

Molecular and biological characterization of a newly discovered *Kayfunavirus* bacteriophage targeting multidrug-resistant *Escherichia coli* from swine feces
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Supplementary Table S1. Functional genomic annotation of *Escherichia* phage vECPPW10

CDSs	CDS_POSITION	Amino acid sequence	PHASTEST analysis	Results of BLASTp analysis								
			Protein Product	Protein Product	Organism	Score	Total Score	Query Cover	E value	Percent identity	Accession Length	Accession
CDS1	complement(874..2637)	LSKDLVARQALMTARMKADFVFIFVLWKALSLPVPTRCQIDMCKKLAAGDNNRRFILQAFRGI GKSLFTCGFVVWKLWNNPDLKFMIVSASKERADANSIFIKRIIDLMPQLQELKPKQGQRDAVIS FDVGPAPKPDHSPSVKSVGITGQLTGSRADILIADDVEVPNNSATQAARDRLSELVKFEEDAILKPG GTTIYLGTPOQNEIMTLRYLELEGRGYTTITTPAARYPRDRKDQWSYGDRLAPMLQAELEEDPEAFYVW RPTDEVRFDDIDKEREISYGYKAGFALQFMNLNPNLSDAEKYPLKRLDLIVADLDPASSPMVYVQ WLPNPQNKRREDVPYVGLMGDSYHTYQTVGSAFSSYTQKILVIDPSGRGKDETGAVYVLQNLNG YIFAMEVGGMRGGYEDSTLEALAKIGRKWKVNEYVIEGNFGDGMYLELFKPVAARIHPAAVTE VKSKGQKELRICDVLEPIMGSHRLIVNAAAIQDYQASADKDGVRNPISLFLYQMTRISRERGA LAHDDRLDALAIGVQFFVESMAKDANKGEREVTEEWLEEQMENPRKGFESIHTFEWDNGVRVVT HDTDDDELGLGSYVTFH	PHAGE_Escher_vB_EcoP_F_NC_047808: hypothetical protein; PP_00034: phage; -	terminase large subunit [Escherichia phage 6925]	Escherichia phage 6925	1211	1211	100%	0.00E+00	99.15%	587	UT175182.1
CDS2	complement(2634..3083)	MLEFLKRAAPWLLAAVMFAGGYHTANNKWEAKVNAEYTSNLKASEDTRLAVQAEVNKSKVR FQDEMSLEGSTDRIIADLQSDNKRILRVKPTSGTTQSDGRCVIASIELDERDAKRLIAIGVKG DKWIKALQDVTVALQQDKEATH	PHAGE_Escher_Vec13_NC_048023: endopeptidase Rz; PP_00035; phage; -	Rz-like spanin [Escherichia phage PSK1]	Escherichia phage PSK1	300	300	100%	2.00E-102	97.99%	149	XAO35749.1
CDS3	complement(3186..3449)	MTQMDLEKFLMLDTERARLMLQDLRDSKRSQOLYNAIEKLLARHNFVLSKVSVEKTLAD MEALNAEYDKVLSATENDNTGGVQ	PHAGE_Escher_ST31_NC_047829: DNA packaging protein, small subunit; PP_0003	terminase small subunit [Escherichia phage ElsieAttenhofer_Bas105]	Escherichia phage ElsieAttenhofer_Bas105	169	169	97%	2.00E-52	100.00%	84	XPK40850.1
CDS4	complement(3446..3640)	MIELDFKNEVLKASPIVGTAAADGASRFFFGLTNLNEWFYVAAIAYTVVQIGVLVYTIKGGGKT phage; -	PHAGE_Escher_Vec13_NC_048023: type II holin; PP_00037; phage; -	class II holin [Escherichia phage Mt1B1_P3]	Escherichia phage Mt1B1_P3	124	124	100%	2.00E-35	98.46%	65	QNJ49131.1
CDS5	complement(3800..5995)	MSTITQFSGNTHYRIEFDYLARTFVVVTLVNSSNPMTNMRVLVGRDYYRFNPTMIEMLVDSQG FDIVRIHQRTGTDLVDFRNGSVLTASDLTNSLQAIHIAEEGRDQTVDLAKEYADAAGSSAGN AKDSEDEARRIAESIKASGKIGYITRRSEKGFNITTWNEVLLWEEDSDYRWGDTLPKNVPTGS TPESSGGIGVGAWVSVGDASLRHLASKGLYSIGELDSVSGFYGLYGRDTSRVKLKSWSDDYI LVTGKGPTTGGEFIFVTPMPKTSHHNGGTIISPSVYSSIAFLAGTGESDPSGSGCWWRDFDGPIN ALWFGAVGDGVTDNSAQLAAFRNVAVAQTDKRRGYIPAGIYAYATGPNFAVKGVIHFGDGK NNTILKSTSGCAFKFDGNGVYDVYVENIGIEGHANTQHILYVENSSHILMNRNLREAS PTTGKVMNSLLWTVASVFENITYSINEQPVTNKPYVGLVLTGPSRNLKSTANLFINIMEGVGGT GIRLNDTDLNTFTIGTSEANGTYGITSSGSRQNKVFVGMGFEANGTADLLDGGQDTVLENCYTG KSIIVLLSSRRARIVGGLHERIEMQSGCSAANIENLTVNYFDTGSGGIVDSGTNSSFRNVFDLDA NAYVYPTKLROPIVTASPTFTYNTTGEYQNVLTGTGTVTSIQFNRGGSQTVTGMTSGFVMLAP GDSLIVSYSVAPTMSMVMGMNNIV	PHAGE_Escher_LM33_P1_NC_031937: Phage tail fibers; PP_00038: phage; -	tail protein [Escherichia phage Baskent_phicol_1]	Escherichia phage Baskent_phicol_1	437	437	31%	4.00E-139	91.67%	718	XCD08726.1
CDS6	complement(6062..10450)	MATRGIRNNLGNLRVSKDQWEGAVDGDGAFVIFDPSGESVRLAKNLQSYGRQGYDSIEKH NRWAPPNENDTQSYINSVVAATGIPATQSLDSDPDTLSLQAIGYHETGSRYDPEVYRKGVA RALNGISPKTPPVSAANVFDAITGLKAKPKVALGENLPTAAGLNIEGQSPAPNESFGEFMYKST GETMQEREDRSTWFGGAATAEAEVKNMSMVGAIRAGQTEDSLDVIGDFNPTRWNNHKWSRE ELDQIRNAGVLPQYYGVITGSGPQNLTLEINLALENQKLDQEKAKAGVGAQLAAGVIGAGVDP LTVYPAGQVKGKGLVKNMFTVAASQSGALAGVSEMARTSVAGGDIAHVAEAILGGALFGGG MTAIAADGLRALGQNTNEFAGPATRLAEARETARNTDQDLSRLPIQDGEQTFSHQGYKFAIDVP NEPGSVRLDEGSLIGENPLNPKTRQYFDEVIEPERAAAGVNLGGLTEGLKLLRSENPIERGAA DLVRSPTGMQSGASGKIGTTASDVFERLRAVDHFRYNDIDDAVTEALKDPYFQTAFWRDNSAL REDVYKRYVALAIEDSGSNLSELTPEGLKYVYDMLKNQFDKREMMENPAMFGRDITDAKSIFFG SRFKGTYVPVVYSSQMKQLYNELGSPALQEAIKSWLTSYASRPEVKARVDEMLAEQLRAS QPAAGKTGTASNHRSSVEAARDQMKLDDAATAQIDKVAELKDVLNTAEKRVADREKLLQN SKDRLDSHEAKLKELEKLAAPNSKTIPTVKIESRQMIEQKSHVRIINTERLDYMKGQADKVR DRITKATTEAESAFAAAKQKSSVDGQDITSGETTSGNSQAAPVETMDMVEKYANDKAYGI SHITQFERSSVMEENLGLVLENNMLEARNLFDNMETLPMKQFQSVNSLREWDMDKVPFA YNNRINGDIAIMAGCTGKTIKEMKDLVETMMNKAAGDDGKLKEVSTRLDRTLKILTRARRDGA DDAAAFATVMRTMDLSFFAKNAYMGVQNLTEIGGMLARGNVRAMLHGVPMFRDLAFRNKK VGASEIKDLHNVLFGKELDDSRPSKQDVIDRLRSYDLGRGAATALGTAKYYTGELAVRSPLT KVNLNGTNYLLDAGRQGLSDIVEHSLTGSKRKFDDRWLKTAGISNEQWNGIKSLIRESVTRGP DGKYTIKDKKAFSQDPRAMDLWRMGDTIADETLLRPYKLSNMDAKAYGPIAKTVLQFKNFVI KSINGRTMRTFYNAKNNRAIDAAALSTVMSMGLAGIYYMAQAHVKAAYAMQDGRDRDYLKQ ALDPTMIGYASLSRSSHLGGPLGVANILGGIAGYEDTKMLRSSILPRSPTEKPERAIAYGAATSDP VMNVNGLFLEQVAPFGYAAANVGASAYNLAGYLYKADTRVNERDYMTGMYNLTRELVPNDPIT QKLLLGTFEEQHIIKD	PHAGE_Escher_NC_A_NC_048163: protein inside capsid D; PP_00039: phage; -	internal virion protein with endolysin domain [Escherichia phage ST31]	Escherichia phage ST31	2909	2909	100%	0.00E+00	96.37%	1462	YP_009790653.1
CDS7	complement(10455..12737)	MASNIESALANRTMGRGRAPGKTIAVNYYQAASVQAPTGDSGLARALTNFVESGTGLYKQFKD EEKTRADERSNEIIRKLTPOQRREAIQNGTLYQDDPYAMEALRVKTRGNAFAVDDENVKIQ NGEFTRTQDMEEYRHQRLQDAAKSYAEEAGINPTDEFFQGFNDNITDRNIAIYGSFNKYFSKQ SEETAMLNTRIEMNSFLNDGLMRSPESGKTFMAYLRDGLTTAAIPSDQRAREVITQTVRDAIQ KSGGSNFLQVQGERITLNGVDATIEEIVGPDVFNAAYVEAQGTIEKLVAKYQEDLALGVQSAI LQDDPTIGLAQIQKLEQNNLLQPGEEHTPQRQMLNAAEASLLEAVKRKSAEQAKENTKLIQTQN KQLVDQVYQRLACGDNSTNYEDLPVSDATGEFKSRSDMNNYASAKLQIQDQMDPIEAAKDA QKVALLRADTNNGPNRANFOTLTQDAAGGEWAQAVIRGQYDDPKMKRFESLRRAYTQDPSFA ALYPDQAQLFSTFDQMDKMGDLDPQTMIEADKQAASQSRMRMESDKAWQELKNDNRNKKDL RIPTSLDASARKVWDSWYYRTGNADDTAQQTQRWLNENTVTFQSEGS DGKSGIMVSKHQILV GDNLESWQVGRDIIDTARKQLIKANPWVNSQLSVFEQNGSIFLQDATGTIRIYDKELVGKLY REQQKEQDAAAYQAERDANKRARIVWTKAAGDKRRADREDNIEKRGGMYNDVSLGIANV LIGKE	PHAGE_Enterov_KIF_NC_007456: internal virion protein C; PP_00040: phage; -	internal virion protein [Escherichia phage vB_EcoP-101120B1-2]	Escherichia phage vB_EcoP-101120B1-2	1529	1529	100%	0.00E+00	98.29%	760	QZI79807.1
CDS8	complement(12749..13303)	MSVAGATMSASQQAEGAIDAQNRQAQEMVKQMNYSDANLKMQRDLKEQQMAELTET TLNGVRNQGMVRAAAVESGLEGNSMDRIERQVEGDTYKVERGITESYNRDYAAIFGNRIANIE NTKSAIRGGRIIKTSPLAHLNVSASAGMQGYAAGKSISGASSSGGAAPISAAKGTPTGHS	PHAGE_Citrob_SH3_NC_031123: internal virion protein B; PP_00041: phage; -	internal (core) protein [Escherichia phage p091]	Escherichia phage p091	363	363	100%	5.00E-126	97.28%	187	WMM35653.1
CDS9	complement(13321..13791)	MYIRKATPEVDHYHFLWLSADDVNECKANAYGSTVGLSERLLKHLSPSSVLTNGVGEVFAVG GNGQGDNVWFLTSLGNLNRKPREKREFIKRISEYRDLMLDQYGTWNYVWSGKNKSHIKFLKLLG AKFHDDWTVSPVTGERFQLFTISKEDVCVNP	PHAGE_Escher_vB_EcoP_F_NC_047808: internal virion protein A; PP_00042: pha	internal virion protein [Escherichia phage ZG49]	Escherichia phage ZG49	224	224	69%	2.00E-72	99.07%	134	YP_009787290.1

CDS10	complement(1368..16225)	MPLTQSIKLNKGGISQQPDLRFSDDQGESQVNCWSSSEDLGQKRPPTVFKRRLLDIVGSNPKFIH LINRDEQEQY YIVFNGSNQIVVDLSGNQYVSGAVDY VKSSNPRDDIRVVTYADYTFVVNRRKV VVKGGSEKSHSGYNRKARALINLRGGQYGRTLKVINGGVKVSHKLPAGNDAENDPPKVD QAQGAALRDLVAAAYPITFTDLGSGFLITLTPSGTNNINSVETEDGYANQLISPLDVTQTSKSLPL AAPNGYIKIQGQENSSADEYVYMYDSNTKTKWETVPEPVVGTGFDNTMPHALVROSDGSEF KTLDWSKRGAGNDNTNPMPSYVDATINDVFFYRNRLGFLSGENVMSSRSASYFAFPKSVATLS DDDDPIDVAVSHPRISILKYAVPFSQILLWSDEVQFMVSTSGVLTAKSQILDVGSEFALGDNRAP FAVGRSVFFSAPRGFSITSIKRYFAVADVSVDKADDDTTGHVLSYIPNGVFDIQGTGTYICVN STGAYNRIYIYKFLFKDGVQLQASWSHWEFPKDDKLASASIGSTMFIYRQHGQGV DIEHLKFIK EATDLPEPYRLHVDISKVSMVIPIGSYNADTYKTTVDIGAA YGGNAPSPGRYYLIDSQGAYVDL GDLTISISTVILNGDWSGRTVFIGRSY LMSYKFSRLIKIEDDSGTQSEDGRLQLRRAWINYKDT GALRLJVRNGERFVNTFNGYTLGQQTIGTNGDGGYRFAMNGNALTSLTLES DYPTPVSVIG CGWEASYAKKARSV	PHAGE_Enterok1F_NC_007456: tail tube; PP_00043; phage; -	non-contractile tail tubular protein [Escherichia phage vB_EcoP-22664BS1]	Escherichia phage vB_EcoP-22664BS1	1585	1585	100%	0	98.22%	785	QZ178486.1
CDS11	complement(16235..16462)	MASHNLKIHRRHFQIQLGLKTAELRLNDRDFKVGDWLILNEWNDNGYTGQQVARKVHVHSDV GDIAEGYVIMSMI	PHAGE_Escher_ST31_NC_047829: hypothetical protein; PP_00044; phage; -	RNA-binding protein [Escherichia phage EcoDS1]	Escherichia phage EcoDS1	154	154	100%	1.00E-46	96%	75	YP_002003774.1
CDS12	complement(16462..17028)	MAQYIPLNANDDLDAINDMLAAIGEPAVLQLDEGNADISNAQRILHRVNRQVQAKGWNFNINE AAILTPDKONRIRFLPSYLRVMTAGATSYYSNMGGYLDLSTQSTFTDPTITVELVEMKPFSE MPVYFRDVIYTKASREFNAKFFGSEPELILREQEALYQQVMEYEMDTGRYNNMMSDIGRD	PHAGE_Escher_ZG49_NC_047777: tail tubular protein A; PP_00045; phage; -	tail tubular protein [Escherichia phage Baskent_phicoli_1]	Escherichia phage Baskent_phicoli_1	388	388	100%	7.00E-136	98.94%	188	XCD08719.1
CDS13	complement(17353..18402)	MANVPGQKIGTDGQKGSSSDALALFLKFVAGEVLTAFTRRSVTADKHIVRTIQNGKSAQFPV MGRITSGVYLAPGERLSDRRKGIKHTKVITIDGLLTADVMIFDIEDAMNHYDVAGEYSNQLGE ALAIADGVALAEAMAILCNLPSASNENIAGLTASVLEVKKADLNTPAKLGEAIIIGQLTIARAK LTANYVPAGDRIFYTTPDNYSAILAALMPNAAANYAALIDPETGNIRNVMGFVVVEVPHILTQGG AGETKAGADGITIASGQKHAFPA TAGGDTKV ALDNNVGLFSHRSASVGTKLRLDALERDRDVID AQGDILVGYAMGHGGLRPEAAGALVFTAAAGG	PHAGE_Citrob_SH3_NC_031123: major capsid protein; PP_00046; phage; -	major capsid protein [Escherichia phage pO91]	Escherichia phage pO91	685	685	99%	0.00E+00	97.69%	347	WMM35647.1
CDS14	complement(18350..19489)	VNAPWAVTDWQVVVFPINDLKENDLMSQSVYAEFGVSSNAITGSVEDLNEHQKSMLEQDVAV RGGDDAITFKLEANEAEA TEEDGNVETEEDGESDDEESTDGEQPEFIELGDAPKDLTESVT ALDENEAAFDMMVSSA VEA GKVTADAITAIEAYAKDGLKSDASAKLQEAQGYTKRFVDSFV RGQEALAQY AAGV VRYAGGAEQFNRLIYHLESDNPSTREALEAIVRKDIAITKALLNLAGKT LGKAVGVYKPKRTITITQAKPVVAPKSPKTEAFSSKADMIKAMSDPRYLRDAKYTMEVRAKVAA SSL	PHAGE_Escher_ST31_NC_047829: capsid and scaffold protein; PP_00047; phage; -	capsid assembly protein [Escherichia phage vB_EcoA_ASO2B]	Escherichia phage vB_EcoA_ASO2B	577	577	92%	0.00E+00	97.62%	294	UAW58420.1
CDS15	complement(19523..21091)	MAEREGFAAEGAKAVYDRLNKGRQPYETRAQNCAAVTIPSLPKESDNSSTEYVTPWQAVGA RCLNNLAAKIMLALFQSPWMRLTVSEYAKTISQDSEAAARYDEGLAMVIEYTLMA YMETNS FRVPLFEALKQIVSNCNLLYIPPEIQGYTSPMRMYRLYSYVYQORDAFGNVLQVITLKDVAESA LPEDVKSQUNAEDYEPDTELEVYTHIRQDDDEYLR YEEVEGIEVAGTEGSPYLTACPYIPVPMRV LDGEDYGRSYCEEYLGDLNSLETITAITKMAKVASKVVGVLVNPNGITQPRRLNKAATGEFVAG RVEDINFLQTLTKGQDFTIAKSVADAIQRLGWAFLNSAVQRNAERVTAEERYVAGELEATLG GVYSVQSQELQLPIVRVLMNQLQSA GMIPELPKEAVEPTVSTGLEALGRGQDLEKLTQAVNMM TGLQPLAQDPDINLPTLKLRLNLALGIDTAGLLLTQDEKIQRMAEQSAQGA VVNGASAAAGANM GAAVGGQAGEDMAQA	PHAGE_Escher_YZ1_NC_047927: head to tail connector; PP_00048; phage; -	head-tail adaptor [Escherichia phage ST31]	Escherichia phage ST31	1055	1055	100%	0.00E+00	99%	522	YP_009790644.1
CDS16	complement(21102..21350)	VGKSISAKFKVVKSTLGTVGLGADDA PKVVEAQTPAAPVEVPNDKVEDVIETTASDEKKV RSGKRSRL	PHAGE_Escher_ST31_NC_047829: virion assembly protein; PP_00001; phage; -	host range and adsorption protein [Escherichia phage ST31]	Escherichia phage ST31	131	131	100%	1.00E-45	97.14%	82	YP_009790642.1
CDS17	complement(21343..21765)	MLPYLNSREGRHMCACRLWEDGQSNFKSFEDFKVHTYRMADEFDGEETYTYDVGQPVAYLY MLATTSWHRPTPLGLDSIVAIRDSQSSRKVLETVRHIVNEECKRWGLGWYSRIKHVSGSVDIVT TKCVSTNKEINRG	PHAGE_Citrob_SH3_NC_031123: hypothetical protein; PP_00002; phage; -	hypothetical protein 22664BS1_047 [Escherichia phage vB_EcoP-22664BS1]	Escherichia phage vB_EcoP-22664BS1	291	291	100%	7.00E-99	97%	140	QZ178477.1
CDS18	complement(21770..21994)	MCFSPKISTPKPSVQAPAPLSEEVASVDIGAESDVTNETIKGDKLKVKESAPKDKSSVSRA MRASGVNMG	PHAGE_Escher_ST31_NC_047829: DUF5476 family protein; PP_00003; phage; -	DUF5476 family protein [Escherichia phage BUCT788]	Escherichia phage BUCT788	145	145	100%	2.00E-43	98.65%	74	XTB81123.1
CDS19	complement(22009..22281)	MAINAIENVVKQLQEERLDVPNISQAISQIHLVLFNASYAEKMGVISLLKQQGYSDAIFAGFIG LQYCSDTLSDAISAMRRELKDTVQFD	PHAGE_Escher_YZ1_NC_047927: DUF2717 domain-containing protein; PP_00004; p	hypothetical protein AHPLHJF_00014 [Escherichia phage SR04]	Escherichia phage SR04	185	185	100%	2.00E-58	100.00%	90	WLW38337.1
CDS20	complement(22492..23361)	MTSNKKIALVLDGDYLVFSSMAAAEDETWDGDDIWTICDHAKARRILENTIAEIVKKRKAWK DAKIVMCFITDANWRKDVLPYKANRKGSRKPVGYKKFAEYMA DPFNSFLRPTLEGDDC MGICIRPQIVGCDHIALVLSQCDKGTIPNCIEFWLTIGELSHITAEADYWHMEQTIKGDITDG YGGIPGMGEDITRAFLDEPYVYVQESRELKTGRNKGOIKTEWKVYPKREDMTLWDCMVTLLAA KAGMTEEELLVQAQVARICRASDYDPKSKVILWTPSV	PHAGE_Escher_ZG49_NC_047777: exodeoxyribonuclease; PP_00005; phage; -	exonuclease [Escherichia phage 216EcoI046PP]	Escherichia phage 216EcoI046PP	593	593	100%	0	98.27%	289	WWT42867.1
CDS21	complement(23689..23973)	MAITKRIRVSFDLKMVNSKEETMCRQLAEVTKAYAEGEKLDGLQFAMVKAAIESGPESAIEI AVKKYVKKELMYAFDDHQFGVSNLRFVQ	PHAGE_Cronob_Dev2_NC_023558: hypothetical protein; PP_00006; phage; -	hypothetical protein [Escherichia phage KM02]	Escherichia phage KM02	167	167	100%	3.00E-51	87.23%	94	XFA12263.1
CDS22	complement(23973..24146)	MGEYRKDELQIACTQELAIERTVEIAQLAMRKVGEFYNFKCVLDTGEGKIGPTWKECH	PHAGE_Escher_K1F_NC_007636: gp5.4 protein; PP_00007; phage; -	DNA polymerase [Escherichia phage Ro451w]	Escherichia phage Ro451w	120	120	100%	4.00E-34	100.00%	57	YP_009818275.1
CDS23	complement(24146..24646)	MRGKKLILEATEGCIPTSHKLNQDGYFRKRTNGVLEMVYHRTLWTKANGPIEGFEVDHIKCHN RACCNVEIHLVQLDRDLSHVKTNQERYAARKLEARDYVWETGCTGKLAIEVNFVSFAACGW IESGRRRDY PKGVGPVWRPRNPKRQTYTSTKDDIVRIHQ	PHAGE_Escher_K1F_NC_007636: gp5.3 protein; PP_00008; phage; -	HNH endonuclease [Escherichia phage K1F]	Escherichia phage K1F	265	265	77%	2.00E-88	97.66%	131	YP_338109.1
CDS24	complement(24656..24775)	MYTAGKETSRTWHGCINIMVHIKSGELGELLMGQYRAKP	hypothetical; PP_00009; -	hypothetical protein (Escherichia phage vB_EcoP_PPW10)								
CDS25	complement(24726..26744)	MFLKSIWCSDIETNGLLDTSYQHFCHGLVLAESNETIKYGVAPMVGI VGGFKFYVHKVEEIAA SPDGMVLVHNGINVDYPAIDKLKRLYFGKRFNFKHKMIDTLVLGRLMYPNIKFSMDGAVGA GRLPPKMMGROSLEAWGYRLGEMKGEYKHIDYVAKCKAEGIEYKAGDEWLPSQEMLDYNNV QDQVVTTLALFKFLTKDY YFQSEQAFDQIYALRLIHDAAWTCAMERNYGMNTEMVIEGLY RELTVKRAELLDLKRLTSGSPHAPKAGKGEFKFIPRTPKDLPKYPRVVPKVGSVFKCKPKKA QRLGLEPCEFSRDMTEGAPITPTIYVEFNPGSGDHLAKVLMERGWEPVDFDTDTGKPVVDDEL FHVKLPAEAAQACVELREYLVVQKRIGQAAEGKNAWIKLVGPDGRMHGNSPCGAVTGRAT HSSPNMAQVPANGAPYGETCGRGAFAAWNKKDGNPDPIQVGV DASGLELRCCLGNRAAPFD GGDYAKTVVEGDHIVANAVNAGLAPNVPRDKSNHHDHAFRNNAKTFIYFLY GAGA AKIGLI VGGGKKEGSALMKKFIEGTPAIKDLREAVSSTLISDSKVVVDGENIVKWKRRWLRLGDRRIHIR SPHSALNALQGDGAVVCKHWIVETERMLEEAGYVHGWE GDFAYMAWVH	PHAGE_Escher_vB_EcoP_F_NC_047808: thermostable DNA polymerase I; PP_00010;	hypothetical protein AHPLHJF_00021 [Escherichia phage SR04]	Escherichia phage SR04	1379	1379	100%	0	98.66%	723	WLW38344.1

CDS26	complement(26984..28684)	MSYDQDDSESVFLYHTQPCDGGSSDANGVYSDGHQFCFACDPSVAWKKGDMELTEGYTPSG GRKQVSNLLITGENAGRVYPLPRLSLSMEICKKYSYVWGNMGGMKVQVADYVDRSGTKVGG QKVRDAEKNFTAIGSVKSDMLFGSQLWNGGKKIVITEGIDALSVAQVQDGKYPVVSPLGAK SAKKAMAAANLEYLDQFEIHLFDMDEPGRQAIEDAAPVLPAGRVKVAFIGYKDNAALQA KDFKATDADWNAKPVPAQVYSAASLGDRTREAMLEAETGLMSSCTTLNAMTLGARAGEL DMVTSGSGMGKSTVRLQLLEWVGSGGKRVGMALEAAVEETVQDLGLDNNVRLRQSKELKQ AILEDGRFDEWYDKLFGDDKFIHLYDSFAESEEDTLFASKL5MV DGLDCD VILLDHISIV VSGME DNSDERKTIDIRMLTKKFAKTKGVVVVICHILKNPEKGKSHHEGRPV5ITDLRSGS GALLRQ LSD TIALERNQQGDTPNIVQLRLKCRFTGETGVAGHLEYNKTTGWLEPIHFTSSGSEEDSGSWEDND F	PHAGE_Escher_K1F_NC_007636: gp4A protein; PP_00011; phage; -	toprim domain-containing protein [Escherichia phage K1F]	Escherichia phage K1F	1162	1162	100%	0.00E+00	98.76%	566	YP_424934.1
CDS27	complement(28753..28968)	MIKLIELGLRVLVVRGYRRAAVLERKVEKKTADGAADAALADKLTIASLEAGMKARQADTKA DQLSKFFK	PHAGE_Citrob_SH3_NC_031123: hypothetical protein; PP_00012; phage; -	hypothetical protein UFJFEcSw4_00022 [Escherichia phage UFJF_EcSw4]	Escherichia phage UFJF_EcSw4	133	133	100%	2.00E-38	98.57%	71	XJP09158.1
CDS28	complement(28993..29463)	VEIIMGSKVQFMPRK2TD AIFVHCSATKPEMDIGVDITRMWHKQQGWLDAGYHFIIKRDRGTVE EGRPVNVVGSHVKDWNKSVGVCLVGGINDKGQFEANFTPAQMNSLRSKLADKLVLYPQAEI KAHHIDVAPKACPSFDLQRWLSTNELVTSDRG	PHAGE_Escher_ZG49_NC_047777: N-acetyl-muramoyl-L-alanine amidase; PP_00013;	amidase [Escherichia phage ZG49]	Escherichia phage ZG49	306	306	97%	1.00E-104	95%	152	YP_009787273.1
CDS29	complement(29496..29825)	MESDCIEWTNSRNKNGYGRKFRGQSMGAHRAAWIETNGAIPGGLVVRHKCDNRACVNIHIL ELGTQEENMMDCSVCRITFNKLKLTEDVDRDITSETLKFMAEKYSVS	PHAGE_Enterо_13a_NC_011045: gp7.7; PP_00014; phage; -	hypothetical protein [Escherichia phage ZH4]	Escherichia phage ZH4	136	136	60%	5.00E-39	95.38%	80	ULF48599.1
CDS30	complement(29815..30285)	MTRRAITVDLSLTSVCCGFEEOQEVFVRHICKTTNPSDGLWDISRDKGCWITAMYGKRKLF IDAGKRTGEKKTQVLPASSVPVTVKREVLTDIKIGVQTFIVHKGKPEDEVYVKISKSHVFNHKR LQMHTIDSQRQSHLNLNVVEIVYNGK	PHAGE_Escher_K1F_NC_007636: gp3.2 protein; PP_00015; phage; -	hypothetical protein [Escherichia phage Mt1B1_P3]	Escherichia phage Mt1B1_P3	141	141	54%	3.00E-39	92.86%	156	QNJ49156.1
CDS31	complement(30285..30737)	MATRSMSRSGH5VGIYRSGLEAKNOQEWLEKNGVKA EYEMYKIAIYTIPOS LHTYCPDFVLPNGIIV ETKGIFAVEDRKKHLLEKQHPELDRIRFVSSRSKLYKGSPTTYGAWCEKNGFYADKFIPIV E LREATVHLSGLIPKKGVK	PHAGE_Escher_PE3_1_NC_024379: endonuclease; PP_00016; phage; -	endonuclease I [Escherichia phage HC13]	Escherichia phage HC13	298	298	100%	2.00E-101	93%	151	URY99501.1
CDS32	complement(30719..31168)	MATVIESIKORLIVVSGSWCLFTGCVNNKGYGQIRHNGKTMLAHRVA YELITGEEPNGLVHTTC DTPLCNPEHITVGTOLDNLDQMRNKG RVNPHVPGCKGMSKLTDTKVKEIRSSSLTQRQL ATYGVSGPTQIGKILRTRWHVA	PHAGE_Yersin_YpsP_G_NC_047940: host range protein; PP_00017; phages; -	HNH homing endonuclease [Escherichia phage HC13]	Escherichia phage HC13	299	299	99%	7.00E-102	96.62%	149	URY99500.1
CDS33	complement(31168..31866)	MAKEQLKTTTTPVAGIVPYA WLNKADTKFNERGEHKVNLTFDLSNPVKRMIDV LQKHDDA YAKALADHEKNPPQVQRGKKPIEPREGDMPWIENGDGTVMKFKCFASYLKDGKSEPIVIRFY DTDAKLIRDVPNIGAGSKLKVFKFVLPFKWNAATGASVQLQLEKCLLVLEKKEWKGDGAGGDDG GWDGDEDLDTGYKASTDGGDDGDDGDDGSEGGDDSSSGGDYDF	PHAGE_Escher_ZG49_NC_047777: ssDNA-binding protein; PP_00018; phage; -	single-stranded DNA-binding protein [Escherichia phage vB_EcoP-PM129]	Escherichia phage vB_EcoP-PM129	469	469	100%	1.00E-166	99.57%	232	QZJ84325.1
CDS34	complement(31925..32083)	MTDVEKKYIVIELEGRVQSFEVVPYAKSLEEA TLKSQEYEDAGFVVGRI RPET	PHAGE_Escher_ZG49_NC_047777: host RNA polymerase inhibitor; PP_00019; phag	RNA polymerase inhibitor [Escherichia phage ZG49]	Escherichia phage ZG49	105	105	100%	7.00E-28	100.00%	58	YP_009787269.1
CDS35	complement(32171..32398)	MTHEELKAVGVKRRALSFYRSYKALRKGMLFASLGHSEYYDYLDPFAYMKTPSMIIRVEEYD HISDDCMVNRYA	PHAGE_Escher_Vec13_NC_048023: hypothetical protein; PP_00020; phages; -	hypothetical protein HO177_gp16 [Escherichia phage Vec13]	Escherichia phage Vec13	152	152	100%	7.00E-46	97.33%	75	YP_009807339.1
CDS36	complement(32388..32714)	MSHYESKTCYERYDAYRCGVSTPHPVAVADDGVRKPSHYQVDFGVEIEIARSMVTSEFRFG CMGNVLKYRLRAGKKSILATMEKDMAKAEFYGELYEKHKDKCYDA	PHAGE_Escher_Vec13_NC_048023: hypothetical protein; PP_00021; phage; -	nucleotide kinase [Escherichia phage Vec13]	Escherichia phage Vec13	159	159	72%	8.00E-48	99%	111	YP_009807338.1
CDS37	complement(32714..32968)	MSKNLMFNRYSSTFHLSNPPFACIKRNEKLGYFGKAIKLSPTVFALITPSKAEARQKRETNFV YYTKWPRVRLFVEVKEVF	PHAGE_Escher_K1F_NC_007636: gp1.6 protein; PP_00022; phage; -	hypothetical protein [Escherichia phage BUCT788]	Escherichia phage BUCT788	170	170	100%	8.00E-53	96.43%	86	XTB81154.1
CDS38	complement(33075..33305)	VYDHNRPDSNVNRIENLRCTQAVNL TNVPTSRHCQSGEKYVQYQKSTGRWQLRIKRSYGTFD TIAEAAVLRDSL	PHAGE_Escher_PE3_1_NC_024379: hypothetical protein; PP_00023; phage; -	HNH endonuclease [Escherichia phage PH1061]	Escherichia phage PH1061	160	160	100%	2.00E-48	100%	126	WKV16783.1
CDS39	complement(33466..34515)	MTTITKTNPHRAVDYSIESGVKKALEAAGSLEAEVKYDGVRLNIPVPIGTETQWLSRESKELPAL SHLSNPASROHIEGVYTRADDWVSGKLMIDGEGVNVGVGDENSGGLIRYKVRDHI KNHEFAVGGTDPDKSRKLEFNILKPEHKKVYVGIIDNVLDQKAEQPHSVTRLKA EA AIVPLIQ KYFPEDWVLSSEHTVFSLDELTDLYEKKREEGHEGLVKDPLGRWKRGGKSGMKMKPSEEA DGHVVRPIWGTGLTNEGLVIGDFVLENGMEVSATNISRALMSFTENVKSDPDYKGWAC QITYMEETPSGLLRHPSDFDQWRGTEDDPTVKI	PHAGE_Escher_ZG49_NC_047777: DNA ligase; PP_00024; phage; -	DNA ligase [Escherichia phage SR04]	Escherichia phage SR04	597	597	100%	0.00E+00	86%	351	WLW38357.1
CDS40	complement(34493..34777)	MGRLSYGNLNAKCAACNLRYQLDAVISQEFDPA5RQECMKLRVEDRAGNIFALETFAHIDE DVLNTATDFLNGLADQLDTRWNHNDNDYQN	PHAGE_Escher_Ro45w_NC_048136: hypothetical protein; PP_00025; phage; -	dGTPase inhibitor; target for F exclusion [Escherichia phage Ro45w]	Escherichia phage Ro45w	167	167	89%	1.00E-51	95%	87	YP_009818261.1
CDS41	complement(34782..35000)	MINPNVNVYWRFNHMYQNTINFERIRERQKTEYIYIPKGRKLNKTRGGGVKGAFNR AEGKDSL VNREKYLVG A	PHAGE_Enterо_EcpYZU01_NC_048135: hypothetical protein; PP_00026; phage; -	hypothetical protein HOS81_gp08 [Escherichia phage YZ1]	Escherichia phage YZ1	113	113	82%	1.00E-30	94.92%	59	YP_009798530.1
CDS42	complement(35132..35332)	MQFAHRVSNVSGGNKVTVTTVAGKGLVKVTMVPTGTAKAKCISQELIQVIQVSHKEALRE EATK	PHAGE_Escher_Vec13_NC_048023: hypothetical protein; PP_00035; phage; -	MAG; hypothetical protein [Enterobacter phage ENC31]	Enterobacter phage ENC31	129	129	100%	1.00E-45	98.48%	66	UIW11706.1
CDS43	complement(35349..38030)	MSVISIDKIDFSDVSN5AIEPFLNLANHYGQDLAVKQLQLEHEAYTEGERRFIKNIERQTERGELA DNQVAKPLMOTLVPTIAKAFREWHIEGPDGKSSTSRPSVAFMLSDTEKAVKDRSLISAESAAIL ILKVILSKLVKPEGPIPTMASAIGRTLEDIRGRIRDKEQEHFKAIAENLNKRAGSVYKKAYM QAVETSMLEQOQLEDAGWTGWSPTAEVHVGIKMLEIVIQSTQLVELKRYGAGNAADVEMVHL SDFWVKKMAQRGFSLAGIAPVYQPCVVPKPWTGVVGGYVAKGRRLPLRLIRLGSKSAVARY EDVYMPEVYDAVNIIQNTPWKVNKKVLDVVNMVEKLNNTPIDDIPQMEPLKPEDYVGETEEDL KA WKKAAGIYRREKARQSRRLSLSFIVNQANKFSQFKAIWFPYNMDWRGRVYA VPMFNPQ GNDMQKGLLTLAVGKPIGADGFKWLKVHGANCAGVDKVTFEERIKWVEDNHDNIMAAKAP MDSIEWWKGKLDSPHCFLAFCEYAGVMHHGLSYSCSLPIAFDGCSSGIQHFSAMLRDHIGGHIA VNLTPSGKQODVYRSDNDEJELKVLVNGTDNEMVTHIEDKKTGETERLKLGTRELARQWLTY GMSRKVTKRSYMTLAYGSKKEYGADQVYEDIVMPAIDSGSGAMFTEPRQASRFMAKMIWEA VSVTVVAAVDAMKWLQGA AKLLAAEVKDKKTGELKPKCLPVHVVTPDGFVPVWQERYKKDIT RLNLMFGSGFNLPQTVNKGKTKKLDKHKGESGISPNFVHSQDGSHLRKTTVVHTHRKYGVMSF AVIHDSFGTIPADAELYFRGVRET MVETVYRDNDVLLDFYEQFEYQLHESQRDKLPKPKGKLN IEDILSSDF AFA	PHAGE_Escher_ST31_NC_047829: RNA polymerase; PP_00028; phage; -	DNA-directed RNA polymerase [Escherichia phage P762]	Escherichia phage P762	1833	1833	100%	0.00E+00	98%	893	QUR34664.1
CDS44	complement(38128..38520)	MNMANLVHAMD5TSLHTITDKNGV EWKYVGTDPRGRNYWEKTGNKNTAYVHRHSSHTARQ QOQERDRVLQARLLAEGHSEQMCLAYGGRPITDDGKLLVSGWKAIDQRSTIKTHTHGDFSHLH ANQLICK	PHAGE_Enterо_EcoDS1_NC_011042: gp0.38; PP_00029; phage; -	gp0.38 [Escherichia phage EcoDS1]	Escherichia phage EcoDS1	253	253	100%	2.00E-84	92.31%	132	YP_002003740.1
CDS45	complement(38520..38723)	MTMSLALLAIGYGLIAYVLVKDIIHKARKVYKFNVYRLGRWTVRQPNGRFMRNLANVWDIAT LGSCLK	PHAGE_Citrob_SH4_NC_031018: hypothetical protein; PP_00030; phage; -	hypothetical protein HFBEMICV_CDS0005 [Escherichia phage 216Eco046PP]	protein HFBEMICV_CDS0005 [Escherichia phage 216Eco046PP]	127	127	97%	2.00E-36	95.38%	65	WWT42843.1
CDS46	38840..39289	MQVVIFEATCQLDDLSSITLHFYRDGCHLGYSKSTSQNLNCIAYRLVFGPEIFTSKVVNVAVYFF GWLAA NCYSVAKGKLTIRPLRPVAA YALRRYVEVTGHLRKHVKSRRATLRLAHVQVCLYS YFKIYRVAAVSSCVHEICILC	hypothetical; PP_00046	hypothetical protein (Escherichia phage vB_EcoP_PPW10)								
CDS47	complement(39345..39494)	MYTYGLCQHHTVNARIMVKNQNLNHDAA MRHLKAVYDGRKRIHDSLSHAK	PHAGE_Citrob_CR44b_NC_023576: hypothetical protein; PP_00032; phage; -	hypothetical protein [Escherichia phage P762]	hypothetical protein [Escherichia phage P762]	90.5	90.5	92%	3.00E-22	93.33%	48	YP_009798525.1
CDS48	complement(39488..40012)	MKLGIGGAFTKCYLDCGKRVLLVSSDPKECMAWGWFPESPLFPEVKMIEVGYT EMDYIPPTR GLKAHLDDQWQLYQVLRDCFSPSPVFSRPAELYHRWYEIFQA AHRSDTETVREGLMDVLM ALDACANFGSDIQFEISPRNRAIN GKLLVDCFLVSKLQEVSSRW	PHAGE_Escher_YZ1_NC_047927: hypothetical protein; PP_00033; phage; -	hypothetical protein HOR80_gp01 [Escherichia phage ST31]	Escherichia phage ST31	291	291	82%	2.00E-90	95.77%	142	YP_009790616.1

Supplementary TableS2. Efficacy of *Escherichia* phage vECPW10 in lysing MDR *E. coli* isolates and its efficacy of plating (EOP) of the phage

Strain	Phage vECPW10	
	Lytic Activity	EOP
MDR <i>E. coli</i> PPW021	+	Moderate (0.14)
MDR <i>E. coli</i> PPW022	+	High (0.71)
MDR <i>E. coli</i> PPW023	-	-
MDR <i>E. coli</i> PPW024	-	-
MDR <i>E. coli</i> PPW025	+	Moderate (0.11)
MDR <i>E. coli</i> PPW026	-	-
MDR <i>E. coli</i> PPW027	+	High (Host = 1)
MDR <i>E. coli</i> PPW028	+	High (0.91)
MDR <i>E. coli</i> PPW029	-	-
MDR <i>E. coli</i> PPW030	-	-
MDR <i>E. coli</i> PPW031	-	-
MDR <i>E. coli</i> PPW032	-	-
MDR <i>E. coli</i> PPW033	-	-
MDR <i>E. coli</i> PPW034	-	-
MDR <i>E. coli</i> PPW035	-	-
MDR <i>E. coli</i> PPW036	+	High (0.56)
MDR <i>E. coli</i> PPW037	-	-
MDR <i>E. coli</i> PPW038	-	-
MDR <i>E. coli</i> PPW039	-	-
MDR <i>E. coli</i> PPW040	-	-

Lysis results were recorded as positive (+) when clear zones appeared on the bacterial lawn, and negative (-) when no lysis was observed. An asterisk (*) indicates the host strain used for isolating *Escherichia* phage vECPW10. EOP values were classified into four categories: high ($\text{EOP} \geq 0.5$), moderate ($0.1 \leq \text{EOP} < 0.5$), low ($0.001 < \text{EOP} < 0.1$), and no production ($\text{EOP} \leq 0.001$). All experiments were independently performed in triplicate, with each experiment including duplicate plaque assays, and the entire process was repeated twice.