```
LOCUS       RecA_mobile_element_Copy32783 bp   DNA     linear       20-
DEC-2013
DEFINITION  Vibrio cholerae strain S24.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Vibrio cholerae
  ORGANISM  Vibrio cholerae
            Unclassified.
REFERENCE   1  (bases 1 to 32783)
  AUTHORS   Rapa,R.A.
  TITLE     An integrated mobile genetic element in Vibrio cholerae
provides
            multi-pathway protection from DNA damage
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 32783)
  AUTHORS   Rapa,R.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-DEC-2013) The ithree institute, University of
            Technology, Sydney, Sydney, NSW 2007, Australia
COMMENT     ##Assembly-Data-START##
            Assembly Method       :: NA v. NA
            Sequencing Technology :: Sanger dideoxy sequencing; Illumina
            ##Assembly-Data-END##
FEATURES             Location/Qualifiers
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                     element"
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SVRLDIRRTGAIKEGDEVVGNETRIKVVKNKIAAPFKEANTQILYGKGFNRYGELIDL

GVKHKLVEKSGAWYSYQGDKIGQGKANACKFIEEHSHISQELEAKLREVLLSPVKAEG
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                     /gene="RME002"
                     /allele="ParB-like nuclease"
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IIIWGISDALAFAHTDTGNIRSRANVLEMAGVSVDARVLSQVAMLSKSFEMTANPYAF

RGTQGTSFQPAEILDYVQGKDELAWSVNLVASLAREHKQQIQAPQATLAFAHYLINEK

LKTYEGDEIPINPDMYISNIISGLGQTSIESIEYQVRDYLESIRKESTSYALLCRLSC

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VITLFAMMQISGFSHPFEKKRISKDLTQKNCRVRQELASYPVQVNLLFSPTEPLSQKA

CITLYKKYSQTESNIYAPLIESLNAELPLNTYVKEIADDIALDSFGGMKTSSVRLSVK

DPYVTTEATMIRLVLGAIGGADYQDKNKVDLFGSGPFSAEHIDKIKPYICIFMEAWLD

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                     /note="Proetin with DNA mismatch repair MutL domain"
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KYAATATWYTRRNNENARIVIDSSCIKTYKFQPLDEIEQIKDILNNGSGTSVFLSGIT

SEKSQKIPPIESIIDSLSNEFGWKLIVCSEINISVNGTLLTPPQHKLFQDTIEIDENQ

FSSNIIQWLNKPSGEKSYNYFRDLKDELQHRTLTGFNYKNDFFISGYIQSEWFNDFQA

TSSLNNDFFVDNEKTDGSKVLDKLLKELRKKTDEIYQKFLRERAAQLVDEFESKGYFP

VYKWEQDADRLVRIEHTKKLVTSICVADPSAFNGLKAKQTKIIIALLDRLSTSSENDS

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EGATIEGAKGQVDLFLARKMITVDHSTHDEFIKCTIIEIKRPSVALNKKHLAQAERYA

EVLDKHPAFNDERMRFDIVLVGTKISQNDTQINRRLKDLAGKGGAGLVSGADSRIRVY
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GGNRNVAKIKGHVGLKNKLYYFPAEGDQDIDTALDDVLADQMIAQNKIRYVLTTDFER

FLAWDTATNERLDIDFEVLHRNYSFFLPLVGLEKAILNSEKPADVKAAVKMGKLFDLI

RVHNHLNTPEDIHALNVFLTRLLFCLFAEDTGIFPKKSQFTSAIKSMTSEDGSDLDQF

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IDWHTVCPNSGNEEIYVIGNPPFKGHRGRSDNQRSEMVRVFKGFKSIGLLDYVACWFW

KGAEYIKGTNAELALVSTNSISQGEQVGTLWPSIFNLGVSIHLAYPTFTWANNAKDKA

AVHVVIIGLTAKSKKGLLFERVEEDWHSRVVDSISPYLLEGGKACVLAAKAPLNSSVP

PLLFGNMPNDGGYLLLNRSERDELIAKEPEAKKWIKKVLGADEFLNSKERWCLWLKDA

TKSDLASMPLVLQRIEKVAEKRRKSSDKGTQKLADRPHQFRDLNNPSKYILMPSVSSA

RRRYVPVGVFDESVISTNLNYIIPNGTMYEFAILSSLIHNDWMRLVAGRMKSDYRYSA

SVVYNTFPWITPSDAQRKELEVLAEDILFAREDYPGKTLAELYNPDSMPLGLLSAHQK
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     gene            9247..11268
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     CDS             9247..11268
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                     /allele="Hypothetical"
                     /note="Protein with helicase and phosphorothioation
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                     restriction enzyme domains"
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VSADENSRLGSLIDVLMKQSSAHIIAMTGSYFRGDTVPILLPEDEAKFTKVTYTYYEQ

LNGYKHLKTLGIGYHFYQGRYVNALPSVLDPTRKTIIHIPNVNSVESTKDKYTEVDSI

LEVLGDVMMQDPETGIYQVKCAKTGKTLLVANLVDDSDMRPKVQAYLRNIESAEQMDI

IIALGMAKEGFDWPYCEHVLTIGYRSSMTEIVQIIGRATRDSEGKSHAQFTNLIAQPD

AQDDDVKVSVNNMLKAITTSLLMEQILAPSIQFKPRSQWNGEDLPANTLIVDDTTTSV

SQKVLDILNRGKDEILSALLSKESVVKGAIADTMPAEVINEIELPSVIQTLYPDLEEH

EIEQIRTGVLHSLYIGQKGGLIDGKDLPEDAVIEDGGASYGNGHKSKDNGESGTSNQF
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                     /note="YeeC-like nuclease domain-containing protein"
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LAAQENVQRDKVEDKSLPTELDKSELVTSLDDIFDDDDDGLLEFDAPHLFTKTHVPAE

KKSQPNEIARRQPCAEFHRFSPIFETIQQEIRSGSASLERFRHELQMRVGDVFILNGL

IGYVHSAGERLEGYSSYNARLHLIFENGTEMHMLFQSLTHGLVRDERGCKIIREGESL

EPDDTPVPAGLVYVLATKSTDSALAPYKANLYKVGFTDGKVEERIKYAEKDKTFLEAP

VRVVMTTECYNIDAHKLETLIHGFLGHRRLNVTLKGHAGQYSPREWFYVPLNTVLEVI
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                     /note="Direct repeat for insertion of ISVuv4"
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                     /rpt_unit_seq="ccttaag"
     mobile_element  12877..14083
                     /mobile_element_type="insertion sequence:ISVvu4"
     gene            13036..14025
                     /gene="RME008"
                     /allele="Transposase for ISVvu4"
     CDS             13036..14025
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KGVGRIYQQTFVDTYSKVAFAKLYTTKTPITAADILNDKVLPFFEAHELPMLRILTDR

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YGSIEELQKDLDEWMDYYNNHRTHQGKMCCGRTPIETLEDGKSIWAEKNLAQI"
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     gene            complement(14114..14731)
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     CDS             complement(14114..14731)
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VENSPLTRGEVNEHVANASEEQVIIDQEQTLIRVSSALKLNDPKLRDVDPNVRSQAQQ

FEQVIDKINMMPKLNEERAIASETVKTKSTKAKQDYKNQRVIQGLGNVCEKTNQPIPQ
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     gene            complement(14734..15192)
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SIMKIDHQTKTPTPFFSVDSLVSCIGTDRKPFRELMADAADGEVIKINNKYLIRSDLT
                     KQFLQERSEQPRSCGERARIEATRSIVNEVGKLDYEQVIALLNNKVQGDE"
     gene            complement(15199..15609)
                     /gene="RME011"
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     CDS             complement(15199..15609)
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                     /allele="Hypothetical"
                     /note="DnaJ domain-containing protein"
                     /codon_start=1
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                     /product="Hypothetical Protein"

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EADLQVNLVRTSTDDMAYFKSENDRILFLLLEVDGKRRNQLLGITSEMYEDEDAAKKW
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     repeat_region   15890..15896
                     /note="Direct repeat for insertion of ISVuv4"
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                     /rpt_unit_seq="cctaaat"
     mobile_element  15897..17103
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     CDS             16056..17045
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YGSIEELQKDLDEWMDYYNNHRTHQGKMCCGRTPIETLEDGKSIWAEKNLAQI"
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     gene            complement(17211..17645)
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SoxR"
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     gene            17963..18844
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     CDS             17963..18844
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(DMT)
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FAIALLLLNRVQREHPLIVARNVLTMASIQLIIVALITTTRMTYKAPSPSIFIAVIYL

GVMCAGVVYYLYMTSVKNAGAVFTSMTNYLVPAVGVLIAALVTNESIQTTTWLALGII
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     gene            complement(19225..21105)
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MTSPDRLFKFDKFDSPNKRQAIGELLIGLSDFELYEKRVRLQSLKLALENRIKEIKTI

HSFLGGTIKSVSEINGEIEEKRKEIDALELEVESFSSPSEDGCTEDEVLKNLIVEVQE

ARGKYTASQQEIAKTSFEINDSQMFIESLSRRVKALKETQDTINALSDVAFNHCPACQ

TEVQARPTGCSLCGATKPESENNIDPTFKVRKEIEFQIAESILLIEKKQIRLDEQKVE

SNQLETKLGELERDLEIIRKPQRAVNIQLRQKLSEIGGLRNEIRTLNNSKKEFAKLYG

LYDERDTLQTDFNTLNDEITRLTQRMENELKAKKRKLSEATLSILKADAGHEEIFVDG

SKVEFDFAEDRVTIDDRALFSASSMVYLKNAFRLAMLKCSCEDSSYLYPRFLLMDNIE

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     gene            complement(22683..23939)
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                     /allele="Error prone, lesion bypass DNA polymerase V
                     (UmuC)"
     CDS             complement(22683..23939)
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                     (UmuC)"
                     /note="Error prone, lesion bypass DNA polymerase V
(UmuC)"
                     /codon_start=1
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                     /product="UmuC"

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SFLSFEHSFPAIRSLKEHGMKLRRAVWRECRLPVCVGFGQTLTLAKVANHAAKKIEGY

NGVCVLDSERERKAVLGQLHVSEVWGIGRKLTHRLEMMGINTALKLANYPPALIRKEF

NVEVERTVRELNGQKCKGWDAARADKKQIFSTRSAGQRITDLESLQQALCKHANIASF

KARKQKSLCRVMLCFANSSPFDSPPVARRAVHRFAYPTADVTLITQAASRLAEQLFQQ

DVRFYKIGVGLIDLVDGQHEQPDLFNLTPNNPKLMNVYDTLNNRFGNDAIFLAAQGIT
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     gene            complement(23939..24199)
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     CDS             complement(23939..24199)
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                     /allele="Error-prone repair protein (UmuD)"
                     /note="Error-prone repair protein UmuD"
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/translation="MQDVGIFDKDLLIVDRSLDVQDFDIIVANLNGEFICKQIDLNRR
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     CDS             24984..25739
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DLSRGTIAKKTGVSLDAIDGAIGFLQSTSLISKVEDKGFLANSIRRDLSERLHRYWVI
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     gene            complement(26001..27461)
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PYGKRYLHHDCIPHCESYGSRSPITDTAIESLYDDLDILEAEGDLYRFEFFSTLISLL

EATGIRVSEAANIDTHTIEVLRAQVNASLSGKAIGLDEIISLNKLTINTQSLQAAQAI

YRKSALGSANDQLIWIKIKTTKGKNKDKFRIIPISFTTAQYLIRFYDDYIVNELDRIS

KGLAKVNRAKFGKLFVHPSSHLPMSGIMISRLFYDVFSRKFKSKHKRSPHLFRHRFIT

LLVLQQLKALKTNIGGTQLAILILNRIKGLTGHASIKAMLHYVELAEAELYEDEDESE
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     gene            complement(27465..28181)
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LRQRSANNTLISLIKERDKYASRTLKSYYEDHQTELCKVRTVIKPALRETISNLNKLS
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     gene            complement(28165..30198)
                     /gene="RME022"
                     /allele="Phage integrase"
     CDS             complement(28165..30198)
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domain
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                     /product="Phage integrase"

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