

Figure legends for a supplemental figure

Figure S1. Alignment of amino acid sequences from the 25 relaxases (TraI) in plasmids and SXT/R39 that belong to the MOB_H family. The amino acids sequences of the highly conserved regions (boxed) were aligned.

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10      20      30      40      50      60      70      80      90      100     110     120     130     140     150     160     170     180
R27_IncH1  --MNFRALFLSMQVRFGLFSRRENDVSELMKMDAANFSPAQIIGEQKYTVDPDHPNPEVLKFIETPRRPAIGIQTNE-----CSILSYRDLKHSISMMLAISDGIREDATFTFTNLVLKPLIEYIRWIHLLPASENHHHNGIGGLLSHSLE
R478_IncH12  --MMNFRALYLCIKRILGIFSSQENDATSMVIDISSLSPAQILGDQKYTVDPDHPNPEVLKFIETPRRPAIGIQTNE-----CSILSYRDLKHSISMMLAISDGIREDATFTFTNLVLKPLVEYVRWIHLLPASENHHHNGIGGLLSHSLE
R391_IncJ_   --MFKNLFQTKALPELSSQL-----DADIP-----RYPPFLKGLPASP-----EDLQSQDQELIACLKRVLGFNQRI-----DFQRLIQPCIDHLAAYVHLLPASEHHHHSAGGLLRHSLE
SXT         --MFKNLFQAKALPELSSQL-----DAEIP-----RYPPFLKGLPASP-----EDLQSQDQELIACLKRVLGFNQRI-----DFQRLIQPCIDHLAAYVHLLPASEHHHHSAGGLLRHSLE
pAsa4      --MFGWGGKSGESPOSGRLLPLKMD-----EEDIP-----RIPFFAKGLVPAPI-----DKILATQAEILIEKVRNSLGFTE-----DFNRLVLPVIHRYAAFVHLLPASEAHHHRGAGGLFRHGLE
p1P1202_IncA/C  --MLKALNKIPGGRSGVIETAPASRVLPVKDVE-----DEEIP-----RIPFFAKGLVPAPL-----DKILATQAEILIEKVRNSLGFTE-----DFNRLVLPVIQRYAAFVHLLPASESHHHRGAGGLFRHGLE
pAQU1     --MISSAFKKLPGGRGKKEVVAS-----QVRDLA-----RIPFFAKGLPMAVP-----EYDRLVMPVIGRYAAFVHLLPASEAHHHRGAGGLFRHGLE
PAGI-2_C   -----MLSLFQQRKRPVATATPTPPASDLPKGLM-----REPESAASILLATPRRQKLEHIEWO-----FTSLSRIFOPAVLYRAPLERYAELVQVFPASESHHHAYPGGMIDHGLE
c1c       --MLSLFQQRKRPVVASATPPASNDLPKRL-----REPESAASILLATPRRQKLEHIEWO-----FTSLSRIFOPATLYRAPLERYAELVQVFPASEAHHAYPGGMIDHGLE
PAGI-3_SG  -----MLSLLQQRKRVSPTAGPATPASDSPKRLT-----REPESATALLPRRQKLEHIEWO-----FTSLSRIFOPATLYLAPLERYASLVQVFPASESHHHAYSGGMIDHGLE
PAGI-4_C   -----MELLGTIPRRRQLLENLWOCASLSKQOFEIYRRPLANYAELVQVLPASENHHHHAHPGGMIDHGLE
pKLC102   --MFQLLSWISRKPSPTPTTKAAPGVFL-----LPLSSTALLDTPRRRQLLENLWOCASLSKQOFEIYRRPLANYAELVQVLPASENHHHHAHPGGMIDHGLE
Plasmid2_Ralme_  -----MSTHT-----SMPMAEALLSREASRIALRQYAEVS-----GILLFAVKWLSILTRCADWFSSMLRFAEHAH-----PGGAFRATVE
pMOL28    -----MTH-----HHLTPAALLASHDSRLALRVQYANESD-----DGFRTKWLSVLDRCAAWFSSMPLRPTAEHAH-----PGGAFRATVE
pHG1      -----MHDH-----ELVSRNERIELIAQCANESSR-----EFDRKMWVLIRRCAEWFSSVPPGPDLYRE-----PGSAFRATVE
pBVEI02   -----MFRRLMKRLETSSPEKPTPYA-----VALSGDKLLQPKRTELISRVKRFVSTVEVWNKHLYLAIQFAELVQVFPASEIIHHHSGGLLDHTE
pMAQU02   --MFNRLKTLFSGKRTPKPTVNOIIMPAEV-----VEALTGSGDILRYPPEALGFPVAVG-----EYDEYIQPMLTNFANFVHLLPASEFHHHRAGGLLRHTE
Rts1_IncT  --MFNRLKTLFSGKRTPKPTVNOIIMPAEV-----VEALTGSGDILRYPPEALGFPVAVG-----EYDEYIQPMLTNFANFVHLLPASEFHHHRAGGLLRHTE
pCAR1_IncP7  MRRSKSRHSFSEPSGNSPARHLPGFFSTKILPENETQGGIIPHASFAHMAEKRMPPFSFLKRLMRSERALDZFAHPAEQMTITEIKRYLENHNNWNLRLVPPYQEGYPLVLSVQDFMKNYQHELFRDIILHISVGMGAPDLKLVPELIVNFAELNHLPLASENHHHSGGGLLRHSLE
Plasmid1_Rhofe  --MRFSDVFSFIKRTPKRVIIPVSSVRVGTIIPAMVO-----VVAPESNEPGVRYPPRPMDSGIRLPT-----DQVLTAVQDMLLRLKRNLIAND-----DFERRYLALPRLRAEILNLIIPATRKDHHAGGGLFRHAAT
Plasmid2_Polsp  -----MSIFNI FTRKAAAPLAIPEQRTALANSS-----RWQASKASLEAIIYPLDPLPVIDA-----EQLLHGAEAKLKRIVEIAGGTAS-----EFERLYMTPIRLLASHVHLLPATSSSHSYSGPGLFNMSLD
Plasmid1_Polsp  -----MKTSLLTIIASSLMVSGSMLYLIN-----TRKSTDVSHNDEVAHINQNIWNRFR-----ILMAHELIQVLDLSPQISGKMYMLGLSDNMSKDALPYLEKYIAFVQRLPASESHHHAHPGGMIDHVRTLD
chrom_Neigo_  -----MKTSLLTIIASSLMVSGSMLYLIN-----TRKSTDVSHNDEVAHINQNIWNRFR-----ILMAHELIQVLDLSPQISGKMYMLGLSDNMSKDALPYLEKYIAFVQRLPASESHHHAHPGGMIDHVRTLD
pNPAP01    -----MKTSAKHPKYLFSEMHGDYFAQLLTICVGEHAFRSYQIYPAERLACTVQDPLEN-----SFFAYAGGALQGLLL
Plasmid1_Shesp_  -----MKKIAKLVSLAVRSFLLDGKTPDKNAVRFMFGG-----IETKAVSEELAEETFPVADGVAVNQARIKKS-----NNDLIDMSIRELGLTDIHRDTFNPANLFEYNQVINAQTLVRDVRVANFLSYAHLPLASENHHHAAVGLLARHSLE
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190     200     210     220     230     240     250     260     270     280     290     300     310     320     330     340     350     360
R27_IncH1  VAMISLKNANHSELRRPIGYQDEEVVRRKVLYAAFCIGLVHDAGKVYDL-DIVSLNLS-----EPLTWAPSSQSLLDWAR-----NNNVVEYIHHWRKRI-----ANQHNWSSVFLERILDPVCMFLDRVVKERVYAKMVTALNV-----MAGNDFLSKCVRTSDYYSTGTGDLNV
R478_IncH12  VAILSLKNAHHSLELRPIGYQDEEVVRRKVLYAAFCIGLVHDAGKVYDL-DIVSLNLS-----SPIIWTWPPSSQSLLDWAR-----NDVVEYIHHWRKRI-----ANQHNWSSVFLERILNVPCLAFLDVRNKEVYKSMITALNV-----TGNDFLSKCVRTADFYSTGTGDLNV
R391_IncJ_   VAFWAAQAAEGII FVASGTPVEKKELEPRWRVAAALGGLFHDIGKPVS-----DLSITDED-----GRYQWNPFLLETLSQWITNNSIERYFIWRWDGR-----CKRHEQFSLVLRNVRMPELLAIAWLTQPGFE-----ILQAMLEAIGN-----TDLEHVLSKLVLEADQTSVQRDLKA
SXT         VAFWAAQAAEGII FVASGTPVEKKELEPRWRVAAALGGLFHDIGKPVS-----DLSITDED-----GRYQWNPFLLETLSQWITNNSIERYFIWRWDGR-----CKRHEQFSLVLRNVRMPELLAIAWLTQPGFE-----ILQAMLEAIGN-----TDPEHVLSKLVLEADQTSVQRDLKA
pAsa4      VAFWAAQASESVI FSI EGT PKQRDNE PRWRLASCFSGLLHDVKGPLA-----DVSITDKN-----GVVWNPNYFESLHDWAGRNHVDRYFIWRWREKR-----KRRHEQFSLAVDRI I PVATREYLSSESGE-----IIEAMLEAISG-----TVNQPVTKMLLRADQESVSRDLQK
p1P1202_IncA/C  VAFWAAQASESVI FSI EGT PRERDNE PRWRLASCFSGLLHDVKGPLS-----DVSITDKD-----GSIITWNPYSELHDWAHHEIDRYFIWRWRDR-----KRRHEQFSLAVDRI I PAETREFLSKSGES-----IIEAMLEAISG-----TVNQPVTKMLLRADQESVSRDLQK
pAQU1     VAFWAAQASESVI FSI EGT PRERDNE PRWRLASCFSGLLHDVKGPLS-----DVSITDKD-----GSKTWNPNYSETLVDWAKRNHVSRYFIWRWRDR-----KRRHEQFSLTVERILITPEALELADPDKG-----IIEAMLEAISG-----LRINDPVTKMLLRADQESVSRDLQK
PAGI-2_C   IVAYALKRQSHLLPI GASPEEDQAQAEMWTAAYAAVAAALLHDIGKIVAV-----DLHVELA-----DGSGLWHFWYGLPHQYR-----FRYRDDRE-----YRLHSAATGLLYRQLLDTQDLWLSGYRDL-----WGPLLYVLAGQ-----YHAGTIGELVVQADRASVAQELGG
c1c       IVAYALKRQSHLLPAGSTPEDQAQAQSEAMTAAYAAVAAALLHDIGKIVAV-----DLHVELA-----DGSGLWHFWYGLPHQYR-----FRYRDDRE-----YRLHSAATGLLYRQLLDTQDLWLSGYRDL-----WGPLLYVLAGQ-----YHAGTIGELVVQADRASVAQELGG
PAGI-3_SG  IVAYALKRQSHLLPTGTPEQVIOQAEAMTAAIYAAALLHDIGKIVAV-----DLHVEYG-----DGSGLWHFWYGLPHQYR-----FRYRDDRE-----YRLHSAATGLLYRQVLDLRLDLSRYPPL-----WGPLLYVLAGQ-----YHAGTIGELVVQADRASVAQELGG
PAGI-4_C   IVAYALKVRQTYLLPI GAAPESQSAQEAEMSAAYAAVAAALLHDIGKIVAV-----DLQVELQ-----DGSGLWHFWYGLPHQYR-----FRYRDDRE-----YRLHSAATGLLYRQVLDLRLDLSRYPPL-----WGPLLYVLAGQ-----YHAGTIGELVVQADRASVAQELGG
pKLC102   IVAYALKVRQTYLLPI GAAPESQSAQEAEMSAAYAAVAAALLHDIGKIVAV-----DLQVELQ-----DGSGLWHFWYGLPHQYR-----FRYRDDRE-----YRLHSAATGLLYRQVLDLRLDLSRYPPL-----WGPLLYVLAGQ-----YHAGTIGELVVQADRASVAQELGG
Plasmid2_Ralme_  AAYFAMRLSQAQKFGADQPSERRRMLPEQYLYALFLAACCSRLEDPCR-----HFQFYRDS-----DGAEWI PAAHGAFG-----PWGTSN-----YRVTRREAIQPIERMRTALLAR-----EILGSRERLAFDQSVLTLFQ
pMOL28    AAYFAMRLSQAQKFGADQPSERRRMLPEQYLYALFLAACCSRLEDPCR-----HFQFYRDS-----DGAEWI PAAHGAFG-----PWGTSN-----YRVTRREAIQPIERMRTALLAR-----EILGSRERLAFDQSVLTLFQ
pHG1      AAYFAMRLSQAQKFGADQPSERRRMLPEQYLYALFLAACCSRLEDPCR-----HFQFHRMR-----DGAEWVPAAHGAFG-----AWLGDST-----YRVTRREAIQPIERMRTALLAR-----EILGTRERLAFDQSVLTLFQ
pBVEI02   TAFYAVRISAGGLKTNLTSERRRIEPOYNFVFLAAICSGLDEPYR-----HFDEVRAT-----DQCVWNPVSWHGVAG-----PWLAGTS-----YCVARRATLPLVERMTRGLMAH-----ALVGTCELLSGLDVAQEAIFG
pMAQU02   IALYAGVRI SGGYILPNNAEPESIAESADRWFPAAMIAALLSHDIGKIVAV-----PEQFQIWHVFWYGNIPGGAARFRYFRKRIENTRLA-----CTLHEKSAMSLPRLLSKEAATWLKFDLEL-----ISQLESTISHS-----TFGGQVIAEIVRADQASVSKNQVA
Rts1_IncT  VVLYSITDKASFEDANESPVIKSDRALARWIAVVGVMHDIGKIPIS-----DUDVMDKS-----GHEKHMVAOCLHEWAEKIEREYFIWRSDR-----HERHNTSLTKMTDIPKSLAQLMQEGND-----IYNEALTAGANSFRAVTSRNETGTIFKNIKHKIVAHADSRVSKQDLQR
pCAR1_IncP7  VASITLDGCLTAFADTNEPTARRSMRLRRWYVAGIASGLLDHAGKPLT-----DIRATDFE-----GNQWIVAYOETLHDWSVKNKLTRYFLHWNNSR-----IGNHVQSVLGAQATRI I PPAVQALIEGGD-----IYEAALDAISG-----GSSPDLTKVWADASTKTRDNR
Plasmid1_Rhofe  MAIRSAQSDAGRI FAANEGERIERRQTEAAMRHAALTGITCELEFRPLT-----EMMIFDPK-----GNQWVSVFVAPLTELWAKQGAADRFFVRHKGHD-----RSVANTLSSWAVNVAVNEVSELNNVNSK-----IVETIFGVSSWY-----ITTADNISTMAALINVRVRIYTOQHEI
Plasmid2_Polsp  IALMRAQAAGEKIFVPPESTIEHRHTIGMWRYSAFGLAGLLSGLHPVIG-----QMTIVTVA-----DQTPWKYKVPPLLTHWQCRSADRYPVIWHHEKA-----RVTGAEAGVASAIIVPEIMNLSQITSDIRDLNVAATREEM-----LADNSITGKVLNVI GRUKEVAELQ
Plasmid1_Polsp  -----MEPRWRYICFLAGLLHPIGIPLVR-----MUVSTKG-----GESWPKMHMDITTWAOEAKIDRVVFNWSDSESLEQNKRLGSPPYTASILHKVIGPENGLWLEEGSE-----LITRFLPELVGGS-----ETTSRIAKDVVVMTGWVQVQREEA
chrom_Neigo_  VAALALVASTSQSWPNNAKTEIAKTTAVRYGIMCAALLHDVGTGVTGVPGLFDSAA-----SEKLLMLDPTGSMASAEKQ-----LYRYVEFPDAK-----A-----YSTHAEIAWTFQALVPSVRWQWLATPDE-----LMTLTRNLYSGK-----KDGSPLEQLIKMADTMSVSRDLRS
pNPAP01    AGLTALRDCDGVIFEPSASAQRMELVQRYVAAWCATLA-----GVPLIVDHALLTVN-----DKWFSFVPSSSLWEAEGTGTSGYIIEWKPSK-----NPTPLSGLLILLSSFFVAGQFT-----DFDSSVLQVLSQNSVNPGLTO
Plasmid1_Shesp_  VALFSLRHMASVDIRETKPTDELHGKLRQYAAWVIGLVHDIGKALH-----DMTVQADD-----SVWNQPLENIYDWSGKNQVSRVQVTVNYAD-----HGKHI GLASSMLNTVLTAKAQYLFQTDQ-----LQVAYIETLSGS-----EVNNSLRDSLCKGEARSVHKMDMM
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Fig. S1 Nonaka *et al.*

370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540

R27_IncH1 LR-DPIMGLRSNDAAARAIGTIKHNFTSININNYKTKPMHIIIVNGE VYLNENAFLDVFLSDFAAHKFNFPQGDG KTVLVESLVQRGVVEPYDDER VVHYFIP-GTYSENEIASIFRNIGKLFEFYNLLKLRMLGLIFDSYKTPDSVPGLFSVNANKDFIY DEQKTVTEYRP

R478_IncH12 LR-DPIMGLRSNDAAARAISTIKHNFTSININNYNAKPMHIIIVNGE VYLNENAFLDVFLNDFLHKYFNFPQGEA KTVLVESLVQRGVVEPYDDER VVHYFIP-GIYSENEISNIFRNIGKLFEFYNLLKLRMLGLIFDSYKTPDSVPGLFSVNANKDFIY DEQKTVTEYRP

R391_IncJ QR-ISVDDNALGVVPERYLLDAMRRLASSQWLNVQRDVRVLRKSNSTH LYLWVKSAAKDI IELLAKDKI PGI PRDP DTLADLILIERGLATKSASNE -----RYESLAPEVLIK---DDKPIWLPMLHIVADLLFSSNVPSVRLFSKSEWEATRTQTA EPQSRSSSEHS

SXT QR-ISVDDNALGVVPERYLLDAMRRLASSQWLNVQRDVRVLRKSNSTH LYLWVKSAGKEI IELLAKDKI PGI PRDP DTLADLILIERGLAIKASNE -----RYESLAPEVLIK---DDKPIWLPMLHIVADLLFSSNVPSGVILFNKSEWEATQQTQA EPQSRSSSEHS

pAsa4 NR-LNVDFEFSYGVPERYVFDARLRVKTGKWKVNEPGAKVWHLQCG VFIAWRN-LGDLYDLISHDKI PGI PRDP DTLADLILIERGFVAVNTVQEGKDRAYY-RYWEVLEPMIQ---EAGGSIKILMLRLESNELVFTTEPAVAAGEVVGVDADAVIEL DPDEASDADD

pIPI202_IncA/C SR-LDVDFEFSYGVPERYVFDARLRVKTGKWKVNEPGAKVWHLQCG VFIAWRK-LGDLYDLISHDKI PGI PRDP DTLADLILIERGFVAVNTVQEGKDRAYY-RYWEVLEPMIQ---EAGGSVKILMLRLESNELVFTTEPAVAAGEVVGVDADAVIEL DPDEASDADD

pAQU1 NR-LDVDFEFSYGVPERYVFDALRRLVKTGKWKVNEPGAKVWHLQCG VFI TWKQGASDIYDLITEDKI PGI PRDP DTLADLILIERGFALKNVLPEKGDVYF-RYWEVILPELQEGEEVTKIKMQLMLRLESNELVFTTEPAVAAGEVVGVDADAVIEL DPDEASDADD

PAGI-2_C DP-ARAMAAPKHALQRKLLDGLRYLLKEELKLNQPE-ASDGWLTEDA LVLVSKTVSDKLAHLLSQIGDI PANN TAVFNVLQDHGMQLPTDCKAVWRATY-TSNAGWTHSFTLLRLAPALIWE-AGERPAPFAGTVAIDVAVPNDK---SVAQPAVAETPT

c1c DP-ARAMAAPKHALQRKLLDGLRYLLKEELKLNQPE-ASDGWLTEDA LVLVSKTVSDKLAHLLSQIGDI PANN TAVFNVLQDHGMQLPTDCKAVWRATY-TSAGWTHSFTLLRLAPALIWE-PGERPVPFAGTVAIDVAVPNDK---SVAQPAVAETPT

PAGI-3_SG DP-ARAMAAPKHALQRKLLDGLRYLLKEELKLNQSG-ASDGWLTQDA LVLVSKTVSDKLAHLLSQIGDI PANN TAVFNVLQDHGMQLPTDCKAVWRATY-TSTAGWAHTFTLLRLAPALIWE-GENRPEPFTGTVLIEE---SNDAPAEFS

PAGI-4_C NP-DRALAAPKQSLQRQLADGLRFLVKDKFKLNQPGGSDGWLTQDA LVLVSKPAADQLRAYLLAQIGEGVPSSN APFFNMLQDQAVIQTNAEDKIWIATYI-DNGAGWRNKFTLLKIAPALIWADPAERPIYSVSGSLVIEEGNASPEKPTTCEIPNDP EQRQAPKAM

pKLC102 NP-DRALAAPKQSLQRQLADGLRFLVKDKFKLNQPGGSDGWLTQDA LVLVSKPAADQLRAYLLAQIGEGVPSSN APFFNMLQDQAVIQTNAEDKIWIATYI-DNGAGWRNKFTLLKIAPALIWADPAERPIYSVSGSLVIEEGNASPEKPTTCEIPNDP EQRQAPKAM

Plasmid2_Ralme_pMOL28 -----A INPDRPTG-LETLHKVVRQSIDT LTQFEIKARKAIEFPDSTPV-----TAER

pHG1 -----A INPDRPTG-LETLHKVVRQSIDT LTQFEIKARKAIEFPDSTPV-----TAER

pBVEI02 -----A INPDRPAG-LETLHKVVRQAIEI VTQFELKARRAFAPDTPAPSA-----QALAVDA

pMAQU02 -----A INPTQSPGTGGVESLTHKVVQRQAVT AAEFDRKQRAVFEVPTFAV-----SAIHVAELE

Rts1_IncT NT-GKKADHTNTIPLYEKLIVSLRKLVDGDKRKNPGAAVVWTDGT TWVVSKATMEAVRIQLINEGHSGLPKNV VTLFGLINDHDCVLVNPDDG VVWYAEINDHGKNWQOKLTFLRFKNEI IWPTSQPDMGDTVTPIDRNG-----NPLEISQVVE

pCAR1_IncP7 YSGDAVRASQTGVPIARIIVDAMRLLIKKEEWPKNQAGSLWVTGEG VFIWVGTAVTPIISIVKESGINVPHSAD SLADIMVNHGCLVLSNDDG VWRLAPHILNDKISRQNEKPKNALSCILKVDPVVLE TDDVMPNPTSCRIKLDGWKEFTGAGLTH-----KQSPSRPYV

Plasmid1_Rhofe GS-NNGGNGATGVPPVRLVSDAMLRLLSDGTWIKINTPGGRVWVATDG IYIVVMQGAEEIVSMVLQGVGAVIPRSP DTLIGSLVEHGLAERANSDG VYLWVTPHLLKQPKPALRCMLVNPDIKLFPTPIEFPVSIGLGKQKQKVDIAPNDTAGAANA-----LSEHQDLFG

Plasmid2_Polsp AP-ATYKGLTSGSQLEPYFMDAMRTLLRTGQVQVNTKSGRCHFGADG FVAVWRMGSQIEILHGLHTEKJAGVPTAK ETLAEMMGRAGIISISAPDGS NPHLVRV-SVGSAGMPAVRQLQTEPLALGHLEVPKVAOTLVRNSAKP-----APSVAIPLTK

Plasmid1_Polsp HP-ARGRLTIGTQFEIHLNALRELI EEREKWLNDNPGCLFEGSDG LVAVWRGLEDVTSTIFAKRQLKGMPLSS VTLAEMLQGSQVVIKGTDTGV VHDIVV-----GAEKVVVSAMREKIEPAVLLG-----HLDFQVPS

chrom_Neigo_RRPQAYGRLTVGHILTPLYVMSRSLVNDGKWKPNGLPIDVDSGT VYIWPDAGEEIVROGAREGRDGWPSA ATLAELLKQDGVFETS YGNDGMTEVVDKEGNVLQSYKLLKPTTVIETYEASDYQRAAPKTLSGVLDLDR-----DPLAKAEAKV

pPNAP01 GSRQRFSTAKRKFPIETIMETLKEMLSDRGVHFS IATTAGDLFRKGD VYILMSKNVPDYIRQLRKNQHPAAGSFPADN QRIPTDLFEYRAVIPPENDPHRAINHIEVEFTFMDGKVRNIFSVLCTFNAKLTYPDQVYTFELNGLSEVSAKKEIPDVVVSDEKMTQIQGAEDN

Plasmid1_Shesp SS-----GESSLSKLVRAQEKVKATEKLR-----ISRVFVPGAQVNTVASVQA-----

QW----DRLTGARKMPLAFAFKLQMRMRGWVNEEKADICWLGAE VYVSYPASFNKVMSSLKEGDFNVPMQVG-----KMLEMLVERQLFEPLFEDYSVSGHLHPVTPNPEWTAGIKVVKPKWAGIVVGEDI PQSGHKGKLSLIRDDSLIHYADTGLITLTD-----REPPDQTPAN

550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720

R27_IncH1 VPGRESVTRVTDVNDAIENTPQYGLQLVNGPDAASN-----NII SSENTESITDSLEESGADI SNEIFETQVVTIATDAETVNADEPEQVEEHDERSQHLVLEQHEMILLSAPLPHHAVINIDSVVYLDLDAATALI PGI DEAAFCNGFPQLTYRDSGLDGMIVRDNVNLRLIQL

R478_IncH12 VPGRDVITKITDVTETAVLKVNDLGRSSAS-IDVD-----IHSKNEGSSDDEKKAESNEIDNDTQIVKSEGEAAFPV IPI DEESE-DESAKDTESHVLVNLQHEMILLSAPLSNDYIVCVDAVYPLNIDT MALLPGLDEKAESEEPYFQLTFREGSLDGMIVRDI DDLRLVLQ

R391_IncJ -----DLPEASSI EHRKSTESFSTNSSEQDDELRLASDVNNPQATEN-----APGDGCEKPNNSYDGAISNNVNQVDTAALN-----

SXT -----DLPEASSI ELSNSAESFSTNSSDQDELRLSSDVNHLQATEN-----APGDECEKPNNSYDGAISNNVNQHDAAALN-----

pAsa4 ESAGSMESSLASAEQEMNALAGLFGFDAMEILGGTASDNDATQPAVVDVTPPAKPAKAGGGRGKQAK-----KTPAAPAEQOPEP-----SQEIAKSTPPLAVENPLQAIMDVGGGLDGLDPPFDPAVAGTMSDEPSQALAPEPKQ-----DVANPDNDP-TPNLGLMNVQF

pIPI202_IncA/C EGEAALNDMLLAAEQEAKALAGLFGFDAMEMLKSTS-----DAVEEKPEQKDGAGTPESSKPDAGKKGKPSQKPKSDETKQHPKPEAK-EDLSQPI DI AKNAPLANNPQLAKLDVGGGLDGLDPPFDPAFNAS-----ATTSTSDATNSEIP-----DVAMPKQEQEPKPLGNVQEQ

pAQU1 -----DENSDSLTATPEPIGSLD-DGF-----EIPDFMAAPPSTDSQSEPKGKSTDT-----KTSKNDKADAPKEP-----SAQEIAQTAAPLALDDPLKGLKDAGALGVCDPPFDAGLNTEPDTTQKDKAETPNVPTQESEEDTSLPGIDNIRSGKQRQPKAS

PAGI-2_C -----

c1c -----

PAGI-3_SG -----

PAGI-4_C -----

pKLC102 -----

Plasmid2_Ralme_pMOL28 -----

pHG1 -----

pBVEI02 -----

pMAQU02 -----

Rts1_IncT -----EKPPERVLNVDPPDI LKGGSLPPTDLPDGTVVKRGVIEQKNI VDHMLRMLLSPENAAIKSRNENAKAKAESQDVEASPKPAETSVAP-----

pCAR1_IncP7 -----ADLTGDSGGDTDADSGPTPKPE SASSKARKKKAAPRQAAPVPTTASSGVLSKQAQNPVEDAPVNVDSESAADETAIVSSQPEEALDAE-----

Plasmid1_Rhofe -----

Plasmid2_Polsp -----

Plasmid1_Polsp -----

chrom_Neigo_pPNAP01 -----VTMTKDKMDFLSIQPVTAEQPLPEKNQVTEANSAFDNSMNTAA PAENKSSESEKAKEPDGTIDNLIENFNLEADSEQTESTKSEAEATAENAVN-----

Plasmid1_Shesp -----TAAPTQAPAPATPTPAVAVPQQNGSQTNQSKAQTKKPKKQASARASTNTPAPAPAPATTPSEPAPEKSQVETQVPEQSNTRAPADTKGIVFKMNDTPIVSEPAEAAVIEPTEIAQEMP-----

Fig. S1 (continued) Nonaka *et al.*

730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900

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R27_IncH1_ GDNCGAGVSTSEPRNTSSLKSLFDTS-----MYQLPDIPEAPSVNEAASPPQTPLELPQPRLNVAEAEASSVAEQTNHSE--PDSVIATEYEQGHILEETLDS---DGEAYSDLTLASDSIAEY
R478_IncH12_ GDNCGAGFQLYHEPRRPTTLKSLFNST-----MYQALVINDESSVENAAPRPKQTLLEPPPVRNVAEHSQDVEYHGTDSASATGPKLTEAVEYEHQHLFEKEDDEEHEIDYDFQSLSVSRPVGSC
R391_IncC_ SXT-----LPELAWLPEASSALVMGEQLLIRYPDAVRPWCAPRKLKLAELSQLDWLELDFANPTRKARVTTNDNGVQEQGLLKLKVS
pAsa4 PNFMNDESTGVDGMDLPPAWAIEEIP----SFHAYEAGEVGGQGNQVSEELAG-----ADAPDAKCELLTLMATFGAEPILERAIPVLEGGKATLGEVLCMKGQAVILYPEGARALGAPSEVLTALFHAQAVIPEFVMSGRKRVDFNGVKAIVLTEQLSSAF
pIPI202_IncA/C_ NSLQGDDEF--MFGGSDPEPPSWAIEPLP-----MLTDAP-EQPTHTPEMPHTDNVN-----QHEKDAKTLVLEMLSGYGEASALLLEQAIMPVLEGGKATLGEVLCMKGQAVILYPEGARALGAPSEVLTALFHAQAVIPEFVMPGRKRVDFNGVKAIVLTEQLSSADAV
pAQU1 ANTAASLSPNEFFPGEPSAIFDAPMPMPEDMFAPIDAVPLDAYDYSHEMEEREFEVTEHPHQDAETYSFSQDQKSSDVVDRGHLENVLSGYGAESILKEAIIPLVLDGHKTLGEVLCMKGQAVILYPEGARALGAPAEVLTALFHAQAVIPEFVMPGRKRVDFNGVKAIVLTEQLSSADSVI
PAGI-2_C_ c1c-----GGQESPPEWEGGSAADPIIAPLAEAMPDVMEIDLTMVGMGDSATQODESTIPELSELSATREPAAPPSSIVASSPSSAPAPATPA
PAGI-3_SG_ c1c-----GGQESPPEWEGGSAADPIIAPLAEAMPDVMEIDLTMVGMGDSATQODESTIPELSELSATREPAAPPSSIVASSPSSAPAPATPA
PAGI-4_C_ pKLC102-----DSCDSSPAASTTTLTSS-----TEPADGVDLALLSAPDKGPPPE-----TVICPLSTSSVSEPTTFAQESDAMQPPMPPSPT
Plasmid2_Ralme_ pMOL28-----LRQPATPIAKPSNDIQAIKHSFTDDQEETDDLALLGNINSPPLELDTSHDPAVSPANTRGEEMLQPLGTKEHIDDAPEA
pHG1-----LRQPTPSVAKPSNEMRAIKHSAEQEETDDLALLGNINSPPLELDTSHDPAVSPANTRGEEMLQPLGTKEHIDDAPEA
pBVEI02-----EKAVNPSLAQADAPVPAPPPATSTQHADGKGNVSPAESAGLGSQAQVESPDATASDASAARNVVQLDGARSRLKESLDDPF
pMAQU02-----EKAVNPSLAQADAPVPAPPPATSTQHADGKGNVSPAESAGLGSQAQVESPDATASDASAARNVVQLDGARSRLKESLDDPF
Rts1_IncT_ pCARI_IncP7-----TGASTPPAQARTETAPEVETGATATPEVEEQPETTEADPSSPAGLHQAGSDASQHRASR--NAVQLDGARSRLKAPAEEDPF
Plasmid1_Rhofe_ pCARI_IncP7-----KVESAPPAAPAPAPAEHVITADSSAAVAAGGGAADPEMPLASDSEGARPREVPAVLEQGAPKGDEROMALEHPLAAAV
Plasmid1_Polsp_ pCARI_IncP7-----DDPDPKAGEGHLHQHRETTHNNEYNQTKPKVASGPPVTSKITTAHKEKGAEPPEEAKEQSQVRAQSGKAHGLTSEEPVTEH
chrom_Neigo_ pCARI_IncP7-----AKGKAEALSDDKRSQNKKSEKKAASVPAEKAVPEQTEQDELFGIDNRYNDYFHVDTDEENQETDYLMEQYNNQTCSEHPLAL
pPNAF01-----EEEEAPQEPASLEEMLFIISPHSPADPHQETLSAAEAEISSDLSADPCAGPQGAQELPRQEKIQLSINSIMGGKRT
Plasmid1_Shesp_ pCARI_IncP7-----DIVSVAPALAKEVQELIALLAPKSDLKAKVLESVDQETGEIAPVVASKPAAPPEPKTSAAAPASDVDPKPAVAAKAPSA
pPNAF01-----YKAMVEAQEQLTLAARTVDVAVNTFRAGAAAEQPSALVADAPTQVQVTTSAASANKESSAHKVPPVLUVSTDS
Plasmid1_Shesp_ pCARI_IncP7-----EKKAKPAQANLEVDTPAVSTSPANATVDPETGELIASTEVRNDVSSTDGADLSADSAPEVPAVEVATAPIQPPLALDAPL
pPNAF01-----LVQENIRVEVKTETVDKPRAEVETEDKAPKTIKSGTKASRKLGLFADNRKRLGKTAEPDAQIKTTVTVHQIDISEAVTSLP
Plasmid1_Shesp_ pCARI_IncP7-----LQTVPASTTTESAVIYNTPKAKSISSNENQKILQVVTLNVASEQRTNQININSLTDSKLIKLENDQKLENKSVGPIPKVK
pPNAF01-----VEVSKEKTCIELLIRYLLTANNLTHRAKLDGVDVTLNLSLFEEDQMRGLGFAEAVLKDLMDKLLELDPKPAKIVHVNNKQVYQKLAIVLAK

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910 920 930 940 950 960 970 980 990 1000 1010 1020 1030 1040 1050 1060 1070 1080

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R27_IncH1_ PATDPQSSDFAQLPRETALSVAPEGDLDYSEGAIKPPAPDATGKEIILTSPEPAEDVRETVAAEKASHLSPALARLFAVS-----THAEKKHEQTQEPSVKEVKNPSTSSITVKAPISIEPP-----GAEKEAVEEFTLLNDGEMVTHELYVE
R478_IncH12_ ATSSSVNHKELLSESELPELNREQNADPQGTNERSMDVSVGQENSEPDTEGNCPPAEVVSQTEATATSVMASEPALPVLEESNGEHAPDADKAG---HHLSPALARLFAPTAPVEKQKPNRKNRSDDKAEVQKASPVSGHN--LNSVFASTESQNGEFSLISEGVDVTHELFEVE
R391_IncC_ ISKR-----LIALIDISKQGTPEAAAIQNEEALQPRSRTKTNN-----AQAKEPATRAERKQKPIAPN-----AKSSTDPKVYQRQOM
SXT-----LTSLIDLPKQDAEFAAAIQNEASRPSRETETN-----AQAKEPAKRAERKQKPIAPN-----ANSTDPKVYQRQOM
pAsa4 IAAIKQAEESLGGYQDAFELVASPEVKTQSKNKRQQRKTSRSESGEDSHAASPERAQVEEKRVADAQQLIDVSVPPSPVVDTPPPKVVVPRKESRGKEKVDKPIQAPATTKTPEGTQNLARLPPREQPKPEQSQ--QKQARVIDVG-----NIALPL-----GPDLEPELSPRSVKEET
pIPI202_IncA/C_ IAAIKQAEASMGYQDAFELVSPGLDASKNKAPKQSRKKAQDQKPEVNAQ---KASPEQK-----AKGKDSQPKQKPKKVDVTSVPE-----EQQRKPVQ-----EKQVWARLPKREAQVVAPE--PKVEREKLEK-----HVVREEREDPEVREPEFSPKAINPKPD
pAQU1 KAAIEQAQKDF---DPIREVSAINDKQSGKKAEKAKHSEKKVKSKQTNQSTPKPKKPMAMDISALLPGEQTGRRSSENKRIAQTAQKKGTAAK---TQTEQHNESENSASNEEKQNVSRLLPKRQKPKTTVNVKPKKTRPVSLDFDSDLELPMTKVVGQIDLEDEEKKKQKAKE
PAGI-2_C_ ATTVQPS-----GEHFMAWLKQGIASRRLIINDAKALVHTVSD-----SATAQPS-----GEHFMAWLKQGIASRRLIINDAKALVHTVSD-----TAYLVSQGVFQRY
c1c-----ENGNAS-----GEHFMAWLKQGIASRRLIINDAKALVHTVSD-----TAYLVSQGVFQRY
PAGI-3_SG_ IEDVFMPRSRSTDLGQGFVDMWKSIGIARRLFIINDTKALVHTVDG-----TAMLVTPGIFKRY
PAGI-4_C_ IEDVFMPRSRSTDLGQGFVDMWKSIGIARRLFIINDTKALVHTVDG-----TAMLVTPGIFKRY
pKLC102_ IEDVFMPRSRSTDLGQGFVDMWKSIGIARRLFIINDTKALVHTVDG-----TAMLVTPGIFKRY
Plasmid2_Ralme_ K-----ALAGSSN-----LMREFFKLAQDV
pMOL28_ K-----ALAGSSN-----LMREFFKLAQDV
pHG1_ K-----AIAGTSM-----LMREFFKLSQDA
pBVEI02_ NPPEIRR-----EPGAAPATPAGERFDEILKGAPR-----MISDFMALARQDV
pMAQU02_ WKTAKREVQEDILRENDFLAWLKGIAARRQIRVNEKAPVHILDG-----HVALVTPEIFNLFI
Rts1_IncT_ QERMARAAIQQYEQDERNINQDGAPESSWEKARAKIRQAQDIDGHAVTSDTYPHTESADVSFAFIDDDHHSFAMFNDGPDCAKQILKRLVKERAG---ELFADNYHLFVHKQNEQDEHDYTVLVNAGWVWPKFLEPMDNFQLYKSKPGFLRRRGLMDEIDY
pCARI_IncP7_ PKTTPPAESKKQKDGVEGRVAEVEPCASSILPLADVVSKLTAHECVLLEQQPDLAQKLIATQ-----DPENAALARNKVFVRLGKSSFLAEDIHPLVHAGWLQDITVEGPAALTRTLQSGREGMLTADY
Plasmid1_Rhofe_ KPGIP-----TVEDVDDLQVQETFD-----DMLLELGAHCREV
Plasmid1_Polsp_ VEVGGDS-----SPHGKRRVVDWLKRLKMKKDD-----DTANALGMVLEQSL
Plasmid1_Polsp_ PGCSG-----RIKEAAEVKFSDLVPEIRKEIKT-----TLTIELLGVVIKAW
chrom_Neigo_ ESESAQNGMRELERLRLEPTSSPRPVQVMDSEGLDLSASGVKMAEAEIVS-----ERNLKKQSETESTEIVEDSVKAKHMEARDRGMQFLRWLADLGDGSIAVNRSQATVHIEQGM
pPNAF01_ T-----FWLRLISDEA
Plasmid1_Shesp_ PVGDMLTELQAKADERKARKQKNKALTTEVITSPNSLPTQESSIKVDVIGPKTEVPEQELSPLMPNEVPPSSCHSLMAEVEQDLSLMTDELPE-----PLSEYAREMSLATPENELPWFPTPEEQSMLTDMETVTVVAEAAIETAVEPATTASFTFAEQV

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Fig. S1 (continued) Nonaka *et al.*

1090 1100 1110 1120 1130 1140 1150 1160 1170 1180

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R27_IncH1_ IATMLHQILTKLSGSFKR--KRKNRFMVLTQNTFYITQSCIEKYG---TQLNAPDLFNQLPQYQVTSGAVVNTKCIAFNIPTLVAASDRAKVDIELIINKLKEVGNL
R478_IncH12_ IALVLVHQILSKMEVAFKR--KRKNRFMVSTPNTLYITQSCVEKFG---SQLEAQDLFNKL P QYLVNSGAVI NTKCHAFNMPTLLAASDRAKVDIERIINNLEAGNL
R391_IncJ_ VNEVFKDLPILLTDGDYDPD--VDHSADGIR-----VVIQTTLRQVANAHGIPAGQLLRGISASDECQ--FDEGETVLFTHAKR-----
SXT VSFVKDLPILLTDGDYDPD--VDHSADGIR-----VVIQTTLRQVANAHGIPAGQLLRGISASDQCQ--FDEGETVLFTHAKR-----
pAsa4 VDEALYLPP--KMTPEKA--IQMLKEMIKNRSGRWIVSAVLEEEG---FLTTSDKAFEVIAGEYTGISKHVLGGTLRRAQRRPLLKQRQKLYLEVVDKS-----
pIP1202_IncA/C_ INAEDFLPS--GVTPQKA--LQMLKDMIQKRSGRWIVTPVLEEDG---CLVTSDKAFDMIAGENIGISKHILCGMLSRQRRPLLKQRQKLYLEVNET-----
pAQU1 ISDEDFLPPQSDIDAEEA--IRLLKEMIKNQKGRWIVGPKIKEDG---CLVTSDKALEKVGTGECTNLSKSMRLRALLASGQRRPRMTIRQGNLRLEVE-----
PAGI-2_C_ AQEHPQLAAIARQEKLEP--WQWAQKRFEKLAARHRQASGLNIWT---CHVSGPRKSRQLHGYYLLTQPGALFERVPPNNPYLCLFNEEAGREVS LAAK-----
clc AREHPQVGM LAKQESQDD--WQWVQKRFEKLLQLHRH HINGLNVWA---CSVTGSRKSRQLHGYYLLRDPPLPFGKVPNNPYLSILQSI-----
PAGI-3_SG_ AQEHPQTAAALAKQDQVAD--WQWVQKRFEKLQMHRRQDNGLNIWT---CEVTGPRKSRRLHGYYLVSDPRHIFEEVPLNNPYLQLT-----
PAGI-4_C_ VQEHPEVEKLAQAKETAG--WKLVRQAFQKQGLHRHTSKNLNIWT---IKVSGPRKTKELKAYLLQDPKLIFFPVQPLDNPSLTVITDAEGGVE-----
pKLC102 VQEHPELEKLAQAKETT G--WKLVRQAFQKQGLHRHTSKNLNIWT---IKVSGPRKTKELKAYLLQDPKLIFFPVQPLDNPSLTVITDAEGDVE-----
Plasmid2_Ralme_ ASGKAKVARIDGKVSISK--RSLGNFGLASDTLVEHLRKGKHYLYK---VDGQNI LLVDEVGRLIAPETAS-----
pMOL28 ASGKAKVARIDGKVSISK--RSLGNFGLASDTLVEHLRKGKHYLYK---VDGQNI LLVDEVGRLIAPETAS-----
pHG1 AAGKTKVTRVEGKVAISK--RSLGNYGIASETLIENLRKFKHYLYK---IVGQDI LLVNEVGDLI LPASQABEA-----
pBVIE02 AGGKAKVRWAEKGLVVPK--RTIGGYGVASDTLIEHMRRRNLLL AN---DPTEVTLAPRIGELILERGA-----
pMAQU02 LDKNSLKKRRLYEK RAGDKRVTYTVLQRELEVLDI HQFGTDGQNI V T---VSVEGQRSKSELKVYLLNRACFESLRAFAANPAIKIHL-----
Rts1_IncT_ LSGGTLYKSIYPVDPNKS--YCTDSALYRAIASGILKQTFDNKD---VIAISGSAIRNMAKSLRIDTVTVRFLICYNFDSVSKRGSEHVLVDENIKPYMVS SHE--
pCAR1_IncP7_ SVIYCKLAELDWAIPHL SRLREADIPSELEQAVKSLIEKAVLEEIGSGSEVLSLTTYMLTNVAEQFGITSTSIENAVFCFRDAVKVAKRRKI FVRPLYEELPKK-----
Plasmid1_Rhofe_ AAWRDLWNRGQSSQEF LRTTEGLAVSYAVVNGSAIQLSKIMEALKG---AGYIEISNLNGTQRTLTPIEFPPKKTGLGLVLR TNFARKAGFILE-----
Plasmid2_Polsp_ AYRGDRVKVLDWGVAICVNWLTNTAGYDLADVLNPIERVGV IARN---PQEKGVALVSKVVFSDSPTPRMFAVAVKLDFAAKVGM AIDAKV-----
Plasmid1_Polsp_ RERGEQSTTMRLTDNGAAISIDFLGLTLMRSIPDNANEMASAGLIY---APPDRPGLKVHKVAIPEGSKAKAEIVISRYGCKKGLGL-----
chrom_Neigo_ LLVTPAVFRDYAGGVFNKSDTESLGLTQKGF EALFLHARTKKSSLHRVLT TNGSNRRLFYCYLIPEHNIQHIIQPGSRPQNNTDIKLDES DLLVMEQK-----
pPNAP01 MRLAFKFLPDQEMVDITG---AQLRFQGVVAKEMFELHSSSGFVHS---KVGNTLVRLNKELTAVVQNEFKNLGVTHA-----
Plasmid1_Shesp_ STLSQLKVATGNKSPKEKSKYPPELQVFIGWAMARAGKSGIDL RFG---VIRIQSFALTTYEQEVGLAKKEATSLKRTAGDNAS IATDSNQVAWVMVFETV GIEHE-----

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Fig. S1 (continued) Nonaka *et al.*

Table S1. List of MOB_H plasmids used for phylogenetic analysis of relaxase (TraI) ^a

| Name of plasmid or Mobile element (ME) | Accession number of plasmid or ME | Bacterial source | Relaxase name | Accession no of relaxase | Size of relaxase (aa) | MOB _H Group | Experimental evidence for transfer | Reference |
|--|-----------------------------------|---|-----------------------------------|------------------------------|-----------------------|------------------------|------------------------------------|------------------------|
| R478 | BX664015 | <i>Serratia marcescens</i> | hypothetical protein SMR0211 TraI | NP_941280 | 1050 | H11 | YES | Hedges et al., 1975 |
| R27 | AF250878 | <i>Salmonella typhi</i> | TraI | NP_058333 | 1011 | H11 | YES | Maher & Taylor, 1993 |
| Plasmid 1 | CP000470 | <i>Shewanella</i> sp. ANA-3 | Relaxase | YP_863780 | 941 | H11 | | |
| Rts1 | AP004237 | <i>Proteus vulgaris</i> | TraI | NP_640161 | 892 | H12 | YES | Terawaki, et al., 1967 |
| pCAR1 | AB088420 | <i>Pseudomonas resinovorans</i> | TraI | NP_758664 | 900 | H12 | YES | Shintani et al., 2006 |
| SXT | DQ180350 | <i>Vibrio cholerae</i> | TraI | ABA87024 | 716 | H12 | YES | Waldor et al., 1996 |
| R391 | AY090559 | <i>Providencia rettgeri</i> | TraI | AAM08003 | 716 | H12 | YES | Coetzee et al, 1972 |
| pAQU1 | AB571865 | <i>Photobacterium damsela</i> subsp. <i>damsela</i> | TraI | | 1025 | H12 | YES | This study |
| pIP1202 | CP000603 | <i>Yersinia pestis</i> biovar Orientalis str. IP275 | TraI | YP_001102157 | 992 | H12 | YES | Welch et al., 2007 |
| pAsa4 | CP000645 | <i>Aeromonas salmonicida</i> subsp. <i>salmonicida</i> A449 | Relaxase | YP_001144215 | 1006 | H12 | | |
| clc genomic island | AJ617740 | <i>Pseudomonas putida</i> | hypothetical protein | CAE92900 | 615 | H2 | YES | Mokross et al., 1990 |
| PAGI-2(C) | AF440523 | <i>Pseudomonas aeruginosa</i> strain C | conserved hypothetical protein | AAN62129 | 630 | H2 | | |
| PAGI-3(SG) | AF440524 | <i>Pseudomonas aeruginosa</i> strain SG17M | conserved hypothetical protein | AAN62266 | 600 | H2 | | |
| pKLC102 | AY257538 | <i>Pseudomonas aeruginosa</i> | TraI | AAP22591 | 639 | H2 | YES | Qiu et al., 2006 |
| PAGI-4(C) | AY258138 | <i>Pseudomonas aeruginosa</i> strain C | conserved hypothetical protein | AAP94681 | 608 | H2 | | |
| pMAQU02 | CP000516 | <i>Marinobacter aquaeolei</i> VT8 | Relaxase | YP_957144 | 624 | H2 | | |
| Chromosome | AY803022 | <i>Neisseria gonorrhoeae</i> | TraI | AAW83058 | 850 | H2 | | |
| Plasmid 1 | CP000317 | <i>Polaromonas</i> sp. JS666 | hypothetical protein | YP_551982 | 493 | H3 | | |
| Plasmid 1 | CP000268 | <i>Rhodospirillum rubrum</i> T118 | Relaxase | YP_515952 | 642 | H3 | | |

| | | | | | | | | |
|-----------|---------------------------|--|----------------------|------------------------------|-----|----|-----|------------------------|
| Plasmid 2 | CP000318 | <i>Polaromonas</i> sp. JS666 | hypothetical protein | YP_552224 | 611 | H3 | | |
| pPNAP01 | CP000530 | <i>Polaromonas naphthalenivorans</i> CJ2 | hypothetical protein | YP_973353 | 408 | H3 | | |
| pBVIE02 | CP000618 | <i>Burkholderia vietnamiensis</i> G4 | hypothetical protein | YP_001109781 | 441 | H3 | | |
| pHG1 | AY305378 | <i>Ralstonia eutropha</i> H16 | hypothetical protein | NP_943000 | 418 | H3 | YES | Friedrich et al., 1981 |
| Plasmid 2 | NC_007972 | <i>Ralstonia metallidurans</i> CH34 | hypothetical protein | YP_582117 | 413 | H3 | | |
| pMOL28 | X90708 | <i>Ralstonia metallidurans</i> CH34 | TraI | YP_161633 | 359 | H3 | YES | Mergeay et al., 1985 |

a This list is referred reference no.15.