Table S1. ORFs identified in plasmid pJB12.

Gene name	Position	Length	Direction	Function	Amino acid Identity (GenBank accession number)
repA	30141 - 1198	1419	Reverse	Putative plasmid replicase	88% RepA pMATVIM-7 (CAO91756.1)
parB	1812 - 2027	216	Reverse	Plasmid stabilization and partitioting system	80% ParB pNOR-2000 (AGG19226.1)
parA	2048 - 2680	633	Reverse	Plasmid stabilization and partitioting system	97% ParA pNOR-2000 (AGG19225.1)
res	3052 - 3798	747	Reverse	Putatitve resolvase	74% Res pMATVIM-7 (CAO91761.1)
pJB12.5	3998 - 4540	543	Reverse	Putatitve transposase	100% TnpA pAX22 (YP_008508469.1)
t/at1	4546 - 4941	396	Reverse	Toxin/antitoxin system	100% T/AT2 pAX22 (YP_008508471.1)
t/at2	4938 - 5189	252	Reverse	Toxin/antitoxin system	100% T/AT1 pAX22 (YP_008508470.1)
pJB12.8	5254 - 5937	684	Forward	Putative invertase	100% Putative recombinase pAX22 (YP_008508472.1)
intI1	6284 - 7297	1014	Reverse	Class 1 integrase	100% IntI1 (AAK19119.1)
aacA7	7444 - 7902	459	Forward	Aminoglycoside N(6')-acetyltransferase type 1	100% AAC(6')-II (AAK19120.1)
***bla*$_{VIM-2}$**	8055 - 8855	801	Forward	Metallo-β-lactamase	100% VIM-2 (AAK19121.1)
aacC1	8949 - 9413	465	Forward	3-N-aminoglycoside acetyltransferase	100% AAC(3')-I (AAK19122.1)
aacA4	9534 - 10088	555	Forward	Aminoglycoside N(6')-acetyltransferase type 2	100% AAC(6')-Ib' (AAK19123.1)
qacEΔ1	10257 - 10604	348	Forward	SMR family efflux pump	100% QACEΔ1 (AAK19124.1)
sul1	10598 - 11437	840	Forward	Sulfonamide resistance	100% SUL-1 (AAK19125.1)
orf5	11469 - 12065	597	Forward	Hypothetical protein	100% hypothetical protein (AAK19126.1)

tniB	12034 - 13002	969	Reverse	ATP-binding	95% TniBΔ3 pAX22 (YP_008508481.1)
tniA	13029 - 14744	1716	Reverse	Putative transposase	100% TniA pAX22 (YP_008508482.1)
arsR	14955 - 15287	333	Forward	Metalloregulatory repressor	91% ArsR pAB3 (AKQ28764.1)
arsH	15284 - 16051	768	Forward	Oxidoreductase	95% ArsH pAB3 (AKQ28783.1)
arsC	16048 - 16554	507	Forward	Arsenate reductase	85% Arsenic reductase pAB3 (AKQ28782.1)
arsB	16551 - 17612	1062	Forward	Arsenic pump membrane	95% Arsenic transporter pAB3 (AKQ28781.1)
pJB12.23	17667 – 17969	303	Forward	Putative plasmid stabilization protein	84% Putatitve plasmid stabilization protein pRWC72a (AFV47236.1)
pJB12.24	17966 - 18253	288	Forward	Putatitve plasmid stabilization protein	86% Putatitve plasmid stabilization protein pRWC72a (AFV47237.1)
pJB12.25	18425 - 18796	372	Forward	Hypothetical protein	76% hypothetical protein pMRVIM0713 (AKJ19124.1)
pJB12.26	18793 - 19044	252	Forward	Hypothetical protein	100% Growth regulator HB13 (ERF04107.1)
pJB12.27	19177 - 19473	297	Reverse	Hypothetical protein	100% hypothetical protein HB13 (ERF04108.1)
pJB12.28	19564 - 20493	930	Reverse	Putative serine protease	94% TNCP23 pKLC102 (AAP22630.1)
pJB12.29	20492 - 20770	279	Forward	Hypothetical protein	92% TNCP22b pKLC102 (AAP22629.1)
traA	21227 - 24631	3405	Reverse	Conjugal transfer	94% TraA pNOR-2000 (AGG19209.1)
traC	24690 - 24941	252	Forward	Conjugal transfer	87% TraC pNOR-2000 (AGG19208.1)
traD	24964 - 25185	222	Forward	Conjugal transfer	93% TraD pNOR-2000 (AGG19207.1)
traG	25220 - 27742	2523	Forward	Conjugal transfer	93% TraG pNOR-2000 (AGG19206.1)
pJB12.34	27752 - 28144	393	Forward	Hypothetical protein	89% hypothetical protein pAMBL1 (AKH45393.1)
kfrA	28316 - 29344	1029	Reverse	Transcriptional regulation	91% KfrA pNOR-2000 (AGG19205.1)

pJB12.36	29547 - 29855	309	Reverse	Hypothetical protein	96% hypothetical protein pMRVIM0713 (AKJ19104.1)