

Table S2. ORFs in plasmid pNDM-BJ01 and the gene homologies in GenBank

ORF No.	Location (start-stop)	Size (aa.)	Best match (accession no.)	Organism	Similarity (%)
pNDM-BJ01_1	454-3444	996	putative MobA/MobL protein (ZP_05359481)	<i>Acinetobacter radioresistens</i> SK82	886/972 (91%)
pNDM- BJ01_2	3459-4703	414	hypothetical protein (YP_974073)	<i>Acidovorax</i> sp. JS42	230/381 (60%)
pNDM- BJ01_3	4714-5166	150	predicted protein (ZP_06073950)	<i>Acinetobacter radioresistens</i> SH164	67/79 (85%)
pNDM- BJ01_4	5569-5288	93	hypothetical protein (YP_004111389)	<i>Desulfurispirillum indicum</i> S5	20/28 (71%)
pNDM- BJ01_5	5761-6078	105	transposase IS3/IS911 family protein (ZP_06067871)	<i>Acinetobacter junii</i> SH205	105/105 (100%)
pNDM- BJ01_6	6189-6905	238	transposase insB (ADX04036)	<i>Acinetobacter baumannii</i> 1656-2	238/238 (100%)
pNDM- BJ01_7	7011-7790	259	aminoglycoside 3'-phosphotransferase (ZP_07238512)	<i>Acinetobacter baumannii</i> AB058	257/259 (99%)
pNDM- BJ01_8	7942-8967	341	IS30 family transposase ISAbA125 (AEH43777)	<i>Escherichia coli</i>	341/341 (100%)
pNDM- BJ01_9	9068-9880	270	New Delhi metallo-beta-lactamase-1 (ADP20459)	<i>Escherichia coli</i>	270/270 (100%)
pNDM- BJ01_10	9884-10249	121	bleomycin resistance protein (AEH43775)	<i>Escherichia coli</i>	121/121 (100%)
pNDM- BJ01_11	10254-10892	212	phosphoribosylanthranilate isomerase (ADY00042)	<i>Escherichia coli</i>	196/200 (98%)
pNDM- BJ01_12	10903-11934	343	tat twin-arginine translocation pathway signal sequence domain protein (ZP_08267023)	<i>Brevundimonas diminuta</i> ATCC 11568	163/188 (87%)
pNDM- BJ01_13	12346-11939	135	periplasmic divalent cation tolerance protein (YP_003374846)	<i>Xanthomonas albilineans</i> GPE PC73	76/100 (76%)
pNDM- BJ01_14	12462-12752	96	chaperonin Cpn10 (YP_004145503)	<i>Pseudoxanthomonas suwonensis</i> 11-1	90/96 (94%)
pNDM- BJ01_15	12808-14448	546	chaperonin GroEL (YP_001481444)	<i>Escherichia coli</i> APEC O1	515/533 (97%)
pNDM- BJ01_16	14967-16166	399	transposase InsE (YP_001481445)	<i>Escherichia coli</i> APEC O1	380/388 (98%)
pNDM- BJ01_17	16954-17979	341	IS30 family transposase ISAbA125 (ZP_08442521)	<i>Acinetobacter baumannii</i> 6014059	341/341 (100%)
pNDM- BJ01_18	19241-18594	215	resolvase (YP_001966417)	<i>Moraxella bovis</i> Epp63	126/205 (61%)
pNDM- BJ01_19	19801-21513	570	hypothetical protein (YP_025329)	<i>Pseudomonas alcaligenes</i>	125/207 (60%)
pNDM- BJ01_20	21992-21510	160	thermonuclease (ZP_06064599)	<i>Acinetobacter johnsonii</i> SH046	95/158 (60%)
pNDM- BJ01_21	22653-22192	153	hypothetical protein (ZP_05359512)	<i>Acinetobacter radioresistens</i> SK82	41/67 (61%)
pNDM- BJ01_22	23357-22716	213	Type IV secretion system protein (ZP_05359511)	<i>Acinetobacter radioresistens</i> SK82	204/213 (96%)
pNDM- BJ01_23	26065-23354	903	putative type IV secretion system protein VirB4 (ZP_05359510)	<i>Acinetobacter radioresistens</i> SK82	818/903 (91%)

Table S2. Continued

ORF No.	Location (start-stop)	Size (aa.)	Best match (accession no.)	Organism	Similarity (%)
pNDM- BJ01_24	27097-26381	238	soluble lytic murein transglycosylase (ZP_05359508)	<i>Acinetobacter radioresistens</i> SK82	201/240 (84%)
pNDM- BJ01_25	28872-27355	505	conserved hypothetical protein (ZP_05359506)	<i>Acinetobacter radioresistens</i> SK82	467/502 (93%)
pNDM- BJ01_26	30122-28869	417	putative transglycosylase (ZP_05359505)	<i>Acinetobacter radioresistens</i> SK82	391/415 (94%)
pNDM- BJ01_27	30650-30198	150	hypothetical protein (ZP_05359504)	<i>Acinetobacter radioresistens</i> SK82	132/152 (87%)
pNDM- BJ01_28	31028-30654	124	hypothetical protein (ZP_05359503)	<i>Acinetobacter radioresistens</i> SK82	89/98 (91%)
pNDM- BJ01_29	31989-30952	345	P-type DNA transfer ATPase VirB11 (ZP_05359502)	<i>Acinetobacter radioresistens</i> SK82	312/341 (91%)
pNDM- BJ01_30	33384-32005	459	VirB10 protein (ZP_05359501)	<i>Acinetobacter radioresistens</i> SK82	393/462 (85%)
pNDM- BJ01_31	34123-33386	245	VirB9 protein (ZP_05359500)	<i>Acinetobacter radioresistens</i> SK82	232/245 (95%)
pNDM- BJ01_32	34926-34138	262	hypothetical protein (ZP_05359501)	<i>Acinetobacter radioresistens</i> SK82	226/262 (86%)
pNDM- BJ01_33	36011-34926	361	TrbL/VirB6 plasmid conjugal transfer protein (ZP_05359498)	<i>Acinetobacter radioresistens</i> SK82	321/361 (89%)
pNDM- BJ01_34	36456-36019	145	hypothetical protein (ZP_05359497)	<i>Acinetobacter radioresistens</i> SK82	106/122 (87%)
pNDM- BJ01_35	36796-36425	123	hypothetical protein (ZP_05359496)	<i>Acinetobacter radioresistens</i> SK82	100/118 (85%)
pNDM- BJ01_36	38674-39363	229	cobyrinic Acid a,c-diamide synthase (ZP_05359494)	<i>Acinetobacter radioresistens</i> SK82	205/229 (90%)
pNDM- BJ01_37	39360-39764	134	hypothetical protein (ZP_05359493)	<i>Acinetobacter radioresistens</i> SK82	117/130 (90%)
pNDM- BJ01_38	41433-40405	342	hypothetical protein (ABS89902)	<i>Acinetobacter baumannii</i> ATCC 17978	235/388 (61%)
pNDM- BJ01_39	41821-42126	101	hypothetical protein (ZP_05359485)	<i>Acinetobacter radioresistens</i> SK82	68/99 (69%)
pNDM- BJ01_40	42352-42747	131	hypothetical protein	-	-
pNDM- BJ01_41	43010-43651	213	conserved hypothetical protein (ZP_05359484)	<i>Acinetobacter radioresistens</i> SK82	136/199 (68%)
pNDM- BJ01_42	43882-44355	157	hypothetical protein (ZP_05359486)	<i>Acinetobacter radioresistens</i> SK82	116/156 (74%)
pNDM- BJ01_43	44589-45416	275	DNA primase TraC (ZP_07358230)	<i>Desulfovibrio</i> sp. 3_1_syn3	183/255 (72%)
pNDM- BJ01_44	45478-45714	78	Putative uncharacterized protein (ADX05351)	<i>Acinetobacter baumannii</i> 1656-2	65/74 (88%)
pNDM- BJ01_45	45875-46297	140	hypothetical protein (ZP_05359483)	<i>Acinetobacter radioresistens</i> SK82	102/128 (80%)
pNDM- BJ01_46	47274-46738	178	hypothetical protein (ZP_05359482)	<i>Acinetobacter radioresistens</i> SK82	159/175 (91%)