

highlights the need to further investigate the infectivity and pathophysiology of the virus located in the often neglected capillary compartment. These findings provide new information on this biologic compartment, which plays a key role in vectorborne transmission and transmission dynamics. Moreover, these observations, if validated with more patients and extended to other vectorborne infections, will be vital for preventing and controlling the transmission of Zika virus and other arboviruses.

Institutional review board approval was granted by the Comité de Protection des Personnes Sud-Méditerranée I corresponding to the following study “Etude descriptive prospective de la maladie à virus Zika au sein de la communauté de défense des Forces Armées en Guyane” and was registered February 2016 under the number RCB: 2016-A00394-47. Written informed consent was obtained from each patient as required by the Comité de Protection des Personnes Sud-Méditerranée I.

This work was funded by the Direction Centrale du Service de Santé des Armées (grant agreement 2016RC10) and supported by the European Virus Archive Goes Global project, which has received funding (grant agreement 653316) from the European Union’s Horizon 2020 Research and Innovation Program. Funding sources played no role in study design, patient recruitment, data collection, analysis and interpretation of the data, or writing of the manuscript or the decision to submit it for publication.

Dr. Matheus is a research assistant at the Institute Pasteur de la Guyane, French Guiana, with research interests in the diagnosis and pathophysiology of arboviruses. She is currently studying viral emergence, particularly that of a hantavirus in French Guiana.

## References

- Petersen LR, Jamieson DJ, Honein MA. Zika virus. *N Engl J Med*. 2016;375:294–5.
- Waggoner JJ, Gresh L, Vargas MJ, Ballesteros G, Tellez Y, Soda KJ, et al. Viremia and clinical presentation in Nicaraguan patients infected with Zika virus, chikungunya virus, and dengue virus. *Clin Infect Dis*. 2016;63:1584–90. <http://dx.doi.org/10.1093/cid/ciw589>
- Chouin-Carneiro T, Vega-Rua A, Vazeille M, Yebakima A, Girod R, Goindin D, et al. Differential susceptibilities of *Aedes aegypti* and *Aedes albopictus* from the Americas to Zika virus. *PLoS Negl Trop Dis*. 2016;10:e0004543. <http://dx.doi.org/10.1371/journal.pntd.0004543>
- Callahan JD, Wu SJ, Dion-Schultz A, Mangold BE, Peruski LF, Watts DM, et al. Development and evaluation of serotype- and group-specific fluorogenic reverse transcriptase PCR (TaqMan) assays for dengue virus. *J Clin Microbiol*. 2001;39:4119–24. <http://dx.doi.org/10.1128/JCM.39.11.4119-4124.2001>
- Panning M, Grywna K, van Esbroeck M, Emmerich P, Drosten C. Chikungunya fever in travelers returning to Europe from the Indian Ocean region, 2006. *Emerg Infect Dis*. 2008;14:416–22. <http://dx.doi.org/10.3201/eid1403.070906>
- Hamel R, Dejarnac O, Wichit S, Ekchariyawat P, Neyret A, Luplertlop N, et al. Biology of Zika virus infection in human skin cells. *J Virol*. 2015;89:8880–96. <http://dx.doi.org/10.1128/JVI.00354-15>

Address for correspondence: Séverine Matheus, Institut Pasteur de la Guyane, Centre National de Référence des Arbovirus, laboratoire associé, 23 ave Pasteur, BP 6010-97306 Cayenne CEDEX, French Guiana; email: smatheus@pasteur-cayenne.fr

## Detection of Spotted Fever Group *Rickettsia* DNA by Deep Sequencing

Rikki M.A. Graham, Steven Donohue, Jamie McMahon, Amy V. Jennison

Author affiliations: Queensland Department of Health, Coopers Plains, Queensland, Australia (R.M.A. Graham, J. McMahon, A.V. Jennison); Townsville Public Health Unit, Townsville, Queensland, Australia (S. Donohue)

DOI: <https://doi.org/10.3201/eid2311.170474>

After conventional molecular and serologic testing failed to diagnose the cause of illness, deep sequencing identified spotted fever group *Rickettsia* DNA in a patient’s blood sample. Sequences belonged to *R. honei*, the causative agent of Flinders Island spotted fever. Next-generation sequencing is proving to be a useful tool for clinical diagnostics.

When conventional laboratory tests cannot identify an etiologic agent, unbiased deep sequencing performed directly on a clinical sample has the potential to identify a probable cause of disease. We used deep sequencing to detect spotted fever group (SFG) *Rickettsia* DNA in the blood of a patient for whom diagnosis was not possible through conventional molecular and serologic testing.

In late 2016, a middle-aged woman was admitted to a regional hospital in Queensland, Australia, after 2 weeks of mild cough, myalgia, fever, and lethargy. The day before admission, she experienced a blanching rash and pains in her feet, after which her condition deteriorated and a definite petechial rash appeared. Chest radiographs showed atelectasis on 1 side. Meningococcal septicemia was suspected, and the patient was transferred to intensive care with septic shock. Despite treatment with inotropes and several antimicrobial drugs (including ceftriaxone, vancomycin, meropenem, doxycycline), the patient died the next morning.

Clinical testing did not identify an infectious disease agent in the patient’s blood; serologic test results

for *Rickettsia* were negative. Because a limited amount of specimen remained for testing, we applied an unbiased deep-sequencing approach. We extracted DNA from the blood sample by using the MasterPure Complete DNA Purification Kit (Epicenter, Madison, WI, USA) and sequenced with the Ion Torrent PGM (Personal Genome Machine) workflow by using the Ion PGM IC 200 Kit and the Ion 316 Chip Kit, version 2 (Life Technologies, Carlsbad, CA, USA). A total of 3,627,903 sequences were generated and trimmed by using a minimum quality score of Q15 and minimum length of 50 bp. Of the reads generated, 251 matched bacterial DNA sequences (uploaded to GenBank as Bioproject PRJEB21107). The rest either matched human genome sequences and were filtered out (3,619,386 reads) or were unclassified (8,252 reads).

We analyzed the reads for bacterial DNA by using 3 metagenomics tools: Kraken (1), PathoScope (2), and One Codex (<https://www.onecodex.com>). All 3 analyses returned similar results;  $\approx 80\%$  of classified reads (208/251 reads, 53,958 total nucleotides) matched sequences from SFG *Rickettsia* spp.; the remainder gave low-number, low-quality matches to other bacteria. Screening of reads for sequences matching 5 rickettsial genes (*rrs*, *ompA*, *ompB*, *gltA*, and *sca4*) found 1 read mapping to the *ompB* gene (online Technical Appendix, <https://wwwnc.cdc.gov/EID/article/23/11/17-0474-Techapp1.pdf>). This read was a 100% match (272/272 nt) to *R. honei ompB* (GenBank accession nos. AF123724.1, AF123711.1). The next highest match was to *R. parkerii ompB* (accession no. KY113111.1) at 99% (270/272 nt). We confirmed the presence of SFG *Rickettsia* DNA in the DNA extract of the sample by nested PCR and performed Sanger sequencing by using the Invitrogen SuperScript III One-Step RT-PCR system with primers (3) and in-house nested primers.

To narrow down the identification to species level, we further analyzed sequences matching *Rickettsia* spp. We downloaded all *Rickettsia* genomes available at the National Center for Biotechnology Information (<https://www.ncbi.nlm.nih.gov/>), complete and draft, and used them as reference sequences for mapping of the reads in CLC Genomics Workbench 8 (QIAGEN Aarhus, Silkeborgvej, Denmark). We discarded reads mapping to  $>1$  genome, collected the remaining reads that mapped uniquely to a single genome, and noted the genome to which they mapped. Of the 208 reads, 67 mapped to  $>1$  genome, 1 did not map to any of the genomes and was subsequently identified as matching that of the human reference genome, 3 were unique matches to *R. conorii* (AJUR01, GenBank accession no. NC\_003103), 1 was a unique match to *R. sibirica* (accession no. NZ\_AHZB01000018), and 151 were unique matches to *R. honei* (accession no. NZ\_AJTT00000000) (online Technical Appendix) (4). Mapping of the 208 sequencing reads revealed that 207 (99.6%) reads mapped

to the *R. honei* genome, giving 1.43% coverage of the genome, and 168 (80.7%) reads mapped to the *R. australis* (accession no. NC\_017058) genome, representing 0.03% coverage of the genome.

The main causes of SFG rickettsioses in Australia are *R. australis* and *R. honei*, which cause Queensland tick typhus and Flinders Island spotted fever, respectively (5). The rickettsial DNA in the blood sample we describe most closely matched sequences from *R. honei* and had a relatively low level of similarity to sequences from *R. australis*. *R. honei* was initially reported only in the southern states of Australia; however, a genetic variant known as the “marmionii” strain has since been reported in eastern and northern parts of the country (6). Unfortunately, the genome of *R. honei* “marmionii” has not been sequenced, and the genes used to differentiate between *R. honei* and *R. honei* “marmionii” were not covered by the sequences generated from the sample. Therefore, we could not confirm which strain of *R. honei* was in the sample.

Flinders Island spotted fever is reportedly associated with relatively mild illness (5). However, our detection of *R. honei* DNA in the blood of a deceased patient, in the absence of positive *Rickettsia* serologic test results, is suggestive of acute infection with this agent. This case demonstrates the potential of deep sequencing for identifying unknown etiologic agents, particularly when other methods have not done so.

### Acknowledgments

We thank the Townsville Public Health Unit of Pathology Queensland and the Public Health Virology Laboratory at Queensland Health Forensic and Scientific Services for performing routine testing.

Dr. Graham is a senior scientist in the Molecular Epidemiology Unit of the Queensland Department of Health Public Health Microbiology Laboratory at Forensic and Scientific Services. Her work involves research into the potential of whole-genome sequencing as a tool for public health microbiology.

### References

1. Wood DE, Salzberg SL. Kraken: ultrafast metagenomic sequence classification using exact alignments. *Genome Biol.* 2014;15:R46. <http://dx.doi.org/10.1186/gb-2014-15-3-r46>
2. Hong C, Manimaran S, Shen Y, Perez-Rogers JF, Byrd AL, Castro-Nallar E, et al. PathoScope 2.0: a complete computational framework for strain identification in environmental or clinical sequencing samples. *Microbiome.* 2014;2:33. <http://dx.doi.org/10.1186/2049-2618-2-33>
3. Webb L, Carl M, Malloy DC, Dasch GA, Azad AF. Detection of murine typhus infection in fleas by using the polymerase chain reaction. *J Clin Microbiol.* 1990;28:530–4.
4. Xin D, El Karkouri K, Robert C, Raoult D, Fournier P-E. Genomic comparison of *Rickettsia honei* strain RBT and other *Rickettsia* species. *J Bacteriol.* 2012;194:4145. <http://dx.doi.org/10.1128/JB.00802-12>

5. Graves S, Stenos J. Rickettsioses in Australia. *Ann N Y Acad Sci*. 2009;1166:151–5. <http://dx.doi.org/10.1111/j.1749-6632.2009.04530.x>
6. Unsworth NB, Stenos J, Graves SR, Faa AG, Cox GE, Dyer JR, et al. Flinders Island spotted fever rickettsioses caused by “marmionii” strain of *Rickettsia honei*, eastern Australia. *Emerg Infect Dis*. 2007;13:566–73. <http://dx.doi.org/10.3201/eid1304.050087>

Address for correspondence: Rikki M.A. Graham, Public Health Microbiology, Public and Environmental Health, Department of Health, Forensic and Scientific Services, PO Box 594, Archerfield, QLD 4108, Australia; email: rikki.graham@health.qld.gov.au

## ***Chlamydia trachomatis*** **Biovar L2 Infection in Women** **in South Africa**

**Remco P.H. Peters,<sup>1</sup> Ronan Doyle,<sup>1</sup>  
Mathys J. Redelinghuys, James A. McIntyre,  
Georges M. Verjans, Judith Breuer,  
Marleen M. Kock**

Author affiliations: University of Pretoria, Pretoria, South Africa (R.P.H. Peters, M.J. Redelinghuys, M.M. Kock); Maastricht University Medical Centre, Maastricht, the Netherlands (R.P.H. Peters); Anova Health Institute, Johannesburg, South Africa (R.P.H. Peters, J.A. McIntyre); University College London, London, United Kingdom (R. Doyle, J. Breuer); University of Cape Town, Cape Town, South Africa (J.A. McIntyre); Erasmus Medical Centre, Rotterdam, the Netherlands (G.M. Verjans); National Health Laboratory Service, Pretoria (M.M. Kock)

DOI: <https://doi.org/10.3201/eid2311.170758>

We detected *Chlamydia trachomatis* biovar L2 in vaginal swab specimens of 7 women with vaginal discharge in South Africa. Whole-genome sequencing directly from clinical specimens identified a closely related cluster of strains. The clinical role of this infection in the context of syndromic management should be clarified.

Infection with *Chlamydia trachomatis* biovar L is known as lymphogranuloma venereum (LGV). This infection usually presents as genital ulcers, followed by an invasion of the lymphatic system resulting in buboes, painful swelling of lymph nodes (1). In the past 2 decades, another

manifestation of LGV has emerged in North America and Europe: rectal LGV infection causing proctocolitis among men who have sex with men (MSM) (1). In this population, urethral LGV also occurs (2).

There have been only sporadic reports of rectal and genital LGV infection in women living in the industrialized world (3,4). Cross-sectional studies from France, Switzerland, and the Netherlands did not detect biovar L in specimens from women with genital or rectal *C. trachomatis* infection (1,5–7). Because lymphatic manifestation has become relatively rare, LGV infection is considered an outbreak mainly among MSM in Europe and North America (1). Lymphatic LGV is endemic to Africa, but before our study, it was unknown whether *C. trachomatis* biovar L infections occurred in women in Africa. Thus, we determined the prevalence of this infection in South Africa.

To determine whether genital *C. trachomatis* biovar L infections occur in women living in South Africa, we analyzed 82 DNA samples extracted from vaginal swab specimens that were positive by a molecular detection assay for *C. trachomatis* infection at the Department of Medical Microbiology at the University of Pretoria. The Faculty of Health Sciences Research Ethics Committee at the University of Pretoria approved the studies in which these specimens were collected. These swab specimens had been collected during 2012–2016 from women attending different healthcare settings: a mobile health clinic in rural Mopani District (n = 52) and 3 departments at the academic hospital in Pretoria: obstetrics and gynecology clinic (n = 14), antiretroviral treatment clinic (n = 10), and sexually transmitted infection (STI) clinic (n = 6). We assessed the presence of LGV in these genital specimens by using specific PCRs for *C. trachomatis* serovar L and serovar L2b (8). For positive PCR results, we confirmed the diagnosis by conducting whole-genome sequencing (WGS) of *C. trachomatis* directly from the clinical specimen as described elsewhere (9).

Whereas *C. trachomatis* biovar L-specific PCR showed positive results for 7 specimens obtained from women at the antiretroviral treatment (n = 5) and STI (n = 2) clinics in Pretoria, we did not detect LGV in any of the 52 specimens from women in Mopani District. All PCR test results for serovar L2b were negative. The 7 women with genital LGV all had vaginal discharge and were co-infected with another STI (Table).

WGS confirmed LGV (*ompA* sequence identical to those of the *C. trachomatis* L2 434/BU reference strain) in 4 cases with good mean read depth ( $\geq 12$ ) and high genome coverage ( $>98\%$ ). The 4 sequences clustered well with the L2 sequences previously published and away from L1 and L2b sequences. For 1 specimen, the mean read depth

<sup>1</sup>These authors contributed equally to this article.

# Detection of Spotted Fever Group *Rickettsia* DNA by Deep Sequencing

## Technical Appendix

**Technical Appendix Table.** Characteristics of sequence reads mapping to *Rickettsia honei*

Read name	Sequence length	% ID	GenBank accession no.	nt coordinates	Sequence
700666F:214:CA2UUANXX:8:2211:4818:11819_1:N:0:TAGG CATG+CTCTCTAT_(reversed) LH08G:00089:01332	125	100	NZ_AJTT01000001	102663 to 102787	AGCTTTTCAGTTTCAGTAATGATAGCTGTTTTACTTTGGAAATAAAGAGCTTTACC GATTAACCTCAGTGCTTACTACATTAGTATCTCTTGCAAAAAATTCACGAGGTAAA GGGATTAGTTTATTC
LH08G:00103:02050	294	98.98	NZ_AJTT01000001	58385 to 58675	CACGCAGCAAGTCTTGATTTACCGTTCCGGGAGGACCAACATTTAAAGGTTA TGCCATCTGATGCTGCAATTTCTAAAGCTTGTTTAGCAATTTTTGACCTTTTTA TATCTTTAAAATCGGGATAATTTATCGCCTCATCTTGAGCTTAGCTTCCGGAGG AGTTAAAACTTGTGAACCTTTAAAATGATTTACTAATTCAATTAATTAACCTGCA ACAAGTATATTATCATTACCCGACCAAGCAACTCCGAGCTGTTTTACTTGAAC AAATCAGACCTTTACCTC
LH08G:00199:02115	405	96.79	NZ_AJTT01000001	235861 to 236252	TTAGCTGATTCTAACATAGCTTTTTCTAATGGTTTTTTAATATCCATCACTTCATC TTCCGCTTAAGCCATTACGTTTTTTCGTCGTTTCACCTGCTCTACTTGAGACTCAC TTAAATCTCTGGCAAACCAATTTAAAATTTTATGAATGAAAATTAATTAATAAACTT ATAAAAAAGAATTGTATTTTTTTTCATAGAAGAGGTCCTGATCGTAATTTTTCATCA GGGATTTTCAGTTATGAACCTTGAAGGATAAGAACGGACTATTTTCATAAAATATT TTTTCTGCTTTCAGCATGAGTAATGTAGAGGTTCTTTTTGGCTCTCGTAATACC GACATAAGCAATGCGGCGTTCTTTCTAAGCCTTTTTTCGCCGTTCTTCGTTCTA GAGATCTTTTGAGACGGA
LH08G:00260:02605	268	99.627	NZ_AJTT01000001	173179 to 173445	GAGGGTAGAGCGTCCAGCCCGTTCCTGGCCACCCTCAACAAAAGCTGATCCC ATAAGTAAAAGAAAAGCAGGCACTAGTAGCCAAAATGATATTGTTAAGGCGT GGAAATGCCATATCGGGAGCCCTATTAACAGAGGTACGAAATAATTACCAAAG CCACTGAACAAAAGCCGGCATAATCAATAAAGAATACCATAATAACCGCATGTGC TGTGATAAGCACGTTATATAGCTGGAAATCATGATTTAAGAAAAGTCCGCGCGG CAAGTTTTAGACTAGGTATATTTAATATTGAATCATTAAATCCATTTAATTTTTTAA GACCTCGTACTTCTGCACGTTTTTGTGCTACTTCCATGCTAGGCTTGCTGAAAT CTAGATATATTTTTCGGCATTTTTTATCTTTAAGTCTCGGCAAGATAAAATAG TCGAATCACCAGTCCGCGCCGCTGCTATTAAGCATCAAAAATTAATTTAAAAT TTCTTTTCTTGATATAGAAAATGGTTAATTCTCCTAAGAACTACCCGCATGTT GCAAGTAAATATCTTTTTCTTGATTTGGGTC
LH08G:00384:01842	310	99.032	NZ_AJTT01000001	304717 to 305023	CTTTTTGTATCTCTATATTGTACAGTATCAAAATTTGCTGCTACATCAAGCATAGAT GTATCATCGATGTTATGTATATATCTATCTGATTTCAGCAGAAGTAAAGTGGCTAG GGTTAGCATAAGAAATAATAAGTTTATATGCTTCTGGATAAAATGACGTAATGGC ATGATGTAACCTAACAAAATTTATAGCTGTTCTTAGATGCTAAAAT

Read name	Sequence length	% ID	GenBank accession no.	nt coordinates	Sequence
LH08G:00577:01769	208	96.172	NZ_AJTT01000001	341663 to 341864	GTTATAAAAAATAAATTTTCGTCATAGAGAAAAGTCTAGCATAACAATGCATTA GTAATTTAAATTTGTCAATATCAAGTTCATTGAAATTTATAAGCCTTTTGTGCGT AATTTTCTGCTTTCTCATAAAAAGATTTATCATATAAAGTTTTGCTAGATTTTTG CTACCGTAAAAACAATTCCTTTAGATGTAATAAGTTTTT
LH08G:00579:02051	362	100	NZ_AJTT01000001	124494 to 124855	GATACATAAATAATGCCATACTTTCAACAGGAGCATATTTAAGCCAATCATCAAT GCTAATACTATTACCTTTTGATTTTGATTTTTCTCACCATTTTCATGAAGAATA ACTCATAACATAACTGCACCGGCGGCTTTCTCCTAGGATTCGGCAATTTCCG AATAAAGACGAGCATTTGCCAAATGGTCTTTGCCGTACATCTCATAATCGACTTT AAGCGCAGCCCAACGCATACCAAAATCCGGCTTCCACTGTAATTTGCAATGCC TCCCGTTACCGGTACTTCTATATAATTACCGGCTTTGTCTTTATACGTTACAGTG CCTGCTTTAGCATCCCATTTCTCTATAGGTA
LH08G:00581:02966	309	99.029	NZ_AJTT01000001	218033 to 218339	GTAGGAATTGCTGTTTTGCTTATATTTTTATTATAATTAATGCAGAAACACTTTG GTGGCTTGCAGTTGGCTCATCCTTAATAATTATTGGAACATCTAATGATTCAGGA TTAAGTAACTTATTTTCGGTAATCCAATAACATATTTCTAGATCAAATTTGATA TGCTTTATACCTTTCTGCTTTAACTACAGAATTGTTGTAGCATATTACTGGATTT TATCCAACCTTTATGGCTTAAATTTGCTACTTCGGTTACAATAGCTACTATTTT GCATTATATAATTGAATTTACCAGCTCGCC
LH08G:00660:02650	139	97.744	NZ_AJTT01000001	347909 to 348039	ATGATAATATCTTGCAAATTTAGATATTTTAGGAGTATTTCCCCTAAATATCTAT TTATCTAGTTGATTTAAGAGTTTCTGTAATAAATTTGAATTTAGCAAGTCAAGA TGCTTTTTTAGCTAAAATTGAATTAAG
LH08G:00737:02796	261	99.237	NZ_AJTT01000001	242578 to 242838	ACAATATTTTTTTGGTACAGCGTCGTTCCAGAAAGCTTGATACAAGTGAATTTCT GACATGCGCCTTTGCTCACGTAATTTTGTACGTTCCGAGGCTCAGTCGTCAA TTCATCTTGTCTAAAGCTTTCTGAATCTAGCTCTATCCACTTCTATTTTATTATTG TAAAAAAGTTGCTACAAATTTAATTAATGTATTAATTAATAAAGAATCAAA AATATTAAGAAAATTTTTAGCAAACGGCATCATTATGCGG
LH08G:00813:00255	253	100	NZ_AJTT01000001	301855 to 302107	AGCAAAAATTAAGAATATAATAAGGCTAAATCTGAGCTCGAAGAAGCAATAAT TTAAGCTAGAAGTGGGACTTGATAATGCCACTTTGAAATGATGAAGACGAA ATATACACTCTTGAATAATCGTTACCAAACTTGAAAGAGCCGTAATAATGCTT TATTACCAAAAGATGATGCGGATAGTAAAAGTGCTATTATTGAAGTTAGAGCAG GAAGCGCGGAGAGAAGCGGCACCTTTTTGCTGCC
LH08G:00820:01524	258	100	NZ_AJTT01000001	81173 to 81430	ATTATCCATACACTTTGGCTTAAGTAACTTTTACCAGACTGCATAGGTAATAGT GTAACATGCGGTCTTATAATAAAAATGAATATTAGGATGTTGTAATGCATAATTAT AGAAAAAATAGTGATAATTTAAGAAAGTAGAACCTCCTTCATATAAATCTCTATTT TTAAATGATAATTTCCATCTAGGAAGCCATAAAAATGTTTTCCGAGTTTTGGTTTT CTTTAATATTATAATTTCTTACTTCATAGTATGGTTG
LH08G:00832:00648	282	98.94	NZ_AJTT01000001	200820 to 201101	AAGATTTACCCGTTACTTTACCTGATGATGTAATTTTACCGGTACCGGTAATCC GCTTGATCATCATCCTAGTTGGAACATGTTAATTGTCCGAAATGCGATAAGCC GGCTGTGCGTGAAACCGATACTTTTATACATTTTTTGAATCACTTGGTATTTT ACGAGATATTGCAATAGCAATGTTACAGAGATGACTGATAAAAAAGCTTGTGATT ACTGGCTACCGGTCGATAAATATATAGCGGCATTAACATGCGGTAATGCATT TATTATATG
LH08G:00880:03124	260	100	NZ_AJTT01000001	302965 to 303224	AAAATTTCTTAAGACCGAAAAACAATAATTTATTACCTGATCCTTTTCATCTACTT GATATGGAAAAAGCTGTAGATAGAACCCTTACAGCTATTTTAAATAACCAAAAA TATGTATCTTCGCCGATTATGATGTAGACGGTGTACTTTCAGCCGCTTACTTA AAAAATTTTTAGAGATTTAAATATACTATGTGACATTTATGTTCTCGTATA GCTGAAGGATACGGTCCAACCTCTTTTGTATGCAAAAA
LH08G:00901:00649	283	98.233	NZ_AJTT01000001	16343 to 16620	CTTATTAACCATAATTTTCGTTAATACCGTCTTCAGCAATAAATGTTTAAAGGAA GTA AAAACGTCCTAAGGCTGCAAAATCTTCATTCATTTCAATACCTTCGATTTTA

Read name	Sequence length	% ID	GenBank accession no.	nt coordinates	Sequence
LH08G:00911:00432	271	98.893	NZ_AJTT01000001	354716 to 354983	ATAAAACGGCTTTTGGGAATTTATAATCCTTATTAACATATATTCTAACCGGCGT ACCTTGATTAACCGTTGTCGTCGGCTTAAACTGCTGCTGAGTTATCATATTTTTT TACAACATTCGTTTACATCCGTAAAAAGCTTGAGTAGAAGCTTTGTTGTGCTTTG CGTCCG
LH08G:00932:00966	290	98.966	NZ_AJTT01000001	370114 to 370400	AGTATTTAAACTTCTATAAATTTTCGCTCAAAAAACAAGTAATAGATTGTAGTAAC GAATATAAAGTTATCTACTCACTTCAAAAAATTAGATATAGACTCGCTAATTACGG TTCGTGATCCTCGTTATGCTAAGCTTGGTTTCCGCTCAATAAATAAGCTCGATGT CATACCGCTGTGCGGTATCCAGACAATAATTAATAAAGACTGGACCCCGTGGT CAAGCCACAGGGTGACAGAGGGGGGAACCGCCCCCTCAACAACATCTCC CTATACCCCAAATGCTGAAAAAGACTGTTTTAATTCATCTTCCCTATTATTCATA CTAAAACAGATGCAAAACATAATACTTGGCTTCACATAGTTCGCACTGATTTGCT CGGATAAGGAATTAACAAGAGTTTATAGACGGTGATATAAACTCAATTACCCATT TTACACTTTAGAACAAGATTTTTCTGATTCTCCTTTATGGTACTACACACTTTTT CTCTAAACCTTTATCTTACTGGATCGGTCACGTTTTATACCATTAATAATTGATCAT GAGCGTAAAAACA
LH08G:00996:01347	265	100	NZ_AJTT01000001	261795 to 262059	AAAATATTACCAGTTAGTATAGGAGCATTATTAAGGTGCGAAGTTTGCCTTCA CTAATCCCGTAAATAGTTATAATCTTGTTAAACTTGAAGCTCCTCTGATATATAT CTTGATTCAAAGTTTCAAAAATCTGTTCTTGAAAAATCTGAAATATAGGATTTTCT AAAAAAGCATGCCGATGATTTACCAAAAATAGGACAAATCTTAGCAAAAGCAGG TTTTAGAGAATTTCAAGATAAGAGTGCTTTAGATGAAAAGGGAC
LH08G:01008:02633	232	99.138	NZ_AJTT01000001	82660 to 82889	CTAATTATTAGTGCAGAAGAAAATCTATTTTTCTAAAGCTCTATAGAAAATTTAA ACAATAAACTAACATTTTATAAATTTTTTAAAGTTATGACAACCTAGAAAAG ATAAACCTCTAAATATTTATCATACTTTAGTTTCCATTATATACCTGTCTATAATG GGGCTAATTATAGAAAAGACTATAAATAGTGCTTTAGCACAACTTTACAAAA ATATTGAA
LH08G:01016:02876	294	98.639	NZ_AJTT01000001	273506 to 273795	TTGATTTTAGAGGAAGAATTTTCTATATTACTGGGGTTAATCGTCATTATTTGGT CTAACCTATCTTGCTATTGGCTAGAGTTATATATTAAGATTGTCTAAATTTAAGT CAAGTTAAAAATCAAATTAATGAGTAATTATTGGTTAAATATTTATAAAACCAA GAGGTATAAGTTCTGCTCAACTGTTAGCATAGTAAAAAATACTAGGTAAA ACCAAGATAGGACATGCCGGTACTTTAGACGTAGAAGCGGAAGGAATATTACC GTTTGCCGTAGGTGAAGCT
LH08G:01054:02101	244	98.086	NZ_AJTT01000001	148127 to 148333	TTTCGTGTATTAGTGTTAACTTAATAGGAGAAAAACCTCTTATGCCATTTCCGC GAAATCCGGAATCCAGTACTTTAAAGCTTTTTAAAGCTCGATTTATCTTGCTTT ACCCCTAGATTTCTGCTTTCGCAGGAATAACATCATACACTGATTTCAAAAAGAG ATTAACATGAAAAATTTATAAATATTTAGTTTTTACCTGGTTTTTACGTAATA TTAGTTAAGTGTTAACGGTGAA
LH08G:01072:01642	222	99.099	NZ_AJTT01000001	203673 to 203893	GGAGTAGCTGCTCCAAATGAGCAGGTGTTAATCACCCTAACAAAACCTTTGTT GTCATCCCGCGACTTGATCGCGGGATCCAGTCTTTTTTAATTTTTTTTGGATAC CGTGGTCAAGTCACGGTATGACACAGAACGCGTTTTTTCGATCCGCACAACAAC ATTATTGATTCAAAGGAATTAATAATCATTATGACTATAAAAAATTTATCAAAATG ACCT
LH08G:01247:00947	73	100	NZ_AJTT01000001	351245 to 351317	CTTGCCACCTGAATATCGTTGCAACTATAAGTAAGTTAATTATCGAACACATTA TTGCAGTTGATCAAACT
LH08G:01297:00604	245	99.592	NZ_AJTT01000001	366937 to 367180	AATGTTTTTAAAGTTTTTCTGAATACACTATAATTACATCATTTGTAACATTAAGC GAATTCCTTAAATACCATTTCAAGCATTGGAACCTCCACCGACTTTATGCATTA TCGGTAAATCGGACTCCATTCTAGTACCTTTACCGGCTGCTAAAATAATTTTGG ATAATTTGCATCGTTATAAGTCATGGTTCTCCTTGTATTATTTTCGTAACATCATC AGATAACTCATAATTTCCAAAA

Read name	Sequence length	% ID	GenBank accession no.	nt coordinates	Sequence
LH08G:01318:02288	287	99.306	NZ_AJTT01000001	7990 to 8276	CTCTATTCATAATATCTGAAAAAGATCGTACAAATTCTGTTGCTCTAATAATTTGT GCCATATTTTATCCTCAAAAATAATTACCATATTTATACCTTTTGATACTTCAAGATT TGGTACGTCAAATTTCCGGGATTCGCCTGTGCTCACTATTGTACGCTGTGTAGGC GCACTGCTTATTTTGACTTCCAACCTTTGAAGTATCTACGGTATACATATTATATG ATTATGTGTAGATTATGTAATAATGTTTATGTAATATAAGCTAAAAATTCTCTGAT TAAGATTTGA
LH08G:01333:00336	374	97.861	NZ_AJTT01000001	258664 to 259030	TTATCTAAAGCACTCTTATCTTGAAATTCTCTAAAGCCCGCATTGCTAAGATTT GACCTATTTTAGGCAAATCATCCGAATGTTTTTTTTAAAAAATTTCCCATATTGGA GATTTTTTAAAGAAGTGATTTTTGAAATTCGGATCAAGATATATCTTAGAAGAG TTAGCAAGCTTAACAAGATTATAAGTATTTACAGGATTAGTTAAAAATAAGTCTT GCTCCGAGTAATATCGTTCTTAAGCTTATACTCTTTGAAGATGATAAGTCCTGAA TTGCACTCTTGTAGTACTTTATTAGCTTTAGAAGAAGATAAAAAATTTTCTACAAC TTTTGATAGTGTTTAATTATTTATAACAACCATAAAATTCAC
LH08G:01354:00365	286	99.65	NZ_AJTT01000001	262020 to 262305	GAGGTTTTTGTAATATATCATCAAAAGCTTTTATATAGTCGCTGGAAAGTATTTCA GTTATGTAATTCGCAATATCGTTACCTTTTTTCATTAATAAAATTTTCAAGCAATTTT ATCCGTGGATAACATTCCTAATGTTTTAGAAGTACTTTATTATAGTCCGGTACT TCTTGCTTTATCTCAAGTGCAATTTTTTGAAGGCTTTTAAAGTACAGCATCATTTTT AAAAATTCTTTTAGTATTTCCGAGTCCCTTTTCATCTAAAGCACTCTTATCTTGAA ATTCTCT
LH08G:01360:02559	261	100	NZ_AJTT01000001	366624 to 366884	TCAATTATTTTATTCAACCATTGCGGAGTATTTCAGTATCCAATAAATATAGCATCT AATGAAGATGTTTTAGAGGCAGTCATAGAAGCCGGGGGCATGATATTATATCC GATGATACCACCACATAAATCTATACGGATATTGAAAAATTTCTCTAAAGTTCTAG AATTTTTAACTGGCAAATACGGCATACCTGAAGATTCTGATATATAGGCTGGATCC CATTAAATACAATAATTATAGATGATAAGGAAAAAGCTGAAA
LH08G:01418:00298	332	100	NZ_AJTT01000001	246549 to 246880	GATAGTTATATTATCGCCTATTTCTACCGGTCCGTTAAACCTTGAAGCATGAATT ACACTACCGTCTTGTATGTTAGTATTATTTCTATTTTTATCGATTCAACGTCGCC TCTAAGAACCGTATTAACCAAATGCTTGAATTACTACCTTTTCAACATCTCCT ATTAAGAGCTGCTTTCGGCAATATATGCACTTTTATCGATTCTTGGCGTAACTC CTTTGTAAGGGATAATGAGCATTAAATTATAATCTACCCAAGAAATATTACCGTCT TTACGATAATAAATATATTGATACGATCATTATTTATTTTTAAATACTACTGC TAGAAAAATAATCATTGAACGTGTCAGATCAGTATCGATACCTTGTGAATAATA TTTTAAATTTTCATTGACTTAGCATTACCAAAGTATTAATTTTTGTTAAGGTTTAGT AAATTCTGAACCGTCAACAATTTATTAATATATTGGAGGAAGGTTATGAGTAAA AGTAAGGCTATTGAAAATAACGGTATTAGTAATACCAATAGTCCAATGGTAAATA TATGGCCCCAAGACCGGAAGGAGTAAACCTACCTGTGTAGTAATTACTTATTC TGTAAGCAAGGATATTAAGGCTGTTTCGTGAAGTATTGGATGAGCGAGGTGCAA GTGTTTCATTACATAATTGATA
LH08G:01483:00337	349	99.143	NZ_AJTT01000001	117122 to 117469	ATAATAAGTTTATATGCTTCTGGATAAAATGACGTAATGGCATGATGTAACCCTA ACAAATATAGCTGTTCTTAGATGCTAAAATTTGATTTTTATTTGTCATATTTTTTA GTTTTTATAAAAATTTTTTATTAGCTTATTCAAAGCTGTTGTGGGTCAATTGTGAAT AATATTCAGATGGTAAAGACATGTTTTATATCCTATCAAGTTGCTATTATTTTCATG GTAATATGTTTTATAATAAATAGTATATCTTTCTATTTGTAAAGAAATAATTTTAAAT TACAAACGAACATTAACATCTTTATTAAGCTCTCTTATCTACCTCCCAATCATTA TTAATCTGAAAACATAAAATTTATTGGAAAA
LH08G:01503:00952	368	98.113	NZ_AJTT01000001	22507 to 22873	ATATATGCTTCAGGAAGATATGCCTTAATATATTCCATATCAGATGCGTTTTTTAA TAAATAGGGTGATACAAATCTAGTATGTCCTTACCGCTTCTTTTATAATTAGCA AATGAGTAAGCAACACAAATACCGTAGTCATTTAATAAATGCTTGTGTCTTGTCT



Read name	Sequence length	% ID	GenBank accession no.	nt coordinates	Sequence
LH08G:01673:02121	312	99.359	NZ_AJTT01000001	247493 to 247802	GTTGAATGTTGTTTTGCAGATCCACAGCTCTTAAAGCATATAATATCTGTTCTC TTGTTGCTTGAATAGAAACATCATCTGAAGC ATTAATAAATCTATCTTCTACTATTCATACTAATGATTTAATATCAAAAATCAATGA GTTAAACCTTGATAACGAGATTTTCAGGAATTAAGTTTCAGCTTCCTTTGCCAAGC TCCATAGATAAAAAATAAAATTTTATCGGCAGTATCACCTTCTAAAGATATCGATG GTTTCCACCCTTTAAATGTCGGTTACTTACATAGCGGAATTAGTCAAGGCTTTAT TCCCTGCACTGCTCTTGGTTGCTTGCAGCTATAAAAAAATACGAACATAATTT AACCGGTAAAAAACGTTGTAATTATTGGACGCTCA
LH08G:01752:01279	215	99.074	NZ_AJTT01000001	366307 to 366521	CACTAAATTAATTCGTGAAATAGTTACTGCAGCTAAAACCGGTTCTTCTAATAAC CCTGAAAATAATCCACGTCTTAGAAAATGCTTTAACCGCTGCACGTAGTCAAAAT CTCCCTAAAGAAAGATAGATAAAGCTATTAATAGTGCGAATGATTCTTCTAATA ACGAAAATTATACAAGAAATAGATATGAAGGTTATGCACCGAATGTATTG TCTATATTTTCTCTGCCCCAAATATTAGCAAGATAAAGAAGTGCTAACGAAT CGCTCCCACCAGATACTGCAATCGATATTTTAGATAAGCCAAAATTACCTATTAG ATTATTGATATTATACTCAAATTTTTCATATAGCATGGTTGAAAAATGTTAGTATT GTAAAGTGTGGATATTGTGGTCAAACCTAGTAGTATGTCATTTCCGCGTAGG CGGGACGTTGTGCATGGCTCTTATGTCATTCTCGCAAAGCAGGAATCCAGA AAAAAAGTATAAATACAGCAAATTTCTGAAATTAAGCTCGATTTAT
LH08G:01910:02516	322	97.059	NZ_AJTT01000001	138157 to 138477	GAAAGCTTTACTTTAATTCCTCCGAAAATATGAAGCAGCTCTAAAACATTTTGAG AATATAGGTATTACTGCGGATGTAAAAGTACTTACAAAAAATGCTAGCTAAT AAAGATAAAGTAGTTCTTGATCTCACAAAAGGTATAGAAAGTCTCTTTGCCAAAA ACAAAGTTACTAGGATAAAGGTGAAGCTAAAATTAGCTCTAGTAATAATCGTTG AAGTAAATAAAGAGCAAATTAAGCCAAAATATCCTAATTACTACAGGTTCCAG CGTCATAGAA
LH08G:02102:01594	285	99.298	NZ_AJTT01000001	359185 to 359467	GTATTAACGGTTCTATTTGTGACGAGAATGAGGAGAATAATAAATGCTGTCATT TTAGCGTACC GGTTAATAGAGATTTCAATGACCCTGTAATGTATTGAGAGAAG CAATATGCAAATGAAGACTTTATTGTTACTGTTGTGTA GCCAAAGAACGGTGGGAAGAAATAATTTTACTAATAGCTAAAGCTTCTCTATT ATTTCCCTAAGCACACTAATTAATATTGGTTATGAAGAAAATTATCGGATTATT TTTTGTAATTATACTTACTGCAATAAGTACTAGTATCTTA GAATTATGAAATATCATTTTTTCAAAGTAGGGCATTAAAGCAACTCGCTTAGTTG CTCTAAATGCTTTAAGTACATGCTTTAAGTATGTGTTTTACATTAAGAAAA CAGAGGGCTTAAGT
NB501781:2:HGMVWAFX:3: 21506:4952:12115_1:N:0:TAG GCATG+ATAGAGAG	149	99.32	NZ_AJTT01000001	252942 to 253088	ATATGGTGCTAATCGGATATACTCGATCCTGACGGTCAAATGGTCCATGACAAG GAAGCAATTTATGAACCTCTGAAAGCTCTTTTTAACGCTTGAATCCACATTGCGT AAGAATGATTACAAGAAAATTAAGGCTATTGACAAGAAAGATTAGCTGCATTTG TTCAATGGAAAGCAGCAATATTACCGGTTGTAAGGATGTTTCTAAGGATGAGT ATATAAAAAAGCCTATTAGAATATAAATTTTTCAAATCAAATGAGTTTGGATT CGGATGATTCTAATAAAAACAACCATTAATAG
NB501781:2:HGMVWAFX:4: 21504:24946:16382_1:N:0:TA GGCATG+ATAGAGAG	151	100	NZ_AJTT01000001	198785 to 198935	TCCTAACTCTAATAAAAAAGTTTTAATATTATCTATTAATTTTCTAAATCTC GTTCTATTTTACCTTGAATATCTAAAAATCTAAGTTATATGGTTCTTTTATA ATCGACCTGGCTAAATCGGACTGTAGCTCAGGTAAGTATTTGAAAAGTTATTT TATACCTTTGCTGAGCTTTTTCATGTTAAATTAC
700666F:214:CA2UUANXX:8: 1207:11637:88986_1:N:0:TAG GCATG+CTCTCTAT_(reverse d)	125	100	NZ_AJTT01000002	94923 to 95047	TGGGTATAATTATAAAGTTCAATTTAGTATTTTCCCTTTTATGACGGGCATAGTCTT GAGATACAAATAATCATATGAACGATATGCTATATTAATACTCTCCACCAAAGA GCATAAAATACTGCCAGTAAATCATGGAAGATAAAGATTATTAGCGTTCTTAT CGCTGAAAGATTCTATTAATCAATGATTTTCTGAAGTAATACTATCAATCGC
LH08G:00117:01579	305	99.016	NZ_AJTT01000002	112641 to 112942	
LH08G:00213:00620	202	97.03	NZ_AJTT01000002	189029 to 189225	
LH08G:00276:02094	303	99.67	NZ_AJTT01000002	114637 to 114938	



Read name	Sequence length	% ID	GenBank accession no.	nt coordinates	Sequence
LH08G:00319:00921	308	99.676	NZ_AJTT01000002	145726 to 146034	CGGAATCATACCGAGTAAAAATACAAATTACAGTCAATTTAAAGTCATTTAACTTT ATCGAATTTTAAAAAATAAATACCTAA AAAATATATTTTATATGGATTGGTTAGAGAGCTAAAATTTGCGTTTGAAGATATAA AAATTCATGATTTTCAATGCCGGAAACTCAAATTTGATACGGTTAATTGGGAAACC GAAACAACAACAAATTTACTGTCTAAGTAATTTTCATTATAAACTTATTTTCATATAAG AGAAGTAAAAGATTTTATTGCTAATATAATCTAGCAATGCATTTACTGCACATATA ATCGGTGATAATAATTATAACCTAATAAAGAATGATAGTACGTATTATATGATTGA ATCTAGTTGCGATAAAGATTAGTTTATTG
LH08G:00347:00812	376	98.143	NZ_AJTT01000002	168719 to 169090	GAAATGTCCTTCTAATACCGTCCAAGATACGGAAAAGAATGCAGAGTCTTGATT TGAGGGCAATATGTCATTCTGCGAAAAGCAGGAATCCAGTATCCTTAATGTCAC CCCCGTGGGCTTGACCACGGGGGGCAAATAATAAAAAAATACTAATAATATTA GTATTTTTAGCTGGATCCCCGTGATCAAGTCGCGGGATGATAAATGATAAACC TATCCACGCCACAAGGCCTACGCGGGGATGACATAGCAATGCTGTAATGACGC GATAAAAAACATAAACTTAAAAATAAAAGTGCAGAAAAGTTTAAATCAAAAATGGT TGTGTATAAGTTGTATAATGGTCATAGCGACGATTGTTATAGGGGGGATAAC TAAATAGTTGCCCTCTTAGTTCTGTGTTAATTTCTGCTGGATAAATAGAAATAGT GGCTATTTTCTTTAAATATCCTCACCAATTTATATATTAGATGATCACTGAAAA TACTTCTTTTTCTAACAACATTAAGAACTTATCTTTATTATCAGCTGCATGAGAT AAAAGATATTTTTCAGTTGTAATACTACTTACGTAATTAATATCACTTGCTGCTAT TTTAAGAGCTAATCCTTTGTTTAGGAATAGAGGTTTATTTTTATATTGTTCTGCTT AACGGATCGTCTGT
LH08G:00422:02472	293	99.317	NZ_AJTT01000002	197112 to 197402	GTTTGAATAGTAAACTCGATAGGGCTACTTGCATTCTGCTAACCATTGAACGT GGATCCATAGCGTAAATCGACATGCCCGTATTTTCAGAAAACCTGCTTATTTAAC ATATTCCTAATAGTTTCTTGGGAACAAGAACGCTCACCCCAATTTTTTAGAGGAA TGAATCCAAAAACGTTATCGCTACCGCCTGCACCTATTACCATCAGATAACCTA ATATATCTTTATAATTAGCAAGGATTTTTTCGGCTCTTTCACTACTTTAGTAGAA GATTTCTAAATTAGAACCCTCAGGACCTTTAAGAGAAAATGTAAGCATCCATCA TCTTCTGGGGTACGAAAATGTTTTGAGTAAATTTAAAA AGCTGATTTTAAAGCAAGAACGGCAAATAGCAGTCGGTATCGATTTTGGCACTAC TAACTCATTAATAGCTATTGCAGCTAATAGACAAGTTACAGTGATTAATCTATA GATGATAAAGAATTAATCCCAACTACTATAGATTTTACAAGTAACAATTTTACTAT AGGTAATAATAAAGGACTGCGTTCTATTAAGAACTATTTTCGTTAAAAAATAAAA GAAATCTAAATACTCCGGCATCTTTTTCGTTAGTTAAAGTTATATCAT GACATTGCACTAAATCCACTTATAGACACTGGCATCATATTAAGGCTAACTA TGCATTCCTTAACTCGACAGTTACTTAAAAATAAATAAGCAAGAAAGATATAACC AAACTGAGCAAATACGATCGTACAAAAATGAACATATAATCTTTAATAATTATAT CTAATACTTCATCAAACGTAGTTTTACGATAAAG
LH08G:00512:02380	367	99.728	NZ_AJTT01000002	42143 to 42508	TAATTTTTGAGTGGCATTTTTACGGGCAATATTTTTTCGTTTTCTTACTGATTC TAAACTCAGCAATGCTAATTACATGCTCAAGTAAATTAGTAGCTAAAGCTTTTATC GCTACTAAGAAAATGGTCAAAATGATCTTTTATTATATTCGACCGGTTTACTT ACACCGTTTGATACTAATTTTTCTTAGTTTGTCTTGAAAAGACGGCTCAGCTA TAAAAATAGAAAAGTACGACACTTGCAGTTTCTAAAAATA CGAGTGGCTCACGATTCACCCACAAGATATTATTTATAATAAGTTAATTAGTTTG CCGTTAAATTTAATCAAAAATAAAAAAGCTTCTTTTTATTGCACCGCATTTTTAC TTTTAGACATATTAGCAAATAATGATAGCCCTATTATACGCACACTACTATAGATAAA AATCTGCAAGCTGCTATAGAACAACAAGTTCCGGCTATATTAATGATCGGACA AAATATGGCATTAAATAATGCCTCAGTAATTCCTATTGATTTTACTACTATGGAAGT GCTTGCAAGTATTGGCTCCGGAGAGTTTTTTAATA
LH08G:00520:01570	270	99.248	NZ_AJTT01000002	90561 to 90825	AGCTGATTTTAAAGCAAGAACGGCAAATAGCAGTCGGTATCGATTTTGGCACTAC TAACTCATTAATAGCTATTGCAGCTAATAGACAAGTTACAGTGATTAATCTATA GATGATAAAGAATTAATCCCAACTACTATAGATTTTACAAGTAACAATTTTACTAT AGGTAATAATAAAGGACTGCGTTCTATTAAGAACTATTTTCGTTAAAAAATAAAA GAAATCTAAATACTCCGGCATCTTTTTCGTTAGTTAAAGTTATATCAT GACATTGCACTAAATCCACTTATAGACACTGGCATCATATTAAGGCTAACTA TGCATTCCTTAACTCGACAGTTACTTAAAAATAAATAAGCAAGAAAGATATAACC AAACTGAGCAAATACGATCGTACAAAAATGAACATATAATCTTTAATAATTATAT CTAATACTTCATCAAACGTAGTTTTACGATAAAG
LH08G:00565:02879	201	100	NZ_AJTT01000002	101209 to 101409	TAATTTTTGAGTGGCATTTTTACGGGCAATATTTTTTCGTTTTCTTACTGATTC TAAACTCAGCAATGCTAATTACATGCTCAAGTAAATTAGTAGCTAAAGCTTTTATC GCTACTAAGAAAATGGTCAAAATGATCTTTTATTATATTCGACCGGTTTACTT ACACCGTTTGATACTAATTTTTCTTAGTTTGTCTTGAAAAGACGGCTCAGCTA TAAAAATAGAAAAGTACGACACTTGCAGTTTCTAAAAATA CGAGTGGCTCACGATTCACCCACAAGATATTATTTATAATAAGTTAATTAGTTTG CCGTTAAATTTAATCAAAAATAAAAAAGCTTCTTTTTATTGCACCGCATTTTTAC TTTTAGACATATTAGCAAATAATGATAGCCCTATTATACGCACACTACTATAGATAAA AATCTGCAAGCTGCTATAGAACAACAAGTTCCGGCTATATTAATGATCGGACA AAATATGGCATTAAATAATGCCTCAGTAATTCCTATTGATTTTACTACTATGGAAGT GCTTGCAAGTATTGGCTCCGGAGAGTTTTTTAATA
LH08G:00664:02910	259	100	NZ_AJTT01000002	135550 to 135808	TAATTTTTGAGTGGCATTTTTACGGGCAATATTTTTTCGTTTTCTTACTGATTC TAAACTCAGCAATGCTAATTACATGCTCAAGTAAATTAGTAGCTAAAGCTTTTATC GCTACTAAGAAAATGGTCAAAATGATCTTTTATTATATTCGACCGGTTTACTT ACACCGTTTGATACTAATTTTTCTTAGTTTGTCTTGAAAAGACGGCTCAGCTA TAAAAATAGAAAAGTACGACACTTGCAGTTTCTAAAAATA CGAGTGGCTCACGATTCACCCACAAGATATTATTTATAATAAGTTAATTAGTTTG CCGTTAAATTTAATCAAAAATAAAAAAGCTTCTTTTTATTGCACCGCATTTTTAC TTTTAGACATATTAGCAAATAATGATAGCCCTATTATACGCACACTACTATAGATAAA AATCTGCAAGCTGCTATAGAACAACAAGTTCCGGCTATATTAATGATCGGACA AAATATGGCATTAAATAATGCCTCAGTAATTCCTATTGATTTTACTACTATGGAAGT GCTTGCAAGTATTGGCTCCGGAGAGTTTTTTAATA
LH08G:00685:00592	312	98.718	NZ_AJTT01000002	80051 to 80358	CGAGTGGCTCACGATTCACCCACAAGATATTATTTATAATAAGTTAATTAGTTTG CCGTTAAATTTAATCAAAAATAAAAAAGCTTCTTTTTATTGCACCGCATTTTTAC TTTTAGACATATTAGCAAATAATGATAGCCCTATTATACGCACACTACTATAGATAAA AATCTGCAAGCTGCTATAGAACAACAAGTTCCGGCTATATTAATGATCGGACA AAATATGGCATTAAATAATGCCTCAGTAATTCCTATTGATTTTACTACTATGGAAGT GCTTGCAAGTATTGGCTCCGGAGAGTTTTTTAATA

Read name	Sequence length	% ID	GenBank accession no.	nt coordinates	Sequence
LH08G:00800:02828	356	98.603	NZ_AJTT01000002	76876 to 77230	TGTTTGTGAATTGCGTTATTATTTGGGTTTCCTAAGAATATTGTATGCCATAAG CATTGCATCTCGTTGTTTTTGAAGCAAAGTTCGTTCCCTGGGCCCATATATA AATCATATTTTATAGGCTTTTCAGCCTTATTTATAAGACTGTCATAACATTTTAA TATAGAGTCTAATTTTATTCTTTCTATAAAATATGATGCTGGGTCTTCACGTA CCTAGTTAAATAGCGTATCGTCGATTTTATTGTACATTTCTTAAAGTCTTCATTA CATGTTAAGCTGCATTATAATTAACATAAGCTTCATTATAATCTTCTGCTTCGCTC AATATATCGCCTATTTTAGAGT
LH08G:00811:02060	260	99.615	NZ_AJTT01000002	173770 to 174028	GCTTTATGGGGTTTGCCGGTAGTTTATATTATTGAAAATAACGAATATTCGATGG GGACGTCTGTAGCACGTTCTACCTTTATGCGTGATTTATATAAGAAAAGGGGCAT CGTTTGGGATTAAGGATTTTCAGTTAGACGGTATGGATTTTGAAGAAATGTATG ACGGCTCTAAGCAAGCAGCCGAGTATGTTAGAGAAAATAGCTTTCCTCTGATAT TAGAGGTAAAACTTATCGTTATCGTGGGCATTCGACTGTCGG
LH08G:00904:02287	276	98.551	NZ_AJTT01000002	170805 to 171077	AAATATGGTAATAAAGAAATAATGCCGTATAGTAAATATATGTTCTTGATGCTA ATAATATATGTTTATCTGAAAAAATTTTTGGTCAAGAGATTAAGTTAGAAGCAA AATTACCGTTTTATTTAATAGACGCTTACATAACTTGTCTTAAAGGTAATTTG TAGTCGATCCGGTACTCGAGTCTCATGTTAAGTGTACGCTGTGGTTCTGCGT TCCGTGTCTCCTTCAAATTTCTTTTTTATTAGCTGCGTTATGTAAGACGTCTATT TAACATTAGCAATATTTAGTATATTGAAAGAAGTATTAACGATTCGGCAACGA AGTCAAAATTTGAGTTATTTGGAGCTTAACTGAAACAGTACGTATAAATCCTAGT TTAGCCCAAGAGACATTAATAATTTGAATACACTACTTAATAACCTAGTAATT ATATTGAATTCACAATCGCCAAAATCCTAGGTTGGATAATACAATAAACCCCAA TATATCACATGACGCATCTAAAATACTGAAAAATTTATTTAG
LH08G:00929:00391	262	100	NZ_AJTT01000002	196215 to 196476	CTAAAAATAATGGAAATCCCGGAAAGCTAGAAGTAAGAACATTAGATTAGGTGC AGAAACAGATTTAGGGTACTATCAAACACTTGTAACTTTAGAAGAAAGGAAA AGTTCACTTGAGTCTTTAGCATTATTTTCAGAAGCAAAGCATGATAAAGCACAAT TAATGATAAAAGCTGAGAATATTTGGAATAGACTAAAAGATGATGATGTAATAAA GCAAAATTTCAAGGCAAGCTTTAACTTTAAATAATAAAATGCCAACAAGGAATTT TTTTAAAGAGCTATTTAATGAAGAAGAACATAATGCAATAGACCGTTAAACTATA CTTTTG
LH08G:01004:01941	335	99.403	NZ_AJTT01000002	82901 to 83234	TAAAGCCGGTGAGAAAGTGGGTATTGTGCGGGAATTCATTAGGTAGTGGTAAATC CACTTTAATTGCATTATTATTGAAAAATTTAAGCCGGAATTTGCGCATATTATAAT CGATAACCAAAGCCTTTACAATACTTCTTTGACAGCTGTGGGAGCAGATATC ATTAATTCCTCAAGATATTATGCTTTTTTCATCGCTCA
LH08G:01195:02415	201	100	NZ_AJTT01000002	127231 to 127431	TAAATCAACATTTAGCTTAAAGTATTTATTTTTTAAAATTCGATAAAAGTTAAATGA CTTTATTTGACTGTAATTTGTATTTTATCTCGGTATGATTCGGCGATTGATAGTA TATTACTTCAAGAAAATCATTGATTTTAAATAGAATCTTTTCAGCGA
LH08G:01210:01821	157	97.452	NZ_AJTT01000002	114802 to 114954	ATTCAGTTGACACGGATTTCAAAGAGAGTTAGCAATAAAGACTTAAAGGAAAGG AAAAAACTAAAAGCATTAAATTGTAGAAGAAGTTTTGAGAAATATACAACAAAA ATGCAGATGCACCTTGATGGTAATATAAATCAATTAGCTCAAGCTATAAAGAAGG CACCAATATTGAGTTCATAGGTCCTAAAAGAGAAGTAGCAAGTGGTATAGATCA GGAACAAGAAATCTATGTGTTAGAATGAATCAAGATG
LH08G:01267:00554	256	99.609	NZ_AJTT01000002	84100 to 84354	TTTCTTCAGCAGTTGGCTCTCGCTTTGTGCTTTATACATCGCTTCACCAATTTT CATGCTAGCTGCAGTTAACTTTCCGGTCTTTTTCTTTAATCAAAGCAGTATCTTC CGACTCAAGCACGGCTTTAAAGCGGCTAGTGTCTTCTTCAAACAGCTCCTTTATC GTCTGATGATAATTTATCGCCATATTCTGTAAGAGTTTTTTTTCAGTGAATAAATC AAACTATCGGCAGC
LH08G:01288:02068	234	99.145	NZ_AJTT01000002	65637 to 65868	CCGATTCTCTTAATCTCCCACTTAACTTAAACCCCGCTATCTTCATATACTTTCT GCCGGACGAAATCACCTAAATCTTCTAAATCCTTAGCGGTAGCATCACCATTAT
LH08G:01422:02299	310	100	NZ_AJTT01000002	157879 to 158188	

Read name	Sequence length	% ID	GenBank accession no.	nt coordinates	Sequence
LH08G:01567:00542	283	98.233	NZ_AJTT01000002	25976 to 26253	TTATCATAAAATTACAATGAAGTTCTGACATCGAAGCACCCGCCTATTCTATAGCC TCTAAGCCCCGCTTTTGTCAATAAGTTCCCAAGATTTACGCCCTTCAGGATTTGC AAAAGTACTACCGCCCGTACGCTCTTTAATAGGCTGTGTAGATGATCTTGCCTT ATTTATTTTCATTTCATCCGTAATAATATATTTTCACTAT TCAGTGAATTTACTTGATAGCGTAACCCGTGGAAGCTTACGGGAGTAAAATACC GCTTTCACAAGTTGCTTCTCTATCCACACCTGATGCACGAACAATTAACGTGCA GGTTTGGGATAAATCTATGGTATCATCGGTAGAGAAAGGAATTACGATAGCAAA TCTTGGCTTAACTCCTGCAACGGACGGTCAATTAATCAGACTGCCGATACCGGT TTTAAACTGAAGAAAGACGTAAGAAGTGGTAAACTTGTCTAATAAATACGGT GAAAGTATACTAA
LH08G:01579:01219	245	100	NZ_AJTT01000002	98497 to 98741	GTAATTGCAGCTTTTCGTTAGTTTTAGGGAAGTAGTAATTAATAACCGTACTATAT ATTTACTCAATAAAGCAAGAGATAGAGCTCATATTTTACTAGGACTAACTATTGC CGTTAGTAATATCGATGAAATAATACGTATTTAAAACCTTCAAATGACCCGAAT GCAGCTAAACAAGAATTAATGGCTCGTCAGTGGGAAGCATTAAATATCCTACCG CTTGTAAGTTGGTTGATGATAAAG
LH08G:01648:02712	190	98.936	NZ_AJTT01000002	188231 to 188416	TCCCTGCTAATGAAAAAATCTGCAAGACATTCTTATATCAAAATACCTATCAATT CCGATACTCAAAATATAGAGGCTGCAGATAAAGAGGACGGATATAATAGGATGA GGCTTGGCATAGATAGAGATTGCAAGAGCAGTAGCAACTAAAAAACTTGATAA GCAAATATCTAGCCTAACATATGAAG
LH08G:01694:00924	330	99.698	NZ_AJTT01000002	125784 to 126114	TTTCATATCATACCTGCGTGCCCTTGTTCATGACTCTTATGTCTTCCCGCAAAA GCGGGAATCCAGTACCTTAAAACCTTTATTTGAAAAGTAAAATTTATAAAAAAAT CTTGGTCTAAAAGATTTTTTTGGAAAGCTCGATTTATCTCGCTTTACCCTGGATT CCCACCTTCGCGAGAATGACATCGATCCTTAAGTTGTCACCCATATCGCATCAA GGGAATGACATTATTGTAGATAATCTATTAATATATTAGTATCAAAGGTAGCCGT TCCACTCATTACATAATTTAGCCTGATATTCTACACTATCTAGATTTTTATCTTTC AATAACTTTTTCAGGATTCTCAATAAGCTGCTTAATTTTTACCAAGAACGATACTC CTTCTTTCCGTCAATTATACGATGATCGTAAGATAAAGTATATACATCATCGG ACGTATTTCAATTTTACCGTCTATAACTACAGCTCTTTCCCTCGGTTTTATGTAAG CCTAGAATACCTGATTGAGGAGGATTAATATCGGTGTAGACAATAATGAGCCAT ATACGCCCTCCGTTAGAAATCGAGAATGTCCACCTGACAAATCAGCCATAGAAA GCTTAACCCTCACGAGCTTGTTTAGCCAAAATTCCTATAGCTTTCTCCACTTCGG CAAATCCCATTTTATCGGCATCCCTAACACCCGGTACAACAGCCCTTGCCTGT TCCGACAG
LH08G:01773:01731	203	100	NZ_AJTT01000002	116592 to 116794	ATAGGTATTGTGGGGTTATATCTTTACTTGAAGGAAAGATTATATACTACGCATT GGTTTCAATATTGGTATATATTAATGTCACCTTCAGGTTTTATTGCAGTACTTGC CGTTTGGTTTCGTAACCGAGGTAGGTAGACAACCTTATATAGTATATAAATTTTTA AAAACCGTGGATACGGTATCACCGGTAACCGGCAATA
LH08G:01821:03034	311	99.045	NZ_AJTT01000002	154963 to 155276	TTTTATAATTGATCAAAATGTTTTAGAAATGACTGTTAATGAACTTGTCCGCAACC CAAACCTTAAAGTTAGCCGTTAATATTTCAAATATAGGAACAGGCGTGAAGCTTTA TGGGAAATAGCAGAAAACCTTATTAAGGCTCATAATGTTCCGGATCGTTTAATTA TTGAAATTACGGAAACTTCTTTCAATCAGCATTACGATAAAAATAACTTTATTTATT AATAAACTACGTAAGTACGGATGTAATGTCATTAGACGATTTTGGTGCGGGTT TTACTTCGTTTAAACAACCTTCAAAGCTTACCATTG
LH08G:01889:02706	393	98.728	NZ_AJTT01000002	109861 to 110249	GAAGAATTAACCACCTAAAAATAAATACATTATCAGAACTTTATGCAGGAAA TTCATAAATCTATGCATAAATTAACAACAGCAAATCAGAAAAGATATCATCCCTAA AATTGCTAAAAATTATAACTAAACAACTAAAGTGTATGTATAGATGAGTTTGAA ATTAAAGATATTACTGATGCAATGATAATCGGTAGATTATTAATGAATTAATAAA GCAAAAATTTTTATTTTTATAACTTCTAACACGAGTCCCAATAATCTGTACAAAAG

Read name	Sequence length	% ID	GenBank accession no.	nt coordinates	Sequence
LH08G:01959:01839	372	99.194	NZ_AJTT01000002	127037 to 127405	ACGGATTACAACGAGAATCTTTCTTACCTTTTATAAAGATAATCAATAATACATTT TATGTTAAATATCTAGACTAATTCACATGAATTATCGATTTGATAAAGCGTTAAT AGT CTATGGAACCTTAAAGACTTTTTAGAAGATATAGCAGCGTTTTCGCTCCACCTTTAC AATCATGCAAATCCCACAAGATACTGTAGATAAAAAATGCTGCTGAATTAATAAAT CTTCAAAGGGGAGATTATATTTAAGGATATATCGTTTGCTTATAAAGAGGGGAG TAGTGTATTCCAGTCTCTTAATTTGTATATTAAGCCGGTGAGAAAGTGGGTATT GTCGGGAATTCATTAGGTAGTGGTAAATCCACTTTAATTGCATTATTATTGAAAA ATTTTTAAGCCGGAATTTGCGATATTATAATCGATAACCAAAGCCTTTACAATAC TTTTCTTTGACAGCCTGTGGGAGCAGATATCATTTAATTCCTC TTTTTTATATTGATCAACAAGCTTATTAACCTTTTTCTTGTCTTCCGGTAGTTTTG AAATATTTTACGAATATTTGGCATTGTTTCTCTCTTATAAAGTTAAAAACAT ATTAATTTACATTATATATATTTTTTTATATATTTTTTTTATACAAGAAAAAATTT AATAGAAATTAACCTTTGAACGCAGCCTTAATACATAAGAAAGCTAAAAAATTT CGTAATTCCTTGACGTGCAAGCACGTGTGAGCTATTAAGTCTCTCT
LH08G:01985:01148	269	98.507	NZ_AJTT01000002	13347 to 13610	TAGCCACCATTATGTTTGTAAACCAACGCCATCTCCGTTAAACTTAAGGTTGGTA CGCGAGTTATTGCATTAGATATTATCTTAGCGTTTGTCTTCAATATATTTACTG GTGAATTTATCTATACCATTTTTATCTATAGCAGTACCGTATACAAAATTCCTAA CCCCGAAGTAGCCAAATACTTCAACTTTAGTTGCTTCAAGCTTGAGTAAAA AGCTTTATTTGTTCACTCTCCATA
LH08G:02060:02022	249	100	NZ_AJTT01000002	38275 to 38523	AGGTAATTTATGTGCGTGGATCGCAGGAATCCAAAAACATTTAATGCAACCCCG TGGCTTGACCACGGGGTCTAGAAAAACAAATTTATATTAATAATTTTAGTATTT TTAACTAGATTCCGC
700666F:214:CA2UJANXX:8: 1212:1167:48524_1:N:0:TAGG CATG+CTCTCTAT LH08G:00104:01732	125 234	100 98.298	NZ_AJTT01000003 NZ_AJTT01000003	10090 to 10214 94226 to 94457	ACATATAAAGACCTGCATACAAAGGACTTAACCTTTGATAAACTGAAGGACATA AGATACATTATGGATCCTAAGACACAGTTAATCAGCAAATAAACTATTACTCCT ATACTAAAATTAGCTAATTAAGAATAAACGCATATCCACTAACGGATCATCAATT TAAGTTGGCGTAACGTAAGGTAACATTATTGAGTAACACAATGCCAATTAATAG CATTCCGCCGGATG
LH08G:00249:01567	320	98.438	NZ_AJTT01000003	60594 to 60908	CATATCATTATTGAAGTTTCATATAATAAAAGTAGCGGTATTGCAAGAGCAAAC GGCTTAAATGTCAGGAGGCGTTAATATTCCTGCAATAATAAAGTTAATTACCAC GGCAATGCATCTTTTTGCTTTAAGTGTGGTACCTTAACATTTTTAGTATATTT AATATCATTATCACAACCTGGCAGCTGAAAGGCGACTCCAAAAGCAATAATTAAT GAATAACTAAATTTAGATACTCGCTAATTCCTGCTTCCAAAATATCGGTACGAT CATATCACTGTTTTTACAAAACATAAAGAAAAAATTCCAAGCT
LH08G:00430:02505	386	98.187	NZ_AJTT01000003	67256 to 67636	AGTAAGACAATAAACTTTAACATTAATTTAAAATGCGACCTGAATTTATTCATTTA AGAACTCAAAGCTCTTATTCTTTTTCTAGAAAGTGCAATTAACGATTGAGAAGGTA GTAGAACTTGCTTCATCGAATAAAATGCCTGCTATTTGTTTGGCAGATAAGGGA AATTTATTCGGCTCATTAGAGTTTGCATTATGTGCAGTAAAAAAGGACTGCAGC CGATACACGGGATTTCTAAATATAAAATACGATATAGATATTTTTGCTACAATT TTTGTCTTATCGCTAAAGATGAAACTGGTTATAAAAATTTACTCAAATTAAGT CTTACTTTTTACTAAAAATGATCGTAAGATATGCGATCACATTGCTTTTTGAAG
LH08G:00524:01912	296	96.939	NZ_AJTT01000003	123597 to 123881	TGAAGAAATTTTACAAAAACAAAAATGCTTGAATTTTTAAATGAATATGAAAAC CCTTTTAGCTGAGATTTACAAATAGGACATTTTCACTGCTTCGGCTTTTTTACTT AATAATGATAAACTAAATTTTTATTGATGCAACCATAAAAAAGCTTGATAAGTGG CTTCAACCAGGTGGTCATTGTGATGGAGATAGTAATATTAATTAAGTACGGTT AAAGAAGCTATAGAAGAATCCGGAATTAATGAAATCAAACGATAAAAATTAAGGA GAATTTTTGAATATAGAAC

Read name	Sequence length	% ID	GenBank accession no.	nt coordinates	Sequence
LH08G:00803:02840	351	97.721	NZ_AJTT01000003	95748 to 96090	GATAGTCAATATCTGTGTAACAAGGATTAATATCTCAAATATTTCTATAATGCTT TCTTTATATTCTTCAGACTTGGGATTTGCTGTTTCGTATAAATTGTTATTAAGCGTG CAAAGTTGCTGATAGTCTGAAAACATCATCCACCGCCAAGACTCTTACATATTT TCATGCAATATTCGCTTGAAGAATCTAAGTTTTATTGCCTATAGCGGATGGGG AATTTAATTTTACAATTTTATTATTTAAATTTAGTTAGTGGTAGTATTGAGAATTCA TATTCCTTAATTAGATTTTGTAGTTTTATAATATCATGTAATTTATTTATTTTTTA TAACCTCATCGAATAT
LH08G:00830:01910	224	98.661	NZ_AJTT01000003	133965 to 134185	GCTGTTGTTTTCTTGTCTTCCAATAGTTTTCTTTTTCTTCTCTACTTGTGT GTTTCTAGTCTTGTCTTTTGTCTTTCATATTTCTTTTCTGCTTTTTTTTGGTTA TAGTTTTTATTTCTGTACAGATATTCATTAATTATTTTTAAATGTTGCCTCGCCTAT GTTGTGCCAAGGAAGATAAAGCGACGTTAAAGATTGATTACCGCTTAAGCTTGT GGAGTATCAAACGTTGTTGTATCATTAGGACGTTTATCAAAATCAACTCCCATGA TTTTAGGAATAACGTCACCAGCACGTTGCAGGAATACATAATCCTTAATCCGCA AATCTTTTCGTGCAATTTCTTGAAATTAATGTAATGTTGCTCTGCTAACAGTTAC CCCCGCCTATTTCTATGGGTTCAAGTTCGGCTACCGCGTTAACGTACCAGTTC TACCAATCTGTACAGTAATAGAAAGTAACTTTGTGTCCTATTATTGCAGGAAA TTTATGAGCGGTAGCAAAGCGTGGACTTCGTGCAATAA
LH08G:00869:03108	311	99.678	NZ_AJTT01000003	154896 to 155205	TTTTAAATGTTTTATTATTGATGAAAGGAATTGTTTTCTAAGCATTTAAATAGTA CCATGAAAATTAGAAACATAACGTCTAATTCAGTATAGAAAGAAAAACGAAC AAAGTCAAACGCTTTGTCTCGTGCTGCAACTATAATCGCATGATTTTTTTAAG CGTCCGGTCAAATCATCGTTAGTAACTACATAATCATACTCATTAGAATGTGAT ATTTGTTTTGTGCCGACTGCATACGTAATTTTATTGCTTCTTCAATTATCGGTGCG CTCATTTTCTTAAGCGTTGTTCCAATACT
LH08G:00948:00904	306	99.673	NZ_AJTT01000003	84836 to 85140	GAAGCTATGCAAGCAAGTAGTCAAATCCACCAATATAATCAAGATTTAGGTAATT GTGTGGATAACTTCCAAAGATATCAAACTTACCGGTAAAGCTTCTAAAGGTGT ATGTGAAATAATATAACATTCTAAAAGCTGTAACATATAGTTGCAGCTTTTGTAT CATTTTGAATTAAGCTCGAAAGACCTATTGCCTGTATTTTGTCTGACAATTTAAA GCTAATCTCACCTGGA
LH08G:00952:02658	237	99.578	NZ_AJTT01000003	86156 to 86392	TACTTGCGCTAATTTTTTGTCTATTACCCTTACGAATAACCCGTTTATTATGCTAG ATGCAAGCGGTAACATGATGATCATTATGCAAATATTTTATGATACATCATTATCCC CACATCTGATTAATGTCGGTAATTTTAAATGGAGCCTTTATTACGGAAATATATTA GTAATATTGC
LH08G:01087:02301	176	100	NZ_AJTT01000003	47693 to 47868	TCTAGGGTTTTAAAAGGCTTTAAGCCTGACGGTAAACAAATTTGGACTTCTAAAG AAGCTATGATACCGCAGCATGTGCCGAAATCTATGATTATTGTCCGGCTCAGGTG CAATCGGTATAGAATTCGCTTCGTTTTATAATAGTATTTGGTGTGGATGTTACCG TAATTGAGGCACATAATAGAATTATTGTCTGCTGAAGAATTAT
LH08G:01116:01184	207	99.01	NZ_AJTT01000003	29085 to 29284	TATATGCGGCTCTAAATTTCTTATAACAGTTCCTTTGGTCTGTATTTTTCTTA CTTTCATTAATTTATATTTATAGCAAATACATAGCTTTGGATTTAACCTATATCTT TCAGCTTACCGATATAGTT
LH08G:01471:00458	132	99.213	NZ_AJTT01000003	45049 to 45174	AAATAATTGGTAATTTATAAGATTTACTATAACTTTTAAAGTTAAATAATAA TCGCAATACTCTTAAATAGGGCAGATGTCGCAATTGGGTTTTCTAGCTTTGCATA TATATCTGCCGTGTAGAATTAGCCAGTATGGGCATGCGTTAGCCATTTTTTAT CGATAATCTGCAGTAGCTCTTTTTTCTACTATTTTCAGGAGTACCGCTTTAGCAA GCCGATTCTGTTGGCTACTAAAGA
LH08G:01892:02986	248	99.194	NZ_AJTT01000003	116847 to 117093	TCATTGCGAGGAAATTACGAAGTAATTGACGAAGCAATCAGGATATTTGACG AGATTGCCACGCAGCCTACGGCTGCTCGCAATGACAACCTCGGTATCCATGCGG GTGATGCCCGCAGAAATACATCGATCTTTAATATATAATTTTT
NB501781:2:HGMVWAFX:2: 11108:16748:12433_1:N:0:TA GGCATG+ATAGAGAG	151	100	NZ_AJTT01000003	42082 to 42232	TCATTGCGAGGAAATTACGAAGTAATTGACGAAGCAATCAGGATATTTGACG AGATTGCCACGCAGCCTACGGCTGCTCGCAATGACAACCTCGGTATCCATGCGG GTGATGCCCGCAGAAATACATCGATCTTTAATATATAATTTTT

Read name	Sequence length	% ID	GenBank accession no.	nt coordinates	Sequence
NB501781.2:HGMVWAFX:2: 21106:13745:11822_1:N:0:TA GGCATG+ATAGAGAG	151	100	NZ_AJTT01000003	1055 to 1205	TTCTTAGATTTTAAATGCAAAAAACGGTACGGTAAACATTAATAACAATGTAATG TTGCGGGAACAGTCCAAAATACCGGCGGTAATAACGGTACGTTAATAGTTT TAGGTGCAAGTAATCTTAATAGAGTAAACGGGATTGCTATGT
700666F:214:CA2UUANXX:8: 1105:6238:13850_1:N:0:TAGG CATG+CTCTCTAT	125	100	NZ_AJTT01000004	123325 to 123449	CCTAATAGATTATCAAACGATACTCAAATAGTACCGGGACTACATGCTTCTGTAG AAAATAGCTTTAGCAATAAGCAACCTAAGGTGAAAGCTAGATTTATTTGGGCAG ATAATTACTTTGAGAA
700666F:214:CA2UUANXX:8: 2114:8166:42837_1:N:0:TAGG CATG+CTCTCTAT	125	100	NZ_AJTT01000004	70849 to 70973	CAATTAATATTATAAATTACACTTTATAAATTATGTAACCTGTCTATAATAACTAA TTAGTAATTAAGTTATTTAAAGTTTCGATGAATAATAGGTCTAAGTTCAATTTTTTA TCTGCTATTTCA
LH08G:00129:00502	269	100	NZ_AJTT01000004	64050 to 64318	GCAAAATCCGGTATAGTTATAAATCTTATCATATTAATTCAGATTTATATTTCAAT ATTAATGCATCTAAAATTGCTATGGTTTCAGCATCCAAATCGCCAGAAAAATTAC TAGGACGAAAATGCATTTGAAACGAAATTATAATATCTTTCATTTTAGAGTCTAAA ATTTTGGTAACTTCAAGTTTATAACCGTATGTAATAAATTTTGTGAATTGCTGC AATATCGGTTATGTCGACTGCGGCAATAGATCGTTAAACACCTGT
LH08G:00174:00921	272	100	NZ_AJTT01000004	154704 to 154975	TGAACTAAATCAGGGTAAAGGTAAGAAACAAACGAAATATGCAAAATACCCCT AAGAAAAATGAAGTAATAACATAAAACACGTTTTCTTGCTTTAAAATATCGCAGA GCTTAACATAAATTACCATAGCGATTATGGCAGAAGGTAGTACTATATATGTTTT TAAGAACTTATTGCTTCTGCTCCTATATCTGTTACTACAAACCCGCTTTAATTG AACGAAGCGTTGAGTAGTTTAAATAAATAACAGAACATCATAAAGCCATAGG
LH08G:00219:01406	195	99.487	NZ_AJTT01000004	65172 to 65365	CCCGTGGCTTGACCACAATATTTAGAGAAATAACTTGAATAGTCAAATTTACTA AATCCTGCAATCAAATAGCGGGAGATGACAGGGGCTGAATTGATCCACACAGT CAATGCCTGCTCGCAATGACGAAAAATACACTATAAACTAAGTCTTTAGCTTC CTTTTACTTAGTCTAGCTTTGCGGTTTTTTG
LH08G:00314:02276	289	96.181	NZ_AJTT01000004	58769 to 59047	TAACTCATTCAATATTATTATTAAGCAAGGCAATGGGTTATTTGCTTTATGAGGA TAAGTACATGCCACTTAAGCCTTCTATATTTAATTTAAAGTTAACACTTCCTCT TCTGCCAATCTTAATTGCATCGCCTATTTCTTTTTTCAAGTAGGTTACCCGAC AATAGCAAAATTTATCTTATATCCTTGATCATAAATATTGACAGATTTCTTTAT ACCATGCTTTTGTCTTTTCCCTCTTTCACATCTAGTAAGTAAAGAACTAATGG AACCCTTTTAA
LH08G:00420:00401	207	100	NZ_AJTT01000004	65318 to 65524	TGCTTGCTTTAGATAATAGTGAGCGTGTGTTTTAAAAAAGATCGTATAGAATA TTGGCTTGGCACCAGGTGCTAAACCAACTGAGCGAGTCGCAAAATTTATTGAGCA AGCGGGTGTACTCTTCTGAGAAAGTTAAAAAGGAAATGGAAGTAAAGCAAA AAACCGCAAAGCTAGACTAAGTAAAAAGGAAGCTAAAGAAGCTT
LH08G:00456:01603	256	99.609	NZ_AJTT01000004	88760 to 89014	TAAATTTTTAATAAGTTTTGTTGTTTTCTTGCAATAATTCCTTACCTCGGCAA ATGCTTTGTCCGTATCTGCGTAGCTTGCAGCCATTTCCATTATTATCAGCAC GAATAATCATCTCAGGTGGCAGCAGCTTAATAAACTCTAGAGAACTGCTATTAT GCCTTTTTGGATGCAAGCATTAAACATGCTCTCCGAATTTTATCAATAGAGTT AATATTTTCTCAAACATTTCTTGGAATAAGCTCTAT
LH08G:00479:02448	249	100	NZ_AJTT01000004	154629 to 154877	AAAAATGACAATTATCTTTGGAAGTAAAGGTAATTTGGCCTATAGAAAGAT ATGAAAATAAGAAAGTTTCTTCTATGGCGTTTATGATGTTCTGTATTTTAAAC TACTCAACGCTTCTTCAATTAAGACGGGTTTGTAGTAACAGATATAGGAGCA GAAGCAATAAGTTTCTTAAAAACATATATAGTACTACCTTCTGCCATAATCGCTA TGGTAATTTATGTTAAGCTCTGCGATTT
LH08G:00595:00466	205	96.098	NZ_AJTT01000004	105735 to 105931	GAAGTTACATTAGAAATTAACAAAAAATACAAAAGAATGTTTTGAATAAAATAT ATATTAATGCTGCTAAAGATAAGTGAATAGTAAGTTCTCAATCTTAGGAAATTG GGGGGTGCAAGGCTATTTAGGTGATAGATATTTTATAGCAAAAACAAGTAAAG TTTTTATCTGACCTTAAAAAATATAGAAAATAGCTAAAA

Read name	Sequence length	% ID	GenBank accession no.	nt coordinates	Sequence
LH08G:00622:00271	266	99.248	NZ_AJTT01000004	60676 to 60940	ACCCTTAAAAGTATGATCAGCAGTTTAAAGTTTGATGTAATTGTTACTAATTGCCATT TTCTCAAACATCACTAAAAAACTAGCAAAAACGGCAAAAACATAACAGAAAAT CATATAACTTCTCTTTTTAAATAACGGCATTGCAAAAATAACGGTGATGCTGTT TGTGTTTTGCATTGCCTGCAAAATTTAAAAGAGGGTGGTAGAATGGCATTGGTA GTACCTGAAGGGTCTTATTCAGAAAAGACACCGCTGCTGTTCCGTC
LH08G:00812:01794	217	100	NZ_AJTT01000004	26095 to 26311	CATTACTTTTGATAATGTCTATAGCATCAAGACTTATATCGTTGCAATTACATTA GCATTTGGTAACTACATAATAGACTGATAGCAATGCAGCCGCTACCTGTGCCA AGTTCTAGGATATTTAAGAATTTGTCATTGCAGTTTTCGTTATGTCATTCCCGC GAAAGCAGGGATCCGGTCGCTTTTTTCTGGATCCCGCTTTCGCGGGAATG GAGAAGGGATAATCATATCATTAGTTTATCTAATTTTTGCTCTTCTGTTAGCTCT TTTTTACCGGTTTCTAAAAAATTTTTCAAATTACAAGCATCTGTAGATAAAGT TTAACAACATCAATATTATAATCTTATTATTGACAAGTCTTTGATCTTCTAATGT CTTCATTGTAATAGCATTAAACAAATGATTTGTCATATTTAGATTTATACACA AAA
LH08G:00834:01577	228	99.123	NZ_AJTT01000004	51094 to 51319	CATGTAGTCCCGGTAATTTGAGTATCGTTTGATAATCTATTAGGAGCGGTTAA TTTTATGCCTGCAATCCCTGTAGTTAAGTTACCGGACTTACCAGCGACATACATA TTATTCACACCTGTACCGGTTTGTCTGCAGTATAAGTATATCCATTAGGAACAAAT CCATCTCCATTACTCATCTCAAATTTGATAGGGCGGTACATCATTCGCGGTG TGAAACCCTATTAATTAATCAACAATTTGTACCGAATGCCGATGGGAGATTTT GAAAAAACTATACCGCTTCTCCTAAAGCATTATAGTAATATTACCTCAAGTA CTACATCA
LH08G:01093:03061	337	99.703	NZ_AJTT01000004	123035 to 123370	GATATTAGTAATTAATAATTTTACTGATATCCTCTAAGAAGAAATATAATTTTT TTAATATTGACACTTCTTAATTTAGTAGTATGATGTAATTACCATGAAACATGG CAATTACGTATATAAAAAAGAGGTAAGTTTATGAGCAATAGCAATTATGAAAAACA TATACAAAAGCATTTAATTTGTTTTTCAGAAGCAACCAATTCTGCCTATTCAGCCG TAAATACTTTTTTAAACTACCTAATGTATTTAATAAATCTCCTACTATTATTTCTT TAATTTTTCTAAAACAGCAAC
LH08G:01130:00477	302	98.675	NZ_AJTT01000004	133188 to 133486	TACGCTTGTGTACGCTGCGGTGCTGCGTTCCGTGCTCCTTTAAATTCCTCTCT ATAAACTGGTTTGGAAAAATTGTCTAATATAATCTGCATCCTTTAGCTAATTTTTG CCTAATAACATTTTCGTCTATATTTATCAGATGAATTTGAACATCCTTTCAAACCTA TTTTATATTTATGACTGACTAAATTTCTACT
LH08G:01200:03346	198	97.475	NZ_AJTT01000004	138841 to 139033	TACTTTTTTCCAGACAACCTCAACATCTATCCCCATTTTTCTTTTTCTAAGTCGGA GATAATACACATATTGCTTCATTTGGTAAGCAGTGATAAATGAAAAAGGGGG GGTAGAATCCGATTGAATTTCCGGTTGTATATACTCCTGCAATGGCAATGGGA ATAATTTCATAAAATTTATTCATCGTTATTATAATAGATTACAGGATTATTATTTGTT CTTGAAAATAAGATGCTAATAGTTCCCTTATTTACTTTTCACTTTTTTATAGAATTTT TGATAGCA
LH08G:01395:01645	286	97.909	NZ_AJTT01000004	88415 to 88696	AATATAAACATGGGATAGTATTATACACGATTGCCGATCAAGAACTCCGAAAAA CTTTAACGAAATTTTGCTATGAATTAATAATCCATGATTTCTGTAATAGGTAAA ATTATTAAGAAATGTCTGTTTTTTTTCAGGTATTGAAATAGAAAAAGAACAGAATT ACAATTATAAATTTGATAAAACTTATTTTGTACACTTAATGCCATAGATTATGCT ATAAGACATGACGACGGACAAATGCTTAATGAATTATCAGAGGCTGATATAATAT TAATAGGTCCTTCTAGAACTTCTAAGACACCGACTTCCGATTTCTAGCGTATAA CGTTTTAAAAGCTGCTAATATTCCTTATGTTTATAAATGCCCCCTTTCTGATTTTT AAG
LH08G:01446:03084	391	99.225	NZ_AJTT01000004	77026 to 77411	ATTCACAATCAGCATCTCGGTACTTAATCCATAAATTTGGGGATTTTTAAGTAA ATTAACTTGTTCTCGTTTTGCTGAAATATGTTTTAATATTTCTTGGTATATTTGATT TAGTTTCTTATCAACTTTCTTATATTCTGCAGCGACACAATAATTCATGTCACCGT
LH08G:01533:00837	279	99.283	NZ_AJTT01000004	144101 to 144377	



Read name	Sequence length	% ID	GenBank accession no.	nt coordinates	Sequence
LH08G:01668:00801	198	98.99	NZ_AJTT01000004	76552 to 76747	GTGTCATGGTATTATTACAATCAACAGAAAATAATTGCTTTTTTTCATTATTTTAT CATTITTTTAAAAATAATTAATTAAGAATCACACACCGTGACGTTCTGCAATTA TTAAATAAATAGTTTGTGGATAAAATGTGAATAAATATCATTITTTCTTTGAAA AATAGTCTTTTCTAAGCTAGAATGAATTTTACACTTAATTATCCACTTGTATA TTCATTACAACTTATGTGAATAAATAATTAATAACCTATATTTTTAAGAAAATTT TAATGAAAATTTTGTGGATAATCTCTGT
LH08G:01741:01988	263	100	NZ_AJTT01000004	9014 to 9276	ATCCACGTTCTACGGTTGGAACATAACGGAATTTACGATTATCTTAGGTTATT ATATGCAAGGGTGGGTATTCCTTACTCTCCGGCAACCGGTCTCCGATACATAG CCAAACAGTTTCTGAGATGGTAGATATAATTAACGAACTACCTAAGGGTACGAA AATATATTTACTCGCTCCTATTGTTAGAGGACATAAGGGTGAGTTCAAGCGTGA AATTATGAATTTGAAAAGCAAGGCTTTCAGAAATTAATAGTTAAC
LH08G:01837:01796	230	98.696	NZ_AJTT01000004	124826 to 125052	GTTACTTCTTTCTTAACCGGCTGTAGCTTTTGTATTTGCTTTTTTAAATTATCGA AAATTGATTTTTATTTTTTGTATCGAAGCGGAATTTCTGTATAAATTTGAAAA GCTTGGTAGTTTCAGGGATTAATGCGGGCTTGTAGCTCTTCTTGACTAACCA TTAAGCTTATATTAAGAGCAGGTTTTCAGTAAACCTTGCAAAATTTGCAGCAATCATC GGTATCTAT
NB501781:2:HGMVWAFX:4: 21410:9055:4052_1:N:0:TAGG CATG+ATAGAGAG	151	100	NZ_AJTT01000004	71988 to 72138	GAACAAAGATTTACCGGTGTTGCTTTTCAGCTACAATTTTGCAATAGCGATATTCG GCGGAACCTCACCTATATTTCTCGTTGGCTTGTAGAGCGCACAGGCTTATTTT ATGCTCCGGCTTTTTATATTATGATTATTGCTGTCGTATTTT
700666F:214:CA2UUANXX:8: 1310:15115:58891_1:N:0:TAG GCATG+CTCTCTAT_(reverse d)	125	100	NZ_AJTT01000005	47603 to 47727	CCGTTTCGGTTTAGCCTTAGATGACAAAGGCCATAGTCTTTTACCGTTACCTCC TGCCATAATCACCGGTTTTATTAGACTCCTTGCCATAACCTCCTTAAAGGTAATT TGTATACCTTTGATAC
700666F:214:CA2UUANXX:8: 2311:18340:31562_1:N:0:TAG GCATG+CTATCTAT_(reverse d)	125	100	NZ_AJTT01000005	78091 to 78215	ATTAATTAACCGATTGCGATGCAGGAAGGGTTAAATTTCTCTATACGTGAAGG TGGTAGAACAGTGGGTGCCGGCGTAGTAACATAAATAAATTAATTGATTTTA TAAATACCTATTATTT
LH08G:00199:02588*	272	100	NZ_AJTT01000005	3892 to 4163	GAAGATTATTATATGCTGCAGTATTAGTTGCATTTACAAATGTTGTAACGTTCTG ACCTACACCCGGTGCAACTCCAACCGGACTATTTGCGATATCATTAGTAACTAC GTTTTCTGCATTGTTAGTACGTGTTATTACATAATCTTGGTTAGCAGCACGTA AAACCGTAATTTACGAAACGATTACTTCCGGTTACAGCAAAGTTGGGACCTCCT AAAGTACCGTTAAATCTAGCACACCTTGGATTAAAGTATAAAGTTTGTGTACCA CAAATGGAGCGAATAGAATGGCAAGACCTATAAAGAAGAAAATAAATATGCCA CACTCACTAGAATAGTCGGTAATAATGTAGCACAAATAATTTCAATAAATAT AGGATTACAATCATTAAAAGGTTCTAAAGATTCCGGTCAATCAGATCCAAGATAG GA
LH08G:00350:00627	165	100	NZ_AJTT01000005	95517 to 95681	GGATTATAGAAGTAAAATCGATAAAAATCTTTTTTATCAGCAATATTAGGTTGAAG TAACATATTATACGCAGTAGAATTAATGGGTCCTATTTTTAGACAATCCCCTAAT TTAGCTGCTATTTAATGAATATTAAGGAATTTTATTAGTCTTCCATGACTCCA AGCCATCTTCTGAATCCAAGCAAGATATCCTTCAATGTTCACTATGTCTGGTCCAA CTATTTTTAATAATGTGTGGATTTTTCTTCCCTTCTATACAGTGAATCATTACT TTCGTTAAATCATCAATATGAATAGGTTGAAATTGTTGTAACCATCACCTATTAA AGGAATAAATACGGTAATGTTGCAAGAGCCTAAATAGCGAGGTACCACCATAA CAACCGCCTGCTGT
LH08G:00551:02828	401	99.499	NZ_AJTT01000005	24341 to 24739	ACAAATTGCGCATATTGATCAGAGGATAATTCTACTAATAAGGCATAATAGACAA TAATATAATCTTAATACCATAGCCGCTTAAATTTAAAAAATACACTATAATAGCAA TTATAAATTTAGTAAGGAGCTGGGTTAAAAAATTTTTAATTGAAGTAGTGTATGG CCTATTGTAGTAATGATTTTATAAC
LH08G:00753:00799	191	99.476	NZ_AJTT01000005	101236 to 101426	ACAAATTGCGCATATTGATCAGAGGATAATTCTACTAATAAGGCATAATAGACAA TAATATAATCTTAATACCATAGCCGCTTAAATTTAAAAAATACACTATAATAGCAA TTATAAATTTAGTAAGGAGCTGGGTTAAAAAATTTTTAATTGAAGTAGTGTATGG CCTATTGTAGTAATGATTTTATAAC

Read name	Sequence length	% ID	GenBank accession no.	nt coordinates	Sequence
LH08G:01200:02029	304	100	NZ_AJTT01000005	30588 to 30891	GATATAGTCATTGTGAGTTACTGCGAGGTGTTGTTGCATGGCTCGTTTTATGTTAT GCCTGCGCAGGTCTTGTGTTGTGGACCGAAAAACCCGTTTCGGTGTATGCCGT GGCTTGACCACGATATCCAAAAACACAACCTCAAATACTAAAATTTAATGTTT TAAACTGGATCCCGCATCAAGTCGCGGGATGACAGTTAGGAAACTGGTCCAC GCAACAAAGCATTCCCGCTTTTGTGGGAATGACATCGGAAGGCTAAACTATAAA ACAACTTTTCTAGGCAATGCTCAATTTCAATAA
LH08G:01287:00555	110	97.273	NZ_AJTT01000005	134197 to 134303	CAACTGAAAGCTTTTTATTCTCGTATGATGATTCTATTATTAGACTTCTTGCATA ACCTATCTTAGAAAGAGGGACTTGAAAGAAAAACGGTAAGCACTTGCCACCGCA ACTAAATTTTAACTTAAATATAGGACAAAAATATGGCTCAAAAACCAAATTTTC TAAAAAAATTAATTTCCGCAGGGTTGGTAACCTGCTTCTACAGCTACCATAGTAGC CAGTTTTGCAGGTTACGCTATGGGTGCTGCTATACAGCAGAATAGAATAACAAA CGGAGCTGCTACAACCTGTTGATGGTGTGGGATTTGACCAAATGCCGCTCCTG CAGATGTTGCAGTTGCTCTAAATGCAGTTATTACTGCTAATGCTAATAATGGTAT TACTTTAAAATCTCCAGCCGGTAGTTTTAACGGTTTTGCTTTTAAACTGCAAAA CAATTTAGTAG
LH08G:01331:00575	339	98.525	NZ_AJTT01000005	260 to 596	ACCGTATAAAACTTTATCGCCTACTTTTAGCTCTAAAGGATGAATTCGCCTTTT TTATTACGAATACCATTACCTACGGCTACTATTTTACCTTGCAATCGGCTTTTCTT TTACAGTATCCGGAATAATAATCCACCTTTAGTTTTTCTTCTGTTCCGATAGGC TTTTATTGCAATTTCTATCATGTAATGGTTTTAAAAGACATTTTGACCTCCAATT TATTTGAACCTAACACACGCTTATAATAACTAAAACCTAAAATTTACTTTAAGCCT TACTTAAATTAAGAGCCGATAAAAAATTCATTATGCAAAACTACCTTACCTTGCGG CATTTGTCAATAAACATGTCAATAACATGCAAGAGAAAGTATTACTTCTGAAAC TAATCTATCATATTACTATTTTGTCACTATTTAAGTTAATTATCTAATAAAATAT AATGA
LH08G:01354:00607	218	100	NZ_AJTT01000005	103977 to 104194	AAATCTTCCTCTACAGCTTCAACTGCTTGCACTTCCGGTACAAAAATGTTAAGCA TGGACTCAATGCCGTTTTTTAATGTGATGGTGGAACTAGGCATCAAGGCATG CACCACGAAGTGCTAATTTAACTACACCGTTTTTCAAAGCTTTATAGATTATGTC GCCGCCGTCTGTGCAACAGATGGACGCACCCTAGTTTCAATAATCT CAAGTCCGTCATTTTCGCTTCTTGAAGCCAAATATCAAGTATAACTGCAGAGA CCGGTTTTTCGGAAAGTATTTAAGGGCTTGAGTACTATTAGCGGCAACCTTAG GGTTAAAACCTTCATCTTTCAAATTTGCAGCAATGAGATTTGCTATACTCTCTTC ATCGTCTACTATTAACATCTAGTTGTGACATTACAATTTACCTTAAAAATATTA ATACTAGGTTCTTACGTAATTTGCTAATTTAATATTTTACGATATTTTTTA GCGAAAAATTAATAA
LH08G:01628:02693	228	100	NZ_AJTT01000005	65377 to 65604	TACTACATTATGATCAAAATTTTATAGAAAAACACGATGTAATTCTACGCTTAAAT TCTCTATATCCCAATCTTCTCTATAAGAGCCTACCGGCATGAAAGTTAATACTAT CTTTTTGGCGAGTTCCTCAGTAGTACTATTTAAGAAAACGTGACTATCTTTAGAT TTAATAATTTTCAGTTACGTTGTCTCGTATATT AGTTCTTGGAAGTTTAAAGGTGTTAACCATAAAGTAGTCGAGATATTGATTGAT AGCTTAAACAGCGAAAAAATATCTGTGGAAGATTGTAAGCAAGTAGGACT ATCTCCGCTATTCTAGATGTTGAAGATTTAATAGAAGCTGCATATTCTTTAGAGG TAGCATCAAGCGGTCTTTGAACGTCCGTTAGTAAAGTTTGAATAATATAATAGAT TTTTAGAAAAGAGAAGTTAAAATCAAACCTTAAAGAATTATTGAACGGCAAAACTT ATTATTTAGCTAATCTATGCATTTTAAATATAGTAATTTTCTAATAGACCTTTC CCAAGCGTCGCTTCTAGAGATAATTTATACGTGATTTCCGTACTCGACTCTTCA CGTATTTCTATATATGCTGTGGTGTGTGCCGTGCTCCGTTAAATTCCTCTC TATAAGTTTGGTTTGGGAAGAGGTTCTAATAAGAATATATAAAAAATACCTTAAA AAGCAATATTAATAATTTTATATAAATTTAATA
LH08G:01989:01385	211	100	NZ_AJTT01000005	69712 to 69922	AAATCTTCCTCTACAGCTTCAACTGCTTGCACTTCCGGTACAAAAATGTTAAGCA TGGACTCAATGCCGTTTTTTAATGTGATGGTGGAACTAGGCATCAAGGCATG CACCACGAAGTGCTAATTTAACTACACCGTTTTTCAAAGCTTTATAGATTATGTC GCCGCCGTCTGTGCAACAGATGGACGCACCCTAGTTTCAATAATCT CAAGTCCGTCATTTTCGCTTCTTGAAGCCAAATATCAAGTATAACTGCAGAGA CCGGTTTTTCGGAAAGTATTTAAGGGCTTGAGTACTATTAGCGGCAACCTTAG GGTTAAAACCTTCATCTTTCAAATTTGCAGCAATGAGATTTGCTATACTCTCTTC ATCGTCTACTATTAACATCTAGTTGTGACATTACAATTTACCTTAAAAATATTA ATACTAGGTTCTTACGTAATTTGCTAATTTAATATTTTACGATATTTTTTA GCGAAAAATTAATAA
LH08G:00023:01565	289	100	NZ_AJTT01000006	54341 to 54629	TACTACATTATGATCAAAATTTTATAGAAAAACACGATGTAATTCTACGCTTAAAT TCTCTATATCCCAATCTTCTCTATAAGAGCCTACCGGCATGAAAGTTAATACTAT CTTTTTGGCGAGTTCCTCAGTAGTACTATTTAAGAAAACGTGACTATCTTTAGAT TTAATAATTTTCAGTTACGTTGTCTCGTATATT AGTTCTTGGAAGTTTAAAGGTGTTAACCATAAAGTAGTCGAGATATTGATTGAT AGCTTAAACAGCGAAAAAATATCTGTGGAAGATTGTAAGCAAGTAGGACT ATCTCCGCTATTCTAGATGTTGAAGATTTAATAGAAGCTGCATATTCTTTAGAGG TAGCATCAAGCGGTCTTTGAACGTCCGTTAGTAAAGTTTGAATAATATAATAGAT TTTTAGAAAAGAGAAGTTAAAATCAAACCTTAAAGAATTATTGAACGGCAAAACTT ATTATTTAGCTAATCTATGCATTTTAAATATAGTAATTTTCTAATAGACCTTTC CCAAGCGTCGCTTCTAGAGATAATTTATACGTGATTTCCGTACTCGACTCTTCA CGTATTTCTATATATGCTGTGGTGTGTGCCGTGCTCCGTTAAATTCCTCTC TATAAGTTTGGTTTGGGAAGAGGTTCTAATAAGAATATATAAAAAATACCTTAAA AAGCAATATTAATAATTTTATATAAATTTAATA
LH08G:00130:00422	198	98.99	NZ_AJTT01000006	27847 to 28042	TACTACATTATGATCAAAATTTTATAGAAAAACACGATGTAATTCTACGCTTAAAT TCTCTATATCCCAATCTTCTCTATAAGAGCCTACCGGCATGAAAGTTAATACTAT CTTTTTGGCGAGTTCCTCAGTAGTACTATTTAAGAAAACGTGACTATCTTTAGAT TTAATAATTTTCAGTTACGTTGTCTCGTATATT AGTTCTTGGAAGTTTAAAGGTGTTAACCATAAAGTAGTCGAGATATTGATTGAT AGCTTAAACAGCGAAAAAATATCTGTGGAAGATTGTAAGCAAGTAGGACT ATCTCCGCTATTCTAGATGTTGAAGATTTAATAGAAGCTGCATATTCTTTAGAGG TAGCATCAAGCGGTCTTTGAACGTCCGTTAGTAAAGTTTGAATAATATAATAGAT TTTTAGAAAAGAGAAGTTAAAATCAAACCTTAAAGAATTATTGAACGGCAAAACTT ATTATTTAGCTAATCTATGCATTTTAAATATAGTAATTTTCTAATAGACCTTTC CCAAGCGTCGCTTCTAGAGATAATTTATACGTGATTTCCGTACTCGACTCTTCA CGTATTTCTATATATGCTGTGGTGTGTGCCGTGCTCCGTTAAATTCCTCTC TATAAGTTTGGTTTGGGAAGAGGTTCTAATAAGAATATATAAAAAATACCTTAAA AAGCAATATTAATAATTTTATATAAATTTAATA
LH08G:00515:01357	273	99.632	NZ_AJTT01000006	74345 to 74615	AGTTCTTGGAAGTTTAAAGGTGTTAACCATAAAGTAGTCGAGATATTGATTGAT AGCTTAAACAGCGAAAAAATATCTGTGGAAGATTGTAAGCAAGTAGGACT ATCTCCGCTATTCTAGATGTTGAAGATTTAATAGAAGCTGCATATTCTTTAGAGG TAGCATCAAGCGGTCTTTGAACGTCCGTTAGTAAAGTTTGAATAATATAATAGAT TTTTAGAAAAGAGAAGTTAAAATCAAACCTTAAAGAATTATTGAACGGCAAAACTT ATTATTTAGCTAATCTATGCATTTTAAATATAGTAATTTTCTAATAGACCTTTC CCAAGCGTCGCTTCTAGAGATAATTTATACGTGATTTCCGTACTCGACTCTTCA CGTATTTCTATATATGCTGTGGTGTGTGCCGTGCTCCGTTAAATTCCTCTC TATAAGTTTGGTTTGGGAAGAGGTTCTAATAAGAATATATAAAAAATACCTTAAA AAGCAATATTAATAATTTTATATAAATTTAATA
LH08G:00539:02467	256	99.219	NZ_AJTT01000006	88920 to 89173	AGTTCTTGGAAGTTTAAAGGTGTTAACCATAAAGTAGTCGAGATATTGATTGAT AGCTTAAACAGCGAAAAAATATCTGTGGAAGATTGTAAGCAAGTAGGACT ATCTCCGCTATTCTAGATGTTGAAGATTTAATAGAAGCTGCATATTCTTTAGAGG TAGCATCAAGCGGTCTTTGAACGTCCGTTAGTAAAGTTTGAATAATATAATAGAT TTTTAGAAAAGAGAAGTTAAAATCAAACCTTAAAGAATTATTGAACGGCAAAACTT ATTATTTAGCTAATCTATGCATTTTAAATATAGTAATTTTCTAATAGACCTTTC CCAAGCGTCGCTTCTAGAGATAATTTATACGTGATTTCCGTACTCGACTCTTCA CGTATTTCTATATATGCTGTGGTGTGTGCCGTGCTCCGTTAAATTCCTCTC TATAAGTTTGGTTTGGGAAGAGGTTCTAATAAGAATATATAAAAAATACCTTAAA AAGCAATATTAATAATTTTATATAAATTTAATA

Read name	Sequence length	% ID	GenBank accession no.	nt coordinates	Sequence
LH08G:00988:02633	327	100	NZ_AJTT01000006	31603 to 31929	ACTCCCCCTTGATACCTACATACCAAATCTTACAGAGTCAAGATTTTGTAAATTTTT CTTTAAGTCTACCAGCGATGTGCCTGCTACTAGCTTTCCATATCGCCTGCCTAT CTGCATAGTCTGAGTGCCTAGCTGGTATAAATTTAATGCCTGATCTAGAACATC AAGCCATTGCGTACCATTTTTATGTATTAAGTGATTGGCAAGCTTTGCAGTGTAG CTTAAATCTTCTGTATGCCAATATGTATTGTATGCCAGCTTGCATTGTAGTAGA TAGATAGAGGATTTAGCTGTCATTACCTATTATATCGACTTCGCTCTAAAT
LH08G:01328:01305	274	99.635	NZ_AJTT01000006	98551 to 98823	TCTAGAAAAATTTCCAGAAAGAAGTTGGAACGGATGATATTGTTAGTGTACTCCA AGTCAATTAGGTCTAGCTAAAAAAGCTAAACAAAAAGACCAAGATTTATTAATAA TAGATGAAGAAGATCTAAACATATAAAGAATCTAAAGAAAAAGGTTATGAAGCC TACTCAAACACTGCAGTTAGTGTGTTAATAAAAAAGTCTACACCGCTAAAAAT GAGATAATAAATGAACCAAGCAACAAGAAGCTTACAACCTAAGTAATTAATCAGT AGCATAGATAATATAGCAATTATCTTTATTAATTAATAATTAATAGGATAGTAATT ACCTATAATTAATTTGCTGATATTGAATAAAACAATAACCATACCTATTTTTGAGG CAGCATTGAAATAAGTAACCGAAGTAATCGGTGATCCTTCATATACGTCAGGGA CCCCAAAAATGGAGTGGAAACACTTGAGAGTTTTAAAGAAAA
LH08G:01472:00458	205	100	NZ_AJTT01000006	99316 to 99520	GTGGATTTAGATATTGGAACAATTTAATGACGATCCGATCCATTTATTTCCGT TTATGCTATGCATTTCTTAAGCGAGGGCGCAACTAGATATTTAGCCGTTCCAAG TGATACATTTAATCAAGGTATTTACTATTTAGAGAATATGGCTAACAGATCAATAA ACTCCTTAGATGAAGCAAGAGAAAAAGGCATATGCGGTTTTATCTTTGACGCAAA ACAGCGTTATTACTACAAGCTATATTGCAAATTTTTAAATATTTAGACGAGTAC CATAAAA
LH08G:01636:03017	282	100	NZ_AJTT01000006	62415 to 62696	AGCAAAATTTCTTTTTGTAAATGCAATTTTTACTATAAGATAGTTAGGTTATAT ATTAGAATCCAAGTTATTAACATAAAATGAGATATGAATTTTATGTACCCCATATT AGACTTAGAAAGAAATAGAAAAAGCTTTTTTGGCTTAGAGAGTTTAGTATCAGAA AGTAATTTATCGGTTTGTGATTTAGTGTTCCT
LH08G:01751:03116	201	97.015	NZ_AJTT01000006	96058 to 96252	TTGTCACGCAGCCTATGGCTGCTCGCAATGACGATTTGGTATCCATGCAAAGCC TTAAGCAGGAATGATATCGATTGTTCTCTCAATTCTAATACAAGCTTTTTCTAGC TCTTCCATAGAAGTAG
700666F:214:CA2UUANXX:8: 1109:9570:7533_1:N:0:TAGG CATG+CTCTCTAT	125	100	NZ_AJTT01000007	42739 to 42863	TGAAGAGTTGAAGTCGCCTGAACTAATATTGCTACTTTTCCACTAGTATCATCAG ATACCTGTTGTCTGTGTACCTCATCTTGTCTGTAATTGCTTCAGTTTTGAA TGACACATCAATAGCTTTCATCTTCGTTTTCTAAAATATATCTTTTTTAATTTCTT CGTCAGTGGTGCCTATTGCTTTCTTCTAATTTCTTTCATCAGTTGCATACCCTT TATCGTCTTCATCACTAGATCTTAATG
LH08G:00493:02627	249	99.197	NZ_AJTT01000007	30847 to 31093	GACAGACAGGCATTTATAATGTTTTAACTGCTGCATAAAATATAGGTAACCATTT ATCCGGATCATTGCCGTGTTTCTCTCAATTTGATCGAGCAATATTACAGTCTCA ACTCTACCGGATAAAAAACTGATTTATGTTATCCATATCATCTAAGCTAACTTTT GCCACTACAGCA
LH08G:00605:00996	178	98.876	NZ_AJTT01000007	59163 to 59338	AGAGTAGGCACTCCAAGCGTGCAGAAGCAGCGGCTGCTTCTACGCCTGCATG TCCACCGCTATAACTATTACGTCATATTTTAGCATTAAATTTCTATAATTTTCAG ATTTATTAAGAAAAAATTTCTATTTCTTTTTTCGCACATTTTTCAGTATCTGAACC ATGAATACTATTAGCCTCAATTGATTCGCCTAAATCTTTTTCTA
LH08G:00669:00823	208	99.519	NZ_AJTT01000007	1664 to 1870	TACCGAATCACGTATGACGGAAATATGTACGTTATTAATGGAGGACATCGATAA AGATACGGTAGATTTTCGCCCTACTTATGATGGTCCGATTTAGAACCGGTAAT AATGCCGGCAAGTTTTCCGAATTTACTAGCTAATGGTTCTGAAGGGATAGCAGT CGGTATGGCAACCAATATACCGCCGATAATTTACATGAGCTTTTGTGATGCTCT AATACATTTAATCAACCATCCGAAAGCTGAAATTAACGATATAATGAACTTTTGT CAAAGTCTGATTTCCCGACCGCGGCATAATTTATTGATAAAGCTGAAGTTAT TAATGCT
LH08G:00671:00991	332	99.699	NZ_AJTT01000007	15458 to 15788	

Read name	Sequence length	% ID	GenBank accession no.	nt coordinates	Sequence
LH08G:00721:01865	328	99.695	NZ_AJTT01000007	52489 to 52815	CCTAATAAATATTGCTGAATAATATGTTTTGTTGGATTTTCATTTAAAGAGCGATT AGGTATATTTTTATTTTTAGTGAAATCAAAGCCTTTATAAAGTACAGGAGTATTAC TTCCTATACTTAAATGTACTTGTCTAGCAGCGGTTGTTTTATCCTCTCTATCCGG AACAGTTACCTGTTATTGGATCAAATATAATTCTAATGGGGCTCCCTTGTCTTC TATATCTGCAGATTTTATATTTACGTTAAAGTGGTTAGTTAATTCCTTGTGTTACTT TACGAATATTACCATCTGATACCGCAATTTGATACTGCAGATCTATCACG
LH08G:00727:00743	311	99.678	NZ_AJTT01000007	49313 to 49622	GCGAGTATTATAGGTACTATCGGGTATGAGGTATTAACCTTGGTAGTAGA TACAAAAGAAAAGTATATCGGGTAGATATCTGTGTACATACCATGGCTTGACCACG GTATCCAGAAAAAATTA AAAAGACTGGATCCCGCGATCAAGTCGCGGGATGA CATTAGATGTTACTGGATTCCCTGCTTGCGCAGAAAATGACATAGCGTACTTAAATT AAATAGAAAAAATACAAATGTTATTCAATATAGCTAATTCGGTCGGTAAACGTAC TGTAAGTTTGCACAAAGTGTAGGTAGTTTTCTCTATT
LH08G:00910:00305	279	99.642	NZ_AJTT01000007	40345 to 40622	TAAAGATACATTACGGTAGAGACGGAAAATTAATAAGTTATCGTTGCCAAACC CACCTATAATTTTTATAACCAATGGTATCCGGCCTAACCGTTTGTAAGGTGA ATTATGTTCTTTGCCTATAAGTAGTAGGTATTATAGGTATTGAAATAAGAAAATAC TAGAAAATAACGGAAGTATAGAAATCAGTCACGTAGACCCTGAATTTACTATAGA GCTTTTAGGAGAATAAGAGTTTTTAGTTAAATTTTATCAAAGAACTTCGTTAATT ACT
LH08G:00990:02358	303	99.67	NZ_AJTT01000007	50872 to 51173	ACTATTACGCATTTTCATCTTTACTACCGTACCATTTAATTTTTCTTGATAAATCA TAGCTACTTCTTTAGCTATTTTTGCGGCACTAATCATATCATGAGTTATAGTAATC GTAGTTGCCTCTAACTCTTCTTGTATTTTTATAATTAATTCGTTGATAACATTTGC CATGATAGGATCAAGCCCTGTGGTCGGTTCATCAAGCAATAAAATCGACGGTGT ACTACAAATAGCCCTAGCAAGGGCTACTCTTTTTTGCATTCTCCCGATAATTC GGCAGGGTAAAGCTCGAGTATTCTAG
LH08G:01166:02332	83	98.75	NZ_AJTT01000007	47634 to 47712	AAAAATTTCTCTACTTGTATCTGAGTGTAAATCAATAGTAATTACATGGTTTACTC CGAGCTTCTCTAAAAATCTGCTACTT
LH08G:01538:00955	329	98.784	NZ_AJTT01000007	50655 to 50979	G TTCATCAAGCAATAAAATCGACGGTGTACTACAAATAGCCCTAGCAAGGGCTA CTCTTTTTGCATTCTCCCGATAATTCGGCAGGGTAAAGCTCGAGTATTCTAG GAGATAAACCAACGGCATTAAAGCTTGCACCGGCAAGGTCGTTTTTTTTCTTTCT TAGATAATTTTTTAAATCTCGAAAGTAATATATCACGTATATTTAAGGAGTCAAA TAATGCTCCGCCTTGAATAAAAAAACCTATACCATCCATAATCTCAAATTTTTT GTTTACTTGAGATATCTGGATTTCTACATTATCAATAAAAAATTTTACCTTTATC TATACAAGAAATTTTTGAGAGCTGGGTTAAACTAATGATCTCGTCTTGCTGC AACCTATGGTGGTAGTTACTTTTTATGATCACGATGTTTTCGGTATATGATTATG GTTTCTACGGTAAATGTCAATATAAGAGCAAGTTAATTCACAATAGTATAGAAGA CAAAAATTC AAGG
LH08G:01900:01532	178	98.876	NZ_AJTT01000007	61066 to 61241	GGCAAATGATTTCTAGATTACTAATTAGTAAAGATGTTTGTAGTTTTGATAATGTA AGCCAAGTGGTTAATTTGGTTTTCAAGGCAAGATAGTGCATTCTTTCAGTTTTCAAG TAGGAATGTATAAAATAGTTACGGCTTTTCTAACTTTATATGTTATGTTTTTTGGC TTTAAACTATTACTTGCAGGTGAAGTGCCGCCAAAAAGTGAGTATATAAATTTTA TATTGAAAATGATATTCGTAACCTATTTTTCAATA
LH08G:02043:01078	257	100	NZ_AJTT01000007	60308 to 60564	GTA AATATCCGCATCTACTATCCCGACTCGGTAATTTGCTAGACTTAACTGTTGA GCGATAAGAGCAGATATTGTAGATTTTCCGACTCCGCCTTACCTGACGCTACT AAGATAATTTTTTTTA
700666F:214:CA2UUANXX:8: 1108:8596:42754_1:N:0:TAGG CATG+CTCTCTAT	125	100	NZ_AJTT01000008	25142 to 25266	GTAAATATCCGCATCTACTATCCCGACTCGGTAATTTGCTAGACTTAACTGTTGA GCGATAAGAGCAGATATTGTAGATTTTCCGACTCCGCCTTACCTGACGCTACT AAGATAATTTTTTTTA
LH08G:00129:01101	116	100	NZ_AJTT01000008	20602 to 20717	ATTTAGACGTGCATCCAGTACTCGCATCCTCACGTACTGCGGGGCAAGTGCT TCCGTGTCTCTTTAAATTCCTCTCTATAAGCGAATTTGGCAAGATGTCTATTAG TCATTTTT

Read name	Sequence length	% ID	GenBank accession no.	nt coordinates	Sequence
LH08G:00238:00771	252	100	NZ_AJTT01000008	17949 to 18200	CTTGTAAGGATCGTGATATATTAAGGTTTGAGCCGCACAAATTAATAGAAGGTT GCTTGCTTGCAAGCTTTGCTATAGGAGCGAATAATTGTTATATCTATATTAGAGG TGAGTTTTATAATGAAGCCTCTAATATTCAGCGTGCCTTAGATGAAGCCTATAAA GAAGGGTTAATAGGAAAGAATTCCTGCGGTTTCGGGTTTTGATTGTAATATTTATT TACATCGTGGGGCGGGTGCTTATATTTGTGGTG
LH08G:01472:03357	329	100	NZ_AJTT01000008	39709 to 40037	AGCCGTTTAACGGTAGTATAGTAATAATAAAAAATTTGTTATTTTAAGCATTTGT ATCAGTTTAAATATATTAACCTGTATTATAAAAGGAGAATTAAGGTTAAGAT CAGAAAAACCGGTAGCAGTAGAGGATATTGTAATATTTATAAAGAATCGCCCT CTATAATTACTCATTATCACGGGTTAACCGTTAGTCAAGTGAGTTCGCTTAG AGAATCACTTAAATCTAAAGAAGCAGGTTTTAAAGTAGTTAAAAATACTTTAGCA AAAATAGCTGCAAATCAAACAGGGCTTAATAGTATTGCTAATTTATTTGCGGG
LH08G:00343:01258	271	100	NZ_AJTT01000009	20861 to 21131	AGTAAAATATTAGAACTTGAAGCGGAATCCCGCACGGAATTCGGTACGGGAGC AGCAAGAGCATTAGAAGAGCAGGGCGTGTTCCGGCTATTATTTATGGAGCTG GTAAAACACCTGTTAGTATTTCTTTGGAAGAAAAGGAAATAACTAAATATTATAG AAAGCCGGCTTTTATCTCTCAGTTAATTAATTTAACAATTGATAAGAAAAAATATA AAGTATTGCCGAAGGCTGTAGAATTACATCCTGTTACGGATATAGTACGCCATG CCCTAAAATATCTCAAAGCGAAATAGCAGAATTGCCCGCTATTTTCGTTATTACGT GATCCTGAAAAACATCATGTAAGGAGCTTCTTCCTCAGAGCTTAAACAAAAG GTTGAAGAGTTATTA
700666F:214:CA2UUANXX:8: 1215:13592:16288_1:N:0:TAG GCATG+CTCTCTAT	125	99.2	NZ_AJTT01000010	7225 to 7349	

\*Gene name: *ompB*.