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.

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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.

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

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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; ≈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.

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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.

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Chlamydia trachomatis Biovar L2 Infection in Women in South Africa

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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 (≥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

[1]These authors contributed equally to this article.

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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:TAGGCATG+CTCTCTAT_(reversed)	125	100	NZ_AJTT01000001	102663 to 102787	AGCTTTCAGTTTCAGTAATGATAGCTGTTTTACTTTGGAAATAAAGAGCTTTACCGATTAACTCAGTGCTTACTACATTAGTATCTCTTGCAAAAAATTCACGAGGTAAAGGGATTAGTTTATTC
LH08G:00089:01332	294	98.98	NZ_AJTT01000001	58385 to 58675	CACGCAGCAAGTCTTGATTTACCGGTTCCGGGAGGACCAAACATTAAAAGGTTATGCCATCTGATGCTGCAATTTCTAAAGCTTGTTTAGCAATTTTTTTGACCTTTTTATATCTTTAAAATCGGGATAATTTATCGCCTCATCTTGTAGCTTAGCTTCCGGAGGAGTTAAAAACTTGTGAACCTTTAAAATGATTTACTAATTCAATTAAATTACCTGCAACAAGTATATTATCATTACCCGACCAAGCAACTTCCGAGCTGTTTTTACTTGAACAAATCAGACCTTTACCTC
LH08G:00103:02050	405	96.79	NZ_AJTT01000001	235861 to 236252	TTAGCTGATTCTAACATAGCTTTTTCTAATGGTTTTTTAATATCCATCACTTCATCTTCGCTTAAGCCATTACGTTTTTTCGTCGTTTCACCTGCTCTACTTGAGACTCACTTAAATCTCTGGCAAACCAATTTAAAATTTTATGAATGAAAATTAATTAAAAACTTATAAAAAAGAATTGTATTTTTTTTCATAGAAGAGGTCCTGATCGTAATTTTCATCAGGGATTTTCAGTTATGAACCTTGAAGGATAAGAACGGACTATTTCATAAAATATTTTTTCTGCTTTCAGCATGAGTAATGTAGAGGTTCTTTTTTGGCTCTCGTAATACCGACATAAGCAATGCGGCGTTCTTCTTCTAAGCCTTTTTTCGCCGTCTTCGTCTAGAGATCTTTTGAGACGGA
LH08G:00199:02115	268	99.627	NZ_AJTT01000001	173179 to 173445	GAGGGTAGAGCGTCCAGCCCGTTCCTGGCCCACCGTCAACAAAAGCTGATCCCATAAGTAAAAGAAAAGCAGGCACTAGTAGCCAAAAACTGATATTGTTAAGGCGTGGAAATGCCATATCGGGAGCCCCTATTAACAGAGGTACGAAATAATTACCAAAGCCACTGAACAAAGCCGGCATAATCAATAAAGAATACCATAATAACCGCATGTGCTGTGATAAGCACGTTATATAGCTGGAAATCATGATTTAAGAAAGTGCCGCCGG
LH08G:00260:02605	310	99.032	NZ_AJTT01000001	304717 to 305023	CAAGTTTTAGACTAGGTATATTTAATATTGAATCATTAATCCATTTAATATTTTTAAGACCTCGTACTTCTGCACGTTTTTGTGCTACTTCCATGCTAGGCTTGCTGAAATCTAGATATATTATTTTCGGCATTTTTTATCTTTTAACTGCTCGGCAAGATAAATAGTCGAATCACCGGTGCCGCCGCCTGCTATTAAGCATCTAAAATTATTATTAAAATTTTCTTTTCCTTGATATAGAAAATGGTTTAATTCTCCTAAGAACTCACCGCATGTTGCAAGTAAATATTCTTTTTTCTTGATTTGGGTC
LH08G:00384:01842	213	99.531	NZ_AJTT01000001	22382 to 22593	CTTTTTGTATCTCTATATTGTACAGTATCAAAATTGCTGCTACATCAAGCATAGATGTATCATCGATGTTATGTATATATCTATCGTATTCAGCAGAAGTAAAGTGGCTAGGGTTAGCATAAGAAATAATAAGTTTATATGCTTCTGGATAAAATGACGTAATGGCATGATGTAACCCTAACAAATTTATAGCTGTTCTTAGATGCTAAAATT

Read name	Sequence length	% ID	GenBank accession no.	nt coordinates	Sequence
LH08G:00577:01769	208	96.172	NZ_AJTT01000001	341663 to 341864	GTTATAAAAATAAATTTCGTCCATAGAGAAAGTCTAGCATAACAATGCATTAAAA GTAATTTAAATTTGTCAATATCAAGTTCATTGAAATTTATAAGCCTTTTGTTGCGT AATTTTCTGCTTTCTCATAAAAAGATTTATCATATAAAGTTTTTGCTAGATTTTTTG CTACCGTAAAAAACAAATTCTTTAGATGTAATAAGTTTTT
LH08G:00579:02051	362	100	NZ_AJTT01000001	124494 to 124855	GATACATAAATAATGCCATACTTTCAACAGGAGCATATTTAAGCCAATCATCAAT GCTAATACTATTACCTTTTGATTTTGATATTTTCTCACCATTTTCATCTAAGAATA ACTCATAACATAACTGCACCGGCGGCTTTCCTCCTAGGATTCGGCAAATTTCCG AATAAAGACGAGCATTTGCCAAATGGTCTTTGCCGTACATCTCATAATCGACTTT AAGCGCAGCCCAACGCATACCAAAATCCGGCTTCCACTGTAATTTGCAATGCCC TCCCGTTACCGGTACTTCTATATAATTACCGGCTTTGTCTTTATACGTTACAGTG CCTGCTTTAGCATCCCATTTCTCTATAGGTACT
LH08G:00581:02966	309	99.029	NZ_AJTT01000001	218033 to 218339	GTAGGAATTGCTGTTTTTGCTTATATTTTTATTATAATTAATGCAGAAACACTTTG GTGGCTTGCAGTTGGCTCATCCTTAATAATTATTGGAACATCTAATGATTCAGGA TTAAGTAAACTTATTTTCGGTAATCCAATAACATATTTTCTAGATCAAATTTCATA TGCTTTATACCTTTCTGCTTTAACTACAGAATTGTTTGTAGCATATTACTGGATTT TATCCAACTCCTTTATGGCTTAAATTTGCTACTTCGGTTACAATAGCTACTATTTT GCATTATATAATTGAATTTACCAGCTCGCC
LH08G:00660:02650	139	97.744	NZ_AJTT01000001	347909 to 348039	ATGATAATATCTTGCAAATTTAGATATTTTAGGAGTATATTCCCCTAAATATCTAT TTATCTAGTTGATTTAAGAGGTTATCTGTAAATAAATTGTAATTAGCAAGTCAAGA TGCTTTTTTAGCTAAAATTGAATTAAG
LH08G:00737:02796	261	99.237	NZ_AJTT01000001	242578 to 242838	ACAATATTTTTTTGGTACAGCGTCGTTCAGAAAGCTTGATACAAGTGAATTTTCT GACATGCGCCTTTGCTCACGTACTTTTTGTACGTTCCGCAGGCTCAGTCGTCAA TTCATCTTGTCTAAAGCTTTCTGAATCTAGCTCTATCCACTTCTATTTTATTATTG TAAAAAAGTTGCTACAAATTATTAATTAAATGTATTAATATTAATAAAGAATCAAA AATATTAAGAAAATTTTTAGCAAACGGCATCATTATGCGG
LH08G:00813:00255	253	100	NZ_AJTT01000001	301855 to 302107	AGCAAAAATTAAAGAATATAATAAGGCTAAATCTGAGCTCGAAGAAGCAAATAAT TTTAAGCTAGAAGTGGGACTTGATAATGCCACTTTAGAAATGATTGAAGACGAA ATATACACTCTTGAAAATTCGTTACCAAAACTTGAAAGAGCCGTAAAAATTGCTT TATTACCAAAAGATGATGCGGATAGTAAAAGTGCTATTATTGAAGTTAGAGCAG GAAGCGGCGGAGAAGAAGCGGCACTTTTTGCTGCC
LH08G:00820:01524	258	100	NZ_AJTT01000001	81173 to 81430	ATTATCCATATCACTTTGGCTTAAGTAACTTTTACCGACTGCATAGGTAAATAGT GTAACATGCGGTCTTATAATAAAATGAATATTAGGATGTTGTAATGCATAATTAT AGAAAAAATAGTGATAATTTAAGAAAGTAGAACCTCCTTCATATAAATCTCTATTT TTAAATGATAATTCCCATCTAGGAAGCCATAAAATGGTTTCCGAGTTTGGTTTTT CTTTAATATTATAATTTCTTACTTCATAGTATGGTTG
LH08G:00832:00648	282	98.94	NZ_AJTT01000001	200820 to 201101	AAGATTTACCCGTTACTTTACCTGATGATGTAAATTTTGACGGTCACGGTAATCC GCTTGATCATCATCCTAGTTGGAAACATGTTAATTGTCCGAAATGCGATAAGCC GGCTGTGCGTGAAACCGATACTTTTGATACATTTTTTTGAATCACTTGGTATTTT ACGAGATATTGCAATAGCAATGTTACAGAGATGACTGATAAAAAAGCTTGTGATT ACTGGCTACCGGTCGATAAATATATAGGCGGCATTAAACATGCGGTAATGCATT TATTATATG
LH08G:00880:03124	260	100	NZ_AJTT01000001	302965 to 303224	AAAATTTCTTAAGACCGAAAATCAAAAATTTATTACCTGATCCTTTTCATCTACTT GATATGGAAAAAGCTGTAGATAGAACCGTTACAGCTATTTTAAATAACCAAAAAA TATGTATCTTCGCCGATTATGATGTAGACGGTGCTACTTCAGCCGCCTTACTTA AAAATATTTTTAGAGATTTAAATATACTATGTGACATTTATGTTCCTGATCGTATA GCTGAAGGATACGGTCCAACTCCTTTTGCTATGCAAAAA
LH08G:00901:00649	283	98.233	NZ_AJTT01000001	16343 to 16620	CTTATTAACCATAATTTCGTTAATACCGTCTTCAGCAAATAAATGTTTAAAAGGAA GTAAAAACGTCTCTAAGGCTGCAAATTCTTCATTCATTTCATTACCTTCGATTTTA

Read name	Sequence length	% ID	GenBank accession no.	nt coordinates	Sequence
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LH08G:00911:00432	271	98.893	NZ_AJTT01000001	354716 to 354983	AGTATTTAAACTTCTATAAATTTCGCTCAAAAATACAAGTAATAGATTGTAGTAAC GAATATAAAGTTATCTACTCACTTCAAAAATTAGATATAGACTCGCTAATTACGG TTCGTGATCCTCGTTATGCTAAGCTTGGTTTCCGCTCAATAAATAAGCTCGATGT CATACCGCTGTGCGGTATCCAGACAATAATTAAAAAAAGACTGGACCCCGTGGT CAAGCCACAGGGTGACAGAGGGGGGAACCGCCCCCCCTCAACAACATCTCC
LH08G:00932:00966	290	98.966	NZ_AJTT01000001	370114 to 370400	CTATACCCCAAATGCTGAAAAAGACTGTTTTAATTCATCTTTCCCTATTATTCATA CTAAAACAGATGCAAAACATAATACTTGGCTTCACATAGTTCGCACTGATTTGCT CGGATAAGGAATTACAAGAGTTTATAGACGGTGATATAAAACTCAATTACCCATT TTACACTTTAGAACAAGATTTTTTCTGATTCTCCTTTATGGTACTACACACTTTTT CTCTAAACCTTTATCTTACTGGATCGGTCACGTTTTATACCATTAAAATTGATCAT GAGCGTAAAACA
LH08G:00996:01347	265	100	NZ_AJTT01000001	261795 to 262059	AAAATATTACCAGTTAGTATAGGAGCATTATTAAAAGGTGCGAAGTTTGCCTTCA CTAATCCCGTAAATAGTTATAATCTTGTTAAACTTGCAAGCTCCTCTGATATATAT CTTGATTCAAAGTTTCAAAAATCTGTTCTTGAAAAATCTGAAATATAGGATTTTCT AAAAAAGCATGCCGATGATTTACCAAAAATAGGACAAATCTTAGCAAAAGCAGG TTTTAGAGAATTTCAAGATAAGAGTGCTTTAGATGAAAAGGGAC
LH08G:01008:02633	232	99.138	NZ_AJTT01000001	82660 to 82889	CTAATTATTAGTGCAGAAGAAAAATCTATTTTTCTAAAGCTCTATAGAAAATTTAA AACAATAAAACTAACATTTTATAAATTATTTTTAAAAGTTATGACAACTAGAAAAG ATAAACCTCTAAATATTTATCATACTTTAGTTTCCATTATTATACCTGTCTATAATG GGGCTAATTATATGAAAGAAGCTATAAATAGTGCTTTAGCACAAACTTTACAAAA ATATTGAA
LH08G:01016:02876	294	98.639	NZ_AJTT01000001	273506 to 273795	TTGATTTTAGAGGAAGAATTTTCTATATTACTGGGGTTAATCGTCATTATTTGGT CTAACCTATCTTGCTATTGGCTAGAGTTATATATTAAAGATTGTCTAAATTTAAGT CAAGTTAAAAATCAAATTAAAATGAGTAATTATTGGTTAAATATTTATAAAACCAA GAGGTATAAGTTCTGCTCAACTTGTTAGCATAGTAAAAAAAAAATACTAGGTAAA ACCAAGATAGGACATGCCGGTACTTTAGACGTAGAAGCGGAAGGAATATTACC GTTTGCCGTAGGTGAAGCT
LH08G:01054:02101	244	98.086	NZ_AJTT01000001	148127 to 148333	TTTCGTGTATTAGTGTTAACTTAATAGGAGAAAAAACCTCTTATGCCATTTCCGC GAAATCCGGAATCCAGTACTTTAAAGCTTTTTAAAAGCTCGATTTATCTTGCTTT ACCCCTAGATTTCTGCTTTCGCAGGAATAACATCATATCACTGATTCAAAAAGAG ATTAACATGAAAAATTTTATAAAATATTTAGTTTTTTACCTGGTTTTCACGTACTAA TTAGTTAAGTGGTAACGGTGAA
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LH08G:01247:00947	73	100	NZ_AJTT01000001	351245 to 351317	CTTGCCACCTGAATATCGTTGCAACTATAAGTAAGTTAATTATCGAACACATTAA TTGCAGTTGATCAAAACT
LH08G:01297:00604	245	99.592	NZ_AJTT01000001	366937 to 367180	AATGTTTTTTAAGTTTTTTCTGAATACACTATAATTACATCATTTGTAACATTAAGC GAATTCTTTAATACCATTTCAAGCATTGGAACTCCACCGACTTTATGCATTACTT TCGGTAAATCGGACTCCATTCTAGTACCTTTACCGGCTGCTAAAATAATTATTTG ATAATTTGCATCGTTATAAGTCATGGTTCTCCTTGTATTATTTCGTAAACATCATC AGATAACTCATAATTCCCAAAA

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LH08G:01318:02288	287	99.306	NZ_AJTT01000001	7990 to 8276	CTCTATTCATAATATCTGAAAAAGATCGTACAAATTCTGTTGCTCTAATAATTTGT GCCATATTTATCCTCAAAAATAATTACCATATTTATACCTTTGATACTTCAAGATT TGGTACGTCAAATTTCGGGATTCGCCTGTGCTCACTATTGTACGCTGTGTAGGC GCACTGCTTATTTTGACTTCCAACTTTGAAGTATCTACGGTATACATATTATATG ATTATGTGTAGATTATGTAAATATGTTTATGTAATATAAGCTAAAAATTCTCTGAT TAAGATTTGA
LH08G:01333:00336	374	97.861	NZ_AJTT01000001	258664 to 259030	TTATCTAAAGCACTCTTATCTTGAAATTCTCTAAAGCCCGCATTTGCTAAGATTT GACCTATTTTAGGCAAATCATCCGAATGTTTTTTTTAAAAAATTTCCCATATTGGA GATTTTTTTAAGAAGTGATTTTTGAAATTCCGGATCAAGATATATCTTAGAAGAG TTAGCAAGCTTAACAAGATTATAAGTATTTACAGGATTAGTTAAAAATAAGTCTT GCTCCGAGTAATATCGTTCTTAAGCTTATACTCTTTGAAGATGATAAGTCCTGAA TTGCACTCTTTAGTACTTTATTAGCTTTAGAAGAAGATAAAAATTTTTCTACAACT TTTTGATAGTGTTTAATTATTTATAACAACCATAAAATTCAC
LH08G:01354:00365	286	99.65	NZ_AJTT01000001	262020 to 262305	GAGGTTTTTGTAATATATCATCAAAAGCTTTTATATAGTCGCTTGGAAGTATTTCA GTTATGTAATTCGCAATATCGTTACCTTTTTCATTAAAAAATTTTCAGCAATTTTT ATCCGTGGATAACATTCCTAATGTTTTAGAAGTTACTTTATTATAGTCCGGTACT TCTTGCTTTATCTCAAGTGCAATTTTTTGAAGGCTTTTAAGTACAGCATCATTTTT AAAACATTCTTTTAGTATTTCGAGTCCCTTTTCATCTAAAGCACTCTTATCTTGAA ATTCTCT
LH08G:01360:02559	261	100	NZ_AJTT01000001	366624 to 366884	TCAATTATTTATTCAACCATTGCGGAGTTATTCAGTATCCAATAAATATAGCATCT AATGAAGATGTTTTAGAGGCAGTCATAGAAGCCGGGGGGCATGATATTATATCC GATGATACCACCCATACAATCTATACGGATATTGAAAATTTCTCTAAAGTTCTAG AATTTTTAACTGGCAAATACGGCATACCTGAAGATTCGTATATAGGCTGGATCC CATTAAATACAATAATTATAGATGATAAGGAAAAAGCTGAAA
LH08G:01418:00298	332	100	NZ_AJTT01000001	246549 to 246880	GATAGTTATATTATCGCCTATTTCTACCGGTCCGTTAAACCTTGAAGCATGAATT ACACTACCGTCTTGTATGTTAGTATTATTTCCTATTTTTATCGATTCAACGTCGCC TCTAAGAACCGTATTAAACCAAATGCTTGAATTACTACCTATTTCAACATCTCCT ATTAAAGAGCTGCTTTCGGCAATATATGCACTTTTATCGATTCTTGGCGTAACTC CTTTGTAAGGGATAATGAGCATTAATTATAATCTACCCAAGAAATATTACCGTCT TTACGATAATAAACTATATTGATACGATCATTATTTATATTTTTAAATACTACTGC
LH08G:01483:00337	349	99.143	NZ_AJTT01000001	117122 to 117469	TAGAAAAAATAATCATTGAACGTGTCAGATCAGTATCGATACCTTGTGAATAATA TTTAAATTTTCATTGACTTAGCATTACCAAAGTATTAATTTTTGTTAAGGTTTAGT AAATTCTGAACCGTCAACAATTTATTAAATATATTGGAGGAAGGTTATGAGTAAA AGTAAGGCTATTGAAAATAACGGTATTAGTAATACCAATAGTCCAATGGTAAATA TATGGCCCCAAGACCGGAAGGAGTAAAACCTACCTGTGTAGTAATTACTTATTC TGTAAGCAAGGATATTAAGGCTGTTCGTGAAGTATTGGATGAGCGAGGTGCAA GTGTTCATTACATAATTGATA
LH08G:01503:00952	368	98.113	NZ_AJTT01000001	22507 to 22873	ATAATAAGTTTATATGCTTCTGGATAAAATGACGTAATGGCATGATGTAACCCTA ACAAATTATAGCTGTTCTTAGATGCTAAAATTTGATTTTATTTCGTCATATTTTTTA GTTTTTATAAAATTTTTTTATTAGCTTATTCAAAGCTGTTGTGGGTCATTGTGAAT AATATTCAGATGGTAAAGACATGTTTTATATCCTATCAAGTTGCTATTATTTCATG GTAATATGTTTTATAATAAATAGTATATCTTTCTATTTGTAAAGAAATAATTTTAAT TACAAACGAACATTAACATCTTTATTAAGCTCTCTTATCTACCTCCCAAATCATTA TTAATCTGAAAACATAAATTTATTGGAAAAA
LH08G:01617:00382	252	100	NZ_AJTT01000001	183939 to 184190	ATATATGCTTCAGGAAGATATGCCTTAATATATTCCATATCAGATGCGTTTTTTAA TAAATAGGGTGATACAAATTCTAGTATGTCCTTACCGCTTCTTTTATAATTAGCA AATGAGTAAGCAACACAAATACCGTAGTCATTTAATAAATGCTTGTGTCTTGTCT

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LH08G:01673:02121	312	99.359	NZ_AJTT01000001	247493 to 247802	ATTAATAAATCTATCTTCTACTATTCATACTAATGATTTAATATCAAAAATCAATGA GTTAAACCTTGATAACGAGATTTCAGGAATTATAGTTCAGCTTCCTTTGCCAAGC TCCATAGATAAAAATAAAATTTTATCGGCAGTATCACCTTCTAAAGATATCGATG GTTTCCACCCTTTAAATGTCGGTTACTTACATAGCGGAATTAGTCAAGGCTTTAT TCCCTGCACTGCTCTTGGTTGTCTTGCAGCTATAAAAAAAATACGAACATAATTT AACCGGTAAAAAACGTTGTAATTATTGGACGCTCA
LH08G:01752:01279	215	99.074	NZ_AJTT01000001	366307 to 366521	CACTAAATTAATTCGTGAAATAGTTACTGCAGCTAAAACCGGTTCTTCTAATAAC CCTGAAAATAATCCACGTCTTAGAAATGCTTTAACCGCTGCACGTAGTCAAAAT CTCCCTAAAGAAAGAATAGATAAAGCTATTAATAGTGCGAATGATTCTTCTAATA ACGAAAATTATACAAGAAATTAGATATGAAGGTTATGCACCGAATGTATTG
LH08G:01910:02516	322	97.059	NZ_AJTT01000001	138157 to 138477	TCTATATTATTTTTCTCTGCCCAAATATTAGCAAGATAAAGAAGTGCTAACGAAT CGCTCCCACCAGATACTGCAATCGATATTTTAGATAAGCCAAAATTACCTATTAG ATTATTGATATTATACTCAAATTTTTCATATAGCATGGTTGAAAAATGTTAGTATT GTAAAGTGTTTGGATATTGTGGTCAAACTTAGTAGTATGTCATTTCCGCGTAGG CGGGACGTTGTTGCATGGCTCTTATGTCATTCCTGCGAAAGCAGGAATCCAGA AAAAAAAGTATAAATACAGCAAATTCTTGAAATTAAAAGCTCGATTTAT
LH08G:02102:01594	285	99.298	NZ_AJTT01000001	359185 to 359467	GAAAGCTTTACTTAATTCTTCCGAAAAATATGAAGCAGCTCTAAAACATTTTGAG AATATAGGTATTACTGCGGATGTAAAACTAGACTTACAAAAAAATGCTAGCTAAT AAAGATAAAGTAGTTCTTGATCTCACAAAAGGTATAGAAAGTCTCTTTGCCAAAA ACAAAGTTACTAGGATAAAAGGTGAAGCTAAAATTAGCTCTAGTAATAATCGTTG AAGTAAATAAAGAGCAAATTAAAGCCAAAAATATCCTAATTACTACAGGTTCCAG CGTCATAGAA
NB501781:2:HGMVWAFXX:3:21506:4952:12115_1:N:0:TAGGCATG+ATAGAGAG	149	99.32	NZ_AJTT01000001	252942 to 253088	GTATTAAACGGTTCTATTTGTGACGAGAATGAGGAGAATAATAAATGCTGTCATT TTAGCGTACCGGTTAATAGAGATTTCAATGACCCTGTAATTGATTTAGGAGAAG CAATATGCAAATGAAGACTTTATTGTTACTCCTGTGTGTA
NB501781:2:HGMVWAFXX:4:21504:24946:16382_1:N:0:TAGGCATG+ATAGAGAG	151	100	NZ_AJTT01000001	198785 to 198935	GCCAAAGAACGGTGGGAAGAAATAATTTTTGACTAATAGCTAAAGCTTCTCTATT ATTTCCCTTAAGCACACTAATTAAATATTGGTTATGAAGAAAATTATCGGATTATT TTTTGTAATTATACTTAGTGCAATAAGTACTAGTATCTTA
700666F:214:CA2UUANXX:8:1207:11637:88986_1:N:0:TAGGCATG+CTCTCTAT_(reversed)	125	100	NZ_AJTT01000002	94923 to 95047	GAATTATGAAATATCATTTTTTCAAAAGTAGGGCATTAAGCAACTCGCTTAGTTG CTCTAAATGTCTTTAAGTACATGCTTTAAGTATGTGTTTTCACATTACTAGAAAAA CAGAGGGCTTAAGT
LH08G:00117:01579	305	99.016	NZ_AJTT01000002	112641 to 112942	ATATGGTGCTAATCGGATATACTCGATCCTGACGGTCAAATGGTCCATGACAAG GAAGCAATTTATGAACCTCTGAAAGCTCTTTTTAACGCTTGAATCCACATTGCGT AAGAATGATTACAAGAAAATTAAGGCTATTGACAAGAAAGATTTAGCTGCATTTG TTCAATGGAAAGCAGCAATATTACCGGTTGTAAAAGATGTTTCTAAGGATGAGT ATATAAAAAAGCCTATTAGAACTATATAATATTTTCAAATCAAATGAGTTTGGATT CGGATGATTCTAATAAAACAACCATTAATAG
LH08G:00213:00620	202	97.03	NZ_AJTT01000002	189029 to 189225	TCCTAACTCTAATAAAAAAGTTTTTAATATTATCTATTAATTTATTTTCTAAATCTC GTTCTATTATTTTACCTTGAATATCTAAAAATTCTAAGTTATATGGTTCTTTTTATA ATCGACCTGGCTAAATCGGACTGTAGCTCAGGTAAAGTATTGGAAAAGTTATTT TATACCTTTCGCTGAGCTTTTCATGTTAAATTAC
LH08G:00276:02094	303	99.67	NZ_AJTT01000002	114637 to 114938	TGGGTATAATTATAAAGTTCATTTAGTATTTTCCCTTTTATGACGGGCATAGTCTT GAGATACAAATAATCATATGAACGATATGCTATATTAATACTCTCCCACCAAAGA GCATAAAATACTGCCCAGTAAATCATGGAAGATAAAAGATTATTAGCGTTCTTAT CGCTGAAAGATTCTATTAAATCAATGATTTTCTGAAGTAATATACTATCAATCGC

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LH08G:00347:00812	376	98.143	NZ_AJTT01000002	168719 to 169090	GAAATGTCCTTCTAATACCGTCGAAGATACGGAAAAGAATGCAGAGTCTTGATT TGAGGGCAATATGTCATTCCTGCGAAAGCAGGAATCCAGTATCCTTAATGTCAC CCCCGTGGGCTTGACCACGGGGGGCAAAATAATAAAAAAATACTAATAATATTA GTATTTTTTAGCTGGATCCCCGTGATCAAGTCGCGGGATGATAAATGATAAACC TATCCACGCCACAAGGCCTACGCGGGGATGACATAGCAATGCTGTAATGACGC GATAAAAAACATAAACTTAAAATAAAAGTGCAGAAAAGTTTAATTACAAAATGGT TGTGTATAAGTTGTATAATGGTCATAGCGACGATTGTTATAGGGGGGATAAC
LH08G:00422:02472	293	99.317	NZ_AJTT01000002	197112 to 197402	TAAATAGTTGCCCTCTTAGTTCTGTGTTAATTTCTGCTGGATAAATAGAAATAGT GGCTATTTTCTTTAAATTATCCTCACCAAATTTATATATTAGATGATCACTGAAAA TACTTCTTTTTTCTAACAACATTAAGAACTTATCTTTATTATCAGCTGCATGAGAT AAAAGATATTTTTCAGTTGTAATACTACTTACGTAATTAATATCACTTGCTGCTAT TTTAAGAGCTAATCCTTTGTTTAGGAATAGAGGTTTATTTTTATATTGTTCTGCTT AACGGATCGTCTGT
LH08G:00512:02380	367	99.728	NZ_AJTT01000002	42143 to 42508	GTTTGAATAGTAAACTCGATAGGGCTACTTGCATTCCTGCTAACCATTGAACGT GGATCCATAGCGTAAATCGACATGCCCGGTATTTCAGAAAACTGCTTATTTAAC ATATTCTTAATAGTTTCTTGGGAACAAGAACGCTCACCCCAATTTTTTAGAGGAA TGAATCCAAAAACGTTATCGCTACCGCCTGCACCTATTACCATCAGATAACCTA ATATATCTTTATAATTAGCAAGGATTTTTTCGGCTTCTTTCACTACTTTAGTAGAA GATTTCTAAATTAGAACCTTCAGGACCTTTAAGAGAAACTTGTAAGCATCCATCA TCTTCTTGGGGTACGAAAATGTTTTGAGTAAATTTAAAA
LH08G:00520:01570	270	99.248	NZ_AJTT01000002	90561 to 90825	AGCTGATTTTAAGCAAGAACGGCAAATAGCAGTCGGTATCGATTTTGGCACTAC TAACTCATTAATAGCTATTGCAGCTAATAGACAAGTTACAGTGATTAAATCTATA GATGATAAAGAATTAATCCCAACTACTATAGATTTTACAAGTAACAATTTTACTAT AGGTAATAATAAAGGACTGCGTTCTATTAAAAGACTATTCGGTAAAACATTAAAA GAAATTCTAAATACTCCGGCATCTTTTTTCGTTAGTTAAAGTTATATCAT
LH08G:00565:02879	201	100	NZ_AJTT01000002	101209 to 101409	GACATTGCACTAAATCCACTTATAGACACTGGCATCATATTACTAAGGCTAACTA TGCATTCCTTAACTCGACAGTTACTTAAAATAAAATAAGCAAGAAAGATATAACC AAACTGAGCAAATACGATCGTCACAAAAATGAACATATAATCTTTAATAATTATAT CTAATACTTCATCAAACTGTAGTTTTACGATAAAG
LH08G:00664:02910	259	100	NZ_AJTT01000002	135550 to 135808	TAATTTTTGAGTGGCATTTTTACGGGCAATATTTTTTTCGTTTTTCTTACTGATTC TAAACTCAGCAATGCTAATTACATGCTCAAGTAAATTAGTAGCTAAAGCTTTATC GCTACTAAGAAAATGGTCAAAATGATCTTTTATTATATTCTCGACCGGTTTACTT ACACCGTTTGATACTAATTTTTCCTTAGTTTGTCCTTGAAAAGACGGCTCAGCTA TAAAAATAGAAAGTACGACACTTGCGGTTTCTAAAATA
LH08G:00685:00592	312	98.718	NZ_AJTT01000002	80051 to 80358	CGAGTGGCTCACGATTCACCCACAAGATATTATTTATAATAAGTTAATTAGTTTG CCGGTTAAATTTAATCAAAATAAAAAAGCTTCCTTTTTATTGCACCGCATTTTTAC TTTTAGACATATTAGCAAATAATGATAGCCCTATTATACGCACTACTATAGATAAA AATCTGCAAGCTGCTATAGAACAACAAGTTCGGCTATATATTAATGATCGGACA AAATATGGCATTAATAATGCCTCAGTAATTCTTATTGATTTTACTACTATGGAAGT GCTTGCAAGTATTGGCTCCGGAGAGTTTTTTAATA

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LH08G:00811:02060	260	99.615	NZ_AJTT01000002	173770 to 174028	GCTTTATGGGGTTTGCCGGTAGTTTATATTATTGAAAATAACGAATATTCGATGG GGACGTCTGTAGCACGTTCTACCTTTATGCGTGATTTATATAAGAAAGGGGCAT CGTTTGGGATTAAAGGATTTCAGTTAGACGGTATGGATTTTGAAGAAATGTATG ACGGCTCTAAGCAAGCAGCCGAGTATGTTAGAGAAAATAGCTTTCCTCTGATAT TAGAGGTAAAAACTTATCGTTATCGTGGGCATTCGACTGTCCG
LH08G:00904:02287	276	98.551	NZ_AJTT01000002	170805 to 171077	AAATATGGTAATAAAGAAATAATGCCGTATAGTAAATATATGTTCTTGCATGCTA ATAATATATGTTTATCTGAAAAAAATTTTTTGGTCAAGAGATTAAGTTAGAAGCAA AATTACCGTTTTATTTTAATAGACGTCTTACATAACTTGCTTCTAAAGGTAATTTG TACGTCGATCCGGTACTCGAGTCCTCATGTTAAGTGTACGCTGTGGTTCTGCGT TCCGTGTCTCCTTCAAATTTCTTTTTTATTAGCTGCGTTATGTAAGACGTCTATT
LH08G:00929:00391	262	100	NZ_AJTT01000002	196215 to 196476	TAACATTAGCAATATTTAGTATATTGAAAGAAGTATTAAACGATTCCGGCAACGA AGTCAAAATTGTAGTTATTTGGAGCTTAACTGAAACAGTACGTATAAATCCTAGT TTAGCCCAAGAGACATTAAAAATATTGAATACACTACTTAATAACCCTAGTAATT ATATTGAATTCACAATCGCCAAAATCCTAGGTTGGATAATACAAATAAACCCCAA TATATCACATGACGCATCTAAAATACTGAAAAATTTATTTAG
LH08G:01004:01941	335	99.403	NZ_AJTT01000002	82901 to 83234	CTAAAAATAATGGAAATCCCGGAAAGCTAGAAGTAAGAACATTAGATTAGGTGC AGAAACAGATTTAGGGATTACTATCAAAACACTTGTAACTTTAGAAGAAAGGAAA AGTTCACTTGAGTCTTTAGCATTATTTTCAGAAGCAAAGCATGATAAAGCACAAT TAATGATAAAAGCTGAGAATATTTGGAATAGACTAAAAGATGATGATGTAATAAA GCAAATTTCAAGGCAAGCTTTAACTTTAAATAATAAAATAGCCAACAAGGAATTT TTTTAAAGAGCTATTTAATGAAGAAGAACATAATGCAATAGACCGTTAAACTATA CTTTTG
LH08G:01195:02415	201	100	NZ_AJTT01000002	127231 to 127431	TAAAGCCGGTGAGAAAGTGGGTATTGTCGGGAATTCATTAGGTAGTGGTAAATC CACTTTAATTGCATTATTATTGAAAAATTTTAAGCCGGAATTTGCGATATTATAAT CGATAACCAAAGCCTTTACAATACTTCCTTTGACAGCCTGTGGGAGCAGATATC ATTAATTCCTCAAGATATTATGCTTTTTCATCGCTCA
LH08G:01210:01821	157	97.452	NZ_AJTT01000002	114802 to 114954	TAAATCAACATTTAGCTTAAGTATTTATTTTTTAAAATTCGATAAAGTTAAAATGA CTTTATTTGACTGTAATTTGTATTTTATCTCGGTATGATTCCGGCGATTGATAGTA TATTACTTCAAGAAAATCATTGATTTTAATAGAATCTTTCAGCGA
LH08G:01267:00554	256	99.609	NZ_AJTT01000002	84100 to 84354	ATTCAGTTGACACGGATTTCAAAAGAGAGTTAGCAATAAAGACTTAAGGAAAGG AAAAAACTAAAAGCATTAATTGTAGAAGAAGTTTTTGAGAAATATACAACTAAAA ATGCAGATGCACTTGATGGTAATATAAATCAATTAGCTCAAGCTATAAAAGAAGG CACCAATATTGAGTTCATAGGTCCTAAAAGAGAAGTAGCAAGTGGTATAGATCA GGAAACAAGAAATCTATGTGTTAGAATGAATCAAGATG
LH08G:01288:02068	234	99.145	NZ_AJTT01000002	65637 to 65868	TTTCTTCAGCAGGTTGGCTCTCGCTTTGTGCTTTATACATCGCTTCACCAATTTT CATGCTAGCTGCAGTTAAACTTTCGGTCTTTTTCTTTAATCAAAGCAGTATCTTC CGACTCAAGCACGGCTTTTAAAGCGGCTAGTGCTTCTTCAACAGCTCCTTTATC GTCTGATGATAATTTATCGCCATATTCTGTAAGAGTTTTTTTCAGTAGAATAAACT AAACTATCGGCAGC
LH08G:01422:02299	310	100	NZ_AJTT01000002	157879 to 158188	CCGATTCTCTTAATCTCCCACTCTAACTTAACCCCGCTATCTTCATATACTTTCT GCCGGACGAAATCACCTAAATCTTCTAAATCCTTAGCGGTAGCATCACCATTAT

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LH08G:01567:00542	283	98.233	NZ_AJTT01000002	25976 to 26253	TCAGTGAATTTACTTGATAGCGTAACCCGTGGAAGCTTACGGGAGTAAAATACC GCTTTCACAAGTTGCTTCTCTATCCACACCTGATGCACGAACAATTAACGTGCA GGTTTGGGATAAATCTATGGTATCATCGGTAGAGAAAGGAATTACGATAGCAAA TCTTGGCTTAACTCCTGCAACGGACGGTCAATTAATCAGACTGCCGATACCGGT TTTAAACTGAAGAAAGACGTAAAGAACTGGTAAAACTTGCTCAATAAATACGGT GAAAGTATACTAA
LH08G:01579:01219	245	100	NZ_AJTT01000002	98497 to 98741	GTAATTGCAGCTTTCGTTAGTTTTAGGGAAGTAGTAATTACTAACCGTACTATAT ATTTACTCAATAAAGCAAGAGATAGAGCTCATATTTTACTAGGACTAACTATTGC CGTTAGTAATATCGATGAAATAATACGTATTATTAAAACTTCAAATGACCCGAAT GCAGCTAAACAAGAATTAATGGCTCGTCAGTGGGAAGCATTAAATATCCTACCG CTTGTAAAGTTGGTTGATGATAAAGC
LH08G:01648:02712	190	98.936	NZ_AJTT01000002	188231 to 188416	TCCCTGCTAATGAAAAAAATCTGCAAGACATTCTTATATCAAAATACCTATCAATT CCGATACTCAAAATATAGAGGCTGCAGATAAAGAGGACGGATATAATAGGATGA GGCTTGGCATAGATAGAGATTGCAAGAGCAGTAGCAACTAAAAAAACTTGATAA GCAAATATCTAGCCTAACATATGAAG
LH08G:01694:00924	330	99.698	NZ_AJTT01000002	125784 to 126114	TTTCATATCATACCTGCGTGCCCTTGTTGCATGACTCTTATGTCTTCCCGCAAAA GCGGGAATCCAGTACCTTAAAACTTTATTTGAAAAGTAAAATTTATAAAAAAAAT CTTGGTCTAAAAGATTTTTTTGGAAAGCTCGATTTATCTCGCTTTACCCTGGATT CCCACCTTCGCGAGAATGACATCGATCCTTAAGTTGTCACCCATATGCGATCAA GGGAATGACATTATTGTAGATAATCTATTAATATATTAGTATCAAAGGTAGCCGT TCCACTCATTACATAATTTAGCCTGATATTCTACACTATCTAGATTTTTATCTTTC
LH08G:01766:00833	390	99.235	NZ_AJTT01000002	55480 to 55870	AATAACTTTTCAGGATTCTCAATAAGCTGCTTAATTTTTACCAAGAACGATACTC CTTCTTTTCCGTCAATTATACGATGATCGTAAGATAAAGCTATATACATCATCGG ACGTATTTCAATTTTACCGTCTATAACTACAGCTCTTTCCTCGGTTTTATGTAAG CCTAGAATACCTGATTGAGGAGGATTAATATCGGTGTAGACAATAATGAGCCAT ATACGCCTCCGTTAGAAATCGAGAATGTCCCACCTGACAAATCAGCCATAGAAA GCTTAACCCTCACGAGCTTGTTTAGCCAAAATTCCTATAGCTTTCTCCACTTCGG CAAATCCCATTTTATCGGCATCCCTAACAACCGGTACAACAGCCCTTGCGCTGT TCCGACAG
LH08G:01773:01731	203	100	NZ_AJTT01000002	116592 to 116794	ATAGGTATTGTGGGGTTATATCTTTACTTGAAGGAAAGATTATATACTACGCATT GGTTTCAATATTGGTATATATTAATGTCACCTTCAGGTTTTATTGCAGTACTTGC CGGTTGGTTCGTAACCGAGGTAGGTAGACAACCTTATATAGTATATAATATTTTA AAAACCGTGGATACGGTATCACCGGTACTCGGCAAATA
LH08G:01821:03034	311	99.045	NZ_AJTT01000002	154963 to 155276	TTTTATAATTGATCAAATTGTTTTAGAAATGACTGTTAATGAACTTGTCCGCAACC CAAACTTAAAGTTAGCCGTTAATATTTCAAATATAGGAACAGGCGTGAAGCTTTA TGGGAAATAGCAGAAAACTTATTAAAAGCTCATAATGTTCGGGATCGTTTAATTA TTGAAATTACGGAAACTTCTTTCAATCAGCATTACGATAAAATAACTTTATTTATT AATAAACTACGTAAGTACGGATGTAAATTGCATTAGACGATTTTGGTGCGGGTT TTACTTCGTTTAAACAACTTCAAAGCTTACCATTG
LH08G:01889:02706	393	98.728	NZ_AJTT01000002	109861 to 110249	GAAGAATTAACCACACCTAAAATAATAATACATTATCAGAACTTTATGCAGGAAA TTCATAAATCTATGCATAAATTACAAACAGCAAATCAGAAAGATATCATCCCTAA AATTGCTAAAAATTATAACTAAACAAACTAAAGTGTTATGTATAGATGAGTTTGAA ATTAAAGATATTACTGATGCAATGATAATCGGTAGATTATTTAATGAATTAATAAA GCAAAATATTTTTATTTTTATAACTTCTAACACGAGTCCCAATAATCTGTACAAAG

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LH08G:01985:01148	269	98.507	NZ_AJTT01000002	13347 to 13610	TTTTTTATATTGATCAACAAGCTTATTAACTTTTTCTTGTTCTTCCGGTAGTTTTGAAATATTTTCAGCAATATTTGGCATTTGTTTCTCTTCTCTTATAAAGTTAAAACATATTAATTTACATTATATATATATTTTTTATATATTTTTTTTATACAAGAAAAAACTTTAATAGAAATTAACCTTTGAACGCAGCCTTAATACCTAAGAAAGTCTAAAAAATTTCGTAATTCTTGACGTGCAAGCACGTGTGAGCTATTAAATGCTCT
LH08G:02060:02022	249	100	NZ_AJTT01000002	38275 to 38523	TAGCCACCATTATGTTTGTAACCAACGCCATCTCCCGTTAAACTTAAGGTTGGTACGCGAGTTATTGCATTAGATATTATCTTAGCGTTTGTTCCTTCAATATATTTACTGGTGAATTTATCTATACCATTTTTATCTATAGCAGTACCGTATACAAAACTTCCTAACCCCGAAGTAGCCAAATACTCTTCAACTTTAGTTGCTTCATGAGCTTGAGTAAAAAGCTTTATTTGTTCATTACTCTCCATA
700666F:214:CA2UUANXX:8:1212:1167:48524_1:N:0:TAGGCATG+CTCTCTAT	125	100	NZ_AJTT01000003	10090 to 10214	AGGTAATTTATGTGCGTGGATCGCAGGAATCCAAAAACATTTAATGCAACCCCGTGGCTTGACCACGGGGTCTAGAAAAACAAATTATTATATTAATAATTTTAGTATTTTTAACTAGATTCCGC
LH08G:00104:01732	234	98.298	NZ_AJTT01000003	94226 to 94457	ACATATAAAGACCTGCATACAAAGGACTTAACCCTTTGATAAACTGAAGGACATAAGATACATTATGGATCCTAAGACACACGTTAATCAGCAAATAAACTATTACTCCTATACTAAAATTAGCTAATTAAGAATAAACGCATATCCACTAACGGATCATCAATTTAAGTTGGCGTAACGTAAGGTAACTATTATTGAGTAACACAATGCCAATTAATAGCATTCCGCCGGATG
LH08G:00249:01567	320	98.438	NZ_AJTT01000003	60594 to 60908	CATATCATTATTGAAGTTTCATATAATAAAAGTAGCGGTATTGCAAGAGCAAACTGGCTTAAAATGTCAGGAGGCGTTAATATTCCTGCAATAATAAAGTTAATTACCACGGCAATGCATCTTTTTTGCTTTAAGTGTTTGTACCTTAACTATTTTTAGTATATTTAATATCATTATCACAACTGGCAGCTGAAAGGCGACTCCAAAAGCAATAATTAAATGAATAACTAAATTTAGATACTCGCTAATTCTTGCTTCCAAAACTATCGGTACGATCATATCACTGTTTTTACAAAACATAAAGAAAAAAATTCCAAGCT
LH08G:00430:02505	386	98.187	NZ_AJTT01000003	67256 to 67636	AGTAAGACAATAAACTTTAACATTAATTTAAAATGCGACCTGAATTTATTCATTTAAGAACTCAAAGCTCTTATTCTTTTTCTAGAAAGTGCATTAACGATTGAGAAGGTAGTAGAACTTGCTTCATCGAATAAAATGCCTGCTATTTGTTTGGCAGATAAGGGAAATTTATTCGGCTCATTAGAGTTTGCATTATGTGCAGTAAAAAAAGGACTGCAGCCGATACACGGAGTTATTCTAAATATAAAATACGATATAGATATTTTTGCTACAATTTTTGTCTTATCGCTAAAGATGAAACTGGTTATAAAAATTTACTCAAATTATCAAGTCTTACTTTTTTACTAAAAAATGATCGTAAGATATGCGATCACATTGCTTTTGAAG
LH08G:00524:01912	296	96.939	NZ_AJTT01000003	123597 to 123881	TGAAGAAATTGTTACAAAAACAAAAAATGCTTGAATTTTTAAATGAATATGAAAACCCTTTTAGCTGAGATTTACAAATAGGACATTTTCACTGCTTCGGCTTTTTTTACTTAATAATGATAAAACTAAATTTTTATTGATGCAACCATAAAAAGCTTGATAAGTGGCTTCAACCAGGTGGTCATTGTGATGGAGATAGTAATATATTAAATGTAGCGGTTAAAGAAGCTATAGAAGAATCCGGAATTAATGAAATCAAAACGATAAAATTAAGGAGAATTTTTTGAATATAGAAC

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LH08G:00803:02840	351	97.721	NZ_AJTT01000003	95748 to 96090	GATAGTCAATATCTGTGTAACAAGGATTAAATATCTCAAATATTTCTATAATGCTT TCTTTATATTCTTCAGACTTGGGATTTGCTGTTCGTATAATTGTTATTAAGCGTG CAAAGTTGCTGATAGTCTGAAAACTATCATCCACCGCCAAGACTCTTACATATTT TCATGCAATATTCCGCTTGAAGAATCTAAGTTTTATTGCCTATAGCGGATGGGG AATTTAATTTTACAATTTCATTATTTAAATTTAGTTAGTGGTAGTATTGAGAATTCA TATTCCTTAATTAGATTTTGCTAGTTTTATAATATCATGTAAATTATTTTATTTTTTA TAACTTCATCGAATAT
LH08G:00830:01910	224	98.661	NZ_AJTT01000003	133965 to 134185	GCTGTTGTTTTTCTTGTTCTTCCAATAGTTTTCTTTTTTCTTCCTCTACTTGTTGT GTTTCTAGTTCTTGCTTTTGCTGTTCTTCATATTTCTTTTCTGCTTTTTTTTGGTTA TAGTTTTTATTTCTGTACAGATATTCATTAATTATTTTTAAATGTTGCCTCGCCTAT GTTGTGCCAAGGAAGATAAAGCGACGTTAAAGATTGATTACCGCTTAAGCTTGT
LH08G:00869:03108	311	99.678	NZ_AJTT01000003	154896 to 155205	GGAGTATCAAACGTTGTTGTATCATTAGGACGTTTATCAAAATCAACTCCCATGA TTTTAGGAATAACGTCACCAGCACGTTGCAGGAATACATAATCCTTAATCCGCA AATCTTTTCGTGCAATTTCTTGGAAATTATGTAATGTTGCTCTGCTAACAGTTAC CCCCGCCTATTTCTATGGGTTCAAGTTCGGCTACCGGCGTTAACGTACCAGTTC TACCAATCTGTACAGTAATAGAAAGTAACTTTGTTTGTCCTATTATTGCAGGAAA TTTATGAGCGGTAGCAAAGCGTGGACTTCGTGCAATAA
LH08G:00948:00904	306	99.673	NZ_AJTT01000003	84836 to 85140	TTTTAAAATGTTTTATTATTGATGAAAGGAATTGTTTTCTAAGCATTTAAATTAGTA CCATGAAAATTAGAAACATAACGTCTAATTCTCAGTATAGAAAGAAAAAACGAAC AAAGTCAAAACGCTTTGTCTCGTGCTGCAACTATAATCGCATGTATTTTTTTAAG CGTCCGGTCAAAATCATCGTTAGTAACTACATAATCATACTCATTAGAATGTGAT ATTTCGTTTTGTGCCGACTGCATACGTAATTTTATTGCTTCTTCATTATCGGTCG CTCTATTTCTTAAGCGTTGTTCCAATACT
LH08G:00952:02658	237	99.578	NZ_AJTT01000003	86156 to 86392	GAAGCTATGCAAGCAAGTAGTCAAATCCACCAATATAATCAAGATTTAGGTAATT GTGTGGATAATACTTCCAAAGATATCAAACTTACCGGTAAAGCTTCTAAAGGTGT ATGTGAAATAATATAACATTCTAAAAGCTGTAACTATATAGTTGCAGCTTTTGTAT CATTTTGAATTAAGCTCGAAAGACCTATTGCCTGTATTTTGTCTGACAATTTAAA GCTAATCTCACCTGGA
LH08G:01087:02301	176	100	NZ_AJTT01000003	47693 to 47868	TACTTGCGCTAATTTTTTGTCTATTACCCTTACGAATAACCCGTTTATTATGCTAG ATGCAAGCGGTAACATGATGATCATTATGCAAATATTTTGATACATCATTATCCC CACATCTGATTAATGTCGGTAATTTTAATGGAGCCTTTATTACGGAAATATATTA GTAATATTGC
LH08G:01116:01184	207	99.01	NZ_AJTT01000003	29085 to 29284	TCTAGGGTTTTAAAAGGCTTTAAGCCTGACGGTAAACAAATTTGGACTTCTAAAG AAGCTATGATACCGCAGCATGTGCCGAAATCTATGATTATTGTCGGCTCAGGTG CAATCGGTATAGAATTCGCTTCGTTTTATAATAGTATTTGGTGTGGATGTTACCG TAATTGAGGCACATAATAGAATTATTGTCTGCTGAAGAATTAT
LH08G:01471:00458	132	99.213	NZ_AJTT01000003	45049 to 45174	TATATGCGGCTCTTAAATTCTTCTTATACACGTTCTTTGGTTCTGTATTTTTCTTA CTTTCATTAATTTATATTTATAGCAAAATACATAGCTTTGGATTTAACCTATATCTT TCAGCTTACCGATATAGTT
LH08G:01892:02986	248	99.194	NZ_AJTT01000003	116847 to 117093	AAATAATTGGTAATTTATAAGATTTACTATAACTTTTATTTAAGGTTAAAATAATAA TCGCAATACTCTTTAATAGGGCAGATGTCGCAATTGGGTTTTCTAGCTTTGCATA TATATCTGCCGTGTAGAATTAGCCAGTGATGGGCATGCGTTAGCCATTTTTTAT CGATAATCTGCAGTAGCTCTTTTTTCTACTATTTCAGGAGTACCGCCTTTAGCAA GCCCGATTCTGTTGGCTACTCTAAAGA
NB501781:2:HGMVWAFXX:2:11108:16748:12433_1:N:0:TAGGCATG+ATAGAGAG	151	100	NZ_AJTT01000003	42082 to 42232	TCATTGCGAGGAAATTACGAAGTAATTGACGAAGCAATCTCAGGATATTTGACG AGATTGCCACGCAGCCTACGGCTGCTCGCAATGACAACTCGGTATCCATGCGG GTGATGCCCCGCAGAAATACATCGATCTTTAATATATAATTTTT

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NB501781:2:HGMVWAFXX:2:21106:13745:11822_1:N:0:TAGGCATG+ATAGAGAG	151	100	NZ_AJTT01000003	1055 to 1205	TTCTTAGATTTTAATGCAAAAAACGGTACGGTAACATTAAATAACAATGTAAATGTTGCGGGAACAGTCCAAAATACCGGCGGTACTAATAACGGTACGTTAATAGTTTTAGGTGCAAGTAATCTTAATAGAGTAAACGGGATTGCTATGT
700666F:214:CA2UUANXX:8:1105:6238:13850_1:N:0:TAGGCATG+CTCTCTAT	125	100	NZ_AJTT01000004	123325 to 123449	CCTAATAGATTATCAAACGATACTCAAATAGTACCGGGACTACATGCTTCTGTAGAAAATAGCTTTAGCAATAAGCAACCTAAGGTGAAAGCTAGATTTATTTGGGCAGATAATTACTTTGAGAA
700666F:214:CA2UUANXX:8:2114:8166:42837_1:N:0:TAGGCATG+CTCTCTAT	125	100	NZ_AJTT01000004	70849 to 70973	CAATTAAATATTATAAATTACACTTTATAAATTATGTAACTTGTCTATAATAACTAATTAGTAATTAAGTTATTTAAAGTTCGATGAATAATAGGTCTAAGTTCATTTTTTTATCTGCTATTTCA
LH08G:00129:00502	269	100	NZ_AJTT01000004	64050 to 64318	GCAAAATCCGGTATAGTTATAAATCTTATCATATTAATTCAGATTTATATTTCAATATTAATGCATCTAAAATTGCTATGGTTTCAGCATCCAAATCGCCAGAAAAATTACTAGGACGAAAATGCATTTGAAACGAAATTATAATATCTTTCATTTTAGAGTCTAAAATTTTGGTAACTTCAAGTTTATAACCGTATGTAATAAATTTTTGCTGAATTGCTGCAATATCGGTTATGTCGACTTGCGGCAATAGATCGTTAAACACCTGT
LH08G:00174:00921	272	100	NZ_AJTT01000004	154704 to 154975	TGAACTAAATCAGGGTAAGGGTAAAGAACAAACGCAAATAATGCAAAATACCCTAAGAAAAATGAAGTAATAACATAAAACACGTTTTCTTGCTTTAAAATATCGCAGAGCTTAACATAAATTACCATAGCGATTATGGCAGAAGGTAGTACTATATATGTTTTTAAGAAACTTATTGCTTCTGCTCCTATATCTGTTACTACAAACCCGTCTTTAATTGAACGAAGCGTTGAGTAGTTTAATAAAATACAGAACATCATAAACGCCATAGG
LH08G:00219:01406	195	99.487	NZ_AJTT01000004	65172 to 65365	CCCGTGGCTTGACCACAATATTTAGAGAAATAACTTGTAATAGTCAAATTTACTAAATCCTGCAATCAAATAGCGGGAGATGACAGGGGCTGAATTGATCCACACAGTCAATGCCTGCTCGCAATGACGAAAAATACACTATAAACTAAGCTTCTTTAGCTTCCTTTTTACTTAGTCTAGCTTTGCGGTTTTTTG
LH08G:00314:02276	289	96.181	NZ_AJTT01000004	58769 to 59047	TAACTCATTCAATATTATTATTAAGCAAGGCAATGGGTTATTTGCTTTATGAGGATAAGCTACATGCCCACTTAAGCCTTCTATATTTAATTTAAAGTTAACACTTCCTCTTCTGCCAATCTTAATTGCATCGCCTATTTCTTTTTTCACAAGTAGGTTCACCGACAATAGCAAAATTTTATCTTATATCCTTGATCATAAATATATTGCAGCATTTCTTTATACCATGCTTTTGTCTTTTTCCCTCTTTCACATCTAGTAAGTAAAGAAACTAATGGAACCCTTTTAA
LH08G:00420:00401	207	100	NZ_AJTT01000004	65318 to 65524	TGCTTGCTTTAGATAATAGTGAGCGTGTTGTTTTAAAAAAAGATCGTATAGAATATTGGCTTGGCACCGGTGCTAAACCAACTGAGCGAGTCGCAAAATTTATTGAGCAAGCGGGTGTTACTCTTCCTGAGAAAGTTAAAAAGGAAATGGAAGTGAAAGCAAAAAACCGCAAAGCTAGACTAAGTAAAAAGGAAGCTAAAGAAGCTT
LH08G:00456:01603	256	99.609	NZ_AJTT01000004	88760 to 89014	TAAATTTTTTAATAAGTTTTGTTGTTTTTCTTGCAATAATTCCCTTACCTCGGCAAATGCTTTGTCCGTATCTGCGTAGCTTGCAGCCATATTCCCATTATTATCAGCACGAATAATCATCTCAGGTGGCAGCAGCTTAATAAACTCTAGAGAAACTGCTATTATGCCTTTTTTGGATGCAAGCATTAACAATGTCCTTCCGAATTTTATCAATAGAGTTAATATTTTCCTCAAACATTCTTGGAATAAGCTCTAT
LH08G:00479:02448	249	100	NZ_AJTT01000004	154629 to 154877	AAAAATGACAATTATCTTTCGGAACTAAGCAAGGTAATTTGGCCTATAGAAAGATATGAAAATAAGAAGTTTCTTCCTATGGCGTTTATGATGTTCTGTATTTTATTAAACTACTCAACGCTTCGTTCAATTAAAGACGGGTTTGTAGTAACAGATATAGGAGCAGAAGCAATAAGTTTCTTAAAAACATATATAGTACTACCTTCTGCCATAATCGCTATGGTAATTTATGTTAAGCTCTGCGATATT
LH08G:00595:00466	205	96.098	NZ_AJTT01000004	105735 to 105931	GAAGTTACATTAGAAATTAAACAAAAAAATACAAAAGAATGTTTTGAATAAAATATATATTAATGCTGCTAAAGATAAGTGGAATAGTAAGTTCTCAATCTTAGGAAATTGGGGGGTGCAAGGCTATTTAGGTGATAGATATTTTATAGCAAAAACAACTAGGAATTTTTATCTGACCTTAAAAAAATATAGAAAATAGCTAAAA

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LH08G:00622:00271	266	99.248	NZ_AJTT01000004	60676 to 60940	ACCCTTAAAACTGATCAGCAGTTAAAGTTTGATGTAATTGTTACTAATTGCCATTTTCTCAAACTATCACTAAAAAAACTAGCAAAAACGGCAAAACTATAACAGAAAATCATATAACTTCTCTTTTTAAATAACGGCATTGCAAAAAATAACGGTGATGCTGTTTGTGTTTTGCATTGCCTGCAAAATTTAAAAGAGGGTGGTAGAATGGCATTGGTAGTACCTGAAGGGTTCTTATTCAGAAAAGACACCGCTGCTGTTCGTCA
LH08G:00812:01794	217	100	NZ_AJTT01000004	26095 to 26311	CATTACTTTTGATAATGTCTATAGCATCAAGACTTATATCGGTTGCAATTACATTAGCATTTGGTAACTCACATAATAGACTGATAGCAATGCAGCCGCTACCTGTGCCAAGTTCTAGGATATTTAAGAATTTGTCATTGCAGTTTTCGCTTATGTCATTCCCGCGAAAGCAGGGATCCGGTCGCTTTTTTTCTGGATTCCCGCTTTCGCGGGAATG
LH08G:00834:01577	228	99.123	NZ_AJTT01000004	51094 to 51319	GAGAAGGGATAATCATATCATTTAGTTTATCTAATTTTTGCTCTTCTGTTAGCTCTTTTTTACCGGTTTCTAAAAAATTTTTTCAAATTACAAGCATCTTGTAGATAAAGTTTAACAACATCAATATTATAATCTTATTATTGACAAGTTCTTTGATCTTCTTAATGTCTTCATTGTAAATAGCATTAAACAAATTGATTTCGTCATATTTAGATTTATACACAAAA
LH08G:01093:03061	337	99.703	NZ_AJTT01000004	123035 to 123370	CATGTAGTCCCGGTACTATTTGAGTATCGTTTGATAATCTATTAGGAGCGGTTAATTTTATGCCTGCAATCCCTGTAGTTAAGTTACCGGACTTACCAGCGACATACATATTATTCACACCTGTACCGGTTTGCTGCAGTATAAGTATATCCATTAGGAACAAATCCATCTCCATTACTCATCCTCAAAATTGATAGGGCGGCTACATCATTCGCCGTGTGAACCCTATTAATATTAATCACAATATTTGTACCGAATGCCGTAGGGAGATTTTGAAAAAACTATACCGCTTTCTCCTAAAGCATTTATAGTAATATTACCTTCAAGTACTACATCA
LH08G:01130:00477	302	98.675	NZ_AJTT01000004	133188 to 133486	GATATTAGTAATTAAAAATTTATTTACTGATATCCTCTAAGAAGAAATATAATTTTTTTAATATTGACACTTCTTAATTTAGTAGTATGATATGTAATTACCATGAAACATGGCAATTACGTATATAAAAAAGAGGTAAGTTTATGAGCAATAGCAATTATGAAAACATATACAAAAGCATTTAATTGTTTTTCAGAAGCAACCAATTCTGCCTATTCAGCCGTAAATACTTTTTTAAAACTACCTAATGTATTTAATAAATATCCTACTATTATTTCTTTAATTTTTTCTAAAACAGCAAC
LH08G:01200:03346	198	97.475	NZ_AJTT01000004	138841 to 139033	TACGCTTGTGTACGCTGCGGTGCTGCGTTCCGTGTCTCCTTTAAATTCCTCTCTATAAACTGGTTTGGAAAAATTGTCTAATATAATCTGCATCCTTTAGCTAATTTTTGCCTAATAACATTTCGTCTATATTTATCAGATGAATTTGAACTCATCTTCAAACCTATTTTATATTTATGACTGACTAAATATTCTACT
LH08G:01395:01645	286	97.909	NZ_AJTT01000004	88415 to 88696	TACTTTTTTCCAGACAACTCAACATCTATCCCCCATTTTTCATTTTCTAAGTCGGAGATAATACACATATTGCTTCATTTGGTAAGCAGTGATAAATGTAAAAAAGGGGGGGTAGAATCCGATTGAATTTCCGGTTGTATATACTCCTGCAATGGCAAATGGGAATAATTTCATAAAATTATTCATCGTTATTATAATAGATTCAGGATTATTATTTTGTTCTTGTAAATAAGATGCTAATAGTTCCTTATTTACTTTCACTTTTTTTATAGAATTTTTGATAGCA
LH08G:01446:03084	391	99.225	NZ_AJTT01000004	77026 to 77411	AATATAAACATGGGATAGTATTATACACGATTGCCGATCAAGAACTCCGAAAAACTTTAACGAAATTTTGCTATGAATTAAAAATTCCATGTATTTCTGTAATAGGTAAAATTATTAAAGAAATGTCTGTTTTTTTCAGGTATTGAAATAGAAAAAGAACAGAATTACAATTATAAATTTGATAAAACTTATTTTGATACACTTAATGCCATAGATTATGCTATAAGACATGACGACGGACAAATGCTTAATGAATTATCAGAGGCTGATATAATATTAATAGGTCCTTCTAGAACTTCTAAGACACCGACTTCCGTATTTCTAGCGTATAACGGTTTAAAAGCTGCTAATATTCCTTATGTTTATAATTGCCCCCTTTCTGATTTTTAAG
LH08G:01533:00837	279	99.283	NZ_AJTT01000004	144101 to 144377	ATTCACAATCAGCATCTCGGTACTTAATCCATAAATTTGGGGATTTTTTAAGTAAATTAACTTGTTCTCGTTTGTCTGAAATATGTTTTAATATTTCTTGGTATATTTGATTTAGTTTCTTATCAACTTTCTTATATTCTGCAGCGACACAATAATTCATGTCACCGT

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LH08G:01741:01988	263	100	NZ_AJTT01000004	9014 to 9276	ATCCACGTTCTACGGTTGGAACTATAACGGAAATTTACGATTATCTTAGGTTATT ATATGCAAGGGTGGGTATTCCTTACTCTCCGGCAACCGGTCTTCCGATACATAG CCAAACAGTTTCTGAGATGGTAGATATAATTAACGAACTACCTAAGGGTACGAA AATATATTTACTCGCTCCTATTGTTAGAGGACATAAGGGTGAGTTCAAGCGTGA AATTATGAATTTGAAAAAGCAAGGCTTTCAGAAATTAATAGTTAAC
LH08G:01837:01796	230	98.696	NZ_AJTT01000004	124826 to 125052	GTTACTTCTTTCTTAACCGGCTGTAGCTTTTGTATTTGCTTTTTTTAAATTATCGA AAATTGATTTTTATTTTTTTGATCTGAAGCGGAATTTCTGTATAAATTTTGAAAAA GCTTGGTAGTTTCAGGGATTAAATGCGGGCTTGTTAGCTCTTCTTGACTAACCA TTAAGCTTATATTAAGAGCAGGTTCAGTAAACCTTGCAAAATTGCAGCAATCATC GGTATCTAT
NB501781:2:HGMVWAFXX:4:21410:9055:4052_1:N:0:TAGGCATG+ATAGAGAG	151	100	NZ_AJTT01000004	71988 to 72138	GAACAAAGATTTACCGGTGTTGCTTTCAGCTACAATTTTGCAATAGCGATATTCG GCGGAACTTCACCTATTATTTCTCGTTGGCTTGTAGAGCGCACAGGCTTATTTT ATGCTCCGGCTTTTTATATTATGATTATTGCTGTCGTATTTT
700666F:214:CA2UUANXX:8:1310:15115:58891_1:N:0:TAGGCATG+CTCTCTAT_(reversed)	125	100	NZ_AJTT01000005	47603 to 47727	CCGTTTCGGTTTAGCCTTAGATGACAAAGGCCATAGTCTTTTACCGTTACCTCC TGCCATAATCACCGGTTTTATTAGACTCCTTGCATAACCTCCTTTAAAGGTAATT TGTATACCTTTGATAC
700666F:214:CA2UUANXX:8:2311:18340:31562_1:N:0:TAGGCATG+CTATCTAT_(reversed)	125	100	NZ_AJTT01000005	78091 to 78215	ATTAATTAAACCGATTGCGATGCAGGAAGGGTTAAAATTCTCTATACGTGAAGG TGGTAGAACAGTGGGTGCCGGCGTAGTAACTAAAATAAATAATTAATTGATTTTA TAAATACCTATTATTT
LH08G:00199:02588*	272	100	NZ_AJTT01000005	3892 to 4163	GAAGATTATTATATGCTGCAGTATTAGTTGCATTTACAAATGTTGTAACGTTCTG ACCTACACCCGGTGCAACTCCAAACGGACTATTTGCGATATCATTAGTAACTAC GTTTTCTGCATTGTTAGTACGTGTTATTACATAATCTTGGTTAGCAGCACGTATT AAACCGTAATTTACGAAACGATTACTTCCGGTTACAGCAAAGTTGGGACCTCCT AAAGTACCGTTAAATCTAGCACCACCTTGGATTAAAGTATAAGTTTGTGTACCA
LH08G:00350:00627	165	100	NZ_AJTT01000005	95517 to 95681	CAAATGGAGCGAATAGAATGGCAAGACCTATAAAAGAAGAAAATAAATATGCCA CACTCACTAGAATAGTCGGTAATAATGTAGCACAAATAATTTCATCAATAAATAT AGGATTACAATCATTAAAAGGTTCTAAAGATTCGGTCAATCAGATCCAAGATAG GA
LH08G:00551:02828	401	99.499	NZ_AJTT01000005	24341 to 24739	GGATTATAGAAGTAAAATCGATAAAATCTTTTTTATCAGCAATATTAGGTTGAAG TAACATATTATACGCAGTAGAATTAATGGGTCCTATTTTTAGACAATCCCCTAAT TTAGCTGCTATTTTAATGAATATTAAAGGAATTTTTATTAGTCTTCCATGACTCCA AGCCATCTTCTGAATCCAAGCAAGATATCCTTCATGTTCACTATGTCTGGTCCAA CTATTTTTAATAATGTGTGGATTTTTCCTTCCCTTTCTATACAGTGAATCATTACT TTCGTTAAATCATCAATATGAATAGGTTGAAATTGTTGTAAACCATCACCTATTAA AGGAATAAAATACGGTAATGTTGCAAGAGCCTAAATAGCGAGGTACCACCATAA CAACCGCCTGCTGT
LH08G:00753:00799	191	99.476	NZ_AJTT01000005	101236 to 101426	ACAAATTGCGCATATTGATCAGAGGATAATTCTACTAATAAGGCATAATAGACAA TAATATAATCTTAATACCATAGCCGCTTAAATTTAAAAAATACACTATAATAGCAA TTATAAATTGAGTAAGGAGCTGGGTTAAAAAATTTTTAATTGAAGTAGTGTATGG CCTATTGTAGTAATGATTTTATAAC

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LH08G:01287:00555	110	97.273	NZ_AJTT01000005	134197 to 134303	CAACTGAAAGCTTTTTATTCTCGTATGATGATTCCTATTATTAGACTTCTTGCATA ACCTATCTTAGAAAGAGGGACTTGAAAGAAAAACGGTAAGCACTTGCCACCGCA
LH08G:01331:00575	339	98.525	NZ_AJTT01000005	260 to 596	ACTAAATTTTTAACTTAAATATAGGACAAAAATTATGGCTCAAAAACCAAATTTTC TAAAAAAATTAATTTCCGCAGGGTTGGTAACTGCTTCTACAGCTACCATAGTAGC CAGTTTTGCAGGTTCAGCTATGGGTGCTGCTATACAGCAGAATAGAATAACAAA CGGAGCTGCTACAACTGTTGATGGTGTGGGATTTGACCAAAATGCCGCTCCTG CAGATGTTGCAGTTGCTCTAAATGCAGTTATTACTGCTAATGCTAATAATGGTAT TACTTTAAAATCTCCAGCCGGTAGTTTTAACGGTTTTGCTTTTAAATACTGCAAA CAATTTAGTAG
LH08G:01354:00607	218	100	NZ_AJTT01000005	103977 to 104194	ACCGTATAAAACTTTATCGCCTACTTTTAGCTCTAAAGGATGAATTTCGCCTTTT TTATTACGAATACCATTACCTACGGCTACTATTTCACCTTGCATCGGCTTTTCTT TTACAGTATCCGGAATAATAATTCCACCTTTAGTTTTTTCTTCTTGTTCGATAGGC TTTATTGCAATTCTATCATGTAATGGTTTAAAAGACATTTTGACCTCCAATT
LH08G:01628:02693	228	100	NZ_AJTT01000005	65377 to 65604	TATTTGAACTTAACACACGCTTATAATAACTAAAACTTAAATTTTACTTTAAGCCT TACTTAAATTAAGAGCCGATAAAAATTCATTATGCAAAACTACCTTACCTTGCGG CATTTGTCAATAAACATGTCAATAACATGCAAGAGAAAGTATTACTTCCTGAAAC TAATCTATCATATTATTACTATTTTGTCACTATTTAAGTTAATTATCTAATAAATAT AATGA
LH08G:01989:01385	211	100	NZ_AJTT01000005	69712 to 69922	AAATCTTCCTCTACAGCTTCAACTGCTTGCACTTCCGGTACAAAATGTTTAAGCA TGGACTCAATGCCGTTTTTTAATGTGATGGTGGAACTAGGACATCCAAGGCATG CACCACGAAGTGCTAATTTAACTACACCGTTTTCAAAGCCTTTATAGATTATGTC GCCGCCGTCTTGTGCAACAGATGGACGCACCCTAGTTTCAATAATCT
LH08G:00023:01565	289	100	NZ_AJTT01000006	54341 to 54629	CAAGTCCGTCAATTTCGCTTCCTTGAAGCCAAATATCAAGTATAACTGCAGAGA CCGGTTTTTCGGAAAGTATTTTAAGGGCTTGAGTACTATTAGCGGCAACCTTAG GGTTAAAACCTTCATCTTTCAAATTTGCAGCAATGAGATTTCGTATACTCTCTTC ATCGTCTACTATTAAAACATCTAGTTGTGACATTACAATTTACCTTAAAAATATTA ATACTAGGTTCTTACGTACTATTGCTAATTGATTTAATATTTTACGATATTTTTTA GCGAAAATTAATAA
LH08G:00130:00422	198	98.99	NZ_AJTT01000006	27847 to 28042	TACTACATTATGATCAAATTTTATAGAAAAAACACGATGTAATTCTACGCTTAAAT TCTCTATATCCCAATCTTCTCTATAAGAGCCTACCGGCATGAAAGTTAATACTAT CTTTTTGGCGAGTTCCTCAGTAGTACTATTTAAGAAAACGTGACTATCTTTAGAT TTAATAATTTCAGTTACGTTGTCTCGTATATT
LH08G:00515:01357	273	99.632	NZ_AJTT01000006	74345 to 74615	AGTTCTTGTGAAGTTTAAAGGTGTTAACCATAAAGTAGTCGAGATATTGATTGAT AGCTTAAACAGCGAAAAAATATCTGTGGAAGATTGTACTAAAGCAAGTAGGACT ATCTCCGCTATTCTAGATGTTGAAGATTTAATAGAAGCTGCATATTCTTTAGAGG TAGCATCAAGCGGTCTTTGAACGTCCGTTAGTAAAGTTTGAAAATTATAATAGAT TTTTAGAAAGAGAAGTTAAAATCAAACTTAAAGAATTATTGAACGGCAAAACTT
LH08G:00539:02467	256	99.219	NZ_AJTT01000006	88920 to 89173	ATTATTTTAGCTAATCTATGCATTTTTAAATATAGTAATTTTCTAATAGACCTCTTC CCAAGCGTCGCTTCTAGAGATAATTTATACGTCGATTCGGTACTCGCATCTTCA CGTATTTCTATATATGCTGTGGTGCTGTGTCCCGTGTCTCCGTTAAATTCCTCTC TATAAGTTTGGTTTGGGAAGAGGTTCTAATAAGAATATATAAAAATACCCTTAAA AAGCAATATTAATAATTTTATATAAATTATTAATA

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LH08G:00988:02633	327	100	NZ_AJTT01000006	31603 to 31929	ACTCCCCTTGATACCTACATACCAAATCTTACAGAGTCAAGATTTTGTAAATTTTTCTTTAAGTCTACCAGCGATGTGCCTGCTACTAGCTTTCCTATATCGCCTGCTATCTGCATAGTCTGAGTGCCTAGCTGGTATAAATTTAATGCCTGATCTAGAACATCAAGCCATTGCGTACCATTTTTATGTATTAAGTGATTGGCAAGCTTTGCAGTGTAGCTTAAATCTTCTTGTATGCCAATATGTATTGTATGCCAGCTTGCATTGTAGTAGATAGATAGAGGATTTAGCTGTCATTACCTATTATATCGACTTCGTCCTCTAAAT
LH08G:01328:01305	274	99.635	NZ_AJTT01000006	98551 to 98823	TCTAGAAAAATTTCAGAAAGAAGTTGGAACGGATGATATTGTTAGTGTTACTCCAAGTCAATTAGGTCTAGCTAAAAAAGCTAAACAAAAAGACCAAGATTTATTAAAATTAGATGAAGAAGATCTAAAACATATAAAGAATCTAAAAGAAAAGGTTATGAAGCCTACTCAAACTACTGCAGTTAGTGTTGTTAATAAAAAAGTCTACACCGGCTAAAATGAGATAATAAATGAACCAAGCAACAAGAAGCTTACAACTAAGTAATTAATCAGT
LH08G:01472:00458	205	100	NZ_AJTT01000006	99316 to 99520	AGCATAGATAATATAGCAATTATCTTTATTAAATTATAATTAATAGGATAGTAATTACCTATAATTAATTTGCTGATATTGAATAAAACAATAACCATACCTATTTTTGAGGCAGCATTGAAATAAGTAACCGAAGTAATCGGTGATCCTTCATATACGTCAGGGACCCAAAAATGGAGTGGAACACTTGAGAGTTTAAAGAAAA
LH08G:01636:03017	282	100	NZ_AJTT01000006	62415 to 62696	GTGGATTTAGATATTGGAACAATTTTAATGACGATTCCGATCCATTTATTTCCGTTTATGCTATGCATTTCTTAAGCGAGGGCGCAACTAGATATTTAGCCGTTCCAAGTGATACATTTAATCAAGGTATTTACTATTTAGAGAATATGGCTAACAGATCAATAAACTCCTTAGATGAAGCAAGAGAAAAGGCATATGCGGTTTATATCTTGACGCAAAACAGCGTTATTACTACAAGCTATATTGCAAATATTTTAAAATATTTAGACGAGTACCATAAAA
LH08G:01751:03116	201	97.015	NZ_AJTT01000006	96058 to 96252	AGCAAAATTTCTTTTTTGTAATGCAATATTTTTACTATAAGATAGTTAGGTTATATATTAGAATCCAAGTTATTAACTAAAATGAGATATGAATTTTATGTACCCCCATATTAGACTTAGAAAGAAATAGAAAAAGCTTTTTTGGCTTAGAGAGTTTAGTATCAGAAAGTAATTTATCGGTTTAGTGATTTAGTGTTGCCT
700666F:214:CA2UUANXX:8:1109:9570:7533_1:N:0:TAGGCATG+CTCTCTAT	125	100	NZ_AJTT01000007	42739 to 42863	TTGTCACGCAGCCTATGGCTGCTCGCAATGACGATTTGGTATCCATGCAAAGCCTTAAGCAGGAATGATATCGATTGTTCTCTCAATTCTAATACAAGCTTTTTCTAGCTCTTCCATAGAAGTAG
LH08G:00493:02627	249	99.197	NZ_AJTT01000007	30847 to 31093	TGAAGAGTTGAAGTCGCCTGAACTAATATTGCTACTTTTCCACTAGTATCATCAGATACCTGTTGTCTCTGTGTCACCTCATCTTGTTCTGTAATTGCTTCAGTTTTGAATGACACATCAATAGCTTCATCTTCGCTTTTCTAAAACTATATCTTTTTTTAATTCTTCGTCAGTGGTGCTTATTGCTTTCTTCTAATTCTTCTTCATCAGTTGCATACCCTTTATCGTCTTCATCACTAGATCTTAATG
LH08G:00605:00996	178	98.876	NZ_AJTT01000007	59163 to 59338	GACAGACAGGCATTTATAATGTTTTAACTGCTGCATAAAATATAGGTAACCATTTATCCGGATCATTGCCGTGTTTCTCTCTAATTTGATCGAGCAATATTACAGTCTCAACTCTACCGGATAAAAACACTGATTTATGTTATCCATATCATCTAAGCTAACTTTTGCCACTACAGCA
LH08G:00669:00823	208	99.519	NZ_AJTT01000007	1664 to 1870	AGAGTAGGCACTCCAAGACGTGCAGAAGCAGCGGCTGCTTCTACGCCTGCATGTCCACCGCCTATAACTATTACGTCATATTTTAGCATTAATTATTCTATAATTTCAGATTTATTAAAGAAAAATTCTATTTCTCTTTTTCGCACTATTTTCACTATCTGAACCATGAATACTATTAGCCTCAATTGATTCGCCTAAATCTTTTCTA
LH08G:00671:00991	332	99.699	NZ_AJTT01000007	15458 to 15788	TACCGAATCACGTATGACGGAAATATGTACGTTATTAATGGAGGACATCGATAAAGATACGGTAGATTTTCGCCCTACTTATGATGGTTCCGATTTAGAACCGGTAATAATGCCGGCAAGTTTTCCGAATTTACTAGCTAATGGTTCTGAAGGGATAGCAGTCGGTATGGCAACCAATATACCGCCGCATAATTTACATGAGCTTTGTGATGCTCTAATACATTTAATCAACCATCCGAAAGCTGAAATTAACGATATAATGAACTTTTGTCAAAGGTCCTGATTTCCCGACCGGCGGCATAATTATTGATAAAGCTGAAGTTATTAATGCT

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LH08G:00721:01865	328	99.695	NZ_AJTT01000007	52489 to 52815	CCTAATAAATATTGCTGAATAATATGTTTTTGTTGGATTTCATTTAAAGAGCGATTAGGTATATTTTTATTTTTAGTGAAATCAAAAGCTTTATAAAGTACAGGAGTATTACTTCCTATACTTAAATGTACTTGTCTAGCAGCGGTTGTTTTATCCTCTCTATCCGGAACAGTTACCTGTTATTGGATCAAATATAATTCCTAATGGGGCTCCCTTGTCTTCTATATCTGCAGATTTTATATTTACGTTAAAGTGGTTAGTTAATTCTTGTGTTACTTTACGAATATTACCATCTGATACCGCAATTTGATACTGCAGATCTATCACG
LH08G:00727:00743	311	99.678	NZ_AJTT01000007	49313 to 49622	GCGAGTATTATAGGTACTATCGGGTATGAGGTATTAACTACCCTTGGTAGTAGATACAAAAGAAAGTATATCGGGTAGATATCTGTGTCATACCATGGCTTGACCACGGTATCCAGAAAAAAATTAAAAAAGACTGGATCCCGCGATCAAGTCGCGGGATGACATTAGATGTTACTGGATTCCTGCTTGCGCAGAAATGACATAGCGTACTTAAATTAAATAGAAAAAATACAAATGTTATTCAATATAGCTAATTCGGTCGGTAAACGTACTGTAAAGTTTGCACAAAGTGTAGGTAGTTTTTCTCTATT
LH08G:00910:00305	279	99.642	NZ_AJTT01000007	40345 to 40622	TAAAGATACATTACGGTAGAGACGGAAAATTAAATAAGTTATCGTTGCCAAACCCACCTATAATTTTTCATAACCAATGGTATCCGGCCTTAACCGTTTGTAAAGGTGAATTATGTTCTTTGCCTATAAGTAGTAGGTATTATAGGTATTTGAATAAGAAAATACTAGAAAATAACGGAAGTATAGAAATCAGTCACGTAGACCCTGAATTTACTATAGAGCTTTTAGGAGAATAAGAGTTTTTAGTTAAATTTTATCAAAGAAACTTCGTTAATTACT
LH08G:00990:02358	303	99.67	NZ_AJTT01000007	50872 to 51173	ACTATTACGCATTTCATCTTTACTACCGTACCATTTAATTTTTCCTTGATAAATCATAGCTACTTCTTTAGCTATTTTTGCGGCACTAATCATATCATGAGTTATAGTAATCGTAGTTGCCTCTAACTCTTCTTGTATTTTTATAATTAATTCGTTGATAACATTTGCCATGATAGGATCAAGCCCTGTGGTCGGTTCATCAAGCAATAAAATCGACGGTGTACTACAAATAGCCCTAGCAAGGGCTACTCTTTTTTTGCATTCCTCCCGATAATTCGGCAGGGTAAAGCTCGAGTATTCTAG
LH08G:01166:02332	83	98.75	NZ_AJTT01000007	47634 to 47712	AAAAATTTCTCTACTTGTATCTGAGTGTAAATCAATAGTAATTACATGGTTTACTCCGAGCTTCTCTAAAAAATCTGCTACTT
LH08G:01538:00955	329	98.784	NZ_AJTT01000007	50655 to 50979	GTTCATCAAGCAATAAAATCGACGGTGTACTACAAATAGCCCTAGCAAGGGCTACTCTTTTTTGCATTCCTCCCGATAATTCGGCAGGGTAAAGCTCGAGTATTCTAGGAGATAAACCAACGGCATTAAGCTTTGCACCGGCAAGGTCGTTTTTTTTCTTTCTTAGATAATTTTTTTAATCTCGAAAGTAATATTATCACGTATATTTAAGGAGTCAAATAATGCTCCGCCTTGGAATAAAAAAACCTATACCATCCATAATCTCAAATTTTTTGTTTACTTGAGATATCTTGGATTTCTACATTATCAATAAAAATTTTACCTTTATC
LH08G:01900:01532	178	98.876	NZ_AJTT01000007	61066 to 61241	TATACAAGAAATTATTTTGAGAGCTGGGTTAAACTAATGATCTCGTTCTTGCTGCAACCTATGGTGGTAGTTACTTTTTATGATCACGATGTTTTCGGTATATGATTATGGTTTCTACGGTAAATGTCAATATAAGAGCAAGTTAATTCACAATAGTATAGAAGACAAAAATTCAAGG
LH08G:02043:01078	257	100	NZ_AJTT01000007	60308 to 60564	GGCAAATGATTTCTAGATTACTAATTAGTAAAGATGTTTGTAGTTTTGATAATGTAAGCCAAGTGGTTAATTTGGTTTCAAGGCAAGATAGTGCATTCTTTCAGTTTCAAGTAGGAATGTATAAAATAGTTACGGCTTTTCTAACTTTATATGTTATGTTTTTTGGCTTTAAACTATTACTTGCAGGTGAAGTGCCGCCAAAAAGTGAGTATATAAATTTTATATTGAAAATGATATTCGTAACTTATTTTTCAATA
700666F:214:CA2UUANXX:8:1108:8596:42754_1:N:0:TAGGCATG+CTCTCTAT	125	100	NZ_AJTT01000008	25142 to 25266	GTAAATATCCGCATCTACTATCCCGACTCGGTAATTTGCTAGACTTAACTGTTGAGCGATAAGAGCAGATATTGTAGATTTTCCGACTCCGCCTTTACCTGACGCTACTAAGATAATTTTTTTTA
LH08G:00129:01101	116	100	NZ_AJTT01000008	20602 to 20717	ATTTAGACGTCGATCCAGTACTCGCATCCTCACGTACTGCGGCGGCAAGTGCTTCCGTGTCTCCTTTAAATTCCTCTCTATAAGCGAATTTGGCAAGATGTCTATTAGTCATTTTT

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LH08G:00238:00771	252	100	NZ_AJTT01000008	17949 to 18200	CTTGTAAGGATCGTGATATATTAAGGTTTGAGCCGCACAAATTAATAGAAGGTT GCTTGCTTGCAAGCTTTGCTATAGGAGCGAATAATTGTTATATCTATATTAGAGG TGAGTTTTATAATGAAGCCTCTAATATTCAGCGTGCCTTAGATGAAGCCTATAAA GAAGGGTTAATAGGAAAGAATTCTTGCGGTTCGGGTTTTGATTGTAATATTTATT TACATCGTGGGGCGGGTGCTTATATTTGTGGTG
LH08G:01472:03357	329	100	NZ_AJTT01000008	39709 to 40037	AGCCGTTTAACGGTAGTATAGTAATAATAAAAAATTTTGTTATTTTAAGCATTTGT ATCAGTTTAAATATATTAAACTGTATTATAAAAGGAGAATTAAAAGGTGTTAAGAT CAGAAAAACCGGTAGCAGTAGAGGATATTGTAAATATTTATAAAGAATCGCCCT CTATAATTATTACTCATTATCACGGGTTAACCGTTAGTCAAGTGAGTTCGCTTAG AGAATCACTTAAATCTAAAGAAGCAGGTTTTAAAGTAGTTAAAAATACTTTAGCA AAAATAGCTGCAAATCAAACAGGGCTTAATAGTATTGCTAATTTATTTGCGGG
LH08G:00343:01258	271	100	NZ_AJTT01000009	20861 to 21131	AGTGAAATATTAGAACTTGAAGCGGAATCCCGCACGGAATTCGGTACGGGAGC AGCAAGAGCATTAAGAAGAGCAGGGCGTGTTCCGGCTATTATTTATGGAGCTG GTAAAACACCTGTTAGTATTTCTTTGGAAGAAAAGGAAATAACTAAATATTATAG AAAGCCGGCTTTTATCTCTCAGTTAATTAATTTAACAATTGATAAGAAAAAATATA AAGTATTGCCGAAGGCTGTAGAATTACATCCTGTTACGGATATAGTACGCCATG
700666F:214:CA2UUANXX:8:1215:13592:16288_1:N:0:TAGGCATG+CTCTCTAT	125	99.2	NZ_AJTT01000010	7225 to 7349	CCCTAAAATATCTCAAAGCGAAATAGCAGAATTGCCGCCTATTTCGTTATTACGT GATCCTGAAAAACATCATGTAAAAGGAGCTTCTTCCTCAGAGCTTAAACAAAAG GTTGAAGAGTTATTAA

*Gene name: *ompB*.