

MPhil Thesis – 2012

Candidate	Kenneth Douglas Doig
Student No.	197821835
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Supervisors	A/Prof. Tim Stinear ¹ Dr. Torsten Seemann ² Prof. Richard Strugnell ¹
Department	Microbiology and Immunology
Faculty	Medicine, Dentistry and Health Sciences The University of Melbourne

1. Department of Microbiology and Immunology, University of Melbourne, Parkville, Australia
2. Victorian Bioinformatics Consortium, Monash University, Clayton, Australia

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Abstract

Buruli ulcer is a neglected tropical disease which is prevalent in Western Africa. Its etiological agent, *Mycobacteria ulcerans* occurs in a wide range of hosts and environments across the world. In contrast to its progenitor *Mycobacteria marinum*, the bacteria and related strains produce a toxin mycolactone, an immunosuppressive polyketide which gives rise to its pathogenicity. Bacterial pathogenesis has a number of hallmarks such as; an evolutionary bottleneck, insertion sequence (IS) expansion, pseudogene increase, genome reduction, horizontal gene transfers (HGT) and adaption to a new niche. *M. ulcerans* shows all of these characteristics and is a fine model for gaining a deeper understanding of the mechanics of bacterial pathogenesis in general and specifically for *M. ulcerans* and related strains. This research analyses the genomic makeup of 35 isolates that produce mycolactone and five *M. marinum* isolates. Such analysis have recently become possible through the rapid technological development of high throughput sequencing (HTS) allowing whole genome sequences of all isolates to be compared and contrasted.

Nucleotide level comparisons of the isolates has enumerated a core set of SNPs and allowed a detailed phylogeny of the isolates to be revealed showing the clonal nature of the mycolactone producing isolates that have evolved from the marine dwelling *M. marinum*. Also highlighted were two distinct bottlenecks, both accompanied by IS expansion, genome reduction and HGT. The first bottleneck acquired the pMUM001 virulence plasmid that confers the ability to synthesis mycolactone. A second bottleneck resulted in the creation of the more pathogenic clonal groups of isolates present in Africa and Australia, which are responsible for the majority of global Buruli ulcer cases. Genome reduction has resulted in the loss of at least 185 genes with cell wall genes being overrepresented. The balance of the cell wall genes show further signs of adaptive selection suggesting remodelling of the cell wall in response to its new niche or environment. Locating the numerous ISs within the isolates indicated the virulence plasmid pMUM001 to be the likely source of the ISs, which in turn confers genome plasticity on the bacteria.

A most recent common ancestor of *M. marinum* has given rise to *M. ulcerans* and all mycolactone-producing mycobacteria that are specialized variants and have evolved to live in niche environments. Analysis of the genes that have been lost, the genes retained, and the genes now under selective pressure suggest these environments might be dark, aerobic, and extracellular. The bacterial characteristics of *M. ulcerans* such as, slow growth, production of an immune suppressor, cell wall remodelling, loss or modification of cell wall antigens, and biofilm-forming ability all provide a survival advantage in these environments.

This research provides a detailed investigation into the genetic makeup and biological impact of this group of Mycobacteria and will allow better understanding of the transmission of Buruli ulcer and their reservoirs.

Declaration

This is to certify that:

- (i) the thesis comprises only my original work towards the MPhil except where indicated in the Preface,
- (ii) due acknowledgement has been made in the text to all other material used,
- (iii) the thesis is less than 50,000 words in length, exclusive of tables, maps, bibliographies and appendices.

Signed: _____ Date: _____

Kenneth Douglas Doig

Preface

The following paper is a publication arising from research completed for this thesis:

Doig KD, Holt KE, Fyfe JA, Lavender CJ, Eddyani M, Portaels F, Yeboah-Manu D, Pluschke G, Seemann T, Stinear TP: **On the origin of *Mycobacterium ulcerans*, the causative agent of buruli ulcer.** *BMC Genomics* 2012, **13**(1):258.

The author contributions were as follows: K.Doig co-wrote the manuscript, analysed the data and performed the bioinformatic analysis. T.Seemann wrote some of the analysis tools. K.Holt carried out the Bayesian analysis and co-wrote the manuscript. J.Fyfe and C.Lavender provided materials and assisted with study design. M.Eddyani, F.Portaels, D.Yeboah-Manu, G.Pluschke provided materials and co-wrote the manuscript. T.Stinear conceived the study, analysed the biological data and co-wrote the manuscript. All authors read and approved the final manuscript.

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Table of Contents

1. INTRODUCTION	6
1.1 OVERVIEW.....	6
1.2 RESEARCH AIMS.....	6
1.3 THE BIOLOGICAL AND TECHNOLOGICAL STUDY CONTEXT	7
1.3.1 <i>Insights from Comparative Genomics of Bacterial Pathogens</i>	7
1.3.2 <i>The Study Bacteria: Mycobacterium ulcerans and Mycobacterium marinum</i>	13
1.3.3 <i>Short Read Sequencing, Assembly and Alignment</i>	15
1.4 THESIS OUTLINE	19
2. METHODS	20
2.1 BACTERIAL ISOLATES AND SEQUENCING.....	20
2.2 READ MAPPING	21
2.3 DE NOVO ASSEMBLY OF SHORT READ SEQUENCES	21
2.3.1 <i>Analysis of de novo Assembly Parameters</i>	21
2.3.2 <i>Locating Repeat Regions Within de novo Contigs</i>	22
2.3.3 <i>De novo Assembly Limitations</i>	23
2.4 CORE AND PAN GENOME ANALYSIS.....	24
2.5 SNP ANALYSIS.....	25
2.6 DN/DS ANALYSIS.....	25
2.7 PSEUDOGENE IDENTIFICATION	26
3. RESULTS.....	27
3.1 SHORT READ DE NOVO ASSEMBLY OPTIMISATION	27
3.2 ISOLATE SELECTION AND SEQUENCE ANALYSIS STRATEGY	30
3.3 MYCOLACTONE-PRODUCING MYCOBACTERIA FORM A MONOPHLETIC GROUP.....	34
3.4 GEOGRAPHICAL RESTRICTION OF <i>M. ULCERANS</i> OVER SHORT TIME SCALES.....	37
3.5	39
3.5 MYCOLACTONE-PRODUCING MYCOBACTERIA SHOULD BE CONSIDERED A SINGLE SPECIES – <i>M. ULCERANS</i>	39
3.6 GENOMIC FEATURES OF <i>M. ULCERANS</i>	40
3.7 IMPACT OF IS2404 AND IS2606 ON <i>M. ULCERANS</i> GENOME ARCHITECTURE	44
3.8 <i>M. ULCERANS</i> GENES UNDER SELECTIVE PRESSURE.....	45
3.9 CODON BIAS AND tRNA USAGE	46
4. DISCUSSION OF RESULTS.....	48
5. CONCLUSION AND FUTURE DIRECTIONS	50
6. REFERENCES	52

7. ABBREVIATIONS	61
8. TABLES	62

List of Figures

Figure 1 Hallmarks of pathogenesis	9
Figure 2 Workflow Schematic.....	20
Figure 3 Schematic of IS region identification.....	23
Figure 4 Schematic of Pan-Core genome	25
Figure 5 Paired-end Assembly Simulation.....	28
Figure 6 Read Coverage Assembly Simulation.....	29
Figure 7 <i>De novo</i> assembly parameters for <i>M. ulcerans</i> Agy99	30
Figure 8 Comparative genome content of isolates to references <i>M. marinum</i> and <i>M. ulcerans</i>	32
Figure 9 Comparative genome content of plasmid pMUM001.....	33
Figure 10 Open genome analysis.....	34
Figure 11 MuMC phylogenomic analysis	36
Figure 12 African isolates tree and map	38
Figure 13 Percentage DNA difference between isolates	39
Figure 14 Percentage Venn diagrams, showing DNA shared and unique among isolates	42
Figure 15 Inferred pseudogenes and deleted genes	44
Figure 16 IS2404 and IS2606 distribution among isolates.....	45
Figure 17 Codon Usage and tRNA Counts for reference genomes.....	47

List of Tables

Table 1 Some common bacterial pathogens	13
Table 2 Isolates used in this study	62
Table 3 Noteworthy genes or loci absent in the <i>M. ulcerans</i> MRCA.....	64
Table 4 Strain Table and Summary Statistics.....	65
Table 5 <i>M. ulcerans</i> specific CDS and features.....	66
Table 6 High dN/dS CDS and CDS with high non-synonymous SNPs.....	67
Table 7 <i>M. marinum</i> orthologs of <i>M. tuberculosis</i> T-cell antigens.....	80
Table 8 Core SNPs	81
Table 9 Diagnostic Regions.....	81
Table 10 Ancestral Pseudogenes	81

1. Introduction

1.1 Overview

The majority of life's biochemical diversity appears in microbes, in particular the Bacteria. A wide range of nutritional and metabolic adaptations has allowed them to occupy nearly all possible habitats on earth. Underlying this diversity is a pool of genetic material undergoing continuous modification from which new adaptations and traits can arise.

Among microorganisms, the bacteria form the largest group and contain the pathogens that have been responsible for much of human illness throughout recorded history. Naturally, bacterial pathogens have been the focus of intense medical research. Within the last decade, there have been enormous advances in this research, triggered by the human genome project and the subsequent development of high throughput sequencing technologies. These developments have allowed bacterial genomes to be elucidated and analysed with unprecedented detail. This research is revealing many of the mechanisms for modifying genomes and the basis for bacterial diversity.

Darwin's original 'descent with modification' theory required three elements for natural selection to occur; heritable traits that could be passed from parent to offspring, the variation of those traits and an environment that could only support a limited number of the offspring. This theory has stood the test of time and this research seeks to extend its coverage and show evolution in the microcosm of important strains within the genus of the bacteria called *Mycobacterium*.

1.2 Research Aims

The primary aim of this research is to better understand the pathogenesis, genomic architecture and evolution of the species *Mycobacterium ulcerans* and its progenitor *Mycobacterium marinum*.

The occurrence of Buruli ulcer, an infectious disease caused by *Mycobacterium ulcerans*, is associated with wetlands across the world, mostly in tropical regions but also some temperate climates. *M. ulcerans* is a slow growing bacterium and has been found in a wide range of organisms including humans, fish, frogs, possums as well as aquatic insects and invertebrates. The epidemiology of Buruli ulcer is poorly understood despite a number of surveys to isolate *M. ulcerans* from the environment which have only yielded inconclusive results. A number of vectors have been proposed including mosquitoes and other aquatic insects. *Mycobacterium marinum* is a close relative of *M. ulcerans* but in contrast, it is ubiquitous and fast growing pathogen of fish and amphibians. Genetic comparisons suggest *M. ulcerans* evolved from an *M. marinum* progenitor. As a relative of *Mycobacterium tuberculosis*, *M. marinum* is used as a model organism to study *M. tuberculosis*. *M. marinum* has the characteristics of both a specialist bacterium adapted to live in the intracellular environment within organisms such as free living aquatic amoeba and vertebrate hosts as well as a generalist living in changing extracellular environments.

The development of high throughput genomic sequencing in the last six years has allowed the differences and similarities between DNA of related organisms to be explored at nucleotide level. Genome comparisons have helped illuminate the mechanisms of pathogenesis, some of which are summarised in section 1.3.1. The research described in this thesis will undertake similar comparisons to try and elucidate the mechanism by which *M. ulcerans* has become both pathogenic and more virulent compared to its progenitor *M. marinum*. These genetic comparisons will also allow investigation of the evolution of *M. ulcerans* and the processes involved.

A total of 35 mycolactone-producing mycobacteria (MPM) and five *M. marinum* isolates were chosen to give a high-resolution view of the genetic differences between the isolates. The isolates cover a diverse range of source regions, source hosts and species designations. A key goal of the research is to highlight both the DNA segments and the genes overlapping these segments that allow these characteristics (region, host and species) to be discriminated. These segments will provide the basis for molecular tests to detect and distinguish new isolates in the future.

A number of isolates in this research are being studied for the first time. This research will characterise their features as well as making their data available to the wider research community through the NCBI Sequence Read Archive [1].

One approach to understanding the evolution of pathogenesis in a group of bacteria is the characterisation of their most recent common ancestor (MRCA). This study will identify the key genomic features of the *M. ulcerans* MRCA - pseudogenes, genomic deletions, single nucleotide polymorphisms (SNPs) and its distribution of insertion sequences (ISs). The presence or absence of these features in the MRCA will give insights into attributes of the bacterium that were probably present when the organism became pathogenic and hence intrinsic to its change of role from a generalist bacteria into a specialised pathogen.

1.3 *The Biological and Technological Study Context*

The framework for this study is bounded on one side by the diversity of bacterial pathogens and their strategies to survive and on the other by the technological resources available to investigate and understand these strategies. The following section examines, firstly, many of the well-known human pathogens and secondly, the available sequencing technologies and their attendant software tools.

1.3.1 *Insights from Comparative Genomics of Bacterial Pathogens*

Bacterial pathogens such as *M. ulcerans* and their progenitors have many environments within which their genomes are evolving and adapting. This adaption involves a wide variety of different genetic mechanisms. A review of the general evolutionary pathways used by bacteria is presented in the following sections.

The pre-genomic view of evolution was that DNA change occurs slowly through the accumulation of inherited mutations. However, recent advances in DNA sequencing and the advent of high throughput genomics has shown that bacteria have dynamic genomes that participate in rapid DNA gains, losses and rearrangements [2]. This interchange of DNA occurs through many mechanism including transfer of plasmids, bacteriophages, transposons, and also homologous recombination between close relatives who collectively hold a diverse set of genes known as the pan genome [3]. Such DNA exchange, sometimes referred to as horizontal gene transfer (HGT), is a major force in bacterial genome evolution. This dynamic, adaptive capacity of bacteria allows them to rapidly change in response to environmental pressures and has led to their colonisation of almost every niche on the planet [2].

The evolution of bacterial pathogens from a non-pathogenic progenitor is often the result of acquiring clusters of virulence genes on plasmids or via HGT on pathogenicity islands (PAI) [4]. HGT allows bacteria to directly acquire genes, and hence their functions, that are already evolved and have survived selective pressures in other bacteria. These genes may encode traits that allow a newly created pathogen to colonise and survive in a new niche. Hence, with a single step the non-pathogen can acquire virulence [5]. The majority of protein family expansions in bacteria come from HGT rather than gene duplication. This is in contrast to eukaryotes where gene duplication followed by specialisation is regarded as the main source of new gene functions [6].

A review by Bentley and Parkhill [2] covered key aspects of bacteria and observed that the smallest genomes tend to be restricted to stable niches while the larger ones tend to occupy highly complex and variable environments. A number of sets of data were put forward suggesting that environmental pressures largely dictated genome size and content. In particular, genome reduction and loss of gene function can be due to adaption to a simplified more stable environment. Human pathogens which have recently been acquired from another niche, exhibit genome reduction and tend to have a large number of pseudogenes. This is seen as being the result of accelerated genetic drift caused by evolutionary bottlenecks through a niche change [7]. Such bottlenecks may occur multiple times as a pathogen is transmitted between hosts. Inactivated genes that were probably required for adaption in the old niche are superfluous or even disadvantageous (antivirulence genes) in the new niche.

Often niche changes are accompanied by an expansion of mobile genetic elements such as insertion sequences (IS). These are small DNA segments that are capable of autonomously moving or copying within or between replicons. The expansion of ISs may have been suppressed previously through selective pressure but in a new niche, with a reduced population, the relaxed selection pressure allows IS expansion. This usually also coincides with genome rearrangements, deletions and insertions causing loss of gene functions [8]. Repeats in the form of ISs may also result in new gene functions through duplications, stochastic switching of gene expression and homologous recombination generating high rates of sequence variation [9].

Bacterial pathogens may accumulate a series of irreversible genomic defects or deletions by recurrent bottlenecks when they pass from host to host. This process is commonly referred to as

Muller's ratchet [10] and occurs when there are small population sizes and low recombination rates. This process is often active in the genome reduction of pathogen genomes [11].

Pathoadaption through gene loss is where the loss of gene function improves a pathogens ability to survive in a new niche. The loss of gene function may occur through either DNA alterations of the gene via point mutations or deletions or alternatively by the suppression of gene expression through modification of its promoter or 5'UTR preventing its transcription or translation. It may not be clear whether the loss of a gene is due to its antivirulence properties or from just being superfluous. The characteristics of an antivirulence gene are; firstly, the gene must be present and expressed in closely related or ancestral species occupying the non-virulent ancestral niche but absent (or mutated) from pathogenic strains that colonize a new niche and second, expression of the antivirulence gene by the pathogen in a new niche must attenuate virulence and/or inhibit fitness. [4].

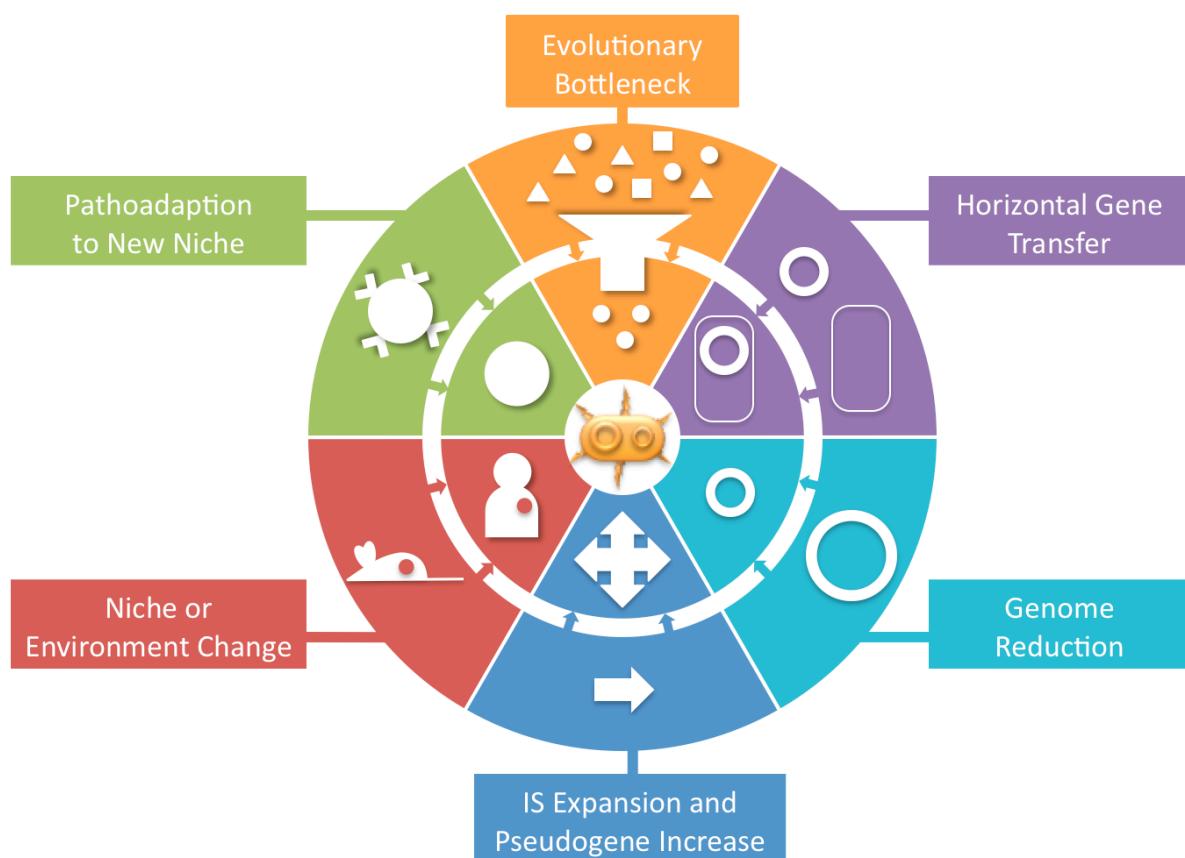


Figure 1 Hallmarks of pathogenesis

Schematic showing common hallmarks of bacterial pathogenesis.

The following section provides a brief summary of a range of bacterial pathogens. While these pathogens do not necessarily closely match the study organisms, they cover much of the diversity human pathogens and provide a context for this genomic study.

The section highlights the common traits of pathogenesis: pathogen emergence from a closely related avirulent organism; evidence of an evolutionary bottleneck (new niche); virulence acquisition via a PAI and HGT or via plasmid; IS expansion; chromosomal rearrangements;

genome reduction; pseudogene accumulation; and pathoadaption (See Figure 1). Each of the pathogens below displays many of these traits. The pathogens are summarised in **Table 1**. This study has identified these traits within the pathogens of this research.

1.3.1.1 *Mycobacterium tuberculosis*

Strains of one of the most widespread and frequently lethal bacterial pathogens, *M. tuberculosis* [12], are highly clonal with their nucleotide sequences 99.9% identical [13]. This clonality is the result of the bacteria undergoing an extreme bottleneck in the recent past [14]. This bottleneck and reduced population size has led to weakened selective pressure and an increase in the effect of genetic drift - the change in frequency of a gene variant due to random sampling. This is shown through extensive lateral gene transfers and genome reduction in strains of the *M. tuberculosis* complex (MTBC) [15, 16]. There is also evidence that it has undergone pathoadaption and lost potential antigens (while gaining other genes) to become more virulent [17]. The genomic changes have resulted in MTBC becoming a specialised primate pathogen without an environmental niche [16].

The origins of *M. tuberculosis* have been long debated, not least because of its apparent failure to fit some of the common traits of pathogenesis. A recent opinion paper [18] has suggested an evolutionary scenario placing *M. tuberculosis* as a terminal host specialised organism that has evolved from the common ancestor of all mycobacteria. Here the evolution is seen in two phases, the first, a dynamic phase with HGT, duplications and deletions and a second clonal phase with deletions and pathoadaption. The second phase of reductive evolution is suggested to take place over a long timescale.

1.3.1.2 *Mycobacterium leprae*

Leprosy is a human neurological disease caused by *Mycobacterium leprae* [19]. Along with Tuberculosis, *M. leprae* is one the best known of the mycobacteria and its genome exhibits an extreme case of reductive evolution with a very high percentage of pseudogenes (36.5%). When compared with *M. tuberculosis*, *M. leprae* shows extensive loss of function of genes no longer required in its human host niche. *M. leprae* also has an extremely low coding density of less than 50% compared with the usual coding density of bacteria of between 85% and 90%. The genome reduction has resulted from many recombination events between repetitive regions (including many ISs) spread throughout the genome. The resulting genome is the smallest amongst known mycobacteria, and the slowest growing, with a doubling time of ~14 days.

1.3.1.3 *Rickettsias*

Rickettsia are an intracellular parasite that causes a number of human diseases including typhus transmitted via body louse and ticks [20]. The genome is small (1.1–1.4 Mb) and has a high proportion of non-coding DNA (24%) including a number of pseudogenes. The small genome size shows extensive gene decay as a result of shedding genes whose functions are no longer required in a niche that is rich in nutrients, amino acids and nucleotides. The loss of genes encoding biosynthetic functions can be compensated for by an increase in the complement of

transport functions to absorb resources from the surrounding environment. A consequence of this specialisation is that the organism cannot be cultivated in a cell-free medium [11].

1.3.1.4 *Shigella*

Shigella species are the etiological agents of dysentery and shigellosis and causes over a million deaths per year worldwide [21]. There are four main species of *Shigella* (*S. dysenteriae*, *S. flexneri*, *S. boydii* and *S. sonnei*) that have emerged from *Escherichia coli* independently in an example of convergent evolution. All *Shigella* species contain a large 220kbp “invasion” plasmid that encodes conserved virulence genes including a specialised protein secretion system for intracellular persistence. Additionally, the chromosome contains virulence genes that have been acquired by HGT from bacteriophages. The *Shigella* genome has a large number of ISs (300-700) and over 200 pseudogenes - hallmarks of reductive evolution. The ISs have mediated many gene deletions and insertions and caused extensive genome rearrangements. There is also evidence of pathoadaption through the loss of genes encoding cell surface antigens that may allow for better host immune system evasion [4, 22].

1.3.1.5 *Typhi*

Salmonella enterica serovar Typhi (Typhi) is the cause of typhoid, a disease caused by the ingestion of contaminated food or water. Typhi is highly clonal and has ongoing loss of gene function, which is consistent with increased genetic drift within a small population caused by evolutionary bottlenecks. Typhi has around 200 pseudogenes and a number of ISs and seven prophage-like elements [23]. Virulence is due to several *Salmonella* pathogenicity islands acquired through HGT together with key gene function loss. In addition there are multi-drug resistant isolates whose resistance is conferred by a plasmid (IncH1) carrying a set of antimicrobial resistance genes [24]. A recent comparison of 19 Typhi isolates using next generation sequencing (NGS) of DNA has succeeded in identifying homoplasic SNPs (SNPs showing convergent evolution by occurring in multiple isolates independently) showing antibiotic resistance to fluoroquinolones within the gene *gyrA* [23]. Acquiring antibiotic resistance is a form of pathoadaption where the organism responds to the use of antibiotics within the host environment.

1.3.1.6 *Bordetella pertussis*

The strictly human pathogen *B. pertussis* is the cause of whooping cough and has evolved from its ancestor *B. bronchiseptica* that has a broad host range. *B. pertussis* has undergone extensive genome changes from *B. bronchiseptica*: the gain of 261 ISs; the creation of 340 pseudogenes; the loss of 1.3 Mb of DNA and 150 chromosomal rearrangements. *B. pertussis* isolates show little genetic variation, common with bacteria that have passed through an evolutionary bottleneck. In contrast to other human pathogens, there is little evidence of exogenous genes conferring virulence; instead, virulence seems to be the result of large scale gene inactivation. For example, the loss of genes encoding cell surface antigens may have allowed for better evasion of the host immune system [25].

1.3.1.7 *Streptococcus pneumonia*

Pneumonia is one of the top ten causes of death in the United States and is caused by the gram-positive bacterium *Streptococcus pneumonia*. It has a small genome of 2.1 Mb containing 84 ISs making up 5% of the genome. These ISs have led to many genomic rearrangements [26]. *S. pneumonia* can adopt a biofilm mode of growth which increases the likelihood of HGT and inter species DNA transfers. These features enable the pathogen to generate diversity at a faster rate than the host's adaptive immune system, making clearance of the bacteria difficult. Comparative genomic analysis of 17 isolates of *S. pneumonia* has highlighted the high variation between isolates showing that only 46% of orthologous gene clusters are conserved across the isolates. This supports the distributed genome hypothesis where a pathogenic bacterium has a large pool of genes (the pan genome) on which it can draw for genetic diversity [27]. The PMEN1 strain of *S. pneumonia* has also been shown to have developed resistance to some antibiotics via rapid evolution resulting from interactions between vaccines and the bacteria [28].

1.3.1.8 *Yersina pestis*

Yersina pestis, the agent of the bubonic plague, is a human pathogen originating in rodents and cats and can be transmitted to humans by tick bites [29]. It is closely related to *Y. pseudotuberculosis* and *Y. enterolitica*, and their genomes are ~4.6 Mb in size and contain 60-139 ISs, 50-150 pseudogenes and 3-5 prophage regions. Isolates show little genetic variation and all contain horizontally acquired loci with high densities of virulence genes. *Y. pestis* contains the greatest number of ISs and pseudogenes, reflecting a change in niche combined with plasmid acquisition. The plasmid pMT1 is highly similar to the Typhi plasmid pHCM2 and suggests a shared gene pool or DNA transfer.

1.3.1.9 *Staphylococcus aureus*

Staphylococcus aureus is a common bacteria causing a wide range of diseases and presenting considerable problems in hospital environments due to antibiotic resistance in some strains, for example, methicillin-resistant *S. aureus* (MRSA). The bacteria have a 2.8 Mb genome that contains 2 bacteriophages, 5 ISs or fragments, a plasmid, 2 genomic islands and a staphylococcal chromosomal cassette (SCC) [30]. The strains of the bacteria are highly clonal but vary with the content of HGT acquired elements. Through HGT, MRSA has acquired the *SCCmec* mobile genetic element that encodes resistance to methicillin and other antibiotics and has been imported on at least 20 different occasions underscoring the convergent evolution aspect of bacterial genomes and the rapid change in function a PAI confers [31]. A recent study of 63 MRSA strains allowed very fine-grain analysis of SNPs and also showed the global transmission of the strains via modern transport, such as planes, and, at the local level, down to the spread of strains within a Thai hospital [32]. The application of NGS technology at the hospital level will, in the future, allow for highly granular tracking of infectious disease transmission.

Pathogen	Size Mb	Disease	Likely Progenitor	Size Mb	Genetic element encoding virulence
<i>Mycobacterium tuberculosis</i>	4.4	Tuberculosis			chromosome
<i>Mycobacterium leprae</i>	3.2	Leprosy	<i>M. tuberculosis</i> ancestor	4.4	chromosome
<i>Mycobacterium ulcerans</i>	5.6	Buruli ulcer	<i>M. marinum</i>	6.6	plasmid
<i>Rickettsias</i>	1.1-1.4	Epidemic typhus	<i>R. candensis</i> (?)	1.1	chromosome
<i>Shigella</i>	4.4-4.8	Dysentery, shigellosis	<i>Escherichia coli</i>	4.6	plasmid, bacteriophage
<i>Salmonella enterica</i> serovar <i>typhi</i>	4.8-5.1	Typhoid fever	<i>S. enterica</i>	4.6-5.1	pathogenicity islands
<i>Bordetella pertussis</i>	4.1	Whooping cough	<i>B. bronchiseptica</i>	5.3	chromosome
<i>Streptococcus pneumoniae</i>	2.1	Pneumonia			pathogenicity islands
<i>Yersina pestis</i>	4.6	Plague			plasmid
<i>Staphylococcus aureus</i>	2.8	Suppuration			bacteriophage

Table 1 Some common bacterial pathogens

List of common bacterial pathogens and their features.

1.3.2 The Study Bacteria: *Mycobacterium ulcerans* and *Mycobacterium marinum*

The genomes of *Mycobacterium ulcerans* and *Mycobacterium marinum* are closely related, sharing >98% overall nucleotide identity [33], but cause very different kinds of infections in humans. *M. marinum* causes minor skin infections, characterised by intracellular bacteria and the granulomatous lesions that are features of infection common to many mycobacterial pathogens, notably *Mycobacterium tuberculosis* [16]. In contrast, *M. ulcerans* causes Buruli ulcer (BU), a slowly progressing, ulcerative disease characterized by necrosis of subcutaneous tissue. BU has a characteristic histopathology with large numbers of extracellular bacteria present during the acute phase of the infection, and a marked lack of inflammatory response in advanced infection. This unusual pathology is principally mediated by an immunosuppressive polyketide called mycolactone, which is not produced by *M. marinum* or *M. tuberculosis*. In BU patients, mycolactone is present in cutaneous lesions but also diffuses and can be detected in serum [34, 35].

Two main features differentiate the genomes of *M. ulcerans* and *M. marinum*. The first is the large 170kb pMUM plasmid, found in *M. ulcerans* but absent from *M. marinum* [36, 37]. This plasmid harbours three large genes (*mlsA1*: 51 kb, *mlsA2*: 7.2 kb, *mlsB*: 43 kb) that encode the polyketide synthases (PKSs) required for mycolactone synthesis [16]. The second is the insertion sequence (IS) IS2404 that is absent from *M. marinum* but present in high copy number (>200) in *M. ulcerans* genomes. IS2404 expansion in the *M. ulcerans* genome has led to the inactivation of many genes through disruption of coding and promoter sequences and has mediated the deletion of about 1 Mb of DNA from *M. ulcerans* compared with *M. marinum* [33]. Together with loss of

DNA, there is also evidence of extensive loss of gene function in *M. ulcerans* - the genome of *M. ulcerans* isolate Agy99 harbours 771 pseudogenes, while the *M. marinum* genome harbours only 65. Acquisition of foreign DNA, IS expansion, pseudogene accumulation and genome reduction are features in common with bacterial populations that have passed through an evolutionary bottleneck [19, 20, 23, 25, 27, 29], suggesting there has been constriction of population size during adaptation to a new, niche environment. Previous analysis of the *M. ulcerans* Agy99 genome showed deletion or inactivation of genes expressing potent T-cell antigens, and genes required for pigment biosynthesis, anaerobiosis, and intracellular growth [33]. This profile suggested a bacterium that has adapted to a dark, extracellular environment where slow growth, loss of immunogens and production of an immunosuppressive molecule provide a selective advantage [33, 38]. In contrast, its progenitor, *M. marinum*, has the characteristics of both a specialist bacterium that can persist within an intracellular environment as well as a generalist that can survive in extracellular conditions. A niche environment for *M. ulcerans* has not yet been demonstrated although the recent discovery that Australian native possums inhabiting BU endemic areas appear to harbour the bacteria in their gastrointestinal tracts raises some interesting possibilities [39].

The species definition of *M. ulcerans* has recently been challenged by the discovery of variously named mycobacteria that also make mycolactones but are not always associated with BU. These mycobacteria, isolated from humans, fish and frogs in diverse geographic locations (Japan, the Mediterranean, Israel, Belgium and the United States), have been variously named *Mycobacterium shinshuense*, *Mycobacterium marinum*, *Mycobacterium pseudoshottsii*, and “*Mycobacterium liflandii*”, the latter an unofficial species name with no standing in nomenclature [40-44]. Studies of these isolates using an 8-gene multi locus sequence typing (MLST) scheme and patterns of genome deletion suggest they evolved from a *M. marinum* common ancestor and subsequently diverged into two principal lineages [45, 46]. These mycolactone-producing *Mycobacterium* (MPM) lineages have been termed “classical” and “ancestral”. The “classical” MPM lineage includes *M. ulcerans* isolates associated with BU from Australia, South East Asia and Africa while the “ancestral” lineage includes the fish and frog isolates as well as *M. ulcerans* BU isolates from Japan, China, Mexico, Surinam and French Guiana [45, 47]. It was recently proposed that based on their genetic coherence all MPM should be renamed *M. ulcerans*, a proposition that will be revisited in this research [48].

Comparative genomic analysis of closely related bacteria has facilitated dramatic improvements in the understanding of bacterial pathogen evolution [49]. Low-coverage 454 and Illumina sequencing of three *M. ulcerans* isolates from Ghana and a single isolate from Japan demonstrated the capacity of high throughput sequencing to differentiate *M. ulcerans* co-circulating in a geographic region [50]. This research will report on the sequencing and analysis of whole genomes from a diversity of isolates that are representative of what is defined as the *M. ulcerans*-*M. marinum* complex (abbreviated hereafter as MuMC). That is, mycobacteria previously identified as *M. marinum*, *M. ulcerans* and other MPM that share >97% nucleotide identity based on MLST [45, 48]. The isolates studied in this research include mycobacteria isolated from humans, possums, a bilby (small Australian mammal), fish, frogs, an insect and an

armadillo from diverse geographic locations. Whole genome comparisons were used to reveal the phylogenomic relationship among these mycobacteria, enabling the investigation of the hypothesis that all MPM (including *M. ulcerans*) are derived from a common ancestor. The genome comparisons strongly supported this hypothesis and showed that the niche-adapted genomic signature of *M. ulcerans* caused by reductive evolution was established in the progenitor of all MPM before their intercontinental dispersal. This research also identifies DNA segments that could be used to develop molecular diagnostic tools to distinguish MPM causing BU from other members of the MuMC.

1.3.3 ***Short Read Sequencing, Assembly and Alignment***

High-throughput sequencing has become a key enabling technology for the molecular analysis of an organisms DNA or RNA. This study's primary data sources are the sequence reads derived from whole genome DNA of bacteria, giving a nucleotide level view of their makeup. To understand the quality and nature of the data, a review of sequencing technologies and the downstream processing of sequenced data was undertaken.

1.3.3.1 *Next Generation Sequencing Platforms*

Up until 2005, genome sequencing was mostly carried out using automated Sanger sequencing with capillary electrophoresis [51]. From 2005 onwards, there has been a series of technological advances that have resulted in increasingly faster and cheaper DNA sequencing platforms becoming available. These platforms are collectively referred to as either next generation sequencing (NGS) platforms or second-generation platforms (with Sanger sequencing being first generation) [52]. More generically, the methods are referred to as high-throughput sequencing. NGS platforms are able to generate large volumes of sequencing data relatively cheaply compared to Sanger sequencing. Additionally, the reads are typically short (20-700bp) compared to Sanger platforms, which generate longer reads (800-1,200 bp). More recently, platforms such as Roche's 454 and Pacific Bio are generating reads longer than Sanger sequencing.

The major commercially available NGS platforms are briefly described here. All platforms rely on sequentially adding nucleotides to a template strand of sampled DNA. The platforms vary in how the template is prepared, whether modified or natural nucleotides are added and in the method of detecting which bases are added.

One of the first commercial NGS platforms released was the Roche/454 platform [53] which uses pyrosequencing as its sequencing process and emulsion PCR as its template amplification step. The most widely used NGS platforms are the Illumina GA and HiSeq [54] which use reversible nucleotide terminators as their sequencing process and solid phase bridge PCR as the template amplification step. Life Technologies is a company formed through a number of mergers and it markets both the SOLiD and the Ion Torrent [55] platforms. The SOLiD platform uses sequencing by ligation for its sequencing process and emulsion PCR as its template amplification step. The Ion torrent platform also uses emulsion PCR for template amplification and the semiconductor detection of hydrogen ion release for sequencing detection. The resulting

read data from SOLiD is encoded as a sequence of four colours, each colour representing one of four possible dinucleotides. This encoding gives the SOLiD platform some ability to detect errors by reading the same DNA base multiple times in a run, however, the encoding must be interpreted by downstream processing software and a number of software packages don't support this format. The Helicos BioSciences Heliscope platform uses reversible terminators and requires no template amplification step [56]. Compared with the Illumina platform, the Heliscope has a higher error rate [52]. The Polonator G.007 platform is the cheapest platform and its open architecture allows it to use alternative NGS chemistries [57]. The most recently released platform is the Pacific Biosciences RS platform which requires no amplification step and sequences using a modified polymerase constrained within a detector well [58], and can produce reads as long as 20kb but with very high error rates of 15% and above.

Both the more recent platforms, Ion Torrent and Pacific Biosciences, use semiconductor detection methods rather than the optical detection methods of the earlier NGS platforms. This may allow these platforms to increase scalability and performance with increased chip densities in the future.

All platforms, except for Pacific Biosciences and Helicos, require a template amplification step that introduces biases in the DNA fragments available for sequencing. This step also adds costs (additional reagents) and additional time onto sequencing runs. All NGS platforms produce much shorter reads than Sanger sequencing which makes *de novo* assembly of the whole genome more difficult due to the increased likelihood of the same read being generated from multiple locations in the source genome [59]. Such repetitive regions of the genome cannot be unambiguously joined together to create a contiguous *de novo* assembly. Of the above platforms, the Polonator platform has the shortest reads (26 bases) while the Pacific BioSciences has the longest (964 average bases), however, Pacific BioSciences also has the highest error rates [52]. Short read length can be compensated for, in many applications, by generating short reads from both ends of longer DNA fragments [60]. This technique is called paired end sequencing when the DNA fragment is a 200-500bp section of source DNA. An alternative technique, called mate paired sequencing, constructs a pseudo sequence of circularised fragments of 2-5kb in size from the source DNA. These fragments are then sequenced with the paired end technique to yield two reads that are either 200-500bp apart or 2-5kb apart if they span the junction of the circularised fragments. A greater distance separating a pair of reads allows the sequencing technique and downstream pipelines to better resolve ambiguous features such as a repetitive genomic regions.

The rapid development of NGS platforms is continuing and will result in platforms with longer read length, cheaper cost, lower running expenses and improved error characteristics. Two companies with platforms currently under development are Oxford Nanopore Technologies [61] and GnuBio [62]. GnuBio uses droplet microfluidics developed by Harvard University which reduces the preparation and sequencing time as well as cost of sequencing. The Oxford Nanopore technology GridION platform operates by threading single DNA strands through nano-scale pores and detecting the sequence of nucleotides as they pass. Of all the above

platforms, the Oxford Nanopore has perhaps the greatest potential for producing reads of comparable length to Sanger sequencing [61] and is expected to release a platform in late 2012.

1.3.3.2 De Novo Sequence Assembly

In parallel with the development of NGS platforms, the analysis of the resulting sequencing data has required new bioinformatics techniques and software to be developed. This software has primarily arisen from the research community and has a wide range of quality, applicability and utility. Here, the common *de novo* assemblers are reviewed.

De novo assembly of sequencing data is required when no reference genome exists for a sequenced organism, or to find novel genomic DNA not present in the reference. For example, in bacteria, novel horizontal genome transfers may occur in a strain but are not present in the reference.

The task of reconstructing a genome from millions of short NGS reads is a more complex problem to the one encountered in assembling Sanger sequencing data. The problem is different both quantitatively (many more shorter reads to be merged) and qualitatively (far higher rates of genome misassembly and loss within regions of >85% identity [63]). The problem can be framed as a graph construction problem where the nodes represent the reads (or part thereof) and the edges represent the overlap between the reads [64]. The graph is typically represented as a de Bruijn graph of K-mers extracted from the input reads. Alternative graph strategies create an overlap/layout/consensus graph. In both cases these represent the same information as shown in the paper by Myers [64] where he presents the concept of a ‘string graph’ contracted from overlapping reads.

The common strategy of current *de novo* NGS assemblers is to construct a directed graph from the sequencing reads, apply a series of heuristics to simplify the graph, and then trace a final path through the graph. Heuristics include; pruning short graph spurs, collapsing simple paths to a single node, collapsing graph bubbles based on comparing branch read counts and simplifying the graph based on read pair distances [65]. The effectiveness of these heuristics determines the quality of resulting assembly as measured by various assembly metrics such as evaluated by the GAGE review [66]. The final step of an assembler is to take the reduced graph and traverse it with a path (visiting each edge at least once) and output contigs and scaffolds representing the original genome that produced the reads [60, 67]. Segments of the original genome can be derived from the constructed graph by threading a path through the graph and concatenating the sequence of reads traversed. Graph traversals are not unique and result in multiple possible fragments (contigs) from a single graph. The goal of *de novo* assembly algorithms is to optimise the constructed graph, and its traversal, according to criteria for resolving ambiguities arising from the input data.

As assemblers continue develop and the NGS read characteristics improve, objective assembler benchmarking is required to compare them. A recent evaluation of assemblers was undertaken, on Illumina data from four diverse genomes (*S. aureus*, *R. sphaeroides*, *B. impatiens* and Human chromosome 14), to compare key assembly metrics [66]. This evaluation used publicly available

data from the Short Read Archive [1] and published the algorithm parameters used for each assembler making it possible to better compare other assemblers and new assemblers still under development. The assemblers reviewed were; Abyss [68], ALLPATHS-LG [69], Bambus2 [70], CABOG [71], MSR-CA [72], SGA [73], SOAPdenovo [74] and Velvet [75, 76]. One of the most commonly used metrics of assembly performance is the N50 size of the contigs produced. N50 is the length of the contig such that 50% of the total assembly length is contained in contigs of length N50 or greater. As this metric doesn't reflect the errors that may be within the contigs, the evaluation broke up the assembly contigs at any point containing a mis-join or an indel greater than five bases and recomputed a corrected N50. For each of the genomes assembled, the assembler with the highest corrected N50 size was; *S. aureus* – ALLPATHS-LG, *R. sphaeroides* – ALLPATHS-LG, *B. impatiens* – SOAPdenovo and Human chromosome 14 - CABOG. One of the more serious types of assembly error is where a contig is incorrectly joined to a contig from a distant part of the genome. ALLPATHS-LG and SOAPdenovo had the fewest of these type of errors while Velvet had the most. The overall conclusion of the evaluation was that ALLPATHS-LG represented the best compromise between the size of contigs and the error rate.

All genomes contain repetitive regions that provide technical challenges to assemblers [59]. Sequenced repeat regions longer than the read length will generate identical reads that, to the assembler, appear to come from a single source but in fact come from multiple locations. These repeat regions manifest themselves in assembly graphs as nodes with multiple incoming edges and multiple outgoing edges making graph traversal ambiguous. Assemblers attempt to resolve repeats using paired-end reads that overlap the repeat region. Many of today's assemblers can use paired-end reads to help disambiguate graph traversal, however assembly errors can still occur. Typical errors include; a mis-join of two distant sections of the genome that are adjacent to the same repeat, the collapsed assembly of tandem repeat regions and the creation of isolated contigs that should be joined to other contigs. A conservative assembler will break the assembly at repetitive branch points leading to a more fragmented assembly while a more aggressive assembler may create larger contigs but incorporate more errors. Ultimately, large correct assemblies of repetitive genomes will require longer reads from future sequencing technologies [59] or reverting to the Sanger based PCR and primer walking methods.

1.3.3.3 Short Read Alignment

A major application of NGS sequencing is to look for variation between genomes. Such variations can take a number of forms such as: single base changes (SNPs), small insertions and deletion (indels), the relocation or copying of large DNA segments (large scale polymorphisms) and different number of tandem repeats (copy number variations - CNVs). This can be achieved by the alignment of the reads against a reference sequence using short read alignment software. Some of the current implementations of short read aligners are Bfast [77], Bowtie [78], BWA [79], MAQ [80], Mosaik [81], mrFAST [82], SOAPAligner [83], ZOOM [83] and SHRiMP [84]. These packages have been reviewed here [85, 86]. These programs generally use either spaced seed alignment [80] or suffix tree algorithms [87]. Some aligners such as BWA also use traditional alignment algorithms such as the Smith-Waterman dynamic programming algorithm.

Suffix tree algorithms, in their basic form, only allow for exact alignment but not indels. The alignment of reads allowing for an indel may be handled as a dynamic programming post processing step or with extensions the basic algorithm (SHRiMP) or with a separate alignment program (SOAPindel). The suffix tree algorithms are more memory efficient and can store the index for the human reference genome in less than 2Gb in addition to being faster by a factor of 30 than spaced seed aligners [86], but has the disadvantage of needing to perform a local alignment step to find indels. The 1000 Genomes Project uses multiple aligners (BFAST, BWA, MAQ) to detect variants in the human genome [88].

When aligning a read from a repetitive region, there will be more than one location to which the read can be mapped in the reference. The alignment software can adopt one of four choices for dealing with reads that map to multiple locations [59]. First, the reads can be discarded and only the unique region of the genome will be mapped. Second, only the best match is reported which may not be the correct choice due to variations in the repeats. The third alternative is to report all alignments up to a maximum number. Finally, a match can be randomly selected from closely scoring alignments. The strategy used may lead to incorrect detection of genome variants, in particular, within or near repeat regions.

1.4 Thesis Outline

The remainder of this thesis covers the detail of research methods, results, discussion and conclusions. Section 2 Methods covers the method details of the bioinformatic techniques and processes used in the research. Section 2.1 Bacterial Isolates and Sequencing describes the source and preparation of the research data. The sequence data was then aligned to reference genomes as described in Section 2.2 Read Mapping. Detection of novel, non-reference sequences are covered in Section 2.3 *De novo* Assembly of Short Read Sequences. Further downstream processing of both read mapped data and *de novo* sequences is covered in Sections 2.4, 2.5 and 2.6. The methods used for pseudogene identification are found in Section 2.7. The results section (Section 3) covers the studies key findings comprising; optimising *de novo* sequencing (Section 3.1), the selection of study isolates (Section 3.2) and the implications of the derived phylogenetic tree (Section 3.3). The isolates relationships are further examined within the African clades (Section 3.4) and the implications of their close identity (Section 3.5). The results then cover the genomic architecture of the isolates and the effect of mobile elements (Sections 3.6 and 3.7 respectively). The final results sections examine selective pressure on the genes (Section 3.8) and codon and tRNA usage (Section 3.9). Finally, section 4 discusses the implications of the results and Section 5 covers research conclusions and directions for future work.

2. Methods

Several different bioinformatics methods were used to analyse the sequence data. The workflow developed is summarised in Figure 2 and involved analysis of sequence differences and similarities between all strains. A alignment-to-reference approach was applied together with *de novo* assembly of the sequenced reads. A summary of the isolate data is presented in Table 4, including the number of reads and the *de novo* assembly statistics for each strain.

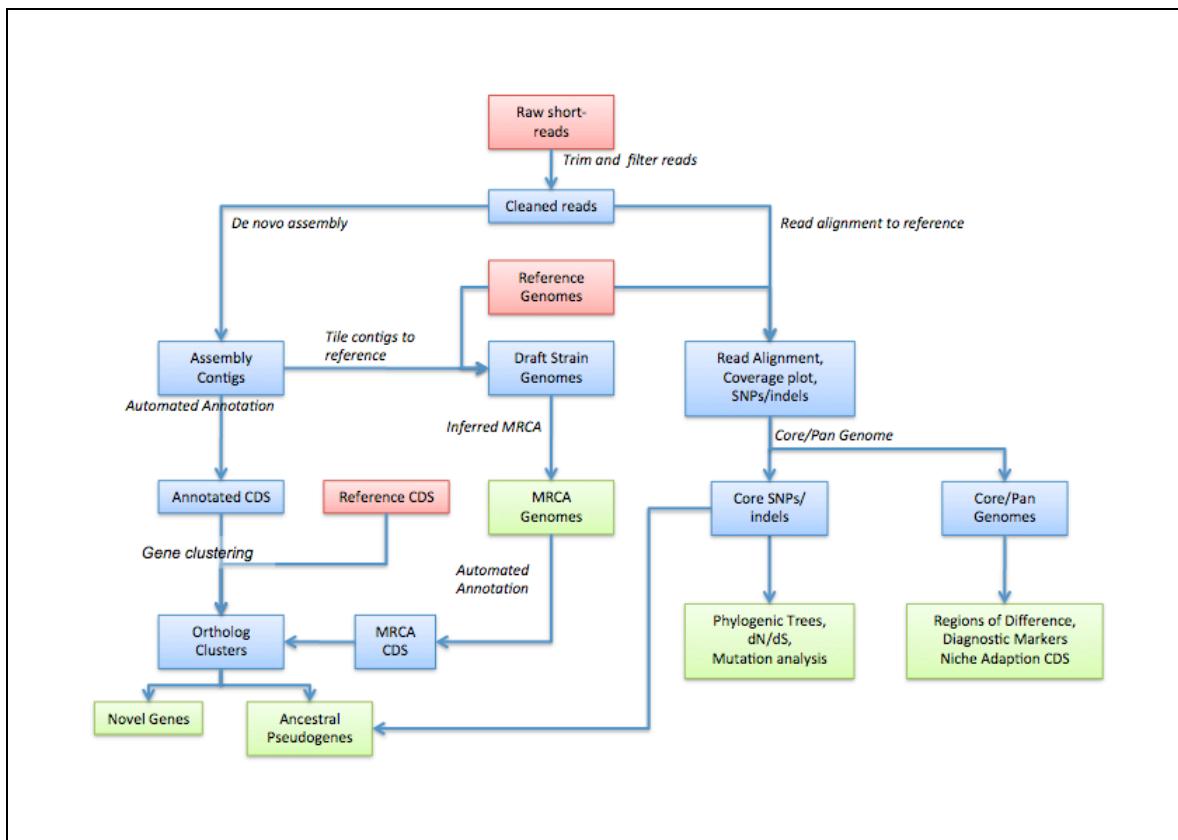


Figure 2 Workflow Schematic

Schematic of the workflow with intermediate stages of the data shown in blue boxes. The inputs to the process are shown in red and comprise the annotated reference genomes and the short read sequencing data of the study isolates. The results are shown in green and include the phylogeny of the complex, novel CDS within each of the isolates, core and accessory genomes of the complex and putative ancestral pseudogenes.

2.1 Bacterial Isolates and Sequencing

The isolates of *M. ulcerans* and *M. marinum* used in this study are described in Table 2. Genomic DNA was prepared from at least 50 mg (wet weight) cell pellets, harvested from mycobacteria that were cultivated on egg-yolk agar media as described in [89].

Genome sequencing of the isolates (except for Mu_DL045) was performed using an Illumina GAIIX DNA sequencer with 36, 76, or 100 cycle paired-end chemistry, generating read lengths of 35-101 nucleotides at a coverage of x16-x240 mean read depth per isolate. Sequencing statistics are provided in Table 4. Mu_DL045 was sequenced using the Ion Torrent platform to generate single-ended reads. Read data for the study isolates (Mu_06-3845, Mu_06-3846, Mu_07-1082, Mu_113, Mu_119, Mu_74, Mu_81, Mu_93, Mu_05142109, Mu_JKD8170, Mu_08009899, Mu_JKD8049) had been previously deposited in the NCBI Sequence Read Archive (SRA) under accession number SRP004497 [1].

Prior to further analysis, reads were filtered to remove those containing ambiguous base calls, any reads <24 nucleotides in length and reads containing only homopolymers. All Illumina reads were trimmed from the 3' end removing bases with a Read Segment Quality Control Indicator "B".

2.2 **Read Mapping**

An Python utility called Nesoni [90], which uses SHRiMP 2 [84] for read alignment, was used to map sequence reads to reference genomes. Nesoni identified SNPs and indels up to ~10bp and predicted the consequences of SNPs and indels on CDS (protein-coding DNA sequence), e.g. frameshifts, premature stop codons and non-synonymous codon changes. Five reference genomes and fragments were used for read mapping (sequence name, Genbank accession number): (*M. ulcerans* Agy99, CP000325), (*M. marinum* strain "M", CP000854), (*pMUM001* plasmid, BX649209), (*pMUM002* plasmid, EU271968) and (*pMUM003* plasmid, EU271967). To facilitate comparison of *M. marinum* and *M. ulcerans* reference genomes using Nesoni, short read data for *M. marinum* "M" was simulated via *in silico* shredding of the reference genome to generate a set of 100bp short reads (read depth x15, insert length 280bp) using a utility function available within Nesoni. Average read depth and the number of SNPs detected by mapping to *M. ulcerans* Agy99 and *M. marinum* "M" are given in Table 4.

The number of reads mapping to unique regions of the plasmids was used to infer plasmid copy number. The ratio of the mode of read depth for the reference plasmid, (*pMUM002* for Mu_06-3844, Mu_CC240299, Mu_JKD8071, Mu_L15, Mu_1G897 and *pMUM001* for all other *M. ulcerans* strains), was compared to the mode of read depth for the chromosome. The mode was used as the statistic of centrality instead of the mean as the distribution of read depths for NGS reads can be skewed by large regions of repeated sequences in the genome.

2.3 **De novo Assembly of Short Read Sequences**

2.3.1 **Analysis of de novo Assembly Parameters**

To assess the effect of assembly parameters on the quality of assembly produced, a number of *de novo* assemblies were run using Velvet (version 0.7.55) [75] with input data of synthetically generated short reads. The reads were generated using the 'simulate' mode of MAQ (version

0.7.1) [80]. This allowed the creation of short read data sets that could be adjusted for read length, average insert size (the outer distance between paired read ends), standard deviation of insert size and error profile of the read bases. The insert size varied for each read pair and followed a Gaussian distribution with a user supplied mean and standard deviation as described in Section 3.1.

Sets of synthetic short reads were generated, with a Perl script written for this study, which took either existing Genbank genomes or random strings from the alphabet of {a,t,c,g}. The script allowed the generated strings to be modified to simulate various cases of genome modification. The string generated could be modified with user specified parameters controlling; the number of repeated segments, proportion of inverted repeats, the length of repeats, the variation in repeat length, whether the repeats were tandem and the length of the generated synthetic genome. This allowed a number of the most common conditions that impact assembly quality to be simulated in a controlled fashion. Synthetic short read data was generated from both Genbank genomes and synthetic genomes to create input data sets for assembly. The synthetic reads were assembled using Velvet and compared to the original genome to assess the impact of various Velvet assembly parameters and simulated read parameters. The results may be found in Section 3.1.

2.3.2 Locating Repeat Regions Within de novo Contigs

The hundreds of copies of the ISs, IS2404 and IS2606, within the *M. ulcerans* isolates was problematic and restricted the ability of Velvet to assemble long contigs. The read size of 36-101 bp plus the size of the paired-end read insert (220-240 bp) was much less than the length of the ISs (1365-1444bp). Alignment of all annotated copies of IS2404 from the reference showed there was considerable variation between the IS copies. This variation, which was also present in IS2606, prevented the assembly of a single contig covering the whole of IS2404 and resulted in a series of fragmented segments that could not be reliably mapped back to the IS. This fragmentation necessitated an alternative strategy to identify location of the ISs flanking of the non-IS contigs.

To identify the IS disrupted contigs, the reads for an isolate were mapped to consensus IS2404 and IS2606 sequences as paired end reads. The unpaired reads (where one read maps onto the IS but the other is unmapped) were *de novo* assembled to find the DNA segments that flank the ISs in the genome. These flanking segments were then aligned back to the original *de novo* assembled contigs. This analysis demonstrated that half, (51% - 11% s.d.), of the contig breakpoints terminated at either IS2404 or IS2606. This process is shown schematically in Figure 3.

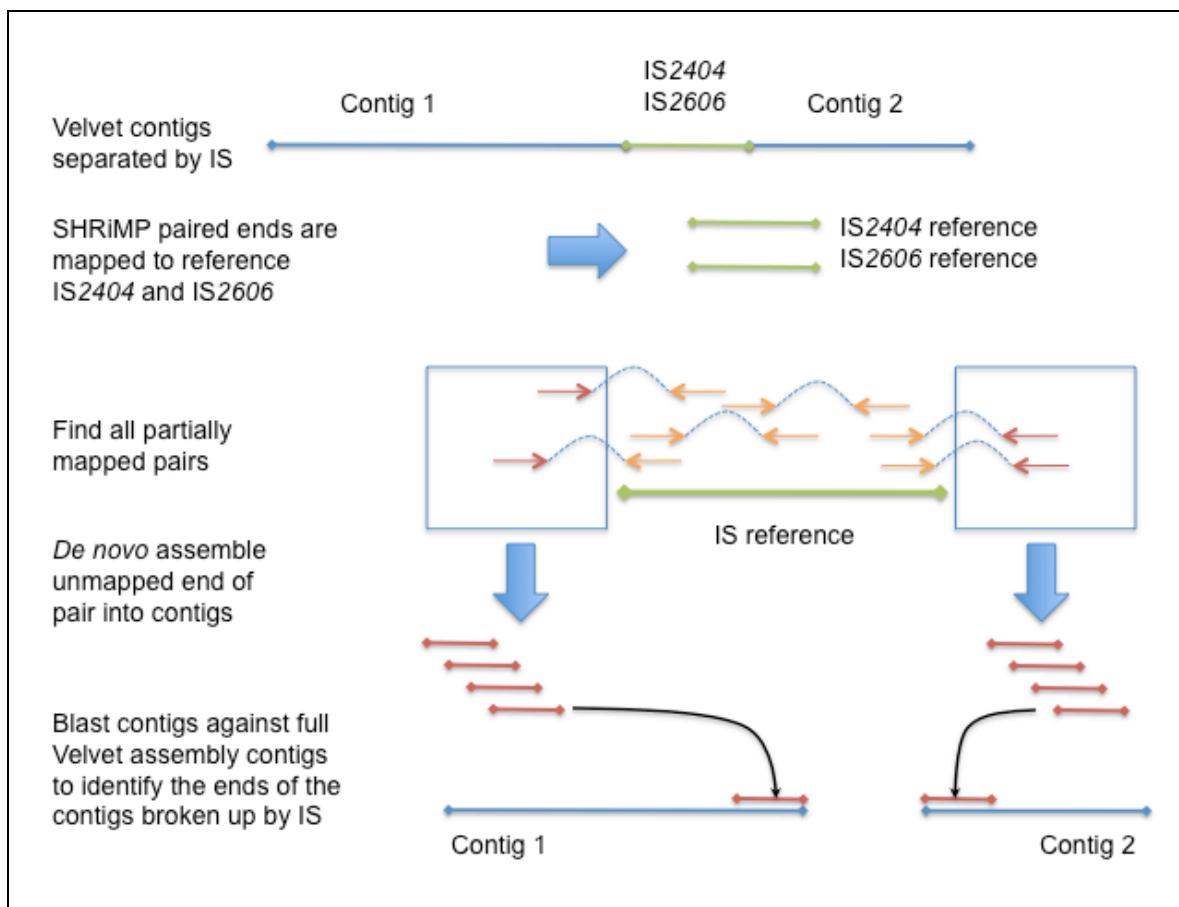


Figure 3 Schematic of IS region identification

A schematic of the method used to identify the de novo assembled contigs abutting an IS2404 or IS2606 insertion sequence.

To identify the orientation of the ISs, both reference ISs were split in half to make four distinct reference sequences (IS2404C, IS2404N, IS2606C and IS2606N). Reads from all isolates were then separately mapped against both ends of the ISs, a total of four mappings per isolate. The unmapped reads of the read pairs were then de novo assembled to provide a set of contigs that could be aligned against the *M. ulcerans* reference genome to locate and orient the position of the ISs within the reference.

2.3.3 De novo Assembly Limitations

The short read data from isolates, were assembled using Velvet [75] with the help of VelvetOptimiser [91] to select appropriate parameter values for k-mer size, expected coverage and coverage cutoff. The Velvet assemblies yielded an average N50 of 18,399 bp; assembly statistics are given in Table 4.

The analysis of repeat regions in the previous section demonstrated that half of the contig breakpoints terminated at either IS2404 or IS2606 in the reference genome. Hence, the IS repeat regions greatly limited the length of *de novo* contigs that could be achieved. Mycobacterial genomes also contain hundreds of PE/PPE genes [92]. The PE and PPE are two highly

polymorphic families that are found in *M. tuberculosis* and may be involved in the evasion of host immune responses. These genes pose problems for sequencing, read mapping and assembly due to their repetitive, high G+C sequences at the 3' end of the gene. In the future, better sequencing platform chemistries will allow these regions to be adequately sequenced. Hence PE/PPE genes were excluded from most downstream analysis including SNP calling and gene content analysis.

After *de novo* assembly of reads, the resulting contigs were annotated using Prokka, an open-source bacterial genome annotation pipeline [<http://vibc bioinformatics.com>] using BioPerl [93], Aragorn [94], RNAmmer [95], Prodigal [96], SignalP [97], BLAST+ [98] and HMMER3 [99].

2.4 Core and Pan Genome Analysis

The core genome was defined as all positions in the reference genomes that were covered by three or more reads in all isolates; this information was derived from coverage plots generated by Nesoni. The set of genomic material conserved in one set of isolates, A, but absent from a second disjoint set of isolates, B, was obtained by taking the core genome of A (all positions conserved among A) and removing any bases present in B. This process is shown schematically in Figure 4 where A is the set of *M. ulcerans* isolates and B is the set of *M. marinum* isolates.

To define the pan genome genes, all CDSs annotated in the reference or *de novo* assembly contigs were subjected to ortholog clustering. CDS were translated to amino acid sequences and clustered using CD-Hit [100] with a 70% amino acid sequence identity threshold. A core set of *M. ulcerans* CDS was defined by identifying all clusters containing a *M. ulcerans* reference CDS and one or more CDS fragments, with a combined length within 15% of the reference sequence, from each *M. ulcerans* sequenced isolate.

To assess the completeness of the set of study isolates, the median number of new genes added to the pan genome for every additional genome was calculated, using 1,000 permutations of the study isolates (*M. ulcerans* and *M. marinum*). A trend was modelled by fitting a power curve to estimate the exponent, indicating whether the pan genome is 'open' or 'closed' [3, 101].

To look for a temporal signal, the tools Path-O-Gen v1.3 (Temporal Signal Investigation Tool) and Beast (<http://beast.bio.ed.ac.uk> - Bayesian analysis) were used. These tools were used to try and identify a molecular clock on the core genome alignment using the year of strain isolation as the time parameter. No statistically significant signal was detected.

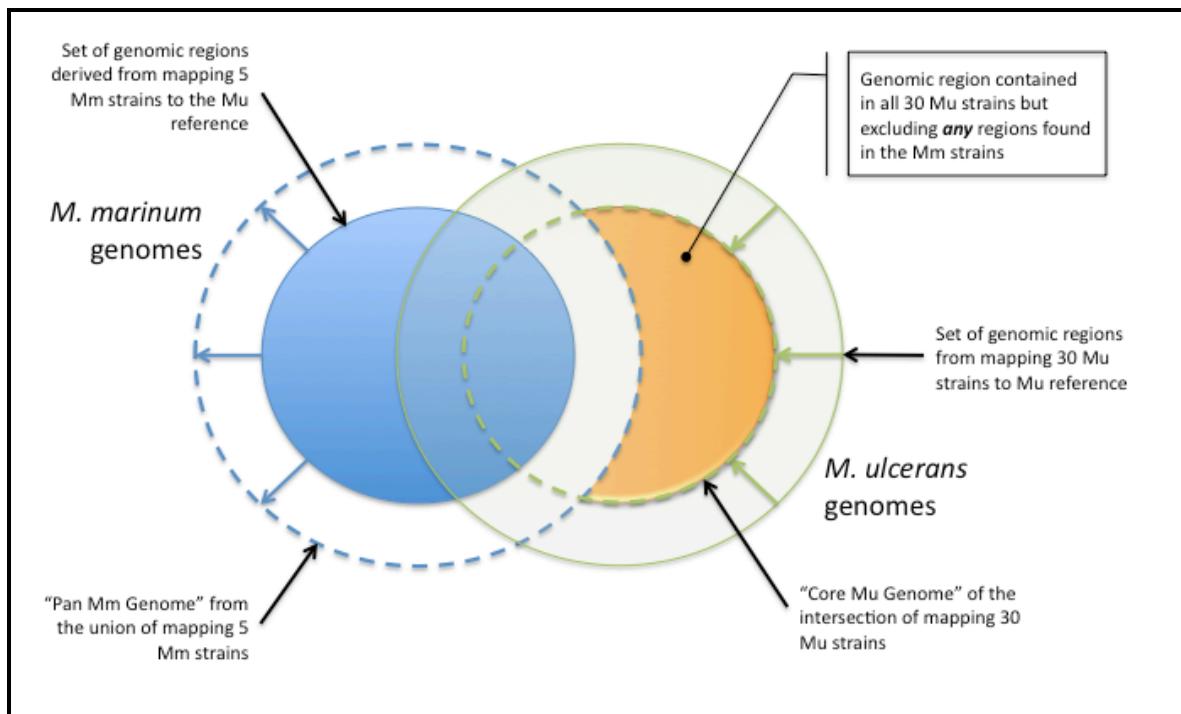


Figure 4 Schematic of Pan-Core genome

*Schematic of the process of finding conserved genomic regions in *M. ulcerans* isolates that are not present in any *M. marinum* isolates (orange segment). The blue region is the core genome of *M. marinum*.*

2.5 SNP Analysis

Variant sites (SNPs and indels) identified using Nesoni with a minimum of six reads required for calling a variant. Nesoni was also used to identify the core genome and variants present in all strains were concatenated to form a multiple alignment. A minimum of three reads per strain were required for a position to be included in the core alignment. A phylogenomic tree was constructed from the multiple alignment using SplitsTree4 (neighbour-joining tree based on uncorrected P distances) [102]. All major bifurcations had >95% bootstrap support based on 1,000 runs. The tree shown in Figure 11 is based on core SNPs identified using *M. marinum* "M" as the reference and present in all strains. SNPs were classified by their position on the annotated references of *M. ulcerans* Agy99 and *M. marinum* "M" and identified as 'intergenic', 'coding' or 'pseudogene'; 'coding' SNPs were further divided into synonymous, non-synonymous or non-sense SNPs. All SNPs called within annotated ISs or PE/PPE genes were excluded from SNP analysis due to the unreliability of read mapping in repetitive regions [23, 32].

2.6 dN/dS Analysis

The relative rates of change at synonymous and non-synonymous sites (dN/dS) within protein coding regions was calculated using the BioPerl [93] module Bio::Align::DNAStatistics and the PyCogent toolkit [103]. The dN/dS analysis was performed for both individual CDS (using

BioPerl and PyCogent) and for aggregate concatenated CDS (using PyCogent). To test for selection across multiple isolates using multiple CDS, analysis was restricted to an alignment of DNA sequences from all CDS that were present, without a premature stop codon, in all isolates (2,379 CDS). This alignment, together with an unweighted neighbour-joining tree of the isolates, was provided as input to PyCogent modules that calculated the dN/dS values across subsets of the isolates. The CNF (conditional nucleotide frequency) codon substitution model [104] was used for all analyses as it overcomes biases in other models that result from naturally occurring sequence compositions. A representative set of study isolates was used: *M. marinum*: Mm_1726, Mm_99/84, Mm_99/87, Mm_99/89; *M. ulcerans* lineage 1: Mu_CC40299, Mu_JKD8071, Mu_DL045, Mu_1G897; *M. ulcerans* lineage 2: Mu_8765; *M. ulcerans* lineage 3: Mu_05142109, Mu_Agy99. This alignment, together with the corresponding subset of the tree and a codon substitution model, was used to create a likelihood function (LF) which models selection using the PyCogent framework [103]. By specifying how the dN/dS parameter values of the model vary, optimisation of the LF can estimate dN/dS across the whole tree, a sub branch of isolates or individual isolates. The dN/dS metric cannot identify CDS that contained only non-synonymous SNPs but have no synonymous SNPs. As an alternative method of identifying CDS with an overabundance of non-synonymous SNPs, the average difference between the number of non-synonymous and synonymous SNPs normalised for the length of CDS was calculated. Functional groups used to classify CDS were defined by the reference genome annotations and based on COG v2.0 / CDD groupings [105].

2.7 Pseudogene Identification

In order to identify the pseudogenes in the *M. ulcerans* MRCA, the CDS SNP changes that were common in all *M. ulcerans* isolates but not present in any *M. marinum* isolates, were examined. All PE/PPE, ISs and *M. marinum* pseudogenes were excluded from this analysis. The remaining *M. marinum* CDSs were examined to determine whether the SNPs called by read mapping the *M. ulcerans* isolates onto *M. marinum* resulted in a change to the CDS that would be likely to render it inactive within the *M. ulcerans* isolates; namely (i) indels that result in frame-shifts, (ii) premature stop codons truncating encoded protein, (iii) a change to the start codon, (iv) an IS insertion or (v) a deletion of whole or part of the CDS.

3. Results

3.1 Short Read de novo Assembly Optimisation

De novo assembly of short read sequencing data attempts to reconstruct a genome without reference to an existing genome. This allows novel DNA transcripts to be constructed for which a reference may not exist. This approach is needed for comparative genomics even if a reference exists as a sequenced isolate may have acquired DNA that is different from the reference.

Prior to using actual sequenced data, a number of experiments were run using simulated reads generated from both the *M. ulcerans* Agy99 reference as well as random strings of simulated DNA (see Section 2.3.1). This allowed the controlled verification of assembly parameters where the results of *de novo* assembly were known.

The short read length of NGS can be compensated for in many applications by generating short reads from either end of longer DNA fragments [60]. This technique is called paired end sequencing or mate paired sequencing. When used with deep sequencing coverage of a genome, it allows the assembler to join contigs into longer segments and assemble the genome around repeat regions shorter than the length of the read pairs plus the insert segment length that separates the reads. In other words, a repeat region in a genome of x bp, will not break up the *de novo* assembly if read pair sequencing is used with a read segment length (length of two reads plus insert length) greater than x bp. This was demonstrated with a synthetic genome containing a single 200 bp repeat which was used to generate a short read datasets with 36 bp reads and an insert size varying from 170 bp to 230 bp. Once the insert length exceeded 200 bp, the assembly created two contigs, one for the full length of the synthetic genome and one for repeat region. See Figure 5.

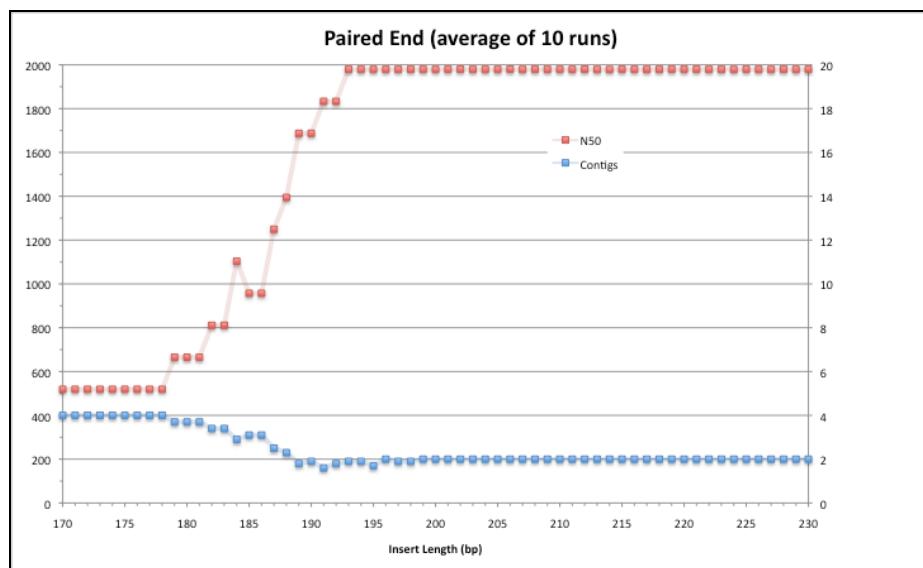


Figure 5 Paired-end Assembly Simulation

Assembly statistics (N50 - red line (lhs scale), number of contigs - blue line (rhs scale)) with simulated reads and varying insert length. A simulated genome of 2,000 bp containing a 200 bp repeat region is fully resolved if the insert length is greater than the repeat length (200bp). The data is the average of 10 runs. Assembly parameters: read length 36 bp, kmer 21, coverage 100x, insert length s.d. = (insert length)/10.

Short read sequencing introduces errors in the reads that impact the ability of assemblers to correctly reconstruct genomes. To assess the impact of read errors, a 100,000 bp random sequence (of As,Ts,Gs and Cs) was created. Synthetic reads were then created from this sequence with a range of error rates from 0.0 to 0.1. Here, an error rate of 0.1 is equivalent to one base in every 10 being mutated from the reference sequence. The average assembly N50 value was then plotted against read coverage values from 10x to 150x. An average N50 over 50 assemblies was taken to smooth the statistical variation. See Figure 6. The results suggest that for typical Illumina sequencing error rates of between 1% and 0.1%, (error=0.01 and 0.001), there was no improvement in N50 for a coverage greater than around 50x.

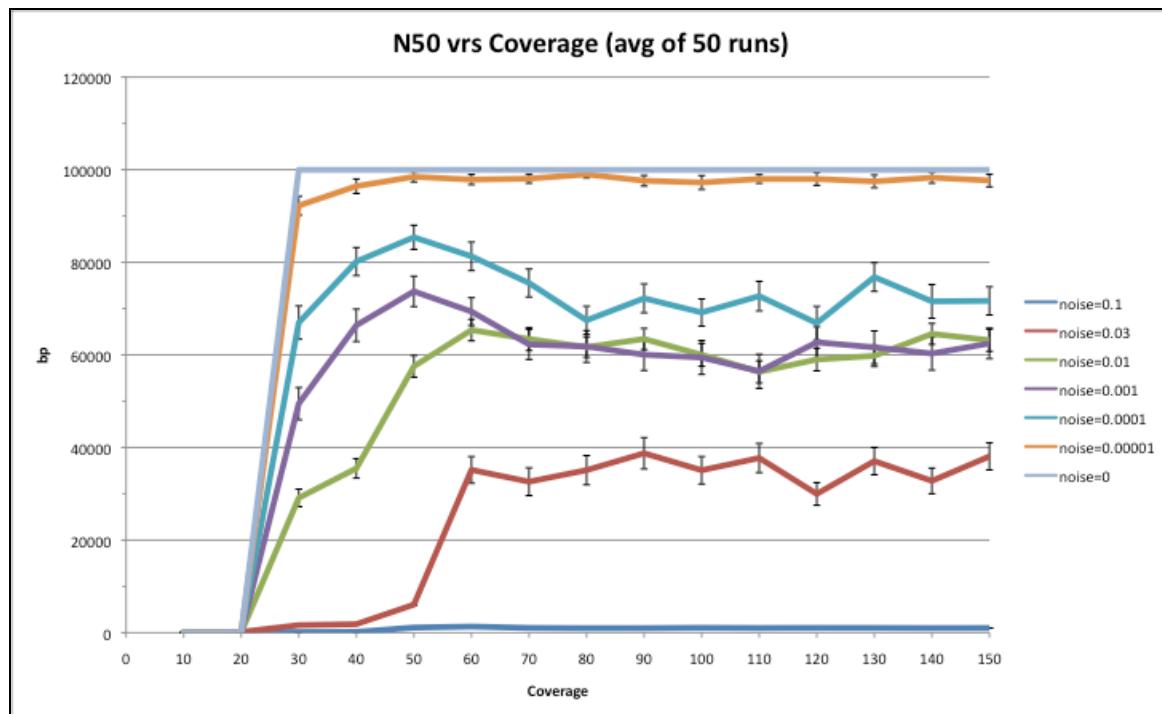


Figure 6 Read Coverage Assembly Simulation

Assembly N50 statistics with simulated reads against genome coverage and varying error rates. A simulated genome of 100,000 bp was used to generate simulated single ended reads with error rates from 0 to 0.1. An error rate of 0.1 is equivalent to one base in ten being mutated from the reference sequence. The data is the average of 50 runs. Assembly parameters: read length 50 bp, kmer 31, insert length 240 bp, insert length s.d.= 20.

To evaluate the effect of larger insert lengths on assembly quality, a large number of simulated paired-end read sets were generated by varying the insert length, (distance between read pairs), from 300 bp to 4,500 bp. The reads were generated from the *M. ulcerans* Agy99 reference genome with a coverage of 60x. The read sets were then assembled with Velvet (assembly parameters: read length 50 bp, kmer 31, insert length s.d.= (insert length)/10). The resulting assembly metrics are shown in Figure 7 and demonstrate the large improvement in assembly contiguity as insert length increases. There is a significant improvement in assembly quality when the average insert size of the simulated reads exceeds the length of the repeated IS2404 (1,368 bp)/IS2606 (1,438 bp) sequences. An even greater improvement can be seen when the average insert size exceeds the length the sum of the two ISs (~ 2,800 bp). This is due to the frequent occurrence of IS2404 appearing adjacent to IS2606 in the Agy99 genome. When the insert size exceeds the length of IS2606 abutting an IS2404, the assembler is able to join the contigs on either sides of the pair and create a more contiguous assembly.

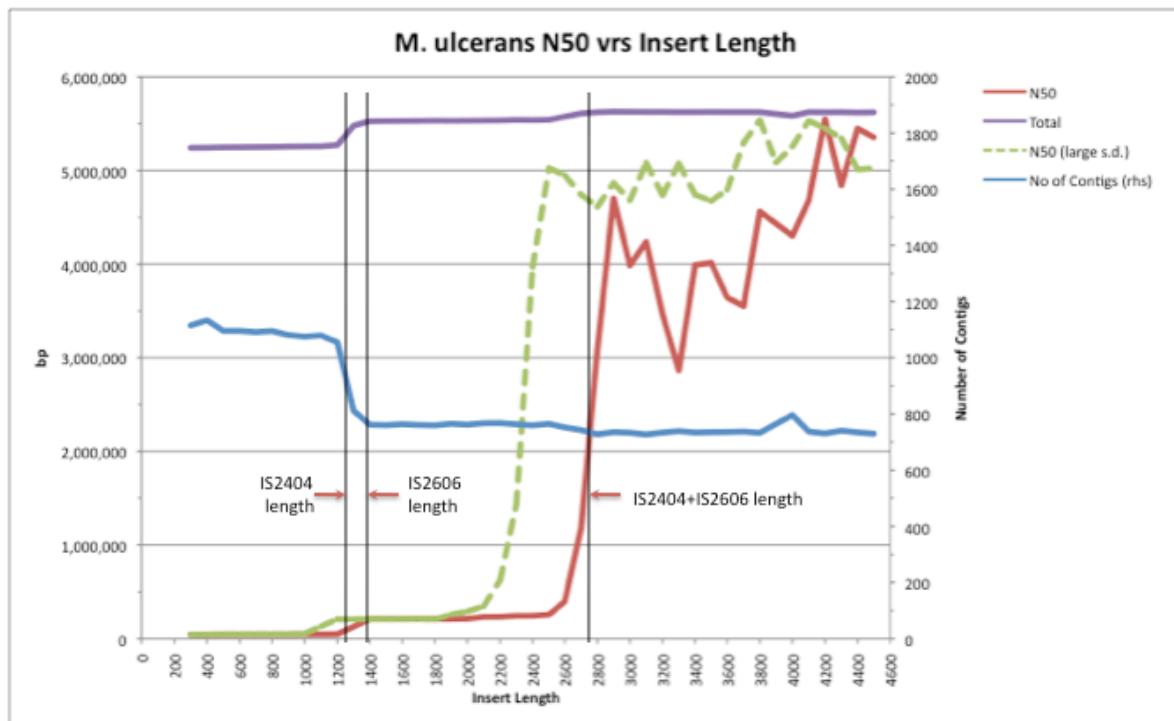


Figure 7 *De novo* assembly parameters for *M. ulcerans* Agy99

Variation of Velvet assembly metrics against the average paired read insert size. The assembly metrics shown are; total length of contigs (purple), N50 (red) and number of contigs (blue (rhs axis)) for the assembly of *M. ulcerans* Agy99 from simulated reads. The default standard deviation for the insert length is 1/10 of the insert length. Also shown is the N50 (green) of an assembly where a more variable insert length was simulated by the reads and the standard deviation was one third of the insert length.

3.2 Isolate Selection and Sequence Analysis Strategy

In order to capture as much diversity as possible within the MuMC and minimise phylogenetic discovery bias [106], 35 mycobacteria isolates were selected from diverse members of the MuMC for whole genome sequencing. These isolates were recovered from a range of host organisms including humans, possums, fish, frogs, an insect and an armadillo and include representatives of all the major MuMC sequence types defined by MLST [107]. The majority of isolates belong to the two dominant human pathogenic clades of MPM, namely *M. ulcerans* from Africa and Australia, however MPMs that have been given various species names such as *M. marinum*, *M. pseudoshottsii* and *M. liflandii* were also represented. One genome was sequenced using Ion Torrent technology (single ended sequencing) and the remainder using Illumina GAIIX paired-end sequencing (Table 2 and Table 4). For each isolate, genes were identified and annotated within *de novo* assembled contigs and then subjected to ortholog clustering by homology searches. Reads and contigs were aligned to both the *M. marinum* "M" and *M. ulcerans* Agy99 reference chromosomes (Figure 8) and the *M. ulcerans* Agy99 pMUM001 plasmid (Figure 9).

To assess how well the collection of isolates represents the genetic diversity of the MuMC, modelling of the pan genome was performed. The number of novel genes discovered with the addition of each new genome using a *de novo* assembly and an ortholog clustering approach was used (see Section 2.4). The trend was assessed by fitting a power curve to estimate the exponent, which is indicative of whether the pan genome is ‘open’ or ‘closed’ ($y=519.8 x^{-0.712}$, $R^2 = 0.997$) [3, 101]. The MuMC isolates indicated an open pan genome (exponent > -1), meaning that the total number of genes would continue to increase if more isolates were included (Figure 10). Based on the model, it was predicted that further sequencing within the MuMC would, on average, reveal fewer than 42 new coding sequences (CDS) per additional isolate. The core set of conserved orthologous clusters of CDS for the study isolates was found to be 3,305 CDS and modelling predicted that additional sequencing would result in no further reduction in core genome size. The pan genome of all CDS within MuMC is 11,073 CDS highlighting the fact that individual isolates contain less than a third of the total genes within the complex. This is a common feature of bacterial pathogens (see Section 1.3.1).

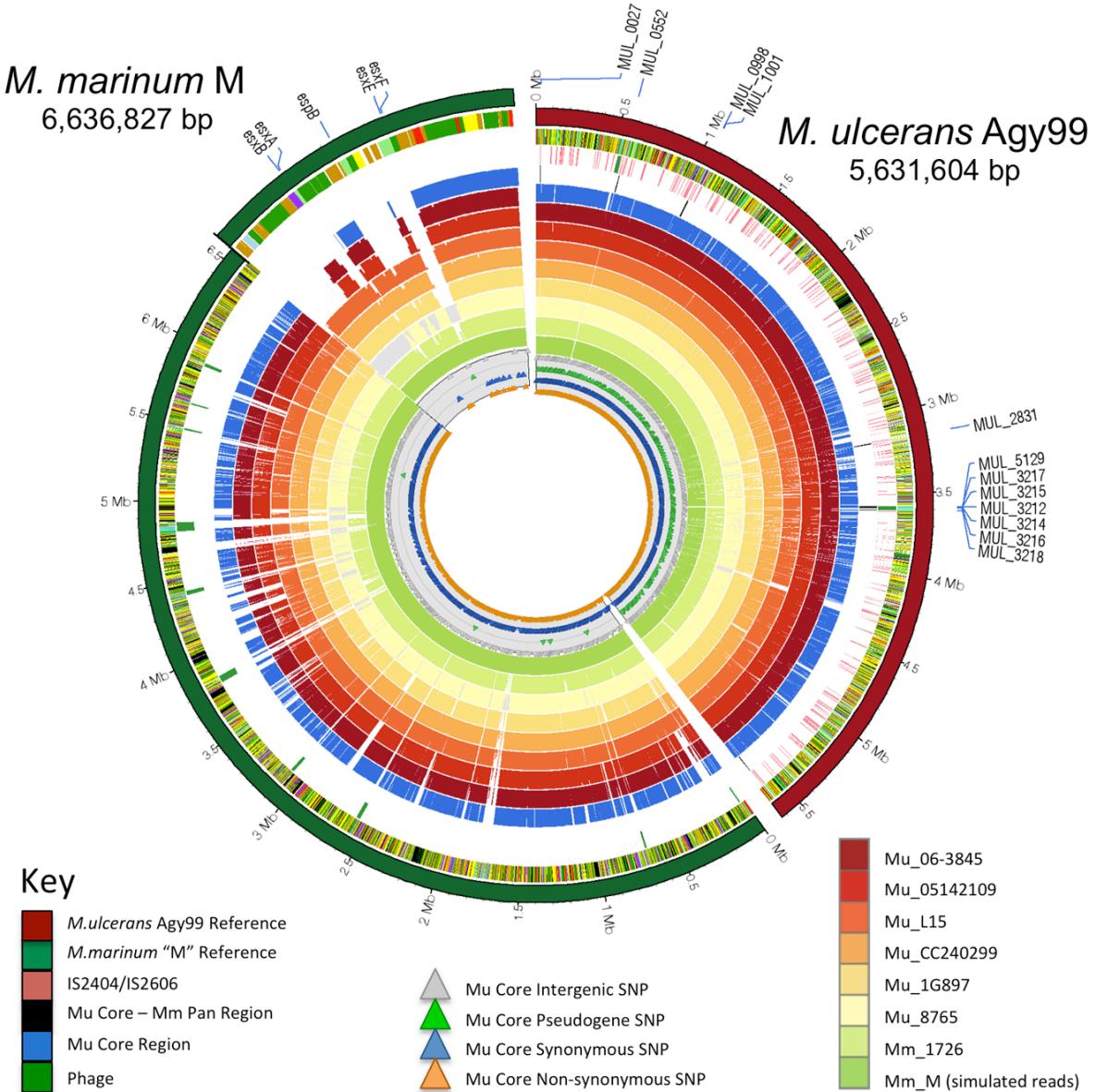


Figure 8 Comparative genome content of isolates to references *M. marinum* and *M. ulcerans*

Circos [108] plot of *de novo* assembled contigs, for a representative sample of the study isolates, mapped against the reference genomes of *M. marinum* "M" (dark green) and *M. ulcerans* Agy99 (dark red). The key below the figure describes the content. Moving inwards, the tracks are genes coloured by functional group (lipid metabolism – black, insertion seqs – aqua, others – green). The next track marks insertion sequences in pink. The remaining tracks show selected isolates and their coverage when *de novo* contigs are mapped against the reference. The isolates moving inwards are: Mu_06-3845 (Benin), Mu_05142109 (Australia), Mu_L15 (USA), Mu_CC240299 (Israel), Mu_1G897 (French Guiana), Mu_8765 (Japan), Mm_1726 (USA) and *M. marinum* "M". The SNPs present in the *M. ulcerans* core genome are marked by type with coloured triangles in the innermost rings. The 12 loci overlapping the core *M. ulcerans* – pan *M. marinum* regions are shown with the outer most labels MUL_nnnn. The *M. marinum* region spanning the

Esx-1 locus is scaled up x30 to highlight how it has been successively affected by deletion and is no longer part of the core *M. ulcerans* genome (blue circle).

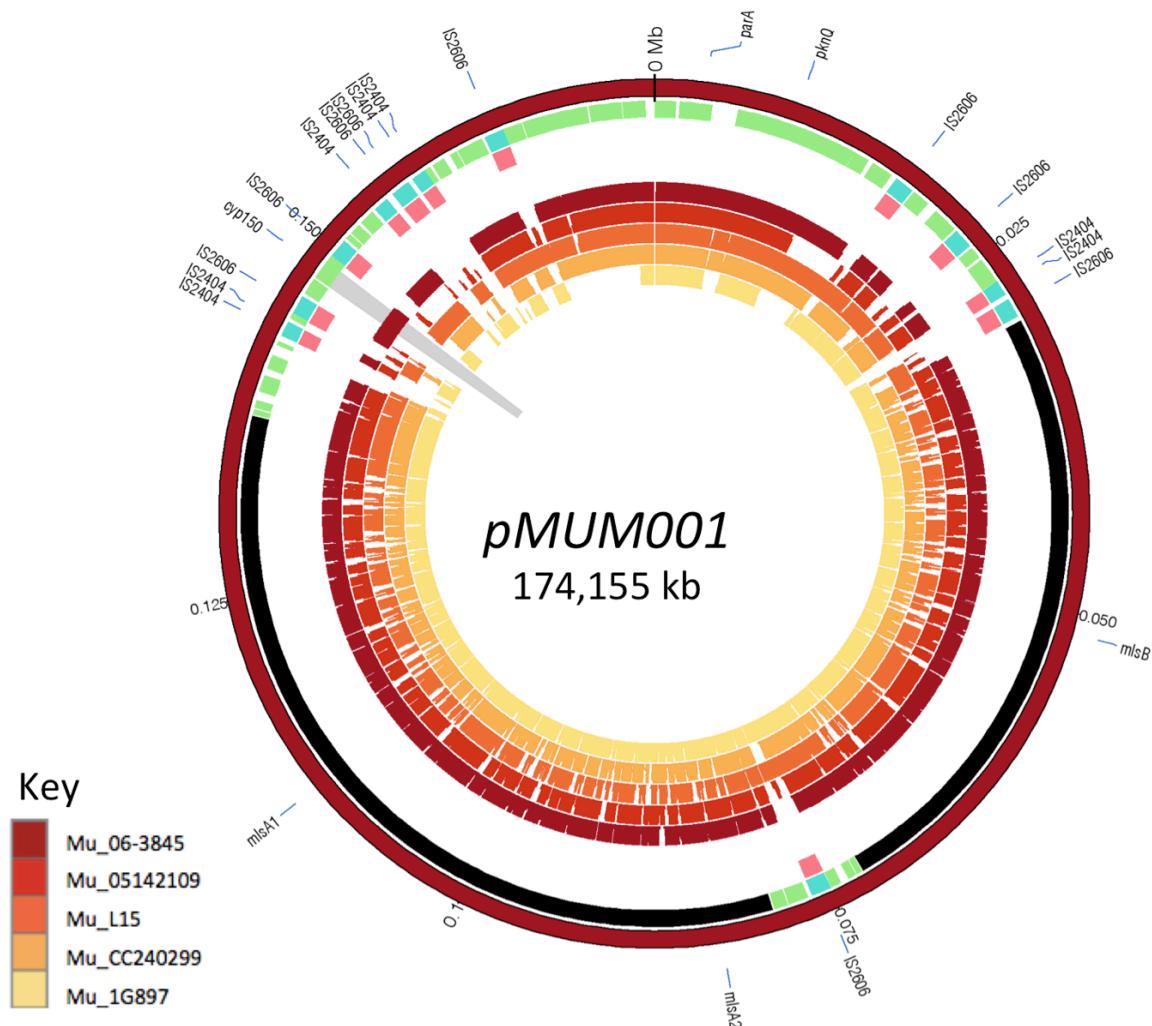


Figure 9 Comparative genome content of plasmid pMUM001

Circos [108] plot of *de novo* assembled contigs, for a sample of the study isolates, mapped against reference chromosome plasmid pMUM001. ISs and known genes are labelled in the outermost ring. Moving inwards, the tracks are genes coloured by functional group (lipid metabolism – black, insertion seqs – aqua, others – green). The next track marks insertion sequences in pink. The remaining tracks show selected isolates and their coverage when *de novo* contigs are mapped against the reference. The isolates moving inwards are: Mu_06-3845 (Benin), Mu_05142109 (Australia), Mu_L15 (USA), Mu_CC240299 (Israel), Mu_1G897 (French Guiana). The cyp150 gene (mup053) has been highlighted (grey wedge) to show its presence only in the African isolates and absence in other isolates.

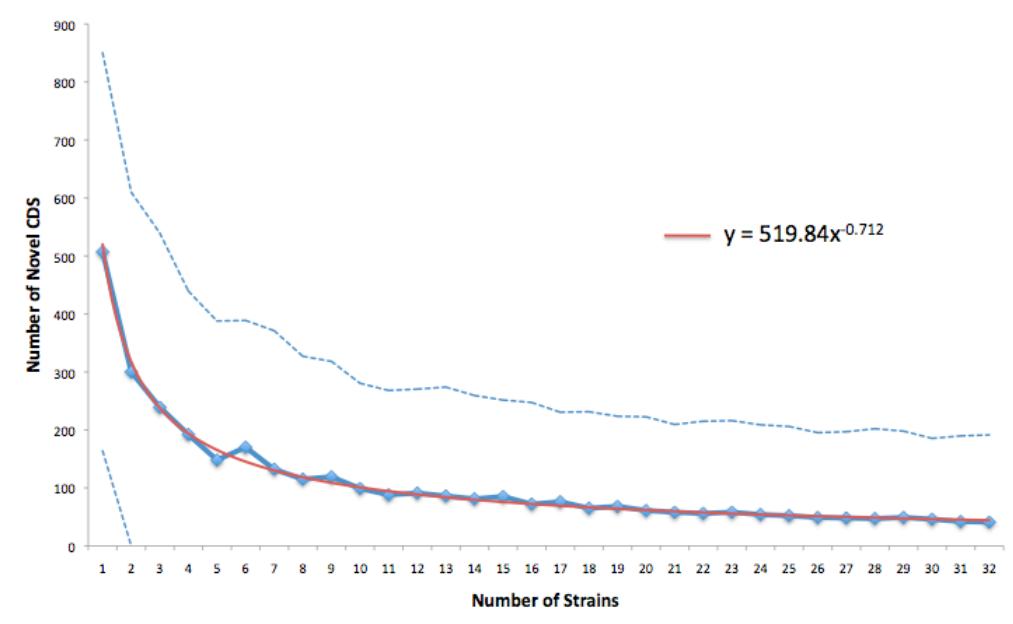


Figure 10 Open genome analysis

Median number of novel genes added per isolate (solid blue line) and the fitted power law model (solid red line, equation inset). The median is for 1,000 random orderings of 32 of the study isolates. The dashed blue lines shows the +/- 1 standard deviation from the median.

3.3 *Mycolactone-producing Mycobacteria Form a Monophyletic Group*

The most sensitive method to identify a core set of conserved nucleotide positions among a set of genomes is by mapping reads to a reference genome. The major advantages of this approach, compared to *de novo* assembly and ortholog clustering, is its independence from gene annotation and orthology and high (single nucleotide) resolution. Hence sequencing reads were mapped from each isolate to the *M. marinum* "M" reference and defined the MuMC core genome as the set of *M. marinum* "M" nucleotide positions that were covered by at least three reads from every isolate. Repeat regions and regions spanning PE/PPE genes were excluded from this analysis due to ambiguous read mapping and poor coverage, respectively. A core of 4,362,138 bp (65.7%) was found and 3,318 CDS of *M. marinum* "M" were present in all 35 mycobacteria of the complex.

Within this core genome, 128,463 variable nucleotide positions were identified among the sequenced MuMC genomes. These were randomly distributed around the chromosome (see Figure 8) and were used to infer a distance-based neighbour joining phylogenetic tree (see Figure 11). The tree topology confirms the relationships previously inferred between isolates by

the lower-resolution MLST approach [107] and indicates that all mycolactone producing isolates (i.e. the MPM) belong to a single clonal group that diverged from a common *M. marinum* progenitor (Figure 11, root of red tree). In keeping with this observation, the MPM were relatively homogeneous with 0.06% median genome nucleotide divergence (interquartile range 0-0.37%) compared with *M. marinum* isolates with 0.86% nucleotide divergence (0.59%-0.87%) (Figure 11). Within the MPM, at least three deep branching lineages were observed comprising, Lineage 1: one human isolate from South America and globally distributed fish and frog isolates; Lineage 2: a single *M. ulcerans* human isolate from Japan; and Lineage 3: *M. ulcerans* human and other animal isolates from Africa and Australia. Lineage 3 corresponds to the previously reported “classical” MPM lineage, while the “ancestral” MPM lineage is refined here by Lineages 1 and 2 [45]. The confirmation of a close genetic relationship between BU-causing MPM isolates from Africa and Australia (4,511 SNP differences) suggests that findings from studies of BU transmission in Australia may find corollaries in African BU endemic settings. Interestingly, there were even fewer nucleotide differences between some of the Lineage 1 isolates. For example, *M. pseudoshottsii* and Mu_DL045, isolated two years apart from fish in the USA and Greece respectively, were separated by only 590 SNPs. Similarly, Mu_CC240299 and Mu_06-3844, isolated seven years and thousands of kilometres apart in Belgium and Israel, were separated by only 40 SNPs. These data indicate that clones of these mycolactone-producing ectotherm-infecting mycobacteria are circulating worldwide.

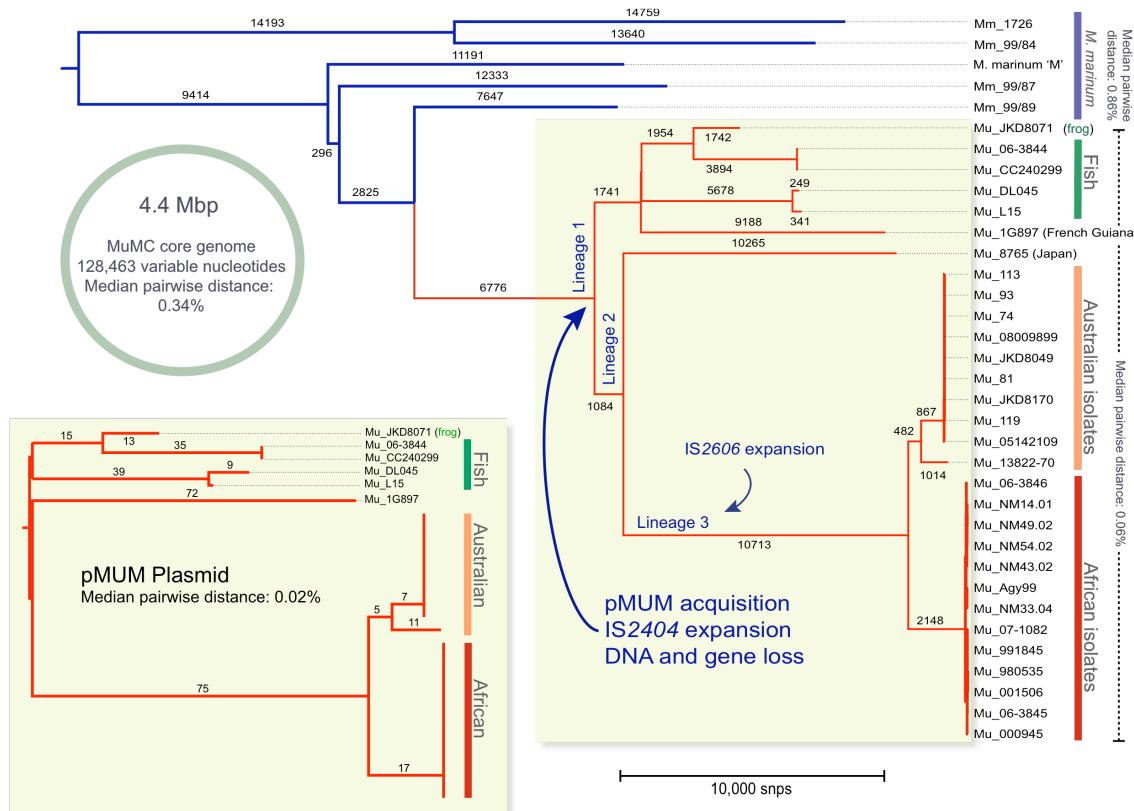


Figure 11 MuMC phylogenomic analysis

Neighbour joining dendrogram based on 128,463 variable nucleotide positions common across 35 sequenced isolates produced by SplitsTree4 [109] using uncorrected 'P' distances. The tree was rooted using *M. tuberculosis* as an outgroup. The major clustering of isolates are *M. marinum* isolates (4) – blue; Fish and frog isolates (5) – green; Japanese isolate (1) – Mu_8765; French Guiana isolate – Mu_1G897; Australian isolates (10) – orange; African isolates (13) – red. The scale bars show the median pairwise divergence for the set of isolates they span. The isolates that produce mycolactone are highlighted with a pale yellow background. The inset shows the pMUM plasmid SNP tree of 315 SNPs with edge lengths and a topology matching the corresponding isolates in the main tree. The details of the isolates can be found in Table 2.

The same approach was used to construct a phylogenetic tree for the mycolactone plasmid pMUM001. No pMUM001 sequences were detected among the four *M. marinum* isolates or *M. ulcerans* isolate Mu_8765 (Lineage 2), indicating that the plasmid was absent from these isolates. Mu_8765 has previously been reported to have lost its plasmid during laboratory passage [50]. All other MPM isolates carried the plasmid, confirming the central role of pMUM001 in the evolution of this complex. A total of 315 pMUM001 SNPs were identified among the MPM isolates, permitting construction of a distance-based phylogenetic tree for the plasmid (Figure 11, inset). The plasmid phylogenetic tree closely matches both the topology and

relative branch lengths of the core chromosome tree, consistent with co-evolution of the plasmid and chromosome in each lineage [107]. By comparing read depths for plasmid and chromosome (see Section 2.2), it was estimated that the average pMUM copy number was 1.8 copies per bacteria (range 1.3 for Mu_CC240299 to 3.1 for Mu_JKD8071).

3.4 ***Geographical Restriction of *M. ulcerans* Over Short Time Scales***

Through the core genome SNP comparisons it was possible to compare isolates within localised geographic regions. Using the same read-mapping approach as described above, a 5,190,533 bp core genome was defined together with a phylogeny for the subset of 13 isolates from Benin and Ghana (Figure 12 African isolates tree and map). Only 396 variable nucleotide positions were identified, with an average pairwise distance of 160 SNPs differentiating isolates between Ghana and Benin. However, Mu_06-3846 isolated in the Couffo valley in Benin, clustered with the isolates from Ghana. The other six isolates from Benin originated from the Zou/Ouémé valley. A previous study has demonstrated a genetic difference between *M. ulcerans* from these two river basins [110]. An explanation for the apparent clustering of the Couffo strain (Mu_06-3846) with the Ghanaian strains could be obtained by sequencing more isolates from the Couffo valley, from Togo (*i.e.* the area between the Couffo valley in Benin and Ghana) and Ghana. The population structure revealed in Figure 12 indicates localized clonal expansion in Ghana and Benin, suggesting that most BU infections in these areas result from local transmission of a single circulating clone, with only occasional transfer of clones between geographic areas. The environmental isolate *M. ulcerans* Mu_06-3845, obtained from an aquatic insect in Benin, clustered with the BU Zou/Ouémé Benin isolates but is distinct from a human isolate obtained from the same region at the same time (Mu_001506). Among this limited set of isolates from the Zou/Ouémé valley in Benin, no finer-scale geographical clustering was observed. This is consistent with a previous study of isolates from an area of comparable size in Ghana [111].

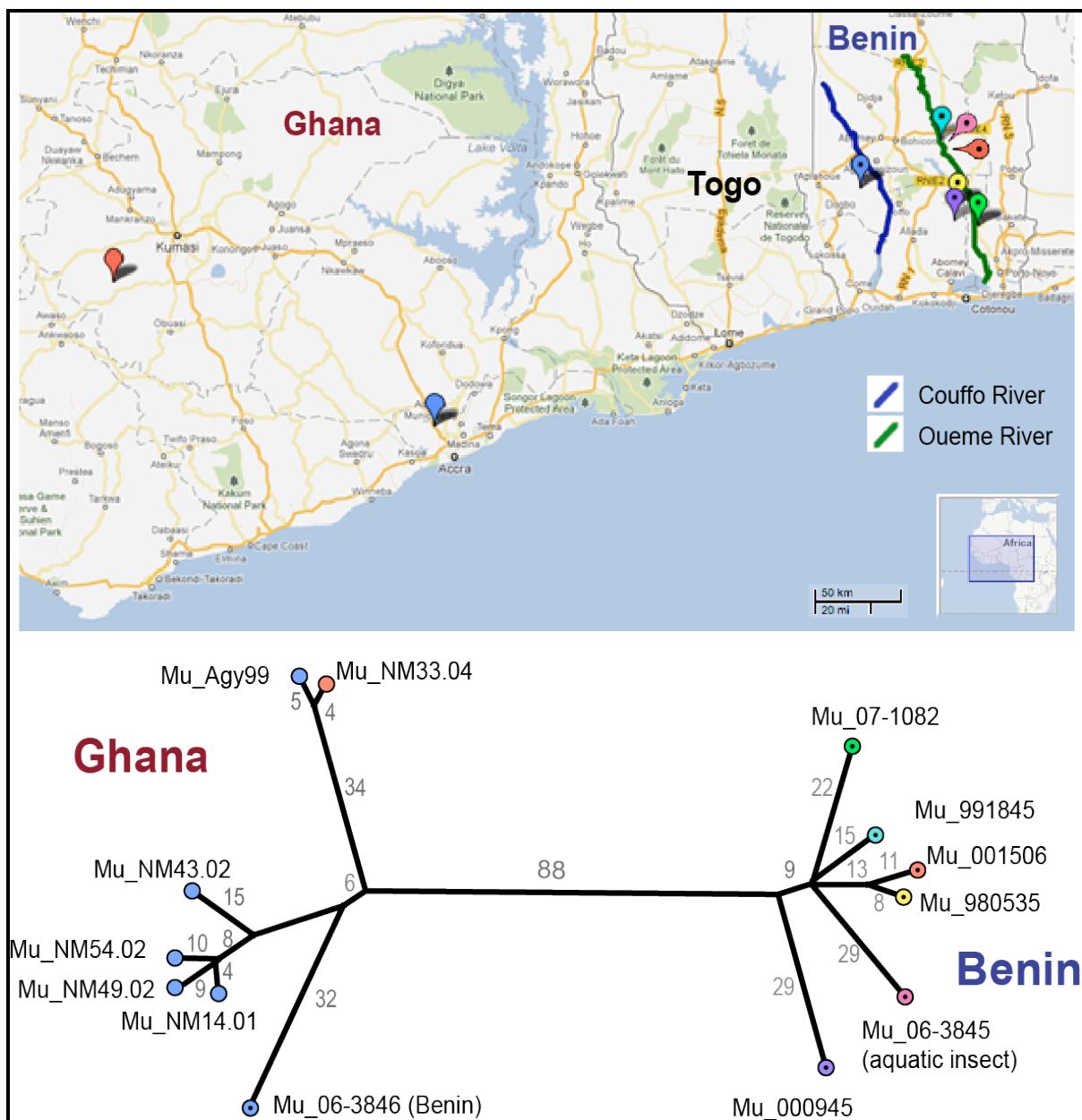


Figure 12 African isolates tree and map

Unrooted neighbour joining tree produced by SplitsTree4 [109] using uncorrected ‘P’ distances and based on 396 variable common nucleotide positions from a core of 5,190,553 bp among the 13 isolates from Ghana and Benin. The map shows their geographic distribution with pin colours corresponding to the tree nodes. The isolate Mu_06-3846 is from Benin but clusters with the Ghanian isolates (see text). Map produced using Google Maps.

3.5 Mycolactone-producing Mycobacteria Should Be Considered a Single Species – *M. ulcerans*

A pairwise DNA re-association value greater than 70% is a common criterion for assigning a bacterium to a particular species. This corresponds to approximately 95% genome-wide average nucleotide identity (ANI) [112]. A genome-wide ANI of 97% among all genome pairs was calculated for the study isolates, which might suggest the entire complex, including *M. marinum* and *M. ulcerans*, should be considered a single species. However, *M. ulcerans* is clearly differentiated from other *M. marinum* by genomic and phenotypic features. To compare the ANI with genomic deletions, the proportion of *M. marinum* and *M. ulcerans* reference genome sequence covered by each isolate of the MuMC (Figure 13) was calculated. The plot shows that MPM isolates are clearly differentiated from *M. marinum* by their gene content, with less than 90% of genomic sequence conserved between MPM and *M. marinum* isolates. In contrast to other pathogens such as *Shigella*, which has four main variants that have emerged independently [21] (see Section 1.3.1.4), it appears that MPM have evolved only once through the acquisition of the virulence plasmid pMUM and IS expansion. Hence the data confirm both high genomic coherence and a common ancestry among all the MPM, supporting the previous argument that all MPM should be considered *M. ulcerans* [48]. Hereafter all MPM are referred to as *M. ulcerans*.

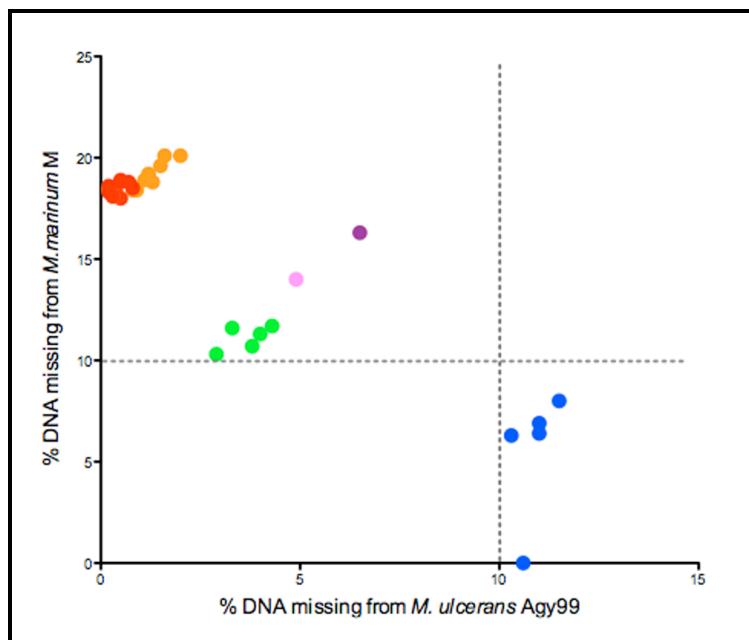


Figure 13 Percentage DNA difference between isolates

Scatter Plot showing the percentages of DNA missing from references M. marinum "M" (y-axis) and M. ulcerans Agy99 and pMUM001 plasmid (x-axis). The percent missing is calculated by taking the number of zero coverage positions in the short read mapping to reference and dividing by total length of the reference. The dotted lines show the percentage missing from either reference to distinguish the M. marinum isolates from the MPM isolates. The clusterings

are coloured as follows with the number in each cluster in brackets; *M. marinum* isolates (5) – blue, Fish and frog isolates (5) – green, Japanese isolate (1) – pink, French Guiana isolates – purple, Australian isolates (10) – gold, African Isolates (13) – red.

To estimate divergence dates for particular lineages of the MuMC, the potential temporal signal in the sequence data was investigated (see methods Section 2.4). However, while the phylogenetic inferences were highly robust (100% bootstrap values for major branches of the tree, Figure 11) no linear correlation between branch length and year of isolation was observed. It is suspected that there is variation in the effective number of generations per year across the complex, perhaps related to different niches, reservoirs or modes of living. Such variation has recently been observed in *M. tuberculosis* [113]. The lack of a temporal signal in these data raises doubts around previous estimates of divergence time that have assumed a constant molecular clock rate among the lineages of the complex [50, 114].

3.6 Genomic Features of *M. ulcerans*

M. ulcerans isolates have specific characteristics such as the ability to produce mycolactones and the expression of Hsp18, an immunodominant small heat shock protein that appears to play a role in biofilm formation [89]. It was sought to identify the set of genomic features, including mutations and differences in gene content, that may explain phenotypic differences between *M. ulcerans* and *M. marinum* and provide potential diagnostic markers for the strains of *M. ulcerans*.

The ancestral SNPs that differentiate the most recent common ancestor (MRCA) of *M. ulcerans* from the rest of *M. marinum* were investigated. These may have played a role in evolution of the distinctive phenotypic characteristics of *M. ulcerans*. Using *M. marinum* “M” as a reference, 4,170 such SNPs (including small indels) were identified, spanning the entire chromosome and comprising 607 intergenic, 2,254 synonymous, 1,301 non-synonymous and eight SNPs occurring within pseudogenes (Figure 8, Table 8). For example, in *M. ulcerans* the ‘C’ nucleotide in *M. marinum* “M” position 3,616,191 has been substituted with the dinucleotide ‘AT’. This intergenic insertion occurs within a promoter region and leads to de-repression of *hsp18* through down-regulation of its specific repressor *hspR_2* [89], contributing to the expression of Hsp18 that is recognised as a characteristic phenotype of *M. ulcerans*. This list of mutations will be important for research exploring the functional characteristics that distinguish *M. ulcerans* from other mycobacteria. The identification of these SNPs is also the foundation for evaluation of evolutionary forces acting on specific genes (see Section 3.8).

The loss of UV-protecting pigment genes from *M. marinum* has been shown in a previous study [33] and has suggested that the new niche of *M. ulcerans* is protected from sunlight and so doesn’t require the production of light-inducible carotenoids generated at the *crtB* locus. Inspection of the locus in all study isolates shows that the *crtI* gene is disabled by a premature STOP codon in all the African and Australian isolates but not in the other isolates suggesting that only lineage 3 requires a dark protected niche.

Chromosomal regions that were conserved within *M. ulcerans* but absent from *M. marinum* were investigated. A total of 11 DNA segments of up to 2,688 bp in length were identified, overlapping 15 CDS (total 10,256 bp) (Figure 14A). The locations of these CDS on the *M. ulcerans* chromosome are shown in Figure 8 and their annotations are described in Table 5. These *M. ulcerans*-specific chromosomal genes include: seven genes from prophage phiMU02, a phage-like polymerase (MUL_0027), a putative lipase (MUL_2832) and six hypothetical proteins. Hence other than the pMUM plasmid, ISs and phiMU02 as already described, *M. ulcerans* isolates have few other species-specific DNA elements and is instead characterised by gene loss. However, the eight identified *M. ulcerans*-specific genes may be important for the ecology of *M. ulcerans* and warrant further investigation. Also investigated were differences in gene content between *M. ulcerans* isolated from different geographic locations or from different hosts (Figure 14B and C, Table 9). The core genome of *M. ulcerans* isolates known to infect humans comprised a strict subset of the core genome of fish and frog isolates. Nine CDS were found that were only in the fish/frog isolates and may be assumed to be superfluous for *M. ulcerans* infections in humans, although care needs to be exercised as there were only five fish and frog isolates on which to base this assumption. The products of the nine CDS include five hypothetical proteins, three putative hydrogenases and a putative oxononanoate synthase (BioF2_5). A total of 76 CDS were conserved in *M. ulcerans* lineages 1 and 2 but absent from lineage 3 (which contains only African and Australian BU isolates) (Figure 14C). These data suggest that the African and Australian BU isolates, which represent the majority of the global burden of BU infection in humans, have undergone further reductive evolution. This may be associated with additional adaptation to a more specialised niche, or genetic drift associated with passing through an evolutionary bottleneck. The 76 genes lost (Table 9) include some involved in metabolic and respiratory processes, which may be no longer required in the more restricted environment occupied by lineage 3 isolates [115]. Also investigated were novel *M. ulcerans* genes not present in the reference genome (Agy99, an African BU isolate from Lineage 3) via annotation and comparison of de novo assemblies of the novel isolates. The African and Australian isolates, also from Lineage 3, had no novel CDS apart from a putative integrase in six of the ten Australian isolates. The remaining *M. ulcerans* isolates from other lineages had many more novel CDS as follows; Mu_JKD8071 (128), Mu_06-3844 (93), Mu_CC240299 (93), Mu_L15 (13), Mu_1G897 (8), Mu_8765 (3). The numbers of novel CDS largely reflects the isolates' similarity to the reference genomes as shown in Figure 13.

Figure 14 also shows the largest segments of DNA that could be used to discriminate between isolates by species, host and region (genomic locations are listed in Table 9). For example, to discriminate between a *M. ulcerans* and a *M. marinum* isolate, there is a 2,688 bp segment that is present in all *M. ulcerans* isolates and absent from all other *M. marinum* isolates. Together with previously described deletions, these DNA segments could provide the basis of a set of DNA diagnostic tests to identify the species, host or region of an unknown isolate.

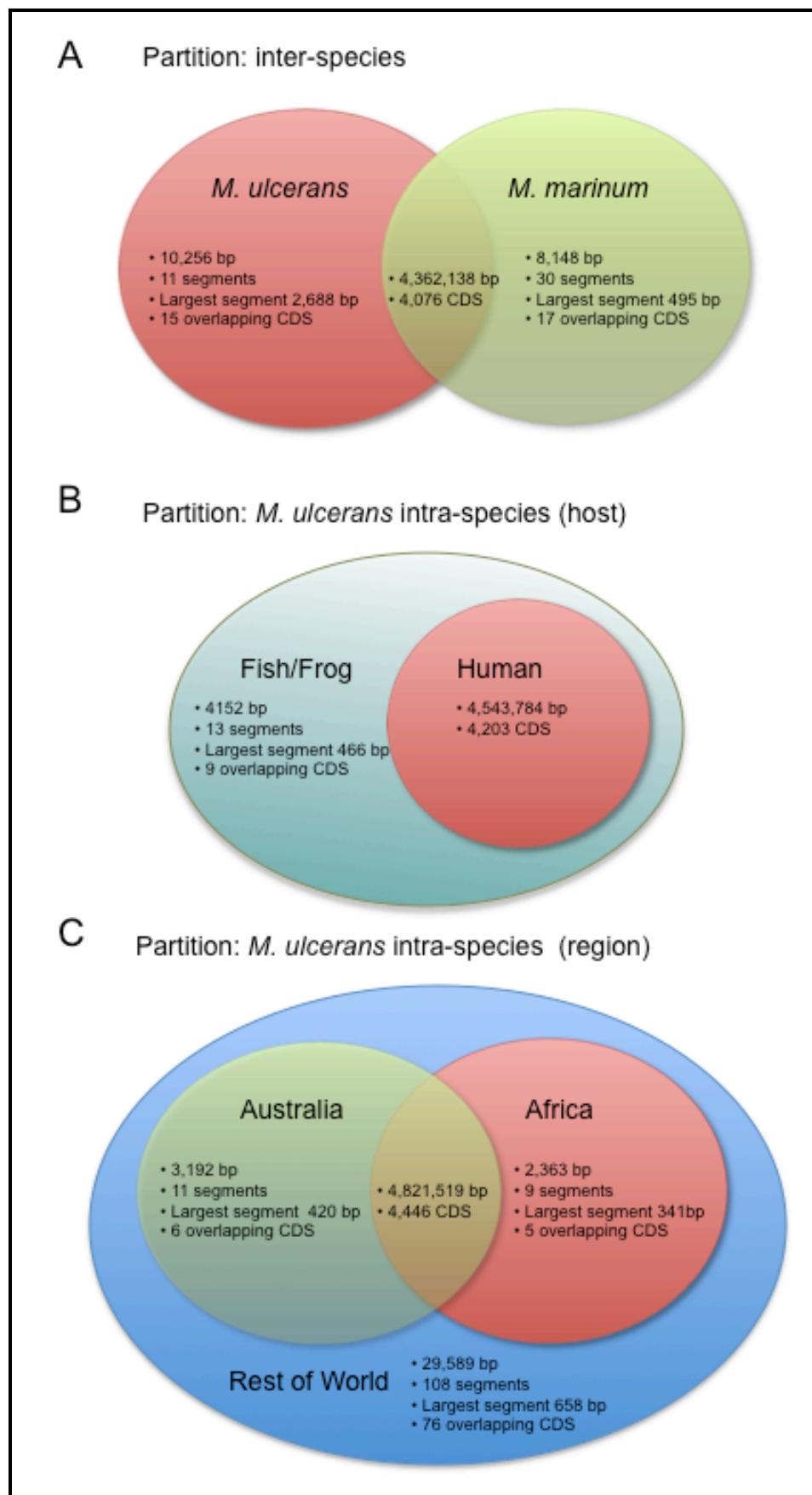


Figure 14 Percentage Venn diagrams, showing DNA shared and unique among isolates

Venn diagrams showing the unique genomic material in the isolates when partitioned by species, host and region. All regions were identified by finding the core genome of the isolates within the set and removing the pan genome of all isolates excluded from the set. The unique material for each partition is shown as total size in base pairs, number of segments in partition with a minimum size of 200bp, the length of the largest segment and the number of CDS with an overlap of >10%. The intersection of the sets was determined by finding the core genome of the union of the sets of isolates and shows the size of the core and the number of CDS with an overlap of >10%. (A) Shows the partition between all 30 *M. ulcerans* isolates and four *M. marinum* isolates. (B) Shows the partition between the four *M. ulcerans* fish and frog host isolates and the *M. ulcerans* human host isolates. The human host isolates are a strict subset of the fish and frog isolates with no unique DNA. (C) Shows the partitioning between the 10 Australian and 13 African *M. ulcerans* isolates and their separation from the isolates from the rest of the world (6 isolates). The combined African and Australian isolates have no unique DNA when compared to the rest of the world isolates.

The *M. ulcerans* Agy99 reference contains the second highest percentage (13.8%) of pseudogenes within a diverse set of 64 prokaryotic genomes [116]. *M. leprae* has the highest percentage (36.5%) and represents an extreme case of genome reduction combined with loss of function. The pseudogenes present within the MRCA of the *M. ulcerans* isolates provide insights into the loss of function that may have been instrumental in the adaptation of *M. ulcerans* from the more generalist *M. marinum*. MRCA pseudogenes were inferred by assuming the inactivation of *M. marinum* CDS (intact in all *M. marinum* strains) via mutations in the *M. ulcerans* isolates affecting start codons, creating frame-shifts or introducing premature stop codons. This analysis resulted in a list of 185 putative ancestral pseudogenes and/or deletions that were identified in all *M. ulcerans* isolates, of which 83 were absent in Agy99 due to gene deletion (Table 10). Hence at least 25% of the pseudogenes present in *M. ulcerans* Agy99 - or lost from this isolate by deletion - are shared by all extant *M. ulcerans* isolates and indicates that significant remodelling and adaptation through reductive evolution was occurring in the *M. ulcerans* MRCA before the global radiation of the species. The number of inferred pseudogenes and deleted genes per isolate is shown in Figure 15 and shows that lineage 3 strains have all lost substantially more coding potential than lineage 1 strains. An examination of the distribution of these ancestral pseudogenes by functional group shows that CDS belonging to one specific group, "cell wall and cell wall processes", are significantly overrepresented (35%, compared with ~22% for all CDS in *M. marinum* "M" and *M. ulcerans* Agy99). Table 3 summarizes some of the key CDS losses that may have played a role in the early adaptive responses of *M. ulcerans* following the acquisition of pMUM and a pathway of reductive evolution. It includes the loss of CDS required for synthesis of selenocysteine-containing proteins, anaerobic respiration, stress responses, intracellular survival, acylation of lipoproteins and biosynthesis of isoprenoids.

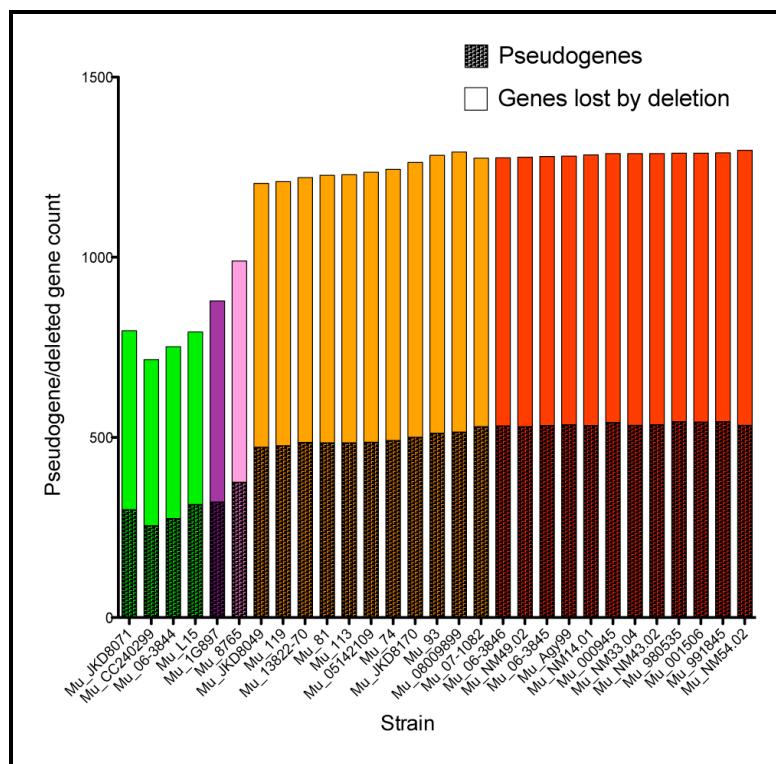


Figure 15 Inferred pseudogenes and deleted genes

Counts of inferred pseudogenes and deleted genes among the study isolates. The counts were inferred by analysis of SNPs that would render *M. marinum* reference CDS inactive and read coverage mapping showing partially or fully deleted CDS. The isolates are coloured by groups; African isolates – red, Australian isolates – gold, French Guiana isolate – purple, Japanese isolate – pink, fish and frog isolates – green.

3.7 Impact of IS2404 and IS2606 on M. ulcerans Genome Architecture

A key differentiator between *M. marinum* and *M. ulcerans* is the presence of multiple copies of IS2404 and IS2606 in *M. ulcerans* that has led to genome plasticity and remodelling. The copy number of these IS in each isolate was estimated and confirmed that neither IS was present in any of the *M. marinum* isolates, as reported previously [33]. It was found that *M. ulcerans* genomes from Lineages 1 and 2 had only 1-4 copies of IS2606, while a massive expansion has occurred in Lineage 3 resulting in 63-98 copies per genome (Figure 16). Conversely, a large number (41-81) of novel IS2404 insertions in Lineage 1 and 2 isolates (relative to the Agy99 reference) were identified, but only a single novel IS2404 insertion in 9 out of the 23 Lineage 3 isolates. These data confirm that ISs are continuing to modify the *M. ulcerans* genome. The sequence data of lineage 1 isolates Mu_CC240299 and Mu_06-3844 each contain a single copy of IS2606 that could be located only within the pMUM plasmid (see methods Section 2.3.2) and no copies were found within the chromosome. As well as containing IS2404, the pMUM plasmid contains between one and eight copies of IS2606 and is therefore the likely original source of both IS2404 and IS2606 in *M. ulcerans* chromosomes.

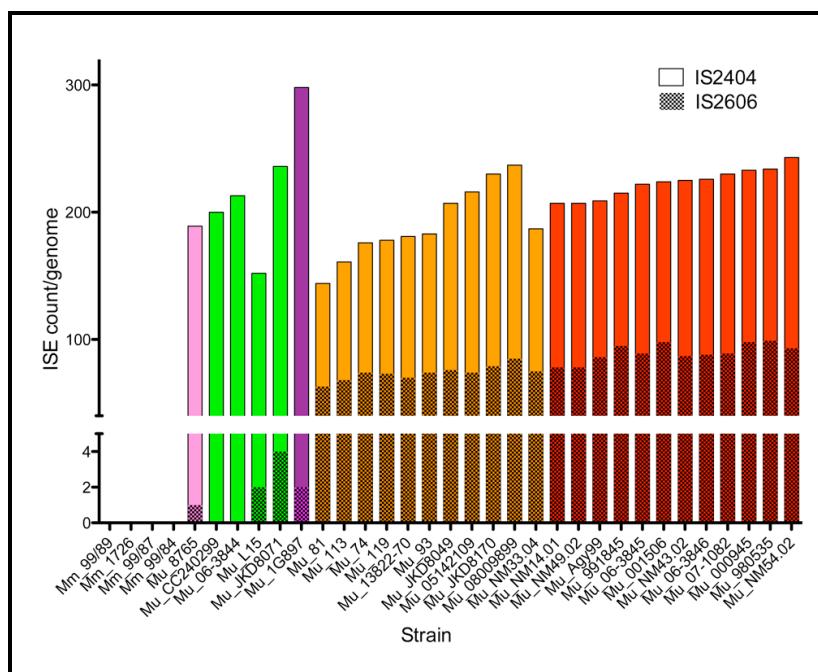


Figure 16 IS2404 and IS2606 distribution among isolates

Counts of IS2404 and IS2606 among the study isolates. The counts were inferred from coverage of reads mapping to each IS. The isolates are coloured by groups; African isolates – red, Australian isolates – gold, French Guiana isolate – purple, Japanese isolate – pink, fish and frog isolates – green. IS2404 and IS2606 were not detected in the non-MPM *M. marinum* isolates.

3.8 M. ulcerans Genes Under Selective Pressure

Identification of CDS that are under selective pressure can give insights into the specific nature of the environment(s) an organism encounters. The ratio dN/dS is the number of non-synonymous substitutions per non-synonymous site (dN) to the number of synonymous substitutions per synonymous site (dS); hence dN/dS>1 implies diversifying selection, while dN/dS<1 implies purifying selection through loss of mutations that cause changes at the protein level. To compare selection in the *M. marinum* isolates against the *M. ulcerans* isolates, two likelihood function (LF) models were generated that compared a constant dN/dS across all isolates against a model where dN/dS differed across the tree. The dN/dS value across a core set of 2,379 CDS for the full tree was 0.181 (constant model) while the values for the differing sub-branches (varying model) were 0.093 for *M. marinum* isolates, 0.484 for African Lineage 3 *M. ulcerans* isolates, 0.515 for Australian Lineage 3 *M. ulcerans* isolates and 0.459 for *M. ulcerans* lineages 1-2. This is consistent with relaxation of purifying selection in *M. ulcerans* compared to *M. marinum* (log likelihood ratio statistic = 8988.6, degrees of freedom=63, $p < 1e-6$), however the younger age of *M. ulcerans* could also explain this result [117]. This dN/dS variation was consistent across all annotated functional groups: (*M. ulcerans* isolates dN/dS, *M. marinum* isolates dN/dS) conserved hypotheticals (0.538, 0.191), cell wall and cell processes (0.524, 0.165), lipid metabolism (0.484, 0.160), regulatory proteins (0.470, 0.160), intermediate

metabolism (0.469, 0.148), information pathways (0.402, 0.128). Next, dN/dS at the level of individual CDS was compared. The model parameter start values were taken from the LF and the tree previously used to compare regions using the full set of CDS. This improved the ability of the new LF to be optimised more rapidly and reliably. Of the 2,379 CDS examined, 172 CDS had a dN/dS > 1 for the *M. ulcerans* isolates (Table 6). This set was dominated by two functional groups, ‘cell wall and cell processes’ (44 CDS) and ‘conserved hypotheticals’ (56 CDS). Notable CDS in this set of genes under diversifying selection included *esxE* and *esxF* that encode WXG100 domains and are orthologs of the secreted T-cell antigens EsxA and EsxB. The stress response sigma factor *sigM* was also identified as under diversifying selection, perhaps indicating remodelling of the SigM regulon in *M. ulcerans* [16] (Figure 8). In *M. tuberculosis*, *sigM* appears to positively regulate *esxE* and *esxF* expression while negatively regulating certain non-ribosomal peptide synthetases and polyketide synthase genes involved in biosynthesis of cell wall lipids [118, 119]. Lipoproteins, another class of cell wall-associated molecule, also featured among the genes displaying evidence of diversifying selection (*lppN*, *lppD*, *lprA*) and perhaps links to the predicted loss of Lgt activity and the ability to acylate prolipoproteins (Table 3).

To capture additional CDS not covered by the above method, CDS were examined that contained only non-synonymous SNPs, preventing calculation of a dN/dS ratio, or were not core to *M. ulcerans*. A list was compiled of CDS with an overabundance of non-synonymous SNPs, sorted by the difference between non-synonymous and synonymous SNPs normalised for gene length (see Section 2.5). The 50 most variable proteins mirrored the dominant functional groupings of the high dN/dS analysis (Table 6), including *esxE/F* as well as enoyl-CoA hydratase *echA4_2* and *ssp*. *Ssp* (signal peptide protease IV) is a serine protease required for digestion of cleaved signal peptides, indicating that *M. ulcerans* may be under pressure to modify its secretome. Also of interest is *mymT*, encoding a copper-binding protein, a cytoplasmic metallothionein which in *M. tuberculosis*, sequesters excess copper in the bacterial cell [120].

The close relationship between *M. tuberculosis* and the MuMC suggested the investigation of whether the orthologous human T cell epitopes for *M. tuberculosis* were conserved in *M. ulcerans*. The genes encoding antigens in human pathogens tend to be under diversifying selection in order to evade host immunity and it has been suggested that this is not the case with *M. tuberculosis* [121]. It was found that there were 20 MuMC orthologs (>80% AA identity) of the 86 human T-cell antigens in *M. tuberculosis* H37Rv (Table 7). These orthologs all had very low dN/dS ratios (*M. marinum* isolates median 0.05, range 0.15, *M. ulcerans* isolates median 0.17, range 0.95) suggesting that these CDS are also under purifying selection in the MuMC as they are in *M. tuberculosis*.

3.9 Codon Bias and tRNA Usage

Both the reference genomes of *M. ulcerans* and *M. marinum* were analysed for the presence of tRNA genes and the usage of their corresponding codons using Aragorn [94]. A significant

variation of tRNA and codon usage between the genomes may indicate a change in rate at which codons are translated and changes in expression levels. No such variation was found in codon usage with the percentage variation between *M. ulcerans* and *M. marinum* being 0.00%, s.d. 0.09% (See Figure 17). This indicates that the translation of codons has been unaffected, at least over the timeframes of *M. ulcerans* speciation.

There was also found to be almost no difference between *M. ulcerans* and *M. marinum* tRNA counts with *M. ulcerans* containing one less tRNA (TGA stop codon) out of a total 46 tRNA genes (See Figure 17). It is interesting to note that *M. marinum* contains only one tRNA stop codon gene and that with the loss of this TGA tRNA gene, *M. ulcerans* contain no tRNAs coding for a stop codon. It is not known whether this absence has any affect on the ability of the genome to efficiently carry out translation or cell growth.

It is also noted that for both genomes, there is only one out of the 16 possible tRNA genes that have a 'T' in the third base position. There is also a reduced usage of these codons within the genomes CDSs and similarly low usage of codons with an 'A' in the third base position. This presumably reflects the GC rich (*M. ulcerans* 65.5%, *M. marinum* 66.1%) content of the genomes with increased use of GC rich codons within CDSs.

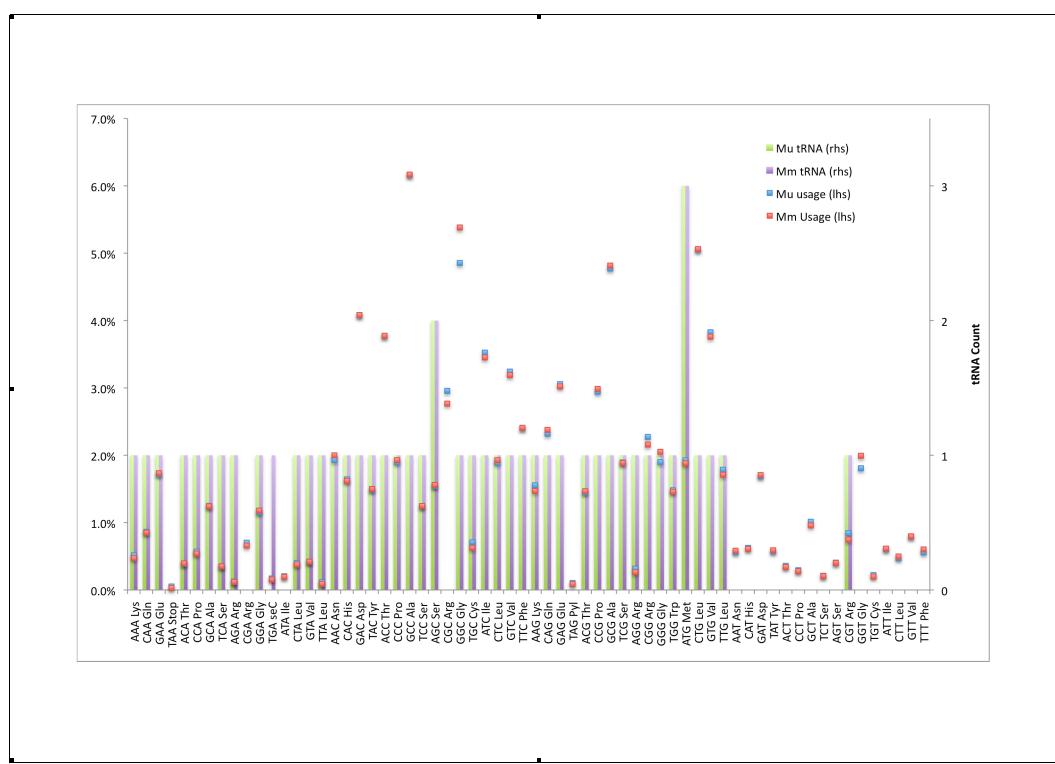


Figure 17 Codon Usage and tRNA Counts for reference genomes

The counts of tRNA genes (right hand axis) for the reference genomes *M. ulcerans* Agy99 (green bars) and *M. marinum* "M" (purple bars). tRNA genes are ordered along the horizontal axis by the third, second then first base of the codon to more clearly show the tRNA bias towards a G/C third base in the genomes. The codon usage in percent (left hand axis) is shown for both *M. ulcerans* Agy99 (blue squares) and *M. marinum* "M" (red squares).

4. Discussion of Results

Whole genome sequencing and the comparison of this large collection of isolates has shown that all mycolactone-producing mycobacteria (collectively referred to in this study as *M. ulcerans*) evolved from a common *M. marinum* progenitor by a combination of horizontal gene transfer (pMUM and phage), IS-mediated deletion and point mutation (Figure 11). These evolutionary processes resulted in extensive gene loss (185 CDS), changes in gene expression (e.g. *hsp18* and possibly *sigM*) and likely changes in gene function through positive selection, establishing *M. ulcerans* as a highly specialized, niche-adapted mycobacterium. The study data indicate these changes were followed by global dispersal of *M. ulcerans* and further diversification and adaptive evolution.

Study of the types of genes gained, lost or modified in conjunction with other experimental evidence provides some evidence regarding the nature of the niche environment in which the *M. ulcerans* MRCA was able to flourish and in which today's isolates still survive. Most significant among the DNA gained was the pMUM plasmid. The acquisition of this plasmid occurred early in the evolution of *M. ulcerans* as demonstrated by the congruent tree topologies inferred from chromosome and plasmid sequence alignments (Figure 11). The synthesis of mycolactone, a potent immunosuppressive small molecule encoded in the pMUM plasmid, probably gave a population of *M. marinum* cells the ability to persist in a place their generalist relatives could not. In previous research, it has been described how recombination and gene conversion has shaped the unusually repetitive gene structure of the mycolactone PKS, such that the 110 kb, three-gene PKS locus on pMUM comprises only 10 kb of unique sequence. This unusual gene structure, and the resulting instability, strongly suggests intense selection acting on *M. ulcerans* populations to maintain mycolactone production [36, 122, 123].

The loss of the mevalonate pathway for synthesis of isoprenoid lipids was originally observed in the genome of *M. ulcerans* Agy99 [33]. In the current study it is shown that this trait was established in the *M. ulcerans* MRCA and was probably a key adaptive responses of the bacterium following the acquisition of pMUM (Table 3). It is possible that loss of this metabolic capacity freed essential resources for critical mycolactone synthesis or alternatively that these pathways and metabolites were redundant in the niche environment occupied by *M. ulcerans*. Other potentially significant gene losses in *M. ulcerans* include selenocysteine synthase (*selA*), required for the synthesis of proteins containing selenocysteine, and the linked genes encoding the alpha and beta subunits of a putative selenocysteine-containing formate dehydrogenase, with a possible role in anaerobic growth; mutations that suggest the *M. ulcerans* MRCA lost the ability to grow anaerobically.

It is also striking that CDS associated with the intracellular lifestyle of mycobacterial pathogens such as *M. marinum* and *M. tuberculosis* have been lost in *M. ulcerans*. Genes predicted to be inactive include four phospholipase enzymes (PlcB_2,3,5&6) and *cueO* (Table 3). As well as

playing roles in intracellular replication in other bacteria, these CDS are also components of the bacterial cell wall. There appears to have been significant selective pressure on *M. ulcerans* to reduce or change its cell wall and cell surface antigenic profile. In this respect another noteworthy pseudogene conserved in *M. ulcerans* is *lgt* (MUL_1594). *Lgt* is a prolipoprotein diacylglycerol transferase that acylates prolipoproteins at a conserved N-terminal cysteine [124]. An *lgt* mutation in *Staphylococcus aureus* causes growth rate attenuation, an accumulation of prolipoproteins in the culture supernatant, and reduced activation of innate immune responses [125, 126]. The loss of *lgt* in *M. ulcerans* might therefore lead to aberrantly or non-acylated lipoproteins with reduced immunogenicity, like the *S. aureus* mutant.

The modification of the cell wall appears to have continued in the BU-associated *M. ulcerans* lineage 3 genomes, which contain an additional 589 pseudogenes or deleted regions of which 30% are predicted to have encoded antigens or cell wall associated proteins, including EsxA_2, EsxA_3, and Hspx_1. The deep branching lineage and clonal nature of the African and Australian lineage 3 isolates, which are most commonly involved in human infections, have the signature of passing through a second evolutionary bottleneck: gene deletions, further loss of gene function, chromosomal rearrangements and the expansion of another IS (IS2606 from the pMUM plasmid). Each of the *M. ulcerans* lineages probably represents different ecotypes, reflecting adaptation to related but distinct niche environments. It may be that each lineage is best described as an *M. ulcerans* ecovar.

There is a compelling correlation between genes undergoing positive selection as revealed by dN/dS analysis and those CDS inactivated or deleted (Table 6, Table 10), with mutations in all these groups skewed towards CDS involved in cell wall and lipid biosynthesis. These patterns point to significant selective pressures acting on *M. ulcerans* populations to devote resources (substrate and energy) towards the synthesis of mycolactones and modification of cell wall structures. Intriguingly, many of the cell wall metabolites lost via mutation are known to be highly antigenic in other mycobacteria. One interpretation of these observations is that the bacteria are responding to pressures from a host immune system, a point argued in a previous study [127]. When one further considers that mycolactone is a potent immune suppressor with apparent specificity for a mammalian microRNA that controls T-cell chemotaxis [128], this in turn leads to the idea that the niche occupied by *M. ulcerans* is a higher organism with a complex immune system. The discovery that Australian possums inhabiting BU endemic areas are susceptible to BU disease and harbour large number of *M. ulcerans* in their gastrointestinal tracts is consistent with this idea [129]. Although these arguments are not consistent with the significant lack of variation seen among *M. ulcerans* proteins with putative T-cell epitopes (Table 7), where an immune escape hypothesis would predict hypervariability not hyperconservation in these regions.

This study has also reinforced the close relationship between isolate origin and genotype for *M. ulcerans* strains that cause Buruli ulcer, notably those from Africa and Australia, where multiple isolates from one region were sequenced. The complete resolution of strain differences afforded by whole genome sequencing has shown how the genotype of *M. ulcerans* strains from two

African countries correlate with place of origin. Isolates from the east of Benin are distinct from isolates in the West of the country or from a different country (Figure 12). These findings suggest, as also demonstrated in a previous study in Ghana, that *M. ulcerans* transmission and microevolution generally occurs at a local level and therefore the source of the bacterium is somewhat fixed within a local region [111]. This observation should guide future thinking regarding the source of the bacteria in BU endemic areas, indicating that animal reservoirs of *M. ulcerans* are not likely to be particularly mobile. Although, one should also consider that the relative paucity of genomic difference between isolates from Ghana and Benin also reflects the relatively recent spread of the bacteria across this entire region. Efforts to establish the rate of mutation of these isolates or genome analysis of a more temporally and spatially diverse collection of isolates from this region might help estimate the amount of time *M. ulcerans* has been extant in West Africa.

5. Conclusion and Future Directions

This research has given a comprehensive insight into the *M. ulcerans*-*M. marinum* complex (MuMC). The isolates examined in the study covered a wide geographical diversity, and while future studies should include *M. ulcerans* isolates from other endemic countries together with more *M. marinum* isolates, whole genome sequencing of 35 isolates across the genetic diversity of the complex has yielded nucleotide-level granular detail of each isolate and their relatedness to each other. It has been shown that all MPM are a single lineage whose divergence from *M. marinum* was characterised by the acquisition of the pMUM plasmid, which conferred the ability to synthesise mycolactones and is largely responsible for the immune evasion properties of *M. ulcerans*. The plasmid has been identified as the likely origin of IS2606 that was then introduced into the chromosome. This was then followed by IS2606 expansion in the African and Australian isolates and extensive loss and modification of gene function, consistent with an evolutionary bottleneck and adaptation to a new niche. It is also likely that IS2404 originated from the plasmid and was present in the *M. ulcerans* MRCA prior to its expansion into all *M. ulcerans* isolate chromosomes.

Based on these shared features it is proposed that all members of the MPM lineage should be considered *M. ulcerans*. Further, it is suggested that *M. ulcerans* sublineages (such as the three identified in this study) can be considered *M. ulcerans* ecovars.

Examination of the classes of genes lost and modified in the *M. ulcerans* MRCA suggests a bacterial population occupying a niche environment that is aerobic and possibly extracellular given the number of genes known to be involved in intracellular survival lost from *M. ulcerans* [33, 38, 107]. Support for an extracellular niche is also found in two separate studies showing *M. ulcerans* elaborates a mycolactone-rich extracellular matrix and specifically expresses a surface protein that promotes adherence during initial stages of biofilm formation [89, 130]. Furthermore, it is hard to ignore the striking depletion of immunogens and modification of cell-wall proteins in *M. ulcerans* that may be subject to interactions with the immune defences of a host organism.

This study has clarified the understanding of the origins of an emerging human pathogen, provided important insights to help in the search for the reservoir(s) of this pathogen and generated a significant resource for future research. It is clear that *M. ulcerans* is not a generalist, saprophytic mycobacterium but a highly specialized occupant of a protected niche. This concept should be considered in ongoing research efforts to pinpoint the reservoir(s) of *M. ulcerans* and to understand the transmission of BU.

The rapid technological development of next generation sequencing platforms over the past few years is likely to continue. In the near future, we are likely to see machines that are able to produce longer and more accurate sequences with less cost and less total sequencing time.

It is foreseeable that single molecule sequencing of DNA and RNA will be routinely performed in real-time at negligible cost and allow hospitals to regularly screen patients for bacterial pathogens. Analogous to the computer revolution of the last few decades, sequencing will be integrated into all aspects of the healthcare and life sciences and, optimistically, provide the tools to combat the bacterial pathogens that have been mankind's constant companion.

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7. Abbreviations

ANI	Average nucleotide identity
BU	Buruli ulcer
CDS	Protein-coding DNA sequence.
HGT/LGT	Horizontal gene transfer/Lateral gene transfer
Indel	Insertion or deletion in genome
IS	Insertion sequence
LF	Likelihood function
MLST	Multi-locus sequence typing
MPM	Mycolactone producing mycobacteria
MRCA	Most Recent Common Ancestor
MTBC	<i>Mycobacterium tuberculosis</i> complex
MuMC	<i>Mycobacterium ulcerans-Mycobacterium marinum</i> complex
N50	The length of the contig such that 50% of the assembly is contained in contigs of length N50 or greater
PKS	Polyketide synthase

8. Tables

Note: Table 1 appears in main text.

Table 2 Isolates used in this study

Additional sequencing and assembly data in Table 4

Identifier	Alternate identifier	Origin	Source	Year isolated	Reference
<i>M. ulcerans</i> isolates					
Mu_06-3845	ITM001441	Houedja, Ouinhi, Zou, Benin	Aquatic insect	2000	[110]
Mu_06-3846	ITM971116	Lalo, Lalo, Couffo, Benin	Human	1997	This study
Mu_07-1082	ITM030216	Adjohoun, Adjohoun, Ouémé, Benin	Human	2003	This study
Mu_1G897		Cayenne, French Guiana	Human	1990	[131]
Mu_Agy99		Ga District, Ghana	Human	1999	[33]
Mu_NM14.01		Ga District, Ghana	Human	2001	[111]
Mu_NM33.04		Amansie West District, Ghana	Human	2004	[111]
Mu_NM43.02		Ga District, Ghana	Human	2002	[111]
Mu_NM49.02		Ga District, Ghana	Human	2002	[111]
Mu_NM54.02		Ga District, Ghana	Human	2002	[111]
Mu_DL045		Greece	Fish	2002	[44]
Mu_001506	ITM001506	Wokon, Ouinhi, Zou, Benin	Human	2000	This study
Mu_980535	ITM980535	Djigbé, Zé, Atlantique, Benin	Human	1998	This study
Mu_000945	ITM000945	Hwegoudo, Zé, Atlantique, Benin	Human	2000	This study
Mu_991845	ITM991845	Sagon, Ouinhi, Zou, Benin	Human	1999	This study
Mu_CC240299		Israel	Fish	1999	[44]
Mu_06-3844	ITM063844	Belgium	Fish	2006	[132]
Mu_8765 (<i>M. shinshuense</i>)	ITM8765	Japan	Human	1980	[133]
Mu_JKD8071 (" <i>M. liflandii</i> " 128FXT)		USA	Frog	2004	[134]
Mu_L15 (<i>M. pseudoshottsii</i> L15)		USA	Fish	2004	[42]
Mu_13822-70		Queensland, Australia	Human	1971	[135]
Mu_113	05152838	Point Lonsdale, Australia	Human	2005	This study
Mu_119	05159089	Frankston, Australia	Human	2005	This study

Identifier	Alternate identifier	Origin	Source	Year isolated	Reference
Mu_74	04140710	Point Lonsdale, Australia	Human	2004	This study
Mu_81	04149669	Point Lonsdale, Australia	Human	2004	This study
Mu_93	05131622	St Leonards, Australia	Human	2005	This study
Mu_05142109		East Gippsland, Australia	Possum	2005	This study
Mu_JKD8170		Point Lonsdale, Australia	Possum	2008	This study
Mu_08009899		Point Lonsdale, Australia	Human	2008	This study
Mu_JKD8049		Point Lonsdale, Australia	Human	2004	This study
<i>M. marinum</i> isolates					
Mm_99/89		NSW, Australia	Human	1994	[135]
Mm_99/84		Western Australia	Bilby (<i>Macrotis lagotis</i>)	1999	[135]
Mm_99/87		Western Australia	Human	1996	[135]
Mm_1726		Louisiana, USA	Armadillo	1986	[136]

Table 3 Noteworthy genes or loci absent in the *M. ulcerans* MRCA

Gene(s)	Locus_tag(s)	Comments	Reference
<i>selA</i>	MMAR_5190 MMAR_5194 MMAR_5195 MMAR_2615	selenocysteine synthase, required for the synthesis of proteins containing selenocysteine. Formate dehydrogenase alpha and beta subunits, selenocysteine-containing. Likely role in anaerobic growth. Anaerobic dehydrogenase (possible nitrate reductase)	[33] [33]
<i>lgt</i>	MMAR_2416	Key role in lipoprotein synthesis. Lgt acylates prolipoproteins. Lgt mutant of <i>S. aureus</i> is less immunogenic.	[124, 126, 137]
<i>plcB_2</i> , <i>plcB_5</i> , <i>plcB_6</i> , <i>plcB_3</i>	MMAR_1485 MMAR_3656 MMAR_4722 MMAR_0284	<i>M. marinum</i> has six plc genes. Four of these are absent in all <i>M. ulcerans</i> . Phospholipase C enzymes can cause direct or indirect enzymatic hydrolysis of host cell membrane phospholipids and appear important for mycobacterial intracellular survival.	[138]
<i>cstA</i>	MMAR_1616	Carbon starvation protein, CstA. In <i>E. coli</i> , <i>cstA</i> encodes a peptide transporter and is induced by carbon starvation. Maybe part of a redundant stress response system in <i>M. ulcerans</i> .	[139]
<i>cueO</i>	MMAR_1618	Multicopper oxidases protect against oxidative stress. This enzyme has functions in tolerance copper, and iron and manganese oxidation in a range of bacteria. It catalyses the oxidation of cuprous copper, ferrous iron and diphenolic compounds. In <i>Salmonella</i> , a <i>cueO</i> deletion mutant is less virulent in mouse model.	[140]
<i>idsB1</i> , <i>idsB2</i> , <i>idsA1</i>	MMAR_3212, MMAR_3219 MMAR_5095	Catalyzes the trans-addition of three molecules of IPP onto DMAPP to form geranylgeranyl pyrophosphate which is a precursor of the ether-linked lipids. Impact here of diverting all isoprenoid biosynthesis to the non-mevalonate pathway is not known. Possibly more favourable energetically if spending cellular resources on mycolactone synthesis.	[33]

Table 4 Strain Table and Summary Statistics

Group	Identifier	Origin	Source	Year isolated	No. Reads obtained	Read Length	Read Coverage	SNP differences compared to Mu_Agy99	SNP differences compared to Mm_M	De novo assembly contig N50	De novo assembly Total Mbp
<i>M. ulcerans</i>	Mu_06-3845	Houedja, Benin	Aquatic insect	2000	13,607,626	36	75	397	49991	23454	5.25
<i>isolates</i>	Mu_06-3846	Lalo, Benin	Human	1997	11,883,560	36	65	235	49668	21239	5.23
	Mu_07-1082	Adjohoun, Benin	Human	2003	11,878,192	36	67	461	49742	21022	5.23
	Mu_1G897	Cayenne, French Guiana	Human	1990	11,880,384	36	67	31912	45491	16703	5.36
	Mu_Agy99	Ga District, Ghana	Human	1999	29,658,550	36	155	113	50423	20349	5.25
	Mu_NM14.01	Ga District, Ghana	Human	2001	31,500,650	36	111	266	49836	15490	5.26
	Mu_NM33.04	Amansie West District, Ghana	Human	2004	25,636,102	36	95	127	49986	26629	5.28
	Mu_NM43.02	Ga District, Ghana	Human	2002	31,063,938	36	104	269	49749	15228	5.23
	Mu_NM49.02	Ga District, Ghana	Human	2002	29,918,112	36	119	292	49763	15221	5.22
	Mu_NM54.02	Ga District, Ghana	Human	2002	29,472,426	36	83	241	49716	22055	5.28
	Mu_DL045	Greece	Fish	2002	2,580,587(1)	108(2)	38			(3)	(3)
	Mu_001506	Wokon, Benin	Human	2000	20,554,068	101	232	470	53145	25681	5.30
	Mu_980535	Djigbé, Benin	Human	1998	22,820,034	101	270	474	53296	28010	5.30
	Mu_000945	Hwegoudo, Benin	Human	2000	19,987,930	101	234	456	52843	25375	5.29
	Mu_991845	Houedja, Benin	Human	1999	13,904,158	101	164	467	52671	30187	5.31
	Mu_CC240299	Israel	Fish	1999	12,838,320	76	84	30376	45929	18548	5.82
	Mu_06-3844	Belgium	Fish	2006	19,328,186	76	107	30736	46510	20371	5.85
	Mu_8765 (M. shinshuense)	Japan	Human	1980	4,259,424	76	17	28690	45300	9480	5.44
	Mu_JKD8071 (M. lflandii 128FXT)	USA	Frog	2004	29,946,082	36	102	27020	42362	16619	5.87
	Mu_L15 (M. pseudoshottsi L15)	USA	Fish	2004	12,635,600	76	87	30445	46474	12240	5.77
	Mu_13822-70	Queensland, Australia	Human	1971	12,965,226	76	92	6603	49932	18461	5.25
	Mu_113	Point Lonsdale, Australia	Human	-	8,111,266	76	32	6451	48570	13487	5.24
	Mu_119	Frankston, Australia	Human	-	9,982,652	76	45	6524	49397	15331	5.23
	Mu_74	Point Lonsdale, Australia	Human	-	19,841,064	76	47	5887	48071	13821	5.20
	Mu_81	Point Lonsdale, Australia	Human	-	7,573,714	76	32	6295	48489	18253	5.24
	Mu_93	St Leonards, Australia	Human	-	9,393,130	76	28	5760	46693	13965	5.21
	Mu_05142109	East Gippsland, Australia	Possum	2005	30,564,548	36	120	6106	48910	17945	5.23
	Mu_JKD8170	Point Lonsdale, Australia	Possum	2008	33,261,846	75	190	6314	50135	15659	5.25
	Mu_08009899	Point Lonsdale, Australia	Human	2004	7,786,752	36	27	5447	45780	12355	5.21
	Mu_JKD8049	Point Lonsdale, Australia	Human	2004	10,921,914	36	63	5919	48727	23130	5.25
<i>M. marinum</i>	Mm_99/89	NSW, Australia	Human	1994	3,396,470	100	23	38017	34786	6816	5.97
<i>isolates</i>	Mm_99/84	Western Australia	Bilby	1999	12,904,538	76	31	81361	76645	21576	6.31
	Mm_99/87	Western Australia	Human	1996	10,810,668	76	60	51196	41217	29125	6.11
	Mm_1726	South Carolina, USA	Armadillo	1986	12,740,914	76	31	83226	76624	18314	6.07
(1)	Average read length										
(2)	Single ended										
(3)	Not assembled due to low quality coverage										

Isolates used in this study with sequencing summary statistics.

Table 5 *M. ulcerans* specific CDS and features

List of *M. ulcerans* Agy99 reference annotated features found in all *M. ulcerans* isolates but not found in any of the *M. marinum* isolates.

Table 6 High dN/dS CDS and CDS with high non-synonymous SNPs

High dN/dS CDS - Mm and Mu strains. Compares Mm and Mu strains showing genes in Mu with dN/dS > 1.0

M.marinum locus	Mm dn/dS	Mu dN/dS	log likelihood	CDS Length	(non- syn) / length	Average Mu non	Average Mu syn	Gene	Functional Group	Gene Product
MMAR_5465	0.38	2.87	-474.37	291	0.0184	7.14	1.79	esxE	cell wall and cell processes	EsaT-6 like protein EsxE
MMAR_3508	0.46	1.56	-758.02	507	0.0099	7.86	2.83		Conserved hypotheticals	conserved hypothetical secreted protein
MMAR_3026	0.41	1.62	-303.61	231	0.0084	1.97	0.03		Conserved hypotheticals	conserved hypothetical protein
MMAR_4020	0.80	1.44	-1,398.15	897	0.0083	8.03	0.59	echA4_2	lipid metabolism	enoyl-CoA hydratase EchA4_2
MMAR_5466	2.97	1.05	-480.16	312	0.0083	5.74	3.16	esxF	cell wall and cell processes	EsaT-6 like protein EsxF
MMAR_5358	0.07	1.11	-1,700.28	1,146	0.0073	8.79	0.45		conserved hypotheticals	conserved hypothetical membrane protein
MMAR_1628	0.33	1.34	-543.84	357	0.0065	3.10	0.79		conserved hypotheticals	conserved hypothetical protein
MMAR_3002	0.66	1.37	-1,994.88	1,287	0.0063	10.03	1.97		PE/PPE	PPE family protein
MMAR_3366	0.23	1.41	-920.23	534	0.0059	3.24	0.07	lppN	cell wall and cell processes	lipoprotein LppN
MMAR_2212	0.40	1.42	-1,217.79	825	0.0059	5.76	0.86		intermediary metabolism and respiration	methyltransferase
MMAR_1996	0.13	1.23	-998.85	687	0.0055	3.83	0.07		conserved hypotheticals	conserved hypothetical protein

M.marinum locus	Mm dn/dS	Mu dN/dS	log likelihood	CDS Length	(non- syn) / length	Average Mu non	Average Mu syn	Gene	Functional Group	Gene Product
MMAR_2753	0.31	1.18	-2,073.71	1,290	0.0053	10.34	3.45	treS_1	intermediary metabolism and respiration	trehalose synthase TreS_1
MMAR_1083	0.06	3.04	-1,171.10	861	0.0053	5.59	1.00		conserved hypotheticals	conserved hypothetical protein
MMAR_3450	0.04	1.05	-435.56	300	0.0052	1.62	0.07		cell wall and cell processes	conserved hypothetical membrane protein
MMAR_4299	0.08	1.18	-726.29	516	0.0051	2.72	0.07		conserved hypotheticals	conserved hypothetical protein
MMAR_5486	1.54	1.22	-869.10	519	0.0051	3.52	0.86		conserved hypotheticals	conserved hypothetical protein
MMAR_2061	0.50	1.48	-672.97	441	0.0050	4.17	1.97		conserved hypotheticals	conserved hypothetical protein
MMAR_1128	0.28	1.90	-623.78	438	0.0050	3.00	0.83		cell wall and cell processes	conserved hypothetical membrane protein
MMAR_4809	0.15	1.86	-593.01	375	0.0046	3.76	2.03	crtYd	lipid metabolism	lycopene cyclase CrtYd
MMAR_3191	0.24	1.63	-1,343.68	957	0.0045	9.91	5.64	ftsQ	cell wall and cell processes	cell division protein FtsQ
MMAR_3644	1.02	2.33	-688.76	417	0.0044	1.86	0.03		conserved hypotheticals	conserved hypothetical protein
MMAR_0144	0.09	1.17	-561.58	417	0.0041	1.72	0.03		cell wall and cell processes	conserved hypothetical membrane protein
MMAR_1669	0.34	1.42	-1,112.90	780	0.0040	3.93	0.79		lipid metabolism	lysophospholipase
MMAR_2115	0.19	1.25	-1,054.30	693	0.0040	3.79	1.03		cell wall and cell processes	hypothetical secreted protein
MMAR_4925	0.20	1.40	-618.26	438	0.0039	1.76	0.03		intermediary metabolism and respiration	4-carboxymuconolactone decarboxylase
MMAR_3109	0.20	1.25	-1,400.25	882	0.0038	5.47	2.09		intermediary metabolism and respiration	dehydrogenase
MMAR_3241	0.10	1.18	-944.14	639	0.0038	3.48	1.07		cell wall and cell processes	conserved transmembrane protein
MMAR_4850	0.22	1.14	-1,333.47	906	0.0038	10.21	6.79		lipid metabolism	O-methyltransferase
MMAR_1934	0.08	4.30	-923.45	642	0.0037	3.14	0.76		conserved hypotheticals	conserved hypothetical protein
MMAR_2060	0.36	1.77	-1,425.38	948	0.0035	4.41	1.07			catalase

M.marinum locus	Mm dn/dS	Mu dN/dS	log likelihood	CDS Length	(non- syn) / length	Average Mu non	Average Mu syn	Gene	Functional Group	Gene Product
MMAR_1976	0.17	1.21	-1,018.39	726	0.0034	3.52	1.03		conserved hypotheticals	conserved hypothetical protein
MMAR_1985	0.20	1.61	-894.79	696	0.0033	2.34	0.03		conserved hypotheticals	conserved protein
MMAR_1383	0.35	1.23	-426.00	264	0.0033	0.90	0.03		unknown	hypothetical protein
MMAR_1570	0.60	1.08	-891.86	645	0.0033	2.59	0.48		cell wall and cell processes	conserved hypothetical secreted protein
MMAR_3745	0.34	1.16	-1,212.43	846	0.0032	3.72	1.03		conserved hypotheticals	conserved protein
MMAR_3300	0.31	1.29	-739.36	513	0.0032	2.66	1.03		cell wall and cell processes	conserved hypothetical membrane protein
MMAR_2419	0.04	1.10	-1,048.72	756	0.0031	2.48	0.10	cut1	cell wall and cell processes	cutinase Cut1
MMAR_3188	0.31	1.24	-1,176.98	786	0.0031	5.52	3.07		conserved hypotheticals	conserved protein
MMAR_1222	0.26	2.48	-1,299.96	888	0.0031	3.79	1.03		conserved hypotheticals	conserved hypothetical protein
MMAR_4088	0.04	2.17	-1,543.82	915	0.0031	2.97	0.14	atpG	intermediary metabolism and respiration	ATP synthase gamma chain AtpG
MMAR_2661	0.17	1.40	-758.14	564	0.0029	1.69	0.03		conserved hypotheticals	conserved hypothetical protein
MMAR_0965	0.24	1.28	-986.86	717	0.0028	2.10	0.07	gloB		glyoxalase II GloB
MMAR_0902	0.07	1.51	-785.56	525	0.0028	3.28	1.79		cell wall and cell processes	conserved hypothetical membrane protein
MMAR_1633	0.65	2.17	-783.17	531	0.0027	2.45	1.00		conserved hypotheticals	conserved hypothetical protein
MMAR_0716	0.13	1.20	-947.27	624	0.0027	2.52	0.83	mutT3	information pathways	mutator protein MutT3
MMAR_0062	0.19	1.58	-1,185.02	765	0.0027	7.24	5.17		regulatory proteins	transcriptional regulatory protein (probably GntR-family)
MMAR_3363	0.59	1.27	-1,016.59	627	0.0027	3.72	2.03		conserved hypotheticals	conserved hypothetical protein
MMAR_4311	0.13	1.16	-976.24	720	0.0027	2.72	0.79		cell wall and cell processes	integral membrane protein
MMAR_1544	0.13	1.02	-979.21	618	0.0027	2.48	0.83		conserved hypotheticals	conserved hypothetical protein

M.marinum locus	Mm dn/dS	Mu dN/dS	log likelihood	CDS Length	(non- syn) / length	Average Mu non	Average Mu syn	Gene	Functional Group	Gene Product
MMAR_4158	0.43	1.48	-1,243.57	849	0.0026	2.31	0.07	citE_1	intermediary metabolism and respiration	citrate (pro-3s)-lyase (beta subunit) CitE_1
MMAR_1737	0.18	2.86	-957.54	684	0.0026	1.83	0.07	ung	information pathways	uracil-DNA glycosylase Ung
MMAR_1725	0.07	1.25	-938.14	702	0.0026	1.86	0.07		regulatory proteins	transcriptional regulatory protein
MMAR_2008	0.19	1.20	-513.45	381	0.0025	1.00	0.03		conserved hypotheticals	conserved hypothetical protein
MMAR_0494	0.16	1.50	-1,065.77	789	0.0024	3.86	2.00	glpQ2	intermediary metabolism and respiration	glycerophosphoryl diester phosphodiesterase GlpQ2
MMAR_0553	0.04	1.38	-1,307.76	792	0.0024	4.83	2.97	tam	intermediary metabolism and respiration	trans-aconitate methyltransferase Tam
MMAR_2018	0.03	1.92	-1,014.81	744	0.0022	2.69	1.03		conserved hypotheticals	conserved hypothetical protein
MMAR_2234	0.07	1.10	-1,123.37	804	0.0022	1.83	0.07		conserved hypotheticals	conserved hypothetical protein
MMAR_2030	0.01	2.00	-1,758.05	1,290	0.0021	2.76	0.03	arsA	cell wall and cell processes	arsenic-transport integral membrane protein ArsA
MMAR_0551	0.14	1.35	-1,363.41	1,014	0.0021	2.14	0.03		cell wall and cell processes	conserved transmembrane protein
MMAR_0473	0.20	1.69	-1,035.17	768	0.0021	1.90	0.31		intermediary metabolism and respiration	methyltransferase
MMAR_1935	0.15	1.54	-1,514.74	1,026	0.0020	4.34	2.28		intermediary metabolism and respiration	oxidoreductase
MMAR_3354	0.20	1.16	-2,401.85	1,449	0.0020	8.28	5.38	Int	cell wall and cell processes	apolipoprotein n-acyltransferase Lnt
MMAR_2077	0.19	1.31	-1,225.57	894	0.0020	2.86	1.10		conserved hypotheticals	conserved hypothetical protein
MMAR_4787	0.18	4.96	-1,272.75	879	0.0019	1.72	0.03		cell wall and cell processes	transport system kinase
MMAR_2153	0.05	1.23	-1,105.39	786	0.0019	5.55	4.07		conserved hypotheticals	conserved hypothetical protein
MMAR_1244	0.09	1.53	-582.80	387	0.0019	1.76	1.03		cell wall and cell processes	conserved hypothetical membrane protein

M.marinum locus	Mm dn/dS	Mu dN/dS	log likelihood	CDS Length	(non- syn) / length	Average Mu non	Average Mu syn	Gene	Functional Group	Gene Product
MMAR_5096	0.24	2.41	-850.66	534	0.0018	1.00	0.03	gpmB	intermediary metabolism and respiration	fructose-2 6-bisphosphatase GpmB
MMAR_2309	0.02	1.13	-1,901.63	1,257	0.0017	5.19	3.05	udgL	intermediary metabolism and respiration	UDP-glucose 6-dehydrogenase UdgL
MMAR_4692	0.15	1.56	-601.12	432	0.0017	1.76	1.03		cell wall and cell processes	conserved hypothetical secreted protein
MMAR_1355	0.19	1.11	-1,159.08	786	0.0016	2.14	0.86	lipV	intermediary metabolism and respiration	lipase LipV
MMAR_2497	0.24	1.22	-1,403.15	1,011	0.0016	1.66	0.03		intermediary metabolism and respiration	phosphatase
MMAR_5111	0.14	1.15	-1,199.76	843	0.0016	3.17	1.83	folP1	intermediary metabolism and respiration	dihydropteroate synthase 1 FolP1
MMAR_1678	0.13	1.67	-957.53	696	0.0015	2.10	1.03		cell wall and cell processes	conserved hypothetical membrane protein
MMAR_1268	0.22	1.18	-1,025.64	657	0.0015	2.03	1.07		conserved hypotheticals	conserved hypothetical regulatory protein
MMAR_1836	0.13	1.21	-1,678.08	1,209	0.0015	2.59	0.83	dxr	intermediary metabolism and respiration	1-deoxy-D-xylulose 5-phosphate reductoisomerase Dxr
MMAR_0821	0.02	1.91	-1,094.36	795	0.0014	1.93	0.79		conserved hypotheticals	conserved hypothetical protein
MMAR_3760	0.06	1.10	-1,372.22	870	0.0014	2.38	1.14		regulatory proteins	Sir2-like regulatory protein
MMAR_1362	0.23	2.55	-1,143.37	726	0.0014	1.07	0.03	lpqQ	cell wall and cell processes	lipoprotein LpqQ
MMAR_4152	0.03	1.02	-991.66	741	0.0014	1.83	0.79	lprA	cell wall and cell processes	lipoprotein LprA
MMAR_5149	0.13	1.01	-1,195.57	858	0.0013	3.31	2.21	serB	cell wall and cell processes	phosphoserine phosphatase SerB
MMAR_3741	0.07	1.40	-1,474.81	1,050	0.0013	3.45	2.10		conserved hypotheticals	conserved hypothetical protein
MMAR_4139	0.17	1.06	-2,537.32	1,749	0.0013	6.28	4.07	oppA	cell wall and cell processes	periplasmic oligopeptide-binding lipoprotein OppA
MMAR_2720	0.10	1.60	-580.78	417	0.0012	0.55	0.03		regulatory proteins	transcriptional regulatory protein

M.marinum locus	Mm dn/dS	Mu dN/dS	log likelihood	CDS Length	(non- syn) / length	Average Mu non	Average Mu syn	Gene	Functional Group	Gene Product
MMAR_1025	0.18	2.34	-2,319.21	1,437	0.0012	6.83	5.07		intermediary metabolism and respiration	dehydrogenase
MMAR_4971	0.13	1.60	-1,903.80	1,245	0.0012	7.38	5.86	bioF2	intermediary metabolism and respiration	8-amino-7-oxononanoate synthase BioF2
MMAR_2762	0.16	1.07	-803.91	495	0.0012	4.72	4.14		conserved hypotheticals	conserved hypothetical protein
MMAR_3724	0.04	1.09	-2,618.02	1,917	0.0011	3.53	1.43	lepA	intermediary metabolism and respiration	GTP-binding protein LepA
MMAR_4217	0.18	1.25	-893.48	675	0.0011	1.79	1.07		intermediary metabolism and respiration	methyltransferase
MMAR_4119	0.28	1.64	-1,038.73	645	0.0011	1.72	1.03		cell wall and cell processes	conserved hypothetical membrane protein
MMAR_2455	0.13	2.18	-1,094.11	783	0.0010	3.62	2.86		cell wall and cell processes	transmembrane protein
MMAR_4115	0.12	1.26	-1,063.41	648	0.0010	1.66	1.03		regulatory proteins	conserved hypothetical regulatory protein
MMAR_5049	0.30	1.33	-1,565.45	1,149	0.0009	2.10	1.10	fadE30	lipid metabolism	acyl-CoA dehydrogenase FadE30
MMAR_1712	0.02	2.19	-1,280.55	1,032	0.0008	1.86	1.00	ilvC	intermediary metabolism and respiration	ketol-acid reductoisomerase IlvC
MMAR_0846	0.37	1.32	-731.68	537	0.0008	1.24	0.83		cell wall and cell processes	conserved transmembrane protein
MMAR_1211	0.16	1.27	-1,229.08	912	0.0007	1.69	1.03		cell wall and cell processes	chitinase
MMAR_1042	0.21	1.29	-1,016.16	705	0.0006	2.28	1.83		conserved hypotheticals	conserved protein
MMAR_3309	0.27	1.47	-755.49	495	0.0006	1.29	0.98	ptpA	regulatory proteins	phosphotyrosine protein phosphatase PtpA
MMAR_0786	0.06	1.12	-362.05	276	0.0006	0.17	0.00		cell wall and cell processes	conserved hypothetical membrane protein
MMAR_1905	0.56	1.17	-1,660.06	1,176	0.0005	2.69	2.07		PE/PPE	PPE family protein
MMAR_3367	0.29	1.83	-723.23	399	0.0005	0.24	0.03		conserved hypotheticals	conserved hypothetical protein
MMAR_0726	0.07	1.16	-2,279.59	1,512	0.0005	5.28	4.55	lpqL	intermediary metabolism and respiration	lipoprotein aminopeptidase LpqL

M.marinum locus	Mm dn/dS	Mu dN/dS	log likelihood	CDS Length	(non- syn) / length	Average Mu non	Average Mu syn	Gene	Functional Group	Gene Product
MMAR_1848	0.17	2.99	-655.26	432	0.0005	0.21	0.00		cell wall and cell processes	conserved hypothetical membrane protein
MMAR_0667	0.02	1.29	-1,561.37	1,116	0.0005	1.86	1.34		intermediary metabolism and respiration	glycosyl hydrolase
MMAR_1076	0.31	1.58	-750.92	549	0.0004	1.03	0.79		conserved hypotheticals	conserved protein
MMAR_2123	0.20	1.39	-794.44	555	0.0003	1.21	1.03	apt	intermediary metabolism and respiration	adenine phosphoribosyltransferase Apt
MMAR_5128	0.08	1.03	-614.19	489	0.0002	1.10	1.00	ppa	intermediary metabolism and respiration	inorganic pyrophosphatase Ppa
MMAR_3817	0.04	1.04	-3,608.38	2,580	0.0002	6.10	5.66	pepN	intermediary metabolism and respiration	aminopeptidase N PepN
MMAR_1973	0.06	2.07	-613.46	441	-0.0001	0.97	1.00		conserved hypotheticals	conserved protein
MMAR_0396	0.24	1.03	-1,644.24	1,170	-0.0001	4.48	4.59		lipid metabolism	acyl-CoA transferase
MMAR_0763	0.25	1.33	-731.48	516	-0.0001	0.93	1.00		conserved hypotheticals	conserved hypothetical protein
MMAR_1555	0.15	1.78	-663.05	477	-0.0002	0.93	1.03		regulatory proteins	transcriptional regulatory protein
MMAR_5033	0.10	2.68	-1,577.43	1,176	-0.0002	2.72	3.00	fadA5	lipid metabolism	acetyl-CoA acetyltransferase FadA5
MMAR_5230	0.27	1.06	-964.53	708	-0.0002	1.59	1.76	cobQ2	intermediary metabolism and respiration	cobyric acid synthase CobQ2
MMAR_2646	0.06	1.62	-1,743.96	1,242	-0.0002	3.55	3.86		conserved hypotheticals	conserved protein
MMAR_3648	0.29	1.97	-724.64	453	-0.0003	0.69	0.83		cell wall and cell processes	conserved hypothetical protein
MMAR_1781	0.08	2.22	-820.33	594	-0.0003	0.59	0.79		conserved hypotheticals	conserved hypothetical protein
MMAR_4386	0.19	1.05	-603.49	435	-0.0004	0.86	1.03		cell wall and cell processes	conserved membrane protein
MMAR_2793	0.13	4.21	-443.00	327	-0.0004	0.90	1.03		conserved hypotheticals	conserved hypothetical protein
MMAR_1024	0.05	1.28	-2,165.50	1,413	-0.0005	3.17	3.83		cell wall and cell processes	membrane glycosyl transferase

M.marinum locus	Mm dn/dS	Mu dN/dS	log likelihood	CDS Length	(non- syn) / length	Average Mu non	Average Mu syn	Gene	Functional Group	Gene Product
MMAR_2434	0.12	1.04	-1,754.11	1,227	-0.0006	4.86	5.59	coaE	intermediary metabolism and respiration	dephospho-CoA kinase CoaE
MMAR_1603	0.17	1.05	-1,978.06	1,266	-0.0006	2.14	2.90		conserved hypotheticals	conserved hypothetical protein
MMAR_4052	0.09	1.1	-1,401.94	1,032	-0.0007	3.45	4.14	mce3B_1		MCE-family protein Mce3B_1
MMAR_2356	0.04	1.05	-4,626.71	3,201	-0.0007	9.66	11.93	ileS	information pathways	isoleucyl-tRNA synthetase IleS
MMAR_0522	0.23	1.74	-773.62	546	-0.0008	0.62	1.03	aac		aminoglycoside 2'-N-acetyltransferase Aac
MMAR_2025	0.18	1.44	-1,695.29	1,206	-0.0008	3.79	4.72		information pathways	SAM-dependent methyltransferase
MMAR_5054	0.08	1.03	-1,676.67	1,176	-0.0008	3.31	4.24	aspB	intermediary metabolism and respiration	aspartate aminotransferase AspB
MMAR_3453	0.23	1.24	-1,621.76	1,200	-0.0008	5.10	6.07		intermediary metabolism and respiration	aminotransferase
MMAR_2595	0.17	2.32	-1,576.47	1,128	-0.0008	2.14	3.07		cell wall and cell processes	hypothetical membrane protein
MMAR_4076	0.22	1.3	-638.15	468	-0.0009	1.93	2.34	gloA_1	intermediary metabolism and respiration	glyoxalase GloA_1
MMAR_0842	0.18	1.03	-1,905.04	1,422	-0.0010	3.41	4.90	hemA	intermediary metabolism and respiration	glutamyl-tRNA reductase HemA
MMAR_3861	0.11	1.13	-1,001.83	621	-0.0011	2.45	3.14		regulatory proteins	conserved hypothetical regulatory protein
MMAR_2300	0.07	1.02	-1,443.34	975	-0.0012	3.86	5.03		conserved hypotheticals	conserved hypothetical membrane protein
MMAR_4150	0.21	1.02	-472.58	333	-0.0012	0.38	0.79		cell wall and cell processes	conserved hypothetical secreted protein
MMAR_0499	0.06	2.52	-1,619.69	1,194	-0.0015	2.28	4.03	lpqI	cell wall and cell processes	conserved lipoprotein LpqI
MMAR_4513	0.32	1.05	-1,140.10	762	-0.0016	7.12	8.36		conserved hypotheticals	conserved hypothetical protein
MMAR_1587	0.05	1.05	-928.98	624	-0.0017	1.97	3.03		conserved hypotheticals	conserved hypothetical protein

M.marinum locus	Mm dn/dS	Mu dN/dS	log likelihood	CDS Length	(non- syn) / length	Average Mu non	Average Mu syn	Gene	Functional Group	Gene Product
MMAR_5475	0.15	1.05	-893.58	588	-0.0018	5.10	6.14	sigM	information pathways	alternative RNA polymerase sigma factor SigM
MMAR_2374	0.07	1.84	-1,712.85	1,281	-0.0020	3.52	6.03	ilvA	intermediary metabolism and respiration	threonine dehydratase IlvA
MMAR_0441	0.11	1.67	-734.66	540	-0.0020	0.97	2.03		conserved hypotheticals	conserved hypothetical protein
MMAR_3010	0.04	1.02	-1,472.02	966	-0.0022	2.00	4.10		conserved hypotheticals	conserved membrane protein
MMAR_3365	0.05	1.4	-846.56	558	-0.0023	1.72	3.00		conserved hypotheticals	conserved hypothetical protein
MMAR_1635	0.03	1.09	-877.17	654	-0.0023	0.28	1.79		regulatory proteins	transcriptional regulatory protein (TetR-family)
MMAR_4332	0.18	1.47	-853.27	606	-0.0024	1.00	2.45		conserved hypotheticals	conserved hypothetical protein
MMAR_2796	0.09	1.44	-1,885.68	1,278	-0.0024	9.93	13.00	cinA		competence/damage-inducible protein CinA
MMAR_5027	0.03	1.54	-1,577.35	1,161	-0.0025	1.07	4.00	ltp2_1	lipid metabolism	acetyl-CoA acetyltransferase (PaaJ-like) Ltp2_1
MMAR_4507	0.28	1.59	-1,535.74	960	-0.0031	15.31	18.28		conserved hypotheticals	conserved hypothetical protein
MMAR_0597	0.21	1.81	-648.61	417	-0.0031	6.69	8.00		conserved hypotheticals	conserved hypothetical protein
MMAR_4581	0.06	2.65	-1,151.42	792	-0.0032	2.52	5.03		intermediary metabolism and respiration	short-chain type dehydrogenase/reductase
MMAR_3227	0.12	1.1	-532.61	390	-0.0035	2.66	4.03		conserved hypotheticals	conserved hypothetical protein
MMAR_2802	0.28	1.67	-743.62	519	-0.0038	3.07	5.03		cell wall and cell processes	conserved membrane protein
MMAR_5039	0.08	1.49	-1,009.29	744	-0.0038	0.97	3.79	echA20	lipid metabolism	enoyl-CoA hydratase EchA20
MMAR_3039	0.15	1.16	-2,295.29	1,542	-0.0040	7.52	13.66		intermediary metabolism and respiration	conserved membrane-bound oxidoreductase
MMAR_2506	0.02	1.39	-1,364.25	942	-0.0042	1.10	5.07	xerD	insertion seqs and phages	integrase/recombinase XerD
MMAR_4951	0.13	1.08	-1,882.96	1,215	-0.0043	1.59	6.86		conserved hypotheticals	conserved protein

M.marinum locus	Mm dn/dS	Mu dN/dS	log likelihood	CDS Length	(non-syn) / length	Average Mu non	Average Mu syn	Gene	Functional Group	Gene Product
MMAR_5009	0.07	2.72	-1,270.43	891	-0.0047	1.59	5.79		conserved hypotheticals	conserved hypothetical oxidoreductase
MMAR_4864	0.13	2.86	-1,456.32	963	-0.0056	6.34	11.76	mshD	lipid metabolism	mycothiol acetyltransferase MshD
MMAR_2436	0.05	1.14	-647.99	477	-0.0060	1.14	4.00		conserved hypotheticals	conserved hypothetical protein
MMAR_4863	0.06	2.27	-1,540.06	1,107	-0.0061	5.21	12.00	phoS3	cell wall and cell processes	phosphate-binding protein 3 precursor PhoS3
MMAR_4024	0.11	1.21	-1,189.29	810	-0.0065	3.10	8.34	echA16_1	lipid metabolism	enoyl-CoA hydratase EchA16_1
MMAR_4413	0.15	1.34	-1,692.78	1,200	-0.0066	8.97	16.83		conserved hypotheticals	conserved hypothetical protein
MMAR_5480	0.05	1.26	-1,144.67	732	-0.0074	5.34	10.79		conserved hypotheticals	conserved hypothetical protein
MMAR_3275	0.12	2.69	-897.03	537	-0.0079	1.76	6.00		conserved hypotheticals	conserved hypothetical protein
MMAR_5336	0.02	1.04	-1,257.44	843	-0.0080	3.07	9.83	rfbE	cell wall and cell processes	O-antigen/lipopolysaccharide transport ATP-binding protein ABC transporter RfbE
MMAR_3292	0.17	1.08	-924.23	639	-0.0092	2.97	8.83		conserved hypotheticals	conserved hypothetical protein
MMAR_4517	0.21	1.79	-1,064.45	783	-0.0098	8.03	15.69		conserved hypotheticals	conserved hypothetical protein
MMAR_4437	0.07	1.24	-1,040.76	705	-0.0098	4.10	11.03		cell wall and cell processes	conserved hypothetical membrane protein
MMAR_2739	0.03	1.06	-1,462.76	1,002	-0.0110	0.93	12.00	adhA	intermediary metabolism and respiration	alcohol dehydrogenase AdhA
MMAR_4504	0.07	1.09	-2,161.79	1,476	-0.0112	26.69	43.17		cell wall and cell processes	conserved hypothetical membrane protein
MMAR_2794	0.07	1.08	-705.49	495	-0.0121	1.52	7.48	lppD	cell wall and cell processes	lipoprotein LppD
MMAR_2803	0.18	1.27	-592.86	426	-0.0130	2.24	7.76		cell wall and cell processes	conserved hypothetical membrane protein

M.marinum locus	Mm dn/dS	Mu dN/dS	log likelihood	CDS Length	(non- syn) / length	Average Mu non	Average Mu syn	Gene	Functional Group	Gene Product
MMAR_5300	0.08	1.63	-1,115.89	681	-0.0132	1.28	10.28	proW		osmoprotectant (glycine betaine/carnitine/choline/L-proline) transport integral membrane protein ABC transporter ProW
MMAR_3018	0.14	1.35	-1,047.25	516	-0.0213	8.90	19.86		intermediary metabolism and respiration	gluconate kinase

M. marinum CDS with large normalised difference bw ns-SNPs and syn-SNPs

delta / length	locus	Average non	sd_non	Average syn	sd_syn	delta	CDS length	gene	fgroup	product	ortholog	mulocus
0.0380	MMAR_3274	10.72	0.64	2.07	0.25	8.66	228		cell wall and cell processes	conserved hypothetical secreted protein	MON01355	MUL_1355
0.0266	MMAR_5583	4.55	1.07	-	-	4.55	171	mymT	intermediary metabolism and respiration	Copper-binding metallothionein MymT	MON21859	MUL_5128
0.0250	MMAR_2549	14.66	1.29	3.31	0.46	11.34	453		unknown	hypothetical protein	MON06430	MUL_5090
0.0235	MMAR_5558	9.91	1.32	2.57	0.34	7.34	312		unknown	hypothetical protein	MON03769	MUL_3769
0.0228	MMAR_4018	11.52	2.08	4.00	0.83	7.52	330		unknown	hypothetical protein	MON03883	MUL_3883
0.0216	MMAR_5174	5.45	0.50	-	-	5.45	252		conserved hypotheticals	conserved hypothetical protein	MON04261	MUL_4261
0.0209	MMAR_0674	5.48	1.96	0.03	0.18	5.45	261		conserved hypotheticals	conserved hypothetical protein	MON02839	MUL_2839
0.0195	MMAR_1878	11.66	2.19	1.90	0.30	9.76	501		conserved hypotheticals	conserved hypothetical protein	MON02106	MUL_2106
0.0185	MMAR_5454	26.00	4.30	9.45	1.28	16.55	897		cell wall and cell processes	conserved hypothetical transmembrane protein	MON05045	MUL_5045
0.0184	MMAR_5465	7.14	2.52	1.79	0.41	5.34	291	esxE	cell wall and cell processes	EsaT-6 like protein EsxE	MON05054	MUL_5054
0.0182	MMAR_5469	6.79	0.41	1.07	0.25	5.72	315		conserved hypotheticals	conserved hypothetical protein	MON05058	MUL_5058
0.0161	MMAR_5571	5.66	1.12	1.93	0.36	3.72	231		conserved hypotheticals	conserved hypothetical protein	MON02379	MUL_2379
0.0157	MMAR_0039	5.69	1.12	0.97	0.18	4.72	300		conserved hypotheticals	conserved hypothetical protein	MON00038	MUL_0038
0.0140	MMAR_3428	9.93	2.85	4.72	1.34	5.21	372		conserved hypotheticals	conserved hypothetical protein	MON02703	MUL_2703
0.0138	MMAR_5548	5.55	0.97	2.07	0.25	3.48	252		cell wall and cell processes	conserved hypothetical secreted protein	MON05031	MUL_5031
0.0136	MMAR_5359	8.17	1.56	1.10	0.30	7.07	519		cell wall and cell processes	conserved hypothetical secreted protein	MON04978	MUL_4978
0.0131	MMAR_0246	10.97	2.92	0.10	0.40	10.86	831		cell wall and cell processes	conserved hypothetical membrane protein	MON04867	MUL_4867
0.0127	MMAR_3675	3.00	0.51	0.07	0.22	2.93	231		conserved hypotheticals	conserved hypothetical protein	MON03618	MUL_3618
0.0126	MMAR_2911	9.44	2.65	5.01	1.50	4.43	351		conserved hypotheticals	conserved hypothetical protein	MON02861	MUL_2861
0.0116		4.76	0.50	0.86	0.43	3.90	336		conserved	conserved hypothetical	MON01988	MUL_1988

delta / length	locus	Average non	sd_non	Average syn	sd_syn	delta	CDS length	gene	fgroup	product	ortholog	mulocus
	MMAR_1745								hypotheticals	protein		
0.0113	MMAR_0050	4.93	0.69	1.28	0.64	3.66	324		cell wall and cell processes	conserved hypothetical secreted protein	MON00049	MUL_0049
0.0108	MMAR_5549	4.48	0.90	1.00	-	3.48	321		conserved hypotheticals	conserved hypothetical protein	MON00788	MUL_0788
0.0107	MMAR_1332	6.03	1.13	1.17	0.38	4.86	456		cell wall and cell processes	conserved hypothetical membrane protein	MON02547	MUL_2547
0.0104	MMAR_2889	7.90	0.96	1.97	0.32	5.93	573		cell wall and cell processes	conserved Mce associated membrane protein	MON02863	MUL_2863
0.0101	MMAR_5544	1.79	0.41	0.79	0.41	1.00	99		unknown	hypothetical protein	MON04906	MUL_4906
0.0100	MMAR_0302	10.93	4.40	3.07	0.25	7.86	789		intermediary metabolism and respiration	short-chain type dehydrogenase/reductase	MON30271	MUL_4820
0.0099	MMAR_3508	7.86	0.63	2.83	0.38	5.03	507		cell wall and cell processes	conserved hypothetical secreted protein	MON02761	MUL_2761
0.0099	MMAR_4936	2.93	0.45	0.10	0.40	2.83	285		conserved hypotheticals	conserved hypothetical protein	MON00469	MUL_0469
0.0099	MMAR_3183	9.10	1.86	3.48	0.97	5.62	567		conserved hypotheticals	hypothetical alanine rich protein	MON03491	MUL_3491
0.0097	MMAR_2899	2.59	0.81	-	-	2.59	267		conserved hypotheticals	conserved hypothetical protein	MON02856	MUL_2856
0.0094	MMAR_3953	9.47	1.20	1.16	0.40	8.31	885		conserved hypotheticals	conserved hypothetical protein	MON03808	MUL_3808
0.0094	MMAR_3544	10.21	3.00	2.86	0.82	7.34	783		conserved hypotheticals	conserved hypothetical protein	MON02775	MUL_2775
0.0094	MMAR_2498	1.66	0.71	-	-	1.66	177		conserved hypotheticals	conserved hypothetical protein	MON01682	MUL_1682
0.0092	MMAR_5543	2.34	1.81	0.14	0.51	2.21	240		unknown	hypothetical protein	MON00133	MUL_0133
0.0091	MMAR_5545	6.00	1.23	2.00	-	4.00	438		conserved hypotheticals	conserved hypothetical protein	MON00290	MUL_0290
0.0089	MMAR_5556	3.62	1.00	0.83	0.38	2.79	315		unknown	hypothetical protein	MON04235	MUL_4235
0.0088	MMAR_4996	6.48	0.81	0.10	0.30	6.38	723		conserved hypotheticals	conserved hypothetical protein	MON04071	MUL_4071
0.0088	MMAR_2901	3.24	0.62	-	-	3.24	369		conserved hypotheticals	conserved hypothetical protein	MON02858	MUL_2858
0.0087	MMAR_4295	1.28	0.74	-	-	1.28	147		conserved hypotheticals	conserved hypothetical protein	MON01003	MUL_1003
0.0084	MMAR_2785	3.41	1.13	0.93	0.25	2.48	294		cell wall and cell processes	conserved hypothetical membrane protein	MON01141	MUL_1141

delta / length	locus	Average non	sd_non	Average syn	sd_syn	delta	CDS length	gene	fgroup	product	ortholog	mulocus
0.0084	MMAR_3026	1.97	0.18	0.03	0.18	1.93	231		conserved hypotheticals	conserved hypothetical protein	MON02267	MUL_2267
0.0083	MMAR_3022	4.41	1.16	1.76	0.68	2.66	318		conserved hypotheticals	conserved hypothetical protein	MON02263	MUL_2263
0.0083	MMAR_4020	8.03	1.90	0.59	0.56	7.45	897	echA4_2	lipid metabolism	enoyl-CoA hydratase EchA4_2	MON03885	MUL_3885
0.0083	MMAR_5466	5.74	0.95	3.16	0.51	2.59	312	esxF	cell wall and cell processes	EsaT-6 like protein EsxF	MON05055	MUL_5055
0.0083	MMAR_4111	3.83	0.38	0.45	0.50	3.38	408		intermediary metabolism and respiration	pyridoxamine 5'-phosphate oxidase	MON03977	MUL_3977
0.0079	MMAR_2372	1.83	0.38	-	-	1.83	231		unknown	hypothetical protein	MON01548	MUL_1548
0.0079	MMAR_3582	3.10	0.40	1.00	-	2.10	267		unknown	hypothetical protein	MON06458	MUL_5087
0.0078	MMAR_0248	13.50	2.05	6.81	0.70	6.69	861		intermediary metabolism and respiration	short-chain type dehydrogenase/reductase	MON04865	MUL_4865
0.0077	MMAR_1056	17.93	3.89	4.14	0.43	13.79	1,803	sspA	cell wall and cell processes	signal peptide peptidase IV SppA	MON00815	MUL_0815
0.0076	MMAR_2773	8.38	0.61	3.76	0.50	4.62	609		cell wall and cell processes	conserved secreted protein	MON02974	MUL_2974

List of core *M. marinum* CDS with dN/dS > 1.0 in representative *M. ulcerans* isolates (Mm_1726, Mm_99/84, Mm_99/87, Mm_99/89, Mu_CC40299, Mu_JKD8071, Mu_DL045, Mu_1G897, Mu_8765, Mu_05142109, Mu_Agy99).

Table 7 *M. marinum* orthologs of *M. tuberculosis* T-cell antigens

H37Rv locus	Mm Locus	Mu Locus	Percent identity	Match Length	Gene	Functional Group	Product	Comment
Rv0222	MMAR_0465	MUL_1114	91.34	254	echA1	lipid metabolism	enoyl-CoA hydratase EchA1	
Rv0287	MMAR_3001		85.57	97	esxG_1	cell wall and cell processes	EsaT-6 like protein EsxG_1	missing Mu_Agy99, paralog in Mm
Rv0287	MMAR_0546	MUL_1209	91.75	97	esxG	cell wall and cell processes	EsaT-6 like protein EsxG	
Rv0309	MMAR_0559	MUL_1223	88.07	218		cell wall and cell processes	conserved exported protein	
Rv0440	MMAR_0759	MUL_1393	95.07	527	groEL2		60 kDa chaperonin 2 GroEL2	
Rv0670	MMAR_0999	MUL_0751	86.51	252	end	information pathways	endonuclease iv (apurinase) End	
Rv1157c	MMAR_4294	MUL_1004	91.37	139		cell wall and cell processes	conserved hypothetical secreted protein	only 34% of CDS matches
Rv1256c	MMAR_4184	MUL_4486	86.53	401	cyp130A4P	intermediary metabolism and respiration	cytochrome P450 130A4 Cyp130A4	pseudogene in Mu_Agy99
Rv1280c	MMAR_4139	MUL_4002	81.31	567	oppA	cell wall and cell processes	periplasmic oligopeptide-binding lipoprotein OppA	
Rv1291c	MMAR_4121	MUL_3987	81.42	113		cell wall and cell processes	conserved hypothetical secreted protein	
Rv1461	MMAR_2266	MUL_1862	94.47	253		conserved hypotheticals	conserved protein	only 52% of CDS matches
Rv2182c	MMAR_3226	MUL_3537	89.07	247		lipid metabolism	1-acylglycerol-3-phosphate O-acyltransferase	
Rv2476c	MMAR_3829	MUL_3756	84.26	1626	gdh	intermediary metabolism and respiration	NAD-dependent glutamate dehydrogenase Gdh	pseudogene in Mu_Agy99
Rv2715	MMAR_1997	MUL_3358	85.04	341		intermediary metabolism and respiration	conserved hypothetical hydrolase	
Rv3207c	MMAR_1351	MUL_2528	84.86	284		conserved hypotheticals	conserved hypothetical protein	
Rv3296	MMAR_1238	MUL_2649	83.81	1532	lhr	information pathways	ATP-dependent helicase Lhr	pseudogene in Mu_Agy99
Rv3803c	MMAR_5367	MUL_4986	85.38	301	fbpD	cell wall and cell processes	secreted Mpt51/Mpb51 antigen protein FbpD	
Rv3804c	MMAR_5368	MUL_4987	84.64	332	fbpA	cell wall and cell processes	secreted antigen 85-A FbpA	
Rv3846	MMAR_5396	MUL_5018	96.62	207	sodA		superoxide dismutase [fe] SodA	
Rv3871	MMAR_5446	MUL_5038	92.72	591		conserved hypotheticals	conserved hypothetical protein	pseudogene in Mu_Agy99

List of *M. tuberculosis* T cell antigens with orthologs in *M. marinum* "M" and *M. ulcerans* Agy99. Orthologs have > 80% amino acid identity.

Table 8 Core SNPs

- (a) Core SNPs - Reference *M. marinum* "M"
- (b) Core SNPs – Reference *M. ulcerans* Agy99

Table 9 Diagnostic Regions

- (a) Core Diagnostic Segments - Reference *M. marinum* "M"
- (b) Core Diagnostic CDS - Reference *M. marinum* "M"
- (c) Core Diagnostic CDS – Reference *M. ulcerans* Agy99

Table 10 Ancestral Pseudogenes

Table 8 (a)

Core SNPs - Reference M. marinum "M"

Notes:

1. SNP types, syn: synonymous SNP, non:non-synonymous SNP, int: Intergenic SNP
2. Gap for intergenic SNPs: nearest CDS within 150bp of snpos
3. Functional groups from genbank reference CP000854

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
1329	syn	GA	MMAR_0001	-		information pathways	chromosomal replication initiator protein DnaA
5568	syn	TC	MMAR_0005	-		information pathways	DNA gyrase (subunit B) GyrB
8580	syn	CG	MMAR_0006	-		information pathways	DNA gyrase (subunit A) GyrA
8620	syn	CT	MMAR_0006	-		information pathways	DNA gyrase (subunit A) GyrA
8694	syn	TC	MMAR_0006	-		information pathways	DNA gyrase (subunit A) GyrA
9217	syn	CT	MMAR_0006	-		information pathways	DNA gyrase (subunit A) GyrA
9393	syn	CT	MMAR_0006	-		information pathways	DNA gyrase (subunit A) GyrA
11259	int	CT		104	MMAR_0008	conserved hypothetical	conserved hypothetical protein
11265	int	AG		98	MMAR_0008	conserved hypothetical	conserved hypothetical protein
11280	int	CT		83	MMAR_0008	conserved hypothetical	conserved hypothetical protein
11366	non	GA	MMAR_0008	-		conserved hypothetical	conserved hypothetical protein
11989	syn	GC	MMAR_0008	-		conserved hypothetical	conserved hypothetical protein
12189	non	GA	MMAR_0008	-		conserved hypothetical	conserved hypothetical protein
12428	syn	CA	MMAR_0009	-		regulatory proteins	transcriptional regulator
12597	non	GA	MMAR_0009	-		regulatory proteins	transcriptional regulator
13056	int	GA	MMAR_0009	68	MMAR_0009	regulatory proteins	transcriptional regulator
13378	non	CG	MMAR_0010	-		conserved hypothetical	conserved hypothetical protein
14360	non	GC	MMAR_0012	-		cell wall and cell processes	conserved hypothetical membrane protein
16304	syn	CG	MMAR_0015	-		intermediary metabolism and respiration	anthranilate synthase component II TrpG
16307	syn	CG	MMAR_0015	-		intermediary metabolism and respiration	anthranilate synthase component II TrpG
17182	syn	TC	MMAR_0016	-		regulatory proteins	serine/threonine-protein kinase B PknB
17647	syn	CT	MMAR_0016	-		regulatory proteins	serine/threonine-protein kinase B PknB
17650	syn	GC	MMAR_0016	-		regulatory proteins	serine/threonine-protein kinase B PknB
18695	syn	GA	MMAR_0017	-		regulatory proteins	serine/threonine-protein kinase a PknA
21412	syn	AT	MMAR_0019	-		cell wall and cell processes	cell division protein RodA
21904	non	CG	MMAR_0019	-		cell wall and cell processes	cell division protein RodA
26835	int	TC		-			
33755	non	GA	MMAR_0030	-		intermediary metabolism and respiration	shortchain dehydrogenase
33911	syn	GT	MMAR_0030	-		intermediary metabolism and respiration	shortchain dehydrogenase
35564	syn	AG	MMAR_0032	-		conserved hypothetical	conserved hypothetical protein
35873	syn	GA	MMAR_0032	-		conserved hypothetical	conserved hypothetical protein
35935	syn	AG	MMAR_0032	-		conserved hypothetical	conserved hypothetical protein
36214	syn	TC	MMAR_0033	-		cell wall and cell processes	conserved hypothetical membrane protein
36541	syn	GA	MMAR_0033	-		cell wall and cell processes	conserved hypothetical membrane protein
36564	non	CT	MMAR_0033	-		cell wall and cell processes	conserved hypothetical membrane protein
36616	non	CT	MMAR_0033	-		cell wall and cell processes	conserved hypothetical membrane protein
38665	syn	GC	MMAR_0035	-		cell wall and cell processes	ABC transporter permease
50024	syn	C-	MMAR_0050	-		conserved hypothetical	conserved hypothetical secreted protein
50025	syn	T-	MMAR_0050	-		conserved hypothetical	conserved hypothetical secreted protein
50064	syn	CT	MMAR_0051	-		conserved hypothetical	conserved hypothetical protein
52673	syn	CT	MMAR_0053	-		conserved hypothetical	conserved hypothetical protein
56490	syn	CA	MMAR_0057	-		information pathways	leucyl-tRNA synthetase LeuS
56958	syn	CT	MMAR_0057	-		information pathways	leucyl-tRNA synthetase LeuS
58296	syn	CT	MMAR_0057	-		information pathways	leucyl-tRNA synthetase LeuS
58641	int	TC		21	MMAR_0057	information pathways	leucyl-tRNA synthetase LeuS
58720	non	GT	MMAR_0058	-		intermediary metabolism and respiration	short-chain type oxidoreductase
59520	non	CT	MMAR_0059	-		regulatory proteins	transcriptional regulatory protein
59593	syn	CT	MMAR_0059	-		regulatory proteins	transcriptional regulatory protein
60087	syn	GA	MMAR_0060	-		cell wall and cell processes	glutamine ABC transporter ATP-binding protein
60811	non	CG	MMAR_0061	-		cell wall and cell processes	ABC transporter permease protein GinQ
61642	syn	TG	MMAR_0061	-		cell wall and cell processes	ABC transporter permease protein GinQ
64202	int	TC		17	MMAR_0063	intermediary metabolism and respiration	oxidoreductase
64417	syn	C-	MMAR_0064	-		lipid metabolism	hydrolase
64418	syn	G-	MMAR_0064	-		lipid metabolism	hydrolase
64419	syn	T-	MMAR_0064	-		lipid metabolism	hydrolase
66636	syn	GA	MMAR_0066	-		conserved hypothetical	conserved hypothetical protein
71270	syn	CA	MMAR_0070	-		cell wall and cell processes	conserved hypothetical transmembrane protein
71276	syn	GA	MMAR_0070	-		cell wall and cell processes	conserved hypothetical transmembrane protein
71294	syn	GA	MMAR_0070	-		cell wall and cell processes	conserved hypothetical transmembrane protein
73934	syn	AG	MMAR_0073	-		information pathways	single-strand binding protein Ssb
75568	int	GA		121	MMAR_0076	information pathways	replicative DNA helicase DnaB
76375	syn	CG	MMAR_0076	-		information pathways	replicative DNA helicase DnaB
94180	non	TC	MMAR_0093	-		cell wall and cell processes	integral membrane efflux protein ErmB
94403	syn	GA	MMAR_0093	-		cell wall and cell processes	integral membrane efflux protein ErmB
94643	syn	GA	MMAR_0093	-		cell wall and cell processes	integral membrane efflux protein ErmB
94862	syn	CA	MMAR_0093	-		cell wall and cell processes	integral membrane efflux protein ErmB
164389	non	CT	MMAR_0134	-		conserved hypothetical	conserved hypothetical protein
164450	non	AG	MMAR_0134	-		conserved hypothetical	conserved hypothetical protein
164531	non	AG	MMAR_0134	-		conserved hypothetical	conserved hypothetical protein
164818	syn	CT	MMAR_0135	-		information pathways	ADP-ribosyl pyrophosphatase RppH
166249	non	CT	MMAR_0136	-		cell wall and cell processes	conserved hypothetical integral membrane protein
166790	syn	CT	MMAR_0137	-		conserved hypothetical	conserved hypothetical protein
167310	syn	GA	MMAR_0138	-		conserved hypothetical	conserved hypothetical protein
168473	syn	CT	MMAR_0139	-		lipid metabolism	acyl-CoA dehydrogenase FadE6_1
178146	non	CG	MMAR_0148	-		cell wall and cell processes	glycosyltransferase
178403	int	GA		65	MMAR_0148	cell wall and cell processes	glycosyltransferase
181072	non	GA	MMAR_0151	-		virulence; detoxification; adaptation	enhanced intracellular survival protein Eis1
181180	non	AT	MMAR_0151	-		virulence; detoxification; adaptation	enhanced intracellular survival protein Eis1
188803	syn	CG	MMAR_0158	-		intermediary metabolism and respiration	isocitrate dehydrogenase [NADP] Icd2
190047	int	TC		-			
190453	int	GC		79	MMAR_0159	cell wall and cell processes	conserved hypothetical membrane protein
190908	non	GT	MMAR_0159	-		cell wall and cell processes	conserved hypothetical membrane protein
190996	non	AG	MMAR_0159	-		cell wall and cell processes	conserved hypothetical membrane protein
192164	syn	CT	MMAR_0161	-		cell wall and cell processes	conserved hypothetical membrane protein
192623	syn	CT	MMAR_0161	-		cell wall and cell processes	conserved hypothetical membrane protein

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
193227	Int	GT	MMAR_0162	34	MMAR_0162	cell wall and cell processes	conserved hypothetical transmembrane protein
194160	syn	CT	MMAR_0162	-		cell wall and cell processes	conserved hypothetical transmembrane protein
195032	non	CG	MMAR_0163	-		conserved hypotheticals	conserved protein
208458	non	CG	MMAR_0177	-			MCE-family protein Mce6A
208985	syn	GC	MMAR_0177	-			MCE-family protein Mce6A
209938	non	GC	MMAR_0178	-			MCE-family protein Mce6B
210139	non	AG	MMAR_0178	-			MCE-family protein Mce6B
210655	non	GA	MMAR_0179	-			MCE-family protein Mce6C
211279	syn	CT	MMAR_0179	-			MCE-family protein Mce6C
214393	non	AG	MMAR_0182	-			MCE-family protein Mce6F
214458	syn	CG	MMAR_0182	-			MCE-family protein Mce6F
235619	non	TC	MMAR_0205	-		intermediary metabolism and respiration	flavoprotein
236004	syn	CT	MMAR_0205	-		intermediary metabolism and respiration	flavoprotein
236700	syn	CT	MMAR_0207	-		intermediary metabolism and respiration	L-serine dehydratase SdaA
236799	syn	AG	MMAR_0207	-		intermediary metabolism and respiration	L-serine dehydratase SdaA
236838	non	CG	MMAR_0207	-		intermediary metabolism and respiration	L-serine dehydratase SdaA
238164	non	CT	MMAR_0208	-		intermediary metabolism and respiration	serine hydroxymethyltransferase GlyA2
238735	non	CA	MMAR_0208	-		intermediary metabolism and respiration	serine hydroxymethyltransferase GlyA2
239383	syn	TC	MMAR_0209	-		intermediary metabolism and respiration	glycine cleavage system H protein GcvH_1
240073	non	TC	MMAR_0210	-		intermediary metabolism and respiration	aminomethyltransferase GcvT_1ne
240145	non	CT	MMAR_0210	-		intermediary metabolism and respiration	aminomethyltransferase GcvT_1ne
241000	syn	CT	MMAR_0211	-		intermediary metabolism and respiration	glycine dehydrogenase GcvB_1
244490	non	CA	MMAR_0212	-		conserved hypotheticals	conserved hypothetical oxidoreductase
244665	syn	TC	MMAR_0212	-		conserved hypotheticals	conserved hypothetical oxidoreductase
244821	syn	TC	MMAR_0212	-		conserved hypotheticals	conserved hypothetical oxidoreductase
253269	non	GA	MMAR_0220	-		conserved hypotheticals	conserved hypothetical protein
253565	non	CA	MMAR_0220	-		conserved hypotheticals	conserved hypothetical protein
253599	syn	GA	MMAR_0220	-		conserved hypotheticals	conserved hypothetical protein
253785	syn	CT	MMAR_0220	-		conserved hypotheticals	conserved hypothetical protein
253799	non	GT	MMAR_0220	-		conserved hypotheticals	conserved hypothetical protein
254100	syn	CT	MMAR_0220	-		conserved hypotheticals	conserved hypothetical protein
254772	non	CT	MMAR_0221	-		conserved hypotheticals	conserved hypothetical protein
254850	non	GA	MMAR_0221	-		conserved hypotheticals	conserved hypothetical protein
255194	syn	GC	MMAR_0221	-		conserved hypotheticals	conserved hypothetical protein
257289	syn	CA	MMAR_0224	-		regulatory protein	transcriptional regulatory protein
260533	non	AG	MMAR_0228	-		conserved hypotheticals	conserved hypothetical protein
261595	non	TG	MMAR_0229	-		cell wall and cell processes	conserved hypothetical protein
261644	Int	TC	MMAR_0229	39	MMAR_0229	cell wall and cell processes	conserved hypothetical protein
261874	non	GC		-		intermediary metabolism and respiration	dioxygenase
262276	syn	GT		-		intermediary metabolism and respiration	dioxygenase
262792	syn	CT		-		intermediary metabolism and respiration	dioxygenase
263024	non	CT		-		cell wall and cell processes	cation transporter p-type ATPase CtpA_1
263202	syn	GA		-		cell wall and cell processes	cation transporter p-type ATPase CtpA_1
263744	non	CT		-		cell wall and cell processes	cation transporter p-type ATPase CtpA_1
265035	syn	GT		-		cell wall and cell processes	cation transporter p-type ATPase CtpA_1
265241	non	CT		-		cell wall and cell processes	cation transporter p-type ATPase CtpA_1
266223	syn	CT		-		conserved hypotheticals	conserved hypothetical protein
268400	non	AG	MMAR_0236	-		conserved hypotheticals	conserved hypothetical protein
270215	syn	CT	MMAR_0239	-		intermediary metabolism and respiration	monoxygenase
281363	Int	CA	MMAR_0251	109	MMAR_0251	intermediary metabolism and respiration	bifunctional Mta/Sah nucleosidase Mtn
283338	non	GA		-		intermediary metabolism and respiration	bifunctional Mta/Sah nucleosidase Mtn
283565	syn	CT		-		intermediary metabolism and respiration	bifunctional Mta/Sah nucleosidase Mtn
284077	Int	AC		50	MMAR_0251	intermediary metabolism and respiration	bifunctional Mta/Sah nucleosidase Mtn
286420	syn	GC		-		cell wall and cell processes	conserved transmembrane transport protein MmpL5_4
286957	syn	GA		-		cell wall and cell processes	conserved transmembrane transport protein MmpL5_4
287677	syn	CT		-		cell wall and cell processes	conserved transmembrane transport protein MmpL5_4
287914	syn	CT		-		cell wall and cell processes	conserved transmembrane transport protein MmpL5_4
288178	syn	CT		-		cell wall and cell processes	conserved transmembrane transport protein MmpL5_4
288451	syn	AC		-		cell wall and cell processes	conserved transmembrane transport protein MmpL5_4
288692	non	AG	MMAR_0255	-		cell wall and cell processes	conserved transmembrane transport protein MmpL5_4
290139	non	GA	MMAR_0256	-		lipid metabolism	non-ribosomal peptide synthetase
290251	syn	GT	MMAR_0256	-		lipid metabolism	non-ribosomal peptide synthetase
290341	syn	GA	MMAR_0256	-		lipid metabolism	non-ribosomal peptide synthetase
290521	syn	CG	MMAR_0256	-		lipid metabolism	non-ribosomal peptide synthetase
290943	syn	AG	MMAR_0256	-		lipid metabolism	non-ribosomal peptide synthetase
291374	non	CA	MMAR_0256	-		lipid metabolism	non-ribosomal peptide synthetase
292221	non	GA	MMAR_0256	-		lipid metabolism	non-ribosomal peptide synthetase
292534	syn	CT	MMAR_0256	-		lipid metabolism	non-ribosomal peptide synthetase
292606	syn	AG	MMAR_0256	-		lipid metabolism	non-ribosomal peptide synthetase
292889	non	GA	MMAR_0256	-		lipid metabolism	non-ribosomal peptide synthetase
293020	syn	AG	MMAR_0256	-		lipid metabolism	non-ribosomal peptide synthetase
293026	non	GT	MMAR_0256	-		lipid metabolism	non-ribosomal peptide synthetase
293187	syn	GC	MMAR_0257	-		conserved hypotheticals	conserved hypothetical protein
293479	syn	GT	MMAR_0258	-		lipid metabolism	fatty-acid-CoA ligase FadD10
294058	syn	GA	MMAR_0258	-		lipid metabolism	fatty-acid-CoA ligase FadD10
294691	syn	GA	MMAR_0258	-		lipid metabolism	fatty-acid-CoA ligase FadD10
297517	Int	TC	MMAR_0269	51	MMAR_0269	cell wall and cell processes	conserved membrane protein
299602	syn	GA		-		cell wall and cell processes	cation transporter p-type ATPase a CtpA
301549	syn	GA		-		cell wall and cell processes	cation transporter p-type ATPase a CtpA
301716	non	CT		-		cell wall and cell processes	cation transporter p-type ATPase a CtpA
302038	syn	CT		-		cell wall and cell processes	cation transporter p-type ATPase a CtpA
303408	syn	GA		-		cell wall and cell processes	conserved hypothetical secreted protein
306293	syn	GC	MMAR_0269	-		cell wall and cell processes	cation-transporter p-type ATPase B CtpB
306465	non	GA	MMAR_0269	-		cell wall and cell processes	cation-transporter p-type ATPase B CtpB
306596	syn	GT	MMAR_0269	-		cell wall and cell processes	cation-transporter p-type ATPase B CtpB
306754	non	CT	MMAR_0269	-		cell wall and cell processes	cation-transporter p-type ATPase B CtpB
307161	non	GA	MMAR_0269	-		cell wall and cell processes	cation-transporter p-type ATPase B CtpB
307730	syn	GA	MMAR_0269	-		cell wall and cell processes	cation-transporter p-type ATPase B CtpB
308745	Int	CT	MMAR_0269	51	MMAR_0269	cell wall and cell processes	cation-transporter p-type ATPase B CtpB
331764	non	TC		-		conserved hypotheticals	conserved hypothetical protein
333380	syn	CT		-		conserved hypotheticals	conserved protein
334334	non	GA	MMAR_0294	-		information pathways	SOS ribosomal protein L31 RsmB_1
334844	syn	TC	MMAR_0295	-		intermediary metabolism and respiration	short-chain type dehydrogenase/reductase
338236	syn	CT	MMAR_0297	-		cell wall and cell processes	cation-transporter ATPase I CtpI
338410	syn	TC	MMAR_0297	-		cell wall and cell processes	cation-transporter ATPase I CtpI

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
342740	Int	A-		11	MMAR_0298	conserved hypotheticals	conserved protein
346596	syn	TC	MMAR_0302	-		intermediary metabolism and respiration	short-chain type dehydrogenase/reductase
348046	non	GA	MMAR_0303	-		lipid metabolism	acyl-CoA synthetase
348190	syn	CT	MMAR_0303	-		lipid metabolism	acyl-CoA synthetase
349485	non	CG	MMAR_0305	-		conserved hypotheticals	conserved hypothetical protein
349938	non	CA	MMAR_0305	-		conserved hypotheticals	conserved hypothetical protein
351228	non	GC	MMAR_0306	-		intermediary metabolism and respiration	short-chain type dehydrogenase/reductase
351510	non	AC	MMAR_0306	-		intermediary metabolism and respiration	short-chain type dehydrogenase/reductase
352553	syn	CT	MMAR_0307	-		intermediary metabolism and respiration	dixygenase
352929	syn	CT	MMAR_0307	-		intermediary metabolism and respiration	dixygenase
354799	non	AT	MMAR_0309	-		intermediary metabolism and respiration	monooxygenase
354807	syn	CT	MMAR_0309	-		intermediary metabolism and respiration	monooxygenase
359550	syn	CT	MMAR_0312	-		intermediary metabolism and respiration	transmembrane acyltransferase
362438	Int	CT		85	MMAR_0314	conserved hypotheticals	conserved hypothetical protein
362766	syn	GA	MMAR_0315	-		cell wall and cell processes	divalent cation-transport integral membrane protein
363631	non	GT	MMAR_0315	-		cell wall and cell processes	divalent cation-transport integral membrane protein
364115	non	AC	MMAR_0315	-		cell wall and cell processes	divalent cation-transport integral membrane protein
364555	syn	CT	MMAR_0316	-		cell wall and cell processes	conserved hypothetical secreted protein
366396	syn	CT	MMAR_0318	-		intermediary metabolism and respiration	oxalyl-CoA decarboxylase OxaC
368857	syn	CT	MMAR_0319	-		lipid metabolism	fatty-acid-CoA ligase FadD7
369780	non	TA	MMAR_0319	-		lipid metabolism	fatty-acid-CoA ligase FadD7
370022	non	GA	MMAR_0320	-		cell wall and cell processes	conserved hypothetical membrane protein
370263	non	GT	MMAR_0320	-		cell wall and cell processes	conserved hypothetical membrane protein
372031	syn	GC	MMAR_0321	-		information pathways	elongation factor G FusA2
372954	syn	TC	MMAR_0322	-		conserved hypotheticals	conserved hypothetical protein
375216	syn	CT	MMAR_0325	-			trehalose synthase TreS
379343	syn	CA	MMAR_0328	-		cell wall and cell processes	secreted antigen 85-C FbpC
380587	Int	CT		14	MMAR_0329	intermediary metabolism and respiration	phosphoesterase
382055	syn	CT	MMAR_0331	-		lipid metabolism	acyl-CoA dehydrogenase FadE1
382227	non	AG	MMAR_0331	-		lipid metabolism	acyl-CoA dehydrogenase FadE1
382801	non	CT	MMAR_0331	-		lipid metabolism	acyl-CoA dehydrogenase FadE1
387314	syn	TC	MMAR_0335	-		intermediary metabolism and respiration	flavodoxin oxidoreductase
387859	non	GA	MMAR_0336	-		lipid metabolism	linoleyl-CoA desaturase DesA3_2
389463	syn	CT	MMAR_0337	-		conserved hypotheticals	conserved hypothetical protein
393177	syn	TG	MMAR_0341	-		conserved hypotheticals	conserved hypothetical protein
394436	syn	AG	MMAR_0342	-			epoxide hydrolase Ephf
395070	syn	GA	MMAR_0343	-		intermediary metabolism and respiration	zinc-dependent alcohol dehydrogenase
396377	non	CG	MMAR_0345	-		regulatory proteins	transcriptional regulatory protein
396420	syn	CT	MMAR_0345	-		regulatory proteins	transcriptional regulatory protein
396495	syn	CT	MMAR_0345	-		regulatory proteins	transcriptional regulatory protein
398840	Int	CG		1	MMAR_0348	conserved hypotheticals	conserved hypothetical protein
398908	non	CT	MMAR_0348	-		conserved hypotheticals	conserved hypothetical protein
399880	syn	CT	MMAR_0349	-		intermediary metabolism and respiration	oxidoreductase
404634	non	TC	MMAR_0354	-		conserved hypotheticals	conserved protein
406909	syn	GA	MMAR_0357	-		intermediary metabolism and respiration	O-Methyltransferase
406954	syn	CT	MMAR_0357	-		intermediary metabolism and respiration	O-Methyltransferase
440315	non	CT	MMAR_0374	-		lipid metabolism	acyl-CoA dehydrogenase FadE2
440316	non	TG	MMAR_0374	-		lipid metabolism	acyl-CoA dehydrogenase FadE2
440731	Int	TC		79	MMAR_0375	conserved hypotheticals	conserved hypothetical protein
441091	syn	CA	MMAR_0375	-		conserved hypotheticals	conserved hypothetical protein
441690	Int	CG		64	MMAR_0376	conserved hypotheticals	conserved protein
442159	non	TC	MMAR_0376	-		conserved hypotheticals	conserved protein
442285	Int	CG		61	MMAR_0376	conserved hypotheticals	conserved protein
445807	syn	CT	MMAR_0381	-		regulatory proteins	transcriptional regulatory protein (possibly TetR-family)
446293	Int	CT		11	MMAR_0382	PE/PE	PE-PGRS family protein
446385	Int	TC		95	MMAR_0381	regulatory proteins	transcriptional regulatory protein (possibly TetR-family)
449432	Int	TC		53	MMAR_0383	PE/PE	PE family protein
450744	Int	AG		-			
452148	non	TA	MMAR_0385	-		conserved hypotheticals	conserved hypothetical protein
452478	syn	CT	MMAR_0386	-		conserved hypotheticals	conserved hypothetical protein
455469	syn	TC	MMAR_0388	-		intermediary metabolism and respiration	oxidoreductase
455749	syn	AG	MMAR_0389	-		regulatory proteins	conserved hypothetical regulatory protein
456308	syn	GA	MMAR_0390	-		conserved hypotheticals	conserved hypothetical protein
456815	syn	CA	MMAR_0390	-		conserved hypotheticals	conserved hypothetical protein
457867	Int	TC		48	MMAR_0392	conserved hypotheticals	conserved hypothetical protein
460081	syn	TC	MMAR_0394	-		conserved hypotheticals	conserved hypothetical protein
460230	non	CT	MMAR_0394	-		conserved hypotheticals	conserved hypothetical protein
460641	syn	CT	MMAR_0395	-		conserved hypotheticals	conserved hypothetical protein
460662	syn	GA	MMAR_0395	-		conserved hypotheticals	conserved hypothetical protein
461634	Int	CT		74	MMAR_0396	lipid metabolism	acyl-CoA transferase
464691	non	GA	MMAR_0399	-		intermediary metabolism and respiration	cytochrome P450 191A3 Cyp191A3
465167	syn	CT	MMAR_0399	-		intermediary metabolism and respiration	cytochrome P450 191A3 Cyp191A3
466047	syn	CG	MMAR_0400	-		intermediary metabolism and respiration	dehydrogenase
467040	non	CG	MMAR_0401	-		conserved hypotheticals	conserved hypothetical protein
468090	non	CG	MMAR_0403	-		intermediary metabolism and respiration	monoxygenase
468573	syn	AG	MMAR_0403	-		intermediary metabolism and respiration	monoxygenase
469089	syn	GA	MMAR_0403	-		intermediary metabolism and respiration	monoxygenase
469263	non	GA	MMAR_0403	-		intermediary metabolism and respiration	monoxygenase
470354	syn	GC	MMAR_0404	-		intermediary metabolism and respiration	esterase LipW
470770	non	GT	MMAR_0405	-		intermediary metabolism and respiration	zinc-type alcohol dehydrogenase (E subunit) AdhE
471785	syn	CA	MMAR_0406	-		conserved hypotheticals	conserved hypothetical protein
472925	non	TC	MMAR_0408	-		regulatory proteins	transcriptional regulatory protein (probably GntR-family)
477654	syn	CT	MMAR_0412	-			MCE-family protein Mce1A
478376	syn	CT	MMAR_0413	-			MCE-family protein Mce1B
479482	syn	GA	MMAR_0414	-		virulence; detoxification; adaptation	MCE-family protein Mce1C
479630	syn	CT	MMAR_0414	-		virulence; detoxification; adaptation	MCE-family protein Mce1C
479977	syn	CT	MMAR_0414	-		virulence; detoxification; adaptation	MCE-family protein Mce1C
481422	syn	GA	MMAR_0415	-			MCE-family protein Mce1D
481737	syn	GT	MMAR_0415	-			MCE-family protein Mce1D
481745	syn	GA	MMAR_0415	-			MCE-family protein Mce1D
482543	syn	CA	MMAR_0416	-			MCE-family lipoprotein LprK (MCE-family lipoprotein Mce1E)
483140	syn	GA	MMAR_0416	-			MCE-family lipoprotein LprK (MCE-family lipoprotein Mce1E)
483344	non	GA	MMAR_0416	-			MCE-family lipoprotein LprK (MCE-family lipoprotein Mce1E)
484009	syn	TC	MMAR_0417	-			MCE-family protein Mce1F
484108	syn	GT	MMAR_0417	-			MCE-family protein Mce1F

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
484123	syn	CG	MMAR_0417	-		MCE-family protein Mce1F	
484351	syn	GA	MMAR_0417	-		MCE-family protein Mce1F	
484487	syn	CT	MMAR_0417	-		MCE-family protein Mce1F	
485440	non	GC	MMAR_0418	-		cell wall and cell processes	conserved Mce associated membrane protein
485667	non	GA	MMAR_0418	-		cell wall and cell processes	conserved Mce associated membrane protein
487655	non	AG	MMAR_0421	-		cell wall and cell processes	conserved Mce associated membrane protein
487710	syn	AG	MMAR_0421	-		cell wall and cell processes	conserved Mce associated membrane protein
492279	non	GC	MMAR_0425	-		conserved hypotheticals	conserved protein
492590	non	TC	MMAR_0425	-		conserved hypotheticals	conserved protein
493299	non	CG	MMAR_0425	-		conserved hypotheticals	conserved protein
493706	non	AG	MMAR_0426	-		information pathways	alternative RNA polymerase sigma factor SigG
496646	syn	CT	MMAR_0430	-		intermediary metabolism and respiration	beta-glucosidase BolS
503649	syn	GA	MMAR_0432	-		intermediary metabolism and respiration	dihydroxy-acid dehydratase IlvD
504956	int	CT	113 MMAR_0433	44 MMAR_0436		conserved hypotheticals	conserved hypothetical protein
507516	int	CA				regulatory protein	transcriptional regulatory protein
508232	syn	GC	MMAR_0437	-		intermediary metabolism and respiration	oxidoreductase
509207	syn	G-	MMAR_0437	-		intermediary metabolism and respiration	oxidoreductase
512339	syn	GA	MMAR_0438	-		intermediary metabolism and respiration	zinc metalloprotease
513735	syn	AG	MMAR_0440	-		cell wall and cell processes	conserved transmembrane protein
520320	syn	GT	MMAR_0445	-		cell wall and cell processes	conserved transmembrane protein
522238	syn	GA	MMAR_0446	-		cell wall and cell processes	conserved transmembrane transport protein MmpL3
524110	non	TC	MMAR_0447	-		conserved hypotheticals	conserved hypothetical protein
524350	syn	GC	MMAR_0447	-		conserved hypotheticals	conserved hypothetical protein
525527	int	CT	77 MMAR_0449			conserved hypotheticals	conserved hypothetical protein
525755	non	TC				conserved hypotheticals	conserved hypothetical protein
526936	non	CT	MMAR_0449	-		cell wall and cell processes	conserved secreted protein
529389	syn	GC	MMAR_0451	-		intermediary metabolism and respiration	iron-regulated phosphoenolpyruvate carboxykinase [GTP] PckA
530163	syn	GC	MMAR_0451	-		intermediary metabolism and respiration	iron-regulated phosphoenolpyruvate carboxykinase [GTP] PckA
533193	non	CT	MMAR_0454	-		cell wall and cell processes	conserved hypothetical membrane protein
534433	non	TC	MMAR_0455	-		lipid metabolism	acyl-CoA dehydrogenase FadE3_2
534585	syn	CT	MMAR_0456	-		conserved hypotheticals	conserved protein
534774	syn	AG	MMAR_0456	-		conserved hypotheticals	conserved protein
536347	psd	CT	MMAR_0457	-		conserved hypotheticals	C-term conserved hypothetical protein pseudogene
538191	int	GA	70 MMAR_0459			conserved hypotheticals	conserved hypothetical protein
538196	int	AT				conserved hypotheticals	conserved hypothetical protein
538697	syn	TC	MMAR_0460	-		cell wall and cell processes	conserved hypothetical membrane protein
540344	non	CT	MMAR_0461	-		cell wall and cell processes	conserved hypothetical transmembrane protein
540956	syn	CG	MMAR_0462	-		cell wall and cell processes	conserved hypothetical transmembrane protein
548102	non	GT	MMAR_0468	-		lipid metabolism	fatty-acid-CoA ligase
549619	syn	GT	MMAR_0469	-		lipid metabolism	peptide synthetase
550703	non	GC	MMAR_0469	-		lipid metabolism	peptide synthetase
551631	non	CT	MMAR_0469	-		lipid metabolism	peptide synthetase
552257	syn	CA	MMAR_0469	-		lipid metabolism	peptide synthetase
552554	non	AG	MMAR_0469	-		lipid metabolism	peptide synthetase
554550	int	GA	20 MMAR_0471			lipid metabolism	enoyl-CoA hydratase
555407	int	CG				intermediary metabolism and respiration	aldehyde dehydrogenase
556347	non	GA	MMAR_0472	-		intermediary metabolism and respiration	aldehyde dehydrogenase
556873	non	TC	MMAR_0472	-		intermediary metabolism and respiration	aldehyde dehydrogenase
557380	non	AG	MMAR_0473	-		intermediary metabolism and respiration	aldehyde dehydrogenase
558110	syn	GT	MMAR_0474	-		cell wall and cell processes	methyltransferase
559258	non	GT	MMAR_0475	-		cell wall and cell processes	glycosyltransferase
559266	syn	GA	MMAR_0475	-		cell wall and cell processes	conserved transmembrane protein
560199	syn	AT	MMAR_0475	-		cell wall and cell processes	conserved transmembrane protein
561016	syn	CG	MMAR_0476	-		cell wall and cell processes	conserved membrane protein
562691	syn	AG	MMAR_0477	-		intermediary metabolism and respiration	integral membrane acyltransferase
578862	int	CT	-				
578866	int	GC	-				
583599	non	TC	MMAR_0493	-		cell wall and cell processes	conserved hypothetical membrane protein
583790	non	AC	MMAR_0493	-		cell wall and cell processes	conserved hypothetical membrane protein
584237	syn	AG	MMAR_0494	-		intermediary metabolism and respiration	glycerophosphoryl ester phosphodiesterase GlpQ2
585681	syn	CT	MMAR_0496	-		cell wall and cell processes	conserved transmembrane protein
590269	non	CT	MMAR_0498	-		cell wall and cell processes	conserved hypothetical small secreted protein
590325	syn	GC	MMAR_0498	-		cell wall and cell processes	conserved hypothetical small secreted protein
593978	non	AG	MMAR_0502	-		cell wall and cell processes	conserved membrane protein
594366	syn	GA	MMAR_0502	-		cell wall and cell processes	conserved membrane protein
596856	syn	CT	MMAR_0504	-		lipid metabolism	acyl-CoA acyltransferase FadA2
597303	syn	GA	MMAR_0504	-		lipid metabolism	acyl-CoA acyltransferase FadA2
597945	syn	GA	MMAR_0505	-		lipid metabolism	acyl-CoA dehydrogenase FadE5
600166	int	CT	76 MMAR_0506			intermediary metabolism and respiration	oxidoreductase
602646	int	TC				conserved hypotheticals	conserved hypothetical protein
602654	int	CT	35 MMAR_0509			conserved hypotheticals	conserved hypothetical protein
607878	syn	TC	MMAR_0515	-		heat shock protein Hsp	-
608106	int	CT	131 MMAR_0516			intermediary metabolism and respiration	nitrile reductase [NAD(P)H] large subunit [fad flavoprotein] NirB
615425	int	AG				amino-glycoside 2'-N-acetyltransferase Aac	
616886	int	GA	12 MMAR_0524			conserved hypotheticals	conserved hypothetical protein
618150	non	GC	MMAR_0525	-		cell wall and cell processes	periplasmic iron-transport lippoprotein
618462	syn	CT	MMAR_0525	-		cell wall and cell processes	periplasmic iron-transport lippoprotein
619392	syn	CT	MMAR_0526	-		cell wall and cell processes	integral membrane nitrite extrusion protein NarU
619964	non	TA	MMAR_0526	-		cell wall and cell processes	integral membrane nitrite extrusion protein NarU
622756	syn	GA	MMAR_0528	-		lipid metabolism	fatty-acid-CoA ligase FadD2
626507	syn	TC	MMAR_0530	-		lipid metabolism	acyl-CoA dehydrogenase FadE6
632347	non	GA	MMAR_0537	-		conserved hypotheticals	conserved hypothetical protein
633111	syn	GC	MMAR_0537	-		conserved hypotheticals	conserved hypothetical protein
633119	non	GC	MMAR_0537	-		conserved hypotheticals	conserved hypothetical protein
635739	non	GT	MMAR_0539	-		lipid metabolism	O-Methyltransferase
639915	int	CT	119 MMAR_0540			hypothetical protein	
640239	syn	GA				cell wall and cell processes	conserved membrane protein
645427	int	AG	-				
646720	non	TG	MMAR_0548	-		conserved hypotheticals	conserved protein
652037	syn	CT	MMAR_0552	-		cell wall and cell processes	conserved hypothetical membrane protein
652809	syn	CT	MMAR_0553	-		intermediary metabolism and respiration	trans-aconitate methyltransferase Tam
653317	syn	GA	MMAR_0554	-		intermediary metabolism and respiration	sulfatase
653494	non	GA	MMAR_0554	-		intermediary metabolism and respiration	sulfatase
653496	non	TG	MMAR_0554	-		intermediary metabolism and respiration	sulfatase
654052	non	CT	MMAR_0554	-		intermediary metabolism and respiration	sulfatase

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
654323	non	TC	MMAR_0554	-		intermediary metabolism and respiration	sulfatase
654526	syn	CT	MMAR_0554	-		intermediary metabolism and respiration	sulfatase
655352	non	CT	MMAR_0555	-		intermediary metabolism and respiration	oxidoreductase
655425	non	CT	MMAR_0555	-		intermediary metabolism and respiration	oxidoreductase
657487	syn	CT	MMAR_0559	-		cell wall and cell processes	conserved exported protein
658693	non	CG	MMAR_0561	-		conserved hypotheticals	conserved hypothetical protein
659450	syn	CG	MMAR_0561	-		conserved hypotheticals	conserved hypothetical protein
659462	non	TA	MMAR_0561	-		conserved hypotheticals	conserved hypothetical protein
663841	syn	GA	MMAR_0565	-		cell wall and cell processes	conserved membrane protein
696639	non	GA	MMAR_0595	-		regulatory protein	transcriptional regulatory protein
697427	syn	CT	MMAR_0596	-		cell wall and cell processes	conserved integral membrane transport protein
697447	syn	GA	MMAR_0596	-		cell wall and cell processes	conserved integral membrane transport protein
698805	syn	AC	MMAR_0597	-		conserved hypotheticals	conserved hypothetical protein
699427	non	AG	MMAR_0598	-		intermediary metabolism and respiration	pyrrolidone-carboxylate peptidase Pcp
699467	syn	CT	MMAR_0598	-		intermediary metabolism and respiration	pyrrolidone-carboxylate peptidase Pcp
699563	syn	CG	MMAR_0598	-		intermediary metabolism and respiration	pyrrolidone-carboxylate peptidase Pcp
699573	non	TG	MMAR_0598	-		intermediary metabolism and respiration	pyrrolidone-carboxylate peptidase Pcp
699736	int	CT	119 MMAR_0598	-		intermediary metabolism and respiration	pyrrolidone-carboxylate peptidase Pcp
700284	syn	CT		-		conserved hypotheticals	conserved hypothetical secreted protein
701007	syn	CT	MMAR_0600	-		intermediary metabolism and respiration	deoxyxytidine triphosphate deaminase Dcd
702974	int	TC	93 MMAR_0601	-		cell wall and cell processes	conserved hypothetical membrane protein
705935	syn	GA		-		intermediary metabolism and respiration	UDP-glucose dehydrogenase UdgA
707783	non	GA	MMAR_0606	-		intermediary metabolism and respiration	alpha-D-glucose-1-phosphate thymidylyl-transferase RmlA
709608	int	GA	141 MMAR_0608	PE/PPE		cell wall and cell processes	PE-PGRS family protein
711138	int	CT		41 MMAR_0608	PE/PPE	cell wall and cell processes	PE-PGRS family protein
714868	syn	CT	MMAR_0610	-		intermediary metabolism and respiration	aspartate aminotransferase AspC
714946	syn	TC	MMAR_0610	-		intermediary metabolism and respiration	aspartate aminotransferase AspC
718544	non	CG	MMAR_0611	-		intermediary metabolism and respiration	iron-sulphur-binding reductase
722594	int	AG	141 MMAR_0613	conserved hypotheticals		cell wall and cell processes	conserved hypothetical protein
726939	syn	CT		MMAR_0615	-	cell wall and cell processes	conserved hypothetical protein InIA
727140	syn	TG	MMAR_0615	-		cell wall and cell processes	conserved hypothetical protein InIA
727895	syn	CG	MMAR_0616	-		cell wall and cell processes	isoniazid inducible protein InIC
728012	syn	CT	MMAR_0616	-		cell wall and cell processes	isoniazid inducible protein InIC
728093	syn	CT	MMAR_0616	-		cell wall and cell processes	isoniazid inducible protein InIC
728297	syn	CT	MMAR_0616	-		cell wall and cell processes	isoniazid inducible protein InIC
728309	syn	GA	MMAR_0616	-		cell wall and cell processes	isoniazid inducible protein InIC
728477	syn	CG	MMAR_0616	-		cell wall and cell processes	isoniazid inducible protein InIC
728598	syn	CT	MMAR_0616	-		cell wall and cell processes	isoniazid inducible protein InIC
732466	syn	CT	MMAR_0620	-		cell wall and cell processes	conserved hypothetical lipoprotein LpgJ
733286	non	CG	MMAR_0621	-		intermediary metabolism and respiration	carbon monoxide dehydrogenase (small chain) CoxS_3
733418	syn	CT	MMAR_0621	-		intermediary metabolism and respiration	carbon monoxide dehydrogenase (small chain) CoxS_3
734157	syn	CA	MMAR_0622	-		intermediary metabolism and respiration	aerobic-type carbon monoxide dehydrogenase CoxM_3
734291	non	CG	MMAR_0622	-		intermediary metabolism and respiration	aerobic-type carbon monoxide dehydrogenase CoxM_3
735698	syn	GT	MMAR_0623	-		intermediary metabolism and respiration	aerobic-type carbon monoxide dehydrogenase CoxL_3
736080	non	GC	MMAR_0623	-		intermediary metabolism and respiration	aerobic-type carbon monoxide dehydrogenase CoxL_3
736859	int	TC	148 MMAR_0623	intermediary metabolism and respiration		cell wall and cell processes	aerobic-type carbon monoxide dehydrogenase CoxL_3
738252	syn	CG		MMAR_0627	-	cell wall and cell processes	L-asparagine permease AnsP1_1
739284	syn	CT	MMAR_0627	-		cell wall and cell processes	L-asparagine permease AnsP1_1
752744	syn	CT	MMAR_0637	-		chaperone protein DnaK	chaperone protein DnaK
753437	syn	TC	MMAR_0637	-		chaperone protein DnaK	chaperone protein DnaK
753704	syn	CT	MMAR_0637	-		chaperone protein DnaK	chaperone protein DnaK
754339	syn	TC	MMAR_0638	-		GrpE protein (Hsp-70 cofactor)	GrpE protein (Hsp-70 cofactor)
754585	syn	CT	MMAR_0638	-		chaperone protein DnaJ	chaperone protein DnaJ
755080	syn	TC	MMAR_0639	-		chaperone protein DnaJ	chaperone protein DnaJ
755287	syn	CA	MMAR_0639	-		chaperone protein DnaJ	chaperone protein DnaJ
755545	syn	GC	MMAR_0639	-		chaperone protein DnaJ	chaperone protein DnaJ
755723	syn	TC	MMAR_0639	-		chaperone protein DnaJ	chaperone protein DnaJ
755764	syn	TC	MMAR_0639	-		chaperone protein DnaJ	chaperone protein DnaJ
755848	syn	CA	MMAR_0639	-		chaperone protein DnaJ	chaperone protein DnaJ
755854	syn	TC	MMAR_0639	-		chaperone protein DnaJ	chaperone protein DnaJ
774548	int	CT	49 MMAR_0642	PE/PPE		cell wall and cell processes	PPE family protein
774786	int	AG		-		cell wall and cell processes	L-asparagine permease AnsP1_1
776587	non	AG	MMAR_0643	-		conserved hypotheticals	conserved hypothetical protein
776894	non	CT	MMAR_0644	-		intermediary metabolism and respiration	monoxygenase
776909	syn	CT	MMAR_0644	-		intermediary metabolism and respiration	monoxygenase
777969	int	CT	116 MMAR_0644	intermediary metabolism and respiration		monoxygenase	monoxygenase
777970	int	CG		117 MMAR_0644	intermediary metabolism and respiration	monoxygenase	monoxygenase
778130	int	AG	50 MMAR_0645	intermediary metabolism and respiration		endopeptidase ATP binding protein (chain B) CipB	endopeptidase ATP binding protein (chain B) CipB
778314	syn	CA		MMAR_0645	-	endopeptidase ATP binding protein (chain B) CipB	endopeptidase ATP binding protein (chain B) CipB
778752	syn	GT	MMAR_0645	-		endopeptidase ATP binding protein (chain B) CipB	endopeptidase ATP binding protein (chain B) CipB
779913	syn	GA	MMAR_0645	-		endopeptidase ATP binding protein (chain B) CipB	endopeptidase ATP binding protein (chain B) CipB
780129	syn	TG	MMAR_0645	-		endopeptidase ATP binding protein (chain B) CipB	endopeptidase ATP binding protein (chain B) CipB
781706	int	AC	785025	-		intermediary metabolism and respiration	RNA methyltransferase
785025	syn	GT	MMAR_0651	-		intermediary metabolism and respiration	RNA methyltransferase
785372	non	CT	MMAR_0651	-		intermediary metabolism and respiration	RNA methyltransferase
785376	syn	CG	MMAR_0651	-		intermediary metabolism and respiration	RNA methyltransferase
785701	int	GA	63 MMAR_0652	cell wall and cell processes		protein transport protein SecE2	conserved hypothetical protein
787850	syn	CT		MMAR_0654	-	conserved hypotheticals	conserved hypothetical protein
788390	syn	CA	MMAR_0655	-		intermediary metabolism and respiration	carbon monoxide dehydrogenase (medium chain) CoxM
788403	non	GC	MMAR_0655	-		intermediary metabolism and respiration	carbon monoxide dehydrogenase (medium chain) CoxM
789008	syn	TC	MMAR_0655	-		intermediary metabolism and respiration	carbon monoxide dehydrogenase (medium chain) CoxM
789633	syn	CT	MMAR_0657	-		intermediary metabolism and respiration	carbon monoxide dehydrogenase (large chain) CoxL
790254	syn	GA	MMAR_0657	-		intermediary metabolism and respiration	carbon monoxide dehydrogenase (large chain) CoxL
790747	syn	CT	MMAR_0657	-		intermediary metabolism and respiration	carbon monoxide dehydrogenase (large chain) CoxL
792339	non	GT	MMAR_0659	-		conserved hypotheticals	conserved hypothetical protein
793095	non	AG	MMAR_0659	-		conserved hypotheticals	conserved hypothetical protein
794616	non	CT	MMAR_0661	-		intermediary metabolism and respiration	membrane oxidoreductase
795888	syn	CG	MMAR_0662	-		cell wall and cell processes	protein containing VWA domain
796027	non	GA	MMAR_0662	-		cell wall and cell processes	protein containing VWA domain
799438	syn	CT	MMAR_0665	-		cell wall and cell processes	ethanolamine transporter
808148	syn	TC	MMAR_0672	-		conserved hypotheticals	conserved protein
810483	non	GA	MMAR_0676	-		intermediary metabolism and respiration	glycolipid transferase
812651	syn	GA	MMAR_0679	-		conserved hypotheticals	conserved hypothetical protein
812677	syn	GA	MMAR_0679	-		conserved hypotheticals	conserved hypothetical protein
813001	non	CT	MMAR_0679	-		conserved hypotheticals	conserved hypothetical protein

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
815084	non	AG	MMAR_0681	-		conserved hypothetical	conserved hypothetical protein
836004	syn	TG	MMAR_0701	-		intermediary metabolism and respiration	conserved hypothetical oxidoreductase
836990	non	CT	MMAR_0702	-		intermediary metabolism and respiration	monoxygenase-like hypothetical protein
836998	non	CG	MMAR_0702	-		intermediary metabolism and respiration	monoxygenase-like hypothetical protein
837136	non	GC	MMAR_0702	-		intermediary metabolism and respiration	monoxygenase-like hypothetical protein
839191	non	AC	MMAR_0703	-		intermediary metabolism and respiration	FMNH2-utilizing oxygenase
839777	syn	CT	MMAR_0704	-		cell wall and cell processes	conserved transmembrane transport protein MmpL1
852321	syn	GC	MMAR_0708	-		cell wall and cell processes	beta lactamase-like protein
853571	non	GC	MMAR_0709	-		intermediary metabolism and respiration	F420-dependent glucose-6-phosphate dehydrogenase Fgd1
853685	syn	CT	MMAR_0709	-		intermediary metabolism and respiration	F420-dependent glucose-6-phosphate dehydrogenase Fgd1
853790	syn	GA	MMAR_0709	-		intermediary metabolism and respiration	F420-dependent glucose-6-phosphate dehydrogenase Fgd1
854733	syn	CT	MMAR_0710	-		intermediary metabolism and respiration	phosphate acetyltransferase Pta
856564	syn	CT	MMAR_0711	-		intermediary metabolism and respiration	acetate kinase AckA
857093	non	CG	MMAR_0711	-		intermediary metabolism and respiration	acetate kinase AckA
857098	syn	CT	MMAR_0711	-		intermediary metabolism and respiration	acetate kinase AckA
857260	int	CT	146 MMAR_0712	-		conserved hypothetical	conserved hypothetical protein
858241	non	AC		-		conserved hypothetical	conserved hypothetical protein
861462	syn	AG		-		cell wall and cell processes	glutamine-binding lipoprotein GlnH
862553	syn	CT		-		cell wall and cell processes	conserved hypothetical membrane protein
863259	non	CG		-		information pathways	mutator protein MutT3
864121	syn	CG		-		intermediary metabolism and respiration	thiamine-phosphate pyrophosphorylase ThiE
866198	syn	CT		-		intermediary metabolism and respiration	thiamin biosynthesis protein ThiG
871982	syn	TC		-		intermediary metabolism and respiration	lipoprotein aminopeptidase LpQ_1
884068	syn	CT		-		intermediary metabolism and respiration	thiamine biosynthesis protein ThiC
884648	syn	CG		-		regulatory protein	conserved hypothetical regulatory protein
889755	syn	GC		-		conserved hypothetical	conserved hypothetical protein
889810	int	TC		39	MMAR_0740	cell wall and cell processes	metal cation transporting p-type ATPase CtpH
891481	syn	CT		-		cell wall and cell processes	metal cation transporting p-type ATPase CtpH
892708	syn	CT		-		cell wall and cell processes	metal cation transporting p-type ATPase CtpH
892798	syn	GT	MMAR_0740	-		cell wall and cell processes	metal cation transporting p-type ATPase CtpH
901674	non	AG	MMAR_0750	-		cell wall and cell processes	MFS transporter
902660	int	GA	72 MMAR_0750	-		cell wall and cell processes	MFS transporter
902917	syn	GA		-		conserved hypothetical	conserved hypothetical protein
903019	syn	CT		-		conserved hypothetical	conserved hypothetical protein
903177	non	AG		-		conserved hypothetical	conserved hypothetical protein
904913	syn	GA		-		cell wall and cell processes	conserved ATPase
905923	syn	CA		-		lipid metabolism	CDP-diacylglycerol--serine o-phosphatidyltransferase PssA
910778	syn	GA		-		intermediary metabolism and respiration	molybdopterin biosynthesis protein MoeA2
910874	syn	GT		-		intermediary metabolism and respiration	molybdopterin biosynthesis protein MoeA2
910936	non	GT		-		intermediary metabolism and respiration	molybdopterin biosynthesis protein MoeA2
911314	non	CT		-		intermediary metabolism and respiration	molybdopterin biosynthesis protein MoeA2
912728	syn	CG		-		intermediary metabolism and respiration	dehydrogenase/reductase
912881	non	GC		-		intermediary metabolism and respiration	dehydrogenase/reductase
914739	non	AC		-		intermediary metabolism and respiration	60 kDa chaperonin 2 GroEL2
917500	non	AG		-		intermediary metabolism and respiration	D-AMINO acid aminohydrolase
917582	syn	CT	MMAR_0762	-		intermediary metabolism and respiration	D-AMINO acid aminohydrolase
918995	syn	CT	MMAR_0762	-		intermediary metabolism and respiration	D-AMINO acid aminohydrolase
924334	non	GA	MMAR_0769	-		conserved hypothetical	conserved hypothetical protein
924474	syn	TG	MMAR_0769	-		conserved hypothetical	conserved hypothetical protein
924749	non	TC	MMAR_0769	-		conserved hypothetical	conserved hypothetical protein
924997	non	GT	MMAR_0770	-		cell wall and cell processes	oxidoreductase
925049	syn	GA	MMAR_0770	-		cell wall and cell processes	oxidoreductase
925397	syn	GA	MMAR_0770	-		cell wall and cell processes	oxidoreductase
925451	syn	AC	MMAR_0770	-		cell wall and cell processes	oxidoreductase
925510	syn	GA	MMAR_0770	-		cell wall and cell processes	oxidoreductase
925526	syn	GA	MMAR_0770	-		cell wall and cell processes	oxidoreductase
925727	syn	TC	MMAR_0770	-		cell wall and cell processes	oxidoreductase
933165	syn	GA	MMAR_0775	-		cell wall and cell processes	conserved transmembrane transport protein - MmpL family
934854	int	AG	37 MMAR_0777	-		cell wall and cell processes	conserved secreted protein
936546	non	GA		-		intermediary metabolism and respiration	peptidase
937589	syn	GA		-		intermediary metabolism and respiration	peptidase
943468	syn	AG		-		intermediary metabolism and respiration	dihydrodipamide dehydrogenase Lpd
946763	syn	AG		-		conserved hypothetical	conserved protein
946790	syn	CT		-		conserved hypothetical	conserved protein
949584	int	CT		27	MMAR_0791	conserved hypothetical	conserved hypothetical protein
949779	int	CT		86	MMAR_0792	intermediary metabolism and respiration	isocitrate lyase Icl
950551	syn	CT		-		intermediary metabolism and respiration	isocitrate lyase Icl
955920	syn	GA		-		regulatory protein	transcriptional regulatory protein (possibly TetR-family)
959399	non	CA	MMAR_0801	-		cell wall and cell processes	conserved transmembrane protein
962980	int	GT	149 MMAR_0807	-		conserved hypothetical	conserved hypothetical protein
969615	syn	CT		-		conserved hypothetical	conserved hypothetical protein
970468	non	GT		-		cell wall and cell processes	UDP-N-acetylenzymuroylglucosamine reductase MurB
971718	syn	CT		-		cell wall and cell processes	conserved lipoprotein LprQ
975326	syn	GA		-		intermediary metabolism and respiration	mannosyltransferase
975385	non	GA		-		intermediary metabolism and respiration	mannosyltransferase
976394	non	CT	MMAR_0813	-		conserved hypothetical	conserved hypothetical protein
984306	non	GT	MMAR_0821	-		conserved hypothetical	conserved hypothetical protein
985030	syn	CT	MMAR_0822	-		conserved hypothetical	conserved protein
988631	syn	CG	MMAR_0826	-		cell wall and cell processes	pyrrolidine-5-carboxylate reductase ProC
989285	syn	CG	MMAR_0826	-		cell wall and cell processes	pyrrolidine-5-carboxylate reductase ProC
992196	non	CG	MMAR_0830	-		conserved hypothetical	conserved protein
993187	syn	GA	MMAR_0831	-		lipid metabolism	cyclopropane-fatty-acyl-phospholipid synthase 2 CmaA2
995577	syn	CA	MMAR_0834	-		intermediary metabolism and respiration	carbon monoxide dehydrogenase (small chain) CoxS_1
995480	syn	CT	MMAR_0834	-		intermediary metabolism and respiration	carbon monoxide dehydrogenase (small chain) CoxS_1
996086	non	AT	MMAR_0835	-		intermediary metabolism and respiration	carbon monoxide dehydrogenase (medium chain) CoxM_1
998217	non	AG	MMAR_0836	-		cell wall and cell processes	carbon monoxide dehydrogenase (large chain) CoxL_1
998822	syn	CT	MMAR_0836	-		cell wall and cell processes	carbon monoxide dehydrogenase (large chain) CoxL_1
998638	syn	GA	MMAR_0836	-		cell wall and cell processes	carbon monoxide dehydrogenase (large chain) CoxL_1
100912	non	TC	MMAR_0842	-		intermediary metabolism and respiration	glutamyl-tRNA reductase HemA
1007357	syn	CT	MMAR_0842	-		intermediary metabolism and respiration	glutamyl-tRNA reductase HemA
1009437	syn	GA	MMAR_0844	-		intermediary metabolism and respiration	urophyrin-III-C-methyltransferase HemD
10105465	non	CA	MMAR_0845	-		intermediary metabolism and respiration	delta-aminoelevulinic acid dehydratase HemB
1042938	int	CT	44 MMAR_0853	-		conserved hypothetical	conserved hypothetical protein
1044253	syn	CT		-		cell wall and cell processes	membrane acyltransferase

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
1044304	syn	GA	MMAR_0854	-	cell wall and cell processes	membrane acyltransferase	
1049205	syn	GA	MMAR_0859	-	unknown	universal stress protein UspA	
1049658	syn	CT	MMAR_0859	-	unknown	universal stress protein UspA	
1051029	syn	CT	MMAR_0860	-	cell wall and cell processes	metal cation-transporting p-type ATPase F CtpF	
1052936	syn	CT	MMAR_0861	-	intermediary metabolism and respiration	glycine-sarcosine methyltransferase	
1052992	non	AG	MMAR_0861	-	intermediary metabolism and respiration	glycine-sarcosine methyltransferase	
1053573	syn	CT	MMAR_0861	-	intermediary metabolism and respiration	glycine-sarcosine methyltransferase	
1056991	int	GA	13 MMAR_0863	cell wall and cell processes	keto-pantoate reductase ApbA		
1057745	non	TC		intermediary metabolism and respiration	mandelate racemase		
1058156	int	CA	5 MMAR_0864	intermediary metabolism and respiration	mandelate racemase		
1058464	non	AT		conserved hypothetical	conserved hypothetical protein		
1058481	non	TA	MMAR_0866	-	conserved hypothetical	conserved hypothetical protein	
1060495	int	AT	130 MMAR_0869	cell wall and cell processes	amino acid permease		
1060936	syn	GA		cell wall and cell processes	amino acid permease		
1061093	non	A-	MMAR_0869	-	cell wall and cell processes	amino acid permease	
1064282	non	CA	MMAR_0872	-	cell wall and cell processes	thioredoxin protein (thiol-disulfide interchange protein)	
1064436	syn	CT	MMAR_0872	-	cell wall and cell processes	thioredoxin protein (thiol-disulfide interchange protein)	
1066508	syn	TC	MMAR_0874	-	conserved hypothetical	ResB-family protein	
1066609	syn	CT	MMAR_0874	-	conserved hypothetical	ResB-family protein	
1066792	syn	TC	MMAR_0874	-	conserved hypothetical	ResB-family protein	
1068549	non	AG	MMAR_0876	-	conserved hypothetical	conserved hypothetical protein	
1073810	syn	TG	MMAR_0882	-	intermediary metabolism and respiration	UDP-glucose 4-epimerase GalE3	
1075255	syn	GA	MMAR_0883	-	cell wall and cell processes	conserved membrane protein	
1076271	non	GA	MMAR_0884	-	cell wall and cell processes	conserved hypothetical membrane protein	
1076444	syn	CA	MMAR_0884	-	cell wall and cell processes	conserved hypothetical membrane protein	
1079857	non	CT	MMAR_0887	-	cell wall and cell processes	conserved hypothetical membrane protein	
1080736	syn	CA	MMAR_0888	-	intermediary metabolism and respiration	O-succinylbenzoic acid-CoA ligase MenE	
1083714	non	CT	MMAR_0892	-	intermediary metabolism and respiration	Glyoxalase	
1084717	int	GA	13 MMAR_0893	conserved hypothetical	conserved protein		
1085029	syn	TC		intermediary metabolism and respiration	dehydrogenase		
1090214	syn	TC	MMAR_0898	-	cell wall and cell processes	conserved hypothetical protein	
1090702	non	CG	MMAR_0899	-	intermediary metabolism and respiration	muconate cycloisomerase MenC	
1090711	syn	AC	MMAR_0899	-	intermediary metabolism and respiration	muconate cycloisomerase MenC	
1092759	non	GA	MMAR_0901	-	intermediary metabolism and respiration	bifunctional 2-succinyl-6-hydroxy-2-4-cyclohexadiene-1-carboxylate synthase MenD	
1093052	non	AC	MMAR_0901	-	intermediary metabolism and respiration	bifunctional 2-succinyl-6-hydroxy-2-4-cyclohexadiene-1-carboxylate synthase MenD	
1093784	syn	CT	MMAR_0901	-	intermediary metabolism and respiration	bifunctional 2-succinyl-6-hydroxy-2-4-cyclohexadiene-1-carboxylate synthase MenD	
1096562	syn	CT	MMAR_0905	-	conserved hypothetical	conserved hypothetical protein	
1101611	syn	CT	MMAR_0910	-	intermediary metabolism and respiration	FAD-linked oxidoreductase	
1102384	syn	CT	MMAR_0911	-	intermediary metabolism and respiration	polypropenyl diphosphate synthetase GrcC1	
1103435	non	AG	MMAR_0912	-	intermediary metabolism and respiration	peptidase heat shock protein X HspX	
1105561	syn	GT	MMAR_0913	-	intermediary metabolism and respiration	transmembrane carbonic anhydrase SulP	
1105891	int	CA	73 MMAR_0914	intermediary metabolism and respiration	transmembrane carbonic anhydrase SulP 1		
1105892	int	AG		intermediary metabolism and respiration	transmembrane carbonic anhydrase SulP 1		
1106936	syn	CG	MMAR_0914	-	intermediary metabolism and respiration	transmembrane carbonic anhydrase SulP 1	
1118116	non	AG	MMAR_0921	-	cell wall and cell processes	ABC-type transporter	
1119233	non	TG	MMAR_0921	-	cell wall and cell processes	ABC-type transporter	
1120127	syn	CT	MMAR_0922	-	cell wall and cell processes	ABC transporter ATP-binding protein	
1120241	syn	GA	MMAR_0922	-	cell wall and cell processes	ABC transporter ATP-binding protein	
1120488	non	CT	MMAR_0923	-	regulatory proteins	transcriptional regulator	
1140513	int	GA	118 MMAR_0937	information pathways	peptide amidase GatA 1		
1144436	non	TC		intermediary metabolism and respiration	galactokinase GalK		
1144570	syn	GA	MMAR_0941	-	intermediary metabolism and respiration	galactokinase GalK	
1144606	non	GA	MMAR_0941	-	intermediary metabolism and respiration	galactokinase GalK	
1145292	non	CT	MMAR_0941	-	intermediary metabolism and respiration	galactokinase GalK	
1145350	syn	CT	MMAR_0941	-	intermediary metabolism and respiration	galactokinase GalK	
1146243	syn	GC	MMAR_0942	-	regulatory proteins	regulatory protein	
1150470	int	AG	62 MMAR_0943	-	information pathways	transcriptional regulator	
1150740	int	GA		PE/PPE	PE-PGRS family protein		
1152093	non	GC	MMAR_0945	-	cell wall and cell processes	conserved hypothetical membrane protein	
1155080	syn	GC	MMAR_0946	-	conserved hypothetical	conserved hypothetical protein	
1161441	syn	AG	MMAR_0952	-	cell wall and cell processes	alpha-1,2-mannosidase	
1165050	psd	TC	MMAR_0953	-	conserved hypothetical	C-term conserved hypothetical protein pseudogene	
1168647	syn	GT	MMAR_0956	-	information pathways	exodeoxyribonuclease V (alpha chain) RecD	
1169287	syn	AG	MMAR_0956	-	information pathways	exodeoxyribonuclease V (alpha chain) RecD	
1169740	non	GA	MMAR_0957	-	information pathways	exodeoxyribonuclease V (beta chain) RecB	
1169774	non	AT	MMAR_0957	-	information pathways	exodeoxyribonuclease V (beta chain) RecB	
1170894	syn	TC	MMAR_0957	-	information pathways	exodeoxyribonuclease V (beta chain) RecB	
1174121	non	GA	MMAR_0958	-	information pathways	exodeoxyribonuclease V (gamma chain) RecC	
1174192	non	GC	MMAR_0958	-	information pathways	exodeoxyribonuclease V (gamma chain) RecC	
1174274	non	GT	MMAR_0958	-	information pathways	exodeoxyribonuclease V (gamma chain) RecC	
1176184	non	AC	MMAR_0959	-	intermediary metabolism and respiration	nitroreductase	
1177457	syn	CT	MMAR_0961	-	cell wall and cell processes	conserved hypothetical transmembrane protein	
1177627	non	AC	MMAR_0961	-	cell wall and cell processes	conserved hypothetical transmembrane protein	
1179268	syn	GA	MMAR_0963	-	cell wall and cell processes	conserved hypothetical membrane protein	
1179934	int	GA	28 MMAR_0965	-	glyoxalase II Glob		
1181047	int	AG		27 MMAR_0966	conserved hypothetical	conserved protein	
1181975	non	GA	MMAR_0968	-	conserved hypothetical	conserved protein	
1187873	non	-C	MMAR_0976	-	information pathways	conserved hypothetical protein	
1188903	non	GA	MMAR_0977	-	lipid metabolism	methoxy mycolic acid synthase 4 MmaA4	
1192066	non	TC	MMAR_0981	-	intermediary metabolism and respiration	lipase/esterase LipG1	
1192112	syn	CG	MMAR_0981	-	intermediary metabolism and respiration	lipase/esterase LipG1	
1194500	int	CA	100 MMAR_0982	conserved hypothetical	conserved hypothetical protein		
1195195	syn	CT		intermediary metabolism and respiration	lipase/esterase LipG2		
1195199	syn	AG	MMAR_0983	-	intermediary metabolism and respiration	lipase/esterase LipG2	
1196945	int	CT	82 MMAR_0985	intermediary metabolism and respiration	alpha-mannosidase		
1197261	non	CT		intermediary metabolism and respiration	alpha-mannosidase		
1199251	non	CT	MMAR_0985	-	intermediary metabolism and respiration	alpha-mannosidase	
1200069	non	CT	MMAR_0985	-	intermediary metabolism and respiration	alpha-mannosidase	
1201665	int	AG	101 MMAR_0989	PE/PPE	PE-PGRS family protein		
1204195	int	GT		PE/PPE	PE-PGRS family protein		
1204295	int	GA	29 MMAR_0989	PE/PPE	PE-PGRS family protein		
1208790	syn	CT		information pathways	SOS ribosomal protein L7/L12 RplL		
1208997	syn	GC	MMAR_0992	-	regulatory proteins	transcriptional regulatory protein	
1209173	non	AC	MMAR_0992	-	regulatory proteins	transcriptional regulatory protein	
1209190	non	GT	MMAR_0992	-	regulatory proteins	transcriptional regulatory protein	

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
1209311	non	TC	MMAR_0992	-		regulatory proteins	transcriptional regulatory protein
1209447	syn	AG	MMAR_0992	-		regulatory proteins	transcriptional regulatory protein
1209477	non	CA	MMAR_0992	-		regulatory proteins	transcriptional regulatory protein
1209519	syn	CG	MMAR_0992	-		regulatory proteins	transcriptional regulatory protein
1209522	syn	AG	MMAR_0992	-		regulatory proteins	transcriptional regulatory protein
1209543	syn	AG	MMAR_0992	-		regulatory proteins	transcriptional regulatory protein
1209546	non	CG	MMAR_0992	-		regulatory proteins	transcriptional regulatory protein
1209666	syn	CT	MMAR_0992	-		regulatory proteins	transcriptional regulatory protein
1210108	syn	TC	MMAR_0993	-		intermediary metabolism and respiration	dioxygenase
1210547	non	AC	MMAR_0993	-		intermediary metabolism and respiration	dioxygenase
1210797	non	CG	MMAR_0993	-		intermediary metabolism and respiration	dioxygenase
1211391	int	GT	143	MMAR_0993		intermediary metabolism and respiration	dioxygenase
1213926	syn	CT				information pathways	DNA-directed RNA polymerase beta subunit RpoB
1214131	syn	TC	MMAR_0995	-		information pathways	DNA-directed RNA polymerase beta subunit RpoB
1215285	non	CG	MMAR_0995	-		information pathways	DNA-directed RNA polymerase beta subunit RpoB
1216975	syn	CT	MMAR_0996	-		information pathways	DNA-directed RNA polymerase beta chain RpoC
1217140	syn	CG	MMAR_0996	-		information pathways	DNA-directed RNA polymerase beta chain RpoC
1217179	syn	CT	MMAR_0996	-		information pathways	DNA-directed RNA polymerase beta chain RpoC
1220020	syn	CG	MMAR_0996	-		information pathways	DNA-directed RNA polymerase beta chain RpoC
1221097	int	TC	105	MMAR_5546		PE/PGRS family protein	PE/PGRS family protein
1221115	int	AG				PE/PGRS family protein	PE/PGRS family protein
1222646	non	CG	MMAR_0997	-		intermediary metabolism and respiration	ceramidase
1223241	syn	AG	MMAR_0997	-		intermediary metabolism and respiration	ceramidase
1223457	int	TC	118	MMAR_0997		intermediary metabolism and respiration	ceramidase
1223662	syn	TC				conserved hypotheticals	conserved hypothetical protein
1224435	int	GA	49	MMAR_0999		information pathways	endonuclease iv (apurinase) End
1227530	syn	CT				lipid metabolism	acyl-CoA dehydrogenase
1233817	int	TC	134	MMAR_1006		cell wall and cell processes	conserved transmembrane protein MmpS5
1234708	syn	AG				cell wall and cell processes	conserved hypothetical membrane protein
1241355	non	GA	MMAR_1015	-		cell wall and cell processes	conserved membrane protein
1241439	non	AG	MMAR_1015	-		cell wall and cell processes	conserved membrane protein
1241458	syn	TG	MMAR_1015	-		cell wall and cell processes	conserved membrane protein
1241620	syn	TC	MMAR_1015	-		cell wall and cell processes	conserved membrane protein
1241686	syn	CT	MMAR_1015	-		cell wall and cell processes	conserved membrane protein
1241845	syn	GA	MMAR_1015	-		cell wall and cell processes	conserved membrane protein
1241957	non	GA	MMAR_1015	-		cell wall and cell processes	conserved membrane protein
1242248	non	TA	MMAR_1016	-		intermediary metabolism and respiration	short-chain dehydrogenase/reductase
1242549	syn	CA	MMAR_1016	-		intermediary metabolism and respiration	short-chain dehydrogenase/reductase
1242677	syn	GC	MMAR_1016	-		intermediary metabolism and respiration	short-chain dehydrogenase/reductase
1243421	syn	CA	MMAR_1017	-		intermediary metabolism and respiration	ferredoxin reductase
1243583	syn	CT	MMAR_1017	-		intermediary metabolism and respiration	ferredoxin reductase
1243586	syn	CT	MMAR_1017	-		intermediary metabolism and respiration	ferredoxin reductase
1243979	syn	CA	MMAR_1017	-		intermediary metabolism and respiration	ferredoxin reductase
1244356	int	CT	74	MMAR_1017		intermediary metabolism and respiration	ferredoxin reductase
1244357	int	TC				intermediary metabolism and respiration	ferredoxin reductase
1244414	non	AG	MMAR_1018	-		conserved hypotheticals	conserved hypothetical protein
1244561	syn	CT	MMAR_1018	-		conserved hypotheticals	conserved hypothetical protein
1247546	syn	CT	MMAR_1021	-		intermediary metabolism and respiration	coenzyme PQQ synthesis protein E_PqqE
1247621	syn	GC	MMAR_1021	-		intermediary metabolism and respiration	coenzyme PQQ synthesis protein E_PqqE
1249362	non	AG	MMAR_1023	-		intermediary metabolism and respiration	Creatinine amidohydrolase
1249523	syn	CT	MMAR_1023	-		intermediary metabolism and respiration	Creatinine amidohydrolase
1251479	non	TC	MMAR_1025	-		intermediary metabolism and respiration	dehydrogenase
1253380	int	GA	84	MMAR_1026		regulatory protein	transcriptional regulator (TetR family)
1255557	int	GA				PE/PGRS family protein	PE/PGRS family protein
1255854	int	CT	141	MMAR_1027		PE/PGRS family protein	PE/PGRS family protein
1263720	non	GA				information pathways	50S ribosomal protein L3 RplC
1263804	non	AG	MMAR_1032	-		information pathways	50S ribosomal protein L4 RplD
1263835	non	CT	MMAR_1032	-		information pathways	50S ribosomal protein L4 RplD
1269189	syn	AG	MMAR_1041	-		intermediary metabolism and respiration	arylsulfatase AtsA
1269298	syn	TC	MMAR_1041	-		intermediary metabolism and respiration	arylsulfatase AtsA
1269422	non	CT	MMAR_1041	-		intermediary metabolism and respiration	arylsulfatase AtsA
1269756	syn	AG	MMAR_1041	-		intermediary metabolism and respiration	arylsulfatase AtsA
1270398	syn	GT	MMAR_1041	-		intermediary metabolism and respiration	arylsulfatase AtsA
1270931	non	TG	MMAR_1042	-		conserved hypotheticals	conserved protein
1271003	non	AG	MMAR_1042	-		conserved hypotheticals	conserved protein
1271504	syn	CT	MMAR_1043	-		conserved hypotheticals	conserved protein
1271633	syn	AG	MMAR_1043	-		conserved hypotheticals	conserved protein
1271912	syn	GT	MMAR_1043	-		conserved hypotheticals	conserved protein
1272164	syn	GA	MMAR_1043	-		conserved hypotheticals	conserved protein
1272359	syn	GA	MMAR_1043	-		conserved hypotheticals	conserved protein
1272564	non	GA	MMAR_1044	-		cell wall and cell processes	conserved transmembrane protein
1277746	syn	CA	MMAR_1054	-		information pathways	50S ribosomal protein L15 RplO
1277863	non	GA	MMAR_1054	-		information pathways	50S ribosomal protein L15 RplO
1278680	syn	CA	MMAR_1055	-		intermediary metabolism and respiration	flavin-dependent oxidoreductase
1278969	int	GA	49	MMAR_1056		cell wall and cell processes	protease iv_Ssp
1279206	syn	GC				cell wall and cell processes	protease iv_Ssp
1279271	non	CG	MMAR_1056	-		cell wall and cell processes	protease iv_Ssp
1279325	non	AC	MMAR_1056	-		cell wall and cell processes	protease iv_Ssp
1280050	non	CG	MMAR_1056	-		cell wall and cell processes	protease iv_Ssp
1281222	syn	CT	MMAR_1057	-		intermediary metabolism and respiration	O-methyltransferase
1282198	syn	CT	MMAR_1058	-		intermediary metabolism and respiration	O-methyltransferase
1282806	syn	TC	MMAR_1059	-		intermediary metabolism and respiration	O-methyltransferase
1282824	syn	CT	MMAR_1059	-		intermediary metabolism and respiration	O-methyltransferase
1283340	syn	CT	MMAR_1059	-		intermediary metabolism and respiration	O-methyltransferase
1284302	psd	TA	MMAR_1060	-		intermediary metabolism and respiration	N-term short-chain type dehydrogenase Adh_1_pseudogene
1284385	psd	AG	MMAR_1060	-		intermediary metabolism and respiration	N-term short-chain type dehydrogenase Adh_1_pseudogene
1284739	psd	GA	MMAR_1060	-		intermediary metabolism and respiration	C-term short-chain dehydrogenase Adh_1_pseudogene
1286719	syn	GA	MMAR_1063	-		regulatory proteins	transcriptional regulatory protein
1286853	non	GC	MMAR_1063	-		regulatory proteins	transcriptional regulatory protein
1286927	non	GA	MMAR_1063	-		regulatory proteins	transcriptional regulatory protein
1287718	syn	CT	MMAR_1064	-		intermediary metabolism and respiration	L-fucose-1-phosphate aldolase FucA
1287865	non	GA	MMAR_1064	-		intermediary metabolism and respiration	L-fucose-1-phosphate aldolase FucA
1288386	syn	CG	MMAR_1065	-		intermediary metabolism and respiration	D-3-PHOSPHOGLYCERATE dehydrogenase SerA2
1289041	non	TC	MMAR_1065	-		intermediary metabolism and respiration	D-3-PHOSPHOGLYCERATE dehydrogenase SerA2
1290025	non	TC	MMAR_1066	-		intermediary metabolism and respiration	D-xylulose-kinase (xylulokinase) XylB

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
1290826	non	GC	MMAR_1067	-		conserved hypotheticals	conserved protein
1293727	syn	CT	MMAR_1070	-		cell wall and cell processes	preprotein translocase SecY
1300199	syn	GA	MMAR_1078	-		lipid metabolism	acyl-CoA dehydrogenase FadE9
1300951	syn	GA	MMAR_1079	-		intermediary metabolism and respiration	methylmalonate semialdehyde dehydrogenase MmsA
1301611	syn	GA	MMAR_1079	-		intermediary metabolism and respiration	methylmalonate semialdehyde dehydrogenase MmsA
1302346	syn	GA	MMAR_1079	-		intermediary metabolism and respiration	methylmalonate semialdehyde dehydrogenase MmsA
1303079	syn	GA	MMAR_1080	-		cell wall and cell processes	transmembrane carbohydrate transport protein
1306565	syn	CT	MMAR_1083	-		conserved hypotheticals	conserved hypothetical protein
1310844	syn	TC	MMAR_1090	-		information pathways	DNA-directed RNA polymerase (alpha chain) RpoA
1312160	syn	CT	MMAR_1092	-		information pathways	pseudouridine synthase a TruA
1312309	syn	CT	MMAR_1092	-		information pathways	pseudouridine synthase a TruA
1312573	non	TC	MMAR_1093	-		cell wall and cell processes	D-serine/D-alanine/glycine transporter CycA
1312996	non	GT	MMAR_1093	-		cell wall and cell processes	D-serine/D-alanine/glycine transporter CycA
1313213	syn	GA	MMAR_1093	-		cell wall and cell processes	D-serine/D-alanine/glycine transporter CycA
1313282	syn	CA	MMAR_1093	-		cell wall and cell processes	D-serine/D-alanine/glycine transporter CycA
1313549	syn	AG	MMAR_1093	-		cell wall and cell processes	D-serine/D-alanine/glycine transporter CycA
1313726	syn	AG	MMAR_1093	-		cell wall and cell processes	D-serine/D-alanine/glycine transporter CycA
1314055	int	TC	48 MMAR_1093	cell wall and cell processes		D-serine/D-alanine/glycine transporter CycA	
1314058	int	GC		51 MMAR_1093	cell wall and cell processes	D-serine/D-alanine/glycine transporter CycA	
1314352	int	TC	74 MMAR_1094	PE/PPE		PPE family protein	
1316177	non	GA					
1318889	syn	GT	MMAR_1097	-		cell wall and cell processes	cutinase precursor Cut4
1319008	non	CT	MMAR_1097	-		cell wall and cell processes	cutinase precursor Cut4
1321112	non	CT	MMAR_1099	-		cell wall and cell processes	conserved hypothetical membrane protein
1321432	non	GA	MMAR_1099	-		cell wall and cell processes	conserved hypothetical membrane protein
1322349	non	CT	MMAR_1100	-		intermediary metabolism and respiration	membrane-anchored serine protease (mycosin) MycP4
1322755	non	AG	MMAR_1100	-		intermediary metabolism and respiration	membrane-anchored serine protease (mycosin) MycP4
1324467	syn	GA	MMAR_1101	-		cell wall and cell processes	conserved hypothetical membrane protein
1326674	syn	CT	MMAR_1102	-		cell wall and cell processes	conserved membrane protein
1327935	non	GC	MMAR_1102	-		cell wall and cell processes	conserved membrane protein
1328031	non	GA	MMAR_1102	-		cell wall and cell processes	conserved membrane protein
1328171	syn	TC	MMAR_1102	-		cell wall and cell processes	conserved membrane protein
1328379	non	GC	MMAR_1103	-		conserved hypotheticals	conserved hypothetical protein
1328618	non	GC	MMAR_1103	-		conserved hypotheticals	conserved hypothetical protein
1329219	non	CT	MMAR_1103	-		conserved hypotheticals	conserved hypothetical protein
1331499	int	CT	76 MMAR_1108	intermediary metabolism and respiration		phosphomannomutase MrsA	
1333439	non	GT					
133726	syn	GA	MMAR_1110	-		conserved hypotheticals	conserved hypothetical protein
1338381	syn	GA	MMAR_1110	-		conserved hypotheticals	conserved hypothetical protein
1335352	non	CA	MMAR_1111	-		intermediary metabolism and respiration	coenzyme F420-dependent oxidoreductase
1336441	syn	GA	MMAR_1112	-		conserved hypotheticals	conserved protein
1336826	non	GT	MMAR_1113	-		cell wall and cell processes	conserved hypothetical transmembrane protein
1337164	int	TC	82 MMAR_1114	intermediary metabolism and respiration		glucosamine-fructose-6-phosphate aminotransferase GlmS	
1337806	syn	GT				intermediary metabolism and respiration	glucosamine-fructose-6-phosphate aminotransferase GlmS
1337818	syn	CA	MMAR_1114	-		intermediary metabolism and respiration	glucosamine-fructose-6-phosphate aminotransferase GlmS
1338325	syn	GT	MMAR_1114	-		intermediary metabolism and respiration	glucosamine-fructose-6-phosphate aminotransferase GlmS
1338650	non	GC	MMAR_1114	-		intermediary metabolism and respiration	glucosamine-fructose-6-phosphate aminotransferase GlmS
1340630	syn	CA	MMAR_1116	-		cell wall and cell processes	conserved hypothetical transmembrane protein
1345418	syn	GA	MMAR_1120	-		cell wall and cell processes	conserved hypothetical hydrolase
1348426	syn	GA	MMAR_1124	-			O-sialoglycoprotein endopeptidase Gcp (glycoprotease)
1349965	syn	CT	MMAR_1126	-			60 kDa chaperone (GroEL1)
1361233	syn	CT	MMAR_1134	-		information pathways	alternative RNA polymerase sigma-D factor SigD
1361553	non	GA	MMAR_1135	-		conserved hypotheticals	conserved hypothetical protein
1361789	syn	CG	MMAR_1135	-		conserved hypotheticals	conserved hypothetical protein
1364497	syn	CT	MMAR_1137	-		intermediary metabolism and respiration	inosine-5'-monophosphate (imp) dehydrogenase Guab2
1364737	syn	CT	MMAR_1137	-		intermediary metabolism and respiration	inosine-5'-monophosphate (imp) dehydrogenase Guab2
1365967	int	CT	12 MMAR_1138	intermediary metabolism and respiration		inosine-5'-monophosphate (imp) dehydrogenase Guab3	
1366028	int	GA					
1370985	syn	GC	MMAR_1142	-		regulatory proteins	transcriptional regulator
1371223	non	CT	MMAR_1142	-		regulatory proteins	transcriptional regulator
1372243	syn	CT	MMAR_1143	-		intermediary metabolism and respiration	glycosyl hydrolase
1375718	non	GA	MMAR_1146	-		cell wall and cell processes	integral membrane transport protein
1377314	int	CT	44 MMAR_1146	cell wall and cell processes		integral membrane transport protein	
1379329	syn	CT				intermediary metabolism and respiration	GMP synthase Guaa
1379400	syn	AG	MMAR_1148	-		intermediary metabolism and respiration	GMP synthase Guaa
1380470	int	G-	71 MMAR_1150	conserved hypotheticals		conserved protein	
1383129	non	CT				intermediary metabolism and respiration	Inosine-uridine nucleoside hydrolase IunH
1383960	syn	GA	MMAR_1153	-		lipid metabolism	short-chain dehydrogenase AcrA1
1383968	non	CT	MMAR_1153	-		lipid metabolism	short-chain dehydrogenase AcrA1
1383990	syn	CT	MMAR_1153	-		lipid metabolism	short-chain dehydrogenase AcrA1
1385038	non	GA	MMAR_1153	-		lipid metabolism	short-chain dehydrogenase AcrA1
1385072	non	CT	MMAR_1153	-		lipid metabolism	short-chain dehydrogenase AcrA1
1387722	syn	AG	MMAR_1156	-			trehalose-6-phosphate phosphatase OtsB2
1387867	non	CT	MMAR_1156	-			trehalose-6-phosphate phosphatase OtsB2
1388202	syn	AG	MMAR_1156	-			trehalose-6-phosphate phosphatase OtsB2
1388726	syn	GA	MMAR_1156	-			trehalose-6-phosphate phosphatase OtsB2
1388934	syn	CT	MMAR_1157	-		conserved hypotheticals	conserved hypothetical protein
1388955	syn	TC	MMAR_1157	-		conserved hypotheticals	conserved hypothetical protein
1389015	syn	GA	MMAR_1157	-		conserved hypotheticals	conserved hypothetical protein
1389144	syn	CT	MMAR_1157	-		conserved hypotheticals	conserved hypothetical protein
1389252	syn	CT	MMAR_1157	-		conserved hypotheticals	conserved hypothetical protein
1389318	syn	AG	MMAR_1157	-		conserved hypotheticals	conserved hypothetical protein
1389753	syn	GA	MMAR_1157	-		conserved hypotheticals	conserved hypothetical protein
1389767	non	GC	MMAR_1157	-		conserved hypotheticals	conserved hypothetical protein
1389745	syn	TC	MMAR_1158	-		information pathways	DNA polymerase III alpha chain DnaE2
1392277	syn	CT	MMAR_1158	-		information pathways	DNA polymerase III alpha chain DnaE2
1393505	non	GA	MMAR_1158	-		information pathways	DNA polymerase III alpha chain DnaE2
1395977	syn	CT	MMAR_1164	-		information pathways	methyltransferase
1401620	non	TG	MMAR_1165	-		regulatory proteins	conserved hypothetical regulatory protein
1401269	syn	GA	MMAR_1165	-		regulatory proteins	conserved hypothetical regulatory protein
1402738	syn	CT	MMAR_1165	-		regulatory proteins	conserved hypothetical regulatory protein
1402857	syn	CA	MMAR_1166	-		conserved hypotheticals	conserved hypothetical protein
1405035	int	AG					
1405178	int	AC		-			
1405767	non	CT	MMAR_1170	-		lipid metabolism	fatty-acid-CoA ligase FadD29_1

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
1405899	non	AG	MMAR_1170	-		lipid metabolism	fatty-acid-CoA ligase FadD29_1
1406532	syn	AC	MMAR_1170	-		lipid metabolism	fatty-acid-CoA ligase FadD29_1
1406939	non	CT	MMAR_1170	-		lipid metabolism	fatty-acid-CoA ligase FadD29_1
1413537	non	CG	MMAR_1173	-		cell wall and cell processes	conserved transmembrane ATP-binding protein ABC transporter
1415845	syn	GA	MMAR_1174	-		cell wall and cell processes	conserved transmembrane ATP-binding protein ABC transporter
1416334	syn	TC	MMAR_1174	-		cell wall and cell processes	conserved transmembrane ATP-binding protein ABC transporter
1421445	int	GA	89 MMAR_1180	lipid metabolism	Fatty acyl-AMP ligase FadD28_1 and polyketide synthase		
1421809	syn	GC		lipid metabolism	Fatty acyl-AMP ligase FadD28_1 and polyketide synthase		
1421827	syn	CG		lipid metabolism	Fatty acyl-AMP ligase FadD28_1 and polyketide synthase		
1423581	non	CT		lipid metabolism	Fatty acyl-AMP ligase FadD28_1 and polyketide synthase		
1424053	syn	CT		lipid metabolism	Fatty acyl-AMP ligase FadD28_1 and polyketide synthase		
1425400	syn	GA		lipid metabolism	Fatty acyl-AMP ligase FadD28_1 and polyketide synthase		
1426042	syn	GC		lipid metabolism	Fatty acyl-AMP ligase FadD28_1 and polyketide synthase		
1426183	non	CG		lipid metabolism	Fatty acyl-AMP ligase FadD28_1 and polyketide synthase		
1429840	syn	CA	MMAR_1180	-		lipid metabolism	Fatty acyl-AMP ligase FadD28_1 and polyketide synthase
1430198	non	CA	MMAR_1180	-		lipid metabolism	Fatty acyl-AMP ligase FadD28_1 and polyketide synthase
1430233	syn	TA	MMAR_1180	-		lipid metabolism	Fatty acyl-AMP ligase FadD28_1 and polyketide synthase
1430413	syn	CG	MMAR_1180	-		lipid metabolism	Fatty acyl-AMP ligase FadD28_1 and polyketide synthase
1431588	non	AG	MMAR_1181	-		cell wall and cell processes	hypothetical secreted protein
1431608	syn	GA	MMAR_1181	-		cell wall and cell processes	hypothetical secreted protein
1431776	non	TC	MMAR_1182	-		cell wall and cell processes	exported protein
1432082	non	CG	MMAR_1182	-		cell wall and cell processes	exported protein
1432447	syn	CT	MMAR_1183	-		intermediary metabolism and respiration	methyltransferase
1433163	syn	AG	MMAR_1184	-		intermediary metabolism and respiration	homoserine O-acetyltransferase MetA
1434533	syn	GA	MMAR_1185	-		intermediary metabolism and respiration	O-acetylhomoserine sulfhydrylase MetC
1437234	non	TC	MMAR_1187	-		cell wall and cell processes	conserved membrane protein
1439457	syn	CA	MMAR_1189	-		cell wall and cell processes	conserved integral membrane protein
1440783	syn	AG	MMAR_1190	-		cell wall and cell processes	n-acetylglucosamine-6-phosphate deacetylase NagA
1441020	syn	AG	MMAR_1190	-		cell wall and cell processes	n-acetylglucosamine-6-phosphate deacetylase NagA
1441029	syn	AG	MMAR_1190	-		cell wall and cell processes	n-acetylglucosamine-6-phosphate deacetylase NagA
1457628	non	GA	MMAR_1200	-		intermediary metabolism and respiration	succinate dehydrogenase (iron-sulphur protein subunit) SdhB
1461098	syn	GA	MMAR_1204	-		intermediary metabolism and respiration	cytidine deaminase Cdd
1463481	syn	GA	MMAR_1206	-		intermediary metabolism and respiration	adenosine deaminase Add
1471616	syn	CA	MMAR_1210	-		intermediary metabolism and respiration	allantoinase Ale
1472968	syn	AT	MMAR_1212	-		cell wall and cell processes	conserved hypothetical membrane protein
1473229	syn	GC	MMAR_1212	-		cell wall and cell processes	conserved hypothetical membrane protein
1474751	non	TC	MMAR_1213	-		conserved hypotheticals	conserved hypothetical 13E12 repeat family protein
1474902	non	TC	MMAR_1213	-		conserved hypotheticals	conserved hypothetical 13E12 repeat family protein
1475457	non	CA	MMAR_1213	-		conserved hypotheticals	conserved hypothetical 13E12 repeat family protein
1476506	non	CT	MMAR_1214	-		conserved hypotheticals	conserved hypothetical protein
1476810	syn	CA	MMAR_1214	-		conserved hypotheticals	conserved hypothetical protein
1479564	non	AC	MMAR_1217	-		intermediary metabolism and respiration	uracil phosphoribosyltransferase Upp
1479858	syn	CT	MMAR_1217	-		intermediary metabolism and respiration	uracil phosphoribosyltransferase Upp
1479972	non	GT	MMAR_1217	-		intermediary metabolism and respiration	uracil phosphoribosyltransferase Upp
1481009	non	TG	MMAR_1218	-		intermediary metabolism and respiration	phosphomannomutase PmmB
1483112	syn	GA	MMAR_1220	-		intermediary metabolism and respiration	amidohydrolase AmbB
1483274	syn	AG	MMAR_1220	-		intermediary metabolism and respiration	amidohydrolase AmbB
1489685	syn	CT	MMAR_1225	-		intermediary metabolism and respiration	glycerol-3-phosphate dehydrogenase GlpD2
1492334	non	CT	MMAR_1227	-		conserved hypotheticals	conserved hypothetical protein
1492683	syn	CT	MMAR_1228	-		cell wall and cell processes	metal cation transporting p-type ATPase CtpH_1
1493256	syn	CA	MMAR_1228	-		cell wall and cell processes	metal cation transporting p-type ATPase CtpH_1
1495452	syn	AG	MMAR_1228	-		cell wall and cell processes	metal cation transporting p-type ATPase CtpH_1
1497749	non	AG	MMAR_1229	-		regulatory protein	phosphate-transport system transcriptional regulatory protein PhoY1
1498370	non	TA	MMAR_1230	-		cell wall and cell processes	magnesium and cobalt transport transmembrane protein CorA_1
1498497	syn	GC	MMAR_1230	-		cell wall and cell processes	magnesium and cobalt transport transmembrane protein CorA_1
1498562	syn	CT	MMAR_1230	-		cell wall and cell processes	magnesium and cobalt transport transmembrane protein CorA_1
1500608	non	AG	MMAR_1232	-		intermediary metabolism and respiration	arylsulfatase AtsB (aryl-sulfate sulphohydrolase)
1500626	non	AG	MMAR_1232	-		intermediary metabolism and respiration	arylsulfatase AtsB (aryl-sulfate sulphohydrolase)
1501091	non	CA	MMAR_1232	-		intermediary metabolism and respiration	arylsulfatase AtsB (aryl-sulfate sulphohydrolase)
1502521	non	CT	MMAR_1232	-		intermediary metabolism and respiration	arylsulfatase AtsB (aryl-sulfate sulphohydrolase)
1502820	non	AG	MMAR_1232	-		intermediary metabolism and respiration	arylsulfatase AtsB (aryl-sulfate sulphohydrolase)
1502980	non	CT	MMAR_1232	-		intermediary metabolism and respiration	arylsulfatase AtsB (aryl-sulfate sulphohydrolase)
1504979	int	CT	74 MMAR_1235 PE/PE	intermediary metabolism and respiration	arylsulfatase AtsB (aryl-sulfate sulphohydrolase)		
1505030	int	AT		intermediary metabolism and respiration	PPE family protein		
1505056	int	CT		intermediary metabolism and respiration	PPE family protein		
1505522	int	CT		intermediary metabolism and respiration	PPE family protein		
1506438	syn	TC	MMAR_1236	-		lipid metabolism	esterase lipoprotein LpqC
1507707	syn	GA	MMAR_1237	-		information pathways	endonuclease viii Nei
1508626	non	GA	MMAR_1238	-		information pathways	ATP-dependent helicase Lhr
1510962	non	CG	MMAR_1238	-		information pathways	ATP-dependent helicase Lhr
1511399	non	TG	MMAR_1238	-		information pathways	ATP-dependent helicase Lhr
1511797	non	GA	MMAR_1238	-		information pathways	ATP-dependent helicase Lhr
1513574	syn	CG	MMAR_1240	-		intermediary metabolism and respiration	pipecideine-6-carboxylic acid dehydrogenase Pcd
1516901	non	GA	MMAR_1243	-		intermediary metabolism and respiration	L-lysine-epsilon-aminotransferase Lat
1517771	syn	CT	MMAR_1243	-		intermediary metabolism and respiration	L-lysine-epsilon-aminotransferase Lat
1518837	int	A-	41 MMAR_1245 conserved hypothetical	intermediary metabolism and respiration	mycobacterial conserved protein UsfY		
1518838	int	C-		intermediary metabolism and respiration	mycobacterial conserved protein UsfY		
1518898	int	C-	102 MMAR_1245 conserved hypothetical	intermediary metabolism and respiration	mycobacterial conserved protein UsfY		
1518928	int	TA		intermediary metabolism and respiration	mycobacterial conserved protein UsfY		
1518931	int	CT	132 MMAR_1245 conserved hypothetical	intermediary metabolism and respiration	mycobacterial conserved protein UsfY		
1521194	int	GA		intermediary metabolism and respiration	transcriptional regulatory protein		
1521219	int	GA	59 MMAR_1249 regulatory proteins	intermediary metabolism and respiration	transcriptional regulatory protein		
1521723	int	CT		intermediary metabolism and respiration	transcriptional regulatory protein		
152258	syn	CT	MMAR_1250	-		peptide synthetase Nrp (peptide synthase)	
1523928	non	GT	MMAR_1250	-		peptide synthetase Nrp (peptide synthase)	
1527625	syn	CT	MMAR_1250	-		peptide synthetase Nrp (peptide synthase)	
1527636	non	CA	MMAR_1250	-		peptide synthetase Nrp (peptide synthase)	
1527912	syn	GA	MMAR_1250	-		peptide synthetase Nrp (peptide synthase)	
1527918	non	CA	MMAR_1250	-		peptide synthetase Nrp (peptide synthase)	
1528214	non	GA	MMAR_1250	-		peptide synthetase Nrp (peptide synthase)	
1531987	syn	CT	MMAR_1251	-		intermediary metabolism and respiration	bifunctional protein acetyl-/propionyl-coenzyme a carboxylase (alpha chain) AccA3
1534808	syn	GT	MMAR_1254	-		information pathways	nucleotide-binding protein
1534973	syn	GC	MMAR_1254	-		information pathways	nucleotide-binding protein
1535012	syn	CT	MMAR_1254	-		information pathways	nucleotide-binding protein
1535671	non	CA	MMAR_1256	-		intermediary metabolism and respiration	propionyl-CoA carboxylase beta chain 5 AccD5

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
1535673	syn	CG	MMAR_1256	-		intermediary metabolism and respiration	propionyl-CoA carboxylase beta chain 5 AccD5
1537678	non	CT	MMAR_1257	-		intermediary metabolism and respiration	bifunctional protein BirA
1537689	syn	TC	MMAR_1257	-		intermediary metabolism and respiration	bifunctional protein BirA
1537697	syn	AG	MMAR_1257	-		intermediary metabolism and respiration	bifunctional protein BirA
1548715	non	CT	MMAR_1267	-		intermediary metabolism and respiration	acyl-CoA transferase
1551605	non	CT	MMAR_1269	-		lipid metabolism	Acyl esterase
1551883	syn	AG	MMAR_1269	-		lipid metabolism	Acyl esterase
1561539	syn	GA	MMAR_1279	-		information pathways	DNA methylase
1562154	non	CA	MMAR_1279	-		information pathways	DNA methylase
1562155	non	AC	MMAR_1279	-		information pathways	DNA methylase
1565330	Int	CG	81 MMAR_1281	intermediary metabolism and respiration	F420 biosynthesis protein FbiA		
1570243	syn	GA	MMAR_1287	-		intermediary metabolism and respiration	mannose-6-phosphate isomerase ManA
1572283	non	GA	MMAR_1288	-		conserved hypotheticals	conserved hypothetical protein
1573156	non	TC	MMAR_1289	-		conserved hypotheticals	conserved hypothetical protein
1577323	syn	CG	MMAR_1294	-		regulatory proteins	transcriptional regulatory protein (probably TetR-family)
1584985	syn	CT	MMAR_1300	-		regulatory proteins	two component sensory transduction histidine kinase MtrB
1586127	syn	CT	MMAR_1301	-		cell wall and cell processes	conserved lipoprotein LpB
1586532	syn	GA	MMAR_1301	-		cell wall and cell processes	conserved lipoprotein LpB
1587056	non	CT	MMAR_1301	-		cell wall and cell processes	conserved lipoprotein LpB
1587243	syn	CT	MMAR_1301	-		cell wall and cell processes	conserved lipoprotein LpB
1592927	syn	CT	MMAR_1305	-		cell wall and cell processes	preprotein translocase SecA1 1 subunit
1595559	non	GA	MMAR_1306	-		cell wall and cell processes	conserved transmembrane transport protein
1596206	non	GA	MMAR_1306	-		cell wall and cell processes	conserved transmembrane transport protein
1598248	syn	GT	MMAR_1309	-		cell wall and cell processes	conserved membrane transport protein
1598683	syn	TC	MMAR_1309	-		cell wall and cell processes	conserved membrane transport protein
1598857	non	GC	MMAR_1309	-		cell wall and cell processes	conserved membrane transport protein
1598858	non	GT	MMAR_1309	-		cell wall and cell processes	conserved membrane transport protein
1600262	syn	AG	MMAR_1311	-		conserved hypotheticals	conserved hypothetical protein
1602796	Int	CG	126 MMAR_1314	intermediary metabolism and respiration	oxidoreductase		
1604290	syn	CT	MMAR_1315	-		lipid metabolism	linoleoyl-CoA desaturase DesA3
1604293	syn	TC	MMAR_1315	-		lipid metabolism	linoleoyl-CoA desaturase DesA3
1604338	non	GC	MMAR_1315	-		lipid metabolism	linoleoyl-CoA desaturase DesA3
1609071	syn	GA	MMAR_1319	-		conserved hypotheticals	conserved hypothetical protein
1617643	syn	TC	MMAR_1324	-		cell wall and cell processes	conserved hypothetical membrane protein
1624299	non	TC	MMAR_1331	-		conserved hypotheticals	conserved hypothetical alanine and proline rich protein
1625093	syn	GA	MMAR_1331	-		conserved hypotheticals	conserved hypothetical alanine and proline rich protein
1625262	non	CT	MMAR_1331	-		conserved hypotheticals	conserved hypothetical alanine and proline rich protein
1625451	non	TC	MMAR_1331	-		conserved hypotheticals	conserved hypothetical alanine and proline rich protein
1625636	syn	GA	MMAR_1331	-		conserved hypotheticals	conserved hypothetical alanine and proline rich protein
1625726	syn	TC	MMAR_1331	-		conserved hypotheticals	conserved hypothetical alanine and proline rich protein
1626274	non	CA	MMAR_1332	-		cell wall and cell processes	conserved hypothetical membrane protein
1626297	non	TC	MMAR_1332	-		cell wall and cell processes	conserved hypothetical membrane protein
1626333	non	CT	MMAR_1332	-		cell wall and cell processes	conserved hypothetical membrane protein
1626441	Int	GA	9 MMAR_1332	cell wall and cell processes	conserved hypothetical membrane protein		
1627327	Int	AT		intermediary metabolism and respiration	iron-regulated short-chain dehydrogenase/reductase		
1628397	non	GA	MMAR_1335	-		regulatory proteins	anti-sigma factor
1629238	syn	CT	MMAR_1337	-		regulatory proteins	sensor kinase from two component regulatory system
1629370	syn	CA	MMAR_1337	-		regulatory proteins	sensor kinase from two component regulatory system
1633122	non	GA	MMAR_1341	-		intermediary metabolism and respiration	acetyltransferase
1634473	non	AG	MMAR_1343	-		intermediary metabolism and respiration	phosphoglycerate mutase Gpm2
1635250	non	AC	MMAR_1344	-		information pathways	Soj/ParA-related protein
1639543	syn	CT	MMAR_1347	-		conserved hypotheticals	conserved hypothetical protein
1640195	syn	GC	MMAR_1348	-		conserved hypotheticals	conserved hypothetical threonine and proline rich protein
1641402	syn	GT	MMAR_1350	-		regulatory proteins	transcriptional regulator TetR family
1641862	syn	TC	MMAR_1351	-		conserved hypotheticals	conserved hypothetical protein
1641889	syn	CT	MMAR_1351	-		conserved hypotheticals	conserved hypothetical protein
1642182	non	GA	MMAR_1351	-		conserved hypotheticals	conserved hypothetical protein
1645174	non	AG	MMAR_1354	-		information pathways	DNA-methyltransferase (modification methylase)
1646110	Int	CA	41 MMAR_1356	conserved hypotheticals	conserved hypothetical protein		
1647192	non	GA	MMAR_1357	-		cell wall and cell processes	conserved hypothetical membrane protein
1648816	syn	CT	MMAR_1358	-		information pathways	ATP-dependent DNA helicase
1651005	syn	CA	MMAR_1359	-		information pathways	ATP-dependent DNA helicase
1651795	non	GC	MMAR_1359	-		information pathways	ATP-dependent DNA helicase
1652246	non	CT	MMAR_1359	-		information pathways	ATP-dependent DNA helicase
1652871	syn	GA	MMAR_1359	-		information pathways	ATP-dependent DNA helicase
1653072	syn	CT	MMAR_1359	-		information pathways	ATP-dependent DNA helicase
1653143	non	CG	MMAR_1359	-		information pathways	ATP-dependent DNA helicase
1653225	syn	AG	MMAR_1359	-		information pathways	ATP-dependent DNA helicase
1655333	syn	CT	MMAR_1361	intermediary metabolism and respiration	NADH pyrophosphatase NudC		
1655914	syn	TG	MMAR_1361	-		intermediary metabolism and respiration	NADH pyrophosphatase NudC
1656115	syn	CA	MMAR_1361	-		intermediary metabolism and respiration	NADH pyrophosphatase NudC
1660560	syn	GC	MMAR_1366	-		cell wall and cell processes	conserved ATP-binding protein ABC transporter
1662320	non	CT	MMAR_1368	-		conserved hypotheticals	conserved hypothetical protein
1663075	non	AC	MMAR_1369	-		conserved hypotheticals	conserved hypothetical protein
1663906	non	CG	MMAR_1369	-		conserved hypotheticals	conserved hypothetical protein
1665286	syn	GC	MMAR_1370	-		information pathways	serine protease
1665316	syn	CT	MMAR_1370	-		serine protease	serine protease
1665334	syn	CT	MMAR_1370	-		serine protease	serine protease
1665373	syn	AC	MMAR_1370	-		serine protease	serine protease
1665490	syn	GT	MMAR_1370	-		serine protease	serine protease
1665548	non	GT	MMAR_1370	-		serine protease	serine protease
1665550	syn	TA	MMAR_1370	-		serine protease	serine protease
1665579	Int	CA	117 MMAR_1371	cell wall and cell processes	conserved transmembrane protein		
1666403	syn	GA	MMAR_1371	-		cell wall and cell processes	conserved transmembrane protein
1667495	syn	GT	MMAR_1371	-		cell wall and cell processes	conserved transmembrane protein
1668095	syn	GC	MMAR_1371	-		cell wall and cell processes	conserved transmembrane protein
1669196	non	CG	MMAR_1372	-		conserved hypotheticals	conserved hypothetical protein
1669668	syn	AG	MMAR_1372	-		conserved hypotheticals	conserved hypothetical protein
1672363	syn	CT	MMAR_1374	-		information pathways	FK-506 binding protein peptidyl-prolyl cis-trans isomerase
1672498	non	GC	MMAR_1374	-		information pathways	FK-506 binding protein peptidyl-prolyl cis-trans isomerase
1674333	syn	CT	MMAR_1375	intermediary metabolism and respiration	arylsulfatase AtsD 1		
1674537	syn	GC	MMAR_1375	intermediary metabolism and respiration	arylsulfatase AtsD 1		
1674612	syn	GA	MMAR_1375	intermediary metabolism and respiration	arylsulfatase AtsD 1		
1674765	syn	GA	MMAR_1375	intermediary metabolism and respiration	arylsulfatase AtsD 1		
1674856	non	GA	MMAR_1375	intermediary metabolism and respiration	arylsulfatase AtsD 1		

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
1675167	syn	GA	MMAR_1375	-		intermediary metabolism and respiration	arylsulfatase AtsD_1
1675379	non	CT	MMAR_1376	-		conserved hypothetical	conserved hypothetical protein
1675558	non	AG	MMAR_1376	-		conserved hypothetical	conserved hypothetical protein
1676229	syn	CT	MMAR_1377	-		conserved hypothetical	conserved hypothetical protein
1676694	syn	CT	MMAR_1377	-		conserved hypothetical	conserved hypothetical protein
1676790	int	AG		48	MMAR_1377	conserved hypothetical	conserved hypothetical protein
1677711	syn	CG	MMAR_1378	-		regulatory protein	transcriptional regulatory protein
1677780	syn	AG	MMAR_1378	-		regulatory protein	transcriptional regulatory protein
1678501	syn	CT	MMAR_1379	-		conserved hypothetical	conserved protein
1678585	syn	TC	MMAR_1379	-		conserved hypothetical	conserved protein
1678826	non	AG	MMAR_1379	-		conserved hypothetical	conserved protein
1680526	non	CG	MMAR_1380	-		intermediary metabolism and respiration	methylisocitrate lyase 2
1680594	syn	CT	MMAR_1380	-		intermediary metabolism and respiration	methylisocitrate lyase 2
1681822	non	CA	MMAR_1381	-		intermediary metabolism and respiration	citrate synthase T_GltA1
1682571	syn	AC	MMAR_1382	-		conserved hypothetical	conserved hypothetical protein
1683339	syn	TC	MMAR_1384	-		conserved hypothetical	conserved hypothetical protein
1684368	int	AG		61	MMAR_1386	unknown	hypothetical protein
1685084	non	GT	MMAR_1387	-		intermediary metabolism and respiration	monoamine oxidase
1685321	syn	GT	MMAR_1387	-		intermediary metabolism and respiration	monoamine oxidase
1685441	syn	TG	MMAR_1387	-		intermediary metabolism and respiration	monoamine oxidase
1685448	non	TC	MMAR_1387	-		intermediary metabolism and respiration	monoamine oxidase
1686482	syn	GT	MMAR_1388	-			non-heme haloperoxidase Hpx
1687585	non	AG	MMAR_1389	-		intermediary metabolism and respiration	flavin-containing monoamine oxidase AofH (amine oxidase)
1687668	syn	CT	MMAR_1389	-		intermediary metabolism and respiration	flavin-containing monoamine oxidase AofH (amine oxidase)
1687941	syn	GA	MMAR_1389	-		intermediary metabolism and respiration	flavin-containing monoamine oxidase AofH (amine oxidase)
1689593	non	AG	MMAR_1390	-		intermediary metabolism and respiration	oxidoreductase
1693831	syn	TC	MMAR_1393	-		conserved hypothetical	conserved hypothetical protein
1695455	syn	GA	MMAR_1394	-		regulatory proteins	transcriptional regulatory protein (probably TetR-family)
1781333	int	TA		118	MMAR_1469	PE/PE	PPE family protein
1781352	int	AC		99	MMAR_1469	PE/PE	PPE family protein
1781353	int	TA		98	MMAR_1469	PE/PE	PPE family protein
1781484	int	GA		33	MMAR_1469	PE/PE	PPE family protein
1781911	non	TC	MMAR_1470	-		intermediary metabolism and respiration	NADH dehydrogenase I (chain N) NuO _N (NADH-ubiquinone oxidoreductase chain N)
1792830	syn	TG	MMAR_1478	-		intermediary metabolism and respiration	NADH dehydrogenase I (chain F) NuO _F (NADH-ubiquinone oxidoreductase chain F)
1793999	syn	CT	MMAR_1479	-		intermediary metabolism and respiration	NADH dehydrogenase I (chain E) NuO _E (NADH-ubiquinone oxidoreductase chain E)
1796536	syn	CT	MMAR_1482	-		intermediary metabolism and respiration	NADH dehydrogenase I (chain B) NuO _B (NADH-ubiquinone oxidoreductase chain B)
1796575	syn	CT	MMAR_1482	-		intermediary metabolism and respiration	NADH dehydrogenase I (chain B) NuO _B (NADH-ubiquinone oxidoreductase chain B)
1801286	non	CG	MMAR_1487	-		conserved hypothetical	conserved protein
1801430	syn	CT	MMAR_1487	-		conserved hypothetical	conserved protein
1801535	syn	AG	MMAR_1487	-		conserved hypothetical	conserved protein
1802007	non	CT	MMAR_1488	-		conserved hypothetical	conserved hypothetical protein
1802014	syn	CA	MMAR_1488	-		conserved hypothetical	conserved hypothetical protein
1802525	syn	AG	MMAR_1490	-		conserved hypothetical	conserved hypothetical protein
1804319	non	AG	MMAR_1491	-		lipid metabolism	acyl-CoA dehydrogenase FadE12_3
1806667	non	CT	MMAR_1494	-		conserved hypothetical	conserved protein
1820322	non	CT	MMAR_1505	-		intermediary metabolism and respiration	acetaldehyde dehydrogenase MhpF
1820329	non	GC	MMAR_1505	-		intermediary metabolism and respiration	acetaldehyde dehydrogenase MhpF
1820338	non	GA	MMAR_1505	-		intermediary metabolism and respiration	acetaldehyde dehydrogenase MhpF
1820341	non	CA	MMAR_1505	-		intermediary metabolism and respiration	acetaldehyde dehydrogenase MhpF
1820349	non	CG	MMAR_1506	-		intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
1820412	non	AG	MMAR_1506	-		intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
1820444	syn	GC	MMAR_1506	-		intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
1820492	syn	CG	MMAR_1506	-		intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
1820522	syn	TC	MMAR_1506	-		intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
1820613	non	AG	MMAR_1506	-		intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
1820630	non	GA	MMAR_1506	-		intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
1820660	syn	GT	MMAR_1506	-		intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
1820696	non	CT	MMAR_1506	-		intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
1820738	syn	GC	MMAR_1506	-		intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
1820748	non	TC	MMAR_1506	-		intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
1820778	non	CT	MMAR_1506	-		intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
1820779	non	GT	MMAR_1506	-		intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
1820813	syn	CT	MMAR_1506	-		intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
1820853	non	CA	MMAR_1506	-		intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
1820900	syn	TC	MMAR_1506	-		intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
1820901	non	CT	MMAR_1506	-		intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
1820915	syn	GA	MMAR_1506	-		intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
1820924	syn	AC	MMAR_1506	-		intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
1821149	syn	TC	MMAR_1506	-		intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
1821197	syn	GC	MMAR_1506	-		intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
1821200	syn	GA	MMAR_1506	-		intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
1821302	syn	CG	MMAR_1506	-		intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
1821538	non	AG	MMAR_1507	-		intermediary metabolism and respiration	alpha-acetoactate decarboxylase
1821775	non	AC	MMAR_1507	-		intermediary metabolism and respiration	alpha-acetoactate decarboxylase
1821911	syn	CT	MMAR_1507	-		intermediary metabolism and respiration	alpha-acetoactate decarboxylase
1822148	syn	CG	MMAR_1507	-		intermediary metabolism and respiration	alpha-acetoactate decarboxylase
1824508	non	GC	MMAR_1509	-		lipid metabolism	acyl-CoA dehydrogenase FadE23
1824551	syn	CG	MMAR_1509	-		lipid metabolism	acyl-CoA dehydrogenase FadE23
1825430	syn	CT	MMAR_1510	-		lipid metabolism	acyl-CoA dehydrogenase FadE24
1825668	non	GA	MMAR_1510	-		lipid metabolism	acyl-CoA dehydrogenase FadE24
1825763	syn	GA	MMAR_1510	-		lipid metabolism	acyl-CoA dehydrogenase FadE24
1825884	non	CG	MMAR_1510	-		lipid metabolism	acyl-CoA dehydrogenase FadE24
1826024	syn	TC	MMAR_1510	-		lipid metabolism	acyl-CoA dehydrogenase FadE24
1826727	non	GC	MMAR_1511	-		intermediary metabolism and respiration	monophosphatase
1828149	int	GA		-			
1829145	int	GT		-			
1834043	non	GA	MMAR_1517	-		regulatory proteins	two component sensor histidine kinase DevS
1834024	non	CT	MMAR_1517	-		regulatory proteins	two component sensor histidine kinase DevS
184175	syn	GC	MMAR_1517	-		regulatory proteins	two component sensor histidine kinase DevS
1839323	int	AG		121	MMAR_1523	conserved hypothetical	conserved hypothetical protein
1839628	non	TG	MMAR_1523	-		conserved hypothetical	conserved hypothetical protein
1840019	syn	CG	MMAR_1523	-		conserved hypothetical	conserved hypothetical protein
1842138	syn	AG	MMAR_1525	-		intermediary metabolism and respiration	alkylidihydroxacetonephosphate synthase AppS
1842468	non	GA	MMAR_1525	-		intermediary metabolism and respiration	alkylidihydroxacetonephosphate synthase AppS
1843300	syn	GA	MMAR_1526	-		intermediary metabolism and respiration	NADPH:adenodoxin oxidoreductase FprA_1

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
1843948	syn	TC	MMAR_1526	-		intermediary metabolism and respiration	NADPH:adrenodoxin oxidoreductase FprA_1
1846270	syn	GT	MMAR_1529	-		cell wall and cell processes	conserved hypothetical membrane protein
1846471	non	TG	MMAR_1529	-		cell wall and cell processes	conserved hypothetical membrane protein
1847571	syn	CG	MMAR_1531	-		cell wall and cell processes	cell division protein FtsX
1848144	syn	CT	MMAR_1531	-		cell wall and cell processes	cell division protein FtsX
1848960	non	CT	MMAR_1533	-		cell wall and cell processes	conserved hypothetical membrane protein
1851967	non	TC	MMAR_1534	-		conserved hypotheticals	conserved protein
1852149	int	AG		26	MMAR_1534	conserved hypotheticals	conserved protein
1852175	int	-G		52	MMAR_1534	conserved hypotheticals	conserved protein
185280	int	G-		-			
1852682	non	CT	MMAR_1535	-		cell wall and cell processes	conserved ATPase
1853388	syn	GC	MMAR_1535	-		cell wall and cell processes	conserved ATPase
1853457	syn	CT	MMAR_1535	-		cell wall and cell processes	conserved ATPase
1854545	non	AC	MMAR_1536	-		conserved hypotheticals	conserved hypothetical protein
1854776	syn	CT	MMAR_1537	-		conserved hypotheticals	conserved protein
1854807	syn	CT	MMAR_1537	-		conserved hypotheticals	conserved protein
1855346	syn	CA	MMAR_1537	-		conserved hypotheticals	conserved protein
1860841	int	GT		36	MMAR_1543	cell wall and cell processes	conserved membrane protein
1861210	syn	TG	MMAR_1543	-		cell wall and cell processes	conserved membrane protein
1862250	int	TC		48	MMAR_1545	conserved hypotheticals	conserved hypothetical protein
1862373	non	CA	MMAR_1545	-		conserved hypotheticals	conserved hypothetical protein
1862569	non	CT	MMAR_1545	-		conserved hypotheticals	conserved hypothetical protein
1862661	non	AG	MMAR_1545	-		conserved hypotheticals	conserved hypothetical protein
1870556	int	G-		88	MMAR_1551	conserved hypotheticals	conserved hypothetical protein
1870952	int	GA		29	MMAR_1552	cell wall and cell processes	conserved hypothetical secreted protein
1879647	syn	AG	MMAR_1561	-		intermediary metabolism and respiration	tRNA delta(2)-isopentenylpyrophosphate transferase MiaA_1
1880044	non	C-	MMAR_1568	-		intermediary metabolism and respiration	short-chain type dehydrogenase/reductase
1888281	syn	AG	MMAR_1569	-		regulatory proteins	conserved hypothetical regulatory protein
1888703	non	CT	MMAR_1569	-		regulatory proteins	conserved hypothetical regulatory protein
1894820	syn	CA	MMAR_1575	-		intermediary metabolism and respiration	conserved oxidoreductase
1895397	int	CT		139	MMAR_1576	unknown	hypothetical protein
1895404	int	GA		132	MMAR_1576	unknown	hypothetical protein
1896403	syn	GT	MMAR_1577	-		intermediary metabolism and respiration	hydrolase
1896580	non	GC	MMAR_1577	-		intermediary metabolism and respiration	hydrolase
1896672	non	CT	MMAR_1577	-		intermediary metabolism and respiration	hydrolase
1897450	syn	AG	MMAR_1577	-		intermediary metabolism and respiration	hydrolase
1897883	non	TA	MMAR_1578	-		conserved hypotheticals	conserved hypothetical protein
1898518	syn	GT	MMAR_1579	-		conserved hypotheticals	conserved hypothetical protein
1901315	non	CT	MMAR_1580	-		intermediary metabolism and respiration	dehydrogenase
1901441	non	AG	MMAR_1580	-		intermediary metabolism and respiration	dehydrogenase
1902368	non	TC	MMAR_1581	-		cell wall and cell processes	conserved hypothetical membrane protein
1903311	int	GA		25	MMAR_1581	cell wall and cell processes	conserved hypothetical membrane protein
1903397	int	CT		111	MMAR_1581	cell wall and cell processes	conserved hypothetical membrane protein
1903509	non	CT	MMAR_1582	-		conserved hypotheticals	conserved hypothetical protein
1903538	non	GT	MMAR_1582	-		conserved hypotheticals	conserved hypothetical protein
1903726	syn	GA	MMAR_1582	-		conserved hypotheticals	conserved hypothetical protein
1903804	syn	CT	MMAR_1582	-		conserved hypotheticals	conserved hypothetical protein
1904125	syn	CT	MMAR_1582	-		conserved hypotheticals	conserved hypothetical protein
1904192	syn	TC	MMAR_1582	-		conserved hypotheticals	conserved hypothetical protein
1904265	non	AG	MMAR_1582	-		conserved hypotheticals	conserved hypothetical protein
1904326	syn	AG	MMAR_1582	-		conserved hypotheticals	conserved hypothetical protein
1904344	syn	TG	MMAR_1582	-		conserved hypotheticals	conserved hypothetical protein
1904356	syn	AG	MMAR_1582	-		conserved hypotheticals	conserved hypothetical protein
1904456	syn	CT	MMAR_1582	-		conserved hypotheticals	conserved hypothetical protein
1905801	int	AG		20	MMAR_1583	intermediary metabolism and respiration	citrate lyase beta subunit Cte_2
1905893	syn	GA	MMAR_1584	-		conserved hypotheticals	conserved hypothetical protein
1908896	non	AG	MMAR_1587	-		conserved hypotheticals	conserved hypothetical protein
1909715	non	GA	MMAR_1588	-		conserved hypotheticals	conserved hypothetical protein
1911219	non	GC	MMAR_1591	-		intermediary metabolism and respiration	phosphoglucomutase PgmA
1911940	syn	CT	MMAR_1591	-		intermediary metabolism and respiration	phosphoglucomutase PgmA
1913061	non	AG	MMAR_1592	-		unknown	hypothetical protein
1936561	int	CG		-			
1936672	int	AT		-			
1936819	int	TC		137	MMAR_1601	PE/PPE	PE-PGRS family protein
1937158	int	CT		-			
1937482	non	CT	MMAR_1602	-		intermediary metabolism and respiration	oxidoreductase GMC-type
1937684	syn	CT	MMAR_1602	-		intermediary metabolism and respiration	oxidoreductase GMC-type
1938365	non	CT	MMAR_1602	-		intermediary metabolism and respiration	oxidoreductase GMC-type
1938975	non	CT	MMAR_1602	-		intermediary metabolism and respiration	oxidoreductase GMC-type
1939268	syn	GT	MMAR_1602	-		intermediary metabolism and respiration	oxidoreductase GMC-type
1940679	int	CA		77	MMAR_1603	conserved hypotheticals	conserved hypothetical protein
1943412	non	GA	MMAR_1606	-		lipid metabolism	fatty-acid-CoA ligase
1945741	non	GT	MMAR_1607	-		intermediary metabolism and respiration	succinate-semialdehyde dehydrogenase [NADP+] dependent PutA_2
1945833	non	GC	MMAR_1607	-		intermediary metabolism and respiration	succinate-semialdehyde dehydrogenase [NADP+] dependent PutA_2
1947932	non	GA	MMAR_1608	-		intermediary metabolism and respiration	hydrolase
1949112	non	CG	MMAR_1610	-		unknown	hypothetical protein
1953301	syn	TC	MMAR_1615	-		information pathways	chaperone protein DnaK1
1953626	syn	CT	MMAR_1616	-		intermediary metabolism and respiration	carbon starvation protein CstA
1954472	syn	GA	MMAR_1616	-		intermediary metabolism and respiration	carbon starvation protein CstA
1962224	non	CT	MMAR_1623	-		information pathways	ATP-dependent DNA ligase LigB
1962337	non	TG	MMAR_1623	-		information pathways	ATP-dependent DNA ligase LigB
1962812	syn	AG	MMAR_1624	-		intermediary metabolism and respiration	short-chain type dehydrogenase/reductase
1963638	syn	AC	MMAR_1625	-		lipid metabolism	acyl-CoA dehydrogenase FadE22
1964391	non	CT	MMAR_1625	-		lipid metabolism	acyl-CoA dehydrogenase FadE22
1966074	non	CG	MMAR_1626	-		regulatory proteins	transcriptional regulator
1966193	syn	CT	MMAR_1626	-		regulatory proteins	transcriptional regulator
1967125	syn	CG	MMAR_1627	-		intermediary metabolism and respiration	methyltransferase
1967144	non	CT	MMAR_1628	-		conserved hypotheticals	conserved hypothetical protein
1967511	non	CT	MMAR_1628	-		conserved hypotheticals	conserved hypothetical protein
1968706	non	GA	MMAR_1629	-		intermediary metabolism and respiration	acetyl-CoA acetyltransferase
1969591	syn	CT	MMAR_1630	-		regulatory proteins	transcriptional regulatory protein
1970679	syn	TC	MMAR_1631	-		conserved hypotheticals	conserved hypothetical protein
1970683	non	AG	MMAR_1631	-		conserved hypotheticals	conserved hypothetical protein
1972003	syn	AC	MMAR_1633	-		conserved hypotheticals	conserved hypothetical protein
1975396	syn	CT	MMAR_1636	-		intermediary metabolism and respiration	short chain alcohol dehydrogenase/reductase

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
1975402	non	AG	MMAR_1636	-		intermediary metabolism and respiration	short chain alcohol dehydrogenase/reductase
1989245	non	CG	MMAR_1643	-		regulatory proteins	transcriptional regulatory protein (probably AsnC-family)
1989289	syn	CT	MMAR_1643	-		regulatory proteins	transcriptional regulatory protein (probably AsnC-family)
1989467	non	GA	MMAR_1643	-		regulatory proteins	transcriptional regulatory protein (probably AsnC-family)
1991600	syn	GA	MMAR_1644	-		intermediary metabolism and respiration	monoxygenase
1992922	syn	CA	MMAR_1647	-		information pathways	ribonucleoside-diphosphate reductase (beta chain) NrdF2
1993878	non	TC	MMAR_1648	-		conserved hypotheticals	conserved protein
1995201	syn	AG	MMAR_1649	-		intermediary metabolism and respiration	NADP-dependent alcohol dehydrogenase Adh
1995264	non	CT	MMAR_1649	-		intermediary metabolism and respiration	NADP-dependent alcohol dehydrogenase Adh
2000019	syn	CT	MMAR_1653	-		regulatory protein	transcriptional regulatory protein
2002301	non	TG	MMAR_1655	-		cell wall and cell processes	oxidoreductase
2002711	syn	CA	MMAR_1655	-		cell wall and cell processes	oxidoreductase
2003256	syn	GA	MMAR_1656	-		intermediary metabolism and respiration	formate hydrogenase HycD
2003736	non	GC	MMAR_1657	-		intermediary metabolism and respiration	hydrogenase HycP
2006702	syn	CG	MMAR_1659	-		intermediary metabolism and respiration	formate hydrogenase HycE
2007949	syn	CT	MMAR_1660	-		cell wall and cell processes	conserved ATP-binding protein ABC transporter
2008884	syn	GC	MMAR_1661	-		conserved hypotheticals	conserved hypothetical protein
2010426	syn	GC	MMAR_1663	-		conserved hypotheticals	conserved hypothetical protein
2013960	syn	AG	MMAR_1667	-		conserved hypotheticals	conserved membrane protein
2015462	int	CT	20 MMAR_1669			lipid metabolism	lysophospholipase
2017431	non	CT				intermediary metabolism and respiration	DNA photolyase PhrI
2019287	syn	CT	MMAR_1673	-		cell wall and cell processes	conserved transmembrane transport protein
2019987	non	GT	MMAR_1673	-		cell wall and cell processes	conserved transmembrane transport protein
2020996	int	AG	119 MMAR_1674			cell wall and cell processes	penicillin-binding protein
2022008	syn	CT				cell wall and cell processes	penicillin-binding protein
2022101	syn	CT	MMAR_1674	-		cell wall and cell processes	penicillin-binding protein
2022127	non	CT	MMAR_1674	-		cell wall and cell processes	penicillin-binding protein
2024021	syn	AG	MMAR_1677	-		conserved hypotheticals	conserved hypothetical protein
2024087	syn	AG	MMAR_1677	-		conserved hypotheticals	conserved hypothetical protein
2024184	int	AT	22 MMAR_1677			conserved hypotheticals	conserved hypothetical protein
2024789	non	AC				cell wall and cell processes	conserved hypothetical membrane protein
2024940	non	CT	MMAR_1678	-		cell wall and cell processes	conserved hypothetical membrane protein
2025316	non	GC	MMAR_1679	-		cell wall and cell processes	conserved hypothetical membrane protein
2026065	syn	CA	MMAR_1679	-		cell wall and cell processes	conserved hypothetical membrane protein
2027251	non	CT	MMAR_1680	-		intermediary metabolism and respiration	dehydrogenase/reductase
2028023	syn	GA	MMAR_1681	-		intermediary metabolism and respiration	transferase
2028227	syn	AG	MMAR_1681	-		intermediary metabolism and respiration	transferase
2029946	non	TC	MMAR_1682	-		conserved hypotheticals	conserved protein
2030918	syn	CT	MMAR_1683	-		conserved hypotheticals	conserved hypothetical protein
2035438	syn	GA	MMAR_1688	-		conserved hypotheticals	conserved hypothetical protein
2035482	non	GA	MMAR_1688	-		conserved hypotheticals	conserved hypothetical protein
2035663	syn	TC	MMAR_1688	-		conserved hypotheticals	conserved hypothetical protein
2035993	syn	GA	MMAR_1689	-		intermediary metabolism and respiration	cysteine desulfurase IscS
2036029	syn	GT	MMAR_1689	-		intermediary metabolism and respiration	cysteine desulfurase IscS
2036323	syn	TC	MMAR_1689	-		intermediary metabolism and respiration	cysteine desulfurase IscS
2037561	syn	CA	MMAR_1690	-		information pathways	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase TrmU
2041698	int	AG	130 MMAR_1693			intermediary metabolism and respiration	methyltransferase
2042187	syn	CT				information pathways	DNA ligase [NAD dependent] LigA
2042625	syn	CT	MMAR_1694	-		information pathways	DNA ligase [NAD dependent] LigA
2044428	syn	TG	MMAR_1695	-		regulatory protein	regulatory protein
2044609	int	CG	22 MMAR_1695			regulatory protein	glutamyl-tRNA (Gln) amidotransferase (subunit A) GatA
2051631	syn	CA				information pathways	6-phosphofructokinase PfkA
2052045	syn	TA	MMAR_1703	-		intermediary metabolism and respiration	information pathways
2053547	non	AG	MMAR_1704	-		information pathways	glutamyl-tRNA(Gln) amidotransferase (subunit B) GatB
2053564	non	GA	MMAR_1704	-		information pathways	glutamyl-tRNA(Gln) amidotransferase (subunit B) GatB
2054388	syn	TC	MMAR_1704	-		information pathways	glutamyl-tRNA(Gln) amidotransferase (subunit B) GatB
2056277	syn	AG	MMAR_1706	-		cell wall and cell processes	conserved lipoprotein Lpp2
2058441	syn	AG	MMAR_1710	-		intermediary metabolism and respiration	acetolactate synthase (large subunit) IlvB1
2058922	syn	CT	MMAR_1710	-		intermediary metabolism and respiration	acetolactate synthase (large subunit) IlvB1
2062041	non	GT	MMAR_1713	-		conserved hypotheticals	conserved protein
2062421	syn	CT	MMAR_1713	-		conserved hypotheticals	conserved protein
2063871	non	CA	MMAR_1714	-		intermediary metabolism and respiration	alanine rich dehydrogenase
2065608	int	AG	50 MMAR_1716			intermediary metabolism and respiration	3-isopropylmalate dehydrogenase LeuB
2065721	non	GA				intermediary metabolism and respiration	3-isopropylmalate dehydrogenase LeuB
2066071	syn	TC	MMAR_1716	-		intermediary metabolism and respiration	3-isopropylmalate dehydrogenase LeuB
2069121	syn	TC	MMAR_1719	-		information pathways	glutamyl-tRNA synthetase GtsS
2070399	syn	CT	MMAR_1719	-		information pathways	glutamyl-tRNA synthetase GtsS
2073475	non	GA	MMAR_1722	-		cell wall and cell processes	conserved transmembrane transport protein MmpL1_1
2073695	syn	GA	MMAR_1722	-		cell wall and cell processes	conserved transmembrane transport protein MmpL1_1
2074033	non	CT	MMAR_1722	-		cell wall and cell processes	conserved transmembrane transport protein MmpL1_1
2074034	syn	GC	MMAR_1722	-		cell wall and cell processes	conserved transmembrane transport protein MmpL1_1
2076028	non	TC	MMAR_1724	-		intermediary metabolism and respiration	8-amino-7-oxononanoate synthase BioF2_2
2077406	int	AG	22 MMAR_1726			intermediary metabolism and respiration	3-isopropylmalate dehydratase (large subunit) LeuC
2078827	syn	TC				intermediary metabolism and respiration	3-isopropylmalate dehydratase (large subunit) LeuC
2079210	non	GA	MMAR_1726	-		intermediary metabolism and respiration	3-isopropylmalate dehydratase (large subunit) LeuC
2080549	syn	GT	MMAR_1727	-		intermediary metabolism and respiration	3-isopropylmalate dehydratase (small subunit) LeuD
2082819	syn	GA	MMAR_1730	-		intermediary metabolism and respiration	polyphosphate kinase Ppk
2087282	syn	AG	MMAR_1733	-		intermediary metabolism and respiration	d-alanine-D-alanine ligase DdIA
2087612	syn	GT	MMAR_1733	-		intermediary metabolism and respiration	d-alanine-D-alanine ligase DdIA
2087831	syn	GA	MMAR_1733	-		intermediary metabolism and respiration	d-alanine-D-alanine ligase DdIA
2091450	syn	CT	MMAR_1738	-		intermediary metabolism and respiration	oxidoreductase
2092051	non	CT	MMAR_1739	-		intermediary metabolism and respiration	nitroreductase
2096311	syn	GT	MMAR_1742	-		information pathways	ATP-dependent DNA helicase RecG
2098270	non	TG	MMAR_1744	-		intermediary metabolism and respiration	oxidoreductase
2100748	non	GA	MMAR_1747	-		cell wall and cell processes	conserved membrane protein
2101188	non	CG	MMAR_1748	-		cell wall and cell processes	conserved integral membrane protein
2102400	non	GA	MMAR_1749	-		intermediary metabolism and respiration	pyruvate carboxylase Pca
2103893	syn	CT	MMAR_1749	-		intermediary metabolism and respiration	pyruvate carboxylase Pca
2103894	syn	CT	MMAR_1749	-		intermediary metabolism and respiration	pyruvate carboxylase Pca
2105449	syn	GT	MMAR_1750	-		intermediary metabolism and respiration	pyruvate carboxylase Pca
2106140	syn	CT	MMAR_1751	-		intermediary metabolism and respiration	methyltransferase
2106265	syn	AC	MMAR_1751	-		intermediary metabolism and respiration	phosphopantetheine adenylyltransferase KdtB
2113110	syn	TC	MMAR_1758	-		intermediary metabolism and respiration	phosphopantetheine adenylyltransferase KdtB
2114423	int	CT	22 MMAR_1758			intermediary metabolism and respiration	ketoreductase
2114432	int	AG				intermediary metabolism and respiration	

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
2116705	non	CG	MMAR_1759	-		lipid metabolism	fatty acyl-AMP ligase FadD29
2118047	syn	GA	MMAR_1761	-		lipid metabolism	fatty-acid-CoA ligase FadD22
2126250	int	TC		144	MMAR_1762	lipid metabolism	polyketide synthase Pks15/1
2126256	int	TC		-			
2131250	syn	CT	MMAR_1765	-		lipid metabolism	fatty acyl-AMP ligase FadD28
2132761	syn	CT	MMAR_1766	-		intermediary metabolism and respiration	methyltransferase
2133078	int	CT		86	MMAR_1766	intermediary metabolism and respiration	methyltransferase
2133301	int	CT		-			
2138013	syn	CT	MMAR_1767	-		lipid metabolism	multifunctional mycocerosic acid synthase membrane-associated Mas
2139618	syn	TC	MMAR_1767	-		lipid metabolism	multifunctional mycocerosic acid synthase membrane-associated Mas
2145177	non	CT	MMAR_1772	-		lipid metabolism	phenolphthiocerol synthesis type-I polyketide synthase PpsE
2147759	syn	GA	MMAR_1772	-		lipid metabolism	phenolphthiocerol synthesis type-I polyketide synthase PpsE
2148203	syn	CT	MMAR_1772	-		lipid metabolism	phenolphthiocerol synthesis type-I polyketide synthase PpsE
2153620	syn	CT	MMAR_1773	-		lipid metabolism	phenolphthiocerol synthesis type-I polyketide synthase PpsD
2153984	syn	GA	MMAR_1774	-		lipid metabolism	phenolphthiocerol synthesis type-I polyketide synthase PpsC
2157129	syn	CG	MMAR_1774	-		lipid metabolism	phenolphthiocerol synthesis type-I polyketide synthase PpsC
2159795	syn	GA	MMAR_1774	-		lipid metabolism	phenolphthiocerol synthesis type-I polyketide synthase PpsC
2171179	non	CT	MMAR_1777	-		lipid metabolism	fatty acyl-AMP ligase FadD26
2175750	non	AG	MMAR_1783	-		information pathways	formamidopyrimidine-DNA glycosylase Fpg
2178082	syn	CT	MMAR_1785	-		cell wall and cell processes	chromosome partition protein Smc
2181228	syn	TA	MMAR_1786	-		cell wall and cell processes	cell division protein FtsY
2184450	non	CT	MMAR_1789	-		intermediary metabolism and respiration	uridylyltransferase GlnD
2189832	syn	CT	MMAR_1792	-		cell wall and cell processes	signal recognition particle protein Ffh
2190423	syn	AG	MMAR_1792	-		cell wall and cell processes	signal recognition particle protein Ffh
2193703	int	CT		79	MMAR_1794	regulatory protein	transmembrane serine/threonine-protein kinase I PknI
2194310	syn	CA	MMAR_1795	-		intermediary metabolism and respiration	D-AMINO acid aminohydrolase
2194874	syn	GA	MMAR_1795	-		intermediary metabolism and respiration	D-AMINO acid aminohydrolase
2195129	syn	GC	MMAR_1795	-		intermediary metabolism and respiration	D-AMINO acid aminohydrolase
2196772	non	CT	MMAR_1797	-		cell wall and cell processes	D-alanyl-D-glutamate carboxypeptidase DacB
2197422	syn	GC	MMAR_1798	-		conserved hypotheticals	conserved hypothetical protein
2200666	syn	GC	MMAR_1803	-		cell wall and cell processes	conserved alanine rich lipoprotein LppW
2201931	syn	GA	MMAR_1805	-		cell wall and cell processes	signal peptidase I LepB
2201964	syn	AG	MMAR_1805	-		cell wall and cell processes	signal peptidase I LepB
2204008	syn	C-	MMAR_1808	-		conserved hypotheticals	conserved hypothetical protein
2206249	syn	CG	MMAR_1810	-		cell wall and cell processes	UDP-glucose 4-epimerase GalE4
2206357	syn	TC	MMAR_1810	-		cell wall and cell processes	UDP-glucose 4-epimerase GalE4
2207315	non	TC	MMAR_1811	-		intermediary metabolism and respiration	formate dehydrogenase family accessory protein FdhD
2208493	syn	GA	MMAR_1813	-		conserved hypotheticals	conserved hypothetical protein
2208760	syn	AG	MMAR_1813	-		conserved hypotheticals	conserved hypothetical protein
2209048	non	GT	MMAR_1813	-		conserved hypotheticals	conserved hypothetical protein
2209240	syn	CT	MMAR_1813	-		conserved hypotheticals	conserved hypothetical protein
2209342	syn	GA	MMAR_1813	-		conserved hypotheticals	conserved hypothetical protein
2210286	syn	CA	MMAR_1814	-		cell wall and cell processes	conserved hypothetical membrane protein
2211236	syn	AG	MMAR_1815	-		intermediary metabolism and respiration	mycobactin utilization protein VnuB
2211460	non	GA	MMAR_1815	-		intermediary metabolism and respiration	mycobactin utilization protein VnuB
2212174	non	CT	MMAR_1816	-		intermediary metabolism and respiration	L-lactate dehydrogenase (cytochrome) LldD1_1
2212186	non	AG	MMAR_1816	-		intermediary metabolism and respiration	L-lactate dehydrogenase (cytochrome) LldD1_1
2213030	syn	TC	MMAR_1816	-		intermediary metabolism and respiration	L-lactate dehydrogenase (cytochrome) LldD1_1
2214626	int	CT		39	MMAR_1818	conserved hypotheticals	conserved hypothetical protein
2214826	int	AG		66	MMAR_1819	information pathways	30S ribosomal protein S2 RpsB
2216880	syn	CT	MMAR_1821	-		intermediary metabolism and respiration	amidase AmiC
2221018	non	CT	MMAR_1825	-		regulatory protein	transcriptional regulatory protein
2221081	int	G-		26	MMAR_1825	regulatory protein	transcriptional regulatory protein
2221082	int	C-		27	MMAR_1825	regulatory proteins	transcriptional regulatory protein
2223281	non	GT	MMAR_1828	-		lipid metabolism	integral membrane phosphatidate cytidylyltransferase CdsA
2231825	syn	CT	MMAR_1832	-		cell wall and cell processes	conserved integral membrane protein
2231829	non	CT	MMAR_1832	-		cell wall and cell processes	conserved integral membrane protein
2231861	syn	CG	MMAR_1832	-		cell wall and cell processes	conserved integral membrane protein
2238469	syn	CT	MMAR_1838	-		lipid metabolism	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase Ispg
2238969	syn	CT	MMAR_1838	-		lipid metabolism	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase Ispg
2243302	non	GA	MMAR_1842	-		intermediary metabolism and respiration	methionine aminopeptidase MapB
2243624	int	AG		115	MMAR_1842	intermediary metabolism and respiration	methionine aminopeptidase MapB
2244082	non	CT	MMAR_1843	-		cell wall and cell processes	conserved hypothetical membrane protein
2244083	non	TC	MMAR_1843	-		cell wall and cell processes	conserved hypothetical membrane protein
2244995	non	GT	MMAR_1844	-		intermediary metabolism and respiration	amidotransferase
2244996	non	GT	MMAR_1844	-		intermediary metabolism and respiration	amidotransferase
2245175	int	GC		35	MMAR_1844	intermediary metabolism and respiration	amidotransferase
2245660	int	CT		-			
2245710	int	CT		-			
2248180	int	AC		48	MMAR_1847	PE/PPE	PPE family protein
2248260	int	CT		32	MMAR_1847	PE/PPE	PPE family protein
2248363	int	TG		135	MMAR_1847	PE/PPE	PPE family protein
2249559	int	CG		-			
2250241	int	TG		23	MMAR_1849	PE/PPE	PPE family protein
2250295	int	CT		31	MMAR_1849	PE/PPE	PPE family protein
2250302	int	AG		38	MMAR_1849	PE/PPE	PPE family protein
2250325	int	AG		61	MMAR_1849	PE/PPE	PPE family protein
2250404	int	AG		140	MMAR_1849	PE/PPE	PPE family protein
2250420	int	GT		-			
2250449	int	GA		-			
2250452	int	AG		-			
2250516	int	TC		-			
2250652	int	TC		-			
2250709	int	CA		-			
2251066	int	TC		11	MMAR_1850	PE/PPE	PE-PGRS family protein
2289754	non	AG	MMAR_1878	-		conserved hypotheticals	conserved hypothetical protein
2290086	syn	TG	MMAR_1878	-		conserved hypotheticals	conserved hypothetical protein
2293751	non	CA	MMAR_1881	-		intermediary metabolism and respiration	malate:quinone oxidoreductase Mgo
2296786	syn	AC	MMAR_1884	-		intermediary metabolism and respiration	cob(I)alamin adenosyltransferase CobD
2299299	syn	CT	MMAR_1885	-		intermediary metabolism and respiration	multifunctional enzyme siroheme synthase CysG
2302890	syn	CT	MMAR_1887	-		cell wall and cell processes	integral membrane effl. protein EfpA
2302977	syn	CA	MMAR_1889	-		information pathways	prolyl-tRNA synthetase ProS
2303453	syn	CG	MMAR_1889	-		information pathways	prolyl-tRNA synthetase ProS
2303790	syn	TC	MMAR_1889	-		conserved hypotheticals	conserved hypothetical alanine rich protein
2303991	syn	GC	MMAR_1889	-		conserved hypotheticals	conserved hypothetical alanine rich protein

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
2311559	syn	CT	MMAR_1897	-		information pathways	DNA-damage-inducible protein F DinF
2321939	syn	TC	MMAR_1907	-		conserved hypothetical	conserved hypothetical protein
2328535	syn	GA	MMAR_1912	-		conserved hypothetical	conserved hypothetical protein
2328828	non	AT	MMAR_1913	-		conserved hypothetical	conserved hypothetical protein
2333158	non	GA	MMAR_1917	-		information pathways	tRNA pseudouridine synthase B TruB
2334202	syn	CA	MMAR_1918	-		cell wall and cell processes	lipid-transfer protein Ltp1
2334409	syn	TC	MMAR_1918	-		cell wall and cell processes	lipid-transfer protein Ltp1
2335481	syn	CT	MMAR_1919	-		lipid metabolism	acyl-CoA dehydrogenase FadE21
2335643	syn	GA	MMAR_1919	-		lipid metabolism	acyl-CoA dehydrogenase FadE21
2336128	syn	TC	MMAR_1920	-		regulatory protein	transcriptional repressor SirR
2336946	syn	AG	MMAR_1921	-		intermediary metabolism and respiration	bifunctional fad synthetase/riboflavin biosynthesis protein RibF
2337768	syn	CT	MMAR_1921	-		intermediary metabolism and respiration	bifunctional fad synthetase/riboflavin biosynthesis protein RibF
2337814	syn	CT	MMAR_1921	-		intermediary metabolism and respiration	bifunctional fad synthetase/riboflavin biosynthesis protein RibF
2339564	int	AG	53 MMAR_1925			information pathways	bifunctional protein polyribonucleotide nucleotidyltransferase GpsI
2340753	syn	GA				information pathways	bifunctional protein polyribonucleotide nucleotidyltransferase GpsI
2341260	syn	GT				information pathways	bifunctional protein polyribonucleotide nucleotidyltransferase GpsI
2343031	syn	TC				intermediary metabolism and respiration	zinc protease PepR
2344756	syn	GA				intermediary metabolism and respiration	secreted L-alanine dehydrogenase Ald (40 kDa antigen)
2348035	non	TC	MMAR_1932	-		short-chain dehydrogenase EphD_1	
2355956	non	AG	MMAR_1939	-		cell wall and cell processes	conserved hypothetical secreted protein
2364075	non	CG	MMAR_1948	-		lipid metabolism	fatty acid-CoA ligase FadD13_1
2364935	non	CA	MMAR_1948	-		lipid metabolism	fatty acid-CoA ligase FadD13_1
2367788	syn	CT	MMAR_1951	-		lipid metabolism	bifunctional protein acetyl-/propionyl-coenzyme a carboxylase (alpha chain) AccA3_1
2368517	syn	CT	MMAR_1951	-		lipid metabolism	bifunctional protein acetyl-/propionyl-coenzyme a carboxylase (alpha chain) AccA3_1
2368962	non	GT	MMAR_1951	-		lipid metabolism	bifunctional protein acetyl-/propionyl-coenzyme a carboxylase (alpha chain) AccA3_1
2369484	non	GC	MMAR_1951	-		lipid metabolism	bifunctional protein acetyl-/propionyl-coenzyme a carboxylase (alpha chain) AccA3_1
2372466	syn	CG	MMAR_1953	-		lipid metabolism	acyl-CoA dehydrogenase FadE34_1
2372589	non	CA	MMAR_1953	-		lipid metabolism	acyl-CoA dehydrogenase FadE34_1
2372844	syn	AG	MMAR_1953	-		lipid metabolism	acyl-CoA dehydrogenase FadE34_1
2374574	non	TG	MMAR_1955	-		intermediary metabolism and respiration	alanine rich hydrolase
2374575	non	GT	MMAR_1955	-		intermediary metabolism and respiration	alanine rich hydrolase
2375669	syn	CT	MMAR_1956	-		intermediary metabolism and respiration	thymidylate synthase ThyA
2375747	syn	CT	MMAR_1956	-		intermediary metabolism and respiration	thymidylate synthase ThyA
2376914	syn	CT	MMAR_1958	-		conserved hypothetical	conserved hypothetical protein
2377665	non	AG	MMAR_1958	-		conserved hypothetical	conserved hypothetical protein
2378849	non	GT	MMAR_1959	-		information pathways	type I restriction/modification system DNA methylase HsdM
2378948	non	AG	MMAR_1959	-		information pathways	type I restriction/modification system DNA methylase HsdM
2379671	non	CG	MMAR_1960	-		information pathways	type I restriction/modification system specificity determinant HsdS (5 protein)
2380707	non	CT	MMAR_1961	-		intermediary metabolism and respiration	thymidylate synthase ThyX
2387414	syn	GT	MMAR_1967	-		cell wall and cell processes	cell division transmembrane protein FtsK
2392162	syn	CT	MMAR_1973	-		conserved hypothetical	conserved protein
2393318	syn	GA	MMAR_1974	-		intermediary metabolism and respiration	glycosyl transferase
2393809	syn	GA	MMAR_1975	-		conserved hypothetical	conserved hypothetical protein
2394395	syn	GC	MMAR_1976	-		conserved hypothetical	conserved hypothetical protein
2396347	int	CT	66 MMAR_1979			conserved hypothetical	conserved hypothetical protein
2396844	syn	CT				conserved hypothetical	conserved hypothetical protein
2396901	non	CT				conserved hypothetical	conserved hypothetical protein
2398505	syn	CT				cell wall and cell processes	conserved membrane protein
2399580	non	GA				conserved hypothetical	conserved protein
2402337	int	CT	138 MMAR_1983			cell wall and cell processes	conserved hypothetical membrane protein
2405435	syn	CT				information pathways	tRNA delta(2)-isopentenylpyrophosphate transferase MiaA
2409162	syn	CA				lipid metabolism	acyl-CoA dehydrogenase FadE20
2409855	syn	CG				lipid metabolism	acyl-CoA dehydrogenase FadE20
2412259	syn	CT				cell wall and cell processes	conserved transmembrane alanine and glycine rich protein
2412559	syn	TC	MMAR_1991	-		cell wall and cell processes	conserved transmembrane alanine and glycine rich protein
2414301	non	AG	MMAR_1992	-		regulatory protein	repressor LexA
2414641	int	-T	65 MMAR_1992			regulatory protein	repressor LexA
2416309	syn	GA				conserved hypothetical	conserved hypothetical protein
2416796	non	CG				conserved hypothetical	conserved hypothetical protein
2417220	non	GA				conserved hypothetical	conserved hypothetical protein
2417807	syn	TC				intermediary metabolism and respiration	conserved hypothetical hydrolase
2420610	syn	GA	MMAR_2000	-		intermediary metabolism and respiration	soluble pyridine nucleotide transhydrogenase SthA
2422159	non	CG	MMAR_2001	-		conserved hypothetical	conserved hypothetical protein
2422746	non	CT	MMAR_2001	-		conserved hypothetical	conserved hypothetical protein
2423140	syn	GC	MMAR_2002	-		regulatory protein	iron-dependent repressor and activator IdeR
2424302	non	CT	MMAR_2003	-		information pathways	RNA polymerase sigma factor SigB
2426134	syn	GA	MMAR_2006	-		cell wall and cell processes	conserved membrane protein
2427072	int	GT	124 MMAR_2007			conserved hypothetical	conserved hypothetical protein
2431366	syn	CT				information pathways	RNA polymerase sigma factor SigA
2433836	syn	GA				cell wall and cell processes	conserved hypothetical secreted protein
2433986	syn	AG				cell wall and cell processes	conserved hypothetical secreted protein
2434570	syn	TG				conserved hypothetical	conserved protein
2436534	syn	GA	MMAR_2019	-		conserved hypothetical	conserved hypothetical protein
2436685	syn	GA	MMAR_2019	-		conserved hypothetical	conserved hypothetical protein
2441117	syn	CT	MMAR_2024	-		cell wall and cell processes	conserved integral membrane alanine valine and leucine rich protein
2443646	syn	GT	MMAR_2026	-		cell wall and cell processes	antibiotic-transport ATP-binding protein ABC transporter
2443687	non	GA	MMAR_2026	-		cell wall and cell processes	antibiotic-transport ATP-binding protein ABC transporter
2444830	syn	CG	MMAR_2027	-		cell wall and cell processes	antibiotic-transport integral membrane leucine and valine rich protein ABC transporter
2448816	syn	GA	MMAR_2031	-		conserved hypothetical	conserved protein
2449354	syn	GA	MMAR_2032	-		intermediary metabolism and respiration	1-deoxy-D-xylulose 5-phosphate synthase Dxs1
2456078	psd	GA	MMAR_2034	-		intermediary metabolism and respiration	N-Term 1-deoxy-D-xylulose 5-phosphate synthase Dxs1A - pseudogene
2456462	psd	CT	MMAR_2034	-		intermediary metabolism and respiration	C-term 1-deoxy-D-xylulose 5-phosphate synthase Dxs1A - pseudogene
2458134	non	GC	MMAR_2036	-		conserved hypothetical	conserved protein
245900	syn	GC	MMAR_2038	-		intermediary metabolism and respiration	uroporphyrinogen decarboxylase HemE
2460173	syn	GA	MMAR_2038	-		intermediary metabolism and respiration	uroporphyrinogen decarboxylase HemE
2461624	syn	CT	MMAR_2039	-		intermediary metabolism and respiration	protoporphyrinogen oxidase HemY
2461746	non	AT	MMAR_2039	-		intermediary metabolism and respiration	protoporphyrinogen oxidase HemY
2462265	syn	GA	MMAR_2040	-		conserved hypothetical	conserved hypothetical protein
2464344	syn	CT	MMAR_2042	-		unknown	conserved hypothetical protein (SelR family)
2464487	syn	TC	MMAR_2043	-		cell wall and cell processes	conserved transmembrane protein
2464545	syn	GA	MMAR_2043	-		cell wall and cell processes	conserved transmembrane protein
2464633	non	CT	MMAR_2043	-		cell wall and cell processes	conserved transmembrane protein
2466428	syn	TG	MMAR_2044	-		conserved hypothetical	conserved hypothetical membrane protein
2466834	syn	GA	MMAR_2045	-		information pathways	bifunctional enzyme riboflavin biosynthesis protein RibD
2468555	syn	CT	MMAR_2046	-		conserved hypothetical	conserved hypothetical protein

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
2468570	syn	CG	MMAR_2046	-		conserved hypotheticals	conserved hypothetical protein
2468576	syn	CT	MMAR_2046	-		conserved hypotheticals	conserved hypothetical protein
2469447	non	CG	MMAR_2047	-		cell wall and cell processes	exported alanine and valine rich protein
2472723	syn	CT	MMAR_2051	-		conserved hypotheticals	conserved hypothetical protein
2475107	Int	GA		67	MMAR_2052	cell wall and cell processes	amino acid transporter
2478105	Int	TA		110	MMAR_2053	PE/PPE	PE-PGRS family protein
2482785	Int	CG		26	MMAR_2060		catalase
2483775	Int	CT		17	MMAR_2060		catalase
2484078	syn	AG	MMAR_2061	-		conserved hypotheticals	conserved hypothetical protein
2484161	non	CG	MMAR_2061	-		conserved hypotheticals	conserved hypothetical protein
2484490	non	AT	MMAR_2062	-		conserved hypotheticals	conserved hypothetical protein
2485470	syn	TC	MMAR_2063	-		cell wall and cell processes	transmembrane protein DedA
2486855	syn	CT	MMAR_2064	-		lipid metabolism	fatty-acid-CoA ligase
2498808	syn	CG	MMAR_2073	-		conserved hypotheticals	conserved hypothetical membrane protein
2499015	syn	GT	MMAR_2073	-		conserved hypotheticals	conserved hypothetical membrane protein
2500245	syn	C-	MMAR_2074	-		unknown	conserved hypothetical protein
2500246	non	C-	MMAR_2074	-		unknown	conserved hypothetical protein
2500707	non	GA	MMAR_2075	-		cell wall and cell processes	conserved transmembrane alanine and leucine rich protein
2501381	syn	CT	MMAR_2075	-		cell wall and cell processes	conserved transmembrane alanine and leucine rich protein
2502109	syn	AG	MMAR_2076	-		conserved hypotheticals	conserved hypothetical protein
2502712	syn	GA	MMAR_2076	-		conserved hypotheticals	conserved hypothetical protein
2503165	syn	GC	MMAR_2077	-		conserved hypotheticals	conserved hypothetical protein
2504974	syn	CA	MMAR_2079	-		cell wall and cell processes	integral membrane nitrite extrusion protein NarK3
2506420	non	TC	MMAR_2080	-		intermediary metabolism and respiration	ferredoxin FdxA_1
2507126	syn	CG	MMAR_2081	-		regulatory protein	transcriptional regulator
2507447	non	GA	MMAR_2082	-		cell wall and cell processes	conserved hypothetical membrane protein
2510397	non	TG	MMAR_2086	-		intermediary metabolism and respiration	oxidoreductase
2511255	non	AC	MMAR_2087	-		conserved hypotheticals	conserved hypothetical protein
2511260	syn	CT	MMAR_2087	-		conserved hypotheticals	conserved hypothetical protein
2511348	Int	CG		103	MMAR_2088	information pathways	threonyl-tRNA synthetase ThrS
2513886	non	AG	MMAR_2089	-		conserved hypotheticals	conserved protein
2514804	syn	GC	MMAR_2090	-		lipid metabolism	pi synthase PgsA1
2515124	syn	CT	MMAR_2091	-		lipid metabolism	acyltransferase
2515277	syn	CT	MMAR_2091	-		lipid metabolism	acyltransferase
2515463	syn	CT	MMAR_2091	-		lipid metabolism	acyltransferase
2515601	syn	CT	MMAR_2091	-		lipid metabolism	acyltransferase
2516464	syn	TC	MMAR_2092	-		lipid metabolism	alpha-mannosyltransferase PimA
2518109	Int	GA		34	MMAR_2094	intermediary metabolism and respiration	pyridoxine biosynthesis protein SnzP
2518787	syn	CG	MMAR_2094	-		intermediary metabolism and respiration	pyridoxine biosynthesis protein SnzP
2536492	syn	AG	MMAR_2104	-		intermediary metabolism and respiration	spermidine synthase SpeE
2541934	syn	CT	MMAR_2111	-		information pathways	Holliday junction DNA helicase RuvB
2546409	non	AG	MMAR_2114	-		cell wall and cell processes	hypothetical membrane protein
2546908	syn	GT	MMAR_2115	-		cell wall and cell processes	hypothetical secreted protein
2550246	syn	AG	MMAR_2117	-		lipid metabolism	fatty-acid-CoA ligase FadD9
2550322	non	TA	MMAR_2117	-		lipid metabolism	fatty-acid-CoA ligase FadD9
2550369	syn	GA	MMAR_2117	-		lipid metabolism	fatty-acid-CoA ligase FadD9
2550739	non	TG	MMAR_2117	-		lipid metabolism	fatty-acid-CoA ligase FadD9
2551260	syn	AG	MMAR_2117	-		lipid metabolism	fatty-acid-CoA ligase FadD9
2553024	syn	GA	MMAR_2117	-		lipid metabolism	fatty-acid-CoA ligase FadD9
2553546	syn	GA	MMAR_2118	-		intermediary metabolism and respiration	4-aminobutyrate aminotransferase GabT
2554458	non	TA	MMAR_2118	-		intermediary metabolism and respiration	4-aminobutyrate aminotransferase GabT
2554962	Int	AG		25	MMAR_2119	cell wall and cell processes	conserved membrane protein secretion factor YajC
2559486	syn	GC	MMAR_2122	-		cell wall and cell processes	ABC-type dipeptide transport system periplasmic component
2561629	syn	CT	MMAR_2124	-		intermediary metabolism and respiration	GTP pyrophosphokinase RelA
2562210	syn	GA	MMAR_2124	-		intermediary metabolism and respiration	GTP pyrophosphokinase RelA
2562565	non	AG	MMAR_2124	-		intermediary metabolism and respiration	GTP pyrophosphokinase RelA
2562891	syn	CT	MMAR_2124	-		intermediary metabolism and respiration	GTP pyrophosphokinase RelA
2564346	Int	GC		80	MMAR_2126	cell wall and cell processes	Zn-dependent glyoxylase
2564503	syn	CT	MMAR_2126	-		cell wall and cell processes	Zn-dependent glyoxylase
2566963	non	CG	MMAR_2128	-		insertion seqs and phages	conserved 13E12 repeat family protein
2567166	non	CT	MMAR_2128	-		insertion seqs and phages	conserved 13E12 repeat family protein
2589794	Int	CT		48	MMAR_2148	conserved hypotheticals	conserved hypothetical protein
2590059	non	CT	MMAR_2148	-		conserved hypotheticals	conserved hypothetical protein
2592740	syn	CT	MMAR_2150	-		lipid metabolism	esterase (alpha-beta hydrolase superfamily)
2597103	non	CG	MMAR_2155	-		cell wall and cell processes	conserved membrane glycine rich protein
2597111	non	CT	MMAR_2155	-		cell wall and cell processes	conserved membrane glycine rich protein
2599051	syn	GT	MMAR_2158	-		information pathways	aspartyl-tRNA synthetase AspS
2599075	syn	GT	MMAR_2158	-		information pathways	aspartyl-tRNA synthetase AspS
2599354	syn	CT	MMAR_2158	-		information pathways	aspartyl-tRNA synthetase AspS
2600709	syn	CT	MMAR_2159	-		conserved hypotheticals	conserved hypothetical protein
2601152	syn	-G	MMAR_2160	-		cell wall and cell processes	transmembrane alanine and valine and leucine rich protein
2602475	Int	GA		55	MMAR_2161	conserved hypotheticals	conserved hypothetical protein
2606349	syn	CA	MMAR_2164	-		conserved hypotheticals	conserved hypothetical alanine and leucine rich protein
2613887	non	CT	MMAR_2168	-		conserved hypotheticals	conserved hypothetical protein
2613939	non	TG	MMAR_2168	-		conserved hypotheticals	conserved hypothetical protein
2615298	syn	GA	MMAR_2170	-		information pathways	alanyl-tRNA synthetase AlaS
2615915	non	TC	MMAR_2170	-		information pathways	alanyl-tRNA synthetase AlaS
2617878	syn	CT	MMAR_2171	-		conserved hypotheticals	conserved hypothetical protein
2617983	syn	AG	MMAR_2171	-		conserved hypotheticals	conserved hypothetical protein
2622628	syn	CT	MMAR_2177	-		intermediary metabolism and respiration	3-dehydroquinate synthase AroB
2623066	syn	GT	MMAR_2177	-		intermediary metabolism and respiration	3-dehydroquinate synthase AroB
2623117	syn	CT	MMAR_2177	-		intermediary metabolism and respiration	3-dehydroquinate synthase AroB
2623165	syn	AG	MMAR_2177	-		intermediary metabolism and respiration	3-dehydroquinate synthase AroB
2625177	syn	CT	MMAR_2180	-		intermediary metabolism and respiration	cytoplasmic peptidase PepQ
2626922	non	CG	MMAR_2182	-		information pathways	N utilization substance protein NusB
2628534	syn	GC	MMAR_2184	-		intermediary metabolism and respiration	amino acid decarboxylase
2632528	non	GA	MMAR_2187	-		cell wall and cell processes	beta-lactamase
2633262	non	CT	MMAR_2187	-		cell wall and cell processes	beta-lactamase
263544	syn	CT	MMAR_2185	-		cell wall and cell processes	conserved lipoprotein LprF
2635510	syn	CG	MMAR_2189	-		cell wall and cell processes	conserved membrane protein
2635972	syn	GA	MMAR_2189	-		cell wall and cell processes	conserved membrane protein
2636574	syn	CG	MMAR_2190	-		lipid metabolism	chalcone/stilbene synthase
2638567	non	CG	MMAR_2191	-		intermediary metabolism and respiration	glycolipid sulfotransferase
2638798	syn	CT	MMAR_2192	-		intermediary metabolism and respiration	glycolipid sulfotransferase
2639125	syn	TC	MMAR_2192	-		intermediary metabolism and respiration	glycolipid sulfotransferase

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
2642303	syn	TC	MMAR_2196	-		intermediary metabolism and respiration	dihydroorotate PyrC
2642514	non	GA	MMAR_2196	-		intermediary metabolism and respiration	dihydroorotate PyrC
2642684	syn	AG	MMAR_2196	-		intermediary metabolism and respiration	dihydroorotate PyrC
2643814	syn	CG	MMAR_2197	-		cell wall and cell processes	secreted protein
2643898	syn	AG	MMAR_2197	-		cell wall and cell processes	secreted protein
2645107	syn	CT	MMAR_2199	-		intermediary metabolism and respiration	carbamoyl-phosphate synthase large chain Carb
2645371	syn	GA	MMAR_2199	-		intermediary metabolism and respiration	carbamoyl-phosphate synthase large chain Carb
2645977	syn	CT	MMAR_2199	-		intermediary metabolism and respiration	carbamoyl-phosphate synthase large chain Carb
2647102	syn	CT	MMAR_2199	-		intermediary metabolism and respiration	carbamoyl-phosphate synthase large chain Carb
2654894	non	GA	MMAR_2206	-		cell wall and cell processes	conserved hypothetical secreted protein
2655188	syn	TA	MMAR_2207	-		intermediary metabolism and respiration	monooxygenase
2655667	non	CA	MMAR_2207	-		intermediary metabolism and respiration	monooxygenase
2655811	non	TC	MMAR_2207	-		intermediary metabolism and respiration	monooxygenase
2656799	non	CT	MMAR_2208	-		lipid metabolism	lipase LipH
2657255	syn	GA	MMAR_2208	-		lipid metabolism	lipase LipH
2662259	non	CA	MMAR_2212	-		intermediary metabolism and respiration	methyltransferase
2662455	Int	AC	73 MMAR_2212	intermediary metabolism and respiration		methyltransferase	
2663770	syn	GC		intermediary metabolism and respiration		methyltransferase	
2665503	non	GT		information pathways		Fmu protein	
2669902	syn	GA		cell wall and cell processes		aminoglycosides/tetracycline-transport integral membrane protein	
2671921	syn	AG		intermediary metabolism and respiration		riboflavin biosynthesis protein RibA2	
2672366	non	CT		intermediary metabolism and respiration		riboflavin biosynthesis beta chain RibA2	
2673283	non	GT		intermediary metabolism and respiration		riboflavin synthase beta chain RibH	
2674503	syn	CG	MMAR_2226	-		insertion seqs and phages	conserved 13E12 repeat family protein
2684032	non	GC	MMAR_2233	-		lipid metabolism	long-chain-fatty-acid-CoA ligase FadD12
2684779	syn	CT	MMAR_2233	-		lipid metabolism	long-chain-fatty-acid-CoA ligase FadD12
2688838	non	CA	MMAR_2236	-		cell wall and cell processes	conserved hypothetical membrane protein
2690388	non	AG	MMAR_2237	-		intermediary metabolism and respiration	dehydrogenase
2694042	non	GC	MMAR_2240	-		intermediary metabolism and respiration	phosphoglycerate kinase Ppk
2694169	syn	TC	MMAR_2240	-		intermediary metabolism and respiration	phosphoglycerate kinase Ppk
2695034	syn	GA	MMAR_2241	-		intermediary metabolism and respiration	triophosphate isomerase Tpi
2695352	syn	GT	MMAR_2241	-		intermediary metabolism and respiration	triophosphate isomerase Tpi
2698879	syn	CT	MMAR_2243	-		cell wall and cell processes	cationic amino acid transport integral membrane protein
2699407	syn	GA	MMAR_2243	-		cell wall and cell processes	cationic amino acid transport integral membrane protein
2700127	Int	GA	135 MMAR_2244	regulatory proteins		transcriptional regulatory protein (probably GntR-family)	
2700666	syn	CT		regulatory proteins		transcriptional regulatory protein (probably GntR-family)	
2701466	syn	G-		cell wall and cell processes		conserved hypothetical membrane protein	
2704163	syn	GT		intermediary metabolism and respiration		phosphoenolpyruvate carboxylase Ppc	
271020	syn	AG		intermediary metabolism and respiration		transaldolase Tal	
2710776	syn	GC		intermediary metabolism and respiration		transaldolase Tal	
2720849	non	AG	MMAR_2258	-		regulatory proteins	transcriptional activator protein
2721561	non	AT	MMAR_2259	-		intermediary metabolism and respiration	quinone reductase Qor
2721735	syn	GA	MMAR_2259	-		intermediary metabolism and respiration	quinone reductase Qor
2722155	syn	CG	MMAR_2259	-		intermediary metabolism and respiration	quinone reductase Qor
2722455	syn	GT	MMAR_2260	-		conserved hypotheticals	conserved hypothetical protein
2722492	non	GA	MMAR_2260	-		conserved hypotheticals	conserved hypothetical protein
2723046	syn	GA	MMAR_2260	-		conserved hypotheticals	conserved hypothetical protein
2723624	non	AG	MMAR_2261	-		cell wall and cell processes	unidentified antibiotic-transport integral membrane ABC transporter
2726115	syn	GC	MMAR_2264	-		cell wall and cell processes	conserved integral membrane protein
2726859	syn	CG	MMAR_2264	-		cell wall and cell processes	conserved integral membrane protein
2729886	syn	GA	MMAR_2266	-		conserved hypotheticals	conserved protein
2730176	syn	CT	MMAR_2267	-		conserved hypotheticals	conserved protein
2730542	syn	CT	MMAR_2267	-		conserved hypotheticals	conserved protein
2730839	syn	CT	MMAR_2267	-		conserved hypotheticals	conserved protein
2731852	syn	CT	MMAR_2268	-		cell wall and cell processes	conserved ATP-binding protein ABC transporter
2732514	syn	CT	MMAR_2269	-		intermediary metabolism and respiration	cysteine desulfurase Csd
2732580	syn	GA	MMAR_2269	-		intermediary metabolism and respiration	cysteine desulfurase Csd
2734141	Int	GT	117 MMAR_2272	PE/PE		PE-PGRS family protein	
2736855	syn	AG		lipid metabolism		acyl-CoA dehydrogenase FadE15	
2738907	Int	GA		136 MMAR_2274	PE/PE	PE-PGRS family protein	
2739187	syn	TC		cell wall and cell processes		cation transporter p-type ATPase D CtpD	
2739553	syn	GA		cell wall and cell processes		cation transporter p-type ATPase D CtpD	
2739577	syn	AG		cell wall and cell processes		cation transporter p-type ATPase D CtpD	
2740456	syn	CA		cell wall and cell processes		cation transporter p-type ATPase D CtpD	
2746007	syn	GA	MMAR_2282	-		intermediary metabolism and respiration	acitomate hydratase Acm
2746557	non	TA	MMAR_2282	-		intermediary metabolism and respiration	acitomate hydratase Acm
2746748	syn	TC	MMAR_2282	-		intermediary metabolism and respiration	acitomate hydratase Acm
2747033	syn	TC	MMAR_2282	-		intermediary metabolism and respiration	acitomate hydratase Acm
2752612	syn	CG	MMAR_2286	-		regulatory proteins	transcriptional regulatory protein MoxR1
2754973	non	GA	MMAR_2289	-		lipid metabolism	3'-oxoacyl-[acyl-carrier protein] reductase FabG1
2755188	syn	CT	MMAR_2289	-		lipid metabolism	3'-oxoacyl-[acyl-carrier protein] reductase FabG1
2755533	syn	CT	MMAR_2289	-		lipid metabolism	3'-oxoacyl-[acyl-carrier protein] reductase FabG1
2757217	syn	CG	MMAR_2291	-		intermediary metabolism and respiration	ferrochelatase HemZ
2758149	non	TC	MMAR_2292	-		conserved hypotheticals	conserved hypothetical protein
2767113	syn	TC	MMAR_2302	-		lipid metabolism	methylmalonyl-CoA mutase small subunit MutA
2767746	syn	GC	MMAR_2302	-		lipid metabolism	methylmalonyl-CoA mutase small subunit MutA
2769488	syn	CT	MMAR_2303	-		lipid metabolism	methylmalonyl-CoA mutase large subunit MutB
2771418	syn	GA	MMAR_2304	-		cell wall and cell processes	LAO/AO transport system kinase
2773164	syn	CT	MMAR_2305	-		intermediary metabolism and respiration	conserved hypothetical esterase LipL
2776356	Int	GT	78 MMAR_2309	intermediary metabolism and respiration		UDP-glucose 6-dehydrogenase UdgL	
2839363	non	GC		intermediary metabolism and respiration		UDP-glycosyltransferase	
2843780	Int	CG					
2843744	syn	CT	MMAR_2356	-		information pathways	isoleucyl-tRNA synthetase IleS
2844064	non	GA	MMAR_2356	-		information pathways	isoleucyl-tRNA synthetase IleS
2845735	syn	GA	MMAR_2356	-		information pathways	isoleucyl-tRNA synthetase IleS
2845796	non	GA	MMAR_2356	-		information pathways	isoleucyl-tRNA synthetase IleS
2845987	syn	AG	MMAR_2356	-		information pathways	isoleucyl-tRNA synthetase IleS
2846119	syn	TC	MMAR_2357	-		conserved hypotheticals	conserved hypothetical protein
2847023	non	TG	MMAR_2357	-		conserved hypotheticals	conserved hypothetical protein
2847697	non	CA	MMAR_2358	-		conserved hypotheticals	conserved hypothetical protein
2848595	syn	GC	MMAR_2359	-		information pathways	DNA polymerase IV DinB 1
2849001	syn	CT	MMAR_2359	-		information pathways	DNA polymerase IV DinP 1
2851955	syn	GC	MMAR_2362	-		intermediary metabolism and respiration	pseudouridine synthase RluA-family
2852030	Int	A-	6 MMAR_2362	intermediary metabolism and respiration		pseudouridine synthase RluA-family	

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
2852126	syn	CT	MMAR_2363	-		conserved hypothetical	conserved hypothetical protein
2853887	non	CT	MMAR_2365	-		intermediary metabolism and respiration	bacterial-like globin GlbN
2856745	non	CG	MMAR_2368	-		conserved hypothetical	conserved protein
2856795	syn	AG	MMAR_2368	-		conserved hypothetical	conserved protein
2857026	non	CT	MMAR_2369	-		information pathways	DNA polymerase III alpha subunit DnaE1
2857884	syn	CG	MMAR_2369	-		information pathways	DNA polymerase III alpha subunit DnaE1
2857932	syn	TC	MMAR_2369	-		information pathways	DNA polymerase III alpha subunit DnaE1
2864412	non	AC	MMAR_2372	-		unknown	hypothetical protein
2869227	syn	GA	MMAR_2377	-		intermediary metabolism and respiration	maltooligosyltrehalose trehalohydrolase TreZ
2869836	syn	CT	MMAR_2377	-		intermediary metabolism and respiration	maltooligosyltrehalose trehalohydrolase TreZ
2871270	non	GA	MMAR_2378	-		intermediary metabolism and respiration	maltooligosyltrehalose synthase TreY
2872275	non	GA	MMAR_2378	-		intermediary metabolism and respiration	maltooligosyltrehalose synthase TreY
2875373	syn	CT	MMAR_2380	-		cell wall and cell processes	conserved hypothetical membrane protein
2876081	syn	CG	MMAR_2380	-		cell wall and cell processes	conserved hypothetical membrane protein
2878774	non	CA	MMAR_2383	-		intermediary metabolism and respiration	adenosylmethionine-8-amino-7-oxononanoate aminotransferase BioA
2881640	syn	CT	MMAR_2385	-		intermediary metabolism and respiration	dethiobiotin synthetase BioD
2882710	non	CT	MMAR_2387	-		intermediary metabolism and respiration	biotin synthase BioB
2884970	non	GT	MMAR_2389	-		cell wall and cell processes	conserved hypothetical membrane protein
2886469	syn	AG	MMAR_2390	-		conserved hypothetical	conserved hypothetical protein
2890371	syn	GA	MMAR_2393	-		intermediary metabolism and respiration	nicotinate-nucleotide pyrophosphatase NadC
2893748	syn	TC	MMAR_2397	-		intermediary metabolism and respiration	imidazole glycerol-phosphate dehydratase HisB
2896104	syn	TC	MMAR_2400	-		intermediary metabolism and respiration	inositol-monophosphatase ImpA
2896197	syn	CT	MMAR_2400	-		intermediary metabolism and respiration	inositol-monophosphatase ImpA
2896347	syn	AG	MMAR_2400	-		intermediary metabolism and respiration	inositol-monophosphatase ImpA
2897313	syn	GA	MMAR_2402	-		intermediary metabolism and respiration	phosphoribosyl-AMP 1' 6 cyclohydrolase HisI
2897543	int	GA	76 MMAR_2403	intermediary metabolism and respiration	deacylase		
2898183	syn	CT		intermediary metabolism and respiration	deacylase		
2898747	non	CT		intermediary metabolism and respiration	conserved hypothetical		
2900270	non	CG		cell wall and cell processes	conserved hypothetical		
2900439	non	CT		cell wall and cell processes	cyanophycinase CphB		
2902192	non	AC		cell wall and cell processes	cyanophycinase CphB		
2907623	syn	GA		regulatory proteins	ligase Mur-family		
2910132	non	GT	MMAR_2411	-		intermediary metabolism and respiration	anchored-membrane serine/threonine-protein kinase PknF_1
2912344	syn	TC	MMAR_2413	-		intermediary metabolism and respiration	indole-3-glycerol phosphate synthase TrpC
2913369	syn	CT	MMAR_2414	-		intermediary metabolism and respiration	tryptophan synthase beta subunit TrpB
2913905	syn	TC	MMAR_2414	-		intermediary metabolism and respiration	tryptophan synthase beta subunit TrpB
2914528	syn	TC	MMAR_2415	-		intermediary metabolism and respiration	tryptophan synthase alpha subunit TrpA
2919279	non	CG	MMAR_2420	-		intermediary metabolism and respiration	pyruvate kinase PykA
2927022	non	TC	MMAR_2425	-		cell wall and cell processes	integral membrane cytochrome D ubiquinol oxidase (subunit II) CydB
2927278	non	CT	MMAR_2425	-		cell wall and cell processes	integral membrane cytochrome D ubiquinol oxidase (subunit II) CydB
2928769	syn	CT	MMAR_2426	-		cell wall and cell processes	integral membrane cytochrome D ubiquinol oxidase (subunit I) CydA
2931841	syn	CT	MMAR_2429	-		regulatory proteins	two-component system transcriptional regulator
2933158	syn	CT	MMAR_2430	-		lipid metabolism	nonspecific lipid-transfer protein
2933364	syn	CT	MMAR_2431	-		conserved hypothetical	conserved hypothetical protein
2934702	syn	AG	MMAR_2432	-		information pathways	DNA polymerase I PolA
2938256	syn	CT	MMAR_2433	-		information pathways	ribosomal protein S1 RpsA
2938383	non	GC	MMAR_2434	-		intermediary metabolism and respiration	dephospho-CoA kinase CoAE
2938730	syn	AT	MMAR_2434	-		intermediary metabolism and respiration	dephospho-CoA kinase CoAE
2938818	non	AG	MMAR_2434	-		intermediary metabolism and respiration	dephospho-CoA kinase CoAE
2940064	non	CT	MMAR_2435	-		conserved hypothetical	conserved hypothetical protein
2940344	syn	CA	MMAR_2436	-		conserved hypothetical	conserved hypothetical protein
2943148	non	AC	MMAR_2438	-		cell wall and cell processes	drug efflux membrane protein
2944130	non	CT	MMAR_2438	-		cell wall and cell processes	drug efflux membrane protein
2946135	non	GA	MMAR_2439	-		cell wall and cell processes	conserved transmembrane protein
2946280	int	CT	114 MMAR_2440	cell wall and cell processes	iron-regulated conserved protein		
2947766	non	AG		conserved hypothetical	conserved protein		
2949006	syn	AG		information pathways	excinuclease ABC (subunit A-DNA-binding ATPase) UvrA		
2949537	syn	GT		information pathways	excinuclease ABC (subunit A-DNA-binding ATPase) UvrA		
2950125	syn	CT		information pathways	excinuclease ABC (subunit A-DNA-binding ATPase) UvrA		
2950239	syn	TC		information pathways	excinuclease ABC (subunit A-DNA-binding ATPase) UvrA		
2951769	non	CG		regulatory proteins	transmembrane serine/threonine-protein kinase		
2952190	syn	GA	MMAR_2444	-		regulatory proteins	transmembrane serine/threonine-protein kinase
2954200	non	CT	MMAR_2446	-		cell wall and cell processes	conserved hypothetical membrane protein
2954968	non	AT	MMAR_2446	-		cell wall and cell processes	conserved hypothetical membrane protein
2955078	int	AG	34 MMAR_2446	cell wall and cell processes	conserved hypothetical membrane protein		
2963584	syn	GA		conserved hypothetical	conserved hypothetical protein		
2966699	syn	CT		information pathways	phenylalanyl-tRNA synthetase beta chain PheT		
2967818	syn	CT		information pathways	phenylalanyl-tRNA synthetase beta chain PheT		
2968996	int	GA		23 MMAR_2457	information pathways	phenylalanyl-tRNA synthetase beta chain PheT	
2970457	int	TC					
2971220	non	GT	95 MMAR_2458 PE/PPE				
2972552	int	AG					
2982638	non	GA					
2982959	int	CA					
2984191	syn	AC		intermediary metabolism and respiration	N-acetyl-gamma-glutamyl-phosphate reductase ArgC		
2984773	syn	GA		intermediary metabolism and respiration	glutamate N-acetyltransferase ArgJ		
2984935	syn	GT		intermediary metabolism and respiration	glutamate N-acetyltransferase ArgJ		
2985349	syn	GA	MMAR_2463	-		intermediary metabolism and respiration	glutamate N-acetyltransferase ArgJ
2986440	syn	CT	MMAR_2464	-		intermediary metabolism and respiration	acetylglutamate kinase ArgB
2987597	syn	CA	MMAR_2465	-		intermediary metabolism and respiration	acetylornithine amino transferase ArgD
2987722	non	CT	MMAR_2465	-		intermediary metabolism and respiration	acetylornithine amino transferase ArgD
2987836	non	CA	MMAR_2465	-		intermediary metabolism and respiration	acetylornithine amino transferase ArgD
2988627	non	CT	MMAR_2466	-		intermediary metabolism and respiration	ornithine carbamoyltransferase anabolic ArgF
2989354	syn	CT	MMAR_2468	-		intermediary metabolism and respiration	argininosuccinate synthase ArgG
2990350	syn	CT	MMAR_2468	-		intermediary metabolism and respiration	argininosuccinate synthase ArgG
2991445	syn	GC	MMAR_2469	-		intermediary metabolism and respiration	argininosuccinate lyase ArgH
2991449	syn	CT	MMAR_2469	-		intermediary metabolism and respiration	argininosuccinate lyase ArgH
2992469	syn	TC	MMAR_2470	-		lipid metabolism	chalcone synthase Pks10
2993493	non	AC	MMAR_2471	-		lipid metabolism	polyketide synthase Pks7
2995297	syn	CT	MMAR_2471	-		lipid metabolism	polyketide synthase Pks7
2996805	syn	CT	MMAR_2471	-		lipid metabolism	polyketide synthase Pks7
2997104	non	CG	MMAR_2471	-		lipid metabolism	polyketide synthase Pks7
2997817	syn	CT	MMAR_2471	-		lipid metabolism	polyketide synthase Pks7
2997882	non	GA	MMAR_2471	-		lipid metabolism	polyketide synthase Pks7
2998462	syn	GT	MMAR_2471	-		lipid metabolism	polyketide synthase Pks7

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
3000162	non	CT	MMAR_2472	-		lipid metabolism	polyketide synthase Pks8
3000225	syn	CT	MMAR_2472	-		lipid metabolism	polyketide synthase Pks8
3001198	syn	TC	MMAR_2472	-		lipid metabolism	polyketide synthase Pks8
3001364	non	TC	MMAR_2472	-		lipid metabolism	polyketide synthase Pks8
3001474	non	AC	MMAR_2472	-		lipid metabolism	polyketide synthase Pks8
3003394	non	GT	MMAR_2472	-		lipid metabolism	polyketide synthase Pks8
3003429	syn	CG	MMAR_2472	-		lipid metabolism	polyketide synthase Pks8
3004641	syn	CA	MMAR_2472	-		lipid metabolism	polyketide synthase Pks8
3005123	non	CT	MMAR_2472	-		lipid metabolism	polyketide synthase Pks8
3006692	syn	GA	MMAR_2473	-		lipid metabolism	polyketide synthase Pks9
3006815	non	AT	MMAR_2473	-		lipid metabolism	polyketide synthase Pks9
3008318	syn	GA	MMAR_2473	-		lipid metabolism	polyketide synthase Pks9
3008746	non	TC	MMAR_2473	-		lipid metabolism	polyketide synthase Pks9
3009176	int	CT	MMAR_2474	143		lipid metabolism	chalcone synthase Pks11_1
3009873	syn	CG		-		lipid metabolism	chalcone synthase Pks11_1
3010092	syn	CT		-		lipid metabolism	chalcone synthase Pks11_1
3010573	syn	CT		-		intermediary metabolism and respiration	cytochrome P450 139A3 Cyp139A3
3010924	non	AT		-		intermediary metabolism and respiration	cytochrome P450 139A3 Cyp139A3
3012549	syn	CT		-		cell wall and cell processes	ABC transporter ATP-binding protein
3014263	int	CT		-			
3015299	non	GC	MMAR_2477	-		intermediary metabolism and respiration	D-AMINO acid oxidase Aao_1
3019291	non	CT	MMAR_2480	-		intermediary metabolism and respiration	lactoylglutathione lyase GloA
3025187	non	CT	MMAR_2486	-		cell wall and cell processes	antibiotic resistance ABC transporter efflux system ATP-binding protein
3025476	syn	GA	MMAR_2486	-		cell wall and cell processes	antibiotic resistance ABC transporter efflux system ATP-binding protein
3037122	non	TC	MMAR_2493	-		conserved hypotheticals	conserved hypothetical protein
3037278	syn	AG	MMAR_2493	-		conserved hypotheticals	conserved hypothetical protein
3037473	non	CT	MMAR_2493	-		conserved hypotheticals	conserved hypothetical protein
3042354	syn	CT	MMAR_2499	-			cytotoxin/hemolysin Tya
3043215	non	GA	MMAR_2500	-		intermediary metabolism and respiration	inorganic polyphosphate/ATP-NAD kinase PpnK
3043415	syn	CT	MMAR_2500	-		intermediary metabolism and respiration	inorganic polyphosphate/ATP-NAD kinase PpnK
3043578	non	CT	MMAR_2500	-		intermediary metabolism and respiration	inorganic polyphosphate/ATP-NAD kinase PpnK
3048871	syn	GT	MMAR_2504	-		intermediary metabolism and respiration	CTP synthase PyrG
3050024	syn	GC	MMAR_2505	-		information pathways	NUDIX hydrolase
3051457	syn	CG	MMAR_2506	-		insertion seqs and phages	integrase/recombinase XerD
3051486	int	GA	MMAR_2506	5		insertion seqs and phages	integrase/recombinase XerD
3051572	syn	CT		-		intermediary metabolism and respiration	O-methyltransferase
3051857	syn	TC		-		intermediary metabolism and respiration	O-methyltransferase
3051884	syn	AG		-		intermediary metabolism and respiration	O-methyltransferase
3051923	syn	GC		-		intermediary metabolism and respiration	O-methyltransferase
3051956	syn	GA	MMAR_2507	-		intermediary metabolism and respiration	O-methyltransferase
3052010	syn	CT	MMAR_2507	-		intermediary metabolism and respiration	O-methyltransferase
3052013	non	CT	MMAR_2507	-		intermediary metabolism and respiration	O-methyltransferase
3052106	syn	GA	MMAR_2507	-		intermediary metabolism and respiration	O-methyltransferase
3052110	non	TG	MMAR_2507	-		intermediary metabolism and respiration	O-methyltransferase
3052263	int	CT	MMAR_2508	137		intermediary metabolism and respiration	myo-inositol-1-phosphate synthase
3052267	int	TC		133		intermediary metabolism and respiration	myo-inositol-1-phosphate synthase
3053485	syn	CA		-		intermediary metabolism and respiration	myo-inositol-1-phosphate synthase
3055398	non	CT		-		intermediary metabolism and respiration	sugar phosphate isomerasers/epimerases
3056203	syn	CT	MMAR_2511	-		intermediary metabolism and respiration	metal dependant hydrolase
3056533	non	AG	MMAR_2511	-		intermediary metabolism and respiration	metal dependant hydrolase
3056635	syn	TC	MMAR_2511	-		intermediary metabolism and respiration	metal dependant hydrolase
3057737	non	AG	MMAR_2512	-		conserved hypotheticals	conserved hypothetical protein
3058137	non	GA	MMAR_2513	-		conserved hypotheticals	conserved hypothetical protein
3058327	non	CT	MMAR_2513	-		conserved hypotheticals	conserved hypothetical protein
3058599	non	CG	MMAR_2513	-		conserved hypotheticals	conserved hypothetical protein
3059048	syn	AG	MMAR_2513	-		conserved hypotheticals	conserved hypothetical protein
3060570	syn	GT	MMAR_2515	-		cell wall and cell processes	integral membrane drug efflux protein
3061146	non	CG	MMAR_2515	-		cell wall and cell processes	integral membrane drug efflux protein
3063057	int	GC	MMAR_2517	112			
3063640	int	GA		112		PE/PPE	PPE family protein
3077063	syn	AG		-		conserved hypotheticals	conserved hypothetical protein
3077764	syn	TC		-		information pathways	ATPase involved in chromosome partitioning (Sj family)
3078142	syn	CT		-		information pathways	ATPase involved in chromosome partitioning (Sj family)
3078621	syn	GA		-		conserved hypotheticals	conserved hypothetical protein
3079049	syn	GC		-		regulatory proteins	transcriptional regulator
3079172	syn	CG		-		regulatory proteins	transcriptional regulator
3080708	non	GC		-		intermediary metabolism and respiration	cytidylate kinase Cmk
3081083	syn	CT		-		intermediary metabolism and respiration	cytidylate kinase Cmk
3081352	syn	AG		-		intermediary metabolism and respiration	GTP-binding protein EngA
3102168	int	CG	MMAR_2550	69		cell wall and cell processes	conserved transmembrane protein
3102169	non	GC		70		cell wall and cell processes	conserved transmembrane protein
3102333	int	TC		54		MMAR_2551 PE/PPE	PE-PGRS family protein
3102401	int	TG		14		MMAR_2551 PE/PPE	PE-PGRS family protein
3103751	int	AG		-			
3104252	int	CT		87		MMAR_2551 PE/PPE	PE-PGRS family protein
3104320	int	TC		102		MMAR_2552 cell wall and cell processes	conserved hypothetical membrane protein
3105276	int	GC		63		MMAR_2552 cell wall and cell processes	conserved hypothetical membrane protein
3105343	int	AG		130		MMAR_2552 cell wall and cell processes	conserved hypothetical membrane protein
3105366	int	GC		67		MMAR_2553 cell wall and cell processes	hypothetical secreted protein
3105394	int	AG		39		MMAR_2553 cell wall and cell processes	hypothetical secreted protein
3105395	int	GA		38		MMAR_2553 cell wall and cell processes	hypothetical secreted protein
3105746	int	AC		44		MMAR_2553 cell wall and cell processes	hypothetical secreted protein
3106321	int	TC		24		MMAR_2554 cell wall and cell processes	conserved hypothetical secreted protein
3106344	int	CG		117		MMAR_2554 cell wall and cell processes	conserved hypothetical secreted protein
3107308	non	TG	MMAR_2557	-		intermediary metabolism and respiration	aldose 1-epimerase
3110321	int	CG		-			
3113132	int	AT		-			
3113482	int	AT	MMAR_2564	37		lipid metabolism	polypropenyl synthetase IdsB
3113575	syn	CT		-		lipid metabolism	polypropenyl synthetase IdsB
3114133	syn	GT		-		lipid metabolism	polypropenyl synthetase IdsB
3114491	non	CT		-		lipid metabolism	polypropenyl synthetase IdsB
3115432	syn	CT		-		unknown	hypothetical protein
3115701	syn	AC		-		unknown	hypothetical protein
3115886	int	GC		26		MMAR_2565 unknown	hypothetical protein
3116309	non	CT	MMAR_2566	-		intermediary metabolism and respiration	conserved hypothetical hydrolase

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
3116347	non	TC	MMAR_2566	-		intermediary metabolism and respiration	conserved hypothetical hydrolase
3118194	non	AG	MMAR_2568	-		intermediary metabolism and respiration	carbohydrate phosphorylase
3118204	non	TC	MMAR_2568	-		intermediary metabolism and respiration	carbohydrate phosphorylase
3118256	syn	GA	MMAR_2568	-		intermediary metabolism and respiration	carbohydrate phosphorylase
3118370	syn	CT	MMAR_2568	-		intermediary metabolism and respiration	carbohydrate phosphorylase
3118436	syn	TG	MMAR_2568	-		intermediary metabolism and respiration	carbohydrate phosphorylase
3118472	non	CT	MMAR_2568	-		intermediary metabolism and respiration	carbohydrate phosphorylase
3119627	syn	GA	MMAR_2568	-		intermediary metabolism and respiration	carbohydrate phosphorylase
3119747	syn	CG	MMAR_2568	-		intermediary metabolism and respiration	carbohydrate phosphorylase
3119888	syn	GA	MMAR_2568	-		intermediary metabolism and respiration	carbohydrate phosphorylase
3120104	int	CT		115	MMAR_2568	intermediary metabolism and respiration	carbohydrate phosphorylase
3120470	syn	AG	MMAR_2569	-		cell wall and cell processes	conserved hypothetical secreted protein
3120850	int	CT		48	MMAR_2569	cell wall and cell processes	conserved hypothetical secreted protein
3121077	non	AG	MMAR_2570	-		intermediary metabolism and respiration	conserved hypothetical hydrolase/amidase
3121774	syn	CA	MMAR_2570	-		intermediary metabolism and respiration	conserved hypothetical hydrolase/amidase
3122587	syn	GA	MMAR_2571	-		intermediary metabolism and respiration	succinate-semialdehyde dehydrogenase [NADP+] dependent (SsdH) GabD2
3123079	syn	CG	MMAR_2571	-		intermediary metabolism and respiration	succinate-semialdehyde dehydrogenase [NADP+] dependent (SsdH) GabD2
3125210	int	CT		49	MMAR_2573	conserved hypotheticals	conserved protein
3125235	int	TG		24	MMAR_2573	conserved hypotheticals	conserved protein
3126555	syn	CT	MMAR_2574	-		cell wall and cell processes	sugar transporter
3126933	syn	CT	MMAR_2574	-		cell wall and cell processes	sugar transporter
3127389	syn	AG	MMAR_2574	-		cell wall and cell processes	sugar transporter
3127503	syn	AG	MMAR_2574	-		cell wall and cell processes	sugar transporter
3128954	int	TC		-			
3129505	syn	GT	MMAR_2576	-		regulatory proteins	serine/threonine-protein kinase transcriptional regulatory protein PknK
3129586	syn	CT	MMAR_2576	-		regulatory proteins	serine/threonine-protein kinase transcriptional regulatory protein PknK
3129733	syn	GA	MMAR_2576	-		regulatory proteins	serine/threonine-protein kinase transcriptional regulatory protein PknK
3129745	syn	GA	MMAR_2576	-		regulatory proteins	serine/threonine-protein kinase transcriptional regulatory protein PknK
3130270	syn	CT	MMAR_2576	-		regulatory proteins	serine/threonine-protein kinase transcriptional regulatory protein PknK
3131839	non	G-	MMAR_2576	-		regulatory proteins	serine/threonine-protein kinase transcriptional regulatory protein PknK
3132059	non	TC	MMAR_2576	-		regulatory proteins	serine/threonine-protein kinase transcriptional regulatory protein PknK
3132238	syn	AG	MMAR_2576	-		regulatory proteins	serine/threonine-protein kinase transcriptional regulatory protein PknK
3132971	syn	CG	MMAR_2577	-		conserved hypotheticals	conserved hypothetical protein
3133042	non	CT	MMAR_2577	-		conserved hypotheticals	conserved hypothetical protein
3134885	non	CT	MMAR_2578	-		cell wall and cell processes	metal cation transporter p-type ATPase a CtpF
3135249	syn	GC	MMAR_2578	-		cell wall and cell processes	metal cation transporter p-type ATPase a CtpF
3135777	syn	CT	MMAR_2578	-		cell wall and cell processes	metal cation transporter p-type ATPase a CtpF
3136936	non	CT	MMAR_2579	-		cell wall and cell processes	amino acid transporter PotE
3137012	syn	GC	MMAR_2579	-		cell wall and cell processes	amino acid transporter PotE
3137180	syn	CT	MMAR_2579	-		cell wall and cell processes	amino acid transporter PotE
3137219	syn	TG	MMAR_2579	-		cell wall and cell processes	amino acid transporter PotE
3140062	syn	CT	MMAR_2581	-		regulatory proteins	transmembrane serine/threonine-protein kinase E PknE
3140503	non	CG	MMAR_2582	-		cell wall and cell processes	conserved hypothetical transmembrane protein
3140531	non	TC	MMAR_2582	-		cell wall and cell processes	conserved hypothetical transmembrane protein
3140933	non	GA	MMAR_2582	-		cell wall and cell processes	conserved hypothetical transmembrane protein
3142145	syn	GA	MMAR_2583	-		cell wall and cell processes	sodium/hydrogen exchanger (antiporter)
3145180	syn	GA	MMAR_2585	-		information pathways	transcriptional accessory protein Tex
3150070	non	CT	MMAR_2588	-		cell wall and cell processes	conserved hypothetical membrane protein
3150496	int	TC		144	MMAR_2589	lipid metabolism	Z-decaprenyl diphosphate synthase
3151980	syn	AG	MMAR_2590	-		conserved hypotheticals	conserved hypothetical protein
3152070	non	TC	MMAR_2590	-		conserved hypotheticals	conserved hypothetical protein
3152490	syn	GT	MMAR_2590	-		conserved hypotheticals	conserved hypothetical protein
3152931	int	GA		-			
3153939	int	TC		-			
3161079	syn	TC	MMAR_2593	-		cell wall and cell processes	divalent cation-transport integral membrane protein
3162357	syn	TC	MMAR_2594	-		cell wall and cell processes	conserved secreted protein
3168610	syn	CT	MMAR_2598	-		conserved hypotheticals	conserved hypothetical protein
3168676	syn	CT	MMAR_2598	-		conserved hypotheticals	conserved hypothetical protein
3169350	syn	GA	MMAR_2599	-		conserved hypotheticals	conserved hypothetical protein
3169572	syn	CG	MMAR_2599	-		conserved hypotheticals	conserved hypothetical protein
3172404	int	GA		110	MMAR_2602	unknown	hypothetical protein
3175146	non	CT	MMAR_2605	-		intermediary metabolism and respiration	anaerobic dehydrogenase
3186032	int	CT		94	MMAR_2612	cell wall and cell processes	conserved transmembrane ATP-binding protein ABC transporter
3187226	syn	CT	MMAR_2612	-		cell wall and cell processes	conserved transmembrane ATP-binding protein ABC transporter
3187847	syn	AC	MMAR_2612	-		cell wall and cell processes	conserved transmembrane ATP-binding protein ABC transporter
3187868	syn	GA	MMAR_2612	-		cell wall and cell processes	conserved transmembrane ATP-binding protein ABC transporter
3187907	syn	TA	MMAR_2612	-		cell wall and cell processes	conserved transmembrane ATP-binding protein ABC transporter
3188034	non	AG	MMAR_2612	-		cell wall and cell processes	conserved transmembrane ATP-binding protein ABC transporter
3188790	int	GC		31	MMAR_2612	cell wall and cell processes	conserved transmembrane ATP-binding protein ABC transporter
3188825	non	GA	MMAR_2613	-		cell wall and cell processes	conserved membrane protein
3188829	syn	GC	MMAR_2613	-		cell wall and cell processes	conserved membrane protein
3189117	syn	GA	MMAR_2613	-		cell wall and cell processes	conserved membrane protein
3189706	syn	GC	MMAR_2614	-		cell wall and cell processes	conserved hypothetical membrane protein
3189780	non	TG	MMAR_2614	-		cell wall and cell processes	conserved hypothetical membrane protein
3190183	syn	CT	MMAR_2614	-		cell wall and cell processes	conserved hypothetical membrane protein
3191344	non	TG	MMAR_2616	-		conserved hypotheticals	conserved hypothetical protein
3192087	syn	CT	MMAR_2616	-		conserved hypotheticals	conserved hypothetical protein
3192138	syn	CT	MMAR_2616	-		conserved hypotheticals	conserved hypothetical protein
3192386	non	CG	MMAR_2616	-		conserved hypotheticals	conserved hypothetical protein
3193753	non	CA	MMAR_2618	-		intermediary metabolism and respiration	amidohydrolase
3196518	int	GA		143	MMAR_2621	lipid metabolism	esterase/lipase
3196649	int	GA		13	MMAR_2621	lipid metabolism	esterase/lipase
3197142	non	GA	MMAR_2621	-		lipid metabolism	esterase/lipase
3197373	non	AG	MMAR_2621	-		lipid metabolism	esterase/lipase
3197869	syn	CT	MMAR_2622	-		intermediary metabolism and respiration	flavin-binding monooxygenase
3198046	syn	CT	MMAR_2622	-		intermediary metabolism and respiration	flavin-binding monooxygenase
3198195	non	TC	MMAR_2622	-		intermediary metabolism and respiration	flavin-binding monooxygenase
3199516	syn	TC	MMAR_2623	-		intermediary metabolism and respiration	flavin-binding monooxygenase
3200065	syn	CT	MMAR_2623	-		intermediary metabolism and respiration	conserved short-chain dehydrogenase
3200195	syn	CT	MMAR_2623	-		intermediary metabolism and respiration	conserved short-chain dehydrogenase
3200903	syn	TC	MMAR_2624	-		intermediary metabolism and respiration	conserved short-chain dehydrogenase
3202317	non	TG	MMAR_2625	-		lipid metabolism	conserved hypothetical protein
3203276	int	AG		130	MMAR_2626	conserved hypotheticals	conserved hypothetical protein
3203706	non	GA	MMAR_2626	-		conserved hypotheticals	conserved hypothetical protein
3204008	syn	CT	MMAR_2626	-		conserved hypotheticals	conserved hypothetical protein

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
3204851	syn	GA	MMAR_2626	-		conserved hypotheticals	conserved hypothetical protein
3205295	int	GA					
3205509	int	TC		72	MMAR_2627	intermediary metabolism and respiration	oxidoreductase
3205517	int	CT		64	MMAR_2627	intermediary metabolism and respiration	oxidoreductase
3205721	syn	GA	MMAR_2627	-		intermediary metabolism and respiration	oxidoreductase
3207799	syn	GT	MMAR_2628	-		conserved hypotheticals	conserved hypothetical protein
3208066	int	GA		-			
3208145	int	GT		-			
3209319	syn	CT	MMAR_2629	-		intermediary metabolism and respiration	glycosyl transferase
3209385	syn	TC	MMAR_2629	-		intermediary metabolism and respiration	glycosyl transferase
3209969	syn	TG	MMAR_2630	-		cell wall and cell processes	conserved hypothetical membrane protein
3210429	syn	CG	MMAR_2630	-		cell wall and cell processes	conserved hypothetical membrane protein
3210937	syn	CT	MMAR_2631	-		intermediary metabolism and respiration	cytochrome P450 143A3 Cyp143A3
3211459	syn	CT	MMAR_2631	-		intermediary metabolism and respiration	cytochrome P450 143A3 Cyp143A3
3212256	syn	GA	MMAR_2632	-		cell wall and cell processes	conserved membrane protein
3213537	syn	CT	MMAR_2633	-		intermediary metabolism and respiration	short-chain type dehydrogenase/reductase
3214000	int	AG		51	MMAR_2634	conserved hypotheticals	conserved hypothetical protein
3215204	non	CG	MMAR_2634	-		conserved hypotheticals	conserved hypothetical protein
3218164	syn	GA	MMAR_2638	-		regulatory protein	transcriptional regulatory protein (probably AcrR-family)
3223553	int	CG		113	MMAR_2646	conserved hypotheticals	conserved protein
3223554	int	CG		112	MMAR_2646	conserved hypotheticals	conserved protein
3242093	syn	CT	MMAR_2657	-		intermediary metabolism and respiration	isochorismatase family protein
3242308	non	CT	MMAR_2657	-		intermediary metabolism and respiration	isochorismatase family protein
3244793	non	CA	MMAR_2660	-		cell wall and cell processes	conserved hypothetical membrane protein
3245247	int	CT		145	MMAR_2660	cell wall and cell processes	conserved hypothetical membrane protein
3247635	syn	GT	MMAR_2663	-		intermediary metabolism and respiration	4-alpha-glucanotransferase MalQ
3248799	int	CT		34	MMAR_2663	intermediary metabolism and respiration	4-alpha-glucanotransferase MalQ
3249569	syn	GA	MMAR_2664	-		cell wall and cell processes	conserved membrane protein
3250288	non	TC	MMAR_2664	-		cell wall and cell processes	conserved membrane protein
3250520	syn	GA	MMAR_2664	-		cell wall and cell processes	conserved membrane protein
3254346	non	TA	MMAR_2665	-		conserved hypotheticals	conserved Ftsk/SpoIIIIE family protein
3259989	int	GC		54	MMAR_2672	conserved hypotheticals	conserved hypothetical protein
3260470	int	AT		107	MMAR_2672	conserved hypotheticals	conserved hypothetical protein
3260552	int	CT		-			
3268026	syn	CT	MMAR_2680	-		conserved hypotheticals	conserved protein
3268398	syn	AG	MMAR_2680	-		conserved hypotheticals	conserved protein
3269808	int	GA		60	MMAR_2680	conserved hypotheticals	conserved protein
3270482	int	C-		-			
3270543	int	CT		106	MMAR_2681	PE/PPE	PPE family protein
3271712	int	G-		-			
3271850	int	AG		67	MMAR_2681	PE/PPE	PPE family protein
3271997	int	GC		80	MMAR_2681	PE/PPE	PPE family protein
3272776	int	TC		-			
3273346	int	CG		104	MMAR_2682	PE/PPE	PPE family protein
3273353	int	TC		111	MMAR_2682	PE/PPE	PPE family protein
3273904	int	AG		-			
3275481	int	AG		-			
3278084	int	GT		-			
3289760	int	CT		59	MMAR_2696	cell wall and cell processes	drug-transport transmembrane ATP-binding protein ABC transporter
3289909	syn	GC	MMAR_2696	-		cell wall and cell processes	drug-transport transmembrane ATP-binding protein ABC transporter
3290063	non	AG	MMAR_2696	-		cell wall and cell processes	drug-transport transmembrane ATP-binding protein ABC transporter
3292370	non	GC	MMAR_2697	-		intermediary metabolism and respiration	acetolactate synthase IlvG
3293728	non	CG	MMAR_2698	-		cell wall and cell processes	preprotein translocase ATPase SecA2
3293929	syn	CT	MMAR_2698	-		cell wall and cell processes	preprotein translocase ATPase SecA2
3294880	syn	GT	MMAR_2698	-		cell wall and cell processes	preprotein translocase ATPase SecA2
3295075	syn	CT	MMAR_2698	-		cell wall and cell processes	preprotein translocase ATPase SecA2
3299326	non	CT	MMAR_2703	-		intermediary metabolism and respiration	glycine cleavage system H protein GcvH
3303289	non	GA	MMAR_2708	-		intermediary metabolism and respiration	glycine dehydrogenase GcvB
3304046	syn	GA	MMAR_2708	-		intermediary metabolism and respiration	glycine dehydrogenase GcvB
3304951	non	AG	MMAR_2708	-		intermediary metabolism and respiration	glycine dehydrogenase GcvB
3308984	syn	GC	MMAR_2711	-		intermediary metabolism and respiration	hydrolase
3309192	syn	CT	MMAR_2711	-		intermediary metabolism and respiration	hydrolase
3310697	syn	CG	MMAR_2712	-		cell wall and cell processes	conserved membrane protein
3311296	non	AG	MMAR_2712	-		cell wall and cell processes	conserved membrane protein
3311623	syn	CT	MMAR_2713	-		intermediary metabolism and respiration	malate synthase G GlcB
3312893	non	AG	MMAR_2713	-		intermediary metabolism and respiration	malate synthase G GlcB
3316910	syn	AG	MMAR_2716	-		cell wall and cell processes	conserved hypothetical membrane protein
3318778	syn	GA	MMAR_2717	-		intermediary metabolism and respiration	inosine-5'-monophosphate dehydrogenase Guab1
3320879	syn	CT	MMAR_2718	-		intermediary metabolism and respiration	6-phosphogluconate dehydrogenase Gnd1
3321044	syn	GC	MMAR_2718	-		intermediary metabolism and respiration	6-phosphogluconate dehydrogenase Gnd1
3321864	syn	AG	MMAR_2719	-		cell wall and cell processes	conserved hypothetical transmembrane protein
3323242	int	CT		46	MMAR_2721	conserved hypotheticals	conserved hypothetical protein
3323342	non	GC	MMAR_2721	-		conserved hypotheticals	conserved hypothetical protein
3324338	syn	GA	MMAR_2723	-		intermediary metabolism and respiration	urease beta subunit UreB
3324386	syn	GA	MMAR_2723	-		intermediary metabolism and respiration	urease beta subunit UreB
3326154	syn	CG	MMAR_2725	-		intermediary metabolism and respiration	urease accessory protein UreF
3328916	syn	CA	MMAR_2728	-		intermediary metabolism and respiration	NADH dehydrogenase Ndh
3329886	syn	CT	MMAR_2729	-		intermediary metabolism and respiration	oxidoreductase
3332436	non	AC	MMAR_2732	-		cell wall and cell processes	molybdenum-transport integral membrane protein ABC transporter ModB
3333235	non	CT	MMAR_2733	-		lipid metabolism	O-methyltransferase Omt
3333720	syn	CG	MMAR_2733	-		lipid metabolism	O-methyltransferase Omt
3334122	int	GA		132	MMAR_2734	intermediary metabolism and respiration	conserved hypothetical protein
3335842	syn	CG	MMAR_2735	-		unknown	hypothetical protein
3336911	non	GA	MMAR_2736	-		cell wall and cell processes	molybdenum-transport ATP-binding protein ABC transporter ModC
3336641	non	GA	MMAR_2736	-		cell wall and cell processes	molybdenum-transport ATP-binding protein ABC transporter ModC
3337233	int	CT		67	MMAR_2737	cell wall and cell processes	alanine and proline rich secreted protein Apa
3340672	int	TC		51	MMAR_2740	cell wall and cell processes	conserved hypothetical membrane protein
3343737	syn	GA	MMAR_2742	-		intermediary metabolism and respiration	D-xylulose 5-phosphate Xfp
3344115	syn	GA	MMAR_2742	-		intermediary metabolism and respiration	D-xylulose 5-phosphate Xfp
3344505	syn	TC	MMAR_2743	-		intermediary metabolism and respiration	short-chain type dehydrogenase
3345845	int	GA		70	MMAR_2744	lipid metabolism	acyl transferase
3345956	syn	CT	MMAR_2745	-		lipid metabolism	acyl-CoA transferase/dehydratase
3346024	syn	GA	MMAR_2745	-		lipid metabolism	acyl-CoA transferase/dehydratase
3346195	syn	CG	MMAR_2745	-		lipid metabolism	acyl-CoA transferase/dehydratase
3347551	non	CG	MMAR_2745	-		lipid metabolism	acyl-CoA transferase/dehydratase

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
3347596	syn	CT	MMAR_2745	-		lipid metabolism	acyl-CoA transferase/dehydratase
3347642	syn	GA	MMAR_2745	-		lipid metabolism	acyl-CoA transferase/dehydratase
3348749	syn	CT	MMAR_2746	-		conserved hypotheticals	conserved hypothetical protein
3349055	syn	CT	MMAR_2746	-		conserved hypotheticals	conserved hypothetical protein
3349415	syn	CT	MMAR_2746	-		conserved hypotheticals	conserved hypothetical protein
3350331	syn	GA	MMAR_2747	-		conserved hypotheticals	conserved hypothetical protein
3351195	syn	CT	MMAR_2747	-		conserved hypotheticals	conserved hypothetical protein
3353770	syn	TC	MMAR_2751	-		Lon ATP-dependent Lon protease	Lon ATP-dependent Lon protease
3355064	non	GA	MMAR_2751	-			Lon ATP-dependent Lon protease
3356825	syn	CG	MMAR_2752	-		intermediary metabolism and respiration	L-lactate dehydrogenase (cytochrome) LldD2
3357208	non	CT	MMAR_2752	-		intermediary metabolism and respiration	L-lactate dehydrogenase (cytochrome) LldD2
3357296	syn	AG	MMAR_2752	-		intermediary metabolism and respiration	L-lactate dehydrogenase (cytochrome) LldD2
3358224	syn	CT	MMAR_2753	-		intermediary metabolism and respiration	trehalose synthase TreS 1
3358342	non	TC	MMAR_2753	-		intermediary metabolism and respiration	trehalose synthase TreS 1
3358430	non	GT	MMAR_2753	-		intermediary metabolism and respiration	trehalose synthase TreS 1
3358921	syn	GA	MMAR_2754	-			alkyl hydroperoxide reductase D protein AhpD
3363216	int	GT		49	MMAR_2760	conserved hypotheticals	conserved hypothetical protein
3363222	int	GA		55	MMAR_2760	conserved hypotheticals	conserved hypothetical protein
3363308	int	GA		141	MMAR_2760	conserved hypotheticals	conserved hypothetical protein
3366036	syn	GC	MMAR_2763	-		intermediary metabolism and respiration	glutamine synthetase GlnA3
3366066	syn	AG	MMAR_2763	-		intermediary metabolism and respiration	glutamine synthetase GlnA3
3366351	syn	CT	MMAR_2764	-		conserved hypotheticals	conserved hypothetical protein
3366532	non	CA	MMAR_2764	-		conserved hypotheticals	conserved hypothetical protein
3366559	non	TC	MMAR_2764	-		conserved hypotheticals	conserved hypothetical protein
3366562	non	AG	MMAR_2764	-		conserved hypotheticals	conserved hypothetical protein
3366564	non	CG	MMAR_2764	-		conserved hypotheticals	conserved hypothetical protein
3366634	non	AG	MMAR_2764	-		conserved hypotheticals	conserved hypothetical protein
3366637	non	GA	MMAR_2764	-		conserved hypotheticals	conserved hypothetical protein
3366648	syn	CT	MMAR_2764	-		conserved hypotheticals	conserved hypothetical protein
3366676	non	CG	MMAR_2764	-		conserved hypotheticals	conserved hypothetical protein
3366762	syn	AG	MMAR_2764	-		conserved hypotheticals	conserved hypothetical protein
3366795	non	TC	MMAR_2764	-		conserved hypotheticals	conserved hypothetical protein
3366879	syn	CA	MMAR_2764	-		conserved hypotheticals	conserved hypothetical protein
3366881	non	GA	MMAR_2764	-		conserved hypotheticals	conserved hypothetical protein
3366921	syn	TC	MMAR_2764	-		conserved hypotheticals	conserved hypothetical protein
3366963	syn	TA	MMAR_2764	-		conserved hypotheticals	conserved hypothetical protein
3366966	syn	AG	MMAR_2764	-		conserved hypotheticals	conserved hypothetical protein
3366972	syn	GA	MMAR_2764	-		conserved hypotheticals	conserved hypothetical protein
3366982	non	GA	MMAR_2764	-		conserved hypotheticals	conserved hypothetical protein
3367008	syn	TC	MMAR_2764	-		conserved hypotheticals	conserved hypothetical protein
3367011	syn	GA	MMAR_2764	-		conserved hypotheticals	conserved hypothetical protein
3367089	syn	CT	MMAR_2764	-		conserved hypotheticals	conserved hypothetical protein
3367098	syn	GA	MMAR_2764	-		conserved hypotheticals	conserved hypothetical protein
3367188	syn	GA	MMAR_2764	-		conserved hypotheticals	conserved hypothetical protein
3367218	non	GC	MMAR_2764	-		conserved hypotheticals	conserved hypothetical protein
3367260	syn	CA	MMAR_2764	-		conserved hypotheticals	conserved hypothetical protein
3367263	syn	AG	MMAR_2764	-		conserved hypotheticals	conserved hypothetical protein
3367323	syn	TC	MMAR_2764	-		conserved hypotheticals	conserved hypothetical protein
3367326	syn	GA	MMAR_2764	-		conserved hypotheticals	conserved hypothetical protein
3367377	syn	AT	MMAR_2764	-		conserved hypotheticals	conserved hypothetical protein
3367382	non	GA	MMAR_2764	-		conserved hypotheticals	conserved hypothetical protein
3367385	non	GA	MMAR_2764	-		conserved hypotheticals	conserved hypothetical protein
3367392	syn	GA	MMAR_2764	-		conserved hypotheticals	conserved hypothetical protein
3367406	non	GA	MMAR_2764	-		conserved hypotheticals	conserved hypothetical protein
3367408	syn	CT	MMAR_2764	-		conserved hypotheticals	conserved hypothetical protein
3367410	syn	TG	MMAR_2764	-		conserved hypotheticals	conserved hypothetical protein
3367413	non	CG	MMAR_2764	-		conserved hypotheticals	conserved hypothetical protein
3367421	non	CG	MMAR_2764	-		conserved hypotheticals	conserved hypothetical protein
3367423	non	AG	MMAR_2764	-		conserved hypotheticals	conserved hypothetical protein
3367429	non	AT	MMAR_2764	-		conserved hypotheticals	conserved hypothetical protein
3367438	non	GA	MMAR_2764	-		conserved hypotheticals	conserved hypothetical protein
3367467	non	AG	MMAR_2765	-		intermediary metabolism and respiration	conserved hypothetical amidase
3367486	non	GC	MMAR_2765	-		intermediary metabolism and respiration	conserved hypothetical amidase
3367497	non	AG	MMAR_2765	-		intermediary metabolism and respiration	conserved hypothetical amidase
3367540	non	CT	MMAR_2765	-		intermediary metabolism and respiration	conserved hypothetical amidase
3367551	non	GT	MMAR_2765	-		intermediary metabolism and respiration	conserved hypothetical amidase
3367562	syn	GC	MMAR_2765	-		intermediary metabolism and respiration	conserved hypothetical amidase
3367565	syn	AG	MMAR_2765	-		intermediary metabolism and respiration	conserved hypothetical amidase
3367583	syn	AG	MMAR_2765	-		intermediary metabolism and respiration	conserved hypothetical amidase
3367589	non	CA	MMAR_2765	-		intermediary metabolism and respiration	conserved hypothetical amidase
3367664	syn	CG	MMAR_2765	-		intermediary metabolism and respiration	conserved hypothetical amidase
3368501	non	CG	MMAR_2765	-		intermediary metabolism and respiration	conserved hypothetical amidase
3378091	syn	GA	MMAR_2772	-		cell wall and cell processes	resuscitation-promoting factor-like protein
3379890	int	TC		58	MMAR_2774	intermediary metabolism and respiration	oxidoreductase
3381700	int	GT		68	MMAR_2776	conserved hypotheticals	conserved hypothetical protein
3391669	int	GA		98	MMAR_2788	cell wall and cell processes	conserved hypothetical membrane protein
3393776	non	CA	MMAR_2789	-		intermediary metabolism and respiration	monoxygenase
3393904	non	CT	MMAR_2790	-		intermediary metabolism and respiration	dehydrogenase
3394226	syn	GA	MMAR_2790	-		intermediary metabolism and respiration	dehydrogenase
3395191	syn	CT	MMAR_2791	-		conserved hypotheticals	conserved protein
3396377	int	CG		132	MMAR_2793	conserved hypotheticals	conserved hypothetical protein
3397062	non	TG	MMAR_2794	-		cell wall and cell processes	lipoprotein LppD
3398769	syn	GA	MMAR_2796	-		cell wall and cell processes	competence/damage-inducible protein CinA
3402088	non	AG	MMAR_2799	-		cell wall and cell processes	conserved hypothetical membrane protein
3402230	int	CT		59	MMAR_2799	cell wall and cell processes	conserved hypothetical membrane protein
3402273	int	AG		102	MMAR_2799	cell wall and cell processes	conserved hypothetical membrane protein
3413195	non	TG	MMAR_2813	-		intermediary metabolism and respiration	dehydrogenase
3414156	syn	GA	MMAR_2814	-		lipid metabolism	oxidoreductase FadB5
3417333	non	GA	MMAR_2819	-		conserved hypotheticals	conserved hypothetical protein
3417379	non	AG	MMAR_2819	-		conserved hypotheticals	conserved hypothetical protein
3417461	non	CT	MMAR_2819	-		conserved hypotheticals	conserved hypothetical protein
3417525	non	GC	MMAR_2819	-		conserved hypotheticals	conserved hypothetical protein
3418056	syn	CT	MMAR_2821	-		intermediary metabolism and respiration	isocitrate lyase AceA
3419513	non	GC	MMAR_2821	-		intermediary metabolism and respiration	isocitrate lyase AceAb
3464111	syn	TC	MMAR_2859	-		intermediary metabolism and respiration	conserved hypothetical oxidoreductase

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
3467055	non	GC	MMAR_2862	-		lipid metabolism	acyl-CoA dehydrogenase FadE17
3471158	non	TC	MMAR_2865	-		intermediary metabolism and respiration	oxygenase
3471931	non	GC	MMAR_2865	-		intermediary metabolism and respiration	oxygenase
3472208	non	CT	MMAR_2865	-		intermediary metabolism and respiration	oxygenase
3472209	non	TC	MMAR_2865	-		intermediary metabolism and respiration	oxygenase
3473067	syn	CA	MMAR_2866	-			epoxide hydrolase EphB
3473945	non	GA	MMAR_2867	-		intermediary metabolism and respiration	conserved hypothetical oxidoreductase
3474451	syn	CT	MMAR_2867	-		intermediary metabolism and respiration	conserved hypothetical oxidoreductase
3476070	syn	GT	MMAR_2869	-		intermediary metabolism and respiration	short-chain type dehydrogenase/reductase
3477182	int	TG		17	MMAR_2870	cell wall and cell processes	conserved hypothetical membrane protein
3477187	int	CG		22	MMAR_2870	cell wall and cell processes	conserved hypothetical membrane protein
3477314	int	CT		149	MMAR_2870	cell wall and cell processes	conserved hypothetical membrane protein
3477924	int	CT		-			
3478262	syn	GC	MMAR_2872	-		cell wall and cell processes	multidrug transport integral membrane protein Mmr-like
3479653	non	CG	MMAR_2873	-		regulatory protein	transcriptional repressor (probably TetR-family) Mce3R
3481213	non	TC	MMAR_2875	-		intermediary metabolism and respiration	aldehyde dehydrogenase
3481281	syn	AG	MMAR_2875	-		intermediary metabolism and respiration	aldehyde dehydrogenase
3481515	syn	GA	MMAR_2875	-		intermediary metabolism and respiration	aldehyde dehydrogenase
3481542	syn	GC	MMAR_2875	-		intermediary metabolism and respiration	aldehyde dehydrogenase
3481635	syn	GC	MMAR_2875	-		intermediary metabolism and respiration	aldehyde dehydrogenase
3481746	syn	AG	MMAR_2875	-		intermediary metabolism and respiration	aldehyde dehydrogenase
3482280	syn	AC	MMAR_2875	-		intermediary metabolism and respiration	aldehyde dehydrogenase
3487412	syn	TC	MMAR_2881	-			conserved hypothetical integral membrane protein YrbE3B
3488210	non	CG	MMAR_2882	-			MCE-family protein Mce3A
3488715	syn	GA	MMAR_2882	-			MCE-family protein Mce3A
3489075	int	AG		51	MMAR_2882		MCE-family protein Mce3A
3489378	syn	AG	MMAR_2883	-			MCE-family protein Mce3B
3491400	non	CG	MMAR_2884	-		unknown	MCE-family protein Mce3C
3492070	syn	GA	MMAR_2885	-			MCE-family protein Mce3D
3492112	syn	CA	MMAR_2885	-			MCE-family protein Mce3D
3492140	non	GA	MMAR_2885	-			MCE-family protein Mce3D
3505414	non	TG	MMAR_2899	-		conserved hypothetical	conserved hypothetical protein
3517444	int	GA		81	MMAR_2913	cell wall and cell processes	glycine betaine transport integral membrane protein BetP
3517667	non	TG	MMAR_2914	-			catalase-peroxidase-peroxynitritase T KatG
3519935	syn	GA	MMAR_2915	-		regulatory proteins	ferric uptake regulation protein FurA
3520292	int	CT		-			
3520797	syn	GC	MMAR_2916	-		conserved hypothetical	conserved protein
3541730	syn	CT	MMAR_2936	-		lipid metabolism	fatty-acid-CoA ligase FadD9_1
3542297	syn	GA	MMAR_2936	-		lipid metabolism	fatty-acid-CoA ligase FadD9_1
3543605	syn	TC	MMAR_2936	-		lipid metabolism	fatty-acid-CoA ligase FadD9_1
3543816	syn	CT	MMAR_2936	-		lipid metabolism	fatty-acid-CoA ligase FadD9_1
3545641	syn	GA	MMAR_2938	-		intermediary metabolism and respiration	nitroreductase
3545686	syn	CT	MMAR_2938	-		intermediary metabolism and respiration	nitroreductase
3547674	int	CT		71	MMAR_2941	regulatory proteins	membrane-anchored serine/threonine-protein kinase
3549223	syn	GA	MMAR_2941	-		regulatory proteins	membrane-anchored serine/threonine-protein kinase
3552655	int	GT		-			
3552838	int	CA		143	MMAR_2944	PE/PPE	PPE family protein
3552847	int	GC		134	MMAR_2944	PE/PPE	PPE family protein
3555558	int	GC		149	MMAR_2947	information pathways	HrpA-like helicase
3555793	syn	-G	MMAR_2947	-		information pathways	HrpA-like helicase
3557290	syn	TA	MMAR_2947	-		information pathways	HrpA-like helicase
3558551	syn	CA	MMAR_2947	-		information pathways	HrpA-like helicase
3558913	syn	GA	MMAR_2947	-		information pathways	HrpA-like helicase
3559751	int	CA		103	MMAR_2947	information pathways	HrpA-like helicase
3564932	syn	CT	MMAR_2951	-		cell wall and cell processes	chitinase/cellulase
3568393	non	GA	MMAR_2968	-		conserved hypothetical	conserved hypothetical protein
3594453	syn	GA	MMAR_2971	-		intermediary metabolism and respiration	O-methyltransferase
3615703	int	GA		128	MMAR_2989	conserved hypothetical	conserved protein
3615969	syn	CT	MMAR_2990	-		regulatory protein	heat shock protein transcriptional repressor HspR_2
3616191	int	-A		76	MMAR_2990	regulatory proteins	heat shock protein transcriptional repressor HspR_2
3616191	int	CT		76	MMAR_2990	regulatory proteins	heat shock protein transcriptional repressor HspR_2
3617199	syn	GA	MMAR_2992	-		intermediary metabolism and respiration	GTP cyclohydrolase I FolE_1
3617629	non	CG	MMAR_2992	-		intermediary metabolism and respiration	GTP cyclohydrolase I FolE_1
3620305	non	TC	MMAR_2996	-		conserved hypothetical	conserved hypothetical protein
3620593	syn	CT	MMAR_2997	-		information pathways	alternative RNA polymerase sigma factor
3621440	syn	CG	MMAR_2998	-		cell wall and cell processes	conserved hypothetical membrane protein
3624167	int	GA		-			
3624398	int	AG		-			
3624410	int	GA		-			
3624416	int	GA		-			
3627666	int	CT		62	MMAR_3006	PE/PPE	PPE family protein
3629637	syn	GA	MMAR_3007	-		conserved hypothetical	conserved hypothetical protein
3630133	non	GA	MMAR_3007	-		conserved hypothetical	conserved hypothetical protein
3633431	syn	AG	MMAR_3010	-		conserved hypothetical	conserved membrane protein
3635350	syn	GA	MMAR_3012	-		cell wall and cell processes	sugar ABC transporter
3636242	syn	CG	MMAR_3013	-		cell wall and cell processes	ABC-type sugar transport integral membrane protein
3637281	non	AG	MMAR_3014	-		cell wall and cell processes	sugar-binding lipoprotein
3637354	non	CT	MMAR_3014	-		cell wall and cell processes	sugar-binding lipoprotein
3637789	non	GC	MMAR_3014	-		cell wall and cell processes	sugar-binding lipoprotein
3641432	non	GC	MMAR_3019	-		conserved hypothetical	conserved hypothetical protein
3641478	syn	GA	MMAR_3019	-		conserved hypothetical	conserved hypothetical protein
3642411	non	CA	MMAR_3019	-		conserved hypothetical	conserved hypothetical protein
3644201	non	AT	MMAR_3020	-		lipid metabolism	carboxylesterase Upf
3644207	non	TC	MMAR_3020	-		lipid metabolism	carboxylesterase Upf
3645438	non	GC	MMAR_3022	-		conserved hypothetical	conserved hypothetical protein
3646545	int	GC		97	MMAR_3024	cell wall and cell processes	conserved membrane protein
3647695	non	GT	MMAR_3024	-		cell wall and cell processes	conserved membrane protein
3649440	int	CT		37	MMAR_3024	cell wall and cell processes	conserved membrane protein
3649914	syn	GT	MMAR_3025	-		lipid metabolism	polyketide synthase Pks12
3653392	syn	GC	MMAR_3025	-		lipid metabolism	polyketide synthase Pks12
3653749	non	TG	MMAR_3025	-		lipid metabolism	polyketide synthase Pks12
3653705	syn	GC	MMAR_3025	-		lipid metabolism	polyketide synthase Pks12
3655611	non	AT	MMAR_3025	-		lipid metabolism	polyketide synthase Pks12
3657105	syn	GA	MMAR_3025	-		lipid metabolism	polyketide synthase Pks12
3658708	non	AG	MMAR_3025	-		lipid metabolism	polyketide synthase Pks12

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
3659652	non	GA	MMAR_3025	-		lipid metabolism	polyketide synthase Pks12
3660243	syn	GA	MMAR_3025	-		lipid metabolism	polyketide synthase Pks12
3662090	int	TC		51	MMAR_3025	lipid metabolism	polyketide synthase Pks12
3663164	syn	GA	MMAR_3027	-		conserved hypothetical	conserved hypothetical protein
3663539	syn	AG	MMAR_3028	-		cell wall and cell processes	C-term polyrenol-monophosphomannose synthase Ppm1B
3663551	syn	GA	MMAR_3028	-		cell wall and cell processes	C-term polyrenol-monophosphomannose synthase Ppm1B
3665701	non	GC	MMAR_3029	-		cell wall and cell processes	N-term polyrenol-monophosphomannose synthase Ppm1A
3666021	syn	GA	MMAR_3029	-		cell wall and cell processes	N-term polyrenol-monophosphomannose synthase Ppm1A
3666319	syn	CG	MMAR_3030	-		conserved hypothetical	conserved hypothetical protein
3666958	syn	GA	MMAR_3030	-		conserved hypothetical	conserved hypothetical protein
3667520	non	TC	MMAR_3030	-		conserved hypothetical	conserved hypothetical protein
3668203	syn	CG	MMAR_3031	-		cell wall and cell processes	conserved hypothetical membrane protein
3669223	non	CG	MMAR_3032	-		conserved hypothetical	conserved hypothetical protein
3669225	non	GT	MMAR_3032	-		conserved hypothetical	conserved hypothetical protein
3669226	non	GA	MMAR_3032	-		conserved hypothetical	conserved hypothetical protein
3669671	non	TG	MMAR_3033	-		cell wall and cell processes	conserved hypothetical membrane protein
3671069	non	GA	MMAR_3033	-		cell wall and cell processes	conserved hypothetical membrane protein
3671933	syn	GA	MMAR_3034	-		cell wall and cell processes	conserved transmembrane protein
3672296	syn	GA	MMAR_3034	-		cell wall and cell processes	conserved hypothetical membrane protein
3672878	non	GA	MMAR_3035	-		cell wall and cell processes	conserved hypothetical membrane protein
3673254	syn	GA	MMAR_3035	-		cell wall and cell processes	conserved hypothetical membrane protein
3673535	non	TC	MMAR_3035	-		cell wall and cell processes	conserved hypothetical membrane protein
3673598	non	CT	MMAR_3035	-		cell wall and cell processes	conserved hypothetical membrane protein
3673936	syn	CA	MMAR_3036	-		conserved hypothetical	conserved hypothetical protein
3674478	syn	GC	MMAR_3037	-		intermediary metabolism and respiration	cobalamin biosynthesis protein CobN
3675559	non	AG	MMAR_3037	-		intermediary metabolism and respiration	cobalamin biosynthesis protein CobN
3675675	syn	GC	MMAR_3037	-		intermediary metabolism and respiration	cobalamin biosynthesis protein CobN
3677303	syn	GA	MMAR_3037	-		intermediary metabolism and respiration	cobalamin biosynthesis protein CobN
3677345	non	TC	MMAR_3037	-		intermediary metabolism and respiration	cobalamin biosynthesis protein CobN
3677400	syn	GA	MMAR_3037	-		intermediary metabolism and respiration	cobalamin biosynthesis protein CobN
3677493	syn	CA	MMAR_3037	-		intermediary metabolism and respiration	cobalamin biosynthesis protein CobN
3678749	syn	GC	MMAR_3039	-		intermediary metabolism and respiration	conserved membrane-bound oxidoreductase
3679050	non	GA	MMAR_3039	-		intermediary metabolism and respiration	conserved membrane-bound oxidoreductase
3680754	syn	CA	MMAR_3041	-		conserved hypothetical	conserved hypothetical protein
3684256	syn	GC	MMAR_3043	-		intermediary metabolism and respiration	adenylate cyclase
3684769	syn	TC	MMAR_3043	-		intermediary metabolism and respiration	adenylate cyclase
3684775	syn	GA	MMAR_3043	-		intermediary metabolism and respiration	adenylate cyclase
3684828	non	CT	MMAR_3043	-		intermediary metabolism and respiration	adenylate cyclase
3685061	non	GT	MMAR_3043	-		intermediary metabolism and respiration	adenylate cyclase
3685144	syn	GA	MMAR_3043	-		intermediary metabolism and respiration	adenylate cyclase
3685373	syn	CT	MMAR_3043	-		intermediary metabolism and respiration	adenylate cyclase
3686058	non	GC	MMAR_3044	-		intermediary metabolism and respiration	cobalamin biosynthesis protein CobN
3690388	non	GC	MMAR_3048	-		cell wall and cell processes	conserved transmembrane transport protein MmpL5_5
3693944	int	CT		41	MMAR_3050	cell wall and cell processes	class a beta-lactamase BlaC
3694213	syn	CT	MMAR_3050	-		cell wall and cell processes	class a beta-lactamase BlaC
3694614	non	GA	MMAR_3050	-		cell wall and cell processes	class a beta-lactamase BlaC
3694812	non	TA	MMAR_3050	-		cell wall and cell processes	class a beta-lactamase BlaC
3696662	syn	GC	MMAR_3053	-		intermediary metabolism and respiration	precorrin-4 C11-methyltransferase CobM
3697147	syn	GC	MMAR_3054	-		intermediary metabolism and respiration	precorrin-6y methyltransferase CobL
3698224	non	CT	MMAR_3054	-		intermediary metabolism and respiration	precorrin-6y methyltransferase CobL
3698316	syn	TC	MMAR_3055	-		intermediary metabolism and respiration	short chain dehydrogenase
3698322	syn	CT	MMAR_3055	-		intermediary metabolism and respiration	short chain dehydrogenase
3698361	syn	CT	MMAR_3055	-		intermediary metabolism and respiration	short chain dehydrogenase
3698664	syn	AG	MMAR_3055	-		intermediary metabolism and respiration	short chain dehydrogenase
3698712	syn	CG	MMAR_3055	-		intermediary metabolism and respiration	short chain dehydrogenase
3698718	syn	AG	MMAR_3055	-		intermediary metabolism and respiration	short chain dehydrogenase
3698721	syn	AG	MMAR_3055	-		intermediary metabolism and respiration	short chain dehydrogenase
3698727	syn	AG	MMAR_3055	-		intermediary metabolism and respiration	short chain dehydrogenase
3699229	syn	TC	MMAR_3056	-		conserved hypothetical	conserved protein
3699940	int	GA		126	MMAR_3057	PE/PE	N-term PPE family protein pseudogene
3710545	syn	GA	MMAR_3066	-		conserved hypothetical	conserved hypothetical protein
3710617	syn	GT	MMAR_3066	-		conserved hypothetical	conserved hypothetical protein
3710737	syn	AG	MMAR_3066	-		conserved hypothetical	conserved hypothetical protein
3711522	syn	TC	MMAR_3067	-		conserved hypothetical	conserved hypothetical protein
3712056	syn	CT	MMAR_3067	-		conserved hypothetical	conserved hypothetical protein
3712414	syn	CT	MMAR_3068	-		conserved hypothetical	conserved protein
3712924	syn	AG	MMAR_3068	-		conserved hypothetical	conserved protein
3712942	non	GC	MMAR_3068	-		conserved hypothetical	conserved protein
3712999	syn	TC	MMAR_3068	-		conserved hypothetical	conserved protein
3713067	syn	GA	MMAR_3068	-		conserved hypothetical	conserved protein
3713284	syn	GA	MMAR_3068	-		conserved hypothetical	conserved protein
3713320	syn	GA	MMAR_3068	-		conserved hypothetical	conserved protein
3713479	syn	TC	MMAR_3068	-		conserved hypothetical	conserved protein
3714372	non	TC	MMAR_3068	-		conserved hypothetical	conserved protein
3714687	non	CG	MMAR_3068	-		conserved hypothetical	conserved protein
3716372	syn	GC	MMAR_3069	-		conserved hypothetical	conserved hypothetical protein
3716788	non	AG	MMAR_3070	-		conserved hypothetical	conserved hypothetical alanine and proline rich protein
3717025	syn	GC	MMAR_3070	-		conserved hypothetical	conserved hypothetical alanine and proline rich protein
3717271	syn	GA	MMAR_3070	-		conserved hypothetical	conserved hypothetical alanine and proline rich protein
3720818	non	TC	MMAR_3072	-		conserved hypothetical	conserved alanine and proline rich protein
3723110	non	AG	MMAR_3074	-		conserved hypothetical	conserved hypothetical protein
3723220	syn	TC	MMAR_3074	-		conserved hypothetical	conserved hypothetical protein
3723451	syn	GT	MMAR_3074	-		conserved hypothetical	conserved hypothetical protein
3723535	syn	GA	MMAR_3074	-		conserved hypothetical	conserved hypothetical protein
3723535	syn	CG	MMAR_3074	-		conserved hypothetical	conserved hypothetical protein
3726333	syn	CT	MMAR_3076	-		information pathways	5'-3' exonuclease
3726453	syn	GC	MMAR_3076	-		information pathways	5'-3' exonuclease
3729444	syn	CA	MMAR_3078	-		information pathways	ATP-dependent DNA helicase HelY
3729482	syn	GC	MMAR_3078	-		information pathways	ATP-dependent DNA helicase HelY
3729718	non	TC	MMAR_3078	-		information pathways	ATP-dependent DNA helicase HelY
3729745	syn	GA	MMAR_3078	-		information pathways	ATP-dependent DNA helicase HelY
3730763	syn	GA	MMAR_3079	-		cell wall and cell processes	sec-independent protein translocase transmembrane protein TatC
3733074	non	CT	MMAR_3082	-		conserved hypothetical	conserved protein
3733146	syn	GC	MMAR_3082	-		conserved hypothetical	conserved protein
3734705	syn	CT	MMAR_3083	-		conserved hypothetical	conserved hypothetical protein

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
3735288	non	TA	MMAR_3084	-		intermediary metabolism and respiration	proteasome (alpha subunit) PrcA
3735489	non	CT	MMAR_3084	-		intermediary metabolism and respiration	proteasome (alpha subunit) PrcA
3738844	int	CT		74	MMAR_3087	conserved hypothetical	conserved protein
3741833	non	CG	MMAR_3090	-		conserved hypothetical	conserved hypothetical protein
3742128	syn	GC	MMAR_3090	-		conserved hypothetical	conserved hypothetical protein
3742149	syn	GT	MMAR_3090	-		conserved hypothetical	conserved hypothetical protein
3742858	syn	GA	MMAR_3091	-		intermediary metabolism and respiration	ATPase
3744553	syn	TC	MMAR_3092	-		cell wall and cell processes	conserved lipoprotein LppK
3744612	syn	TG	MMAR_3092	-		cell wall and cell processes	conserved lipoprotein LppK
3744621	syn	GT	MMAR_3092	-		cell wall and cell processes	conserved lipoprotein LppK
3745716	non	GT	MMAR_3094	-		intermediary metabolism and respiration	RNA methyltransferase
3745896	syn	GA	MMAR_3094	-		intermediary metabolism and respiration	RNA methyltransferase
3746334	syn	GA	MMAR_3095	-		information pathways	conserved hypothetical protein
3746457	syn	CA	MMAR_3095	-		information pathways	conserved hypothetical protein
3746721	syn	GA	MMAR_3095	-		information pathways	conserved hypothetical protein
3746907	syn	TC	MMAR_3095	-		information pathways	conserved hypothetical protein
3746994	syn	GA	MMAR_3095	-		information pathways	conserved hypothetical protein
3747233	syn	CA	MMAR_3096	-		conserved hypothetical	conserved hypothetical protein
3747329	syn	GC	MMAR_3096	-		conserved hypothetical	conserved hypothetical protein
3747701	syn	AC	MMAR_3096	-		conserved hypothetical	conserved hypothetical protein
3747853	non	AC	MMAR_3096	-		conserved hypothetical	conserved hypothetical protein
3748112	non	GT	MMAR_3097	-		lipid metabolism	non-ribosomal peptide synthetase
3748142	syn	GA	MMAR_3097	-		lipid metabolism	non-ribosomal peptide synthetase
3748160	syn	TC	MMAR_3097	-		lipid metabolism	non-ribosomal peptide synthetase
3748193	non	GA	MMAR_3097	-		lipid metabolism	non-ribosomal peptide synthetase
3748194	non	CA	MMAR_3097	-		lipid metabolism	non-ribosomal peptide synthetase
3785645	syn	CG	MMAR_3103	-		intermediary metabolism and respiration	ATP phosphoribosyltransferase HisG
3789143	int	AG		-			
3789261	int	GA		100	MMAR_3106	PE/PPE	PPE family protein
3789849	int	CT		-			
3790232	int	GA		-			
3790829	int	GA		29	MMAR_3106	PE/PPE	PPE family protein
3793168	syn	CG	MMAR_3108	-		cell wall and cell processes	FAD-dependent oxidoreductase
3793734	non	CT	MMAR_3109	-		intermediary metabolism and respiration	dehydrogenase
3795404	syn	GA	MMAR_3110	-		information pathways	cysteinyl-tRNA synthetase MshC
3795486	syn	TC	MMAR_3110	-		information pathways	cysteinyl-tRNA synthetase MshC
3795495	syn	GA	MMAR_3110	-		information pathways	cysteinyl-tRNA synthetase MshC
3796954	non	CT	MMAR_3111	-		intermediary metabolism and respiration	succinate-semialdehyde dehydrogenase [NADP+] dependent GabD1_1
3798940	non	AG	MMAR_3113	-		conserved hypothetical	conserved hypothetical protein
3799254	syn	AG	MMAR_3114	-		conserved hypothetical	conserved protein
3800220	non	CT	MMAR_3115	-		conserved hypothetical	conserved hypothetical protein
3800679	syn	CT	MMAR_3116	-		cell wall and cell processes	conserved transmembrane protein
3802031	syn	GT	MMAR_3118	-		cell wall and cell processes	conserved lipoprotein LppL
3802559	syn	GT	MMAR_3118	-		cell wall and cell processes	conserved lipoprotein LppL
3803311	non	GT	MMAR_3120	-		intermediary metabolism and respiration	dihydrodorotate dehydrogenase PyrD
3804395	int	GA		8	MMAR_3120	intermediary metabolism and respiration	dihydrodorotate dehydrogenase PyrD
3885463	int	GT		70	MMAR_3185	cell wall and cell processes	conserved secreted antigen Wag31
3886541	syn	GA	MMAR_3187	-		conserved hypothetical	conserved hypothetical protein
3886611	non	TC	MMAR_3187	-		conserved hypothetical	conserved hypothetical protein
3894282	syn	CT	MMAR_3194	-		cell wall and cell processes	FtsW-like protein FtsW
3894949	non	GT	MMAR_3194	-		cell wall and cell processes	FtsW-like protein FtsW
3896020	non	TC	MMAR_3195	-		cell wall and cell processes	UDP-N-acetylglucosaminyldalanine-D-glutamate ligase MurD
3896357	non	CG	MMAR_3195	-		cell wall and cell processes	UDP-N-acetylglucosaminyldalanine-D-glutamate ligase MurD
3897336	non	AT	MMAR_3196	-		cell wall and cell processes	phospho-N-acetylglucosaminyldalanyl-D-glutamyl-2'-6'-diaminopimelate-D-alanyl-D-alanyl ligase MurX
3897795	syn	TC	MMAR_3197	-		cell wall and cell processes	UDP-N-acetylglucosaminyldalanyl-D-glutamyl-2'-6'-diaminopimelate-D-alanyl-D-alanyl ligase MurF
3898542	syn	AT	MMAR_3197	-		cell wall and cell processes	UDP-N-acetylglucosaminyldalanyl-D-glutamate-2'-6'-diaminopimelate ligase MurF
3900880	int	AC		102	MMAR_3198	cell wall and cell processes	UDP-N-acetylglucosaminyldalanyl-D-glutamate-2'-6'-diaminopimelate ligase MurE
3902693	int	CA		-			
3905036	syn	GA	MMAR_3200	-		cell wall and cell processes	penicillin-binding membrane protein PbpB
3909395	syn	CT	MMAR_3205	-		conserved hypothetical	conserved hypothetical protein
3913040	syn	CA	MMAR_3209	-		cell wall and cell processes	conserved hypothetical membrane protein
3913844	syn	GA	MMAR_3209	-		cell wall and cell processes	conserved hypothetical membrane protein
3914510	syn	CG	MMAR_3209	-		cell wall and cell processes	conserved hypothetical membrane protein
3916877	syn	GT	MMAR_3212	-		lipid metabolism	polypropenyl synthetase IdsB_2
3916882	non	CA	MMAR_3212	-		lipid metabolism	polypropenyl synthetase IdsB_2
3918059	non	CG	MMAR_3213	-		lipid metabolism	hydroxymethylglutaryl-coenzyme a synthase PksG
3918396	syn	GA	MMAR_3213	-		lipid metabolism	hydroxymethylglutaryl-coenzyme a synthase PksG
3918771	int	CT		43	MMAR_3213	lipid metabolism	hydroxymethylglutaryl-coenzyme a synthase PksG
3919365	syn	GC	MMAR_3214	-		lipid metabolism	hydroxymethylglutaryl-coenzyme a (HMG-CoA) reductase
3919398	syn	GA	MMAR_3214	-		lipid metabolism	hydroxymethylglutaryl-coenzyme a (HMG-CoA) reductase
3920603	non	AG	MMAR_3215	-		lipid metabolism	phosphomevalonate kinase
3920771	syn	TC	MMAR_3215	-		lipid metabolism	phosphomevalonate kinase
3920926	syn	GA	MMAR_3215	-		lipid metabolism	phosphomevalonate kinase
3921046	syn	CT	MMAR_3216	-		lipid metabolism	diphosphomevalonate decarboxylase
3921058	syn	GA	MMAR_3216	-		lipid metabolism	diphosphomevalonate decarboxylase
3921559	syn	CT	MMAR_3216	-		lipid metabolism	diphosphomevalonate decarboxylase
3922393	non	CG	MMAR_3218	-		intermediary metabolism and respiration	isopentenyl-diphosphate delta-isomerase Idi.
3923405	syn	AG	MMAR_3218	-		intermediary metabolism and respiration	isopentenyl-diphosphate delta-isomerase Idi.
3925076	int	CG		-			
3925753	syn	CT	MMAR_3220	-		lipid metabolism	terpene cyclase
3926210	syn	CT	MMAR_3220	-		lipid metabolism	terpene cyclase
3926347	syn	GA	MMAR_3220	-		lipid metabolism	terpene cyclase
3926530	int	AT		-			
3926756	non	GC	MMAR_3221	-		lipid metabolism	3-oxoacyl-[acyl-carrier-protein] synthase III FabH_1
3930344	syn	GA	MMAR_3224	-		conserved hypothetical	conserved hypothetical membrane protein
3931738	syn	GA	MMAR_3225	-		cell wall and cell processes	conserved hypothetical integral membrane protein
3931804	syn	CT	MMAR_3225	-		cell wall and cell processes	conserved hypothetical integral membrane protein
3932637	int	CT		44	MMAR_3228	conserved hypothetical	conserved hypothetical protein
3949048	non	GT	MMAR_3234	-		cell wall and cell processes	conserved hypothetical secreted protein
3947628	syn	GT	MMAR_3240	-		intermediary metabolism and respiration	ubiquinol-cytochrome C reductase QcrB
3952034	syn	AG	MMAR_3244	-		intermediary metabolism and respiration	transmembrane cytochrome C oxidase (subunit II) CtaC
3952607	syn	GA	MMAR_3244	-		intermediary metabolism and respiration	transmembrane cytochrome C oxidase (subunit II) CtaC
3953955	non	AG	MMAR_3245	-		intermediary metabolism and respiration	asparagine synthetase AsnB
3954637	syn	GA	MMAR_3245	-		intermediary metabolism and respiration	asparagine synthetase AsnB
3956672	non	CT	MMAR_3247	-		conserved hypothetical	conserved protein

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
3956759	non	GA	MMAR_3247	-		conserved hypotheticals	conserved protein
3956965	non	GA	MMAR_3247	-		conserved hypotheticals	conserved protein
3957369	non	GA	MMAR_3248	-		conserved hypotheticals	conserved protein
3962722	non	GT	MMAR_3254	-		cell wall and cell processes	conserved hypothetical integral membrane protein
3968608	syn	CT	MMAR_3258	-		intermediary metabolism and respiration	leucyl aminopeptidase PepB
3969444	non	CG	MMAR_3259	-			short-chain dehydrogenase EphD
3970336	syn	GA	MMAR_3259	-			short-chain dehydrogenase EphD
4040898	syn	GA	MMAR_3275	-		conserved hypotheticals	conserved hypothetical protein
4041875	syn	CT	MMAR_3277	-		conserved hypotheticals	conserved hypothetical protein
4041887	syn	GC	MMAR_3277	-		conserved hypotheticals	conserved hypothetical protein
4042034	int	TC		51	MMAR_3277	conserved hypotheticals	conserved hypothetical protein
4042041	int	GC		58	MMAR_3277	conserved hypotheticals	conserved hypothetical protein
4042044	int	AG		61	MMAR_3277	conserved hypotheticals	conserved hypothetical protein
4042237	int	CT		-			
4042256	int	TA		-			
4049073	non	CA	MMAR_3283	-		cell wall and cell processes	drugs-transport transmembrane ATP-binding protein ABC transporter
4050438	non	TG	MMAR_3284	-		cell wall and cell processes	drugs-transport transmembrane ATP-binding protein ABC transporter
4051732	non	GA	MMAR_3285	-		intermediary metabolism and respiration	lipoate biosynthesis protein B LipB
4054570	non	AC	MMAR_3289	-		intermediary metabolism and respiration	glutamine synthetase GlnA1
4055095	syn	CG	MMAR_3289	-		intermediary metabolism and respiration	glutamine synthetase GlnA1
4055170	syn	CT	MMAR_3289	-		intermediary metabolism and respiration	glutamine synthetase GlnA1
4058751	syn	CT	MMAR_3291	-		intermediary metabolism and respiration	conserved hypothetical protein
4060152	syn	GA	MMAR_3293	-		intermediary metabolism and respiration	glutamate-ammonia-lyase adenylyltransferase GlnE
4060875	syn	CG	MMAR_3293	-		intermediary metabolism and respiration	glutamate-ammonia-lyase adenylyltransferase GlnE
4061643	syn	CG	MMAR_3293	-		intermediary metabolism and respiration	glutamate-ammonia-lyase adenylyltransferase GlnE
4061916	syn	CT	MMAR_3293	-		intermediary metabolism and respiration	glutamate-ammonia-lyase adenylyltransferase GlnE
4062873	syn	GA	MMAR_3293	-		intermediary metabolism and respiration	glutamate-ammonia-lyase adenylyltransferase GlnE
4063255	syn	CT	MMAR_3294	-		intermediary metabolism and respiration	glutamine synthetase GlnA2
4065514	non	GA	MMAR_3295	-		cell wall and cell processes	exported protease
4065780	syn	CT	MMAR_3295	-		cell wall and cell processes	exported protease
4068239	syn	GA	MMAR_3297	-		cell wall and cell processes	exported protease
4068947	syn	GA	MMAR_3297	-		cell wall and cell processes	exported protease
4071154	non	AT	MMAR_3299	-		intermediary metabolism and respiration	3-methyl-2-oxobutanate hydroxymethyltransferase PanB
4073020	syn	GA	MMAR_3301	-		conserved hypotheticals	conserved protein
4073271	non	CG	MMAR_3301	-		conserved hypotheticals	conserved protein
4074082	syn	CT	MMAR_3301	-		conserved hypotheticals	conserved protein
4075594	int	TC		56	MMAR_3303 PE/PE	PE/PGRS family protein	PE-PGRS family protein
4078237	int	CG		98	MMAR_3303 PE/PE	PE-PGRS family protein	PE-PGRS family protein
4079012	int	GC		83	MMAR_3304	conserved hypotheticals	conserved hypothetical protein
4081072	syn	CT	MMAR_3306	-		conserved hypotheticals	conserved hypothetical protein
4081788	non	CT	MMAR_3306	-		conserved hypotheticals	conserved hypothetical protein
4083424	int	GA		15	MMAR_3308	conserved hypotheticals	conserved hypothetical protein
4084414	non	CG	MMAR_3309	-		regulatory proteins	phosphotyrosine protein phosphatase PtpA
4085397	syn	AG	MMAR_3311	-		intermediary metabolism and respiration	cobalamin biosynthesis transmembrane protein CobD
4087129	syn	GA	MMAR_3312	-		conserved hypotheticals	conserved hypothetical protein
4110075	syn	GA	MMAR_3329	-		conserved hypotheticals	conserved hypothetical protein
4110199	non	AG	MMAR_3329	-		conserved hypotheticals	conserved hypothetical protein
4110813	syn	CT	MMAR_3330	-		conserved hypotheticals	conserved hypothetical protein
4111535	syn	TC	MMAR_3330	-		conserved hypotheticals	conserved hypothetical protein
4112379	syn	GA	MMAR_3331	-			peroxidoxin AhpC
4113459	syn	TG	MMAR_3333	-		cell wall and cell processes	conserved hypothetical protein
4115320	syn	TC	MMAR_3334	-		intermediary metabolism and respiration	pyruvate dehydrogenase E1 component AceE
4118179	syn	TC	MMAR_3336	-		lipid metabolism	malonyl CoA-acyl carrier protein transacylase FabD
4120086	syn	CT	MMAR_3338	-		lipid metabolism	3-oxoacyl-[acyl-carrier protein] synthase 1 KasA
4121307	syn	TC	MMAR_3339	-		lipid metabolism	3-oxoacyl-[acyl-carrier protein] synthase 2 KasB
4124734	non	GA	MMAR_3342	-		intermediary metabolism and respiration	glycerol-3-phosphate dehydrogenase GlpD1
4124815	non	TG	MMAR_3342	-		intermediary metabolism and respiration	glycerol-3-phosphate dehydrogenase GlpD1
4125909	syn	CT	MMAR_3342	-		intermediary metabolism and respiration	glycerol-3-phosphate dehydrogenase GlpD1
4128869	syn	GC	MMAR_3345	-		conserved hypotheticals	conserved hypothetical protein
4129014	non	TC	MMAR_3345	-		conserved hypotheticals	conserved hypothetical protein
4131349	syn	GA	MMAR_3348	-		conserved hypotheticals	conserved hypothetical protein
4138562	syn	GA	MMAR_3355	-		intermediary metabolism and respiration	oxidoreductase
4140731	non	GA	MMAR_3357	-		conserved hypotheticals	conserved hypothetical protein
4140818	non	AC	MMAR_3357	-		conserved hypotheticals	conserved hypothetical protein
4142668	syn	GA	MMAR_3358	-		conserved hypotheticals	conserved hypothetical proline rich protein
4142794	syn	CT	MMAR_3358	-		conserved hypotheticals	conserved hypothetical proline rich protein
4142930	int	AC		104	MMAR_3358	conserved hypotheticals	conserved hypothetical proline rich protein
4145742	syn	TC	MMAR_3361	-		intermediary metabolism and respiration	cytochrome P450 124A1 Cyp124A1
4147471	non	GA	MMAR_3363	-		conserved hypotheticals	conserved hypothetical protein
4147485	syn	GT	MMAR_3363	-		conserved hypotheticals	conserved hypothetical protein
4147600	non	GA	MMAR_3363	-		conserved hypotheticals	conserved hypothetical protein
4148001	syn	GA	MMAR_3363	-		conserved hypotheticals	conserved hypothetical protein
4149008	non	GA	MMAR_3364	-		cell wall and cell processes	conserved hypothetical membrane protein
4149045	syn	GC	MMAR_3364	-		cell wall and cell processes	conserved hypothetical membrane protein
4149380	int	TC		134	MMAR_3365	conserved hypotheticals	conserved hypothetical protein
4150038	non	GA	MMAR_3365	-		conserved hypotheticals	conserved hypothetical protein
4152051	syn	GT	MMAR_3370	-		cell wall and cell processes	conserved transport protein
4214549	syn	AC	MMAR_3415	-		cell wall and cell processes	phosphate-transport permease PitB
4214550	non	AG	MMAR_3415	-		cell wall and cell processes	phosphate-transport permease PitB
4216795	syn	GA	MMAR_3416	-		intermediary metabolism and respiration	ferredoxin-dependent nitrite/sulphite reductase NirA
4217482	non	CT	MMAR_3416	-		intermediary metabolism and respiration	ferredoxin-dependent nitrite/sulphite reductase NirA
4220054	syn	GC	MMAR_3419	-		regulatory proteins	transcription regulator (LysR family)
4230294	int	CT		-			
423268	syn	CA	MMAR_3430	-		conserved hypotheticals	conserved hypothetical protein
4237361	syn	CG	MMAR_3433	-		intermediary metabolism and respiration	oxidoreductase
4240113	non	GA	MMAR_3436	-		conserved hypotheticals	conserved hypothetical protein
4242119	int	AG		37	MMAR_3437	cell wall and cell processes	conserved integral membrane transport protein YjcE
4242130	int	TC		48	MMAR_3437	cell wall and cell processes	conserved integral membrane transport protein YjcE
4242330	syn	CT	MMAR_3438	-		regulatory proteins	transcriptional regulatory protein (probably TetR-family)
4245605	non	TC	MMAR_3441	-		conserved hypotheticals	conserved hypothetical protein
4250913	int	CT		126	MMAR_3445	lipid metabolism	CDP-diacylglycerol pyrophosphatase Cdh
4252177	syn	CT	MMAR_3448	-		conserved hypotheticals	conserved hypothetical protein
4252207	non	TC	MMAR_3448	-		conserved hypotheticals	conserved hypothetical protein
4252241	non	AG	MMAR_3448	-		conserved hypotheticals	conserved hypothetical protein
4254504	int	AT		50	MMAR_3450	cell wall and cell processes	conserved hypothetical membrane protein

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
4258910	non	CA	MMAR_3454	-		regulatory proteins	conserved hypothetical regulatory protein
4313785	syn	GA	MMAR_3506	-		cell wall and cell processes	conserved hypothetical membrane protein
4313967	syn	GT	MMAR_3507	-		regulatory proteins	transcriptional regulator (IclR family)
4314635	syn	CT	MMAR_3507	-		regulatory proteins	transcriptional regulator (IclR family)
4314895	Int	CT		138	MMAR_3508	conserved hypotheticals	conserved hypothetical secreted protein
4316023	non	CG	MMAR_3509	-		intermediary metabolism and respiration	short-chain alcohol dehydrogenase
4318162	syn	CT	MMAR_3511	-		intermediary metabolism and respiration	acyl-CoA dehydrogenase
4318808	non	AG	MMAR_3512	-		intermediary metabolism and respiration	acyl-CoA dehydrogenase
4318875	syn	CT	MMAR_3512	-		intermediary metabolism and respiration	acyl-CoA dehydrogenase
4319121	syn	GA	MMAR_3512	-		intermediary metabolism and respiration	acyl-CoA dehydrogenase
4319409	syn	CT	MMAR_3512	-		intermediary metabolism and respiration	acyl-CoA dehydrogenase
4319474	non	CG	MMAR_3513	-		intermediary metabolism and respiration	oxidoreductase
4319656	non	CT	MMAR_3513	-		intermediary metabolism and respiration	oxidoreductase
4319915	non	GA	MMAR_3513	-		intermediary metabolism and respiration	oxidoreductase
4320760	syn	GA	MMAR_3514	-		intermediary metabolism and respiration	oxidoreductase
4321212	Int	GA		138	MMAR_3514	intermediary metabolism and respiration	oxidoreductase
4325243	Int	AG		53	MMAR_3518	intermediary metabolism and respiration	rubredoxin RubB_1
4326021	syn	GA	MMAR_3519	-		regulatory proteins	transcriptional regulatory protein (probably TetR-family)
4326027	syn	CT	MMAR_3519	-		regulatory proteins	transcriptional regulatory protein (probably TetR-family)
4326560	syn	GC	MMAR_3520	-		conserved hypotheticals	conserved hypothetical protein
4327249	non	GT	MMAR_3521	-			chaperone protein HtpG
4328388	non	CA	MMAR_3521	-			chaperone protein HtpG
4328562	syn	TA	MMAR_3521	-			chaperone protein HtpG
4328631	syn	AC	MMAR_3521	-			chaperone protein HtpG
4329380	non	AC	MMAR_3522	-		regulatory proteins	transcriptional regulatory protein (LuxR-family)
4331105	non	TC	MMAR_3522	-		regulatory proteins	transcriptional regulatory protein (LuxR-family)
4331205	syn	CA	MMAR_3522	-		regulatory proteins	transcriptional regulatory protein (LuxR-family)
4331274	syn	TC	MMAR_3522	-		regulatory proteins	transcriptional regulatory protein (LuxR-family)
4331279	non	GA	MMAR_3522	-		regulatory proteins	transcriptional regulatory protein (LuxR-family)
4331341	non	AG	MMAR_3522	-		regulatory proteins	transcriptional regulatory protein (LuxR-family)
4331593	non	TC	MMAR_3522	-		regulatory proteins	transcriptional regulatory protein (LuxR-family)
4379448	syn	CT	MMAR_3560	-		regulatory proteins	transcriptional regulatory protein
4379617	Int	AC		86	MMAR_3560	regulatory proteins	transcriptional regulatory protein
4379866	non	GA	MMAR_3561	-		intermediary metabolism and respiration	oxidoreductase
4380817	non	GC	MMAR_3562	-		conserved hypotheticals	conserved hypothetical protein
4384761	syn	GA	MMAR_3566	-			membrane-associated phospholipase C 2 PicB
4385524	syn	GA	MMAR_3566	-			membrane-associated phospholipase C 2 PicB
4385858	Int	CT		-			
4401147	Int	AC		39	MMAR_3581	PE/PPE	PE-PGRS family protein
4403350	Int	CT		113	MMAR_3581	PE/PPE	PE-PGRS family protein
4403396		GT		-			
4403684	non	AG	MMAR_3582	-		unknown	hypothetical protein
4403727	non	TC	MMAR_3582	-		unknown	hypothetical protein
4403800	non	CA	MMAR_3582	-		unknown	hypothetical protein
4404212	non	GA	MMAR_3583	-		cell wall and cell processes	conserved hypothetical membrane protein
4404308	syn	TC	MMAR_3583	-		cell wall and cell processes	conserved hypothetical membrane protein
4404503	syn	GA	MMAR_3583	-		cell wall and cell processes	conserved hypothetical membrane protein
4404947	syn	G-	MMAR_3584	-		insertion seqs and phages	phage-related integrase
4404948	non	T-	MMAR_3584	-		insertion seqs and phages	phage-related integrase
4404949	non	C-	MMAR_3584	-		insertion seqs and phages	phage-related integrase
4405376	syn	GT	MMAR_3584	-		insertion seqs and phages	phage-related integrase
4405377	syn	AG	MMAR_3584	-		insertion seqs and phages	phage-related integrase
4405556	syn	CA	MMAR_3585	-		insertion seqs and phages	phage-related integrase
4433765	syn	GA	MMAR_3610	-		unknown	hypothetical protein
4434099	syn	GC	MMAR_3611	-		conserved hypotheticals	conserved hypothetical protein
4434188	non	CT	MMAR_3611	-		conserved hypotheticals	conserved hypothetical protein
4435064	syn	TC	MMAR_3612	-		cell wall and cell processes	metal cation transporter p-type ATPase a
4435872	non	GA	MMAR_3612	-		cell wall and cell processes	metal cation transporter p-type ATPase a
4436930	syn	CT	MMAR_3612	-		cell wall and cell processes	metal cation transporter p-type ATPase a
4438348	syn	GA	MMAR_3613	-		cell wall and cell processes	conserved hypothetical secreted protein
4438435	syn	GC	MMAR_3613	-		cell wall and cell processes	conserved hypothetical secreted protein
4439013	non	GA	MMAR_3614	-		conserved hypotheticals	conserved hypothetical protein
4439067	syn	GA	MMAR_3614	-		conserved hypotheticals	conserved hypothetical protein
4439305	non	AG	MMAR_3614	-		conserved hypotheticals	conserved hypothetical protein
4439554	non	GA	MMAR_3614	-		conserved hypotheticals	conserved hypothetical protein
4439863	syn	CT	MMAR_3615	-		cell wall and cell processes	conserved membrane protein
4440057	non	TC	MMAR_3615	-		cell wall and cell processes	conserved membrane protein
4440643	syn	CT	MMAR_3615	-		cell wall and cell processes	conserved membrane protein
4440748	syn	CA	MMAR_3615	-		cell wall and cell processes	conserved membrane protein
4441665	syn	AG	MMAR_3616	-		cell wall and cell processes	conserved protein
4442961	syn	AG	MMAR_3617	-		cell wall and cell processes	sugar-transport integral membrane protein ABC transporter UspA
4443447	non	CG	MMAR_3618	-		cell wall and cell processes	sugar-transport integral membrane protein ABC transporter UspB
4443508	syn	CA	MMAR_3618	-		cell wall and cell processes	sugar-transport integral membrane protein ABC transporter UspB
4444278	syn	GA	MMAR_3619	-		cell wall and cell processes	periplasmic sugar-binding lipoprotein UspC
4444587	syn	CT	MMAR_3619	-		cell wall and cell processes	periplasmic sugar-binding lipoprotein UspC
4446165	non	CG	MMAR_3620	-		conserved hypotheticals	conserved hypothetical protein
4446735	syn	CA	MMAR_3621	-		cell wall and cell processes	cationic amino acid transport integral membrane protein RocE
4447806	syn	CT	MMAR_3621	-		cell wall and cell processes	cationic amino acid transport integral membrane protein RocE
4449891	non	GC	MMAR_3623	-		conserved hypotheticals	conserved hypothetical protein
4449919	syn	TC	MMAR_3623	-		conserved hypotheticals	conserved hypothetical protein
4450018	syn	AG	MMAR_3623	-		conserved hypotheticals	conserved hypothetical protein
4457059	non	AG	MMAR_3629	-		cell wall and cell processes	conserved hypothetical membrane protein
4457076	syn	GC	MMAR_3629	-		cell wall and cell processes	conserved hypothetical membrane protein
4457592	syn	GA	MMAR_3629	-		cell wall and cell processes	conserved hypothetical membrane protein
4457613	syn	GA	MMAR_3629	-		cell wall and cell processes	conserved hypothetical membrane protein
4457694	non	TC	MMAR_3629	-		cell wall and cell processes	conserved hypothetical membrane protein
4460554	non	GA	MMAR_3631	-		lipid metabolism	acyl-CoA dehydrogenase
4460743	syn	CT	MMAR_3631	-		lipid metabolism	acyl-CoA dehydrogenase
4464478	Int	GT		59	MMAR_3638	cell wall and cell processes	lipoprotein LppP
4477807	non	GC	MMAR_3638	-		cell wall and cell processes	lipoprotein LppP
4478197	Int	GA		-			
4483290	non	GA	MMAR_3640	-		cell wall and cell processes	adenylyl cyclase
4483335	syn	TC	MMAR_3640	-		cell wall and cell processes	adenylyl cyclase
4490859	syn	CA	MMAR_3643	-		cell wall and cell processes	[NAD] dependent malate oxidoreductase Mez
4493571	syn	CT	MMAR_3647	-		cell wall and cell processes	thioredoxin ThiX

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
4495311	syn	CT	MMAR_3650	-		information pathways	DNA primase DnaG
4498764	syn	TC	MMAR_3652	-		cell wall and cell processes	conserved hypothetical secreted protein
4501353	int	GA		72	MMAR_3654	cell wall and cell processes	EsaT-6 like protein EsxP_2
4516149	syn	CT	MMAR_3667	-		information pathways	glycyl-tRNA synthetase GlyS
4516215	syn	GC	MMAR_3667	-		information pathways	glycyl-tRNA synthetase GlyS
4516683	syn	GA	MMAR_3667	-		information pathways	glycyl-tRNA synthetase GlyS
4517420	int	A-		146	MMAR_3668	regulatory proteins	transcriptional regulatory protein (probably ArsR-family)
4517513	int	AG		141	MMAR_3667	information pathways	glycyl-tRNA synthetase GlyS
4518062	syn	AG	MMAR_3669	-		regulatory proteins	Zinc uptake regulation protein Zur
4518587	syn	AG	MMAR_3670	-		conserved hypotheticals	conserved hypothetical protein
4518613	non	CT	MMAR_3670	-		conserved hypotheticals	conserved hypothetical protein
4518646	syn	GA	MMAR_3670	-		conserved hypotheticals	conserved hypothetical protein
4518788	syn	TC	MMAR_3670	-		conserved hypotheticals	conserved hypothetical protein
4518853	syn	GC	MMAR_3671	-		cell wall and cell processes	undecaprenyl diphosphate synthase
4519084	syn	GA	MMAR_3671	-		cell wall and cell processes	undecaprenyl diphosphate synthase
4520267	syn	GT	MMAR_3672	-		information pathways	recombination protein O RecO
4521429	non	GT	MMAR_3673	-		intermediary metabolism and respiration	amidas AmiA2
4521570	non	GA	MMAR_3673	-		intermediary metabolism and respiration	amidas AmiA2
4523305	syn	CA	MMAR_3676	-		cell wall and cell processes	conserved hypothetical membrane protein
4530518	syn	GC	MMAR_3684	-		regulatory proteins	heat shock protein transcriptional repressor HrcA
4532473	syn	GC	MMAR_3686	-		conserved hypotheticals	conserved hypothetical protein
4533393	syn	AG	MMAR_3687	-		information pathways	alternative RNA polymerase sigma factor SigJ-like
4534231	int	GT		66	MMAR_3688	cell wall and cell processes	low molecular weight antigen Cfp2
4535878	non	AG	MMAR_3689	-		intermediary metabolism and respiration	phenyloxazoline synthase MbtB
4539120	non	GC	MMAR_3690	-		intermediary metabolism and respiration	non-ribosomal peptide synthetase MbtF
4539357	non	CA	MMAR_3690	-		intermediary metabolism and respiration	non-ribosomal peptide synthetase MbtF
4539473	syn	GA	MMAR_3690	-		intermediary metabolism and respiration	non-ribosomal peptide synthetase MbtF
4540478	non	TA	MMAR_3690	-		intermediary metabolism and respiration	non-ribosomal peptide synthetase MbtF
4541119	non	CT	MMAR_3690	-		intermediary metabolism and respiration	non-ribosomal peptide synthetase MbtF
4544082	syn	GA	MMAR_3691	-		intermediary metabolism and respiration	non-ribosomal peptide synthetase MbtE
4544244	non	GA	MMAR_3691	-		intermediary metabolism and respiration	non-ribosomal peptide synthetase MbtE
4546717	non	GT	MMAR_3691	-		intermediary metabolism and respiration	non-ribosomal peptide synthetase MbtE
4547676	int	CT		122	MMAR_3692	conserved hypotheticals	conserved hypothetical protein
4550814	syn	AG	MMAR_3695	-		lipid metabolism	polyketide synthase MbtD
4554026	non	AT	MMAR_3697	-		intermediary metabolism and respiration	lysine-N-oxygenase MbtG
4556268	syn	CT	MMAR_3698	-		cell wall and cell processes	bifunctional enzyme MbtA: salicyl-AMP ligase (SAL-AMP ligase) + salicyl-S-ACP synthetase
4556895	syn	TG	MMAR_3698	-		cell wall and cell processes	bifunctional enzyme MbtA: salicyl-AMP ligase (SAL-AMP ligase) + salicyl-S-ACP synthetase
4558006	syn	CT	MMAR_3699	-		intermediary metabolism and respiration	acetyl hydrolase MbtJ
4558202	syn	CA	MMAR_3700	-		cell wall and cell processes	short-chain membrane-associated dehydrogenase
4561846	syn	CT	MMAR_3703	-		regulatory proteins	conserved hypothetical transcriptional regulator
4561934	non	AG	MMAR_3703	-		regulatory proteins	conserved hypothetical transcriptional regulator
4562039	non	AG	MMAR_3703	-		regulatory proteins	conserved hypothetical transcriptional regulator
4564191	syn	CT	MMAR_3705	-		conserved hypotheticals	conserved hypothetical protein
4564479	int	AG		50	MMAR_3706	intermediary metabolism and respiration	Isochorismate synthase MbtI
4568661	syn	AG	MMAR_3709	-		intermediary metabolism and respiration	oxygen-independent coproporphyrinogen III oxidase HemN
4571672	non	AC	MMAR_3711	-		intermediary metabolism and respiration	3'-phosphadenosine 5'-phosphosulfate reductase CysH
4572282	syn	GA	MMAR_3712	-		cell wall and cell processes	conserved hypothetical protein
4573418	syn	CT	MMAR_3713	-		intermediary metabolism and respiration	gamma-glutamyltranspeptidase precursor GgtB
4573853	syn	CT	MMAR_3713	-		intermediary metabolism and respiration	gamma-glutamyltranspeptidase precursor GgtB
4574630	syn	GA	MMAR_3713	-		intermediary metabolism and respiration	gamma-glutamyltranspeptidase precursor GgtB
4575742	non	GC	MMAR_3714	-		cell wall and cell processes	conserved hypothetical membrane protein
4576188	non	GA	MMAR_3714	-		cell wall and cell processes	conserved hypothetical membrane protein
4576625	non	CG	MMAR_3714	-		cell wall and cell processes	conserved hypothetical membrane protein
4578016	syn	CA	MMAR_3716	-		cell wall and cell processes	sulfate-transport integral membrane protein ABC transporter CysW
4578053	non	TC	MMAR_3716	-		cell wall and cell processes	sulfate-transport integral membrane protein ABC transporter CysW
4579428	syn	TC	MMAR_3717	-		cell wall and cell processes	sulfate-transport integral membrane protein ABC transporter CysT
4581428	syn	GC	MMAR_3720	-		intermediary metabolism and respiration	FAD-dependent oxidoreductase
4581754	non	GC	MMAR_3720	-		intermediary metabolism and respiration	FAD-dependent oxidoreductase
4583517	syn	CT	MMAR_3721	-		intermediary metabolism and respiration	conserved hypothetical glycosyl hydrolase
4583682	syn	CG	MMAR_3721	-		intermediary metabolism and respiration	conserved hypothetical glycosyl hydrolase
4584066	syn	TG	MMAR_3721	-		intermediary metabolism and respiration	conserved hypothetical glycosyl hydrolase
4584870	syn	CA	MMAR_3722	-		cell wall and cell processes	conserved hypothetical lipoprotein LppR
4585267	non	TC	MMAR_3722	-		cell wall and cell processes	conserved hypothetical lipoprotein LppR
4585275	syn	AG	MMAR_3722	-		cell wall and cell processes	conserved hypothetical lipoprotein LppR
4585299	syn	GT	MMAR_3722	-		cell wall and cell processes	conserved hypothetical lipoprotein LppR
4590674	int	TC		-			
4596423	syn	CG	MMAR_3732	-		conserved hypotheticals	conserved hypothetical protein
4597565	int	AG		45	MMAR_3733	information pathways	30S ribosomal protein S20 RpsT
4600998	non	CG	MMAR_3736	-		cell wall and cell processes	conserved hypothetical membrane protein ComEA
4601691	syn	GA	MMAR_3737	-		lipid metabolism	acyl-CoA dehydrogenase Fad17_1
4606012	non	TC	MMAR_3740	-			enhanced intracellular survival protein Eis
4606268	syn	GA	MMAR_3740	-			enhanced intracellular survival protein Eis
4607329	syn	CA	MMAR_3741	-		conserved hypotheticals	conserved hypothetical protein
4608861	syn	CT	MMAR_3743	-		cell wall and cell processes	conserved membrane protein MmpSS_1
4608900	non	TC	MMAR_3743	-		cell wall and cell processes	conserved membrane protein MmpSS_1
4617496	non	GA	MMAR_3751	-		conserved hypotheticals	conserved hypothetical protein
4620656	non	TG	MMAR_3754	-		cell wall and cell processes	conserved hypothetical membrane protein
4620932	non	GA	MMAR_3754	-		cell wall and cell processes	conserved hypothetical membrane protein
4621552	non	TG	MMAR_3754	-		cell wall and cell processes	conserved hypothetical membrane protein
4621712	syn	GA	MMAR_3754	-		cell wall and cell processes	conserved hypothetical membrane protein
4624045	int	AG		124	MMAR_3755	intermediary metabolism and respiration	adenylate or guanylate cyclase
4625519	syn	CG	MMAR_3757	-		intermediary metabolism and respiration	adenylate or guanylate cyclase
4625521	syn	GA	MMAR_3757	-		intermediary metabolism and respiration	adenylate or guanylate cyclase
4626519	syn	TC	MMAR_3757	-		intermediary metabolism and respiration	adenylate or guanylate cyclase
4626783	non	-CA	MMAR_3757	-		intermediary metabolism and respiration	adenylate or guanylate cyclase
4634346	int	GA		55	MMAR_3760	regulatory proteins	Sir2-like regulatory protein
4634350	int	AG		59	MMAR_3760	regulatory proteins	Sir2-like regulatory protein
4634351	int	GC		60	MMAR_3760	regulatory proteins	Sir2-like regulatory protein
4634455	non	GA	MMAR_3761	-		intermediary metabolism and respiration	cytochrome P450 268A2 Cyp268A2
4634699	non	GA	MMAR_3761	-		intermediary metabolism and respiration	cytochrome P450 268A2 Cyp268A2
4635468	non	TC	MMAR_3761	-		intermediary metabolism and respiration	cytochrome P450 268A2 Cyp268A2
4635548	syn	TC	MMAR_3761	-		intermediary metabolism and respiration	cytochrome P450 268A2 Cyp268A2
4635559	non	AC	MMAR_3761	-		intermediary metabolism and respiration	cytochrome P450 268A2 Cyp268A2
4635718	int	TG		81	MMAR_3761	intermediary metabolism and respiration	cytochrome P450 268A2 Cyp268A2
4635719	int	CA		82	MMAR_3761	intermediary metabolism and respiration	cytochrome P450 268A2 Cyp268A2

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
4635898	syn	CT	MMAR_3762	-		regulatory proteins	transcriptional regulatory protein (AcrR family)
4636069	non	CT	MMAR_3762	-		regulatory proteins	transcriptional regulatory protein (AcrR family)
4636158	syn	GA	MMAR_3762	-		regulatory proteins	transcriptional regulatory protein (AcrR family)
4636353	syn	TC	MMAR_3762	-		regulatory proteins	transcriptional regulatory protein (AcrR family)
4636458	Int	CA		54	MMAR_3762	regulatory proteins	transcriptional regulatory protein (AcrR family)
4641725	Int	GA		-			
4642922	syn	GA	MMAR_3764	-		intermediary metabolism and respiration	glutamate 5-kinase protein ProB
4642976	syn	CT	MMAR_3764	-		intermediary metabolism and respiration	glutamate 5-kinase protein ProB
4644094	non	CT	MMAR_3765	-		intermediary metabolism and respiration	GTP1/OBG-family GTP-binding protein Obg
4644562	syn	GT	MMAR_3765	-		intermediary metabolism and respiration	GTP1/OBG-family GTP-binding protein Obg
4648584	syn	GA	MMAR_3768	-		intermediary metabolism and respiration	ribonuclease E Rne
4653855	syn	CT	MMAR_3772	-		information pathways	valyl-tRNA synthetase protein ValS
4655432	non	AG	MMAR_3774	-		cell wall and cell processes	conserved hypothetical membrane protein
4655436	non	TC	MMAR_3774	-		cell wall and cell processes	conserved hypothetical membrane protein
4656735	syn	CT	MMAR_3775	-		cell wall and cell processes	conserved membrane protein
4656888	syn	TC	MMAR_3775	-		cell wall and cell processes	conserved membrane protein
4720958	syn	GA	MMAR_3801	-		intermediary metabolism and respiration	molybdopterin-quanine dinucleotide biosynthesis protein a Mba
4721508	Int	CT		1	MMAR_3802	intermediary metabolism and respiration	pyruvate:ferredoxin oxidoreductase PorB beta subunit
4721508	Int	CT		1	MMAR_3801	intermediary metabolism and respiration	molybdopterin-quanine dinucleotide biosynthesis protein a Mba
4722154	syn	GA	MMAR_3802	-		intermediary metabolism and respiration	pyruvate:ferredoxin oxidoreductase PorB beta subunit
4722181	syn	GA	MMAR_3802	-		intermediary metabolism and respiration	pyruvate:ferredoxin oxidoreductase PorB beta subunit
4723501	syn	TC	MMAR_3803	-		intermediary metabolism and respiration	pyruvate:ferredoxin oxidoreductase PorA alpha subunit
4723654	syn	GA	MMAR_3803	-		intermediary metabolism and respiration	pyruvate:ferredoxin oxidoreductase PorA alpha subunit
4724804	Int	TG		139	MMAR_3804	cell wall and cell processes	conserved integral membrane transport protein
4726014	syn	GA	MMAR_3804	-		cell wall and cell processes	conserved integral membrane transport protein
4726941	syn	GA	MMAR_3805	-			ATP-dependent CLP protease ATP-binding subunit ClpX
4730637	syn	TC	MMAR_3808	-		intermediary metabolism and respiration	ATP-dependent CLP protease proteolytic subunit 1 ClpP1
4733150	non	GA	MMAR_3810	-		lipid metabolism	esterase/lipase LipP
4740407	Int	TG		23	MMAR_3817	intermediary metabolism and respiration	aminopeptidase N PepN
4740901	non	GA	MMAR_3817	-		intermediary metabolism and respiration	aminopeptidase N PepN
4741000	non	GA	MMAR_3817	-		intermediary metabolism and respiration	aminopeptidase N PepN
4741923	syn	TG	MMAR_3817	-		intermediary metabolism and respiration	aminopeptidase N PepN
4742908	non	TG	MMAR_3817	-		intermediary metabolism and respiration	aminopeptidase N PepN
4744201	non	GT	MMAR_3820	-		conserved hypotheticals	conserved hypothetical protein
4744202	non	CT	MMAR_3820	-		conserved hypotheticals	conserved hypothetical protein
4744228	syn	CT	MMAR_3820	-		conserved hypotheticals	conserved hypothetical protein
4746335	syn	CT	MMAR_3822	-		intermediary metabolism and respiration	alpha-glucosidase AgIa
4747054	non	AG	MMAR_3823	-			membrane-associated phospholipase C 2 PlcB_1
4748580	non	CT	MMAR_3824	-		lipid metabolism	cholesterol oxidase precursor ChoD_1
4749800	syn	GA	MMAR_3824	-		lipid metabolism	cholesterol oxidase precursor ChoD_1
4749878	syn	AG	MMAR_3824	-		lipid metabolism	cholesterol oxidase precursor ChoD_1
4751324	non	GC	MMAR_3825	-		cell wall and cell processes	drug-transport integral membrane protein
4752132	syn	CT	MMAR_3826	-		intermediary metabolism and respiration	molybdopterin biosynthesis protein MoeY_1
4752631	non	TA	MMAR_3826	-		intermediary metabolism and respiration	molybdopterin biosynthesis protein MoeY_1
4753038	syn	CT	MMAR_3826	-		intermediary metabolism and respiration	molybdopterin biosynthesis protein MoeY_1
4755104	non	AG	MMAR_3827	-		conserved hypotheticals	conserved protein
4756624	non	TC	MMAR_3829	-		intermediary metabolism and respiration	NAD-dependent glutamate dehydrogenase Gdh
4757048	syn	GA	MMAR_3829	-		intermediary metabolism and respiration	NAD-dependent glutamate dehydrogenase Gdh
4758218	syn	GA	MMAR_3829	-		intermediary metabolism and respiration	NAD-dependent glutamate dehydrogenase Gdh
4759652	syn	GA	MMAR_3829	-		intermediary metabolism and respiration	NAD-dependent glutamate dehydrogenase Gdh
4760135	non	GC	MMAR_3829	-		intermediary metabolism and respiration	NAD-dependent glutamate dehydrogenase Gdh
4760646	syn	GA	MMAR_3830	-		cell wall and cell processes	ATP-binding component of an ABC transporter
4762375	syn	CT	MMAR_3831	-		information pathways	single-stranded DNA-binding protein
4762786	Int	TG		7	MMAR_3831	information pathways	single-stranded DNA-binding protein
4763088	Int	AC		-			
4763604	non	CG	MMAR_3832	-		lipid metabolism	membrane-bound C-5 sterol desaturase Erg3_2
4764146	non	TC	MMAR_3832	-		lipid metabolism	membrane-bound C-5 sterol desaturase Erg3_2
4764198	syn	CG	MMAR_3832	-		lipid metabolism	membrane-bound C-5 sterol desaturase Erg3_2
4764243	syn	AT	MMAR_3832	-		lipid metabolism	membrane-bound C-5 sterol desaturase Erg3_2
4764369	Int	AG		48	MMAR_3832	lipid metabolism	membrane-bound C-5 sterol desaturase Erg3_2
4765948	syn	CA	MMAR_3833	-		lipid metabolism	glycerol-3-phosphate acyltransferase PlsB2
4767819	syn	GC	MMAR_3834	-		lipid metabolism	bifunctional transmembrane phospholipid biosynthesis enzyme PlsC
4767978	syn	GC	MMAR_3834	-		lipid metabolism	bifunctional transmembrane phospholipid biosynthesis enzyme PlsC
4770302	Int	CT		145	MMAR_3835	cell wall and cell processes	conserved hypothetical membrane protein
4771605	syn	AT	MMAR_3836	-		lipid metabolism	carboxylesterase LipQ
4772401	non	GC	MMAR_3837	-		cell wall and cell processes	cutinase precursor
4773170	non	CT	MMAR_5558	-		unknown	hypothetical protein
4773207	non	GA	MMAR_5558	-		unknown	hypothetical protein
4774228	non	TC	MMAR_3838	-		intermediary metabolism and respiration	cobyrinic acid synthase CobQ1
4774865	syn	CG	MMAR_3838	-		intermediary metabolism and respiration	cobyrinic acid synthase CobQ1
4775267	Int	CA		-			
4778878	non	GA	MMAR_3842	-		intermediary metabolism and respiration	dihydrolipoamide S-acetyltransferase E2 component PdhC
4780727	syn	GA	MMAR_3844	-		intermediary metabolism and respiration	pyruvate dehydrogenase E1 component (alpha subunit) PdhA
4781502	Int	AG		123	MMAR_3845	intermediary metabolism and respiration	citrate (pro-3s)-lyase (beta subunit) CitE
4782467	syn	TC	MMAR_3846	-		intermediary metabolism and respiration	conserved protein
4783618	syn	CT	MMAR_3847	-		lipid metabolism	acyl-CoA dehydrogenase FadE19
4784546	non	GA	MMAR_3848	-		lipid metabolism	acyl-/propionyl-coenzyme a carboxylase alpha chain AccA1
4784953	syn	GT	MMAR_3848	-		lipid metabolism	acyl-/propionyl-coenzyme a carboxylase alpha chain AccA1
4786068	syn	GA	MMAR_3848	-		lipid metabolism	acyl-/propionyl-coenzyme a carboxylase alpha chain AccA1
4786167	non	GC	MMAR_3849	-		lipid metabolism	acyl-/propionyl-CoA carboxylase (beta subunit) AccD1
4790143	non	GT	MMAR_3852	-		lipid metabolism	fatty-acid-CoA ligase FadD35
4790253	syn	AG	MMAR_3852	-		lipid metabolism	fatty-acid-CoA ligase FadD35
4793193	syn	GA	MMAR_3855	-		cell wall and cell processes	conserved integral membrane leucine and alanine rich protein
4794193	syn	TC	MMAR_3856	-		intermediary metabolism and respiration	short-chain-type dehydrogenase/reductase
4794940	syn	GA	MMAR_3856	-		intermediary metabolism and respiration	short-chain-type dehydrogenase/reductase
4797149	syn	GA	MMAR_3858	-		conserved hypotheticals	conserved hypothetical protein
4797424	syn	TA	MMAR_3858	-		conserved hypotheticals	conserved hypothetical protein
4798144	non	AG	MMAR_3860	-		cell wall and cell processes	conserved hypothetical membrane protein
4798775	non	GC	MMAR_3860	-		cell wall and cell processes	conserved hypothetical membrane protein
4799999	non	GA	MMAR_3860	-		cell wall and cell processes	conserved hypothetical membrane protein
4801685	non	TG	MMAR_3863	-		cell wall and cell processes	conserved hypothetical integral ABC-type transport protein
4802492	syn	TC	MMAR_3864	-			Mce protein Mce5A
4804719	syn	CA	MMAR_3866	-			Mce family protein Mce5C
4806209	non	GA	MMAR_3867	-			Mce family protein Mce5D
4806532	syn	CT	MMAR_3867	-			Mce family protein Mce5D

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
4806898	non	AG	MMAR_3868	-		Mce family protein Mce5E	
4807789	non	GC	MMAR_3868	-		Mce family protein Mce5E	
4807825	syn	TC	MMAR_3868	-		Mce family protein Mce5E	
4807962	syn	CA	MMAR_3868	-		Mce family protein Mce5E	
4808766	non	GA	MMAR_3869	-		Mce family protein Mce5F	
4811282	non	CA	MMAR_3872	-	cell wall and cell processes	conserved lipoprotein LppS	
4811380	syn	GA	MMAR_3872	-	cell wall and cell processes	conserved lipoprotein LppS	
4870616	non	TA	MMAR_3953	-	conserved hypothetical	conserved hypothetical protein	
4871196	non	TG	MMAR_3953	-	conserved hypothetical	conserved hypothetical protein	
4871244	int	GC	32 MMAR_3953	conserved hypothetical	conserved hypothetical protein		
4873306	non	CT		conserved hypothetical	conserved membrane protein		
4878691	non	TC		cell wall and cell processes	conserved hypothetical protein		
4878943	non	GC		cell wall and cell processes	conserved hypothetical protein		
4880394	syn	CT		lipid metabolism	fatty acid synthase Fas		
4882686	syn	GA		lipid metabolism	fatty acid synthase Fas		
4882713	syn	CT		lipid metabolism	fatty acid synthase Fas		
4884867	syn	GA		lipid metabolism	fatty acid synthase Fas		
4885166	non	TC		lipid metabolism	fatty acid synthase Fas		
4885730	non	GA		lipid metabolism	fatty acid synthase Fas		
4886235	syn	GA		lipid metabolism	fatty acid synthase Fas		
4888314	syn	GC		lipid metabolism	fatty acid synthase Fas		
4888731	syn	GC		lipid metabolism	fatty acid synthase Fas		
4888764	syn	TC		lipid metabolism	fatty acid synthase Fas		
4889929	syn	GC		cell wall and cell processes	conserved hypothetical secreted protein		
4890554	non	GA	MMAR_3964	-	intermediary metabolism and respiration	ring-hydroxylating dioxygenase large terminal subunit	
4890930	non	AG	MMAR_3964	-	intermediary metabolism and respiration	ring-hydroxylating dioxygenase large terminal subunit	
4891936	non	CA	MMAR_3965	-	intermediary metabolism and respiration	NAD-dependent aldehyde dehydrogenase	
4892712	syn	CT	MMAR_3965	-	intermediary metabolism and respiration	NAD-dependent aldehyde dehydrogenase	
4894064	non	GA	MMAR_3968	-	conserved hypothetical	conserved protein	
4894122	syn	GA	MMAR_3968	-	conserved hypothetical	conserved protein	
4894725	int	CG	13 MMAR_3968	conserved hypothetical	conserved protein		
4894947	int	TG		-			
4895031	int	GC		-			
4899111	non	GC	MMAR_3971	-	intermediary metabolism and respiration	oxidoreductase	
4899171	non	GC	MMAR_3971	-	intermediary metabolism and respiration	oxidoreductase	
4899297	syn	GT	MMAR_3971	-	intermediary metabolism and respiration	oxidoreductase	
4899333	syn	GT	MMAR_3971	-	intermediary metabolism and respiration	oxidoreductase	
4904047	syn	AG	MMAR_3973	-	intermediary metabolism and respiration	ferredoxin Fdx1	
4904819	non	CT	MMAR_3974	-	conserved hypothetical	conserved hypothetical acyl-CoA transferase	
4904856	syn	CT	MMAR_3974	-	conserved hypothetical	conserved hypothetical acyl-CoA transferase	
4904904	non	CG	MMAR_3974	-	conserved hypothetical	conserved hypothetical acyl-CoA transferase	
4905108	syn	GA	MMAR_3974	-	conserved hypothetical	conserved hypothetical acyl-CoA transferase	
4905421	non	GC	MMAR_3974	-	conserved hypothetical	conserved hypothetical acyl-CoA transferase	
4907070	syn	CG	MMAR_3975	-	regulatory protein	transcriptional regulatory protein (FadR family)	
4958068	non	GA	MMAR_4019	-	regulatory protein	transcriptional regulatory protein	
4958850	non	GC	MMAR_4020	-	lipid metabolism	enoyl-CoA hydratase EchA4_2	
4960153	int	GA	86 MMAR_4021	conserved hypothetical	conserved hypothetical protein		
4960596	non	GC		lipid metabolism	enoyl-CoA hydratase EchA10_1		
4961508	syn	GC		lipid metabolism	enoyl-CoA hydratase EchA11_1		
4962720	non	GT		lipid metabolism	long-chain fatty-acid CoA ligase		
4963693	syn	TC		lipid metabolism	long-chain fatty-acid CoA ligase		
4964065	syn	CT		lipid metabolism	long-chain fatty-acid CoA ligase		
4964507	syn	GA		lipid metabolism	fatty-acid-CoA ligase FadD35_1		
4965416	syn	CG		lipid metabolism	fatty-acid-CoA ligase FadD35_1		
4965474	non	GA		lipid metabolism	fatty-acid-CoA ligase FadD35_1		
4965609	non	TC		lipid metabolism	fatty-acid-CoA ligase FadD35_1		
4965621	non	CA		lipid metabolism	fatty-acid-CoA ligase FadD35_1		
4965795	non	GT	MMAR_4027	-	lipid metabolism	fatty-acid-CoA ligase	
4965842	non	AT	MMAR_4027	-	lipid metabolism	fatty-acid-CoA ligase	
4966678	non	AT	MMAR_4027	-	lipid metabolism	fatty-acid-CoA ligase	
4966684	syn	GC	MMAR_4027	-	lipid metabolism	fatty-acid-CoA ligase	
4967324	int	AG	110 MMAR_4027	lipid metabolism	fatty-acid-CoA ligase		
4967664	non	TG		cell wall and cell processes	conserved hypothetical secreted protein		
4968454	syn	GA		regulatory proteins	transcriptional regulatory protein (probably GntR-family)		
4969577	syn	GA		lipid metabolism	acyl-CoA dehydrogenase		
4969954	syn	GT	MMAR_4030	-	lipid metabolism	acyl-CoA dehydrogenase	
4971746	non	TC	MMAR_4032	-	lipid metabolism	beta-ketoacyl CoA thiolase	
4971812	non	AT	MMAR_4032	-	lipid metabolism	beta-ketoacyl CoA thiolase	
4972984	non	TC	MMAR_4033	-	lipid metabolism	3'-oxoacyl-[acyl-carrier protein] reductase FabG	
4973059	syn	AG	MMAR_4033	-	lipid metabolism	3'-oxoacyl-[acyl-carrier protein] reductase FabG	
4975524	non	TG	MMAR_4035	-	conserved hypothetical	conserved hypothetical protein	
4978827	syn	AG	MMAR_4037	-	cell wall and cell processes	transmembrane ATP-binding protein ABC transporter	
4981483	int	G-	17 MMAR_4039	cell wall and cell processes	conserved hypothetical membrane protein		
4981740	syn	TC		intermediary metabolism and respiration	Ham1-related NTPase		
4981916	non	CA		intermediary metabolism and respiration	Ham1-related NTPase		
4982209	int	AT		intermediary metabolism and respiration	Ham1-related NTPase		
4983234	syn	GA	MMAR_4042	-	information pathways	ribonuclease RphA	
4983477	syn	GA	MMAR_4042	-	information pathways	ribonuclease RphA	
4984427	syn	CA	MMAR_4043	-	conserved hypothetical	conserved hypothetical metal-dependent hydrolase	
4984609	non	GC	MMAR_4043	-	conserved hypothetical	conserved hypothetical metal-dependent hydrolase	
4992669	non	GA	MMAR_4051	-	Mce family protein Mce3A_1		
4993289	syn	CT	MMAR_4051	-	Mce family protein Mce3A_1		
4996465	non	AT	MMAR_4054	-	Mce family protein Mce3D_1		
4996723	syn	CG	MMAR_4054	-	Mce family protein Mce3D_1		
4997548	non	TC	MMAR_4055	-	Mce family lipoprotein LprM_1		
5001403	syn	GA	MMAR_4058	-	cell wall and cell processes	glutamate racemase MurI	
5008441	syn	CT	MMAR_4068	-	intermediary metabolism and respiration	nicotinic acid phosphoribosyltransferase PncB	
5014664	non	GA	MMAR_4070	-	intermediary metabolism and respiration	glycogen phosphorylase GlgP	
5013320	syn	CT	MMAR_4071	-	intermediary metabolism and respiration	conserved glycosidase	
5016325	syn	TG	MMAR_4072	-	intermediary metabolism and respiration	1,4-alpha-glucan branching enzyme GlgB	
5019799	syn	GA	MMAR_4074	-	intermediary metabolism and respiration	thioredoxin	
5020414	syn	TC	MMAR_4075	-	lipid metabolism	acetyl-CoA acetyltransferase FadA4	
5020677	syn	GA	MMAR_4073	-	lipid metabolism	acetyl-CoA acetyltransferase FadA4	
5020738	syn	CT	MMAR_4073	-	lipid metabolism	acetyl-CoA acetyltransferase FadA4	
5021091	non	AG	MMAR_4075	-	lipid metabolism	acetyl-CoA acetyltransferase FadA4	

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
5023819	syn	CA	MMAR_4078	-		intermediary metabolism and respiration	adenylate cyclase
5029881	syn	CT	MMAR_4082	-		information pathways	methylated-DNA--protein-cysteine methyltransferase Ogt
5031579	int	GA		-			
5032082	int	GA		-			
5035683	int	GA	62 MMAR_4083	cell wall and cell processes		UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA	
5037212	syn	TC	MMAR_4084	-		intermediary metabolism and respiration	cobalamin adenosyltransferase
5038198	int	GA		6 MMAR_4086		intermediary metabolism and respiration	ATP synthase epsilon chain AtpC
5042513	syn	CA	MMAR_4089	-		intermediary metabolism and respiration	ATP synthase alpha chain AtpA
5042988	syn	GC	MMAR_4090	-		intermediary metabolism and respiration	ATP synthase delta chain AtpH
5043030	syn	GA	MMAR_4090	-		intermediary metabolism and respiration	ATP synthase delta chain AtpH
5043258	syn	GC	MMAR_4090	-		intermediary metabolism and respiration	ATP synthase delta chain AtpH
5043656	non	CA	MMAR_4090	-		intermediary metabolism and respiration	ATP synthase delta chain AtpH
5045780	non	CG	MMAR_4094	-		cell wall and cell processes	conserved hypothetical membrane protein
5048822	syn	GA	MMAR_4097	-		intermediary metabolism and respiration	modification methylase HemK
5049135	non	CT	MMAR_4097	-		intermediary metabolism and respiration	modification methylase HemK
5051337	syn	CT	MMAR_4100	-		information pathways	transcription termination factor Rho
5051736	syn	CT	MMAR_4100	-		information pathways	transcription termination factor Rho
5051823	syn	CT	MMAR_4100	-		information pathways	transcription termination factor Rho
5053703	syn	AG	MMAR_4101	-		intermediary metabolism and respiration	homoserine kinase ThrB
5054411	syn	GA	MMAR_4102	-		intermediary metabolism and respiration	threonine synthase ThrC
5054775	syn	GA	MMAR_4102	-		intermediary metabolism and respiration	threonine synthase ThrC
5056520	syn	TC	MMAR_4104	-		intermediary metabolism and respiration	diaminopimelate decarboxylase LysA
5056841	syn	GA	MMAR_4104	-		intermediary metabolism and respiration	diaminopimelate decarboxylase LysA
5057701	non	TC	MMAR_4104	-		intermediary metabolism and respiration	diaminopimelate decarboxylase LysA
5057873	non	AG	MMAR_4105	-		information pathways	arginyl-tRNA synthetase ArgS
5058039	non	TC	MMAR_4105	-		information pathways	arginyl-tRNA synthetase ArgS
5063984	int	GA		86 MMAR_4109	PE/PPE	PE-PGRS family protein	
5066615	non	CG	MMAR_4110	-		intermediary metabolism and respiration	aldehyde dehydrogenase
5067956	non	GT	MMAR_4111	-		intermediary metabolism and respiration	pyridoxamine 5'-phosphate oxidase
5068121	non	CT	MMAR_4111	-		intermediary metabolism and respiration	pyridoxamine 5'-phosphate oxidase
5068122	non	TC	MMAR_4111	-		intermediary metabolism and respiration	pyridoxamine 5'-phosphate oxidase
5068224	syn	GA	MMAR_4112	-		conserved hypotheticals	conserved hypothetical protein
5068448	non	GA	MMAR_4112	-		conserved hypotheticals	conserved hypothetical protein
5069239	syn	CA	MMAR_4113	-		intermediary metabolism and respiration	haloalkane dehalogenase DhaA
5069814	non	GT	MMAR_5521	-		intermediary metabolism and respiration	peptidase S15
5070549	syn	GA	MMAR_5521	-		intermediary metabolism and respiration	peptidase S15
5074244	non	TA	MMAR_4118	-		cell wall and cell processes	conserved hypothetical membrane permease
5077337	non	GA	MMAR_4120	-		intermediary metabolism and respiration	adenylate cyclase
5078016	int	GC		64 MMAR_4122	cell wall and cell processes	conserved hypothetical membrane protein	
5083161	syn	CT	MMAR_4126	-		conserved hypotheticals	conserved hypothetical transport protein
5084955	int	CT		97 MMAR_4128	intermediary metabolism and respiration	flavin-dependent oxidoreductase	
5085400	syn	AG	MMAR_4128	-		intermediary metabolism and respiration	flavin-dependent oxidoreductase
5085424	syn	CT	MMAR_4128	-		intermediary metabolism and respiration	flavin-dependent oxidoreductase
5085511	syn	CT	MMAR_4128	-		intermediary metabolism and respiration	flavin-dependent oxidoreductase
5085513	syn	AG	MMAR_4128	-		intermediary metabolism and respiration	flavin-dependent oxidoreductase
5085748	syn	GA	MMAR_4128	-		intermediary metabolism and respiration	flavin-dependent oxidoreductase
5085981	syn	GT	MMAR_4129	-		intermediary metabolism and respiration	glyoxalase GlaO 2
5086426	int	AT		59 MMAR_4130	conserved hypotheticals	conserved hypothetical protein	
5087384	int	CT		66 MMAR_4132	intermediary metabolism and respiration	bifunctional enzyme CysN/CysC: sulfate adenyltransferase (subunit 1) + adenylsulfate kinase	
5087588	syn	GA	MMAR_4132	-		intermediary metabolism and respiration	bifunctional enzyme CysN/CysC: sulfate adenyltransferase (subunit 1) + adenylsulfate kinase
5089596	syn	AG	MMAR_4133	-		intermediary metabolism and respiration	sulfate adenyltransferase subunit 2 CysD
5090166	syn	AG	MMAR_4133	-		intermediary metabolism and respiration	sulfate adenyltransferase subunit 2 CysD
5093704	syn	GC	MMAR_4138	-		cell wall and cell processes	oligopeptide-transport ATP-binding protein ABC transporter OppD
5094142	syn	CG	MMAR_4138	-		cell wall and cell processes	oligopeptide-transport ATP-binding protein ABC transporter OppD
5094688	syn	GA	MMAR_4138	-		cell wall and cell processes	oligopeptide-transport ATP-binding protein ABC transporter OppD
5095985	non	CG	MMAR_4139	-		cell wall and cell processes	periplasmic oligopeptide-binding lipoprotein OppA
5098941	syn	CT	MMAR_4141	-		intermediary metabolism and respiration	dehydrogenase fad flavoprotein Gmc oxidoreductase
5099643	syn	GA	MMAR_4141	-		intermediary metabolism and respiration	dehydrogenase fad flavoprotein Gmc oxidoreductase
5101033	syn	GA	MMAR_4142	-		conserved hypotheticals	conserved hydrolase
5101157	non	CT	MMAR_4142	-		conserved hypotheticals	conserved hydrolase
5101989	non	GT	MMAR_4142	-		conserved hypotheticals	conserved hydrolase
5102296	syn	AC	MMAR_4142	-		conserved hypotheticals	conserved hydrolase
5102650	syn	GA	MMAR_4142	-		conserved hypotheticals	conserved hydrolase
5107162	non	GA	MMAR_4147	-		cell wall and cell processes	transmembrane ATP-binding protein ABC transporter
5107522	non	GT	MMAR_4147	-		cell wall and cell processes	transmembrane ATP-binding protein ABC transporter
5109416	syn	GA	MMAR_4148	-		cell wall and cell processes	transmembrane ATP-binding protein ABC transporter
5111415	int	GA		100 MMAR_4149	PE/PPE	PE-PGRS family protein	
5111501	int	AG		14 MMAR_4149	PE/PPE	PE-PGRS family protein	
512010	int	GA		-			
5115799	syn	GA	MMAR_4155	-		regulatory proteins	transcriptional regulatory protein EmbR
5116426	syn	GA	MMAR_4155	-		regulatory proteins	transcriptional regulatory protein EmbR
5116573	syn	CA	MMAR_4155	-		regulatory proteins	transcriptional regulatory protein EmbR
5116970	int	CT		55 MMAR_4155	regulatory proteins	transcriptional regulatory protein EmbR	
5118257	syn	GT	MMAR_4156	-		regulatory proteins	transmembrane serine/threonine-protein kinase H PknH
5118782	non	GT	MMAR_4156	-		regulatory proteins	transmembrane serine/threonine-protein kinase H PknH
5119064	int	GT		6 MMAR_4156	regulatory proteins	transmembrane serine/threonine-protein kinase H PknH	
5119696	non	AG	MMAR_4157	-		regulatory proteins	transcriptional regulatory protein (LysR family)
5121583	syn	GA	MMAR_4159	-		intermediary metabolism and respiration	conserved hydrolase
5122075	non	CT	MMAR_4160	-		intermediary metabolism and respiration	acetyl-CoA hydrolase/transferase
5122180	non	GA	MMAR_4160	-		intermediary metabolism and respiration	acetyl-CoA hydrolase/transferase
5123237	syn	CT	MMAR_4161	-		lipid metabolism	acyl-CoA dehydrogenase FadE3
5135531	int	CT		145 MMAR_4171	regulatory proteins	transmembrane serine/threonine-protein kinase	
5139462	syn	GT	MMAR_4171	-		regulatory proteins	transmembrane serine/threonine-protein kinase
5139463	syn	GC	MMAR_4173	-		intermediary metabolism and respiration	adenylate cyclase
5140149	syn	GA	MMAR_4174	-		regulatory proteins	anchored-membrane serine/threonine-protein kinase PknF
5140308	syn	TG	MMAR_4174	-		regulatory proteins	anchored-membrane serine/threonine-protein kinase PknF
5141211	non	CG	MMAR_4174	-		regulatory proteins	anchored-membrane serine/threonine-protein kinase PknF
5141687	syn	CG	MMAR_4175	-		regulatory proteins	anchored-membrane serine/threonine-protein kinase PknF
5143237	syn	CT	MMAR_4176	-		cell wall and cell processes	conserved hypothetical membrane protein
5144620	non	GA	MMAR_4179	-		intermediary metabolism and respiration	amidase Amb2
5146415	syn	AG	MMAR_4180	-		intermediary metabolism and respiration	monoxygenase
5150102	int	GA		23 MMAR_4183	intermediary metabolism and respiration	oxidoreductase	
5151029	non	GA	MMAR_4184	-		intermediary metabolism and respiration	cytochrome P450 130A4 Cyp130A4
5151080	syn	CT	MMAR_4184	-		intermediary metabolism and respiration	cytochrome P450 130A4 Cyp130A4

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
5152113	Int	AC	MMAR_4185	6	MMAR_4185	regulatory proteins	transcriptional regulatory protein
5157194	Syn	GA	MMAR_4188	-		intermediary metabolism and respiration	integral membrane acyltransferase
5157529	Syn	TC	MMAR_4189	-		information pathways	cold-shock DEAD-Box protein DeaD
5160233	Int	GA	MMAR_4190	38	MMAR_4190	cell wall and cell processes	lipoprotein LprE
5160291	non	AG	MMAR_4191	-		conserved hypothetical	conserved hypothetical protein
5162996	non	CG	MMAR_4191	-		conserved hypothetical	conserved hypothetical protein
5165542	non	GC	MMAR_4192	-		cell wall and cell processes	drug-transport integral membrane protein
5165682	Int	GA	MMAR_4192	108	MMAR_4192	cell wall and cell processes	drug-transport integral membrane protein
5166155	Syn	CT	MMAR_4193	-		cell wall and cell processes	conserved membrane protein
5166157	non	TA	MMAR_4193	-		cell wall and cell processes	conserved membrane protein
5168168	Syn	GA	MMAR_4194	-		intermediary metabolism and respiration	alpha-ketoglutarate decarboxylase Kgd
5169083	Syn	CA	MMAR_4194	-		intermediary metabolism and respiration	alpha-ketoglutarate decarboxylase Kgd
5169155	Syn	CG	MMAR_4194	-		intermediary metabolism and respiration	alpha-ketoglutarate decarboxylase Kgd
5169614	Syn	CT	MMAR_4194	-		intermediary metabolism and respiration	alpha-ketoglutarate decarboxylase Kgd
5169788	Syn	CG	MMAR_4194	-		intermediary metabolism and respiration	alpha-ketoglutarate decarboxylase Kgd
5170112	non	GA	MMAR_4194	-		intermediary metabolism and respiration	alpha-ketoglutarate decarboxylase Kgd
5171481	Int	CT	MMAR_4195	28	MMAR_4195	intermediary metabolism and respiration	short-chain type dehydrogenase/reductase
5172412	Syn	GA	MMAR_4197	-		intermediary metabolism and respiration	[NAD] dependent malate oxidoreductase Mez_1
5172662	Syn	CG	MMAR_4197	-		intermediary metabolism and respiration	[NAD] dependent malate oxidoreductase Mez_1
5172713	non	CG	MMAR_4197	-		intermediary metabolism and respiration	[NAD] dependent malate oxidoreductase Mez_1
5174795	Int	AG	MMAR_4199	104	MMAR_4199	cell wall and cell processes	magnesium and cobalt transport transmembrane protein CorA
5175786	Syn	GA	MMAR_4199	-		cell wall and cell processes	magnesium and cobalt transport transmembrane protein CorA
5175900	Syn	CA	MMAR_4199	-		cell wall and cell processes	magnesium and cobalt transport transmembrane protein CorA
5176265	Syn	CG	MMAR_4200	-		intermediary metabolism and respiration	F420-dependent glucose-6-phosphate dehydrogenase Fgd2
5176640	Syn	TC	MMAR_4200	-		intermediary metabolism and respiration	F420-dependent glucose-6-phosphate dehydrogenase Fgd2
5177096	Syn	CA	MMAR_4200	-		intermediary metabolism and respiration	F420-dependent glucose-6-phosphate dehydrogenase Fgd2
5177652	Syn	AC	MMAR_4201	-		cell wall and cell processes	GabA permease GabP_1
5178875	Int	GA	MMAR_4201	39	MMAR_4201	cell wall and cell processes	GabA permease GabP_1
5178936	Int	GT	MMAR_4201	100	MMAR_4201	cell wall and cell processes	GabA permease GabP_1
5178954	Int	CG	MMAR_4201	118	MMAR_4201	cell wall and cell processes	GabA permease GabP_1
5178988	Int	CT	MMAR_4202	130	MMAR_4202	cell wall and cell processes	conserved hypothetical membrane protein
5179543	non	GA	MMAR_4202	-		cell wall and cell processes	conserved hypothetical membrane protein
5179867	non	CG	MMAR_4203	-		cell wall and cell processes	sugar-transport ATP-binding protein ABC transporter SugC
5179870	Syn	CT	MMAR_4203	-		cell wall and cell processes	sugar-transport ATP-binding protein ABC transporter SugC
5180053	Syn	CT	MMAR_4203	-		cell wall and cell processes	sugar-transport ATP-binding protein ABC transporter SugC
5180539	Syn	GC	MMAR_4203	-		cell wall and cell processes	sugar-transport ATP-binding protein ABC transporter SugC
5180554	Syn	CT	MMAR_4203	-		cell wall and cell processes	sugar-transport ATP-binding protein ABC transporter SugC
5181693	non	AG	MMAR_4204	-		cell wall and cell processes	sugar-transport integral membrane protein ABC transporter SugB
5181727	non	TA	MMAR_4204	-		cell wall and cell processes	sugar-transport integral membrane protein ABC transporter SugB
5181735	Int	GC	MMAR_4205	6	MMAR_4205	cell wall and cell processes	sugar-transport integral membrane protein ABC transporter SugA
5182053	Syn	GT	MMAR_4205	-		cell wall and cell processes	sugar-transport integral membrane protein ABC transporter SugA
5182204	non	CA	MMAR_4205	-		cell wall and cell processes	sugar-transport integral membrane protein ABC transporter SugA
5182389	Syn	CT	MMAR_4205	-		cell wall and cell processes	sugar-transport integral membrane protein ABC transporter SugA
5182637	non	TG	MMAR_4205	-		cell wall and cell processes	sugar-transport integral membrane protein ABC transporter SugA
5182638	non	CG	MMAR_4205	-		cell wall and cell processes	sugar-transport integral membrane protein ABC transporter SugA
5187651	Syn	GC	MMAR_4211	-		cell wall and cell processes	membrane protein
5187948	Syn	CA	MMAR_4211	-		cell wall and cell processes	membrane protein
5193894	Syn	AG	MMAR_4217	-		intermediary metabolism and respiration	methyltransferase
5195127	Int	AC		-			
5198830	Syn	CG	MMAR_4221	-		cell wall and cell processes	tetronasin-transport integral membrane protein ABC transporter
5199629	non	GA	MMAR_4221	-		cell wall and cell processes	tetronasin-transport integral membrane protein ABC transporter
5199922	non	TG	MMAR_4221	-		cell wall and cell processes	tetronasin-transport integral membrane protein ABC transporter
5200149	Int	CA	MMAR_4222	27	MMAR_4222	cell wall and cell processes	conserved integral membrane protein
5209692	Syn	GA	MMAR_4230	-		conserved hypothetical	conserved hypothetical protein
5210433	Syn	CA	MMAR_4231	-		intermediary metabolism and respiration	dihydropteroate synthase 2 FolP2
5211650	Syn	GA	MMAR_4232	-		lipid metabolism	fatty-acid-CoA ligase FadD6
5212301	Syn	GA	MMAR_4232	-		lipid metabolism	fatty-acid-CoA ligase FadD6
5216798	non	GA	MMAR_4236	-		intermediary metabolism and respiration	transferase
5216906	non	CG	MMAR_4236	-		intermediary metabolism and respiration	transferase
5217499	Syn	CT	MMAR_4236	-		intermediary metabolism and respiration	transferase
5217675	non	AT	MMAR_4236	-		intermediary metabolism and respiration	transferase
5217956	Syn	GA	MMAR_4237	-		regulatory proteins	conserved hypothetical regulatory protein
5218094	Syn	GA	MMAR_4237	-		regulatory proteins	conserved hypothetical regulatory protein
5218497	Int	GA		-			
5219829	Syn	AG	MMAR_4238	-		cell wall and cell processes	conserved integral membrane transport protein
5220953	Int	AG	MMAR_4239	117	MMAR_4239	conserved hypothetical	conserved hypothetical protein
5221065	Int	TG	MMAR_4239	5	MMAR_4239	conserved hypothetical	conserved hypothetical protein
5223972	Syn	CG	MMAR_4242	-		regulatory proteins	transcriptional regulatory protein
5224317	Syn	CT	MMAR_4242	-		regulatory proteins	transcriptional regulatory protein
5224395	Syn	TC	MMAR_4242	-		regulatory proteins	transcriptional regulatory protein
5224425	Syn	TC	MMAR_4242	-		regulatory proteins	transcriptional regulatory protein
5226477	Syn	CT	MMAR_4243	-		lipid metabolism	fatty-acid-CoA synthetase FadD36
5230327	non	AG	MMAR_4247	-		conserved hypothetical	conserved hypothetical protein
5230795	non	TC	MMAR_4247	-		conserved hypothetical	conserved hypothetical protein
5232131	Syn	CT	MMAR_4250	-		lipid metabolism	keto acyl-CoA thiolase Ltp2
5233228	non	GC	MMAR_4251	-		regulatory proteins	transcriptional regulator
5233356	Syn	AG	MMAR_4251	-		regulatory proteins	transcriptional regulator
5234918	Syn	CT	MMAR_4253	-		intermediary metabolism and respiration	pyrrole-5-carboxylate dehydrogenase RocA
5236699	Syn	CT	MMAR_4254	-		conserved hypothetical	conserved hypothetical protein
5236771	Syn	CG	MMAR_4254	-		conserved hypothetical	conserved hypothetical protein
5237629	Syn	GA	MMAR_4254	-		conserved hypothetical	conserved hypothetical protein
5237659	Syn	GC	MMAR_4254	-		conserved hypothetical	conserved hypothetical protein
5238877	Syn	AC	MMAR_4256	-		conserved hypothetical	conserved hypothetical protein
5259087	non	GA	MMAR_4271	-		conserved hypothetical	conserved hypothetical protein
5259667	non	GT	MMAR_4271	-		conserved hypothetical	conserved hypothetical protein
5259839	Syn	GA	MMAR_4271	-		conserved hypothetical	conserved hypothetical protein
5260222	Int	AG		-			
5260796	Syn	GA	MMAR_4272	-		cell wall and cell processes	conserved hypothetical membrane protein
5261020	Syn	GA	MMAR_4272	-		cell wall and cell processes	conserved hypothetical membrane protein
5261027	non	AG	MMAR_4272	-		cell wall and cell processes	conserved hypothetical membrane protein
5262239	non	TC	MMAR_4272	-		cell wall and cell processes	conserved hypothetical membrane protein
5262419	non	GA	MMAR_4272	-		cell wall and cell processes	conserved hypothetical membrane protein
5262883	Syn	CT	MMAR_4272	-		cell wall and cell processes	conserved hypothetical membrane protein
5263343	Syn	AG	MMAR_4273	-		intermediary metabolism and respiration	aminotransferase
5263382	Syn	CA	MMAR_4273	-		intermediary metabolism and respiration	aminotransferase

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
5264707	syn	TC	MMAR_4274	-		intermediary metabolism and respiration	ferredoxin FdxC
5268322	int	GC		37	MMAR_4278	PE/PPE	PE-PGRS family protein
5271189	int	CT		-			
5271369	int	TA		-			
5271715	syn	GC	MMAR_4279	-		intermediary metabolism and respiration	F420 biosynthesis protein FbiC
5271727	syn	CG	MMAR_4279	-		intermediary metabolism and respiration	F420 biosynthesis protein FbiC
5272396	syn	GA	MMAR_4279	-		intermediary metabolism and respiration	F420 biosynthesis protein FbiC
5273246	non	TC	MMAR_4279	-		intermediary metabolism and respiration	F420 biosynthesis protein FbiC
5273629	syn	GC	MMAR_4279	-		intermediary metabolism and respiration	F420 biosynthesis protein FbiC
5273643	syn	GA	MMAR_4279	-		intermediary metabolism and respiration	F420 biosynthesis protein FbiC
5275890	syn	GA	MMAR_4283	-		intermediary metabolism and respiration	N-acetyl-1-D-myo-inosyl-2-amino-2-deoxy-alpha-D-glucopyranoside deacetylase MshB
5276156	non	TC	MMAR_4283	-		intermediary metabolism and respiration	N-acetyl-1-D-myo-inosyl-2-amino-2-deoxy-alpha-D-glucopyranoside deacetylase MshB
5276784	int	GA		92	MMAR_4284	regulatory protein	transcriptional regulatory protein
5276898	non	TC	MMAR_4284	-		regulatory proteins	transcriptional regulatory protein
5277100	syn	CG	MMAR_4284	-		regulatory proteins	transcriptional regulatory protein
5277771	int	GA		-			
5277840	int	GA		-			
5278017	int	AG		-			
5278232	int	AG		-			
5282017	syn	GA	MMAR_4288	-		cell wall and cell processes	conserved lipoprotein LpqW
5283383	non	CT	MMAR_4289	-		information pathways	GTP-binding translation elongation factor TypA
5283614	syn	GA	MMAR_4289	-		information pathways	GTP-binding translation elongation factor TypA
5284849	syn	GA	MMAR_4289	-		information pathways	GTP-binding translation elongation factor TypA
5285033	syn	GA	MMAR_4289	-		information pathways	GTP-binding translation elongation factor TypA
5286189	non	GC	MMAR_4291	-		conserved hypotheticals	conserved hypothetical protein
5286253	syn	CT	MMAR_4291	-		conserved hypotheticals	conserved hypothetical protein
5286837	non	AG	MMAR_4292	-		cell wall and cell processes	conserved transmembrane protein
5287259	non	CT	MMAR_4292	-		cell wall and cell processes	conserved transmembrane protein
5287266	syn	CA	MMAR_4292	-		cell wall and cell processes	conserved transmembrane protein
5287414	non	TC	MMAR_4292	-		cell wall and cell processes	conserved transmembrane protein
5290408	syn	GA	MMAR_4296	-		conserved hypotheticals	conserved protein
5290441	non	GA	MMAR_4296	-		conserved hypotheticals	conserved protein
5290900	syn	GT	MMAR_4298	-		conserved hypotheticals	conserved protein
5290953	non	AG	MMAR_4298	-		conserved hypotheticals	conserved protein
5292314	syn	-C	MMAR_4300	-		lipid metabolism	O-methyltransferase Omt_2
5292388	syn	AG	MMAR_4300	-		lipid metabolism	O-methyltransferase Omt_2
5292551	syn	CT	MMAR_4300	-		lipid metabolism	O-methyltransferase Omt_2
5293801	int	CT		61	MMAR_4303	conserved hypotheticals	conserved hypothetical protein
5293821	int	AG		67	MMAR_4302	regulatory protein	transcriptional regulatory protein
5294435	syn	GC	MMAR_4303	-		conserved hypotheticals	conserved hypothetical protein
5294438	syn	AG	MMAR_4303	-		conserved hypotheticals	conserved hypothetical protein
5295073	syn	CG	MMAR_4304	-		regulatory proteins	transcriptional regulatory protein (probably TetR-family)
5296212	non	CT	MMAR_4305	-		cell wall and cell processes	conserved transmembrane transport protein MmpL13
5297803	int	CT		94	MMAR_4306	conserved hypotheticals	conserved hypothetical protein
5298104	int	TC		85	MMAR_4307	intermediary metabolism and respiration	short-chain type dehydrogenase/reductase
5298411	syn	GA	MMAR_4307	-		intermediary metabolism and respiration	short-chain type dehydrogenase/reductase
5299012	non	AG	MMAR_4308	-		lipid metabolism	alpha-methylacyl-CoA racemase Mcr
5301185	syn	AC	MMAR_4310	-		intermediary metabolism and respiration	oxidoreductase
5302163	syn	CT	MMAR_4310	-		intermediary metabolism and respiration	oxidoreductase
5302399	non	CG	MMAR_4310	-		intermediary metabolism and respiration	oxidoreductase
5302473	non	TC	MMAR_4310	-		intermediary metabolism and respiration	oxidoreductase
5306323	syn	GA	MMAR_4315	-		intermediary metabolism and respiration	oxidoreductase
5306683	syn	CT	MMAR_4315	-		intermediary metabolism and respiration	oxidoreductase
5307218	int	AG		70	MMAR_4315	intermediary metabolism and respiration	oxidoreductase
5313298	int	GC		102	MMAR_4316	PE/PPE	PE-PGRS family protein
5313416	int	GA		-			
5314088	non	CA	MMAR_4317	-		lipid metabolism	enoyl-CoA hydratase EchA1_1
5314778	syn	CT	MMAR_4318	-		lipid metabolism	acetyl-CoA acyltransferase FadA6_3
5315722	int	AC		-			
5315994	int	CT		118	MMAR_4319	PE/PPE	PPE family protein
5321850	int	CG		86	MMAR_4320	PE/PPE	PPE family protein
5323614	int	GT		19	MMAR_4321	PE/PPE	PE family protein
5324409	syn	GA	MMAR_4322	-		intermediary metabolism and respiration	aldehyde dehydrogenase NAD dependent AldA_2
5325096	syn	GA	MMAR_4322	-		intermediary metabolism and respiration	aldehyde dehydrogenase NAD dependent AldA_2
5333318	int	GA		68	MMAR_4328	intermediary metabolism and respiration	5-methyltetrahydropteroxytriglutamate--homocysteine methyltransferase MetE
5334646	non	GA	MMAR_4328	-		intermediary metabolism and respiration	5-methyltetrahydropteroxytriglutamate--homocysteine methyltransferase MetE
5336087	syn	GA	MMAR_4329	-		cell wall and cell processes	conserved hypothetical membrane protein
5340473	syn	AG	MMAR_4333	-		conserved hypotheticals	conserved hypothetical protein
5340565	non	GC	MMAR_4333	-		conserved hypotheticals	conserved hypothetical protein
5345240	syn	GA	MMAR_4338	-		intermediary metabolism and respiration	6-phosphogluconate dehydrogenase decarboxylating Gnd2
5345300	syn	GA	MMAR_4338	-		intermediary metabolism and respiration	6-phosphogluconate dehydrogenase decarboxylating Gnd2
5349197	syn	GA	MMAR_4342	-		conserved hypotheticals	conserved hypothetical protein
5359476	syn	GA	MMAR_4353	-		information pathways	GTP binding protein
5362014	syn	GA	MMAR_4355	-		lipid metabolism	4-hydroxy-3-methylbut-2-enyl diphosphate reductase IspH
5362125	syn	CT	MMAR_4355	-		lipid metabolism	4-hydroxy-3-methylbut-2-enyl diphosphate reductase IspH
5363726	syn	CT	MMAR_4357	-		information pathways	exodeoxyribonuclease VII (large subunit) XseA
5364023	syn	GA	MMAR_4357	-		information pathways	exodeoxyribonuclease VII (large subunit) XseA
5365347	syn	GA	MMAR_4359	-		intermediary metabolism and respiration	cholesterol dehydrogenase
5369501	int	TG		34	MMAR_4363	conserved hypotheticals	hypothetical carboxylesterase
5370093	syn	TC	MMAR_4363	-		conserved hypotheticals	hypothetical carboxylesterase
5370807	syn	CT	MMAR_4363	-		conserved hypotheticals	hypothetical carboxylesterase
5373615	syn	GA	MMAR_4366	-		conserved hypotheticals	conserved protein
5373687	syn	GT	MMAR_4366	-		conserved hypotheticals	conserved protein
5378053	syn	GA	MMAR_4370	-		cell wall and cell processes	conserved hypothetical transmembrane protein
5378456	syn	TC	MMAR_4370	-		cell wall and cell processes	conserved hypothetical transmembrane protein
5379990	syn	CG	MMAR_4371	-		intermediary metabolism and respiration	glycosyl hydrolase
5383008	syn	GA	MMAR_4375	-		intermediary metabolism and respiration	serine hydroxymethyltransferase 1 GlyA1
5387729	non	AG	MMAR_4379	-		cell wall and cell processes	conserved hypothetical transmembrane protein
5388699	syn	AG	MMAR_4379	-		cell wall and cell processes	conserved hypothetical transmembrane protein
5388338	int	CT		78	MMAR_4381	intermediary metabolism and respiration	hemolysin like protein
5391845	syn	GT	MMAR_4383	-		cell wall and cell processes	conserved transmembrane protein
5391861	syn	CT	MMAR_4383	-		cell wall and cell processes	conserved transmembrane protein
5394009	syn	CA	MMAR_4385	-		mycothiol conjugate amidase Mca	
5396659	non	CA	MMAR_4388	-		intermediary metabolism and respiration	cystathione gamma-synthase MetB (cos)
5396674	syn	GA	MMAR_4388	-		intermediary metabolism and respiration	cystathione gamma-synthase MetB (cos)

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
5397184	syn	TC	MMAR_4389	-		cell wall and cell processes	proline-rich antigen Pra
5398592	non	GT	MMAR_4390	-		intermediary metabolism and respiration	cystathione beta-synthase Cbs
5398731	non	GA	MMAR_4390	-		intermediary metabolism and respiration	cystathione beta-synthase Cbs
5400350	syn	GA	MMAR_4391	-		intermediary metabolism and respiration	lipase LipU
5403001	Int	TC		120	MMAR_4394	cell wall and cell processes	conserved hypothetical transmembrane protein
5403646	syn	GA	MMAR_4394	-		cell wall and cell processes	conserved hypothetical transmembrane protein
5404912	syn	CT	MMAR_4395	-		lipid metabolism	envol-CoA hydrolase EchA9
5407785	non	AG	MMAR_4397	-		cell wall and cell processes	conserved hypothetical transmembrane protein
5411123	Int	CT		128	MMAR_4399	PE/PPE	PE-PGRS family protein
5413823	syn	GA	MMAR_4400	-		conserved hypothetical	conserved hypothetical protein
5415148	syn	GA	MMAR_4402	-		cell wall and cell processes	lipoprotein LpV
5415739	syn	GA	MMAR_4403	-		conserved hypothetical	conserved hypothetical protein
5416429	syn	TC	MMAR_4403	-		conserved hypothetical	conserved hypothetical protein
5416967	syn	GA	MMAR_4404	-		cell wall and cell processes	conserved hypothetical protein
5417370	Int	CG		23	MMAR_4404	cell wall and cell processes	conserved hypothetical protein
5417631	non	GA	MMAR_4405	-		conserved hypothetical	conserved hypothetical protein
5417792	non	TC	MMAR_4405	-		conserved hypothetical	conserved hypothetical protein
5424419	syn	CT	MMAR_4410	-		intermediary metabolism and respiration	arylsulfatase AsiA
5424548	syn	TC	MMAR_4410	-		intermediary metabolism and respiration	arylsulfatase AsiA
5424617	syn	GA	MMAR_4410	-		intermediary metabolism and respiration	arylsulfatase AsiA
5425291	non	GA	MMAR_4410	-		intermediary metabolism and respiration	arylsulfatase AsiA
5425802	syn	CT	MMAR_4411	-		conserved hypothetical	conserved hypothetical protein
5459385	non	GA	MMAR_4438	-		cell wall and cell processes	conserved hypothetical transmembrane protein
5477264	non	GA	MMAR_4457	-		intermediary metabolism and respiration	hydantoin racemase
5477412	Int	GA		77	MMAR_4458	conserved hypothetical	conserved hypothetical protein
5478937	syn	CA	MMAR_4460	-		conserved hypothetical	conserved hypothetical protein
5482364	Int	CT		-			
5482386	Int	CT		139	MMAR_4464	conserved hypothetical	conserved hypothetical protein
5483194	syn	CA	MMAR_4464	-		conserved hypothetical	conserved hypothetical protein
5487342	Int	CG		52	MMAR_4465	information pathways	TRANSCRIPTION-REPAIR coupling factor Mfd (TrcF)
5487345	Int	CG		55	MMAR_4465	information pathways	TRANSCRIPTION-REPAIR coupling factor Mfd (TrcF)
5487346	Int	CG		56	MMAR_4465	information pathways	TRANSCRIPTION-REPAIR coupling factor Mfd (TrcF)
5488206	Int	GA		-			
5490375	non	GA	MMAR_4468	-		intermediary metabolism and respiration	ribose-phosphate pyrophosphokinase PrsA
5490617	syn	TC	MMAR_4468	-		intermediary metabolism and respiration	ribose-phosphate pyrophosphokinase PrsA
5492598	psd	CT	MMAR_4471	-		intermediary metabolism and respiration	N-term oxidoreductase pseudogene
5492910	Int	GA		108	MMAR_4471	intermediary metabolism and respiration	N-term oxidoreductase pseudogene
5492982	Int	CT		123	MMAR_4472	information pathways	50S ribosomal protein L25 RplY
5494561	syn	AG	MMAR_4474	-		cell wall and cell processes	conserved membrane protein
5497808	syn	GC	MMAR_4476	-		lipid metabolism	polyketide synthase Pks16
5497970	syn	GA	MMAR_4476	-		lipid metabolism	polyketide synthase Pks16
5500044	syn	GA	MMAR_4477	-		intermediary metabolism and respiration	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase IspE
5501039	non	GA	MMAR_4478	-		information pathways	dimethyladenosine transferase KsgA
5501932	syn	TC	MMAR_4479	-		cell wall and cell processes	resuscitation-promoting factor RpB
5502075	non	GC	MMAR_4479	-		cell wall and cell processes	resuscitation-promoting factor RpB
5504105	syn	CT	MMAR_4481	-		information pathways	methionyl-tRNA synthetase MetS
5504384	syn	TC	MMAR_4481	-		information pathways	methionyl-tRNA synthetase MetS
5504570	syn	CT	MMAR_4481	-		information pathways	methionyl-tRNA synthetase MetS
5510575	syn	GA	MMAR_4485	-		cell wall and cell processes	conserved hypothetical secreted protein
5511603	non	CG	MMAR_4486	-		intermediary metabolism and respiration	dehydrogenase
5513909	syn	GA	MMAR_4488	-		intermediary metabolism and respiration	para-aminobenzoate synthase component PabD
5519417	syn	CG	MMAR_4492	-		intermediary metabolism and respiration	arginine deiminase ArcA
5520546	non	CT	MMAR_4493	-		conserved hypothetical	conserved hypothetical protein
5523907	syn	AG	MMAR_4497	-		intermediary metabolism and respiration	methyltransferase
5523910	syn	GA	MMAR_4497	-		intermediary metabolism and respiration	methyltransferase
5524416	syn	AG	MMAR_4499	-		cell wall and cell processes	conserved hypothetical membrane protein
5524518	syn	GA	MMAR_4499	-		cell wall and cell processes	conserved hypothetical membrane protein
5524530	syn	GA	MMAR_4499	-		cell wall and cell processes	conserved hypothetical membrane protein
5524877	non	CG	MMAR_4499	-		cell wall and cell processes	conserved hypothetical membrane protein
5524878	non	CA	MMAR_4499	-		cell wall and cell processes	conserved hypothetical membrane protein
5524936	syn	AG	MMAR_4499	-		cell wall and cell processes	conserved hypothetical membrane protein
5524978	syn	GA	MMAR_4499	-		cell wall and cell processes	conserved hypothetical membrane protein
5525064	syn	GA	MMAR_4499	-		cell wall and cell processes	conserved hypothetical membrane protein
5525318	syn	GA	MMAR_4500	-		cell wall and cell processes	conserved hypothetical protein
5525342	syn	TC	MMAR_4500	-		cell wall and cell processes	conserved hypothetical protein
5525375	syn	CT	MMAR_4500	-		cell wall and cell processes	conserved hypothetical protein
5525477	syn	GA	MMAR_4500	-		cell wall and cell processes	conserved hypothetical protein
5525735	non	CA	MMAR_4500	-		cell wall and cell processes	conserved hypothetical protein
5526639	Int	GC		-			
5527880	non	GC	MMAR_4502	-		cell wall and cell processes	teichoic acid biosynthesis protein
5528087	syn	AG	MMAR_4502	-		cell wall and cell processes	teichoic acid biosynthesis protein
5531264	syn	CT	MMAR_4504	-		cell wall and cell processes	conserved hypothetical membrane protein
5531810	syn	TC	MMAR_4505	-		cell wall and cell processes	glycosyltransferase
5532252	non	GA	MMAR_4505	-		cell wall and cell processes	glycosyltransferase
5533039	non	GA	MMAR_4505	-		cell wall and cell processes	glycosyltransferase
5534597	non	AC	MMAR_4507	-		conserved hypothetical	conserved hypothetical protein
5537869	syn	GA	MMAR_4509	-		conserved hypothetical	conserved hypothetical protein
5538179	non	GA	MMAR_4509	-		conserved hypothetical	conserved hypothetical protein
5538645	non	GC	MMAR_4509	-		conserved hypothetical	conserved hypothetical protein
5540827	non	CT	MMAR_4512	-		intermediary metabolism and respiration	predicted amidohydrolase
5543369	non	GT	MMAR_4515	-		cell wall and cell processes	conserved hypothetical transmembrane protein
5543390	non	AC	MMAR_4515	-		cell wall and cell processes	conserved hypothetical transmembrane protein
5546716	non	GA	MMAR_4515	-		cell wall and cell processes	conserved hypothetical transmembrane protein
5546732	non	CT	MMAR_4517	-		conserved hypothetical	conserved hypothetical protein
5548307	non	TC	MMAR_4518	-		cell wall and cell processes	conserved hypothetical transmembrane protein
5549548	syn	TA	MMAR_4520	-		intermediary metabolism and respiration	mybldopterin biosynthesis protein MoeA1
5551791	non	CG	MMAR_4522	-		conserved hypothetical	conserved hypothetical protein
5551833	non	CT	MMAR_4522	-		conserved hypothetical	conserved hypothetical protein
5553377	syn	GA	MMAR_4523	-		conserved hypothetical	conserved hypothetical protein
5553374	non	GC	MMAR_4524	-		cell wall and cell processes	conserved hypothetical serine rich protein
5554815	syn	GA	MMAR_4527	-		intermediary metabolism and respiration	conserved hypothetical membrane protein
5555162	non	CA	MMAR_4527	-		intermediary metabolism and respiration	serine protease PepD
5556729	syn	CT	MMAR_4528	-		regulatory proteins	serine protease PepD
5556729	syn	CA	MMAR_4528	-		regulatory proteins	two component sensor kinase MprB
5557050	syn	GA	MMAR_4528	-		regulatory proteins	two component sensor kinase MprB

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
5558460	Int	AG	MMAR_4530	139	MMAR_4530	information pathways	50S ribosomal protein L32 RpmF
5558675	non	GC	MMAR_4530	-		information pathways	50S ribosomal protein L32 RpmF
5559091	syn	CT	MMAR_4531	-		conserved hypothetical	conserved hypothetical protein
5559280	non	GT	MMAR_4531	-		conserved hypothetical	conserved hypothetical protein
5559297	non	CA	MMAR_4531	-		conserved hypothetical	conserved hypothetical protein
5559298	non	CG	MMAR_4531	-		conserved hypothetical	conserved hypothetical protein
5560549	non	GA	MMAR_4531	-		conserved hypothetical	conserved hypothetical protein
5560789	non	AT	MMAR_4532	-		intermediary metabolism and respiration	acyl-CoA dehydrogenase FadE13
5561118	syn	GT	MMAR_4532	-		intermediary metabolism and respiration	acyl-CoA dehydrogenase FadE13
5561322	syn	AG	MMAR_4532	-		intermediary metabolism and respiration	acyl-CoA dehydrogenase FadE13
5561463	syn	CT	MMAR_4532	-		intermediary metabolism and respiration	acyl-CoA dehydrogenase FadE13
5563405	syn	GA	MMAR_4533	-		lipid metabolism	acyl-/propionyl-CoA carboxylase (beta subunit) AccD2
5565920	non	CA	MMAR_4535	-		lipid metabolism	acyl-CoA dehydrogenase FadE12
5568714	syn	AG	MMAR_4539	-		conserved hypothetical	conserved hypothetical protein
5568811	syn	CG	MMAR_4540	-		conserved hypothetical	conserved hypothetical protein
5569027	syn	CT	MMAR_4540	-		conserved hypothetical	conserved hypothetical protein
5569675	syn	CT	MMAR_4540	-		conserved hypothetical	conserved hypothetical protein
5570891	syn	CT	MMAR_4541	-		intermediary metabolism and respiration	magnesium chelatase
5570999	syn	CT	MMAR_4541	-		intermediary metabolism and respiration	magnesium chelatase
5571263	non	AG	MMAR_4541	-		intermediary metabolism and respiration	magnesium chelatase
5574292	non	TC	MMAR_4543	-		intermediary metabolism and respiration	5'-phosphoribosylglycaminide formyltransferase PurN
5575881	syn	CA	MMAR_4544	-		cell wall and cell processes	conserved integral membrane protein
5576023	non	CG	MMAR_4545	-		cell wall and cell processes	conserved transmembrane protein
5578186	non	TC	MMAR_4547	-		lipid metabolism	thiolase
5578254	syn	GA	MMAR_4547	-		lipid metabolism	thiolase
5579073	syn	GA	MMAR_4547	-		lipid metabolism	thiolase
5579817	int	CG		-			
5579870	int	TC		-			
5582706	syn	GC	MMAR_4550	-		intermediary metabolism and respiration	succinyl-CoA synthetase (beta chain) SucC
5583021	syn	CT	MMAR_4550	-		intermediary metabolism and respiration	succinyl-CoA synthetase (beta chain) SucC
5584012	syn	GA	MMAR_4551	-		conserved hypothetical	conserved hypothetical protein
5584903	syn	GT	MMAR_4552	-		conserved hypothetical	conserved hypothetical protein
5584980	non	GT	MMAR_4552	-		conserved hypothetical	conserved hypothetical protein
5587232	syn	TC	MMAR_4553	-		information pathways	ATP-dependent DNA helicase II UvrD1
5591774	syn	AG	MMAR_4557	-		intermediary metabolism and respiration	glucose-6-phosphate isomerase Pgi
5591777	syn	AG	MMAR_4557	-		intermediary metabolism and respiration	glucose-6-phosphate isomerase Pgi
5592265	non	TC	MMAR_4557	-		intermediary metabolism and respiration	glucose-6-phosphate isomerase Pgi
5592542	syn	TA	MMAR_4557	-		intermediary metabolism and respiration	glucose-6-phosphate isomerase Pgi
5592758	non	CA	MMAR_4557	-		intermediary metabolism and respiration	glucose-6-phosphate isomerase Pgi
5596210	int	GC		-			
5597422	int	GA		-			
5599399	int	CT	125 MMAR_4562	PE/PPE		PE-PGRS family protein	
5599737	syn	CG	MMAR_4563	-		conserved hypothetical	conserved hypothetical protein
5600169	syn	TC	MMAR_4563	-		conserved hypothetical	conserved hypothetical protein
5600258	syn	GT	MMAR_4563	-		conserved hypothetical	conserved hypothetical protein
5602101	syn	AG	MMAR_4565	-		intermediary metabolism and respiration	monoxygenase
5603192	int	GT		-			
5604493	syn	AC	MMAR_4568	-		intermediary metabolism and respiration	conserved hypothetical oxidoreductase
5604706	syn	TA	MMAR_4568	-		intermediary metabolism and respiration	conserved hypothetical oxidoreductase
5605220	syn	GA	MMAR_4569	-		lipid metabolism	enoyl-CoA hydratase EchA12_2
5605334	syn	CT	MMAR_4569	-		lipid metabolism	enoyl-CoA hydratase EchA12_2
5605550	syn	CT	MMAR_4569	-		lipid metabolism	enoyl-CoA hydratase EchA12_2
5606824	non	GA	MMAR_4570	-		conserved hypothetical	conserved hypothetical protein
5610316	syn	GC	MMAR_4572	-		intermediary metabolism and respiration	bifunctional enzyme: 2-hydroxyhepta-2-4-diene-1-7-dioate isomerase (HHDD isomerase) + cyclase/dehydrase
5612793	syn	CT	MMAR_4573	-		intermediary metabolism and respiration	ATP dependent DNA ligase
5613817	non	GA	MMAR_4574	-		intermediary metabolism and respiration	fructokinase PfkB
5615022	syn	CT	MMAR_4575	-		conserved hypothetical	conserved hypothetical protein
5615370	syn	CT	MMAR_4576	-		cell wall and cell processes	periplasmic phosphate-binding lipoprotein PstS2
5616525	int	TC	75 MMAR_4577	regulatory proteins			
5616774	non	CT	MMAR_4577	-		transmembrane serine/threonine-protein kinase D PknD	
5617022	syn	CG	MMAR_4577	-		regulatory proteins	transmembrane serine/threonine-protein kinase D PknD
5619510	non	AG	MMAR_4578	-		cell wall and cell processes	phosphate-transport integral membrane ABC transporter PstA1
5620075	non	TG	MMAR_4579	-		cell wall and cell processes	phosphate-transport integral membrane ABC transporter PstC2
5620212	non	GC	MMAR_4579	-		cell wall and cell processes	phosphate-transport integral membrane ABC transporter PstC2
5623237	non	GA	MMAR_4582	-		conserved hypothetical	conserved hypothetical protein
5624070	non	TG	MMAR_4583	-		conserved hypothetical	conserved hypothetical protein
5624514	non	GA	MMAR_4583	-		conserved hypothetical	conserved hypothetical protein
5625055	syn	GT	MMAR_4584	-		cell wall and cell processes	divalent cation-transport integral membrane protein MntH
5626544	non	GT	MMAR_4585	-		cell wall and cell processes	conserved hypothetical secreted protein
5626599	int	AG	106 MMAR_4586	unknown		conserved hypothetical protein	
5627048	non	GA	MMAR_4586	-		unknown	conserved hypothetical protein
5646139	int	GT		-			
5649759	int	GA		-			
5649789	int	AC		-			
5650473	syn	AG	MMAR_4610	-		cell wall and cell processes	conserved hypothetical membrane protein
5650661	non	AG	MMAR_4610	-		cell wall and cell processes	conserved hypothetical membrane protein
5650935	int	AT	48 MMAR_4610	cell wall and cell processes		conserved hypothetical membrane protein	
5651001	int	AG	114 MMAR_4610	cell wall and cell processes		conserved hypothetical membrane protein	
5651101	int	CA	100 MMAR_4611	PE/PPE		PE family protein	
5651172	int	TA	29 MMAR_4611	PE/PPE		PE family protein	
5651197	int	TC	4 MMAR_4611	PE/PPE		PE family protein	
5651212	int	GC	11 MMAR_4611	PE/PPE		PE family protein	
5651449	int	TC	60 MMAR_4612	PE/PPE		PE family protein	
5651742	int	GA		-			
5651766	int	GC		-			
5652025	int	AG		-			
5652026	int	GA		-			
5652582	int	CG		-			
5652639	int	CT		-			
5652648	int	AG	129 MMAR_4612	PE/PPE		PPE family protein	
5653717	syn	AT	MMAR_4613	-		lipid metabolism	lipid carrier protein or keto acyl-CoA thiolase
5653975	syn	GC	MMAR_4613	-		lipid metabolism	lipid carrier protein or keto acyl-CoA thiolase
5654558	syn	TC	MMAR_4614	-		intermediary metabolism and respiration	dioxygenase
5654582	syn	GC	MMAR_4614	-		intermediary metabolism and respiration	dioxygenase
5654729	non	CT	MMAR_4614	-		intermediary metabolism and respiration	dioxygenase

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
5656745	int	TC		44	MMAR_4617	conserved hypotheticals	conserved hypothetical protein
5656948	syn	GA	MMAR_4619	-		conserved hypotheticals	conserved hypothetical protein
5659107	non	AG	MMAR_4619	-		conserved hypotheticals	conserved protein
5659631	syn	CT	MMAR_4620	-		conserved hypotheticals	conserved hypothetical protein
5671556	syn	TA	MMAR_4622	-		cell wall and cell processes	metal cation transporter ATPase p-type CtpE
5672842	syn	GA	MMAR_4623	-		cell wall and cell processes	conserved hypothetical penicillin binding protein
5672947	syn	CA	MMAR_4623	-		cell wall and cell processes	conserved hypothetical penicillin binding protein
5673098	non	AT	MMAR_4623	-		cell wall and cell processes	conserved hypothetical penicillin binding protein
5673460	non	TC	MMAR_4624	-		conserved hypotheticals	conserved protein
5676816	int	GA		39	MMAR_4626	lipid metabolism	acyl-coenzyme A carboxyl transferase (subunit beta) AccD3
5677534	int	GA		-			
5677698	int	GA		127	MMAR_4627	cell wall and cell processes	conserved two-domain transmembrane protein
5680271	syn	CT	MMAR_4628	-		intermediary metabolism and respiration	8-amino-7-oxononanoate synthase BioF2_1
5680818	int	CG		1	MMAR_4629	intermediary metabolism and respiration	cysteine synthase B CysM
5682747	non	TC	MMAR_4630	-		cell wall and cell processes	membrane-bound C-5 sterol desaturase Erg3_1
5683431	non	GA	MMAR_4631	-		regulatory proteins	transcriptional regulatory protein
5686320	syn	CG	MMAR_4634	-		regulatory protein	two component sensor histidine kinase PrrB
5689647	syn	CT	MMAR_4638	-		conserved hypotheticals	conserved protein
5690732	non	CT	MMAR_4639	-		intermediary metabolism and respiration	oxidoreductase
5691046	non	CT	MMAR_4639	-		intermediary metabolism and respiration	oxidoreductase
5691212	syn	CT	MMAR_4639	-		intermediary metabolism and respiration	oxidoreductase
5693277	non	CA	MMAR_4641	-		intermediary metabolism and respiration	monooxygenase
5696046	syn	CT	MMAR_4643	-		intermediary metabolism and respiration	citrate synthase II CitA
5696277	syn	TC	MMAR_4643	-		intermediary metabolism and respiration	citrate synthase II CitA
5696786	int	AG		35	MMAR_4643	intermediary metabolism and respiration	citrate synthase II CitA
5696855	syn	AG	MMAR_4644	-		cell wall and cell processes	conserved hypothetical exported protein
5698585	int	CT		-			
5698778	int	AC		-			
5698868	int	CT		-			
5698910	int	AG		-			
5699093	int	AG		-			
5699258	int	GA		-			
5699344	int	GA		-			
5699366	int	AT		-			
5699656	int	AG		139	MMAR_4645	conserved hypotheticals	conserved protein
5699677	int	GA		118	MMAR_4645	conserved hypotheticals	conserved protein
5700024	non	GA	MMAR_4645	-		conserved hypotheticals	conserved protein
5704231	syn	CT	MMAR_4648	-		intermediary metabolism and respiration	phosphoserine aminotransferase SerC
5704243	syn	AG	MMAR_4648	-		intermediary metabolism and respiration	phosphoserine aminotransferase SerC
5705126	syn	GA	MMAR_4649	-		conserved hypotheticals	conserved hypothetical protein
5705970	non	CG	MMAR_4651	-		intermediary metabolism and respiration	rRNA methyltransferase
5706006	non	CT	MMAR_4651	-		intermediary metabolism and respiration	rRNA methyltransferase
5706193	syn	AG	MMAR_4651	-		intermediary metabolism and respiration	rRNA methyltransferase
5706196	non	GT	MMAR_4651	-		intermediary metabolism and respiration	rRNA methyltransferase
5706480	non	CG	MMAR_4652	-		regulatory proteins	transcriptional regulatory protein (possibly marR-family)
5706645	syn	CG	MMAR_4652	-		regulatory proteins	transcriptional regulatory protein (possibly marR-family)
5708054	non	GA	MMAR_4655	-		cell wall and cell processes	conserved protein
5708056	syn	AG	MMAR_4655	-		cell wall and cell processes	conserved protein
5708164	syn	GC	MMAR_4655	-		cell wall and cell processes	conserved protein
5709759	syn	GT	MMAR_4656	-		cell wall and cell processes	conserved transmembrane protein
5710074	syn	TA	MMAR_4656	-		cell wall and cell processes	conserved transmembrane protein
5711817	non	GT	MMAR_4658	-		conserved hypotheticals	conserved hypothetical protein
5713082	syn	GA	MMAR_4660	-		lipid metabolism	acyl-CoA dehydrogenase FadE10
5714165	syn	CT	MMAR_4660	-		lipid metabolism	acyl-CoA dehydrogenase FadE10
5714311	non	CT	MMAR_4660	-		lipid metabolism	acyl-CoA dehydrogenase FadE10
5714600	syn	CT	MMAR_4660	-		lipid metabolism	acyl-CoA dehydrogenase FadE10
5714792	syn	GC	MMAR_4660	-		lipid metabolism	acyl-CoA dehydrogenase FadE10
5717058	non	AG	MMAR_4663	-		intermediary metabolism and respiration	molybdenum cofactor biosynthesis protein A2 MoaA2
5717583	int	TC		-			
5719041	int	CA		27	MMAR_4666	intermediary metabolism and respiration	molybdenum cofactor biosynthesis protein E2 MoaE2
5719287	syn	AG	MMAR_4666	-		intermediary metabolism and respiration	molybdenum cofactor biosynthesis protein E2 MoaE2
5719365	syn	GA	MMAR_4666	-		intermediary metabolism and respiration	molybdenum cofactor biosynthesis protein E2 MoaE2
5719673	syn	GC	MMAR_4667	-		intermediary metabolism and respiration	molybdopterin biosynthesis Moq protein
5720161	syn	AC	MMAR_4668	-		intermediary metabolism and respiration	molybdenum cofactor biosynthesis protein C 2 MoaC2
5721193	syn	CA	MMAR_4670	-		conserved hypotheticals	conserved hypothetical protein
5721667	syn	GA	MMAR_4670	-		conserved hypotheticals	conserved hypothetical protein
5722073	syn	CT	MMAR_4670	-		conserved hypotheticals	conserved hypothetical protein
5722794	non	AC	MMAR_4670	-		conserved hypotheticals	conserved hypothetical protein
5722888	syn	GA	MMAR_4670	-		conserved hypotheticals	conserved hypothetical protein
5722970	non	TA	MMAR_4670	-		conserved hypotheticals	conserved hypothetical protein
5723126	int	GA		79	MMAR_4670	conserved hypotheticals	conserved hypothetical protein
5724173	syn	GA	MMAR_4671	-		information pathways	DNA helicase Erc3
5725501	int	GC		129	MMAR_4672	conserved hypotheticals	conserved hypothetical protein
5725520	int	T-		110	MMAR_4672	conserved hypotheticals	conserved hypothetical protein
5726207	non	TG	MMAR_4673	-		conserved hypotheticals	conserved protein
5726649	syn	CG	MMAR_4673	-		conserved hypotheticals	conserved protein
5727228	syn	GA	MMAR_4674	-		regulatory proteins	transcriptional regulator
5727682	non	CT	MMAR_4675	-		cell wall and cell processes	membrane-associated oxidoreductase
5727695	non	AT	MMAR_4675	-		cell wall and cell processes	membrane-associated oxidoreductase
5727714	syn	GA	MMAR_4675	-		cell wall and cell processes	membrane-associated oxidoreductase
5728062	non	CG	MMAR_4675	-		cell wall and cell processes	membrane-associated oxidoreductase
5732803	non	TG	MMAR_4678	-		intermediary metabolism and respiration	aminotransferase
5733532	syn	GT	MMAR_4678	-		intermediary metabolism and respiration	aminotransferase
5735505	syn	CT	MMAR_4681	-		lipid metabolism	fatty-acid-CoA racemase Far
5736099	non	GA	MMAR_4682	-		conserved hypotheticals	conserved hypothetical protein
5738191	int	GA		8	MMAR_4684	conserved hypotheticals	conserved hypothetical protein
5738968	syn	CA	MMAR_4686	-		cell wall and cell processes	conserved hypothetical membrane protein
5739094	syn	CT	MMAR_4686	-		cell wall and cell processes	conserved hypothetical membrane protein
5739788	syn	AG	MMAR_4687	-		cell wall and cell processes	conserved hypothetical membrane protein
5739794	syn	CT	MMAR_4687	-		cell wall and cell processes	conserved hypothetical membrane protein
5739921	syn	GA	MMAR_4687	-		cell wall and cell processes	conserved hypothetical membrane protein
5740112	non	AT	MMAR_4687	-		cell wall and cell processes	conserved hypothetical membrane protein
5740373	non	AG	MMAR_4687	-		cell wall and cell processes	conserved hypothetical membrane protein
5740417	non	CG	MMAR_4687	-		cell wall and cell processes	conserved hypothetical membrane protein
5740433	non	CT	MMAR_4687	-		cell wall and cell processes	conserved hypothetical membrane protein

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
5740645	int	CA		67	MMAR_4688	lipid metabolism	fatty-acid-CoA ligase FadD3_2
5740646	int	TA		66	MMAR_4688	lipid metabolism	fatty-acid-CoA ligase FadD3_2
5741057	syn	AG	MMAR_4688	-		lipid metabolism	fatty-acid-CoA ligase FadD3_2
5741084	syn	AG	MMAR_4688	-		lipid metabolism	fatty-acid-CoA ligase FadD3_2
5741195	syn	GC	MMAR_4688	-		lipid metabolism	fatty-acid-CoA ligase FadD3_2
5741240	syn	TC	MMAR_4688	-		lipid metabolism	fatty-acid-CoA ligase FadD3_2
5741388	non	TC	MMAR_4688	-		lipid metabolism	fatty-acid-CoA ligase FadD3_2
5741936	syn	AG	MMAR_4688	-		lipid metabolism	fatty-acid-CoA ligase FadD3_2
5741991	non	TC	MMAR_4688	-		lipid metabolism	fatty-acid-CoA ligase FadD3_2
5742020	syn	CT	MMAR_4688	-		lipid metabolism	fatty-acid-CoA ligase FadD3_2
5742412	syn	GA	MMAR_4689	-		conserved hypotheticals	amidohydrolase
5743171	syn	GT	MMAR_4689	-		conserved hypotheticals	amidohydrolase
5743717	non	AC	MMAR_4690	-		cell wall and cell processes	conserved lipoprotein
5744222	syn	GA	MMAR_4691	-		lipid metabolism	enoyl-CoA hydratase EchA8_2
5744262	non	GA	MMAR_4691	-		lipid metabolism	enoyl-CoA hydratase EchA8_2
5746661	non	CG	MMAR_4694	-		intermediary metabolism and respiration	cytochrome P450 150A6 Cyp150A6
5746725	syn	GC	MMAR_4694	-		intermediary metabolism and respiration	cytochrome P450 150A6 Cyp150A6
5766186	non	AG	MMAR_4715	-		lipid metabolism	3-oxoacyl-[acyl-carrier protein] reductase
5766415	syn	CA	MMAR_4715	-		lipid metabolism	3-oxoacyl-[acyl-carrier protein] reductase
5766466	syn	CG	MMAR_4715	-		lipid metabolism	3-oxoacyl-[acyl-carrier protein] reductase
5766804	int	GA		77	MMAR_4716	intermediary metabolism and respiration	ferredoxin
5767674	syn	AT	MMAR_4717	-		intermediary metabolism and respiration	cytochrome P450 188A3 Cyp188A3
5768558	int	TG		98	MMAR_4717	intermediary metabolism and respiration	cytochrome P450 188A3 Cyp188A3
5769067	non	GT	MMAR_4718	-		lipid metabolism	acyl-CoA dehydrogenase
5769113	syn	AG	MMAR_4718	-		lipid metabolism	acyl-CoA dehydrogenase
5770957	syn	GA	MMAR_4720	-		conserved hypotheticals	conserved hypothetical protein
5771250	non	TC	MMAR_4720	-		conserved hypotheticals	conserved hypothetical protein
5771448	int	CG		128	MMAR_4720	conserved hypotheticals	conserved hypothetical protein
5771495	syn	AC	MMAR_4721	-		intermediary metabolism and respiration	nitroreductase
5802665	int	TA		118	MMAR_4752	information pathways	transcriptional regulatory protein
5802685	int	AG		98	MMAR_4752	information pathways	transcriptional regulatory protein
5803265	syn	CT	MMAR_4752	-		information pathways	transcriptional regulatory protein
5803657	int	AG		13	MMAR_4753	intermediary metabolism and respiration	cytochrome P450 189A7 Cyp189A7
5804011	syn	GA	MMAR_4753	-		intermediary metabolism and respiration	cytochrome P450 189A7 Cyp189A7
5804560	syn	GA	MMAR_4753	-		intermediary metabolism and respiration	cytochrome P450 189A7 Cyp189A7
5804643	non	CG	MMAR_4753	-		intermediary metabolism and respiration	cytochrome P450 189A7 Cyp189A7
5804644	non	GT	MMAR_4753	-		intermediary metabolism and respiration	cytochrome P450 189A7 Cyp189A7
5804663	non	GA	MMAR_4753	-		intermediary metabolism and respiration	cytochrome P450 189A7 Cyp189A7
5805334	syn	GA	MMAR_4754	-		intermediary metabolism and respiration	short-chain type dehydrogenase/reductase
5805499	syn	GA	MMAR_4754	-		intermediary metabolism and respiration	short-chain type dehydrogenase/reductase
5806710	syn	GC	MMAR_4756	-		intermediary metabolism and respiration	oxidoreductase
5806889	non	CT	MMAR_4756	-		intermediary metabolism and respiration	oxidoreductase
5809090	non	TA	MMAR_4758	-		lipid metabolism	enoyl-CoA hydratase EchA4_1
5809922	non	TC	MMAR_4758	-		lipid metabolism	enoyl-CoA hydratase EchA4_1
5810047	syn	GA	MMAR_4758	-		lipid metabolism	enoyl-CoA hydratase EchA4_1
5810080	syn	TC	MMAR_4758	-		lipid metabolism	enoyl-CoA hydratase EchA4_1
5810919	syn	GT	MMAR_4759	-		intermediary metabolism and respiration	aminopeptidase
5811376	non	GA	MMAR_4759	-		intermediary metabolism and respiration	aminopeptidase
5811377	non	CA	MMAR_4759	-		intermediary metabolism and respiration	aminopeptidase
5811549	syn	CT	MMAR_4759	-		intermediary metabolism and respiration	aminopeptidase
5811798	syn	GA	MMAR_4759	-		intermediary metabolism and respiration	aminopeptidase
5811997	syn	CT	MMAR_4760	-		intermediary metabolism and respiration	dipeptidase
5812628	non	GT	MMAR_4760	-		intermediary metabolism and respiration	dipeptidase
5812947	non	CG	MMAR_4760	-		intermediary metabolism and respiration	dipeptidase
5813430	syn	GA	MMAR_4761	-		conserved hypotheticals	conserved hypothetical protein
5814310	syn	CG	MMAR_4761	-		conserved hypotheticals	conserved hypothetical protein
5815268	syn	TC	MMAR_4762	-		intermediary metabolism and respiration	cytochrome P450 105Q4 Cyp105Q4
5815540	non	CA	MMAR_4762	-		intermediary metabolism and respiration	cytochrome P450 105Q4 Cyp105Q4
5815765	syn	AC	MMAR_4763	-		intermediary metabolism and respiration	ferredoxin
5816526	int	CT		86	MMAR_4765	intermediary metabolism and respiration	short chain dehydrogenase
5816550	int	TC		62	MMAR_4765	intermediary metabolism and respiration	short chain dehydrogenase
5816818	non	TG	MMAR_4765	-		intermediary metabolism and respiration	short chain dehydrogenase
5816861	syn	CG	MMAR_4765	-		intermediary metabolism and respiration	short chain dehydrogenase
5816945	syn	GC	MMAR_4765	-		intermediary metabolism and respiration	short chain dehydrogenase
5817056	syn	GA	MMAR_4765	-		intermediary metabolism and respiration	short chain dehydrogenase
5818366	int	AT		49	MMAR_4767	cell wall and cell processes	conserved integral membrane transport protein
5818973	syn	CT	MMAR_4767	-		cell wall and cell processes	conserved integral membrane transport protein
5819078	syn	CT	MMAR_4767	-		cell wall and cell processes	conserved integral membrane transport protein
5819126	syn	AG	MMAR_4767	-		cell wall and cell processes	conserved integral membrane transport protein
5819207	syn	GT	MMAR_4767	-		cell wall and cell processes	conserved integral membrane transport protein
5819274	non	AG	MMAR_4767	-		cell wall and cell processes	conserved integral membrane transport protein
5819510	syn	CT	MMAR_4767	-		cell wall and cell processes	conserved integral membrane transport protein
5819785	non	AG	MMAR_4768	-		intermediary metabolism and respiration	cysteine synthase a CysK2
5820349	syn	GA	MMAR_4768	-		intermediary metabolism and respiration	cysteine synthase a CysK2
5821286	syn	CT	MMAR_4769	-		cell wall and cell processes	lipoprotein LpgS
5823245	syn	GA	MMAR_4771	-		cell wall and cell processes	conserved membrane protein
5823262	non	GA	MMAR_4771	-		cell wall and cell processes	conserved membrane protein
5826271	syn	AG	MMAR_4774	-		intermediary metabolism and respiration	monooxygenase
5827488	syn	CG	MMAR_4775	-		intermediary metabolism and respiration	dehydrogenase
5827569	syn	GA	MMAR_4775	-		intermediary metabolism and respiration	dehydrogenase
5827578	non	CG	MMAR_4775	-		intermediary metabolism and respiration	dehydrogenase
5827580	non	TA	MMAR_4775	-		intermediary metabolism and respiration	dehydrogenase
5827647	syn	TC	MMAR_4775	-		intermediary metabolism and respiration	dehydrogenase
5829577	non	TG	MMAR_4776	-		intermediary metabolism and respiration	extradiol dioxygenase MhpB
5829749	syn	AG	MMAR_4776	-		intermediary metabolism and respiration	extradiol dioxygenase MhpB
5837943	syn	AG	MMAR_4783	-		regulatory proteins	two component sensor kinase
5839561	non	CT	MMAR_4785	-		cell wall and cell processes	integral membrane protein
5841249	int	TC		14	MMAR_4786	PE/PPE	PE-PGRS family protein
5841298	int	GA		83	MMAR_4786	PE/PPE	PE-PGRS family protein
5843778	non	AT	MMAR_4789	-		intermediary metabolism and respiration	proline iminopeptidase Pip
5844171	non	AG	MMAR_4789	-		intermediary metabolism and respiration	proline iminopeptidase Pip
5845945	syn	CT	MMAR_4791	-		lipid metabolism	acyl-CoA dehydrogenase
5847280	non	CA	MMAR_4792	-		lipid metabolism	acyl-CoA dehydrogenase
5847376	non	AC	MMAR_4792	-		lipid metabolism	acyl-CoA dehydrogenase
5847534	syn	GA	MMAR_4793	-		lipid metabolism	acyl-CoA synthetase

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
5850602	syn	AG	MMAR_4796	-		intermediary metabolism and respiration	oxidoreductase
5850995	syn	CA	MMAR_4796	-		intermediary metabolism and respiration	oxidoreductase
5851019	syn	AT	MMAR_4796	-		intermediary metabolism and respiration	oxidoreductase
5851256	non	GT	MMAR_4797	-		lipid metabolism	methylmalonyl-CoA mutase alpha subunit McmA2b
5851576	syn	CG	MMAR_4797	-		lipid metabolism	methylmalonyl-CoA mutase alpha subunit McmA2b
5852039	non	TC	MMAR_4798	-		lipid metabolism	methylmalonyl-CoA mutase beta subunit McmA2a
5852532	non	AG	MMAR_4798	-		lipid metabolism	methylmalonyl-CoA mutase beta subunit McmA2a
5852959	syn	GA	MMAR_4798	-		lipid metabolism	methylmalonyl-CoA mutase beta subunit McmA2a
5853088	syn	CT	MMAR_4798	-		lipid metabolism	methylmalonyl-CoA mutase beta subunit McmA2a
5853410	syn	CG	MMAR_4799	-		conserved hypotheticals	conserved hypothetical protein
5853742	syn	GA	MMAR_4799	-		conserved hypotheticals	conserved hypothetical protein
5854204	int	CT		48	MMAR_4799	conserved hypotheticals	conserved hypothetical protein
5854823	non	CT	MMAR_4800	-		cell wall and cell processes	conserved lipoprotein LpgR
5855259	non	GA	MMAR_4801	-		unknown	hypothetical membrane protein
5858853	syn	GA	MMAR_4806	-		lipid metabolism	phytoene dehydrogenase CrtI
5860919	syn	GC	MMAR_4807	-		lipid metabolism	phytoene synthase CrtB
5861069	syn	TC	MMAR_4807	-		lipid metabolism	phytoene synthase CrtB
5865677	non	GA	MMAR_4812	-		intermediary metabolism and respiration	isopentenyl pyrophosphate isomerase type 2 Idi2
5867087	syn	GA	MMAR_4814	-		conserved hypotheticals	conserved hypothetical protein
5867201	syn	GT	MMAR_4814	-		conserved hypotheticals	conserved hypothetical protein
5868365	syn	GA	MMAR_4815	-		cell wall and cell processes	L-asparagine permease AnsP1
5871023	non	GA	MMAR_4818	-		intermediary metabolism and respiration	short chain dehydrogenase/reductase
5871436	non	AC	MMAR_4819	-		conserved hypotheticals	conserved hypothetical protein
5872456	syn	CT	MMAR_4820	-		conserved hypotheticals	conserved hypothetical protein
5872873	syn	AG	MMAR_4820	-		conserved hypotheticals	conserved hypothetical protein
5873145	syn	CT	MMAR_4821	-		conserved hypotheticals	conserved hypothetical protein
5876832	int	A-		9	MMAR_4823	cold shock protein A CspA	
5877140	syn	GC	MMAR_4824	-		information pathways	ATP-dependent RNA helicase RhlE1
5878409	syn	CA	MMAR_4824	-		information pathways	ATP-dependent RNA helicase RhlE1
5879133	int	CT		72	MMAR_5579	conserved hypotheticals	conserved hypothetical protein
5879346	int	GA					
5879999	syn	GA	MMAR_4825	-		intermediary metabolism and respiration	5-methyltetrahydrofolate--homocysteine methyltransferase MetH
5880098	syn	CA	MMAR_4825	-		intermediary metabolism and respiration	5-methyltetrahydrofolate--homocysteine methyltransferase MetH
5880542	syn	CG	MMAR_4825	-		intermediary metabolism and respiration	5-methyltetrahydrofolate--homocysteine methyltransferase MetH
5881346	syn	CT	MMAR_4825	-		intermediary metabolism and respiration	5-methyltetrahydrofolate--homocysteine methyltransferase MetH
5881994	syn	CT	MMAR_4825	-		intermediary metabolism and respiration	5-methyltetrahydrofolate--homocysteine methyltransferase MetH
5883293	int	GC		9	MMAR_4825	intermediary metabolism and respiration	5-methyltetrahydrofolate--homocysteine methyltransferase MetH
5883295	int	TG		11	MMAR_4825	intermediary metabolism and respiration	5-methyltetrahydrofolate--homocysteine methyltransferase MetH
5883411	int	CT		127	MMAR_4825	intermediary metabolism and respiration	5-methyltetrahydrofolate--homocysteine methyltransferase MetH
5905123	syn	GC	MMAR_4849	-		conserved hypotheticals	conserved hypothetical protein
5906225	non	GA	MMAR_4850	-		lipid metabolism	O-methyltransferase
5906747	int	AC		62	MMAR_4851	conserved hypotheticals	deaminase
5906756	int	GA		53	MMAR_4851	conserved hypotheticals	deaminase
5906849	non	AT	MMAR_4851	-		conserved hypotheticals	deaminase
5907342	int	CT		33	MMAR_4851	conserved hypotheticals	deaminase
5911651	non	GC	MMAR_4857	-		regulatory proteins	transcriptional regulator
5913162	syn	CG	MMAR_4858	-		conserved hypotheticals	conserved hypothetical protein
5914728	syn	CA	MMAR_4859	-		cell wall and cell processes	phosphate-transport system regulatory protein PhoY2
5915070	syn	GA	MMAR_4859	-		cell wall and cell processes	phosphate-transport system regulatory protein PhoY2
5915835	syn	GA	MMAR_4860	-		cell wall and cell processes	phosphate-transport ATP-binding protein ABC transporter PhoT
5917197	syn	GA	MMAR_4862	-		cell wall and cell processes	phosphate-transport integral membrane ABC transporter PstC2_1
5918981	syn	TC	MMAR_4863	-		cell wall and cell processes	phosphate-binding protein 3 precursor PhoS3
5921224	int	GA					
5921502	non	GA	MMAR_4866	-		conserved hypotheticals	conserved protein
5922014	syn	GC	MMAR_4866	-		conserved hypotheticals	conserved protein
5923083	non	GA	MMAR_4868	-		intermediary metabolism and respiration	thiosulfate sulfurtransferase CysA2
5923202	syn	CT	MMAR_4868	-		intermediary metabolism and respiration	thiosulfate sulfurtransferase CysA2
5925650	non	AG	MMAR_4872	-		conserved hypotheticals	conserved hypothetical protein
5928733	int	CT		77	MMAR_4873	intermediary metabolism and respiration	amino acid aminotransferase PabC
5929033	syn	GA	MMAR_4874	-		conserved hypotheticals	conserved hypothetical protein
5931976	int	CA		33	MMAR_4876	cell wall and cell processes	metal cation transporter p-type ATPase CtpV
5932458	non	GA	MMAR_4877	-		conserved hypotheticals	conserved hypothetical protein
5932459	non	GA	MMAR_4877	-		conserved hypotheticals	conserved hypothetical protein
5932813	syn	AG	MMAR_4878	-		conserved hypotheticals	conserved hypothetical protein
5932897	syn	GA	MMAR_4878	-		conserved hypotheticals	conserved hypothetical protein
5933520	non	TC	MMAR_4878	-		conserved hypotheticals	conserved hypothetical protein
5934661	non	GA	MMAR_4880	-		intermediary metabolism and respiration	5'-phosphoribosyl-5-aminoimidazole synthetase PurM
5935783	syn	CT	MMAR_4881	-		intermediary metabolism and respiration	amidophosphoribosyltransferase PurF
5936584	syn	TC	MMAR_4881	-		intermediary metabolism and respiration	amidophosphoribosyltransferase PurF
5938709	non	CA	MMAR_4884	-		cell wall and cell processes	lipoprotein
5939719	syn	GC	MMAR_4884	-		cell wall and cell processes	lipoprotein
5942358	syn	GA	MMAR_4886	-		conserved hypotheticals	conserved hypothetical protein
5942481	syn	GA	MMAR_4886	-		conserved hypotheticals	conserved hypothetical protein
5943298	syn	GA	MMAR_4888	-		intermediary metabolism and respiration	phosphoribosylformylglycinamide synthase II PurL
5944443	syn	GC	MMAR_4888	-		intermediary metabolism and respiration	phosphoribosylformylglycinamide synthase II PurL
5944624	non	TC	MMAR_4888	-		intermediary metabolism and respiration	phosphoribosylformylglycinamide synthase II PurL
5944939	syn	GA	MMAR_4888	-		intermediary metabolism and respiration	phosphoribosylformylglycinamide synthase II PurL
5947338	syn	AG	MMAR_4891	-		intermediary metabolism and respiration	aminopeptidase PepC
5948772	syn	GA	MMAR_4892	-		conserved hypotheticals	conserved hypothetical protein
5950378	int	AC		49	MMAR_4894	intermediary metabolism and respiration	dihydrodipamide dehydrogenase LpdB
5952053	syn	AG	MMAR_4895	-		conserved hypotheticals	conserved hypothetical protein
5952999	syn	CT	MMAR_4897	-		intermediary metabolism and respiration	phosphoribosylformylglycinamide synthase I PurQ
5953011	syn	TC	MMAR_4897	-		intermediary metabolism and respiration	phosphoribosylformylglycinamide synthase I PurQ
5953241	syn	GA	MMAR_4897	-		intermediary metabolism and respiration	phosphoribosylformylglycinamide synthase I PurQ
5953718	syn	GA	MMAR_4898	-		conserved hypotheticals	conserved protein
5957736	int	AG		88	MMAR_4902	regulatory proteins	conserved hypothetical regulatory protein
5960607	syn	GA	MMAR_4905	-		cell wall and cell processes	integral membrane drug efflux protein
5961122	syn	GC	MMAR_4905	-		cell wall and cell processes	integral membrane drug efflux protein
5960349	non	GC	MMAR_4905	-		cell wall and cell processes	integral membrane drug efflux protein
5961814	int	GA		63	MMAR_4907	cell wall and cell processes	conserved membrane protein
5963160	non	GA	MMAR_4908	-		intermediary metabolism and respiration	protease II (oligopeptidase B) PtrB
5963163	non	GA	MMAR_4908	-		intermediary metabolism and respiration	protease II (oligopeptidase B) PtrB
5963455	syn	GC	MMAR_4908	-		intermediary metabolism and respiration	protease II (oligopeptidase B) PtrB
5963511	syn	GT	MMAR_4908	-		intermediary metabolism and respiration	protease II (oligopeptidase B) PtrB
5964359	non	GA	MMAR_4908	-		intermediary metabolism and respiration	protease II (oligopeptidase B) PtrB

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
5964552	syn	GA	MMAR_4909	-		intermediary metabolism and respiration	phosphoribosylaminoimidazole- succinocarboxamide synthase PurC
5966418	syn	CG	MMAR_4911	-		intermediary metabolism and respiration	Zn-dependent alcohol dehydrogenase AdhX
5967055	int	GA		26	MMAR_4912	intermediary metabolism and respiration	aldehyde dehydrogenase
5967055	int	GA		26	MMAR_4911	intermediary metabolism and respiration	Zn-dependent alcohol dehydrogenase AdhX
5968125	syn	GA	MMAR_4912	-		intermediary metabolism and respiration	aldehyde dehydrogenase
5971812	non	GA	MMAR_4915	-		intermediary metabolism and respiration	cytochrome P450_126A3 Cyp126A3
5971979	syn	GA	MMAR_4915	-		intermediary metabolism and respiration	cytochrome P450_126A3 Cyp126A3
5972063	syn	GA	MMAR_4915	-		intermediary metabolism and respiration	cytochrome P450_126A3 Cyp126A3
5972480	syn	GA	MMAR_4915	-		intermediary metabolism and respiration	cytochrome P450_126A3 Cyp126A3
5972711	syn	GA	MMAR_4915	-		intermediary metabolism and respiration	cytochrome P450_126A3 Cyp126A3
5972768	syn	GT	MMAR_4915	-		intermediary metabolism and respiration	cytochrome P450_126A3 Cyp126A3
5972783	syn	GA	MMAR_4915	-		intermediary metabolism and respiration	cytochrome P450_126A3 Cyp126A3
5974785	non	CT	MMAR_4917	-		conserved hypothetical	conserved hypothetical protein
5974963	syn	GT	MMAR_4917	-		conserved hypothetical	conserved hypothetical protein
5980445	syn	GA	MMAR_4921	-		intermediary metabolism and respiration	molybdopterin biosynthesis protein Moey
5981454	non	CT	MMAR_4922	-		conserved hypothetical	conserved hypothetical protein
5982784	non	GA	MMAR_4923	-		regulatory protein	serine/threonine-protein kinase PknF_2
5983142	syn	GC	MMAR_4923	-		regulatory protein	serine/threonine-protein kinase PknF_2
5984352	syn	CT	MMAR_4924	-		intermediary metabolism and respiration	phosphoribosylamine-glycine ligase PurD
5988981	int	TC		127	MMAR_4928	intermediary metabolism and respiration	NAD-dependent aldehyde dehydrogenase AldA
5989002	int	CA		148	MMAR_4928	intermediary metabolism and respiration	NAD-dependent aldehyde dehydrogenase AldA
5989004	int	AC		56	MMAR_4929	conserved hypothetical	conserved hypothetical protein
5989019	int	GA		41	MMAR_4929	conserved hypothetical	conserved hypothetical protein
5989377	syn	CG	MMAR_4929	-		conserved hypothetical	conserved hypothetical protein
5993113	non	AT	MMAR_4932	-		intermediary metabolism and respiration	cytochrome P450_51B1 Cyp51B1
5993347	int	AG		5	MMAR_4933	intermediary metabolism and respiration	ferredoxin
5994003	int	CT		110	MMAR_4934	conserved hypothetical	conserved hypothetical protein
5994389	syn	CT	MMAR_4935	-		intermediary metabolism and respiration	zinc-containing alcohol dehydrogenase NAD-dependent AdhB
5996176	non	CA	MMAR_4938	-		unknown	hypothetical secreted protein
5996975	non	TC	MMAR_4938	-		unknown	hypothetical secreted protein
5997902	int	CT		110	MMAR_4939	PE/PE	PE-PGRS family protein
5998445	int	GA		-			
6003392	non	GA	MMAR_4944	-		conserved hypothetical	conserved hypothetical oxidoreductase
6004773	non	GC	MMAR_4945	-		intermediary metabolism and respiration	carbon monoxide dehydrogenase
6006199	non	GA	MMAR_4945	-		intermediary metabolism and respiration	carbon monoxide dehydrogenase
6007731	non	GT	MMAR_4947	-		conserved hypothetical	conserved hypothetical protein
6008260	syn	CT	MMAR_4948	-		conserved hypothetical	conserved protein
6009547	syn	GT	MMAR_4949	-		cell wall and cell processes	xanthine/uracil permease
6011872	non	TC	MMAR_4950	-		intermediary metabolism and respiration	arylsulfatase AtsD
6013154	int	GC		12	MMAR_4951	conserved hypothetical	conserved protein
6025271	int	AC		55	MMAR_4961	cell wall and cell processes	conserved membrane protein
6025277	int	AG		61	MMAR_4961	cell wall and cell processes	conserved membrane protein
6027785	non	CG	MMAR_4965	-		cell wall and cell processes	conserved hypothetical membrane protein
6028334	syn	GT	MMAR_4965	-		cell wall and cell processes	conserved hypothetical membrane protein
6028698	int	CT		35	MMAR_4966	cell wall and cell processes	conserved hypothetical membrane protein CpsA
6028906	syn	CT	MMAR_4966	-		cell wall and cell processes	conserved hypothetical membrane protein CpsA
6028966	syn	CA	MMAR_4966	-		cell wall and cell processes	conserved hypothetical membrane protein CpsA
6032092	non	CT	MMAR_4969	-		lipid metabolism	acyl carrier protein
6032483	syn	GA	MMAR_4970	-		lipid metabolism	acyl-coenzyme A synthetase
6033085	non	CT	MMAR_4970	-		lipid metabolism	acyl-coenzyme A synthetase
6033985	int	GC		102	MMAR_4970	lipid metabolism	acyl-coenzyme A synthetase
6034665	non	CG	MMAR_4971	-		intermediary metabolism and respiration	B-amino-7-oxononanoate synthase BioF2
6035636	syn	GC	MMAR_4972	-		lipid metabolism	enoyl-CoA hydratase EchA13_1
6035675	syn	CA	MMAR_4972	-		lipid metabolism	enoyl-CoA hydratase EchA13_1
6037948	non	GC	MMAR_4974	-		cell wall and cell processes	phosphate-transport ATP-binding protein ABC transporter PstB
6041073	syn	AG	MMAR_4975	-		cell wall and cell processes	conserved transmembrane transport protein MmpL_family
6045789	non	GA	MMAR_4982	-			MCE-family protein Mcf4F
6052041	syn	GA	MMAR_4986	-			MCE-family protein Mcf4B
6064988	non	GA	MMAR_4996	-		conserved hypothetical	conserved hypothetical protein
6075193	syn	GA	MMAR_5001	-		lipid metabolism	fatty-acid-CoA ligase FadD19_1
6076081	syn	GA	MMAR_5002	-		lipid metabolism	enoyl-CoA hydratase EchA19
6076286	syn	CT	MMAR_5002	-		lipid metabolism	enoyl-CoA hydratase EchA19
6076421	non	AG	MMAR_5002	-		lipid metabolism	enoyl-CoA hydratase EchA19
6089571	syn	CT	MMAR_5015	-		intermediary metabolism and respiration	conserved hypothetical oxidoreductase
6089694	syn	AG	MMAR_5015	-		intermediary metabolism and respiration	conserved hypothetical oxidoreductase
6090614	syn	CT	MMAR_5016	-		conserved hypothetical	conserved hypothetical protein
6093422	non	TC	MMAR_5019	-		conserved hypothetical	conserved hypothetical protein
6095072	syn	GA	MMAR_5020	-		intermediary metabolism and respiration	glutamate--cysteine ligase Gcs2
6095420	syn	GA	MMAR_5020	-		intermediary metabolism and respiration	glutamate--cysteine ligase Gcs2
6095793	non	GT	MMAR_5020	-		intermediary metabolism and respiration	glutamate--cysteine ligase Gcs2
6096209	syn	TC	MMAR_5020	-		intermediary metabolism and respiration	glutamate--cysteine ligase Gcs2
6099965	syn	GC	MMAR_5024	-		intermediary metabolism and respiration	conserved hypothetical dehydrogenase
6101382	syn	TG	MMAR_5025	-		intermediary metabolism and respiration	conserved hypothetical dehydratase (MaoC-like)
6101511	syn	CT	MMAR_5025	-		intermediary metabolism and respiration	conserved hypothetical dehydratase (MaoC-like)
6103016	int	CT		84	MMAR_5027	lipid metabolism	acyl-CoA acyltransferase (PaaJ-like) Ltp2_1
6103040	int	GT		71	MMAR_5026	conserved hypothetical	conserved hypothetical protein
6103946	syn	CT	MMAR_5027	-		lipid metabolism	acyl-CoA acyltransferase (PaaJ-like) Ltp2_1
6104272	syn	GA	MMAR_5028	-		conserved hypothetical	conserved hypothetical protein
6105321	syn	GA	MMAR_5029	-		conserved hypothetical	conserved hypothetical protein
6105386	non	CT	MMAR_5029	-		conserved hypothetical	conserved hypothetical protein
6105595	non	TC	MMAR_5029	-		conserved hypothetical	conserved hypothetical protein
6105823	syn	CA	MMAR_5030	-		lipid metabolism	acyl-CoA dehydrogenase FadE29
6106144	syn	TC	MMAR_5030	-		lipid metabolism	acyl-CoA dehydrogenase FadE29
6106909	syn	GA	MMAR_5032	-		intermediary metabolism and respiration	cytochrome P450_125A7 Cyp125A7
6108987	syn	CA	MMAR_5032	-		intermediary metabolism and respiration	cytochrome P450_125A7 Cyp125A7
6109002	syn	AG	MMAR_5032	-		intermediary metabolism and respiration	cytochrome P450_125A7 Cyp125A7
6109303	syn	GC	MMAR_5033	-		lipid metabolism	acyl-CoA acyltransferase FadA5
6110221	non	CG	MMAR_5033	-		lipid metabolism	acyl-CoA acyltransferase FadA5
6110656	non	TA	MMAR_5035	-		conserved hypothetical	conserved hypothetical protein
6112361	syn	GA	MMAR_5037	-		intermediary metabolism and respiration	short-chain type dehydrogenase/reductase
6113052	non	GT	MMAR_5037	-		intermediary metabolism and respiration	short-chain type dehydrogenase/reductase
6118368	syn	AG	MMAR_5042	-		intermediary metabolism and respiration	2-nitropropane dioxygenase
6118612	non	GC	MMAR_5042	-		intermediary metabolism and respiration	2-nitropropane dioxygenase
6119006	non	TC	MMAR_5043	-		intermediary metabolism and respiration	electron transfer protein FdxB
6120851	syn	GA	MMAR_5043	-		intermediary metabolism and respiration	electron transfer protein FdxB

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
6129058	int	TC		69	MMAR_5048	intermediary metabolism and respiration	short chain dehydrogenase
6129062	int	TC		65	MMAR_5048	intermediary metabolism and respiration	short chain dehydrogenase
6129066	-	-C		61	MMAR_5048	intermediary metabolism and respiration	short chain dehydrogenase
6129076	int	GA		51	MMAR_5048	intermediary metabolism and respiration	short chain dehydrogenase
6129436	syn	AG	MMAR_5048	-		intermediary metabolism and respiration	short chain dehydrogenase
6129441	syn	GA	MMAR_5048	-		intermediary metabolism and respiration	short chain dehydrogenase
6129451	syn	GA	MMAR_5048	-		intermediary metabolism and respiration	short chain dehydrogenase
6129898	syn	CT	MMAR_5048	-		intermediary metabolism and respiration	short chain dehydrogenase
6131490	non	CA	MMAR_5050	-		lipid metabolism	fatty-acid-CoA ligase FadD3
6131605	non	GA	MMAR_5050	-		lipid metabolism	fatty-acid-CoA ligase FadD3
6132318	syn	CT	MMAR_5050	-		lipid metabolism	fatty-acid-CoA ligase FadD3
6135324	non	CG	MMAR_5053	-		lipid metabolism	acyl-CoA dehydrogenase FadE33
6137614	non	GC	MMAR_5055	-		intermediary metabolism and respiration	arylamine N-acetyltransferase Nat
6138899	syn	AG	MMAR_5057	-		cell wall and cell processes	conserved lipoprotein DsbF
6140281	non	TA	MMAR_5059	-		cell wall and cell processes	conserved hypothetical peptidase M48 like-protein
6141737	syn	CT	MMAR_5061	-		cell wall and cell processes	conserved hypothetical secreted protein
6141877	non	AG	MMAR_5061	-		cell wall and cell processes	conserved hypothetical secreted protein
6142497	non	GA	MMAR_5062	-		intermediary metabolism and respiration	conserved hypothetical oxidase
6143777	syn	TC	MMAR_5064	-		intermediary metabolism and respiration	2-hydroxy-6-OXO-6-phenylhexa-2-4-dienoate hydrolase BphD
6144143	syn	GT	MMAR_5064	-		intermediary metabolism and respiration	2-hydroxy-6-OXO-6-phenylhexa-2-4-dienoate hydrolase BphD
6144625	syn	CA	MMAR_5065	-		intermediary metabolism and respiration	acyl-CoA dehydrogenase
6147742	non	CA	MMAR_5068	-		lipid metabolism	acyl-CoA dehydrogenase FadE34
6148322	syn	CT	MMAR_5068	-		lipid metabolism	acyl-CoA dehydrogenase FadE34
6148670	syn	GA	MMAR_5068	-		lipid metabolism	acyl-CoA dehydrogenase FadE34
6151167	non	CT	MMAR_5070	-		regulatory protein	transcriptional regulatory protein (purp family)
6153298	syn	AG	MMAR_5072	-		cell wall and cell processes	ATPase component of an ABC-type transport system
6153636	syn	AG	MMAR_5073	-		cell wall and cell processes	permease component of an ABC-type transporter
6153666	syn	AG	MMAR_5073	-		cell wall and cell processes	permease component of an ABC-type transporter
6155866	syn	TC	MMAR_5075	-		cell wall and cell processes	conserved hypothetical lipoprotein
6157197	syn	AG	MMAR_5077	-		intermediary metabolism and respiration	conserved hypothetical Zn-dependent hydrolase
6159306	syn	CT	MMAR_5079	-		information pathways	tRNA/RNA methyltransferase
6159761	non	GA	MMAR_5079	-		information pathways	tRNA/RNA methyltransferase
6160294	non	GA	MMAR_5080	-		information pathways	cysteinyl-tRNA synthetase 1 CysS1
6161971	non	CA	MMAR_5082	-		intermediary metabolism and respiration	4-diphosphocytidyl-2'-methyl-D-erythritol pyrophosphokinase IspD
6165032	syn	AG	MMAR_5085	-		information pathways	DNA repair protein RadA
6166097	syn	CT	MMAR_5086	-		information pathways	conserved hypothetical RuvA-like protein
6167491	int	CT		69	MMAR_5088	intermediary metabolism and respiration	carboxic anhydrase
6168577	syn	CA	MMAR_5089	-		information pathways	adenine glycosylase MutY
6170845	syn	GA	MMAR_5092	-		cell wall and cell processes	conserved hypothetical lipoprotein LpqF
6171565	non	GC	MMAR_5092	-		cell wall and cell processes	conserved hypothetical lipoprotein LpqF
6172523	syn	GA	MMAR_5094	-		cell wall and cell processes	conserved integral membrane transport protein
6180339	syn	GA	MMAR_5100	-		intermediary metabolism and respiration	ATP-dependent protease ATP-binding subunit ClpC1
6182501	syn	CT	MMAR_5102	-		information pathways	[lysyl]-tRNA synthetase 1 LysS
6182545	non	GA	MMAR_5102	-		information pathways	[lysyl]-tRNA synthetase 1 LysS
6184735	syn	GA	MMAR_5104	-		intermediary metabolism and respiration	aspartate 1-decarboxylase precursor PanD
6185023	syn	CG	MMAR_5105	-		intermediary metabolism and respiration	pantoate-beta-alanine ligase PanC
6187183	non	CT	MMAR_5107	-		cell wall and cell processes	conserved transmembrane protein rich in alanine, arginine and proline
6187950	non	CG	MMAR_5107	-		cell wall and cell processes	conserved transmembrane protein rich in alanine, arginine and proline
6189029	syn	CT	MMAR_5109	-		intermediary metabolism and respiration	2-amino-4-hydroxy-6-hydroxymethylidihydropteridine pyrophosphokinase FolK
6189033	non	AT	MMAR_5109	-		intermediary metabolism and respiration	2-amino-4-hydroxy-6-hydroxymethylidihydropteridine pyrophosphokinase FolK
6189527	non	GC	MMAR_5110	-		intermediary metabolism and respiration	dihydroopterin aldolase FolB
6189654	non	TC	MMAR_5111	-		intermediary metabolism and respiration	dihydroopterate synthase 1 FolP1
6192062	syn	AG	MMAR_5113	-		membrane-bound protease FtsH	
6194738	syn	GA	MMAR_5115	-		intermediary metabolism and respiration	monooxygenase
6197445	int	CT		-		intermediary metabolism and respiration	
6197915	int	TC		142	MMAR_5118	PE/PPE	PE family protein
6203718	syn	GC	MMAR_5125	-		cell wall and cell processes	cell cycle protein MesJ
6205224	non	GC	MMAR_5126	-		conserved hypotheticals	conserved hypothetical protein
6207497	syn	CT	MMAR_5128	-		intermediary metabolism and respiration	inorganic pyrophosphatase Ppa
6208220	syn	CT	MMAR_5129	-		cell wall and cell processes	conserved hypothetical membrane protein
6208806	int	AG		92	MMAR_5129	cell wall and cell processes	conserved hypothetical membrane protein
6209790	syn	GA	MMAR_5130	-		cell wall and cell processes	conserved hypothetical membrane protein
6211114	syn	GA	MMAR_5132	-		cell wall and cell processes	conserved hypothetical membrane protein
6217513	syn	AC	MMAR_5136	-		conserved hypotheticals	conserved protein
6218282	syn	GA	MMAR_5137	-		cell wall and cell processes	adenylate cyclase
6218810	syn	GA	MMAR_5137	-		cell wall and cell processes	adenylate cyclase
6223762	syn	GC	MMAR_5141	-		information pathways	DEAD/DEAH box helicase
6224673	non	GC	MMAR_5141	-		information pathways	DEAD/DEAH box helicase
6225253	syn	CA	MMAR_5141	-		information pathways	DEAD/DEAH box helicase
6226234	int	GA		90	MMAR_5142	conserved hypotheticals	conserved protein
6226515	syn	CT	MMAR_5142	-		conserved hypotheticals	conserved protein
6226575	syn	TC	MMAR_5142	-		conserved hypotheticals	conserved protein
6226880	non	GA	MMAR_5142	-		conserved hypotheticals	conserved protein
6227152	non	GA	MMAR_5142	-		conserved hypotheticals	conserved protein
6228135	non	CA	MMAR_5144	-		conserved hypotheticals	conserved hypothetical membrane protein
6228201	non	CA	MMAR_5144	-		conserved hypotheticals	conserved hypothetical membrane protein
6229227	non	AC	MMAR_5146	-		cell wall and cell processes	conserved hypothetical membrane protein
6230120	non	CT	MMAR_5147	-		conserved hypotheticals	conserved hypothetical protein
6230644	non	GA	MMAR_5147	-		conserved hypotheticals	conserved hypothetical protein
6230986	syn	GA	MMAR_5148	-		conserved hypotheticals	conserved hypothetical protein
6231693	non	GA	MMAR_5148	-		conserved hypotheticals	conserved hypothetical protein
6231971	int	TC		1	MMAR_5148	conserved hypotheticals	conserved hypothetical protein
6232091	int	CG		121	MMAR_5148	conserved hypotheticals	conserved hypothetical protein
6232267	int	GA		-		cell wall and cell processes	
6233583	non	GA	MMAR_5556	-		unknown	hypothetical protein
6236413	syn	GA	MMAR_5152	-		cell wall and cell processes	dipeptide-transport integral membrane protein ABC transporter DppC
6238594	syn	AG	MMAR_5154	-		cell wall and cell processes	periplasmic dipeptide-binding lipoprotein DppA
6240411	non	AT	MMAR_5155	-		intermediary metabolism and respiration	acetyl-coenzyme A synthetase Acs
6241593	non	AC	MMAR_5155	-		intermediary metabolism and respiration	acetyl-coenzyme A synthetase Acs
6241733	non	CG	MMAR_5155	-		intermediary metabolism and respiration	acetyl-coenzyme A synthetase Acs
6241945	syn	GA	MMAR_5155	-		intermediary metabolism and respiration	acetyl-coenzyme A synthetase Acs
6242947	syn	CT	MMAR_5157	-		cell wall and cell processes	conserved hypothetical protease
6246421	syn	CT	MMAR_5161	-		cell wall and cell processes	membrane-anchored thioredoxin-like protein
6248022	syn	CT	MMAR_5163	-		cell wall and cell processes	conserved hypothetical membrane protein

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
6248866	non	GT	MMAR_5165	-		intermediary metabolism and respiration	conserved hypothetical Zn-dependent hydrolase
6249014	syn	CT	MMAR_5165	-		intermediary metabolism and respiration	conserved hypothetical Zn-dependent hydrolase
6249671	syn	AG	MMAR_5165	-		intermediary metabolism and respiration	conserved hypothetical Zn-dependent hydrolase
6249721	syn	TC	MMAR_5166	-		intermediary metabolism and respiration	conserved protein with endoribonuclease L-PSP domain
6249910	syn	CG	MMAR_5166	-		intermediary metabolism and respiration	conserved protein with endoribonuclease L-PSP domain
6249946	syn	GA	MMAR_5166	-		intermediary metabolism and respiration	conserved protein with endoribonuclease L-PSP domain
6249988	syn	GA	MMAR_5166	-		intermediary metabolism and respiration	conserved protein with endoribonuclease L-PSP domain
6252348	syn	TC	MMAR_5169	-		intermediary metabolism and respiration	anion transporter ATPase
6253352	int	AC	MMAR_5171	93		cell wall and cell processes	bifunctional membrane-associated penicillin-binding protein 1A/1B PonA2
6253960	syn	GC		-		cell wall and cell processes	bifunctional membrane-associated penicillin-binding protein 1A/1B PonA2
6254203	syn	GC		-		cell wall and cell processes	bifunctional membrane-associated penicillin-binding protein 1A/1B PonA2
6254290	syn	CT		-		cell wall and cell processes	bifunctional membrane-associated penicillin-binding protein 1A/1B PonA2
6254860	syn	GA		-		cell wall and cell processes	bifunctional membrane-associated penicillin-binding protein 1A/1B PonA2
6255991	syn	GA	MMAR_5172	-		cell wall and cell processes	conserved membrane protein
6256663	syn	CG	MMAR_5172	-		cell wall and cell processes	conserved membrane protein
6257748	syn	CT	MMAR_5173	-		intermediary metabolism and respiration	cysteine synthase CysK
6259717	non	GC	MMAR_5175	-		intermediary metabolism and respiration	cytochrome P450 137A2 Cyp137A2
6260574	syn	GA	MMAR_5177	-		cell wall and cell processes	conserved hypothetical membrane protein
6275988	int	GC	MMAR_5193	48		conserved hypotheticals	conserved hypothetical protein
6276357	syn	G-		-		intermediary metabolism and respiration	formate dehydrogenase alpha subunit selenocysteine-containing
6277180	syn	GA		-		intermediary metabolism and respiration	formate dehydrogenase beta subunit selenocysteine-containing
6278146	syn	CT	MMAR_5195	-		intermediary metabolism and respiration	formate dehydrogenase alpha subunit selenocysteine-containing
6282690	syn	GC	MMAR_5199	-		cell wall and cell processes	conserved membrane protein
6282902	non	AC	MMAR_5199	-		cell wall and cell processes	conserved membrane protein
6284994	syn	TC	MMAR_5202	-		regulatory proteins	methanol dehydrogenase transcriptional regulatory protein MoxR
6289082	int	CT	MMAR_5206	92		regulatory proteins	PadR-like transcriptional regulatory protein
6289132	int	CT		92	MMAR_5205	cell wall and cell processes	conserved hypothetical membrane protein
6289133	int	TC		93	MMAR_5205	cell wall and cell processes	conserved hypothetical membrane protein
6293483	syn	CT	MMAR_5208	-		intermediary metabolism and respiration	glycerol kinase Gpk
6294098	syn	AG	MMAR_5208	-		intermediary metabolism and respiration	glycerol kinase Gpk
6294885	syn	AG	MMAR_5209	-		conserved hypotheticals	conserved hypothetical protein
6294942	syn	CG	MMAR_5209	-		conserved hypotheticals	conserved hypothetical protein
6295071	syn	AG	MMAR_5209	-		conserved hypotheticals	conserved hypothetical protein
6295385	non	AG	MMAR_5209	-		conserved hypotheticals	conserved hypothetical protein
6295404	syn	GC	MMAR_5209	-		conserved hypotheticals	conserved hypothetical protein
6295584	non	GA	MMAR_5209	-		conserved hypotheticals	conserved hypothetical protein
6295706	non	CG	MMAR_5209	-		conserved hypotheticals	conserved hypothetical protein
6298890	syn	GA	MMAR_5213	-		conserved hypotheticals	conserved hypothetical protein
6299099	syn	GT	MMAR_5213	-		conserved hypotheticals	conserved hypothetical protein
6302073	non	CT	MMAR_5216	-		cell wall and cell processes	conserved hypothetical secreted protein
6302853	syn	CT	MMAR_5217	-		catalase KatE	
6304260	int	GC	MMAR_5217	106		catalase KatE	
6305468	syn	CT		-		cell wall and cell processes	conserved hypothetical secreted protein
6305718	non	GC		-		cell wall and cell processes	conserved hypothetical secreted protein
6306167	syn	GT		-		cell wall and cell processes	conserved hypothetical secreted protein
6306356	syn	CT		-		cell wall and cell processes	conserved hypothetical secreted protein
6306438	non	GA		-		cell wall and cell processes	conserved hypothetical secreted protein
6306445	non	CA		-		cell wall and cell processes	conserved hypothetical secreted protein
6307215	syn	GC	MMAR_5221	-		intermediary metabolism and respiration	aspartate-semialdehyde dehydrogenase Asd
6315887	non	CG	MMAR_5225	-		intermediary metabolism and respiration	2-isopropylmalate synthase LeuA
6318140	non	TC	MMAR_5227	-		cell wall and cell processes	conserved hypothetical membrane protein
6318508	syn	GA	MMAR_5228	-		information pathways	DNA polymerase III (epsilon subunit) DnaQ
6318846	non	CT	MMAR_5228	-		information pathways	DNA polymerase III (epsilon subunit) DnaQ
6319996	non	CA	MMAR_5229	-		cell wall and cell processes	UDP-N-acetylglucosamine tripeptidase synthase
6321668	non	AC	MMAR_5231	-		information pathways	recombination protein RecR
6323913	syn	CG	MMAR_5235	-		intermediary metabolism and respiration	conserved hypothetical dehydrogenase
6324009	syn	AG	MMAR_5235	-		intermediary metabolism and respiration	conserved hypothetical dehydrogenase
6324066	syn	TC	MMAR_5235	-		intermediary metabolism and respiration	conserved hypothetical dehydrogenase
6324124	non	AG	MMAR_5235	-		intermediary metabolism and respiration	conserved hypothetical dehydrogenase
6324162	syn	TC	MMAR_5235	-		intermediary metabolism and respiration	conserved hypothetical dehydrogenase
6324760	non	GA	MMAR_5235	-		intermediary metabolism and respiration	conserved hypothetical dehydrogenase
6324798	syn	TC	MMAR_5235	-		intermediary metabolism and respiration	conserved hypothetical dehydrogenase
6326569	non	GA	MMAR_5237	-		cell wall and cell processes	conserved hypothetical membrane protein
6330536	syn	GA	MMAR_5241	-		regulatory proteins	conserved transcriptional regulator
6330653	syn	CG	MMAR_5241	-		regulatory proteins	conserved transcriptional regulator
6330698	syn	GT	MMAR_5241	-		regulatory proteins	conserved transcriptional regulator
6330848	syn	GA	MMAR_5241	-		regulatory proteins	conserved transcriptional regulator
6331660	non	GC	MMAR_5242	-		cell wall and cell processes	conserved membrane protein
6331681	syn	CA	MMAR_5242	-		cell wall and cell processes	conserved membrane protein
6331858	syn	GA	MMAR_5242	-		cell wall and cell processes	conserved membrane protein
6332820	syn	CT	MMAR_5243	-		lipid metabolism	enoyl-CoA hydratase EchA3
6333336	syn	CG	MMAR_5244	-		cell wall and cell processes	19 kDa lipoprotein antigen precursor LpqH-like
6333504	syn	CT	MMAR_5244	-		cell wall and cell processes	19 kDa lipoprotein antigen precursor LpqH-like
6333807	non	TG	MMAR_5245	-		conserved hypotheticals	conserved hypothetical protein
6333971	syn	CT	MMAR_5245	-		conserved hypotheticals	conserved hypothetical protein
6334045	non	GA	MMAR_5245	-		conserved hypotheticals	conserved hypothetical protein
6334108	non	AG	MMAR_5245	-		conserved hypotheticals	conserved hypothetical protein
6334382	syn	GC	MMAR_5245	-		conserved hypotheticals	conserved hypothetical protein
6334436	non	AT	MMAR_5245	-		conserved hypotheticals	conserved hypothetical protein
6334524	non	CG	MMAR_5245	-		conserved hypotheticals	conserved hypothetical protein
6334618	non	CT	MMAR_5245	-		conserved hypotheticals	conserved hypothetical protein
6334709	syn	AG	MMAR_5245	-		conserved hypotheticals	conserved hypothetical protein
6335192	syn	TG	MMAR_5245	-		conserved hypotheticals	conserved hypothetical protein
6335354	syn	GT	MMAR_5245	-		conserved hypotheticals	conserved hypothetical protein
6336281	non	AG	MMAR_5246	-		conserved hypotheticals	conserved hypothetical protein
6336656	syn	AG	MMAR_5246	-		conserved hypotheticals	conserved hypothetical protein
6336869	syn	TC	MMAR_5247	-		conserved hypotheticals	conserved hypothetical protein
6337064	syn	CT	MMAR_5247	-		conserved hypotheticals	conserved hypothetical protein
6337397	non	GT	MMAR_5248	-		conserved hypotheticals	conserved hypothetical protein
6337639	non	AG	MMAR_5248	-		conserved hypotheticals	conserved hypothetical protein
6337758	non	GT	MMAR_5248	-		conserved hypotheticals	conserved hypothetical protein
6337777	syn	CG	MMAR_5248	-		conserved hypotheticals	conserved hypothetical protein
6337919	non	GA	MMAR_5248	-		conserved hypotheticals	conserved hypothetical protein
6337978	syn	CT	MMAR_5248	-		conserved hypotheticals	conserved hypothetical protein
6338159	non	CG	MMAR_5248	-		conserved hypotheticals	conserved hypothetical protein

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
6338260	syn	TC	MMAR_5248	-		conserved hypotheticals	conserved hypothetical protein
6338320	syn	AG	MMAR_5248	-		conserved hypotheticals	conserved hypothetical protein
6338507	syn	CT	MMAR_5248	-		conserved hypotheticals	conserved hypothetical protein
6338539	syn	GA	MMAR_5248	-		conserved hypotheticals	conserved hypothetical protein
6338551	syn	GA	MMAR_5248	-		conserved hypotheticals	conserved hypothetical protein
6338638	syn	CT	MMAR_5248	-		conserved hypotheticals	conserved hypothetical protein
6338675	syn	CT	MMAR_5248	-		conserved hypotheticals	conserved hypothetical protein
6338733	syn	CT	MMAR_5249	-		conserved hypotheticals	conserved hypothetical protein
6339246	syn	CT	MMAR_5249	-		conserved hypotheticals	conserved hypothetical protein
6339265	non	GA	MMAR_5249	-		conserved hypotheticals	conserved hypothetical protein
6339826	non	GA	MMAR_5249	-		conserved hypotheticals	conserved hypothetical protein
6339867	int	GA		24	MMAR_5249	conserved hypotheticals	conserved hypothetical protein
6365715	int	TC		13	MMAR_5275	lipid metabolism	long-chain-fatty-acid-CoA ligase FadD15_1
6366643	syn	CG	MMAR_5275	-		lipid metabolism	long-chain-fatty-acid-CoA ligase FadD15_1
6366826	syn	GA	MMAR_5275	-		lipid metabolism	long-chain-fatty-acid-CoA ligase FadD15_1
6366967	syn	GA	MMAR_5275	-		lipid metabolism	long-chain-fatty-acid-CoA ligase FadD15_1
6367691	int	CT		100	MMAR_5276	regulatory protein	transcriptional regulatory protein (probably AraC/XylS-family)
6368880	int	CA		70	MMAR_5276	regulatory protein	transcriptional regulatory protein (probably AraC/XylS-family)
6371398	non	CT	MMAR_5278	-		cell wall and cell processes	conserved hypothetical membrane protein
6371649	syn	AG	MMAR_5279	-		intermediary metabolism and respiration	monoxygenase-like flavoprotein
6373536	non	CT	MMAR_5280	-		conserved hypotheticals	conserved hypothetical protein
6374292	non	GA	MMAR_5280	-		conserved hypotheticals	conserved hypothetical protein
6374394	syn	CT	MMAR_5280	-		conserved hypotheticals	conserved hypothetical protein
6374485	syn	TC	MMAR_5281	-		lipid metabolism	short chain dehydrogenase
6374494	syn	TC	MMAR_5281	-		lipid metabolism	short chain dehydrogenase
6375159	non	CG	MMAR_5281	-		lipid metabolism	short chain dehydrogenase
6375635	non	CT	MMAR_5282	-		intermediary metabolism and respiration	D-3-PHOSPHOGLYCERATE dehydrogenase SerA4
6375771	syn	CG	MMAR_5282	-		intermediary metabolism and respiration	D-3-PHOSPHOGLYCERATE dehydrogenase SerA4
6376170	syn	CG	MMAR_5282	-		intermediary metabolism and respiration	D-3-PHOSPHOGLYCERATE dehydrogenase SerA4
6376251	syn	CA	MMAR_5282	-		intermediary metabolism and respiration	D-3-PHOSPHOGLYCERATE dehydrogenase SerA4
6376657	syn	CA	MMAR_5283	-		lipid metabolism	non-ribosomal peptide synthetase
6376819	syn	GA	MMAR_5283	-		lipid metabolism	non-ribosomal peptide synthetase
6377584	syn	CT	MMAR_5283	-		lipid metabolism	non-ribosomal peptide synthetase
6382083	int	CA		44	MMAR_5286	PE/PE	PE family protein
6387383	non	AG	MMAR_5291	-		cell wall and cell processes	conserved hypothetical membrane protein
6387919	int	GA		59	MMAR_5292	conserved hypotheticals	conserved hypothetical protein
6396390	syn	TA	MMAR_5295	-		intermediary metabolism and respiration	cytidine/deoxycytidine deaminase
6396932	syn	GA	MMAR_5296	-		conserved hypotheticals	conserved protein
6397553	non	AC	MMAR_5297	-		intermediary metabolism and respiration	prephenate dehydrogenase TyrA
6397983	syn	GT	MMAR_5297	-		intermediary metabolism and respiration	prephenate dehydrogenase TyrA
6398085	syn	CT	MMAR_5297	-		intermediary metabolism and respiration	prephenate dehydrogenase TyrA
6400975	non	CG	MMAR_5301	-			osmoprotectant transport ATP-binding protein ABC transporter ProV
6403769	syn	GA	MMAR_5304	-		lipid metabolism	acyl-CoA dehydrogenase FadE36
6404592	syn	CT	MMAR_5305	-		conserved hypotheticals	conserved hypothetical protein
6404717	non	GC	MMAR_5305	-		conserved hypotheticals	conserved hypothetical protein
6404767	int	CT		5	MMAR_5305	conserved hypotheticals	conserved hypothetical protein
6404932	int	TC					
6416782	syn	CT	MMAR_5310	-		intermediary metabolism and respiration	short-chain type dehydrogenase/reductase
6416787	non	GA	MMAR_5310	-		intermediary metabolism and respiration	short-chain type dehydrogenase/reductase
6417085	syn	TC	MMAR_5310	-		intermediary metabolism and respiration	short-chain type dehydrogenase/reductase
6417494	non	AC	MMAR_5311	-		lipid metabolism	acyl-CoA dehydrogenase FadE1_1
6430474	syn	GA	MMAR_5323	-		intermediary metabolism and respiration	O-methyltransferase
6430479	non	CT	MMAR_5323	-		intermediary metabolism and respiration	O-methyltransferase
6432510	int	GA		59	MMAR_5325	conserved hypotheticals	conserved hypothetical protein
6432534	int	AG		83	MMAR_5325	conserved hypotheticals	conserved hypothetical protein
6432554	int	GA		103	MMAR_5325	conserved hypotheticals	conserved hypothetical protein
6433139	syn	CG	MMAR_5326	-		intermediary metabolism and respiration	histidinol-phosphate aminotransferase HisC2
6433223	syn	CT	MMAR_5326	-		intermediary metabolism and respiration	histidinol-phosphate aminotransferase HisC2
6435103	syn	AG	MMAR_5329	-		intermediary metabolism and respiration	enoyl-CoA hydratase EchA21
6435517	syn	TG	MMAR_5329	-		intermediary metabolism and respiration	enoyl-CoA hydratase EchA21
6440346	syn	GA	MMAR_5332	-		intermediary metabolism and respiration	oxidoreductase
6440876	int	GA		35	MMAR_5333	intermediary metabolism and respiration	aminotransferase
6441153	syn	GA	MMAR_5333	-		intermediary metabolism and respiration	aminotransferase
6441535	syn	CG	MMAR_5333	-		intermediary metabolism and respiration	aminotransferase
6444433	syn	CT	MMAR_5335	-		conserved hypotheticals	conserved protein
6445559	non	AG	MMAR_5336	-		cell wall and cell processes	O-antigen/lipopolysaccharide transport ATP-binding protein ABC transporter RfbE
6457723	syn	CA	MMAR_5345	-		conserved hypotheticals	conserved hypothetical protein
6462102	non	AG	MMAR_5349	-		conserved hypotheticals	conserved hypothetical protein
6462842	syn	GA	MMAR_5350	-		conserved hypotheticals	conserved hypothetical protein
6467197	non	AG	MMAR_5354	-		cell wall and cell processes	conserved hypothetical transmembrane protein
6467322	syn	GT	MMAR_5354	-		cell wall and cell processes	conserved hypothetical transmembrane protein
6467557	non	CA	MMAR_5354	-		cell wall and cell processes	conserved hypothetical transmembrane protein
6467565	syn	GA	MMAR_5354	-		cell wall and cell processes	conserved hypothetical transmembrane protein
6468116	syn	CT	MMAR_5355	-		cell wall and cell processes	integral membrane indolylaceteyltransferase EmbC
6468497	syn	TC	MMAR_5355	-		cell wall and cell processes	integral membrane indolylaceteyltransferase EmbC
6468782	syn	GA	MMAR_5355	-		cell wall and cell processes	integral membrane indolylaceteyltransferase EmbC
6469154	syn	CT	MMAR_5355	-		cell wall and cell processes	integral membrane indolylaceteyltransferase EmbC
6469664	syn	TA	MMAR_5355	-		cell wall and cell processes	integral membrane indolylaceteyltransferase EmbC
6470112	non	AG	MMAR_5355	-		cell wall and cell processes	integral membrane indolylaceteyltransferase EmbC
6473548	syn	GT	MMAR_5356	-		cell wall and cell processes	integral membrane indolylaceteyltransferase EmbA
6474016	syn	CT	MMAR_5356	-		cell wall and cell processes	integral membrane indolylaceteyltransferase EmbA
6474687	syn	CT	MMAR_5357	-		cell wall and cell processes	integral membrane indolylaceteyltransferase EmbB
6475452	syn	CT	MMAR_5357	-		cell wall and cell processes	integral membrane indolylaceteyltransferase EmbB
6476758	non	GC	MMAR_5357	-		cell wall and cell processes	integral membrane indolylaceteyltransferase EmbC
6477749	syn	CT	MMAR_5357	-		cell wall and cell processes	integral membrane indolylaceteyltransferase EmbB
6477744	syn	AG	MMAR_5357	-		cell wall and cell processes	integral membrane indolylaceteyltransferase EmbB
6479404	syn	TC	MMAR_5359	-		cell wall and cell processes	conserved hypothetical secreted protein
6479658	non	AG	MMAR_5359	-		cell wall and cell processes	conserved hypothetical secreted protein
6479700	non	GA	MMAR_5359	-		cell wall and cell processes	conserved hypothetical secreted protein
6482328	int	CG	MMAR_5361	-		lipid metabolism	acyl-CoA dehydrogenase FadE35
6482569	int	GT		99	MMAR_5361	lipid metabolism	acyl-CoA dehydrogenase FadE35
6489269	syn	GC	MMAR_5363	-		lipid metabolism	propionyl-CoA carboxylase beta chain 4 AccD4_1
6490327	syn	CT	MMAR_5364	-		lipid metabolism	polyketide synthase Pks13
6490885	syn	GT	MMAR_5364	-		lipid metabolism	polyketide synthase Pks13

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
6492164	non	GT	MMAR_5364	-		lipid metabolism	polyketide synthase Pks13
6493452	non	CG	MMAR_5364	-		lipid metabolism	polyketide synthase Pks13
6495112	syn	GC	MMAR_5364	-		lipid metabolism	polyketide synthase Pks13
6495536	syn	GA	MMAR_5365	-		lipid metabolism	fatty acyl-AMP ligase FadD32
6496112	syn	CA	MMAR_5365	-		lipid metabolism	fatty acyl-AMP ligase FadD32
6496130	syn	CT	MMAR_5365	-		lipid metabolism	fatty acyl-AMP ligase FadD32
6496553	syn	GA	MMAR_5365	-		lipid metabolism	fatty acyl-AMP ligase FadD32
6498801	int	GA	11 MMAR_5367	cell wall and cell processes		secreted MptS1/MptS1 antigen protein FbpD	
6499130	syn	GA		cell wall and cell processes		secreted MptS1/MptS1 antigen protein FbpD	
6500127	syn	GA		cell wall and cell processes		secreted antigen 85-A FbpA	
6500535	syn	GA		cell wall and cell processes		secreted antigen 85-A FbpA	
6500731	non	GA		cell wall and cell processes		secreted antigen 85-A FbpA	
6500864	non	GA		cell wall and cell processes		secreted antigen 85-A FbpA	
6501040	int	GA		cell wall and cell processes		secreted antigen 85-A FbpA	
6505972	syn	CT	MMAR_5372	-		intermediary metabolism and respiration	bifunctional UDP-galactofuranosyl transferase GifT
6514539	syn	GA	MMAR_5380	-		intermediary metabolism and respiration	phosphotransferase
6514710	syn	TC	MMAR_5380	-		intermediary metabolism and respiration	phosphotransferase
6514835	syn	G-	MMAR_5380	-		intermediary metabolism and respiration	phosphotransferase
6515272	non	GA	MMAR_5381	-		conserved hypothetical	UDP-MurNAc hydroxylase NamH
6515598	syn	GA	MMAR_5381	-		conserved hypothetical	UDP-MurNAc hydroxylase NamH
6516557	syn	CG	MMAR_5382	-		conserved hypothetical	conserved hypothetical protein
6519320	non	GT	MMAR_5385	-		cell wall and cell processes	conserved hypothetical membrane protein
6520516	non	TG	MMAR_5386	-		information pathways	seryl-tRNA synthetase SerS
6521897	non	CA	MMAR_5387	-		cell wall and cell processes	conserved hypothetical membrane protein
6524084	syn	AG	MMAR_5390	-		intermediary metabolism and respiration	prephenate dehydratase PheA
6527069	syn	CT	MMAR_5393	-		intermediary metabolism and respiration	bacterioferritin BfrB
6528508	syn	GA	MMAR_5395	-		cell wall and cell processes	conserved hypothetical transmembrane protein
6528866	syn	GA	MMAR_5395	-		cell wall and cell processes	conserved hypothetical transmembrane protein
6531025	int	TC	122 MMAR_5397	cell wall and cell processes		conserved hypothetical membrane protein	conserved hypothetical membrane protein
6535879	syn	GT		-		intermediary metabolism and respiration	monooxygenase EthA
6535924	non	GC		-		intermediary metabolism and respiration	monooxygenase EthA
6536533	syn	GT		-		intermediary metabolism and respiration	monooxygenase EthA
6536572	syn	GT		-		intermediary metabolism and respiration	monooxygenase EthA
6536613	non	TA		-		intermediary metabolism and respiration	monooxygenase EthA
6537702	syn	GA		-		regulatory protein	transcriptional regulatory repressor protein (TetR-family) EthR
6539564	syn	GC	MMAR_5407	-		conserved hypothetical	conserved hypothetical PHP domain protein
6540186	syn	AC	MMAR_5408	-		cell wall and cell processes	conserved hypothetical membrane protein
6540195	syn	GT	MMAR_5408	-		cell wall and cell processes	conserved hypothetical membrane protein
6540435	syn	CG	MMAR_5408	-		cell wall and cell processes	conserved hypothetical membrane protein
6540897	non	AG	MMAR_5548	-		cell wall and cell processes	conserved hypothetical secreted protein
6542032	non	GA	MMAR_5410	-		conserved hypothetical	conserved hypothetical protein
6542374	syn	AC	MMAR_5410	-		conserved hypothetical	conserved hypothetical protein
6543007	int	CT	107 MMAR_5411	conserved hypothetical		conserved hypothetical protein	conserved hypothetical protein
6543045	int	CT		conserved hypothetical		conserved hypothetical protein	conserved hypothetical protein
6544486	non	CG		-		intermediary metabolism and respiration	NADH-dependent glutamate synthase (small subunit) GltD
6546989	syn	GC		-		intermediary metabolism and respiration	ferredoxin-dependent glutamate synthase [NADPH] (large subunit) GltB
6547250	syn	CA		-		intermediary metabolism and respiration	ferredoxin-dependent glutamate synthase [NADPH] (large subunit) GltB
6547352	syn	GA		-		intermediary metabolism and respiration	ferredoxin-dependent glutamate synthase [NADPH] (large subunit) GltB
6547619	syn	AG		-		intermediary metabolism and respiration	ferredoxin-dependent glutamate synthase [NADPH] (large subunit) GltB
6547736	syn	GA		-		intermediary metabolism and respiration	ferredoxin-dependent glutamate synthase [NADPH] (large subunit) GltB
6548019	non	GC		-		intermediary metabolism and respiration	ferredoxin-dependent glutamate synthase [NADPH] (large subunit) GltB
6548738	syn	AT		-		intermediary metabolism and respiration	ferredoxin-dependent glutamate synthase [NADPH] (large subunit) GltB
6548993	syn	CT		-		intermediary metabolism and respiration	ferredoxin-dependent glutamate synthase [NADPH] (large subunit) GltB
6550502	int	TC		-		intermediary metabolism and respiration	ferredoxin-dependent glutamate synthase [NADPH] (large subunit) GltB
6551175	int	TC	127 MMAR_5413	intermediary metabolism and respiration		ferredoxin-dependent glutamate synthase [NADPH] (large subunit) GltB	
6593288	syn	GC		-		cell wall and cell processes	conserved hypothetical alanine and proline rich membrane protein
6594257	syn	AG		-		cell wall and cell processes	conserved hypothetical alanine and proline rich membrane protein
6595715	non	AC		-		cell wall and cell processes	conserved hypothetical transmembrane protein
6596147	int	CT		-		cell wall and cell processes	conserved hypothetical transmembrane protein
6596815	non	GT		-		cell wall and cell processes	conserved hypothetical alanine rich secreted protein
6597714	non	CG		-		cell wall and cell processes	conserved hypothetical transmembrane protein
6606558	int	TC		-		cell wall and cell processes	C-term conserved hypothetical membrane protein pseudogene
6612119	non	CT		-		ADP-ribosyltransferase	ADP-ribosyltransferase
6612127	non	GC		-		ADP-ribosyltransferase	ADP-ribosyltransferase
6612129	non	CA		-		ADP-ribosyltransferase	ADP-ribosyltransferase
6612398	syn	TC	MMAR_5465	-		cell wall and cell processes	EsaT'-like protein EsxE
6612426	non	CT	MMAR_5465	-		cell wall and cell processes	EsaT'-like protein EsxE
6612718	non	CT	MMAR_5466	-		cell wall and cell processes	EsaT'-like protein EsxF
6612761	non	TC	MMAR_5466	-		cell wall and cell processes	EsaT'-like protein EsxF
6614139	syn	CT	MMAR_5468	-		conserved hypothetical	conserved hypothetical protein
6615113	syn	AG	MMAR_5468	-		conserved hypothetical	conserved hypothetical protein
6615308	syn	GA	MMAR_5468	-		conserved hypothetical	conserved hypothetical protein
6615364	non	TC	MMAR_5468	-		conserved hypothetical	conserved hypothetical protein
6615655	int	CA	107 MMAR_5468	conserved hypothetical		conserved hypothetical	conserved hypothetical protein
6615893	non	TC		-		conserved hypothetical	conserved hypothetical protein
6616747	non	GA		-		conserved hypothetical	conserved hypothetical protein
6617112	syn	CT		-		information pathways	poly(A) polymerase PcaN
6618129	syn	CG	MMAR_5471	-		information pathways	poly(A) polymerase PcaN
6619555	syn	GA	MMAR_5473	-		cell wall and cell processes	conserved hypothetical secreted protein
6620183	non	CG	MMAR_5473	-		cell wall and cell processes	conserved hypothetical secreted protein
6621978	syn	CG	MMAR_5474	-		cell wall and cell processes	conserved transmembrane protein
6622287	syn	CG	MMAR_5474	-		cell wall and cell processes	conserved transmembrane protein
6623716	non	CT	MMAR_5474	-		cell wall and cell processes	conserved transmembrane protein
6625250	syn	CT	MMAR_5475	-		information pathways	alternative RNA polymerase sigma factor SigM
6625262	non	GA	MMAR_5475	-		information pathways	alternative RNA polymerase sigma factor SigM
6627052	non	GC	MMAR_5477	-		intermediary metabolism and respiration	thioredoxin reductase TrxB2
6630312	int	CG	60 MMAR_5480	conserved hypothetical		conserved hypothetical	conserved hypothetical protein
6630317	syn	GC		-		cell wall and cell processes	chromosome partitioning protein ParB
6630694	syn	GA		-		cell wall and cell processes	chromosome partitioning protein ParB
6631215	syn	TC		-		cell wall and cell processes	chromosome partitioning protein ParB
6633331	syn	AG	MMAR_5483	-		cell wall and cell processes	glucose-inhibited division protein B Gid
6633732	syn	GA	MMAR_5484	-		conserved hypothetical	conserved protein
6634358	non	GA	MMAR_5485	-		cell wall and cell processes	conserved transmembrane protein
6634421	non	TC	MMAR_5485	-		cell wall and cell processes	conserved transmembrane protein
6636756	int	AG	-		conserved hypothetical	conserved transmembrane protein	

Table 8 (b)

Core SNPs - Reference M. ulcerans Agy99

Notes: 1. SNP types, syn: synonymous SNP, non:non-synonymous SNP, int: Intergenic SNP
 2. Gap for intergenic SNPs: nearest CDS within 150bp of snpos
 3. Functional groups from genbank reference CP000325

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
1329	syn	AG	MUL_0001	-		information pathways	chromosomal replication initiator protein DnaA
5565	syn	CT	MUL_0005	-		information pathways	DNA gyrase (subunit B) GyrB
8578	syn	GC	MUL_0006	-		information pathways	DNA gyrase (subunit A) GyrA
8618	syn	TC	MUL_0006	-		information pathways	DNA gyrase (subunit A) GyrA
8692	syn	CT	MUL_0006	-		information pathways	DNA gyrase (subunit A) GyrA
9215	syn	TC	MUL_0006	-		information pathways	DNA gyrase (subunit A) GyrA
9391	syn	TC	MUL_0006	-		information pathways	DNA gyrase (subunit A) GyrA
11257	int	TC		104	MUL_0010	conserved hypothetical	conserved hypothetical protein
11263	int	GA		98	MUL_0010	conserved hypothetical	conserved hypothetical protein
11278	int	TC		83	MUL_0010	conserved hypothetical	conserved hypothetical protein
11364	non	AG	MUL_0010	-		conserved hypothetical	conserved hypothetical protein
11987	syn	CG	MUL_0010	-		conserved hypothetical	conserved hypothetical protein
12187	non	AG	MUL_0010	-		conserved hypothetical	conserved hypothetical protein
12426	syn	AC	MUL_0011	-		regulatory proteins	transcriptional regulator
12595	non	AG	MUL_0011	-		regulatory proteins	transcriptional regulator
13054	int	AG		68	MUL_0011	regulatory proteins	transcriptional regulator
13368	non	GC	MUL_0012	-		conserved hypothetical	conserved hypothetical protein
14359	non	CG	MUL_0014	-		cell wall and cell processes	conserved hypothetical membrane protein
14454	syn	AC	MUL_0014	-		cell wall and cell processes	conserved hypothetical membrane protein
16303	syn	GC	MUL_0017	-		intermediary metabolism and respiration	anthranilate synthase component II TrpG
16306	syn	GC	MUL_0017	-		intermediary metabolism and respiration	anthranilate synthase component II TrpG
17181	syn	CT	MUL_0018	-		regulatory proteins	serine/threonine-protein kinase B PknB
17646	syn	TC	MUL_0018	-		regulatory proteins	serine/threonine-protein kinase B PknB
17649	syn	CG	MUL_0018	-		regulatory proteins	serine/threonine-protein kinase B PknB
18695	syn	AG	MUL_0019	-		regulatory proteins	serine/threonine-protein kinase A PknA
20911	syn	GC	MUL_0020	-		cell wall and cell processes	penicillin-binding protein PbpA
21411	syn	TA	MUL_0021	-		cell wall and cell processes	cell division protein RodA
21903	syn	GC	MUL_0021	-		cell wall and cell processes	cell division protein RodA
29869	non	AG	MUL_0028	-		intermediary metabolism and respiration	shortchain dehydrogenase
30025	syn	TG	MUL_0028	-		intermediary metabolism and respiration	shortchain dehydrogenase
31675	psd	GA	MUL_0030	-		conserved hypothetical	C-term conserved hypothetical secreted protein_pseudogene
31983	psd	AG	MUL_0030	-		conserved hypothetical	N-term conserved hypothetical secreted protein_pseudogene
32045	psd	GA	MUL_0030	-		conserved hypothetical	N-term conserved hypothetical secreted protein_pseudogene
32324	non	CT	MUL_0032	-		cell wall and cell processes	conserved hypothetical membrane protein
32650	non	AG	MUL_0032	-		cell wall and cell processes	conserved hypothetical membrane protein
32673	non	TC	MUL_0032	-		cell wall and cell processes	conserved hypothetical membrane protein
32725	non	TC	MUL_0032	-		cell wall and cell processes	conserved hypothetical membrane protein
34774	syn	CG	MUL_0034	-		cell wall and cell processes	ABC transporter permease
46132	int	-CT		63	MUL_0049	conserved hypothetical	conserved hypothetical secreted protein
46170	syn	TC	MUL_0050	-		conserved hypothetical	conserved hypothetical protein
48778	syn	TC	MUL_0052	-		conserved hypothetical	conserved hypothetical protein
52596	syn	AC	MUL_0055	-		information pathways	leucyl-tRNA synthetase LeuS
53064	syn	TC	MUL_0055	-		information pathways	leucyl-tRNA synthetase LeuS
54402	syn	TC	MUL_0056	-		information pathways	leucyl-tRNA synthetase LeuS
54747	int	CT		21	MUL_0056	information pathways	leucyl-tRNA synthetase LeuS
54826	non	TG	MUL_0057	-		intermediary metabolism and respiration	short-chain-type oxidoreductase
55626	non	TC	MUL_0058	-		regulatory proteins	transcriptional regulatory protein
55699	non	TC	MUL_0058	-		regulatory proteins	transcriptional regulatory protein
56193	psd	AG	MUL_0059	-		cell wall and cell processes	C-term glutamine ABC transporter ATP-binding protein_pseudogene
56922	psd	GC	MUL_0060	-		cell wall and cell processes	C-term ABC transporter permease protein GinQ_pseudogene
57079	psd	GC	MUL_0060	-		cell wall and cell processes	C-term ABC transporter permease protein GinQ_pseudogene
57751	psd	CT	MUL_0060	-		cell wall and cell processes	N-term ABC transporter permease protein GinQ_pseudogene
60315	psd	CT		17	MUL_0062	intermediary metabolism and respiration	oxidoreductase
60530	syn	CGT	MUL_0063	-		lipid metabolism	hydrolase
62701	syn	AG	MUL_0065	-		conserved hypothetical	conserved hypothetical protein
67335	syn	AC	MUL_0069	-		cell wall and cell processes	conserved hypothetical transmembrane protein
67341	syn	AC	MUL_0069	-		cell wall and cell processes	conserved hypothetical transmembrane protein
67359	syn	AG	MUL_0069	-		cell wall and cell processes	conserved hypothetical transmembrane protein
69999	syn	GA	MUL_0072	-		information pathways	single-strand binding protein Ssb
71622	int	AG		121	MUL_0075	information pathways	replicative DNA helicase DnaB
72429	syn	GC	MUL_0075	-		information pathways	replicative DNA helicase DnaB
78859	psd	CT	MUL_0082	-		cell wall and cell processes	C-term integral membrane efflux protein EmrB_pseudogene
78986	psd	CG	MUL_0082	-		cell wall and cell processes	C-term integral membrane efflux protein EmrB_pseudogene
79082	psd	AG	MUL_0082	-		cell wall and cell processes	C-term integral membrane efflux protein EmrB_pseudogene
79321	psd	AG	MUL_0082	-		cell wall and cell processes	N-term integral membrane efflux protein EmrB_pseudogene
79321	psd	AG	MUL_0082	-		cell wall and cell processes	C-term integral membrane efflux protein EmrB_pseudogene
79540	psd	AC	MUL_0082	-		cell wall and cell processes	N-term integral membrane efflux protein EmrB_pseudogene
79540	psd	AC	MUL_0082	-		cell wall and cell processes	C-term integral membrane efflux protein EmrB_pseudogene
80960	syn	TG	MUL_0084	-		conserved hypothetical	conserved hypothetical protein
87012	syn	GC	MUL_0089	-		conserved hypothetical	conserved hypothetical protein
88964	non	CT	MUL_0091	-		cell wall and cell processes	L-rhamnosyltransferase
90090	syn	AG	MUL_0093	-		conserved hypothetical	conserved protein
92988	syn	CG	MUL_0095	-		intermediary metabolism and respiration	aminotransferase
93370	syn	TC	MUL_0095	-		intermediary metabolism and respiration	aminotransferase
93647	int	TC		35	MUL_0095	intermediary metabolism and respiration	aminotransferase
94177	syn	TC	MUL_0096	-		intermediary metabolism and respiration	oxidoreductase
106747	psd	AG	MUL_0107	-		cell wall and cell processes	N-term ethanolamine transporter_pseudogene
110160	non	TC	MUL_0110	-		cell wall and cell processes	protein containing VWA domain
110299	syn	CG	MUL_0110	-		cell wall and cell processes	protein containing VWA domain
111341	non	AG	MUL_0111	-		intermediary metabolism and respiration	membrane oxidoreductase
113092	non	CT	MUL_0113	-		conserved hypothetical	conserved hypothetical protein
113248	non	AC	MUL_0113	-		conserved hypothetical	conserved hypothetical protein

SNP position	SNP type	Nucleotide change <ref><snp>	Distance to nearest locus	Nearby Locus	Functional group	Product
114579	syn	AG	MUL_0115	-	intermediary metabolism and respiration	carbon monoxide dehydrogenase (large chain) CoxL
115932	syn	TC	MUL_0115	-	intermediary metabolism and respiration	carbon monoxide dehydrogenase (large chain) CoxL
116553	syn	AG	MUL_0115	-	intermediary metabolism and respiration	carbon monoxide dehydrogenase (large chain) CoxL
117178	psd	GA	MUL_0117	-	intermediary metabolism and respiration	C-term carbon monoxide dehydrogenase (medium chain) - pseudogene CoxM
117784	psd	GC	MUL_0117	-	intermediary metabolism and respiration	mid-section carbon monoxide dehydrogenase (medium chain) - pseudogene CoxM
117797	psd	TG	MUL_0117	-	intermediary metabolism and respiration	mid-section carbon monoxide dehydrogenase (medium chain) - pseudogene CoxM
118336	syn	AG	MUL_0118	-	conserved hypothetical	C-term conserved hypothetical protein - pseudogene
120503	int	TC	63 MUL_0120	cell wall and cell processes		protein transport protein SecE2
120826	syn	CG	MUL_0121	-	intermediary metabolism and respiration	RNA methyltransferase
120832	non	AG	MUL_0121	-	intermediary metabolism and respiration	RNA methyltransferase
121179	syn	AC	MUL_0121	-	intermediary metabolism and respiration	RNA methyltransferase
124498	int	GT		-		
126075	syn	CA	MUL_0127	-		endopeptidase ATP binding protein (chain B) CipB
126291	syn	TC	MUL_0127	-		endopeptidase ATP binding protein (chain B) CipB
127452	syn	AC	MUL_0127	-		endopeptidase ATP binding protein (chain B) CipB
127890	syn	TG	MUL_0127	-		endopeptidase ATP binding protein (chain B) CipB
128074	int	CT	50 MUL_0127	cell wall and cell processes		endopeptidase ATP binding protein (chain B) CipB
128234	int	CG	117 MUL_0128	intermediary metabolism and respiration		monoxygenase
128235	int	AG	116 MUL_0128	intermediary metabolism and respiration		monoxygenase
129395	syn	AG	MUL_0128	intermediary metabolism and respiration		monoxygenase
129617	non	CT	MUL_0129	-	conserved hypothetical	conserved hypothetical protein
141257	non	AG	MUL_0138	-	intermediary metabolism and respiration	5-methyltetrahydropteroyltriglutamate-- homocysteine methyltransferase MetE
142585	non	AG	MUL_0138	-	intermediary metabolism and respiration	5-methyltetrahydropteroyltriglutamate-- homocysteine methyltransferase MetE
144026	syn	AG	MUL_0139	-	cell wall and cell processes	conserved hypothetical membrane protein
148412	psd	GA	MUL_0143	-	conserved hypothetical	C-term conserved hypothetical protein - pseudogene
148504	psd	CG	MUL_0143	-	conserved hypothetical	C-term conserved hypothetical protein - pseudogene
153178	syn	AG	MUL_0148	-	intermediary metabolism and respiration	6-phosphogluconate dehydrogenase decarboxylating Gnd2
153239	syn	AG	MUL_0148	-	intermediary metabolism and respiration	6-phosphogluconate dehydrogenase decarboxylating Gnd2
157137	syn	AG	MUL_5079	-	conserved hypothetical	conserved hypothetical protein
158994	syn	CT	MUL_0155	-	intermediary metabolism and respiration	dioxygenase
159016	syn	CG	MUL_0155	-	intermediary metabolism and respiration	dioxygenase
159165	non	TC	MUL_0155	-	intermediary metabolism and respiration	dioxygenase
161181	int	CT	44 MUL_0158	conserved hypothetical		conserved hypothetical protein
161384	syn	AG	MUL_0158	-	conserved hypothetical	conserved hypothetical protein
163545	non	GA	MUL_0160	-	conserved hypothetical	conserved protein
164069	syn	TC	MUL_0161	-	conserved hypothetical	conserved hypothetical protein
168877	syn	AG	MUL_0166	-	information pathways	GTP binding protein
171410	syn	AG	MUL_0168	-	lipid metabolism	4-hydroxy-3-methylbut-2-enyl diphosphate reductase IspH
171521	syn	TC	MUL_0168	-	lipid metabolism	4-hydroxy-3-methylbut-2-enyl diphosphate reductase IspH
173122	syn	TC	MUL_0170	-	information pathways	exodeoxyribonuclease VII (large subunit) XseA
173419	syn	AG	MUL_0170	-	information pathways	exodeoxyribonuclease VII (large subunit) XseA
174743	syn	AG	MUL_0172	-	intermediary metabolism and respiration	cholesterol dehydrogenase
177729	int	GT	34 MUL_0176	conserved hypothetical		C-term hypothetical carboxylesterase - pseudogene
178321	psd	CT	MUL_0176	-	conserved hypothetical	C-term hypothetical carboxylesterase - pseudogene
179036	psd	TC	MUL_0176	-	conserved hypothetical	N-term hypothetical carboxylesterase - pseudogene
181844	syn	AG	MUL_0179	-	conserved hypothetical	conserved protein
181916	syn	TG	MUL_0179	-	conserved hypothetical	conserved protein
186262	psd	AG	MUL_0183	-	cell wall and cell processes	C-term conserved hypothetical transmembrane protein - pseudogene
186686	psd	CT	MUL_0183	-	cell wall and cell processes	N-term conserved hypothetical transmembrane protein - pseudogene
188220	syn	GC	MUL_0184	-	intermediary metabolism and respiration	glycosyl hydrolase
191233	syn	AG	MUL_0188	-	intermediary metabolism and respiration	serine hydroxymethyltransferase 1 GlvA1
195606	syn	GA	MUL_0192	-	cell wall and cell processes	conserved hypothetical transmembrane protein
195975	syn	GA	MUL_0192	-	cell wall and cell processes	conserved hypothetical transmembrane protein
197724	int	TC	78 MUL_0194	intermediary metabolism and respiration		hemolysin-like protein
199732	syn	TG	MUL_0196	-	cell wall and cell processes	conserved transmembrane protein
199747	syn	TC	MUL_0196	-	cell wall and cell processes	conserved transmembrane protein
201895	syn	AC	MUL_0198	-		mycothiol conjugate amidase Mca
204545	syn	AC	MUL_0201	-	intermediary metabolism and respiration	cystathione gamma-synthase MetB (cgs)
204560	syn	AG	MUL_0201	-	intermediary metabolism and respiration	cystathione gamma-synthase MetB (cgs)
205070	syn	CT	MUL_0202	-	cell wall and cell processes	proline-rich antigen homolog Pra
206433	non	TG	MUL_0203	-	intermediary metabolism and respiration	cystathione beta-synthase Cbs
206572	non	AG	MUL_0203	-	intermediary metabolism and respiration	cystathione beta-synthase Cbs
210865	int	CT	120 MUL_0208	cell wall and cell processes		conserved hypothetical transmembrane protein
211510	syn	AG	MUL_0208	-	cell wall and cell processes	conserved hypothetical transmembrane protein
212776	syn	TC	MUL_0209	-	lipid metabolism	enoyl-CoA hydratase EchA9
215648	syn	GA	MUL_0211	-	cell wall and cell processes	conserved hypothetical transmembrane protein
218163	int	TC	128 MUL_0213	PE/PPG		N-term PE-PGRS family protein - pseudogene
221493	syn	AG	MUL_0215	-	conserved hypothetical	conserved hypothetical protein
222836	syn	AG	MUL_0217	-	cell wall and cell processes	lipoprotein Lpp1
232427	non	AG	MUL_0218	-	conserved hypothetical	conserved hypothetical protein
224117	syn	CT	MUL_0218	-	conserved hypothetical	conserved hypothetical protein
224653	psd	AG	MUL_0219	-	cell wall and cell processes	N-term conserved hypothetical protein - pseudogene
225056	int	GC	23 MUL_0219	cell wall and cell processes		N-term conserved hypothetical protein - pseudogene
225317	non	AG	MUL_0220	-	conserved hypothetical	conserved hypothetical protein
225484	non	CT	MUL_0220	-	conserved hypothetical	conserved hypothetical protein
232223	syn	TC	MUL_0227	-	intermediary metabolism and respiration	arylsulfatase AsIA
232352	syn	CT	MUL_0227	-	intermediary metabolism and respiration	arylsulfatase AsIA
232421	non	AG	MUL_0227	-	intermediary metabolism and respiration	arylsulfatase AsIA
233607	psd	TC	MUL_0228	-	conserved hypothetical	C-term conserved hypothetical protein - pseudogene
241813	syn	AT	MUL_0233	-	cell wall and cell processes	metal cation transporter ATPase p-type CtpE
243098	psd	AG	MUL_0234	-	cell wall and cell processes	N-term conserved hypothetical protein - pseudogene
243204	psd	AC	MUL_0234	-	cell wall and cell processes	N-term conserved hypothetical protein - pseudogene
243355	psd	TA	MUL_0234	-	cell wall and cell processes	N-term conserved hypothetical protein - pseudogene
243717	non	CT	MUL_0235	-	conserved hypothetical	conserved protein
247429	int	G-		-		
247801	int	AG		-		
247965	int	AG	127 MUL_0240	cell wall and cell processes		conserved two-domain transmembrane protein
250539	syn	TC	MUL_0241	-	intermediary metabolism and respiration	8-amino-7-oxononanoate synthase BioF2_1
251050	int	GC	1 MUL_0242	intermediary metabolism and respiration	cysteine synthase B CysM	
252990	psd	CT	MUL_0244	-	lipid metabolism	C-term membrane-bound C-5 sterol desaturase Erg3_1 - pseudogene
253674	syn	AG	MUL_0245	-	regulatory proteins	transcriptional regulatory protein
256583	syn	GC	MUL_0249	-	regulatory proteins	two component sensor histidine kinase PrrB

SNP position	SNP type	Nucleotide change <ref><snp>	Distance to nearest locus	Nearby Locus	Functional group	Product
259912	syn	TC	MUL_0253	-	conserved hypotheticals	conserved protein
260997	non	TC	MUL_0254	-	intermediary metabolism and respiration	oxidoreductase
261137	non	TG	MUL_0254	-	intermediary metabolism and respiration	oxidoreductase
261311	non	TC	MUL_0254	-	intermediary metabolism and respiration	oxidoreductase
261477	syn	TC	MUL_0254	-	intermediary metabolism and respiration	oxidoreductase
263542	non	AC	MUL_0256	-	intermediary metabolism and respiration	monooxygenase
266900	syn	TC	MUL_0259	-	intermediary metabolism and respiration	citrate synthase II CitA
267131	syn	CT	MUL_0259	-	intermediary metabolism and respiration	citrate synthase II CitA
267640	int	GA	35 MUL_0259	-	intermediary metabolism and respiration	citrate synthase II CitA
267709	psd	GA	MUL_0260	-	cell wall and cell processes	C-term exported protein - pseudogene
271948	int	TC		-		
272233	int	GA		-		
272455	int	GA		-		
272620	int	AG		-		
272706	int	AG		-		
272728	int	TA		-		
272998	int	GA	139 MUL_0263	conserved hypotheticals	conserved protein	
273019	int	AG	118 MUL_0263	conserved hypotheticals	conserved protein	
273365	non	AG	MUL_0263	conserved hypotheticals	conserved protein	
277573	syn	TC	MUL_0266	-	intermediary metabolism and respiration	phosphoserine aminotransferase SerC
277585	syn	GA	MUL_0266	-	intermediary metabolism and respiration	phosphoserine aminotransferase SerC
278448	syn	AG	MUL_0267	-	conserved hypotheticals	conserved hypothetical protein
279312	non	GC	MUL_0269	-	intermediary metabolism and respiration	tRNA methyltransferase
279348	non	TC	MUL_0269	-	intermediary metabolism and respiration	tRNA methyltransferase
279535	syn	GA	MUL_0269	-	intermediary metabolism and respiration	tRNA methyltransferase
279538	non	TC	MUL_0269	-	intermediary metabolism and respiration	tRNA methyltransferase
279923	non	GC	MUL_0270	-	regulatory proteins	transcriptional regulatory protein (possibly marR-family)
279987	syn	GC	MUL_0270	-	regulatory proteins	transcriptional regulatory protein (possibly marR-family)
281393	non	AG	MUL_0273	-	cell wall and cell processes	transcriptional regulatory protein (possibly marR-family)
281395	syn	GA	MUL_0273	-	cell wall and cell processes	conserved protein
281503	syn	CG	MUL_0273	-	cell wall and cell processes	conserved protein
283098	syn	TG	MUL_0274	-	cell wall and cell processes	conserved transmembrane protein
283413	syn	AT	MUL_0274	-	cell wall and cell processes	conserved transmembrane protein
285155	non	TG	MUL_0276	-	conserved hypotheticals	conserved hypothetical protein
285361	non	CA	MUL_0277	-	conserved hypotheticals	conserved hypothetical protein
286419	syn	AG	MUL_0278	-	lipid metabolism	acyl-CoA dehydrogenase Fad10
287502	syn	TC	MUL_0278	-	lipid metabolism	acyl-CoA dehydrogenase Fad10
287648	non	TC	MUL_0278	-	lipid metabolism	acyl-CoA dehydrogenase Fad10
287937	syn	TC	MUL_0278	-	lipid metabolism	acyl-CoA dehydrogenase Fad10
288129	syn	CG	MUL_0278	-	lipid metabolism	acyl-CoA dehydrogenase Fad10
290394	non	GA	MUL_0281	-	intermediary metabolism and respiration	molybdenum cofactor biosynthesis protein A2 MoaA2
290920	int	CT	130 MUL_0282	intermediary metabolism and respiration	molybdenum cofactor biosynthesis protein D 2 MoaD2	
292084	int	AC	27 MUL_0284	intermediary metabolism and respiration	molybdenum cofactor biosynthesis protein E2 MoaE2	
292330	syn	GA	MUL_0284	-	intermediary metabolism and respiration	molybdenum cofactor biosynthesis protein E2 MoaE2
292408	syn	AG	MUL_0284	-	intermediary metabolism and respiration	molybdenum cofactor biosynthesis protein E2 MoaE2
292525	syn	AC	MUL_0284	-	intermediary metabolism and respiration	molybdenum cofactor biosynthesis protein E2 MoaE2
292716	syn	CG	MUL_0285	-	intermediary metabolism and respiration	molybdopterin biosynthesis Moa protein
293204	syn	CA	MUL_0286	-	intermediary metabolism and respiration	molybdenum cofactor biosynthesis protein C 2 MoaC2
294240	syn	AC	MUL_0288	-	conserved hypotheticals	conserved hypothetical protein
294714	syn	AG	MUL_0288	-	conserved hypotheticals	conserved hypothetical protein
295120	syn	TC	MUL_0288	-	conserved hypotheticals	conserved hypothetical protein
295841	non	CA	MUL_0288	-	conserved hypotheticals	conserved hypothetical protein
295935	syn	AG	MUL_0288	-	conserved hypotheticals	conserved hypothetical protein
296017	non	AT	MUL_0288	-	conserved hypotheticals	conserved hypothetical protein
296145	int	CG	53 MUL_0289	information pathways	DNA helicase Ercc3	
296173	int	AG	79 MUL_0288	conserved hypotheticals	conserved hypothetical protein	
297220	syn	AG	MUL_0289	-	information pathways	DNA helicase Ercc3
298548	int	CG	128 MUL_0291	conserved hypotheticals	conserved hypothetical protein	
298567	int	-T	109 MUL_0291	conserved hypotheticals	conserved hypothetical protein	
299254	non	GT	MUL_0292	-	conserved hypotheticals	conserved protein
299696	syn	GC	MUL_0292	-	conserved hypotheticals	conserved protein
300275	syn	AG	MUL_0293	-	regulatory proteins	transcriptional regulator
300729	non	TC	MUL_0294	-	cell wall and cell processes	membrane-associated oxidoreductase
300742	non	TA	MUL_0294	-	cell wall and cell processes	membrane-associated oxidoreductase
300761	syn	AG	MUL_0294	-	cell wall and cell processes	membrane-associated oxidoreductase
301109	non	GC	MUL_0294	-	cell wall and cell processes	membrane-associated oxidoreductase
305791	non	GT	MUL_0297	-	intermediary metabolism and respiration	aminotransferase
306521	syn	TG	MUL_0297	-	intermediary metabolism and respiration	aminotransferase
308054	psd	TC	MUL_0300	-	lipid metabolism	C-term fatty-acid-CoA racemase Far - pseudogene
309117	non	AG	MUL_0301	-	conserved hypotheticals	conserved hypothetical protein
309149	non	TC	MUL_0301	-	conserved hypotheticals	conserved hypothetical protein
311209	int	AG	8 MUL_0303	conserved hypotheticals	conserved hypothetical protein	
311976	syn	AC	MUL_0305	-	cell wall and cell processes	conserved hypothetical membrane protein
312102	syn	TC	MUL_0305	-	cell wall and cell processes	conserved hypothetical membrane protein
312796	syn	GA	MUL_0306	-	cell wall and cell processes	conserved hypothetical membrane protein
312842	syn	TC	MUL_0306	-	cell wall and cell processes	conserved hypothetical membrane protein
312929	syn	AG	MUL_0306	-	cell wall and cell processes	conserved hypothetical membrane protein
313120	non	TA	MUL_0306	-	cell wall and cell processes	conserved hypothetical membrane protein
313381	int	GA	15 MUL_0306	cell wall and cell processes	conserved hypothetical membrane protein	
313425	int	GC	59 MUL_0306	cell wall and cell processes	conserved hypothetical membrane protein	
313441	int	TC	75 MUL_0306	cell wall and cell processes	conserved hypothetical membrane protein	
313654	int	AC	67 MUL_0307	lipid metabolism	C-term fatty-acid-CoA ligase FadD3_2 - pseudogene	
313655	int	AT	66 MUL_0307	lipid metabolism	C-term fatty-acid-CoA ligase FadD3_2 - pseudogene	
314066	psd	GA	MUL_0307	-	lipid metabolism	C-term fatty-acid-CoA ligase FadD3_2 - pseudogene
314093	psd	GA	MUL_0307	-	lipid metabolism	C-term fatty-acid-CoA ligase FadD3_2 - pseudogene
314204	psd	CG	MUL_0307	-	lipid metabolism	C-term fatty-acid-CoA ligase FadD3_2 - pseudogene
314249	psd	CT	MUL_0307	-	lipid metabolism	C-term fatty-acid-CoA ligase FadD3_2 - pseudogene
314397	psd	CT	MUL_0307	-	lipid metabolism	C-term fatty-acid-CoA ligase FadD3_2 - pseudogene
314944	psd	GA	MUL_0307	-	lipid metabolism	N-term fatty-acid-CoA ligase FadD3_2 - pseudogene
315006	psd	CT	MUL_0307	-	lipid metabolism	N-term fatty-acid-CoA ligase FadD3_2 - pseudogene
315035	int	TC	128 MUL_0308	conserved hypotheticals	amidohydrolase	

SNP position	SNP type	Nucleotide change <ref><snp>	Distance to nearest locus	Nearby Locus	Functional group	Product
315427	syn	AG	MUL_0308	-	conserved hypotheticals	amidohydrolase
316186	syn	TG	MUL_0308	-	conserved hypotheticals	amidohydrolase
316732	non	CA	MUL_0309	-	cell wall and cell processes	conserved lipoprotein
317237	syn	AG	MUL_0310	-	lipid metabolism	enoyl-CoA hydratase EchA8_2
317277	non	AG	MUL_0310	-	lipid metabolism	enoyl-CoA hydratase EchA8_2
319593	syn	GC	MUL_0314	-	intermediary metabolism and respiration	cytochrome P450_150A6 Cyo150A6
319657	non	CG	MUL_0314	-	intermediary metabolism and respiration	cytochrome P450_150A6 Cyo150A6
320819	non	GA	MUL_0315	-	lipid metabolism	3-oxoacyl-[acyl-carrier protein] reductase FabG2
321048	syn	AC	MUL_0315	-	lipid metabolism	3-oxoacyl-[acyl-carrier protein] reductase FabG2
321099	syn	GC	MUL_0315	-	lipid metabolism	3-oxoacyl-[acyl-carrier protein] reductase FabG2
321437	Int.	AG	77 MUL_0316	intermediary metabolism and respiration	ferredoxin	
322307	syn	TA		intermediary metabolism and respiration	cytochrome P450_188A3 Cyo188A3	
323190	psd	GT		lipid metabolism	C-term acyl-CoA dehydrogenase - pseudogene	
323700	psd	TG		lipid metabolism	C-term acyl-CoA dehydrogenase - pseudogene	
323700	psd	TG		lipid metabolism	N-term acyl-CoA dehydrogenase - pseudogene	
323747	psd	GA		lipid metabolism	C-term acyl-CoA dehydrogenase - pseudogene	
323747	psd	GA		lipid metabolism	N-term acyl-CoA dehydrogenase - pseudogene	
325591	syn	AG	MUL_0320	-	conserved hypotheticals	conserved hypothetical protein
325884	non	CT	MUL_0320	-	conserved hypotheticals	conserved hypothetical protein
326093	Int.	GC	138 MUL_0320	conserved hypotheticals	conserved hypothetical protein	
326139	Int.	CA				
329545	Int.	GA		98 MUL_0323	information pathways	transcriptional regulatory protein
330125	syn	TC		13 MUL_0324	information pathways	transcriptional regulatory protein
330517	Int.	GA		intermediary metabolism and respiration	cytochrome P450_189A7 Cyo189A7	
330971	syn	AG		intermediary metabolism and respiration	cytochrome P450_189A7 Cyo189A7	
331420	syn	AG		intermediary metabolism and respiration	cytochrome P450_189A7 Cyo189A7	
331503	non	GC		intermediary metabolism and respiration	cytochrome P450_189A7 Cyo189A7	
331504	non	CG		intermediary metabolism and respiration	cytochrome P450_189A7 Cyo189A7	
331523	non	AG		intermediary metabolism and respiration	cytochrome P450_189A7 Cyo189A7	
332194	psd	AG		intermediary metabolism and respiration	N-term short-chain type dehydrogenase/reductase - pseudogene	
332350	psd	AG		intermediary metabolism and respiration	N-term short-chain type dehydrogenase/reductase - pseudogene	
333569	syn	CG		intermediary metabolism and respiration	oxidoreductase	
333748	non	TC	MUL_0327	-	intermediary metabolism and respiration	oxidoreductase
335205	non	TA	MUL_0328	-	acyl-CoA metabolism	acyl-CoA transferase
336766	psd	AT	MUL_0329	-	lipid metabolism	C-term enoyl-CoA hydratase EchA4_1 - pseudogene
336781	psd	CT	MUL_0329	-	lipid metabolism	C-term enoyl-CoA hydratase EchA4_1 - pseudogene
336906	psd	AG	MUL_0329	-	lipid metabolism	C-term enoyl-CoA hydratase EchA4_1 - pseudogene
336939	psd	CT	MUL_0329	-	lipid metabolism	C-term enoyl-CoA hydratase EchA4_1 - pseudogene
337778	syn	TG	MUL_0330	-	intermediary metabolism and respiration	aminopeptidase
338235	non	AG	MUL_0330	-	intermediary metabolism and respiration	aminopeptidase
338236	non	AC	MUL_0330	-	intermediary metabolism and respiration	aminopeptidase
338408	syn	TC	MUL_0330	-	intermediary metabolism and respiration	aminopeptidase
338657	syn	AG	MUL_0330	-	intermediary metabolism and respiration	aminopeptidase
338856	syn	TC	MUL_0331	-	intermediary metabolism and respiration	dipeptidase
339423	syn	AC	MUL_0331	-	intermediary metabolism and respiration	dipeptidase
339487	non	TG	MUL_0331	-	intermediary metabolism and respiration	dipeptidase
339806	non	GC	MUL_0331	-	intermediary metabolism and respiration	dipeptidase
340305	psd	AG	MUL_0332	-	conserved hypotheticals	C-term conserved hypothetical protein - pseudogene
341168	psd	GC	MUL_0332	-	conserved hypotheticals	N-term conserved hypothetical protein - pseudogene
342126	syn	CT	MUL_0333	-	intermediary metabolism and respiration	cytochrome P450_10504 Cyo10504
342398	non	AC	MUL_0333	-	intermediary metabolism and respiration	cytochrome P450_10504 Cyo10504
342623	syn	CA	MUL_0334	-	intermediary metabolism and respiration	ferredoxin
343384	Int.	TC	87 MUL_0336	intermediary metabolism and respiration	short chain dehydrogenase	
343408	Int.	CT		intermediary metabolism and respiration	short chain dehydrogenase	
343677	non	GT	MUL_0336	-	intermediary metabolism and respiration	short chain dehydrogenase
343720	syn	GC	MUL_0336	-	intermediary metabolism and respiration	short chain dehydrogenase
343804	syn	CG	MUL_0336	-	intermediary metabolism and respiration	short chain dehydrogenase
343915	syn	AG	MUL_0336	-	intermediary metabolism and respiration	short chain dehydrogenase
345227	Int.	TA	49 MUL_0338	cell wall and cell processes	conserved integral membrane transport protein	
345834	syn	TC		cell wall and cell processes	conserved integral membrane transport protein	
345939	syn	TC	MUL_0338	-	cell wall and cell processes	conserved integral membrane transport protein
345987	syn	GA	MUL_0338	-	cell wall and cell processes	conserved integral membrane transport protein
346068	syn	TG	MUL_0338	-	cell wall and cell processes	conserved integral membrane transport protein
346135	non	GA	MUL_0338	-	cell wall and cell processes	conserved integral membrane transport protein
346371	syn	TC	MUL_0338	-	cell wall and cell processes	conserved integral membrane transport protein
346645	psd	GA	MUL_0339	-	intermediary metabolism and respiration	C-term cysteine synthase a CysK2 - pseudogene
346645	psd	GA	MUL_0339	-	intermediary metabolism and respiration	N-term cysteine synthase a CysK2 - pseudogene
347211	psd	AG	MUL_0339	-	intermediary metabolism and respiration	N-term cysteine synthase a CysK2 - pseudogene
348147	syn	TC	MUL_0340	-	cell wall and cell processes	lipoprotein LpqS
350106	syn	AG	MUL_0342	-	cell wall and cell processes	conserved membrane protein
350123	syn	AG	MUL_0342	-	cell wall and cell processes	conserved membrane protein
350565	syn	AC	MUL_0342	-	cell wall and cell processes	conserved membrane protein
353132	syn	GA	MUL_0345	-	intermediary metabolism and respiration	monooxygenase
354349	syn	GC	MUL_0346	-	intermediary metabolism and respiration	dehydrogenase
354430	syn	AG	MUL_0346	-	intermediary metabolism and respiration	dehydrogenase
354439	non	GC	MUL_0346	-	intermediary metabolism and respiration	dehydrogenase
354441	non	AT	MUL_0346	-	intermediary metabolism and respiration	dehydrogenase
354508	syn	CT	MUL_0346	-	intermediary metabolism and respiration	dehydrogenase
356258	non	GT	MUL_0347	-	intermediary metabolism and respiration	extradiol dioxygenase MhpB
356610	syn	GA	MUL_0347	-	intermediary metabolism and respiration	extradiol dioxygenase MhpB
362732	psd	GA	MUL_0352	-	regulatory protein	N-term two component sensor kinase - pseudogene
364343	non	TC	MUL_0354	-	cell wall and cell processes	integral membrane protein
365999	Int.	CT	127 MUL_0354	cell wall and cell processes	integral membrane protein	
366068	Int.	AG		cell wall and cell processes	integral membrane protein	
368548	Int.	TA	83 MUL_0355	lipid metabolism	PE/PGRS family protein family_protein	
368949	non	GA		intermediary metabolism and respiration	beta-ketoacyl CoA thiolase	
370723	syn	TC	MUL_0360	-	lipid metabolism	acyl-CoA dehydrogenase
372058	non	AC	MUL_0361	-	lipid metabolism	acyl-CoA dehydrogenase
372155	syn	CA	MUL_0361	-	lipid metabolism	acyl-CoA dehydrogenase
372313	syn	AG	MUL_0362	-	lipid metabolism	acyl-CoA synthetase
372318	syn	AG	MUL_0362	-	lipid metabolism	acyl-CoA synthetase
375382	syn	GA	MUL_0365	-	intermediary metabolism and respiration	oxidoreductase

SNP position	SNP type	Nucleotide change <ref><snp>	Distance to nearest locus	Nearby Locus	Functional group	Product
375775	syn	AC	MUL_0365	-	intermediary metabolism and respiration	oxidoreductase
375799	syn	TA	MUL_0365	-	intermediary metabolism and respiration	oxidoreductase
376036	non	TG	MUL_0366	-	lipid metabolism	methylmalonyl-CoA mutase alpha subunit McmA2b
376356	syn	GC	MUL_0366	-	lipid metabolism	methylmalonyl-CoA mutase alpha subunit McmA2b
376819	non	CT	MUL_0367	-	lipid metabolism	methylmalonyl-CoA mutase beta subunit McmA2a
377312	non	GA	MUL_0367	-	lipid metabolism	methylmalonyl-CoA mutase beta subunit McmA2a
377637	syn	CG	MUL_0367	-	lipid metabolism	methylmalonyl-CoA mutase beta subunit McmA2a
377739	syn	AG	MUL_0367	-	lipid metabolism	methylmalonyl-CoA mutase beta subunit McmA2a
377868	syn	TC	MUL_0367	-	lipid metabolism	methylmalonyl-CoA mutase beta subunit McmA2a
378191	syn	GC	MUL_0368	-	conserved hypothetical	conserved hypothetical protein
378523	non	AG	MUL_0368	-	conserved hypothetical	conserved hypothetical protein
378985	int	TC	48 MUL_0368	conserved hypothetical	conserved hypothetical protein	
385018	psd	AG		conserved hypothetical	conserved hypothetical protein	
387084	syn	CG		lipid metabolism	N-term phytene dehydrogenase CrtI_pseudogene	
387234	syn	CT		lipid metabolism	phytene synthase CrtB	
391838	non	AG	MUL_0380	-	intermediary metabolism and respiration	isopentenyl pyrophosphate isomerase type 2 IdI2
393246	syn	AG	MUL_0382	-	conserved hypothetical	conserved hypothetical protein
393360	syn	TG	MUL_0382	-	conserved hypothetical	conserved hypothetical protein
394524	syn	AG	MUL_0383	-	cell wall and cell processes	L-asparagine permease AnsP1
398575	psd	AG	MUL_0386	-	unknown	C-term short chain dehydrogenase/reductase - pseudogene
398653	psd	AG	MUL_0388	-	conserved hypothetical	N-term conserved hypothetical protein - pseudogene
398987	psd	CA	MUL_0388	-	conserved hypothetical	C-term conserved hypothetical protein - pseudogene
398987	psd	CA	MUL_0388	-	conserved hypothetical	N-term conserved hypothetical protein - pseudogene
400007	syn	TC	MUL_0389	-	conserved hypothetical	conserved hypothetical protein
400424	syn	GA	MUL_0389	-	conserved hypothetical	conserved hypothetical protein
400695	psd	TC	MUL_0390	-	conserved hypothetical	N-term conserved hypothetical protein_pseudogene
404171	int	A	8 MUL_0392	cell shock protein alpha CspA	ATP-dependent RNA helicase RhlE1	
405747	syn	AG		information pathways	hypothetical protein	
406471	int	TC	72 MUL_0394	intermediary metabolism and respiration	5-methyltetrahydrofolate--homocysteine methyltransferase Meth	
406584	int	AG		intermediary metabolism and respiration	5-methyltetrahydrofolate--homocysteine methyltransferase Meth	
407337	syn	AG	MUL_0395	-	intermediary metabolism and respiration	5-methyltetrahydrofolate--homocysteine methyltransferase Meth
407436	syn	AC	MUL_0395	-	intermediary metabolism and respiration	5-methyltetrahydrofolate--homocysteine methyltransferase Meth
407880	syn	GC	MUL_0395	-	intermediary metabolism and respiration	5-methyltetrahydrofolate--homocysteine methyltransferase Meth
408684	syn	TC	MUL_0395	-	intermediary metabolism and respiration	5-methyltetrahydrofolate--homocysteine methyltransferase Meth
409332	syn	TC	MUL_0395	-	intermediary metabolism and respiration	5-methyltetrahydrofolate--homocysteine methyltransferase Meth
410631	int	CG	9 MUL_0395	intermediary metabolism and respiration	5-methyltetrahydrofolate--homocysteine methyltransferase Meth	
410633	int	GT		intermediary metabolism and respiration	5-methyltetrahydrofolate--homocysteine methyltransferase Meth	
410749	int	TC	127 MUL_0395	intermediary metabolism and respiration	5-methyltetrahydrofolate--homocysteine methyltransferase Meth	
414586	syn	TC		conserved hypothetical	conserved protein	
415063	syn	TC	MUL_0401	-	intermediary metabolism and respiration	phosphoribosylformylglycinamide synthase I PurQ
415287	syn	GA	MUL_0401	-	intermediary metabolism and respiration	phosphoribosylformylglycinamide synthase I PurQ
415305	syn	AG	MUL_0401	-	intermediary metabolism and respiration	phosphoribosylformylglycinamide synthase I PurQ
416251	syn	CT	MUL_0403	-	conserved hypothetical	conserved hypothetical protein
417926	int	GT	1 MUL_0404	intermediary metabolism and respiration	dihydrodipamide dehydrogenase LpdB	
419533	syn	TC		conserved hypothetical	conserved hypothetical protein	
420967	psd	CT	MUL_0407	-	intermediary metabolism and respiration	mid-section aminopeptidase PepC_pseudogene
423390	syn	TC	MUL_0410	-	intermediary metabolism and respiration	phosphoribosylformylglycinamide synthase II PurL
423705	non	GA	MUL_0410	-	intermediary metabolism and respiration	phosphoribosylformylglycinamide synthase II PurL
423896	syn	GC	MUL_0410	-	intermediary metabolism and respiration	phosphoribosylformylglycinamide synthase II PurL
425031	syn	TC	MUL_0410	-	intermediary metabolism and respiration	phosphoribosylformylglycinamide synthase II PurL
425848	syn	TC	MUL_0412	-	conserved hypothetical	conserved hypothetical protein
425971	syn	TC	MUL_0412	-	conserved hypothetical	conserved hypothetical protein
428610	psd	GC	MUL_0414	-	cell wall and cell processes	C-term lipoprotein pseudogene
429524	psd	TG	MUL_0414	-	cell wall and cell processes	N-term lipoprotein pseudogene
429619	psd	TG	MUL_0414	-	cell wall and cell processes	N-term lipoprotein pseudogene
431744	syn	GA	MUL_0417	-	intermediary metabolism and respiration	amidophosphoribosyltransferase PurF
432545	syn	AG	MUL_0417	-	intermediary metabolism and respiration	amidophosphoribosyltransferase PurF
433667	non	TC	MUL_0418	-	intermediary metabolism and respiration	5'-phosphoribosyl-5-aminoimidazole synthetase PurM
434765	non	GA	MUL_0420	-	conserved hypothetical	conserved hypothetical protein
435388	syn	TC	MUL_0420	-	conserved hypothetical	conserved hypothetical protein
435472	syn	CT	MUL_0420	-	conserved hypothetical	conserved hypothetical protein
435826	psd	TC	MUL_0421	-	conserved hypothetical	N-terminal conserved hypothetical protein - pseudogene
435826	psd	TC	MUL_0421	-	conserved hypothetical	C-term hypothetical membrane protein - pseudogene
435827	psd	TC	MUL_0421	-	conserved hypothetical	C-term hypothetical membrane protein - pseudogene
435827	psd	TC	MUL_0421	-	conserved hypothetical	N-terminal conserved hypothetical protein - pseudogene
436310	int	TG	33 MUL_0423	cell wall and cell processes	metal cation transporter p-type ATPase CtpV	
436877	syn	CG		cell wall and cell processes	metal cation transporter p-type ATPase CtpV	
437390	syn	TC	MUL_0423	-	cell wall and cell processes	metal cation transporter p-type ATPase CtpV
439253	syn	TC	MUL_0425	-	conserved hypothetical	conserved hypothetical protein
439553	int	AG	77 MUL_0426	intermediary metabolism and respiration	amino acid aminotransferase PabC	
442637	psd	CT		conserved hypothetical	N-term conserved hypothetical protein pseudogene	
445085	syn	AG	MUL_0432	-	intermediary metabolism and respiration	thiosulfate sulfurtransferase CysA2
445204	non	TC	MUL_0432	-	intermediary metabolism and respiration	thiosulfate sulfurtransferase CysA2
446270	syn	GC	MUL_0434	-	conserved hypothetical	conserved protein
446782	non	TC	MUL_0434	-	conserved hypothetical	conserved protein
447060	int	TC	-	intermediary metabolism and respiration	phosphate-binding protein 3 precursor PhoS3	
449303	syn	GA	MUL_0437	-	cell wall and cell processes	C-terminal phosphate-transport integral membrane ABC transporter PstC2_1_pseudogene
451088	psd	TC	MUL_0438	-	cell wall and cell processes	phosphate-transport ATP-binding protein ABC transporter PhoT
452450	syn	TC	MUL_0440	-	cell wall and cell processes	phosphate-transport system regulatory protein PhoY2
453214	syn	TC	MUL_0441	-	cell wall and cell processes	phosphate-transport system regulatory protein PhoY2
453556	syn	TG	MUL_0441	-	cell wall and cell processes	C-term conserved hypothetical protein pseudogene
455122	psd	CG	MUL_0442	-	conserved hypothetical	transcriptional regulator
456633	non	GC	MUL_0444	-	regulatory proteins	transcriptional regulator
460881	int	AG	33 MUL_0449	conserved hypothetical	deaminase	
460928	non	TC		conserved hypothetical	deaminase	
461182	non	AT	MUL_0449	-	conserved hypothetical	deaminase
461275	int	TC	53 MUL_0449	conserved hypothetical	deaminase	
461284	int	GT		conserved hypothetical	deaminase	
461806	non	TC	MUL_0450	-	lipid metabolism	O-methyltransferase
465329	non	GC	MUL_0453	-	conserved hypothetical	conserved protein
466620	non	GA	MUL_0454	-	intermediary metabolism and respiration	arylsulfatase AtsD
468944	psd	AC	MUL_0455	-	unknown	mid-section xanthine/uracil permease pseudogene

SNP position	SNP type	Nucleotide change <ref><snp>	Distance to nearest locus	Nearby Locus	Functional group	Product
470233	syn	AG	MUL_0456	-	conserved hypothetical	conserved protein
470762	non	AC	MUL_0457	-	conserved hypothetical	conserved hypothetical protein
472293	non	TC	MUL_0459	-	intermediary metabolism and respiration	carbon monoxide dehydrogenase
473719	non	GC	MUL_0459	-	intermediary metabolism and respiration	carbon monoxide dehydrogenase
474868	non	TC	MUL_0460	-	conserved hypothetical	conserved hypothetical protein
479815	Int	TC	-	97 MUL_0466	PE/PP	N-term PE PGRS family protein - pseudogene
480350	Int	AG	-	110 MUL_0466	PE/PP	N-term PE PGRS family protein - pseudogene
481285	non	GA	MUL_0467	-	unknown	hypothetical secreted protein
482084	non	TG	MUL_0467	-	unknown	hypothetical secreted protein
483871	syn	AG	MUL_0470	-	intermediary metabolism and respiration	zinc-containing alcohol dehydrogenase NAD-dependent AdhB
484257	Int	AG	-	110 MUL_0471	conserved hypothetical	conserved hypothetical protein
484913	Int	CT	-	5 MUL_0472	intermediary metabolism and respiration	ferredoxin
485147	non	AT	MUL_0473	-	intermediary metabolism and respiration	cytochrome P450 51B1 Cyp51B1
488883	syn	CG	MUL_0476	-	conserved hypothetical	conserved hypothetical protein
489245	Int	TC	-	-	-	-
489260	Int	GT	-	-	-	-
489262	Int	TG	-	149 MUL_0477	intermediary metabolism and respiration	NAD-dependent aldehyde dehydrogenase AldA
489284	Int	GA	-	127 MUL_0477	intermediary metabolism and respiration	NAD-dependent aldehyde dehydrogenase AldA
493911	syn	AG	MUL_0481	-	intermediary metabolism and respiration	phosphoribosylamine-glycine ligase PurD
495121	syn	GC	MUL_0482	-	regulatory proteins	serine/threonine-protein kinase PknF_2
495479	non	TC	MUL_0482	-	regulatory proteins	serine/threonine-protein kinase PknF_2
496829	non	AG	MUL_0483	-	conserved hypothetical	conserved hypothetical protein
497828	syn	TC	MUL_0484	-	intermediary metabolism and respiration	molybdopterin biosynthesis protein Moey
504484	syn	AC	MUL_0489	-	intermediary metabolism and respiration	conserved hypothetical protein
504562	non	AG	MUL_0489	-	conserved hypothetical	conserved hypothetical protein
505654	syn	TC	MUL_0491	-	intermediary metabolism and respiration	cytochrome P450 126A3 Cyp126A3
505676	syn	AC	MUL_0491	-	intermediary metabolism and respiration	cytochrome P450 126A3 Cyp126A3
506709	syn	TA	MUL_0491	-	intermediary metabolism and respiration	cytochrome P450 126A3 Cyp126A3
506736	syn	TC	MUL_0491	-	intermediary metabolism and respiration	cytochrome P450 126A3 Cyp126A3
506857	syn	TC	MUL_0491	-	intermediary metabolism and respiration	cytochrome P450 126A3 Cyp126A3
507384	syn	TC	MUL_0491	-	intermediary metabolism and respiration	cytochrome P450 126A3 Cyp126A3
507468	syn	TC	MUL_0491	-	intermediary metabolism and respiration	cytochrome P450 126A3 Cyp126A3
507635	non	TC	MUL_0491	-	intermediary metabolism and respiration	cytochrome P450 126A3 Cyp126A3
511322	syn	TC	MUL_0494	-	intermediary metabolism and respiration	aldehyde dehydrogenase
512392	Int	TC	-	26 MUL_0495	intermediary metabolism and respiration	Zn-dependent alcohol dehydrogenase AdhX
512392	Int	TC	-	26 MUL_0494	intermediary metabolism and respiration	aldehyde dehydrogenase
513029	syn	CG	MUL_0495	-	intermediary metabolism and respiration	Zn-dependent alcohol dehydrogenase AdhX
514895	syn	TC	MUL_0497	-	intermediary metabolism and respiration	phosphoribosylaminoimidazole succinocarboxamide synthase PurC
515088	non	TC	MUL_0498	-	intermediary metabolism and respiration	protease II (oligopeptidase B) PtrB
515936	syn	AC	MUL_0498	-	intermediary metabolism and respiration	protease II (oligopeptidase B) PtrB
515992	syn	GC	MUL_0498	-	intermediary metabolism and respiration	protease II (oligopeptidase B) PtrB
516284	non	TC	MUL_0498	-	intermediary metabolism and respiration	protease II (oligopeptidase B) PtrB
516287	non	TC	MUL_0498	-	intermediary metabolism and respiration	protease II (oligopeptidase B) PtrB
517633	Int	TC	-	63 MUL_0499	cell wall and cell processes	conserved membrane protein
519097	non	GC	MUL_0501	-	cell wall and cell processes	integral membrane drug efflux protein
519324	syn	GC	MUL_0501	-	cell wall and cell processes	integral membrane drug efflux protein
519369	syn	TC	MUL_0501	-	cell wall and cell processes	integral membrane drug efflux protein
521710	non	CT	MUL_0503	-	conserved hypothetical	conserved hypothetical integral membrane protein
542974	psd	CG	MUL_0534	-	conserved hypothetical	N-term conserved hypothetical protein pseudogene
562557	syn	AG	MUL_0554	-	regulatory proteins	transcriptional regulatory protein
563300	psd	TC	MUL_0555	-	cell wall and cell processes	N-terminal conserved integral membrane transport protein - pseudogene
563320	psd	AG	MUL_0555	-	cell wall and cell processes	N-terminal conserved integral membrane transport protein - pseudogene
564678	syn	CA	MUL_0556	-	conserved hypothetical	conserved hypothetical protein
565316	psd	GA	MUL_0558	-	intermediary metabolism and respiration	C-terminal pyrrolidine-carboxylate peptidase Pcp - pseudogene
565356	psd	TC	MUL_0558	-	intermediary metabolism and respiration	C-terminal pyrrolidine-carboxylate peptidase Pcp - pseudogene
565452	psd	GC	MUL_0558	-	intermediary metabolism and respiration	C-terminal pyrrolidine-carboxylate peptidase Pcp - pseudogene
565462	psd	GT	MUL_0558	-	intermediary metabolism and respiration	C-terminal pyrrolidine-carboxylate peptidase Pcp - pseudogene
565625	Int	TC	-	119 MUL_0558	intermediary metabolism and respiration	C-terminal pyrrolidine-carboxylate peptidase Pcp - pseudogene
566173	syn	TC	MUL_0559	-	conserved hypothetical	conserved hypothetical secreted protein
566896	syn	TC	MUL_0560	-	intermediary metabolism and respiration	deoxyctydine triphosphate deaminase Dcd
566892	Int	CT	-	104 MUL_0562	unknown	hypothetical protein
571702	psd	AG	MUL_0565	-	intermediary metabolism and respiration	C-term UDP-glucose 6-dehydrogenase UdgA pseudogene
573550	non	AG	MUL_0568	-	intermediary metabolism and respiration	alpha-D-glucose-1-phosphate thymidylate transferase RmlA
574970	Int	AG	-	141 MUL_0570	PE/PP	PE PGRS family protein
580706	syn	TC	MUL_0573	-	intermediary metabolism and respiration	aspartate aminotransferase AspC
580784	syn	CT	MUL_0573	-	intermediary metabolism and respiration	aspartate aminotransferase AspC
584373	non	GC	MUL_0574	-	intermediary metabolism and respiration	iron-sulphur-binding reductase
591042	Int	GA	-	142 MUL_0579	cell wall and cell processes	conserved hypothetical membrane protein InIB
595261	syn	TC	MUL_0580	-	cell wall and cell processes	conserved hypothetical protein InIA
595462	syn	GT	MUL_0580	-	cell wall and cell processes	conserved hypothetical protein InIA
596205	syn	GC	MUL_0581	-	cell wall and cell processes	isoniazid inducible gene protein InIC
596322	syn	TC	MUL_0581	-	cell wall and cell processes	isoniazid inducible gene protein InIC
596403	syn	TC	MUL_0581	-	cell wall and cell processes	isoniazid inducible gene protein InIC
596607	non	TC	MUL_0581	-	cell wall and cell processes	isoniazid inducible gene protein InIC
596619	non	AG	MUL_0581	-	cell wall and cell processes	isoniazid inducible gene protein InIC
596787	syn	GC	MUL_0581	-	cell wall and cell processes	isoniazid inducible gene protein InIC
596908	syn	TC	MUL_0581	-	cell wall and cell processes	isoniazid inducible gene protein InIC
600728	syn	TC	MUL_0585	-	cell wall and cell processes	conserved hypothetical lipoprotein LpJ
601542	psd	GC	MUL_0586	-	intermediary metabolism and respiration	N-term carbon monoxide dehydrogenase - pseudogene
601674	psd	TC	MUL_0586	-	intermediary metabolism and respiration	N-term carbon monoxide dehydrogenase - pseudogene
602413	syn	AC	MUL_0587	-	intermediary metabolism and respiration	aerobic-type carbon monoxide dehydrogenase CoxM_2
602547	non	GC	MUL_0587	-	intermediary metabolism and respiration	aerobic-type carbon monoxide dehydrogenase CoxM_2
603954	syn	TG	MUL_0588	-	intermediary metabolism and respiration	aerobic-type carbon monoxide dehydrogenase CoxL_2
604336	non	CG	MUL_0588	-	intermediary metabolism and respiration	aerobic-type carbon monoxide dehydrogenase CoxL_2
605115	Int	CT	-	148 MUL_0588	intermediary metabolism and respiration	aerobic-type carbon monoxide dehydrogenase CoxL_2
606588	psd	GC	MUL_0591	-	cell wall and cell processes	C-term L-asparagine permease AcpP2 - pseudogene
607621	psd	TC	MUL_0591	-	cell wall and cell processes	N-term L-asparagine permease AcpP2 - pseudogene
607850	Int	TG	-	107 MUL_0591	cell wall and cell processes	N-term L-asparagine permease AcpP2 - pseudogene
608601	syn	TC	MUL_0593	-	chaperone protein DnaK	chaperone protein DnaK
609294	syn	CT	MUL_0593	-	chaperone protein DnaK	chaperone protein DnaK
609561	syn	TC	MUL_0593	-	chaperone protein DnaK	chaperone protein DnaK
610196	syn	CT	MUL_0594	-	GrpE protein (Hsp-70 cofactor)	GrpE protein (Hsp-70 cofactor)

SNP position	SNP type	Nucleotide change <ref><snp>	Distance to nearest locus	Nearby Locus	Functional group	Product
610442	syn	TC	MUL_0594	-		GroF protein (Hsp-70 cofactor)
610937	syn	CT	MUL_0595	-		chaperone protein DnaJ
611144	syn	AC	MUL_0595	-		chaperone protein DnaJ
611402	syn	CG	MUL_0595	-		chaperone protein DnaJ
611580	syn	CT	MUL_0595	-		chaperone protein DnaJ
611621	syn	CT	MUL_0595	-		chaperone protein DnaJ
611705	syn	AC	MUL_0595	-		chaperone protein DnaJ
611711	syn	CT	MUL_0595	-		chaperone protein DnaJ
625310	Int	TC	44 MUL_0605		conserved hypotheticals	conserved hypothetical protein
626646	syn	TC		cell wall and cell processes		membrane acyltransferase
626697	syn	AG		cell wall and cell processes		membrane acyltransferase
631596	syn	AG		unknown		conserved hypothetical protein
632065	non	TC		unknown		conserved hypothetical protein
633436	syn	TC		cell wall and cell processes		metal cation-transporting p-type ATPase F_CtpF
635344	psd	TC		intermediary metabolism and respiration		N-term glycine-sarcosine methyltransferase pseudogene
635400	psd	GA		intermediary metabolism and respiration		N-term glycine-sarcosine methyltransferase pseudogene
635981	psd	TC		intermediary metabolism and respiration		N-term glycine-sarcosine methyltransferase pseudogene
640760	Int	AG		intermediary metabolism and respiration		N-term mandelate racemase - pseudogene
641513	psd	CT		intermediary metabolism and respiration		N-term mandelate racemase - pseudogene
641925	Int	AC		intermediary metabolism and respiration		N-term mandelate racemase - pseudogene
642233	non	TA		conserved hypotheticals		conserved hypothetical protein
642250	non	AT		conserved hypotheticals		conserved hypothetical protein
642465	Int	TA		84 MUL_0621		unknown
644706	psd	AG		cell wall and cell processes		N-term conserved hypothetical protein - pseudogene
644706	psd	AG		cell wall and cell processes		N-term amino acid permease - pseudogene
644863	psd	A		cell wall and cell processes		C-term amino acid permease - pseudogene
644863	psd	A		cell wall and cell processes		C-term amino acid permease - pseudogene
649051	non	AG		cell wall and cell processes		thioredoxin protein (thiol-disulfide interchange protein)
64825	syn	TC		cell wall and cell processes		thioredoxin protein (thiol-disulfide interchange protein)
65277	syn	CT		conserved hypotheticals		ResB-family protein
650376	syn	TC		conserved hypotheticals		ResB-family protein
650561	syn	CT		conserved hypotheticals		ResB-family protein
652319	psd	GA		conserved hypotheticals		C-term conserved hypothetical protein - pseudogene
652319	psd	GA		conserved hypotheticals		N-term conserved hypothetical protein - pseudogene
657580	syn	GT		intermediary metabolism and respiration		UDP-glucose 4-epimerase GalE3
659025	syn	AG		cell wall and cell processes		conserved membrane protein
660041	non	AG		cell wall and cell processes		conserved hypothetical membrane protein
660214	syn	AC		cell wall and cell processes		conserved hypothetical membrane protein
663501	non	TC		cell wall and cell processes		conserved hypothetical membrane protein
664380	syn	AC		intermediary metabolism and respiration		O-succinylbenzoic acid-CoA ligase MenE
667375	syn	TC		intermediary metabolism and respiration		Glyoxalase
668378	Int	AG	13 MUL_0646	conserved hypotheticals		conserved protein
668690	syn	CT		intermediary metabolism and respiration		dehydrogenase
673876	syn	CT		cell wall and cell processes		conserved hypothetical protein
674364	non	GC		intermediary metabolism and respiration		muconate cyclotomerase MenC
674375	syn	CA		intermediary metabolism and respiration		muconate cyclotomerase MenC
676421	non	AG		intermediary metabolism and respiration		bifunctional 2-succinyl-6-hydroxy-2-4-cyclohexadiene-1-carboxylate synthase MenD
677446	syn	TC		intermediary metabolism and respiration		bifunctional 2-succinyl-6-hydroxy-2-4-cyclohexadiene-1-carboxylate synthase MenD
680224	syn	TC		conserved hypotheticals		conserved hypothetical protein
685284	syn	TC		intermediary metabolism and respiration		FAD-linked oxidoreductase
686057	syn	TC		intermediary metabolism and respiration		polypropenyl diphosphate synthetase GrcC1
687108	non	GA		peptidase heat shock protein X HspX		peptidase heat shock protein X HspX
689234	syn	TG		intermediary metabolism and respiration		transmembrane carbonic anhydrase Sulp
689564	Int	AC	73 MUL_0666	intermediary metabolism and respiration		transmembrane carbonic anhydrase Sulp 1
689565	Int	GA		intermediary metabolism and respiration		transmembrane carbonic anhydrase Sulp 1
690609	syn	GC		intermediary metabolism and respiration		intermediary metabolism and respiration
693949	psd	AG		intermediary metabolism and respiration		C-term lantibiotic modifying enzyme - pseudogene
699562	non	GA		cell wall and cell processes		ABC-type transporter
700679	non	GT		cell wall and cell processes		ABC-type transporter
701573	syn	TC		cell wall and cell processes		ABC transporter ATP-binding protein
701687	syn	AG		cell wall and cell processes		ABC transporter ATP-binding protein
701934	non	TC		regulatory proteins		transcriptional regulator
717274	Int	AG	118 MUL_0689	information pathways		peptide amidase GatA 1
718997	non	CT		intermediary metabolism and respiration		galactokinase GalK
719131	syn	AG		intermediary metabolism and respiration		galactokinase GalK
719167	non	AG		intermediary metabolism and respiration		galactokinase GalK
719853	non	TC		intermediary metabolism and respiration		galactokinase GalK
719911	syn	TC		intermediary metabolism and respiration		galactokinase GalK
720804	syn	CG		regulatory proteins		transcriptional regulator
723885	Int	GA				
724155	Int	AG	62 MUL_0694	PE/PPe		N-term PE-PGRS - pseudogene
725517	psd	CG		cell wall and cell processes		C-term conserved hypothetical membrane protein - pseudogene
728515	psd	CG		conserved hypotheticals		C-term conserved hypothetical protein - pseudogene
734879	psd	GA		cell wall and cell processes		C-term conserved hypothetical secreted protein - pseudogene
738488	Int	CT				
742086	syn	TG		information pathways		exodeoxyribonuclease V (alpha chain) RecD
742726	syn	GA		information pathways		exodeoxyribonuclease V (alpha chain) RecD
743179	non	AG		information pathways		exodeoxyribonuclease V (beta chain) RecB
743213	non	TA		information pathways		exodeoxyribonuclease V (beta chain) RecB
744333	syn	CT		information pathways		exodeoxyribonuclease V (beta chain) RecB
747560	syn	AG		information pathways		exodeoxyribonuclease V (gamma chain) RecC
747631	non	CG		information pathways		exodeoxyribonuclease V (gamma chain) RecC
747713	non	TG		information pathways		exodeoxyribonuclease V (gamma chain) RecC
749623	non	CA		intermediary metabolism and respiration		nitroreductase
750894	psd	TC		cell wall and cell processes		N-term conserved hypothetical transmembrane protein - pseudogene
751064	psd	CA		cell wall and cell processes		N-term conserved hypothetical transmembrane protein - pseudogene
752705	syn	AG		cell wall and cell processes		conserved hypothetical membrane protein
753371	Int	AG	124 MUL_0714	cell wall and cell processes		conserved hypothetical membrane protein
754475	Int	GA		conserved hypotheticals		conserved protein
755403	non	AG		conserved hypotheticals		conserved protein
761298	Int	C-	9 MUL_5083	information pathways		conserved hypothetical protein_pseudogene
762330	non	AG		lipid metabolism		methoxy mycolic acid synthase 4 MmaA4

SNP position	SNP type	Nucleotide change <ref><snp>	Distance to nearest locus	Nearby Locus	Functional group	Product
765505	non	CT	MUL_0733	-	intermediary metabolism and respiration	lipase/esterase LinG1
765551	syn	GC	MUL_0733	-	intermediary metabolism and respiration	lipase/esterase LinG1
767939	int	AC	70	MUL_0734	conserved hypothetical	conserved hypothetical protein
768634	non	TC	MUL_0735	-	intermediary metabolism and respiration	lipase/esterase LinG2
768718	non	GA	MUL_0735	-	intermediary metabolism and respiration	lipase/esterase LinG2
770385	int	TC	82	MUL_0737	intermediary metabolism and respiration	alpha-mannosidase
770702	non	TC	MUL_0737	-	intermediary metabolism and respiration	alpha-mannosidase
772692	non	TC	MUL_0737	-	intermediary metabolism and respiration	alpha-mannosidase
774110	non	TC	MUL_0737	-	intermediary metabolism and respiration	alpha-mannosidase
774136	syn	AG	MUL_0737	-	intermediary metabolism and respiration	alpha-mannosidase
776039	int	CA	85	MUL_0739	intermediary metabolism and respiration	carbohydrate kinase
776273	int	GA	101	MUL_0740	PE/PPE	PE-PGRS family protein
776304	int	TG	70	MUL_0740	PE/PPE	PE-PGRS family protein
776403	int	AG	29	MUL_0740	PE/PPE	PE-PGRS family protein
779722	syn	TC	MUL_0742	-	information pathways	50S ribosomal protein L7/L12, RplL
779929	syn	CG	MUL_0743	-	regulatory proteins	transcriptional regulatory protein
780105	non	CA	MUL_0743	-	regulatory proteins	transcriptional regulatory protein
780122	non	TG	MUL_0743	-	regulatory proteins	transcriptional regulatory protein
780243	non	CT	MUL_0743	-	regulatory proteins	transcriptional regulatory protein
780279	syn	GA	MUL_0743	-	regulatory proteins	transcriptional regulatory protein
780409	non	AC	MUL_0743	-	regulatory proteins	transcriptional regulatory protein
780451	syn	GC	MUL_0743	-	regulatory proteins	transcriptional regulatory protein
780454	syn	GA	MUL_0743	-	regulatory proteins	transcriptional regulatory protein
780475	syn	GA	MUL_0743	-	regulatory proteins	transcriptional regulatory protein
780478	non	GC	MUL_0743	-	regulatory proteins	transcriptional regulatory protein
780598	syn	TC	MUL_0743	-	regulatory proteins	transcriptional regulatory protein
781040	syn	CT	MUL_0744	-	intermediary metabolism and respiration	dehydrogenase
781479	non	CA	MUL_0744	-	intermediary metabolism and respiration	dehydrogenase
781729	non	CC	MUL_0744	-	intermediary metabolism and respiration	dehydrogenase
782323	int	TG	143	MUL_0744	intermediary metabolism and respiration	dehydrogenase
784656	syn	TC	MUL_0746	-	information pathways	DNA-directed RNA polymerase beta subunit RpoB
785063	syn	CT	MUL_0746	-	information pathways	DNA-directed RNA polymerase beta subunit RpoB
786217	syn	GC	MUL_0746	-	information pathways	DNA-directed RNA polymerase beta subunit RpoB
787907	syn	TC	MUL_0747	-	information pathways	DNA-directed RNA polymerase beta chain RpoC
758072	syn	GC	MUL_0747	-	information pathways	DNA-directed RNA polymerase beta chain RpoC
788111	syn	TC	MUL_0747	-	information pathways	DNA-directed RNA polymerase beta chain RpoC
790952	syn	GC	MUL_0747	-	information pathways	DNA-directed RNA polymerase beta chain RpoC
792030	int	CT	105	MUL_0748	PE/PPE	PE-PGRS family protein
792048	int	GA	87	MUL_0748	PE/PPE	PE-PGRS family protein
793579	psd	GC	MUL_0749	-	intermediary metabolism and respiration	C-term ceramidas - pseudogene
793579	psd	GC	MUL_0749	-	intermediary metabolism and respiration	N-term ceramidas - pseudogene
794196	psd	GA	MUL_0749	-	intermediary metabolism and respiration	N-term ceramidas - pseudogene
794412	int	CT	118	MUL_0749	intermediary metabolism and respiration	N-term ceramidas - pseudogene
794617	psd	CT	MUL_0750	-	conserved hypothetical	N-term conserved hypothetical protein - pseudogene
795391	int	AG	49	MUL_0751	information pathways	endonuclease (apurinase) End
798465	syn	TC	MUL_0753	-	lipid metabolism	acyl-CoA dehydrogenase
804758	int	CT	134	MUL_0758	cell wall and cell processes	conserved transmembrane protein MmpS5
805649	non	GA	MUL_0760	-	cell wall and cell processes	conserved hypothetical membrane protein
807239	int	CT	66	MUL_0762	regulatory proteins	transcription regulator TetR family
812297	non	AG	MUL_0767	-	cell wall and cell processes	conserved membrane protein
812381	non	GA	MUL_0767	-	cell wall and cell processes	conserved membrane protein
812400	syn	GT	MUL_0767	-	cell wall and cell processes	conserved membrane protein
812562	syn	CT	MUL_0767	-	cell wall and cell processes	conserved membrane protein
812628	syn	TC	MUL_0767	-	cell wall and cell processes	conserved membrane protein
812787	syn	AG	MUL_0767	-	cell wall and cell processes	conserved membrane protein
812899	non	AG	MUL_0767	-	cell wall and cell processes	conserved membrane protein
813190	int	AT	38	MUL_0768	intermediary metabolism and respiration	short-chain dehydrogenase/reductase
813489	syn	AC	MUL_0768	-	intermediary metabolism and respiration	short-chain dehydrogenase/reductase
813617	syn	CG	MUL_0768	-	intermediary metabolism and respiration	short-chain dehydrogenase/reductase
814361	syn	AC	MUL_0769	-	intermediary metabolism and respiration	ferredoxin reductase
814523	syn	TC	MUL_0769	-	intermediary metabolism and respiration	ferredoxin reductase
814526	syn	TC	MUL_0769	-	intermediary metabolism and respiration	ferredoxin reductase
814919	syn	AC	MUL_0769	-	intermediary metabolism and respiration	ferredoxin reductase
815287	syn	TA	MUL_0769	-	intermediary metabolism and respiration	ferredoxin reductase
815295	syn	TC	MUL_0769	-	intermediary metabolism and respiration	ferredoxin reductase
815296	syn	CT	MUL_0769	-	intermediary metabolism and respiration	ferredoxin reductase
815353	non	GA	MUL_0769	-	intermediary metabolism and respiration	ferredoxin reductase
815500	syn	TC	MUL_0770	-	conserved hypothetical	conserved hypothetical protein
818485	syn	TC	MUL_0773	-	intermediary metabolism and respiration	coenzyme PQQ synthesis protein E_PqqE
818560	syn	CG	MUL_0773	-	intermediary metabolism and respiration	coenzyme PQQ synthesis protein E_PqqE
820303	non	GA	MUL_0775	-	intermediary metabolism and respiration	Creatinine amidohydrolase
820464	syn	TC	MUL_0775	-	intermediary metabolism and respiration	Creatinine amidohydrolase
822420	non	CT	MUL_0777	-	intermediary metabolism and respiration	dehydrogenase
826498	int	AG	147	MUL_0779	PE/PPE	N-term PPE family protein pseudogene
829625	int	TC	-	-	-	-
837470	non	AG	MUL_0790	-	information pathways	50S ribosomal protein L3 RplC
837554	non	GA	MUL_0791	-	information pathways	50S ribosomal protein L4 RplD
837585	non	TC	MUL_0791	-	information pathways	50S ribosomal protein L4 RplD
842939	psd	GA	MUL_0800	-	intermediary metabolism and respiration	mid-section arylsulfatase AtsA - pseudogene
843048	psd	CT	MUL_0800	-	intermediary metabolism and respiration	mid-section arylsulfatase AtsA - pseudogene
843188	psd	TC	MUL_0800	-	intermediary metabolism and respiration	mid-section arylsulfatase AtsA - pseudogene
843188	psd	TC	MUL_0800	-	unknown	mid-section arylsulfatase AtsA - pseudogene
843522	psd	GA	MUL_0800	-	unknown	mid-section arylsulfatase AtsA - pseudogene
844163	psd	TG	MUL_0800	-	intermediary metabolism and respiration	C-term arylsulfatase AtsA - pseudogene
844696	non	GT	MUL_0801	-	conserved hypothetical	conserved protein
844768	non	GA	MUL_0801	-	conserved hypothetical	conserved protein
845269	psd	TC	MUL_0802	-	conserved hypothetical	N-term conserved hypothetical protein - pseudogene
845398	psd	GA	MUL_0802	-	conserved hypothetical	N-term conserved hypothetical protein - pseudogene
845677	psd	TG	MUL_0802	-	conserved hypothetical	C-term conserved hypothetical protein - pseudogene
845677	psd	TG	MUL_0802	-	conserved hypothetical	N-term conserved hypothetical protein - pseudogene
845931	psd	AG	MUL_0802	-	conserved hypothetical	C-term conserved hypothetical protein - pseudogene
846126	int	AG	139	MUL_0803	cell wall and cell processes	conserved transmembrane protein

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
846233	Int	CT	-	32	MUL_0803	cell wall and cell processes	conserved transmembrane protein
846331	non	AG	MUL_0803	-		cell wall and cell processes	conserved transmembrane protein
851513	syn	AC	MUL_0813	-		information pathways	50S ribosomal protein L15 RplO
851630	non	AG	MUL_0813	-		information pathways	50S ribosomal protein L15 RplO
852447	syn	AC	MUL_0814	-		intermediary metabolism and respiration	flavin-dependent oxidoreductase
852736	Int	AG	-	49	MUL_0815	cell wall and cell processes	protease iv Ssp
852973	syn	CG	MUL_0815	-		cell wall and cell processes	protease iv Ssp
853038	non	GC	MUL_0815	-		cell wall and cell processes	protease iv Ssp
853092	non	CA	MUL_0815	-		cell wall and cell processes	protease iv Ssp
853817	non	GC	MUL_0815	-		cell wall and cell processes	protease iv Ssp
854989	non	TC	MUL_0816	-		intermediary metabolism and respiration	O-methyltransferase
855965	syn	TC	MUL_0817	-		intermediary metabolism and respiration	O-methyltransferase
856573	syn	CT	MUL_0818	-		intermediary metabolism and respiration	O-methyltransferase
856696	syn	TC	MUL_0818	-		intermediary metabolism and respiration	O-methyltransferase
857107	syn	TC	MUL_0818	-		intermediary metabolism and respiration	O-methyltransferase
858069	syn	AT	MUL_0819	-		intermediary metabolism and respiration	short-chain dehydrogenase Adh 1
858152	non	GA	MUL_0819	-		intermediary metabolism and respiration	short-chain dehydrogenase Adh 1
858507	syn	AG	MUL_0819	-		intermediary metabolism and respiration	D-3-phosphoglycerate dehydrogenase SerA2
860487	syn	AG	MUL_0821	-		regulatory proteins	transcriptional regulatory protein
860621	non	CG	MUL_0821	-		regulatory proteins	transcriptional regulatory protein
860845	non	AG	MUL_0821	-		regulatory proteins	transcriptional regulatory protein
861486	syn	TC	MUL_0822	-		intermediary metabolism and respiration	L-fuculose-1-phosphate aldolase FucA
861633	syn	AG	MUL_0822	-		intermediary metabolism and respiration	L-fuculose-1-phosphate aldolase FucA
862154	syn	GC	MUL_0823	-		intermediary metabolism and respiration	D-3-phosphoglycerate dehydrogenase SerA2
862309	non	TT	MUL_0823	-		intermediary metabolism and respiration	D-3-phosphoglycerate dehydrogenase SerA2
864594	non	CG	MUL_0825	-		conserved hypothetical	conserved protein
867494	syn	TC	MUL_0828	-		cell wall and cell processes	proton-translocase SecY
869472	syn	AG	MUL_0830	-		intermediary metabolism and respiration	methionine aminopeptidase MapA
873965	syn	AG	MUL_0836	-		lipid metabolism	acyl-CoA dehydrogenase FadE9
874716	syn	AG	MUL_0837	-		intermediary metabolism and respiration	methylmalonate semialdehyde dehydrogenase MmsA
875378	syn	AG	MUL_0837	-		intermediary metabolism and respiration	methylmalonate semialdehyde dehydrogenase MmsA
876113	syn	AG	MUL_0837	-		intermediary metabolism and respiration	methylmalonate semialdehyde dehydrogenase MmsA
876846	syn	AG	MUL_0838	-		cell wall and cell processes	transmembrane carbohydrate transport protein
880330	syn	TC	MUL_0841	-		conserved hypothetical	conserved hypothetical protein
884609	syn	CT	MUL_0848	-		information pathways	DNA-directed RNA polymerase (alpha chain) RpoA
885925	syn	TC	MUL_0850	-		information pathways	pseudouridine synthase a TruA
886074	syn	TC	MUL_0850	-		information pathways	pseudouridine synthase a TruA
886338	non	CT	MUL_0851	-		cell wall and cell processes	D-serine/D-alanine/glycine transporter CvcA
886773	non	TG	MUL_0851	-		cell wall and cell processes	D-serine/D-alanine/glycine transporter CvcA
886990	syn	AG	MUL_0851	-		cell wall and cell processes	D-serine/D-alanine/glycine transporter CvcA
887059	syn	AC	MUL_0851	-		cell wall and cell processes	D-serine/D-alanine/glycine transporter CvcA
887326	syn	GA	MUL_0851	-		cell wall and cell processes	D-serine/D-alanine/glycine transporter CvcA
887503	syn	GA	MUL_0851	-		cell wall and cell processes	D-serine/D-alanine/glycine transporter CvcA
887832	Int	CT	-	45	MUL_0851	cell wall and cell processes	D-serine/D-alanine/glycine transporter CvcA
887835	Int	CG	-	48	MUL_0851	cell wall and cell processes	D-serine/D-alanine/glycine transporter CvcA
888129	Int	CT	-	74	MUL_5078	PE/PPE	PPE family protein
889953	Int	AG	-	112	MUL_0852	PE/PPE	N-term PPE family protein - pseudogene
892666	syn	TG	MUL_0855	-		cell wall and cell processes	cutinase precursor Cut4
892785	non	TC	MUL_0855	-		cell wall and cell processes	cutinase precursor Cut4
894889	non	TC	MUL_0857	-		cell wall and cell processes	conserved hypothetical membrane protein
895209	non	AG	MUL_0857	-		cell wall and cell processes	conserved hypothetical membrane protein
896126	non	TC	MUL_0858	-		intermediary metabolism and respiration	membrane anchored serine protease (mycosin) Mcp4
896532	syn	GA	MUL_0858	-		intermediary metabolism and respiration	membrane anchored serine protease (mycosin) Mcp4
898244	syn	AG	MUL_0859	-		cell wall and cell processes	conserved hypothetical membrane protein
900451	syn	TC	MUL_0860	-		cell wall and cell processes	conserved membrane protein
901712	non	CG	MUL_0860	-		cell wall and cell processes	conserved membrane protein
901808	non	AG	MUL_0860	-		cell wall and cell processes	conserved membrane protein
901948	syn	CT	MUL_0860	-		cell wall and cell processes	conserved membrane protein
902156	non	CG	MUL_0861	-		conserved hypothetical	conserved hypothetical protein
902395	non	CG	MUL_0861	-		conserved hypothetical	conserved hypothetical protein
902996	non	TC	MUL_0861	-		conserved hypothetical	conserved hypothetical protein
905276	Int	TC	-	76	MUL_0866	intermediary metabolism and respiration	phosphomannomutase MrsA
907216	non	TG	MUL_0868	-		conserved hypothetical	conserved hypothetical protein
907503	syn	AG	MUL_0868	-		conserved hypothetical	conserved hypothetical protein
907608	syn	AG	MUL_0868	-		conserved hypothetical	conserved hypothetical protein
909128	psd	AC	MUL_0869	-		intermediary metabolism and respiration	N-term cytochrome F420-dependent oxidoreductase pseudogene
910217	syn	AG	MUL_0870	-		conserved hypothetical	conserved protein
910602	psd	TG	MUL_0871	-		cell wall and cell processes	C-term conserved hypothetical transmembrane protein pseudogene
910940	Int	CT	-	82	MUL_0872	intermediary metabolism and respiration	glucosamine-fructose-6-phosphate aminotransferase GlnS
911582	syn	TG	MUL_0872	-		intermediary metabolism and respiration	glucosamine-fructose-6-phosphate aminotransferase GlnS
911594	syn	AC	MUL_0872	-		intermediary metabolism and respiration	glucosamine-fructose-6-phosphate aminotransferase GlnS
912101	syn	TG	MUL_0872	-		intermediary metabolism and respiration	glucosamine-fructose-6-phosphate aminotransferase GlnS
912426	non	CG	MUL_0872	-		intermediary metabolism and respiration	glucosamine-fructose-6-phosphate aminotransferase GlnS
915782	syn	AC	MUL_0876	-		cell wall and cell processes	conserved hypothetical membrane protein
920570	syn	AG	MUL_0880	-		cell wall and cell processes	conserved hypothetical hydrolase
923578	syn	AG	MUL_0884	-			O-sialoglycoprotein endopeptidase Gcp (glycoprotease)
925117	syn	TC	MUL_0886	-			60 kDa chaperone (GroEL1)
937851	syn	TC	MUL_0897	-		information pathways	alternative RNA polymerase sigma-D factor SqiD
938171	non	AG	MUL_0898	-		conserved hypothetical	conserved hypothetical protein
938407	syn	GC	MUL_0898	-		conserved hypothetical	conserved hypothetical protein
941114	syn	TC	MUL_0900	-		intermediary metabolism and respiration	inosine-5'-monophosphate (imp) dehydrogenase Guab2
941354	syn	TC	MUL_0900	-		intermediary metabolism and respiration	inosine-5'-monophosphate (imp) dehydrogenase Guab2
942584	Int	TC	-	12	MUL_0901	intermediary metabolism and respiration	inosine-5'-monophosphate (imp) dehydrogenase Guab3
942645	Int	AG	-	108	MUL_0902	PE/PPE	PPE family protein
943920	Int	CG	-				
947602	syn	CG	MUL_0905	-		regulatory proteins	transcriptional regulator
947840	non	TC	MUL_0905	-		regulatory proteins	transcriptional regulator
948860	syn	TC	MUL_0906	-		intermediary metabolism and respiration	glycosyl hydrolase
953122	non	AG	MUL_0911	-		cell wall and cell processes	integral membrane transport protein
954718	Int	TC	-	44	MUL_0911	cell wall and cell processes	integral membrane transport protein
956733	syn	TC	MUL_0913	-		intermediary metabolism and respiration	GMP synthase GuA
956804	syn	GA	MUL_0913	-		intermediary metabolism and respiration	GMP synthase GuA

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
957886	Int	-G		37	MUL_0914	cell wall and cell processes	conserved hypothetical secreted protein
957886	Int	-G		37	MUL_0915	conserved hypothetical	conserved protein
960544	psd	TC	MUL_0917	-		intermediary metabolism and respiration	C-term inosine-uridine nucleoside hydrolase <i>IunH</i> - pseudogene
961375	syn	AG	MUL_0918	-		lipid metabolism	short-chain dehydrogenase <i>AcrA1</i>
961383	non	TC	MUL_0918	-		lipid metabolism	short-chain dehydrogenase <i>AcrA1</i>
961405	syn	TC	MUL_0918	-		lipid metabolism	short-chain dehydrogenase <i>AcrA1</i>
962453	non	AG	MUL_0918	-		lipid metabolism	short-chain dehydrogenase <i>AcrA1</i>
962487	non	TC	MUL_0918	-		lipid metabolism	short-chain dehydrogenase <i>AcrA1</i>
965137	syn	GA	MUL_0921	-			trehalose-6-phosphate phosphatase <i>OtsB2</i>
965282	non	TC	MUL_0921	-			trehalose-6-phosphate phosphatase <i>OtsB2</i>
965617	syn	GA	MUL_0921	-			trehalose-6-phosphate phosphatase <i>OtsB2</i>
966141	syn	AG	MUL_0921	-			trehalose-6-phosphate phosphatase <i>OtsB2</i>
966349	psd	TC	MUL_0922	-		conserved hypotheticals	C-term conserved hypothetical protein - pseudogene
966370	psd	CT	MUL_0922	-		conserved hypotheticals	C-term conserved hypothetical protein - pseudogene
966430	psd	AG	MUL_0922	-		conserved hypotheticals	C-term conserved hypothetical protein - pseudogene
966559	psd	TC	MUL_0922	-		conserved hypotheticals	C-term conserved hypothetical protein - pseudogene
966667	psd	TC	MUL_0922	-		conserved hypotheticals	C-term conserved hypothetical protein - pseudogene
966733	psd	GA	MUL_0922	-		conserved hypotheticals	C-term conserved hypothetical protein - pseudogene
967168	psd	AG	MUL_0922	-		conserved hypotheticals	C-term conserved hypothetical protein - pseudogene
967412	psd	CG	MUL_0922	-		conserved hypotheticals	N-term conserved hypothetical protein - pseudogene
968975	syn	CT	MUL_0923	-		information pathways	DNA polymerase III alpha chain <i>DnaE2</i>
969707	syn	TC	MUL_0923	-		information pathways	DNA polymerase III alpha chain <i>DnaE2</i>
970935	non	AG	MUL_0923	-		information pathways	DNA polymerase III alpha chain <i>DnaE2</i>
976623	syn	GT	MUL_0929	-		conserved hypotheticals	conserved hypothetical protein
977840	syn	GC	MUL_0931	-		conserved hypotheticals	conserved hypothetical protein
977870	syn	TC	MUL_0931	-		conserved hypotheticals	conserved hypothetical protein
978728	syn	CG	MUL_0931	-		conserved hypotheticals	conserved hypothetical protein
978900	syn	AG	MUL_0931	-		conserved hypotheticals	conserved hypothetical protein
980581	syn	AG	MUL_0932	-		intermediary metabolism and respiration	pyrrole-5-carboxylate dehydrogenase <i>RocA</i>
982145	syn	CT	MUL_0934	-		regulatory proteins	transcriptional regulator
982236	non	GC	MUL_0934	-		regulatory proteins	transcriptional regulator
983368	syn	AG	MUL_0935	-		lipid metabolism	ketothiolase <i>Ltp2</i>
984704	non	GA	MUL_0938	-		conserved hypotheticals	conserved hypothetical protein
985172	non	CT	MUL_0938	-		conserved hypotheticals	conserved hypothetical protein
989021	syn	AG	MUL_0943	-		lipid metabolism	fatty-acid-CoA synthetase <i>FadD36</i>
991073	syn	GA	MUL_0944	-		regulatory proteins	transcriptional regulatory protein
991103	syn	GA	MUL_0944	-		regulatory proteins	transcriptional regulatory protein
991181	syn	AG	MUL_0944	-		regulatory proteins	transcriptional regulatory protein
991526	syn	CG	MUL_0944	-		regulatory proteins	transcriptional regulatory protein
994433	non	CA	MUL_0948	-		conserved hypotheticals	conserved hypothetical protein
994545	non	CT	MUL_0948	-		conserved hypotheticals	conserved hypothetical protein
995682	syn	CT	MUL_0949	-		cell wall and cell processes	conserved integral membrane transport protein
998396	non	TC	MUL_0951	-		unknown	hypothetical protein
998799	syn	TC	MUL_0952	-		regulatory proteins	conserved hypothetical regulatory protein
998937	syn	TC	MUL_0952	-		regulatory proteins	conserved hypothetical regulatory protein
999218	non	AT	MUL_0953	-		intermediary metabolism and respiration	transferase
999394	syn	AG	MUL_0953	-		intermediary metabolism and respiration	transferase
999987	non	CG	MUL_0953	-		intermediary metabolism and respiration	transferase
1000095	non	TC	MUL_0953	-		intermediary metabolism and respiration	transferase
1000958	syn	GC	MUL_0954	-		intermediary metabolism and respiration	succinyl-diaminopimelate desuccinylase <i>DapE</i>
1004592	syn	TC	MUL_0957	-		lipid metabolism	fatty-acid-CoA ligase <i>FadD6</i>
1005243	syn	TC	MUL_0957	-		lipid metabolism	fatty-acid-CoA ligase <i>FadD6</i>
1006460	syn	TG	MUL_0958	-		intermediary metabolism and respiration	dihydropteroate synthase 2 <i>FolP2</i>
1007201	syn	TC	MUL_0959	-		conserved hypotheticals	conserved hypothetical protein
1016614	Int	GC		142	MUL_0966	insertion seqs and phages	transposase for IS2606
1018380	Int	TG		13	MUL_0967	PE/PP	PE family protein
1019174	psd	AG	MUL_0969	-		intermediary metabolism and respiration	C-term aldehyde dehydrogenase NAD dependent <i>AldA</i> 2 - pseudogene
1019861	psd	AG	MUL_0969	-		intermediary metabolism and respiration	C-term aldehyde dehydrogenase NAD dependent <i>AldA</i> 2 - pseudogene
1021898	Int	GT		-			
1022842	syn	AG	MUL_0971	-		lipid metabolism	acetyl-CoA acetyltransferase <i>FadA6</i> 3
1023532	non	TG	MUL_0972	-		lipid metabolism	enoyl-CoA hydratase <i>EchA1</i>
1024204	Int	TC		-			
1024322	Int	GC		102	MUL_0973	PE/PPE	N-term PE-PGRS family protein - pseudogene
1033216	syn	AG	MUL_0979	-		intermediary metabolism and respiration	oxidoreductase
1033576	syn	TC	MUL_0979	-		intermediary metabolism and respiration	oxidoreductase
1037454	psd	GA	MUL_0984	-		intermediary metabolism and respiration	C-term oxidoreductase - pseudogene
1037528	psd	CG	MUL_0984	-		intermediary metabolism and respiration	C-term oxidoreductase - pseudogene
1037764	psd	AG	MUL_0984	-		intermediary metabolism and respiration	C-term oxidoreductase - pseudogene
1038741	psd	GT	MUL_0984	-		intermediary metabolism and respiration	N-term oxidoreductase - pseudogene
1040914	non	CT	MUL_0986	-		lipid metabolism	alpha-methylacyl-CoA racemase <i>Mcr</i>
1041515	syn	TC	MUL_0987	-		intermediary metabolism and respiration	short-chain type dehydrogenase/reductase
1041822	Int	GA		85	MUL_0987	intermediary metabolism and respiration	short-chain type dehydrogenase/reductase
1042123	Int	AG		94	MUL_0988	conserved hypotheticals	conserved hypothetical protein
1043714	non	AG	MUL_0989	-		cell wall and cell processes	conserved transmembrane transport protein <i>MmpL13</i>
1044853	syn	CG	MUL_0990	-		regulatory proteins	transcriptional regulatory protein (probably TetR-family)
1045488	syn	CT	MUL_0991	-		conserved hypotheticals	conserved hypothetical protein
1045491	syn	GC	MUL_0991	-		conserved hypotheticals	conserved hypothetical protein
1046105	Int	CT		67	MUL_0992	regulatory proteins	transcriptional regulatory protein
1046125	Int	AG		61	MUL_0991	conserved hypotheticals	conserved hypothetical protein
1047375	psd	AG	MUL_0994	-		lipid metabolism	C-term O-methyltransferase <i>Omt</i> 2 - pseudogene
1047538	psd	CT	MUL_0994	-		lipid metabolism	C-term O-methyltransferase <i>Omt</i> 2 - pseudogene
1047613	psd	G-	MUL_0994	-		lipid metabolism	N-term O-methyltransferase <i>Omt</i> 2 - pseudogene
1048974	non	CT	MUL_0996	-		conserved hypotheticals	conserved protein
1049027	syn	AC	MUL_0996	-		conserved hypotheticals	conserved protein
1049486	Int	TC		86	MUL_0997	conserved hypotheticals	conserved hypothetical protein
1049519	Int	TC		119	MUL_0997	conserved hypotheticals	conserved hypothetical protein
1049538	Int	AC		138	MUL_0997	conserved hypotheticals	conserved hypothetical protein
1049539	Int	GA		139	MUL_0997	conserved hypotheticals	conserved hypothetical protein
1049540	Int	TC		140	MUL_0997	conserved hypotheticals	conserved hypothetical protein
1049545	Int	CA		145	MUL_0997	conserved hypotheticals	conserved hypothetical protein
10507046	non	GA	MUL_1006	-		cell wall and cell processes	conserved transmembrane protein
1057194	syn	TG	MUL_1006	-		cell wall and cell processes	conserved transmembrane protein

SNP position	SNP type	Nucleotide change <ref><snp>	Distance to nearest locus	Nearby Locus	Functional group	Product
1057201	non	AG	MUL_1006	-	cell wall and cell processes	conserved transmembrane protein
1057623	non	CT	MUL_1006	-	cell wall and cell processes	conserved transmembrane protein
1058207	syn	AG	MUL_1007	-	conserved hypothetical	conserved hypothetical protein
1058271	non	GC	MUL_1007	-	conserved hypothetical	conserved hypothetical protein
1059427	syn	TC	MUL_1009	-	information pathways	GTP-binding translation elongation factor TypA
1059561	syn	TC	MUL_1009	-	information pathways	GTP-binding translation elongation factor TypA
1059796	syn	GC	MUL_1009	-	information pathways	GTP-binding translation elongation factor TypA
1060846	syn	TC	MUL_1009	-	information pathways	GTP-binding translation elongation factor TypA
1061077	non	AG	MUL_1009	-	information pathways	GTP-binding translation elongation factor TypA
1062440	syn	TC	MUL_1010	-	cell wall and cell processes	conserved lipoprotein LpoW
1069048	int.	CT		-		
1069263	int.	CT		-		
1069440	int.	TC		-		
1069509	int.	TC		-		
1070171	psd	CG	MUL_1016	-	regulatory proteins	N-term transcriptional regulatory protein - pseudogene
1070373	psd	GA	MUL_1016	-	regulatory proteins	N-term transcriptional regulatory protein - pseudogene
1070487	int.	TC	89 MUL_1016	-	regulatory proteins	N-term transcriptional regulatory protein - pseudogene
1071114	non	GA	MUL_1017	-	intermediary metabolism and respiration	N-acetyl-1-D-myo-inositol-2-amino-2-deoxy-alpha-D-glucopyranoside deacetylase MshB
1071380	syn	TC	MUL_1017	-	intermediary metabolism and respiration	N-acetyl-1-D-myo-inositol-2-amino-2-deoxy-alpha-D-glucopyranoside deacetylase MshB
1073648	syn	TC	MUL_1020	-	intermediary metabolism and respiration	F420 biosynthesis protein FbiC
1073662	syn	GC	MUL_1020	-	intermediary metabolism and respiration	F420 biosynthesis protein FbiC
1074045	non	GA	MUL_1020	-	intermediary metabolism and respiration	F420 biosynthesis protein FbiC
1074895	syn	TC	MUL_1020	-	intermediary metabolism and respiration	F420 biosynthesis protein FbiC
1075564	syn	CG	MUL_1020	-	intermediary metabolism and respiration	F420 biosynthesis protein FbiC
1075575	syn	CC	MUL_1020	-	intermediary metabolism and respiration	F420 biosynthesis protein FbiC
1075922	int.	TA		-		
1076103	int.	AG		-		
1078013	int.	GG	37 MUL_1021	PE/PPE	PE/PPE	PE-PGK family protein
1082431	syn	GA	MUL_1025	-	intermediary metabolism and respiration	ferredoxin FdxC
1083756	syn	TG	MUL_1026	-	intermediary metabolism and respiration	ammonotransferase
1083795	syn	CT	MUL_1026	-	intermediary metabolism and respiration	ammonotransferase
1084255	psd	AG	MUL_1027	-	cell wall and cell processes	C-term conserved hypothetical membrane protein - pseudogene
1084339	psd	CG	MUL_1027	-	cell wall and cell processes	C-term conserved hypothetical membrane protein - pseudogene
1084719	psd	TC	MUL_1027	-	cell wall and cell processes	C-term conserved hypothetical membrane protein - pseudogene
1084899	psd	GA	MUL_1027	-	cell wall and cell processes	C-term conserved hypothetical membrane protein - pseudogene
1086113	psd	CT	MUL_1027	-	cell wall and cell processes	N-term conserved hypothetical membrane protein - pseudogene
1086120	psd	TC	MUL_1027	-	cell wall and cell processes	N-term conserved hypothetical membrane protein - pseudogene
1086342	psd	TC	MUL_1027	-	cell wall and cell processes	N-term conserved hypothetical membrane protein - pseudogene
1086918	int.	CT	49 MUL_1028	conserved hypothetical	conserved hypothetical	N-term conserved hypothetical protein - pseudogene
1087302	psd	TC	MUL_1028	-	conserved hypothetical	N-term conserved hypothetical protein - pseudogene
1087474	psd	AC	MUL_1028	-	conserved hypothetical	N-term conserved hypothetical protein - pseudogene
1088054	psd	TC	MUL_1028	-	conserved hypothetical	C-term conserved hypothetical protein - pseudogene
1093005	int.	CT	53 MUL_1033	PE/PPE	PE/PPE	N-term PE family protein - pseudogene
1094317	int.	GA		-		
1095733	non	AT	MUL_1035	-	conserved hypothetical	conserved hypothetical protein
1096063	psd	TC	MUL_1036	-	conserved hypothetical	N-term conserved hypothetical protein - pseudogene
1099053	syn	CT	MUL_1038	-	intermediary metabolism and respiration	oxidoreductase
1099333	syn	GA	MUL_1039	-	regulatory proteins	conserved hypothetical regulatory protein
1099892	psd	AG	MUL_1040	-	conserved hypothetical	C-term conserved hypothetical protein - pseudogene
1100399	psd	AC	MUL_1040	-	conserved hypothetical	N-term conserved hypothetical protein - pseudogene
1101440	psd	CT	MUL_1042	-	conserved hypothetical	N-term conserved hypothetical protein - pseudogene
1103653	syn	CT	MUL_1044	-	conserved hypothetical	conserved hypothetical protein
1103802	non	TC	MUL_1044	-	conserved hypothetical	conserved hypothetical protein
1104213	syn	TC	MUL_1045	-	conserved hypothetical	conserved hypothetical protein
1104234	syn	AG	MUL_1045	-	conserved hypothetical	conserved hypothetical protein
1105206	int.	TC	74 MUL_1046	lipid metabolism	acyl-CoA transferase	
1108264	non	AG	MUL_1049	-	intermediary metabolism and respiration	cytochrome P450 191A3 Cyp191A3
1108740	syn	TC	MUL_1049	-	intermediary metabolism and respiration	cytochrome P450 191A3 Cyp191A3
1109620	psd	GC	MUL_1050	-	intermediary metabolism and respiration	C-term dehydrogenase - pseudogene
1110613	non	GC	MUL_1051	-	conserved hypothetical	conserved hypothetical protein
1111663	syn	GC	MUL_1053	-	intermediary metabolism and respiration	monooxygenase
1112146	syn	GA	MUL_1053	-	intermediary metabolism and respiration	monooxygenase
1112662	syn	AG	MUL_1053	-	intermediary metabolism and respiration	monooxygenase
1112836	non	AG	MUL_1053	-	intermediary metabolism and respiration	monooxygenase
1113927	syn	CG	MUL_1054	-	intermediary metabolism and respiration	esterase LipW
1114343	psd	TG	MUL_1055	-	intermediary metabolism and respiration	C-term zinc-type alcohol dehydrogenase (E subunit) AdhE_pseudogene
1115359	syn	AC	MUL_1056	-	conserved hypothetical	conserved hypothetical protein
1116499	non	CT	MUL_1058	-	regulatory proteins	transcriptional regulatory protein (probably GntR-family)
1120638	syn	TC	MUL_1062	-		MCE-family protein Mce1A
1121960	syn	TC	MUL_1063	-		MCE-family protein Mce1B
1123066	syn	AG	MUL_1064	-	virulence; detoxification; adaptation	MCE-family protein Mce1C
1123504	syn	TC	MUL_1064	-	virulence; detoxification; adaptation	MCE-family protein Mce1C
1123561	syn	TC	MUL_1064	-	virulence; detoxification; adaptation	MCE-family protein Mce1C
1125006	syn	AG	MUL_1065	-		MCE-family protein Mce1D
1125321	syn	TG	MUL_1065	-		MCE-family protein Mce1D
1125330	syn	AG	MUL_1065	-		MCE-family protein Mce1D
1126127	syn	AC	MUL_1066	-		MCE-family lipoprotein LprK (MCE-family lipoprotein Mce1E)
1126724	syn	AG	MUL_1066	-		MCE-family lipoprotein LprK (MCE-family lipoprotein Mce1E)
1126928	syn	AG	MUL_1066	-		MCE-family lipoprotein LprK (MCE-family lipoprotein Mce1E)
1127593	syn	CT	MUL_1067	-		MCE-family protein Mce1F
1127692	syn	TG	MUL_1067	-		MCE-family protein Mce1F
1127707	syn	GC	MUL_1067	-		MCE-family protein Mce1F
1127935	syn	AG	MUL_1067	-		MCE-family protein Mce1F
1128071	syn	TC	MUL_1067	-		MCE-family protein Mce1F
1128918	non	AC	MUL_1068	-	cell wall and cell processes	conserved Mce-associated membrane protein
1128949	non	CG	MUL_1068	-	cell wall and cell processes	conserved Mce-associated membrane protein
1129176	syn	AG	MUL_1068	-	cell wall and cell processes	conserved Mce-associated membrane protein
1131164	non	GA	MUL_1071	-	cell wall and cell processes	conserved Mce-associated membrane protein
1131219	syn	GA	MUL_1071	-	cell wall and cell processes	conserved Mce-associated membrane protein
1135763	non	CG	MUL_1075	-	conserved hypothetical	conserved protein
1136074	non	CT	MUL_1075	-	conserved hypothetical	conserved protein
1136783	non	GC	MUL_1075	-	conserved hypothetical	conserved protein

SNP position	SNP type	Nucleotide change <ref><snp>	Distance to nearest locus	Nearby Locus	Functional group	Product
1137190	non	GA	MUL_1076	-	information pathways	alternative RNA polymerase sigma factor SigG
1140130	Int	TC	-	46 MUL_1080	intermediary metabolism and respiration	beta-glucosidase BglS
1146427	Syn	AG	MUL_1082	-	intermediary metabolism and respiration	dihydroxy-acid dehydratase IlvD
1147734	Int	TC	-	113 MUL_1083	conserved hypotheticals	conserved hypothetical protein
1150267	Int	AC	-	65 MUL_1086	regulatory proteins	transcriptional regulatory protein
1150983	psd	CG	MUL_1087	-	intermediary metabolism and respiration	N-term oxidoreductase - pseudogene
1151958	psd	-G	MUL_1087	-	intermediary metabolism and respiration	N-term oxidoreductase - pseudogene
1155089	Syn	AG	MUL_1088	-	intermediary metabolism and respiration	zinc metalloprotease
1156485	Syn	GA	MUL_1090	-	cell wall and cell processes	conserved transmembrane protein
1163069	psd	TG	MUL_1095	-	cell wall and cell processes	C-term conserved transmembrane protein - pseudogene
1164987	Syn	AG	MUL_1096	-	cell wall and cell processes	conserved transmembrane transport protein MmpL3
1166859	Evo	CT	MUL_1097	-	conserved hypotheticals	conserved hypothetical protein
1167099	Evo	CG	MUL_1097	-	conserved hypotheticals	conserved hypothetical protein
1168524	non	CT	MUL_1099	-	conserved hypotheticals	conserved hypothetical protein
1169705	non	TC	MUL_1100	-	cell wall and cell processes	conserved secreted protein
1172158	Evo	CG	MUL_1101	-	intermediary metabolism and respiration	iron-regulated phosphoenolpyruvate carboxykinase [GTP] PckA
1172932	Evo	CG	MUL_1101	-	intermediary metabolism and respiration	iron-regulated phosphoenolpyruvate carboxykinase [GTP] PckA
1175921	Int	TC	-	96 MUL_1104	cell wall and cell processes	conserved hypothetical membrane protein
1178537	psd	CT	MUL_1105	-	lipid metabolism	N-term acyl-CoA dehydrogenase FadE3 - 2 - pseudogene
1178689	Evo	TC	MUL_1107	-	conserved hypotheticals	conserved protein
1178878	Evo	GA	MUL_1107	-	conserved hypotheticals	conserved protein
1180450	psd	TC	MUL_1108	-	conserved hypotheticals	C-term conserved hypothetical protein - pseudogene
1181483	Syn	GT	MUL_1109	-	conserved hypotheticals	conserved hypothetical protein
1182315	Int	AG	-	70 MUL_1109	conserved hypotheticals	conserved hypothetical protein
1182320	Int	TA	-	75 MUL_1109	conserved hypotheticals	conserved hypothetical protein
1182631	psd	CT	MUL_5097	-	cell wall and cell processes	mid-section conserved hypothetical membrane protein pseudogene
1184476	non	TC	MUL_1110	-	cell wall and cell processes	conserved hypothetical transmembrane protein
1185691	Syn	GC	MUL_1111	-	cell wall and cell processes	conserved hypothetical transmembrane protein
1192237	non	TG	MUL_1117	-	lipid metabolism	fatty-acid-CoA ligase
1193754	psd	TG	MUL_1118	-	lipid metabolism	N-term peptide synthetase Nrp_pseudogene
1194636	psd	CG	MUL_1118	-	lipid metabolism	N-term peptide synthetase Nrp_pseudogene
1195765	psd	TC	MUL_1118	-	lipid metabolism	N-term peptide synthetase Nrp_pseudogene
1196392	psd	AC	MUL_1118	-	lipid metabolism	C-term peptide synthetase Nrp_pseudogene
1196689	psd	GA	MUL_1118	-	lipid metabolism	C-term peptide synthetase Nrp_pseudogene
1198685	Int	AG	-	65 MUL_1121	lipid metabolism	enoyl-CoA hydratase
1199542	Int	GC	-	43 MUL_1122	intermediary metabolism and respiration	aldehyde dehydrogenase
1200482	Syn	AG	MUL_1122	-	intermediary metabolism and respiration	aldehyde dehydrogenase
1201008	non	CT	MUL_1122	-	intermediary metabolism and respiration	aldehyde dehydrogenase
1201515	non	GA	MUL_1123	-	intermediary metabolism and respiration	methyltransferase
1202245	Syn	TG	MUL_1124	-	cell wall and cell processes	glycosyltransferase
1203401	Syn	AG	MUL_1125	-	cell wall and cell processes	conserved transmembrane protein
1204331	Syn	AG	MUL_1125	-	cell wall and cell processes	conserved transmembrane protein
1204334	Syn	TA	MUL_1125	-	cell wall and cell processes	conserved transmembrane protein
1205151	Syn	GC	MUL_1126	-	cell wall and cell processes	conserved membrane protein
1206626	Syn	GA	MUL_1127	-	intermediary metabolism and respiration	integral membrane acyltransferase
1218500	Syn	TG	MUL_1140	-	cell wall and cell processes	conserved hypothetical membrane protein
1218524	Syn	AC	MUL_1140	-	cell wall and cell processes	conserved hypothetical membrane protein
1221138	Int	AG	-	74 MUL_1144	cell wall and cell processes	conserved hypothetical membrane protein
1234626	Int	TC	-			
1234630	Int	CG	-			
1239264	non	CT	MUL_1156	-	cell wall and cell processes	conserved hypothetical membrane protein
1239455	non	CA	MUL_1156	-	cell wall and cell processes	conserved hypothetical membrane protein
1239902	Syn	GA	MUL_1157	-	intermediary metabolism and respiration	glycerophosphoryl diester phosphodiesterase GlpQ2
1241346	Syn	TC	MUL_1159	-	cell wall and cell processes	conserved transmembrane protein
1245934	non	TC	MUL_1161	-	cell wall and cell processes	conserved hypothetical small secreted protein
1245990	Syn	CG	MUL_1161	-	cell wall and cell processes	conserved hypothetical small secreted protein
1248091	non	TC	MUL_1164	-	cell wall and cell processes	conserved transmembrane protein
1248296	Syn	CG	MUL_1164	-	cell wall and cell processes	conserved transmembrane protein
1249525	non	GA	MUL_1165	-	cell wall and cell processes	conserved membrane protein
1249913	Syn	AG	MUL_1165	-	cell wall and cell processes	conserved membrane protein
1252403	Syn	TC	MUL_1167	-	lipid metabolism	acyl-CoA acyltransferase FadA2
1252850	Syn	AG	MUL_1167	-	lipid metabolism	acyl-CoA acyltransferase FadA2
1253479	Syn	AG	MUL_1168	-	lipid metabolism	acyl-CoA dehydrogenase FadE5
1255701	Int	TC	-	76 MUL_1169	intermediary metabolism and respiration	oxidoreductase
1257526	Int	CT	-	27 MUL_5125	conserved hypotheticals	conserved hypothetical protein
1257534	Int	TC	-	35 MUL_5125	conserved hypotheticals	conserved hypothetical protein
1264134	Syn	CT	MUL_1178	-		heat shock protein Hsp
1264362	Int	TC	-	103 MUL_1178		heat shock protein Hsp
1271668	Int	GA	-	16 MUL_1185		aminoglycoside 2'-N-acetyltransferase Aac
1273129	Int	AG	-	12 MUL_1187	conserved hypotheticals	conserved hypothetical protein
1274393	non	CG	MUL_1188	-	cell wall and cell processes	periplasmic iron-transport lipoprotein
1274705	Syn	TC	MUL_1188	-	cell wall and cell processes	periplasmic iron-transport lipoprotein
1275635	Syn	TC	MUL_1189	-	cell wall and cell processes	integral membrane nitrite extrusion protein NarU
1276207	non	AT	MUL_1189	-	cell wall and cell processes	integral membrane nitrite extrusion protein NarU
1278999	Syn	AG	MUL_1191	-	lipid metabolism	fatty-acid-CoA ligase FadD2
1281900	Syn	AG	MUL_1194	-	lipid metabolism	acyl-CoA dehydrogenase FadE6
1282752	Syn	CT	MUL_1194	-	lipid metabolism	acyl-CoA dehydrogenase FadE6
1288592	non	AG	MUL_1201	-	conserved hypotheticals	conserved hypothetical protein
1289346	Syn	CG	MUL_1201	-	conserved hypotheticals	conserved hypothetical protein
1289364	non	CG	MUL_1201	-	conserved hypotheticals	conserved hypothetical protein
1292001	psd	TG	MUL_1203	-	lipid metabolism	mid-section O-Methyltransferase - pseudogene
1292177	Int	TC	-	119 MUL_5109	unknown	hypothetical protein
1296518	Syn	AG	MUL_1206	-	cell wall and cell processes	conserved membrane protein
1301728	Int	GA	-			
1303021	non	GT	MUL_1211	-	conserved hypotheticals	conserved protein
1308338	Syn	TC	MUL_1215	-	cell wall and cell processes	conserved hypothetical membrane protein
1309210	Syn	TC	MUL_1216	-	intermediary metabolism and respiration	trans-aconitase methyltransferase Tam
1309618	Syn	AG	MUL_1217	-	intermediary metabolism and respiration	sulfatase
1309795	non	AG	MUL_1217	-	intermediary metabolism and respiration	sulfatase
1309797	non	GT	MUL_1217	-	intermediary metabolism and respiration	sulfatase
1310353	non	TC	MUL_1217	-	intermediary metabolism and respiration	sulfatase
1310624	non	CT	MUL_1217	-	intermediary metabolism and respiration	sulfatase

SNP position	SNP type	Nucleotide change <ref><snp>	Distance to nearest locus	Nearby Locus	Functional group	Product
1310827	syn	TC	MUL_1217	-	intermediary metabolism and respiration	sulfatase
1311653	non	TC	MUL_1218	-	intermediary metabolism and respiration	oxidoreductase
1311726	non	TC	MUL_1218	-	intermediary metabolism and respiration	oxidoreductase
1313786	syn	TC	MUL_1223	-	cell wall and cell processes	conserved exported protein
1314992	non	GC	MUL_1225	-	conserved hypotheticals	conserved hypothetical protein
1315749	syn	GC	MUL_1225	-	conserved hypotheticals	conserved hypothetical protein
1315761	non	AT	MUL_1225	-	conserved hypotheticals	conserved hypothetical protein
1331908	syn	AG	MUL_1233	-	lipid metabolism	acyl-CoA dehydrogenase
1332147	non	TC	MUL_1233	-	lipid metabolism	acyl-CoA dehydrogenase
1335005	psd	GA	MUL_1235	-	cell wall and cell processes	N-term conserved hypothetical membrane protein - pseudogene
1335028	psd	TC	MUL_1235	-	cell wall and cell processes	N-term conserved hypothetical membrane protein - pseudogene
1335109	psd	TC	MUL_1235	-	cell wall and cell processes	N-term conserved hypothetical membrane protein - pseudogene
1337007	psd	GC	MUL_1235	-	cell wall and cell processes	C-term conserved hypothetical membrane protein - pseudogene
1344047	syn	CT	MUL_1242	-	conserved hypotheticals	conserved hypothetical protein
1344146	syn	GA	MUL_1242	-	conserved hypotheticals	conserved hypothetical protein
1344174	non	GC	MUL_1242	-	conserved hypotheticals	conserved hypothetical protein
1346259	syn	AG	MUL_1244	-	cell wall and cell processes	cationic amino acid transport integral membrane protein RocE
1347330	syn	TG	MUL_1244	-	cell wall and cell processes	cationic amino acid transport integral membrane protein RocE
1347900	non	CG	MUL_1245	-	conserved hypotheticals	conserved hypothetical protein
1349478	syn	AG	MUL_1246	-	cell wall and cell processes	periplasmic sugar-binding lipoprotein UspC
1349787	syn	TC	MUL_1246	-	cell wall and cell processes	periplasmic sugar-binding lipoprotein UspC
1350557	syn	TG	MUL_1247	-	cell wall and cell processes	sugar-transport integral membrane protein ABC transporter UspB
1350618	non	CG	MUL_1247	-	cell wall and cell processes	sugar-transport integral membrane protein ABC transporter UspB
1351104	syn	CT	MUL_1248	-	cell wall and cell processes	sugar-transport integral membrane protein ABC transporter UspB
1352400	syn	CT	MUL_1249	-	cell wall and cell processes	sugar-transport integral membrane protein ABC transporter UspA
1353317	syn	TG	MUL_1250	-	cell wall and cell processes	conserved protein
1353422	syn	AG	MUL_1250	-	cell wall and cell processes	conserved membrane protein
1354008	non	GA	MUL_1250	-	cell wall and cell processes	conserved membrane protein
1354202	syn	AG	MUL_1250	-	cell wall and cell processes	conserved membrane protein
1354511	psd	TC	MUL_1251	-	conserved hypotheticals	N-term conserved hypothetical protein - pseudogene
1354760	psd	CT	MUL_1251	-	conserved hypotheticals	N-term conserved hypothetical protein - pseudogene
1354997	psd	TC	MUL_1251	-	conserved hypotheticals	C-term conserved hypothetical protein - pseudogene
1355051	psd	TC	MUL_1251	-	conserved hypotheticals	C-term conserved hypothetical protein - pseudogene
1355629	syn	GC	MUL_1252	-	cell wall and cell processes	conserved hypothetical secreted protein
1355716	syn	TC	MUL_1252	-	cell wall and cell processes	conserved hypothetical secreted protein
1356167	int	TA	116	MUL_1253	conserved hypotheticals	conserved hypothetical protein
1357134	syn	AG	MUL_1254	-	cell wall and cell processes	metal cation transporter p-type ATPase a
1358192	non	TC	MUL_1254	-	cell wall and cell processes	metal cation transporter p-type ATPase a
1359000	syn	GA	MUL_1254	-	cell wall and cell processes	metal cation transporter p-type ATPase a
1359876	non	AG	MUL_1255	-	conserved hypotheticals	conserved hypothetical protein
1359965	syn	GC	MUL_1255	-	conserved hypotheticals	conserved hypothetical protein
1360298	syn	TC	MUL_1256	-	unknown	hypothetical protein
1361165	int	GC	129	MUL_1258	cell wall and cell processes	mid-section conserved transmembrane transport protein MmpL4 - pseudogene
1370870	syn	AC	MUL_1269	-	cell wall and cell processes	conserved ion transport protein
1372884	non	TC	MUL_1275	-	conserved hypotheticals	conserved hypothetical protein
1373913	psd	TC	MUL_1276	-	cell wall and cell processes	N-term conserved hypothetical membrane protein pseudogene
1373950	psd	TC	MUL_1276	-	cell wall and cell processes	N-term conserved hypothetical membrane protein pseudogene
1376333	syn	TC	MUL_1280	-	conserved hypotheticals	conserved hypothetical protein
1376734	non	TC	MUL_1280	-	conserved hypotheticals	conserved hypothetical protein
1376849	syn	AC	MUL_1280	-	conserved hypotheticals	conserved hypothetical protein
1376863	non	TC	MUL_1280	-	conserved hypotheticals	conserved hypothetical protein
1378592	syn	GA	MUL_1282	-	intermediary metabolism and respiration	cytochrome P450 124A1 Cyp124A1
1381423	int	GT	93	MUL_1285	conserved hypotheticals	N-term conserved hypothetical proline rich protein - pseudogene
1381548	psd	AG	MUL_1285	-	conserved hypotheticals	N-term conserved hypothetical proline rich protein - pseudogene
1381694	int	TC	59	MUL_1285	conserved hypotheticals	N-term conserved hypothetical proline rich protein - pseudogene
1383545	int	GT	119	MUL_1285	conserved hypotheticals	C-term conserved hypothetical proline rich protein - pseudogene
1383632	non	TC	MUL_1286	-	conserved hypotheticals	conserved hypothetical protein
1385801	non	TC	MUL_1288	-	intermediary metabolism and respiration	oxidoreductase
1391331	syn	TC	MUL_1294	-	conserved hypotheticals	conserved hypothetical protein
1393667	non	GA	MUL_1297	-	conserved hypotheticals	conserved hypothetical protein
1393812	syn	GC	MUL_1297	-	conserved hypotheticals	conserved hypothetical protein
1396772	syn	AG	MUL_1300	-	intermediary metabolism and respiration	glycerol-3-phosphate dehydrogenase GlpD1
1397866	non	CA	MUL_1300	-	intermediary metabolism and respiration	glycerol-3-phosphate dehydrogenase GlpD1
1397947	non	TC	MUL_1300	-	intermediary metabolism and respiration	glycerol-3-phosphate dehydrogenase GlpD1
1401374	syn	GA	MUL_1303	-	lipid metabolism	3-oxoacyl-[acyl-carrier protein] synthase 2 KasB
1402595	syn	AG	MUL_1304	-	lipid metabolism	3-oxoacyl-[acyl-carrier protein] synthase 1 KasA
1404502	syn	GA	MUL_1306	-	lipid metabolism	malonyl CoA-acyl carrier protein thioacylase FabD
1407361	syn	GA	MUL_1308	-	intermediary metabolism and respiration	pyruvate dehydrogenase E1 component AceE
1409222	syn	CA	MUL_1309	-	cell wall and cell processes	conserved hypothetical protein
1410302	syn	TC	MUL_1311	-		peroxiredoxin AhpF
1411146	syn	GA	MUL_1313	-	conserved hypotheticals	conserved hypothetical protein
1411868	syn	AG	MUL_1313	-	conserved hypotheticals	conserved hypothetical protein
1412482	psd	CT	MUL_1314	-	conserved hypotheticals	C-term conserved hypothetical protein - pseudogene
1412606	psd	TC	MUL_1314	-	conserved hypotheticals	C-term conserved hypothetical protein - pseudogene
1413941	syn	TC	MUL_1316	-	conserved hypotheticals	conserved hypothetical protein
1415673	syn	CT	MUL_1317	-	intermediary metabolism and respiration	cobalamin biosynthesis transmembrane protein CobD
1416656	syn	CG	MUL_1319	-	regulatory proteins	phosphotyrosine protein phosphatase PtpA
1417646	int	TC	-			
1419282	non	AG	MUL_1322	-	conserved hypotheticals	conserved hypothetical protein
1419998	syn	AG	MUL_1322	-	conserved hypotheticals	conserved hypothetical protein
1421327	syn	CG	MUL_1324	-	conserved hypotheticals	conserved hypothetical protein
1422058	int	GC	83	MUL_1324	conserved hypotheticals	conserved hypothetical protein
1422828	int	CG	98	MUL_1326	PE/PPe	N-term PE-PGRS family protein - pseudogene
1425046	int	GA	56	MUL_1326	PE/PPe	C-term PE-PGRS family protein - pseudogene
1426548	syn	AG	MUL_1328	-	conserved hypotheticals	conserved protein
1427359	non	CG	MUL_1328	-	conserved hypotheticals	conserved protein
1427610	non	TC	MUL_1328	-	conserved hypotheticals	conserved protein
1429473	non	GA	MUL_1330	-	intermediary metabolism and respiration	3-methyl-2-oxobutanate hydroxymethyltransferase PanB
1429476	non	AT	MUL_1330	-	intermediary metabolism and respiration	3-methyl-2-oxobutanate hydroxymethyltransferase PanB
1429477	syn	CT	MUL_1330	-	intermediary metabolism and respiration	3-methyl-2-oxobutanate hydroxymethyltransferase PanB
1431682	syn	TC	MUL_1332	-	cell wall and cell processes	exported protease
1432390	syn	TC	MUL_1332	-	cell wall and cell processes	exported protease

SNP position	SNP type	Nucleotide change <ref><snp>	Distance to nearest locus	Nearby Locus	Functional group	Product
1434852	syn	AG	MUL_1334	-	cell wall and cell processes	exported protease
1435118	non	TC	MUL_1334	-	cell wall and cell processes	exported protease
1437327	syn	AG	MUL_1335	-	intermediary metabolism and respiration	glutamine synthetase GlnA2
1437759	syn	TC	MUL_1336	-	intermediary metabolism and respiration	glutamate-ammonia-lyase adenylyltransferase GlnF
1438716	syn	AG	MUL_1336	-	intermediary metabolism and respiration	glutamate-ammonia-lyase adenylyltransferase GlnF
1438989	syn	CG	MUL_1336	-	intermediary metabolism and respiration	glutamate-ammonia-lyase adenylyltransferase GlnF
1439757	syn	CG	MUL_1336	-	intermediary metabolism and respiration	glutamate-ammonia-lyase adenylyltransferase GlnF
1440480	syn	TC	MUL_1336	-	intermediary metabolism and respiration	glutamate-ammonia-lyase adenylyltransferase GlnE
1441878	syn	AG	MUL_1338	-	intermediary metabolism and respiration	glutamate-ammonia-lyase adenylyltransferase GlnE
1445459	syn	AG	MUL_1340	-	intermediary metabolism and respiration	glutamine synthetase GlnA1
1445534	syn	CG	MUL_1340	-	intermediary metabolism and respiration	glutamine synthetase GlnA1
1446059	non	GT	MUL_1340	-	intermediary metabolism and respiration	glutamine synthetase GlnA1
1448899	non	TC	MUL_1344	-	intermediary metabolism and respiration	lipoate biosynthesis protein B LipB
1450193	non	CA	MUL_1345	-	cell wall and cell processes	drugs-transport transmembrane ATP-binding protein ABC transporter
1451559	psd	TG	MUL_1346	-	cell wall and cell processes	N-term drugs-transport transmembrane ATP-binding protein ABC transporter - pseudogene
1458342	int	TA		-		
1458361	int	AG		-		
1458554	int	CT		61 MUL_1352	conserved hypothetical	conserved hypothetical protein
1458557	int	GC		58 MUL_1352	conserved hypothetical	conserved hypothetical protein
1458564	int	GA		51 MUL_1352	conserved hypothetical	conserved hypothetical protein
1458711	syn	GC	MUL_1352	-	conserved hypothetical	conserved hypothetical protein
1458723	syn	AG	MUL_1352	-	conserved hypothetical	conserved hypothetical protein
1459700	syn	TC	MUL_1354	-	conserved hypothetical	conserved hypothetical protein
1460355	non	AG	MUL_1355	-	cell wall and cell processes	conserved hypothetical secreted protein
1471181	syn	TC	MUL_1364	-	intermediary metabolism and respiration	adenosine deaminase Add
1473564	syn	TC	MUL_1366	-	intermediary metabolism and respiration	cysteine deaminase Cdd
1477016	non	TC	MUL_1370	-	intermediary metabolism and respiration	methane dehydrogenase (iron-sulphur protein subunit) SdhB
1490555	non	GA	MUL_1382	-	cell wall and cell processes	MFS transporter
1497542	int	AG		72 MUL_1382	cell wall and cell processes	MFS transporter
1497795	syn	AG	MUL_1383	-	conserved hypothetical	conserved hypothetical protein
1497801	syn	TC	MUL_1383	-	conserved hypothetical	conserved hypothetical protein
1488059	non	GA	MUL_1383	-	conserved hypothetical	conserved hypothetical protein
1489795	syn	AG	MUL_1384	-	cell wall and cell processes	conserved ATPase
1490808	syn	AC	MUL_1385	-	lipid metabolism	CDP-diacylglycerol-serine o-phosphatidyltransferase PssA
1491512	syn	TC	MUL_1386	-	lipid metabolism	phosphatidylserine decarboxylase Psd
1496013	syn	AG	MUL_1390	-	intermediary metabolism and respiration	molybdopterin biosynthesis protein MoeA2
1496109	syn	TG	MUL_1390	-	intermediary metabolism and respiration	molybdopterin biosynthesis protein MoeA2
1496171	non	TG	MUL_1390	-	intermediary metabolism and respiration	molybdopterin biosynthesis protein MoeA2
1496549	non	TC	MUL_1390	-	intermediary metabolism and respiration	molybdopterin biosynthesis protein MoeA2
1497975	syn	GC	MUL_1391	-	intermediary metabolism and respiration	dehydrogenase/reductase
1499986	non	CA	MUL_1393	-		60 kDa chaperonin 2 GroEL2
1502752	non	GA	MUL_1396	-	intermediary metabolism and respiration	D-amino acid aminohydrolase
1502834	syn	TC	MUL_1396	-	intermediary metabolism and respiration	D-amino acid aminohydrolase
1504247	syn	TC	MUL_1396	-	intermediary metabolism and respiration	D-amino acid aminohydrolase
1509587	non	AG	MUL_1403	-	conserved hypothetical	conserved hypothetical protein
1509727	syn	GT	MUL_1403	-	conserved hypothetical	conserved hypothetical protein
1510002	int	CT		48 MUL_1403	conserved hypothetical	conserved hypothetical protein
1510250	non	TG	MUL_1404	-	cell wall and cell processes	oxidoreductase
1510302	syn	AG	MUL_1404	-	cell wall and cell processes	oxidoreductase
1510650	syn	AG	MUL_1404	-	cell wall and cell processes	oxidoreductase
1510704	syn	CA	MUL_1404	-	cell wall and cell processes	oxidoreductase
1510763	syn	AG	MUL_1404	-	cell wall and cell processes	oxidoreductase
1510773	syn	AG	MUL_1404	-	cell wall and cell processes	oxidoreductase
1510779	syn	AG	MUL_1404	-	cell wall and cell processes	oxidoreductase
1510980	syn	CT	MUL_1404	-	cell wall and cell processes	oxidoreductase
1515548	psd	AG	MUL_1409	-	cell wall and cell processes	mid-section conserved MmpL4-like transmembrane transport protein - pseudogene
1518681	int	GA		37 MUL_1413	cell wall and cell processes	conserved secreted protein
1520373	psd	AG	MUL_1415	-	intermediary metabolism and respiration	C-term peptidase - pseudogene
1521437	psd	AG	MUL_1415	-	intermediary metabolism and respiration	N-term peptidase - pseudogene
1531368	non	GC	MUL_1424	-	cell wall and cell processes	conserved transmembrane ATP-binding protein ABC transporter
1533674	psd	AG	MUL_1425	-	cell wall and cell processes	N-term conserved transmembrane ATP-binding protein ABC transporter - pseudogene
1534163	psd	CT	MUL_1425	-	cell wall and cell processes	N-term conserved transmembrane ATP-binding protein ABC transporter - pseudogene
1539273	int	AG		89 MUL_1432	lipid metabolism	fatty-acyl AMP ligase FadD28_1
1539637	syn	CG	MUL_1432	-	lipid metabolism	fatty-acyl AMP ligase FadD28_1
1539655	syn	GC	MUL_1432	-	lipid metabolism	fatty-acyl AMP ligase FadD28_1
1541409	psd	TC	MUL_1433	-	lipid metabolism	N-term polyketide synthase - pseudogene
1543228	psd	AG	MUL_1433	-	lipid metabolism	N-term polyketide synthase - pseudogene
1543870	psd	CG	MUL_1433	-	lipid metabolism	N-term polyketide synthase - pseudogene
1544011	psd	GC	MUL_1433	-	lipid metabolism	N-term polyketide synthase - pseudogene
1547681	psd	AC	MUL_1433	-	lipid metabolism	C-term polyketide synthase - pseudogene
1548039	psd	AC	MUL_1433	-	lipid metabolism	C-term polyketide synthase - pseudogene
1548074	psd	AT	MUL_1433	-	lipid metabolism	C-term polyketide synthase - pseudogene
1548254	psd	GC	MUL_1433	-	lipid metabolism	C-term polyketide synthase - pseudogene
1549429	non	GA	MUL_1434	-	cell wall and cell processes	hypothetical secreted protein
1549449	syn	AG	MUL_1434	-	cell wall and cell processes	hypothetical secreted protein
1549617	non	CT	MUL_1435	-	cell wall and cell processes	exported protein
1549923	int	GC		116 MUL_1436	intermediary metabolism and respiration	methyltransferase
1550288	syn	TC	MUL_1436	-	intermediary metabolism and respiration	methyltransferase
1551004	syn	GA	MUL_1437	-	intermediary metabolism and respiration	homoserine O-acetyltransferase MetA
1552374	syn	AG	MUL_1438	-	intermediary metabolism and respiration	O-acetylhomoserine sulfhydrylase MetC
1555090	non	CT	MUL_1440	-	cell wall and cell processes	conserved membrane protein
1557313	syn	AC	MUL_1442	-	cell wall and cell processes	conserved integral membrane protein
1558639	syn	GA	MUL_1443	-	cell wall and cell processes	n-acetylgalactosamine-6-phosphate deacetylase NagA
1558876	syn	GA	MUL_1443	-	cell wall and cell processes	n-acetylglucosamine-6-phosphate deacetylase NagA
1558885	syn	GA	MUL_1443	-	cell wall and cell processes	n-acetylglucosamine-6-phosphate deacetylase NagA
1572786	int	TC		72 MUL_1455	cell wall and cell processes	EsaT-6 like protein EsvP_2
1575375	psd	GA	MUL_1457	-	cell wall and cell processes	N-term conserved transmembrane protein - pseudogene
1578828	syn	AG	MUL_1459	-	information pathways	DNA primase DnaG
1580568	syn	AG	MUL_1463	-	cell wall and cell processes	thioredoxin Thlx
1583280	syn	TG	MUL_1467	-	cell wall and cell processes	[NAD] dependent malate oxidoreductase Mez
1592327	non	GA	MUL_1472	-	cell wall and cell processes	adenylate cyclase
1592373	int	TC		30 MUL_1472	cell wall and cell processes	adenylate cyclase

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
1597464	int	TC		-			
1597754	non	GC	MUL_1475	-		cell wall and cell processes	lipoprotein LppP
1598183	int	AC		59	MUL_1475	cell wall and cell processes	lipoprotein LppP
1598704	int	AG		6	MUL_1476	cell wall and cell processes	N-term nitrite extrusion protein 1 NarK1 - pseudogene
1598984	snp	CT	MUL_1477	-		cell wall and cell processes	cation transporter: p-type ATPase D CtpD
1599350	snp	AG	MUL_1477	-		cell wall and cell processes	cation transporter: p-type ATPase D CtpD
1599374	snp	GA	MUL_1477	-		cell wall and cell processes	cation transporter: p-type ATPase D CtpD
1600253	snp	AC	MUL_1477	-		cell wall and cell processes	cation transporter: p-type ATPase D CtpD
1605809	snp	TG	MUL_1484	-		intermediary metabolism and respiration	aconitate hydratase Acn
1605824	snp	AG	MUL_1484	-		intermediary metabolism and respiration	aconitate hydratase Acn
1606374	non	AT	MUL_1484	-		intermediary metabolism and respiration	aconitate hydratase Acn
1606565	snp	CT	MUL_1484	-		intermediary metabolism and respiration	aconitate hydratase Acn
1606850	snp	CT	MUL_1484	-		intermediary metabolism and respiration	aconitate hydratase Acn
1612429	snp	GC	MUL_1488	-		regulatory proteins	transcriptional regulatory protein MoxR
1614791	non	AG	MUL_1491	-		lipid metabolism	3'-oxoacyl-[acyl-carrier protein] reductase FabG1
1615006	snp	TC	MUL_1491	-		lipid metabolism	3'-oxoacyl-[acyl-carrier protein] reductase FabG1
1615351	snp	TC	MUL_1491	-		lipid metabolism	3'-oxoacyl-[acyl-carrier protein] reductase FabG1
1617034	snp	GC	MUL_1493	-		intermediary metabolism and respiration	ferrocelatase HemZ
1617966	non	CT	MUL_1494	-		conserved hypotheticals	conserved hypothetical protein
1622566	int	CT		-			
1628379	snp	CT	MUL_1505	-		lipid metabolism	methylmalonyl-CoA mutase small subunit MutA
1629012	snp	CG	MUL_1505	-		lipid metabolism	methylmalonyl-CoA mutase small subunit MutA
1630754	snp	TC	MUL_1506	-		lipid metabolism	methylmalonyl-CoA mutase large subunit MutB
1632684	snp	AG	MUL_1507	-		cell wall and cell processes	LAO/AO transport system kinase
1634430	psd	TC	MUL_1508	-		intermediary metabolism and respiration	C-term esterase_LipI - pseudogene
1635911	int	TG		78	MUL_1511	intermediary metabolism and respiration	UDP-glucose 4-dehydrogenase UdgL
1652149	snp	CG	MUL_1529	-		intermediary metabolism and respiration	UDP-glycosyltransferase
1655565	int	CG		-			
1656129	snp	TC	MUL_1532	-		information pathways	isoleucy-tRNA synthetase IleS
1656849	non	AG	MUL_1532	-		information pathways	isoleucy-tRNA synthetase IleS
1658520	snp	AG	MUL_1532	-		information pathways	isoleucy-tRNA synthetase IleS
1658575	non	AG	MUL_1532	-		information pathways	isoleucy-tRNA synthetase IleS
1658772	snp	GA	MUL_1532	-		information pathways	isoleucy-tRNA synthetase IleS
1659504	psd	CT	MUL_1533	-		conserved hypotheticals	C-term conserved hypothetical protein pseudogene
1659807	psd	GT	MUL_1533	-		conserved hypotheticals	C-term conserved hypothetical protein pseudogene
1659807	snp	GT	MUL_1533	-		conserved hypotheticals	N-term conserved hypothetical protein pseudogene
1660240	int	TC		52	MUL_1533	conserved hypotheticals	N-term conserved hypothetical protein pseudogene
1660481	non	AC	MUL_1534	-		conserved hypotheticals	conserved hypothetical protein
1661380	snp	CG	MUL_1535	-		information pathways	DNA polymerase IV_DinP1
1661785	snp	TC	MUL_1535	-		information pathways	DNA polymerase IV_DinP1
1664739	non	CG	MUL_1538	-		intermediary metabolism and respiration	pseudouridine synthase RluA-family
1664815	snp	-A	MUL_1538	-		intermediary metabolism and respiration	pseudouridine synthase RluA-family
1664910	snp	TC	MUL_1538	-		intermediary metabolism and respiration	pseudouridine synthase RluA-family
1666673	non	TC	MUL_1541	-		intermediary metabolism and respiration	bacterial-like globin GlbN
1669127	int	TC		61	MUL_1543	lipid metabolism	ketoadic reductase
1669522	non	GC	MUL_1544	-		conserved hypotheticals	conserved protein
1669572	snp	GA	MUL_1544	-		conserved hypotheticals	conserved protein
1669803	snp	TC	MUL_1545	-		information pathways	DNA polymerase III_alpha subunit DnaE1
1670661	snp	GC	MUL_1545	-		information pathways	DNA polymerase III_alpha subunit DnaE1
1670709	snp	CT	MUL_1545	-		information pathways	DNA polymerase III_alpha subunit DnaE1
1677189	non	CA	MUL_1548	-		unknown	hypothetical protein
1681905	snp	AG	MUL_1553	-		intermediary metabolism and respiration	maltooligosyltrehalose trehalohydrolase TreZ
1682514	snp	TC	MUL_1553	-		intermediary metabolism and respiration	maltooligosyltrehalose trehalohydrolase TreZ
1683948	non	AG	MUL_1554	-		intermediary metabolism and respiration	maltooligosyltrehalose synthase TreY
1684953	non	AG	MUL_1554	-		intermediary metabolism and respiration	maltooligosyltrehalose synthase TreY
1688051	snp	TC	MUL_1556	-		cell wall and cell processes	conserved hypothetical membrane protein
1688759	snp	GC	MUL_1556	-		cell wall and cell processes	conserved hypothetical membrane protein
1691452	non	AC	MUL_1559	-		intermediary metabolism and respiration	adenosylmethionine-8-amino-7-oxononanoate aminotransferase BioA
1694318	snp	TC	MUL_1561	-		intermediary metabolism and respiration	dethiobiotin synthetase BioD
1695388	non	TC	MUL_1563	-		intermediary metabolism and respiration	biotin synthase BioB
1697648	snp	TG	MUL_1566	-		cell wall and cell processes	conserved hypothetical membrane protein
1699147	snp	GA	MUL_1567	-		conserved hypotheticals	conserved hypothetical protein
1703049	snp	AG	MUL_1570	-		intermediary metabolism and respiration	nicotinate-nucleotide pyrophosphatase NadC
1706426	snp	CT	MUL_1574	-		intermediary metabolism and respiration	imidazole glycerol-phosphate dehydratase HisB
1708782	snp	CT	MUL_1577	-		intermediary metabolism and respiration	inositol-monophosphatase ImpA
1708875	snp	TC	MUL_1577	-		intermediary metabolism and respiration	inositol-monophosphatase ImpA
1709025	snp	GA	MUL_1577	-		intermediary metabolism and respiration	inositol-monophosphatase ImpA
1709991	snp	AG	MUL_1579	-		intermediary metabolism and respiration	phosphoribosyl-AMP 1,6 cyclohydrolase HisF
1710221	int	AG		76	MUL_1580	intermediary metabolism and respiration	deacetylase
1710861	snp	TC	MUL_1580	-		intermediary metabolism and respiration	deacetylase
1715771	psd	GC	MUL_1583	-		cell wall and cell processes	N-term cyanophycinase CphB - pseudogene
1715940	psd	TC	MUL_1583	-		cell wall and cell processes	N-term cyanophycinase CphB - pseudogene
1717703	psd	CA	MUL_1585	-		cell wall and cell processes	mid-section UDP-N-acetylglucosamine tripeptidase pseudogene
1720255	int	AG		24	MUL_1586	regulatory protein	N-term anchored-membrane serine/threonine-protein kinase PknF 1 - pseudogene
1722766	non	TG	MUL_1589	-		intermediary metabolism and respiration	anthranilate synthase component I TrpE
1724976	snp	CT	MUL_1591	-		intermediary metabolism and respiration	indole-3-glycerol phosphate synthase TrpC
1726003	snp	TC	MUL_1592	-		intermediary metabolism and respiration	tryptophan synthase beta subunit TrpB
1726539	snp	CT	MUL_1592	-		intermediary metabolism and respiration	tryptophan synthase beta subunit TrpB
1727162	snp	CT	MUL_1593	-		intermediary metabolism and respiration	tryptophan synthase alpha subunit TrpA
1731671	non	GC	MUL_1598	-		intermediary metabolism and respiration	pyruvate kinase PykA
1739416	non	CT	MUL_1603	-		cell wall and cell processes	integral membrane cytochrome D ubiquinol oxidase (subunit II) CvdB
1739672	non	TC	MUL_1603	-		cell wall and cell processes	integral membrane cytochrome D ubiquinol oxidase (subunit II) CvdB
1741163	psd	TC	MUL_1604	-		cell wall and cell processes	N-term integral membrane cytochrome D ubiquinol oxidase (subunit I) CvdA - pseudogene
1744236	snp	TC	MUL_1608	-		regulatory protein	two-component system transcriptional regulator
1745553	snp	TC	MUL_1609	-		lipid metabolism	Nonspecific lipid-transferring protein
1745759	snp	TC	MUL_1610	-		conserved hypotheticals	conserved hypothetical protein
1747097	snp	GA	MUL_1611	-		information pathways	DNA polymerase I PolA
1750651	snp	TC	MUL_1612	-		information pathways	ribosomal protein S1 RpsA
1750778	non	CG	MUL_1613	-		intermediary metabolism and respiration	dephospho-CoA kinase CoaE
1751125	snp	TA	MUL_1613	-		intermediary metabolism and respiration	dephospho-CoA kinase CoaE
1751213	non	GA	MUL_1613	-		intermediary metabolism and respiration	dephospho-CoA kinase CoaE
1752456	non	TC	MUL_1614	-		conserved hypotheticals	conserved hypothetical protein

SNP position	SNP type	Nucleotide change <ref><snp>	Distance to nearest locus	Nearby Locus	Functional group	Product
1752734	syn	AC	MUL_1615	-	conserved hypothetical	conserved hypothetical protein
1756520	non	TC	MUL_1617	-	cell wall and cell processes	dnug efflux membrane protein
1758525	int	AG	-	63 MUL_1618	cell wall and cell processes	conserved transmembrane protein
1758670	int	TC	-	114 MUL_1619	conserved hypothetical	iron-regulated conserved protein
1760157	non	GA	MUL_1621	-	conserved hypothetical	conserved protein
1761397	syn	GA	MUL_1622	-	information pathways	excinuclease ABC (subunit A-DNA-binding ATPase) UvrA
1761928	syn	TG	MUL_1622	-	information pathways	excinuclease ABC (subunit A-DNA-binding ATPase) UvrA
1762516	syn	TC	MUL_1622	-	information pathways	excinuclease ABC (subunit A-DNA-binding ATPase) UvrA
1762630	syn	CT	MUL_1622	-	information pathways	excinuclease ABC (subunit A-DNA-binding ATPase) UvrA
1764160	psd	GC	MUL_1623	-	regulatory proteins	C-term transmembrane serine/threonine-protein kinase - pseudogene
1764581	psd	AG	MUL_1623	-	regulatory proteins	C-term transmembrane serine/threonine-protein kinase - pseudogene
1766590	non	TC	MUL_1625	-	cell wall and cell processes	conserved hypothetical membrane protein
1767358	non	TA	MUL_1625	-	cell wall and cell processes	conserved hypothetical membrane protein
1767468	int	GA	-	28 MUL_1626	information pathways	lysyl-tRNA synthetase 2 LysX
1775974	syn	AG	MUL_1633	-	conserved hypothetical	conserved hypothetical protein
1779089	exp	TC	MUL_1636	-	information pathways	phenylalanyl-tRNA synthetase_beta chain PheT
1781386	int	AG	-	23 MUL_1636	information pathways	phenylalanyl-tRNA synthetase_beta chain PheT
1784187	int	CT	-	-	-	-
1784950	int	TG	-	95 MUL_1637	PE/PPe	C-term PE-PGRS family protein - pseudogene
1786283	int	GA	-	-	-	-
1794759	int	AC	-	-	-	-
1795991	syn	CA	MUL_1644	-	intermediary metabolism and respiration	N-acetyl-gamma-glutamyl-phosphate reductase ArgC
1796573	syn	AG	MUL_1645	-	intermediary metabolism and respiration	glutamate N-acetyltransferase ArgJ
1797735	syn	TG	MUL_1645	-	intermediary metabolism and respiration	glutamate N-acetyltransferase ArgJ
1797149	syn	AG	MUL_1645	-	intermediary metabolism and respiration	glutamate N-acetyltransferase ArgJ
1798240	syn	TC	MUL_1646	-	intermediary metabolism and respiration	aspartylglutamate kinase ArgB
1799397	syn	AG	MUL_1647	-	intermediary metabolism and respiration	acetylornithine aminotransferase ArgD
1799522	non	TC	MUL_1647	-	intermediary metabolism and respiration	acetylornithine aminotransferase ArgD
1799636	non	AC	MUL_1647	-	intermediary metabolism and respiration	acetylornithine aminotransferase ArgD
1800427	non	TC	MUL_1648	-	intermediary metabolism and respiration	ornithine carbonyltransferase_anabolic ArgF
1801537	syn	TC	MUL_1650	-	intermediary metabolism and respiration	argininosuccinate synthase ArgG
1802150	syn	TC	MUL_1650	-	intermediary metabolism and respiration	argininosuccinate synthase ArgG
1803230	syn	CG	MUL_1651	-	intermediary metabolism and respiration	argininosuccinate lyase ArgH
1803234	syn	TC	MUL_1651	-	intermediary metabolism and respiration	argininosuccinate lyase ArgH
1804262	psd	CT	MUL_1652	-	lipid metabolism	mid-section chalcone synthase_Pks10_pseudogene
1805284	psd	CA	MUL_1653	-	lipid metabolism	N-term polyketide synthase Pks7_pseudogene
1807087	psd	TC	MUL_1653	-	lipid metabolism	mid-section polyketide synthase Pks7_pseudogene
1808596	psd	TC	MUL_1653	-	lipid metabolism	mid-section polyketide synthase Pks7_pseudogene
1808894	psd	GC	MUL_1653	-	lipid metabolism	C-term polyketide synthase Pks7_pseudogene
1809607	psd	TC	MUL_1653	-	lipid metabolism	C-term polyketide synthase Pks7_pseudogene
1809672	psd	AG	MUL_1653	-	lipid metabolism	C-term polyketide synthase Pks7_pseudogene
1810252	psd	TG	MUL_1653	-	lipid metabolism	C-term polyketide synthase Pks7_pseudogene
1811951	psd	TC	MUL_1654	-	lipid metabolism	mid-section polyketide synthase Pks8_pseudogene
1812014	psd	TC	MUL_1654	-	lipid metabolism	mid-section polyketide synthase Pks8_pseudogene
1812986	psd	CT	MUL_1654	-	lipid metabolism	C-term polyketide synthase Pks8_pseudogene
1813152	psd	CT	MUL_1654	-	lipid metabolism	C-term polyketide synthase Pks8_pseudogene
1813262	psd	CA	MUL_1654	-	lipid metabolism	C-term polyketide synthase Pks8_pseudogene
1815182	psd	TG	MUL_1654	-	lipid metabolism	C-term polyketide synthase Pks8_pseudogene
1815217	psd	GC	MUL_1654	-	lipid metabolism	C-term polyketide synthase Pks8_pseudogene
1816429	psd	AC	MUL_1654	-	lipid metabolism	C-term polyketide synthase Pks8_pseudogene
1816911	psd	TC	MUL_1654	-	lipid metabolism	C-term polyketide synthase Pks8_pseudogene
1818480	syn	AG	MUL_1655	-	lipid metabolism	polyketide synthase Pks9
1818603	non	TA	MUL_1655	-	lipid metabolism	polyketide synthase Pks9
1820106	syn	AG	MUL_1655	-	lipid metabolism	polyketide synthase Pks9
1820534	non	CT	MUL_1655	-	lipid metabolism	polyketide synthase Pks9
1820964	int	TC	-	143 MUL_1656	lipid metabolism	chalcone synthase_Pks11
1821661	syn	GC	MUL_1656	-	lipid metabolism	chalcone synthase_Pks11
1821880	syn	TC	MUL_1656	-	lipid metabolism	chalcone synthase_Pks11
1822358	psd	TC	MUL_1657	-	intermediary metabolism and respiration	C-term cytochrome P450_139A3_Cyp139A3P_pseudogene
1822709	psd	TA	MUL_1657	-	intermediary metabolism and respiration	C-term cytochrome P450_139A3_Cyp139A3P_pseudogene
1822709	psd	TA	MUL_1657	-	intermediary metabolism and respiration	N-term cytochrome P450_139A3_Cyp139A3P_pseudogene
1824333	syn	TC	MUL_1658	-	cell wall and cell processes	ABC transporter ATP-binding protein
1825952	int	TC	-	-	-	-
1826998	non	CG	MUL_1659	-	intermediary metabolism and respiration	D-amino acid oxidase Aao_1
1831001	non	TC	MUL_1662	-	intermediary metabolism and respiration	lactoylglutathione lyase GlaO
1833694	int	GA	-	139 MUL_1664	conserved hypothetical	conserved hypothetical protein
1835347	non	TC	MUL_1666	-	cell wall and cell processes	antibiotic resistance ABC transporter_efflux system_ATP-binding protein
1835636	syn	AG	MUL_1666	-	cell wall and cell processes	antibiotic resistance ABC transporter_efflux system_ATP-binding protein
1840603	non	CT	MUL_1677	-	conserved hypothetical	conserved hypothetical protein
1848219	syn	GA	MUL_1677	-	conserved hypothetical	conserved hypothetical protein
1848414	non	TC	MUL_1677	-	conserved hypothetical	conserved hypothetical protein
1853292	syn	TC	MUL_1683	-	cytotoxin/hemolysin	TlyA
1854153	non	AG	MUL_1684	-	intermediary metabolism and respiration	inorganic polyphosphate/ATP-NAD kinase PpnK
1854353	syn	TC	MUL_1684	-	intermediary metabolism and respiration	inorganic polyphosphate/ATP-NAD kinase PpnK
1854516	non	TC	MUL_1684	-	intermediary metabolism and respiration	inorganic polyphosphate/ATP-NAD kinase PpnK
1859809	syn	TG	MUL_1688	-	intermediary metabolism and respiration	CTP synthase_PvG
1860962	syn	CG	MUL_1689	-	information pathways	NUDIX hydrolase
1862395	syn	GC	MUL_1690	-	insertion seqs and phages	integrase/recombinase_XerD
1862424	int	AG	-	5 MUL_1690	insertion seqs and phages	integrase/recombinase_XerD
1862510	syn	TC	MUL_1691	-	intermediary metabolism and respiration	O-methyltransferase
1862795	syn	CT	MUL_1691	-	intermediary metabolism and respiration	O-methyltransferase
1862822	syn	GA	MUL_1691	-	intermediary metabolism and respiration	O-methyltransferase
1862861	syn	CG	MUL_1691	-	intermediary metabolism and respiration	O-methyltransferase
1862894	syn	AG	MUL_1691	-	intermediary metabolism and respiration	O-methyltransferase
1862948	syn	TC	MUL_1691	-	intermediary metabolism and respiration	O-methyltransferase
1862951	syn	TC	MUL_1691	-	intermediary metabolism and respiration	O-methyltransferase
1863044	int	AG	-	25 MUL_1691	intermediary metabolism and respiration	O-methyltransferase
1863048	int	GT	-	29 MUL_1691	intermediary metabolism and respiration	O-methyltransferase
1863201	int	TC	-	137 MUL_1692	intermediary metabolism and respiration	myo-inositol-1-phosphate synthase
1863205	int	CT	-	133 MUL_1692	intermediary metabolism and respiration	myo-inositol-1-phosphate synthase
1864420	syn	AC	MUL_1692	-	intermediary metabolism and respiration	myo-inositol-1-phosphate synthase

SNP position	SNP type	Nucleotide change <ref><snp>	Distance to nearest locus	Nearby Locus	Functional group	Product
1866333	non	TC	MUL_1694	-	intermediary metabolism and respiration	sugar phosphate isomerases/epimerases
1867138	syn	TC	MUL_1695	-	intermediary metabolism and respiration	metal dependant hydrolase
1867468	non	GA	MUL_1695	-	intermediary metabolism and respiration	metal dependant hydrolase
1867570	syn	CT	MUL_1695	-	intermediary metabolism and respiration	metal dependant hydrolase
1868665	psd	GA	MUL_1696	-	conserved hypothetical	C-term conserved hypothetical protein pseudo gene
1869065	non	AG	MUL_1697	-	conserved hypothetical	conserved hypothetical protein
1869255	non	TC	MUL_1697	-	conserved hypothetical	conserved hypothetical protein
1869527	non	GC	MUL_1697	-	conserved hypothetical	conserved hypothetical protein
1869976	syn	GA	MUL_1697	-	conserved hypothetical	conserved hypothetical protein
1872874	psd	TG	MUL_1700	-	cell wall and cell processes	C-term multidrug resistance membrane efflux protein EmrB_2 pseudogene
1873450	psd	GC	MUL_1700	-	cell wall and cell processes	C-term multidrug resistance membrane efflux protein EmrB_2 pseudogene
1875362	Int.	CG				
1875945	Int.	AG	112	MUL_1702	PE/PPF	PPE family protein
1891739	syn	TC	MUL_1716	-	information pathways	Holliday junction DNA helicase RuvB
1895933	non	GA	MUL_1719	-	cell wall and cell processes	hypothetical membrane protein
1896432	syn	TG	MUL_1720	-	cell wall and cell processes	hypothetical secreted protein
1899298	syn	GA	MUL_1722	-	lipid metabolism	fatty-acid-CoA ligase FadD9
1899374	non	AT	MUL_1722	-	lipid metabolism	fatty-acid-CoA ligase FadD9
1899421	syn	AG	MUL_1722	-	lipid metabolism	fatty-acid-CoA ligase FadD9
1899791	non	GT	MUL_1722	-	lipid metabolism	fatty-acid-CoA ligase FadD9
1900312	syn	GA	MUL_1722	-	lipid metabolism	fatty-acid-CoA ligase FadD9
1902076	syn	AG	MUL_1722	-	lipid metabolism	fatty-acid-CoA ligase FadD9
1902598	syn	AG	MUL_1723	-	intermediary metabolism and respiration	4-aminobutyrate aminotransferase GabT
1903510	non	AT	MUL_1723	-	intermediary metabolism and respiration	4-aminobutyrate aminotransferase GabT
1904014	Int.	GA	25	MUL_1724	cell wall and cell processes	4-aminobutyrate aminotransferase GabT
1908539	syn	CG	MUL_1727	-	cell wall and cell processes	conserved membrane protein secretion factor YajC
1908551	syn	GC	MUL_1727	-	cell wall and cell processes	ABC-type dipeptide transport system periplasmic component
1910603	syn	TC	MUL_1729	-	intermediary metabolism and respiration	GTP pyrophosphokinase RelA
1911265	syn	AG	MUL_1729	-	intermediary metabolism and respiration	GTP pyrophosphokinase RelA
1911616	non	GA	MUL_1729	-	intermediary metabolism and respiration	GTP pyrophosphokinase RelA
1911944	syn	TG	MUL_1729	-	intermediary metabolism and respiration	GTP pyrophosphokinase RelA
1913399	syn	CG	MUL_1730	-	information pathways	GTP pyrophosphokinase RelA
1913556	syn	TC	MUL_1731	-	information pathways	peptidyl-prolyl cis-trans isomerase B PpiB
1916017	psd	GC	MUL_1733	-	insertion seqs and phages	Zn-dependent glyoxalase
1916017	psd	GC	MUL_1733	-	insertion seqs and phages	N-term conserved 13E12 repeat family protein pseudogene
1916220	psd	TC	MUL_1733	-	insertion seqs and phages	C-term conserved 13E12 repeat family protein pseudogene
1916356	psd	AG	MUL_1733	-	insertion seqs and phages	C-term conserved 13E12 repeat family protein pseudogene
1917174	Int.	TC	48	MUL_1734	conserved hypothetical	conserved hypothetical protein
1917439	non	TC	MUL_1734	-	conserved hypothetical	conserved hypothetical protein
1920120	syn	TC	MUL_1736	-	lipid metabolism	esterase (alpha-beta hydrolase superfamily)
1924510	syn	GC	MUL_1740	-	cell wall and cell processes	conserved membrane glycine rich protein
1924518	non	TC	MUL_1740	-	cell wall and cell processes	conserved membrane glycine rich protein
1926458	syn	TG	MUL_1743	-	information pathways	aspartyl-tRNA synthetase AspS
1926761	syn	TC	MUL_1743	-	information pathways	aspartyl-tRNA synthetase AspS
1928116	psd	TC	MUL_5095	-	conserved hypothetical	N-term conserved hypothetical protein pseudogene
1928122	C-	MUL_5095	-		conserved hypothetical	N-term conserved hypothetical protein pseudogene
1928364	Int.	G-	119	MUL_5095	conserved hypothetical	C-term conserved hypothetical protein pseudogene
1929705	Int.	AG	55	MUL_1745	conserved hypothetical	conserved hypothetical protein
1933579	syn	AC	MUL_1748	-	conserved hypothetical	conserved hypothetical alanine and leucine rich protein
1939404	non	TC	MUL_1752	-	conserved hypothetical	conserved hypothetical protein
1939456	syn	GT	MUL_1752	-	conserved hypothetical	conserved hypothetical protein
1940816	syn	AG	MUL_1754	-	information pathways	alanyl-tRNA synthetase AlaS
1941433	non	CT	MUL_1754	-	information pathways	alanyl-tRNA synthetase AlaS
1943396	syn	TC	MUL_1755	-	conserved hypothetical	conserved hypothetical protein
1943501	syn	GA	MUL_1755	-	conserved hypothetical	conserved hypothetical protein
1948147	syn	TC	MUL_1761	-	intermediary metabolism and respiration	3-dehydroquinate synthase AroB
1948585	syn	TG	MUL_1761	-	intermediary metabolism and respiration	3-dehydroquinate synthase AroB
1948636	syn	TC	MUL_1761	-	intermediary metabolism and respiration	3-dehydroquinate synthase AroB
1948684	syn	GA	MUL_1761	-	intermediary metabolism and respiration	3-dehydroquinate synthase AroB
1950836	syn	TC	MUL_1764	-	intermediary metabolism and respiration	cytoplasmic peptidase PepQ
1952441	non	GC	MUL_1766	-	information pathways	N utilization substance protein NusB
1954053	psd	CG	MUL_1769	-	intermediary metabolism and respiration	N-term amino acid decarboxylase pseudogene
1954053	psd	CG	MUL_1769	-	intermediary metabolism and respiration	C-term amino acid decarboxylase pseudogene
1958046	non	AG	MUL_1772	-	cell wall and cell processes	beta-lactamase
1958780	non	TC	MUL_1772	-	cell wall and cell processes	beta-lactamase
1960162	syn	TC	MUL_1773	-	cell wall and cell processes	conserved lipoprotein LprF
1961028	syn	GC	MUL_1774	-	cell wall and cell processes	conserved membrane protein
1961490	syn	AG	MUL_1774	-	cell wall and cell processes	conserved membrane protein
1962092	syn	GC	MUL_1775	-	lipid metabolism	chalcone/stilbene synthase
1964085	non	GC	MUL_1776	-	intermediary metabolism and respiration	glycolipid sulfotransferase
1964315	non	TC	MUL_1776	-	intermediary metabolism and respiration	glycolipid sulfotransferase
1964642	syn	CT	MUL_1777	-	intermediary metabolism and respiration	glycolipid sulfotransferase
1967819	syn	CT	MUL_1781	-	intermediary metabolism and respiration	dihydroorotate PyrC
1968030	non	AG	MUL_1781	-	intermediary metabolism and respiration	dihydroorotate PyrC
1968200	syn	GA	MUL_1781	-	intermediary metabolism and respiration	dihydroorotate PyrC
1969318	syn	GC	MUL_1782	-	cell wall and cell processes	secreted protein
1969402	syn	GA	MUL_1782	-	cell wall and cell processes	secreted protein
1970611	Int.	TC	61	MUL_1784	intermediary metabolism and respiration	carbamoyl-phosphate synthase large chain CarbB
1970875	syn	AG	MUL_1784	-	intermediary metabolism and respiration	carbamoyl-phosphate synthase large chain CarbB
1971481	syn	TC	MUL_1784	-	intermediary metabolism and respiration	carbamoyl-phosphate synthase large chain CarbB
1972606	syn	TC	MUL_1784	-	intermediary metabolism and respiration	carbamoyl-phosphate synthase large chain CarbB
1980388	non	AG	MUL_1792	-	cell wall and cell processes	conserved hypothetical secreted protein
1980683	syn	AT	MUL_1793	-	intermediary metabolism and respiration	monooxygenase
1981162	non	AC	MUL_1793	-	intermediary metabolism and respiration	monooxygenase
1981306	non	CT	MUL_1793	-	intermediary metabolism and respiration	monooxygenase
1982294	non	TC	MUL_1794	-	lipid metabolism	lipase LipH
1982750	syn	AG	MUL_1794	-	lipid metabolism	lipase LipH
1987754	non	AC	MUL_1798	-	intermediary metabolism and respiration	methyltransferase
1987950	Int.	CA	73	MUL_1798	intermediary metabolism and respiration	methyltransferase
1990640	syn	CG	MUL_1801	-	intermediary metabolism and respiration	methyltransferase
1992373	non	TG	MUL_1803	-	information pathways	Fmu_nprotein
1996772	syn	AG	MUL_1806	-	cell wall and cell processes	aminoglycosides/tetracycline-transport integral membrane protein

SNP position	SNP type	Nucleotide change <ref><snp>	Distance to nearest locus	Nearby Locus	Functional group	Product
1998791	syn	GA	MUL_1809	-	intermediary metabolism and respiration	riboflavin biosynthesis protein RibA2
1999236	non	TC	MUL_1809	-	intermediary metabolism and respiration	riboflavin biosynthesis protein RibA2
2000153	non	TG	MUL_1810	-	intermediary metabolism and respiration	riboflavin synthase beta chain RibH
2001373	Int	GC	75 MUL_1812	cell wall and cell processes	cell wall and cell processes	lipoprotein LnrH
2008992	syn	AC	MUL_1818	-	conserved hypothetical	conserved hypothetical protein
2010896	psd	CG	MUL_1820	-	lipid metabolism	N-term long-chain-fatty-acid-CoA ligase FadD12 - pseudogene
2011643	psd	TC	MUL_1820	-	lipid metabolism	N-term long-chain-fatty-acid-CoA ligase FadD12 - pseudogene
2017078	psd	AC	MUL_1825	-	cell wall and cell processes	N-term conserved hypothetical membrane protein - pseudogene
2018629	non	GA	MUL_1826	-	intermediary metabolism and respiration	dehydrogenase
2022091	non	CG	MUL_1829	-	intermediary metabolism and respiration	phosphoglycerate kinase Pfk
2022218	syn	CT	MUL_1829	-	intermediary metabolism and respiration	phosphoglycerate kinase Pfk
2023083	syn	AG	MUL_1830	-	intermediary metabolism and respiration	triosephosphate isomerase Tpi
2023401	syn	TG	MUL_1830	-	intermediary metabolism and respiration	triosephosphate isomerase Tpi
2026933	psd	TC	MUL_1832	-	cell wall and cell processes	C-term cationic amino acid transport integral membrane protein - pseudogene
2027461	psd	AG	MUL_1832	-	cell wall and cell processes	C-term cationic amino acid transport integral membrane protein - pseudogene
2028181	Int	AG	142 MUL_1832	cell wall and cell processes	N-term cationic amino acid transport integral membrane protein - pseudogene	
2028720	syn	TC	MUL_1833	-	regulatory proteins	transcriptional regulatory protein (probably GntR-family)
2029348	syn	GT	MUL_1834	-	cell wall and cell processes	conserved hypothetical membrane protein
2029520	Int	-G	-	cell wall and cell processes	conserved hypothetical membrane protein	
2023246	syn	TG	MUL_1826	-	intermediary metabolism and respiration	phosphoglycoluruvate carboxylase
2038971	syn	GA	MUL_1843	-	intermediary metabolism and respiration	transaldolase Tal
2039727	syn	CG	MUL_1843	-	intermediary metabolism and respiration	transaldolase Tal
2055716	non	GA	MUL_1854	-	regulatory proteins	transcriptional activator protein
2056428	non	TA	MUL_1855	-	intermediary metabolism and respiration	quinone reductase Qor
2056602	syn	AG	MUL_1855	-	intermediary metabolism and respiration	quinone reductase Qor
2057022	syn	CC	MUL_1855	-	intermediary metabolism and respiration	quinone reductase Qor
2057322	syn	TG	MUL_1826	-	conserved hypothetical	conserved hypothetical protein
2057352	non	AG	MUL_1856	-	conserved hypothetical	conserved hypothetical protein
2057913	syn	AG	MUL_1856	-	conserved hypothetical	conserved hypothetical protein
2058491	non	GA	MUL_1857	-	cell wall and cell processes	unidentified antibiotic-transport integral membrane ABC transporter
2060582	syn	CG	MUL_1860	-	cell wall and cell processes	conserved integral membrane protein
2061726	syn	CC	MUL_1860	-	cell wall and cell processes	conserved integral membrane protein
2064753	syn	AG	MUL_1862	-	conserved hypothetical	conserved protein
2065043	syn	TC	MUL_1863	-	conserved hypothetical	conserved protein
2065409	syn	TC	MUL_1863	-	conserved hypothetical	conserved protein
2065706	syn	TC	MUL_1863	-	conserved hypothetical	conserved protein
2066719	syn	TC	MUL_1864	-	cell wall and cell processes	conserved ATP-binding protein ABC transporter
2067381	syn	TC	MUL_1865	-	intermediary metabolism and respiration	cysteine desulfurase Csd
2067447	syn	AG	MUL_1865	-	intermediary metabolism and respiration	cysteine desulfurase Csd
2069008	Int	TG	117 MUL_1868	PE/PE	N-term PE-PGRS family protein - pseudogene	
2071722	syn	GA	MUL_1869	-	lipid metabolism	acyl-CoA dehydrogenase FadE15
2080485	non	GC	MUL_1879	-	regulatory proteins	transcriptional regulatory protein (probably AsnC-family)
2080529	syn	TC	MUL_1879	-	regulatory proteins	transcriptional regulatory protein (probably AsnC-family)
2080707	non	AG	MUL_1879	-	regulatory proteins	transcriptional regulatory protein (probably AsnC-family)
2082840	syn	AG	MUL_1880	-	intermediary metabolism and respiration	monoxygenase
2084161	syn	AC	MUL_1883	-	information pathways	ribonucleoside-diphosphate reductase (beta chain) NrdF2
2085117	Int	CT	95 MUL_1883	information pathways	ribonucleoside-diphosphate reductase (beta chain) NrdF2	
2086440	syn	GA	MUL_1885	-	intermediary metabolism and respiration	NADP-dependent alcohol dehydrogenase Adh
2086503	syn	TC	MUL_1885	-	intermediary metabolism and respiration	NADP-dependent alcohol dehydrogenase Adh
2089240	syn	AG	MUL_1887	-	intermediary metabolism and respiration	cytochrome C oxidase polypeptide I CtaB
2094850	non	GT	MUL_1892	-	cell wall and cell processes	oxidoreductase
2095263	syn	AC	MUL_1892	-	cell wall and cell processes	oxidoreductase
2095808	syn	AG	MUL_1893	-	intermediary metabolism and respiration	formate hydrogenlyase HydC
2096288	non	CG	MUL_1894	-	intermediary metabolism and respiration	hydrogenase HydP
2099253	psd	GC	MUL_1896	-	intermediary metabolism and respiration	mid-section formate hydrogenase HydE - pseudogene
2100497	syn	TC	MUL_1897	-	cell wall and cell processes	conserved ATP-binding protein ABC transporter
2101432	syn	CG	MUL_1898	-	conserved hypothetical	conserved hypothetical protein
2101947	syn	TC	MUL_1899	-	lipid metabolism	enoyl-CoA hydratase EchA17
2102974	syn	CG	MUL_1900	-	conserved hypothetical	conserved hypothetical protein
2106510	syn	GA	MUL_1903	-	conserved hypothetical	conserved membrane protein
2108012	Int	TC	20 MUL_1905	lipid metabolism	lysophospholipase	
2109981	non	TC		intermediary metabolism and respiration	DNA photolyase Phr1	
2111837	syn	TC		cell wall and cell processes	conserved transmembrane transport protein	
2112537	non	TG		cell wall and cell processes	conserved transmembrane transport protein	
2112607	non	GC		cell wall and cell processes	conserved transmembrane transport protein	
2113546	Int	GA		cell wall and cell processes	N-term penicillin-binding protein pseudogene	
2114558	psd	TC		cell wall and cell processes	C-term penicillin-binding protein pseudogene	
2114651	psd	TC		cell wall and cell processes	C-term penicillin-binding protein pseudogene	
2114677	psd	TC		cell wall and cell processes	C-term penicillin-binding protein pseudogene	
2117945	psd	GA		conserved hypothetical	C-term conserved hypothetical protein pseudogene	
2118011	psd	GA		conserved hypothetical	C-term conserved hypothetical protein pseudogene	
2118108	Int	TA		conserved hypothetical	C-term conserved hypothetical protein pseudogene	
2118713	non	CA	MUL_1916	-	cell wall and cell processes	conserved hypothetical membrane protein
2118864	non	TC	MUL_1916	-	cell wall and cell processes	conserved hypothetical membrane protein
2119239	psd	CG	MUL_1917	-	cell wall and cell processes	N-term conserved hypothetical membrane protein pseudogene
2119986	psd	AC	MUL_1917	-	cell wall and cell processes	N-term conserved hypothetical membrane protein pseudogene
2121174	non	TC	MUL_1918	-	intermediary metabolism and respiration	dehydrogenase/reductase
2121946	syn	AG	MUL_1919	-	intermediary metabolism and respiration	transferase
2122150	syn	GA	MUL_1919	-	intermediary metabolism and respiration	transferase
2123869	non	CT	MUL_1920	-	conserved hypothetical	conserved protein
2124841	syn	TC	MUL_1921	-	conserved hypothetical	conserved hypothetical protein
2129318	psd	AG	MUL_1926	-	conserved hypothetical	C-term conserved hypothetical protein pseudogene
2129362	psd	AG	MUL_1926	-	conserved hypothetical	C-term conserved hypothetical protein pseudogene
2129543	psd	CT	MUL_1926	-	conserved hypothetical	C-term conserved hypothetical protein pseudogene
2129873	syn	AG	MUL_1927	-	intermediary metabolism and respiration	cysteine desulfurase IcsC
2129909	syn	TG	MUL_1927	-	intermediary metabolism and respiration	cysteine desulfurase IcsC
2130203	syn	CT	MUL_1927	-	intermediary metabolism and respiration	cysteine desulfurase IcsC
2131441	syn	AC	MUL_1928	-	information pathways	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase TrmU
2136954	Int	GA	130 MUL_1931	intermediary metabolism and respiration	C-term methyltransferase pseudogene	
2137443	syn	TC		information pathways	DNA ligase [NAD dependent] LigA	
2137881	syn	TC	MUL_1933	-	information pathways	DNA ligase [NAD dependent] LigA
2139684	syn	GT	MUL_1934	-	regulatory proteins	regulatory protein

SNP position	SNP type	Nucleotide change <ref><snp>	Distance to nearest locus	Nearby Locus	Functional group	Product
2139865	int	GC	22	MUL_1934	regulatory protein	
2145640	syn	AC	MUL_1939	-	information pathways	glutamyl-tRNA (Gln) amidotransferase (subunit A) GatA
2146054	syn	AT	MUL_1940	-	intermediary metabolism and respiration	6-phosphofructokinase PfkA
2147332	non	GA	MUL_1941	-	information pathways	glutamyl-tRNA(Gln) amidotransferase (subunit B) GatB
2147349	non	AG	MUL_1941	-	information pathways	glutamyl-tRNA(Gln) amidotransferase (subunit B) GatB
2148173	syn	CT	MUL_1941	-	information pathways	glutamyl-tRNA(Gln) amidotransferase (subunit B) GatB
2150061	syn	GA	MUL_1943	-	cell wall and cell processes	conserved lipoprotein LpnZ
2152225	syn	GA	MUL_1947	-	intermediary metabolism and respiration	acetolactate synthase (large subunit) IlvB1
2152706	syn	TC	MUL_1947	-	intermediary metabolism and respiration	acetolactate synthase (large subunit) IlvB1
2155825	non	TG	MUL_1950	-	conserved hypotheticals	conserved protein
2156205	syn	TC	MUL_1950	-	conserved hypotheticals	conserved protein
2157678	psd	AC	MUL_1951	-	intermediary metabolism and respiration	mid-section alanine rich dehydrogenase_pseudogene
2158521	evn	CT	MUL_1952	-	intermediary metabolism and respiration	D-3-phosphoglycerate dehydrogenase SerA1
2158525	evn	CT	MUL_1952	-	intermediary metabolism and respiration	D-3-phosphoglycerate dehydrogenase SerA1
2159415	int	GA	50 MUL_1953	intermediary metabolism and respiration	3-isopropylmalate dehydrogenase LeuB	
2159528	non	AG		intermediary metabolism and respiration	3-isopropylmalate dehydrogenase LeuB	
2159878	evn	CT		intermediary metabolism and respiration	3-isopropylmalate dehydrogenase LeuB	
2162815	evn	CT		information pathways	glutamyl-tRNA synthetase GtsS	
2164093	evn	TC		information pathways	glutamyl-tRNA synthetase GtsS	
2167169	psd	AG		cell wall and cell processes	C-term conserved transmembrane transport protein MmpL1_pseudogene	
2167389	psd	AG		cell wall and cell processes	C-term conserved transmembrane transport protein MmpL1_pseudogene	
2167727	psd	TC		cell wall and cell processes	C-term conserved transmembrane transport protein MmpL1_pseudogene	
2167728	psd	CG		cell wall and cell processes	C-term conserved transmembrane transport protein MmpL1_pseudogene	
2172599	non	CT		intermediary metabolism and respiration	8-amino-7-oxononanoic acid synthase_BioF2_2	
2173570	int	GA		intermediary metabolism and respiration		
2175391	syn	CT	MUL_1968	-	intermediary metabolism and respiration	3-isopropylmalate dehydrogenase (large subunit) LeuC
2175774	non	AG	MUL_1968	-	intermediary metabolism and respiration	3-isopropylmalate dehydrogenase (large subunit) LeuC
2177113	syn	TG	MUL_1969	-	intermediary metabolism and respiration	3-isopropylmalate dehydrogenase (small subunit) LeuD
2179410	syn	AG	MUL_1972	-	intermediary metabolism and respiration	polyphosphate kinase Ppk
2183873	syn	GA	MUL_1976	-	intermediary metabolism and respiration	d-alanine-D-alanine ligase DdlA
2184203	syn	TG	MUL_1976	-	intermediary metabolism and respiration	d-alanine-D-alanine ligase DdlA
2184422	syn	AG	MUL_1976	-	intermediary metabolism and respiration	d-alanine-D-alanine ligase DdlA
2188041	psd	TC	MUL_1981	-	intermediary metabolism and respiration	N-term oxidoreductase_pseudogene
2188641	syn	TC	MUL_1982	-	intermediary metabolism and respiration	nitroreductase
2189375	int	-A	99 MUL_1983	information pathways	50S ribosomal protein L28 RpmB2_1	
2192903	syn	TG		information pathways	A1P-dependent DNA helicase RecG	
2194858	non	GT		intermediary metabolism and respiration	oxidoreductase	
2197337	non	AG		cell wall and cell processes	conserved membrane protein	
2197777	non	GC		cell wall and cell processes	conserved integral membrane protein	
2198499	syn	AG		intermediary metabolism and respiration	pyruvate carboxylase Pca	
2200572	syn	TC		intermediary metabolism and respiration	pyruvate carboxylase Pca	
2200573	syn	TC		intermediary metabolism and respiration	pyruvate carboxylase Pca	
2202038	syn	TG		cell wall and cell processes	Methyltransferase	
2202729	syn	TC	MUL_1994	-	intermediary metabolism and respiration	phosphopantetheine adenylyltransferase KdtB
2202855	syn	CA	MUL_1994	-	intermediary metabolism and respiration	phosphopantetheine adenylyltransferase KdtB
2209703	int	CT	10 MUL_2001	intermediary metabolism and respiration	N-term ketoreductase_pseudogene	
2211016	int	TC		-		
2211025	int	GA		-		
2213297	non	GC	MUL_2002	-	lipid metabolism	fatty-acyl AMP ligase FadD29
2214639	syn	AG	MUL_2004	-	lipid metabolism	fatty-acid-CoA ligase FadD22
2222842	int	CT	144 MUL_2005	lipid metabolism	polyketide synthase Pks15/1	
2222848	int	CT		-		
2227842	syn	TC	MUL_2008	-	lipid metabolism	fatty-acyl AMP ligase FadD28
2229356	syn	TC	MUL_2009	-	intermediary metabolism and respiration	methyltransferase
2229674	int	TC	123 MUL_2009	intermediary metabolism and respiration	methyltransferase	
2229896	int	TC		-		
2234632	syn	TC	MUL_2010	-	lipid metabolism	multifunctional mycocerosic acid synthase membrane-associated Mas
2236237	syn	CT	MUL_2010	-	lipid metabolism	multifunctional mycocerosic acid synthase membrane-associated Mas
2236510	int	GC	39 MUL_2010	lipid metabolism	multifunctional mycocerosic acid synthase membrane-associated Mas	
2241796	non	TC		lipid metabolism	phenolthiocerol synthesis type-I polyketide synthase PpsE	
2244378	syn	AG	MUL_2015	-	lipid metabolism	phenolthiocerol synthesis type-I polyketide synthase PpsE
2244622	syn	TC	MUL_2015	-	lipid metabolism	phenolthiocerol synthesis type-I polyketide synthase PpsE
2250239	syn	TC	MUL_2016	-	lipid metabolism	phenolthiocerol synthesis type-I polyketide synthase PpsD
2250603	syn	AG	MUL_2017	-	lipid metabolism	phenolthiocerol synthesis type-I polyketide synthase PpsC
2253748	syn	GC	MUL_2017	-	lipid metabolism	phenolthiocerol synthesis type-I polyketide synthase PpsC
2256414	syn	AG	MUL_2017	-	lipid metabolism	phenolthiocerol synthesis type-I polyketide synthase PpsC
2267798	non	TC	MUL_2020	-	lipid metabolism	fatty-acyl AMP ligase Fad26
2275107	non	GA	MUL_2031	-	information pathways	formamidopyrimidine-DNA glycosylase Fpg
2277440	syn	TC	MUL_2033	-	cell wall and cell processes	chromosome partition protein Smc
2280586	syn	AT	MUL_2034	-	cell wall and cell processes	cell division protein FtsY
2283798	psd	TC	MUL_2037	-	intermediary metabolism and respiration	N-term [protein-PII] uridyltransferase GlnD_pseudogene
2289178	syn	TC	MUL_2040	-	cell wall and cell processes	signal recognition particle protein Ffh
2289769	syn	GA	MUL_2040	-	cell wall and cell processes	signal recognition particle protein Ffh
2293035	int	TC	80 MUL_2042	regulatory protein	transmembrane serine/threonine-protein kinase I PknI	
2293642	syn	AC		intermediary metabolism and respiration	D-amino acid aminohydrolase	
2294206	syn	AG	MUL_2043	-	intermediary metabolism and respiration	D-amino acid aminohydrolase
2294461	syn	CG	MUL_2043	-	intermediary metabolism and respiration	D-amino acid aminohydrolase
2296104	non	TC	MUL_2045	-	cell wall and cell processes	D-alanyl-D-alanine carboxypeptidase DacB
2296754	syn	CG	MUL_2046	-	conserved hypotheticals	conserved hypothetical protein
2299997	syn	CG	MUL_2051	-	cell wall and cell processes	conserved alanine rich lipoprotein LppW
2301262	syn	AG	MUL_2053	-	cell wall and cell processes	signal peptidase I LepB
2301295	syn	GA	MUL_2053	-	cell wall and cell processes	signal peptidase I LepB
2303334	psd	-C	MUL_2056	-	conserved hypotheticals	N-term conserved hypothetical protein_pseudogene
2303334	psd	-C	MUL_2056	-	conserved hypotheticals	C-term conserved hypothetical protein_pseudogene
2305574	syn	GC	MUL_2058	-	cell wall and cell processes	conserved hypothetical membrane protein
2305682	syn	CT	MUL_2058	-	cell wall and cell processes	conserved hypothetical membrane protein
2306640	non	CT	MUL_2059	-	intermediary metabolism and respiration	formate dehydrogenase family accessory protein FdhD
2307818	psd	AG	MUL_2061	-	conserved hypotheticals	N-term conserved hypothetical protein_pseudogene
2308085	psd	GA	MUL_2061	-	conserved hypotheticals	N-term conserved hypothetical protein_pseudogene
2308373	psd	TG	MUL_2061	-	conserved hypotheticals	N-term conserved hypothetical protein_pseudogene
2308565	psd	TC	MUL_2061	-	conserved hypotheticals	N-term conserved hypothetical protein_pseudogene
2308667	psd	AG	MUL_2061	-	conserved hypotheticals	N-term conserved hypothetical protein_pseudogene

SNP position	SNP type	Nucleotide change <ref><snp>	Distance to nearest locus	Nearby Locus	Functional group	Product
2309611	syn	AC	MUL_2062	-	cell wall and cell processes	conserved hypothetical membrane protein
2310561	syn	GA	MUL_2063	-	intermediary metabolism and respiration	mycobactin utilization protein VnuB
2310785	non	AG	MUL_2063	-	intermediary metabolism and respiration	mycobactin utilization protein VnuB
2311499	bsd	TC	MUL_2064	-	intermediary metabolism and respiration	N-term L-lactate dehydrogenase (cytochrome) LldD1_1_pseudogene
2311511	bsd	GA	MUL_2064	-	intermediary metabolism and respiration	N-term L-lactate dehydrogenase (cytochrome) LldD1_1_pseudogene
2312353	bsd	CT	MUL_2064	-	intermediary metabolism and respiration	C-term L-lactate dehydrogenase (cytochrome) LldD1_1_pseudogene
2313938	int	TC		81 MUL_2067	information pathways	30S ribosomal protein S2 RpsB
2316192	syn	TC	MUL_2069	-	intermediary metabolism and respiration	amidase AmiC
2320330	int	TC		23 MUL_2073	regulatory proteins	transcriptional regulatory protein
2322591	non	TG	MUL_2076	-	lipid metabolism	integral membrane phosphatidate cytidyltransferase CdsA
2326268	syn	TC	MUL_2080	-	cell wall and cell processes	conserved integral membrane protein
2326372	non	TC	MUL_2080	-	cell wall and cell processes	conserved integral membrane protein
2326304	syn	GC	MUL_2080	-	cell wall and cell processes	conserved integral membrane protein
2334287	syn	TC	MUL_2087	-	lipid metabolism	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase IspG
2334538	syn	TC	MUL_2087	-	lipid metabolism	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase IspG
2334787	syn	TC	MUL_2087	-	lipid metabolism	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase IspG
2339120	syn	AG	MUL_2091	-	intermediary metabolism and respiration	methionine aminopeptidase MapB
2339442	int	GA		115 MUL_2091	intermediary metabolism and respiration	methionine aminopeptidase MapB
2339897	non	TC	MUL_2092	-	cell wall and cell processes	conserved hypothetical membrane protein
2339898	non	CT	MUL_2092	-	cell wall and cell processes	conserved hypothetical membrane protein
2340810	non	TG	MUL_2093	-	intermediary metabolism and respiration	amidotransferase
2340811	non	TG	MUL_2093	-	intermediary metabolism and respiration	amidotransferase
2340990	int	CG		35 MUL_2093	intermediary metabolism and respiration	amidotransferase
2341475	int	TC		-	-	-
2341525	int	TC		-	-	-
2343995	int	CA		48 MUL_2096	PE/PPE	PPE family protein
2344075	int	TC		32 MUL_2096	PE/PPE	PPE family protein
2344178	int	GT		135 MUL_2096	PE/PPE	PPE family protein
2345374	int	GC		-	-	-
2346055	int	GT		23 MUL_2098	PE/PPE	N-term PPE family protein pseudogene
2346110	int	TC		31 MUL_2098	PE/PPE	N-term PPE family protein pseudogene
2346117	int	GA		38 MUL_2098	PE/PPE	N-term PPE family protein pseudogene
2346140	int	GA		61 MUL_2098	PE/PPE	N-term PPE family protein pseudogene
2346219	int	GA		140 MUL_2098	PE/PPE	N-term PPE family protein pseudogene
2346235	int	TG		-	-	-
2346264	int	AG		-	-	-
2346265	int	AG		-	-	-
2346267	int	GA		-	-	-
2346305	int	AG		-	-	-
2346332	int	CT		-	-	-
2346473	int	CT		-	-	-
2346694	int	AC		146 MUL_2099	PE/PPE	C-term PE-PGRS family protein pseudogene
2351866	int	T-		-	-	-
2351868	int	GA		-	-	-
2352202	int	GT		142 MUL_2107	cell wall and cell processes	N-term drug-transport integral membrane protein pseudogene
2355874	non	AC	MUL_2109	-	intermediary metabolism and respiration	malate:quinone oxidoreductase Mqo
2358907	syn	CA	MUL_2112	-	intermediary metabolism and respiration	cob(I)alamin adenosyltransferase CobO
2361278	syn	TC	MUL_2114	-	intermediary metabolism and respiration	multifunctional enzyme siroheme synthase CysG
2362469	syn	TC	MUL_2115	-	cell wall and cell processes	integral membrane efflux protein EfpA
2365156	syn	AC	MUL_2116	-	information pathways	prolyl-tRNA synthetase ProS
2365632	syn	GC	MUL_2116	-	information pathways	prolyl-tRNA synthetase ProS
2365969	syn	CT	MUL_2117	-	conserved hypotheticals	conserved hypothetical alanine rich protein
2366170	syn	CG	MUL_2117	-	conserved hypotheticals	conserved hypothetical alanine rich protein
2373732	syn	TC	MUL_2125	-	information pathways	DNA-damage-inducible protein F DifF
2379476	bsd	CT	MUL_2131	-	conserved hypotheticals	C-term conserved hypothetical protein pseudogene
2386073	syn	AG	MUL_2136	-	conserved hypotheticals	conserved hypothetical protein
2386366	bsd	TA	MUL_2137	-	conserved hypotheticals	N-term conserved hypothetical protein pseudogene
2391326	non	AG	MUL_2142	-	information pathways	tRNA pseudouridine synthase B TruB
2392370	syn	AC	MUL_2143	-	cell wall and cell processes	lipid-transfer protein Ltp1
2392577	syn	CT	MUL_2143	-	cell wall and cell processes	lipid-transfer protein Ltp1
2393649	syn	TC	MUL_2144	-	lipid metabolism	acyl-CoA dehydrogenase FadE21
2393811	syn	AG	MUL_2144	-	lipid metabolism	acyl-CoA dehydrogenase FadE21
2394296	syn	CT	MUL_2145	-	regulatory proteins	transcriptional repressor SirR
2395114	syn	GA	MUL_2146	-	intermediary metabolism and respiration	bifunctional fad synthetase/riboflavin biosynthesis protein RibF
2395936	syn	TC	MUL_2146	-	intermediary metabolism and respiration	bifunctional fad synthetase/riboflavin biosynthesis protein RibF
2395982	syn	TC	MUL_2146	-	intermediary metabolism and respiration	bifunctional fad synthetase/riboflavin biosynthesis protein RibF
2397733	int	GA		80 MUL_2150	information pathways	bifunctional protein polyribonucleotide nucleotidylyltransferase GpsI
2398922	syn	AG	MUL_2150	-	information pathways	bifunctional protein polyribonucleotide nucleotidylyltransferase GpsI
2399429	syn	TG	MUL_2150	-	information pathways	bifunctional protein polyribonucleotide nucleotidylyltransferase GpsI
2402576	bsd	CT	MUL_2151	-	intermediary metabolism and respiration	C-term zinc protease PepR pseudogene
2404301	syn	AG	MUL_2154	-	intermediary metabolism and respiration	secreted L-alanine dehydrogenase Ald (40 kDa antigen)
2407576	bsd	CT	MUL_2158	-	intermediary metabolism and respiration	N-term short-chain dehydrogenase EhdD 1 pseudogene
2415496	non	GA	MUL_2165	-	cell wall and cell processes	conserved hypothetical secreted protein
2418196	bsd	GC	MUL_2168	-	lipid metabolism	C-term chain-fatty-acid-CoA ligase FadD13 1 pseudogene
2419044	bsd	AC	MUL_2168	-	lipid metabolism	C-term chain-fatty-acid-CoA ligase FadD13 1 pseudogene
2422217	bsd	TC	MUL_2171	-	lipid metabolism	N-term bifunctional protein acetyl-/propionyl-coenzyme a carboxylase (alpha chain) AccA3 1 pseudogene
2422946	bsd	TC	MUL_2171	-	lipid metabolism	N-term bifunctional protein acetyl-/propionyl-coenzyme a carboxylase (alpha chain) AccA3 1 pseudogene
2423391	bsd	TG	MUL_2171	-	lipid metabolism	N-term bifunctional protein acetyl-/propionyl-coenzyme a carboxylase (alpha chain) AccA3 1 pseudogene
2423913	bsd	CG	MUL_2171	-	lipid metabolism	N-term bifunctional protein acetyl-/propionyl-coenzyme a carboxylase (alpha chain) AccA3 1 pseudogene
2428321	bsd	AC	MUL_2174	-	lipid metabolism	C-term acyl-CoA dehydrogenase FadE34 1 pseudogene
2428576	bsd	GA	MUL_2174	-	lipid metabolism	C-term acyl-CoA dehydrogenase FadE34 1 pseudogene
2430306	non	GT	MUL_2177	-	intermediary metabolism and respiration	alanine rich hydrolase
2430307	non	TG	MUL_2177	-	intermediary metabolism and respiration	alanine rich hydrolase
2431401	syn	TC	MUL_2178	-	intermediary metabolism and respiration	thymidylate synthase ThyA
2431479	syn	TC	MUL_2178	-	intermediary metabolism and respiration	thymidylate synthase ThyA
2432646	syn	TC	MUL_2180	-	conserved hypotheticals	conserved hypothetical protein
2433397	non	GA	MUL_2180	-	conserved hypotheticals	conserved hypothetical protein
2434582	syn	TG	MUL_2181	-	information pathways	C-term type I restriction/modification system DNA methylase HsdM pseudogene
2434681	bsd	GA	MUL_2181	-	information pathways	C-term type I restriction/modification system DNA methylase HsdM pseudogene
2435404	bsd	GC	MUL_2182	-	information pathways	C-term type I restriction/modification system specificity determinant HsdS (S protein) pseudogene
2436440	non	TC	MUL_2183	-	intermediary metabolism and respiration	thymidylate synthase ThyX

SNP position	SNP type	Nucleotide change <ref><snp>	Distance to nearest locus	Nearby Locus	Functional group	Product
2439512	bsd	TG	MUL_2187	-	cell wall and cell processes	N-term conserved hypothetical membrane protein _pseudogene
2439600	bsd	TC	MUL_2187	-	cell wall and cell processes	N-term conserved hypothetical membrane protein _pseudogene
2440194	snp	GC	MUL_2188	-	conserved hypotheticals	conserved protein
2440691	Int	AG		-	regulatory proteins	feric uptake regulation protein FurA
2441056	snp	TC	MUL_2189	-	regulatory proteins	catalase-peroxidase-peroxynitritase T KatG
2443324	hon	CA	MUL_2190	-	cell wall and cell processes	glycine betaine transport integral membrane protein BetP
2443547	hon	TC	MUL_2191	-	cell wall and cell processes	glycine betaine transport integral membrane protein BetP
2445250	snp	TG	MUL_2191	-	lipid metabolism	mid-section fatty-acid-CoA ligase FadD9_pseudogene
2451054	Int	AG		109 MUL_2195	lipid metabolism	C-term fatty-acid-CoA ligase FadD9_pseudogene
2452363	psd	CT	MUL_2195	-	lipid metabolism	C-term fatty-acid-CoA ligase FadD9_pseudogene
2452574	psd	TC	MUL_2195	-	lipid metabolism	C-term fatty-acid-CoA ligase FadD9_pseudogene
2454398	snp	AG	MUL_2198	-	intermediary metabolism and respiration	nitroreductase
2454444	snp	TC	MUL_2198	-	intermediary metabolism and respiration	nitroreductase
2455670	Int	TC		71 MUL_2200	regulatory proteins	membrane-anchored serine/threonine-protein kinase
2457219	snp	AG	MUL_2200	-	regulatory proteins	membrane-anchored serine/threonine-protein kinase
2460317	Int	TG		57 MUL_2203	PE/PPE	N-term PPE family protein _pseudogene
2460317	Int	TG		57 MUL_2203	PE/PPE	C-term PPE family protein _pseudogene
2460500	Int	AC		143 MUL_2203	PE/PPE	N-term PPE family protein _pseudogene
2460509	Int	CG		134 MUL_2203	PE/PPE	N-term PPE family protein _pseudogene
2460767	Int	TG		124 MUL_2203	PE/PPE	N-term PPE family protein _pseudogene
2463023	Int	CG		24 MUL_2205	conserved hypotheticals	conserved protein
2463258	Int	G-		-	information pathways	mid-section HrpA-like helicases _pseudogene
2464756	psd	AT	MUL_2206	-	information pathways	mid-section HrpA-like helicases _pseudogene
2466016	psd	AC	MUL_2206	-	information pathways	mid-section HrpA-like helicases _pseudogene
2466016	psd	AC	MUL_2206	-	information pathways	C-term HrpA-like helicases _pseudogene
2466378	psd	AG	MUL_2206	-	information pathways	C-term HrpA-like helicases _pseudogene
2467219	Int	AC		106 MUL_2206	information pathways	C-term HrpA-like helicases _pseudogene
2471760	snp	TC	MUL_2210	-	cell wall and cell processes	chitinase/cellulase
2475123	snp	GA	MUL_2214	-	intermediary metabolism and respiration	dihydrodiprolamide dehydrogenase Lpd
2483358	snp	AG	MUL_2223	-	conserved hypotheticals	conserved hypothetical protein
2484424	psd	AG	MUL_2224	-	intermediary metabolism and respiration	N-term O-methyltransferase _pseudogene
2485867	Int	AG		128 MUL_2228	conserved hypotheticals	conserved protein
2487133	psd	TC	MUL_2229	-	regulatory proteins	C-term heat shock protein transcriptional repressor HspR_2 _pseudogene
2488731	Int	A-		100 MUL_2231	insertion seqs and phages	C-term transposase for IS2404
2489750	Int	AG		-	intermediary metabolism and respiration	GTP cyclohydrolase I FoIE_1
2490179	hon	GC	MUL_2233	-	intermediary metabolism and respiration	carboxylesterase Ldt
2492855	hon	CT	MUL_2237	-	conserved hypotheticals	carboxylesterase Ldt
2493143	snp	TC	MUL_2238	-	information pathways	alternative RNA polymerase sigma factor
2493991	snp	GC	MUL_2239	-	cell wall and cell processes	conserved hypothetical membrane protein
2496735	Int	AG		-	intermediary metabolism and respiration	carboxylesterase Ldt
2496966	Int	GA		-	intermediary metabolism and respiration	carboxylesterase Ldt
2496978	Int	AG		-	intermediary metabolism and respiration	carboxylesterase Ldt
2496984	Int	AG		-	intermediary metabolism and respiration	carboxylesterase Ldt
2499818	Int	TC		62 MUL_2248	PE/PPE	C-term PPE family protein - pseudogene
2499906	Int	AG		26 MUL_2248	PE/PPE	C-term PPE family protein - pseudogene
2500298	Int	G-		5 MUL_2248	PE/PPE	N-term PPE family protein _pseudogene
2500299	Int	A-		6 MUL_2248	PE/PPE	N-term PPE family protein _pseudogene
2501459	snp	AG	MUL_2249	-	conserved hypotheticals	conserved hypothetical protein
2501955	hon	AG	MUL_2249	-	conserved hypotheticals	conserved hypothetical protein
2505244	snp	GA	MUL_2251	-	conserved hypotheticals	conserved membrane protein
2507163	snp	AG	MUL_2253	-	cell wall and cell processes	sugar ABC transporter
2508055	snp	GC	MUL_2254	-	cell wall and cell processes	ABC-type sugar transport integral membrane protein
2509094	psd	GA	MUL_2255	-	cell wall and cell processes	C-term sugar-binding lipoprotein - pseudogene
2509167	psd	TC	MUL_2255	-	cell wall and cell processes	N-term sugar-binding lipoprotein - pseudogene
2509167	psd	TC	MUL_2255	-	cell wall and cell processes	C-term sugar-binding lipoprotein - pseudogene
2509604	psd	CG	MUL_2255	-	cell wall and cell processes	N-term sugar-binding lipoprotein - pseudogene
2512774	psd	TA	MUL_2260	-	conserved hypotheticals	C-term conserved hypothetical protein - pseudogene
2513247	psd	CG	MUL_2260	-	conserved hypotheticals	C-term conserved hypothetical protein - pseudogene
2513293	psd	AG	MUL_2260	-	conserved hypotheticals	C-term conserved hypothetical protein - pseudogene
2514227	psd	AC	MUL_2260	-	conserved hypotheticals	N-term conserved hypothetical protein - pseudogene
2515851	hon	TA	MUL_2261	-	lipid metabolism	carboxylesterase Ldt
2516097	hon	CT	MUL_2261	-	lipid metabolism	carboxylesterase Ldt
2517246	hon	CG	MUL_2263	-	conserved hypotheticals	conserved hypothetical protein
2518456	Int	CG		97 MUL_2265	cell wall and cell processes	conserved membrane protein
2519505	hon	TG	MUL_2265	-	cell wall and cell processes	conserved membrane protein
2521250	Int	TC		37 MUL_2265	cell wall and cell processes	conserved membrane protein
2521724	snp	TG	MUL_2266	-	lipid metabolism	polyketide synthase Pks12
2524202	snp	CG	MUL_2266	-	lipid metabolism	polyketide synthase Pks12
2525059	hon	GT	MUL_2266	-	lipid metabolism	polyketide synthase Pks12
2527421	hon	TA	MUL_2266	-	lipid metabolism	polyketide synthase Pks12
2528915	snp	AG	MUL_2266	-	lipid metabolism	polyketide synthase Pks12
2530518	hon	GA	MUL_2266	-	lipid metabolism	polyketide synthase Pks12
2531474	snp	AG	MUL_2266	-	lipid metabolism	polyketide synthase Pks12
2532065	snp	AG	MUL_2266	-	lipid metabolism	polyketide synthase Pks12
2533912	Int	CT		51 MUL_2266	lipid metabolism	polyketide synthase Pks12
2534986	snp	AG	MUL_2268	-	conserved hypotheticals	conserved hypothetical protein
2535361	snp	GA	MUL_2269	-	cell wall and cell processes	C-term polyenol-monophosphomannose synthase Ppm1B
2535373	snp	AG	MUL_2269	-	cell wall and cell processes	C-term polyenol-monophosphomannose synthase Ppm1B
2537523	hon	CG	MUL_5127	-	cell wall and cell processes	N-term polyenol-monophosphomannose synthase Ppm1A
2537843	Int	AG		130 MUL_5127	cell wall and cell processes	N-term polyenol-monophosphomannose synthase Ppm1A
2538141	snp	GC	MUL_2270	-	conserved hypotheticals	conserved hypothetical protein
2538780	snp	AG	MUL_2270	-	conserved hypotheticals	conserved hypothetical protein
2539342	hon	CT	MUL_2270	-	conserved hypotheticals	conserved hypothetical protein
2540025	snp	GC	MUL_2271	-	cell wall and cell processes	conserved hypothetical membrane protein
2541045	hon	GC	MUL_2272	-	conserved hypotheticals	conserved hypothetical protein
2541047	hon	TG	MUL_2272	-	conserved hypotheticals	conserved hypothetical protein
2541048	hon	AG	MUL_2272	-	conserved hypotheticals	conserved hypothetical protein
2541493	hon	GT	MUL_2273	-	cell wall and cell processes	conserved hypothetical membrane protein
2542892	hon	AG	MUL_2273	-	cell wall and cell processes	conserved hypothetical membrane protein
2543754	snp	AG	MUL_2274	-	cell wall and cell processes	conserved transmembrane protein
2544117	snp	AG	MUL_2274	-	cell wall and cell processes	conserved transmembrane protein
2544699	hon	AG	MUL_2275	-	cell wall and cell processes	conserved hypothetical membrane protein

SNP position	SNP type	Nucleotide change <ref><snp>	Distance to nearest locus	Nearby Locus	Functional group	Product
2545075	syn	AG	MUL_2275	-	cell wall and cell processes	conserved hypothetical membrane protein
2545356	non	CT	MUL_2275	-	cell wall and cell processes	conserved hypothetical membrane protein
2545419	non	TC	MUL_2275	-	cell wall and cell processes	conserved hypothetical membrane protein
2545757	non	AC	MUL_2276	-	conserved hypotheticals	conserved hypothetical protein
2546239	syn	CG	MUL_2277	-	intermediary metabolism and respiration	cobalamin biosynthesis protein CobN
2547320	non	GA	MUL_2277	-	intermediary metabolism and respiration	cobalamin biosynthesis protein CobN
2547436	syn	CG	MUL_2277	-	intermediary metabolism and respiration	cobalamin biosynthesis protein CobN
2549064	syn	AG	MUL_2277	-	intermediary metabolism and respiration	cobalamin biosynthesis protein CobN
2549106	non	CT	MUL_2277	-	intermediary metabolism and respiration	cobalamin biosynthesis protein CobN
2549161	syn	AG	MUL_2277	-	intermediary metabolism and respiration	cobalamin biosynthesis protein CobN
2549254	syn	AC	MUL_2277	-	intermediary metabolism and respiration	cobalamin biosynthesis protein CobN
2550529	syn	CG	MUL_2279	-	intermediary metabolism and respiration	conserved membrane-bound oxidoreductase
2550830	non	AG	MUL_2279	-	intermediary metabolism and respiration	conserved membrane-bound oxidoreductase
2553909	syn	AC	MUL_2283	-	conserved hypotheticals	conserved hypothetical protein
2557285	psd	CG	MUL_2285	-	intermediary metabolism and respiration	N-term adenylate cyclase_pseudogene
2557411	psd	CG	MUL_2285	-	intermediary metabolism and respiration	N-term adenylate cyclase_pseudogene
2557924	psd	CT	MUL_2285	-	intermediary metabolism and respiration	N-term adenylate cyclase_pseudogene
2557930	psd	AG	MUL_2285	-	intermediary metabolism and respiration	N-term adenylate cyclase_pseudogene
2557983	psd	TC	MUL_2285	-	intermediary metabolism and respiration	N-term adenylate cyclase_pseudogene
2558216	psd	TG	MUL_2285	-	intermediary metabolism and respiration	N-term adenylate cyclase_pseudogene
2558299	psd	AG	MUL_2285	-	intermediary metabolism and respiration	mid-section adenylate cyclase_pseudogene
2558528	psd	TC	MUL_2285	-	intermediary metabolism and respiration	mid-section adenylate cyclase_pseudogene
2559213	non	CG	MUL_2288	-	intermediary metabolism and respiration	cobalamin biosynthesis protein
2559475	non	TG	MUL_2288	-	intermediary metabolism and respiration	cobalamin biosynthesis protein
2563543	psd	CG	MUL_2292	-	cell wall and cell processes	C-term conserved transmembrane transport protein MmpL4_7 - pseudogene
2567097	int	TC	41	MUL_2294	cell wall and cell processes	class a beta-lactamase BlaC
2567365	syn	TC	MUL_2294	-	cell wall and cell processes	class a beta-lactamase BlaC
2567767	non	AG	MUL_2294	-	cell wall and cell processes	class a beta-lactamase BlaC
2567965	non	AT	MUL_2294	-	cell wall and cell processes	class a beta-lactamase BlaC
2569815	syn	CG	MUL_2297	-	intermediary metabolism and respiration	precornin-4 C11-methyltransferase CobM
2570300	syn	CG	MUL_2298	-	intermediary metabolism and respiration	precornin-6v methyltransferase CobL
2571275	syn	AG	MUL_2298	-	intermediary metabolism and respiration	precornin-6v methyltransferase CobL
2571371	non	TC	MUL_2298	-	intermediary metabolism and respiration	precornin-6v methyltransferase CobL
2571469	syn	CT	MUL_2299	-	intermediary metabolism and respiration	short chain dehydrogenase
2571475	syn	TC	MUL_2299	-	intermediary metabolism and respiration	short chain dehydrogenase
2571514	syn	TC	MUL_2299	-	intermediary metabolism and respiration	short chain dehydrogenase
2571817	syn	GA	MUL_2299	-	intermediary metabolism and respiration	short chain dehydrogenase
2571865	syn	GC	MUL_2299	-	intermediary metabolism and respiration	short chain dehydrogenase
2571871	syn	GA	MUL_2299	-	intermediary metabolism and respiration	short chain dehydrogenase
2571874	syn	GA	MUL_2299	-	intermediary metabolism and respiration	short chain dehydrogenase
2571880	syn	GA	MUL_2299	-	intermediary metabolism and respiration	short chain dehydrogenase
2572382	syn	CT	MUL_2300	-	conserved hypotheticals	conserved protein
2573094	int	AG	49	MUL_2302	conserved hypotheticals	C-term conserved hypothetical protein - pseudogene
2584262	psd	AG	MUL_2311	-	conserved hypotheticals	conserved hypothetical
2584334	psd	TG	MUL_2311	-	conserved hypotheticals	N-term conserved hypothetical protein pseudogene
2584454	psd	GA	MUL_2311	-	conserved hypotheticals	N-term conserved hypothetical protein pseudogene
2584454	psd	GA	MUL_2311	-	conserved hypotheticals	C-term conserved hypothetical protein - pseudogene
2585240	syn	CT	MUL_2312	-	conserved hypotheticals	conserved hypothetical protein
2585774	syn	TC	MUL_2312	-	conserved hypotheticals	conserved hypothetical protein
2586132	syn	TC	MUL_2313	-	conserved hypotheticals	conserved protein
2586642	syn	GA	MUL_2313	-	conserved hypotheticals	conserved protein
2586660	non	CG	MUL_2313	-	conserved hypotheticals	conserved protein
2586717	syn	CT	MUL_2313	-	conserved hypotheticals	conserved protein
2586785	syn	AG	MUL_2313	-	conserved hypotheticals	conserved protein
2587002	syn	AG	MUL_2313	-	conserved hypotheticals	conserved protein
2587038	syn	AG	MUL_2313	-	conserved hypotheticals	conserved protein
2587197	syn	CT	MUL_2313	-	conserved hypotheticals	conserved protein
2588069	non	CT	MUL_2313	-	conserved hypotheticals	conserved protein
2588384	non	GC	MUL_2313	-	conserved hypotheticals	conserved protein
2590069	syn	CG	MUL_2314	-	conserved hypotheticals	conserved hypothetical protein
2590485	non	GA	MUL_2315	-	conserved hypotheticals	conserved hypothetical alanine and proline rich protein
2590721	syn	CG	MUL_2315	-	conserved hypotheticals	conserved hypothetical alanine and proline rich protein
2590967	syn	AG	MUL_2315	-	conserved hypotheticals	conserved hypothetical alanine and proline rich protein
2594513	non	CT	MUL_2318	-	conserved hypotheticals	conserved alanine and proline rich protein
2595000	non	TC	MUL_2318	-	conserved hypotheticals	conserved alanine and proline rich protein
2595250	int	AG	103	MUL_2318	conserved hypotheticals	conserved alanine and proline rich protein
2596314	non	GA	MUL_2320	-	conserved hypotheticals	conserved hypothetical protein
2596424	syn	CT	MUL_2320	-	conserved hypotheticals	conserved hypothetical protein
2596655	syn	TG	MUL_2320	-	conserved hypotheticals	conserved hypothetical protein
2596739	syn	AG	MUL_2320	-	conserved hypotheticals	conserved hypothetical protein
2596889	syn	GC	MUL_2320	-	conserved hypotheticals	conserved hypothetical protein
2598162	non	GC	MUL_2321	-	intermediary metabolism and respiration	dipeptidase PepF
2599537	syn	TC	MUL_2322	-	information pathways	5'-3' exonuclease
2599657	syn	CG	MUL_2322	-	information pathways	5'-3' exonuclease
2600231	syn	AG	MUL_2323	-	cell wall and cell processes	conserved membrane protein
2602488	syn	AC	MUL_2324	-	information pathways	ATP-dependent DNA helicase HelY
2602686	syn	CG	MUL_2324	-	information pathways	ATP-dependent DNA helicase HelY
2602922	non	CT	MUL_2324	-	information pathways	ATP-dependent DNA helicase HelY
2602950	syn	AG	MUL_2324	-	information pathways	ATP-dependent DNA helicase HelY
2603967	syn	AG	MUL_2325	-	cell wall and cell processes	sec-independent protein translocase transmembrane protein TatC
2606278	non	TC	MUL_2328	-	conserved hypotheticals	conserved protein
2606350	syn	CG	MUL_2328	-	conserved hypotheticals	conserved protein
2607909	syn	TC	MUL_2329	-	conserved hypotheticals	conserved hypothetical protein
2608492	non	AT	MUL_2330	-	intermediary metabolism and respiration	proteasome (alpha subunit) PrcA
2608693	non	TC	MUL_2330	-	intermediary metabolism and respiration	proteasome (alpha subunit) PrcA
2610229	syn	GT	MUL_2332	-	conserved hypotheticals	conserved protein
2612048	int	TC	74	MUL_2333	conserved hypotheticals	conserved protein
2614810	non	GC	MUL_2336	-	conserved hypotheticals	conserved hypothetical protein
2615108	syn	CG	MUL_2336	-	conserved hypotheticals	conserved hypothetical protein
2615129	syn	TG	MUL_2336	-	conserved hypotheticals	conserved hypothetical protein
2615838	syn	AG	MUL_2337	-	intermediary metabolism and respiration	ATPase
2617533	syn	CT	MUL_2338	-	cell wall and cell processes	conserved lipoprotein LppK

SNP position	SNP type	Nucleotide change <ref><snp>	Distance to nearest locus	Nearby Locus	Functional group	Product
2617592	syn	GT	MUL_2338	-	cell wall and cell processes	conserved lipoprotein LppK
2617601	syn	TG	MUL_2338	-	cell wall and cell processes	conserved lipoprotein LppK
2618697	non	TG	MUL_2340	-	intermediary metabolism and respiration	RNA methyltransferase
2618872	syn	AG	MUL_2340	-	intermediary metabolism and respiration	RNA methyltransferase
2619315	syn	AG	MUL_2341	-	information pathways	conserved hypothetical protein
2619438	syn	AC	MUL_2341	-	information pathways	conserved hypothetical protein
2619702	syn	AG	MUL_2341	-	information pathways	conserved hypothetical protein
2619738	syn	CG	MUL_2341	-	information pathways	conserved hypothetical protein
2619888	syn	CT	MUL_2341	-	information pathways	conserved hypothetical protein
2619975	syn	AG	MUL_2341	-	information pathways	conserved hypothetical protein
2620214	syn	AC	MUL_2342	-	conserved hypotheticals	conserved hypothetical protein
2620310	syn	CG	MUL_2342	-	conserved hypotheticals	conserved hypothetical protein
2620682	syn	CA	MUL_2342	-	conserved hypotheticals	conserved hypothetical protein
2620834	non	CA	MUL_2342	-	conserved hypotheticals	conserved hypothetical protein
2621021	psd	CG	MUL_2345	-	conserved hypotheticals	C-term peptide synthetase pseudogene
2621093	psd	TG	MUL_2345	-	conserved hypotheticals	C-term peptide synthetase pseudogene
2621123	psd	AG	MUL_2345	-	conserved hypotheticals	C-term peptide synthetase pseudogene
2621141	psd	CT	MUL_2345	-	conserved hypotheticals	C-term peptide synthetase pseudogene
2621174	psd	AG	MUL_2345	-	conserved hypotheticals	C-term peptide synthetase pseudogene
2621175	psd	AC	MUL_2345	-	conserved hypotheticals	C-term peptide synthetase pseudogene
2639538	syn	GC	MUL_2352	-	intermediary metabolism and respiration	ATP phosphotransferase HisG
2642613	Int	GA		-		
2642731	Int	AG		99 MUL_2355	PE/PPE	N-term PPE family protein - pseudogene
2643317	Int	TC		-		
2643700	Int	AG		-		
2644397	psd	AG	MUL_2356	-	intermediary metabolism and respiration	C-term 5-methyltetrahydrofolate--homocysteine methyltransferase Meth_1 pseudogene
2646555	syn	GC	MUL_2358	-	cell wall and cell processes	FAD-dependent oxidoreductase
2647323	non	TC	MUL_2359	-	intermediary metabolism and respiration	dehydrogenase
2648892	syn	AG	MUL_2360	-	information pathways	cysteinyl-tRNA synthetase MshC
2648974	syn	CT	MUL_2360	-	information pathways	cysteinyl-tRNA synthetase MshC
2649883	syn	AG	MUL_2360	-	information pathways	cysteinyl-tRNA synthetase MshC
2650509	non	TC	MUL_2361	-	intermediary metabolism and respiration	succinate-semialdehyde dehydrogenase [NADP+] dependent GabD1_1
2652495	non	GA	MUL_2363	-	conserved hypotheticals	conserved hypothetical protein
2652809	syn	GA	MUL_2364	-	conserved hypotheticals	conserved protein
2653775	non	TC	MUL_2365	-	conserved hypotheticals	conserved hypothetical protein
2654234	syn	TC	MUL_2366	-	cell wall and cell processes	conserved transmembrane protein
2655600	syn	TG	MUL_2368	-	cell wall and cell processes	conserved lipoprotein LppL
2656128	syn	TG	MUL_2368	-	cell wall and cell processes	conserved lipoprotein LppL
2656880	non	TG	MUL_2370	-	intermediary metabolism and respiration	dehydorotate dehydrogenase PvdR
2657964	Int	AG		8 MUL_2370	intermediary metabolism and respiration	dehydorotate dehydrogenase PvdR
2672483	non	CT	MUL_2387	-	conserved hypotheticals	conserved hypothetical protein
2672575	non	AG	MUL_2387	-	conserved hypotheticals	conserved hypothetical protein
2672771	Int	TG		66 MUL_2387	conserved hypotheticals	conserved hypothetical protein
2672894	Int	GA		27 MUL_2388	conserved hypotheticals	conserved hypothetical protein
2673934	syn	CA	MUL_2389	-	cell wall and cell processes	conserved membrane protein
2674303	Int	AC		36 MUL_2389	cell wall and cell processes	conserved membrane protein
2679437	syn	TG	MUL_2397	-	conserved hypotheticals	conserved protein
2679976	syn	AG	MUL_2397	-	conserved hypotheticals	conserved protein
2680007	syn	AG	MUL_2397	-	conserved hypotheticals	conserved protein
2680239	non	GT	MUL_2398	-	conserved hypotheticals	conserved hypothetical protein
2681327	syn	AG	MUL_2399	-	cell wall and cell processes	conserved ATPase
2681396	syn	GC	MUL_2399	-	cell wall and cell processes	conserved ATPase
2682102	non	AG	MUL_2399	-	cell wall and cell processes	conserved ATPase
2682503	Int	-C-		-		
2682608	Int	C-		53 MUL_2400	conserved hypotheticals	N-term conserved hypothetical protein pseudogene
2682635	Int	CT		26 MUL_2400	conserved hypotheticals	N-term conserved hypothetical protein pseudogene
2682817	psd	GA	MUL_2400	-	conserved hypotheticals	N-term conserved hypothetical protein pseudogene
2690003	psd	AG	MUL_2403	-	conserved hypotheticals	C-terminal conserved hypothetical membrane protein pseudogene
2690819	syn	AG	MUL_2408	-	cell wall and cell processes	cell division protein FtsX
2691392	syn	CG	MUL_2408	-	cell wall and cell processes	cell division protein FtsX
2692279	syn	CT	MUL_2410	-	cell wall and cell processes	conserved hypothetical membrane protein
2692492	non	CA	MUL_2410	-	cell wall and cell processes	conserved hypothetical membrane protein
2692693	non	AC	MUL_2410	-	cell wall and cell processes	conserved hypothetical membrane protein
2695015	syn	GA	MUL_2413	-	intermediary metabolism and respiration	NADPH:adrenodoxin oxidoreductase FprA_1
2695663	syn	TC	MUL_2413	-	intermediary metabolism and respiration	NADPH:adrenodoxin oxidoreductase FprA_1
2696495	Int	TC		-		
2700288	syn	CG	MUL_2416	-	conserved hypotheticals	conserved hypothetical protein
2700679	non	CA	MUL_2416	-	conserved hypotheticals	conserved hypothetical protein
2700984	Int	CT		121 MUL_2416	conserved hypotheticals	conserved hypothetical protein
2706135	syn	GC	MUL_2422	-	regulatory proteins	two component sensor histidine kinase DevS
2706286	non	AG	MUL_2422	-	regulatory proteins	two component sensor histidine kinase DevS
2706307	non	TC	MUL_2422	-	regulatory proteins	two component sensor histidine kinase DevS
2713986	Int	AC		-		
2714613	Int	TC		-		
2716405	non	GC	MUL_2430	-	intermediary metabolism and respiration	monophosphatase
2717108	syn	GA	MUL_2431	-	lipid metabolism	acyl-CoA dehydrogenase FadE24
2717246	non	CG	MUL_2431	-	lipid metabolism	acyl-CoA dehydrogenase FadE24
2717369	syn	TC	MUL_2431	-	lipid metabolism	acyl-CoA dehydrogenase FadE24
2717464	non	TC	MUL_2431	-	lipid metabolism	acyl-CoA dehydrogenase FadE24
2717702	syn	AG	MUL_2431	-	lipid metabolism	acyl-CoA dehydrogenase FadE24
2718581	syn	CG	MUL_2432	-	lipid metabolism	acyl-CoA dehydrogenase FadE23
2718624	non	GC	MUL_2432	-	lipid metabolism	acyl-CoA dehydrogenase FadE23
2720984	syn	CG	MUL_2434	-	intermediary metabolism and respiration	alpha-acetylactate decarboxylase
2721221	syn	AG	MUL_2434	-	intermediary metabolism and respiration	alpha-acetylactate decarboxylase
2721357	non	GT	MUL_2434	-	intermediary metabolism and respiration	alpha-acetylactate decarboxylase
2721594	non	CT	MUL_2434	-	intermediary metabolism and respiration	alpha-acetylactate decarboxylase
2721830	syn	CG	MUL_2435	-	intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
2721932	syn	TC	MUL_2435	-	intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
2721935	syn	GC	MUL_2435	-	intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
2721983	syn	GA	MUL_2435	-	intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
2722028	syn	GT	MUL_2435	-	intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
2722217	syn	TC	MUL_2435	-	intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase

SNP position	SNP type	Nucleotide change <ref><snp>	Distance to nearest locus	Nearby Locus	Functional group	Product
2722231	syn	AG	MUL_2435	-	intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
2722232	syn	GA	MUL_2435	-	intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
2722279	non	TG	MUL_2435	-	intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
2722319	syn	AG	MUL_2435	-	intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
2722353	non	AC	MUL_2435	-	intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
2722354	non	AG	MUL_2435	-	intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
2722384	syn	GA	MUL_2435	-	intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
2722394	non	GC	MUL_2435	-	intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
2722436	non	AG	MUL_2435	-	intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
2722472	non	AC	MUL_2435	-	intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
2722502	non	TC	MUL_2435	-	intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
2722519	non	CT	MUL_2435	-	intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
2722610	non	GA	MUL_2435	-	intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
2722640	syn	CG	MUL_2435	-	intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
2722688	syn	GC	MUL_2435	-	intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
2722720	non	CT	MUL_2435	-	intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
2722783	non	CG	MUL_2435	-	intermediary metabolism and respiration	4-hydroxy-2-oxovalerate aldolase
2722791	non	TG	MUL_2436	-	intermediary metabolism and respiration	acetaldehyde dehydrogenase MhpF
2722794	non	TC	MUL_2436	-	intermediary metabolism and respiration	acetaldehyde dehydrogenase MhpF
2722803	non	GC	MUL_2436	-	intermediary metabolism and respiration	acetaldehyde dehydrogenase MhpF
2722810	non	AG	MUL_2436	-	intermediary metabolism and respiration	acetaldehyde dehydrogenase MhpF
2735303	non	AG	MUL_2446	-	conserved hypothetical	conserved protein
2737651	psd	CT	MUL_2449	-	lipid metabolism	N-term acyl-CoA dehydrogenase FadE12_3 - pseudogene
2739445	syn	CT	MUL_2450	-	conserved hypothetical	conserved hypothetical protein
2739556	syn	TG	MUL_2451	-	conserved hypothetical	conserved hypothetical protein
2739563	non	AG	MUL_2451	-	conserved hypothetical	conserved hypothetical protein
2740433	syn	CT	MUL_2452	-	conserved hypothetical	conserved protein
2740549	syn	AG	MUL_2452	-	conserved hypothetical	conserved protein
2740684	non	CG	MUL_2452	-	conserved hypothetical	conserved protein
2748142	syn	AG	MUL_2460	-	intermediary metabolism and respiration	NADH dehydrogenase I (chain B) NuoB (NADH-ubiquinone oxidoreductase chain B)
2748181	syn	AG	MUL_2460	-	intermediary metabolism and respiration	NADH dehydrogenase I (chain B) NuoB (NADH-ubiquinone oxidoreductase chain B)
2750716	syn	AG	MUL_2463	-	intermediary metabolism and respiration	NADH dehydrogenase I (chain E) NuoE (NADH-ubiquinone oxidoreductase chain E)
2751887	syn	CA	MUL_2464	-	intermediary metabolism and respiration	NADH dehydrogenase I (chain F) NuoF (NADH-ubiquinone oxidoreductase chain F)
2761312	syn	AG	MUL_2471	-	intermediary metabolism and respiration	NADH dehydrogenase I (chain M) NuoM (NADH-ubiquinone oxidoreductase chain M)
2762806	non	GA	MUL_2472	-	intermediary metabolism and respiration	NADH dehydrogenase I (chain N) NuoN (NADH-ubiquinone oxidoreductase chain N)
2763233	int	TC	33	MUL_2473	PE/PPE	C-term PPE family protein pseudogene
2763364	int	TA	98	MUL_2473	PE/PPE	C-term PPE family protein pseudogene
2763365	int	GT	99	MUL_2473	PE/PPE	C-term PPE family protein pseudogene
2763384	int	TA	109	MUL_2473	PE/PPE	C-term PPE family protein pseudogene
2771756	syn	TC	MUL_2482	-	regulatory proteins	transcriptional regulatory protein (probably TetR-family)
2773380	syn	GA	MUL_2483	-	conserved hypothetical	conserved hypothetical protein
2777198	non	CT	MUL_2486	-	intermediary metabolism and respiration	oxidoreductase
2778850	syn	TC	MUL_2487	-	intermediary metabolism and respiration	flavin-containing monooxygenase AofH (amine oxidase)
2779123	syn	AG	MUL_2487	-	intermediary metabolism and respiration	flavin-containing monooxygenase AofH (amine oxidase)
2779206	non	CT	MUL_2487	-	intermediary metabolism and respiration	flavin-containing monooxygenase AofH (amine oxidase)
2780309	syn	AC	MUL_2488	-	intermediary metabolism and respiration	non-heme haloperoxidase Hpx
2781342	syn	GA	MUL_2489	-	intermediary metabolism and respiration	monooxygenase oxidase
2781349	syn	CA	MUL_2489	-	intermediary metabolism and respiration	monooxygenase oxidase
2781469	syn	AC	MUL_2489	-	intermediary metabolism and respiration	monooxygenase oxidase
2781706	syn	AC	MUL_2489	-	intermediary metabolism and respiration	monooxygenase oxidase
2782422	int	CT	61	MUL_5120	unknown	hypothetical protein
2783450	syn	GA	MUL_2491	-	conserved hypothetical	conserved hypothetical protein
2784245	syn	GT	MUL_2493	-	conserved hypothetical	conserved hypothetical protein
2784994	non	TG	MUL_2494	-	intermediary metabolism and respiration	citrate synthase I GltA1
2786222	psd	AG	MUL_2495	-	intermediary metabolism and respiration	C-term methylisocitrate lyase 2 - pseudogene
2786290	psd	CG	MUL_2495	-	intermediary metabolism and respiration	C-term methylisocitrate lyase 2 - pseudogene
2787989	non	CT	MUL_2496	-	conserved hypothetical	conserved protein
2788230	syn	GA	MUL_2496	-	conserved hypothetical	conserved protein
2788314	syn	AG	MUL_2496	-	conserved hypothetical	conserved protein
2789035	syn	CT	MUL_2497	-	regulatory protein	transcriptional regulatory protein
2789104	syn	CG	MUL_2497	-	regulatory protein	transcriptional regulatory protein
2790025	int	CT	48	MUL_2498	conserved hypothetical	conserved hypothetical protein
2790121	syn	AG	MUL_2498	-	conserved hypothetical	conserved hypothetical protein
2790589	syn	AG	MUL_2498	-	conserved hypothetical	conserved hypothetical protein
2791260	syn	CT	MUL_2499	-	conserved hypothetical	conserved hypothetical protein
2791439	non	AG	MUL_2499	-	conserved hypothetical	conserved hypothetical protein
2791649	syn	TC	MUL_2500	-	intermediary metabolism and respiration	arylsulfatase AtSD 1
2791960	non	TC	MUL_2500	-	intermediary metabolism and respiration	arylsulfatase AtSD 1
2792051	syn	TC	MUL_2500	-	intermediary metabolism and respiration	arylsulfatase AtSD 1
2792204	syn	TC	MUL_2500	-	intermediary metabolism and respiration	arylsulfatase AtSD 1
2792279	syn	GC	MUL_2500	-	intermediary metabolism and respiration	arylsulfatase AtSD 1
2792483	syn	AG	MUL_2500	-	intermediary metabolism and respiration	arylsulfatase AtSD 1
2794435	non	GC	MUL_2502	-	information pathways	FK-506 binding protein peptidyl-prolyl cis-trans isomerase
2794451	syn	AG	MUL_2502	-	information pathways	FK-506 binding protein peptidyl-prolyl cis-trans isomerase
2795284	non	CT	MUL_2504	-	conserved hypothetical	conserved hypothetical protein
2795756	non	CG	MUL_2504	-	conserved hypothetical	conserved hypothetical protein
2796857	syn	GC	MUL_2505	-	cell wall and cell processes	conserved transmembrane protein
2797457	syn	AC	MUL_2505	-	cell wall and cell processes	conserved transmembrane protein
2798549	syn	TC	MUL_2505	-	cell wall and cell processes	conserved transmembrane protein
2799373	int	TG	117	MUL_2505	cell wall and cell processes	conserved transmembrane protein
2799396	syn	TA	MUL_2506	-	serine protease	serine protease
2799404	non	AC	MUL_2506	-	serine protease	serine protease
2799462	syn	AC	MUL_2506	-	serine protease	serine protease
2799579	syn	GT	MUL_2506	-	serine protease	serine protease
2799618	syn	AG	MUL_2506	-	serine protease	serine protease
2799636	syn	AG	MUL_2506	-	serine protease	serine protease
2799666	syn	GC	MUL_2506	-	serine protease	serine protease
2801046	non	CG	MUL_2507	-	conserved hypothetical	conserved hypothetical protein
2801877	non	GT	MUL_2507	-	conserved hypothetical	conserved hypothetical protein
2802632	non	AG	MUL_2508	-	conserved hypothetical	conserved hypothetical protein
2804392	syn	GC	MUL_2510	-	cell wall and cell processes	conserved ATP-binding protein ABC transporter
2813147	syn	TG	MUL_2518	-	intermediary metabolism and respiration	NADH pyrophosphatase NudC

SNP position	SNP type	Nucleotide change <ref><snp>	Distance to nearest locus	Nearby Locus	Functional group	Product
2813348	syn	CA	MUL_2518	-	intermediary metabolism and respiration	NADH pyrophosphatase NudC
2813929	syn	AG	MUL_2518	-	intermediary metabolism and respiration	NADH pyrophosphatase NudC
2815981	syn	CT	MUL_2520	-	information pathways	ATP-dependent DNA helicase
2816063	non	CG	MUL_2520	-	information pathways	ATP-dependent DNA helicase
2816134	syn	AG	MUL_2520	-	information pathways	ATP-dependent DNA helicase
2816335	syn	TC	MUL_2520	-	information pathways	ATP-dependent DNA helicase
2816960	non	AG	MUL_2520	-	information pathways	ATP-dependent DNA helicase
2817411	non	GC	MUL_2520	-	information pathways	ATP-dependent DNA helicase
2818201	syn	TG	MUL_2520	-	information pathways	ATP-dependent DNA helicase
2820390	syn	AG	MUL_2521	-	information pathways	ATP-dependent DNA helicase
2822014	non	TC	MUL_2522	-	cell wall and cell processes	conserved hypothetical membrane protein
2823096	int	TG	41 MUL_2523	-	conserved hypotheticals	conserved hypothetical protein
2824032	non	CT		-	information pathways	DNA-methyltransferase (modification methylase)
2827024	non	TC	MUL_2528	-	conserved hypotheticals	conserved hypothetical protein
2827317	exp	AG	MUL_2528	-	conserved hypotheticals	conserved hypothetical protein
2827344	exp	GA	MUL_2528	-	conserved hypotheticals	conserved hypothetical protein
2827804	exp	AC	MUL_2529	-	regulatory proteins	transcriptional regulator TetR family
2829664	exp	AG	MUL_2529	-	conserved hypotheticals	conserved hypothetical protein
2833957	non	GT	MUL_2525	-	information pathways	Sol/ParA-related protein
2834734	non	CT	MUL_2526	-	intermediary metabolism and respiration	phosphoglycerate mutase Gpm2
2836085	non	TC	MUL_2528	-	intermediary metabolism and respiration	acetyltransferase
2839837	syn	TG	MUL_2542	-	regulatory proteins	sensor kinase from two component regulatory system
2839969	syn	AG	MUL_2542	-	regulatory proteins	sensor kinase from two component regulatory system
2840810	non	TC	MUL_2544	-	regulatory proteins	anti-sigma factor
2841880	int	AT	35 MUL_2546	-	intermediary metabolism and respiration	iron-regulated short-chain dehydrogenase/reductase
2842765	int	TC		-	cell wall and cell processes	conserved hypothetical membrane protein
2842914	non	GA	MUL_2547	-	cell wall and cell processes	conserved hypothetical membrane protein
2842937	non	TG	MUL_2547	-	cell wall and cell processes	conserved hypothetical membrane protein
2843485	psd	GA	MUL_2548	-	cell wall and cell processes	conserved hypothetical - pseudogene
2843575	psd	TC	MUL_2548	-	cell wall and cell processes	C-term conserved hypothetical protein - pseudogene
2843760	psd	GA	MUL_2548	-	cell wall and cell processes	conserved hypothetical - pseudogene
2843949	psd	AG	MUL_2548	-	cell wall and cell processes	C-term conserved hypothetical protein - pseudogene
2844118	psd	TC	MUL_2548	-	cell wall and cell processes	C-term conserved hypothetical protein - pseudogene
2844850	psd	TC	MUL_2548	-	cell wall and cell processes	C-term conserved hypothetical protein - pseudogene
2844850	psd	TC	MUL_2548	-	cell wall and cell processes	N-term conserved hypothetical protein - pseudogene
2844914	psd	GA	MUL_2548	-	cell wall and cell processes	conserved hypothetical N-term conserved hypothetical protein - pseudogene
2851571	syn	GA	MUL_2555	-	cell wall and cell processes	conserved hypothetical membrane protein
2858945	syn	TC	MUL_2561	-	cell wall and cell processes	conserved hypothetical protein
2863676	syn	GC	MUL_2565	-	lipid metabolism	linoleoyl-CoA desaturase DesA3
2863721	syn	GA	MUL_2565	-	lipid metabolism	linoleoyl-CoA desaturase DesA3
2863724	syn	AG	MUL_2565	-	lipid metabolism	linoleoyl-CoA desaturase DesA3
2865218	int	CG	126 MUL_2566	-	intermediary metabolism and respiration	oxidoreductase
2867751	psd	CT		-	conserved hypotheticals	N-term conserved hypothetical protein pseudogene
2869154	non	AC	MUL_2572	-	cell wall and cell processes	conserved membrane transport protein
2869155	non	GC	MUL_2572	-	cell wall and cell processes	conserved membrane transport protein
2869329	syn	GA	MUL_2572	-	cell wall and cell processes	conserved membrane transport protein
2869764	syn	AC	MUL_2572	-	cell wall and cell processes	conserved membrane transport protein
2871854	psd	TC	MUL_2575	-	cell wall and cell processes	C-term conserved transmembrane transport protein - pseudogene
2871854	psd	TC	MUL_2575	-	cell wall and cell processes	N-term conserved transmembrane transport protein - pseudogene
2872500	psd	TC	MUL_2575	-	cell wall and cell processes	N-term conserved transmembrane transport protein - pseudogene
2874427	psd	AG	MUL_2575	-	cell wall and cell processes	N-term conserved transmembrane transport protein - pseudogene
2875132	syn	AG	MUL_2576	-	cell wall and cell processes	preprotein translocase SecA1 1 subunit
2880821	syn	AG	MUL_2580	-	cell wall and cell processes	conserved lipoprotein Lpb
2881008	non	AG	MUL_2580	-	cell wall and cell processes	conserved lipoprotein Lpb
2881532	syn	TC	MUL_2580	-	cell wall and cell processes	conserved lipoprotein Lpb
2881937	syn	AG	MUL_2580	-	cell wall and cell processes	conserved lipoprotein Lpb
2883079	syn	AG	MUL_2581	-	regulatory proteins	two component sensory transduction histidine kinase MtrB
2894772	syn	CG	MUL_2593	-	regulatory proteins	transcriptional regulatory protein (probably TetR-family)
2898818	non	GA	MUL_2598	-	conserved hypotheticals	conserved hypothetical protein
2899691	non	TC	MUL_2599	-	conserved hypotheticals	conserved hypothetical protein
2901728	syn	TC	MUL_2600	-	intermediary metabolism and respiration	mannose-6-phosphate isomerase ManA
2906641	int	CG	81 MUL_2606	-	intermediary metabolism and respiration	F420 biosynthesis protein FbiA
2909817	non	TG		-	information pathways	DNA methylase
2910432	syn	TC	MUL_2608	-	information pathways	DNA methylase
2920088	psd	CT	MUL_2618	-	lipid metabolism	C-terminal acyl esterase pseudogene
2920366	psd	AG	MUL_2618	-	lipid metabolism	C-terminal acyl esterase pseudogene
2923275	non	AG	MUL_2621	-	intermediary metabolism and respiration	acyl-CoA transferase
2934292	syn	CT	MUL_2631	-	intermediary metabolism and respiration	bifunctional protein BirA
2934300	syn	GA	MUL_2631	-	intermediary metabolism and respiration	bifunctional protein BirA
2934311	non	AG	MUL_2631	-	intermediary metabolism and respiration	bifunctional protein BirA
2936316	syn	CG	MUL_2632	-	intermediary metabolism and respiration	propionyl-CoA carboxylase beta chain 5 AccD5
2936318	non	TG	MUL_2632	-	intermediary metabolism and respiration	propionyl-CoA carboxylase beta chain 5 AccD5
2936977	syn	AG	MUL_2634	-	information pathways	nucleotide-binding protein
2937016	non	GC	MUL_2634	-	information pathways	nucleotide-binding protein
2937181	syn	AC	MUL_2634	-	information pathways	nucleotide-binding protein
2940002	syn	AG	MUL_2637	-	intermediary metabolism and respiration	bifunctional protein acetyl-/propionyl-coenzyme a carboxylase (alpha chain) AccA3
2943774	non	TC	MUL_2638	-	lipid metabolism	peptidyl synthetase Nrp (peptide synthase)
2944070	non	TG	MUL_2638	-	lipid metabolism	peptidyl synthetase Nrp (peptide synthase)
2944316	syn	TC	MUL_2638	-	lipid metabolism	peptidyl synthetase Nrp (peptide synthase)
2944350	non	TG	MUL_2638	-	lipid metabolism	peptidyl synthetase Nrp (peptide synthase)
2944363	syn	AG	MUL_2638	-	lipid metabolism	peptidyl synthetase Nrp (peptide synthase)
2948045	non	AC	MUL_2638	-	lipid metabolism	peptidyl synthetase Nrp (peptide synthase)
2949392	syn	AG	MUL_2638	-	lipid metabolism	peptidyl synthetase Nrp (peptide synthase)
2950245	int	AG	38 MUL_2638	-	lipid metabolism	peptidyl synthetase Nrp (peptide synthase)
2950751	int	TC		-	regulatory proteins	transcriptional regulatory protein
2950776	int	TC	MUL_2639	-	regulatory proteins	transcriptional regulatory protein
2953039	int	AG	132 MUL_2642	-	conserved hypotheticals	mycobacterial conserved protein UsfY
2953042	int	TA		-	conserved hypotheticals	mycobacterial conserved protein UsfY
2953131	int	-GT	40 MUL_2642	-	conserved hypotheticals	mycobacterial conserved protein UsfY
2954196	syn	AG		-	intermediary metabolism and respiration	L-lysine-epsilon-aminotransferase Lat
2955066	syn	TC	MUL_2644	-	intermediary metabolism and respiration	L-lysine-epsilon-aminotransferase Lat
2958393	syn	CG	MUL_2647	-	intermediary metabolism and respiration	piperideine-6-carboxylic acid dehydrogenase Pcd

SNP position	SNP type	Nucleotide change <ref><snp>	Distance to nearest locus	Nearby Locus	Functional group	Product
2958792	syn	CG	MUL_2647	-	intermediary metabolism and respiration	o-perideine-6-carboxylic acid dehydrogenase Pcd
2960170	psd	TC	MUL_2649	-	information pathways	N-term ATP-dependent helicase I hr - pseudogene
2960568	psd	CA	MUL_2649	-	information pathways	N-term ATP-dependent helicase I hr - pseudogene
2961005	psd	CG	MUL_2649	-	information pathways	N-term ATP-dependent helicase I hr - pseudogene
2963343	psd	TC	MUL_2649	-	information pathways	C-term ATP-dependent helicase I hr - pseudogene
2964262	syn	TC	MUL_2650	-	information pathways	endonuclease VIII Nei
2965531	syn	GA	MUL_2651	-	lipid metabolism	esterase lipoprotein LpqC
2968312	Int	AG	MUL_2655	-		
2968338	Int	AT	MUL_2655	125	PE/PPe	N-term PPE family protein pseudogene
2968389	Int	AG	MUL_2655	74	PE/PPe	N-term PPE family protein pseudogene
2970381	non	AG	MUL_2658	-	intermediary metabolism and respiration	arylsulfatase AtSB (aryl-sulfate sulphohydrolase)
2970387	non	AG	MUL_2658	-	intermediary metabolism and respiration	arylsulfatase AtSB (aryl-sulfate sulphohydrolase)
2970547	non	CT	MUL_2658	-	intermediary metabolism and respiration	arylsulfatase AtSB (aryl-sulfate sulphohydrolase)
2970846	non	AG	MUL_2658	-	intermediary metabolism and respiration	arylsulfatase AtSB (aryl-sulfate sulphohydrolase)
2972276	non	TG	MUL_2658	-	intermediary metabolism and respiration	arylsulfatase AtSB (aryl-sulfate sulphohydrolase)
2972729	non	CT	MUL_2658	-	intermediary metabolism and respiration	arylsulfatase AtSB (aryl-sulfate sulphohydrolase)
2972747	non	CT	MUL_2658	-	intermediary metabolism and respiration	arylsulfatase AtSB (aryl-sulfate sulphohydrolase)
2974793	psd	AG	MUL_2660	-	cell wall and cell processes	C-term magnesium and cobalt transport transmembrane protein CorA 1 pseudogene
2974858	psd	GC	MUL_2660	-	cell wall and cell processes	C-term magnesium and cobalt transport transmembrane protein CorA 1 pseudogene
2974985	psd	TA	MUL_2660	-	cell wall and cell processes	N-term magnesium and cobalt transport transmembrane protein CorA 1 pseudogene
2975606	non	CT	MUL_2662	-	regulatory proteins	phosphate-transport system transcriptional regulatory protein PhoY1
2977903	psd	CT	MUL_2663	-	cell wall and cell processes	N-term metal cation transporting p-type ATPase CtpH 1 - pseudogene
2979113	psd	AG	MUL_2663	-	cell wall and cell processes	N-term metal cation transporting p-type ATPase CtpH 1 - pseudogene
2980096	psd	TG	MUL_2663	-	cell wall and cell processes	C-term metal cation transporting p-type ATPase CtpH 1 - pseudogene
2980098	psd	TG	MUL_2663	-	cell wall and cell processes	C-term metal cation transporting p-type ATPase CtpH 1 - pseudogene
2980671	psd	AG	MUL_2663	-	cell wall and cell processes	C-term metal cation transporting p-type ATPase CtpH 1 - pseudogene
2981020	psd	AG	MUL_2664	-	conserved hypotheticals	C-terminal conserved hypothetical protein pseudogene
2983670	syn	AG	MUL_2667	-	intermediary metabolism and respiration	glycerol-3-phosphate dehydrogenase GlpD2
2985842	syn	GT	MUL_2668	-	intermediary metabolism and respiration	dihydroxyacetone dehydrogenase LpdA
2990081	syn	CT	MUL_2672	-	intermediary metabolism and respiration	amidohydrolase Amb1
2990243	syn	TC	MUL_2672	-	intermediary metabolism and respiration	amidohydrolase Amb1
2992345	non	CA	MUL_2674	-	intermediary metabolism and respiration	phosphomannose mutase PmmB
2993383	syn	AC	MUL_2675	-	intermediary metabolism and respiration	uracil phosphoribosyltransferase Upp
2993497	syn	AG	MUL_2675	-	intermediary metabolism and respiration	uracil phosphoribosyltransferase Upp
2993791	non	GT	MUL_2675	-	intermediary metabolism and respiration	uracil phosphoribosyltransferase Upp
2996517	syn	TG	MUL_2678	-	conserved hypotheticals	conserved hypothetical protein
2996621	non	AG	MUL_2678	-	conserved hypotheticals	conserved hypothetical protein
2997870	non	TG	MUL_2679	-	conserved hypotheticals	conserved hypothetical 13E12 repeat family protein
2998425	non	GA	MUL_2679	-	conserved hypotheticals	conserved hypothetical 13E12 repeat family protein
2998580	syn	GA	MUL_2679	-	conserved hypotheticals	conserved hypothetical 13E12 repeat family protein
3000102	syn	GC	MUL_2680	-	cell wall and cell processes	conserved hypothetical membrane protein
3000363	Int	AT	MUL_2680	96	cell wall and cell processes	conserved hypothetical membrane protein
3001715	syn	TG	MUL_2682	-	intermediary metabolism and respiration	allantocase Aic
3012988	syn	CA	MUL_2694	-	cell wall and cell processes	phosphate-transport permease PttB
3012989	non	GA	MUL_2694	-	cell wall and cell processes	phosphate-transport permease PttB
3014872	psd	AG	MUL_2695	-	intermediary metabolism and respiration	C-term ferredoxin-dependent nitrite/sulphite reductase NirA pseudogene
3015559	psd	TC	MUL_2695	-	intermediary metabolism and respiration	C-term ferredoxin-dependent nitrite/sulphite reductase NirA pseudogene
3018131	syn	CG	MUL_2698	-	regulatory proteins	transcription regulator (LysR family)
3021794	Int	TC	MUL_2701	-		
3025126	syn	AC	MUL_2705	-	conserved hypotheticals	conserved hypothetical protein
3027760	syn	GC	MUL_2707	-	intermediary metabolism and respiration	oxidoreductase
3030512	psd	AG	MUL_2711	-	conserved hypotheticals	C-term conserved hypothetical protein - pseudogene
3033864	Int	GA	MUL_2712	37	cell wall and cell processes	C-term conserved integral membrane transport protein YicE - pseudogene
3033875	Int	CT	MUL_2712	48	cell wall and cell processes	C-term conserved integral membrane transport protein YicE - pseudogene
3034075	syn	TC	MUL_2714	-	regulatory proteins	transcriptional regulatory protein (probably TetR-family)
3037350	non	CT	MUL_2717	-	conserved hypotheticals	conserved hypothetical protein
3040097	Int	TC	MUL_2719	126	lipid metabolism	CDP-diacylglycerol pyrophosphatase Cdh
3041361	non	TC	MUL_2721	-	conserved hypotheticals	conserved hypothetical protein
3041391	non	CT	MUL_2722	-	conserved hypotheticals	conserved hypothetical protein
3041425	non	GA	MUL_2722	-	conserved hypotheticals	conserved hypothetical protein
3043687	Int	TA	MUL_2724	50	cell wall and cell processes	conserved hypothetical membrane protein
3048093	non	AC	MUL_2728	-	regulatory proteins	conserved hypothetical regulatory protein
3066714	non	CT	MUL_2743	-	regulatory proteins	Transcriptional regulatory protein (LuxR-family)
3066776	non	TC	MUL_2743	-	regulatory proteins	Transcriptional regulatory protein (LuxR-family)
3066781	syn	GA	MUL_2743	-	regulatory proteins	Transcriptional regulatory protein (LuxR-family)
3066850	syn	TG	MUL_2743	-	regulatory proteins	Transcriptional regulatory protein (LuxR-family)
3066950	non	GA	MUL_2743	-	regulatory proteins	Transcriptional regulatory protein (LuxR-family)
3068675	non	GT	MUL_2743	-	regulatory proteins	Transcriptional regulatory protein (LuxR-family)
3069423	syn	GT	MUL_2744	-		
3069492	syn	TA	MUL_2744	-		
3069666	syn	TG	MUL_2744	-		
3070805	non	AC	MUL_2744	-		
3071494	syn	GC	MUL_2745	-	conserved hypotheticals	conserved hypothetical protein
3072027	syn	AG	MUL_2746	-	regulatory proteins	transcriptional regulatory protein (probably TetR-family)
3072033	syn	TC	MUL_2746	-	regulatory proteins	transcriptional regulatory protein (probably TetR-family)
3072811	Int	CT	MUL_2747	53	intermediary metabolism and respiration	rubredoxin RubB 1
3078286	Int	TC	MUL_2753	138	intermediary metabolism and respiration	oxidoreductase
3078680	syn	TC	MUL_2753	-	intermediary metabolism and respiration	oxidoreductase
3079527	syn	TC	MUL_2755	-	intermediary metabolism and respiration	oxidoreductase
3079786	non	AG	MUL_2755	-	intermediary metabolism and respiration	oxidoreductase
3079968	non	CG	MUL_2755	-	intermediary metabolism and respiration	oxidoreductase
3080033	syn	AG	MUL_2756	-	intermediary metabolism and respiration	acyl-CoA dehydrogenase
3080321	syn	TC	MUL_2756	-	intermediary metabolism and respiration	acyl-CoA dehydrogenase
3080567	syn	AG	MUL_2756	-	intermediary metabolism and respiration	acyl-CoA dehydrogenase
3080634	non	CT	MUL_2756	-	intermediary metabolism and respiration	acyl-CoA dehydrogenase
3081307	syn	AG	MUL_2757	-	intermediary metabolism and respiration	acyl-CoA dehydrogenase
3083464	psd	CG	MUL_2760	-	intermediary metabolism and respiration	C-term short-chain alcohol dehydrogenase - pseudogene
3084592	Int	AG	MUL_2762	29	regulatory proteins	transcriptional regulator (IclR family)
3084852	syn	AG	MUL_2762	-	regulatory proteins	transcriptional regulator (IclR family)
3085520	non	AC	MUL_2762	-	regulatory proteins	transcriptional regulator (IclR family)
3121286	syn	TC	MUL_2793	-	regulatory proteins	transcriptional regulatory protein
3121455	Int	CA	MUL_2793	86	regulatory proteins	transcriptional regulatory protein

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3121704	non	AG	MUL_2794	-	intermediary metabolism and respiration	oxidoreductase
3122655	non	CG	MUL_2795	-	conserved hypotheticals	conserved hypothetical protein
3126599	syn	AG	MUL_2799	-	membrane-associated phospholipase C 2 PlcB	membrane-associated phospholipase C 2 PlcB
3127362	syn	AG	MUL_2799	-	membrane-associated phospholipase C 2 PlcB	membrane-associated phospholipase C 2 PlcB
3127386	syn	CA	MUL_2799	-	membrane-associated phospholipase C 2 PlcB	membrane-associated phospholipase C 2 PlcB
3127696	Int	TC				
3130488	syn	AG	MUL_2803	-	intermediary metabolism and respiration	thiamin biosynthesis protein ThiG
3132565	syn	CG	MUL_2806	-	intermediary metabolism and respiration	thiamine-phosphate pyrophosphorylase ThiE
3133427	non	CG	MUL_2807	-	information pathways	mutator protein MutT3
3134133	syn	AG	MUL_2808	-	cell wall and cell processes	conserved hypothetical membrane protein
3135224	syn	CT	MUL_2809	-	cell wall and cell processes	glutamine-binding lipoprotein GinH
3138445	non	GT	MUL_2811	-	conserved hypotheticals	conserved hypothetical protein
3139426	Int	AG	MUL_2811	146	conserved hypotheticals	conserved hypothetical protein
3139588	syn	AG	MUL_2812	-	intermediary metabolism and respiration	acetate kinase AckA
3139593	non	CG	MUL_2812	-	intermediary metabolism and respiration	acetate kinase AckA
3140122	syn	AG	MUL_2812	-	intermediary metabolism and respiration	acetate kinase AckA
3141954	psd	AG	MUL_2813	-	intermediary metabolism and respiration	N-term phosphate acetyltransferase Pta - pseudogene
3142897	syn	TC	MUL_2814	-	intermediary metabolism and respiration	F420-dependent glucose-6-phosphate dehydrogenase Fd1
3143002	syn	AG	MUL_2814	-	intermediary metabolism and respiration	F420-dependent glucose-6-phosphate dehydrogenase Fd1
3143116	non	GC	MUL_2814	-	intermediary metabolism and respiration	F420-dependent glucose-6-phosphate dehydrogenase Fd1
3144204	syn	GC	MUL_2815	-	cell wall and cell processes	beta lactamase-like protein
3147257	psd	AG	MUL_2817	-	cell wall and cell processes	C-term conserved transmembrane transport protein MmpL1_1 pseudogene
3147843	psd	GT	MUL_2817	-	cell wall and cell processes	C-term conserved transmembrane transport protein MmpL1_1 pseudogene
3149896	psd	GC	MUL_2819	-	intermediary metabolism and respiration	C-term coenzyme F420-dependent reductase - pseudogene
3150034	psd	GG	MUL_2819	-	intermediary metabolism and respiration	C-term coenzyme F420-dependent reductase - pseudogene
3150034	psd	GG	MUL_2819	-	intermediary metabolism and respiration	N-term coenzyme F420-dependent reductase - pseudogene
3150042	psd	AG	MUL_2819	-	intermediary metabolism and respiration	N-term coenzyme F420-dependent reductase - pseudogene
3150042	psd	AG	MUL_2819	-	intermediary metabolism and respiration	C-term coenzyme F420-dependent reductase - pseudogene
3152403	psd	CA	MUL_2823	-	intermediary metabolism and respiration	C-term coenzyme F420-dependent reductase - pseudogene
3161589	non	CT	MUL_2833	-	conserved hypotheticals	mid-term conserved hypothetical oxidoreductase - pseudogene
3163672	non	AG	MUL_2835	-	conserved hypotheticals	conserved hypothetical protein
3163995	non	TC	MUL_2835	-	conserved hypotheticals	conserved hypothetical protein
3164022	syn	TC	MUL_2835	-	conserved hypotheticals	conserved hypothetical protein
3166190	non	TC	MUL_2838	-	intermediary metabolism and respiration	glycolipid sulfotransferase
3168525	syn	GA	MUL_2841	-	conserved hypotheticals	conserved protein
3172299	psd	AG	MUL_2845	-	lipid metabolism	N-term fatty-acid-CoA ligase FadD29_1 - pseudogene
3172706	psd	GT	MUL_2845	-	lipid metabolism	N-term fatty-acid-CoA ligase FadD29_1 - pseudogene
3173339	psd	CT	MUL_2845	-	lipid metabolism	N-term fatty-acid-CoA ligase FadD29_1 - pseudogene
3173471	psd	AG	MUL_2845	-	lipid metabolism	N-term fatty-acid-CoA ligase FadD29_1 - pseudogene
3174061	Int	GT		108	MUL_2845	lipid metabolism
3174204	Int	CT				
3176385	syn	TG	MUL_2849	-	conserved hypotheticals	conserved hypothetical protein
3176504	syn	AG	MUL_2850	-	regulatory proteins	conserved hypothetical regulatory protein
3176640	non	GT	MUL_2850	-	regulatory proteins	conserved hypothetical regulatory protein
3177953	syn	TC	MUL_2850	-	regulatory proteins	conserved hypothetical regulatory protein
3178722	non	CA	MUL_2850	-	regulatory proteins	conserved hypothetical regulatory protein
3179855	syn	AG	MUL_2851	-	information pathways	methyltransferase
3184220	non	GT	MUL_2856	-	conserved hypotheticals	conserved hypothetical protein
3193189	non	TC	MUL_2867	-		MCE-family protein Mce3D
3193217	syn	TG	MUL_2867	-		MCE-family protein Mce3D
3193259	syn	TC	MUL_2867	-		MCE-family protein Mce3D
3193929	psd	CG	MUL_2868	-		C-term MCE-family protein Mce3C pseudogene
3195951	syn	CT	MUL_2869	-		MCE-family protein Mce3B
3196254	Int	CT		51	MUL_2870	C-term MCE-family protein Mce3A pseudogene
3196614	psd	TC	MUL_2870	-		C-term MCE-family protein Mce3A pseudogene
3197119	psd	CG	MUL_2870	-		N-term MCE-family protein Mce3A pseudogene
3197917	syn	GA	MUL_2871	-		conserved hypothetical integral membrane protein Yrb3B
3203046	syn	GT	MUL_2877	-	intermediary metabolism and respiration	aldehyde dehydrogenase
3203580	syn	CT	MUL_2877	-	intermediary metabolism and respiration	aldehyde dehydrogenase
3203691	syn	GC	MUL_2877	-	intermediary metabolism and respiration	aldehyde dehydrogenase
3203784	syn	GC	MUL_2877	-	intermediary metabolism and respiration	aldehyde dehydrogenase
3203811	syn	TC	MUL_2877	-	intermediary metabolism and respiration	aldehyde dehydrogenase
3204045	syn	CT	MUL_2877	-	intermediary metabolism and respiration	aldehyde dehydrogenase
3204113	non	GA	MUL_2877	-	intermediary metabolism and respiration	aldehyde dehydrogenase
3205673	non	CG	MUL_2880	-	regulatory proteins	transcriptional repressor (probably TetR-family) Mce3R
3207069	syn	GC	MUL_2881	-	cell wall and cell processes	multidrugs-transport integral membrane protein Mmr-like
3207362	Int	AT		132	MUL_2881	cell wall and cell processes
3207407	Int	AG				multidrugs-transport integral membrane protein Mmr-like
3208015	Int	AG		130	MUL_2882	conserved hypotheticals
3208142	psd	CG	MUL_2884	-	conserved hypotheticals	conserved hypothetical protein
3208147	psd	CA	MUL_2884	-	conserved hypotheticals	N-terminal conserved hypothetical membrane protein - pseudogene
3209258	syn	AC	MUL_2885	-	intermediary metabolism and respiration	short-chain type dehydrogenase/reductase
3210877	syn	AG	MUL_2887	-	intermediary metabolism and respiration	conserved hypothetical oxidoreductase
3211383	non	TC	MUL_2887	-	intermediary metabolism and respiration	conserved hypothetical oxidoreductase
3212256	syn	TG	MUL_2888	-		epoxide hydrolase EphB
3213116	non	GA	MUL_2889	-	intermediary metabolism and respiration	oxygenase
3213117	non	AG	MUL_2889	-	intermediary metabolism and respiration	oxygenase
3213944	non	GC	MUL_2889	-	intermediary metabolism and respiration	oxygenase
3214167	non	GA	MUL_2889	-	intermediary metabolism and respiration	oxygenase
3218269	non	GC	MUL_2892	-	lipid metabolism	acyl-CoA dehydrogenase FadE17
3221232	non	GA	MUL_2895	-	intermediary metabolism and respiration	conserved hypothetical oxidoreductase
3248834	syn	AG	MUL_2924	-	cell wall and cell processes	conserved hypothetical membrane protein
3249120	non	GA	MUL_2924	-	cell wall and cell processes	conserved hypothetical membrane protein
3249262	Int	TC		59	MUL_2924	cell wall and cell processes
3249305	Int	GA		102	MUL_2924	cell wall and cell processes
3254443	psd	CA	MUL_2931	-	unknown	N-term hypothetical protein - pseudogene
3256455	syn	AC	MUL_2933	-	regulatory proteins	transcriptional regulatory protein (TetR-family)
3257752	non	GT	MUL_2934	-	intermediary metabolism and respiration	dehydrogenase
3258713	syn	AG	MUL_2935	-	lipid metabolism	oxidoreductase FadB5
3261881	psd	AG	MUL_2940	-	conserved hypotheticals	C-term conserved hypothetical protein - pseudogene
3261937	psd	GA	MUL_2940	-	conserved hypotheticals	C-term conserved hypothetical protein - pseudogene
3262019	psd	TC	MUL_2940	-	conserved hypotheticals	C-term conserved hypothetical protein - pseudogene

SNP position	SNP type	Nucleotide change <ref><snp>	Distance to nearest locus	Nearby Locus	Functional group	Product
3262083	psd	CG	MUL_2940	-	conserved hypothetical	C-term conserved hypothetical protein - pseudogene
3264390	snp	TC	MUL_2943	-	intermediary metabolism and respiration	isocitrate lyase AceAb
3265447	non	CG	MUL_2943	-	intermediary metabolism and respiration	isocitrate lyase AceAb
3280834	snp	TC	MUL_2956	-	complement/damage-inducible protein CinA	
3282478	non	CA	MUL_2958	-	cell wall and cell processes	lipoprotein LpdD
3283163	int	CG		132 MUL_2959	conserved hypothetical	conserved hypothetical protein
3284346	snp	AG	MUL_2961	-	conserved hypothetical	conserved protein
3285311	snp	TC	MUL_2962	-	intermediary metabolism and respiration	dehydrogenase
3285633	non	AG	MUL_2962	-	intermediary metabolism and respiration	dehydrogenase
3285761	psd	TG	MUL_2963	-	intermediary metabolism and respiration	C-term monooxygenase - pseudogene
3294701	int	AC		68 MUL_2971	conserved hypothetical	conserved hypothetical protein
3296511	int	GA		49 MUL_2973	intermediary metabolism and respiration	oxidoreductase
3298310	snp	TC	MUL_2975	-	cell wall and cell processes	resuscitation-promoting factor-like protein
3310374	psd	CG	MUL_2987	-	unknown	
3311211	psd	CG	MUL_2987	-	intermediary metabolism and respiration	N-term amidase pseudogene
3311286	psd	TG	MUL_2987	-	intermediary metabolism and respiration	N-term amidase pseudogene
3311292	psd	CT	MUL_2987	-	intermediary metabolism and respiration	N-term amidase pseudogene
3311310	psd	CT	MUL_2987	-	intermediary metabolism and respiration	N-term amidase pseudogene
3311313	psd	GC	MUL_2987	-	intermediary metabolism and respiration	N-term amidase pseudogene
3311324	psd	AC	MUL_2987	-	intermediary metabolism and respiration	N-term amidase pseudogene
3311335	psd	AG	MUL_2987	-	intermediary metabolism and respiration	N-term amidase pseudogene
3311378	psd	CT	MUL_2987	-	intermediary metabolism and respiration	N-term amidase pseudogene
3311389	psd	GC	MUL_2987	-	intermediary metabolism and respiration	N-term amidase pseudogene
3311408	psd	CT	MUL_2987	-	intermediary metabolism and respiration	N-term amidase pseudogene
3311437	non	TC	MUL_2988	-	conserved hypothetical	conserved hypothetical protein
3311445	non	AT	MUL_2988	-	conserved hypothetical	conserved hypothetical protein
3311452	non	CT	MUL_2988	-	conserved hypothetical	conserved hypothetical protein
3311454	non	CG	MUL_2988	-	conserved hypothetical	conserved hypothetical protein
3311462	non	CG	MUL_2988	-	conserved hypothetical	conserved hypothetical protein
3311465	snp	CA	MUL_2988	-	conserved hypothetical	conserved hypothetical protein
3311467	snp	AG	MUL_2988	-	conserved hypothetical	conserved hypothetical protein
3311469	non	TC	MUL_2988	-	conserved hypothetical	conserved hypothetical protein
3311483	snp	TC	MUL_2988	-	conserved hypothetical	conserved hypothetical protein
3311490	non	TC	MUL_2988	-	conserved hypothetical	conserved hypothetical protein
3311493	non	TC	MUL_2988	-	conserved hypothetical	conserved hypothetical protein
3311498	snp	AT	MUL_2988	-	conserved hypothetical	conserved hypothetical protein
3311549	snp	TC	MUL_2988	-	conserved hypothetical	conserved hypothetical protein
3311552	snp	GA	MUL_2988	-	conserved hypothetical	conserved hypothetical protein
3311612	snp	CT	MUL_2988	-	conserved hypothetical	conserved hypothetical protein
3311615	snp	TG	MUL_2988	-	conserved hypothetical	conserved hypothetical protein
3311657	non	GC	MUL_2988	-	conserved hypothetical	conserved hypothetical protein
3311687	snp	TC	MUL_2988	-	conserved hypothetical	conserved hypothetical protein
3311777	snp	TC	MUL_2988	-	conserved hypothetical	conserved hypothetical protein
3311786	snp	AG	MUL_2988	-	conserved hypothetical	conserved hypothetical protein
3311864	snp	TC	MUL_2988	-	conserved hypothetical	conserved hypothetical protein
3311867	snp	GA	MUL_2988	-	conserved hypothetical	conserved hypothetical protein
3311893	non	TC	MUL_2988	-	conserved hypothetical	conserved hypothetical protein
3311903	snp	TC	MUL_2988	-	conserved hypothetical	conserved hypothetical protein
3311909	snp	CT	MUL_2988	-	conserved hypothetical	conserved hypothetical protein
3311912	snp	TA	MUL_2988	-	conserved hypothetical	conserved hypothetical protein
3311954	snp	GA	MUL_2988	-	conserved hypothetical	conserved hypothetical protein
3311994	non	TC	MUL_2988	-	conserved hypothetical	conserved hypothetical protein
3311996	non	TG	MUL_2988	-	conserved hypothetical	conserved hypothetical protein
3312080	non	GA	MUL_2988	-	conserved hypothetical	conserved hypothetical protein
3312113	snp	CT	MUL_2988	-	conserved hypothetical	conserved hypothetical protein
3312199	non	CG	MUL_2988	-	conserved hypothetical	conserved hypothetical protein
3312227	snp	AG	MUL_2988	-	conserved hypothetical	conserved hypothetical protein
3312238	non	TC	MUL_2988	-	conserved hypothetical	conserved hypothetical protein
3312241	non	CT	MUL_2988	-	conserved hypothetical	conserved hypothetical protein
3312311	non	CG	MUL_2988	-	conserved hypothetical	conserved hypothetical protein
3312316	non	CT	MUL_2988	-	conserved hypothetical	conserved hypothetical protein
3312343	non	GA	MUL_2988	-	conserved hypothetical	conserved hypothetical protein
3312524	snp	AG	MUL_2988	-	conserved hypothetical	conserved hypothetical protein
3312809	psd	CT	MUL_2989	-	intermediary metabolism and respiration	C-term glutamine synthetase GlnA3 - pseudogene
3312839	psd	GC	MUL_2989	-	intermediary metabolism and respiration	C-term glutamine synthetase GlnA3 - pseudogene
3316944	int	TC		-	conserved hypothetical	conserved hypothetical protein
3317030	int	TC		75 MUL_2994	conserved hypothetical	conserved hypothetical protein
3317036	int	AC		69 MUL_2994	conserved hypothetical	conserved hypothetical protein
3321357	snp	TC	MUL_3000	-	alkyl hydroperoxide reductase D protein AhpD	
3321848	non	AC	MUL_3001	-	intermediary metabolism and respiration	trehalose synthase TreS 1
3321936	non	GA	MUL_3001	-	intermediary metabolism and respiration	trehalose synthase TreS 1
3322054	snp	AG	MUL_3001	-	intermediary metabolism and respiration	trehalose synthase TreS 1
3322982	snp	CT	MUL_3002	-	intermediary metabolism and respiration	L-lactate dehydrogenase (cytochrome) LldD2
3323070	non	AG	MUL_3002	-	intermediary metabolism and respiration	L-lactate dehydrogenase (cytochrome) LldD2
3323453	snp	CG	MUL_3002	-	intermediary metabolism and respiration	L-lactate dehydrogenase (cytochrome) LldD2
3325214	non	TC	MUL_3003	-	intermediary metabolism and respiration	Lon ATP-dependent Lon protease
3326508	snp	GA	MUL_3003	-		Lon ATP-dependent Lon protease
3329083	snp	AG	MUL_3007	-	conserved hypothetical	conserved hypothetical protein
3329947	snp	TC	MUL_3007	-	conserved hypothetical	conserved hypothetical protein
3330863	snp	AG	MUL_3008	-	conserved hypothetical	conserved hypothetical protein
3331223	snp	AG	MUL_3008	-	conserved hypothetical	conserved hypothetical protein
3331529	snp	AG	MUL_3008	-	conserved hypothetical	conserved hypothetical protein
3332636	int	TC		91 MUL_3009	lipid metabolism	N-term acyl-CoA transferase/dehydratase pseudogene
3332682	int	AG		82 MUL_3009	lipid metabolism	C-term acyl-CoA transferase/dehydratase pseudogene
3332727	psd	CG	MUL_3009	-	lipid metabolism	N-term acyl-CoA transferase/dehydratase pseudogene
3334083	psd	CG	MUL_3009	-	lipid metabolism	N-term acyl-CoA transferase/dehydratase pseudogene
3334254	psd	TC	MUL_3009	-	lipid metabolism	N-term acyl-CoA transferase/dehydratase pseudogene
3334322	psd	AG	MUL_3009	-	lipid metabolism	N-term acyl-CoA transferase/dehydratase pseudogene
3334433	int	TC		70 MUL_3010	lipid metabolism	acyltransferase
3335723	snp	GA	MUL_3011	-	intermediary metabolism and respiration	short-chain type dehydrogenase
3336163	snp	TC	MUL_3012	-	intermediary metabolism and respiration	D-xylulose 5-phosphate Xfp

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
3336541	syn	TC	MUL_3012	-		intermediary metabolism and respiration	D-xylulose 5-phosphate Xfp
3338501	int	AG		40	MUL_3012	intermediary metabolism and respiration	D-xylulose 5-phosphate Xfp
3339424	int	GA		-			
3342793	int	AG		67	MUL_3017	cell wall and cell processes	alanine and proline rich secreted protein Ana
3343385	non	TC	MUL_3018	-		cell wall and cell processes	molybdenum-transport ATP-binding protein ABC transporter ModC
3343949	int	TC		15	MUL_3018	cell wall and cell processes	molybdenum-transport ATP-binding protein ABC transporter ModC
3344184	syn	CG	MUL_5112	-		unknown	hypothetical protein
3345916	int	TC		144	MUL_3019	intermediary metabolism and respiration	conserved hypothetical protein
3346318	syn	CG	MUL_3020	-		lipid metabolism	O-methyltransferase Omt
3346803	non	AG	MUL_3020	-		lipid metabolism	O-methyltransferase Omt
3347601	non	GT	MUL_3021	-		cell wall and cell processes	molybdenum-transport integral membrane protein ABC transporter ModB
3350150	syn	AG	MUL_3024	-		intermediary metabolism and respiration	oxidoreductase
3351120	env	TG	MUL_3025	-		intermediary metabolism and respiration	NADH dehydrogenase Ndh
3352382	env	CG	MUL_3028	-		intermediary metabolism and respiration	urease accessory protein UreF
3355650	env	TC	MUL_3030	-		intermediary metabolism and respiration	urease beta subunit UreB
3355698	env	TC	MUL_3030	-		intermediary metabolism and respiration	urease beta subunit UreB
3356694	non	GC	MUL_3032	-		conserved hypothetical	conserved hypothetical protein
3356793	int	TG		45	MUL_3032	conserved hypothetical	conserved hypothetical protein
3356794	int	AG		46	MUL_3032	conserved hypothetical	conserved hypothetical protein
3358172	env	CT	MUL_3034	-		cell wall and cell processes	conserved hypothetical transmembrane protein
3358992	env	GC	MUL_3035	-		intermediary metabolism and respiration	6-phosphogluconate dehydrogenase Gnd1
3359157	syn	AG	MUL_3035	-		intermediary metabolism and respiration	6-phosphogluconate dehydrogenase Gnd1
3361258	syn	TC	MUL_3036	-		intermediary metabolism and respiration	inosine-5'-monophosphate dehydrogenase GuaB1
3363126	psd	CT	MUL_3037	-		cell wall and cell processes	C-term conserved hypothetical membrane protein pseudogene
3363289	non	GG	MUL_3039	-		intermediary metabolism and respiration	acetolactate synthase InvA
3365347	non	GC	MUL_3040	-		cell wall and cell processes	preprotein translocase ATPase SecA2
3365548	syn	TC	MUL_3040	-		cell wall and cell processes	preprotein translocase ATPase SecA2
3366449	syn	TG	MUL_3040	-		cell wall and cell processes	preprotein translocase ATPase SecA2
3366694	syn	TC	MUL_3040	-		cell wall and cell processes	preprotein translocase ATPase SecA2
3370944	non	TC	MUL_3045	-		intermediary metabolism and respiration	glycine cleavage system H protein GcvH
3374807	non	AG	MUL_3050	-		intermediary metabolism and respiration	glycine dehydrogenase GcvB
3375664	syn	AG	MUL_3050	-		intermediary metabolism and respiration	glycine dehydrogenase GcvB
3376569	non	GA	MUL_3050	-		intermediary metabolism and respiration	glycine dehydrogenase GcvB
3380233	syn	CG	MUL_3053	-		intermediary metabolism and respiration	hydrolase
3380441	syn	TC	MUL_3053	-		intermediary metabolism and respiration	hydrolase
3381946	syn	GC	MUL_3054	-		cell wall and cell processes	conserved membrane protein
3382545	non	GA	MUL_3054	-		cell wall and cell processes	conserved membrane protein
3382872	syn	TC	MUL_3055	-		intermediary metabolism and respiration	malate synthase G Gcb
3384142	non	GA	MUL_3055	-		intermediary metabolism and respiration	malate synthase G Gcb
3390791	non	CT	MUL_3059	-		cell wall and cell processes	drug-transport transmembrane ATP-binding protein ABC transporter
3391094	int	AG		59	MUL_3059	cell wall and cell processes	drug-transport transmembrane ATP-binding protein ABC transporter
3406912	int	AC		-			
3409515	int	CT		-			
3411092	int	CT		-			
3411644	int	GA		111	MUL_3075	PE/PPE	C-term PPE family protein - pseudogene
3411651	int	CG		104	MUL_3075	PE/PPE	C-term PPE family protein - pseudogene
3412221	int	GA		75	MUL_3075	PE/PPE	N-term PPE family protein - pseudogene
3413001	int	GC		31	MUL_3075	PE/PPE	N-term PPE family protein - pseudogene
3413148	int	CT		-			
3413283	int	-C		-			
3414454	int	AG		106	MUL_3076	PE/PPE	PPE family protein
3414515	int	-G		-			
3415188	int	TC		60	MUL_3077	conserved hypothetical	conserved protein
3416598	syn	CT	MUL_3077	-		conserved hypothetical	conserved protein
3416970	syn	AG	MUL_3077	-		conserved hypothetical	conserved protein
3424463	int	AG		-			
3424545	int	AT		-			
3426400	int	GC		54	MUL_3086	conserved hypothetical	conserved hypothetical protein
3432074	non	TA	MUL_3092	-		conserved hypothetical	conserved hypothetical
3435906	syn	TC	MUL_3093	-		cell wall and cell processes	conserved membrane protein
3436138	non	GA	MUL_3093	-		cell wall and cell processes	conserved membrane protein
3436857	syn	TC	MUL_3093	-		cell wall and cell processes	conserved membrane protein
3437626	int	AG		34	MUL_3094	intermediary metabolism and respiration	4-alpha-D-glucanotransferase MalQ
3438790	syn	AC	MUL_3094	-		intermediary metabolism and respiration	4-alpha-D-glucanotransferase MalQ
3441178	int	AG		145	MUL_3097	conserved hypothetical	N-term conserved hypothetical protein pseudogene
3441632	psd	TG	MUL_3097	-		conserved hypothetical	N-term conserved hypothetical protein pseudogene
3444118	psd	AG	MUL_3099	-		intermediary metabolism and respiration	Mid section isochorismatase family protein - pseudogene
3444236	psd	AG	MUL_3099	-		intermediary metabolism and respiration	C-term isochorismatase family protein - pseudogene
3444236	psd	AG	MUL_3099	-		intermediary metabolism and respiration	Mid section isochorismatase family protein - pseudogene
3444483	psd	GA	MUL_3099	-		intermediary metabolism and respiration	C-term isochorismatase family protein - pseudogene
3448028	syn	AG	MUL_3101	-		conserved hypothetical	conserved hypothetical protein
3448464	int	AG		94	MUL_3102	intermediary metabolism and respiration	N-term oxidoreductase - pseudogene
3448677	psd	GC	MUL_3102	-		intermediary metabolism and respiration	N-term oxidoreductase - pseudogene
3448678	psd	CT	MUL_3102	-		intermediary metabolism and respiration	N-term oxidoreductase - pseudogene
3448686	psd	TC	MUL_3102	-		intermediary metabolism and respiration	N-term oxidoreductase - pseudogene
3448890	psd	AG	MUL_3102	-		intermediary metabolism and respiration	N-term oxidoreductase - pseudogene
3450968	syn	TG	MUL_3103	-		conserved hypothetical	conserved hypothetical protein
3451235	int	AG		-			
3451314	int	TG		-			
3452490	syn	TC	MUL_3104	-		intermediary metabolism and respiration	glycosyl transferase
3452556	syn	CT	MUL_3104	-		intermediary metabolism and respiration	glycosyl transferase
3453140	syn	GT	MUL_3105	-		cell wall and cell processes	conserved hypothetical membrane protein
3453600	syn	GC	MUL_3105	-		cell wall and cell processes	conserved hypothetical membrane protein
3454108	syn	TC	MUL_3106	-		intermediary metabolism and respiration	cytochrome P450 143A3 Cyp143A3
3454630	syn	TC	MUL_3106	-		intermediary metabolism and respiration	cytochrome P450 143A3 Cyp143A3
3455427	syn	AG	MUL_3107	-		cell wall and cell processes	conserved membrane protein
3456708	syn	TC	MUL_3108	-		intermediary metabolism and respiration	short-chain type dehydrogenase/reductase
3457170	int	GA		51	MUL_3109	conserved hypothetical	N-term conserved hypothetical protein - pseudogene
3458375	psd	GC	MUL_3109	-		conserved hypothetical	C-term conserved hypothetical protein - pseudogene
3461332	syn	AG	MUL_3113	-		regulatory proteins	transcriptional regulatory protein (probably AcrR-family)
3466536	int	GC		113	MUL_3122	conserved hypothetical	conserved protein
3466537	int	GC		112	MUL_3122	conserved hypothetical	conserved protein

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
3483456	psd	AG	MUL_3135	-		conserved hypothetical	mid portion conserved hypothetical secreted protein_pseudogene
3483758	Int	TC		76	MUL_3135	conserved hypothetical	N-terminal conserved hypothetical protein_pseudogene
3484185	Int	CT		82	MUL_3135	conserved hypothetical	N-terminal conserved hypothetical protein_pseudogene
3485114	psd	CA	MUL_3137	-		lipid metabolism	N-term fatty-acid-CoA ligase FadD1_pseudogene
3486530	snp	GA	MUL_3138	-		conserved hypothetical	conserved hypothetical protein
3487237	snp	AG	MUL_3139	-		intermediary metabolism and respiration	conserved short-chain dehydrogenase
3487368	snp	AG	MUL_3139	-		intermediary metabolism and respiration	conserved short-chain dehydrogenase
3487447	snp	GA	MUL_3139	-		intermediary metabolism and respiration	conserved short-chain dehydrogenase
3489251	psd	GA	MUL_3140	-		intermediary metabolism and respiration	C-term flavin-binding monooxygenase - pseudogene
3489400	psd	AG	MUL_3140	-		intermediary metabolism and respiration	C-term flavin-binding monooxygenase - pseudogene
3489577	psd	AG	MUL_3140	-		intermediary metabolism and respiration	C-term flavin-binding monooxygenase - pseudogene
3489864	Int	CT		26	MUL_3140	intermediary metabolism and respiration	C-term flavin-binding monooxygenase - pseudogene
3490304	non	TC	MUL_3141	-		lipid metabolism	esterase/lipase
3490798	psn	TC	MUL_3141	-		lipid metabolism	esterase/lipase
3490928	Int	TC		110	MUL_3141	lipid metabolism	esterase/lipase
3492615	non	TG	MUL_3143	-		intermediary metabolism and respiration	amidohydrolase
3493982	non	CG	MUL_3145	-		conserved hypothetical	conserved hypothetical protein
3494230	snp	AG	MUL_3145	-		conserved hypothetical	conserved hypothetical protein
3494281	snp	AG	MUL_3145	-		conserved hypothetical	conserved hypothetical protein
3495024	snp	CA		108	MUL_3145	conserved hypothetical	conserved hypothetical protein
3496185	snp	AG	MUL_3147	-		cell wall and cell processes	conserved hypothetical membrane protein
3496588	non	CA	MUL_3147	-		cell wall and cell processes	conserved hypothetical membrane protein
3496662	snp	GC	MUL_3147	-		cell wall and cell processes	conserved hypothetical membrane protein
3497251	snp	TC	MUL_3148	-		cell wall and cell processes	conserved membrane protein
3497535	snp	GC	MUL_3148	-		cell wall and cell processes	conserved membrane protein
3497543	non	TC	MUL_3148	-		cell wall and cell processes	conserved membrane protein
3497578	Int	GC		30	MUL_3149	cell wall and cell processes	conserved transmembrane ATP-binding protein ABC transporter
3498333	non	CT	MUL_3149	-		cell wall and cell processes	conserved transmembrane ATP-binding protein ABC transporter
3498460	snp	TA	MUL_3149	-		cell wall and cell processes	conserved transmembrane ATP-binding protein ABC transporter
3498499	snp	TC	MUL_3149	-		cell wall and cell processes	conserved transmembrane ATP-binding protein ABC transporter
3498520	snp	GT	MUL_3149	-		cell wall and cell processes	conserved transmembrane ATP-binding protein ABC transporter
3499141	snp	AG	MUL_3149	-		cell wall and cell processes	conserved transmembrane ATP-binding protein ABC transporter
3500335	Int	AG		73	MUL_3149	cell wall and cell processes	conserved transmembrane ATP-binding protein ABC transporter
3507708	psd	AG	MUL_3154	-		intermediary metabolism and respiration	N-term anaerobic dehydrogenase_pseudogene
3510449	Int	TC		110	MUL_3157	unknown	hypothetical protein
3512880	snp	CG	MUL_3161	-		conserved hypothetical	conserved hypothetical protein
3513502	snp	TC	MUL_3161	-		conserved hypothetical	conserved hypothetical protein
3514176	Int	AG		41	MUL_3161	conserved hypothetical	conserved hypothetical protein
3514242	Int	AG		125	MUL_3162	conserved hypothetical	conserved hypothetical protein
3519295	snp	GA	MUL_3166	-		cell wall and cell processes	conserved secreted protein
3520573	snp	GA	MUL_3167	-		cell wall and cell processes	divalent cation-transport integral membrane protein
3525970	Int	GA		-		cell wall and cell processes	conserved transmembrane ATP-binding protein ABC transporter
3527419	snp	AC	MUL_3170	-		conserved hypothetical	conserved hypothetical protein
3527839	snp	GA	MUL_3170	-		conserved hypothetical	conserved hypothetical protein
3527929	snp	CT	MUL_3170	-		conserved hypothetical	conserved hypothetical protein
3529413	Int	GA		144	MUL_3171	lipid metabolism	Z'-decaprenyl diphosphate synthase
3529839	non	AG	MUL_3172	-		cell wall and cell processes	conserved hypothetical membrane protein
3534729	snp	TC	MUL_3175	-		information pathways	transcriptional accessory protein Tex
3537764	snp	TC	MUL_3177	-		cell wall and cell processes	sodium/hydrogen exchanger (antipporter)
3538976	non	TC	MUL_3178	-		cell wall and cell processes	conserved hypothetical transmembrane protein
3539378	non	GA	MUL_3178	-		cell wall and cell processes	conserved hypothetical transmembrane protein
3539406	non	CG	MUL_3178	-		cell wall and cell processes	conserved hypothetical transmembrane protein
3541070	non	AC	MUL_3180	-		regulatory proteins	transmembrane serine/threonine-protein kinase E PknE
3544066	snp	CA	MUL_3182	-		cell wall and cell processes	amino acid transporter PotE
3544105	snp	AG	MUL_3182	-		cell wall and cell processes	amino acid transporter PotE
3544273	snp	GC	MUL_3182	-		cell wall and cell processes	amino acid transporter PotE
3544349	non	AG	MUL_3182	-		cell wall and cell processes	amino acid transporter PotE
3545508	psd	AG	MUL_3183	-		cell wall and cell processes	C-term metal cation transporter p-type ATPase a CtpF_pseudogene
3546036	psd	GC	MUL_3183	-		unknown	N-term metal cation transporter p-type ATPase a CtpF_pseudogene
3546400	psd	AG	MUL_3183	-		unknown	N-term metal cation transporter p-type ATPase a CtpF_pseudogene
3548243	non	AG	MUL_3184	-		conserved hypothetical	conserved hypothetical protein
3548314	snp	CG	MUL_3184	-		conserved hypothetical	conserved hypothetical protein
3549047	psd	CT	MUL_3185	-		regulatory proteins	N-term serine/threonine-protein kinase transcriptional regulatory protein PknK - pseudogene
3549226	psd	GA	MUL_3185	-		regulatory proteins	N-term serine/threonine-protein kinase transcriptional regulatory protein PknK - pseudogene
3549445	psd	-C	MUL_3185	-		regulatory proteins	N-term serine/threonine-protein kinase transcriptional regulatory protein PknK - pseudogene
3551014	psd	AG	MUL_3185	-		regulatory proteins	C-term serine/threonine-protein kinase transcriptional regulatory protein PknK - pseudogene
3551539	psd	TC	MUL_3185	-		regulatory proteins	C-term serine/threonine-protein kinase transcriptional regulatory protein PknK - pseudogene
3551551	psd	TC	MUL_3185	-		regulatory proteins	C-term serine/threonine-protein kinase transcriptional regulatory protein PknK - pseudogene
3551698	psd	AG	MUL_3185	-		regulatory proteins	C-term serine/threonine-protein kinase transcriptional regulatory protein PknK - pseudogene
3551779	psd	AC	MUL_3185	-		regulatory proteins	C-term serine/threonine-protein kinase transcriptional regulatory protein PknK - pseudogene
3551815	Int	A-		31	MUL_3186	PE/PPe	PE-PGRS family protein
3551816	Int	C-		30	MUL_3186	PE/PPe	PE-PGRS family protein
3551817	Int	C-		29	MUL_3186	PE/PPe	PE-PGRS family protein
3551818	Int	T-		28	MUL_3186	PE/PPe	PE-PGRS family protein
3551819	Int	G-		27	MUL_3186	PE/PPe	PE-PGRS family protein
3551820	Int	G-		26	MUL_3186	PE/PPe	PE-PGRS family protein
3551820	Int	G-		26	MUL_3185	regulatory proteins	C-term serine/threonine-protein kinase transcriptional regulatory protein PknK - pseudogene
3551821	Int	T-		27	MUL_3185	regulatory proteins	C-term serine/threonine-protein kinase transcriptional regulatory protein PknK - pseudogene
3551822	Int	TC		28	MUL_3185	regulatory proteins	C-term serine/threonine-protein kinase transcriptional regulatory protein PknK - pseudogene
3551823	Int	TA		29	MUL_3185	regulatory proteins	C-term serine/threonine-protein kinase transcriptional regulatory protein PknK - pseudogene
3551827	Int	GA		33	MUL_3185	regulatory proteins	C-term serine/threonine-protein kinase transcriptional regulatory protein PknK - pseudogene
3551828	Int	CA		34	MUL_3185	regulatory proteins	C-term serine/threonine-protein kinase transcriptional regulatory protein PknK - pseudogene
3552337	Int	GA		-			
3553788	snp	CT	MUL_3187	-		cell wall and cell processes	sugar transporter
3553902	snp	CT	MUL_3187	-		cell wall and cell processes	sugar transporter
3554358	snp	AG	MUL_3187	-		cell wall and cell processes	sugar transporter
3554736	snp	AG	MUL_3187	-		cell wall and cell processes	sugar transporter
3556056	Int	CA		24	MUL_3188	conserved hypothetical	conserved protein
3556081	Int	AG		49	MUL_3188	conserved hypothetical	conserved protein
3558212	snp	CG	MUL_3190	-		intermediary metabolism and respiration	succinate-semialdehyde dehydrogenase [NADP+] dependent (SsdH) GabD2
3558704	snp	TC	MUL_3190	-		intermediary metabolism and respiration	succinate-semialdehyde dehydrogenase [NADP+] dependent (SsdH) GabD2
3559517	snp	TG	MUL_3191	-		intermediary metabolism and respiration	conserved hypothetical hydrolase/amidase

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
3560214	non	CT	MUL_3191	-		intermediary metabolism and respiration	conserved hypothetical hydrolase/amidase
3560441	Int	AG		48	MUL_3192	cell wall and cell processes	conserved hypothetical secreted protein
3560821	syn	CT	MUL_3192	-		cell wall and cell processes	conserved hypothetical secreted protein
3561187	Int	AG		61	MUL_3193	intermediary metabolism and respiration	N-term carbohydrate phosphorlyase - pseudogene
3561403	psd	TC	MUL_3193	-		intermediary metabolism and respiration	N-term carbohydrate phosphorlyase - pseudogene
3561544	psd	CG	MUL_3193	-		intermediary metabolism and respiration	N-term carbohydrate phosphorlyase - pseudogene
3561664	psd	TC	MUL_3193	-		intermediary metabolism and respiration	N-term carbohydrate phosphorlyase - pseudogene
3562818	psd	AG	MUL_3193	-		intermediary metabolism and respiration	N-term carbohydrate phosphorlyase - pseudogene
3562854	psd	CA	MUL_3193	-		intermediary metabolism and respiration	N-term carbohydrate phosphorlyase - pseudogene
3562919	Int	AG		61	MUL_3193	intermediary metabolism and respiration	N-term carbohydrate phosphorlyase - pseudogene
3563033	psd	TC	MUL_3193	-		intermediary metabolism and respiration	mid-section carbohydrate phosphorlyase - pseudogene
3563085	psd	GA	MUL_3193	-		intermediary metabolism and respiration	mid-section carbohydrate phosphorlyase - pseudogene
3563095	psd	CT	MUL_3193	-		intermediary metabolism and respiration	mid-section carbohydrate phosphorlyase - pseudogene
3564683	non	AG	MUL_3195	-		intermediary metabolism and respiration	conserved hypothetical hydrolase
3564867	syn	AG	MUL_3195	-		intermediary metabolism and respiration	conserved hypothetical hydrolase
3564944	non	GA	MUL_3195	-		intermediary metabolism and respiration	conserved hypothetical hydrolase
3564982	non	AG	MUL_3195	-		intermediary metabolism and respiration	conserved hypothetical hydrolase
3565405	Int	GC		26	MUL_3196	unknown	hypothetical protein
3565590	syn	GT	MUL_3196	-		unknown	hypothetical protein
3565858	syn	AG	MUL_3196	-		unknown	hypothetical protein
3566800	non	AG	MUL_3197	-		lipid metabolism	polypropyl synthetase IdsB
3567158	syn	AC	MUL_3197	-		lipid metabolism	polypropyl synthetase IdsB
3567716	syn	AG	MUL_3197	-		lipid metabolism	polypropyl synthetase IdsB
3567809	Int	AT		37	MUL_3197	lipid metabolism	polypropyl synthetase IdsB
3568159	Int	AT		44	MUL_3198	information pathways	translation initiation inhibitor
3568160	Int	CG		43	MUL_3198	information pathways	translation initiation inhibitor
3575083	Int	CG		117	MUL_3206	cell wall and cell processes	conserved hypothetical secreted protein
3575176	Int	GA		24	MUL_3206	cell wall and cell processes	conserved hypothetical secreted protein
3575551	Int	GT		57	MUL_3206	cell wall and cell processes	conserved hypothetical secreted protein
3575802	Int	TC		38	MUL_3207	cell wall and cell processes	hypothetical secreted protein
3575803	Int	CT		39	MUL_3207	cell wall and cell processes	hypothetical secreted protein
3575931	Int	GC		67	MUL_3207	cell wall and cell processes	hypothetical secreted protein
3575954	Int	CT		90	MUL_3207	cell wall and cell processes	hypothetical secreted protein
3576021	Int	GC		103	MUL_3208	cell wall and cell processes	conserved hypothetical membrane protein
3576977	Int	GA		101	MUL_3208	cell wall and cell processes	conserved hypothetical membrane protein
3577045	Int	AG		138	MUL_3209	PE/PPE	C-term PE-PGRS family protein - pseudogene
3577546	Int	CT		-			
3578897	Int	CA		14	MUL_3209	PE/PPE	N-term PE-PGRS family protein - pseudogene
3578965	Int	GA		54	MUL_3209	PE/PPE	N-term PE-PGRS family protein - pseudogene
3579087	Int	CG		-			
3579114	Int	CG		-			
3608418	syn	CT	MUL_3232	-		intermediary metabolism and respiration	GTP-binding protein EngA
3608687	syn	AG	MUL_3233	-		intermediary metabolism and respiration	cytidylate kinase Cmk
3609062	non	GC	MUL_3233	-		intermediary metabolism and respiration	cytidylate kinase Cmk
3610598	syn	CG	MUL_3235	-		regulatory proteins	transcriptional regulator
3610721	syn	TC	MUL_3235	-		regulatory proteins	transcriptional regulator
3611149	syn	TC	MUL_3236	-		conserved hypotheticals	conserved hypothetical protein
3611628	syn	AG	MUL_3237	-		information pathways	ATPase involved in chromosome partitioning (Soi family)
3612006	syn	GA	MUL_3237	-		information pathways	ATPase involved in chromosome partitioning (Soi family)
3612707	psd	CT	MUL_3238	-		conserved hypotheticals	C-term conserved hypothetical protein pseudogene
3627770	syn	CG	MUL_3250	-		intermediary metabolism and respiration	pyridoxine biosynthesis protein SnzP
3628448	syn	TC	MUL_3250	-		intermediary metabolism and respiration	pyridoxine biosynthesis protein SnzP
3630093	syn	GA	MUL_3252	-		lipid metabolism	alpha-mannosyltransferase PimA
3630956	syn	AG	MUL_3253	-		lipid metabolism	acyltransferase
3631094	syn	AG	MUL_3253	-		lipid metabolism	acyltransferase
3631280	syn	AG	MUL_3253	-		lipid metabolism	acyltransferase
3631433	syn	AG	MUL_3253	-		lipid metabolism	acyltransferase
3631753	syn	GC	MUL_3254	-		lipid metabolism	pi synthase PsgA1
3632671	non	CT	MUL_3255	-		conserved hypotheticals	conserved protein
3635209	Int	CG		103	MUL_3256	information pathways	threonyl-tRNA synthetase ThrS
3635297	syn	AG	MUL_3257	-		conserved hypotheticals	conserved hypothetical protein
3635302	non	GT	MUL_3257	-		conserved hypotheticals	conserved hypothetical protein
3636160	psd	CA	MUL_3258	-		intermediary metabolism and respiration	C-term oxidoreductase - pseudogene
3639105	non	TC	MUL_3262	-		cell wall and cell processes	conserved hypothetical membrane protein
3639426	syn	CG	MUL_3263	-		regulatory proteins	transcriptional regulator
3640132	non	GA	MUL_3264	-		intermediary metabolism and respiration	ferredoxin FdxA_1
3641578	syn	TG	MUL_3265	-		cell wall and cell processes	integral membrane nitrite extrusion protein NarK3
3643387	syn	GC	MUL_3267	-		conserved hypotheticals	conserved hypothetical protein
3643840	psd	TC	MUL_3268	-		conserved hypotheticals	C-term conserved hypothetical protein - pseudogene
3644442	Int	CT		-			
3645170	syn	AG	MUL_3269	-		cell wall and cell processes	conserved transmembrane alanine and leucine rich protein
3645844	Int	TC		60	MUL_5091	unknown	C-term hypothetical protein pseudogene
3646303	psd	-GTG	MUL_5091	-		unknown	C-term hypothetical protein pseudogene
3647533	syn	AC	MUL_3271	-		conserved hypotheticals	conserved hypothetical membrane protein
3647740	syn	CG	MUL_3271	-		conserved hypotheticals	conserved hypothetical membrane protein
3655670	syn	AG	MUL_3279	-		lipid metabolism	fatty-acid-CoA ligase
3657055	syn	GA	MUL_3280	-		cell wall and cell processes	transmembrane protein DedA
3658037	Int	AT		10	MUL_3281	conserved hypotheticals	mid-section conserved hypothetical protein - pseudogene
3658037	Int	AT		10	MUL_3281	conserved hypotheticals	N-term conserved hypothetical protein - pseudogene
3658388	non	CG	MUL_3282	-		conserved hypotheticals	conserved hypothetical protein
3658471	syn	CT	MUL_3282	-		conserved hypotheticals	conserved hypothetical protein
3658774	Int	AG		17	MUL_3283	catalase	catalase
3659764	Int	CG		26	MUL_3283	catalase	catalase
3666605	Int	TA		110	MUL_3292	PE/PPE	PE-PGRS family protein
3669226	Int	TC		52	MUL_3297	cell wall and cell processes	N-term amino acid transporter - pseudogene
3671609	syn	AG	MUL_3298	-		conserved hypotheticals	conserved hypothetical protein
3674886	non	CG	MUL_3302	-		cell wall and cell processes	exported alanine and valine rich protein
3675757	syn	AG	MUL_3304	-		conserved hypotheticals	conserved hypothetical protein
3675763	syn	CG	MUL_3304	-		conserved hypotheticals	conserved hypothetical protein
3675778	syn	AG	MUL_3304	-		conserved hypotheticals	conserved hypothetical protein
3677499	syn	TC	MUL_3305	-		information pathways	bifunctional enzyme riboflavin biosynthesis protein RihD
3677904	Int	CA		72	MUL_3306	conserved hypotheticals	C-term conserved hypothetical membrane protein- pseudogene

SNP position	SNP type	Nucleotide change <ref><snp>	Distance to nearest locus	Nearby Locus	Functional group	Product
3679699	non	AG	MUL_3307	-	cell wall and cell processes	conserved transmembrane protein
3679786	snp	TC	MUL_3307	-	cell wall and cell processes	conserved transmembrane protein
3680798	snp	AG	MUL_3308	-	unknown	conserved hypothetical protein (SelR family)
3682068	snp	TC	MUL_3310	-	conserved hypotheticals	conserved hypothetical protein
3682587	non	AT	MUL_3311	-	intermediary metabolism and respiration	protoporphyrinogen oxidase HemY
3682709	snp	AG	MUL_3311	-	intermediary metabolism and respiration	protoporphyrinogen oxidase HemY
3684160	snp	TC	MUL_3312	-	intermediary metabolism and respiration	protoporphyrinogen decarboxylase HemE
3684523	snp	GC	MUL_3312	-	intermediary metabolism and respiration	protoporphyrinogen decarboxylase HemE
3686199	non	GC	MUL_3314	-	conserved hypotheticals	conserved protein
3687871	psd	AG	MUL_3316	-	intermediary metabolism and respiration	C-term 1-deoxy-D-xylulose 5-phosphate synthase Dxs1A - pseudogene
3695033	snp	TC	MUL_3320	-	conserved hypotheticals	conserved protein
3699934	snp	CG	MUL_3325	-	cell wall and cell processes	antibiotic-transport integral membrane leucine and valine rich protein ABC transporter
3700177	psd	TC	MUL_3326	-	cell wall and cell processes	N-term antibiotic-transport ATP-binding protein ABC transporter - pseudogene
3700218	psd	AC	MUL_3326	-	cell wall and cell processes	N-term antibiotic-transport ATP-binding protein ABC transporter - pseudogene
3702729	snp	AG	MUL_3328	-	cell wall and cell processes	conserved integral membrane alanine, valine and leucine rich protein
3707162	snp	TC	MUL_3333	-	conserved hypotheticals	conserved hypothetical protein
3707313	snp	TC	MUL_3333	-	conserved hypotheticals	conserved hypothetical protein
3708324	snp	CA	MUL_3335	-	intermediary metabolism and respiration	deoxyuridine 5'-triphosphate nucleotidohydrolase DutT
3708921	snp	TA	MUL_3336	-	cell wall and cell processes	conserved hypothetical membrane protein
3709286	snp	CA	MUL_3327	-	conserved hypotheticals	conserved protein
3709870	snp	CT	MUL_3328	-	cell wall and cell processes	conserved hypothetical secreted protein
3710020	snp	TC	MUL_3328	-	cell wall and cell processes	conserved hypothetical secreted protein
3712490	snp	AG	MUL_3341	-	information pathways	RNA polymerase sigma factor SigA
3716675	int	AC	124 MUL_3346	conserved hypotheticals	conserved hypothetical protein	
3717613	snp	TC		cell wall and cell processes	conserved membrane protein	
3719445	non	AG		information pathways	RNA polymerase sigma factor SigB	
3720607	snp	GC		respiratory protein	non-dependent repressor and activator IdeR	
3724001	psd	AG		conserved hypotheticals	C-term conserved hypothetical protein - pseudogene	
3724588	psd	CG		conserved hypotheticals	N-term conserved hypothetical protein - pseudogene	
3724513	psd	TC		intermediary metabolism and respiration	C-term soluble pyridine nucleotide transhydrogenase SthA - pseudogene	
3727316	snp	GA		intermediary metabolism and respiration	intermediate metabolism and respiration C-term soluble pyridine nucleotide transhydrogenase SthA - pseudogene	
3727802	non	TC		conserved hypotheticals	conserved hypothetical hydrolase	
3728326	non	CG		conserved hypotheticals	conserved hypothetical protein	
3728613	non	TC		conserved hypotheticals	conserved hypothetical protein	
3730481	int	A-	66 MUL_3363	regulatory proteins	regulator LexA	
3730822	snp	CT		regulatory proteins	repressor LexA	
3732567	snp	GA		cell wall and cell processes	conserved transmembrane alanine and glycine rich protein	
3732867	snp	AG		cell wall and cell processes	conserved transmembrane alanine and glycine rich protein	
3737340	snp	TG		lipid metabolism	acyl-CoA dehydrogenase FadE20	
3738977	snp	TG		intermediary metabolism and respiration	GTP-binding protein Hfx	
3741067	snp	AG		information pathways	tRNA delta(2)-isopentenylpyrophosphate transferase MiaA	
3744166	int	AG		cell wall and cell processes	N-term conserved membrane hypothetical protein pseudogene	
3746922	non	TC		conserved hypotheticals	conserved protein	
3747997	snp	AG		cell wall and cell processes	conserved membrane protein	
3749601	snp	AG		conserved hypotheticals	conserved hypothetical protein	
3749658	snp	AG		conserved hypotheticals	conserved hypothetical protein	
3750155	int	AG	66 MUL_3378	conserved hypotheticals	conserved hypothetical protein	
3752107	snp	GC		conserved hypotheticals	conserved hypothetical protein	
3752693	snp	TC		conserved hypotheticals	conserved hypothetical protein	
3753184	snp	TC		intermediary metabolism and respiration	glycosyl transferase	
3754340	non	AG		conserved hypotheticals	conserved protein	
3759089	snp	AC		cell wall and cell processes	cell division transmembrane protein FtsK	
3767018	non	CT		intermediary metabolism and respiration	short chain alcohol dehydrogenase/reductase	
3767024	snp	AG		intermediary metabolism and respiration	short chain alcohol dehydrogenase/reductase	
3770417	snp	GT		conserved hypotheticals	conserved hypothetical protein	
3771737	non	CT		conserved hypotheticals	conserved hypothetical protein	
3771741	snp	GA		conserved hypotheticals	conserved hypothetical protein	
3772829	psd	AG		regulatory proteins	C-term transcriptional regulatory protein - pseudogene	
3773713	non	TC	MUL_3406	intermediary metabolism and respiration	acyl-CoA acetyltransferase	
3776284	non	AG	MUL_3408	conserved hypotheticals	conserved hypothetical protein	
3776481	non	AG	MUL_3408	conserved hypotheticals	conserved hypothetical protein	
3776670	snp	CG	MUL_3409	intermediary metabolism and respiration	methyltransferase	
3777602	snp	AG	MUL_3410	regulatory proteins	transcriptional regulator	
3777721	non	CG	MUL_3410	regulatory proteins	transcriptional regulator	
3779404	non	AG	MUL_3411	lipid metabolism	acyl-CoA dehydrogenase FadE22	
3780156	snp	GT	MUL_3411	lipid metabolism	acyl-CoA dehydrogenase FadE22	
3780983	snp	CT	MUL_3412	intermediary metabolism and respiration	short-chain type dehydrogenase/reductase	
3781458	non	CA	MUL_3413	information pathways	ATP-dependent DNA ligase LqB	
3781571	non	AG	MUL_3413	information pathways	ATP-dependent DNA ligase LqB	
3791947	psd	TC	MUL_3421	intermediary metabolism and respiration	C-term carbon starvation protein a homolog CstA - pseudogene	
3792793	snp	AG	MUL_3421	intermediary metabolism and respiration	C-term carbon starvation protein a homolog CstA - pseudogene	
3793116	snp	GA	MUL_3422	information pathways	chaperone protein DnaK1	
3797307	non	CG	MUL_3427	-	hypothetical protein	
3800587	non	GC	MUL_3430	intermediary metabolism and respiration	succinate-semialdehyde dehydrogenase [NADP+] dependent PutA_2	
3800679	snp	AC	MUL_3430	intermediary metabolism and respiration	succinate-semialdehyde dehydrogenase [NADP+] dependent PutA_2	
3802846	non	TC	MUL_3431	lipid metabolism	fatty-acid-CoA ligase	
3805578	int	TG	77 MUL_3434	conserved hypotheticals	conserved hypothetical protein	
3806989	snp	AC		intermediary metabolism and respiration	oxidoreductase GMC-type	
3807282	non	AG		intermediary metabolism and respiration	oxidoreductase GMC-type	
3807892	snp	AG		intermediary metabolism and respiration	oxidoreductase GMC-type	
3808573	snp	AG		intermediary metabolism and respiration	oxidoreductase GMC-type	
3808775	non	AG		intermediary metabolism and respiration	oxidoreductase GMC-type	
3809099	int	AG		intermediary metabolism and respiration	oxidoreductase GMC-type	
3809438	int	GA		intermediary metabolism and respiration	N-term PE-PGRS family protein - pseudogene	
3809585	int	AT		-		
3811384	int	TC		-		
3818042	psd	CT	MUL_5117	unknown	C-term hypothetical protein pseudogene	
3819161	snp	AG	MUL_3442	intermediary metabolism and respiration	phosphoglucomutase PomA	
3819882	non	GC	MUL_3442	intermediary metabolism and respiration	phosphoglucomutase PomA	
3822779	non	TC	MUL_3446	conserved hypotheticals	conserved hypothetical protein	
3823598	non	CT	MUL_3447	conserved hypotheticals	conserved hypothetical protein	
3826603	psd	TC	MUL_3450	conserved hypotheticals	C-term conserved hypothetical protein - pseudogene	

SNP position	SNP type	Nucleotide change <ref><snp>	Locus	Distance to nearest locus	Nearby Locus	Functional group	Product
3826695	Int	CT	20 MUL_3451	-		intermediary metabolism and respiration	citrate lyase beta subunit CitE_2
3828040	syn	AG	MUL_3452	-		conserved hypothetical	conserved hypothetical protein
3828140	syn	CT	MUL_3452	-		conserved hypothetical	conserved hypothetical protein
3828152	syn	CA	MUL_3452	-		conserved hypothetical	conserved hypothetical protein
3828170	syn	CT	MUL_3452	-		conserved hypothetical	conserved hypothetical protein
3828231	non	CT	MUL_3452	-		conserved hypothetical	conserved hypothetical protein
3828304	syn	GA	MUL_3452	-		conserved hypothetical	conserved hypothetical protein
3828371	syn	AG	MUL_3452	-		conserved hypothetical	conserved hypothetical protein
3828692	syn	AG	MUL_3452	-		conserved hypothetical	conserved hypothetical protein
3828770	syn	TC	MUL_3452	-		conserved hypothetical	conserved hypothetical protein
3828958	non	AC	MUL_3452	-		conserved hypothetical	conserved hypothetical protein
3828987	non	AG	MUL_3452	-		conserved hypothetical	conserved hypothetical protein
3829099	Int	AG		111 MUL_3453		cell wall and cell processes	conserved hypothetical membrane protein
3829185	Int	TC		25 MUL_3453		cell wall and cell processes	conserved hypothetical membrane protein
3830128	non	GA	MUL_3453	-		cell wall and cell processes	conserved hypothetical membrane protein
3831055	psd	CT	MUL_3454	-		intermediary metabolism and respiration	N-term dehydrogenase pseudogene
3831181	psd	AG	MUL_3454	-		intermediary metabolism and respiration	N-term dehydrogenase pseudogene
3833966	psd	AC	MUL_3455	-		conserved hypothetical	C-term conserved hypothetical protein - pseudogene
3833966	psd	AC	MUL_3455	-		conserved hypothetical	N-term conserved hypothetical protein - pseudogene
3834601	non	TA	MUL_3456	-		conserved hypothetical	conserved hypothetical protein
3835034	syn	CT	MUL_3457	-		intermediary metabolism and respiration	hydrolase
3835812	non	AG	MUL_3457	-		intermediary metabolism and respiration	hydrolase
3835904	non	GC	MUL_3457	-		intermediary metabolism and respiration	hydrolase
3836081	syn	AC	MUL_3457	-		intermediary metabolism and respiration	hydrolase
3837081	Int	TC		132 MUL_5118		unknown	N-term hypothetical protein pseudogene
3837088	Int	AG		139 MUL_5118		unknown	N-term hypothetical protein pseudogene
3837665	syn	TG	MUL_3458	-		intermediary metabolism and respiration	conserved oxidoreductase
3843789	non	AG	MUL_3464	-		regulatory proteins	conserved hypothetical regulatory protein
3844211	syn	CT	MUL_3464	-		regulatory proteins	conserved hypothetical regulatory protein
3844447	psd	AG	MUL_3465	-		intermediary metabolism and respiration	mid-chain short-chain type dehydrogenase/reductase - pseudogene
3848986	syn	CT	MUL_3469	-		intermediary metabolism and respiration	tRNA delta(2')-isopentenyl pyrophosphate transferase MiaA_1
3857722	Int	TC		123 MUL_3478		cell wall and cell processes	conserved hypothetical secreted protein
3858144	Int	C		95 MUL_3479		conserved hypothetical	conserved hypothetical protein
3872978	Int	TG		70 MUL_3493		cell wall and cell processes	conserved secreted antigen Wag31
3874056	syn	AG	MUL_3495	-		conserved hypothetical	conserved hypothetical protein
3874126	non	CT	MUL_3495	-		conserved hypothetical	conserved hypothetical protein
3876424	syn	GA	MUL_3498	-		cell wall and cell processes	cel division protein FtsZ
3881797	syn	TC	MUL_3502	-		cell wall and cell processes	FtsW-like protein FtsW
3882464	non	TG	MUL_3502	-		cell wall and cell processes	FtsW-like protein FtsW
3883535	non	CT	MUL_3503	-		cell wall and cell processes	UDP-N-acetyl muramoylalanine-D-glutamate ligase MurD
3883872	non	GC	MUL_3503	-		cell wall and cell processes	UDP-N-acetyl muramoylalanine-D-glutamate ligase MurD
3884851	non	TA	MUL_3504	-		cell wall and cell processes	phospho-N-acetyl muramoyl pentapeptidetransferase MurX
3885310	syn	CT	MUL_3505	-		cell wall and cell processes	UDP-N-acetyl muramoylalanyl-D-glutamyl-2'-6'-diaminopimelate-D-alanyl-D-alanyl ligase MurF
3886057	syn	TA	MUL_3505	-		cell wall and cell processes	UDP-N-acetyl muramoylalanyl-D-glutamyl-2'-6'-diaminopimelate-D-alanyl-D-alanyl ligase MurF
3888385	non	CA	MUL_3506	-		cell wall and cell processes	UDP-N-acetyl muramoylalanyl-D-glutamate-2'-6'-diaminopimelate ligase MurE
3888454	Int	-A		47 MUL_3506		cell wall and cell processes	UDP-N-acetyl muramoylalanyl-D-glutamate-2'-6'-diaminopimelate ligase MurE
3892534	syn	AG	MUL_3508	-		cell wall and cell processes	penicillin-binding membrane protein PbpB
3896687	syn	TC	MUL_3513	-		conserved hypothetical	conserved hypothetical protein
3900532	Int	AC		127 MUL_3517		cell wall and cell processes	conserved hypothetical membrane protein
3901336	syn	AG	MUL_3517	-		cell wall and cell processes	conserved hypothetical membrane protein
3902002	syn	GC	MUL_3517	-		cell wall and cell processes	conserved hypothetical membrane protein
3904370	Int	TG		-			
3904375	Int	AC		-			
3906425	psd	GC	MUL_3521	-		lipid metabolism	N-term hydroxymethylglutaryl-coenzyme A synthase PksG pseudogene
3906762	psd	AG	MUL_3521	-		lipid metabolism	N-term hydroxymethylglutaryl-coenzyme A synthase PksG pseudogene
3907428	syn	AG	MUL_3522	-		lipid metabolism	hydroxymethylglutaryl-coenzyme A (HMG-CoA) reductase
3907731	syn	CG	MUL_3522	-		lipid metabolism	hydroxymethylglutaryl-coenzyme A (HMG-CoA) reductase
3907764	syn	AG	MUL_3522	-		lipid metabolism	hydroxymethylglutaryl-coenzyme A (HMG-CoA) reductase
3909137	syn	CT	MUL_3523	-		lipid metabolism	phosphomevalonate kinase
3909292	syn	AG	MUL_3523	-		lipid metabolism	phosphomevalonate kinase
3909412	syn	TC	MUL_3524	-		lipid metabolism	diphosphomevalonate decarboxylase
3909424	syn	AG	MUL_3524	-		lipid metabolism	diphosphomevalonate decarboxylase
3909925	syn	TC	MUL_3524	-		lipid metabolism	diphosphomevalonate decarboxylase
3913135	psd	GC	MUL_3526	-		intermediary metabolism and respiration	N-term isopentenyl-diphosphate delta-isomerase Idi - pseudogene
3914817	Int	GC		-			
3915494	psd	TC	MUL_3529	-		lipid metabolism	N-term terpene cyclase - pseudogene
3915951	psd	TC	MUL_3529	-		lipid metabolism	C-term terpene cyclase - pseudogene
3916088	psd	AG	MUL_3529	-		lipid metabolism	C-term terpene cyclase - pseudogene
3916271	Int	TA		-			
3916497	non	CG	MUL_3531	-		lipid metabolism	3-oxoacyl-[acyl-carrier-protein] synthase III FabH_1
3917404	syn	TA	MUL_3531	-		lipid metabolism	3-oxoacyl-[acyl-carrier-protein] synthase III FabH_1
3921640	non	AG	MUL_3535	-		conserved hypothetical	conserved hypothetical membrane protein
3923073	syn	AG	MUL_3536	-		cell wall and cell processes	conserved hypothetical integral membrane protein
3923139	syn	TC	MUL_3536	-		cell wall and cell processes	conserved hypothetical integral membrane protein
3925882	Int	TC		92 MUL_3539		conserved hypothetical	conserved hypothetical protein
3932058	non	TG	MUL_3545	-		cell wall and cell processes	conserved hypothetical secreted protein
3938971	syn	TG	MUL_3553	-		intermediary metabolism and respiration	ubiquinol-cytochrome C reductase OcrB
3943377	syn	GA	MUL_3557	-		intermediary metabolism and respiration	transmembrane cytochrome C oxidase (subunit II) CtaC
3943950	syn	AG	MUL_3557	-		intermediary metabolism and respiration	transmembrane cytochrome C oxidase (subunit II) CtaC
3945298	non	GA	MUL_3558	-		intermediary metabolism and respiration	asparagine synthetase AsnB
3945980	syn	AG	MUL_3558	-		intermediary metabolism and respiration	asparagine synthetase AsnB
3948014	non	TC	MUL_3560	-		conserved hypothetical	conserved protein
3948101	non	AG	MUL_3560	-		conserved hypothetical	conserved protein
3948307	non	AG	MUL_3560	-		conserved hypothetical	conserved protein
3948711	non	AG	MUL_3561	-		conserved hypothetical	conserved protein
3955441	non	TG	MUL_3569	-		cell wall and cell processes	conserved hypothetical integral membrane protein
3961325	syn	TC	MUL_3573	-		intermediary metabolism and respiration	leucyl aminopeptidase PepB
3962159	non	GC	MUL_3574	-		intermediary metabolism and respiration	short-chain dehydrogenase EhdB
3963051	syn	AG	MUL_3574	-		short-chain dehydrogenase EhdB	short-chain dehydrogenase EhdB
3971527	Int	AG		-			
3971812	psd	TG	MUL_5084	-		insertion seqs and phages	N-term phage-related integrase pseudogene
3971991	non	CT	MUL_3581	-		insertion seqs and phages	phage-related integrase

SNP position	SNP type	Nucleotide change <ref><snp>	Distance to nearest locus	Nearby Locus	Functional group	Product
3971992	syn	AC	MUL_3581	-	insertion seqs and phages	phage-related integrase
3972858	syn	TC	MUL_3582	-	cell wall and cell processes	conserved hypothetical membrane protein
3973053	syn	GA	MUL_3582	-	cell wall and cell processes	conserved hypothetical membrane protein
3973149	syn	TC	MUL_3582	-	cell wall and cell processes	conserved hypothetical membrane protein
3973284	int	TG	100 MUL_3582	cell wall and cell processes	conserved hypothetical membrane protein	conserved hypothetical membrane protein
3973561	non	TG	MUL_5087	-	unknown	hypothetical protein
3973634	non	GA	MUL_5087	-	unknown	hypothetical protein
3973677	non	CT	MUL_5087	-	unknown	hypothetical protein
3976756	syn	AT	MUL_3587	-	intermediary metabolism and respiration	lipoprotein aminopeptidase LpqL
3979340	psd	CT	MUL_3588	-	intermediary metabolism and respiration	C-term lipoprotein aminopeptidase LpqL_1 - pseudogene
3995710	syn	TC	MUL_3600	-	intermediary metabolism and respiration	thiamine biosynthesis protein ThIC
3996290	syn	GC	MUL_3601	-	regulatory proteins	conserved hypothetical regulatory protein
4001396	syn	CG	MUL_3604	-	conserved hypotheticals	conserved hypothetical protein
4001451	int	CT	39 MUL_3605	cell wall and cell processes	C-term metal cation transporting p-type ATPase CtpH - pseudogene	C-term metal cation transporting p-type ATPase CtpH - pseudogene
4003122	psd	TC	MUL_3605	-	cell wall and cell processes	C-term metal cation transporting p-type ATPase CtpH - pseudogene
4004349	psd	TC	MUL_3605	-	cell wall and cell processes	C-term metal cation transporting p-type ATPase CtpH - pseudogene
4004438	psd	TG	MUL_3605	-	cell wall and cell processes	C-term metal cation transporting p-type ATPase CtpH - pseudogene
4011361	syn	TC	MUL_3610	-	information pathways	Glycyl-tRNA synthetase GlyS
4011427	syn	CG	MUL_3610	-	information pathways	Glycyl-tRNA synthetase GlyS
4011895	syn	AG	MUL_3610	-	information pathways	Glycyl-tRNA synthetase GlyS
4012632	int	A	145 MUL_3611	regulatory proteins	transcriptional regulatory protein (probably ArsR-family)	transcriptional regulatory protein (probably ArsR-family)
4012724	int	GA	53 MUL_3611	regulatory proteins	transcriptional regulatory protein (probably ArsR-family)	transcriptional regulatory protein (probably ArsR-family)
4013273	syn	GA	MUL_3612	-	regulatory proteins	Zinc uptake regulation protein Zur
4013798	syn	GA	MUL_3613	-	conserved hypotheticals	conserved hypothetical protein
4013824	non	TC	MUL_3613	-	conserved hypotheticals	conserved hypothetical protein
4013857	syn	AG	MUL_3613	-	conserved hypotheticals	conserved hypothetical protein
4013998	syn	TT	MUL_3613	-	conserved hypotheticals	conserved hypothetical protein
4014064	syn	CG	MUL_3614	-	cell wall and cell processes	undecaprenyl diphosphate synthase Upps
4014295	non	AG	MUL_3614	-	cell wall and cell processes	undecaprenyl diphosphate synthase Upps
4015478	syn	TG	MUL_3615	-	information pathways	recombination protein O RecO
4016640	non	TC	MUL_3616	-	intermediary metabolism and respiration	amidase AmiA2
4016781	non	AG	MUL_3616	-	intermediary metabolism and respiration	amidase AmiA2
4018516	psd	AC	MUL_3619	-	cell wall and cell processes	N-term conserved hypothetical membrane protein - pseudogene
4018516	psd	AC	MUL_3619	-	cell wall and cell processes	C-term conserved hypothetical membrane protein - pseudogene
4025751	syn	CG	MUL_3627	-	regulatory proteins	heat shock protein transcriptional repressor HrcA
4027706	syn	CG	MUL_3629	-	conserved hypotheticals	conserved hypothetical protein
4028626	syn	GA	MUL_3630	-	information pathways	alternative RNA polymerase sigma factor SigJ-like
4029465	int	TG	66 MUL_3631	cell wall and cell processes	N-term low molecular weight antigen Ctp2 - pseudogene	N-term low molecular weight antigen Ctp2 - pseudogene
4034354	non	CG	MUL_3633	-	intermediary metabolism and respiration	non-ribosomal peptide synthetase MbtF
4034591	non	AC	MUL_3633	-	intermediary metabolism and respiration	non-ribosomal peptide synthetase MbtF
4034707	syn	AG	MUL_3633	-	intermediary metabolism and respiration	non-ribosomal peptide synthetase MbtF
4035712	non	AT	MUL_3633	-	intermediary metabolism and respiration	non-ribosomal peptide synthetase MbtF
4036353	non	TC	MUL_3633	-	intermediary metabolism and respiration	non-ribosomal peptide synthetase MbtF
4039316	syn	AG	MUL_3634	-	intermediary metabolism and respiration	non-ribosomal peptide synthetase MbtE
4039478	non	AG	MUL_3634	-	intermediary metabolism and respiration	non-ribosomal peptide synthetase MbtE
4041951	non	TG	MUL_3634	-	intermediary metabolism and respiration	non-ribosomal peptide synthetase MbtE
4042910	int	TC	122 MUL_3635	conserved hypotheticals	conserved hypothetical protein	conserved hypothetical protein
4046048	syn	GA	MUL_3638	-	lipid metabolism	polyketide synthase MbtD
4049260	non	TA	MUL_3640	-	intermediary metabolism and respiration	lysine-N-oxygenase MbtG
4051502	syn	TC	MUL_3641	-	cell wall and cell processes	bifunctional enzyme MbtA: salicyl-AMP ligase (SAL-AMP ligase) + salicyl-S-ACP synthetase
4052129	syn	GT	MUL_3641	-	cell wall and cell processes	bifunctional enzyme MbtA: salicyl-AMP ligase (SAL-AMP ligase) + salicyl-S-ACP synthetase
4052321	syn	TC	MUL_3642	-	intermediary metabolism and respiration	acetyl hydrolase MbtJ
4053427	syn	AC	MUL_3643	-	cell wall and cell processes	short-chain membrane-associated dehydrogenase
4055316	syn	TC	MUL_3645	-	regulatory proteins	conserved hypothetical transcriptional regulator
4055509	non	GA	MUL_3645	-	regulatory proteins	conserved hypothetical transcriptional regulator
4057661	non	TC	MUL_3647	-	conserved hypotheticals	conserved hypothetical protein
4075949	int	GA	50 MUL_3648	intermediary metabolism and respiration	isochorismate synthase MbtI	isochorismate synthase MbtI
4058833	syn	CA	MUL_3648	-	intermediary metabolism and respiration	isochorismate synthase MbtI
4062130	syn	GA	MUL_3651	-	intermediary metabolism and respiration	oxygen-independent coproporphyrinogen III oxidase HemN
4065140	non	CA	MUL_3653	-	intermediary metabolism and respiration	3'-phosphoadenosine 5'-phosphosulfate reductase CysH
4065750	non	AG	MUL_3654	-	cell wall and cell processes	conserved hypothetical protein
4066887	psd	TC	MUL_3655	-	intermediary metabolism and respiration	N-term gamma-glutamyltranspeptidase precursor GtbB - pseudogene
4067322	psd	TC	MUL_3655	-	intermediary metabolism and respiration	N-term gamma-glutamyltranspeptidase precursor GtbB - pseudogene
4068125	psd	AG	MUL_3655	-	intermediary metabolism and respiration	C-term gamma-glutamyltranspeptidase precursor GtbB - pseudogene
4069237	psd	CG	MUL_3656	-	cell wall and cell processes	N-term conserved hypothetical membrane protein - pseudogene
4069683	psd	AG	MUL_3656	-	cell wall and cell processes	N-term conserved hypothetical membrane protein - pseudogene
4070120	psd	GC	MUL_3656	-	cell wall and cell processes	N-term conserved hypothetical membrane protein - pseudogene
4071512	syn	AC	MUL_3659	-	cell wall and cell processes	sulfate-transport integral membrane protein ABC transporter CysW
4071549	non	CT	MUL_3659	-	cell wall and cell processes	sulfate-transport integral membrane protein ABC transporter CysW
4072924	syn	CT	MUL_3660	-	cell wall and cell processes	sulfate-transport integral membrane protein ABC transporter CysT
4075250	non	CG	MUL_3663	-	intermediary metabolism and respiration	FAD-dependent oxidoreductase
4077013	syn	TC	MUL_3664	-	intermediary metabolism and respiration	conserved hypothetical glycosyl hydrolase
4077178	syn	GC	MUL_3664	-	intermediary metabolism and respiration	conserved hypothetical glycosyl hydrolase
4077562	syn	GT	MUL_3664	-	intermediary metabolism and respiration	conserved hypothetical glycosyl hydrolase
4078366	syn	AC	MUL_3665	-	cell wall and cell processes	conserved hypothetical lipoprotein LprD
4078763	non	CT	MUL_3665	-	cell wall and cell processes	conserved hypothetical lipoprotein LprD
4078771	syn	GA	MUL_3665	-	cell wall and cell processes	conserved hypothetical lipoprotein LprD
4078795	syn	TG	MUL_3665	-	cell wall and cell processes	conserved hypothetical lipoprotein LprD
4084170	int	CT	-	-	-	conserved hypothetical lipoprotein LprD
4089544	syn	GC	MUL_3675	-	conserved hypotheticals	conserved hypothetical protein
4090685	int	GA	44 MUL_3676	information pathways	30S ribosomal protein S20 RpsT	30S ribosomal protein S20 RpsT
4093583	syn	CT	MUL_3679	-	cell wall and cell processes	conserved hypothetical membrane metal-binding protein ComEC
4095509	non	GC	MUL_3680	-	cell wall and cell processes	conserved hypothetical membrane protein ComEA
4096202	syn	AG	MUL_3681	-	lipid metabolism	acyl-CoA dehydrogenase FadE17_1
4100524	psd	CT	MUL_3684	-	-	N-term enhanced intracellular survival protein Eis - pseudogene
4100780	psd	AG	MUL_3684	-	-	N-term enhanced intracellular survival protein Eis - pseudogene
4101841	syn	AC	MUL_3685	-	conserved hypotheticals	conserved hypothetical protein
4103373	syn	TC	MUL_3687	-	cell wall and cell processes	conserved membrane protein MmpSS_1
4103412	syn	CT	MUL_3687	-	cell wall and cell processes	conserved membrane protein MmpSS_1
4112009	non	AG	MUL_3694	-	conserved hypotheticals	conserved hypothetical protein
4115170	non	GT	MUL_3697	-	cell wall and cell processes	conserved hypothetical membrane protein
4115446	syn	AG	MUL_3697	-	cell wall and cell processes	conserved hypothetical membrane protein

SNP position	SNP type	Nucleotide change <ref><snp>	Distance to nearest locus	Nearby Locus	Functional group	Product
4116066	non	GT	MUL_3697	-	cell wall and cell processes	conserved hypothetical membrane protein
4116226	syn	AG	MUL_3697	-	cell wall and cell processes	conserved hypothetical membrane protein
4118559	int	GA	-	42 MUL_3699	cell wall and cell processes	conserved hypothetical membrane protein
4120033	psd	GC	MUL_3700	-	intermediary metabolism and respiration	C-term adenylate and quanilate cyclase, pseudogene
4120035	psd	AG	MUL_3700	-	intermediary metabolism and respiration	C-term adenylate and quanilate cyclase, pseudogene
4121034	psd	CT	MUL_3700	-	intermediary metabolism and respiration	mid-section adenylate and quanilate cyclase, pseudogene
4121297	psd	C-	MUL_3700	-	intermediary metabolism and respiration	mid-section adenylate and quanilate cyclase, pseudogene
4121298	psd	A-	MUL_3700	-	intermediary metabolism and respiration	mid-section adenylate and quanilate cyclase, pseudogene
4130366	int	AG	-	55 MUL_3706	regulatory proteins	Sir2-like regulatory protein
4130370	int	GA	-	59 MUL_3706	regulatory proteins	Sir2-like regulatory protein
4130371	int	CG	-	60 MUL_3706	regulatory proteins	Sir2-like regulatory protein
4130374	int	GC	-	63 MUL_3706	regulatory proteins	Sir2-like regulatory protein
4130545	psd	AG	MUL_3707	-	intermediary metabolism and respiration	C-term cytochrome P450_268A2 Cyp268A2P pseudogene
4130719	psd	AG	MUL_3707	-	intermediary metabolism and respiration	C-term cytochrome P450_268A2 Cyp268A2P pseudogene
4131487	psd	CT	MUL_3707	-	intermediary metabolism and respiration	N-term cytochrome P450_268A2 Cyp268A2P pseudogene
4131567	psd	CT	MUL_3707	-	intermediary metabolism and respiration	N-term cytochrome P450_268A2 Cyp268A2P pseudogene
4131578	psd	CA	MUL_3707	-	intermediary metabolism and respiration	N-term cytochrome P450_268A2 Cyp268A2P pseudogene
4131737	int	GT	-	81 MUL_3707	intermediary metabolism and respiration	N-term cytochrome P450_268A2 Cyp268A2P pseudogene
4131738	int	AC	-	82 MUL_3707	intermediary metabolism and respiration	N-term cytochrome P450_268A2 Cyp268A2P pseudogene
4131937	syn	TC	MUL_3708	-	regulatory proteins	transcriptional regulatory protein (AcrR family)
4132088	non	TC	MUL_3708	-	regulatory proteins	transcriptional regulatory protein (AcrR family)
4132177	syn	AG	MUL_3708	-	regulatory proteins	transcriptional regulatory protein (AcrR family)
4132372	syn	CT	MUL_3708	-	regulatory proteins	transcriptional regulatory protein (AcrR family)
4132477	int	AC	-	54 MUL_3708	regulatory proteins	transcriptional regulatory protein (AcrR family)
4136424	int	AG	-			
4137145	non	CT	MUL_3711	-	intermediary metabolism and respiration	glutamate 5-kinase protein ProB
4137713	syn	AG	MUL_3711	-	intermediary metabolism and respiration	glutamate 5-kinase protein ProB
4137767	syn	TC	MUL_3711	-	intermediary metabolism and respiration	glutamate 5-kinase protein ProB
4138885	syn	TC	MUL_3712	-	intermediary metabolism and respiration	GTP/GDP-family GTP-binding protein Obq
4139353	syn	TG	MUL_3712	-	intermediary metabolism and respiration	GTP/GDP-family GTP-binding protein Obq
4143289	syn	AG	MUL_3715	-	intermediary metabolism and respiration	ribonuclease E Rne
4148560	syn	TC	MUL_3719	-	information pathways	valyl-tRNA synthetase protein ValS
4150137	non	GA	MUL_3721	-	cell wall and cell processes	conserved hypothetical membrane protein
4150140	non	AG	MUL_3721	-	cell wall and cell processes	conserved hypothetical membrane protein
4150141	non	CT	MUL_3721	-	cell wall and cell processes	conserved hypothetical membrane protein
4151440	syn	TC	MUL_3722	-	cell wall and cell processes	conserved membrane protein
4151593	syn	CT	MUL_3722	-	cell wall and cell processes	conserved membrane protein
4153551	int	TC	-	2 MUL_3724	intermediary metabolism and respiration	molybdopterin-quanine dinucleotide biosynthesis protein a MobA
4154197	syn	AG	MUL_3725	-	intermediary metabolism and respiration	pyruvate:ferredoxin oxidoreductase PorB beta subunit
4154224	syn	AG	MUL_3725	-	intermediary metabolism and respiration	pyruvate:ferredoxin oxidoreductase PorB beta subunit
4155544	syn	CT	MUL_3726	-	intermediary metabolism and respiration	pyruvate:ferredoxin oxidoreductase PorA alpha subunit
4155697	syn	AG	MUL_3726	-	intermediary metabolism and respiration	pyruvate:ferredoxin oxidoreductase PorA alpha subunit
4156860	int	GT	-	139 MUL_3727	cell wall and cell processes	conserved integral membrane transport protein
4158076	syn	AG	MUL_3727	-	cell wall and cell processes	conserved integral membrane transport protein
4158997	syn	AG	MUL_3728	-	intermediary metabolism and respiration	ATP-dependent CLP protease ATP-binding subunit ClpX
4162693	syn	CT	MUL_3731	-	intermediary metabolism and respiration	ATP-dependent CLP protease proteolytic subunit 1 ClpP1
4165206	int	AG	-	9 MUL_3735	lipid metabolism	esterase/lipase LipD
4171871	int	GT	-	23 MUL_3742	intermediary metabolism and respiration	aminopeptidase N PepN
4172365	non	AG	MUL_3742	-	intermediary metabolism and respiration	aminopeptidase N PepN
4172464	non	AG	MUL_3742	-	intermediary metabolism and respiration	aminopeptidase N PepN
4173387	syn	GT	MUL_3742	-	intermediary metabolism and respiration	aminopeptidase N PepN
4174372	non	GT	MUL_3742	-	intermediary metabolism and respiration	aminopeptidase N PepN
4175721	non	TG	MUL_3745	-	conserved hypotheticals	conserved hypothetical protein
4175722	non	TC	MUL_3745	-	conserved hypotheticals	conserved hypothetical protein
4175748	syn	TC	MUL_3745	-	conserved hypotheticals	conserved hypothetical protein
4177856	psd	TC	MUL_3747	-	intermediary metabolism and respiration	C-term alpha-glucosidase AglA pseudogene
4178575	psd	GA	MUL_3748	-		N-term membrane-associated phospholipase C PlcB_1 pseudogene
4180102	non	TC	MUL_3749	-	lipid metabolism	cholesterol oxidase precursor ChoD_1
4181322	syn	AG	MUL_3749	-	lipid metabolism	cholesterol oxidase precursor ChoD_1
4181400	syn	GA	MUL_3749	-	lipid metabolism	cholesterol oxidase precursor ChoD_1
4182846	psd	CG	MUL_3750	-	cell wall and cell processes	mid-section drug-transport integral membrane protein pseudogene
4183665	psd	TC	MUL_3751	-	intermediary metabolism and respiration	C-term molybdopterin biosynthesis protein MoeV_1 pseudogene
4184164	psd	AT	MUL_3751	-	intermediary metabolism and respiration	C-term molybdopterin biosynthesis protein MoeV_1 pseudogene
4184571	psd	TC	MUL_3751	-	intermediary metabolism and respiration	C-term molybdopterin biosynthesis protein MoeV_1 pseudogene
4188026	non	GA	MUL_3754	-	conserved hypotheticals	conserved protein
4189546	psd	CT	MUL_3756	-	intermediary metabolism and respiration	C-term NAD-dependent glutamate dehydrogenase Gdh pseudogene
4189970	psd	AG	MUL_3756	-	intermediary metabolism and respiration	C-term NAD-dependent glutamate dehydrogenase Gdh pseudogene
4191161	psd	AG	MUL_3756	-	intermediary metabolism and respiration	C-term NAD-dependent glutamate dehydrogenase Gdh pseudogene
4192595	psd	AG	MUL_3756	-	intermediary metabolism and respiration	C-term NAD-dependent glutamate dehydrogenase Gdh pseudogene
4193077	psd	CG	MUL_3756	-	intermediary metabolism and respiration	C-term NAD-dependent glutamate dehydrogenase Gdh pseudogene
4193588	syn	AG	MUL_3757	-	cell wall and cell processes	N-term NAD-dependent glutamate dehydrogenase Gdh pseudogene
4195317	syn	TC	MUL_3758	-	information pathways	ATP-binding component of an ABC transporter
4195728	int	GT	-	28 MUL_3758	information pathways	single-stranded DNA-binding protein
4197924	psd	GC	MUL_3762	-	lipid metabolism	N-term membrane-bound C-5 sterol desaturase Erg3_2 pseudogene
4198464	psd	CT	MUL_3762	-	lipid metabolism	C-term membrane-bound C-5 sterol desaturase Erg3_2 pseudogene
4198516	psd	GC	MUL_3762	-	lipid metabolism	C-term membrane-bound C-5 sterol desaturase Erg3_2 pseudogene
4198561	psd	TA	MUL_3762	-	lipid metabolism	C-term membrane-bound C-5 sterol desaturase Erg3_2 pseudogene
4198687	int	GA	-	101 MUL_3763	lipid metabolism	N-term glycerol-3-phosphate acyltransferase PlsB2 pseudogene
4200270	psd	AC	MUL_3763	-	lipid metabolism	N-term glycerol-3-phosphate acyltransferase PlsB2 pseudogene
4202111	syn	CG	MUL_3764	-	lipid metabolism	bifunctional transmembrane phospholipid biosynthesis enzyme PlsC
4202270	syn	CG	MUL_3764	-	lipid metabolism	bifunctional transmembrane phospholipid biosynthesis enzyme PlsC
4204612	int	TC	-	124 MUL_3765	cell wall and cell processes	conserved hypothetical membrane protein
4205915	syn	TA	MUL_3766	-	lipid metabolism	carboxylesterase LipQ
4206711	psd	CG	MUL_3768	-	cell wall and cell processes	N-term cutinase precursor pseudogene
4207479	non	TC	MUL_3769	-	unknown	hypothetical protein
4208537	non	CT	MUL_3770	-	intermediary metabolism and respiration	cobric acid synthase CobQ1
4209174	syn	GC	MUL_3770	-	intermediary metabolism and respiration	cobric acid synthase CobQ1
4209576	int	AC	-			
4212531	non	AG	MUL_3773	-	intermediary metabolism and respiration	dihydrolipopamide S-acetyltransferase E2 component PdhC
4214380	syn	AG	MUL_3775	-	intermediary metabolism and respiration	pyruvate dehydrogenase E1 component (alpha subunit) PdhA
4215155	int	GA	-	123 MUL_3776	intermediary metabolism and respiration	citrate (pmo-3s)-lase (beta subunit) ClfE
4216120	syn	CT	MUL_3777	-	intermediary metabolism and respiration	conserved protein

SNP position	SNP type	Nucleotide change <ref><snp>	Distance to nearest locus	Nearby Locus	Functional group	Product
4217271	syn	TC	MUL_3728	-	lipid metabolism	acyl-CoA dehydrogenase FadE19
4218199	non	AG	MUL_3729	-	lipid metabolism	acyl-/propionyl-coenzyme a carboxylase alpha chain ArcA1
4218606	syn	TG	MUL_3729	-	lipid metabolism	acyl-/propionyl-coenzyme a carboxylase alpha chain ArcA1
4219721	syn	AG	MUL_3729	-	lipid metabolism	acyl-/propionyl-coenzyme a carboxylase alpha chain ArcA1
4219820	psd	CG	MUL_3780	-	lipid metabolism	C-term acetyl-/propionyl-CoA carboxylase (beta subunit) AccD1_pseudogene
4225221	psd	TG	MUL_3783	-	lipid metabolism	N-term fatty-acid-CoA ligase FadD35_pseudogene
4225331	psd	GA	MUL_3783	-	lipid metabolism	N-term fatty-acid-CoA ligase FadD35_pseudogene
4228595	syn	AG	MUL_3787	-	cell wall and cell processes	conserved integral membrane leucine and alanine rich protein
4229271	syn	CT	MUL_3788	-	intermediary metabolism and respiration	short-chain type dehydrogenase/reductase
4230018	syn	AG	MUL_3788	-	intermediary metabolism and respiration	short-chain type dehydrogenase/reductase
4231134	psd	AG	MUL_3789	-	conserved hypothetical	N-term conserved hypothetical protein_pseudogene
4231410	psd	AT	MUL_3789	-	conserved hypothetical	N-term conserved hypothetical protein_pseudogene
4232760	non	GA	MUL_3792	-	cell wall and cell processes	conserved hypothetical membrane protein
4232761	non	CG	MUL_3792	-	cell wall and cell processes	conserved hypothetical membrane protein
4232985	non	AG	MUL_3792	-	cell wall and cell processes	conserved hypothetical membrane protein
4235671	psd	GT	MUL_3795	-		C-term YrbE family protein YrbE5B_pseudogene
4236478	syn	CT	MUL_3796	-		Mce protein_Mce5A
4238705	syn	AC	MUL_3798	-		Mce family protein_Mce5C
4240195	psd	AG	MUL_3799	-		C-term Mce family protein Mce5D_pseudogene
4240518	psd	TC	MUL_3799	-		C-term Mce family protein Mce5D_pseudogene
4240884	non	GA	MUL_3800	-		Mce family protein_Mce5E
4241775	non	CG	MUL_3800	-		Mce family protein_Mce5E
4241811	syn	CT	MUL_3800	-		Mce family protein_Mce5E
4241948	syn	AC	MUL_3800	-		Mce family protein_Mce5E
4242682	syn	TC	MUL_3801	-		Mce family protein_Mce5F
4242752	non	AG	MUL_3801	-		Mce family protein_Mce5F
4245247	non	AC	MUL_3804	-	cell wall and cell processes	conserved lipoprotein LppS
4245345	syn	AG	MUL_3804	-	cell wall and cell processes	conserved lipoprotein LppS
4247255	non	AT	MUL_3808	-	conserved hypothetical	conserved hypothetical protein
4247835	non	GT	MUL_3808	-	conserved hypothetical	conserved hypothetical protein
4247884	int	CG	32 MUL_3808	conserved hypothetical	conserved hypothetical	conserved hypothetical protein
4249946	non	TC		conserved hypothetical	conserved membrane protein	conserved membrane protein
4255352	psd	CT		cell wall and cell processes	C-term conserved hypothetical membrane protein_pseudogene	
4255604	psd	CG		cell wall and cell processes	C-term conserved hypothetical membrane protein_pseudogene	
4257055	syn	TC		lipid metabolism	fatty acid synthase_Fas	
4259347	syn	AG	MUL_3818	-	lipid metabolism	fatty acid synthase_Fas
4259374	syn	TC	MUL_3818	-	lipid metabolism	fatty acid synthase_Fas
4261528	syn	AG	MUL_3818	-	lipid metabolism	fatty acid synthase_Fas
4261827	non	CT	MUL_3818	-	lipid metabolism	fatty acid synthase_Fas
4262391	non	AG	MUL_3818	-	lipid metabolism	fatty acid synthase_Fas
4262896	syn	AG	MUL_3818	-	lipid metabolism	fatty acid synthase_Fas
4264975	syn	CG	MUL_3818	-	lipid metabolism	fatty acid synthase_Fas
4265392	syn	CG	MUL_3818	-	lipid metabolism	fatty acid synthase_Fas
4265425	syn	CT	MUL_3818	-	lipid metabolism	fatty acid synthase_Fas
4266592	syn	CG	MUL_3819	-	cell wall and cell processes	conserved hypothetical secreted protein
4267217	non	AG	MUL_3820	-	intermediary metabolism and respiration	ring-hydroxylating dioxygenase large terminal subunit
4267593	non	GA	MUL_3820	-	intermediary metabolism and respiration	ring-hydroxylating dioxygenase large terminal subunit
4268600	psd	AC	MUL_3821	-	intermediary metabolism and respiration	N-term NAD-dependent aldehyde dehydrogenase_pseudogene
4269376	psd	TC	MUL_3821	-	intermediary metabolism and respiration	N-term NAD-dependent aldehyde dehydrogenase_pseudogene
4270728	syn	AG	MUL_3824	-	conserved hypothetical	conserved hypothetical
4270786	syn	AG	MUL_3824	-	conserved hypothetical	conserved protein
4271390	int	GC	-	-	-	-
4271502	int	GA	-	-	-	-
4271612	int	GT	-	-	-	-
4271696	int	CG	-	-	-	-
4277361	non	CG	MUL_3829	-	intermediary metabolism and respiration	oxidoreductase
4277421	non	CG	MUL_3829	-	intermediary metabolism and respiration	oxidoreductase
4277547	syn	TG	MUL_3829	-	intermediary metabolism and respiration	oxidoreductase
4277583	syn	TG	MUL_3829	-	intermediary metabolism and respiration	oxidoreductase
4278384	syn	GA	MUL_3830	-	intermediary metabolism and respiration	ferredoxin Fdx1
4279156	psd	TC	MUL_3831	-	conserved hypothetical	C-term conserved hypothetical protein_pseudogene
4279193	psd	TC	MUL_3831	-	conserved hypothetical	mid-section conserved hypothetical protein_pseudogene
4279241	psd	GC	MUL_3831	-	conserved hypothetical	mid-section conserved hypothetical protein_pseudogene
4279274	psd	AG	MUL_3831	-	conserved hypothetical	mid-section conserved hypothetical protein_pseudogene
4279445	psd	AG	MUL_3831	-	conserved hypothetical	mid-section conserved hypothetical protein_pseudogene
4279758	psd	CG	MUL_3831	-	conserved hypothetical	mid-section conserved hypothetical protein_pseudogene
4281407	syn	GC	MUL_3832	-	regulatory proteins	transcriptional regulatory protein (FadR family)
4304079	non	AG	MUL_3884	-	regulatory proteins	transcriptional regulatory protein
4341561	non	CG	MUL_3885	-	lipid metabolism	enoyl-CoA hydratase_EchA4_2
4342864	int	AG	86 MUL_3886	conserved hypothetical	lipid metabolism	enoyl-CoA hydratase_EchA4_2
4343307	non	CG		-	lipid metabolism	enoyl-CoA hydratase_EchA10_1
4344219	syn	CG		-	lipid metabolism	enoyl-CoA hydratase_EchA11_1
4345431	non	TG		-	lipid metabolism	long-chain fatty-acid CoA ligase
4346404	syn	CT		-	lipid metabolism	long-chain fatty-acid CoA ligase
4346776	syn	TC		-	lipid metabolism	long-chain fatty-acid CoA ligase
4347218	psd	AG		-	lipid metabolism	N-term fatty-acid-CoA ligase FadD35_1_pseudogene
4348126	psd	GC		-	lipid metabolism	C-term fatty-acid-CoA ligase FadD35_1_pseudogene
4348184	psd	AG	MUL_3891	-	lipid metabolism	C-term fatty-acid-CoA ligase FadD35_1_pseudogene
4348319	psd	CT	MUL_3891	-	lipid metabolism	C-term fatty-acid-CoA ligase FadD35_1_pseudogene
4348331	psd	AC	MUL_3891	-	lipid metabolism	C-term fatty-acid-CoA ligase FadD35_1_pseudogene
4348505	psd	TG	MUL_3892	-	lipid metabolism	N-term fatty-acid-CoA ligase_pseudogene
4348552	psd	TA	MUL_3892	-	lipid metabolism	N-term fatty-acid-CoA ligase_pseudogene
4349388	psd	TA	MUL_3892	-	lipid metabolism	N-term fatty-acid-CoA ligase_pseudogene
4349554	psd	CG	MUL_3892	-	lipid metabolism	C-term long-chain fatty-acid CoA ligase_pseudogene
4350034	int	GA	110 MUL_3892	lipid metabolism	C-term long-chain fatty-acid CoA ligase_pseudogene	
4350374	non	GT	MUL_3893	-	cell wall and cell processes	conserved hypothetical secreted protein
4351164	syn	AG	MUL_3894	-	regulatory proteins	transcriptional regulatory protein (probably GntR-family)
4352287	syn	AG	MUL_3895	-	lipid metabolism	acyl-CoA dehydrogenase
4352664	syn	TG	MUL_3895	-	lipid metabolism	acyl-CoA dehydrogenase
4354456	psd	CT	MUL_3897	-	lipid metabolism	C-term beta-ketoacyl CoA thiolase_pseudogene
4354522	psd	TA	MUL_3897	-	lipid metabolism	C-term beta-ketoacyl CoA thiolase_pseudogene
4355693	non	CT	MUL_3898	-	lipid metabolism	3-oxoacyl-[acyl-carrier protein] reductase FabG

SNP position	SNP type	Nucleotide change <ref><snp>	Distance to nearest locus	Nearby Locus	Functional group	Product
4355768	syn	GA	MUL_3898	-	lipid metabolism	3-oxoacyl-[acyl-carrier protein] reductase FabG
4357344	psd	GT	MUL_3900	-	conserved hypotheticals	N-term conserved hypothetical protein_pseudogene
4360646	syn	GA	MUL_3902	-	cell wall and cell processes	transmembrane ATP-binding protein ABC transporter
4363298	Int	-G	13	MUL_3905	cell wall and cell processes	conserved hypothetical membrane protein
4363554	syn	CT	MUL_3906	-	intermediary metabolism and respiration	Ham1-related NTPase
4363730	hon	AC	MUL_3906	-	intermediary metabolism and respiration	Ham1-related NTPase
4364023	Int	TA	104	MUL_3906	intermediary metabolism and respiration	Ham1-related NTPase
4365048	syn	AG	MUL_3908	-	information pathways	ribonuclease RphA
4365291	syn	AG	MUL_3908	-	information pathways	ribonuclease RphA
4366241	syn	AC	MUL_3909	-	conserved hypotheticals	conserved hypothetical metal-dependent hydrolase
4366423	hon	CG	MUL_3909	-	conserved hypotheticals	conserved hypothetical metal-dependent hydrolase
4374483	hon	AG	MUL_3918	-	MCE-family protein Mce3A_1	MCE-family protein Mce3A_1
4375103	syn	TC	MUL_3918	-	MCE-family protein Mce3A_1	MCE-family protein Mce3A_1
4378260	hon	TA	MUL_3921	-	MCE-family protein Mce3D_1	MCE-family protein Mce3D_1
4378545	syn	GC	MUL_3921	-	MCE-family protein Mce3D_1	MCE-family protein Mce3D_1
4379347	hon	CT	MUL_3922	-	MCE-family lipoprotein LprM_1	MCE-family lipoprotein LprM_1
4383190	syn	AG	MUL_3925	-	cell wall and cell processes	glutamate racemase MurI
4387958	syn	TC	MUL_3932	-	intermediary metabolism and respiration	nicotinic acid phosphoribosyltransferase PncB
4391181	syn	AG	MUL_3934	-	intermediary metabolism and respiration	cyclooenzyme phosphorylase GlqP
4392367	syn	TC	MUL_3935	-	intermediary metabolism and respiration	concerned glycosidase
4395842	syn	GT	MUL_3936	-	intermediary metabolism and respiration	1,4-alpha-glucan branching enzyme GlgB
4398225	syn	AG	MUL_3937	-	intermediary metabolism and respiration	thioredoxin
4398840	syn	CT	MUL_3938	-	lipid metabolism	acetyl-CoA acetyltransferase FadA4
4399103	syn	AG	MUL_3938	-	lipid metabolism	acetyl-CoA acetyltransferase FadA4
4399164	syn	TC	MUL_3938	-	lipid metabolism	acetyl-CoA acetyltransferase FadA4
4399517	hon	GA	MUL_3938	-	lipid metabolism	acetyl-CoA acetyltransferase FadA4
4403569	psd	AC	MUL_3942	-	intermediary metabolism and respiration	N-term adenylyl cyclase pseudogene
4409357	syn	TC	MUL_3946	-	information pathways	methylated-DNA-protein-cysteine methyltransferase Out
4411055	Int	AG	62	MUL_3950	cell wall and cell processes	UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurA
4411558	Int	AG	-	-	intermediary metabolism and respiration	cobalamin adenosyltransferase
4415163	Int	AG	-	-	ATP synthase epsilon chain AtpC	ATP synthase epsilon chain AtpC
4416692	syn	CT	MUL_3951	6	ATP synthase alpha chain AtpA	ATP synthase alpha chain AtpA
4417578	Int	AG	-	-	ATP synthase delta chain AtpH	ATP synthase delta chain AtpH
4422008	syn	AC	MUL_3956	-	ATP synthase epsilon chain AtpC	ATP synthase epsilon chain AtpC
4422483	syn	CG	MUL_3957	-	ATP synthase delta chain AtpH	ATP synthase delta chain AtpH
4422525	syn	AG	MUL_3957	-	ATP synthase delta chain AtpH	ATP synthase delta chain AtpH
4422753	syn	CG	MUL_3957	-	ATP synthase delta chain AtpH	ATP synthase delta chain AtpH
4423151	hon	AC	MUL_3957	-	ATP synthase delta chain AtpH	ATP synthase delta chain AtpH
4425275	hon	GC	MUL_3961	-	cell wall and cell processes	conserved hypothetical membrane protein
4428316	syn	AG	MUL_3964	-	intermediary metabolism and respiration	modification methylase HemK
4428629	hon	TC	MUL_3964	-	intermediary metabolism and respiration	modification methylase HemK
4429539	syn	CA	MUL_3965	-	information pathways	peptide chain release factor 1 PrfA
4430831	syn	TC	MUL_3967	-	information pathways	transcription termination factor Rho
4430897	syn	TG	MUL_3967	-	information pathways	transcription termination factor Rho
4431230	syn	TC	MUL_3967	-	information pathways	transcription termination factor Rho
4431317	syn	TC	MUL_3967	-	information pathways	transcription termination factor Rho
4433197	syn	GA	MUL_3968	-	intermediary metabolism and respiration	homoserine kinase ThrB
4433905	syn	AG	MUL_3969	-	intermediary metabolism and respiration	threonine synthase ThrC
4434269	syn	AG	MUL_3969	-	intermediary metabolism and respiration	threonine synthase ThrC
4436014	syn	CT	MUL_3971	-	intermediary metabolism and respiration	diaminopimelate decarboxylase LysA
4436335	syn	AG	MUL_3971	-	intermediary metabolism and respiration	diaminopimelate decarboxylase LysA
4437195	hon	CT	MUL_3971	-	intermediary metabolism and respiration	diaminopimelate decarboxylase LysA
4437367	hon	GA	MUL_3972	-	information pathways	arginyl-tRNA synthetase ArgS
4437533	hon	CT	MUL_3972	-	information pathways	arginyl-tRNA synthetase ArgS
4439265	Int	TA	-	-	PE/PPE	PE-PGRS family protein
4440003	Int	AG	74	MUL_3975	intermediary metabolism and respiration	pyridoxamine 5'-phosphate oxidoreductase-related protein
4443975	hon	TG	MUL_3977	-	conserved hypotheticals	conserved hypothetical protein
4444140	Int	TC	79	MUL_3978	conserved hypotheticals	conserved hypothetical protein
4444141	Int	CT	78	MUL_3978	conserved hypotheticals	conserved hypothetical protein
4444243	syn	AG	MUL_3978	-	conserved hypotheticals	conserved hypothetical protein
4444467	hon	AG	MUL_3978	-	conserved hypotheticals	conserved hypothetical protein
4445258	syn	AC	MUL_3979	-	intermediary metabolism and respiration	haloalkane dehalogenase DhaA
4445833	syn	TG	MUL_3980	-	intermediary metabolism and respiration	peptidase S15
4446568	syn	AG	MUL_3980	-	intermediary metabolism and respiration	peptidase S15
4450262	hon	AT	MUL_3984	-	cell wall and cell processes	conserved hypothetical membrane permease
4453358	hon	AG	MUL_3986	-	intermediary metabolism and respiration	adenylyl cyclase
4453628	hon	CG	MUL_3987	-	cell wall and cell processes	conserved hypothetical secreted protein
4454037	Int	CG	64	MUL_3988	cell wall and cell processes	N-term conserved hypothetical membrane protein pseudogene
4456044	psd	TC	MUL_3989	-	N-term conserved hypothetical transport protein	N-term conserved hypothetical transport protein pseudogene
4457848	Int	TC	97	MUL_3991	intermediary metabolism and respiration	flavin-dependent oxidoreductase
4457984	syn	AG	MUL_3991	-	intermediary metabolism and respiration	flavin-dependent oxidoreductase
4458293	syn	GA	MUL_3991	-	intermediary metabolism and respiration	flavin-dependent oxidoreductase
4458317	syn	TC	MUL_3991	-	intermediary metabolism and respiration	flavin-dependent oxidoreductase
4458404	syn	TC	MUL_3991	-	intermediary metabolism and respiration	flavin-dependent oxidoreductase
4458406	syn	GA	MUL_3991	-	intermediary metabolism and respiration	flavin-dependent oxidoreductase
4458641	syn	AG	MUL_3991	-	intermediary metabolism and respiration	flavin-dependent oxidoreductase
4458874	hon	TG	MUL_3992	-	intermediary metabolism and respiration	glyoxalase GlaB_2
4459319	Int	TA	59	MUL_3993	conserved hypotheticals	conserved hypothetical protein
4460277	Int	TC	66	MUL_3995	intermediary metabolism and respiration	bifunctional enzyme CysN/CysC: sulfate adenylyltransferase (subunit 1) + adenylylsulfate kinase
4460481	syn	AG	MUL_3995	-	intermediary metabolism and respiration	bifunctional enzyme CysN/CysC: sulfate adenylyltransferase (subunit 1) + adenylylsulfate kinase
4462489	syn	GA	MUL_3996	-	intermediary metabolism and respiration	sulfate adenylyltransferase subunit 2 CysD
4463059	syn	GA	MUL_3996	-	intermediary metabolism and respiration	sulfate adenylyltransferase subunit 2 CysD
4466597	syn	CG	MUL_4001	-	cell wall and cell processes	oligoopeptide-transport ATP-binding protein ABC transporter OppD
4467035	syn	GC	MUL_4001	-	cell wall and cell processes	oligoopeptide-transport ATP-binding protein ABC transporter OppD
4467581	syn	AG	MUL_4001	-	cell wall and cell processes	oligoopeptide-transport ATP-binding protein ABC transporter OppD
4468878	hon	GC	MUL_4002	-	cell wall and cell processes	periplasmic oligopeptide-binding lipoprotein OppA
4471832	syn	TC	MUL_4004	-	intermediary metabolism and respiration	dehydrogenase fad flavoprotein Gmc oxidoreductase
4472534	syn	AG	MUL_4004	-	intermediary metabolism and respiration	dehydrogenase fad flavoprotein Gmc oxidoreductase
4473924	syn	AG	MUL_4005	-	conserved hypotheticals	conserved hydrolase
4474048	hon	TC	MUL_4005	-	conserved hypotheticals	conserved hydrolase
4474880	hon	TG	MUL_4005	-	conserved hypotheticals	conserved hydrolase
4475187	syn	CA	MUL_4005	-	conserved hypotheticals	conserved hydrolase

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4475541	syn	AG	MUL_4005	-	conserved hypotheticals	conserved hydrolase
4480053	non	AG	MUL_4010	-	cell wall and cell processes	transmembrane ATP-binding protein ABC transporter
4480413	non	TG	MUL_4010	-	cell wall and cell processes	transmembrane ATP-binding protein ABC transporter
4482307	syn	AG	MUL_4011	-	cell wall and cell processes	transmembrane ATP-binding protein ABC transporter
448296	int	AG		100 MUL_4012	PE/PPe	N-term PE-PGRS family protein pseudogene
4484382	int	GA		14 MUL_4012	PE/PPe	N-term PE-PGRS family protein pseudogene
4484891	int	AG		-		
4488680	syn	AG	MUL_4018	-	regulatory proteins	transcriptional regulatory protein EmbR
4489307	syn	AG	MUL_4018	-	regulatory proteins	transcriptional regulatory protein EmbR
4489454	syn	AC	MUL_4018	-	regulatory proteins	transcriptional regulatory protein EmbR
4489851	int	TC		55 MUL_4018	regulatory proteins	transcriptional regulatory protein EmbR
4491149	psd	TG	MUL_4019	-	regulatory proteins	C-term transmembrane serine/threonine-protein kinase H PknH pseudogene
4491674	psd	TG	MUL_4019	-	regulatory proteins	C-term transmembrane serine/threonine-protein kinase H PknH pseudogene
4491956	int	TG		6 MUL_4019	regulatory proteins	C-term transmembrane serine/threonine-protein kinase H PknH pseudogene
4492587	non	GA	MUL_4020	-	regulatory proteins	transcriptional regulatory protein (LysR family)
4494474	syn	AG	MUL_4022	-	intermediary metabolism and respiration	conserved dehydratase
4494966	non	TC	MUL_4023	-	intermediary metabolism and respiration	acyl-CoA hydrolase/transferase
4495071	non	AG	MUL_4023	-	intermediary metabolism and respiration	acyl-CoA hydrolase/transferase
4496128	syn	TC	MUL_4024	-	lipid metabolism	acyl-CoA dehydrogenase FadE3
4505560	int	CA		55 MUL_4024	cell wall and cell processes	conserved membrane protein
4505565	int	GA		61 MUL_4024	cell wall and cell processes	conserved membrane protein
4508073	non	GC	MUL_4038	-	cell wall and cell processes	conserved hypothetical membrane protein
4508622	syn	TG	MUL_4038	-	cell wall and cell processes	conserved hypothetical membrane protein
4508885	int	TG		95 MUL_4040	cell wall and cell processes	conserved hypothetical membrane protein CpsA
4509193	syn	TC	MUL_4040	-	cell wall and cell processes	conserved hypothetical membrane protein CpsA
4509253	syn	AC	MUL_4040	-	cell wall and cell processes	conserved hypothetical membrane protein CpsA
4512378	non	TC	MUL_4043	-	cell wall and cell processes	conserved hypothetical membrane protein CpsA
4512770	syn	AG	MUL_4044	-	lipid metabolism	acyl carrier protein
4513327	non	TG	MUL_4044	-	lipid metabolism	acyl-coenzyme A synthetase
4514277	int	CG		102 MUL_4044	lipid metabolism	acyl-coenzyme A synthetase
4514952	non	GC	MUL_4045	-	intermediary metabolism and respiration	8-amino-7-oxononanoate synthase BioF2
4515023	psd	CG	MUL_4046	-	lipid metabolism	C-term enoyl-CoA hydratase EchA13 1 pseudogene
4515962	psd	AC	MUL_4046	-	lipid metabolism	C-term enoyl-CoA hydratase EchA13 1 pseudogene
4516231	psd	CG	MUL_4046	-	lipid metabolism	N-term enoyl-CoA hydratase EchA13 1 pseudogene
4516231	psd	CG	MUL_4046	-	lipid metabolism	C-term enoyl-CoA hydratase EchA13 1 pseudogene
4519315	psd	GA	MUL_4049	-	cell wall and cell processes	C-term conserved transmembrane transport protein pseudogene
4524032	non	AG	MUL_4057	-		MCE-family protein Mcf4F
4530284	syn	AG	MUL_4061	-		MCE-family protein Mcf4B
4540313	non	AG	MUL_4071	-	conserved hypotheticals	conserved hypothetical protein
4545009	syn	AG	MUL_4075	-	lipid metabolism	fatty-acid-CoA ligase FadD19 1
4545897	syn	AG	MUL_4076	-	lipid metabolism	enoyl-CoA hydratase EchA19
4546102	syn	TC	MUL_4076	-	lipid metabolism	enoyl-CoA hydratase EchA19
4546237	non	GA	MUL_4076	-	lipid metabolism	enoyl-CoA hydratase EchA19
4559378	syn	TC	MUL_4089	-	intermediary metabolism and respiration	conserved hypothetical oxidoreductase
4559501	non	GA	MUL_4089	-	intermediary metabolism and respiration	conserved hypothetical oxidoreductase
4560421	syn	TC	MUL_4090	-	conserved hypotheticals	conserved hypothetical protein
4563229	non	CT	MUL_4093	-	conserved hypotheticals	conserved hypothetical protein
4564879	syn	AG	MUL_4094	-	intermediary metabolism and respiration	glutamate--cysteine ligase Gcs2
4565227	syn	AG	MUL_4094	-	intermediary metabolism and respiration	glutamate--cysteine ligase Gcs2
4565600	non	TG	MUL_4094	-	intermediary metabolism and respiration	glutamate--cysteine ligase Gcs2
4566016	syn	CT	MUL_4094	-	intermediary metabolism and respiration	glutamate--cysteine ligase Gcs2
4569772	syn	CG	MUL_4098	-	intermediary metabolism and respiration	conserved hypothetical dehydrogenase
4571189	syn	GT	MUL_4099	-	intermediary metabolism and respiration	conserved hypothetical dehydratase (MaoC-like)
4571318	syn	TC	MUL_4099	-	intermediary metabolism and respiration	conserved hypothetical dehydratase (MaoC-like)
4572823	int	TC		84 MUL_4101	lipid metabolism	acyl-CoA acetyltransferase (PaaJ-like) Ltp2 1
4572847	int	TG		71 MUL_4100	conserved hypotheticals	conserved hypothetical protein
4573753	syn	TC	MUL_4101	-	lipid metabolism	acyl-CoA acetyltransferase (PaaJ-like) Ltp2 1
4574079	syn	AG	MUL_4102	-	conserved hypotheticals	conserved hypothetical protein
4575126	syn	AG	MUL_4103	-	conserved hypotheticals	conserved hypothetical protein
4575193	non	TC	MUL_4103	-	conserved hypotheticals	conserved hypothetical protein
4575402	non	CT	MUL_4103	-	conserved hypotheticals	conserved hypothetical protein
4575628	syn	AC	MUL_4104	-	lipid metabolism	acyl-CoA dehydrogenase FadE29
4575961	syn	CT	MUL_4104	-	lipid metabolism	acyl-CoA dehydrogenase FadE29
4578716	syn	AG	MUL_4106	-	intermediary metabolism and respiration	cytochrome P450 125A7 Cyp125A7
4578794	syn	AC	MUL_4106	-	intermediary metabolism and respiration	cytochrome P450 125A7 Cyp125A7
4578809	syn	GA	MUL_4106	-	intermediary metabolism and respiration	cytochrome P450 125A7 Cyp125A7
4579110	syn	CG	MUL_4107	-	lipid metabolism	acyl-CoA acetyltransferase FadA5
4580028	non	GC	MUL_4107	-	lipid metabolism	acyl-CoA acetyltransferase FadA5
4580708	non	AT	MUL_4109	-	conserved hypotheticals	conserved hypothetical protein
4582190	syn	AG	MUL_4111	-	intermediary metabolism and respiration	short-chain-type dehydrogenase/reductase
4582881	non	TG	MUL_4111	-	intermediary metabolism and respiration	short-chain-type dehydrogenase/reductase
4588233	syn	GA	MUL_4116	-	intermediary metabolism and respiration	2-nitropropane dioxygenase
4588477	non	CG	MUL_4116	-	intermediary metabolism and respiration	2-nitropropane dioxygenase
4588871	non	CT	MUL_4117	-	intermediary metabolism and respiration	electron transfer protein FdxB
4590716	syn	AG	MUL_4117	-	intermediary metabolism and respiration	electron transfer protein FdxB
4597783	int	CT		70 MUL_4124	intermediary metabolism and respiration	short chain dehydrogenase
4597787	int	CT		66 MUL_4124	intermediary metabolism and respiration	short chain dehydrogenase
4597791	int	C-		62 MUL_4124	intermediary metabolism and respiration	short chain dehydrogenase
4597802	int	AG		51 MUL_4124	intermediary metabolism and respiration	short chain dehydrogenase
4598162	syn	GA	MUL_4124	-	intermediary metabolism and respiration	short chain dehydrogenase
4598167	syn	AG	MUL_4124	-	intermediary metabolism and respiration	short chain dehydrogenase
4598177	syn	AG	MUL_4124	-	intermediary metabolism and respiration	short chain dehydrogenase
4598624	syn	TC	MUL_4124	-	intermediary metabolism and respiration	short chain dehydrogenase
4600216	syn	AC	MUL_4126	-	lipid metabolism	fatty-acid-CoA ligase FadD3
4600331	non	AG	MUL_4126	-	lipid metabolism	fatty-acid-CoA ligase FadD3
4601044	syn	TC	MUL_4126	-	lipid metabolism	fatty-acid-CoA ligase FadD3
4604050	non	GC	MUL_4129	-	lipid metabolism	acyl-CoA dehydrogenase FadE33
4606340	non	CG	MUL_4131	-	intermediary metabolism and respiration	arylamine N-acetyltransferase Nat
4609036	non	AT	MUL_4135	-	cell wall and cell processes	conserved hypothetical peptidase M48 like-protein
4610492	syn	TC	MUL_4137	-	cell wall and cell processes	conserved hypothetical secreted protein
4610632	non	GA	MUL_4137	-	cell wall and cell processes	conserved hypothetical secreted protein
4611252	non	AG	MUL_4138	-	intermediary metabolism and respiration	conserved hypothetical oxidase

SNP position	SNP type	Nucleotide change <ref><snp>	Distance to nearest locus	Nearby Locus	Functional group	Product
4612532	syn	CT	MUL_4140	-	intermediary metabolism and respiration	2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydrolase BphD
4613380	syn	AC	MUL_4141	-	intermediary metabolism and respiration	acyl-CoA dehydrogenase
4616497	non	AC	MUL_4144	-	lipid metabolism	acyl-CoA dehydrogenase FadE34
4617077	syn	TC	MUL_4144	-	lipid metabolism	acyl-CoA dehydrogenase FadE34
4617425	syn	AG	MUL_4144	-	lipid metabolism	acyl-CoA dehydrogenase FadE34
4619922	non	TC	MUL_4146	-	regulatory proteins	transcriptional regulatory protein (PurR family)
4622053	syn	GA	MUL_4148	-	cell wall and cell processes	ATP component of an ABC-type transport system
4622391	syn	GA	MUL_4149	-	cell wall and cell processes	permease component of an ABC-type transporter
4622421	syn	GA	MUL_4149	-	cell wall and cell processes	permease component of an ABC-type transporter
4624621	syn	CT	MUL_4151	-	cell wall and cell processes	conserved hypothetical lipoprotein
4625952	syn	GA	MUL_4153	-	intermediary metabolism and respiration	conserved hypothetical Zn-dependent hydrolase
4628061	syn	TC	MUL_4155	-	information pathways	tRNA/rRNA methyltransferase
4628516	non	AG	MUL_4155	-	information pathways	tRNA/rRNA methyltransferase
4629049	non	AG	MUL_4156	-	information pathways	cysteinyl-tRNA synthetase tLysS1
4630726	non	AC	MUL_4158	-	intermediary metabolism and respiration	4-diphosphocidyl-2C-methyl-D-erythritol synthase IspD
4633792	psd	GA	MUL_4161	-	information pathways	C-term DNA repair protein RadA_pseudogene
4634857	syn	TC	MUL_4162	-	information pathways	conserved hypothetical RuvA-like protein
4636251	Int	TC	69 MUL_4164	intermediary metabolism and respiration	carbonic anhydrase	
4637337	syn	AC	MUL_4165	information pathways	adenine glycosylase MutY	
4639605	syn	AG	MUL_4168	cell wall and cell processes	conserved hypothetical lipoprotein LpoF	
4640325	non	CG	MUL_4168	cell wall and cell processes	conserved hypothetical lipoprotein LpoF	
4641283	syn	AG	MUL_4170	cell wall and cell processes	conserved integral membrane transport protein	
4650406	syn	AG	MUL_4178	intermediary metabolism and respiration	ATP-dependent protease ATP-binding subunit CipC1	
4653944	syn	TC	MUL_4181	-	information pathways	tysyl-tRNA synthetase tLysS
4653988	non	AG	MUL_4181	-	information pathways	tysyl-tRNA synthetase tLysS
4656178	syn	AG	MUL_4183	-	intermediary metabolism and respiration	aspartate 1-decarboxylase precursor Pand
4656465	syn	GC	MUL_4184	-	intermediary metabolism and respiration	partate- α -beta-alanine ligase PanC
4658235	non	TC	MUL_4186	-	cell wall and cell processes	conserved transmembrane protein rich in alanine, arginine and proline
4659393	syn	GC	MUL_4186	-	cell wall and cell processes	conserved transmembrane protein rich in alanine, arginine and proline
4660472	syn	TC	MUL_4188	-	intermediary metabolism and respiration	2-amino-4-hydroxy-6-hydroxymethylidihydropyridine pyrophosphokinase FolK
4660475	non	TA	MUL_4188	-	intermediary metabolism and respiration	2-amino-4-hydroxy-6-hydroxymethylidihydropyridine pyrophosphokinase FolK
4660970	non	CG	MUL_4189	-	intermediary metabolism and respiration	dihydropteropterin aldolase FolB
4661097	non	CT	MUL_4190	-	intermediary metabolism and respiration	dihydropteroate synthase 1 FolP1
4663487	syn	GA	MUL_4192	-	membrane-bound protease RtsH	
4666163	syn	AG	MUL_4194	-	intermediary metabolism and respiration	monoxygenase
4667865	Int	TC	142 MUL_4196	monooxygenase		
4668335	Int	CT		PE/PPE	PE family protein	
4672369	syn	CG	MUL_4201	cell wall and cell processes	cell cycle protein MesJ	
4673875	non	CG	MUL_4202	conserved hypotheticals	conserved hypothetical protein	
4676148	syn	TC	MUL_4204	intermediary metabolism and respiration	inorganic pyrophosphatase Ppa	
4676871	syn	TC	MUL_4205	cell wall and cell processes	conserved hypothetical membrane protein	
4679887	syn	AG	MUL_4207	cell wall and cell processes	conserved hypothetical membrane protein	
4681211	syn	AG	MUL_4209	cell wall and cell processes	conserved hypothetical membrane protein	
4681349	Int	CG	cell wall and cell processes	conserved hypothetical membrane protein		
4692102	syn	CA	MUL_4220	conserved hypotheticals	conserved protein	
4692871	syn	AG	MUL_4221	12 MUL_4209	cell wall and cell processes	adenylate cyclase
4693399	syn	AG	MUL_4221		cell wall and cell processes	adenylate cyclase
4698351	psd	CG	MUL_4225		information pathways	N-term DEAD/DEAH box helicase pseudogene
4699225	psd	CG	MUL_4225		information pathways	mid-section DEAD/DEAH box helicase pseudogene
4699805	psd	AC	MUL_4225		information pathways	mid-section DEAD/DEAH box helicase pseudogene
4700788	Int	AG	90 MUL_4226	conserved hypotheticals	conserved protein	
4701069	syn	TC	MUL_4226	conserved hypotheticals	conserved protein	
4701129	syn	CT	MUL_4226	conserved hypotheticals	conserved protein	
4701434	non	AG	MUL_4226	conserved hypotheticals	conserved protein	
4701706	non	AG	MUL_4226	conserved hypotheticals	conserved protein	
4702687	syn	AC	MUL_4229	1 MUL_4233	conserved hypotheticals	conserved hypothetical membrane protein
4702753	syn	AC	MUL_4229		conserved hypotheticals	conserved hypothetical membrane protein
4703778	non	CA	MUL_4231		cell wall and cell processes	conserved hypothetical membrane protein
4704671	non	TC	MUL_4232		conserved hypotheticals	conserved hypothetical protein
4705195	non	AG	MUL_4232		conserved hypotheticals	conserved hypothetical protein
4705537	syn	AG	MUL_4233		conserved hypotheticals	conserved hypothetical protein
4706244	non	AG	MUL_4233		conserved hypotheticals	conserved hypothetical protein
4706522	Int	CT	1 MUL_4233	conserved hypotheticals	conserved hypothetical protein	
4706642	Int	GC	121 MUL_4233	conserved hypotheticals	conserved hypothetical protein	
4706820	Int	AG	121 MUL_4233	conserved hypotheticals	conserved hypotheticals	
4708136	non	AG	MUL_4235	unknown	hypothetical protein	
4710966	syn	AG	MUL_4238	cell wall and cell processes	dipeptide-transport integral membrane protein ABC transporter DppC	
4711179	syn	AT	MUL_4238	cell wall and cell processes	dipeptide-transport integral membrane protein ABC transporter DppC	
4713151	syn	GA	MUL_4240	cell wall and cell processes	periplasmic dipeptide-binding lipoprotein DppA	
4714594	non	TA	MUL_4241	intermediary metabolism and respiration	acetyl-coenzyme A synthetase Acs	
4715164	syn	CA	MUL_4241	intermediary metabolism and respiration	acetyl-coenzyme A synthetase Acs	
4716148	non	GC	MUL_4241	intermediary metabolism and respiration	acetyl-coenzyme A synthetase Acs	
4716286	syn	AG	MUL_4241	intermediary metabolism and respiration	acetyl-coenzyme A synthetase Acs	
4716499	syn	AG	MUL_4242	intermediary metabolism and respiration	conserved hypothetical protease	
4717500	syn	TC	MUL_4243	93 MUL_4257	cell wall and cell processes	conserved membrane protein
4720972	syn	TC	MUL_4247		cell wall and cell processes	membrane-anchored thioredoxin-like protein
4722573	syn	TC	MUL_4249		cell wall and cell processes	conserved hypothetical membrane protein
4723437	non	TG	MUL_4251		intermediary metabolism and respiration	conserved hypothetical Zn-dependent hydrolase
4723565	syn	TC	MUL_4251		intermediary metabolism and respiration	conserved hypothetical Zn-dependent hydrolase
4724222	syn	GA	MUL_4251		intermediary metabolism and respiration	conserved hypothetical Zn-dependent hydrolase
4724272	syn	CT	MUL_4252		intermediary metabolism and respiration	conserved protein with endoribonuclease L-PSP domain
4724461	syn	GC	MUL_4252		intermediary metabolism and respiration	conserved protein with endoribonuclease L-PSP domain
4724497	syn	AG	MUL_4252		intermediary metabolism and respiration	conserved protein with endoribonuclease L-PSP domain
4724539	syn	AG	MUL_4252		intermediary metabolism and respiration	conserved protein with endoribonuclease L-PSP domain
4726899	syn	CT	MUL_4255		intermediary metabolism and respiration	anion transporter ATPase
4727902	Int	CA	93 MUL_4257	intermediary metabolism and respiration	bifunctional membrane-associated penicillin-binding protein 1A/1B PonA2	
4728510	syn	CG	MUL_4257	cell wall and cell processes	bifunctional membrane-associated penicillin-binding protein 1A/1B PonA2	
4728753	syn	CG	MUL_4257	cell wall and cell processes	bifunctional membrane-associated penicillin-binding protein 1A/1B PonA2	
4728840	syn	TC	MUL_4257	cell wall and cell processes	bifunctional membrane-associated penicillin-binding protein 1A/1B PonA2	
4729410	syn	AG	MUL_4257	cell wall and cell processes	bifunctional membrane-associated penicillin-binding protein 1A/1B PonA2	
4730552	syn	AG	MUL_4258	cell wall and cell processes	conserved membrane protein	

SNP position	SNP type	Nucleotide change <ref><snp>	Distance to nearest locus	Nearby Locus	Functional group	Product
4732309	syn	TC	MUL_4259	-	intermediary metabolism and respiration	cysteine synthase CysK
4734302	psd	CG	MUL_4262	-	intermediary metabolism and respiration	C-term cytochrome P450_137A2 Cyo137A2P pseudogene
4734302	psd	CG	MUL_4262	-	intermediary metabolism and respiration	N-term cytochrome P450_137A2 Cyo137A2P pseudogene
4735159	syn	AG	MUL_4264	-	cell wall and cell processes	conserved hypothetical membrane protein
4736851	Int	CG	48 MUL_4266	-	conserved hypotheticals	C-term conserved hypothetical protein pseudogene
4737220	psd	-G	MUL_4267	-	intermediary metabolism and respiration	C-term formate dehydrogenase alpha subunit selenocysteine-containing pseudogene
4737220	psd	-G	MUL_4267	-	intermediary metabolism and respiration	N-term formate dehydrogenase alpha subunit selenocysteine-containing pseudogene
4738042	psd	AG	MUL_4268	-	intermediary metabolism and respiration	N-term formate dehydrogenase beta subunit selenocysteine-containing pseudogene
4739007	psd	TC	MUL_4268	-	intermediary metabolism and respiration	mid-section formate dehydrogenase beta subunit selenocysteine-containing pseudogene
4743549	syn	CG	MUL_4272	-	cell wall and cell processes	conserved membrane protein
4743761	non	CA	MUL_4272	-	cell wall and cell processes	conserved membrane protein
4745853	syn	CT	MUL_4275	-	regulatory proteins	methanol dehydrogenase transcriptional regulatory protein MoxR2
4749941	Int	TC	42 MUL_4278	-	cell wall and cell processes	conserved hypothetical membrane protein
4749991	non	TC	MUL_4279	-	regulatory proteins	Padf-like transcriptional regulatory protein
4749992	non	CT	MUL_4279	-	regulatory proteins	Padf-like transcriptional regulatory protein
4753976	syn	TC	MUL_4281	-	intermediary metabolism and respiration	glycerol kinase GlkP
4754591	syn	GA	MUL_4281	-	intermediary metabolism and respiration	conserved hypotheticals
4755378	psd	GA	MUL_4282	-	conserved hypotheticals	N-term conserved hypothetical protein pseudogene
4755378	psd	GA	MUL_4282	-	conserved hypotheticals	C-term conserved hypothetical protein pseudogene
4755435	psd	GC	MUL_4282	-	conserved hypotheticals	C-term conserved hypothetical protein pseudogene
4755563	psd	GA	MUL_4282	-	conserved hypotheticals	N-term conserved hypothetical protein pseudogene
4755563	psd	GA	MUL_4282	-	conserved hypotheticals	C-term conserved hypothetical protein pseudogene
4755877	psd	GA	MUL_4282	-	conserved hypotheticals	C-term conserved hypothetical protein pseudogene
4755895	psd	GC	MUL_4282	-	conserved hypotheticals	C-term conserved hypothetical protein pseudogene
4756076	psd	AG	MUL_4282	-	conserved hypotheticals	C-term conserved hypothetical protein pseudogene
4756198	psd	GC	MUL_4282	-	conserved hypotheticals	C-term conserved hypothetical protein pseudogene
4759382	syn	AG	MUL_4286	-	conserved hypotheticals	conserved hypothetical protein
4762591	syn	TG	MUL_4286	-	conserved hypotheticals	conserved hypothetical protein
4762563	non	TC	MUL_4290	-	cell wall and cell processes	conserved hypothetical secreted protein
4763133	syn	TC	MUL_4291	-	catalase KatE	catalase KatE
4764738	Int	CG	94 MUL_4291	-	catalase KatE	catalase KatE
4767011	syn	TC	MUL_4295	-	cell wall and cell processes	conserved hypothetical secreted protein
4767261	non	CG	MUL_4295	-	cell wall and cell processes	conserved hypothetical secreted protein
4767710	syn	TG	MUL_4295	-	cell wall and cell processes	conserved hypothetical secreted protein
4767740	syn	AG	MUL_4295	-	cell wall and cell processes	conserved hypothetical secreted protein
4767899	syn	TC	MUL_4295	-	cell wall and cell processes	conserved hypothetical secreted protein
4767981	non	AG	MUL_4295	-	cell wall and cell processes	conserved hypothetical secreted protein
4767988	non	AC	MUL_4295	-	cell wall and cell processes	conserved hypothetical secreted protein
4768758	syn	CG	MUL_4296	-	intermediary metabolism and respiration	aspartate-semialdehyde dehydrogenase Asd
4777431	non	GC	MUL_4300	-	intermediary metabolism and respiration	2-isopropylmalate synthase LeuA
4779684	Int	CT	72 MUL_4302	-	cell wall and cell processes	conserved hypothetical membrane protein
4780052	syn	AG	MUL_4303	-	information pathways	DNA polymerase III (epsilon subunit) DnaQ
4780390	non	TC	MUL_4303	-	information pathways	DNA polymerase III (epsilon subunit) DnaQ
4781540	non	AC	MUL_4304	-	cell wall and cell processes	UDP-N-acetylglucosamine tripeptidase synthase
4783212	non	CA	MUL_4306	-	information pathways	recombination protein RecR
4785457	syn	GC	MUL_4310	-	intermediary metabolism and respiration	conserved hypothetical dehydrogenase
4785553	syn	GA	MUL_4310	-	intermediary metabolism and respiration	conserved hypothetical dehydrogenase
4785610	syn	CT	MUL_4310	-	intermediary metabolism and respiration	conserved hypothetical dehydrogenase
4785668	non	GA	MUL_4310	-	intermediary metabolism and respiration	conserved hypothetical dehydrogenase
4785706	syn	CT	MUL_4310	-	intermediary metabolism and respiration	conserved hypothetical dehydrogenase
4786304	non	AG	MUL_4310	-	intermediary metabolism and respiration	conserved hypothetical dehydrogenase
4786342	syn	CT	MUL_4310	-	intermediary metabolism and respiration	conserved hypothetical dehydrogenase
4788111	non	AG	MUL_4312	-	cell wall and cell processes	conserved hypothetical membrane protein
4790427	syn	AG	MUL_4315	-	information pathways	DNA polymerase III (subunit gamma/tau) DnaZK
4792042	syn	AG	MUL_4316	-	regulatory proteins	conserved transcriptional regulator
4792159	syn	GC	MUL_4316	-	regulatory proteins	conserved transcriptional regulator
4792204	syn	TG	MUL_4316	-	regulatory proteins	conserved transcriptional regulator
4792354	syn	AG	MUL_4316	-	regulatory proteins	conserved transcriptional regulator
4793165	syn	CG	MUL_4318	-	cell wall and cell processes	conserved membrane protein
4793187	syn	AC	MUL_4318	-	cell wall and cell processes	conserved membrane protein
4793364	syn	AG	MUL_4318	-	cell wall and cell processes	conserved membrane protein
4794299	syn	TC	MUL_4319	-	lipid metabolism	enoyl-CoA hydratase EchA3 1
4794815	syn	GC	MUL_4320	-	cell wall and cell processes	19 kDa lipoprotein antigen precursor LpqH-like
4794983	syn	TC	MUL_4320	-	cell wall and cell processes	19 kDa lipoprotein antigen precursor LpqH-like
4795286	psd	GT	MUL_4321	-	conserved hypotheticals	N-term conserved hypothetical protein pseudogene
4795450	psd	TC	MUL_4321	-	conserved hypotheticals	N-term conserved hypothetical protein pseudogene
4795523	psd	AG	MUL_4321	-	conserved hypotheticals	N-term conserved hypothetical protein pseudogene
4795585	psd	GA	MUL_4321	-	conserved hypotheticals	N-term conserved hypothetical protein pseudogene
4795860	psd	CG	MUL_4321	-	conserved hypotheticals	mid-section conserved hypothetical protein pseudogene
4795914	psd	TA	MUL_4321	-	conserved hypotheticals	mid-section conserved hypothetical protein pseudogene
4796002	psd	GC	MUL_4321	-	conserved hypotheticals	mid-section conserved hypothetical protein pseudogene
4796096	psd	TC	MUL_4321	-	conserved hypotheticals	mid-section conserved hypothetical protein pseudogene
4796178	psd	GA	MUL_4321	-	conserved hypotheticals	mid-section conserved hypothetical protein pseudogene
4796670	Int	GT	30 MUL_4321	-	conserved hypotheticals	mid-section conserved hypothetical protein pseudogene
4796682	Int	TG	42 MUL_4321	-	conserved hypotheticals	mid-section conserved hypothetical protein pseudogene
4797538	psd	GA	MUL_4322	-	conserved hypotheticals	C-term conserved hypothetical protein pseudogene
4797538	psd	GA	MUL_4322	-	conserved hypotheticals	N-term conserved hypothetical protein pseudogene
4797915	psd	GA	MUL_4322	-	conserved hypotheticals	C-term conserved hypothetical protein pseudogene
4798126	psd	CT	MUL_4323	-	conserved hypotheticals	C-term conserved hypothetical protein pseudogene
4798321	psd	TC	MUL_4323	-	conserved hypotheticals	C-term conserved hypothetical protein pseudogene
4798891	non	TG	MUL_4324	-	conserved hypotheticals	conserved hypothetical protein pseudogene
4798893	non	GA	MUL_4324	-	conserved hypotheticals	conserved hypothetical protein
4799012	non	GA	MUL_4324	-	conserved hypotheticals	conserved hypothetical protein
4799031	syn	GC	MUL_4324	-	conserved hypotheticals	conserved hypothetical protein
4799173	non	AG	MUL_4324	-	conserved hypotheticals	conserved hypothetical protein
4799232	syn	TC	MUL_4324	-	conserved hypotheticals	conserved hypothetical protein
4799413	non	GC	MUL_4324	-	conserved hypotheticals	conserved hypothetical protein
4799514	syn	CT	MUL_4324	-	conserved hypotheticals	conserved hypothetical protein
4799574	syn	GA	MUL_4324	-	conserved hypotheticals	conserved hypothetical protein
4799761	syn	TC	MUL_4324	-	conserved hypotheticals	conserved hypothetical protein
4799793	syn	AG	MUL_4324	-	conserved hypotheticals	conserved hypothetical protein

SNP position	SNP type	Nucleotide change <ref><snp>	Distance to nearest locus	Nearby Locus	Functional group	Product	
4799805	syn	AG	MUL_4324	-	conserved hypotheticals	conserved hypothetical protein	
4799892	syn	TC	MUL_4324	-	conserved hypotheticals	conserved hypothetical protein	
4799929	syn	TC	MUL_4324	-	conserved hypotheticals	conserved hypothetical protein	
4799987	syn	TC	MUL_4325	-	conserved hypotheticals	conserved hypothetical protein	
4800500	syn	TC	MUL_4325	-	conserved hypotheticals	conserved hypothetical protein	
4800519	non	AG	MUL_4325	-	conserved hypotheticals	conserved hypothetical protein	
4801080	non	AG	MUL_4325	-	conserved hypotheticals	conserved hypothetical protein	
4801121	int	AG	38_MUL_4326	cell wall and cell processes	N-term conserved hypothetical membrane protein_pseudogene		
4824113	int	CT	13_MUL_4349	lipid metabolism	long-chain-fatty-acid-CoA ligase FadD15_1		
4825041	syn	GC	MUL_4349	lipid metabolism	long-chain-fatty-acid-CoA ligase FadD15_1		
4825224	syn	AG	MUL_4349	lipid metabolism	long-chain-fatty-acid-CoA ligase FadD15_1		
4825365	syn	AG	MUL_4349	lipid metabolism	long-chain-fatty-acid-CoA ligase FadD15_1		
4826088	int	TC	100_MUL_4350	regulatory proteins	transcriptional regulatory protein (probably AraC/XylS-family)		
4827276	int	TG	69_MUL_4350	regulatory proteins	transcriptional regulatory protein (probably AraC/XylS-family)		
4827277	int	AC	70_MUL_4350	regulatory proteins	transcriptional regulatory protein (probably AraC/XylS-family)		
4828536	non	TC	MUL_4351	cell wall and cell processes	conserved hypothetical membrane protein		
4828787	syn	GA	MUL_4352	-	intermediary metabolism and respiration	monooxygenase-like flavoprotein	
4830674	non	TC	MUL_4353	-	conserved hypotheticals	conserved hypothetical protein	
4831430	non	AG	MUL_4353	-	conserved hypotheticals	conserved hypothetical protein	
4831532	syn	TC	MUL_4353	-	conserved hypotheticals	conserved hypothetical protein	
4831623	syn	CT	MUL_4354	lipid metabolism	short chain dehydrogenase		
4831632	syn	CT	MUL_4354	lipid metabolism	short chain dehydrogenase		
4832297	non	GC	MUL_4354	lipid metabolism	short chain dehydrogenase		
4832775	non	TC	MUL_4355	intermediary metabolism and respiration	D-3-phosphoglycerate dehydrogenase SerA4		
4832911	syn	GC	MUL_4355	intermediary metabolism and respiration	D-3-phosphoglycerate dehydrogenase SerA4		
4833310	syn	GC	MUL_4355	intermediary metabolism and respiration	D-3-phosphoglycerate dehydrogenase SerA4		
4833391	syn	AC	MUL_4355	intermediary metabolism and respiration	D-3-phosphoglycerate dehydrogenase SerA4		
4833797	syn	AC	MUL_4356	lipid metabolism	nri-ribosomal peptide synthetase		
4833959	syn	AG	MUL_4356	lipid metabolism	nri-ribosomal peptide synthetase		
4838886	syn	TA	MUL_4358	-	conserved hypotheticals	conserved hypothetical protein	
4839223	int	AC	44_MUL_4359	PE/PPe	PE family protein		
4844523	non	GA	MUL_4364	cell wall and cell processes	conserved hypothetical membrane protein		
4845058	int	AG	58_MUL_4365	conserved hypotheticals	conserved hypothetical protein		
4851427	syn	AG	MUL_4371	-	conserved hypotheticals	conserved protein	
4851502	syn	TC	MUL_4371	-	conserved hypotheticals	conserved protein	
4852048	non	CA	MUL_4372	-	intermediary metabolism and respiration	prephenate dehydrogenase TyrA	
4852478	syn	TG	MUL_4372	-	intermediary metabolism and respiration	prephenate dehydrogenase TyrA	
4852580	syn	TC	MUL_4372	-	intermediary metabolism and respiration	prephenate dehydrogenase TyrA	
4855469	psd	GC	MUL_4376	lipid metabolism	N-term osmoprotectant transport ATP-binding protein ABC transporter ProV_pseudogene		
4858269	psd	AG	MUL_4379	-	lipid metabolism	N-term acyl-CoA dehydrogenase FadE36_pseudogene	
4859092	syn	TC	MUL_4380	-	conserved hypotheticals	conserved hypothetical protein	
4859267	int	TC	89_MUL_4380	conserved hypotheticals	conserved hypothetical protein		
4859354	int	CT	-	-	-	-	
4859433	int	CT	-	-	-	-	
4863723	non	GC	MUL_4383	-	conserved hypotheticals	conserved hypothetical protein	
4865184	syn	TC	MUL_4384	-	intermediary metabolism and respiration	short-chain type dehydrogenase/reductase	
4865189	non	AG	MUL_4384	-	intermediary metabolism and respiration	short-chain type dehydrogenase/reductase	
4865487	syn	CT	MUL_4384	-	intermediary metabolism and respiration	short-chain type dehydrogenase/reductase	
4865896	non	CA	MUL_4385	-	lipid metabolism	acyl-CoA dehydrogenase FadE1_1	
4885298	syn	AG	MUL_4402	-	intermediary metabolism and respiration	O-methyltransferase	
4885303	non	TC	MUL_4402	-	intermediary metabolism and respiration	O-methyltransferase	
4887333	int	AG	59_MUL_4404	conserved hypotheticals	conserved hypothetical protein		
4887357	int	GA	83_MUL_4404	conserved hypotheticals	conserved hypothetical protein		
4887377	int	AG	103_MUL_4404	conserved hypotheticals	conserved hypothetical protein		
4887962	syn	GC	MUL_4407	-	intermediary metabolism and respiration	histidinol-phosphate aminotransferase HisC2	
4888046	syn	TC	MUL_4407	-	intermediary metabolism and respiration	histidinol-phosphate aminotransferase HisC2	
4889927	syn	GA	MUL_4410	-	intermediary metabolism and respiration	Fusion of enoyl-CoA hydratase EchA21 and lipase LipE	
4890341	syn	GT	MUL_4410	-	intermediary metabolism and respiration	Fusion of enoyl-CoA hydratase EchA21 and lipase LipE	
4898557	syn	GA	MUL_4416	-	intermediary metabolism and respiration	glucose-6-phosphate isomerase PgI	
4898560	syn	GA	MUL_4416	-	intermediary metabolism and respiration	glucose-6-phosphate isomerase PgI	
4899048	non	CT	MUL_4416	-	intermediary metabolism and respiration	glucose-6-phosphate isomerase PgI	
4899325	syn	AT	MUL_4416	-	intermediary metabolism and respiration	glucose-6-phosphate isomerase PgI	
4899541	non	AC	MUL_4416	-	intermediary metabolism and respiration	glucose-6-phosphate isomerase PgI	
4902830	int	GA	33_MUL_4420	PE/PPe	C-term PE-PGRS family protein_pseudogene		
4902983	int	CG	-	-	-	-	
4904095	int	AG	39_MUL_4420	PE/PPe	N-term PE-PGRS family protein_pseudogene		
4905928	int	TC	116_MUL_4421	PE/PPe	N-term PE-PGRS family protein_pseudogene		
4906276	syn	GC	MUL_4422	-	conserved hypotheticals	conserved hypothetical protein	
4906708	syn	CT	MUL_4422	-	conserved hypotheticals	conserved hypothetical protein	
4906797	syn	TG	MUL_4422	-	conserved hypotheticals	conserved hypothetical protein	
4908640	non	GA	MUL_4425	-	intermediary metabolism and respiration	monoxygenase	
4909731	int	TG	-	-	-	-	
4911032	psd	CA	MUL_4428	-	intermediary metabolism and respiration	N-term oxidoreductase_pseudogene	
4911245	psd	AT	MUL_4428	-	intermediary metabolism and respiration	N-term oxidoreductase_pseudogene	
4911760	syn	AG	MUL_4429	-	lipid metabolism	enoyl-CoA hydratase EchA12_2	
4911874	syn	TC	MUL_4429	-	lipid metabolism	enoyl-CoA hydratase EchA12_2	
4912090	non	TC	MUL_4429	-	lipid metabolism	enoyl-CoA hydratase EchA12_2	
4913391	non	AG	MUL_4430	-	conserved hypotheticals	conserved hypothetical protein	
4916809	psd	CG	MUL_4433	-	intermediary metabolism and respiration	mid-section bifunctional enzyme: 2-hydroxyhepta-2,4-diene-1-dioate isomerase (HHDD isomerase) + cyclase	
4919287	syn	TC	MUL_4434	-	intermediary metabolism and respiration	ATP dependent DNA ligase	
4920311	non	AG	MUL_4435	-	intermediary metabolism and respiration	fructokinase_PkB	
4921516	syn	TC	MUL_4436	-	conserved hypotheticals	conserved hypothetical protein	
4921859	syn	TC	MUL_4437	-	cell wall and cell processes	periplasmic phosphate-binding lipoprotein PstS2	
4923023	int	CT	45_MUL_4438	regulatory proteins	N-term transmembrane serine/threonine-protein kinase D PkND_pseudogene		
4923277	psd	TC	MUL_4438	-	regulatory proteins	C-term transmembrane serine/threonine-protein kinase D PkND_pseudogene	
4923277	psd	TC	MUL_4438	-	regulatory proteins	N-term transmembrane serine/threonine-protein kinase D PkND_pseudogene	
4923519	psd	GC	MUL_4438	-	regulatory proteins	C-term transmembrane serine/threonine-protein kinase D PkND_pseudogene	
4925102	-C	MUL_4438	-	regulatory proteins	C-term transmembrane serine/threonine-protein kinase D PkND_pseudogene		
4926006	non	GA	MUL_4439	-	cell wall and cell processes	phosphate-transport integral membrane ABC transporter PstA1	
4926571	non	GT	MUL_4440	-	cell wall and cell processes	phosphate-transport integral membrane ABC transporter PstC2	
4926708	non	CG	MUL_4440	-	cell wall and cell processes	phosphate-transport integral membrane ABC transporter PstC2	
4929733	psd	AG	MUL_4443	-	conserved hypotheticals	N-term conserved hypothetical protein_pseudogene	

SNP position	SNP type	Nucleotide change <ref><snp>	Distance to nearest locus	Nearby Locus	Functional group	Product
4930565	non	GT	MUL_4444	-	conserved hypothetical	conserved hypothetical protein
4931009	non	AG	MUL_4444	-	conserved hypothetical	conserved hypothetical protein
4931550	syn	TG	MUL_4445	-	cell wall and cell processes	divalent cation-transport integral membrane protein MntH
4933039	non	TG	MUL_4446	-	cell wall and cell processes	conserved hypothetical secreted protein
4933094	int	GA		106 MUL_4447	conserved hypothetical	conserved protein
4933543	non	AG	MUL_4447	-	conserved hypothetical	conserved protein
4941514	int	TG		-		
4942307	int	AG		-		
4945278	int	CA		-		
4945965	syn	GA	MUL_4461	-	cell wall and cell processes	conserved hypothetical membrane protein
4946153	non	GA	MUL_4461	-	cell wall and cell processes	conserved hypothetical membrane protein
4946427	int	TA		48 MUL_4461	cell wall and cell processes	conserved hypothetical membrane protein
4946493	int	GA		114 MUL_4461	cell wall and cell processes	conserved hypothetical membrane protein
4946593	int	AC		100 MUL_4462	PE/PPE	PE family protein
4946664	int	AT		29 MUL_4462	PE/PPE	PE family protein
4946689	int	CT		4 MUL_4462	PE/PPE	PE family protein
4946704	int	CG		11 MUL_4462	PE/PPE	PE family protein
4946941	int	CT		57 MUL_4463	PE/PPE	PPE family protein
4947234	int	AG		-		
4947258	int	CG		-		
4947517	int	GA		-		
4947519	int	AG		-		
4948074	int	GC		-		
4948104	int	TC		-		
4948140	int	GA		129 MUL_4463	PE/PPE	PPE family protein
4949209	psd	TA	MUL_4464	-	lipid metabolism	N-term lipid carrier protein or keto acyl-CoA thiolase - pseudogene
4949467	psd	CG	MUL_4464	-	lipid metabolism	N-term lipid carrier protein or keto acyl-CoA thiolase - pseudogene
4953755	int	TC		145 MUL_4468	regulatory proteins	C-term transmembrane serine/threonine-protein kinase pseudogene
4955737	psd	TG	MUL_4468	-	regulatory proteins	C-term transmembrane serine/threonine-protein kinase pseudogene
4957690	syn	CG	MUL_4470	-	intermediary metabolism and respiration	adenylate cyclase
4958375	syn	AG	MUL_4471	-	regulatory proteins	anchored-membrane serine/threonine-protein kinase PknF
4958535	non	GT	MUL_4471	-	regulatory proteins	anchored-membrane serine/threonine-protein kinase PknF
4959097	non	GC	MUL_4471	-	regulatory proteins	anchored-membrane serine/threonine-protein kinase PknF
4959438	syn	GC	MUL_4471	-	regulatory proteins	anchored-membrane serine/threonine-protein kinase PknF
4964908	psd	GC	MUL_4477	-	cell wall and cell processes	C-term conserved hypothetical membrane protein pseudogene
4966458	syn	TC	MUL_4478	-	intermediary metabolism and respiration	amidase AmbZ
4968041	non	AG	MUL_4481	-	intermediary metabolism and respiration	monooxygenase
4969636	non	GA	MUL_4482	-	intermediary metabolism and respiration	oxidoreductase
4973321	int	AG		23 MUL_4485	intermediary metabolism and respiration	oxidoreductase
4974247	psd	AG	MUL_4486	-	intermediary metabolism and respiration	C-term cytochrome P450 130A4 Cyp130A4P pseudogene
4974298	psd	TC	MUL_4486	-	intermediary metabolism and respiration	C-term cytochrome P450 130A4 Cyp130A4P pseudogene
4975331	int	CA		6 MUL_4487	regulatory proteins	transcriptional regulatory protein
4978519	int	TG		121 MUL_4492	intermediary metabolism and respiration	integral membrane acyltransferase
4979657	syn	AG	MUL_4492	-	intermediary metabolism and respiration	integral membrane acyltransferase
4979992	psd	CT	MUL_4493	-	information pathways	C-term cold-shock DEAD-Box protein a homolog DeaD pseudogene
4982295	int	AG		45 MUL_4495	conserved hypothetical	conserved hypothetical protein
4982353	non	GA	MUL_4495	-	conserved hypothetical	conserved hypothetical protein
4985058	non	GC	MUL_4495	-	conserved hypothetical	conserved hypothetical protein
4988872	psd	CG	MUL_4496	-	cell wall and cell processes	N-term drug-transport integral membrane protein pseudogene
4989012	int	AG		108 MUL_4496	cell wall and cell processes	N-term drug-transport integral membrane protein pseudogene
4989485	syn	TC	MUL_4499	-	cell wall and cell processes	conserved membrane protein
4989487	non	AT	MUL_4499	-	cell wall and cell processes	conserved membrane protein
4991496	syn	AG	MUL_4500	-	intermediary metabolism and respiration	alpha-ketoglutarate decarboxylase Kdg
4992411	syn	AC	MUL_4500	-	intermediary metabolism and respiration	alpha-ketoglutarate decarboxylase Kdg
4992483	syn	GC	MUL_4500	-	intermediary metabolism and respiration	alpha-ketoglutarate decarboxylase Kdg
4992942	syn	TC	MUL_4500	-	intermediary metabolism and respiration	alpha-ketoglutarate decarboxylase Kdg
4993116	syn	GC	MUL_4500	-	intermediary metabolism and respiration	alpha-ketoglutarate decarboxylase Kdg
4993440	syn	AG	MUL_4500	-	intermediary metabolism and respiration	alpha-ketoglutarate decarboxylase Kdg
4994809	int	TC		28 MUL_4501	intermediary metabolism and respiration	short-chain-type dehydrogenase/reductase
4995740	syn	AG	MUL_4503	-	intermediary metabolism and respiration	[NAD] dependent malate oxidoreductase Mez 1
4995990	syn	GC	MUL_4503	-	intermediary metabolism and respiration	[NAD] dependent malate oxidoreductase Mez 1
4996041	non	GC	MUL_4503	-	intermediary metabolism and respiration	[NAD] dependent malate oxidoreductase Mez 1
4998123	int	GA		104 MUL_4505	cell wall and cell processes	N-term magnesium and cobalt transport transmembrane protein CorA - pseudogene
5000490	psd	AG	MUL_4505	-	cell wall and cell processes	C-term magnesium and cobalt transport transmembrane protein CorA - pseudogene
5000604	psd	AC	MUL_4505	-	cell wall and cell processes	C-term magnesium and cobalt transport transmembrane protein CorA - pseudogene
5000969	syn	GC	MUL_4507	-	intermediary metabolism and respiration	F420-dependent glucose-6-phosphate dehydrogenase Fgd2
5001344	syn	CT	MUL_4507	-	intermediary metabolism and respiration	F420-dependent glucose-6-phosphate dehydrogenase Fgd2
5001800	syn	AC	MUL_4507	-	intermediary metabolism and respiration	F420-dependent glucose-6-phosphate dehydrogenase Fgd2
5002356	syn	CA	MUL_4508	-	cell wall and cell processes	GabA permease Gabp 1
5003579	int	AG		39 MUL_4508	cell wall and cell processes	GabA permease Gabp 1
5003640	int	TG		100 MUL_4508	cell wall and cell processes	GabA permease Gabp 1
5003658	int	GC		118 MUL_4508	cell wall and cell processes	GabA permease Gabp 1
5003692	int	TC		129 MUL_4509	cell wall and cell processes	conserved hypothetical membrane protein
5004246	non	AG	MUL_4509	-	cell wall and cell processes	conserved hypothetical membrane protein
5004569	psd	GC	MUL_4510	-	cell wall and cell processes	C-term sugar-transport ATP-binding protein ABC transporter SugC - pseudogene
5004572	psd	TC	MUL_4510	-	cell wall and cell processes	C-term sugar-transport ATP-binding protein ABC transporter SugC - pseudogene
5004755	psd	TC	MUL_4510	-	cell wall and cell processes	N-term sugar-transport ATP-binding protein ABC transporter SugC - pseudogene
5005241	psd	CG	MUL_4510	-	cell wall and cell processes	N-term sugar-transport ATP-binding protein ABC transporter SugC - pseudogene
5005256	psd	TC	MUL_4510	-	cell wall and cell processes	N-term sugar-transport ATP-binding protein ABC transporter SugC - pseudogene
5005926	syn	GC	MUL_4511	-	cell wall and cell processes	sugar-transport integral membrane protein ABC transporter SugB
5006395	syn	GA	MUL_4512	-	cell wall and cell processes	sugar-transport integral membrane protein ABC transporter SugA
5006429	non	AT	MUL_4512	-	cell wall and cell processes	sugar-transport integral membrane protein ABC transporter SugA
5006437	non	CG	MUL_4512	-	cell wall and cell processes	sugar-transport integral membrane protein ABC transporter SugA
5006783	syn	TG	MUL_4512	-	cell wall and cell processes	sugar-transport integral membrane protein ABC transporter SugA
5006934	non	AC	MUL_4512	-	cell wall and cell processes	sugar-transport integral membrane protein ABC transporter SugA
5007119	syn	TC	MUL_4512	-	cell wall and cell processes	sugar-transport integral membrane protein ABC transporter SugA
5007367	non	GT	MUL_4512	-	cell wall and cell processes	sugar-transport integral membrane protein ABC transporter SugA
5007368	non	GC	MUL_4512	-	cell wall and cell processes	sugar-transport integral membrane protein ABC transporter SugA
5008326	syn	CG	MUL_4514	-	cell wall and cell processes	membrane protein
5008623	syn	AC	MUL_4514	-	cell wall and cell processes	membrane protein
5014602	syn	GA	MUL_4520	-	intermediary metabolism and respiration	methyltransferase
5015836	int	CA		114 MUL_4521	PE/PPE	mid-section PPE family protein - pseudogene

SNP position	SNP type	Nucleotide change <ref><snp>	Distance to nearest locus	Nearby Locus	Functional group	Product
5016424	psd	TC	MUL_4522	-	cell wall and cell processes	N-term tetronasin-transport integral membrane protein ABC transporter - pseudogene
5016709	psd	GC	MUL_4522	-	cell wall and cell processes	C-term tetronasin-transport integral membrane protein ABC transporter - pseudogene
5017508	psd	AG	MUL_4522	-	cell wall and cell processes	C-term tetronasin-transport integral membrane protein ABC transporter - pseudogene
5017868	psd	GT	MUL_4522	-	cell wall and cell processes	C-term tetronasin-transport integral membrane protein ABC transporter - pseudogene
5018025	int	AC	-	27 MUL_4523	cell wall and cell processes	conserved integral membrane protein
5026114	int	CT	-	-	conserved hypothetical	conserved protein
5033932	syn	GA	MUL_4533	-	conserved hypothetical	conserved protein
5033959	syn	TC	MUL_4533	-	conserved hypothetical	conserved protein
5036753	int	TC	-	27 MUL_4535	conserved hypothetical	conserved hypothetical protein
5036948	int	TC	-	86 MUL_4536	intermediary metabolism and respiration	isocitrate lyase Icl
5037720	syn	TC	MUL_4536	-	intermediary metabolism and respiration	isocitrate lyase Icl
5041997	syn	AG	MUL_4540	-	regulatory proteins	transcriptional regulatory protein (possibly TetR-family)
5045476	non	AC	MUL_4544	-	cell wall and cell processes	conserved transmembrane protein
5050303	int	TG	-	149 MUL_4551	conserved hypothetical	conserved hypothetical protein
5050638	syn	TC	MUL_4551	-	conserved hypothetical	conserved hypothetical protein
5051491	non	TG	MUL_4552	-	cell wall and cell processes	UDP-N-acetylglucosamine reductase MurB
5052742	syn	TC	MUL_4553	-	cell wall and cell processes	conserved hypothetical LprQ
5056350	syn	AG	MUL_4556	-	intermediary metabolism and respiration	mannosyltransferase
5056409	non	AG	MUL_4556	-	intermediary metabolism and respiration	mannosyltransferase
5057418	non	TC	MUL_4557	-	conserved hypothetical	conserved hypothetical protein
5065211	non	TG	MUL_4565	-	conserved hypothetical	conserved hypothetical protein
5065925	syn	TC	MUL_4566	-	conserved hypothetical	conserved protein
5069536	syn	GC	MUL_4570	-	cell wall and cell processes	pyrrole-5-carboxylate reductase ProC
5070190	syn	GC	MUL_4570	-	cell wall and cell processes	pyrrole-5-carboxylate reductase ProC
5073101	non	GC	MUL_4574	-	conserved hypothetical	conserved protein
5074092	syn	AG	MUL_4575	-	lipid metabolism	cyclopropane-fatty-acyl-phospholipid synthase 2 CmaA2
5076261	syn	AC	MUL_4578	-	intermediary metabolism and respiration	carbon monoxide dehydrogenase (small chain) CoxS_1
5078384	syn	TC	MUL_4578	-	intermediary metabolism and respiration	carbon monoxide dehydrogenase (small chain) CoxS_1
5078590	non	TA	MUL_4579	-	intermediary metabolism and respiration	carbon monoxide dehydrogenase (medium chain) CoxM_1
5079121	non	GA	MUL_4580	-	cell wall and cell processes	carbon monoxide dehydrogenase (large chain) CoxL_1
5079476	syn	TC	MUL_4580	-	cell wall and cell processes	carbon monoxide dehydrogenase (large chain) CoxL_1
5079542	syn	AG	MUL_4580	-	cell wall and cell processes	carbon monoxide dehydrogenase (large chain) CoxL_1
5099044	non	CT	MUL_4598	-	intermediary metabolism and respiration	glutamyl-tRNA reductase HemA
5099489	syn	TC	MUL_4598	-	intermediary metabolism and respiration	glutamyl-tRNA reductase HemA
5101569	syn	AG	MUL_4600	-	intermediary metabolism and respiration	urophorophyrin-III C-methyltransferase HemD
5102778	non	AC	MUL_4601	-	intermediary metabolism and respiration	delta-aminolevulinic acid dehydratase HemB
5119222	non	AG	MUL_4617	-	cell wall and cell processes	conserved hypothetical transmembrane protein
5126188	non	AG	MUL_4626	-	intermediary metabolism and respiration	hydantoin racemase
5126359	non	AG	MUL_4626	-	intermediary metabolism and respiration	hydantoin racemase
5126507	int	AG	-	77 MUL_4627	conserved hypothetical	conserved hypothetical protein
5126689	syn	TG	MUL_4627	-	conserved hypothetical	conserved hypothetical protein
5128028	syn	AC	MUL_4629	-	conserved hypothetical	conserved hypothetical protein
5131455	int	TC	-	-	conserved hypothetical	conserved hypothetical protein
5131477	int	TC	-	139 MUL_4633	conserved hypothetical	conserved hypothetical protein
5132285	syn	AC	MUL_4633	-	conserved hypothetical	conserved hypothetical protein
5136433	int	GC	-	52 MUL_4634	information pathways	TRANSCRIPTION-REPAIR coupling factor Mfd (TrcF)
5136436	int	GC	-	55 MUL_4634	information pathways	TRANSCRIPTION-REPAIR coupling factor Mfd (TrcF)
5136437	int	GC	-	56 MUL_4634	information pathways	TRANSCRIPTION-REPAIR coupling factor Mfd (TrcF)
5137297	int	AG	-	-	conserved hypothetical	conserved hypothetical protein
5139466	non	AG	MUL_4638	-	intermediary metabolism and respiration	ribose-phosphate pyrophosphokinase PrsA
5139708	syn	CT	MUL_4638	-	intermediary metabolism and respiration	ribose-phosphate pyrophosphokinase PrsA
5141689	psd	TC	MUL_4641	-	intermediary metabolism and respiration	N-term oxidoreductase - pseudogene
5143376	int	AG	-	9 MUL_4641	intermediary metabolism and respiration	C-term oxidoreductase - pseudogene
5143474	int	TC	-	123 MUL_4643	information pathways	50S ribosomal protein L25 RplY
5145053	syn	GA	MUL_4645	-	cell wall and cell processes	conserved membrane protein
5148208	syn	CG	MUL_4648	-	lipid metabolism	polyketide synthase Pks16
5148370	syn	AG	MUL_4648	-	lipid metabolism	polyketide synthase Pks16
5150444	syn	AG	MUL_4649	-	intermediary metabolism and respiration	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase Ispe
5151439	non	AG	MUL_4650	-	information pathways	dimethyladenosine transferase KsgA
5152332	syn	CT	MUL_4651	-	cell wall and cell processes	resuscitation-promoting factor RpfB
5152475	non	CG	MUL_4651	-	cell wall and cell processes	resuscitation-promoting factor RpfB
5154505	syn	TC	MUL_4654	-	information pathways	methionyl-tRNA synthetase MetS
5154784	syn	CT	MUL_4654	-	information pathways	methionyl-tRNA synthetase MetS
5154970	syn	TC	MUL_4654	-	information pathways	methionyl-tRNA synthetase MetS
5155755	non	CG	MUL_4655	-	intermediary metabolism and respiration	serine acetyltransferase CysE_1
5156769	psd	AG	MUL_4656	-	cell wall and cell processes	N-term conserved hypothetical secreted protein - pseudogene
5158708	non	GC	MUL_4658	-	intermediary metabolism and respiration	dehydrogenase
5161016	syn	AG	MUL_4660	-	intermediary metabolism and respiration	para-aminobenzoate synthase component PabD
5166524	syn	GC	MUL_4664	-	intermediary metabolism and respiration	arginine deiminase ArcA
5167653	non	TC	MUL_4665	-	conserved hypothetical	conserved hypothetical protein
5171014	syn	GA	MUL_4668	-	intermediary metabolism and respiration	methyltransferase
5171017	syn	AG	MUL_4668	-	intermediary metabolism and respiration	methyltransferase
5171146	syn	TG	MUL_4669	-	conserved hypothetical	conserved hypothetical protein
5171523	syn	GA	MUL_4670	-	cell wall and cell processes	conserved hypothetical membrane protein
5171625	syn	AG	MUL_4670	-	cell wall and cell processes	conserved hypothetical membrane protein
5171637	syn	AG	MUL_4670	-	cell wall and cell processes	conserved hypothetical membrane protein
5171942	non	GC	MUL_4670	-	cell wall and cell processes	conserved hypothetical membrane protein
5171943	non	AC	MUL_4670	-	cell wall and cell processes	conserved hypothetical membrane protein
5172001	syn	GA	MUL_4670	-	cell wall and cell processes	conserved hypothetical membrane protein
5172043	syn	AG	MUL_4670	-	cell wall and cell processes	conserved hypothetical membrane protein
5172129	syn	AG	MUL_4670	-	cell wall and cell processes	conserved hypothetical membrane protein
5172383	syn	AG	MUL_4671	-	cell wall and cell processes	conserved hypothetical protein
5172407	syn	CT	MUL_4671	-	cell wall and cell processes	conserved hypothetical protein
5172440	syn	TC	MUL_4671	-	cell wall and cell processes	conserved hypothetical protein
5172542	syn	AG	MUL_4671	-	cell wall and cell processes	conserved hypothetical protein
5172800	non	AC	MUL_4671	-	cell wall and cell processes	conserved hypothetical protein
5172841	int	T-	-	14 MUL_4671	cell wall and cell processes	conserved hypothetical protein
5173710	int	CG	-	-	cell wall and cell processes	teichoic acid biosynthesis protein
5174951	syn	CG	MUL_4673	-	cell wall and cell processes	teichoic acid biosynthesis protein
5175158	syn	GA	MUL_4673	-	cell wall and cell processes	teichoic acid biosynthesis protein
5178335	syn	TC	MUL_4675	-	cell wall and cell processes	conserved hypothetical membrane protein
5178881	syn	CT	MUL_4676	-	cell wall and cell processes	glycosyltransferase

SNP position	SNP type	Nucleotide change <ref><snp>	Distance to nearest locus	Nearby Locus	Functional group	Product
5178866	syn	TC	MUL_4676	-	cell wall and cell processes	glycosyltransferase
5179323	non	AG	MUL_4676	-	cell wall and cell processes	glycosyltransferase
5180110	non	AG	MUL_4676	-	cell wall and cell processes	glycosyltransferase
5181668	non	CA	MUL_4678	-	conserved hypotheticals	conserved hypothetical protein
5184949	syn	AG	MUL_4680	-	conserved hypotheticals	conserved hypothetical protein
5185259	non	AG	MUL_4680	-	conserved hypotheticals	conserved hypothetical protein
5185725	non	CG	MUL_4680	-	conserved hypotheticals	conserved hypothetical protein
5187541	syn	GA	MUL_4683	-	intermediary metabolism and respiration	predicted amidohydrolase
5187907	non	TC	MUL_4683	-	intermediary metabolism and respiration	predicted amidohydrolase
5190447	non	TG	MUL_4685	-	cell wall and cell processes	conserved hypothetical transmembrane protein
5190457	non	GC	MUL_4685	-	cell wall and cell processes	conserved hypothetical transmembrane protein
5190468	non	CA	MUL_4685	-	cell wall and cell processes	conserved hypothetical transmembrane protein
5190794	non	AG	MUL_4685	-	cell wall and cell processes	conserved hypothetical transmembrane protein
5193415	non	TC	MUL_4688	-	conserved hypotheticals	conserved hypothetical protein
5195220	non	TC	MUL_4690	-	cell wall and cell processes	conserved hypothetical transmembrane protein
5195384	non	CT	MUL_4690	-	cell wall and cell processes	conserved hypothetical transmembrane protein
5196626	syn	AT	MUL_4692	-	intermediary metabolism and respiration	molybdoferro biosynthesis protein MoeA1
5198869	non	GC	MUL_4694	-	conserved hypotheticals	conserved hypothetical protein
5198913	syn	TC	MUL_4694	-	conserved hypotheticals	conserved hypothetical protein
5199665	syn	AG	MUL_4695	-	conserved hypotheticals	conserved hypothetical serine rich protein
5200467	non	CG	MUL_4696	-	cell wall and cell processes	conserved hypothetical membrane protein
5201908	syn	AG	MUL_4699	-	intermediary metabolism and respiration	serine protease Pept
5202255	non	AC	MUL_4699	-	intermediary metabolism and respiration	serine protease PeptB
5203823	syn	TC	MUL_4700	-	regulatory proteins	two component sensor kinase MprB
5203838	syn	AC	MUL_4700	-	regulatory proteins	two component sensor kinase MprB
5204144	syn	AG	MUL_4700	-	regulatory proteins	two component sensor kinase MprB
5205554	Int	GA	139	MUL_4702	information pathways	50S ribosomal protein L32 RpmF
5205769	non	CG	MUL_4702	-	information pathways	50S ribosomal protein L32 RpmF
5206185	syn	TC	MUL_4703	-	conserved hypotheticals	conserved hypothetical protein
5206374	non	TG	MUL_4703	-	conserved hypotheticals	conserved hypothetical protein
5207024	non	AC	MUL_4703	-	conserved hypotheticals	conserved hypothetical protein
5207022	non	GC	MUL_4703	-	conserved hypotheticals	conserved hypothetical protein
5207643	syn	AG	MUL_4703	-	conserved hypotheticals	conserved hypothetical protein
5207883	non	TA	MUL_4704	-	intermediary metabolism and respiration	acyl-CoA dehydrogenase FadE13
5208158	syn	AG	MUL_4704	-	intermediary metabolism and respiration	acyl-CoA dehydrogenase FadE13
5208212	syn	TG	MUL_4704	-	intermediary metabolism and respiration	acyl-CoA dehydrogenase FadE13
5208416	syn	GA	MUL_4704	-	intermediary metabolism and respiration	acyl-CoA dehydrogenase FadE13
5208557	syn	TC	MUL_4704	-	intermediary metabolism and respiration	acyl-CoA dehydrogenase FadE13
5210499	syn	AG	MUL_4705	-	lipid metabolism	acetyl-/propionyl-CoA carboxylase (beta subunit) AccD2
5213014	non	AC	MUL_4707	-	lipid metabolism	acetyl-CoA dehydrogenase FadE12
5215601	syn	GA	MUL_4709	-	conserved hypotheticals	conserved hypothetical protein
5215698	syn	GC	MUL_4710	-	conserved hypotheticals	conserved hypothetical protein
5215914	syn	TC	MUL_4710	-	conserved hypotheticals	conserved hypothetical protein
5216562	syn	TC	MUL_4710	-	conserved hypotheticals	conserved hypothetical protein
5217778	syn	TC	MUL_4711	-	intermediary metabolism and respiration	magnesium chelatase
5217886	syn	TC	MUL_4711	-	intermediary metabolism and respiration	magnesium chelatase
5218150	syn	GA	MUL_4711	-	intermediary metabolism and respiration	magnesium chelatase
5221179	non	CT	MUL_4713	-	intermediary metabolism and respiration	5'-phosphoribosylpyrimidinamide formyltransferase PurN
5222750	syn	AC	MUL_4714	-	cell wall and cell processes	conserved integral membrane protein
5222892	non	GC	MUL_4715	-	cell wall and cell processes	conserved transmembrane protein
5225046	Int	CT	MUL_4717	-	lipid metabolism	thiolase
5225114	syn	AG	MUL_4717	-	lipid metabolism	thiolase
5225933	syn	AG	MUL_4717	-	lipid metabolism	thiolase
5226677	Int	GC	-	-	-	-
5226730	Int	CT	-	-	-	-
5229520	syn	CG	MUL_4720	-	intermediary metabolism and respiration	succinyl-CoA synthetase (beta chain) SucC
5229835	syn	TC	MUL_4720	-	intermediary metabolism and respiration	succinyl-CoA synthetase (beta chain) SucC
5230817	syn	AG	MUL_4721	-	conserved hypotheticals	conserved hypothetical protein
5231708	syn	TG	MUL_4722	-	conserved hypotheticals	conserved hypothetical protein
5234037	syn	CT	MUL_4723	-	information pathways	ATP-dependent DNA helicase II UvrD1
5240775	Int	GA	136	MUL_4726	PE/PPe	mid-section PE family protein_pseudogene
5240867	Int	AG	11	MUL_4726	PE/PPe	C-term PE family protein_pseudogene
5241353	syn	AG	MUL_4731	-	regulatory proteins	transcriptional regulatory protein (possibly TetR-family)
5244875	Int	CG	61	MUL_4736	conserved hypotheticals	conserved protein
5245001	non	GA	MUL_4736	-	conserved hypotheticals	conserved protein
5245470	Int	CG	64	MUL_4736	conserved hypotheticals	conserved protein
5246069	syn	TG	MUL_4737	-	conserved hypotheticals	conserved hypothetical protein
5246429	Int	GA	79	MUL_4737	conserved hypotheticals	conserved hypothetical protein
5246844	psd	CA	MUL_4738	-	lipid metabolism	N-term acyl-CoA dehydrogenase FadE2_pseudogene
5246845	psd	AG	MUL_4738	-	lipid metabolism	N-term acyl-CoA dehydrogenase FadE2_pseudogene
5249320	syn	AG	MUL_4742	-	cell wall and cell processes	conserved membrane protein
5280776	syn	AG	MUL_4762	-	conserved hypotheticals	O-Methyltransferase
5280821	syn	TC	MUL_4762	-	conserved hypotheticals	O-Methyltransferase
5283096	non	GA	MUL_4766	-	conserved hypotheticals	conserved protein
5287877	syn	AG	MUL_4771	-	intermediary metabolism and respiration	oxidoreductase
5288849	non	AG	MUL_4772	-	conserved hypotheticals	conserved hypothetical protein
5288917	Int	CG	1	MUL_4772	conserved hypotheticals	conserved hypothetical protein
5291261	syn	AG	MUL_4775	-	regulatory proteins	transcriptional regulatory protein
5291336	syn	AG	MUL_4775	-	regulatory proteins	transcriptional regulatory protein
5291379	non	CG	MUL_4775	-	regulatory proteins	transcriptional regulatory protein
5292686	syn	TC	MUL_4777	-	intermediary metabolism and respiration	zinc-dependent alcohol dehydrogenase
5293320	syn	CT	MUL_4778	-	epoxide hydrolase EphF	-
5294580	psd	CA	MUL_4779	-	conserved hypotheticals	N-term conserved hypothetical protein_pseudogene
5294580	psd	CA	MUL_4779	-	conserved hypotheticals	C-term conserved hypothetical protein_pseudogene
5298282	syn	AG	MUL_4783	-	conserved hypotheticals	conserved hypothetical protein
5300431	syn	GA	MUL_4786	-	intermediary metabolism and respiration	flavodoxin oxidoreductase
5304940	non	AG	MUL_4790	-	lipid metabolism	acyl-CoA dehydrogenase FadE1
5305514	non	CT	MUL_4790	-	lipid metabolism	acyl-CoA dehydrogenase FadE1
5305686	syn	AG	MUL_4790	-	lipid metabolism	acyl-CoA dehydrogenase FadE1
5307154	Int	AG	14	MUL_4792	intermediary metabolism and respiration	phosphoesterase
5308398	syn	TG	MUL_4793	-	cell wall and cell processes	secreted antigen 85-C FbpC
5312526	syn	AG	MUL_4797	-	trehalose synthase TreS	-

SNP position	SNP type	Nucleotide change <ref><snp>	Distance to nearest locus	Nearby Locus	Functional group	Product
5314788	syn	GA	MUL_4800	-	conserved hypothetical	conserved hypothetical protein
5315711	psd	GC	MUL_4801	-	information pathways	N-term elongation factor G FusA2 pseudogene
5317481	non	AC	MUL_4802	-	cell wall and cell processes	conserved hypothetical membrane protein
5317722	non	TC	MUL_4802	-	cell wall and cell processes	conserved hypothetical membrane protein
5317964	non	TA	MUL_4803	-	lipid metabolism	fatty-acid-CoA ligase FadD7
5318887	syn	AG	MUL_4803	-	lipid metabolism	fatty-acid-CoA ligase FadD7
5321348	syn	AG	MUL_4804	-	intermediary metabolism and respiration	oxalyl-CoA decarboxylase OxaC
5323188	syn	AG	MUL_4806	-	cell wall and cell processes	conserved hypothetical secreted protein
5323628	non	GT	MUL_4807	-	cell wall and cell processes	divalent cation-transport integral membrane protein
5324112	non	AC	MUL_4807	-	cell wall and cell processes	divalent cation-transport integral membrane protein
5324977	syn	TC	MUL_4807	-	cell wall and cell processes	divalent cation-transport integral membrane protein
5325305	int	AG	85 MUL_4808	-	conserved hypothetical	conserved hypothetical protein
5328193	syn	AG		-	intermediary metabolism and respiration	transmembrane acyltransferase
5332936	syn	AG	MUL_4813	-	intermediary metabolism and respiration	monooxygenase
5332944	non	AT	MUL_4813	-	intermediary metabolism and respiration	monooxygenase
5334814	psd	AG	MUL_4815	-	intermediary metabolism and respiration	N-term dioxygenase pseudogene
5335190	psd	AG	MUL_4815	-	intermediary metabolism and respiration	N-term dioxygenase pseudogene
5336234	psd	GT	MUL_4816	-	intermediary metabolism and respiration	N-term short-chain type dehydrogenase/reductase pseudogene
5336516	psd	GC	MUL_4816	-	intermediary metabolism and respiration	N-term short-chain type dehydrogenase/reductase pseudogene
5337806	non	TG	MUL_4817	-	conserved hypothetical	conserved hypothetical protein
5338259	non	CG	MUL_4817	-	conserved hypothetical	conserved hypothetical protein
5339554	psd	AG	MUL_4819	-	lipid metabolism	N-term fatty-acid-CoA ligase pseudogene
5339698	psd	TC	MUL_4819	-	lipid metabolism	N-term fatty-acid-CoA ligase pseudogene
5341148	syn	GA	MUL_4820	-	intermediary metabolism and respiration	short-chain type dehydrogenase/reductase
5346110	int	T	78 MUL_4825	-	conserved hypothetical	conserved protein
5350441	syn	GA		-	cell wall and cell processes	cation-transporter ATPase I CtpI
5350615	syn	AG	MUL_4826	-	cell wall and cell processes	cation-transporter ATPase I CtpI
5354007	syn	GA	MUL_4828	-	intermediary metabolism and respiration	short-chain type dehydrogenase/reductase
5354517	non	TC	MUL_4829	-	information pathways	50S ribosomal protein L31 RpmE_1
5355471	syn	AG	MUL_4830	-	conserved hypothetical	conserved protein
5356087	non	GA	MUL_4835	-	conserved hypothetical	conserved hypothetical protein
5366627	int	AG	51 MUL_4845	-	cell wall and cell processes	cation-transporter p-type ATPase B CtpB
5367432	syn	TC		-	cell wall and cell processes	cation-transporter p-type ATPase B CtpB
5368001	non	TC	MUL_4845	-	cell wall and cell processes	cation-transporter p-type ATPase B CtpB
5368408	non	AG	MUL_4845	-	cell wall and cell processes	cation-transporter p-type ATPase B CtpB
5368566	syn	AC	MUL_4845	-	cell wall and cell processes	cation-transporter p-type ATPase B CtpB
5368667	non	TC	MUL_4845	-	cell wall and cell processes	cation-transporter p-type ATPase B CtpB
5368869	syn	GC	MUL_4845	-	cell wall and cell processes	cation-transporter p-type ATPase B CtpB
5371781	syn	TC	MUL_4848	-	cell wall and cell processes	conserved hypothetical secreted protein
5373151	syn	AG	MUL_4850	-	cell wall and cell processes	cation transporter p-type ATPase a CtpA
5373473	non	AG	MUL_4850	-	cell wall and cell processes	cation transporter p-type ATPase a CtpA
5373640	syn	TC	MUL_4850	-	cell wall and cell processes	cation transporter p-type ATPase a CtpA
5375599	syn	TC	MUL_4851	-	cell wall and cell processes	conserved membrane protein
5377684	int	GA	-	-	-	-
5380510	syn	TC	MUL_4856	-	lipid metabolism	fatty-acid-CoA ligase FadD10
5381143	syn	TC	MUL_4856	-	lipid metabolism	fatty-acid-CoA ligase FadD10
5381722	syn	AC	MUL_4856	-	lipid metabolism	fatty-acid-CoA ligase FadD10
5382014	syn	GC	MUL_4857	-	conserved hypothetical	conserved hypothetical protein
5382175	syn	AC	MUL_4858	-	lipid metabolism	non-ribosomal peptide synthetase
5382181	syn	CT	MUL_4858	-	lipid metabolism	non-ribosomal peptide synthetase
5382312	non	TC	MUL_4858	-	lipid metabolism	non-ribosomal peptide synthetase
5382595	syn	CT	MUL_4858	-	lipid metabolism	non-ribosomal peptide synthetase
5382667	non	AG	MUL_4858	-	lipid metabolism	non-ribosomal peptide synthetase
5382980	non	TC	MUL_4858	-	lipid metabolism	non-ribosomal peptide synthetase
5383827	non	TG	MUL_4858	-	lipid metabolism	non-ribosomal peptide synthetase
5384258	syn	CT	MUL_4858	-	lipid metabolism	non-ribosomal peptide synthetase
5384680	syn	CG	MUL_4858	-	lipid metabolism	non-ribosomal peptide synthetase
5384860	syn	TC	MUL_4858	-	lipid metabolism	non-ribosomal peptide synthetase
5384950	syn	AC	MUL_4858	-	lipid metabolism	non-ribosomal peptide synthetase
5385062	non	TC	MUL_4858	-	lipid metabolism	non-ribosomal peptide synthetase
5386509	psd	CT	MUL_4859	-	cell wall and cell processes	C-term conserved transmembrane transport protein MmpL4_6 pseudogene
5386750	psd	GT	MUL_4859	-	cell wall and cell processes	C-term conserved transmembrane transport protein MmpL4_6 pseudogene
5387287	psd	AG	MUL_4859	-	cell wall and cell processes	C-term conserved transmembrane transport protein MmpL4_6 pseudogene
5387524	psd	AG	MUL_4859	-	cell wall and cell processes	C-term conserved transmembrane transport protein MmpL4_6 pseudogene
5387896	psd	AT	MUL_4859	-	cell wall and cell processes	N-term conserved transmembrane transport protein MmpL4_6 pseudogene
5388244	psd	TC	MUL_4859	-	cell wall and cell processes	N-term conserved transmembrane transport protein MmpL4_6 pseudogene
5388781	psd	GC	MUL_4859	-	cell wall and cell processes	N-term conserved transmembrane transport protein MmpL4_6 pseudogene
5390299	int	GC	70 MUL_4860	-	lipid metabolism	ketoadyl reductase
5391124	int	GT		-	intermediary metabolism and respiration	bifunctional Mta/Sah nucleosidase Mtn
5391636	syn	AG	MUL_4862	-	intermediary metabolism and respiration	bifunctional Mta/Sah nucleosidase Mtn
5391863	non	TC	MUL_4862	-	intermediary metabolism and respiration	bifunctional Mta/Sah nucleosidase Mtn
5392036	int	TG	109 MUL_4862	-	intermediary metabolism and respiration	bifunctional Mta/Sah nucleosidase Mtn
5394052	syn	TC		-	intermediary metabolism and respiration	short-chain type dehydrogenase/reductase
5404988	psd	AG	MUL_4874	-	intermediary metabolism and respiration	N-term monooxygenase pseudogene
5406802	non	CT	MUL_4877	-	conserved hypothetical	conserved hypothetical protein
5408980	syn	AG	MUL_4881	-	conserved hypothetical	conserved hypothetical protein
5409962	psd	AG	MUL_4883	-	cell wall and cell processes	N-term cation transporter p-type ATPase a CtpA_1 pseudogene
5410168	psd	AC	MUL_4883	-	cell wall and cell processes	N-term cation transporter p-type ATPase a CtpA_1 pseudogene
5411459	psd	AG	MUL_4883	-	cell wall and cell processes	C-term cation transporter p-type ATPase CtpA_1 pseudogene
5412001	psd	TC	MUL_4883	-	cell wall and cell processes	C-term cation transporter p-type ATPase CtpA_1 pseudogene
5412179	psd	AG	MUL_4883	-	cell wall and cell processes	C-term cation transporter p-type ATPase CtpA_1 pseudogene
5412441	syn	AG	MUL_4884	-	intermediary metabolism and respiration	diroxigenase
5412927	syn	AC	MUL_4884	-	intermediary metabolism and respiration	diroxigenase
5413329	non	GC	MUL_4884	-	intermediary metabolism and respiration	diroxigenase
5413559	int	GA	39 MUL_4885	-	cell wall and cell processes	conserved hypothetical protein
5413608	non	CA		-	cell wall and cell processes	conserved hypothetical protein
5414670	non	CT	MUL_4886	-	conserved hypothetical	conserved hypothetical protein
5417576	syn	TG	MUL_4890	-	regulatory proteins	transcriptional regulatory protein
5419671	syn	GC	MUL_4893	-	conserved hypothetical	conserved hypothetical protein
5420015	non	TC	MUL_4893	-	conserved hypothetical	conserved hypothetical protein
5420093	non	AG	MUL_4893	-	conserved hypothetical	conserved hypothetical protein
5420765	psd	AG	MUL_4894	-	conserved hypothetical	N-term conserved hypothetical protein pseudogene

SNP position	SNP type	Nucleotide change <ref><snp>	Distance to nearest locus	Nearby Locus	Functional group	Product
5421066	psd	AC	MUL_4894	-	conserved hypothetical	N-term conserved hypothetical protein_pseudogene
5421080	psd	AG	MUL_4894	-	conserved hypothetical	N-term conserved hypothetical protein_pseudogene
5427982	non	CT	MUL_4900	-	intermediary metabolism and respiration	flavoprotein
5428367	snp	TC	MUL_4900	-	intermediary metabolism and respiration	flavoprotein
5429063	snp	TC	MUL_4901	-	intermediary metabolism and respiration	L-serine dehydratase SdaA
5429162	snp	GA	MUL_4901	-	intermediary metabolism and respiration	L-serine dehydratase SdaA
5429201	non	GC	MUL_4901	-	intermediary metabolism and respiration	L-serine dehydratase SdaA
5430527	non	TC	MUL_4902	-	intermediary metabolism and respiration	L-serine dehydratase SdaA
5431098	non	AC	MUL_4902	-	intermediary metabolism and respiration	serine hydroxymethyltransferase GlyA2
5431746	snp	CT	MUL_4903	-	intermediary metabolism and respiration	glycine cleavage system H protein GcvH_1
5432436	psd	CT	MUL_4904	-	intermediary metabolism and respiration	C-term aminomethyltransferase GcvT_1_pseudogene
5432508	psd	TC	MUL_4904	-	intermediary metabolism and respiration	C-term aminomethyltransferase GcvT_1_pseudogene
5433364	psd	TC	MUL_4905	-	intermediary metabolism and respiration	C-term glycine dehydrogenase GcvB1_pseudogene
5436856	psd	AC	MUL_4907	-	conserved hypothetical	C-term conserved hypothetical protein_pseudogene
5437031	psd	CT	MUL_4907	-	conserved hypothetical	C-term conserved hypothetical protein_pseudogene
5437187	psd	CT	MUL_4907	-	conserved hypothetical	C-term conserved hypothetical protein_pseudogene
5440306	Int	GT	39 MUL_4909	PE/PPE	PE-PGRS family protein	
5445340	snp	CG	MUL_4914	-	MCE-family protein MceF	
5445405	non	CT	MUL_4914	-	MCE-family protein MceF	
5448519	snp	AG	MUL_4917	-	MCE-family protein MceC	
5449143	non	TC	MUL_4917	-	MCE-family protein MceC	
5449659	non	CT	MUL_4918	-	MCE-family protein MceB	
5449860	non	GC	MUL_4918	-	MCE-family protein MceB	
5450813	snp	GC	MUL_4919	-	MCE-family protein MceA	
5451340	non	GG	MUL_4919	-	MCE-family protein MceA	
5464765	non	GG	MUL_4933	-	conserved protein	
5465538	snp	AG	MUL_4934	cell wall and cell processes	conserved hypothetical	
5465571	Int	AG	34 MUL_4934	cell wall and cell processes	conserved hypothetical transmembrane protein	
5467175	snp	AG	MUL_4935	-	cell wall and cell processes	conserved hypothetical transmembrane protein
5467634	snp	AG	MUL_4935	-	cell wall and cell processes	conserved hypothetical membrane protein
5468802	Int	CT	141 MUL_4938	cell wall and cell processes	conserved hypothetical membrane protein	
5468890	Int	AC	53 MUL_4938	cell wall and cell processes	conserved hypothetical membrane protein	
5469345	Int	GC	79 MUL_4938	cell wall and cell processes	conserved hypothetical membrane protein	
5469751	Int	GA	-	cell wall and cell processes	conserved hypothetical membrane protein	
5470995	snp	CG	MUL_4939	intermediary metabolism and respiration	isocitrate dehydrogenase [NADP] Icd2	
5478620	psd	AT	MUL_4946	-	virulence; detoxification; adaptation	C-term enhanced intracellular survival protein Eis1_pseudogene
5478728	psd	TC	MUL_4946	-	virulence; detoxification; adaptation	C-term enhanced intracellular survival protein Eis1_pseudogene
5481397	Int	TC	65 MUL_4949	cell wall and cell processes	glycosyltransferase	
5481654	non	CG	MUL_4949	cell wall and cell processes	glycosyltransferase	
5491326	snp	AG	MUL_4958	-	lipid metabolism	acyl-CoA dehydrogenase FadE6_1
5492489	snp	TC	MUL_4959	-	conserved hypothetical	conserved hypothetical protein
5493009	snp	AG	MUL_4960	-	conserved hypothetical	conserved hypothetical protein
5493550	non	AG	MUL_4961	cell wall and cell processes	conserved hypothetical intergral membrane protein	
5494981	snp	AG	MUL_4962	information pathways	ADP-ribose pyrophosphatase RppH	
5495268	non	CT	MUL_4963	-	conserved hypothetical	conserved hypothetical protein
5495349	non	CT	MUL_4963	-	conserved hypothetical	conserved hypothetical protein
5495410	non	AG	MUL_4963	-	conserved hypothetical	conserved hypothetical protein
5499154	psd	TC	MUL_4966	-	conserved hypothetical	C-term conserved hypothetical protein_pseudogene
5499187	psd	GA	MUL_4966	-	conserved hypothetical	C-term conserved hypothetical protein_pseudogene
5499927	snp	AG	MUL_4967	-	conserved hypothetical	conserved hypothetical protein
5504282	non	GA	MUL_4971	cell wall and cell processes	conserved hypothetical transmembrane protein	
5504407	snp	TG	MUL_4971	cell wall and cell processes	conserved hypothetical transmembrane protein	
5504642	non	AC	MUL_4971	cell wall and cell processes	conserved hypothetical transmembrane protein	
5504650	snp	AG	MUL_4971	cell wall and cell processes	conserved hypothetical transmembrane protein	
5505201	snp	TC	MUL_4972	-	cell wall and cell processes	integral membrane indolylacetlyinositol arabinosyltransferase EmbC
5505582	snp	CT	MUL_4972	-	cell wall and cell processes	integral membrane indolylacetlyinositol arabinosyltransferase EmbC
5505867	snp	AG	MUL_4972	-	cell wall and cell processes	integral membrane indolylacetlyinositol arabinosyltransferase EmbC
5506239	snp	TC	MUL_4972	-	cell wall and cell processes	integral membrane indolylacetlyinositol arabinosyltransferase EmbC
5506749	snp	AT	MUL_4972	-	cell wall and cell processes	integral membrane indolylacetlyinositol arabinosyltransferase EmbC
5507197	non	GA	MUL_4972	-	cell wall and cell processes	integral membrane indolylacetlyinositol arabinosyltransferase EmbC
5510276	snp	TC	MUL_4973	-	cell wall and cell processes	integral membrane indolylacetlyinositol arabinosyltransferase EmbA
5510633	snp	TG	MUL_4973	-	cell wall and cell processes	integral membrane indolylacetlyinositol arabinosyltransferase EmbA
5511101	snp	TC	MUL_4973	-	cell wall and cell processes	integral membrane indolylacetlyinositol arabinosyltransferase EmbA
5511772	snp	TC	MUL_4974	-	cell wall and cell processes	integral membrane indolylacetlyinositol arabinosyltransferase EmbB
5512537	snp	TC	MUL_4974	-	cell wall and cell processes	integral membrane indolylacetlyinositol arabinosyltransferase EmbB
5513843	non	CG	MUL_4974	-	cell wall and cell processes	integral membrane indolylacetlyinositol arabinosyltransferase EmbB
5514694	snp	TC	MUL_4974	-	cell wall and cell processes	integral membrane indolylacetlyinositol arabinosyltransferase EmbB
5514829	snp	GA	MUL_4974	-	cell wall and cell processes	integral membrane indolylacetlyinositol arabinosyltransferase EmbB
5517864	Int	CT	28 MUL_4978	cell wall and cell processes	conserved hypothetical secreted protein	
5518118	non	GA	MUL_4978	-	cell wall and cell processes	conserved hypothetical secreted protein
5518120	non	AG	MUL_4978	-	cell wall and cell processes	conserved hypothetical secreted protein
5520635	psd	GA	MUL_4980	-	lipid metabolism	C-term acyl-CoA dehydrogenase FadE35_pseudogene
5520789	Int	GC	99 MUL_4980	lipid metabolism	C-term acyl-CoA dehydrogenase FadE35_pseudogene	
5521030	Int	TG	-	lipid metabolism		
5524859	snp	CG	MUL_4982	lipid metabolism	propionyl-CoA carboxylase beta chain 4 AccD4_1	
5525917	snp	TC	MUL_4983	-	lipid metabolism	polyketide synthase Pks13
5526475	snp	TG	MUL_4983	-	lipid metabolism	polyketide synthase Pks13
5526523	snp	TC	MUL_4983	-	lipid metabolism	polyketide synthase Pks13
5527748	non	TG	MUL_4983	-	lipid metabolism	polyketide synthase Pks13
5529036	non	GC	MUL_4983	-	lipid metabolism	polyketide synthase Pks13
5530696	snp	CG	MUL_4983	-	lipid metabolism	polyketide synthase Pks13
5531120	snp	AG	MUL_4984	-	lipid metabolism	fatty-acyl AMP ligase FadD32
5531696	snp	AC	MUL_4984	-	lipid metabolism	fatty-acyl AMP ligase FadD32
5531714	snp	TC	MUL_4984	-	lipid metabolism	fatty-acyl AMP ligase FadD32
5532137	snp	AG	MUL_4984	-	lipid metabolism	fatty-acyl AMP ligase FadD32
5534385	Int	AG	11 MUL_4986	cell wall and cell processes	secreted Mp51/Mpb51 antigen protein FbpD	
5534714	snp	AG	MUL_4986	cell wall and cell processes	secreted Mp51/Mpb51 antigen protein FbpD	
5535711	snp	AG	MUL_4987	cell wall and cell processes	secreted antigen 85-A FbpA	
5536119	snp	AG	MUL_4987	cell wall and cell processes	secreted antigen 85-A FbpA	
5536315	non	AG	MUL_4987	cell wall and cell processes	secreted antigen 85-A FbpA	
5536448	non	AG	MUL_4987	cell wall and cell processes	secreted antigen 85-A FbpA	
5536624	Int	AG	134 MUL_4987	cell wall and cell processes	secreted antigen 85-A FbpA	

SNP position	SNP type	Nucleotide change <ref><snp>	Distance to nearest locus	Nearby Locus	Functional group	Product
5541576	syn	TC	MUL_4992	-	intermediary metabolism and respiration	bifunctional UDP-galactofuranosyl transferase GIFT
5550140	syn	AG	MUL_5000	-	intermediary metabolism and respiration	phosphotransferase
5550311	syn	CT	MUL_5000	-	intermediary metabolism and respiration	phosphotransferase
5550436	syn	-G	MUL_5000	-	intermediary metabolism and respiration	phosphotransferase
5550872	non	AG	MUL_5001	-	conserved hypothetical	UDP-MurNAc hydroxylase NamH
5551198	syn	AG	MUL_5001	-	conserved hypothetical	UDP-MurNAc hydroxylase NamH
5552157	syn	GC	MUL_5002	-	conserved hypothetical	conserved hypothetical protein
5554887	non	TG	MUL_5005	-	cell wall and cell processes	conserved hypothetical membrane protein
5556083	non	GT	MUL_5006	-	information pathways	serV-tRNA synthetase SerS
5557502	non	AC	MUL_5007	-	cell wall and cell processes	conserved hypothetical membrane protein
5559683	syn	GA	MUL_5011	-	intermediary metabolism and respiration	prephenate dehydratase PheA
5562678	Int.	TC	1 MUL_5014		intermediary metabolism and respiration	bacterioferritin BfrB
5564117	syn	AG	MUL_5016	-	cell wall and cell processes	conserved hypothetical transmembrane protein
5564495	syn	AG	MUL_5016	-	cell wall and cell processes	conserved hypothetical transmembrane protein
5566634	Int.	CT	95 MUL_5018		superoxide dismutase [fe] SodA	
5571496	syn	TG	MUL_5026	-	intermediary metabolism and respiration	monooxygenase EthA
5571541	non	CG	MUL_5026	-	intermediary metabolism and respiration	monooxygenase EthA
5572150	syn	TG	MUL_5026	-	intermediary metabolism and respiration	monooxygenase EthA
5572189	syn	TG	MUL_5026	-	intermediary metabolism and respiration	monooxygenase EthA
5572230	non	AT	MUL_5026	-	intermediary metabolism and respiration	monooxygenase EthA
5573319	syn	AG	MUL_5027	-	regulatory proteins	transcriptional regulatory repressor protein (TetR-family) EthR
5575181	syn	CG	MUL_5029	-	conserved hypothetical	conserved hypothetical PHP domain protein
5575803	psd	CA	MUL_5030	-	cell wall and cell processes	C-term conserved hypothetical membrane protein pseudogene
5575812	psd	TG	MUL_5030	-	cell wall and cell processes	N-term conserved hypothetical membrane protein pseudogene
5575812	psd	TG	MUL_5030	-	cell wall and cell processes	C-term conserved hypothetical membrane protein pseudogene
5576051	psd	CG	MUL_5030	-	cell wall and cell processes	N-term conserved hypothetical membrane protein pseudogene
5576153	non	GA	MUL_5031	-	cell wall and cell processes	conserved hypothetical secreted protein
5577649	syn	AG	MUL_5033	-	conserved hypothetical	conserved hypothetical protein
5577983	non	CA	MUL_5033	-	conserved hypothetical	conserved hypothetical protein
5578051	Int.	TC	107 MUL_5034		conserved hypothetical	conserved hypothetical protein
5578617	Int.	TG	105 MUL_5034		conserved hypothetical	conserved hypothetical protein
5578653	Int.	TC	69 MUL_5034		conserved hypothetical	conserved hypothetical protein
5580094	syn	GC	MUL_5036	-	intermediary metabolism and respiration	NADH-dependent glutamate synthase (small subunit) GltD
5582597	syn	CG	MUL_5037	-	intermediary metabolism and respiration	ferredoxin-dependent glutamate synthase [NADPH] (large subunit) GltB
5582658	syn	AC	MUL_5037	-	intermediary metabolism and respiration	ferredoxin-dependent glutamate synthase [NADPH] (large subunit) GltB
5582960	syn	AG	MUL_5037	-	intermediary metabolism and respiration	ferredoxin-dependent glutamate synthase [NADPH] (large subunit) GltB
5583227	syn	GA	MUL_5037	-	intermediary metabolism and respiration	ferredoxin-dependent glutamate synthase [NADPH] (large subunit) GltB
5583344	syn	AG	MUL_5037	-	intermediary metabolism and respiration	ferredoxin-dependent glutamate synthase [NADPH] (large subunit) GltB
5583627	non	CG	MUL_5037	-	intermediary metabolism and respiration	ferredoxin-dependent glutamate synthase [NADPH] (large subunit) GltB
5584346	syn	TA	MUL_5037	-	intermediary metabolism and respiration	ferredoxin-dependent glutamate synthase [NADPH] (large subunit) GltB
5584601	syn	TC	MUL_5037	-	intermediary metabolism and respiration	ferredoxin-dependent glutamate synthase [NADPH] (large subunit) GltB
5586110	Int.	CT	127 MUL_5037		intermediary metabolism and respiration	ferredoxin-dependent glutamate synthase [NADPH] (large subunit) GltB
5586783	psd	CT	MUL_5038	-	conserved hypothetical	mid-section conserved hypothetical protein pseudogene
5595097	psd	CG	MUL_5042	-	cell wall and cell processes	C-term conserved hypothetical alanine and proline rich membrane protein pseudogene
5596075	psd	GA	MUL_5042	-	cell wall and cell processes	C-term conserved hypothetical alanine and proline rich membrane protein pseudogene
5597544	psd	CA	MUL_5043	-	cell wall and cell processes	C-term conserved hypothetical transmembrane protein pseudogene
5597976	Int.	TC	76 MUL_5043		cell wall and cell processes	C-term conserved hypothetical transmembrane protein pseudogene
5598343	psd	TG	MUL_5044	-	cell wall and cell processes	C-term conserved hypothetical alanine rich secreted protein pseudogene
5598577	psd	TG	MUL_5044	-	cell wall and cell processes	C-term conserved hypothetical alanine rich secreted protein pseudogene
5599476	non	GC	MUL_5045	-	cell wall and cell processes	conserved hypothetical transmembrane protein
5601349	psd	CT	MUL_5047	-	cell wall and cell processes	N-term conserved hypothetical membrane protein pseudogene
5606886	psd	TC	MUL_5053	-	conserved hypothetical	N-term ADP-ribosyltransferase pseudogene
5606894	psd	CG	MUL_5053	-	conserved hypothetical	N-term ADP-ribosyltransferase pseudogene
5606896	psd	AC	MUL_5053	-	conserved hypothetical	N-term ADP-ribosyltransferase pseudogene
5607165	syn	CT	MUL_5054	-	cell wall and cell processes	EsaT-6 like protein EsxE
5607193	non	TC	MUL_5054	-	cell wall and cell processes	EsaT-6 like protein EsxE
5607485	non	TC	MUL_5055	-	cell wall and cell processes	EsaT-6 like protein EsxF
5607528	non	CT	MUL_5055	-	cell wall and cell processes	EsaT-6 like protein EsxF
5608906	syn	TC	MUL_5057	-	conserved hypothetical	conserved hypothetical protein
5609880	syn	GA	MUL_5057	-	conserved hypothetical	conserved hypothetical protein
5610075	syn	AG	MUL_5057	-	conserved hypothetical	conserved hypothetical protein
5610131	non	CT	MUL_5057	-	conserved hypothetical	conserved hypothetical protein
5610422	Int.	AC	5610422 MUL_5057		conserved hypothetical	
5610661	non	CT	MUL_5058	-	conserved hypothetical	conserved hypothetical protein
5611880	syn	TC	MUL_5060	-	information pathways	poly(A) polymerase PcnA
5612897	syn	GC	MUL_5060	-	information pathways	poly(A) polymerase PcnA
5614323	syn	AG	MUL_5062	-	cell wall and cell processes	conserved hypothetical secreted protein
5614951	non	GC	MUL_5062	-	cell wall and cell processes	conserved hypothetical secreted protein
5616746	syn	GC	MUL_5063	-	cell wall and cell processes	conserved transmembrane protein
5617055	syn	GC	MUL_5063	-	cell wall and cell processes	conserved transmembrane protein
5618484	non	TC	MUL_5063	-	cell wall and cell processes	conserved transmembrane protein
5620108	syn	TC	MUL_5064	-	information pathways	alternative RNA polymerase sigma factor SigM
5620594	non	AG	MUL_5064	-	information pathways	alternative RNA polymerase sigma factor SigM
5621820	non	CG	MUL_5066	-	intermediary metabolism and respiration	thioredoxin reductase TrxB2
5625081	Int.	GC	60 MUL_5069		conserved hypothetical	conserved hypothetical protein
5625547	syn	CG	MUL_5070	-	cell wall and cell processes	chromosome partitioning protein ParB
5625664	syn	AG	MUL_5070	-	cell wall and cell processes	chromosome partitioning protein ParB
5625985	syn	CT	MUL_5070	-	cell wall and cell processes	chromosome partitioning protein ParB
5628102	syn	GA	MUL_5072	-	cell wall and cell processes	glucose-inhibited division protein B Gid
5628503	syn	AG	MUL_5073	-	conserved hypothetical	conserved protein
5629130	non	AG	MUL_5074	-	cell wall and cell processes	conserved transmembrane protein
5629193	non	CT	MUL_5074	-	cell wall and cell processes	conserved transmembrane protein
5631533	Int.	GA	5631533 MUL_5074		conserved hypothetical	

Strain Groupings used in Pan/Core genome Analysis

Strain Identifier	Pan Core Group prefix used in tables						
	Species Groups		Host Groups		Region Groups		
	mm - M.marinum strains	mu - M.ulcerans strains	hs - Human host strains	fi - Fish/frog host strains	au - Australian strains	af - African strains	rw - Rest of world strains
Mm_M	✓						
Mm_1726	✓						
Mm_99/84	✓						
Mm_99/87	✓						
Mm_99/89	✓						
Mu_06-3845		✓				✓	
Mu_001506		✓		✓		✓	
Mu_NM49.02		✓	✓	✓		✓	
Mu_06-3846		✓	✓	✓		✓	
Mu_07-1082		✓	✓	✓		✓	
Mu_Agy99		✓	✓	✓		✓	
Mu_NM14.01		✓	✓	✓		✓	
Mu_NM33.04		✓	✓	✓		✓	
Mu_NM43.02		✓	✓	✓		✓	
Mu_NM54.02		✓	✓	✓		✓	
Mu_980535		✓	✓	✓		✓	
Mu_000945		✓	✓	✓		✓	
Mu_991845		✓	✓	✓		✓	
Mu_13822-70		✓	✓		✓		
Mu_113		✓	✓		✓		
Mu_119		✓	✓		✓		
Mu_74		✓	✓		✓		
Mu_81		✓	✓		✓		
Mu_93		✓	✓		✓		
Mu_08009899		✓	✓		✓		
Mu_JKD8049		✓	✓		✓		
Mu_JKD8170		✓	✓		✓		
Mu_05142109		✓	✓		✓		
Mu_8765		✓	✓				✓
Mu_1G897		✓	✓				✓
Mu_L15		✓		✓			✓
Mu_CC240299		✓		✓			✓
Mu_06-3844		✓		✓			✓
Mu_JKD8071		✓		✓			✓

Table 9(a)

Pan Core Diagnostic Segments

Legend	Description
muref	Agy99 reference used for mapping reads
mmref	M.marinum "M" used for mapping reads
afcore, afpan	African strains core and pan genomes see Strain Groups tab
aucore, aupan	Australian strains core and pan genomes see Strain Groups tab
rwcore, rwpan	Non African/Australian strains core and pan genomes see Strain Groups tab
hscore, hspan	Human host strains core and pan genomes see Strain Groups tab
ficore, fipan	Fish and Frog host strains core and pan genomes see Strain Groups tab

Reference	Core Group	Pan Group	Start	End	Length
mmref	afcore	aupan	1000555	1000793	239
mmref	afcore	aupan	1849456	1849656	201
mmref	afcore	aupan	1849933	1850205	273
mmref	afcore	aupan	1850223	1850466	244
mmref	afcore	aupan	5326769	5327041	273
mmref	afcore	aupan	5352871	5353211	341
mmref	afcore	aupan	5353230	5353506	277
mmref	afcore	aupan	5456139	5456420	282
mmref	afcore	aupan	5456441	5456673	233
mmref	afcore	rwaupan	5353230	5353506	277
mmref	afcore	rwpan	232264	232494	231
mmref	afcore	rwpan	1814194	1814432	239
mmref	afcore	rwpan	2715724	2716002	279
mmref	afcore	rwpan	3708030	3708435	406
mmref	afcore	rwpan	3859125	3859566	442
mmref	afcore	rwpan	3974957	3975287	331
mmref	afcore	rwpan	3975305	3976052	748
mmref	afcore	rwpan	4156363	4157198	836
mmref	afcore	rwpan	4157225	4157693	469
mmref	afcore	rwpan	4158765	4159010	246
mmref	afcore	rwpan	4161882	4163015	1134
mmref	afcore	rwpan	4163126	4163349	224
mmref	afcore	rwpan	4929772	4930507	736
mmref	afcore	rwpan	4930549	4930782	234
mmref	afcore	rwpan	4930905	4931560	656
mmref	afcore	rwpan	4932069	4932393	325
mmref	afcore	rwpan	4933173	4933441	269
mmref	afcore	rwpan	4933460	4933987	528
mmref	afcore	rwpan	4935372	4935598	227
mmref	afcore	rwpan	4935849	4936083	235
mmref	afcore	rwpan	5353030	5353506	477
mmref	afcore	rwpan	6425416	6425726	311
mmref	afcore	rwpan	6425788	6426006	219
mmref	aucore	afpan	763629	763857	229
mmref	aucore	afpan	2903776	2904176	401
mmref	aucore	afpan	2904333	2904752	420
mmref	aucore	afpan	3176629	3176830	202
mmref	aucore	afpan	3509602	3509812	211
mmref	aucore	afpan	3509831	3510067	237
mmref	aucore	afpan	3512942	3513150	209
mmref	aucore	afpan	5131876	5132114	239
mmref	aucore	afpan	5367108	5367428	321

Reference	Core Group	Pan Group	Start	End	Length
mmref	aucore	afrpan	6022361	6022765	405
mmref	aucore	afrpan	6265420	6265737	318
mmref	aucore	rwpans	232270	232494	225
mmref	aucore	rwpans	1814194	1814432	239
mmref	aucore	rwpans	2715724	2716002	279
mmref	aucore	rwpans	3708030	3708435	406
mmref	aucore	rwpans	3859125	3859566	442
mmref	aucore	rwpans	3974957	3975287	331
mmref	aucore	rwpans	3975305	3976052	748
mmref	aucore	rwpans	4156363	4157198	836
mmref	aucore	rwpans	4157225	4157693	469
mmref	aucore	rwpans	4161882	4163015	1134
mmref	aucore	rwpans	4163126	4163349	224
mmref	aucore	rwpans	4929772	4930507	736
mmref	aucore	rwpans	4930549	4930782	234
mmref	aucore	rwpans	4930905	4931560	656
mmref	aucore	rwpans	4932069	4932393	325
mmref	aucore	rwpans	4933173	4933441	269
mmref	aucore	rwpans	4933460	4933987	528
mmref	aucore	rwpans	4935372	4935598	227
mmref	aucore	rwpans	4935849	4936083	235
mmref	aucore	rwpans	6425416	6425726	311
mmref	aucore	rwpans	6425788	6426006	219
mmref	ficore	hspan	1408269	1408641	373
mmref	ficore	hspan	1408933	1409162	230
mmref	ficore	hspan	2264998	2265263	266
mmref	ficore	hspan	2268995	2269104	210
mmref	ficore	hspan	2272846	2273211	366
mmref	ficore	hspan	2274818	2275254	437
mmref	ficore	hspan	3514257	3514722	466
mmref	ficore	hspan	3781467	3781881	415
mmref	ficore	hspan	4168636	4168853	218
mmref	ficore	hspan	4173459	4173772	314
mmref	ficore	hspan	4176477	4176767	291
mmref	ficore	hspan	4181910	4182247	338
mmref	ficore	hspan	6198678	6198905	228
mmref	mmccore	mupans	144521	144746	226
mmref	mmccore	mupans	231848	232048	201
mmref	mmccore	mupans	688611	688814	204
mmref	mmccore	mupans	689527	689873	347
mmref	mmccore	mupans	815672	815955	284
mmref	mmccore	mupans	842973	843221	249
mmref	mmccore	mupans	843784	844278	495
mmref	mmccore	mupans	844536	844854	319
mmref	mmccore	mupans	1129924	1130288	365
mmref	mmccore	mupans	2816832	2817164	333
mmref	mmccore	mupans	2819026	2819247	222
mmref	mmccore	mupans	2822885	2823084	200
mmref	mmccore	mupans	2824000	2824250	251
mmref	mmccore	mupans	2825396	2825614	219
mmref	mmccore	mupans	3409908	3410157	250
mmref	mmccore	mupans	3411240	3411490	251
mmref	mmccore	mupans	3978693	3978893	201
mmref	mmccore	mupans	4158386	4158630	245
mmref	mmccore	mupans	4163723	4163952	230
mmref	mmccore	mupans	5241664	5242107	444
mmref	mmccore	mupans	5242317	5242589	273

Reference	Core Group	Pan Group	Start	End	Length
mmref	mmcore	mupan	5242716	5242931	216
mmref	mmcore	mupan	5242966	5243379	414
mmref	mmcore	mupan	5665784	5666041	258
mmref	mmcore	mupan	6554200	6554429	230
mmref	mmcore	mupan	6556730	6556932	203
mmref	mmcore	mupan	6562451	6562786	336
mmref	mmcore	mupan	6563644	6563843	200
mmref	mmcore	mupan	6565842	6566045	204
mmref	mmcore	mupan	6609482	6609759	278
mmref	rwcore	afaupan	131420	131638	219
mmref	rwcore	afaupan	135621	135837	217
mmref	rwcore	afaupan	136831	137055	225
mmref	rwcore	afaupan	139822	140088	267
mmref	rwcore	afaupan	140476	140702	227
mmref	rwcore	afaupan	140727	141026	300
mmref	rwcore	afaupan	141260	141508	249
mmref	rwcore	afaupan	143047	143252	206
mmref	rwcore	afaupan	143337	143675	339
mmref	rwcore	afaupan	153831	154255	425
mmref	rwcore	afaupan	157778	157981	204
mmref	rwcore	afaupan	161510	161781	272
mmref	rwcore	afaupan	161801	162247	447
mmref	rwcore	afaupan	310294	310545	252
mmref	rwcore	afaupan	310566	310897	332
mmref	rwcore	afaupan	311696	312353	658
mmref	rwcore	afaupan	313353	313639	287
mmref	rwcore	afaupan	318612	318811	200
mmref	rwcore	afaupan	319214	319425	212
mmref	rwcore	afaupan	319816	320184	369
mmref	rwcore	afaupan	320233	320611	379
mmref	rwcore	afaupan	322989	323244	256
mmref	rwcore	afaupan	601172	601389	218
mmref	rwcore	afaupan	929443	929860	418
mmref	rwcore	afaupan	930405	930706	302
mmref	rwcore	afaupan	1109912	1110116	205
mmref	rwcore	afaupan	1779326	1779567	242
mmref	rwcore	afaupan	1882020	1882229	210
mmref	rwcore	afaupan	1882649	1882866	218
mmref	rwcore	afaupan	1882899	1883190	292
mmref	rwcore	afaupan	1933417	1933622	206
mmref	rwcore	afaupan	1933672	1934029	358
mmref	rwcore	afaupan	2317257	2317501	245
mmref	rwcore	afaupan	2318759	2318993	235
mmref	rwcore	afaupan	2535527	2535903	377
mmref	rwcore	afaupan	2775446	2775646	201
mmref	rwcore	afaupan	3499225	3499446	222
mmref	rwcore	afaupan	3499737	3499978	242
mmref	rwcore	afaupan	3508271	3508497	227
mmref	rwcore	afaupan	3525530	3525773	244
mmref	rwcore	afaupan	3525925	3526128	204
mmref	rwcore	afaupan	3527327	3527566	240
mmref	rwcore	afaupan	3538179	3538624	446
mmref	rwcore	afaupan	3573583	3573820	238
mmref	rwcore	afaupan	3573840	3574164	325
mmref	rwcore	afaupan	3584774	3585046	273
mmref	rwcore	afaupan	3594896	3595104	209
mmref	rwcore	afaupan	3595347	3595578	232

Reference	Core Group	Pan Group	Start	End	Length
mmref	rwcore	afaupan	3595924	3596129	206
mmref	rwcore	afaupan	3602379	3602578	200
mmref	rwcore	afaupan	3607361	3607595	235
mmref	rwcore	afaupan	3610662	3610954	293
mmref	rwcore	afaupan	3613129	3613443	315
mmref	rwcore	afaupan	3974029	3974294	266
mmref	rwcore	afaupan	3974317	3974531	215
mmref	rwcore	afaupan	4226184	4226500	317
mmref	rwcore	afaupan	4228831	4229067	237
mmref	rwcore	afaupan	4229823	4230129	307
mmref	rwcore	afaupan	4278376	4278643	268
mmref	rwcore	afaupan	4279150	4279361	212
mmref	rwcore	afaupan	4280629	4280844	216
mmref	rwcore	afaupan	4286077	4286284	208
mmref	rwcore	afaupan	4291294	4291661	368
mmref	rwcore	afaupan	4292260	4292478	219
mmref	rwcore	afaupan	4293542	4293878	337
mmref	rwcore	afaupan	4295183	4295409	227
mmref	rwcore	afaupan	4300827	4301028	202
mmref	rwcore	afaupan	4305290	4305522	233
mmref	rwcore	afaupan	4306641	4306877	237
mmref	rwcore	afaupan	4308373	4308603	231
mmref	rwcore	afaupan	4310899	4311415	517
mmref	rwcore	afaupan	4313042	4313284	243
mmref	rwcore	afaupan	4313310	4313536	227
mmref	rwcore	afaupan	4474589	4474841	253
mmref	rwcore	afaupan	4475033	4475302	270
mmref	rwcore	afaupan	4475331	4475582	252
mmref	rwcore	afaupan	4501579	4501903	325
mmref	rwcore	afaupan	4560251	4560464	214
mmref	rwcore	afaupan	4627867	4628075	209
mmref	rwcore	afaupan	5080045	5080395	351
mmref	rwcore	afaupan	5080950	5081228	279
mmref	rwcore	afaupan	5197389	5197677	289
mmref	rwcore	afaupan	5325535	5325975	441
mmref	rwcore	afaupan	5432810	5433094	285
mmref	rwcore	afaupan	5433469	5433682	214
mmref	rwcore	afaupan	5437146	5437456	311
mmref	rwcore	afaupan	5439868	5440082	215
mmref	rwcore	afaupan	5443096	5443300	205
mmref	rwcore	afaupan	5443495	5443715	221
mmref	rwcore	afaupan	5445027	5445407	381
mmref	rwcore	afaupan	5445509	5445839	331
mmref	rwcore	afaupan	5445967	5446284	318
mmref	rwcore	afaupan	5748169	5748388	220
mmref	rwcore	afaupan	5750779	5751190	412
mmref	rwcore	afaupan	5751230	5751489	260
mmref	rwcore	afaupan	5758673	5758932	260
mmref	rwcore	afaupan	5761712	5761926	215
mmref	rwcore	afaupan	5762681	5762992	312
mmref	rwcore	afaupan	5772140	5772399	260
mmref	rwcore	afaupan	5776621	5777023	403
mmref	rwcore	afaupan	5777394	5777657	264
mmref	rwcore	afaupan	5778368	5778622	255
mmref	rwcore	afaupan	5780577	5780877	301
mmref	rwcore	afaupan	5783319	5783526	208
mmref	rwcore	afaupan	5793344	5793552	209

Reference	Core Group	Pan Group	Start	End	Length
mmref	rwcore	afaupan	5831393	5831645	253
mmref	rwcore	afaupan	5956568	5956819	252
mmref	rwcore	afaupan	6459560	6459793	234
mmref	rwcore	aften	131420	131638	219
mmref	rwcore	aften	132393	132645	253
mmref	rwcore	aften	135621	135837	217
mmref	rwcore	aften	136831	137055	225
mmref	rwcore	aften	139822	140088	267
mmref	rwcore	aften	140476	140702	227
mmref	rwcore	aften	140727	141026	300
mmref	rwcore	aften	141260	141508	249
mmref	rwcore	aften	143047	143252	206
mmref	rwcore	aften	143337	143675	339
mmref	rwcore	aften	153831	154255	425
mmref	rwcore	aften	157778	157981	204
mmref	rwcore	aften	161433	162247	815
mmref	rwcore	aften	310294	310545	252
mmref	rwcore	aften	310566	310897	332
mmref	rwcore	aften	311696	312353	658
mmref	rwcore	aften	313353	313639	287
mmref	rwcore	aften	318612	318850	239
mmref	rwcore	aften	319214	319425	212
mmref	rwcore	aften	319816	320184	369
mmref	rwcore	aften	320233	320611	379
mmref	rwcore	aften	322989	323244	256
mmref	rwcore	aften	601172	601393	222
mmref	rwcore	aften	763629	763857	229
mmref	rwcore	aften	831946	832171	226
mmref	rwcore	aften	929443	929860	418
mmref	rwcore	aften	930405	930706	302
mmref	rwcore	aften	1109912	1110116	205
mmref	rwcore	aften	1360709	1360922	214
mmref	rwcore	aften	1779326	1779567	242
mmref	rwcore	aften	1882020	1882229	210
mmref	rwcore	aften	1882649	1882866	218
mmref	rwcore	aften	1882899	1883246	348
mmref	rwcore	aften	1932893	1933106	214
mmref	rwcore	aften	1933280	1933622	343
mmref	rwcore	aften	1933672	1934029	358
mmref	rwcore	aften	2317257	2317501	245
mmref	rwcore	aften	2318759	2318993	235
mmref	rwcore	aften	2535455	2535903	449
mmref	rwcore	aften	2775446	2775646	201
mmref	rwcore	aften	2903776	2904176	401
mmref	rwcore	aften	3176629	3176830	202
mmref	rwcore	aften	3498341	3498589	249
mmref	rwcore	aften	3499225	3499446	222
mmref	rwcore	aften	3499737	3499978	242
mmref	rwcore	aften	3508271	3508497	227
mmref	rwcore	aften	3509602	3509812	211
mmref	rwcore	aften	3522320	3522632	313
mmref	rwcore	aften	3525530	3525773	244
mmref	rwcore	aften	3525925	3526128	204
mmref	rwcore	aften	3527327	3527566	240
mmref	rwcore	aften	3529402	3529694	293
mmref	rwcore	aften	3538179	3538624	446
mmref	rwcore	aften	3573583	3573820	238

Reference	Core Group	Pan Group	Start	End	Length
mmref	rwcore	afrpan	3573840	3574164	325
mmref	rwcore	afrpan	3584774	3585080	307
mmref	rwcore	afrpan	3594890	3595104	215
mmref	rwcore	afrpan	3595347	3595578	232
mmref	rwcore	afrpan	3595842	3596129	288
mmref	rwcore	afrpan	3602379	3602578	200
mmref	rwcore	afrpan	3607361	3607595	235
mmref	rwcore	afrpan	3610662	3610954	293
mmref	rwcore	afrpan	3613129	3613605	477
mmref	rwcore	afrpan	3974029	3974294	266
mmref	rwcore	afrpan	3974317	3974531	215
mmref	rwcore	afrpan	4226184	4226501	318
mmref	rwcore	afrpan	4228831	4229115	285
mmref	rwcore	afrpan	4229823	4230129	307
mmref	rwcore	afrpan	4278337	4278643	307
mmref	rwcore	afrpan	4279150	4279361	212
mmref	rwcore	afrpan	4280629	4280844	216
mmref	rwcore	afrpan	4281351	4281581	231
mmref	rwcore	afrpan	4286077	4286284	208
mmref	rwcore	afrpan	4291294	4291661	368
mmref	rwcore	afrpan	4292260	4292478	219
mmref	rwcore	afrpan	4293542	4293878	337
mmref	rwcore	afrpan	4295183	4295409	227
mmref	rwcore	afrpan	4300827	4301028	202
mmref	rwcore	afrpan	4305290	4305522	233
mmref	rwcore	afrpan	4306641	4306877	237
mmref	rwcore	afrpan	4308373	4308603	231
mmref	rwcore	afrpan	4310899	4311415	517
mmref	rwcore	afrpan	4311788	4312115	328
mmref	rwcore	afrpan	4313042	4313284	243
mmref	rwcore	afrpan	4313310	4313536	227
mmref	rwcore	afrpan	4474589	4474841	253
mmref	rwcore	afrpan	4475033	4475302	270
mmref	rwcore	afrpan	4475331	4475582	252
mmref	rwcore	afrpan	4501579	4501903	325
mmref	rwcore	afrpan	4560251	4560464	214
mmref	rwcore	afrpan	4627867	4628075	209
mmref	rwcore	afrpan	5080045	5080395	351
mmref	rwcore	afrpan	5080950	5081228	279
mmref	rwcore	afrpan	5131876	5132114	239
mmref	rwcore	afrpan	5184723	5184952	230
mmref	rwcore	afrpan	5186864	5187063	200
mmref	rwcore	afrpan	5197389	5197677	289
mmref	rwcore	afrpan	5325535	5325975	441
mmref	rwcore	afrpan	5367108	5367428	321
mmref	rwcore	afrpan	5432810	5433094	285
mmref	rwcore	afrpan	5433469	5433682	214
mmref	rwcore	afrpan	5434140	5434369	230
mmref	rwcore	afrpan	5437146	5437456	311
mmref	rwcore	afrpan	5439868	5440082	215
mmref	rwcore	afrpan	5443096	5443300	205
mmref	rwcore	afrpan	5443495	5443715	221
mmref	rwcore	afrpan	5445027	5445407	381
mmref	rwcore	afrpan	5445509	5445839	331
mmref	rwcore	afrpan	5445959	5446284	326
mmref	rwcore	afrpan	5748065	5748388	324
mmref	rwcore	afrpan	5750779	5751190	412

Reference	Core Group	Pan Group	Start	End	Length
mmref	rwcore	african	5751230	5751489	260
mmref	rwcore	african	5758673	5758932	260
mmref	rwcore	african	5761712	5761926	215
mmref	rwcore	african	5762681	5762992	312
mmref	rwcore	african	5765735	5766082	348
mmref	rwcore	african	5772138	5772399	262
mmref	rwcore	african	5776621	5777023	403
mmref	rwcore	african	5777394	5777657	264
mmref	rwcore	african	5778368	5778622	255
mmref	rwcore	african	5780576	5780877	302
mmref	rwcore	african	5783300	5783526	227
mmref	rwcore	african	5793344	5793562	219
mmref	rwcore	african	5795162	5795425	264
mmref	rwcore	african	5831393	5831645	253
mmref	rwcore	african	5956568	5956819	252
mmref	rwcore	african	6022361	6022765	405
mmref	rwcore	african	6265420	6265737	318
mmref	rwcore	african	6269417	6269640	224
mmref	rwcore	african	6459453	6459796	344
mmref	rwcore	african	91425	91667	243
mmref	rwcore	african	130716	131127	412
mmref	rwcore	african	131416	132160	745
mmref	rwcore	african	132180	132588	409
mmref	rwcore	african	132946	133231	286
mmref	rwcore	african	134783	135060	278
mmref	rwcore	african	135525	136027	503
mmref	rwcore	african	136490	136802	313
mmref	rwcore	african	136825	137055	231
mmref	rwcore	african	137697	137900	204
mmref	rwcore	african	137919	138128	210
mmref	rwcore	african	138796	139005	210
mmref	rwcore	african	139023	139245	223
mmref	rwcore	african	139440	139720	281
mmref	rwcore	african	139738	140094	357
mmref	rwcore	african	140120	140402	283
mmref	rwcore	african	140425	141026	602
mmref	rwcore	african	141064	141595	532
mmref	rwcore	african	141615	141826	212
mmref	rwcore	african	141888	142103	216
mmref	rwcore	african	143030	143253	224
mmref	rwcore	african	143274	144210	937
mmref	rwcore	african	145431	145652	222
mmref	rwcore	african	145753	145991	239
mmref	rwcore	african	147128	148026	899
mmref	rwcore	african	148279	148556	278
mmref	rwcore	african	148753	149101	349
mmref	rwcore	african	150297	150632	336
mmref	rwcore	african	150767	151702	936
mmref	rwcore	african	152437	153042	606
mmref	rwcore	african	153269	153685	417
mmref	rwcore	african	153831	154280	450
mmref	rwcore	african	154456	154658	203
mmref	rwcore	african	156291	156495	205
mmref	rwcore	african	156562	156946	385
mmref	rwcore	african	157323	157571	249
mmref	rwcore	african	157660	158059	400
mmref	rwcore	african	158078	158317	240

Reference	Core Group	Pan Group	Start	End	Length
mmref	rwcore	aupan	158344	158657	314
mmref	rwcore	aupan	159045	159286	242
mmref	rwcore	aupan	159780	160153	374
mmref	rwcore	aupan	160285	160762	478
mmref	rwcore	aupan	160932	161150	219
mmref	rwcore	aupan	161169	161486	318
mmref	rwcore	aupan	161510	161781	272
mmref	rwcore	aupan	161801	162248	448
mmref	rwcore	aupan	258357	258715	359
mmref	rwcore	aupan	310053	311020	968
mmref	rwcore	aupan	311051	311279	229
mmref	rwcore	aupan	311448	313132	1685
mmref	rwcore	aupan	313166	313651	486
mmref	rwcore	aupan	314944	315215	272
mmref	rwcore	aupan	315251	315691	441
mmref	rwcore	aupan	316293	316776	484
mmref	rwcore	aupan	316808	317117	310
mmref	rwcore	aupan	317552	317870	319
mmref	rwcore	aupan	317993	318577	585
mmref	rwcore	aupan	318600	318814	215
mmref	rwcore	aupan	318834	319584	751
mmref	rwcore	aupan	319816	320184	369
mmref	rwcore	aupan	320207	320693	487
mmref	rwcore	aupan	320713	321087	375
mmref	rwcore	aupan	321341	321598	258
mmref	rwcore	aupan	322465	322699	235
mmref	rwcore	aupan	322918	323263	346
mmref	rwcore	aupan	323283	323504	222
mmref	rwcore	aupan	600870	601532	663
mmref	rwcore	aupan	830834	831603	770
mmref	rwcore	aupan	831849	832052	204
mmref	rwcore	aupan	928918	929998	1081
mmref	rwcore	aupan	930394	930927	534
mmref	rwcore	aupan	1109901	1110116	216
mmref	rwcore	aupan	1111084	1111291	208
mmref	rwcore	aupan	1140646	1141047	402
mmref	rwcore	aupan	1141967	1142179	213
mmref	rwcore	aupan	1142208	1142501	294
mmref	rwcore	aupan	1373605	1373872	268
mmref	rwcore	aupan	1615187	1615427	241
mmref	rwcore	aupan	1779326	1779567	242
mmref	rwcore	aupan	1849456	1849656	201
mmref	rwcore	aupan	1856348	1856548	201
mmref	rwcore	aupan	1881037	1881987	951
mmref	rwcore	aupan	1882007	1882231	225
mmref	rwcore	aupan	1882306	1882513	208
mmref	rwcore	aupan	1882550	1883190	641
mmref	rwcore	aupan	1883277	1883560	284
mmref	rwcore	aupan	1883667	1883935	269
mmref	rwcore	aupan	1883987	1884323	337
mmref	rwcore	aupan	1931807	1932012	206
mmref	rwcore	aupan	1932402	1932688	287
mmref	rwcore	aupan	1932707	1933021	315
mmref	rwcore	aupan	1933084	1933380	297
mmref	rwcore	aupan	1933417	1933646	230
mmref	rwcore	aupan	1933671	1934041	371
mmref	rwcore	aupan	1934067	1934608	542

Reference	Core Group	Pan Group	Start	End	Length
mmref	rwcore	aupan	2316643	2317057	415
mmref	rwcore	aupan	2317256	2317652	397
mmref	rwcore	aupan	2317871	2318127	257
mmref	rwcore	aupan	2318637	2319031	395
mmref	rwcore	aupan	2319481	2319826	346
mmref	rwcore	aupan	2382310	2382514	205
mmref	rwcore	aupan	2382533	2383294	762
mmref	rwcore	aupan	2487361	2487814	454
mmref	rwcore	aupan	2535035	2535507	473
mmref	rwcore	aupan	2535527	2536077	551
mmref	rwcore	aupan	2607949	2608195	247
mmref	rwcore	aupan	2608213	2608644	432
mmref	rwcore	aupan	2609241	2609453	213
mmref	rwcore	aupan	2774426	2774799	374
mmref	rwcore	aupan	2774821	2775031	211
mmref	rwcore	aupan	2775445	2775653	209
mmref	rwcore	aupan	2832139	2832463	325
mmref	rwcore	aupan	2832487	2833016	530
mmref	rwcore	aupan	2833077	2833310	234
mmref	rwcore	aupan	3400597	3401352	756
mmref	rwcore	aupan	3498449	3498816	368
mmref	rwcore	aupan	3499225	3499695	471
mmref	rwcore	aupan	3499727	3500074	348
mmref	rwcore	aupan	3507626	3507978	353
mmref	rwcore	aupan	3508260	3508503	244
mmref	rwcore	aupan	3508531	3508983	453
mmref	rwcore	aupan	3509002	3509565	564
mmref	rwcore	aupan	3522694	3522984	291
mmref	rwcore	aupan	3523196	3523490	295
mmref	rwcore	aupan	3524817	3525124	308
mmref	rwcore	aupan	3525159	3525501	343
mmref	rwcore	aupan	3525527	3525901	375
mmref	rwcore	aupan	3525925	3526130	206
mmref	rwcore	aupan	3526152	3526525	374
mmref	rwcore	aupan	3526797	3527245	449
mmref	rwcore	aupan	3527327	3527592	266
mmref	rwcore	aupan	3527614	3528017	404
mmref	rwcore	aupan	3528434	3528641	208
mmref	rwcore	aupan	3528663	3528998	336
mmref	rwcore	aupan	3529953	3530182	230
mmref	rwcore	aupan	3530807	3531090	284
mmref	rwcore	aupan	3531243	3531546	304
mmref	rwcore	aupan	3532033	3532370	338
mmref	rwcore	aupan	3532389	3532591	203
mmref	rwcore	aupan	3533892	3534370	479
mmref	rwcore	aupan	3534393	3535117	725
mmref	rwcore	aupan	3535221	3535478	258
mmref	rwcore	aupan	3535536	3536098	563
mmref	rwcore	aupan	3536307	3536918	612
mmref	rwcore	aupan	3537642	3537865	224
mmref	rwcore	aupan	3538073	3538804	732
mmref	rwcore	aupan	3539442	3539689	248
mmref	rwcore	aupan	3545777	3545985	209
mmref	rwcore	aupan	3546009	3546535	527
mmref	rwcore	aupan	3573583	3574248	666
mmref	rwcore	aupan	3584774	3585046	273
mmref	rwcore	aupan	3585657	3585861	205

Reference	Core Group	Pan Group	Start	End	Length
mmref	rwcore	aupan	3594896	3595193	298
mmref	rwcore	aupan	3595215	3595585	371
mmref	rwcore	aupan	3595816	3596129	314
mmref	rwcore	aupan	3596396	3596597	202
mmref	rwcore	aupan	3596809	3597010	202
mmref	rwcore	aupan	3600365	3600867	503
mmref	rwcore	aupan	3600891	3601427	537
mmref	rwcore	aupan	3601489	3602034	546
mmref	rwcore	aupan	3602109	3602732	624
mmref	rwcore	aupan	3604643	3604930	288
mmref	rwcore	aupan	3604956	3605228	273
mmref	rwcore	aupan	3605253	3605989	737
mmref	rwcore	aupan	3606058	3606574	517
mmref	rwcore	aupan	3606997	3607237	241
mmref	rwcore	aupan	3607262	3607598	337
mmref	rwcore	aupan	3607670	3607893	224
mmref	rwcore	aupan	3607922	3608473	552
mmref	rwcore	aupan	3609353	3609625	273
mmref	rwcore	aupan	3609752	3610113	362
mmref	rwcore	aupan	3610654	3611127	474
mmref	rwcore	aupan	3611388	3611624	237
mmref	rwcore	aupan	3612053	3612398	346
mmref	rwcore	aupan	3612419	3613095	677
mmref	rwcore	aupan	3613114	3613777	664
mmref	rwcore	aupan	3613797	3614198	402
mmref	rwcore	aupan	3614224	3614470	247
mmref	rwcore	aupan	3614513	3614818	306
mmref	rwcore	aupan	3614968	3615287	320
mmref	rwcore	aupan	3782224	3782610	387
mmref	rwcore	aupan	3783584	3783834	251
mmref	rwcore	aupan	3784191	3784632	442
mmref	rwcore	aupan	3942582	3942823	242
mmref	rwcore	aupan	3974010	3974531	522
mmref	rwcore	aupan	4088088	4088503	416
mmref	rwcore	aupan	4088892	4089422	531
mmref	rwcore	aupan	4095817	4096136	320
mmref	rwcore	aupan	4097090	4097293	204
mmref	rwcore	aupan	4097638	4097949	312
mmref	rwcore	aupan	4098151	4098460	310
mmref	rwcore	aupan	4099030	4099272	243
mmref	rwcore	aupan	4099343	4099638	296
mmref	rwcore	aupan	4099722	4099941	220
mmref	rwcore	aupan	4100395	4100755	361
mmref	rwcore	aupan	4101298	4101525	228
mmref	rwcore	aupan	4101628	4101998	371
mmref	rwcore	aupan	4102353	4102603	251
mmref	rwcore	aupan	4102851	4103117	267
mmref	rwcore	aupan	4103974	4104180	207
mmref	rwcore	aupan	4107638	4107906	269
mmref	rwcore	aupan	4108193	4108435	243
mmref	rwcore	aupan	4108636	4108840	205
mmref	rwcore	aupan	4109130	4109462	333
mmref	rwcore	aupan	4226114	4226500	387
mmref	rwcore	aupan	4226699	4226916	218
mmref	rwcore	aupan	4228518	4229067	550
mmref	rwcore	aupan	4229758	4230138	381
mmref	rwcore	aupan	4277289	4277529	241

Reference	Core Group	Pan Group	Start	End	Length
mmref	rwcore	aupan	4278128	4278355	228
mmref	rwcore	aupan	4278376	4278774	399
mmref	rwcore	aupan	4279036	4279365	330
mmref	rwcore	aupan	4279487	4279954	468
mmref	rwcore	aupan	4279986	4280299	314
mmref	rwcore	aupan	4280319	4280520	202
mmref	rwcore	aupan	4280564	4280851	288
mmref	rwcore	aupan	4281599	4281799	201
mmref	rwcore	aupan	4281957	4282243	287
mmref	rwcore	aupan	4282265	4282499	235
mmref	rwcore	aupan	4282873	4283576	704
mmref	rwcore	aupan	4283618	4283903	286
mmref	rwcore	aupan	4283922	4284152	231
mmref	rwcore	aupan	4284171	4284419	249
mmref	rwcore	aupan	4284625	4284956	332
mmref	rwcore	aupan	4285013	4285266	254
mmref	rwcore	aupan	4285323	4285751	429
mmref	rwcore	aupan	4286036	4286284	249
mmref	rwcore	aupan	4287561	4287830	270
mmref	rwcore	aupan	4287848	4288084	237
mmref	rwcore	aupan	4288546	4288953	408
mmref	rwcore	aupan	4289087	4289454	368
mmref	rwcore	aupan	4290594	4290972	379
mmref	rwcore	aupan	4291049	4291702	654
mmref	rwcore	aupan	4292144	4292656	513
mmref	rwcore	aupan	4293192	4293878	687
mmref	rwcore	aupan	4293897	4294430	534
mmref	rwcore	aupan	4294838	4295416	579
mmref	rwcore	aupan	4295777	4296054	278
mmref	rwcore	aupan	4296091	4296317	227
mmref	rwcore	aupan	4296344	4296598	255
mmref	rwcore	aupan	4296620	4296904	285
mmref	rwcore	aupan	4297368	4298011	644
mmref	rwcore	aupan	4298727	4299241	515
mmref	rwcore	aupan	4300345	4300791	447
mmref	rwcore	aupan	4300811	4301041	231
mmref	rwcore	aupan	4301562	4301795	234
mmref	rwcore	aupan	4302330	4302580	251
mmref	rwcore	aupan	4302614	4303087	474
mmref	rwcore	aupan	4303107	4303481	375
mmref	rwcore	aupan	4303590	4304071	482
mmref	rwcore	aupan	4304157	4304400	244
mmref	rwcore	aupan	4304483	4304992	510
mmref	rwcore	aupan	4305204	4305530	327
mmref	rwcore	aupan	4305661	4305974	314
mmref	rwcore	aupan	4306072	4306934	863
mmref	rwcore	aupan	4307229	4307491	263
mmref	rwcore	aupan	4308358	4308603	246
mmref	rwcore	aupan	4309376	4309589	214
mmref	rwcore	aupan	4309881	4310137	257
mmref	rwcore	aupan	4310177	4310411	235
mmref	rwcore	aupan	4310896	4311767	872
mmref	rwcore	aupan	4311788	4312115	328
mmref	rwcore	aupan	4312333	4312577	245
mmref	rwcore	aupan	4313005	4313284	280
mmref	rwcore	aupan	4313303	4313556	254
mmref	rwcore	aupan	4431871	4432104	234

Reference	Core Group	Pan Group	Start	End	Length
mmref	rwcore	aupan	4474589	4475622	1034
mmref	rwcore	aupan	4476542	4476780	239
mmref	rwcore	aupan	4501414	4501934	521
mmref	rwcore	aupan	4560088	4560474	387
mmref	rwcore	aupan	4560502	4561104	603
mmref	rwcore	aupan	4561127	4561536	410
mmref	rwcore	aupan	4627849	4628316	468
mmref	rwcore	aupan	5079926	5080664	739
mmref	rwcore	aupan	5080792	5081613	822
mmref	rwcore	aupan	5081638	5081934	297
mmref	rwcore	aupan	5081962	5082230	269
mmref	rwcore	aupan	5082253	5082476	224
mmref	rwcore	aupan	5127792	5128173	382
mmref	rwcore	aupan	5128192	5128572	381
mmref	rwcore	aupan	5183560	5183795	236
mmref	rwcore	aupan	5184584	5184789	206
mmref	rwcore	aupan	5184808	5185026	219
mmref	rwcore	aupan	5185481	5185705	225
mmref	rwcore	aupan	5186081	5186451	371
mmref	rwcore	aupan	5186857	5187204	348
mmref	rwcore	aupan	5196725	5197062	338
mmref	rwcore	aupan	5197080	5197370	291
mmref	rwcore	aupan	5197389	5197680	292
mmref	rwcore	aupan	5198109	5198352	244
mmref	rwcore	aupan	5325526	5326326	801
mmref	rwcore	aupan	5351748	5352432	685
mmref	rwcore	aupan	5430030	5430272	243
mmref	rwcore	aupan	5430299	5430856	558
mmref	rwcore	aupan	5430877	5431221	345
mmref	rwcore	aupan	5431830	5432310	481
mmref	rwcore	aupan	5432782	5433216	435
mmref	rwcore	aupan	5433242	5433828	587
mmref	rwcore	aupan	5436211	5436669	459
mmref	rwcore	aupan	5437024	5437517	494
mmref	rwcore	aupan	5437572	5437796	225
mmref	rwcore	aupan	5438106	5438542	437
mmref	rwcore	aupan	5438790	5439053	264
mmref	rwcore	aupan	5439074	5439492	419
mmref	rwcore	aupan	5439514	5440082	569
mmref	rwcore	aupan	5440292	5440588	297
mmref	rwcore	aupan	5441542	5441933	392
mmref	rwcore	aupan	5442767	5443345	579
mmref	rwcore	aupan	5443495	5443895	401
mmref	rwcore	aupan	5443917	5444389	473
mmref	rwcore	aupan	5444419	5444693	275
mmref	rwcore	aupan	5444717	5444932	216
mmref	rwcore	aupan	5445027	5445477	451
mmref	rwcore	aupan	5445507	5445949	443
mmref	rwcore	aupan	5445967	5446284	318
mmref	rwcore	aupan	5446302	5446838	537
mmref	rwcore	aupan	5446858	5447141	284
mmref	rwcore	aupan	5627540	5627933	394
mmref	rwcore	aupan	5695498	5695713	216
mmref	rwcore	aupan	5747901	5748149	249
mmref	rwcore	aupan	5748169	5748389	221
mmref	rwcore	aupan	5748417	5748634	218
mmref	rwcore	aupan	5749109	5749512	404

Reference	Core Group	Pan Group	Start	End	Length
mmref	rwcore	aupan	5749565	5749802	238
mmref	rwcore	aupan	5750186	5750437	252
mmref	rwcore	aupan	5750631	5751197	567
mmref	rwcore	aupan	5751219	5751496	278
mmref	rwcore	aupan	5751617	5751820	204
mmref	rwcore	aupan	5751889	5752107	219
mmref	rwcore	aupan	5752128	5752342	215
mmref	rwcore	aupan	5752561	5752910	350
mmref	rwcore	aupan	5753621	5753829	209
mmref	rwcore	aupan	5753848	5754095	248
mmref	rwcore	aupan	5754117	5754757	641
mmref	rwcore	aupan	5754778	5755024	247
mmref	rwcore	aupan	5755076	5755300	225
mmref	rwcore	aupan	5755730	5756065	336
mmref	rwcore	aupan	5756469	5756852	384
mmref	rwcore	aupan	5757331	5757614	284
mmref	rwcore	aupan	5757717	5757984	268
mmref	rwcore	aupan	5758003	5758244	242
mmref	rwcore	aupan	5758274	5758603	330
mmref	rwcore	aupan	5758625	5758933	309
mmref	rwcore	aupan	5759020	5759320	301
mmref	rwcore	aupan	5759464	5759670	207
mmref	rwcore	aupan	5759695	5759923	229
mmref	rwcore	aupan	5759945	5760355	411
mmref	rwcore	aupan	5760788	5761040	253
mmref	rwcore	aupan	5761696	5762039	344
mmref	rwcore	aupan	5762630	5763096	467
mmref	rwcore	aupan	5763125	5763366	242
mmref	rwcore	aupan	5763384	5763674	291
mmref	rwcore	aupan	5763743	5763970	228
mmref	rwcore	aupan	5765724	5765926	203
mmref	rwcore	aupan	5772140	5772399	260
mmref	rwcore	aupan	5773952	5774159	208
mmref	rwcore	aupan	5774354	5774580	227
mmref	rwcore	aupan	5774656	5775344	689
mmref	rwcore	aupan	5775426	5776100	675
mmref	rwcore	aupan	5776518	5777073	556
mmref	rwcore	aupan	5777382	5777858	477
mmref	rwcore	aupan	5778076	5778284	209
mmref	rwcore	aupan	5778303	5778727	425
mmref	rwcore	aupan	5778750	5779021	272
mmref	rwcore	aupan	5779393	5779729	337
mmref	rwcore	aupan	5780162	5780550	389
mmref	rwcore	aupan	5780577	5781156	580
mmref	rwcore	aupan	5781648	5782071	424
mmref	rwcore	aupan	5782102	5782323	222
mmref	rwcore	aupan	5783319	5783787	469
mmref	rwcore	aupan	5783895	5784133	239
mmref	rwcore	aupan	5784510	5784750	241
mmref	rwcore	aupan	5784770	5784995	226
mmref	rwcore	aupan	5786776	5787042	267
mmref	rwcore	aupan	5788006	5788412	407
mmref	rwcore	aupan	5788775	5789113	339
mmref	rwcore	aupan	5789131	5789362	232
mmref	rwcore	aupan	5790639	5790964	326
mmref	rwcore	aupan	5790987	5791206	220
mmref	rwcore	aupan	5791231	5791562	332

Reference	Core Group	Pan Group	Start	End	Length
mmref	rwcore	aupan	5791655	5792006	352
mmref	rwcore	aupan	5792418	5792702	285
mmref	rwcore	aupan	5792913	5793552	640
mmref	rwcore	aupan	5794149	5794907	759
mmref	rwcore	aupan	5794926	5795295	370
mmref	rwcore	aupan	5795618	5795952	335
mmref	rwcore	aupan	5795970	5796275	306
mmref	rwcore	aupan	5796585	5796816	232
mmref	rwcore	aupan	5830680	5831013	334
mmref	rwcore	aupan	5831032	5831372	341
mmref	rwcore	aupan	5831390	5831648	259
mmref	rwcore	aupan	5831901	5832345	445
mmref	rwcore	aupan	5955243	5955562	320
mmref	rwcore	aupan	5956535	5957242	708
mmref	rwcore	aupan	6003628	6003835	208
mmref	rwcore	aupan	6268779	6269229	451
mmref	rwcore	aupan	6269250	6269596	347
mmref	rwcore	aupan	6270465	6270700	236
mmref	rwcore	aupan	6459328	6459793	466
mmref	rwcore	aupan	6591553	6591922	370
mmref	rwcore	aupan	6600209	6600454	246
mmref	rwcore	aupan	6600543	6601197	655
mmref	rwcore	aupan	6603964	6604178	215
mmref	rwcore	aupan	6604530	6604935	406
mmref	rwcore	aupan	6605979	6606254	276
muref	afcore	aupan	2686073	2686821	749
muref	afcore	aupan	5084322	5084556	235
muref	afcore	aupan	5088824	5089323	500
muref	afcore	aupan	5113348	5113716	369
muref	afcore	rwpan	1364934	1365256	323
muref	afcore	rwpan	1365603	1366184	582
muref	afcore	rwpan	2581758	2581977	220
muref	afcore	rwpan	2670704	2671117	414
muref	afcore	rwpan	3006422	3006643	222
muref	afcore	rwpan	3007575	3007787	213
muref	afcore	rwpan	3010888	3011635	748
muref	afcore	rwpan	3011665	3012026	362
muref	afcore	rwpan	3012150	3012360	211
muref	afcore	rwpan	3966796	3967063	268
muref	afcore	rwpan	3967253	3967809	557
muref	afcore	rwpan	4309729	4310174	446
muref	afcore	rwpan	4310633	4310839	207
muref	afcore	rwpan	4312616	4312946	331
muref	afcore	rwpan	4313265	4313718	454
muref	afcore	rwpan	4314787	4315133	347
muref	afcore	rwpan	4876793	4877102	310
muref	aucore	rwpan	1364934	1365256	323
muref	aucore	rwpan	1365603	1366184	582
muref	aucore	rwpan	2581758	2581977	220
muref	aucore	rwpan	2670704	2671117	414
muref	aucore	rwpan	3010888	3011635	748
muref	aucore	rwpan	3011665	3012026	362
muref	aucore	rwpan	3012150	3012360	211
muref	aucore	rwpan	3966796	3967063	268
muref	aucore	rwpan	3967253	3967809	557
muref	aucore	rwpan	4309729	4310174	446
muref	aucore	rwpan	4310633	4310839	207

Reference	Core Group	Pan Group	Start	End	Length
muref	aucore	rwpn	4312616	4312946	331
muref	aucore	rwpn	4313265	4313718	454
muref	aucore	rwpn	4314787	4315133	347
muref	aucore	rwpn	4876793	4877102	310
muref	mucore	mmpan	28485	29165	681
muref	mucore	mmpan	561265	561869	605
muref	mucore	mmpan	1049949	1050456	508
muref	mucore	mmpan	10527111	1053020	310
muref	mucore	mmpan	3159879	3160205	327
muref	mucore	mmpan	3160226	3160815	590
muref	mucore	mmpan	3582965	3583445	481
muref	mucore	mmpan	3584923	3587610	2688
muref	mucore	mmpan	3587806	3590026	2221
muref	mucore	mmpan	3605316	3606912	1597
muref	mucore	mmpan	5606397	5606644	248
muref	rwcore	aupan	2686265	2686821	557

Table 9(b)

M.marinum "M" Reference: Pan Core Regions

Reference	Core Group	Pan Group	feature	start	end	length	strand	locus	product	pseudo	ortholog	pct_overlap
mmref	afcore	aupan	CDS	1848921	1849787	867	-1	MMAR_1533	conserved hypothetical membrane protein	0	MON02403	23.18
mmref	afcore	aupan	CDS	1849784	1852123	2340	-1	MMAR_1534	conserved protein	0	MON02400	22.09
mmref	afcore	aupan	CDS	5326176	5327018	843	-1	MMAR_4323	transposase	0	MON06532	29.66
mmref	afcore	aupan	CDS	5353161	5354540	1380	1	MMAR_4347	conserved hypothetical alanine and glycine rich protein	0	MON04588	23.77
mmref	afcore	aupan	CDS	5456235	5456615	381	-1	MMAR_4435	conserved hypothetical membrane protein	0	MON04612	94.75
mmref	afcore	rwaupan	CDS	5353161	5354540	1380	1	MMAR_4347	conserved hypothetical alanine and glycine rich protein	0	MON04588	20.07
mmref	afcore	rwpan	CDS	1814049	1815083	1035	-1	MMAR_1500	conserved hypothetical membrane protein	0	MON02437	23.09
mmref	afcore	rwpan	CDS	3974940	3975905	966	-1	MMAR_3263	ATP-binding protein ABC transporter	0	MON03577	96.48
mmref	afcore	rwpan	CDS	4157159	4157638	480	-1	MMAR_3376	6-pyruvoyl tetrahydrobiopterin synthase	0	MON01264	94.58
mmref	afcore	rwpan	CDS	4158378	4159550	1173	-1	MMAR_3378	PPE family protein	0	MON02686	20.97
mmref	afcore	rwpan	CDS	4162042	4163643	1602	-1	MMAR_3381	conserved hypothetical protein	0	MON02693	74.78
mmref	afcore	rwpan	CDS	4292188	4930423	1236	-1	MMAR_3992	acyl-CoA dehydrogenase	0	MON03854	52.75
mmref	afcore	rwpan	CDS	4930420	4931580	1161	-1	MMAR_3993	acyl-CoA dehydrogenase	0	MON03855	84.24
mmref	afcore	rwpan	CDS	4931749	4932573	825	1	MMAR_3994	conserved hypothetical alanine-rich protein	0	MON03858	39.39
mmref	afcore	rwpan	CDS	4933516	4934742	1227	1	MMAR_3996	cytochrome P450 187A4 Cyp187A4	0	MON03860	38.47
mmref	afcore	rwpan	CDS	4934739	4935893	1155	1	MMAR_3997	zinc-containing alcohol dehydrogenase NAD dependent	0	MON03861	23.55
mmref	afcore	rwpan	CDS	4935923	4936750	828	-1	MMAR_3998	short chain dehydrogenase	0	MON30444	19.44
mmref	afcore	rwpan	CDS	5353161	5354540	1380	1	MMAR_4347	conserved hypothetical alanine and glycine rich protein	0	MON04588	25.07
mmref	afcore	rwpan	CDS	6425173	6425496	324	-1	MMAR_5319	conserved hypothetical protein	0	MON04395	25
mmref	afcore	rwpan	CDS	6425540	6425962	423	-1	MMAR_5320	conserved hypothetical protein	0	MON04396	85.58
mmref	aucore	afpan	misc_feature	2903223	2906122	2900	1		MURD55_2900bp	0		28.31
mmref	aucore	afpan	misc_feature	3507422	3513150	5729	1		MURD69_5729bp	0		11.47
mmref	aucore	afpan	CDS	3509697	3509957	261	1	MMAR_2905	hypothetical protein	0	MON06442	93.1
mmref	aucore	afpan	CDS	3513110	3513208	99	1	MMAR_2909	N-term conserved hypothetical oxidoreductase, putative	1	MON02862	41.41
mmref	aucore	afpan	CDS	5130970	5132823	1854	1	MMAR_4169	transmembrane serine/threonine-protein kinase	0	MON04019	12.89
mmref	aucore	afpan	misc_feature	5366953	5369485	2533	1		MURD124_2533bp	0		12.67
mmref	aucore	afpan	misc_feature	6021901	6023211	1311	1		MURD136_1311bp	0		30.89
mmref	aucore	afpan	CDS	6022093	6022575	483	-1	MMAR_4957	hypothetical protein	0	MON06169	44.51
mmref	aucore	afpan	CDS	6022708	6023094	387	1	MMAR_4958	hypothetical secreted protein	0	MON06550	14.99
mmref	aucore	afpan	CDS	6265076	6267304	2229	1	MMAR_5186	sensor-component of a two-component regulator	0	MON05596	14.27
mmref	aucore	rwpan	CDS	1814049	1815083	1035	-1	MMAR_1500	conserved hypothetical membrane protein	0	MON02437	23.09
mmref	aucore	rwpan	CDS	3974940	3975905	966	-1	MMAR_3263	ATP-binding protein ABC transporter	0	MON03577	96.48
mmref	aucore	rwpan	CDS	4157159	4157638	480	-1	MMAR_3376	6-pyruvoyl tetrahydrobiopterin synthase	0	MON01264	94.58
mmref	aucore	rwpan	CDS	4162042	4163643	1602	-1	MMAR_3381	conserved hypothetical protein	0	MON02693	74.78
mmref	aucore	rwpan	CDS	4929188	4930423	1236	-1	MMAR_3992	acyl-CoA dehydrogenase	0	MON03854	52.75
mmref	aucore	rwpan	CDS	4930420	4931580	1161	-1	MMAR_3993	acyl-CoA dehydrogenase	0	MON03855	84.24
mmref	aucore	rwpan	CDS	4931749	4932573	825	1	MMAR_3994	conserved hypothetical alanine-rich protein	0	MON03858	39.39
mmref	aucore	rwpan	CDS	4933516	4934742	1227	1	MMAR_3996	cytochrome P450 187A4 Cyp187A4	0	MON03860	38.47
mmref	aucore	rwpan	CDS	4934739	4935893	1155	1	MMAR_3997	zinc-containing alcohol dehydrogenase NAD dependent	0	MON03861	23.55
mmref	aucore	rwpan	CDS	4935923	4936750	828	-1	MMAR_3998	short chain dehydrogenase	0	MON30444	19.44
mmref	aucore	rwpan	CDS	6425173	6425496	324	-1	MMAR_5319	conserved hypothetical protein	0	MON04395	25
mmref	aucore	rwpan	CDS	6425540	6425962	423	-1	MMAR_5320	conserved hypothetical protein	0	MON04396	85.58
mmref	ficore	hspan	CDS	1407389	1409836	2448	1	MMAR_1171	8-amino-7-oxononanoate synthase BioF2_5	0	MON02843	24.63
mmref	ficore	hspan	misc_feature	1408047	1409392	1346	1		MURD26_1346bp	0		44.8
mmref	ficore	hspan	CDS	2264067	2265215	1149	-1	MMAR_1857	hydrogenase-forming protein, HypD	0	MON06020	18.97
mmref	ficore	hspan	CDS	2265227	2265499	273	-1	MMAR_1858	hydrogenase maturation factor, HypC	0	MON06395	13.55
mmref	ficore	hspan	CDS	2272669	2273328	660	-1	MMAR_1866	conserved hypothetical protein	0	MON06023	55.45
mmref	ficore	hspan	CDS	2273948	2274922	975	-1	MMAR_1868	conserved hypothetical protein	0	MON06399	10.77
mmref	ficore	hspan	CDS	2274926	2276725	1800	-1	MMAR_1869	nickel/iron-hydrogenase I large subunit, HydA	0	MON06025	18.28
mmref	ficore	hspan	misc_feature	3514257	3515182	926	1		MURD70_926bp	0		50.32
mmref	ficore	hspan	CDS	3514344	3515207	864	1	MMAR_2912	conserved hypothetical hydrolase or acyltransfer	0	MON05281	43.87

Reference	Core Group	Pan Group	feature	start	end	length	strand	locus	product	pseudo	ortholog	pct_overlap
mmref	ficore	hspan	misc feature	3781467	3785215	3749	1	MURD78	37 bp	0		11.07
mmref	ficore	hspan	CDS	4167635	4168903	1269	1	MMAR_3385	conserved hypothetical protein	0	MON06076	17.18
mmref	ficore	hspan	CDS	4181725	4182126	402	-1	MMAR_3396	conserved hypothetical protein	0	MON05386	53.98
mmref	mmcore	mupan	CDS	144293	145480	1188	1	MMAR_0119	conserved hypothetical membrane protein	0	MON05981	19.02
mmref	mmcore	mupan	CDS	688441	689655	1215	-1	MMAR_0586	conserved hypothetical protein	0	MON05985	27.41
mmref	mmcore	mupan	CDS	815627	816274	648	-1	MMAR_0684	conserved hypothetical regulatory protein	0	MON05138	43.83
mmref	mmcore	mupan	misc feature	840415	850622	10208	1	MURD12	10208bp	0		10.41
mmref	mmcore	mupan	CDS	842939	844708	1770	1	MMAR_0706	fatty acyl-AMP ligase Fadd30	0	MON05149	51.81
mmref	mmcore	mupan	CDS	1129286	1130005	720	1	MMAR_0931	hypothetical protein	0	MON06489	11.39
mmref	mmcore	mupan	CDS	2824080	2825516	1437	-1	MMAR_2343	conserved hypothetical protein	0	MON05250	20.32
mmref	mmcore	mupan	misc feature	3409154	3411750	2597	1	MURD64	2597bp	0		19.29
mmref	mmcore	mupan	CDS	3409293	3410231	939	1	MMAR_2810	conserved hypothetical protein	0	MON05268	26.62
mmref	mmcore	mupan	CDS	3410231	3411364	1134	1	MMAR_2811	conserved hypothetical membrane protein	0	MON06436	11.02
mmref	mmcore	mupan	CDS	4158378	4159550	1173	-1	MMAR_3378	PPE family protein	0	MON02686	20.89
mmref	mmcore	mupan	CDS	4163700	4164473	774	-1	MMAR_3382	conserved hypothetical membrane protein	0	MON06075	29.72
mmref	mmcore	mupan	CDS	5241011	5241811	801	1	MMAR_4258	monophosphatase CysO-like	0	MON05507	18.48
mmref	mmcore	mupan	misc feature	5241176	5243989	2814	1	MURD116	2814bp	0		47.87
mmref	mmcore	mupan	CDS	5242294	5242998	705	1	MMAR_4259	bifunctional enzyme CysN/CysC-like: sulfate ade	0	MON05508	74.04
mmref	mmcore	mupan	CDS	5243079	5244002	924	1	MMAR_4260	glycolipid sulfotransferase	0	MON05509	32.58
mmref	mmcore	mupan	CDS	6554276	6555361	1086	1	MMAR_5416	conserved hypothetical transmembrane protein	0	MON05609	14.18
mmref	mmcore	mupan	CDS	6562512	6563717	1206	1	MMAR_5423	conserved hypothetical transmembrane protein	0	MON05616	28.94
mmref	mmcore	mupan	CDS	6563707	6564747	1041	1	MMAR_5424	conserved hypothetical transmembrane protein	0	MON05617	13.16
mmref	mmcore	mupan	CDS	6565895	6566314	420	-1	MMAR_5426	hypothetical membrane protein	0	MON06554	35.95
mmref	rwcore	afaupan	CDS	130639	132027	1389	1	MMAR_0104	conserved hypothetical protein	0	MON05978	15.77
mmref	rwcore	afaupan	CDS	139721	140698	978	1	MMAR_0112	haloalkane dehalogenase DhaA_1	0	MON03979	50.1
mmref	rwcore	afaupan	CDS	140862	141167	306	-1	MMAR_0113	hypothetical protein	0	MON06097	53.92
mmref	rwcore	afaupan	CDS	142815	143285	471	-1	MMAR_0117	conserved hypothetical protein	0	MON05089	43.74
mmref	rwcore	afaupan	CDS	150923	154276	3354	1	MMAR_0123	transcriptional regulatory protein (LuxR-family)	0	MON05094	12.67
mmref	rwcore	afaupan	CDS	160372	161910	1539	-1	MMAR_0131	monoxygenase hydroxylase, subunit A (AamH)	0		24.82
mmref	rwcore	afaupan	CDS	162067	162729	663	1	MMAR_0132	two component transcriptional regulatory protein	0	MON05099	27.3
mmref	rwcore	afaupan	CDS	309447	310718	1272	-1	MMAR_0272	cytochrome P450 226B1 Cyp226B1	0	MON04843	31.84
mmref	rwcore	afaupan	misc feature	309901	324932	15032	1	MURD6	15032bp	0		19.59
mmref	rwcore	afaupan	CDS	311150	312412	1263	-1	MMAR_0273	amidohydrolase	0	MON05119	52.1
mmref	rwcore	afaupan	CDS	312399	313694	1296	-1	MMAR_0274	cytochrome P450 271A1 Cyp271A1	0	MON05120	22.15
mmref	rwcore	afaupan	CDS	317703	318719	1017	-1	MMAR_0278	conserved hypothetical protein	0	MON06361	10.62
mmref	rwcore	afaupan	CDS	318780	319523	744	-1	MMAR_0279	conserved hypothetical membrane protein	0	MON06259	32.8
mmref	rwcore	afaupan	CDS	319581	320576	996	-1	MMAR_0280	non-plant terpene cyclase (C1 class)	0	MON05123	71.59
mmref	rwcore	afaupan	CDS	601170	602420	1251	1	MMAR_0508	conserved integral membrane protein	0	MON01170	17.43
mmref	rwcore	afaupan	misc_feature	926912	932606	5695	1	MURD13	5695bp	0		12.64
mmref	rwcore	afaupan	CDS	929771	930508	738	1	MMAR_0773	conserved hypothetical regulatory protein	0	MON03947	26.29
mmref	rwcore	afaupan	CDS	1108935	1110431	1497	1	MMAR_0916	trypsin-like serine protease	0	MON00668	13.69
mmref	rwcore	afaupan	misc feature	1880808	1885688	4881	1	MURD36	4881bp	0		14.75
mmref	rwcore	afaupan	CDS	1881688	1882923	1236	-1	MMAR_1564	cytochrome P450 276A1 Cyp276A1	0	MON05199	36.65
mmref	rwcore	afaupan	CDS	1882994	1883767	774	-1	MMAR_1565	conserved hypothetical methyltransferase	0	MON06198	25.45
mmref	rwcore	afaupan	CDS	1933569	1934207	639	1	MMAR_1597	transcriptional regulatory protein	0	MON05203	64.48
mmref	rwcore	afaupan	CDS	2316939	2317883	945	-1	MMAR_1902	thioredoxin reductase TrxB2_2	0	MON05217	25.93
mmref	rwcore	afaupan	CDS	2534389	2536353	1965	1	MMAR_2103	PE-PGRS family protein	0	MON05222	19.19
mmref	rwcore	afaupan	misc feature	2774426	2776190	1765	1	MURD53	1765bp	0		11.39
mmref	rwcore	afaupan	CDS	3498706	3499398	693	-1	MMAR_2894	PE family protein	0	MON05275	25.11
mmref	rwcore	afaupan	CDS	3507458	3508471	1014	-1	MMAR_2903	conserved hypothetical NADP-dependent oxidore	0	MON05277	19.82
mmref	rwcore	afaupan	CDS	3525354	3525632	279	1	MMAR_2921	conserved hypothetical protein	0	MON06056	36.92
mmref	rwcore	afaupan	CDS	3525739	3526422	684	1	MMAR_2922	conserved hypothetical O-methyltransferase	0	MON05284	34.94
mmref	rwcore	afaupan	CDS	3526403	3527455	1053	-1	MMAR_2923	conserved hypothetical membrane protein	0	MON06057	12.25
mmref	rwcore	afaupan	CDS	3527466	3528224	759	-1	MMAR_2924	SAM-dependent methyltransferase	0	MON05285	13.31
mmref	rwcore	afaupan	CDS	3536853	3538514	1662	1	MMAR_2933	PE-PGRS family protein	0	MON04399	20.22
mmref	rwcore	afaupan	CDS	3538558	3539199	642	-1	MMAR_2934	cutinase Cfp21	0	MON06730	10.44
mmref	rwcore	afaupan	CDS	3573899	3574927	1029	-1	MMAR_2959	Zn-dependent alcohol dehydrogenase	0	MON05298	25.85

Reference	Core Group	Pan Group	feature	start	end	length	strand	locus	product	pseudo	ortholog	pct_overlap
mmref	rwcore	afaupan	CDS	3584821	3585843	1023	1	MMAR_2965	predicted ATPase/kinase, NadR	0	MON06450	22.09
mmref	rwcore	afaupan	CDS	3594195	3595016	822	-1	MMAR_2971	O-methyltransferase	0	MON05306	14.72
mmref	rwcore	afaupan	CDS	3595313	3596377	1065	1	MMAR_2972	conserved hypothetical sugar transport protein	0	MON06451	41.13
mmref	rwcore	afaupan	CDS	3601884	3602636	753	1	MMAR_2977	acyl-ACP thioesterase, FatA	0	MON05309	26.56
mmref	rwcore	afaupan	CDS	3607311	3608681	1371	1	MMAR_2982	conserved hypothetical transmembrane protein	0	MON05314	17.14
mmref	rwcore	afaupan	CDS	3610187	3610858	672	-1	MMAR_2984	transcriptional regulatory protein (TetR-family)	0	MON05316	29.32
mmref	rwcore	afaupan	CDS	3613045	3614589	1545	1	MMAR_2987	3-(3-hydroxy-phenyl) propionate hydroxylase	0	MON05318	20.39
mmref	rwcore	afaupan	misc_feature	3974006	3974948	943	1		MURD81, 943bp	0		51.01
mmref	rwcore	afaupan	CDS	3974086	3974850	765	-1	MMAR_3262	integral membrane protein ABC transporter	0	MON05357	55.42
mmref	rwcore	afaupan	misc_feature	4225185	4230172	4988	1		MURD89, 88bp	0		17.26
mmref	rwcore	afaupan	CDS	4228833	4230482	1650	-1	MMAR_3427	PE family protein	0	MON00967	32.85
mmref	rwcore	afaupan	CDS	4277637	4278530	894	-1	MMAR_3473	ketoacyl-acyl carrier protein synthase III	0	MON06078	17.34
mmref	rwcore	afaupan	CDS	4278514	4279614	1101	-1	MMAR_3474	ketoacyl-acyl carrier protein synthase III	0	MON05410	31.06
mmref	rwcore	afaupan	CDS	4291071	4291502	432	-1	MMAR_3484	heat shock protein HspX_1	0	MON06222	48.38
mmref	rwcore	afaupan	CDS	4292151	4292423	273	-1	MMAR_3486	hypothetical protein	0	MON06079	60.07
mmref	rwcore	afaupan	CDS	4293932	4295731	1800	1	MMAR_3488	acetyl-coenzyme A synthetase Acs_1	0	MON05420	12.61
mmref	rwcore	afaupan	CDS	4299906	4301507	1602	1	MMAR_3494	PE-PGRS family protein	0	MON05426	12.61
mmref	rwcore	afaupan	CDS	4304715	4305572	858	-1	MMAR_3499	flavodoxin oxidoreductase	0	MON05428	27.16
mmref	rwcore	afaupan	CDS	4306787	4307368	582	-1	MMAR_3501	conserved hypothetical membrane protein	0	MON06474	15.64
mmref	rwcore	afaupan	CDS	4311086	4311457	372	-1	MMAR_3504	conserved hypothetical protein	0	MON06081	88.71
mmref	rwcore	afaupan	CDS	4312975	4313838	864	-1	MMAR_3506	conserved hypothetical membrane protein	0	MON06082	54.4
mmref	rwcore	afaupan	misc_feature	4473209	4477073	3865	1		MURD98, 3865bp	0		20.05
mmref	rwcore	afaupan	CDS	4474722	4475495	774	1	MMAR_3636	methylase	0	MON05454	71.71
mmref	rwcore	afaupan	CDS	4501414	4501731	318	-1	MMAR_3655	conserved hypothetical protein	0	MON06486	48.11
mmref	rwcore	afaupan	CDS	4559937	4561448	1512	1	MMAR_3702	Flavin-binding monooxygenase	0	MON05466	14.15
mmref	rwcore	afaupan	misc_feature	4559939	4561693	1755	1		MURD101, 1755bp	0		12.19
mmref	rwcore	afaupan	misc_feature	5079529	5082660	3132	1		MURD110, 3132bp	0		20.11
mmref	rwcore	afaupan	CDS	5079599	5080225	627	-1	MMAR_4123	conserved hypothetical protein	0	MON06525	28.87
mmref	rwcore	afaupan	CDS	5080318	5080845	528	-1	MMAR_4124	conserved hypothetical secreted protein	0	MON05497	14.77
mmref	rwcore	afaupan	CDS	5080996	5081532	537	-1	MMAR_4125	NUDIX hydrolase	0	MON05498	43.39
mmref	rwcore	afaupan	CDS	5196932	5197570	639	1	MMAR_4219	transcriptional regulator	0	MON05503	28.48
mmref	rwcore	afaupan	CDS	5197560	5198507	948	1	MMAR_4220	unidentified antibiotic-transport ATP-binding prot	0	MON05504	12.45
mmref	rwcore	afaupan	misc_feature	5325526	5326782	1257	1		MURD121, 1257bp	0		35.08
mmref	rwcore	afaupan	CDS	5433015	5433791	777	-1	MMAR_4417	conserved hypothetical membrane protein	0	MON05517	37.84
mmref	rwcore	afaupan	CDS	5435560	5438004	2445	1	MMAR_4420	aminomethyltransferase GcvT_2	0	MON05519	12.72
mmref	rwcore	afaupan	CDS	5439150	5440298	1149	1	MMAR_4422	dioxygenase	0	MON05520	18.71
mmref	rwcore	afaupan	CDS	5442929	5443999	1071	-1	MMAR_4426	transcriptional regulatory protein	0	MON05524	39.78
mmref	rwcore	afaupan	CDS	5444274	5445830	1557	1	MMAR_4427	dehydrogenase fad flavoprotein Gmc oxidoreduct	0	MON05525	45.15
mmref	rwcore	afaupan	CDS	5445832	5446710	879	-1	MMAR_4428	haloalkane dehalogenase	0	MON05526	37.09
mmref	rwcore	afaupan	CDS	5748117	5748929	813	-1	MMAR_4697	conserved hypothetical membrane protein	0	MON06160	27.06
mmref	rwcore	afaupan	CDS	5750550	5750840	291	1	MMAR_4700	conserved hypothetical secreted protein	0	MON05537	21.31
mmref	rwcore	afaupan	CDS	5750867	5751283	417	-1	MMAR_4701	conserved hypothetical secreted protein	0	MON05538	90.65
mmref	rwcore	afaupan	CDS	5758697	5759728	1032	-1	MMAR_4709	MCE-family protein	0	MON05545	22.87
mmref	rwcore	afaupan	CDS	5761022	5761867	846	-1	MMAR_4711	conserved hypothetical membrane protein	0	MON05547	18.44
mmref	rwcore	afaupan	CDS	5776024	5777169	1146	1	MMAR_4725	conserved hypothetical metal-dependent hydrol	0	MON05555	35.17
mmref	rwcore	afaupan	CDS	5777171	5777563	393	1	MMAR_4726	conserved hypothetical protein	0	MON06544	43.26
mmref	rwcore	afaupan	CDS	5777560	5778447	888	1	MMAR_4727	conserved hypothetical hydrolase	0	MON05556	20.05
mmref	rwcore	afaupan	CDS	5778462	5778935	474	-1	MMAR_4728	conserved hypothetical protein	0	MON06162	33.97
mmref	rwcore	afaupan	CDS	5780322	5780618	297	1	MMAR_4730	ferredoxin	0	MON05558	14.14
mmref	rwcore	afaupan	misc_feature	5830307	5832376	2070	1		MURD134, 2070bp	0		12.22
mmref	rwcore	afaupan	CDS	5831537	5832403	867	-1	MMAR_4778	2-hydroxy-6-OXO-6-phenylhexa-2,4-dienoate hy	0	MON05576	12.57
mmref	rwcore	afaupan	CDS	5956016	5956654	639	1	MMAR_4901	Zn-dependent hydrolases	0	MON06549	13.62
mmref	rwcore	afaupan	misc_feature	5956071	5957506	1436	1		MURD155, 1436bp	0		17.55
mmref	rwcore	afaupan	misc_feature	6458356	6460277	1922	1		MURD149, 1922bp	0		12.17
mmref	rwcore	afaupan	CDS	6458741	6459727	987	1	MMAR_5346	dTDP-glucose-4,6-dehydratase, RmlB_1	0	MON06346	17.02
mmref	rwcore	afpan	CDS	130639	132027	1389	1	MMAR_0104	conserved hypothetical protein	0	MON05978	15.77
mmref	rwcore	afpan	CDS	139721	140698	978	1	MMAR_0112	haloalkane dehalogenase DhaA_1	0	MON03979	50.1

Reference	Core Group	Pan Group	feature	start	end	length	strand	locus	product	pseudo	ortholog	pct_overlap
mmref	rwcore	afrpan	CDS	140862	141167	306	-1	MMAR_0113	hypothetical protein	0	MON06097	53.92
mmref	rwcore	afrpan	CDS	142815	143285	471	-1	MMAR_0117	conserved hypothetical protein	0	MON05089	43.74
mmref	rwcore	afrpan	CDS	150923	154276	3354	1	MMAR_0123	transcriptional regulatory protein (LuxR-family)	0	MON05094	12.67
mmref	rwcore	afrpan	CDS	160372	161910	1539	-1	MMAR_0131	monooxygenase hydroxylase, subunit A (AamH)	0		31.06
mmref	rwcore	afrpan	CDS	162067	162729	663	1	MMAR_0132	two component transcriptional regulatory protein	0	MON05099	27.3
mmref	rwcore	afrpan	CDS	309447	310718	1272	-1	MMAR_0272	cytochrome P450 226B1 Cyp226B1	0	MON04843	31.84
mmref	rwcore	afrpan	misc feature	309901	324932	15032	1		MURD6, 15032bp	0		19.85
mmref	rwcore	afrpan	CDS	311150	312412	1263	-1	MMAR_0273	amidohydrolase	0	MON05119	52.1
mmref	rwcore	afrpan	CDS	312399	313694	1296	-1	MMAR_0274	cytochrome P450 271A1 Cyp271A1	0	MON05120	22.15
mmref	rwcore	afrpan	CDS	317703	318719	1017	-1	MMAR_0278	conserved hypothetical protein	0	MON06361	10.62
mmref	rwcore	afrpan	CDS	318780	319523	744	-1	MMAR_0279	conserved hypothetical membrane protein	0	MON06259	38.04
mmref	rwcore	afrpan	CDS	319581	320576	996	-1	MMAR_0280	non-plant terpene cyclase (C1 class)	0	MON05123	71.59
mmref	rwcore	afrpan	CDS	601170	602420	1251	1	MMAR_0508	conserved integral membrane protein	0	MON01170	17.75
mmref	rwcore	afrpan	CDS	830917	832158	1242	-1	MMAR_0696	Conserved lipoprotein, LpqK	0	MON06338	17.15
mmref	rwcore	afrpan	misc feature	926912	932606	5695	1		MURD13, 5695bp	0		12.64
mmref	rwcore	afrpan	CDS	929771	930508	738	1	MMAR_0773	conserved hypothetical regulatory protein	0	MON03947	26.29
mmref	rwcore	afrpan	CDS	1108935	1110431	1497	1	MMAR_0916	trypsin-like serine protease	0	MON0668	13.69
mmref	rwcore	afrpan	misc feature	1359740	1360922	1183	1		MURD24, 1183bp	0		18.09
mmref	rwcore	afrpan	CDS	1360001	1360873	873	1	MMAR_1133	conserved hypothetical protein	0	MON06375	18.9
mmref	rwcore	afrpan	misc feature	1880808	1885688	4881	1		MURD36, 4881bp	0		15.9
mmref	rwcore	afrpan	CDS	1881688	1882923	1236	-1	MMAR_1564	cytochrome P450 276A1 Cyp276A1	0	MON05199	36.65
mmref	rwcore	afrpan	CDS	1882994	1883767	774	-1	MMAR_1565	conserved hypothetical methyltransferase	0	MON06198	32.69
mmref	rwcore	afrpan	CDS	1932650	1933411	762	1	MMAR_1596	conserved hypothetical protein	0	MON05202	45.41
mmref	rwcore	afrpan	CDS	1933569	1934207	639	1	MMAR_1597	transcriptional regulatory protein	0	MON05203	64.48
mmref	rwcore	afrpan	CDS	2316939	2317883	945	-1	MMAR_1902	thioredoxin reductase TrxB2_2	0	MON05217	25.93
mmref	rwcore	afrpan	CDS	2534389	2536353	1965	1	MMAR_2103	PE-PGRS family protein	0	MON05222	22.85
mmref	rwcore	afrpan	misc feature	2774426	2776190	1765	1		MURD53, 1765bp	0		11.39
mmref	rwcore	afrpan	misc feature	2903223	2906122	2900	1		MURD55, 2900bp	0		13.83
mmref	rwcore	afrpan	CDS	3498254	3498532	279	-1	MMAR_2893	hypothetical protein	0	MON06053	68.82
mmref	rwcore	afrpan	CDS	3498706	3499398	693	-1	MMAR_2894	PE family protein	0	MON05275	25.11
mmref	rwcore	afrpan	CDS	3507458	3508471	1014	-1	MMAR_2903	conserved hypothetical NADP-dependent oxidore	0	MON05277	19.82
mmref	rwcore	afrpan	CDS	3509697	3509957	261	1	MMAR_2905	hypothetical protein	0	MON06442	44.44
mmref	rwcore	afrpan	misc feature	3521798	3531905	10108	1		MURD71, 10108bp	0		12.8
mmref	rwcore	afrpan	CDS	3522027	3522881	855	-1	MMAR_2918	thiosulfate sulfotransferase	0	MON05282	36.61
mmref	rwcore	afrpan	CDS	3525354	3525632	279	1	MMAR_2921	conserved hypothetical protein	0	MON06056	36.92
mmref	rwcore	afrpan	CDS	3525739	3526422	684	1	MMAR_2922	conserved hypothetical O-methyltransferase	0	MON05284	34.94
mmref	rwcore	afrpan	CDS	3526403	3527455	1053	-1	MMAR_2923	conserved hypothetical membrane protein	0	MON06057	12.25
mmref	rwcore	afrpan	CDS	3527466	3528224	759	-1	MMAR_2924	SAM-dependent methyltransferase	0	MON05285	13.31
mmref	rwcore	afrpan	CDS	3536853	3538514	1662	1	MMAR_2933	PE-PGRS family protein	0	MON04399	20.22
mmref	rwcore	afrpan	CDS	3538558	3539199	642	-1	MMAR_2934	cutinase Cfp21	0	MON06730	10.44
mmref	rwcore	afrpan	CDS	3573899	3574927	1029	-1	MMAR_2959	Zn-dependent alcohol dehydrogenase	0	MON05298	25.85
mmref	rwcore	afrpan	CDS	3584821	3585843	1023	1	MMAR_2965	predicted ATPase/kinase, NadR	0	MON06450	25.42
mmref	rwcore	afrpan	CDS	3594195	3595016	822	-1	MMAR_2971	O-methyltransferase	0	MON05306	15.45
mmref	rwcore	afrpan	CDS	3595313	3596377	1065	1	MMAR_2972	conserved hypothetical sugar transport protein	0	MON06451	48.83
mmref	rwcore	afrpan	CDS	3601884	3602636	753	1	MMAR_2977	acyl-ACP thioesterase, FatA	0	MON05309	26.56
mmref	rwcore	afrpan	CDS	3607311	3608681	1371	1	MMAR_2982	conserved hypothetical transmembrane protein	0	MON05314	17.14
mmref	rwcore	afrpan	CDS	3610187	3610858	672	-1	MMAR_2984	transcriptional regulatory protein (TetR-family)	0	MON05316	29.32
mmref	rwcore	afrpan	CDS	3613045	3614589	1545	1	MMAR_2987	3-(3-hydroxy-phenyl) propionate hydroxylase	0	MON05318	30.87
mmref	rwcore	afrpan	misc feature	3974006	3974948	943	1		MURD81, 943bp	0		51.01
mmref	rwcore	afrpan	CDS	3974086	3974850	765	-1	MMAR_3262	integral membrane protein ABC transporter	0	MON05357	55.42
mmref	rwcore	afrpan	misc feature	4225185	4230172	4988	1		MURD89, 88bp	0		18.24
mmref	rwcore	afrpan	CDS	4228833	4230482	1650	-1	MMAR_3427	PE family protein	0	MON00967	35.76
mmref	rwcore	afrpan	misc feature	4271366	4313737	42372	1		MURD92, 42372bp	0		10.72
mmref	rwcore	afrpan	CDS	4277637	4278530	894	-1	MMAR_3473	ketoacyl-acyl carrier protein synthase III	0	MON06078	21.7
mmref	rwcore	afrpan	CDS	4278514	4279614	1101	-1	MMAR_3474	ketoacyl-acyl carrier protein synthase III	0	MON05410	31.06
mmref	rwcore	afrpan	CDS	4280736	4282184	1449	-1	MMAR_3476	conserved hypothetical protein	0	MON06470	23.46
mmref	rwcore	afrpan	CDS	4291071	4291502	432	-1	MMAR_3484	heat shock protein HspX_1	0	MON06222	48.38

Reference	Core Group	Pan Group	feature	start	end	length	strand	locus	product	pseudo	ortholog	pct_overlap
mmref	rwcore	afrpan	CDS	4292151	4292423	273	-1	MMAR_3486	hypothetical protein	0	MON06079	60.07
mmref	rwcore	afrpan	CDS	4293932	4295731	1800	1	MMAR_3488	acetyl-coenzyme a synthetase Acs_1	0	MON05420	12.61
mmref	rwcore	afrpan	CDS	4299906	4301507	1602	1	MMAR_3494	PE-PGRS family protein	0	MON05426	12.61
mmref	rwcore	afrpan	CDS	4304715	4305572	858	-1	MMAR_3499	flavodoxin oxidoreductase	0	MON05428	27.16
mmref	rwcore	afrpan	CDS	4306787	4307368	582	-1	MMAR_3501	conserved hypothetical membrane protein	0	MON06474	15.64
mmref	rwcore	afrpan	CDS	4311086	4311457	372	-1	MMAR_3504	conserved hypothetical protein	0	MON06081	88.71
mmref	rwcore	afrpan	CDS	4311592	4312929	1338	1	MMAR_3505	conserved hypothetical hydrolase	0	MON05431	24.51
mmref	rwcore	afrpan	CDS	4312975	4313838	864	-1	MMAR_3506	conserved hypothetical membrane protein	0	MON06082	54.4
mmref	rwcore	afrpan	misc_feature	4473209	4477073	3865	1		MURD98, 3865bp	0		20.05
mmref	rwcore	afrpan	CDS	4474722	4475495	774	1	MMAR_3636	methylase	0	MON05454	71.71
mmref	rwcore	afrpan	CDS	4501414	4501731	318	-1	MMAR_3655	conserved hypothetical protein	0	MON06486	48.11
mmref	rwcore	afrpan	CDS	4559937	4561448	1512	1	MMAR_3702	Flavin-binding monooxygenase	0	MON05466	14.15
mmref	rwcore	afrpan	misc_feature	4559939	4561693	1755	1		MURD101, 1755bp	0		12.19
mmref	rwcore	afrpan	misc_feature	5079529	5082660	3132	1		MURD110, 3132bp	0		20.11
mmref	rwcore	afrpan	CDS	5079599	5080225	627	-1	MMAR_4123	conserved hypothetical protein	0	MON06525	28.87
mmref	rwcore	afrpan	CDS	5080318	5080845	528	-1	MMAR_4124	conserved hypothetical secreted protein	0	MON05497	14.77
mmref	rwcore	afrpan	CDS	5080996	5081532	537	-1	MMAR_4125	NUDIX hydrolase	0	MON05498	43.39
mmref	rwcore	afrpan	CDS	5130970	5132823	1854	1	MMAR_4169	transmembrane serine/threonine-protein kinase	0	MON04019	12.89
mmref	rwcore	afrpan	misc_feature	5183384	5187439	4056	1		MURD113, 4056bp	0		10.6
mmref	rwcore	afrpan	CDS	5184862	5185530	669	1	MMAR_4208	proline and glycine rich transmembrane protein	0	MON05502	13.6
mmref	rwcore	afrpan	CDS	5186934	5187464	531	1	MMAR_4210	conserved hypothetical membrane protein	0	MON06530	24.48
mmref	rwcore	afrpan	CDS	5196932	5197570	639	1	MMAR_4219	transcriptional regulator	0	MON05503	28.48
mmref	rwcore	afrpan	CDS	5197560	5198507	948	1	MMAR_4220	unidentified antibiotic-transport ATP-binding prot	0	MON05504	12.45
mmref	rwcore	afrpan	misc_feature	5325526	5326782	1257	1		MURD121, 1257bp	0		35.08
mmref	rwcore	afrpan	misc_feature	5366953	5369485	2533	1		MURD124, 2533bp	0		12.67
mmref	rwcore	afrpan	misc_feature	5430030	5456138	26109	1		MURD127, 26109bp	0		10.41
mmref	rwcore	afrpan	CDS	5433015	5433791	777	-1	MMAR_4417	conserved hypothetical membrane protein	0	MON05517	37.84
mmref	rwcore	afrpan	CDS	5433875	5434498	624	-1	MMAR_4418	transcriptional regulatory protein	0	MON05518	36.86
mmref	rwcore	afrpan	CDS	5435560	5438004	2445	1	MMAR_4420	aminomethyltransferase GcvT_2	0	MON05519	12.72
mmref	rwcore	afrpan	CDS	5439150	5440298	1149	1	MMAR_4422	dioxygenase	0	MON05520	18.71
mmref	rwcore	afrpan	CDS	5442929	5443999	1071	-1	MMAR_4426	transcriptional regulatory protein	0	MON05524	39.78
mmref	rwcore	afrpan	CDS	5444274	5445830	1557	1	MMAR_4427	dehydrogenase fad flavoprotein Gmc oxidoreduct	0	MON05525	45.15
mmref	rwcore	afrpan	CDS	5445832	5446710	879	-1	MMAR_4428	haloalkane dehalogenase	0	MON05526	38
mmref	rwcore	afrpan	misc_feature	5747903	5766082	18180	1		MURD132, 18180bp	0		11.72
mmref	rwcore	afrpan	CDS	5748117	5748929	813	-1	MMAR_4697	conserved hypothetical membrane protein	0	MON06160	33.46
mmref	rwcore	afrpan	CDS	5750550	5750840	291	1	MMAR_4700	conserved hypothetical secreted protein	0	MON05537	21.31
mmref	rwcore	afrpan	CDS	5750867	5751283	417	-1	MMAR_4701	conserved hypothetical secreted protein	0	MON05538	90.65
mmref	rwcore	afrpan	CDS	5758697	5759728	1032	-1	MMAR_4709	MCE-family protein	0	MON05545	22.87
mmref	rwcore	afrpan	CDS	5761022	5761867	846	-1	MMAR_4711	conserved hypothetical membrane protein	0	MON05547	18.44
mmref	rwcore	afrpan	CDS	5776024	5777169	1146	1	MMAR_4725	conserved hypothetical metal-dependent hydrola	0	MON05555	35.17
mmref	rwcore	afrpan	CDS	5777171	5777563	393	1	MMAR_4726	conserved hypothetical protein	0	MON06544	43.26
mmref	rwcore	afrpan	CDS	5777560	5778447	888	1	MMAR_4727	conserved hypothetical hydrolase	0	MON05556	20.05
mmref	rwcore	afrpan	CDS	5778462	5778935	474	-1	MMAR_4728	conserved hypothetical protein	0	MON06162	33.97
mmref	rwcore	afrpan	CDS	5780322	5780618	297	1	MMAR_4730	ferredoxin	0	MON05558	14.48
mmref	rwcore	afrpan	CDS	5794267	5795547	1281	1	MMAR_4744	dioxygenase	0	MON17599	20.61
mmref	rwcore	afrpan	misc_feature	5830307	5832376	2070	1		MURD134, 2070bp	0		12.22
mmref	rwcore	afrpan	CDS	5831537	5832403	867	-1	MMAR_4778	2-hydroxy-6-OXO-6-phenylhexa-2,4-dienoate hy	0	MON05576	12.57
mmref	rwcore	afrpan	CDS	5956016	5956654	639	1	MMAR_4901	Zn-dependent hydrolases	0	MON06549	13.62
mmref	rwcore	afrpan	misc_feature	5956071	5957506	1436	1		MURD155, 1436bp	0		17.55
mmref	rwcore	afrpan	misc_feature	6021901	6023211	1311	1		MURD136, 1311bp	0		30.89
mmref	rwcore	afrpan	CDS	6022093	6022575	483	-1	MMAR_4957	hypothetical protein	0	MON06169	44.51
mmref	rwcore	afrpan	CDS	6022708	6023094	387	1	MMAR_4958	hypothetical secreted protein	0	MON06550	14.99
mmref	rwcore	afrpan	CDS	6265076	6267304	2229	1	MMAR_5186	sensor-component of a two-component regulator	0	MON05596	14.27
mmref	rwcore	afrpan	misc_feature	6458356	6460277	1922	1		MURD149, 1922bp	0		17.9
mmref	rwcore	afrpan	CDS	6458741	6459727	987	1	MMAR_5346	dTDP-glucose-4,6-dehydratase, RmlB_1	0	MON06346	27.86
mmref	rwcore	aupan	CDS	90890	91492	603	-1	MMAR_0088	transcriptional regulator	0	MON00080	11.28
mmref	rwcore	aupan	misc_feature	95649	163719	68071	1		MURD3, 68071bp	0		24.6

Reference	Core Group	Pan Group	feature	start	end	length	strand	locus	product	pseudo	ortholog	pct_overlap
mmref	rwcore	aupan	CDS	130639	132027	1389	1	MMAR_0104	conserved hypothetical protein	0	MON05978	73.72
mmref	rwcore	aupan	CDS	132134	132397	264	-1	MMAR_0105	conserved hypothetical protein	0	MON05979	92.8
mmref	rwcore	aupan	CDS	132604	133635	1032	-1	MMAR_0106	conserved hypothetical protein	0	MON05085	27.71
mmref	rwcore	aupan	CDS	133857	134909	1053	1	MMAR_0107	cellobiohydrolase a (1,4-beta-cellobiosidase a) C	0	MON06354	12.06
mmref	rwcore	aupan	CDS	135051	135656	606	1	MMAR_0108	transcriptional regulatory protein	0	MON05086	23.43
mmref	rwcore	aupan	CDS	135771	136856	1086	1	MMAR_0109	conserved hypothetical protein	0	MON06229	55.43
mmref	rwcore	aupan	CDS	137017	138456	1440	1	MMAR_0110	oxidoreductase	0	MON01431	31.46
mmref	rwcore	aupan	CDS	138493	139467	975	-1	MMAR_0111	PE family protein	0	MON05087	47.28
mmref	rwcore	aupan	CDS	139721	140698	978	1	MMAR_0112	haloalkane dehalogenase DhaA_1	0	MON03979	93.46
mmref	rwcore	aupan	CDS	140862	141167	306	-1	MMAR_0113	hypothetical protein	0	MON06097	87.91
mmref	rwcore	aupan	CDS	141538	141798	261	-1	MMAR_0115	conserved hypothetical membrane protein	0	MON06355	92.72
mmref	rwcore	aupan	CDS	141795	142814	1020	-1	MMAR_0116	conserved hypothetical membrane protein	0	MON05088	24.31
mmref	rwcore	aupan	CDS	142815	143285	471	-1	MMAR_0117	conserved hypothetical protein	0	MON05089	50.11
mmref	rwcore	aupan	CDS	143631	144206	576	-1	MMAR_0118	regulatory protein	0	MON05090	100
mmref	rwcore	aupan	CDS	145613	147001	1389	1	MMAR_0120	conserved hypothetical protein	0	MON05091	20.09
mmref	rwcore	aupan	CDS	147163	149505	2343	1	MMAR_0121	formate dehydrogenase H	0	MON05092	63.64
mmref	rwcore	aupan	CDS	149522	150760	1239	-1	MMAR_0122	cytochrome P450 279A2 Cyp279A2	0	MON05093	27.12
mmref	rwcore	aupan	CDS	150923	154276	3354	1	MMAR_0123	transcriptional regulatory protein (LuxR-family)	0	MON05094	67.05
mmref	rwcore	aupan	CDS	154332	155273	942	-1	MMAR_0124	quinone oxidoreductase	0	MON05095	21.55
mmref	rwcore	aupan	CDS	155864	156622	759	-1	MMAR_0126	conserved hypothetical protein	0	MON05096	35.05
mmref	rwcore	aupan	CDS	156692	157801	1110	-1	MMAR_0127	zinc-containing alcohol dehydrogenase NAD-dependent	0	MON05097	58.2
mmref	rwcore	aupan	CDS	157936	158958	1023	-1	MMAR_0128	oxidoreductase	0	MON05098	66.28
mmref	rwcore	aupan	CDS	158967	159284	318	-1	MMAR_0129	monooxygenase effector, MmoB/DmpM family.	0	MON05982	75.47
mmref	rwcore	aupan	CDS	159281	160372	1092	-1	MMAR_0130	monooxygenase hydroxylase, subunit B (AamH)	0	MON06356	42.86
mmref	rwcore	aupan	CDS	160372	161910	1539	-1	MMAR_0131	monooxygenase hydroxylase, subunit A (AamH)	0		85.12
mmref	rwcore	aupan	CDS	162067	162729	663	1	MMAR_0132	two component transcriptional regulatory protein	0	MON05099	27.45
mmref	rwcore	aupan	CDS	258629	259237	609	1	MMAR_0226	conserved hypothetical protein	0	MON04888	14.29
mmref	rwcore	aupan	CDS	309447	310718	1272	-1	MMAR_0272	cytochrome P450 226B1 Cyp226B1	0	MON04843	52.36
mmref	rwcore	aupan	misc_feature	309901	324932	15032	1	MURD6_15032bp		0		60.12
mmref	rwcore	aupan	CDS	311150	312412	1263	-1	MMAR_0273	amidohydrolase	0	MON05119	86.7
mmref	rwcore	aupan	CDS	312399	313694	1296	-1	MMAR_0274	cytochrome P450 271A1 Cyp271A1	0	MON05120	94.14
mmref	rwcore	aupan	CDS	314855	316708	1854	-1	MMAR_0276	1-deoxy-D-xylulose 5-phosphate synthase Dxs2	0	MON05122	60.9
mmref	rwcore	aupan	CDS	316705	317706	1002	-1	MMAR_0277	LytB-related protein LytB2	0	MON06360	53.59
mmref	rwcore	aupan	CDS	317703	318719	1017	-1	MMAR_0278	conserved hypothetical protein	0	MON06361	85.84
mmref	rwcore	aupan	CDS	318780	319523	744	-1	MMAR_0279	conserved hypothetical membrane protein	0	MON06259	97.45
mmref	rwcore	aupan	CDS	319581	320576	996	-1	MMAR_0280	non-plant terpene cyclase (C1 class)	0	MON05123	74.6
mmref	rwcore	aupan	CDS	320584	321972	1389	-1	MMAR_0281	cytochrome P450 183B1 Cyp183B1	0	MON05124	53.49
mmref	rwcore	aupan	CDS	321985	322974	990	-1	MMAR_0282	polypropenyl synthetase IdsB_3	0	MON05125	29.49
mmref	rwcore	aupan	CDS	600855	601163	309	1	MMAR_0507	hypothetical membrane protein	0	MON06362	95.15
mmref	rwcore	aupan	CDS	601170	602420	1251	1	MMAR_0508	conserved integral membrane protein	0	MON01170	29.02
mmref	rwcore	aupan	CDS	830263	830913	651	-1	MMAR_0695	conserved hypothetical secreted protein	0	MON04889	12.29
mmref	rwcore	aupan	CDS	830917	832158	1242	-1	MMAR_0696	Conserved lipoprotein, LpqK	0	MON06338	71.74
mmref	rwcore	aupan	misc_feature	926912	932606	5695	1	MURD13_5695bp		0		28.36
mmref	rwcore	aupan	CDS	929036	929455	420	-1	MMAR_0772	conserved membrane protein MmpS4_2	0	MON02293	100
mmref	rwcore	aupan	CDS	929771	930508	738	1	MMAR_0773	conserved hypothetical regulatory protein	0	MON03947	46.48
mmref	rwcore	aupan	CDS	930767	931213	447	1	MMAR_0774	conserved membrane protein	0	MON30285	36.02
mmref	rwcore	aupan	CDS	1108935	1110431	1497	1	MMAR_0916	trypsin-like serine protease	0	MON00668	14.43
mmref	rwcore	aupan	misc_feature	1109898	1112078	2181	1	MURD18_2181bp		0		19.44
mmref	rwcore	aupan	CDS	1110460	1111968	1509	-1	MMAR_0917	Flavin-binding monooxygenase	0	MON05026	13.78
mmref	rwcore	aupan	CDS	1140594	1141985	1392	1	MMAR_0938	cytochrome P450 135B4 Cyp135B4	0	MON06348	30.24
mmref	rwcore	aupan	misc_feature	1140646	1142845	2200	1	MURD21_2200bp		0		41.32
mmref	rwcore	aupan	CDS	1141970	1143139	1170	-1	MMAR_0939	oxidoreductase	0	MON00690	43.08
mmref	rwcore	aupan	CDS	1373721	1374461	741	-1	MMAR_1144	hydrolase	0	MON00908	20.51
mmref	rwcore	aupan	misc_feature	1614900	1616091	1192	1	MURD30_1192bp		0		20.22
mmref	rwcore	aupan	CDS	1848921	1849787	867	-1	MMAR_1533	conserved hypothetical membrane protein	0	MON02403	23.18
mmref	rwcore	aupan	CDS	1856202	1857965	1764	-1	MMAR_1538	PE family protein	0	MON02395	11.39
mmref	rwcore	aupan	CDS	1880466	1881233	768	-1	MMAR_1562	conserved hypothetical protein	0	MON03468	25.65

Reference	Core Group	Pan Group	feature	start	end	length	strand	locus	product	pseudo	ortholog	pct_overlap
mmref	rwcore	aupan	misc feature	1880808	1885688	4881	1		MURD36, 4881bp	0		59.72
mmref	rwcore	aupan	CDS	1881230	1881691	462	-1	MMAR_1563	conserved hypothetical protein	0	MON06012	100
mmref	rwcore	aupan	CDS	1881688	1882923	1236	-1	MMAR_1564	cytochrome P450 276A1 Cyp276A1	0	MON05199	89.56
mmref	rwcore	aupan	CDS	1882994	1883767	774	-1	MMAR_1565	conserved hypothetical methyltransferase	0	MON06198	75.19
mmref	rwcore	aupan	CDS	1884059	1885648	1590	-1	MMAR_1566	2-methylthioadenine synthetase, MiaB	0	MON03378	16.67
mmref	rwcore	aupan	CDS	1931701	1932657	957	1	MMAR_1595	O-methyltransferase	0	MON05201	48.28
mmref	rwcore	aupan	CDS	1932650	1933411	762	1	MMAR_1596	conserved hypothetical protein	0	MON05202	85.43
mmref	rwcore	aupan	CDS	1933569	1934207	639	1	MMAR_1597	transcriptional regulatory protein	0	MON05203	92.33
mmref	rwcore	aupan	misc feature	2314125	2320127	6003	1		MURD43, 6003bp	0		30.15
mmref	rwcore	aupan	CDS	2315827	2316909	1083	1	MMAR_1901	ABC-type sugar transport protein, ATPase compo	0	MON02252	24.65
mmref	rwcore	aupan	CDS	2316939	2317883	945	-1	MMAR_1902	thioredoxin reductase TrxB2_2	0	MON05217	55.98
mmref	rwcore	aupan	CDS	2317933	2318682	750	-1	MMAR_1903	enoyl-CoA hydratase, EchA16_2	0	MON06402	32.13
mmref	rwcore	aupan	CDS	2318976	2320172	1197	1	MMAR_1904	PPE family protein	0	MON05218	33.58
mmref	rwcore	aupan	CDS	2382069	2383745	1677	1	MMAR_1963	conserved hypothetical hydrolase	0	MON03394	57.66
mmref	rwcore	aupan	misc feature	2382095	2383477	1383	1		MURD46, 1383bp	0		69.92
mmref	rwcore	aupan	misc feature	2487027	2489505	2479	1		MURD48, 2479bp	0		18.31
mmref	rwcore	aupan	CDS	2487522	2488151	630	-1	MMAR_2065	chloramphenicol 3-O-phosphotransferase	0	MON06404	46.51
mmref	rwcore	aupan	misc feature	2530506	2536379	5874	1		MURD50, 5874bp	0		17.43
mmref	rwcore	aupan	CDS	2534389	2536353	1965	1	MMAR_2103	PE-PGRS family protein	0	MON05222	52.11
mmref	rwcore	aupan	CDS	2607291	2610641	3351	-1	MMAR_2165	transglutaminase family protein	0	MON01749	26.62
mmref	rwcore	aupan	misc feature	2607774	2609449	1676	1		MURD52, 1676bp	0		52.98
mmref	rwcore	aupan	CDS	2773695	2775599	1905	-1	MMAR_2307	hypothetical trans-membrane protein	0	MON01510	38.85
mmref	rwcore	aupan	misc feature	2774426	2776190	1765	1		MURD53, 1765bp	0		44.99
mmref	rwcore	aupan	CDS	2832079	2832642	564	1	MMAR_2345	conserved hypothetical protein	0	MON06350	85.28
mmref	rwcore	aupan	CDS	2832775	2833908	1134	1	MMAR_2346	conserved hypothetical dioxygenase	0	MON05253	41.98
mmref	rwcore	aupan	misc feature	3400597	3401557	961	1		MURD63, 961bp	0		78.67
mmref	rwcore	aupan	CDS	3400686	3401753	1068	1	MMAR_2798	amidohydrolase	0	MON02923	62.45
mmref	rwcore	aupan	misc feature	3496566	3505190	8625	1		MURD68, 8625bp	0		13.76
mmref	rwcore	aupan	CDS	3498254	3498532	279	-1	MMAR_2893	hypothetical protein	0	MON06053	30.11
mmref	rwcore	aupan	CDS	3498706	3499398	693	-1	MMAR_2894	PE family protein	0	MON05275	41.13
mmref	rwcore	aupan	misc feature	3507422	3513150	5729	1		MURD69, 5729bp	0		28.17
mmref	rwcore	aupan	CDS	3507458	3508471	1014	-1	MMAR_2903	conserved hypothetical NADP-dependent oxidore	0	MON05277	55.72
mmref	rwcore	aupan	CDS	3508570	3509427	858	1	MMAR_2904	conserved hypothetical O-methyltransferase	0	MON05278	97.9
mmref	rwcore	aupan	misc feature	3521798	3531905	10108	1		MURD71, 10108bp	0		46.23
mmref	rwcore	aupan	CDS	3522027	3522881	855	-1	MMAR_2918	thiosulfate sulfotransferase	0	MON05282	21.99
mmref	rwcore	aupan	CDS	3523014	3523709	696	-1	MMAR_2919	conserved hypothetical protein	0	MON06055	42.39
mmref	rwcore	aupan	CDS	3525354	3525632	279	1	MMAR_2921	conserved hypothetical protein	0	MON06056	91.04
mmref	rwcore	aupan	CDS	3525739	3526422	684	1	MMAR_2922	conserved hypothetical O-methyltransferase	0	MON05284	93.57
mmref	rwcore	aupan	CDS	3526403	3527455	1053	-1	MMAR_2923	conserved hypothetical membrane protein	0	MON06057	66.57
mmref	rwcore	aupan	CDS	3527466	3528224	759	-1	MMAR_2924	SAM-dependent methyltransferase	0	MON05285	69.96
mmref	rwcore	aupan	CDS	3528218	3529477	1260	-1	MMAR_2925	conserved hypothetical glycosyltransferase	0	MON05286	43.17
mmref	rwcore	aupan	CDS	3529642	3530742	1101	-1	MMAR_2926	glycine/D-amino acid oxidase	0		20.89
mmref	rwcore	aupan	CDS	3530907	3531320	414	-1	MMAR_2927	conserved hypothetical protein	0	MON05287	63.29
mmref	rwcore	aupan	CDS	3531548	3532876	1329	1	MMAR_2928	PPE family protein	0	MON05288	40.71
mmref	rwcore	aupan	CDS	3533667	3534935	1269	-1	MMAR_2930	cytochrome P450 147G1 Cyp147G1	0	MON05290	80.54
mmref	rwcore	aupan	CDS	3534978	3536381	1404	-1	MMAR_2931	ferredoxin reductase	0	MON05291	73.79
mmref	rwcore	aupan	CDS	3536378	3536593	216	-1	MMAR_2932	ferredoxin reductase FdxD	0	MON05292	100
mmref	rwcore	aupan	CDS	3536853	3538514	1662	1	MMAR_2933	PE-PGRS family protein	0	MON04399	44.04
mmref	rwcore	aupan	CDS	3538558	3539199	642	-1	MMAR_2934	cutinase Cfp21	0	MON06730	38.47
mmref	rwcore	aupan	CDS	3539304	3540569	1266	-1	MMAR_2935	conserved hypothetical protein	0	MON02193	19.59
mmref	rwcore	aupan	misc feature	3545777	3546535	759	1		MURD72, 759bp	0		96.97
mmref	rwcore	aupan	CDS	3545896	3546441	546	1	MMAR_2939	transcriptional regulatory protein	0	MON05943	95.79
mmref	rwcore	aupan	CDS	3573899	3574927	1029	-1	MMAR_2959	Zn-dependent alcohol dehydrogenase	0	MON05298	34.01
mmref	rwcore	aupan	CDS	3584821	3585843	1023	1	MMAR_2965	predicted ATPase/kinase, NadR	0	MON06450	40.37
mmref	rwcore	aupan	misc feature	3588986	3598713	9728	1		MURD74, 9728bp	0		14.26
mmref	rwcore	aupan	CDS	3594195	3595016	822	-1	MMAR_2971	O-methyltransferase	0	MON05306	14.72
mmref	rwcore	aupan	CDS	3595313	3596377	1065	1	MMAR_2972	conserved hypothetical sugar transport protein	0	MON06451	55.12

Reference	Core Group	Pan Group	feature	start	end	length	strand	locus	product	pseudo	ortholog	pct_overlap
mmref	rwcore	aupan	CDS	3596523	3597854	1332	1	MMAR_2973	PE-PGRS family protein	0	MON05307	20.8
mmref	rwcore	aupan	misc feature	3600365	3615287	14923	1		MURD75, 14923bp	0		64.91
mmref	rwcore	aupan	CDS	3600432	3601874	1443	1	MMAR_2976	conserved hypothetical protein	0	MON06452	94.18
mmref	rwcore	aupan	CDS	3601884	3602636	753	1	MMAR_2977	acyl-ACP thioesterase, FatA	0	MON05309	90.17
mmref	rwcore	aupan	CDS	3604789	3605397	609	1	MMAR_2979	transcriptional regulatory protein (probably TetR-family)	0	MON05311	91.95
mmref	rwcore	aupan	CDS	3605418	3606500	1083	1	MMAR_2980	conserved hypothetical protein	0	MON05312	93.72
mmref	rwcore	aupan	CDS	3606541	3607323	783	1	MMAR_2981	20-beta-hydroxysteroid dehydrogenase FabG3_1	0	MON30270	43.04
mmref	rwcore	aupan	CDS	3607311	3608681	1371	1	MMAR_2982	conserved hypothetical transmembrane protein	0	MON05314	77.61
mmref	rwcore	aupan	CDS	3608847	3609758	912	1	MMAR_2983	conserved hypothetical protein	0	MON05315	30.7
mmref	rwcore	aupan	CDS	3610187	3610858	672	-1	MMAR_2984	transcriptional regulatory protein (TetR-family)	0	MON05316	30.51
mmref	rwcore	aupan	CDS	3610941	3612113	1173	1	MMAR_2985	2,3-dihydroxybiphenyl-1,2-dioxygenase BphC_1	0	MON06243	41.35
mmref	rwcore	aupan	CDS	3612110	3613048	939	1	MMAR_2986	2-hydroxyhepta-2,4-diene-1,7-dioate isomerase	0	MON05317	97.87
mmref	rwcore	aupan	CDS	3613045	3614589	1545	1	MMAR_2987	3-(3-hydroxy-phenyl) propionate hydroxylase	0	MON05318	93.27
mmref	rwcore	aupan	CDS	3614654	3615127	474	1	MMAR_2988	conserved hypothetical acetyltransferase	0	MON05319	68.57
mmref	rwcore	aupan	misc feature	3781467	3785215	3749	1		MURD78, 37 bp	0		28.81
mmref	rwcore	aupan	CDS	3781744	3783345	1602	1	MMAR_3100	integral membrane drug efflux protein, ErmB_1	0	MON05321	24.16
mmref	rwcore	aupan	CDS	3783385	3784764	1380	-1	MMAR_3101	dihydroripoamide dehydrogenase Lpd_1	0	MON05322	50.22
mmref	rwcore	aupan	CDS	3941645	3943669	2025	1	MMAR_3235	conserved hypothetical protein	0	MON03547	11.95
mmref	rwcore	aupan	misc feature	3974006	3974948	943	1		MURD81, 943bp	0		55.36
mmref	rwcore	aupan	CDS	3974086	3974850	765	-1	MMAR_3262	integral membrane protein ABC transporter	0	MON05357	58.3
mmref	rwcore	aupan	CDS	4087255	4088184	930	-1	MMAR_3313	conserved membrane protein	0	MON01315	10.43
mmref	rwcore	aupan	misc feature	4088065	4109675	21611	1		MURD84, 21611bp	0		25.85
mmref	rwcore	aupan	CDS	4088273	4089397	1125	-1	MMAR_3314	conserved hypothetical hydrolase	0	MON05367	65.51
mmref	rwcore	aupan	CDS	4095830	4096024	195	-1	MMAR_3318	conserved hypothetical protein	0	MON06072	100
mmref	rwcore	aupan	CDS	4097273	4098307	1035	-1	MMAR_3320	transcriptional regulatory protein (probably AraC)	0	MON05369	47.34
mmref	rwcore	aupan	CDS	4098380	4099801	1422	-1	MMAR_3321	hypothetical protein	0	MON05370	49.23
mmref	rwcore	aupan	CDS	4099812	4100825	1014	-1	MMAR_3322	pyruvate dehydrogenase E1 component (beta subunit)	0	MON05371	48.42
mmref	rwcore	aupan	CDS	4100822	4101883	1062	-1	MMAR_3323	pyruvate dehydrogenase E1 component (alpha subunit)	0	MON05372	45.57
mmref	rwcore	aupan	CDS	4101943	4102944	1002	-1	MMAR_3324	nucleoside-diphosphate-sugar epimerase	0	MON05949	40.02
mmref	rwcore	aupan	CDS	4107646	4108728	1083	1	MMAR_3328	zinc-dependent alcohol dehydrogenase AdhE2_1	0	MON05375	55.12
mmref	rwcore	aupan	CDS	4108765	4110237	1473	1	MMAR_3329	conserved hypothetical protein	0	MON06228	27.77
mmref	rwcore	aupan	misc feature	4225185	4230172	4988	1		MURD89, 88bp	0		30.79
mmref	rwcore	aupan	CDS	4226483	4227715	1233	1	MMAR_3425	conserved hypothetical protein	0	MON05402	19.14
mmref	rwcore	aupan	CDS	4228833	4230482	1650	-1	MMAR_3427	PE family protein	0	MON00967	37.33
mmref	rwcore	aupan	misc feature	4271366	4313737	42372	1		MURD92, 42372bp	0		48.87
mmref	rwcore	aupan	CDS	4276737	4277630	894	1	MMAR_3472	haloalkane dehalogenase	0	MON30242	26.96
mmref	rwcore	aupan	CDS	4277637	4278530	894	-1	MMAR_3473	ketoacyl-acyl carrier protein synthase III	0	MON06078	42.84
mmref	rwcore	aupan	CDS	4278514	4279614	1101	-1	MMAR_3474	ketoacyl-acyl carrier protein synthase III	0	MON05410	65.3
mmref	rwcore	aupan	CDS	4279643	4280632	990	-1	MMAR_3475	conserved hypothetical protein	0	MON05411	90.61
mmref	rwcore	aupan	CDS	4280736	4282184	1449	-1	MMAR_3476	conserved hypothetical protein	0	MON06470	37.61
mmref	rwcore	aupan	CDS	4282316	4283212	897	-1	MMAR_3477	conserved hypothetical membrane protein	0	MON05412	58.42
mmref	rwcore	aupan	CDS	4283515	4284330	816	1	MMAR_3478	conserved hypothetical membrane protein	0	MON05413	90.56
mmref	rwcore	aupan	CDS	4284352	4286001	1650	-1	MMAR_3479	two component sensor histidine kinase	0	MON05414	65.64
mmref	rwcore	aupan	CDS	4287104	4287868	765	-1	MMAR_3481	conserved hypothetical membrane protein	0	MON05416	38.04
mmref	rwcore	aupan	CDS	4288010	4288981	972	-1	MMAR_3482	phosphofructokinase, PfkB_1	0	MON06471	49.69
mmref	rwcore	aupan	CDS	4289010	4291052	2043	-1	MMAR_3483	conserved hypothetical protein	0	MON06300	36.76
mmref	rwcore	aupan	CDS	4291071	4291502	432	-1	MMAR_3484	heat shock protein HspX_1	0	MON06222	100
mmref	rwcore	aupan	CDS	4292151	4292423	273	-1	MMAR_3486	hypothetical protein	0	MON06079	100
mmref	rwcore	aupan	CDS	4292633	4293613	981	-1	MMAR_3487	conserved hypothetical protein	0	MON05419	45.46
mmref	rwcore	aupan	CDS	4293932	4295731	1800	1	MMAR_3488	acetyl-coenzyme a synthetase Acs_1	0	MON05420	59.89
mmref	rwcore	aupan	CDS	4295731	4296735	1005	1	MMAR_3489	pyruvate dehydrogenase E1 component (alpha subunit)	0	MON05421	87.16
mmref	rwcore	aupan	CDS	4296732	4297709	978	1	MMAR_3490	pyruvate dehydrogenase E1 component (beta subunit)	0	MON05422	52.66
mmref	rwcore	aupan	CDS	4297706	4298947	1242	1	MMAR_3491	pyruvate dehydrogenase (E2 component)	0	MON05423	42.43
mmref	rwcore	aupan	CDS	4298955	4299212	258	1	MMAR_3492	conserved hypothetical protein	0	MON05424	100
mmref	rwcore	aupan	CDS	4299906	4301507	1602	1	MMAR_3494	PE-PGRS family protein	0	MON05426	42.32
mmref	rwcore	aupan	CDS	4302197	4302670	474	-1	MMAR_3496	conserved hypothetical protein	0	MON06472	64.98
mmref	rwcore	aupan	CDS	4302667	4303959	1293	-1	MMAR_3497	coenzyme F420-reducing hydrogenase, alpha subunit	0	MON06738	90.18

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mmref	rwcore	aupan	CDS	4303959	4304714	756	-1	MMAR_3498	coenzyme F420-reducing hydrogenase, gamma subunit	0	MON06080	77.91
mmref	rwcore	aupan	CDS	4304715	4305572	858	-1	MMAR_3499	flavodoxin oxidoreductase	0	MON05428	70.51
mmref	rwcore	aupan	CDS	4305565	4306695	1131	-1	MMAR_3500	ferredoxin	0	MON06473	82.94
mmref	rwcore	aupan	CDS	4306787	4307368	582	-1	MMAR_3501	conserved hypothetical membrane protein	0	MON06474	49.48
mmref	rwcore	aupan	CDS	4307430	4308431	1002	-1	MMAR_3502	conserved hypothetical protein	0	MON05429	13.57
mmref	rwcore	aupan	CDS	4308580	4310913	2334	-1	MMAR_3503	metal cation transporter p-type ATPase	0	MON05430	32.05
mmref	rwcore	aupan	CDS	4311086	4311457	372	-1	MMAR_3504	conserved hypothetical protein	0	MON06081	100
mmref	rwcore	aupan	CDS	4311592	4312929	1338	1	MMAR_3505	conserved hypothetical hydrolase	0	MON05431	55.98
mmref	rwcore	aupan	CDS	4312975	4313838	864	-1	MMAR_3506	conserved hypothetical membrane protein	0	MON06082	61.81
mmref	rwcore	aupan	CDS	4431723	4432574	852	1	MMAR_3608	conserved hypothetical protein	0	MON06485	27.46
mmref	rwcore	aupan	misc feature	4473209	4477073	3865	1	MURD98_3865bp		0		32.94
mmref	rwcore	aupan	CDS	4474722	4475495	774	1	MMAR_3636	methylase	0	MON05454	100
mmref	rwcore	aupan	CDS	4475790	4477313	1524	-1	MMAR_3637	integral membrane nitrite extrusion protein NarK	0	MON05455	15.68
mmref	rwcore	aupan	CDS	4501414	4501731	318	-1	MMAR_3655	conserved hypothetical protein	0	MON06486	100
mmref	rwcore	aupan	CDS	4559937	4561448	1512	1	MMAR_3702	Flavin-binding monooxygenase	0	MON05466	86.77
mmref	rwcore	aupan	misc feature	4559939	4561693	1755	1	MURD101_1755bp		0		79.77
mmref	rwcore	aupan	misc feature	5079529	5082660	3132	1	MURD110_3132bp		0		75.06
mmref	rwcore	aupan	CDS	5079599	5080225	627	-1	MMAR_4123	conserved hypothetical protein	0	MON06525	47.85
mmref	rwcore	aupan	CDS	5080318	5080845	528	-1	MMAR_4124	conserved hypothetical secreted protein	0	MON05497	75.95
mmref	rwcore	aupan	CDS	5080996	5081532	537	-1	MMAR_4125	NUDIX hydrolase	0	MON05498	100
mmref	rwcore	aupan	CDS	5081791	5083542	1752	1	MMAR_4126	conserved hypothetical transport protein	0	MON03989	36.36
mmref	rwcore	aupan	misc feature	5127780	5132764	4985	1	MURD111_85bp		0		15.31
mmref	rwcore	aupan	CDS	5182646	5184082	1437	-1	MMAR_4206	sugar-binding lipoprotein LpqY	0	MON04513	16.42
mmref	rwcore	aupan	misc feature	5183384	5187439	4056	1	MURD113_4056bp		0		39.57
mmref	rwcore	aupan	CDS	5184862	5185530	669	1	MMAR_4208	proline and glycine rich transmembrane protein	0	MON05502	32.14
mmref	rwcore	aupan	CDS	5185630	5186937	1308	1	MMAR_4209	transport transmembrane protein	0	MON06529	40.37
mmref	rwcore	aupan	CDS	5186934	5187464	531	1	MMAR_4210	conserved hypothetical membrane protein	0	MON06530	51.04
mmref	rwcore	aupan	misc feature	5195466	5198515	3050	1	MURD114_3050bp		0		38.2
mmref	rwcore	aupan	CDS	5196932	5197570	639	1	MMAR_4219	transcriptional regulator	0	MON05503	94.52
mmref	rwcore	aupan	CDS	5197560	5198507	948	1	MMAR_4220	unidentified antibiotic-transport ATP-binding protein	0	MON05504	38.5
mmref	rwcore	aupan	misc feature	5325526	5326782	1257	1	MURD121_1257bp		0		63.72
mmref	rwcore	aupan	CDS	5326176	5327018	843	-1	MMAR_4323	transposase	0	MON06532	17.91
mmref	rwcore	aupan	misc feature	5351130	5352870	1741	1	MURD122_1741bp		0		39.35
mmref	rwcore	aupan	CDS	5351761	5352753	993	-1	MMAR_4346	PPE family protein	0	MON05514	67.67
mmref	rwcore	aupan	CDS	5429919	5430704	786	-1	MMAR_4414	conserved hypothetical protein	0	MON05516	82.57
mmref	rwcore	aupan	misc feature	5430030	5456138	26109	1	MURD127_26109bp		0		39
mmref	rwcore	aupan	CDS	5430837	5431349	513	1	MMAR_4415	conserved hypothetical protein	0	MON06241	71.15
mmref	rwcore	aupan	CDS	5431369	5432955	1587	-1	MMAR_4416	conserved hypothetical secreted protein	0	MON06533	41.27
mmref	rwcore	aupan	CDS	5433015	5433791	777	-1	MMAR_4417	conserved hypothetical membrane protein	0	MON05517	96.78
mmref	rwcore	aupan	CDS	5435560	5438004	2445	1	MMAR_4420	aminomethyltransferase GcvT_2	0	MON05519	48.18
mmref	rwcore	aupan	CDS	5438011	5439153	1143	1	MMAR_4421	conserved hypothetical dehydrogenase	0	MON06535	68.33
mmref	rwcore	aupan	CDS	5439150	5440298	1149	1	MMAR_4422	dioxygenase	0	MON05520	79.98
mmref	rwcore	aupan	CDS	5440310	5441140	831	1	MMAR_4423	transcriptional regulatory protein	0	MON05521	33.57
mmref	rwcore	aupan	CDS	5441306	5442022	717	1	MMAR_4424	conserved hypothetical secreted protein	0	MON05522	54.67
mmref	rwcore	aupan	CDS	5442125	5442868	744	-1	MMAR_4425	methylase	0	MON05523	13.71
mmref	rwcore	aupan	CDS	5442929	5443999	1071	-1	MMAR_4426	transcriptional regulatory protein	0	MON05524	84.13
mmref	rwcore	aupan	CDS	5444274	5445830	1557	1	MMAR_4427	dehydrogenase fad flavoprotein Gmc oxidoreductase	0	MON05525	88.76
mmref	rwcore	aupan	CDS	5445832	5446710	879	-1	MMAR_4428	haloalkane dehalogenase	0	MON05526	96.13
mmref	rwcore	aupan	CDS	5626705	5627766	1062	1	MMAR_4586	conserved hypothetical protein	0	MON04447	21.37
mmref	rwcore	aupan	CDS	5627794	5628612	819	1	MMAR_4587	conserved hypothetical oxidoreductase	0	MON04219	17.09
mmref	rwcore	aupan	CDS	5747515	5748120	606	-1	MMAR_4696	cytochrome C oxidase subunit III	0	MON00312	36.3
mmref	rwcore	aupan	misc feature	5747903	5766082	18180	1	MURD132_18180bp		0		56.72
mmref	rwcore	aupan	CDS	5748117	5748929	813	-1	MMAR_4697	conserved hypothetical membrane protein	0	MON06160	58.06
mmref	rwcore	aupan	CDS	5748932	5749681	750	-1	MMAR_4698	conserved hypothetical membrane protein	0	MON06161	69.47
mmref	rwcore	aupan	CDS	5749769	5750350	582	1	MMAR_4699	transcriptional regulatory protein	0	MON05536	34.19
mmref	rwcore	aupan	CDS	5750550	5750840	291	1	MMAR_4700	conserved hypothetical secreted protein	0	MON05537	72.16
mmref	rwcore	aupan	CDS	5750867	5751283	417	-1	MMAR_4701	conserved hypothetical secreted protein	0	MON05538	94.96

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mmref	rwcore	aupan	CDS	5751435	5752169	735	1	MMAR_4702	conserved hypothetical membrane protein	0	MON05539	71.7
mmref	rwcore	aupan	CDS	5752166	5752696	531	1	MMAR_4703	conserved hypothetical membrane protein	0	MON05540	58.95
mmref	rwcore	aupan	CDS	5752798	5753301	504	1	MMAR_4704	conserved hypothetical secreted protein	0	MON06543	22.42
mmref	rwcore	aupan	CDS	5753337	5754968	1632	-1	MMAR_4705	MCE-family protein	0	MON05541	78.98
mmref	rwcore	aupan	CDS	5754969	5756201	1233	-1	MMAR_4706	MCE-family lipoprotein	0	MON05542	50.04
mmref	rwcore	aupan	CDS	5756198	5757625	1428	-1	MMAR_4707	MCE-family protein	0	MON30258	46.78
mmref	rwcore	aupan	CDS	5757622	5758704	1083	-1	MMAR_4708	MCE-family protein	0	MON05544	84.95
mmref	rwcore	aupan	CDS	5758697	5759728	1032	-1	MMAR_4709	MCE-family protein	0	MON05545	75.48
mmref	rwcore	aupan	CDS	5759725	5761002	1278	-1	MMAR_4710	MCE-family protein	0	MON05546	64.55
mmref	rwcore	aupan	CDS	5761022	5761867	846	-1	MMAR_4711	conserved hypothetical membrane protein	0	MON05547	22.58
mmref	rwcore	aupan	CDS	5761910	5762716	807	-1	MMAR_4712	conserved hypothetical membrane protein	0	MON05548	26.89
mmref	rwcore	aupan	CDS	5763034	5764239	1206	-1	MMAR_4713	conserved hypothetical dehydratase	0	MON05549	68.33
mmref	rwcore	aupan	misc feature	5771630	5799568	27939	1		MURD133, 27939bp	0		44.84
mmref	rwcore	aupan	CDS	5774113	5774580	468	1	MMAR_4723	conserved hypothetical secreted protein	0	MON05553	58.55
mmref	rwcore	aupan	CDS	5774873	5775976	1104	1	MMAR_4724	conserved hypothetical metal-dependent hydrolase	0	MON05554	92.66
mmref	rwcore	aupan	CDS	5776024	5777169	1146	1	MMAR_4725	conserved hypothetical metal-dependent hydrolase	0	MON05555	55.24
mmref	rwcore	aupan	CDS	5777171	5777563	393	1	MMAR_4726	conserved hypothetical protein	0	MON06544	46.31
mmref	rwcore	aupan	CDS	5777560	5778447	888	1	MMAR_4727	conserved hypothetical hydrolase	0	MON05556	73.54
mmref	rwcore	aupan	CDS	5778462	5778935	474	-1	MMAR_4728	conserved hypothetical protein	0	MON06162	95.36
mmref	rwcore	aupan	CDS	5778988	5780325	1338	1	MMAR_4729	NADH dehydrogenase I (chain F) (NADH-ubiquinol oxidoreductase)	0	MON05557	39.99
mmref	rwcore	aupan	CDS	5780322	5780618	297	1	MMAR_4730	ferredoxin	0	MON05558	91.25
mmref	rwcore	aupan	CDS	5780754	5782409	1656	1	MMAR_4731	3-ketoacyl-CoA thiolase	0	MON30253	63.35
mmref	rwcore	aupan	CDS	5783436	5784638	1203	1	MMAR_4733	cytochrome P450 190A3 Cyp190A3	0	MON05560	59.85
mmref	rwcore	aupan	CDS	5784649	5784840	192	1	MMAR_4734	ferredoxin FdxD_2	0	MON05561	90.1
mmref	rwcore	aupan	CDS	5786777	5786965	189	-1	MMAR_4736	ferredoxin	0	MON05563	100
mmref	rwcore	aupan	CDS	5786962	5788233	1272	-1	MMAR_4737	cytochrome P450 150A5 Cyp150A5	0	MON05564	24.29
mmref	rwcore	aupan	CDS	5788342	5788845	504	-1	MMAR_4738	conserved hypothetical protein	0	MON05565	28.17
mmref	rwcore	aupan	CDS	5788842	5789447	606	-1	MMAR_4739	transcriptional regulatory protein (possibly TetR-like)	0	MON05566	83.17
mmref	rwcore	aupan	CDS	5790807	5791973	1167	-1	MMAR_4741	acyl-CoA dehydrogenase FadE12_1	0	MON30252	88.17
mmref	rwcore	aupan	CDS	5792084	5793382	1299	-1	MON30253	metal-dependent amidohydrolase	0	MON05569	58.12
mmref	rwcore	aupan	CDS	5793711	5794259	549	1	MMAR_4743	conserved hypothetical protein	0	MON30247	20.22
mmref	rwcore	aupan	CDS	5794267	5795547	1281	1	MMAR_4744	dioxygenase	0	MON17599	78.92
mmref	rwcore	aupan	CDS	5795531	5795866	336	1	MMAR_4745	conserved hypothetical protein	0	MON06163	74.11
mmref	rwcore	aupan	CDS	5795870	5797090	1221	1	MMAR_4746	imidazolonepropionase	0	MON17597	50.86
mmref	rwcore	aupan	CDS	5829822	5831537	1716	-1	MMAR_4777	conserved hypothetical hydroxylase	0	MON06293	47.96
mmref	rwcore	aupan	misc feature	5830307	5832376	2070	1		MURD134, 2070bp	0		66.62
mmref	rwcore	aupan	CDS	5831537	5832403	867	-1	MMAR_4778	2-hydroxy-6-OXO-6-phenylhexa-2,4-dienoate hydrolase	0	MON05576	64.24
mmref	rwcore	aupan	CDS	5955311	5956030	720	-1	MMAR_4900	conserved hypothetical secreted protein	0	MON00505	35
mmref	rwcore	aupan	CDS	5956016	5956654	639	1	MMAR_4901	Zn-dependent hydrolases	0	MON06549	18.78
mmref	rwcore	aupan	misc feature	5956071	5957506	1436	1		MURD155, 1436bp	0		49.3
mmref	rwcore	aupan	CDS	5956734	5957648	915	-1	MMAR_4902	conserved hypothetical regulatory protein	0	MON03983	55.63
mmref	rwcore	aupan	CDS	6003001	6004167	1167	1	MMAR_4944	conserved hypothetical oxidoreductase	0	MON00460	17.82
mmref	rwcore	aupan	CDS	6268894	6269448	555	-1	MMAR_5188	conserved hypothetical protein	0	MON05944	96.4
mmref	rwcore	aupan	CDS	6269640	6270656	1017	-1	MMAR_5189	thiamine-monophosphate kinase	0	MON05598	18.88
mmref	rwcore	aupan	tRNA	6270689	6270779	91	1	MMAR_5533	tRNA-SeC(p) anticodon TCA	0		13.19
mmref	rwcore	aupan	misc feature	6458356	6460277	1922	1		MURD149, 1922bp	0		24.25
mmref	rwcore	aupan	CDS	6458741	6459727	987	1	MMAR_5346	dTDP-glucose-4,6-dehydratase, RmlB_1	0	MON06346	40.53
mmref	rwcore	aupan	misc feature	6589253	6592034	2782	1		MURD152, 2782bp	0		13.3
mmref	rwcore	aupan	CDS	6591497	6591784	288	1	MMAR_5450	6 kDa early secretory antigenic target EsxA (Esa)	0	MON05639	80.56
mmref	rwcore	aupan	misc feature	6597919	6606254	8336	1		MURD153, 8336bp	0		21.57
mmref	rwcore	aupan	CDS	6598333	6600663	2331	-1	MMAR_5455	conserved hypothetical alanine and proline rich protein	0	MON05640	15.74
mmref	rwcore	aupan	CDS	6601072	6601419	348	-1	MMAR_5456	conserved hypothetical protein	0	MON04590	36.21
mmref	rwcore	aupan	CDS	6602919	6604316	1398	-1	MMAR_5458	conserved hypothetical membrane protein	0	MON05643	15.38
mmref	rwcore	aupan	CDS	6604313	6605719	1407	-1	MMAR_5459	membrane-anchored serine protease (mycosin),	0	MON05644	28.86
mmref	rwcore	aupan	CDS	6605910	6606470	561	-1	MMAR_5460	C-term conserved hypothetical membrane protein	1	MON15971	49.2

Table 9(c)

Agy99 Reference: Pan Core Regions

Reference	Core Group	Pan Group	feature	start	end	length	strand	locus	product	pseudo	ortholog	pct_overlap
muref	afcore	aupan	CDS	2685734	2686387	654	1	MUL_2400	C-term conserved hypothetical protein, pseudogene	1	MON02400	48.2
muref	afcore	aupan	CDS	2686384	2686962	579	1	MUL_2403	N-terminal conserved hypothetical membrane protein, pseudogene	1	MON02403	75.7
muref	afcore	aupan	CDS	5089096	5089461	366	1	MUL_4588	N-term conserved hypothetical alanine and glycine rich protein - pseu	1	MON04588	62.3
muref	afcore	aupan	CDS	5113284	5113520	237	-1	MUL_4612	conserved hypothetical membrane protein	0	MON04612	73.0
muref	afcore	rwpn	CDS	1365078	1365560	483	1	MUL_1264	6-pyruvoyl tetrahydrobiopterin synthase	0	MON01264	37.1
muref	afcore	rwpn	CDS	2670708	2671169	462	-1	MUL_2385	non-ribosomal peptide synthetase fragment, pseudogene	1	MON05355	88.7
muref	afcore	rwpn	CDS	3006536	3007183	648	-1	MUL_2686	PPE family protein	0	MON02686	16.7
muref	afcore	rwpn	CDS	3007230	3007724	495	-1	MUL_2690	C-terminal PPE family protein, pseudogene	1	MON02690	30.3
muref	afcore	rwpn	CDS	3011053	3012375	1323	-1	MUL_2693	conserved protein	0	MON02693	87.4
muref	afcore	rwpn	CDS	3966440	3967681	1242	-1	MUL_3577	ATP-binding protein ABC transporter	0	MON03577	56.1
muref	afcore	rwpn	CDS	4309152	4310387	1236	-1	MUL_3854	acyl-CoA dehydrogenase	0	MON03854	36.1
muref	afcore	rwpn	CDS	4310384	4311109	726	-1	MUL_3855	C-term acyl-CoA dehydrogenase, pseudogene	1	MON03855	28.5
muref	afcore	rwpn	CDS	4312402	4312920	519	-1	MUL_3855	N-term acyl-CoA dehydrogenase, pseudogene	1	MON03855	58.8
muref	afcore	rwpn	CDS	4313089	4313898	810	1	MUL_3858	conserved hypothetical alanine-rich protein	0	MON03858	56.1
muref	afcore	rwpn	CDS	4314843	4316069	1227	1	MUL_3860	cytochrome P450 187A4 Cyp187A4	0	MON03860	23.7
muref	afcore	rwpn	CDS	4876916	4877053	138	-1	MUL_4396	C-term conserved hypothetical protein, pseudogene	1	MON04396	100.0
muref	aucore	rwpn	CDS	1365078	1365560	483	1	MUL_1264	6-pyruvoyl tetrahydrobiopterin synthase	0	MON01264	37.1
muref	aucore	rwpn	CDS	2670708	2671169	462	-1	MUL_2385	non-ribosomal peptide synthetase fragment, pseudogene	1	MON05355	88.7
muref	aucore	rwpn	CDS	3011053	3012375	1323	-1	MUL_2693	conserved protein	0	MON02693	87.4
muref	aucore	rwpn	CDS	3966440	3967681	1242	-1	MUL_3577	ATP-binding protein ABC transporter	0	MON03577	56.1
muref	aucore	rwpn	CDS	4309152	4310387	1236	-1	MUL_3854	acyl-CoA dehydrogenase	0	MON03854	36.1
muref	aucore	rwpn	CDS	4310384	4311109	726	-1	MUL_3855	C-term acyl-CoA dehydrogenase, pseudogene	1	MON03855	28.5
muref	aucore	rwpn	CDS	4312402	4312920	519	-1	MUL_3855	N-term acyl-CoA dehydrogenase, pseudogene	1	MON03855	58.8
muref	aucore	rwpn	CDS	4313089	4313898	810	1	MUL_3858	conserved hypothetical alanine-rich protein	0	MON03858	56.1
muref	aucore	rwpn	CDS	4314843	4316069	1227	1	MUL_3860	cytochrome P450 187A4 Cyp187A4	0	MON03860	23.7
muref	aucore	rwpn	CDS	4876916	4877053	138	-1	MUL_4396	C-term conserved hypothetical protein, pseudogene	1	MON04396	100.0
muref	mucore	mmpan	misc_feature	28452	29208	757	1		non-IS element not present in <i>Mycobacterium marinum</i> strain M	0		90.0
muref	mucore	mmpan	CDS	28617	29372	756	1	MUL_0027	glycosylase	0	MON00026	72.6
muref	mucore	mmpan	CDS	561042	561290	249	-1	MUL_0551	conserved hypothetical protein	0	MON00551	10.4
muref	mucore	mmpan	misc_feature	561066	561884	819	1		non-IS element not present in <i>Mycobacterium marinum</i> strain M	0		73.9
muref	mucore	mmpan	CDS	561291	561713	423	-1	MUL_0552	conserved hypothetical protein	0	MON00552	100.0
muref	mucore	mmpan	misc_feature	1049570	1050990	1421	1		non-IS element not present in <i>Mycobacterium marinum</i> strain M	0		35.8
muref	mucore	mmpan	CDS	1050322	1050519	198	1	MUL_0998	hypothetical protein	0	MON00998	68.2
muref	mucore	mmpan	misc_feature	1052357	1054054	1698	1		non-IS element not present in <i>Mycobacterium marinum</i> strain M	0		18.3
muref	mucore	mmpan	CDS	1052616	1053740	1125	-1	MUL_1001	hypothetical membrane protein	0	MON01001	27.6
muref	mucore	mmpan	misc_feature	3159068	3161047	1980	1		non-IS element not present in <i>Mycobacterium marinum</i> strain M	0		46.3
muref	mucore	mmpan	CDS	3159788	3159895	108	1	MUL_2830	hypothetical protein	0	MON02830	15.7
muref	mucore	mmpan	CDS	3160001	3160279	279	1	MUL_2831	hypothetical protein	0	MON02831	92.8
muref	mucore	mmpan	CDS	3160372	3161436	1065	1	MUL_2832	lipase LipU_1	0	MON30165	41.7
muref	mucore	mmpan	misc_feature	3582831	3583478	648	1		non-IS element not present in <i>Mycobacterium marinum</i> strain M	0		74.2
muref	mucore	mmpan	CDS	3582899	3583384	486	1	MUL_3212	conserved hypothetical protein	0	MON03212	86.4
muref	mucore	mmpan	misc_feature	3582899	3606951	24053	-1		Prophage phiMU02	0		29.1
muref	mucore	mmpan	misc_feature	3584917	3593219	8303	1		non-IS element not present in <i>Mycobacterium marinum</i> strain M	0		59.1
muref	mucore	mmpan	CDS	3585030	3585779	750	-1	MUL_3214	DNAse (TatD family)	0	MON03214	100.0
muref	mucore	mmpan	CDS	3585779	3587041	1263	-1	MUL_3215	conserved hypothetical protein	0	MON03215	100.0
muref	mucore	mmpan	CDS	3587038	3587910	873	-1	MUL_3216	conserved hypothetical protein	0	MON03216	77.7
muref	mucore	mmpan	CDS	3587910	3589535	1626	-1	MUL_3217	P-loop ATPase	0	MON03217	100.0
muref	mucore	mmpan	CDS	3589712	3590350	639	-1	MUL_3218	zinc metalloprotease	0	MON03218	49.3
muref	mucore	mmpan	misc_feature	3605316	3606912	1597	1		non-IS element not present in <i>Mycobacterium marinum</i> strain M	0		100.0
muref	mucore	mmpan	CDS	3605344	3606948	1605	1	MUL_5129	prophage integrase	0	MON30075	97.8
muref	rwcore	aupan	CDS	2685734	2686387	654	1	MUL_2400	C-term conserved hypothetical protein, pseudogene	1	MON02400	18.8

Reference	Core Group	Pan Group	feature	start	end	length	strand	locus	product	pseudo	ortholog	pct_overlap
muref	rwcore	aupan	CDS	2686384	2686962	579	1	MUL_2403	N-terminal conserved hypothetical membrane protein, pseudogene	1	MON02403	75.7

Table 10

Putative Pseudogenes present in ALL Mu strains

Mm locus	Mu locus	Agy99 Pseudogene	Functional Group	Product
MMAR_0094	MUL_0083	1	cell wall and cell processes	conserved transmembrane transport protein_MmpL5_3
MMAR_0670	MUL_0102	1	cell wall and cell processes	Mg2+ transport transmembrane protein MgtE
MMAR_0655	MUL_0117	1	intermediary metabolism and respiration	carbon monoxide dehydrogenase (medium chain) CoxM
MMAR_4370	MUL_0183	1	cell wall and cell processes	conserved hypothetical transmembrane protein
MMAR_4411	MUL_0228	1	conserved hypotheticals	conserved hypothetical protein
MMAR_4821	MUL_0390	1	conserved hypotheticals	conserved hypothetical protein
MMAR_4858	MUL_0442	1	conserved hypotheticals	conserved hypothetical protein
MMAR_0578	MUL_0543	1	intermediary metabolism and respiration	3-dehydroquinate synthase AroB_1
MMAR_0601	MUL_0561	1	cell wall and cell processes	conserved hypothetical membrane protein
MMAR_0602	MUL_0564	1	conserved hypotheticals	conserved hypothetical membrane protein
MMAR_0612	MUL_0577	1	regulatory proteins	transcriptional regulatory protein
MMAR_0627	MUL_0591	1	cell wall and cell processes	L-asparagine permease AnsP1_1
MMAR_0851	MUL_0600	1	lipid metabolism	non-ribosomal peptide synthetase
MMAR_3270	MUL_0600	1	lipid metabolism	non-ribosomal peptide synthetase
MMAR_3271	MUL_0600	1	lipid metabolism	non-ribosomal peptide synthetase
MMAR_0869	MUL_0622	1	cell wall and cell processes	amino acid permease
MMAR_0928	MUL_0680	1	lipid metabolism	cytochrome P450 189A6 Cyp189A6
MMAR_1096	MUL_0853	1	cell wall and cell processes	conserved hypothetical membrane protein
MMAR_1157	MUL_0922	1	conserved hypotheticals	conserved hypothetical protein
MMAR_4300	MUL_0994	1	lipid metabolism	O-methyltransferase Omt_2
MMAR_4284	MUL_1016	1	regulatory proteins	transcriptional regulatory protein
MMAR_4267	MUL_1031	1	cell wall and cell processes	integral membrane nitrite extrusion protein NarK3_1
MMAR_0437	MUL_1087	1	intermediary metabolism and respiration	oxidoreductase
MMAR_0455	MUL_1105	1	lipid metabolism	acyl-CoA dehydrogenase FadE3_2
MMAR_0539	MUL_1203	1	lipid metabolism	O-Methyltransferase
MMAR_3633	MUL_1229	1	lipid metabolism	peptide synthetase Nrp (peptide synthase)
MMAR_3632	MUL_1232	1	intermediary metabolism and respiration	tryptophan halogenase
MMAR_3609	MUL_1258	1	cell wall and cell processes	conserved transmembrane transport protein MmpL4
MMAR_3358	MUL_1285	1	conserved hypotheticals	conserved hypothetical proline rich protein
MMAR_3283	MUL_1346	1	cell wall and cell processes	drugs-transport transmembrane ATP-binding protein ABC transporter
MMAR_3268	MUL_1358	1	lipid metabolism	nonribosomal peptide synthetase
MMAR_3264	MUL_1361	1	cell wall and cell processes	conserved transmembrane transport protein - MmpL family
MMAR_3266	MUL_1361	1	cell wall and cell processes	conserved transmembrane transport protein - MmpL family
MMAR_1171	MUL_1422	1	intermediary metabolism and respiration	8-amino-7-oxononanoate synthase BioF2_5
MMAR_1180	MUL_1433	1	lipid metabolism	Fatty acyl-AMP ligase FadD28_1 and polyketide synthase
MMAR_2313	MUL_1517	1	cell wall and cell processes	glycosyltransferase LosA
MMAR_2314	MUL_1521	1	conserved hypotheticals	conserved hypothetical
MMAR_2357	MUL_1533	1	conserved hypotheticals	conserved hypothetical protein
MMAR_2416	MUL_1594	1	cell wall and cell processes	prolipoprotein diacylglycerol transferases Lgt
MMAR_2444	MUL_1623	1	regulatory proteins	transmembrane serine/threonine-protein kinase
MMAR_2471	MUL_1653	1	lipid metabolism	polyketide synthase Pks7
MMAR_2472	MUL_1654	1	lipid metabolism	polyketide synthase Pks8
MMAR_2518	MUL_1703	1	lipid metabolism	nonribosomal peptide synthetase
MMAR_2160	MUL_1744	1	cell wall and cell processes	transmembrane alanine and valine and leucine rich protein
MMAR_2256	MUL_1846	1	intermediary metabolism and respiration	protoporphyrinogen oxidase HemY_1
MMAR_4264	MUL_1871	1	conserved hypotheticals	conserved hypothetical protein
MMAR_1722	MUL_1962	1	cell wall and cell processes	conserved transmembrane transport protein MmpL1_1
MMAR_1741	MUL_1984	1	cell wall and cell processes	conserved hypothetical alanine rich membrane protein
MMAR_1808	MUL_2056	1	conserved hypotheticals	conserved hypothetical protein
MMAR_1852	MUL_2102	1	intermediary metabolism and respiration	8-amino-7-oxononanoate synthase BioF2_3

Mm locus	Mul locus	Agy99 Pseudogene	Functional Group	Product
MMAR_2947	MUL_2206	1	information pathways	HrpA-like helicase
MMAR_0569	MUL_2212	1	cell wall and cell processes	conserved hypothetical transmembrane protein
MMAR_2952	MUL_2218	1	conserved hypotheticals	conserved hypothetical protein
MMAR_2954	MUL_2221	1	intermediary metabolism and respiration	dehydrogenase fad flavoprotein Gmc oxidoreductase
MMAR_3043	MUL_2285	1	intermediary metabolism and respiration	adenylate cyclase
MMAR_3066	MUL_2311	1	conserved hypotheticals	conserved hypothetical protein
MMAR_3097	MUL_2345	1	lipid metabolism	non-ribosomal peptide synthetase
MMAR_3098	MUL_2348	1	lipid metabolism	polyketide synthase PKS
MMAR_3099	MUL_2349	1	lipid metabolism	polyketide synthase and peptide synthetase
MMAR_3176	MUL_2385	1	intermediary metabolism and respiration	non-ribosomal peptide synthetase
MMAR_1534	MUL_2400	1	conserved hypotheticals	conserved protein
MMAR_1533	MUL_2403	1	cell wall and cell processes	conserved hypothetical membrane protein
MMAR_1485	MUL_2454	1		membrane-associated phospholipase C 2 PlcB_2
MMAR_1331	MUL_2548	1	conserved hypotheticals	conserved hypothetical alanine and proline rich protein
MMAR_1306	MUL_2575	1	cell wall and cell processes	conserved transmembrane transport protein
MMAR_1230	MUL_2660	1	cell wall and cell processes	magnesium and cobalt transport transmembrane protein CorA_1
MMAR_1228	MUL_2663	1	cell wall and cell processes	metal cation transporting p-type ATPase CtpH_1
MMAR_3547	MUL_2779	1	regulatory proteins	serine/threonine-protein kinase transcriptional regulatory protein
MMAR_3568	MUL_2800	1	cell wall and cell processes	conserved hypothetical proline-rich protein
MMAR_0707	MUL_2816	1	lipid metabolism	polyketide synthase Pks6
MMAR_2884	MUL_2868	1	unknown	MCE-family protein Mce3C
MMAR_2805	MUL_2931	1	unknown	hypothetical protein
MMAR_2830	MUL_2953	1	conserved hypotheticals	conserved hypothetical protein
MMAR_2766	MUL_2981	1	lipid metabolism	non-ribosomal peptide synthetase
MMAR_2745	MUL_3009	1	lipid metabolism	acyl-CoA transferase/dehydratase
MMAR_2660	MUL_3097	1	cell wall and cell processes	conserved hypothetical membrane protein
MMAR_2657	MUL_3099	1	intermediary metabolism and respiration	isochorismatase family protein
MMAR_2626	MUL_3135	1	conserved hypotheticals	conserved hypothetical protein
MMAR_2605	MUL_3154	1	intermediary metabolism and respiration	anaerobic dehydrogenase
MMAR_2576	MUL_3185	1	regulatory proteins	serine/threonine-protein kinase transcriptional regulatory protein PknK
MMAR_2550	MUL_3211	1	cell wall and cell processes	conserved transmembrane protein
MMAR_2084	MUL_3260	1	conserved hypotheticals	conserved hypothetical protein
MMAR_2026	MUL_3326	1	cell wall and cell processes	antibiotic-transport ATP-binding protein ABC transporter
MMAR_1990	MUL_3365	1	cell wall and cell processes	conserved hypothetical integral membrane protein
MMAR_1983	MUL_3373	1	cell wall and cell processes	conserved hypothetical membrane protein
MMAR_1618	MUL_3417	1	intermediary metabolism and respiration	Multicopper oxidase type 1 CueO
MMAR_1616	MUL_3421	1	intermediary metabolism and respiration	carbon starvation protein CstA
MMAR_1605	MUL_3432	1	cell wall and cell processes	conserved hypothetical membrane protein
MMAR_1580	MUL_3454	1	intermediary metabolism and respiration	dehydrogenase
MMAR_3212	MUL_3528	1	lipid metabolism	polyprenyl synthetase IdsB_2
MMAR_3219	MUL_3528	1	lipid metabolism	polyprenyl synthetase IdsB_1
MMAR_3233	MUL_3544	1	cell wall and cell processes	conserved hypothetical secreted protein
MMAR_3257	MUL_3572	1	intermediary metabolism and respiration	adenylate cyclase
MMAR_0738	MUL_3603	1	regulatory proteins	two-component sensor and regulator
MMAR_0740	MUL_3605	1	cell wall and cell processes	metal cation transporting p-type ATPase CtpH
MMAR_3713	MUL_3655	1	intermediary metabolism and respiration	gamma-glutamyltranspeptidase precursor GgtB
MMAR_3656	MUL_3748	1	lipid metabolism	membrane-associated phospholipase C 2 PlcB_5
MMAR_3958	MUL_3813	1	regulatory proteins	two component sensor kinase
MMAR_3960	MUL_3815	1	cell wall and cell processes	conserved hypothetical protein
MMAR_3977	MUL_3838	1	cell wall and cell processes	drug-transport integral membrane protein
MMAR_3993	MUL_3855	1	intermediary metabolism and respiration	acyl-CoA dehydrogenase
MMAR_4027	MUL_3892	1	lipid metabolism	fatty-acid-CoA ligase
MMAR_4078	MUL_3942	1	intermediary metabolism and respiration	adenylate cyclase
MMAR_4169	MUL_4019	1	regulatory proteins	transmembrane serine/threonine-protein kinase H PknH_1
MMAR_4960	MUL_4033	1		peroxidase BpoA
MMAR_5011	MUL_4085	1	cell wall and cell processes	conserved hypothetical secreted protein

Mm locus	Mu locus	Agy99 Pseudogene	Functional Group	Product
MMAR_5095	MUL_4171	1	cell wall and cell processes	multifunctional geranylgeranyl pyrophosphate synthetase IdsA1
MMAR_5195	MUL_4268	1	intermediary metabolism and respiration	formate dehydrogenase beta subunit selenocysteine-containing
MMAR_5254	MUL_4331	1	intermediary metabolism and respiration	membrane-anchored adenylyl cyclase
MMAR_5257	MUL_4331	1	intermediary metabolism and respiration	membrane-anchored adenylyl cyclase
MMAR_5319	MUL_4395	1	conserved hypotheticals	conserved hypothetical protein
MMAR_5320	MUL_4396	1	conserved hypotheticals	conserved hypothetical protein
MMAR_4577	MUL_4438	1	regulatory proteins	transmembrane serine/threonine-protein kinase D PknD
MMAR_4171	MUL_4468	1	regulatory proteins	transmembrane serine/threonine-protein kinase
MMAR_4345	MUL_4475	1	cell wall and cell processes	conserved hypothetical exported protein
MMAR_4192	MUL_4496	1	cell wall and cell processes	drug-transport integral membrane protein
MMAR_4221	MUL_4522	1	cell wall and cell processes	tetronasin-transport integral membrane protein ABC transporter
MMAR_4347	MUL_4588	1	conserved hypotheticals	conserved hypothetical alanine and glycine rich protein
MMAR_4351	MUL_4593	1	conserved hypotheticals	conserved hypothetical alanine and proline rich protein
MMAR_0840	MUL_4596	1	cell wall and cell processes	conserved transmembrane transport protein Mmpl2
MMAR_4489	MUL_4661	1	cell wall and cell processes	conserved hypothetical membrane protein
MMAR_4516	MUL_4687	1	cell wall and cell processes	conserved hypothetical secreted protein
MMAR_0368	MUL_4748	1	lipid metabolism	peptide synthetase Nrp (peptide synthase)
MMAR_0284	MUL_4840	1		membrane-associated phospholipase C 2 PlcB_3
MMAR_0239	MUL_4874	1	intermediary metabolism and respiration	monooxygenase
MMAR_0220	MUL_4894	1	conserved hypotheticals	conserved hypothetical protein
MMAR_0202	MUL_4897	1	conserved hypotheticals	conserved hypothetical alanine and glycine rich protein
MMAR_0203	MUL_4897	1	conserved hypotheticals	conserved hypothetical alanine and glycine rich protein
MMAR_5361	MUL_4980	1	lipid metabolism	acyl-CoA dehydrogenase FadE35
MMAR_5451	MUL_5042	1	cell wall and cell processes	conserved hypothetical alanine and proline rich membrane protein
MMAR_5464	MUL_5053	1		ADP-ribosyltransferase
MMAR_5470	MUL_5059	1	conserved hypotheticals	conserved hypothetical protein
MMAR_0976	MUL_5083	1	information pathways	conserved hypothetical protein
MMAR_2778	MUL_5088	1	unknown	hypothetical protein
MMAR_2074	MUL_5091	1	unknown	conserved hypothetical protein
MMAR_4538	MUL_5093	1	unknown	hypothetical protein
MMAR_2159	MUL_5095	1	conserved hypotheticals	conserved hypothetical protein
MMAR_1946	MUL_5098	1	intermediary metabolism and respiration	conserved hypothetical dehydrogenase
MMAR_1592	MUL_5117	1	unknown	hypothetical protein
MMAR_0586	MUL_5124	1	conserved hypotheticals	conserved hypothetical protein
MMAR_5414	MUL_5126	1	cell wall and cell processes	conserved hypothetical membrane protein
MMAR_0025	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_0026	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_0027	(null)	(null)	intermediary metabolism and respiration	thymidylate synthase ThyA_1
MMAR_0028	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_0029	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_0077	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_0078	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_0079	(null)	(null)	unknown	hypothetical protein
MMAR_0083	(null)	(null)	cell wall and cell processes	amidohydrolase
MMAR_0084	(null)	(null)	intermediary metabolism and respiration	conserved hypothetical short-chain dehydrogenase
MMAR_0085	(null)	(null)	regulatory proteins	transcriptional regulatory protein
MMAR_0089	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_0096	(null)	(null)	unknown	hypothetical protein
MMAR_0098	(null)	(null)	lipid metabolism	polyketide synthase
MMAR_0099	(null)	(null)	intermediary metabolism and respiration	non-ribosomal peptide synthetase
MMAR_0100	(null)	(null)	lipid metabolism	4-hydroxybenzoate synthetase (chorismate lyase)
MMAR_0101	(null)	(null)	lipid metabolism	polyketide synthase PKS
MMAR_0102	(null)	(null)	lipid metabolism	polyketide synthase PKS
MMAR_0103	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_0113	(null)	(null)	unknown	hypothetical protein
MMAR_0117	(null)	(null)	conserved hypotheticals	conserved hypothetical protein

Mm locus	Mu locus	Agy99 Pseudogene	Functional Group	Product
MMAR_0119	(null)	(null)	conserved hypotheticals	conserved hypothetical membrane protein
MMAR_0123	(null)	(null)	regulatory proteins	transcriptional regulatory protein (LuxR-family)
MMAR_0184	(null)	(null)	cell wall and cell processes	conserved hypothetical membrane protein
MMAR_0188	(null)	(null)		6 kDa culture filtrate antigen EsxA_1 (early secreted antigenic target - EsxA)
MMAR_0190	(null)	(null)	unknown	hypothetical protein
MMAR_0193	(null)	(null)	cell wall and cell processes	hypothetical protein
MMAR_0307	(null)	(null)	intermediary metabolism and respiration	dioxygenase
MMAR_0587	(null)	(null)	intermediary metabolism and respiration	short-chain type dehydrogenase/reductase
MMAR_0588	(null)	(null)	unknown	hypothetical protein
MMAR_0590	(null)	(null)	unknown	conserved hypothetical protein
MMAR_0593	(null)	(null)	unknown	hypothetical protein
MMAR_0594	(null)	(null)	unknown	hypothetical protein
MMAR_0628	(null)	(null)	intermediary metabolism and respiration	monooxygenase
MMAR_0629	(null)	(null)	intermediary metabolism and respiration	dehydrogenase
MMAR_0630	(null)	(null)	regulatory proteins	transcriptional regulatory protein
MMAR_0631	(null)	(null)	intermediary metabolism and respiration	potassium-transporting ATPase a subunit KdpA
MMAR_0632	(null)	(null)	cell wall and cell processes	high-affinity K+ transport system ATPase chain B KdpB
MMAR_0633	(null)	(null)	intermediary metabolism and respiration	potassium-transporting ATPase C chain KdpC
MMAR_0634	(null)	(null)	regulatory proteins	two component system response phosphate sensor kinase KdpD
MMAR_0635	(null)	(null)	regulatory proteins	transcriptional regulatory protein KdpE
MMAR_0636	(null)	(null)	unknown	hypothetical protein
MMAR_0684	(null)	(null)	regulatory proteins	conserved hypothetical regulatory protein
MMAR_0686	(null)	(null)	intermediary metabolism and respiration	formate-dependent phosphoribosylglycnamide formyltransferase PurT
MMAR_0690	(null)	(null)	cell wall and cell processes	conserved hypothetical transport protein
MMAR_0706	(null)	(null)	lipid metabolism	fatty acyl-AMP ligase FadD30
MMAR_0775	(null)	(null)	cell wall and cell processes	conserved transmembrane transport protein - MmpL family
MMAR_0931	(null)	(null)	unknown	hypothetical protein
MMAR_1133	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_1405	(null)	(null)	cell wall and cell processes	hypothetical membrane protein
MMAR_1406	(null)	(null)	unknown	hypothetical protein
MMAR_1409	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_1410	(null)	(null)	unknown	hypothetical protein
MMAR_1411	(null)	(null)	cell wall and cell processes	hypothetical membrane protein
MMAR_1413	(null)	(null)	regulatory proteins	conserved hypothetical transcriptional regulatory protein
MMAR_1414	(null)	(null)	intermediary metabolism and respiration	adenylate cyclase CyaA_1
MMAR_1415	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_1419	(null)	(null)	cell wall and cell processes	conserved hypothetical transmembrane protein
MMAR_1420	(null)	(null)	conserved hypotheticals	Carbonic anhydrase CynT
MMAR_1422	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_1423	(null)	(null)	regulatory proteins	anchored-membrane serine/threonine-protein kinase
MMAR_1424	(null)	(null)	unknown	hypothetical protein
MMAR_1426	(null)	(null)	conserved hypotheticals	conserved hypothetical secreted protein
MMAR_1427	(null)	(null)	unknown	hypothetical membrane protein
MMAR_1428	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_1429	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_1430	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_1432	(null)	(null)	cell wall and cell processes	conserved hypothetical membrane protein
MMAR_1438	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_1439	(null)	(null)	unknown	hypothetical protein
MMAR_1443	(null)	(null)	intermediary metabolism and respiration	conserved hypothetical protein
MMAR_1444	(null)	(null)	regulatory proteins	transcriptional regulatory protein (probably TetR/AcrR-family)
MMAR_1448	(null)	(null)	cell wall and cell processes	zinc cation transport ATPase
MMAR_1450	(null)	(null)	unknown	hypothetical protein
MMAR_1454	(null)	(null)	conserved hypotheticals	hypothetical protein
MMAR_1457	(null)	(null)	unknown	hypothetical protein
MMAR_1458	(null)	(null)	conserved hypotheticals	conserved hypothetical protein

Mm locus	Mu locus	Agy99 Pseudogene	Functional Group	Product
MMAR_1459	(null)	(null)	unknown	hypothetical protein
MMAR_1462	(null)	(null)	intermediary metabolism and respiration	conserved hypothetical oxidoreductase
MMAR_1464	(null)	(null)	unknown	hypothetical protein
MMAR_1465	(null)	(null)	unknown	hypothetical protein
MMAR_1868	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_1876	(null)	(null)	lipid metabolism	long-chain acyl-CoA synthetase
MMAR_1900	(null)	(null)	cell wall and cell processes	ABC-type sugar transport protein
MMAR_1942	(null)	(null)	unknown	hypothetical protein
MMAR_1943	(null)	(null)	unknown	conserved hypothetical protein
MMAR_1944	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_1945	(null)	(null)	conserved hypotheticals	conserved hypothetical membrane protein
MMAR_2133	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_2134	(null)	(null)	regulatory proteins	transcriptional regulatory protein
MMAR_2136	(null)	(null)	cell wall and cell processes	conserved hypothetical metal transport protein
MMAR_2137	(null)	(null)	cell wall and cell processes	conserved hypothetical metal transport protein
MMAR_2138	(null)	(null)	intermediary metabolism and respiration	membrane-associated methyltransferase
MMAR_2139	(null)	(null)	regulatory proteins	transcriptional regulatory protein
MMAR_2140	(null)	(null)	cell wall and cell processes	metal cation transporter p-type ATPase
MMAR_2141	(null)	(null)	cell wall and cell processes	conserved hypothetical transmembrane protein
MMAR_2142	(null)	(null)	unknown	hypothetical protein
MMAR_2143	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_2144	(null)	(null)	cell wall and cell processes	conserved hypothetical membrane protein
MMAR_2145	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_2146	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_2315	(null)	(null)	conserved hypotheticals	conserved hypothetical methyltransferase
MMAR_2316	(null)	(null)	regulatory proteins	transcriptional regulator
MMAR_2317	(null)	(null)	intermediary metabolism and respiration	conserved hypothetical O-methyltransferase
MMAR_2318	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_2319	(null)	(null)	cell wall and cell processes	conserved hypothetical transmembrane protein
MMAR_2320	(null)	(null)	cell wall and cell processes	pyridoxal phosphate-dependent enzyme WeeE
MMAR_2323	(null)	(null)	cell wall and cell processes	conserved hypothetical transmembrane protein
MMAR_2340	(null)	(null)	lipid metabolism	probable polyketide synthase Pks5
MMAR_2341	(null)	(null)	lipid metabolism	fatty acyl-AMP ligase FadD25
MMAR_2342	(null)	(null)	cell wall and cell processes	conserved transmembrane transport protein MmpL family
MMAR_2343	(null)	(null)	lipid metabolism	conserved hypothetical protein
MMAR_2344	(null)	(null)	lipid metabolism	polyketide synthase Pks5_1
MMAR_2533	(null)	(null)	conserved hypotheticals	conserved hypothetical secreted protein
MMAR_2535	(null)	(null)	cell wall and cell processes	conserved hypothetical secreted protein
MMAR_2537	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_2538	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_2539	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_2541	(null)	(null)	unknown	conserved hypothetical membrane protein
MMAR_2542	(null)	(null)	unknown	hypothetical protein
MMAR_2543	(null)	(null)	conserved hypotheticals	conserved hypothetical proline-rich protein
MMAR_2545	(null)	(null)	unknown	hypothetical protein
MMAR_2546	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_2607	(null)	(null)	conserved hypotheticals	conserved hypothetical secreted protein
MMAR_2608	(null)	(null)	intermediary metabolism and respiration	copper methylamine oxidase precursor MaoX
MMAR_2609	(null)	(null)	cell wall and cell processes	conserved hypothetical membrane protein
MMAR_2690	(null)	(null)	unknown	hypothetical protein
MMAR_2737	(null)	(null)	cell wall and cell processes	alanine and proline rich secreted protein Apa
MMAR_2810	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_2811	(null)	(null)	cell wall and cell processes	conserved hypothetical membrane protein
MMAR_2831	(null)	(null)	regulatory proteins	transcriptional regulator
MMAR_2840	(null)	(null)	intermediary metabolism and respiration	arylsulfatase AtsD_2
MMAR_2903	(null)	(null)	intermediary metabolism and respiration	conserved hypothetical NADP-dependent oxidoreductase

Mm locus	Mu locus	Agy99 Pseudogene	Functional Group	Product
MMAR_2905	(null)	(null)	unknown	hypothetical protein
MMAR_2906	(null)	(null)	cell wall and cell processes	conserved hypothetical membrane protein
MMAR_2958	(null)	(null)	conserved hypotheticals	macrophage infection protein_MimD
MMAR_2962	(null)	(null)	regulatory proteins	transcriptional regulatory protein
MMAR_2964	(null)	(null)	cell wall and cell processes	conserved transmembrane transport protein
MMAR_2976	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_3073	(null)	(null)	cell wall and cell processes	conserved hypothetical membrane protein
MMAR_3127	(null)	(null)	regulatory proteins	conserved hypothetical regulatory protein
MMAR_3128	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_3130	(null)	(null)	intermediary metabolism and respiration	conserved hypothetical hydrolase
MMAR_3132	(null)	(null)	lipid metabolism	acyl-CoA dehydrogenase
MMAR_3133	(null)	(null)	lipid metabolism	medium chain fatty-acid-CoA ligase FadD14_1
MMAR_3134	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_3135	(null)	(null)	intermediary metabolism and respiration	cytochrome P450 136B2 Cyp136B2
MMAR_3136	(null)	(null)	intermediary metabolism and respiration	monooxygenase
MMAR_3137	(null)	(null)	intermediary metabolism and respiration	esterase/lipase
MMAR_3138	(null)	(null)	intermediary metabolism and respiration	monooxygenase
MMAR_3139	(null)	(null)	intermediary metabolism and respiration	monooxygenase
MMAR_3140	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_3141	(null)	(null)	cell wall and cell processes	short-chain membrane-associated dehydrogenase
MMAR_3142	(null)	(null)	regulatory proteins	transcriptional regulatory protein (possibly TetR-family)
MMAR_3143	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_3144	(null)	(null)	regulatory proteins	transcriptional regulatory protein (possibly Acr-FAMILY)
MMAR_3145	(null)	(null)	cell wall and cell processes	conserved hypothetical membrane protein
MMAR_3146	(null)	(null)	unknown	hypothetical protein
MMAR_3147	(null)	(null)	unknown	conserved hypothetical membrane protein
MMAR_3150	(null)	(null)	intermediary metabolism and respiration	zinc-containing alcohol dehydrogenase NAD-dependent
MMAR_3151	(null)	(null)	lipid metabolism	medium chain fatty-acid-CoA ligase
MMAR_3152	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_3153	(null)	(null)	intermediary metabolism and respiration	ferredoxin reductase
MMAR_3154	(null)	(null)	intermediary metabolism and respiration	cytochrome P450 153A16 Cyp153A16
MMAR_3155	(null)	(null)	intermediary metabolism and respiration	ferredoxin
MMAR_3156	(null)	(null)	regulatory proteins	transcriptional regulatory protein (probably AraC/XylS-family)
MMAR_3158	(null)	(null)	regulatory proteins	transcriptional regulatory protein (probably TetR-family)
MMAR_3159	(null)	(null)	intermediary metabolism and respiration	conserved hypothetical hydrolase
MMAR_3160	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_3161	(null)	(null)	regulatory proteins	transcriptional regulatory protein
MMAR_3162	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_3163	(null)	(null)	intermediary metabolism and respiration	Zn-dependent alcohol dehydrogenase
MMAR_3164	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_3165	(null)	(null)	unknown	hypothetical protein
MMAR_3267	(null)	(null)	cell wall and cell processes	conserved transmembrane protein
MMAR_3319	(null)	(null)	intermediary metabolism and respiration	dehydrogenase
MMAR_3324	(null)	(null)	cell wall and cell processes	nucleoside-diphosphate-sugar epimerase
MMAR_3382	(null)	(null)	cell wall and cell processes	conserved hypothetical membrane protein
MMAR_3383	(null)	(null)	intermediary metabolism and respiration	FabG-like dehydrogenase
MMAR_3384	(null)	(null)	intermediary metabolism and respiration	conserved hypothetical hydroxylase
MMAR_3386	(null)	(null)		Phagosome maturation inhibitor_Pmia
MMAR_3387	(null)	(null)	conserved hypotheticals	conserved hypothetical membrane protein
MMAR_3398	(null)	(null)	regulatory proteins	transmembrane serine/threonine-protein kinase D
MMAR_3399	(null)	(null)	cell wall and cell processes	conserved hypothetical protein
MMAR_3405	(null)	(null)	regulatory proteins	conserved hypothetical regulatory protein
MMAR_3422	(null)	(null)	cell wall and cell processes	conserved hypothetical membrane protein
MMAR_3491	(null)	(null)	intermediary metabolism and respiration	pyruvate dehydrogenase (E2 component)
MMAR_3495	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_3503	(null)	(null)	cell wall and cell processes	metal cation transporter p-type ATPase

Mm locus	Mu locus	Agy99 Pseudogene	Functional Group	Product
MMAR_3569	(null)	(null)	unknown	hypothetical protein
MMAR_3571	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_3572	(null)	(null)	cell wall and cell processes	conserved hypothetical membrane protein
MMAR_3575	(null)	(null)		conserved hypothetical protein
MMAR_3577	(null)	(null)	unknown	hypothetical protein
MMAR_3586	(null)	(null)	unknown	hypothetical protein
MMAR_3587	(null)	(null)	unknown	hypothetical protein
MMAR_3588	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_3591	(null)	(null)	unknown	hypothetical protein
MMAR_3592	(null)	(null)	unknown	hypothetical protein
MMAR_3593	(null)	(null)	unknown	conserved hypothetical secreted protein
MMAR_3594	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_3595	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_3596	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_3601	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_3602	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_3606	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_3658	(null)	(null)	cell wall and cell processes	conserved hypothetical transmembrane protein
MMAR_3778	(null)	(null)	intermediary metabolism and respiration	flavin-dependent oxidoreductase
MMAR_3779	(null)	(null)	intermediary metabolism and respiration	non-ribosomal peptide synthetase
MMAR_3780	(null)	(null)	intermediary metabolism and respiration	monooxygenase
MMAR_3787	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_3790	(null)	(null)	intermediary metabolism and respiration	isochorismatase family protein
MMAR_3794	(null)	(null)	regulatory proteins	transcriptional regulatory protein
MMAR_3796	(null)	(null)	lipid metabolism	type I modular polyketide synthase
MMAR_3797	(null)	(null)	lipid metabolism	type I modular polyketide synthase
MMAR_3798	(null)	(null)	lipid metabolism	type I modular polyketide synthase
MMAR_3799	(null)	(null)	lipid metabolism	type I modular polyketide synthase
MMAR_3800	(null)	(null)	lipid metabolism	beta-ketoacyl synthase-like protein
MMAR_3873	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_3874	(null)	(null)	conserved hypotheticals	conserved hypothetical secreted protein
MMAR_3876	(null)	(null)	unknown	hypothetical protein
MMAR_3877	(null)	(null)	unknown	hypothetical protein
MMAR_3878	(null)	(null)	cell wall and cell processes	conserved hypothetical membrane protein
MMAR_3879	(null)	(null)	conserved hypotheticals	conserved hypothetical bacteriophage protein
MMAR_3880	(null)	(null)	unknown	hypothetical protein
MMAR_3881	(null)	(null)	unknown	hypothetical protein
MMAR_3887	(null)	(null)	unknown	hypothetical protein
MMAR_3889	(null)	(null)	unknown	hypothetical protein
MMAR_3890	(null)	(null)	unknown	hypothetical protein
MMAR_3893	(null)	(null)	unknown	hypothetical protein
MMAR_3894	(null)	(null)	unknown	hypothetical protein
MMAR_3903	(null)	(null)	unknown	hypothetical protein
MMAR_3904	(null)	(null)	unknown	hypothetical protein
MMAR_3905	(null)	(null)	unknown	hypothetical protein
MMAR_3909	(null)	(null)	unknown	hypothetical protein
MMAR_3910	(null)	(null)	unknown	hypothetical protein
MMAR_3911	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_3912	(null)	(null)	regulatory proteins	transcriptional regulatory protein
MMAR_3913	(null)	(null)	unknown	hypothetical protein
MMAR_3914	(null)	(null)	unknown	hypothetical protein
MMAR_3915	(null)	(null)	unknown	hypothetical protein
MMAR_3917	(null)	(null)	unknown	hypothetical protein
MMAR_3924	(null)	(null)	unknown	hypothetical protein
MMAR_3925	(null)	(null)	unknown	hypothetical protein
MMAR_3926	(null)	(null)	information pathways	DNA polymerase III (beta chain) DnaN_1

Mm locus	Mu locus	Agy99 Pseudogene	Functional Group	Product
MMAR_3927	(null)	(null)	information pathways	RecT-family phage protein
MMAR_3929	(null)	(null)	unknown	hypothetical protein
MMAR_3930	(null)	(null)	regulatory proteins	conserved hypothetical regulatory protein
MMAR_3931	(null)	(null)	unknown	hypothetical protein
MMAR_3932	(null)	(null)	cell wall and cell processes	hypothetical secreted protein
MMAR_3933	(null)	(null)	unknown	hypothetical protein
MMAR_3934	(null)	(null)	unknown	hypothetical protein
MMAR_3935	(null)	(null)	unknown	hypothetical protein
MMAR_3936	(null)	(null)	unknown	hypothetical protein
MMAR_3937	(null)	(null)	unknown	hypothetical secreted protein
MMAR_3939	(null)	(null)	unknown	hypothetical protein
MMAR_3940	(null)	(null)	unknown	hypothetical protein
MMAR_3942	(null)	(null)	unknown	hypothetical protein
MMAR_3944	(null)	(null)	unknown	hypothetical protein
MMAR_3947	(null)	(null)	regulatory proteins	transcriptional regulatory protein
MMAR_3948	(null)	(null)	intermediary metabolism and respiration	conserved hypothetical hydrolase
MMAR_3949	(null)	(null)	cell wall and cell processes	conserved hypothetical phage membrane protein
MMAR_3951	(null)	(null)	unknown	hypothetical protein
MMAR_3972	(null)	(null)	intermediary metabolism and respiration	non-ribosomal peptide synthetase
MMAR_4060	(null)	(null)	cell wall and cell processes	conserved hypothetical secreted protein
MMAR_4061	(null)	(null)	cell wall and cell processes	conserved hypothetical transmembrane protein
MMAR_4062	(null)	(null)	cell wall and cell processes	hypothetical membrane protein
MMAR_4079	(null)	(null)	intermediary metabolism and respiration	adenylate cyclase
MMAR_4107	(null)	conserved hypotheticals		conserved hypothetical protein
MMAR_4208	(null)	(null)	cell wall and cell processes	proline and glycine rich transmembrane protein
MMAR_4211	(null)	(null)	cell wall and cell processes	membrane protein
MMAR_4258	(null)	(null)	intermediary metabolism and respiration	monophosphatase CysQ-like
MMAR_4259	(null)	(null)	intermediary metabolism and respiration	bifunctional enzyme CysN/CysC-like: sulfate adenylyltransferase (subunit 1
MMAR_4260	(null)	(null)	intermediary metabolism and respiration	glycolipid sulfotransferase
MMAR_4265	(null)	(null)	cell wall and cell processes	integral membrane nitrite extrusion protein NarK3_4
MMAR_4415	(null)	conserved hypotheticals		conserved hypothetical protein
MMAR_4417	(null)	(null)	cell wall and cell processes	conserved hypothetical membrane protein
MMAR_4429	(null)	(null)	cell wall and cell processes	conserved transmembrane transport protein Mmpl
MMAR_4432	(null)	conserved hypotheticals		conserved hypothetical protein
MMAR_4439	(null)	(null)	unknown	hypothetical protein
MMAR_4440	(null)	conserved hypotheticals		conserved hypothetical protein
MMAR_4441	(null)	(null)	unknown	hypothetical protein
MMAR_4444	(null)	(null)	unknown	hypothetical protein
MMAR_4445	(null)	(null)	unknown	hypothetical protein
MMAR_4446	(null)	(null)	unknown	hypothetical protein
MMAR_4447	(null)	(null)	unknown	hypothetical protein
MMAR_4449	(null)	(null)	unknown	hypothetical protein
MMAR_4450	(null)	(null)	unknown	hypothetical protein
MMAR_4482	(null)	(null)	information pathways	methyltransferase
MMAR_4483	(null)	(null)	intermediary metabolism and respiration	cytochrome P450 135B3 Cyp135B3
MMAR_4588	(null)	(null)	unknown	hypothetical protein
MMAR_4589	(null)	conserved hypotheticals		conserved hypothetical protein
MMAR_4590	(null)	conserved hypotheticals		conserved hypothetical protein
MMAR_4591	(null)	conserved hypotheticals		conserved hypothetical protein
MMAR_4596	(null)	(null)	unknown	hypothetical protein
MMAR_4597	(null)	(null)	unknown	hypothetical protein
MMAR_4697	(null)	(null)	cell wall and cell processes	conserved hypothetical membrane protein
MMAR_4706	(null)	(null)		MCE-family lipoprotein
MMAR_4707	(null)	(null)		MCE-family protein
MMAR_4710	(null)	(null)		MCE-family protein
MMAR_4721	(null)	(null)	intermediary metabolism and respiration	nitroreductase

Mm locus	Mu locus	Agy99 Pseudogene	Functional Group	Product
MMAR_4722	(null)	(null)		membrane-associated phospholipase C 2 PlcB_6
MMAR_4726	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_4744	(null)	(null)	intermediary metabolism and respiration	dioxygenase
MMAR_4749	(null)	(null)	lipid metabolism	acyl-CoA dehydrogenase
MMAR_4828	(null)	(null)	unknown	hypothetical protein
MMAR_4829	(null)	(null)	unknown	hypothetical protein
MMAR_4830	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_4831	(null)	(null)	unknown	hypothetical protein
MMAR_4832	(null)	(null)	regulatory proteins	transcriptional regulatory protein (probably TetR-family)
MMAR_4833	(null)	(null)	intermediary metabolism and respiration	cytochrome P450 123B1 Cyp123B1
MMAR_4834	(null)	(null)	regulatory proteins	transcriptional regulatory protein (TetR family)
MMAR_4835	(null)	(null)	unknown	hypothetical protein
MMAR_4836	(null)	(null)	cell wall and cell processes	conserved transmembrane transport protein MmpL family
MMAR_4837	(null)	(null)	intermediary metabolism and respiration	conserved hypothetical hydrolase
MMAR_4838	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_4839	(null)	(null)	regulatory proteins	transcriptional regulatory protein (TetR-family)
MMAR_5189	(null)	(null)	intermediary metabolism and respiration	thiamine-monophosphate kinase
MMAR_5190	(null)	(null)	information pathways	selenocysteine synthase SelA
MMAR_5191	(null)	(null)	information pathways	selenocysteine-specific translation elongation factor SelB
MMAR_5192	(null)	(null)	cell wall and cell processes	integral membrane transport protein
MMAR_5194	(null)	(null)	intermediary metabolism and respiration	formate dehydrogenase alpha subunit selenocysteine-containing
MMAR_5261	(null)	(null)	cell wall and cell processes	conserved hypothetical secreted protein
MMAR_5262	(null)	(null)	cell wall and cell processes	hypothetical secreted protein
MMAR_5263	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_5346	(null)	(null)	intermediary metabolism and respiration	dTDP-glucose-4 6-dehydratase RmlB_1
MMAR_5415	(null)	(null)	cell wall and cell processes	conserved hypothetical transmembrane protein
MMAR_5416	(null)	(null)	cell wall and cell processes	conserved hypothetical transmembrane protein
MMAR_5418	(null)	(null)	cell wall and cell processes	conserved hypothetical membrane protein
MMAR_5420	(null)	(null)	cell wall and cell processes	conserved hypothetical transmembrane protein
MMAR_5421	(null)	(null)	cell wall and cell processes	conserved hypothetical transmembrane protein
MMAR_5422	(null)	(null)	cell wall and cell processes	conserved hypothetical transmembrane protein
MMAR_5423	(null)	(null)	cell wall and cell processes	conserved hypothetical transmembrane protein
MMAR_5424	(null)	(null)	cell wall and cell processes	conserved hypothetical transmembrane protein
MMAR_5425	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_5426	(null)	(null)	unknown	hypothetical membrane protein
MMAR_5427	(null)	(null)	cell wall and cell processes	conserved hypothetical transmembrane protein
MMAR_5428	(null)	(null)	cell wall and cell processes	conserved hypothetical transmembrane protein
MMAR_5429	(null)	(null)	cell wall and cell processes	conserved hypothetical transmembrane protein
MMAR_5430	(null)	(null)	cell wall and cell processes	conserved hypothetical transmembrane protein
MMAR_5431	(null)	(null)	cell wall and cell processes	conserved hypothetical transmembrane protein
MMAR_5435	(null)	(null)	conserved hypotheticals	conserved hypothetical alanine and glycine rich protein
MMAR_5436	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_5455	(null)	(null)	conserved hypotheticals	conserved hypothetical alanine and proline rich protein
MMAR_5462	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_5463	(null)	(null)	conserved hypotheticals	conserved hypothetical protein
MMAR_5580	(null)	(null)	unknown	hypothetical protein