DIFFERENTIAL GENE EXPRESSION OF CD43 WILDTYPE AND KNOCKOUT MACROPHAGES IN RESPONSE TO MYCOBACTERIAL STIMULATION

by

Audra Helena Vair

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Abstract

Previous studies in our lab show CD43 deficient macrophages have reduced binding and uptake of *M.tb* bacilli but allow increased intracellular bacterial growth within the host macrophage due to decreased TNF-α production. It was also found that there are two heat-shock proteins found on the cell surface of *M.tb* that are capable of binding CD43: Cpn 60.2 and dnaK. The purpose of this study was to determine the intracellular signalling pathways activated by CD43 upon *M.tb* stimulation and to determine if Cpn 60.2 or dnaK could reproduce these responses. An RNA-microarray was performed using mRNA isolated from wildtype (CD43 +/+) and gene-deleted (CD43-/-) bone-marrow derived murine macrophages that had been co-incubated with one of *M.tb*, Cpn 60.2 or dnaK. There was a large quantity of differentially regulated genes for each treatment, ranging from 330 to 990. Only 113 of these genes were statistically significant and shared between treatment types, 21 genes down regulated in the knockout compared to the wild type and 92 genes were up regulated in CD43-/- compared to CD43+/+. Pathway analysis of differential gene expression was performed using lists of statistically significant, differentially-regulated genes, which indicated there were multiple pathways and cellular processes in which several genes were found to be affected by the absence of CD43. The pathways included p38/JNK/Erk MAP kinase signaling functioning, TNF-α post-transcriptional control, cytoskeletal remodeling, phagocytosis and apoptosis. Related genes from both the microarray data and interacting genes from pathway-data associated with TNF-α and apoptosis were selected to both validate the microarray and possibly determine if changes in TNF-related regulation could be controlled by CD43. The microarray indicated several genes involved in TNF-α regulation and apoptosis were differentially expressed in CD43 +/+ and CD43 -/- macrophages. Quantitative Reverse-Transcriptase PCR was used on a selected number of these genes. Differential gene regulation was observed in the Q RT-PCR results; however results conflicted with the microarray. In conclusion, CD43 influences the course of *M.tb* infection within the macrophage, possibly through the regulation of TNF-α and apoptosis. There are implications for CD43-related control of eicosanoid production and cytoskeletal regulation but these observations require further investigation.

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List of abbreviations

AIDS	acquired immune deficiency syndrome
BCG	Bacille Calmette-Guerin
BMDMΦ	bone-marrow derived macrophages
CFU	colony forming units
EMB	ethambutol
HIV	human immunodeficiency virus
IFN-γ	Interferon gamma
INH	isoniazid
KO	knockout
LAM	lipoarabinomannan
LPS	lipopolysaccharide
MΦ	macrophage
MHC	major histocompatability complex
MOI	multiplicity of infection
MTB	*Mycobacterium tuberculosis*
NO	nitric oxide
PIM	phosphatidylinositol
PPD	purified protein derivative
PZA	pyrazinamide
RA	rheumatoid arthritis
RIF	rifampin
RNI	reactive nitrogen intermediates
ROI	reactive oxygen intermediates
STR	streptomycin

Th_1	T-helper cell type 1
Th_2	T-helper cell type 2
TB	Tuberculosis
TNF-α	tumour necrosis factor
WT	wild type
WHO	World Health Organization

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For my Parents

1 Introduction

1.1 *Mycobacterium tuberculosis*

Mycobacterium tuberculosis (*M.tb*) is a member of the genus Mycobacterium and the order Actinomycetales. The bacillus is slim and rod-shaped, 0.2-0.4 x2 to 10 µm in size [1]. The *M.tb* genome consists of a single, circular chromosome of approximately 4 million base pairs, leading to almost 4000 annotated genes [2]. *Mycobacterium bovis* , the 'TB of cattle' has 99.9 % similarity to *M.tb* [2], however another notable mycobacterial pathogen, *M.leprae,* has approximately 1200 fewer annotated genes but is also an obligate parasite. Unable to grow outside of the host environment, it contains what is considered to be the 'essential' mycobacterial genome [3]. First isolated and cultured by Robert Koch in 1882, *Mycobacterium tuberculosis* was one of the first bacteria used to establish Koch's postulates of disease and infection. These statements were four criteria Koch laid out to determine the connection between an infection and the infectious organism [4]:

1. The microorganism must be found in abundance in all organisms suffering from the disease, but should not be found in healthy animals.
2. The microorganism must be isolated from a diseased organism and grown in pure culture.
3. The cultured microorganism should cause disease when introduced into a healthy organism.
4. The microorganism must be re-isolated from the inoculated, diseased experimental host and identified as being identical to the original specific causative agent.

Mycobacterium tuberculosis is a slow growing, non-motile intracellular pathogen that is not known to form spores, is highly resistant to drying and chemical disinfection and has yet to be isolated from an environmental source [1].

1.1.1 *Mycobacterium tuberculosis* biology

Mycobacterium tuberculosis (M.tb) has a complex, lipid-rich cell wall containing mycolic acid, which makes the organism difficult to visualize with common stains. *M.tb* bacillus can be visualized by specialized methods of staining, such as Ziehl-Neelson, carbol fuchsin and Auromin O. Once stained, they become acid-fast. This means *M.tb* bacillus are highly resistant to decolourization with up to 3% hydrochloric acid, ethanol or both [5]. It is the thick, waxy cell wall of *M.tb* that has distinguished it from other virulent organisms. It's unique and highly complex nature is such an integral part of the *M.tb* bacterium, it indicates that it is a determinant of virulence. The cell wall core consists of a peptidoglycan layer covalently linked with arabinogalactan, to which mycolic acids are attached. The extracellular surface layer is composed of free lipids and fatty acid chains containing various cell wall proteins. Such glycolipids are phosphatylinositols (PIMs), the phthiocerol-containing lipids (PDIMS, PAT and DAT), lipomannan and lipoarabinomannan (LAM) [6]. Some of these lipids are thought to be highly correlated with virulence. For example, trehalose 6, 6'-dimycolate (TDM), also known as cord factor, is a mycolic acid that contains glycolipid and is responsible for the characteristic colony morphology of *M.tb* growth on solid media [6]. The outermost layer of the cell wall, commonly known as the capsule, is a loose polysaccharide layer containing both proteins and lipids. Some of these capsular moieties have been shown to be involved in host interactions [7]. The inability most drugs to pass through the cell wall are considered to be one of the main challenges in drug discovery for novel anti- *M.tb* treatments.

1.1.2 Mycobacterium tuberculosis infection

M.tb is spread by aerosol from patients with active pulmonary disease. The dissemination of TB is facilitated by characteristic tissue-destructive immunopathology, which results in the development of necrotic, liquid-filled cavities containing large numbers of bacilli that can erode into bronchi and the airways. Inhalation of just a few bacilli can cause infection, but most infections are either eradicated

completely or remain latent [8]. The first sentinel of the immune system to encounter *M.tb* bacillus is the alveolar macrophage, whereby upon phagocytosis, the bacillus arrests phagosome-lysosome maturation and persists and replicates in the harsh vacuole environment [9, 10]. This cell serves as a double-edged sword in terms of a tubercular infection. An activated macrophage has sufficient anti-microbial function to destroy *M.tb* bacillus, but if the bacteria is not contained and successfully replicates, it can serve as a vehicle for further dissemination and replication within the lung, liver and spleen [10]. However as previously mentioned, the macrophage does contain sufficient anti-microbial properties to contain *M.tb* bacillus when activated. Appropriate conditions for activation and bactericidal activity of the alveolar macrophages are not precisely known, although pro-inflammatory cytokines such as TNF-α and IFN-γ are very important as well as the active metabolite of vitamin D, 1,25-dihydroxyvitamin D [11]. The mechanisms of *M.tb* killing include reactive oxygen intermediate (ROI) and reactive nitrogen intermediate (RNI) production, digestive enzymes of the lysosomal compartment as well as the acidic environment of the lysosome, both of which can be induced by TNF-α production. It is known that bacilli that have been ingested by activated macrophages are incapable of resisting phagosome-lysosome fusion, and succumb to the digestive enzymes and acidic environment of the lysosome [11].

In addition to retarding phagosomal maturation [12], *M.tb* has developed many other mechanisms for defense against host immunity. It is also capable of producing catalase and superoxide dismutase; both of which can neutralize reactive oxygen species which are produced by macrophages and capable of destroying mycobacteria [13]. Pathogenic strains of *M.tb* have been known to deregulate apoptotic activation, leading to cellular necrosis and improved bacterial dissemination.

Apoptosis is also a putative effecter mechanism of the host macrophage to limit replication of the intracellular pathogen [14, 15]. Apoptosis of infected phagocytes may prevent the spread of infection

and reduce viability of intracellular mycobacteria, whereas necrosis, the uncontrolled death and lysis of an infected cell, does not [16, 17]. TNF-α is required for the induction of apoptosis during *M.tb* infection [14] and it has been observed that pathogenic strains of *M.tb* induce less host cell apoptosis than related attenuated strains [14] . This decrease in apoptosis was related to release of soluble TNF-α receptors, a process that is regulated by IL-10 production [18].

When infection has been established in the lung, a tubercle (or granuloma) is formed. This consists of infected alveolar macrophages in the central core, surrounded by mononuclear cells brought in by the pro-inflammatory response initiated by the bacillus including additional 'regular' antimicrobial phagocytes, such as macrophages and neutrophils. This collection of professional phagocytes is then contained by a peripheral 'wall' of lymphocytes and epitheliod cells. It is the containment of the bacteria via these immune cells that build the granuloma. The infected macrophages can fuse together, generating giant cells or they may develop into lipid-rich 'foamy-like' macrophages. This bacterial containment controls dissemination and the infection no longer actively spreads to uninfected bystanders. It is thought that during this stage, the bacteria, though still viable, enter a 'dormant' stage during which time their metabolism alters and slows considerably. Due to the difficult nature of accessing and modeling this environment for research, not a lot is known for certain about this stage of the infection. The replicative state of the bacteria is still under investigation, but it is generally thought to be significantly slowed or perhaps non-existent [19-21].

The granuloma can remain stable and potentially contain the *M.tb* infection for the entire life of the patient although the eventual failure of the containment is usually anticipated by the medical community. The reason for this lapse in containment is not entirely known, but generally the risk of reactivation occurs with increased age, immunosuppression or co-infection with another immune-related infection (such as HIV/AIDS) [8]. Recent cases of TB reactivation following anti-TNF-α

treatment of rheumatoid arthritis indicate a pivotal role for TNF-α in the maintenance of the granuloma [22].

TNF-α blocking agents have been approved for a number of inflammatory afflictions such as chronic arthritis [23]. If an arthritis sufferer has a latent tuberculosis infection and takes such an immune-suppressant, they will experience re-activation of the latent infection as well as a hyper-inflammatory response if taken off the TNF-α blocker. This demonstrates the highly important, yet undeciphered role that intracellular signaling and cytokines have in the control of each stage of infection [22]. When the breakdown of the tubercle occurs, the necrotic, bacteria-filled central core becomes caseous, meaning the tissue within dies and appears soft and white. This necrotic tissue eventually liquefies, and breaks through the bronchial wall and allowing viable bacteria to flow into the host airways and systemic circulation. From the lungs of the actively infected, the densely populated bacterial liquid waits to be coughed into the atmosphere, and perhaps the lungs of another victim [24]. As previously mentioned, the majority of the infected population experiences latent infection as a life-long state, changing only upon the disruption of immune functions [25]. Apart from individuals are those on immunosuppressive drugs, those who suffer from alcoholism, diabetes, nutritional deficiencies, stress and, co-infected with HIV also have higher risk of re-activation of latent disease. AIDS patients with HIV have an increasing risk (10% chance per year) of developing active TB, whereas immunocompetent patients have a 10% lifetime chance. Out of the global 9.2 million new cases and 1.7 million deaths worldwide, more than 13% of cases and more than 11% of those deaths were in HIV-positive individuals [8].

1.1.3 Prevention

Indication of past or present TB infection is typically identified by an initial tuberculin skin test (TST). One's reactivity to purified protein derivative (PPD), is a precipitate of non-species specific molecules obtained from filtrates of sterilized, concentrated cultures. The reaction that ensues reflects

sensitization of a patient to highly antigenic proteins originating from *M.tb* [22, 26]. Sensitization in this case refers to the delayed-type hypersensitivity response of T-cells that recognize and bind the tuberculin antigens, prompting them to release cytokines and chemokines that attract more lymphocytes and macrophages to the site of PPD injection [26]. It is the T_H1 helper subset ($CD4^+$) cells that are responsible for this response.

The cell-mediated response to the injection is measured via the area of induration, palpable raised hardened area around the injection site; in most countries 5-10 mm counts as either a positive or 'intermediate' result, requiring further investigation into patient history and more tests [22]. An unfortunate aspect to this test is the reliance on a fully functioning immune system to demonstrate a positive result. Individuals on immunosuppressive therapies and HIV-positive patients do not always demonstrate a strong reaction, due to CD4+ T-cell depletion, and they are the greatest at-risk groups for active infection [22]. False positives are also common occurrences in certain areas of the globe. Mycobacteria are more common in equatorial regions and many non-tuberculous mycobacterial peptides cross-react with PPD. Individuals vaccinated with Bacille Calmette-Guerin (BCG) also frequently present with a positive result. The ambiguity of the TST is reflected in terms of how to interpret the induration as a reflection of disease state, with national standards for TB control and the experience of the health-care worker providing the service all impacting the interpretation of the reaction. Improvements to this test are currently under examination, utilizing *M.tb*-specific antigens such as ESAT-6 and CFP10 to minimize the impact of cross-reactivity with BCG [27].

Considering the lengthy history between mankind and *Mycobacterium tuberculosis* [28], there is very little that has been found to be effective against infection of this highly evolved pathogen. Overall patient health proves to be the most significant factor in the difference between control of the infection and the establishment of active, replicating bacilli. Where populations typically suffer from poor

nutrition, unclean drinking water and crowded conditions, TB is more common [29]. There is a live, attenuated vaccine currently available, Bacille Calmette-Guerin (BCG), which was developed from a virulent strain of *Mycobacterium bovis*. Over the span of 13 years, it was passaged 230 times over glycerinated bile potato medium [30], resulting in a loss of virulence in animal models and it has been used since the mid-1920's to prevent TB infection. However, its discovery led to the dissemination of the original BCG strain to research centres worldwide. The variety of methodologies for bacterial growth and strain maintenance has resulted in great variation in BCG strains with significant differences in immunogenicity and vaccine efficacy [31-33]. These efficacies range from 0-94% depending on the recipient human population and the BCG substrain used [30, 34]. Despite the evidence for variation of efficacy, there are still a number of sub-strains of BCG used for vaccine purposes [30] with the type one is likely to receive simply depending on geographical location.

Two independent studies, one from the Tuberculosis Research Centre of India [35], and another conducted in Malawi by the Karonga Prevention Trial Group [36], both gave results in which BCG vaccine showed 0% efficacy. The study in Malawi tested the efficacy of this vaccine using single and repeated BCG doses, with an additional group consisting of combined BCG and heat-killed *Mycobacterium leprae.* Individuals lacking a BCG vaccination scar were randomly assigned a prophylaxis and observed for infection over the course of 9 years. Although some protection was afforded by BCG vaccination for *Mycobacterium leprae* infection, there was no evidence that any of the trial vaccines contributed to protection against pulmonary tuberculosis.

Studies in the Chingleput district of south India have also demonstrated 0% efficacy [37]. This study was a double-blind randomized controlled trial initiated in 1968 and carried on for 15 years, using low , high and placebo doses of BCG. Over the 15-year period, the incidence of culture-positive tuberculosis was virtually the same in all three groups; 55, 56 and 54 per 100 000, respectively. There was no trend

worth remarking upon nor statistical significance for the case of protection with BCG vaccination in this study whatsoever.

The reasons that BCG vaccination tends to fail in equatorial climes are based predominantly on the environmental consequences that occur from inhabiting these regions of the globe. Individuals who live within 30 ˚ of the equator are most likely to lack protection from BCG. Skin tests in these countries indicate that almost everyone has been sero-converted to at least one environmental mycobacterial antigen [38]. However in northern latitudes, where environmental mycobacteria are less common, a false positive is correspondingly unusual. The cross-reactivity of the immune response generated by exposure to environmental mycobacterial species, results in very little increased immunological response from BCG vaccination due to previous priming of the T_H1 response by environmental mycobacterial infection [39]. This has led to a theory that BCG is destroyed by the host immune response that has already been primed by the non-pathogenic mycobacterial species before it can establish a greater *M.tb* – specific response. Typically, a T_H1 response is initially desired in a response to *M.tb*, as this induces the production of IFN-γ and TNF-α [40], powerful stimulatory cytokines that activate not only T-cells but surrounding macrophages, enabling them to release nitrous oxide (NO) and commence the anti-microbial response.

The improved understanding of the immune responses to TB has led to a push for better, more comprehensive vaccine strategies. Complimentary 'booster' vaccines to improve BCG efficiency are commonly regarded as the best method of improvement [40]. Primarily consisting of recombinant proteins, these shots would boost $CD4^+$ and cytotoxic $CD8^+$ T-cell response via exposure to additional mycobacterial antigen. Although these have been considered as 'likely unhelpful in countries where there is an already adequate T_H1-cell response following exposure to environmental mycobacteria'[40], some fusion proteins (Mtb72F for example) have been recognized in BCG-vaccinated infants and healthy

individuals from TB endemic regions [41]. This would indicate an ability to prime the immune system beyond that of environmental exposure. Improving cell-specific responses, such as boosting the BCG-induced $CD8^+$ response have also been considered. BCG with improved 'self-destruct' mechanisms would enable MHC class I presentation to occur more readily, thereby improving presentation to this cell type. DNA vaccines that encode specific mycobacterial antigens, such as HSP65, are capable of infecting host-cells and expressing antigen from within, like an intracellular pathogen. These types of vaccines induce both $CD4^+$ and $CD8^+$ T-cell response as well as down regulating T_H2-cell responses in animal models of TB [42, 43].

1.1.4 Treatment

The advent of chemotherapeutic agents against TB came upon the scene mid 20th-century with the use of streptomycin and soon after the capacity of *M.tb* to become drug-resistant became apparent [44]. Current treatment for TB infection includes isoniazid (INH), rifampicin (RMP), pyrazinamide (PZA), ethambutol (EMB), as well as fluoroquinolones (FQs). Short-course chemotherapy achieves good success when all four first-line drugs (INH, RMP, PZA, and EMB) are used concurrently throughout 6 months of treatment. Reduction of the number of drugs used together increases the relapse rate of the patient. It is therefore recommended that with smaller drug combinations, longer courses of drug regimen should be followed [45].

Isoniazid is currently the most commonly used anti-tuberculosis drug, whether on its own or in combinatory treatment [8]. It has been the basis for most effective treatments of TB disease. Typically, INH has a minimum inhibitory concentration of 0.02-0.2 μg/ml for *M.tb*, but is only active against growing bacilli and not active against non-replicating bacteria or in hypoxic conditions, such as may be found with dormant *M.tb* inside a granuloma. Administered as a prodrug, INH is activated by catalase-peroxidase enzyme (KatG) [46], generating a highly reactive species that is effective against multiple

drug-susceptible functions of *M.tb.* The primary target of INH appears to be the enoyl-acyl carrier protein reductase (InhA enzyme) which is involved in elongation of fatty acids in mycolic acid synthesis [47]. Resistance to INH occurs frequently, generally occurring due to the loss of the catalase and peroxidase enzyme encoded by KatG [48].

Rifampicin (RMP) is active against both growing and stationary phase bacilli with low metabolic activity; it has high sterilizing activity in vivo and can shorten TB treatments from over a year to 9 months [49]. RMP binds the β subunit of the RNA polymerase thereby interfering with RNA synthesis.

Pyrazinamide (PZA) can further shorten treatment from 9 months to 6 because of its ability to kill 'persister' bacteria in low pH environments that are not killed by other drugs [49]. It has high bactericidal activity *in vivo* but little if any activity in normal culture conditions near neutral pH. PZA activity is enhanced under low oxygen or anaerobic conditions and is therefore used to treat latent infection [49-51].

Ethambutol (EMB) is used to prevent drug resistance. It is a bacteriostatic agent against growing bacilli only and is ineffective against non-replicating organisms [44]. It's method of action is to interfere with the biosynthesis of arabinogalactan, which comprises part of the cell wall [52].

Aminoglycosides such as streptomycin, kanamycin, amikacin and capreomycin are antibiotics used to treat a number of bacteria, and are also active against *M.tb*. Bactericidal against replicating bacteria, these drugs are not active against non-growing (latent) or intracellular bacteria. These drugs are not typically used as they cannot be administered orally, and their bactericidal activity is comparable to INH [53]. They are only used when the primary agents (INH, RMP, PZA) are ineffective [54].

Ethionamide, prothionamide and thioamides are commonly used anti-mycobacterial drugs and are active against *M.tb, M. avium-intracellulare* and *M.leprae* [44]. They inhibit the same target as INH (the

InhA of the mycolic acid synthesis pathway) [47]. They are used as a second-line therapy for drug-resistant TB, and are administered with multiple agents due to the rapid development of resistance to them when used as a single therapy [54].

The success of a drug-treatment for TB is highly dependent on patient compliance to a regimen of administration of therapy. Unfortunately, this singularly important area is most commonly compromised due to length of treatment, multi-drug side effects and inadequate access to health care. The advent of both multi-drug resistant (MDR) and extremely drug resistant (XDR) –TB has further complicated the situation. MDR-TB describes a tuberculosis strain that is resistant to two or more front-line pharmaceuticals. In these cases, second-line antibiotics (aminoglycocides, thiamides and fluoroquinolones) are added to the drug treatment, increasing the complications and cost involved in patient treatment. XDR-TB strains are now emerging in places such as Asia and Africa [29], as strains that are both resistant to first and second line therapies [55]. Although not yet as common, these strains are even more difficult to treat and are highly challenging to control in even a well-equipped health care system [44].

1.2 Immune response to TB

Due to the complexity of TB infection and disease progression, the interplay of the immune system and bacteria is a delicate balance. Both protective immunity and pathogenesis related to this disease are mediated by the host immune system [56, 57]. The macrophage is both the primary defender against and replicating vector of *M.tb* [58] and the cell-mediated immune response provides support in long term control, but does not provide much in the way of immunological protection against re-infection [57].

1.2.1 Macrophages

The alveolar macrophages are the first line of host-cell defense to TB, being a permanent defense feature of the lung. Animal models have demonstrated, however, that these macrophages are also capable of further dissemination of the bacteria to deeper parts of the lung and other lymphoid tissues [58, 59].

Macrophages have been identified as modulators of the immune response to infections since the early 1960's [60, 61]. They are activated, not only by host signals (interferon γ)[62], but by bacterial moieties as well. For example, lipopolysaccharide, also known as LPS, is a highly stimulating factor found on the external coat of Gram-negative bacteria. The way in which macrophages respond to these types of signals differs depending on the signal nature and source [63]. LPS and IFN-γ induce a 'classical' (currently known as M1) macrophage activation characterized by antimicrobial activities such as production of IL-12, NO and oxygen-derived free radicals. Macrophages exposed to IL-4 and IL-13 produce an alternative cytokine response, increasing production of IL-10 and scavenger receptors. This is known as the 'M2' macrophage that is predominantly involved in immunomodulatory activities [64 6235, 65 7247]. The M2 state has been sub-categorized even further into M2a, M2b and M2c based on the origin of immuno-modulating materials [66]. M2 macrophages have a demonstrated role in parasitic infection [64, 67, 68].

Bacilli may gain entry into the macrophage by a number of methods; there is evidence of receptor-mediated phagocytosis with a number of macrophage ligands [69-71]. Such ligands include complement receptors, mannose receptor, scavenger receptors, CD14, and most recently, CD43 [70, 72]. The consequences of the interactions of each receptor with *M.tb* are not yet well characterized. It is known that some *M.tb* receptor interactions result in pro-inflammatory cytokine production and similar host-defense mechanisms [56]. This reaction is beneficial for both host and bacterium. The activation of

additional immunity increases the probability of infection control and clearance; however the increased inflammation to the site of infection also brings an influx of new cells for infection and dissemination of bacteria.

Macrophages are entirely capable of mediating the inhibition and killing of intracellular pathogens through mechanisms such as the production of reactive nitrogen and reactive oxygen intermediates (RNI, ROI), phagolysosome fusion leading to phagosomal acidification and antigen presentation and macrophage apoptosis, which would lead to bacterial killing and antigen presentation as well [73, 74]. It is the ability of the mycobacterium to evade these host-effecter functions that can dictate the next steps in pathology. More virulent strains of *M.tb* demonstrate higher functionality in terms of these traits: arrest of phagosome-lysosome fusion, down-regulation of apoptotic signals and induction of necrosis [75-77]. The preference of virulent *M.tb* for necrosis versus apoptosis is considered a means of intramacrophage survival [75]. The apoptotic cellular breakdown is considered to contain intracellular replication, and is facilitated during *M.tb* infection by increasing anti-apoptotic signaling within the host macrophage [78].

As previously mentioned, once ingested by the macrophage, the *M.tb* bacillus resides within the phagosome and arrests phagosomal maturation [79]. The bacillus then replicates intracellularly and is either controlled by macrophage and immune activation or continues to replicate and disseminate throughout the lung. The ability of the macrophage to prepare the mycobacterial antigen for presentation to immature T-cells is crucial for the subsequent control of the infection [79].

1.2.2 Cell-mediated immunity

Adaptive immunity develops 2-6 weeks post infection, following the flurry of cytokine and chemokine signals produced by infected macrophages and other affected antigen-presenting cells. By this time, mycobacterial antigens have been presented to T cells, either in the circulation or within the draining

lymph nodes [74, 80] and the T-cell subsets have initialized a response against the infection. As previously mentioned, the type of T-cell response is important not only for the control of an established TB infection, but more so in later stages of the disease. The subtypes most universally recognized for their importance are $CD4^+$ and $CD8^+$ T-cells [74, 81]. The $CD4^+$ T-cell has been recognized for its importance in the control of granuloma development at the site of infection. As previously mentioned, these dormant colonies of bacteria are enclosed by a wall of T and B lymphocytes, as well as monocytes, fibroblasts and multi-nucleated giant cells [82, 83]. The activation and maintenance of this containment is crucial to prevent re-activation of the disease; just as sufficient control of inflammation is important to prevent unnecessary immunopathology.

The observations made of latent TB infections have shown that the cellular responses and cytokines signals that are immunologically important for bacterial containment and elimination in later stages is typically not the same as for the immediate response to the microbe. Studies have shown that interferon-γ (IFN-γ), which promotes further differentiation into T_H1 cells, has a 'plateau' of immune efficiency, and when this is reached, boosters designed to improve this response are ineffectual in terms of protection against *M.tb* if used when IFN-γ levels have already peaked. In patients that have TB, it has been observed that there is a careful balance between the T_H1 and T_H2 responses, demonstrating the complex nature of this infection. In a latent infection, the T_H2 response is somewhat preferable, since heavy infiltration of lymphocytes into the lungs is a main cause of gross pathology [38, 40]. High-dose exposure of *M.tb* induces production of IL-4, a cytokine that inhibits antimicrobial T_H1 production, allowing the bacterium to take advantage of this response [40]. Patients with TB in developing countries have greater amounts of IL-4, compared to controls in northern climates, possibly as a result of the constant exposure to environmental mycobacteria [40].

The $CD4^+$ T-cell is regarded as one of the most important cell populations for the formation of the protective cell wall surrounding the granuloma [84]. Also known as $CD4^+/\alpha\beta/TCR^+$ T-lymphocyte cells, these cells secrete many different immunostimulatory cytokines, such as the aforementioned TNF-α and IFN-γ, as well as IL-12 which is critical to promote additional T_H1 differentiation [40]. Presentation of antigen to immature T-cells initiates differentiation into either T_H1 or T_H2 –type T-cells, defining the immunological response, thus heavily affecting disease outcome. At the initial point of infection, T_H1 is clearly preferable. It is the highly inflammatory, anti-microbial response that releases activation cytokines such as TNF-α, IFN-γ and IL-12. These cytokines activate macrophages to produce Reactive Oxygen Intermediates and Reactive Nitrogen Intermediates (ROI and RNI) which have been shown to eliminate mycobacteria [85, 86] as well as promote phagosomal maturation of the macrophage; a critical step in bacterial killing and antigen presentation. The initial T_H1 response is so important to the control of *M.tb* infection that genetic defects in the receptors of IL-12 or IFN-γ lead to increased susceptibilities and progressive mycobacterial disease [87, 88].

The cytokines of the T_H2 phenotype include IL-6, IL-10 and TGFβ. As previously mentioned, virulent *M. tuberculosis* can stimulate macrophages to secrete certain quantities of these molecules and could act to control (and limit) the T-cell responsiveness. [74, 89-91]. T_H2 cells are more important in parasite-response (such as helminthes) and eosinophil production and activation. They activate B cells to produce antibodies for protein-specific long term immunity and as previously stated, release cytokines that down regulate anti-microbial macrophage functions.

Since *M.tb* infection resides within the endosomal compartment, it was commonly thought that MHC class I presentation was unlikely to occur, and therefore the role of $CD8^+$ T-lymphocytes, also known as cytotoxic killer T-cells, has been historically underappreciated [74]. However, Flynn et al found that deficiencies in MHC I presentation render mice highly susceptible to TB infection, and therefore

could demonstrate a higher role of importance than initially anticipated [92]. $CD8^+$ also migrate to the sites of infection and are also IFN-γ producing cells which are capable of killing infected macrophages [81, 93]; so their role in the initial infection and containment of replicating bacteria might be more important than previously considered. More studies should be performed in this area in order to determine the potentially important roles of MHC class I presentation in *M.tb* infection.

$CD1^+$ 'nonclassically restricted' T-cells are important for receiving antigens presented via the CD1-receptor (instead of MHC-class receptors). CD1 has an altered binding site to MHC 1 and is capable of presenting polar hydrophobic antigens, such as lipids and glycolipids [94] These cells would play a significant role in the presentation of important mycobacterial lipids, such as mycolic acids and phosphatidyl-inosital mannosides (PIM) [95]. These T-cells are also capable of secreting IFN-γ for inflammatory activation and are capable of cytotoxic activities towards *M.tb* infected macrophages [95].

B cells, also known as 'B lymphocytes' play a large role in the humeral immune response. They function primarily to make antibodies against foreign bodies known as antigens. They are not only antibody-producers, but work as antigen-presenting cells and also maintain adaptive immunity via 'memory B cells'. These cells are capable of producing microbe-specific antibodies long after their production was triggered either by infection or vaccination [96] . B cells, particularly in intracellular infection, impact T-cell activation by acting as or upon antigen presenting cells [97]. Many studies involving a variety of intracellular infectious agents have demonstrated susceptibility of B-cell deficient mice, although studies with *M.tb* have been variable, resulting in delay of pathologic progression and diminished immunity, but no dramatic effects [97].

1.3 Bacterial chaperonins and host cell response

Heat shock proteins, or Chaperonins, are historically known as proteins that 'non-enzymatically aid in the folding or refolding of proteins' [63], found intracellularly near the Golgi apparatus. However,

evidence is mounting that these proteins contain alternative functions and are expressed throughout the cell [63, 98].

Current dogma states that these proteins are solely intracellular, and only upon cellular lysis would they be located in the extracellular space. Chaperonins are typically located in or near the cellular endoplasmic reticulum and assist polypeptide folding as soon as the amino acid chain comes out from the ribosomal 'exit' tunnel [63, 99, 100]. However, it has become increasingly apparent in current research, that these proteins are not only secreted, but are capable of having cellular activation capabilities [63]. This idea is not new; a circulating immunosuppressive chaperone known as Early Pregnancy Factor (EPF) was discovered in 1977 [101] and later identified as Chaperonin 10 (also known as Hsp10) by Morton and Cavanagh in 1994 [102]. Since this period, a number of mammalian stress proteins have been characterized as extracellular [63] having been identified in bodily fluids or in cell culture medium. The methods by which HSP secretion occurs are still unknown, but studies have shown that migration via non-ER-Golgi exocytosis is possible [103, 104].

One HSP that has received extensive review in light of these observations is Hsp60. It is highly conserved and found in most all organisms [105] and demonstrates a broad variety of responses in macrophages, depending on its source [63]. These variations of response can result in the stimulation of CD14/TLR2/TLR4-dependant signaling (Human and Chlamydia Hps60) to cytokine production that is TLR2/4/Myd-88-independent (*H. pylori*) to a complete failure to activate macrophages at all [106-108]. Hsp60 in humans is homologous to the GroEL gene in *E.coli* and Hsp65 in *M.tb* [109, 110].

Mycobacterium tuberculosis has 2 Hsp65 variants: Cpn60.1 and Cpn60.2. Cpn60.2 is also known as Hsp65. This protein has been documented to have pro-inflammatory properties for human monocytes [111] and it has been suggested that Cpn60.2 and 60.1 can both be used to induce pro-inflammatory protein production in human monocytes in microgram per milliliter quantities. Cpn60.2 has been

determined to be essential to *M.tb* and no knockout mutant has been created yet. Cpn60.1 however, can be deleted without consequences to bacterial survival and growth, but results in a failure of the mutant to induce granulomatous response [112]. The two proteins share 96% sequence similarity but have differential effects *in vivo* in during the course of infection.

Classical macrophage activation and anti-microbial properties are crucial for the controlling of *M.tb* infection. Tuberculosis, however, is a disease that has been characterized by the ability of virulent *M.tb* to inhibit the antibacterial Th1 response, and instead, patients with tuberculosis infection have been characterized with a Th2 phenotype [40] and specific Hsps like Cpn60.1 have been observed to inhibit the formation of IL-12 p40 subunit; a critical cytokine in the activation of Th1 response [113].

DnaK, from the Hsp 70 family, is important in chaperoning nascent polypeptide chains and is known to assist the folding of newly synthesized polypeptides together [100]. As a protein-folding chaperonin, dnaK is ATP-dependant but not physically tethered to ribosomes. It is monomeric, with an amino-terminal ATPase and carboxy-terminal polypeptide binding domain, capable of recognizing short, hydrophobic polypeptides in extended confirmations [63, 100]. In *Mycobacterium tuberculosis*, Hsp 70 has been documented as stimulatory to human Peripheral Blood Monocytes (PBMs) and produces classical activation; stimulates production of TNF-α, IL-12, NO, CCL3, CCL4 and CCL5 [63]. It is also found to bind to many macrophage receptors, including TLR4, TLR2, CD14 and CD40.

1.4 CD43

CD43, also known as leukosialin or sialophorin, is a glycoprotein expressed by most hematopoietic cells; with the exception of platelets, red blood cells and mature B cells [114, 115]. It is a transmembrane protein containing a large, highly glycosylated extracellular domain, and a membrane-spanning domain and highly conserved cytoplasmic domain [116]. The roles it plays in cellular function are as vast and variable as the types of cells on which it is located [115]. It has been implicated to influence both

adhesive and anti-adhesive cellular properties, cellular differentiation, cytoskeletal changes, apoptosis, intracellular signaling and chemokine signaling[115, 117, 118]. Although there is only a single gene present for CD43, post-translational modifications and protein cleavage provide ample opportunity for a heterogeneous population of structures. These changes result in differentially sialyated forms of the extracellular protein backbone [119].

1.4.1 Structure

Leukosialin (CD43) is made of 400 amino acids in humans and 395 in mice[114, 120]; an extracellular domain of 224 to 234 amino acids (from rat and human, respectively) with an average of one *O*-linked carbohydrate chain per three amino acids that extends approximately 45 nm in length from the cell surface [116]. The extracellular domain contains anywhere from 70 to 85 O-linked carbohydrate chains and over 100 negatively charged sialic acid residues [116]. CD43 exists in two isoforms, 115 kDa and 130 kDa. The 115 kDa isoform contains tetrasaccharide carbohydrate chains and is predominantly found on immature thymocytes and resting monocytes. The 130 kDa form contains hexasaccharide chains and is found on activated T cells and macrophages [117, 121]. The extracellular domain can also be proteolytically cleaved and is commonly found in blood plasma [122]. The differential glycosylation of the amino acid backbone is an essential feature of CD43 for many cell functions, particularly in T cell responses [123, 124].

The cytoplasmic domain is relatively large (123 aa) and demonstrates a higher degree of conservation than the extracellular portion. Mouse and humans demonstrate 65% similarity in the cytoplasmic domain versus 42 % similarity in the extracellular portion [125, 126]. CD43 has longtime been implicated in the involvement of signal transduction, as evidenced by the conservation of the cytoplasmic tail and its ability to become both phosphorylated (and hyperphosphorylated), as well as sulfated [114, 120, 121,

123]. Both sets of post-transcriptional modifications lend themselves to indications of intracellular signaling capabilities.

1.4.2 Expression

CD43 is a single gene transcript; the murine CD43 gene is found on chromosome 7, contained within two exons [120]. The post translational modifications of CD43 demonstrate activation-specific isoforms on certain cell types. Specifically, the differential glycosylation generates glycoproteins of different molecular weights and antibody specificities [119]. T lymphocytes derived from either human or rodent sources express both the 115kDa and 130kDa isoform. Resting T-lymphocytes express tetrasaccharides, but activated human T-cells carry more complex hexasaccharide structures due to a shift in activation of glycosylating enzymes [117].

CD43 can be found on T lymphocytes, B lymphocytes and is highly expressed on polymorphonuclear neutrophils, macrophages, mast cells and NK cells[116, 127-130]. Its expression can vary depending on the activation state of the cell in question; CD43 is expressed on the surface of mature mast cells, but not the monocyte progenitors [127]. Similarly, peritoneal macrophages express CD43 constitutively at low levels, but upon activation, there is a significant positive shift in CD43 expression [128]. Neutrophils experience an opposite effect. When activated, CD43 is shed via proteolysis [130].

It has been demonstrated that activated macrophages also have increased expression of CD43 [131] and increased CD43 expression also appears to correlate with increased TNF alpha production upon immunological challenge [131, 132].

1.4.3 Function

As previously stated, the putative functions of CD43 are diverse and variable within each cell population that they are observed. Initially, it was widely accepted that CD43 acted only as a cell-adhesion molecule [115, 121, 133, 134] but further investigation into the subject revealed that CD43 is also capable of transmitting some form of signals that are able to regulate cellular functions [117, 121, 133, 135, 136]. The methods by which CD43 is altered to induce cellular reaction vary between studies which lead to occasionally confusing results.

Engagement of CD43 with specific monoclonal antibodies regulates integrin-mediated T-cell adhesion and promotes cell aggregation in monocytes and T lymphocytes, suggesting a role in the regulation of integrin function [115, 137, 138].

The intracellular portion has been documented to undergo a number of different modifications, such as ubiquitination and phosphorylation. Phosphorylation of cytoplasmic domain involves src family kinases lyn and hck. The involvement of tyrosine kinase activity associated with CD43 may play a role in the transduction of regulatory signals in neutrophils [133, 139].

CD43 appears to have the capacity to act as an 'activation molecule 'to transduce positive activation signals. Its activation stimulates secretion of chemokines RANTES, MIP-1alpha, MIP-1beta as well as increased tyrosine kinase activity in anti-phosphotyrosine immune complexes of cell lysates [129]. Addition of CD43-specific monoclonal antibody (thus mimicking CD43 stimulation) induces monocyte-dependent T-cell proliferation and homotypic adhesion in T-cells. It also increases hydrogen peroxide production in monocytes, and elevates natural killer T-cell activity [117, 128, 129, 134, 140].

The functioning of CD43 affects T- cell differentiation and T_H2 regulation [141], CD43-/- T-cells demonstrate defects in Ca^{2+} transportation, leading to an enhanced T_H2 response which can be reversed

via the reintroduction of CD43. T_H1 differentiation appears unaffected, but an elevation of T_H2 cytokines was observed [142].

Subpopulations of high CD43-expressing macrophages also express higher quantities of TNF-α than do low CD43-expressing MΦ, 71% versus 32% respectively, and have also been found to have a somewhat antagonistic function upon NF kappa B activation [131, 143]. Additionally, Randhawa et al demonstrated that CD43-/- murine macrophages demonstrated a defect in TNF-alpha production upon stimulation with *Mycobacterium tuberculosis* infection when compared to their wild type counterparts [132].

CD43 has been implicated as a mediator of apoptosis in a number of different cell types; its down-regulation has been linked to caspase 3 activation [132, 144]. The intracellular signaling portion of CD43 has also been shown to be marked by ubiquitin, cleaved and translocated to the nucleus during apoptotic activities [145].

1.4.4 Implications in disease

Although the phenotype for CD43-disrupted individuals is not very dramatic [145], there have been documented changes in CD43 in certain diseases. This is not surprising, given the mounting evidence of the importance of CD43 in states of cellular activation and immunological defense. Glycan structuring alone can affect disease progression and outcome: core2 branches in O-linked oligosaccharides are found in activated T cells (converted from the tetrasaccharide form), and the same structural change is also found on lymphocytes from patients with immunodeficiency conditions (Wiskott –Aldrich and AIDS) [146].

1.5 Introduction of thesis

The information presented in this chapter outlines the importance of TB as a global-concern and *M.tb* as a relevant pathogen. Research into the nature of TB infection and disease progression is not only crucial for world-health but is important for the insights it gives into the nature of the human immune-system and the search for novel methods by which we might be able to treat similar infections and ask relevant questions about disease-control in the human body. TB disease is fascinating because of the possibility of life-long infection being maintained within the host as well as the possibility of reactivation at any time. As we struggle to understand how this bacterium is capable of evading and controlling the host immune response, we are also forced to investigate 'both sides of the coin' of infection and immunity. The failure to provide an adequate vaccine based on current 'immunological-memory' dogma demonstrates that this infection is not quite like any other, and in order to help the millions of people who are infected, it is crucial to understand the interactions between bacillus and host. For *M.tb* in particular, examination of the innate immune system, including macrophage functions, cytokine production and intracellular signals that lead to them, is a critical first-step.

CD43 has been implicated as both an important mediator of cell signaling and immunological functions, as well as an important intermediary of *M.tb* binding and uptake [69, 132, 147]. CD43 is a requirement for fully-efficient binding and uptake of *M.tb* not only in CD43-transfected HeLa cells, but CD43 WT vs. KO macrophages as well [69, 132, 147]. Furthermore, Randhawa et al found that intracellular replication of *M.tb* was enhanced in CD43 KO macrophages, and that this enhancement of growth was controlled only by the addition of recombinant TNF-α. Conversely, CD43 WT macrophages had similar levels of uninhibited growth when anti- TNF-α antibody was added. Decreased levels of apoptosis and increased levels of necrosis were also observed when CD43 KO macrophages were infected with a virulent strain of *Mycobacterium tuberculosis* compared to their CD43 WT counterparts [132].

Chaperonins have been observed as possible modulators of immune responses for some time [148]. Their capabilities to stimulate specific immune-responses have been thoroughly documented for both mammalian and bacterial sources [98] and have been seriously looked at as vaccine-candidates in mycobacterial prophylactic treatments [40, 42]. Mycobacterial proteins Cpn 60.2 and dnaK have both demonstrated CD43-binding capabilities [7], as well as immunomodulatory capacities [42, 149].

The aforementioned cytokine deregulation with the lack of CD43 given *M.tb* stimulus, as well as the potential for immune-control via extracellular chaperonins led us to hypothesize that the two might be related at the junction of the CD43 mucin. We chose to investigate the possible intracellular macrophage signaling pathways affected by CD43 following stimulus with *M.tb,* Cpn 60.2 and dnaK via RNA-microarray and further qualification via quantitative-reverse-transcriptase PCR (q-RT-PCR). We hoped to determine if there were any similarities between the chaperonin-host mRNA expression and *M.tb*-host cellular mRNA expression. Additionally we planned to observe possible trends in macrophage responses with CD43 and without CD43 in all three treatment groups.

2 Methods

2.1 Cell preparation and tissue culture

2.1.1 Mice

Wild-type (WT) control mice (CD43 +/+) and knock-out (KO), CD43 -/- mice backcrossed more than 10 times on C57Bl/6 background were housed in a specific pathogen-free animal facility in micro isolator cages. Experiments were done in accordance with the standards set by the Canadian Council on Animal Care. For all experiments, CD43WT and CD43KO mice were age- and sex-matched homozygous littermates.

2.1.2 Culture of bone-marrow derived macrophages

Bone-Marrow derived Macrophages (BMDMΦ) were isolated from CD43+/+ and CD43 -/- pairs. Mice were euthanized and dissected to remove femurs and tibiae. The ends of the bones were cut and using a 25 gauge needle, the marrow was flushed out with RPMI (RPMI 1640 medium, Gibco, Burlington ON) supplemented with 10% fetal calf serum, 10mM L-glutamine and 10 mM sodium pyruvate), all from Gibco (Burlington ON). Bone marrow washes were pooled and erythrocytes were lysed using 0.17 M ammonium chloride (NH_4Cl, pH 7.2) After washing, cells were re-suspended in supplemented RPMI and incubated in tissue culture-treated flasks (Becton Dickinson Lab ware, Franklin Lakes, NJ) for 3 h at 37°C, 5% CO_2 to deplete non-stem cells by adherence. Non-adherent cells were then washed, re-suspended in bone-marrow media (RPMI + 10% (v/v) L929 cell medium), diluted to 1 million/ml concentration and plated in 125 cm^3 flasks and allowed to differentiate for 7 days at 37°C , 5% CO_2. Media was replenished on day 5.

2.2 Bacterial culture

M. tuberculosis strain H37Rv (TMC #102, ATTCC # 27294) was grown to late log phase in Proskauer & Beck medium supplemented with 0.05% Tween 80 under static conditions with intermittent agitation (every 2 days). Cultures were stored at -80˚C and tested for viability and approximate concentration of bacteria by CFU counts on 7H10 plates.

2.3 Recombinant molecular chaperones

Recombinant Cpn60.2 and DnaK were derived using plasmids pMRLB1 and pMRLB.6, provided through the NIH/NIAID TB Resource Contract (HHSN266200400091c) at Colorado State University. The pMRLB1 (rv0440, Cpn60.2) and pMRLB.6 (rv0350, dnaK) plasmids were designed to include a 6xHiis tag on the gene product and encode for ampicillin resistance. Each of these plasmids was transformed and expressed using BL21Star (DE3) pLysS *E.coli* competent cells (Invitrogen, Carlsbad, CA). These E.coli strains contain the λ DE3 lysogen (prophage) which enhances T7 promoter function. After successful heat shock transformation of pMRLB1 and pMRLB.6 into respective BL21Star (DE3) pLysS bacteria, 1L volumes of transformed *E.coli*, grown at 225 rpm in Miller Acros Organics LB Broth (Fisher Scientific, Ottawa ON), at 37°C, were induced with 120 mg mL^{-1} isopropyl β-D-1-thiogalactopyranoside (IPTG) to express the recombinant proteins at early log phase, and the cultures were then grown to late log phase, over 3-4 hours. Growth phases were evaluated throughout, using optical density at 600nm. After logarithmic growth was exhausted, the cultures were centrifuged using 600 mL centrifuge jars (NalgeNunc, Rochester, NY) spun at 10 000 X g. Sedimented bacteria were then resuspended in bacterial lysis buffer (200µg mL^{-1} Lysozyme (Sigma, Oakville ON), 250 UL^{-1} DNase I (Invitrogen, Burlington ON), one tablet of EDTA-free protease inhibitor cocktail (Roche) dissolved in 1x Binding Buffer (Calbiochem, San Diego, CA) and ≥18 MΩ H_2O). The *E.coli* lysate was then spun down at 48,400 X g for 1 hour and the supernatant was reserved. A His-Bind Resin kit (Novagen, Madison , WI) was used for

recombinant protein purification, as per manufacturer's recommendations, and the proteins were washed in the Ni^{2+} column including a 0.5% (w/v) amidosulfobetaine (ASB) – 14 detergent (Calbiochem, San Diego, CA) treatment to help minimize residual endotoxin presence.

2.4 *In vitro* assay for binding of particles to macrophages and *M.tb* infection

The macrophage monolayer exposure to recombinant *M.tb* proteins DnaK, Cpn 60.2 and *M.tb* was based on previously-described whole-bacterial infection protocols. Bone-marrow derived stem cells were cultured in 125 cm^3 flasks at 15 million cells (1 million cells per ml, 15 mls total) for 7 days at 37°C, 5% CO_2 to allow for maturation into BMDMΦ (See section 2.1.2). On day 7, monolayers were washed with phagocytosis medium (138 mM NaCl, 8.1mM Na_2HPO_4, 1.5 mM KH_2PO_4 , 2.7 mM KCl, 0.6mM $CaCl_2$, 1 mM $MgCl_2$, and 5.5 mM D-glucose, pH 7.4) (PBS-G) twice, and 5ug/ml of either Cpn 60.2, DnaK or PBS-G. Flasks were rocked in an incubator at 7 days at 37°C, 5% CO_2 for 1 hour, and then co-incubated static for an additional two hours. After 3 hours of total co-incubation, the flasks were washed three times with PBS-G and RNA was immediately isolated. For bacterial infection, *M.tb* bacteria were passed through a 25-gauge needle 10 times to disperse the bacterial clumps characteristic of mycobacteria, and diluted to the required concentration using PBS-G. The overlay was removed from BMDMΦ monolayers and replaced with *M. tuberculosis* in PBS-G at multiplicities of infection (MOI) of 20:1 or 30:1 (bacteria: MΦ, CD43 +/+ and CD43-/- respectively). Previously in our lab, Randhawa et al found that CD43 deficient mice did not uptake *M.tb* bacillus as readily as CD43WT mice [72]. It was found that in order to gain the same initial quantities of bacteria within the macrophage itself, 1.5 times more bacteria must be added to the monolayer during the infection. Since this study was an observation of the effects of *M.tb* on the intracellular signaling of the MΦ, it was imperative that approximately the same numbers of bacteria have entered in the cell for both the CD43WT and CD43KO. Tyler Hickey made a similar observation

with the inhibition of bacterial binding and uptake with the blocking of the CD43 extracellular portion using Cpn60.2 [7]. Both of these studies confirm that the addition of 1.5 times more bacteria to CD43KO macrophages is required to obtain similar amounts of intracellular bacilli.

Infected MΦs were incubated as for the hsp-challenged: 1 hour rocking (Nutator, Becton Dickinson, and Mountain View CA) followed by 2 hours stationary at 37˚/5% CO_2. Following infection, monolayers were washed three times with PBS-G and RNA extraction was performed immediately.

2.5 RNA isolation from BMDMΦ

RNA was isolated using a trizol-chloroform extraction followed by a secondary purification using RNeasy RNA purification columns (Qiagen, Mississauga, ON). Wash media was removed by pipetting and 3 ml of Trizol (Invitrogen) was added directly to a flask containing 1.5 x 10^7 BMDMΦ, which was then incubated at room temperature for 2-3 minutes until the monolayer had sufficiently lysed in the flask. The sample was then subdivided into 1 ml aliquots, to which 200µl of chloroform was added and the sample was shaken vigorously for 15 seconds and incubated at RT for 2-5 minutes. Samples were then centrifuged at 13 000 rpm (12 000 g) for 15 minutes at 2-8 °C. The aqueous phase was then extracted and transferred to separate 1.5 ml RNAse-free tubes, to which 350 µl β2-mercaptoethanol-free RLT buffer (Qiagen, Oakville ON) was added. Samples were homogenized by pipetting. 100% Ethanol was then added to the RNA-RLT buffer mix and the subdivided RNA solutions were re-pooled in a treatment-specific manner and transferred into RNeasy filter-columns. The columns were centrifuged at 11 000 rpm for 15 seconds and the flow through was discarded. This process was repeated until the entire sample had passed through the filter. Columns were washed with 500 µl RPE buffer, centrifuged for 15 seconds at 11 000 rpm again, and collection tubes were changed. The RNA sample-columns were washed a final time with 500 µl of RPE buffer and 35 µl of RNase-free water was added. The RNA columns were centrifuged at 11 000 rpm for 90 seconds, and this step was repeated with an additional

30 µl of RNase-free water. RNA quality and quantity was assessed using conventional spectrometry and Bioanalyzer methods.

2.6 RNA amplification

After RNA quality was confirmed using an Agilent 2100 bioanalyzer system from Agilent Technologies, aliquots of 1 µg total RNA were subdivided and stored at -80 °C. Amplification of the mRNA from the 1 µg total RNA aliquots was performed using a Message Amp II kit from Applied Biosciences. RNA was amplified according to manufacturer's instructions. Samples were thawed and 1 µl of T7 Oligo (dT) was added to the 1 µg total RNA aliquot. Sufficient RNAse-free water was added to bring the total volume to 12 µl. Samples were incubated for 10 minutes at 70°C in an Eppendorf Mastercycle, spun for 10 seconds to gather sample at the bottom of the tubes and incubated on ice. Each reaction then had 2 µl 10X first strand buffer, 1 µl of ribonuclease inhibitor, 4 µl dNTP mix and 1 µl of reverse transcriptase added. Reactions were incubated for 2 hours at 42°C in an Eppendorf Mastercycle thermocycler, spun and incubated on ice again. The cDNA that was produced from this reverse-transcriptase reaction immediately underwent RNA amplification; 63 µl of nuclease-free water, 10 µl of 10X second strand buffer, 4 µl dNTP mix, 2 µl DNA polymerase and 1 µl of RNAse H were added to all cDNA samples then incubated at 16 °C for 2 hours. cDNA filter cartridges and subsequent solutions were prepped during this time: cDNA filter cartridges were co-located in 2ml wash (Eppendorf) tubes and 50 µl of cDNA binding buffer was added to each filter cartridge and incubated for a minimum of 5 minutes. When the cDNA amplification was complete, 250 µl of cDNA binding buffer was added to each cDNA sample, mixed via gentle pipetting and transferred into an equilibrated cDNA filter cartridge. Samples were then centrifuged for 1 minute at 10 000Xg, flow through discarded and the centrifugation step repeated. Filters were then transferred to cDNA elution tubes and 10 µl of nuclease-free water (preheated to 50° C) was added and samples were left for 2 minutes and then centrifuged for 1.5 min at 10 000 Xg.

Another 10 µl of pre-heated nuclease-free water was added, incubated and eluted a second time. The eluate was then incubated on ice. A dNTP solution of T7 ATP, T7 CTP, T7 GTP, T7 UTP and T7 10x Reaction buffer and T7 Enzyme Mix was added to each sample, as per manufacturer's instructions. The cDNA samples were then incubated for 14 hours at 37°C, during which the cDNA was transcribed into amplified RNA (aRNA). Reactions were stopped by addition of 60µl of nuclease-free water and gently vortexed to mix. RNA was then purified by the addition of 350 µl of aRNA binding buffer, thoroughly mixed and passed through an aRNA filter cartridge and centrifuged for 1 minute at 10 000 Xg. 650 µl of aRNA wash buffer was applied to the filter and the sample was spun again for 1 minute at 10 000 Xg. After an additional spin to assure the removal of any trace ethanol, the filter was then transferred into a clean microfuge tube and the centre of the filter was re-hydrated with 50µl of pre-heated (60°C) nuclease-free water. Rehydrated columns were left at room temperature for 2 minutes and centrifuged for 1.5 minutes at 10 000 g. A second elution was performed with another 50µl aliquot of nuclease-free water. Samples of aRNA totaling 100 µl were quantified using a spectrophotometer, diluted to an approximate concentration of 1 µg/µl, aliquotted into 10 µl volumes and stored at -80°C until needed.

2.7 RNA micro-array application

Amplified RNA aliquots were transported to the Vancouver Prostate Centre Microarray Facility at 2660 Oak Street, Vancouver, BC V6H 3Z6. All microarray applications (Labeling, Hybridization, Scanning and Analysis) took place at this location, by members of the Stokes lab (Audra Vair, Sharlene Eivemark). CD43KO and CD43WT RNA samples of the same biological replicate and treatment were directly compared using opposing dyes and 'dye swap' normalizations were performed.

2.7.1 Labeling and purification of nucleic acid

In a 1.5 ml microfuge tube, 2-3 µg of amplified RNA was added to 2µl of 10x labelling buffer and enough nuclease-free water to complete the 20 µl reaction volumes. Tubes were incubated in for 5 minutes at

95°C and then tubes were spun briefly to gather sample at the bottom of the tube and placed on ice for a minimum of 1 minute. 1 µl of Cy3 or Cy5 fluorescent label was added to the reaction and mixed by pipetting. From here on, samples were shielded from light to avoid quenching of the dyes. Samples were then incubated for 1 hour at 37°C to incorporate dyes. After 1 hour of incubation, labeled aRNA was purified using the CyScribe GFX Purification kit (GE Healthcare, formerly Amersham biosciences) (Baie d'Urfe, Quebec) as per manufacturer's directions. 500 µl of capture buffer was added to the purification column and labeled aRNA was mixed with the capture buffer by pipetting 4-5 times. Columns were spun at 13 000 rpm for 30 seconds and the flow-through was discarded. 600 µl of wash buffer was added to each column and spun for 13 000 rpm for 30 seconds, flow through was discarded. Columns were washed twice more in the same fashion and finally spun for an additional 10 seconds to remove any residual wash buffer. Columns were then transferred to clean 1.5 ml microfuge tubes. 30 µl of pre-heated (to 65°C) elution buffer was then added to the centre of the column and samples were then incubated at room-temperature (25°C) and spun at 13 000 rpm for 1 minute. A second addition of 30 µl of elution buffer was applied, incubated and centrifuged. Dye incorporation was then measured using a Nanodrop Spectrophotometer. RNA concentration, A260/280 ratio and dye incorporation were all calculated using these readings. 30pmol of dye per RNA sample was calculated and used to hybridize to the microarray.

2.7.2 Microarray chip hybridization

Operon OpArray, Mouse Genome Oligo Set version 4.0 (Eurofins MWG Operon, Hunstville AL) glass slides were given a pre-hybridization treatment, whereby they were incubated in 1x Saline-Sodium Citrate (SSC) buffer (150mM sodium chloride, 300mM trisodium citrate, pH 7.0) for 45 minutes at 50˚C. Slides were then washed with distilled water three times and dipped in 100% isopropanol 10 times. Slides were dried by centrifugation in a 50 ml falcon tube for 2 minutes at 2 000 xg.

In a clean, nuclease-free tube, the Cy3 and Cy5 samples from CD43KO and CD43WT macrophages (same co-incubation medium) were combined and an equal volume of Genesphere Hybridization buffer (2x formamide) was added and tubes were subsequently incubated at 80°C for 10 minutes. Hybridization cassettes were arranged (for the containment of the glass sides and sample), glass slides were placed inside and glass coverslips gently placed on top. After the 10 minute incubation was terminated, the sample was gently applied to the slide, between glass slide and coverslip, making sure to avoid bubbles. Arrays were incubated overnight in a 53°C hybridization oven. Cassettes were then disassembled and washed in the first wash buffer (2x SSC/0.2%SDS) at 65°C for 15 minutes. The second wash (2xSSC) was pre-warmed to 50°C and slides were removed from wash 1 and incubated in wash 2 for 15 minutes (while shaking). Samples were then transferred to a room-temperature third wash buffer, 0.2X SSC and shaken for 15 minutes and subsequently dried by centrifugation as before (2 000 xg for 2 minutes) Slides were scanned using the ScanArray Express from Perkin Elmer (Waltham, MA) and images were analyzed using Imagene ™ (BioDiscovery, El Segundo, CA). After scanning, slides were stored shielded from light at -20°C.

2.8 Microarray analysis- Genespring GX analysis

Microarray analysis was done using Genespring GX ®. Samples were subjected to dye-swap normalization and average signal was recorded. Gene lists were first subjected to a confidence filter (Students t-test) between triplicate biological samples; All genes with p-value greater than 0.05 were rejected as poorly-replicating results. The model for relative RNA quantization was the 'Inactive cross-gene error' model and 'significant differential regulation' was set to be 1.2 times above or 0.833 times below that of the wild-type, reference sample.

2.8.1 Ingenuity ™ pathways analysis

Lists of statistically significant, differentially regulated genes were subjected to a rigorous database analysis via Ingenuity ™ (version 8.0, accessed April 17-May 15, 2009), an online- program that investigates annotated genes of interest and presents the candidate genes that share canonical cell-signaling pathways, both at the tissue and sub-cellular level. Statistical significance of the differential regulation of each candidate pathway is given by a relative comparison of total candidate genes vs. 'listed' pathway genes, which is updated online weekly. Pathways and genes were selected from this list based on relativity to the research question and past observations.

2.9 Quantitative RT-PCR

Two-step quantitative RT-PCR was performed on original, non amplified samples of RNA from storage in the -80˚C freezer. Copy-DNA (cDNA) was performed first and quantitative PCR was applied to the cDNA.

2.9.1 Copy-DNA (cDNA) synthesis

Original (non-amplified) samples of RNA from storage in the -80˚C freezer. 1 µg of RNA (to a maximum of 11 µl) was added to a mix of 1 µl of Oligo dT, 1 µl of 10 µM dNTP. Sufficient RNAse-free DNAse-free water was added to a final volume of 13 µl. Samples were then incubated for 10 minutes at 60˚C and put on ice for minimum of 1 minute. A second master mix consisting of 4µl of first strand synthesis buffer, 1 µl of 0.1 M DTT, 1µl RNAse-Out and 1 µl of Superscript III was added per tube of sample. Samples were centrifuged briefly to collect at the bottom of the tube and then incubated for one hour at 42˚C. cDNA was aliquotted and diluted 1:8 in nuclease-free water prior to qPCR analysis.

2.9.2 Quantitative PCR-primer design and quality analysis

Gene-specific primers for Quantitative RT-PCR amplification were ordered from Invitrogen (Invitrogen, Carlsbad, CA) in 25 nanomolar quantities, desalted. They were resuspended to give a 100µM concentration stock solution in pH 8, 10 µM, and filter-sterilized Tris buffer. Primers were then subjected to a trial PCR to test specificity, using the same temperature and timing of the Q-PCR machine to be used. cDNA created from the reference control group (PBS-G CD43WT) amplified RNA was used to test primer specificity. Each amplification run consisted of 10 minutes at 95 ˚C, 2 minutes at 52˚ C, 60 seconds at 60˚ C and 15 seconds at 95˚C, the later three temperatures repeating in cycle 40 times. The PCR master mix consisted of a 20 µl reaction (as is reflective of the sybr-green qPCR reaction) containing the following (per tube): 2µl of magnesium-free PCR buffer (Invitrogen) , 1.6 µl 10 µM dNTP, 1.2 µl 50 µM $MgCl_2$, 0.5 µl of sense and antisense primers, 0.2 µl of Taq , 12 µl H_2O and 1 µl of template cDNA. PCR product was visualized on a 5% agarose gel with 1% SybrSafe additive, and compared to a 100bp DNA ladder for product size and specificity.

2.9.3 Quantitative-RT-PCR efficiency and protocol

Template cDNA was generated by combining 1 aliquot from all three biological reps of CD43+/+, PBS-G incubated cDNA samples. This master-combination was then diluted 2-fold from 1:1 dilution to 1:32 dilution in RNASE/DNASE-free water and used as a template for determining quantitative RT-PCR efficiency. One µl of each cDNA sample was pipetted into 1 well of a 96-well PCR plate, to which a master mix consisting of 8.5 µl of Nuclease-free water, 9.5 µl of Sybr Green, 0.5 µl of sense primer and 0.5 µl of antisense primer was added. Plates were sealed using clear plastic cap-strips and spun at 4 000 g for 5 minutes at 4˚C to ensure proper mixing and to displace any bubbles. The plates were then analyzed in an Applied Biosystems 7300 Real-Time PCR system, whereby they were incubated at 50˚ C for 2 minutes, then incubated at 90˚C for 10 minutes, then cycled through a PCR amplification of 15

seconds at 95 ˚C and 60.0˚C for 1 minute, 40 times. Dissociation cycles were added to the end of every run in order to ensure appropriate binding and amplification of a single-gene target.

2.9.4 RNA isolation for additional qPCR samples

For tissue culture and infection details, refer to sections 2.1.2 and 2.4. BMDMΦ from both CD43+/+ and CD43-/- mice, seeded at 4 million per flask and adhered to $75cm^3$ flasks were removed from CO_2 incubator and washed three times with 5mls of PBS-G. One ml of Trizol was added to each flask and adherent cells were then harvested with a cell scraper, transferred to a 1.5 ml RNase-free microfuge tube and frozen until RNA extraction could take place (an average of 5 days later). Frozen tubes of Trizol were then thawed at room temperature for 5-10 minutes. 200 µl of chloroform was added to each sample, shaken vigorously for 10-15 seconds and then incubated for 3-5 minutes sitting static at room temperature. Tubes were then centrifuged at 13 000 rpm for 15 minutes at 4˚C. The aqueous layer was then transferred into a new tube containing 500 µl of >96% ethanol and incubated at -80˚C for a minimum of 4 hours and up to 7 days. Samples in ethanol were then removed from the freezer, thawed and spun at 13 000 rpm for 20 minutes at 4 ˚C. The supernatant was poured off and discarded and the pellet was washed in 500ul of 75% ethanol, spun at 13000 rpm for 1 minute a 4˚C, the supernatant was poured off and the pellet was washed in 500 µl of 96% ethanol, spun for 1 minutes at 13 000 rpm and the wash was discarded. RNA pellets were then allowed to air-dry for a maximum of 5 minutes, and resuspended in 100 µl of RNase-free water and then cleaned using the RNeasy kit from Qiagen. Three hundred fifty µl of RLT buffer was added to the re-suspended RNA sample and mixed by gentle pipetting. Two hundred fifty µl of 96% ethanol were then added, mixed a second time and the entire solution was added to an RNeasy column. Columns were spun according to manufacturer's instructions, 15 seconds at 8 000 Xg. Eluate was discarded, and columns were washed twice with 500 µl of RPE buffer and spun for 15 seconds at 8 000 Xg each time. After the second wash, the columns were

spun for a longer, 2 minute period. Dry columns were then transferred to clean , RNase-free microfuge tubes and filters were hydrated with 30 µl of water, incubated at room temperature for 1 minute, and spun for 1 minute at 8 000 Xg. Eluate was carefully removed and re-applied to the column, incubated a second time at room-temperature and respun. RNA quantity was then measured by Nanodrop and aliquotted into approximate quantities of 1µg per tube and stored at -80°C.

2.9.5 Quantitative reverse-transcriptase PCR analysis

Q-RT-PCR analysis was performed using Relative Expression Software Tool (REST) 2009 from Qiagen (Oakville, ON). Quantitative Cycle (Cq) values were exported from the ABI 7300 Q-PCR thermocycler and entered into this program in a treatment-specific manner for each biological replicate. Gene expression was normalized to the expression average of three reference genes, glyceraldehyde 3-phosphate dehydrogenase (GAPDH), beta actin and 18S ribosomal RNA (18s rRNA). CD43 KO expression of each gene was compared to that of the WT control for each biological replicate. All relative expression values were then averaged and statistics were performed using Student's t-test to determine significance.

Chapter 3: Differential gene expression between CD43 WT and KO macrophages exposed to *M.tb,* Cpn 60.2 and dnaK

3.1 Introduction

Gene-expression microarrays are a common method of observing global changes in gene expression. Typically consisting of a glass slide (referred to as a chip) upon which thousands of spots of DNA oligonucleotides are embedded. Each oligonucleotide (probe) is especially designed to bind a portion of a single gene or gene transcript variant. The microarray used in this study was RNA-specific, and therefore the probes coded for expressed sequence tags (ESTs) of the genome, both annotated (for functional proteins) and non-annotated. There must be a treatment and control sample for every cell type and/or treatment studied. In the current study, there were separate controls for the two areas of interest, the first being the affect of CD43 on cellular functioning and the second being the effects of *M.tb* infection on these macrophages versus hsp stimulation. The controls were as follows, 1) CD43 WT (control), for normalizing the differential CD43KO macrophage gene expression and 2) stimulated versus unstimulated macrophages. The isolated RNA must be labelled with two different fluorophores to visualize the binding on the chip and to differentiate signals between control and experimental RNA populations. The two differentially-labelled RNA sets (KO and WT) are then hybridized onto the same oligonucleotide chip. During this process, the labelled mRNA will bind their specific oligonucleotide sequence and emit a fluorescent signal which is then read by a 'chip-reader', specialized piece of fluorometric machinery. The chip is read in the two optimal wavelengths of the 'competing' (control and experimental) dyes, and individual levels of fluorescence are quantified for each oligonucleotide spot. The levels of the fluorescent signal (representing quantities of RNA) are first normalized within the chip, by comparing values of technical replicate spots. The treatment sample is then normalized to the

control sample, and final values are assigned to each gene transcript. In order to control for preferential binding or signaling of one dye over another, an additional method of normalization control, known as the 'dye swap' method is commonly used. This involves dividing one population of RNA and binding both dyes to it separately and then treating two glass slides with the opposing dye types. For example, of two slides used, one will have 'Cy5' control and 'Cy3' experimental and other slide will have 'Cy5' experimental and 'Cy3' control. The two sets of normalized RNA values (from within the chip) are then compared and normalized to each other (chip-to-chip), in order to reduce possible error generated by chemistry. This secondary normalization is performed in the microarray data-analysis program. These programs are designed to deal with large quantities of data as our microarray chips have over 35 000 spots on them, representing approximately 25 000 different genes. In our experiment, dye-swap normalization was performed. The gene-expression lists are then filtered based on whatever criteria the researcher chooses, with the predominant two being 1) a filter based on relative gene expression, in which a minimal level of relative difference between the experimental and control samples is set, and 2) a filter based on statistical significance. This current study filtered data on both criteria, however a preferred stringency was set for confidence between biological replicates (p-value of 0.05 or less) and the relative changes in expression had lower cutoffs than generally used (1.2 or 0.833 fold difference).

In order to validate the data that was generated using the microarray, quantitative reverse-transcriptase polymerase chain reaction (Q RT-PCR) was employed on specific genes selected from the microarray. Q RT-PCR is a highly specific and sensitive method to measure differential RNA levels, compared to a whole-genome microarray. This method involves the use of gene-specific primers and fluorescent markers in the way of either a gene-specific probe, which fluoresces upon cleavage by the polymerase, or Sybr green dye, a specially formulated dye that intercalates in double-stranded (and therefore amplified) DNA. Both methods measure the amount of amplification that occurs for a specific gene in a single PCR reaction, the fluorescence of which is measured and analyzed on a specialized plate-reading

thermocycler. Relative values of amplification of genes of interest are compared to genes of reference, which are then compared to the other experimental samples in the study. Because the primers must bind and amplify specific sections of the mRNA, and it is the amplified cDNA that is measured, this method is more specific than a microarray, where nonspecific binding of the single probe to mRNA sequence is more common and background binding must be taken into account.

The genes that are examined do not necessarily have to be the focus of the study itself, but their levels of relative expression are compared to those in the microarray. It is ideal to see similar trends of expression with perhaps a higher level of expression in the Q RT-PCR, eg. 2 fold up-regulations in microarray can become 200-fold up regulation in Q RT-PCR. To find the levels of mRNA for a specific gene being exactly the same for the two methods is relatively uncommon; one usually looks for trend similarities between datasets.

3.2 Rationale

Previous research indicated that CD43 is an important element in macrophage interactions with *M.tb* bacterial invasion, cytokine signaling and apoptosis [72, 131, 132, 143, 145, 147]. Previous studies also indicate that the heat shock protein Cpn 60.2 is primarily responsible for the bacterial interaction with CD43. In addition, dnaK is another heat shock protein found on the M.tb capsule and also demonstrates binding capabilities with CD43 [7].

Two separate studies by Randhawa et al. explored the impact of CD43 deficiency in M.tb infection. It was first demonstrated that there was a deficiency in bacterial binding and uptake of M.tb , which could be countered for at initial infection by increasing the multiplicity of infection 1.5 times, for example from 20:1 to 30:1 for CD43KO macrophages [72]. Once internalized, there was a relative increase of intracellular bacterial growth in the CD43KO compared to CD43WT. This phenomenon was maintained *in vivo,* a whole-mouse infection, with a significant increase in bacterial load in the lungs, liver and

spleen, but did not affect mouse survival over the 65-day time-course. This study also demonstrated that there was a gene-dose effect of bacterial binding and uptake, CD43 heterozygote macrophages (CD43 +/-) demonstrated binding and uptake that was intermediate between both CD43WT (CD43+/+) and CD43KO (CD43-/-). A second study demonstrated that inactivated CD43KO macrophages were deficient in pro-inflammatory cytokines TNF-α, IL-12 and IL-6, and that the addition of recombinant TNF-α to CD43KO macrophages controlled the intracellular bacterial growth to levels comparable to CD43WT macrophages [132].

The molecular mechanism for deficient binding and uptake of *M.tb* bacillus to CD43KO macrophages was also explored in our lab, by Tyler Hickey. He found that two heat shock proteins Cpn60.2 and dnaK, were found extracellularly in the *M.tb* capsular material, and were capable of binding the extracellular portion of CD43 [7]. Further study demonstrated that Cpn60.2 was capable of preventing bacterial binding and uptake in a dose-dependent fashion to a maximal inhibition of up to 60% reduction of binding and uptake. DnaK did not demonstrate the same strong affinity for CD43. The concentration at which maximal inhibition of binding and uptake was found was 5μg/ml, which was therefore the concentration of recombinant protein used in the current study. The use of heat shock proteins including Cpn60.2 as immunological stimuli as well as potential vaccine candidates has been well-documented [42, 150, 151], however it has also been found that the concentrations used in this study are lower than those at which maximal stimulation was achieved elsewhere [151].

The microarray was performed with live *M.tb* bacillus, recombinant Cpn 60.2 and dnaK in order to investigate the possibility of specific pathways that are differentially regulated between CD43 KO and WT macrophages and ascertain the ability of Cpn 60.2 and dnaK to stimulate CD43 to differentially regulate mRNA expression compared to *M.tb*.

3.3 Results

3.3.1 CD43 knockout and CD43 wild type macrophages exhibit differential regulation to each other in response to mycobacterial stimuli

The changes in mRNA expression in CD43 WT and CD43 KO macrophages were tested using whole, live *M.tb* bacillus, recombinant Cpn 60.2 and recombinant dnaK on murine BMDMϕ in the absence of serum, for three hours as outlined in the methods, section 2.4. This was done in three independent experiments using three sets of age-matched littermate CD43WT and CD43KO mice. It was determined that (i) the mRNA expression of BMDMϕ is altered when CD43 is disrupted (Table 1), the (ii) differential gene expression between the two genotypes was much higher upon stimulus with *M.tb* than with either dnaK or Cpn60.2, and (iii) that there was a high level of basal differential expression between WT and KO macrophages. The basal levels of differential expression were taken into account for genes and pathways that were selected for further investigation and it was taken into account that trends in expression were enhanced with stimulation compared to the phagocytosis-medium control.

3.3.2 *Mycobacterium tuberculosis*, Cpn 60.2 and dnaK elicit differential responses in CD43-/- and CD43+/+ BMDMφ

In CD43 KO macrophages, there were more genes differentially regulated in response to *M.tb* stimulation than any other co-incubation factor (figure 1 A and B). There were 728 uniquely down-regulated and 940 uniquely up-regulated genes in CD43KO macrophages compared to CD43WT macrophages, in response to *M.tb*, versus 531 and 748 for dnaK and 321 and 843 for Cpn 60.2 (Supplemental Tables 1, 2, 3, 4). There were relatively few genes that were shared in both statistical significance and minimum fold change between the different stimuli, and only one gene shared in both

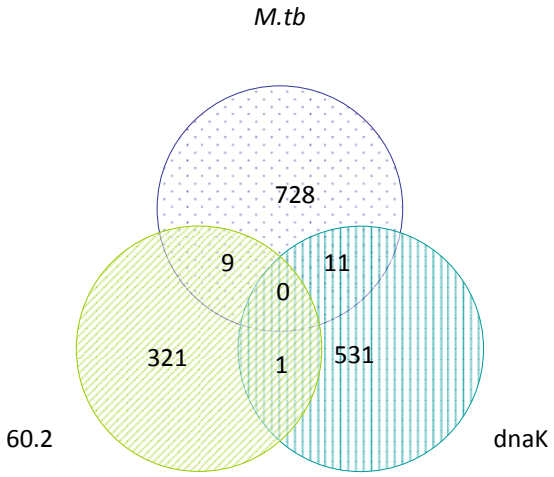
Table 1 Summary of overall changes in differential expression between CD43KO and CD43WT macrophages

Gene Expression	*M. tuberculosis*	Cpn 60.2	dnaK	Phagocytosis medium
Total number of up regulated RNA sequences (KO)	1003	907	805	759
Total number of down regulated RNA sequences (KO)	748	330	543	402
Total number of differentially expressed RNA sequences	1751/38 000	1237/38 000	1348/38 000	1161/38 000

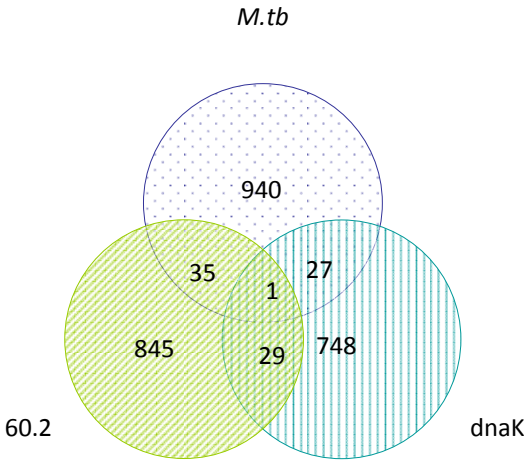
Relative expression is given as CD43KO expression compared to CD43WT control. *M. tuberculosis* infection was performed with an MOI (Multiplicity of Infection) of 20:1 for CD43WT macrophages and 30:1 for CD43KO macrophages, in order to normalize for differential bacterial binding and uptake. Recombinant proteins Cpn60.2 and dnaK were co-incubated with CD43WT or CD43KO macrophages in the phagocytosis medium at a concentration of 5 μg/ml. Genes were filtered based on confidence between biological replicates ($p<0.05$), then normalized expression of either greater than 1.2 (up regulated) or less than 0.8333 (down-regulated) in the CD43KO macrophages compared to CD43WT. Approximately 25 000 genes were represented in the microarray, with 38 000 gene transcripts (genes including transcript variants)

Figure 1 Venn diagram demonstrating the quantities of genes exhibiting differential response with exposure to one of *M.tb* Cpn 60.2 or dnaK

a



b



Genes that are down regulated (a) or up regulated (b) and shared between treatments. Statistically significant based on Confidence between biological replicates (p-value >0.05). Differential expression is of the CD43KO MΦ compared to CD43WT MΦ control. Normalized cutoff values for differential expression are 0.8333 and 1.2 respectively.

statistical significance and minimum fold change in all three stimuli (figure 1B). This gene was a non-annotated region of the mus muscles chromosome 14 genomic contig, flanked by a hypothetical protein and a voltage-dependent calcium channel. DnaK and Cpn 60.2 demonstrated little expressional similarity between each other, when compared to the similarity between either of the recombinant proteins and whole *M.tb* infection. For genes that are down regulated in the knockout, only one gene meets both stringency requirements for both 60.2 and dnaK, however the hsps have 9 and 11 genes in common with whole *M.tb*, respectively (Supplemental Table 5). Up regulated genes were similarly matched in numbers between Cpn 60.2 and dnaK, with 29 genes shared between the two recombinant proteins and 35 and 27 genes shared between *M.tb* and 60.2 or dnak respectively. If reproducibility between biological replicates (statistical significance) specific to each treatment type is disregarded, there are 9 genes up regulated in the knockout compared to the wild type shared between all three treatments (Supplemental Table 5). The lack of similarity in down regulated genes between all three treatment types however indicates that dnaK and 60.2 do not appear to be stimulating the macrophages with the same type of CD43 dependence. There were no apparent relationships between shared genes although many functional categories are shared. There were very few genes that belonged to a unique functional sub-set which was only activated by a single stimulus (Table 2).This initially caused difficulty in determining the true effect that a lack of CD43 had on the intracellular functions of BMDMϕ and how they might be affected by *M.tb,* Cpn60.2 or dnaK.

3.3.3 CD43 deficiency affects multiple signaling pathways

To determine the significance of CD43 in terms of intracellular signaling pathways, a network analysis was performed using an internet-based knowledge network. Using the Ingenuity Systems Pathway Analysis (IPA, http://www.ingenuity.com/) to model potentially significant signaling networks affected by the loss of CD43 when comparing stimulation by Cpn 60.2, dnaK or *M.tb*, it was determined that a

Table 2 Trends in the expression of statistically significant genes shared between different treatments.

Table 2.a Genes up-regulated in CD43KO macrophages compared to CD43WT macrophages shared by dnaK and *M.tb*-treated phagocytes.

Gene Category	Description	Normalized Expression	
Receptors		Dnak	*M.tb*
Olfr770	Olfactory receptor 770	1.913	1.654
Olfr 894	Olfactory receptor 894	1.663	1.391
Signalling proteins		Dnak	*M.tb*
Nek10	Never in Mitosis gene A-related kinase 10, NIMA related kinase 10	2.276	1.356
EG209380	Similar to Very Large Inducible GTPase 1	1.827	1.624
Rgs17	Regulator of G-protein signaling	1.746	1.339
Plxna2	Plexin A2, Multicellular organismal development, receptor activity	1.468	1.528
Mark2	Map/Microtubule affinity-regulated kinase 2, Par-1, Mark2-cell differentiation amino acid phosphorylation	1.368	1.545
Chemokines		Dnak	*M.tb*
Irf2bp2	Interferon regulatory factor 2 binding protein 2, negative regulation of Interferon transcription from RNA polymerase II promoter	1.342	1.345
Transporters		Dnak	*M.tb*
Clca5	Chloride channel, calcium activated 5- chloride transport/ligand-gated ion channel activity	1.936	2.451
Transcription/Translation		Dnak	*M.tb*
Similar to short coil-coil protein		2.119	1.433
LAzip	HCF-binding transcription factor, CREB/ATF bZIP transcription factor, Zf, LAZip, tyrosine kinase-associate leucine zipper protein LAZipII, Mus Musclus, CREB/ATF bZIP transcription factor	1.459	1.343
coiled-coil domain containing 25		1.421	1.411
Structural		Dnak	*M.tb*
Col9a2	procallagen, typ IX, alpha 2, cell adhesion, phosphate transport, skeletal development	1.94	1.346

The genes in the above table were determined to be statistically significant in both dnaK and *M.tb* – challenged macrophages and observed to share the same trend in expression profile. Expression values provided are of CD43KO macrophages compared to CD43WT macrophage control. Macrophages were infected with an MOI of 20:1 for CD43WT and 30:1 CD43KO. Macrophages were co-incubated with dnaK at a concentration of 5 µg/ml.

Table 2.b Genes up-regulated in CD43KO macrophages compared to CD43WT macrophages shared by Cpn 60.2 and *M.tb* treated phagocytes

Gene Category	Description	Normalized Expression	
Receptors		60.2	*M.tb*
V1rb1	Vomonasal receptor B1, Vn2, V1RA5	1.701	1.477
Olf609	MOR9-1	1.722	1.454
Olfr818	Olfactory receptor 818	1.631	1.462
5-Ht2b	5-hydroxytryptamine (serotonin) receptor 2b	1.400	1.460
Chemokines		60.2	*M.tb*
Card11	Caspase recruitment domain family member 11, BIMP3, CARMA1, endocytosis , positive regulation of I-kappa B kinase, NF-kappa B cascade, postitive regulation of interleukin-2 biosynthetic process`	1.496	1.888
Transporters		60.2	*M.tb*
Gabrr1	Gamma-aminobutyric acid receptor, subunit rho 1' chloride transport-gamma aminobutyric acid signaling pathway, ion transport	1.678	1.842
Guk1	Guanylate kinase 1, atp binding, guanylate kinase activity, transferase activity, pruine metabolism	1.266	1.709
Transcription/Translation		60.2	*M.tb*
AT rich interactive domain 5A (Mrf1 like, modulator recognition factor 1) Arid5a,		1.603	1.836
Ayp1	ribonuclease H2, subunit C, Rnase H2c	1.370	1.346
ZccHc17	Putative S1 RNA binding domain protein, predicted riken cdna, zinc finger cchc domain containing 17	1.266	1.539
Cell differentiation/growth		60.2	*M.tb*
Fgfr-1	Basic fibroblast growth factor receptor 1 precursor	1.834	1.502
Structural		60.2	*M.tb*
krtap6-1	Keratin associate protein 6-1	1.297	2.288
	Dynein axonemal, heavy chain 10	1.292	1.387
Plasma Membrane		60.2	*M.tb*
Tmem 139	Transmembrane protain 139, integral to membrane	1.756	1.763
Mir 16	Membrane interacting protein of RGS16, g-coupled receptor protein signaling pathway, glycerol metabolic process	1.462	1.535
Metabolism		60.2	*M.tb*
Gdpd3	glycerophosphodiester phosphodiesterase domain containing 3, glycerol metabolic process	2.235	6.843
Ech1	Enyol coenzyme A hydratase 1, proxisomal/mitochondrial dienyol-coa isomerase , fatty acid metabolic process, lipid metabolism	1.432	1.227
Ubiquitin/proteasome		60.2	*M.tb*
Usp37	Ubiquitin specific peptidase 37, cystein - type peptidase activity	2.068	1.811

The genes in the above table were determined to be statistically significant in both Cpn60.2 and *M.tb* –challenged macrophages and observed to share the same trend in expression profile. Expression values provided are of CD43KO macrophages compared to CD43WT macrophage control. Macrophages were infected with an MOI of 20:1 for CD43WT and 30:1 CD43KO. Macrophages were co-incubated with Cpn60.2 at a concentration of 5 μg/ml

Table 2.c Genes up-regulated in CD43KO macrophages compared to CD43WT macrophages shared by dnaK and Cpn 60.2 treated phagocytes

Gene Category	Description	Normalized Expression	
Receptors		60.2	Dnak
Asgr2	asialoglycoprotein receptor 2 (Asgr2)	1.785	2.424
F2rl2	Proteinase activated receptor 3 precursor (PAR-3) (Thrombin receptor- like 2) (Coagulation factor II receptor-like 2). [Source:Uniprot/SWISSPROT;Acc:O08675]	1.459	1.860
Antxr1	anthrax toxin receptor 1	1.270	1.462
Ssr4	Signal sequence receptor Delta, Trap, endoplasmic reticulum receptor activity, integral to the membrane	1.3	1.21
Signalling proteins		60.2	Dnak
Wnt16	Wnt-16 protein precursor, wingles-related MMTV integration site 16, Wnt receptor signaling pathway, calcium modulating pathway	1.423	2.548
Insl6	Insulin-like 6, homone activity	1.452	1.822
Rragd	Ras-related GTP bindin D, GTP binding, nucleotide binding, protein binding	1.408	1.750
Adhesion		60.2	Dnak
Caspr4	Contactin associated protein-like 4 precursor (cell-recognition protein)	1.297	2.763
Transporters		60.2	Dnak
GluR-2	Glutamate receptor 2, precursor GluR-2, GluR-B, GluR-K2, glutamate receptor , ionotropic, AMPA2, Gria2, potassium ion transport	2.240	1.987
Copg	Coatomer protein complex, subunit gamma, isoform 2 is encoded by transcript variant, transporter activity, structural molecule activity	1.428	1.673
Transcription/Translation		60.2	Dnak
Brunol4	Bruno-like 4, RNA binding protein	2.796	2.551
Ccdc57	Coilded-coil domain containing 57	1.347	2.330
SCR2_MOUSE	Scratch homolog 2 zinc finger protein, Similar to Transcriptional repressor scratch 2	3.024	2.329
4931407K02Rik	CAP-binding protein complex interacting protein 1	2.120	2.256
Smug1	Single strand selective monofunctional uracil DNA glycosylase, dna-repair, base-exision repair	1.715	1.829
Pelp1	Proline, glutamic acid and leucine rich protein 1, Mus musclus praline, glutamic acid and leucin e rich protein 1	1.897	1.693
Structural		60.2	Dnak
Myo5c	myosin VC	1.502	1.931
Vill	Villin-like protein, Villp, actin bidning, barbed-end actin filament capping, cytoskeleton organization and biogenesis	1.489	1.331
Plasma Membrane		60.2	Dnak
Clec2e	C lectin-related protein A, sugar binding	1.617	2.923

The genes in the above table were determined to be statistically significant in both dnaK and Cpn 60.2 –incubated samples and observed to share the same trend in expression profile. Expression values provided are of CD43KO macrophages compared to CD43WT macrophage control. Macropahges were co-incubated with recombinant protein concentrations of 5µg/ml.

Table 2.d Genes down-regulated in CD43KO macrophages compared to CD43WT macrophages shared by *M.tb* and dnaK treated phagocytes

Gene Category	Description	Normalized Expression	
Downregulated Receptors		Dnak	*M.tb*
Ager	advanced glycosylation end product-specific receptor precursor (receptor for advanced glycosylation end product)	0.714	0.583
Enzymes			
Peci	Peroxisomal 3, 2-trans-enyol-CoA isomerase	0.764	0.802
Phospho2	Phosphatase, orphan2, novel protein containing a putative phosphatase domain	0.640	0.807
Signalling proteins			
Psd4	Pleckstrin and Sec7 domain containing 4, regulation of ARF protein signal transduction, guanyl-nucleotide exchange factor activity	0.706	0.782
Adhesion			
Comp	Cartilage oligomeric matrix protein , Calcium ion binding, protein binding	0.540	0.557
Transcription/Translation			
EST AI449063	putative nucleic acid binding protein RY-1	0.558	0.659

The genes in the above table were determined to be statistically significant in both dnaK and *M.tb* – incubated samples and observed to share the same trend in expression profile. Expression values provided are of CD43KO macrophages compared to CD43WT macrophage control. Macrophages were infected with *M.tb* at a MOI of 20:1 for CD43WT and 30:1 for CD43KO. Macrophages were co-incubated with dnaK at a concentration of 5µg/ml.

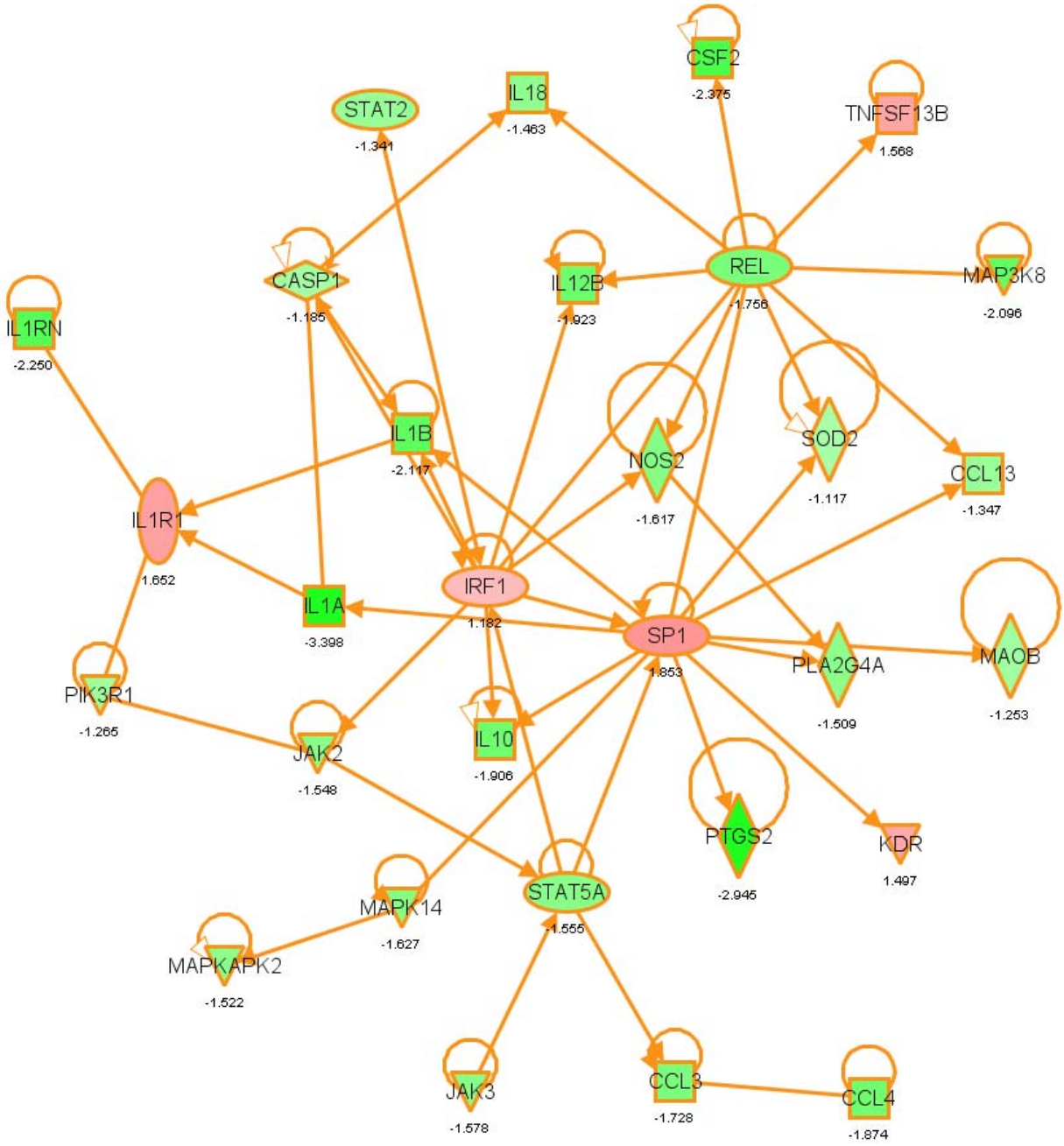
Table 2.e Genes down-regulated in CD43KO macrophages compared to CD43WT macrophages shared by *M.tb* and 60.2 treated phagocytes

Gene Category	Description	Normalized Expression	
Downregulated Receptors		60.2	*M.tb*
Notch 1	Notch gene homolog 1, Mis6, Tan1, Major Type A protein, tranmembrane receptor Notch1, activation regulateds T-cell linieage commitment and early tcell development	0.782	0.572
Epo-R	erythropeoitin receptor precursor	0.623	0.540
Itgam	Integrin alpha - M precursor, Cell surface glycoprotein MAC-1 alpha subunit, CR-3 alpha chain CD11b, leukocyte adhesion receptor MO1	0.613	0.611
Enzymes			
Sps2	Selenophosphate Synthetase 2, Ysg3, Sephs2	0.705	0.831
AMP deaminase 3	AMP deaminase isoform E	0.588	0.687
Signalling proteins			
Lrrc10	Leucine rich repeat containing 10, heart-restricted leucine-rich repeat protein, important in heart development	0.749	0.599
Tle3	Transducin-like enhancer of split 3, homolog of DrosophilaE (spl)	0.638	0.485
MAPKAPK-2	MAP kinase-activated protein kinase 2	0.634	0.657
Plasma Membrane			
Fibronectin leucine Rich transmembrane protein 3		0.518	0.619

The genes in the above table were determined to be statistically significant in both Cpn 60.2 and *M.tb* –incubated samples and observed to share the same trend in expression profile. Expression values provided are of CD43KO macrophages compared to CD43WT macrophage control. Macrophages were infected with *M.tb* at a MOI of 20:1 for CD43WT and 30:1 for CD43KO. Macrophages were co-incubated with Cpn60.2 at a concentration of 5µg/ml.

number of intracellular signaling pathways are potentially affected by CD43 presence or absence. The changes in gene expression (n-fold) for each treatment were analyzed using this program and the most significant molecular and cellular function pathways were examined to determine if there was a functional significance of CD43 in *M.tb*-related stimuli. Maps of inter-connected molecules were generated (example shown in figure 2). However, the details of gene-gene interactions were not clear or particularly detailed using this aspect of the program. For that reason, a more detailed, analytical approach was used. The program is also capable of individually associating specific genes to various cell functions and pathways. Genes that are broadly-used cell signaling molecules would be associated with a number of pathways for example, however statistical significance for the genes of interest when compared to the total number of genes listed in a specific pathway demonstrates the likelihood of true association. A summary of the top five pathways identified from my data as differentially regulated by CD43 is shown in Table 3. Upon investigation with common signaling pathways involving all three stimuli, it appeared that among the top molecular and cellular functions that were differentially expressed were 1) cellular development, 2) growth and proliferation, 3) death, 4) movement and 5) cellular function and maintenance. The master lists of the variety of pathways is quite extensive, and there is a range of statistical significance in terms of the probability that a pathway is associated by chance (or not) based on the total number of genes associated with a specific function compared to the total number of genes in the list of that function. All of the aforementioned molecular and cellular functions had significant p-values of less than 0.05 (range of values provided in table 3). The pathways analysis system tends to sub-categorize genes not only based on cellular functions but disease states and physical disorders. I chose to investigate the pathways based around cellular and molecular functions as opposed to investigating genes that are disease-state specific in order to simplify the search based solely on cellular functionality. Additionally, certain genes transcend various 'categories' and are applicable to a number of cellular functions.

Figure 2 Example of gene-gene interactions related to 'immunity' pathway in Ingenuity ™



The genes presented are associated with the 'Immunity' gene lists and the relative expression values are connected to *M. tuberculosis* infection. Genes are annotated, protein-coding and all linear connections denote direct protein-protein interactions. Data is represented as fold-change in CD43KO macrophages compared to CD43WT macrophages. Green color represents genes that are down regulated in CD43KO macrophages and red color represents genes that are up regulated in CD43WT macrophages.

Table 3 Common Molecular and Cellular Functions related to *M.tb*, hsp65 and dnaK stimulus

Associated Pathway/Function	Number of molecules present from pathway	P-value (Significance of pathway-association)
Cellular Development	381	<0.01
Differentiation of cells	240	<0.001
Development Processes	269	<0.001
Development	207	<0.001
Cell Death	48	<0.001
Growth	39	<0.001
Morphogenesis	73	<0.001
Maturation	39	<0.001
Apoptosis	41	<0.001
Expansion	24	<0.001
Branching Morphogenesis	6	<0.01
Cellular Growth and Proliferation	438	<0.01
Proliferation	340	<0.01
Growth	238	<0.001
Colony formation	68	<0.001
Expansion	24	<0.001
Cell Death	433	<0.01
Cell Death	376	<0.01
Apoptosis	378	<0.001
Survival	143	<0.01
Cytotoxicity	16	<0.001

Killing	7	<0.001
Necrosis	33	<0.001
Inhibition	36	<0.001
Cell viability	45	<0.01
Cellular Movement	258	<0.01
Migration	196	<0.001
Cell Movement	141	<0.001
Infiltration	51	<0.001
Homing	77	<0.01
Mobilization	10	<0.001
Movement	88	<0.001
Chemotaxis	75	<0.01
Invasion	77	<0.01
Emigration	6	<0.001
Chemoattraction	13	<0.001
Recruitment	13	<0.001
Transmigration	17	<0.001
Cellular Function and Maintenance	121	<0.001
Homeostasis	101	<0.001
Function	34	<0.001
Development	93	<0.001
Respiratory Burst	15	<0.001
Cell death	48	<0.001
Apoptosis	41	<0.001
Differentiation	47	<0.001

Pathways determined to be differentially regulated by CD43 when stimulated by three ligands: *M.tb,* Cpn60.2 and dnaK. Pathways listed result from comparing the 3 treatments and selecting those present in two or more of the aforementioned treatment lists. P- values represent statistical significance of the genes provided representing the aforementioned pathway.

Further inspection of these categorized gene lists revealed that eicosanoid signaling, p38 MapK signaling, apoptosis, inflammatory signaling and cytoskeletal remodeling were all differentially regulated pathways between CD43 WT and KO macrophages (Table 4). Because of the previously observed results concerning the role of CD43 in the induction of inflammatory cytokines and apoptosis

[132], further investigation into apoptosis and inflammatory signaling was performed. Networks of directly-relating genes from these pathways were generated, and it was apparent that CD43 KO macrophages induced higher levels of intrinsic apoptosis compared to their WT counterparts, as well as expressed lower quantities of mRNA involved in extrinsic apoptosis and TNF-α production (Table 4.4). Genes from these three areas were chosen as candidates for Q RT-PCR validation.

3.3.4 Confirmation of RNA microarray using Quantitative Reverse-Transcriptase PCR

There were several candidate genes selected for expression analysis (Supplemental, Table 6). The final set of genes (Table 5) were selected on the basis of either being present in the microarray and sharing expression trends in at least two of the three treatments (Cpn60.2, *M.tb* or dnaK). We were also interested in looking at other possible differentially regulated genes in the pathways identified (Table 4) that were not deemed differentially regulated via the microarray analysis (Table 6). As previously mentioned due to earlier observations concerning the differential apoptosis and TNF-α production in CD43KO compared to WT macrophages [132], these areas were of primary interest for further investigation. RNA samples from the dnaK exposed macrophages were omitted from this portion of the study due to the previous lack of evidence for any specific role in the interaction of *M.tb* and macrophages that was mediated by dnaK and CD43 [7]. The same study

Table 4 Pathway-associated gene lists with relative expression data

Table 4.a Cytoskeletal Remodeling-Associated genes

Gene	Relative Expression level per treatment				
	Phagocytosis medium	***M.tb***	**60.2**	**dnaK**	**Gene Function**
ASAP1	1.130	1.03	1.124	0.738	Phospholipid-dependent Arf GTPasse-Activating protein (associated with Src)
CAPN9	0.797	0.726	1.316	0.893	Calpain 9, calcium-dependent cystein endopeptidase. Calcium-ion binding
CAPN11	0.983	1.186	1.555	1.749	Calpain 11, Calcium-dependent thiol protease
GRB7	0.260	1.523	0.658	1.317	Growth factor receptor bound protein 7
ITGAL	1.043	0.766	0.749	1.345	Alpha L integrin
ITGAM	0.937	0.610	0.612	0.916	Alpha M Integrin
ITGAX	1.528	3.859	1.625	1.194	Alpha X Integrin
ITGB2	1.219	1.293	0.710	0.859	Integrin, beta 2
ITGB8	1.199	0.780	0.59342	1.291	Integrin, beta 8
MAP2K1	0.887	1.074	0.788	0.705	Mitogen-activated protein kinase kinase 1
MRAS	0.555	0.726	0.743	0.793	Muscle and microspikes RAS
PIK3CA	0.615	1.339	0.676	0.906	phosphatidylinositol 3-kinase, catalytic alpha polypeptide
PPP1CB	1.049	0.771	0.668	0.862	protein phosphatase 1, catalytic subunit, beta isoform
RAP2A	1.164	1.295	0.878	1.324	member of RAS oncogene family
TLN2	0.605	1.375	0.689	0.565	talin 2, actin assembly
TSPAN3	1.250	0.984	1.079	0.651	tetraspanin 3
TSPAN5	1.041	1.411	0.958	1.003	tetraspanin 5
TTN	0.649	1.622	1.017	1.104	Titin
WAS	0.977	1.198	1.149	1.204	WAS protein family, member 1
ACTR1A	1.198	0.837	0.561	0.947	ARP1 actin-related protein, homolog A
Gsn	1.166	1.312	1.247	1.258	gelsolin (amyloidosis, Finnish type)

Genes filtered on confidence between biological replicates ($p<0.05$) and with expression values of either greater than 1.2 or less than 0.8333 in either *M.tb,* Cpn 60.2 or dnaK-treated CD43KO MΦ compared to CD43WT and associated with cytoskeletal remodelling as determined by Ingenuity.

Table 4.b Mapk/p38signalling-associated genes

Gene	Relative Expression level per treatment				
	Phagocytosis medium	*M.tb*	60.2	dnaK	Gene Function
DUSP1	1.490	0.487	1.174	1.392	dual specificity phosphatase 1
IL1A	0.677	0.294	0.998	1.273	interleukin 1, alpha
IL1B	1.149	0.472	0.614	0.962	interleukin 1, beta
IL1F9	1.488	0.791	1.766	0.445	interleukin 1 family, member 9
IL1R1	1.667	1.652	1.440	2.085	interleukin 1 receptor, type I
IL1RN	0.791	0.444	0.771	1.161	interleukin 1 receptor antagonist
JMJD7-PLA2G4B	1.065	0.779	1.106	1.715	JMJD7-PLA2G4B readthrough
MAP3K7IP2	1.209	1.000	0.872	0.643	mitogen-activated protein kinase kinase kinase 7 interacting protein 2
MAPK14	0.903	0.615	0.791	1.357	mitogen-activated protein kinase 14
MAPKAPK2	0.973	0.657	0.634	1.042	mitogen-activated protein kinase-activated protein kinase 2
MAPKAPK3	1.159	1.020	0.986	1.117	mitogen-activated protein kinase-activated protein kinase 3
MYC	0.091	1.731	1.721	1.903	v-myc myelocytomatosis viral oncogene homolog (avian)
PLA2G4A	1.354	0.663	1.323	1.097	phospholipase A2, group IVA (cytosolic, calcium-dependent)
TGFBR2	0.967	1.503	0.803	1.140	transforming growth factor, beta receptor II (70/80kDa)
TNFRSF1A	1.147	0.967	0.652	1.083	tumor necrosis factor receptor superfamily, member 1A
TNFRSF1B	0.999	0.810	0.551	0.798	tumor necrosis factor receptor superfamily, member 1B
DEDD	0.940	0.500	0.583	1.07	harakiri, BCL2 interacting protein (contains only BH3 domain)
HRK	0.499	0.735	1.405	0.696	tumor necrosis factor receptor superfamily, member 1A
TNFRSF1A	1.147	0.967	0.652	1.083	tumor necrosis factor receptor superfamily, member 1B
Traf1	1.158	0.810	0.981	1.630	TNF receptor-associated factor 1
Traf5	0.867	0.784	1.278	0.565	TNF receptor-associated factor 5
Tnfaip3	1.314	0.432	0.785	0.938	Tumor necrosis factor, alpha-induced protein 3 (Putative DNA binding protein A20)
timp3	1.086	0.673	0.498	0.806	Metalloproteinase inhibitor 3 precursor
zfp36	0.965	0.456	0.614	0.891	zinc finger protein 36, tristetraprolin

Genes filtered on confidence between biological replicates ($p<0.05$) and with expression values of either greater than 1.2 or less than 0.8333 in either *M.tb,* Cpn 60.2 or dnaK-treated cells and associated with MAP-kinase and p38 activity as determined by Ingenuity.

Table 4.c Eicosanoid Signaling

Gene	Relative Expression level per treatment				
	Phagocytosis medium	***M.tb***	**60.2**	**dnaK**	**Gene Function**
PTGFR	1.213	0.708	0.967	0.816	prostaglandin F recptor
PLA2G2D	0.852	1.883	1.612	1.156	phospholipase A2, group IID
PTGS2	0.902	0.340	1.258	1.267	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)
Pla2g4a	1.354	0.663	1.323	1.097	phospholipase A2, group IVA (cytosolic, calcium-dependent)
Pla2g4b	1.065	0.779	1.106	1.715	phospholipase A2, group IVB (cytosolic)
PTGDS	1.198	1.0162	1.265	1.299	prostaglandin D2 synthase 21kDa (brain)
PTGER4	0.542	0.832	0.653	1.464	prostaglandin E receptor 4 (subtype EP4)
PTGES	0.392	0.685	0.878	0.712	prostaglandin E synthase
PTGS2	0.902	0.339	1.258	1.267	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)
Il12b	1.067	0.520	0.528	0.278	interleukin 12B (natural kill cell stimulatory factor 2)
IL18	0.855	0.683	1.0139	1.338	interleukin 18 (interferon-gamma-inducing factor)

Genes filtered on confidence between biological replicates ($p<0.05$) and with expression values of either greater than 1.2 or less than 0.8333 in either *M.tb,* Cpn 60.2 or dnaK-treated cells and associated with Eicosanoid production and metabolism as determined by Ingenuity.

Table 4.d Apoptosis-related signaling

Gene	Relative Expression level per treatment				
	Phagocytosis medium	***M.tb***	**60.2**	**dnaK**	**Gene Function**
Fadd	1.582	0.888	0.895	0.898	Fas (TNFRSF6) -associated via death domain
Adam17	0.999	0.810	0.551	0.798	ADAM metallopeptidase domain 17
CASP7	0.948	1.239	0.461	0.799	caspase 7, apoptosis-related cysteine peptidase
CASP9	0.664	0.238	0.917	1.481	caspase 9, apoptosis-related cysteine peptidase
DAPK1	1.530	0.917	1.142	1.087	death-associated protein kinase 1
DAPK2	1.379	1.611	1.108	1.837	death-associated protein kinase 2
DEDD	0.940	0.500	0.583	1.070	death effector domain containing
HRK	0.499	0.735	1.405	0.696	harakiri, BCL2 interacting protein (contains only BH3 domain)
TNFRSF1A	1.147	0.967	0.652	1.083	tumor necrosis factor receptor superfamily, member 1A
TNFRSF1B	0.999	0.810	0.551	0.798	tumor necrosis factor receptor superfamily, member 1B
Traf1	1.158	0.784	0.981	1.630	TNF receptor-associated factor 1
Tnfaip3	1.314	0.432	0.785	0.938	Tumor necrosis factor, alpha-induced protein 3 (Putative DNA binding protein A20)
timp3	1.086	0.673	0.497	0.806	Metalloproteinase inhibitor 3 precursor
zfp36	0.965	0.456	0.615	0.890	zinc finger protein 36, tristetraprolin
Traf5	0.867	1.327	1.278	0.565	TNF receptor-associated factor 5

Genes filtered on confidence between biological replicates ($p<0.05$) and with expression values of either greater than 1.2 or less than 0.8333 in either *M.tb,* Cpn 60.2 or dnaK-treated cells and associated with Apoptosis as determined by Ingenuity.

Table 5 Confirmation of differential expression of selected genes in RNA microarray using Quantitative Reverse-Transcriptase PCR

	Phagocytosis medium				*M.tb*				Cpn 60.2			
Gene Name	**Microarray**		**q-RT-PCR**		**Microarray**		**q-RT-PCR**		**Microarray**		**q-RT-PCR**	
Common	Normalized	SE	Normalized	SE	Normalized	SE	Normalized	SE	Normalized	SE	Normalized	SE
Zfp36	0.9653	0.32	0.688	0.3496	0.456	0.107	0.7427	0.2717	0.615	0.174	1.042	0.274
Tnfrsf1b	0.9997	0.491	0.733	0.1188	0.81	0.088	1.9613	1.627	0.551	0.123	7.949	3.942
Casp7	0.9479	0.194	0.888	0.0777	1.239	0.26	1.5233	0.6386	0.461	0.1	1.338	0.084
Casp9	0.6642	0.516	0.989	0.2772	0.238	0.576	1.0773	0.5407	0.917	0.452	1.603	0.265

RNA microarray data using amplified mRNA compared to Quantitative RT-PCR data using original RNA sample. Gene expression was normalized with the average expression of three reference genes (GAPDH, 16S rRNA and β-actin) and KO expression is presented in reference to WT control. Data presented is the mean of three biological replicates.

confirmed Cpn60.2 binds with sufficient specificity to CD43 that *M.tb* bacillus binding and uptake is blocked by up to 60% in its presence [7]. Baseline differences in expression between CD43KO and CD43WT macrophages (incubated in phagocytosis medium alone) were not replicated with Q RT-PCR for ¾ genes. Trends in differential expression were replicated with Q RT-PCR in 2 out of 4 of the selected genes when CD43KO macrophages were infected with *M.tb* although none of the trends were maintained in macrophages exposed to Cpn60.2. As measured by Q RT-PCR, gene expression in CD43KO macrophages treated with Cpn 60.2 appeared to be over expressed when compared to the microarray data.

3.3.5 Investigation of specific intracellular signaling pathways using Quantitative RT-PCR

In addition to the genes that were determined to be differentially regulated in the RNA microarray, genes that were not found in the analysis but were related to the pathways of interest were examined for differential expression using Q RT-PCR. The data taken from the microarray analysis appeared to indicate a possible change in TNF-α post-transcriptional control as well as a tendency towards intrinsic apoptosis over extrinsic apoptosis in CD43 KO macrophages when compared to WT. Results from Q RT-PCR (Table 6) indicate that these trends require further investigation. When CD43KO macrophages were stimulated with *M.tb*, there appeared to be an increase in genes related to intrinsic apoptosis, although the quantity of differential expression was not determined to be statistically significant. Cpn60.2 also demonstrated similar trends for 2 of the 3 non-microarray genes.

Additional genes associated with extrinsic apoptosis also appeared to be up-regulated in CD43KO macrophages in the majority of treatments. TNF-α production appeared to be deficient in KO macrophages, but the level of differential expression was not statistically significant.

Table 6 Investigation of specific intracellular signaling pathways using Quantitative RT-PCR

	Phagocytosis medium		*M.tb*		Cpn 60.2	
Gene Name / Related Pathway	**Normalized**	**SE**	**Normalized**	**SE**	**Normalized**	**SE**
Intrinsic Apoptosis						
Bax	1.0572	0.246	1.927	0.811	0.888	0.1313
Casp9	0.9893	0.277	1.077	0.5407	1.6027	0.265
Apaf1	0.8227	0.184	1.259	0.5596	1.7437	0.3319
Extrinsic Apoptosis						
TRADD	0.8693	0.315	0.571	0.1125	1.3655	0.3765
Casp3	0.8157	0.192	1.507	0.1362	1.5583	0.5024
TNF-α production						
TNF-α	1.119	0.184	0.61	0.2312	0.8153	0.3831

Additional genes coding for proteins that had direct protein-protein interactions with the genes and pathways of interest were also investigated for differential regulation. Gene expression was normalized with the average expression of three reference genes (GAPDH, 16S rRNA and β-actin) and KO expression is presented in reference to WT control. Data is the mean of three biological replicates

3.4 Discussion and Summary

Understanding how the host cells interact with *M.tb* during their initial encounter is an important part of gaining understanding of what it takes to establish an infection. Important cytokines, proteins, receptors and their subsequent stimulatory functions such as inducing anti-microbial responses are all vital in this process. Deficiencies in pro-inflammatory cytokines such as TNF-α, IFN-γ and IL-12 have all been shown to result in increased host susceptibility to *M.tb* [132]. Phagocytes play crucial roles as initiators and directors of the immune response, both by cytokine production and antigen presentation. It is known that *M.tb* can evade many of these processes by entering the macrophage and preventing activation [152]. This can be done via binding and uptake through the complement receptors CR1, CR3 or CR4 [153]. Mannose receptor and type A scavenger receptors are also known as 'back door' entries for the bacterium because the binding of these receptors is not directly linked to an inflammatory response [154].

As previously mentioned, research in our lab has demonstrated strong binding interactions between Cpn60.2, an hsp found on the mycobacterial capsular surface, and CD43, a transmembrane glycoprotein found on macrophages [7]. Using Cpn60.2 and dnaK, another capsular hsp with weaker affinity for CD43 [7], we examined the possible changes in intracellular signaling due to CD43 stimulation with the hsps in comparison to whole bacteria to investigate how they relate to each other. Our lab has also previously determined a link between CD43, TNF-α production, control of bacterial infection and increased apoptosis upon infection with *M.tb* [132]. Given the already-known pro-inflammatory capabilities of Cpn60.2 [151], we hypothesized that CD43 stimulation by this hsp could, at least in part, be responsible for the effect of the bacterial interactions with macrophage CD43.

An RNA-microarray was performed by which RNA from bone-marrow derived murine macrophages from CD43 KO and WT mice that had been co-incubated with one of Cpn60.2, dnaK, *M.tb* or phagocytosis

medium (control) was applied to a mouse whole-genome expressed sequence tag array. The initial analysis of this gene-expression array demonstrated that the pattern of differential expression of the genome attributable to CD43 was quite different between all treatment types. This then led us to a more functionally-oriented investigation.

The exploration into differential pathway regulation demonstrated a number of interesting findings. There were many different areas of cellular function possibly regulated by CD43, several of them linked to *in vivo* and *in vitro* results found in our lab[69, 132]. Cell death, morphogenesis, cellular movement, respiratory burst and chemo-attraction were all categories that had a statistically significant number of genes differentially regulated. These areas all had physiological significance in the form of previously published observations, both from our group and others [132, 147]. Other pathways of interest that had high numbers of differentially expressed genes included eicosanoid signaling, p53 and MAPK signaling. All of these processes have been related to cellular function both in general and in reference to microbial infection and activation. Because these signaling mediators are so diversely involved in cellular functions, it is difficult to say if their differential expression is directly related to CD43 or a result of a subsequently differentially regulated process. That being said, these data should not be regarded as insignificant. The scope of this project is such that their investigation could not be conducted, but could be highly relevant to these and other physiological observations made about cells deficient in CD43.

The areas that were investigated further with quantitative RT-PCR were apoptosis and TNF-α regulation, wherein the microarray was partially validated in expression trends with the Q RT-PCR. The trends for the control phagocytosis-medium treatment were similar. Both microarray and Q RT-PCR were around one, and not significantly differentiated. However not all of the genes were consistently validated for *M.tb* and Cpn60.2. Zfp36, a gene responsible for TNF-α mRNA control was down regulated in the CD43 KO macrophages compared to the CD43 WT macrophages with both *M.tb* and

Cpn60.2 in the microarray data, but appeared to be unchanged when examined with Q RT-PCR. Tnfrsf1b had a very interesting expression profile, the microarray data inferred that it would be down regulated in Cpn60.2-incubated CD43KO macrophages but up regulated in *M.tb*-infected CD43KO macrophages. However the Q RT-PCR results demonstrated opposing effects; it appeared to be significantly up regulated in the CD43KO macrophages when stimulated with Cpn60.2 and down regulated in *M.tb* infected macrophages. Caspase 7 gave similar results for Cpn60.2 treatment; it was down regulated in the microarray and up regulated in the Q RT-PCR. In contrast, *M.tb* infected macrophages gave similar results for caspase 7 expressions in the microarray and Q RT-PCR. Caspase 9 was significantly differentially expressed in the microarray analysis of dnaK treated and *M.tb* infected samples and was included in the Q RT-PCR reactions due to its biological significance. Both *M.tb* and Cpn60.2 appear to have opposing expression levels with Q RT-PCR data when the microarray showed down regulation in *M.*tb and unchanged relative expression in Cpn 60.2, but with Q RT-PCR data, unchanged relative expression with *M.tb* and relative up regulation in Cpn60.2. It would appear that the Q-PCR validation of the microarray was inconclusive and that more differentially expressed genes should have been chosen.

The pathway-related genes however did give some interesting results in terms of biological trends. Although no differential expression was statistically significant, both Bax and Apaf1, which are key players in intrinsic apoptosis were up regulated in CD43KO mice when infected with *M.tb*. Apaf1 and Caspase 9 were up regulated in the CD43KO compared to CD43WT when stimulated with Cpn60.2. The genes that had been selected for their involvement in extrinsic apoptosis, TRADD and Tnfrsf1b, both appear to be up regulated in the CD43KO macrophages when exposed to Cpn 60.2 as well, making this story more complex than initially anticipated. TNF-α expression appears to remain higher in the CD43 WT than the CD43KO although this was not statistically significant, it would appear that this pathway could still be affected at the transcriptional level.

It would appear that the genes that had been selected involved in TNF-α production and extrinsic apoptosis appear to be predominantly in agreement with previous studies performed in our lab [132]. *M.tb* infection and CD43 deficiency appears to have a negative effect on the production of TNF-α-associated genes as well one out of the two extrinsic-apoptotic signaling genes. The previous observations made regarding the affects of CD43 lend credit to this trend, but as previously mentioned, the effects of mRNA quantity on protein production are not always directly-linked, and the significance found here may or may not be completely reflective of the biological significance of TNF-α underproduction.

The disconnect between the RNA microarray and Q RT-PCR could be due to a number of factors. The many steps of sample preparation invite a number of sources of error that cannot always be accounted for. Due to the typically low quantities of mRNA that working with primary cell-culture provides, a mRNA amplification was done to a portion of the original RNA sample for the microarray work. The rest of the RNA was stored at -80˚C until such a time that it was required for Quantitative-RT-PCR, which was at least one and a half years later. In the case of *M.tb*-infected macrophages, the RNA was more than two years old at the time of cDNA synthesis. . RNA storage at -80˚ is typically secure up to a year as long as the sample remains undisturbed however contamination of these samples would have gone unchecked after the initial bioanalyzer examination pre-RNA amplification By conventional standards, RNA that is over a year old is too old to use. The possible degradation taken place during this time makes any true verification of RNA-expression somewhat suspect, particularly in the case of the *M.tb*-infected samples.

The Q RT-PCR was also performed on cDNA that was made from original RNA sample, and not amplified RNA that was used in the microarray itself. The amplification process could have had an effect on mRNA

that was present in either very low or very high quantities, with higher concentrations of mRNA being more likely to amplify and lower concentrations being less likely to amplify.

Examination of the technical repeats of the data suggests that at the time of Q-RT-PCR, there was little to indicate errors in reproducibility within a single, aliquotted cDNA sample. That being said however, the manner in which the experiment was set-up could have been altered to lessen the probability of variation between genotypes and biological replicates. The reactions were performed in a genotype-specific manner, then normalized within the plate and compared to their other genotype-plate. Although in-plate normalizations were performed, plate to plate variations could affect the comparisons of relative expression levels. There appears to be inconsistencies between plate values for the reference genes as well as the genes of interest. The differences in gene expression for a CD43WT to CD43KO comparison would be better compared on the same plate, in order to eliminate any error due to run-to-run variation. This would also make it more apparent if a reference gene was not only affected by treatment, but genotype as well; which could be the case in this example. Three reference genes were chosen to lessen the likelihood of this effect, so that target genes could be normalized to an average expression of reference. However the second comparison, of that CD43WT to CD43KO data, could be influenced by the possible changes in expression of the reference genes per genotype.

Previously observed data from Randhawa et al demonstrated both lower amounts of apoptosis and TNF-α production in CD43KO macrophages, when infected with *M.tb* [132]. The molecular data shown here shows the disconnect that is physiologically possible between transcription of a gene, its translation into protein and the biological protein release. TNF-α is a major apoptotic signaling factor in macrophage biology and is crucial in the containment of *M.tb* infection. When TNF-α levels are hindered, either by genomic disruption or protein-inhibition, intracellular replication of *M.tb* increases significantly. This effect is returned to normal upon the addition of recombinant TNF-α. Although current Q-RT-PCR data

suggest that the TNF-α mRNA levels are not statistically significantly different between the KO and WT macrophages, the trend is in agreement with previously published data. It has already been observed *in vitro* that these results are physiologically significant to the survival of the host cell and the subsequent life cycle of the bacteria [132]. This could indicate that the significant alterations that occur are at a post-translational level, and involve other signaling enzymes such as kinases and acetylases. The post-translational modification sites for CD43 are well-documented [115, 119, 120, 145] The alternate pathways that were differentially regulated included several kinase-related pathways.

An interesting result that was found but left unexplored was the differentially-related eicoasnoid signaling. Several enzymes in the prostaglandin synthesis pathway were differentially regulated between CD43 KO and WT macrophages. Although phospholipase A2 (Pla2g2d) appeared to be up regulated in KO macrophages, subsequent enzymes such as Prostaglandin-endoperozide synthase 2 which helps break down the arachadonic acid produced by phospholipase A2, is only up regulated in Cpn60.2-treated macrophages compared to *M.tb*-infected macrophages. Additionally, prostaglandin E synthase , *ptges*, is down regulated in both Cpn60.2 treated and *M.tb*-infected CD43 KO macrophages. There have been studies that demonstrate *ptges* knockout mice are more susceptible to *M.tb* [155] , however this observation is based on the theory that the bacterium inhibits prostaglandin-E_2 mediated plasma membrane repair in the lysosome. If this mechanism disruption was a factor in CD43 KO mice, it could help to explain the observed increased necrosis in CD43 KO macrophages, as observed previously in our lab [132].

Cytoskeletal remodeling was also differentially affected between the two genotypes. Previous studies have already determined a link between CD43 deficiency and impaired binding and uptake of *M.tb* bacillus [69, 147]. Blocking of CD43 on the host surface with Cpn60.2 also prevents bacterial entry into the macrophage [7], indicating that CD43 is not only a player in cytokine production and intracellular

regulation, but in the very beginnings of bacteria-host interactions. It has not yet been determined what the link is between CD43, cytoskeletal modifications and phagocytosis but our microarray determined that there are differentially regulated genes related to these processes.

Recently, Kumar et al [156] performed a similar type of study to ours, using a genome-wide bank of siRNAs for macrophages, infecting them with *M.tb* and observing the resulting growth patterns. Several genes from their study that were up regulated by *M.tb* infection were also significantly differentially regulated in this study as well. *EMP2, SLC26A11, ST8SIA4* and *TLR8* were all up regulated in the CD43WT macrophages upon infection with *M.tb* compared to the CD43KO counterparts in the microarray performed. The investigation in the study of Kumar et al also focused on pathway-analysis, and found that autophagy is a key process in the control of intracellular replication. The aforementioned, shared genes all produce protein products that interact within the autophagy pathway, but having both inhibitory and stimulatory roles for autophagy in the cell. It was observed that *M.tb* can possibly partially control the advent of autophagy from within the cell via manipulation of intracellular signaling. Some of the aforementioned proteins, EMP2 and ST8SIA4 are down regulated in infected macrophages that are stimulated by IFN-γ, further indicating a possible role in their importance to control of intracellular infection. Autophagy and apoptosis are tightly regulated intracellular functions. The former is a signal for the cell to begin 'digesting itself', usually instigated in times of severe cell stress and nutrient-deprivation, whereas the latter, apoptosis, is also a path which the cell controls from within, initiating the dismantling of intracellular structures within a highly organized procedure. It is clear to see that both of these processes would be detrimental to the successful replication of *M.tb* bacillus within its host macrophage niches, and therefore must be managed in some way. The inability to carry out either of these functions could very possibly be detrimental to the chances of survival for the host cell and certainly result in a less than optimal control of infection.

4 Conclusions and future directions

4.1 Conclusions

Mycobacterium tuberculosis is the etiological agent of TB, an infection that has plagued mankind for centuries. It is capable of evading host defenses without any initial detrimental effects to host or pathogen, enabling successful intracellular replication and efficient dissemination. Although the advent of antimicrobial treatments gave hope to the millions of sufferers worldwide, it is evident that none of these treatments is without weakness, and drug-resistance is a common phenomenon [55]. The best prophylaxis for infection that we have is the vaccine BCG. The efficacy of this vaccine has been documented to be inconsistent: it varies from 0% to 80%[157] [31-33]. Most disturbingly, it shows the least protection in equatorial climes, inhabited by people who need protection from *M.tb* the most [40]. The main reasons for this effect are predominantly related to cross-antigen reactivity with environmental mycobacteria, which are more prevalent in southern climes. The already primed immune system easily kills the attenuated *Mycobacterium bovis*, BCG, (thus compromising its efficacy) but is still ineffectual against the more pathogenic *Mycobacterium tuberculosis.* Subsequent infection with *M.tb* ensues and the immune system is only activated enough to simply contain the infection at the latent stage, offering no protection from the re-activation that commonly occurs with age and infirmity.

Additional vaccines have been developed as 'booster' shots, to further prime the immune system and initiate stronger activation responses. Subunit and DNA-based vaccines are in the forefront of this field, using highly antigenic *M.tb*-specific proteins. These vaccines are intended to both further stimulate the host immune response as well as generate a more species-specific defense. Mycobacterial HSPs such as Cpn60.2, ESAT-6 and 85kDa are common players in these studies. Fusion proteins of one or more of these HSPs are regularly developed and tested for improved efficacy. T-cell responses vary depending

on the stimulus used, and it has been surmised that gaining the appropriate balance of CD4+ and CD8+ T-cell response with a vaccine could be the key to attaining effective prophylaxis [40].

The intricate interactions between *M.tb* and the host immune system over the course of a possible life-long infection present a unique challenge in terms of improving the host immune response. The ability of *M.tb* to survive and manipulate the adaptive and cell-mediated sides of immunity demonstrates a need to better understand these interactions, so that we may eventually be able to use them to the host advantage. Understanding the initial macrophage-host interaction is key to finding the mediating factors that can control the balance of power between the host and pathogen. The research presented here is an investigation into the possible role of macrophage CD43 in the regulation of the host response to *M.tb* infection and to bacterial HSPs located on the cell surface.

Previously published results show both the ability of Cpn 60.2 and dnaK to demonstrate immunomodulatory functions [151, 158] as well as evidence suggesting a prominent role of CD43 in *M.tb*-macrophage association and mediation of bacterial growth [7, 72, 132, 147]. Additional studies demonstrated binding of Cpn 60.2 and dnaK to the CD43 extracellular domain and the ability of exogenous Cpn 60.2 to significantly block the binding and uptake of bacteria by CD43 WT macrophages [7]. This was of interest because it provided possible evidence for a direct ligand-receptor signaling mechanism of CD43 within *M.tb* infection.

The purpose of this current study was to determine if Cpn 60.2 or dnaK were either entirely or partially responsible for mediating the cellular responses previously observed *in vitro* between *M.tb* and CD43 WT macrophages versus CD43 KO macrophages and to determine other possible functions of CD43 when stimulated by mycobacterial ligands. These responses included differential cytokine responses and bacterial binding and uptake, which could involve a number of possible areas of cellular control. To gain a broader understanding of the intracellular differences between CD43 KO and WT

macrophages, we performed an RNA microarray on mRNA isolated from CD43 KO and WT BMDMϕ that had been either infected with *M.tb* or co-incubated with one of Cpn 60.2 or dnaK. The differential expression was then examined between WT and KO for each treatment, and expression profiles of KO macrophages were compared between treatments. Results from this study showed that there were a great number of transcriptional differences between WT and KO macrophages as a whole, despite CD43 KO mice being typically described as phenotypically unremarkable in a passive, unstimulated state [145]. There were more differences than similarities between *M.tb* and either HSP in the expression profiles they induced. However a number of shared functional categories and signaling pathways were elucidated. CD43 deficiency combined with bacterial ligand stimulation led to differential regulation of a variety of areas of cellular regulation including intracellular signaling molecules such as p53/MapK, cytoskeletal maintenance, eicosanoid production, TNF-α production and apoptosis.

Previously published *in vitro* results [132, 147] implicated CD43 has a strong affect on apoptosis and TNF-α production and so the latter two categories were chosen for further investigation using quantitative RT-PCR. In terms of differential change of gene expression between CD43 KO and CD43WT macrophages, the data obtained lacks statistical significance. It would appear, however, that some of the trends that were observed in the microarray are supported by the Q RT-PCR, although not for all treatments. This is somewhat anticipated, because both Cpn 60.2 and dnaK have different cytokine expression profiles and binding affinity for CD43 and *M.tb* is clearly more likely to induce greater transcriptional changes than a single purified protein.

The Q RT-PCR results were not entirely consistent with the microarray results. Gene expression (as measured by Q RT-PCR) was not consistently differentially regulated between Cpn60.2 and *M.tb,* and expression values did not entirely reflect those of the microarray. However, additional genes from implicated pathways were investigated and these results demonstrated trends that indicated some of

the observed pathways are directly affected by the loss of CD43. Intrinsic apoptotic signaling and TNF-α production both demonstrate trends and, as previously mentioned, the statistical insignificance in differential mRNA levels between CD43KO and CD43WT macrophages could indicate that the significant alterations that occur are at a post-translational level, and involve other signaling enzymes. As mentioned additionally in the discussion, there were a number of unexplored pathways that showed promise as CD43-related factors. These findings however, would have to be verified using additional tests at either RNA or protein levels, but using fresher samples, with an altered study set-up.

The results presented indicate that CD43 is capable of inducing changes in intracellular signaling which control a variety of cellular functions. Stimulation of its extracellular domain with *Mycobacterium tuberculosis* and mycobacterial proteins induce a variety of responses, some of which have been closely connected to *in vitro* observed results. Not surprisingly, there is no known single pathway to infection protection from *M.tb.* It has a unique and complex relationship with its host, but through this study and similar investigations, these pathways might be elucidated and their connections employed for the benefit of the host.

4.2 Future directions

The body of this work examines the initial steps of intracellular change upon infection. There is some *in vitro*, *in vivo* and protein-level work previously done involving CD43 and *Mycobacterium tuberculosis*, that shows CD43 deficiency results in reduced bacterial binding and uptake and reduced pro-inflammatory cytokine production leading to increased intracellular replication of the bacterium *in vitro* and increased bacterial load of the organs *in vivo* [72, 132]. Cpn60.2 and dnaK from *Mycobacterium tuberculosis* both have been shown to bind the extracellular portion of CD43, and the co-incubation of CD43WT macrophages with recombinant Cpn 60.2 can partially block *M.tb* tuberculosis in a dose-

dependent manner [7]. This study has demonstrated the capability of Cpn60.2 to initiate changes in the transcriptional response of CD43 WT and KO macrophages, but in order to determine physiological significance, these interactions should also be validated on a protein-level. It is still not entirely clear if Cpn60.2 is also capable of affecting TNF-α production via CD43 stimulation. Even though the RNA microarray and Q RT-PCR indicated post-translational trends that support this contention, these changes were not statistically significant and their impact on protein production and release (in terms of CD43-related TNF-α) is not yet known. Because of its broad-ranging immunostimulatory nature, TNF-α has a tightly-regulated production pathway. More genes involved in this production pathway, both those found in the microarray study and those not, could be examined using Q RT-PCR. Adam17, TIMP3 and tnfaip3 were all differentially expressed in the microarray and are closely involved with TNF-α production. It would be interesting to see if the production of any of these proteins was highly deregulated due to CD43 disruption, and contribute to the understanding of how CD43 and TNF-α are linked during macrophage activation.

Since it had been previously demonstrated that CD43 deficiency resulted in reduced TNF-α production as well as reduced apoptosis and increased levels of necrosis *in vitro* [132] only apoptosis and TNF-α were further examined in this study. Other affected signaling pathways, such as prostaglandin synthesis, and MAPK activation have previously been shown to also have important roles in *M.tb* infection, affecting cytokine production, plasma membrane stability and endosome function [155]. Our group observed that the lack of CD43-mediated TNF-α production resulted in increased mycobacterial growth, decreased apoptosis and increased necrosis [132]. Divangahi et al showed that lack of prostaglandin E_2 (PGE_2) prevents membrane repair and induces necrosis. Their study investigated the ability of virulent *M.tb* to down regulate PGE_2 leading to the result of increased necrosis and decreased apoptosis. It is possible that there is a similar link in CD43KO mice, with decreased PGE_2 production, leading to the increased necrosis that was previously observed by Randhawa et al [132]. Our Q RT-PCR

data showed an elevated level of caspase 3 mRNA in CD43KO macrophages when infected with *M.tb* or co-incubated with Cpn60.2. Although Randhawa et al found relatively decreased caspase 3 activity, these findings should be validated further, through additional Q RT-PCR experiments using more recent samples and perhaps involving increased Cpn60.2 concentrations. Another caspase 3 activity assay could also be performed, using both *M.tb* infection and Cpn60.2 co-incubation as stimuli for apoptotic activities. It would be interesting to investigate the link between differential caspase 3 mRNA production, protein production and activity in CD43KO macrophages versus CD43WT. The possible link between prostaglandin and necrosis could be further investigated by looking at the potential differential levels of prostaglandin production within these two genotypes in relation to the differential levels of apoptosis during *M.tb* infection and Cpn60.2 stimulation using ELISA.

Cytoskeletal remodeling was also differentially affected between the two macrophage genotypes. Previous studies have already determined a link between CD43 deficiency and impaired binding and uptake of *M.tb* bacillus. Blocking of CD43 on the host surface with Cpn60.2 also prevents bacterial entry into the macrophage, indicating that CD43 is not only a player in cytokine production and intracellular regulation, but in the very beginnings of bacteria-host interactions. It has not yet been determined what the link is between CD43, bacterial binding, cytoskeletal modifications and phagocytosis. A simple assay that could be done to investigate the possible cytoskeletal defects in CD43KO mice would be a mobility assay involving CD43KO and CD43WT macrophages: investigating their ability to move towards a chemo attractant while adhered on a solid surface. Latex beads are also commonly used in studies involving phagocytes; to investigate the ability of CD43KO macrophages to phagocytose latex beads, coating the beads in different proteins, such as Cpn60.2 or dnaK to improve or impair binding could also be performed.

Similarly, a number of genes found to be statistically differentially regulated in our study have been linked to the results of other groups interested in host-macrophage interactions with *M.tb*. As previously mentioned, Kumar et al [156] have recently made a case for the importance of autophagy in the control of *M.tb* infection and replication. This pathway involves cytoskeletal remodeling as well as a significant involvement of intracellular signaling molecules (due to tight internal regulation). It is feasible to further investigate the differential expression of the genes that are commonly shared between the two studies, to fully explore the possibility of a link between these observations. Q RT-PCR analysis on EMP2, SLC26A11, ST8SIA4 and TLR8 to verify possible differential expression between CD43KO and CD43WT would be a good starting point to investigate the possible links between these two studies.

Lastly, it has yet to be determined if the observed differential changes in mRNA expression mediated by CD43 are a result of its functionality as a single signaling molecule, or its possible work in conjunction with an adapter protein. The concentrations of recombinant Cpn60.2 and dnaK used to elucidate transcriptional response (5 μg/ml) were sufficient to block bacterial binding and uptake [7], but not to produce optimal cytokine response previously observed with Cpn60.2 (10μg/ml) [151]. That being said, differential responses between CD43KO and CD43WT macrophages were observed and several genes relating to apoptosis were shared in expression levels in the Q RT-PCR data. The intracellular tail of CD43 has the capacity to maintain a phosphorylation or ubiquitin signal, but has no known kinase activity of its own. It is possible that it works in conjunction with additional adaptor proteins. More detailed work involving CD43-binding moieties (such as Cpn60.2) and macrophages at the protein-level could further deduce the roles of CD43 as a possible receptor on its own or as a partner in a larger intracellular signaling network. The data provided indicates many possible CD43 interactions previously unconsidered. Although CD43KO mice appear to be normal, their ability to regain and maintain homeostasis appears altered. An investigation with differential dosage of Cpn60.2 and *M.tb* infection could be performed, using the two known stimulatory concentrations (5 and 10μg/ml) of Cpn60.2, *M.tb*

infections with normalized quantities of bacteria (MOI of 20:1 for CD43WT and 30:1 for CD43KO) looking at specific cellular functions of interest such as apoptotic activity, as previously described. Transfection of CD43KO macrophages with CD43 that has had an altered intracellular tail could determine if the regions of phosphorylation (Ser76 for example, [159]) are necessary for specific cellular functions or not.

Additional experiments that would give strength to these findings might include additional quantitative RT-PCR experiments using RNA that has not been in storage for so long, and altering the plate setup to accommodate both sets of comparison data on a single plate, to minimize variation. Since the microarray that was performed was a direct comparison of CD43WT and CD43KO gene expression, it would be prudent to include both genotypes on a single plate, as well as space enough to include a small dilution-set to measure PCR efficiency with each run. Using the REST program, gene concentration is calculated using PCR efficiency first then the relative expression is calculated by the differences in concentrations. Calculations using this method would be more accurate (per plate) if a separate PCR efficiency was performed in each instance. Although this would reduce the number of genes examined per experiment, the data gained from these changes would be more reliable.

Many studies have demonstrated an important role of the macrophage in *M.tb* infection. It is the first cell to encounter *M. tuberculosis*, the first line of direct defense, and the first cell to initiate the cytokine cascade. The ability to produce an appropriate cytokine response is crucial for the activation as well as infiltration of incoming immune cells to the site of infection. Furthermore, the ability to appropriately regulate tissue homeostasis with functions such as autophagy and apoptosis is vital for gaining the upper hand and controlling intracellular replication. It has been shown that CD43 has multiple possible roles in this process, and is potentially important for macrophage function in the state of infection. Understanding the factors that impact host-response in *M.tb* infection is imperative in developing novel

prophylactic treatments. Species-specific stimulation of immunity can be improved by knowing more about the factors of stimulation and cell activation from within the immune system as well as the bacterial interactions.

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Supplementary Table 1. Statistically significant, differentially regulated genes in the incubation medium microarray analysis

	Normalized Expression					
Common	**Incubation Medium (protein-incubation)**	**Incubation Medium (infection)**	***M.tb***	**60.2**	**dnaK**	**Description**
Jam4	0.775	0.807	1.275	0.841	0.591	cell adhesion molecule JCAM; immunoglobulin superfamily, member 5. [Source:RefSeq;Acc:NM_028078]
Comt	0.802	2.348	1.15	1.068	0.766	Catechol O-methyltransferase, membrane-bound form (EC 2.1.1.6) (MB- COMT) [Contains: Catechol O-methyltransferase, soluble form (S-COMT)]. [Source:Uniprot/SWISSPROT;Acc:O88587]
Dbt	0.586	1.316	0.922	1.194	0.834	Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial precursor (EC 2.3.1.168) (Dihydrolipoyllysine-residue (2-methylpropanoyl)transferase) (E2) (Dihydrolipoamide branched chain transacylase) (BCKAD E2 subunit). [Source:Uniprot/SWISSPROT;Acc:P53395]
Mkrn2	0.679	0.954	1.528	1.014	1.076	Makorin 2. [Source:Uniprot/SWISSPROT;Acc:Q9ERV1]
Grasp	1.744	1.485	1.627	1.062	1.03	GRP1 (general receptor for phosphoinositides 1)-associated scaffold protein; GRP1-associated scaffold protein. [Source:RefSeq;Acc:NM_019518]
C1d	0.673	0.825	1.08	0.888	1.33	nuclear DNA-binding protein; C1D protein; small unique nuclear co-repressor. [Source:RefSeq;Acc:NM_020558]
Cd52	0.547	1.633	1.387	0.989	1.906	CAMPATH-1 antigen precursor (CD52 antigen) (Lymphocyte differentiation antigen B7). [Source:Uniprot/SWISSPROT;Acc:Q64389]
Luzp1	0.764	1.38	1.169	1.106	0.658	leucine zipper protein 1. [Source:RefSeq;Acc:NM_024452]
Slc13a2	2.193	0.621	0.658	0.961	0.995	Solute carrier family 13, member 2 (Renal sodium/dicarboxylate cotransporter) (Na()/dicarboxylate cotransporter 1) (NaDC-1). [Source:Uniprot/SWISSPROT;Acc:Q9ES88]
Agpat3	0.738	1.812	1.096	1.165	0.957	1-acylglycerol-3-phosphate O-acyltransferase 3. [Source:RefSeq;Acc:NM_053014]
Lsr	1.505	1.113	0.626	1.289	1.393	liver-specific bHLH-Zip transcription factor; Lisch7 protein. [Source:RefSeq;Acc:NM_017405]
Gramd1a	1.31	0.608	0.639	1.261	0.853	GRAM domain containing 1A
Cyp51	2.268	0.954	1.1	0.998	0.825	cytochrome P450, 51.
Itfg2	1.776	1.117	1.233	1.012	0.995	integrin alpha FG-GAP repeat containing 2
Coasy	1.464	1.213	1.121	1.259	1.135	Bifunctional coenzyme A synthase (CoA synthase) [Includes: Phosphopantetheine adenylyltransferase (EC 2.7.7.3) (Pantetheine- phosphate adenylyltransferase) (PPAT) (Dephospho-CoA pyrophosphorylase); Dephospho-CoA kinase (EC 2.7.1.24) (DPCK)

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Vwf	1.645	1.346	1.134	1.326	1.173	von Willebrand factor. [Source:RefSeq;Acc:NM_011708]
Supt6h	2.772	0.035	0.576	0.736	1.315	suppressor of Ty 6 homolog. [Source:RefSeq;Acc:NM_009297]
Narfl	0.731	0.851	0.951	0.984	0.969	nuclear prelamin A recognition factor-like. [Source:RefSeq;Acc:NM_026238]
Tmem143	0.537	1.087	1.238	0.62	1.191	transmembrane protein 143; synonyms: AI481604, 2310076O21Rik; Mus musculus transmembrane protein 143 (Tmem143), mRNA.
Btbd6	1.449	1.251	1.052	0.992	1.139	BTB/POZ domain containing protein 6. [Source:Uniprot/SWISSPROT;Acc:Q8K2J9]
Prkar2a	0.545	0.831	1.03	0.949	0.8	cAMP-dependent protein kinase type II-beta regulatory chain (Fragment). [Source:Uniprot/SWISSPROT;Acc:P31324]
Cyp17a1	1.382	0.747	0.907	0.805	0.885	Cytochrome P450 17A1 (EC 1.14.99.9) (CYPXVII) (P450-C17) (P450c17) (Steroid 17-alpha-hydroxylase/17,20 lyase). [Source:Uniprot/SWISSPROT;Acc:P27786]
expressed sequence AI413414 (AI413414)	1.73	2.38	1.563	1.205	0.617	expressed sequence AI413414 (AI413414)
Cp	1.478	0.486	0.666	0.934	1.341	Ceruloplasmin precursor (EC 1.16.3.1) (Ferroxidase). [Source:Uniprot/SWISSPROT;Acc:Q61147]
Brd8	1.438	0.749	1.275	1.068	1.052	bromodomain containing 8. [Source:RefSeq;Acc:NM_030147]
Fancl	0.724	1.295	1.07	1.098	0.955	Ubiquitin ligase protein PHF9 (EC 6.3.2.-) (Proliferation of germ cells protein). [Source:Uniprot/SWISSPROT;Acc:Q9CR14]
Rpgrip1	0.726	1.563	0.902	0.819	0.749	X-linked retinitis pigmentosa GTPase regulator-interacting protein 1 (RPGR-interacting protein 1).
Dlst	1.624	0.975	1.182	0.676	0.913	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex). [Source:RefSeq;Acc:NM_030225]
Pgf	0.687	1.103	1.056	1.315	0.918	Placenta growth factor precursor (PlGF). [Source:Uniprot/SWISSPROT;Acc:P49764]
Grap	0.684	1.776	0.908	1.008	1.029	GRB2-related adaptor protein. [Source:RefSeq;Acc:NM_027817]
Prdx2	0.733	1.191	1.163	0.962	1.171	Peroxiredoxin 2 (EC 1.11.1.-) (Thioredoxin peroxidase 1) (Thioredoxin- dependent peroxide reductase 1) (Thiol-specific antioxidant protein) (TSA). [Source:Uniprot/SWISSPROT;Acc:Q61171]
Polr2a	0.616	2.04	1.772	1.269	0.906	DNA-directed RNA polymerase II largest subunit

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
RIP3_MOUSE	2.401	1.598	0.447	1.653	0.529	Rho-interacting protein 3 (p116RIP) (RIP3). [Source:Uniprot/SWISSPROT;Acc:P97434]
Fcer2a	0.349	1.187	1.228	1.382	1.119	Low affinity immunoglobulin epsilon Fc receptor (Lymphocyte IGE receptor) (Fc-epsilon-RII) (CD23). [Source:Uniprot/SWISSPROT;Acc:P20693]
Pvalb	2.426	1.276	1.379	0.456	1.16	Parvalbumin alpha. [Source:Uniprot/SWISSPROT;Acc:P32848]
Ranbp1	0.803	1.034	1.139	1.124	1.048	Ran-specific GTPase-activating protein (Ran binding protein 1) (RANBP1). [Source:Uniprot/SWISSPROT;Acc:P34022]
Mmp8	1.497	1.12	1.113	0.893	1.121	Neutrophil collagenase precursor (EC 3.4.24.34) (Matrix metalloproteinase-8) (MMP-8) (Collagenase 2). [Source:Uniprot/SWISSPROT;Acc:O70138]
Nr2c2	1.296	1.061	0.496	1.114	0.858	Orphan nuclear receptor TR4 (Orphan nuclear receptor TAK1). [Source:Uniprot/SWISSPROT;Acc:P49117]
Otx1	0.465	0.851	2.286	1.353	1.755	Homeobox protein OTX1. [Source:Uniprot/SWISSPROT;Acc:P80205]
Dnase1	2.511	1.167	0.798	0.457	0.795	Deoxyribonuclease I precursor (EC 3.1.21.1) (DNase I). [Source:Uniprot/SWISSPROT;Acc:P49183]
Eps8l1	0.6	1.31	0.653	0.682	1.47	epidermal growth factor receptor pathway substrate 8-like protein 1. [Source:RefSeq;Acc:NM_026146]
Pak6	2.225	1.467	1.202	1.097	0.811	p21 (CDKN1A)-activated kinase 6
Herpud2	1.203	1.215	1.271	1.05	0.976	HERPUD family member 2
Mgst1	0.66	1.334	1.308	0.81	1.103	Microsomal glutathione S-transferase 1 (EC 2.5.1.18) (Microsomal GST- 1) (Microsomal GST-I). [Source:Uniprot/SWISSPROT;Acc:Q91VS7]
Hipk1	1.265	1.006	0.947	0.971	0.524	Homeodomain-interacting protein kinase 1 (EC 2.7.1.-). [Source:Uniprot/SWISSPROT;Acc:O88904]
Apobec3	1.59	1.21	0.803	0.75	1.415	DNA dC->dU editing enzyme APOBEC-3 (EC 3.5.4.-) (Apolipoprotein B editing complex 3) (Arp3) (CEM15) (CEM-15). [Source:Uniprot/SWISSPROT;Acc:Q99J72]
Ccdc109a	2.247	1.278	0.939	0.966	0.71	PREDICTED: similar to chromosome 10 open reading frame 42 (LOC215999)
BY749370	1.894	0.715	0.684	0.578	2.45	hypothetical protein
Wnt2	0.66	1.072	1.138	0.771	0.96	Wnt-2 protein precursor (IRP protein) (INT-1 related protein). [Source:Uniprot/SWISSPROT;Acc:P21552]
BC048079	0.619	1.135	1.36	1.17	0.795	hypothetical protein
ENSMUSG00000011263	2.715	0.511	1.231	0.46	0.516	hypothetical protein
BC040201	0.511	0.914	1.16	1.338	1.195	hypothetical protein

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Q9D2E9	1.779	0.609	0.864	0.904	2.028	hypothetical protein
Slc41a1	1.77	0.931	0.64	0.893	0.713	solute carrier family 41, member 1. [Source:RefSeq;Acc:NM_173865]
Pten	1.646	0.992	0.983	0.98	0.966	Phosphatidylinositol-3,4,5-trisphosphate 3-phosphatase PTEN (EC 3.1.3.67) (Mutated in multiple advanced cancers 1). [Source:Uniprot/SWISSPROT;Acc:O08586]
Q9DA53	0.547	0.745	0.759	0.858	1.137	hypothetical protein
Pax5	1.883	0.988	1.569	2.691	0.928	Paired box protein Pax-5 (B-cell specific transcription factor) (BSAP). [Source:Uniprot/SWISSPROT;Acc:Q02650]
Mrps25	0.689	1.198	1.141	1.229	1.785	Mitochondrial 28S ribosomal protein S25 (S25mt) (MRP-S25). [Source:Uniprot/SWISSPROT;Acc:Q9D125]
Hoxa2	1.608	0.903	1.451	1.483	0.746	Homeobox protein Hox-A2 (Hox-1.11) (Hox1.11). [Source:Uniprot/SWISSPROT;Acc:P31245]
Pdcd2	1.451	0.982	1.226	1.105	1.054	Programmed cell death protein 2 (Zinc finger protein Rp-8). [Source:Uniprot/SWISSPROT;Acc:P46718]
AK131125	1.565	1.71	0.8	1.274	0.638	hypothetical protein
ENSMUSG00000014786	0.36	0.238	0.822	1.552	0.868	hypothetical protein
ENSMUSG00000015002	1.499	0.161	0.968	0.28	0.858	hypothetical protein
Hmgb3	1.289	0.793	0.912	0.93	0.968	High mobility group protein 4 (HMG-4) (High mobility group protein 2a) (HMG-2a). [Source:Uniprot/SWISSPROT;Acc:O54879]
Zdhhc12	0.762	1.029	0.957	0.854	1.083	Zinc finger DHHC domain containing protein 12. [Source:Uniprot/SWISSPROT;Acc:Q8VC90]
ENSMUSG00000015542	0.705	0.963	1.337	1.296	1.384	hypothetical protein
Nkx2-5	0.547	0.8	1.043	0.728	0.866	Homeobox protein Nkx-2.5 (Homeobox protein NK-2 homolog E) (Cardiac- specific homeobox) (Homeobox protein CSX). [Source:Uniprot/SWISSPROT;Acc:P42582]
Dgat2l3	0.495	0.718	0.621	0.275	1.206	diacylglycerol O-acyltransferase 2-like 3
ENSMUSG00000016082	1.601	1.191	1.115	1.267	1.126	hypothetical protein
Lonrf3	0.608	0.995	1.342	1.36	1.664	ring finger protein 127
Matn4	1.227	0.597	0.73	0.788	0.586	Matrilin-4 precursor (MAT-4). [Source:Uniprot/SWISSPROT;Acc:O89029]
Eef1a2	1.371	0.891	0.411	1.277	1.633	Elongation factor 1-alpha 2 (EF-1-alpha-2) (Elongation factor 1 A-2) (eEF1A-2) (Statin S1). [Source:Uniprot/SWISSPROT;Acc:P27706]
Q9CZJ0	2.17	0.257	0.642	1.158	1.148	hypothetical protein
XM_149454	0.692	1.531	0.927	1.343	1.041	PREDICTED: RIKEN cDNA 1700042G07 gene (1700042G07Rik)

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Exosc10	1.222	0.926	0.854	1.159	0.58	Polymyositis/scleroderma autoantigen 100 kDa (Autoantigen PM/Scl 2) (P100 polymyositis-scleroderma overlap syndrome associated autoantigen homolog). [Source:Uniprot/SWISSPROT;Acc:P56960]
Nek8	1.606	0.621	1.279	1.173	0.818	Serine/threonine-protein kinase Nek8 (EC 2.7.1.37) (NimA-related protein kinase 8). [Source:Uniprot/SWISSPROT;Acc:Q91ZR4]
Akap1	0.447	0.813	1.01	0.911	0.982	A kinase anchor protein 1, mitochondrial precursor (Protein kinase A anchoring protein 1) (PRKA1) (Dual specificity A-Kinase anchoring protein 1) (D-AKAP-1) (Spermatid A-kinase anchor protein) (S-AKAP). [Source:Uniprot/SWISSPROT;Acc:O08715]
6330403K07Rik	1.616	2.049	1.363	2.009	0.765	UGS148 protein. [Source:RefSeq;Acc:NM_134022]
Ncor1	1.539	1.129	0.929	1.004	0.92	Nuclear receptor corepressor 1 (N-CoR1) (N-CoR) (Retinoid X receptor interacting protein 13) (RIP13). [Source:Uniprot/SWISSPROT;Acc:Q60974]
Slc2a4	0.713	1.065	1.521	0.588	1.098	Solute carrier family 2, facilitated glucose transporter, member 4 (Glucose transporter type 4, insulin-responsive) (GT2). [Source:Uniprot/SWISSPROT;Acc:P14142]
Zfpn1a1	0.659	1.126	0.768	1.159	1.12	DNA-binding protein Ikaros (Lymphoid transcription factor LyF-1). [Source:Uniprot/SWISSPROT;Acc:Q03267]
Smyd4	2.17	1.039	0.695	1.145	0.566	SET and MYND domain containing 4. [Source:RefSeq;Acc:NM_177009]
Tm4sf5	0.701	0.569	1.022	0.89	1.167	transmembrane 4 superfamily member 5. [Source:RefSeq;Acc:NM_029360]
Slc35b4	1.264	0.951	0.928	1.057	1.171	solute carrier family 35, member B4 (Slc35b4)
Trip10	0.463	0.995	0.618	1.035	0.665	thyroid hormone receptor interactor 10; Cdc42 interacting protein-4. [Source:RefSeq;Acc:NM_134125]
Slc6a8	1.367	0.876	1.242	1.031	1.01	solute carrier family 6 (neurotransmitter transporter, creatine), member 8; creatine transporter. [Source:RefSeq;Acc:NM_133987]
ENSMUSG00000019770	1.737	1.578	1.12	1.046	1.34	PREDICTED: similar to nesprin 1 isoform longer; synaptic nuclei expressed gene 1; nesprin 1; enaptin (LOC432424)
Trdn	2.631	0.972	0.715	0.273	1.153	Cardiac triadin isoform 3. [Source:Uniprot/SPTREMBL;Acc:Q8VIN7]
1700021F05Rik	0.557	1.173	0.817	1.041	1.268	hypothetical protein LOC67851
Ppil6	1.777	5.461	1.487	0.289	1.023	2900084F20Rik protein (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase).
Dcbld1	1.424	0.951	0.598	1.159	1.199	discoidin, CUB and LCCL domain containing 1. [Source:RefSeq;Acc:NM_025705]

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Ros1	2.321	0.992	0.913	1.105	0.448	Ros1 proto-oncogene. [Source:RefSeq;Acc:NM_011282]
Ube2d1	0.721	0.892	0.971	0.905	0.858	Ubiquitin-conjugating enzyme E2-17 kDa 1 (EC 6.3.2.19) (Ubiquitin- protein ligase) (Ubiquitin carrier protein) (E2(17)KB 1). [Source:Uniprot/SWISSPROT;Acc:P61080]
Tmpo	0.716	1.627	0.675	0.841	1.578	Lamina-associated polypeptide 2 isoforms beta/delta/epsilon/gamma (Thymopoietin isoforms beta/delta/epsilon/gamma) (TP beta/delta/epsilon/gamma). [Source:Uniprot/SWISSPROT;Acc:Q61029]
Epb4.1l2	0.739	2.119	1.615	0.908	0.923	Band 4.1-like protein 2 (Generally expressed protein 4.1) (4.1G). [Source:Uniprot/SWISSPROT;Acc:O70318]
ENSMUSG00000020069	0.647	0.887	1.032	1.077	1.159	PREDICTED: similar to heterogeneous nuclear ribonucleoprotein H3 isoform a (LOC432467)
Ddit4	0.584	0.856	0.523	0.707	0.968	HIF-1 responsive RTP801; dexamethasone-induced gene 2. [Source:RefSeq;Acc:NM_029083]
ENSMUSG00000020177	2.441	1.347	0.532	1.3	0.664	hypothetical protein
Mpg	0.554	1.017	0.829	0.962	1.176	DNA-3-methyladenine glycosylase (EC 3.2.2.21) (3-methyladenine DNA glycosidase) (ADPG) (3-alkyladenine DNA glycosylase) (N-methylpurine- DNA glycosirase). [Source:Uniprot/SWISSPROT;Acc:Q04841]
4930524B15Rik	1.907	2.058	0.975	0.796	0.308	hypothetical protein LOC67592
Cpeb4	1.564	0.973	0.982	0.94	1.023	cytoplasmic polyadenylation element binding protein 4
Acsl6	0.696	0.903	0.851	1.107	1.074	Long-chain-fatty-acid--CoA ligase 6 (EC 6.2.1.3) (Long-chain acyl-CoA synthetase 6) (LACS 6). [Source:Uniprot/SWISSPROT;Acc:Q91WC3]
Kremen	0.553	1.672	1.037	1.903	0.82	Kremen protein 1 precursor (Kringle-containing protein marking the eye and the nose) (Dickkopf receptor). [Source:Uniprot/SWISSPROT;Acc:Q99N43]
Nefh	0.472	0.814	1.206	0.937	0.753	Neurofilament triplet H protein (200 kDa neurofilament protein) (Neurofilament heavy polypeptide) (NF-H). [Source:Uniprot/SWISSPROT;Acc:P19246]
4921536K21Rik	1.56	1.168	0.911	0.488	0.478	hypothetical protein LOC67430

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Patz1	1.671	1.208	0.871	0.686	1.339	zinc finger protein 278; transcription factor (MAZ-related) MAZR; POZ-AT hook-zinc finger protein. [Source:RefSeq;Acc:NM_019574]
2810021J22Rik	1.462	0.66	1.561	1.095	0.781	hypothetical protein LOC69944
Arsg	1.717	0.318	0.646	0.353	1.029	Arylsulfatase G
Rnaseh1	1.433	1.832	0.868	1.118	0.892	Ribonuclease H1 (EC 3.1.26.4) (RNase H1). [Source:Uniprot/SWISSPROT;Acc:O70338]
Dus4l	0.532	1.024	1.086	0.599	0.793	protein similar to E.coli yhdg and R. capsulatus nifR3. [Source:RefSeq;Acc:NM_028002]
Klf11	0.722	1.664	1.316	0.983	1.037	Transforming growth factor-beta-inducible early growth response protein 3 (TGFB-inducible early growth response protein 3) (TIEG-3) (TGFB-inducible early growth response protein 2b). [Source:Uniprot/SWISSPROT;Acc:Q8K1S5]
Ccl11	0.381	1.358	0.499	1.604	1.041	Eotaxin precursor (Small inducible cytokine A11) (CCL11) (Eosinophil chemotactic protein). [Source:Uniprot/SWISSPROT;Acc:P48298]
Nf1	1.576	0.875	0.893	0.888	1.27	Neurofibromin (Neurofibromatosis-related protein NF-1). [Source:Uniprot/SWISSPROT;Acc:Q04690]
1700012C15Rik	1.572	0.936	0.971	1.131	0.83	hypothetical protein LOC76390
Aanat	0.698	2.309	0.753	0.904	2.636	Serotonin N-acetyltransferase (EC 2.3.1.87) (Aralkylamine N- acetyltransferase) (AA-NAT) (Serotonin acetylase). [Source:Uniprot/SWISSPROT;Acc:O88816]
Mfsd11	0.723	1.068	1.005	0.935	1.159	major facilitator superfamily domain containing 11
Hoxb9	1.88	0.865	0.958	1.159	0.699	Homeobox protein Hox-B9 (Hox-2.5). [Source:Uniprot/SWISSPROT;Acc:P20615]
1500010J02Rik	1.536	1.599	0.994	1.262	1.321	hypothetical protein LOC68964 isoform a
Stat5b	1.488	1.313	1.043	1.029	0.92	Signal transducer and activator of transcription 5B. [Source:Uniprot/SWISSPROT;Acc:P42232]
Gstz1	1.4	1.132	0.92	0.852	0.832	Maleylacetoacetate isomerase (EC 5.2.1.2) (MAAI) (Glutathione S- transferase zeta 1) (EC 2.5.1.18) (GSTZ1-1). [Source:Uniprot/SWISSPROT;Acc:Q9WVL0]
D12Ertd551e	1.823	0.859	1.004	0.969	1.563	hypothetical protein
Mlh3	1.429	0.98	0.891	1.005	1.178	Similar to mutL (E. coli) homolog 3. [Source:Uniprot/SPTREMBL;Acc:Q99L38]
Gli3	2.432	2.313	1.06	1.196	1.882	Zinc finger protein GLI3. [Source:Uniprot/SWISSPROT;Acc:Q61602]

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Prl	1.773	0.836	1.362	2.186	0.914	Prolactin precursor (PRL). [Source:Uniprot/SWISSPROT;Acc:P06879]
Tcfap2a	1.467	0.856	0.998	0.456	0.545	Transcription factor AP-2 alpha (AP2-alpha) (Activating enhancer- binding protein 2 alpha) (Activator protein-2) (AP-2). [Source:Uniprot/SWISSPROT;Acc:P34056]
Tbc1d7	0.685	0.794	1.609	0.994	1.053	TBC1 domain family, member 7. [Source:RefSeq;Acc:NM_025935]
Fbp2	1.661	1.128	1.271	1.187	0.858	Fructose-1,6-bisphosphatase isozyme 2 (EC 3.1.3.11) (D-fructose-1,6- bisphosphate 1-phosphohydrolase) (FBPase) (RAE-30). [Source:Uniprot/SWISSPROT;Acc:P70695]
Auh	0.715	0.806	0.796	0.827	1.044	Methylglutaconyl-CoA hydratase, mitochondrial precursor (EC 4.2.1.18) (AU-specific RNA-binding enoyl-CoA hydratase) (AU-binding enoyl-CoA hydratase) (muAUH). [Source:Uniprot/SWISSPROT;Acc:Q9JLZ3]
Zfp369	1.482	1.247	1.031	0.985	0.559	zinc finger protein 369; neurotrophin receptor interacting factor 2. [Source:RefSeq;Acc:NM_178364]
Dapk1	1.53	0.975	0.917	1.142	1.087	Death-associated protein kinase 1 (EC 2.7.1.37) (DAP kinase 1). [Source:Uniprot/SWISSPROT;Acc:Q80YE7]
Dapk1	1.708	0.991	1.335	0.954	0.986	Death-associated protein kinase 1 (EC 2.7.1.37) (DAP kinase 1). [Source:Uniprot/SWISSPROT;Acc:Q80YE7]
2900041A09Rik	0.584	1.743	0.973	1.339	1.066	hypothetical protein
Otp	1.594	0.798	0.936	0.381	1.357	Homeobox protein orthopedia. [Source:Uniprot/SWISSPROT;Acc:O09113]
Q80VX9	0.748	1.427	1.218	1.246	1.075	Retinal pigment (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q80VX9]
Ppwd1	1.944	0.903	0.758	0.801	1.18	peptidylprolyl isomerase domain and WD repeat containing 1
ENSMUSG00000021775	0.488	0.987	0.935	0.682	1.36	hypothetical protein
Usp54	1.83	1.318	0.758	0.856	0.921	ubiquitin specific protease 54. [Source:RefSeq;Acc:NM_030180]
Camk2g	1.386	1.466	1.242	1.142	1.324	Calcium/calmodulin-dependent protein kinase type II gamma chain (EC 2.7.1.123) (CaM-kinase II gamma chain) (CaM kinase II gamma subunit) (CaMK-II gamma subunit). [Source:Uniprot/SWISSPROT;Acc:Q923T9]
Glt8d1	1.862	1.741	0.918	0.812	0.898	glycosyltransferase 8 domain containing 1
3425401B19Rik	2.162	0.563	0.775	0.863	1.23	hypothetical protein
Rnaseh2b	1.448	1.387	0.935	0.6	1.15	2610207P08Rik protein (Similar to hypothetical 35.1 kDa protein). [Source:Uniprot/SPTREMBL;Acc:Q9D014]

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Gdf10	2.46	2.024	1.226	2.172	1.024	Bone morphogenetic protein 3b precursor (BMP-3b) (Growth/differentiation factor 10) (GDF-10). [Source:Uniprot/SWISSPROT;Acc:P97737]
BC051457	1.452	1.124	0.55	0.758	1.099	hypothetical protein
Dnajc15	1.264	1.248	1.246	1.127	1.109	DnaJ (Hsp40) homolog, subfamily D, member 1. [Source:RefSeq;Acc:NM_025384]
Q8BWQ9	1.438	1.277	0.554	1.433	0.542	Ubiquitin carboxyl-terminal esterase L3. [Source:Uniprot/SPTREMBL;Acc:Q8BWQ9]
Gzme	1.427	0.694	1.187	0.923	0.998	Granzyme E precursor (EC 3.4.21.-) (Cytotoxic cell protease 3) (CCP3) (CTL serine protease 2) (D12) (Cytotoxic serine protease 2) (MCSP2). [Source:Uniprot/SWISSPROT;Acc:P08884]
1500005A01Rik	0.665	0.93	1.334	0.942	0.821	UPF0172 protein C14orf122 homolog. [Source:Uniprot/SWISSPROT;Acc:Q9DB76]
Q8BWX0	0.385	0.503	1.183	0.873	0.824	Similar to HCDI protein. [Source:Uniprot/SPTREMBL;Acc:Q8BWX0]
Ugt3a2	1.292	0.763	1.06	2.227	0.775	UDP glycosyltransferases 3 family, polypeptide A2
Khdrbs3	1.272	1.062	0.811	0.964	0.843	KH domain containing, RNA binding, signal transduction associated 3; etoile. [Source:RefSeq;Acc:NM_010158]
Zfat1	1.511	1.432	0.837	1.175	1.229	zinc finger protein 406; zinc finger protein 403. [Source:RefSeq;Acc:NM_198644]
Ttc35	1.297	0.987	1.012	0.999	0.928	tetratricopeptide repeat domain 35
Fbxo32	1.306	1.242	1.225	0.878	1.082	F-box only protein 32 (Muscle atrophy F-box protein) (MAFbx) (Atrogin- 1). [Source:Uniprot/SWISSPROT;Acc:Q9CPU7]
Zhx1	0.773	1.302	1.214	0.824	0.819	Zinc fingers and homeoboxes protein 1. [Source:Uniprot/SWISSPROT;Acc:P70121]
Slc25a17	1.299	0.954	0.978	1.036	1.122	Peroxisomal membrane protein PMP34 (34 kDa peroxisomal membrane protein) (Solute carrier family 25, member 17). [Source:Uniprot/SWISSPROT;Acc:O70579]
Cacna1i	2.09	0.693	0.739	0.792	0.549	calcium channel, voltage-dependent, alpha 1I subunit
ENSMUSG00000022416	1.611	0.666	1.191	1.035	0.952	hypothetical protein
Adamts20	5.149	0.808	0.855	0.513	0.824	ADAMTS-20 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase with thrombospondin motifs 20) (ADAM-TS 20) (ADAM-TS20). [Source:Uniprot/SWISSPROT;Acc:P59511]
D15Wsu75e	1.514	1.352	0.941	0.878	1.273	D15Wsu75e protein. [Source:RefSeq;Acc:NM_134095]

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Txndc11	0.55	0.882	1.161	0.648	0.977	thioredoxin domain containing 11 isoform 1
Zfp263	1.425	0.899	0.832	0.868	0.746	zinc finger protein 263; kruppel-associated box-zinc finger protein NT2. [Source:RefSeq;Acc:NM_148924]
ENSMUSG00000022591	0.301	0.197	1.436	1.068	0.411	hypothetical protein
Muc19	1.532	0.533	0.908	0.296	1.717	mucin 19
ENSMUSG00000022647	0.281	1.792	1.157	0.715	0.271	hypothetical protein
Retnlb	2.311	1.412	1.104	0.884	0.978	Resistin-like beta precursor (RELMbeta) (Cysteine-rich secreted protein FIZZ2) (Cysteine-rich secreted protein A12-beta). [Source:Uniprot/SWISSPROT;Acc:Q99P86]
Stxbp5l	1.957	0.829	0.734	1.063	1.213	syntaxin binding protein 5-like
Cxadr	0.6	2.246	0.878	0.818	0.441	Coxsackievirus and adenovirus receptor homolog precursor (mCAR). [Source:Uniprot/SWISSPROT;Acc:P97792]
Cxadr	1.525	0.941	0.351	0.75	0.649	Coxsackievirus and adenovirus receptor homolog precursor (mCAR). [Source:Uniprot/SWISSPROT;Acc:P97792]
Enah	2.157	0.942	0.769	0.857	1.093	Enabled protein homolog (NPC derived proline-rich protein 1) (NDPP-1). [Source:Uniprot/SWISSPROT;Acc:Q03173]
Igfbp6	0.65	1.074	0.981	1.314	0.874	Insulin-like growth factor binding protein 6 precursor (IGFBP-6) (IBP- 6) (IGF-binding protein 6). [Source:Uniprot/SWISSPROT;Acc:P47880]
ENSMUSG00000023147	0.539	0.6	1.153	1.057	0.399	tryptophan rich basic protein. [Source:RefSeq;Acc:NM_207301]
ENSMUSG00000023159	0.055	4.673	1.091	0.194	1.121	Cea17 protein (Fragment). [Source:Uniprot/SPTREMBL;Acc:O08932]
ENSMUSG00000023387	1.838	0.353	0.829	0.784	2.12	hypothetical protein
ENSMUSG00000023528	0.411	0.826	1.714	0.93	1.332	Homeobox protein Pem (Placenta and embryonic expression protein). [Source:Uniprot/SWISSPROT;Acc:P52651]
Iqcf3	1.58	0.24	0.469	0.985	1.501	IQ motif containing F3
Slc5a7	1.36	0.446	0.591	0.809	0.847	solute carrier family 5 (choline transporter), member 7. [Source:RefSeq;Acc:NM_022025]
Clic5	1.541	1.178	0.817	0.304	1.235	Chloride intracellular channel protein 5. [Source:Uniprot/SWISSPROT;Acc:Q8BXK9]
Tmprss3	2.198	1.082	0.918	0.849	1.313	Transmembrane protease, serine 3 (EC 3.4.21.-). [Source:Uniprot/SWISSPROT;Acc:Q8K1T0]

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
DP30_MOUSE	0.721	1.404	1.461	1.098	0.734	Dpy-30-like protein. [Source:Uniprot/SWISSPROT;Acc:Q99LT0]
Qpct	0.608	1.354	0.935	0.885	1.132	Similar to glutaminyl-peptide cyclotransferase precursor. [Source:Uniprot/SPTREMBL;Acc:Q8BH20]
Luc7l	1.375	1.675	0.968	1.682	0.998	Putative RNA-binding protein Luc7-like 1. [Source:Uniprot/SWISSPROT;Acc:Q9CYI4]
ENSMUSG00000024194	0.742	0.632	1.021	0.899	1.148	divalent cation tolerant protein CUTA. [Source:RefSeq;Acc:NM_026307]
Map3k8	0.606	0.579	0.477	0.854	0.764	Mitogen-activated protein kinase kinase kinase 8 (EC 2.7.1.37) (COT proto-oncogene serine/threonine-protein kinase) (C-COT) (Cancer Osaka thyroid oncogene). [Source:Uniprot/SWISSPROT;Acc:Q07174]
Cox7a2l	0.64	0.976	0.889	0.662	0.813	Cytochrome c oxidase subunit VIIa-related protein, mitochondrial precursor (Silica-induced protein 81) (SIG-81) (SIG81). [Source:Uniprot/SWISSPROT;Acc:Q61387]
Wdr46	0.687	0.895	1.119	1.125	0.838	WD-repeat protein BING4. [Source:Uniprot/SWISSPROT;Acc:Q9Z0H1]
Atp6v1g2	2.385	0.608	0.852	0.86	0.956	Vacuolar ATP synthase subunit G 2 (EC 3.6.3.14) (V-ATPase G subunit 2) (Vacuolar proton pump G subunit 2) (V-ATPase 13 kDa subunit 2). [Source:Uniprot/SWISSPROT;Acc:Q9WTT4]
Zfp521	0.676	0.82	1.593	0.991	0.474	zinc finger protein 521; ecotropic viral integration site 3. [Source:RefSeq;Acc:NM_145492]
ENSMUSG00000024459	0.436	1.937	0.802	0.522	0.544	hypothetical protein
Rab27b	1.92	0.948	0.743	0.75	0.797	Ras-related protein Rab-27B. [Source:Uniprot/SWISSPROT;Acc:Q99P58]
1110032A13Rik	0.807	1.411	0.961	0.968	0.904	hypothetical protein LOC68731
ENSMUSG00000024593	2.226	0.834	1.022	0.899	0.923	hypothetical protein
Tmc1	1.772	0.999	1.352	1.464	0.537	Transmembrane cochlear-expressed protein 1 (Beethoven protein) (Deafness protein). [Source:Uniprot/SWISSPROT;Acc:Q8R4P5]
Lipf	1.571	0.791	0.825	0.392	1.081	Triacylglycerol lipase, gastric precursor (EC 3.1.1.3) (Gastric lipase) (GL). [Source:Uniprot/SWISSPROT;Acc:Q9CPP7]
Ppp2r5b	0.499	0.622	1.485	0.707	1.012	protein phosphatase 2, regulatory subunit B (B56), beta isoform. [Source:RefSeq;Acc:NM_198168]
Il33	0.677	2.516	0.765	0.91	1.131	interleukin 33
Q8BXH7	1.376	0.836	0.951	0.871	1.134	TANKYRASE-related protein (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8BXH7]

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Fosl1	0.639	1.92	1.095	0.628	1.319	Fos-related antigen-1 (FRA-1). [Source:Uniprot/SWISSPROT;Acc:P48755]
Tcf7l2	1.242	1.282	0.576	1.058	1.006	Transcription factor 7-like 2 (HMG box transcription factor 4) (T- cell-specific transcription factor 4) (TCF-4) (mTCF-4). [Source:Uniprot/SWISSPROT;Acc:Q924A0]
Tcf7l2	1.483	1.101	1.078	1.594	1.065	Transcription factor 7-like 2 (HMG box transcription factor 4) (T- cell-specific transcription factor 4) (TCF-4) (mTCF-4). [Source:Uniprot/SWISSPROT;Acc:Q924A0]
Trub1	1.432	1.24	0.999	0.723	0.873	TruB pseudouridine (psi) synthase homolog 1 isoform 1
Slc18a2	0.339	0.952	0.912	0.959	0.996	Synaptic vesicular amine transporter (Monoamine transporter) (Vesicular amine transporter 2) (VAT2) (Solute carrier family 18 member 2). [Source:Uniprot/SWISSPROT;Acc:Q8BRU6]
Bnc1	1.572	0.746	1.855	1.055	2.126	Zinc finger protein basonuclin 1. [Source:Uniprot/SWISSPROT;Acc:O35914]
Mms19l	1.457	1.415	1.06	0.856	0.946	MMS19 (MET18 S. cerevisiae)-like. [Source:RefSeq;Acc:NM_028152]
Entpd7	0.63	0.772	1.544	1.045	0.839	ectonucleoside triphosphate diphosphohydrolase; lysosomal apyrase-like 2. [Source:RefSeq;Acc:NM_053103]
Tlx1	3.757	1.143	1.123	0.415	0.645	T-cell leukemia homeobox protein 1 (Homeobox protein Hox-11) (Homeobox TLX-1). [Source:Uniprot/SWISSPROT;Acc:P43345]
Zfhx4	0.691	0.861	0.822	0.547	0.729	zinc finger homeodomain 4. [Source:RefSeq;Acc:NM_030708]
Hsd17b10	0.743	1.034	1.045	0.999	1.137	3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HADH) (Endoplasmic reticulum-associated amyloid beta-peptide binding protein). [Source:Uniprot/SWISSPROT;Acc:O08756]
Huwe1	1.749	1.508	1.109	1.176	0.831	Upstream regulatory element binding protein 1 (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8BNJ7]
Jarid1c	1.849	0.461	1.262	1.256	1.52	Jumonji/ARID domain-containing protein 1C (SmcX protein) (Xe169 protein). [Source:Uniprot/SWISSPROT;Acc:P41230]
Gpr143	1.726	1.346	1.037	1.166	0.87	G protein-coupled receptor 143 (Ocular albinism type 1 protein homolog) (MOA1). [Source:Uniprot/SWISSPROT;Acc:P70259]
Cdk2	0.546	0.837	0.779	0.715	0.999	Cell division protein kinase 2 (EC 2.7.1.37). [Source:Uniprot/SWISSPROT;Acc:P97377]
Cdk2	1.537	1.143	0.728	1.089	0.827	Cell division protein kinase 2 (EC 2.7.1.37). [Source:Uniprot/SWISSPROT;Acc:P97377]
Q9D7M0	1.203	1.229	0.974	1.033	1.555	hypothetical protein

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Hras1	1.775	0.191	0.933	0.724	0.583	Transforming protein P21/H-Ras-1 (c-H-ras). [Source:Uniprot/SWISSPROT;Acc:Q61411]
Mir	1.389	0.628	0.782	0.699	0.928	c-mir, cellular modulator of immune recognition (Mir)
Akap13	1.487	1.171	0.746	1.25	1.26	Type II cAMP-dependent protein kinase anchoring protein Ht31 (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q924X9]
Plk4	0.501	0.985	1.186	1.062	1.109	polo-like kinase 4 isoform sak-a; serine/threonine kinase 18. [Source:RefSeq;Acc:NM_011495]
Sec61a2	1.937	0.866	0.641	1.024	0.594	Protein transport protein Sec61 alpha subunit isoform 2 (Sec61 alpha- 2). [Source:Uniprot/SWISSPROT;Acc:Q9JLR1]
ENSMUSG00000025861	1.834	1.29	1.144	1.087	0.327	hypothetical protein
Gria4	1.566	1.108	1.619	1.115	1.515	Glutamate receptor 4 precursor (GluR-4) (GluR4) (GluR-D) (Glutamate receptor ionotropic, AMPA 4). [Source:Uniprot/SWISSPROT;Acc:Q9Z2W8]
Eya1	0.47	0.841	1.015	0.677	1.437	Eyes absent homolog 1 (EC 3.1.3.48). [Source:Uniprot/SWISSPROT;Acc:P97767]
Slco5a1	1.511	0.92	1.494	0.485	1.108	solute carrier organic anion transporter family, member 5A1. [Source:RefSeq;Acc:NM_172841]
Crygf	0.624	0.815	0.714	1.265	0.831	crystallin, gamma F. [Source:RefSeq;Acc:NM_027010]
Ica1l	0.524	1.048	1.14	0.93	1.386	Ica69-related protein. [Source:RefSeq;Acc:NM_027407]
ENSMUSG00000026023	0.735	0.683	1.023	1.04	1.034	hypothetical protein
Pdcl3	1.783	0.616	1.047	1.46	1.012	IAP-associated factor VIAF1. [Source:RefSeq;Acc:NM_026850]
1700024G10Rik	0.623	1.342	1.577	1.266	1.408	hypothetical protein LOC71849 isoform 1
4930544G21Rik	0.549	0.406	1.341	0.176	1.295	sphingosine kinase type 1-interacting protein. [Source:RefSeq;Acc:NM_172430]
Slc23a3	1.512	2.109	0.546	0.834	1.372	solute carrier family 23 (nucleobase transporters), member 3; yolk sac permease-like molecule 1. [Source:RefSeq;Acc:NM_194333]
Rnpepl1	1.274	1.189	0.978	1.124	0.926	arginyl aminopeptidase (aminopeptidase B)-like 1. [Source:RefSeq;Acc:NM_181405]
Capn10	1.633	0.81	0.658	1.494	1.102	Calpain 10 (EC 3.4.22.-) (Calcium-activated neutral proteinase 10) (CANP 10). [Source:Uniprot/SWISSPROT;Acc:Q9ESK3]
F13b	1.751	1.207	1.409	1.812	0.632	Coagulation factor XIII B chain precursor (Protein-glutamine gamma- glutamyltransferase B chain) (Transglutaminase B chain). [Source:Uniprot/SWISSPROT;Acc:Q07968]

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3110009E18Rik	0.658	1.299	0.8	0.89	1.118	hypothetical protein LOC73103
Cacna1s	1.503	0.687	1.108	1.688	0.504	Voltage-dependent L-type calcium channel, alpha-1S subunit (Calcium channel, L type, alpha-1 polypeptide, isoform 3, skeletal muscle). [Source:Uniprot/SPTREMBL;Acc:Q02789]
Fcamr	1.285	0.843	0.714	0.94	0.761	Fc receptor, IgA, IgM, high affinity. [Source:RefSeq;Acc:NM_144960]
Stx6	1.469	1.226	1.015	1.247	0.681	Syntaxin 6. [Source:Uniprot/SWISSPROT;Acc:Q9JKK1]
Ahctf1	1.704	0.92	1.04	1.253	0.935	transcription factor ELYS. [Source:RefSeq;Acc:NM_026375]
Uck2	0.78	1.008	0.945	1.101	1.025	Uridine-cytidine kinase 2 (EC 2.7.1.48) (UCK 2) (Uridine monophosphokinase 2) (Cytidine monophosphokinase 2). [Source:Uniprot/SWISSPROT;Acc:Q99PM9]
Abl2	1.823	1.535	1.04	0.502	0.433	Protein tyrosine kinase (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q61055]
Ptpn14	1.442	1.824	1.249	0.775	0.781	Protein tyrosine phosphatase, non-receptor type 14 (EC 3.1.3.48) (Protein-tyrosine phosphatase PTP36). [Source:Uniprot/SWISSPROT;Acc:Q62130]
Nuf2	1.764	1.314	0.671	0.872	1.35	NUF2R protein. [Source:RefSeq;Acc:NM_023284]
Fmo3	0.493	0.74	0.662	1.237	0.863	Dimethylaniline monooxygenase [N-oxide forming] 3 (EC 1.14.13.8) (Hepatic flavin-containing monooxygenase 3) (FMO 3) (Dimethylaniline oxidase 3). [Source:Uniprot/SWISSPROT;Acc:P97501]
ENSMUSG00000026702	1.29	1.003	0.822	1.268	1.207	hypothetical protein
Q9D5L1	0.634	0.893	0.822	0.741	1.14	hypothetical protein
Q9D362	2.175	1.393	1.254	1.445	1.063	hypothetical protein
Gbgt1	0.623	1.577	0.333	1.209	0.793	globoside alpha-1,3-N-acetylgalactosaminyltransferase 1; forssman glycolipid synthetase. [Source:RefSeq;Acc:NM_139197]
Phf19	1.992	1.832	0.882	1.541	0.42	PHD finger protein 19
ENSMUSG00000026927	1.29	1.095	1.279	0.911	0.948	hypothetical protein
Q8CBV3	0.668	1.619	0.896	0.31	1.065	hypothetical protein
Q9D5S3	1.548	0.301	1.007	1.021	1.261	hypothetical protein
Wdr85	1.407	0.102	1.008	1.27	0.305	WD40 repeat domain 85
Pkp4	1.325	0.9	0.816	1.031	1.176	Neural PLAKOPHILIN-related ARM repeat protein

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Ssfa2	1.364	0.95	0.955	0.817	1.071	Sperm-specific antigen 2. [Source:Uniprot/SWISSPROT;Acc:Q922B9]
Stk39	0.482	0.65	1.008	1.095	0.633	STE20/SPS1-related proline-alanine rich protein kinase (EC 2.7.1.37) (Ste-20 related kinase) (Serine/threonine-protein kinase 39). [Source:Uniprot/SWISSPROT;Acc:Q9Z1W9]
ENSMUSG00000027063	1.685	1.204	1.313	0.076	1.58	hypothetical protein
4933404M02Rik	1.432	0.815	0.943	0.91	1.058	hypothetical protein LOC66748
Elf5	1.553	0.769	0.776	1.073	0.591	E74-like factor 5. [Source:RefSeq;Acc:NM_010125]
Duoxa2	0.505	0.904	1.509	0.647	1.443	similar to Numb-interacting homolog protein. [Source:RefSeq;Acc:NM_025777]
F2	1.583	0.668	0.786	1.924	1.032	Prothrombin precursor (EC 3.4.21.5). [Source:Uniprot/SWISSPROT;Acc:P19221]
Cdan1	1.269	0.993	1.387	1.171	0.768	Codanin 1 (Fragment). [Source:Uniprot/SWISSPROT;Acc:Q8CC12]
Cdc25b	1.92	0.993	0.984	1.136	0.899	M-phase inducer phosphatase 2 (EC 3.1.3.48) (Dual specificity phosphatase Cdc25B). [Source:Uniprot/SWISSPROT;Acc:P30306]
Dusp2	0.706	0.438	0.338	0.988	0.837	Dual specificity protein phosphatase 2 (EC 3.1.3.48) (EC 3.1.3.16) (Dual specificity protein phosphatase PAC-1). [Source:Uniprot/SWISSPROT;Acc:Q05922]
ENSMUSG00000027371	1.334	2.55	1.111	1.314	1.088	hypothetical protein
Tgm3	0.397	0.988	1.026	0.267	0.934	Protein-glutamine glutamyltransferase E precursor (EC 2.3.2.13) (TGase E) (TGE) (TG(E)) (Transglutaminase 3). [Source:Uniprot/SWISSPROT;Acc:Q08189]
9230104L09Rik	1.388	0.874	1.879	1.294	1.076	9230104L09Rik protein (Cystatin E2). [Source:Uniprot/SPTREMBL;Acc:Q9D264]
2310046K01Rik	0.644	0.726	1.363	0.84	0.502	hypothetical protein LOC69698
Bpil1	1.432	1.15	0.899	1.286	0.914	Bactericidal/permeability-increasing protein-like 1 precursor. [Source:Uniprot/SWISSPROT;Acc:Q8C1E1]
Rab22a	1.36	1.828	0.702	1.189	0.912	Ras-related protein Rab-22A (Rab-22) (Rab-14). [Source:Uniprot/SWISSPROT;Acc:P35285]
C030019F02Rik	2.197	1.655	0.936	1.786	0.727	hypothetical protein LOC58237
0610011L14Rik	1.301	1.127	1.011	1.188	1.389	hypothetical protein LOC68295
Gnb4	0.715	0.876	1.105	1.071	0.739	Guanine nucleotide-binding protein beta subunit 4 (Transducin beta chain 4). [Source:Uniprot/SWISSPROT;Acc:P29387]

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Ect2	1.522	0.361	1.299	0.902	0.868	ECT2 protein (Epithelial cell transforming sequence 2 oncogene). [Source:Uniprot/SWISSPROT;Acc:Q07139]
Trpc4	1.499	0.525	1.653	0.574	0.63	Short transient receptor potential channel 4 (TrpC4) (Receptor- activated cation channel TRP4) (Capacitative calcium entry channel Trp4). [Source:Uniprot/SWISSPROT;Acc:Q9QUQ5]
Postn	0.316	1.232	0.573	1.907	0.869	Periostin precursor (PN) (Osteoblast specific factor 2) (OSF-2). [Source:Uniprot/SWISSPROT;Acc:Q62009]
Dhx36	1.253	0.941	0.91	0.626	1.012	DEAH (Asp-Glu-Ala-His) box polypeptide 36. [Source:RefSeq;Acc:NM_028136]
Gfm	1.552	1.005	1.197	1.245	0.95	Elongation factor G 1, mitochondrial precursor (mEF-G 1) (Elongation factor G1). [Source:Uniprot/SWISSPROT;Acc:Q8K0D5]
Kcnab1	2.112	0.283	1.367	1.241	0.238	Voltage-gated potassium channel beta-1 subunit (K channel beta-1 subunit) (Kv-beta-1). [Source:Uniprot/SWISSPROT;Acc:Q63277]
Shox2	2.106	1.157	0.378	1.241	1.162	Short stature homeobox protein 2 (Homeobox protein Og12X) (OG-12) (Paired family homeodomain protein Prx3). [Source:Uniprot/SWISSPROT;Acc:P70390]
Gpsm2	1.698	1.198	1.07	1.349	0.932	Pins; pins homolog (Drosophia). [Source:RefSeq;Acc:NM_029522]
Slc16a4	1.452	0.174	1.365	1.271	1.601	solute carrier family 16, member 4. [Source:RefSeq;Acc:NM_146136]
4933434E20Rik	0.817	1.075	1.166	1.061	0.92	NICE-3 protein. [Source:RefSeq;Acc:NM_025762]
Adar	1.265	0.967	0.888	1.156	1.238	Double-stranded RNA-specific adenosine deaminase (EC 3.5.4.-) (DRADA) (RNA adenosine deaminase 1). [Source:Uniprot/SWISSPROT;Acc:Q99MU3]
Lef1	1.913	0.854	0.998	0.89	1.241	Lymphoid enhancer binding factor 1 (LEF-1). [Source:Uniprot/SWISSPROT;Acc:P27782]
Lrat	2.146	1.148	1.035	0.345	1.587	Lecithin retinol acyltransferase (EC 2.3.1.135) (Phosphatidylcholine-- retinol O-acyltransferase) (Phosphatidylcholine-retinol-O- acyltransferase). [Source:Uniprot/SWISSPROT;Acc:Q9JI60]
Bcar3	1.437	0.928	1.008	1.39	0.84	breast cancer anti-estrogen resistance 3. [Source:RefSeq;Acc:NM_013867]
Zcd2	0.487	1.569	0.561	0.454	0.856	zinc finger, CDGSH-type domain 2
Asph	1.243	1.158	1.023	1.139	1.16	aspartyl beta-hydroxylase; calsequestrin-binding protein. [Source:RefSeq;Acc:NM_023066]
D3Ertd250e	1.41	0.714	0.919	0.583	1.716	hypothetical protein

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Clca2	0.582	0.587	0.353	1.821	1.429	chloride channel calcium activated 2. [Source:RefSeq;Acc:NM_030601]
Ppp3r2	1.438	1.144	0.769	1.116	0.58	Calcineurin B subunit isoform 2 (Protein phosphatase 2B regulatory subunit 2) (Protein phosphatase 3 regulatory subunit B alpha isoform 2). [Source:Uniprot/SWISSPROT;Acc:Q63811]
Tmeff1	1.848	0.342	0.895	0.814	0.835	transmembrane protein with EGF-like and two follistatin-like domains 1; tomoregulin-1; tomoregulin-like. [Source:RefSeq;Acc:NM_021436]
Aco1	1.383	1.372	0.805	0.835	0.89	Iron-responsive element binding protein 1 (IRE-BP 1) (Iron regulatory protein 1) (IRP1) (Ferritin repressor protein) (Aconitate hydratase) (EC 4.2.1.3) (Citrate hydro-lyase) (Aconitase). [Source:Uniprot/SWISSPROT;Acc:P28271]
Dab1	1.593	0.61	0.497	1.447	1.461	Disabled homolog 1. [Source:Uniprot/SWISSPROT;Acc:P97318]
Cc2d1b	1.314	0.928	1.085	1.161	1.008	coiled-coil and C2 domain containing 1B
Podn	3.388	0.885	0.722	0.679	0.61	podocan. [Source:RefSeq;Acc:NM_172874]
0610037L13Rik	1.367	1.17	0.76	0.668	0.933	hypothetical protein LOC74098
Tmem48	0.695	1.213	1.461	0.737	0.845	transmembrane protein 48
Gale	1.759	1.224	0.824	0.977	1.49	UDP-glucose 4-epimerase (EC 5.1.3.2) (Galactowaldenase) (UDP-galactose 4-epimerase). [Source:Uniprot/SWISSPROT;Acc:Q8R059]
BC057625	1.261	1.345	0.792	0.96	0.94	RIKEN cDNA C230096C10; KIAA0090 protein-like. [Source:RefSeq;Acc:NM_146157]
Tmem54	1.727	0.745	0.527	0.614	1.808	beta-casein-like protein. [Source:RefSeq;Acc:NM_025452]
Cnksr1	2.521	0.698	0.7	0.242	1.139	connector enhancer of kinase suppressor of Ras 1
Trappc3	0.74	1.124	1.043	0.911	1.057	Trafficking protein particle complex subunit 3 (BET3 homolog). [Source:Uniprot/SWISSPROT;Acc:O55013]
Slc9a1	1.342	1.149	1.092	1.395	1.116	Sodium/hydrogen exchanger 1 (Na()/H() exchanger 1) (NHE-1). [Source:Uniprot/SWISSPROT;Acc:Q61165]
D4Ertd196e	1.237	1.023	1.345	1.152	0.935	hypothetical protein LOC52174
Arhgef19	0.595	0.758	1.062	1.026	1.053	Rho guanine nucleotide exchange factor (GEF) 19
Acot7	1.28	0.838	0.947	0.891	0.935	Cytosolic acyl coenzyme A thioester hydrolase (EC 3.1.2.2) (Long chain acyl-CoA thioester hydrolase) (CTE-II) (Brain acyl-CoA hydrolase). [Source:Uniprot/SWISSPROT;Acc:Q91V12]
Galntl5	0.592	0.891	0.441	2.039	0.763	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 15.

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Galntl5	0.592	0.891	0.441	2.039	0.763	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 15. [Source:RefSeq;Acc:NM_026449]
Slc2a5	0.702	1.224	1.295	1.102	0.598	Solute carrier family 2, facilitated glucose transporter, member 5 (Glucose transporter type 5, small intestine) (Fructose transporter). [Source:Uniprot/SWISSPROT;Acc:Q9WV38]
Agtrap	0.775	0.746	1.034	1.197	1.236	angiotensin II receptor-associated protein; angiotensin II receptor, type I; AT1 receptor. [Source:RefSeq;Acc:NM_009642]
Q9D4N2	1.834	2.555	0.233	0.764	1.937	PREDICTED: similar to hypothetical protein FLJ36119 (LOC433814)
Noc2l	1.394	1.116	1.059	1.034	0.756	UPF0120 protein DKFZp564C186 homolog. [Source:Uniprot/SWISSPROT;Acc:Q9WV70]
Pcdh7	0.616	0.258	1.174	0.479	0.83	protocadherin 7; BH-protocadherin (brain-heart); BH-protocadherin. [Source:RefSeq;Acc:NM_018764]
ENSMUSG00000029165	1.699	1.561	1.457	1.639	1.359	hypothetical protein
Dhx15	1.337	1.028	0.782	0.872	0.693	Putative pre-mRNA splicing factor RNA helicase (DEAH box protein 15). [Source:Uniprot/SWISSPROT;Acc:O35286]
Pdgfra	1.245	1.538	1.307	1.704	0.783	Alpha platelet-derived growth factor receptor precursor (EC 2.7.1.112) (PDGF-R-alpha). [Source:Uniprot/SWISSPROT;Acc:P26618]
Tpst2	1.295	1.179	1.113	0.732	1.035	Protein-tyrosine sulfotransferase 2 (EC 2.8.2.20) (Tyrosylprotein sulfotransferase-2) (TPST-2). [Source:Uniprot/SWISSPROT;Acc:O88856]
Pitpnm2	0.54	1.491	1.772	0.98	1.918	retinal degeneration B2 homolog; retinal degeneration B2 homolog (Drosophila). [Source:RefSeq;Acc:NM_011256]
Bcl7a	1.631	0.898	0.959	0.866	1.302	B-cell CLL/lymphoma 7A. [Source:RefSeq;Acc:NM_029850]
Brap	1.352	0.647	0.716	0.999	1.137	BRCA1 associated protein. [Source:RefSeq;Acc:NM_028227]
Morn3	2.182	1.043	0.749	0.925	1.073	MORN repeat containing 3
ENSMUSG00000029483	1.453	0.201	1.04	1.266	0.602	PREDICTED: similar to KIAA1906 protein (LOC208151)
4933411G11Rik	0.405	3.383	0.953	1.416	1.17	hypothetical protein LOC330228
Glcci1	0.523	1.831	0.956	1.069	1.689	glucocorticoid induced transcript 1; testhymin; thymocyte/spermatocyte selection 1. [Source:RefSeq;Acc:NM_133236]
4921511K06Rik	1.225	0.997	0.807	1.696	1.029	hypothetical protein LOC232664 isoform 1

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Gars	1.279	1.16	1.053	1.04	1.067	Glycyl-tRNA synthetase (EC 6.1.1.14) (Glycine--tRNA ligase) (GlyRS). [Source:Uniprot/SWISSPROT;Acc:Q9CZD3]
Q9D1U9	0.465	0.96	0.755	0.909	0.616	hypothetical protein
Tcrb-V13	1.531	0.8	1.023	1.408	1.013	T-cell receptor beta-2 chain C region. [Source:Uniprot/SWISSPROT;Acc:P01851]
Tgfa	1.694	4.122	1.207	0.891	1.922	Transforming growth factor alpha precursor (TGF-alpha) (EGF-like TGF) (ETGF) (TGF type 1). [Source:Uniprot/SWISSPROT;Acc:P48030]
Add2	1.53	1.415	0.905	0.99	1.34	Beta adducin (Erythrocyte adducin beta subunit) (Add97). [Source:Uniprot/SWISSPROT;Acc:Q9QYB8]
Cml5	1.39	0.414	1.068	1.104	1.122	camello-like 5. [Source:RefSeq;Acc:NM_023493]
Bmp10	1.46	1.136	0.946	0.237	0.541	Bone morphogenetic protein 10 precursor (BMP-10). [Source:Uniprot/SWISSPROT;Acc:Q9R229]
Edem1	1.345	0.72	0.852	0.887	1.117	ER degradation-enhancing alpha-mannosidase-like. [Source:Uniprot/SWISSPROT;Acc:Q925U4]
A2m	2.306	1.55	0.65	0.508	1.413	alpha-2-macroglobulin. [Source:RefSeq;Acc:NM_175628]
Gdf3	1.633	1.952	1.604	1.479	1.056	Growth/differentiation factor 3 precursor (GDF-3) (VG-1-related protein 2). [Source:Uniprot/SWISSPROT;Acc:Q07104]
Rasgef1a	0.543	2.631	0.589	0.995	1.79	PREDICTED: RasGEF domain family, member 1A ()
Klra5	3.327	1.557	1.175	2.337	0.371	Killer cell lectin-like receptor 5 (T-cell surface glycoprotein Ly- 49E) (Ly49-E antigen) (Lymphocyte antigen 49E). [Source:Uniprot/SWISSPROT;Acc:Q60652]
Klra2	0.611	0.769	0.718	0.985	1.016	Killer cell lectin-like receptor 2 (T-cell surface glycoprotein Ly- 49B) (Ly49-B antigen) (Lymphocyte antigen 49B). [Source:Uniprot/SWISSPROT;Acc:Q60660]
Atf7ip	0.587	0.829	0.705	0.842	1.204	activating transcription factor 7 interacting protein; ATFa-associated Modulator. [Source:RefSeq;Acc:NM_019426]
Q9CW36	0.744	0.642	1.133	0.948	1.41	hypothetical protein
Clec2h	1.304	0.325	0.576	1.067	0.995	C-type lectin related f. [Source:RefSeq;Acc:NM_053165]
Tarsl2	0.478	1.002	1.193	1.248	0.434	BBP-like protein 2. [Source:RefSeq;Acc:NM_026795]
Furin	1.494	0.936	1.368	0.907	1.683	Furin precursor (EC 3.4.21.75) (Paired basic amino acid residue cleaving enzyme) (PACE) (Dibasic processing enzyme). [Source:Uniprot/SWISSPROT;Acc:P23188]
ENSMUSG00000030563	2.101	0.993	1.432	1.42	0.97	hypothetical protein
ENSMUSG00000030563	0.636	1.617	0.926	1.184	2.585	hypothetical protein

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Det1	0.724	1.489	0.759	1.074	1.061	de-etiolated homolog 1
Coq7	0.741	0.806	0.659	1.256	0.973	Ubiquinone biosynthesis protein COQ7 homolog (Coenzyme Q biosynthesis protein 7 homolog) (Timing protein clk-1 homolog). [Source:Uniprot/SWISSPROT;Acc:P97478]
Xylt1	0.633	1.503	0.573	0.627	0.811	xylosyltransferase 1; xylosyltransferase I. [Source:RefSeq;Acc:NM_175645]
Nfatc2ip	1.935	0.987	0.961	0.875	1.107	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2 interacting protein; nuclear factor of activated T-cells, cytoplasmic 2 interacting protein. [Source:RefSeq;Acc:NM_010900]
Arhgap17	0.49	0.239	1.171	1.019	0.857	nadrin; neuron-associated developmentally regulated protein; WW domain-binding protein 15. [Source:RefSeq;Acc:NM_144529]
Itgax	1.528	5.087	3.859	1.625	1.194	Integrin alpha-X precursor (Leukocyte adhesion glycoprotein p150,95 alpha chain) (Leukocyte adhesion receptor p150,95) (CD11c). [Source:Uniprot/SWISSPROT;Acc:Q9QXH4]
Ush1c	1.306	0.99	1.623	1.123	1.563	Harmonin (Usher syndrome 1C protein homolog) (PDZ domain-containing protein). [Source:Uniprot/SWISSPROT;Acc:Q9ES64]
Ptpn5	1.985	0.558	1.392	0.791	1.736	Protein-tyrosine phosphatase, non-receptor type 5 (EC 3.1.3.48) (Protein-tyrosine phosphatase striatum-enriched) (STEP) (Neural- specific protein-tyrosine phosphatase). [Source:Uniprot/SWISSPROT;Acc:P54830]
Ilk	1.295	1.404	1.059	1.026	0.849	Integrin-linked protein kinase (EC 2.7.1.37). [Source:Uniprot/SWISSPROT;Acc:O55222]
Fadd	1.582	1.149	0.888	0.895	0.898	FADD protein (FAS-associating death domain-containing protein) (Mediator of receptor induced toxicity). [Source:Uniprot/SWISSPROT;Acc:Q61160]
Cacna1f	2.327	0.851	1.25	0.933	0.605	Voltage-dependent L-type calcium channel alpha-1F subunit (Voltage- gated calcium channel alpha subunit Cav1.4). [Source:Uniprot/SWISSPROT;Acc:Q9JIS7]
Wdr13	2.325	1.094	0.947	1.059	1.033	WD-repeat protein 13. [Source:Uniprot/SWISSPROT;Acc:Q91V09]
ENSMUSG00000031178	1.627	0.736	0.887	0.948	1.361	hypothetical protein
Pak3	2.398	0.737	0.584	1.521	1.155	Serine/threonine-protein kinase PAK 3 (EC 2.7.1.37) (p21-activated kinase 3) (PAK-3) (Beta-PAK) (CDC42/RAC effector kinase PAK-B). [Source:Uniprot/SWISSPROT;Acc:Q61036]
Chic1	1.247	2.31	1.318	1.285	1.21	Cysteine-rich hydrophobic domain 1 (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8CBW7]

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Zfp275	1.65	0.945	1.063	1.186	1.178	Zinc finger protein 275. [Source:RefSeq;Acc:NM_031494]
UIP1_MOUSE	1.821	2.126	0.645	0.599	0.921	26S proteasome-associated UCH37 interacting protein 1. [Source:Uniprot/SWISSPROT;Acc:Q8BKT8]
Asb11	2.481	2.105	0.615	1.417	0.439	ankyrin repeat and SOCS box-containing protein 11. [Source:RefSeq;Acc:NM_026853]
Asb11	1.294	1.151	0.461	1.1	0.668	ankyrin repeat and SOCS box-containing protein 11. [Source:RefSeq;Acc:NM_026853]
Mcf2l	2.206	1.774	0.694	1.052	1.511	Guanine nucleotide exchange factor DBS (DBL's big sister) (MCF2 transforming sequence-like protein). [Source:Uniprot/SWISSPROT;Acc:Q64096]
Sorbs2	1.828	0.885	1.02	0.843	1.288	Similar to ARG/ABL-interacting protein ARGBP2A. [Source:Uniprot/SPTREMBL;Acc:Q8BJL6]
Pdlim3	0.543	0.243	1.078	1.415	1.273	PDZ and LIM domain 3; actinin alpha 2 associated LIM protein. [Source:RefSeq;Acc:NM_016798]
Tnpo2	1.337	2.093	0.816	1.056	0.8	Transportin 2 (Karyopherin beta-2b). [Source:Uniprot/SWISSPROT;Acc:Q99LG2]
2010004A03Rik	1.413	0.857	0.921	0.947	0.702	hypothetical protein LOC76527
Cngb1b	2.307	1.225	1.152	1.319	1.307	LOC333329 protein (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q80XL8]
Rab3a	1.299	0.822	0.347	0.799	0.719	Ras-related protein Rab-3A. [Source:Uniprot/SWISSPROT;Acc:P05713]
Cdh5	0.566	0.559	1.191	3.202	0.847	Vascular endothelial-cadherin precursor (VE-cadherin) (Cadherin-5). [Source:Uniprot/SWISSPROT;Acc:P55284]
Cep57	0.512	1.392	0.838	0.99	0.935	translokin; testis-specific protein 57. [Source:RefSeq;Acc:NM_026665]
Folr4	0.507	2.814	0.522	1.147	1.091	folate receptor 4 (delta). [Source:RefSeq;Acc:NM_022888]
Panx1	1.274	1.469	1.217	0.89	0.951	Pannexin 1. [Source:Uniprot/SWISSPROT;Acc:Q9JIP4]
ENSMUSG00000031936	1.489	1.624	0.882	1.006	2.122	hypothetical protein
4932417I16Rik	0.691	1.177	1.325	0.697	0.376	hypothetical protein LOC234740
Galnt2	1.519	0.784	0.944	0.769	0.578	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2; ppGaNTase-T2. [Source:RefSeq;Acc:NM_139272]
Ets1	2.04	2.581	2.079	2.682	0.7	C-ets-1 protein (p54). [Source:Uniprot/SWISSPROT;Acc:P27577]
Dcps	0.771	0.821	0.864	1.254	0.949	histidine triad protein member 5; mRNA decapping enzyme. [Source:RefSeq;Acc:NM_027030]
Icam5	2.367	1.23	0.745	0.742	0.856	Intercellular adhesion molecule-5 precursor (ICAM-5) (Telencephalin).

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Myo1e	1.49	2.038	1.296	0.913	0.913	Myosin If. [Source:Uniprot/SWISSPROT;Acc:P70248]
Htr3a	2.173	1.148	0.526	0.735	1.695	5-hydroxytryptamine 3 receptor precursor (5-HT-3) (Serotonin-gated ion channel receptor) (5-HT3R). [Source:Uniprot/SWISSPROT;Acc:P23979]
Q8K1X6	1.327	1.45	0.838	0.776	0.944	hypothetical protein
Cyp1a2	3.38	0.539	0.856	1.771	0.515	Cytochrome P450 1A2 (EC 1.14.14.1) (CYPIA2) (P450-P2/P450-P3). [Source:Uniprot/SWISSPROT;Acc:P00186]
Plscr1	0.685	1.411	0.971	0.752	1.032	Phospholipid scramblase 1 (PL scramblase 1) (Ca(2)-dependent phospholipid scramblase 1) (Transplantability associated protein 1) (TRA1) (NOR1). [Source:Uniprot/SWISSPROT;Acc:Q9JJ00]
Car12	0.532	0.807	0.428	0.973	0.99	Carbonic anhydrase XII precursor (EC 4.2.1.1) (Carbonate dehydratase XII) (CA-XII). [Source:Uniprot/SWISSPROT;Acc:Q8CI85]
Ttc21a	1.869	2.162	1.18	2.297	1.517	hypothetical protein
Ube1dc1	0.628	1.297	0.729	0.807	1.128	ubiquitin-activating enzyme E1-domain containing 1. [Source:RefSeq;Acc:NM_025692]
1700080E11Rik	0.63	0.493	1.372	0.613	1.162	hypothetical protein LOC73532
Abcc10	0.598	1.369	0.821	0.502	0.801	ATP-binding cassette, sub-family C, member 10 isoform mrp7A; multidrug resistance-associated protein 7. [Source:RefSeq;Acc:NM_145140]
Ncb5or	0.769	0.911	0.843	1.107	0.743	NADPH cytochrome B5 oxidoreductase; cytochrome b-type NAD(P)H oxidoreductase. [Source:RefSeq;Acc:NM_024195]
ENSMUSG00000032896	2.014	0.926	1.146	1.184	0.87	hypothetical protein
ENSMUSG00000032899	1.571	1.195	0.918	1.188	1.042	NOK kinase. [Source:RefSeq;Acc:NM_172891]
Fshr	0.733	0.892	0.998	0.73	0.611	Follicle stimulating hormone receptor precursor (FSH-R) (Follitropin receptor). [Source:Uniprot/SWISSPROT;Acc:P35378]
ENSMUSG00000032999	1.564	1.384	0.371	1.575	1.781	hypothetical protein
Rnf125	1.554	0.466	0.839	1.187	0.925	ring finger protein 125. [Source:RefSeq;Acc:NM_026301]
Mgll	0.75	1.315	1.132	0.769	0.78	Monoglyceride lipase (EC 3.1.1.23). [Source:Uniprot/SWISSPROT;Acc:O35678]
Jmjd2a	0.614	1.061	0.643	1.69	0.862	Jumonji domain containing protein 2A (Fragment). [Source:Uniprot/SWISSPROT;Acc:Q8BW72]

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Caskin1	1.493	1.152	2.673	1.378	0.859	CASK interacting protein 1. [Source:RefSeq;Acc:NM_027937]
D930015E06Rik	1.632	0.967	0.768	0.724	0.229	hypothetical protein LOC229473
Mga	1.383	0.989	1.089	1.565	0.809	MAX-interacting protein; Max dimerization protein 5. [Source:RefSeq;Acc:NM_013720]
Msi2h	1.294	0.745	1.019	0.927	0.804	Musashi homolog 2 (Drosophila) (
ENSMUSG00000034064	1.468	0.728	1.05	0.999	0.75	hypothetical protein
Sfrs2	0.732	1.146	1.07	0.857	1.006	Splicing factor, arginine/serine-rich 2 (Splicing factor SC35) (SC-35) (Splicing component, 35 kDa) (PR264 protein). [Source:Uniprot/SWISSPROT;Acc:Q62093]
Ccnd3	0.492	0.981	0.729	0.811	1.059	G1/S-specific cyclin D3. [Source:Uniprot/SWISSPROT;Acc:P30282]
ENSMUSG00000034201	0.493	0.633	1.241	1.955	0.549	GAS2-related protein isoform beta; GAS2-related protein. [Source:RefSeq;Acc:NM_144560]
Golgb1	1.489	0.725	0.824	1.095	0.911	PREDICTED: golgi autoantigen, golgin subfamily b, macrogolgin 1 (Golgb1)
2810012G03Rik	1.867	0.636	1.31	2.243	0.88	family 53, member C protein
Tulp4	1.576	1.846	0.997	1.166	1.271	Tubby-like protein 4 (Tubby superfamily protein). [Source:Uniprot/SWISSPROT;Acc:Q9JIL5]
Sfrs3	0.634	0.686	0.593	0.747	1.1	Splicing factor. [Source:Uniprot/SPTREMBL;Acc:Q8C3H6]
BC022224	0.542	0.281	1.165	1.217	1.145	short-chain dehydrogenase/reductase
Uaca	0.78	1.067	0.82	1.359	0.584	nuclear membrane binding protein NUCLING. [Source:RefSeq;Acc:NM_028283]
BC018507	0.738	1.086	1.072	1.121	1.026	hypothetical protein LOC218333 isoform 1
D030011N01Rik	1.358	0.917	0.596	1.107	1.169	hypothetical protein LOC245596
ENSMUSG00000034731	2.548	2.059	1.478	0.496	1.112	hypothetical protein
Glis1	0.462	1.286	0.85	1.018	1.124	GLIS family zinc finger 1; Glis1 Kruppel-like zinc finger protein; GLI-Kruppel family member GLI6; zinc finger transcription factor Gli5. [Source:RefSeq;Acc:NM_147221]
ENSMUSG00000034807	1.244	1.061	1.089	1.045	0.928	hypothetical protein
AK173222	1.543	0.92	0.515	1.652	1.44	hypothetical protein
Dhcr24	0.761	1.742	0.808	0.843	0.772	24-dehydrocholesterol reductase; 3-beta-hydroxysterol delta-24 reductase; seladin-1. [Source:RefSeq;Acc:NM_053272]
Otoa	2.03	1.674	0.505	1.397	1.719	otoancorin. [Source:RefSeq;Acc:NM_139310]
1700020L24Ri	1.66	0.776	0.656	2.03	0.501	hypothetical protein LOC66330

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Common	**Incubation Medium (protein-incubation)**	**Incubation Medium (infection)**	***M.tb***	**60.2**	**dnaK**	**Description**
L40632	1.21	1.216	0.514	0.839	1.005	ankyrin 3, epithelial (Ank3), transcript variant 2
Nhedc2	2.053	0.988	1.048	0.669	0.667	Na+/H+ exchanger domain containing 2
3110001I20Rik	1.445	0.975	0.81	1.167	0.984	hypothetical protein LOC70354
AW146020	1.583	1.097	1.449	1.488	1.062	hypothetical protein LOC330361
Elmod2	1.348	1.061	1.109	1.195	0.845	ELMO domain containing 2
Kcnk15	1.498	0.654	0.807	0.378	1.534	potassium channel, subfamily K, member 15
Impg2	1.627	0.951	1.242	0.383	1.168	sialoprotein associated with cones and rods proteoglycan. [Source:RefSeq;Acc:NM_174876]
Cops4	1.852	1.122	1.076	0.788	1.035	COP9 signalosome subunit 4; COP9 (constitutive photomorphogenic), subunit 4 (Arabidopsis); COP9 complex S4. [Source:RefSeq;Acc:NM_012001]
Pcsk7	1.289	1.098	0.92	1.062	1.139	Proprotein convertase subtilisin/kexin type 7 precursor (EC 3.4.21.-) (Proprotein convertase PC7) (Subtilisin/kexin-like protease PC7) (Prohormone convertase PC7) (Subtilisin-like proprotein convertase 7) (SPC7). [Source:Uniprot/SWISSPROT;Acc:Q61139]
EMSY_MOUSE	0.489	0.707	0.714	0.752	0.82	EMSY protein. [Source:Uniprot/SWISSPROT;Acc:Q8BMB0]
Galm	0.646	0.985	1.212	0.891	1.594	aldose 1-epimerase. [Source:RefSeq;Acc:NM_176963]
Ankrd11	1.591	0.971	0.752	1.069	0.804	ankyrin repeat domain 11 isoform 1
Ndufa3	1.804	1.036	1.009	1.304	1.417	NADH-ubiquinone oxidoreductase B9 subunit (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-B9) (CI-B9). [Source:Uniprot/SWISSPROT;Acc:Q9CQ91]
Prkx	1.565	0.758	0.762	1.08	1.626	Serine/threonine-protein kinase PRKX (EC 2.7.1.37) (PKA-related protein kinase). [Source:Uniprot/SWISSPROT;Acc:Q922R0]
Palm	1.703	1.026	0.803	0.74	1.781	Paralemmin. [Source:Uniprot/SWISSPROT;Acc:Q9Z0P4]
BC021523	1.463	1.498	0.685	1.209	0.967	hypothetical protein LOC223752
Dock4	2.628	0.977	1.246	0.989	1.046	Dedicator of cytokinesis protein 4. [Source:Uniprot/SWISSPROT;Acc:P59764]
Dnajb5	1.387	1.061	0.949	0.807	1.089	DnaJ homolog subfamily B member 5 (Heat shock protein Hsp40-3) (Heat shock protein cognate 40) (Hsc40). [Source:Uniprot/SWISSPROT;Acc:O89114]

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Slc17a2	1.727	0.826	0.624	1.971	0.658	solute carrier family 17 (sodium phosphate), member 2
Fstl4	0.56	0.582	1.009	1.219	1.178	follistatin-like 4
1700011E24Rik	2.531	0.203	0.433	0.551	0.859	hypothetical protein LOC75467
Cart1	1.583	0.579	0.82	1.333	1.301	cartilage homeo protein 1. [Source:RefSeq;Acc:NM_172553]
Atp13a2	1.28	1.22	1.181	0.907	0.982	Probable cation-transporting ATPase 1 (EC 3.6.3.-) (Fragment). [Source:Uniprot/SWISSPROT;Acc:Q9CTG6]
Tcte3	0.623	0.892	1.085	0.821	1.316	T complex testis-specific protein 2 (TCTEX-2). [Source:Uniprot/SWISSPROT;Acc:P11985]
Zfp39	1.355	0.85	1.238	0.834	0.559	Zinc finger protein 39 (Zfp-39) (CtFIN33) (Fragment). [Source:Uniprot/SWISSPROT;Acc:Q02525]
Inhbb	0.472	0.978	1.224	0.618	1.075	Inhibin beta B chain precursor (Activin beta-B chain) (Fragment). [Source:Uniprot/SWISSPROT;Acc:Q04999]
Ppp1r14a	2.13	0.709	0.362	1.274	0.944	protein phosphatase 1, regulatory (inhibitor) subunit 14A. [Source:RefSeq;Acc:NM_026731]
E330009J07Rik	1.214	0.933	0.478	0.869	0.426	hypothetical protein
D8Ertd354e	1.873	0.526	0.849	1.002	0.678	DNA segment, Chr 8, ERATO Doi 354, expressed (D8Ertd354e)
ENSMUSG00000037263	0.603	1.054	1.06	1.783	1.184	aldehyde dehydrogenase 7-like. [Source:RefSeq;Acc:NM_028545]
4930578C19Rik	1.88	1.215	0.511	1.695	0.406	hypothetical protein LOC75905
Ranbp10	1.563	1.199	0.903	1.17	0.899	Ran-binding protein 10. [Source:RefSeq;Acc:NM_145824]
ENSMUSG00000037482	1.808	1.198	0.979	1.443	1.387	hypothetical protein
Nr0b2	1.692	1.003	0.951	2.245	1.43	Nuclear receptor 0B2 (Orphan nuclear receptor SHP) (Small heterodimer partner). [Source:Uniprot/SWISSPROT;Acc:Q62227]
Nme1	1.245	1.013	1.116	1.107	1.026	Nucleoside diphosphate kinase A (EC 2.7.4.6) (NDK A) (NDP kinase A) (Tumor metastatic process-associated protein) (Metastasis inhibition factor NM23) (NDPK-A) (nm23-M1). [Source:Uniprot/SWISSPROT;Acc:P15532]
Wdtc1	0.723	1.026	0.623	1.178	1.049	WD and tetratricopeptide repeats protein 1. [Source:Uniprot/SWISSPROT;Acc:Q80ZK9]
Ahdc1	2.063	0.544	0.862	0.604	0.476	AT hook, DNA binding motif, containing 1
2810002N01Rik	0.753	1.311	1.369	0.901	0.947	hypothetical protein LOC68020
Mat1a	1.772	0.853	1.292	0.929	1.169	methionine adenosyltransferase I, alpha; S-adenosylmethionine synthetase.

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Fgd3	0.673	1.377	0.663	1.167	0.74	FYVE, RhoGEF and PH domain containing 3; faciogenital dysplasia homolog 3; Fgd1 family, member 3. [Source:RefSeq;Acc:NM_015759]
Nsd1	0.71	1.27	1.156	0.946	1.066	nuclear receptor-binding SET-domain protein 1
Q9D4G7	0.422	1.664	0.606	1.321	1.261	hypothetical protein
Dnahc10	0.753	0.429	1.387	1.292	0.805	PREDICTED: dynein, axonemal, heavy chain 10 ()
AK172909	1.414	1.152	0.932	1.028	0.817	hypothetical protein
Kcnj9	1.282	0.098	0.746	1.3	1.415	G protein-activated inward rectifier potassium channel 3 (GIRK3) (Potassium channel, inwardly rectifying, subfamily J, member 9) (Inwardly rectifier K channel Kir3.3). [Source:Uniprot/SWISSPROT;Acc:P48543]
BC063065	1.493	1.353	1.006	1.112	1.086	hypothetical protein
Spon1	1.754	1.157	1.425	2.249	0.869	spondin 1, (f-spondin) extracellular matrix protein. [Source:RefSeq;Acc:NM_145584]
Hand2	1.848	0.611	0.92	1.876	1.367	Heart- and neural crest derivatives-expressed protein 2 (Deciduum, heart, autonomic nervous system and neural crest derivatives-expressed protein 2) (dHAND) (Helix-loop-helix transcription factor expressed in embryo and deciduum) (Thing-2). [Source:Uniprot/SWISSPROT;Acc:Q61039]
Mical2	2.618	0.3	0.544	0.956	0.691	Protein MICAL-2. [Source:Uniprot/SWISSPROT;Acc:Q8BML1]
Usp5	1.53	0.986	1.141	0.899	0.864	Ubiquitin carboxyl-terminal hydrolase 5 (EC 3.1.2.15) (Ubiquitin thiolesterase 5) (Ubiquitin-specific processing protease 5) (Deubiquitinating enzyme 5) (Isopeptidase T). [Source:Uniprot/SWISSPROT;Acc:P56399]
Fchsd1	1.44	0.971	0.932	1.347	0.897	FCH and double SH3 domains 1. [Source:RefSeq;Acc:NM_175684]
Car14	1.499	0.875	1.026	1.241	0.443	Carbonic anhydrase XIV precursor (EC 4.2.1.1) (Carbonate dehydratase XIV) (CA-XIV). [Source:Uniprot/SWISSPROT;Acc:Q9WVT6]
AI592645	0.585	0.658	0.856	1.094	1.266	PREDICTED: similar to hypothetical protein BC017397 (LOC433627)
Nfe2l1	1.209	1.505	0.922	1.312	0.356	Nuclear factor erythroid 2 related factor 1 (NF-E2 related factor 1) (NFE2-related factor 1) (Nuclear factor, erythroid derived 2, like 1). [Source:Uniprot/SWISSPROT;Acc:Q61985]
Hoxb5	0.552	1.217	0.82	0.944	0.991	Homeobox protein Hox-B5 (Hox-2.1) (MU-1) (H24.1). [Source:Uniprot/SWISSPROT;Acc:P09079]

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Hoxb7	0.49	0.246	1.622	0.528	0.959	Homeobox protein Hox-B7 (Hox-2.3) (MUB1) (MH-22B). [Source:Uniprot/SWISSPROT;Acc:P09024]
Hace1	1.801	0.971	1.366	1.054	0.608	HECT domain and ankyrin repeat containing, E3 ubiquitin protein ligase 1
Tut1	1.521	1.469	1.089	1.073	0.893	RNA binding motif protein 21
Atpbd3	0.674	1.343	0.91	0.625	1.356	ATP binding domain 3
Ube2l3	1.245	0.942	1.071	1.015	1.114	Ubiquitin-conjugating enzyme E2-18 kDa UbcH7 (EC 6.3.2.19) (Ubiquitin- protein ligase) (Ubiquitin carrier protein) (UbcM4) (E2-F1) (L-UBC). [Source:Uniprot/SWISSPROT;Acc:P51966]
Q8BUV4	1.369	1.601	0.686	0.818	1.155	Myosin heavy chain MYR 8 homolog (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8BUV4]
Rln1	1.963	0.683	1.946	0.884	1.373	Prorelaxin 1 precursor. [Source:Uniprot/SWISSPROT;Acc:P47932]
Mycbpap	1.768	0.933	0.822	0.502	0.589	Myc-binding protein-associated protein; AMY1-associating protein 1. [Source:RefSeq;Acc:NM_170671]
Suv39h1	0.594	1.017	0.887	1.379	0.769	Histone-lysine N-methyltransferase, H3 lysine-9 specific 1 (EC 2.1.1.43) (Histone H3-K9 methyltransferase 1) (H3-K9-HMTase 1) (Suppressor of variegation 3-9 homolog 1) (Su(var)3-9 homolog 1) (Position-effect variegation 3-9 homolog). [Source:Uniprot/SWISSPROT;Acc:O54864]
Pomt1	0.563	2.38	0.784	0.73	1.179	Protein O-mannosyl-transferase 1 (EC 2.4.1.109) (Dolichyl-phosphate- mannose--protein mannosyltransferase 1). [Source:Uniprot/SWISSPROT;Acc:Q8R2R1]
Ppl	2.087	0.95	0.335	1.604	1.284	Periplakin. [Source:Uniprot/SWISSPROT;Acc:Q9R269]
Q8BNV6	1.92	0.266	1.262	0.953	0.695	hypothetical protein
Q9CUI4	1.537	2.487	0.58	0.287	1.313	hypothetical protein
Kcne1	1.32	3.222	0.518	0.651	1.51	Potassium voltage-gated channel subfamily E member 1 (IKs producing slow voltage-gated potassium channel beta subunit Mink) (Minimal potassium channel) (Delayed rectifier potassium channel subunit IsK) (mISK). [Source:Uniprot/SWISSPROT;Acc:P23299]
ENSMUSG00000039697	0.529	0.35	0.225	0.286	0.907	hypothetical protein
Trim14	0.506	1.104	1.176	0.794	1.153	PU.1 binding protein Pub. [Source:RefSeq;Acc:NM_029077]

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Lrrc17	0.464	1.155	1.6	3.534	1.049	hypothetical protein
Mrap	0.741	0.918	1.072	0.534	0.797	Fat cell-specific low molecular weight protein (Fat tissue-specific low MW protein). [Source:Uniprot/SWISSPROT;Acc:Q9D159]
Q9D4F2	1.705	0.936	1.455	0.523	0.876	hypothetical protein
LOC620538	1.907	0.522	0.904	1.755	0.595	hypothetical protein
Fmo1	1.532	1.224	1.246	0.872	0.583	Dimethylaniline monooxygenase [N-oxide forming] 1 (EC 1.14.13.8) (Hepatic flavin-containing monooxygenase 1) (FMO 1) (Dimethylaniline oxidase 1). [Source:Uniprot/SWISSPROT;Acc:P50285]
Fbxl4	1.733	0.978	1.275	1.159	0.884	F-box and leucine-rich repeat protein 4. [Source:RefSeq;Acc:NM_172988]
Rabggta	1.325	1.249	0.843	0.964	1.261	Geranylgeranyl transferase type II alpha subunit (EC 2.5.1.60) (Rab geranylgeranyltransferase alpha subunit) (Rab geranyl- geranyltransferase alpha subunit) (Rab GG transferase alpha) (Rab GGTase alpha). [Source:Uniprot/SWISSPROT;Acc:Q9JHK4]
Tsfm	1.327	0.651	0.908	1.098	1.119	Elongation factor Ts, mitochondrial precursor (EF-Ts) (EF-TsMt). [Source:Uniprot/SWISSPROT;Acc:Q9CZR8]
Cblc	1.74	0.544	1.003	0.311	1.06	Casitas B-lineage lymphoma c. [Source:RefSeq;Acc:NM_023224]
Ctdsp2	1.42	0.966	1.225	1.205	0.787	Nuclear LIM interactor-interacting factor 2; NLI-interacting factor 2. [Source:RefSeq;Acc:NM_146012]
ENSMUSG00000040575	0.435	1.321	0.754	0.376	0.995	hypothetical protein
Nlrp1a	1.538	1.529	0.945	1.097	1.267	NACHT, leucine rich repeat and PYD containing 1
ENSMUSG00000040612	2.331	1.544	1.467	0.394	0.814	hypothetical protein
Q9CUV2	0.585	1.754	1.785	1.195	0.464	PREDICTED: similar to restin; cytoplasmic linker protein 50; Reed-Steinberg cell-espressed intermediate filament-associated protein (LOC433773)
Erg	1.313	1.272	1.553	1.228	1.089	Transcriptional regulator ERG. [Source:Uniprot/SWISSPROT;Acc:P81270]
ENSMUSG00000040828	1.973	0.785	1.241	0.212	0.634	hypothetical protein
ENSMUSG00000040936	1.511	1.093	1.285	0.815	1.191	hypothetical protein
Arhgef1	1.397	0.897	0.928	0.788	1.073	Rho guanine nucleotide exchange factor 1 (Lymphoid blast crisis like 2) (Lbc's second cousin). [Source:Uniprot/SWISSPROT;Acc:Q61210]
Npnt	1.562	0.815	1.24	0.593	1.201	nephronectin. [Source:RefSeq;Acc:NM_033525]

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
H2afv	0.799	0.961	1.009	0.986	0.989	Similar to histone H2A.F/Z variant. [Source:Uniprot/SPTREMBL;Acc:Q8R029]
Lonp1	1.424	2.146	0.873	0.79	1.339	1200017E13Rik protein (EC 3.4.21.-) (Mitochondrial Lon protease homolog). [Source:Uniprot/SPTREMBL;Acc:Q9DBP9]
Arhgap12	0.684	1.315	1.199	1.061	0.921	Rho-GTPase-activating protein 12. [Source:Uniprot/SWISSPROT;Acc:Q8C0D4]
Lamp3	1.845	0.561	0.821	0.357	1.31	lysosomal-associated membrane protein 3; dendritic cells-lysosome associated membrane glycoprotein. [Source:RefSeq;Acc:NM_177356]
ENSMUSG00000041482	3.281	1.67	0.46	0.519	0.954	hypothetical protein
Stx3	1.287	1.094	0.92	1.245	1.746	Syntaxin 3. [Source:Uniprot/SWISSPROT;Acc:Q64704]
ENSMUSG00000041546	0.451	1.263	0.364	1.504	0.268	hypothetical protein
Tssk1	1.835	1.573	0.734	0.757	1.232	Serine/threonine-protein kinase 22A (EC 2.7.1.37) (Testis-specific kinase 1) (TSK-1) (Testis-specific serine kinase 1) (TSSK-1). [Source:Uniprot/SWISSPROT;Acc:Q61241]
ENSMUSG00000041735	1.382	0.775	0.917	1.061	0.78	hypothetical protein
Ccrl1	0.704	0.946	0.82	1.019	0.338	chemokine (C-C) receptor-like 1; chemokine receptor CCX-CKR; chemokine receptor CCR11. [Source:RefSeq;Acc:NM_145700]
V1rk1	0.356	0.864	0.12	0.61	0.807	vomeronasal 1 receptor, K1. [Source:RefSeq;Acc:NM_134227]
Rhod	1.422	0.583	1.064	1.495	1.768	Rho-related GTP-binding protein RhoD. [Source:Uniprot/SWISSPROT;Acc:P97348]
ENSMUSG00000042165	0.618	1.424	1.028	0.895	0.989	hypothetical protein
Chchd7	1.561	1.418	0.947	1.106	1.286	coiled-coil-helix-coiled-coil-helix domain containing 7
BC037111	0.524	0.153	0.3	0.939	0.725	hypothetical protein
Prox2	0.561	1.021	1.367	0.749	0.53	prospero homeobox 2
ENSMUSG00000042377	1.619	0.352	0.893	0.577	1.012	hypothetical protein
Atf4	0.729	0.965	0.982	1.322	1.074	Cyclic-AMP-dependent transcription factor ATF-4 (C/EBP-related ATF) (C/ATF) (TAXREB67 homolog). [Source:Uniprot/SWISSPROT;Acc:Q06507]
Zmym6	1.566	0.327	0.449	1.024	0.892	zinc finger protein 258
Agps	0.582	1.285	1.456	0.936	0.964	alkylglycerone phosphate synthase. [Source:RefSeq;Acc:NM_172666]
Acot5	2.983	1.157	0.855	1.098	1.19	acyl-CoA thioesterase 5

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
ENSMUSG00000042420	3.081	0.495	1.345	1.106	0.759	hypothetical protein
Zfp410	1.716	0.808	0.884	0.952	1.225	Zinc finger protein APA-1 (Another partner for ARF 1). [Source:Uniprot/SWISSPROT;Acc:Q8BKX7]
Eif2c4	0.58	0.172	0.735	1.126	0.428	Eukaryotic translation initiation factor 2C 4 (eIF2C 4) (eIF-2C 4) (Piwi/argonaute family protain meIF2C4). [Source:Uniprot/SWISSPROT;Acc:Q8CJF8]
ENSMUSG00000044145	2.132	1.91	1.163	2.346	1.246	hypothetical protein
Maff	1.319	0.526	1.033	1.023	1.809	Transcription factor MafF (V-maf musculoaponeurotic fibrosarcoma oncogene homolog F). [Source:Uniprot/SWISSPROT;Acc:O54791]
Muc1	1.61	1.13	1.011	1.318	1.029	Mucin 1 precursor (Polymorphic epithelial mucin) (PEMT) (Episialin). [Source:Uniprot/SWISSPROT;Acc:Q02496]
Sbk1	1.866	0.876	1.172	1.392	1.338	SH3-binding kinase; CG4945-like. [Source:RefSeq;Acc:NM_145587]
Ifnk	1.274	1.997	0.32	1.742	1.57	interferon kappa precursor. [Source:RefSeq;Acc:NM_199157]
Ccdc52	1.386	1.099	1.53	1.066	0.867	coiled-coil domain containing 52
3222402P14Rik	0.581	0.992	1.15	0.899	0.291	Serine/threonine protein phosphatase 2A. [Source:Uniprot/SPTREMBL;Acc:Q8BVE6]
Arl11	1.697	1.062	1.049	0.928	0.579	ADP-ribosylation factor-like 11; ADP-ribosylation factor-like tumor suppressor protein 1. [Source:RefSeq;Acc:NM_177337]
Q8VEN3	0.814	1.379	1.163	1.257	0.941	hypothetical protein
Leng9	1.271	1.123	1.002	0.684	0.798	leukocyte receptor cluster (LRC) member 9. [Source:RefSeq;Acc:NM_175529]
ENSMUSG00000043566	0.788	1.048	1.013	0.855	1.397	hypothetical protein
Acpl2	1.45	1.3	1.546	0.911	1.122	acid phosphatase-like 2
ENSMUSG00000043705	0.495	0.856	1.282	1.409	0.914	hypothetical protein
Olfr94	2.022	1.083	1.481	0.185	1.242	Olfactory receptor GA_x6K02T2PSCP-1637650-1636712 (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q7TRL0]
Tmem145	1.564	1.193	1.041	0.465	0.536	hypothetical protein LOC330485
ENSMUSG00000043897	0.437	1.053	1.103	1.071	0.789	hypothetical protein
Naalad2	2.187	0.906	1.398	2.278	1.507	N-acetylated-alpha-linked acidic dipeptidase II (EC 3.4.17.21) (NAALADase II) (Fragment). [Source:Uniprot/SWISSPROT;Acc:Q9CZR2]
Q9DCX6	1.396	1.274	1.257	1.563	1.237	hypothetical protein

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BC038822	0.412	0.355	1.4	1.082	0.907	hypothetical protein LOC239647
ENSMUSG00000044357	2.331	0.6	1.142	0.876	1.044	hypothetical protein
ENSMUSG00000044361	1.506	1.143	1.085	1.13	0.589	hypothetical protein
Dsg2	1.996	0.309	1.332	0.987	1.387	Desmoglein 2 precursor. [Source:Uniprot/SWISSPROT;Acc:O55111]
2310022M17Rik	0.653	1.822	0.742	0.803	1.037	hypothetical protein LOC69556
Zfp488	0.459	1.239	1.156	1.153	0.136	zinc finger protein 488
BY715046	2.004	0.563	0.845	0.495	0.828	PREDICTED: similar to Chromosome-associated kinesin KIF4A (Chromokinesin) (LOC238379)
AJ564976	0.555	1.185	1.156	1.15	1.097	PREDICTED: protocadherin 11 X-linked (Pcdh11x)
Rasip1	0.655	1.117	0.785	1.096	0.776	PREDICTED: Ras interacting protein 1 (Rasip1)
BC035295	0.674	0.661	0.63	0.942	1.029	cDNA sequence BC035295; TGF-beta induced apoptosis protein 12. [Source:RefSeq;Acc:NM_153407]
Ly6k	2.728	1.13	0.939	1.085	0.996	2410015A16Rik protein (Similar to cDNA for differentially expressed CO16 gene). [Source:Uniprot/SPTREMBL;Acc:Q9CWP4]
Dok7	1.547	0.273	1.263	1.942	0.766	downstream of tyrosine kinase 7
Fads6	2.018	0.837	1.197	0.847	1.917	fatty acid desaturase domain family, member 6
BC059049	1.341	1.007	1.117	1.036	1.018	PREDICTED: cDNA sequence BC031601 (BC031601)
D630023F18Rik	1.623	1.718	0.633	0.586	1.287	hypothetical protein LOC98303
ENSMUSG00000044831	2.074	0.979	1.39	0.083	0.605	hypothetical protein
Lsm11	0.662	0.679	1.12	0.866	0.689	U7 snRNA-associated Sm-like protein Lsm11. [Source:RefSeq;Acc:NM_028185]
BC050099	1.499	1.084	0.706	0.31	0.944	Cea12 protein (Fragment). [Source:Uniprot/SPTREMBL;Acc:O08927]
ENSMUSG00000044938	2.295	0.935	0.58	2.166	1.579	hypothetical protein
Ubtd2	2.113	1.349	0.861	1.125	0.949	hypothetical protein
Asah3	0.679	1.566	1.846	0.824	1.148	N-acylsphingosine amidohydrolase 3; alkaline ceramidase. [Source:RefSeq;Acc:NM_175731]
1700024P04Rik	0.651	0.332	0.516	1.391	0.76	hypothetical protein
Cetn4	0.636	1.22	0.754	0.329	1.159	centrin 4. [Source:RefSeq;Acc:NM_145825]
Kcng3	1.901	0.9	0.788	1.778	1.466	Potassium voltage-gated channel subfamily G member 3 (Voltage-gated potassium channel subunit Kv6.3) (Kv10.1). [Source:Uniprot/SWISSPROT;Acc:P59053]

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Olfr1445	1.281	0.685	0.846	1.789	1.18	olfactory receptor 1445; olfactory receptor MOR202-7; GA_x6K02T2RE5P-3213352-3214296. [Source:RefSeq;Acc:NM_146699]
AI467606	0.776	1.107	1.005	1.122	1.254	expressed sequence AI467606 (AI467606)
TVB5_MOUSE	3.08	0.677	1.285	1.269	0.519	T-cell receptor beta chain V region C5 precursor (Fragment). [Source:Uniprot/SWISSPROT;Acc:P04213]
ENSMUSG00000045191	2.134	1.515	1.168	0.487	0.799	hypothetical protein 9530053H22 (9530053H22)
Olfr1390	2.081	0.581	1.424	2.496	1.358	olfactory receptor 1390; GA_x6K02T2QP88-6094111-6093176; olfactory receptor MOR256-2. [Source:RefSeq;Acc:NM_147065]
Gpr109a	0.573	0.909	0.605	0.81	1.836	G protein-coupled receptor 109B; putative seven transmembrane spanning receptor; interferon-gamma inducible gene, Puma-g. [Source:RefSeq;Acc:NM_030701]
Penk1	1.685	2.338	1.358	1.053	1.569	Proenkephalin A precursor [Contains: Synenkephalin; Met-enkephalin (Opioid growth factor) (OGF); Met-enkephalin-Arg-Ser-Leu; Leu- enkephalin; Met-enkephalin-Arg-Phe]. [Source:Uniprot/SWISSPROT;Acc:P22005]
Pigz	1.787	0.972	1.174	0.955	0.665	SMP3 mannosyltransferase
Q8C1H0	0.619	2.705	0.361	2.248	0.565	Similar to ribonuclease/angiogenin inhibitor 2 (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8C1H0]
9830130M13Rik	0.575	2.134	1.331	1.336	0.87	hypothetical protein LOC238875
ENSMUSG00000046014	0.774	0.897	0.93	1.213	0.901	hypothetical protein
Psg21	0.673	1.197	0.75	0.998	1.145	pregnancy-specific glycoprotein 21; pregnancy-specific glrcoprotein 21. [Source:RefSeq;Acc:NM_027403]
CB173849	1.976	1.658	0.8	1.393	1.201	PREDICTED: similar to chromosome X open reading frame 22 (LOC434805)
LOC245693	1.96	0.633	1.431	0.837	0.384	similar to Protein C9orf138
Kcnrg	1.533	1.34	0.5	1.378	0.883	potassium channel regulator. [Source:RefSeq;Acc:NM_206974]
Nxph1	2.763	1.14	1.198	0.965	0.966	Neurexophilin 1 precursor (Fragment). [Source:Uniprot/SWISSPROT;Acc:Q61200]
Q8BQU9	2.789	1.237	1.153	1.025	1.122	hypothetical protein
Plaur	1.366	0.699	0.804	0.971	1.318	Urokinase plasminogen activator surface receptor, GPI-anchored form precursor (uPAR) (U-PAR) (CD87 antigen). [Source:Uniprot/SWISSPROT;Acc:P35456]
Adam29	2.265	1.596	1.814	1.715	0.901	a disintegrin and metalloprotease domain 29

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ENSMUSG00000046274	1.789	0.962	1.228	1.21	0.881	hypothetical protein
ENSMUSG00000046295	1.812	0.464	0.905	0.365	1.144	hypothetical protein
ENSMUSG00000046330	0.571	0.893	0.967	1.035	1.161	hypothetical protein
Pcdhb17	2.087	3.8	0.569	1.015	0.747	protocadherin beta 17. [Source:RefSeq;Acc:NM_053142]
ENSMUSG00000046555	1.52	0.686	0.183	0.583	1.509	hypothetical protein
B230396O12Rik	1.541	1.531	0.697	1.208	1.562	hypothetical protein
Q8C9C9	1.456	1.608	0.927	0.213	0.568	hypothetical protein
4732496O08Rik	0.508	1.219	0.755	1.093	0.961	hypothetical protein LOC242736
ENSMUSG00000046940	2.864	2.019	0.579	1.082	0.808	hypothetical protein
Adck2	2.004	1.192	0.734	0.942	0.831	aarF domain containing kinase 2; EST AA408112. [Source:RefSeq;Acc:NM_178873]
Gpr156	1.944	1.196	1.111	0.397	1.213	G protein-coupled receptor 156; GABAB-related G-protein coupled receptor. [Source:RefSeq;Acc:NM_153394]
Muc5ac	1.952	1.318	1.161	1.549	1.23	Muc5AC protein (Fragment). [Source:Uniprot/SPTREMBL;Acc:O88715]
Rnf31	1.359	1.033	0.852	1.204	1.033	RING finger protein 31. [Source:Uniprot/SWISSPROT;Acc:Q924T7]
9130227C08Rik	1.416	1.449	0.799	1.158	0.525	hypothetical protein LOC219094
B3gnt7	0.646	0.75	0.797	0.989	1.364	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7. [Source:RefSeq;Acc:NM_145222]
B3gnt1	0.726	1.429	1.43	1.032	0.877	beta-1,3-N-acetylglucosaminyltransferase bGnT-6. [Source:RefSeq;Acc:NM_175383]
4932411E22Rik	1.477	1.05	1.092	1.057	0.478	hypothetical protein LOC214604
Dmbt1	2.335	1.26	1.016	0.968	0.926	deleted in malignant brain tumors 1; crp-ductin; vomeroglandin; muclin. [Source:RefSeq;Acc:NM_007769]
Neurod4	1.425	0.066	1.558	1.135	1.226	Neurogenic differentiation factor 4 (NeuroD4) (Atonal protein homolog 3) (Helix-loop-helix protein mATH-3) (MATH3). [Source:Uniprot/SWISSPROT;Acc:O09105]
ENSMUSG00000048041	1.461	0.784	0.843	0.387	1.273	hypothetical protein
Ldlrad3	2.138	0.777	0.612	0.216	1.602	low density lipoprotein receptor class A domain containing 3
H1fnt	2.148	1.418	0.745	1.268	1.734	histone H1 variant

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
BC037267	0.623	1.339	1.032	0.996	0.838	hypothetical protein
KV5C_MOUSE	1.907	0.213	1.594	5.065	0.911	Ig kappa chain V-V region K2 precursor (Fragment). [Source:Uniprot/SWISSPROT;Acc:P01635]
LOC232887	1.332	1.242	1.249	0.862	1.386	similar to WD repeat domain 12
Pou4f1	0.824	0.639	1.444	1.595	0.235	POU domain, class 4, transcription factor 1 (Brain-specific homeobox/POU domain protein 3A) (Brn-3A) (Brn-3.0). [Source:Uniprot/SWISSPROT;Acc:P17208]
Naip5	0.742	1.583	0.984	0.752	0.996	Baculoviral IAP repeat-containing protein 1b (Neuronal apoptosis inhibitory protein 2). [Source:Uniprot/SWISSPROT;Acc:Q9QUK4]
Cyp4f13	1.684	0.907	0.689	0.821	0.924	cytochrome P450, family 4, subfamily f, polypeptide 13; cytochrome P450 CYP4F13; cytochrome P450,subfamily IVF, polypeptide 13; leukotriene B4 omega hydroxylase; P450 CYP4F13. [Source:RefSeq;Acc:NM_130882]
Zbtb8	2.207	0.234	0.739	1.396	0.656	Zinc finger and BTB domain containing protein 8. [Source:Uniprot/SWISSPROT;Acc:Q8CII0]
Adam26a	0.62	0.525	1.179	1.701	0.609	ADAM 26 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase domain 26) (Testase 3). [Source:Uniprot/SWISSPROT;Acc:Q9R158]
Nhlh2	1.45	0.21	0.417	1.138	0.757	Helix-loop-helix protein 2 (HEN2) (Nescient helix loop helix 2) (NSCL- 2). [Source:Uniprot/SWISSPROT;Acc:Q64221]
Cypt3	1.279	1.326	0.688	1.68	1.751	basic protein CKT1R1. [Source:RefSeq;Acc:NM_173367]
ENSMUSG00000048849	1.476	1.049	1.142	1.037	1.194	hypothetical protein
ENSMUSG00000048896	0.023	1.537	1.06	0.63	0.219	hypothetical protein
Rnf24	0.62	0.691	1.004	0.476	0.673	ring finger protein 24. [Source:RefSeq;Acc:NM_178607]
Pcdh10	0.584	0.863	1.471	0.847	0.805	protocadherin 10; OL-protocadherin. [Source:RefSeq;Acc:NM_011043]
Wdr22	1.569	0.848	0.654	0.968	0.723	WD-repeat protein 22. [Source:Uniprot/SWISSPROT;Acc:Q80T85]
ENSMUSG00000049109	1.598	1.039	1.03	1.185	0.914	hypothetical protein
Olfr509	0.354	1.167	1.491	0.737	1	olfactory receptor 509; olfactory receptor MOR267-14; GA_x6K02T2PBJ9-10976304-10975339. [Source:RefSeq;Acc:NM_146372]
BC038925	1.836	1.749	1.249	0.788	0.904	hypothetical protein LOC330216
Trappc1	0.745	1.251	1.222	1.003	1.166	trafficking protein particle complex 1
Smcr8	2.414	0.622	0.446	0.978	0.932	Smith-Magenis syndrome chromosome region, candidate 8 homolog. [Source:RefSeq;Acc:NM_175491]

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
C030003D03Rik	0.595	0.977	1.352	0.909	0.643	hypothetical protein LOC77220
2810046L04Rik	1.444	1.232	0.867	0.987	0.749	hypothetical protein LOC212127
Espnl	2.751	2.058	0.619	0.129	0.888	espin-like
ENSMUSG00000049565	2.642	0.567	0.989	0.909	0.261	hypothetical protein 4921525H12 (4921525H12)
Arhgap15	0.631	1.263	1.507	0.698	1.048	Rho GTPase activating protein 15. [Source:RefSeq;Acc:NM_153820]
Fzd4	0.586	0.453	1.868	0.844	0.649	Frizzled 4 precursor (Frizzled-4) (Fz-4) (mFz4). [Source:Uniprot/SWISSPROT;Acc:Q61088]
ENSMUSG00000049815	0.323	1.831	0.965	1.479	1.493	hypothetical protein
Arl4c	0.664	0.716	1.31	0.826	1.245	ADP-ribosylation factor-like protein 7. [Source:Uniprot/SWISSPROT;Acc:P61208]
Zfp697	0.526	1.199	0.91	1.133	1.119	zinc finger protein 697
ENSMUSG00000050196	2.258	1.388	0.875	1.365	0.975	hypothetical protein
2310030N02Rik	1.48	1.15	1.274	0.881	1.055	hypothetical protein
CB316915	2.04	1.569	1.539	1.541	0.675	hypothetical protein
Olfr524	0.669	0.831	1.101	0.555	0.72	Olfactory receptor GA_x6K02T2PBJ9-42354580-42353624. [Source:Uniprot/SPTREMBL;Acc:Q7TRU0]
Hoxd10	2.572	1.609	0.973	1.137	0.662	Homeobox protein Hox-D10 (Hox-4.5) (Hox-5.3). [Source:Uniprot/SWISSPROT;Acc:P28359]
LOC381065	0.407	1.679	0.459	0.786	1.063	similar to U1 small nuclear ribonucleoprotein A (U1 snRNP protein A) (U1A protein) (U1-A)
Olfr1008	2.605	0.485	1.317	0.797	1.31	olfactory receptor 1008; olfactory receptor MOR187-3; GA_x6K02T2Q125-47170431-47171372. [Source:RefSeq;Acc:NM_146866]
ENSMUSG00000050676	0.765	1.179	0.907	1.012	0.994	hypothetical protein
Prkaa1	1.258	1.076	1.376	0.932	1.019	5'-AMP-activated protein kinase (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8BUX6]
Olfr164	1.346	0.226	0.79	1.572	1.372	olfactory receptor 164; olfactory receptor MOR279-2; GA_x54KRFPKG5P-15738260-15737319. [Source:RefSeq;Acc:NM_146451]
AI595036	0.368	1.06	0.961	0.249	0.676	hypothetical protein
Defb6	0.69	0.453	1.637	1.924	1.469	defensin beta 6. [Source:RefSeq;Acc:NM_054074]
Olfr1494	1.778	0.91	1.75	1.719	2.054	olfactory receptor 1494; olfactory receptor MOR266-1; GA_x6K02T2RE5P-4082427-4083374.

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Q8BQ82	3.22	0.886	0.3	1.165	0.424	hypothetical protein
9130014G24Rik	1.765	0.341	0.895	0.46	1.176	hypothetical protein LOC215772
1700014D04Rik	1.907	0.849	0.837	2.594	0.816	hypothetical protein LOC74224
Olfr672	1.532	0.701	1.477	1.672	1.152	olfactory receptor 672; olfactory receptor MOR32-4; odorant receptor S46 gene; GA_x6K02T2PBJ9-7625746-7624808. [Source:RefSeq;Acc:NM_146760]
4930422G04Rik	2.399	1.168	0.981	1.546	0.951	prematurely terminated mRNA decay factor-like isoform 2
9630028B13Rik	1.516	0.598	0.916	1.29	0.594	hypothetical protein LOC319562
2900026A02Rik	1.505	1.191	0.879	0.889	1.234	hypothetical protein LOC243219
Pcdh1	1.86	0.482	0.77	1.017	0.959	protocadherin 1
Ywhag	1.961	1.978	0.756	1.333	0.746	14-3-3 protein gamma. [Source:Uniprot/SWISSPROT;Acc:P61982]
ENSMUSG00000051440	1.539	1.189	0.858	0.917	0.824	hypothetical protein
ENSMUSG00000051452	2.491	0.262	1.433	0.838	1.065	hypothetical protein
Q8CDD5	0.748	0.694	1.172	0.428	0.67	hypothetical protein
Lrrc3	1.506	2.662	0.374	1.238	0.858	Leucine-rich repeat protein LRRC3 precursor. [Source:Uniprot/SWISSPROT;Acc:P59034]
Olfr284	2.008	0.461	1.905	2.301	1.321	olfactory receptor 284; olfactory receptor MOR160-4; GA_x6K02T2NBG7-5395976-5396893. [Source:RefSeq;Acc:NM_146281]
Krtap8-2	1.499	1.037	0.574	1.018	1.617	keratin associated protein 8-2; keratin-associated protein 8.2; keratin-associated protein 8-2; HGTpI alpha. [Source:RefSeq;Acc:NM_010676]
Gli2	1.501	0.68	1.012	0.892	0.859	GLI-Kruppel family member GLI2
AI595101	0.545	3.491	1.037	1.495	1.168	hypothetical protein
1700029F12Rik	1.572	1.094	0.937	0.389	1.589	hypothetical protein LOC66479 isoform 2
Q8R193	1.749	0.775	1.008	0.808	0.828	hypothetical protein
BC013672	1.289	0.958	0.688	1.036	0.885	hypothetical protein
Hbb-bh1	2.175	0.453	1.584	1.018	0.725	Hemoglobin beta-H1 chain (Z protein). [Source:Uniprot/SWISSPROT;Acc:P04444]
Q8C3V1	0.689	0.314	0.67	1.443	1.123	hypothetical protein

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
ENSMUSG00000052256	1.547	1.192	0.891	0.868	1.113	hypothetical protein
ENSMUSG00000052334	1.287	0.269	1.265	1.387	0.961	hypothetical protein
Q8C8F9	2.004	0.889	0.957	1.257	1.375	hypothetical protein
Tcp10a	0.825	0.637	0.915	1.015	1.442	t-complex protein 10b. [Source:RefSeq;Acc:NM_011553]
Dlgh2	2.155	2.006	0.893	0.843	1.503	chapsyn-110; discs large homolog 2. [Source:RefSeq;Acc:NM_011807]
Q8CA86	2.44	0.925	1.073	1.133	1.512	hypothetical protein
ENSMUSG00000052688	0.748	1.666	1.314	0.947	1.531	RAB7-like protein. [Source:RefSeq;Acc:NM_145509]
ENSMUSG00000052699	0.594	0.919	1.166	0.832	1.47	hypothetical protein
ENSMUSG00000052709	1.957	0.574	0.942	0.923	1.823	hypothetical protein
A630001G21Rik	0.645	0.861	1.208	0.686	1.144	hypothetical protein LOC319997 isoform 1
Q8BQS3	1.964	1.292	1.259	1.013	0.695	hypothetical protein
ENSMUSG00000052959	3.093	0.816	1.128	1.856	1.441	hypothetical protein
3110006E14Rik	1.758	1.698	0.873	0.409	1.29	hypothetical protein
ENSMUSG00000052983	0.619	1.503	1.039	0.745	1.065	hypothetical protein
Q8C616	1.689	0.43	0.517	1.253	0.912	hypothetical protein
Q80V88	0.612	0.745	0.932	0.647	1.764	hypothetical protein
Arrdc3	1.434	1.322	0.926	0.739	0.845	arrestin domain containing 3. [Source:RefSeq;Acc:NM_178917]
ENSMUSG00000053327	0.532	1.561	0.724	1.394	0.967	PREDICTED: similar to butyrophilin-like 7 (LOC435523)
Hs6st3	1.739	0.173	0.862	0.374	1.981	heparan sulfate 6-O-sulfotransferase 3. [Source:RefSeq;Acc:NM_015820]
Q8C3U4	1.898	1.24	0.733	1.258	0.83	hypothetical protein
Cdc42bpg	2.142	0.276	1.139	0.948	0.698	CDC42 binding protein kinase gamma (DMPK-like)
Actl7b	1.977	1.018	0.834	1.278	1.619	Actin-like 7b (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q9CVR1]
ENSMUSG00000053712	1.427	0.846	0.765	0.84	0.929	PREDICTED: similar to Rac GTPase-activating protein (LOC382358)
Sox14	1.887	0.25	0.438	0.825	1.086	Transcription factor SOX-14. [Source:Uniprot/SWISSPROT;Acc:Q04892]

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Q8C4A9	0.776	0.573	1.132	0.79	1.239	hypothetical protein
Tdrd9	0.54	2.033	0.485	0.983	1.007	hypothetical protein
ENSMUSG00000054059	0.662	1.387	1.02	0.704	0.575	hypothetical protein
ENSMUSG00000054181	1.568	0.819	0.752	0.899	1.122	hypothetical protein
BC021356	0.556	0.994	1.365	1.09	0.679	hypothetical protein
Cpsf3	0.634	2.15	1.417	0.955	1.265	Cleavage and polyadenylation specificity factor, 73 kDa subunit (CPSF 73 kDa subunit). [Source:Uniprot/SWISSPROT;Acc:Q9QXK7]
Q8CEK0	0.65	1.203	0.869	1.456	1.025	hypothetical protein
OTTMUSG00000016703	0.737	2.313	0.944	1.285	1.327	hypothetical protein
Ugt1a1	0.753	0.646	0.631	0.642	1.369	UDP-glucuronosyltransferase 1-2 precursor, microsomal (EC 2.4.1.17) (UDPGT) (UGT1*0) (UGT1-02) (UGT1.2) (UGT1A2) (Bilirubin specific). [Source:Uniprot/SWISSPROT;Acc:P70691]
Cntnap2	1.512	0.476	0.275	0.225	0.705	contactin associated protein-like 2 isoform a
Q8CB91	0.611	1.316	0.513	0.79	0.555	hypothetical protein
Prkar2a	1.202	0.969	1.206	1.541	0.652	hypothetical protein
Olfr1346	2.04	1.798	1.033	0.977	0.848	olfactory receptor 1346; olfactory receptor MOR103-6; GA_x6K02T2QGBW-3203957-3204898. [Source:RefSeq;Acc:NM_146916]
Naaladl1	1.667	1.751	1.184	1.219	2.368	N-acetylated-alpha-linked acidic dipeptidase like protein. [Source:Uniprot/SPTREMBL;Acc:Q7M758]
ENSMUSG00000055354	0.738	0.633	1.001	1.006	1.445	PREDICTED: similar to chaperonin containing TCP1, subunit 3 (gamma) (LOC230185)
Pprc1	1.601	1.418	0.494	0.959	1.134	MKIAA0595 protein (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q80TW6]
Q8CAX9	0.706	1.609	0.833	1.043	1.227	hypothetical protein
LOC434676	0.643	1.509	1.193	1.882	0.99	hypothetical protein
Q8C683	3.162	0.905	1.682	0.414	0.401	hypothetical protein
Fancm	1.989	1.42	1.209	1.025	1.223	Fanconi anemia, complementation group M
ENSMUSG00000055914	0.523	1.191	1.096	1.92	0.421	hypothetical protein
OTTMUSG00000004461	0.673	1.216	0.904	0.512	0.763	hypothetical protein LOC208820
Irs1	2.02	1.172	0.674	1.858	0.886	Insulin receptor substrate-1. [Source:Uniprot/SWISSPROT;Acc:P35569]

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Eif3s9	1.464	1.059	0.987	1.003	0.984	eukaryotic translation initiation factor 3, subunit 9. [Source:RefSeq;Acc:NM_133916]
ENSMUSG00000056210	2.193	0.998	0.703	0.926	0.712	hypothetical protein
Q8BW29	1.32	1.935	1.037	1.143	0.878	hypothetical protein
Foxk1	2.042	1.475	1.228	0.85	0.816	Forkhead box protein K1 (Myocyte nuclear factor) (MNF). [Source:Uniprot/SWISSPROT;Acc:P42128]
Ppp1r14b	1.314	0.978	1.102	1.214	0.991	protein phosphatase 1, regulatory (inhibitor) subunit 14B; phospholipase c neighboring. [Source:RefSeq;Acc:NM_008889]
Retsat	1.31	1.105	1.094	1.17	0.961	all-trans-13,14-dihydroretinol saturase
ENSMUSG00000056800	0.786	1.133	0.98	1.115	1.685	hypothetical protein
EG384814	1.895	0.902	1.114	0.987	0.59	Testase-7 precursor. [Source:Uniprot/SPTREMBL;Acc:Q7M765]
Gm1008	1.421	0.478	0.79	1.628	0.719	gene model 1008, (NCBI) (Gm1008)
ENSMUSG00000056935	0.492	1.354	1.486	0.254	0.852	PREDICTED: similar to Spindlin homolog (Protein DXF34) (LOC382203)
ENSMUSG00000056952	1.541	0.858	1.458	0.789	0.904	PREDICTED: similar to KIAA0218 (LOC381801)
CA535774	1.576	0.948	2.067	1.743	1.611	PREDICTED: similar to nuclear RNA export factor 3 (LOC245610)
ENSMUSG00000057034	0.435	1.274	0.347	1.053	1.817	hypothetical protein
Fxyd3	0.683	1.863	0.661	1.942	0.52	FXYD domain-containing ion transport regulator 3 precursor (Chloride conductance inducer protein Mat-8) (Mammary tumor 8 kDa protein) (Phospholemman-like). [Source:Uniprot/SWISSPROT;Acc:Q61835]
Maml3	0.562	0.136	0.785	0.499	0.977	mastermind-like 3
ENSMUSG00000057278	0.548	0.207	0.923	1.119	0.631	hypothetical protein
V1rh12	1.428	0.748	0.907	1.37	0.248	vomeronasal 1 receptor, H12. [Source:RefSeq;Acc:NM_134237]
E2f6	1.561	1.327	1.068	1.15	1.148	Transcription factor E2F6 (E2F-6) (E2F-binding site modulating activity protein) (EMA). [Source:Uniprot/SWISSPROT;Acc:O54917]
Q8C8M5	1.875	1.147	0.506	1.047	1.346	hypothetical protein
Ece1	1.318	0.815	1.215	1.131	0.819	endothelin converting enzyme 1. [Source:RefSeq;Acc:NM_199307]
Tufm	1.334	1.695	1.324	1.278	0.946	Tu translation elongation factor, mitochondrial
ENSMUSG00000057579	1.686	0.863	1.091	1.063	2.433	hypothetical protein

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Tas2r131	3.335	1.05	1.092	0.971	1.472	taste receptor, type 2, member 131. [Source:RefSeq;Acc:NM_207030]
BC027243	1.641	1.12	0.746	1.18	0.937	hypothetical protein
ENSMUSG00000057787	1.434	1.028	0.724	0.745	1.111	H-2 class I histocompatibility antigen, D-37 alpha chain precursor. [Source:Uniprot/SWISSPROT;Acc:P06339]
ENSMUSG00000057826	2.023	1.316	1.512	1.189	0.736	hypothetical protein
ENSMUSG00000057859	1.761	0.216	1.738	1.071	0.881	hypothetical protein
AF126456	1.451	1.45	1.104	1.74	2.099	PREDICTED: similar to TRAV9-1 (LOC436541)
Zfp105	0.748	0.92	1.07	1.038	0.315	zinc finger protein 105. [Source:RefSeq;Acc:NM_009544]
ENSMUSG00000058070	0.822	0.656	1.237	0.91	1.753	hypothetical protein
BC047145	1.743	1.183	0.99	0.956	1.255	hypothetical protein
Rpl32-ps	0.664	1.33	1.017	0.92	0.927	60S ribosomal protein L32'. [Source:Uniprot/SWISSPROT;Acc:P17932]
ENSMUSG00000058140	0.46	0.572	0.72	0.853	1.151	hypothetical protein
Sez6l	0.64	0.729	0.321	1.182	2.381	Acupuncture induced gene 1. [Source:Uniprot/SPTREMBL;Acc:Q8C420]
Serpina3k	1.342	1.219	1.569	1.36	2.073	Serine proteinase inhibitor A3K precursor (Contrapsin) (Serpin A3K). [Source:Uniprot/SWISSPROT;Acc:P07759]
ENSMUSG00000058211	2.579	1.294	1.33	0.587	1.276	PREDICTED: similar to RPD3 protein (LOC225805)
Olfr25	1.339	0.789	0.584	0.852	0.955	olfactory receptor 25; olfactory receptor MOR170-4; GA_x6K02T2PVTD-32017922-32018863. [Source:RefSeq;Acc:NM_146870]
Espl1	0.657	2.047	0.743	1.747	1.494	Separin (EC 3.4.22.49) (Separase) (Caspase-like protein ESPL1) (Extra spindle poles-like 1 protein). [Source:Uniprot/SWISSPROT;Acc:P60330]
Q8C1Q6	0.817	0.89	0.92	0.844	0.961	hypothetical protein
Krt6a	1.435	0.351	1.278	0.898	1.782	Keratin, type II cytoskeletal 6 (Cytokeratin 6) (CK 6) (K6 keratin). [Source:Uniprot/SWISSPROT;Acc:P50446]
Tm9sf4	1.208	0.829	0.954	1.059	0.992	transmembrane 9 superfamily protein member 4. [Source:RefSeq;Acc:NM_133847]
Znrf2	1.3	0.857	0.953	0.93	0.946	zinc finger/RING finger 2. [Source:RefSeq;Acc:NM_199143]
ENSMUSG00000058661	2.572	1.087	2.039	0.6	0.588	hypothetical protein
0610030E20Rik	0.764	0.798	1.268	0.84	0.799	hypothetical protein LOC68364 isoform 1

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
LOC435271	0.658	0.975	0.705	0.803	1.517	Schlafen4 (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q9Z0I3]
Q9DAG0	2.072	1.307	1.3	0.562	0.46	PREDICTED: hypothetical gene supported by AK005868; BC048576 (LOC433188)
1500016O10Rik	2.203	0.951	1.592	1.114	1.135	similar to Protein FAM57B isoform 1
ENSMUSG00000058969	0.454	0.735	0.549	1.084	1.293	hypothetical protein
Q8BW33	1.302	1.268	1.177	0.77	0.165	hypothetical protein
ENSMUSG00000059014	0.626	2.304	0.398	0.918	0.528	hypothetical protein
ENSMUSG00000059094	0.381	0.28	1.328	0.761	1.224	hypothetical protein
ENSMUSG00000059114	1.453	1.131	0.85	1.837	0.641	hypothetical protein
Nap1l4	2.673	1.513	1.166	0.768	0.67	nucleosome assembly protein 1-like 4; nucleosome assembly protein 1 like 4. [Source:RefSeq;Acc:NM_008672]
ENSMUSG00000059126	2.068	0.914	2.131	1.782	0.387	hypothetical protein
ENSMUSG00000059171	2.665	2.358	0.656	2.075	0.946	reduced expression 2. [Source:RefSeq;Acc:NM_009051]
C330019L16Rik	1.907	1.164	1.373	1.454	0.818	Mszf88 (Fragment). [Source:Uniprot/SPTREMBL;Acc:O88266]
Q8CDG0	2.804	0.717	0.7	0.62	0.664	hypothetical protein
Gzmd	0.536	0.813	1.379	0.339	0.57	Granzyme D precursor (EC 3.4.21.-). [Source:Uniprot/SWISSPROT;Acc:P11033]
Erbb4	2.086	1.503	0.766	1.75	1.36	v-erb-a erythroblastic leukemia viral oncogene homolog 4 isoform 2
ENSMUSG00000059304	2.093	1.957	0.798	1.212	0.738	hypothetical protein
Taar7d	1.455	0.219	1.332	1.547	1.097	Trace amine receptor 2 (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q80UC9]
Q61883	0.689	1.856	0.809	0.892	0.74	Endogenous mammary tumor virus MTV-9 mRNA envelope gene (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q61883]
Bcas3	0.669	0.888	1.084	0.806	1.12	Breast carcinoma amplified sequence 3 homolog (K20D4). [Source:Uniprot/SWISSPROT;Acc:Q8CCN5]
Syn3	1.556	1.155	0.431	0.882	0.824	synapsin III; synapsin 3. [Source:RefSeq;Acc:NM_013722]
ENSMUSG00000059617	1.62	1.138	0.775	1.119	1.164	PREDICTED: similar to WAP four-disulfide core domain protein 8 precursor (Putative protease inhibitor WAP8) (LOC277343)
Krtap8-1	0.685	0.299	1.104	1.046	0.812	Keratin associated protein 8-1 (Hight-glycine/tyrosine protein keratin) (HGT keratin) (HGTp type I F) (Fragment). [Source:Uniprot/SWISSPROT;Acc:O08633]

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Clec4a4	1.624	1.25	1.06	0.581	0.631	dendritic cell inhibitory receptor 2 (Dcir2)
9930111J21Rik	0.584	1.005	0.723	1.587	1.795	hypothetical protein LOC245240
Gm1077	3.154	1.564	1.138	1.428	1.058	Ig kappa chain V-IV region S107B precursor. [Source:Uniprot/SWISSPROT;Acc:P01680]
ENSMUSG00000059816	1.676	2.899	2.878	0.461	0.983	hypothetical protein
BC043136	1.393	1.621	0.987	1.207	1.69	hypothetical protein
ENSMUSG00000059988	4.126	1.695	1.489	0.94	0.744	hypothetical protein
ENSMUSG00000060027	2.609	0.156	1.014	1.956	0.839	hypothetical protein
Olfr317	1.454	0.801	0.905	2.309	0.341	Olfactory receptor GA_x6K02T2NKPP-680866-681849. [Source:Uniprot/SPTREMBL;Acc:Q7TRZ5]
ENSMUSG00000060301	1.323	0.206	0.988	0.899	0.565	hypothetical protein
Olfr1447	2.342	1.322	0.718	0.882	1.169	olfactory receptor 1447; olfactory receptor MOR202-3; GA_x6K02T2RE5P-3231251-3230331. [Source:RefSeq;Acc:NM_146703]
BM935212	1.717	0.156	0.375	1.381	0.793	hypothetical protein
Tnfrsf19	2.786	0.659	0.474	1.118	0.767	Tumor necrosis factor receptor superfamily member 19 precursor (Toxicity and JNK inducer) (TRADE). [Source:Uniprot/SWISSPROT;Acc:Q9JLL3]
Q9D3T0	0.05	1.383	0.721	1.198	1.358	hypothetical protein
Rpl35a	0.715	1.724	0.81	0.649	0.848	60S ribosomal protein L35a. [Source:Uniprot/SWISSPROT;Acc:O55142]
Hist1h3d	0.75	0.699	0.813	1.003	1.068	Histone H3 (H3.2). [Source:Uniprot/SWISSPROT;Acc:P16105]
Fpr-rs4	2.552	0.505	0.149	1.177	0.407	formyl peptide receptor, related sequence 3. [Source:RefSeq;Acc:NM_008040]
Q8BXF7	2.794	1.001	0.304	0.282	0.694	Similar to tyrosine-protein kinase JAK3. [Source:Uniprot/SPTREMBL;Acc:Q8BXF7]
Olfr51	0.128	1.31	2.156	1.278	0.127	olfactory receptor 51; GA_x6K02T2QP88-4431129-4430206; olfactory receptor MOR129-3. [Source:RefSeq;Acc:NM_146909]
Hba-a1	0.503	2.479	0.801	1.133	1.334	Hemoglobin alpha chain. [Source:Uniprot/SWISSPROT;Acc:P01942]
ENSMUSG00000061049	2.261	1.009	1.212	0.464	0.902	hypothetical protein
EG232801	1.73	0.287	0.381	2.162	0.864	hypothetical protein LOC232801
ENSMUSG00000061203	0.633	0.806	1.374	1.005	1.086	hypothetical protein

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Igk-C	0.484	1.254	0.776	0.879	0.724	Ig kappa chain C region. [Source:Uniprot/SWISSPROT;Acc:P01837]
9030605E09Rik	2.134	1.021	1.718	0.148	0.369	Cytochrome P450. [Source:Uniprot/SPTREMBL;Acc:Q8BVD2]
ENSMUSG00000061384	0.606	0.863	0.627	1.041	0.735	hypothetical protein
ENSMUSG00000061417	1.431	2.039	0.904	0.586	0.346	hypothetical protein
ENSMUSG00000061432	1.495	1.694	0.391	1.4	0.764	hypothetical protein
ENSMUSG00000061490	1.545	0.904	1.051	0.972	1.037	hypothetical protein
ENSMUSG00000061507	1.447	0.294	0.514	2.082	1.307	hypothetical protein
ENSMUSG00000061545	1.395	0.29	0.763	1.601	1.994	hypothetical protein
ENSMUSG00000061597	0.514	0.227	0.31	1.098	1.029	hypothetical protein
HV61_MOUSE	1.717	1.727	2.226	0.626	1.385	Ig heavy chain V region 1B43 precursor. [Source:Uniprot/SWISSPROT;Acc:P18532]
2310047D13Rik	1.412	0.706	2.093	0.904	1.213	whn-dependent transcript 3
Q7M6W0	2.078	0.125	0.145	0.348	1.327	MCP24145. [Source:Uniprot/SPTREMBL;Acc:Q7M6W0]
ENSMUSG00000061756	1.616	1.873	1.126	1.588	0.792	hypothetical protein
Mospd2	1.43	1.386	0.742	0.76	1.019	hypothetical protein
Lcmt2	1.996	1.138	0.844	1.385	1.269	hypothetical protein
ENSMUSG00000061918	3.051	1.414	0.651	2.763	0.971	hypothetical protein
Abca14	1.465	0.828	1.251	0.947	0.451	ATP-binding cassette transporter sub-family A member 14. [Source:RefSeq;Acc:NM_026458]
ENSMUSG00000062122	2.003	0.728	0.718	1.154	1.285	hypothetical protein
ENSMUSG00000062140	1.464	0.479	0.241	0.388	1.097	hypothetical protein
Krt40	1.539	1.105	0.379	2.214	1.321	hypothetical protein
ENSMUSG00000062242	1.665	1.225	1.399	1.299	0.439	hypothetical protein
AA415398	3.035	0.836	1.237	1.092	0.663	hypothetical protein
ENSMUSG00000062299	2.151	0.631	1.22	0.814	0.387	hypothetical protein
Ap3b2	0.784	1.142	1.194	1.139	1.343	Adapter-related protein complex 3 beta 2 subunit (Beta3B-adaptin) (AP-3 complex beta-2 subunit) (Clathrin assembly protein complex 3 beta-2 large chain)

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
ENSMUSG00000062458	1.971	0.909	0.795	0.391	1.34	hypothetical protein
Olfr1411	1.864	1.41	0.962	0.425	0.758	olfactory receptor 1411; olfactory receptor MOR208-3; GA_x6K02T2R7CC-81157497-81156526. [Source:RefSeq;Acc:NM_146490]
ENSMUSG00000062500	0.346	1.466	1.348	0.412	0.705	hypothetical protein
ENSMUSG00000062513	1.996	0.093	0.63	0.889	1.407	hypothetical protein
Zfp398	1.567	1.801	0.952	1.01	0.612	zinc finger protein 398. [Source:RefSeq;Acc:NM_027477]
Mrpplf3	2.585	0.493	0.456	1.536	1	Proliferin 1 precursor (Mitogen-regulated protein 1). [Source:Uniprot/SWISSPROT;Acc:P04095]
Wfdc6b	0.484	0.937	0.924	1.077	1.493	WAP four-disulfide core domain 6
Q9D4U9	0.292	0.7	1.147	0.859	1.022	hypothetical protein
Cav3	2.015	0.649	0.705	0.497	0.71	Caveolin-3 (M-caveolin). [Source:Uniprot/SWISSPROT;Acc:P51637]
ENSMUSG00000062717	0.609	0.957	0.784	0.941	1.213	hypothetical protein
AK129310	0.443	1.48	1.181	0.303	0.813	hypothetical protein
Ppox	1.374	1.19	0.982	1.175	0.595	Protoporphyrinogen oxidase (EC 1.3.3.4) (PPO). [Source:Uniprot/SWISSPROT;Acc:P51175]
Olfr619	1.812	0.616	0.217	1.04	0.945	olfactory receptor 619; olfactory receptor MOR31-5; GA_x6K02T2PBJ9-6326488-6327450. [Source:RefSeq;Acc:NM_147076]
ENSMUSG00000062786	0.769	1.081	1.529	0.538	0.12	hypothetical protein
V1ra1	0.729	1.203	1.095	0.84	0.478	vomeronasal 1 receptor, A1; vomeronasal organ family 1, receptor 1; vomeronasal 1, receptor 1. [Source:RefSeq;Acc:NM_011683]
ENSMUSG00000062875	0.652	0.846	0.757	1.487	0.668	hypothetical protein
ENSMUSG00000062888	0.399	0.496	0.864	1.793	0.531	hypothetical protein
Olfr777	1.805	1.625	1.977	1.865	1.211	olfactory receptor 777; olfactory receptor MOR114-9; GA_x6K02T2PULF-10955551-10954616. [Source:RefSeq;Acc:NM_146544]
ENSMUSG00000062915	1.402	1.31	1.028	1.009	1.164	hypothetical protein
LOC238836	0.555	0.413	1.004	0.861	0.477	hypothetical protein

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Ing2	1.384	0.957	1.16	0.933	0.928	inhibitor of growth family, member 1-like. [Source:RefSeq;Acc:NM_023503]
ENSMUSG00000063091	0.486	1.024	0.872	0.864	1.686	hypothetical protein
Cd300lb	0.723	1.07	0.988	0.6	0.969	gene model 253. [Source:RefSeq;Acc:NM_199221]
ENSMUSG00000063277	1.45	0.374	1.24	0.945	0.824	hypothetical protein
ENSMUSG00000063278	1.781	1.266	0.994	1.084	1.428	PREDICTED: similar to Nonhistone chromosomal protein HMG-17
CN675669	0.41	0.368	0.618	0.872	1.148	hypothetical protein
Q8BPT3	1.613	0.577	0.436	0.2	0.99	Weakly similar to integrin alpha 5 (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8BPT3]
Speer4f	2.852	0.792	1.038	1.299	0.666	spermatogenesis associated glutamate (E)-rich protein 4f
ENSMUSG00000063353	0.644	1.723	1.105	0.871	0.941	hypothetical protein
ENSMUSG00000063464	0.632	0.696	0.764	1.151	0.956	PREDICTED: golgi autoantigen, golgin subfamily b, macrogolgin 1 (Golgb1)
ENSMUSG00000063465	0.466	0.919	1.106	0.665	0.808	PREDICTED: similar to IG KAPPA CHAIN V-V REGION L6 PRECURSOR (LOC243428)
ENSMUSG00000063466	2.959	0.653	1.159	1.973	0.225	PREDICTED: similar to pheromone receptor V3R8 (LOC434142)
ENSMUSG00000063488	3.895	0.451	1.271	0.715	1.044	hypothetical protein
Mzf6d	1.379	0.251	0.578	1.841	1.278	KRAB zinc finger protein 6D (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8CIP9]
Slc22a8	0.595	2.134	1.114	0.935	2.095	solute carrier family 22 member 8; reduced in osteosclerosis transporter; organic anion transporter 3. [Source:RefSeq;Acc:NM_031194]
BF152048	2.015	1.634	0.723	3.74	0.859	PREDICTED: similar to hypothetical protein MGC15606 (LOC208684)
Olfr45	2.964	0.642	0.828	1.389	0.714	olfactory receptor 45; olfactory receptor MOR253-2; GA_x6K02T2PBJ9-42837030-42837962. [Source:RefSeq;Acc:NM_146963]
Rpl7l1	0.813	1.177	1.044	1.105	1.016	ribosomal protein L7-like 1
Prkcc	0.657	0.818	1.157	1.433	0.906	protein kinase C, gamma
Xab1	1.574	0.894	1.114	1.036	1.323	XPA-binding protein 1. [Source:Uniprot/SWISSPROT;Acc:Q8VCE2]
CA463480,BU937311,CN838094,CN833382,BF149562	2.734	1.488	1.117	1.163	1.169	hypothetical protein
ENSMUSG00000064070	2.23	0.791	1.08	0.809	1.198	hypothetical protein

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Cadm2	1.484	1.727	1.625	1.382	0.798	immunoglobulin superfamily, member 4. [Source:RefSeq;Acc:NM_178721]
Krt39	2.536	1.319	1.28	0.691	1.01	type I hair keratin KA35. [Source:RefSeq;Acc:NM_213730]
Olfr559	1.909	1.828	1.047	1.564	0.602	olfactory receptor 559; olfactory receptor MOR11-1; GA_x6K02T2PBJ9-5441154-5440198. [Source:RefSeq;Acc:NM_147112]
Krt2	1.404	1.076	1.11	0.149	1.102	keratin complex 2, basic, gene 17; keratin complex 2, gene 17. [Source:RefSeq;Acc:NM_010668]
Olfr694	0.327	1.423	0.527	1.024	0.387	olfactory receptor 694; olfactory receptor MOR283-9; GA_x6K02T2PBJ9-9067220-9066273. [Source:RefSeq;Acc:NM_146452]
LOC384525	0.62	1.364	1.031	0.876	0.957	similar to ribosomal protein S18
Hist1h2ae	0.622	0.481	0.945	1.108	0.999	histone 1, H2ae
Olfr1082	1.488	0.806	1.547	0.979	0.918	olfactory receptor 1082
XM_489032	1.953	0.96	1.18	1.526	0.519	PREDICTED: hypothetical protein 9330178D15 (9330178D15)
BB168868	1.793	0.752	0.706	0.76	0.643	hypothetical protein
Klra16	2.706	0.788	0.539	1.384	0.887	killer cell lectin-like receptor, subfamily A, member 16
Fgfr4	3.264	1.541	0.785	1.379	1.19	fibroblast growth factor receptor 4
XM_196166	1.289	1.057	0.902	1.498	0.955	PREDICTED: RIKEN cDNA 3300005D01 gene (3300005D01Rik)
BC024836	2.643	0.764	0.898	1.316	0.546	hypothetical protein
Atad2	1.447	1.194	1.131	0.869	0.802	ATPase family, AAA domain containing 2 (Atad2)
Krtap16-3	1.531	0.837	2.093	0.788	1.098	keratin associated protein 16-3
NM_177062	0.408	0.739	0.918	0.559	0.924	RIKEN cDNA 4833444G19 gene (4833444G19Rik)
Nlrp4f	1.314	0.885	0.905	0.834	1.537	NACHT, leucine rich repeat and PYD containing 4F (Nalp4f)
Slc6a11	1.409	2.093	0.993	0.877	0.214	gamma-aminobutyric acid (GABA-A) transporter 4
BB631817	1.933	0.728	0.736	0.356	0.693	hypothetical protein
Ear3	0.666	0.784	1.556	1.053	0.399	eosinophil-associated, ribonuclease A family, member 3 (Ear3)
4933407P14Rik	3.231	0.978	0.927	1.168	1.218	intramembrane protease 5 isoform a
XM_489155	0.634	1.275	0.744	1.28	1.381	PREDICTED: RIKEN cDNA 2310001H17 gene (2310001H17Rik)
Kir3dl2	1.457	0.273	0.717	0.206	0.389	killer immunoglobulin-like receptor-like 2
XM_488968	1.848	0.83	1.01	1.346	0.893	PREDICTED: RIKEN cDNA 1200007C13 gene

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XM_130163	1.249	1.081	1.076	0.922	0.789	PREDICTED: WW domain containing E3 ubiquitin protein ligase 1 (Wwp1)
H1f0	0.82	1.135	0.984	0.985	0.814	H1 histone family, member 0
BY706053	0.613	1.372	1.108	1.782	0.643	hypothetical protein
Alas2	0.558	1.934	1.272	0.83	1.056	aminolevulinic acid synthase 2, erythroid
AV252590	0.395	0.855	0.941	1.363	1.697	hypothetical protein
NM_176967	0.594	0.789	0.791	1.303	1.233	hypothetical protein
XM_488773,XM_489679	1.991	0.252	1.534	1.2	0.589	hypothetical protein
Olfr1231	3.621	1.355	0.643	0.759	0.871	olfactory receptor 1231
Cxcl12	1.631	0.74	0.693	0.746	0.889	stromal cell derived factor 1 isoform alpha precursor
Nedd1	1.653	1.208	0.979	0.892	1.152	neural precursor cell expressed, developmentally down-regulated gene 1
Man2b1	0.695	1.081	0.851	0.916	0.991	mannosidase 2, alpha B1
CK333231	1.62	1.01	0.458	1.156	1.321	hypothetical protein
Defcr-rs7	0.502	2.674	0.698	0.764	1.276	defensin related cryptdin, related sequence 7
Cln6	1.287	1.224	0.808	1.155	1.099	ceroid-lipofuscinosis, neuronal 6
Olfr1270	0.271	1.213	0.898	0.643	0.457	olfactory receptor 1270
Psbpc1	1.553	0.621	0.492	1.499	0.166	prostatic steroid binding protein C1 (Psbpc1)
Ifna6	2.203	1.304	0.884	1.396	1.008	hypothetical protein
BC034085	1.192	1.001	1.043	0.948	0.673	hypothetical protein
Olfr1110	0.708	1.321	0.719	1.194	0.827	olfactory receptor 1110
Krtap3-3	1.741	3.129	1.583	0.559	1.652	keratin associated protein 3-3
NM_177044	3.196	0.557	0.354	2.006	1.292	RIKEN cDNA 9330119M13 gene (9330119M13Rik)
XM_489573	2.111	0.906	1.035	1.491	1.181	PREDICTED: similar to Retrovirus-related POL polyprotein (LOC436367)
Fgd4	0.58	0.692	0.756	1.934	0.488	FYVE, RhoGEF and PH domain containing 4 isoform gamma
Spag4	1.414	0.344	1.048	1.126	1.971	sperm antigen 4
BY720425	0.756	0.531	0.642	0.604	1.088	hypothetical protein
AI508483	0.701	0.973	1.148	0.889	0.903	hypothetical protein
BC033915	1.558	1.22	0.581	0.943	1.116	hypothetical protein LOC70661
Slc16a10	0.552	0.841	0.869	0.691	1.419	solute carrier family 16 (monocarboxylic acid transporters), member 10
Osgep	1.465	0.995	0.905	1.033	1.103	O-sialoglycoprotein endopeptidase
Samd14	1.776	0.758	0.618	1.166	1.375	sterile alpha motif domain containing 14 isoform 1
Il1rl1	0.722	0.797	0.483	0.091	0.919	interleukin 1 receptor-like 1 isoform b

CB845695	0.596	1.416	0.968	1.058	1.031	hypothetical protein
Slc26a1	1.833	1.738	1.001	1.277	1.731	solute carrier family 26 (sulfate transporter), member 1
Arrdc1	0.833	1.377	0.962	0.717	1.212	arrestin domain containing 1
NM_029417	0.717	0.812	1.533	1.197	0.752	RIKEN cDNA 9030605E16 gene (9030605E16Rik)
Supt4h2	0.773	1.257	1.045	0.965	1.047	suppressor of Ty 4 homolog 2
Olfr1019	1.863	0.257	0.169	0.59	0.773	olfactory receptor 1019
NM_177163	1.481	0.865	0.899	1.365	0.662	RIKEN cDNA B330016D10 gene (B330016D10Rik)
V1ri6	3.188	0.18	1.449	3.802	1.351	vomeronasal 1 receptor, I6
BB634620	2.743	0.401	0.738	1.371	1.463	hypothetical protein
Meis1	0.434	2.694	1.106	0.879	1.976	myeloid ecotropic viral integration site 1
AI591942	1.898	1.073	1.244	1.637	1.262	hypothetical protein
Sf3b1	1.166	0.636	0.912	1.124	0.555	splicing factor 3b, subunit 1
BY716121	0.336	0.66	1.257	0.986	0.537	hypothetical protein
XM_488832	1.561	0.896	1.101	0.459	1.74	PREDICTED: RIKEN cDNA C030034I22 gene (C030034I22Rik)

Genes in this table were differentially regulated in the CD43KO macrophages compared to CD43WT macrophages while in incubation medium. Normalized expression cutoff values were 1.2 (upregulated) and 0.833 (downregulated). Genes were also filtered on confidence between the biological replicates ($p<0.05$).

Supplementary table 2. Statistically significant, differentially regulated genes in the Cpn60.2 microarray analysis

	Normalized Expression					
Common	**Incubation Medium (protein-incubation)**	**Incubation Medium (infection)**	***M.tb***	**60.2**	**dnaK**	**Description of Gene Product**
Cav2	1.029	1.225	1.155	0.715	0.98	caveolin 2 (Cav2)
Cdh1	0.936	0.348	0.877	1.352	1.222	cadherin 1 (Cdh1)
Hoxb6	0.382	1.017	0.622	2.002	0.683	homeo box B6 (Hoxb6)
Loxl3	1.29	0.912	1.078	1.288	0.974	lysyl oxidase-like 3 (Loxl3)
Hpn	1.187	1.864	0.898	0.79	0.869	hepsin (Hpn)
Myg1	0.86	0.887	0.581	1.452	0.955	melanocyte proliferating gene 1 (Myg1)
Ube2c	0.668	0.897	0.834	0.787	1.04	ubiquitin-conjugating enzyme E2C (Ube2c)
Irx2	0.886	1.432	0.458	1.879	1.052	Iroquois related homeobox 2 (Drosophila) (Irx2)
Brpf1	1.202	1.441	0.732	0.656	0.957	bromodomain and PHD finger containing, 1 (Brpf1)
Ssr4	0.917	1.203	1.032	1.297	1.21	signal sequence receptor, delta (Ssr4)
Stat6	0.856	1.303	1.192	0.73	0.977	signal transducer and activator of transcription 6 (Stat6)
Ppm1j	0.751	0.969	0.81	0.927	1.552	protein phosphatase 2a, catalytic subunit, zeta isoform (Ppp2cz)
Tmem112	1.111	1.518	0.943	1.493	0.968	hypothetical protein
Slc9a3r2	1.139	0.803	1.071	1.446	1.038	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 2 (Slc9a3r2)
Arrdc2	1.024	0.857	0.923	1.338	0.742	PREDICTED: arrestin domain containing 2 (Arrdc2)
Gsbs	0.677	0.618	1.358	1.757	1.475	G substrate (Gsbs)
Lipe	1.054	0.717	0.592	0.726	0.8	lipase, hormone sensitive (Lipe)
Pafah1b2	0.715	0.805	0.977	0.85	0.971	Platelet-activating factor acetylhydrolase IB beta subunit (
Abcf3	1.069	1.463	1.01	1.2	0.768	ATP-binding cassette, sub-family F (GCN20), member 3 (Abcf3)
Cd79a	0.997	0.784	1.49	1.179	1.319	CD79A antigen (immunoglobulin-associated alpha) (Cd79a)
Inmt	1.039	1.574	0.51	1.515	0.845	indolethylamine N-methyltransferase (Inmt)
Fosb	0.943	1.038	1.185	1.439	1.998	FBJ osteosarcoma oncogene B (Fosb)
Klc4	0.935	1.56	0.84	0.691	0.834	RIKEN cDNA 1200014P03 gene (1200014P03Rik)
Ssbp2	1.039	1.226	1.078	0.736	0.936	single-stranded DNA binding protein 2 (Ssbp2)
Grcc10	0.972	1.502	0.947	1.38	0.984	gene rich cluster, C10 gene (Grcc10)
Mcoln1	0.814	1.073	0.838	0.78	1.03	mucolipin 1 (Mcoln1)
Abca13	0.784	1.143	1.055	1.652	1.758	similar to ATP binding cassette gene, sub-family A (ABC1), member 13; ATP binding cassette transporter A13 (LOC435246)

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description of Gene Product
Cd244	0.377	0.872	1.127	0.402	0.985	CD244 natural killer cell receptor 2B4 (Cd244)
Dlst	1.624	0.975	1.182	0.676	0.913	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) (Dlst)
Cd44	0.456	0.931	0.791	1.813	1.7	CD44 antigen (Cd44)
Slc2a9	0.824	0.904	1.961	0.814	1.058	solute carrier family 2 (facilitated glucose transporter), member 9 (Slc2a9)
RIP3_MOUSE	2.401	1.598	0.447	1.653	0.529	Rho-interacting protein 3 (p116RIP) (RIP3). [Source:Uniprot/SWISSPROT;Acc:P97434]
Ampd3	0.927	1.317	0.687	0.588	1.071	AMP deaminase 3 (EC 3.5.4.6) (AMP deaminase isoform E) (AMP deaminase H-type) (Heart-type AMPD). [Source:Uniprot/SWISSPROT;Acc:O08739]
Ampd3	0.959	1.553	0.819	0.666	0.708	AMP deaminase 3 (Ampd3)
Ncoa2	1.116	0.996	0.94	1.116	1.425	Nuclear receptor coactivator 2 (NCoA-2) (Transcriptional intermediary factor 2) (Glucocorticoid receptor-interacting protein 1) (GRIP-1). [Source:Uniprot/SWISSPROT;Acc:Q61026]
Epor	1.506	0.652	0.54	0.623	0.879	erythropoietin receptor (Epor)
Pvrl4	0.587	0.696	0.999	1.356	1.411	PREDICTED: poliovirus receptor-related 4 (Pvrl4)
Slc4a3	0.901	1.289	1.034	2.139	1.133	Anion exchange protein 3 (Neuronal band 3-like protein). [Source:Uniprot/SWISSPROT;Acc:P16283]
Zfp184	1.346	2.336	0.646	1.874	0.951	zinc finger protein 184 (Kruppel-like) (Zfp184)
Dennd2c	0.997	1.121	0.698	0.775	1.184	RIKEN cDNA A930010I20 gene (A930010I20Rik)
Ccdc124	1.191	1.05	0.949	1.221	0.829	RIKEN cDNA 1810023B24 gene (1810023B24Rik)
Nfib	0.497	0.984	0.928	1.409	2.659	nuclear factor I/B (Nfib)
Hipk1	1.036	0.843	1.158	0.77	0.46	homeodomain interacting protein kinase 1 (Hipk1)
ENSMUSG00000009647	1.832	0.701	0.904	2.196	0.913	
Fxyd5	0.806	1.224	0.991	0.568	1.128	FXYD domain-containing ion transport regulator 5 (Fxyd5)
1300013J15Rik	0.714	0.291	1.282	1.652	0.951	RIKEN cDNA 1300013J15 gene (1300013J15Rik)
Faf1	0.88	1.079	0.901	1.486	1.299	Fas-associated factor 1 (Faf1)
Slc22a13	1.022	0.801	1.216	1.857	1.039	solute carrier family 22 (organic cation transporter), member 13 (Slc22a13)

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description of Gene Product
Phlda2	1.622	1.605	0.685	2.881	0.701	pleckstrin homology-like domain, family A, member 2 (Phlda2)
Kdelr3	0.826	0.844	0.891	1.702	1.068	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3 (Kdelr3)
Rpa3	1.4	1.634	1.084	1.561	1.044	replication protein A3 (Rpa3)
Tnpo3	1.203	0.979	1.06	1.454	0.828	transportin 3 (Tnpo3)
Adh6-ps1	2.769	1.368	1.022	1.715	1.179	
D16H22S680E	0.883	1.528	1.048	0.727	0.994	DNA segment, Chr 16, human D22S680E, expressed (D16H22S680E)
Ndufs2	1.015	1.052	1.044	1.306	1.073	NADH dehydrogenase (ubiquinone) Fe-S protein 2 (Ndufs2)
Dedd	0.94	1.038	0.5	0.583	1.07	death effector domain-containing (Dedd)
2410012H22Rik	0.699	1.12	1.247	1.435	0.805	PREDICTED: RIKEN cDNA 2410012H22 gene (2410012H22Rik)
Adam28	1.215	0.132	0.274	1.437	1.09	a disintegrin and metalloprotease domain 28 (Adam28), transcript variant 1
ENSMUSG00000014786	0.36	0.238	0.822	1.552	0.868	hypothetical protein
Msh3	1.174	2.95	0.721	1.358	1.397	mutS homolog 3 (E. coli) (Msh3)
C920006C10Rik	1.088	1.102	1.019	0.727	0.863	RIKEN cDNA C920006C10 gene (C920006C10Rik)
Ptgds	1.198	1.525	1.016	1.265	1.299	prostaglandin D2 synthase (brain) (Ptgds)
Slc25a13	1.068	1.446	1.311	1.977	1.627	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 13 (Slc25a13)
Lage3	0.857	1.007	1.096	1.311	1.003	RIKEN cDNA 1110049G11 gene (1110049G11Rik)
Zdhhc12	1.01	0.781	0.989	0.947	0.753	zinc finger, DHHC domain containing 12 (Zdhhc12)
Cybb	1.11	1.11	0.756	0.65	0.959	cytochrome b-245, beta polypeptide (Cybb)
Pcolce2	1.084	1.404	0.802	0.454	1.004	procollagen C-endopeptidase enhancer 2 (Pcolce2)
Rnf5	0.944	1.054	1.101	1.16	0.874	ring finger protein 5. [Source:RefSeq;Acc:NM_019403]
ENSMUSG00000015599	1.089	1.212	1.009	1.809	1.782	hypothetical protein
Nfe2l2	0.845	1.195	0.809	0.63	1.126	nuclear factor, erythroid derived 2, like 2 (Nfe2l2)
Adamtsl4	0.852	1.039	1.294	1.817	1.219	thrombospondin repeat containing 1 (Tsrc1)
Fli1	1.133	0.706	0.865	0.497	0.779	Friend leukemia integration 1 (Fli1)

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description of Gene Product
ENSMUSG00000016284	0.982	0.932	1.015	1.406	0.935	
Cd34	1.377	1.596	0.826	1.421	1.308	CD34 antigen (Cd34)
Mapkapk2	0.973	0.955	0.657	0.634	1.042	MAP kinase-activated protein kinase 2 (Mapkapk2)
Rbpjl	1.43	2.131	1.018	1.321	0.854	recombining binding protein suppressor of hairless-like (Drosophila) (Rbpsuhl)
Hnf4g	0.858	0.262	0.736	1.799	0.747	hepatocyte nuclear factor 4, gamma (Hnf4g)
Mmp9	0.853	1.705	0.847	0.606	1.333	matrix metalloproteinase 9 (Mmp9)
Ppp2r5c	1.1	1.176	0.969	0.738	1.022	Serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit, gamma isoform (PP2A, B subunit, B' gamma isoform) (PP2A, B subunit, B56 gamma isoform) (PP2A, B subunit, PR61 gamma isoform) (PP2A, B subunit, R5 gamma isoform) (PP2A, B subunit, B'alpha3 isoform) (Fragment). [Source:Uniprot/SWISSPROT;Acc:Q60996]
Cldn7	1.233	0.684	0.401	1.763	0.903	claudin 7 (Cldn7)
Pelp1	0.829	1.814	0.871	1.897	1.693	RIKEN cDNA 4930563C04 gene (4930563C04Rik)
Pcmt1	1.014	1.349	1.008	1.149	1.043	protein-L-isoaspartate (D-aspartate) O-methyltransferase 1 (Pcmt1)
Slc6a15	0.718	1.026	0.317	1.332	1.631	solute carrier family 6 (neurotransmitter transporter), member 15 (Slc6a15)
1200009F10Rik	0.605	1.034	1.142	1.377	0.884	RIKEN cDNA 1700023M03 gene (1700023M03Rik)
Plxnc1	0.773	1.29	0.619	0.623	0.7	plexin C1 (Plxnc1)
Timp3	1.086	0.781	0.673	0.497	0.806	tissue inhibitor of metalloproteinase 3 (Timp3)
Tcfe2a	0.949	1.642	0.91	1.534	0.86	transcription factor E2a (Tcfe2a)
Dohh	1.058	1.065	1.207	1.247	0.878	RIKEN cDNA 1110033C18 gene (1110033C18Rik)
Pes1	0.961	1.081	1.475	0.746	1.058	pescadillo homolog 1, containing BRCT domain (zebrafish) (Pes1)
Myo1g	1.205	1.082	0.785	1.185	1.452	myosin IG (Myo1g)
Guk1	1.003	1.175	1.709	1.266	0.745	guanylate kinase 1 (Guk1)
Trim11	0.768	0.971	1.12	0.724	0.869	tripartite motif protein 11 (Trim11)
Galnt10	1.287	1.21	0.839	1.74	1.22	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10 (Galnt10)

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description of Gene Product
MYCD_MOUSE	0.091	0.295	1.731	1.721	1.903	myocardin (Myocd)
Pdia6	1.06	1.029	0.99	1.34	0.719	PREDICTED: thioredoxin domain containing 7 (Txndc7)
Adi1	1.035	1.848	1.11	0.831	1.5	expressed sequence AL024210 (AL024210)
Dnmt3a	1.095	1.947	1.392	1.414	1.303	DNA methyltransferase 3A (Dnmt3a), transcript variant 1
Tpo	0.552	1.255	0.779	1.544	0.89	thyroid peroxidase (Tpo)
Mrc2	0.86	1.172	0.659	1.371	0.81	mannose receptor, C type 2 (Mrc2)
Cct6b	1.47	0.187	0.82	1.324	0.336	T-complex protein 1, zeta-2 subunit (TCP-1-zeta-2) (CCT-zeta-2) (Cctz- 2). [Source:Uniprot/SWISSPROT;Acc:Q61390]
Pafah1b1	0.882	0.926	0.931	0.86	1.02	Platelet-activating factor acetylhydrolase IB alpha subunit (PAF acetylhydrolase 45 kDa subunit) (PAF-AH 45 kDa subunit) (PAF-AH alpha) (PAFAH alpha) (Lissencephaly-1 protein) (LIS-1). [Source:Uniprot/SWISSPROT;Acc:P43035]
Camkk1	0.987	0.329	1.782	1.571	1.037	calcium/calmodulin-dependent protein kinase kinase 1, alpha (Camkk1)
Exoc7	1.309	1.133	1.341	1.278	0.834	Exocyst complex component 7 (Exocyst complex component Exo70). [Source:Uniprot/SWISSPROT;Acc:O35250]
Eral1	0.617	1.181	0.968	0.687	0.866	Era (G-protein)-like 1 (E. coli) (Eral1)
Cdc34	0.99	1.767	0.471	0.656	1.442	Ubiquitin-conjugating enzyme E2-32 kDa complementing (EC 6.3.2.19) (Ubiquitin-protein ligase) (Ubiquitin carrier protein) (E2-CDC34). [Source:Uniprot/SWISSPROT;Acc:Q8CFI2]
Dlx4	1.122	0.734	0.955	1.448	1.019	distal-less homeobox 4 (Dlx4)
Sel1l	1	1.652	1.522	0.555	0.844	Sel1 (suppressor of lin-12) 1 homolog (C. elegans) (Sel1h)
Rab15	1.631	0.648	1.221	2.421	1.107	RAB15, member RAS oncogene family (Rab15)
Pygl	1.024	0.834	1.162	0.701	1.002	liver glycogen phosphorylase (Pygl)
Rtn1	0.474	0.564	1.314	1.884	0.88	reticulon 1 (Rtn1), transcript variant 1
Pigh	0.824	0.956	1.082	0.676	1.123	phosphatidylinositol glycan, class H (Pigh)
Gtpbp4	0.999	1.031	1.007	0.658	1.243	GTP binding protein 4 (Gtpbp4)
2610021K21Rik	0.857	1.044	1.565	1.683	1.156	PREDICTED: RIKEN cDNA 2610021K21 gene (2610021K21Rik)
Mtac2d1	0.86	0.276	1.041	1.952	1.196	membrane targeting (tandem) C2 domain containing 1 (Mtac2d1)
Acot3	1.102	1.06	0.888	0.773	0.848	peroxisomal acyl-CoA thioesterase 2A (Pte2a)
Wars	0.806	1.277	0.964	0.799	1.106	tryptophanyl-tRNA synthetase (Wars)

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description of Gene Product
Xrcc3	0.845	0.927	1.06	1.157	1.298	X-ray repair complementing defective repair in Chinese hamster cells 3 (Xrcc3)
Ggps1	1.253	1.269	0.851	1.446	1.209	geranylgeranyl diphosphate synthase 1 (Ggps1)
Prl	1.773	0.836	1.362	2.186	0.914	prolactin (Prl)
Prl7d1	1.358	0.347	1.111	1.616	1.128	proliferin related protein (Plfr)
Tcfap2a	0.664	0.874	1.611	1.5	0.385	transcription factor AP-2, alpha (Tcfap2a)
Mak	0.771	0.225	1.493	1.581	0.991	Serine/threonine-protein kinase MAK (EC 2.7.1.37) (Male germ cell- associated kinase) (Protein kinase RCK). [Source:Uniprot/SWISSPROT;Acc:Q04859]
Rpp40	1.013	1.257	0.916	1.467	1.051	ribonuclease P 40 subunit (human) (Rpp40)
Riok1	0.962	0.752	0.981	1.756	1.161	RIO kinase 1 (yeast) (Riok1)
ENSMUSG00000021430	0.792	1.168	0.763	1.394	1.178	PREDICTED: desmoplakin (Dsp)
Sema4d	1.023	1.106	0.815	0.695	1.431	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D (Sema4d)
Fancc	0.559	0.903	0.865	0.715	0.696	Fanconi anemia, complementation group C (Fancc)
Pdlim7	0.738	0.108	0.801	0.494	1.374	PDZ and LIM domain 7. [Source:RefSeq;Acc:NM_026131]
AI595366	0.814	0.588	1.025	1.45	0.622	PREDICTED: similar to Leucine-rich repeat-containing protein 14 (LOC432779)
Med10	0.942	1.085	0.965	1.25	1.063	DNA segment, Chr 13, Wayne State University 50, expressed (D13Wsu50e)
Cd180	0.913	1.864	1.142	1.394	1.42	lymphocyte antigen 78 (Ly78)
Marveld2	0.662	0.63	1.381	1.555	0.512	MARVEL (membrane-associating) domain containing 2 (Marveld2)
Hmgcr	0.908	0.849	0.112	0.472	1.133	3-hydroxy-3-methylglutaryl-coenzyme A reductase (EC 1.1.1.34) (HMG-CoA reductase) (Fragment). [Source:Uniprot/SWISSPROT;Acc:Q01237]
F2rl2	0.383	0.346	0.485	1.459	1.86	coagulation factor II (thrombin) receptor-like 2 (F2rl2)
Zfyve16	0.984	1.206	1.113	0.742	1.08	zinc finger, FYVE domain containing 16 (Zfyve16)
Comtd1	0.89	0.889	1.722	1.59	0.964	catechol-O-methyltransferase domain containing 1 (Comtd1)
5730469M10Rik	1.063	1.626	0.782	1.807	1.103	RIKEN cDNA 5730469M10 gene (5730469M10Rik)
Anxa7	1.172	0.761	0.757	1.458	1.056	Annexin A7 (Annexin VII) (Synexin).

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description of Gene Product
Ppif	0.915	1.182	1.052	0.587	1.209	peptidylprolyl isomerase F (cyclophilin F) (Ppif)
Galntl2	1.173	1.169	0.952	1.835	0.667	PREDICTED: UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 2 (Galntl2)
Mipep	0.922	0.941	1.163	1.632	1.709	mitochondrial intermediate peptidase. [Source:RefSeq;Acc:NM_027436]
2610206B13 Rik	1.952	0.683	1.44	1.547	1.443	RIKEN cDNA 2610206B13 gene (2610206B13Rik)
Fbxl3	0.95	1.719	1.022	0.69	1.007	F-box and leucine-rich repeat protein 3a (Fbxl3a)
Nup155	1.373	1.463	0.974	2.461	1.196	nucleoporin 155 (Nup155)
Bcl2l2	0.792	1.042	0.998	1.259	0.993	Bcl2-like 2 (Bcl2l2)
Wdr23	1.079	1.003	1.02	1.3	1.103	WD repeat domain 23 (Wdr23)
5730557B15 Rik	0.963	1.442	1.067	1.51	0.883	RIKEN cDNA 5730557B15 gene (5730557B15Rik)
Eny2	0.834	1.367	0.441	1.481	1.821	RIKEN cDNA 1810057B09 gene (1810057B09Rik)
9130401M0 1Rik	1.145	1.116	1.178	1.239	1.254	RIKEN cDNA 9130401M01 gene (9130401M01Rik)
ENSMUSG00 000022393	0.571	0.143	1.124	1.584	1.07	PREDICTED: RIKEN cDNA D930017K21 gene (D930017K21Rik)
Syngr1	0.84	1.344	1.374	1.251	0.636	synaptogyrin 1 (Syngr1), transcript variant 1b
Depdc6	1.23	0.667	1.06	1.226	0.617	DEP domain containing 6 (Depdc6)
4931407K02 Rik	1.707	0.763	0.608	2.12	2.256	RIKEN cDNA 4931407K02 gene (4931407K02Rik)
ENSMUSG00 000022455	0.887	1.084	1.199	1.362	0.702	PREDICTED: RIKEN cDNA 4930521I23 gene (4930521I23Rik)
Txndc11	0.55	0.882	1.161	0.648	0.977	RIKEN cDNA 2810408E11 gene (2810408E11Rik)
ENSMUSG00 000022543	0.792	0.183	1.298	2.123	1.077	PREDICTED: RIKEN cDNA 4930451G09 gene (4930451G09Rik)
Shank3	0.638	0.838	2.188	1.78	0.792	SH3/ankyrin domain gene 3 (Shank3)
ENSMUSG00 000022637	1.004	0.644	0.321	0.638	1.015	hypothetical protein
Pvrl3	0.592	0.424	1.028	1.505	0.988	poliovirus receptor-related 3 (Pvrl3)
Mpv17l	0.719	0.784	0.687	1.664	0.531	Mpv17 transgene, kidney disease mutant-like (Mpv17l)
Gbe1	0.998	0.906	1.106	1.323	0.941	glucan (1,4-alpha-), branching enzyme 1 (Gbe1)

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description of Gene Product
Siat10	1.55	1.518	1.152	1.282	0.794	Type 2 lactosamine alpha-2,3-sialyltransferase (EC 2.4.99.-) (CMP-NeuAc:beta-galactoside alpha-2,3-sialyltransferase VI) (ST3Gal VI) (Sialyltransferase 10). [Source:Uniprot/SWISSPROT;Acc:Q8VIB3]
Ehhadh	0.701	1.111	0.611	1.754	1.435	enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase (Ehhadh)
Pigp	0.252	1.278	1.02	1.651	1.467	Down syndrome critical region homolog 5 (human) (Dscr5)
Gpd1	0.864	0.681	0.927	1.425	1.163	glycerol-3-phosphate dehydrogenase 1 (soluble) (Gpd1)
Lass5	0.545	0.73	1.238	0.696	0.908	longevity assurance homolog 5. [Source:RefSeq;Acc:NM_028015]
D330037H05 Rik	1.307	1.335	1.456	1.651	1.799	PREDICTED: RIKEN cDNA D330037H05 gene (D330037H05Rik)
Pcdhga3	1.796	0.876	1.223	2.453	1.039	protocadherin gamma subfamily A, 3 (Pcdhga3)
Abcc1	1.353	0.735	0.878	0.532	0.762	ATP-binding cassette, sub-family C (CFTR/MRP), member 1 (Abcc1)
Sympk	1.059	1.647	1.062	1.604	1.279	PREDICTED: symplekin (Sympk)
Ceacam14	0.603	0.963	0.983	2.536	0.257	CEA-related cell adhesion molecule 14. [Source:RefSeq;Acc:NM_025957]
Lcn9	0.596	1.154	0.468	1.991	1.003	lipocalin 9 (Lcn9)
Bmp15	0.32	0.504	0.348	2.146	0.875	bone morphogenetic protein 15 (Bmp15)
ENSMUSG00 000023482	1.29	0.664	1.303	0.716	1.146	hypothetical protein
Brp44l	1.018	0.931	0.809	1.384	0.823	Brain protein 44-like protein (Apoptosis-regulating basic protein). [Source:Uniprot/SWISSPROT;Acc:Q9JLG5]
Slc25a27	1.137	2.407	1.246	2.088	0.975	solute carrier family 25, member 27. [Source:RefSeq;Acc:NM_028711]
Mrpl14	0.868	0.865	1.207	1.246	0.943	mitochondrial ribosomal protein L14 (Mrpl14)
2810410M2 0Rik	0.958	1.028	1.188	1.52	0.959	RIKEN cDNA 2810410M20 gene (2810410M20Rik)
Luc7l	1.375	1.675	0.968	1.682	0.998	Luc7 homolog (S. cerevisiae)-like (Luc7l)
Spdef	0.948	1.049	1.044	1.51	0.757	SAM pointed domain containing ets transcription factor; prostate specific ets transcription factor. [Source:RefSeq;Acc:NM_013891]
ENSMUSG00 000024245	2.318	1.539	0.814	1.318	0.491	hypothetical protein

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description of Gene Product
Brunol4	0.425	0.202	0.87	2.796	2.551	bruno-like 4, RNA binding protein. [Source:RefSeq;Acc:NM_133195]
Esco1	1.101	0.514	1.127	0.678	0.677	PREDICTED: RIKEN cDNA A930014I12 gene (A930014I12Rik)
5133400G04 Rik	0.99	0.935	1.172	2.225	0.845	RIKEN cDNA 5133400G04 gene (5133400G04Rik)
Map3k2	1.537	1.331	0.841	0.45	0.872	mitogen activated protein kinase kinase kinase 2 (Map3k2)
Rpp21	0.96	1.536	1.134	1.41	0.911	ribonuclease P 21 subunit (human) (Rpp21)
Hdac3	0.787	0.95	1.171	0.696	1.21	Histone deacetylase 3 (HD3). [Source:Uniprot/SWISSPROT;Acc:O88895]
ENSMUSG00 000024500	0.642	1.099	1.531	2.188	1.454	hypothetical protein
Afg3l2	1.275	0.708	0.985	1.318	0.801	PREDICTED: AFG3(ATPase family gene 3)-like 2 (yeast) (Afg3l2)
D18Ertd653 e	1.317	0.952	0.924	0.577	0.882	DNA segment, Chr 18, ERATO Doi 653, expressed (D18Ertd653e)
Smad2	0.658	1.026	0.999	0.722	0.993	MAD homolog 2 (Drosophila) (Smad2)
Ms4a4c	1.11	1.526	0.896	1.496	1.07	membrane-spanning 4-domains, subfamily A, member 4C (Ms4a4c)
Rnaseh2c	1.024	1.179	1.346	1.37	0.983	RIKEN cDNA 1500026D16 gene (1500026D16Rik)
Tcf7l2	1.483	1.101	1.078	1.594	1.065	Transcription factor 7-like 2 (HMG box transcription factor 4) (T- cell-specific transcription factor 4) (TCF-4) (mTCF-4). [Source:Uniprot/SWISSPROT;Acc:Q924A0]
Tcf7l2	0.882	1.475	1.041	1.112	0.733	transcription factor 7-like 2, T-cell specific, HMG-box (Tcf7l2)
Casp7	0.948	1.294	1.239	0.461	0.8	caspase 7 (Casp7)
Ablim1	0.865	0.75	1.087	1.268	0.859	actin-binding LIM protein 1 (Ablim1)
Actr1a	1.198	0.805	0.837	0.561	0.947	ARP1 actin-related protein 1 homolog A (yeast) (Actr1a)
Slc6a20	1.356	0.227	1.081	1.603	0.86	solute carrier family 6 (neurotransmitter transporter), member 20 (Slc6a20)
Pfkfb1	1.053	1.339	1.306	1.353	0.805	PREDICTED: 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1 (Pfkfb1)
Prdx4	1.072	1.251	1.035	1.439	1.055	peroxiredoxin 4 (Prdx4)
Ube3a	1.25	0.891	1.026	1.469	1.35	Ubiquitin-protein ligase E3A (EC 6.3.2.-) (Oncogenic protein- associated protein E6-AP). [Source:Uniprot/SWISSPROT;Acc:O08759]
Gpr143	1.726	1.346	1.037	1.166	0.87	G protein-coupled receptor 143 (Gpr143)
Rnf41	1.764	1.123	0.776	1.593	1.444	ring finger protein 41 (Rnf41)

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Myo1a	0.59	1.24	1.156	1.852	0.825	PREDICTED: similar to Myosin Ia (Brush border myosin I) (BBM-I) (BBMI) (Myosin I heavy chain) (MIHC) (LOC432516)
Phkg1	1.13	1.33	1.055	1.668	0.494	phosphorylase kinase gamma 1 (Phkg1)
RPOR_MOUSE	1.406	0.655	0.906	0.752	0.635	Regulatory associated protein of mTOR (Raptor) (P150 target of rapamycin (TOR)-scaffold protein). [Source:Uniprot/SWISSPROT;Acc:Q8K4Q0]
Rhot2	1.219	1.261	1.074	1.412	0.674	ras homolog gene family, member T2; mitochondrial Rho 2. [Source:RefSeq;Acc:NM_145999]
Rhot2	0.971	0.496	1.557	0.69	0.82	ras homolog gene family, member T2; mitochondrial Rho 2. [Source:RefSeq;Acc:NM_145999]
ENSMUSG00000025750	0.205	1.049	0.772	0.528	1.49	PREDICTED: RIKEN cDNA 1700026G02 gene (1700026G02Rik)
ENSMUSG00000025808	1.783	0.524	1.108	1.552	1.256	hypothetical protein
Gria4	0.137	2.262	0.784	1.868	0.937	glutamate receptor, ionotropic, AMPA4 (alpha 4) (Gria4)
Lancl1	0.934	1.097	0.864	1.14	1.046	LanC (bacterial lantibiotic synthetase component C)-like 1 (Lancl1)
ENSMUSG00000026004	0.849	1.195	0.953	1.336	1.133	hypothetical protein
Unc50	0.92	0.924	0.948	1.235	1	unc-50 homolog (C. elegans) (Unc50)
Ctdsp1	0.915	1.141	0.699	0.558	1.086	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 1 (Ctdsp1)
ENSMUSG00000026211	1.006	2.059	0.921	2.014	1.359	hypothetical protein
Htr2b	0.928	1.306	1.46	1.4	1.127	5-hydroxytryptamine (serotonin) receptor 2B (Htr2b)
Farslb	1.01	1.389	0.659	0.532	0.816	Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20) (Phenylalanine-- tRNA ligase beta chain) (PheRS). [Source:Uniprot/SWISSPROT;Acc:Q9WUA2]
ENSMUSG00000026301	0.514	0.405	0.926	1.746	1.056	hypothtical protein
Cdh7	1.175	0.97	1.062	1.555	0.762	cadherin 7, type 2. [Source:RefSeq;Acc:NM_172853]

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Serpinb3c	1.21	1.46	0.984	1.521	0.872	serine (or cysteine) proteinase inhibitor, clade B, member 3c. [Source:RefSeq;Acc:NM_201363]
Ptprc	0.248	0.934	1.285	0.574	0.858	protein tyrosine phosphatase, receptor type, C (Ptprc)
Pfkfb2	0.792	0.763	0.894	1.301	0.879	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2 (Pfkfb2)
Rab7l1	0.843	0.96	0.971	1.412	1.216	RAB7, member RAS oncogene family-like 1 (Rab7l1)
Slc45a3	1.854	1.117	1.778	0.61	1.621	RIKEN cDNA 2210413P12 gene (2210413P12Rik)
Rgs5	0.356	0.991	0.975	1.824	0.901	regulator of G-protein signaling 5 (Rgs5)
Mgst3	1.112	1.573	1.355	1.645	0.792	microsomal glutathione S-transferase 3 (Mgst3)
ENSMUSG00000026702	1.29	1.003	0.822	1.268	1.207	hypothetical protein
ENSMUSG00000026729	0.337	1.58	0.458	1.602	1.611	PREDICTED: RIKEN cDNA 4930562F07 gene (4930562F07Rik)
Kif5c	0.76	0.922	1.007	1.415	1.179	kinesin family member 5C (Kif5c)
ENSMUSG00000026784	1.103	1.251	1.261	2.186	1.21	hypothetical protein
Lcn2	0.933	0.549	0.416	1.466	1.161	lipocalin 2 (Lcn2)
Olfm1	0.883	1.287	1.096	0.58	1.125	olfactomedin 1 (Olfm1)
Mrrf	0.608	2.237	0.956	1.593	0.869	mitochondrial ribosome recycling factor. [Source:RefSeq;Acc:NM_026422]
Notch1	1.046	0.705	0.572	0.782	0.634	Notch gene homolog 1 (Drosophila) (Notch1)
Card9	1.269	1.334	0.888	1.412	0.65	PREDICTED: similar to caspase recruitment domain protein 9 (LOC332579)
P2rx3	1.095	1.817	0.889	1.735	0.524	purinergic receptor P2X, ligand-gated ion channel, 3 (P2rx3)
Prg3	2.065	1.716	0.801	1.869	1.588	proteoglycan 3 (Prg3)
Hoxd8	1.172	0.705	0.956	0.653	1.854	PREDICTED: homeo box D8 (Hoxd8)
Gtpbp9	0.901	0.897	0.978	0.657	0.934	RIKEN cDNA 2810409H07 gene (2810409H07Rik)
Sp3	0.916	0.741	0.888	0.531	0.981	trans-acting transcription factor 3 (Sp3)
Lrp4	1.608	0.769	0.929	0.604	1.424	low density lipoprotein receptor-related protein 4 (Lrp4)
Zfp106	1.391	0.999	1.054	1.255	0.875	zinc finger protein 106 (Zfp106)
Tyro3	1.002	0.328	0.792	0.615	1.298	TYRO3 protein tyrosine kinase 3 (Tyro3)
Chac1	1.134	0.481	0.905	1.382	2.524	RIKEN cDNA 1810008K03 gene

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Tgm3	0.397	0.988	1.026	0.267	0.934	transglutaminase 3, E polypeptide (Tgm3)
Bfsp1	0.843	0.668	0.814	3.441	0.797	beaded filament structural protein in lens-CP94 (Bfsp1)
Sall4	0.882	1.665	1.471	1.35	1.555	sal-like 4 (Drosophila) (Sall4), transcript variant a
5530400B04 Rik	0.717	1.023	0.993	1.972	1.378	PREDICTED: RIKEN cDNA 5530400B04 gene (5530400B04Rik)
Pik3ca	0.616	0.906	1.339	0.677	0.906	phosphatidylinositol 3-kinase, catalytic, alpha polypeptide (Pik3ca)
Pld1	0.829	1.298	0.697	0.718	1.094	phospholipase D1 (Pld1)
Trpc3	1.385	1.595	0.752	1.487	0.684	transient receptor potential cation channel, subfamily C, member 3 (Trpc3)
Postn	0.316	1.232	0.573	1.907	0.869	periostin, osteoblast specific factor (Postn)
Efna1	1.2	0.811	0.724	1.774	1.053	ephrin A1 (Efna1)
Vcam1	0.941	1.124	1.075	0.446	1.405	vascular cell adhesion molecule 1 (Vcam1)
1700006A11 Rik	1.928	2.484	1.563	1.793	1	PREDICTED: RIKEN cDNA 1700006A11 gene (1700006A11Rik)
Pitx2	1.031	1.026	0.419	1.728	0.668	paired-like homeodomain transcription factor 2 (Pitx2)
Pitx2	1.299	0.744	0.686	1.754	0.863	paired-like homeodomain transcription factor 2 (Pitx2)
Them5	0.637	0.46	0.646	2.292	0.852	RIKEN cDNA 1110038F21 gene (1110038F21Rik)
Zcd2	0.487	1.569	0.561	0.454	0.856	RIKEN cDNA 1500009M05 gene (1500009M05Rik)
Lphn2	1.114	1.424	0.844	0.663	1.087	PREDICTED: latrophilin 2 (Lphn2)
	0.951	1.853	0.514	1.801	0.741	RIKEN cDNA 1110001A05 gene (1110001A05Rik)
Rragd	0.563	0.895	1.256	1.408	1.75	Ras-related GTP binding D (Rragd)
Gabrr1	0.672	1.21	1.842	1.678	0.361	gamma-aminobutyric acid (GABA-C) receptor, subunit rho 1 (Gabrr1)
2310039E09 Rik	0.877	0.697	0.593	2.473	1.001	RIKEN cDNA 2310039E09 gene (2310039E09Rik)
Dbc1	0.455	1.48	0.633	0.653	0.688	deleted in bladder cancer chromosome region candidate 1 (human) (Dbccr1)
Aqp7	1.605	1.599	0.884	2.019	0.399	aquaporin 7 (Aqp7)
Rmrp	0.699	1.156	1.16	1.366	0.792	hypothetical protein
Tnfrsf1b	1	1.021	0.81	0.551	0.798	tumor necrosis factor receptor superfamily, member 1b (Tnfrsf1b)
0610037L13 Rik	1.367	1.17	0.76	0.668	0.933	RIKEN cDNA 0610037L13 gene (0610037L13Rik)
3110037I16 Rik	0.806	0.951	1.477	0.645	0.865	RIKEN cDNA 3110037I16 gene (3110037I16Rik)
Dyrk2	0.218	0.881	0.991	2.166	0.729	PREDICTED: RIKEN cDNA 1810038L18 gene (1810038L18Rik)

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Trit1	1.279	1.24	0.821	1.465	0.984	tRNA isopentenyltransferase 1 (Trit1)
Toe1	0.717	0.822	0.935	0.772	1.041	RIKEN cDNA 4930584N22 gene (4930584N22Rik)
Nsun4	0.677	1.298	0.424	1.479	1.005	RIKEN cDNA 2810405F18 gene (2810405F18Rik)
Mobkl2c	0.958	1.387	0.964	0.775	1.085	MOB1, Mps One Binder kinase activator-like 2C (yeast) (Mobkl2c)
Capzb	0.891	1.04	1.216	1.763	0.513	F-actin capping protein beta subunit (CapZ beta). [Source:Uniprot/SWISSPROT;Acc:P47757]
Zcchc17	1.185	0.93	1.539	1.266	0.892	RIKEN cDNA 2810055E05 gene (2810055E05Rik)
Khdrbs1	1.157	0.978	1.285	0.619	1.001	KH domain containing, RNA binding, signal transduction associated 1 (Khdrbs1)
Yars	1.664	1.183	0.877	1.212	0.845	hypothetical protein
Slc30a2	1.376	0.787	1.21	1.758	0.692	PREDICTED: solute carrier family 30 (zinc transporter), member 2 (Slc30a2)
Pftk1	1.326	1.218	1.048	1.403	0.895	PFTAIRE protein kinase 1 (Pftk1)
Klhl7	1.487	1.114	0.636	1.938	1.104	SBBI26 homolog. [Source:RefSeq;Acc:NM_026448]
Tas1r3	1.53	0.305	1.35	1.466	0.885	taste receptor, type 1, member 3 (Tas1r3)
ENSMUSG00000029092	1.343	1.279	0.452	1.711	1.831	PREDICTED: RIKEN cDNA 4930435H24 gene (4930435H24Rik)
Htra3	0.977	0.294	1.157	0.565	0.647	serine protease HTRA3 (Htra3)
Rnf4	1.02	0.992	0.861	0.805	0.859	ring finger protein 4 (Rnf4)
Tbc1d1	1.189	1.797	0.833	0.512	1.18	TBC1 domain family, member 1 (Tbc1d1)
Ugdh	0.984	0.933	1	0.769	0.946	UDP-glucose dehydrogenase (Ugdh)
Slc10a4	0.719	1.086	1.209	1.656	0.724	hypothetical protein E130304D01 (E130304D01)
Ppat	1.038	0.843	1.002	1.453	1.279	phosphoribosyl pyrophosphate amidotransferase (Ppat)
Wsb2	0.85	0.969	1.385	0.708	1.203	WD repeat and SOCS box-containing 2 (Wsb2)
Tmem116	1.21	0.64	0.899	0.413	1.09	RIKEN cDNA C030022K24 gene (C030022K24Rik)
Anapc7	1.055	1.024	0.809	0.843	0.916	anaphase promoting complex subunit 7 (Anapc7)
Chek2	0.976	1.553	0.808	0.677	0.793	CHK2 checkpoint homolog (S. pombe) (Chek2)
Mad1l1	0.957	2.026	1.331	1.794	1.175	mitotic arrest deficient 1-like 1 (Mad1l1)
ENSMUSG00000029564	2.418	1.191	0.322	1.304	0.598	hypothetical protein
ENSMUSG00000032812	1.284	0.689	0.808	1.167	1.098	centaurin, delta 2 (Centd2), transcript variant 1

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Tmem106b	0.612	0.955	1.075	0.834	0.965	RIKEN cDNA 2310036D22 gene (2310036D22Rik)
Usp42	1.198	0.671	0.521	0.627	0.737	PREDICTED: RIKEN cDNA A630018G05 gene (A630018G05Rik)
Wnt16	0.792	1.881	1.221	1.423	2.548	wingless-related MMTV integration site 16 (Wnt16)
Sspo	1.316	0.909	0.957	0.626	0.808	subcommissural organ spondin (Scospondin)
ENSMUSG00000029837	0.575	0.688	1.582	0.488	1.167	hypothetical protein
ENSMUSG00000029993	1.328	1.15	1.062	1.214	1.134	hypothetical protein
Add2	0.954	0.802	0.198	1.445	1.31	adducin 2 (beta) (Add2)
Tmf1	0.704	1.495	1.097	1.868	0.629	PREDICTED: similar to TATA element modulatory factor 1 (LOC232286)
Chl1	1.613	1.338	0.826	1.552	1.644	cell adhesion molecule with homology to L1CAM; close homolog of L1. [Source:RefSeq;Acc:NM_007697]
Slc41a3	1.292	1.327	0.845	1.612	0.863	PREDICTED: solute carrier family 41, member 3 (Slc41a3)
Cops7a	0.793	1.314	1.004	1.497	1	COP9 (constitutive photomorphogenic) homolog, subunit 7a; COP9 (constitutive photomorphogenic), subunit 7a (Arabidopsis); COP9 complex S7a. [Source:RefSeq;Acc:NM_012003]
Cops7a	0.904	1.208	1.631	0.809	1.045	COP9 (constitutive photomorphogenic) homolog, subunit 7a (Arabidopsis thaliana) (Cops7a)
Clec2e	0.395	1.074	1.158	1.617	2.923	C lectin-related protein A (Clra)
Mlstd1	1.607	0.795	0.744	1.333	1.621	male sterility domain containing 1 (Mlstd1)
Mbd4	0.942	0.757	0.392	1.572	1.253	methyl-CpG binding domain protein 4 (Mbd4)
Tnfrsf1a	1.147	0.921	0.967	0.652	1.083	tumor necrosis factor receptor superfamily, member 1a (Tnfrsf1a)
D6Wsu163e	0.876	1.092	0.909	1.512	0.611	DNA segment, Chr 6, Wayne State University 163, expressed (D6Wsu163e)
Zdhhc13	0.801	1.121	1.08	1.244	0.704	zinc finger, DHHC domain containing 13 (Zdhhc13)
Ceacam18	1.114	1.205	1.522	1.745	0.88	PREDICTED: RIKEN cDNA 2010110O04 gene (2010110O04Rik)
Chrna7	0.898	0.462	1.434	0.565	1.605	cholinergic receptor, nicotinic, alpha polypeptide 7 (Chrna7)
Abcc10	0.598	1.369	0.821	0.502	0.801	ATP-binding cassette, sub-family C (CFTR/MRP), member 10 (Abcc10), transcript variant mrp7A

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Sema4b	0.886	1.033	1.113	0.646	1.047	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B (Sema4b)
ENSMUSG00000030587	0.54	1.258	0.971	1.607	1.033	hypothetical protein
Fah	0.929	0.965	0.739	0.537	0.867	fumarylacetoacetate hydrolase (Fah)
Xylt1	0.633	1.503	0.573	0.627	0.811	xylosyltransferase 1 (Xylt1)
Pde3b	1.171	0.598	0.728	0.797	0.876	phosphodiesterase 3B, cGMP-inhibited (Pde3b)
Gdpd3	1.478	9.014	6.843	2.235	2.442	RIKEN cDNA 1110015E22 gene (1110015E22Rik)
Cln3	1.07	1.129	0.687	1.206	1.15	ceroid lipofuscinosis, neuronal 3, juvenile (Batten, Spielmeyer-Vogt disease) (Cln3)
BC017158	1.217	1.347	0.961	1.403	0.994	cDNA sequence BC017158 (BC017158)
Itgam	0.937	0.869	0.611	0.613	0.916	integrin alpha M (Itgam)
Fus	1.26	1.327	0.616	0.62	1.338	fusion, derived from t(12;16) malignant liposarcoma (human) (Fus)
Abcc6	1.075	0.249	0.421	2.076	0.468	ATP-binding cassette, sub-family C (CFTR/MRP), member 6 (Abcc6)
Bag3	0.898	1.848	0.651	1.932	1.509	Bcl2-associated athanogene 3 (Bag3)
Fgfr2	1.097	0.54	0.971	1.691	1.641	fibroblast growth factor receptor 2 (Fgfr2), transcript variant 2
Thumpd1	0.894	0.746	1.21	1.32	0.809	THUMP domain containing 1 (Thumpd1)
Art1	0.298	2.301	1.693	1.86	1.079	ADP-ribosyltransferase 1 (Art1)
Q8K3S0	0.441	0.954	0.261	0.526	1.368	PREDICTED: RIKEN cDNA 4930519F16 gene (4930519F16Rik)
Gpm6b	1.824	0.723	1.137	0.616	1.255	glycoprotein m6b (Gpm6b)
Cetn2	1.347	1.2	1.21	0.699	0.705	centrin 2 (Cetn2)
Zfp185	0.493	0.778	0.981	1.474	0.838	zinc finger protein 185 (Zfp185)
Irak1	0.969	1.065	1.022	1.193	0.828	Interleukin-1 receptor-associated kinase 1 (EC 2.7.1.-) (IRAK-1) (IRAK) (Pelle-like protein kinase) (mPLK). [Source:Uniprot/SWISSPROT;Acc:Q62406]
ENSMUSG00000031439	1.152	0.788	0.409	1.77	0.687	hypothetical protein
Vps36	1.023	3.028	1.142	1.401	0.92	RIKEN cDNA 2210415M20 gene (2210415M20Rik)
Polb	0.944	1.04	1.02	1.287	1.444	polymerase (DNA directed), beta (Polb)
Wwc2	0.662	1.224	0.68	1.54	0.788	DNA segment, Chr 8, ERATO Doi 594, expressed (D8Ertd594e)
ENSMUSG00000039722	0.572	0.948	1.177	0.696	0.711	hypothetical protein

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description of Gene Product
Fgfr1	1.79	1.197	1.502	1.834	1.115	Basic fibroblast growth factor receptor 1 precursor (EC 2.7.1.112) (FGFR-1) (bFGF-R) (MFR). [Source:Uniprot/SWISSPROT;Acc:P16092]
Slc7a2	0.767	0.681	0.513	1.651	1.618	Low-affinity cationic amino acid transporter-2 (CAT-2) (CAT2) (TEA protein) (T-cell early activation protein) (20.5). [Source:Uniprot/SWISSPROT;Acc:P18581]
Mt4	0.884	0.893	2.274	1.525	0.823	metallothionein 4 (Mt4)
Cntnap4	1.225	1.516	0.57	1.297	2.763	contactin associated protein 4 (Cntnap4)
1110012M11Rik	1.006	0.881	1.057	1.292	1.153	RIKEN cDNA 1110012M11 gene (1110012M11Rik)
Zdhhc7	0.823	1.219	1.482	0.571	1.069	zinc finger, DHHC domain containing 7 (Zdhhc7)
Nfatc3	0.751	1.684	1.869	0.641	0.821	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3 (Nfatc3)
Nip7	1.147	0.965	1.103	1.266	0.95	RIKEN cDNA 1110017C15 gene (1110017C15Rik)
Fez1	1.099	0.492	0.827	1.445	1.707	fasciculation and elongation protein zeta 1 (zygin I) (Fez1)
Tex9	1.333	0.768	1.607	1.405	2.107	testis expressed gene 9 (Tex9)
Tcf12	0.827	0.058	0.907	0.63	0.882	Transcription factor 12 (Transcription factor HTF-4) (E-box-binding protein) (DNA-binding protein HTF4) (Class A helix-loop-helix transcription factor ME1). [Source:Uniprot/SWISSPROT;Acc:Q61286]
Man2c1	1.236	1.199	0.888	1.308	0.963	mannosidase, alpha, class 2C, member 1 (Man2c1)
Nrg4	0.843	0.462	1.399	1.492	0.909	neuregulin 4 (Nrg4)
Csk	1.198	1.265	1.114	1.23	0.991	c-src tyrosine kinase (Csk)
Mras	0.555	0.83	0.726	0.743	0.793	muscle and microspikes RAS (Mras)
Scap	0.918	1.124	0.982	1.227	1.096	SREBP cleavage activating protein (Scap)
Ltf	1.487	1.021	1.825	0.633	0.832	lactotransferrin (Ltf)
Pdcd6ip	1.177	1.264	0.848	0.536	0.643	programmed cell death 6 interacting protein (Pdcd6ip)
Rpsa	1.08	0.618	0.892	1.511	1.674	laminin receptor 1 (ribosomal protein SA) (Lamr1)
Atp2c1	0.327	1.389	0.748	0.655	1.483	ATPase, Casequestering (Atp2c1)
1700102P08Rik	0.254	1.691	0.774	1.458	1.532	RIKEN cDNA 1700102P08 gene (1700102P08Rik)
Gpr19	1.012	1.047	0.726	1.356	1.116	G protein-coupled receptor 19 (Gpr19)
ENSMUSG00000032776	0.478	1.179	0.909	1.914	1.152	hypothetical protein

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description of Gene Product
Nrip3	0.905	1.393	2.278	2.192	1.407	nuclear receptor interacting protein 3 (Nrip3)
Cdo1	0.967	0.804	1.388	1.376	1.064	cysteine dioxygenase 1, cytosolic (Cdo1)
Nol12	0.463	0.474	1.302	1.737	0.742	expressed sequence C78541 (C78541)
Atg9a	1.904	0.793	0.482	1.54	0.495	expressed sequence AU019532 (AU019532)
Phldb2	1.295	0.57	0.948	0.508	1.101	PREDICTED: similar to pleckstrin homology-like domain, family B, member 2; LL5 beta (LOC436358)
Fbp1	1.627	1.15	1.461	1.54	1.975	fructose bisphosphatase 1 (Fbp1)
Usp37	0.873	1.651	1.811	2.068	1.06	ubiquitin specific protease 37 (Usp37)
Clasp2	0.858	0.725	0.391	1.31	1.357	PREDICTED: CLIP associating protein 2 (Clasp2)
Ctdspl2	0.913	0.848	1.593	1.579	0.805	DNA segment, Chr 2, ERATO Doi 485, expressed (D2Ertd485e)
Antxr1	1.23	1.091	1.539	1.27	1.462	anthrax toxin receptor 1 (Antxr1)
Myo5c	1.691	1.047	0.288	1.502	1.931	Myosin VC (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8BWY8]
Mrcl	1.339	0.993	0.629	2.017	0.615	mannose receptor-like precursor (Mrcl)
Acbd6	0.923	1.637	1.2	1.368	1.164	acyl-Coenzyme A binding domain containing 6 (Acbd6)
BC034090	0.665	0.429	1.276	1.463	1.217	PREDICTED: cDNA sequence BC034090 (BC034090)
ENSMUSG00000033767	0.86	1.421	1.298	1.976	0.676	hypothetical protein
Stonin 1	0.496	0.822	1.134	1.916	2.674	Stonin 1 (Stoned B-like factor). [Source:Uniprot/SWISSPROT;Acc:Q8CDJ8]
Mir16	1.153	2.107	1.534	1.462	1.379	membrane interacting protein of RGS16 (Mir16)
Gria2	1.011	1.24	1.554	2.24	1.987	glutamate receptor, ionotropic, AMPA2 (alpha 2) (Gria2)
Zfp291	0.953	1.294	1.536	0.689	1.128	zinc finger protein 291. [Source:RefSeq;Acc:NM_175536]
ENSMUSG00000034122	0.919	0.985	0.418	0.491	0.565	hypothetical protein
Pomt2	0.293	0.258	1.051	1.125	0.843	protein-O-mannosyltransferase 2 (Pomt2)
Tmem63c	1.041	1.746	0.497	1.733	1.355	RIKEN cDNA 9330187M14 gene (9330187M14Rik)
Gas2l1	0.818	2.051	1.212	0.756	1.359	growth arrest-specific 2 like 1 (Gas2l1)
Mscp	1.135	1.337	0.855	0.752	0.964	mitochondrial solute carrier protein (Mscp)
Slc24a1	0.433	0.658	1.479	1.955	0.812	solute carrier family 24 (sodium/potassium/calcium exchanger), member 1 (Slc24a1)
Tmem5	0.894	1.533	0.449	0.558	1.017	transmembrane protein 5 (Tmem5)

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ENSMUSG00000034832	0.839	0.519	1.109	1.622	1.847	hypothetical protein
Plvap	1.087	0.85	1.402	1.984	0.734	plasmalemma vesicle associated protein (Plvap)
Ncaph	1.001	0.906	0.771	1.128	0.716	barren homolog (Drosophila) (Brrn1)
ENSMUSG00000034951	0.981	0.821	0.97	0.827	1.05	PREDICTED: RIKEN cDNA 5630400E24 gene (5630400E24Rik)
Hrh2	0.873	0.796	0.652	1.475	0.732	Histamine H2 receptor (H2R) (Gastric receptor I). [Source:Uniprot/SWISSPROT;Acc:P97292]
Eif2s3x	1.216	0.889	1.006	0.675	0.891	eukaryotic translation initiation factor 2, subunit 3, structural gene X-linked (Eif2s3x)
ENSMUSG00000035195	2.284	0.642	0.939	1.389	0.83	PREDICTED: similar to P38IP protein (LOC245516)
ENSMUSG00000035201	1.649	0.664	1.606	7.657	1.493	hypothetical protein
Epn1	1.064	1.366	1.107	1.271	0.947	epsin 1 (Epn1)
A930041I02Rik	1.067	1.61	1.766	0.563	0.909	RIKEN cDNA A930041I02 gene (A930041I02Rik)
ENSMUSG00000035271	1.554	1.295	0.764	0.592	1.224	hypothetical protein
Adrb1	1.69	0.142	1.372	1.232	1.117	adrenergic receptor, beta 1 (Adrb1)
ENSMUSG00000035284	0.728	0.539	0.873	1.454	1.092	hypothetical protein
Ror1	1.793	0.484	0.331	2.447	0.955	receptor tyrosine kinase-like orphan receptor 1 (Ror1)
Gdpd5	1.193	1.352	1.019	1.29	1.095	cDNA sequence BC024955 (BC024955)
Nup37	0.81	1.034	0.698	1.477	1.001	nucleoporin 37 (Nup37)
Pdzrn3	0.432	0.301	0.736	2.192	1.152	PDZ domain containing RING finger 3 (Pdzrn3)
Ccl2	0.648	0.77	0.743	1.529	1.809	chemokine (C-C motif) ligand 2 (Ccl2)
Slc25a21	1.687	3.657	0.585	1.291	1.633	solute carrier family 25 (mitochondrial oxodicarboxylate carrier), member 21 (Slc25a21)
BC057893	1.175	1.461	1.504	0.567	1.218	cDNA sequence BC057893 (BC057893)
Aldh1b1	1.367	1.77	1.111	0.596	0.925	aldehyde dehydrogenase 1 family, member B1 (Aldh1b1)
Zswim4	1.303	1.116	0.923	1.703	1.021	zinc finger, SWIM domain containing 4 (Zswim4)
Rnf38	0.96	0.995	0.892	1.436	0.79	ring finger protein 38 (Rnf38)
4930503E14Rik	0.647	1.296	1.863	2.198	0.669	hypothetical protein
Polr3g	1.139	0.884	0.773	0.663	0.829	PREDICTED: polymerase (RNA) III (DNA directed) polypeptide G (Polr3g)

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1110049B09 Rik	0.189	0.669	1.356	3.262	1.049	PREDICTED: RIKEN cDNA 1110049B09 gene (1110049B09Rik)
Birc1f	0.761	0.982	0.661	0.623	0.937	Baculoviral IAP repeat-containing protein 1g (Neuronal apoptosis inhibitory protein 7). [Source:Uniprot/SWISSPROT;Acc:Q9JIB3]
4930432H15 Rik	1.618	1.225	0.996	2.923	1.21	RIKEN cDNA 4930432H15 gene (4930432H15Rik)
Smug1	1.021	1.164	0.731	1.715	1.829	single-strand selective monofunctional uracil DNA glycosylase (Smug1)
Oprs1	1.083	1.777	1.056	0.73	1.053	opioid receptor, sigma 1 (Oprs1)
Hyal3	0.407	0.667	1.5	1.398	1.102	hyaluronidase 3 (Hyal3)
Rab3gap1	0.788	1.186	1.09	0.734	1.082	RIKEN cDNA 4732493F09 gene (4732493F09Rik)
D9Ertd25e	1.063	0.106	1.212	2.08	1.132	acetyl-Coenzyme A acyltransferase 1; 3-ketoacyl-CoA thiolase A; peroxisomal 3-oxoacyl-Coenzyme A thiolase; peroxisomal 3-ketoacyl-CoA thiolase. [Source:RefSeq;Acc:NM_130864]
Acaa1a	0.746	1.129	0.836	0.71	1.019	acetyl-Coenzyme A acyltransferase 1 (Acaa1)
Elf1	0.729	0.88	0.851	0.674	0.911	E74-like factor 1 (Elf1)
Akp3	0.66	0.104	1.652	1.628	0.912	alkaline phosphatase 3, intestine, not Mn requiring (Akp3)
Card11	0.789	1.407	1.888	1.496	0.893	caspase recruitment domain family, member 11 (Card11)
H2-Aa	0.857	1.23	1.332	0.673	0.642	histocompatibility 2, class II antigen A, alpha (H2-Aa)
Nudt1	0.749	0.65	1.286	0.628	1.277	nudix (nucleoside diphosphate linked moiety X)-type motif 1 (Nudt1)
Dennd3	0.169	1.426	1.261	1.311	0.811	PREDICTED: RIKEN cDNA E030003N15 gene (E030003N15Rik)
Micall2	0.411	0.212	0.761	1.371	1.517	RIKEN cDNA A930021H16 gene (A930021H16Rik)
Acaa2	1.049	1.32	1.156	1.172	0.916	acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase) (Acaa2)
ENSMUSG00 000036885	0.943	0.893	1.248	1.324	1.03	PREDICTED: RIKEN cDNA 8430436L14 gene (8430436L14Rik)
Elac1	0.995	0.894	0.775	0.775	1.109	elaC homolog 1 (E. coli) (Elac1)
D4Wsu53e	1.017	1.038	1.145	0.632	0.867	DNA segment, Chr 4, Wayne State University 53, expressed (D4Wsu53e)
Whsc1	0.76	0.918	0.607	1.997	1.123	PREDICTED: Wolf-Hirschhorn syndrome candidate 1 (human) (Whsc1)
Ttc13	1.58	0.868	1.025	1.208	0.621	PREDICTED: tetratricopeptide repeat domain 13 (Ttc13)

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Traf3ip3	1.055	0.698	0.993	1.732	0.894	RIKEN cDNA 6030423D04 gene (6030423D04Rik)
Tap1	0.914	0.765	0.591	0.724	2.027	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP) (Tap1)
Nudt22	1.113	2.072	1.22	1.517	0.783	RIKEN cDNA 0610006K04 gene (0610006K04Rik)
4930578C19 Rik	1.88	1.215	0.511	1.695	0.406	RIKEN cDNA 4930578C19 gene (4930578C19Rik)
Arid5a	0.622	1.009	1.836	1.603	1.55	AT rich interactive domain 5A (Mrf1 like) (Arid5a)
Shank2	0.874	1.493	0.427	2.831	1.037	PREDICTED: SH3/ankyrin domain gene 2 (Shank2)
BC022687	1.068	0.769	0.971	1.328	1.03	cDNA sequence BC022687 (BC022687)
ENSMUSG00 000037627	0.863	1.005	1.125	3.313	1.071	hypothetical protein
Gm8	1.158	1.38	0.978	1.637	0.947	PREDICTED: similar to mitochondrial solute carrier protein (LOC194744)
1110057K04 Rik	1.043	1.177	1.184	0.694	0.987	RIKEN cDNA 1110057K04 gene (1110057K04Rik)
Armc3	1.179	0.848	1.428	1.711	0.186	PREDICTED: armadillo repeat containing 3 (Armc3)
Ckap2	0.812	0.862	0.87	1.571	1.188	Cytoskeleton associated protein 2 (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8BSF0]
Mynn	1.042	1.178	0.727	0.668	0.957	myoneurin (Mynn)
Slc32a1	0.846	0.868	1.096	0.65	1.162	vesicular inhibitory amino acid transporter (Viaat)
ENSMUSG00 000038011	0.753	0.429	1.387	1.292	0.805	PREDICTED: dynein, axonemal, heavy chain 10 (Dnahc10)
Kcnj9	1.282	0.098	0.746	1.3	1.415	G protein-activated inward rectifier potassium channel 3 (GIRK3) (Potassium channel, inwardly rectifying, subfamily J, member 9) (Inwardly rectifier K channel Kir3.3). [Source:Uniprot/SWISSPROT;Acc:P48543]
9630033F20 Rik	1.03	1.249	1.105	0.681	0.893	RIKEN cDNA 9630033F20 gene (9630033F20Rik)
AW456874	1.598	0.89	1.448	1.472	0.992	expressed sequence AW456874 (AW456874)
Mll3	1.059	1.195	1.119	1.338	0.972	PREDICTED: myeloid/lymphoid or mixed-lineage leukemia 3 (Mll3)
Fkbp14	0.951	1.35	0.451	1.351	0.69	FK506 binding protein 14 (Fkbp14)
Crygn	1.636	2.345	1.369	1.438	0.337	crystallin, gamma N (Crygn)
Cer1	1.311	1.225	0.498	1.625	2.233	cerberus 1 homolog (Xenopus laevis) (Cer1)
Cd160	1.223	1.22	0.786	1.608	0.93	CD160 antigen (Cd160)

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ENSMUSG00000038311	1.419	0.097	0.787	1.551	1.311	PREDICTED: RIKEN cDNA 2410017I17 gene (2410017I17Rik)
Edem2	0.876	0.995	0.972	0.697	0.993	RIKEN cDNA 9530090G24 gene (9530090G24Rik)
BC057079	1.209	0.957	1.476	0.71	0.987	PREDICTED: cDNA sequence BC057079 (BC057079)
ENSMUSG00000038377	0.902	1.836	0.702	0.376	1.167	hypothetical protein
Atf5	1.063	0.575	0.96	1.368	1.241	activating transcription factor 5 (Atf5)
BC028528	0.859	1.006	1.26	1.16	1.13	cDNA sequence BC028528 (BC028528)
Reep2	0.791	0.901	1.186	2.76	1.351	cDNA sequence BC020184 (BC020184)
Sp6	0.437	0.701	0.786	1.609	1.092	trans-acting transcription factor 6 (Sp6)
ENSMUSG00000038570	1.889	0.965	1.711	2.182	1.371	hypothetical protein
Samd10	1.062	1.571	1.401	1.115	1.406	sterile alpha motif domain containing 10 (Samd10)
Pold1	0.976	4.817	1.097	1.608	1.392	polymerase (DNA directed), delta 1, catalytic subunit (Pold1)
ENSMUSG00000038672	1.395	0.681	1.541	1.611	1.176	hypothetical protein
ENSMUSG00000038785	1.149	0.28	2.059	1.424	0.652	hypothetical protein
Prc1	0.515	0.52	1.191	1.411	0.571	hypothetical protein
9630058J23Rik	1.772	1.699	0.985	1.432	1.035	RIKEN cDNA 9630058J23 gene (9630058J23Rik)
Tlr4	1.07	0.898	1.026	0.669	1.295	toll-like receptor 4 (Tlr4)
5430433G21Rik	1.36	1.104	0.926	1.24	0.919	PREDICTED: RIKEN cDNA 5430433G21 gene (5430433G21Rik)
Cpa4	0.723	0.285	0.264	2.09	1.013	carboxypeptidase A4 (Cpa4)
Htr5a	1.014	1.29	0.75	1.926	1.074	5-hydroxytryptamine (serotonin) receptor 5A (Htr5a)
Kif7	0.544	1.884	1.177	1.537	0.633	hypothetical protein
ENSMUSG00000039150	3.245	0.399	0.765	1.732	1.242	hypothetical protein
Gpatch2	0.721	1.447	1.203	1.444	0.982	G patch domain containing 2 (Gpatc2)
Rnf122	0.532	1.084	1.163	0.817	0.953	ring finger protein 122 (Rnf122)
	0.289	0.332	1.279	1.676	0.83	RIKEN cDNA 4921511F01 gene (4921511F01Rik)
Sec24c	1.139	0.757	0.979	1.171	1.089	SEC24 related gene family, member C (S. cerevisiae) (Sec24c)
ENSMUSG00000039373	1.27	0.52	0.443	2.003	0.271	hypothetical protein
Pdzd2	0.676	0.958	1.336	0.637	0.861	PREDICTED: PDZ domain containing 3 (Pdzk3)
Prkcbp1	0.823	1.205	0.708	0.607	0.855	protein kinase C binding protein 1

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Btbd12	0.66	0.947	1.038	0.614	1.024	BTB (POZ) domain containing 12 (Btbd12)
Exo1	1.156	1.105	1.18	1.756	1.107	exonuclease 1 (Exo1)
Olig2	0.915	1.054	1.145	0.529	0.667	oligodendrocyte transcription factor 2 (Olig2)
Tera	0.961	1.237	0.773	1.384	1.216	teratocarcinoma expressed, serine rich (Tera)
Olfr391-ps1	0.683	1.408	1.162	2.656	0.239	PREDICTED: similar to olfactory receptor Olr1496 (LOC193058)
Rbms2	1.064	1.158	1.253	1.373	1.427	RNA binding motif, single stranded interacting protein 2 (Rbms2)
Flywch1	1.141	1.249	1.195	1.48	1.028	RIKEN cDNA E030034P13 gene (E030034P13Rik)
Mrps35	0.876	1.07	0.849	0.911	0.898	mitochondrial ribosomal protein S35 (Mrps35)
Abcc8	0.395	1.449	0.484	0.692	1.22	RIKEN cDNA D930031B21 gene (D930031B21Rik)
Ankrd6	1.225	0.202	0.338	1.639	1.155	ankyrin repeat domain 6 (Ankrd6)
Daam2	1.844	0.592	0.97	1.216	0.106	PREDICTED: dishevelled associated activator of morphogenesis 2 (Daam2)
Klhdc4	1.64	1.05	1.064	1.452	0.847	kelch domain containing 4 (Klhdc4)
2610203E10 Rik	0.866	0.991	0.86	1.292	0.767	RIKEN cDNA 2610203E10 gene (2610203E10Rik)
B230220E17 Rik	0.661	1.845	0.472	1.447	1.056	PREDICTED: similar to Cadherin-18 precursor (Cadherin-14) (LOC432937)
Pitpnm3	0.852	0.483	1.14	1.579	0.305	PREDICTED: RIKEN cDNA A330068P14 gene (A330068P14Rik)
Aipl1	1.537	0.655	1.291	1.309	0.903	aryl hydrocarbon receptor-interacting protein-like 1 (Aipl1)
ENSMUSG00 000040693	1.105	1.154	1.439	1.773	1.325	hypothetical protein
Agmat	0.681	0.981	0.969	0.845	0.524	PREDICTED: agmatine ureohydrolase (agmatinase) (Agmat)
Klc3	0.875	1.152	0.947	1.593	1.153	kinesin light chain 3 (Klc3)
Eif4h	0.926	1.499	0.787	0.543	1.119	Williams-Beuren syndrome chromosome region 1 homolog (human) (Wbscr1)
Ints8	1.255	0.486	1.305	0.717	0.994	RIKEN cDNA 2810013E07 gene (2810013E07Rik)
Siah1b	1.218	1.481	0.718	1.695	0.63	seven in absentia 1B (Siah1b)
Lat2	0.798	1.515	1.266	0.783	1.178	Williams-Beuren syndrome chromosome region 5 homolog (human) (Wbscr5)
Dlk1	0.32	0.336	1.065	1.667	0.405	delta-like 1 homolog (Drosophila) (Dlk1)
S100pbp	0.974	1.205	0.763	1.8	1.068	PREDICTED: RIKEN cDNA 4930429A08 gene (4930429A08Rik)
Asgr2	1.018	0.749	1.009	1.785	2.424	asialoglycoprotein receptor 2 (Asgr2)
ENSMUSG00 000040978	0.664	1.51	1.318	1.302	0.699	hypothetical protein

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description of Gene Product
Pla2g2d	0.852	1.034	1.883	1.612	1.156	phospholipase A2, group IID (Pla2g2d)
4930563P21 Rik	1.27	1.107	0.724	4.371	0.429	PREDICTED: RIKEN cDNA 4930563P21 gene (4930563P21Rik)
ENSMUSG00 000041353	1.009	0.966	1.014	1.772	1.72	hypothetical protein
Bbox1	1.083	1.434	1.016	1.898	0.739	butyrobetaine (gamma), 2-oxoglutarate dioxygenase 1 (gamma-butyrobetaine hydroxylase) (Bbox1)
MISS_MOUS E	0.356	1.177	1.062	1.379	1.618	MAPK-interacting and spindle-stabilizing protein. [Source:Uniprot/SWISSPROT;Acc:Q9D7G9]
C7	0.959	0.947	0.908	1.308	1.565	PREDICTED: similar to complement component 7 precursor (LOC383055)
myosin 1H	1.308	0.278	1.347	1.491	1.501	myosin 1H. [Source:RefSeq;Acc:NM_146163]
ENSMUSG00 000042057	0.912	1.381	0.72	0.558	1.164	hypothetical protein
Ankrd47	1	1.167	0.735	1.477	0.995	DNA segment, Chr 17, ERATO Doi 288, expressed (D17Ertd288e)
Cdrt4	0.992	0.725	1.71	1.455	1.931	RIKEN cDNA 1700019I23 gene (1700019I23Rik)
Pglyrp4	1.904	1.466	0.643	1.52	0.781	peptidoglycan recognition protein 4 (Pglyrp4)
Osbpl6	0.951	0.443	0.394	2.336	2.145	oxysterol binding protein-like 6 (Osbpl6)
Tsen2	0.708	1.046	0.828	0.681	0.791	expressed sequence AU067695 (AU067695)
ENSMUSG00 000042454	0.232	0.847	1.421	0.366	1.075	hypothetical protein
Clspn	2.384	0.22	0.647	1.416	0.251	claspin homolog (Xenopus laevis) (Clspn)
Ipo11	1.011	1.371	1.215	1.801	0.514	importin 11 (Ipo11)
ENSMUSG00 000042595	0.176	0.189	1.016	0.705	0.498	hypothetical protein
Arrdc4	1.2	0.487	1.199	0.747	0.477	arrestin domain containing 4 (Arrdc4)
Rnf214	0.764	1.919	0.494	0.544	0.924	RIKEN cDNA D130054N24 gene (D130054N24Rik)
Ints5	1.063	0.745	0.914	0.64	1.179	RIKEN cDNA 1110055N21 gene (1110055N21Rik)
Egflam	0.768	0.639	0.879	3.387	1.033	expressed sequence AU040377 (AU040377)
Upk3b	0.614	0.946	0.854	2.414	0.381	uroplakin 3B (Upk3b)
Tmem186	1.085	0.848	1.19	0.622	0.938	RIKEN cDNA 4432406C05 gene (4432406C05Rik)
Olfr131	1.445	0.367	1.571	0.616	0.568	olfactory receptor 131 (Olfr131)
Leng9	1.271	1.123	1.002	0.684	0.798	leukocyte receptor cluster (LRC) member 9 (Leng9)

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ENSMUSG00000043469	0.642	0.999	1.006	1.239	1.075	hypothetical protein
ENSMUSG00000043656	1.318	0.83	1.111	0.822	0.886	PREDICTED: similar to protease (prosome, macropain) 26S subunit, ATPase 1 (LOC386042)
BC033932	0.211	0.975	1.388	0.708	1.731	PREDICTED: hypothetical gene supported by BC033932 (LOC434325)
V2r2	1.329	1.655	0.892	1.542	0.892	vomeronasal 2, receptor, 2 (V2r2)
E430028B21Rik	1.292	1.182	0.969	0.764	1.45	RIKEN cDNA E430028B21 gene (E430028B21Rik)
ENSMUSG00000043723	1.271	1.105	0.858	1.354	1.11	PREDICTED: similar to 60S ribosomal protein L29 (P23) (LOC382856)
BC038613	0.883	0.677	0.56	0.783	1.199	cDNA sequence BC038613 (BC038613)
ENSMUSG00000043790	1.722	1.596	0.969	0.641	1.35	hypothetical protein
Olfr479	0.867	1.652	0.963	1.545	1.278	Olfactory receptor GA_x6K02T2PBJ9-10384085-10385068. [Source:Uniprot/SPTREMBL;Acc:Q7TRV1]
Edg5	1.142	0.98	1.279	0.658	1.111	endothelial differentiation, sphingolipid G-protein-coupled receptor, 5 (Edg5)
A330049M08Rik	0.533	2.159	1.041	3.525	0.689	RIKEN cDNA A330049M08 gene (A330049M08Rik)
1700029G01Rik	1.199	0.892	0.987	0.672	0.973	RIKEN cDNA 1700029G01 gene (1700029G01Rik)
ENSMUSG00000044058	0.882	0.985	1.143	1.289	1.92	hypothetical protein
ENSMUSG00000044062	1.396	1.274	1.257	1.563	1.237	PREDICTED: RIKEN cDNA 0610009B14 gene (0610009B14Rik)
AI851790	0.889	0.072	0.782	1.778	1.356	expressed sequence AI851790 (AI851790)
Olfr868	1.129	0.918	1.123	2.736	0.556	olfactory receptor 868 (Olfr868)
Nkx2-6	0.928	4.066	0.713	1.542	1.003	NK2 transcription factor related, locus 6 (Drosophila) (Nkx2-6)
Vsig4	1.082	1.689	1.331	2.185	2.113	V-set and immunoglobulin domain containing 4 (Vsig4)
Nhlrc1	1.18	0.797	2.074	0.518	0.932	NHL repeat containing 1 (Nhlrc1)
9630041N07Rik	1.234	1.11	1.343	2.029	1.038	RIKEN cDNA 9630041N07 gene (9630041N07Rik)
Cxxc4	0.635	0.851	0.936	1.621	0.431	CXXC finger 4 (Cxxc4)
Tmem46	1.055	0.807	2.272	1.497	1.223	RIKEN cDNA 9430059P22 gene (9430059P22Rik)
4632419K20Rik	1.239	0.941	0.924	1.412	0.781	RIKEN cDNA 4632419K20 gene (4632419K20Rik)
9130011J15Rik	1.219	1.352	1.231	0.8	0.695	RIKEN cDNA 9130011J15 gene (9130011J15Rik)
Dok7	1.547	0.273	1.263	1.942	0.766	hypothetical protein A930013K19 (A930013K19)

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H1fx	0.595	1.352	0.858	0.543	0.679	H1 histone family, member X (H1fx)
Cetn4	0.636	1.22	0.754	0.329	1.159	centrin 4 (Cetn4)
Kcng3	1.901	0.9	0.788	1.778	1.466	potassium voltage-gated channel, subfamily G, member 3 (Kcng3)
ENSMUSG00000045065	0.898	0.772	1.225	1.379	1.432	RIKEN cDNA 9930022D16 gene (9930022D16Rik)
LOC625662	1.274	0.427	1.314	1.802	1.248	PREDICTED: similar to hypothetical protein (LOC218476)
Cirbp	0.844	1.029	0.832	1.315	1.087	cold inducible RNA binding protein (Cirbp)
Zfp691	0.774	1.788	1.113	1.638	1.119	RIKEN cDNA 6430544H17 gene (6430544H17Rik)
5430407P10Rik	2.135	0.339	0.938	1.679	1.068	RIKEN cDNA 5430407P10 gene (5430407P10Rik)
Hnrph2	1.056	2.006	0.751	0.62	0.788	Heterogeneous nuclear ribonucleoprotein H' (hnRNP H'). [Source:Uniprot/SWISSPROT;Acc:P70333]
ENSMUSG00000045437	0.839	0.611	1.387	2.03	1.304	PREDICTED: similar to BC005685 protein (LOC212970)
ENSMUSG00000045463	1.604	1.259	0.995	0.417	0.595	PREDICTED: similar to testis-specific transporter TST-2; gonad-specific transporter 2 (LOC383605)
2610042O14Rik	1.01	1.343	1.142	1.349	1.042	RIKEN cDNA 2610042O14 gene (2610042O14Rik)
Tssk2	1.332	0.718	1.364	1.397	0.662	serine/threonine kinase 22B (spermiogenesis associated) (Stk22b)
Olfr891	1.857	2.145	1.283	1.876	1.305	olfactory receptor 891 (Olfr891)
Olfr610	0.912	0.848	0.722	1.4	1.701	olfactory receptor 610 (Olfr610)
BC049730	0.638	0.755	0.727	1.88	0.968	PREDICTED: cDNA sequence BC049730 (BC049730)
2310042D19Rik	1.215	1.71	0.456	1.98	1.237	RIKEN cDNA 2310042D19 gene (2310042D19Rik)
Tcf21	1.326	0.227	0.994	1.414	1.264	transcription factor 21 (Tcf21)
ENSMUSG00000045694	1.099	0.843	0.916	0.609	1.141	PREDICTED: similar to 40S ribosomal protein S20 (LOC245676)
F730047E07Rik	1.329	1.087	1.318	1.133	1.117	RIKEN cDNA F730047E07 gene (F730047E07Rik)
Olfr1461	0.893	0.7	0.43	1.133	1.214	olfactory receptor 1461 (Olfr1461)
C80008	1.541	1.129	0.68	1.487	1.385	PREDICTED: similar to DNA segment, Chr 18, Wayne State University 98, expressed (LOC384207)
ENSMUSG00000046009	0.712	1.079	0.637	0.632	0.891	Sepiapterin reductase. [Source:Uniprot/SPTREMBL;Acc:Q62218]
ENSMUSG00000046048	1.976	1.658	0.8	1.393	1.201	PREDICTED: similar to chromosome X open reading frame 22 (LOC434805)
Rp1l1	0.826	1.66	1.111	2.561	2.397	PREDICTED: retinitis pigmentosa 1 homolog (human)-like 1 (Rp1hl1)

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Krt32	1.709	0.306	1.279	1.598	0.429	keratin complex 1, acidic, gene 2 (Krt1-2)
ENSMUSG00000046271	1.181	1.434	1.527	1.508	0.986	hypothetical protein
ENSMUSG00000046321	0.343	0.416	0.376	1.116	0.348	RIKEN cDNA A830061E14 gene (A830061E14Rik)
Dppa3	0.778	0.848	1.389	1.632	0.816	developmental pluripotency-associated 3 (Dppa3)
Ube2v1	0.461	1.935	0.9	0.519	1.103	Similar to ubiquitin-conjugating enzyme E2 variant 1 (EC 6.3.2.19) (Ubiquitin-protein ligase) (Ubiquitin carrier protein). [Source:Uniprot/SPTREMBL;Acc:Q8VEB5]
Olfr609	0.687	1.032	1.454	1.722	0.778	olfactory receptor 609; olfactory receptor MOR9-1; GA_x6K02T2PBJ9-6207735-6206776. [Source:RefSeq;Acc:NM_147082]
B430212C06Rik	1.427	1.753	0.667	0.449	0.484	PREDICTED: RIKEN cDNA B430212C06 gene (B430212C06Rik)
Spin2	1.076	0.254	0.246	1.71	1.692	spindlin-like (Spin2)
Mrgprb1	1.5	1.171	0.963	1.357	1.456	MAS-related GPR, member B1 (Mrgprb1)
Tas2r143	0.401	2.465	1.176	2.078	1.03	taste receptor, type 2, member 143 (Tas2r143)
Gprc5a	0.442	0.718	1.009	1.546	1.644	retinoic acid induced 3 (Rai3)
3110062M04Rik	0.846	2.054	1.004	1.404	0.92	RIKEN cDNA 3110062M04 gene (3110062M04Rik)
Slc39a3	1.149	0.999	1.169	1.281	1.052	solute carrier family 39 (zinc transporter), member 3 (Slc39a3)
ENSMUSG00000046958	1.257	2.354	0.372	2.657	0.422	RIKEN cDNA 4930432E11 gene (4930432E11Rik)
1110032F04Rik	0.743	1.817	1.176	1.795	0.699	PREDICTED: RIKEN cDNA 1110032F04 gene (1110032F04Rik)
Zfp41	0.678	1.014	0.927	1.827	1.129	zinc finger protein 41 (Zfp41)
Mipol1	0.754	0.431	0.607	1.978	0.568	PREDICTED: mirror-image polydactyly gene 1 homolog (human) (Mipol1)
BC048390	0.875	1.025	1.207	2.147	0.852	cDNA sequence BC048390 (BC048390)
Chst9	2.205	1.099	0.495	2.193	1.6	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 (Chst9)
Hist1h2be	0.293	1.013	1.263	1.773	0.502	histone 1, H2be (Hist1h2be)
Zfp286	0.792	0.841	1.061	1.412	1.381	zinc finger protein 286 (Zfp286)
Nr1h4	1.14	1.445	0.525	1.385	0.868	nuclear receptor subfamily 1, group H, member 4 (Nr1h4)
D8Ertd457e	0.811	0.861	1.021	0.624	1.52	DNA segment, Chr 8, ERATO Doi 457, expressed (D8Ertd457e)
Utf1	0.469	0.975	1.315	1.686	0.789	undifferentiated embryonic cell transcription factor 1 (Utf1)

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Olfr685	0.276	1.873	0.954	1.788	1.563	Olfactory receptor GA_x6K02T2PBJ9-7810071-7809121. [Source:Uniprot/SPTREMBL;Acc:Q7TRN7]
Fbxw10	1.512	0.304	0.664	1.475	0.817	PREDICTED: similar to chromosome 17 open reading frame 1A (LOC213980)
Cdca4	0.963	0.888	0.891	0.868	1.2	cell division cycle associated 4 (Cdca4)
LOC381776	0.767	0.762	1.015	1.533	0.606	PREDICTED: similar to Ig V-K167 precursor (LOC381776)
Isg20l2	1.318	1.702	0.779	0.602	0.944	expressed sequence C80587 (C80587)
ENSMUSG00000048143	1.365	0.833	0.692	1.184	0.799	PREDICTED: RIKEN cDNA A030009A09 gene (A030009A09Rik)
Nwd1	1.609	0.384	0.619	1.565	0.517	RIKEN cDNA A230063L24 gene (A230063L24Rik)
Ccdc57	1.292	2.373	0.636	1.347	2.33	PREDICTED: RIKEN cDNA 4933434G05 gene (4933434G05Rik)
Zbtb8	2.207	0.234	0.739	1.396	0.656	zinc finger and BTB domain containing 8 (Zbtb8)
Fbxl13	0.929	1.312	1.103	1.328	0.696	F-box and leucine-rich repeat protein 13 (Fbxl13)
Cxcr6	1.005	1.501	1.956	1.389	1.084	chemokine (C-X-C motif) receptor 6 (Cxcr6)
ENSMUSG00000048559	0.681	1.109	1.442	1.619	1.017	hypothetical protein
Sp8	1.021	0.344	0.763	1.95	1.05	trans-acting transcription factor 8 (Sp8)
Vstm2	1.418	1.361	0.835	1.364	0.461	cDNA sequence BC027127 (BC027127)
BC057371	0.441	1.839	1.011	1.514	1.133	cDNA sequence BC057371 (BC057371)
ENSMUSG00000048903	0.965	0.865	1.089	1.288	1.361	hypothetical protein
A930017N06Rik	1.577	1.06	0.417	2.533	0.979	RIKEN cDNA A930017N06 gene (A930017N06Rik)
Sephs2	1.092	1.039	0.831	0.705	0.864	selenophosphate synthetase 2 (Sephs2)
BC038286	1.231	0.844	0.916	1.218	0.973	cDNA sequence BC038286 (BC038286)
Brd8	0.43	0.839	0.882	1.505	0.452	PREDICTED: hypothetical protein 4933408B17 (4933408B17)
Vkorc1l1	0.854	1.367	0.912	1.275	0.764	vitamin K epoxide reductase complex, subunit 1-like 1 (Vkorc1l1), transcript variant 1
Zfp260	1.394	1.28	1.171	0.74	0.714	zinc finger protein 260 (Zfp260)
ENSMUSG00000049460	0.929	1.062	0.74	0.717	1.276	hypothetical protein
Tmem139	0.617	0.965	1.763	1.756	0.917	RIKEN cDNA A930027H06 gene (A930027H06Rik)
E030049G20Rik	0.561	1.318	0.463	1.599	1.44	RIKEN cDNA E030049G20 gene (E030049G20Rik)
Nlrp10	1.934	0.946	1.326	1.217	0.722	NACHT, leucine rich repeat and PYD containing 10 (Nalp10)

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Lrrc4	1.285	1.561	0.8	1.415	0.836	leucine rich repeat containing 4 (Lrrc4)
4930401F20 Rik	0.598	0.97	1.005	0.567	1.427	RIKEN cDNA 4930401F20 gene (4930401F20Rik)
ENSMUSG00 000049981	1.366	1.129	0.819	2.14	0.396	hypothetical protein
Eid1	1.034	0.904	1.051	0.794	0.953	CREBBP/EP300 inhibitory protein 1 (Cri1)
A830091I15 Rik	1.701	2.364	1.322	3.066	1.16	RIKEN cDNA A830091I15 gene (A830091I15Rik)
Ig kappa chain V-V region J606. [Source:Uniprot/SWISSPROT;Acc:P01652]	0.969	0.863	0.775	1.427	1.919	PREDICTED: similar to IG KAPPA CHAIN V-V REGION L6 PRECURSOR (LOC243428)
Svs3b	0.518	0.927	0.84	1.647	0.728	similar to seminal vesicle secretion 3 (9530004A22Rik)
ENSMUSG00 000050459	0.327	0.404	0.972	1.737	0.23	PREDICTED: RIKEN cDNA 4930470H14 gene (4930470H14Rik)
B230340J04 Rik	0.445	0.462	1.283	2.762	0.97	RIKEN cDNA B230340J04 gene (B230340J04Rik)
ENSMUSG00 000050604	0.516	0.576	1.138	1.316	1.2	hypothetical protein
Olfr1136	0.672	1.493	1.064	0.412	0.749	olfactory receptor 1136 (Olfr1136)
Insl6	1.02	1.103	0.898	1.452	1.822	insulin-like 6 (Insl6)
Sepn1	1.107	1.011	1.626	0.613	1.332	selenoprotein N, 1 (Sepn1)
Hs3st1	0.498	0.282	0.339	0.755	0.751	heparan sulfate (glucosamine) 3-O-sulfotransferase 1 (Hs3st1)
Olfr77	0.968	1.318	1.023	1.394	1.609	olfactory receptor 77 (Olfr77)
Olfr1491	1.714	2.468	0.655	1.213	0.412	olfactory receptor 1491 (Olfr1491)
Commd1	1.012	1.118	1.187	1.337	0.865	COMM domain containing 1 (Commd1)
Flrt3	1.409	0.552	0.619	0.518	0.778	fibronectin leucine rich transmembrane protein 3 (Flrt3)
ENSMUSG00 000051422	1.191	1.427	1.149	1.382	1.424	contactin 2 (Cntn2), transcript variant 1
Rps19bp1	1.062	1.289	1.085	1.387	1.286	RIKEN cDNA 2510038A11 gene (2510038A11Rik)
ENSMUSG00 000051638	0.66	0.298	1.073	2.246	0.811	hypothetical protein
1810063B05 Rik	1.483	1.512	1.212	1.528	0.964	RIKEN cDNA 1810063B05 gene (1810063B05Rik)
ENSMUSG00 000051739	1.836	0.843	1.846	4.364	0.797	hypothetical protein
	1.068	0.257	1.142	2.453	1.057	PREDICTED: similar to KIAA0316 protein (LOC237234)

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4930523C11 Rik	1.012	1.07	0.865	0.629	1.448	PREDICTED: RIKEN cDNA 4930523C11 gene (4930523C11Rik)
Sox12	1.004	0.295	2.168	1.363	1.125	SRY-box containing gene 12 (Sox12)
ENSMUSG00 000051926	0.861	1.246	0.358	1.451	0.587	hypothetical protein
Zfp236	1.366	0.623	0.8	1.249	0.521	PREDICTED: zinc finger protein 236 (Zfp236)
Spats2	1.126	1.251	1.254	0.495	1.023	spermatogenesis associated, serine-rich 2 (Spats2)
Got2	1.11	1.24	0.789	0.543	1.692	Aspartate aminotransferase, mitochondrial precursor (EC 2.6.1.1) (Transaminase A) (Glutamate oxaloacetate transaminase-2). [Source:Uniprot/SWISSPROT;Acc:P05202]
GPR17	0.818	0.336	0.771	1.223	1.553	G protein-coupled receptor GPR17 (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q80UD2]
ENSMUSG00 000052254	0.689	0.314	0.67	1.443	1.123	hypothetical protein
Taf9	1.016	0.954	1.053	1.258	1.004	RIKEN cDNA 4921516M08 gene (4921516M08Rik)
Saps1	1.008	1.469	0.755	0.706	1.087	RIKEN cDNA B430201G11 gene (B430201G11Rik)
Mrgprc11	1.505	2.049	1.502	1.82	1.696	PREDICTED: similar to hypothetical protein C230069C04 (LOC330532)
Immt	1.218	1.175	0.874	0.579	1.008	Mitochondrial inner membrane protein (Mitofilin). [Source:Uniprot/SWISSPROT;Acc:Q8CAQ8]
Vil2	1.159	0.726	0.812	1.342	1.061	villin 2 (Vil2)
ENSMUSG00 000052547	0.758	3.253	1.163	1.415	0.264	hypothetical protein
Adam17	0.938	1.085	1.123	0.683	1.169	a disintegrin and metalloproteinase domain 17 (Adam17)
Atf7	0.915	0.907	0.889	1.529	1.054	hypothetical protein
Traf7	1.022	1.09	1.001	1.157	0.976	Tnf receptor-associated factor 7 (Traf7)
A630001G21 Rik	0.645	0.861	1.208	0.686	1.144	PREDICTED: RIKEN cDNA A630001G21 gene (A630001G21Rik)
Gprk2l	1.056	1.214	1.46	1.608	0.892	G protein-coupled receptor kinase 2, groucho gene related (Drosophila) (Gprk2l)
Clec12a	1.265	1.367	0.893	0.558	1.017	myeloid inhibitory C-type lectin-like receptor (Micl)
2700081O15 Rik	1.264	1.094	0.865	0.756	1.02	RIKEN cDNA 2700081O15 gene (2700081O15Rik)
ENSMUSG00 000053161	3.068	3.035	0.971	2.002	0.738	hypothetical protein

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description of Gene Product
ENSMUSG00000053204	0.626	1.146	1.073	1.899	1.045	hypothetical protein
ENSMUSG00000053249	0.555	0.14	0.947	1.788	1.115	hypothetical protein
Arrdc3	1.434	1.322	0.926	0.739	0.845	arrestin domain containing 3 (Arrdc3)
Rxfp2	0.669	1.103	0.243	1.477	0.775	leucine-rich repeat-containing G protein-coupled receptor 8 (Lgr8)
ENSMUSG00000053544	0.719	0.315	1.832	1.714	1.297	hypothetical protein
Zfand2a	1.116	0.983	1.112	1.19	0.978	expressed sequence AA407930 (AA407930)
LOC434121	0.274	0.281	1.492	1.158	1.947	PREDICTED: similar to sulfotransferase, hydroxysteroid preferring 2; Sulfotransferase hydroxysteroid gene 2 (LOC434121)
Sh3pxd2a	0.894	1.28	0.649	0.472	1.138	SH3 multiple domains 1 (Sh3md1)
ENSMUSG00000053774	1.358	0.76	0.748	1.529	0.844	hypothetical protein
ENSMUSG00000053880	1.735	2.18	0.804	1.573	1.161	hypothetical protein
Ech1	1.09	1.035	1.227	1.432	0.87	enoyl coenzyme A hydratase 1, peroxisomal (Ech1)
Rhox10	1.577	1.174	0.551	1.655	0.659	PREDICTED: similar to C.Elegans Homeobox (28.6 kD) (ceh-36) (LOC434769)
ENSMUSG00000053930	0.391	0.493	1.302	1.849	0.55	PREDICTED: similar to FLJ45455 protein (LOC380702)
Jakmip2	0.475	0.576	0.796	1.425	0.454	PREDICTED: RIKEN cDNA 6430702L21 gene (6430702L21Rik)
Msl2l1	0.737	1.89	0.781	0.683	0.702	PREDICTED: male-specific lethal-2 homolog (Drosophila) (Msl2)
	1.55	1.699	0.729	0.661	1.379	hypothetical protein
Fgfr3	1.306	1.944	1.806	1.931	0.982	Fibroblast growth factor receptor 3 precursor (EC 2.7.1.112) (FGFR-3) (Heparin-binding growth factor receptor). [Source:Uniprot/SWISSPROT;Acc:Q61851]
Fgfr3	1.254	2.133	1.61	2.423	1.179	fibroblast growth factor receptor 3 (Fgfr3)
ENSMUSG00000054283	0.699	1.543	1.169	1.641	1.554	hypothetical protein
ENSMUSG00000054402	1.064	1.474	0.94	2.187	1.251	hypothetical protein
Olfr411	2.046	1.039	1.062	1.696	0.843	olfactory receptor 411 (Olfr411)
Zfp553	1.108	0.998	0.355	0.846	0.946	Zinc finger protein 553
ENSMUSG00000054488	0.652	1.201	1.734	1.608	1.235	hypothetical protein C630010N09 (C630010N09)
Olfr308	0.762	0.597	1.819	0.536	1.564	olfactory receptor 308 (Olfr308)

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description of Gene Product
OTTMUSG00000016703	0.737	2.313	0.944	1.285	1.327	hypothetical protein A830093M07 (A830093M07)
ENSMUSG00000054636	1.075	1.299	1.45	1.337	1.078	hypothetical protein
Msra	1.505	1.197	1.119	1.464	1.054	methionine sulfoxide reductase A (Msra)
	2.157	1.625	1.35	1.997	2.196	cystatin and DUF19 domain-containing protein 1. [Source:RefSeq;Acc:NM_176966]
Prkar2a	1.202	0.969	1.206	1.541	0.652	hypothetical protein
	1.277	0.71	1.121	2.135	0.833	Gamma-aminobutyric-acid receptor gamma-3 subunit precursor (GABA(A) receptor). [Source:Uniprot/SWISSPROT;Acc:P27681]
2700049P18Rik	0.306	0.56	0.882	1.796	0.267	RIKEN cDNA 2700049P18 gene (2700049P18Rik)
Zfp811	0.803	1.066	0.765	1.644	0.777	cDNA sequence BC052046 (BC052046)
ENSMUSG00000055213	1.079	3.267	1.047	1.269	0.258	hypothetical protein
ENSMUSG00000055285	0.848	0.958	1.19	1.708	0.451	hypothetical protein
ENSMUSG00000055321	1.035	1.702	1.115	1.539	0.897	hypothetical protein
Fat2	1.037	0.792	0.378	1.246	1.734	PREDICTED: similar to MEGF1 (LOC245827)
Q9D179	1.288	0.155	1.259	2.797	1.511	hypothetical protein
Cdca7	0.469	1.174	0.939	1.627	0.966	cell division cycle associated 7 (Cdca7)
Slain1	0.865	1.074	0.607	1.384	0.771	RIKEN cDNA 9630044O09 gene (9630044O09Rik)
Usp26	2.199	0.844	0.494	1.899	0.998	ubiquitin specific protease 26 (Usp26)
AF215666	1.175	0.729	1.213	0.657	1.009	lymphocyte specific formin related protein; formin-related gene in leukocytes; formin-like. [Source:RefSeq;Acc:NM_019679]
9030607L17Rik	0.978	0.754	0.997	1.642	1.041	RIKEN cDNA 9030607L17 gene (9030607L17Rik)
LOC384806	0.679	0.629	1.203	1.778	1.334	PREDICTED: similar to testase-8 (LOC384806)
ENSMUSG00000056387	0.809	1.517	0.923	0.593	0.755	hypothetical protein
Gpr116	0.395	0.665	1.079	1.971	0.995	PREDICTED: RIKEN cDNA 8430401C09 gene (8430401C09Rik)
Dlx1	1.243	0.945	0.658	0.74	0.584	Homeobox protein DLX-1. [Source:Uniprot/SWISSPROT;Acc:Q64317]
Ppp1r14b	1.314	0.978	1.102	1.214	0.991	protein phosphatase 1, regulatory (inhibitor) subunit 14B (Ppp1r14b)
Dsg3	1.014	0.492	0.759	1.756	0.446	desmoglein 3 (Dsg3)

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Olfr1350	1.189	1.147	0.714	2.121	0.965	olfactory receptor 1350 (Olfr1350)
Kpna2	0.993	1.144	0.744	0.674	1.183	Importin alpha-2 subunit (Karyopherin alpha-2 subunit) (SRP1-alpha) (RAG cohort protein 1) (Pendulin) (Pore targeting complex 58 kDa subunit) (PTAC58) (Importin alpha P1). [Source:Uniprot/SWISSPROT;Acc:P52293]
Tsnax	1.181	1.094	1.094	1.536	1.079	translin-associated factor X (Tsnax)
ENSMUSG00000057000	1.576	0.948	2.067	1.743	1.611	PREDICTED: similar to nuclear RNA export factor 3 (LOC245610)
HV60_MOUSE	0.565	0.188	1.242	1.711	0.888	PREDICTED: similar to immunoglobulin heavy chain (LOC432699)
Cyp2d13	0.995	0.884	1.124	1.155	1.104	cytochrome P450, family 2, subfamily d, polypeptide 13 (Cyp2d13)
LOC236891	1.398	0.699	1.316	0.61	1.338	PREDICTED: similar to Smage-1 protein (LOC236891)
ENSMUSG00000057141	1.164	0.365	1.059	0.78	1.989	hypothetical protein
Prl3d1	0.309	0.996	1.361	0.756	0.869	chorionic somatomammotropin hormone 1 (Csh1)
Mrps36	0.99	1.27	1.277	1.16	1.048	mitochondrial ribosomal protein S36 (Mrps36)
ENSMUSG00000057283	0.719	0.844	0.689	1.75	0.357	Anti human TNF-alpha light chain variable region (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q9ERZ9]
ENSMUSG00000057289	1.322	0.494	1.408	1.486	1.236	hypothetical protein
Sphk2	1.138	0.922	1.189	1.574	0.753	sphingosine kinase 2 (Sphk2), transcript variant 2
ENSMUSG00000057348	1.044	0.961	1.065	0.413	1.28	hypothetical protein
4922501K12Rik	0.477	1.57	2.076	1.579	0.481	PREDICTED: RIKEN cDNA 4922501K12 gene (4922501K12Rik)
ENSMUSG00000057399	0.259	0.973	1.076	1.673	0.357	hypothetical protein
ENSMUSG00000057544	1.191	0.845	0.996	1.347	0.729	hypothetical protein
Colq	0.435	1.009	0.787	1.349	0.792	Acetylcholinesterase collagenic tail peptide (AChE Q subunit) (Acetylcholinesterase-associated collagen) (Fragment). [Source:Uniprot/SWISSPROT;Acc:O35348]
Bloc1s3	1.178	1.124	1.124	0.753	0.828	biogenesis of lysosome-related organelles complex-1, subunit 3 (Bloc1s3)
ENSMUSG00000057671	0.383	0.438	0.54	1.349	0.91	hypothetical protein
BC049702	0.487	0.805	1.657	1.359	1.165	cDNA sequence BC049702 (BC049702)

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Grm5	1.058	1.145	1.125	2.02	0.487	PREDICTED: glutamate receptor, metabotropic 5 (Grm5)
ENSMUSG00000057853	0.698	0.872	0.417	0.454	2.205	RIKEN cDNA 9630020C08 gene (9630020C08Rik)
Gpr111	0.63	0.744	0.647	1.884	1.09	PREDICTED: similar to G-protein coupled receptor 111 (LOC435529)
ENSMUSG00000057918	1.438	3.239	1.622	1.401	1.6	hypothetical protein
ENSMUSG00000057988	0.411	0.99	1.007	0.57	1.039	hypothetical protein
ENSMUSG00000058004	0.612	1.893	1.436	1.606	0.98	hypothetical protein
Olfr818	0.646	0.921	1.462	1.631	1.233	olfactory receptor 818 (Olfr818)
ENSMUSG00000058119	1.37	0.317	0.511	2.801	1.183	Try10-like trypsinogen precursor. [Source:Uniprot/SPTREMBL;Acc:Q7M754]
Krtap6-1	0.989	0.463	2.288	1.297	1.293	keratin associated protein 6-1 (Krtap6-1)
Amy2	1.501	1.144	0.715	0.807	0.756	amylase 2, pancreatic (Amy2)
Olfr1137	0.708	1.465	0.968	1.366	0.602	Olfactory receptor GA_x6K02T2Q125-49215724-49214792. [Source:Uniprot/SPTREMBL;Acc:Q7TR40]
Q8C1Q6	1.334	0.793	1.416	1.214	0.817	hypothetical protein
LOC241621	0.945	1.219	0.741	0.788	1.044	PREDICTED: similar to ribosomal protein L27a; ribosomal protein L29 homolog (yeast) (LOC241621)
Syt17	0.774	1.115	0.958	1.285	0.889	brain and kidney protein (Bk)
	0.989	0.869	0.72	0.691	0.811	PREDICTED: hypothetical gene supported by NM_028084 (LOC432414)
ENSMUSG00000058512	1.094	1.288	1.48	1.859	1.145	hypothetical protein
Olfr933	0.943	0.68	0.551	2.103	1.258	olfactory receptor 933 (Olfr933)
Cntn2	1.213	0.814	0.883	2.482	0.885	Contactin 2 (Axonin-1) (Axonal glycoprotein TAG-1) (Transient axonal glycoprotein 1) (TAX-1) (Fragment). [Source:Uniprot/SWISSPROT;Acc:Q61330]
V1rb1	0.291	1.22	1.418	1.701	0.438	vomeronasal 1 receptor, B1 (V1rb1)
Zfyve19	0.897	1.243	1.378	0.844	0.604	zinc finger, FYVE domain containing 19 (Zfyve19)
ENSMUSG00000058647	0.994	1.325	0.983	1.741	1.032	hypothetical protein
ENSMUSG00000058687	0.983	1.245	1.326	1.522	1.192	PREDICTED: similar to ribosomal protein L35a (LOC383141)
Olfr846	1.529	0.956	1.003	1.801	0.755	olfactory receptor 846 (Olfr846)
Q9DCF0	0.847	0.351	1.37	1.396	1.263	hypothetical protein
ENSMUSG00000058874	1.238	0.558	0.691	3.139	2.345	hypothetical protein

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Snrp1c	1.028	0.499	0.774	1.961	1.117	PREDICTED: similar to U1 snRNP-specific protein C (LOC432960)
ENSMUSG00000059022	0.924	0.865	0.929	1.673	1.048	hypothetical protein
ENSMUSG00000059024	0.495	1.553	2.035	1.655	0.784	hypothetical protein
Olfr128	0.515	0.474	0.97	0.307	1.485	olfactory receptor 128 (Olfr128)
1110020C03Rik	0.767	1.244	1.172	1.622	0.244	RIKEN cDNA 1110020C03 gene (1110020C03Rik)
Lep	1.252	0.675	0.731	1.923	0.471	leptin (Lep)
Defb4	1.151	1.508	2.352	1.564	1.071	defensin beta 4 (Defb4)
Usp47	1.483	0.966	0.997	0.858	1.466	ubiquitin specific protease 47 (Usp47)
CK332043	0.239	1.498	0.569	1.549	1.828	PREDICTED: similar to hypothetical protein 4930503F14 (LOC433719)
ENSMUSG00000059295	1.732	0.8	0.548	2.341	1.372	RIKEN cDNA 2900060N12 gene (2900060N12Rik)
Taar2	0.368	0.852	0.587	1.959	0.84	PREDICTED: gene model 225, (NCBI) (Gm225)
Cks2	1.124	0.749	0.914	1.302	1.044	CDC28 protein kinase regulatory subunit 2 (Cks2)
ENSMUSG00000059510	0.697	0.746	0.805	1.546	0.83	hypothetical protein
Olfr97	1.637	1.068	0.511	2.624	1.281	olfactory receptor 108; GA_x6K02T2PSCP-1893605-1894534; olfactory receptor MOR156-5. [Source:RefSeq;Acc:NM_146465]
Hydin	1.299	1.388	1.456	3.907	2.291	hydrocephalus inducing (Hydin)
Mug1	0.317	0.28	0.846	1.302	0.865	Murinoglobulin 1 precursor (MuG1). [Source:Uniprot/SWISSPROT;Acc:P28665]
Mug1	1.019	0.98	0.938	1.185	0.808	PREDICTED: similar to Murinoglobulin 1 (LOC434082)
ENSMUSG00000060022	0.873	1.345	1.054	1.231	1.999	hypothetical protein
Rpl3	0.941	1.291	1.209	0.788	1.065	ribosomal protein L3 (Rpl3)
ENSMUSG00000060102	0.769	0.753	1.431	1.617	0.864	PREDICTED: similar to ribosomal protein L30 (LOC383539)
Hist1h2bb	1.147	0.472	0.908	1.577	0.697	histone 1, H2bb (Hist1h2bb)
Lrrc10	0.808	1.156	0.599	0.749	0.981	leucine rich repeat containing 10 (Lrrc10)
Cend1	1.015	0.602	0.442	1.615	2.303	RIKEN cDNA 1500001H12 gene (1500001H12Rik)
	0.766	1.036	0.75	1.696	1.763	TD and POZ domain containing 4 (Tdpoz4)
ENSMUSG00000060257	0.549	0.308	0.36	3.024	2.329	PREDICTED: similar to Transcriptional repressor scratch 2 (Scratch homolog 2 zinc finger protein) (LOC383757)

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Gtf2i	1.296	1.316	1.171	1.39	1.092	PREDICTED: general transcription factor II I (Gtf2i)
ENSMUSG00000060304	0.804	1.857	1.478	1.361	0.3	hypothetical protein
ENSMUSG00000060304	0.787	1.249	1.084	1.32	1.133	hypothetical protein
ENSMUSG00000060315	0.382	0.893	0.69	1.365	1.058	PREDICTED: similar to chaperonin containing TCP1, subunit 3 (gamma) (LOC230185)
ENSMUSG00000060437	1.717	0.156	0.375	1.381	0.793	hypothetical protein
Hist1h3b	1.042	1.153	1.062	1.19	0.953	histone 1, H2ag (Hist1h2ag)
ENSMUSG00000060659	1.118	1.583	1.095	1.892	1.603	PREDICTED: similar to Colorectal mutant cancer protein (MCC protein) (LOC328949)
V1rc8	0.972	1.661	0.359	1.413	0.958	vomeronasal 1 receptor, C8 (V1rc8)
V1rd18	0.466	0.115	1.475	1.949	0.953	vomeronasal 1 receptor, D18 (V1rd18)
ENSMUSG00000060696	0.952	1.138	0.712	1.258	0.811	hypothetical protein
Tcl1b2	0.945	1.745	1.117	1.459	0.729	T-cell leukemia/lymphoma 1B, 2 (Tcl1b2)
Mcpt4	0.622	0.094	1.307	1.608	2.108	mast cell protease-like (Mcptl)
V1re1	1.315	1.193	1.083	1.459	0.649	vomeronasal 1 receptor, E1 (V1re1)
EG232801	1.73	0.287	0.381	2.162	0.864	PREDICTED: hypothetical protein E030017K20 (E030017K20)
ENSMUSG00000061256	1.68	1.015	1.066	1.568	0.873	hypothetical protein
ENSMUSG00000061327	0.828	1.38	1.759	1.767	0.488	hypothetical protein
ENSMUSG00000061341	1.025	1.892	1.507	1.463	1.018	hypothetical protein
Olfr1168	1.588	1.077	0.361	1.73	1.42	olfactory receptor 1168 (Olfr1168)
Q8BUS7	1.055	1.073	1.227	1.339	1.25	WEAKLY similar to L- ribulokinase homolog. [Source:Uniprot/SPTREMBL;Acc:Q8BUS7]
C1qtnf7	0.345	0.795	0.62	0.541	1.57	C1q and tumor necrosis factor related protein 7; C1q and tumor necrosis factor related protein 5. [Source:RefSeq;Acc:NM_175425]
ENSMUSG00000061551	1.119	0.733	0.862	1.439	1.137	PREDICTED: similar to bN312B5.2 (novel protein similar to ribosomal protein L17 (Rpl17)) (LOC435787)
ENSMUSG00000061592	1.005	1.681	1.099	2.236	1.103	hypothetical protein
Pclo	1.151	1.999	1.234	1.148	0.98	piccolo (presynaptic cytomatrix protein) (Pclo)

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ENSMUSG00000061657	0.801	1.739	2.377	1.706	0.705	hypothetical protein
4733401H18Rik	0.824	1.168	1.24	1.509	0.91	RIKEN cDNA 4733401H18 gene (4733401H18Rik)
Cps1	1.624	2.206	0.655	2.812	0.976	PREDICTED: carbamoyl-phosphate synthetase 1 (Cps1)
Rufy4	1.302	2.44	0.899	1.434	0.809	PREDICTED: similar to FLJ46536 protein (LOC435626)
ENSMUSG00000061888	0.287	0.503	0.706	1.984	0.62	hypothetical protein
Csn1s2a	0.456	1.069	1.093	1.932	0.362	casein gamma (Csng)
LOC240669	2.224	1.965	0.463	1.47	0.409	PREDICTED: similar to Histone H1 (LOC240669)
Serpina10	0.814	0.483	1.045	1.397	0.947	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 10 (Serpina10)
Wbscr16	1.592	1.807	1.31	1.436	0.953	Williams-Beuren syndrome chromosome region 16 homolog (human) (Wbscr16)
Sort1	1.022	1.352	0.991	1.345	0.68	sortilin 1 (Sort1)
HV52_MOUSE	0.458	1.38	1.485	1.191	0.921	PREDICTED: similar to monoclonal antibody heavy chain (LOC217930)
Olfr395	1.863	0.809	0.441	1.407	1.23	olfactory receptor 395 (Olfr395)
BC099439	1.506	1.514	0.603	1.724	0.87	PREDICTED: similar to RIKEN cDNA 2210409E12 (LOC217066)
ENSMUSG00000062217	1.825	1.421	0.77	1.807	0.69	PREDICTED: similar to Rpl7a protein (LOC215605)
Olfr170	1.578	0.092	1.188	1.454	1.578	olfactory receptor 170 (Olfr170)
ENSMUSG00000062257	0.966	0.68	1.031	1.455	0.688	hypothetical protein
Itgb1bp1	1.772	0.795	0.302	1.604	0.924	integrin beta 1 binding protein 1 (Itgb1bp1)
ENSMUSG00000062370	1.325	0.699	1.371	0.51	1.087	hypothetical protein
ENSMUSG00000062419	0.921	1.044	1.286	1.31	1.142	PREDICTED: RIKEN cDNA 2310047M15 gene (2310047M15Rik)
ENSMUSG00000062432	1.072	0.805	1.22	1.284	0.895	hypothetical protein
ENSMUSG00000062432	1.085	3.025	1.062	0.718	1.154	hypothetical protein
ENSMUSG00000062511	1.119	1.037	1.069	1.936	0.814	RIKEN cDNA 4930512M02 gene (4930512M02Rik)
ENSMUSG00000062573	1.83	0.138	0.826	1.33	0.608	hypothetical protein
ENSMUSG00000062657	1.696	1.743	0.898	1.421	0.687	PREDICTED: similar to hypothetical protein (LOC245027)
ENSMUSG00000062700	1.652	0.787	0.32	3.231	0.725	PREDICTED: RIKEN cDNA 1700025B11 gene (1700025B11Rik)

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Olfr527	0.707	1.345	2.013	0.693	1.849	Olfactory receptor GA_x6K02T2PBJ9-42486061-42486978. [Source:Uniprot/SPTREMBL;Acc:Q7TRT9]
EG240549	0.47	0.51	0.633	2.487	1.031	PREDICTED: similar to arylacetyl acyl-CoA N-acyltransferase (LOC240549)
ENSMUSG00000062814	1.137	0.996	0.958	1.916	1.093	PREDICTED: synovial sarcoma, X member A, breakpoint 1 (Ssxa1)
Hist1h2an	0.923	0.905	0.856	1.147	1.187	histone 1, H2an (Hist1h2an)
ENSMUSG00000062907	0.854	0.535	0.604	1.49	0.694	hypothatical protein
Ica1	1.04	0.712	1.017	0.587	1.181	islet cell autoantigen 1 (Ica1)
Ica1	1.022	0.583	0.762	1.381	0.964	islet cell autoantigen 1 (Ica1)
TVB3_MOUSE	0.933	1.536	0.971	1.938	0.543	T-cell receptor beta chain V region PHDS203 precursor (Fragment). [Source:Uniprot/SWISSPROT;Acc:P01736]
Pdcd11	0.728	0.234	1.187	1.319	1	hypothetical protein
ENSMUSG00000063251	0.98	0.811	1.571	1.247	1.217	PREDICTED: hypothetical gene supported by NM_026807 (LOC432598)
Cd209b	1.646	0.598	0.655	1.459	1.533	CD209b antigen (Cd209b)
Zfp97	0.686	0.606	0.767	0.536	0.717	zinc finger protein 97. [Source:RefSeq;Acc:NM_011765]
ENSMUSG00000063313	0.879	0.718	1.466	0.521	0.736	hypothetical protein
ENSMUSG00000063427	1.352	0.818	0.781	1.35	0.885	hypothetical protein
1700027L20Rik	0.504	0.53	0.902	0.519	0.935	PREDICTED: similar to transmembrane serine protease 9; polyserase 1 (LOC435631)
Q8BGG1	0.426	1.522	1.291	1.617	1.012	hypothetical protein
LOC623874	1.453	1.479	1.092	1.712	0.386	PREDICTED: cDNA sequence BC042569 (BC042569)
ENSMUSG00000063503	0.965	0.696	1.462	0.632	0.483	hypothetical protein
2010100O12Rik	0.85	1.27	1.291	1.315	0.742	RIKEN cDNA 2010100O12 gene (2010100O12Rik)
Crb1	2.055	0.583	1.097	0.505	0.802	crumbs homolog 1. [Source:RefSeq;Acc:NM_133239]
Cyp2c65	0.688	0.309	2.02	1.371	0.17	PREDICTED: cytochrome P450, family 2, subfamily c, polypeptide 65 (Cyp2c65)
ENSMUSG00000063792	0.953	0.916	0.969	1.734	1.816	hypothetical protein
Nlgn1	0.186	1.811	0.824	1.296	1.301	neuroligin 1 (Nlgn1)
Olfr657	0.457	0.272	1.233	1.998	0.985	olfactory receptor 657 (Olfr657)
ENSMUSG00000063958	0.666	0.593	0.71	1.481	1.023	hypothetical protein

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description of Gene Product
Prkcc	0.657	0.818	1.157	1.433	0.906	protein kinase C, gamma (Prkcc)
Klk8	1.253	1.611	1.166	1.722	0.669	protease, serine, 19 (neuropsin) (Prss19)
Hcst	1.031	0.949	1.214	1.335	0.99	hematopoietic cell signal transducer (Hcst)
Olfr329	1.014	1.743	1.08	1.812	1.487	Olfactory receptor GA_x6K02T2NKPP-882068-883006. [Source:Uniprot/SPTREMBL;Acc:Q7TRZ0]
ENSMUSG00000064286	0.888	0.238	1.007	1.147	0.705	hypothetical protein
Fat3	0.633	0.809	2.534	1.332	0.557	PREDICTED: similar to fat3; fat3 protein (LOC382129)
Crtac1	1.407	0.349	1.518	0.576	0.669	cartilage acidic protein 1 (Crtac1)
Fbxl12	0.426	1.138	0.936	0.079	1.045	F-box and leucine-rich repeat protein 12 (Fbxl12)
BI731946	1.301	0.617	0.965	1.564	1.196	hypothetical protein
AA867261	0.954	1.371	0.892	0.72	1.465	hypothetical protein
CN843074	0.836	1.01	0.907	0.597	1.198	hypothetical protein
BY706310	1.391	0.377	0.934	1.839	1.059	hypothetical protein
ENSMUSG00000055481	0.87	0.362	1.175	0.618	1.334	hypothetical protein
ENSMUSG00000060180	0.755	1.911	2.084	2.421	0.86	hypothetical protein
ENSMUSG00000058818	1.773	0.3	0.781	2.843	0.783	hypothetical protein
ENSMUSG00000053679	1.365	0.97	0.819	0.401	0.701	PREDICTED: protein phosphatase 2 (formerly 2A), regulatory subunit B'', alpha (Ppp2r3a)
ENSMUSG00000038196	0.721	0.468	0.927	0.676	1.519	hypothetical protein
ENSMUSG00000057435	0.941	1.014	1.163	2.444	0.575	hypothetical protein
BC061021	1.715	1.334	0.419	1.508	0.738	RIKEN cDNA 4930465K10 gene (4930465K10Rik)
1110018M03Rik	1.104	1.037	1.442	1.45	0.472	RIKEN cDNA 1110018M03 gene (1110018M03Rik)
Kcnj4	0.719	0.934	0.799	0.536	0.669	potassium inwardly-rectifying channel, subfamily J, member 4 (Kcnj4)
ENSMUSG00000054165	1.544	2.502	0.502	2.68	0.883	hypothetical protein
Dclre1b	0.761	1.186	1.303	0.541	1.093	DNA cross-link repair 1B, PSO2 homolog (S. cerevisiae) (Dclre1b)
ENSMUSG00000051217	1.277	0.786	1.167	1.375	0.891	hypothetical protein
Tac1	1.32	0.696	1.06	0.632	0.773	tachykinin 1 (Tac1)
Copg	0.871	0.663	1.24	1.428	1.673	coatomer protein complex, subunit gamma (Copg)

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description of Gene Product
ENSMUSG00000057131	1.381	1.652	1.152	1.781	0.383	hypothetical protein
ENSMUSG00000057710	0.961	0.895	1.08	0.882	1.075	RIKEN cDNA 9630041A04 gene (9630041A04Rik)
ENSMUSG00000062472	1.157	0.535	0.694	1.666	0.936	PREDICTED: similar to ribosomal protein (LOC240110)
Tubg1	1.182	1.308	1.356	1.441	0.999	tubulin, gamma 1 (Tubg1)
D45210	0.948	1.185	0.748	1.523	0.247	hypothetical protein
BB632145	1.496	0.171	1.228	1.436	1.974	hypothetical protein
BC061212	0.784	1.183	1.211	0.704	1.524	cDNA sequence BC061212 (BC061212)
BU938278	0.167	1.913	0.84	2.19	0.828	hypothetical protein
Upk3a	0.166	1.888	1.754	1.51	0.972	uroplakin 3A (Upk3a)
Fjx1	1.007	1.672	1.24	1.479	0.653	four jointed box 1 (Drosophila) (Fjx1)
Zfp85-rs1	1.106	1.461	1.277	1.617	0.969	zinc finger protein 85, related sequence 1 (Zfp85-rs1)
2310047K21Rik	0.519	0.507	0.386	1.608	1.088	PREDICTED: RIKEN cDNA 2310047K21 gene (2310047K21Rik)
Tle3	0.743	0.713	0.485	0.638	1.239	transducin-like enhancer of split 3, homolog of Drosophila E(spl) (Tle3)
ENSMUSG00000052829	1.041	1.365	0.736	0.494	0.78	hypothetical protein
ENSMUSG00000050258	0.416	1.107	1.588	0.586	0.776	hypothetical protein
ENSMUSG00000050730	1.428	0.636	1.449	0.683	1.461	hypothetical protein
prkcq	0.309	0.659	1.335	0.871	1.661	protein kinase C, theta (Prkcq)
ENSMUSG00000046094	1.104	0.576	1.106	1.355	0.503	hypothetical protein
ENSMUSG00000056745	1.035	2.029	0.993	1.317	0.695	hypothetical protein
ENSMUSG00000003575	0.359	0.501	1.221	2.077	0.731	expressed sequence AI413414 (AI413414)
Smoc2	0.59	1.127	0.866	2.859	2.109	SPARC related modular calcium-binding protein 2 precursor (Secreted modular calcium-binding protein 2) (SMOC-2). [Source:Uniprot/SWISSPROT;Acc:Q8CD91]
ENSMUSG00000064091	0.486	0.494	0.385	1.472	0.701	PREDICTED: similar to RIKEN cDNA 5730509K17 gene (LOC383467)
ENSMUSG00000045339	1.179	1.26	1.272	3.638	0.981	RIKEN cDNA A930104D05 gene (A930104D05Rik)
ENSMUSG00000052959	3.093	0.816	1.128	1.856	1.441	PREDICTED: similar to Filamin C (Gamma-filamin) (Filamin 2) (Protein FLNc) (Actin-binding like protein) (ABP-L) (ABP-280-like protein) (LOC381769)

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description of Gene Product
BE985588	1.033	1.026	0.695	1.302	0.925	hypothetical protein
1700042G07 Rik	0.692	1.531	0.927	1.343	1.041	PREDICTED: RIKEN cDNA 1700042G07 ge\ne (1700042G07Rik)
B930041F14 Rik	1.066	1.036	1.798	1.765	1.057	RIKEN cDNA B930041F14 gene (B930041F14Rik)
ENSMUSG00 000045291	1.269	0.382	2.104	1.913	0.409	RIKEN cDNA E330021D16 gene (E330021D16Rik)
ENSMUSG00 000056469	0.277	0.2	1.085	0.621	1.213	hypothetical protein
C85492	1.224	0.814	0.564	0.737	0.738	expressed sequence C85492 (C85492)
4732460I24	0.951	1.177	0.884	1.414	1.56	PREDICTED: hypothetical protein 4732460I24 (4732460I24)
ENSMUSG00 000038413	1.142	0.808	1.111	1.224	0.795	PREDICTED: similar to myeloid/lymphoid or mixed-lineage leukemia 5 (LOC433854)
ENSMUSG00 000063003	0.559	0.767	1.031	1.301	0.919	hypothetical protein
Ank2	0.912	1.505	1.037	1.675	0.618	ankyrin 2, brain. [Source:RefSeq;Acc:NM_178655]
ENSMUSG00 000062090	1.038	0.919	0.944	1.645	1.027	hypothetical protein
ENSMUSG00 000062787	0.891	0.967	1.544	0.737	1.204	hypothetical protein
ENSMUSG00 000043431	0.356	5.258	0.783	1.631	1.791	PREDICTED: similar to TAR DNA-binding protein-43 (TDP-43) (LOC238191)
ENSMUSG00 000058999	0.658	0.523	0.625	0.557	0.618	hypothetical protein
BF582268	1.026	0.977	1.183	1.411	0.835	hypothetical protein
ENSMUSG00 000053008	0.494	3.206	0.84	1.63	0.832	hypothetical protein
ENSMUSG00 000046759	0.643	0.727	1.323	2.832	0.922	RIKEN cDNA D130079A08 gene (D130079A08Rik)
ENSMUSG00 000056145	0.684	1.022	0.682	0.351	1.034	expressed sequence AI504432 (AI504432)
ENSMUSG00 000046655	1.533	1.452	1.309	2.816	1.12	PREDICTED: similar to gp25L2 protein (LOC227757)
ENSMUSG00 000032536	0.877	0.65	0.893	0.59	1.116	hypothetical protein
Olfr65	0.51	0.765	0.944	3.6	1.257	olfactory receptor 64 (Olfr64)
ENSMUSG00 000056802	0.726	1.388	1.105	2.15	1.281	PREDICTED: hypothetical gene supported by AK086481 (LOC432828)
ENSMUSG00 000034241	0.531	1.931	1.132	0.533	1.122	hypothetical protein
Fbxl5	0.634	1.106	0.895	0.473	0.68	F-box and leucine-rich repeat protein 5 (Fbxl5)
ENSMUSG00 000056210	1.224	1.074	0.973	0.581	0.845	hypothetical protein

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description of Gene Product
ENSMUSG00000045480	0.27	1.346	1.123	0.75	0.846	hypothetical protein
ENSMUSG00000062714	0.225	1.711	1.005	1.556	0.583	hypothetical protein
ENSMUSG00000001061	0.968	1.776	0.663	0.56	1.084	hypothetical protein
ENSMUSG00000038594	1.682	2.05	0.962	1.438	1.388	hypothetical protein
Ppnr	0.856	0.943	0.817	1.735	0.918	per-pentamer repeat gene (Ppnr)
BU935945	0.535	0.373	0.592	1.637	1.04	hypothetical protein
ENSMUSG00000039179	0.884	1.79	0.761	1.631	1.145	PREDICTED: RIKEN cDNA 3300001K11 gene (3300001K11Rik)
1700065D16Rik	1.145	1.309	1.068	1.533	0.529	RIKEN cDNA 1700065D16 gene (1700065D16Rik)
ENSMUSG00000046372	0.805	0.63	1.035	0.706	1.059	PREDICTED: similar to RIKEN cDNA 2510049I19 (LOC384607)
D030034H08	1.029	1.286	0.889	1.412	1.253	hypothetical protein D030034H08 (D030034H08)
ENSMUSG00000049291	1.232	1.042	1.329	0.62	0.699	PREDICTED: similar to marapsin 2 (LOC216797)
Ubie	0.577	1.275	1.018	0.374	1.66	UbiE-YGHL1 fusion protein (Ubie)
ENSMUSG00000047334	0.745	0.642	0.755	0.571	0.966	hypothetical protein LOC280487 (LOC280487)
BM933309	1.698	3.5	1.523	2.012	0.894	hypothetical protein
ENSMUSG00000056415	0.45	0.629	1.08	0.552	0.96	hypothetical protein
ENSMUSG00000058480	0.309	0.853	1.072	1.678	0.985	hypothetical protein
ENSMUSG00000061945	1.01	1.315	1.157	1.288	1.252	hypothetical protein
ENSMUSG00000053913	1.021	1.188	0.953	0.547	1.03	PREDICTED: gene model 734, (NCBI) (Gm734)
ENSMUSG00000051552	2.046	0.774	1.273	1.337	0.362	hypothetical protein
Mak	1.655	1.226	1.202	1.59	0.69	male germ cell-associated kinase (Mak)
ENSMUSG00000047527	0.669	0.621	0.808	1.369	0.846	hypothetical protein
ENSMUSG00000029784	0.827	2.301	0.795	3.18	0.526	hypothetical protein
Frmd4a	1.101	0.814	0.993	1.438	1.307	FERM domain containing 4A (Frmd4a)
ENSMUSG00000063535	1.169	1.032	1.494	1.366	0.985	PREDICTED: RIKEN cDNA 2810409K11 gene (2810409K11Rik)
ENSMUSG00000026195	0.48	1.065	0.944	1.819	0.319	PREDICTED: ATP-binding cassette, sub-family A (ABC1), member 12 (Abca12)
ENSMUSG00000057544	1.657	1.713	1.548	1.966	0.995	hypothetical protein

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description of Gene Product
ENSMUSG00000052466	0.387	0.573	0.876	1.588	0.654	RIKEN cDNA C130057E09 gene (C130057E09Rik)
Olfr740	0.964	0.178	1.725	1.257	0.917	olfactory receptor 740; olfactory receptor MOR106-4; GA_x6K02T2PMLR-6167145-6168080. [Source:RefSeq;Acc:NM_146667]
ENSMUSG00000055999	1.215	0.17	1.059	2.656	1.241	hypothetical protein
ENSMUSG00000059578	0.445	0.235	0.077	0.07	0.579	olfactory receptor 313; olfactory receptor MOR222-2; GA_x6K02T2NKPP-590035-589109. [Source:RefSeq;Acc:NM_146536]
ENSMUSG00000053902	1.691	0.286	0.593	0.177	1.28	hypothetical protein
ENSMUSG00000040086	0.232	1.332	0.829	2.239	0.683	hypothetical protein
ENSMUSG00000033060	0.996	0.829	0.732	1.457	1.067	PREDICTED: LIM domain only 7 (Lmo7)
ENSMUSG00000059515	1.178	1.039	0.291	2.079	0.215	hypothetical protein
ENSMUSG00000059067	0.549	0.309	0.287	0.749	1.078	PREDICTED: similar to ribosomal protein L13 (LOC434255)
Robo1	0.353	0.389	1.03	1.7	0.737	roundabout homolog 1 (Drosophila) (Robo1)
Rpl18	1.126	0.854	0.82	1.284	1.167	ribosomal protein L18 (Rpl18)
ENSMUSG00000062363	0.976	0.189	0.662	1.219	0.947	hypothetical protein
ENSMUSG00000039831	2.274	1.879	0.552	1.367	0.547	PTPL1-associated RhoGAP 1. [Source:RefSeq;Acc:NM_172525]
ENSMUSG00000053095	1.176	0.547	1.656	1.251	0.585	hypothetical protein
ENSMUSG00000042976	1.113	2.074	0.995	1.535	1.954	RIKEN cDNA 9930038B18 gene (9930038B18Rik)
ENSMUSG00000034801	0.814	0.717	1.268	0.678	0.842	hypothetical protein
ENSMUSG00000057246	0.881	0.323	0.911	1.931	1.771	hypothetical protein
ENSMUSG00000054935	0.698	1.235	1.28	1.754	0.872	hypothetical protein
Cacng3	1.06	0.699	0.78	1.435	1.071	calcium channel, voltage-dependent, gamma subunit 3 (Cacng3)
ENSMUSG00000055833	0.678	1.141	0.552	1.47	1.231	hypothetical protein
BY715099,BI113102	0.483	0.952	0.749	0.535	0.652	hypothetical protein
BY715141	0.704	1.851	0.961	1.294	1.332	hypothetical protein
Rnu33	0.667	0.786	0.303	1.552	0.997	RNA, U33 small nucleolar (Rnu33) on chromosome 7

Common	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description of Gene Product
AV252590	0.395	0.855	0.941	1.363	1.697	hypothetical protein
Rprm	1.117	1.392	1.263	1.341	1.267	reprimo, TP53 dependant G2 arrest mediator candidate (Reprimo)
BB615068	0.574	0.809	1.939	1.169	0.941	hypothetical protein
Olfr1019	1.863	0.257	0.169	0.59	0.773	olfactory receptor 1019 (Olfr1019)
AK173324	1.348	1.297	0.565	0.366	1.137	hypothetical protein
Mtap9	0.795	0.356	1.037	0.799	0.856	PREDICTED: RIKEN cDNA 5330427D05 gene (5330427D05Rik)
CB194220	1.092	1.071	1.03	0.802	1.073	hypothetical protein
1700013B16 Rik	0.671	0.82	0.88	1.278	0.719	RIKEN cDNA 1700013B16 gene (1700013B16Rik)
BC019134	1.322	0.357	1.52	0.746	0.922	hypothetical protein
Gcnt1	1.036	2.163	1.156	0.685	0.625	glucosaminyl (N-acetyl) transferase 1, core 2 (Gcnt1)
Olfr713	1.075	0.805	1.066	1.522	0.939	olfactory receptor 713 (Olfr713)
Bves	0.943	0.69	1.171	1.761	0.333	blood vessel epicardial substance (Bves)
Olfr297	0.647	1.399	1.205	3.419	0.817	olfactory receptor 297 (Olfr297)
Ssfa2	0.636	1.421	0.833	0.658	0.586	sperm specific antigen 2 (Ssfa2)
Olfr912	1.113	0.713	0.922	1.391	0.702	olfactory receptor 912 (Olfr912)
BC060256	1.182	1.24	1.28	6.08	1.351	hypothetical protein
Olfr121	1.556	0.975	1.156	1.336	1.263	olfactory receptor 121 (Olfr121)
Vill	1.098	1.297	0.728	1.489	1.331	villin-like (Vill)
Olfr1298	0.821	0.322	0.745	1.588	0.763	olfactory receptor 1298 (Olfr1298)
BC037766	0.808	1.22	1.329	1.611	1.359	hypothetical protein
Eef1g	0.99	1.425	1.066	1.333	0.938	eukaryotic translation elongation factor 1 gamma (Eef1g)
BC060120	2.389	0.782	0.556	1.406	1.589	hypothetical protein
Fbxw16	1.62	0.082	0.677	0.601	1.025	RIKEN cDNA 7420402K12 gene (7420402K12Rik)
Ccdc99	0.895	1.192	0.961	1.344	0.973	RIKEN cDNA 2600001J17 gene (2600001J17Rik)
Klhl12	1.078	0.995	0.931	1.365	0.791	kelch-like 12 (Drosophila) (Klhl12)
BE988845	0.904	0.997	0.928	1.833	1.198	hypothetical protein
Olfr859	1.41	0.135	1.471	2.067	0.95	olfactory receptor 859 (Olfr859)
Fjx1	0.847	1.134	0.979	1.811	1.351	four jointed box 1 (Drosophila) (Fjx1)

Genes in this table were differentially regulated in the CD43KO macrophages compared to CD43WT macrophages while incubated with Cpn60.2. Normalized expression cutoff values were 1.2 (upregulated) and 0.833 (downregulated). Genes were also filtered on confidence between the biological replicates ($p<0.05$).

Supplementary table 3. Statistically significant, differentially regulated genes in CD43KO when co-incubated with *M.tb*

	Normalized Expression					
Gene	**Incubation Medium (Protein-incubation)**	**Incubation Medium (infection)**	***M.tb***	**60.2**	**dnaK**	**Description**
	0.507	0.791	1.376	0.898	1.171	fer (fms/fps related) protein kinase, testis specific 2. [Source:RefSeq;Acc:NM_008000]
Gna12	0.859	0.943	0.668	0.814	0.993	Guanine nucleotide-binding protein, alpha-12 subunit (G alpha 12). [Source:Uniprot/SWISSPROT;Acc:P27600]
Itgb2	1.219	1.167	1.293	0.71	0.86	Integrin beta-2 precursor (Cell surface adhesion glycoproteins LFA-1/CR3/P150,95 beta-subunit) (CD18) (Complement receptor C3 beta- subunit). [Source:Uniprot/SWISSPROT;Acc:P11835]
Comt	0.802	2.348	1.15	1.068	0.766	Catechol O-methyltransferase, membrane-bound form (EC 2.1.1.6) (MB-COMT) [Contains: Catechol O-methyltransferase, soluble form (S-COMT)]. [Source:Uniprot/SWISSPROT;Acc:O88587]
Gcg	0.104	1.448	1.454	1.842	0.175	Glucagon precursor [Contains: Glicentin; Glicentin-related polypeptide (GRPP); Oxyntomodulin (OXY) (OXM); Glucagon; Glucagon-like peptide 1 (GLP-1); Glucagon-like peptide 1(7-37) (GLP-1(7-37)); Glucagon-like peptide 1(7-36) (GLP-1(7-36)); Glucagon-like peptide 2 (GLP-2)]. [Source:Uniprot/SWISSPROT;Acc:P55095]
ENSMUSG00000000568	1.281	1.055	1.261	1.021	1.172	Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich element RNA-binding protein 1). [Source:Uniprot/SWISSPROT;Acc:Q60668]
Dynlt1	0.872	1.294	1.235	0.895	1.109	dynein light chain Tctex-type 1; synonyms: Tctex1, Tctex-1, MGC107110, MGC107111; Mus musculus dynein light chain Tctex-type 1 (Dynlt1), mRNA.
Hk2	1.095	0.547	0.605	0.96	0.953	Hexokinase type II (EC 2.7.1.1) (HK II). [Source:Uniprot/SWISSPROT;Acc:O08528]
Cd52	0.547	1.633	1.387	0.989	1.906	CAMPATH-1 antigen precursor (CD52 antigen) (Lymphocyte differentiation antigen B7). [Source:Uniprot/SWISSPROT;Acc:Q64389]
Hoxb6	0.382	1.017	0.622	2.002	0.683	Homeobox protein Hox-B6 (Hox-2.2) (MH-22A). [Source:Uniprot/SWISSPROT;Acc:P09023]
Slc5a5	0.589	1.768	1.829	0.639	0.3	solute carrier family 5 (sodium iodide symporter), member 5.

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
BC058994	0.184	0.634	0.792	0.599	1.708	Inferred: ubiquitin specific protease (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8CCP4]
Vpreb3	0.896	1.104	1.342	0.344	0.692	pre-B lymphocyte gene 3. [Source:RefSeq;Acc:NM_009514]
Ccl3	1.036	0.998	0.579	0.719	1.339	Small inducible cytokine A3 precursor (CCL3) (Macrophage inflammatory protein 1-alpha) (MIP-1-alpha) (TY-5) (SIS-alpha) (Heparin-binding chemotaxis protein) (L2G25B). [Source:Uniprot/SWISSPROT;Acc:P10855]
Snapap	0.733	1.579	0.633	1.277	0.771	SNARE-associated protein Snapin (Synaptosomal-associated protein 25 binding protein) (SNAP-associated protein). [Source:Uniprot/SWISSPROT;Acc:Q9Z266]
S100a6	1.01	1.298	1.393	1.043	1.399	Calcyclin (Prolactin receptor associated protein) (5B10). [Source:Uniprot/SWISSPROT;Acc:P14069]
Mapk7	0.887	1.304	1.313	1.217	1.546	Mitogen-activated protein kinase 7 (EC 2.7.1.37) (Extracellular signal-regulated kinase 5) (ERK-5) (BMK1 kinase). [Source:Uniprot/SWISSPROT;Acc:Q9WVS8]
ENSMUSG00000001158	2.259	1.347	0.659	1.705	0.558	putative nucleic acid binding protein RY-1; EST AI449063. [Source:RefSeq;Acc:NM_025665]
Dpp9	1.122	0.815	0.879	1.016	0.914	dipeptidylpeptidase 9. [Source:RefSeq;Acc:NM_172624]
Ramp2	0.26	1.83	1.71	1.164	1.586	Receptor activity-modifying protein 2 precursor. [Source:Uniprot/SWISSPROT;Acc:Q9WUP0]
Lsr	1.505	1.113	0.626	1.289	1.393	liver-specific bHLH-Zip transcription factor; Lisch7 protein. [Source:RefSeq;Acc:NM_017405]
Sp1	0.731	1.11	1.853	0.765	1.365	Transcription factor Sp1. [Source:Uniprot/SWISSPROT;Acc:O89090]
Myg1	0.86	0.887	0.581	1.452	0.955	MYG1 protein (Gamm1 protein). [Source:Uniprot/SWISSPROT;Acc:Q9JK81]
Sost	0.951	0.639	2.598	1.064	1.272	Sclerostin precursor. [Source:Uniprot/SWISSPROT;Acc:Q99P68]
Il16	0.863	1.074	1.542	0.639	0.95	interleukin 16. [Source:RefSeq;Acc:NM_010551]

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
AF022889	1.161	1.109	1.714	0.966	1.228	Latent transforming growth factor beta binding protein, isoform 1L precursor (LTBP-1) (Transforming growth factor beta-1 binding protein 1) (TGF-beta1-BP-1). [Source:Uniprot/SWISSPROT;Acc:Q8CG19]
Rapsn	1.34	1.349	1.588	1.069	1.451	43 kDa receptor-associated protein of the synapse (RAPsyn) (Acetylcholine receptor-associated 43 kDa protein) (43 kDa postsynaptic protein). [Source:Uniprot/SWISSPROT;Acc:P12672]
Slc39a13	1.134	0.997	1.31	0.887	1.055	hypothetical protein
Sf3a1	1.153	1.069	1.374	1.113	0.994	splicing factor 3a, subunit 1. [Source:RefSeq;Acc:NM_026175]
Zim1	0.296	1.712	1.745	2.572	1.122	zinc finger, imprinted 1. [Source:RefSeq;Acc:NM_011769]
425O18-1	1.174	1.304	1.393	1.493	1.031	hypothetical protein
Ncan	1.308	0.902	1.547	0.235	0.466	Neurocan core protein precursor (Chondroitin sulfate proteoglycan 3). [Source:Uniprot/SWISSPROT;Acc:P55066]
Slc25a42	0.56	0.94	2.009	1.104	0.701	Similar to R29893_1. [Source:Uniprot/SPTREMBL;Acc:Q8R0Y8]
ENSMUSG00000002578	0.867	0.522	0.586	1.016	1.432	zinc finger protein, subfamily 1A, 4. [Source:RefSeq;Acc:NM_011772]
Akap8l	1.023	2.034	0.614	1.056	1.191	Neighbor of A-kinase anchoring protein 95. [Source:Uniprot/SWISSPROT;Acc:Q9R0L7]
Gnmt	1.599	1.878	1.953	0.985	0.818	glycine N-methyltransferase; glycine N methyl transferase. [Source:RefSeq;Acc:NM_010321]
Il4i1	1.116	0.643	0.486	0.843	0.753	Interleukin-4 induced protein 1 precursor (Fig-1 protein) (mFIG1). [Source:Uniprot/SWISSPROT;Acc:O09046]
Pafah1b2	0.798	1.328	0.732	0.81	0.797	Platelet-activating factor acetylhydrolase IB beta subunit (EC 3.1.1.47) (PAF acetylhydrolase 30 kDa subunit) (PAF-AH 30 kDa subunit) (PAF-AH beta subunit) (PAFAH beta subunit). [Source:Uniprot/SWISSPROT;Acc:Q61206]
Ebi3	0.984	0.8	0.596	0.906	1.033	Interleukin-27 beta chain precursor (IL-27B) (Epstein-Barr virus induced gene 3 protein homolog). [Source:Uniprot/SWISSPROT;Acc:O35228]

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Sult2b1	1.236	1.809	1.448	0.743	0.793	sulfotransferase family, cytosolic, 2B, member 1; hydroxysteroid sulfotransferase. [Source:RefSeq;Acc:NM_017465]
Hck	1.377	0.742	0.777	1.221	1.92	Tyrosine-protein kinase HCK (EC 2.7.1.112) (p56-HCK/p59-HCK) (Hemopoietic cell kinase) (B-cell/myeloid kinase) (BMK). [Source:Uniprot/SWISSPROT;Acc:P08103]
Ccdc65	0.928	1.194	1.399	1.055	0.475	NYD-SP28 protein. [Source:RefSeq;Acc:NM_153518]
Cd79a	0.997	0.784	1.49	1.179	1.319	B-cell antigen receptor complex associated protein alpha-chain precursor (IG-alpha) (MB-1 membrane glycoprotein) (Surface-IGM- associated protein) (Membrane-bound immunoglobulin associated protein) (CD79A). [Source:Uniprot/SWISSPROT;Acc:P11911]
Etv3	1.614	1.081	0.606	1.481	0.691	ets variant gene 3; ETS-domain transcriptional repressor; ETS-domain protein; mitogenic Ets transcriptional suppressor METS. [Source:RefSeq;Acc:NM_012051]
Supt5h	1.016	0.967	0.888	1.013	1.075	suppressor of Ty 5 homolog. [Source:RefSeq;Acc:NM_013676]
Ier3	1.037	0.544	0.516	0.766	0.748	Radiation-inducible immediate-early gene IEX-1 (Immediate early protein GLY96) (Immediate early response 3 protein). [Source:Uniprot/SWISSPROT;Acc:P46694]
Klc4	1.086	1.423	1.263	1.301	0.865	Kinesin-like protein 8. [Source:Uniprot/SWISSPROT;Acc:Q9DBS5]
ENSMUSG00000003617	1.216	0.564	0.407	0.79	1.27	Ceruloplasmin precursor (EC 1.16.3.1) (Ferroxidase). [Source:Uniprot/SWISSPROT;Acc:Q61147]
Stat5a	0.658	0.706	0.643	0.936	0.902	Signal transducer and activator of transcription 5A (Mammary gland factor). [Source:Uniprot/SWISSPROT;Acc:P42230]
Il12b	1.067	0.904	0.52	0.528	0.278	Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte maturation factor 40 kDa subunit) (CLMF p40). [Source:Uniprot/SWISSPROT;Acc:P43432]
Emr1	1.256	1.31	0.815	0.712	0.85	EGF-like module containing mucin-like hormone receptor-like 1 precursor (Cell surface glycoprotein EMR1) (EMR1 hormone receptor)

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Sh2b2	0.852	0.639	0.657	0.96	1.433	SH2 and PH domain-containing adapter protein APS. [Source:Uniprot/SWISSPROT;Acc:Q9JID9]
Ndrg1	1.028	0.724	0.772	0.997	1.605	NDRG1 protein (N-myc downstream regulated gene 1 protein) (Protein Ndr1). [Source:Uniprot/SWISSPROT;Acc:Q62433]
Prlr	0.315	1.678	2.266	1.647	1.168	Prolactin receptor precursor (PRL-R). [Source:Uniprot/SWISSPROT;Acc:Q08501]
Fcer1a	1.305	1.29	0.348	1.235	1.496	High affinity immunoglobulin epsilon receptor alpha-subunit precursor (FCERI) (IGE FC receptor, alpha-subunit) (FC-epsilon RI-alpha). [Source:Uniprot/SWISSPROT;Acc:P20489]
Tbl2	0.851	0.87	0.59	1.375	0.573	Transducin beta-like 2 protein. [Source:Uniprot/SWISSPROT;Acc:Q9R099]
AA536749	0.749	0.796	0.746	0.548	0.998	Rho-interacting protein 3 (p116RIP) (RIP3). [Source:Uniprot/SWISSPROT;Acc:P97434]
Igf1r	0.906	1.083	0.541	0.89	0.728	Insulin-like growth factor I receptor precursor (EC 2.7.1.112). [Source:Uniprot/SWISSPROT;Acc:Q60751]
BC040366	0.927	1.317	0.687	0.588	1.071	AMP deaminase 3 (EC 3.5.4.6) (AMP deaminase isoform E) (AMP deaminase H-type) (Heart-type AMPD). [Source:Uniprot/SWISSPROT;Acc:O08739]
ENSMUSG00000005836	1.244	1.068	0.498	0.894	0.852	Transcription factor GATA-6 (GATA binding factor-6). [Source:Uniprot/SWISSPROT;Acc:Q61169]
Nr2c1	0.776	2.244	0.675	0.55	0.886	nuclear receptor subfamily 2, group C, member 1; orphan receptor, TR2-11; nuclear receptor subfamily 2, group H, member 1. [Source:RefSeq;Acc:NM_011629]
Ctns	1.188	1.218	0.688	1.187	1.321	Cystinosin. [Source:Uniprot/SWISSPROT;Acc:P57757]
Tyrp1	1.719	1.354	1.396	0.693	1.333	5,6-dihydroxyindole-2-carboxylic acid oxidase precursor (EC 1.14.18.-) (DHICA oxidase) (Tyrosinase-related protein 1) (TRP-1) (TRP1) (TRP) (Catalase B) (Brown locus protein). [Source:Uniprot/SWISSPROT;Acc:P07147]
BC003331	1.189	0.806	0.76	0.903	1.042	hypothetical protein LOC226499 isoform 1
Epor	1.506	0.652	0.54	0.623	0.879	Erythropoietin receptor precursor (EPO-R). [Source:Uniprot/SWISSPROT;Acc:P14753]

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Ttc5	0.914	1.071	0.828	1.374	1.164	tetratricopeptide repeat domain 5. [Source:RefSeq;Acc:NM_177625]
Cbfa2t3h	0.459	0.875	0.641	0.92	0.754	core-binding factor, runt domain, alpha subunit 2; translocated to, 3 homolog; CBFA2T3 identified gene homolog (human); core-binding factor, runt domain, alpha subunit 2; translocated to, 3 homolog (human). [Source:RefSeq;Acc:NM_009824]
Fbln1	0.453	1.718	0.64	0.974	0.651	Fibulin-1 precursor (Basement-membrane protein 90) (BM-90). [Source:Uniprot/SWISSPROT;Acc:Q08879]
Mpl	1.352	0.95	1.934	1.082	1.218	Thrombopoietin receptor precursor (TPO-R) (Myeloproliferative leukemia protein) (C-mpl). [Source:Uniprot/SWISSPROT;Acc:Q08351]
Adamts4	1.07	1.276	0.635	0.497	1.074	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 4; aggrecanase-1. [Source:RefSeq;Acc:NM_172845]
Zdhhc24	0.465	1.315	1.272	1.166	1.079	leukocyte receptor cluster (LRC) member 4. [Source:RefSeq;Acc:NM_027476]
BC049789	1.006	0.939	0.707	1.049	1.292	NADPH dependent diflavin oxidoreductase 1. [Source:RefSeq;Acc:NM_178239]
Cyba	0.934	0.823	1.244	0.951	1.087	Cytochrome b-245 light chain (p22 phagocyte B-cytochrome) (Neutrophil cytochrome B, 22 kDa polypeptide) (p22-phox) (p22phox) (Cytochrome B(558) alpha chain) (Cytochrome b558 alpha-subunit) (Superoxide- generating NADPH oxidase light chain subunit). [Source:Uniprot/SWISSPROT;Acc:Q61462]
Itih1	0.934	1.256	0.561	1.161	1.14	Inter-alpha-trypsin inhibitor heavy chain H1 precursor (ITI heavy chain H1) (Inter-alpha-inhibitor heavy chain 1). [Source:Uniprot/SWISSPROT;Acc:Q61702]
Krt23	1.032	1.511	2.233	1.961	0.48	Keratin, type I cytoskeletal 23 (Cytokeratin 23) (K23) (CK 23). [Source:Uniprot/SWISSPROT;Acc:Q99PS0]
Sod2	1.175	3.425	0.895	0.983	1.067	Superoxide dismutase [Mn], mitochondrial precursor (EC 1.15.1.1). [Source:Uniprot/SWISSPROT;Acc:P09671]
Tmco6	1.066	0.992	0.642	1.291	1.186	transmembrane and coiled-coil domains 6; synonym: 2410015B03Rik; Mus musculus transmembrane and coiled-coil domains 6 (Tmco6), mRNA.
Ctnnb1	1.059	1.031	1.867	0.909	0.96	Beta-catenin.

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Slc44a4	0.762	1.15	0.466	0.78	1.329	solute carrier family 44, member 4; synonyms: NG22, 2210409B01Rik; Mus musculus solute carrier family 44, member 4 (Slc44a4), mRNA.
Zfp655	0.988	0.443	0.696	0.908	1.106	zinc finger protein 655; synonyms: KIAA4222, mKIAA4222, 2700038I16Rik, 9030409O18Rik; isoform a is encoded by transcript variant 1; Mus musculus zinc finger protein 655 (Zfp655), transcript variant 1, mRNA.
BC060660	1.157	1.299	0.652	1.103	1.05	hypothetical protein
4930432K21Rik	1.146	1.336	1.688	1.122	0.654	hypothetical protein LOC74666
Rnf151	0.579	1.237	0.487	0.442	1.015	ring finger protein 151; synonyms: AV047371, 1700010O16Rik; Mus musculus ring finger protein 151 (Rnf151), mRNA.
Cldn13	1.97	0.258	1.469	1.326	0.694	Claudin-13. [Source:Uniprot/SWISSPROT;Acc:Q9Z0S4]
Cabp7	0.225	1.225	1.511	1.019	0.783	Calcium-binding protein CaBP7. [Source:Uniprot/SWISSPROT;Acc:Q91ZM8]
Dmap1	1.326	1.46	1.29	0.952	0.869	DNA methyltransferase 1-associated protein 1 (DNMT1-associated protein 1) (DNMAP1) (MAT1-mediated transcriptional repressor). [Source:Uniprot/SWISSPROT;Acc:Q9JI44]
Dazl	1.656	1.32	1.961	0.288	1.567	Deleted in azoospermia-like (DAZ-like autosomal) (Deleted in azoospermia-like 1). [Source:Uniprot/SWISSPROT;Acc:Q64368]
Psen2	1.369	1.606	0.76	1.148	1.149	Presenilin 2 (PS-2) (ALG-3) (Alzheimer disease 4 homolog). [Source:Uniprot/SWISSPROT;Acc:Q61144]
Gabra1	0.968	0.924	2.25	1.297	1.655	Gamma-aminobutyric-acid receptor alpha-1 subunit precursor (GABA(A) receptor). [Source:Uniprot/SWISSPROT;Acc:P18504]
Dhdh	0.651	1.584	0.627	0.686	0.386	dihydrodiol dehydrogenase (dimeric); synonyms: AA591799, 1300018L09Rik; Mus musculus dihydrodiol dehydrogenase (dimeric) (Dhdh), mRNA.
Pgam1	1.266	1.059	1.227	1.047	0.936	Phosphoglycerate mutase 1 (EC 5.4.2.1) (EC 5.4.2.4) (EC 3.1.3.13) (Phosphoglycerate mutase isozyme B) (PGAM-B) (BPG-dependent PGAM 1). [Source:Uniprot/SWISSPROT;Acc:Q9DBJ1]

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Lrrc8e	1.086	0.837	0.59	0.49	0.856	leucine rich repeat containing 8 family, member E; synonyms: C87354, MGC91131, 1810049O03Rik; Mus musculus leucine rich repeat containing 8 family, member E (Lrrc8e), mRNA.
Snapc2	1.08	1.352	0.744	1.263	1.028	small nuclear RNA activating complex, polypeptide 2. [Source:RefSeq;Acc:NM_133968]
Xpo5	1.021	1.258	0.591	0.793	1.189	exportin 5. [Source:RefSeq;Acc:NM_028198]
Ehf	0.794	1.071	0.644	1.426	0.66	ets homologous factor. [Source:RefSeq;Acc:NM_007914]
Retn	1.672	0.659	0.506	0.685	1.002	Resistin precursor (Cysteine-rich secreted protein FIZZ3) (Adipose tissue-specific secretory factor) (ADSF) (Adipose-specific cysteine- rich secreted protein A12-alpha). [Source:Uniprot/SWISSPROT;Acc:Q99P87]
Tmem175	0.864	1.492	1.315	1.017	0.749	transmembrane protein 175; synonyms: AI504381, 3010001K23Rik; Mus musculus transmembrane protein 175 (Tmem175), mRNA.
ORF61	1.012	0.956	0.752	1.029	1.132	Membralin splice variant 2 (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8CIV1]
1810033B17Rik	1.054	1.258	1.246	0.825	1.308	RIKEN cDNA 1810033B17 gene; Mus musculus RIKEN cDNA 1810033B17 gene (1810033B17Rik), mRNA.
0610012D17Rik	0.958	1.252	1.464	0.994	0.991	RIKEN cDNA 0610012D17 gene; synonym: 2410011K15Rik; Mus musculus RIKEN cDNA 0610012D17 gene (0610012D17Rik), mRNA.
Klra8	2.165	1.131	0.615	0.889	1.667	Natural killer cell receptor (Fragment). [Source:Uniprot/SPTREMBL;Acc:O88362]
ENSMUSG00000014444	1.28	1.065	1.208	0.653	1.054	PREDICTED: RIKEN cDNA 2310061F22 gene (2310061F22Rik)
Zfyve20	0.701	1.453	0.536	0.93	1.265	zinc finger, FYVE domain containing 20. [Source:RefSeq;Acc:NM_030081]
Chrne	1.87	1.528	0.426	1.009	0.909	Acetylcholine receptor protein, epsilon chain precursor. [Source:Uniprot/SWISSPROT;Acc:P20782]
Hoxa2	1.608	0.903	1.451	1.483	0.746	Homeobox protein Hox-A2 (Hox-1.11) (Hox1.11). [Source:Uniprot/SWISSPROT;Acc:P31245]
Dll1	1.238	0.635	1.513	0.867	0.351	Delta-like protein 1 precursor (Drosophila Delta homolog 1) (Delta1).

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BC057616	0.706	1.178	2.077	1.084	1.11	PREDICTED: similar to solute carrier family 9 (sodium/hydrogen exchanger), isoform 5 (LOC277973)
ENSMUSG00000014850	0.555	1.971	0.64	1.042	0.579	DNA mismatch repair protein Msh3 (Repair-3 protein) (REP-1). [Source:Uniprot/SWISSPROT;Acc:P13705]
Ppp1cb	1.05	0.676	0.771	0.668	0.863	Serine/threonine protein phosphatase PP1-beta catalytic subunit (EC 3.1.3.16) (PP-1B). [Source:Uniprot/SWISSPROT;Acc:P62141]
Nolc1	1.431	1.118	1.966	0.958	1.467	nucleolar and coiled-body phosphoprotein 1. [Source:RefSeq;Acc:NM_053086]
Gadd45b	0.842	1.055	0.704	1.068	0.838	Growth arrest and DNA-damage-inducible protein GADD45 beta (Negative growth-regulatory protein MyD118) (Myeloid differentiation primary response protein MyD118). [Source:Uniprot/SWISSPROT;Acc:P22339]
Slamf1	0.571	0.56	0.416	0.901	1.411	Signaling lymphocytic activation molecule precursor. [Source:Uniprot/SWISSPROT;Acc:Q9QUM4]
Ager	0.751	0.756	0.583	1.017	0.714	Advanced glycosylation end product-specific receptor precursor (Receptor for advanced glycosylation end products). [Source:Uniprot/SWISSPROT;Acc:Q62151]
Notch4	0.689	1.013	1.692	1.101	1.347	Neurogenic locus notch homolog protein 4 precursor (Notch 4) [Contains: Transforming protein Int-3]. [Source:Uniprot/SWISSPROT;Acc:P31695]
Arnt	0.844	1.014	0.508	0.68	0.919	Aryl hydrocarbon receptor nuclear translocator (ARNT protein) (Dioxin receptor, nuclear translocator) (Hypoxia-inducible factor 1 beta) (HIF-1 beta). [Source:Uniprot/SWISSPROT;Acc:P53762]
ENSMUSG00000015807	0.547	1.236	0.607	0.915	0.961	hypothetical protein
Cd5l	0.929	1.353	1.782	0.899	0.903	CD5 antigen-like precursor (SP-alpha) (CT-2) (Apoptosis inhibitory 6) (Apoptosis inhibitor expressed by macrophages). [Source:Uniprot/SWISSPROT;Acc:Q9QWK4]
Lcorl	0.797	1.225	1.728	1.599	1.262	Mblk1-related protein-1; transcription factor MLR1. [Source:RefSeq;Acc:NM_172153]

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Atp1b4	2.053	0.485	1.395	1.76	1.391	X/potassium-transporting ATPase beta-m chain (X,K-ATPase beta-m subunit). [Source:Uniprot/SWISSPROT;Acc:Q99ME6]
Eef1a2	1.371	0.891	0.411	1.277	1.633	Elongation factor 1-alpha 2 (EF-1-alpha-2) (Elongation factor 1 A-2) (eEF1A-2) (Statin S1). [Source:Uniprot/SWISSPROT;Acc:P27706]
Il19	0.801	0.825	0.412	0.865	1.284	Interleukin 19 (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8CJ70]
Mapkapk2	0.973	0.955	0.657	0.634	1.042	MAP kinase-activated protein kinase 2 (EC 2.7.1.-) (MAPK-activated protein kinase 2) (MAPKAP kinase 2) (MAPKAPK-2) (Fragment). [Source:Uniprot/SWISSPROT;Acc:P49138]
Il10	1.042	0.582	0.525	0.999	0.984	Interleukin-10 precursor (IL-10) (Cytokine synthesis inhibitory factor) (CSIF). [Source:Uniprot/SWISSPROT;Acc:P18893]
Lamp2	1.008	0.715	0.698	0.638	0.949	Lysosome-associated membrane glycoprotein 2 precursor (LAMP-2) (Lysosomal membrane glycoprotein-type B) (LGP-B) (CD107B). [Source:Uniprot/SWISSPROT;Acc:P17047]
Sdc4	0.951	0.88	0.721	0.97	0.675	Syndecan-4 precursor (Ryudocan core protein). [Source:Uniprot/SWISSPROT;Acc:O35988]
Nt5c3l	0.715	1.029	0.621	0.949	0.78	5'-nucleotidase, cytosolic III-like; synonyms: AI841843, 2610037D24Rik, C330027I04Rik; Mus musculus 5'-nucleotidase, cytosolic III-like (Nt5c3l), mRNA.
Ccdc56	1.03	1.239	1.163	1.238	1.071	coiled-coil domain containing 56; synonyms: HSPC009, D11Ertd99e, 1810033A19Rik; Mus musculus coiled-coil domain containing 56 (Ccdc56), mRNA.
ENSMUSG00000017198	0.879	0.875	0.622	1.293	1.025	PREDICTED: similar to ORM1-like 3 (LOC269542)
Nlk	1.012	2.531	1.671	1.155	0.89	nemo like kinase. [Source:RefSeq;Acc:NM_008702]
Stac2	1.222	1.256	1.399	1.145	0.917	SH3 and cysteine rich domain 2; synonyms: 24b2, AW240854, MGC38869, 24b2/STAC2; Mus musculus SH3 and cysteine rich domain 2 (Stac2), mRNA.
Top2b	1.044	0.89	1.304	1.025	1.021	DNA topoisomerase II, beta isozyme (EC 5.99.1.3). [Source:Uniprot/SWISSPROT;Acc:Q64511]

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ENSMUSG00000017652	1.172	0.752	0.702	0.945	1.303	Tumor necrosis factor receptor superfamily member 5 precursor (CD40L receptor) (B-cell surface antigen CD40) (BP50) (CDw40). [Source:Uniprot/SWISSPROT;Acc:P27512]
AB093301	0.789	0.841	0.744	1.519	0.511	Engulfment and cell motility protein 2 (CED-12 homolog A). [Source:Uniprot/SWISSPROT;Acc:Q8BHL5]
Wsb1	1.132	0.812	0.711	0.874	1.18	WD repeat and SOCS box containing protein 1 (WSB-1). [Source:Uniprot/SWISSPROT;Acc:O54927]
Ada	1.249	1.051	1.307	1.438	1.46	Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase). [Source:Uniprot/SWISSPROT;Acc:P03958]
D11Lgp2e	0.983	1.014	0.796	0.906	1.433	hypothetical protein
Hspb9	1.433	0.492	0.387	0.914	0.898	Heat-shock protein beta-9 (HspB9). [Source:Uniprot/SWISSPROT;Acc:Q9DAM3]
Thrap2	1.106	1	0.768	0.84	0.882	thyroid hormone receptor associated protein 2; synonyms: Trap240L, mKIAA1025, 2210413I17Rik, 6330591G05Rik, 9030618F05Rik; Mus musculus thyroid hormone receptor associated protein 2 (Thrap2), mRNA.
Tbx5	1.146	1.246	0.769	0.454	0.956	T-box transcription factor TBX5 (T-box protein 5). [Source:Uniprot/SWISSPROT;Acc:P70326]
Adora2b	1.145	0.473	0.399	0.987	0.984	Adenosine A2b receptor. [Source:Uniprot/SWISSPROT;Acc:Q60614]
ENSMUSG00000018654	0.659	1.126	0.768	1.159	1.12	DNA-binding protein Ikaros (Lymphoid transcription factor LyF-1). [Source:Uniprot/SWISSPROT;Acc:Q03267]
Ndel1	0.939	0.858	0.661	0.893	1.256	NudeL protein; nuclear disribution gene E like; nuclear distribution gene E-like. [Source:RefSeq;Acc:NM_023668]
Unc45b	1.564	1.34	1.534	0.893	0.982	cardiomyopathy associated 4; striated muscle UNC45. [Source:RefSeq;Acc:NM_178680]
Irf1	1.048	1.813	1.182	0.975	1.18	interferon regulatory factor 1; synonyms: Irf-1, AU020929; Mus musculus interferon regulatory factor 1 (Irf1), mRNA.
Csf2	0.269	0.745	0.421	0.917	1.08	Granulocyte-macrophage colony-stimulating factor precursor (GM-CSF) (Colony-stimulating factor) (CSF). [Source:Uniprot/SWISSPROT;Acc:P01587]

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Pelp1	0.829	1.814	0.871	1.897	1.693	proline-, glutamic acid-, leucine-rich protein 1. [Source:RefSeq;Acc:NM_029231]
Ccl4	0.926	0.622	0.534	1.011	1.576	Small inducible cytokine A4 precursor (CCL4) (Macrophage inflammatory protein 1-beta) (MIP-1-beta) (H400 protein) (SIS-gamma) (ACT2). [Source:Uniprot/SWISSPROT;Acc:P14097]
Hoxb1	0.714	0.923	0.655	0.701	2.265	Homeobox protein Hox-B1 (Hox-2.9). [Source:Uniprot/SWISSPROT;Acc:P17919]
Dnase1l1	0.987	1.1	1.271	1.224	0.849	deoxyribonuclease 1-like 1; synonyms: G4.8, AI324885, 2310005K03Rik; DNase X; Mus musculus deoxyribonuclease 1-like 1 (Dnase1l1), mRNA.
Tmem160	0.94	1.375	1.26	1.284	1.017	transmembrane protein 160; synonym: 1810008O21Rik; Mus musculus transmembrane protein 160 (Tmem160), mRNA.
BC045148	0.789	1.148	0.489	0.73	1.068	map kinase phosphatase-like protein MK-STYX. [Source:RefSeq;Acc:NM_029659]
Atp6v0a1	1.264	1.318	1.692	1.003	0.877	Vacuolar proton translocating ATPase 116 kDa subunit a isoform 1 (V- ATPase 116-kDa isoform a1) (Clathrin-coated vesicle/synaptic vesicle proton pump 116 kDa subunit) (Vacuolar proton pump subunit 1) (Vacuolar adenosine triphosphatase subunit Ac116). [Source:Uniprot/SWISSPROT;Acc:Q9Z1G4]
Grb7	0.26	1.313	1.523	0.658	1.317	Growth factor receptor-bound protein 7 (GRB7 adapter protein) (Epidermal growth factor receptor GRB-7). [Source:Uniprot/SWISSPROT;Acc:Q03160]
Slc6a8	1.367	0.876	1.242	1.031	1.01	solute carrier family 6 (neurotransmitter transporter, creatine), member 8; creatine transporter. [Source:RefSeq;Acc:NM_133987]
1110001J03Rik	0.852	1.592	1.272	1.162	0.924	hypothetical protein LOC66117
ENSMUSG00000019763	1.348	0.901	1.481	1.137	1.025	RIKEN cDNA 0610042C05 gene (0610042C05Rik)
Rgs17	1.191	0.548	1.339	1.059	1.746	Regulator of G-protein signaling 17 (RGS17) (Regulator of Gz-selective protein signaling 2). [Source:Uniprot/SWISSPROT;Acc:Q9QZB0]

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Hey2	1.03	1.806	2.312	0.808	1.012	hairy/enhancer-of-split related with YRPW motif 2; hairy-related transcription factor 2; Hairy-E(spl)-related with YRPW motif 2; hairy and enhancer of split related 2. [Source:RefSeq;Acc:NM_013904]
ENSMUSG00000019838	1.121	1.263	1.319	1.134	1.123	solute carrier family 16 (monocarboxylic acid transporters), member 10. [Source:RefSeq;Acc:NM_028247]
ENSMUSG00000019843	0.932	0.768	0.67	1.026	0.864	Proto-oncogene tyrosine-protein kinase FYN (EC 2.7.1.112) (P59-FYN). [Source:Uniprot/SWISSPROT;Acc:P39688]
Tnfaip3	1.314	0.784	0.432	0.785	0.938	Tumor necrosis factor, alpha-induced protein 3 (Putative DNA binding protein A20) (Zinc finger protein A20). [Source:Uniprot/SWISSPROT;Acc:Q60769]
Smpdl3a	0.848	0.862	1.226	0.851	1.168	Acid sphingomyelinase-like phosphodiesterase 3a precursor (EC 3.1.4.-) (ASM-like phosphodiesterase 3a). [Source:Uniprot/SWISSPROT;Acc:P70158]
Mgat4c	1.453	1.498	0.346	3.956	0.615	UDP-N-acetylglucosamine: alpha-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV
Atp2b1	1.255	1.027	1.153	1.089	1.188	plasma membrane calcium ATPase 1
Sgk	1.16	1.296	1.473	0.92	1.126	Serine/threonine-protein kinase Sgk1 (EC 2.7.1.37) (Serum/glucocorticoid-regulated kinase 1). [Source:Uniprot/SWISSPROT;Acc:Q9WVC6]
Arg1	1.412	3.572	2.089	1.221	0.453	Arginase 1 (EC 3.5.3.1) (Liver-type arginase). [Source:Uniprot/SWISSPROT;Acc:Q61176]
2010107G23Rik	0.609	0.37	2.247	0.736	1.091	RIKEN cDNA 2010107G23 gene; synonym: AA545165; Mus musculus RIKEN cDNA 2010107G23 gene (2010107G23Rik), mRNA.
Pcsk4	0.784	0.662	1.557	1.757	1.24	Neuroendocrine convertase 3 precursor (EC 3.4.21.-) (NEC 3) (PC4) (Prohormone convertase 3) (KEX2-like endoprotease 3). [Source:Uniprot/SWISSPROT;Acc:P29121]
Ptprb	1.062	0.955	1.644	1.425	1.113	protein tyrosine phosphatase, receptor type, B; vascular endothelial protein tyrosine phosphatase. [Source:RefSeq;Acc:NM_029928]
Ptprb	0.269	2.32	1.633	1.874	0.621	protein tyrosine phosphatase, receptor type, B; vascular endothelial protein tyrosine phosphatase.

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Csrp2	1.315	0.936	0.549	0.94	1.222	Cysteine and glycine-rich protein 2 (Cysteine-rich protein 2) (CRP2) (Double LIM protein-1) (DLP-1). [Source:Uniprot/SWISSPROT;Acc:P97314]
Phlda1	0.887	0.591	0.443	0.905	1.676	pleckstrin homology-like domain, family A, member 1; T-cell death associated gene. [Source:RefSeq;Acc:NM_009344]
Hmg20b	0.95	1.761	0.728	1.152	1.12	high mobility group 20 B; high mobility group protein 20 B; BRCA2-associated factor 35. [Source:RefSeq;Acc:NM_010440]
Rel	1.375	1.41	0.569	0.726	0.855	C-Rel proto-oncogene protein (C-Rel protein). [Source:Uniprot/SWISSPROT;Acc:P15307]
4933407N01Rik	0.987	1.817	1.451	1.059	1.013	XTP3-transactivated protein B
Fstl3	1.499	1.67	1.549	1.718	1.46	Follistatin-related protein 3 precursor (Follistatin-like 3) (Follistatin-related gene protein). [Source:Uniprot/SWISSPROT;Acc:Q9EQC7]
ENSMUSG00000020358	1.02	1.104	1.277	1.165	0.945	Heterogeneous nuclear ribonucleoprotein A/B (hnRNP A/B) (CArG-binding factor-A) (CBF-A). [Source:Uniprot/SWISSPROT;Acc:Q99020]
Canx	1.042	0.879	0.869	0.809	0.767	Calnexin precursor. [Source:Uniprot/SWISSPROT;Acc:P35564]
Upp1	0.939	0.577	0.407	0.903	0.813	Uridine phosphorylase 1 (EC 2.4.2.3) (UrdPase 1) (UPase 1). [Source:Uniprot/SWISSPROT;Acc:P52624]
ENSMUSG00000020412	1.479	0.75	1.337	1.271	0.948	ASC-1 complex subunit P100. [Source:RefSeq;Acc:NM_029291]
Guk1	1.003	1.175	1.709	1.266	0.745	Guanylate kinase (EC 2.7.4.8) (GMP kinase). [Source:Uniprot/SWISSPROT;Acc:Q64520]
Hs3st3b1	0.824	0.589	1.568	1.444	0.764	D-glycosaminyl 3-O-sulfotransferase-3B. [Source:RefSeq;Acc:NM_018805]
ENSMUSG00000020561	1.242	1.169	0.851	1.447	1.118	TWIST neighbor. [Source:RefSeq;Acc:NM_172253]
BC072598	1.224	1.117	1.316	0.991	1.402	PREDICTED: RIKEN cDNA 4933425L03 gene (4933425L03Rik)
Ntsr2	1.232	1.209	0.416	1.268	0.523	Neurotensin receptor type 2 (NT-R-2) (Low-affinity levocabastine- sensitive neurotensin receptor) (NTRL). [Source:Uniprot/SWISSPROT;Acc:P70310]

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Arsg	1.717	0.318	0.646	0.353	1.029	Arylsulfatase G
Hs1bp3	1.369	1.032	1.281	0.556	1.091	HS1-binding protein 3. [Source:RefSeq;Acc:NM_021429]
ENSMUSG00000020636	0.348	0.523	2.048	1.009	0.7	allantoicase. [Source:RefSeq;Acc:NM_053156]
Mboat2	1.328	1.457	1.581	0.266	1.107	O-acyltransferase (membrane bound) domain containing 2 isoform a
Ddx52	1.291	1.236	0.85	1.001	1.155	DEAD-box protein 52 (EC 3.6.1.-) (Putative ATP-dependent RNA helicase ROK1-like). [Source:Uniprot/SWISSPROT;Acc:Q8K301]
Taf15	1.442	0.439	2.022	1.591	0.453	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor; TATA box binding protein (TBP)-associated factor, RNA polymerase II, N, 68kD (RNA binding protein 56); TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68 kDa. [Source:RefSeq;Acc:NM_027427]
ENSMUSG00000020728	1.143	0.131	2.331	0.808	0.991	hypothetical protein
Slc9a3r1	1.185	0.468	0.457	1.195	1.202	Ezrin-radixin-moesin binding phosphoprotein 50 (EBP50) (Na()/H() exchange regulatory cofactor NHE-RF) (NHERF-1) (Regulatory cofactor of Na()/H() exchanger) (Sodium-hydrogen exchanger regulatory factor 1) (Solute carrier family 9 isoform 3 regulatory factor 1). [Source:Uniprot/SWISSPROT;Acc:P70441]
Nt5c	0.958	1.033	1.291	1.116	1.085	5'(3')-deoxyribonucleotidase, cytosolic type (EC 3.1.3.-) (Cytosolic 5',3'-pyrimidine nucleotidase) (Deoxy-5'-nucleotidase 1) (dNT-1). [Source:Uniprot/SWISSPROT;Acc:Q9JM14]
1300001I01Rik	1.116	1.233	1.434	0.894	0.832	MKIAA0664 protein (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8CHD9]
ENSMUSG00000020757	0.805	0.625	0.705	0.973	1.134	hypothetical protein
ENSMUSG00000020757	0.973	1.991	1.805	0.506	1.032	hypothetical protein

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Exoc7	1.008	1.28	1.179	0.882	0.808	exocyst complex component 7; synonyms: 70kDa, Exo70, sec70, mKIAA1067; exocyst component protein 70 kDa homolog; Mus musculus exocyst complex component 7 (Exoc7), mRNA.
Rhbdf2	1.058	0.842	0.7	1.001	0.897	rhomboid-like protein 6. [Source:RefSeq;Acc:NM_172572]
Wscd1	1.248	2.087	2.108	2.541	0.611	WSC domain containing 1
Nos2	0.494	0.905	0.619	1.094	0.221	Nitric oxide synthase, inducible (EC 1.14.13.39) (NOS, type II) (Inducible NOS) (iNOS) (Macrophage NOS) (MAC-NOS). [Source:Uniprot/SWISSPROT;Acc:P29477]
AK172961	1.368	0.693	0.868	1.143	0.657	sperm associated antigen 9; JNK-associated leucine-zipper. [Source:RefSeq;Acc:NM_027569]
Abcc3	0.962	0.999	1.264	1.28	0.765	Similar to ATP-binding cassette, sub-family C (CFTR/MRP), member 3 (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q80ZK8]
Dvl2	1.178	1.333	0.479	0.873	1.042	Segment polarity protein dishevelled homolog DVL-2 (Dishevelled-2) (DSH homolog 2). [Source:Uniprot/SWISSPROT;Acc:Q60838]
Myh10	0.935	1.229	0.851	1.381	1.126	Myosin heavy chain, smooth muscle isoform (SMMHC). [Source:Uniprot/SWISSPROT;Acc:O08638]
Stx8	0.961	1.239	1.342	1.085	1.219	Syntaxin 8 (Syntaxin-like protein 3I35). [Source:Uniprot/SWISSPROT;Acc:O88983]
Lyzl6	1.164	2.205	0.688	0.708	0.829	lysozyme-like 6; synonyms: Lyc1, 1700023H08Rik; lysozyme-like protein 1; novel protein similar to lysozyme; Mus musculus lysozyme-like 6 (Lyzl6), mRNA.
Gosr2	1.22	0.84	1.202	1.019	1.05	27 kDa Golgi SNARE protein (Golgi SNAP receptor complex member 2) (Membrin). [Source:Uniprot/SWISSPROT;Acc:O35166]
ENSMUSG00000020950	0.191	0.925	1.645	0.662	0.627	Forkhead box protein G1B (Forkhead-related protein FKHL1) (Transcription factor BF-1) (Brain factor 1) (BF1). [Source:Uniprot/SWISSPROT;Acc:Q60987]
Psma6	1.02	0.701	0.842	0.838	1.036	Proteasome subunit alpha type 6 (EC 3.4.25.1) (Proteasome iota chain) (Macropain iota chain) (Multicatalytic endopeptidase complex iota chain). [Source:Uniprot/SWISSPROT;Acc:Q9QUM9]
Akap5	1.249	0.38	1.684	1.427	0.677	similar to A-kinase anchor protein 5 isoform 1

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Six6os1	0.936	0.179	1.236	0.797	0.908	Six6 opposite strand transcript 1
Vrk1	0.998	0.797	1.584	1.692	1.14	vaccinia related kinase 1; synonym: 51PK; isoform a is encoded by transcript variant 1; Mus musculus vaccinia related kinase 1 (Vrk1), transcript variant 1, mRNA.
Zfp36l1	1.695	0.446	0.535	0.823	1.101	Butyrate response factor 1 (TIS11B protein). [Source:Uniprot/SWISSPROT;Acc:P23950]
Pcnx	1.15	1.069	1.257	0.974	1.165	Pecanex-like protein 1 (Pecanex homolog) (Fragment). [Source:Uniprot/SWISSPROT;Acc:Q9QYC1]
Zadh1	0.999	1.174	1.921	0.805	1.141	zinc binding alcohol dehydrogenase, domain containing 1 (Zadh1)
Lrrc16	1.501	1.472	1.553	0.683	1.08	leucine rich repeat containing 16. [Source:RefSeq;Acc:NM_026825]
Tpmt	0.763	1.096	1.54	0.677	1.143	Thiopurine S-methyltransferase (EC 2.1.1.67) (Thiopurine methyltransferase). [Source:Uniprot/SWISSPROT;Acc:O55060]
Peci	1.134	0.995	0.802	0.985	0.764	Peroxisomal 3,2-trans-enoyl-CoA isomerase (EC 5.3.3.8) (Dodecenoyl-CoA delta-isomerase) (D3,D2-enoyl-CoA isomerase). [Source:Uniprot/SWISSPROT;Acc:Q9WUR2]
ENSMUSG00000021458	0.95	0.841	1.747	1.534	0.912	Similar to CDNA FLJ32888 FIS. [Source:Uniprot/SPTREMBL;Acc:Q8BXQ6]
Lman2	1.129	1.233	0.743	0.972	0.805	Vesicular integral-membrane protein VIP36 precursor (Lectin, mannose-binding 2). [Source:Uniprot/SWISSPROT;Acc:Q9DBH5]
Pitx1	0.796	1.309	0.815	1.367	0.979	Pituitary homeobox 1 (Homeobox protein P-OTX) (Pituitary OTX-related factor) (Hindlimb expressed homeobox protein backfoot) (Ptx1). [Source:Uniprot/SWISSPROT;Acc:P70314]
Cxcl14	0.622	1.114	1.271	0.944	1.042	Small inducible cytokine B14 precursor (CXCL14) (Chemokine BRAK) (Kidney-expressed chemokine CXC). [Source:Uniprot/SWISSPROT;Acc:Q9WUQ5]
Gm274	0.74	0.794	2.565	1.031	0.302	PREDICTED: similar to Tesp1 protein (LOC218304)
Cetn3	0.38	1.369	1.212	1.216	0.959	Centrin 3. [Source:Uniprot/SWISSPROT;Acc:O35648]

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ENSMUSG00000021571	0.065	1.405	1.603	1.084	0.643	hypothetical protein
Mrpl36	0.876	1.401	1.188	0.813	0.949	60S ribosomal protein L36, mitochondrial precursor (L36mt). [Source:Uniprot/SWISSPROT;Acc:Q99N90]
Aytl2	1.12	1.372	0.521	0.889	0.601	acyltransferase like 2
ENSMUSG00000021639	0.795	1.2	0.69	0.686	0.993	TFIIH basal transcription factor complex p44 subunit (Basic transcription factor 2 44 kDa subunit) (BTF2-p44) (General transcription factor IIH polypeptide 2). [Source:Uniprot/SWISSPROT;Acc:Q9JIB4]
Serf1	1.263	1.519	1.234	1.022	1.159	small EDRK-rich factor 1 (Serf1)
Cartpt	1.167	0.515	1.542	0.415	0.834	Cocaine- and amphetamine-regulated transcript protein precursor [Contains: CART(1-52); CART(55-102)]. [Source:Uniprot/SWISSPROT;Acc:P56388]
1200014M14Rik	0.454	0.928	1.243	0.994	0.795	hypothetical protein LOC67463
Kif2a	0.955	1.261	1.251	0.793	0.773	kinesin family member 2A (Kif2a)
ENSMUSG00000021704	1.154	1.432	0.625	0.637	0.883	hypothetical protein
Comtd1	0.89	0.889	1.722	1.59	0.964	catechol-O-methyltransferase domain containing 1. [Source:RefSeq;Acc:NM_026965]
Nudt13	1.089	0.339	1.189	0.941	1.091	nudix (nucleoside diphosphate linked moiety X)-type motif 13. [Source:RefSeq;Acc:NM_026341]
1700011H14Rik	0.392	1.546	1.292	2.358	0.355	hypothetical protein LOC67082
Mettl6	1.044	1.26	0.485	1.188	1.222	Methyltransferase-like protein 4 homolog (EC 2.1.1.-). [Source:Uniprot/SWISSPROT;Acc:Q8BVH9]
Cdadc1	1.177	1.375	2.006	1.224	1.214	Protein kinase NYD-SP15 homolog. [Source:Uniprot/SPTREMBL;Acc:Q8BYN1]
Esd	1.275	0.699	0.75	0.604	0.712	esterase D/formylglutathione hydrolase; esterase D; esterase 10. [Source:RefSeq;Acc:NM_016903]
Slc25a30	1.407	0.932	1.351	1.004	0.961	solute carrier family 25, member 30. [Source:RefSeq;Acc:NM_026232]
Wbp4	0.952	1.294	1.311	1.036	1.166	WW domain binding protein 4; formin binding protein 21. [Source:RefSeq;Acc:NM_018765]
Ccdc25	0.762	1.533	1.411	0.533	1.421	coiled-coil domain containing 25

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Nkx3-1	0.745	0.271	1.421	1.043	1.168	Homeobox protein Nkx-3.1. [Source:Uniprot/SWISSPROT;Acc:P97436]
ENSMUSG00000022136	1.124	1.72	1.521	1.061	0.868	DnaJ (Hsp40) homolog, subfamily C, member 3; protein kinase, interferon inducible double stranded RNA dependent inhibitor. [Source:RefSeq;Acc:NM_008929]
Dab2	1.089	0.674	0.643	0.972	0.899	Disabled homolog 2 (DOC-2) (Mitogen-responsive phosphoprotein). [Source:Uniprot/SWISSPROT;Acc:P98078]
C6	1.606	1.096	1.413	1.142	0.414	complement component 6. [Source:RefSeq;Acc:NM_016704]
ENSMUSG00000022222	0.982	1.037	1.465	1.181	0.629	hypothetical protein
Zfpm2	1.547	0.931	0.457	1.226	0.538	Zinc finger protein ZFPM2 (Zinc finger protein multitype 2) (Friend of GATA protein 2) (Friend of GATA-2) (FOG-2) (mFOG-2). [Source:Uniprot/SWISSPROT;Acc:Q8CCH7]
Stk3	0.71	1.145	0.469	0.673	0.606	Serine/threonine-protein kinase 3 (EC 2.7.1.37) (STE20-like kinase MST2) (MST-2) (Mammalian STE20-like protein kinase 2). [Source:Uniprot/SWISSPROT;Acc:Q9JI10]
Eny2	0.834	1.367	0.441	1.481	1.821	e(y)2 protein; DC6 protein; e(y)2 homolog; enhancer of yellow eye homolog (Drosophila); enhancer of yellow 2 homolog (Drosophila). [Source:RefSeq;Acc:NM_175009]
ENSMUSG00000022347	0.892	0.248	1.986	0.726	0.334	hypothetical protein
Atad2	1.46	1.129	3.622	0.935	0.315	ATPase family, AAA domain containing 2. [Source:RefSeq;Acc:NM_153199]
ENSMUSG00000022372	1.471	0.697	0.706	1.342	1.344	SRC-like-adapter (Src-like-adapter protein 1) (mSLAP). [Source:Uniprot/SWISSPROT;Acc:Q60898]
ENSMUSG00000022415	0.84	1.344	1.374	1.251	0.636	Synaptogyrin 1. [Source:Uniprot/SWISSPROT;Acc:O55100]
Syngr1	0.926	1.25	1.364	1.158	0.864	Synaptogyrin 1. [Source:Uniprot/SWISSPROT;Acc:O55100]
Nptxr	0.869	1.056	0.498	0.812	0.901	Neuronal pentraxin receptor. [Source:Uniprot/SWISSPROT;Acc:Q99J85]

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Sh3bp1	1.011	1.017	2.016	1.078	0.714	SH3-domain binding protein 1 (3BP-1). [Source:Uniprot/SWISSPROT;Acc:P55194]
4931407K02Rik	1.707	0.763	0.608	2.12	2.256	CAP-binding protein complex interacting protein 1
Srebf2	0.806	0.77	0.686	1.175	1.347	Sterol regulatory element binding protein 2 (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q925C2]
BC051085	0.776	1.035	1.436	1.074	1.136	ATP-dependent DNA helicase II, 70 kDa subunit (Ku autoantigen protein p70 homolog) (Ku70) (CTC box binding factor 75 kDa subunit) (CTCBF) (CTC75). [Source:Uniprot/SWISSPROT;Acc:P23475]
Col2a1	1.194	0.297	1.552	1.234	0.959	Collagen alpha 1(II) chain precursor [Contains: Chondrocalcin]. [Source:Uniprot/SWISSPROT;Acc:P28481]
Nckap1l	1.25	0.868	1.248	0.43	0.957	NCK associated protein 1 like; synonyms: Hemp1, AI463083, 4930568P13Rik; Mus musculus NCK associated protein 1 like (Nckap1l), mRNA.
ENSMUSG00000022505	0.837	1.607	0.709	0.498	0.669	Epithelial membrane protein-2 (EMP-2) (XMP protein). [Source:Uniprot/SWISSPROT;Acc:O88662]
BC030485	0.863	2.287	1.649	1.334	0.461	Fibroblast growth factor-12 (FGF-12) (Fibroblast growth factor homologous factor 1) (FHF-1) (Myocyte-activating factor). [Source:Uniprot/SWISSPROT;Acc:P61329]
ENSMUSG00000022647	0.802	0.812	0.564	1.37	0.669	hypothetical protein
Prkdc	0.763	1.298	1.367	0.915	1.233	DNA-dependent protein kinase catalytic subunit (EC 2.7.1.37) (DNA- PKcs) (P460). [Source:Uniprot/SWISSPROT;Acc:P97313]
Snai2	1.173	0.749	1.286	1.37	0.855	Zinc finger protein SLUG (Neural crest transcription factor Slug) (Snail homolog 2). [Source:Uniprot/SWISSPROT;Acc:P97469]
P2rxl1	0.899	0.524	1.613	2.257	0.507	P2X purinoceptor 6 (ATP receptor) (P2X6) (Purinergic receptor) (P2XM) (Purinergic receptor P2X-like 1). [Source:Uniprot/SWISSPROT;Acc:O54803]
Sdf2l1	0.96	3.762	1.466	1.092	1.057	Stromal cell-derived factor 2-like protein 1 precursor (SDF2 like protein 1). [Source:Uniprot/SWISSPROT;Acc:Q9ESP1]
ENSMUSG00000022801	1.236	0.956	0.699	0.989	0.896	PREDICTED: similar to leucine-rich repeats and calponin homology (CH) domain containing 3; 2210409B11Rik

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Lmln	1.363	1.116	1.784	1.309	0.779	leishmanolysin-like (metallopeptidase M8 family). [Source:RefSeq;Acc:NM_172823]
AF316548	0.87	0.842	1.222	1.128	1.214	Zinc finger protein 148 (Zinc finger DNA binding protein 89) (Transcription factor ZBP-89) (G-rich box-binding protein) (Beta enolase repressor factor 1) (Transcription factor BFCOL1). [Source:Uniprot/SWISSPROT;Acc:Q61624]
Umps	0.974	1.496	1.649	0.997	0.981	Uridine 5'-monophosphate synthase (UMP synthase) [Includes: Orotate phosphoribosyltransferase (EC 2.4.2.10) (OPRtase); Orotidine 5'- phosphate decarboxylase (EC 4.1.1.23) (OMPdecase)]. [Source:Uniprot/SWISSPROT;Acc:P13439]
Stxbp5l	1.957	0.829	0.734	1.063	1.213	syntaxin binding protein 5-like
Ropn1	0.956	0.907	1.763	0.323	1.559	ropporin, rhophilin associated protein 1; rhophilin-associated oppo protein. [Source:RefSeq;Acc:NM_030744]
ENSMUSG00000022847	0.513	1.185	2.33	0.807	0.496	Thrombopoietin precursor (Megakaryocyte colony stimulating factor) (Myeloproliferative leukemia virus oncogene ligand) (C-mpl ligand) (ML) (Megakaryocyte growth and development factor) (MGDF). [Source:Uniprot/SWISSPROT;Acc:P40226]
ENSMUSG00000022860	0.751	1.22	1.508	1.277	0.803	Chondrolectin precursor (Transmembrane protein MT75). [Source:Uniprot/SWISSPROT;Acc:Q9CXM0]
ENSMUSG00000022875	0.837	0.896	1.811	1.114	1.746	Kininogen precursor [Contains: Bradykinin]. [Source:Uniprot/SWISSPROT;Acc:O08677]
ENSMUSG00000022940	0.713	0.92	1.38	1.078	1.003	Down syndrome critical region protein c; Down syndrome critical region gene c; phosphatidylinositol-glycan-class P. [Source:RefSeq;Acc:NM_019543]
ENSMUSG00000022977	1.041	1.529	1.382	1.16	1.382	PREDICTED: RIKEN cDNA 4921511H13 gene (4921511H13Rik)
ENSMUSG00000022978	0.953	1.064	1.246	1.028	0.803	hypothetical protein
Wnt1	0.905	1.253	1.186	0.65	0.835	Wnt-1 proto-oncogene protein precursor. [Source:Uniprot/SWISSPROT;Acc:P04426]
Tuba1b	0.921	1.099	1.186	1.344	0.81	Tubulin alpha-1 chain (Alpha-tubulin 1). [Source:Uniprot/SWISSPROT;Acc:P05209]

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C230021P08Rik	0.739	1.826	1.622	0.801	1.058	hypothetical protein LOC380969
Ccrn4l	0.956	0.597	0.638	0.625	1.808	Nocturnin (CCR4 protein homolog). [Source:Uniprot/SWISSPROT;Acc:O35710]
Ndufa5	0.975	1.5	1.502	1.034	0.969	NADH-ubiquinone oxidoreductase 13 kDa-B subunit (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-13Kd-B) (CI-13Kd-B) (Complex I subunit B13). [Source:Uniprot/SWISSPROT;Acc:Q9CPP6]
Denr	0.665	0.718	0.539	1.116	0.968	Density-regulated protein (DRP). [Source:Uniprot/SWISSPROT;Acc:Q9CQJ6]
ENSMUSG00000023120	0.933	1.12	0.559	1.297	0.376	hypothetical protein
Sult1c2	1.353	2.352	1.685	1.127	0.898	Sulfotransferase 1C1 (EC 2.8.2.-). [Source:Uniprot/SWISSPROT;Acc:Q9D939]
2610200G18Rik	0.72	1.843	0.797	0.679	1.576	hypothetical protein LOC67149
Ube2j2	0.873	1.19	0.801	1.155	1.108	ubiquitin-conjugating enzyme E2, J2 homolog; ubiquitin conjugating enzyme 6; Ubc6p homolog. [Source:RefSeq;Acc:NM_021402]
Clec4n	1.071	0.709	0.882	0.692	1.334	C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 10. [Source:RefSeq;Acc:NM_020001]
Pisd	1.161	1.816	0.614	1.023	0.446	Phosphatidylserine decarboxylase proenzyme (EC 4.1.1.65) [Contains: Phosphatidylserine decarboxylase alpha chain; Phosphatidylserine decarboxylase beta chain]. [Source:Uniprot/SWISSPROT;Acc:Q8BSF4]
Tpi1	1.122	1.232	2.044	0.987	1.024	Triosephosphate isomerase (EC 5.3.1.1) (TIM). [Source:Uniprot/SWISSPROT;Acc:P17751]
BQ949340	0.411	0.826	1.714	0.93	1.332	Homeobox protein Pem (Placenta and embryonic expression protein). [Source:Uniprot/SWISSPROT;Acc:P52651]
ENSMUSG00000023902	1.22	0.833	1.566	1.095	0.879	hypothetical protein
ENSMUSG00000023951	1.088	1.04	1.231	0.82	1.537	Vascular endothelial growth factor A precursor (VEGF-A) (Vascular permeability factor) (VPF). [Source:Uniprot/SWISSPROT;Acc:Q00731]

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Prph2	1.896	1.654	1.554	0.816	0.625	Peripherin (Retinal degeneration slow protein). [Source:Uniprot/SWISSPROT;Acc:P15499]
Tbn	1.067	0.916	0.655	1.154	0.876	taube nuss. [Source:RefSeq;Acc:NM_022015]
Foxp4	0.8	0.816	0.812	0.901	1.658	winged-helix repressor FOXP4; fork head-related protein like A. [Source:RefSeq;Acc:NM_028767]
Mtch1	1.207	1.122	1.148	1.024	0.908	mitochondrial carrier homolog 1; mitochondrial carrier homolog 1 isoform b. [Source:RefSeq;Acc:NM_019880]
Pim1	1.156	0.837	0.56	1.29	0.813	Proto-oncogene serine/threonine-protein kinase Pim-1 (EC 2.7.1.37). [Source:Uniprot/SWISSPROT;Acc:P06803]
Cryaa	0.538	1.857	1.243	0.994	0.914	Alpha crystallin A chain, major component. [Source:Uniprot/SWISSPROT;Acc:P02490]
Ehd3	0.783	1.312	1.734	0.479	0.886	EH-domain containing 3
Xdh	1.111	1.316	0.721	1.128	0.927	Xanthine dehydrogenase/oxidase [Includes: Xanthine dehydrogenase (EC 1.1.1.204) (XD); Xanthine oxidase (EC 1.1.3.22) (XO) (Xanthine oxidoreductase)]. [Source:Uniprot/SWISSPROT;Acc:Q00519]
Prkcn	0.938	0.994	1.297	0.617	0.804	protein kinase C, nu. [Source:RefSeq;Acc:NM_029239]
Vapa	0.93	0.858	1.252	0.948	0.741	Vesicle-associated membrane protein-associated protein A (VAMP- associated protein A) (VAMP-A) (VAP-A) (33 kDa Vamp-associated protein) (VAP-33). [Source:Uniprot/SWISSPROT;Acc:Q9WV55]
ENSMUSG00000024125	0.133	1.68	1.42	0.933	0.8	Spermine binding protein. [Source:Uniprot/SPTREMBL;Acc:Q9CPP2]
Sbp	1.298	0.864	1.783	1.301	1.031	Prostatic spermine-binding protein precursor (SBP) (Major prostatic secretory glycoprotein) (P25). [Source:Uniprot/SWISSPROT;Acc:P15501]
Dci	1.076	0.863	1.498	0.958	0.873	3,2-trans-enoyl-CoA isomerase, mitochondrial precursor (EC 5.3.3.8) (Dodecenoyl-CoA delta-isomerase). [Source:Uniprot/SWISSPROT;Acc:P42125]
Pigf	0.822	0.892	1.179	0.975	1.241	Phosphatidylinositol-glycan biosynthesis, class F protein (PIG-F). [Source:Uniprot/SWISSPROT;Acc:O09101]
Prss28	0.328	1.15	0.623	0.809	1.149	implantation serine protease 1. [Source:RefSeq;Acc:NM_053259]

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Mrpl28	1.171	0.798	1.313	1.451	1.402	39S ribosomal protein L28, mitochondrial precursor (L28mt) (MRP-L28). [Source:Uniprot/SWISSPROT;Acc:Q9D1B9]
Dusp1	1.49	0.506	0.487	1.174	1.393	Dual specificity protein phosphatase 1 (EC 3.1.3.48) (EC 3.1.3.16) (MAP kinase phosphatase-1) (MKP-1) (Protein-tyrosine phosphatase 3CH134) (Protein-tyrosine phosphatase ERP). [Source:Uniprot/SWISSPROT;Acc:P28563]
Map3k8	0.606	0.579	0.477	0.854	0.764	Mitogen-activated protein kinase kinase kinase 8 (EC 2.7.1.37) (COT proto-oncogene serine/threonine-protein kinase) (C-COT) (Cancer Osaka thyroid oncogene). [Source:Uniprot/SWISSPROT;Acc:Q07174]
BC006037	1.165	1.509	1.324	1.02	0.756	Mitogen-activated protein kinase kinase kinase kinase 3 (EC 2.7.1.37) (MAPK/ERK kinase kinase kinase 3) (MEK kinase kinase 3) (MEKKK 3) (Germinal center kinase related protein kinase) (GLK) (Fragments). [Source:Uniprot/SWISSPROT;Acc:Q99JP0]
Cox7a2l	0.64	0.976	0.889	0.662	0.813	Cytochrome c oxidase subunit VIIa-related protein, mitochondrial precursor (Silica-induced protein 81) (SIG-81) (SIG81). [Source:Uniprot/SWISSPROT;Acc:Q61387]
Thoc1	0.384	1.451	1.314	0.969	0.69	THO complex subunit 1 (Tho1) (Nuclear matrix protein p84). [Source:Uniprot/SWISSPROT;Acc:Q8R3N6]
Myo1f	1.134	1.623	1.358	0.902	0.886	myosin IF (Myo1f)
ENSMUSG00000024319	1.114	1.265	1.49	0.912	1.122	ARE1 homolog. [Source:Uniprot/SPTREMBL;Acc:Q8C754]
Aif1	0.963	1.801	1.473	1.099	1.125	allograft inflammatory factor 1. [Source:RefSeq;Acc:NM_019467]
Riok3	1.261	0.916	0.733	0.866	0.938	RIO kinase 3; sudD, suppressor of bimD6 homolog (Aspergillus nidulans). [Source:RefSeq;Acc:NM_024182]
Jakmip2	0.929	1.771	2.106	0.882	1.182	janus kinase and microtubule interacting protein 2 isoform 1
Mbd1	1.081	0.741	3.384	1.141	0.93	methyl-CpG binding domain protein 1. [Source:RefSeq;Acc:NM_013594]
Sall3	0.208	0.71	0.483	0.364	0.349	Sal-like protein 3 (Spalt-like protein 3) (MSal) (Fragment). [Source:Uniprot/SWISSPROT;Acc:Q62255]

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Pcyox1l	1.037	0.945	1.31	1.108	0.999	prenylcysteine oxidase 1 like
ENSMUSG00000024600	0.862	1.203	0.549	0.617	0.828	hypothetical protein
ENSMUSG00000024646	0.852	1.26	1.214	1.149	0.813	Cytochrome b5. [Source:Uniprot/SWISSPROT;Acc:P56395]
Asrgl1	0.528	1.341	1.442	1.157	0.908	asparaginase like 1. [Source:RefSeq;Acc:NM_025610]
ENSMUSG00000024663	1.101	1.074	1.516	1.217	0.902	RAB3A interacting protein (rabin3)-like 1. [Source:RefSeq;Acc:NM_144538]
Fads2	1.406	2.979	1.749	0.555	1.667	fatty acid desaturase 2; delta-6 fatty acid desaturase. [Source:RefSeq;Acc:NM_019699]
Zfand5	0.993	0.666	0.766	1.004	0.438	Zinc finger protein 216. [Source:Uniprot/SWISSPROT;Acc:O88878]
Tmem2	0.951	1.112	0.559	0.934	1.236	transmembrane protein 2. [Source:RefSeq;Acc:NM_031997]
Rcl1	0.833	0.939	0.631	1.141	0.862	RNA 3'-terminal phosphate cyclase-like protein. [Source:Uniprot/SWISSPROT;Acc:Q9JJT0]
Jak2	1.006	6.378	0.646	1.247	0.676	Tyrosine-protein kinase JAK2 (EC 2.7.1.112) (Janus kinase 2) (JAK-2). [Source:Uniprot/SWISSPROT;Acc:Q62120]
Pip5k1b	0.89	1.387	1.198	0.282	0.9	phosphatidylinositol-4-phosphate 5-kinase, type 1 alpha; PI4P5K-I. [Source:RefSeq;Acc:NM_008846]
Nudt8	0.894	1.269	1.17	1.296	0.835	nudix (nucleoside diphosphate linked moiety X)-type motif 8. [Source:RefSeq;Acc:NM_025529]
Aldh3b1	1.246	0.912	1.441	1.123	0.837	fatty aldehyde dehydrogenase-like; ALDH class 3-like; microsomal aldehyde dehydrogenase-like. [Source:RefSeq;Acc:NM_026316]
Minpp1	1.106	1.203	1.432	1.205	1.083	multiple inositol polyphosphate histidine phosphatase 1. [Source:RefSeq;Acc:NM_010799]
Saps3	1.084	1.128	0.659	0.874	0.93	sporulation-induced transcript 4-associated protein. [Source:RefSeq;Acc:NM_029456]
Smarca2	1.422	0.203	0.432	2.115	1.102	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 (Smarca2), transcript variant 1
Rnaseh2c	1.024	1.179	1.346	1.37	0.983	AYP1. [Source:RefSeq;Acc:NM_026616]

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Mark2	0.765	0.818	1.545	0.771	1.368	MAP/microtubule affinity-regulating kinase 3 (EC 2.7.1.37) (MPK-10) (Fragment). [Source:Uniprot/SWISSPROT;Acc:Q03141]
ENSMUSG00000024985	1.242	1.282	0.576	1.058	1.006	Transcription factor 7-like 2 (HMG box transcription factor 4) (T- cell-specific transcription factor 4) (TCF-4) (mTCF-4). [Source:Uniprot/SWISSPROT;Acc:Q924A0]
ENSMUSG00000025023	1.092	1.091	1.42	0.79	0.514	PREDICTED: hypothetical LOC381232 (LOC381232)
Bnc1	1.572	0.746	1.855	1.055	2.126	Zinc finger protein basonuclin 1. [Source:Uniprot/SWISSPROT;Acc:O35914]
Rfng	1.119	0.942	0.399	0.884	1.369	Beta-1,3-N-acetylglucosaminyltransferase radical fringe (EC 2.4.1.222) (O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase). [Source:Uniprot/SWISSPROT;Acc:O09009]
Hif1an	1.06	0.994	0.757	1.131	0.957	Hypoxia-inducible factor 1 alpha inhibitor (EC 1.14.11.16) (Hypoxia- inducible factor asparagine hydroxylase). [Source:Uniprot/SWISSPROT;Acc:Q8BLR9]
Lbx1	1.376	0.181	3.355	1.049	0.39	Transcription factor LBX1. [Source:Uniprot/SWISSPROT;Acc:P52955]
Car5a	1.01	2.941	0.511	0.564	1.193	Carbonic anhydrase VA, mitochondrial precursor (EC 4.2.1.1) (Carbonate dehydratase VA) (CA-VA) (CA Y). [Source:Uniprot/SWISSPROT;Acc:P23589]
Itgb8	1.199	0.519	0.78	0.593	1.291	PREDICTED: integrin beta 8 (Itgb8)
Padi1	0.438	0.267	1.343	0.726	1.918	Protein-arginine deiminase type I (EC 3.5.3.15) (Peptidylarginine deiminase I). [Source:Uniprot/SWISSPROT;Acc:Q9Z185]
Rabgef1	1.169	0.86	0.672	1.07	0.959	Rab5 GDP/GTP exchange factor (Rabex-5). [Source:Uniprot/SWISSPROT;Acc:Q9JM13]
Dgka	1.014	1.418	1.753	1.086	1.076	Diacylglycerol kinase, alpha (EC 2.7.1.107) (Diglyceride kinase) (DGK- alpha) (DAG kinase alpha) (80 kDa diacylglycerol kinase). [Source:Uniprot/SWISSPROT;Acc:O88673]
2410002I01Rik	0.985	1.171	0.711	1.026	0.794	hypothetical protein LOC78777
Fscn2	0.994	0.986	1.338	1.102	0.157	fascin homolog 2, actin-bundling protein, retinal (Strongylocentrotus purpuratus). [Source:RefSeq;Acc:NM_172802]

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Tmem4	0.998	1.085	1.431	1.206	0.639	transmembrane protein 4; putative secreted protein ZSIG9. [Source:RefSeq;Acc:NM_019953]
Echs1	1.086	1.088	1.342	1.044	0.92	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial. [Source:RefSeq;Acc:NM_053119]
ENSMUSG00000025489	1.696	0.664	0.299	0.648	1.169	haemopoiesis related membrane protein 1; fragilis4. [Source:RefSeq;Acc:NM_053088]
Ifitm1	1.011	0.395	0.426	0.972	1.426	interferon induced transmembrane protein 1; fragilis2; interferon induced transmembrane protein 2 like. [Source:RefSeq;Acc:NM_026820]
ENSMUSG00000025500	1.127	1.087	1.315	0.423	1.34	PREDICTED: RIKEN cDNA 1600016N20 gene (1600016N20Rik)
Taldo1	1.284	1.723	1.136	0.964	1.003	Transaldolase (EC 2.2.1.2). [Source:Uniprot/SWISSPROT;Acc:Q93092]
Tktl2	1.335	1.605	0.585	0.267	0.44	similar to transketolase. [Source:RefSeq;Acc:NM_028927]
1810029B16Rik	0.898	0.875	0.668	0.991	0.853	hypothetical protein LOC66282
Copg2	1.139	1.372	1.412	0.972	1.611	coatomer protein complex, subunit gamma 2
Tmem47	0.862	0.907	0.565	0.687	1.538	transmembrane 4 superfamily member 10. [Source:RefSeq;Acc:NM_138751]
Tgm4	0.873	0.955	1.781	1.085	0.468	transglutaminase 4 (prostate); synonyms: TGP, Eapa1, 9530008N10Rik; experimental autoimmune prostatitis antigen 1; Mus musculus transglutaminase 4 (prostate) (Tgm4), mRNA.
Slc25a10	1.252	1.391	1.245	1.237	1.258	Mitochondrial dicarboxylate carrier. [Source:Uniprot/SWISSPROT;Acc:Q9QZD8]
Ubxd8	1.333	1.219	1.705	1.061	1.279	protein expressed in T-cells and eosinophils in atopic dermatitis
Casp1	0.663	0.882	0.844	1.069	1.182	Interleukin-1 beta convertase precursor (EC 3.4.22.36) (IL-1BC) (IL-1 beta converting enzyme) (ICE) (Interleukin-1 beta converting enzyme) (P45) (Caspase-1) (CASP-1). [Source:Uniprot/SWISSPROT;Acc:P29452]
Kbtbd3	0.423	0.826	1.614	0.75	0.708	Kelch repeat and BTB domain containing protein 3 (BTB and kelch domain containing protein 3). [Source:Uniprot/SWISSPROT;Acc:Q8BHI4]

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ENSMUSG00000025907	1.026	1.321	0.662	0.784	0.75	RB1-inducible coiled-coil 1; coiled coil forming protein 1. [Source:RefSeq;Acc:NM_009826]
Tmem70	1.022	0.912	1.174	1.039	1.081	transmembrane protein 70; synonyms: 1110020A09Rik, 2210416J16Rik; isoform 1 is encoded by transcript variant 1; Mus musculus transmembrane protein 70 (Tmem70), transcript variant 1, mRNA.
Klf7	0.872	0.62	0.649	0.476	1.232	Krueppel-like factor 7. [Source:Uniprot/SWISSPROT;Acc:Q99JB0]
Prei3	0.795	0.815	0.584	1.016	1.222	preimplantation protein 3. [Source:RefSeq;Acc:NM_025283]
Wdr75	0.935	1.22	1.215	0.942	1.032	WD repeat domain 75; synonyms: C77608, FLJ12545, MGC143988, 1300003A18Rik, 2410118I19Rik; Mus musculus WD repeat domain 75 (Wdr75), mRNA.
ENSMUSG00000026023	0.685	1.182	1.668	1.109	0.69	PREDICTED: similar to amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 7 (LOC271697)
Il1r1	1.666	1.274	1.652	1.44	2.085	Interleukin-1 receptor, type I precursor (IL-1R-1) (P80). [Source:Uniprot/SWISSPROT;Acc:P13504]
Tmeff2	0.553	0.819	0.484	1.29	1.218	transmembrane protein with EGF-like and two follistatin-like domains 2. [Source:RefSeq;Acc:NM_019790]
ENSMUSG00000026131	0.983	0.768	0.599	0.902	1.034	Bullous pemphigoid antigen 1, isoforms 6/7 (BPA) (Hemidesmosomal plaque protein) (Dystonia musculorum protein) (Dystonin) (Fragments). [Source:Uniprot/SWISSPROT;Acc:Q60824]
Col9a1	1.316	0.908	1.383	0.87	0.555	Collagen alpha 1(IX) chain precursor. [Source:Uniprot/SWISSPROT;Acc:Q05722]
4921533L14Rik	1.041	1.024	0.496	0.673	0.43	hypothetical protein LOC68187
Ogfrl1	1.298	0.811	1.328	1.33	1.052	opioid growth factor receptor-like 1; synonym: 2210417C17Rik; Mus musculus opioid growth factor receptor-like 1 (Ogfrl1), mRNA.
Bcs1l	0.765	1.299	1.529	0.462	1.132	Mitochondrial chaperone BCS1 (BCS1-like protein). [Source:Uniprot/SWISSPROT;Acc:Q9CZP5]
Htr2b	0.928	1.306	1.46	1.4	1.127	5-hydroxytryptamine 2B receptor (5-HT-2B) (Serotonin receptor 2B) (5- HT-2F) (NP75 protein). [Source:Uniprot/SWISSPROT;Acc:Q02152]

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Nmur1	0.685	0.289	0.688	1.417	1.286	G protein-coupled receptor 66. [Source:RefSeq;Acc:NM_010341]
Farsb	1.292	1.843	1.301	1.08	0.913	Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20) (Phenylalanine-- tRNA ligase beta chain) (PheRS). [Source:Uniprot/SWISSPROT;Acc:Q9WUA2]
AK122456	0.574	0.721	1.493	0.636	0.712	Ankyrin repeat and SOCS box containing protein 1 (ASB-1). [Source:Uniprot/SWISSPROT;Acc:Q9WV74]
Ccdc93	1.523	0.345	0.376	1.366	1.035	coiled-coil domain containing 93 isoform c
R3hdm1	0.976	0.904	1.333	1.195	1.154	MKIAA0029 protein (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q80U91]
Steap3	0.48	0.448	1.671	1.294	1.117	dudulin 2; dudlin 2. [Source:RefSeq;Acc:NM_133186]
Tnni1	1.499	0.697	0.72	0.469	0.701	Troponin I, slow skeletal muscle (Troponin I, slow-twitch isoform). [Source:Uniprot/SWISSPROT;Acc:Q9WUZ5]
Slc45a3	1.854	1.117	1.778	0.61	1.621	Prostein. [Source:Uniprot/SWISSPROT;Acc:Q8K0H7]
ENSMUSG00000026447	1.212	1.202	0.71	1.515	1.667	PREDICTED: similar to Phosphatidylinositol-4-phosphate 3-kinase C2 domain-containing beta polypeptide (Phosphoinositide 3-Kinase-C2-beta) (PtdIns-3-kinase C2 beta) (PI3K-C2beta) (C2-PI3K) (LOC433348)
Ifi202b	1.055	0.267	1.532	0.527	0.531	Interferon-activatable protein 202a (Ifi-202a) (Interferon-inducible protein p202a). [Source:Uniprot/SWISSPROT;Acc:P15091]
ENSMUSG00000026571	1.186	0.95	1.502	0.668	0.437	hypothetical protein
Prrx1	1.256	0.984	1.697	1.094	0.884	Paired mesoderm homeobox protein 1 (PRX-1) (Paired related homeobox protein 1) (Homeobox protein MhoX) (Homeobox protein K-2) (Rhox). [Source:Uniprot/SWISSPROT;Acc:P43271]
Slc30a10	0.529	0.768	1.308	1.062	0.905	solute carrier family 30, member 10
Traf5	0.867	1.085	1.327	1.278	0.565	TNF receptor associated factor 5. [Source:Uniprot/SWISSPROT;Acc:P70191]
Plxna2	0.88	1.203	1.528	1.53	1.468	plexin A2; plexin 2. [Source:RefSeq;Acc:NM_008882]

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Fcgr2b	0.814	0.741	0.751	0.938	1.097	Low affinity immunoglobulin gamma Fc region receptor II precursor (Fc- gamma RII) (FcRII) (IgG Fc receptor II beta) (Fc gamma receptor IIB) (Fc-gamma-RIIB). [Source:Uniprot/SWISSPROT;Acc:P08101]
Epc2	0.99	1.683	1.821	0.879	1.154	enhancer of polycomb homolog 2
Pfkfb3	0.914	0.49	0.376	0.983	1.013	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3; inducible 6-phosphofructo-2-kinase. [Source:RefSeq;Acc:NM_172976]
Lcn2	0.933	0.549	0.416	1.466	1.161	Neutrophil gelatinase-associated lipocalin precursor (NGAL) (P25) (SV- 40 induced 24P3 protein) (Lipocalin 2). [Source:Uniprot/SWISSPROT;Acc:P11672]
Fcnb	0.871	0.654	1.761	0.785	0.902	Ficolin 2 precursor (Collagen/fibrinogen domain-containing protein 2) (Ficolin-B) (Ficolin B) (Serum lectin p35) (EBP-37) (Hucolin) (Fragment). [Source:Uniprot/SWISSPROT;Acc:O70497]
ENSMUSG00000026844	0.542	0.339	1.495	0.668	1.023	Argininosuccinate synthase (EC 6.3.4.5) (Citrulline--aspartate ligase). [Source:Uniprot/SWISSPROT;Acc:P16460]
ENSMUSG00000026863	0.95	0.691	1.771	0.489	0.698	F-box/WD-repeat protein 2 (MD6 protein). [Source:Uniprot/SWISSPROT;Acc:Q60584]
Kynu	0.664	1.917	1.265	0.96	1.071	kynureninase (L-kynurenine hydrolase). [Source:RefSeq;Acc:NM_027552]
Traf1	1.158	0.858	0.784	0.981	1.63	TNF receptor associated factor 1. [Source:Uniprot/SWISSPROT;Acc:P39428]
Rab14	1.394	1.174	0.692	0.915	0.946	Ras-related protein Rab-14. [Source:Uniprot/SWISSPROT;Acc:Q91V41]
Gsn	1.166	1.282	1.312	1.247	1.258	Gelsolin precursor, plasma (Actin-depolymerizing factor) (ADF) (Brevin). [Source:Uniprot/SWISSPROT;Acc:P13020]
Ndufa8	0.967	0.975	1.211	1.09	1.275	NADH-ubiquinone oxidoreductase 19 kDa subunit (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-19KD) (CI-19KD) (Complex I-PGIV) (CI-PGIV). [Source:Uniprot/SWISSPROT;Acc:Q9DCJ5]
Notch1	1.046	0.705	0.572	0.782	0.634	Neurogenic locus notch homolog protein 1 precursor (Notch 1) (Motch A) (mT14) (p300). [Source:Uniprot/SWISSPROT;Acc:Q01705]
Sdccag3	0.938	0.918	0.8	0.977	0.9	serologically defined colon cancer antigen 3 isoform 1

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Rbms1	1.058	1.05	0.861	1.025	0.994	RNA binding motif, single stranded interacting protein 1. [Source:RefSeq;Acc:NM_020296]
Psd4	1.167	1.385	0.782	0.882	0.706	pleckstrin and Sec7 domain containing 4
Il1rn	0.791	0.489	0.444	0.771	1.161	Interleukin-1 receptor antagonist protein precursor (IL-1ra) (IRAP) (IL1 inhibitor) (IL-1RN). [Source:Uniprot/SWISSPROT;Acc:P25085]
BI731739	1.027	1.419	0.74	1.559	1.321	hypothetical protein
Lass6	0.883	0.747	0.717	0.612	1.34	longevity assurance homolog 6. [Source:RefSeq;Acc:NM_172856]
Phospho2	0.843	0.965	0.807	0.943	0.64	phosphatase, orphan 2
ENSMUSG00000027099	1.321	1.362	1.498	1.207	1.021	Metaxin 2. [Source:Uniprot/SWISSPROT;Acc:O88441]
B230118H07Rik	0.797	1.379	2.108	0.717	1.059	RIKEN cDNA B230118H07 gene (B230118H07Rik)
Sema6d	1.112	1.068	0.519	0.501	1.972	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6D isoform 1; semaphorin 6D. [Source:RefSeq;Acc:NM_172537]
Q9D518	0.832	2.436	1.834	0.682	2.051	hypothetical protein
Jag1	0.592	1.204	0.424	0.735	1.189	Jagged 1 precursor (Jagged1). [Source:Uniprot/SWISSPROT;Acc:Q9QXX0]
Q9CVX9	2.103	1.653	1.664	0.97	1.11	hypothetical protein
Cdan1	1.269	0.993	1.387	1.171	0.768	Codanin 1 (Fragment). [Source:Uniprot/SWISSPROT;Acc:Q8CC12]
Dusp2	0.706	0.438	0.338	0.988	0.837	Dual specificity protein phosphatase 2 (EC 3.1.3.48) (EC 3.1.3.16) (Dual specificity protein phosphatase PAC-1). [Source:Uniprot/SWISSPROT;Acc:Q05922]
Mrps5	0.969	1.217	1.319	1.121	1.083	Mitochondrial 28S ribosomal protein S5 (MRP-S5). [Source:Uniprot/SWISSPROT;Acc:Q99N87]
Il1b	1.15	0.646	0.472	0.615	0.962	Interleukin-1 beta precursor (IL-1 beta). [Source:Uniprot/SWISSPROT;Acc:P10749]
Il1a	0.677	0.415	0.294	0.998	1.273	Interleukin-1 alpha precursor (IL-1 alpha). [Source:Uniprot/SWISSPROT;Acc:P01582]
Cst3	0.967	1.22	1.231	0.961	0.848	Cystatin C precursor (Cystatin 3). [Source:Uniprot/SWISSPROT;Acc:P21460]
Cdk5rap1	1.108	0.687	0.354	1.431	2.122	CDK5 regulatory subunit associated protein 1 (CDK5 activator-binding protein C42). Source:Uniprot/SWISSPROT;Acc:Q8BTW8

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Rbm38	0.824	0.569	0.529	1.177	1.428	RNA-binding region containing protein 1 (ssDNA binding protein SEB4). [Source:Uniprot/SWISSPROT;Acc:Q62176]
Col9a3	0.455	0.26	2.609	1.041	1.302	Collagen type IX alpha 3 (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q9JKK4]
1110008F13Rik	0.984	1.234	1.384	0.964	1.168	RAB5-interacting protein
Samhd1	1.087	1.31	1.398	1.104	1.368	SAM domain and HD domain-containing protein 1 (Interferon-gamma inducible protein Mg11). [Source:Uniprot/SWISSPROT;Acc:Q60710]
2310007D09Rik	1.436	0.254	0.7	0.988	1.032	hypothetical protein LOC71878
Actl6a	0.833	0.943	1.087	1.149	0.824	53 kDa BRG1-associated factor A (Actin-related protein Baf53a). [Source:Uniprot/SWISSPROT;Acc:Q9Z2N8]
Aadacl1	0.921	0.955	1.284	0.904	0.896	arylacetamide deacetylase-like 1
ENSMUSG00000027702	0.635	0.101	1.518	0.515	0.757	PREDICTED: RIKEN cDNA 1700007J06 gene (1700007J06Rik)
ENSMUSG00000027713	1.68	1.117	1.758	2.434	1.455	hypthothetical protein
Slc7a11	0.932	0.988	0.732	0.796	1.1	Cystine/glutamate transporter (Amino acid transport system xc-) (xCT). [Source:Uniprot/SWISSPROT;Acc:Q9WTR6]
Trpc4	1.499	0.525	1.653	0.574	0.63	Short transient receptor potential channel 4 (TrpC4) (Receptor- activated cation channel TRP4) (Capacitative calcium entry channel Trp4). [Source:Uniprot/SWISSPROT;Acc:Q9QUQ5]
ENSMUSG00000027774	1.552	1.005	1.197	1.245	0.95	Elongation factor G 1, mitochondrial precursor (mEF-G 1) (Elongation factor G1). [Source:Uniprot/SWISSPROT;Acc:Q8K0D5]
Schip1	1.353	0.825	1.535	0.734	0.928	schwannomin interacting protein 1; neurofibromatosis 2 interacting protein. [Source:RefSeq;Acc:NM_013928]
ENSMUSG00000027790	0.413	0.607	1.974	1.46	0.867	hypothetical protein

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
D3Ucla1	1.11	0.935	0.808	0.902	1.244	stress-associated endoplasmic reticulum protein 1; ribosome associated membrane protein 4. [Source:RefSeq;Acc:NM_030685]
Csde1	1.253	0.855	1.258	0.851	1.044	cold shock domain containing E1, RNA binding; synonyms: unr, D3Jfr1, AA960392, BC016898, MGC19174, mKIAA0885; NRAS-related; Mus musculus cold shock domain containing E1, RNA binding (Csde1), mRNA.
Ngfb	1.158	1.011	0.76	1.135	1.654	Beta-nerve growth factor precursor (Beta-NGF). [Source:Uniprot/SWISSPROT;Acc:P01139]
Prpf38b	0.799	0.94	0.694	0.943	1.015	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B
Kcnc4	0.485	0.864	0.649	2.014	0.914	potassium voltage gated channel, Shaw-related subfamily, member 4. [Source:RefSeq;Acc:NM_145922]
Rab13	1.175	1.068	0.527	1.061	1.124	Ras-related protein Rab-13. [Source:Uniprot/SWISSPROT;Acc:Q9DD03]
4933434E20Rik	0.817	1.075	1.166	1.061	0.92	NICE-3 protein. [Source:RefSeq;Acc:NM_025762]
1700006A11Rik	1.928	2.484	1.563	1.793	1	hypothetical protein LOC71824
Accn5	1.331	0.114	1.38	1.381	1.915	amiloride-sensitive cation channel 5, intestinal; amiloride-sensitive Na channel; amiloride-sensitive sodium channel; brain-liver-intestine amiloride-sensitive sodium channel. [Source:RefSeq;Acc:NM_021370]
Rrh	0.786	1.555	1.398	0.951	0.546	Visual pigment-like receptor peropsin. [Source:Uniprot/SWISSPROT;Acc:O35214]
ENSMUSG00000028018	0.628	0.95	0.676	0.645	0.905	hypothetical protein
AK173191, AI608130	0.728	1.541	0.699	1.171	1.1	hypothetical protein
Dnajb4	0.703	0.805	2.004	1.028	0.936	DnaJ homolog subfamily B member 4. [Source:Uniprot/SWISSPROT;Acc:Q9D832]
Ptgfr	1.213	1.345	0.708	0.967	0.816	Prostaglandin F2-alpha receptor (Prostanoid FP receptor) (PGF receptor) (PGF2 alpha receptor). [Source:Uniprot/SWISSPROT;Acc:P43117]

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BU707888	0.451	0.1	1.412	1.124	1.339	Ephrin-A3 (EPH-related receptor tyrosine kinase ligand 3) (LERK-3) (EHK1 ligand) (EHK1-L) (Fragment). [Source:Uniprot/SWISSPROT;Acc:O08545]
ENSMUSG00000028057	0.702	1.312	1.316	1.289	0.822	GTP-binding protein Rit1 (Ras-like protein expressed in many tissues) (Ras-like without CAAX protein 1). [Source:Uniprot/SWISSPROT;Acc:P70426]
Cd1d1	1.139	1.548	1.456	0.511	0.982	T-cell surface glycoprotein CD1d1 precursor (CD1.1 antigen). [Source:Uniprot/SWISSPROT;Acc:P11609]
ENSMUSG00000028100	0.937	0.267	0.564	0.204	0.788	hypothetical protein
Tars2	0.738	1.422	0.705	1.391	0.743	threonyl-tRNA synthetase-like 1
ENSMUSG00000028108	0.834	1.207	1.295	1.135	0.865	Extracellular matrix protein 1 precursor (Secretory component p85). [Source:Uniprot/SWISSPROT;Acc:Q61508]
Pip5k1a	0.918	0.863	0.696	0.963	1.262	phosphatidylinositol-4-phosphate 5-kinase, type 1 beta; PI4P5K-I. [Source:RefSeq;Acc:NM_008847]
F3	1.591	0.813	0.591	3.431	0.382	Tissue factor precursor (TF) (Coagulation factor III). [Source:Uniprot/SWISSPROT;Acc:P20352]
Tspan5	1.041	1.426	1.411	0.959	1.003	Transmembrane 4 superfamily member 9 (Tetraspanin 5) (Tspan-5) (Tetraspan NET-4). [Source:Uniprot/SWISSPROT;Acc:P62080]
Gpr177	1.127	1.03	1.434	0.894	0.768	G protein-coupled receptor 177
Cyr61	1.33	1.221	0.673	0.409	0.588	CYR61 protein precursor (Cysteine-rich, angiogenic inducer, 61) (Insulin-like growth factor-binding protein 10) (3CH61). [Source:Uniprot/SWISSPROT;Acc:P18406]
Lhx8	1.627	0.775	1.719	1.368	0.72	LIM/homeobox protein Lhx8 (LIM homeodomain Lhx7) (L3). [Source:Uniprot/SWISSPROT;Acc:O35652]
Trp53inp1	1.079	1.581	1.635	1.162	0.8	transformation related protein 53 inducible nuclear protein 1; thymus expressed acidic protein; Stress induced protein. [Source:RefSeq;Acc:NM_021897]
Tmem55a	0.764	1.387	1.547	0.995	0.773	transmembrane protein 55A
Atp6v0d2	0.961	2.165	1.916	0.855	0.962	vacuolar proton-translocating ATPase d subunit d2. [Source:RefSeq;Acc:NM_175406]

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Gabrr1	0.672	1.21	1.842	1.678	0.361	Gamma-aminobutyric-acid receptor rho-1 subunit precursor (GABA(A) receptor). [Source:Uniprot/SWISSPROT;Acc:P56475]
Nr4a3	1.255	1.703	1.787	0.465	0.357	Orphan nuclear receptor NR4A3 (Orphan nuclear receptor TEC) (Translocated in extraskeletal chondrosarcoma). [Source:Uniprot/SWISSPROT;Acc:Q9QZB6]
Invs	0.779	1.067	1.442	0.971	0.817	inversin; inversion of embryonic turning. [Source:RefSeq;Acc:NM_010569]
2310002L09Rik	0.554	1.447	1.424	1.359	1.21	hypothetical protein LOC71886
Cd72	1.326	1.531	1.368	1.007	1.587	B-cell differentiation antigen CD72 (Lyb-2). [Source:Uniprot/SWISSPROT;Acc:P21855]
Psip1	1.183	0.876	1.296	0.432	0.92	lens epithelium-derived growth factor; PC4 and SFRS1 interacting protein 2. [Source:RefSeq;Acc:NM_133948]
Laptm5	1.233	1.23	1.13	1.056	0.93	Lysosomal-associated multitransmembrane protein (Retinoic acid- inducible E3 protein). [Source:Uniprot/SWISSPROT;Acc:Q61168]
ENSMUSG00000028590	1.008	1.263	1.521	2.542	1.511	hypothetical protein
Scp2	0.82	1.398	1.417	0.944	0.823	Nonspecific lipid-transfer protein, mitochondrial precursor (NSL-TP) (Sterol carrier protein 2) (SCP-2) (Sterol carrier protein X) (SCP-X) (SCPX). [Source:Uniprot/SWISSPROT;Acc:P32020]
Col9a2	1.593	0.789	1.346	1.016	1.939	Collagen alpha 2(IX) chain precursor. [Source:Uniprot/SWISSPROT;Acc:Q07643]
Ermap	0.308	4.273	2.069	1.122	1.172	erythroblast membrane-associated protein. [Source:RefSeq;Acc:NM_013848]
Kif2c	0.635	0.994	1.507	1.26	1.666	Kinesin-like protein KIF2C (Mitotic centromere-associated kinesin) (MCAK). [Source:Uniprot/SWISSPROT;Acc:Q922S8]
Dmbx1	1.315	0.634	0.596	1.083	0.296	orthodenticle homolog 3; homeobox gene Atx; diencephalon/mesencephalon-expressed brain homeobox 1; orthodenticle 3. [Source:RefSeq;Acc:NM_130865]
BC013476	1.293	0.134	1.578	0.933	1.337	cytochrome P450, family 4, subfamily a, polypeptide 10; cytochrome P450, 4a10. [Source:RefSeq;Acc:NM_010011]
Cyp4a14	0.958	1.29	0.639	0.224	0.712	cytochrome P450, family 4, subfamily a, polypeptide 14; cytochrome P450, 4a14.

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C230096C10Rik	0.729	1.077	0.57	0.767	0.91	RIKEN cDNA C230096C10; KIAA0090 protein-like. [Source:RefSeq;Acc:NM_146157]
BC057625	1.261	1.345	0.792	0.96	0.94	RIKEN cDNA C230096C10; KIAA0090 protein-like. [Source:RefSeq;Acc:NM_146157]
Zcchc17	1.185	0.93	1.539	1.266	0.892	putative S1 RNA binding domain protein; pS1D protein. [Source:RefSeq;Acc:NM_153160]
ENSMUSG00000028786	0.954	2.473	1.749	0.991	1.675	beta-casein-like protein. [Source:RefSeq;Acc:NM_025452]
Eif3s2	1.032	1.281	1.079	1.163	1.077	Eukaryotic translation initiation factor 3 subunit 2 (eIF-3 beta) (eIF3 p36) (eIF3i) (TGF-beta receptor interacting protein 1) (TRIP-1). [Source:Uniprot/SWISSPROT;Acc:Q9QZD9]
Runx3	0.891	0.834	1.148	0.667	1.225	Runt-related transcription factor 3 (Core-binding factor, alpha 3 subunit) (CBF-alpha 3) (Acute myeloid leukemia 2 protein) (Oncogene AML-2) (Polyomavirus enhancer binding protein 2 alpha C subunit) (PEBP2-alpha C) (PEA2-alpha C) (SL3-3 enhancer factor 1 alpha C subunit) (SL3/AKV core-binding factor alpha C subunit). [Source:Uniprot/SWISSPROT;Acc:Q64131]
ENSMUSG00000028851	1.025	1.148	1.374	0.989	1.037	nuclear distribution gene C homolog. [Source:RefSeq;Acc:NM_010948]
Csf3r	1.164	1.078	0.542	0.88	1.133	Granulocyte colony stimulating factor receptor precursor (G-CSF-R). [Source:Uniprot/SWISSPROT;Acc:P40223]
Acot7	0.692	0.792	0.597	1.121	1.165	Cytosolic acyl coenzyme A thioester hydrolase (EC 3.1.2.2) (Long chain acyl-CoA thioester hydrolase) (CTE-II) (Brain acyl-CoA hydrolase). [Source:Uniprot/SWISSPROT;Acc:Q91V12]
ENSMUSG00000028946	0.304	1.059	0.45	1.793	0.965	Transcription factor HES-3 (Hairy and enhancer of split 3). [Source:Uniprot/SWISSPROT;Acc:Q61657]
Tas1r1	0.847	0.721	1.496	1.105	0.664	sweet taste receptor T1r; candidate taste receptor T1R1; G protein-coupled receptor 70. [Source:RefSeq;Acc:NM_031867]

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Uts2	0.907	1.208	1.422	0.831	0.471	Urotensin II precursor (U-II) (UII). [Source:Uniprot/SWISSPROT;Acc:Q9QZQ3]
Errfi1	1.417	0.838	0.724	0.95	1.665	Mitogen-inducible gene 6 protein homolog (Mig-6). [Source:Uniprot/SWISSPROT;Acc:Q99JZ7]
ENSMUSG00000029038	0.979	1.156	0.872	0.773	1.175	hypothetical protein
ENSMUSG00000029047	0.34	1.036	1.489	0.544	1.015	hypothetical protein
ENSMUSG00000029059	1.132	1.217	1.271	1.234	1.485	hypothetical protein
Nadk	1.052	0.916	1.133	0.839	1.168	Putative inorganic polyphosphate/ATP-NAD kinase (EC 2.7.1.23) (Poly(P)/ATP NAD kinase). [Source:Uniprot/SWISSPROT;Acc:P58058]
Sdf4	1.056	0.737	1.162	1.045	1.022	45 kDa calcium-binding protein precursor (Cab45) (Stromal cell-derived factor 4) (SDF-4). [Source:Uniprot/SWISSPROT;Acc:Q61112]
ENSMUSG00000029096	1.243	1.119	0.398	0.949	0.783	Probable serine protease HTRA3 precursor (EC 3.4.21.-) (Toll- associated serine protease). [Source:Uniprot/SWISSPROT;Acc:Q9D236]
Hgfac	0.816	1.271	1.554	0.312	1.026	Hepatocyte growth factor activator precursor (EC 3.4.21.-) (HGF activator) (HGFA). [Source:Uniprot/SWISSPROT;Acc:Q9R098]
Pcdh7	1.04	0.863	0.798	1.157	0.919	protocadherin 7; BH-protocadherin (brain-heart); BH-protocadherin. [Source:RefSeq;Acc:NM_018764]
Zfp509	0.891	1.479	1.47	1.113	1.26	Weakly similar to zinc finger protein 177. [Source:Uniprot/SPTREMBL;Acc:Q8BXX2]
Nrbp1	1.281	1.476	0.712	0.814	0.8	nuclear receptor binding protein; HLS7-interacting protein kinase. [Source:RefSeq;Acc:NM_147201]
ENSMUSG00000029165	1.699	1.561	1.457	1.639	1.359	hypothetical protein
Dhx15	1.337	1.028	0.782	0.872	0.693	Putative pre-mRNA splicing factor RNA helicase (DEAH box protein 15). [Source:Uniprot/SWISSPROT;Acc:O35286]

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Olfr109	0.801	0.938	0.482	0.978	0.71	olfactory receptor 109; GA_x6K02T2PSCP-1914078-1915022; olfactory receptor MOR250-1. [Source:RefSeq;Acc:NM_146835]
BC057606	1.012	0.884	1.588	1.134	0.803	Similar to lymphocyte activation-associated protein. [Source:Uniprot/SPTREMBL;Acc:Q8R334]
BC004084	1.128	1.33	1.293	1.181	0.916	glucosamine-6-phosphate deaminase 2; oscillin; glucosamine-6-phosphate isomerase. [Source:RefSeq;Acc:NM_027681]
Gabra4	0.254	0.265	1.933	0.517	0.567	Gamma-aminobutyric-acid receptor alpha-4 subunit precursor (GABA(A) receptor). [Source:Uniprot/SWISSPROT;Acc:Q9D6F4]
ENSMUSG00000029215	0.418	0.64	0.619	1.12	0.814	hypothetical protein
Rest	1.076	2.561	1.517	0.665	1.014	RE1-silencing transcription factor. [Source:RefSeq;Acc:NM_011263]
AW496103	0.802	0.792	0.532	0.871	1.31	Zinc finger protein Gfi-1 (Growth factor independence-1). [Source:Uniprot/SWISSPROT;Acc:P70338]
ENSMUSG00000029280	0.911	0.81	0.712	1.11	1.065	Submaxillary gland androgen regulated protein 1 precursor (Salivary protein MSG1). [Source:Uniprot/SWISSPROT;Acc:Q61900]
Cdc7	1.803	0.592	1.988	1.512	1.166	Cell division cycle 7-related protein kinase (EC 2.7.1.-) (CDC7- related kinase) (muCdc7). [Source:Uniprot/SWISSPROT;Acc:Q9Z0H0]
BC050858	0.773	1.3	1.216	1.196	1.409	RasGEF domain family, member 1B; GPI-gamma 4. [Source:RefSeq;Acc:NM_145839]
Prkg2	1.852	1.049	1.695	0.724	1.666	cGMP-dependent protein kinase 2 (EC 2.7.1.37) (CGK 2) (cGKII) (Type II cGMP-dependent protein kinase). [Source:Uniprot/SWISSPROT;Acc:Q61410]
Cxcl1	0.781	0.379	0.262	0.793	0.508	Growth regulated alpha protein precursor (CXCL1) (Platelet-derived growth factor-inducible protein KC) (Secretory protein N51) [Contains: (KC(5-72)) (KC-T) (Hematopoietic synergistic factor) (HSF)]. [Source:Uniprot/SWISSPROT;Acc:P12850]

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Eif2b1	0.857	1.609	1.796	1.526	0.916	Translation initiation factor eIF-2B alpha subunit (eIF-2B GDP-GTP exchange factor). [Source:Uniprot/SWISSPROT;Acc:Q99LC8]
Mphosph9	1.086	1.362	1.401	0.657	1.201	M-phase phosphoprotein 9 isoform 1
U90926	1.108	0.41	0.263	1.273	1.336	Putative TNF-resistance related protein. [Source:Uniprot/SPTREMBL;Acc:O08546]
Asahl	1.242	0.996	1.386	0.961	1.245	N-acylsphingosine amidohydrolase (acid ceramidase)-like. [Source:RefSeq;Acc:NM_025972]
Scarb2	1.008	1.436	1.406	1.042	0.913	scavenger receptor class B, member 2; CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 2; LIMP II. [Source:RefSeq;Acc:NM_007644]
Wdr66	1.028	0.609	2.046	1.19	1.312	WD repeat domain 66
Camkk2	1.085	1.681	0.811	1.112	0.989	calcium/calmodulin-dependent protein kinase kinase 2, beta. [Source:RefSeq;Acc:NM_145358]
St7	1.182	0.823	0.598	0.759	0.796	suppression of tumorigenicity 7; family with sequence similarity 4, subfamily A, member 2. [Source:RefSeq;Acc:NM_022332]
Uncx4.1	1.463	0.657	1.731	1.211	0.666	Unc4.1 homeobox. [Source:RefSeq;Acc:NM_013702]
Tes	0.866	0.823	0.704	0.746	1.218	Testin (TES1/TES2). [Source:Uniprot/SWISSPROT;Acc:P47226]
Pomp	0.934	0.908	1.235	1.092	1.291	proteasome maturation protein
Perq1	1.065	0.698	0.647	1.053	0.872	PERQ amino acid rich with GYF domain protein 1. [Source:Uniprot/SWISSPROT;Acc:Q99MR1]
Asns	1.316	0.808	0.756	1.044	1.374	Asparagine synthetase [glutamine-hydrolyzing] (EC 6.3.5.4) (Glutamine-dependent asparagine synthetase). [Source:Uniprot/SWISSPROT;Acc:Q61024]
Cald1	1.052	0.588	1.556	0.898	0.858	caldesmon 1; EST AI195384. [Source:RefSeq;Acc:NM_145575]
ENSMUSG00000029875	1.405	1.033	0.543	3.643	1.263	hypothetical protein
Mrps33	0.838	0.873	1.073	0.979	0.571	Mitochondrial 28S ribosomal protein S33 (S33mt) (MRP-S33) (Ganglioside-induced differentiation-associated-protein 3). [Source:Uniprot/SWISSPROT;Acc:Q9D2R8]
Mkrn1	1.115	1.265	1.27	1.027	0.791	Makorin 1.

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Tbxas1	0.842	1.215	1.241	0.905	1.145	Thromboxane-A synthase (EC 5.3.99.5) (TXA synthase) (TXS) (TS). [Source:Uniprot/SWISSPROT;Acc:P36423]
ENSMUSG00000030055	1.392	0.96	1.671	0.903	0.894	Ras-related protein Rab. [Source:RefSeq;Acc:NM_133717]
Frmd4b	0.952	0.888	0.509	1.086	1.015	GRP1-binding protein GRSP1; GRP1 binding protein GRSP1; Golgi-associated band 4.1-like. [Source:RefSeq;Acc:NM_145148]
ENSMUSG00000030067	0.954	0.709	0.662	0.87	0.944	Forkhead box protein P1 (Forkhead-related transcription factor 1). [Source:Uniprot/SWISSPROT;Acc:P58462]
Rybp	0.803	0.851	0.681	0.889	1.391	RING1 and YY1 binding protein
Bhlhb2	1.272	1.101	0.742	0.994	1.503	Class B basic helix-loop-helix protein 2 (bHLHB2) (Stimulated with retinoic acid 13) (E47 interaction protein 1) (eipl). [Source:Uniprot/SWISSPROT;Acc:O35185]
ENSMUSG00000030154	0.888	0.484	2.034	0.899	1.745	NKR-P1F. [Source:RefSeq;Acc:NM_153094]
Olr1	1.587	1.542	1.413	0.946	0.399	oxidized low density lipoprotein (lectin-like) receptor 1; oxidised low density lipoprotein (lectin-like) receptor 1. [Source:RefSeq;Acc:NM_138648]
Klra1	0.999	1.157	0.469	1.931	1.477	Killer cell lectin-like receptor 4 (T-cell surface glycoprotein Ly- 49D) (Ly49-D antigen) (Lymphocyte antigen 49D). [Source:Uniprot/SWISSPROT;Acc:Q60651]
Klra4	1.659	2.721	1.675	0.771	1.651	Killer cell lectin-like receptor 4 (T-cell surface glycoprotein Ly- 49D) (Ly49-D antigen) (Lymphocyte antigen 49D). [Source:Uniprot/SWISSPROT;Acc:Q60651]
Klra2	0.611	0.769	0.718	0.985	1.016	Killer cell lectin-like receptor 2 (T-cell surface glycoprotein Ly- 49B) (Ly49-B antigen) (Lymphocyte antigen 49B). [Source:Uniprot/SWISSPROT;Acc:Q60660]
Dusp16	0.946	0.658	0.504	0.952	1.102	dual specificity phosphatase 16. [Source:RefSeq;Acc:NM_181320]
ENSMUSG00000030203	0.698	0.522	0.718	0.982	0.781	dual specificity phosphatase 16. [Source:RefSeq;Acc:NM_181320]
Ldhb	1.096	0.903	1.276	0.878	1.08	L-lactate dehydrogenase B chain (EC 1.1.1.27) (LDH-B) (LDH heart subunit) (LDH-H). [Source:Uniprot/SWISSPROT;Acc:P16125]
Mtmr14	1.016	0.857	0.764	0.961	1.183	myotubularin related protein 14

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Ergic2	1.035	1.306	0.585	0.684	0.901	PTX1 protein isoform 1
Tspan9	1.01	1.549	2.154	1.488	1.096	tetraspan NET-5
Tead4	1.067	0.48	0.554	0.803	0.564	Transcriptional enhancer factor TEF-3 (TEA domain family member 4) (TEAD-4) (ETF-related factor-2) (ETFR-2) (TEF-1-related factor 1) (TEF-1-related factor FR-19) (RTEF-1). [Source:Uniprot/SWISSPROT;Acc:Q62296]
Strn4	1.006	1.238	0.894	0.947	0.789	Striatin 4 (Zinedin). [Source:Uniprot/SWISSPROT;Acc:P58404]
Dmwd	0.115	0.644	1.813	1.112	0.994	Dystrophia myotonica-containing WD repeat motif protein (DMR-N9 protein). [Source:Uniprot/SWISSPROT;Acc:Q08274]
ENSMUSG00000030424	0.917	0.734	0.733	0.858	1.178	hypothetical protein
Asb7	1.242	1.422	0.747	1.061	1.057	Ankyrin repeat and SOCS box containing protein 7 (ASB-7). [Source:Uniprot/SWISSPROT;Acc:Q91ZU0]
H47	0.977	1.274	1.307	1.515	0.981	Selenoprotein S (Minor histocompatibility antigen H47). [Source:Uniprot/SWISSPROT;Acc:Q9BCZ4]
Tjp1	1.242	1.219	0.79	1.147	1.165	Tight junction protein ZO-1 (Zonula occludens 1 protein) (Zona occludens 1 protein) (Tight junction protein 1). [Source:Uniprot/SWISSPROT;Acc:P39447]
ENSMUSG00000030529	1.385	1.092	0.743	0.827	0.795	hypothetical protein
BY455730	1.042	1.132	1.305	1.158	1.065	Isocitrate dehydrogenase [NADP], mitochondrial precursor (EC 1.1.1.42) (Oxalosuccinate decarboxylase) (IDH) (NADP+specific ICDH) (IDP) (ICD- M). [Source:Uniprot/SWISSPROT;Acc:P54071]
ENSMUSG00000030554	2.279	1.171	0.358	0.644	1.036	desmuslin isoform H. [Source:RefSeq;Acc:NM_201639]
Tyrobp	0.943	1.317	1.174	0.903	1.139	TYRO protein tyrosine kinase-binding protein precursor (DNAX- activation protein 12) (KAR-associated protein). [Source:Uniprot/SWISSPROT;Acc:O54885]
Mfge8	0.864	2.427	1.707	1.068	0.789	Lactadherin precursor (Milk fat globule-EGF factor 8) (MFG-E8) (MFGM) (Sperm surface protein SP47) (MP47). [Source:Uniprot/SWISSPROT;Acc:P21956]

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Coq7	0.741	0.806	0.659	1.256	0.973	Ubiquinone biosynthesis protein COQ7 homolog (Coenzyme Q biosynthesis protein 7 homolog) (Timing protein clk-1 homolog). [Source:Uniprot/SWISSPROT;Acc:P97478]
Fchsd2	0.899	0.506	0.685	0.965	1.133	FCH and double SH3 domains 2; cDNA sequence BC034086; SH3 multiple domains 3. [Source:RefSeq;Acc:NM_199012]
Gdpd3	1.478	9.014	6.843	2.235	2.442	glycerophosphodiester phosphodiesterase domain containing 3
Cln3	1.07	1.129	0.687	1.206	1.15	CLN3 protein (Battenin). [Source:Uniprot/SWISSPROT;Acc:Q61124]
Lat	1.131	0.87	1.644	0.892	0.506	Linker for activation of T cells (36 kDa phospho-tyrosine adaptor protein) (pp36) (p36-38). [Source:Uniprot/SWISSPROT;Acc:O54957]
M27960	1.096	0.727	0.7	0.925	1.096	Interleukin-4 receptor alpha chain precursor (IL-4R-alpha). [Source:Uniprot/SWISSPROT;Acc:P16382]
Prkrir	0.573	1.495	1.65	0.637	0.592	52 kDa repressor of the inhibitor of the protein kinase (p58IPK- interacting protein) (58 kDa interferon-induced protein kinase- interacting protein) (P52rIPK) (THAP domain protein 0). [Source:Uniprot/SWISSPROT;Acc:Q9CUX1]
Itgam	0.937	0.869	0.611	0.613	0.916	Integrin alpha-M precursor (Cell surface glycoprotein MAC-1 alpha subunit) (CR-3 alpha chain) (CD11b) (Leukocyte adhesion receptor MO1). [Source:Uniprot/SWISSPROT;Acc:P05555]
Itgax	1.528	5.087	3.859	1.625	1.194	Integrin alpha-X precursor (Leukocyte adhesion glycoprotein p150,95 alpha chain) (Leukocyte adhesion receptor p150,95) (CD11c). [Source:Uniprot/SWISSPROT;Acc:Q9QXH4]
Itgal	1.043	1.102	0.767	0.749	1.345	Integrin alpha-L precursor (Leukocyte adhesion glycoprotein LFA-1 alpha chain) (LFA-1A) (Leukocyte function associated molecule 1, alpha chain) (CD11a). [Source:Uniprot/SWISSPROT;Acc:P24063]
Ush1c	1.306	0.99	1.623	1.123	1.563	Harmonin (Usher syndrome 1C protein homolog) (PDZ domain-containing protein). [Source:Uniprot/SWISSPROT;Acc:Q9ES64]

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Rgs10	0.917	1.644	1.745	1.02	1.299	Regulator of G-protein signaling 10 (RGS10). [Source:Uniprot/SWISSPROT;Acc:Q9CQE5]
Dctn5	1.17	0.821	0.63	1.109	0.764	dynactin 5; dynactin 4; p25 dynactin subunit. [Source:RefSeq;Acc:NM_021608]
Fxc1	0.94	0.915	1.164	0.982	0.996	Mitochondrial import inner membrane translocase subunit TIM9 B. [Source:Uniprot/SWISSPROT;Acc:Q9WV96]
2310008H09Rik	1.144	0.926	1.222	1.177	0.983	TSG118.1 protein. [Source:RefSeq;Acc:NM_023197]
Cask	1.46	0.75	1.243	0.891	1.153	Peripheral plasma membrane protein CASK (EC 2.7.1.-) (Calcium/calmodulin-dependent serine protein kinase). [Source:Uniprot/SWISSPROT;Acc:O70589]
BC051034	1.128	0.841	0.798	1.024	0.757	suppression of tumorigenicity 5 isoform 1. [Source:RefSeq;Acc:NM_001001326]
ENSMUSG00000031088	1.116	1.16	1.766	1.067	0.982	hypothetical protein
Rbmx	0.76	1.179	1.171	1.031	0.867	RNA binding motif protein, X chromosome. [Source:RefSeq;Acc:NM_011252]
Glod5	1.381	0.785	0.344	2.775	1.112	glyoxalase domain containing 5
Dynlt3	0.925	1.339	1.242	1.044	0.971	T-complex associated-testis-expressed 1-like (Protein 91/23). [Source:Uniprot/SWISSPROT;Acc:P56387]
Fundc2	1.151	1.285	1.217	1.118	0.961	FUN14 domain containing 2
Rab39b	1.347	0.761	0.537	0.954	0.273	Ras-related protein Rab-39B. [Source:Uniprot/SWISSPROT;Acc:Q8BHC1]
ENSMUSG00000031207	0.426	0.856	0.624	0.67	1.144	Moesin (Membrane-organizing extension spike protein). [Source:Uniprot/SWISSPROT;Acc:P26041]
Atrx	0.95	0.784	1.37	0.985	2.322	Transcriptional regulator ATRX (X-linked nuclear protein) (Heterochromatin protein 2) (HP1 alpha-interacting protein) (HP1-BP38 protein). [Source:Uniprot/SWISSPROT;Acc:Q61687]
Rs1	0.775	1.903	1.914	0.854	1.084	Retinoschisin precursor (X-linked juvenile retinoschisis protein homolog). [Source:Uniprot/SWISSPROT;Acc:Q9Z1L4]
BC031147	0.809	1.88	1.364	1.181	0.634	PREDICTED: cDNA sequence BC031147 (BC031147)
AV324811	1.342	0.264	1.455	0.914	1.052	X-linked myotubular myopathy gene 1. [Source:Uniprot/SPTREMBL;Acc:Q8BSI3]

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Gabre	0.564	0.211	2.161	1.001	1.489	gamma-aminobutyric acid (GABA-A) receptor, subunit epsilon. [Source:RefSeq;Acc:NM_017369]
Ctps2	0.799	0.855	1.076	0.735	1.055	cytidine 5'-triphosphate synthase 2; CTP synthetase homolog. [Source:RefSeq;Acc:NM_018737]
Uchl5ip	0.725	1.538	0.789	1.159	1.451	26S proteasome-associated UCH37 interacting protein 1. [Source:Uniprot/SWISSPROT;Acc:Q8BKT8]
Zfp92	0.546	1.415	1.672	2.35	0.708	Zinc finger protein 92 (Zfp-92). [Source:Uniprot/SWISSPROT;Acc:Q62396]
G6pdx	0.982	1.312	1.187	0.957	0.873	Glucose-6-phosphate 1-dehydrogenase X (EC 1.1.1.49) (G6PD). [Source:Uniprot/SWISSPROT;Acc:Q00612]
Plp1	1	0.792	0.59	0.815	1.087	Myelin proteolipid protein (PLP) (Lipophilin). [Source:Uniprot/SWISSPROT;Acc:P60202]
F7	1.198	1.504	1.374	1.354	1.229	Coagulation factor VII precursor (EC 3.4.21.21) (Serum prothrombin conversion accelerator). [Source:Uniprot/SWISSPROT;Acc:P70375]
Gpr124	1.441	0.733	0.581	0.947	0.883	Probable G protein-coupled receptor 124 precursor (Tumor endothelial marker 5). [Source:Uniprot/SWISSPROT;Acc:Q91ZV8]
Tnfsf13b	0.602	0.852	1.568	0.784	0.957	Tumor necrosis factor ligand superfamily member 13B (B cell-activating factor) (BAFF). [Source:Uniprot/SWISSPROT;Acc:Q9WU72]
ENSMUSG00000031508	0.992	1.021	1.506	1.228	0.623	Ankyrin repeat domain protein 10. [Source:Uniprot/SWISSPROT;Acc:Q99LW0]
Ap3m2	0.672	1.555	0.841	1.136	1.078	adaptor-related protein complex 3, mu 2 subunit. [Source:RefSeq;Acc:NM_029505]
Adam3	1.473	1.481	1.393	0.948	0.844	a disintegrin and metalloprotease domain 3 (cyritestin); cyritestin. [Source:RefSeq;Acc:NM_009619]
BC010200	1.79	1.197	1.502	1.834	1.115	Basic fibroblast growth factor receptor 1 precursor (EC 2.7.1.112) (FGFR-1) (bFGF-R) (MFR). [Source:Uniprot/SWISSPROT;Acc:P16092]
Fgl1	0.347	2.266	1.435	1.371	1.312	fibrinogen-like protein 1. [Source:RefSeq;Acc:NM_145594]
Klhl2	1.034	1.372	1.562	0.535	1.162	kelch-like 2, Mayven

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
F11	0.75	1.054	0.499	1.602	2.044	Coagulation factor XI precursor (EC 3.4.21.27) (Plasma thromboplastin antecedent) (PTA) (FXI). [Source:Uniprot/SWISSPROT;Acc:Q91Y47]
Gins3	1.165	1.681	1.506	0.965	0.78	GINS complex subunit 3 (Psf3 homolog)
ENSMUSG00000031684	1.172	1.546	0.585	0.816	0.64	hypothetical protein
Gab1	1.291	0.778	0.749	1.015	0.772	GRB2-associated binding protein 1 (GRB2-associated binder-1). [Source:Uniprot/SWISSPROT;Acc:Q9QYY0]
St3gal2	1.411	1.459	1.551	1.302	0.999	CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,3-sialyltransferase (EC 2.4.99.-) (Beta-galactoside alpha-2,3-sialyltransferase) (Alpha 2,3-ST) (Gal-NAc6S) (Gal-beta-1,3-GalNAc-alpha-2,3-sialyltransferase) (ST3GalA.2) (SIAT4-B) (ST3Gal II). [Source:Uniprot/SWISSPROT;Acc:Q11204]
Cox4nb	1.116	1.487	1.684	1.155	0.966	Neighbor of COX4. [Source:Uniprot/SWISSPROT;Acc:O70378]
Mbtps1	0.83	1.154	1.246	1.074	0.77	Membrane-bound transcription factor site-1 protease precursor (EC 3.4.21.-) (Site-1 protease) (Subtilisin/kexin isozyme-1) (SKI-1) (Sterol-regulated luminal protease). [Source:Uniprot/SWISSPROT;Acc:Q9WTZ2]
Hsbp1	0.931	1.147	1.427	0.976	0.975	heat shock factor binding protein 1. [Source:RefSeq;Acc:NM_024219]
2310079N02Rik	1.044	1.151	1.197	1.092	1.355	hypothetical protein LOC66566
Cyb5b	0.965	1.308	1.145	0.864	1.457	cytochrome b5 outer mitochondrial membrane precursor. [Source:RefSeq;Acc:NM_025558]
Mre11a	0.936	1.181	1.978	0.753	0.821	Double-strand break repair protein MRE11A (MRE11 homolog 1) (MmMRE11A). [Source:Uniprot/SWISSPROT;Acc:Q61216]
ENSMUSG00000031933	0.507	2.814	0.522	1.147	1.091	folate receptor 4 (delta). [Source:RefSeq;Acc:NM_022888]
Panx1	1.518	1.866	1.764	0.908	1.356	Pannexin 1. [Source:Uniprot/SWISSPROT;Acc:Q9JIP4]

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ENSMUSG00000031960	1.397	1.174	0.552	0.917	1.271	Alanyl-tRNA synthetase (EC 6.1.1.7) (Alanine--tRNA ligase) (AlaRS). [Source:Uniprot/SWISSPROT;Acc:Q8BGQ7]
Acad8	0.905	1.009	1.163	1.028	0.86	Acyl-CoA dehydrogenase family member 8, mitochondrial precursor (EC 1.3.99.-) (ACAD-8) (Isobutyryl-CoA dehydrogenase). [Source:Uniprot/SWISSPROT;Acc:Q9D7B6]
Agt	1.119	0.867	1.311	2.309	1.112	Angiotensinogen precursor [Contains: Angiotensin I (Ang I); Angiotensin II (Ang II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin II)]. [Source:Uniprot/SWISSPROT;Acc:P11859]
Capn9	0.797	1.4	0.726	1.317	0.894	Calpain 9 (EC 3.4.22.-) (Digestive tract-specific calpain) (nCL-4). [Source:Uniprot/SWISSPROT;Acc:Q9D805]
2810004N23Rik	1.171	1.26	1.937	1.285	1.113	hypothetical protein LOC66523
Snx19	0.979	1.289	1.362	1.055	1.028	sorting nexin 19. [Source:RefSeq;Acc:NM_028874]
Birc3	1.072	0.78	0.773	0.927	1.045	Baculoviral IAP repeat-containing protein 3 (Inhibitor of apoptosis protein 1) (MIAP1) (MIAP-1). [Source:Uniprot/SWISSPROT;Acc:O08863]
Abhd12	0.986	1.141	1.241	1.012	0.788	abhydrolase domain containing 12
Ddx25	0.467	1.258	1.491	2.989	1.399	ATP-dependent RNA helicase DDX25 (DEAD-box protein 25) (Gonadotropin-regulated testicular RNA helicase). [Source:Uniprot/SWISSPROT;Acc:Q9QY15]
ENSMUSG00000032134	1.356	1.61	1.63	1.033	1.29	hypothetical protien
BC044786	0.829	1.021	1.788	2.627	1.206	cAMP-dependent 3',5'-cyclic phosphodiesterase 4A (EC 3.1.4.17). [Source:Uniprot/SWISSPROT;Acc:O89084]
Carm1	0.914	0.657	1.951	0.337	1.269	coactivator-associated arginine methyltransferase 1; protein arginine methyltransferase. [Source:RefSeq;Acc:NM_021531]
Sh3bgrl2	0.275	1.101	0.721	1.178	0.759	SH3 domain-binding glutamic acid-rich-like protein 2. [Source:Uniprot/SWISSPROT;Acc:Q8BG73]

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Grg-3	0.909	0.811	0.586	1.472	0.77	Transducin-like enhancer protein 3 (ESG) (Grg-3). [Source:Uniprot/SWISSPROT;Acc:Q08122]
Pstpip1	0.687	0.92	0.797	1.021	1.046	proline-serine-threonine phosphatase-interacting protein 1. [Source:RefSeq;Acc:NM_011193]
Dapk2	1.379	1.831	1.611	1.108	1.837	Death-associated protein kinase 2 (EC 2.7.1.37) (DAP kinase 2) (DAP- kinase related protein 1) (DRP-1). [Source:Uniprot/SWISSPROT;Acc:Q8VDF3]
Spg21	1.118	1.061	1.341	1.053	1.148	spastic paraplegia 21 homolog. [Source:RefSeq;Acc:NM_138584]
ENSMUSG00000032407	0.931	0.919	0.598	1.086	1.405	hypothetical protein
Tfdp2	0.934	1.662	1.821	1.229	0.855	Transcription factor Dp-2 (E2F dimerization partner 2) (Dp-3). [Source:Uniprot/SWISSPROT;Acc:Q64163]
Tgfbr2	0.967	1.5	1.503	0.803	1.14	TGF-beta receptor type II precursor (EC 2.7.1.37) (TGFR-2) (TGF-beta type II receptor). [Source:Uniprot/SWISSPROT;Acc:Q62312]
Cldn18	1.109	0.623	1.712	0.698	0.45	Claudin-18. [Source:Uniprot/SWISSPROT;Acc:P56857]
Ptgs2	0.902	0.382	0.34	1.258	1.267	Prostaglandin G/H synthase 2 precursor (EC 1.14.99.1) (Cyclooxygenase -2) (COX-2) (Prostaglandin-endoperoxide synthase 2) (Prostaglandin H2 synthase 2) (PGH synthase 2) (PGHS-2) (PHS II) (Glucocorticoid- regulated inflammatory cyclooxygenase) (Gripghs) (TIS10 protein) (Macrophage activation-associated marker protein P71/73) (PES-2). [Source:Uniprot/SWISSPROT;Acc:Q05769]
Ltf	1.487	1.021	1.825	0.633	0.832	Lactotransferrin precursor (Lactoferrin). [Source:Uniprot/SWISSPROT;Acc:P08071]
Trib1	1.002	1.217	0.67	0.76	1.11	tribbles homolog 1. [Source:RefSeq;Acc:NM_144549]
Nktr	0.992	0.897	0.864	1.245	1.163	NK-tumor recognition protein (Natural-killer cells cyclophilin-related protein) (NK-TR protein). [Source:Uniprot/SWISSPROT;Acc:P30415]
ENSMUSG00000032562	0.623	1.168	1.325	1.533	1.25	Guanine nucleotide-binding protein G(i), alpha-2 subunit (Adenylate cyclase-inhibiting G alpha protein). [Source:Uniprot/SWISSPROT;Acc:P08752]

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
ENSMUSG00000032565	1.048	1.308	0.438	0.897	1.024	hypothetical protein
Cish	1.175	0.893	0.441	1.108	0.949	Cytokine-inducible SH2-containing protein (CIS) (CIS-1) (Suppressor of cytokine signaling) (SOCS). [Source:Uniprot/SWISSPROT;Acc:Q62225]
Bsn	2.139	0.99	1.372	0.982	1.906	bassoon; presynaptic cytomatrix protein. [Source:RefSeq;Acc:NM_007567]
AK173072	1.044	1.334	1.702	1.47	0.887	hypothetical protein
ENSMUSG00000032654	1.536	1.518	1.931	1.235	1.61	hypothetical protein
Troap	0.477	1.063	0.697	1.106	0.75	Weakly similar to trophinin-associated protein. [Source:Uniprot/SPTREMBL;Acc:Q8BWP3]
Tas2r140	0.736	1.701	1.834	1.882	0.892	Putative taste receptor type 2 member 40 (T2r40) (mt2r64). [Source:Uniprot/SWISSPROT;Acc:Q7TQA4]
Fanca	1.713	0.854	0.706	1.129	1.045	Fanconi anemia, complementation group A. [Source:RefSeq;Acc:NM_016925]
P2ry2	0.939	0.781	0.68	0.947	1.238	P2Y purinoceptor 2 (P2Y2) (P2U purinoceptor 1) (P2U1) (ATP receptor) (Purinergic receptor). [Source:Uniprot/SWISSPROT;Acc:P35383]
ENSMUSG00000033083	0.976	1.184	0.739	1.612	1.168	TBC1 domain family, member 4. [Source:RefSeq;Acc:NM_173380]
Rnf125	0.489	0.633	1.258	1.016	0.297	ring finger protein 125. [Source:RefSeq;Acc:NM_026301]
AK129187	0.614	1.061	0.643	1.69	0.862	Jumonji domain containing protein 2A (Fragment). [Source:Uniprot/SWISSPROT;Acc:Q8BW72]
L31398	0.9	1.953	0.599	0.838	1.124	Dynamin 2 (EC 3.6.5.5) (Dynamin UDNM). [Source:Uniprot/SWISSPROT;Acc:P39054]
Usp37	0.873	1.651	1.811	2.068	1.06	ubiquitin specific protease 37
Frrs1	1.188	1.078	1.112	1.187	0.972	stromal cell derived factor receptor 2. [Source:RefSeq;Acc:NM_009146]
BQ715189	0.84	0.643	1.432	0.455	1.028	hypothetical protein
Pnkd	0.976	1.249	1.382	1.098	0.834	brain protein 17; trans-activated by hepatitis C virus core protein 2; myofibrillogenesis regulator 1.

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Upb1	1.167	0.828	0.577	0.974	1.181	ureidopropionase, beta. [Source:RefSeq;Acc:NM_133995]
ENSMUSG00000033509	0.849	1.175	0.608	1.567	1.311	hypothetical protein
Znrf1	0.826	0.695	0.614	0.892	1.16	zinc ring finger protein 1; peripheral nerve injury protein nin283; ring finger protein 42. [Source:RefSeq;Acc:NM_133206]
Caskin1	1.493	1.152	2.673	1.378	0.859	CASK interacting protein 1. [Source:RefSeq;Acc:NM_027937]
Ptplad1	1.325	1.248	1.232	1.072	0.809	butyrate-induced transcript 1. [Source:RefSeq;Acc:NM_021345]
Acbd6	0.923	1.637	1.2	1.368	1.164	acyl-Coenzyme A binding domain containing 6. [Source:RefSeq;Acc:NM_028250]
Sfxn5	1.195	0.783	1.219	0.953	1.188	Sideroflexin 5. [Source:Uniprot/SWISSPROT;Acc:Q925N0]
Emx1	0.952	1.423	1.711	0.122	0.82	Homeobox protein EMX1 (Fragment). [Source:Uniprot/SWISSPROT;Acc:Q04742]
St18	0.238	0.663	0.597	0.961	1.063	suppression of tumorigenicity 18; breast carcinoma. [Source:RefSeq;Acc:NM_173868]
Exoc6b	0.631	0.832	0.609	0.886	1.364	Weakly similar to RSEC15. [Source:Uniprot/SPTREMBL;Acc:Q8C203]
Tlr13	0.839	2.247	1.404	0.869	1.175	toll-like receptor 13. [Source:RefSeq;Acc:NM_205820]
Rbm35b	0.295	0.646	1.476	0.95	1.2	RNA binding motif protein 35b
Foxh1	1.072	1	1.146	1.174	1.753	Forkhead box protein H1 (Forkhead activin signal transducer 1) (Fast- 1) (Forkhead activin signal transducer 2) (Fast-2). [Source:Uniprot/SWISSPROT;Acc:O88621]
ENSMUSG00000033869	1.298	0.89	1.557	0.891	1.128	hypothetical protein
Mir16	1.153	2.107	1.534	1.462	1.379	membrane interacting protein of RGS16. [Source:RefSeq;Acc:NM_019580]
ENSMUSG00000033924	1.057	0.912	1.508	1.153	1.107	hypothetical protein
6720456B07Rik	0.73	1.186	1.362	0.695	0.854	hypothetical protein LOC101314
ENSMUSG00000033941	0.595	1.242	0.734	0.706	1.396	hypothetical protein

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
BC058639	1.007	0.997	0.683	1.241	0.76	182 kDa tankyrase 1-binding protein (Fragment). [Source:Uniprot/SWISSPROT;Acc:P58871]
BC050789	0.758	1.173	1.615	1.316	1.031	cDNA sequence BC050789 (BC050789)
6430527G18Rik	0.786	0.749	0.847	0.631	0.891	hypothetical protein LOC238330
Hsdl1	0.65	0.645	1.343	0.937	1.473	hydroxysteroid dehydrogenase like 1
Mrps17	0.94	1.02	1.447	0.984	0.904	28S ribosomal protein S17, mitochondrial precursor (MRP-S17). [Source:Uniprot/SWISSPROT;Acc:Q9CQE3]
ENSMUSG00000034226	0.618	1.053	0.612	1.024	1.516	ras homolog gene family, member V. [Source:RefSeq;Acc:NM_145530]
ENSMUSG00000034255	1	0.947	0.6	1.32	0.807	hypothetical protein
Batf	1.073	0.707	0.71	1.206	0.982	ATF-like basic leucine zipper transcription factor B-ATF. [Source:Uniprot/SWISSPROT;Acc:O35284]
ENSMUSG00000034437	0.634	0.686	0.593	0.747	1.1	Splicing factor. [Source:Uniprot/SPTREMBL;Acc:Q8C3H6]
ENSMUSG00000034579	1.572	0.961	1.645	1.366	0.37	hypothetical protein
Tmem109	1.183	0.987	1.286	0.902	0.968	mitsugumin 23. [Source:RefSeq;Acc:NM_134142]
Pbx2	0.73	0.496	1.999	0.978	0.954	pre B-cell leukemia transcription factor 2
Ttyh2	1.258	1.4	1.251	1.012	1.129	tweety homolog 2. [Source:RefSeq;Acc:NM_053273]
ENSMUSG00000034731	2.548	2.059	1.478	0.496	1.112	hypothetical protein
ENSMUSG00000034753	1.014	1.092	1.23	0.988	1.003	hypothetical protein
Unc13a	1.286	1.141	1.495	2.291	0.357	unc-13 homolog A
AK173222	1.543	0.92	0.515	1.652	1.44	PREDICTED: cDNA sequence BC053460 (BC053460)
Ap1gbp1	1.377	0.963	0.687	1.228	1.061	AP1 gamma subunit binding protein 1; EST AF007009. [Source:RefSeq;Acc:NM_194341]

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ENSMUSG00000034951	1.217	1.686	1.416	1.035	1.075	PREDICTED: RIKEN cDNA 5630400E24 gene (5630400E24Rik)
1700047I17Rik	1.063	0.933	0.669	1.257	0.892	hypothetical protein LOC73385
Anapc13	0.898	0.976	1.302	1.204	0.96	anaphase promoting complex subunit 13. [Source:RefSeq;Acc:NM_181394]
Rrp12	1.003	1.337	0.574	0.948	0.68	ribosomal RNA processing 12 homolog
Oma1	0.698	1.164	1.529	0.91	1.073	OMA1 homolog, zinc metallopeptidase
Ints6	0.895	1.088	0.717	0.99	0.981	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26; Notch2-like. [Source:RefSeq;Acc:NM_008715]
Tanc1	0.457	0.702	1.492	1.572	0.631	MKIAA1728 protein (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8CHA0]
Arl6ip5	0.974	4.739	1.254	0.964	0.947	ADP-ribosylation factor-like 6 interacting protein 5; ADP-ribosylation-like factor 6 interacting protein 5. [Source:RefSeq;Acc:NM_022992]
Leprot	1.14	0.986	1.22	0.971	1.19	Leptin receptor gene-related protein (OB-R gene related protein) (OB- RGRP). [Source:Uniprot/SWISSPROT;Acc:O89013]
Hel308	1.451	2.237	2.405	1.518	1.572	DNA helicase HEL308 (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8R4K9]
ENSMUSG00000035266	0.943	0.801	0.423	0.924	1.115	DNA helicase HEL308 (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8R4K9]
Hpse	1.202	1.433	1.242	1.051	0.95	heparanase; endoglycosidase heparanase. [Source:RefSeq;Acc:NM_152803]
ENSMUSG00000035335	0.865	0.971	0.566	1.162	1.13	hypothetical protein
Nfkbiz	1.454	0.368	0.235	0.898	1.012	expreexpressed sequence AA408868; molecule possessing ankyrin-repeats induced by lipopolysaccharide; IkappaB-zeta. [Source:RefSeq;Acc:NM_030612]
Ptplb	0.455	0.921	0.831	1.223	0.933	protein tyrosine phosphatase-like protein PTPLB. [Source:RefSeq;Acc:NM_023587]
Shq1	1.448	1.547	2.013	1.928	0.737	SHQ1 homolog
Ccl2	0.648	0.77	0.743	1.529	1.809	Small inducible cytokine A2 precursor (CCL2) (Monocyte chemotactic protein 1) (MCP-1) (Monocyte chemoattractant protein-1) (Platelet- derived growth factor-inducible protein JE). [Source:Uniprot/SWISSPROT;Acc:P10148]
Gm93	1.454	0.943	2.354	1.499	1.444	hypothetical protein LOC225497

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CA465142	1.474	0.854	1.594	0.967	2.392	hypothetical protein
Muc20	1.445	1.772	0.713	0.958	1.462	mucin 20; cDNA sequence BC026367. [Source:RefSeq;Acc:NM_146071]
ENSMUSG00000035666	0.883	0.982	1.406	0.769	0.954	General transcription factor 3C polypeptide 4 (EC 2.3.1.48) (Transcription factor IIIC-delta subunit) (TF3C-delta) (TFIIIC 90 kDa subunit) (TFIIIC 90). [Source:Uniprot/SWISSPROT;Acc:Q8BMQ2]
Tnfsf9	0.684	0.515	0.465	1.164	1.2	Tumor necrosis factor ligand superfamily member 9 (4-1BB ligand) (4- 1BBL). [Source:Uniprot/SWISSPROT;Acc:P41274]
Hmha1	1.075	1.33	1.156	0.908	0.795	minor histocompatibility antigen HA-1
ENSMUSG00000035714	1.077	0.451	1.273	1.442	0.982	hypothetical protein
Bbs10	1.222	0.36	1.919	1.236	0.982	hypothetical protein LOC71769 isoform 1
Dync1li2	1.28	1.867	1.429	1.044	1.061	dynein, cytoplasmic, light intermediate polypeptide 2
ENSMUSG00000035778	1.301	0.79	0.385	0.957	0.584	N-acetyllactosaminide alpha-1,3-galactosyltransferase (EC 2.4.1.87) (Galactosyltransferase) (UDP-galactose:beta-D-galactosyl-1,4-N-acetyl-D-glucosaminide alpha-1,3-galactosyltransferase). [Source:Uniprot/SWISSPROT;Acc:P23336]
Mlc1	0.477	1.2	1.764	1.503	1.313	Membrane protein MLC1. [Source:Uniprot/SWISSPROT;Acc:Q8VHK5]
Krt25	1.169	1.073	0.386	2.071	0.559	keratin 25A
Pawr	0.952	0.95	0.527	1.287	0.41	PRKC, apoptosis, WT1, regulator
ENSMUSG00000035916	1.617	1.17	0.631	3.074	1.096	PREDICTED: protein tyrosine phosphatase, receptor type, Q (Ptprq)
Myf6	2.156	1.171	0.779	1.596	1.67	Myogenic factor 6 (Myf-6) (Herculin). [Source:Uniprot/SWISSPROT;Acc:P15375]
D030022P06Rik	1.24	0.729	1.434	1.572	0.71	Snf2-related CBP activator protein isoform 1
Fnip1	1.036	0.972	0.669	0.981	0.484	MKIAA1961 protein (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q80T72]
ENSMUSG00000036016	0.906	0.582	0.765	0.703	0.618	PREDICTED: similar to putative pheromone receptor (LOC224546)

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Dnajb5	0.647	0.758	0.561	1.156	1.216	DnaJ homolog subfamily B member 5 (Heat shock protein Hsp40-3) (Heat shock protein cognate 40) (Hsc40). [Source:Uniprot/SWISSPROT;Acc:O89114]
Slc2a6	1.196	0.844	0.785	1.031	0.797	solute carrier family 2 (facilitated glucose transporter), member 6. [Source:RefSeq;Acc:NM_172659]
Slain2	1.036	1.034	1.49	1.01	0.726	SLAIN motif family, member 2
Metap2	1.107	0.881	1.224	1.035	0.818	Methionine aminopeptidase 2 (EC 3.4.11.18) (MetAP 2) (Peptidase M 2) (Initiation factor 2 associated 67 kDa glycoprotein) (p67) (p67eIF2). [Source:Uniprot/SWISSPROT;Acc:O08663]
ENSMUSG00000036120	0.761	0.933	1.792	1.168	0.5	DNA-binding protein RFXANK (Regulatory factor X subunit B) (RFX-B) (Regulatory factor X-associated ankyrin-containing protein) (Ankyrin repeat-containing adapter protein Tvl-1). [Source:Uniprot/SWISSPROT;Acc:Q9Z205]
Meox2	0.807	1.15	2.256	1.575	1.422	Homeobox protein MOX-2 (Mesenchyme homeobox 2). [Source:Uniprot/SWISSPROT;Acc:P32443]
Pphln1	0.713	0.805	0.471	0.944	1.308	Periphilin 1. [Source:Uniprot/SWISSPROT;Acc:Q8K2H1]
Hist1h1c	0.948	1.198	1.553	1.15	0.998	Histone H1.2 (H1 VAR.1) (H1C). [Source:Uniprot/SWISSPROT;Acc:P15864]
Ndufa13	0.832	1.589	1.285	1.201	0.895	NADH-ubiquinone oxidoreductase B16.6 subunit (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-B16.6) (CI-B16.6) (Gene associated with retinoic-interferon-induced mortality 19 protein) (GRIM-19) (Cell death-regulatory protein GRIM-19). [Source:Uniprot/SWISSPROT;Acc:Q9ERS2]
2810433K01Rik	1.471	1.525	1.688	2.328	0.669	hypothetical protein LOC66468
Snapc4	0.889	0.915	1.205	0.744	0.754	small nuclear RNA activating complex, polypeptide 4. [Source:RefSeq;Acc:NM_172339]
Fsip2	0.506	0.809	0.658	0.933	0.759	similar to FLJ44048 protein
AV275869	1.43	3.069	1.658	1.212	0.857	Hypothetical protein
ENSMUSG00000036466	0.735	1.177	1.673	1.206	0.666	hypothetical protein
AK122555	1.062	0.154	1.356	0.942	1.466	hypothetical protien

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ENSMUSG00000036480	1.746	0.198	0.524	1.95	0.601	PREDICTED: RIKEN cDNA 1700027L20 gene (1700027L20Rik)
Card11	0.789	1.407	1.888	1.496	0.893	caspase recruitment domain family, member 11. [Source:RefSeq;Acc:NM_175362]
2310005P05Rik	1.005	1.234	0.619	0.74	1.786	hypothetical protein LOC67484
Tcte3	1.349	1.033	1.411	0.778	1.42	T complex testis-specific protein 2 (TCTEX-2). [Source:Uniprot/SWISSPROT;Acc:P11985]
Olfr701	0.9	0.568	1.509	1.349	0.728	olfactory receptor 701; olfactory receptor MOR283-1; GA_x6K02T2PBJ9-9195805-9196755. [Source:RefSeq;Acc:NM_028910]
Mbd5	0.871	0.837	1.46	1.227	1.209	methyl-CpG binding domain protein 5
ENSMUSG00000036849	0.566	0.784	1.396	2.859	0.836	hypothetical protien
Phkb	0.917	1.518	0.564	0.823	0.85	phosphorylase kinase beta
C1qb	0.771	0.948	1.381	0.785	0.679	Complement C1q subcomponent, B chain precursor. [Source:Uniprot/SWISSPROT;Acc:P14106]
4930549C01Rik	1.313	0.097	0.533	2.422	0.883	hypothetical protein LOC67663
Htr1d	1.155	1.492	1.891	1.239	1.219	5-hydroxytryptamine 1D receptor (5-HT-1D) (Serotonin receptor 1D). [Source:Uniprot/SWISSPROT;Acc:Q61224]
Clca5	0.958	0.1	2.451	1.303	1.936	chloride channel calcium activated 5
ENSMUSG00000036969	1.761	0.852	1.784	1.939	0.373	T-cell receptor beta chain V region 3H.25 precursor. [Source:Uniprot/SWISSPROT;Acc:P01734]
BC020990	0.933	1.474	1.492	1.383	1.209	Probable transcription factor PML. [Source:Uniprot/SWISSPROT;Acc:Q60953]
Otud4	0.575	1.845	0.678	0.628	0.526	MKIAA1046 protein (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q80TL3]
Tenc1	0.861	0.792	0.699	0.859	0.897	C1 domain-containing phosphatase and tensin-like protein; tensin 2. [Source:RefSeq;Acc:NM_153533]
Myom3	1.425	0.805	1.671	1.346	1.849	myomesin family, member 3
Nodal	0.62	0.937	1.569	2.357	0.431	Nodal precursor. [Source:Uniprot/SWISSPROT;Acc:P43021]
ENSMUSG00000037188	1.781	0.929	1.263	1.752	1.089	hypothetical protien

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Prf1	0.979	1.139	1.107	0.175	0.718	Perforin 1 precursor (P1) (Lymphocyte pore forming protein) (Cytolysin). [Source:Uniprot/SWISSPROT;Acc:P10820]
Clic4	1.329	1.252	0.83	1.115	1.004	Chloride intracellular channel protein 4 (mc3s5/mtCLIC). [Source:Uniprot/SWISSPROT;Acc:Q9QYB1]
ENSMUSG00000037243	0.636	1.787	1.799	1.743	0.762	hypothetical protein
ENSMUSG00000037331	0.631	1.393	1.328	1.317	0.952	hypothetical protein
2410018C17Rik	1.006	0.965	1.357	1.021	0.591	dorsal neural-tube nuclear protein
Arid5a	0.622	1.009	1.836	1.603	1.55	modulator recognition factor I. [Source:RefSeq;Acc:NM_145996]
Rps6kc1	0.952	0.759	0.583	1.103	1.054	Weakly similar to RSK-like protein. [Source:Uniprot/SPTREMBL;Acc:Q8BLK9]
ENSMUSG00000037600	1.034	1.318	0.594	1.27	1.307	Similar to TATA box binding protein. [Source:Uniprot/SPTREMBL;Acc:Q8C1Q5]
Tnfrsf23	1.023	0.811	0.807	0.99	0.993	Tumor necrosis factor receptor superfamily member 23 precursor (Tumor necrosis factor receptor p60 homolog 1) (TNF receptor family member SOB) (Decoy TRAIL receptor 1) (TNF receptor homolog 1). [Source:Uniprot/SWISSPROT;Acc:Q9ER63]
ENSMUSG00000037618	1.294	1.919	1.533	0.705	0.602	hypothetical protein
ENSMUSG00000037640	0.586	0.951	1.824	1.337	1.378	Zinc finger protein 60 (Zfp-60) (Zinc finger protein Mfg-3). [Source:Uniprot/SWISSPROT;Acc:P16374]
Zcd1	1	1.422	1.213	1.14	0.895	Uncharacterized hematopoietic stem/progenitor cells protein MDS029 homolog. [Source:Uniprot/SWISSPROT;Acc:Q91WS0]
Mrps26	1.082	1.135	1.557	1.144	1.199	mitochondrial ribosomal protein S26
A930025D01Rik	0.811	1.648	1.585	1.125	1.604	hypothetical protein LOC319513
ENSMUSG00000037792	1.633	1.006	1.695	1.046	0.957	hypothetical protein

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
BC048715	0.632	2.004	0.355	0.515	1.059	hypothetical protein
Zfp365	1.76	0.064	2.671	1.258	0.443	zinc finger protein 365. [Source:RefSeq;Acc:NM_178679]
EG244495	0.432	0.511	1.66	0.427	0.054	similar to tripin
ENSMUSG00000037884	0.388	0.216	0.428	1.77	0.878	PREDICTED: RIKEN cDNA 1700017G19 gene (1700017G19Rik)
ENSMUSG00000037955	0.305	1.043	0.713	0.414	0.984	hypothetical protein
ENSMUSG00000038011	0.753	0.429	1.387	1.292	0.805	PREDICTED: dynein, axonemal, heavy chain 10 (Dnahc10)
Csf3	1.448	0.522	0.313	1.231	0.647	Granulocyte colony-stimulating factor precursor (G-CSF). [Source:Uniprot/SWISSPROT;Acc:P09920]
Als2cr4	1.015	1.286	1.257	1.08	1.086	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 4 isoform 2
Stox2	0.647	1.017	0.588	0.839	1.183	storkhead box 2
Cd84	0.988	4.894	1.678	0.966	1.061	CD84 antigen. [Source:RefSeq;Acc:NM_013489]
Prdm1	0.442	1.01	0.66	0.523	0.939	PR-domain zinc finger protein 1 (Beta-interferon gene positive- regulatory domain I binding factor) (BLIMP-1). [Source:Uniprot/SWISSPROT;Acc:Q60636]
BC057600	1.32	1.16	0.646	1.238	1.676	scavenger receptor class F, member 1 (Scarf1)
Serpinf2	0.963	2.434	0.557	1.222	0.52	Alpha-2-antiplasmin precursor (Alpha-2-plasmin inhibitor) (Alpha-2-PI) (Alpha-2-AP). [Source:Uniprot/SWISSPROT;Acc:Q61247]
BC058965	1.321	1.935	2.131	1.082	1.199	Neurogenic differentiation factor 2 (NeuroD2) (NeuroD-related factor) (NDRF). [Source:Uniprot/SWISSPROT;Acc:Q62414]
Trpm4	1.011	0.887	0.811	1.173	0.813	transient receptor potential cation channel, subfamily M, member; transient receptor potential ion channel melastatin subgroup member 4. [Source:RefSeq;Acc:NM_175130]
Ostm1	0.918	0.735	0.839	0.551	0.963	osteopetrosis associated transmembrane protein 1; grey-lethal; grey lethal osteroperosis; grey lethal osteopetrosis. [Source:RefSeq;Acc:NM_172416]

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Snx25	0.306	0.752	1.769	0.968	1.758	sorting nexin 25
Spsb2	0.817	1.109	1.367	0.887	0.937	gene rich cluster, C9 gene. [Source:RefSeq;Acc:NM_013539]
Nos1ap	0.636	1.569	1.987	1.327	0.396	C-terminal PDZ domain ligand of neuronal nitric oxide synthase
BC058633	0.765	1.047	0.687	1.078	1.464	Transcription factor Dp-1 (E2F dimerization partner 1) (DRTF1-polypeptide-1). [Source:Uniprot/SWISSPROT;Acc:Q08639]
Parp12	0.781	0.963	0.673	1.037	1.506	Zinc finger CCCH type domain containing protein 1. [Source:Uniprot/SWISSPROT;Acc:Q8BZ20]
Grtp1	0.366	1.144	1.607	0.622	0.888	GH regulated TBC protein 1. [Source:RefSeq;Acc:NM_025768]
Rgs4	0.671	0.714	0.732	0.988	1.383	Regulator of G-protein signaling 4 (RGS4). [Source:Uniprot/SWISSPROT;Acc:O08899]
Tmc3	1.423	0.765	0.496	1.011	1.154	transmembrane channel-like gene family 3. [Source:RefSeq;Acc:NM_177695]
BC028528	0.859	1.006	1.26	1.16	1.13	L259. [Source:RefSeq;Acc:NM_153513]
ENSMUSG00000038598	1.233	0.825	1.792	1.242	0.437	PREDICTED: similar to chromosome 9 open reading frame 84 (LOC242489)
Slc35f1	0.688	0.471	0.727	0.83	0.565	solute carrier family 35, member F1; DUF6 containing protein. [Source:RefSeq;Acc:NM_178675]
Samd10	1.062	1.571	1.401	1.115	1.406	sterile alpha motif domain containing 10
ENSMUSG00000038608	0.449	0.992	0.585	0.382	0.809	Dedicator of cytokinesis protein 10 (Fragment). [Source:Uniprot/SWISSPROT;Acc:Q8BZN6]
ENSMUSG00000038615	0.955	1.263	0.686	0.927	1.073	Nuclear factor erythroid 2 related factor 1 (NF-E2 related factor 1) (NFE2-related factor 1) (Nuclear factor, erythroid derived 2, like 1). [Source:Uniprot/SWISSPROT;Acc:Q61985]
Dgki	0.466	0.367	1.543	0.463	1.327	diacylglycerol kinase, iota
Gmeb2	0.759	0.842	0.601	0.971	1.383	Glucocorticoid modulatory element binding protein 2 (GMEB-2) (Fragment). [Source:Uniprot/SWISSPROT;Acc:P58929]
Txndc8	3.02	0.767	1.603	1.369	0.878	thioredoxin domain containing 8
4930504E06Rik	0.99	1.181	0.872	0.925	0.885	RIKEN cDNA 4930504E06; cDNA sequence, clone 2-4; NF-E2 inducible protein. [Source:RefSeq;Acc:NM_133858]
Hoxb7	0.49	0.246	1.622	0.528	0.959	Homeobox protein Hox-B7 (Hox-2.3) (MUB1) (MH-22B). [Source:Uniprot/SWISSPROT;Acc:P09024]

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Irs2	1.192	0.517	0.563	0.914	1.487	Insulin receptor substrate-2 (IRS-2) (4PS). [Source:Uniprot/SWISSPROT;Acc:P81122]
Sccpdh	0.753	1.053	0.803	0.992	0.669	saccharopine dehydrogenase (putative)
ENSMUSG00000038939	0.353	1.466	1.918	1.253	0.603	hypothetical protein
ENSMUSG00000038942	0.521	0.197	0.791	0.719	1.485	PREDICTED: discs, large homolog 5 (Drosophila) (Dlg5)
BC059808	0.796	0.762	0.726	0.85	0.994	protein regulator of cytokinesis 1. [Source:RefSeq;Acc:NM_145150]
Timm8b	0.882	1.283	1.199	1.216	1.011	Mitochondrial import inner membrane translocase subunit TIM8 B (Deafness dystonia protein 2 homolog). [Source:Uniprot/SWISSPROT;Acc:P62077]
Hrh3	0.766	0.84	0.717	1.194	1.012	Histamine H3 receptor (HH3R). [Source:Uniprot/SWISSPROT;Acc:P58406]
ENSMUSG00000039138	1.337	1.089	1.618	0.7	0.472	RIKEN cDNA 4930591A17 gene (4930591A17Rik)
H28	0.559	0.16	0.468	0.792	1.353	histocompatibility 28
C230093N12Rik	1.179	1.493	1.485	1.139	0.902	early estrogen-induced gene 1 protein
Metrnl	1.107	0.749	1.092	0.988	1.325	meteorin, glial cell differentiation regulator-like
Svs1	1.225	0.365	0.572	0.799	0.936	seminal vesicle-secreted protein I. [Source:RefSeq;Acc:NM_172888]
Il18	0.855	0.817	0.683	1.014	1.338	Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor) (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma). [Source:Uniprot/SWISSPROT;Acc:P70380]
Tbce	1.26	0.852	0.823	0.852	0.992	tubulin-specific chaperone e; progressive motor neuropathy. [Source:RefSeq;Acc:NM_178337]
ENSMUSG00000039245	1.036	1.29	0.605	0.982	0.643	hypothetical protein
Spdyb	0.279	1.937	1.367	1.104	0.732	speedy B
ENSMUSG00000039335	0.289	0.332	1.279	1.676	0.83	Nyd-sp12 protein; spermatogenesis-related protein. [Source:RefSeq;Acc:NM_029150]
Hlx1	1.139	0.558	0.656	0.908	1.248	Homeobox protein HLX1. [Source:Uniprot/SWISSPROT;Acc:Q61670]
BC060723	0.435	1.191	0.639	0.653	0.745	Similar to UBINUCLEIN (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8BNC3]

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Asb6	0.887	1.035	0.776	0.667	0.781	Ankyrin repeat and SOCS box containing protein 6 (ASB-6). [Source:Uniprot/SWISSPROT;Acc:Q91ZU1]
ENSMUSG00000039488	0.828	0.287	0.415	1.07	1.491	PREDICTED: contactin 5 (Cntn5)
ENSMUSG00000039555	0.846	0.363	1.355	1.588	1.914	hypothetical protein
5730528L13Rik	1.274	0.862	0.749	1.386	0.979	hypothetical protein LOC66665
ENSMUSG00000039779	1.159	0.965	0.649	1.474	0.775	PREDICTED: RIKEN cDNA 2210407G14 gene (2210407G14Rik)
Sft2d1	0.899	0.897	1.268	0.945	1.369	hypothetical protein LOC106489
Zfp335	0.787	0.589	0.578	1.217	0.491	zinc finger protein 335
Heca	0.818	0.84	0.578	0.702	0.779	headcase homolog
Slc26a11	0.966	1.319	1.313	1.164	1.273	anion exchanger Slc26a11. [Source:RefSeq;Acc:NM_178743]
Hip1	0.325	1.314	1.444	0.583	0.687	huntingtin interacting protein 1. [Source:RefSeq;Acc:NM_146001]
Zc3h12d	0.821	0.763	0.709	0.908	1.545	zinc finger CCCH-type containing 12D
Stat2	1.259	0.818	0.745	1.028	1.282	Signal transducer and activator of transcription 2. [Source:Uniprot/SWISSPROT;Acc:Q9WVL2]
Cacna2d1	1.029	1.439	1.881	0.93	1.076	Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta subunits precursor. [Source:Uniprot/SWISSPROT;Acc:O08532]
Gpr176	1.253	0.689	0.548	0.973	0.834	gene model 1012; Similar to putative G protein coupled receptor. [Source:RefSeq;Acc:NM_201367]
Maob	1.18	1.449	0.798	1.51	1.013	amine oxidase (flavin-containing). [Source:RefSeq;Acc:NM_172778]
Fmo2	1.187	0.995	1.789	0.914	0.502	flavin-containing monooxygenase 2. [Source:RefSeq;Acc:NM_018881]
Pacsin1	1.234	0.42	1.532	1.472	1.303	Protein kinase C and casein kinase substrate in neurons protein 1. [Source:Uniprot/SWISSPROT;Acc:Q61644]
Trim7	0.952	1.031	1.419	2.15	0.881	tripartite motif protein 7. [Source:RefSeq;Acc:NM_053166]
Zzef1	0.55	1.208	0.651	0.872	1.011	zinc finger, ZZ-type with EF hand domain 1
Aqr	1.204	1.043	1.384	1.044	0.922	aquarius. [Source:RefSeq;Acc:NM_009702]

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Abhd13	0.985	1.165	1.373	0.95	0.762	abhydrolase domain containing 13
ENSMUSG00000040422	4.816	1.694	1.564	1.359	0.967	Mg310 protein (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q9ER85]
ENSMUSG00000040434	1.522	1.242	2.124	0.953	0.88	glycosyltransferase-like 1B; glycoslytransferase-like 1B. [Source:RefSeq;Acc:NM_172670]
ENSMUSG00000040451	0.677	0.617	0.601	0.686	0.98	Phosphatidylcholine:ceramide cholinephosphotransferase 1 (EC 2.7.-.-) (Sphingomyelin synthase 1). [Source:Uniprot/SWISSPROT;Acc:Q8VCQ6]
ENSMUSG00000040498	0.534	2.853	0.375	0.28	0.513	hypothetical protein
Tlr8	1.107	0.948	0.5	0.984	1.255	Toll-like receptor 8 precursor. [Source:Uniprot/SWISSPROT;Acc:P58682]
Cldn3	1.103	1.861	1.925	1.333	1.708	Claudin-3 (Clostridium perfringens enterotoxin receptor 2) (CPE- receptor 2) (CPE-R 2). [Source:Uniprot/SWISSPROT;Acc:Q9Z0G9]
ENSMUSG00000040573	0.373	1.061	1.618	1.24	1.391	hyupothetical protein
ENSMUSG00000040573	1.1	0.996	1.227	0.947	0.785	hypothetical protein
ENSMUSG00000040597	1.108	0.925	0.664	0.175	1.299	hypothetical protien
Tmem51	1.13	0.956	1.392	1.28	1.139	transmembrane protein 51
4933426K21Rik	1.952	0.096	0.771	1.691	1.515	hypothetical protein LOC108653
St8sia4	1.158	0.849	0.692	1.011	0.312	CMP-N-acetylneuraminate-poly-alpha-2,8-sialyl transferase (EC 2.4.99.-) (Alpha-2,8-sialyltransferase 8D) (ST8Sia IV) (Polysialyltransferase-1). [Source:Uniprot/SWISSPROT;Acc:Q64692]
Cd53	1.066	1.115	0.855	1.019	1.119	Leukocyte surface antigen CD53 (Cell surface glycoprotein CD53). [Source:Uniprot/SWISSPROT;Acc:Q61451]
Lat2	0.798	1.515	1.266	0.783	1.178	Williams-Beuren syndrome chromosome region 5 homolog; Williams-Beuren syndrome chromosome region 15 homolog (human). [Source:RefSeq;Acc:NM_022964]

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Eml2	0.838	0.817	0.756	1.023	1.054	echinoderm microtubule associated protein like 2 isoform 1
ENSMUSG00000040838	0.528	0.32	1.685	1.118	1.698	PREDICTED: similar to hypothetical protein (LOC217236)
Bsdc1	1.351	1.064	0.509	0.721	1.183	BSD domain containing 1
ENSMUSG00000041067	1.908	0.772	0.411	1.202	0.928	hypothetical protein
Nbl1	0.252	1.15	1.465	1.333	0.926	Neuroblastoma suppressor of tumorigenicity 1 precursor (Zinc finger protein DAN) (N03). [Source:Uniprot/SWISSPROT;Acc:Q61477]
Osgin2	1.534	0.793	0.693	0.839	0.865	oxidative stress induced growth inhibitor family member 2
Otud3	0.982	1.182	1.64	0.865	1.069	OTU domain containing 3
ENSMUSG00000041224	0.425	1.003	1.987	1.431	1.423	hypothetical protein
Ssr2	0.801	1.129	1.097	1	0.969	signal sequence receptor, beta. [Source:RefSeq;Acc:NM_025448]
Pik3r1	1.06	0.703	0.79	0.78	0.667	Phosphatidylinositol 3-kinase regulatory alpha subunit (PI3-kinase p85-alpha subunit) (PtdIns-3-kinase p85-alpha) (PI3K). [Source:Uniprot/SWISSPROT;Acc:P26450]
Mmrn2	0.565	1.529	1.974	1.307	1.224	elastin microfibril interfacer 3. [Source:RefSeq;Acc:NM_153127]
ENSMUSG00000041482	3.281	1.67	0.46	0.519	0.954	RIKEN cDNA 9430028L06 gene (9430028L06Rik)
ENSMUSG00000041540	0.601	1.35	0.713	1.17	0.669	Transcription factor SOX-5. [Source:Uniprot/SWISSPROT;Acc:P35710]
ENSMUSG00000041607	0.482	1.673	1.36	0.426	0.696	Myelin basic protein (MBP) (Myelin A1 protein). [Source:Uniprot/SWISSPROT;Acc:P04370]
BC006965	1.933	1.718	1.518	0.605	0.927	cDNA sequence BC006965 (BC006965)
1810011H11Rik	0.939	1.282	0.746	0.995	1.049	hypothetical protein LOC69069 isoform 1
Moap1	1.029	1.583	0.665	0.781	1.132	modulator of apoptosis 1 (Moap1)
Cpsf2	0.894	1.088	1.183	1.103	0.894	Cleavage and polyadenylation specificity factor, 100 kDa subunit (CPSF 100 kDa subunit). [Source:Uniprot/SWISSPROT;Acc:O35218]

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Lad1	1.352	0.698	0.889	1.058	1.343	Ladinin 1 (Lad-1) (Linear IgA disease autoantigen). [Source:Uniprot/SWISSPROT;Acc:P57016]
Il17f	1.222	1.398	0.467	1.394	1.271	interleukin 17F. [Source:RefSeq;Acc:NM_145856]
S100a10	0.971	1.114	1.188	1.163	1.263	Calpactin I light chain (p10 protein) (p11) (Cellular ligand of annexin II). [Source:Uniprot/SWISSPROT;Acc:P08207]
Ssh1	0.896	1.074	0.467	0.844	0.928	slingshot-like 1; slingshot 1L. [Source:RefSeq;Acc:NM_198109]
Cdrt4	0.992	0.725	1.71	1.455	1.931	CMT1A duplicated region transcript 4
Adrbk2	1.465	0.82	0.687	1.138	0.936	Beta-adrenergic receptor kinase 2. [Source:Uniprot/SPTREMBL;Acc:Q8BX71]
Trem1	1.372	0.873	0.5	0.851	0.792	triggering receptor expressed on myeloid cells 1; triggering receptor expressed in monocytes 1. [Source:RefSeq;Acc:NM_021406]
ENSMUSG00000042371	1.331	1.029	1.318	0.962	0.803	hypothetical protein
ENSMUSG00000042420	1.112	0.639	1.828	0.966	0.892	hypothetical protein
BC051701	1.168	0.19	1.902	1.41	1.301	hypothetical protein
ENSMUSG00000042487	1.046	0.684	0.723	0.915	1.08	hypothetical protein
Nek10	0.455	0.738	1.356	1.152	2.276	NIMA (never in mitosis gene a)- related kinase 10
ENSMUSG00000042590	0.996	0.257	0.6	1.035	1.774	importin 11. [Source:RefSeq;Acc:NM_029665]
Dcst1	1.134	1.258	1.987	1.384	0.431	DC-STAMP domain containing 1
Zc3h12a	1.131	0.604	0.538	1.118	0.88	zinc finger CCCH type containing 12A
Sipa1l1	1.173	0.745	0.468	0.832	1.012	signal-induced proliferation-associated 1 like 1. [Source:RefSeq;Acc:NM_172579]
Trafd1	1.102	0.87	0.607	0.734	1.292	FLN29 gene product. [Source:RefSeq;Acc:NM_172275]
BC065049	0.312	1.063	0.246	0.647	1.04	TRIFIC. [Source:Uniprot/SPTREMBL;Acc:Q7TNM2]
ENSMUSG00000042825	1.142	0.855	0.642	1.105	1.115	hypothetical protein
Trim72	1.147	0.189	0.399	0.491	2.047	tripartite motif-containing 72

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D0H4S114	1.645	0.339	0.653	0.707	1.383	neuronal protein 3.1
Wrnip1	0.873	0.724	1.657	0.726	0.999	hypothetical protein
ENSMUSG00000042933	1.039	2.65	1.592	0.869	0.923	hypothetical protein
Rfwd3	0.924	1.008	1.399	0.813	1.093	ring finger and WD repeat domain 3
ENSMUSG00000042970	0.208	1.52	0.531	0.974	0.845	hypothetical protein
ENSMUSG00000043001	0.622	1.417	2.292	2.245	1.379	PREDICTED: similar to SH2/SH3 adaptor protein (LOC384630)
BU939258, BU946147	1.288	1.9	1.297	1.571	0.503	hypothetical protein
ENSMUSG00000043062	0.82	1.002	1.23	1.027	1.098	NADH-ubiquinone oxidoreductase 15 kDa subunit (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-15 kDa) (CI-15 kDa). [Source:Uniprot/SWISSPROT;Acc:Q99LY9]
A530016L24Rik	1.754	0.94	0.611	0.379	0.412	hypothetical protein LOC319942
Mobk1b	0.873	0.861	0.68	0.656	0.825	Mob4B protein. [Source:RefSeq;Acc:NM_145571]
Upf2	0.907	1.312	1.663	0.749	0.963	UPF2 regulator of nonsense transcripts homolog
ENSMUSG00000043278	0.958	1.041	0.688	0.906	2.221	PREDICTED: similar to chromosome 14 open reading frame 29 isoform c (LOC435306)
Olfr131	1.445	0.367	1.571	0.616	0.568	olfactory receptor 131; GA_x6K02T2PSCP-2531299-2530355; olfactory receptor MOR256-4. [Source:RefSeq;Acc:NM_146867]
Pcdhb19	0.841	1.002	0.604	1.019	0.962	protocadherin beta 19. [Source:RefSeq;Acc:NM_053144]
BC070413, BC058970	0.952	0.183	1.631	0.829	0.823	PER1 interacting protein of the SUPRACHIAMATIC NUCLEUS homolog (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8BKR8]
Usp31	1.179	1.125	0.712	1.073	1.062	RIKEN cDNA 2810449C13 gene (2810449C13Rik)
Rab9b	1.533	0.793	1.46	1.079	0.815	RAB9B, member RAS oncogene family. [Source:RefSeq;Acc:NM_176971]
ENSMUSG00000043531	0.969	0.553	0.652	1.108	1.355	VPS10 domain-containing receptor SorCS1 precursor (mSorCS). [Source:Uniprot/SWISSPROT;Acc:Q9JLC4]
AU042671	0.491	0.835	1.503	1.127	1.447	hypothetical protein LOC269700 isoform 1

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E330026B02Rik	1.307	1.71	1.23	1.008	1.216	hypothetical protein LOC245026
ENSMUSG00000043754	1.118	0.713	1.186	1.188	0.914	hypothetical protein
Serf2	0.994	0.87	1.481	0.988	0.869	Small EDRK-rich factor 2 (4F5rel) (h4F5rel) (Gastric cancer-related protein VRG107). [Source:Uniprot/SWISSPROT;Acc:O75918]
BU583135	1.019	0.741	1.403	1.447	0.288	Mouse ATPB2 gene. [Source:Uniprot/SPTREMBL;Acc:Q99386]
Mglap	0.242	0.706	1.385	0.944	1.051	hypothetical protein
ENSMUSG00000043932	1.445	0.394	0.406	1.696	0.739	hypothetical protein
Olfr1497	1.208	0.671	0.687	1.081	0.371	olfactory receptor 1497; olfactory receptor MOR212-1; GA_x6K02T2RE5P-4127765-4126821. [Source:RefSeq;Acc:NM_146741]
ENSMUSG00000044138	0.789	1.28	1.512	1.248	1.843	SIRP beta 1 isoform 2; SIRP beta 1. [Source:RefSeq;Acc:NM_198405]
Lsm8	1.065	1	1.251	1.049	1.084	U6 snRNA-associated Sm-like protein LSm8. [Source:RefSeq;Acc:NM_133939]
9030611K07Rik	1.361	0.426	0.413	1.379	1.154	RIKEN cDNA 9030611K07
Gm566	1.09	0.648	0.525	1.423	1.559	hypothetical protein
ENSMUSG00000044233	1.103	0.922	1.67	0.478	1.255	PREDICTED: similar to zinc finger protein 353 (LOC384044)
Ctla2a	0.815	0.555	0.797	0.743	1.088	CTLA-2-beta protein precursor (Fragment). [Source:Uniprot/SWISSPROT;Acc:P12400]
ENSMUSG00000044260	1.265	0.902	1.78	0.895	0.878	hypothetical protein
Crb3	1.185	1.302	1.853	2.625	1.617	crumbs homolog 3. [Source:RefSeq;Acc:NM_177638]
BU938071	1.054	0.892	0.598	1.181	0.733	hypothetical protein
ENSMUSG00000044348	2.215	1.58	1.387	1.926	0.369	PREDICTED: similar to mitochondrial carrier triple repeat 1 (LOC434854)
ENSMUSG00000044356	0.361	0.801	1.517	1.263	2.786	Weakly similar to CDNA FLJ31726 FIS (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8C020]

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
1110002B05Rik	0.786	0.817	1.369	1.18	0.871	hypothetical protein LOC104725
Olfr1112	0.739	1.491	2.624	2.479	0.584	olfactory receptor 1112; olfactory receptor MOR264-6; GA_x6K02T2Q125-48676316-48677272. [Source:RefSeq;Acc:NM_146661]
ENSMUSG00000044544	1.329	1.437	1.506	1.471	0.522	PREDICTED: RIKEN cDNA 4921513I03 gene (4921513I03Rik)
ENSMUSG00000044550	0.991	1.098	1.582	0.7	0.51	hypothetical protein
BC035295	0.674	0.661	0.63	0.942	1.029	cDNA sequence BC035295; TGF-beta induced apoptosis protein 12. [Source:RefSeq;Acc:NM_153407]
BC025147	1.292	0.553	0.598	0.83	0.286	Partitioning defective-6 homolog beta (PAR-6 beta) (PAR-6B). [Source:Uniprot/SWISSPROT;Acc:Q9JK83]
Zbtb7c	1.124	1.364	0.629	0.832	1.063	zinc finger and BTB domain containing 36
E230025N22Rik	0.931	0.803	1.743	0.717	1.575	hypothetical protein LOC240216
Zfp36	0.965	0.645	0.456	0.615	0.891	Tristetraproline (TTP) (TIS11A protein) (TIS11) (Zinc finger protein 36) (Zfp-36) (Growth factor-inducible nuclear protein NUP475) (TPA induced sequence 11). [Source:Uniprot/SWISSPROT;Acc:P22893]
Pamci	0.623	1.492	1.586	0.993	1.043	peptidylglycine alpha-amidating monooxygenase COOH-terminal interactor. [Source:RefSeq;Acc:NM_146240]
ENSMUSG00000044936	1.646	1.053	1.197	1.72	0.824	hypothetical protein
ENSMUSG00000044976	0.83	0.758	1.652	0.829	1.241	hypothetical protein
Asah3	0.679	1.566	1.846	0.824	1.148	N-acylsphingosine amidohydrolase 3; alkaline ceramidase. [Source:RefSeq;Acc:NM_175731]
2810002I04Rik	0.945	1.758	1.275	1.208	1.847	hypothetical protein LOC72350
LOC625662	1.274	0.427	1.314	1.802	1.248	PREDICTED: similar to hypothetical protein (LOC218476)
ENSMUSG00000045114	0.861	1.147	1.35	0.565	0.774	hypothetical protein

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Olfr620	0.98	1.585	0.483	1.244	1.226	olfactory receptor 620; olfactory receptor MOR4-1; GA_x6K02T2PBJ9-6335095-6334154. [Source:RefSeq;Acc:NM_146812]
ENSMUSG00000045184	0.154	1.028	0.511	0.678	0.62	hypothetical protein
Olfr123	1.307	2.893	1.609	2.291	0.737	olfactory receptor 123; GA_x6K02T2PSCP-2255106-2256035; olfactory receptor MOR256-9. [Source:RefSeq;Acc:NM_146630]
Rln3	0.819	1.273	1.737	1.136	2.087	Relaxin 3 precursor (Prorelaxin M3) (Insulin-like peptide INSL7) (Insulin-like peptide 7). [Source:Uniprot/SWISSPROT;Acc:Q8CHK2]
Gpr20	1.077	0.739	1.687	1.197	1.771	G protein-coupled receptor 20. [Source:RefSeq;Acc:NM_173365]
ENSMUSG00000045330	0.752	2.17	1.609	1.901	0.471	PREDICTED: RIKEN cDNA 4933402E13 gene (4933402E13Rik)
Kcnk13	1.286	2.104	1.382	0.978	1.202	Potassium channel subfamily K member 13 (Tandem pore domain halothane inhibited potassium channel 1) (THIK-1). [Source:Uniprot/SWISSPROT;Acc:Q8R1P5]
ENSMUSG00000045437	0.839	0.611	1.387	2.03	1.304	PREDICTED: similar to BC005685 protein (LOC212970)
Gprin3	2.02	1.398	2.116	0.813	1.517	GPRIN family member 3
Gpr109a	0.573	0.909	0.605	0.81	1.836	G protein-coupled receptor 109B; putative seven transmembrane spanning receptor; interferon-gamma inducible gene, Puma-g. [Source:RefSeq;Acc:NM_030701]
Cdc42ep2	0.735	0.919	0.832	1.09	1.161	CDC42 effector protein (Rho GTPase binding) 2; centrosomal protein 2; Cdc42 effector protein 2. [Source:RefSeq;Acc:NM_026772]
Pqlc3	1.057	1.117	1.519	1.07	1.098	PQ loop repeat containing 3
Thtpa	0.467	1.139	1.311	0.714	0.884	Thiamine-triphosphatase (EC 3.6.1.28) (ThTPase). [Source:Uniprot/SWISSPROT;Acc:Q8JZL3]
Prr8	1.225	1.199	1.859	0.959	1.35	hypothetical protein LOC381626 isoform 1

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Olfr552	0.732	0.909	1.538	0.107	1.111	olfactory receptor 552; olfactory receptor MOR28-1; GA_x6K02T2PBJ9-5323062-5324015. [Source:RefSeq;Acc:NM_147102]
ENSMUSG00000045823	1.236	0.928	1.228	1.159	1.002	PREDICTED: RIKEN cDNA 1110019J04 gene (1110019J04Rik)
ENSMUSG00000045842	0.96	0.71	1.588	1.047	1.081	hypothetical protein
EG226957	0.86	2.178	1.152	0.375	0.902	similar to RNA and export factor binding protein 2
Clec14a	0.226	1.042	1.843	2.067	0.93	C-type lectin domain family 14, member a
Prdm12	2.138	1.086	2.159	0.588	1.91	PR domain containing 12
Onecut2	1.565	0.798	2.337	0.403	1.633	one cut domain, family member 2; transcription factor ONECUT2. [Source:RefSeq;Acc:NM_194268]
ENSMUSG00000046014	0.744	0.71	0.778	0.791	0.803	hypothetical protein
ENSMUSG00000046110	0.714	1.215	0.713	1.628	0.991	hypothetical protein
AV312086	0.866	1.104	0.782	0.891	0.424	hypothetical protein LOC225929
EG432460	1.581	0.756	2.241	1.111	2.556	hypothetical protein
Gldn	0.29	1.624	0.442	1.596	1.027	collomin; olfactomedin-related protein; cancer related gene - liver 2. [Source:RefSeq;Acc:NM_177350]
Pnma2	1.183	1.428	2.019	1.027	1.113	Paraneoplastic antigen Ma2 homolog. [Source:Uniprot/SWISSPROT;Acc:Q8BHK0]
Plaur	1.366	0.699	0.804	0.971	1.318	Urokinase plasminogen activator surface receptor, GPI-anchored form precursor (uPAR) (U-PAR) (CD87 antigen). [Source:Uniprot/SWISSPROT;Acc:P35456]
Adam29	2.265	1.596	1.814	1.715	0.901	a disintegrin and metalloprotease domain 29; a disintegrin and metalloproteinase domain 29. [Source:RefSeq;Acc:NM_175939]
ENSMUSG00000046361	1.331	1.226	1.575	0.821	1.529	PREDICTED: RIKEN cDNA 2810416G20 gene (2810416G20Rik)
ENSMUSG00000046396	0.687	1.032	1.454	1.722	0.778	olfactory receptor 609; olfactory receptor MOR9-1; GA_x6K02T2PBJ9-6207735-6206776.

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
ENSMUSG00000046401	0.429	1.213	1.731	0.907	1.101	hypothetical protein
BC022651	0.92	0.776	1.943	0.72	0.766	hypothetical protein LOC330460
ENSMUSG00000046707	0.827	2.391	1.677	0.962	1.348	Casein kinase II, alpha' chain (CK II) (EC 2.7.1.37). [Source:Uniprot/SWISSPROT;Acc:O54833]
ENSMUSG00000046720	1.303	1.617	0.777	1.119	1.466	PREDICTED: similar to RIKEN cDNA 1700108L22 (LOC384865)
Cdc42se1	0.948	1.261	1.517	0.863	0.672	small protein effector 1 of Cdc42. [Source:RefSeq;Acc:NM_172395]
ENSMUSG00000046764	0.542	1.788	1.782	1.601	0.421	RIKEN cDNA A530053G22 gene (A530053G22Rik)
Zfp787	0.517	0.24	1.794	1.082	1.267	TTF-I interacting peptide 20 homolog. [Source:Uniprot/SPTREMBL;Acc:Q8BIF9]
Ckap4	0.691	1.033	1.172	1.007	0.869	Similar to P63 protein (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8BMK4]
Pip5kl1	0.868	1.975	1.602	0.648	0.682	phosphatidylinositol-4-phosphate 5-kinase-like 1; cDNA sequence BC028795; phosphatidylinositol phosphate kinase-like. [Source:RefSeq;Acc:NM_198191]
Cd24a	0.962	0.648	0.669	1.079	1.375	Signal transducer CD24 precursor (M1/69-J11D heat stable antigen) (HSA) (Nectadrin) (LY-52) (X62 heat stable antigen) (R13-AG). [Source:Uniprot/SWISSPROT;Acc:P24807]
Dmrta2	0.437	0.412	1.78	0.339	1.803	doublesex and mab-3 related transcription factor like family A2; doublesex- and mab-3-related transcription factor 5. [Source:RefSeq;Acc:NM_172296]
Hps6	1.673	1.134	0.608	1.401	0.797	Hermansky-Pudlak syndrome 6 protein homolog (Ruby-eye protein) (Ru). [Source:Uniprot/SWISSPROT;Acc:Q8BLY7]
ENSMUSG00000047179	0.934	1.162	1.684	1.954	1.122	hypothetical protien
BC005573	1.534	1.158	1.363	0.867	0.955	Prostaglandin G/H synthase 1 precursor (EC 1.14.99.1) (Cyclooxygenase -1) (COX-1) (Prostaglandin-endoperoxide synthase 1) (Prostaglandin H2 synthase 1) (PGH synthase 1) (PGHS-1) (PHS 1). [Source:Uniprot/SWISSPROT;Acc:P22437]

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
ENSMUSG00000047318	0.886	1.09	1.232	0.879	1.176	reduced expression 2. [Source:RefSeq;Acc:NM_009051]
Cstad	1.404	0.902	2.482	0.647	0.892	CSA-conditional, T cell activation-dependent protein. [Source:RefSeq;Acc:NM_030137]
B3gnt1	0.726	1.429	1.43	1.032	0.877	beta-1,3-N-acetylglucosaminyltransferase bGnT-6. [Source:RefSeq;Acc:NM_175383]
Tgif1	0.948	1.312	1.432	1.031	1.074	5'-TG-3' interacting factor (Homeobox protein TGIF). [Source:Uniprot/SWISSPROT;Acc:P70284]
Gphn	1.051	1.135	0.798	0.882	0.809	gephyrin. [Source:RefSeq;Acc:NM_172952]
A430005L14Rik	0.886	1.169	1.413	0.852	1.059	hypothetical protein LOC97159
Olfr656	1.045	0.958	0.514	2.23	0.383	olfactory receptor 656; olfactory receptor MOR27-1; GA_x6K02T2PBJ9-7245486-7246451. [Source:RefSeq;Acc:NM_147075]
Rps8	0.701	0.94	1.403	0.948	1.29	40S ribosomal protein S8. [Source:Uniprot/SWISSPROT;Acc:P62241]
Ppp1r2	0.93	0.91	0.734	1.268	0.903	protein phosphatase 1, regulatory (inhibitor) subunit 2; protein phosphatase inhibitor 2. [Source:RefSeq;Acc:NM_025800]
AK173329, BC031151	1.224	0.898	0.791	0.853	1.513	hypothetical protein
Cdca4	0.963	0.888	0.891	0.868	1.2	Cell division cycle associated protein 4 (Hematopoietic progenitor protein). [Source:Uniprot/SWISSPROT;Acc:Q9CWM2]
Olfr770	0.265	0.797	1.654	0.576	1.913	olfactory receptor 770; olfactory receptor MOR114-5; GA_x6K02T2PULF-10819232-10818297. [Source:RefSeq;Acc:NM_146863]
D030070L09Rik	1	1.131	0.751	0.982	1.2	RIKEN cDNA D030070L09
Hes5	0.581	0.914	2.222	1.191	1.072	Transcription factor HES-5 (Hairy and enhancer of split 5). [Source:Uniprot/SWISSPROT;Acc:P70120]
BC037267	1.038	0.606	0.504	0.955	1.177	hypothetical protein
ENSMUSG00000048113	1.907	0.213	1.594	5.065	0.911	Ig kappa chain V-V region K2 precursor (Fragment). [Source:Uniprot/SWISSPROT;Acc:P01635]

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Entpd1	1.176	0.867	1.227	0.909	0.833	Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5) (NTPDase1) (Ecto-ATP diphosphohydrolase) (ATPDase) (Lymphoid cell activation antigen) (Ecto-apyrase) (CD39 antigen). [Source:Uniprot/SWISSPROT;Acc:P55772]
Nwd1	1.609	0.384	0.619	1.565	0.517	NACHT and WD repeat domain containing 1
ENSMUSG00000048225	2.094	0.53	1.335	2.742	0.394	hypothetical protein
H2-M10.2	0.446	0.189	1.348	0.516	0.553	histocompatibility 2, M region locus 10.2; major histocompatibility complex class Ib M10.1. [Source:RefSeq;Acc:NM_177923]
ENSMUSG00000048285	0.579	1.183	1.841	0.387	0.109	hypothetical protein
Scrt1	0.584	0.731	1.448	1.393	1.109	Transcriptional repressor scratch 1 (Scratch homolog 1 zinc finger protein) (Scratch 1) (SCRT) (mScrt). [Source:Uniprot/SWISSPROT;Acc:Q99M85]
ENSMUSG00000048440	1.161	1	1.459	0.559	0.414	cytochrome P450, family 4, subfamily f, polypeptide 13; cytochrome P450 CYP4F13; cytochrome P450,subfamily IVF, polypeptide 13; leukotriene B4 omega hydroxylase; P450 CYP4F13. [Source:RefSeq;Acc:NM_130882]
ENSMUSG00000048559	0.681	1.109	1.442	1.619	1.017	hypothetical protein
ENSMUSG00000048621	0.717	0.564	0.511	0.812	1.902	Weakly similar to hypothetical 33.9 kDa protein. [Source:Uniprot/SPTREMBL;Acc:Q8BHV4]
ENSMUSG00000048681	1.116	0.595	0.608	1.393	1.422	hypothetical protein
Dcun1d3	1.033	0.611	0.59	1.294	1.004	DCN1, defective in cullin neddylation 1, domain containing 3
BC022776	0.377	1.267	1.477	0.866	1.227	T-cell specific GTPase. [Source:RefSeq;Acc:NM_011579]
ENSMUSG00000049063	1.073	1.035	1.581	0.759	0.322	Putative per-hexamer repeat protein 3. [Source:Uniprot/SWISSPROT;Acc:P15975]

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Sephs2	1.092	1.039	0.831	0.705	0.864	Selenide,water dikinase 2 (EC 2.7.9.3) (Selenophosphate synthetase 2) (Selenium donor protein 2). [Source:Uniprot/SWISSPROT;Acc:P97364]
AK122503	0.584	0.863	1.471	0.847	0.805	protocadherin 10; OL-protocadherin. [Source:RefSeq;Acc:NM_011043]
BC060946	1.159	0.274	0.428	0.91	0.515	hypothetical protein
Prmt6	0.991	1.304	0.741	1.176	0.795	HMT1 hnRNP methyltransferase-like 6
Ltbp2	0.425	1.115	1.278	1.507	1.125	hypothetical protein
ENSMUSG00000049340	0.975	1.118	0.528	1.147	0.833	hypothetical protein
Olfr173	1.103	1.036	0.483	0.385	1.198	olfactory receptor 173; olfactory receptor MOR184-3; GA_x54KRFPKG5P-54960233-54959268. [Source:RefSeq;Acc:NM_147000]
Gemin4	1.149	1.443	0.5	0.842	1.148	gem (nuclear organelle) associated protein 4. [Source:RefSeq;Acc:NM_177367]
ENSMUSG00000049455	1.086	1.26	1.249	0.486	0.694	PREDICTED: similar to ZNF43 protein (LOC241944)
Olfr1449	1.042	1.166	0.397	0.839	1.415	olfactory receptor 1449; olfactory receptor MOR202-34; GA_x6K02T2RE5P-3264213-3265157. [Source:RefSeq;Acc:NM_146303]
Htr1b	0.507	0.587	1.528	0.854	1.675	5-hydroxytryptamine 1B receptor (5-HT-1B) (Serotonin receptor 1B). [Source:Uniprot/SWISSPROT;Acc:P28334]
Mapk10	0.835	0.472	1.527	1.039	0.432	mitogen activated protein kinase 10 isoform 1
ENSMUSG00000049571	1.291	1.398	1.616	0.93	0.71	hypothetical protein
AF257520, D64160	0.682	0.974	0.666	0.825	1.601	Retinoic acid early inducible protein 1 epsilon precursor (RAE- 1epsilon). [Source:Uniprot/SWISSPROT;Acc:Q9CZQ6]
Zbtb5	0.718	1.026	1.505	0.553	0.857	Zinc finger and BTB domain containing protein 5. [Source:Uniprot/SWISSPROT;Acc:Q7TQG0]
Tmem139	0.617	0.965	1.763	1.756	0.917	transmembrane protein 139; synonym: A930027H06Rik; Mus musculus transmembrane protein 139 (Tmem139), mRNA.

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ENSMUSG00000049696	0.677	0.539	0.722	1.32	0.811	hypothetical protein
Zfp646	1.025	1.016	0.692	0.736	1.094	zinc finger protein 646
Olfr466	0.42	0.401	0.477	0.875	1.802	olfactory receptor 466; olfactory receptor MOR209-1; GA_x6K02T2PB7A-3051266-3052192. [Source:RefSeq;Acc:NM_146819]
ENSMUSG00000049996	0.966	1.238	1.326	1.09	1.25	translocase of outer mitochondrial membrane 7 homolog. [Source:RefSeq;Acc:NM_025394]
D830007B15Rik	0.322	0.883	0.551	0.479	1.126	hypothetical protein LOC330096
4932413O14Rik	0.239	1.79	1.459	0.799	1.08	hypothetical protein LOC320696
Klk6	1.333	0.323	1.554	0.391	1.487	protease, serine, 18; protease, serine, 9; kallikrein 7; protease M; kallikrein 6; kallikrein 29. [Source:RefSeq;Acc:NM_011177]
Prdx6-rs1	1.482	0.741	2.264	0.676	0.77	peroxiredoxin 5 related sequence 1 protein; anti-oxidant protein 2 related sequence 1; peroxiredoxin 5 related sequence 1. [Source:RefSeq;Acc:NM_177256]
ENSMUSG00000050179	1.416	1.817	1.621	1.164	0.985	RIKEN cDNA A930002I21 gene (A930002I21Rik)
ENSMUSG00000050209	0.378	1.021	1.22	0.723	0.855	RIKEN cDNA 6720469N11 gene (6720469N11Rik)
D8Ertd82e	1.324	0.671	0.467	0.547	0.91	hypothetical protein LOC244418
ENSMUSG00000050281	0.371	0.754	1.555	1.087	1.698	olfactory receptor 630; olfactory receptor MOR17-1; GA_x6K02T2PBJ9-6483085-6482126. [Source:RefSeq;Acc:NM_147098]
Neto1	0.43	2.83	2.88	0.321	1.2	neuropilin- and tolloid-like protein 1. [Source:RefSeq;Acc:NM_144946]
CB316915	2.04	1.569	1.539	1.541	0.675	hypothetical protein
Mmp13	0.516	0.751	0.542	1.072	1.001	Collagenase 3 precursor (EC 3.4.24.-) (Matrix metalloproteinase-13) (MMP-13). [Source:Uniprot/SWISSPROT;Acc:P33435]
ENSMUSG00000050583	0.246	1.095	2.033	2.18	0.66	RIKEN cDNA 1700120K04 gene (1700120K04Rik)

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
A130092J06Rik	0.346	0.912	1.684	0.356	0.89	hypothetical protein LOC241303
ENSMUSG00000050600	1.466	2.409	0.869	0.891	0.539	PREDICTED: similar to dJ492J12.1 (novel protein similar to zinc finger protein human immunodeficiency virus type I enhancer-binding protein 1 (HIVEP1)) (LOC241830)
BC048562	0.889	0.921	1.611	1.17	0.643	hypothetical protein LOC434439
Defb19	0.949	0.374	1.741	1.014	0.64	defensin beta 19; testis-specific beta-defensin-like; defensin beta 119; testis specific beta defensin-like. [Source:RefSeq;Acc:NM_145157]
Scg2	1.103	1.951	1.551	1.024	0.884	Secretogranin II precursor (SgII) (Chromogranin C). [Source:Uniprot/SWISSPROT;Acc:Q03517]
Plekhq1	1.309	1.47	1.481	1.116	1.378	PH domain-containing protein homolog
BB511804	1.428	0.636	1.449	0.683	1.461	hypothetical protein
Ptges	0.392	0.764	0.685	0.878	0.712	Prostaglandin E synthase (EC 5.3.99.3) (mPGES-1). [Source:Uniprot/SWISSPROT;Acc:Q9JM51]
ENSMUSG00000050783	1.779	0.28	1.645	0.454	1.16	5-hydroxytryptamine 1F receptor (5-HT-1F) (Serotonin receptor 1F) (5- HT-1E-beta). [Source:Uniprot/SWISSPROT;Acc:Q02284]
Phospho1	0.955	2.077	1.236	0.894	1.036	phosphatase, orphan 1. [Source:RefSeq;Acc:NM_153104]
Rtn4rl2	0.962	1.154	1.333	1.31	1.003	reticulon 4 receptor-like 2; nogo-66 receptor-related protein 2; nogo receptor-like 3; nogo-66 receptor homolog 1. [Source:RefSeq;Acc:NM_199223]
Mtnr1b	2.984	1.385	1.713	1.329	0.72	Melatonin receptor type 1B (Mel-1B-R) (Mel1b melatonin receptor). [Source:Uniprot/SWISSPROT;Acc:Q8CIQ6]
Gja1	1.237	0.413	0.591	1.053	0.809	Gap junction alpha-1 protein (Connexin 43) (Cx43) (Gap junction 43 kDa heart protein). [Source:Uniprot/SWISSPROT;Acc:P23242]
ENSMUSG00000051168	0.647	1.09	1.81	0.276	0.731	hypothetical protein
Gpr119	0.966	0.546	1.385	1.091	1.171	G-protein coupled receptor 119; G protein-coupled receptor 119. [Source:RefSeq;Acc:NM_181751]

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Jagn1	0.965	1.295	1.207	1.042	0.989	jagunal homolog 1
AK129230	0.982	0.424	1.459	0.812	0.751	Rab11 interacting protein Rip11. [Source:Uniprot/SWISSPROT;Acc:Q8R361]
Flrt3	1.409	0.552	0.619	0.518	0.778	fibronectin leucine rich transmembrane protein 3. [Source:RefSeq;Acc:NM_178382]
Plagl2	0.988	0.85	0.592	1.418	0.878	pleiomorphic adenoma gene-like 2; pleomorphic adenoma gene like 2. [Source:RefSeq;Acc:NM_018807]
ENSMUSG00000051413	1.031	0.782	0.53	1.107	0.732	pleiomorphic adenoma gene-like 2; pleomorphic adenoma gene like 2. [Source:RefSeq;Acc:NM_018807]
Crebzf	0.75	0.772	1.343	0.755	1.459	HCF-binding transcription factor Zhangfei; tyrosine kinase-associated leucine zipper protein LAZipII. [Source:RefSeq;Acc:NM_145151]
4733401H21Rik	1.178	1.212	1.404	1.175	1.293	hypothetical protein LOC70831
ENSMUSG00000051483	0.959	1.353	1.239	1.276	1.016	Carbonyl reductase [NADPH] 1 (EC 1.1.1.184) (NADPH-dependent carbonyl reductase 1). [Source:Uniprot/SWISSPROT;Acc:P48758]
Olfr974	0.857	1.305	1.673	0.483	1.383	olfactory receptor 974; olfactory receptor MOR171-1; GA_x6K02T2PVTD-33640290-33641222. [Source:RefSeq;Acc:NM_147107]
Irf2bp2	1.044	2.181	1.345	0.961	1.342	Brain MY039 protein homolog (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8BJC6]
Zfp786	0.891	0.965	0.625	1.081	2.163	zinc finger protein 786
E130306D19Rik	1.526	1.746	4.124	1.129	0.676	hypothetical protein LOC230098
ENSMUSG00000051536	1.177	1.036	2.279	0.963	0.559	Olfactory receptor MOR6-1. [Source:Uniprot/SPTREMBL;Acc:Q8VGZ4]
Cmtm4	0.91	1.042	0.906	1.01	1.541	Chemokine-like factor super family member 4. [Source:Uniprot/SWISSPROT;Acc:Q8CJ61]
BY703358	0.312	1.255	1.632	1.75	1.085	hypothetical protein
B3gnt2	1.07	3.532	0.803	0.869	1.048	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1; beta-1,3-N-acetylglucosaminyltransferase; beta-1,3-N-acetylglucosaminyltransferase 1; UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 6.

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
ENSMUSG00000051658	1.002	1.663	2.023	1.088	2.42	PREDICTED: RIKEN cDNA 4932415A06 gene (4932415A06Rik)
A230078I05Rik	1.307	0.839	1.78	1.142	1.477	hypothetical protein LOC319998
Kcnf1	1.523	1.507	1.868	1.639	1.059	potassium voltage-gated channel, subfamily F, member 1. [Source:RefSeq;Acc:NM_201531]
1100001G20Rik	1.806	0.959	1.468	1.028	0.889	WDNM1-like protein
ENSMUSG00000051788	1.029	1.475	1.443	1.203	1.22	hypothetical protein
AK173159	1.263	0.637	1.558	1.026	0.666	neuroligin 2. [Source:RefSeq;Acc:NM_198862]
ENSMUSG00000051805	1.056	0.483	1.299	1.515	0.373	hypothetical protien
Cd209f	1.397	1.139	1.659	0.813	0.958	hypothetical protein LOC69142 isoform 1
BC067407	1.586	2.276	1.709	1.751	1.181	Transcription factor SOX-6 (SOX-LZ). [Source:Uniprot/SWISSPROT;Acc:P40645]
ENSMUSG00000051928	0.275	0.275	0.696	0.866	0.8	Inositol 1. [Source:Uniprot/SPTREMBL;Acc:Q8C9F0]
ENSMUSG00000051985	0.928	0.916	1.527	0.965	1.622	hypothetical protein
ENSMUSG00000052005	0.678	0.804	0.598	0.479	1.079	IgE-binding protein. [Source:Uniprot/SWISSPROT;Acc:P03975]
Rgs14	0.982	1.505	1.44	0.911	1.268	Regulator of G-protein signaling 14 (RGS14) (RAP1/RAP2 interacting protein). [Source:Uniprot/SWISSPROT;Acc:P97492]
Rnaset2b	1.283	0.733	1.171	1.062	1.051	Ribonuclease T2 precursor (EC 3.1.27.-) (Ribonuclease 6). [Source:Uniprot/SWISSPROT;Acc:Q9CQ01]
Olfr849	0.517	0.228	0.642	2.936	1.319	olfactory receptor 849; olfactory receptor MOR151-1; GA_x6K02T2PVTD-13176842-13177780. [Source:RefSeq;Acc:NM_146527]
Hbb-bh1	2.175	0.453	1.584	1.018	0.725	Hemoglobin beta-H1 chain (Z protein). [Source:Uniprot/SWISSPROT;Acc:P04444]

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Bhlhb8	0.955	1.1	1.966	1.34	0.606	muscle, intestine and stomach expression 1. [Source:RefSeq;Acc:NM_010800]
ENSMUSG00000052351	0.721	0.619	0.684	1.013	0.865	hypothetical protein
ENSMUSG00000052372	1.279	1.16	1.592	1.235	1.325	X-linked interleukin-1 receptor accessory protein-like 1 precursor (IL1RAPL-1). [Source:Uniprot/SWISSPROT;Acc:P59823]
Olfr633	0.915	0.949	0.813	1.03	1.057	olfactory receptor 633; olfactory receptor MOR12-5; GA_x6K02T2PBJ9-6681230-6682168. [Source:RefSeq;Acc:NM_146354]
Olfr720	0.901	0.451	1.824	1.255	1.414	olfactory receptor 720; olfactory receptor MOR274-2; GA_x6K02T2PLTE-6544896-6543946. [Source:RefSeq;Acc:NM_146392]
Bmpr1b	0.335	1.112	1.624	0.763	0.247	Bone morphogenetic protein receptor type IB precursor (EC 2.7.1.37) (Serine/threonine-protein kinase receptor R6) (SKR6) (Activin receptor-like kinase 6) (ALK-6). [Source:Uniprot/SWISSPROT;Acc:P36898]
ENSMUSG00000052537	1.367	1.249	3.079	1.042	1.83	Olfactory receptor GA_x54KRFPKG5P-55416332-55415412. [Source:Uniprot/SPTREMBL;Acc:Q7TS40]
Hist1h1d	1.826	1.468	1.937	2.015	1.002	Histone H1.3 (H1 VAR.4) (H1D). [Source:Uniprot/SWISSPROT;Acc:P43277]
Ccdc79	0.927	0.138	1.832	1.586	1.07	Myb DNA binding domain-containing protein. [Source:RefSeq;Acc:NM_180958]
ENSMUSG00000052659	1.287	1.403	0.693	0.896	1.764	hypothetical protein
ENSMUSG00000052688	0.791	1.223	1.469	1.055	1.766	RAB7-like protein. [Source:RefSeq;Acc:NM_145509]
ENSMUSG00000052728	0.44	1.098	0.575	0.907	0.68	hypothetical protein
A530023O14Rik	0.744	1.145	0.526	0.252	1.241	hypothetical protein LOC244183
Mypn	1.936	0.424	1.526	1.56	1.244	myopalladin
EG245113	1.244	0.901	0.823	0.827	0.864	similar to tissue-type vomeronasal neurons putative pheromone receptor V2R2
F830104D24Rik	1.001	1.903	0.575	1.094	0.998	pheromone receptor-like

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ENSMUSG00000053037	1.891	2.179	1.517	1.157	1.549	hypothetical protein
Socs3	1.008	0.414	0.416	1.062	0.899	Suppressor of cytokine signaling 3 (SOCS-3) (Cytokine-inducible SH2 protein 3) (CIS-3) (Protein EF-10). [Source:Uniprot/SWISSPROT;Acc:O35718]
Gprc2a-rs5	1.991	0.757	1.626	0.862	1.323	G protein-coupled receptor, family C, group 2, member A, related sequence 5
Olfr212	0.433	0.881	2.333	0.411	1.159	olfactory receptor 212
Sec61b	1.021	2.039	1.38	1.189	0.966	Sec61 beta subunit
BC024587	1.179	1.258	1.283	1.002	1.519	PREDICTED: SLAM family member 8 (Slamf8)
ENSMUSG00000053400	0.482	1.65	0.673	0.689	1.753	hypothetical protein
Cbx7	1.116	0.6	0.596	0.864	0.985	Chromobox protein homolog 7. [Source:Uniprot/SWISSPROT;Acc:Q8VDS3]
Mapk14	0.903	1.238	0.615	0.791	1.357	Mitogen-activated protein kinase 14 (EC 2.7.1.37) (Mitogen-activated protein kinase p38alpha) (MAP kinase p38alpha) (CRK1). [Source:Uniprot/SWISSPROT;Acc:P47811]
ENSMUSG00000053470	1.038	1.072	1.383	1.188	0.393	Similar to zinc finger protein (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8K2K4]
ENSMUSG00000053526	1.385	0.613	1.63	0.182	1.231	hypothetical protein
CN664323	0.369	1.523	0.777	1.046	1.418	PREDICTED: similar to dedicator of cytokinesis 11 (LOC434754)
EG209380	1.088	1.088	1.624	1.016	1.827	similar to very large inducible GTPase 1. [Source:RefSeq;Acc:NM_001001318]
D430041B17Rik	0.494	1.074	1.458	0.778	0.767	hypothetical protein LOC232813
ENSMUSG00000053663	1.173	0.788	1.691	2.248	1.169	hypothetical protein
ENSMUSG00000053719	1.23	1.16	1.346	0.727	1.019	Glandular kallikrein K26 precursor (EC 3.4.21.35) (Tissue kallikrein 26) (mGK-26) (Prorenin-converting enzyme 2) (PRECE-2). [Source:Uniprot/SWISSPROT;Acc:P36369]

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Jak3	0.824	0.68	0.634	1.101	0.928	Insulin-like 3 precursor (Leydig insulin-like peptide) (Ley-I-L) (Relaxin-like factor). [Source:Uniprot/SWISSPROT;Acc:O09107]
ENSMUSG00000053815	0.609	1.491	0.481	0.252	0.972	Olfactory receptor GA_x6K02T2PMLR-6326342-6327313. [Source:Uniprot/SPTREMBL;Acc:Q7TRM0]
ENSMUSG00000053839	0.454	0.956	0.501	1.101	1.35	hypothetical protein
BU562831	0.897	1.113	0.596	2.958	0.937	hypothetical protein
Ech1	1.09	1.035	1.227	1.432	0.87	Delta3,5-delta2,4-dienoyl-CoA isomerase, mitochondrial precursor (EC 5.3.3.-). [Source:Uniprot/SWISSPROT;Acc:O35459]
BQ178867	0.391	0.493	1.302	1.849	0.55	PREDICTED: similar to FLJ45455 protein (LOC380702)
ENSMUSG00000053993	1.14	1.39	1.523	0.902	0.471	PREDICTED: similar to Ribosomal protein L3 (LOC242809)
ENSMUSG00000054003	0.899	0.928	1.54	1.163	1.989	hypothetical protein
Krt15	0.652	0.975	1.672	1.494	1.018	Keratin, type I cytoskeletal 15 (Cytokeratin 15) (K15) (CK 15). [Source:Uniprot/SWISSPROT;Acc:Q61414]
Cpsf3	0.634	2.15	1.417	0.955	1.265	Cleavage and polyadenylation specificity factor, 73 kDa subunit (CPSF 73 kDa subunit). [Source:Uniprot/SWISSPROT;Acc:Q9QXK7]
6430604K15Rik	0.745	0.582	0.29	0.865	0.805	hypothetical protein LOC269997
Atpif1	0.992	1.189	1.156	1.521	0.833	ATPase inhibitor, mitochondrial precursor. [Source:Uniprot/SWISSPROT;Acc:O35143]
Sytl5	1.008	1.379	1.511	1.057	1.214	Synaptotagmin-like protein 5. [Source:Uniprot/SWISSPROT;Acc:Q80T23]
Vsnl1	0.516	0.55	0.711	0.319	0.28	Visinin-like protein 1 (VILIP-1) (Neural visinin-like protein 1) (NVL- 1) (NVP-1) (21 kDa CABP) (Neurocalcin alpha) (Hippocalcin-like protein 3) (HLP3). [Source:Uniprot/SWISSPROT;Acc:P28677]
ENSMUSG00000054471	0.862	0.601	1.474	1.03	1.042	hypothetical protein

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Olfr308	0.762	0.597	1.819	0.536	1.564	olfactory receptor 308; olfactory receptor MOR104-1; GA_x6K02T2NHDJ-9786435-9787361. [Source:RefSeq;Acc:NM_146621]
ENSMUSG00000054526	0.718	1.23	0.557	1.207	1.272	Olfactory receptor GA_x6K02T2RE5P-4160554-4159619. [Source:Uniprot/SPTREMBL;Acc:Q7TQQ3]
Muc4	1.023	0.299	0.562	1.117	0.739	mucin 4
ENSMUSG00000054545	0.727	0.722	0.799	1.14	0.791	UDP-glucuronosyltransferase 1-2 precursor, microsomal (EC 2.4.1.17) (UDPGT) (UGT1*0) (UGT1-02) (UGT1.2) (UGT1A2) (Bilirubin specific). [Source:Uniprot/SWISSPROT;Acc:P70691]
ENSMUSG00000054591	0.458	1.401	1.687	0.834	0.714	OBOX4 (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8VHG5]
Xlr	0.837	0.883	1.696	1.022	0.848	X-linked lymphocyte-regulated protein PM1. [Source:Uniprot/SWISSPROT;Acc:P05531]
ENSMUSG00000054636	1.075	1.299	1.45	1.337	1.078	hypothetical protein
Zfp182	1.674	1.781	1.573	0.904	0.706	Finger protein kox14 homolog (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8CCU4]
ENSMUSG00000054743	1.102	1.326	0.727	1.153	1.14	hypothetical protein
ENSMUSG00000054795	0.554	0.971	2.155	0.423	0.804	hypothetical protein
Rnd1	0.638	0.457	0.444	1.256	0.587	Rho family GTPase 1. [Source:RefSeq;Acc:NM_172612]
ENSMUSG00000054931	0.878	1.578	1.545	0.934	1.043	hypothetical protein
ENSMUSG00000054952	1.021	0.747	0.744	0.966	1.039	hypothetical protein
Lrtm2	0.377	0.627	1.297	1.721	1.506	leucine-rich repeats and transmembrane domains 2
ENSMUSG00000055131	1.434	1.412	1.296	0.845	1.998	hypothetical protein
Kcmf1	0.992	0.931	0.915	0.796	0.844	potassium channel modulatory factor DEBT-91; clone DEBT-91. [Source:RefSeq;Acc:NM_019715]

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Wdr6	1.552	1.358	1.524	1.133	0.726	WD repeat domain 6. [Source:RefSeq;Acc:NM_031392]
ENSMUSG00000055323	1.238	1.682	1.452	1.976	1.371	hypothetical protein
ENSMUSG00000055395	0.924	0.477	1.917	0.897	1.367	hypothetical protein
Mtap6	1.011	0.468	1.298	1.134	1.461	microtubule-associated protein 6. [Source:RefSeq;Acc:NM_010837]
ENSMUSG00000055415	0.875	1.042	0.808	1.122	0.973	hypothetical protein
Apob	1.558	1.126	0.465	0.548	0.849	PREDICTED: apolipoprotein B (Apob)
ENSMUSG00000055468	0.557	0.527	2.114	1.556	1.934	hypothetical protein
ENSMUSG00000055596	1.03	1.364	1.575	0.788	1.031	hypothetical protein
E030030I06Rik	1.139	1.125	0.609	1.168	1.098	Weakly similar to cyclin-dependent kinase 6 (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8BLG7]
ENSMUSG00000055660	0.645	1.629	0.786	0.772	1.549	hypothetical protein
ENSMUSG00000055720	1.132	1.219	0.721	0.9	0.979	Ubiquitin-like protein SB132. [Source:Uniprot/SWISSPROT;Acc:Q91W67]
ENSMUSG00000055801	3.162	0.905	1.682	0.414	0.401	hypothetical protein
ENSMUSG00000055956	1.176	1.294	2.941	0.636	1.007	hypothetical protein
Nod2	1.245	1.488	0.71	0.564	1.145	Caspase recruitment domain protein 15 (Nod2 protein). [Source:Uniprot/SWISSPROT;Acc:Q8K3Z0]
BC052328	0.932	1.079	1.214	1.074	0.858	hypothetical protein LOC223433
ENSMUSG00000056080	1.043	0.47	1.369	0.847	0.499	hypothetical protein
AB080741	1.035	1.206	1.389	1.447	0.443	Carbonic anhydrase-related protein 10 (Carbonic anhydrase-related protein X) (CARP X) (CA-RP X).

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ENSMUSG00000056217	0.764	1.154	1.49	0.797	0.425	Weakly similar to mucin-like protein. [Source:Uniprot/SPTREMBL;Acc:Q8BIC0]
Pla2g4a	1.354	0.836	0.663	1.323	1.097	Cytosolic phospholipase A2 (cPLA2) (Phospholipase A2 group IVA) [Includes: Phospholipase A2 (EC 3.1.1.4) (Phosphatidylcholine 2- acylhydrolase); Lysophospholipase (EC 3.1.1.5)]. [Source:Uniprot/SWISSPROT;Acc:P47713]
Ms4a4b	1.189	1.313	0.706	0.925	1.144	membrane-spanning 4-domains, subfamily A, member 4B; lymphocyte antigen 116. [Source:RefSeq;Acc:NM_021718]
1810011O10Rik	0.677	0.777	1.571	1.195	1.424	thyroid cancer-1
ENSMUSG00000056316	0.816	1.416	1.424	1.137	1.276	hypothetical protein
ENSMUSG00000056359	0.97	1.526	1.577	0.357	0.825	PREDICTED: RIKEN cDNA D830013O20 gene (D830013O20Rik)
ENSMUSG00000056460	1.551	0.866	0.521	1.023	2.883	PREDICTED: similar to putative odorant receptor (LOC384749)
ENSMUSG00000056476	1.651	0.578	1.37	2.488	0.504	NOPAR2 homolog. [Source:Uniprot/SPTREMBL;Acc:Q8C9E3]
Cd248	0.921	1.069	1.507	0.82	0.557	CD164 sialomucin-like 1; tumor endothelial marker 1 precursor. [Source:RefSeq;Acc:NM_054042]
ENSMUSG00000056516	0.826	1.262	0.834	0.836	0.875	NADH-ubiquinone oxidoreductase chain 4L (EC 1.6.5.3). [Source:Uniprot/SWISSPROT;Acc:P03903]
ENSMUSG00000056524	0.392	0.974	0.544	1.569	0.973	hypothetical protein
ENSMUSG00000056527	1.267	2.152	1.786	1.367	1.352	hypothetical protein
Olfr1350	1.189	1.147	0.714	2.121	0.965	olfactory receptor 1350; olfactory receptor MOR222-3; GA_x6K02T2QGBW-3300391-3301317. [Source:RefSeq;Acc:NM_146389]
Capg	0.929	1.434	1.21	1.107	1.525	Macrophage capping protein (Myc basic motif homolog-1) (Actin-capping protein GCAP39). [Source:Uniprot/SWISSPROT;Acc:P24452]

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Ash1l	0.24	0.564	0.55	0.738	1.879	Similar to absent, small, or homeotic discs 1 (Drosophila) (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q80VY5]
ENSMUSG00000056850	1.562	0.244	2.498	1.027	0.446	Anti-myosin immunoglobulin light chain variable region (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q9JL78]
Olfr1360	0.267	0.846	1.484	0.518	0.875	olfactory receptor 1360; GA_x6K02T2QHY8-11561962-11562903; olfactory receptor MOR256-10. [Source:RefSeq;Acc:NM_146543]
CN839098	0.641	1.666	0.544	0.821	0.269	hypothetical protein
ENSMUSG00000056952	1.541	0.858	1.458	0.789	0.904	hypothetical protein
4921509E07Rik	1.687	1.7	1.696	2.158	0.58	hypothetical protein LOC70897
Polr2k	0.843	1.052	1.315	1.081	0.627	DNA-directed RNA polymerases I, II, and III 7.0 kDa polypeptide (EC 2.7.7.6) (ABC10-alpha) (RPB7.0) (Metallothionein-I gene transcription activator). [Source:Uniprot/SWISSPROT;Acc:Q63871]
Myh3	1.087	1.818	1.754	0.942	0.326	myosin, heavy polypeptide 3, skeletal muscle, embryonic
Rims2	0.531	3.784	2.46	1.4	0.566	regulating synaptic membrane exocytosis 2
Arih2	1.396	0.967	0.781	1.059	0.81	Ariadne-2 protein homolog (ARI-2) (Triad1 protein) (UbcM4-interacting protein 48). [Source:Uniprot/SWISSPROT;Acc:Q9Z1K6]
Tmem140	1.078	2.035	1.739	1.248	1.141	transmembrane protein 140; synonym: 1110007F12Rik; Mus musculus transmembrane protein 140 (Tmem140), mRNA.
ENSMUSG00000057145	0.326	1.433	1.439	0.704	1.274	hypothetical protein
V1rg3	1.053	1.676	1.469	0.583	0.57	vomeronasal 1 receptor, G3. [Source:RefSeq;Acc:NM_134204]
BC071190	0.942	1.193	1.291	0.926	1.063	hypothetical protein
Olfr1484	0.636	0.56	1.722	1.964	1.296	Putative olfactory receptor 185-3. [Source:Uniprot/SWISSPROT;Acc:Q8VGS1]
ENSMUSG00000057231	1.172	0.322	1.408	1.055	1.21	hypothetical protein

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Gm9	1.539	1.424	0.78	0.628	1.337	hypothetical protein LOC194854
Acaca	1.316	0.744	0.672	0.484	0.898	acetyl-Coenzyme A carboxylase alpha
ENSMUSG00000057481	1.078	0.965	1.268	1.129	1.006	PREDICTED: similar to Small nuclear ribonucleoprotein F (snRNP-F) (Sm protein F) (Sm-F) (SmF) (LOC382887)
ENSMUSG00000057641	0.175	2.278	1.921	3.169	0.886	hypothetical protein
BC057597	0.928	1.104	0.666	0.85	1.047	hypothetical protein
ENSMUSG00000057649	1.592	0.861	0.636	0.535	0.367	hypothetical protein
U42467	0.452	0.458	1.673	0.682	1.271	Leptin receptor precursor (LEP-R) (OB receptor) (OB-R) (B219). [Source:Uniprot/SWISSPROT;Acc:P48356]
CB174439	0.969	0.642	0.78	0.705	0.949	olfactory receptor 1360; GA_x6K02T2QHY8-11561962-11562903; olfactory receptor MOR256-10. [Source:RefSeq;Acc:NM_146543]
ENSMUSG00000057772	0.956	1.249	1.337	0.588	1.79	hypothetical protein
Olfr1446	0.745	0.791	0.548	1.114	0.73	olfactory receptor 1446; olfactory receptor MOR202-2; GA_x6K02T2RE5P-3220047-3219130. [Source:RefSeq;Acc:NM_146704]
ENSMUSG00000057871	1.397	0.811	2.345	1.379	1.3	hypothetical protein
Cyp3a44	1.019	0.153	1.791	1.028	0.342	cytochrome P450, family 3, subfamily a, polypeptide 44
ENSMUSG00000057948	1	0.923	0.735	1.196	1.267	Similar to Munc13-4 protein. [Source:Uniprot/SPTREMBL;Acc:Q80UG7]
ENSMUSG00000057993	0.263	0.731	1.562	0.988	2.169	PROTOCADHERIN-9 homolog (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8C421]
V1rf3	1.144	0.166	1.557	0.346	0.711	vomeronasal 1 receptor, F3. [Source:RefSeq;Acc:NM_134200]
ENSMUSG00000058070	1.099	1.481	1.771	1.418	1.421	hypothetical protein
Olfr818	0.646	0.921	1.462	1.631	1.233	olfactory receptor 818; olfactory receptor MOR110-2; GA_x6K02T2PULF-11624146-11623190.

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Sdhc	1.112	0.887	1.185	1.189	1.052	Succinate dehydrogenase cytochrome b560 subunit, mitochondrial precursor (Integral membrane protein CII-3) (QPS1) (QPs-1). [Source:Uniprot/SWISSPROT;Acc:Q9CZB0]
ENSMUSG00000058124	1.233	0.6	1.837	1.242	0.547	histocompatibility 2, M region locus 10.3. [Source:RefSeq;Acc:NM_201608]
ENSMUSG00000058140	1.235	0.932	0.777	0.872	0.911	hypothetical protein
Krtap6-1	0.989	0.463	2.288	1.297	1.293	keratin associated protein 6-1; keratin-associated protein 6.1; keratin-associated protein 6-1. [Source:RefSeq;Acc:NM_010672]
ENSMUSG00000058210	1.366	0.69	1.857	0.596	1.049	hypothetical protein
ENSMUSG00000058217	0.715	0.757	0.769	0.397	0.714	Melanoma derived growth regulatory protein precursor (Melanoma inhibitory activity) (Cartilage-derived retinoic acid-sensitive protein) (CD-RAP). [Source:Uniprot/SWISSPROT;Acc:Q61865]
ENSMUSG00000058221	1.021	1.117	0.738	1.029	0.835	RNP particle component (Fragment). [Source:Uniprot/SPTREMBL;Acc:O08905]
Grlf1	1.693	0.951	0.784	1.303	1.203	glucocorticoid receptor DNA binding factor 1
ENSMUSG00000058305	1.017	0.197	1.276	1.258	0.734	PREDICTED: similar to IgM(b) heavy pre-chain (AA -18 to 119) (LOC380822)
ENSMUSG00000058324	1.043	0.936	0.683	1.155	0.709	hypothetical protein
ENSMUSG00000058351	1.334	0.793	1.416	1.214	0.817	hypothetical protein
Myh3	0.936	1.481	0.496	1.072	0.957	Myosin heavy chain, fast skeletal muscle, embryonic (Fragment). [Source:Uniprot/SWISSPROT;Acc:P13541]
ENSMUSG00000058430	0.666	1.053	2.066	0.633	1.014	PREDICTED: similar to ribosomal protein L27a; ribosomal protein L29 homolog (yeast) (LOC239245)
V1rc7	0.792	1.9	1.537	1.254	1.451	vomeronasal 1 receptor, C7. [Source:RefSeq;Acc:NM_053237]

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
ENSMUSG00000058442	1.001	2.77	1.858	0.267	1.342	hypothetical protein
Ifitm7	1.292	0.272	0.609	0.579	0.715	interferon induced transmembrane protein 7; interferon induced transmembrane protein like 4 (human); interferon induced transmembrane protein 4 like (human); interferon induced transmembrane protein 4 like. [Source:RefSeq;Acc:NM_028968]
Pcf11	0.831	1.75	1.344	0.323	1.186	pre-mRNA cleavage complex II protein Pcf11
V1rb1	0.291	1.22	1.418	1.701	0.438	vomeronasal 1 receptor, B1. [Source:RefSeq;Acc:NM_053225]
ENSMUSG00000058602	0.597	0.875	0.425	1.041	0.255	hypothetical protein
AY761184	0.775	0.976	0.407	0.543	1.106	PREDICTED: similar to Cryptdin-related protein 1C precursor (CRS1C) (LOC382000)
Zfp110	1.149	1.216	1.475	0.831	0.776	zinc finger protein 110; neurotrophin receptor interacting factor. [Source:RefSeq;Acc:NM_022981]
Wdr49	1.077	0.589	1.464	1.739	1.535	similar to WD repeat domain 49
ENSMUSG00000058654	1.29	1.213	1.475	1.183	1.206	hypothetical protein
ENSMUSG00000058661	2.572	1.087	2.039	0.6	0.588	hypothetical protein
ENSMUSG00000058674	0.515	1.6	1.745	1.412	0.452	hypothetical protein
ENSMUSG00000058736	0.734	1.26	0.76	1.195	1.035	hypothetical protein
Ndufb6	1.108	0.667	1.715	1.321	0.767	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6
ENSMUSG00000058796	0.694	1.222	1.582	0.818	0.483	hypothetical protein
ENSMUSG00000058810	0.831	1.717	0.567	0.638	0.794	hypothetical protein
Olfr146	1.101	0.875	1.465	1.857	1.568	Olfactory receptor 146 (Olfactory receptor 7D) (M15) (Fragment). [Source:Uniprot/SWISSPROT;Acc:Q60884]

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
ENSMUSG00000058934	0.974	0.676	1.586	1.264	1.002	hypothetical protein
ENSMUSG00000058941	0.858	1.126	1.443	1.418	1.136	Olfactory receptor GA_x6K02T2QD9B-18619941-18620882. [Source:Uniprot/SPTREMBL;Acc:Q7TQV9]
ENSMUSG00000059001	0.976	1.011	0.547	1.269	0.907	hypothetical protein
Psg23	0.902	0.941	0.526	1.158	0.791	Cea11 protein (Fragment). [Source:Uniprot/SPTREMBL;Acc:O08926]
Olfr15	0.814	1.596	0.59	0.703	0.158	Olfactory receptor 15 (OR3). [Source:Uniprot/SWISSPROT;Acc:P23275]
Olfr749	1.226	0.969	0.857	1.158	0.895	odorant receptor S1; odorant receptor S1 gene; GA_x6K02T2PMLR-6484046-6483105. [Source:RefSeq;Acc:NM_020288]
ENSMUSG00000059126	2.068	0.914	2.131	1.782	0.387	hypothetical protein
ENSMUSG00000059176	0.89	0.806	1.496	0.734	1.261	hypothetical protein
ENSMUSG00000059200	0.43	3.174	1.934	0.673	1.528	hypothetical protein
ENSMUSG00000059270	0.929	0.67	1.282	1.062	1.818	hypothetical protein
R74862	1.46	0.678	1.554	0.42	1.578	hypothetical protein
Nfkbil2	0.655	0.717	0.54	2.239	0.578	I-kappa-B-related protein
ENSMUSG00000059380	0.852	0.814	0.685	0.594	0.584	hypothetical protein
Ccdc28a	0.154	1.394	1.229	0.596	1.229	coiled-coil domain containing 28A
ENSMUSG00000059564	1.654	0.983	1.197	1.103	1.19	hypothetical protein
Olfr1339	0.489	0.384	1.649	1.243	0.091	olfactory receptor 1339; olfactory receptor MOR258-2; GA_x6K02T2QD9B-18815145-18814198. [Source:RefSeq;Acc:NM_146852]
Nrm	0.904	1.306	0.757	0.963	1.499	nurim (nuclear envelope membrane protein). [Source:RefSeq;Acc:NM_134122]

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Olfr847	1.319	0.918	0.518	0.815	1.374	olfactory receptor 847; olfactory receptor MOR149-2; GA_x6K02T2PVTD-13113073-13112135. [Source:RefSeq;Acc:NM_146525]
Krtap9-1	0.904	0.802	0.476	1.008	1.179	keratin associated protein 9-1; keratin-associated protein 9.1; keratin-associated protein 9-1. [Source:RefSeq;Acc:NM_015741]
Suv420h2	1.054	1.081	0.725	0.925	0.819	suppressor of variegation 4-20 homolog 2
Stk22s1	1.284	0.701	1.353	1.313	1.543	serine/threonine kinase 22 substrate 1 isoform 1
ENSMUSG00000059897	1.952	1.309	0.277	0.774	0.883	PREDICTED: cDNA sequence D10627 (D10627)
Mug1	1.347	0.455	0.471	0.904	0.363	Murinoglobulin 1 precursor (MuG1). [Source:Uniprot/SWISSPROT;Acc:P28665]
BF020696	1.281	0.618	0.48	0.792	0.933	hypothetical protein
ENSMUSG00000059947	0.24	1.432	0.592	0.913	0.856	hypothetical protein
Lsm5	1.283	1.232	0.747	0.952	0.71	LSM5 homolog, U6 small nuclear RNA associated. [Source:RefSeq;Acc:NM_025520]
EG433319	0.918	0.876	2.052	1.072	0.707	similar to ribosomal protein L21
AK173307	1.514	0.855	0.552	1.366	0.968	hypothetical protein
Pop5	0.933	1.653	1.847	0.933	0.838	processing of precursor 5, ribonuclease P/MRP family; RNase MRP/RNase P protein-like; processing of precursor 5, ribonuclease P/MRP family, (S. cerevisiae). [Source:RefSeq;Acc:NM_026398]
Lrrc10	0.808	1.156	0.599	0.749	0.981	leucine-rich repeat-containing 10; leucine-rich repeat protein; leucine-rich containing 10. [Source:RefSeq;Acc:NM_146242]
ENSMUSG00000060256	0.784	0.58	0.812	1.042	1.092	TD and POZ domain containing 4; TD and POZ domain containing gene 4. [Source:RefSeq;Acc:NM_207272]
Olfr894	1.797	1.088	1.391	0.966	1.663	olfactory receptor 894; olfactory receptor MOR170-5; GA_x6K02T2PVTD-31898993-31899934. [Source:RefSeq;Acc:NM_146868]
EG225058	0.878	1.023	1.633	1.174	0.767	similar to ribosomal protein S24

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
ENSMUSG00000060399	3.473	1.262	2.059	0.664	1.229	hypothetical protein
Serpinb3b	1.868	1.634	0.727	0.945	1.039	squamous cell carcinoma antigen 2 related protein 1; serpinb3b. [Source:RefSeq;Acc:NM_198680]
Nlrp9b	0.731	0.9	0.361	0.377	1.266	NACHT, LRR and PYD containing protein 9b
0610040J01Rik	0.933	3.041	1.77	0.698	0.923	hypothetical protein LOC76261
ENSMUSG00000060586	0.771	0.887	1.11	0.911	0.683	H-2 class II histocompatibility antigen, E-B beta chain precursor. [Source:Uniprot/SWISSPROT;Acc:P04230]
Ifitm2	0.753	0.577	0.638	0.72	1.122	interferon induced transmembrane protein 2; interferon induced transmembrane protein, like; interferon induced transmembrane protein 3-like; fragilis R. [Source:RefSeq;Acc:NM_030694]
Nkpd1	0.744	0.837	1.929	0.442	0.865	NTPase, KAP family P-loop domain containing 1
4930595M18Rik	0.465	1.019	2.006	1.134	1.514	hypothetical protein LOC245492
ENSMUSG00000060719	1.162	1.144	1.648	1.737	1.069	Weakly similar to reverse transcriptase. [Source:Uniprot/SPTREMBL;Acc:Q8BIB0]
2410018L13Rik	1.438	1.04	1.695	0.929	1.041	hypothetical protein LOC69732
Olfr17	1.264	1.125	1.809	1.396	0.899	olfactory receptor 17; GA_x6K02T2PBJ9-9470146-9471093; olfactory receptor MOR263-5. [Source:RefSeq;Acc:NM_020598]
ENSMUSG00000060931	0.249	1.098	1.352	1.176	1.372	olfactory receptor 313 (Olfr313)
Slc4a4	1.665	1.448	0.481	0.846	0.728	solute carrier family 4 (anion exchanger), member 4; pancreas sodium bicarbonate cotransporter. [Source:RefSeq;Acc:NM_018760]
Olfr507	0.291	1.008	4.124	0.153	1.335	Putative olfactory receptor 204-7. [Source:Uniprot/SWISSPROT;Acc:Q8VG13]
ENSMUSG00000061019	0.2	1.033	1.433	0.962	2.119	PREDICTED: similar to short coiled-coil protein; short coiled coil protein (LOC433655)
BC059938	0.73	1.094	0.695	0.997	0.948	similar to phosphatidylserine decarboxylase (MGC65558)

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Olfr920	0.726	0.676	1.895	1.633	1.441	olfactory receptor 920; olfactory receptor MOR165-6; GA_x6K02T2PVTD-32458442-32459374. [Source:RefSeq;Acc:NM_146787]
Cbln4	1.287	0.801	0.365	1.046	0.763	Cerebellin-like glycoprotein 1 precursor (Cerebellin 4). [Source:Uniprot/SWISSPROT;Acc:Q8BME9]
ENSMUSG00000061069	0.938	1.015	1.083	0.96	0.978	hypothetical protein
ENSMUSG00000061069	0.839	1.135	1.595	1.258	0.838	PREDICTED: similar to hypothetical protein FLJ38281 (LOC434382)
Blnk	1.042	1.216	1.357	1.013	1.061	B-cell linker; lymphocyte antigen 57. [Source:RefSeq;Acc:NM_008528]
ENSMUSG00000061180	0.862	0.712	1.71	0.846	1.219	hypothetical protein
ENSMUSG00000061181	1.203	1.649	1.397	1.355	0.628	PREDICTED: RIKEN cDNA 2900041A11 gene (2900041A11Rik)
ENSMUSG00000061203	0.269	1.88	0.644	1.901	0.729	hypothetical protein
Tmprss11d	1.085	0.839	1.343	0.92	0.499	airway trypsin-like protease precursor. [Source:RefSeq;Acc:NM_145561]
ENSMUSG00000061334	0.908	0.978	0.533	0.793	0.842	Friend virus susceptibility 4. [Source:RefSeq;Acc:NM_010245]
Csn1s2b	0.863	0.524	0.664	0.479	0.304	Epsilon casein precursor. [Source:Uniprot/SWISSPROT;Acc:P02664]
EG329070	1.881	0.864	1.134	0.936	1.51	hypothetical protein C230050L11 (C230050L11)
ENSMUSG00000061496	1.4	0.288	2.124	0.837	1.563	hypothetical protein
ENSMUSG00000061612	1.717	1.727	2.226	0.626	1.385	Ig heavy chain V region 1B43 precursor. [Source:Uniprot/SWISSPROT;Acc:P18532]
Olfr845	1.139	1.673	0.698	1.494	1.101	olfactory receptor 845; GA_x6K02T2PVTD-13076685-13077623; olfactory receptor MOR150-2. [Source:RefSeq;Acc:NM_207145]
BE456855	0.765	4.668	1.698	2.074	0.688	PREDICTED: hypothetical LOC381452 (LOC381452)

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
ENSMUSG00000061719	0.424	0.96	1.759	1.123	0.322	hypothetical protein
ENSMUSG00000061722	0.904	0.117	0.496	0.559	0.278	hypothetical protein
ENSMUSG00000061741	0.722	0.491	1.951	0.532	0.679	hypothetical protein
Rps17	0.743	1.001	1.195	0.646	0.834	40S ribosomal protein S17. [Source:Uniprot/SWISSPROT;Acc:P06584]
AA871410	0.937	0.143	2.47	1.161	1.02	Cryptdin-5 precursor. [Source:Uniprot/SWISSPROT;Acc:P28312]
ENSMUSG00000061907	1.018	0.265	3.373	0.958	0.691	Ig delta chain C region secreted form. [Source:Uniprot/SWISSPROT;Acc:P01881]
BC052495	0.239	0.346	0.168	1.669	0.829	Serum amyloid A-1 protein precursor. [Source:Uniprot/SWISSPROT;Acc:P05366]
Saa1	0.467	0.462	0.522	0.995	1.544	Serum amyloid A-1 protein precursor. [Source:Uniprot/SWISSPROT;Acc:P05366]
ENSMUSG00000062009	1.554	1.436	0.775	0.802	1.005	hypothetical protein
Athl1	1.147	0.958	1.514	1.13	0.852	ATH1, acid trehalase-like 1
Blcap	1.161	0.962	0.873	0.859	1.236	Bladder cancer-associated protein (Bladder cancer 10 kDa protein) (Bc10). [Source:Uniprot/SWISSPROT;Acc:O60629]
ENSMUSG00000062058	0.872	0.508	1.515	1.293	0.965	L1Md-9 repetitive sequence. [Source:Uniprot/SPTREMBL;Acc:Q04365]
ENSMUSG00000062063	1.068	0.845	1.327	1.186	0.94	zinc finger protein 617; Zinc finger protein s11-6. [Source:RefSeq;Acc:NM_133358]
Zfp617	1.284	0.968	0.456	1.357	1.306	zinc finger protein 617; Zinc finger protein s11-6. [Source:RefSeq;Acc:NM_133358]
ENSMUSG00000062068	0.353	1.103	0.611	0.664	0.984	hypothetical protein
ENSMUSG00000062080	0.68	0.702	0.557	0.67	0.926	Single chain Fv (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q99NG4]
CB174114, CB174399	1.667	0.337	1.652	1.346	1.376	olfactory receptor 943; olfactory receptor MOR171-44; GA_x6K02T2PVTD-32881408-32882343. [Source:RefSeq;Acc:NM_146326]

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
1700061J05Rik	1.585	1.029	1.951	1.366	1.549	hypothetical protein LOC73376
Tgif2	0.462	0.507	0.89	0.81	1.619	TGFB-induced factor 2; TALE family homeobox. [Source:RefSeq;Acc:NM_173396]
ENSMUSG00000062199	2.505	0.128	1.418	0.885	0.338	Olfactory receptor GA_x6K02T2RE5P-3645346-3644423. [Source:Uniprot/SPTREMBL;Acc:Q7TQR2]
Rapgef2	0.345	0.977	0.714	1.188	1.182	Rap guanine nucleotide exchange factor 2 (PDZ domain containing guanine nucleotide exchange factor 1) (PDZ-GEF1) (Fragment). [Source:Uniprot/SWISSPROT;Acc:Q8CHG7]
ENSMUSG00000062265	0.773	1.052	0.589	0.439	0.941	hypothetical protein
ENSMUSG00000062275	0.377	0.952	0.375	0.983	0.304	hypothetical protein
Rpl17	1.89	0.84	1.173	0.778	0.392	60S ribosomal protein L17 (L23). [Source:Uniprot/SWISSPROT;Acc:Q9CPR4]
Cytl1	1.044	0.728	1.375	1.556	1.548	cytokine like 1
ENSMUSG00000062333	0.798	0.797	1.581	1.252	1.189	hypothetical protein
Serpinb2	1.208	0.571	0.497	1.119	0.962	Plasminogen activator inhibitor-2, macrophage (PAI-2). [Source:Uniprot/SWISSPROT;Acc:P12388]
ENSMUSG00000062365	1.355	0.416	1.37	1.476	1.006	hypothetical protein
ENSMUSG00000062396	1.231	2.025	0.533	1.441	1.271	hypothetical protein
ENSMUSG00000062406	0.393	0.515	0.331	1.122	0.439	hypothetical protein
ENSMUSG00000062408	0.647	1.103	3.167	1.204	1.859	hypothetical protein
ENSMUSG00000062419	0.921	1.044	1.286	1.31	1.142	PREDICTED: RIKEN cDNA 2310047M15 gene (2310047M15Rik)

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
V1ra8	0.706	1.224	1.909	1.632	1.514	vomeronasal 1 receptor, A8. [Source:RefSeq;Acc:NM_053223]
ENSMUSG00000062574	0.746	1.266	0.702	1.763	0.907	Ig kappa chain V-V region MOPC 149. [Source:Uniprot/SWISSPROT;Acc:P01636]
Olfr724	0.456	0.091	0.493	0.384	1.554	olfactory receptor 724 (Olfr724)
ENSMUSG00000062645	0.994	1.267	0.486	0.976	0.939	hypothetical protein
BY707471	0.978	0.863	0.577	0.891	0.662	hypothetical protein
Znhit2	1.151	1.05	1.367	0.783	1.024	Protein C11orf5 homolog (Protein FON). [Source:Uniprot/SWISSPROT;Acc:Q9QY66]
Zfp512	1.105	0.657	0.61	1.067	0.933	zinc finger protein 512. [Source:RefSeq;Acc:NM_172993]
Chia	0.684	1.512	1.379	0.32	1.811	Acidic mammalian chitinase precursor (EC 3.2.1.14) (AMCase) (YNL). [Source:Uniprot/SWISSPROT;Acc:Q91XA9]
Aurkaip1	1.095	1.257	1.345	1.279	1.184	Aurora-A kinase interacting protein. [Source:Uniprot/SWISSPROT;Acc:Q9DCJ7]
Klhl24	0.889	0.725	0.659	0.789	0.97	DRE1 protein. [Source:RefSeq;Acc:NM_029436]
Slc31a1	1.093	1.31	0.731	0.976	0.904	solute carrier family 31, member 1. [Source:RefSeq;Acc:NM_175090]
Kdr	1.128	1.006	1.497	0.98	1.402	Vascular endothelial growth factor receptor 2 precursor (EC 2.7.1.112) (VEGFR-2) (Protein-tyrosine kinase receptor flk-1) (Fetal liver kinase 1) (Kinase NYK). [Source:Uniprot/SWISSPROT;Acc:P35918]
BB661454	0.49	0.223	2.421	1.52	1.254	hypothetical gene supported by AK085556 (LOC330776)
Lrrc40	0.848	1.108	1.528	0.894	1.137	leucine rich repeat containing 40
Klk1b8	1.233	0.226	2.348	1.727	1.013	Glandular kallikrein K8 precursor (EC 3.4.21.35) (Tissue kallikrein 8) (mGK-8). [Source:Uniprot/SWISSPROT;Acc:P07628]
Defcr21	0.999	0.589	1.655	1.305	1.361	defensin-related cryptdin 21
Bbs5	0.667	0.788	1.444	1.025	1.173	Bardet-Biedl syndrome 5
Speer2	1.982	1.033	1.646	1.286	0.348	spermatogenesis associated glutamate (E)-rich protein 2; SPEER 2; sperm-associated glutamate (E)-rich protein 2; spermatogenic-associated glutamate (E)-rich protein 2. [Source:RefSeq;Acc:NM_173069]

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
ENSMUSG00000063184	1.178	1.378	0.585	0.827	0.824	hypothetical protein
Olfr107	0.835	1.396	0.609	1.657	0.447	olfactory receptor 107; GA_x6K02T2PSCP-1867165-1868094; olfactory receptor MOR156-3. [Source:RefSeq;Acc:NM_146511]
ENSMUSG00000063196	1.255	4.141	0.769	0.896	0.442	hypothetical protein
Gpr84	0.937	1.538	0.632	1.042	1.11	G protein-coupled receptor 84; orphan G protein-coupled receptor 84. [Source:RefSeq;Acc:NM_030720]
ENSMUSG00000063253	1.179	0.303	1.336	1.1	0.991	short coiled-coil protein; short coiled coil protein SCOCO; short coiled coil protein. [Source:RefSeq;Acc:NM_019708]
Gja9	0.524	1.419	0.697	0.705	1.165	Gap junction alpha-9 protein (Connexin 36) (Cx36). [Source:Uniprot/SWISSPROT;Acc:O54851]
Zfp35	1.19	1.065	1.887	0.814	1.283	Zinc finger protein 35 (Zfp-35). [Source:Uniprot/SWISSPROT;Acc:P15620]
ENSMUSG00000063340	0.65	0.271	0.691	1.435	0.559	hypothetical protein
Olfr969	0.348	4.688	1.692	0.814	1.111	olfactory receptor 969; olfactory receptor MOR171-7; GA_x6K02T2PVTD-33492981-33493916. [Source:RefSeq;Acc:NM_146826]
ENSMUSG00000063367	0.813	0.724	1.582	0.777	1.162	hypothetical protein
ENSMUSG00000063402	1.304	1.145	1.801	1.226	1.597	hypothetical protein
Tmc4	0.988	0.837	0.684	0.613	0.609	transmembrane channel-like gene family 4
BC042569	0.545	1.115	1.703	1.709	1.59	hypothetical protein
ENSMUSG00000063496	0.92	0.845	0.701	0.87	1.597	PREDICTED: similar to 60S ribosomal protein L9 (LOC241737)
Sema3e	0.283	0.633	1.51	0.726	1.723	Semaphorin 3E precursor (Semaphorin H) (Sema H). [Source:Uniprot/SWISSPROT;Acc:P70275]
ENSMUSG00000063647	1.107	1.567	0.567	0.644	1.015	hypothetical protein

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
ENSMUSG00000063663	0.863	1.034	1.334	1.54	1.253	Unclassifiable. [Source:Uniprot/SPTREMBL;Acc:Q8C7D5]
ENSMUSG00000063710	1.04	1.022	0.444	1.073	1.119	hypothetical protein
Olfr282	1.119	0.983	0.437	0.441	0.714	olfactory receptor 282; olfactory receptor MOR160-2; GA_x6K02T2NBG7-5293798-5292872. [Source:RefSeq;Acc:NM_146457]
Psrc1	1.062	1.02	0.691	0.58	0.396	differential display and activated by p53; p53-regulated DDA3. [Source:RefSeq;Acc:NM_019976]
ENSMUSG00000063889	0.971	0.829	0.63	0.623	0.901	cAMP responsive element modulator. [Source:Uniprot/SWISSPROT;Acc:P27699]
ENSMUSG00000063889	0.723	0.946	0.687	0.948	0.875	cAMP responsive element modulator. [Source:Uniprot/SWISSPROT;Acc:P27699]
ENSMUSG00000063918	0.727	0.992	1.845	0.922	1.094	hypothetical protein
ENSMUSG00000064075	0.908	0.988	0.756	0.966	0.915	hypothetical protein
Vrk2	0.745	1.689	1.398	0.86	1.329	Serine/threonine-protein kinase VRK2 (EC 2.7.1.37) (Vaccinia-related kinase 2). [Source:Uniprot/SWISSPROT;Acc:Q8BN21]
Vrk2	0.681	1.038	1.395	1.155	0.875	Serine/threonine-protein kinase VRK2 (EC 2.7.1.37) (Vaccinia-related kinase 2). [Source:Uniprot/SWISSPROT;Acc:Q8BN21]
Olfr291	0.669	0.496	1.469	0.839	0.569	olfactory receptor 291; olfactory receptor MOR254-2; GA_x6K02T2NHDJ-11231385-11230438. [Source:RefSeq;Acc:NM_146415]
ENSMUSG00000064169	1.415	1.832	0.687	0.979	1.052	Olfactory receptor GA_x6K02T2PSCP-1855511-1856437 (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q7TRK5]
2410137M14Rik	1.161	0.874	0.45	0.385	1.217	hypothetical protein LOC76797
Siva1	0.912	1.024	1.25	1.024	1.161	Apoptosis regulatory protein Siva (CD27-binding protein) (CD27BP). [Source:Uniprot/SWISSPROT;Acc:O54926]
BB207239	1.101	1.236	1.721	0.443	0.859	hypothetical protein

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
BB664636	0.686	0.832	1.461	1.122	1.056	hypothetical protein
Zfp516	1.153	1.266	1.981	1.386	0.763	zinc finger protein 516
BB638112	0.812	0.852	1.803	1.102	0.809	hypothetical protein
Cnga1	0.558	1.322	0.735	0.664	0.422	cyclic nucleotide gated channel alpha 1
Hrk	0.499	1.282	0.735	1.405	0.696	BH3 interacting (with BCL2 family) domain, apoptosis agonist (Bid3)
Ypel3	0.926	1.16	1.198	0.899	0.739	yippee-like 3
Mcts2	1.316	0.965	1.608	0.969	1.097	malignant T cell amplified sequence 2
BE985588	1.033	1.026	0.695	1.302	0.925	hypothetical protein
G0s2	1.759	0.66	2.765	0.855	0.638	G0/G1 switch gene 2
Trnah2	1.282	0.995	1.539	1.057	1.107	histidine transfer RNA 2 (Trnah2)
Ugt3a2	0.845	0.871	1.433	1.788	0.913	UDP glycosyltransferases 3 family, polypeptide A2
Rps18	0.929	0.268	0.725	0.617	0.9	ribosomal protein S18 (Rps18)
BC024751	1.318	1.102	1.375	0.908	1.334	hypothetical protein
Fxyd6	0.78	0.867	1.382	1.067	0.964	FXYD domain-containing ion transport regulator 6
BE651378	1.5	0.139	2.674	1.042	0.595	hypothetical protein
Nap1l2	0.535	0.544	0.387	1.037	0.462	nucleosome assembly protein 1-like 2
Rbbp9	0.477	1.041	0.598	0.981	1.257	retinoblastoma binding protein 9
Ddx5	0.979	1.067	0.728	1.039	0.813	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5
Azi2	0.851	0.853	0.805	0.935	1.039	5-azacytidine induced 2 isoform a
BG100585	1.146	1.963	1.682	1.114	1.089	hypothetical protein
Ptgfrn	0.779	0.842	0.659	1.182	0.917	prostaglandin F2 receptor negative regulator precursor
Golt1b	0.885	1.143	0.729	0.846	0.875	golgi transport 1 homolog B
Rnf121	0.61	1.767	1.146	0.869	1.191	ring finger protein 121
BY715546	0.986	2.186	0.769	1.337	1.641	hypothetical protein
Zfp364	0.728	1.203	1.173	1.061	0.789	zinc finger protein 364 (Zfp364)
BC060127	1.238	0.787	0.645	1.319	0.964	hypothetical protein
Vill	1.098	1.297	0.728	1.489	1.331	villin-like
Ugt1a5	0.304	1.895	2.154	0.409	0.635	UDP glucuronosyltransferase 1 family, polypeptide A5
A730080H06Rik	1.427	2.518	1.81	1.15	1.524	PREDICTED: RIKEN cDNA A730080H06 gene (A730080H06Rik)
LOC432971	1.166	1.199	0.669	0.774	0.846	PREDICTED: hypothetical gene supported by AK038224 (LOC432971)

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
2810038L03Rik	1.03	1.358	1.524	1.218	1.247	PREDICTED: RIKEN cDNA 2810038L03 gene (2810038L03Rik)
2310067E19Rik	0.921	1.281	0.694	1.162	0.948	RIKEN cDNA 2310067E19 gene (2310067E19Rik)
Tle3	0.743	0.713	0.485	0.638	1.239	transducin-like enhancer protein 3 isoform 2
BB634600	1.845	0.947	1.845	0.827	1.392	hypothetical protein
BY715638	1.093	0.771	1.926	1.134	1.148	hypothetical protein
Htatip2	1.165	1.226	1.238	1.11	0.772	HIV-1 tat interactive protein 2, homolog
Dbx2	0.512	1.217	1.323	1.625	0.999	developing brain homeobox 2
1810027O10Rik	0.964	1.114	1.244	1.049	1.154	hypothetical protein LOC69186
Krtap16-3	1.531	0.837	2.093	0.788	1.098	keratin associated protein 16-3
AK122557	1.152	0.833	0.551	1.014	1.612	hypothetical protein
Tbrg3	1.188	1.182	0.557	1.099	0.255	transforming growth factor beta regulated gene 3 (Tbrg3)
Hes3	1.629	0.605	0.451	2.822	0.822	hairy and enhancer of split 3
B930095G15Rik	0.738	0.84	1.841	0.881	0.416	RIKEN cDNA B930095G15 gene (B930095G15Rik)
BB637831	1.095	1.443	1.25	1.534	0.303	hypothetical protein
BY720915	0.213	0.675	1.267	0.641	1.153	hypothetical protein
Unc84b	0.802	1.017	1.227	1.29	1.033	unc-84 homolog B
Comp	0.921	0.211	0.557	1.242	0.54	cartilage oligomeric matrix protein
1700029J07Rik	1.014	1.345	2.091	1.333	1.393	hypothetical protein LOC69479
AK172983	0.914	1.117	1.175	1.039	0.927	hypothetical protein
Arbp	0.672	0.848	0.782	1.06	0.86	acidic ribosomal phosphoprotein P0
BY716031	0.307	1.277	0.615	0.48	1.073	hypothetical protein
BB631109	0.855	0.935	0.644	1.319	1.208	hypothetical protein
Olfr725	1.192	1.416	0.793	1.387	0.886	olfactory receptor 725
BC048857	0.992	0.667	0.609	0.876	1.236	hypothetical protein
Olfr140	0.682	0.896	0.598	1.16	0.848	olfactory receptor 140
Mrgpra1	0.455	0.057	1.727	1.15	1.328	MAS-related GPR, member A1
Plscr1	1.023	0.823	0.822	0.867	1.273	phospholipid scramblase 1
AV088569	0.649	0.863	1.622	1.017	1.104	titin isoform N2-A

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
Mtus1	0.569	0.857	0.391	1.02	0.905	mitochondrial tumor suppressor 1 isoform 1
Olfr3	0.866	2.957	1.394	1.731	0.334	olfactory receptor 3
Olfr1086	0.512	0.785	0.43	1.212	1.127	olfactory receptor 1086
CF586374	1.051	1.688	0.634	0.772	0.609	hypothetical protein
2310006M14Rik	1.307	1.598	0.363	0.307	1.631	hypothetical protein LOC76422
9330155M09Rik	1.035	0.813	1.714	1.19	2.066	hypothetical protein LOC320756
AK129174	1.179	0.539	0.751	1.368	0.804	hypothetical protein
BY705863	0.972	0.857	0.52	0.99	1.278	hypothetical protein
Kcne1l	0.977	0.871	1.384	1.155	0.754	potassium voltage-gated channel, Isk-related family, member 1-like
Ifi202b	0.205	0.731	2.205	0.068	1.047	interferon activated gene 202B
Ttc30a1	0.241	0.633	0.644	2.607	1.025	tetratricopeptide repeat domain 30A1
Defcr-rs2	0.754	0.854	0.592	0.992	0.728	defensin related cryptdin, related sequence 2
Disc1	0.725	0.806	1.794	0.864	1.481	disrupted in schizophrenia 1 (Disc1)
Vpreb1	1.155	1.269	0.422	0.982	1.24	pre-B lymphocyte gene 1
BY709238	1.143	0.665	1.966	1.48	0.956	hypothetical protein
BC066049	1.203	1.464	0.561	1.02	1.823	PREDICTED: RIKEN cDNA C130040D06 gene (C130040D06Rik)
LOC433426	0.643	1.067	1.389	1.814	1.204	hypothetical protein
0610007C21Rik	1.201	1.075	1.281	1.007	0.914	apoptosis related protein APR-3 isoform 2
Prdm16	0.709	0.908	1.242	1.13	0.858	transcription factor MEL1
Cox6b2	0.961	1.037	0.61	1.214	1.074	cytochrome c oxidase subunit VIb, testis-specific isoform
Tdg	0.73	1.843	2.105	1.896	1.178	thymine DNA glycosylase isoform 2
Tnfrsf4	1.921	1.459	0.584	0.667	0.631	tumor necrosis factor receptor superfamily, member 4
Klhl7	1.081	0.901	1.451	0.915	1.272	SBBI26 protein
Ky	0.357	0.658	0.568	0.487	0.743	Kyphoscoliosis
BC070449	1.101	0.795	0.696	0.886	0.756	hypothetical protein
Kctd12	0.926	0.413	0.645	0.749	0.936	potassium channel tetramerization domain containing 12
2310005E10Rik	1.035	1.404	1.354	1.142	1.28	aldo-keto reductase family 1, member B10
BC067008	0.373	1.3	1.817	1.176	0.788	hypothetical protein

Gene	Incubation Medium (Protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Description
CF907745, BY721136	0.798	1.299	1.374	0.882	1.363	hypothetical protein
BM937289	0.987	0.986	1.444	0.923	0.985	hypothetical protein
LOC433932	1.459	1.141	1.605	2.181	0.718	PREDICTED: hypothetical gene supported by AK031827 (LOC433932)
Erdr1	0.743	7.334	4.982	1.025	1.467	erythroid differentiation regulator 1

Genes in this table were differentially regulated in the CD43KO macrophages compared to CD43WT macrophages while incubated with *M.tb*. Normalized expression cutoff values were 1.2 (upregulated) and 0.833 (downregulated). Genes were also filtered on confidence between the biological replicates ($p<0.05$).

Supplementary table 4. Statistically significant, differentially expressed in CD43KO macrophages co-incubated with dnaK

	Normalized Expression					
Gene	**Incubation Medium (protein-incubation)**	**Incubation Medium (infection)**	***M.tb***	**60.2**	**dnaK**	**Product**
Cdc45l	0.781	0.8964	1.206	0.949	1.573	cell division cycle 45 homolog (S. cerevisiae)-like
Pih1d2	1.428	0.7635	1.172	1.654	0.6604	PIH1 domain containing 2
Scnn1g	1.268	1.6599	1.022	1.45	0.5743	sodium channel, nonvoltage-gated 1 gamma
Pemt	1.226	0.8399	1.082	0.772	1.6186	phosphatidylethanolamine N-methyltransferase
Myo18a	0.795	1.2406	0.81	1.402	0.5808	myosin XVIIIa
1300007F04 Rik	1.043	1.173	0.836	1.003	0.6441	hypothetical protein LOC67477
Sult5a1	0.317	0.2069	1.018	1.003	1.7837	sulfotransferase family 5A, member 1
Bcl11a	0.377	1.141	1.226	0.347	1.6741	B-cell CLL/lymphoma 11A (zinc finger protein)
Mmp11	0.858	1.0153	1.012	0.725	0.7454	matrix metalloproteinase 11
0610009O03 Rik	1.327	1.0531	1.055	1.029	0.5484	tetracycline transporter-like protein
ENSMUSG00 000001158	2.259	1.3474	0.659	1.705	0.558	putative nucleic acid binding protein RY-1; EST AI449063. [Source:RefSeq;Acc:NM_025665]
Tmem79	1.465	0.9552	1.694	0.506	2.068	hypothetical protein LOC71913
Col1a1	1.314	1.3827	0.497	0.828	1.5757	procollagen, type I, alpha 1
Brpf1	1.233	1.2618	0.972	1.058	0.6385	bromodomain containing 1
Ubl3	0.867	1.1261	1.049	0.852	0.827	ubiquitin-like 3
BU707566	1.639	1.1517	0.498	0.593	0.386	PREDICTED: similar to low density lipoprotein receptor-related protein 3 (LOC435965)
Ssr4	0.917	1.2034	1.032	1.297	1.2099	signal sequence receptor, delta
Rgs20	0.98	0.7851	1.592	1.1	1.3786	regulator of G-protein signaling 20
Tiam1	0.728	0.8293	1.062	1.064	1.2636	T-cell lymphoma invasion and metastasis 1
Zfpn1a4	0.867	0.5216	0.586	1.016	1.4315	zinc finger protein, subfamily 1A, 4. [Source:RefSeq;Acc:NM_011772]
Prkcm	1.714	0.3852	1.188	1.203	2.1455	protein kinase C, mu

Gene	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Product
Tpra40	0.855	0.9224	0.95	0.897	1.278	transmembrane domain protein regulated in adipocytes; transmembrane domain protein regulated in adipocytes 40 kDa. [Source:RefSeq;Acc:NM_011906]
Arrdc2	1.024	0.8575	0.923	1.338	0.7417	arrestin domain containing 2
Bscl2	1.005	0.8932	0.979	0.752	1.6089	Bernardinelli-Seip congenital lipodystrophy 2 homolog; G protein gamma 3 linked gene. [Source:RefSeq;Acc:NM_008144]
B3gat3	1	1.2038	1.144	1.343	0.6631	beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase I)
Nob1	0.65	2.1831	0.755	1.037	1.4414	nin one binding protein
Stat3	1.162	0.8446	0.528	1.041	0.6687	Signal transducer and activator of transcription 3 (Acute-phase response factor). [Source:Uniprot/SWISSPROT;Acc:P42227]
ENSMUSG00000004360	0.61	1.4893	0.531	1.07	0.3622	PREDICTED: RIKEN cDNA 9330159F19 gene (9330159F19Rik)
Ctse	0.887	0.8004	0.638	0.89	0.5806	cathepsin E preproprotein
Lim2	0.445	0.8646	1.434	0.883	1.7961	lens intrinsic membrane protein 2
Sgce	0.98	1.1041	0.533	1.111	1.855	sarcoglycan, epsilon
Emr1	1.245	0.8576	1.173	0.817	1.4808	EGF-like module containing, mucin-like, hormone receptor-like sequence 1
Dgkq	1.278	0.5038	1.138	0.765	1.8108	diacylglycerol kinase, theta
Matk	0.239	0.5707	0.844	0.324	1.9046	Megakaryocyte-associated tyrosine-protein kinase (EC 2.7.1.112) (Tyrosine-protein kinase CTK) (Protein kinase NTK). [Source:Uniprot/SWISSPROT;Acc:P41242]
Map2k1	0.887	0.8041	1.074	0.789	0.7052	mitogen activated protein kinase kinase 1
ENSMUSG00000004996	0.947	2.0088	1.498	1	1.2382	hypothetical protein

Gene	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Product
2410018C20Rik	0.598	1.6103	1.307	1.158	1.7039	hypothetical protein LOC67873
Ndrg1	1.028	0.7238	0.772	0.997	1.6053	N-myc downstream regulated gene 1
Slc1a3	0.88	0.4375	0.986	1.656	1.7383	solute carrier family 1 (glial high affinity glutamate transporter), member 3
RIP3_MOUSE	2.401	1.5978	0.447	1.653	0.5286	Rho-interacting protein 3 (p116RIP) (RIP3). [Source:Uniprot/SWISSPROT;Acc:P97434]
Cic	0.883	1.8265	1.444	0.661	1.7491	capicua homolog
Sh2d1a	1.104	0.6656	1.355	1.402	1.9869	SH2 domain protein 1A
Prl4a1	2.452	1.255	0.906	1.26	0.294	prolactin family 4, subfamily a, member 1
Trh	0.781	0.9237	0.824	0.809	1.4992	thyrotropin releasing hormone
Prg4	1.163	1.6907	0.517	1.062	2.6522	similar to proteoglycan 4
Ndp52	1.349	1.7515	0.918	1.465	0.3998	nuclear domain 10 protein 52 like 1
Aamp	0.982	1.157	0.978	0.823	0.832	angio-associated migratory protein
Them2	0.864	0.8707	1.559	1.148	1.5124	thioesterase superfamily member 2
Neu1	0.72	1.0427	1.055	0.709	1.4188	neuraminidase 1
Ceacam9	1.253	1.6651	0.961	0.742	2.2055	CEA-related cell adhesion molecule 9
Homer1	1.311	1.0377	0.711	1.333	1.6421	Homer protein homolog 1 (VASP/Ena related gene up-regulated during seizure and LTP) (Vesl-1). [Source:Uniprot/SWISSPROT;Acc:Q9Z2Y3]
Rabl5	0.916	1.4414	1.152	0.973	1.3046	RAB, member of RAS oncogene family-like 5
1700008O03Rik	0.949	0.8082	0.844	1.372	0.7076	hypothetical protein LOC69349 isoform 1
CXZ1_MOUSE	1.204	1.1304	1.359	0.84	1.8097	hypothetical protein
ENSMUSG00000008142	1.002	1.7021	1.325	0.842	1.7394	hypothetical protein
Clstn3	0.314	0.7949	1.469	0.379	0.6995	calsyntenin 3
Spib	0.442	0.4059	0.384	1.669	1.4723	Ets transcription factor Spi-B (Fragment). [Source:Uniprot/SPTREMBL;Acc:O35906]

Gene	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Product
Nutf2	1.097	1.1003	1.282	0.957	1.775	nuclear transport factor 2
D15Ertd785e	0.898	1.1511	0.87	0.924	0.6549	hypothetical protein
ENSMUSG00000008813	0.375	1.2577	0.431	2.482	1.7644	
Gnat2	0.87	0.9529	0.706	1.637	1.9273	guanine nucleotide binding protein, alpha transducing 2
Lpo	1.146	1.8231	0.977	0.417	0.3846	lactoperoxidase
Slc16a12	0.874	1.0408	0.722	0.6	0.073	solute carrier family 16 (monocarboxylic acid transporters), member 12
Kcnq1	0.444	2.3386	1.079	0.947	0.4718	Potassium voltage-gated channel subfamily KQT member 1 (Voltage-gated potassium channel subunit Kv7.1) (IKs producing slow voltage-gated potassium channel alpha subunit KvLQT1) (KQT-like 1). [Source:Uniprot/SWISSPROT;Acc:P97414]
Q9D3A7	1.598	0.7602	1.228	0.144	1.6903	hypothetical protein
G0s2	0.53	1.2335	0.674	1.296	2.0413	Putative lymphocyte G0/G1 switch protein 2 (G0S2-like protein). [Source:Uniprot/SWISSPROT;Acc:Q61585]
BY749370	1.894	0.7149	0.684	0.578	2.45	hypothetical protein
Nat6	0.975	1.3393	0.48	1.173	1.5048	N-acetyltransferase 6
Rassf1	0.922	0.9664	1.091	1.06	1.2791	Ras association (RalGDS/AF-6) domain family 1
Mcoln2	1.112	1.1024	0.822	1.039	1.2735	mucolipin 2 (Mcoln2), transcript variant 2
ENSMUSG00000011263	2.715	0.5106	1.231	0.46	0.516	hypothetical protein
ENSMUSG00000011350	0.517	0.2215	1.181	0.557	1.9916	hypothetical protein
Evi5	0.937	1.1827	1.069	1.052	0.4824	ecotropic viral integration site 5
Pcqap	1.205	1.0664	0.991	0.928	0.6793	positive cofactor 2, glutamine/Q-rich-associated protein isoform a
Tmem175	0.864	1.4918	1.315	1.017	0.7493	hypothetical protein LOC72392

Gene	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Product
BC059896	1.067	1.2447	1.054	1.024	1.6374	RIKEN cDNA 2410002F23 gene (2410002F23Rik)
2210415F13 Rik	1.502	2.1163	0.852	1.037	0.417	RIKEN cDNA 2210415F13
Glis2	0.994	0.7031	0.751	0.809	0.6928	GLIS family zinc finger 2
Ankrd28	1.002	1.0902	0.647	0.707	0.6959	ankyrin repeat domain 28
Mrps25	1.131	1.1985	1.419	0.843	0.6396	mitochondrial ribosomal protein S25
Mrps25	0.689	1.1982	1.141	1.229	1.785	Mitochondrial 28S ribosomal protein S25 (S25mt) (MRP-S25). [Source:Uniprot/SWISSPROT;Acc:Q9D125]
6330569M22Rik	1.324	1.3247	0.795	0.712	2.1332	hypothetical protein LOC229707
E2f4	1.134	1.0731	0.773	0.566	2.0437	E2F transcription factor 4
Ubl4	0.955	1.4576	1.034	1.073	1.2104	ubiquitin-like 4
Golga7	0.877	1.4318	1.09	1.041	0.7787	golgi autoantigen, golgin subfamily a, 7
Ager	0.751	0.7557	0.583	1.017	0.7138	advanced glycosylation end product-specific receptor
Lpl	1.04	1.3609	1.294	1.23	1.7298	Lipoprotein lipase precursor (EC 3.1.1.34) (LPL). [Source:Uniprot/SWISSPROT;Acc:P11152]
Serac1	0.294	1.5996	0.774	0.513	1.7597	serine active site containing 1 isoform 2
Plekho1	0.917	2.2068	1.358	0.902	1.2296	TNF intracellular domain-interacting protein
Map3k7ip2	1.209	0.9787	1	0.872	0.6431	mitogen-activated protein kinase kinase kinase 7 interacting protein 2
Gnrh1	1.153	1.7638	0.926	1.464	0.6597	gonadotropin releasing hormone
Dstn	1.556	1.1035	0.955	1.055	1.5729	destrin
Skiv2l2	1.341	1.1461	1.098	0.924	0.6886	superkiller viralicidic activity 2-like 2
Odz1	0.218	0.9127	1.079	0.93	2.4539	odd Oz/ten-m homolog 1
Hsd11b1	0.795	1.0164	1.154	0.888	1.9583	hydroxysteroid 11-beta dehydrogenase 1
Th1l	0.997	1.2938	0.843	0.79	0.6449	TH1 homolog
Slmo2	1.12	1.1477	0.97	1.089	1.3761	slowmo homolog 2
Lnx2	0.875	1.4444	1.032	1.002	1.3873	PDZ domain containing ring finger 1

Gene	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Product
Slpi	0.978	1.1348	1.09	0.927	2.1649	secretory leukocyte protease inhibitor
Sdc4	0.951	0.8798	0.721	0.97	0.6749	syndecan 4
Nbr1	1.181	1.0383	0.911	1.022	0.6864	neighbor of Brca1 gene 1
Cntnap1	0.956	0.6846	0.621	1.561	1.7376	contactin associated protein 1
Aldoc	1.107	1.0261	0.96	1.191	1.331	PREDICTED: aldolase 3, C isoform (Aldoc)
Q99J70	0.842	1.7666	1.056	0.427	2.0659	hypothetical protein
Serinc3	1.525	1.1203	0.812	0.552	1.4537	tumor differentially expressed protein 1
Etv4	0.856	1.0778	0.804	2.318	2.1113	ets variant gene 4 (E1A enhancer binding protein, E1AF)
Slc12a7	0.843	1.2828	1.385	0.888	1.5178	Solute carrier family 12 member 7 (Electroneutral potassium-chloride cotransporter 4) (K-Cl cotransporter 4). [Source:Uniprot/SWISSPROT;Acc:Q9WVL3]
Slc12a4	1.076	1.0312	0.907	1.264	0.6323	solute carrier family 12, member 4
Cadps2	1.374	0.9597	0.628	0.701	0.3956	Ca2+dependent activator for secretion protein 2; cerebellum postnatal development associated protein 2. [Source:RefSeq;Acc:NM_153163]
h2bc	0.948	0.8807	1.187	0.963	1.4348	histone 1, H2bc; H2B histone family, member S. [Source:RefSeq;Acc:NM_023422]
Mfng	1.24	1.4054	1.07	1.279	0.7209	O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase
Zkscan6	0.874	1.0558	0.77	1.255	1.3467	zinc finger protein 535
Mrm1	1.562	1.8109	1.394	0.92	0.6258	mitochondrial rRNA methyltransferase 1 homolog
Q7TMU3	0.822	1.0042	1.036	1.047	1.7453	hypothetical protein
Dullard	1.05	0.9632	1.061	0.87	0.5998	Dullard homolog
2810408A11Rik	1.021	0.8624	0.895	0.882	0.6553	hypothetical protein LOC70419
Atox1	0.819	0.9535	1.361	0.767	1.2125	antioxidant protein 1

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Zfpn1a1	1.103	1.6756	0.819	0.611	1.654	DNA-binding protein Ikaros (Lymphoid transcription factor LyF-1). [Source:Uniprot/SWISSPROT;Acc:Q03267]
Slc25a35	1.09	1.2011	0.967	1.212	1.7472	solute carrier family 25, member 35
Smyd4	2.17	1.0391	0.695	1.145	0.5661	SET and MYND domain containing 4
Pelp1	0.829	1.814	0.871	1.897	1.6928	proline-, glutamic acid-, leucine-rich protein 1
Hoxb1	0.714	0.923	0.655	0.701	2.2647	homeobox B1
Prl8a1	1.263	0.1509	0.73	1.223	0.3229	placental prolactin-like protein C delta
Rgs17	1.191	0.5475	1.339	1.059	1.7461	regulator of G-protein signaling 17
Stxbp5	1.034	1.1835	0.885	0.856	0.6335	tomosyn isoform 1
Ltv1	0.749	1.1808	0.985	0.623	1.964	LTV1 homolog
Rev3l	1.268	0.9887	0.877	0.756	0.5259	REV3-like, catalytic subunit of DNA polymerase zeta RAD54 like
ENSMUSG00000019928	0.793	1.1454	0.853	1.091	1.4644	hypothetical protein
Cdc2a	0.931	1.7686	1.005	0.954	0.6182	cell division cycle 2 homolog A
Wdr51b	1.319	1.505	1.111	0.672	1.8763	WD repeat domain 51B
Tmpo	0.716	1.6267	0.675	0.841	1.5779	thymopoietin isoform alpha
Hbs1l	1.092	1.1444	0.912	0.986	0.7239	Hbs1-like; eukaryotic release factor 3. [Source:RefSeq;Acc:NM_019702]
Epb4.1l2	0.493	0.9891	1.013	0.937	1.4973	Band 4.1-like protein 2 (Generally expressed protein 4.1) (4.1G). [Source:Uniprot/SWISSPROT;Acc:O70318]
Fgd6	0.934	1.2147	0.653	0.85	1.5976	FYVE, RhoGEF and PH domain containing 6
Socs2	1.688	0.9472	0.759	1.352	0.6131	suppressor of cytokine signaling 2
Usp15	0.712	1.8278	0.864	0.933	1.5147	ubiquitin specific protease 15
Peli1	0.652	0.9839	0.958	0.694	1.2479	pellino 1
Grb10	1.252	1.6019	1.559	1.539	2.3852	growth factor receptor bound protein 10
Cabin1	1.145	0.8591	0.257	1.007	1.7534	calcineurin binding protein 1
ENSMUSG00000020213	1.29	0.937	0.862	0.525	2.1176	hypothetical protein
Slc36a2	0.738	0.8604	0.588	0.655	1.8445	tramdorin 1

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Guk1	1.003	1.175	1.709	1.266	0.7453	guanylate kinase 1
ENSMUSG00000020460	0.992	0.8758	0.97	1.232	1.5422	hypothetical protein
Pold2	0.621	1.0489	0.796	1.18	1.7285	polymerase (DNA directed), delta 2, regulatory subunit
Butr1	2.213	0.9538	0.928	0.445	0.4962	butyrophilin related 1
Znhit3	1.35	1.2299	1.375	0.966	1.7162	thyroid hormone receptor interactor 3
Smc6	0.846	1.0535	1.166	1.2	1.4737	SMC6 protein
Apob	1.273	0.2054	0.645	1.285	1.9814	apolipoprotein B
1700012B07Rik	2.168	0.8338	1.293	1.678	1.8263	hypothetical protein LOC69324 isoform 1
Ttc15	0.489	1.237	1.244	0.623	1.9719	Tetratricopeptide repeat protein 15 (TPR repeat protein 15). [Source:Uniprot/SWISSPROT;Acc:Q8K2L8]
ENSMUSG00000020666	0.878	0.7643	0.9	1.153	0.5281	hypothetical protein
ENSMUSG00000020696	1.965	1.0001	0.817	0.776	0.624	fring; rififylin. [Source:RefSeq;Acc:NM_026097]
Ddx42	1.11	1.0943	1.006	0.959	0.7939	DEAD (Asp-Glu-Ala-Asp) box polypeptide 42
Polg2	0.967	1.4043	0.851	1.081	1.2336	polymerase (DNA directed), gamma 2, accessory subunit
Atp2a3	0.789	0.3645	0.817	1.019	1.8158	ATPase, Ca++ transporting, ubiquitous
9830002I17Rik	0.876	1.3399	0.881	2.025	0.5153	hypothetical protein LOC77577
Aanat	0.698	2.3087	0.753	0.904	2.6356	arylalkylamine N-acetyltransferase
Cpd	0.792	1.3439	0.822	0.918	0.6328	carboxypeptidase D
Nr1d1	0.952	0.4796	1.244	1.165	0.7821	nuclear receptor subfamily 1, group D, member 1
Krt1-12	1.142	0.4243	1.73	0.611	2.6703	Keratin, type I cytoskeletal 12 (Cytokeratin 12). [Source:Uniprot/SWISSPROT;Acc:Q64291]
Klhl28	1.017	0.9044	0.876	1.333	1.4533	BTB (POZ) domain containing 5

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Fkbp3	1.104	0.7444	0.824	1.387	1.4763	FK506-binding protein 3 (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase) (25 kDa FKBP) (FKBP-25) (Rapamycin- selective 25 kDa immunophilin). [Source:Uniprot/SWISSPROT;Acc:Q62446]
Tshr	0.658	1.119	1.208	0.722	1.4366	Thyrotropin receptor precursor (TSH-R) (Thyroid stimulating hormone receptor). [Source:Uniprot/SWISSPROT;Acc:P47750]
Tshr	0.37	1.3445	0.954	0.503	2.3305	thyroid stimulating hormone receptor
1110034A24Rik	0.985	0.9892	1.198	0.882	0.5841	hypothetical protein LOC109065
Zc3h14	1.102	1.0816	1.61	0.832	0.6716	nuclear protein UKp68 isoform a
Zmynd11	0.948	1.3328	0.645	0.846	0.5433	zinc finger, MYND domain containing 11
Akr1c12	1.154	1.0486	1.416	0.906	1.5085	aldo-keto reductase family 1, member C12; aldo-keto reductase AKR1C12. [Source:RefSeq;Acc:NM_013777]
Lrrc16	1.197	0.2404	1.481	0.882	0.1064	leucine rich repeat containing 16
Prpf4b	0.918	1.3685	0.897	0.849	0.5223	PRP4 pre-mRNA processing factor 4 homolog B
Peci	1.134	0.9949	0.802	0.985	0.7642	peroxisomal delta3, delta2-enoyl-Coenzyme A isomerase
Ror2	0.892	2.0726	1.045	1.066	1.7621	receptor tyrosine kinase-like orphan receptor 2
Nsd1	0.817	2.2941	1.072	1.035	1.3958	nuclear receptor-binding SET-domain protein 1
1700001L19Rik	0.797	0.7321	0.69	1.022	1.7947	hypothetical protein LOC69315
Q9D3K5	1.153	1.4526	1.247	0.916	0.5859	hypothetical protein
Slc9a3	0.379	0.6918	0.913	0.634	1.5919	solute carrier family 9 (sodium/hydrogen exchanger), member 3

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ENSMUSG00000021575	1.156	1.0673	0.287	1.271	1.6574	aryl-hydrocarbon receptor repressor. [Source:RefSeq;Acc:NM_009644]
F2rl2	0.383	0.3459	0.485	1.459	1.8603	coagulation factor II (thrombin) receptor-like 2
F2rl1	1.464	1.2224	1.359	1.039	0.5589	coagulation factor II (thrombin) receptor-like 1
Depdc1b	0.572	0.9403	1.343	0.806	0.3447	DEP domain containing 1B
Hcn1	1.073	0.8128	0.821	1.013	0.5994	hyperpolarization-activated, cyclic nucleotide-gated K+ 1
Dusp13	1.093	0.9045	0.88	0.937	2.1825	dual specificity phosphatase 13 isoform 2
Ap3m1	1.107	1.6521	1.124	0.865	0.6981	adaptor-related protein complex 3, mu 1 subunit
Ppif	0.915	1.1818	1.052	0.587	1.2088	peptidylprolyl isomerase F
Asb14	1.618	2.3391	0.982	2.219	2.218	ankyrin repeat and SOCS box-containing protein 14
Sema3g	0.641	0.302	0.93	1.658	2.2084	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3G
Tnnc1	1.127	1.5949	0.92	1.06	1.9711	troponin C, cardiac/slow skeletal
Esd	0.637	1.299	1.052	0.652	0.5828	esterase D/formylglutathione hydrolase; esterase D; esterase 10. [Source:RefSeq;Acc:NM_016903]
1200011I18Rik	0.512	1.1914	0.994	0.511	1.5829	hypothetical protein LOC67467
Ccdc25	0.762	1.5334	1.411	0.533	1.4209	coiled-coil domain containing 25
D14Ertd581e	0.92	1.1538	0.937	1.061	0.4076	progesterone-induced blocking factor 1 isoform a
Dok2	0.934	0.7691	1.3	1.033	2.2305	docking protein 2
Med4	0.916	0.8243	0.838	1.093	1.3566	vitamin D receptor interacting protein
Ednrb	0.936	1.7616	0.575	0.564	0.6046	Endothelin B receptor precursor (ET-B) (Endothelin receptor Non- selective type). [Source:Uniprot/SWISSPROT;Acc:P48302]
C9	0.881	0.8799	0.952	1.412	0.4461	complement component 9

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Dab2	1.037	0.6326	0.662	0.968	0.5687	Disabled homolog 2 (DOC-2) (Mitogen-responsive phosphoprotein). [Source:Uniprot/SWISSPROT;Acc:P98078]
Jub	0.486	0.7265	1.175	1.141	2.0753	ajuba
Oxct1	0.957	1.1907	1.379	0.8	0.6774	3-oxoacid CoA transferase 1
Slc22a17	0.444	1.029	0.639	1.172	0.5179	solute carrier family 22 (organic cation transporter), member 17
Adcy4	1.147	1.0248	1.417	0.753	0.6143	adenylate cyclase 4
5730557B15Rik	0.946	1.1832	1.231	0.969	1.4754	hypothetical protein LOC67434 isoform 2
Myc	0.918	1.0779	1.004	0.694	1.4933	myc proto-oncogene protein
Ddef1	1.13	1.1283	1.03	1.124	0.7378	development and differentiation enhancing
ENSMUSG00000022408	1.24	2.2701	0.406	0.317	0.4083	hypthetical protein
Enpp2	1.369	0.65	0.912	1.411	0.6381	ectonucleotide pyrophosphatase/phosphodiesterase 2
4931407K02Rik	1.707	0.7633	0.608	2.12	2.2565	CAP-binding protein complex interacting protein 1
Pde1b	0.952	0.7727	0.827	1.102	0.7668	phosphodiesterase 1B, Ca2+-calmodulin dependent
Glycam1	0.921	0.2607	1.013	0.847	1.8244	glycosylation dependent cell adhesion molecule 1
Q9CZN4	1.256	1.2434	0.927	0.942	0.4928	hypothetical protein
Anks3	1.422	1.3489	0.996	0.581	1.2997	ankyrin repeat and sterile alpha motif domain containing 3
Ly6e	0.555	0.5195	1.154	1.101	1.5248	Lymphocyte antigen Ly-6E precursor (Thymic shared antigen-1) (TSA-1) (Stem cell antigen 2). [Source:Uniprot/SWISSPROT;Acc:Q64253]
Nat13	0.975	1.3815	0.896	0.932	1.4433	Mak3p homolog
Pmm2	1.15	1.2721	1.032	0.977	1.303	phosphomannomutase 2
Muc13	1.658	0.8447	1.31	0.614	2.5538	mucin 13, epithelial transmembrane

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D16Ertd472e	0.986	0.9435	1.144	1.161	1.67	hypothetical protein LOC67102
Samsn1	1.322	1.2491	0.713	0.799	2.0076	SAM domain, SH3 domain and nuclear localization signals, 1
Atp5j	0.851	1.1396	1.125	1.094	1.3833	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F
Ets2	1.496	0.9779	0.828	1.161	1.8922	E26 avian leukemia oncogene 2, 3' domain
Kpna1	0.861	2.1968	1.573	0.82	0.7501	karyopherin (importin) alpha 1
Dhh	1.497	1.2904	0.643	0.372	0.4354	desert hedgehog
Slc11a2	1	1.1453	0.936	1.067	1.2401	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2
Krt6b	0.959	0.7299	0.662	0.569	2.0043	keratin complex 2, basic, gene 6b
Mospd1	1.086	0.9658	0.958	1.02	0.7841	motile sperm domain containing 1
Ivns1abp	1.102	0.8887	1.143	0.909	0.6021	influenza virus NS1A binding protein isoform 2
Ccl25	1.171	0.8488	1.02	0.758	1.4895	chemokine (C-C motif) ligand 25
Cd4	0.608	0.3604	0.83	0.603	1.4043	CD4 antigen
Gnb3	1.024	0.762	1.117	0.761	2.802	guanine nucleotide-binding protein, beta-3 subunit
1700010I14Rik	0.999	0.9007	0.914	1.135	1.5084	hypothetical protein LOC66931
2610036F08Rik	1.28	1.0282	0.807	1.267	1.9523	hypothetical protein LOC75424
ENSMUSG00000023900	1.38	0.8916	1.236	1.095	0.6217	hypothetical protein
Pgc	0.4	0.6881	0.835	1.043	0.6541	progastricsin (pepsinogen C)
ENSMUSG00000024018	1.415	0.7213	0.957	0.785	1.3751	hypothetical protein
Arhgap28	1.208	0.8078	1.014	1.277	0.8015	Rho GTPase activating protein 28
DP30_MOUSE	0.721	1.4043	1.461	1.098	0.734	Dpy-30-like protein. [Source:Uniprot/SWISSPROT;Acc:Q99LT0]
Birc6	1.094	0.8204	1.061	0.723	0.7009	baculoviral IAP repeat-containing 6
Vapa	0.93	0.8583	1.252	0.948	0.7405	vesicle-associated membrane protein, associated protein A
Ralbp1	0.98	1.3105	1.043	1.11	0.7377	ralA binding protein 1
ORF19	0.7	0.7774	0.877	0.981	1.2631	hypothetical protein LOC68767

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BC054438	1.304	0.7004	1.757	1.156	0.4886	cDNA sequence BC054438
Epc1	1.118	1.366	0.816	0.881	1.2902	enhancer of polycomb homolog 1 isoform 1
4930403J07 Rik	1.16	1.2417	0.478	1.307	2.2472	hypothetical protein LOC75773 isoform 1
Brunol4	0.425	0.202	0.87	2.796	2.5511	bruno-like 4, RNA binding protein. [Source:RefSeq;Acc:NM_133195]
Brunol4	0.278	0.8348	1.576	1.167	2.1667	bruno-like 4, RNA binding protein
Slc39a7	0.964	0.9486	1.003	0.951	0.8066	solute carrier family 39, member 7
Dsc2	1.395	0.9062	0.901	1.475	0.6547	desmocollin 2
Bat4	0.983	1.2168	0.831	1.006	1.467	HLA-B associated transcript 4
Taf4b	0.73	0.9719	0.327	1.458	1.4517	TAF4B RNA polymerase II, TATA box binding protein (TBP)-associated factor
2810439F02 Rik	0.819	1.2011	0.794	0.666	1.233	hypothetical protein LOC72747
H2-M10.1	2.308	0.7327	0.886	0.85	0.5545	histocompatibility 2, M region locus 10.1
Cplx4	1.256	1.5974	0.487	1.098	1.3754	complexin 4
Afg3l2	1.275	0.7081	0.985	1.318	0.8008	AFG3(ATPase family gene 3)-like 2
Q9D2T6	1.18	0.4527	0.901	1.245	2.5035	hypothetical protein
Pde6a	1.115	1.0442	1.002	0.994	1.3887	phosphodiesterase 6A, cGMP-specific, rod, alpha
Lmnb1	1.019	0.9374	0.822	0.797	1.7831	lamin B1
ENSMUSG00000024593	0.516	0.7202	0.718	1.519	2.0652	hypothetical protein
Pdgfrb	1.141	1.2156	0.908	1.083	1.3775	platelet derived growth factor receptor, beta polypeptide
1700025F22 Rik	1.235	0.7974	1.105	0.724	1.9994	hypothetical protein LOC69416
Ms4a8a	1.368	0.7133	1.055	1.243	0.6032	membrane-spanning 4-domains, subfamily A, member 8A
Tmem132a	1.032	1.0343	0.99	1.087	0.5658	heat shock 70kDa protein 5 binding protein 1
Ddb1	1.043	1.2004	1.039	1.094	0.7504	damage specific DNA binding protein 1
BC020020	1.271	1.347	1.132	0.954	0.6499	hypothetical protein
Lipk	0.952	0.6331	0.766	0.434	1.9191	lipase-like, ab-hydrolase domain containing 2

Gene	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Product
Tjp2	0.718	1.2574	1.575	1.024	0.5995	Tight junction protein ZO-2 (Zonula occludens 2 protein) (Zona occludens 2 protein) (Tight junction protein 2). [Source:Uniprot/SWISSPROT;Acc:Q9Z0U1]
Slc25a45	0.724	1.2898	0.804	0.874	1.3271	solute carrier family 25, member 45
Rps6kb2	0.865	1.1322	1.014	1.181	1.3099	ribosomal protein S6 kinase, polypeptide 2
Banf1	1.013	1.3551	1.025	1.228	0.8187	barrier to autointegration factor 1
Adrbk1	1.116	1.0607	1.056	0.954	0.7828	adrenergic receptor kinase, beta 1
Htatip	0.673	1.0778	1.092	0.606	1.3613	HIV-1 tat interactive protein, homolog
Zfp162	1.189	0.8607	0.945	1.084	1.6729	Splicing factor 1 (Zinc finger protein 162) (Transcription factor ZFM1) (mZFM) (Zinc finger gene in MEN1 locus) (Mammalian branch point binding protein mBBP) (BBP) (CW17). [Source:Uniprot/SWISSPROT;Acc:Q64213]
Mark2	0.765	0.8178	1.545	0.771	1.3677	MAP/microtubule affinity-regulating kinase 2 isoform 1
Smc3	0.894	1.1893	0.952	1.021	0.6515	chondroitin sulfate proteoglycan 6
Pdcd4	1.039	1.0922	1.041	0.775	0.7544	programmed cell death 4
Tcf7l2	0.882	1.4755	1.041	1.112	0.7334	transcription factor 7-like 2, T-cell specific, HMG-box
1110012N22Rik	1.54	0.4189	1.595	1.041	0.5246	hypothetical protein LOC68515 isoform 1
Sectm1a	1.131	0.9723	0.873	0.512	0.6735	secreted and transmembrane 1A
Ribc1	1.043	0.8081	1.167	1.331	1.5222	RIB43A domain with coiled-coils 1
AA049260	0.958	1.3367	0.889	0.654	0.6656	PREDICTED: similar to ITI-like protein (LOC382247)
Abhd6	0.942	1.0338	1.222	0.535	2.9315	abhydrolase domain containing 6
Padi4	0.973	1.2725	1.402	1.486	1.525	peptidyl arginine deiminase, type IV
Obfc2b	1.205	1.4623	0.755	0.753	2.6014	oligonucleotide/oligosaccharide-binding fold containing 2B
Tmem4	0.998	1.0851	1.431	1.206	0.6385	transmembrane protein 4
Tmem89	0.399	0.5193	1.577	1.132	1.2584	hypothetical protein LOC69384

Gene	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Product
Stau2	1.623	0.942	0.83	1.129	0.5234	staufen (RNA binding protein) homolog 2; staufen (Drosophila, RNA-binding protein) homolog 2. [Source:RefSeq;Acc:NM_025303]
Ctla4	1.58	1.3815	1.148	0.253	0.468	cytotoxic T-lymphocyte-associated protein 4
Mpp4	1.598	0.9983	1.27	1.057	1.9441	membrane protein, palmitoylated 4
Il1rl2	1.679	1.0367	0.659	1.208	0.4367	interleukin 1 receptor-like 2
Inpp4a	1.566	1.9859	0.303	0.601	0.3743	inositol polyphosphate-4-phosphatase, type I; inositol polyphosphate-4-phosphatase, type I, 107kD. [Source:RefSeq;Acc:NM_172971]
Fn1	1.031	0.7835	0.902	0.936	1.4066	fibronectin 1
Nppc	1.783	0.4293	0.577	0.737	0.478	natriuretic peptide precursor type C
Gpr35	0.971	0.6976	0.763	1.216	0.5939	G protein-coupled receptor 35
ENSMUSG00000026304	1.133	1.0507	0.771	0.497	0.4057	hypothetical protein
Cdh7	0.618	0.8047	1.085	0.935	1.744	cadherin 7, type 2
Tmem9	0.919	0.4748	0.844	0.679	1.5965	transmembrane protein 9
Arl8a	1.283	1.291	1.046	1.099	1.7862	ADP-ribosylation factor-like 10B
Ube2t	1.114	1.6357	1.17	1.134	0.6681	ubiquitin-conjugating enzyme E2T (putative)
Cyb5r1	0.825	1.1276	1.017	1.012	0.7954	cytochrome b5 reductase 1 (B5R.1)
Stx6	1.469	1.2257	1.015	1.247	0.681	Syntaxin 6. [Source:Uniprot/SWISSPROT;Acc:Q9JKK1]
Lamc1	0.914	1.0407	0.763	1.026	0.5022	laminin, gamma 1
Cabc1	1.227	0.8117	0.827	1.146	1.4508	chaperone, ABC1 activity of bc1 complex like
Pou2f1	1.048	0.8552	0.997	1.006	0.538	POU domain, class 2, transcription factor 1 (Octamer-binding transcription factor 1) (Oct-1) (OTF-1) (NF-A1). [Source:Uniprot/SWISSPROT;Acc:P25425]
Mark1	1.055	1.8353	0.833	0.612	1.9078	MAP/microtubule affinity-regulating kinase 1

Gene	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Product
Angel2	1.102	1.0052	1.109	0.872	1.322	D1Ertd396e protein
Traf5	0.867	1.0855	1.327	1.278	0.5654	Tnf receptor-associated factor 5
Plxna2	0.88	1.2032	1.528	1.53	1.4679	plexin A2
3110001A13 Rik	0.997	1.0042	0.774	0.798	0.6422	hypothetical protein LOC66540
Fmo4	0.27	1.8042	1.598	0.326	0.5414	flavin containing monooxygenase 4
Nek6	1.102	0.7194	0.796	0.99	1.2713	NIMA (never in mitosis gene a)-related expressed kinase 6
2010311D03 Rik	0.967	0.995	1.11	1.151	0.704	hypothetical protein LOC109129
Dpm2	0.865	1.5933	0.904	1.177	1.3444	dolichol-phosphate (beta-D) mannosyltransferase 2
Tsc1	0.57	0.9549	0.616	1.078	1.5572	tuberous sclerosis 1
Gpd2	1.054	1.0495	1.062	1.066	1.5425	Glycerol-3-phosphate dehydrogenase, mitochondrial precursor (EC 1.1.99.5) (GPD-M) (GPDH-M). [Source:Uniprot/SWISSPROT;Acc:Q64521]
ENSMUSG00000026845	0.875	0.2251	0.583	0.782	2.1409	hypothetical protein
5730472N09 Rik	0.665	0.4646	1.408	0.656	0.3876	hypothetical protein LOC108958
Sh3glb2	0.686	1.7316	1.646	0.898	1.6529	SH3-domain GRB2-like endophilin B2
Gapvd1	1.071	1.3324	1.023	1.096	0.6985	GTPase activating protein and VPS9 domains 1
Traf1	1.158	0.8578	0.784	0.981	1.6297	Tnf receptor-associated factor 1
Stom	0.641	1.1435	0.929	1.078	1.3569	erythrocyte protein band 7.2
Lcn3	0.855	1.2705	0.851	0.84	1.6793	lipocalin 3
Lcn12	0.409	1.7801	0.358	0.57	1.7629	lipocalin 12
Psd4	1.167	1.3848	0.782	0.882	0.7063	pleckstrin and Sec7 domain containing 4
ENSMUSG00000027070	2.457	1.0436	1.36	1.01	2.6593	hypothetical protein
Lrp2	0.381	1.5612	1.335	0.44	1.7488	similar to low density lipoprotein receptor-related protein 2 isoform 2
Timm10	0.88	1.4066	1.162	1.026	1.4999	translocase of inner mitochondrial membrane 13 homolog a
Phospho2	0.843	0.9655	0.807	0.943	0.6402	phosphatase, orphan 2

Gene	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Product
Zc3h15	1.185	1.0019	1.01	0.907	0.7412	erythropoietin 4 immediate early response
Hoxd8	1.172	0.7054	0.956	0.653	1.854	homeo box D8
Pax6	0.427	1.5551	0.568	0.507	0.5091	paired box gene 6
Tcp11l1	1.458	0.9885	0.767	1.13	0.6907	t-complex 11 like 1
Mtap1a	1.204	0.8605	0.837	0.74	0.1239	microtubule-associated protein 1 A
Ttbk1	0.721	1.4839	1.149	0.234	0.5142	tau tubulin kinase 1; tau-tubulin kinase. [Source:RefSeq;Acc:NM_080788]
Ndufaf1	0.873	1.623	0.87	0.845	1.3293	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 1
Prnd	0.872	1.6864	1.037	1.432	1.6777	Major prion protein precursor (PrP) (PrP27-30) (PrP33-35C). [Source:Uniprot/SWISSPROT;Acc:P04925]
Slc27a2	3.029	1.2326	0.852	0.945	1.4668	solute carrier family 27 (fatty acid transporter), member 2
Stard7	0.852	0.7958	0.668	1.017	0.5647	START domain containing 7
Q9D6K0	0.775	0.1957	0.928	1.096	0.7392	ENSMUSG00000027389
Ttl	1.122	2.091	1.065	0.752	1.515	tubulin tyrosine ligase
Slc20a1	0.834	0.9022	0.786	1.009	1.4125	solute carrier family 20, member 1
8430406I07 Rik	1.286	1.3624	0.677	0.834	1.3757	hypothetical protein LOC74528
Cdk5rap1	1.108	0.6869	0.354	1.431	2.1225	CDK5 regulatory subunit associated protein 1
Car13	0.894	0.9734	0.97	1.134	1.5238	carbonic anhydrase 13
Car3	1.093	0.4652	0.645	1.957	0.4925	Carbonic anhydrase III (EC 4.2.1.1) (Carbonate dehydratase III) (CA- III). [Source:Uniprot/SWISSPROT;Acc:P16015]
Pcmtd2	0.801	1.242	0.919	0.667	0.7305	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2
Mfsd1	1.036	0.7697	0.981	1.012	0.7316	major facilitator superfamily domain containing 1
Crct1	1.381	0.8391	0.818	1.815	1.4185	cysteine-rich C-terminal 1
C77668	0.844	1.3077	0.85	0.967	1.461	expressed sequence C77668 (C77668), transcript variant 1

Gene	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Product
Il6ra	1.135	0.9148	0.971	0.826	3.5844	Interleukin-6 receptor alpha chain precursor (IL-6R-alpha) (IL-6R 1). [Source:Uniprot/SWISSPROT;Acc:P22272]
Ndst3	1.127	0.5515	0.814	1.528	0.505	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 3. [Source:RefSeq;Acc:NM_031186]
Snx7	0.92	0.9921	0.911	0.674	1.4158	sorting nexin 7
Pdgfc	1.011	1.1537	0.935	0.847	1.6318	platelet-derived growth factor, C polypeptide
Chd1l	0.907	1.2433	0.882	1.045	0.748	chromodomain helicase DNA binding protein 1-like
Col24a1	0.989	0.696	0.386	0.419	2.1536	ENSMUSG00000028197
Gem	0.712	1.0751	0.682	0.479	2.2971	GTP binding protein (gene overexpressed in skeletal muscle)
Rragd	0.563	0.8949	1.256	1.408	1.7498	Ras-related GTP binding D
Mdn1	0.797	1.0573	0.937	1.264	0.6112	PREDICTED: similar to Midasin (MIDAS-containing protein) (LOC433691)
1300002K09 Rik	0.66	1.1692	1.121	1.038	1.7324	hypothetical protein LOC74152
Bspry	0.601	0.5875	1.384	1.233	2.1896	B-box and SPRY domain containing
B4galt1	0.946	1.0042	1.208	1.041	0.7289	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 1
Rmrp	0.699	1.1564	1.16	1.366	0.7915	hypothetical protein
Usp24	0.645	0.9152	1.533	1.352	0.5404	ubiquitin specific protease 24 isoform 1
Itgb3bp	2.384	0.199	1.753	0.45	2.9125	integrin beta 3 binding protein
Lrrc42	1.083	1.227	1.134	1.161	0.7034	leucine rich repeat containing 42
2210012G02 Rik	0.691	0.8158	0.764	0.492	1.5162	hypothetical protein LOC66526
Col9a2	1.593	0.7889	1.346	1.016	1.9393	procollagen, type IX, alpha 2
Kcnq4	1.879	1.9053	0.973	1.022	1.6947	potassium voltage-gated channel, subfamily Q, member 4
Q9D9N6	1.922	1.573	1.071	1.712	2.7723	hypothetical protein
ENSMUSG00000028739	0.173	0.8726	1.061	1.633	1.8918	hypothetical protein
Tmem54	0.938	0.793	0.923	0.908	1.6835	beta-casein-like protein

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2410081M15Rik	0.73	1.6804	0.536	1.099	0.5263	zinc finger and BTB domain containing 8
Slc30a2	1.376	0.787	1.21	1.758	0.6918	solute carrier family 30 (zinc transporter), member 2
Nudc	1.06	1.3429	1.175	1.083	0.7319	nuclear distribution gene C homolog (Aspergillus) (Nudc)
2310005N01Rik	0.847	0.6348	1.168	0.974	0.7252	hypothetical protein LOC70088
Fgr	1.009	1.3911	1.002	0.811	1.7307	proto-oncogene tyrosine-protein kinase Fgr
ENSMUSG00000028881	1.123	1.2834	1.163	0.944	1.7649	hypothetical protein
Casp9	0.664	0.2788	0.238	0.917	1.4808	caspase 9
Padi2	1.364	1.0933	1.02	1.129	1.4008	peptidyl arginine deiminase, type II
Abcf2	1.092	1.4354	0.988	0.689	0.6668	ATP-binding cassette, sub-family F (GCN20), member 2
Ube4b	1.177	0.8119	0.899	0.983	0.6366	ubiquitination factor E4B
Lzic	1.925	1.3046	0.66	0.819	1.3291	leucine zipper and CTNNBIP1 domain containing
Ccnl2	0.77	0.9577	1.275	0.861	1.4193	cyclin L2 isoform 1; Paneth cell enhanced expression. [Source:RefSeq;Acc:NM_207678]
Q9D5I1	1.343	1.2785	0.452	1.711	1.8313	PREDICTED: RIKEN cDNA 4930435H24 gene (4930435H24Rik)
Q8BKW4	0.921	1.7877	1.244	1.251	0.5265	hypothetical protein
Klhl5	1.012	0.8844	1.588	1.134	0.8027	Similar to lymphocyte activation-associated protein. [Source:Uniprot/SPTREMBL;Acc:Q8R334]
Tec	1.332	1.4617	1.036	1.069	1.2373	cytoplasmic tyrosine kinase, Dscr28C related
AI586015	0.88	1.0604	0.837	0.897	1.482	BCR downstream signaling 1
Ugt2b36	1.024	1.0711	0.888	0.961	1.6831	UDP glucuronosyltransferase 2 family, polypeptide B36
Smr2	1.315	0.9744	0.641	1.184	1.811	Salivary protein MSG2, isoform alpha precursor [Contains: SMR1-like peptide]. [Source:Uniprot/SPTREMBL;Acc:O09133]

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Nudt9	1.018	0.9259	1.277	1.156	1.2551	nudix (nucleoside diphosphate linked moiety X)-type motif 9
6330548G22 Rik	0.5	1.1322	0.645	1.313	1.4684	U11/U12 snRNP 35K
Camkk2	0.433	1.6586	1.106	1.418	1.778	calcium/calmodulin-dependent protein kinase kinase 2, beta. [Source:RefSeq;Acc:NM_145358]
Ep400	1.839	1.3407	1.05	1.427	0.6131	Domino. [Source:RefSeq;Acc:NM_029337]
Gal3st4	1.009	0.7089	1.15	0.361	0.5245	galactose-3-O-sulfotransferase 4
Rpo1-3	0.897	0.8451	0.891	1.079	1.311	RNA polymerase 1-3 isoform 1
C130038G02 Rik	0.77	1.6438	0.811	1.074	1.6567	hypothetical protein LOC77521 isoform b
Wnt16	0.792	1.8812	1.221	1.423	2.5477	wingless-related MMTV integration site 16
Cutl1	0.638	0.8589	0.971	1.006	1.3283	CCAAT displacement protein isoform b
Bcdin3	0.982	0.99	0.919	0.999	0.8204	bin3, bicoid-interacting 3, homolog
Sec8l1	0.967	1.2311	1.116	1.111	1.2371	Exocyst complex component Sec8. [Source:Uniprot/SWISSPROT;Acc:O35382]
Fkbp9	1.246	1.4421	1.004	0.992	0.6284	FK506 binding protein 9
Mrps33	0.838	0.8729	1.073	0.979	0.5708	mitochondrial ribosomal protein S33 isoform 1
Gkn1	0.795	2.0664	0.667	1.014	0.4879	gastrokine 1
ENSMUSG00000030134	0.543	2.6314	0.589	0.995	1.7902	PREDICTED: RasGEF domain family, member 1A (Rasgef1a)
Bms1	1.171	1.0348	1.195	1.045	0.6963	BMS1-like, ribosome assembly protein
Prpmp5	0.461	0.5903	0.193	1.332	1.7226	proline-rich protein MP5
Clec2e	0.395	1.0744	1.158	1.617	2.9225	C-type lectin domain family 2, member e
Clec1b	0.113	0.4057	0.907	0.702	2.4062	C-type lectin domain family 1, member b
Erc1	0.628	1.2401	0.957	0.525	2.3316	Rab6-interacting protein 2 isoform 2
Plcz1	1.5	1.163	1.014	2.54	2.7796	phospholipase C, zeta 1
ENSMUSG00000030295	2.256	1.0873	1.283	0.252	2.5033	hypothetical protein

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ENSMUSG00000030304	1.016	1.4586	1.383	0.856	2.4776	hypothetical protein
Vamp1	1.352	1.1954	0.628	0.803	0.471	vesicle-associated membrane protein 1 isoform a
Strn4	1.006	1.2379	0.894	0.947	0.7891	zinedin isoform 1
4933421I07Rik	1.295	0.7871	1	1.057	0.7292	hypothetical protein LOC71162
ENSMUSG00000030465	1.224	1.1651	1.054	1.039	1.5623	hypothetical protein
Zdhhc13	0.801	1.1208	1.08	1.244	0.7045	zinc finger, DHHC domain containing 13
Mef2a	0.443	0.832	1.195	0.94	0.8313	Myocyte-specific enhancer factor 2A. [Source:Uniprot/SWISSPROT;Acc:Q60929]
4632434I11Rik	0.719	1.0246	0.72	1.136	1.7265	hypothetical protein LOC74041
Art2b	0.196	0.1235	0.873	1.177	0.498	ADP-ribosyltransferase 2b
Vkorc1	1.006	1.0829	1.02	1.31	1.3872	vitamin K epoxide reductase complex, subunit 1
Abcc6	1.075	0.2488	0.421	2.076	0.4677	ATP-binding cassette, sub-family C, member 6
Fxc1	1.036	0.9752	0.714	1.244	1.7679	Mitochondrial import inner membrane translocase subunit TIM9 B. [Source:Uniprot/SWISSPROT;Acc:Q9WV96]
Lyrm1	1.015	0.7025	0.877	1.013	2.2099	LYR motif containing 1
Uros	0.427	1.3783	0.703	1.212	2.1295	uroporphyrinogen III synthase
Usp11	0.962	0.3709	0.962	1.185	2.0323	ubiquitin specific protease 11
Oraov1	1.219	0.6765	0.853	0.832	1.3484	oral cancer overexpressed 1
Tnni2	1.018	1.0494	0.839	1.346	1.5376	troponin I, skeletal, fast 2
Elf4	1.023	0.5996	0.863	0.982	0.6669	E74-like factor 4
Lmo6	0.962	1.0595	0.898	1.23	0.6792	LIM domain only 6
Was	0.977	1.4656	1.198	1.149	1.2043	Wiskott-Aldrich syndrome homolog
Heph	0.581	1.0523	1.125	0.179	0.5015	hephaestin isoform 1
Q8K3S0	0.441	0.9539	0.261	0.526	1.3679	Ppnx protein. [Source:Uniprot/SPTREMBL;Acc:Q8K3S0]

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Q8BSI3	0.83	2.7912	0.683	1.384	2.0351	X-linked myotubular myopathy gene 1. [Source:Uniprot/SPTREMBL;Acc:Q8BSI3]
Xlr4	1.415	0.8156	1.205	0.729	1.5623	X-linked lymphocyte-regulated 4. [Source:RefSeq;Acc:NM_021365]
Dsip1	0.806	0.7944	1.066	1.498	1.7809	Glucocorticoid-induced leucine zipper protein. [Source:Uniprot/SWISSPROT;Acc:Q9Z2S7]
Q9CZ75	1.152	0.7876	0.409	1.77	0.6872	hypothetical protein
Tpte	1.726	0.1247	0.532	0.302	1.2003	transmembrane phosphatase with tensin homology isoform C. [Source:RefSeq;Acc:NM_181851]
Ankrd10	1.035	1.4025	1.265	0.809	0.6485	ankyrin repeat domain 10
Q80ZU4	0.948	1.1446	0.944	1.346	0.6845	hypothetical protein
Adam5	0.514	0.3011	0.77	1.086	0.4605	a disintegrin and metalloprotease domain 5
Pou4f2	0.706	1.094	1.205	0.436	1.5573	POU domain, class 4, transcription factor 2
Hp	0.95	0.6114	0.505	0.781	2.4707	haptoglobin
Pmfbp1	0.867	1.0703	0.74	1.147	0.6454	polyamine modulated factor 1 binding protein 1
Cntnap4	1.225	1.5155	0.57	1.297	2.7626	contactin associated protein 4
Crispld2	0.594	0.1039	1.431	1.248	2.5927	LCCL domain containing cysteine-rich secretory protein 2
Car7	1.732	3.2027	1.291	0.417	1.7303	carbonic anhydrase 7
Cbfb	1.151	1.3215	1.021	0.995	0.6617	core binding factor beta
Cyb5b	0.965	1.3083	1.145	0.864	1.4571	cytochrome b5 outer mitochondrial membrane precursor
Chst5	0.968	1.5357	1.225	1.053	0.3522	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 5
Jam3	0.885	1.2739	0.717	1.247	2.271	junction adhesion molecule 3
Pdgfd	0.486	0.6442	0.445	0.683	0.684	platelet-derived growth factor, D polypeptide
Pdgfd	0.258	1.3717	0.814	0.94	2.2453	platelet-derived growth factor, D polypeptide

Gene	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Product
Usp2	1.175	0.6208	1.345	1.087	1.3497	Ubiquitin carboxyl-terminal hydrolase 2 (EC 3.1.2.15) (Ubiquitin thiolesterase 2) (Ubiquitin-specific processing protease 2) (Deubiquitinating enzyme 2) (41 kDa ubiquitin-specific protease). [Source:Uniprot/SWISSPROT;Acc:O88623]
Oaf	1.979	1.3485	0.758	0.692	1.4059	out at first
Pou2f3	0.458	1.3562	1.102	0.292	2.9404	POU domain, class 2, transcription factor 3 (Octamer-binding transcription factor 11) (Oct-11) (Epoc-1). [Source:Uniprot/SWISSPROT;Acc:P31362]
1600029D21Rik	0.968	0.8972	0.993	1.282	2.7118	placenta expressed transcript 1
Slc37a2	0.902	1.1575	1.096	1.077	0.7302	solute carrier family 37 (glycerol-3-phosphate transporter), member 2
Yipf2	1.175	1.1057	1.06	1.054	1.2682	Yip1 domain family, member 2
Tmod2	1.035	1.234	0.454	0.513	2.6603	tropomodulin 2
Stoml1	0.85	1.101	0.994	0.904	1.302	stomatin-like 1
Lactb	0.789	1.0823	0.956	1.008	1.2833	lactamase, beta
Slc25a36	1.294	1.6923	1.722	1.098	0.6252	solute carrier family 25, member 36
Kif9	0.288	1.9109	1.544	0.628	2.4736	kinesin family member 9
ENSMUSG00000032490	0.5	1.4697	0.704	0.522	0.5806	PREDICTED: RIKEN cDNA 4921524K10 gene (4921524K10Rik)
Pdcd6ip	1.177	1.2641	0.848	0.536	0.6432	programmed cell death 6 interacting protein
Fbxl2	1.133	1.8411	0.803	0.93	1.3278	F-box and leucine-rich repeat protein 2
Axud1	0.608	0.6973	0.818	0.798	1.3274	AXIN1 up-regulated 1
Usp4	0.988	0.8986	0.991	1.079	0.8021	ubiquitin specific protease 4 (proto-oncogene)
Pon2	0.892	1.198	1.053	0.938	0.7783	paraoxonase 2

Gene	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Product
Pon2	1.015	1.2144	0.939	1.126	0.6739	Serum paraoxonase/arylesterase 2 (EC 3.1.1.2) (EC 3.1.8.1) (PON 2) (Serum aryldialkylphosphatase 2) (A-esterase 2) (Aromatic esterase 2). [Source:Uniprot/SWISSPROT;Acc:Q62086]
Ankrd15	0.883	1.1415	1.049	0.984	1.6168	ankyrin repeat domain 15
Abtb2	1.592	0.9453	1.006	1.432	1.6862	ankyrin repeat and BTB (POZ) domain containing 2
Zfp414	1.308	1.1548	0.844	0.95	1.5499	zinc finger protein 414
ENSMUSG00000032808	1.767	0.8127	1.269	1.133	0.5886	hypothetical protein
ENSMUSG00000032849	0.907	1.0553	0.398	0.423	1.8156	hypothetical protein
Pkd1	0.935	0.7212	0.813	0.701	0.6181	polycystin 1
Ccdc85a	1.148	0.538	1.321	1.405	0.5547	coiled-coil domain containing 85A
ENSMUSG00000032999	1.564	1.3841	0.371	1.575	1.781	hypothetical protein
Accn4	0.824	0.1364	0.626	1.824	2.3433	amiloride-sensitive cation channel 4, pituitary
Entpd6	1.207	0.9492	0.951	0.742	1.6795	ectonucleoside triphosphate diphosphohydrolase 6
Arid2	0.635	1.885	1.053	0.918	0.6592	AT rich interactive domain 2 (Arid-rfx like)
Slc35a4	0.86	0.7808	0.835	0.853	0.7715	solute carrier family 35, member A4
Chst2	1.144	1.0054	1.102	0.963	0.532	carbohydrate sulfotransferase 2
Rtp4	1.349	0.7328	1.065	1.355	2.7371	receptor transporting protein 4
AI427515	0.866	1.5601	0.817	1.081	1.6486	hypothetical protein LOC270097
Antxr1	1.23	1.0907	1.539	1.27	1.4617	anthrax toxin receptor 1
Prnpip1	1.412	1.434	1.156	1.097	0.8326	prion protein interacting protein 1
ENSMUSG00000033441	1.208	1.4068	0.893	0.5	1.6322	hypothetical protein
Myo5c	1.691	1.0467	0.288	1.502	1.9306	Myosin VC (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8BWY8]
Pcgf3	0.547	1.0445	0.797	0.894	0.5752	polycomb group ring finger 3
Spr	0.964	1.4572	1.15	1.383	0.7355	sepiapterin reductase

Gene	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Product
LOC435392	0.681	0.3782	1.026	0.88	1.7462	similar to ribosomal protein L31
ENSMUSG00000033788	0.661	1.7093	0.733	0.937	0.5349	hypothetical protein
Atp7a	1.524	1.1567	0.968	0.867	0.8323	ATPase, Cu++ transporting, alpha polypeptide
SALF_MOUSE	0.496	0.8221	1.134	1.916	2.6744	Stonin 1 (Stoned B-like factor). [Source:Uniprot/SWISSPROT;Acc:Q8CDJ8]
Pla2g4b	1.065	0.9136	0.779	1.106	1.7154	phospholipase A2, group IVB
6330503K22Rik	0.856	1.4604	1.063	0.907	2.0779	CP110 protein
Q8BV95	0.928	0.8611	1.084	1.598	1.8926	CDNA FLJ12851 FIS. [Source:Uniprot/SPTREMBL;Acc:Q8BV95]
Gria2	1.011	1.2402	1.554	2.24	1.9874	glutamate receptor, ionotropic, AMPA 2 isoform 2
Chchd4	0.961	1.6596	1.129	1.021	1.313	coiled-coil-helix-coiled-coil-helix domain containing 4. [Source:RefSeq;Acc:NM_133928]
Rhov	0.618	1.0527	0.612	1.024	1.5162	ras homolog gene family, member V. [Source:RefSeq;Acc:NM_145530]
Jundm2	1.416	0.8351	0.915	1.158	1.5729	Jun dimerization protein 2
Cyp4a12	0.64	0.5851	1.387	1.419	0.3131	cytochrome P450, family 4, subfamily a, polypeptide 12
4632417N05Rik	2.105	0.933	1.092	1.065	0.7945	RIKEN cDNA 4632417N05
Brip1	1.538	1.1024	0.943	0.672	2.4144	BRCA1 interacting protein C-terminal helicase 1. [Source:RefSeq;Acc:NM_178309]
Tulp4	1.576	1.8455	0.997	1.166	1.2708	tubby like protein 4
Spata6	1.065	1.1991	1.216	1.15	0.6389	HASH. [Source:RefSeq;Acc:NM_026470]
Uaca	0.78	1.0673	0.82	1.359	0.5845	nuclear membrane binding protein NUCLING
Gja7	0.894	1.2782	1.088	1.241	1.7181	gap junction membrane channel protein alpha 7
Morc2a	1.157	0.8616	1.064	0.76	0.7101	microrchidia 2A
Ccpg1	1.14	1.2248	1.194	1.091	0.7853	cell cycle progression 8 protein. [Source:RefSeq;Acc:NM_028181]

Gene	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Product
ENSMUSG00000034623	1.076	0.5766	1.011	1.209	2.5681	hypothetical protein
Cib3	1.374	1.639	1.221	0.737	1.7598	similar to DNA-dependent protein kinase catalytic subunit-interacting protein 3 isoform 1
Gnat1	0.955	1.1122	1.057	0.311	2.4228	guanine nucleotide binding protein, alpha transducing 1
Cxcl10	1.16	1.6943	1.044	1.487	2.5934	chemokine (C-X-C motif) ligand 10
ENSMUSG00000034865	0.728	0.957	1.162	0.928	2.0815	PREDICTED: bromo domain-containing protein disrupted in leukemia (Brodl)
BY707822	0.979	1.2962	0.389	3.661	1.9302	hypothetical protein
Ncaph	1.001	0.9055	0.771	1.128	0.716	barren homolog
Ttc22	0.417	1.0389	0.262	0.238	2.6518	tetratricopeptide repeat domain 22
Dapk3	1.085	1.3856	0.77	0.869	0.6722	death-associated kinase 3
Wdr78	1.041	0.6724	3.169	1.678	2.0336	WD repeat domain 78
ENSMUSG00000035129	0.98	0.8809	0.831	0.349	1.5703	PREDICTED: similar to farnesyl diphosphate farnesyl transferase 1; squalene synthase (LOC432824)
Zc3h12c	0.843	0.509	1.16	1.243	0.0784	similar to zinc finger CCCH type containing 12A
Chrnb4	1.149	1.31	1.175	1.024	2.3539	cholinergic receptor, nicotinic, beta polypeptide 4
Kcnk15	1.498	0.6536	0.807	0.378	1.5341	potassium channel, subfamily K, member 15
ENSMUSG00000035258	0.894	1.059	0.828	1.022	0.7165	hypothetical protein
Plekhj1	1.462	0.8309	1.171	0.846	1.6983	hypothetical protein
Dennd1a	1.189	1.206	0.838	1.397	1.522	DENN/MADD domain containing 1A
Thyn1	1.025	1.3275	1.249	0.888	0.6564	thymocyte protein Thy28
1810020D17Rik	1.007	0.8227	0.94	0.946	0.6487	hypothetical protein LOC66273
Sbno2	1.01	0.3186	0.749	0.82	0.632	strawberry notch homolog
Hmha1	1.075	1.3303	1.156	0.908	0.7949	minor histocompatibility antigen HA-1
ENSMUSG00000035714	1.302	1.4344	0.956	1.166	2.5628	hypothetical protein
Prkx	1.565	0.7578	0.762	1.08	1.6255	protein kinase, X-linked

Gene	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Product
Grin3b	1.692	1.4537	0.414	1.151	0.4375	glutamate receptor, ionotropic, NMDA3B
Palm	1.703	1.0258	0.803	0.74	1.7806	paralemmin
Rab6ip1	1.006	0.7727	1.11	1.139	0.7382	Rab6 interacting protein 1
4632404H22 Rik	0.665	1.4022	0.894	0.631	1.6129	hypothetical protein LOC78755
Smug1	1.021	1.164	0.731	1.715	1.8292	single-strand selective monofunctional uracil DNA glycosylase
Dgkb	1.258	0.8705	0.56	0.625	0.4954	diacylglycerol kinase, beta. [Source:RefSeq;Acc:NM_178681]
Slc9a3	1.229	1.9869	1.508	1.098	3.3762	solute carrier family 9 (sodium/hydrogen exchanger), member 3
Q9D4C8	1.698	0.5996	1.01	0.471	1.5146	hypothetical protein
ENSMUSG00 000036288	1.19	0.8296	0.982	0.988	0.7386	hypothetical protein
Alpi	0.9	0.7107	1.516	0.773	1.9883	alkaline phosphatase, intestinal
Ttyh3	0.396	0.1665	1.039	0.794	0.4764	tweety 3
2310005P05 Rik	1.005	1.2342	0.619	0.74	1.7857	hypothetical protein LOC67484
Rfxap	1.223	0.8873	1.321	1.043	0.6287	regulatory factor X-associated protein
Cab39	1.025	1.2605	0.861	0.84	0.6476	MO25 protein. [Source:Uniprot/SWISSPROT;Acc:Q06138]
Q9D5V3	0.284	0.3128	1.01	2.361	0.6648	hypothetical protein
Kif15	1.264	1.0114	0.971	1.362	1.8309	kinesin-like 7
ENSMUSG00 000036842	0.705	1.0325	0.572	1.401	1.4248	hypothetical protein
Mrpl55	0.659	1.0718	0.897	0.605	1.3522	mitochondrial ribosomal protein L55
BC053749	1.097	0.866	1.129	1.114	1.8152	hypothetical protein LOC333193
Kirrel2	0.566	2.2651	0.849	2.039	1.4053	kin of IRRE-like 2
Clca5	0.958	0.1002	2.451	1.303	1.936	chloride channel calcium activated 5
Tfb1m	0.731	0.7378	1.11	0.722	0.6825	transcription factor B1, mitochondrial
BC038156	0.921	1.2238	0.887	0.941	0.6686	hypothetical protein LOC270135
ENSMUSG00 000037079	1.077	1.403	1.477	0.822	1.3981	hypothetical protein
BC057552	0.783	1.092	0.929	1.287	1.7053	hypothetical protein LOC212123

Gene	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Product
Syn1	0.221	1.0972	1.114	0.266	0.5214	synapsin I
Rkhd2	1.536	0.9019	1.111	0.895	1.36	ring finger and KH domain containing 2
D8Ertd354e	1.873	0.5259	0.849	1.002	0.6777	DNA segment, Chr 8, ERATO Doi 354, expressed (D8Ertd354e)
ENSMUSG00000037263	1.023	1.4488	1.521	1.109	1.4631	aldehyde dehydrogenase 7-like. [Source:RefSeq;Acc:NM_028545]
Tmem97	0.867	1.3726	0.738	1.003	1.553	hypothetical protein LOC69071
ENSMUSG00000037290	0.488	0.9367	0.969	0.713	0.4737	PREDICTED: similar to C5orf4 protein (LOC216763)
Ttc13	1.58	0.8681	1.025	1.208	0.6205	tetratricopeptide repeat domain 13
Bag4	0.673	1.2284	0.91	0.824	0.6905	BCL2-associated athanogene 4
2410018C17Rik	1.006	0.9649	1.357	1.021	0.591	dorsal neural-tube nuclear protein
Paqr7	0.971	0.6571	0.632	0.994	1.665	progestin and adipoQ receptor family member VII
Azin1	0.876	0.8172	1.036	1.125	1.5268	antizyme inhibitor 1
1700029I01Rik	0.986	0.6937	0.851	0.994	1.5132	hypothetical protein LOC70005
Bclaf1	0.856	1.2673	1.092	0.754	0.622	BCL2-associated transcription factor 1 isoform 2
ENSMUSG00000037770	1.047	1.5559	0.735	1.041	0.6546	cDNA sequence BC013481 (BC013481)
Gm806	1.128	0.1743	1.07	1.022	0.2255	hypothetical protein LOC328250
LOC244495	0.432	0.5107	1.66	0.427	0.054	similar to tripin
Pcdh18	1.136	1.2975	0.808	1.09	1.5614	protocadherin 18
Dhx38	1.176	0.3973	1.267	0.91	1.6516	DEAH (Asp-Glu-Ala-His) box polypeptide 38
Slc24a2	1.226	1.2513	1.19	0.631	0.6192	solute carrier family 24 (sodium/potassium/calcium exchanger), member 2. [Source:RefSeq;Acc:NM_172426]
Centd1	0.639	1.3309	1.229	0.633	2.3878	centaurin, delta 1 isoform 1
ENSMUSG00000038011	1.217	2.9658	0.858	0.276	0.5034	PREDICTED: dynein, axonemal, heavy chain 10 (Dnahc10)
Q8CE32	1.107	1.3905	1.001	0.905	1.2894	PREDICTED: RIKEN cDNA B430108F07 gene (B430108F07Rik)
Tmem16b	1.745	1.9414	1.231	2.643	2.0338	transmembrane protein 16B
CF749571	0.898	0.9958	1.429	1.857	1.3301	hypothetical protein

Gene	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Product
Mphosph9	0.285	1.353	1.066	1.362	2.131	M-phase phosphoprotein 9 isoform 1
1810054D07 Rik	0.872	0.5294	0.982	1	1.4887	hypothetical protein LOC69863
Slc43a2	0.864	1.3989	0.915	1.046	0.6411	solute carrier family 43, member 2
Sema7a	0.465	0.7255	0.786	0.586	1.8905	semaphorin 7A
Nol1	1.267	1.0354	0.839	0.848	0.5641	nucleolar protein 1
ENSMUSG00 000038377	0.553	0.3815	1.233	1.127	0.0801	hypothetical protein
Txnip	1.103	1.2292	1.653	0.781	0.5878	hypothetical protein
Foxf2	0.904	1.2255	1.068	0.54	0.6676	forkhead box F2
Polr2l	0.868	1.4474	1.116	1.117	1.4782	DNA-directed RNA polymerase II 7.6 kDa polypeptide (EC 2.7.7.6) (RPB10) (RPB7.6) (RPABC5). [Source:Uniprot/SWISSPROT;Acc:P52436]
BC021785	1.358	0.3111	1.404	0.182	0.6075	hypothetical protein LOC215928
Srd5a2	0.76	0.3077	1.31	2.44	0.4689	steroid 5 alpha-reductase 2
Pcid2	1.206	1.3366	0.719	1.222	1.4758	PCI domain containing 2
Pcid2	1.13	1.1365	0.752	0.924	1.2465	PCI domain containing 2
Ift172	0.946	1.0126	1.386	0.999	1.3253	intraflagellar transport 172 protein
ENSMUSG00 000038570	0.262	1.4731	0.875	2.442	1.3915	hypothetical protein
Gmeb2	0.759	0.842	0.601	0.971	1.3829	glucocorticoid modulatory element binding protein 2
Scgb3a2	1.451	0.6914	1.145	1.596	1.65	secretoglobin, family 3A, member 2
1700106N22 Rik	0.877	0.822	0.668	0.709	1.7389	hypothetical protein LOC73582
Muted	1.112	1.1609	1.078	1.259	0.7106	muted
4930526H21 Rik	0.844	1.1599	0.421	0.687	1.5263	hypothetical protein LOC75136 isoform 1
2610034B18 Rik	0.635	0.8132	1.097	0.948	0.7047	hypothetical protein LOC70420
Osbpl2	0.801	1.1982	0.778	1.131	0.672	oxysterol-binding protein-like protein 2
Zfp503	1.101	0.8315	1.253	0.89	1.6846	zinc-finger protein NOLZ1
Q80VW6	1.113	1.6903	1.399	1.143	1.9953	hypothetical protein
Sec24d	0.879	1.1849	0.949	1.046	0.5089	SEC24 related gene family, member D

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ENSMUSG00000039272	1.611	0.7799	1.1	1.303	0.6047	hypothetical protein
Cdk5rap2	1.32	1.2609	1.044	1.489	3.2823	CDK5 regulatory subunit associated protein 2
Tsga10ip	1.068	1.5441	1.256	0.852	0.7661	Similar to CDNA FLJ32880 FIS (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8C1H4]
Q9D2E5	1.461	2.8566	0.898	0.972	2.1619	hypothetical protein
Fbxl18	1.554	0.749	1.192	1.179	1.3399	F-box and leucine-rich repeat protein 18
BC046331	0.568	1.2767	0.844	1.6	1.6023	glycine-, glutamate-, thienylcyclohexylpiperidine-binding protein
Prkrip1	0.519	1.3466	1.062	1.107	1.6108	Prkr interacting protein 1 (IL11 inducible)
Olig2	0.683	1.5083	1.233	0.923	1.9019	Oligodendrocyte transcription factor 2. [Source:Uniprot/SWISSPROT;Acc:Q9EQW6]
Q80TA9	0.81	1.2427	0.92	0.839	1.2495	MKIAA1632 protein (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q80TA9]
ENSMUSG00000039895	1.215	1.0065	0.939	1.044	2.0912	hypothetical protein
Ptger4	0.542	0.8313	0.833	0.653	1.4644	prostaglandin E receptor 4, subtype EP4
Ccdc40	1.216	1.3901	0.675	1.391	0.6189	coiled-coil domain containing 40
Gnaz	4.006	1.6748	1.156	2.789	1.7559	guanine nucleotide binding protein, alpha z subunit
Cox15	1.294	0.9153	0.716	1.314	0.6894	COX15 homolog, cytochrome c oxidase assembly protein
Bat2d	0.967	1.0668	0.964	1.012	1.7909	BAT2 domain containing 1 isoform 1
Tm7sf3	1.067	0.8861	1.025	0.797	1.6791	transmembrane 7 superfamily member 3
ENSMUSG00000040272	1.027	0.9523	1.273	0.991	0.5913	1-aminocyclopropane-1-carboxylate synthase. [Source:RefSeq;Acc:NM_183220]
Cdk6	0.849	1.3408	0.379	1.021	0.5035	cyclin-dependent kinase 6

Gene	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Product
ENSMUSG00000040494	1.543	1.0601	0.387	0.501	0.4257	hypothetical protein
Apoc1	0.939	1.6539	0.897	0.925	1.6074	apolipoprotein C-I
ENSMUSG00000040590	0.44	1.208	0.945	1.161	1.8644	hypothetical protein
Dok4	0.746	0.7796	0.311	1.114	0.6753	docking protein 4
Limd2	0.807	1.0326	0.949	0.784	1.4311	LIM domain containing 2
C1qtnf4	1.16	1.23	1.474	1.202	1.7001	C1q and tumor necrosis factor related protein 4
Psme4	0.765	0.6297	0.854	0.845	0.6906	proteasome (prosome, macropain) activator subunit 4
Ccr6	0.713	0.5265	0.528	0.57	0.5755	chemokine (C-C motif) receptor 6
Mgl2	0.799	1.2429	1.02	1.098	0.6197	macrophage galactose N-acetyl-galactosamine specific lectin 2
ENSMUSG00000040953	1.033	0.7848	0.449	1.204	1.8208	hypothetical protein
Asgr2	1.018	0.7486	1.009	1.785	2.4235	asialoglycoprotein receptor 2
Bub3	1.028	1.2213	0.931	0.986	0.6271	Mitotic checkpoint protein BUB3 (WD-repeat type I transmembrane protein A72.5). [Source:Uniprot/SWISSPROT;Acc:Q9WVA3]
ENSMUSG00000041190	1.39	0.2568	1.254	2.903	0.505	hypothetical protein
Sox15	0.44	1.5906	0.865	0.816	0.5602	SRY-box 15
Serpina3g	1.204	1.0508	0.407	1.457	1.8013	Spi2 proteinase inhibitor (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q62259]
BC075677	0.382	0.9768	0.164	0.641	2.0579	hypothetical protein
5330439B14Rik	1.07	1.7363	0.881	0.84	1.8377	hypothetical protein LOC321015
ENSMUSG00000041618	0.975	1.1158	0.941	0.934	0.296	hypothetical protein

Gene	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Product
Slco1a5	0.877	2.2703	1.89	1.778	3.0872	Solute carrier organic anion transporter family member 1A5 (Solute carrier family 21 member 7) (Sodium-independent organic anion transporter 3) (Organic anion transporting polypeptide 3). [Source:Uniprot/SWISSPROT;Acc:Q91YY5]
ENSMUSG00000041759	0.147	0.3678	1.044	1.096	3.3319	hypothetical protein
Enc1	1.162	0.2602	0.858	1.207	0.627	ectodermal-neural cortex 1
ENSMUSG00000041866	0.799	1.0749	1.036	1.004	0.5534	hypothetical protein
Ipo9	0.94	0.9403	1.099	0.775	0.4899	importin 9
ENSMUSG00000041885	0.926	0.981	0.841	0.917	0.2901	hypothetical protein
Pigs	0.905	1.2446	1.103	0.92	1.275	phosphatidylinositol glycan, class S homolog
Abhd14b	1.042	1.2476	1.007	1.105	1.2378	abhydrolase domain containing 14b
Svop	0.646	1.0099	0.846	1.094	1.5832	SV2 related protein
Tekt3	1.041	0.4663	1.432	1.136	0.5727	tektin 3
Isl1	1.029	1.5507	0.788	1.243	1.8327	ISL1 transcription factor, LIM/homeodomain (islet 1)
Dhx29	1.128	0.9276	0.813	1.177	0.6942	DEAH (Asp-Glu-Ala-His) box polypeptide 29
Zmym4	1.389	1.3043	1.258	1.235	1.3977	similar to zinc finger protein 262
Reln	0.315	0.8077	1.062	1.258	2.7584	Reelin precursor (EC 3.4.21.-) (Reeler protein). [Source:Uniprot/SWISSPROT;Acc:Q60841]
Reln	1.008	1.0431	0.854	0.648	1.8169	reelin precursor
ENSMUSG00000042466	1.166	0.833	0.192	1.095	0.6027	hypothetical protein
Tcfap2e	0.665	0.629	0.686	0.594	1.7409	transcription factor AP-2, epsilon

Gene	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Product
Eif2c4	0.58	0.1722	0.735	1.126	0.4277	Eukaryotic translation initiation factor 2C 4 (eIF2C 4) (eIF-2C 4) (Piwi/argonaute family protain meIF2C4). [Source:Uniprot/SWISSPROT;Acc:Q8CJF8]
Acn9	0.686	1.1286	1.062	0.944	1.4395	ACN9 homolog
Adprhl2	0.556	1.6562	0.789	0.931	0.6745	ecto ADP-ribosylhydrolase
ENSMUSG00000042567	1.934	0.1768	0.806	1.115	0.6009	hypothetical protein
Nek10	0.455	0.7377	1.356	1.152	2.2764	NIMA (never in mitosis gene a)-related kinase 10
Nek10	1.284	1.7023	0.52	1.076	0.5334	NIMA (never in mitosis gene a)-related kinase 10
Ipo11	1.011	1.3713	1.215	1.801	0.5136	importin 11
Maff	1.319	0.5258	1.033	1.023	1.8086	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein F
Susd5	0.925	1.1574	1.356	0.597	0.5446	hypothetical protein
Obfc1	1.325	1.2829	1.071	1.097	1.4664	oligonucleotide/oligosaccharide-binding fold containing 1
Ppp1r3a	0.986	0.6498	0.792	1.879	2.3844	protein phosphatase 1, regulatory (inhibitor) subunit 3A
Id1	0.652	1.6515	0.809	1.611	1.4484	inhibitor of DNA binding 1
Bex2	0.851	0.6725	0.518	0.346	2.2109	brain expressed X-linked 2
Tmem102	0.93	1.155	1.256	1.756	0.4783	hypothetical protein LOC380705
Serpinb6b	0.91	0.9922	1.185	0.843	1.7218	serine (or cysteine) proteinase inhibitor, clade B, member 6b
Trp53rk	0.967	1.2777	0.92	0.839	1.7179	Nori-2 protein
Olfr957	0.441	0.2744	0.766	0.783	2.2034	olfactory receptor 957
ENSMUSG00000043007	1.288	1.9005	1.297	1.571	0.5031	hypothetical protein
BC025833	0.596	1.175	1.568	0.824	2.9684	hypothetical protein LOC213989
ENSMUSG00000043269	0.965	0.9725	1.083	1.406	1.3814	hypothetical protein

Gene	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Product
ENSMUSG00000043278	0.958	1.0406	0.688	0.906	2.2206	PREDICTED: similar to chromosome 14 open reading frame 29 isoform c (LOC435306)
Q8BQM7	1.45	1.2701	0.775	1.385	0.6385	hypothetical protein
Gpr135	0.877	0.6523	0.648	1.222	0.4165	G protein-coupled receptor 135
Eif3s1	0.923	1.3999	0.96	0.978	1.3946	eukaryotic translation initiation factor 3, subunit 1 alpha; merged. [Source:RefSeq;Acc:NM_144545]
Gja12	0.52	0.8728	1.184	0.645	1.4742	gap junction membrane channel protein alpha 12; connexin 47. [Source:RefSeq;Acc:NM_080454]
Krt34	0.917	1.0965	0.609	1.334	1.8042	keratin complex 1, acidic, gene 4
LOC216394	2.022	0.9244	0.426	0.276	1.7023	similar to sentrin 18
Q9CX41	0.764	0.7549	0.542	1.082	1.9343	hypothetical protein
BC033932	0.211	0.9748	1.388	0.708	1.7307	hypothetical protein
V2r2	0.784	0.5143	1.441	0.452	2.1334	vomeronasal 2, receptor, 2; vomeronasal organ family 2, receptor, 2. [Source:RefSeq;Acc:NM_009492]
Rtn4r	1.607	0.8261	1.374	1.77	1.3928	nogo receptor
Olfr550	0.724	0.5322	0.977	0.748	0.4887	olfactory receptor 550
ENSMUSG00000043897	1.235	1.611	1.071	1.058	0.324	hypothetical protein
Trp53bp1	1.158	1.2771	1.511	0.929	0.6456	transformation related protein 53 binding protein 1
A330049M08Rik	0.533	2.1594	1.041	3.525	0.6887	hypothetical protein LOC230822
Olfr544	0.939	0.6624	1.058	1.301	0.5777	olfactory receptor 544
Pura	1.106	1.5513	1.043	0.856	0.794	purine rich element binding protein A
Q8BLW1	0.626	0.6741	1.169	0.906	1.7063	hypothetical protein
Il1f9	1.489	0.616	0.792	1.767	0.4452	interleukin 1 family, member 9
Pcsk9	0.641	0.9209	1.317	1.73	1.9676	proprotein convertase subtilisin/kexin type 9
Neurog3	1.257	1.0613	0.758	0.906	0.6002	neurogenin 3
ENSMUSG00000044513	1.207	0.9389	1.794	2.007	1.624	hypothetical protein
AY074887	0.727	0.754	1.043	0.455	2.452	cleft palate-related protein 1

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Lsm11	0.662	0.6794	1.12	0.866	0.6892	U7 snRNA-associated Sm-like protein Lsm11
ENSMUSG00000044938	2.295	0.9352	0.58	2.166	1.5794	hypothetical protein
Olfr669	0.912	0.5995	1.805	1.017	0.6862	olfactory receptor 669
Olfr711	1.263	0.8756	0.841	0.727	2.2855	olfactory receptor 711
ENSMUSG00000045065	0.898	0.7723	1.225	1.379	1.4322	hypothetical protein
E130308A19Rik	0.831	1.4114	1.272	0.717	0.5068	hypothetical protein LOC230259 isoform 1
Olfr594	0.641	1.1132	1.105	0.887	1.4515	olfactory receptor 594
Atxn2	1	0.8821	0.434	0.778	0.4616	ataxin 2
Olfr1255	1.203	0.8921	0.956	0.563	1.89	olfactory receptor 1255
AI467606	0.776	1.1066	1.005	1.122	1.2544	hypothetical protein LOC101602
Zfp574	1.07	2.7604	0.926	0.738	0.746	zinc finger protein 574
ENSMUSG00000045357	0.391	0.9493	0.935	1.069	1.7634	hypothetical protein
Tnfrsf26	0.659	0.8568	0.841	1.075	1.7824	tumor necrosis factor receptor superfamily, member 26
ENSMUSG00000045544	1.381	0.2223	0.978	1.197	2.0357	hypothetical protein
Fpr1	1.153	1.4241	0.825	0.856	1.9034	formyl peptide receptor 1
ENSMUSG00000045614	0.774	1.1794	1.003	1.073	0.6215	
Tssc4	0.941	1.2589	1.136	1.119	0.697	tumor-suppressing subchromosomal transferable fragment 4. [Source:RefSeq;Acc:NM_020285]
B3gat1	1.602	1.2954	1.095	0.452	0.1202	Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 1 (EC 2.4.1.135) (Beta-1,3-glucuronyltransferase 1) (Glucuronosyltransferase-P) (GlcAT-P) (UDP-GlcUA:glycoprotein beta- 1,3-glucuronyltransferase) (GlcUAT-P) (Fragment). [Source:Uniprot/SWISSPROT;Acc:Q9CW73]
ENSMUSG00000046064	0.844	0.7979	1.004	1.18	0.6934	hypothetical protein

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Lrrc8d	0.946	1.3568	0.888	1.003	0.7419	leucine rich repeat containing 5
Jrk	1.018	1.3715	1.649	0.976	0.5951	jerky
ENSMUSG00000046720	1.303	1.6174	0.777	1.119	1.4659	
ENSMUSG00000046797	0.833	0.5728	0.93	1.192	1.8022	
ENSMUSG00000046976	0.945	0.9559	0.936	1.06	0.8162	
Spata2	0.892	0.9598	0.748	1.21	1.4904	spermatogenesis associated 2
BC037048	0.886	1.0821	0.806	1.287	1.6221	TICAM-1; TIR domain-containing adaptor inducing interferon-beta. [Source:RefSeq;Acc:NM_174989]
Ttn	0.677	0.243	1.298	1.925	0.4399	titin; connectin; muscular dystrophy with myositis. [Source:RefSeq;Acc:NM_027369]
Defb9	0.348	2.596	1.167	1.033	2.3401	defensin beta 9
Dmbt1	0.742	1.1993	0.999	1.801	0.344	hypothetical protein
Slfnl1	0.562	0.8735	1.137	1.056	0.3906	schlafen like 1
Frat2	1.281	3.0991	1.184	0.65	1.6943	frequently rearranged in advanced T-cell lymphomas 2
D19Wsu162e	0.795	1.5128	0.531	0.728	0.5305	hypothetical protein LOC226178
Olfr770	0.265	0.7965	1.654	0.576	1.9129	olfactory receptor 770
Tnrc6b	0.965	1.6897	0.737	0.831	0.634	trinucleotide repeat containing 6b isoform 1
BY728099	1.562	0.2712	0.971	1.257	0.4741	hypothetical protein
ENSMUSG00000047905	0.955	1.0008	0.827	0.793	1.2208	hypothetical protein
BC037442	0.887	0.972	1.091	1.047	0.7332	hypothetical protein
Npm2	1.649	0.5036	1.773	1.381	2.1222	nucleophosmin/nucleoplasmin 2
Grem1	1.159	1.4493	1.19	0.775	1.8063	gremlin 1; down-regulated in v-mos-transformed cells; Gremlin1; cysteine knot superfamily 1, BMP antagonist 1. [Source:RefSeq;Acc:NM_011824]
ENSMUSG00000048110	0.807	0.9245	1.347	1.121	0.679	hypothetical protein
Arid4a	1.417	1.1066	1.36	0.735	0.6145	retinoblastoma-binding protein 1
CN31_MOUSE	0.579	1.1834	1.841	0.387	0.1087	hypothetical protein

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Olfr556	1.681	1.3567	0.848	0.428	0.1677	olfactory receptor 556
Fgfbp1	1.911	0.3004	0.758	0.45	1.5872	fibroblast growth factor binding protein 1
Osr1	1.143	1.5088	0.955	1.269	1.9998	odd-skipped related 1
Ccdc57	1.292	2.373	0.636	1.347	2.33	coiled-coil domain containing 57
ENSMUSG00000048473	0.617	1.3729	1.012	1.129	0.3812	hypothetical protein
ENSMUSG00000048509	1.534	0.7181	0.71	1.164	0.625	hypothetical protein
Dock7	1.385	1.1653	0.41	1.201	0.4417	dedicator of cytokinesis 7
Q8BHV4	0.717	0.5637	0.511	0.812	1.9022	Weakly similar to hypothetical 33.9 kDa protein. [Source:Uniprot/SPTREMBL;Acc:Q8BHV4]
P2ry6	0.855	0.7926	0.597	0.769	0.6626	pyrimidinergic receptor P2Y, G-protein coupled, 6
Olfr202	0.969	1.6671	0.953	0.475	1.2492	olfactory receptor 202
Vps37c	0.908	1.1404	0.838	1.068	1.5417	vacuolar protein sorting 37C
Hexim1	1.311	0.7157	0.973	1.118	1.9748	hexamethylene bis-acetamide inducible 1
Olfr1366	0.468	0.2369	0.293	1.27	0.4588	olfactory receptor 1366
E430004N04Rik	0.608	0.6882	1.129	0.859	0.0785	hypothetical protein LOC210757
Es31	0.315	1.7315	0.634	2.163	1.4176	esterase 31 isoform 1
Olfr572	0.997	0.5851	0.842	1.258	1.7517	olfactory receptor 572; olfactory receptor MOR10-2; GA_x6K02T2PBJ9-5638785-5639741. [Source:RefSeq;Acc:NM_147089]
ENSMUSG00000049460	0.929	1.0624	0.74	0.717	1.2758	hypothetical protein
ENSMUSG00000049672	0.94	0.7859	0.374	0.726	0.7273	hypothetical protein
Olfr250	1.679	1.7372	1.136	0.309	1.8875	olfactory receptor 250
9130218O11Rik	1.424	0.2773	0.879	1.813	0.4308	hypothetical protein LOC328561
Olfr728	1.295	0.3538	0.884	1.079	0.4234	Olfactory receptor GA_x6K02T2PMLR-5831021-5830086. [Source:Uniprot/SPTREMBL;Acc:Q7TRM6]

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Prss18	0.877	1.4375	1.084	3.433	0.6996	protease, serine, 18; protease, serine, 9; kallikrein 7; protease M; kallikrein 6; kallikrein 29. [Source:RefSeq;Acc:NM_011177]
Akap4	1.049	1.5313	0.479	1.068	0.7034	A-kinase anchor protein 4 precursor (Major fibrous sheath protein) (FSC1) (AKAP82) (p82). [Source:Uniprot/SWISSPROT;Acc:Q60662]
ENSMUSG00000050103	0.814	1.0483	0.885	1.002	1.5712	hypothetical protein
2810002O09Rik	0.391	0.7343	0.804	1.01	2.0263	RIKEN cDNA 2810002O09
AK172894	0.806	1.087	1.219	1.115	0.6262	Septin 6. [Source:Uniprot/SWISSPROT;Acc:Q9R1T4]
C77080	1.264	2.3284	0.841	0.802	1.3995	hypothetical protein LOC97130
Hamp1	1.269	1.1979	1.065	0.867	1.8919	hepcidin antimicrobial peptide 1
BC062109	1.55	1.1891	1.101	0.468	1.4337	hypothetical protein LOC231503
Vamp8	0.915	0.9302	1.055	1.189	1.4746	vesicle-associated membrane protein 8
AI314180	1.336	1.1244	1.142	1.043	0.5523	hypothetical protein LOC230249
Olfr1494	1.778	0.9105	1.75	1.719	2.0537	olfactory receptor 1494
Insl6	1.02	1.1029	0.898	1.452	1.8219	insulin-like 6
Prkca	0.895	0.8182	1.075	1.168	1.2994	protein kinase C, alpha
AI595406	0.47	1.8741	0.964	0.554	2.0754	similar to fibrillarin
ENSMUSG00000051107	0.725	1.0297	1.321	1.368	0.7137	PREDICTED: similar to hypothetical protein LOC349236 (LOC432759)
Mrgprd	1.044	2.3222	0.881	0.517	3.9719	MAS-related GPR, member D
Six1	0.618	1.1489	0.403	1.083	1.6042	sine oculis homeobox homolog 1
Crebzf	0.75	0.7722	1.343	0.755	1.4594	HCF-binding transcription factor Zhangfei
Irf2bp2	1.044	2.1806	1.345	0.961	1.3417	similar to interferon regulatory factor 2 binding protein 2 isoform 1
Pcdhb2	2.427	0.9686	1.018	1.007	1.8852	protocadherin beta 2
Rap2a	1.164	1.2614	1.295	0.878	1.3249	RAP2A, member of RAS oncogene family

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5830482F20 Rik	0.661	1.0389	0.366	0.825	0.4948	hypothetical protein LOC320435
Q8BN39	0.736	0.8479	0.601	0.445	1.8453	hypothetical protein
Q8CC28	0.698	1.4921	1.395	1.217	1.2854	hypothetical protein
Q8C9R4	0.904	0.9843	0.648	1.792	1.8278	hypothetical protein
Cd177	0.64	0.9276	0.996	0.65	1.9681	CD177 antigen
Tln2	0.605	0.8751	1.375	0.689	0.5656	talin 2
Pmp2	1.603	1.1342	0.919	0.744	3.7983	Myelin P2 protein. [Source:Uniprot/SWISSPROT;Acc:P24526]
4930504O13 Rik	0.254	0.2633	0.467	2.07	0.4579	hypothetical protein LOC403200
ENSMUSG00000052652	0.703	0.6699	0.755	0.146	1.4287	PREDICTED: similar to kappa immunoglobulin (LOC435902)
Rnf103	1.418	1.1907	0.949	0.969	0.673	ring finger protein 103
Q9JLA5	1.194	0.8741	1.2	0.342	0.7773	Fibroblast growth factor homologous factor 2 isoform 1P' (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q9JLA5]
Q8C3B6	0.885	0.8367	0.978	2.476	1.9693	hypothetical protein
1700030K09 Rik	1.276	2.1862	1.109	0.85	1.6452	hypothetical protein LOC72254
ENSMUSG00000052812	0.501	2.121	1.117	0.467	2.0551	hypothetical protein
Rnf144	0.971	0.5944	0.977	1.405	1.3892	ring finger protein 144
ENSMUSG00000052951	1.356	1.1259	1.448	0.444	1.9361	hypothetical protein C130021I20 (C130021I20)
Cyp2f2	0.313	0.4456	0.673	1.074	1.8042	cytochrome P450, family 2, subfamily f, polypeptide 2
Trim10	2.036	1.1813	0.347	1.056	1.362	tripartite motif protein 10
CA751297	1.643	1.4691	1.389	0.888	2.6073	ENSMUSG00000052999
1300003B13 Rik	0.98	1.014	0.392	1.04	0.4816	hypothetical protein LOC74149
Q8BPB4	1.189	0.4809	0.982	0.621	0.7004	hypothetical protein
Fes	1.06	1.5122	0.747	0.393	1.4218	hypothetical protein
4930563E19 Rik	0.633	1.3328	0.493	1.522	2.0891	hypothetical protein LOC71227

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Zfy1	1.185	2.0374	1.176	0.428	0.1478	Zinc finger Y-chromosomal protein 1. [Source:Uniprot/SWISSPROT;Acc:P10925]
Q80V88	0.612	0.7447	0.932	0.647	1.7635	hypothetical protein
ENSMUSG00000053347	0.978	1.0688	1.055	0.942	2.4911	hypothetical protein
4930432O21Rik	0.847	0.5998	0.946	0.772	1.3971	hypothetical protein LOC74670
D8Ertd319e	0.482	1.6499	0.673	0.689	1.7525	hypothetical protein
Cntnap2	1.162	2.456	1.323	1.547	2.1828	contactin associated protein-like 2 isoform a
Q8C312	0.791	0.9289	1.902	1.32	0.5995	hypothetical protein
EG209380	1.088	1.0882	1.624	1.016	1.8272	hypothetical protein LOC209380
Q8C7Z7	0.98	1.7207	0.906	1.574	1.3008	hypothetical protein
Q9D5G7	1.275	0.8476	0.859	1.632	2.1154	hypothetical protein
Q8BR98	1.179	0.207	0.694	1.133	1.7395	hypothetical protein
ENSMUSG00000053721	0.946	0.4099	1.59	1.134	1.441	hypothetical protein
Q8C3P1	1.101	0.9341	0.767	0.256	0.533	hypothetical protein
Tusc1	0.971	1.2563	1.109	0.536	2.0168	tumor suppressor candidate 1
Olfr234	0.376	1.237	0.829	1.044	0.5797	olfactory receptor 234
ENSMUSG00000054042	0.396	0.8776	0.754	1.193	1.3746	hypothetical protein
BF301743	1.224	0.9588	0.803	1.201	0.6133	hypothetical protein
ENSMUSG00000054198	0.568	1.327	0.936	0.76	2.3265	hypothetical protein
C330019G07Rik	0.735	1.5053	1.059	0.752	0.7249	hypothetical protein LOC215476
Cadps	1.02	0.3148	0.392	1.242	1.5263	Ca<2+>dependent activator protein for secretion isoform 1
Lycat	0.58	0.8501	0.592	0.853	1.6143	lysocardiolipin acyltransferase
Tmem62	0.98	2.47	1.161	1.065	1.6127	transmembrane protein 62
Dedd2	0.99	1.5091	1.186	0.98	0.6963	DNA-binding death effector domain-containing protein 2 (DED-containing protein FLAME-3). [Source:Uniprot/SWISSPROT;Acc:Q8QZV0]
Zfp82	0.197	0.9561	0.76	1.109	1.7742	zinc finger protein 82. [Source:RefSeq;Acc:NM_177889]

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Mgmt	0.927	1.2727	1.169	0.453	0.4962	Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63) (6-O-methylguanine-DNA methyltransferase) (MGMT) (O-6-methylguanine-DNA- alkyltransferase). [Source:Uniprot/SWISSPROT;Acc:P26187]
Slc8a1	0.675	1.5663	0.817	0.922	1.5743	Sodium/calcium exchanger 1 precursor (Na()/Ca(2)-exchange protein 1). [Source:Uniprot/SWISSPROT;Acc:P70414]
Slc8a1	0.884	1.1793	0.541	0.708	0.6151	Sodium/calcium exchanger 1 precursor (Na()/Ca(2)-exchange protein 1). [Source:Uniprot/SWISSPROT;Acc:P70414]
Irs4	0.889	0.8076	0.877	0.525	1.6659	insulin receptor substrate 4
Slc2a9	0.961	0.9447	0.944	0.505	0.6918	solute carrier family 2, member 9 isoform b
ENSMUSG00000054752	2.157	1.6255	1.35	1.997	2.1959	cystatin and DUF19 domain-containing protein 1. [Source:RefSeq;Acc:NM_176966]
Akr1c20	1.194	0.6776	1.06	0.164	1.6869	aldo-keto reductase family 1, member C20. [Source:RefSeq;Acc:NM_054080]
Akr1c20	1.437	0.6739	1.34	1.993	0.386	aldo-keto reductase family 1, member C20
Prkar2a	1.202	0.9689	1.206	1.541	0.6523	hypothetical protein
ENSMUSG00000054958	0.735	0.5896	0.861	0.266	1.8567	hypothetical protein
Cntn1	1.323	1.7355	1.52	2.024	3.0207	contactin 1

Gene	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Product
Ep300	1.631	1.4552	1.168	0.723	0.5145	P300 transcription coactivator homolog. [Source:Uniprot/SPTREMBL;Acc:Q8BJ14]
Adh1	0.891	0.8022	0.918	0.252	1.6577	alcohol dehydrogenase 1 (class I)
4933427D06Rik	1.811	0.9407	0.797	0.707	0.3195	hypothetical protein LOC232217
Q8C5Y9	0.77	1.2337	0.933	1.055	0.6036	hypothetical protein
ENSMUSG00000055451	0.315	0.6258	1.343	0.774	0.4043	hypothetical protein
ENSMUSG00000055551	0.789	1.1106	1.704	0.869	0.414	PREDICTED: similar to ARF-GAP, RHO-GAP, ankyrin repeat and plekstrin homology domains-containing protein 3; phosphoinositide binding protein; PtdIns(3,4,5)P3-binding protein (LOC381942)
Loxl4	1.063	1.3437	1.194	1.612	2.1915	Lysyl oxidase-like 4. [Source:Uniprot/SPTREMBL;Acc:Q8C5D5]
6030429G01Rik	0.965	0.5516	1.118	1.111	1.759	hypothetical protein LOC436022
Q8C3D3	1.176	0.9977	1.111	1.24	1.2886	PREDICTED: hypothetical gene supported by AK086247 (LOC432939)
Cnot10	0.779	1.2475	0.885	1.138	0.6993	CCR4-NOT transcription complex, subunit 10
Aarsd1	0.759	1.209	1.176	1.363	1.2065	alanyl-tRNA synthetase domain containing 1
Q8CBS8	0.562	2.7681	1.158	2.277	1.314	hypothetical protein
ENSMUSG00000056415	0.423	1.0187	1.183	1.103	1.84	hypothetical protein
ENSMUSG00000056460	1.551	0.8658	0.521	1.023	2.8829	PREDICTED: similar to putative odorant receptor (LOC384749)
ENSMUSG00000056505	0.647	0.4293	0.768	1.089	0.3794	hypothetical protein
BU961992	1.14	1.5378	1.519	0.768	0.7379	hypothetical protein
ENSMUSG00000056531	1.021	1.2109	0.897	1.01	0.6182	
Capg	0.929	1.434	1.21	1.107	1.5248	gelsolin-like capping protein

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A730036I17Rik	0.482	0.868	1.333	0.861	0.5187	hypothetical protein LOC329513
Ttc26	1.276	0.8062	1.812	1.434	0.2889	tetratricopeptide repeat domain 26
Ash1l	0.24	0.5637	0.55	0.738	1.8785	absent, small, or homeotic discs 1
CN839098	0.641	1.6661	0.544	0.821	0.2686	hypothetical protein
ENSMUSG00000056932	0.709	1.1662	0.773	0.994	0.5005	hypothetical protein
Ces3	0.147	0.6935	1.395	1.558	1.8769	carboxylesterase 3
Q9DAI7	1.192	0.9821	0.943	1.219	1.3823	hypothetical protein
ENSMUSG00000057141	1.164	0.3652	1.059	0.78	1.9893	hypothetical protein
Olfr10	1.505	1.6233	1.43	1.024	0.5978	olfactory receptor 10
Hist1h2bj	0.861	0.822	0.814	0.971	1.9461	histone 1, H2bj
ENSMUSG00000057204	0.777	2.2856	1.549	1.063	0.4993	hypothetical protein
ENSMUSG00000057325	0.383	1.2702	1.043	1.818	3.1008	PREDICTED: similar to repetin (LOC435204)
Ryr3	0.496	0.7499	1.613	2.044	0.6806	ryanodine receptor 3; calcium release channel isoform 3. [Source:RefSeq;Acc:NM_177652]
E2f6	0.639	0.5581	0.708	0.768	1.9585	Transcription factor E2F6 (E2F-6) (E2F-binding site modulating activity protein) (EMA). [Source:Uniprot/SWISSPROT;Acc:O54917]
Akap13	0.943	1.5498	1.397	1.287	0.593	A kinase (PRKA) anchor protein 13 isoform 1
ENSMUSG00000057497	1.081	1.0754	0.946	1.076	0.502	hypothetical protein
Spop	0.871	0.9551	0.986	1.021	0.7757	speckle-type POZ protein
Lmcd1	1.27	1.399	0.98	1.014	1.4373	LIM and cysteine-rich domains 1
BC062127	1.15	1.712	0.818	0.314	0.506	hypothetical protein LOC331188
ENSMUSG00000057625	1.119	0.5093	1.112	0.242	2.0443	hypothetical protein
BC057597	0.861	1.2853	1.058	0.93	2.1036	PREDICTED: expressed sequence AL022779 (AL022779)
BY726890,BY707279	1.342	0.289	1.287	0.982	0.4212	PREDICTED: similar to class II bHLH protein ASCL4 (LOC382393)
BG295588	0.874	1.3967	1.206	1.154	1.3897	hypothetical protein

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ENSMUSG00000057776	1.196	0.7179	1.445	0.669	1.4302	hypothetical protein
ENSMUSG00000057805	2.737	1.3831	0.955	1.48	2.0091	hypothetical protein
ENSMUSG00000057869	1.156	0.9372	1.064	1.159	0.8041	hypothetical protein
Ifna9	0.187	0.9134	1.072	0.846	0.3138	interferon alpha family, gene 9
Cacnb2	2.931	1.4677	1.158	0.551	0.4484	calcium channel, voltage-dependent, beta 2 subunit
ENSMUSG00000057970	0.742	0.7068	1.018	1.285	1.8641	hypothetical protein
Ssty1	1.185	0.4804	0.433	0.305	1.4254	spermiogenesis specific transcript on the Y 1
Sez6l	0.64	0.729	0.321	1.182	2.3811	seizure related 6 homolog like
ENSMUSG00000058208	1.119	0.9116	0.48	1.399	0.5808	hypothetical protein
Olfr318	1.595	1.2311	0.796	0.788	1.6382	olfactory receptor 318
ENSMUSG00000058226	2.091	1.0013	1.374	1.358	1.7944	hypothetical protein
Espl1	0.657	2.0467	0.743	1.747	1.4937	extra spindle poles-like 1
Dock1	0.757	0.5752	1.794	0.904	2.054	Dedicator of cytokinesis protein 1 (180 kDa protein downstream of CRK) (DOCK180) (Fragments). [Source:Uniprot/SWISSPROT;Acc:Q8BUR4]
ENSMUSG00000058340	0.935	0.4924	0.571	0.824	1.4173	hypothetical protein
ENSMUSG00000058416	1.218	0.8016	1.012	0.296	3.2322	hypothetical protein
ENSMUSG00000058461	0.797	0.9469	1.382	0.667	0.5255	hypothetical protein
BC027787	0.862	1.41	0.628	0.899	1.5845	hypothetical protein
Capn11	0.984	1.6655	1.187	1.556	1.7498	calpain 11
Zfyve19	0.897	1.2427	1.378	0.844	0.6041	zinc finger, FYVE domain containing 19
Kcnj14	0.422	1.8778	1.588	0.838	2.4826	potassium inwardly-rectifying channel J14. [Source:RefSeq;Acc:NM_145963]

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Art1	0.853	1.7189	0.715	0.647	2.9173	GPI-linked NAD(P)()--arginine ADP-ribosyltransferase 1 precursor (EC 2.4.2.31) (Mono(ADP-ribosyl)transferase) (YAC-1). [Source:Uniprot/SWISSPROT;Acc:Q60935]
Cds2	1.101	1.1702	0.758	0.852	0.7376	phosphatidate cytidylyltransferase 2
Olfr952	1.453	1.7221	1.119	1.463	2.5235	olfactory receptor 952
ENSMUSG00000058877	1.328	0.1976	0.504	0.904	2.4818	PREDICTED: similar to ribosomal protein S2 (LOC219180)
ENSMUSG00000058882	0.649	1.0804	0.518	1.94	3.0688	hypothetical protein
Olfr1037	1.67	0.8057	1.123	1.87	0.6741	olfactory receptor 1040; GA_x6K02T2Q125-47615732-47614791. [Source:RefSeq;Acc:NM_207561]
ENSMUSG00000059014	0.626	2.3038	0.398	0.918	0.5281	hypothetical protein
Crim2	1.2	0.5223	0.582	0.41	1.5817	cysteine rich BMP regulator 2 (chordin like)
ENSMUSG00000059022	0.274	0.8624	0.535	1.617	2.0085	hypothetical protein
ENSMUSG00000059049	1.187	0.8586	1.019	0.434	1.8004	hypothetical protein
ENSMUSG00000059050	0.908	0.7547	1.521	0.445	1.6526	hypothetical protein
ENSMUSG00000059118	1.154	1.6221	0.611	0.337	2.5549	hypothetical protein
ENSMUSG00000059164	0.799	1.2166	1.787	0.916	3.0244	hypothetical protein
AK122363	0.964	1.1764	0.877	0.76	0.4206	PREDICTED: similar to mKIAA0749 protein (LOC328602)
Usp47	1.483	0.9664	0.997	0.858	1.4658	ubiquitin specific protease 47. [Source:RefSeq;Acc:NM_133758]

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Vpreb2	1.248	1.0997	0.989	0.557	0.1476	Immunoglobulin omega chain precursor (VpreB2 protein). [Source:Uniprot/SWISSPROT;Acc:P13373]
BY720157	0.762	0.1666	1.095	0.466	2.321	PREDICTED: similar to RIKEN cDNA 2510010F15 (LOC432649)
ENSMUSG00000059306	1.086	2.62	1.062	1.239	0.4292	hypothetical protein
V1rc23	1.094	0.5475	0.995	0.398	1.5778	vomeronasal 1 receptor, C23
AI586361	0.99	0.8535	1.512	0.118	0.5169	hypothetical protein
Q8CBZ5	1.044	1.5632	0.956	1.071	0.5076	SCAN-KRAB-zinc finger gene 1 (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8CBZ5]
BY720985	0.329	0.4865	1.129	1.582	0.5872	hypothetical protein
ENSMUSG00000059563	0.929	0.8597	1.287	0.809	1.204	hypothetical protein
ENSMUSG00000059611	1.351	0.2348	0.355	1.06	1.871	PREDICTED: similar to UBE2D3 (LOC236864)
TVA3_MOUSE	2.41	0.0552	0.885	0.876	1.4928	T-cell receptor alpha chain V region CTL-F3 precursor. [Source:Uniprot/SWISSPROT;Acc:P06323]
Hist1h2bf	0.997	1.0167	1.17	1.097	1.4231	histone 1, H2bf
Cbx3	0.869	1.5775	1.217	1.018	0.5958	chromobox homolog 3
Dscr1l2	1.243	0.6006	1.049	0.877	1.6597	Down syndrome critical region gene 1-like 2
Olfr781	0.44	0.6953	1.195	0.553	1.5428	olfactory receptor 781
Olfr145	0.729	1.0555	1.363	0.953	0.7866	Olfactory receptor 7C (K21) (Fragment). [Source:Uniprot/SWISSPROT;Acc:Q60882]
Ddefl1	0.979	0.5595	0.889	0.82	0.7789	development and differentiation enhancing factor-like 1
ENSMUSG00000059861	1.327	1.0229	1.313	0.745	0.4489	PREDICTED: similar to glyceraldehyde 3-phosphate dehydrogenase (LOC385339)

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ENSMUSG00000059881	0.815	0.3712	0.892	0.803	2.16	PREDICTED: similar to ribosomal protein L21 (LOC218274)
9030607L17Rik	1.197	1.0972	0.646	1.103	0.5626	hypothetical protein LOC71564
ENSMUSG00000059965	0.8	1.0882	0.356	0.492	0.3925	hypothetical protein
ENSMUSG00000059994	0.752	1.0657	0.65	1.54	1.8538	Fc receptor-like protein 1; BXMAS1-like protein 1. [Source:RefSeq;Acc:NM_178165]
V1rh14	1.569	0.1453	0.368	1.491	0.4679	vomeronasal 1 receptor, H14
Defcr-rs12	0.619	0.3799	0.712	0.391	2.7494	Cryptdin-related protein 4C-1 precursor (CRS4C). [Source:Uniprot/SWISSPROT;Acc:P17534]
ENSMUSG00000060103	1.795	1.0859	1.291	0.502	1.8527	PREDICTED: similar to Translocase of outer mitochondrial membrane 20 homolog (LOC385481)
ENSMUSG00000060163	1.367	0.3259	0.225	0.608	0.5818	PREDICTED: similar to Cox7a2l protein (LOC435890)
Zdhhc8	0.92	0.9792	0.675	1.107	0.6741	PREDICTED: similar to zinc finger, DHHC domain containing 8; zinc finger, DHHC domain like containing 1 (LOC328639)
Refbp2	2.103	0.2274	0.614	1.122	0.6143	RNA and export factor binding protein 2
SCR2_MOUSE	0.549	0.3082	0.36	3.024	2.3285	Transcriptional repressor scratch 2 (Scratch homolog 2 zinc finger protein). [Source:Uniprot/SWISSPROT;Acc:Q8BTH6]
Hist1h2ah	1.798	0.2414	1.142	0.925	0.7742	Histone H2A.g (H2A/g) (H2A.3). [Source:Uniprot/SWISSPROT;Acc:P20671]
Zfp26	0.947	0.8314	0.57	0.878	2.1415	Zinc finger protein 26 (Zfp-26) (mKR3 protein) (Fragment). [Source:Uniprot/SWISSPROT;Acc:P10076]
Q8BQ58	0.462	1.8666	0.585	1.066	0.421	hypothetical protein
Olfr894	1.797	1.0878	1.391	0.966	1.6628	olfactory receptor 894

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Bckdha	0.446	0.4108	0.779	0.858	0.73	branched chain ketoacid dehydrogenase E1, alpha polypeptide
EG330602	1.118	0.2965	1.125	2.15	2.1289	hypothetical protein LOC330602
2410018L13 Rik	1.33	0.6925	1.388	0.979	1.9074	hypothetical protein LOC69732
Q8BX20	0.77	0.6626	0.787	0.803	1.3421	Eukaryotic translation initiation factor 1A. [Source:Uniprot/SPTREMBL;Acc:Q8BX20]
4930522H14 Rik	1.159	1.4691	0.973	0.93	3.1613	hypothetical protein LOC67646
Speer3	1.361	0.9411	0.95	1.371	0.1482	spermatogenesis associated glutamate (E)-rich protein 3
ENSMUSG00000060620	1.003	1.124	0.976	1.235	1.4667	hypothetical protein
Igl-5	0.569	1.3287	0.954	1.58	0.6097	Ig lambda-5 chain C region. [Source:Uniprot/SWISSPROT;Acc:P20764]
ENSMUSG00000060643	1.259	1.2158	0.841	0.899	1.6027	hypothetical protein
Cd302	1.157	0.9648	1.039	0.826	1.3628	CD302 antigen
Gstp1	0.846	1.0429	1.218	1.123	1.6182	glutathione S-transferase, pi 1
Olfr32	0.724	0.663	1.021	0.568	1.8973	Olfactory receptor MOR226-1. [Source:Uniprot/SPTREMBL;Acc:Q8VF96]
Ceacam20	0.903	0.3346	1.027	0.287	0.5758	CEA-related cell adhesion molecule 20
ENSMUSG00000061019	0.2	1.0331	1.433	0.962	2.1194	PREDICTED: similar to short coiled-coil protein; short coiled coil protein (LOC433655)
ENSMUSG00000061069	0.896	0.7256	1.153	0.718	0.4868	hypothetical protein
ENSMUSG00000061069	0.89	0.8825	0.89	0.788	2.2561	hypothetical protein
ENSMUSG00000061087	1.068	0.1537	1.286	0.854	0.6025	hypothetical protein
M20876	0.599	0.4939	1.327	1.722	0.5606	hypothetical protein

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ENSMUSG00000061204	0.974	0.212	1.263	0.981	0.6396	hypothetical protein
ENSMUSG00000061315	0.892	0.8152	0.95	1.257	0.6536	hypothetical protein
Olfr771	0.783	0.8248	0.788	0.871	0.6017	olfactory receptor 771
Ifna12	1.114	1.4845	1.589	1.632	3.4928	interferon alpha family, gene 12
Obscn	0.439	2.4415	0.848	1.349	0.5134	PREDICTED: obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF (Obscn)
Obscn	1.312	1.2557	0.977	1.286	1.7378	hypothetical protein
Orm2	0.504	0.6248	0.902	0.758	1.448	Alpha-1-acid glycoprotein 2 precursor (AGP 2) (Orosomucoid 2) (OMD 2). [Source:Uniprot/SWISSPROT;Acc:P07361]
ENSMUSG00000061647	0.187	0.3116	1.312	0.431	0.3912	hypothetical protein
ENSMUSG00000061734	1.047	0.5601	0.52	1.001	2.6683	hypothetical protein
ENSMUSG00000061861	0.595	1.5816	0.737	2.228	0.5513	hypothetical protein
ENSMUSG00000061869	0.963	0.8375	1.273	0.8	1.4531	hypothetical protein
BC048679	1.3	1.2167	1.032	1.193	2.0338	hypothetical protein LOC210321
Q8C5Y8	0.372	1.5471	1.326	1.498	2.2201	hypothetical protein
ENSMUSG00000061916	0.795	0.5836	0.608	0.737	1.7472	hypothetical protein
ENSMUSG00000061945	1.01	1.3151	1.157	1.288	1.2517	hypothetical protein
BE864673	0.873	0.9189	0.872	0.905	2.1801	hypothetical protein
Olfr815	1.094	0.067	0.897	1.486	1.5914	olfactory receptor 815
LOC209589	0.806	2.2795	0.642	3.145	0.5207	similar to 40S ribosomal protein S7 (S8)
ENSMUSG00000061987	1.04	0.3748	1.022	0.691	1.3538	hypothetical protein
Sort1	0.512	1.1625	0.965	0.375	3.3602	sortilin 1
Chrac1	0.925	1.1042	1.174	0.75	0.663	chromatin accessibility complex 1
ENSMUSG00000062102	0.994	0.3205	0.525	1.104	1.703	hypothetical protein
Olfr1373	1.54	0.5748	1.014	1.041	0.5687	olfactory receptor 1373

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ENSMUSG00000062230	0.742	0.198	0.302	0.694	0.3994	PREDICTED: similar to V2r2 protein (LOC232873)
Psma5	1.117	1.1671	1.143	0.81	0.8136	proteasome (prosome, macropain) subunit, alpha type 5
BY706896	2.576	1.7985	0.863	1.043	1.5176	hypothetical protein
Q8C8R7	1.776	0.9329	0.587	1.377	1.3664	hypothetical protein
Reg3a	0.431	0.136	0.684	2.501	0.5153	regenerating islet-derived 3 alpha
ENSMUSG00000062350	1.268	0.4853	1.508	0.301	0.5489	hypothetical protein
ENSMUSG00000062415	0.765	0.7808	1.103	1.058	2.1873	hypothetical protein
LOC384081	0.886	1.0206	0.806	1.212	0.7269	similar to 60S acidic ribosomal protein P1
Q8CBM3	0.973	1.5818	1.161	0.586	2.4807	Itchy (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8CBM3]
Q9D5J7	0.357	0.6461	1.039	1.405	1.9119	PREDICTED: RIKEN cDNA 4930431F12 gene (4930431F12Rik)
Slp	0.729	2.0717	1.334	2.723	1.4695	sex-limited protein (Slp)
Spaca4	0.266	0.88	0.754	1.543	0.6468	sperm acrosomal membrane protein 14
Atp5g2	0.76	0.9086	1.182	1.191	1.5677	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2
ENSMUSG00000062685	0.588	1.2741	1.141	1.12	1.7461	hypothetical protein
ENSMUSG00000062714	0.225	1.7113	1.005	1.556	0.583	hypothetical protein
Ppox	1.374	1.1901	0.982	1.175	0.5949	protoporphyrinogen oxidase
Olfr619	1.56	1.9447	0.375	2.434	1.8801	olfactory receptor 619
LOC243433	1.378	0.8236	0.608	1.125	0.3351	similar to Ig kappa chain V region EV15 precursor
4833420G17Rik	1.804	1.2236	1.007	0.979	0.4532	hypothetical protein LOC67392
Tas2r110	1.2	1.971	0.485	0.501	0.611	taste receptor, type 2, member 110
ENSMUSG00000062956	1.112	0.7768	1.257	1.598	0.6563	hypothetical protein
ENSMUSG00000063009	0.973	1.201	1.024	1.474	0.6422	hypothetical protein

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ENSMUSG00000063158	1.271	0.6665	1.186	1.089	0.3928	hypothetical protein
Ptpmt1	1.034	1.0975	1.125	1.226	1.2292	PTEN-like phosphatase
ENSMUSG00000063261	1.681	1.1621	0.431	1.105	2.3762	hypothetical protein
LOC383436	0.623	0.8515	0.911	0.953	1.3613	similar to 60S acidic ribosomal protein P1 isoform 1
ENSMUSG00000063346	0.841	1.7185	0.67	0.915	2.0818	PREDICTED: RIKEN cDNA 9630047L19 gene (9630047L19Rik)
Stk24	1.164	1.0605	1.059	1.094	0.7391	serine/threonine protein kinase 24
ENSMUSG00000063418	1.102	0.8928	0.875	0.968	0.6639	hypothetical protein
ENSMUSG00000063433	1.327	1.1467	1.547	3.57	2.3227	hypothetical protein
Hbb-ar	1.077	0.1344	0.759	0.485	1.9441	olfactory receptor 65; GA_x6K02T2PBJ9-6648196-6649143. [Source:RefSeq;Acc:NM_013617]
Mdn1	1.55	1.033	1.368	1.15	2.593	similar to Midasin (MIDAS-containing protein) isoform 1
Mzf6d	1.101	1.4001	1.58	0.893	0.6289	KRAB zinc finger protein 6D (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8CIP9]
ENSMUSG00000063792	0.953	0.9161	0.969	1.734	1.8163	hypothetical protein
Olfr376	0.355	1.8975	0.333	1.379	1.9844	olfactory receptor 376
Adamtsl1	1.462	1.8975	0.497	0.367	2.0473	ADAMTS-like 1 isoform 2
Scgb3a1	0.688	1.7425	1.539	0.841	1.7157	Uteroglobin-related protein 2 precursor (Cytokine HIN-1) (High in normal-1) (Secretoglobin family 3A member 1) (Pneumo secretory protein 2) (PnSP-2). [Source:Uniprot/SWISSPROT;Acc:Q920D7]
ENSMUSG00000064083	1.041	1.1235	0.668	0.537	0.1124	hypothetical protein
Abpa	0.787	0.5242	0.669	0.904	1.9032	androgen binding protein alpha
ENSMUSG00000064209	0.833	0.9215	1.053	1.44	2.238	hypothetical protein

Gene	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Product
ENSMUSG00000064234	0.769	1.2309	0.951	0.959	1.2289	hypothetical protein
2210021J22Rik	0.99	1.1124	0.764	1.168	1.4578	hypothetical protein LOC72355
V1rd21	0.293	0.8949	1.177	2.133	0.4132	vomeronasal 1 receptor, D21 (V1rd21)
BE650314	0.792	0.8202	0.737	1.113	1.6051	hypothetical protein
CN838631	1.639	1.6321	1.585	1.47	0.557	hypothetical protein
Krt74	0.98	1.5539	1.163	1.446	1.9812	type II keratin Kb37
AI315385,AI573699	0.195	0.2273	0.617	0.72	0.4335	hypothetical protein
A430089I19Rik	0.378	0.1383	0.875	0.904	1.6937	hypothetical protein LOC331195
BB233194	0.457	0.8629	1.416	1.022	0.5619	hypothetical protein
Olfr103	0.986	0.7733	1.083	1.127	1.7667	olfactory receptor 103
BB804796	0.732	1.1666	1.439	0.849	1.2818	hypothetical protein
C1r	0.968	0.7032	1.045	1.328	1.7744	complement component 1, r subcomponent
6030408B16Rik	0.36	0.2573	1.465	0.513	1.2108	hypothetical protein LOC77717
Gria1	0.252	0.6705	1.151	0.663	1.8487	glutamate receptor, ionotropic, AMPA1 (alpha 1)
Vill	1.098	1.2967	0.728	1.489	1.331	villin-like
Comp	0.921	0.2107	0.557	1.242	0.5399	cartilage oligomeric matrix protein
AI606402	1.995	1.5406	1.123	1.482	0.1109	hypothetical protein
Dclre1c	1.287	1.0171	0.807	0.917	1.3697	DNA cross-link repair 1A, PSO2 homolog isoform 1
XM_488955	0.993	0.9305	1.107	0.887	1.3145	PREDICTED: hypothetical protein C230060E24 (C230060E24)
BB632145	1.496	0.1712	1.228	1.436	1.9743	hypothetical protein
XM_358611, XM_359418	0.634	1.2511	0.753	0.834	0.606	PREDICTED: RIKEN cDNA 9530048O09 gene (9530048O09Rik)
Rpa2	0.867	1.4451	1.091	0.812	0.446	replication protein A2
Olfr1040	1.556	1.2554	1.031	1.384	2.1866	olfactory receptor 1040
Copg	0.871	0.6629	1.24	1.428	1.6729	coatomer protein complex, subunit gamma isoform 2
Foxl1	0.987	0.8607	0.367	0.451	1.8804	forkhead box L1
Larp1	1.218	0.9511	1.078	0.978	1.4921	la related protein

Gene	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Product
Nrp2	0.24	0.8216	1.106	1.172	1.4338	neuropilin 2 isoform 3 precursor
BB186558	0.907	0.228	0.585	1.613	1.841	hypothetical protein
Kcnk10	0.238	2.2569	0.789	1.002	1.7345	potassium channel, subfamily K, member 10
9830001H06 Rik	0.919	0.8642	1.074	0.848	1.4618	hypothetical protein LOC320706
AY461596	0.651	0.9902	1.267	0.971	0.5262	solute carrier organic anion transporter family, member 6b1 (Slco6b1)
XM_488773, XM_489679	1.991	0.2517	1.534	1.2	0.5886	PREDICTED: RIKEN cDNA A230028O05 gene (A230028O05Rik)
Dlgap4	0.982	1.6282	1.032	0.96	1.3854	discs, large homolog-associated protein 4 isoform a
XM_489027	1.048	1.3774	0.763	1.436	2.1492	PREDICTED: hypothetical gene supported by AK035802 (LOC433658)
NM_183219	1.293	2.8233	1.014	0.72	0.6557	hypothetical protein B230218O03 (B230218O03)
Fbxo3	0.77	0.8968	0.985	0.732	0.5958	F-box only protein 3 isoform 2
Olfr1290	0.202	0.5889	1.643	0.453	0.436	olfactory receptor 1290
XM_488949	1.793	1.5517	1.417	1.049	2.7736	PREDICTED: hypothetical gene supported by AK036400 (LOC433455)
BC060238	1.094	1.0192	0.899	1.059	0.6687	hypothetical protein
Hist1h2bc	0.93	0.9002	1.243	1.119	1.4835	histone 1, H2bc
Col8a2	0.771	0.7895	1.028	0.549	1.7654	procollagen, type VIII, alpha 2
AV280521	1.248	0.1222	1.556	1.686	2.0026	hypothetical protein
NM_177163	1.481	0.8647	0.899	1.365	0.6619	RIKEN cDNA B330016D10 gene (B330016D10Rik)
Tcp10b	0.409	1.9103	1.105	0.313	1.6026	t-complex protein 10b
4931406H21 Rik	0.891	1.7112	0.346	0.715	0.6667	hypothetical protein LOC77592
Pcdhga9	0.331	0.5724	1.042	0.958	1.6619	protocadherin gamma subfamily A, 9
Kctd17	0.963	1.1124	1.145	1.259	1.5348	potassium channel tetramerisation domain containing 17 isoform 1
Olfr1061	0.296	0.7575	0.938	1.836	2.1528	olfactory receptor 1061
BC060736	1.089	0.6513	1.029	2.574	2.2838	hypothetical protein
NM_008038	0.89	0.9208	0.843	0.865	2.4312	formyl peptide receptor, related sequence 1 (Fpr-rs1)
Smad9	0.624	0.4254	0.649	1.607	1.48	MAD homolog 9

Gene	Incubation Medium (protein-incubation)	Incubation Medium (infection)	*M.tb*	60.2	dnaK	Product
BE648109	0.809	1.0657	1.134	0.308	0.0613	hypothetical protein
Tlr9	0.968	0.7025	1.2	0.713	1.5235	toll-like receptor 9
2600009E05 Rik	1.004	1.1602	0.849	1	0.7736	hypothetical protein LOC77006
AF515450	0.209	0.4656	0.838	1.42	1.8418	hypothetical protein
Adamts10	1.196	2.5082	0.987	0.558	1.8533	a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 10
Es2el	1.022	1.1039	0.959	1.186	1.3165	DiGeorge syndrome critical region protein 14 isoform 1
Nudcd2	0.549	1.2893	1.174	0.828	1.3564	NudC domain containing 2
BG101268	1.193	0.5999	1.382	0.727	1.5526	hypothetical protein
Meis1	0.434	2.6939	1.106	0.879	1.9765	myeloid ecotropic viral integration site 1
Olfr1471	1.679	2.0891	0.94	0.901	2.11	olfactory receptor 1471
2010309E21 Rik	1.213	0.943	1.245	0.925	1.5206	hypothetical protein LOC66488
XM_488629	0.427	0.9421	0.671	0.76	0.602	PREDICTED: hypothetical gene supported by AK031661 (LOC432641)
BC069935	0.525	1.3952	0.965	0.948	1.4717	similar to proline rich protein MP4 (MGC78233)
Ckt2	1.94	1.3468	1.001	1.345	1.8464	CKT2 protein
A830080D01 Rik	1.097	0.7629	0.956	1.15	0.6288	hypothetical protein LOC382252
BI456154	0.669	2.1737	0.808	1.769	2.4115	hypothetical protein
BY716593	1.205	1.3983	1.102	0.297	1.7426	hypothetical protein
1700110N18 Rik	0.588	1.0458	1.45	1.46	1.5915	hypothetical protein LOC73569
U72672	0.906	0.333	0.528	0.864	2.1987	angiogenin, ribonuclease A family, member 3 (Ang3)
AK173328	0.856	1.1789	0.605	0.616	2.2679	hypothetical protein
XM_110264, XM_128555	0.6	0.9025	0.928	1.158	1.6002	PREDICTED: similar to hypothetical protein FLJ31364; homolog of yeast EME1 endonuclease; essential meiotic endonuclease 1 homolog 2 (S. pombe); essential meiotic endonuclease 1 homolog (S. pombe)
NM_001004 163	0.635	1.1691	0.965	0.927	0.4426	gene model 1553, (NCBI) (Gm1553)

Genes in this table were differentially regulated in the CD43KO macrophages compared to CD43WT macrophages while incubated with dnaK. Normalized expression cutoff values were 1.2 (upregulated) and 0.833 (downregulated). Genes were also filtered on confidence between the biological replicates ($p<0.05$).

Supplementary Table 5. Genes that are statistically significant, differentially expressed and shared between multiple treatments.

Differential Expression	Normalized Expression						
CD43KO>CD43 WT	Incubation Medium (protein-incubation)	Incubation Medium (Infection)	*M.tb*	60.2	dnaK	Gene	Product (if known)
***M.tb* and dnaK**	0.721	0.255	1.525	1.371	2.874	(unnamed, Expressed Sequence Tag)	
	1.265	0.552	1.47	1.673	2.771	(unnamed, Expressed Sequence Tag)	
	0.455	0.738	1.356	1.152	2.276	Nek10	PREDICTED: similar to hypothetical protein FLJ32685 (LOC238944)
	0.2	1.033	1.433	0.962	2.119	ENSMUSG00000061019	PREDICTED: similar to short coiled-coil protein; short coiled coil protein (LOC433655)
	1.525	1.935	1.76	1.684	2.074	(unnamed, Expressed Sequence Tag)	
	1.593	0.789	1.346	1.016	1.939	Col9a2	procollagen, type IX, alpha 2 (Col9a2)
	0.958	0.1	2.451	1.303	1.936	Clca5	expressed sequence AI586120 (AI586120)
	0.265	0.797	1.654	0.576	1.913	Olfr770	olfactory receptor 770 (Olfr770)
	1.834	1.922	1.785	2.059	1.851	(unnamed, Expressed Sequence Tag)	
	0.798	0.712	1.542	0.765	1.846	(unnamed, Expressed Sequence Tag)	
	1.088	1.088	1.624	1.016	1.827	EG209380	similar to very large inducible GTPase 1 (LOC209380)
	1.191	0.548	1.339	1.059	1.746	Rgs17	regulator of G-protein signaling 17 (Rgs17)
	1.185	1.524	1.556	0.917	1.719	(unnamed, Expressed Sequence Tag)	
	1.308	1.004	1.564	0.843	1.696	(unnamed, Expressed Sequence Tag)	
	1.202	0.119	1.278	1.431	1.689	(unnamed, Expressed Sequence Tag)	
	0.525	0.867	2.229	0.337	1.672	(unnamed, Expressed Sequence Tag)	
	1.797	1.088	1.391	0.966	1.663	Olfr894	olfactory receptor 894 (Olfr894)
	1.929	0.452	1.51	0.802	1.584	(unnamed, Expressed Sequence Tag)	
	1.822	1.177	1.943	1.433	1.567	(unnamed, Expressed Sequence Tag)	

CD43KO>CD43 WT	Incubation Medium (protein-incubation)	Incubation Medium (Infection)	*M.tb*	60.2	dnaK	Gene	Product (if known)
***M.tb* and dnaK**	0.929	1.434	1.21	1.107	1.525	Capg	capping protein (actin filament), gelsolin-like (Capg)
	0.761	1.231	1.277	0.888	1.48	(unnamed, Expressed Sequence Tag)	
	0.88	1.203	1.528	1.53	1.468	Plxna2	plexin A2 (Plxna2)
	0.75	0.772	1.343	0.755	1.459	Crebzf	HCF-binding transcription factor Zhangfei (Zf)
	0.762	1.533	1.411	0.533	1.421	Ccdc25	RIKEN cDNA 2610528H13 gene (2610528H13Rik)
	0.765	0.818	1.545	0.771	1.368	Mark2	MAP/microtubule affinity-regulating kinase 2 (Mark2)
	1.044	2.181	1.345	0.961	1.342	Irf2bp2	PREDICTED: interferon regulatory factor 2 binding protein 2 (Irf2bp2)
	1.723	0.154	1.639	1.573	1.303	(unnamed, Expressed Sequence Tag)	

	Normalized Expression						
CD43KO>CD43 WT	Incubation Medium (protein-incubation)	Incubation Medium (Infection)	*M.tb*	60.2	dnaK	Gene	Product (if known)
***M.tb* and cpn60.2**	1.478	9.014	6.843	2.235	2.442	Gdpd3	RIKEN cDNA 1110015E22 gene (1110015E22Rik)
	0.873	1.651	1.811	2.068	1.06	Usp37	ubiquitin specific protease 37 (Usp37)
	0.956	1.102	1.88	2.051	1.213	(unnamed, Expressed Sequence Tag)	
	0.839	0.611	1.387	2.03	1.304	ENSMUSG00000045437	PREDICTED: similar to BC005685 protein (LOC212970)
	0.605	0.645	1.778	2.029	1.472	(unnamed, Expressed Sequence Tag)	
	0.391	0.493	1.302	1.849	0.55	XM_354612	PREDICTED: similar to FLJ45455 protein (LOC380702)

CD43KO>CD43 WT	Incubation Medium (protein-incubation)	Incubation Medium (Infection)	*M.tb*	60.2	dnaK	Gene	Product (if known)
***M.tb* and cpn60.2**	1.79	1.197	1.502	1.834	1.115	Fgfr1	Basic fibroblast growth factor receptor 1 precursor (EC 2.7.1.112) (FGFR-1) (bFGF-R) (MFR). [Source:Uniprot/SWISSPROT;Acc:P16092]
	1.274	0.427	1.314	1.802	1.248	LOC625662	PREDICTED: similar to hypothetical protein (LOC218476)
	1.37	0.531	1.346	1.794	1.312	(unnamed, Expressed Sequence Tag)	
	1.928	2.484	1.563	1.793	1	1700006A11Rik	hypothetical protein LOC71824
	0.617	0.965	1.763	1.756	0.917	Tmem139	transmembrane protein 139; synonym: A930027H06Rik; Mus musculus transmembrane protein 139 (Tmem139), mRNA.
	0.687	1.032	1.454	1.722	0.778	Olfr609	olfactory receptor 609; olfactory receptor MOR9-1; GA_x6K02T2PBJ9-6207735-6206776. [Source:RefSeq;Acc:NM_147082]
	0.291	1.22	1.418	1.701	0.438	V1rb1	vomeronasal 1 receptor, B1
	0.672	1.21	1.842	1.678	0.361	Gabrr1	gamma-aminobutyric acid (GABA-C) receptor, subunit rho 1
	0.289	0.332	1.279	1.676	0.83	ENSMUSG00000039335	Nyd-sp12 protein; spermatogenesis-related protein. [Source:RefSeq;Acc:NM_029150]
	0.646	0.921	1.462	1.631	1.233	Olfr818	olfactory receptor 818
	0.681	1.109	1.442	1.619	1.017	Q8CER6	hypothetical protein
	0.622	1.009	1.836	1.603	1.55	Arid5a	modulator recognition factor I
	0.89	0.889	1.722	1.59	0.964	Comtd1	catechol-O-methyltransferase domain containing 1
	0.789	1.407	1.888	1.496	0.893	Card11	caspase recruitment domain family, member 11
	1.153	2.107	1.534	1.462	1.379	Mir16	membrane interacting protein of RGS16

CD43KO>CD43 WT	Incubation Medium (protein-incubation)	Incubation Medium (Infection)	*M.tb*	60.2	dnaK	Gene	Product (if known)
***M.tb* and cpn60.2**	0.992	0.725	1.71	1.455	1.931	Cdrt4	CMT1A duplicated region transcript 4
	1.09	1.035	1.227	1.432	0.87	Ech1	enoyl coenzyme A hydratase 1, peroxisomal
	0.928	1.306	1.46	1.4	1.127	Htr2b	5-hydroxytryptamine (serotonin) receptor 2B
	0.89	0.771	2.077	1.384	1.435	(unnamed, Expressed Sequence Tag)	
	1.024	1.179	1.346	1.37	0.983	Rnaseh2c	AYP1 protein
	1.075	1.299	1.45	1.337	1.078	Q8BTE2	hypothetical protein
	0.553	1.611	1.44	1.32	1.041	(unnamed, Expressed Sequence Tag)	
	0.921	1.044	1.286	1.31	1.142	ENSMUSG00000062419	PREDICTED: RIKEN cDNA 2310047M15 gene (2310047M15Rik)
	0.989	0.463	2.288	1.297	1.293	Krtap6-1	keratin associated protein 6-1
	0.753	0.429	1.387	1.292	0.805	ENSMUSG00000038011	PREDICTED: dynein, axonemal, heavy chain 10 (Dnahc10)
	1.185	0.93	1.539	1.266	0.892	Zcchc17	putative S1 RNA binding domain protein
	1.003	1.175	1.709	1.266	0.745	Guk1	guanylate kinase 1
	0.84	1.344	1.374	1.251	0.636	Syngr1	synaptogyrin 1 (Syngr1), transcript variant 1b
	1.334	0.793	1.416	1.214	0.817	Q8C1Q6	hypothetical protein

	Normalized Expression						
CD43KO>CD43 WT	**Incubation Medium (protein-incubation)**	**Incubation Medium (Infection)**	***M.tb***	**60.2**	**dnaK**	**Gene**	**Product (if known)**
cpn60.2 and dnaK	0.395	1.074	1.158	1.617	2.923	Clec2e	C lectin-related protein A (Clra)
	1.225	1.516	0.57	1.297	2.763	Cntnap4	contactin associated protein 4 (Cntnap4)
	0.496	0.822	1.134	1.916	2.674	SALF_MOUSE	Stonin 1 (Stoned B-like factor). [Source:Uniprot/SWISSPROT;Acc:Q8CDJ8]
	0.425	0.202	0.87	2.796	2.551	Brunol4	bruno-like 4, RNA binding protein. [Source:RefSeq;Acc:NM_133195]

CD43KO>CD43 WT	Incubation Medium (protein-incubation)	Incubation Medium (Infection)	*M.tb*	60.2	dnaK	Gene	Product (if known)
cpn60.2 and dnaK	0.792	1.881	1.221	1.423	2.548	Wnt16	wingless-related MMTV integration site 16 (Wnt16)
	1.018	0.749	1.009	1.785	2.424	Asgr2	asialoglycoprotein receptor 2 (Asgr2)
	1.292	2.373	0.636	1.347	2.33	Ccdc57	PREDICTED: RIKEN cDNA 4933434G05 gene (4933434G05Rik)
	0.549	0.308	0.36	3.024	2.329	SCR2_MOUSE	Transcriptional repressor scratch 2 (Scratch homolog 2 zinc finger protein). [Source:Uniprot/SWISSPROT;Acc:Q8BTH6]
	1.707	0.763	0.608	2.12	2.256	4931407K02Rik	RIKEN cDNA 4931407K02 gene (4931407K02Rik)
	2.157	1.625	1.35	1.997	2.196	ENSMUSG00000054752	cystatin and DUF19 domain-containing protein 1. [Source:RefSeq;Acc:NM_176966]
	1.011	1.24	1.554	2.24	1.987	Gria2	glutamate receptor, ionotropic, AMPA2 (alpha 2) (Gria2)
	1.496	0.171	1.228	1.436	1.974	BB632145	hypothetical protein
	2.054	0.916	1.05	1.746	1.955	(unnamed, Expressed Sequence Tag)	
	1.691	1.047	0.288	1.502	1.931	Myo5c	Myosin VC (Fragment). [Source:Uniprot/SPTREMBL;Acc:Q8BWY8]
	0.383	0.346	0.485	1.459	1.86	F2rl2	coagulation factor II (thrombin) receptor-like 2 (F2rl2)
	1.343	1.279	0.452	1.711	1.831	Q9D5I1	PREDICTED: RIKEN cDNA 4930435H24 gene (4930435H24Rik)
	1.021	1.164	0.731	1.715	1.829	Smug1	single-strand selective monofunctional uracil DNA glycosylase (Smug1)
	1.02	1.103	0.898	1.452	1.822	Insl6	insulin-like 6 (Insl6)
	0.953	0.916	0.969	1.734	1.816	ENSMUSG00000063792	hypothetical protein
	0.563	0.895	1.256	1.408	1.75	Rragd	Ras-related GTP binding D (Rragd)
	0.82	1.265	1.234	1.336	1.732	(unnamed, Expressed Sequence Tag)	
	0.829	1.814	0.871	1.897	1.693	Pelp1	RIKEN cDNA 4930563C04 gene (4930563C04Rik)

CD43KO>CD43 WT	Incubation Medium (protein-incubation)	Incubation Medium (Infection)	*M.tb*	60.2	dnaK	Gene	Product (if known)
cpn60.2 and dnaK	0.871	0.663	1.24	1.428	1.673	Copg	coatomer protein complex, subunit gamma (Copg)
	1.23	1.091	1.539	1.27	1.462	Antxr1	anthrax toxin receptor 1 (Antxr1)
	0.898	0.772	1.225	1.379	1.432	ENSMUSG00000045065	RIKEN cDNA 9930022D16 gene (9930022D16Rik)
	1.428	1.337	0.838	1.513	1.431	(unnamed, Expressed Sequence Tag)	
	1.098	1.297	0.728	1.489	1.331	Vill	villin-like (Vill)
	1.01	1.315	1.157	1.288	1.252	ENSMUSG00000061945	hypothetical protein
	0.917	1.203	1.032	1.297	1.21	Ssr4	signal sequence receptor, delta (Ssr4)

	Normalized Expression						
CD43KO>CD43 WT	**Incubation Medium (protein-incubation)**	**Incubation Medium (Infection)**	***M.tb***	**60.2**	**dnaK**	**Gene**	**Product (if known)**
Shared upregulated all	0.792	1.881	1.221	1.423	2.548	Wnt16	wingless-related MMTV integration site 16 (Wnt16)
	2.157	1.625	1.35	1.997	2.196	ENSMUSG00000054752	cystatin and DUF19 domain-containing protein 1. [Source:RefSeq;Acc:NM_176966]
	1.011	1.24	1.554	2.24	1.987	Gria2	glutamate receptor, ionotropic, AMPA2 (alpha 2) (Gria2)
	1.496	0.171	1.228	1.436	1.974	BB632145	hypothetical protein
	0.563	0.895	1.256	1.408	1.75	Rragd	Ras-related GTP binding D (Rragd)
	0.82	1.265	1.234	1.336	1.732	(unnamed, Expressed Sequence Tag)	
	0.871	0.663	1.24	1.428	1.673	Copg	coatomer protein complex, subunit gamma (Copg)
	1.23	1.091	1.539	1.27	1.462	Antxr1	anthrax toxin receptor 1 (Antxr1)
	0.898	0.772	1.225	1.379	1.432	ENSMUSG00000045065	RIKEN cDNA 9930022D16 gene (9930022D16Rik)

CD43KO<CD43 WT	Normalized Expression						
Shared between *M.tb* and 60.2	Incubation Medium (protein-incubation)	Incubation Medium (Infection)	*M.tb*	60.2	dnaK	Common	Product
	1.046	0.705	0.572	0.782	0.634	Notch1	Notch gene homolog 1
	0.808	1.156	0.599	0.749	0.981	Lrrc10	leucine rich repeat containing 10
	1.092	1.039	0.831	0.705	0.864	Sephs2	selenophosphate synthetase 2
	0.743	0.713	0.485	0.638	1.239	Tle3	transducin-like enhancer protein 3 isoform 2
	0.973	0.955	0.657	0.634	1.042	Mapkapk2	MAP kinase-activated protein kinase 2
	1.506	0.652	0.54	0.623	0.879	Epor	erythropoietin receptor
	0.937	0.869	0.611	0.613	0.916	Itgam	integrin alpha M isoform 2 precursor
	0.927	1.317	0.687	0.588	1.071	Ampd3	AMP deaminase 3 (EC 3.5.4.6) (AMP deaminase isoform E) (AMP deaminase H-type) (Heart-type AMPD). [Source:Uniprot/SWISSPROT;Acc:O08739]
	1.409	0.552	0.619	0.518	0.778	Flrt3	fibronectin leucine rich transmembrane protein 3

CD43KO<CD43 WT	Normalized Expression						
Shared between *M.tb* and dnaK	Incubation Medium (protein-incubation)	Incubation Medium (Infection)	*M.tb*	60.2	dnaK	Common	Product
	1.134	0.995	0.802	0.985	0.764	Peci	peroxisomal delta3, delta2-enoyl-Coenzyme A isomerase
	0.751	0.756	0.583	1.017	0.714	Ager	advanced glycosylation end product-specific receptor
	1.167	1.385	0.782	0.882	0.706	Psd4	pleckstrin and Sec7 domain containing 4
	0.951	0.88	0.721	0.97	0.675	Sdc4	syndecan 4
	0.843	0.965	0.807	0.943	0.64	Phospho2	phosphatase, orphan 2
CD43KO<CD43 WT	Incubation Medium (protein-incubation)	Incubation Medium (Infection)	*M.tb*	60.2	dnaK	Common	Product

Shared between *M.tb* and dnaK	0.99	0.825	0.666	1.01	0.611	(unnamed, Expressed Sequence Tag)	
	0.836	1.142	0.654	1.026	0.568	(unnamed, Expressed Sequence Tag)	
	2.259	1.347	0.659	1.705	0.558	ENSMUSG00000001158	putative nucleic acid binding protein RY-1; EST AI449063. [Source:RefSeq;Acc:NM_025665]
	0.921	0.211	0.557	1.242	0.54	Comp	cartilage oligomeric matrix protein
	0.667	0.807	0.466	1.064	0.525	(unnamed, Expressed Sequence Tag)	
	0.641	1.666	0.544	0.821	0.269	ENSMUSG00000056867	hypothetical protein

	Normalized Expression						
CD43KO<CD43 WT	**Incubation Medium (protein-incubation)**	**Incubation Medium (Infection)**	***M.tb***	**60.2**	**dnaK**	**Common**	**Product**
Shared between cpn 60.2 and dnaK	1.177	1.264	0.848	0.536	0.643	Pdcd6ip	programmed cell death 6 interacting protein

Genes were statistically significant as determined by the Confidence filter (between biological replicates, p-value >0.05) and shared in differential expression trend (upregulated greater than or equal to 1.2, or downregulated less than or equal to 0.833) between two or more treatment-types.

Supplementary table 6. Primer sequences for genes selected for quantitative RT-PCR and their sources

Gene	Function	Forward Primer	Reverse Primer	Source
Found in Micorarray				
TNF-related (extrinsic) apoptosis				
Zfp36	TNF-α expression regulator	cctctgcaactctggtctcc	ttctcaggagaggcttcgac	In-house
Tnfrsf1b	TNF-receptor 1 beta. Involved in TNF-related apoptotic signalling	taccaagggtggcatctctc	agggcttctttttcctctgc	In-house
Intrinsic Apoptosis				
Meox2		aaatgcaggcatctcgagtc	cgttcgctttctccaatttc	In-house
Casp9	Activating caspase for intrinsic apoptotic signalling	tgcacttcctctcaaggcaggacc	tccaaggtctccatgtaccaggagc	In-house

Gene	Function	Forward Primer	Reverse Primer	Source
Not found in Microarray				
Extrinsic Apoptosis				
Tradd	Tnfrsf1a associated death domain. Binds caspase 8, FADD and other TNF receptors	ggagtctgcggtagacaagg	tcagagctgtccccactctc	In-house
Casp7	Extrinsic-apoptosis activating caspase	acttcgagtcccagtctgatg	ttctcagctgaagggtggtc	In-house
Casp3	Final apoptosis activating caspase	tgtcactcgctctggtacg	aaatgacccctcatcacca	Chen, M. et al. Minocyclin inhibits caspase-1 and caspase-3 expression and delays mortality in a transgenic mouse model of Huntington Disease. *Nature Medicine.* 6:7. 2000.

Gene	Function	Forward Primer	Reverse Primer	Source
TNF	Cytokine involved in systemic inflammation and apoptotic cell death	tctcatgcaccaccatcaag	ccactctccctttgcagaac	In-house

Gene	Function	Forward Primer	Reverse Primer	Source
Intrinsic Apoptosis				
Bax	Pro-apoptotic protein from the Bcl-2 family of proteins.	aaactggtgctcaaggccct	agcagccgctcacggag	In-house
Apaf1	Protein that interacts directly with caspase 9 and Bcl2, forming the apoptosome.	cagcaaacgagaggaaaagc	accatctgcagaccaggaac	In-house

Gene	Function	Forward Primer	Reverse Primer	Source
Reference Genes				
Beta Actin		ttgctgacaggatgcagaag	acatctgctggaaggt	In-house
18S rRNA		aaacggctaccacatccaag	caattacagggcctcgaaag	In-house
GapdH		tgcgacttcaacagcaactc	atgtaggccatgaggtccac	In-house

Genes selected were either found to be statistically significant and differentially regulated in the microarray or related to pathways of interest within the microarray. Primer sequences that were developed in house were generated using primer3 software.

Supplementary Table 7. Functionally characterized genes that are differentially expressed and shared in multiple treatments

Genes/Pathway	Functions and Interactions	present in microarray
TNF-Related (extrinsic) apoptosis		
Tnfaip3	*Gene co-transcribed with TNF-α. Levels of Tnfaip3 mRNA closely correspond to those of TNF-α*	yes
Zfp36	*TNF-α translation regulator*	yes
Adam17	*TNF-α cleaving enzyme*	yes
Dedd	*Death-domain containing protein, involved in the transfer of apoptosis signal from the TNF-α receptor*	yes
Tnfrsf1b	*TNF-receptor β. Involved in TNF-related apoptotic signalling.*	yes
Trib1	*Negative regulator of NF and IL-6 dependant signalling*	yes
Tradd	*Tnfrsf1a-associated death domain. Binds caspase 8, FADD, TNF-receptors*	no
Casp7	*Activating caspase. Involved in both intrinsic and extrinsic signalling. Cleaved by caspases 3,10 and 9.*	yes
Fadd	*Fas-associated Death Domain. Interacts with Tradd and DISC (death-inducing signalling complex)*	no
Caspase 3	*Final apoptosis activating caspase (for both extrinisc and intrinsic pathways)*	no
Intrinsic Apoptosis		
Meox2	*Shown to interact in Bax-mediated apoptosis*	yes
Casp9	*Activating caspase for intrinsic apoptotic signalling*	yes
Bax	*Protein from the Bcl-2 family, pro-apoptotic protein*	no
Bcl2	*Protein that governs mitochondrial membrane permeabilization, anti-apoptotic*	no
Bcl2l10	*Bcl2-like 10. Interacts with Bak12 and apaf1 during intrinsic apoptosis*	no
Apaf1	*Relates to Caspase 9 activation, interacts directly with caspase 9 and Bcl2*	no
Cytoskeletal Remodelling		
Gsn	*Gelsolin, Actin-remodelling protein. Regulated by Caspase 3 activity.*	yes
Itgam	*Alpha M-Integrin. Complement component 3 receptor 3 subunit.*	yes
FAK	*Focal adhesion kinase, becomes phosphorylated (and activated) during integrin-mediated signalling*	no
Grb2	*Adapter protein binds FAK and may activate MAPK pathway*	no
Talin	*Intermediatry integrin-binding protein that mediates ITGAM to Actin and facilitates cytoskeletal remodelling*	no
Paxillan	*Intermediatry integrin-binding protein that mediates ITGAM to Actin and facilitates cytoskeletal remodelling*	no
Vinculin	*Intermediatry integrin-binding protein that mediates ITGAM to Actin and facilitates cytoskeletal remodelling*	no