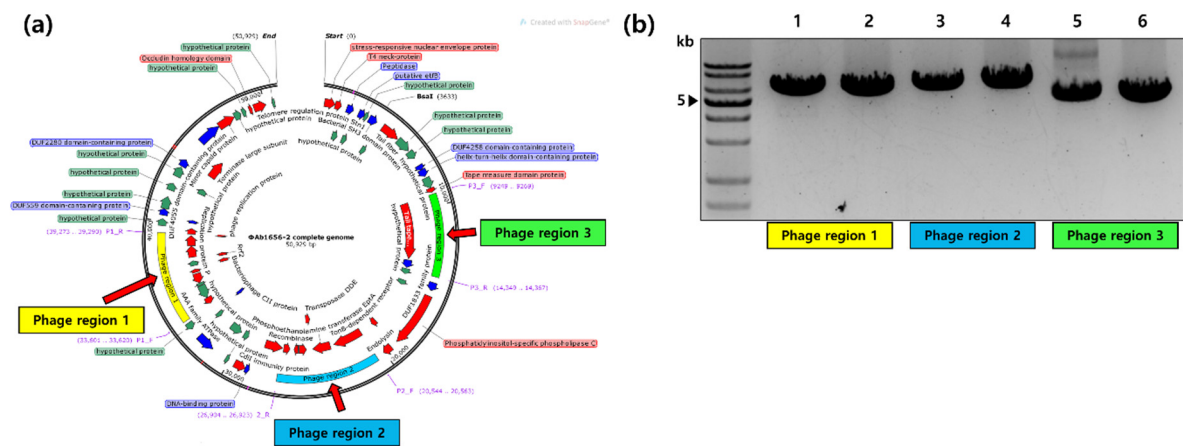**(a)**

(b)

Figure S1. Identification of ΦAb1656-2 genome from ΦAb1656-2 and *A. baumannii* 1656-2 by PCR. (a) Location of phage regions in the whole phage sequence. (b) The phage regions was amplified using *A. baumannii* 1656-2 chromosomal DNA as templates in lane 1, 3, 5 and ΦAb1656-2 genomic DNA as templates in lane 2, 4, 6. The PCR amplicon size of phage regions are 6.4 kb, 6.4 kb and 5.1 kb, respectively.
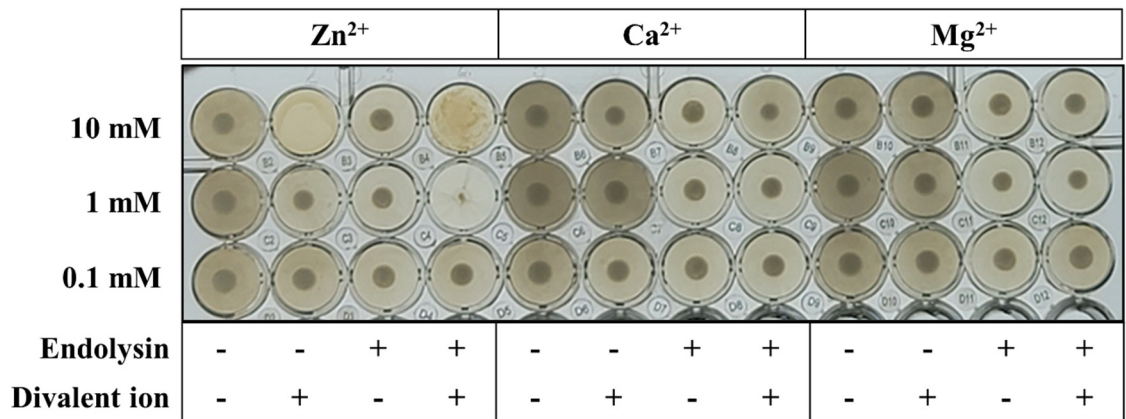
Supplementary Figure 2.

Figure S2. Effects of divalent cation ions on the antibacterial activity of AbEndolysin. The concentration of AbEndolysin was fixed, and the divalent ions Zn^{2+}, Ca^{2+}, and Mg^{2+} were used at concentrations of 0.1 mM, 1 mM, and 10 mM, respectively. Total volume of each well was fixed as 200 µl with fresh MHB.
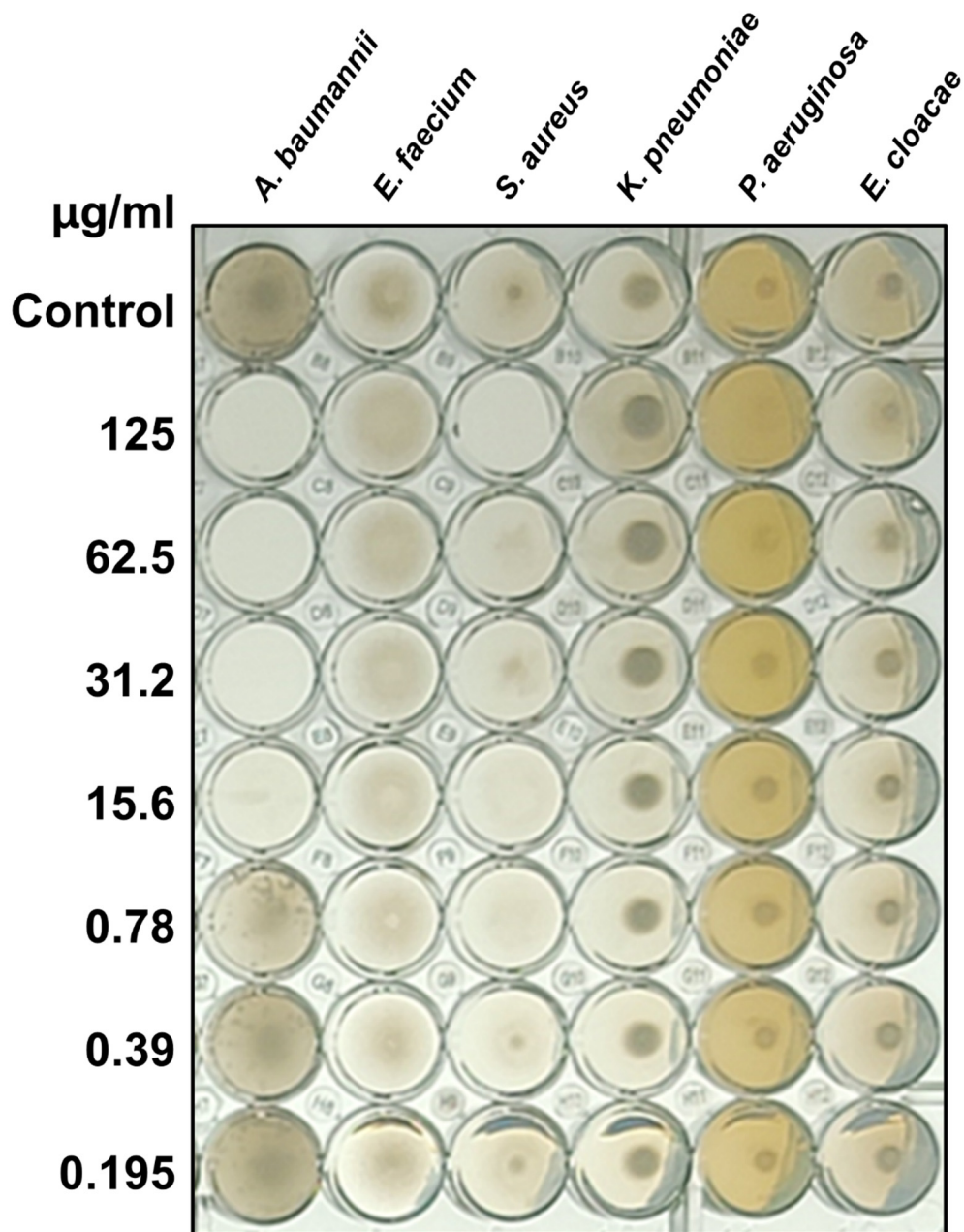
Supplementary Figure 3.

Figure S3. Antibacterial activity test of AbEndolysin against ESKAPE pathogens. AbEndolysin antibacterial activity against ESKAPE pathogens (*Enterococcus faecium* (clinical strain), *Staphylococcus aureus* ATCC 33591*, Klebsiella pneumoniae* ATCC 13883, *A. baumannii* ATCC 17978, *Pseudomons aeruginosa* ATCC 27853 and *Enterobacter cloacae* (clinical strain)). AbEndolysin was serially diluted two-fold from the highest concentration of 125 µg/ml to confirm its inhibitory concentration. Fresh bacterial culture in MHB was used as control.

Supplementary Figure 4.

(a)

>YP_009882155.1 LysAb54
>APD20282.1 endolysin [Acinetobacter phage AM24]
>AJG41873.1 endolysin [Acinetobacter phage RL-2015]
>YP_009624620.1 endolysin [Acinetobacter phage vB_AbaP_D2]
>YP_009190475.1 putative endolysin [Acinetobacter phage vB_AbaP_PD-6A3]
>YP_008058242.1 EF hand domain protein [Acinetobacter phage Abp1]
>YP_009610435.1 endolysin [Acinetobacter phage vB_AbaP_B5]
>HM755898.1 Acinetobacter phage phiAB2 endolysin (lysAB2) gene
>ADX62345.1 endolysin [Acinetobacter phage phiAB2]
>YP_008060133.1 putative endolysin [Acinetobacter phage AB3]
>KF548002.1 Acinetobacter phage ABP-01 putative endolysin (lysABP-01) gene
>KF548003.1 Acinetobacter phage ABP-04 putative endolysin (lysABP-04) gene
>AZF88457.1 endolysin [Acinetobacter phage TAC1]
>QXM18610.1 endolysin [Acinetobacter phage Phab24]

(b)

>YP_009882155.1 LysAb54
>APD20282.1 endolysin [Acinetobacter phage AM24]
>AJG41873.1 endolysin [Acinetobacter phage RL-2015]
>YP_009624620.1 endolysin [Acinetobacter phage vB_AbaP_B5]
>YP_009190475.1 putative endolysin [Acinetobacter phage vB_AbaP_PD-6A3]
>YP_008058242.1 EF hand domain protein [Acinetobacter phage Abp1]
>YP_009610435.1 endolysin [Acinetobacter phage vB_AbaP_B5]
>HM755898.1 Acinetobacter phage phiAB2 endolysin (lysAB2) gene
>ADX62345.1 endolysin [Acinetobacter phage phiAB2]
>YP_008060133.1 putative endolysin [Acinetobacter phage AB3]
>KF548002.1 Acinetobacter phage ABP-01 putative endolysin (lysABP-01) gene
>KF548003.1 Acinetobacter phage ABP-04 putative endolysin (lysABP-04) gene
>AZF88457.1 endolysin [Acinetobacter phage TAC1]
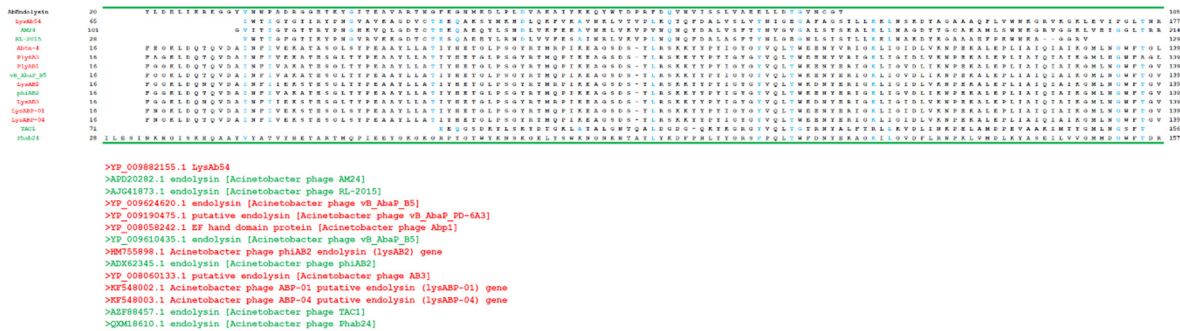>QXM18610.1 endolysin [Acinetobacter phage Phab24]

Figure S4. Multiple sequence alignment of AbEndolysin with another *Acinetobacter* phage derived endolysin. Thirteen *Acinetobacter* phage derived endolysins amino acid sequence was compared. Red letters (Abtn-4, ply6A3, plyAB1, LysAB2, LysAB3, LysABP-01 and LysABP-04) indicate reported endolysins and green letters (vB_AbP_B5, phiAB2, TAC1, Phab24, AM24 and RL-2015) indicate endolysins sequence obtained from the NCBI protein database.

Table S1: list for the genome predicted 68 putative ORFs

Protein_ID	Start	End	Strand	Product	Protein Seq
phageDNA_00001	192	857	+	stress-responsive nuclear envelope protein	MKIIYTRIAAAAALETGIIANPDYYENPNLKAKEVIIYGNYPKIQKDYESLEVPVEVRKLEVPQKTTLATVNVAVGITPELQAVMDDAKAECEKVVEENTQLKQKIAILEQAGGNQSELLSENSRLKDAAVLADKALKDAEAQVVGIKTEFEAFKNDIPAMQARIAELEAGKAAENPATETAANDFENWSNDQLKEYLASKNIGYKPSATKAELLKLIPKE*
phageDNA_00002	862	1251	+	T4 neck-protein	MSFITVDDANSILGSDFAPDSDKARLVKLANVWMKNRIGFVPDPIDPLLKDAACEIIKGILAKVIYNGKEQQLKRKKVKADSVESEKEFQDGSEAISSFEQIAIDFIDSLDLKDPNASFNGFGIPLYRA*
phageDNA_00003	1208	1621	+	hypothetical protein Peptidase	MQVLMALAYHFTGHDMGLRDEIQADIAEAFNDDLADAIHTFTCERISKTNWDPKTETYVEKVENYSGRGVLFGSYSQYEIQTLGVLATDKKATVLQNEVTMTPKIEDEWLTALGSFRVINIQQDPANTIWKCQLRKV*
phageDNA_00004	1600	2034	+	hypothetical protein	MSASKSVGAKMVNPDYVPEWYISPFQHVQYTLARNQLHMDLLFEDMDKADQFLDMGADAQVSTFSDGAYAIVQIGDTADKDRIQVYGLLLHEAVHVWQKIKKLMGEREPSSEFEAYSIQAIAQDLFKMYEESEVNDGMEGEKAN*
phageDNA_00005	2006	2374	+	hypothetical protein	MGWKGKKPTEFSFDVSKAAEDQVKHIVMDTVQSLVNLSPVDTGAYRASHIVSVGSADFGVREPETNPINDAAIQAMKIKLGNLVYIQNNKAYGPRLENGWSDQAPQGIYGLTFNFISQKYGG*
phageDNA_00006	2382	2774	+	putative Electron transfer flavoprotein subunit beta (etfB)	MTLEQTRQAIIDRMQSFTGIAQERIQYPNAPDFTVPTKGVWCRLTIAGGPSFTSGIADKPCTRRTGNIMIQCFDRLHTGEKAVTVLSDALLAHFEYFTIEHLECLNGQSIYAGKDADFIQYNVSIGYKVN*
phageDNA_00007	2776	2994	+	hypothetical protein	MSCMLTLEEIEIKRQELERHLEDVMSVELSKWQSENKLCVSDVNIRLANVVSLGGPKHNVVTGVSVDLDNEL*
phageDNA_00008	3103	3624	+	bacterial SH3 domain protein	MKKSTLGWGAAGLVALGIFGSGNDNSPKQTSDSENAQSAVEEVIESKYINTNSLNIRDKPNGQVVGKLGRGEKVDIYEMKGNWARISLNSSSPQWLSTKLLCETDGCFKQKSRSTTSNNYQALKSHPHHSERKQKKTYYDSDCSCAVVDYCVGPRGGHYCITSGGNKRYKPRY*
phageDNA_00009	3721	4074	+	hypothetical protein	MSNFVFKRGDTFNLNLQLVDMDEALQYPPDDVRRAIDLTGYTFTSQVKALADGATVATLTCTALSQSTQKGWLNIKSSASTATWPLGLCQMDIKAVVSGTTQHTETLTFQVIDGVTA*
phageDNA_00010	4074	5252	+	putative tail fiber	MANLVFKFSWDHRPFPYNASQGKRQFMLPFASGIPNLAPNFSQVVGTAAISQGGTGATTAAGARANLGAAASGVNSDISELKGLTTPLSISQGGLGADNAQTARMNLGLGTAAVLASTTSQYDPTPGRALRVGDWGIGAEGSRVSDMVAPLNNGFFRTDDTLTNDTGNSIGPYGFFLHCTRRSMGLYTNGSHSFGLGKAASYSALKYRFNNSGTWSNWFNLLTAQNTTTDGNGFIKAASPVVKLFQSHIELNNDAAKQPITFDKLGTGDYLIKGSLGFAQEGWYIEVPKDANGNTVVAVEYSTLENGDLSIKTYKRKFDVEKAAIVADLENPLDIPEGRWIDIRLHEEPEPEPEEPLSETPVDFQPTNLSQAVAAAMNGVEPPEISETDETL*
phageDNA_00011	5305	6222	+	hypothetical protein	MSSGAKIRLYACEEAVLGTTPANPVWYTVRRVTDSLTENVTTEDSSEVVDSRFRQQAVVTEAEVTGQLEFELSLGTFDLFLNVLAFNNNWAANALSFGGGVRKSLTLVKVFEDIGQVFIYRGIQVNTGEMTIQTTGKITGNFGLVGSSFTRQQVNPVTNPIPASTRPLVSMPNVEKLLINGQSIQGKACLQTLTINFSNNLEAIRCIGSGKYTPEFYLEKMMDIGVNANFMFSATSASWIDAIKTRDVFTLTFDITDTKGSKSYSFNFPQLEVKEANHPDGGGDDIITIDINFAQVRTSPTIVRALV*
phageDNA_00012	6292	6807	+	hypothetical protein	MALKVGIIKSSDVSKWCEYKGADGDVQAEFKVRGIAYKPFQVAIERAGNQISSKGYDVMVKDEDAKLYHELLMDACAAHLIEDWKGVVFAEIVDGKTVESEKPYTPENASKLLNLGDIGISIWLFIKEQAQKIQEDADKDKALILGKSWSSTNTKKRMRRKRRTKSSKSSS*
phageDNA_00013	7310	7609	+	DUF4258 domain-containing protein	MCLTLTEAKQKLRAFARDTSKIKLTAHAKERMKERCISMKQIICCFEHGDITEGPYPNTRGDCQLNVSVRTAGEYITTAVAIKQSENGEFSVVVTTFRE*
phageDNA_00014	7618	8076	+	helix-turn-helix domain-containing protein	MYHYEECGLSNIWLRNGFTIENDEDYGELVSIESVHELHNAIGLFLITQKPDLNGEEIRFLRKELNLSQKNLAGLLGVSETSIRHWEADRGLIGKPTELLLRALYKEHVQDGDGKLRSMIESLNHQERTLVPSEISFSYGNNHSWHQTNCEIA*
phageDNA_00015	8181	8861	+	hypothetical protein	MKKILAAGLIGLGLVGCATPAYNYQAIPKNISKPPIGSVNKAFVGDQMLEQGMVVDREVLNVPENIKISFAYSLTSGIYLKTGKNEKGQYFQPFNTVSGGGMVQKNPLADPFKVVMLDTEGKLCVVTVFNAKNCTDKHQATMKTVAIASDNSFQQTLIYSGKFGNKINVGYREFSSNQARPAFNNDVEYDLSQSKQIGYKGALLEVIDATNQDITYKVLKNFNKVD*
phageDNA_00016	8863	9126	+	tape measure domain protein	MSAPQYKPMRESEVCNAIGVWVLIALGFIAGFLFILAFGRIEVASYYGKETVWSGVMIATGIGIFNGFLAGYLFQKVASILRYHENK*
phageDNA_00017	9254	13564	+	tail tape measure protein	MAQESRLVIVIDSQNAERNARNLGNELVSIERKGEFASKSMDSLSVATRALAGHMAGLLTVGSAISKMDTYTGLQNRLKLVTNNQVELNKATEDTFRIAQKTYSAWDSVLQVYQRFSDNAKTLNLTMDDTARLTETVSKAVAISGASAEAADAALVQFGQALASGTLRGEELNSVMEQTPALAKAIAKGMGITVGELRSVAAEGKITSQEIVKALRNVESDVDALFAKTDITIGQSLTLLNNEITKFVGEAGKGSGAAQVLAGSVQTLASNLDLADGALVVGIGYITRAILMKSAAIKEGMASTLASRQASVLNAQAEYAEATAALNAKAHELANVRATNAETQAKFGATAAATRYAQAQAAVTAATNAGTAAQIKLNTATSIAGRLAKGAFGLIGGWAGVATLGVMGLAAAYSYFNNKAEEAKQKLAEQAKVAEKADEELKKLTQNDKAKAVVNDLTTTAFNAQNKALEKSSRAVGSALIDIENYARGNREVEKISQEARTGTISYTEAIERLNKIKLPTDLYENLKKQAAQYDDNASKASLKAREILKLIRLVEVKLGSNEAQNAAIQHQKQADLALQNTATEAEKATKALQDYQKQKDSVIDSIYHSGWLDKGYTVAQMAILELQKAKGMSAILSKDEIDSALRNLKIIEEQQEREDKLTEAKRKQTQEIEKQAKLTKRLVGISGQSGIGTGPHLDVRYGGSLSGQKVSNEHLARLQAGGKPLTSYKISSNYGPRKAPTKGASSFHKGIDFSMPEGTPITTNVAVKDIKTWYDSKGGQYVSEVIFECGVSLKLLHQSPKMQSKVKGGASKGSDKAAGDIQSQLERQQDLQRSLENEVASEVGRINNNRKARLEDVDKANFSPERTAEIKAEINRRADNDIAIAKQALRTKLEDYKEFQKTEEQLLEESFNRKKFNAAHDLELSKFEQKQAVELLEQDKQQELGLLKLAQEQRLFQARLSLLSETQAMQERYRLEREEILKNTKLSIEERQKLIALSKANQDKETRDKVNNAVQNWSGGIQADMNGTGEFFRQDQERFSRLNAANDLADSQFAATDLDEKNGLDVLNAHMIEAGLIKQQDFENRKTAIIQAAQDQRNQIAAEYAQNAQDIEDKYHQDRLNAQIALGGQMMGSLTSMFGSMFGEQSKAYKIMFAADKAYAIAAAGISIQQSIAKAASVGFPANIPLIASAIAQGASIIANIRAIKDQGFADGGYTGSGGKYQPAGIVHKGEVVWSQEDIKRWGGVGLVEKMRKSANPEAFLNNNALADSVMRRAMMSSSAFIESQKQADIFNQPVQDTQIYKGNRDTPKLASSGNLDLFHDGKVYFSSNGLVQDRSNLDDVQDFTLGSTSRPQAEMMPSIEPASPTINFKIEVINQVSGATVEAEQLDEQTVRIIVKDELDKQLPRTVPKLVSDQIANPNSTISRSLTENTTARRNRT*
phageDNA_00018	13655	14242	+	Prokaryotic membrane lipoprotein lipid attachment	MKKIIVISTTLLGLTGCAIPAVNNLVRSTNMYQDDVSGNTANLRVYRSNIPMVQFYITYQNNEGEKISKNLITKQISNNLTKYGSMHEPKKLNMPKPTISLNNGEEFFEFKVPANKKLTFRLTSVIGSTTMYSCDVKMDYQLERNGNYELIRLKQIKDFVNPALLTEPSQDEAYCKFVVKEIFEDGKETIIKSIS*
phageDNA_00019	14335	14733	+	hypothetical protein	MYKLKLNPQTSGYGVTPGDDVKRQQMDGGRGRYYIDVKRNSHIVDVNWNLSKTDFNKMMAFWRVYQNKPASFYADLVIDQGTRQQYLCNFIPNSFKTNEVNGNLYRVNAQLEVVQNQPNLNADIALIKDWEV*
phageDNA_00020	14733	15239	+	DUF1833 family protein	MDNEYAKFFFNRKVDVYQLECIELSHPSFMNTYRVVRNDDRGVYVQHKEGSGQVYYEFLPVSIQRSGMLGDLDQTLTVSISGLGDVMPDEFERVIEGQYPDVKPTVNYRIYSSDNLNSPMFYLLGLQLSSVAMNHKAVTFKAESPRLNTTKTGDIFALDRFSGLKGAI*
phageDNA_00021	15236	15598	+	hypothetical protein	MKSHDHLLDRQYDEDHYNCVHFVHEAAMDLYGIDRAEALELFMQPKGKITFLSSRLKLLNPLPMPKEGCIVAFHPRQRNKPPHVGLFRGQKILHLMESGVTYLPEEVVMEMGFNRVSYYD*
phageDNA_00022	15591	19016	+	Phosphatidylinositol-specific phospholipase C	MIKVIYKKDALSEEKTIEQAQTIGQWLTSKYEHMPEHVRIFHTTSNMDHAEISFANEVTPKNAYDLKQDFLPGTFIVVNPKWVAAIVSIVISIAIAFLMPTPSIAQTTQNTNQSSSANNELSNRENKIRVNGRIADNYGAGWNTPDLIAVPYKVYENNVEVEHVVGCIGRGHYKINGAYDGETNIVDIAGASVEVFRPGVDIVSGEPYFSLGTEITTPPLTVQHQTSVNGQVLRPADTQSLEGTNYLHFAYPNEILRATANNTDLTTKFVSNDRVEITNASFTFNGQTFDLNGTYSVLSVADDRMTLSNPAAVNANWLKLKELNNQQTAALSPKISSIGEKWIGPFILDNVERSRVLCNFVATNGLYTVSSGGYQAAVHVTIEVEVTPVNESGAAIGNPMLKQIILKGSAKSRQTVCATLDMVTFQQRCSVRARRLTPTPTVTTVVDEVKWQALYGAAYPLQSTVYEHETVFRARTYATTGALSVKSRKINFDLQRMLPTYKNGAMTTELYPTSFADALVSMALDDKGRRSISEIDLENIYRTNDVVYFGTPKAAEFCTTIDDTNLSFEELVTNLCDKHVYFERPTDNSVMLFNFRNIIPDSYKHDLTFGVMDDYGGLVYEYTDPTDDSRINIYLPDKGAANPKEVKSVGVRNKWQAHFNAYNNNKKMKRFQRKSITFDAAPESELLVLRDRIAVADYRNGIHGSGEVVQQEGLVLTLSHDVDFIAGKSYVIYLQMADGTVDLIPVTPGSAKNKVVLGRLPNGALKLSPDDFVNTIYTVVNDDTKGSLPYLVAKREPVDQFSNTITAINYDERYYLNDKDFIDVPVDSPIYIRYDQLDINLARLYQMQRGDLPTTGEISFVVESGALVSSSSYRPETRFVYKFDYNSSPPKQEFIAPAATELPAIDTGEFPPDLVVNLTKGAVVGRCGDGGLPHLAFGAWESDPDYNFTKTRRDGFQGAPGLLNRHSKLNLIIDGGTLARGGSGGGATPSGIYTGLSYGVQGIPGGAGAPFGRVMTGGPISSDSQDWRWYFGSYFNVLKITDAEASVPGKGYRTQNDRYGSPLSGDGGNWGERGTKSTNDGTWNWKYHGTTEGQPGPGGPAIVGVAPLTTQLINGGKILQTL*
phageDNA_00023	19084	19473	+	Ammonia monooxygenase/methane monooxygenase	MEPVSTSGFTALLKLYGIAIMVTLAVGLVAAVVLMTRMPRSPQEWAVGLICTVVSSLAGGSFIIVKWGLHEWVTDVWGMIALGGFFFVCGLPGWALVRWIFNFIDKQEGKTIVEVIKEFKKARKDIENS*
phageDNA_00024	19473	20060	+	Endolysin	MPPSGGFLHLKETEMNIEQYLDELIKREGGYVNNPADRGGETKYGITEAVARTNGFKGNMKDLPLDVAKAIYKKQYWTDPRFDQVNVISSLVAEELLDTGVNCGTGFAKPLLQRALNLLNNQGKAGWPDLTVDGIYGPATLNALKTYLAKRGKDGEKVLVRVLNIMQGQRYIEICERNPSQEQFFYGWIANRVVI*
phageDNA_00025	20542	22860	+	TonB-dependent receptor	MKPLAALPLIFAIGQVQAEERIAILKPLVFKANALKEKNYYVDKEKVESSNTIGDALKNITGIQSTSFGPNAGAPVIRSLSGNRVGVIENGEFINGMNAFSGNINIPFDPIFIEKVIVNKNTDNIRYGGNAIGGSVQIESGLIPKKIEEKPNKLDIVFRKGFNDFDVKGFNFNINDQKNWSTNIRYSEYISSYKPGNSKAKLCEDQIFSNSGGINSLAAASCQKDSRYKDAHSYPYIDKFMTENPDWADGDFSFYTDKPTSIWGGKTYINRKNPEYIPNTPQNTIKKINTDVTPNYFKKLGNSYAQNENIGFGTTYFFDKGFIGLSADKKKSEYGVPGFSLQNQSFADSYETLPVGVKIDQNRFVLNSNFIQPISSAEEISLNFQQLSNKSGEYVGTAKANEYKIDNQLIELIMKQSSFKGLDGILGFSLKNRNIEGSGTQRYLPNVSTISKAIFLQEELNIKQFTLNTGYRFERIEHELQDNDFKLARNASNSRIENRKYNLNQYFIGGEYKVNNFINLKVDYGISERAPEVNELYSSNVHYSVMAQEEGDQNLKPEKSKSLEGLMFLMWNNWVMQLVGYQMDFENYMYLSHSGVAVQNRLPLKYWKQTDTDVKQFEIDLIYDFNLAHIGNIKLGGLADFVNKKAVNPTDIRLANDGVYLPNMPTNRYGMFLEWRNDSWKGKISSIYYDEPRYLGKNVIQEVPLSGYNLLEFKIDKKLKIKNASFDIFLNGTNLLNEEARPQNSPLKYIAPLPGRAFQLGITMHI*
phageDNA_00026	23142	24527	-	Phosphoethanolamine transferase EptA	MALNVFKFKKICKDVTLLNFNLLLSIWLGLFLNIGFFKIIHQLTPYNGIIKSVLFLGATLVILIAAYNLIFQLINWKWTAKIFAILLIFIGGFSSYFVNTLGVIISPDQIQMMVQTDVSEFTDLISLRFVLWTVFFVILPIFLITQVKFKQEKASRLLLKKVFSLVASFAVVGVLLFTYYVDFAAIFREHRDLKGMISPQNSISSLMSYYHKKAPKKNLPLVIYGQDAHQVQQVQKNLPKLMILVVGETARAESFSLNGYAKNTNPELSKQDIFNFSQVSSCGTATAVSVPCMFSGMPRVDYDEQLASHREGLLDIAKRAGYQVTWIDNNSGCKACDRVEQYQIPENLKKKWCKDGECYDDILIDSLKQYLATIAKDDDRPRLIVLHQVGSHGPAYYKRAPEAYQPFKPTCDTNAIQGCSQTELLNSYDNTIVYTDHVLSQMILCTRQISQNPYPIRVLPS*
phageDNA_00027	24489	24935	-	Transposase DDE	MVGRVKLYISALQLENGELLLVVSPQFNANAIQDYALRWEIETLFSCLKGRGFNLENTRLTDPRRVKKLIAVLAISFCWCYLTGEWQHDQKKAIKIKKHGRLSMSLFRYGLDYVQMAIQRLIGFGKKEEFKEILAILRRQNPDRIRVL*
phageDNA_00028	25010	25579	-	TnpA (transposase)	MTHLNELYLILNKYLKWNKSHLKCFALIMLVIILKQTCNLSSASKALPIKCLPQSFYRRMQRFFAGQYFDYRQISQLIFNMFSFDQVQLTLDRTNWKWGKRNINILMLAIVYRGIAIPILWTLLNKRGNSDTKERIALIQRFIAIFGKDRIVNVFADREFIGEQWFTWLIEQDINFCIRVKKTSLSPII*
phageDNA_00029	25654	25977	+	Phosphoethanolamine transferase EptA	MINTLKEISKYQTGLWYLSDHGESTGEHGLYLHGSPYAIAPSQQTHVPMIMVFSESWKQHNLAQVNCLSQQTKQKLSQDNLFPSLLSLLDVKTQVVNNKLDMLSQCK*
phageDNA_00030	26288	26776	+	SEL1-like repeat protein	MKKIFLAALATIGLQACTTPYQEMGASGGVEATIIDDNVFQVRASVNGYTHKSIANQYALRKAAEVSKSLGCSYFSAINNTSQSYNQNISKVDAGLKTTPNGVYYVSSAGTQYKLIKPSRNNTYVCFNEKPNTVLPGLIYNVKYVLGSPMPTGKFKVPNSWR*
phageDNA_00031	26866	28239	-	Recombinase	MAQHIKFTKSVIDSIPLSEEKGIFYRDTVTIGFGLCVGKTKSYFAEKKMPNGKSKRKVIGKHGVYTLEQARTEAKRLLILMDEGVDPVKQKRDLRASAIQNDALQKLVPTLSEAYQYYKLRKKLAETSLIAYDGCIENYFSDWKDLKLDQITSAMIIDRHLKLSKASPSRANLASKFLHALFNHTISRYKDESGNKILNIKNPVVIVKEEKAFNKKRRKGHVRADQREAWALAVATTYWMGEQNDFRAYTNQDFLFLLALTGYPREAESVEWKNVDLQFGTIKINTKNHEDLLLPMGDTLWHIMRERKKRAGDNKVYFTDRNGVSHISDRRAARDKVTENSGIEFTFHDLRRTFGTIANSLAIGSYTIKRLINHTTDDDDNDVTDGYIQVSFDDLKKAMNMIEDVIISEPVKALIKSRLYFEKNESRNQAQELINHHIQVLDNFKMAGQILDF*
phageDNA_00032	28674	28937	-	DNA-binding protein	MSRLTKLDRMTHAEKEAAKKEFWEAADNQTFPPETVAIVMHVSLPWLQKKRCEGGGIPFSKPHKRQVNYMKSDVLAYIEQNKMAHTA*
phageDNA_00033	28938	29660	-	CdiI immunity protein	MSESTLWAVAMRPEGYSPFKQTPAASKEIAERAVERYRKMHEKEGNNFFLEIFDDVIKVQKWHGSRKDHIKNLFYVESWFSEPMYQCFDLKTAERVFKFDEIVICYKKGSAPLVTKSFDEAKLFYGSSETGFKYQIQPIEPPENLFNWFHPDIELFDTIEEGAEAYTREQWAQLQMNLRVEIETQLLDYDEIPNIPEDAVVWPNWKPEPPEQGLFLIAAFDSEDGPVLWWANPKAESKEK*
phageDNA_00034	29657	30064	-	hypothetical protein	MTGNERIPFESQFKTTEIFKRESAIRKNDILAFSETMNGYFNIVTNDAWQLWNKAKAETVPDTPTPSVTLTCAELKEAFDFGAPDGEKDQFQMETEMTIKWLQDGYDGEGYYCWYADLPEEGCIKLGVSESGAEG*
phageDNA_00035	30065	30280	-	hypothetical protein	MLGFMYYLQLLGYVIVRQGMDQAMFLTKHYAVPVAWRRITIDYHNRLNKPAQQLYKEFVEWTKEEYAEMVA*

Locus	Start	End	Strand	Product	Sequence
phageDNA_00036	30318	31250	-	hypothetical protein	MKILNKVEAKLAWANGELLLVNNTERRNGWEPFNPYDFGFDVFDKFEFQLKPRTIFIGEFEVPEPLRVAPEKGSTCSYPSPTVELGVQQFKWNGSKGQLRMLQHGQVHSSFDNAFAHCCAIIKISGGEFAEDILKLLNKPTEEVEEEKPSESHAESLKVKNSKPEVVEKAQTAE PAIESETADSEYQKKLDTLLQRVKDSKTPDEVNAVYRYTRTWSDKQMEPLLLATHKRLEELEKSKAQATEPPSLMVQIQNAPDLTTLDALEIDVAARDPQIQSRLMDFVKKRRFELENPTSTPLQEAEPDYLLGDGF*
phageDNA_00037	31247	32383	-	ATP-binding protein	MRIRKMALPIITADQTLLVQAIIVYLYADPGLGKSSMGFTAEKAISFDFDRGAHRTGELRRGAVVQVQQWSDVANLTPQDLAPYKTVVIDTVGAMLECIKTHLLLTANNRQKDGSLKLKAQGLANQTFKQYINTLJSLGKDVVFIAHASEDQNGDQIIYRPDLGGKNRNELYRIAD LMGYLTTVTTGEGKNARVINFKPSPTHHAKNSGALGGETGEVWVPDLKAHPTFLADLITQAKDHINTLTPAQLAAAKAQEELENWKQSCEEAEHAGDLNQLTESLDKEHMYYQNMRQAMLMRAKALNCTFDKQRGTWISPPEFNGISDQQRDELQNFIAERGLDVKTVCE HFGIDALIQIEAAKLTAVKQEIETLAKTGMTA*
phageDNA_00038	32380	32703	-	hypothetical protein	MSNFKKHPDGYMSFLGRDDKGLYSVRIGWQVYASNANGSVLYKVKDGVKTPLNVFRFQTSYPKVWNELTQEIDFQRRKQLAIKLRETNIPTYDRKAYKQKRGFTGSR*
phageDNA_00039	32696	32986	-	Ubiquitin-Binding Zinc Finger	MKDYNCPTCKKMIPVDRSKIKAGDEVSFCRVTQSSKSARFSSREGIVNCREGDVVLVKYRKEIIPLNIRDVSPVDAPSPLTYAFVGTCECKEAEHV*
phageDNA_00040	32986	33426	-	hypothetical protein	MNVKTFSNKHKVTGVTAIAVLVALSSCEYRTANSSVPSNYSYESEQVVASEYELLAVKKTGEKSGEAVIRIDGFKLNVSFDFDGVADSYGVAGSDFTTAEITNLAIDSVTDLSGKSFNDFTNHDDHKNINILLAGYIDRNNWLEAA*
phageDNA_00041	33635	34138	-	Actinobacterial Holin-X	MAKRYLPFYNNARFIALVLVGLFAIFSIIFKYLELNITINLVQFSFVLLLPLSQIYLAYKGMLDALKLDGLNQSERDRLTSTVDIRSKSSLYVAMLFIILVFSMYILNLLGLLSAKHLLALILSVGLTSIFSFFLAWSDLREISLLEKTLKDRKESREAKAKVLSNK*
phageDNA_00042	34140	35192	-	hypothetical protein	MNPTQYFRAIREEEIMSKTVVKDKTVHYKKVDFLKGANLGQLLKAQLLDKDSFYYKAINRQQFVSATKDDFILINHASSHQSMFFGELIVESGKAQAVLKIDSDDATEFPIKTYLTDDLPDDEDGVDATEVVRKEFIDSVLYFGVIDNHVAIIQSRSLTARTLESYLGWLLGEAAK ALPENSALILKDAPNPTVKQKLESTPAKTISISSGIGSTELQPVHTVESSIPAKIDYKIEDNVVDVLKSAFGVDLENLKLEDGLDDANLKLKLTLTYNRKTSKSGQKVIDTVASSMRHNDDYVITLEDGTKVTADNLKMSGKISVETINNKVYNDGLKVQLYNWMTTNINFGD*
phageDNA_00043	35199	35414	-	hypothetical protein	MDNSKRPINQIIARINDAAKHGEALVLTAEEVKILSKDIGDKVFIPVLTNEQVVQLVKEGKLGHKINNTKD*
phageDNA_00044	35429	36193	-	LexA (CI repressor)	MNTLAERLRYAMEVLPPKKIKGVELARAVGVKPPSVSDWLSGKSKTMEGENLLRASKFLNVNPSWLASGTGEIQSSTRDKFKQLDIEAFKKKYNISDSDEALLFSTIIEKPFTPSSKRWVPVKAYSKMGMDGYFTDMGYEGNAGDGYVPTHSAGPRAYGIKGTGDSMFPAIR NGWYVVCDPDADLVPNEFVQVCLKDGRCTIKEFVGINGGVLSLLSVNGGERFFFEMDEVESITAITDIVPPSQHRQEHPYSH*
phageDNA_00045	36302	36553	+	Cro	MNDAQLIDKLGGVTAVARLLGITPPSVSGWKAIPLDKKIRLAVIAEDLGLTTRKELFPDNYQDIWIELRPQTTKSRNLGSLTA*
phageDNA_00046	36564	36884	+	Bacteriophage CII protein	MSKVSNELPASASNNESLILQALNTSNQRQVAEKVGIDASTLSRMKNDKKNNGLTEIEFISSLLTAIGLKVVPESDVYCSPEIAEATRVYLAHAFTSPEYMRILFK*
phageDNA_00047	36841	37215	+	hypothetical protein	MHSLHLNTCGFYSNKKPLPAGTGVVRHSNEVDQMNTNNLSEQPIELNSPDFLIGDVVVLTKECRSFKSNDLFEVKNKTLTRLWTIKSENHLILVSSKEIRTATVAELNAKRRLTKAEQALAEVS*
phageDNA_00048	37212	37511	+	Iron-dependent Transcriptional regulator	MNSQFKYKPEYKQTQEIQSFFDPALVILNELHDRNRKNLRAKGYDENNAAITREEFSQTMAQRFRINQWLAGQIVNSLANADLVQKFGGYVKPKVGVHE*
phageDNA_00049	37504	38385	+	Bacteriophage replication protein O	MSNFVPNSFQVPNAFVDEVLNKISDAACKIYLVICRKTRGWNKEMDSISLTQFEEITGKSRPTVVKCLNELIKVGLVVEQPSTIHGNTFKLGNDTSVGLVLKFPSKNFLLPEIYGQTSKNSLPLLVKNFNYTSKNFLPLLVKIFNTQSITIKNNSQSNKKINKKREPVSEKPKSEKPT EFNPRLVELPACVDPELWNNFVDMRISIKKPLSENAVKLILKKLISFGPLANQSLENSIIGNYQGVFEPRQNQIQENPQSHNVPEEPGYFTQMYAESNRSNVIDVTPVSQDFGGY*
phageDNA_00050	38388	39188	+	Replication protein P	MNELAPFESFLKELIAAYRTKYAVQFNKNFPVEGKNAVPMQIVEQQLAKALVGVTPNQLQRGLALFYASTNTYMPNFAEFRAMCMGDDWWSAEKAWVKACEYTQISQHKKVTLPDGREQNQEITTLTKFVLDQVYSLIQDGEMYKAKMEFIKIYDEYKAEAQLKGKTQAWY QEPILLAQKNEQKVHKPVSNDEAQKHLQSLMERLKINGRKPVPVQKLKAKEKEPELKQELGPDPFDNPHEYAEMCRREGMPIPRNILKLIDGANI*
phageDNA_00051	39185	39319	+	putative phage replication protein	MNKFEILAWGLLISFFTAAISGAVVWWWLARKELDEKGASHESN*
phageDNA_00052	39288	39728	+	Ribosomal protein L7/L12 C-terminal domain	MRKEPAMKATKLIRDKGLQYAKEIVDSAPDNATEWNEGYEFQCGQSVEISPADREKYFVDLVELKRLVESLKIINDLGGVEKLTPAFITTDKHVGYTHVRMVGNGRLSFLDDFCDFIPDGSISIKRVMTAIRDHESIYGGGESHAN*
phageDNA_00053	39718	40140	+	hypothetical protein	MPTRYNTGEYSYDLEYHYGDMSASMEMLRARLIELLTPHLSGRYVKWREAYFTWFTKCGGDSGWMFCVGPHEFHIDGALRRYYSGSIDITYNQKDRYFLVGEKKKVKCKACKGFGFIRDDGWGHIDKCEMCDAEKGASHE*
phageDNA_00054	40133	40357	+	carbohydrate binding domain-containing protein	MSEFEGKSGKWAWEIQKEQQAKVEELQKRLDGALKETQYALQYVEEDMRGNHEFLQMAMIRTLKAIEQVLKGGA*
phageDNA_00055	40357	40758	+	DUF559 domain-containing protein	MSSVSIAEYRKLFPIKKNKKRRSAKQVARQPSVGEVVLATHLRACKIGFEQEYKFHPERKWRADFLIKGSKILIEVEGGIWSGGRHTRGKGYLGDMEKYNSAAMMGFTVLRFSTEQVKSGMALKQIELLIKGK*
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phageDNA_00058	42460	42894	+	hypothetical protein	MDSTEYFWLTRKKEPKTKPKSRPLPKAKQKYLEAEATLKEELEDLAIGFESKFQPIHTKHWRFDFHIVKLRLLIEIEGGPWSGGRGGKLSNKAWSLNRYDHAEEMGYKIERFHPDSILSGYVINWIKSELARIEDGADQTISTD*
phageDNA_00059	42863	43504	+	hypothetical protein	MEQIRPFPPTDFIDQAEEEEAIRLTPAPDLKKWVVANYLTIGGPIYNPDHDHIAELLHDNDEFLAFAWASSAYKSKQAMVLGQCEKVMFNVGGWRKARQEQQMRDWFGFVPTYLITVDASFCERANDTEFCYLLEHELYHIGVMRDEDGEIVYSDSSGLPKHYLAGHDVEEF IGVVKRYGPSKNVKRLIEVAKNPPFVSNLDISKCCGNCVIN*
phageDNA_00060	43563	44033	+	DUF2280 domain-containing protein	MATLKEPVKIFIVQSLACRDTPQEVAELVKQEFGVDIDRVQVATYDPTKVAGKNLSKKYVELFEKTRDEFDKGLIDIPIANKYYRLKQYQRQLEKTRNVKTALKILEQAAKDIGGQFTNRQEITGKDGGPVQTVNSEIPVPMEDYLKARREVLDEY*
phageDNA_00061	44023	45450	+	Terminase large subunit	MSTDAARDKAIRIEAQEDLYFFTRYMFKERRGYKWMQNWIHHLEICEALMKVYRGEIKRLIINVPPRYSKTEIAVINFMAWCFGKNPDCEFIHISYSAMILAANNAFQIRTLVQEEAYRKVFPELTLRDDSKAKDFWRTSQGGVCYATGTGGTITGFGAGKLRKGFGGCIIIDDPH KAHEASSKTIREGVIDWFQNTLESRTNSPDTPIIVIMQRLHEDDLAGWLLGDRKDGVPVAGGNGEVWEHLCLSAIQEDGSALWPAKHNIQKLRLMEQAAPYVFAGQYRQMPSPPAGGFFKPDNIQVDALPADVVKQVRAWDFGATENEGDFTVGVREALGADGFTYIVDV TRGQLGPDNVNKRLEQTAKIDGKKVSVRLPQDPGQAGKSQASSFVKLLAGYSVIAKPISGDKLTRAQPFAAQVNVGNVRMLKGEWNKDFIDELRHFPNGTHDDQVDAASDAFNELHEGFEAFFADMGFAR*
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phageDNA_00063	46900	48003	+	Minor capsid protein	MATDIKKLFEVLTQHQAYLYRASSKTVNELLALFNDDTSKMLSKLRDLLDELNESEKVALAGGKYTTSNLREIRDLIAQWFASVNLALPEAFAVSATALAVYEANYVAKLYGAKINKPDGEKLFLSAKKVPLAGGALVDDLLSRIAESARQKVEYAIRDGINSGKTNQEIVQRIRG TKRLNYEDGILNGTKTDIERTVRTVRSHVANQAYLNSFNQIGFEYVRFVSVLDGRTSKLCASLDGSVWEINDPAKRVPPLHPNCRSILVPVEKDGQLVGERPFVMDERRVKDIPKEERSQLIGQLDANTTFKEFFKKTDDFFQREWLGPKRFKLYKDGKFDFDKFFDPEGRFY SLDDLRKLDEKAFKKLGL*
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phageDNA_00065	48539	48781	+	hypothetical protein	MSESKVRHLVLKRVSDKSSHLALCDEETGIPLAGLTAVKMNCSVFEGPATITATFDVGGPQGIRLVGDEPRQKVWSAKET*
phageDNA_00066	48999	49190	+	Occludin homology domain	MPSPIIQYFQYEHLPEHLQQVSKPIGDLARQMDEQLPDGPEKSTGLRKLLEAKDAFVRQALSK*
phageDNA_00067	49304	50071	+	Telomere regulation protein Stn1	MKLKTVTIDGKVYAEVDGDKPIYIHDDGKEMPHDAPHSVATIARLNNEAKTHREAKEAAEKALKAFEGIEDPAAAKKALQTIQNLDDKKLVDAGEVEKVKAEAIKAVEEKYAPIVAQRDALEASLHKELIGGGFARSKYIQDNIAVPVDMVQATFGHHFKIEEGKVVAYDPNGEKI YSRVRPGELANVDEALESLVGGYQHKDLILKGGKGTGGGFQGGGKGGAPTGMKRSEMSVSQKADYIKEHGNDAFLKLPN*
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  AUTHORS   Kim,K., Islam,M.M. and Shin,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-JUL-2021) Dept. of Microbiology, Kyungpook National
            University, 680 Gussaboseong ro, Daegu, Daegu 41944, South Korea
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Table S2: Oligonucleotides used in this study

Primers	Oligonucleotide sequence (5'→3')	Use	
Phage1_F	GGTGGTGGGTAGATTAGATG	Confirmation of	Phage region 1
Phage1_R	CATCAAGCTCTTTACGCG		
Phage2_F	GAAACCTTTGGCAGCTTTAC	Confirmation of	Phage region 2
Phage2_R	CCACCACATTCAAGTGTTAG		
Phage3_F	GTAAAATGGCACAAGAATCCC	Confirmation of	Phage region 3
Phage3_R	GCTGGTCTGAGGATTTAGC		