

International Journal of Environmental Research and Public Health



Supplementary Materials: The Occurrence of the Colistin Resistance Gene *mcr-1* in the Haihe River (China)

Dong Yang 1,† , Zhigang Qiu 1,† , Zhiqiang Shen 1,† , Hong Zhao 2 , Min Jin 1 , Huaying Li 3 , Weili Liu 1 and Jun-Wen Li 1,*

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CATCGC	GGACAATCTC GGACAATCTC	GG · · · · · · ·		GTEGTGETETT	GGCGCGATGCTACTG	Primers T _m differer Forward Primer Reverse Primer Upper Oligo Lower Oligo Monovalent Cation Free Mg(2+) Total Na(+) Equivala ATCACCACGCTGTTA TAGTGGTCCGACAA	Concer 200.0 200.0 200.0 200.0 200.0 200.0 200.0 50.0 0.7 ent: 155.8 TCATCG	ntration nM nM nM mM 3 mM	Commer	CTAAAGCCT GATTTCGGA		AACGATAATI	ATCATGGGCGC

Figure S1. The scores of product, prime and probe in Oligo 7.0.

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Figure S2. Cont.

Sequ	iences producing significant alignments:						
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4 1	lignments EDownload - GenBank Graphics Distance tree of results Description	Max	Total	Query	E	Ident	Accessio
		score 36.2		cover 100%			KX711707.1
	Escherichia coli strain FS170G plasmid pFS170G, complete sequence Escherichia coli strain C9Z4 plasmid pC9Z4, complete sequence	36.2	36.2	100%	3.7		KX711706.1
	Escherichia coli strain GD65 plasmid pGD65-4, complete sequence	36.2	36.2	100%	3.7		KY075660.1
	Escherichia coli strain GD80 plasmid pGD80-2, complete sequence	36.2	36.2	100%	3.7	100%	KY075659.
	Escherichia coli strain WH03 plasmid pWH03-3, complete seguence	36.2	36.2	100%	3.7		KY075655.
	Escherichia coli strain Lishui 12 plasmid pLishui 12-2, complete sequence	36.2		100%	3.7		KY075653.
	Escherichia coli strain GD46 plasmid pGD46-3, complete sequence Escherichia coli strain FS13228 plasmid pFS13228, complete sequence	36.2 36.2		100% 100%	3.7		KY075652.
	Escharichia coli FS13Z2S contig 2 genomic sequence	36.2	36.2	100%	3.7		KY421935.
	Escherichia coli FS13Z2S contig 1 genomic sequence	36.2		100%	3.7		KY421934.
1	Klebsiella pneumoniae strain KP2442 plasmid pKP2442_1c330, complete sequence	36.2	36.2	100%	3.7		KX434879.
	Salmonella enterica subsp. enterica serovar Typhimurium strain YL14P053 plasmid pMCR16_P053, complete sequence	36.2		100%	3.7		KY352406.
	Salmonella enterica subsp. enterica strain R150626 plasmid pR150626, complete sequence	36.2	36.2	100%	3.7		KY120366.
	Salmonella enterica subsp. enterica strain P111 plasmid pP111, complete sequence Escherichia coli strain Ec72H phosphoethanolamine-lipid A transferase MCR-1 (mcr-1) gene, partial cds	36.2 36.2	36.2 36.2	100% 100%	3.7		KY120365. KX216852.
	Escherichia coli strain UCHEC1613 plasmid pMCR_WCHEC1613, complete seguence	36.2					CP019214.
	Escherichia coli strain 2018C-3936C1 plasmid pMCR-1-CT, complete sequence	36.2					CP018773
	Escherichia coli SLK172 plasmid pSLK172-1, complete seguence	36.2	36.2	100%	3.7	100%	CP017632
	Escherichia coli strain HYEC7 plasmid pHYEC7-mcr1, complete sequence	36.2		100%	3.7		KX518745.
	Escherichia coli strain IMP163 plasmid pMCR-1-P3, complete sequence	36.2			3.7		KX880944.
	Escherichia coli strain EHS30-1 plasmid pEHS30-1, complete sequence	36.2		100% 100%			KX772391.1
	Escherichia coli strain E15004 plasmid pE15004, complete seguence Salmonella enterica strain Z3195 plasmid pHIVZ3195 seguence	36.2	36.2	100%	3.7		KX257482.
	Salmonella enterica strain SH36 plasmid pHNSH36 sequence	36.2	36.2	100%	3.7		KX257480
	Escherichia coli strain C002-121 plasmid pC002-121, complete sequence	36.2	36.2	100%	3.7	100%	KU647721.
1	Escherichia coli strain MCR1_NJ plasmid pMCR1-NJ-incX4, complete seguence	36.2		100%	3.7		KX447768.1
	Escherichia coli strain OW3E1 plasmid pOW3E1, complete sequence	36.2		100%			KX129783.
	Escherichia coli strain S38 plasmid pS38, complete sequence Klabsiella pneumoniae strain KP-6884 nlasmid nMCP1 2./T. complete sequence	36.2 36.2		100% 100%	3.7		KX129782.
	Klebsiella pneumoniae strain KP-6884 plasmid pMCR1 2-17, complete sequence Escherichia coli strain EC2 plasmid pEC2-4, complete sequence	36.2		100%	3.7		CP016184
	Escherichia coli isolate W2 isolate genome assembly, plasmid: pW2-mcr	36.2		100%	3.7		LT838201.1
	Escheritchia coli strain ICBEC13AM plasmid pICBEC13AM, complete sequence	36.2		100%	3.7		KY770025.
)	Escherichia coli strain ICBEC3AM plasmid pICBEC3AM, complete sequence	36.2		100%	3.7		KY770024.
	Escherichia coli strain ICBEC2AM plasmid pICBEC2AM, complete sequence	36.2	36.2	100%	3.7		KY770023
	Escherichia coli strain WCHEC1604 plasmid pMCR_WCHEC1604-IncX4, complete sequence	36.2	36.2	100%	3.7		KY218739.1
	Escherichia coli strain W5-6 phosphoethanolaminelipid Atransferase MCR-1 (mcr-1) gene, partial cds	36.2		100%	3.7		
	Escherichia coli strain W2-5 phosphoethanolamine—lipid A transferase MCR-1 (mcr-1) gene, partial cds Escherichia coli strain BE2-5 phosphoethanolamine—lipid A transferase MCR-1 (mcr-1) gene, partial cds	36.2		100%			KY218738. KY218737.
	Escherichia coli plasmid pMRY15-131_2 DNA, complete genome, strain: MRY15-131	36.2		100%	3.7		AP017622.
	Escherichia coli plasmid pMRY15-117_2 DNA, complete genome, strain: MRY15-117	36.2		100%	3.7	100%	AP017619.1
	Escherichia coli plasmid pMRY16-002_4 DNA, complete genome, strain: 20Ec-P-124	36.2	36.2	100%	3.7	100%	AP017614.
	Escherichia coli DNA, genomic structure surrounding mcr-1 gene, strain: RYU2912C-1	36.2	36.2	100%	3.7	100%	LC228070
	Escherichia coli plasmid pKT2378 DNA, complete sequence, strain: KT2378	36.2		100%			LC227558
	Escherichia coli strain HKSH_MCR_161114268_EC phosphoethanolamine lipid A transferase (mcr1) gene, mcr1.9 allele, complete cds	36.2	36.2	100%	3.7		KY685071.
	Escherichia coli strain HKBH_MCR_161103180_EC phosphoethanolamine lipid A transferase (mcr1) gene, mcr1.8 allele, comptete cds Escherichia coli strain pPY1 plasmid pPY1, comptete sequence	36.2 36.2	36.2 36.2	100% 100%	3.7		KY685070.
	Eschrichia coli strain EC590, complete genome	36.2	108	100%	3.7		CP016182
	Citrobacter braakii strain CA-26 plasmid pCA-26, complete sequence	36.2	36.2	100%	3.7	100%	KY624633.
	Escherichia coli strain GD53 plasmid pGD53-3, complete sequence	36.2	36.2	100%	3.7	100%	KY075662.1
	Escherichia coli strain GD65 plasmid pGD65-3, complete sequence	36.2	36.2	100%	3.7		KY075661.1
	Escherichia coli strain WH07 plasmid pWH07-3, complete sequence	36.2		100%	3.7		KY075658
	Escherichia coli strain WH09 plasmid pWH09-3, complete sequence Escherichia coli strain WH13 plasmid pWH13-4, complete sequence	36.2		100% 100%	3.7		KY075657.1 KY075656.1
	Escherichia coli strain Lishui142 plasmid pLishui142-1, complete sequence	36.2	36.2	100%	3.7		KY075654.1
	Escherichia coli strain GD23 plasmid pGD23-3, complete sequence	36.2		100%	3.7		KY075651.1
	Escherichia coli strain GD17 plasmid pGD17-2, complete sequence	36.2	36.2	100%	3.7	100%	KY075650.1
	Escherichia coli FS13Z28 contig 3 genomic sequence	36.2			3.7		KY421936.1
	Escherichia coli strain ST101 phosphoethanolamine transferase (mcr-1.8) gene, complete cds	36.2		100%			KY683842
	Escherichia coli strain C2-007R phosphoethanolamine-lipid A transferase (mcr-1) gene, partial cds	36.2 36.2		100% 100%	3.7		KY013597.1
	Escherichia coli strain MDR_56 plasmid pMCR1-NY, complete sequence Cloning vector pGDP2, complete sequence	36.2		100%	3.7		KX859085.
	Salmonella enterica subsp. enterica serovar Typhimurium YL14P053 pMCR16_P053 mcr-1 gene for phosphoethanolamine-lipid A transferase MCR-1.6, complete CDS	36.2		100%	3.7		NG_05289
	Escherichia coli HeN867 pHeNE867 mcr-1 gene for phosphoethanolamine—lipid A transferase MCR-1.3, complete CDS	36.2					NG_05286
	Escherichia coli WCHEC1606 mcr-1 gene for phosphoethanolamine-lipid A transferase MCR-1.4, complete CDS	36.2					NG_05266
	Escherichia coli 1256822 mcr-1 gene for phosphoethanolamine-lipid A transferase MCR-1.5, complete CDS	36.2					NG_052663
	Escherichia coli strain EC111 plasmid pEC111, complete sequence	36.2					KY471146.
	Escherichia coli strain EC019 plasmid pEC019, complete sequence Escharichia coli strain EC008 plasmid pEC008, complete sequence	36.2		100%			KY471145.
	Escherichia coli strain EC006 plasmid pEC006, complete seguence Escherichia coli strain WCHEC1604 phosphoethanolamineilpid A transferase MCR-1.7 (mcr-1) gene, mcr-1.7 allele, complete cds	36.2					KY488488.
	Escherichia coli ParA (parA), hypothetical protein (pCF132_02), hypothetical protein (pCF132_03), Mcr1 (mcr1), and Pap2 (pap2) genes, complete cds	36.2					KY550359.1
	Escherichia coli ParA (parA), hypothetical protein (pCF1-2_02), hypothetical protein (pCF1-2_03), Mcr1 (mcr1), and Pap2 (pap2) genes, complete cds	36.2					KY550358.1
	Escherichia coli ParA (parA), hypothetical protein (pCF131_02), hypothetical protein (pCF131_03), Mcr1 (mcr1), and Pap2 (pap2) genes, complete cds	36.2					KY550357.1
	Escherichia coli strain A434-59 plasmid phosphoethanolamine-lipid A transferase MCR-1 (mcr-1) gene, complete cds	36.2					KX242348.
	Escherichia coli plasmid pEc_04HAE12, complete sequence	36.2			3.7		KX592672.
	Salmonella Typhimurium strain HSHLJ1 plasmid pHSHLJ1-MCR1, complete sequence	36.2 36.2					KX856066.1 KY012276.1
	Escherichia coli strain 19HAE25 plasmid pEc_18HAE25, complete sequence Escherichia coli strain 27COE18 plasmid pEc_27COE18, complete sequence	36.2					KY012276.
	Escherichia coli strain 2/COE16 plasmid pec_2/COE16, complete sequence Escherichia coli strain 20COE13 plasmid pec_20COE13, complete sequence						KY012274.
	Salmonella enterica subsp. enterica strain NG14043 plasmid pNG14043, complete sequence						KY120364
	Salmonella enterica subsp. enterica strain C214 plasmid pC214, complete sequence	36.2	36.2	100%	3.7	100%	KY120363.
	Escherichia coli strain MRSN346355 plasmid pMRSN346355_55, complete sequence	36.2					CP018124
	Escherichia coli strain MRSN346638 plasmid pMRSN346639_64.5, complete sequence	36.2					CP018118
	Escherichia coli strain MRSN346595 plasmid pMRSN346595_64.5, complete sequence	36.2					CP018112.
	Escherichia coli strain MRSN352231 plasmid pMR0716_mcr1, complete sequence Escherichia coli nikB, mcr-1, pap2, ydfA topB genes for relaxase, phosphoethanolamine transferase, putative PAP family transmembrane protein, hemolysin activation pro	36.2		100% 100%			CP018106.
	Escherichia coli nikB, mcr-1, pap2, ydlA, topB genes for relaxase, phosphoethanolamine transferase, putative PAP family transmembrane protein, hemolysin activation pro Klebsiella pneumoniae strain WCHKP1511 plasmid pMCR_1511, complete sequence	36.2					KX377410.
	Cronobacter sakazakii strain WF-5-19C plasmid pWF-5-19C_mcr-1, complete sequence	36.2					KX505142.
	Escherichia coli strain WF-5-19 plasmid pWF-5-19, partial sequence	36.2					KX505141.
	Escherichia coli strain E15017_00 plasmid pE15017_00, complete sequence	36.2	36.2	100%	3.7	100%	KX772778.
	Escherichia coli transposase (tnpA), MCR-1 (mcr-1), hypothetical protein, and transcriptional regulator (ydfA) genes, complete cds	36.2					KX886345.
	Salmonella enterica strain SH138 plasmid pHNSH138 sequence	36.2					KX257481.
	Escherichia coli strain ICBEC7P plasmid pICBEC7Pmcr, complete sequence	36.2					CP017246
	Escherichia coli strain 210221272 plasmid pSLy21, complete sequence	36.2					CP016405.
	Escherichia coli strain GD-8 plasmid pECGD-8-33, complete seguence	36.2 36.2		100% 100%			KX254343.
	Escherichia coli strain JS-61 plasmid pECJS-61-63, complete sequence						KX254342.
9		36.2					A CONTRACTOR OF T
0	Escherichia coli strain JS-B60 plasmid pECJS-B60-267, complete sequence Escherichia coli strain NDM132 plasmid pist insertion sequence ISApit integrase (int) gene, complete cds; mcr-1 (mcr-1) and hypothetical protein genes, complete cds; i	36.2					KX458104.1
	Eschericha coll strain J2-B60 (Jasmid pECJ8-B60-287, complete seguence Escherichia coll strain NDM132 plasmid plat i maericon seguenci 13Acti i integrase (m) gene, complete cds, mcr-1 (mcr-1) and hypothetical protein genes, complete cds, i National proteinmanes MP-884 unnamed5 mcr-1 gene for phosphosthanolarmin—bipl A transferase MCR-12, complete CDS	36.2	36.2	100%	3.7	100%	KX458104. NG_051170

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Download → <u>GenBank</u> <u>Graphics</u> Escherichia coli strain FS170G plasmid pFS170G, c	complete sequence	e	Vext 🔺 Previous 🛦 Description
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Escherichia coli strain CSZ4 plasmid pCSZ4, compl Sequence ID: KX711706.1 Length: 33309 Number of Matc			Related Information
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Sbjet 4834 CATCOCOGACAATCTCOG 4817			
Download - <u>GenBank</u> <u>Graphics</u>			🔻 Next 🔺 Previous 🛦 Description
Escherichia coli strain GD65 plasmid pGD65-4, con Sequence ID: <u>KY075660.1</u> Length: 33305 Number of Matc	nplete sequence :hes: 1		Related Information
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Escherichia coli strain GD80 plasmid pGD80-2, con Sequence ID: KY075659.1 Length: 241033 Number of Mat	nplete sequence tches: 1		
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Download v <u>GenBank</u> <u>Graphics</u> Escherichia coli strain Lishui12 plasmid pLishui12-2	, complete sequer	nce	▼ Next ▲ Previous ▲ Description
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Escherichia coli strain GD46 plasmid pGD46-3, con Sequence 10: <u>KY075652.1</u> Length: 33302 Number of Mate Range 1: 4617 to 4634 <u>GenBank</u> <u>Graphics</u> Score <u>Expect Identities</u>	hes: 1 Gaps	V Next Match A Previous Match Strond Plus/Minus	
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Escherichia coli strain GD46 plasmid pGD46-3, con Sequence ID: <u>KV076652.1</u> Length: 33302 Number of Matc Range 1: 4617 to 4634 <u>GenBank</u> <u>Graphics</u> Score <u>Expect Identities</u> 36.2 bits(18) 3.7 18/18(100%)	hes: 1 Gaps	Strand	
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Escherichia coli strain GD46 plasmid pGD46-3, con Sequence ID: <u>KY076652-1</u> Length: 33302 Humber of Matc Range 1: 4617 to 4634 <u>GenBank Graphics</u> Score Expect Identifies 3.2. bits(18) 3.7 Id/18(100%) 9avgr 1 <u>c417000000000000000000000000000000000000</u>	Gaps 0/18(0%)	Strand Plus/Minus	Related Information
Escherichia coli strain GD46 plasmid pGD46-3, con Sequence ID: <u>KY076652-1</u> Length: 33302 Humber of Matc Range 1: 4617 to 4634 <u>GenBank Graphics</u> Score Expect Identifies 3.2. bits(18) 3.7 16/18(100%) 9avry 1 <u>CATCOVIDENTITON</u> 18 Shjet 4634 CATCOVIDENTITON 4617 Elowindoad ~ <u>GenBank Graphics</u> Elowindoad ~ <u>GenBank Graphics</u> Elowindoad ~ <u>GenBank Graphics</u> Sequence ID: <u>KY4210371</u> Length: 236355 Number of Mat Range 1: 162519 to 162536 <u>GenBank Graphics</u> Score Expect Identifies	ches: 1 Gaps 0/18(0%) i, complete sequer tches: 1 Gaps	Strand Plus/Minus nce V Next Match & Previous Match Strand	Related Information ▼ Next ▲ Previous ▲ Description
Escherichia coli strain GD48 plasmid pGD46-3, con Sequence ID: <u>KY0756521</u> Length: 33302 Humber of Matc Range 1: 4617 to 4634 <u>GenBank</u> <u>Graphics</u> Score <u>Expect</u> Identities 3.2. bis(18) 3.7. 16/18(100%) 0ery 1 <u>CATC0004644TCT000</u> 4617 Bj.et. 4634 <u>CATC0004644TCT000</u> 4617 Escherichia coli strain FS1322S plasmid pFS1322S Escherichia coli strain FS1322S plasmid pFS1322S Sequence IB: <u>KY012971</u> Length: 23555 Number of Mat Range 1: 162519 to 162536 <u>GenBank</u> <u>Graphics</u> Score <u>Expect</u> Identities 3.2. bis(10) 3.7. 16/18(100%)	Gaps 0/18(0%)	Strand Plus/Minus nce V Next Match 🔺 Previous Match	Related Information ▼ Next ▲ Previous ▲ Description
Escherichia coli strain GD48 plasmid pGD46-3, con Sequence ID: <u>KY0756521</u> Length: 33302 Humber of Matc Range 1: 4617 to 4634 <u>GenBank</u> <u>Graphics</u> Score <u>Expect</u> Identifies 3.2. bis(3) 3.7. 16/18(100%) 0wry 1 <u>CATC00004AMTCT000</u> 4617 Sbjet 4634 <u>CATC0004AMTCT000</u> 4617 Escherichia coli strain FS1322S plasmid pFS1322S Escherichia coli strain FS1322S plasmid pFS1322S Sequence ID: <u>KY012971</u> Length: 23355 Number of Mat Range 1: 162519 to 162536 <u>GenBank</u> <u>Graphics</u> Socre <u>Expect</u> Identifies Jos2 bis(18) 3.7. 19/18(100%)	ches: 1 Gaps 0/18(0%) i, complete sequer tches: 1 Gaps	Strand Plus/Minus nce V Next Match & Previous Match Strand	Related Information ▼ Next ▲ Previous ▲ Description
Escherichia coli strain CD46 plasmid pGD46-3, con Sequence Ib: <u>KY0756521</u> 1. english: 3302 Humber of Matc Range 1: 4617 to 4634 <u>GenBank Graphics</u> Score Expect Identifies 3.2 bits(18) 3.7 Id/16(100%) Beary 1 <u>CATCROVERNATIONS</u> 4617 Bownoad ~ <u>GenBank Graphics</u> Escherichia coli strain FS1322S plasmid pFS1322S Sequence Ib: <u>KY421937.1</u> Length: 23535 Number of Mat Range 1: 62519 to 162536 <u>GenBank Graphics</u> Score Expect Identifies 3.2 bits(18) 3.7 Id/16(100%) Bowr 1 <u>CATCROVERNATIONS</u> 18 Bits 18258 HATCROVERNATIONS 18 Bits	Gaps 0/18(0%) , complete sequer ches: 1 Gaps 0/18(0%)	Strand Plus/Minus nce V Next Match & Previous Match Strand	Related Information ▼ Next ▲ Previous ▲ Description Related Information
Escherichia coli strain GD48 plasmid pGD46-3, con Sequence ID: <u>KY075652-1</u> Length: 33302 Humber of Matc Range 1: 4617 to 4634 <u>GenBank Graphics</u> Score Expect Identifies 3-2. bits(1) 3-7. 19/18(100%) 9erry 1 CATCOCOMENTICOM 4617 Stjet 4634 CATGOCOMENTICOM 4617 Stjet 4634 CATGOCOMENTICOM 4617 Escherichia coli strain FS1322S plasmid pFS1322S Sequence ID: <u>KY141971</u> Length: C3355 Number of Mat Range 1: 162519 to 162536 GenBank Graphics Score Sequence ID: <u>KY141971</u> Length: G3555 Number of Mat Range 1: 162519 to 162536 GenBank Graphics Score Sore 1: 62536 GenBank Graphics Score 1: 62539 Control 1000% Job 1000% Jo	ce	Strand Plus/Minus ICCe ▼ Next Match ▲ Previous Match Strand Plus/Minus	Related Information ▼ Next ▲ Previous ▲ Description Related Information
Escherichia coli strain GD48 plasmid pGD46-3, con Sequence ID: <u>KY075652-1</u> Length: 33302 Humber of Matc Score Expect Identifies Score Expect Identifies Sole bis(10) 3.7 19/18(100%) Genery 1 CATCOCOMPARTICOM 4617 Stat 4634 CATCOCOMPARTICOM 4617 Sole Expect Identifies Soce Expect Identifies Soce Sole CATCOCOMPARTICOM 16519 Sole 16536 CATCOCOMPARTICOM 16519 Soce 154295 Contig 2 genomic sequent Sequence ID: KY421935-1 Length: 20590 Humber of Matc Range 1: 4490 to 8507 <u>CenBank Graphics</u> Soce 2 Expect Identifies	Gaps 0/18(0%) complete sequer ches: 1 Gaps 0/18(0%) CCE hes: 1 Gaps	Strand Plus/Minus ICC V Next Match A Previous Match Strand Plus/Minus V Next Match A Previous Match Strand	Related Information ▼ Next ▲ Previous ▲ Description Related Information ▼ Next ▲ Previous ▲ Description
Escherichia coli strain GD46 plasmid pGD46-3, con Sequence ID: KY075652_1 Renge 1: 4617 to 4634 Gembark Display Score Expect Identifies Boynet Echericia col Strain FS13225 Sequence ID: KY4219371 Length Carbon Score Expect 1 Identifies Score Expect 1 Identifies Score Expectial control Bownload GenBank Graphics Escheri	ce ce chos: 1 Caps 0/18(0%) Class 0/18(0%)	Strand Plus/Minus NCC ▼ Next Match ▲ Previous Match Strand Plus/Minus ▼ Next Match ▲ Previous Match	Related Information ▼ Next ▲ Previous ▲ Description Related Information ▼ Next ▲ Previous ▲ Description
Escherichia coli strain GD46 plasmid pGD46-3, con Sequence ID: KY075652_1 Renge 1: 4617 to 4634 Gembark Display Score Expect Identifies Boynet Echericia col Strain FS13225 Sequence ID: KY4219371 Length Carbon Score Expect 1 Identifies Score Expect 1 Identifies Score Expectial control Bownload GenBank Graphics Escheri	Gaps 0/18(0%) complete sequer ches: 1 Gaps 0/18(0%) CCE hes: 1 Gaps	Strand Plus/Minus ICC V Next Match A Previous Match Strand Plus/Minus V Next Match A Previous Match Strand	Related Information ▼ Next ▲ Previous ▲ Description Related Information ▼ Next ▲ Previous ▲ Description
Escherichia coli strain GD46 plasmid pGD46-3, con Sequence ID: KY075652.1 Length: 3302 Number of Matc Range 1: 4617 to 463.4 GenBank Graphics Score Expect Identifies 3.2. bits(18) 3.7. 16/18(100%) Baytet 4634 CARCEWARTCOM 4617 Convended ~ GenBank Graphics Escherichia coli strain FS1322S plasmid pFS1322S Sequence ID: KY421937.1 Length: 236355 Number of Mat Range 1: 162519 to 162336 GenBank Graphics Score Expect Identifies 3.2. bits(18) 3.7. 16/18(100%) Download ~ GanBank Graphics Escherichia coli FS1322S contig 2 genomic sequen 34.2 bits(18) 3.7. 16/18(100%) Download ~ GanBank Graphics Escherichia coli FS1322S contig 2 genomic sequen Sequence ID: KY421935.1 Length: 2899 Commic Score Identifies Score Expect Identifies Score Score Figure Identifies Score Score Identifies Score Identifies Sco	Gaps 0/18(0%) c, complete sequer 0/18(0%) c, complete sequer 0/18(0%) ce 0/18(0%) Gaps 0/18(0%)	Strand Plus/Minus ICC V Next Match A Previous Match Strand Plus/Minus V Next Match A Previous Match Strand	Related Information ▼ Next ▲ Previous ▲ Description Related Information ▼ Next ▲ Previous ▲ Description Related Information
Escherichia coli strain CD46 plasmid pGD46-3, con Sequence ID: KY075652_1 L english: 3302: Humber of Matc Range 1: 4617 to 4634 <u>GenBank Graphics</u> Score Expect Identifies 3.2 bit(10) Bayst 431 CMT070240MTT000 18 Bownold ~ GenBank Graphics Escherichia coli strain FS13225 plasmid pFS13225 Sequence ID: KY421937_1 Length: 23535 Humber of Matc Range 1: 62519 to 162536 GenBank Graphics Score Expect Identifies 3.2 bit(18) 3.7 110/18(100%) Bownold ~ GenBank Graphics Escherichia coli FS13222 contig 2 genomic sequence Bownold ~ GenBank Graphics Escherichia coli FS13222 contig 2 genomic sequence Bownold ~ GenBank Graphics Escherichia coli FS13222 contig 2 genomic sequence Bownold ~ GenBank Graphics Escherichia coli FS13222 contig 2 genomic sequence Bownold ~ GenBank Graphics Escherichia coli FS13222 contig 1 genomic sequence Boyact 18530 Ch100000AMTT000 18519 Bownold ~ GenBank Graphics Escherichia coli FS13225 contig 1 genomic sequence Boyact (185) Sover Identifies Sover Expect Identifies Sover Expect Identifies Sover Expect Identifies Escherichia coli FS13225 contig 1 genomic sequence Boyact (185) Sover Expect Identifies Sover Expect Identifies Escherichia coli FS13225 contig 1 genomic sequence Boyact (185) Sover Expect Identifies Sover Expect Identifies Escherichia coli FS13225 contig 1 genomic sequence Boyact (185) Sover Identifies Boyact Contig Sover Identifies Boyact Identifies Boyact Contig Sover Identifies Boyact Identifies Boyac	ce	Strand Plus/Minus ICC V Next Match A Previous Match Strand Plus/Minus V Next Match A Previous Match Strand	Related Information ✓ Next ▲ Previous ▲ Description Related Information Related Information ✓ Next ▲ Previous ▲ Description
Escherichia coli Strain GD46 plasmid pGD46-3, con Sequence ID: KY075652-1 Length: 33302 Humber of Matc Score Expect Identifies Score Expect Identifies Sol 2 bits(10) 3.7 10/18(100%) Bayet 4634 CATC0004AACTC00 4617 Commond ~ GenBank Graphics Escherichia coli Strain FS1322S plasmid pFS1322S Sequence ID: KY421337.1 Length: 26355 Number of Matc Range 1: 162519 to 162536 GenBank Graphics Score Expect Identifies 30.2 bits(10) 3.7 10/18(100%) Pary 1 CATC0004AACTC00 18 Boyet 16258 CATC0004ACTC00 18 Boyet 16259 10 10 507 GenBank Graphics Score Expect Identifies Escherichia coli FS1322S contig 2 genomic sequen Sequence ID: KY421355.1 Length: 2099 Humber of Matc Boyet 600 CATC0004AACTC00 18 Boyet 600 CATC0004AACTC00 18 Boyet 600 FS1322S contig 1 Boyet 600 FS132S FS13 Boyet 600 FS132S FS13 Boyet 600 F	ce	Strand Plus/Minus ICC V Next Match A Previous Match Strand Plus/Minus V Next Match A Previous Match Strand	Related Information ▼ Next ▲ Previous ▲ Description Related Information ▼ Next ▲ Previous ▲ Description
Escherichia coli strain GD46 plasmid pGD46-3, con Sequence ID: KY075652.1 Length: 3302 Humber of Matc Range 1: 4617 to 4634 GenBank Graphics Score Expect Identifies 3.7 16/18(100%) Baytet 4634 CARCEWARTCOM 4617 Convended ~ GenBank Graphics Escherichia coli strain FS1322S plasmid pFS1322S Sequence ID: KY2139271 Length: 23535 Humber of Matc Range 1: 62519 to 162336 GenBank Graphics Score Expect Identifies 34.2 bfs(18) 3.7 16/18(100%) Baytet 16255 Contg 2 genomic sequence Sequence ID: KY2139271 Length: 23635 Baytet 16255 Contg 2 genomic sequence Sequence ID: KY2139271 Length: 2090 Baytet 16255 Contg 2 genomic sequence Sequence ID: KY213951 Length: 2090 Baytet 16255 Contg 2 genomic sequence Sequence ID: KY213951 Length: 2090 Baytet 16255 Contg 2 genomic sequence Sequence ID: KY213951 Length: 2090 Baytet 16255 Contg 2 genomic sequence Sequence ID: KY213951 Length: 2090 Baytet 16255 Contg 2 genomic sequence Sequence ID: KY213951 Length: 2090 Baytet 16255 Contg 2 genomic sequence Sequence ID: KY213951 Length: 4912 Humber of Matc Range 1: 3940 to 39263 GenBank Graphics Escherichia coli FS1322S contg 1 genomic sequence Baytet 6507 CANDOWARTCOM 180 Baytet 6507 CANDOW	Gaps 0/18(0%) . complete sequenches: 1 Gaps . Gaps 0/18(0%) Cce Gaps . des: 1 Gaps . complete: 1 Cce	Strand PLspMinus ICC V Next Match ▲ Previous Match V Next Match ▲ Previous Match	Related Information ✓ Next ▲ Previous ▲ Description Related Information Related Information ✓ Next ▲ Previous ▲ Description
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Escherichia coli strain GD46 plasmid pGD46-3, con Sequence ID: KY075652.1 Length: 3302 Humber of Matc Range 1: 4617 to 4634 GenBank Graphics Score Expect Identifies 3.7 16/18(100%) Derry 1 CATCOMMANTICO 18 Biyet 4634 CATCOMMANTICO 461T Elowinoad ~ GenBank Graphics Escherichia coli strain FS1322S plasmid pFS1322S Score Expect Identifies 3.7 16/18(100%) Derry 1 CATCOMMANTICO 18 Biyet 16254 CATCOMMANTICO 18 Biyet 16254 CatCommand FS1322S Score Expect Identifies Biowinoad ~ GenBank Graphics Escherichia coli FS1322S contig 2 genomic sequen Biget 16255 (contig 2 genomic sequen Sequence ID: KY21357.1 Length: 2090 Mumber of Matc Range 1: 3490 to 8507 GenBank Graphics Score Expect Identifies Score Expect Identifies Score CatCommand Graphics Escherichia coli FS1322S contig 2 genomic sequen Sequence ID: KY21357.1 Length: 2090 Number of Matc Range 1: 3490 to 8507 GenBank Graphics Score CatCommand FS1322S contig 1 genomic sequen Bib; KY21335.1 Length: 4912 Humber of Matc Range 1: 39246 to 39263 GenBank Graphics Escherichia coli FS1322S contig 1 genomic sequen Bib; KY21335.1 Length: 4912 Humber of Matc Range 1: 39246 to 39263 GenBank Graphics Escherichia coli FS1322S contig 1 genomic sequen Bib; KY21335.1 Length: 4912 Humber of Matc Range 1: 39246 to 39263 GenBank Graphics Score Expect Identifies Score Score Identifies Score Score Identifies Score Score Score Identifies Score Score Score Identifies Score Score Identifies Score Score Score Identifies Score Identifies Score Score Identifies Score Identifies Score Identifies Score Identifies Score Identifies Score Identifie	Gaps 0/18(0%) 0/18(0%) 0/18(0%) c, complete sequer 0/18(0%) Cce Gaps 0/18(0%) 0/18(0%) Cce Cce hes: 1 Gaps Cce Cce Gaps 0/18(0%)	Strand Plus,Minus	Related Information ✓ Next ▲ Previous ▲ Description Related Information ✓ Next ▲ Previous ▲ Description Related Information ✓ Next ▲ Previous ▲ Description
Escherichia coli strain GD46 plasmid pGD46-3, con Sequence ID: KY075652.1 Length: 3302 Humber of Matc Range 1: 4617 to 4634 GenBank Graphics Score Expect Identifies 3.7 16/18(100%) Baytet 4634 CARCEWARTCOM 4617 Convended ~ GenBank Graphics Escherichia coli strain FS1322S plasmid pFS1322S Sequence ID: KY2139271 Length: 23535 Humber of Matc Range 1: 62519 to 162336 GenBank Graphics Score Expect Identifies 34.2 bfs(18) 3.7 16/18(100%) Baytet 16255 Contg 2 genomic sequence Sequence ID: KY2139271 Length: 23635 Baytet 16255 Contg 2 genomic sequence Sequence ID: KY2139271 Length: 2090 Baytet 16255 Contg 2 genomic sequence Sequence ID: KY213951 Length: 2090 Baytet 16255 Contg 2 genomic sequence Sequence ID: KY213951 Length: 2090 Baytet 16255 Contg 2 genomic sequence Sequence ID: KY213951 Length: 2090 Baytet 16255 Contg 2 genomic sequence Sequence ID: KY213951 Length: 2090 Baytet 16255 Contg 2 genomic sequence Sequence ID: KY213951 Length: 2090 Baytet 16255 Contg 2 genomic sequence Sequence ID: KY213951 Length: 4912 Humber of Matc Range 1: 3940 to 39263 GenBank Graphics Escherichia coli FS1322S contg 1 genomic sequence Baytet 6507 CANDOWARTCOM 180 Baytet 6507 CANDOW	Gaps 0/18(0%) 0/18(0%) 0/18(0%) c, complete sequer 0/18(0%) Cce Gaps 0/18(0%) 0/18(0%) Cce Cce hes: 1 Gaps Cce Cce Gaps 0/18(0%)	Strand Plus,Minus	Related Information ✓ Next ▲ Previous ▲ Description Related Information Related Information ✓ Next ▲ Previous ▲ Description
Escherichia coli strain CD-46 plasmid pGD463, con sequence ID: KY075652,1 Length: 3302: Humber of Matc Renge 1: 4617 to 4634 GenBank Graphics Score Expect Identifies 3.2 bit(10) Bayst 4634 CHICOMANTION 4017 Bownload ~ GenBank Graphics Escherichia coli strain FS13225 plasmid pFS13225 Sequence ID: KY421937,1 Length: 23535 Humber of Matc Renge 1: 162519 to 162536 GenBank Graphics Score Expect Identifies 3.2 bit(18) 3.7 10/18(100%) Boynload ~ GenBank Graphics Score Expect Identifies 3.2 bit(18) 3.7 10/18(100%) Boynload ~ GenBank Graphics Escherichia coli FS13225 contg 2 genomic sequent Boynload ~ GenBank Graphics Escherichia coli FS13225 contg 2 genomic sequent Boynload ~ GenBank Graphics Escherichia coli FS13225 contg 2 genomic sequent Boynload ~ GenBank Graphics Escherichia coli FS13225 contg 1 genomic sequent Boynload & GenBank Graphics Escherichia coli FS13225 contg 1 genomic sequent Boynload & GenBank Graphics Escherichia coli FS13225 contg 1 genomic sequent Boynload & GenBank Graphics Escherichia coli FS13225 contg 1 genomic sequent Boynload & GenBank Graphics Escherichia coli FS13225 contg 1 genomic sequent Boynload & GenBank Graphics Escherichia coli FS13225 contg 1 genomic sequent Boynload & GenBank Graphics Escherichia coli FS13225 contg 1 genomic sequent Boynload & GenBank Graphics Escherichia coli FS13225 contg 1 genomic sequent Boynload & GenBank Graphics Escherichia coli FS13225 contg 1 genomic sequent Sequence ID: KY42193.1 Length: 45912 Humber of Matc Renge 1: 39246 to 39263 GenBank Graphics Score Boynload & GenBank Graphics Escherichia coli FS13225 contg 1 genomic sequent Sequent DB: KY42193.1 Length: 45912 Humber of Matc Renge 1: 39246 to 39263 GenBank Graphics Score Boynload & GenBank Graphics Score Boynload	Gaps 0/18(0%) 0/18(0%) 0/18(0%) c, complete sequer 0/18(0%) Cce Gaps 0/18(0%) 0/18(0%) Cce Cce hes: 1 Gaps Cce Cce Gaps 0/18(0%)	Strand Plus,Minus	Related Information V Next Previous Description Related Information
Escherichia coli strain GD46 plasmid pGD46-3, con Sequence ID: <u>KY076652.1</u> Length: 3302 Humber of Matc Range 1: 4617 to 4634 <u>GenBank Graphics</u> Score Expect Identifies 3.2. bit(18) 3.7 16/18(100%) 9ary 1 <u>CMT000000000000000000000000000000000000</u>	Gaps 0/18(0%) 0/18(0%) 0/18(0%) c, complete sequer 0/18(0%) Cce Gaps 0/18(0%) 0/18(0%) Cce Cce hes: 1 Gaps Cce Cce Gaps 0/18(0%)	Strand Plus,Minus	Related Information ✓ Next ▲ Previous ▲ Description Related Information Related Information ✓ Next ▲ Previous ▲ Description

Figure S2. BLASTN analysis of primer M-F.

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NIH U.S. National Library of Medicine NCBI N	tional Center for Biotechnology Information						Sign ir	n to NCBI
BLAST [®] » blastn suite » RID-FVEYNP1N014			ł	Home	Recent Results	Saved Str	rategies	Help
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Job title: Nucleotide Sequence (22 letters)								
RID FVEYNP1N014 (Expires on 04-25 16: Query ID Id[Query_171885 Description None Molecule type nucleic acid Query Length 22 Other reports: <u>> Search Summary [Taxonomy reports</u>			nr Nucleotide collection (nt BLASTN 2.6.0+ ▷ <u>Citatio</u>					
⊖ <u>Graphic Summary</u>	New Designing or Testing PCR Primers? T	'ry your search in Primer-B	LAST. GO					
	Distribution of the top 103 Blast H Mouse over to see the title, Color key for all of 40 40-50 50- 1 4 8	click to show alignments						

Figure S3. Cont.

	ences producing significant alignments:						
	: <u>All None</u> Selected.0 Ignments (BDownload - CarrEank Graphics Distance tree of results						0
	Description	Max	Total	Query cover	E	Ident	Accession
1	scherichia coll isolate Wi2 isolate genome assembly, plasmid, pWi2-mcr					100%	LT838201.1
	acherichia coli strain ICBEC13AM plasmid pICBEC13AM, complete sequence	44.1	44.1	100%	0.023	100%	KY770025.1
	acherichia coli strain ICREC3AM plasmid pICREC3AM, complete sequence						KY770024.1
	scherichia coli strain ICBEC2AM plasmid pICBEC2AM, complete seguence						KY770023.1
	ischenchia coli sirain WCHEC1604 plasmis pMCR_WCHEC1604-IncK4, complete sequence ischenchia coli sirain W5-6 phosphoethanolamine-lipid A transferare MCR-1 (mcr-1) gene, partial coli						KY218739.1
	scherichia coli strain VI2-5 phosphorethanolamine-lipid A transferase MCR-1 (mcr-1) gene, parlial cda						KY218738.1
	scherichia coll strain BE2-5 phosphoethanolaminelipid A transferase MCR-1 (mcr-1) gene, partial cds						KY218737.1
	acherichia coli plasmid pMRY15-131_2 DNA, complete genome, strain: MRY15-131	44.1	44.1	100%	0.023	100%	AP017622.1
							AP017619.1
							AP017614.1
							LC228070.1 LC227558.1
							KY685071.1
	acherichia coli strain HKSH_MCR_161103180_EC phosphoethanolamine ligid A transferase (mcr1) gene, mcr1.8 allele, complete cda						KY685070.1
	scherichia coli strain pPY1 plasmid pPY1, complete sequence	44.1	44.1	100%	0.023	100%	KX711708.1
	scherichia coli strain EC590, complete genome	44.1	132	100%	0.023	100%	CP016182.2
	itrobacter braakii strain CA-26 plasmid pCA-26, complete sequence						KY624633.1
	scherichia coli strain GD53 plasmid pGD53-3, complete sequence						KY075662.1
	scherichia coli strain GD85 plasmid pGD85-3, complete seguence						KY075661.1
	acherichia coli strain WH07 planmid pWH07-3, complete seguence						KY075658.1 KY075657.1
	acherichia coli strain WH09 plaamid pWH09-3, complete seguence iacherichia coli strain WH13 plaamid pWH13-4, complete seguence						KY075656.1
	acherichia coli strain Lishui 142 plasmid plushui 142-1, complete sequence						KY075654 1
							KY075651.1
	scherichia coli strain GD17 plasmid pGD17-2, complete sequence						KY075650.1
	acherichia coli FS13228 contig 3 genomic sequence						KY421936.1
	acherichia coli strain ST101 phosphoethanolamine transferase (mcr-1.8) gene, complete cda						KY683842.1
	acherichia coli strain C2-007R phosphoethanolamine-lipid A transferase (mcr-1) gene, partial cda						KY013597.1
	scherichia coli strain MDR_56 plasmid pMCR1-NY, complete sequence						CP019908.1
	loning vector pGDP2, complete sequence						H0(859085.1
	almonella enterica subsp. enterica serovar Typhimurium YL,14P053 pMCR15_P053 mcr-1 gene for phosphoethanolamine—lipid A transferase MCR-1.5, complete CDS acherichia coli HeN887 pHeNE857 mcr-1 gene for phosphoethanolamine—lipid A transferase MCR-1.3, complete CDS						NG_052893.1
							NG_052664.
							NG_052663
							KY471146.1
1.1	scherichia coli strain EC019 plasmid pEC019, complete sequence	44.1	44.1	100%	0.023	100%	KY471145.1
1 1							<u>KY471144.1</u>
8 1	acherichia coli strain WCHEC1604 phosphoethanolamine-lipid A transferase MCR-1.7 (mcr-1) gene, mcr-1.7 allele, complete cda	44.1	44.1	100%	0.023	100%	KY488488.1
							KY550359.1
							KY550358.1
							KY550357.1
							KX242348.1 KX592672.1
	schenchia coli plasmid pEc_0444E12, complete sequence almonella Typhimunium strain HBHL/11 plasmid pHBHL/11-MCR1, complete sequence						KX856066.1
	scherichia coli strain 18H4E25 plaamid pEc_18H4E25, complete sequence						KY012276.1
	scherichia coli strain 27COE 18 plasmid pEc_ 27COE 18, complete seguence						KY012275.1
	scherichia coli strain 20C0E13 plasmid pEc. 20C0E13, complete seguence						KY012274.1
	almonella enterica subsp. enterica strain NG14043 plasmid pNG14043, complete sequence	44.1	44.1	100%	0.023	100%	KY120354.1
8	almonella enterica subsp. enterica strain C214 plasmid pC214, complete sequence	44.1	44.1	100%	0.023	100%	KY120353.1
	acherichia coli strain MRSN246355 plasmid pMRSN346355_65.5, complete sequence	44.1	44.1	100%	0.023	100%	CP018124.1
	scherichia coli strain MRSN346638 plasmid pMRSN346538_64.5, complete seguence						CP018118.1
	scherichia coli strain MRSN346595 plasmid pMRSN346595_64.5, complete sequence						CP018112.1
	acherichia coli atrain MRSR352231 plaamid pMR0716_mcr1, comptete aeguence ischerichia coli nik8, mcr1, pap2, ydA, top8 genes for relaxase, phosphoethanolamine transferase, putative PAP family transmembrane protein, hemolysin activation pr						CP018106.1
	accentra con nes, nor-1, papz, yok, tope genes tor relaxase, prospholemanotamine transferase, putative PAP family transmemotiane protein, nemotysin activation pr Jebsiella pneumoniae strain WCHKP1511 plasmid pMCR_1511, complete sequence						K0(377410.1
	zonobacter sakazakii strain WF-5-19C plasmid pWF-5-19C_mg-1, complete sequence						KX505142.1
	scherichia coli strain WE-5-19 plasmid pWE-5-19, partial sequence						KX505141.1
	scherichia coli strain E15017_00 plasmid pE15017_00, complete seguence	44.1	44.1	100%	0.023	100%	KX772778.1
		44.1	44.1	100%	0.023	100%	KX886345.1
1	almonella enterica strain SH138 plasmid pHNSH138 sequence	44.1	44.1	100%	0.023	100%	KX257481.1
	scherichia coli strain ICBEC7P plasmid pICBEC7Pmcr, complete seguence						CP017246.1
	scherichia coli strain 210221272 plasmid pSLy21, complete sequence						CP016405.1
	acherichia coll strain GD-8 stasmit pECGD-8-33, complete sequence						KX254343.1
	acherichia coli strain JS-61 plasmid pECJS-61-63, complete sequence						KX254342.1
	acherichia coli atrain JS-860 plaamid pECJS-869-287, complete seguence acherichia coli atrain NDM132 plaamid piis1 insertion seguence ISAp11 integrase (int) gene, complete cds; mcr-1 (mcr-1) and hypothetical protein genes, complete cds;						KX458104.1
							NG_051170.1
	acherichia coli strain 0177 H21 plasmid unnamed4, complete seguence						CP016550.1
	scherichia coli plasmid unnamed1. complete sequence						KX528699.1
	scherichia coli strain 59 plasmid pECJ9-59-244, compléte sequence	44.1	44.1	100%	0.023	100%	KX084394.1
1	acherichia coli strain 61 plasmid pECJS-61-63, complete sequence	44.1	44.1	100%	0.023	100%	KX084393.1
1	acherichia coli strain 865 plasmid pECJS-865-33, complete seguence						KX084392.1
	scherichia coli strain BA76 plasmid pBA76-MCR-1, complete sequence						KX013540.1
	scherichia coli strain BA77 plasmid pBA77-MCR-1, complete sequence						KXI013539.1
	scherichia coli strain ABC149 plasmid pABC149-MCR-1, complete sequence						KX013538.1
	Juyera ascorbata strain WCH1410 plasmid pMCR_1410, complete sequence scherichia coli strain KPR1 plasmid nKP81.BEF complete sequence						KU922754.1 KU994859.1
	scherichia coli strain KP81 plasmid pKP81-BE, complete seguence acherichia coli plasmid pK9457-3-BE, complete seguence						KU994859.1 KU353730.1
	acherichia coli prasma pKH457-3-ae, complete seguence iacherichia coli strain H229B plasmid pH229B, complete seguence						KX129784.1
	scherichia coli strain 742/06 praemid pr22.14-2, complete sequence						CP016187.1
	scherichia coli strain EC13 plasmid pEC13-1, complete seguence						CP016186 1
	acherichia coli strain EC5 plasmid pEC5-1, complete sequence	44.1	44.1	100%	0.023	100%	CP0161851
1	scherichia coll strain EC2_1 plasmid pEC2_1-4, complete sequence						CP016183.1
1	acherichia coli strain FS170G plasmid pFS170G, complete seguence						KX711707.1
	ischerichia coli strain CSZ4 plasmid pCSZ4, complete sequence						KX711706.1
	scherichla coli strain GD65 plasmid pGD65-4, complete sequence						KY075650.1
	ischerichia coli strain GD80 ptasmid pGD80-2, complete seguence						KY075659.1
	scherichia coli strain WH03 plasmid pWH03-3, complete sequence						KY075655.1
	scherichia coli strain Lishui 12 plasmid pLishui 12-2, complete sequence						KY075653.1
	acherichia coli atrain GD46 piaamid pGD45.3, complete seguence acherichia coli atrain FS13225 piaamid pFS13225, complete seguence						KY075652.1 KY421937.1
							KY421935.1
							KY421933.1
1.1	Jebsiella preumoniae strain KP2442 plasmid pKP2442_1c330, complete sequence						KX434879.1
1	almonella enterica subsp. enterica serovar Typhimunum strain YL14P053 plasmid pMCR16_P053, complete sequence	44.1	44.1	100%	0.023	100%	KY352406.1
	almonetla enterca subsp. enterca serovar Typhimurum strain YL 14P053 plasmid pMCR16_P053, complete sequence acherichia coli atrain EH530-1 plasmid pEH530-1, complete sequence						KY352406.1 KX772391.1
		44.1	44.1	100%	0.023	100%	

Figure S3. Cont.

ments			New Designing or	Testing PCR Primers? Try your search in Primer-BLAST.	
Download - Gen	Bank Granbico				Next & Drainur, & Descriptions
Escherichia coli is	solate WI2 isolat	e genome assembly,	plasmid: pWl2-n	ncr	🔻 Next 🔺 Previous 🛓 Descriptions
Range 1: 25333 1		304 Number of Matches ank <u>Graphics</u>	c 1	Vext Match 🔺 Previous Match	Related Information
Score 44.1 bits(22)	Expect 0.023	Identities 22/22(100%)	Gaps 0/22(0%)	Strand Plus/Minus	
Query 1 AAATC. Sbjet 25354 AAATC	AACACAGGETTTAGCAC	22 25333			
	train ICBEC13A	M plasmid pICBEC13		quence	▼ Next ▲ Previous ▲ Descriptions
Sequence ID: KY770 Range 1: 29166		975 Number of Matches	s: 1	🔻 Next Match 🔺 Previous Match	Related Information
Score 44.1 bits(22)	Expect 0.023	Identities 22/22(100%)	Gaps 0/22(0%)	Strand Plus/Minus	
	AACACAGGCTTTAGCAC				
Sbjet 29187 AAATC	AACACAGGCTTTAGCAC	29166			
Bownload - Gen Escherichia.coli s		I plasmid plCBEC3A	V complete segu	ence	▼ Next ▲ Previous ▲ Descriptions
Sequence ID: KY770	1024.1 Length: 33	304 Number of Matche		Vext Match 🛦 Previous Match	Related Information
Range 1: 27406 1 Score 44.1 bits(22)	Expect 0.023	Identities 22/22(100%)	Gaps 0/22(0%)	Strand Plus/Minus	
Query 1 AMATC Sbjct 27427 AMATC			-//		
Sbjet 27427 ÁÁÁÍĆ	AACACAGGCTTTAGCAC	27406			
Bownload ~ Gen		I plasmid pICBEC2A	u complete segu	ence	Vext 🛦 Previous 🛓 Descriptions
Sequence ID: KY770	1023.1 Length: 33	051 Number of Matche			Related Information
Range 1: 27153 1 Score 44.1 bits(22)	Expect 0.023	Identities	Gaps 0/22(0%)	Vext Match Previous Match Strand Plus/Minus	
44.1 DR5(22) Query 1 AAATC. Sbjet 27174 AAATC		22/22(100%) 22	0/22(0%)	Pius/Minus	
Sbjet 27174 AAATC	AACACAGGCTTTAGCAC	27153			
Download - Gen					🔻 Next 🔺 Previous 🛓 Descriptions
Escherichia coli s Sequence ID: KY582	train WCHEC16 848.1 Length: 31	304 plasmid pMCR_V 229 Number of Matche	VCHEC1604-IncX s: 1	4, complete sequence	Related Information
Range 1: 3666 to Score	Expect	Identities	Gaps	Vext Match A Previous Match	
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Sbjet 3687 AAAICA	ACACAGGCTTTAGCAC	3666			
Bownload - Gen	Bank Graphics				🔻 Next 🔺 Previous 🛓 Descriptions
Escherichia coli s	train W5-6 phos	sphoethanolaminelip 18 Number of Matches:		VICR-1 (mcr-1) gene, partial cds	
Range 1: 178 to 1	199 GenBank			Vext Match 🔺 Previous Match	Related Information
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Figure S3. BLASTN analysis of primer M-R.

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Graphic Summary	New Designing or Testing PCR Primers? Try your search in Primer-BLAST. (0)				
	Distribution of the top 103 Blast Hits on 100 subject sequences Mouse over to see the title, click to show alignments Color key for alignment scores 40 0 00 0 50 0 0 0 0 0 0 0 0 0 0 0 0 0 0				

Figure S4. Cont.

	iences producing significant alignments:						
elec A	t: A <u>ll None</u> Selected.0 Agriments (B)Download – Ganflank: Graphics: Distance tree of results						
	Description			Query cover		Ident	Accession
	Escherichia coli isolate WI2 isolate genome assembly, plasmid. pWI2-mor					100%	LT838201.1
	Escherichia coli strain ICBEC13AM plasmid pICBEC13AM, complete seguence						KY770025.1
	Escherichia coli strain ICBEC3AM plasmid pICBEC3AM, complete sequence						KY770024.1
	Escherichia coli strain ICBEC24M plasmid pICBEC24M, complete sequence						KY770023.1
	Escherichia coli strain WCHEC1504 plasmid pMCR_WCHEC1504-InCX4, complete sequence Escherichia coli strain W5-8 phosphoethanolamine—lipid A transferase MCR-1 (mcr-1) gene, pattal cdg	46.1	46.1				KY582848 1
	Escherichia coll strain W2-9 phosphoethanolamine-lipid A transferase MCR-1 (mcr-1) gene, partial cos						KY218738.1
	Escherichia coli strain BE2-5 phosphoethanolamine-lipid A transferase MCR-1 (mcr-1) gene, partial cds						KY218737.1
	Escherichia coli plasmid pMRY15-131_2 DNA, complete genome, strain: MRY15-131	46.1	46.1	100%	0.006	100%	AP017622.1
	Escherichia coli plasmid pMRY15-117_2 DNA, complete genome, straim MRY15-117						AP017619.1
	Escherichia coli plasmid pMRY16-002_4 DNA, complete genome, straim 20Ec-P-124						AP017614.1
	Escherichia coli DNA, genomic structure sumounding mor-1 gene, straim RVU2912C-1 Escherichia coli plasmid pKT2378 DNA, complete sequence, straim KT2378						LC228070.1
	Escherichia coli prasmio pri 12576 Urer, comprete sequence, sitain. N72378 Escherichia coli strain HKSH_MCR_161114268_EC phosphoethanolamine lipid A transferase (mcr1) gene, mcr1.9 allele, complete cds						KY685071.1
	Escherichia coll strain HKSH_MCR_161103180_EC phosphoethanolamine lipid A transferase (mcr1) gene, mcr1 8 allele, complete cds		46.1				KY685070.1
1	Escherichia coli strain pPY1 plasmid pPY1, complete sequence	46.1	46.1	100%	0.006	100%	KX711708.1
	Escherichia coli strain FS170G plasmid pFS170G, complete sequence		46.1				KX711707.1
	Escherichia coli strain CSZ4 plasmid pCSZ4, complete sequence						KX711706.1
	Escherichia coli strain EC599, complete genome Citrobacter brasili strain CA-26 plasmid pCA-26, complete seguence						CP016182.2 KY624633.1
	Escherichia coli strain GD53 plasmid pGD53-3, complete sequence						KY075662.1
	Escherichia coli strain GD65 plasmid pGD65-3, complete sequence						KY075661 1
	Escherichia coli strain GD65 plasmid pGD65-4, complete sequence	46.1	46.1	100%	0.006	100%	KY075660.1
8 1	Escherichia coli strain GD80 plasmid pGD80-2, complete sequence						KY075659.1
	Escherichia coli strain WH07 plasmid pWH07-3, complete sequence						KY075658.1
	Escherichia coli strain WH09 plasmid pWH09-3, complete sequence		46.1				KY075657.1
	Escherichia coli strain WH13 plasmid pWH13-4, complete sequence Escherichia coli etrain WH12 plasmid pWH13-4, complete sequence						KY075656 1
	Escherichia coli strain WHO3 plasmid pWHO3-3, complete sequence Escherichia coli strain Lishui142 plasmid pLishui142-1, complete sequence						KY075655.1 KY075654.1
	escherichia coli strain Lishui 142 plasmid pLishui 142-1, complete sequence Escherichia coli strain Lishui 12 plasmid pLishui 12-2, complete sequence						KY075653 1
	Escherichia coll strain GD46 plasmid pGD46-3, complete seguence						KY075652 1
	Escherichia coli strain GD23 plasmid pGD23-3, complete sequence	46.1	46.1	100%	0.006	100%	KY075651.1
1	Escherichia coli strain GD17 plasmid pGD17-2, complete sequence						KY075650 1
	Escherichia coli strain FS13Z2S plasmid pFS13Z2S, complete sequence		46.1				KY421937.1
	Escherichia coli F813228 contig 3 genomic sequence		46.1				KY421936.1
	Escherichia coli F813228 config 2 genomic sequence		46.1				KY421935.1
	Escherichia coli FS13228 contig 1 genomic sequence Escherichia coli strain ST101 phosphoethansiamine transferase (mc-1.8) gene, complete cds	40.1	40.1				KY683842.1
	Escherichia coli strain C2-007R phosphoethanolamine-lipid A transferase (mor-1) gene, partial cds						KY013597.1
	Escherichia coli strain MDR_56 plasmid pMCR1-NY, complete sequence						CP019908.1
	Cloning vector pGDP2, complete sequence						KX859085.1
	Salmonella enterica subsp. enterica serovar Typhimurium YL14P053 pMCR16_P053 mcr-1 gene for phosphoethanolamine-lipid Atransferase MCR-1.6, complete CDS	46.1	46.1	100%	0.006	100%	NG_052893
1	Escherichia coll HeN867 pHeNE867 mor-1 gene for phosphoethanolamine-lipid A transferase MCR-1.3, complete CDS	46.1	45.1	100%	0.006	100%	NG_052861
	Escherichia coli WCHEC1606 mcr-1 gene for phosphoethanolamine-lipid A transferase MCR-1.4, complete CDS						NG_052664
	Escherichia coli 1256822 mm-1 gene for phosphoethanolamine-lipid A transferase MCR-1.5, complete CDS						NG_052663
	Escherichia coli strain EC111 plasmid pEC111, complete sequence Escherichia coli strain EC019 plasmid pEC019, complete sequence		46.1				KY471146.1
	Escherichia coli strain Ecolo plasmid pEColo, complete sequence						KY471144.1
	Escherichia coli strain WCHEC1604 phosphoethanolamine–lipid A transferase MCR-1.7 (mcr-1) gene, mcr-1.7 allele, complete cds						KY488488.1
	Sebsiella pneumoniae strain KP2442 plasmid pKP2442_1c330, complete sequence						KX434879.1
1	Escherichia coli ParA (parA), hypothetical protein (pCF132_02), hypothetical protein (pCF132_03), Mcr1 (mcr1), and Pap2 (pap2) genes, complete cds.	46.1	46.1	100%	0.006	100%	KY550359 1
	Escherichia coli ParA (parA), hypothetical protein (pCF1-2_02), hypothetical protein (pCF1-2_03). Mcr1 (mcr1), and Pap2 (pap2) genes, complete cds						KY550358_1
	Escherichia coli ParA (parA), hypothetical protein (pCF131_02), hypothetical protein (pCF131_03), Mor1 (mor1), and Pap2 (pap2) genes, complete cds						KY550357.1
	Escherichia coli strain A434-59 plasmid phosphoethanolamine-lipid A transferase MCR-1 (mcr-1) gene, complete cds						KX242348.1
	Escherichia coli plasmid pEC_04H4E12, complete sequence Salmonella enterica subsp. enterica serovar Typhimurium strain YL 14P063 plasmid pMCR16_P053, complete sequence	46.1	46.1				KY352406.1
	Salmonella Typhimulum strain HSHLJ1 plasmid pHSHLJ1-MCR1, complete sequence		46.1				KX856066.1
	Escherichia coli strain 18HAE25 plasmid pEc_18HAE25, complete seguence	46.1	46.1				KY012276.1
	Escherichia coli strain 27COE18 plasmid pEc_27COE18, complete sequence	46.1	46.1	100%	0.006	100%	KY012275 1
ij	Escherichia coli strain 20COE13 plasmid pEc_20COE13, complete seguence	46.1	46.1	100%	0.006	100%	KY012274.1
	Salmonella enterica subsp. enterica strain R150625 plasmid pR150626, complete sequence						KY120366.1
	Salmonella enterica subsp. enterica strain P111 plasmid pP111, complete sequence						KY120365.1
1	Salmonella enterica subsp. enterica strain NG14043 plasmid pNG14043, complete sequence	46.1					KY120364.1
	Salmonella enterica subap, enterica strain C214 plaamid pC214, complete sequence Escherichia coli strain IIRSN346355 plasmid pMRSN346355_65 5, complete sequence	40.1	40.1	10076	0.000	100.10	KY120363.1 CP018124.1
	Escherichia coli strain MKSNI346335 plasmid pMKSNI346336_65.5, complete sequence Escherichia coli strain MRSNI346638 plasmid pMRSNI346638_64.5, complete sequence						CP018124
	Escherichia coli strain MRSN346595 plasmid pMRSN346595_64.5, complete seguence						CP018112.1
	Escherichia coli strain NRSN352231 plasmid pMR0716_mcr1, complete sequence						CP018106.1
	Escherichia coli strain EHS30-1 plasmid pEHS30-1, complete seguence						KX772391.1
	Escherichia coli nikB, mcr-1, pap 2, ydA, topB genes for relaxase, phosphoethanolamine transferase, putative PAP family transmembrane protein, hemotysin adivation pr						
	Klebsiella pneumoniae strain WCHKP1511 plasmid pMCR_1511, complete seguence						K0(377410.1
	Cronobacter sakazakii strain WF-5-19C plasmid pWF-5-19C_mp-1. complete sequence						KX505142.1
	Escherichia coli strain WF-5-19 plasmid pWF-5-19, partial sequence Escherichia coli strain F15017. 00 ellasmid eF15017. 00 complete sequence						KX505141.1 KX772778.1
	Escherichia coli strain E15017_00 piasmid pE15017_00, complete sequence Escherichia coli strain E15004 piasmid pE15004, complete sequence						KX772778.1
	Escherichia coli transposase (thpA). MCR-1 (mcr-1), hypothetical protein, and transcriptional regulator (vdfA) genes, complete cds						KX886345 1
	Salmonella enterica strain Z319S plasmid pH0/Z319S seguence						KX257482.1
	Salmonella enterica strain SH138 plasmid pHN8H138 sequence						KX257481.1
	Salmonella enterica strain SH36 plasmid pHNSH36 sequence						KX257480.1
	Escherichia coli strain ICBEC7P plasmid pICBEC7Pmcr, complete seguence						CP017246.1
	Escherichia coli strain 210221272 plasmid pSLy21, complete sequence						CP016405.1
	Escherichia coli strain CO02-121 plasmid pCO02-121, complete sequence						KU647721.2
	Escherichia coli strain GD-8 plasmid pECGD-8-33. complete sequence Escherichia coli strain JS-61 plasmid pECJS-61-63. complete sequence						KX254343.1
	Escherichia coli strain JS-61 plasmid pECJS-61-63, complete sequence Escherichia coli strain JS-860 plasmid pECJS-860-267, complete sequence						KX254342.1
	Escherichia coli strain NDM132 plasmid pis1 insertion sequence ISApI1 integrase (int) gene, complete cds, mcr-1 (mcr-1) and hypothetical protein genes, complete cds,						
	Escherichia coli strain MCR1_NJ plasmid pMCR1-NJ-incX4, complete sequence						KX447768.1
	Nebstella pneumoniae KP-6894 unnamed5 mcr-1 gene for phosphoethanolamine-lipid A transferase MCR-1.2, complete CDS						NG_051170
	Escherichia coli strain 0177:H21 plasmid unnamed4, complete sequence						CP016550.1
	Escherichia coli plasmid unnamed1, complete sequence						KX528699.1
	Escherichia coli strain 59 plasmid pECJS-59-244, complete seguence						KX084394.1
	Escherichia coli strain 61 plasmid pECUS-61-63, complete sequence						KX084393.1
	Escherichia coli strain 865 plasmid pECJS-865-33, complete seguence						KX084392.1
	Escherichia coli strain BA76 plasmid pBA764/CR-1, complete sequence						KX013540.1
	Escherichia coli strain BA77 plasmid pBA77-MCR-1, complete sequence Escherichia coli strain ABC148 plasmid nABC148.4/CR-1 complete sequence						KX013539.1 KX013538.1
	Escherichia coli strain ABC149 plasmid pABC14948CR-1, complete sequence Kluvvera ascorbata strain WCH1410 plasmid pMCR_1410, complete sequence						KU922754.1
	Nuvvera ascotbala strain VKUH1410 plasmid pMCHL_1410, complete sequence Escherichia coli strain KP81 plasmid pMP81-BE, complete sequence						KU922754.1
	Escherichia coli plasmid pKH457.3-8E, complete sequence						KU353730.1
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Figure S4. BLASTN analysis of primer M-Probe.

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7 KP347127.txt	
8 s-P.txt	
q s1.txt	CATCGCGGACAATCTCGGCTITGTGCTGACGATCGCTGTGCTGT
s2.txt	CATCGCGGACAATCTCGGGCTTTGTGCTGACGATCGCTGTCGTGCTGTTGTGGCGCGATGCTACTGATCACCGCGCTGTTATCATCGTATCGCCTAAAGCCTGTGTTGATTT
10 52.txt	CATCGCGGACAATCTCGGGCTTTGTGCTGACGATCGCTGTCGTGCTCTTTGGCGCGATGCTACTGATCACCACGCTGTTATCATCGCTATGTGCTAAAGCCTGTTGATTT
11 34.txt	CATCCCCGGCAATCICCGGCTTTGIGCTGGCGATCGCTGCTGCTGCTGCTGCTGATCACCACGCGCTGTTATCACCGCTGATCGCTAATGGCTAAAGCCTGGTTGATTT
	CALCEGEGGAAATCLEGECTI TERELTBAGAT GELTETETETETETETETETETETETATETATETATETATE
12 s5.txt s6.txt	
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ST.CAC	CATCGCGGACAATCTCGGCTTTGTGCTGACGATCGCTGTCGTGCGTG
14 s8.txt	CATCGCGGACAATCTCGGCTTTGTGCTGACGATCGCTGTCGTGCTGTCGTGCTCTTGGCGCGATGCTACCAACGACGCTGTTATCATCGTATCGCTATGTGCTAAAGCCTGTGTTGATTT
15 s9.txt	CATCGCGGACAATCTCGGCTTTGGCTGACGATCGCTGTCGTGCGTG
s10.txt	CATCGCGGACAATCTCGGCTTTGGCTGACGATCGCTGTCGTGCTCTTGGCGCGATGCTACTGATCACCACGCTGTTATCATCGTATCGCTAAAGCCTGTGTTGATTT
16 s11.txt	CATCGCGGGACAATCTCGGCTTTGGCTGACGATCGCTGTCGTGGCGCGCGATGCTACTGATCACCACGCTGTTACCATCGTATCGCTAAAGCCTGTGTTGATTT
17 s12.txt	CATCGCGGGACAATCTCGGCTTTGGCTGACGATCGCTGTCGTGCTCTTTGGCGCGATGCTACTGATCACCGCTGTTACATCGTTACGCTATGTGCTAAAGCCTGTGTTGATTT
10 s13.txt	CMTCGCGGACANTCTCGGCTTTGTGCTGACGATCGCTGTCGTGCTCTTTGGCGCGATGCTACTGATCACCACGCTGTTATCATCGCTATGGCTAAGGCCTGTGTGATTT
18 \$13.txt	CATCGCGGACAATCTCGGGCTTTGTGCTGACGATCGCTGTCGTGCTCTTTGGCGCGATGCTACTGATCACCGCGCTGTTATCATCGTATCGCCTATGTGCTAAAGCCTGTGTTGATTT.
19 s15.txt	CATCGCGGACAATCTCGGCTTTGTGCTGACGATCGCTGTCGTGCTCTTTGGCGCGATGCTACTGATCACCACGCTGTTATCATCGTATCGCTATGTGCTAAAGCCTGTGTTGATTT
20 s16.txt	CATCECEGACAATCICEGECTITEIGCEACGATCECIECEIGCECTITIEGCECEGATECTACICACCACGCEGITATCATCECEATCECEATEGECTAAAGCCIEFEITEATTT
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s18.txt	
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Ready	Channel 1 Empty

Figure S5. Alignment of the sequences of qPCR products and the *mcr-1* gene sequence: (KP347127: the *mcr-1* gene sequence reported by Liu and colleagues, s-P: positive control, s-1–s-18: water samples).

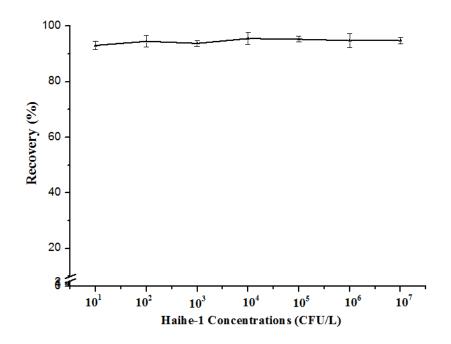


Figure S6. Recovery of Haihe-1 strain (101 CFU/L-107 CFU/L) spiked into 10L PBS

S11 of S13

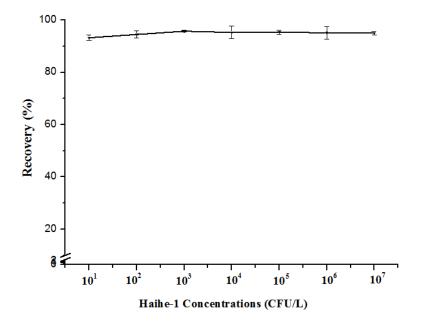


Figure S7. Recovery of Haihe-1 strain (10¹CFU/L–10⁷CFU/L) spiked into 10L sterilized waster sample.

Univariate Analysis of Variance

) I	Ν
site	HD	6
	HE	6
	HU	6
time	Apr	3
	Feb	3
	Jan	3
	June	3
	Mar	3
	May	3

Tests of Between-Subjects Effects

Source	Type III Sum of Squares	df	Mean Square	F	Sig.	
Corrected Model	3.920 ^a	7	.560	6.287	.005	
Intercept	339.259	1	339.259	3808.794	.000	
site	2.576	2	1.288	14.459	.001	
time	1.344	5	.269	3.019	.065	
Error	.891	10	.089			
Total	344.070	18				
Corrected Total	4.811	17				

a. R Squared = .815 (Adjusted R Squared = .685)

Figure S8. The multiple comparisons result of ANOVA.

Post Hoc Tests

site

Multiple Comparisons

Dependent Variable:	IgGC
---------------------	------

Bonferroni

(I) site	(J) site	Mean Difference (I- J)	Std. Error	Sig.	95% Confidence Interval	
					Lower Bound	Upper Bound
HD HE HU	HE	644917	.1723104	.011	-1.139460	150373
	HU	.253731	.1723104	.515	240812	.748275
HE HD HU	HD	.644917	.1723104	.011	.150373	1.139460
	HU	.898648	.1723104	.001	.404105	1.393192
HU	HD	253731	.1723104	.515	748275	.240812
	HE	898648	.1723104	.001	-1.393192	404105

Based on observed means.

The error term is Mean Square(Error) = .089.

*. The mean difference is significant at the 0.05 level.

Figure S9. The deviance analysis result of ANOVA.



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