.02196	0.096304	0.161983	0.507342	0.550228	0	0.556978	0.103433	11.89919	0.404931	0	0.090488	0.07427	0.15322	0.051084	0.595263
LY_3_1.525 562_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	adeJ	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
WF_3_1.32 5272_2	k__Bacteria; p__Firmicutes; c__Bacilli	aminoglycosi de	aph2-le	0	0	0.019747	0.06472	0	0.025396	1.203441	0.291022	0.587713	0.371161	0	0	0	0	0.021986	0	0.025581
WH_2_1.17 294_5	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Enterobacterales; f__Enterobacteriaceae	multidrug	TolC	0.584632	0.016279	0.080112	0.034252	0.575182	0.441969	0.015603	0.637594	0.138933	10.96729	0.36742	0.012759	0.093761	0.140564	0.111546	0.037141	0.502743

gene_id	JN_3_1	LC_2_1	LC_3_1	LC_1_1	LY_3_1	LY_2_1	LY_1_1	QD_2_1	QD_3_1	QD_1_1	RZ_1_1	RZ_2_1	RZ_3_1	TA_2_1	TA_3_1	TA_1_1	WF_3_1	WF_2_1	WF_1_1	WH_2_1	WH_1_1
DZ_3_1.90371_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ZZ_3_1.439226_1	1.228175	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ZZ_3_1.125637_2	0	0.036375	0	0	0	0.082057	0	0.042257	0	0	0	0.166919	0	0	0	0	0	0	0	0	0
WF_1_1.93743_1	1.001663	5.595011	4.181269	4.28741	9.346862	7.655957	14.44821	6.128776	7.120951	5.501143	8.480573	7.853308	0.109816	7.268618	2.187896	0.474204	6.018017	5.423333	3.225647	2.441738	1.963511
WH_2_1.58031_7	0.098302	11.29877	0	0.975285	0.248571	0.241185	0.227042	0.248354	0.139544	0.131419	0.044462	9.361514	0	1.048388	17.65147	1.036863	0.565349	0.099751	0	12.60996	0.15488
WH_2_1.58031_8	0	8.895728	0.048013	0.97974	0.276603	0.179142	0.165694	0.313863	0.102309	0.259687	0	6.947487	0.030481	0.655126	12.53885	0.632363	0.560424	0	0	9.09214	0.132782
LY_3_1.525562_1	0	0	0	0	0.353014	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.147479
WF_3_1.325272_2	0.025494	0.067558	0	0.057735	0	0	0	0.078596	0	0	0	0.119098	0.442396	0.076244	0.026318	0.077212	0.432034	0	0.030624	0	0
WH_2_1.17294_5	0.10444	8.408629	0.058704	0.794823	0.202727	0.144454	0.080747	0.108287	0.147044	0.088727	0.023032	5.294686	0	0.476851	10.20028	0.687121	0.603488	0.069411	0.015992	7.932846	0.124937

gene_id	WH_3_1	YT_1_1	YT_3_1	YT_2_1	ZB_1_1	ZB_2_1	ZB_3_1	ZZ_2_1	ZZ_3_1	ZZ_1_1
DZ_3_1.90371_1	0	0	0	0	0	0	0	0	0	0
ZZ_3_1.439226_1	0	0	0	0	0	0	0	0	0	0
ZZ_3_1.125637_2	0	0	0	0	0	0	0	0	0.490796	0
WF_1_1.93743_1	5.28865	4.723971	24.03645	9.342099	3.44063	3.876731	3.865697	11.33305	14.4227	7.508549
WH_2_1.58031_7	0.090299	6.991557	0.496271	0.31748	0.125638	0	0.059237	0.105567	0	3.708441
WH_2_1.58031_8	0	4.834508	0.182086	0.131458	0.049664	0	0.04447	0.060077	0.019829	2.579349
LY_3_1.525562_1	0	0	0	0	0	0	0	0	0	0
WF_3_1.325272_2	0.023076	0	0	0	0	0	0.220322	0	0.027982	0
WH_2_1.17294_5	0.023452	3.835225	0.218006	0.059997	0.110342	0	0.081636	0.01473	0.04377	2.102438

gene_id	Taxonomy	ARG_Category	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
HZ_1_1.171883_3	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacterales; f__Enterobacteriaceae	unclassified	sdiA	0.711955	0	0.114271	0.18043	0.493178	0.543315	0	0.631151	0.104686	8.947031	0.389902	0	0.059599	0.23177	0.031794	0	0.667101
DY_3_1.259888_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacterales; f__Enterobacteriaceae	unclassified	DNA-binding_protein_H-NS	1.372449	0	0.427378	0.13397	0.964766	1.84635	0	1.3109	0	17.80585	0.794106	0	0.221793	0.113195	0	0	0.485538
RZ_2_1.441359_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Aeromonadales; f__Aeromonadaceae; g__Aeromonas; s__Aeromonas hydrophila	beta-lactam	AER-1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ZZ_3_1.397568_2	k__Bacteria; p__Firmicutes	vancomycin	vanR	0.190195	0.220248	0	0	0.67721	0	0	0	0.228765	0	0	0.225201	0	0	0	0.556795	0
WH_2_1.56747_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacterales; f__Enterobacteriaceae	multidrug	acrA	0.031383	0	0	0	0.021788	0.059731	0	0.046096	0	0.351778	0	0	0	0	0	0	0
TA_2_1.490820_1	k__Bacteria; p__Firmicutes; c__Bacilli	macrolide-lincosamide-streptogramin	lsa	0	0	0	0	0	0	0.386866	0.170975	0	0	0	0	0	0	0	0	0
TA_3_1.181660_11	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia; s__Escherichia fergusonii	multidrug	mdtH	0.026469	0	0	0	0.036913	0.083761	0	0	0	0.049542	0.018217	0.016434	0	0.028028	0	0	0
QD_2_1.94232_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia	kasugamycin	kasugamycin_resistance_protein_ksgA	0.226309	0	0.076814	0	0.200814	0.097856	0	0.160891	0	3.193535	0.051541	0	0.040121	0.082828	0.042722	0.0479	0.047251
WH_3_1.224231_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	beta-lactam	OXA-236	0.142236	0	0.832967	0	0	0	0	0	0	0.511539	0	0	0	0	0	0	0

gene_id	JN_3_1	LC_2_1	LC_3_1	LC_1_1	LY_3_1	LY_2_1	LY_1_1	QD_2_1	QD_3_1	QD_1_1	RZ_1_1	RZ_2_1	RZ_3_1	TA_2_1	TA_3_1	TA_1_1	WF_3_1	WF_2_1	WF_1_1	WH_2_1	WH_1_1
HZ_1_1.17 1883_3	0.109684	7.237118	0	1.057791	0.111836	0.235587	0.140992	0.042125	0.038766	0.128161	0.032783	5.923377	0	0.211641	9.640179	0.310739	0.413994	0.037637	0	7.74182	0.038567
DY_3_1.25 9888_2	0.510452	14.52715	0	1.605431	0.37841	0	0	0.125097	0.107823	0.492182	0	10.7145	0	2.174969	25.61007	1.41055	1.3062	0	0	14.35569	0.132082
RZ_2_1.441 359_2	0	0	0	0	0	0	0	0	0.025035	0	0	0.813737	0	0	0	0	0	0	0	0	0
ZZ_3_1.397 568_2	0	0	0	0	0	0	0.393216	0	0	0	0.461519	0	0	0	0	0	0.226816	0	0	0	0
WH_2_1.56 747_2	0	0.230765	0	0	0	0	0	0	0.020187	0	0	0.081323	0	0.039759	0.020758	0.020242	0	0	0	0.499341	0
TA_2_1.490 820_1	0	0.149621	0	0	0	0	0	0.34187	0	0	0	0.174629	0	0.375302	0	0	0.162479	0	0	0	0.359112
TA_3_1.181 660_11	0	0.014983	0	0	0	0	0	0.017444	0	0	0	0	0	0.033409	0.578365	0	0.049642	0	0	0	0
QD_2_1.94 232_1	0	1.887263	0	0.267973	0.098516	0.23721	0.075001	0.24601	0	0	0.044027	1.776094	0	0	4.046363	0.098069	0.392765	0.049432	0.056444	2.182698	0.051146
WH_3_1.22 4231_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0.194372	0	0	0	0	0	0	1.45891

gene_id	Taxonomy	ARG_Catego ry	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
ZB_3_1.118 575_1	k__Bacteria; p__Bacteroidetes	tetracycline	tet36	0.012274	0.019348	0	0.32597	0	0.015521	1.253177	1.287797	0.030214	1.717971	0.0169	0	0	0	0	0.163559	0.015815
J_3_1.4350 3_10	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales	bacitracin	bacA	0.021983	0.033558	0.021848	0.141934	0.120756	0.028068	0.132515	0	0	0	0.060356	0.108618	0.136608	0.778366	0.875643	0.108436	0.225477
DZ_2_1.48 462_15	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales; f__Lachnospiraceae; g__Lacrimispora; s__Lacrimispora celerecrescens	chloramphe nicol	chloramph enicol_and _florfenicol _resistance _gene	0.032911	0	0.016217	0	0	0.062686	2.681312	0.615307	0.373621	1.131301	0	0.022248	0	0	0	0	0
YT_2_1.490 019_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Enterobacterales; f__Enterobacteriaceae	fosmidomyci n	rosB	0.326985	0	0	0	0	0.817546	0	0.944653	0.321165	3.380231	0.546419	0	0	0.331626	0	0	0
LY_3_1.468 053_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	mexT	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TA_1_1.220 725_3	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales; f__Lachnospiraceae	aminoglycosi de	aph2-II	2.913828	2.418584	4.734526	4.785291	14.64473	1.974713	16.03602	4.988831	19.32962	6.950284	17.68354	2.455449	5.073554	9.456678	9.20797	2.883467	14.31451
WF_3_1.21 0435_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia	beta-lactam	OXA-58	0.200017	0	0.176767	0.143391	0	0.028382	0.234396	1.261515	0.40935	21.42765	0	0	0	0	0	0	0.085469
DZ_3_1.52 362_8	k__Bacteria; p__Proteobacteria; c__Epsilonproteobacteri a; o__Campylobacterales; f__Campylobacteraceae; g__Campylobacter; s__Campylobacter coli	macrolide- lincosamide- streptogrami n	macA	0	0.022105	0	0	0	0.017874	0	1.423948	0	0	0	0	0	0	0	0	0
WH_3_1.96 15_2	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides; s__Bacteroides pectinophilus CAG:437	bacitracin	bacA	0	0	0.202096	0.239124	0	0	0	0	0	0	0	0	0	0.606491	0	0	0

[illegible]

gene_id	WH_3_1	YT_1_1	YT_3_1	YT_2_1	ZB_1_1	ZB_2_1	ZB_3_1	ZZ_2_1	ZZ_3_1	ZZ_1_1
ZB_3_1.118575_1	0.084411	0	0.057987	0.043133	0.065608	0	1.129567	0	0.139289	0.015806
J_3_1.43503_10	0.10208	0.159693	0.155984	0.129577	0.038027	0.085207	0.069312	0.0311	0.030777	0
DZ_2_1.48462_15	0.026735	0	0	0	0	0	0.260603	0.035148	0.162474	0
YT_2_1.490019_1	0	1.85135	0	0	0	0	0.220216	0	0.230686	1.357418
LY_3_1.468053_1	0	0	0	0	0	0	0	0	0	0
TA_1_1.220725_3	9.982215	1.36742	6.169225	2.740131	2.965396	2.946562	3.79835	5.477855	4.927491	4.428192
WF_3_1.210435_1	0.490347	0.032282	0.026283	0	0.038415	0	0	0.031432	0.715393	0
DZ_3_1.52362_8	0	0	0	0	0	0	0	0	0	0
WH_3_1.9615_2	0.450524	0.243187	0	0	0	0	0	0	0	0

[illegible]

[illegible]

gene_id	Taxonomy	ARG_Catego ry	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
YT_2_1.252 91_3	k__Bacteria; p__Bacteroidetes; c__Bacteroidia	macrolide- lincosamide- streptogrami n	ermF	2.068473	2.532372	2.254559	0.880559	8.930377	2.723798	1.535229	2.767703	1.835387	3.2858	1.796282	3.114234	3.196276	6.990475	6.473846	2.594164	1.863635
LC_3_1.649 4_2	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales	aminoglycosi de	ant9-I	4.607651	9.915858	8.166977	3.768745	5.461045	5.71974	4.307183	4.003027	2.797753	1.711989	4.81844	1.854386	6.100098	7.34235	5.239587	6.528227	9.202545
BZ_2_1.138 551_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Enterobacterales; f__Enterobacteriaceae	multidrug	mdtA	0.66946	0	0.055482	0.056657	0.381047	0.516096	0.034493	0.318599	0.111752	8.393831	0.281307	0	0.057729	0.071887	0.098878	0.027446	0.336441
TA_3_1.981 09_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia	multidrug	mdtG	0.090455	0	0	0	0	0	0	0.043407	0	0.742896	0	0	0	0	0	0	0
LC_2_1.195 956_1	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales	tetracycline	tetQ	2.221103	3.074011	2.218234	0.371719	0.667227	0.665629	0.570473	0.656032	1.110685	0.122645	1.13555	0.295117	1.70857	0.717337	1.060844	1.975396	1.668784
QD_1_1.72 288_3	k__Bacteria; p__Firmicutes	vancomycin	vanR	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ZZ_3_1.186 933_2	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales	tetracycline	tetQ	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HZ_3_1.34 0437_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia	trimethopri m	dfrA14	0.193654	0	0	0.373054	0.082586	0.256875	0	0.266691	0	5.897098	0.175063	0	0.214213	0	0	0	0.162041
WH_1_1.31 1742_4	k__Bacteria; p__Firmicutes	vancomycin	vanG	0.032256	0.075298	0.146868	0	0	0.020473	0	0	0.019833	0	0	0	0.313239	0.188843	0.106195	0	0
HZ_3_1.56 13_4	k__Bacteria; p__Firmicutes; c__Bacilli	macrolide- lincosamide- streptogrami n	ermA	0.07013	0	0.116414	0.676504	0	0.484592	1.544878	1.089059	0.832215	3.332593	0	0.231359	0	0.125674	0.155511	0.028901	0.029949
LY_1_1.647 45_2	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales; f__Clostridiaceae; g__Butyrivicoccus; s__Butyrivicoccus sp. AM42-5AC	vancomycin	vanU	0.977892	0	1.076594	0.81515	0.694269	0	0	0	0	0	0	0	0.508834	0.509922	1.65788	0	0
BZ_1_1.205 165_19	k__Bacteria; p__Firmicutes	vancomycin	vanG	0.103659	0	1.663299	0.124103	0.070691	0	0	0.037526	0	0.064055	0.035532	0	0.695027	0.223775	0.144314	0	0

gene_id	JN_3_1	LC_2_1	LC_3_1	LC_1_1	LY_3_1	LY_2_1	LY_1_1	QD_2_1	QD_3_1	QD_1_1	RZ_1_1	RZ_2_1	RZ_3_1	TA_2_1	TA_3_1	TA_1_1	WF_3_1	WF_2_1	WF_1_1	WH_2_1	WH_1_1
YT_2_1.25291_3	0.575955	1.119312	3.36286	1.395569	7.669633	12.9267	7.970613	0.634489	0.662283	1.183768	13.21649	0	0.569833	5.23603	4.482023	0	6.567333	3.952554	1.549286	1.237513	2.450479
LC_3_1.6494_2	1.869711	8.401598	3.336651	6.751431	3.979041	6.46953	8.517646	1.992633	3.572842	7.335924	6.547248	6.61259	0	6.24762	4.288372	0.778275	6.060386	4.666418	2.417942	2.737377	3.576632
BZ_2_1.138551_2	0.101153	5.899339	0	0.795489	0.119569	0.15974	0.134048	0.104774	0.117998	0.09839	0.012759	4.281756	0	0.314183	8.54815	0.438661	0.298165	0.030675	0	5.826353	0.061434
TA_3_1.98109_1	0	0.135854	0	0	0	0	0	0	0	0	0	0.155822	0	0	0.832365	0	0	0.039863	0	0	0
LC_2_1.195956_1	0.826336	1.048138	0.620605	1.388077	2.261947	2.491161	1.838753	1.59213	1.342168	1.813715	1.06324	1.720232	0.074408	1.445561	0.927363	0.080565	0.586357	1.825794	0.177856	0.368133	0.304511
QD_1_1.72288_3	0	0	0	0	0	0	0	0	0.616105	1.105325	0	0	0	0	0	0	0	0	0	0	0
ZZ_3_1.186933_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.412179	0	0	0
HZ_3_1.340437_2	0.252582	5.473651	0	0.538526	0	0.16211	0.129576	0.083331	0.298448	0	0.077923	0.165882	0	0.438392	0.083641	0.168284	0	0	0	0.981812	0
WH_1_1.311742_4	0	0	0	0	0.021211	0	0.031837	0	0.082903	0	0	0	0	0	0	0	0	0	0	0	0.605373
HZ_3_1.5613_4	0.149766	0.10554	0.079678	0.135546	0	0.655205	0.115588	0.920482	0.687214	0	0.37563	0.393149	2.20765	1.765449	0.092461	0.181267	2.178418	0.093456	0.607454	1.844627	0.411682
LY_1_1.64745_2	0	0	0.527452	0	0	0	1.51677	0	0.616105	0	0	0	0	0	0	0.616249	0	0	0	0	1.159267
BZ_1_1.205165_19	0.099746	0.11691	0	0.037315	0.067947	0	0.102609	0	0.130205	0	0	0	0	0	0.170647	0.067024	0	0.034432	0.039463	0.030507	0.872631

gene_id	WH_3_1	YT_1_1	YT_3_1	YT_2_1	ZB_1_1	ZB_2_1	ZB_3_1	ZZ_2_1	ZZ_3_1	ZZ_1_1
YT_2_1.25291_3	1.831446	4.514442	5.609574	2.51771	1.862124	1.94378	5.572776	12.41439	7.502116	3.088943
LC_3_1.6494_2	5.80206	6.606613	19.50679	8.025905	4.181361	3.734047	3.382021	7.631947	9.961155	5.85182
BZ_2_1.138551_2	0.038972	2.92586	0.147406	0.119557	0	0	0.108277	0.032546	0.032233	1.929812
TA_3_1.98109_1	0	0.217629	0	0	0	0	0	0	0	0.076935
LC_2_1.195956_1	0.583996	1.644478	2.21796	1.777125	0.590031	0.637345	0.753766	1.788026	1.710748	2.070547
QD_1_1.72288_3	0	0	0	0	0	0	0	0	0	0
ZZ_3_1.186933_2	0	0	0	0	0	0	0	0	2.179998	0
HZ_3_1.340437_2	0.078938	0.635844	0	0	0	0	0.098531	0	0	0.567048
WH_1_1.311742_4	0.018582	0	0.058962	0.018941	0	0.021069	0	0.206497	0.045519	0
HZ_3_1.5613_4	0.163118	0.067851	0	0.137915	0	0	2.10388	0.033013	0.065333	0.11972
LY_1_1.64745_2	1.739738	0	0	0	0	0	0	0	0	0
BZ_1_1.205165_19	0.423366	0.037534	0.091987	0.061258	0	0	0	0.10944	0	0

gene_id	Taxonomy	ARG_Catego ry	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
BZ_1_1.205 165_17	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Streptococcus; s__Streptococcus agalactiae	vancomycin	vanW	0.068938	0	1.555383	0.036987	0.031502	0	0.034602	0	0	0	0	0	0.480127	0.123464	0.127315	0	0
HZ_3_1.27 5921_2	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Weeksellaceae; g__Elizabethkingia; s__Elizabethkingia anophelis	chloramphenicol	catB	0	0	0	0	0	0	0	0	0	0.87549	0	0	0	0	0	0	0
DZ_2_1.15 8066_1	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales; f__Thermohalobacteraceae; g__Clostridiisalibacter; s__Clostridiisalibacter paucivorans*	macrolide-lincosamide-streptogramin	mefA	0.028819	0	0	0	0	0	0.852068	0.106015	0.035454	0.431141	0	0	0	0.015285	0	0	0
BZ_1_1.460 775_4	k__Bacteria; p__Proteobacteria; c__Epsilonproteobacteria; o__Campylobacterales; f__Campylobacteraceae; g__Campylobacter; s__Campylobacter jejuni	aminoglycoside	bifunctional_aminoglycoside_N-acetyltransferase_and_aminoglycoside_phosphotransferase	0	0	0.319749	0.354178	1.954729	0.321591	0.444525	0	1.849159	0.063717	1.237211	0.905552	0	0	0	0.321225	0.152808
QD_2_1.48 2039_1	k__Bacteria; p__Firmicutes	tetracycline	tetW	2.54445	5.442381	3.205823	2.570883	8.05504	1.618174	1.485229	7.31546	2.110414	1.945185	5.188457	3.366329	0.832693	6.871449	6.249567	2.254834	1.276854
WH_2_1.44 6329_3	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Pasteurellales; f__Pasteurellaceae; g__Pasteurella; s__Pasteurella multocida	aminoglycoside	aadA	0	0	0	0	0	0	0	0	0	0.523749	0	0	0	0	0	0	0
ZB_3_1.285 632_1	k__Bacteria; p__Firmicutes	macrolide-lincosamide-streptogramin	vatB	0.111763	0	0	0	0.272126	0	0	0	0	0	0.150862	0.53182	0	0.258236	0.401265	0	0

gene_id	JN_3_1	LC_2_1	LC_3_1	LC_1_1	LY_3_1	LY_2_1	LY_1_1	QD_2_1	QD_3_1	QD_1_1	RZ_1_1	RZ_2_1	RZ_3_1	TA_2_1	TA_3_1	TA_1_1	WF_3_1	WF_2_1	WF_1_1	WH_2_1	WH_1_1
BZ_1_1.205 165_17	0	0.181578	0.026114	0.033183	0	0.058561	0	0	0.116246	0.025554	0	0	0	0	0	0	0.028615	0	0.035146	0.027066	0.349337
HZ_3_1.27 5921_2	0	0	0	0	0	0.407104	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DZ_2_1.15 8066_1	0	0	0.049367	0.020983	0	0.128943	0	0.132888	0.148758	0	0	0.056024	0.047084	0	0	0.167244	0	0	0.066976	0	0
BZ_1_1.460 775_4	0.395932	0.067857	0.338198	0.254229	0.078803	0.076394	3.045651	0.157114	0.212238	0.293037	0	0	0	0	0.157712	0.079166	0	0	0.088096	0	0.082441
QD_2_1.48 2039_1	1.859247	1.487687	1.944512	1.614103	0.573412	3.473907	1.549793	2.845617	2.36295	3.117181	1.47254	0.774467	0.394032	2.37983	3.032642	0.195959	1.435144	0.364779	0.824987	1.943082	0.760935
WH_2_1.44 6329_3	0	0.048142	0	0.060773	0	0.271275	0	0	0	0	0	0	0	0	0	0	0.052981	0	0	0.402823	0
ZB_3_1.285 632_1	0.144855	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.137881	0	0	0

gene_id	WH_3_1	YT_1_1	YT_3_1	YT_2_1	ZB_1_1	ZB_2_1	ZB_3_1	ZZ_2_1	ZZ_3_1	ZZ_1_1
BZ_1_1.205 165_17	0.293803	0	0.078991	0.027107	0	0.029634	0	0.032468	0.032128	0
HZ_3_1.27 5921_2	0	0	0	0	0	0	0	0	0	0
DZ_2_1.15 8066_1	0.049689	0	0	0.016904	0	0	0.137156	0	0	0
BZ_1_1.460 775_4	0.074046	0.085732	0.128945	1.46759	0.094344	0	0	0.164131	0.080977	0.458255
QD_2_1.48 2039_1	1.682112	1.015915	5.034965	2.410394	3.352696	2.016057	1.130141	7.893221	3.864479	1.820853
WH_2_1.44 6329_3	0	0	0.050863	0	0	0	0	0	0	0
ZB_3_1.285 632_1	0.560432	0	0	0.137689	0	0.127188	0.336978	0	0	0.138557

gene_id	Taxonomy	ARG_Catego ry	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
TA_3_1.279 274_2	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Oceanobacillus; s__Oceanobacillus rekensis	quinolone	norB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
QD_2_1.79 131_1	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus	vancomycin	vanS	1.089584	0	0	5.633415	0	1.428937	5.692001	18.48869	26.51833	14.41327	0.718373	0	0	0.570006	0	0	0
WH_2_1.55 199_1	k__Bacteria; p__NA; c__NA; o__NA; f__NA; g__NA; s__uncultured bacterium T3_7_42578	tetracycline	tetL	1.331955	0.034584	5.456743	7.667337	9.703709	22.84871	26.91472	3.329707	38.90308	6.356787	18.66056	10.28509	12.33631	10.14891	11.35321	17.51822	0.224998
TA_3_1.212 391_6	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia; s__Escherichia fergusonii	unclassified	sdiA	0	0	0	0	0	0.033883	0.039675	0.038232	0.097235	0	0	0	0	0.02854	0	0	0
WH_2_1.48 4385_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Enterobacterales; f__Enterobacteriaceae	multidrug	mdtM	0.094807	0.021199	0	0	0.056632	0.085744	0	0.019953	0	1.222237	0.018641	0	0	0	0.0148	0	0.018044
TA_2_1.338 264_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Alteromonadales; f__Pseudoalteromonada ceae; g__Pseudoalteromonas; s__Pseudoalteromonas sp. 58	tetracycline	tet31	0.025961	0	0.012725	0.387037	0	0.016426	0.039407	0.095693	0.047922	0.1944	0	0	0.013244	0	0	0	0
RZ_3_1.289 94_2	k__Bacteria; p__Firmicutes; c__Tissierellia; o__Tissierellales; f__Peptoniphilaceae; g__Anaerococcus	bacitracin	bacA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
JN_3_1.317 635_1	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae	aminoglycosi de	aadD	0.160856	0	0.251606	4.253848	0.567039	31.77917	11.78541	2.205103	2.341628	15.62562	0.031536	1.475133	0.452949	1.080744	0.814818	0.255504	0.119907

gene_id	JN_3_1	LC_2_1	LC_3_1	LC_1_1	LY_3_1	LY_2_1	LY_1_1	QD_2_1	QD_3_1	QD_1_1	RZ_1_1	RZ_2_1	RZ_3_1	TA_2_1	TA_3_1	TA_1_1	WF_3_1	WF_2_1	WF_1_1	WH_2_1	WH_1_1
TA_3_1.279 274_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.342492	0	0	0	0	0	0
QD_2_1.79 131_1	0	0	0	1.474612	0	0.616286	0	18.46998	0.712246	0	0	5.537725	1.204572	3.435669	0	4.109029	24.61043	0	0	1.955413	0
WH_2_1.55 199_1	10.08505	31.0212	12.22396	11.10953	0.489766	0.963545	7.452546	12.6934	2.175073	1.99415	2.763703	6.793825	0.505732	1.418875	31.28522	0.567936	5.004593	15.11988	37.67329	2.659442	1.713893
TA_3_1.212 391_6	0	0.059588	0	0	0	0	0	0	0	0	0	0	0	0	0.947189	0	0.065707	0	0	0	0
WH_2_1.48 4385_1	0	0.766246	0	0.05922	0.017827	0.017319	0.026689	0.01785	0.034943	0	0	0.75367	0	0.051058	0.779925	0.017462	0.050796	0	0	1.193512	0.018335
TA_2_1.338 264_2	0	0.014696	0	0.056785	0.034178	0.199229	0	0.017111	0	0	0	0.185098	0	0.491327	0	0	0.11362	0	0	0	0.017572
RZ_3_1.289 94_2	0	0	0.026409	0	0	0	0	0	0	0	0	0	1.278459	0	0	0	0	0	0	0	0
JN_3_1.317 635_1	0.529959	0.233457	4.282694	3.351529	0	3.630765	0.204493	11.31269	11.91519	0.051109	0.656623	3.508216	39.41816	4.121272	2.839561	1.811394	4.034658	0.857831	5.623409	3.220851	4.264656

gene_id	WH_3_1	YT_1_1	YT_3_1	YT_2_1	ZB_1_1	ZB_2_1	ZB_3_1	ZZ_2_1	ZZ_3_1	ZZ_1_1
TA_3_1.279 274_2	0	0	0	0	0	0	0	0	0	0
QD_2_1.79 131_1	2.554041	0	0	0	1.00266	0	0	0	0	0
WH_2_1.55 199_1	0.120337	1.234062	3.231506	4.462909	8.263252	26.53219	6.115597	0.191953	0.519315	5.410095
TA_3_1.212 391_6	0	0	0.031263	0	0	0	0.0415	0.037169	0	0.033774
WH_2_1.48 4385_1	0	0.256967	0.031999	0.031758	0	0	0	0	0	0.171759
TA_2_1.338 264_2	0	0	0	0	0	0	0.082466	0.037153	0.036792	0.033421
RZ_3_1.289 94_2	0	0	0	0	0	0	0.10981	0	0	0
JN_3_1.317 635_1	1.148588	0.233517	0.163072	1.111401	0.158524	0	39.1021	0.746773	0.771082	0.088283

gene_id	Taxonomy	ARG_Catego ry	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
TA_2_1.248 28_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	adeJ	0.054302	0	0.044549	0.048315	0	0	0	0.025517	0	0.276073	0	0	0.028782	0.023915	0.006169	0	0.029178
JN_1_1.571 02_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Enterobacterales; f__Morganellaceae; g__Proteus; s__Proteus mirabilis	chloramphe nicol	floR	1.119494	0.370906	0.950514	0.468783	1.61411	0.267623	0.853575	1.43223	0.65377	1.209752	0	0	0	0	0.124169	0.552011	0.067663
DZ_2_1.13 9474_2	k__Bacteria; p__Firmicutes k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales; f__Oscillospiraceae; g__Oscillibacter; s__Oscillibacter ruminantium	tetracycline	tetT	0.022193	0	0.007124	0.308602	0	0.904853	6.968585	0.784284	0.559961	1.986084	0	1.618575	0	0.023078	0.007937	0	0.047341
DZ_2_1.22 2497_1	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales; f__Oscillospiraceae; g__Oscillibacter; s__Oscillibacter ruminantium	macrolide- lincosamide- streptogrami n	vatB	0	0	0	0.058279	0	0	0.449073	0.053741	0	0.092409	0	0	0	0	0	0	0
HZ_3_1.88 878_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter; s__Acinetobacter sichuanensis	multidrug	adeJ	0	0	0	0	0	0	0	0	0	0.285048	0	0	0	0	0	0	0
TA_3_1.804 48_4	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia	macrolide- lincosamide- streptogrami n	macB	0.044214	0	0	0	0.051923	0	0	0.010952	0.018161	0.055418	0	0	0	0.01547	0	0	0
JN_2_1.147 5_1	k__Bacteria; p__Firmicutes k__Bacteria;	tetracycline	tetW	3.093071	5.549905	1.064453	6.310193	11.09636	2.042247	2.251027	2.332232	4.44598	6.054269	7.11667	7.38447	1.67227	2.553556	1.473535	1.451774	1.872422
HZ_3_1.55 841_2	p__Proteobacteria; c__Gammaproteobacter ia	aminoglycosi de	aac6-31	0	0	0	0	0	0	0	0	0.940135	0.466182	0	0	0	0	0	0	0
YT_3_1.146 309_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia	aminoglycosi de	aph6-I	0.651638	0	0.454693	5.288039	0.554969	0.516095	1.624772	5.034945	3.477138	23.22548	0.678522	0.083244	0.372661	0.493903	0.29836	0.676764	0.633637

gene_id	JN_3_1	LC_2_1	LC_3_1	LC_1_1	LY_3_1	LY_2_1	LY_1_1	QD_2_1	QD_3_1	QD_1_1	RZ_1_1	RZ_2_1	RZ_3_1	TA_2_1	TA_3_1	TA_1_1	WF_3_1	WF_2_1	WF_1_1	WH_2_1	WH_1_1
TA_2_1.24828_2	0.014501	0	0	0	0.007535	0	0	0.030157	0	0	0	0.022607	0	0.263624	0.446037	0	0	0	0	0.209018	0.400491
JN_1_1.57102_1	0.069735	1.356762	3.23568	0.826441	0	0	0.268177	0.069525	0	0	0	0.803424	0	0.431607	0	0	0.849413	0.205128	0.235413	0.251285	0
DZ_2_1.139474_2	0.456427	0	1.995265	0.400689	0.009667	0.920544	0.021614	0.4261	2.692741	0	0.081954	0.313878	25.17269	1.913427	0.019462	1.377825	0.599522	0.169231	1.342501	0.216448	0.009917
DZ_2_1.222497_1	0	0	0	0	0	0	0	0	0	0	0.088054	0	0	0	0	0	0	0	0	0	0
HZ_3_1.88878_1	0	0	0	0.008553	0	0.00747	0	0.107811	0	0	0	0.015122	0	0	0	0	0	0	0	0.006882	0.007881
TA_3_1.80448_4	0	0.008357	0	0.021611	0	0	0.007244	0	0	0	0	0	0	0.009219	0.626153	0.018974	0.046182	0	0.01154	0	0
JN_2_1.1475_1	3.909411	3.761022	1.917119	6.399916	3.8522	2.584741	1.597732	3.348608	2.984736	5.855392	3.24797	2.028841	0	1.637614	1.912518	4.837575	3.681672	7.607732	4.873008	4.484994	7.953486
HZ_3_1.55841_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
YT_3_1.146309_2	0.172672	4.227471	0.051086	1.460882	0.412872	2.020001	0.310993	3.158919	0.597478	0.07488	0.589059	7.080064	0.251566	4.615025	4.225835	2.380753	2.324052	0.749401	0.309545	11.5943	1.369689

gene_id	WH_3_1	YT_1_1	YT_3_1	YT_2_1	ZB_1_1	ZB_2_1	ZB_3_1	ZZ_2_1	ZZ_3_1	ZZ_1_1
TA_2_1.24828_2	0.006489	0	0	0	0	0	0	0	0	0
JN_1_1.57102_1	0.064852	0.076048	0.190949	1.290025	0.084778	0.065446	0	0.875789	0	0
DZ_2_1.139474_2	0.116863	0	0.054719	0.034233	0.039787	0.05842	12.24171	0.052829	0.304354	0.009463
DZ_2_1.222497_1	0	0	0	0	0	0	0	0	0	0
HZ_3_1.88878_1	0.006621	0	0	0	0	0	0	0	0	0
TA_3_1.80448_4	0	0.032492	0.026095	0	0.013333	0	0.023517	0	0.021048	0.009515
JN_2_1.1475_1	6.832446	0.46324	1.083406	4.960834	4.125685	5.646869	1.447231	4.941059	6.801752	1.778053
HZ_3_1.55841_2	0	0	0	0	0	0	0	0	0	0
YT_3_1.146309_2	1.647857	2.28454	0.239174	0.423967	0.116437	0.029005	0.424914	1.367205	2.410524	1.355079

gene_id	Taxonomy	ARG_Catego ry	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
TA_3_1.181 702_1	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus; s__Enterococcus asini	multidrug	multidrug_t ransporter	0	0	0	0	0	0	0	0	0.155333	0.456709	0	0	0	0	0	0	0
JN_2_1.420 506_1	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Limosilactobacillus; s__Limosilactobacillus fermentum	macrolide- lincosamide- streptogrami n	ermT	4.600935	0	5.431484	9.880873	5.927714	91.28213	7.39234	6.007437	5.099715	3.933326	0.409603	1.966509	2.563808	22.4346	25.08758	42.29533	0.942092
DZ_2_1.93 493_2	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales	tetracycline	tetP	0.303099	0.178804	0.284789	0.795658	0.370486	0.877853	6.842912	1.494407	0.932107	1.864335	0.382771	1.174885	0.425375	0.348175	0.220319	0.351779	0.146294
DZ_2_1.93 493_3	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales; f__Lachnospiraceae; g__Anaerobium; s__Anaerobium acetethvlicum*	tetracycline	tetP	0	0	0.091906	0	0.212154	0	10.12127	0.574727	0	1.894262	0	0	0	0	0	0	0
WH_2_1.20 9095_1	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales; f__Clostridiaceae; g__Butyricicoccus; s__Butyricicoccus sp. AM05-1	chlorampe nicol	catD	0.838846	0.05388	0.414329	0	0.247753	0.191963	0.05514	0.158429	0.453131	0.045385	0.202392	0	0.039342	0.365889	0.167601	0.046965	0.471108
WF_1_1.50 6424_1	k__Bacteria; p__Firmicutes	vancomycin	vanG	0	0	0	0	0	0	0.202963	0	0	0	0	0.091484	0	0	0	0.142283	0
HZ_2_1.14 3391_2	k__Bacteria; p__Actinobacteria; c__Actinomycetia	macrolide- lincosamide- streptogrami n	ermX	0.019834	0	0	0.869737	0.05468	0.833793	1.497065	0.839938	0.560486	4.706552	0.490426	0.638245	0.102341	0.106058	0.131253	0.073086	0.280029
WF_3_1.42 2234_4	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	mexT	0	0	0	0	0	0	0.079161	0	0	5.403193	0	0	0	0	0	0	0
BZ_1_1.278 992_1	k__Bacteria; p__Firmicutes	macrolide- lincosamide- streptogrami n	vatB	0	0	0.352944	0	0	0.219413	0	0	0.099397	0	0	0	0	0	0	0	0

gene_id	JN_3_1	LC_2_1	LC_3_1	LC_1_1	LY_3_1	LY_2_1	LY_1_1	QD_2_1	QD_3_1	QD_1_1	RZ_1_1	RZ_2_1	RZ_3_1	TA_2_1	TA_3_1	TA_1_1	WF_3_1	WF_2_1	WF_1_1	WH_2_1	WH_1_1
TA_3_1.181702_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.326775	0	0	0	0	0	0
JN_2_1.420506_1	0.954996	36.71778	49.75059	26.13121	0.77442	7.586386	24.50434	1.362199	10.90292	0.091565	1.965963	1.68861	4.534738	4.134889	15.49519	1.90336	13.65371	31.00924	24.64644	10.0694	6.473286
DZ_2_1.93493_2	1.623948	0.642879	1.692141	0.920257	0.555233	0.547079	0.372817	1.013647	1.639591	0.315412	1.161713	0.637933	0.876895	1.082481	1.454639	5.670269	1.594911	0.903148	1.723563	0.819502	1.040489
DZ_2_1.93493_3	0	0	0.187583	0	0	0	0	0.218129	0	0	0.208545	0.109351	0.223485	0	0.109471	0	0.103485	0	0	0.363248	0
WH_2_1.209095_1	0.047781	0.499528	0.166991	0.316511	0.04837	0	0.294469	0.241661	0.090695	0	0	0.238897	0	0.630223	0	0	0.366743	0.485687	0.16641	0.217503	0.401683
WF_1_1.506424_1	0	0	0	0	0	0	0.037152	0	0	0	0.16816	0	0	0	0	0	0	0	0.241891	0	0
HZ_2_1.143391_2	0.819477	0.345	0.09032	0.559495	0.234479	0.354236	0.078353	0.886433	0.101075	0.065708	0.135417	0.540744	0.66639	3.708723	0.080907	0.260588	3.833203	0.557369	0.548619	0.350626	0.214897
WF_3_1.422234_4	0	0	0	0.025329	0	0.155933	0	3.856492	0	0	0.197855	0.971636	0	0.044323	0.069183	0	0.23952	0	0	4.345761	0.023624
BZ_1_1.278992_1	0	0	0	0	0	0	0	0.210254	0	0	0	0	0	0	0.105508	0.321251	0	0	0.116209	0	0

[illegible]

gene_id	Taxonomy	ARG_Catego ry	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
HZ_1_1.41 1672_2	k__Bacteria; p__NA; c__NA; o__NA; f__NA; g__NA; s__uncultured bacterium	aminoglycosi de	rmtF	0	0.401152	0	0	0	0	0.479324	0	0	0	0.880476	0.392483	0.708579	0	0	1.302946	0
DZ_2_1.15 8246_1	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales	macrolide- lincosamide- streptogrami n	mefA	0	0	0	0	0	0	0.753692	0.266691	0	0.077655	0	0	0	0	0	0	0
WH_1_1.14 5467_2	k__Bacteria; p__Firmicutes	vancomycin	vanG	0.032256	0	0	0	0	0	0	0	0	0	0	0	0.033083	0	0	0	0
DY_2_1.43 163_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Xanthomonadales; f__Xanthomonadaceae; g__Luteimonas; s__Luteimonas sp. YGD11-2	multidrug	multidrug_t ransporter	0	0	0	1.308804	0	0	0.051042	0	0	0	0	0	0.034638	0	0	0	0
ZZ_3_1.428 46_2	k__Bacteria; p__Firmicutes	macrolide- lincosamide- streptogrami n	lsa	0.77364	0.537679	0.433678	0.646136	1.525986	1.11804	1.049712	1.504165	0.904981	0	0.513025	1.390949	1.229729	1.15167	0.881763	1.450529	1.515046
TA_3_1.679 7_5	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia; s__Escherichia fergusonii	multidrug	mdtP	0.083747	0.016604	0	0	0.117367	0.039644	0	0.046469	0.051561	0.03927	0	0	0	0	0	0	0
DZ_3_1.29 502_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter; s__Acinetobacter baumannii	chloramphe nicol	catB	0	0	0	0.320281	0	0	0.051069	0.293934	0.209508	0.550773	0	0	0	0.074817	0.115681	0	0
WH_1_1.63 6_12	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales	chloramphe nicol	catA	0	0	0	0	2.336916	0	0	0	0	0	0	0	0	0	0	0.25224	0
DY_3_1.14 898_1	k__Bacteria; p__Synergistetes; c__Synergistia; o__Synergistales; f__Synergistaceae; g__Cloacibacillus; s__Cloacibacillus porcorum	tetracycline	tetracycline _resistance _protein	5.042791	7.341671	3.694521	7.304103	13.24648	4.392017	4.815422	5.426959	4.282132	5.093159	5.891557	7.439881	7.099322	7.192643	6.820985	6.535085	3.930478

gene_id	JN_3_1	LC_2_1	LC_3_1	LC_1_1	LY_3_1	LY_2_1	LY_1_1	QD_2_1	QD_3_1	QD_1_1	RZ_1_1	RZ_2_1	RZ_3_1	TA_2_1	TA_3_1	TA_1_1	WF_3_1	WF_2_1	WF_1_1	WH_2_1	WH_1_1
HZ_1_1.41 1672_2	0.371928	0.361741	0.359006	0.886018	0	1.93919	0	0	0	2.328902	0	2.16186	0	0	0.736768	0.822266	0	0	0.470043	0.40095	0.793512
DZ_2_1.15 8246_1	0	0	0	0	0	0.081055	0	0.083331	0	0	0	0.082941	0	0	0	0.084142	0	0	0	0.226572	0
WH_1_1.14 5467_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.041615	0	0	0	0	0.327566
DY_2_1.43 163_1	0	0	0	0	0.022176	0	0	0	0	0	0.019112	0	0	0	0	0	0	0	0	0	0
ZZ_3_1.428 46_2	0.891227	0.852251	0.831502	1.042271	0	0.441865	0.805362	0	0.905762	0	0	0.506449	0.470585	0	0.746156	0	0.9018	0.477352	1.131306	0.470044	1.73407
TA_3_1.679 7_5	0	0.035582	0	0	0	0	0	0.013814	0	0.011325	0	0	0	0.013158	0.608008	0.026975	0.026208	0.014165	0.04895	0	0
DZ_3_1.29 502_1	0	0.038501	0	0.04888	0	0	0	0.044716	0	0	0	0.132532	0	0.485822	0.044906	0.044339	0.339306	0	0	0.160882	0.092784
WH_1_1.63 6_12	0	0	0	0.047713	0	0	0	0	0	0	0.154865	0	0	0	0	0	0	0.087922	0	0	1.266854
DY_3_1.14 898_1	6.465584	7.542437	5.676467	5.839637	4.007915	7.966145	3.42076	5.869165	6.15551	5.276369	4.054773	5.831761	0.459351	4.336419	4.395787	1.938158	4.493761	6.597868	6.376903	6.264217	4.990499

gene_id	WH_3_1	YT_1_1	YT_3_1	YT_2_1	ZB_1_1	ZB_2_1	ZB_3_1	ZZ_2_1	ZZ_3_1	ZZ_1_1
HZ_1_1.41 1672_2	0	0.451086	0	0.406503	0	0.376131	0	0.479935	0	0
DZ_2_1.15 8246_1	0	0	0	0	0	0	0	0	0	0
WH_1_1.14 5467_2	0.132253	0	0.019059	0	0	0	0	0	0	0
DY_2_1.43 163_1	0	0	0	0	0	0	0	0.024017	0	0
ZZ_3_1.428 46_2	0.978101	0.528288	0.602644	0.443071	2.202398	0.821503	0.606958	1.165437	1.992307	1.393291
TA_3_1.679 7_5	0	0.030696	0.024724	0.012249	0	0	0.033323	0.01503	0.029774	0.067472
DZ_3_1.29 502_1	0.040374	0	0	0	0	0	0.053409	0.047671	0	0.043566
WH_1_1.63 6_12	0	0	0	0	0	0	0	0	0	0
DY_3_1.14 898_1	4.131711	3.052295	4.853365	3.543367	6.050126	5.527453	3.163791	9.070161	8.161271	6.582581

gene_id	Taxonomy	ARG_Catego ry	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
LY_3_1.632 918_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	adeJ	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HZ_1_1.17 900_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Enterobacterales; f__Enterobacteriaceae	multidrug	mdtN	0	0	0	0	0	0	0	0	0	0	0.350138	0	0	0	0	0.158139	0
HZ_3_1.20 0051_1	k__Bacteria; p__Firmicutes	macrolide- lincosamide- streptogrami n	mefA	0.217518	0.469215	0.253635	0.112352	0.094762	0.120449	2.533181	0.320301	0.306656	1.354833	0.093518	0.033741	0.027758	0.057589	0.074255	0.132119	0.105061
RZ_2_1.821 88_7	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Enterobacterales; f__Enterobacteriaceae	bacitracin	bacA	0.855081	0.03515	0.092033	0.074367	0.570167	0.590791	0	0.604707	0.141861	11.01929	0.380568	0	0.047961	0.223546	0.128065	0.057116	0.503406
DZ_2_1.30 3189_1	k__Bacteria; p__Firmicutes	tetracycline	tetM	0	0	0	0.097142	0	0	0.986065	0.185783	0.082281	0	0	0.081521	0	0	0	0	0
RZ_2_1.247 533_4	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	mexT	0	0	0	0.028645	0	0	0.052998	1.129452	0.129235	0.087167	0	0	0	0	0	0	0
RZ_1_1.312 182_1	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales	beta-lactam	CfxA2	5.713558	3.731741	6.373439	0.449171	2.842682	0.547089	1.121627	0.476097	0.359441	0.61561	2.120743	0.256409	3.015732	1.998099	2.243359	1.882312	3.571875
DY_2_1.53 130_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	adeJ	0	0	0	0.397461	0	0	0	0	0	0	0	0	0	0	0	0	0
YT_3_1.289 789_1	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales; f__Lachnospiraceae; g__NA; s__Lachnospiraceae bacterium	tetracycline	tet40	0	0	0	0	0	0	0	0	0	0	0	0	0.320071	0	0	0	0

[illegible]

gene_id	WH_3_1	YT_1_1	YT_3_1	YT_2_1	ZB_1_1	ZB_2_1	ZB_3_1	ZZ_2_1	ZZ_3_1	ZZ_1_1
LY_3_1.632 918_1	0	0	0	0	0	0	0	0	0	0
HZ_1_1.17 900_2	0	0	0	0	0.16301	0	0.172373	0	0	0
HZ_3_1.20 0051_1	0.031206	0.120066	0.128427	0.159326	0.120575	0.035676	0.151006	0.097245	0.134699	0.122418
RZ_2_1.821 88_7	0	3.656535	0.13667	0.081792	0.039841	0	0.109196	0.065296	0.032306	1.953147
DZ_2_1.30 3189_1	0	0	0	0	0	0	0.515679	0	0	0
RZ_2_1.247 533_4	0.040443	0	0	0	0.06144	0	0	0.024929	0.172749	0
RZ_1_1.312 182_1	0.951529	1.442152	5.080332	2.30793	0.205642	2.668218	0.13032	5.912106	4.295597	0.532705
DY_2_1.53 130_1	0	0	0	0	0	0	0	0	0	0
YT_3_1.289 789_1	0	0.401443	0	0	0	0	0	0	0	0

[illegible]

gene_id	JN_3_1	LC_2_1	LC_3_1	LC_1_1	LY_3_1	LY_2_1	LY_1_1	QD_2_1	QD_3_1	QD_1_1	RZ_1_1	RZ_2_1	RZ_3_1	TA_2_1	TA_3_1	TA_1_1	WF_3_1	WF_2_1	WF_1_1	WH_2_1	WH_1_1
WF_3_1.15 537_2	0.058209	0	0	0	0	0	0	0	0.028753	0	0	0	0	0	0	0.058721	2.26377	0.030303	0.034766	0	0
BZ_2_1.492 354_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ZZ_1_1.784 76_4	0.078434	7.414803	0.023839	0.638114	0.141898	0.195414	0.115766	0.183924	0.091028	0.119012	0.030973	4.786051	0	0.269589	9.10103	0.552984	0.423534	0.01883	0.032573	6.408062	0.103947
HZ_3_1.45 9449_1	0.020265	0.017959	0	0	0	0	0	0.271737	0	0	0	0.082275	0	0.181068	0.021	0	0	0	0	0.168517	0.021496
BZ_2_1.302 05_24	0.114957	5.643057	0.025817	0.659261	0.04459	0.144414	0.088866	0.074424	0.04401	0.110057	0.025374	4.170197	0.012162	0.340806	7.567808	0.407133	0.437712	0.030507	0.035131	5.554399	0.076365
HZ_2_1.18 7828_2	0.049276	0.065325	0	0	0	0.07376	0	0	0.122906	0	0.021909	0	0.021336	0.122725	0.076351	0.024878	0.048063	0	0.029636	0	0
WH_1_1.33 8076_1	0	0	0	0	0	0.199202	0	0	0	0	0	0	0	0	0.203915	0	0	0	0	0	1.907349
BZ_1_1.518 850_1	0.428508	1.52221	0.043887	1.277475	0.151893	0.916233	0.114156	2.065229	0.410172	0.127511	0.043818	4.3203	0.618737	3.622474	2.300858	3.132275	3.584984	0.619271	0.355626	3.126174	0.836416
QD_1_1.24 6718_2	0	0	0	0	0	0	0	0	0	0.196344	0	0	0	0	0.880298	0	0	0	0	1.048668	0

[illegible]

gene_id	Taxonomy	ARG_Cat egory	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
J_3_1.166216_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Psychrobacter	bacitracin	bacA	0	0	0	0	0	0	0	0	0	0	0	0	0.36321	1.072089	0.389015	0	0
WH_3_1.30470_1	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales	beta-lactam	OXA-209	0	0	0.164983	0.061893	0	0	0	0.057276	0	0	0	0	0	0	0	0	0
LY_2_1.434330_3	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides; s__Bacteroides propionicifaciens	tetracycline	tet36	0.043581	0.069881	0.240033	0.440494	0.030713	0.036561	4.262011	3.907269	0.098458	8.375205	0.050084	0.063362	0.022024	0.030493	0.039325	0.488333	0.093837
TA_3_1.215856_4	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae; g__Escherichia	multidrug	TolC	0.051544	0	0	0	0.057805	0	0	0.045771	0.038083	0	0.014203	0	0	0.021737	0	0	0
RZ_2_1.254673_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria	multidrug	mexD	0	0	0	1.353288	0	0	0	0	0	0.381497	0	0	0	0	0	0	0
HZ_3_1.382995_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	mexT	0	0	0	0	0	0	0	0	0	0.359991	0	0	0	0	0	0	0
HZ_3_1.61018_3	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae; g__Escherichia; s__Escherichia coli	multidrug	emrE	0.598878	0	0	0	0.231479	0.237539	0	0.082921	0.072907	3.887613	0	0	0	0	0.139627	0	0.225979
TA_2_1.275528_6	k__Bacteria; p__Firmicutes	chloramphenicol	chloramphenicol_and _florfenicol_resistance_gene	0.030214	0	0.014858	0.049742	0	0.019158	2.654964	0.77727	0.576044	1.769442	0	0.112428	0	0.032084	0.016547	0	0.019438
YT_1_1.114569_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae	unclassified	DNA-binding_transcriptional_regulator_gadX	1.263867	0	0.160113	0.258906	0.72455	1.009566	0.034602	0.902088	0.310336	15.74062	0.693785	0	0.095358	0.246928	0.305557	0.056779	1.001177

gene_id	JN_3_1	LC_2_1	LC_3_1	LC_1_1	LY_3_1	LY_2_1	LY_1_1	QD_2_1	QD_3_1	QD_1_1	RZ_1_1	RZ_2_1	RZ_3_1	TA_2_1	TA_3_1	TA_1_1	WF_3_1	WF_2_1	WF_1_1	WH_2_1	WH_1_1
J_3_1.1662 16_2	0	0	0	0	0	0	0	0	0	0	0	0	0	1.13938	0	0	0	0	0	0	0.406241
WH_3_1.30 470_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.23681	0
LY_2_1.434 330_3	0.08308	0.016475	0.083287	0.511269	0.028741	2.392763	0.035699	0.412699	0.371868	0.02341	0.12182	1.093469	0.177679	2.871127	0	0.065457	0.437015	0.009866	0.182031	1.467272	0.019657
TA_3_1.215 856_4	0	0.070083	0	0	0	0	0.02029	0	0	0	0	0	0	0	0.779142	0.026562	0.02581	0	0	0	0
RZ_2_1.254 673_2	0	0	0	0	0	0	0	0	0	0	0	0.473183	0	0.408373	0	0	0	0	0	0	0
HZ_3_1.38 2995_1	0	0	0	0.032289	0	0	0	0.088032	0	0	0	0.028915	0	0	0	0	0	0	0	0	0
HZ_3_1.61 018_3	0	4.029677	0	0.3343	0.07768	0	0.120036	0	0.13968	0	0	3.84949	0	0.161887	4.727978	0.468051	0.734459	0	0	3.154195	0.162501
TA_2_1.275 528_6	0.096382	0	0.103471	0.35174	0	0.231685	0	0.378048	0.467104	0	0	0.333328	4.684039	0.631041	0	0.136398	0.41523	0.02033	0.140289	0.142562	0
YT_1_1.114 569_2	0.176629	14.00742	0.104456	1.561885	0.432992	0.263523	0.454428	0.181003	0.20343	0.178881	0.026265	10.49492	0.051544	0.765391	18.27217	1.306579	0.915667	0.122547	0.070293	12.66434	0.093387

gene_id	WH_3_1	YT_1_1	YT_3_1	YT_2_1	ZB_1_1	ZB_2_1	ZB_3_1	ZZ_2_1	ZZ_3_1	ZZ_1_1
J_3_1.1662 16_2	0	0	0	0	0	0	0	0	0	0
WH_3_1.30 470_1	0.911738	0	0	0	0	0	0	0	0	0
LY_2_1.434 330_3	0.264701	0.032029	0.102885	0.050887	0.092023	0.019302	2.493169	0.073304	0.68474	0.093789
TA_3_1.215 856_4	0	0.030232	0.012173	0	0	0	0.032819	0.014804	0	0.026579
RZ_2_1.254 673_2	0	0	0	0	0	0	0	0	0	0
HZ_3_1.38 2995_1	0	0	0	0	0	0	0	0	0	0
HZ_3_1.61 018_3	0	1.01052	0.284359	0.072282	0	0	0	0	0	0.8254
TA_2_1.275 528_6	0.156425	0	0.01785	0	0	0.039547	1.221555	0.086245	0.213482	0
YT_1_1.114 569_2	0.053423	5.904642	0.43486	0.162644	0.118893	0.029634	0.072393	0.064937	0.064257	3.501876

gene_id	Taxonomy	ARG_Category	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
TA_3_1.117420_3	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia; s__Escherichia fergusonii	polymyxin	arnA	0.007212	0	0	0	0.040664	0.01815	0	0.032161	0.017774	0.036161	0.009946	0	0	0.022705	0	0	0.009317
RZ_3_1.88093_2	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales	macrolide-lincosamide-streptogramin	ermG	0	0	0.027755	0.879434	0.037642	0.462096	0.24917	0	0	0.170835	0	0.034079	0	0	0	0	0
J_1_1.262845_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Psychrobacter	bacitracin	bacA	0.028865	0	0	0	0	0	0	0	0	0	0	0	0.090732	0.156482	0.387195	0	0
ZB_2_1.416404_1	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales; f__Clostridiaceae; g__Clostridium	bacitracin	bacA	0	0	0.090085	0	0	0	0	0.06193	0	0	0	0	0	0	0	0	0
DZ_3_1.147792_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	adeJ	0	0	0	0	0	0	0	0.356703	0	0	0	0	0	0	0	0	0
LC_3_1.180941_4	k__Bacteria; p__Firmicutes; c__Tissierellia; o__Tissierellales; f__Peptoniphilaceae; g__Anaerococcus; s__Anaerococcus lactolyticus	bacitracin	bacA	0	0	0	0.102293	0.028981	0.537544	7.86389	0.061432	0.02588	0.235215	0	0.578301	0	0	0	0	0
QD_2_1.57677_11	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Weeksellaceae; g__Empedobacter; s__Empedobacter falsenii	beta-lactam	metallo-beta-lactamase	0	0	0	0.046926	0	0	0	0.042797	0	3.691808	0	0	0	0	0	0	0
RZ_2_1.429200_3	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales; f__Clostridiaceae; g__Clostridium	bacitracin	bacA	0.201119	0.579235	0.266661	0.036033	0	0	0.168332	0.39023	0.082319	0.221533	0.122693	0.137986	0	0.071969	0	0	0.028645

gene_id	JN_3_1	LC_2_1	LC_3_1	LC_1_1	LY_3_1	LY_2_1	LY_1_1	QD_2_1	QD_3_1	QD_1_1	RZ_1_1	RZ_2_1	RZ_3_1	TA_2_1	TA_3_1	TA_1_1	WF_3_1	WF_2_1	WF_1_1	WH_2_1	WH_1_1
TA_3_1.117 420_3	0	0.024537	0	0	0	0	0.007089	0	0	0	0	0.00936	0	0	0.661899	0.027595	0.03616	0	0.011297	0	0
RZ_3_1.880 93_2	0	0	0.156877	0.119378	0.036271	0.035211	0.054842	0.108815	0.277044	0	0	0.071567	0.220936	1.000187	1.238625	0.179066	0.103213	0	0.126133	0.097732	0.075025
J_1_1.2628 45_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0.164544	0	0	0	0	0	0	0.391172
ZB_2_1.416 404_1	0	0.098334	0	0.06203	0.114242	0	0.043673	0.114082	0.052861	0	0.051597	0	0	0.115942	0	0.056907	0	0	0.065004	0	0.059448
DZ_3_1.14 7792_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
LC_3_1.180 941_4	0.889876	0	0.671166	0.335308	0	0.053734	0	0.166094	2.408921	0	0.120089	0.02727	2.347555	1.709935	0	2.449871	0.866509	0.19708	0.807952	0	0
QD_2_1.57 677_11	0	0	0	0.042623	0	0.226583	0	0.933479	0	0	0.102852	0.076777	0	0	0	0	0.258247	0	0	1.85255	0
RZ_2_1.429 200_3	0.314757	0.10092	0.304848	0.129157	0.439944	0.085442	0.066271	0.205408	0.169817	0.049631	0.255188	0.375901	0.125036	0.171598	0.058951	1.328149	0.222671	0.208708	0.44474	0	0.272433

gene_id	WH_3_1	YT_1_1	YT_3_1	YT_2_1	ZB_1_1	ZB_2_1	ZB_3_1	ZZ_2_1	ZZ_3_1	ZZ_1_1
TA_3_1.117 420_3	0	0.021202	0.017025	0	0	0	0.011509	0.010398	0	0.009312
RZ_3_1.880 93_2	0	0	0.032762	0.098269	0	0	0.825316	0	0	0.035363
J_1_1.2628 45_1	0	0	0	0	0	0	0	0	0	0
ZB_2_1.416 404_1	0	0	0	0	0.071142	0.265293	0	0	0	0
DZ_3_1.14 7792_1	0	0	0	0	0	0	0	0	0	0
LC_3_1.180 941_4	0.244304	0	0.099657	0.049648	0	0	4.154792	0	0	0
QD_2_1.57 677_11	0.174218	0	0	0	0.050225	0	0.046541	0	0.082333	0
RZ_2_1.429 200_3	0.103816	0.129828	0.105713	0.1054	0.347516	1.961943	0.140872	0.0316	0	1.202317

[illegible]

gene_id	JN_3_1	LC_2_1	LC_3_1	LC_1_1	LY_3_1	LY_2_1	LY_1_1	QD_2_1	QD_3_1	QD_1_1	RZ_1_1	RZ_2_1	RZ_3_1	TA_2_1	TA_3_1	TA_1_1	WF_3_1	WF_2_1	WF_1_1	WH_2_1	WH_1_1
DZ_2_1.44 059_10	0	0.023302	0.023541	0.030069	0	0.026331	0	0.05428	0.026801	0	0	0.013337	0.022092	0.025842	0	0	0.012873	0	0	0.036421	0
J_3_1.4912 07_9	0.754027	1.857177	1.529981	1.008668	5.139788	3.047396	5.708457	2.885781	1.669041	2.681469	5.790556	1.393348	0	5.650528	0.951043	0.302519	1.126797	3.304565	1.262418	2.896265	0.553703
WH_2_1.23 4989_1	0	0	0	0	0	0	0	0.23567	0	0	0	0	0	0.082215	0	0	0	0	0	0.28447	0
HZ_2_1.21 6882_3	0.052823	0	0.328834	0	0	0	0	0	0.078742	0	0.023515	0	20.59762	0.264853	0	0	0	0	0.126724	0	0
WH_2_1.23 4614_1	0	0	0	0.314962	0	0	0	0	0.251618	0	0	0.311012	0	0.318509	0	0	0	0	0	0.569832	0
QD_2_1.24 4209_2	0	0	0	0	0	0	0	1.531031	0	0	0	0	0	0	0	0	0	0	0	0	0
QD_3_1.56 0176_1	0.196943	0	0	0	0	0	0	0	0.204151	0	0.058709	0	0	0	0	0	0	0.068021	0	0	0
WF_3_1.11 5822_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5.56944	0.066396	0.03806	0	0

gene_id	Taxonomy	ARG_Catego ry	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
TA_1_1.307845_2	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae; g__Staphylococcus	multidrug	norA	0	0	0	0	0	0	0	0.062097	0.017298	0.052599	0	0.01745	0	0	0	0	0
YT_1_1.75739_14	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Enterobacterales; f__Enterobacteriaceae	multidrug	acrB	0.511631	0	0.078384	0.130443	0.435021	0.470759	0.026071	0.426417	0.105154	8.655868	0.200104	0	0.047171	0.071278	0.073547	0.015274	0.446857
DZ_3_1.337161_1	k__Bacteria; p__Firmicutes	macrolide- lincosamide- streptogrami n	lsa	3.566184	3.461559	0.240062	4.329707	9.768336	1.845444	1.903361	3.614628	3.003698	2.462495	7.179108	4.599368	2.559658	2.356128	1.63249	1.164925	4.445447
WH_2_1.234358_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Vibrionales; f__Vibrionaceae; g__Vibrio; s__Vibrio vulnificus	rifamycin	ADP- ribosylating _transferas e_arr	0.03923	0	0.119939	0.120582	0	0.203504	0	0.222822	0.143739	1.674973	0.106985	0	0.041772	0.129443	0	0	0.149352
WF_3_1.56933_2	k__Bacteria; p__Firmicutes; c__Bacilli	tetracycline	tetS	0.029856	0.01196	0.029027	0	0	0.009403	0.330034	0.532373	0.165552	0.299345	0	0.018601	0.007547	0.007836	0	0.008964	0.202476
WH_1_1.256155_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Moraxellales; f__Moraxellaceae; g__Psychrobacter	multidrug	mexT	0.017521	0.027142	0.017296	0	0	0	0	0	0	0	0	0	0.108072	0.149385	0.096295	0	0.022516
YT_1_1.114569_5	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Enterobacterales; f__Enterobacteriaceae	multidrug	mdtF	0.725307	0	0.046448	0.132088	0.575901	0.471226	0.039604	0.541892	0.095581	9.954555	0.339764	0	0.082525	0.10378	0.134605	0.020627	0.452914
LY_3_1.131126_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	adeJ	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
WH_1_1.213635_2	k__Bacteria; p__Firmicutes	vancomycin	vanW	0	0	0.075745	0	0.090141	0.094705	0	0	0	0	0	0	0.079191	0	0	0	0
WH_1_1.213635_1	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus	vancomycin	vanY	0	0.665254	0	0	0	0	0	0	0	0.597991	0	0	0	0	0	0	0

gene_id	JN_3_1	LC_2_1	LC_3_1	LC_1_1	LY_3_1	LY_2_1	LY_1_1	QD_2_1	QD_3_1	QD_1_1	RZ_1_1	RZ_2_1	RZ_3_1	TA_2_1	TA_3_1	TA_1_1	WF_3_1	WF_2_1	WF_1_1	WH_2_1	WH_1_1
TA_1_1.307845_2	0	0	0	0	0	0	0	0.018526	0.018159	0.01533	0	0.018223	0	0	0	0.290085	0.087868	0	0	0	0
YT_1_1.75739_14	0.091976	6.578382	0.024486	0.664723	0.163245	0.17024	0.146522	0.189955	0.10712	0.097412	0.009495	4.255928	0.008981	0.350421	8.391297	0.405889	0.465447	0.041692	0.046962	6.361787	0.069217
DZ_3_1.337161_1	6.405284	5.47203	3.459455	5.771803	1.895095	4.014403	1.995049	2.443281	3.067639	2.675269	0.77642	3.11088	0	2.328727	4.534741	2.257918	3.574641	2.647188	1.48315	4.757554	1.18922
WH_2_1.234358_1	0	1.144278	0	0.167078	0	0.198453	0.038971	0	0.047743	0	0	0.404206	0	0.257277	0	0	0.145363	0	0	1.058027	0
WF_3_1.56933_2	0.047434	0	0	0.043774	0.019688	0.0574	0	0.078894	0	0	0.008348	0.029059	0.07167	0.382916	0.227912	0.076876	2.674867	0	0	0.308594	0.333301
WH_1_1.256155_1	0	0	0	0	0.023033	0	0	0	0	0	0	0	0	0.111298	0	0	0	0	0	0	0.474526
YT_1_1.114569_5	0.043837	7.451453	0.049597	0.641899	0.159626	0.149609	0.097517	0.142808	0.091346	0.129336	0.02885	5.411121	0.004548	0.381814	8.832476	0.683304	0.483957	0.035316	0.06794	6.70111	0.128519
LY_3_1.131126_2	0	0	0	0	0.456204	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
WH_1_1.213635_2	0	0	0.078772	0	0	0	0	0.091573	0	0	0	0	0	0	0	0	0.086854	0	0	0	0.289126
WH_1_1.213635_1	0	0	0	0	0	0	0.49281	0	0	0	0	0	0	0.608379	0	0	0	0	0	0	1.128078

[illegible]

gene_id	Taxonomy	ARG_Category	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
RZ_1_1.140794_1	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales; f__Clostridiaceae; g__Clostridium; s__Clostridium beiierinckii	tetracycline	tetP	0.037564	0.019867	0.024281	0.145865	0.034652	0.079805	6.080253	0.348216	0.092764	0.314554	0.034146	0.094621	0.03778	0.02558	0.013769	0	0.016255
DZ_3_1.397169_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	mexT	0	0	0	0.057289	0	0	0.052998	0.564726	0.215391	0.174334	0	0	0	0	0	0	0
QD_2_1.416875_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	adeJ	0	0	0	0	0	0	0.183155	0	0	0.06455	0	0	0	0	0	0	0
ZZ_1_1.452208_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae; g__Escherichia	multidrug	mdfA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TA_3_1.23256_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria	aminoglycoside	aac3-VI	0	0	0	0	0.032749	0	0	0	0	0.14808	0	0	0	0	0	0	0
QD_2_1.47153_29	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter; s__Acinetobacter sp. B51(2017)	multidrug	adeJ	0	0	0	0	0	0	0.019371	0.100883	0	1.289506	0	0	0	0	0	0	0.01093
WF_3_1.80771_3	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae	multidrug	mdtD	0.445291	0.017203	0.095521	0.072411	0.441092	0.301744	0.016514	0.378151	0.147095	7.507797	0.224415	0	0.04417	0.068758	0.106397	0.013124	0.315379
WF_3_1.449841_1	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae	tetracycline	tetQ	2.67263	5.449899	2.26456	0.628688	0.994995	1.818143	1.47498	1.685117	2.276122	0.504489	2.13543	0.532471	4.018855	0.987548	3.341129	2.131252	2.835999

gene_id	JN_3_1	LC_2_1	LC_3_1	LC_1_1	LY_3_1	LY_2_1	LY_1_1	QD_2_1	QD_3_1	QD_1_1	RZ_1_1	RZ_2_1	RZ_3_1	TA_2_1	TA_3_1	TA_1_1	WF_3_1	WF_2_1	WF_1_1	WH_2_1	WH_1_1
RZ_1_1.140794_1	0.144708	0	0.200707	0.073621	0.109271	0.082377	0	0.067469	1.258946	0.013714	0.472757	0.114501	0.136373	0.078979	0.082859	0.562578	0.109281	0.067502	0.235217	0.059004	0.086771
DZ_3_1.397169_2	0	0.316966	0	0	0	0.044744	0	0.253591	0	0	0	0.499256	0	0.066779	0.069479	0	0.087472	0	0	0.041317	0.023726
QD_2_1.416875_1	0	0	0	0	0	0	0	0.32871	0	0	0.019613	0	0	0.021967	0	0	0	0	0	0.101976	0
ZZ_1_1.452208_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TA_3_1.23256_1	0	0.054006	0	0	0	0	0	0	0	0	0	0	0	0	0.28386	0	0	0	0	0	0
QD_2_1.47153_29	0	0.373951	0	0.012425	0.005576	0	0	0.7432	0	0	0.014108	0.274082	0	0.015778	1.142821	0	0	0	0	3.267288	0
WF_3_1.80771_3	0.055312	6.06039	0.012428	0.555465	0.143083	0.180731	0.082726	0.114636	0.056538	0.082316	0.036613	3.994743	0	0.368802	6.787542	0.391768	0.421382	0.073446	0	5.397103	0.0294
WF_3_1.449841_1	0.258056	2.087101	1.975567	1.776017	4.79842	2.835539	0.908385	1.021658	1.664937	1.507758	1.728767	1.787551	0	1.332996	1.190708	0.570679	2.630279	3.15407	0.902679	1.117461	0.510475

gene_id	WH_3_1	YT_1_1	YT_3_1	YT_2_1	ZB_1_1	ZB_2_1	ZB_3_1	ZZ_2_1	ZZ_3_1	ZZ_1_1
RZ_1_1.140794_1	0.109847	0	0.044499	0.02906	0.066354	0.315973	0.201565	0.108059	0.071341	0.225997
DZ_3_1.397169_2	0.020221	0	0	0	0.03072	0	0	0.024929	0.419534	0
QD_2_1.416875_1	0	0	0	0	0	0	0	0	0	0
ZZ_1_1.452208_2	0	0	0	0	0	0	0	0	0	1.77808
TA_3_1.23256_1	0	0	0	0	0	0	0	0	0	0
QD_2_1.47153_29	0	0	0	0	0	0	0	0	0.006058	0
WF_3_1.80771_3	0.062131	2.324067	0.256515	0.025422	0.038874	0	0.05184	0.015586	0.015437	1.411603
WF_3_1.449841_1	1.060899	1.480855	2.339479	2.593654	0.909336	0.387314	1.290989	4.72928	1.687835	1.418039

gene_id	Taxonomy	ARG_Catego ry	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
TA_3_1.143 551_3	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia	multidrug	mdtH	0	0	0	0	0	0	0	0.019632	0	0.016621	0	0	0	0	0	0	0
QD_2_1.21 6771_15	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Cytobacillus; s__Cytobacillus eiseniae	tetracycline	tetL	0	0	0	0	0	0	0.11973	0.133049	0	0.253112	0	0	0	0	0	0	0.014507
DZ_2_1.10 3394_1	k__Bacteria; p__Firmicutes	vancomycin	vanG	0	0	0	0.036219	0	0	0.384249	0	0.082772	0	0	0.055496	0	0	0	0	0
WF_3_1.19 1191_4	k__Bacteria; p__Proteobacteria	aminoglycosi de	aph3-I	0.125222	0	0.451416	1.28569	0	0.19298	0.679505	0.582479	0.616324	64.83956	0.068881	0	0.07844	0.162439	0.30707	0	0.032145
RZ_2_1.477 775_7	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Enterobacterales; f__Enterobacteriaceae	polymyxin	arnA	0.640509	0	0.063082	0.109357	0.37614	0.326695	0	0.375212	0.071098	8.516737	0.2387	0	0.05102	0.083348	0.093702	0.008661	0.51245
WF_2_1.89 612_1	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales	bacitracin	bacA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
QD_2_1.19 6415_2	k__Bacteria; p__Firmicutes	vancomycin	vanD	0	0	0	0	0	0	0	0.042797	0	0.036613	0	0	0	0	0	0	0.07588
HZ_3_1.44 7557_1	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus	vancomycin	vanE	0	0	0	0	0	0	0	0	0.05806	0.3806	0	0	0	0	0	0	0
HZ_3_1.95 347_2	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus; s__Enterococcus hirae	multidrug	EmrB- QacA_famil y_major_fa cilitator_tra nsporter	0	0	0	0	0	0	0	0.215697	0	0.196424	0	0	0	0	0	0	0
J_1_1.2735 87_3	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia; s__Escherichia coli	multidrug	emrE	0.200873	0	0	0	0.238555	0	0	0.258913	0	0.716028	0	0	0	0	0.241631	0	0.484823

gene_id	JN_3_1	LC_2_1	LC_3_1	LC_1_1	LY_3_1	LY_2_1	LY_1_1	QD_2_1	QD_3_1	QD_1_1	RZ_1_1	RZ_2_1	RZ_3_1	TA_2_1	TA_3_1	TA_1_1	WF_3_1	WF_2_1	WF_1_1	WH_2_1	WH_1_1
TA_3_1.143 551_3	0	0.015081	0	0	0	0	0	0	0	0	0	0.069072	0	0	0.413812	0	0	0	0	0	0
QD_2_1.21 6771_15	0	0	0	0	0	0	0	1.365629	0	0	0	0.627446	0	0.113282	0	0	0.014081	0	0	0.358633	0
DZ_2_1.10 3394_1	0	0	0	0	0.029491	0	0	0	0	0	0.208991	0	0	0	0	0	0.027987	0	0.126462	0	0
WF_3_1.19 1191_4	0.032206	0.02833	0	0.434265	0.065861	0.927225	0	0.592904	0	0	0	0.227342	0.028375	1.130582	0.099254	0.032468	0.468653	0.066795	0.26801	0.325238	0.272192
RZ_2_1.477 775_7	0.109983	6.715076	0.024809	0.581703	0.142687	0.240353	0.093563	0.104826	0.076234	0.131701	0.008063	4.440051	0.007669	0.288658	8.739616	0.47344	0.452281	0.02939	0.022594	6.28934	0.087829
WF_2_1.89 612_1	0	0	0	0	1.482622	0	0	0	0	0	0	0	0	0	0	0	0	0.739729	0	0	0
QD_2_1.19 6415_2	0	0	0	0	0	0	0	0.23337	0	0.033543	0	0	0	0	0	0	0	0	0	0	0
HZ_3_1.44 7557_1	0	0	0	0.034128	0	0.030126	0	0	0	0	0	0	0	0.030327	0	0.030565	0.058881	0	0	0	0
HZ_3_1.95 347_2	0	0	0	0	0	0	0	0.208861	0	0	0	0.431218	0	0	0	0	0	0	0	0	0
J_1_1.2735 87_3	0	1.105819	0	0.540189	0.255134	0	0	0	0.211602	0	0	0.524133	0.255545	0.273267	1.258092	0	0.718146	0	0	2.394588	0

[illegible]

gene_id	Taxonomy	ARG_Catego ry	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
LY_3_1.140 957_1	k__Bacteria; p__Firmicutes	macrolide- lincosamide- streptogrami n	ermA	1.858349	1.290261	2.257316	5.865959	2.503863	0.678185	6.530795	2.329915	2.311215	2.018567	3.306311	3.901247	7.24225	6.528498	3.908883	8.254379	2.957337
TA_3_1.219 154_3	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia	aminoglycosi de	ant3-lh- aac6-IId	0	0	0.079599	0.476967	0	0.085378	0.256185	0.913134	0	1.976108	0	0	0	0	0	0	0.185117
ZZ_2_1.185 395_1	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales	tetracycline	tetQ	4.537255	6.572521	4.009133	0.968224	1.379852	1.474174	1.012325	0.913454	1.401521	1.312748	2.841751	1.225449	2.923051	1.498953	2.380527	4.917294	2.66632
RZ_2_1.111 624_1	k__Bacteria; p__Proteobacteria; c__Betaproteobacteria; o__Burkholderiales; f__Oxalobacteraceae; g__Oxalobacter; s__Oxalobacter formigenes	bacitracin	bacA	0.022722	0	0	0.182995	0.124653	0	0.034222	0	0	0.140744	0.06237	0	0.070687	0	0	0	0
LC_1_1.319 667_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Enterobacterales; f__Enterobacteriaceae	multidrug	mdtC	0.489143	0	0.046562	0.104047	0.291262	0.356753	0	0.331507	0.080904	6.146063	0.211308	0.00546	0.0352	0.059422	0.056596	0.02612	0.260322
ZZ_2_1.352 72_1	k__Bacteria; p__Firmicutes	tetracycline	tetM	5.227264	3.334104	3.280216	3.492982	6.555811	4.361627	4.256107	3.058959	8.981727	2.005599	3.349111	7.45259	5.774216	8.751077	8.454925	3.30753	3.773363
QD_2_1.25 8713_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia; s__Escherichia coli	aminoglycosi de	aac3-II	0.247435	0	0.052352	0.173289	0.09782	0	0.187088	0.517749	0.43452	11.16536	0	0.021888	0.127215	0.0942	0.116587	0	0.13626
ZB_1_1.264 04_2	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae	bacitracin	bacA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.099115	0	0
HZ_2_1.20 7077_19	k__Bacteria; p__Firmicutes; c__Tissierellia; o__Tissierellales; f__Peptoniphilaceae; g__Anaerococcus	bacitracin	bacA	0	0	0	0	0	0	0.187779	0	0	0	0	1.490245	0	0	0	0	0
ZZ_1_1.277 99_6	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Enterobacterales; f__Enterobacteriaceae	multidrug	mdtB	0.407674	0.007175	0.060043	0.090336	0.357825	0.289161	0.027092	0.363721	0.087428	6.82997	0.275238	0	0.057955	0.074099	0.071679	0.026465	0.212127

gene_id	JN_3_1	LC_2_1	LC_3_1	LC_1_1	LY_3_1	LY_2_1	LY_1_1	QD_2_1	QD_3_1	QD_1_1	RZ_1_1	RZ_2_1	RZ_3_1	TA_2_1	TA_3_1	TA_1_1	WF_3_1	WF_2_1	WF_1_1	WH_2_1	WH_1_1
LY_3_1.140957_1	4.605517	0.878224	1.254175	2.786533	3.457728	15.47497	13.42988	2.799825	2.212178	1.43674	11.94793	1.558917	1.645731	3.001729	1.885835	10.45484	6.779797	0.734744	11.14155	1.241816	1.394984
TA_3_1.219154_3	0	0	0.037404	0.146047	0.086592	0.865613	0	0.094135	0.081801	0	0.038386	0.163837	0.115426	0.254402	0.623603	0	0.246386	0	0	0.44728	0.264655
ZZ_2_1.185395_1	0.841535	1.390182	1.944206	1.81732	4.490876	2.736588	2.514968	1.969093	2.172292	3.509945	2.670964	2.651536	0.040316	3.583417	1.450843	0.225908	1.414529	3.504254	0.615886	1.379815	0.795477
RZ_2_1.111624_1	0	0.051302	0	0.098459	0.029819	0.028955	0	0.029832	0.08626	0	0	0.264592	0	0.029097	0	0	0	0.151514	0	0	0
LC_1_1.319667_1	0.044405	4.976583	0.025118	0.410604	0.080844	0.08419	0.098781	0.104155	0.05204	0.102738	0	3.215446	0	0.234167	6.088783	0.32637	0.32935	0.041732	0.006881	4.35039	0.071008
ZZ_2_1.35272_1	6.709308	3.225937	4.609968	4.12965	6.287579	2.938849	4.509114	5.195635	3.954728	7.480448	8.123615	4.115565	0.307007	2.58172	3.012379	4.255627	2.860494	4.455085	6.668029	6.625976	5.703353
QD_2_1.258713_2	0	1.61855	0	0.179579	0.023232	0.406177	0.017441	0.744099	0.067895	0.019424	0.02005	0.663824	0.019464	0.471635	6.170346	0.02281	0.419083	0.023711	0	4.876051	0.526531
ZB_1_1.26404_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HZ_2_1.207077_19	0.079644	0	0	0.030024	0	0	0	0	0.026375	0	0	0	0	0.052975	0	0	0.025859	0.221864	0.031838	0	0
ZZ_1_1.27799_6	0.067483	4.969305	0.005089	0.521317	0.087752	0.108036	0.095727	0.123104	0.064429	0.066333	0.034546	3.352715	0.004669	0.237341	6.986564	0.44467	0.316976	0.042277	0.062738	4.876112	0.04796

gene_id	WH_3_1	YT_1_1	YT_3_1	YT_2_1	ZB_1_1	ZB_2_1	ZB_3_1	ZZ_2_1	ZZ_3_1	ZZ_1_1
LY_3_1.140 957_1	1.083119	1.492227	3.386962	3.23082	5.078116	3.290165	3.001072	11.28825	18.51644	9.121091
TA_3_1.219 154_3	0.187128	0	0	0	0.166227	0	0	0	0.423241	0
ZZ_2_1.185 395_1	1.057361	2.137026	4.455777	3.434556	0.957446	1.088852	1.978456	3.917917	6.710882	2.569538
RZ_2_1.111 624_1	0.158419	0	0.107494	0.053598	0.039217	0	0	0	0.222034	0
LC_1_1.319 667_1	0.004963	2.447675	0.129025	0.035683	0.015978	0	0.048978	0.018989	0.006272	1.4132
ZZ_2_1.352 72_1	4.627428	5.503218	3.187367	4.171092	8.361939	9.747238	4.559595	3.12004	7.891252	5.810555
QD_2_1.25 8713_2	0.183615	0.334948	0.02089	0.020777	0	0	0.027962	0.075425	0.522655	0.249659
ZB_1_1.264 04_2	0	0	0	0	0.618501	0	0	0	0	0
HZ_2_1.20 7077_19	0	0	0.024531	0	0	0.026867	0	0	0	0
ZZ_1_1.277 99_6	0.015084	2.506728	0.073202	0.072305	0.032369	0	0.056706	0.05771	0.006354	1.14607

gene_id	Taxonomy	ARG_Catego ry	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
WH_3_1.69 620_1	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales	vancomycin	vanR	0.088483	0	0.207573	0.093225	0.199898	0.03794	0	0.042498	0.036144	0.036353	0	0	0.185619	0.288086	0.165005	0.147526	0.075337
WH_1_1.23 3240_1	k__Bacteria; p__Firmicutes	vancomycin	vanU	0	0	4.946513	0	0	0	0	0	0	0	0	0	1.040294	0	0.566601	0	0
LC_2_1.690 06_1	k__Bacteria; p__Firmicutes	tetracycline	tetP	1.543536	1.167683	1.221508	2.418121	1.034859	1.98333	3.33807	5.061739	2.446952	5.364088	1.207079	4.019464	1.988541	0.914069	0.525331	1.361503	0.811449
HZ_3_1.46 8774_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Pasteurellales; f__Pasteurellaceae; g__Pasteurella; s__Pasteurella multocida	aminoglycosi de	aadA	0	0	0	0	0	0	0.147106	0	0	0.849331	0	0	0	0	0	0	0
DY_2_1.37 2958_2	k__Bacteria; p__Proteobacteria	chloramphenicol	floR	0	0	0	0.309264	0	0	0	0	0	0	0	0	0	0	0	0	0
DZ_1_1.27 5248_1	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae; g__Staphylococcus	bacitracin	bcrA	0	0	0	0	0	0	0.06773	0.129102	0.471284	0.055772	0	0	0	0	0	0	0
LY_3_1.432 261_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	major_facili tator_super family_tran sporter	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
QD_2_1.25 0378_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	adeC	0.02178	0	0	0	0	0	0.016558	0.048311	0	4.315185	0	0	0	0	0	0	0.014042
QD_2_1.25 0378_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	adeJ	0.025316	0	0.004082	0	0	0	0.090302	0.012597	0.010406	3.850768	0	0	0	0	0	0	0
QD_2_1.50 462_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	emrB	0	0	0	0	0	0	0.043563	0	0	0.179216	0	0	0	0	0	0	0

gene_id	JN_3_1	LC_2_1	LC_3_1	LC_1_1	LY_3_1	LY_2_1	LY_1_1	QD_2_1	QD_3_1	QD_1_1	RZ_1_1	RZ_2_1	RZ_3_1	TA_2_1	TA_3_1	TA_1_1	WF_3_1	WF_2_1	WF_1_1	WH_2_1	WH_1_1
WH_3_1.69620_1	0	0.033229	0	0.082628	0.077241	0	0.20467	0.038616	0.220457	0.166413	0.136097	0	0	0	0.193915	0	0.073255	0.039024	0	0	1.918657
WH_1_1.233240_1	0	1.089515	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2.974521
LC_2_1.69006_1	4.830328	1.67795	5.276832	1.85583	3.460603	1.87992	1.957957	3.842734	4.524601	1.019428	3.935009	2.881724	2.749539	3.217909	3.694828	19.00987	7.816254	2.367348	7.003662	1.981985	2.726826
HZ_3_1.468774_1	0	0	0	0	0	0.2679	0	0	0	0	0	0	0	0	0	0	0	0	0	0.479578	0
DY_2_1.372958_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DZ_1_1.275248_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0.09123	0.059846	0	0	0	0	0	0
LY_3_1.432261_1	0	0	0	0	0.619241	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.071831
QD_2_1.250378_1	0	0	0	0.047738	0.028693	0.167275	0	4.181036	0.014171	0	0.024475	0.776743	0	0.068496	0.057744	0.014032	0.286215	0	0	3.278212	0
QD_2_1.250378_2	0	0	0	0.037236	0	0.113723	0	4.089862	0	0	0.051667	0.673004	0	0.092355	0.022438	0	0.185365	0	0.013279	2.885155	0.034248
QD_2_1.50462_2	0	0	0	0	0	0	0	0.418759	0	0	0	0	0	0.037593	0	0	0	0	0	0.171011	0

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gene_id	Taxonomy	ARG_Catego ry	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
DZ_3_1.47 9598_2	k__Bacteria; p__Proteobacteria; c__Epsilonproteobacteri a; o__Campylobacterales; f__Campylobacteraceae; g__Campylobacter; s__Campylobacter coli	multidrug	cmeA	0	0	0	0	0	0	0	1.96931	0	0	0.020706	0	0	0	0	0	0
DZ_3_1.47 9598_1	k__Bacteria; p__Proteobacteria; c__Epsilonproteobacteri a; o__Campylobacterales; f__Campylobacteraceae; g__Campylobacter; s__Campylobacter coli	multidrug	cmeB	0	0.007609	0.004554	0	0.00666	0	0	1.57005	0	0	0.006492	0	0.009468	0	0	0	0
ZB_3_1.122 684_7	k__Bacteria; p__Firmicutes; c__Bacilli n	macrolide- lincosamide- streptogrami n	mphB	0.121318	0	0.039295	0.511612	0	0.60647	2.14338	0.347567	0.828305	1.10812	0	0.441562	0.040936	0.296963	0.371885	0	0.025457
RZ_1_1.321 054_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Aeromonadales; f__Succinivibrionaceae	unclassified	cAMP- regulatory_ protein	0	0	0	0	0	0	0.052357	0	0	0	0	0	0	0	0	0.1331	0
QD_2_1.40 2813_4	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia	sulfonamide	sul2	0.642103	0.098205	0.531332	12.34378	0.706139	0.273115	1.967755	5.693208	1.025571	54.16383	0.499585	0.105789	0.642234	0.29828	0.47323	0.790972	0.374338
RZ_2_1.414 425_1	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides	beta-lactam	class_A_bet a- lactamase	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
RZ_3_1.864 26_1	k__Bacteria; p__Firmicutes; c__Tissierellia; o__Tissierellales; f__Peptoniphilaceae; g__Anaerococcus	bacitracin	bacA	0	0	0	0	0	0	0	0	0	0	0	0.071517	0	0	0	0	0
WH_2_1.34 1013_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	adeC	0	0	0	0.0256	0	0	0.023587	1.04092	0.134054	0.07758	0	0	0	0	0	0	0.04006

gene_id	JN_3_1	LC_2_1	LC_3_1	LC_1_1	LY_3_1	LY_2_1	LY_1_1	QD_2_1	QD_3_1	QD_1_1	RZ_1_1	RZ_2_1	RZ_3_1	TA_2_1	TA_3_1	TA_1_1	WF_3_1	WF_2_1	WF_1_1	WH_2_1	WH_1_1
DZ_3_1.47 9598_2	0	0	0	0	0	0	0	0	0	0	0	0.039007	0	0	0	0	0	0	0	0	0
DZ_3_1.47 9598_1	0	0	0	0	0	0	0	0	0	0	0.00524	0	0	0	0	0	0	0	0.007396	0	0.006363
ZB_3_1.122 684_7	0.152209	0.02241	1.326845	0.476127	0.026053	0.751444	0	2.059654	1.869884	0.080286	0	0.3338	2.447865	1.316399	4.031732	0.153666	0.838247	0	0.640055	0.678015	0.501036
RZ_1_1.321 054_2	0	0	0	0	0	0	0	0	0	0	0.857379	0	0	0	0	0	0	0	0	0	0
QD_2_1.40 2813_4	0.054795	5.785503	0.04869	1.509282	0.337205	5.02321	0.084603	5.932363	0.434691	0.142408	0.414981	7.736678	0.023874	3.318946	5.365206	0.193536	2.363455	0.200121	0.229693	20.90524	2.482931
RZ_2_1.414 425_1	0	0.02669	0	0	0	0	0	0	0.029862	0	0	0.39771	0	0.121309	0.031176	0	0	0	0	0.111405	0
RZ_3_1.864 26_1	0	0	0	0	0	0	0	0	0	0	0	0	0.682872	0	0	0	0	0	0	0	0
WH_2_1.34 1013_2	0	0.105693	0	0.022648	0	0	0	0.061553	0	0	0	0.462357	0	0	0.0206	0	0.01945	0	0	0.293842	0

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gene_id	Taxonomy	ARG_Category	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
WH_1_1.412251_4	k_Bacteria; p_Proteobacteria	multidrug	mexT	0.087606	0	0.051887	0.085934	0	0	0	0.025669	0.021539	0.588379	0	0	0	0.018673	0	0	0.090063
TA_1_1.225618_7	k_Bacteria; p_Proteobacteria; c_Gammaproteobacteria; o_Enterobacteriales; f_Enterobacteriaceae; g_Escherichia; s_Escherichia coli	multidrug	mdtM	0.46693	0.018492	0.034264	0.038821	0.392588	0.353847	0.017738	0.586259	0.086219	7.526775	0.20899	0	0.035654	0.086331	0.076328	0.014126	0.300403
RZ_2_1.73245_3	k_Bacteria; p_Proteobacteria; c_Gammaproteobacteria; o_Enterobacteriales; f_Enterobacteriaceae	chloramphenicol	catB	0	0	0	0.113977	0	0	0.035592	0.206115	0	0.29277	0.032448	0	0.122809	0	0	0	0.030294
ZZ_3_1.145207_1	k_Bacteria; p_Firmicutes; c_Tissierellia; o_Tissierellales; f_Peptoniphilaceae; g_Helcococcus; s_Helcococcus kunzii	tetracycline	tetT	0.049821	0	0.043039	0.651297	0	2.505322	15.31887	1.111266	1.174166	5.196898	0	4.724432	0.011195	0.043469	0.056165	0.013305	0.063348
DY_2_1.263954_1	k_Bacteria; p_Proteobacteria; c_Gammaproteobacteria; o_Xanthomonadales; f_Xanthomonadaceae; g_Luteimonas; s_Luteimonas sp. YGD11-2	multidrug	multidrug_transporter	0	0	0	0.524736	0	0	0	0.063831	0	0	0	0	0	0	0	0	0
HZ_3_1.316502_10	k_Bacteria; p_Proteobacteria; c_Gammaproteobacteria; o_Moraxellales; f_Moraxellaceae; g_Acinetobacter; s_Acinetobacter larvae	multidrug	mexT	0	0	0	0	0	0	0	0	0	11.77218	0	0	0	0	0	0	0
DZ_3_1.157167_1	k_Bacteria; p_Proteobacteria; c_Gammaproteobacteria; o_Moraxellales; f_Moraxellaceae; g_Acinetobacter	multidrug	adeJ	0	0	0	0	0	0	0	0.379279	0	0	0	0	0	0	0	0	0
LY_1_1.275318_1	k_Bacteria; p_Bacteroidetes; c_Bacteroidia; o_Bacteroidales	tetracycline	tetQ	6.636175	9.990896	7.272193	2.53255	4.623523	2.180297	3.847789	1.971242	4.093599	1.871509	5.207099	3.301713	5.270512	3.147233	3.605895	7.341369	4.703771

gene_id	JN_3_1	LC_2_1	LC_3_1	LC_1_1	LY_3_1	LY_2_1	LY_1_1	QD_2_1	QD_3_1	QD_1_1	RZ_1_1	RZ_2_1	RZ_3_1	TA_2_1	TA_3_1	TA_1_1	WF_3_1	WF_2_1	WF_1_1	WH_2_1	WH_1_1
WH_1_1.412251_4	0	0.01981	0	0	0	0	0	0.069161	0	0	0	0	0	0.311635	1.27379	0	0.043736	0	0	0.309876	0.83042
TA_1_1.225618_7	0.014869	6.798086	0	0.715848	0.107622	0.194192	0.183896	0.16936	0.060722	0.063308	0.065661	4.325689	0	0.26462	7.821719	0.586742	0.335915	0	0.018161	5.917408	0.015801
RZ_2_1.73245_3	0	0	0	0.034128	0	0.060252	0	0	0	0	0	1.404356	0	0.121309	0.034168	0	0.02944	0	0	0.139257	0
ZZ_3_1.145207_1	1.000696	0	4.45538	1.007947	0.039845	1.227129	0.023481	0.948087	8.044444	0	0.085657	0.646694	59.63836	4.221949	0.055026	2.420955	1.688216	0.313303	3.263905	0.235425	0
DY_2_1.263954_1	0	0	0	0	0	0	0	0	0	0	0	0.018741	0	0	0	0	0	0	0	0	0
HZ_3_1.316502_10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DZ_3_1.157167_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.052542	0
LY_1_1.275318_1	2.33609	3.131033	3.562884	3.440042	5.080248	6.495357	8.798111	4.489097	3.496139	5.648423	4.017177	6.638104	0.06744	4.479715	2.320999	0.784108	3.343931	5.806956	2.335964	2.284032	2.15288

gene_id	WH_3_1	YT_1_1	YT_3_1	YT_2_1	ZB_1_1	ZB_2_1	ZB_3_1	ZZ_2_1	ZZ_3_1	ZZ_1_1
WH_1_1.41 2251_4	0	0	0	0	0	0	0	0	0	0.022502
TA_1_1.225 618_7	0.06685	2.856899	0.193013	0.027338	0	0.015379	0.01856	0	0.016573	1.624905
RZ_2_1.732 45_3	0	0	0	0	0	0	0	0.100159	0.297315	0.060549
ZZ_3_1.145 207_1	0.284291	0	0.111277	0.21182	0.126515	0.114794	32.18293	0.157351	0.536719	0.073885
DY_2_1.26 3954_1	0	0	0	0	0	0	0	0	0	0
HZ_3_1.31 6502_10	0	0	0	0	0	0	0	0	0	0
DZ_3_1.15 7167_1	0	0	0	0	0	0	0	0	0	0
LY_1_1.275 318_1	2.956199	4.934388	10.40161	5.590913	2.359141	2.688877	4.474683	7.095546	8.322494	3.502517

gene_id	Taxonomy	ARG_Catego ry	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
DZ_2_1.457742_1	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Streptococcus; s__Streptococcus suis	aminoglycoside	aadE	0	0	0	0	0	0	0.91436	0	0	0	0.81207	0	0	0	0	0	0
WF_2_1.220514_3	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae; g__Staphylococcus; s__Staphylococcus aureus	aminoglycoside	streptomycin_resistance_protein	0.195484	0	0.019355	0.666562	0.161776	0.525966	1.379138	2.078242	1.133091	2.749127	0.053709	0.145085	0	0.167168	0.086201	0	0.075279
WF_1_1.307223_1	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales; f__Lachnospiraceae; g__Lacrimispora; s__Lacrimispora celerecrescens	chloramphenicol	chloramphenicol_and_florfenicol_resistance_gene	0.103202	0	0	0.153741	0	0	1.850242	0.325889	0.285372	1.174502	0	0.056947	0	0	0	0	0.065165
TA_3_1.80448_3	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae; g__Escherichia	macrolide-lincosamide-streptogramin	macA	0.01494	0	0.01469	0	0.124635	0.05683	0	0.021968	0	0.018618	0	0	0	0.015861	0	0	0
WH_2_1.318180_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	mexB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TA_2_1.499240_1	k__Bacteria; p__Bacteroidetes	macrolide-lincosamide-streptogramin	erm35	0	0	0	0.038623	0	0	1.122599	1.432683	0	1.137981	0	0.11878	0	0	0	0	0
JN_1_1.183884_1	k__Bacteria; p__Bacteroidetes	tetracycline	tet36	0.06769	0.360186	0	1.068561	0	0.089964	6.606633	6.130825	0.411406	9.104948	0	0.081521	0	0	0	1.289434	0.169673
HZ_2_1.413653_2	k__Bacteria; p__Actinobacteria	tetracycline	tetracycline_resistance_protein	2.475818	2.688364	1.607406	2.26486	2.825829	2.705816	2.632498	4.900838	2.318967	2.613319	3.262217	4.390347	3.855799	1.826746	1.495152	2.872753	2.035197
YT_1_1.117428_4	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae	fosmidomycin	rosB	0.495368	0.014051	0.102983	0.177263	0.495281	0.3744	0.013417	0.418741	0.114564	8.741434	0.240511	0	0.07141	0.096437	0.095601	0.010605	0.295656

gene_id	JN_3_1	LC_2_1	LC_3_1	LC_1_1	LY_3_1	LY_2_1	LY_1_1	QD_2_1	QD_3_1	QD_1_1	RZ_1_1	RZ_2_1	RZ_3_1	TA_2_1	TA_3_1	TA_1_1	WF_3_1	WF_2_1	WF_1_1	WH_2_1	WH_1_1
DZ_2_1.457742_1	0	0	0	0	0	0.688271	0	0.765515	0.827747	0	0	0	3.37087	0	0	0	0	0	0	0.729769	0
WF_2_1.220514_3	0.149987	0.022088	0.155801	0.566432	0.051358	0.299274	0	0.760773	1.02173	0.021572	0.022234	0.272074	0.698479	2.389775	0.826084	2.464368	22.50044	1.179318	0.300512	0.115192	1.217959
WF_1_1.307223_1	0	0	0.096111	0.080556	0	0	0	0.492928	0.184732	0	0	0.344895	0.26731	0.243588	0	0.134223	0.090361	0	0.152236	0.285528	0
TA_3_1.80448_3	0	0.016905	0	0	0	0	0.014728	0	0	0	0	0	0	0.018906	0.553574	0	0.037334	0	0.023129	0	0
WH_2_1.318180_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.220221	0
TA_2_1.499240_1	0	0	0.218692	0.659703	0.031574	0.36789	0.02381	0	0.364363	0	0.082662	0.12454	0.379366	0.525077	0	0.062225	0.389467	0	0.036754	0.056689	0
JN_1_1.183884_1	0	0	0.150182	1.314549	0	4.160891	0	0.959998	0.311153	0	0.081935	3.043474	0.173752	3.411983	0	0.264813	0.910459	0	0.19465	2.692044	0
HZ_2_1.413653_2	2.696076	3.571434	2.7058	2.86122	1.742428	1.523936	1.223549	3.24617	2.563705	3.127177	1.279906	3.536645	0.210233	2.101661	1.659816	2.070822	1.87904	3.337555	2.57026	4.086738	2.197693
YT_1_1.117428_4	0.033613	6.007918	0.032676	0.567533	0.127745	0.157989	0.112634	0.104692	0.046084	0.089063	0.039482	4.131929	0	0.3203	8.308269	0.57422	0.540699	0.047774	0.02753	5.923779	0.086173

gene_id	WH_3_1	YT_1_1	YT_3_1	YT_2_1	ZB_1_1	ZB_2_1	ZB_3_1	ZZ_2_1	ZZ_3_1	ZZ_1_1
DZ_2_1.45 7742_1	0	0	0	0	0	0	0.933731	0	0	0
WF_2_1.22 0514_3	0.113165	0.056908	0.046219	0	0.238435	0.025371	4.390016	0.693499	0.247109	0.351083
WF_1_1.30 7223_1	0.098992	0	0	0	0	0	0.158886	0.105628	0	0.06512
TA_3_1.804 48_3	0	0.021827	0	0	0	0	0.047381	0	0.042234	0
WH_2_1.31 8180_1	0	0	0	0	0	0	0	0	0	0
TA_2_1.499 240_1	0.196135	0	0	0	0	0	1.780375	0	0.067208	0
JN_1_1.183 884_1	1.162219	0	0.24106	0.328118	0.206821	0	1.856443	0.090822	1.074666	0.169674
HZ_2_1.41 3653_2	3.473613	1.799814	0.979689	2.116982	2.421534	2.542258	1.9205	2.793963	2.677131	2.785919
YT_1_1.117 428_4	0.040209	3.163059	0.218404	0.092666	0	0	0.031119	0.063375	0.012791	1.847858

gene_id	Taxonomy	ARG_Catego ry	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
LY_3_1.690 132_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	oprM	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
WH_2_1.20 871_1	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Niallia; s__Niallia nealsonii	chloramphenicol	cat_chloramphenicol acetyltransferase	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DZ_2_1.16 4749_1	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales	vancomycin	vanR	0	0	0	0	0	0	0.512957	0	0	0	0	0.146846	0	0	0	0.080306	0
DY_3_1.15 0334_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Enterobacteriales; f__Enterobacteriaceae; g__Klebsiella; s__Klebsiella pneumoniae	aminoglycoside	aadA	1.297282	0.350859	0.372328	11.88109	1.587465	1.365501	0.510629	7.753071	1.589796	32.43916	1.370769	0.232935	0.402314	0.381871	0.457929	0.207684	1.162545
TA_1_1.772 5_6	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Streptococcus	tetracycline	tetM	0.714403	0.170445	0.42962	2.479275	1.08346	3.08775	14.83034	4.803424	3.376665	12.07539	0.425356	1.042118	0.461674	0.588152	0.427662	0.239325	0.838461
RZ_2_1.438 444_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	adeJ	0	0	0	0.050207	0	0	0.064502	0.8944	0.114468	0.074216	0	0	0	0	0	0	0.00546
YT_1_1.369 237_1	k__Bacteria; p__Proteobacteria; c__Epsilonproteobacteri a; o__Campylobacterales; f__Campylobacteraceae; g__Campylobacter	beta-lactam	OXA-61	0.099833	0.075469	0.124593	0	0.034098	0.351566	0	1.773246	0	0	0.102692	0	0	0.107601	0.027737	0.309474	0.223648
TA_2_1.495 585_1	k__Bacteria; p__Proteobacteria	trimethoprim	dfrA16	0	0	0.071818	1.554271	0	0	0.295819	1.393369	0.246844	6.584829	0	0.163043	0.150239	0	0.079481	0	0.169673
ZB_3_1.858 06_3	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales	macrolide-lincosamide-streptogramin	lsa	0.061696	0	0.030119	0.515048	0	0	0.391064	0.639187	0.189933	4.475118	0	0	0	0	0	0	0.053054

gene_id	JN_3_1	LC_2_1	LC_3_1	LC_1_1	LY_3_1	LY_2_1	LY_1_1	QD_2_1	QD_3_1	QD_1_1	RZ_1_1	RZ_2_1	RZ_3_1	TA_2_1	TA_3_1	TA_1_1	WF_3_1	WF_2_1	WF_1_1	WH_2_1	WH_1_1
LY_3_1.690 132_2	0	0	0	0	0.880983	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
WH_2_1.20 871_1	0	0	0	0	0	0	0	0.313012	0	0	0	0.088354	0	0	0	0	0	0	0	0.361985	0
DZ_2_1.16 4749_1	0	0	0	0	0.078803	0.076394	0.182754	0	0	0	0.073075	0	0	0	0	0	0	0	0.175984	0	0
DY_3_1.15 0334_2	0	13.37923	0.653233	2.598692	0.247318	0.258783	0.278778	1.69525	0.576871	0.207385	0	13.02979	0.145304	2.915635	13.37725	0.160802	2.535148	0.437259	0.434513	15.85284	1.096058
TA_1_1.772 5_6	1.390688	7.47156	1.348292	1.432217	0.29242	2.22168	2.786873	8.745467	3.137769	0.545618	0.92666	3.574403	2.786036	3.966835	4.86881	3.235362	22.05244	0.50735	2.114945	5.434599	3.507701
RZ_2_1.438 444_2	0	0.287329	0	0.049648	0	0	0	0.066986	0.00558	0.004503	0	0.45475	0	0.015762	0.011219	0	0.047659	0	0	0.38401	0
YT_1_1.369 237_1	0	0.028157	0.084993	0	0.425487	0	0.148179	0.261909	0.031419	0	0.371889	0.161393	0	0	0	0.12907	0	0.066396	0.03806	0	0
TA_2_1.495 585_1	0.088341	0	0	0.187793	0	0.424581	0	1.221816	0.076381	0	0	1.914105	0.086876	0.368863	5.706339	0.264813	0.496614	0	0.097325	2.058622	0.091769
ZB_3_1.858 06_3	0.052353	0.011651	0	0.21048	0.027099	0.039496	0	1.940522	0.522625	0	0.092363	0.786874	0	0.400552	1.567986	0.05299	0.283197	0	0.208411	2.173106	0.47318

gene_id	WH_3_1	YT_1_1	YT_3_1	YT_2_1	ZB_1_1	ZB_2_1	ZB_3_1	ZZ_2_1	ZZ_3_1	ZZ_1_1
LY_3_1.690 132_2	0	0	0	0	0	0	0	0	0	0
WH_2_1.20 871_1	0	0	0	0	0	0	0	0	0	0
DZ_2_1.16 4749_1	0	0	0	0	0	0	0	0.082065	0	0
DY_3_1.15 0334_2	0.783336	3.452349	0.333746	0.608714	0	0	0.586288	1.659316	1.123605	1.973378
TA_1_1.772 5_6	0.673121	2.279034	1.061262	0.983694	0.985174	1.020764	18.03002	0.813626	2.420494	1.908672
RZ_2_1.438 444_2	0.043076	0	0	0	0.00771	0	0	0.006107	0.169454	0.005457
YT_1_1.369 237_1	0.058175	0.614996	0.590537	0.147399	0.078055	0.160337	0.0785	0.422115	0.034803	0
TA_2_1.495 585_1	0.498094	0	0	0	0.10341	0	0	0.726573	0.358222	0.254511
ZB_3_1.858 06_3	0.905219	0	0.060711	0.02406	0	0.013583	0.802046	0	0	0.039769

gene_id	Taxonomy	ARG_Cat egory	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
TA_3_1.185941_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia	multidrug	emrD	0.028416	0	0	0	0.01978	0.018001	0	0.020912	0.034959	0.070861	0.019551	0	0	0	0	0	0
LC_2_1.261073_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	adeJ	0	0	0	0.01501	0	0	0	0.203256	0.014982	0.05208	0	0	0	0	0	0	0
WF_1_1.377144_2	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae; g__Staphylococcus; s__Staphylococcus aureus	macrolide-lincosamide-streptogramin	vgaE	0.047626	0	0.064931	0.748071	0.013352	0.743708	1.027944	0.549603	0.855153	2.225637	0.078645	0.142043	0.009649	0.07011	0.051663	0.02293	0
HZ_3_1.284296_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter; s__Acinetobacter defluvii	multidrug	adeC	0	0	0	0	0	0	0	0	0	0.291902	0	0	0	0	0	0	0
J_3_1.65345_1	k__Bacteria; p__Firmicutes	tetracycline	tet32	0.36203	0.454159	0.202391	1.130601	0.837169	0.289075	0.42841	0.719532	0.521548	0.342936	0.82227	0.476251	0.237358	0.391783	0.284287	0.593816	0.389956
DZ_2_1.43713_4	k__Bacteria; p__Firmicutes	macrolide-lincosamide-streptogramin	ermTR	0	0	0	0.088501	0	0.107391	1.337833	0.563536	0.341809	0.859918	0	0.137236	0	0	0.062224	0	0
ZB_3_1.36171_4	k__Bacteria; p__Firmicutes; c__Tissierellia; o__Tissierellales; f__Peptoniphilaceae; g__Anaerococcus; s__Anaerococcus lactolyticus	bacitracin	bacA	0	0	0	0	0	0.026877	2.605598	0	0	0	0	4.769961	0	0	0	0	0
BZ_3_1.322292_1	k__Bacteria; p__Firmicutes	tetracycline	tetW	0.195443	0	0	0	0.232006	1.053366	0.558825	1.008513	0	0	0.263191	0	1.750181	0	0.231501	0	0
QD_3_1.571453_1	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae; g__Staphylococcus; s__Staphylococcus aureus	macrolide-lincosamide-streptogramin	ermC	0	0	0.026438	0.084232	0.035675	0	0	1.050792	0.098723	0.685038	0	0.065111	0	0	0.088281	0.03285	0.035028

gene_id	JN_3_1	LC_2_1	LC_3_1	LC_1_1	LY_3_1	LY_2_1	LY_1_1	QD_2_1	QD_3_1	QD_1_1	RZ_1_1	RZ_2_1	RZ_3_1	TA_2_1	TA_3_1	TA_1_1	WF_3_1	WF_2_1	WF_1_1	WH_2_1	WH_1_1
TA_3_1.185941_1	0	0	0.016227	0	0	0	0	0.01872	0	0	0	0	0	0	0.684626	0.018321	0.071028	0	0	0	0
LC_2_1.261073_1	0	0.194022	0	0	0	0.009584	0	0	0	0	0	0.155809	0	0.063711	0.014266	0	0	0	0	0.033985	0
WF_1_1.377144_2	0.07261	0.086235	0.381223	0.431426	0	0.20708	0.028072	0.715695	1.117303	0	0.010668	0.148058	1.324856	1.611592	0.492025	0.061257	2.084377	0	0.623547	0.044925	0.579253
HZ_3_1.284296_2	0	0	0	0	0	0	0	0.137658	0	0	0	0	0	0	0	0.033948	0.032643	0	0	0	0.035568
J_3_1.65345_1	0.262529	0.726699	0.496446	0.465906	0.612832	0.22174	0.28672	0.261111	0.215729	0.247177	0.159178	0.459774	0.007981	0.249485	0.419956	0.15534	0.290402	0.478799	0.193777	0.408657	0.226667
DZ_2_1.43713_4	0.071594	0	0.063175	0.200294	0	0.319055	0	0.328661	0.057924	0	0.03208	0.360279	0.763208	0.12116	0	0.360607	0.207828	0	0	0.0984	0
ZB_3_1.36171_4	0.175664	0	0.928528	0.24386	0	0	0	0	0.802974	0	0.072053	0	8.263987	0.026913	0	0	0.840251	0.112617	0.420136	0	0
BZ_3_1.322292_1	0	0	0	0	0.745105	0	0.202196	0.489387	0	0	0	0	0	0.266439	0	0	0	0	0	0	0
QD_3_1.571453_1	0	0.029794	0	0.0392	0.034631	0	0	0	1.356194	0.029609	0	0.035031	0.02987	0.483794	7.694802	0.17089	0.851991	0.549869	0.048226	0	0.905635

gene_id	WH_3_1	YT_1_1	YT_3_1	YT_2_1	ZB_1_1	ZB_2_1	ZB_3_1	ZZ_2_1	ZZ_3_1	ZZ_1_1
TA_3_1.185941_1	0	0.020769	0.016786	0	0	0	0	0.020301	0.020102	0
LC_2_1.261073_1	0.019091	0	0	0	0.025664	0	0	0	0.026173	0
WF_1_1.377144_2	0.108633	0.013955	0.033691	0.102019	0.017094	0	23.60412	0.027346	0.040631	0.061334
HZ_3_1.284296_2	0	0	0	0	0	0	0	0	0	0
J_3_1.65345_1	0.191849	0.504538	0.44125	0.364007	0.852237	0.40287	0.351836	0.440495	0.883878	0.505261
DZ_2_1.43713_4	0	0	0	0	0	0	0.408595	0	0	0
ZB_3_1.36171_4	0	0	0.024914	0	0	0.081807	1.828261	0	0	0
BZ_3_1.322292_1	0.487839	0.263477	0	0	0.274668	0	0	0.262271	0	0.479977
QD_3_1.571453_1	0.030852	0	0	0.031237	0.090202	0	0.08536	0.222289	0.03677	0.033774

gene_id	Taxonomy	ARG_Catego ry	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
WH_1_1.53 551_2	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales; f__Oscillospiraceae; g__Flavonifractor; s__Flavonifractor sp. An306	vancomycin	vanR	0	0	0	0	0	0	0	0	0	0	0	0	0.473855	0	0	0	0
TA_1_1.219 618_7	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae; g__Staphylococcus	unclassified	truncated_ putative_re sponse_reg ulator_ArIR	0	0	0	0	0	0	0	0.189851	0	0.040691	0	0	0	0	0	0	0
HZ_3_1.46 1332_1	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus; s__Enterococcus hirae	aminoglycosi de	aac6-II	0	0	0	0	0	0	0	0	0	0.725955	0	0	0	0	0	0	0
WH_3_1.56 181_2	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales	tetracycline	tetQ	11.50461	7.07182	14.97001	1.125089	6.757717	5.009004	3.81404	0	5.335161	2.415437	16.22607	2.338828	9.174084	6.089164	8.730032	9.001623	7.777648
WF_3_1.42 5636_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia	beta-lactam	PSE-1	0.019642	0	0	0.446832	0	0.02502	0.088968	0.460193	0.12067	2.884326	0	0	0	0.021195	0.064973	0	0.050426
YT_3_1.571 624_7	k__Bacteria; p__Bacteroidetes	beta-lactam	CfxA3	3.658574	7.384377	6.129579	2.281657	5.722478	2.746361	3.741757	0.595412	1.887744	1.758325	1.432946	2.62655	1.286859	3.749172	3.148017	4.241481	2.373866
DY_2_1.13 0686_3	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides; s__Bacteroides xvlanisolvens	beta-lactam	CfxA2	41.2864	20.37726	58.11297	4.395686	18.9071	8.880125	8.568707	5.297078	6.086997	6.870542	17.26307	2.618898	24.53859	16.79822	18.61629	23.03528	25.27062
DZ_3_1.49 8710_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia; s__Escherichia coli	multidrug	mdtP	0.273946	0.017292	0.053357	0.113849	0.116105	0.219652	0	0.259362	0.061794	4.213108	0.132229	0	0.01219	0.117562	0.147604	0.013196	0.184069
DZ_1_1.41 2213_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia	trimethopri m	dfrA20	0	0	0.059236	0.08328	0	0	0	0.236019	0.206833	0.684131	0	0	0	0	0	0	0

gene_id	JN_3_1	LC_2_1	LC_3_1	LC_1_1	LY_3_1	LY_2_1	LY_1_1	QD_2_1	QD_3_1	QD_1_1	RZ_1_1	RZ_2_1	RZ_3_1	TA_2_1	TA_3_1	TA_1_1	WF_3_1	WF_2_1	WF_1_1	WH_2_1	WH_1_1
WH_1_1.53 551_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.017057
TA_1_1.219 618_7	0	0	0	0	0	0	0	0	0.040901	0	0	0	0	0	0.043461	0.514563	0.164193	0	0	0	0
HZ_3_1.46 1332_1	0	0	0	0	0	0	0	0	0	0	0	0.198822	0	0	0	0	0	0	0	0	0
WH_3_1.56 181_2	2.211952	6.216787	2.091064	2.626788	2.476636	12.30281	9.960466	5.654841	2.585239	2.136552	22.78406	4.784614	0	5.83226	0.784625	2.411829	2.997986	4.95761	0	3.904528	1.545116
WF_3_1.42 5636_1	0	0.022194	0	0	0.051605	0.273603	0	0.335675	0.050071	0	0.022345	0.762878	0	0.175242	3.901501	0	0.440871	0	0	0.722195	0.026602
YT_3_1.571 624_7	1.063921	3.017069	2.538349	1.975372	3.551389	5.235169	8.089309	1.20916	1.561924	1.262581	1.724334	2.56053	0.019464	2.043552	0.700801	0.47901	2.842768	1.517525	1.989111	1.271107	1.124233
DY_2_1.13 0686_3	2.358779	5.631564	4.678757	4.572876	17.06557	34.69444	76.97168	9.823285	7.539135	11.51634	67.65449	5.339899	0.216614	21.60633	2.24247	0.487649	11.41206	12.73339	7.594281	4.121836	7.713893
DZ_3_1.49 8710_1	0.029072	4.215723	0	0.202051	0.055228	0	0.063082	0.116305	0.043141	0.076208	0.012271	2.526554	0	0.135817	4.027665	0.115086	0.274634	0.040567	0	2.336746	0.014566
DZ_1_1.41 2213_2	0	0	0	0.158385	0.073477	0.142473	0	0.190321	0	0	0	0.436738	0	0.838103	0.073561	0	0.5776	0	0	0.72888	0

gene_id	WH_3_1	YT_1_1	YT_3_1	YT_2_1	ZB_1_1	ZB_2_1	ZB_3_1	ZZ_2_1	ZZ_3_1	ZZ_1_1
WH_1_1.53 551_2	0	0	0	0	0	0	0	0	0	0
TA_1_1.219 618_7	0	0	0	0	0	0	0	0	0	0
HZ_3_1.46 1332_1	0	0	0	0	0	0	0	0	0	0
WH_3_1.56 181_2	5.076966	1.911272	18.80766	8.458097	0	3.21387	2.902736	14.37447	9.762145	9.242499
WF_3_1.42 5636_1	0.022732	0	0	0	0	0	0.031025	0.027871	0.386204	0
YT_3_1.571 624_7	2.894151	3.916561	5.874851	5.20149	1.300886	2.187696	2.208998	5.983697	4.430264	2.841477
DY_2_1.13 0686_3	11.65629	9.584898	28.00845	29.02269	3.09514	13.9334	4.670762	31.48827	28.41937	13.62167
DZ_3_1.49 8710_1	0.016026	2.024174	0.097392	0.076663	0	0.014406	0	0.015668	0	1.083708
DZ_1_1.41 2213_2	0.068658	0	0	0	0.17756	0	0.173649	0	0.07577	0.071256

gene_id	Taxonomy	ARG_Catego ry	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
DY_2_1.372958_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacterales; f__Enterobacteriaceae; g__Enterobacter; s__Enterobacter sp. MGH 10	sulfonamide	sul1	0	0	0	1.069282	0	0	0	0	0	0	0	0	0	0	0	0	0
ZZ_3_1.362065_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	adeJ	0	0	0	0.045621	0	0	0.013773	0.207712	0.03317	0.15909	0	0	0	0	0	0	0.011674
LY_2_1.334528_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria	beta-lactam	PSE-1	0	0	0	0.220141	0	0	0	0.422857	0	2.326531	0.223823	0	0.375314	0.375754	0.395981	0	0
LC_2_1.195679_3	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__NA; g__Exiguobacterium; s__Exiguobacterium sp. S3-2	macrolide-lincosamide-streptogramin	mphB	0.404269	0.518348	0.373307	0.515375	0.02734	0.303235	0.932137	0.434458	0.46301	0.492498	2.152418	0.269844	0.122809	0.509077	0.612516	0.341069	0.81463
QD_3_1.533368_1	k__Bacteria; p__Actinobacteria	tetracycline	tetW	5.411065	4.101827	2.798905	4.632886	7.919156	3.444819	5.221134	3.86648	5.202506	4.397229	6.19667	6.736984	7.620488	4.220279	4.388809	4.33398	3.561034
DZ_1_1.74387_1	k__Bacteria; p__Bacteroidetes	beta-lactam	CfxA2	34.64496	36.81903	41.18859	12.26956	42.60876	11.31374	9.022815	13.64352	29.90414	11.65702	22.42294	13.41709	17.91121	12.98422	14.83208	21.99017	26.39863
TA_1_1.378630_6	k__Bacteria; p__Firmicutes; c__Tissierellia; o__Tissierellales; f__Peptoniphilaceae; g__Helcococcus; s__Helcococcus kunzii	tetracycline	tetT	0.04498	0	0	0.982411	0.042299	2.329687	20.69211	1.186584	1.946785	5.293689	0.013852	5.197266	0	0.119283	0.101801	0	0.071809
LY_3_1.264828_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Psychrobacter; s__Psychrobacter pasteurii	multidrug	mexT	0.134926	0	0	0.16575	0	0.064276	0	0.321511	0.373256	0.482699	0	0	0	0	0	0	0
TA_3_1.292611_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia	multidrug	mdtK	0.022567	0	0	0	0.047371	0.028511	0	0.016677	0.041675	0.042302	0	0	0	0	0	0	0

gene_id	JN_3_1	LC_2_1	LC_3_1	LC_1_1	LY_3_1	LY_2_1	LY_1_1	QD_2_1	QD_3_1	QD_1_1	RZ_1_1	RZ_2_1	RZ_3_1	TA_2_1	TA_3_1	TA_1_1	WF_3_1	WF_2_1	WF_1_1	WH_2_1	WH_1_1
DY_2_1.372958_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ZZ_3_1.362065_2	0	0.058524	0	0.01324	0	0	0	0.052496	0	0	0	0.299786	0	0.015231	0.03282	0	0.027992	0	0	0.084092	0
LY_2_1.334528_1	0	0	0	0.447352	0	0.971411	0	0	0	0	0	0.215609	0	0.457853	2.445978	0	0.596287	0	0	0.747873	0
LC_2_1.195679_3	0.481995	0.336148	2.099935	1.321888	0.468958	0.177118	0.372178	1.538223	1.56666	0.919911	0.180556	0.564893	0.176035	0.657456	0.549999	0.384165	0.469876	0.345038	0.51814	1.285629	0
QD_3_1.533368_1	4.27917	5.742079	3.880744	4.818074	2.744448	2.920732	2.80442	4.365782	5.238601	3.665228	2.650966	4.647311	0.529897	3.552823	3.929228	3.205396	4.233557	5.492292	4.570416	3.860443	4.505384
DZ_1_1.74387_1	8.243559	18.9828	12.56839	14.99032	16.34517	10.26756	26.29239	10.62042	16.3731	11.29377	8.496568	8.013157	0.120657	32.27815	7.566669	5.56072	14.3949	19.10613	9.369641	7.413071	16.78004
TA_1_1.378630_6	1.375627	0.034176	5.248303	1.897024	0.029839	2.418977	0.087382	1.08468	10.13487	0	0.215268	0.934963	74.40509	5.349023	0.083045	4.909092	2.729645	0.557369	3.42208	0.30554	0.027213
LY_3_1.264828_2	0	0	0	0.196003	0.243933	0.02154	0	0.022197	0	0	0	0.109236	0.037046	0.684974	0	0	0.126333	0	0.078101	0.119328	0
TA_3_1.292611_2	0	0.051125	0	0	0	0	0	0	0	0	0	0	0	0	0.687948	0	0.01412	0	0	0	0

gene_id	WH_3_1	YT_1_1	YT_3_1	YT_2_1	ZB_1_1	ZB_2_1	ZB_3_1	ZZ_2_1	ZZ_3_1	ZZ_1_1
DY_2_1.37 2958_1	0	0	0	0	0	0	0	0	0	0
ZZ_3_1.362 065_2	0	0	0	0	0	0	0	0.01301	0.22872	0
LY_2_1.334 528_1	0	0	0	0	0	0	0	0	0	0
LC_2_1.195 679_3	0.459198	0.923677	1.266257	0.875557	0.552508	0.154374	2.119618	0.365775	0.278485	0.432503
QD_3_1.53 3368_1	4.988495	4.502086	3.509493	3.932865	4.439329	5.599783	3.560019	6.437717	7.827829	4.692374
DZ_1_1.74 387_1	18.26447	19.22972	26.182	27.56547	7.719691	7.440132	13.11938	6.385655	11.47933	11.31933
TA_1_1.378 630_6	0.487571	0.044233	0.191305	0.18299	0.028412	0.160692	36.83527	0.260495	0.496363	0.088035
LY_3_1.264 828_2	0	0	0	0.019816	0.02963	0	0.160207	0	0.023776	0.173341
TA_3_1.292 611_2	0	0.016533	0.013326	0	0	0	0.071787	0.016184	0	0

gene_id	Taxonomy	ARG_Catego ry	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
ZZ_2_1.246 493_2	k__NA; p__NA; c__NA; o__NA; f__NA; g__NA; s__uncultured organism	tetracycline	tetW	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
QD_2_1.39 5528_3	k__Bacteria; p__Actinobacteria; c__Actinomycetia; o__Corynebacteriales; f__Corynebacteriaceae; g__Corynebacterium; s__Corynebacterium glutamicum	tetracycline	tetZ	0.025472	0	0	1.012372	0.035554	0.241698	0.661875	0.817867	2.507868	4.494657	0.43821	0.25311	0.116902	0	0	0.015442	0.131256
DZ_2_1.10 1208_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	adeJ	0	0	0	0	0	0	0.195916	0	0	0.054582	0	0	0	0	0	0	0
J_2_1.3036 14_8	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales; f__Clostridiaceae; g__Clostridium; s__Clostridium sp. SN20	macrolide- lincosamide- streptogrami n	vatB	0	0.052607	0.073214	0	0.338184	0	0	0.102943	0	0	0	0.044151	0.420526	0	0.040725	0.091259	0
TA_3_1.274 882_1	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Bacillaceae; g__Fredinandcohnia; s__Fredinandcohnia aciditolerans	macrolide- lincosamide- streptogrami n	ermG	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ZB_2_1.104 482_2	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales	bacitracin	bacA	0	0	0	0.035484	0	0	0.099386	0	0.080987	0	0	0	0	0	0	0.054218	0
WH_1_1.42 7849_1	k__Bacteria; p__Firmicutes	vancomycin	vanB	0	0.031648	0	0	0	0	0	0	0	0	0	0	0.02133	0	0	0	0
WH_1_1.42 7849_2	k__Bacteria; p__Firmicutes	vancomycin	vanH	0.022722	0.069206	0.022608	0.036599	0.031163	0	0	0	0	0	0	0	0.047124	0	0	0	0
QD_2_1.32 5012_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	mexT	0	0	0	0	0	0	0	0	0	0.62232	0	0	0	0	0	0	0

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gene_id	Taxonomy	ARG_Catego ry	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
DY_2_1.82798_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Cellvibrionales; f__Cellvibrionaceae; g__Cellvibrio; s__Cellvibrio mixtus	multidrug	mexD	0	0	0	0.451096	0	0	0	0	0	0	0	0	0	0	0	0	0
WH_2_1.90264_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	mexB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ZB_1_1.383066_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae; g__Escherichia; s__Escherichia coli	macrolide-lincosamide-streptogramin	ermB	0.387362	0	0	3.711932	1.592399	3.071444	2.32134	0.17198	0.294668	1.667928	0.995236	1.391664	1.432403	2.2913	1.253284	2.352399	1.457198
QD_2_1.449153_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	adeJ	0	0	0	0	0	0	0.127766	0	0	0	0	0	0	0	0	0	0
TA_2_1.497377_2	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacteriales; f__Enterobacteriaceae	trimethoprim	dfrA17	0.230594	0	0	1.126091	0.09945	0.14963	0.285824	0.218822	0.188055	2.965566	0.367442	0.141034	0.040929	0.042284	0.043576	0	0.14658
DZ_3_1.14281_1	k__Bacteria; p__Bacteroidetes	macrolide-lincosamide-streptogramin	ermF	0	0	0	0	0	0	0	2.074724	0	0	0	0	0	0	0	0	0
ZB_1_1.313233_3	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales	macrolide-lincosamide-streptogramin	vatE	2.297285	0	4.128287	10.5165	16.3989	125.4618	2.128739	3.435477	3.750081	5.683201	3.331488	18.56541	3.757748	7.083693	8.008158	67.76894	0.576326
WH_2_1.23994_2	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Weeksellaceae; g__Empedobacter; s__Empedobacter falsenii	beta-lactam	metallo-beta-lactamase	0	0	0	0	0	0	0	0	0	0.199194	0	0	0	0	0	0	0

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gene_id	Taxonomy	ARG_Catego ry	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
RZ_3_1.324 35_4	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia	multidrug	qacEdelta1	0.166196	0	0.743702	24.82817	0.592669	2.240563	3.948199	13.12774	18.80874	31.74906	2.462053	1.376921	1.501254	0.943766	0.395981	0	1.211011
HZ_3_1.24 3725_1	k__Bacteria; p__Bacteroidetes; c__Flavobacteriia; o__Flavobacteriales; f__Flavobacteriaceae; g__Myroides	beta-lactam	MUS-1	0	0	0	0	0	0	0	0	0	0.30605	0	0	0	0	0	0	0
HZ_3_1.38 1468_2	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus; s__Enterococcus asini	multidrug	multidrug_t ransporter	0	0	0	0	0	0	0	0	0	0.616673	0	0	0	0	0	0	0
DZ_1_1.23 1770_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia; s__Escherichia coli	aminoglycosi de	aadA	0.02407	0	0.023999	0.733831	0	0	0.072426	0.314491	0.38407	1.519218	0.132085	0	0	0.025908	0	0	0.400746
TA_1_1.106 179_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Pseudomonadales; f__Pseudomonadaceae; g__Pseudomonas; s__Pseudomonas aeruginosa	aminoglycosi de	aadA	0	0	0	0.35929	0	0	0.060759	0.058766	0.346218	0.024986	0.027649	0	0	0	0	0	0
RZ_2_1.491 61_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia	aminoglycosi de	aac6-I	0	0	0.074536	1.474489	0	0	0.179576	0.859432	0.309606	2.503823	0.113967	0	0.042886	0.111093	0.022951	0	0.042941
ZB_3_1.405 409_1	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae	tetracycline	tetS	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HZ_3_1.17 6079_2	k__Bacteria; p__Firmicutes	tetracycline	tetP	0.012539	0	0.036854	0	0	0	1.009146	0.369987	0	0.360054	0	0	0	0	0	0	0
TA_1_1.110 627_3	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae; g__Staphylococcus	bacitracin	bacA	0	0	0	0	0	0	0	0.061124	0	0.104008	0	0.025908	0	0	0	0	0

gene_id	JN_3_1	LC_2_1	LC_3_1	LC_1_1	LY_3_1	LY_2_1	LY_1_1	QD_2_1	QD_3_1	QD_1_1	RZ_1_1	RZ_2_1	RZ_3_1	TA_2_1	TA_3_1	TA_1_1	WF_3_1	WF_2_1	WF_1_1	WH_2_1	WH_1_1
RZ_3_1.32435_4	1.379834	5.863772	0.179924	3.097138	0.847354	4.446293	0.684584	5.952244	1.227626	0.418135	0.203518	15.121	1.949529	14.57724	6.69361	6.622983	10.72426	1.211585	0.685777	14.94902	2.594463
HZ_3_1.243725_1	0	0	0	0	0	0	0	0	0	0	0	0.040142	0	0	0	0	0	0	0	0	0
HZ_3_1.381468_2	0	0	0	0	0	0	0	0	0	0	0	0.094501	0	0	0	0	0.08979	0	0	0	0
DZ_1_1.231770_1	0	0.217295	0	0.104164	0	0.091972	0	0.536947	0.091091	0	0	0.871781	0.054195	0.432416	0.095175	0.12445	0.269631	0	0	2.777666	0.130435
TA_1_1.106179_1	0.02575	0	0	0.029148	0	0.077029	0	0	0.051254	0	0	0.208461	0.178836	0.179722	0.053153	0.441902	0.100381	0	0	0.071165	0.027263
RZ_2_1.49161_1	0	0.196409	0	0.047078	0	0.419592	0	0.428592	0	0	0	1.177417	0	0.332331	0.099994	0	0.831395	0.055466	0.031838	0.976685	0
ZB_3_1.405409_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HZ_3_1.176079_2	0	0	0	0	0	0.032081	0	0.082662	0	0	0.028247	0.097528	0	0.01581	0	0.032326	0.031365	0	0	0.429145	0
TA_1_1.110627_3	0	0	0	0	0	0	0	0	0.026634	0	0	0	0	0	0.027665	0.595625	0.208987	0	0	0	0

gene_id	WH_3_1	YT_1_1	YT_3_1	YT_2_1	ZB_1_1	ZB_2_1	ZB_3_1	ZZ_2_1	ZZ_3_1	ZZ_1_1
RZ_3_1.324 35_4	8.915945	3.785022	0.196618	0.412124	0.491534	0	2.012145	10.38639	4.85759	3.23624
HZ_3_1.24 3725_1	0	0	0	0	0	0	0	0	0	0
HZ_3_1.38 1468_2	0	0	0	0	0	0	0	0	0	0
DZ_1_1.23 1770_1	0.39227	0.034913	0.056945	0	0.082753	0.030977	0.03788	0.305662	0.134416	0.308066
TA_1_1.106 179_1	0.023311	0	0	0	0.035014	0	0.095345	0.028545	0.028252	0
RZ_2_1.491 61_1	0.286391	0.043064	0.024967	0.024438	0	0	0.1637	0.558547	0.195831	0.186205
ZB_3_1.405 409_1	0	0	0	0	0	0	1.880712	0	0	0
HZ_3_1.17 6079_2	0.014378	0	0.014811	0	0.044648	0	0.239086	0	0.017781	0
TA_1_1.110 627_3	0	0	0	0	0	0	0	0.059386	0.029386	0

gene_id	Taxonomy	ARG_Catego ry	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
RZ_2_1.492 009_1	k__Bacteria; p__Firmicutes; c__Erysipelotrichia; o__Erysipelotrichales; f__Coprobacillaceae; g__Coprobacillus	tetracycline	tet32	0	0.64302	0.115057	0.162684	0	0	0	0.460385	0.469804	0.096622	0.07802	0.467225	0	0	0	0.07213	0.277724
WH_1_1.31 1742_3	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Streptococcus; s__Streptococcus agalactiae	vancomycin	vanW	0.022979	0	0.022874	0	0	0	0	0	0	0.028462	0	0	0.166876	0.222235	0.127315	0.028389	0
WH_3_1.42 0078_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Enterobacteriales; f__Enterobacteriaceae	aminoglycosi de	ant2-I	0	0	0.236305	1.356596	0.044941	0.129297	0.348892	0.478355	1.308092	1.603348	0.182623	0.040948	0.10572	0	0	0	0.212705
ZZ_1_1.118 488_6	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Limosilactobacillus; s__Limosilactobacillus mucosae	bacitracin	bacA	0	0	0	0.035127	0	0.083281	0.03278	0	0	0	0.029857	0	0	0.069977	0	0.026807	0.027886
BZ_1_1.205 165_18	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Streptococcus; s__Streptococcus agalactiae	vancomycin	vanG	0	0	1.00984	0.052946	0.022377	0	0.048839	0	0.019833	0.02008	0.022181	0	0.30104	0.051292	0.194495	0	0
LY_3_1.620 973_1	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales; f__Clostridiaceae; g__Clostridium	bacitracin	bacA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TA_3_1.679 7_3	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Enterobacteriales; f__Enterobacteriaceae; g__Escherichia	multidrug	mdtN	0.033045	0	0	0	0.022908	0.083927	0	0	0.020316	0.04113	0.04544	0	0	0.017582	0	0	0

gene_id	JN_3_1	LC_2_1	LC_3_1	LC_1_1	LY_3_1	LY_2_1	LY_1_1	QD_2_1	QD_3_1	QD_1_1	RZ_1_1	RZ_2_1	RZ_3_1	TA_2_1	TA_3_1	TA_1_1	WF_3_1	WF_2_1	WF_1_1	WH_2_1	WH_1_1
RZ_2_1.492009_1	0	0.245707	0.430409	0	0.071536	0	0	0.071355	0.259405	0.722841	0	1.559029	0.068738	0.148017	0.214891	0.143361	0	0	0	0.064496	0.074729
WH_1_1.311742_3	0	0.02594	0.078342	0.033183	0	0.02928	0.022721	0	0.087184	0	0	0.089192	0	0	0	0	0	0	0.035146	0.027066	0.988636
WH_3_1.420078_1	0.128955	0	0	0.190851	0	0.321713	0	0.349023	0.041211	0	0	0.301658	0	0.782209	0.133988	0.345886	1.158673	0.087922	0.050265	0.510965	0.09049
ZZ_1_1.118488_6	0.306271	0	0	0	0.171294	0.055447	0.042987	0.028565	0.055166	0	0.024814	0.028144	0	0.055615	0.028693	0.16857	0.027095	0	0	0.051242	0.26512
BZ_1_1.205165_18	0.082359	0.1277	0	0	0	0.020604	0.047695	0	0.020736	0	0.018257	0	0	0	0.085326	0	0	0	0	0.019021	0.246299
LY_3_1.620973_1	0	0	0	0	1.174371	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TA_3_1.6797_3	0	0.018686	0	0	0	0	0	0	0	0	0	0	0	0.020959	0.78656	0	0	0	0	0	0

gene_id	WH_3_1	YT_1_1	YT_3_1	YT_2_1	ZB_1_1	ZB_2_1	ZB_3_1	ZZ_2_1	ZZ_3_1	ZZ_1_1
RZ_2_1.492009_1	0	0.07801	0.062581	0.066291	0.086733	0	0	0	0	0
WH_1_1.311742_3	0	0.03336	0.027179	0	0	0	0.036196	0	0.032128	0
WH_3_1.420078_1	0.95341	0	0.039528	0	0.055821	0	0.104255	0.884335	0.184083	0.212547
ZZ_1_1.118488_6	0	0.094806	0	0	0.037646	0	0	0.030776	0.243653	0.306549
BZ_1_1.205165_18	0.204392	0	0	0	0	0	0.025549	0.023731	0	0
LY_3_1.620973_1	0	0	0	0	0	0	0	0	0	0
TA_3_1.6797_3	0	0.024108	0	0	0	0	0.10466	0.047076	0.023303	0.04246

gene_id	Taxonomy	ARG_Catego ry	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
TA_2_1.126 657_2	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Planococcaceae; g__Metalysinibacillus; s__Metalysinibacillus jejuensis	vancomycin	vanS	0	0	0.228855	0.141909	0	0	11.36804	0	0.126447	0.371845	0	0	0	0	0	0	0
HZ_3_1.25 1018_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	chloramphe nicol	cmIA	0	0	0	0	0	0	0	0.055049	0.023131	0.444337	0	0	0	0	0	0	0.024171
QD_2_1.69 332_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	mexT	0	0	0	0	0	0	0.166064	0	0	0.068413	0	0	0	0	0	0	0
LY_1_1.285 82_1	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus; s__Enterococcus hirae	tetracycline	tet32	0.56564	0.273084	0.316328	0.684116	0.366774	0.938166	0.266463	0.237026	0.550104	0.39503	2.015458	0.398628	0.425083	0.414062	0.605041	0.194067	0.328924
TA_3_1.144 733_7	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia	multidrug	mdtE	0.042327	0	0	0	0.019645	0.035749	0	0	0.017358	0	0	0	0	0.01496	0	0	0
LY_3_1.271 529_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	mexB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
QD_1_1.47 0896_1	k__Bacteria; p__Firmicutes	vancomycin	vanR	0.129567	0.094484	0.088289	0	0.039706	0	0	0	0.107687	0	0.441442	0	0	0	0	0	0
BZ_2_1.170 030_1	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides	beta-lactam	metallo- beta- lactamase	1.57942	0	1.608091	0	0	0	0	0	0	0	0	0	0	0.028932	0	0	0

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gene_id	Taxonomy	ARG_Cat egory	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
WH_3_1.230898_1	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales; f__Oscillospiraceae; g__Ruminococcus; s__Ruminococcus bromii	vancomycin	vanW	0.190195	0	0	0.506239	0	0	0	0.245599	0	0	0	0	0	0.21345	0.225529	0	0
TA_2_1.36012_1	k__Bacteria; p__Firmicutes; c__Bacilli	macrolide-lincosamide-streptogramin	lsa	0	0	0	0	0	0	0.790059	0	0.629168	0	0	0	0	0	0	0	0
WH_2_1.266091_7	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Moraxellales; f__Moraxellaceae; g__Acinetobacter	multidrug	mexT	0	0	0	0	0	0	0	0.051339	0	1.351091	0	0.021701	0	0	0	0	0.022516
ZB_3_1.57831_2	k__Bacteria; p__Firmicutes	macrolide-lincosamide-streptogramin	ermTR	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TA_1_1.232481_1	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae; g__Staphylococcus	macrolide-lincosamide-streptogramin	msrA	0	0	0	0.017339	0	0	0	0.107606	0	0.090931	0	0	0	0	0	0	0
WF_2_1.340290_1	k__Bacteria; p__Firmicutes	macrolide-lincosamide-streptogramin	mphB	1.085834	0.183786	0.315955	0.09708	0	0.050792	1.383957	0.552942	0.220392	0.668089	1.532434	0.295804	0.231177	0.042638	0.065959	0.367292	1.765087
TA_3_1.181660_21	k__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Enterobacterales; f__Enterobacteriaceae; g__Escherichia	multidrug	mdtG	0.026128	0	0	0	0.072897	0.033067	0	0.01926	0.016077	0.032607	0.035968	0	0	0	0.014266	0	0
WF_3_1.179423_5	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae; g__Staphylococcus	macrolide-lincosamide-streptogramin	vgaA	0	0	0	0	0	0.023991	0	1.127391	0.011714	0.119018	0.026215	0	0	0.020031	0.010333	0	0

gene_id	JN_3_1	LC_2_1	LC_3_1	LC_1_1	LY_3_1	LY_2_1	LY_1_1	QD_2_1	QD_3_1	QD_1_1	RZ_1_1	RZ_2_1	RZ_3_1	TA_2_1	TA_3_1	TA_1_1	WF_3_1	WF_2_1	WF_1_1	WH_2_1	WH_1_1
WH_3_1.230898_1	0.234894	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.230522	0.261849	0	0
TA_2_1.360012_1	0	0	0	0	0	0	0	0	0	0	0	0.675992	0	0.671357	0	0	0	0	0	0	0.63095
WH_2_1.266091_7	0	0.49526	0	0	0	0	0	1.083525	0	0	0	0.385788	0	0.02226	1.296949	0	0	0	0	4.276295	0
ZB_3_1.57831_2	0	0	0	0	0	0	0	0	0.163291	0	0	0	0	0.294011	0	0	0	0	0.173827	0	0
TA_1_1.232481_1	0	0.01177	0	0	0	0.0133	0.010223	0.013708	0.027069	0	0	0.013473	0	0	0.041321	0.495795	0.104031	0	0	0	0
WF_2_1.340290_1	0.546183	0.247713	1.236488	0.288673	0.821126	0.177981	0.549862	0.838355	0.25387	0.330225	0.022683	0.528297	0.110599	0.813273	0.236861	0.630816	0.173956	0.240018	0.275617	1.409369	0.107977
TA_3_1.181660_21	0	0	0	0	0.017199	0	0.01287	0	0	0	0	0	0	0.016485	0.519052	0	0.049006	0	0	0	0
WF_3_1.179423_5	0	0.021559	0.010892	0.027834	0	0.012181	0.009357	0	0.024837	0	0	0	0	0	0	0.269529	0.500309	0	0	0	0.115851

gene_id	WH_3_1	YT_1_1	YT_3_1	YT_2_1	ZB_1_1	ZB_2_1	ZB_3_1	ZZ_2_1	ZZ_3_1	ZZ_1_1
WH_3_1.230898_1	0.950086	0.256534	0	0.236217	0	0.210251	0	0	0	0
TA_2_1.360012_1	0	0	0	0	0	0	0	0	0	0
WH_2_1.266091_7	0	0	0	0	0	0	0	0	0	0
ZB_3_1.57831_2	0.145811	0.084542	0	0	0	0	0.243516	0	0.159761	0
TA_1_1.232481_1	0	0.015231	0	0	0	0	0	0.074582	0.014774	0.013391
WF_2_1.340290_1	0.207681	0.406063	0.664727	0.879969	0.381603	0.206806	0.40917	0.141356	0.280164	1.840681
TA_3_1.181660_21	0	0	0.015432	0	0	0	0.041496	0	0	0
WF_3_1.179423_5	0.021727	0	0	0	0.017094	0	0.0909	0.082037	0.013544	0.061334

[illegible]

[illegible]

[illegible]

[illegible]

gene_id	JN_3_1	LC_2_1	LC_3_1	LC_1_1	LY_3_1	LY_2_1	LY_1_1	QD_2_1	QD_3_1	QD_1_1	RZ_1_1	RZ_2_1	RZ_3_1	TA_2_1	TA_3_1	TA_1_1	WF_3_1	WF_2_1	WF_1_1	WH_2_1	WH_1_1
YT_3_1.274 490_2	0	0	0	0	0.326464	0	0.268371	0.320908	0	0	0	0	0	0	0	0	0	0	0	0.310659	0
TA_3_1.380 69_1	0	0.084836	0	0	0	0	0	0	0	0	0	0.195736	0	0	1.081082	0	0	0	0	0	0
TA_1_1.217 258_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.338103	0.036401	0	0	0	0
WF_2_1.11 4998_1	0.744935	0.409843	5.911934	2.968496	0.063522	2.744668	0.263482	5.115196	7.625494	0	0.055448	1.440517	29.25123	7.956015	1.180763	0.845075	11.6325	0.483534	5.840584	8.981642	2.525884
DZ_2_1.23 274_1	0	0	0	0	0	0.103537	0	0.035552	0.033979	0	0	0.070139	0	0	0	0	0	0	0	0.031927	0
QD_3_1.18 75_1	0.472194	1.575663	1.38734	1.770237	0	0.179765	0.151014	1.077966	1.704754	0.013891	0.02879	0.828139	9.554489	3.529095	0.236914	0.01647	4.037849	2.604362	1.865294	0.482465	0.345896
ZZ_3_1.934 73_1	0	0	0.500066	0	0	0	0	0	0	0	0.51326	0	0	0	0.568675	0	0	0	0	0	0

gene_id	WH_3_1	YT_1_1	YT_3_1	YT_2_1	ZB_1_1	ZB_2_1	ZB_3_1	ZZ_2_1	ZZ_3_1	ZZ_1_1
YT_3_1.274490_2	0	0	0.305533	0	0	0	0	1.074986	0.658397	0
TA_3_1.38069_1	0	0	0	0	0	0	0	0	0	0
TA_1_1.217258_1	0	0	0	0	0	0	0	0.020802	0	0
WF_2_1.114998_1	1.468656	0.175587	0.229145	0.31445	0.208028	0.062307	56.50151	0.512383	0.371778	0.402845
DZ_2_1.23274_1	0	0	0	0	0	0	0.042586	0	0.037718	0
QD_3_1.1875_1	1.348177	0.056091	0.58856	0.254513	0.022729	0.016797	1.116238	1.079047	0.815015	0
ZZ_3_1.93473_1	0	0	0	0	0	0	0	0.723593	0.603816	0.55614

gene_id	Taxonomy	ARG_Catego ry	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
DZ_2_1.52 03_3	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales	vancomycin	vanR	0	0	0	0	0	0	0.59114	0	0	0	0	0	0	0	0	0	0
HZ_2_1.23 2612_1	k__Bacteria; p__Bacteroidetes; c__Bacteroidia; o__Bacteroidales	macrolide- lincosamide- streptogrami n	ermF	102.1565	92.08531	94.31932	68.90579	97.90812	73.57564	88.79068	98.05786	109.1308	52.40004	88.32085	47.45792	104.9199	98.31964	99.54516	134.9977	103.862
QD_3_1.72 454_1	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales; f__Clostridiaceae; g__Clostridium	bacitracin	bacA	0	0	0	0	0	0	0	0	0	0	0	0	0.045011	0	0	0	0
WH_1_1.40 9118_1	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae; g__Staphylococcus	multidrug	norA	0	0	0	0	0	0	0	0.02765	0	0.070481	0	0	0	0.04039	0	0	0
TA_2_1.126 198_5	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Planococcaceae; g__Metalysinibacillus; s__Metalysinibacillus jejuensis	bacitracin	bacA	0	0	0.04548	0	0	0	5.196042	0.033229	0	0.113219	0	0	0	0	0	0	0
HZ_3_1.80 883_1	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus; s__Enterococcus hiraе	multidrug	EmrB- QacA_famil y_major_fa cilitator_tra nsporter	0	0	0	0	0	0	0	0	0.029896	0.301397	0	0	0	0	0	0	0
J_1_1.3833 63_1	k__Bacteria; p__Firmicutes	vancomycin	vanW	0	0	0	0	0	0	0	0	0	0	0	0	0	0.062901	0.25917	0	0
DY_2_1.34 6591_1	k__Bacteria; p__Proteobacteria	chloramphe nicol	floR	0	0	0	0.42347	0	0	0	0	0	0	0	0	0	0	0	0	0
DY_1_1.13 3438_6	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Enterobacterales; f__Enterobacteriaceae	multidrug	emrD	0.766899	0	0.147689	0.067848	0.438465	0.467766	0.020755	0.362722	0.0505	9.928461	0.357755	0	0.097822	0.11597	0.074765	0.033232	0.334695
QD_3_1.55 3759_2	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales	bacitracin	bacA	0	0	0.034352	0	0.045649	0	0	0	0	0	0	0	0.143453	0.074158	0.076443	0	0

gene_id	JN_3_1	LC_2_1	LC_3_1	LC_1_1	LY_3_1	LY_2_1	LY_1_1	QD_2_1	QD_3_1	QD_1_1	RZ_1_1	RZ_2_1	RZ_3_1	TA_2_1	TA_3_1	TA_1_1	WF_3_1	WF_2_1	WF_1_1	WH_2_1	WH_1_1
DZ_2_1.5203_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HZ_2_1.232612_1	23.59599	68.46737	70.57	137.8458	96.06656	154.1898	104.1906	47.06814	69.59265	56.03637	76.99764	124.0519	2.010208	104.0618	49.08772	3.411048	74.02712	149.5472	53.50505	72.75159	56.42724
QD_3_1.72454_1	0	0	0	0	0	0	0	0	0.305266	0	0	0	0	0	0	0	0	0	0	0	0.056982
WH_1_1.409118_1	0	0	0	0	0	0	0	0	0.024143	0	0	0	0	0	0	0.12206	0.023587	0	0	0	0.281695
TA_2_1.126198_5	0	0	0.025969	0.066001	0	0.058234	0.022592	2.849893	0.086719	0	0.026112	0.206948	0	0.526797	0	0.029527	0.085365	0	0.244686	0.51137	0
HZ_3_1.80883_1	0	0	0	0	0	0	0	0.03196	0	0	0	0.063014	0	0.031272	0	0	0	0	0	0	0
J_1_1.383363_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.228618
DY_2_1.346591_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DY_1_1.133438_6	0.087218	7.309391	0.046889	0.897116	0.126048	0.227416	0.121322	0.144234	0.07074	0.193756	0	5.252976	0	0.449267	8.525051	0.652667	0.376248	0.092206	0.084878	7.362061	0.130347
QD_3_1.553759_2	0	0	0	0.096969	0.04437	0	0	0	0.209238	0	0.118186	0	0	0	0	0	0	0	0.051064	0	0

gene_id	WH_3_1	YT_1_1	YT_3_1	YT_2_1	ZB_1_1	ZB_2_1	ZB_3_1	ZZ_2_1	ZZ_3_1	ZZ_1_1
DZ_2_1.5203_3	0.035658	0	0	0	0	0	0	0	0	0
HZ_2_1.232612_1	81.83084	101.7094	164.3235	90.32357	28.90125	19.39664	74.92371	165.7069	147.8412	123.4027
QD_3_1.72454_1	0	0	0	0	0	0.156954	0	0	0	0
WH_1_1.409118_1	0	0	0	0	0	0	0	0	0	0.048535
TA_2_1.126198_5	0.053113	0	0.135126	0	0	0	1.151886	0	0.159765	0
HZ_3_1.80883_1	0	0	0	0	0	0	0	0	0	0.062344
J_1_1.383363_1	0	0	0	0	0	0	0	0	0	0
DY_2_1.346591_1	0	0	0	0	0	0	0	0	0	0
DY_1_1.133438_6	0.047131	2.662269	0.193942	0.144369	0.072812	0.03591	0.065148	0.078245	0.03874	1.918989
QD_3_1.553759_2	0.040022	0	0	0	0	0.171528	0	0	0	0

gene_id	Taxonomy	ARG_Catego ry	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
BZ_1_1.205 165_14	k__Bacteria; p__Firmicutes; c__Clostridia; o__Eubacteriales; f__Oscillospiraceae; g__NA; s__[Eubacterium] siraenum	vancomycin	vanR	0	0	1.663916	0	0	0.038226	0.044497	0	0	0	0	0.10959	0.561142	0.129019	0.033253	0	0
DY_2_1.26 0109_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia	chloramphenicol	floR	0	0	0.122091	0.511856	0	0	0	0.161487	0	0	0	0	0	0	0	0	0
YT_1_1.190 058_7	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Enterobacteriales; f__Enterobacteriaceae; g__Escherichia; s__Escherichia coli	aminoglycoside	aph3-I	0.648259	0.027142	0.674313	3.94192	0.291004	0.289977	1.192465	3.619949	3.249204	17.70756	0.457637	0.065103	0.378252	0.345996	0.405971	0.471415	0.247673
WH_2_1.21 5386_1	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales	bacitracin	bacA	0	0	0	0	0	0	0	0	0	0.089583	0	0.089904	0	0	0	0	0
HZ_3_1.40 2263_2	k__Bacteria; p__Firmicutes; c__Bacilli; o__Bacillales; f__Staphylococcaceae; g__Staphylococcus	unclassified	truncated_ putative_re sponse_reg ulator_ArIR	0	0	0	0	0	0	0	0.234081	0	0.103377	0	0	0	0	0.103159	0	0
TA_3_1.374 00_6	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Enterobacteriales; f__Enterobacteriaceae; g__Escherichia	multidrug	multidrug_t ransporter	0.025908	0	0.004179	0	0.079541	0.032509	0	0.038671	0.015974	0.021623	0.00596	0	0	0.013536	0	0	0
TA_3_1.144 733_8	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia; o__Enterobacteriales; f__Enterobacteriaceae; g__Escherichia	multidrug	mdtF	0.04318	0	0	0	0.024474	0.037927	0	0.01289	0.015974	0.016274	0.00596	0	0	0.009024	0.009312	0	0
HZ_3_1.23 077_1	k__Bacteria; p__Proteobacteria; c__Gammaproteobacter ia	beta-lactam	VEB-6	0	0	0	0	0	0	0.060759	0.058766	0	0.649632	0	0	0	0	0	0	0
ZB_2_1.380 10_4	k__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Streptococcaceae; g__Streptococcus; s__Streptococcus suis	macrolide- lincosamide- streptogramin	ermT	3.015367	0	5.457397	6.62057	5.882098	90.53177	6.508784	5.954793	5.588478	3.82183	0.116214	2.29818	2.278214	25.826	24.71511	41.23123	0.358698

gene_id	JN_3_1	LC_2_1	LC_3_1	LC_1_1	LY_3_1	LY_2_1	LY_1_1	QD_2_1	QD_3_1	QD_1_1	RZ_1_1	RZ_2_1	RZ_3_1	TA_2_1	TA_3_1	TA_1_1	WF_3_1	WF_2_1	WF_1_1	WH_2_1	WH_1_1
BZ_1_1.205 165_14	0	0.401637	0	0	0	0	0.058902	0	0	0	0	0	0.034117	0.076914	0.078127	0	0	0	0	0	0.040265
DY_2_1.26 0109_1	0	0	0	0	0	0	0	0	0	0	0	0.224466	0	0	0	0	0	0	0	0	0
YT_1_1.190 058_7	0.134304	2.939811	0.060488	1.303418	0.138197	1.543183	0.051868	2.573564	0.201997	0.01925	0.536554	5.592392	0.077143	3.306486	3.361609	1.718526	1.902462	0.211597	0.243171	8.773315	1.161942
WH_2_1.21 5386_1	0	0	0	0	0	0	0	0	0	0	0.091145	0	0	0.307844	0	0	0	0	0	0.437839	0
HZ_3_1.40 2263_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.114821	0	0	0	0	0.234306
TA_3_1.374 00_6	0	0.03921	0.00496	0.006351	0	0	0.01272	0.017138	0	0.00461	0	0.011214	0	0.016133	0.766147	0.016665	0.032515	0.005886	0.013588	0	0
TA_3_1.144 733_8	0	0.009803	0	0	0	0	0.00424	0.005713	0	0	0	0	0	0	0.579797	0.016665	0.037934	0	0.013588	0	0
HZ_3_1.23 077_1	0	0	0	0.058296	0	0.282439	0	0.026456	0	0	0	0	0	0	0	0	0.075286	0	0	0.545599	0
ZB_2_1.380 10_4	0.732036	29.59643	53.13854	27.54211	0.48797	6.555678	9.589209	0.735033	9.268042	0.304543	2.999833	1.665048	3.574864	3.169458	3.311003	0.097576	9.756795	29.45458	22.15382	1.881058	4.70804

gene_id	WH_3_1	YT_1_1	YT_3_1	YT_2_1	ZB_1_1	ZB_2_1	ZB_3_1	ZZ_2_1	ZZ_3_1	ZZ_1_1
BZ_1_1.205165_14	0.278749	0	0	0.035201	0	0	0	0	0	0
DY_2_1.260109_1	0	0	0	0	0	0	0	0	0	0
YT_1_1.190058_7	1.16275	1.313933	0.165672	0.185358	0.092161	0.068485	0.360412	1.071093	1.505285	0.7858
WH_2_1.215386_1	0.277143	0	0	0	0	0	0	0	0	0
HZ_3_1.402263_2	0	0	0	0	0	0	0	0	0	0
TA_3_1.37400_6	0	0.006362	0.02038	0	0	0	0.041447	0.006249	0.006193	0.011169
TA_3_1.144733_8	0	0.025447	0.03057	0	0	0	0.013816	0.006249	0.012386	0.033506
HZ_3_1.23077_1	0.046621	0	0	0	0	0	0	0.028545	0.084755	0
ZB_2_1.38010_4	1.019117	84.68764	5.860344	15.43132	0.633209	4.573886	8.225111	0.399055	1.318041	0.394649

gene_id	Taxonomy	ARG_Catego ry	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
ZB_1_1.229090_1	k__Bacteria	macrolide-lincosamide-streptogramin	mefA	0	0	0	0	0	0.33572	0	0	0.716984	0	0	0	0	0	0	0.488244	0
ZB_1_1.316188_1	k__Bacteria	tetracycline	tetracycline_resistance_protein	0.213198	0	0.235669	0.134063	0.129639	0.14057	0.294221	0	0.111129	0.121349	0	0.125968	0.117936	0.351107	0.122172	0.14602	0
YT_1_1.270548_2	k__Bacteria	chloramphenicol	cat_chloramphenicol_acetyltransferase	0.205321	0	0.069314	0.427042	0.4141	0.398038	1.07244	1.371693	2.262682	4.11879	0	0.545514	0.90458	0.374084	0.154241	0.043172	1.071095
YT_1_1.353064_6	k__Bacteria	multidrug	emrA	0.845941	0	0.081682	0.068738	0.521585	0.298602	0.021036	0.428849	0.085313	9.132231	0.400796	0	0.07085	0.132287	0.09097	0.016849	0.249965
YT_3_1.419007_1	k__Bacteria	beta-lactam	ROB-1	0.033104	0.048764	0.368153	0	0.178379	0	0	0.047463	0	0.081382	0.181149	0	0.209618	0	0.03724	0	0
YT_2_1.466938_4	k__Bacteria	tetracycline	tetX2	0	0	0	0	1.279215	0	0	0	0.785822	0	1.489233	0.643868	0.273019	2.861656	2.335585	0.788436	0
TA_2_1.217316_1	k__Bacteria	chloramphenicol	cat_chloramphenicol_acetyltransferase	0	0	0	0.161374	0.092759	0.089231	2.108499	0.224083	0.08451	0.802279	0	0	1.971773	0.301945	0.268042	0	0
TA_2_1.258516_1	k__Bacteria	beta-lactam	OXA-10	0	0	0	0	0	0.03176	0.037298	0.2878	0.121766	0.464418	0	0	0	0	0	0	0
TA_2_1.277408_1	k__Bacteria	tetracycline	tetX2	5.277115	6.68215	5.152395	14.1126	3.071676	2.231962	6.409831	8.109838	3.173844	13.72942	7.434007	3.023278	4.352583	4.520781	5.927088	6.554004	2.952593
TA_2_1.327749_1	k__Bacteria	aminoglycoside	aadE	0	0	0	0	0	0	0.12339	0	0	0.096159	0	0	0	0	0	0	0
ZB_3_1.255882_2	k__Bacteria	vancomycin	vanS	0.250424	0	0	0.726751	0	0.414692	1.646719	3.024375	3.884988	3.166766	0	0	0	0	0	0	0
ZB_3_1.378667_1	k__Bacteria	aminoglycoside	aadA	0.103202	0	0	0.260158	0	0	0.265652	0.106695	0.580155	0.448241	0	0	0.045191	0	0	0	0
ZB_3_1.389856_5	k__Bacteria	macrolide-lincosamide-streptogramin	lnuB	1.627103	1.125215	5.693583	3.264874	2.947374	4.2237	32.1508	7.024844	17.36203	10.52066	1.64344	9.066106	3.190182	1.596456	1.221377	1.954478	1.149233
LC_1_1.266010_3	k__Bacteria	tetracycline	tet44	12.72041	7.354081	9.110728	26.06615	6.913021	14.07089	13.26973	5.930914	8.440927	12.25675	25.45525	15.52872	21.67101	13.34352	17.96276	20.58516	13.90269
LC_1_1.314362_2	k__Bacteria	multidrug	emrB	0.538263	0	0.085934	0.081819	0.439424	0.407413	0.014894	0.34791	0.072316	7.554376	0.242745	0	0.069529	0.092788	0.116996	0.023606	0.315618
LC_1_1.446053_12	k__Bacteria	multidrug	mdtH	0.519536	0	0.065332	0.066135	0.241472	0.1855	0	0.21595	0.016392	6.694275	0.220039	0	0.081596	0.056432	0.087316	0.032338	0.256708
LC_1_1.446752_2	k__Bacteria	aminoglycoside	aac6-I	1.822402	0.122586	2.276101	0.457574	6.152134	0.279559	1.653206	1.757649	2.625502	0.942306	0.936198	0.732731	6.498081	2.375641	1.487063	0.068806	0.435302
LC_1_1.465964_3	k__Bacteria	tetracycline	tetH	0.329912	0	0.272361	0.483256	0	0	0	0.998917	0.607496	0	0	0	0	0.335506	0.364394	0	0

gene_id	JN_3_1	LC_2_1	LC_3_1	LC_1_1	LY_3_1	LY_2_1	LY_1_1	QD_2_1	QD_3_1	QD_1_1	RZ_1_1	RZ_2_1	RZ_3_1	TA_2_1	TA_3_1	TA_1_1	WF_3_1	WF_2_1	WF_1_1	WH_2_1	WH_1_1
ZB_1_1.229090_1	0	0	0	0	0	0.437477	0	0.463646	0	0	0	0	0	0	0	0	0	0	0	0	0
ZB_1_1.316188_1	0.271683	0	0.11481	0.182844	0.277984	0.133729	0.10162	0	0	0.264694	0	0.114912	0	0.407898	0.249671	0	0	0	0.311465	0	0
YT_1_1.270548_2	0.264547	0	1.468346	0.439921	0.17896	0.43419	0.781522	1.1179	0.548251	0.117094	0.635903	0.48595	0.119795	0.356845	0.089812	0.798094	4.071673	1.170761	2.161868	0.361985	0.510311
YT_1_1.353064_6	0.053051	6.778987	0.031683	0.606144	0.164267	0.195046	0.163986	0.201023	0.107512	0.120914	0	4.996768	0	0.254514	9.078601	0.500685	0.468036	0.037378	0.043007	6.545355	0.037548
YT_3_1.419007_1	0	0.037256	0	0	0	0.16808	0.131426	0.043277	0.040901	0	0.076771	0	0	0	0	0	0	0	0.049875	0	0
YT_2_1.466938_4	0	0	0	0.835454	2.182031	0	1.478081	0	0	0	1.358253	0.650554	0	0	0.38475	0	0	0	0.571782	0.632463	0
TA_2_1.217316_1	0	0	0	0	0	0.247381	0	0.090278	0.212519	0	0.040099	0	0.040313	0.405048	0.289082	0.973031	0.415823	0	0.155665	0.081121	0.233937
TA_2_1.258516_1	0	0	0	0.121896	0	0.207619	0	0	0	0	0	0.127284	0.027998	0.096405	0.032685	0	0	0.033001	0	0.467316	0.033607
TA_2_1.277408_1	2.551226	3.571427	3.884095	4.811584	9.68013	9.005209	6.286073	4.810034	3.773828	3.766569	2.663563	7.844323	0.101893	6.11537	2.491541	0.485257	1.71876	5.371998	2.074489	7.230434	2.946875
TA_2_1.327749_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0.1251	0	0	0	0	0	0	0
ZB_3_1.255882_2	0	0	0.069626	0.610254	0	0.078658	0	3.23515	0.145257	0	0	0.965454	0.079554	0.509203	0.08118	1.305281	2.607763	0	0	0.36629	0.084922
ZB_3_1.378667_1	0.199015	0.041823	0	0	0	1.080428	0	0.164182	0	0	0.088499	0	0	0	0	0.260773	0	0	0	4.475493	0
ZB_3_1.389856_5	13.58532	4.296375	6.821577	6.213812	3.390031	2.194437	1.274754	23.14617	6.67298	2.866404	5.659684	7.42483	6.770115	6.321165	13.23809	24.07236	3.901009	4.191849	8.679981	9.188622	3.24178
LC_1_1.266010_3	21.33228	10.07327	18.14984	24.72928	10.59077	15.59178	12.00257	13.92638	24.22446	20.22011	8.653081	11.9057	7.638652	22.62264	6.998943	17.616	21.6951	14.20515	14.95756	7.499033	22.90884
LC_1_1.314362_2	0.112083	5.989121	0.044822	0.701481	0.141874	0.187987	0.182953	0.12918	0.127693	0.137432	0	4.074973	0	0.362185	7.96352	0.416025	0.453401	0.03976	0.061079	5.8345	0.039736
LC_1_1.446053_12	0.016982	5.461795	0.030444	0.548382	0.122751	0.153327	0.104995	0.035116	0.103416	0.130513	0.015021	3.690287	0	0.353145	6.128293	0.505919	0.349765	0.017964	0	5.566042	0.018034
LC_1_1.446752_2	0.666185	0.628669	0.289224	2.491691	0.223729	1.573395	0.574429	0.335144	1.244408	0.199608	0.353096	0.939953	0	1.020031	0.504766	0	2.074762	0.894227	0.254863	0.302043	0.75646
LC_1_1.465964_3	0	0	0	0	0	0	0	0	0	0	0	0.312924	0	1.467996	0	0	0	0	0.314728	0	0.26521

gene_id	WH_3_1	YT_1_1	YT_3_1	YT_2_1	ZB_1_1	ZB_2_1	ZB_3_1	ZZ_2_1	ZZ_3_1	ZZ_1_1
ZB_1_1.229090_1	0	0	0	0	0	0	0	0	0	0
ZB_1_1.316188_1	0.128942	0	0.134689	0.125683	0	0.234568	0	0	0.103914	0.117609
YT_1_1.270548_2	0.161498	1.329547	0.486382	2.480487	0.399649	1.641903	2.35001	0.143013	0.188529	0.304959
YT_1_1.353064_6	0	2.494124	0.114682	0.162623	0.049177	0	0	0.09912	0	1.873659
YT_3_1.419007_1	0	0.047677	0.196018	0.078617	0.055409	0	0	0.245798	0	0.042169
YT_2_1.466938_4	0	0	2.014022	2.943292	0	0.277773	0.554736	2.506924	0	0.665965
TA_2_1.217316_1	0.040734	0	0	0	0.05753	0.043565	0.425323	0.192235	0.047515	0.307506
TA_2_1.258516_1	0	0.071919	0	0.029297	0	0	0	0	0.089312	0.045188
TA_2_1.277408_1	3.041592	4.487087	6.604733	6.146525	2.783377	0.955928	3.503072	6.933809	7.933224	2.666419
TA_2_1.327749_1	0	0	0	0	0	0	0.08357	0	0	0
ZB_3_1.255882_2	0.61139	0	0	0	0.38708	0	0.765374	0	0.166521	0
ZB_3_1.378667_1	0	0	0	0	0.169542	0.075761	0.314291	0.605634	0	0
ZB_3_1.389856_5	1.754535	6.178275	0.990647	3.637303	8.215036	10.27557	9.213738	0.540291	0.768479	14.82353
LC_1_1.266010_3	40.4072	22.37057	10.29102	21.04761	18.38675	12.07555	15.99092	11.50815	20.14707	4.289421
LC_1_1.314362_2	0.044727	3.100753	0.208002	0.05723	0.05272	0.01294	0.06234	0.084382	0.027861	1.539636
LC_1_1.446053_12	0.045871	2.796614	0.141629	0.078156	0.047319	0	0.063456	0.019056	0.018871	1.165941
LC_1_1.446752_2	1.987135	0.613173	0.610359	0.538447	0.837851	0.373366	0.398935	0.768579	0.292096	0.815572
LC_1_1.465964_3	0	0	0.370231	0	1.018498	0	0	0	0	0

gene_id	Taxonomy	ARG_Catego ry	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
LC_3_1.417 820_2	k__Bacteria	aminoglycosi de	bifunctiona l_aminogly coside_N- acetyltransf erase_and_ aminoglyco side_phosp hottransfera se	0.555772	0.743836	1.452145	0.738356	5.513833	0.257233	3.433042	2.173189	4.342275	0.637801	1.071253	0.572058	5.622319	3.138789	2.855159	1.465716	0.470889
LC_3_1.504 636_1	k__Bacteria	aminoglycosi de	aad9	0.026594	0	0	0.042371	0	0	0.878459	0.038474	0.032623	0.098551	0	2.358702	0	0.11494	0.029628	0	0
WF_1_1.40 6733_2	k__Bacteria	bacitracin	bacA	0	0	0	0	0	0	0.111704	0	0.045423	0	0.15237	0.022874	0	0	0	0.203772	0
WF_1_1.50 0520_1	k__Bacteria	tetracycline	tetL	3.873625	0	9.522547	12.08341	17.87613	36.75377	29.83646	4.870964	64.87875	12.81325	24.81908	15.44593	19.79746	12.65747	17.82021	34.20173	0.258761
TA_2_1.456 829_1	k__Bacteria	chloramphe nicol	catB	0	0	0	0	0	0	0	0.205116	0.189889	0	0	0	0	0	0	0.218715	0
ZB_3_1.154 163_1	k__Bacteria	tetracycline	tetW	8.056827	7.39905	5.125706	9.836601	11.8443	6.700634	7.39828	8.672304	6.101746	9.062571	9.453757	10.85897	9.082993	6.494247	5.924245	8.522115	12.30815
TA_1_1.341 581_1	k__Bacteria	multidrug	multidrug_ ABC_transp orter	0.016323	0	0	0	0	0	0	0.095815	0	0.142239	0	0	0	0	0	0	0
TA_1_1.361 418_3	k__Bacteria	multidrug	mdfA	0.713926	0	0.076353	0.064506	0.470867	0.22997	0	0.574156	0.047922	8.826996	0.268038	0	0.026488	0.096178	0.028346	0.031491	0.300956
DY_1_1.50 6095_3	k__Bacteria	multidrug	acrA	0.771997	0	0.079734	0.201586	0.396425	0.394424	0.020549	0.638505	0.133321	10.07133	0.316904	0	0.069157	0.071741	0.133203	0	0.52321
RZ_2_1.270 447_9	k__Bacteria	tetracycline	tetB	0.353869	0.06181	0.064256	0.043405	0.054845	0.116114	0.039785	0.135244	0.064514	2.943985	0.10825	0	0.107	0.20881	0.157444	0	0.168807
RZ_2_1.283 885_1	k__Bacteria	chloramphe nicol	floR	0.038072	0	0.193945	1.064294	0	0.049391	0	0.271095	0	0.140076	0	0	0.040521	0.251188	0.086291	0	0.193642
RZ_2_1.289 863_1	k__Bacteria	beta-lactam	NPS-1	0	0	0	0.05338	0	0	0	0	0	0.042051	0	0	0	0	0	0	0
BZ_1_1.330 760_1	k__Bacteria	tetracycline	tetX1	2.420828	0.451074	1.302464	0.309016	0.220588	0.383477	0.873916	1.102561	0.248178	0.323356	1.229327	0.375487	2.520007	1.666096	1.05636	1.384451	0.278205
DZ_3_1.23 3882_2	k__Bacteria	beta-lactam	OXA-2	0.022347	0.068145	0.222218	0.324294	0	0.085625	0.26933	1.951151	0.082319	0.498449	0.09202	0	0	0.04798	0	0.027575	0.085935
DZ_3_1.32 9151_1	k__Bacteria	multidrug	norA	0	0	0	0	0	0	0	0.297561	0	0	0	0	0	0	0	0	0.053312
DZ_3_1.36 8523_1	k__Bacteria	aminoglycosi de	aph3-I	0	0	0	0.037183	0	0	0.452343	0.839872	0	0.085865	0	0	0	0	0	0	0
QD_2_1.49 5585_3	k__Bacteria	aminoglycosi de	aadE	18.26187	21.41862	13.91523	24.03721	32.14774	29.96699	28.10132	14.68204	26.55323	19.05743	24.10603	29.88819	28.5826	26.73051	26.99711	22.38959	9.445239
YT_1_1.214 12_2	k__Bacteria	tetracycline	tetW	0	0	0	0	0	0	0	0	0	0	0	0.267779	0	0	0	0	0
YT_1_1.546 71_4	k__Bacteria	unclassified	transcriptio nal_regulat ory_protein _CpxR_cpx R	1.025161	0	0.151726	0.285388	0.653196	0.543349	0	0.520879	0.110865	14.48694	0.412866	0	0.189969	0.098269	0.10131	0.03775	0.53893
YT_1_1.114 569_6	k__Bacteria	multidrug	mdtE	0.592579	0.066316	0.1247	0.186358	0.510783	0.589858	0	0.456928	0.086792	10.79409	0.252407	0	0.072111	0.074798	0.077154	0.01715	0.399582
WH_2_1.31 6074_7	k__Bacteria	beta-lactam	OXA-360	0	0	0	0	0	0	0	0	0	1.070773	0	0	0.450266	0	0	0	0

gene_id	JN_3_1	LC_2_1	LC_3_1	LC_1_1	LY_3_1	LY_2_1	LY_1_1	QD_2_1	QD_3_1	QD_1_1	RZ_1_1	RZ_2_1	RZ_3_1	TA_2_1	TA_3_1	TA_1_1	WF_3_1	WF_2_1	WF_1_1	WH_2_1	WH_1_1
LC_3_1.417820_2	0.796716	1.147345	0.820607	1.777653	0.160446	1.76656	0.509014	0.266032	1.663501	0.665458	0.065618	1.702876	0.058834	0.444772	0.3766	0	1.3853	0.74864	0.71439	0.769607	8.786783
LC_3_1.504636_1	0	0	0.452403	0.191341	0	0.203043	0	0.034861	0.133409	0	0	0	6.222234	0.23981	0.280112	0	0.198397	0.035306	0.242738	0.031303	0.036035
WF_1_1.406733_2	0.047238	0	0	0	0	0	0	0	0.023617	0	0.251849	0	0	0	0	0	0.115269	0	0.483726	0	0
WF_1_1.500520_1	21.73214	44.48232	19.97629	13.40986	0.328234	2.662637	19.16805	30.36113	5.245178	5.437488	8.25881	10.2118	2.010636	2.605534	6.823149	1.764936	15.39251	23.00903	49.50295	2.636432	4.116884
TA_2_1.456829_1	0	0	0	0	0	0	0	0	0	0	0	0	0.206597	0.652878	0	0	0	0	0	0	0
ZB_3_1.154163_1	8.789228	8.348575	8.946326	9.052028	4.135565	6.879506	4.414973	6.456269	7.139629	5.80568	6.774727	9.599852	0.355401	5.722298	5.071567	1.84258	5.86357	10.90143	8.286478	6.684552	7.99791
TA_1_1.341581_1	0	0	0	0	0	0	0	0	0.020968	0.017886	0	0	0	0	0	0.421441	0.061157	0	0	0	0
TA_1_1.361418_3	0.049634	6.619397	0	0.794991	0.119623	0.199229	0.089508	0.171985	0.084038	0.169436	0.014629	4.392157	0	0.360306	8.164242	0.401612	0.454481	0.052535	0.020155	6.693266	0.087859
DY_1_1.506095_3	0.051803	7.706626	0	0.848773	0.213928	0.138554	0.106757	0.184286	0.105081	0.191758	0.030553	5.346816	0.029417	0.461778	10.46588	0.576259	0.457437	0.033355	0.021011	7.575311	0.11001
RZ_2_1.270447_9	0.066825	1.276057	0	0.248423	0.034508	0.100575	0.051645	0.051828	0.118758	0.1269	0	3.924649	0.014212	0.115776	2.377952	0.05069	0.065552	0	0	1.237259	0
RZ_2_1.283885_1	0	0	0	0.054183	0	0.048237	0.037859	0	0	0.043806	0	0.294694	0	0	0	0	0	0	0.056944	0.312458	0
RZ_2_1.289863_1	0	0	0	0	0	0	0	0	0	0	0	0.284601	0	0	0	0	0	0	0	0.080551	0
BZ_1_1.330760_1	0.664111	1.206735	1.069609	0.839321	0.379233	0.521294	1.065175	3.099978	0.688008	2.09122	0.374271	1.064555	0.015695	0.491946	0.095363	0	0.378165	4.521811	0.468834	0.696986	0.351152
DZ_3_1.233882_2	0	0	0	0	0	0	0.02209	0.029344	0	0.024816	0	0.231323	0	0.142998	0.117903	0.115491	0.055668	0.029815	0.034211	0.184266	0
DZ_3_1.329151_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DZ_3_1.368523_1	0	0	0	0	0	0	0	0	0	0	0	0.119597	0	0	0	0	0.057552	0	0	0	0.062613
QD_2_1.495585_3	16.13322	31.2804	24.44637	36.11745	6.174336	17.8259	19.58417	11.09075	25.13902	11.95553	11.88596	18.82968	8.973871	15.3183	16.01366	7.557937	16.03836	29.73586	20.73608	15.65823	35.0911
YT_1_1.21412_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
YT_1_1.54671_4	0	10.2698	0.170626	1.513331	0.236839	0.34484	0.17938	0.157864	0.262525	0.170375	0	6.9029	0.034678	0.546773	14.37542	0.70253	0.748672	0	0	9.260982	0.08173
YT_1_1.114569_6	0.125954	7.744624	0.112804	0.513781	0.25995	0.144305	0.208566	0.167312	0.127539	0.06066	0	5.54067	0.015352	0.267479	9.241389	0.564002	0.576565	0.057026	0.065609	7.296572	0.133707
WH_2_1.316074_7	0	0	0	0	0	0	0	0	0	0	0	0	0	1.651685	6.320201	0	0	0	0	0.520029	3.545587

[illegible]

gene_id	Taxonomy	ARG_Catego ry	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
WH_2_1.40 8065_3	k__Bacteria	macrolide- lincosamide- streptogrami n	mphB	0.019834	0	0.019648	0.032211	0	0	0.059883	0.492386	0.048738	0.221624	0	0	0.040936	0.021212	0	0	0.025457
WH_2_1.46 2308_2	k__Bacteria	aminoglycosi de	rmtB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
QD_2_1.32 7714_1	k__Bacteria	tetracycline	tetM	0	0	0	0	0.585066	0	0	0	0	0	0.32789	0	0	0	0	0	0
DY_2_1.22 2001_3	k__Bacteria	tetracycline	tetA	0.013589	0.042656	0.026669	0.658066	0.132533	0	0	0	0.033442	0.033904	0.112221	0.033741	0	0.028794	0.029702	0.033004	0
DY_2_1.27 9453_4	k__Bacteria	macrolide- lincosamide- streptogrami n	ermC	0.108158	0	0.021487	1.083477	0.089445	0.331496	1.695625	3.250844	7.420514	3.609318	0.148493	0.374151	0.022391	0.092789	0.239219	0.079974	0.553765
DY_2_1.28 6448_1	k__Bacteria	aminoglycosi de	aadA	0.023649	0	0	0.493902	0	0	0	0	0	0	0	0	0	0	0	0	0
DY_2_1.40 5890_1	k__Bacteria	chloramphe nicol	floR	0	0	0	0.879434	0	0	0	0	0.033949	0	0.037935	0	0	0	0	0	0
DY_2_1.43 1058_1	k__Bacteria	tetracycline	tetD	0	0	0.019747	0.388322	0	0	0	0	0	0.024744	0	0	0	0	0	0	0
HZ_1_1.35 6127_1	k__Bacteria	tetracycline	tetW	0.510494	0.070151	0.103421	0.576276	0.470462	0	0	0.568086	0	0.335579	0.205897	0.123362	0.323561	0	0	0.064556	0.439558
HZ_1_1.43 1301_2	k__Bacteria	kasugamycin	kasugamycin_resistanc e_protein_ ksgA	0.855081	0	0.046016	0.074367	0.443968	0.383999	0	0.403345	0.028372	8.872381	0.285418	0	0.119847	0.074562	0.051222	0	0.178116
WF_1_1.20 017_1	k__Bacteria	tetracycline	tetW	5.572786	1.238422	8.144985	11.45993	19.07374	40.4683	12.77629	2.79811	77.62554	4.164412	30.28718	18.02223	20.94663	19.65086	22.93403	28.23404	0.975131
YT_2_1.380 52_1	k__Bacteria	tetracycline	tetQ	22.25727	21.56085	16.45826	16.32489	28.88005	11.67948	18.16953	8.410981	13.22287	9.258658	17.46188	16.47068	18.17291	13.9933	17.21893	22.49348	16.36209
HZ_3_1.19 2412_2	k__Bacteria	chloramphe nicol	catA	0.033376	0	0	0	0	0	0.049842	0	0	0.697297	0	0	0	0	0	0	0
HZ_3_1.19 5409_2	k__Bacteria	multidrug	qacG	0	0	0	0	0.245409	0	0	2.392918	0	0.736717	0.277974	0	0	0	0.243942	0.283835	0
HZ_3_1.19 8611_1	k__Bacteria	multidrug	acrB	0	0	0	0.008799	0.007349	0	0	0.026634	0	0.189992	0	0	0	0	0	0	0
HZ_3_1.21 2865_2	k__Bacteria	aminoglycosi de	aph6-I	0	0	0	0.205664	0.091529	0	0	0	0	0.606577	0.097933	0	0	0	0	0	0
HZ_3_1.25 3421_2	k__Bacteria	chloramphe nicol	catQ	0.066752	0.049123	0.101274	0	0	0	7.326731	0.52619	0.040876	1.353577	0.091312	0	0	0.072877	0	0	0
HZ_3_1.27 4915_1	k__Bacteria	aminoglycosi de	aph2-III	0.077814	0.029944	0	0.063255	0.107334	0.322083	0.558144	0.227388	0.717111	0.483191	0.080179	0.024066	0.100314	0.062379	0.021444	0.095512	0.32466
HZ_3_1.29 9343_1	k__Bacteria	multidrug	multidrug_t ransporter	0	0	0	0	0	0	0	0.048214	0.041212	0.289444	0	0	0	0	0	0	0
HZ_3_1.30 4962_2	k__Bacteria	tetracycline	tetC	0.553728	0.096125	0.065809	0.10208	0.043919	0.210137	0.243362	0.140205	0.039899	5.667628	0.089135	0	0.137377	0.106551	0.292905	0	0.166134
HZ_3_1.35 3829_1	k__Bacteria	aminoglycosi de	aadE	0	0	0	0	0	0	0	0	0	0.115469	0	0.109171	0	0	0	0	0
HZ_3_1.35 4829_1	k__Bacteria	macrolide- lincosamide- streptogrami n	ermTR	0	0	0	0	0	0	0.064241	0.122614	0	0.317349	0	0	0	0	0	0	0

gene_id	JN_3_1	LC_2_1	LC_3_1	LC_1_1	LY_3_1	LY_2_1	LY_1_1	QD_2_1	QD_3_1	QD_1_1	RZ_1_1	RZ_2_1	RZ_3_1	TA_2_1	TA_3_1	TA_1_1	WF_3_1	WF_2_1	WF_1_1	WH_2_1	WH_1_1
WH_2_1.40 8065_3	0	0	0	0	0	0	0	0.052143	0	0.021903	0	0.077031	0	0.050574	0.025102	0	0.098921	0	0	2.617677	0.053724
WH_2_1.46 2308_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.279898	0
QD_2_1.32 7714_1	0	1.341219	0.262994	0.327915	0	0	12.18186	0.303833	0.518543	0	0	0.320051	1.203026	0.326499	1.519694	0	10.80537	0	0	1.172207	8.385944
DY_2_1.22 2001_3	0.08663	0	0.077629	0.079217	0	0.376152	0.026779	0.017909	0.182595	0.014801	0.030657	0.035228	0.01476	0	0.017993	0	0.271813	0.091598	0.063241	0.049988	0.091983
DY_2_1.27 9453_4	0.110771	0.317566	0.270615	1.562704	0.170388	0.358503	0.021378	1.807025	1.504259	0.07195	0.09871	0.895105	1.409541	3.828607	51.71481	0.363247	5.432802	0.64493	0.662596	0.433928	2.126133
DY_2_1.28 6448_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.027851	0
DY_2_1.40 5890_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.032577	0
DY_2_1.43 1058_1	0	0	0	0	0	0	0	0	0.025387	0	0	0.051605	0	0	0	0	0	0	0	0	0
HZ_1_1.35 6127_1	0.394222	0.285436	0.113364	0.070479	0	0.126419	1.258144	2.831544	0.059339	0.234927	0	0.064249	0.062693	0.065434	0.904946	0.19363	2.089629	0.065356	0.750659	0.642758	2.847244
HZ_1_1.43 1301_2	0.088824	7.155805	0	0.956476	0.121298	0.11887	0.137114	0.12124	0.116872	0.231367	0.026419	4.32046	0	0.562622	8.5054	0.328365	0.534839	0	0.03534	6.618422	0.093919
WF_1_1.20 017_1	22.27271	48.77972	19.05645	17.40669	0.903161	4.107863	8.486305	20.00695	3.546937	7.937472	6.144926	6.834974	1.004002	1.148378	1.643857	1.748014	4.706116	26.53827	60.99133	1.921415	3.273493
YT_2_1.380 52_1	6.428093	10.82586	15.91058	14.03512	19.69909	24.25165	23.00146	10.78822	20.0638	10.87457	16.83774	10.42662	0.173355	13.25597	10.59274	4.617187	15.62499	18.66014	11.85898	6.240211	12.80501
HZ_3_1.19 2412_2	0	0.338037	0	0	0	0	0	0	0	0	0	0.129282	0	0.043448	0.043814	0	0	0	0	0.588519	0
HZ_3_1.19 5409_2	0	0	0	0	0	0.503235	0	1.291192	0	0	0	0	0	0.280355	1.809388	0.81038	1.72175	0	0	0	1.579902
HZ_3_1.19 8611_1	0.013181	0.107319	0	0	0	0	0	0	0	0	0	0.051233	0	0.022983	0	0.015525	0	0	0	0.204747	0.007023
HZ_3_1.21 2865_2	0	0.24173	0	0	0	0	0	0.465455	0	0	0	0	0	0	0.280276	0	0	0	0	0	0
HZ_3_1.25 3421_2	0.08597	0.112679	0.263938	0.095426	0	0.084722	0.03313	0.218139	1.566037	0	0.387163	0.129282	0	0.043448	0.043814	0.043236	0.37243	0.043961	0	0.313877	0.045245
HZ_3_1.27 4915_1	0.099507	0.021983	0.155062	0.16913	0	0	0.096049	1.687985	0.19845	0.107322	0.066374	0.025186	0.776704	0.371813	0.282616	0.025117	0.09704	0.156264	0.119646	1.215206	0.079039
HZ_3_1.29 9343_1	0	0	0	0	0	0	0	0.043985	0	0	0	0	0	0	0.044172	0	0	0	0	0	0
HZ_3_1.30 4962_2	0.041932	2.566943	0	0.372797	0.085216	0.289476	0.064645	0.085183	0.040293	0.037013	0	5.959728	0	0.254091	4.726229	0.042187	0.080796	0.042942	0	1.83819	0
HZ_3_1.35 3829_1	0	0	0	0	0	0	0	0	0	0	0	0	0.111271	0.161266	0	0	0	0	0.066345	0	0
HZ_3_1.35 4829_1	0.056121	0	0	0	0	0	0	0	0.05235	0	0.102027	0.103257	0	0.057312	0	0	0	0	0.064353	0.050873	0

gene_id	Taxonomy	ARG_Catego ry	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
HZ_3_1.38 0283_2	k__Bacteria	macrolide- lincosamide- streptogrami n	macB	0.501095	0	0.085962	0.136515	0.259615	0.38754	0.022473	0.284733	0.099886	8.666368	0.252586	0	0.074494	0.085087	0.111728	0.035395	0.399201
HZ_3_1.38 0283_3	k__Bacteria	macrolide- lincosamide- streptogrami n	macA	0.608498	0	0.058304	0.073307	0.268119	0.413659	0.067438	0.460719	0.145949	8.895298	0.365385	0	0.075892	0.062969	0.048713	0	0.268439
YT_2_1.170 644_2	k__Bacteria	macrolide- lincosamide- streptogrami n	lnuA	0.755314	0	0.201371	21.18013	1.661385	6.490376	5.769788	1.31454	3.544174	4.21605	1.292878	1.775522	0.070232	0.21657	0.148737	0.65488	1.668466
YT_2_1.183 102_1	k__Bacteria	tetracycline	tetW	0.929155	0	0.096298	1.304167	0.312942	0	0.137157	0.838772	0.179542	0.265019	0.181127	0	0.055822	0	0	0	0.396223
LC_2_1.370 711_2	k__Bacteria	macrolide- lincosamide- streptogrami n	mefA	37.49854	27.8857	36.27726	11.84629	28.96742	22.38001	10.11931	15.41276	13.35132	10.27345	20.83033	9.451606	14.07271	19.35206	18.97791	20.94781	34.2495
LC_2_1.406 032_6	k__Bacteria	chloramph enicol_exp orter	chloramph enicol_exp orter	0.055283	0.021674	0.067832	6.279743	0	0.840188	1.844895	3.48955	9.910783	7.722369	0.779087	0.274488	0.227195	0	0.031216	0.302225	0.498235
RZ_3_1.522 24_1	k__Bacteria	aminoglycosi de	aadE	0.079723	0.051058	0.191788	0.717597	0.079292	1.466709	1.088892	0.748971	0.371995	1.383213	0.245687	0.725419	0.679347	0.146926	0.135573	0.971288	0.143399
RZ_3_1.564 17_1	k__Bacteria	aminoglycosi de	aac6-I	0.540318	0.550243	1.185732	0.781445	2.301877	0.792582	2.244079	1.429562	2.84111	0.823415	3.00909	0.614312	2.554659	1.349988	0.968064	0.525985	1.433001
LC_3_1.486 71_3	k__Bacteria	tetracycline	tet44	28.7878	29.14171	27.60395	86.08635	17.77405	41.68319	40.13668	30.97272	28.97593	40.65164	50.10642	47.18165	43.95467	36.04967	32.94336	45.28358	38.44464
DY_1_1.16 5812_1	k__Bacteria	tetracycline	tetW	19.44243	9.226744	22.22492	34.24732	52.77016	82.61604	36.42432	10.72005	138.5217	13.91226	61.06203	41.68214	47.51055	46.62414	51.56076	64.75257	11.62308
DY_1_1.19 5988_2	k__Bacteria	unclassified	coblalamin _adenolsylt ransferase	0.864357	0	0.042135	0.06301	0.492192	0.589125	0.12218	0.525352	0.100635	9.845744	0.280871	0	0.132106	0.090937	0.140563	0	0.470286
DY_1_1.26 7452_4	k__Bacteria	quinolone	qnrS	0.874967	0	0.034052	0.31546	1.132299	1.515423	0.050244	1.157135	0.329696	23.04946	0.414274	0.041281	0	0.257291	0.113667	0.212054	0.986153
DY_1_1.28 7276_3	k__Bacteria	tetracycline	tet40	0	0	0	0	0	0.791369	0	0	0	0	0	0	0	0	0	0	0
WF_3_1.21 6767_2	k__Bacteria	tetracycline	tetP	0.335325	0.362316	0.410956	0.503183	0.34932	0.357762	1.400645	1.419349	0.224571	1.462405	0.150792	0.782953	0.044209	0.053556	0.031574	0.144753	0.178929
WF_3_1.22 5747_1	k__Bacteria	aminoglycosi de	aadA	0	0	0	0.759359	0	0	0	0.245599	0	0.225531	0.512306	0	0	0.21345	0	0	0
WF_3_1.24 6216_1	k__Bacteria	multidrug	multidrug_ ABC_transp orter	0	0	0	0	0.037399	0	0	0.039728	0	0	0	0.033852	0	0	0	0	0
HZ_2_1.26 7577_1	k__Bacteria	tetracycline	tetW	11.43076	13.09947	5.807226	14.14084	7.159565	9.873034	6.721913	10.49109	11.42693	10.42909	15.07884	18.00785	15.39851	13.13712	8.639423	19.94687	9.714446
ZZ_1_1.388 420_1	k__Bacteria	multidrug	acrB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
LC_1_1.489 392_1	k__Bacteria	trimethopri m	dfrA15	0	0	0	0.971419	0	0.269893	0.295819	0.74313	0.246844	0.731666	0.366899	0.081521	0	0	0	0	0
QD_3_1.29 1453_1	k__Bacteria	chloramph enicol	catD	0	0	0	0.057322	0	0	0	0	0	0	0	0	0	0.162618	0	0	0.047111

gene_id	JN_3_1	LC_2_1	LC_3_1	LC_1_1	LY_3_1	LY_2_1	LY_1_1	QD_2_1	QD_3_1	QD_1_1	RZ_1_1	RZ_2_1	RZ_3_1	TA_2_1	TA_3_1	TA_1_1	WF_3_1	WF_2_1	WF_1_1	WH_2_1	WH_1_1
HZ_3_1.38 0283_2	0.056195	5.95382	0.042246	0.563236	0.106912	0.103898	0.072439	0.097367	0.116054	0.079187	0.016481	4.336545	0	0.322684	8.034124	0.42692	0.471055	0.070058	0.023081	5.785531	0.049858
HZ_3_1.38 0283_3	0.018921	6.629884	0.050798	0.690509	0.039027	0.113777	0.02924	0.175137	0.076478	0.09719	0.033517	4.76779	0	0.581305	8.232105	0.516457	0.501063	0.059887	0.022964	6.039868	0.040159
YT_2_1.170 644_2	4.630475	1.915289	7.708175	0.440882	0.658883	0.159677	0.701552	3.498057	1.692983	0.307954	0.542	0.695474	2.595028	2.806813	4.66501	11.27619	67.76571	6.05599	2.846923	1.099595	3.448516
YT_2_1.183 102_1	0.950816	0.350657	0.343686	0.140638	0	0.444347	3.143848	2.617138	0.524795	0.026288	0	0	0.203012	0.095849	2.000111	0.029882	3.651961	0.073066	1.95233	1.38662	5.947356
LC_2_1.370 711_2	8.746578	22.05725	15.02371	18.32842	21.65895	25.65628	30.55278	9.8379	11.38766	24.67501	25.47468	28.40735	0.333632	25.56354	14.25189	4.256353	23.77735	23.83566	11.84534	18.03369	11.88554
LC_2_1.406 032_6	0.458201	0.688212	0.063153	1.22835	0.14552	0.494798	0.081717	3.708662	0.285755	0.150346	0.077973	1.952493	0.689689	6.560483	0.695298	3.752257	8.897377	1.095053	0.621526	1.190376	0.598726
RZ_3_1.522 24_1	0.351383	0.349443	0.802031	0.640633	0.029023	0.183567	0.249898	0.246086	0.422114	0	0.790565	0.392626	1.654842	0.642554	0.340964	0.61749	1.066537	0.267568	0.47931	0.152466	0.32415
RZ_3_1.564 17_1	0.318716	0.756864	0.11236	0.571737	0.723123	0.941031	0.108151	0.543113	0.918709	0.447617	0.291213	2.592585	0.454192	0.695589	0.447651	0.319242	0.362994	0.399176	0.305417	0.51814	0.959775
LC_3_1.486 71_3	77.29933	39.82404	61.17343	76.3546	27.84944	65.04021	45.21142	48.60597	101.5063	47.59707	21.43563	28.98173	14.19819	53.18332	29.94246	55.61676	68.48417	45.3739	53.87516	32.77312	66.04154
DY_1_1.16 5812_1	52.60062	93.49034	49.00018	34.34667	14.94566	20.99116	35.22968	55.23445	19.92849	21.05335	29.68034	21.41038	4.229658	7.701126	9.830414	5.630307	26.60656	53.36515	117.3291	10.28858	19.89215
DY_1_1.19 5988_2	0.05322	8.374493	0	0.876082	0.161084	0.104178	0.204885	0.107263	0.199763	0.095385	0	5.739768	0	0.433823	11.33934	0.64099	0.457824	0	0	7.862476	0.055825
DY_1_1.26 7452_4	0.043348	16.07234	0	2.112335	0.220031	0.213539	0.334085	0.395862	0	0.153339	0.039053	9.861219	0	1.095675	13.12516	0.174389	0.783249	0.132935	0.050662	24.96425	0.136863
DY_1_1.28 7276_3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
WF_3_1.21 6767_2	0.453958	0.256274	0.937094	0.213792	1.401714	0.252281	0.193471	0.89578	0.824628	0.217435	0.350484	0.6906	0.387681	0.750124	1.065912	5.081041	1.324335	0.356446	1.060312	0.516679	0.331312
WF_3_1.22 5747_1	0	0	0.205585	0	0	0.232686	0	0	0	0	0	0	0	0	0	0.248913	0.907263	0.230522	0	0.226183	0
WF_3_1.24 6216_1	0	0.061992	0	0	0	0	0	0	0.034411	0	0	0	0.031328	0	0	0.071234	0.273374	0	0.041771	0	0
HZ_2_1.26 7577_1	15.81949	9.997975	11.04151	13.09289	11.53562	10.19566	9.018061	10.87917	8.97938	16.62311	12.80011	12.33628	0.749029	11.38334	14.08829	9.335871	12.3854	9.753331	13.27586	12.873	18.15549
ZZ_1_1.388 420_1	0	0.273527	0	0	0	0	0	0	0	0	0	0.105261	0	0	0	0	0	0	0	0	0
LC_1_1.489 392_1	0	0	0	0.563378	0	0.254748	0.068002	0.959998	0	0	0	1.21739	0.43438	0.092216	0	0	1.158766	0	0	0.316711	0
QD_3_1.29 1453_1	0	0.041627	0	0.052752	0	0.046935	0.441704	0	0.317434	0	0.388632	0	0	0	0	0	0.183371	0	0.05547	0	0.100421

gene_id	WH_3_1	YT_1_1	YT_3_1	YT_2_1	ZB_1_1	ZB_2_1	ZB_3_1	ZZ_2_1	ZZ_3_1	ZZ_1_1
HZ_3_1.38 0283_2	0.02518	2.96757	0.147873	0.12047	0.026666	0.019578	0.011759	0.053114	0	1.883901
HZ_3_1.38 0283_3	0.034114	3.411265	0.122663	0	0.052437	0.038844	0.02352	0.021175	0.020966	1.515601
YT_2_1.170 644_2	0.077663	1.963407	1.207407	0.922089	0.892509	1.144958	3.143732	0.856099	0.253349	2.100352
YT_2_1.183 102_1	0.438529	0.319725	1.245771	1.301561	0.058093	0	0.499273	0	0.391483	0
LC_2_1.370 711_2	24.08092	24.2492	34.08402	25.03174	13.11295	3.579592	5.037857	31.06567	36.33687	26.57135
LC_2_1.406 032_6	3.095299	0.040418	0.114291	0.162064	0.269591	0.14507	0.767743	3.931766	0.684751	0.782501
RZ_3_1.522 24_1	0.441424	0.159105	0.177555	0.238763	0.300664	0.567656	2.072853	0.71733	0.338292	0.264254
RZ_3_1.564 17_1	1.602741	0.069873	0.664843	0.309382	0.485673	0.191153	1.059495	1.499496	0.334123	0.481517
LC_3_1.486 71_3	83.3881	61.84071	39.10107	58.22272	119.9245	42.44442	44.92437	27.57511	41.19005	12.73782
DY_1_1.16 5812_1	13.34135	28.02152	18.55037	25.53706	40.28659	109.4964	17.6631	10.40359	10.80568	32.41982
DY_1_1.19 5988_2	0	4.005908	0.341546	0.063719	0	0	0.127764	0	0.056176	2.61068
DY_1_1.26 7452_4	0	6.334121	0.159384	0.279822	0.056238	0	0.052548	0	0	3.214182
DY_1_1.28 7276_3	0	0	0	0	0	0	0	0	0	0
WF_3_1.21 6767_2	0.141133	0.460726	0.120464	0.178748	0.527694	1.491485	1.081845	0.129666	0.145765	2.635493
WF_3_1.22 5747_1	0.237522	0	0	0	0	0	0	0	0.483257	0
WF_3_1.24 6216_1	0	0	0	0	0	0	0	0	0.03821	0
HZ_2_1.26 7577_1	10.2469	8.53267	6.861549	11.27993	8.634131	15.28933	6.21655	7.043912	10.629	13.02977
ZZ_1_1.388 420_1	0	0	0	0	0	0	0	0	0	0.306729
LC_1_1.489 392_1	0.083016	0	0	0	0.206821	0	0.206271	0.181643	0.179111	0.424185
QD_3_1.29 1453_1	0.482382	0	0.043875	0	0	0.093062	0	0.205621	0.30488	0

gene_id	Taxonomy	ARG_Cate gory	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
QD_3_1.310732_1	k__Bacteria	tetracycline	tetW	0	0	0	0.689932	0	2.658337	0.3989	0	2.863333	1.681826	0	0.187774	0	0	0	1.356203	0
WH_1_1.278758_3	k__Bacteria	tetracycline	tetX5	0.312133	0	0.195651	0.393679	0.041741	0	0.347028	2.801449	0.275251	6.379481	0	0	0.057453	0	0	0	0.07296
WH_1_1.347555_1	k__Bacteria	vancomycin	vanS	0	0	0	0.100197	0.021152	0	0	0	0	0.05689	0	0	0	0	0	0.018538	0
WH_1_1.347555_2	k__Bacteria	vancomycin	vanR	0.033104	0	0	0	0	0	0	0	0	0.040691	0	0	0.034936	0.036126	0	0.041676	0.084399
WH_1_1.414632_2	k__Bacteria	beta-lactam	mecI	0	0	0	0	0	0	0	0	0	0.19129	0	0	0	0	0	0	0
JN_1_1.327467_5	k__Bacteria	aminoglycoside	aadE	16.54794	13.68667	19.48057	69.41235	13.40569	22.89509	29.50498	21.72704	22.68876	33.00698	30.76776	32.66477	31.52353	24.65952	20.04652	36.40464	26.9067
JN_1_1.331757_1	k__Bacteria	tetracycline	tet44	0.057386	0	0	0.084283	0	0.075728	0	0.079696	0.20969	0	0	0	0	0	0	0	0.072261
JN_1_1.366419_1	k__Bacteria	macrolide-lincosamide-streptogramin	ermG	0	0	0	0	0	0.663595	0.746648	0.67069	1.190558	0	0	1.21037	0.5482	0.523428	0	1.903003	0
ZZ_1_1.4732_1	k__Bacteria	aminoglycoside	aadE	0.144081	0.072356	0	0.583099	0.107044	0.20708	0.381365	0	0.325126	0.388911	0.325159	0.1571	0.646979	0.077503	0.065016	0.130237	0.44704
ZZ_1_1.34043_5	k__Bacteria	trimethoprim	dfrA12	1.018092	0	0.188857	0.78801	1.234555	0.791798	0	0.91213	0.072907	14.9554	0.406509	0	0.065879	0	0.139627	0.079038	1.054567
WH_3_1.7135_5	k__Bacteria	aminoglycoside	aph4-I	0.066632	0	0	0.382214	0.092362	0.04237	0.277322	0.806326	2.262731	1.574941	0.114528	0.020642	0.0855	0.01773	0.018346	0	0.064248
WH_3_1.7135_7	k__Bacteria	aminoglycoside	aac3-IV	0.071784	0	0	0.384103	0.032749	0.153049	0.432041	0.799118	2.202793	1.80658	0.558074	0	0.07459	0.051499	0.053103	0	0.153235
JN_2_1.365238_1	k__Bacteria	aminoglycoside	aph3-I	0.191185	0.080121	0.441855	2.705495	0.333914	1.247595	1.354885	3.432987	2.244126	15.321	0.35519	0.085345	0.141579	0.256869	0.15139	0.105275	0.75265
JN_2_1.420103_2	k__Bacteria	multidrug	mdtP	0.44932	0	0.030433	0.130698	0.268005	0.216306	0	0.229613	0.043537	5.576752	0.150756	0	0.072842	0.085048	0.066955	0	0.414364
QD_1_1.34437_1	k__Bacteria	bleomycin	bleomycin_resistance_protein	0.619608	0.112314	0.383274	1.019131	0	12.65741	4.344055	2.14551	3.64686	15.68272	0.239185	1.692996	0.498774	1.01983	0.736972	0.120613	0.219982
QD_1_1.65089_1	k__Bacteria	tetracycline	tet32	0.013321	0.020927	0.013066	0.022045	0	0	0.020216	0.019637	0	0.049864	0.037962	0	0	0	0	0	0
JN_2_1.500035_3	k__Bacteria	multidrug	mdtG	0.509537	0	0.051236	0.086541	0.309811	0.380273	0	0.327412	0.016077	8.044686	0.250856	0	0.079986	0.06915	0.014266	0	0.370157
HZ_3_1.4764_1	k__Bacteria	beta-lactam	NPS-1	0	0	0	0.058279	0	0	0	0.053741	0	0.462022	0	0	0	0	0	0	0
HZ_3_1.47187_1	k__Bacteria	tetracycline	tetT	0	0	0	0.130735	0	0.447305	5.814024	0.242788	0.530436	0.582484	0	2.150143	0.046029	0	0	0	0
HZ_3_1.55841_1	k__Bacteria	beta-lactam	OXA-10	0.07221	0	0	0.308981	0	0	0	0	0	1.157691	0	0	0	0	0	0	0.030827
HZ_3_1.89108_34	k__Bacteria	tetracycline	tetH	0.093867	0	0.135058	0.13311	0.056084	0.016977	0.427304	0.328928	0.370572	4.16545	0	0	0.027383	0.02894	0.029851	0	0
ZB_2_1.119174_2	k__Bacteria	tetracycline	tetO	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
LY_1_1.412505_1	k__Bacteria	chloramphenicol	catD	0.03703	0.057287	0.71566	0.22929	1.255079	0.143972	0	0.212255	0.271879	0.136154	0.151794	0.272001	0.078685	0.081309	0.0419	0.140895	0.047111

gene_id	JN_3_1	LC_2_1	LC_3_1	LC_1_1	LY_3_1	LY_2_1	LY_1_1	QD_2_1	QD_3_1	QD_1_1	RZ_1_1	RZ_2_1	RZ_3_1	TA_2_1	TA_3_1	TA_1_1	WF_3_1	WF_2_1	WF_1_1	WH_2_1	WH_1_1
QD_3_1.31 0732_1	0.163266	0	2.856056	0.936593	0	0	0	0.075758	1.540308	0	0	0	0	0	0	0	0	0.711831	3.451917	0	0
WH_1_1.27 8758_3	0.042147	2.050798	0	0.229792	0	0.470848	0	8.02121	0	0	0.080207	3.721831	0	0.724448	3.442785	0	0.767215	0	0.024306	14.8848	1.429485
WH_1_1.34 7555_1	0	0.017221	0	0	0	0.038902	0	0.020046	0	0	0	0	0	0	0.18125	0	0.019015	0	0	0	0.370935
WH_1_1.34 7555_2	0.042628	0.037256	0.037404	0	0	0	0	0.043277	0	0	0.038386	0	0	0	0.086923	0	0	0	0	0.038916	0.673124
WH_1_1.41 4632_2	0	0	0	0	0	0	0	0.203585	0	0	0	0	0	0	0	0	0	0	0	0	0.635783
JN_1_1.327 467_5	51.88622	31.80465	42.8555	45.23978	16.51039	46.78794	26.35226	25.91269	70.08345	35.59097	14.88051	23.29133	10.19026	34.54037	14.69745	37.11015	45.37738	36.61728	35.67134	18.78808	51.89026
JN_1_1.331 757_1	0	0	0	0	0	0	0.057462	0	0	0.068776	0	0	0	0	0	0	0	0	0	0	0
JN_1_1.366 419_1	0.558946	0.544757	0	2.026747	0.63798	1.196119	0.518035	0.616157	2.026796	0	0.554002	0.644595	0	0	0.615875	0	0.581522	1.268089	1.502587	1.20607	1.189809
ZZ_1_1.473 2_1	0.143163	0.185063	0.537557	0.299072	0.040364	0.274253	0.10194	0.285079	0.829171	0.139625	0.039969	0.1411	1.072541	0.681928	0.088114	0.367354	0.622202	0	0.714809	0.424821	0
ZZ_1_1.340 43_5	0	11.98258	0	1.420775	0.155361	0.150612	0.420127	0.542115	0.06984	0.072088	0	8.77602	0	0.242831	18.04702	0.156017	1.467562	0.22981	0.086913	15.16699	0.08125
WH_3_1.71 35_5	0.129622	1.320799	0	0.048476	0	0.212764	0.032864	0.517134	0.064145	0	0.018871	0.517895	0	1.669672	0.396486	0.236433	0.436774	0	0.025721	1.414333	0.135335
WH_3_1.71 35_7	0.153342	1.458206	0.027177	0.138085	0	0.213348	0	0.47333	0.060389	0	0	0.340475	0	1.673543	0.9462	0.36734	0.240814	0.127464	0	1.41988	0.226913
JN_2_1.365 238_1	0.308009	7.454667	0.019638	1.408612	0.203795	2.221428	0.203926	4.283337	0.309099	0.075643	0.15622	5.286899	0.32191	3.368246	2.345355	2.289343	1.67694	0.393034	0.239149	13.2297	0.796558
JN_2_1.420 103_2	0.039669	3.991481	0.03567	0.479191	0.09082	0.106389	0.093346	0.189723	0.040113	0.084888	0	2.980656	0	0.300141	5.566743	0.506166	0.300941	0.017612	0.016193	4.804551	0.111452
QD_1_1.34 437_1	0.577262	3.542298	2.824104	1.956814	0	1.326347	0.35807	8.383074	7.683009	0.441607	0.325761	5.700065	40.63272	2.596313	3.640182	0.347111	2.548973	0.110571	2.505823	8.600987	0.597732
QD_1_1.65 089_1	0	0	0.015227	0	0.140288	0.017036	0	0.035116	0.017235	0.203019	0	0.155412	0	0.016816	0	0	0.016657	0.017972	0	0	0
JN_2_1.500 035_3	0.016652	6.224673	0.044791	0.642331	0.143258	0.167088	0.141565	0.172208	0.101475	0.085279	0.029451	4.212811	0	0.320157	7.584993	0.48827	0.310373	0.052016	0.020282	5.770574	0.10611
HZ_3_1.47 64_1	0	0	0	0	0	0	0	0	0	0	0.044027	0.124463	0	0	0	0	0	0	0	0.132789	0
HZ_3_1.47 187_1	0.726874	0.144427	2.595087	0.791122	0	0.054535	0	0.22182	2.47817	0	0	0.055291	21.19712	1.748817	0.056085	1.406045	0.759126	0.223557	1.363778	0.107873	0
HZ_3_1.55 841_1	0	0.298781	0	0.124684	0	0.074401	0	0	0	0	0	0.094419	0.027098	0.135622	0	0	0.119836	0	0	0	0
HZ_3_1.89 108_34	0.017095	0.01518	0	0.195458	0.052954	1.66339	0	0.866009	0.104072	0	0.060488	0.12653	0.043668	0.767577	0.071026	0	0.406924	0	0.124844	1.851252	0.13309
ZB_2_1.119 174_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
LY_1_1.412 505_1	0.047781	0	0.37573	0.105504	0.09674	0	0.331278	0.096664	0.136043	0.170027	0.106118	0.191117	0	0.387829	0.339746	0	0	0.097137	0.22188	0	0.10043

gene_id	WH_3_1	YT_1_1	YT_3_1	YT_2_1	ZB_1_1	ZB_2_1	ZB_3_1	ZZ_2_1	ZZ_3_1	ZZ_1_1
QD_3_1.310732_1	0	0	0	0.187523	0.101024	0.389573	0	0	0	0
WH_1_1.278758_3	0.560091	0	0.039272	0	0.086976	0	0	0.044383	0.587463	0.136776
WH_1_1.347555_1	0	0	0	0	0.05375	0	0	0	0	0
WH_1_1.347555_2	0	0	0	0	0.110818	0	0	0	0	0
WH_1_1.414632_2	0	0	0	0	0	0	0	0	0	0
JN_1_1.327467_5	59.36642	40.60411	22.74062	37.11021	67.53533	24.24616	33.73632	16.288	32.72267	13.80515
JN_1_1.331757_1	0.069676	0	0	0	0.089841	0	0	0	0	0
JN_1_1.366419_1	0	0.724498	1.794692	0	0	0	0	0	1.317114	0
ZZ_1_1.4732_1	0.348592	0.102551	0.096638	0.168257	0.05766	0.269	0.640955	0.272559	0	0.299839
ZZ_1_1.34043_5	0.437434	7.101545	0.142179	0.216846	0	0	0.275028	0.242848	0	3.463574
WH_3_1.7135_5	1.01644	0	0.059059	0	0.029284	0	0.079131	0.4039	0.30537	0.078475
WH_3_1.7135_7	1.505103	0.034711	0.028304	0	0	0	0.037661	0.472754	0.367534	0.061254
JN_2_1.365238_1	0.973654	4.108374	0.223921	0.12145	0.241808	0.022453	0.218079	1.397375	2.014343	0.707853
JN_2_1.420103_2	0.032276	1.740572	0.079087	0.024324	0	0	0.066138	0.044749	0.044323	1.057844
QD_1_1.34437_1	0.548751	7.245675	0.315158	0.432806	0.26009	0	29.03321	0.585984	0.691127	3.307389
QD_1_1.65089_1	0	0	0	0	0.071009	0	0	0	0	0.068585
JN_2_1.500035_3	0.02998	2.828907	0.108024	0.09187	0.023221	0	0.062243	0	0.018512	1.589859
HZ_3_1.4764_1	0	0	0	0	0	0	0	0	0	0
HZ_3_1.47187_1	0.204776	0.122635	0.101727	0	0.069821	0	9.642811	0.059121	0.287101	0
HZ_3_1.55841_1	0	0	0	0	0.124129	0	0	0	0.081271	0.202588
HZ_3_1.89108_34	0.2309	0	0.032546	0	0	0.017608	0.338227	0	0.341874	0.172587
ZB_2_1.119174_2	0	0	0	0	0	0.517293	0	0	0	0
LY_1_1.412505_1	0.219264	0	0.219375	0.264621	0.061282	0.046732	0.057664	0.102811	0.15244	0.1883

gene_id	Taxonomy	ARG_Catego ry	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
DZ_2_1.10 3798_7	k__Bacteria	aminoglycosi de	bifunctiona l_aminogly coside_N- acetyltransf erase_and_ aminoglyco side_phosp hottransfera se	0.840011	0.470427	2.391738	4.469213	3.117606	4.833947	41.04414	6.916233	18.43035	15.06024	1.561594	6.641803	4.596097	3.759606	2.856287	3.484857	2.444437
DZ_2_1.12 8704_3	k__Bacteria	aminoglycosi de	aph2-II	1.707081	0.305243	2.130549	0.419787	8.431841	0.282185	1.810103	2.063591	2.398885	0.732745	0.987165	1.041663	5.588414	2.133434	1.680923	0.132956	0.334983
DZ_2_1.14 4665_3	k__Bacteria	macrolide- lincosamide- streptogrami n	ermF	0	0	0	0	0	0	1.411876	0	0	0	0	0	0	0	0	0.605974	0
DZ_2_1.19 6269_1	k__Bacteria	aminoglycosi de	aadE	0	0	0	0	0	0	0.440597	0.120197	0	0.207281	0	0	0	0	0	0	0
DZ_2_1.27 8765_2	k__Bacteria	aminoglycosi de	aad9	0	0	0	0	0	0	0.596765	0	0	0	0	0.091768	0	0	0	0	0
QD_3_1.33 080_1	k__Bacteria	tetracycline	tetracycline _resistance _protein	2.063366	2.016704	0.815515	0.943465	2.28022	2.326514	1.47478	1.826446	1.392141	2.263277	2.603615	3.054645	1.790401	1.084884	0.985697	1.371812	2.414824
QD_3_1.14 2953_1	k__Bacteria	tetracycline	tet32	1.016483	0.868531	0.482814	0.111642	0.460733	1.377901	0.360949	0.560382	0.57721	0.750114	0.808298	0.650971	0.289256	0.261442	0.197745	2.471603	0.435206
QD_3_1.14 8531_2	k__Bacteria	tetracycline	tetO	14.51406	8.980542	11.89331	9.571586	14.17184	10.50141	9.499395	11.47184	13.80718	7.195484	17.47299	10.07813	15.90031	25.01266	26.69025	7.225284	24.74723
QD_3_1.16 0146_1	k__Bacteria	bacitracin	bacA	0.020747	0.031799	0.164644	0	0	0	0.281666	0	0	0	0	0.076938	0.021443	0.710994	0.504092	0.051052	0.266163
LC_3_1.178 463_3	k__Bacteria	macrolide- lincosamide- streptogrami n	mefA	31.1118	34.78634	33.74017	7.656447	22.97002	15.65566	9.308571	9.427237	10.18725	7.317458	15.46609	7.095385	15.39571	12.23782	11.99894	20.08959	26.11104
LC_3_1.191 714_2	k__Bacteria	aminoglycosi de	aadE	1.688314	0.623137	4.72492	5.149518	2.867336	8.539254	38.34149	9.394264	16.40494	13.70863	1.803664	10.56526	1.897644	1.088217	1.125725	1.144715	1.409186
TA_2_1.966 65_2	k__Bacteria	aminoglycosi de	rmtF	0.080457	0.103804	0.086496	0.225427	0	0.107619	0.116462	0.109045	0	0	0.435197	0	0.090264	0	0	0.108873	0
WH_3_1.45 0889_1	k__Bacteria	trimethopri m	dfrA1	0.04116	0	0	0.18903	0	0	0.244361	0.408607	0.251588	1.760243	0.11234	0	0.044035	0	0	0	0.052254
WH_2_1.62 89_6	k__Bacteria	aminoglycosi de	ant9-I	1.726523	0.718131	4.521652	4.293134	2.914428	10.30064	36.17349	5.597123	15.03533	10.89606	1.94368	11.11749	2.800161	0.610519	0.629993	1.78414	1.151179
WH_2_1.42 612_4	k__Bacteria	macrolide- lincosamide- streptogrami n	ermC	0	0	0	0	0	0	0	5.765164	0	2.050089	0	0	0	0	0	0	0
WH_2_1.54 063_11	k__Bacteria	aminoglycosi de	aadA	0.043967	0	0.087394	0.319352	0	0.056135	0.165644	0.19204	0.134979	0.953713	0.030178	0	0.022768	0.023587	0	0	0.028185
WH_2_1.71 813_1	k__Bacteria	multidrug	mdtK	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
WH_2_1.84 160_4	k__Bacteria	chloramphe nicol	chloramph enicol_exp orter	0	0	0	0.041596	0	0	0.095202	0.018499	0.030865	0.8766	0	0	0	0	0	0	0.03231

gene_id	JN_3_1	LC_2_1	LC_3_1	LC_1_1	LY_3_1	LY_2_1	LY_1_1	QD_2_1	QD_3_1	QD_1_1	RZ_1_1	RZ_2_1	RZ_3_1	TA_2_1	TA_3_1	TA_1_1	WF_3_1	WF_2_1	WF_1_1	WH_2_1	WH_1_1
DZ_2_1.10 3798_7	4.91877	0.975474	7.244998	5.776676	0.948237	3.158574	0.795401	8.339731	13.23261	0.817011	2.996928	3.266713	145.4318	12.0704	4.655062	5.725659	6.664694	1.812513	8.091287	3.051873	5.807815
DZ_2_1.12 8704_3	0.556808	0.987477	0.292028	2.491027	0.456779	1.143075	0.402385	0.33847	1.316769	0.330819	0.697531	0.55329	0.118971	1.363029	0.558111	0.055045	2.739029	0.777467	0.26518	0.22789	0.913244
DZ_2_1.14 4665_3	0	0	0	0	0	0	0	0	0	0	0.52682	0	0	0	0	0	0	0.598163	0	0	0
DZ_2_1.19 6269_1	0	0	0	0.060163	0	0.053697	0	0	0	0	0	0.054718	0	0	0	0	0	0	0	0	0
DZ_2_1.27 8765_2	0.031808	0	0	0	0	0	0	0	0	0	0	0	0.447963	0.031867	0	0	0.246923	0	0.037836	0	0
QD_3_1.33 080_1	1.940512	2.789563	2.515302	2.624359	1.947421	0.492661	0.704943	2.406983	1.358562	2.587824	0.752493	3.114594	0.124386	1.230145	1.465983	0.621304	1.126601	2.044162	2.214285	1.830725	1.789679
QD_3_1.14 2953_1	1.377692	1.158126	1.144703	0.645145	0.593476	0.132853	0.649569	0.581127	0.605614	2.740371	0.117869	1.012427	0.008195	1.026226	0.490047	1.046952	0.128382	1.259122	0.580662	4.099937	0.500808
QD_3_1.14 8531_2	12.9065	7.817897	11.22548	18.96232	19.05297	9.458335	11.94349	14.06786	9.937914	11.67978	17.72045	9.798818	1.37722	18.56074	4.755925	5.174446	7.009628	17.88902	15.59701	10.07062	13.64996
QD_3_1.16 0146_1	0	0	0	0	0.190709	0.282845	0.573909	0.163567	0.211001	0.022957	2.883052	0	0.046179	0	0	0	0.051717	0	0.573134	0	0
LC_3_1.178 463_3	5.994357	16.56843	10.31231	13.84414	20.31425	17.47064	26.72518	9.692158	11.65342	16.34466	20.89665	19.18657	0.210017	22.10368	7.558736	2.560514	17.30426	16.43066	8.589206	11.19214	6.904911
LC_3_1.191 714_2	10.57874	3.312865	10.06721	5.904776	1.889911	4.200183	1.743572	12.47202	17.49612	2.493963	6.07795	3.319856	57.1687	8.944466	12.07725	21.87369	12.54779	5.195957	10.4063	11.4551	1.719105
TA_2_1.966 65_2	0.21011	0.179031	0	0.110705	0	0.100627	0	0.103245	0.271597	0.09961	0	0.20665	0	0.442761	0	0.21019	0.09795	0	0.114217	0.094121	0
WH_3_1.45 0889_1	0	0.046215	0	0.408838	0.107389	0.468803	0	0.214526	0.049941	0	0	0.318402	0	0.216912	0	0.053416	0.813909	0	0.18386	0.19326	0.055825
WH_2_1.62 89_6	9.969187	2.962626	9.939988	4.470764	2.420032	3.489387	1.567049	10.52048	15.85568	2.317792	4.43675	3.365301	58.97059	9.911791	9.947217	19.39758	6.626178	4.28467	7.941657	12.99797	2.787267
WH_2_1.42 612_4	0	0	0	0.379316	0	0	0	0	0.647868	0	0	0.369081	1.043657	2.719117	1.286093	0	0.336333	0	0	2.031582	0.852593
WH_2_1.54 063_11	0	0.049645	0	0.158877	0	0.280216	0	0.086614	0.027866	0	0	0	0	0.365549	0	0	0.547712	0	0.033673	1.449783	0.029778
WH_2_1.71 813_1	0	0	0	0	0	0	0	0.200841	0	0	0	0	0	0	0	0	0	0	0	0.483677	0
WH_2_1.84 160_4	0	0	0	0	0	0.016041	0	0.115727	0	0	0	0.130051	0	0.03162	0	0	0.031365	0	0	1.504131	0.050921

gene_id	WH_3_1	YT_1_1	YT_3_1	YT_2_1	ZB_1_1	ZB_2_1	ZB_3_1	ZZ_2_1	ZZ_3_1	ZZ_1_1
DZ_2_1.10 3798_7	5.568751	5.174984	2.398181	1.612311	1.171904	3.257191	45.71444	2.692178	3.948967	2.396352
DZ_2_1.12 8704_3	2.430156	0.349954	0.943976	0.678267	0.414374	0.339268	0.266179	0.326249	0.271407	0.991407
DZ_2_1.14 4665_3	0	0.681816	0	0	0	0	0	0	0	0
DZ_2_1.19 6269_1	0	0	0	0	0	0	0	0	0.05784	0
DZ_2_1.27 8765_2	0	0	0	0	0	0	1.170443	0	0	0
QD_3_1.33 080_1	0.957428	2.460725	0.808327	1.06319	1.831922	1.322409	2.280991	2.020248	1.543464	3.102465
QD_3_1.14 2953_1	0.339169	0.385441	0.475776	1.227749	0.993879	0.22798	0.391609	0.124101	0.138585	1.367175
QD_3_1.14 8531_2	14.40717	12.76905	14.85286	10.4084	19.55197	23.96655	8.090504	19.70232	11.37589	9.701267
QD_3_1.16 0146_1	0.144272	0	0.098125	0.073314	0.216129	2.579235	0	0.117589	1.425616	0
LC_3_1.178 463_3	16.04845	18.84021	29.04511	22.98201	9.336015	3.474708	7.333639	22.55471	24.07596	21.16818
LC_3_1.191 714_2	2.732762	7.783895	1.312347	2.269675	6.994991	10.88964	41.00069	1.527652	1.279486	10.61022
TA_2_1.966 65_2	0	0.1121	0.09551	0	0	0	0	0	0	0
WH_3_1.45 0889_1	0.784187	0	0.048792	0	0	0.051336	0.063882	0.341081	0.617935	0.117421
WH_2_1.62 89_6	2.944578	4.90688	1.314742	2.149033	5.047309	7.313659	32.57953	1.034955	1.12319	9.446256
WH_2_1.42 612_4	0	0.760609	0	0	0	0	0.458219	0	0	0
WH_2_1.54 063_11	0.22968	0	0	0	0.038027	0	0	0.0311	0	0.056333
WH_2_1.71 813_1	0	0	0	0	0	0	0	0	0	0
WH_2_1.84 160_4	0	0	0	0	0.022324	0	0	0	0.017781	0

gene_id	Taxonomy	ARG_Category	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
WH_2_1.126969_3	k__Bacteria	trimethoprim	dfrA1	0.676897	0	0.143636	3.302825	0	0.269893	0.986065	4.459526	2.056898	45.60497	0.091725	0.081521	0.375598	0.385777	0.71533	0	0.169466
WH_2_1.167430_2	k__Bacteria	chloramphenicol	cmlA	0.4416	0	0.024725	0.585826	0.369909	0.287297	0.134104	0.576983	0.232925	9.096501	0.086855	0	0.077192	0.026696	0.027538	0.015295	0.481853
LC_1_1.191335_1	k__Bacteria	tetracycline	tetQ	2.034104	1.197876	0.591573	1.106701	0.160967	0.168526	1.206778	0	0.231986	0.07651	2.582652	0.473059	1.623852	1.155038	2.010532	1.26663	0.638543
TA_1_1.36884_6	k__Bacteria	multidrug	mdtL	0.82136	0.021674	0.135664	0.20554	0.616121	0.455108	0.020965	0.508708	0.357098	10.28235	0.361395	0	0	0.11718	0.105763	0.033581	0.58721
TA_1_1.37010_3	k__Bacteria	macrolide-lincosamide-streptogramin	mefA	30.34343	38.05183	38.12904	8.50874	24.11441	15.59388	9.359362	11.35489	12.30858	8.528989	14.657	6.892803	16.08779	11.7902	11.70276	19.61188	23.71249
TA_1_1.68055_1	k__Bacteria	macrolide-lincosamide-streptogramin	lsa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
TA_1_1.168754_1	k__Bacteria	multidrug	multidrug_ABC_transporter	0	0	0	0	0.050412	0	0	0.107482	0	0.138614	0	0	0	0	0	0	0
TA_1_1.190872_1	k__Bacteria	aminoglycoside	ant9-I	0.116213	0.035336	0.023362	0.523365	0	0.354836	2.78027	0.91879	1.257684	1.976648	0.226409	0.189063	0.096493	0.124929	0.10242	0.028729	0.02978
QD_2_1.73865_12	k__Bacteria	tetracycline	tet39	0.02727	0	0.01338	0.202887	0	0	0.165488	0.953087	0.033554	14.86239	0	0	0.069633	0	0	0	0.05267
LC_2_1.136158_3	k__Bacteria	beta-lactam	CTX-M-55	0.020961	0	0	0	0.057673	0	0	0.030562	0	0.13001	0	0	0	0	0	0	0.053777
LC_2_1.159899_1	k__Bacteria	beta-lactam	CTX-M-14	0	0	0.0624	0	0.057673	0	0	0.030562	0	0.260021	0	0	0.065017	0.022455	0	0	0.16133
LC_2_1.196754_1	k__Bacteria	aminoglycoside	aac6-I	0.030607	0	0	0	0	0.078914	0.141128	0	0.031938	0	0	0	0.032164	0	0.034246	0	0
LC_2_1.210076_3	k__Bacteria	multidrug	mdtN	0.726982	0	0.048855	0.162536	0.481066	0.410999	0.025008	0.509034	0.060948	8.251693	0.175656	0	0.033914	0.123074	0.14506	0	0.403616
DZ_3_1.4107_3	k__Bacteria	tetracycline	tetA	0.565698	0.063376	0.079195	1.144787	0.46886	0.469863	0.061244	1.025119	0.182105	10.55429	0.370366	0.050112	0.027475	0.085506	0.0294	0.071928	0.416012
DZ_3_1.5006_2	k__Bacteria	multidrug	mexT	0	0	0	0	0	0	0	0.214963	0	0	0	0	0	0	0	0	0
DZ_3_1.84682_1	k__Bacteria	chloramphenicol	cat_chloramphenicol_acetyltransferase	0	0	0	0	0	0	0.184242	0.198325	0	0.101997	0	0	0	0	0.05093	0	0
DY_2_1.795_1	k__Bacteria	sulfonamide	sul1	0	0	0	1.098966	0	0	0.101763	0	0	0.167792	0	0	0	0	0	0	0
DY_2_1.27721_1	k__Bacteria	tetracycline	tetO	20.86245	19.63316	18.14574	17.70766	19.57907	23.0043	21.29419	16.81733	24.65869	10.83106	17.36141	21.63249	27.42823	37.40724	36.35359	16.37029	27.8418
DY_2_1.29007_1	k__Bacteria	tetracycline	tetM	3.266457	2.833588	2.904437	4.34034	5.256603	3.100066	3.760189	3.452393	2.975185	1.729546	3.029184	4.193901	3.294547	6.627354	5.351489	1.866162	4.24101
DY_2_1.34088_3	k__Bacteria	tetracycline	tetG	0.013821	0.043349	0.135664	3.311482	0.077015	0.035008	0.062894	0.630949	0.017005	0.689503	0.152166	0.034311	0.028241	0.043942	0.045327	0	0.088971
DY_2_1.125027_1	k__Bacteria	macrolide-lincosamide-streptogramin	ereA	0	0	0	0.184076	0	0	0	0	0	0	0	0	0	0	0	0	0
DY_2_1.130463_1	k__Bacteria	beta-lactam	GES-5	0	0	0	1.109596	0	0	0	0	0	0	0	0	0	0	0	0	0

gene_id	JN_3_1	LC_2_1	LC_3_1	LC_1_1	LY_3_1	LY_2_1	LY_1_1	QD_2_1	QD_3_1	QD_1_1	RZ_1_1	RZ_2_1	RZ_3_1	TA_2_1	TA_3_1	TA_1_1	WF_3_1	WF_2_1	WF_1_1	WH_2_1	WH_1_1
WH_2_1.126969_3	0	2.206145	0	1.220653	0.087594	3.481616	0.136003	3.466696	0.155576	0	0	3.999995	0.08838	3.504199	3.506356	0.176542	1.22455	0.171886	0.19465	23.03415	1.612189
WH_2_1.167430_2	0	5.708894	0.014423	0.533749	0.016613	0.274378	0.062136	0.365965	0.114459	0.082098	0	5.206219	0.027319	0.38185	8.975614	0.113848	0.552269	0.017029	0	7.051138	0.102477
LC_1_1.191335_1	0	0.141873	0.777234	0.176896	1.482797	0.953144	1.721992	0.246266	0.147216	1.077842	1.528882	0.08168	0.08093	0.502268	1.156011	0.331378	0.77846	0.729121	0.183672	0.2975	0.20947
TA_1_1.36884_6	0.070493	8.454009	0.063153	0.664517	0.25466	0.282742	0.190662	0.145699	0.053579	0.242084	0.031189	5.768694	0	0.366656	9.985205	0.766282	0.811971	0.074506	0.021432	6.951667	0.093551
TA_1_1.37010_3	6.461141	16.5356	10.58858	13.56865	19.0757	16.79099	26.53835	9.627901	13.77656	16.48456	17.48718	21.37262	0.357232	21.16547	8.066704	4.475859	21.26881	15.41264	10.53446	10.2847	10.12262
TA_1_1.68055_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.559318	0	0	0	0	0
TA_1_1.168754_1	0	0.042393	0	0	0	0	0	0	0.046119	0.043364	0	0	0	0	0	0.439492	0.140044	0	0	0	0
TA_1_1.190872_1	0.269665	0.05247	0.158455	0.248423	0.030497	0.53493	0.022984	0.458161	0.53014	0	0.157596	0.180419	4.331566	0.935721	0.311116	1.534701	1.272812	0.030978	0.463846	1.095857	0.220408
QD_2_1.73865_12	0.017385	0.308803	0	0.099349	0.071786	0.383571	0	9.841286	0	0.014853	0.076905	1.060387	0.029624	0.258304	2.682908	0.01758	0.306869	0	0	7.714094	1.592665
LC_2_1.136158_3	0	2.063767	0	0	0	0	0	0	0.053269	0	0	0.05426	0	0	0	0	0.07837	0	0	0.148189	0
LC_2_1.159899_1	0	0.520863	0	0	0	0	0	0	0	0.023205	0.02389	0.515472	0	0	0.027665	0	0.026123	0	0	0.493964	0
LC_2_1.196754_1	0	0.986532	0	0.103078	0	0.09879	0.03035	0.044178	0	0	0	0.21042	0	0.097624	0.040238	0	0.0452	0	0	0.090699	0.04573
LC_2_1.210076_3	0.084388	7.146955	0.018845	0.840336	0.19554	0.232146	0.097785	0.173986	0.127287	0.090563	0	4.877314	0	0.46109	8.348347	0.5969	0.515744	0.088786	0	6.370208	0.178976
DZ_3_1.4107_3	0.06861	9.800407	0.06149	0.862725	0.123967	0.223664	0.132556	0.248247	0.104406	0.07325	0.440019	3.53778	0	0.662716	8.37496	0.104077	0.67399	0.145146	0.020875	8.325939	0.072853
DZ_3_1.5006_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.098846	0	0	0	0	0	0.153438
DZ_3_1.84682_1	0.156426	0	0	0.114578	0	0.068939	0	0.105055	0	0	0	0.052021	0	0	0.45493	0.11731	0.163462	0.052712	0	0	0
DY_2_1.795_1	0	0.077945	0	0	0	0	0	0.090099	0	0	0	0.269513	0	0	0	0	0	0	0	0	0
DY_2_1.27721_1	29.39445	17.52025	23.84738	19.35244	33.00523	11.99892	26.50029	25.46263	17.59352	22.13526	27.93859	17.68735	1.893795	16.58748	11.68861	14.40174	19.76137	22.08809	24.25956	19.29035	23.60761
DY_2_1.29007_1	5.541223	3.258444	2.796609	2.224604	3.638499	3.847827	1.737928	3.078344	3.712974	1.262763	1.977961	1.814763	0.782295	2.956176	4.130956	1.906504	1.028654	2.397182	3.744357	1.403452	3.988963
DY_2_1.34088_3	0.017623	0.031287	0.031576	0.100684	0.07276	0.070685	0.068094	0.091062	0.035719	0	0.077973	1.271843	0	0.157138	0	0	0.190036	0.037253	0	1.255603	0.01871
DY_2_1.125027_1	0	0	0	0	0	0	0	0.082089	0	0	0	0	0	0	0	0	0	0	0	0.074375	0
DY_2_1.130463_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

[illegible]

gene_id	Taxonomy	ARG_Catego ry	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
DY_2_1.13 9949_2	k__Bacteria	chloramphe nicol	floR	0.04138	0.020801	0	1.492252	0	0.053727	0.083851	0.367903	0.016286	0.301729	0.109305	0	0	0.028028	0	0.082321	0.017045
DY_2_1.15 3879_3	k__Bacteria	aminoglycosi de	bifunctiona l_aminogly coside_N- acetyltransf erage_and_ aminoglyco side_phosp hotransfera se	0	0	0	1.122988	0	0	0	0	0	0	0	0	0	0	0	0	0
DY_2_1.15 6429_2	k__Bacteria	chloramphe nicol	floR	0	0	0.114428	1.277181	0	0	0	0	0.126447	0	0.282199	0	0	0	0	0	0
DY_2_1.17 1467_2	k__Bacteria	aminoglycosi de	aadA	0	0	0	1.04861	0	0	0	0.035145	0	0	0	0	0	0	0	0	0
DY_2_1.19 3521_1	k__Bacteria	chloramphe nicol	floR	0	0	0	0.590089	0	0	0	0.041345	0	0	0	0	0	0	0	0	0
JN_1_1.175 047_3	k__Bacteria	chloramphe nicol	chloramph enicol_exp orter	5.963864	0.06811	14.9368	26.50354	22.73138	35.53115	32.11638	14.00225	40.12169	20.28507	1.968804	4.757315	45.44595	16.85538	18.42083	69.02029	0.789867
JN_1_1.190 355_3	k__Bacteria	chloramphe nicol	cat_chlora mphenicol_ acetyltransf erage	17.59108	14.50959	17.27109	50.18048	111.8774	13.09646	26.73394	46.36359	20.56317	28.41298	44.06954	50.97846	48.74286	15.3415	16.02916	18.73848	29.90449
WH_1_1.26 536_2	k__Bacteria	aminoglycosi de	aadA	0.615818	0.05299	0.185408	5.835124	0.687486	0.607609	0.817013	2.929475	3.661027	16.32271	0.515771	0.169267	0.122809	0.290923	0.168843	0.062616	1.055256
DZ_1_1.20 5547_1	k__Bacteria	macrolide- lincosamide- streptogrami n	ermB	0.276392	0.348309	0.200009	0	0	0.495076	0	0	0.3348	0	0	0	0.104001	0	0	0.125878	0
DZ_1_1.23 3906_2	k__Bacteria	beta-lactam	CARB-8	0.182065	0	0.040103	0.328162	0	0.103135	0	0.442879	0.894692	0.728146	0	0	0.125341	0.28142	0.156275	0	0
TA_3_1.668 14_1	k__Bacteria	bacitracin	bcrA	0	0	0	0.036987	0	0	0	0.033411	0.11405	0	0	0	0	0	0	0	0
TA_3_1.127 815_2	k__Bacteria	chloramphe nicol	cat_chlora mphenicol_ acetyltransf erage	6.102028	0	2.136006	9.127686	12.3849	3.393558	0	2.443087	5.388305	2.43712	11.75184	5.82954	16.79111	5.901171	4.29597	3.615084	3.748884
TA_3_1.143 492_1	k__Bacteria	multidrug	bicyclomyci n- multidrug_ efflux_prot ein bcr	0.839251	0	0.104532	0.13227	0.42722	0.489045	0.020216	0.451532	0.098355	9.008718	0.259993	0	0.095196	0.070539	0.101868	0	0.326002
TA_3_1.171 468_2	k__Bacteria	aminoglycosi de	ant9-I	0.025428	0	0	0.243872	0	0.618955	0.573208	0.478987	0.0624	0.251493	0.096645	0	0.052977	0.054851	0	0	0.195256
TA_3_1.196 563_1	k__Bacteria	beta-lactam	TEM-1	1.210951	0.032897	0.363285	0.417322	1.094188	0.768865	0.064876	1.253922	0.26426	26.08904	0.26588	0	0.222677	0.622895	0.428238	0.053022	1.043199
JN_3_1.147 56_9	k__Bacteria	tetracycline	tetW	32.1194	23.44347	21.53096	53.18635	48.2554	56.96312	30.10291	25.78987	76.77453	31.50327	57.24509	56.57035	48.08783	34.54953	35.66707	50.60193	28.92477

gene_id	JN_3_1	LC_2_1	LC_3_1	LC_1_1	LY_3_1	LY_2_1	LY_1_1	QD_2_1	QD_3_1	QD_1_1	RZ_1_1	RZ_2_1	RZ_3_1	TA_2_1	TA_3_1	TA_1_1	WF_3_1	WF_2_1	WF_1_1	WH_2_1	WH_1_1
DY_2_1.13 9949_2	0	0.185588	0.046676	0	0.017422	0.050778	0.013038	0.034889	0	0	0	0.434994	0	0.033412	0	0	0.117789	0.017849	0	0.342936	0
DY_2_1.15 3879_3	0	0	0	0	0	0	0	0	0.860011	0	0	0	0	0	0	0	0	0	0	0	0
DY_2_1.15 6429_2	0	0	0	0	0.134413	0	0	0.133187	0	0	0	0.134517	0	0	0	0	0	0	0	0	0
DY_2_1.17 1467_2	0	0	0	0	0	0	0	0	0	0	0	0	0	0.031078	0	0	0.030136	0	0	0	0
DY_2_1.19 3521_1	0	0	0	0	0	0	0	0	0	0	0	0.03704	0	0	0	0	0	0	0	0	0
JN_1_1.175 047_3	7.38763	86.70899	6.461028	11.68133	0.198201	3.962108	12.90762	11.75335	6.350775	1.651738	3.873439	4.60773	1.063627	3.309736	25.04148	0.719964	133.5983	26.23001	88.10715	15.23571	44.94018
JN_1_1.190 355_3	19.1863	41.25209	25.4895	58.00841	5.238698	26.17646	24.51333	38.47115	49.3602	19.40504	13.84626	23.98794	1.598371	58.46372	23.14981	4.610057	63.11165	55.89037	27.49778	16.64486	38.15687
WH_1_1.26 536_2	0.196324	12.44402	0.038948	1.552501	0.200465	0.830283	0.168498	1.986957	0.262801	0.16871	0	10.36907	0.337866	2.174885	13.56706	1.879135	2.383581	0.275147	0.095644	20.52003	0.68659
DZ_1_1.20 5547_1	0	0.102374	0.101267	0.12663	0	0.114956	0.09328	0	0.102041	0	0.113182	0	0	0	0.118204	0	0.11216	0	0	0	0.124324
DZ_1_1.23 3906_2	0	0	0	0.615103	0.132847	0.438657	0	0.053174	0	0	0.023032	0.078561	0.067421	1.522588	0.026708	0	0.807019	0	0.124273	0.166877	0.520574
TA_3_1.668 14_1	0	0	0	0	0	0.02928	0	0	0	0	0	0	0	0.073554	0.242394	0.029695	0	0	0	0	0
TA_3_1.127 815_2	3.827397	0	5.287483	17.23191	5.554031	1.828766	6.581903	4.770328	5.487804	4.651394	3.873786	9.269665	0	14.00119	7.847886	2.933772	7.696639	9.034912	0	6.107467	4.347588
TA_3_1.143 492_1	0.050947	7.637222	0	0.407801	0.140287	0.13629	0.157493	0.140466	0.086175	0.072507	0.030042	5.47394	0	0.302696	8.949256	0.480894	0.466353	0.035929	0.020673	6.482557	0.162304
TA_3_1.171 468_2	0.032615	0	0.028856	0.073262	0	0.03237	0.025165	0.033348	0.191852	0	0	0.032883	0.028762	0.032697	0.770384	0.62468	5.978247	0.135214	0	0.059872	0.757928
TA_3_1.196 563_1	0.165265	16.71685	0.024472	1.306853	0.028248	0.192025	0.382748	0.367436	0.409574	0.310053	0.024543	4.538973	0.02401	0.797587	9.46258	0.166773	1.018775	0.203878	0.065963	13.45832	0.087435
JN_3_1.147 56_9	51.11803	66.4985	45.88078	42.81836	21.29912	24.41084	25.94078	48.38676	28.04179	33.44936	17.75655	34.51539	3.639294	18.80098	39.49678	15.7964	35.29477	54.86373	71.3093	32.08668	40.56711

gene_id	WH_3_1	YT_1_1	YT_3_1	YT_2_1	ZB_1_1	ZB_2_1	ZB_3_1	ZZ_2_1	ZZ_3_1	ZZ_1_1
DY_2_1.13 9949_2	0	0	0	0	0.023511	0	0	0	0.094096	0.03407
DY_2_1.15 3879_3	1.438862	0	0	0	0	0	0	0	0	0
DY_2_1.15 6429_2	0	0	0	0	0	0	0	0	0.134893	0
DY_2_1.17 1467_2	0	0	0	0	0	0	0	0	0	0
DY_2_1.19 3521_1	0	0	0	0	0	0	0	0	0	0
JN_1_1.175 047_3	20.68038	12.65254	5.672289	10.83992	5.019097	1.503315	1.949254	2.637296	3.177305	0.48474
JN_1_1.190 355_3	52.20471	15.13545	19.76247	19.15345	21.2146	25.73469	28.46487	32.9472	31.44932	17.26569
WH_1_1.26 536_2	0.815709	4.484016	0.201847	0.120416	0.276097	0	0.356051	1.536512	1.154076	2.617619
DZ_1_1.20 5547_1	0.114834	0	0	0.451083	0	0	0	0	0	0.114656
DZ_1_1.23 3906_2	0	0	0.023918	0	0.105535	0	0.159688	0.057366	0.056777	0.259434
TA_3_1.668 14_1	0	0	0	0	0	0	0	0	0	0
TA_3_1.127 815_2	13.20453	1.456545	2.611588	2.392819	0	0	0	13.12669	9.030018	7.467688
TA_3_1.143 492_1	0.01529	3.597463	0.078683	0.07808	0.023659	0	0.063456	0.057169	0.018871	1.988958
TA_3_1.171 468_2	0.029653	0.036843	0	0	0.043533	0	0.199862	0.250715	0.177174	0.065041
TA_3_1.196 563_1	0.199706	7.980565	0.152666	0.380369	0	0	0.101802	0.152294	0.060286	2.426672
JN_3_1.147 56_9	27.59263	27.89583	22.82612	31.64792	41.49491	67.06709	28.33017	22.93459	25.09012	45.27208

gene_id	Taxonomy	ARG_Cate gory	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
JN_3_1.32912_1	k__Bacteria	tetracycline	tetracycline_resistance_protein	41.90266	45.49923	23.21335	50.19749	56.2624	39.00862	35.59622	39.76601	39.36176	37.79307	49.0219	55.79333	42.49752	31.98993	30.02533	40.379	39.84102
HZ_1_1.88083_2	k__Bacteria	unclassified	16S_rRNA_methylase	0.133504	0	0.033758	0	0.463502	0	0	0.143506	0	0.082035	0.913117	0.163792	0	0.072877	0.112685	0.04204	0
DY_3_1.2294_1	k__Bacteria	tetracycline	tetW	0.529333	0	0	1.812334	0	0.697461	0	0	0	0	0.698381	1.283636	0.546954	0.553482	0	0.663916	0.633799
DY_3_1.69798_2	k__Bacteria	vancomycin	vanY	0.063613	0	0	0	0.515312	0	0	0	0	0.078269	0	0	0.066986	0	0	0	0.040573
DY_3_1.82104_2	k__Bacteria	sulfonamide	sul3	1.033383	0	0.0978	0.196371	1.005184	0.784184	0	1.351442	0.240608	19.34777	0.470609	0	0.127444	0.158368	0.299381	0.124104	1.390067
HZ_3_1.408157_11	k__Bacteria	multidrug	adeJ	0.004228	0	0	0	0	0	0	0	0	9.071317	0	0.005279	0	0	0	0	0
HZ_3_1.410400_1	k__Bacteria	chloramphenicol	cat_chloramphenicol_acetyltransferase	0	0	0	0	0	0.089231	0.360437	0	0	0.465586	0	0	0	0	0	0	0
WF_3_1.86991_3	k__Bacteria	tetracycline	tetK	0	0	0	0.056051	0.047114	0	0.034115	1.161006	0.096704	0.462767	0.030912	0.083704	0	0.082925	0.061104	0	0
ZZ_1_1.196949_1	k__Bacteria	tetracycline	tetW	0	0	0	0	0.603895	0	0	0	0.523252	0	0	0	0	0	0	0	0
DY_3_1.375115_2	k__Bacteria	tetracycline	tetW	40.54578	34.8626	25.84053	46.48378	94.33467	24.25818	37.30272	28.85351	27.9501	36.08416	43.6255	60.60607	50.80142	25.11346	26.27496	60.7707	21.41393
HZ_2_1.46274_2	k__Bacteria	tetracycline	tetW	4.84231	5.443412	2.089829	4.782934	6.623092	3.629518	2.436406	4.673697	3.241424	4.208103	4.932497	5.521799	3.96917	2.563391	2.255807	4.772917	5.064249
HZ_2_1.78082_1	k__Bacteria	tetracycline	tetW	5.576705	5.003901	0	3.158046	5.788276	1.302844	0.946912	1.642835	1.600981	2.299193	0.833698	0	4.811775	2.59485	0.700492	3.330324	2.312427
DZ_1_1.47489_1	k__Bacteria	macrolide-lincosamide-streptogramin	ermC	0	0	0.439413	1.042436	0	0	0.279413	10.08513	0.705101	3.47994	0.526383	0	0.437545	0.218726	0	0	0.236113
ZZ_3_1.330421_14	k__Bacteria	bacitracin	bacA	0	0	0	0.034265	0	0	0	0	0	0	0	0	0	0	0	0	0
WF_2_1.103862_1	k__Bacteria	tetracycline	tetA	0.114771	0	0.120255	0.300216	0.222745	0.227183	0	0.356738	0	5.756816	0	0	0	0	0.133439	0.120429	0
WF_2_1.260382_1	k__Bacteria	beta-lactam	class_A_beta-lactamase	0	0	0	0	0.030347	0	0	0.032176	0	0.10958	0	0	0	0.02372	0	0	0
WF_2_1.267156_4	k__Bacteria	aminoglycoside	aph3-III	138.4544	82.73831	121.5536	181.6442	498.5066	208.1208	197.8314	112.4009	231.4702	140.5526	187.142	95.96253	360.3434	213.8401	209.3274	202.7234	84.40223
QD_1_1.226235_1	k__Bacteria	aminoglycoside	bifunctional_aminoglycoside_N-acetyltransferase_and_aminoglycoside_phosphotransferase	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
LY_3_1.463041_1	k__Bacteria	aminoglycoside	aadE	0.038355	0.443187	0	0	0	0	0.202761	0.925029	0.219403	0.095288	0.02635	1.305088	0.019769	0.040979	0.063394	7.874173	0.024623

gene_id	JN_3_1	LC_2_1	LC_3_1	LC_1_1	LY_3_1	LY_2_1	LY_1_1	QD_2_1	QD_3_1	QD_1_1	RZ_1_1	RZ_2_1	RZ_3_1	TA_2_1	TA_3_1	TA_1_1	WF_3_1	WF_2_1	WF_1_1	WH_2_1	WH_1_1
JN_3_1.32912_1	43.87589	48.00352	46.07745	44.91403	34.83378	34.36953	25.17642	39.46803	41.12981	40.28086	20.36812	42.69615	2.954778	30.54911	41.70768	23.47658	39.47055	46.61049	43.86433	44.38511	44.67111
HZ_1_1.88083_2	0	0.03756	0	0.047713	0	0.042361	0	0	0	0	0	0	0	0	0.306697	0	0	0	0	0	0.226224
DY_3_1.2294_1	0	0.575414	0.573469	0.715271	0.675946	0.600955	0.544874	0.654399	0	0	0	0	0.579955	1.342716	0	0	0.61385	0	0.800471	0	0
DY_3_1.69798_2	0	0	0	0.045538	0	0	0	0	0	0	0	0	0	0.082608	0	0	0	0	0	0.0374	0.215561
DY_3_1.82104_2	0.031419	15.50914	0.027825	1.733079	0	0.936237	0.170204	0.48227	0.271074	0.246109	0	12.37336	0	0.50348	23.61173	0.031679	1.25035	0.065228	0.037396	15.90411	0.232405
HZ_3_1.408157_11	0	0.004799	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
HZ_3_1.410400_1	0	0.038824	0	0	0	0	0	0	0.297527	0	0	0	0	0.315037	0	0.268313	0.042769	0.317778	0	0.04056	0.046787
WF_3_1.86991_3	0.01429	0.025422	0.025675	0.032783	0.029563	0.043086	0	0.029606	0.218864	0.012159	0	0.116412	0.012092	0	1.11548	5.971907	1.418241	1.365312	0	0.026492	0.506808
ZZ_1_1.196949_1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
DY_3_1.375115_2	26.95387	42.85843	30.3333	36.05767	17.20102	54.15646	26.29464	19.9616	39.44828	36.06016	20.71601	39.61213	2.85884	28.64565	30.28078	14.58681	47.23817	49.66896	35.87581	28.51187	39.82495
HZ_2_1.46274_2	3.940139	5.359038	4.20188	5.251308	2.612717	2.277911	1.946611	3.14204	3.863379	4.003452	2.022525	5.288602	0.216604	3.656767	3.698822	2.315473	3.689272	4.435564	3.576282	4.818567	3.323905
HZ_2_1.78082_1	0.735278	5.16481	4.765394	6.897751	0.818002	1.084145	0	4.889236	3.16487	6.084512	2.094586	1.555049	0	3.766445	3.133539	3.160239	1.285796	0	7.781158	2.080794	1.280047
DZ_1_1.47489_1	0.240552	0.645642	0	0.52563	0.248368	0.23879	0	0	0.41152	0.730231	0	0.764319	0	5.058074	32.30309	0.51165	7.92202	5.684869	0.269227	0.232736	5.024359
ZZ_3_1.330421_14	0	0	0	0	0	0	0	0.055651	0	0	0.096588	0	0	0	0	0	0	0	0.129926	0	0
WF_2_1.103862_1	0	4.759438	0.063982	0.642395	0	0	0.114924	0.222844	0	0.137537	0.274996	1.783892	0	0.463004	4.676243	0.074717	0.565325	0.294259	0	3.960647	0
WF_2_1.260382_1	0	0.024957	0	0	0	0.028173	0	0	0.02801	0.049064	0	0	0	0	0.116631	0.028557	0.027533	0.29499	0	0.026038	0.05988
WF_2_1.267156_4	87.30923	300.8052	184.8149	317.1294	27.20876	132.2978	126.8538	71.09417	238.8208	46.91778	47.67046	105.5931	92.34942	98.84028	116.3113	37.26433	197.6201	296.6313	238.4172	153.1684	272.5011
QD_1_1.226235_1	0	0	0	0	0	0	0	0	0	0.182673	0	0	0	0	0	0	0	0	0	0	0.107288
LY_3_1.463041_1	1.839047	0	0	0	0.229882	0	0	0	0.02447	0	0.525554	0.049661	0	0	0	8.319252	0	0.051366	0.265495	0.022604	0

gene_id	WH_3_1	YT_1_1	YT_3_1	YT_2_1	ZB_1_1	ZB_2_1	ZB_3_1	ZZ_2_1	ZZ_3_1	ZZ_1_1
JN_3_1.32912_1	35.76518	28.11798	25.98839	30.18487	46.5873	37.07948	30.74754	39.635	41.96605	51.22977
HZ_1_1.88083_2	36.25324	0.048059	0	0	0	0	0.052127	0	0	0
DY_3_1.2294_1	1.245752	0	0.632547	0	0.966575	0	0	2.53189	0	1.26998
DY_3_1.69798_2	0	0	0	0.037736	0.053439	0	0	0	0	0
DY_3_1.82104_2	0.371064	11.33166	0.202931	0.347246	0	0	0.346976	0	0.170964	5.021926
HZ_3_1.408157_11	0	0	0	0	0.007726	0	0	0.00612	0	0
HZ_3_1.410400_1	0	0	0.040878	0	0.05753	0	0.053851	0.048059	0	0.087859
WF_3_1.86991_3	0.025689	0	0.026504	0	0.060178	0	0.017848	0.917439	0.207235	0.375934
ZZ_1_1.196949_1	0	0	0	0	0	0	0	0	0	0
DY_3_1.375115_2	32.00766	15.58769	21.3913	24.12484	17.0256	34.22618	23.82258	54.29705	59.80216	34.02946
HZ_2_1.46274_2	3.593845	3.647947	2.082273	3.001652	3.890627	3.277273	3.62789	4.418487	4.065064	5.316801
HZ_2_1.78082_1	1.799572	3.016199	0.748809	0	3.63918	3.454424	2.023596	2.912285	4.227712	4.412106
DZ_1_1.47489_1	0.731759	0.263477	0	0	0.549335	0	0	1.835899	0.248298	0.959955
ZZ_3_1.330421_14	0	0	0	0	0	2.356896	0	0.343262	0.74211	0
WF_2_1.103862_1	0.069676	1.567286	0.136228	0	0	0	0	0.077822	0.098364	0.565692
WF_2_1.260382_1	0	0	0	0	0	0	0	0.06253	0.03094	0
WF_2_1.267156_4	273.5526	140.9599	116.8399	144.7369	57.77642	50.19055	70.68457	181.1849	156.0129	70.50571
QD_1_1.226235_1	0	0	0	0	0	0	0	0	0	0
LY_3_1.463041_1	0.022181	0	0	0	3.044553	1.1707	0.242427	0	0	0.12304

gene_id	Taxonomy	ARG_Catego ry	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
WH_3_1.12 0153_1	k__Bacteria	aminoglycosi de	aac6-I	9.707234	5.257115	9.459786	9.788712	31.47367	7.700488	24.2287	8.842947	50.06905	13.80125	43.91967	5.80013	15.1929	27.19882	31.43817	5.03536	39.8112
J_3_1.3517 1_2	k__Bacteria	chloramphenicol	chloramphenicol_exp orter	2.50195	1.470111	3.577338	17.85616	4.845189	1.454497	7.083366	16.31152	10.26781	55.47253	1.31704	0.065103	13.24182	6.05835	5.501899	6.747703	4.895398
J_3_1.3600 0_1	k__Bacteria	tetracycline	tetX2	5.316442	4.129077	5.633443	4.663267	2.21819	2.277567	4.637305	2.863371	2.380318	5.611345	6.204905	1.952102	5.013016	4.622235	3.77953	6.235946	2.153253
DY_3_1.10 7443_11	k__Bacteria	beta-lactam	OXA-85	3.10747	3.226898	6.608826	0	8.271139	0.127041	0.111893	0.863401	0.091325	0.368187	0.170114	0	0.59371	0.053459	0.082685	1.573431	1.047978
DY_3_1.17 2650_2	k__Bacteria	chloramphenicol	cat_chloramphenicol_ acetyltransferase	0.03422	0.150696	0.173285	0.320281	0.552134	0.132679	0.255343	0.096681	0.293311	2.162934	0.140395	0.041963	0.072366	0.112225	0.115681	0.172634	0.043598
LY_2_1.149 988_1	k__Bacteria	tetracycline	tetM	0.943487	0.355769	0.912791	4.232354	1.336848	5.999508	20.34324	6.485185	5.666583	21.694	0.234748	1.869317	0.535192	0.924646	0.878396	0.227278	1.735764
LY_2_1.238 523_1	k__Bacteria	aminoglycosi de	aadE	0.042807	0	0.021253	0.138418	0.029422	0.054623	1.355334	0.592565	0.315503	1.639859	0	0.105789	0.199314	0.070028	0.023662	0	0
LY_2_1.254 322_4	k__Bacteria	polymyxin	mcr-1	0	0	0.026746	0	0.064244	0.069189	0.013927	0.108474	0	0.011449	0	0	0.055641	0	0	0.055092	0.059026
LY_3_1.160 787_3	k__Bacteria	tetracycline	tet44	0.564342	0.246737	0.427672	0.222193	1.032909	0.682536	0.067057	0.929816	0.144503	0.055614	0.093579	0.356194	0.007816	0.13847	0.047621	0.140801	1.271721
J_2_1.2223 58_8	k__Bacteria	bacitracin	bacA	0.08472	0	0.315363	0.034265	0	0	0.255509	0	0.026014	0	0.058165	0	5.189984	0.136184	0.023407	0.02608	0
J_2_1.2507 76_1	k__Bacteria	unclassified	sdiA	0.136485	0	0	0	0.195842	0.104641	0	0.248103	0	5.001815	0	0	0.152871	0.194987	0.080857	0	0.228925
J_2_1.3747 15_3	k__Bacteria	aminoglycosi de	aph2-II	3.706606	2.48256	5.091409	22.65796	29.46983	2.840182	13.20764	4.760081	6.943051	6.204742	7.440406	5.032533	14.78067	7.52435	5.331843	6.803462	3.481369
YT_1_1.386 301_2	k__Bacteria	multidrug	acrB	0.012687	0	0.006157	0	0.035818	0.015951	0	0.033595	0	0.205672	0.026252	0	0.006402	0	0	0	0
ZZ_3_1.156 972_1	k__Bacteria	tetracycline	tet44	2.230266	1.93912	2.627612	3.213247	0.64023	8.234904	2.560223	4.173031	2.195646	1.587	13.82629	2.297373	0.489316	0.982192	1.061587	2.768747	3.292194
RZ_2_1.742 3_5	k__Bacteria	unclassified	cAMP-regulatory_ protein	1.297565	0.052607	0.256249	0.167836	1.159489	0.98111	0	0.823548	0.176463	16.22477	0.591177	0	0.267607	0.23707	0.244349	0	0.917574
RZ_2_1.354 56_4	k__Bacteria	macrolide-lincosamide- streptogramin	mphA	0.079725	0	0.078989	0.03236	0.137348	0.025396	0	0.203716	0	0.148464	0.027379	0	0.020572	0	0.043972	0	0
RZ_2_1.491 61_4	k__Bacteria	chloramphenicol	catB	0.180217	0	0.073214	2.237796	0	0.280002	0.268563	0.875019	0.573506	2.34303	0.09853	0	0.03823	0.079023	0.040725	0	0.091757
RZ_2_1.182 431_1	k__Bacteria	trimethoprim	dfrA5	0	0	0	0.313078	0	0	0	0.100365	0	0.088096	0	0	0	0	0	0	0.09199
BZ_2_1.637 647_3	k__Bacteria	aminoglycosi de	aadE	94.2682	59.40937	90.9829	75.44345	78.86287	47.42156	52.33411	57.0075	54.76796	57.5085	70.70067	50.61823	88.52995	44.0975	43.64719	56.84016	46.26398
LC_2_1.491 52_2	k__Bacteria	tetracycline	tetY	0	0	0	0.977433	0	0.017504	0.041929	0.093592	0	2.460565	0.019021	0	0.028241	0	0	0	0
LY_1_1.172 199_1	k__Bacteria	tetracycline	tet32	0.227378	0.38483	0.139243	0.108128	0.03798	0.704798	0.308052	0.33363	0.19347	0.27173	0.224457	0.376272	0.118892	0.237378	0.26879	0.708584	0.045153
JN_2_1.120 405_1	k__Bacteria	chloramphenicol	catD	7.517066	2.87722	7.834613	18.11391	26.01491	4.46231	6.396217	4.277579	9.651697	11.02942	8.63666	9.248474	13.76785	7.602368	7.362699	6.951489	8.150172
ZZ_2_1.444 2_3	k__Bacteria	aminoglycosi de	aadE	10.96152	12.4202	11.33356	25.97992	30.7676	37.14398	22.63194	14.34424	54.54546	18.04828	20.97462	15.03151	35.34523	17.60002	17.53125	19.41955	11.99077
ZZ_2_1.109 30_3	k__Bacteria	aminoglycosi de	aph2-II	0.255888	0.189396	0.548742	0.266131	1.461634	0.282185	1.02973	0.317665	0.958224	0.31666	0.063489	0.028692	1.72362	0.321797	0.362075	0.132956	0.233324

gene_id	JN_3_1	LC_2_1	LC_3_1	LC_1_1	LY_3_1	LY_2_1	LY_1_1	QD_2_1	QD_3_1	QD_1_1	RZ_1_1	RZ_2_1	RZ_3_1	TA_2_1	TA_3_1	TA_1_1	WF_3_1	WF_2_1	WF_1_1	WH_2_1	WH_1_1
WH_3_1.12 0153_1	7.057044	8.240099	6.905663	21.02582	5.159566	12.78641	5.307354	4.773674	9.209182	5.703855	2.986527	2.964996	1.430042	9.357077	6.981599	1.890886	6.149106	9.936427	7.629665	3.697039	24.42401
J_3_1.3517 1_2	0.267298	20.69443	6.441876	5.133329	0.172538	7.113458	3.045351	11.37559	1.821512	0.185386	1.764503	12.90437	0.127912	7.884028	3.283516	0.05069	16.30007	15.4432	5.513945	26.13458	2.624825
J_3_1.3600 0_1	1.145763	4.010825	3.373087	3.214932	5.521393	6.883008	4.74502	4.767266	3.408262	3.811497	2.594953	4.928641	0.084788	2.810898	1.651248	0.252953	1.304011	4.995471	1.95583	4.169808	1.351324
DY_3_1.10 7443_11	0	0.391804	0.02816	0.035757	0.097594	0	1.487157	3.181395	0.18743	0.443174	0.056852	0.096247	0	0.732939	0.098054	0	0.030865	0.099003	0.718891	0.292072	1.142648
DY_3_1.17 2650_2	0.176187	0.038501	0.154563	0.244401	0	0.043419	0.080226	0.134148	0	0.117094	0.039744	0.088354	0	0.226725	0.179624	0	0.424133	0.270176	0.102946	0.080441	1.062986
LY_2_1.149 988_1	1.258958	7.26578	1.811555	2.504276	0.524755	3.147991	1.827674	14.03161	5.804511	0.458705	0.903266	5.136954	4.913743	9.035346	8.788345	5.136972	58.9942	0.740424	3.869534	9.986179	3.568595
LY_2_1.238 523_1	0.109589	0.024273	0.09738	0.123819	0.056201	0.736791	0	0.477981	0.190177	0	0.024409	0.249302	0.310362	0.110176	0	1.382403	0.186694	0	0.032813	0.303227	0.028991
LY_2_1.254 322_4	0	0.020735	0	0.053554	0	0.398342	0	0	0.011953	0	0	0	0	0	0	0.023561	0	0	0.028571	0	0.024757
LY_3_1.160 787_3	0.228731	0.20779	0.310934	0.429886	1.722367	0.206673	0.141859	0.280838	0.384865	0.392104	0.032782	0.057069	0.007797	0.23839	0.544924	0.056614	0.064305	0.081479	0.080349	0.216448	0.31034
J_2_1.2223 58_8	0	0	0	0.030638	0	0.459101	0.146497	0	0.107594	0	0.961108	0	0	0	0	0	0.079181	0	0.357297	0	0
J_2_1.2507 76_1	0	3.041933	0.076281	0.107141	0	0.214839	0.069137	0.343135	0.229553	0.167953	0	2.415131	0	0.116693	4.572648	0.140129	0.276776	0.08741	0	3.750377	0
J_2_1.3747 15_3	1.87252	4.186046	3.360819	10.0549	1.006307	7.295132	6.625345	3.955368	9.376504	8.31974	1.347159	2.088635	0.321411	7.025765	3.134245	0.345239	9.742203	6.305135	4.816072	1.595725	11.35954
YT_1_1.386 301_2	0	0.077582	0	0	0	0	0	0	0.008346	0	0	0.036214	0	0.029251	0.008426	0.030012	0	0	0	0.252017	0
ZZ_3_1.156 972_1	6.750833	2.616857	4.961554	3.656376	5.148174	3.473462	2.407102	3.953443	7.356298	4.036086	1.633322	3.720447	1.083086	4.762743	1.205719	8.507374	3.688229	2.564122	2.205066	2.371936	2.364915
RZ_2_1.742 3_5	0.092969	12.88693	0.081316	1.542373	0.141288	0.274209	0.286516	0.376509	0.176951	0.495384	0	9.531487	0	0.753849	13.94936	1.214758	0.580316	0.28514	0.108141	11.22369	0.04887
RZ_2_1.354 56_4	0	3.265861	0	0.057735	0	0	0	0.026199	0	0	0.022683	0.464447	0	0.025415	0.026318	0	0.223657	0.053337	0	0.963069	0
RZ_2_1.491 61_4	0	1.053783	0	0.10279	0.047096	0.776926	0	0.376509	0.044238	0.041282	0.083943	1.255915	0.084667	0.800965	0.141786	0.093443	0.357118	0.047329	0	0.338797	0.04887
RZ_2_1.182 431_1	0	0.081953	0	0	0	0	0	0	0	0	0	0.567006	0	0.10075	0	0.096035	0	0	0	0.258172	0
BZ_2_1.637 647_3	49.50413	66.58821	49.10199	65.11444	31.36989	38.89349	57.10723	41.48034	53.44097	46.59319	36.37922	45.54044	5.424285	46.00152	49.79641	22.54194	64.74841	65.6442	49.90617	73.48095	66.49696
LC_2_1.491 52_2	0	0.39778	0	0.081273	0	0.055174	0	0.425373	0	0	0	0.299991	0	0.215974	0.349628	0	0.034552	0	0	0.074867	0.137328
LY_1_1.172 199_1	0.279447	0.219551	0.473494	0.047204	0.384739	0.060274	0.196608	0.465003	0.171962	0.352425	0.023953	0.172611	0.01594	0.07449	0.165841	0.370833	0.052415	0.488612	0.081659	0.339325	0.143412
JN_2_1.120 405_1	4.921422	17.6013	7.138863	17.93563	1.257614	5.207787	6.184348	3.624908	10.56602	2.677921	1.684072	5.733521	0.523745	16.23216	3.640138	0.816194	17.51271	19.38564	8.875219	2.697038	14.41583
ZZ_2_1.444 2_3	17.5594	24.59517	15.9868	42.02996	8.055633	13.2074	10.04405	12.89447	15.99811	8.584831	8.310338	11.38411	19.56561	12.08731	19.2507	11.92008	15.45382	21.51311	31.5387	9.048243	15.67418
ZZ_2_1.109 30_3	0.138432	0.284715	0.051654	0.307196	0.165395	0.474532	0.026244	0.270027	0.220853	0.136289	0.081578	1.166514	0.238701	0.331494	0	0.334866	0.167994	0.031696	0.198602	0.1991	0.259043

gene_id	WH_3_1	YT_1_1	YT_3_1	YT_2_1	ZB_1_1	ZB_2_1	ZB_3_1	ZZ_2_1	ZZ_3_1	ZZ_1_1
WH_3_1.12 0153_1	32.38305	3.340861	11.3816	3.785	6.066854	5.668898	5.673596	18.57974	8.389971	10.95719
J_3_1.3517 1_2	4.233	5.263331	1.785374	3.666038	1.118054	0.051659	0.582722	3.138849	5.64724	2.079244
J_3_1.3600 0_1	1.937972	4.227541	7.891762	4.271106	1.881733	0.618258	2.699614	4.486728	4.267292	2.068024
DY_3_1.10 7443_11	3.0349	0.035959	1.37925	3.544913	0.127643	0.063761	0.156059	0.104904	0.069194	0
DY_3_1.17 2650_2	0.183205	0.049242	0.162127	0.243961	0	0	0.053409	0	0	0
LY_2_1.149 988_1	1.146761	1.876028	1.213538	1.041491	0.906802	0.488868	45.63764	1.445935	1.604618	2.997904
LY_2_1.238 523_1	0.124139	0.03111	0	0	0.22253	0.027683	0.405097	0	0.179931	0.082296
LY_2_1.254 322_4	0.010442	0	0	0.010693	0	0	0	0	0	0
LY_3_1.160 787_3	0.317199	0.215443	0.328748	0.316668	5.837482	0.214208	0.105259	0.211315	0.083741	0.596186
J_2_1.2223 58_8	0.392974	0	0.075134	0	0	0.356275	0	0.089984	0	0
J_2_1.2507 76_1	0	1.955275	0.080261	0.081407	0.104849	0	0	0	0	0.688714
J_2_1.3747 15_3	17.76074	2.147614	8.189883	5.916795	1.16344	3.842327	7.370025	8.878273	6.769146	3.240815
YT_1_1.386 301_2	0	0.304471	0	0	0	0	0.010131	0	0	0.069914
ZZ_3_1.156 972_1	4.600774	5.645776	3.0229	5.359535	14.53715	1.859172	2.50587	1.031059	1.888851	1.301374
RZ_2_1.742 3_5	0.127887	5.749046	0.341609	0.25729	0.119638	0	0.056173	0.050097	0	3.667516
RZ_2_1.354 56_4	0	1.566241	0.047129	0	0	0	0.031475	0	0.083945	0.025565
RZ_2_1.491 61_4	0.298402	0.103586	0	0.042882	0.059819	0	0	0.601165	1.485727	0.137532
RZ_2_1.182 431_1	0	0.308804	0	0	0	0	0	0	0	0
BZ_2_1.637 647_3	72.01701	39.63056	67.96394	63.96091	47.48764	44.06916	30.81923	55.10529	38.35717	44.65243
LC_2_1.491 52_2	0	0	0.048982	0	0	0	0	0	0.160319	0
LY_1_1.172 199_1	0.043194	0.259903	0.191417	0.35206	0.257824	0.105233	0.111445	0.102987	0.066992	0.444749
JN_2_1.120 405_1	17.24225	6.805425	7.987492	5.510454	4.657463	3.862092	5.362787	4.833466	2.743921	3.48759
ZZ_2_1.444 2_3	17.14964	21.83185	13.26151	11.13359	16.56533	19.76305	33.57548	15.84637	8.697157	15.19368
ZZ_2_1.109 30_3	0.2316	0.030787	0.198379	0.11562	0.601046	0.026098	0.433019	0.472999	0.237119	0.351026

gene_id	Taxonomy	ARG_Catego ry	ARG	BZ_2_1	BZ_3_1	BZ_1_1	DY_2_1	DY_3_1	DY_1_1	DZ_2_1	DZ_3_1	DZ_1_1	HZ_3_1	HZ_1_1	HZ_2_1	J_2_1	J_3_1	J_1_1	JN_1_1	JN_2_1
ZZ_2_1.156 849_1	k__Bacteria	beta-lactam	ROB-1	0	0.076726	0.05837	0.164599	0	0	0	0	0	0.067515	0.151725	0	0.061083	0	0	0	0
ZZ_2_1.231 411_1	k__Bacteria	tetracycline	tetW	26.69121	32.52587	15.11762	31.98531	37.33847	26.76985	24.13576	26.44826	26.03722	26.04531	31.10919	37.9898	27.74988	19.32711	17.48204	21.43871	27.20476
BZ_2_1.421 826_4	k__Bacteria	tetracycline	tetD	0.287982	0.120146	0.208996	0	0	0	0	0.257101	0.116218	7.006846	0.129623	0	0.108539	0	0	0	0

gene_id	JN_3_1	LC_2_1	LC_3_1	LC_1_1	LY_3_1	LY_2_1	LY_1_1	QD_2_1	QD_3_1	QD_1_1	RZ_1_1	RZ_2_1	RZ_3_1	TA_2_1	TA_3_1	TA_1_1	WF_3_1	WF_2_1	WF_1_1	WH_2_1	WH_1_1
ZZ_2_1.156849_1	0	0.062417	0	0.078166	0	0.140569	0.167614	0.072305	0	0	0	0	0.069808	0	0	0	0	0	0	0	0
ZZ_2_1.231411_1	27.97604	32.77371	35.31288	32.61012	23.96235	23.26206	17.83989	26.89678	27.6356	31.17786	12.4761	32.58185	1.818594	26.41847	21.81338	18.36852	23.5811	29.39025	25.51155	29.20471	24.23325
BZ_2_1.421826_4	0	2.878621	0	0.393351	0	0.119677	0	0.122572	0.105831	0	0	7.731977	0	0	8.261926	0.125563	0.11634	0.119377	0	1.799044	0

gene_id	WH_3_1	YT_1_1	YT_3_1	YT_2_1	ZB_1_1	ZB_2_1	ZB_3_1	ZZ_2_1	ZZ_3_1	ZZ_1_1
ZZ_2_1.156849_1	0	0	0.198779	0	0	0	0	0.506035	0.074806	0.070312
ZZ_2_1.231411_1	24.24523	16.79412	18.83513	21.27152	30.88793	21.78028	21.88515	32.30968	32.78772	35.50741
BZ_2_1.421826_4	0	0.978178	0	0.117671	0	0.110687	0.434578	0	0	1.998528