



Letter to the Editor

Detection of OXA-58-producing *Acinetobacter bereziniae* in Brazil

Sir,

Acinetobacter bereziniae, formerly *Acinetobacter* genospecies 10, has gained attention due to its emergence as a causative agent of healthcare-associated infection. Importantly, *A. bereziniae* isolates harbouring genes encoding resistance to multiple antimicrobial agents, including carbapenems, located mainly on mobile genetic elements, have been increasingly reported [1].

The widespread mechanism of carbapenem resistance in *Acinetobacter* spp. is mediated by the production of carbapenem-hydrolysing class D β -lactamases (CHDLs). In particular, carbapenem resistance in *A. bereziniae* has been previously associated with the expression of metallo- β -lactamases (IMP, VIM, SIM and NDM types) or overexpression of variants of the intrinsic OXA-228-like [1]. To date, the *bla*_{OXA-58} gene has only been detected in one *A. bereziniae* isolate each in Ireland and Portugal [1,2]. In Brazil, the *bla*_{OXA-58} gene has been detected sporadically in *A. baumannii* and *A. seifertii*. Herein, we report the first detection of an OXA-58-producing *A. bereziniae* (Ac374/14) in Brazil.

Strain Ac374/14 was isolated from an endotracheal aspirate sample (10^6 CFU/mL) obtained from an 83-year-old female patient diagnosed with ventilator-associated pneumonia in August 2014. Species identification was confirmed by *rpoB* gene sequencing [3]. Antimicrobial susceptibility testing was performed according to Clinical and Laboratory Standards Institute (CLSI) M100-S28 and M07-A9 guidelines. The antimicrobial susceptibility profile is reported in Table 1, demonstrating a multidrug-resistant phenotype. Carbapenemase production was confirmed by the CarbAcinet NP test. Multiplex PCR assay revealed that the isolate possessed a *bla*_{OXA-58-like} gene but was negative for other CHDL genes analysed [4]. Nucleotide analysis of this amplicon showed 100% identity with a known *bla*_{OXA-58} sequence (GenBank accession no. **CP028560.1**/*Acinetobacter* sp.).

Whole-genome sequencing of *A. bereziniae* Ac374/14 was performed on an Illumina MiSeq platform (Illumina Inc., San Diego, CA, USA) using a 300-bp paired-end library, which generated 4 663 604 reads. These reads were subjected to trimming and filtering using CLC Genomics Workbench software v.11.0.1, in which reads with an average Phred quality of <30 and with one or more ambiguities were removed. Finally, reads with a size of <50 bp as well as the last 10 nucleotides of the 3' end of each read were removed. After trimming, 4 660 646 reads were used in the assembly, which generated a genome coverage corresponding to ca. 233-fold based on the reference genome size of 4 509 124 bp for *A. bereziniae* strain XH901 (accession no. **CP018259.1**). The genome of

Ac374/14 was assembled using CLC Genomics Workbench software v.11.0.1 and a total of 242 contigs were generated, comprising a total length of 4 837 458 bp with coverage depth of 160, an N_{50} value of 45.186, a maximum length of 154 002 bp, a minimum length of 579 bp and a G + C content of 38.1%. Annotation of the draft assembly was performed using Rapid Annotation using Subsystem Technology (RAST) v.2.0 (available from rast.nmpdr.org/), which included 4572 coding genes and 77 RNA genes.

The acquired antimicrobial resistance genes were identified using ResFinder 3.0 (<https://cge.cbs.dtu.dk/services/ResFinder/>) available from the Center for Genomic Epidemiology. Resistome analysis revealed the presence of genes encoding resistance to β -lactams (*bla*_{OXA-58}, *bla*_{OXA-257} and *bla*_{CARB-49}), aminoglycosides [*aph* (3')-VIa, *ant*(2'')-Ia], phenicols (*floR*) and sulfonamides (*sullI*). Furthermore, according to RAST, point mutations in the *parC*, *parE*, *gyrA* and *gyrB* genes and the presence of *bla*_{AmpC} gene responsible for fluoroquinolone and intrinsic β -lactam resistance, respectively, were observed. Moreover, efflux pumps families [resistance-nodulation-cell division (RND), major facilitator superfamily (MFS), multidrug and toxic compound extrusion (MATE) and ATP-binding cassette (ABC) superfamily] were identified.

Based on in silico analysis, the *bla*_{OXA-58} gene was found to be flanked on either side by insertion sequence *IS**Aba3*. However, the upstream *IS**Aba3* sequence was interrupted by *IS**Aba125*, resembling that previously reported in *Acinetobacter* genospecies 3 [5]. The downstream *IS**Aba3* sequence was followed *ampC* and *rep* sequences; the presence of a *rep* sequence indicates that the *bla*_{OXA-58} gene may be located in a plasmid (Supplementary Fig. S1).

A cluster of genes associated with colicin E (*crbC*-like, *creB*, *creC* and *creD*), colicin V and bacteriocin production (*dedA*, *dedE*, R1, R3, R4, R5, R8 and *purF*) as well as genes associated with invasion and intercellular resistance, including active virulence operons involved in protein synthesis (rv0682, rv0683, rv0684, rv0685, rv1641, rv1642 and rv1643), DNA transcription (rv0667 and rv0668), quinolinate biosynthesis (rv1594, rv1595 and rv1596) and internalin-like protein were found. The virulence factors detected in a manual inspection of the 242 contigs are included in Table 1. In addition, the presence of adhesin genes *ompA* and *bap* may be associated with the strong biofilm-producer phenotype of *A. bereziniae* strain Ac374/14. Biofilm formation was evaluated using the crystal violet staining method in polystyrene plates following 24 h of incubation at 37 °C, using *A. baumannii* ATCC 19606 and brain-heart infusion broth as positive and negative controls, respectively.

The draft genome sequence of *A. bereziniae* Ac374/14 has been deposited in DDBJ/EMBL/GenBank under accession no. **QWV01000000**. The version described in this paper is the first version (**QWV01000000**).

Table 1Phenotypic and molecular characteristics of extensively drug-resistant *Acinetobacter bereziniae* strain Ac374/14.

Phenotypic characteristics	Antimicrobial susceptibility profile	R: TZP, SXT, IPM, MEM, CRO, FEP, GEN, AMK, CIP I: CAZ, LVX S: SAM, COL, PMB, TGC
Molecular characteristics	Carbapenemase production	Positive
	Biofilm formation capability	Strong biofilm producer
Molecular characteristics	Resistance genes	β -Lactams: <i>bla</i> _{OXA-58} , <i>bla</i> _{OXA-257} , <i>bla</i> _{CARB-49} , <i>ampC</i> Aminoglycosides: <i>aph(3')-VIa</i> , <i>ant(2'')-Ia</i> Phenicol: <i>floR</i> Sulfonamides: <i>sullI</i>
	Mutations in topoisomerases	GyrA: Ser84Phe GyrB: Ile171Val ParC: Ser84Phe ParE: Asn532Ala
Molecular characteristics	Efflux systems	ABC-type efflux pump (MacAB–TolC tripartite efflux pump) RND-type efflux pumps (CmeABC, AdeABC and AdelJK) AcrB multidrug efflux pump MATE family efflux pumps MFS transporters
	Virulence factors	Adhesin Alginate biosynthesis protein Alkaline phosphatase family protein BapA prefix-like domain-containing protein BrnT family toxin DotU family type IV/VI secretion system protein Haemolysin III family protein OmpA family protein Patatin-like phospholipase family protein Phospholipase (C and D) ShlB/FhaC/HecB family haemolysin secretion/activation protein Type I secretion C-terminal target domain-containing protein Type II/IV secretion system protein Type II secretion system F family protein Type II secretion system protein (GspD, GspE, GspF, GspG, GspI, GspJ) Type II toxin–antitoxin system (HipA family toxin, RelB/DinJ family antitoxin, VapC family toxin, YafQ family toxin) Type VI secretion system-associated protein (Hcp, TagF, TssA, TssE, TssF, TssG, TssH, TssK, TssM, VgrG) Zeta toxin

R, resistant; I, intermediate; S, susceptible; TZP, piperacillin/tazobactam; SXT, trimethoprim/sulfamethoxazole; IPM, imipenem; MEM, meropenem; CRO, ceftriaxone; FEP, cefepime; GEN, gentamicin; AMK, amikacin; CIP, ciprofloxacin; CAZ, ceftazidime; LVX, levofloxacin; SAM, ampicillin/sulbactam; COL, colistin; PMB, polymyxin B; TGC, tigecycline; ABC, ATP-binding cassette; RND, resistance–nodulation–cell division; MATE, multidrug and toxic compound extrusion; MFS, major facilitator superfamily.

Funding

This work was supported by the Programa de Pesquisa para o SUS: Gestão Compartilhada em Saúde (PPSUS)/Fundação Araucária/SESA-PR/MS/CNPq [agreement 035/2017 - protocol 48.045 - PPSUS / 2015]; and Pro-Reitoria de Pesquisa e Pós Graduação (PROPPG) of the Universidade Estadual de Londrina (UEL). This work was part of the MSc dissertation of LSF.

Competing interests

None declared.

Ethical approval

Not required.

Appendix A. Supplementary data

Supplementary material related to this article can be found, in the online version, at doi:<https://doi.org/10.1016/j.jgar.2019.08.011>.

References

- [1] Grosso F, Silva L, Sousa C, Ramos H, Quineteira S, Peixe L. Extending the reservoir of *bla*_{IMP-5}: the emerging pathogen *Acinetobacter bereziniae*. *Future Microbiol* 2015;10:1609–13, doi:<http://dx.doi.org/10.2217/fmb.15.88>.

- [2] Boo TW, Crowley B. Detection of *bla*_{OXA-58} and *bla*_{OXA-23-like} genes in carbapenem-susceptible *Acinetobacter* clinical isolates: should we be concerned? *J Med Microbiol* 2009;58:839–41, doi:<http://dx.doi.org/10.1099/jmm.0.008904-0>.
- [3] La Scola B, Gundi VA, Khamis A, Raoult D. Sequencing of the *rpoB* gene and flanking spacers for molecular identification of *Acinetobacter* species. *J Clin Microbiol* 2006;44:827–32, doi:<http://dx.doi.org/10.1128/JCM.44.3.827-832.2006>.
- [4] Woodford N, Ellington MJ, Coelho JM, Turton JF, Ward ME, Brown S, et al. Multiplex PCR for genes encoding prevalent OXA carbapenemases in *Acinetobacter* spp. *Int J Antimicrob Agents* 2006;7:351–3, doi:<http://dx.doi.org/10.1016/j.ijantimicag.2006.01.004>.
- [5] Evans BA, Hamouda A, Townner KJ, Amyes SGB. Novel genetic context of multiple *bla*_{OXA-58} genes in *Acinetobacter* genospecies 3. *J Antimicrob Chemother* 2010;65:1586–8, doi:<http://dx.doi.org/10.1093/jac/dkr334>.

Larissa dos Santos Fávoro
Suelen Balero de Paula-Petroli
Priscila Romanin

Laboratório de Estudos Moleculares e Resistência aos Antimicrobianos, Departamento de Patologia, Análises Clínicas e Patológicas, Universidade Estadual de Londrina - UEL, Londrina - PR, Brazil

Eliandro dos Reis Tavares
Laboratório de Biologia Molecular de Microrganismos, Departamento de Microbiologia, Universidade Estadual de Londrina - UEL, Londrina - PR, Brazil

Renan Augusto Ribeiro
Mariangela Hungria
Laboratório de Biotecnologia do Solo, EMPRAPA Soja, Londrina - PR, Brazil

Admilton Gonçalves de Oliveira Junior
Laboratório de Biotecnologia Microbiana, Departamento de Microbiologia, Universidade Estadual de Londrina - UEL, Londrina - PR, Brazil

Lucy Megumi Yamauchi
Sueli Fumie Yamada-Ogatta
Laboratório de Biologia Molecular de Microrganismos, Departamento de Microbiologia, Universidade Estadual de Londrina - UEL, Londrina - PR, Brazil

Floristher Elaine Carrara-Marroni*
Laboratório de Estudos Moleculares e Resistência aos Antimicrobianos, Departamento de Patologia, Análises Clínicas e Patológicas, Universidade Estadual de Londrina - UEL, Londrina - PR, Brazil

* Corresponding author. Present address: Laboratório de Estudos Moleculares e Resistência aos Antimicrobianos, Ambulatório de Especialidades do Hospital Universitário de Londrina – UEL, Rodovia Celso Garcia Cid, PR 445 Km 179, Campus Universitário, Londrina - PR, 86051-990, Brazil.
E-mail address: floristher@uel.br (F. Carrara-Marroni).

Received 6 May 2019

Available online 23 August 2019

Supplementary Fig. S1. Overview of the genetic context of the *bla*_{OXA-58} gene in *Acinetobacter bereziniae* strain Ac374/14.

<u>JQ690825_ISAba125</u>	GTTTAATTAGGCAATATTTACCTAAAGGGATTGATTTAAATCAGGCAGATCAGCATTATT	60
AC374_contig_122	GTTTAATTAGGCAATATTTACCTAAAGGGATTGATTTAAATCAGGCAGATCAGCATTATT	60
AC374_contig_187	-----	0
AC374_contig_241	-----	0

<u>JQ690825_ISAba125</u>	TAAATCAAGTTGCCATGTCACCTGAATACTCGTCCTAGAAAAGCGTTAGATTGGCTTACAC	120
AC374_contig_122	TAAATCAAGTTGCCATGTCACCTGAATACTCGTCCTAGAAAAGCGTTAGATTGGCTTACAC	120
AC374_contig_187	-----	0
AC374_contig_241	-----	0

<u>JQ690825_ISAba125</u>	CATTAGAGAAAATTTGCTCAGCTTGTGATTATCATAAGACTTTTCAAACGTGCGCACCTC	180
AC374_contig_122	CATTAGAGAAAATTTGCTCAGCTTGTGATTATCATAAGACTTTTCAAACGTGCGCACCTC	180
AC374_contig_187	-----ACCTC	5
AC374_contig_241	-----TC	2

<u>JQ690825_ISAba125</u>	ATGTTTGAATTC-----	192
AC374_contig_122	ATGTTTGAATTCGCCCCATTTTCTTTATACTATCACTGAGGCAGGTTGGACATTTGATT	240
AC374_contig_187	ATGTTTGAATTCGCCCCATTTTCTTTATACTATCACTGAGGCAGGTTGGACATTTGATT	65
AC374_contig_241	ATGTTTGAATTCGCCCCATTTTCTTTATACTATCACTGAGGCAGGTTGGACATTTGATT	62
<u>GU911349_ISAba3</u>	-----GCCCCATTTTCTTTATACTATCACTGAGGCAGGTTGGACATTTGATT	48

AC374_contig_122	GCTAGAGTTATTTGCATTTCTCTATTTTATCAAAATCCAATCGGCTTTTCTTCAGCATA	300
AC374_contig_187	GCTAGAGTTATTTGCATTTCTCTATTTTATCAAAATCCAATCGGCTTTTCTTCAGCATA	125
AC374_contig_241	GCTAGAGTTATTTGCATTTCTCTATTTTATCAAAATCCAATCGGCTTTTCTTCAGCATA	122
<u>GU911349_ISAba3</u>	GCTAGAGTTATTTGCAT-----	65

AC374_contig_122	CTTTTGA AACACTACCAAATTTTAAAGTTGTATATCATGAAATTATTA AAAATATTGAG	360
AC374_contig_187	CTTTTGA AACACTACCAAATTTTAAAGTTGTATATCATGAAATTATTA AAAATATTGAG	185
AC374_contig_241	CTTTTGA AACACTACCAAATTTTAAAGTTGTATATCATGAAATTATTA AAAATATTGAG	182
<u>GU911349_bla_{OXA-58}</u>	-----ATGAAATTATTA AAAATATTGAG	23

AC374_contig_122	TTTAGTTTGCTTAAGCATAAGTATTGGGGCTTGTGCTGAGCATAGTATGAGTCGAGCAA	420
AC374_contig_187	TTTAGTTTGCTTAAGCATAAGTATTGGGGCTTGTGCTGAGCATAGTATGAGTCGAGCAA	245
AC374_contig_241	TTTAGTTTGCTTAAGCATAAGTATTGGGGCTTGTGCTGAGCATAGTATGAGTCGAGCAA	242
<u>GU911349_bla_{OXA-58}</u>	TTTAGTTTGCTTAAGCATAAGTATTGGGGCTTGTGCTGAGCATAGTATGAGTCGAGCAA	83

AC374_contig_122	AACAAGTACAATTCCACAAGTGAATAACTCAATCATCGATCAGAATGTTCAAGCGCTTTT	480
AC374_contig_187	AACAAGTACAATTCCACAAGTGAATAACTCAATCATCGATCAGAATGTTCAAGCGCTTTT	305
AC374_contig_241	AACAAGTACAATTCCACAAGTGAATAACTCAATCATCGATCAGAATGTTCAAGCGCTTTT	302
<u>GU911349_bla_{OXA-58}</u>	AACAAGTACAATTCCACAAGTGAATAACTCAATCATCGATCAGAATGTTCAAGCGCTTTT	143

AC374_contig_122	TAATGAAATCTCAGCTGATGCTGTGTTTGTACATATGATGGTCAAAAATATTA AAAAATA	540
AC374_contig_187	TAATGAAATCTCAGCTGATGCTGTGTTTGTACATATGATGGTCAAAAATATTA AAAAATA	365
AC374_contig_241	TAATGAAATCTCAGCTGATGCTGTGTTTGTACATATGATGGTCAAAAATATTA AAAAATA	362
<u>GU911349_bla_{OXA-58}</u>	TAATGAAATCTCAGCTGATGCTGTGTTTGTACATATGATGGTCAAAAATATTA AAAAATA	203

AC374_contig_122	TGGCACGCATTTAGACCGAGCAAAAACAGCTTATATTCCTGCATCTACATTTAAAATTGC	600
AC374_contig_187	TGGCACGCATTTAGACCGAGCAAAAACAGCTTATATTCCTGCATCTACATTTAAAATTGC	425
AC374_contig_241	TGGCACGCATTTAGACCGAGCAAAAACAGCTTATATTCCTGCATCTACATTTAAAATTGC	422
<u>GU911349_bla_{OXA-58}</u>	TGGCACGCATTTAGACCGAGCAAAAACAGCTTATATTCCTGCATCTACATTTAAAATTGC	263

AC374_contig_122	CAATGCACTAATTGGTTTAGAAAATCATAAAGCAACATCTACAGAAATATTTAAGTGGGA	660
AC374_contig_187	CAATGCACTAATTGGTTTAGAAAATCATAAAGCAACATCTACAGAAATATTTAAGTGGGA	485
AC374_contig_241	CAATGCACTAATTGGTTTAGAAAATCATAAAGCAACATCTACAGAAATATTTAAGTGGGA	482
<u>GU911349_bla_{OXA-58}</u>	CAATGCACTAATTGGTTTAGAAAATCATAAAGCAACATCTACAGAAATATTTAAGTGGGA	323

AC374_contig_122	TGGAAAGCCACGTTTTTTTAAAGCATGGGACAAAGATTTTACTTTGGGCGAAGCCATGCA	720
AC374_contig_187	TGGAAAGCCACGTTTTTTTAAAGCATGGGACAAAGATTTTACTTTGGGCGAAGCCATGCA	545
AC374_contig_241	TGGAAAGCCACGTTTTTTTAAAGCATGGGACAAAGATTTTACTTTGGGCGAAGCCATGCA	542
<u>GU911349_bla_{OXA-58}</u>	TGGAAAGCCACGTTTTTTTAAAGCATGGGACAAAGATTTTACTTTGGGCGAAGCCATGCA	383

AC374_contig_122	***** AGCATCTACAGTGCCTGTATATCAAGAATTGGCACGTCGTATTGGTCCAAGCTTAATGCA	780
AC374_contig_187	AGCATCTACAGTGCCTGTATATCAAGAATTGGCACGTCGTATTGGTCCAAGCTTAATGCA	605
AC374_contig_241	AGCATCTACAGTGCCTGTATATCAAGAATTGGCACGTCGTATTGGTCCAAGCTTAATGCA	602
<u>GU911349_bla_{OXA-58}</u>	AGCATCTACAGTGCCTGTATATCAAGAATTGGCACGTCGTATTGGTCCAAGCTTAATGCA *****	443
AC374_contig_122	AAGTGAATTGCAACGTATTGGTTATGGCAATATGCAATAGGCACGGAAGTTGATCAATT	840
AC374_contig_187	AAGTGAATTGCAACGTATTGGTTATGGCAATATGCAATAGGCACGGAAGTTGATCAATT	665
AC374_contig_241	AAGTGAATTGCAACGTATTGGTTATGGCAATATGCAATAGGCACGGAAGTTGATCAATT	662
<u>GU911349_bla_{OXA-58}</u>	AAGTGAATTGCAACGTATTGGTTATGGCAATATGCAATAGGCACGGAAGTTGATCAATT *****	503
AC374_contig_122	TTGGTTGAAAGGGCCTTTGACAATTACACCTATACAAGAAGTAAAGTTTGTGTATGATTT	900
AC374_contig_187	TTGGTTGAAAGGGCCTTTGACAATTACACCTATACAAGAAGTAAAGTTTGTGTATGATTT	725
AC374_contig_241	TTGGTTGAAAGGGCCTTTGACAATTACACCTATACAAGAAGTAAAGTTTGTGTATGATTT	722
<u>GU911349_bla_{OXA-58}</u>	TTGGTTGAAAGGGCCTTTGACAATTACACCTATACAAGAAGTAAAGTTTGTGTATGATTT *****	563
AC374_contig_122	AGCCCAAGGGCAATTGCCTTTTAAACCTGAAGTTCAGCAACAAGTAAAAGAGATGTTGTA	960
AC374_contig_187	AGCCCAAGGGCAATTGCCTTTTAAACCTGAAGTTCAGCAACAAGTAAAAGAGATGTTGTA	785
AC374_contig_241	AGCCCAAGGGCAATTGCCTTTTAAACCTGAAGTTCAGCAACAAGTAAAAGAGATGTTGTA	782
<u>GU911349_bla_{OXA-58}</u>	AGCCCAAGGGCAATTGCCTTTTAAACCTGAAGTTCAGCAACAAGTAAAAGAGATGTTGTA *****	623
AC374_contig_122	TGTAGAGCGCAGAGGGGAGAATCGTCTATATGCTAAAAGTGGCTGGGGAATGGCTGTAGA	1020
AC374_contig_187	TGTAGAGCGCAGAGGGGAGAATCGTCTATATGCTAAAAGTGGCTGGGGAATGGCTGTAGA	845
AC374_contig_241	TGTAGAGCGCAGAGGGGAGAATCGTCTATATGCTAAAAGTGGCTGGGGAATGGCTGTAGA	842
<u>GU911349_bla_{OXA-58}</u>	TGTAGAGCGCAGAGGGGAGAATCGTCTATATGCTAAAAGTGGCTGGGGAATGGCTGTAGA *****	683
AC374_contig_122	CCCGCAAGTGGGTTGGTATGTGGGTTTTGTTGAAAAGGCAGATGGGCAAGTGGTGGCATT	1080
AC374_contig_187	CCCGCAAGTGGGTTGGTATGTGGGTTTTGTTGAAAAGGCAGATGGGCAAGTGGTGGCATT	905
AC374_contig_241	CCCGCAAGTGGGTTGGTATGTGGGTTTTGTTGAAAAGGCAGATGGGCAAGTGGTGGCATT	902
<u>GU911349_bla_{OXA-58}</u>	CCCGCAAGTGGGTTGGTATGTGGGTTTTGTTGAAAAGGCAGATGGGCAAGTGGTGGCATT *****	743
AC374_contig_122	TGCTTTAAATATGCAATGAAAGCTGGTGATGATATTGCTCTACGTAAACAATTGTCTTT	1140
AC374_contig_187	TGCTTTAAATATGCAATGAAAGCTGGTGATGATATTGCTCTACGTAAACAATTGTCTTT	965
AC374_contig_241	TGCTTTAAATATGCAATGAAAGCTGGTGATGATATTGCTCTACGTAAACAATTGTCTTT	962
<u>GU911349_bla_{OXA-58}</u>	TGCTTTAAATATGCAATGAAAGCTGGTGATGATATTGCTCTACGTAAACAATTGTCTTT *****	803
AC374_contig_122	AGATGTGCTAGATAAGTTGGGTGTTTTTCATTATTTATAA	1200
AC374_contig_187	AGATGTGCTAGATAAGTTGGGTGTTTTTCATTATTTATAA	1025
AC374_contig_241	AGATGTGCTAGATAAGTTGGGTGTTTTTCATTATTTATAA	1022
<u>GU911349_bla_{OXA-58}</u>	AGATGTGCTAGATAAGTTGGGTGTTTTTCATTATTTATAA----- *****	843
AC374_contig_122	ATCTATTTTTGGTAGTGTTCAAAAAGTATGCTGAAGAAAAAGCCGATTGGATTTTGATA	1260
AC374_contig_187	ATCTATTTTTGGTAGTGTTCAAAAAGTATGCTGAAGAAAAAGCCGATTGGATTTTGATA	1085
AC374_contig_241	ATCTATTTTTGGTAGTGTTCAAAAAGTATGCTGAAGAAAAAGCCGATTGGATTTTGATA	1082
AC374_contig_122	AAATAGAGAAATGCAATAAECTCTAGCAATCAAATGTCCAACCTGCCTCAGTGATAGTAT	1320
AC374_contig_187	AAATAGAGAAATGCAATAAECTCTAGCAATCAAATGTCCAACCTGCCTCAGTGATAGTAT	1145
AC374_contig_241	AAATAGAGAAATGCAATAAECTCTAGCAATCAAATGTCCAACCTGCCTCAGTGATAGTAT	1142
<u>KY202456_ISAba3</u>	-----ATGCAATAAECTCTAGCAATCAAATGTCCAACCTGCCTCAGTGATAGTAT *****	50
AC374_contig_122	AAAGAAAAATGGTATCAAAGTAGATGGGAAACAAAACCTATCAGTGCAAAGACTGTAAACG	1380
AC374_contig_187	AAAGAAAAATGGTATCAAAGTAGATGGGAAACAAAACCTATCAGTGCAAAGACTGTAAACG	1205
AC374_contig_241	AAAGAAAAATGGTATCAAAGTAGATGGGAAACAAAACCTATCAGTGCAAAGACTGTAAACG	1202
<u>KY202456_ISAba3</u>	AAAGAAAAATGGTATCAAAGTAGATGGGAAACAAAACCTATCAGTGCAAAGACTGTAAACG *****	110
AC374_contig_122	TCAGTTTATTGGTGATCATGCACCTGAGCTATCTAGGATGTAAGTCAGGTATTACTCGTAA	1440
AC374_contig_187	TCAGTTTATTGGTGATCATGCACCTGAGCTATCTAGGATGTAAGTCAGGTATTACTCGTAA	1265
AC374_contig_241	TCAGTTTATTGGTGATCATGCACCTGAGCTATCTAGGATGTAAGTCAGGTATTACTCGTAA	1262
<u>KY202456_ISAba3</u>	TCAGTTTATTGGTGATCATGCACCTGAGCTATCTAGGATGTAAGTCAGGTATTACTCGTAA *****	170
AC374_contig_122	AATATTACAGTTGATGGTCAGAGGCAGCGGTATACGAGATATTGCTGAAGTTGAGCGCAT	1500
AC374_contig_187	AATATTACAGTTGATGGTCAGAGGCAGCGGTATACGAGATATTGCTGAAGTTGAGCGCAT	1325
AC374_contig_241	AATATTACAGTTGATGGTCAGAGGCAGCGGTATACGAGATATTGCTGAAGTTGAGCGCAT	1322
<u>KY202456_ISAba3</u>	AATATTACAGTTGATGGTCAGAGGCAGCGGTATACGAGATATTGCTGAAGTTGAGCGCAT *****	230

AC374_contig_122	***** CAGTATCGGTAAGTTTACGTACTTTAACTGAATCAACCTATGAAATTCAGCCTCAGCA	1560
AC374_contig_187	CAGTATCGGTAAGTTTACGTACTTTAACTGAATCAACCTATGAAATTCAGCCTCAGCA	1385
AC374_contig_241	CAGTATCGGTAAGTTTACGTACTTTAACTGAATCAACCTATGAAATTCAGCCTCAGCA	1382
<u>KY202456_ISAb3</u>	CAGTATCGGTAAGTTTACGTACTTTAACTGAATCAACCTATGAAATTCAGCCTCAGCA *****	290
AC374_contig_122	AAGTCATTATGAATCTCTCGAAGTAGATGAGTTCCTGGAATTTTGTGGAAATAAAAAGAA	1620
AC374_contig_187	AAGTCATTATGAATCTCTCGAAGTAGATGAGTTCCTGGAATTTTGTGGAAATAAAAAGAA	1445
AC374_contig_241	AAGTCATTATGAATCTCTCGAAGTAGATGAGTTCCTGGAATTTTGTGGAAATAAAAAGAA	1442
<u>KY202456_ISAb3</u>	AAGTCATTATGAATCTCTCGAAGTAGATGAGTTCCTGGAATTTTGTGGAAATAAAAAGAA *****	350
AC374_contig_187	TAAACAATGGCTTATTTTGTTCAAAAGTCATATTTTACCTCGGAGAAACCGGACATTTT	1505
AC374_contig_241	TAAACAATGGCTTATTTTGTTCAAAAGTCATATTTTACCTCGGAGAAACCGGACATTTT	1502
<u>KY202456_ISAb3</u>	TAAACAATGGCTTATTTTGTTCAAAAGTCATATTTTACCTCGGAGAAACCGGACATTTT *****	410
AC374_contig_187	TATTGGTGAGAATATAGACACTTTAAATGGGTTCTAACTACTCTCGTTTCGTATAACAGCC	1565
AC374_contig_241	TATTGGTGAGAATATAGACACTTTAAATGGGTTCTAACTACTCTCGTTTCGTATAACAGCC	1562
<u>KY202456_ISAb3</u>	TATTGGTGAGAATATAGACACTTTAAATGGGTTCTAA ----- *****	447
AC374_contig_187	ATTATGTTAAATAGCTGTTGGGCTAGATGATTTTTATATAAGAAGTTATTTAACAAAAAT	1625
AC374_contig_241	ATTATGTTAAATAGCTGTTGGGCTAGATGATTTTTATATAAGAAGTTATTTAACAAAAAT	1622
<u>NG_055474_ampC</u>	-----ATGATTTTTATATAAGAAGTTATTTAACAAAAAT *****	34
AC374_contig_187	TAATACATATGTAATATTTAGTATATGATATTATATGTTCCATATTTTTTAAAGAAATTT	1685
AC374_contig_241	TAATACATATGTAATATTTAGTATATGATATTATATGTTCCATATTTTTTAAAGAAATTT	1682
<u>NG_055474_ampC</u>	TAATACATATGTAATATTTAGTATATGAGATTATATGTTCCATATTTTTTAAAGAAATTT *****	94
AC374_contig_187	AACTTAATGTTTTTAAATCAGAAATATTTTTTCAAGCAAGCTTCATTACGATGGTTATC	1745
AC374_contig_241	AACTTAATGTTTTTAAATCAGAAATATTTTTTCAAGCAAGCTTCATTACGATGGTTATC	1742
<u>NG_055474_ampC</u>	AACTTAATGTTTTTAAATCAGAAATATTTTTTCAAGCAAGCTTCATTACGATGGTTATC *****	154
AC374_contig_187	GGTTTTGGTATGAATTTAAATGCAAGTGAAGTCAGTCAAAATGAGCAAAATATTGAAAAA	1805
AC374_contig_241	GGTTTTGGTATGAATTTAAATGCAAGTGAAGTCAGTCAAAATGAGCAAAATATTGAAAAA	1802
<u>NG_055474_ampC</u>	GGTTTTGGTATGAATTTAAATGCAAGTGAAGTCAGTCAAAATGAGCAAAATATTGAAAAA *****	214
AC374_contig_187	GTTGTTACCCAATCATTTAAGCCACTTATGGATGAGTATGGTGTAGCTGGTATGGCTATA	1865
AC374_contig_241	GTTGTTACCCAATCATTTAAGCCACTTATGGATGAGTATGGTGTAGCTGGTATGGCTATA	1862
<u>NG_055474_ampC</u>	GTTGTTACCCAATCATTTAAGCCACTTATGGATGAGTATGGTGTAGCTGGTATGGCTATA *****	274
AC374_contig_187	GGCGTAATTTACAACGGTAAAAGTTATGAAAAATATTATGGTGTCCGATCTAAAGATACA	1925
AC374_contig_241	GGCGTAATTTACAACGGTAAAAGTTATGAAAAATATTATGGTGTCCGATCTAAAGATACA	1922
<u>NG_055474_ampC</u>	GGCGTAATTTACAACGGTAAAAGTTATGAAAAATATTATGGTGTCCGATCTAAAGATACA *****	334
AC374_contig_187	AATGAAAGCGTAAATAGTCAGACACTTTTTGAGTTAGGTTCTTTAAGTAAAACTTTACT	1985
AC374_contig_241	AATGAAAGCGTAAATAGTCAGACACTTTTTGAGTTAGGTTCTTTAAGTAAAACTTTACT	1982
<u>NG_055474_ampC</u>	AATGAAAGCGTAAATAGTCAGACACTTTTTGAGTTAGGTTCTTTAAGTAAAACTTTACT *****	394
AC374_contig_187	GCTATTTACGGAACATATGCCAATAATCAAGGTAAAATATCGTTCAACGATCATCCTAGT	2045
AC374_contig_241	GCTATTTACGGAACATATGCCAATAATCAAGGTAAAATATCGTTCAACGATCATCCTAGT	2042
<u>NG_055474_ampC</u>	GCTATTTACGGAACATATGCCAATAATCAAGGTAAAATATCGTTCAACGATCATCCTAGT *****	454
AC374_contig_187	AAATACGTCCCTGCTTTAAAAAATTCAGAAATTGATAAGGTAAATTTATTAGAGTTATTA	2105
AC374_contig_241	AAATACGTCCCTGCTTTAAAAAATTCAGAAATTGATAAGGTAAATTTATTAGAGTTATTA	2102
<u>NG_055474_ampC</u>	AAATACGTCCCTGCTTTAAAAAATTCAGAAATTGATAAGGTAAATTTATTAGAGTTATTA *****	514
AC374_contig_187	ACTTATACAAGTGGCAATTTACCATTACAATCCCAGATAATATCAAACCTGATAAGCAA	2165
AC374_contig_241	ACTTATACAAGTGGCAATTTACCATTACAATCCCAGATAATATCAAACCTGATAAGCAA	2162
<u>NG_055474_ampC</u>	ACTTATACAAGTGGCAATTTACCATTACAATCCCAGATAATATCAAACCTGATAAGCAA *****	574

AC374_contig_187	ATATTAGAGTATTTCAAAAATTGGAAAGTAAAGAATCCTCCTGGTACTTATCGTGAATAC	2225
AC374_contig_241	ATATTAGAGTATTTCAAAAATTGGAAAGTAAAGAATCCTCCTGGTACTTATCGTGAATAC	2222
<u>NG_055474_ampC</u>	ATATTAGAGTATTTCAAAAATTGGAAAGTAAAGAATCCTCCTGGTACTTATCGTGAATAC	634

AC374_contig_187	TCAAATCCAAGTATAGGACTTTTTGGGTATCTAACTGCAAAATCGATGAATGTTTCCTTTC	2285
AC374_contig_241	TCAAATCCAAGTATAGGACTTTTTGGGTATCTAACTGCAAAATCGATGAATGTTTCCTTTC	2282
<u>NG_055474_ampC</u>	TCAAATCCAAGTATAGGACTTTTTGGGTATCTAACTGCAAAATCGATGAATGTTTCCTTTC	694

AC374_contig_187	TCTTCATTATTAGAGAAGACTGTTTTCTCAACTTAATTTGAAACATACATACGTCAAT	2345
AC374_contig_241	TCTTCATTATTAGAGAAGACTGTTTTCTCAACTTAATTTGAAACATACATACGTCAAT	2342
<u>NG_055474_ampC</u>	TCTTCATTATTAGAGAAGACTGTTTTCTCAACTTAATTTGAAACATACATACGTCAAT	754

AC374_contig_187	GTTCCAGAAGCACAAAAACGAACATGCTTTTGGTTATGATGAAAATAATAAGCCAATT	2405
AC374_contig_241	GTTCCAGAAGCACAAAAACGAACATGCTTTTGGTTATGATGAAAATAATAAGCCAATT	2402
<u>NG_055474_ampC</u>	GTTCCAGAAGCACAAAAACGAACATGCTTTTGGTTATGATGAAAATAATAAGCCAATT	814

AC374_contig_187	CGAGTTAATCCTGGTCCATTGTCGGATGAAGCATATGGCGTTAAATCAACACTCCCAGAT	2465
AC374_contig_241	CGAGTTAATCCTGGTCCATTGTCGGATGAAGCATATGGCGTTAAATCAACACTCCCAGAT	2462
<u>NG_055474_ampC</u>	CGAGTTAATCCTGGTCCATTGTCGGATGAAGCATATGGCGTTAAATCAACACTCCCAGAT	874

AC374_contig_187	ATGCTTAAGTTTGTAATTCGAATCTTAATGTAGATACAAATAGCCCTGCTATGAAAAAA	2525
AC374_contig_241	ATGCTTAAGTTTGTAATTCGAATCTTAATGTAGATACAAATAGCCCTGCTATGAAAAAA	2522
<u>NG_055474_ampC</u>	ATGCTTAAGTTTGTAATTCGAATCTTAATGTAGATACAAATAGCCCTGCTATGAAAAAA	934

AC374_contig_187	GCTTACTGGATACACACAAAGGATATTTTAAAGTTTCTGATAGCGGTATGACACAAGCA	2585
AC374_contig_241	GCTTACTGGATACACACAAAGGATATTTTAAAGTTTCTGATAGCGGTATGACACAAGCA	2582
<u>NG_055474_ampC</u>	GCTTACTGGATACACACAAAGGATATTTTAAAGTTTCTGATAGCGGTATGACACAAGCA	994

AC374_contig_187	CTTGGATGGGAAATGTTTTCTTATCCCACTACTTCTGAAATCTACAGGCTAGTAATTTA	2645
AC374_contig_241	CTTGGATGGGAAATGTTTTCTTATCCCACTACTTCTGAAATCTACAGGCTAGTAATTTA	2642
<u>NG_055474_ampC</u>	CTTGGATGGGAAATGTTTTCTTATCCCACTACTTCTGAAATCTACAGGCTAGTAATTTA	1054

AC374_contig_187	TTGGGCTCAAATCCTGTTGTAAAAGAATTATCGCAACCAAATCTAAAGTTTTTCATAAA	2705
AC374_contig_241	TTGGGCTCAAATCCTGTTGTAAAAGAATTATCGCAACCAAATCTAAAGTTTTTCATAAA	2702
<u>NG_055474_ampC</u>	TTGGGCTCAAATCCTGTTGTAAAAGAATTATCGCAACCAAATCTAAAGTTTTTCATAAA	1114

AC374_contig_187	ACAGGTCGACTAATGGCTTTGGGGCGTATGTTTTATTATTCCAGAAGAAGGATTTGGA	2765
AC374_contig_241	ACAGGTCGACTAATGGCTTTGGGGCGTATGTTTTATTATTCCAGAAGAAGGATTTGGA	2762
<u>NG_055474_ampC</u>	ACAGGTCGACTAATGGCTTTGGGGCGTATGTTTTATTATTCCAGAAGAAGGATTTGGA	1174

AC374_contig_187	TTGGTTATGTTAATGAATAAAAAGATACCAAATGTAGATCGTATTAAGGCTGCATATAAT	2825
AC374_contig_241	TTGGTTATGTTAATGAATAAAAAGATACCAAATGTAGATCGTATTAAGGCTGCATATAAT	2822
<u>NG_055474_ampC</u>	TTGGTTATGTTAATGAATAAAAAGATACCAAATGTAGATCGTATTAAGGCTGCATATAAT	1234

AC374_contig_187	GTTTTGAGACATTGAAAAGATAATTAACCTTCTCTAAAATTAACATAAT-----	2874
AC374_contig_241	GTTTTGAGACATTGAAAAGATAATTAACCTTCTCTAAAATTAACATAATACACCTTATAC	2882
<u>NG_055474_ampC</u>	GTTTTGAGACATTGAAAAGATAATTAACCTTCTCTAAAATTAACATAATACACCTTATAC	1294

AC374_contig_122	-----	1637
AC374_contig_187	-----	2874
AC374_contig_241	GAAATGCTCTAAATAGTTGTTTTATTTCATAAATTTATAGTATTAAGTGCAGCCTGATT	2942
<u>NG_055474_ampC</u>	GAAA	

AC374_contig_122	-----	1637
AC374_contig_187	-----	2874
AC374_contig_241	CTTAGCAATCAGGCTTTTTTATGATTTTTCATGTTCCACGCCTATTATTTGACCAATGT	3002
AC374_contig_122	-----	1637
AC374_contig_187	-----	2874

AC374_contig_241	TCCACGATTTTGGTTAGTTTTGATGAATAATCACTTGCTTTGATCTTGGGCTTTCTGGCG	3062
AC374_contig_122	-----	1637
AC374_contig_187	-----	2874
AC374_contig_241	CTGATCCTGCTCCTTTTTAAAGGCTCGTTGATCCATAATGCTGGCCATAATCATGATCGG	3122
AC374_contig_122	-----	1637
AC374_contig_187	-----	2874
AC374_contig_241	AATCCCGATAAATAGAAATGCAATGCCTTGTAGGATCTCTTTCAGTTTTTTCATACGTAA	3182
AC374_contig_122	-----	1637
AC374_contig_187	-----	2874
AC374_contig_241	TGCTCCTTGGGGAGCTTAGTCTTCATCGAATACCGCACTCAGTACTCGCCAAATAAGCT	3242
AC374_contig_122	-----	1637
AC374_contig_187	-----	2874
AC374_contig_241	ACGCTTTTTTCTTGTCTCATGATGTGTCTGTGATACGTTTTTTGGTGCCTTCACTGGTATG	3302
AC374_contig_122	-----	1637
AC374_contig_187	-----	2874
AC374_contig_241	TCTCGTTACTGTGTCATGAGATAATGAATTTGGCTCTATGCTTTTATTTTCAATACTTTC	3362
AC374_contig_122	-----	1637
AC374_contig_187	-----	2874
AC374_contig_241	ACTTGAGTCATCATTTGTTGTGCGAAGGTGTTTCATTGAAATGTCTATTTGGTGTGTCATG	3422
AC374_contig_122	-----	1637
AC374_contig_187	-----	2874
AC374_contig_241	AGACATTTTTTCTTCTGACTCTTTATGTCCTAGCAACAATTGGAAGCGGTCTATTTGGTC	3482
AC374_contig_122	-----	1637
AC374_contig_187	-----	2874
AC374_contig_241	TAAATAGCGTTTCTCACGATCTTTATATGACTCAATCTCCTTTTTTCATAAAATCAACAAG	3542
AC374_contig_122	-----	1637
AC374_contig_187	-----	2874
AC374_contig_241	CTGACGTAAATCTGCATCATCCTTAGATTGATCAACTTCTGTTTTTTTTCATGCTTTTTT	3602
AC374_contig_122	-----	1637
AC374_contig_187	-----	2874
AC374_contig_241	GATTGGCTCTCAAAGCAGCGAATGACTTCTGCAATGTCAAAAAGACCATCTGCGCTTCG	3662
AC374_contig_122	-----	1637
AC374_contig_187	-----	2874
AC374_contig_241	AGATATACGCCCTTCTTTTATAGCCCTATATAGCGTAGAGCGACTAACATTAAAGCGATT	3722
AC374_contig_122	-----	1637
AC374_contig_187	-----	2874
AC374_contig_241	GGATACTTCACTTAGTGATAACTTAGCCATTTACTAAGTCCCTTTTTATTGATGGCATAT	3782
CP023032_repB	----- GTCCTTTTTATTGATGGCATGT ***** * *	23
AC374_contig_122	-----	1637
AC374_contig_187	-----	2874
AC374_contig_241	ATCCCACTTTTTTAGGTATGGGTATAGCTCTTTGAATTGAGCGGGATCTGTAGCATCT	3842
CP023032_repB	ATCCCACTTTTTTAGGTATGGGGATAGTTCTTTGATTTTTTCAGGGTCTGTAGCATCT ***** * * * *	83
AC374_contig_122	-----	1637
AC374_contig_187	-----	2874
AC374_contig_241	CAGCAATACGTACAGCAAACCTGTTGGTAGCTTCTGTACCTTGAGAATATTTCCCATTT	3902
CP023032_repB	CAGCAATACGTACAGCAAACCTGTTGGTAGCTTCTGTACCTTGAGAATATTTCCCATTT *****	143

AC374_contig_122	-----	1637
AC374_contig_187	-----	2874
AC374_contig_241	-----	3962
<u>CP023032_repB</u>	CAGGTAATTCTGAAAGCTTATTAGCAAACATATGACGTTGAGCATCCGTCATTTTTGAAA CAGGTAATTCTGAAAGCTTATTAGCAAACATATGACGTTGAGCATCCGTCATTTTTGAAA *****	203
AC374_contig_122	-----	1637
AC374_contig_187	-----	2874
AC374_contig_241	-----	4022
<u>CP023032_repB</u>	AAAGATCTAGCGTGTTTGGATCTCGCTTATCTGCTATTGGTTGATTCGTTTTCTTTTGT AAAGATCTAGCGTGTTTGGATCTCGCTTATCTGCTATTGGTTGATTCGTTTTCTTTTGT *****	263
AC374_contig_122	-----	1637
AC374_contig_187	-----	2874
AC374_contig_241	-----	4082
<u>CP023032_repB</u>	TGAAGACGAATGAAAAACCTGAAATAGCACGACCTTTTTTATGTTGCTCATATTTAACGG TGAAGGCGAATGAAAAACCTGAAATAGCACGACCTTTTTTATGTTGCTCATATTTAACGG *****	323
AC374_contig_122	-----	1637
AC374_contig_187	-----	2874
AC374_contig_241	-----	4142
<u>CP023032_repB</u>	TAATATCAGAAAGCTCATTAATTTGTTTAAATAGCAATATCTAAAACACGCTTTTTAAAAG TAATATCAGAAAGCTCATTAATTTGTTTAAATAGCAATATCTAAAACACGCTTTTTAAAAG *****	383
AC374_contig_122	-----	1637
AC374_contig_187	-----	2874
AC374_contig_241	-----	4202
<u>CP023032_repB</u>	CCTCCATACGATCATATTCATTAACCTTATACCCAATTGGCTACGAAATTTATTCAACT CCTCCATACGATCATATTCATTAACCTTATACCCAATTGGCTACGAAATTTATTCAACT *****	443
AC374_contig_122	-----	1637
AC374_contig_187	-----	2874
AC374_contig_241	-----	4262
<u>CP023032_repB</u>	CATATATAGGTGTTTTGCCTACAGACTTCCATTGCATTAACAACCTCATAAAGTCGTACAG CATATATAGGTGTTTTGCCTACAGACTTCCATTGCATTAACAACCTCATAAAGTCGTACAG *****	503
AC374_contig_122	-----	1637
AC374_contig_187	-----	2874
AC374_contig_241	-----	4322
<u>CP023032_repB</u>	CATAAACGCTTTTTAAAATCGGAAGTTTTTTTAAAGATGGTAACTAGTAAAATATTGTTCAA CATAAACGCTTTTTAAAATCGGAAGTTTTTTTAAAGATGGTAACTAGTAAAATATTGTTCAA *****	563
AC374_contig_122	-----	1637
AC374_contig_187	-----	2874
AC374_contig_241	-----	4382
<u>CP023032_repB</u>	AGCCATCTATTTTTGTGACATGTTCAATTACAACACGAGTTAATGTTACTAGTATGCGAC AGCCATCTATTTTTGTGACATGTTCAATTACAACACGAGTTAATGTTACTAGTATGCGAC *****	623
AC374_contig_122	-----	1637
AC374_contig_187	-----	2874
AC374_contig_241	-----	4442
<u>CP023032_repB</u>	CTTCACCTTTTCGATAATTAGCATCTTGAATCCAACGACTTTTTGTTAAAGTTCATCTT CTTCACCTTTTCGATAATTAGCATCTTGAATCCAACGACTTTTTGTTAAAGTTCATCTT *****	683
AC374_contig_122	-----	1637
AC374_contig_187	-----	2874
AC374_contig_241	-----	4502
<u>CP023032_repB</u>	CATTGGTAATAGTAAATTTGCTTTTTAAATAAAGAATCTTCTGCCTCAACTAAAGCTAAAT CATTGGTAATAGTAAATTTGCTTTTTAAATAAAGAATCTTCTGCCTCAACTAAAGCTAAAT *****	743
AC374_contig_122	-----	1637
AC374_contig_187	-----	2874
AC374_contig_241	-----	4562
<u>CP023032_repB</u>	AAGCAGCATCAGGTGAAACATTAAGGCTGTAGCATATCTACTAGCATTAGTTCTAATG AAGCAGCATCAGGTGAAACATTAAGGCTGTAGCATATCTACTAGCATTAGTTCTAATG *****	803
AC374_contig_122	-----	1637
AC374_contig_187	-----	2874
AC374_contig_241	-----	4622
<u>CP023032_repB</u>	GTTCTTCTGCTGATAATCCTTGGCCGTGTTTACGAGCATCGACAATAGCGAGCTGTAATA GTTCTTCTGCTGATAATCCTTGGCCGTGTTTACGAGCATCGACAATAGCGAGCTGTAATA *****	863
AC374_contig_122	-----	1637

AC374_contig_187	-----	2874
AC374_contig_241	GGCGAGTTTCACTTAAAGTAAGTGTCTGTAAGGCTTGAACAAGTTTATTGATTTTACGA	4682
<u>CP023032_repB</u>	GGCGAGTTTCACTTAAAGTAAGTGTCTGTAAGGCTTGAACAAGTTTATTGATTTTACGA	983

AC374_contig_122	-----	1637
AC374_contig_187	-----	2874
AC374_contig_241	CTAAGTCGGCCATGTCATTCTATTTAGCAACGGTTTTATTGTGTTGTTATAACAACACAA	4742
<u>CP023032_repB</u>	CTAAGTCGGCCATGTCATTCTATTTAGCAACGGTTTTATTGTGTTGTTATAACAACACAA	983

AC374_contig_122	-----	1637
AC374_contig_187	-----	2874
AC374_contig_241	TAAATATTTGTTGTCAAATTCGAGGAAACGTTGCTATATAACCGAGGAAACGTTGCTAT	4802
<u>CP023032_repB</u>	TAAATATTTGTTGTCAAATTCGAGGAAACGTTGCTATATAACCGAGGAAACGTTGCTAT	1043

AC374_contig_122	-----	1637
AC374_contig_187	-----	2874
AC374_contig_241	ATAACCGAGGAAACGTTGCTATATAACCGAGGAAACGTTGCTATATACTTCTTAAAAGCA	4862
<u>CP023032_repB</u>	ATAACCGAGGAAACGTTGCTATATAACCGAGGAAACGTTGCTATATACTTCTTAAAAGCA	1103

AC374_contig_122	-----	1637
AC374_contig_187	-----	2874
AC374_contig_241	TTGTAATAAAGGGTTTCAGGCCATTTAAAAACATTTAAAAACATTTAAAAATAATTA	4922
<u>CP023032_repB</u>	TTGTAATAAAGGGTTTCAGGCCATTTAAAAACATTTAAAAACATTTAAAAATAATTA	1163

AC374_contig_122	-----	1637
AC374_contig_187	-----	2874
AC374_contig_241	GCCCAAGGAGTGAAAAATTGCCCTATGTTTTCGCTACGCTCAAACCTCTATTGAATCTCGC	4982
<u>CP023032_repB</u>	GCCCAAGGA-----	1172

AC374_contig_122	-----	1637
AC374_contig_187	-----	2874
AC374_contig_241	TTTCGCTCGATTTCGTCGGGGCAATTTTGGCTCATCTCGTTGTGACTTCAATAAAAAGC	5042
AC374_contig_122	-----	1637
AC374_contig_187	-----	2874
AC374_contig_241	AAAAGCACGATGAATTCGCTTCGCTCATAAAGCTTTTTTGCTCGCTACGCTCGGTCTAGG5102	
AC374_contig_122	-----	1637
AC374_contig_187	-----	2874
AC374_contig_241	GGCGAATTTAGCATGAAAAATATAGATTTTCTAGGATCAAGTCATTTAAAAGCGGTTTT	5162
AC374_contig_122	-----	1637
AC374_contig_187	-----	2874
AC374_contig_241	TCAGAGGGTCGATGGTCGAATATTGCTAGTTCGCTCGTAGACTCGCT	5211