

Supplementary material

Table 1: Plasmid description (p138R) and gene identity % respect to the reference plasmid pmatVim-7.

Gene	Position (bp)	Description	Identity with pmatVim-7 %	Nucleotidic change	Aminoacidic change / identity %
<i>p138R-1</i>	252-1163	Partitioning (par)-Resolvase subfamily	100%		
<i>parA</i>	2131-2736	Replication protein	100%		
<i>repA</i>	3823-4650	partitioning-associated protein	100% 98%cover		
<i>relE</i>	6535-6819	Toxin of toxin-antitoxin system	- Absent		
<i>stbE</i>	6816-7094	Antitoxin toxin-antitoxin system	- Absent		
<i>p138R-12</i>	7270-7926	Resolvase	- Absent		
<i>tnpA</i>	7923-10952	Tn3 transposase	- Absent		
<i>merE</i>	11302-11538	Hypothetical mercuric resistance protein	100%		
<i>merD</i>	11535-11900	HTH-type transcriptional regulator <i>merD</i>	100%		
<i>merA</i>	11918-13603	Mercuric reductase	99,94%	A*G /	-, 100%
<i>merP</i>	13675-13950	Mercuric transport periplasmic protein	100%		
<i>merT</i>	13966-14316	Mercuric transport protein	100%		
<i>merR</i>	14388-14822	Mercuric resistance operon regulatory protein	99,08%	T*C , AA*GG, G*T	15R*K, 16T*A, 24P*L, 39T*A 97,22%
<i>kfrA</i>	15006-15911	KfrA transcriptional regulator protein	100%		
<i>traK</i>	16046-16465	Conjugal transfer <i>oriT</i> -binding protein TraK	99,76%	A*-	43,88% identity
<i>traJ</i>	16830-17207	Conjugal transfer <i>oriT</i> -binding protein	100%		
<i>tral</i>	17204-19033	DNA relaxase	100%		
<i>trbJ</i>	19273-20058	Mating pair formation protein/ Conjugal transfer/entry exclusion protein precursor	100%		
<i>trbK</i>	20074-20340	Entry exclusion protein	100%		
<i>trbL</i>	20337-21998	Conjugal protein, TrbL component	100%		
<i>p138R-31</i>	22322-22555	Toxin of toxin-antitoxin system	100%		

<i>pemI</i>	22770-23378	Antitoxin of toxin-antitoxin system	100%		
<i>phd</i>	23375-23740	Antitoxin of toxin-antitoxin system	100%		
<i>doc</i>	23755-24036	Toxin of toxin-antitoxin system	100%		
<i>intI</i>	24680-25693	Integrase IntI-1	99,80%	T*C , C*T	-, 100%
<i>aac-(6')-Ib</i>	25776-26408	aminoglycoside N(6')-acetyltransferase	- Absent		
<i>qacEΔ1</i>	26577-26924	ethidium bromide resistance locus	- Absent		
<i>sul1</i>	26918-27757	sulfonamide resistance locus	- Absent		
<i>radA</i>	28419-28868	DNA repair protein RadA	- Absent		
<i>tnpA</i>	29086-30615	Transposase	- Absent		
<i>catB</i>	31311-31976	Xenobiotic/chloramphenicol-o-acetyltransferase	- Absent		
<i>sul1</i>	32146-32385	sulfonamide resistance locus	- Absent		
<i>gcn5</i>	32515-33013	GCN5-related N-Acetyltransferases	- Absent		
<i>tnpA</i>	33355-34095	Transposase	- Absent		

-Absent: means that this gene is not present on pmatVim-7.

*: means a substitution

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Figure 1. Plasmid comparison between p138R (*A. ruhlandii*) and pmatVim-7 (*P.aeruginosa*). Blank regions indicate no identity areas.

