

**Table 2. Top 10 largest effect markers from genomic prediction on 3 AMR phenotypes (ciprofloxacin, ampicillin trimethoprim/sulfamethoxazole). Effect sizes estimates with GEMMA BSLMM linear model.**

Contig	Position	N_missing	Alpha	Beta	Gamma	Phenotype	Reference_gene	Absolute_effect	Type_marker	Rank	Notes_BLAST
Cluster_7017_+_GCA_00333865. 1_ASM333386v1_+_DHJNCGMO_04403_+_DHJNCGMO_04404_+_+_DP	22	0	4.00E-05	1.133386		1 trimethoprim.sulfamethoxazole		1.133426045	snp	1	Nucleotidyltransferase/aminoglycoside adenylyltransferase familr protein. Sequence hits human ORFeome gateway entry vector
LMHECDEF_04343	248	0	1.89E-05	0.9983141		1 ciprofloxacin	gyrA	0.9983329768	snp	1	Known resistance mutation gyrA
LMHECDEF_04343	259	30	1.56E-05	0.8527291		1 ciprofloxacin	gyrA	0.8527446747	snp	2	Known resistance mutation gyrA
LMHECDEF_01124	239	0	1.60E-05	0.8216989		1 ciprofloxacin	parC	0.8217148641	snp	3	Known resistance mutation Topoisomerase IV
DHJNCGMO_04404	672	0	1.93E-05	0.5636097		1 trimethoprim.sulfamethoxazole	ant1	0.5636290327	snp	2	Aminoglycoside adenylyltransferas (AadA1/ANT(3"))
Cluster_6325_+_GCA_00333945. 1_ASM333394v1_+_MFCAOJAD_04226_+_MFCAOJAD_04227_+_+_CO_R	pres_abs	0	4.42E-05	0.5415463		1 ampicillin		0.5415905408	pres_abs	1	TEM-1 beta lactamase
Cluster_12949_+_GCA_003334065. 1_ASM333406v1_+_FBCKMFHC_03093_+_FBCKMFHC_03094_+_+_CO_F	pres_abs	0	1.87E-05	0.5109123		1 trimethoprim.sulfamethoxazole		0.5109309941	pres_abs	3	Small fragment of DNA
MFCAOJAD_04228	pres_abs	0	3.90E-05	0.4731588		1 ampicillin	group_13207	0.4731978032	pres_abs	2	Tn3 family transposase
Cluster_7829_+_GCA_003334785. 1_ASM333478v1_+_MGCLNDBK_02849_+_MGCLNDBK_02850_+_+_DT	pres_abs	0	3.66E-05	0.4443546		1 ampicillin		0.4443911559	pres_abs		Poor hits (mostly hypothetical protein), DNA-cytosine methyltransferase, nucleotide hits to multiple plasmids
Cluster_7924_+_GCA_00333785. 1_ASM333378v1_+_MGFKKGBB_02404_+_MGFKKGBB_02405_+_+_CO_R	pres_abs	0	2.37E-05	0.7045151	0.57914	1 ciprofloxacin		0.4080365764	pres_abs	4	Fragment of a plasmid, top hit PlncFIB plasmid but many other similar hits
Cluster_6925_+_GCA_00333865. 1_ASM333386v1_+_DHJNCGMO_04404_+_DHJNCGMO_04405_+_+_CO_F	pres_abs	0	1.50E-05	0.4075407		1 trimethoprim.sulfamethoxazole		0.4075557123	pres_abs	4	Protein BLAST hits all hypothetical, but multiple hits on aadA14, aadA16, Aac6'-Ib-cr aminoglycoside resistance targets
MFCAOJAD_02216	pres_abs	0	3.01E-05	0.3652687		1 ampicillin	group_13123	0.3652988227	pres_abs	4	AadA family aminoglycoside 3"-O-nucleotidyltransferase
IPMBBGLD_03535	pres_abs	0	3.72E-05	0.3434706	0.95012	1 ampicillin	group_5777	0.3263754571	pres_abs	5	TnpA transposase, lots of hits for IS91-like element ISVsa3 family transposase
Cluster_8133_+_GCA_00333945. 1_ASM333394v1_+_MFCAOJAD_02210_+_MFCAOJAD_02211_+_+_DP	pres_abs	0	2.50E-05	0.3045247		1 ampicillin		0.3045496766	pres_abs	6	Nucleotide BLAST many hits to Acinetobacter baumannii chromosome regions, BLASTx lots of hits to A. baumannii transposase
MGFKKGBB_02404	pres_abs	0	2.11E-05	0.6981362	0.42087	1 ciprofloxacin	group_12063	0.2938457049	pres_abs	5	Recombinase family protein
Cluster_6004_+_GCA_003333975. 1_ASM333397v1_+_OGHCJOMA_01872_+_OGHCJOMA_01873_+_+_CO_F	pres_abs	0	5.29E-05	0.3741718	0.77751	1 trimethoprim.sulfamethoxazole		0.2909752465	pres_abs	5	Tyrosine-type recombinase/integrase and fragment of plasmid (RCS96_plI)
Cluster_2575_+_GCA_003334145. 1_ASM333414v1_+_KBHDICFF_04012_+_KBHDICFF_04013_+_+_CO_F	257	0	-8.59E-05	-0.3554087	0.79676	1 ampicillin		0.2832613264	snp	7	Putative transposase
MFCAOJAD_04227	219	0	0.0001001314	0.3492993	0.78745	1 ampicillin	tnpR	0.2751558652	snp	8	tnpR resolvase
Cluster_1243_+_GCA_003334245. 1_ASM333424v1_+_CLEHOBFI_04503_+_CLEHOBFI_04504_+_+_DT	445	0	0.0001043991	0.3793977	0.61456	1 ampicillin		0.2332670496	snp	9	DNA primase
Cluster_3086_+_GCA_003333765. 1_ASM333376v1_+_EEIHECBN_04173_+_EEIHECBN_04174_+_+_CO_R	229	0	7.14E-05	0.7162494	0.27923	1 ampicillin		0.2000697003	snp	10	Hypothetical protein
OGOJFKBC_00513	3646	0	-0.0001614178	-0.4708532	0.24562	1 trimethoprim.sulfamethoxazole	rhsC_1	0.1158123808	snp	6	rhs element protein (B/C) function poorly understood
Cluster_11697_+_GCA_003334065. 1_ASM333406v1_+_FBCKMFHC_03096_+_FBCKMFHC_03097_+_+_CO_R	pres_abs	0	0.0001975492	0.3518425	0.21761	1 trimethoprim.sulfamethoxazole		0.07676199563	pres_abs	7	Small fragment of DNA
KFGAJDKJ_01185	162	0	0.0001998558	0.3944848	0.17225	1 trimethoprim.sulfamethoxazole	group_794	0.0681498626	snp	8	DUG987 containing protein, no functional data
OPGBLGHL_00621	268	0	0.000240352	0.3193421	0.18756	1 trimethoprim.sulfamethoxazole	group_10682	0.06013615628	snp	9	EntS/YbdA MFS transporter
Cluster_4369_+_GCA_003333925. 1_ASM333392v1_+_FDNLPHOJ_00345_+_FDNLPHOJ_00346_+_+_CO_F	229	0	0.0001427287	0.4504367	0.11364	1 trimethoprim.sulfamethoxazole		0.05133035529	snp	10	Hypothetical protein
LMHECDEF_03851	258	0	-0.0001222142	-0.8910132	0.03317	1 ciprofloxacin	psd	0.02967712204	snp	6	Phosphatidylserine decarboxylase proenzyme
LMHECDEF_02570	480	0	9.75E-05	0.933703	0.02869	1 ciprofloxacin	treB	0.02688541915	snp	7	Trehalose-specific PTS enzyme: IIB and IIC component;
ONLNHHCL_03732	414	1	-0.000201868	-0.5179818	0.05024	1 ciprofloxacin	yicJ_2	0.02622527363	snp	8	MFS, putative permease.
LMHECDEF_03465	1747	0	0.000147698	0.5166916	0.04764	1 ciprofloxacin	rmlL	0.02476288582	snp	9	Ribosomal RNA large subunit methyltransferase K/L
LMHECDEF_03020	609	0	-9.26E-05	-0.8985856	0.02645	1 ciprofloxacin	trkH	0.02386023664	snp	10	Trk system potassium uptake protein TrkH