

**Table S1.** Characteristics of the plasmids included in the phylogenetic tree of the RepA proteins.

Plasmid name	Strain	Accession number	Country	Size (bp)	Resistance genes	Replicase	Family	Incompatibility group
unnamed1	AR_0353	NZ_CP027173.1	-	41,559	<i>bla</i> <sub>GES-1</sub>	RepA	<i>PriCT-1</i> superfamily	ND
unnamed1	AR_0356	NZ_CP027168.1	-	57,053	<i>bla</i> <sub>KPC-2</sub>	RepA	<i>Rep_3</i> superfamily	ND
unnamed2	AR_0356	NZ_CP027170.1	-	438,531	<i>aadA16</i> , <i>tet</i> (G), <i>qacEΔ1</i> , <i>aac</i> (6')- <i>Ib4</i>	RepA	<i>Rep_3</i> superfamily	ND
unnamed3	AR441	NZ_CP029094.1	-	438,529	<i>aac</i> (6')- <i>Ib4</i> , <i>aadA16</i> , <i>tet</i> (G), <i>sul1</i> , <i>qacEΔ1</i>	RepA	<i>Rep_3</i> superfamily	ND
p1	C79	NZ_CP040685.1	China	40,180	<i>bla</i> <sub>KPC-2</sub>	RepA	<i>HTH</i> superfamily	IncP-6
pF092021-2	F092021	NZ_CP081289.1	China: Henan	32,558	<i>aac</i> (6')- <i>II</i> , <i>bla</i> <sub>IMP-10</sub>	RepA	<i>Rep_3</i> superfamily	ND
unnamed1	P8W	CP081478.1	China: Tianjin	232,884	<i>sul1</i> , <i>cmlA6</i> , <i>qacE</i> , <i>ant</i> (2'')- <i>la</i>	RepA	<i>Rep_3</i> superfamily	ND
pOZ176	PA96	NC_022344.1	Guangzhou, China	500,839	<i>aac</i> (6')- <i>Ib4</i> , <i>aac</i> (6')- <i>Ib4</i> , <i>aac</i> (6')- <i>Ib4</i> , <i>aph</i> (3')- <i>II</i> , <i>sul1</i> , <i>catB8a</i> , <i>bla</i> <sub>OXA-10</sub> , <i>bla</i> <sub>IMP-9</sub> , <i>qacEΔ1</i>	RepA	<i>Rep_3</i> superfamily	IncP-2
pMATVIM-7	P07-406	AM778842.1	USA: Texas	24,179	<i>bla</i> <sub>VIM-7</sub>	RepA	<i>HTH</i> superfamily	ND
pNOR-2000	COL-1	NC_020452.1	France	21,880	<i>qacEΔ1</i> , <i>sul1</i> , <i>bla</i> <sub>VIM-2</sub>	RepA	<i>Rep_3</i> superfamily	ND

pCOL-1	ST308	NC_022346.1	Colombia	31,529	<i>bla</i> <sub>KPC-2</sub>	RepA	<i>HTH</i> <i>superfamily</i>	IncP-6
unnamed	FDAARGOS_570	CP033834.1	USA	36,032	<i>aac</i> (6′)- <i>lb</i> 3, <i>aph</i> (6)- <i>ld</i> , <i>aph</i> (3′′)- <i>Ib</i> , <i>aac</i> (6′)- <i>lb</i> 3, <i>sul</i> 1, <i>bla</i> <sub>OXA-10</sub> , <i>bla</i> <sub>VIM-6</sub> , <i>bla</i> <sub>OXA-10</sub> , <i>qacEΔ</i> 1, <i>cmx</i>	RepA	<i>HTH</i> <i>superfamily</i>	ND
p10265-KPC	10265	NZ_KU578314.1	China	38,939	<i>bla</i> <sub>TEM</sub> , <i>bla</i> <sub>KPC-2</sub>	RepA	<i>HTH</i> <i>superfamily</i>	IncP-6
pCB58	-	NZ_KY630469.1	Porto, Portugal	32,207	<i>aac</i> (6′)- <i>lb</i> 4, <i>aac</i> (3)- <i>Ia</i> , <i>aac</i> (6′)- <i>II</i> , <i>aph</i> (6)- <i>ld</i> , <i>aph</i> (3′′)- <i>Ib</i> , <i>qacEΔ</i> 1, <i>sul</i> 1, <i>bla</i> <sub>VIM-2</sub>	RepA	<i>Rep_3</i> <i>superfamily</i>	ND
pAMBL2	PAO1	NZ_KP873171.1	Madrid	24,133	<i>aadA</i> 1, <i>aac</i> (6′)- <i>lb</i> 4, <i>sul</i> 1, <i>bla</i> <sub>VIM-1</sub> , <i>bla</i> <sub>VIM-1</sub> , <i>bla</i> <sub>VIM-1</sub> , <i>qacEΔ</i> 1	RepA	<i>Rep_3</i> <i>superfamily</i>	ND
pJB37	FFU NA P_PS_37	NZ_KY494864.1	Porto, Portugal	464,804	<i>aac</i> (6′)- <i>II</i> , <i>aac</i> (3)- <i>Ia</i> , <i>aac</i> (6′)- <i>Ib</i> 4, <i>qacEΔ</i> 1, <i>sul</i> 1, <i>bla</i> <sub>VIM-2</sub>	RepA	<i>Rep_3</i> <i>superfamily</i>	IncP-2
pD5170990	D5170990	KX169264.1	Brazil	32,424	<i>sul</i> 1, <i>aac</i> (6′)- <i>II</i> , <i>aph</i> (3′′)- <i>Ib</i> , <i>aph</i> (6)- <i>ld</i> , <i>qacEΔ</i> 1, <i>cmx</i> , <i>bla</i> <sub>KPC-2</sub>	RepA	<i>HTH</i> <i>superfamily</i>	ND

p243931-IMP	243931	NZ_MN208062.1	China; Zhejiang	392,046	<i>msr(E), armA, aph(3')-Ia, aac(6')-Ib4, ARR- 2, mph(E), qnrVC1, sul1, dfrA22, tet(C), bla<sub>OXA-1</sub>, bla<sub>IMP-45</sub>, qacEΔ1, catB3</i>	RepAcin	COG5527 superfamily	ND
p60503-DIM	60503	NZ_MN208063.1	China: Beijing	407,628	<i>catB3, qacEΔ1, aac(6')-IIa, aac(6')-IIa, aac(6')-Ib, aph(3'')-Ib, aadA1, aph(6)-Id, qnrVC6, sul1, dfrA1, dfrB, bla<sub>OXA-4</sub>, bla<sub>DIM</sub></i>	RepA	AAA_25 ATPase	ND
pJB35	-	NZ_MF168945.1	Portugal	31,166	<i>aac(6')-Ib4, aac(6')-II, qacEΔ1, sul1, bla<sub>VIM-2</sub></i>	RepA	Rep_3 superfamily	ND
pCOOP-101	PAcoop101	NZ_MF141039.1	United kingdom	26,108	<i>dfrA1, sul1, aadA22, aac(6')- II, qacEΔ1, bla<sub>VIM-4</sub></i>	RepA	Rep_3 superfamily	ND
pOXA-198	PA41437	NZ_MG958650.1	France	48,978	<i>cmlA1, qacEΔ1, sul1, bla<sub>OXA-198</sub>, aac(6')-II</i>	RepA	PriCT-1 superfamily	ND
pPA2047	2047	NZ_MN082782.1	Argentina	43,660	<i>bla<sub>KPC-2</sub></i>	RepA	PriCT-1 superfamily	ND

pTROUS1	163940	NZ_MK047610.1	France	42,035	<i>aac(6')-Ib</i> , <i>qacEΔ1</i> , <i>sul1</i> , <i>bla</i> <sub>OXA-19</sub> , <i>bla</i> <sub>IMP-63</sub>	RepA	<i>Rep_3</i> <i>superfamily</i>	ND
pMRVIM0713	MRSN17623	KP975076.1	USA	36,032	<i>aac(6')-Ib3</i> , <i>aac(6')-Ib3</i> , <i>aph(6)-Id</i> , <i>aph(3'')-Ib</i> , <i>sul1</i> , <i>bla</i> <sub>OXA-10</sub> , <i>bla</i> <sub>VIM-6</sub> , <i>qacEΔ1</i> , <i>cmx</i>	RepA	<i>HTH</i> <i>superfamily</i>	ND
pNK546b	NK546	NZ_MN583270.1	China: Tianjin	232,884	<i>sul1</i> , <i>qacE</i> , <i>cmlA6</i> , <i>ant(2'')-Ia</i>	RepA	<i>Rep_3</i> <i>superfamily</i>	IncP-7
p1160-VIM	1160	NZ_MF144194.1	China	205,426	<i>msr(E)</i> , <i>aph(3'')-Ib</i> , <i>aph(6)-Id</i> , <i>aac(6')-Ib4</i> , <i>aac(6')-Ib</i> , <i>dfrA42</i> , <i>aadA1</i> , <i>mph(E)</i> , <i>ere(A)</i> , <i>qnrVC6</i> , <i>sul1</i> , <i>bla</i> <sub>VIM-24</sub> , <i>qacEΔ1</i> , <i>catB3</i>	RepA	<i>Rep_3</i> <i>superfamily</i>	IncP-7
p2	ZPPH2	NZ_CP077987.1	China: Hangzhou	35,358	<i>tet(A)</i>	RepA	<i>Rep_3</i> <i>superfamily</i>	ND
p4	ZPPH1	NZ_CP077992.1	China: Hangzhou	35,358	<i>tet(A)</i>	RepA	<i>Rep_3</i> <i>superfamily</i>	ND
pFAHZU40-KPC	FAHZU40	NZ_CP078008.1	China: Hangzhou	28,700	<i>aac(6')-IbΔ</i> , <i>aac(6')-IbΔ</i> , <i>qnrVC4</i> , <i>cmlA5</i> , <i>bla</i> <sub>TEM-1C</sub> , <i>bla</i> <sub>KPC-2</sub>	RepA	<i>Rep_3</i> <i>superfamily</i>	ND
pQZPH41-KPC	QZPH41	NZ_CP064400.1	China: Quzhou	88,210	<i>bla</i> <sub>KPC-2</sub>	RepA	<i>Rep_3</i> <i>superfamily</i>	ND

pPUV-1	NMI804/03	NZ_MT732179.1	Poland	489,508	<i>aadA10, aadA10,</i> <i>aadA10, aadA10,</i> <i>qacEΔ1, sul1,</i> <i>bla<sub>VIM-2</sub>, bla<sub>VIM-2</sub>,</i> <i>bla<sub>VIM-2</sub>, bla<sub>OXA-2</sub>,</i> <i>ant(2'')-la,</i> <i>ant(2'')-la,</i> <i>ant(2'')-la</i>	RepA	<i>Rep_3</i> <i>superfamily</i>	IncP-2
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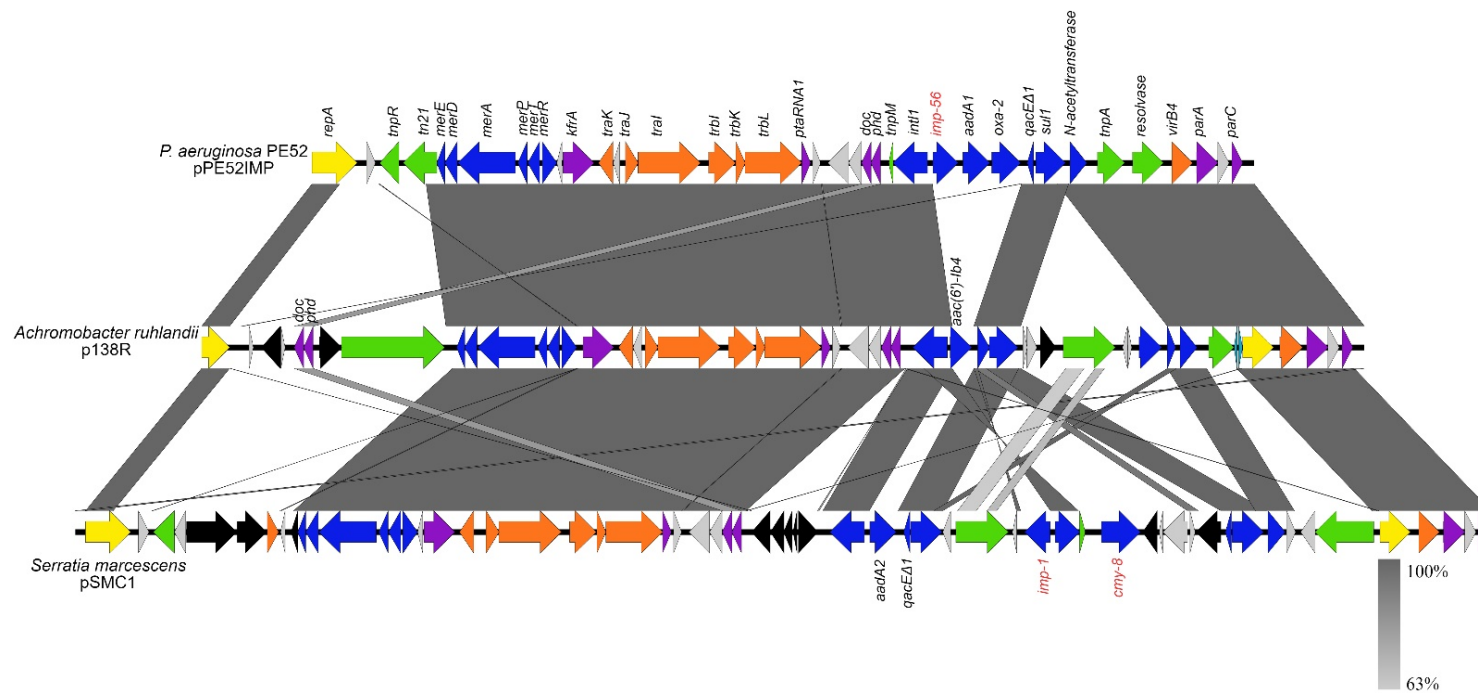
To determine the country of isolation we relied on the information of the submitters in GenBank. Δ symbol indicates a truncated gen.

**Table S2.** Characteristics of *P. aeruginosa* plasmids with similar structure like pPE52IMP.

Strain	Plasmid name	Accession Number	Country	Source	Size (bp)	Resistance genes
FDAARGOS_570	unnamed	CP033834.1	USA	Collection	36,032	<i>aph(3'')-Ib</i> , <i>aph(6)-Id</i> , <i>aac(6')-Ib3</i> , <i>aac(6')-Ib3</i> , <i>sul1</i> , <i>bla<sub>VIM-6</sub></i> , <i>bla<sub>OXA-10</sub></i> , <i>bla<sub>OXA-10</sub></i> , <i>qacEΔ1</i> , <i>cmx</i>
D5170990	pD5170990	KX169264.1	Brazil	Blood	32,424	<i>cmx</i> , <i>qacEΔ1</i> , <i>sul1</i> , <i>bla<sub>KPC-2</sub></i> , <i>aph(6)-Id</i> , <i>aac(6')-II</i> , <i>aph(3'')-Ib</i>
MRSN17623	pMRVIM0713	KP975076.1	USA	Unknown	36,032	<i>aph(3'')-Ib</i> , <i>aac(6')-Ib3</i> , <i>aac(6')-Ib3</i> , <i>aph(6)-Id</i> , <i>sul1</i> , <i>bla<sub>VIM-6</sub></i> , <i>bla<sub>OXA-10</sub></i> , <i>bla<sub>OXA-10</sub></i> , <i>qacEΔ1</i> , <i>cmx</i>
P07-406	pMATVIM-7	AM778842.1	USA: Texas	Clinical isolate	24,179	<i>bla<sub>VIM-7</sub></i>
164130	p4130-KPC	MN336501.1	France	Urine	58,104	<i>aac(6')-Ib4</i> , <i>sul1</i> , <i>bla<sub>KPC-2</sub></i> , <i>bla<sub>KPC-2</sub></i> , <i>qacEΔ1</i> , <i>catB3</i> , <i>bla<sub>OXA-732</sub></i> , <i>bla<sub>OXA-</sub></i>

**Table S3.** Characteristics of plasmids from other bacterial genera with similar structure like pPE52IMP.

Strain	Plasmid name	Accession Number	Country	Source	Size (bp)	Resistance genes
138R	p138R	MK423762.1	Argentina	Patient with cystic fibrosis	34,096	<i>aac(6')-Ib4</i> , <i>qacEΔ1</i> , <i>sul1</i>
SM39	pSMC1	AP013064.1	Japan	Clinical isolate	41,517	<i>aadA2</i> , <i>qacEΔ1</i> , <i>sul1</i> , <i>bla<sub>IMP-1</sub></i> , <i>bla<sub>CMY-8</sub></i>



**Figure S1. Comparison of pPE52IMP with plasmids from other bacterial genera with similar backbone.** This figure was built with Easyfig [44]. Plasmid modules were represented with different colors. Yellow: replication; Purple: stability; Orange: mobilization; Blue: adaptation; Green: transposons; Grey: hypothetical proteins; Black: other genes. The gray color level indicates the percentage of BLAST identity of the plasmids. p138R (accession no. MK423762.1), pSMC1 (accession no. AP013064.1).