THESIS

LOCAL ADAPTATION TO HIGH ALTITUDES FUNCTIONALLY MODIFIES THE INNATE IMMUNE RESPONSE IN DEER MICE

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ABSTRACT

LOCAL ADAPTATION TO HIGH ALTITUDES FUNCTIONALLY MODIFIES THE INNATE IMMUNE RESPONSE IN DEER MICE

Organisms across the tree of life have repeatedly colonized high altitudes, where they are met by environmental challenges including hypoxia, low temperatures, and increased UV exposure. Over evolutionary timescales, many of these populations of high-altitude residents have adapted to these conditions particularly through changes in metabolically demanding physiological systems ranging from the cardiopulmonary and muscular physiology to reproductive function. Although the immune system is also metabolically demanding to maintain and activate, the immune response is an understudied aspect of animal adaptations to high elevations.

In this study, we investigated whether highland-adapted deer mice (*Peromyscus maniculatus*), a model mammal for high elevation adaptation, display immune-specific adaptations. To study local adaptation in immunity, we employed a conventional immune challenge experiment wherein we injected lowland and highland-derived mice in a common garden environment with a standard dose of the bacterial cell wall component, lipopolysaccharide (LPS), to elicit robust activation of host defense. We collected and analyzed both acute phase responses, including circulating blood glucose, serum corticosterone, and the spleen transcriptomic response to LPS, as well as longer-term responses, such as metabolic recovery and fever, for insight into population-specific strategies.

Upon injection of LPS, the metabolic axis of the acute phase response was fundamentally similar between populations. However, highland mice displayed a wider spectrum of body temperatures post-LPS, with an overall more muted fever relative to lowlanders. Behaviorally, we found that lowlanders display a greater degree of sick markers than highlanders do. Using RNAseq, we showed that nearly half of the spleen transcriptome (6202) was LPS-responsive and that many (1052) genes are differentially responsive in a population-specific manner. Importantly, we found nearly 400 genes with additive effects (i.e., population + injection), demonstrating that the transcription response to LPS differs by ancestral origin in a core set of genes. The results of this study unveil key differences in immune regulation strategies affected by the process of high-altitude adaptation.

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1. INTRODUCTION

Novel selective pressures in a given environment can lead to the preservation or improvement of organismal fitness (i.e., survival and reproduction), a process known as local adaptation (Meek et al., 2023). Often, this involves changes in organismal traits or their responses to environmental factors (Wadgymar et al., 2022). However, novel or changing environments rarely present organisms with a single selective pressure that can be addressed by modifying a single trait (Kawecki & Ebert, 2004). Instead, the complexity of dynamic ecosystems and their communities along with the integrated nature of organismal physiology often means that local adaptation involves changes to a combination of morphological, physiological, and behavioral traits (Geber & Griffen, 2003).

High altitude environments (>2500 m) provide a useful setting for studying how environmental challenges interact to modify whole-organism physiology as part of local adaptation (Storz, 2021; Scheinfeldt & Tishkoff, 2010). Although low oxygen (hypoxia) is the major environmental variable that characterizes high altitudes, it is often the interaction between hypoxia and other demands that determines how organisms locally adapt in high elevation environments. For example, for small mammals, environmental hypoxia negatively impacts their capacity to generate heat (thermogenesis), which is more important at high elevations because of their relatively cold temperatures (Murray, 2016; Storz & Cheviron, 2021). Furthermore, high elevation adaptation has been shown to modify a wide range of metabolically intensive physiological systems, including the respiratory, cardiovascular, muscular, and reproductive systems (Storz et al., 2019; Richalet et al, 2024; Wearing et al., 2022; Moore, 2003; Rockwell et al., 2003; Wilsterman et al., 2023; Robertson & Wilsterman, 2020).

One physiological system that has remained largely unexplored in the context of organismal adaptation to high elevations is the immune system. Nonetheless, similarly to the other systems that have received more attention, the immune response is metabolically demanding (Lochmiller & Deerenberg, 2000). Additionally, we know that high elevation environments differ from low elevation environments in pathogen prevalence, diversity, and virulence (Halliday et al., 2021; Ferrell et al., 2017). Specifically, the harsher abiotic environment (i.e., hypoxia and lower temperatures) of high elevations is considered less conducive to the proliferation and spread of etiological agents, including ectoparasites, bacteria, and fungi (Jouda et al., 2004; Aeschlimman et al., 1986; Rizzoli et al., 2002; Siles & Margesin, 2016; Zhang et al., 2024). With this, we might hypothesize that immune systems and responses are likely to be potential targets of selection in the process of local adaptation.

In support of this hypothesis, Jaramillo-Valverde et al. (2024) recently demonstrated that humans living at high altitudes in the Andes display differential expression of immune-related genes compared to lowland-resident humans, confirming that high elevation environments lead to near-term changes in immune surveillance. Furthermore, in small rodents, botfly (*Cuterebrida*e) infections have more severe effects on aerobic capacity at high elevations relative to low altitude residents with similar infections (Wilde et al., 2019). These observations suggest at least that populations living in high versus low elevation environments have different metabolic responses to a similar pathogenic pressure. However, to our knowledge, there are no experimental tests of the extent to which local adaptation of the organism to high elevation environments has altered immune function to-date.

This gap in knowledge is particularly important to address in the near term because we know that, with climate change, key vectors of disease, including ticks and mosquitos, are

expanding into higher elevation environments (Lemoine et al., 2022; Lozano-Fuentes et al., 2012; Eisen et al., 2008). These changes in vector distribution set up the potential for novel interactions between pathogens of concern and hosts with differing immune systems in high elevation environments. Such interactions have already been observed and shown to be important for conservation as well as disease ecology: recent changes in temperature and moisture have allowed mosquitos to expand into higher altitudes in the Hawaiian Islands, leading to novel exposure of high-elevation birds to Hawaiian Avian Malaria (HAM). This novel exposure drove significant decreases in range for some Hawaiian bird species and declines for others (Liao et al., 2017). Therefore, understanding patterns of immune function and infection resiliency associated with local adaptation to high elevations is increasingly important for understanding the effects of climate change on biodiversity with potential ramifications for conservation and community ecology (Semenza et al., 2022; Assis et al., 2024).

The North American deer mouse (*Peromyscus maniculatus*) is a tractable and valuable model for investigating local adaptation in immune function across elevational gradients because it is both an important host species for several zoonotic diseases and an established model species for studying high elevation adaptation. First, deer mice serve as natural reservoirs for many important infectious pathogens that are expanding with climate change, including *Hantavirus*, *Babesia, Yersinia pestis*, and *Borrelia burgdorferi* (Luis et al., 2010; Danforth et al., 2018; Barbour, 2017; Caminade et al., 2019). Second, deer mice inhabit the widest elevational range of any mammal in North America, extending from below sea level in Death Valley to above 4300 meters (Snyder et al., 1982; Bedford & Hoekstra, 2015). Deer mice possess well-characterized genetic and physiological adaptations to these high elevation residences (Storz et al., 2019; Wearing et al., 2022; Schweizer et al., 2019). Finally, there is already some evidence

that adaptation to high elevation environments has resulted in changes to key parts of the immune system in this species: high elevation deer mice possess alternative alleles for both *Ifn-γ* and multiple interleukins (Schweizer et al., 2019; Schweizer et al., 2021), which are genes that play critical roles in the acute immune response to bacterial infection (Gutsmann et al., 2001; Lee & Sulivan, 2001).

In this study, we use deer mice as a model system to investigate whether local adaptation to high elevations has modified physiological responses to and the capacity to cope with an immune challenge in using a common garden experiment. To this end, we challenged lab-bred deer mice descended from high or low elevation populations with a non-infectious immune agent to elicit a standardized acute immune response. We then assayed phenotypic traits to determine whether these two populations exhibit alternative immune response strategies. This experimental approach aims to provide novel insight into how high elevation environments might shape the evolution of the immune system. Furthermore, we hope to gain insight into how those selection gradients may contribute to the integrative physiology that ultimately determines individual fitness and population persistence.

2. MATERIALS AND METHODS

All animal work was carried out under IACUC approved protocols (protocol 4262) at Colorado State University.

2.1 Study population and animal care

All experimental animals were adult males (3-7 months old at the start of experiments) derived from two wild populations of deer mice (*Peromyscus maniculatus)*. The lowland population was trapped in and around Kearney, Nebraska (elevation: 655.9 m; 40.7864 °N, -99.0836 °W). The highland population was trapped on Mt. Blue Sky (formerly Mt. Evans) in Clear Creek County, Colorado (elevation: 4,348 m; 39.5883°N, -105.6438°W). Mice trapped from each population were subsequently used to establish lab-based lines under normoxic conditions. All mice used for experimental work were at least four generations removed from wild-caught individuals. While we recognize that the mice of our experiment are not truly wild (G0), we do refer to their groups with the terms ancestry and population interchangeably, although ancestry is more accurate.

Mice were singly housed throughout the experiments and were given access to food and water *ad libitum*. We supplied each cage with sani-chip bedding, nestlets, and a hut for shelter. Mice were housed on a fixed light-dark cycle of 12:12, with lights off from times 1800 to 0600.

2.2 Experimental procedures

2.2.1 Generalized approach

In total, thirty-four mice (20 lowlanders, 14 highlanders) were subjected to a standardized immune challenge to elicit and quantify their physiological response to infection. In order to induce a controlled febrile and acute phase response, mice received an intraperitoneal injection of the bacterial endotoxin lipopolysaccharide (LPS; O111:B4; Catalogue #: SIAL-L2630-10MG, Neta Scientific) reconstituted in 0.9% NaCl sterile saline at a dose of 10 mg/kg. All injections were performed at the start of the dark (active) cycle (time 1800). LPS is derived from the cell wall of Gram-negative bacteria and can evoke an immune response without infecting the host. LPS injection has been used across mammalian and avian systems to study the immune response (Milovic et al., 2024; Anderson et al., 2022; Nakamori et al., 1994; Liang et al., 2019; D'Alecy & Kluger, 1975; Amaral-Silva et al., 2021; Lennon et al., 2023). Previous work in another *Peromyscus* species suggested that a 10 mg/kg dose induced a robust immune response with full recovery within 7 days (Balderrama-Gutierrez et al., 2021; Milovic et al, 2024); the 50% lethal dose (LD50) was estimated to be well above this at somewhere between 100 and 300 mg/kg in *P. leucopus*.

We conducted an immune challenge experiment involving two separate injection points. Following the first injection, we collected the longer-term data, to include body temperature, food consumption, body weight changes, and sickness behavior; this we refer to as the febrile and recovery response. Following the second injection, we collected hematological measures (blood glucose and serum corticosterone) and spleen transcriptomic data; we refer to this as the

acute phase response. The order in which we discuss these responses follows in this way because the acute phase response required euthanasia.

2.2.2 Febrile and recovery response

To quantify the febrile and recovery responses to LPS injection in deer mice, we inserted a temperature-sensitive Passive Integrated Transponder (PIT-tag; UID Identification Solutions) 10 days prior to the injection of LPS. The PIT-tags were inserted subcutaneously between each mouse's shoulder blades while mice were lightly anesthetized under isoflurane. These PIT-tags allow for near-continuous measurements of body temperature (every 1-2 min) via a custom-built monitoring system (UID Identification Solutions) that uses individual antenna located under each animal's cage linked to a matrix reader that sequentially reads body temperature measured by the PIT-tags.

We established individual baseline daily body temperature rhythms by measuring subcutaneous temperature for 10 consecutive days prior to the first injection of LPS (**Fig. 1**). We also weighed each mouse and the food in their hopper 48 hours prior to experimental injections and on the evening of injections. Animals were injected with LPS in saline at 2.5 mg/mL to administer a 10 mg/kg dose (volume ranges from 62 to 152 μL depending on the mass of each individual of 15 to 38 grams). Following the injection, we weighed the mice and their food every 48 hours for 12 days to track metabolic response and recovery.

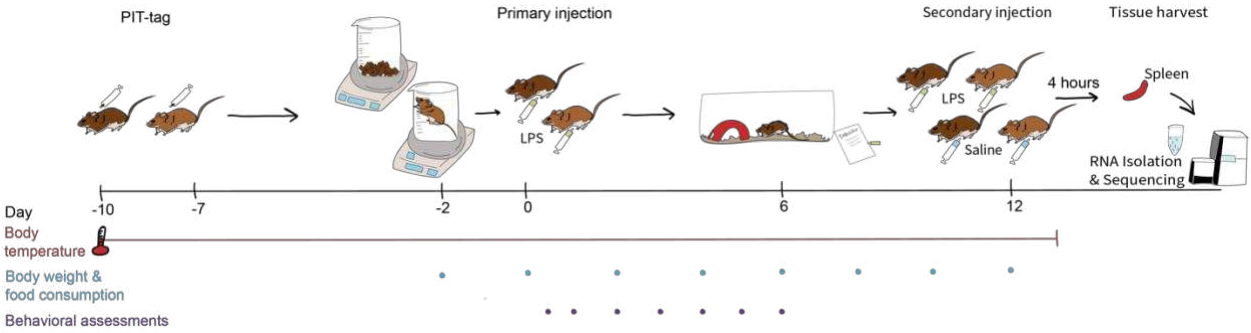

Fig. 1- Experimental design: Study design to assess acute physiological response to LPS in lowland and highland-derived deer mice. Febrile response (n=20), physiological measures (n=34), and spleen transcriptomic data (n=33) were collected through a 12-day immune trial. Individual baseline body temperatures were gathered for ten days prior to the 12-day trial.

To confirm that handling and injection alone did not induce fever or other irregularities in body temperature, we also carried out these procedures with three mice using intraperitoneal injections of the volumetric equivalent of saline only. We collected body temperature from these mice for 6 days following injection and found that saline injection alone had no qualitative effect on normal body temperature (**Fig. S1**).

Additionally, we tracked acute sickness behavior and recovery, through observation of piloerection, optic health, and activity for the first six days following LPS injection. There were 7 observation times: the first occurring at 12 hours after LPS exposure, then at every 24-hour mark post-injection through day 6 (hour 144). For piloerection, we noted if the mouse's hair was smooth or erect. For eye health, the most apparent sign between mice was eye aperture (openness/closure). A mouse's eye aperture could be classified as fully open, half-open (incomplete closure of eyelids), or closed. Eye color and lacrimal discharge was observed but rare and did not last long. Also, we conducted activity assessments. A mouse could be identified as alert, lethargic, or nonmotile. Upon opening the lid of the cage, mouse movement without provocation was considered alert. If no noticeable movement occurred, the mouse's tail was

stroked. Once stroked, if the mouse moved, it was deemed lethargic. The mouse was classifed as nonmotile if no noticeable movement took place after being provoked. Lastly, we looked for shivering when movement halted.

During these experimental trials, two highland-ancestry deer mice unexpectedly died within 48 h of receiving LPS injection (body temperature traces for these individuals are shown in **Fig. S2**). We found no signs of abdominal tears for these animals or other potential reasons for death due to the injection itself. We, therefore, had to halt the febrile and recovery response experiments and were only able to examine the acute phase response for the remaining individuals in the study (see 2.2.3). Nonetheless, we collected febrile and recovery phase responses across 12 lowland- and 8 highland-ancestry mice prior to the deaths of these two highland mice. We provided only one LPS exposure event to the 8 lowland- and 6 highland-ancestry mice that followed this unexpected response in an attempt to reduce animal stress.

2.2.3 Acute phase response

To study the acute phase response, we randomly assigned individuals from highland and lowland populations to either receive an intraperitoneal injection of LPS (10 mg/kg in 0.9% saline, as above) or saline only (**Fig. 1**)**.** We removed food pellets from all cages at the time of injection to allow us to measure fasting blood glucose levels in animals at the time of euthanasia. Four (4) hours after injection (following Balderrama-Gutierrez et al., 2021), we euthanized mice using an isoflurane overdose followed by rapid decapitation and collected a tissue panel from each individual. To limit the potential impact of handling stress on outcome measures (Balcombe et al., 2004), each mouse was euthanized within 3 minutes of lifting their cage.

Injections and tissue collection were completed blind to the injection type. For animals in which we examined the febrile and recovery response prior to the acute phase response, the acute phase response injection was carried out 12 days after the initial injection.

We gathered a panel of tissues and hematological parameters for each mouse. We collected whole blood from which we measured blood glucose (mg/dL) using a glucose meter (HemoCue Glucose 201 Analyzer). Additional whole blood was centrifuged at 5000×g for 10 minutes to collect serum. We also immediately dissected out and weighed the spleen prior to snap freezing it on dry ice. All tissues were stored at –80°C until further processing. In total, we collected tissue panels from 34 mice (20 lowland-ancestry, 14 highland-ancestry), 20 of which also received LPS during the febrile and recovery responses study (see 2.2.2).

2.3 Serum extraction and corticosterone ELISA

Plasma was extracted using solid phase extraction. The extraction columns (C18 Hypersep columns; Part #: 12102052, Agilent) were prepped by running 3 mL of 100% ethanol (Catalogue #: 145615-1L; Beantown Chemical) through them using vacuum filtration. Columns were then equilibrated with 6 mL of deionized (DI) water. Frozen plasma samples were thawed on ice and then 25 µl of serum was added to 10mL of room temperature DI water. For one sample, there was insufficient volume to extract 25 µl and thus 15 µl of sample was used instead. Samples were loaded onto columns and vacuum filtration was used to cycle the total 10 mL of water with the suspended sample. An interference elution step was then run, during which 6 mL of water was run through the columns and discarded. At this point, the collection vials were inserted and 5 mL of methanol was run through each column using vacuum filtration. The vacuum was allowed to run at a high pressure for 2 minutes to collect any remaining sample.

Samples were then dried using nitrogen (N_2) gas at 40°C until methanol was evaporated. Extracted samples were stored at -80°C until assay.

Samples were resuspended in 50% ethanol and then further diluted with assay buffer at room temperature to create a 1:20 dilution with ~5% ethanol. The 1:20 reconstituted sample was further diluted to 1:100 for assay. Corticosterone was quantified using Arbor Assays DetectX Corticosterone ELISA kit (Item No. K014-H5, Ann Arbor, MI). The kit was validated using deer mouse plasma by tests of parallelism and accuracy. Samples were randomized across plates and assayed in triplicate following manufacturer instructions, exceptfive samples which were run across five wells. Samples which initially reached the limit of detection (5 of 33) were rerun at a higher dilution (1:5000) along with samples with the highest coefficients of variance (CVs) (4 of 33). A non-experimental sample of deer mouse serum extracted identically was run across all plates as inter-plate control. Corticosterone concentrations were calculated using a fitted 4-parameter line. The mean intra-assay CV was 6.4% and the inter-assay CV was 13.8%.

2.4 Sample processing for transcriptomic sequencing (RNAseq)

Total RNA was extracted from spleen tissue using a hybrid TRIzol-RNeasy spin column method. The tissue was homogenized with TRIzol in a bead beater (T9424-100ML, Sigma-Aldrich), then chloroform (BJC2432-25ML, VWR) was added to promote phase separation. After the TRIzol phase separation, the aqueous phase was transferred to an RNeasy column to perform column-based purification (74104, Qiagen). Following isolation, RNA concentration and quality were assessed using a Nanodrop spectrophotometer, a Qubit fluorometer (RNA Broad Range Kit Catalog Number: Q10210, Thermo Fisher), and a Tapestation automated electrophoresis system. All RIN scores were > 7.0 (average 9.2), excluding one low quality RNA

sample (RIN: 6.6), which was not sequenced. Isolated RNA samples were then shipped to Novogene for library prep and sequencing.

2.5 Data processing and analysis

2.5.1 Febrile response

The duration of body temperature data read collection ranged from 23 to 36 days among individuals. The data from the two unexpected fatalities post-injection were excluded from all subsequent analysis, however we did process their data as described below for binning and plotting in **Fig. S2**. Our PIT-tag readers collected a read every 1-3 minutes per mouse. All temperature data processing and analyses were conducted in R (2023.12.1+402).

Across these data, erroneous reads (extreme values or NAs) were common due to loss of reader sensitivity, possible interference from nearby readers, or tag malfunction. We, therefore, cleaned each individual's PIT-tag data of erroneous reads prior to further analysis using a rolling window approach (window size = 10 in R packages *zoo* and *lubridate*) (Wilsterman et al., 2025), where each window consisted of consecutive body temperature reads that were then used to calculate a median and standard deviation for that window. We kept reads within a ±1.5 standard deviation of this median temperature. After cleaning, we retained an average of 90.7% (555,199 reads) of the original data for 20 individuals with temperature data and 91.1% (21,963 reads) for the three control mice for further analysis. This translates to an average of 25-41 reads/hour for LPS-injected mice and 23 reads/hour for saline controls.

Previous studies have shown that lowland and highland-derived deer mice exhibit constitutive differences in core body temperature, potentially associated with adaptations to deal with the metabolic costs of thermoregulation (Wearing & Scott, 2022). We, therefore, also

looked for ancestry-specific differences in our deer mice to determine whether and how we should account for such differences in our analyses of the febrile response to LPS. To confirm the presence of ancestry-specific differences in rest-phase body temperature, we calculated daily means, medians, maximums, and minimums during times 0800-1200 (the inactive phase for deer mice in our colony) for the 10 days prior to injection for each individual. We, then, fit a linear mixed effect model (LMM; *lmer* function in the *lme4* package and the *emmeans* package), with random effect of ID, followed by a type 3 ANOVA to obtain statistical values. Lowland-ancestry deer mice maintained a higher average resting phase body temperature relative to highlanders ($F_{1,20} = 6.76$, P= 0.017; **Fig. S3**). This observation is consistent with data from a replicate colony (i.e., mice extracted from the same natural populations; Wearing & Scott, 2022).

To account for these baseline differences between populations in body temperature as well as individual variation in daily temperature rhythms, we employed an analysis method that compared pre-injection to post-injection body temperature values relative to individually-predicted patterns in daily temperature rhythms and then compared these residual values between populations for our statistical analysis. To generate individual-specific residual temperature values, we used pre-injection data from each individual to fit a generalized additive model (GAM) with a spline that accounted for daily rhythms in body temperature. These GAMs were then used to generate predicted values for body temperature at a specific time of day *for each individual*. To determine how LPS injection contributed to departures from expected body temperatures, we then subtracted these time- and individual-specific temperature values from the actual post-injection temperatures that we collected. This generated about 800 residual temperature values per population per day of the experiment (**Table S1**). We then compared these residual temperature values between populations across two time scales: rest (times 0800-1200)

vs active phase (times 2000-2400) and daily. We looked for population differences across the rest and active phases for the first 3 days after injection, and we looked for ancestry-specific 24-hour differences for the first seven days. For both time scales, we used an LMM, with random effect of individual ID, to predict mean body temperature difference between populations, and we used a type 3 ANOVA to calculate F-statistics and P-values.

2.5.2 Metabolic recovery and the acute physiological response

To evaluate population differences in patterns of food consumption and body weight change over the trial period, we fit an LMM with fixed effects of body weight (for body weight change, we instead used day 0 body weight), population, and day, as well as a random effect of mouse ID.

Sickness behavior and recovery assessments were recorded on an ordinal scale for all factors. All behaviors consistent with sickness symptoms were given higher values (i.e. piloerection, lethargy, eye aperture), while healthy behavior was marked as 0 (i.e. smoothed hair, alertness, and eye openness/aperture. The one caveat was that eye closure could be given a 0.5 if the mouse's eyes were only partially open. We also calculated the sum total sickness behavior by adding together each of these sick markers for each individual and averaging by population. Like food consumption and body weight, we used a LMM to test for population differences in each of these markers and total sickness behavior, with mouse ID as a random effect.

Similarly, we used an LMM to test for population differences in blood glucose, serum corticosterone, and spleen weight values with injection and population as fixed effects, and family as a random effect. Spleen weights were adjusted for overall body weight, in that, we included overall body mass in our model.

F-statistics and p-values were determined by a type 3 ANOVA using the LMM output.

2.5.3 Acute phase response: transcriptomic analysis

We generated 336 GB of paired-end raw RNAseq reads (2.6B total reads) from our spleen samples, with each spleen sample having at least 61.7M reads prior to trimming and filtering (sample mean reads = 77.6M). Adapters were trimmed and data was quality checked using *fastp* version 0.23.4. Reads were then mapped to the *Peromyscus maniculatus bairdii* genome (HU_Pman_2.1.3), using *HISAT2* version 2.2.1. We utilized *featureCounts* (within the *Subread* package version 2.0.6) to calculate read counts mapped to genes. Within *featureCounts*, we performed fractional multimapping, which returned 2.3B reads total (average of 68.8M reads per sample; minimum of 51.7M reads). After filtering for low-expressed genes (a minimum of 1 transcript counts per million in each of the 33 samples), we examined differential expression across 13,700 genes.

We tested for differential expression of genes using the model form ~ Population × InjectionType + InjectionNumber, where InjectionNumber refers to whether mice were included in the longer-term febrile and recovery response portion of the experiment – receiving two injections – (20 mice) or only the acute phase analysis where they received one injection (14 mice). Importantly, the difference in number of exposure events could change how gene expression responds to the second LPS injection (Seeley & Ghosh, 2017). We were interested both in genes that showed an ancestry-specific response to injection (i.e., genes that were significant for the Population × InjectionType interaction) and those that differed in expression between populations and were responsive to LPS injections (i.e., additive effects: Population + InjectionType).

In addition to taking a transcriptome-wide approach, we examined a more limited *a priori* list of genes identified in past research as involved in either high-altitude adaptation or the immune response to LPS. Genes included in this list fit at least one of the following categories:

1. Under selection at high-altitudes (two way outliers for PBS and RDA; Schweizer et al., 2021), or
2. Differentially expressed in *Peromyscus leucopus* spleen in response to LPS injection (Balderrama-Gutierrez et al., 2021), or
3. Differentially expressed in *Mus musculus* spleen in response to LPS injection (Balderrama-Gutierrez et al., 2021).

The full *a priori* list comprised 2224 genes (**Table S2**), 857 of which were found in our spleen transcriptome. These genes were subsetted from our filtered data set, after which we performed a Bonferroni-Holmes p-value adjustment for multiple comparisons using *p.adjust*() within this smaller gene set.

To determine whether there were distinct gene functions that represented within our gene sets of interest, we performed Gene Ontology (GO) analyses on upregulated and downregulated genes from each set separately, using R packages *ggrepel*, *edgeR*, and *gprofiler2*. To fit the upregulated or downregulated criteria, the gene had to have a logFC of >0.5 and adjusted p-value below 0.05.

Lastly, we used a Fisher's test (*fisher.test*()) to determine whether there was exceptional overlap between the differentially expressed genes (DEGs) in our dataset and genes that were previously identified as targets of selection at high altitude (Schweizer et al., 2021).

3. RESULTS

3.1 High elevation-ancestry deer mice had a dampened febrile response following LPS exposure.

Overall, we found that LPS disrupts diurnal rhythms of body temperature in both populations. Furthermore, febrile response to LPS injection differed between lowland and highland-adapted deer mice ($F_{1,18}$= 4.65, P= 0.045; **Fig. 2** & **3; Table S3**). Lowlanders had a faster, stronger onset of fever which was sustained throughout both active and rest phases (**Fig. 3A, C**). Conversely, LPS drove a drop in temperature for highlanders during the night (active phase) (**Table S3**).

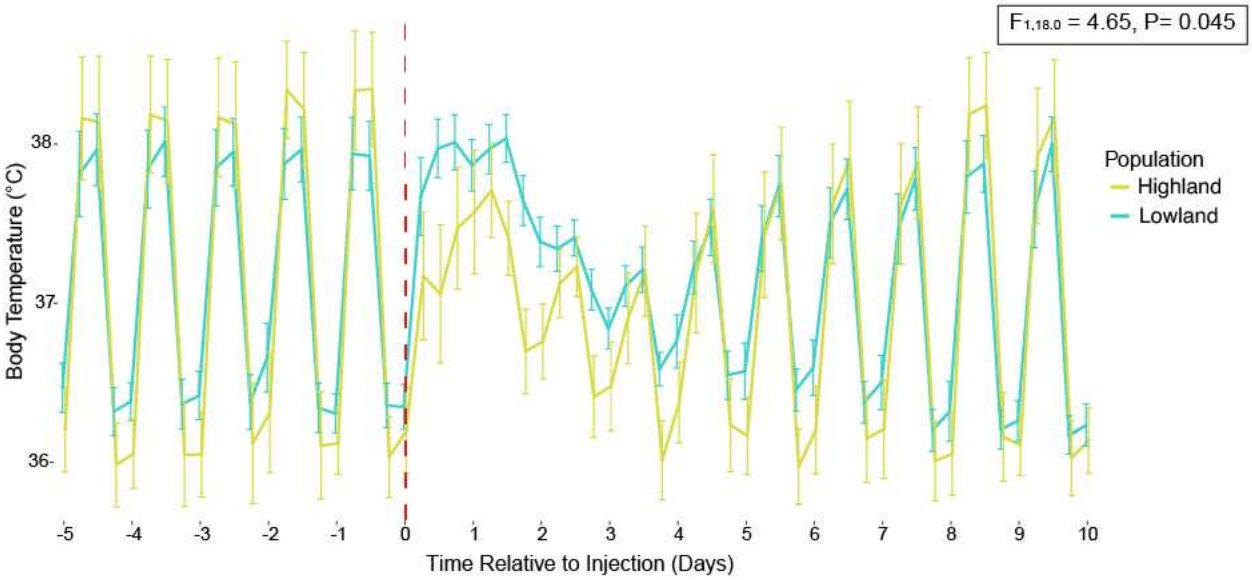

Fig. 2- Pre- and post-injection populational average temperature lines: Effects of LPS on body temperature in 20 deer mice (n= 8 for highlanders and n=12 for lowlanders). Plotted temperatures are the average of six-hour bins per population (± standard error). The first five days depict natural temperature rhythms by population. The red dotted line marks the time of primary LPS injection. An ANOVA type 3 test on the full set of body temperature residuals was used to assess differences between populations in response to LPS injection, after accounting for mouse ID through a linear mixed effect model (test statistic in the top right corner).

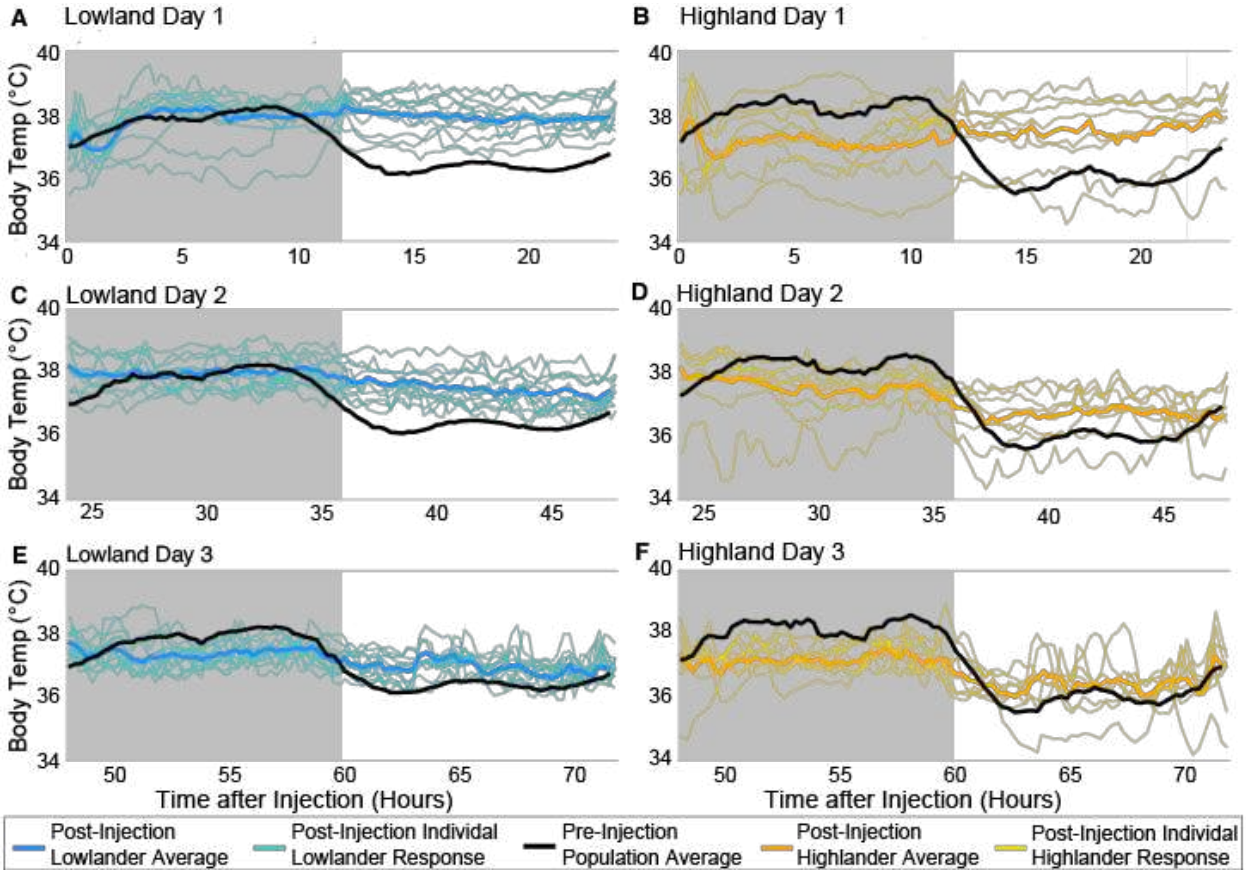

Fig. 3- Pre- and post-LPS exposure body temperature comparison for both populations: (A) Lowlander response to LPS for the first 24 hours following first injection at time 1800, (B) highlander response for the first 24 hours, (C) lowlander temperature changes from 24 to 48 hours post-injection, (D) highlander temperatures 24 to 48 hours after primary exposure to LPS, (E) lowlander response to LPS 48 to 72 hours following injection, and (F) highlander responses for day 3 (48-72 hours) post-injection. Pre-injection/predicted temperatures for each mouse ID were determined using a generalized additive model [GAM] with a cyclic spline. Actual individual responses were plotted for each population. Additionally, both predicted and actual temperatures were separately averaged by population and plotted. The first 12 hours of each plot is shaded to reflect time of activity (i.e. night).

Additionally, the highlander population had a larger range of body temperature values for the first two days especially, such that while some mice experienced fever, others had a more hypothermic response. Thus, we believe highlander fever is highly variable (**Fig. 3**). By day 7,

differences in body temperature residual values between the populations were mostly resolved ($F_{1,18} = 0.483$, $P = 0.496$).

3.2 LPS injection resulted in anorexia and weight loss to a similar degree in lowland and highland-derived deer mice.

The immune challenge resulted in anorexia (suppression of food consumption) for 48 h in both lowland and highland deer mice (**Fig. 4A**). Both populations thereafter began to increase their food intake. There were no differences in the extent of anorexia or recovery food consumption between populations (population × day: $P > 0.8$).

In line with the patterns in food consumption, body weight declined for both populations in the first 48 h following the immune challenge (**Fig. 4B, C**). We observed a significant difference in populations through time (population × day: $F_{1,91.5} = 4.65$, $P = 0.034$), but this was not as significant when we excluded 3 outliers from the lowland population that had extreme body masses at the start (population × day: $F_{6,90} = 1.82$, $P = 0.104$; **Fig. S4**).

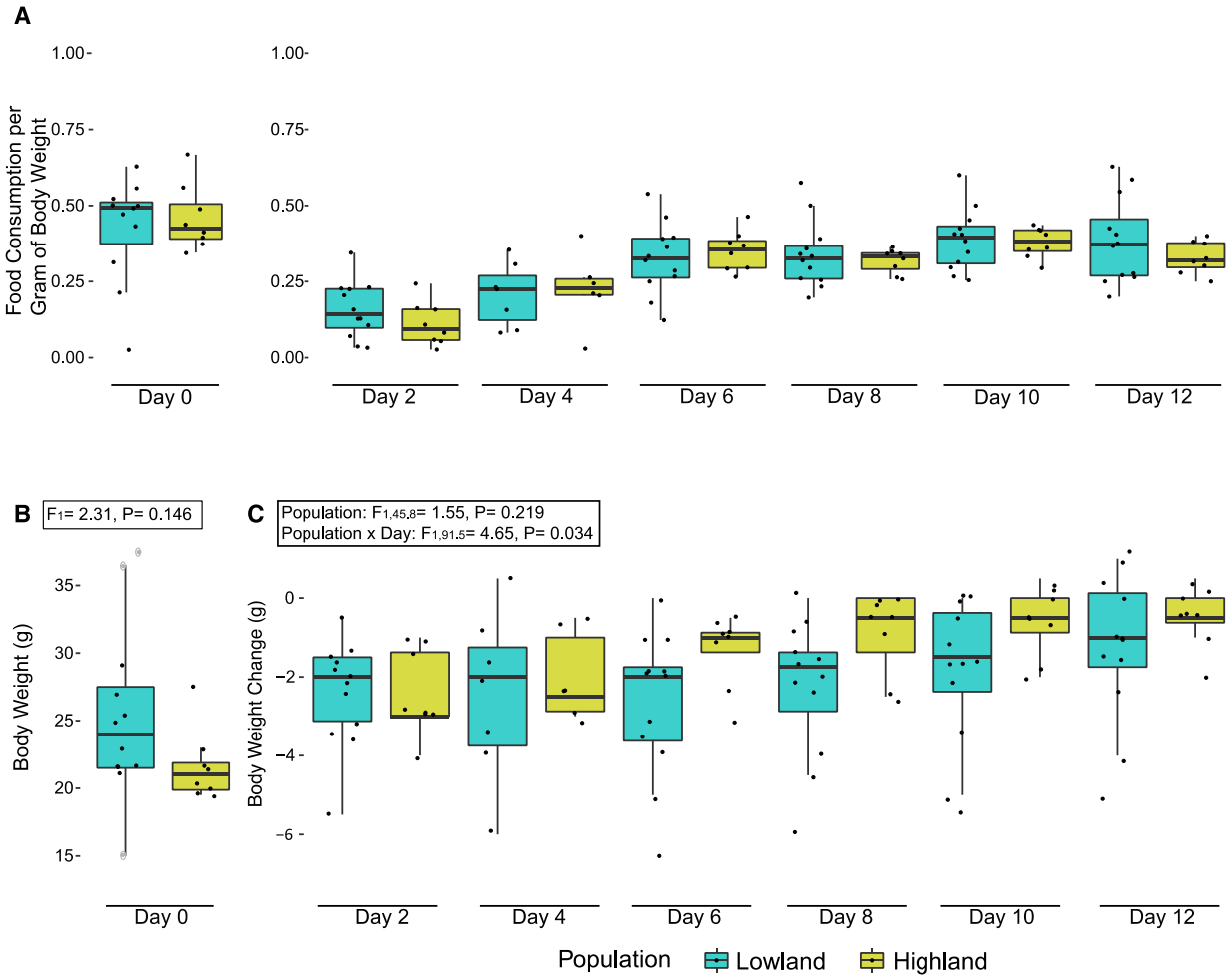

Fig. 4- Anorexia and body weight loss induced by LPS: Both measures were taken on an alternating day basis at the beginning of active phase (time 1800). (A) Food consumption (adjusted for body weight) starting the day of primary injection of LPS and continuing until termination of experiment on Day 12 are separated by population. (B) Initial body weight on day of primary injection and (C) progression of body weight changes (i.e., BWCDay2 = BWDay2 – BWDay0). Three starting body weight values (day 0) that are grey and circled indicate extreme values. Probability values (top left corner for body weight) determined through a type 3 ANOVA with significance attributed to $P < 0.05$; there was no difference between populations in their day 0 or day 2-12 food consumption per gram of mass [(Day 0: $F_1 = 1.79$, $P = 0.199$), (Day 2-12: Population: $F_{1,65.1} = 1.18$, $P = 0.280$; Population × Day: $F_{1,91.6} = 0.019$, $P = 0.890$)]. Mouse ID is accounted for as a random effect for days 2-12.

3.3 Lowlanders appear physically sicker than highlanders.

Lowlanders showed a greater degree of piloerection than highlanders (population: $F_{1,26.5}$= 6.11, P= 0.020; **Fig. 5A**). Eye aperture, lethargy, and shivering were not indicators of differential sickness behavior between populations (P > 0.10; **Fig. 5B-D**). While not considered significant at P < 0.05, the general trend follows that lowlanders exhibit a greater degree of sick markers (population: $F_{1,30.0}$= 2.96, P= 0.096; **Fig. 5E**). Notably, the way sickness behavior changes over the six days of observation is not significantly different between populations (Population × Day: P > 0.3 for all).

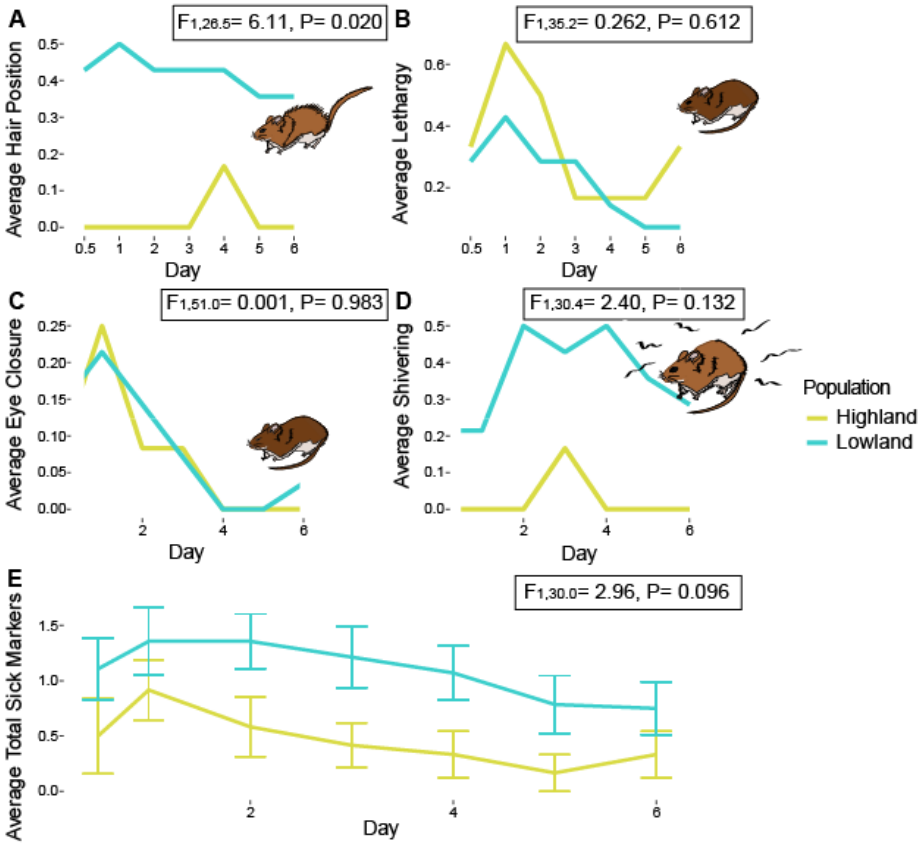

Fig. 5- Sickness behavior: Highland and lowland-ancestry deer mouse behavioral response to lipopolysaccharide (LPS). Sickness behaviors were measured for the first 6 days following LPS exposure. Behaviors were analyzed on an ordinal scale; whereby higher values indicate unhealth. (A) Piloerection, (B) lethargy, (C) eye closure, and (D) shivering were then averaged by

population per collection time. (E) Average total sick markers is the sum of the four behavioral values per individual then averaged by population per collection time. Significance evaluated at $P < 0.05$ through a type 3 ANOVA (test statistic in the top right corner). Mouse ID accounted for as a random effect.

3.4 LPS depletes blood glucose and increases circulating corticosterone.

Four hours following injection, LPS-injected mice had lower blood glucose than saline-injected mice (injection: $F_{1,30} = 5.00$, $P = 0.033$) but there were no population-level or Population × InjectionType interaction differences in this response (population: $F_{1,30} = 0.284$, $P = 0.598$; **Fig. 6A**).

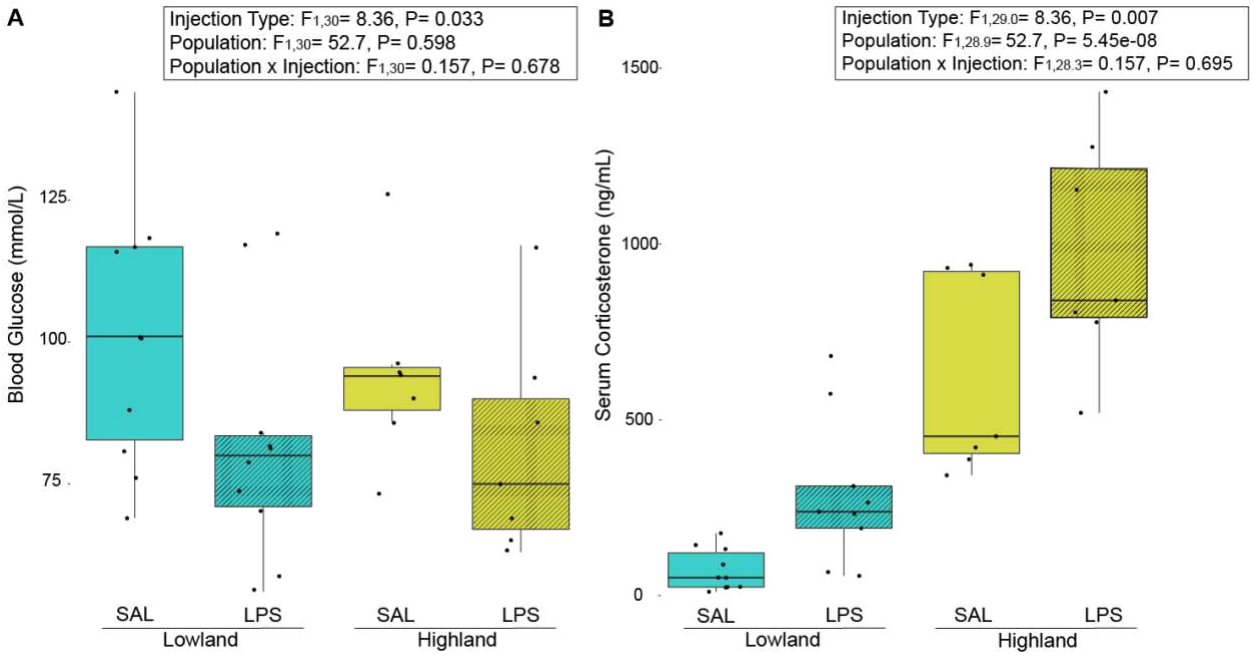

Fig. 6- Hematological measurements: (A) Blood glucose and (B) serum corticosterone collected from lowland and highland-adapted deer mice exposed to saline or LPS four hours prior to tissue harvest. Corticosterone values accounted for its respective dilution factor. Solid boxes are saline controls, while striped boxes represent LPS-injected mice. Significance evaluated at $P < 0.05$ through a type 3 ANOVA (test statistic in the top right corner).

We also found that both populations had elevated corticosterone levels following LPS injection (injection: $F_{1,29.0}$= 8.36, P= 0.007; **Fig. 6B**). Highlanders also had greater basal circulating corticosterone (population: $F_{1,28.9}$= 52.7, P= 5.45e-08). However, there was no interactive effect (population × injection: $F_{1,28.3}$ = 0.157, P= 0.695). We did observe a bimodality in distribution within the highlander saline group. We considered multiple factors that could be the possible source of this trend, including order of dissection, experimental cohort, family, number of injections, and ELISA extraction round. However, none of these explained the bimodality observed in highland-ancestry deer mice following saline injection.

We also measured and compared spleen sizes. However, spleen size did not differ greatly between highland and lowland populations when controlling for body size (population: F_1 = 0.958, P= 0.336; **Fig. S5**).

3.5 Expression patterns of five genes (to include core immune gene *Tnf*) with interactive (population × injection) effects reveal selection on immune strategy.

Among our *a priori* genes of interest, we found a robust and extensive signal of LPS injection: 527 of the 857 genes were differentially expressed in response to injection. This signifies that many of the deer mouse spleen genes that are responsive to LPS, are also responsive in white-footed mice (*Peromyscus leucopus*) and house mice (*Mus musculus*). Of the LPS-responsive *P. leucopus* genes that appeared in our transcriptome, 89% (164/184) were also found to be LPS-responsive in our deer mice. Among house mice, 82% (176/215) of those genes that were LPS-sensitive and occurred in our deer mouse transcriptome were similarly LPS-responsive. Of these LPS-responsive genes, 86 were shared amongst all three species (**Table S4**). This cross-species list includes core immune genes, such as *Tnf* (and a few subtypes of this family), *Il-15ra*, *Il-1b*, and *Tlr2* as well as several understudied immune genes, such as *Parp12,*

Batf2, and *Stat2*. All of these listed genes are upregulated in response to LPS. These findings confirm that a large part of immune gene regulation is conserved among myomorphs.

Additionally, we found 5 LPS-responsive genes that displayed ancestry-specific differences in their transcription following LPS injection from our *a priori* list. These five genes (*Tnfsf10, Slc10a6, Dgat2, Gucy1a2*, and *Klf15*; **Fig. 7**) are strong candidates for understanding how the immune response functionally differs between populations associated with high elevation adaptation. In fact, two of these genes (*Tnfsf10* and *Gucy1a2*) are also known targets of selection within high elevation deer mice (see Schweizer et al. 2019).

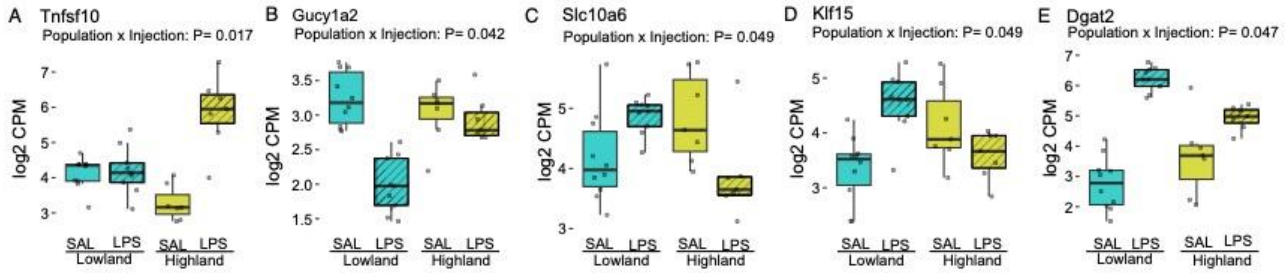

Fig. 7- Splenic gene expression of *a priori* specific genes that have population by injection interactive effects in response to saline vs LPS injection: (A) *Tnfsf10* and (B) *Gucy1a2* are directionally responsive, while remaining relatively nonresponsive in the second population. (C) *Slc201a6* and (D) *Klf15* have opposite responses to LPS between populations. (E) *Dgat2* is upregulated in both populations in response to LPS, but to a greater degree in lowlanders. LPS-injected mice are represented by striped boxes, while saline controls are solid colors. Expression levels are displayed as a log2 of the counts per million (CPM) measure of reads per gene. Significance was determined using voomWithDreamWeights in R package *dream* and linear mixed models with form= Population * Injection Type + Injection Number (test statistic in top right corner; p-value adjustment made specific for the *a priori* list of genes).

We next examined the LPS response and potential for ancestry-specific differences in response within the broader transcriptome. As expected, we found robust evidence of LPS injection across the splenic transcriptome: of the 13,700 filtered genes, 6202 were differentially

expressed in response to the immune challenge. Of these 6202 genes, 3721 had an |logFC| > 0.5. About half (1,848) were upregulated in response to LPS injection, while 1,873 were downregulated.

From the GO analysis, we found over 1000 gene term IDs were enriched among this LPS-sensitive set (928 from the upregulated list; 146 from the downregulated list with $P < 0.05$). The top terms that were enriched among genes upregulated in response to LPS injection were, as expected, immune-related processes, such as response to an external stimulus and cytokine production, and the top downregulated terms for LPS were cellular structure, signaling, and communication **(Tables S5 & S6**).

Although we did not find any genes that were significant for the population × injection interaction after p-value calculation across the whole transcriptome, we did find 1052 genes that were differentially expressed between populations. Of these genes, 63 were found in the *a priori* list. Furthermore, about one third of the population DEGs (386 genes) were *also* responsive to LPS injection (i.e., an additive effect). Of these, 89 upregulated (**Table S7**) and 53 downregulated genes (**Table S8**) also had a |logFC| > 0.5 for both population and injection (**Fig. 8**). We did not find any enriched GO processes in this set. However, the top additive genes are further discussed in the discussion.

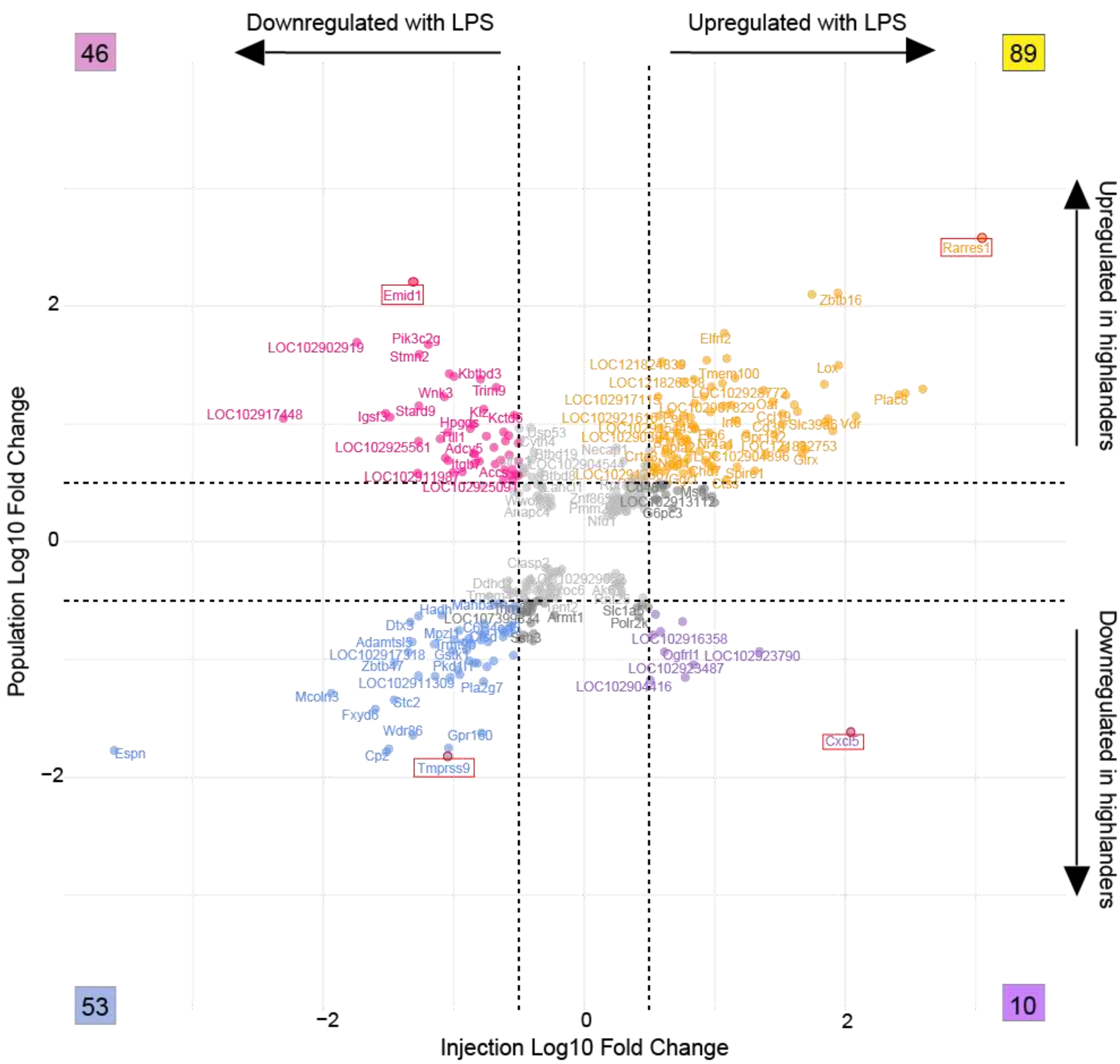

Fig. 8- Volcano plot of the most highly expressed population + injection additive effects: Genes upregulated by LPS injection (positive x axis) are P < 0.05 and logFC > 0.5 for injection differential expression; downregulated genes would have an injection logFC < -0.5 (negative x axis). Genes upregulated by highlanders are P < 0.05 and have a logFC > 0.5 for population (positive y axis), and genes downregulated by highlanders are P < 0.05 and have a logFC < -0.5 (negative y axis). Genes between these logFC cut-offs fall in the gray zone and are considered not significant. Significance determined using the R package *dream* function voomWithDreamWeights in association with linear mixed models with form= Population * Injection Type + Injection Number. Values in the corner of the quadrants indicate the number of genes that fall within its respective quadrant.

Of these additive-effect genes, 20 were previously identified as targets of selection in highland deer mice (Schweizer et al., 2021; **Table S9**). These genes are mostly involved in cell signaling, protein regulation, and transport. Importantly, these genes that show additive effects of population and injection are strong candidates for understanding the basis of population-specific acute phase responses, but not much is known about them currently.

The large-scale of the ancestry-specific differences in expression could also reflect functional differences in the spleen and immune response, even if those genes are not responsive to LPS injection within the experimental time course. Of the 1052 genes differentially expressed by ancestry, 674 had a $|logFC| > 0.5$ where 387 were upregulated and 287 were downregulated in mice with highland ancestry relative to those with lowland-ancestry. Nine GO terms were enriched in those genes that were downregulated in highland ancestry relative to lowland ancestry mice, all of which were related to DNA replication, repair, and modification (**Table S10**). No terms were enriched in the upregulated list.

We found 48 genes with population-specific expression patterns in the high-altitude selection target *a priori* list (Schweizer et al., 2019; Schweizer et al., 2021). However, a Fisher's test revealed that targets of selection were not overrepresented within this set ($P= 0.522$).

4. DISCUSSION

The extent to which the immune system exhibits local adaptation to high elevations is largely unknown (Mazzeo, 2005), even though the immune system is regarded as metabolically demanding (Kominsky et al., 2010) and the abundance of disease vectors is well-known to differ between high and low elevation environments (Zamora-Vilchis et al., 2012; Gilbert, 2010). Here, we investigated this gap in knowledge by using a common-garden experimental design in a model species for high elevation adaptation, the North American deer mouse.

By employing a common-garden design across mice that were generations removed from the wild, we were able to identify differences in their immune responses that were the result of the genetic differences between the populations.

4.1 Highlander febrile strategy reflects the energetic demands of its ancestral environment and appears to be interconnected to the behavioral and glucocorticoid responses.

We found that some of the components of the metabolic response to simulated infection were similar between highland and lowland-ancestry deer mice (food consumption, body weight recovery, and blood glucose).

The reductions in food consumption (anorexia) and subsequent recovery are classic components of the physiological response to apparent infection. Immune challenges shut down an animal's drive to eat through appetite-suppression pathways (Park et al., 2008; Saper & Breder, 1994; Yousefi et al., 2020), often leading to acute weight loss in small-bodied, high metabolism endotherms (Cerami et al., 1985; Owen-Ashley et al., 2006).

The acute drop in blood glucose following injection that we observed in both populations of deer mice is also a common response to LPS-injection and infection. LPS is known to modulate both whole body and tissue glucose metabolism (Lang et al., 1993); furthermore, this effect is not an LPS-specific result, but also found to be the case in response to a wide variety of pathogens (Krapić et al., 2021; Wensveen et al., 2024; Zhang et al., 2023). The reduction in circulating glucose is thought to be associated with the redirection of glucose stores for use in host metabolism (mostly to the spleen and liver) and starving bacterial growth (i.e., the infecting agent) (Lang et al., 1993; Kvidera et al., 2017). Because lowland and highland blood glucose did not differ significantly *within* either saline or LPS-injected groups, our results suggest that glucose homeostasis and regulation in response to apparent infection is largely conserved between the two populations. In line with the food consumption and body mass findings, our data generally suggests that many components of the metabolic response to infection are largely preserved between populations.

Nonetheless, we also observed some notable differences between populations. Most notable and overt were the two unexpected deaths in highland-ancestry individuals that occurred within 48 hours of LPS injection. The cause of these deaths appear consistent with septic shock and liver failure from their body temperature traces; in higher doses of LPS, septic shock is not uncommon in murine models (Lewis et al., 2016). To confirm that sepsis was the true cause of death, we would have needed to take further steps, such as quantifying serum biomarkers and pro-inflammatory cytokines (Wang et al., 2023), measuring their circulating glucose (Zhang et al., 2023), and using antibody-based biosensors (Virzi et al., 2022). Although septic shock should have been extremely unlikely at a 10 mg/kg dosage of LPS (Balderrama-Gutierrez et al., 2021), the two highland-ancestry deaths point to greater sensitivity in highland-ancestry mice to LPS.

At a physiological level, we also observed ancestry-specific patterns in the febrile response and circulating glucocorticoids. Though these data types cannot, on their own, differentiate between ancestry-level differences in sensitivity that could lead to septic shock, they further support that adaptation to high elevations has altered how individuals experience and physiologically respond to immune challenges.

As expected, injection of LPS disrupted the normal daily rhythm of body temperature and induced a febrile response. First, prior to the immune challenge, we observed differences in phase-specific resting temperature which could be attributed to thermogenic adaptations in highland-ancestry deer mice: highlanders have lower resting temperatures (**Fig. S3**), consistent with results from Wearing & Scott, 2022. In the wild, highlanders experience colder temperatures on average, especially during the night (active), compared to lowland populations, which means that highlanders would likely need to spend greater energy on thermogenesis during this phase. Following LPS injection, we saw that lowland-ancestry deer mice displayed greater fever relative to highland ancestry mice during the day 1 and 2 active phases (**Table S3)**. Fever is often most apparent during the rest-phase, as the immune system tends to ramp up when other physiological processes are suppressed (Sheldon & Verhulst, 1996; Lochmiller & Deerenberg, 2000). Since active phase fevers would be especially energetically costly (in thermogenesis) for highlanders, they may suppress the immune-associated febrile response during the night. Alternatively, highlanders may have robust immune activation but are tempering the febrile response, such that mostly non-pyrogenic immune players are activated.

Furthermore, animals that have greater febrile responses may exhibit more sickness behaviors (e.g., inactivity, sleepiness, reduced appetite) as the increased energy required for elevating body temperature may lead to conservation of energy in other organismal processes,

such as behavior (Hart, 2010). For example, increased sleepiness or lethargy frequently coincides with fever as it allows the body to slow down and save energy. Consistent with this, we found that our lowlanders, which had the stronger febrile response, tend to display more sickness behaviors. Of the sickness behaviors we observed, the strongest trends were found for piloerection and shivering. It's important to note that our use of the term "piloerection" may describe a couple of different responses: erect hair may indicate a lack of grooming or may translate to being cold. In the first case, hair may look scruffy or oily due to a lack of grooming because there's more energy involved in muscle movement, and further, the body movement required to groom could result in greater heat loss as the skin surface could become more exposed. Alternatively, keeping the hair erect may reduce heat loss by increasing the insulating properties of the fur (Hart, 2010).

In addition to minimizing thermal losses, clearance of pathogens is expedited by increasing production of heat, which is aided by shivering (Dantzer, 2006). When shivering is activated, it raises the body temperature, and the rate of metabolism is two-threefold higher than the resting level. While this is very energetically costly for the organism, it serves to inhibit pathogen growth (Hart, 2010). Highlanders may favor increased energy conservation to cope with the environmental demands. Therefore, energy conservation in highlanders leads to limiting the febrile response, which may encourage healthy appearance. Maintenance of healthy behaviors, such as being alert, grooming, and exploring is more energetically expensive than the unhealthy alternative.

We also found that serum corticosterone levels universally increase in response to LPS, however the baseline serum corticosterone was much greater in highland ancestry mice when compared to lowland ancestry mice. The difference in baseline corticosterone that we observed

agrees with recent data from replicate colonies (Pranckevicius et al., 2025). These ancestry-dependent differences in circulating corticosterone are thought to be related to differences in whole animal metabolism and adaptations to improve respiratory function under hypoxia (Pranckevicius et al., 2025). Ancestry-dependent differences in corticosterone could thus also be linked to the ancestry-specific regulation of fever that we observed. Endogenous glucocorticoids have been found to modulate fevers induced by LPS in rats, such that LPS-injected rats given a glucocorticoid antagonist have much stronger fevers compared to the rats with undisturbed glucocorticoid levels (Morrow et al., 1993). Therefore, higher corticosterone levels could translate to a more muted fever response, which is what we observed in our highland-ancestry mice.

Follow-up experiments manipulating the time of day at which LPS is provided and manipulations of circulating corticosterone would be necessary to resolve the specific mechanism and potential adaptive value of the patterns we observed here.

4.2 The orchestration of gene expression within lowlanders may allow for greater flexibility of response to LPS than highlanders.

Our transcriptomic analysis revealed both highly conserved as well as notably divergent component of the splenic response to LPS in deer mice.

We found 86 LPS-responsive genes shared across deer mice, white-footed mice, and house mice, with a higher percentage shared (89%) between the *Peromyscus* species. Of the 86 shared genes, a few have well-documented functions that contribute to our understanding of immune regulation. *Il-15ra* (receptor of *Il-15*), *Il-12*, and *Il-1b* are cytokines cornerstone to the maturation and expansion of immune players such as dendritic cells, natural killer (NK) cells, macrophages, and CD4+ T cells (Ma et al., 2003; Mortier et al., 2009). *Tlr2* and *Stat2* are also

heavily involved in immune signaling pathways wherein they mediate the release of cytokines by activating the inflammatory regulator NF-κB (Xu et al., 2016). These genes among others shared in this subset reveal similar strategies for innate immune recovery. Like deer mice, *P. leucopus* and to a lesser degree *M. Musculus* are reservoirs for zoonotic diseases, such as Hantavirus Pulmonary Syndrome (*Hantavirus*; Song et al., 1994; Baek et al., 1988) and Toxoplasmosis (*Toxoplasma gondii*; Lubroth et al., 1983; Salcedo et al., 2021), which lends special insight into the biological processes that are shared between vector host species. Interest lies in comparing the immune response of non-vector species to these animals, so that we can elucidate the specific mechanisms by which vectors protect themselves from (perceived) infection.

We anticipate that genes displaying ancestry-specific differential expression in response to LPS injection with clear roles in the immune response to be the strongest candidates for functional mediators of ancestry-specific immune sensitivities. We found one such gene, *Cxcl5*, that appears to be universally responsive to LPS in myomorphs *and* exhibits ancestry-specific expression in the spleen (**Fig. S7**). Although relatively little is known about the role that *Cxcl5* plays in controlling the immune response, we do know that it is upregulated in the spleen in response to LPS across myomorphs (Balderrama-Gutierrez et al., 2021), and that it plays a critical role in inflammation by regulating neutrophil infiltration and chemotaxis (Lin et al., 2007; Mei et al., 2010). In deer mice, we observed that highlanders have lower expression of *Cxcl5* in the spleen under baseline (saline) conditions, but they upregulate expression to similar levels as lowlanders in response to LPS. This pattern may point to differences in baseline immune system activity; lower *Cxcl5* has been associated with increased autoimmune activity in house mice (Fan et al., 2023). While we know *Cxcl5* to play a role in inflammation, it is not clear by what mechanism it does so, as there is support for both low and high levels of expression

leading to inflammation (Tacke et al., 2011; Roca et al., 2018). Lower expression of *Cxcl5* in other immune tissues, like bone marrow, is also known to contribute to broader immune system phenotypes (Mei et al., 2012), suggesting that the broader tissue characterizations of differences in *Cxcl5* is likely to be valuable in understanding how these ancestry-specific expression patterns shape immune system differences in the integrated organism.

We also identified 5 genes using our *a priori* set that were significant for an interaction between ancestry and injection (**Fig. 7**), suggesting that the degree or direction of differential expression associated with LPS injection for these genes depended on ancestry. Two of these five genes (*Tnfsf10* and *Gucy1a2*) are recognized targets of selection in high elevation deer mice, which specifically attracted our attention. Interestingly, both *Tnfsf10* and *Gucy1a2* were not LPS-responsive in either highland or lowland-ancestry animals: LPS did not alter expression in lowland-ancestry deer mice (median log2 CPM of ~4.2), however it greatly increased *Tnfsf10* expression in highlanders (from median log2 CPM ~3.3 to ~6). Conversely, LPS decreased *Gucy1a2* expression in lowlanders (from median log2 CPM of ~3.2 to ~2), while highlanders displayed constitutively elevated *Gucy1a2* expression (median log2 CPM of ~3). *Tnfsf10* is part of the *Tnf* ligand gene family which is known to regulate apoptosis (both anti- and pro-apoptotic effects). Increased expression of *Tnf* genes leads to the activation of immune transcription factors NF-κB and AP-1, leading to the induction of cytokines, as well as local or global inflammation (Liu, 2005). Comparatively little is known about *Gucy1a2*, though elevated expression of *Gucy1a2* is linked to several illnesses such as heart failure, hypertensive disorder, arthritis, and inflammation in humans (Mosharaf et al., 2022). This suggests that constitutively high expression of *Gucy1a2,* as seen in our highlanders, may be associated with *increased* generalized inflammation or inflammatory responses.

Some of the genes that were significant for the ancestry-by-injection interaction exhibited differential expression in response to LPS in opposing directions (*Slc10a6* and *Klf15*). These patterns point to reliance on a specific set of genes to assist in the mechanisms motivating the integral response. Importantly, reliance on a different set of genes in highland-ancestry mice compared to lowlanders further differentiates these populations, such that they have evolved different mechanisms to handle immune stress. Changes in direction of expression in highland-derived mice might reflect the organism's interaction with factors of the environmental landscape from which they are descended (i.e., relative pathogen presence, hypoxia, interaction of traits being remodeled by adaptation to high-altitudes).

Slc10a6 increased in expression for lowland-ancestry mice but decreased in highland-ancestry mice in response to LPS injection. *Slc10a6* is thought to be involved in bile acid and bile salt transport, and increased expression has been linked to hepatic inflammatory response through its interaction with pro-inflammatory chemokine *CCL5;* while expression of *Slc10a6* does increase in the spleen upon injection of LPS, its effect is most notable in the liver (Kosters et al., 2016). Thus, the patterns we observed in our mice may indicate that lowlanders have greater digestive inflammation than highlanders.

LPS similarly increased *Klf15* expression in lowland-ancestry mice while decreasing expression in highland-ancestry mice. A previous study has found that post-LPS induction, *Klf15* has anti-inflammation and anti-apoptosis effects on mice (Tian et al., 2020), while deficiency may lead to aggressive inflammation for mouse models with vascular diseases (Lu et al., 2013). Therefore, we suspect that with LPS injection, *Klf15* acts to dampen or pacify the lowlander response, while stimulating highlander response.

The final gene that was significant for an ancestry-by-injection effect, *Dgat2*, was upregulated in both populations in response to LPS, but this response was more extreme in lowlanders, suggesting that the LPS-sensitivity of this gene's expression has been suppressed as part of adaptation to high elevations. This gene is involved in triglyceride synthesis, as well as activation of *Tlr7* signaling which triggers the inflammatory regulator NF-κB (Wei et al., 2021). NF-κB has a great deal of control over innate immune processes, such as regulating activation and differentiation of macrophages, dendritic cells, and T cells (Liu et al., 2017). Thus, this difference in expression pattern may translate to increased mobilization and activation of immune players in lowlanders, which may eventually lead to exacerbation of host defense.

We also found many genes with additive effects of LPS-injection and ancestry. Here we focus on those genes where the directional effects were shared. The gene with the greatest increase in expression in response to LPS and differential expression associated with highland-ancestry (highest population and injection logFC) was *Rarres1* (**Fig. 8**). *Rarres1* activates apoptosis in tumor cells, thereby suppressing the spread of tumor cells and promoting healthy cell survival (Wang et al., 2018; Geng et al., 2022; Patel et al., 2022). Highland deer mice thus are likely to display greater apoptotic activity leading to clearance of external threat. In the opposite direction, *Tmprss9* displayed the greatest suppression of expression in response to LPS injection and the greatest down-regulation in highland-ancestry deer mice relative to lowland-ancestry deer mice (lowest logFC for population and injection; **Fig. 8**). *Tmprss9* serves as a protease and may play a role in cancer progression (Fontanil et al., 2014). The fact that we did not find broader functional categories enriched among these genes that were differentially expressed in response to LPS injection and by ancestry suggests that that the remodeling of the immune system in high-altitude deer mice depends on gene-specific, rather than process specific,

modifications. Such changes may reflect constraint on the evolution of immune system pathways or constraint on specific genes, originating from factors of the environment.

These genes with significant ancestry-specific responses to LPS give insight into the transcriptomic interactions guiding immune defense. Lowlanders appear to have expression of genes that lead to a more comprehensive, well-rounded response that may harness more control with the activation and deactivation of inflammation and apoptosis (i.e., upregulation of *Slc10a6, Klf15,* and *Dgat2,* and downregulation of *Gucy1a2*). Highlander response, on the other hand, involves greater expression of pro-apoptosis genes (*Rarres1* and *Tnfsf10*), which should theoretically aid in the clearance of perceived threat faster.

4.3 Future directions

While this project serves as a beneficial starting point to understanding how the immune system has evolved in high altitude environments, we hope to see many follow-on studies which can sharpen our knowledge of this system.

First, a study that addresses the specific (adaptive) immune response would give a more comprehensive view of populational strategies to immune threats. Importantly, our experimental design primarily assessed the non-specific (innate) immune response. Notably, we did find that there were a significant number of genes (1672) that were sensitive to the number of LPS exposures an individual experienced, and some of these effects appeared to be ancestry-specific. These results suggest that the adaptive immune system may also be differentiated as part of the process of adaptation to high elevations. However, our experiment was not specifically designed to evaluate differences in the adaptive immune response and thus we cannot draw robust conclusions about potential differentiation therein. Related, our study only addresses differences

in the immune response to a gram-negative bacterial agent. As such, our study does not and cannot address the full scope of differences in immune system function or speak to which components of the immune system are *most* differentiated and perhaps therefore potentially most interesting. Exploring the immune tactics to a diversity of threats would be a fascinating follow-on study.

Second, future studies should investigate potential for sex differences in the immune response and/or life stage differences, especially those associated with reproduction. Importantly, our experiments focused only on immune function in male deer mice. However, many mammalian systems display sex-specific variation in immunity (Zazara & Arck, 2019; Valdebenito et al., 2021), and deer mice are likely no exception.

Third, a future project based on wild populations would improve our understanding of how natural selection is acting upon the immune system. Our experiments focused on animals that are several generations removed from their natural habitats. Although this common garden design provides a lot of power to detect the effects of genetic differentiation on the immune response, it cannot speak to gene × environment interactions that are likely important for immune system development and function in wild animals. Developing a full understanding of how high elevation adaptation has altered the functional immune response will require studies in wild populations with natural exposure to environmental immune agents that undoubtedly shape how the immune system behaves in natural environments and thus may be exposed to selection.

4.4 Concluding remarks

High elevations present new residents with a complex array of environmental changes, including both abiotic variables like hypoxia and low temperatures, and biotic variables like

modified pressure from predation or immune threats. Historically, most research on organismal adaptation to high elevations has focused on these abiotic challenges. However, our study demonstrates that high elevation-derived North American deer mice also exhibit differentiation in their immune responses, suggesting that these changing biotic stressors are also important selective agents. Our results thus contribute to a broader understanding of how whole organisms adapt to complex environments. Furthermore, as a host for several diseases of concern, understanding spatial variation in the immune responses of deer mouse populations is particularly valuable to helping shape predictions about how these novel host-pathogen interactions might impact disease prevalence and spread under novel climate change conditions.

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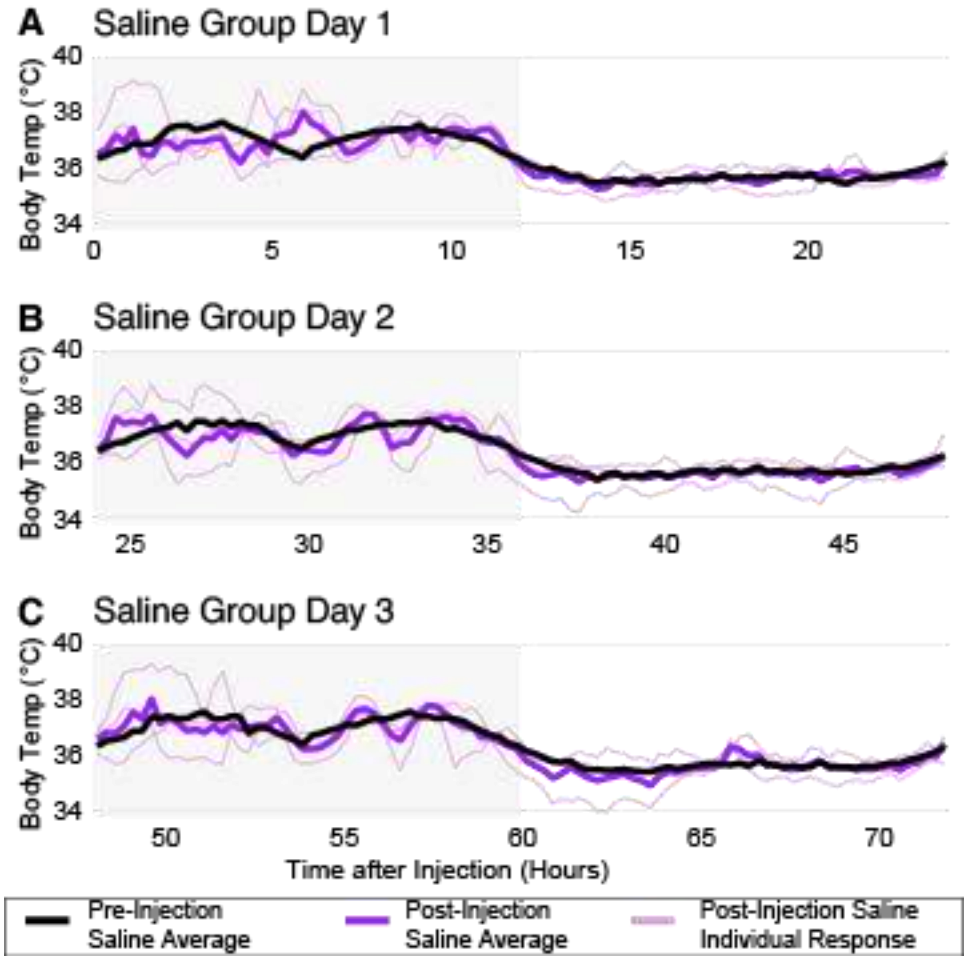
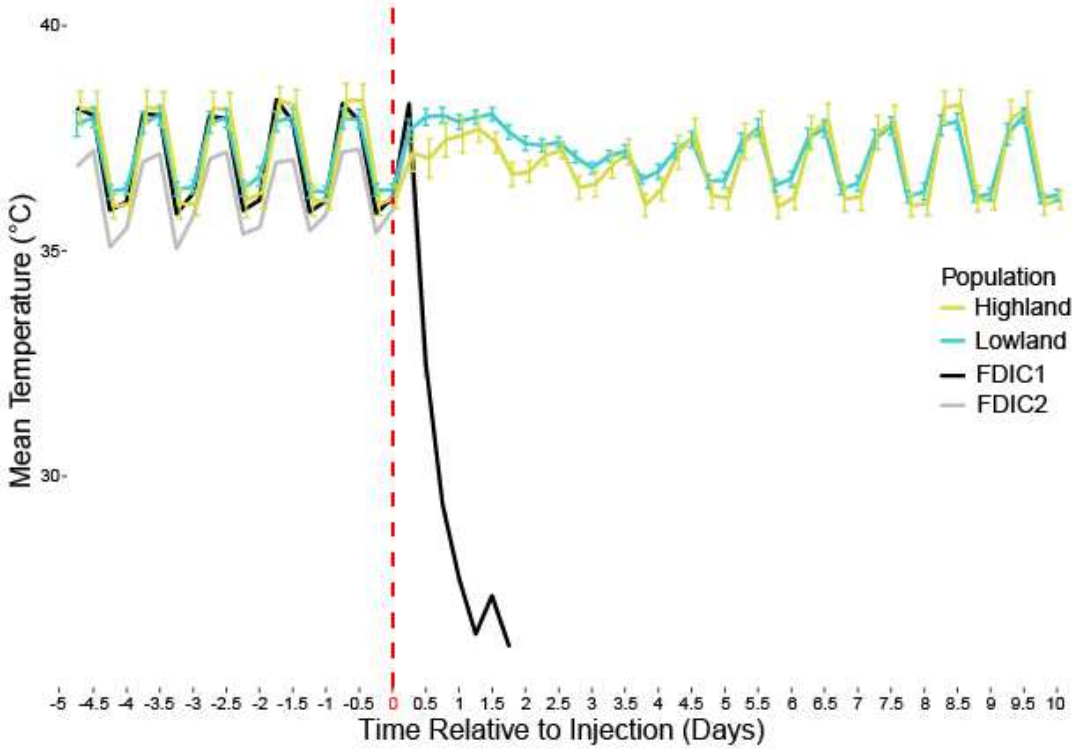
6. APPENDIX

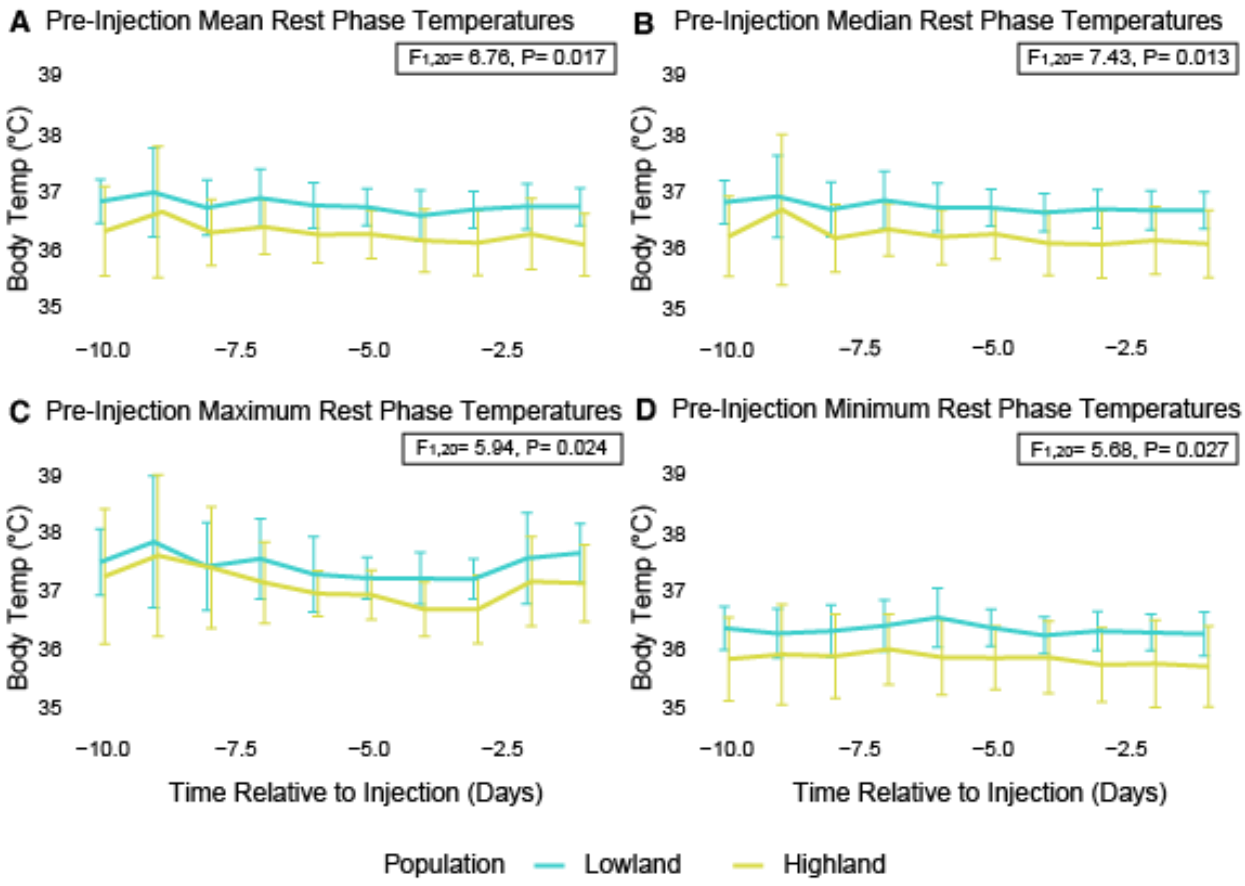
6.1 Supplemental figures



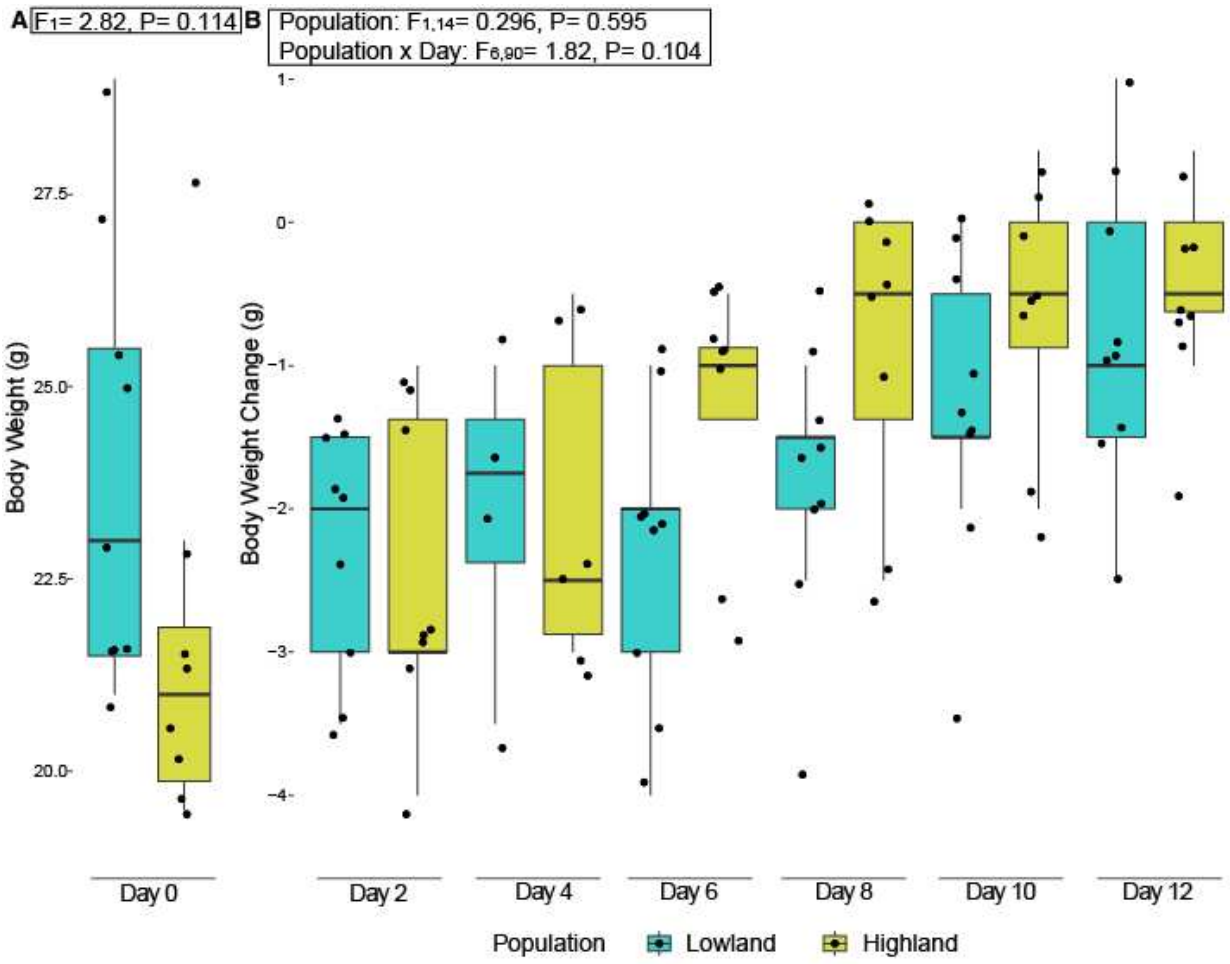
Supplemental Figure 1- Pre- and post-saline injection comparison of body temperatures for the three control mice: (A) The first 24 hours following injection of saline at time 1800, (B) progression of body temperature for hours 24-48 after saline exposure, and (C) day 3 body temperatures for the 3 saline control mice. Pre-injection/predicted temperatures for each mouse ID were determined using a generalized additive model [GAM] with a cyclic spline. Each actual individual response was plotted. Additionally, both predicted and actual temperatures were separately averaged and plotted. The first 12 hours of each plot are shaded to indicate time of activity (i.e. night).



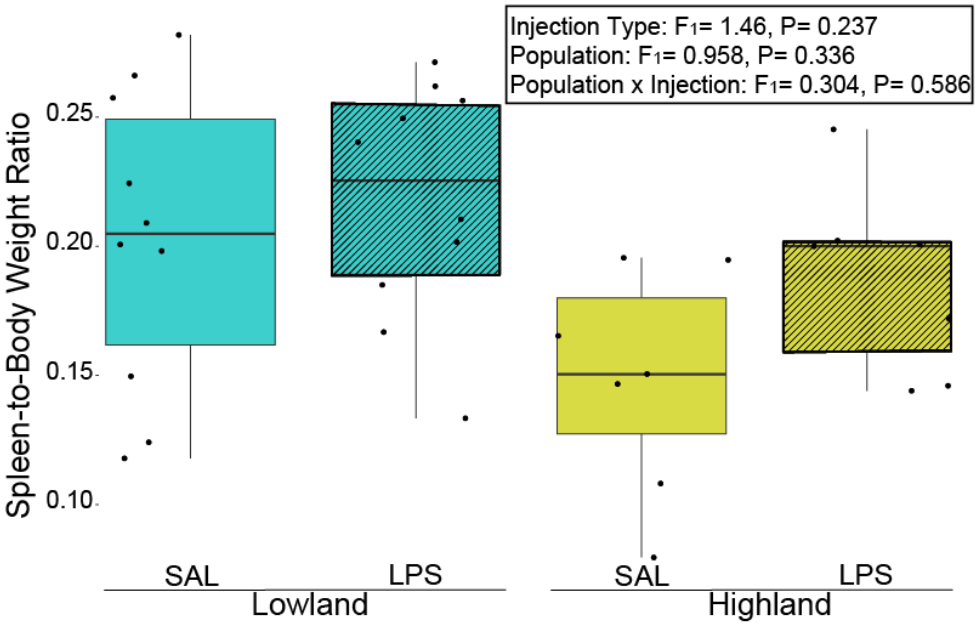
Supplemental Figure 2- Body temperature progression of all mice exposed to LPS, including the two highland mice that died quickly: Body temperature traces of two mice that died unexpectedly from LPS (marked in black and grey lines) compared to the 20 mice (plotted as populational averages) that survived the threat of LPS. Average temperatures for every 6 hours are plotted with standard error bars only for lines of surviving mice (n=8 for highlanders; n=12 for lowlanders). The red dotted line marks the time of primary LPS injection.



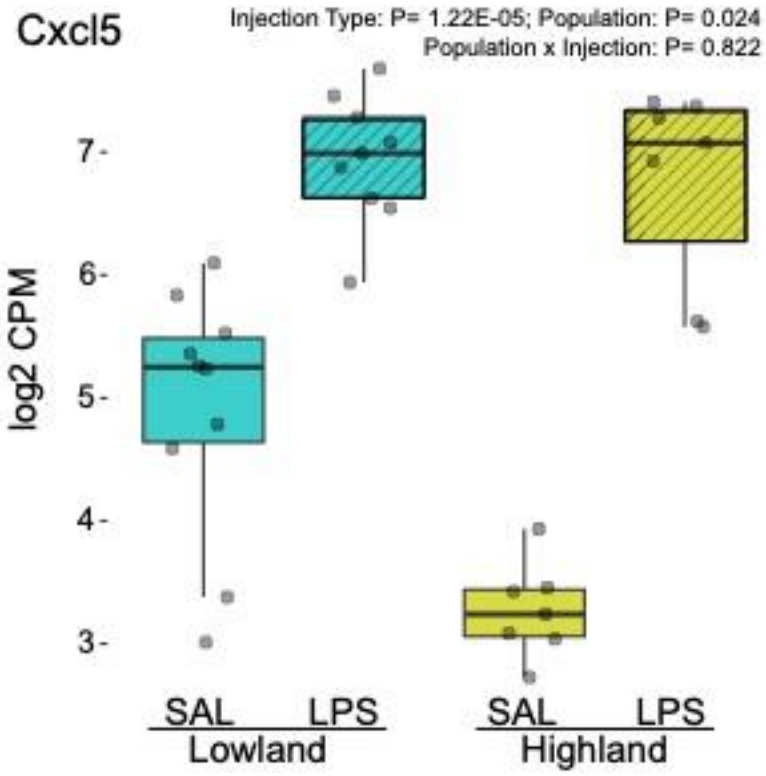
Supplemental Figure 3- Resting body temperature averages between population across the 10 days before primary LPS injection: (A) Mean, (B) median, (C) maximum, and (D) minimum body temperatures were collected for each individual each pre-injection day at time 0800-1200 and averaged for each population. Populational significance (top right) determined through a type 3 ANOVA on each parameter, using LMM output with random effect of mouse ID.



Supplemental Figure 4- Starting body weight and subsequent loss in weight prompted by LPS injection, excluding three outliers. Mouse weight was measured each 48 hours at the start of the mouse's active phase (time point 1800). (A) Initial body weight on day of primary injection and (B) progression of body weight changes (i.e., BWCDay2 = BWDay2 – BWDay0). Three extreme values were excluded from this two-part plot. Probability values (top left corner) determined through a type 3 ANOVA with significance attributed to $P < 0.05$; mouse ID is accounted for as a random effect for days 2-12.



Supplemental Figure 5- Comparison of spleen weights across injection types and populations: Striped boxplots represent LPS-injected mice, while solid boxes are saline controls. Spleen weight was adjusted for overall body weight (i.e. spleen weight/ body weight). Significance was determined via a type 3 ANOVA using raw spleen weight with a fixed effect of body weight (test statistic in the top right corner).



Supplemental Figure 6- Genetic expression of *Cxcl5* in response to control (saline) and LPS injection between lowland and highland-adapted deer mice: LPS-injected mice are represented by striped boxes, while saline controls are solid colors. Expression levels are displayed as a log2 of the counts per million (CPM) measure of reads per gene. Significance was determined using voomWithDreamWeights in R package *dream* and linear mixed models with form= Population * Injection Type + Injection Number (test statistic in the top right corner).

6.2 Supplemental tables

Supplemental Table 1. Average number of residual temperature values per individual for each population for the first six days following cleaning of the data via a rolling window approach.

Day	Population	Average number of residual values per individual
1	Lowland	783.1
	Highland	781
2	Lowland	813.6
	Highland	822.8
3	Lowland	772.6
	Highland	749.5
4	Lowland	779.8
	Highland	776.8
5	Lowland	770.6

	Highland	758.6
6	Lowland	756.8
	Highland	771.3
Daily Average	Lowland	796.1
	Highland	776.6

Supplemental Table 2: Full list of *a priori* genes previously found to be responsive to LPS in *P. leucopus* (abbreviated *P.l*) or *M. musculus* (abbreviated *M.m*) or are under selection at high altitudes in *P. maniculatus* (abbreviated *P.m*.).

Gene ID	Source	Sp.	Gene ID	Source	Sp.	Gene ID	Source	Sp.	Gene ID	Source	Sp.
0610043K17Rik	Balderrama	*M.m*	Oas1g	Balderrama	*M.m*	Nexmif	Balderrama	*P.l*	LOC102913629	Schweizer	*P. m*
1110032F04Rik	Balderrama	*M.m*	Oas1h	Balderrama	*M.m*	Nfkbia	Balderrama	*P.l*	LOC102913816	Schweizer	*P. m*
1190001M18Rik	Balderrama	*M.m*	Oas2	Balderrama	*M.m*	Nfkbiz	Balderrama	*P.l*	LOC102913869	Schweizer	*P. m*
1200007C13Rik	Balderrama	*M.m*	Oasl1	Balderrama	*M.m*	Nim1k	Balderrama	*P.l*	LOC102913898	Schweizer	*P. m*
1600002D24Rik	Balderrama	*M.m*	Oasl2	Balderrama	*M.m*	Nlrc5	Balderrama	*P.l*	LOC102913983	Schweizer	*P. m*
1600014C10Rik	Balderrama	*M.m*	Ogfr	Balderrama	*M.m*	Nlrp3	Balderrama	*P.l*	LOC102914090	Schweizer	*P. m*
1700008H02Rik	Balderrama	*M.m*	Olfr1167	Balderrama	*M.m*	Nnmt	Balderrama	*P.l*	LOC102914280	Schweizer	*P. m*
1700011B04Rik	Balderrama	*M.m*	Olfr1395	Balderrama	*M.m*	Nox1	Balderrama	*P.l*	LOC102914398	Schweizer	*P. m*
1700019C18Rik	Balderrama	*M.m*	Olfr1396	Balderrama	*M.m*	Nppc	Balderrama	*P.l*	LOC102914497	Schweizer	*P. m*
1700022H01Rik	Balderrama	*M.m*	Olfr231	Balderrama	*M.m*	Nr1h4	Balderrama	*P.l*	LOC102914701	Schweizer	*P. m*
1700025N23Rik	Balderrama	*M.m*	Olfr318	Balderrama	*M.m*	Ntrk1	Balderrama	*P.l*	LOC102914718	Schweizer	*P. m*
1700066B17Rik	Balderrama	*M.m*	Olfr362	Balderrama	*M.m*	Oas3	Balderrama	*P.l*	LOC102914774	Schweizer	*P. m*
1810065E05Rik	Balderrama	*M.m*	Olfr56	Balderrama	*M.m*	Oasl	Balderrama	*P.l*	LOC102914793	Schweizer	*P. m*
2210412B16Rik	Balderrama	*M.m*	Olfr596	Balderrama	*M.m*	Olfm4	Balderrama	*P.l*	LOC102914946	Schweizer	*P. m*
2310043L19Rik	Balderrama	*M.m*	Olfr76	Balderrama	*M.m*	Olig1	Balderrama	*P.l*	LOC102915078	Schweizer	*P. m*
2810403G07Rik	Balderrama	*M.m*	Olfr853	Balderrama	*M.m*	Olr1	Balderrama	*P.l*	LOC102915109	Schweizer	*P. m*
2900011O08Rik	Balderrama	*M.m*	Olfr877	Balderrama	*M.m*	Ooep	Balderrama	*P.l*	LOC102915169	Schweizer	*P. m*
4833419F23Rik	Balderrama	*M.m*	Olfr93	Balderrama	*M.m*	Osmr	Balderrama	*P.l*	LOC102915274	Schweizer	*P. m*
4921509O07Rik	Balderrama	*M.m*	Olfr94	Balderrama	*M.m*	Pappa	Balderrama	*P.l*	LOC102915326	Schweizer	*P. m*
4930435F18Rik	Balderrama	*M.m*	Orm1	Balderrama	*M.m*	Pate1	Balderrama	*P.l*	LOC102915382	Schweizer	*P. m*
4930455M05Rik	Balderrama	*M.m*	P2ry2	Balderrama	*M.m*	Pdcd1lg2	Balderrama	*P.l*	LOC102915530	Schweizer	*P. m*
4930478E11Rik	Balderrama	*M.m*	Parp10	Balderrama	*M.m*	Peg10	Balderrama	*P.l*	LOC102915553	Schweizer	*P. m*
4930478L05Rik	Balderrama	*M.m*	Parp12	Balderrama	*M.m*	Penk	Balderrama	*P.l*	LOC102915596	Schweizer	*P. m*

4930503B20Rik	Balderrama	*M.m*	Parp14	Balderrama	*M.m*	Pi15	Balderrama	*P.l*	LOC102915783	Schweizer	*P. m*
4930512B01Rik	Balderrama	*M.m*	Parp9	Balderrama	*M.m*	Pim1	Balderrama	*P.l*	LOC102915842	Schweizer	*P. m*
4930512H18Rik	Balderrama	*M.m*	Pcdh19	Balderrama	*M.m*	Pla1a	Balderrama	*P.l*	LOC102915911	Schweizer	*P. m*
4930540M05Rik	Balderrama	*M.m*	Peak1os	Balderrama	*M.m*	Pla2g2a	Balderrama	*P.l*	LOC102916061	Schweizer	*P. m*
4930546C10Rik	Balderrama	*M.m*	Pfkfb3	Balderrama	*M.m*	Plaur	Balderrama	*P.l*	LOC102916097	Schweizer	*P. m*
4930580E04Rik	Balderrama	*M.m*	Pglyrp3	Balderrama	*M.m*	Plekhs1	Balderrama	*P.l*	LOC102916219	Schweizer	*P. m*
4930599N23Rik	Balderrama	*M.m*	Phf11a	Balderrama	*M.m*	Pml	Balderrama	*P.l*	LOC102916229	Schweizer	*P. m*
4933409D19Rik	Balderrama	*M.m*	Phf11b	Balderrama	*M.m*	Pnoc	Balderrama	*P.l*	LOC102916294	Schweizer	*P. m*
4933421A08Rik	Balderrama	*M.m*	Phf11c	Balderrama	*M.m*	Pnp	Balderrama	*P.l*	LOC102916391	Schweizer	*P. m*
4933432I03Rik	Balderrama	*M.m*	Phf11d	Balderrama	*M.m*	Ppa1	Balderrama	*P.l*	LOC102916413	Schweizer	*P. m*
8030451A03Rik	Balderrama	*M.m*	Phox2a	Balderrama	*M.m*	Ppfia2	Balderrama	*P.l*	LOC102916444	Schweizer	*P. m*
9130230L23Rik	Balderrama	*M.m*	Pik3ap1	Balderrama	*M.m*	Prrg4	Balderrama	*P.l*	LOC102916678	Schweizer	*P. m*
9230110F11Rik	Balderrama	*M.m*	Pkib	Balderrama	*M.m*	Prss37	Balderrama	*P.l*	LOC102916719	Schweizer	*P. m*
A230028O05Rik	Balderrama	*M.m*	Pkp1	Balderrama	*M.m*	Prune2	Balderrama	*P.l*	LOC102916932	Schweizer	*P. m*
A330040F15Rik	Balderrama	*M.m*	Plagl1	Balderrama	*M.m*	Pstpip2	Balderrama	*P.l*	LOC102916970	Schweizer	*P. m*
A3galt2	Balderrama	*M.m*	Plat	Balderrama	*M.m*	Ptpn13	Balderrama	*P.l*	LOC102917074	Schweizer	*P. m*
A430028G04Rik	Balderrama	*M.m*	Platr23	Balderrama	*M.m*	Rab32	Balderrama	*P.l*	LOC102917265	Schweizer	*P. m*
A530046M15Rik	Balderrama	*M.m*	Plet1	Balderrama	*M.m*	Rars	Balderrama	*P.l*	LOC102917596	Schweizer	*P. m*
A630012P03Rik	Balderrama	*M.m*	Plk2	Balderrama	*M.m*	Rasl11b	Balderrama	*P.l*	LOC102917650	Schweizer	*P. m*
A730049H05Rik	Balderrama	*M.m*	Pln	Balderrama	*M.m*	Rassf4	Balderrama	*P.l*	LOC102917876	Schweizer	*P. m*
A930024N18Rik	Balderrama	*M.m*	Plscr1	Balderrama	*M.m*	Rec8	Balderrama	*P.l*	LOC102917904	Schweizer	*P. m*
A930037H05Rik	Balderrama	*M.m*	Pmepa1	Balderrama	*M.m*	Rgs1	Balderrama	*P.l*	LOC102917993	Schweizer	*P. m*
AA467197	Balderrama	*M.m*	Pnp2	Balderrama	*M.m*	Rnase10	Balderrama	*P.l*	LOC102918038	Schweizer	*P. m*
Abtb2	Balderrama	*M.m*	Pnpla1os	Balderrama	*M.m*	Rnf19b	Balderrama	*P.l*	LOC102918218	Schweizer	*P. m*
AC118695.1	Balderrama	*M.m*	Pnpt1	Balderrama	*M.m*	Rnf213	Balderrama	*P.l*	LOC102918219	Schweizer	*P. m*

AC119228.1	Balderrama	*M.m*	Pom121l2	Balderrama	*M.m*	Rtp3	Balderrama	*P.l*	LOC102918499	Schweizer	*P. m*
AC124231.3	Balderrama	*M.m*	Ppfia3	Balderrama	*M.m*	Rtp4	Balderrama	*P.l*	LOC102918677	Schweizer	*P. m*
AC132253.2	Balderrama	*M.m*	Prdx6b	Balderrama	*M.m*	S100a9	Balderrama	*P.l*	LOC102918796	Schweizer	*P. m*
AC147026.1	Balderrama	*M.m*	Prl7d1	Balderrama	*M.m*	Scg2	Balderrama	*P.l*	LOC102918868	Schweizer	*P. m*
AC157784.1	Balderrama	*M.m*	Prm1	Balderrama	*M.m*	Sdc1	Balderrama	*P.l*	LOC102919113	Schweizer	*P. m*
AC160336.1	Balderrama	*M.m*	Prok2	Balderrama	*M.m*	Sds	Balderrama	*P.l*	LOC102919204	Schweizer	*P. m*
AC161438.1	Balderrama	*M.m*	Prr30	Balderrama	*M.m*	Sele	Balderrama	*P.l*	LOC102919257	Schweizer	*P. m*
AC165153.1	Balderrama	*M.m*	Prss23	Balderrama	*M.m*	Selp	Balderrama	*P.l*	LOC102919359	Schweizer	*P. m*
AC167363.2	Balderrama	*M.m*	Prss23os	Balderrama	*M.m*	Sema3a	Balderrama	*P.l*	LOC102919750	Schweizer	*P. m*
Acot4	Balderrama	*M.m*	Psg22	Balderrama	*M.m*	Septin5	Balderrama	*P.l*	LOC102920059	Schweizer	*P. m*
Acta1	Balderrama	*M.m*	Ptgs2	Balderrama	*M.m*	Serpine1	Balderrama	*P.l*	LOC102920188	Schweizer	*P. m*
Adam3	Balderrama	*M.m*	Ptprh	Balderrama	*M.m*	Sgms2	Balderrama	*P.l*	LOC102920196	Schweizer	*P. m*
Adam32	Balderrama	*M.m*	Ptx3	Balderrama	*M.m*	Shox2	Balderrama	*P.l*	LOC102920371	Schweizer	*P. m*
Adamts9	Balderrama	*M.m*	Qrfpr	Balderrama	*M.m*	Sim2	Balderrama	*P.l*	LOC102920506	Schweizer	*P. m*
Adar	Balderrama	*M.m*	Qrich2	Balderrama	*M.m*	Slamf1	Balderrama	*P.l*	LOC102920548	Schweizer	*P. m*
Adgrf2	Balderrama	*M.m*	Rasef	Balderrama	*M.m*	Slamf9	Balderrama	*P.l*	LOC102920571	Schweizer	*P. m*
Adgrg7	Balderrama	*M.m*	Rbm11	Balderrama	*M.m*	Slc15a3	Balderrama	*P.l*	LOC102920647	Schweizer	*P. m*
Adora2b	Balderrama	*M.m*	Reg3g	Balderrama	*M.m*	Slc16a14	Balderrama	*P.l*	LOC102920693	Schweizer	*P. m*
Agrn	Balderrama	*M.m*	Rgs16	Balderrama	*M.m*	Slc28a2	Balderrama	*P.l*	LOC102920805	Schweizer	*P. m*
Ak4	Balderrama	*M.m*	Rhob	Balderrama	*M.m*	Slc28a3	Balderrama	*P.l*	LOC102920815	Schweizer	*P. m*
Akap12	Balderrama	*M.m*	Rhoc	Balderrama	*M.m*	Slc2a6	Balderrama	*P.l*	LOC102920988	Schweizer	*P. m*
Akap2	Balderrama	*M.m*	Rhou	Balderrama	*M.m*	Slc30a1	Balderrama	*P.l*	LOC102921127	Schweizer	*P. m*
Alkal2	Balderrama	*M.m*	Rhov	Balderrama	*M.m*	Slc9a2	Balderrama	*P.l*	LOC102921168	Schweizer	*P. m*
Ank2	Balderrama	*M.m*	Rnd1	Balderrama	*M.m*	Slfn14	Balderrama	*P.l*	LOC102921183	Schweizer	*P. m*
Ankrd66	Balderrama	*M.m*	Rprml	Balderrama	*M.m*	Slpi	Balderrama	*P.l*	LOC102921292	Schweizer	*P. m*
Apol9a	Balderrama	*M.m*	Rtn4rl2	Balderrama	*M.m*	Smtnl1	Balderrama	*P.l*	LOC102921874	Schweizer	*P. m*
Apol9b	Balderrama	*M.m*	Saa1	Balderrama	*M.m*	Socs1	Balderrama	*P.l*	LOC102921878	Schweizer	*P. m*

Areg	Balderrama	*M.m*	Saa2	Balderrama	*M.m*	Socs3	Balderrama	*P.l*	LOC102922071	Schweizer	*P. m*
Arsj	Balderrama	*M.m*	Saa3	Balderrama	*M.m*	Sod2	Balderrama	*P.l*	LOC102922475	Schweizer	*P. m*
Asap3	Balderrama	*M.m*	Samd9l	Balderrama	*M.m*	Sphk1	Balderrama	*P.l*	LOC102922490	Schweizer	*P. m*
Asb13	Balderrama	*M.m*	Samhd1	Balderrama	*M.m*	Srgn	Balderrama	*P.l*	LOC102922517	Schweizer	*P. m*
Asb5	Balderrama	*M.m*	Sct	Balderrama	*M.m*	Srxn1	Balderrama	*P.l*	LOC102922543	Schweizer	*P. m*
Ascc3	Balderrama	*M.m*	Sdc4	Balderrama	*M.m*	Steap2	Balderrama	*P.l*	LOC102922568	Schweizer	*P. m*
Astl	Balderrama	*M.m*	Sema4c	Balderrama	*M.m*	Stra6	Balderrama	*P.l*	LOC102922906	Schweizer	*P. m*
Atf3	Balderrama	*M.m*	Serpina3b	Balderrama	*M.m*	Stx11	Balderrama	*P.l*	LOC102922983	Schweizer	*P. m*
Atp10a	Balderrama	*M.m*	Serpina3c	Balderrama	*M.m*	Sytl3	Balderrama	*P.l*	LOC102923286	Schweizer	*P. m*
Avpr1a	Balderrama	*M.m*	Serpina3f	Balderrama	*M.m*	Tanc1	Balderrama	*P.l*	LOC102923362	Schweizer	*P. m*
AW011738	Balderrama	*M.m*	Serpina3g	Balderrama	*M.m*	Tap1	Balderrama	*P.l*	LOC102923471	Schweizer	*P. m*
AW047730	Balderrama	*M.m*	Serpina3i	Balderrama	*M.m*	Tfec	Balderrama	*P.l*	LOC102923525	Schweizer	*P. m*
AW112010	Balderrama	*M.m*	Serpina3n	Balderrama	*M.m*	Tfpi	Balderrama	*P.l*	LOC102923679	Schweizer	*P. m*
AY761185	Balderrama	*M.m*	Serpinb5	Balderrama	*M.m*	Tgm1	Balderrama	*P.l*	LOC102923707	Schweizer	*P. m*
B3gnt7	Balderrama	*M.m*	Setdb2	Balderrama	*M.m*	Tgm6	Balderrama	*P.l*	LOC102924224	Schweizer	*P. m*
B4galt5	Balderrama	*M.m*	Sh3pxd2b	Balderrama	*M.m*	Thbs1	Balderrama	*P.l*	LOC102924536	Schweizer	*P. m*
Barx2	Balderrama	*M.m*	Six3os1	Balderrama	*M.m*	Timp1	Balderrama	*P.l*	LOC102924668	Schweizer	*P. m*
Batf	Balderrama	*M.m*	Skor1	Balderrama	*M.m*	Tlr2	Balderrama	*P.l*	LOC102924700	Schweizer	*P. m*
Batf2	Balderrama	*M.m*	Slc10a6	Balderrama	*M.m*	Tmcc2	Balderrama	*P.l*	LOC102924798	Schweizer	*P. m*
Bbx	Balderrama	*M.m*	Slc25a22	Balderrama	*M.m*	Tmprss13	Balderrama	*P.l*	LOC102924848	Schweizer	*P. m*
BC026762	Balderrama	*M.m*	Slc26a4	Balderrama	*M.m*	Tnc	Balderrama	*P.l*	LOC102924917	Schweizer	*P. m*
BC035947	Balderrama	*M.m*	Slc26a9	Balderrama	*M.m*	Tnf	Balderrama	*P.l*	LOC102924933	Schweizer	*P. m*
BC147527	Balderrama	*M.m*	Slc39a14	Balderrama	*M.m*	Tnfaip2	Balderrama	*P.l*	LOC102925027	Schweizer	*P. m*
Bcl2a1a	Balderrama	*M.m*	Slc4a4	Balderrama	*M.m*	Tnfaip3	Balderrama	*P.l*	LOC102925569	Schweizer	*P. m*
Bcl2a1b	Balderrama	*M.m*	Slc6a14	Balderrama	*M.m*	Tnfaip6	Balderrama	*P.l*	LOC102925729	Schweizer	*P. m*
Bcl2a1d	Balderrama	*M.m*	Slc9a4	Balderrama	*M.m*	Tnfrsf12a	Balderrama	*P.l*	LOC102925951	Schweizer	*P. m*
Bcl2l14	Balderrama	*M.m*	Slfn1	Balderrama	*M.m*	Tnfsf18	Balderrama	*P.l*	LOC102926234	Schweizer	*P. m*

Bcl3	Balderrama	*M.m*	Slfn2	Balderrama	*M.m*	Tnip1	Balderrama	*P.l*	LOC102926342	Schweizer	*P. m*
Bdkrb1	Balderrama	*M.m*	Slfn4	Balderrama	*M.m*	Tnip3	Balderrama	*P.l*	LOC102926469	Schweizer	*P. m*
Bean1	Balderrama	*M.m*	Slfn5	Balderrama	*M.m*	Tph1	Balderrama	*P.l*	LOC102926599	Schweizer	*P. m*
Bmp10	Balderrama	*M.m*	Slfn5os	Balderrama	*M.m*	Trim10	Balderrama	*P.l*	LOC102926603	Schweizer	*P. m*
Bst2	Balderrama	*M.m*	Slfn8	Balderrama	*M.m*	Trim16	Balderrama	*P.l*	LOC102926642	Schweizer	*P. m*
Btbd16	Balderrama	*M.m*	Slfn9	Balderrama	*M.m*	Trim54	Balderrama	*P.l*	LOC102926817	Schweizer	*P. m*
C230029F24Rik	Balderrama	*M.m*	Slit1	Balderrama	*M.m*	Trim69	Balderrama	*P.l*	LOC102926827	Schweizer	*P. m*
C2cd4b	Balderrama	*M.m*	Slmapos2	Balderrama	*M.m*	Tubb6	Balderrama	*P.l*	LOC102926846	Schweizer	*P. m*
Calca	Balderrama	*M.m*	Smpdl3b	Balderrama	*M.m*	Uba7	Balderrama	*P.l*	LOC102926876	Schweizer	*P. m*
Calhm6	Balderrama	*M.m*	Snx10	Balderrama	*M.m*	Ubd	Balderrama	*P.l*	LOC102926914	Schweizer	*P. m*
Car13	Balderrama	*M.m*	Sox30	Balderrama	*M.m*	Ube2l6	Balderrama	*P.l*	LOC102926916	Schweizer	*P. m*
Car4	Balderrama	*M.m*	Sp100	Balderrama	*M.m*	Unc45b	Balderrama	*P.l*	LOC102926946	Schweizer	*P. m*
Casp4	Balderrama	*M.m*	Sp110	Balderrama	*M.m*	Upp1	Balderrama	*P.l*	LOC102927177	Schweizer	*P. m*
Casr	Balderrama	*M.m*	Spag17os	Balderrama	*M.m*	Usp18	Balderrama	*P.l*	LOC102927215	Schweizer	*P. m*
Ccdc33	Balderrama	*M.m*	Spata31d1b	Balderrama	*M.m*	Vcan	Balderrama	*P.l*	LOC102927216	Schweizer	*P. m*
Ccin	Balderrama	*M.m*	Spdef	Balderrama	*M.m*	Vgf	Balderrama	*P.l*	LOC102927249	Schweizer	*P. m*
Ccl11	Balderrama	*M.m*	Speer4b	Balderrama	*M.m*	Wars	Balderrama	*P.l*	LOC102927285	Schweizer	*P. m*
Ccl12	Balderrama	*M.m*	Spem1	Balderrama	*M.m*	Wnt3	Balderrama	*P.l*	LOC102927424	Schweizer	*P. m*
Ccl17	Balderrama	*M.m*	Spp1	Balderrama	*M.m*	Xaf1	Balderrama	*P.l*	LOC102927726	Schweizer	*P. m*
Ccl2	Balderrama	*M.m*	Sprr1a	Balderrama	*M.m*	Xdh	Balderrama	*P.l*	LOC102927860	Schweizer	*P. m*
Ccl20	Balderrama	*M.m*	Spry4	Balderrama	*M.m*	Zar1	Balderrama	*P.l*	LOC102928024	Schweizer	*P. m*
Ccl3	Balderrama	*M.m*	Stat1	Balderrama	*M.m*	Zc3h12a	Balderrama	*P.l*	LOC102928062	Schweizer	*P. m*
Ccl4	Balderrama	*M.m*	Stat2	Balderrama	*M.m*	Zdhhc2	Balderrama	*P.l*	LOC102928123	Schweizer	*P. m*
Ccl7	Balderrama	*M.m*	Stc1	Balderrama	*M.m*	Zmat1	Balderrama	*P.l*	LOC102928318	Schweizer	*P. m*
Ccn1	Balderrama	*M.m*	Steap1	Balderrama	*M.m*	March6	Schweizer	*P.m*	LOC102928385	Schweizer	*P. m*
Cd69	Balderrama	*M.m*	Steap4	Balderrama	*M.m*	March9	Schweizer	*P.m*	LOC102928410	Schweizer	*P. m*
Cd70	Balderrama	*M.m*	Stfa2	Balderrama	*M.m*	A1bg	Schweizer	*P.m*	LOC102928660	Schweizer	*P. m*

Cd80	Balderrama	*M.m*	Sult6b1	Balderrama	*M.m*	Abcc2	Schweizer	*P.m*	LOC102928670	Schweizer	*P. m*
Cdh15	Balderrama	*M.m*	Sycp2l	Balderrama	*M.m*	Abhd18	Schweizer	*P.m*	LOC102928879	Schweizer	*P. m*
Cdh17	Balderrama	*M.m*	Sycp3	Balderrama	*M.m*	Abhd3	Schweizer	*P.m*	LOC102928913	Schweizer	*P. m*
Cdh6	Balderrama	*M.m*	Tac1	Balderrama	*M.m*	Abhd6	Schweizer	*P.m*	LOC102928917	Schweizer	*P. m*
Cdhr5	Balderrama	*M.m*	Tarm1	Balderrama	*M.m*	Acad8	Schweizer	*P.m*	LOC107399310	Schweizer	*P. m*
Cdx4	Balderrama	*M.m*	Tcam1	Balderrama	*M.m*	Acox2	Schweizer	*P.m*	LOC107400260	Schweizer	*P. m*
Cfap69	Balderrama	*M.m*	Tcp10b	Balderrama	*M.m*	Actl6a	Schweizer	*P.m*	LOC107400365	Schweizer	*P. m*
Ch25h	Balderrama	*M.m*	Tdrd7	Balderrama	*M.m*	Actrt3	Schweizer	*P.m*	LOC107400753	Schweizer	*P. m*
Chil1	Balderrama	*M.m*	Tent4a	Balderrama	*M.m*	Adamts15	Schweizer	*P.m*	LOC107401125	Schweizer	*P. m*
Chl1	Balderrama	*M.m*	Tex12	Balderrama	*M.m*	Adamts8	Schweizer	*P.m*	LOC107401168	Schweizer	*P. m*
Chrdl2	Balderrama	*M.m*	Tgtp1	Balderrama	*M.m*	Adcy8	Schweizer	*P.m*	LOC107401289	Schweizer	*P. m*
Chrm4	Balderrama	*M.m*	Tgtp2	Balderrama	*M.m*	Adgrf4	Schweizer	*P.m*	LOC107401295	Schweizer	*P. m*
Clec2e	Balderrama	*M.m*	Tktl1	Balderrama	*M.m*	Adgrf5	Schweizer	*P.m*	LOC107401301	Schweizer	*P. m*
Clec4d	Balderrama	*M.m*	Tlr3	Balderrama	*M.m*	Adgrg4	Schweizer	*P.m*	LOC107401388	Schweizer	*P. m*
Clic4	Balderrama	*M.m*	Tlr7	Balderrama	*M.m*	Aff2	Schweizer	*P.m*	LOC107401777	Schweizer	*P. m*
Cnksr1	Balderrama	*M.m*	Tmem100	Balderrama	*M.m*	Agap2	Schweizer	*P.m*	LOC107401828	Schweizer	*P. m*
Creb3l1	Balderrama	*M.m*	Tmem132e	Balderrama	*M.m*	Agtr1	Schweizer	*P.m*	LOC107401851	Schweizer	*P. m*
Creb5	Balderrama	*M.m*	Tmem171	Balderrama	*M.m*	Alg5	Schweizer	*P.m*	LOC107402053	Schweizer	*P. m*
Crem	Balderrama	*M.m*	Tmem184b	Balderrama	*M.m*	Alkbh8	Schweizer	*P.m*	LOC107402055	Schweizer	*P. m*
Crybb3	Balderrama	*M.m*	Tmem266	Balderrama	*M.m*	Alms1	Schweizer	*P.m*	LOC107402495	Schweizer	*P. m*
CT009580.1	Balderrama	*M.m*	Tmprss2	Balderrama	*M.m*	Angel2	Schweizer	*P.m*	LOC107402497	Schweizer	*P. m*
Cxcl1	Balderrama	*M.m*	Tnfaip8l3	Balderrama	*M.m*	Angpt1	Schweizer	*P.m*	LOC107402634	Schweizer	*P. m*
Cxcl2	Balderrama	*M.m*	Tnfrsf9	Balderrama	*M.m*	Ankrd13c	Schweizer	*P.m*	LOC107402972	Schweizer	*P. m*
Cxcl3	Balderrama	*M.m*	Tnfsf15	Balderrama	*M.m*	Ankrd50	Schweizer	*P.m*	LOC107402977	Schweizer	*P. m*
Cxcl9	Balderrama	*M.m*	Tnfsf9	Balderrama	*M.m*	Ankrd52	Schweizer	*P.m*	LOC107403033	Schweizer	*P. m*
Cybb	Balderrama	*M.m*	Tnp2	Balderrama	*M.m*	Ankrd60	Schweizer	*P.m*	Lrfn2	Schweizer	*P. m*
D030024E09Rik	Balderrama	*M.m*	Tor1aip2	Balderrama	*M.m*	Anln	Schweizer	*P.m*	Lrig3	Schweizer	*P. m*

D430020J02Rik	Balderrama	*M.m*	Tor3a	Balderrama	*M.m*	Antxr1	Schweizer	*P.m*	Lrp1	Schweizer	*P. m*
D530033B14Rik	Balderrama	*M.m*	Trafd1	Balderrama	*M.m*	Anxa4	Schweizer	*P.m*	Lrrc31	Schweizer	*P. m*
D6Ertd474e	Balderrama	*M.m*	Trem1	Balderrama	*M.m*	Anxa5	Schweizer	*P.m*	Lrrc34	Schweizer	*P. m*
Daxx	Balderrama	*M.m*	Trex1	Balderrama	*M.m*	Anxa7	Schweizer	*P.m*	Lrrc7	Schweizer	*P. m*
Dbx2	Balderrama	*M.m*	Trim21	Balderrama	*M.m*	Ap3m1	Schweizer	*P.m*	Lrrcc1	Schweizer	*P. m*
Ddn	Balderrama	*M.m*	Trim30a	Balderrama	*M.m*	Apbb3	Schweizer	*P.m*	Lrrd1	Schweizer	*P. m*
Ddx60	Balderrama	*M.m*	Trim30b	Balderrama	*M.m*	Aplp2	Schweizer	*P.m*	Lrrtm2	Schweizer	*P. m*
Defb33	Balderrama	*M.m*	Trim30c	Balderrama	*M.m*	Arcn1	Schweizer	*P.m*	Lypd8	Schweizer	*P. m*
Dgkh	Balderrama	*M.m*	Trim30d	Balderrama	*M.m*	Arhgap32	Schweizer	*P.m*	Lztfl1	Schweizer	*P. m*
Dll4	Balderrama	*M.m*	Trim34a	Balderrama	*M.m*	Arhgap42	Schweizer	*P.m*	Mab21l1	Schweizer	*P. m*
Dmkn	Balderrama	*M.m*	Trim34b	Balderrama	*M.m*	Arhgap9	Schweizer	*P.m*	Maml2	Schweizer	*P. m*
Dnase2b	Balderrama	*M.m*	Trpm6	Balderrama	*M.m*	Arhgef12	Schweizer	*P.m*	Maml3	Schweizer	*P. m*
Drd5	Balderrama	*M.m*	Tsx	Balderrama	*M.m*	Arhgef26	Schweizer	*P.m*	Map3k2	Schweizer	*P. m*
Dthd1	Balderrama	*M.m*	U90926	Balderrama	*M.m*	Armc1	Schweizer	*P.m*	Mars	Schweizer	*P. m*
Duoxa2	Balderrama	*M.m*	Ube2ql1	Balderrama	*M.m*	As3mt	Schweizer	*P.m*	Mast4	Schweizer	*P. m*
Dusp16	Balderrama	*M.m*	Unc93a	Balderrama	*M.m*	Asb15	Schweizer	*P.m*	Matn2	Schweizer	*P. m*
Dusp2	Balderrama	*M.m*	Vash1	Balderrama	*M.m*	Asb3	Schweizer	*P.m*	Mbd6	Schweizer	*P. m*
Dusp5	Balderrama	*M.m*	Vdr	Balderrama	*M.m*	Asb4	Schweizer	*P.m*	Mbnl1	Schweizer	*P. m*
E230025N22Rik	Balderrama	*M.m*	Vmn1r76	Balderrama	*M.m*	Ash1l	Schweizer	*P.m*	Mboat2	Schweizer	*P. m*
Ebi3	Balderrama	*M.m*	Vmn2r11	Balderrama	*M.m*	Asxl3	Schweizer	*P.m*	Mc3r	Schweizer	*P. m*
Efcab3	Balderrama	*M.m*	Vmn2r16	Balderrama	*M.m*	Atad2	Schweizer	*P.m*	Mcam	Schweizer	*P. m*
Ehf	Balderrama	*M.m*	Vnn3	Balderrama	*M.m*	Atp11b	Schweizer	*P.m*	Mdm1	Schweizer	*P. m*
Eif2c5	Balderrama	*M.m*	Vwa3b	Balderrama	*M.m*	Atp5b	Schweizer	*P.m*	Mea1	Schweizer	*P. m*
Elovl4	Balderrama	*M.m*	Wfdc17	Balderrama	*M.m*	Atp6ap1	Schweizer	*P.m*	Mecom	Schweizer	*P. m*
En2	Balderrama	*M.m*	Wfdc18	Balderrama	*M.m*	Atp6v0a1	Schweizer	*P.m*	Med12l	Schweizer	*P. m*
Epgn	Balderrama	*M.m*	Wif1	Balderrama	*M.m*	Atp6v0d1	Schweizer	*P.m*	Med20	Schweizer	*P. m*
Epsti1	Balderrama	*M.m*	Zbp1	Balderrama	*M.m*	Avil	Schweizer	*P.m*	Mef2c	Schweizer	*P. m*

Ereg	Balderrama	*M.m*	Zcchc2	Balderrama	*M.m*	Azin1	Schweizer	*P.m*	Megf8	Schweizer	*P. m*
Errfi1	Balderrama	*M.m*	Zfp365	Balderrama	*M.m*	B3gnt9	Schweizer	*P.m*	Mfn1	Schweizer	*P. m*
F830016B08Rik	Balderrama	*M.m*	Zup1	Balderrama	*M.m*	B4galnt1	Schweizer	*P.m*	Mfrp	Schweizer	*P. m*
F830208F22Rik	Balderrama	*M.m*	Ackr1	Balderrama	*P.l*	B4galt6	Schweizer	*P.m*	Mfsd8	Schweizer	*P. m*
Fam110c	Balderrama	*M.m*	Acod1	Balderrama	*P.l*	Baalc	Schweizer	*P.m*	Mgarp	Schweizer	*P. m*
Fam129b	Balderrama	*M.m*	Adamts1	Balderrama	*P.l*	Baz2a	Schweizer	*P.m*	Mib1	Schweizer	*P. m*
Fam25c	Balderrama	*M.m*	Adamts4	Balderrama	*P.l*	Bbs12	Schweizer	*P.m*	Mkrn3	Schweizer	*P. m*
Fam69c	Balderrama	*M.m*	Adm	Balderrama	*P.l*	Bbs9	Schweizer	*P.m*	Mme	Schweizer	*P. m*
Fam83c	Balderrama	*M.m*	Adora2a	Balderrama	*P.l*	Bcl9l	Schweizer	*P.m*	Mmp10	Schweizer	*P. m*
Fap	Balderrama	*M.m*	Agpat4	Balderrama	*P.l*	Bend6	Schweizer	*P.m*	Mmp12	Schweizer	*P. m*
Fcgr4	Balderrama	*M.m*	Aipl1	Balderrama	*P.l*	Birc2	Schweizer	*P.m*	Mon2	Schweizer	*P. m*
Fgf23	Balderrama	*M.m*	Aldh1a2	Balderrama	*P.l*	Blcap	Schweizer	*P.m*	Morc3	Schweizer	*P. m*
Fgf6	Balderrama	*M.m*	Alpk1	Balderrama	*P.l*	Bmper	Schweizer	*P.m*	Mrpl2	Schweizer	*P. m*
Fkbp6	Balderrama	*M.m*	Ankrd1	Balderrama	*P.l*	Brwd1	Schweizer	*P.m*	Mrpl47	Schweizer	*P. m*
Fos	Balderrama	*M.m*	Ankrd2	Balderrama	*P.l*	Bsg	Schweizer	*P.m*	Msh6	Schweizer	*P. m*
Fosl1	Balderrama	*M.m*	Ano2	Balderrama	*P.l*	Bud13	Schweizer	*P.m*	Msrb3	Schweizer	*P. m*
Fosl2	Balderrama	*M.m*	Anxa10	Balderrama	*P.l*	C1qtnf5	Schweizer	*P.m*	Mss51	Schweizer	*P. m*
Foxc2	Balderrama	*M.m*	Anxa2r	Balderrama	*P.l*	C2cd2l	Schweizer	*P.m*	Mtbp	Schweizer	*P. m*
Foxj1	Balderrama	*M.m*	Aoah	Balderrama	*P.l*	Cacna1c	Schweizer	*P.m*	Mtdh	Schweizer	*P. m*
Garem2	Balderrama	*M.m*	Apobec1	Balderrama	*P.l*	Cacna2d1	Schweizer	*P.m*	Mtmr2	Schweizer	*P. m*
Gbp10	Balderrama	*M.m*	Apold1	Balderrama	*P.l*	Cacul1	Schweizer	*P.m*	Mto1	Schweizer	*P. m*
Gbp11	Balderrama	*M.m*	Arg1	Balderrama	*P.l*	Cadm1	Schweizer	*P.m*	Mtss1	Schweizer	*P. m*
Gbp2	Balderrama	*M.m*	Arid5a	Balderrama	*P.l*	Cadps2	Schweizer	*P.m*	Myc	Schweizer	*P. m*
Gbp2b	Balderrama	*M.m*	Arl5c	Balderrama	*P.l*	Camk4	Schweizer	*P.m*	Mycbp2	Schweizer	*P. m*
Gbp3	Balderrama	*M.m*	Bst1	Balderrama	*P.l*	Cand1	Schweizer	*P.m*	Mycn	Schweizer	*P. m*
Gbp4	Balderrama	*M.m*	Btnl2	Balderrama	*P.l*	Casd1	Schweizer	*P.m*	Mynn	Schweizer	*P. m*
Gbp5	Balderrama	*M.m*	C1rl	Balderrama	*P.l*	Casp1	Schweizer	*P.m*	Myo7b	Schweizer	*P. m*

Gbp6	Balderrama	*M.m*	Ca4	Balderrama	*P.l*	Cbfb	Schweizer	*P.m*	Myoz1	Schweizer	*P. m*
Gbp7	Balderrama	*M.m*	Camk2b	Balderrama	*P.l*	Cbl	Schweizer	*P.m*	N4bp2l2	Schweizer	*P. m*
Gbp9	Balderrama	*M.m*	Cartpt	Balderrama	*P.l*	Cbln4	Schweizer	*P.m*	Naa15	Schweizer	*P. m*
Gdap10	Balderrama	*M.m*	Ccl22	Balderrama	*P.l*	Ccdc15	Schweizer	*P.m*	Naaladl2	Schweizer	*P. m*
Gdf15	Balderrama	*M.m*	Ccl5	Balderrama	*P.l*	Ccdc151	Schweizer	*P.m*	Nab2	Schweizer	*P. m*
Gm10309	Balderrama	*M.m*	Ccn4	Balderrama	*P.l*	Ccdc18	Schweizer	*P.m*	Naca	Schweizer	*P. m*
Gm10851	Balderrama	*M.m*	Ccnb1ip1	Balderrama	*P.l*	Ccna1	Schweizer	*P.m*	Nbea	Schweizer	*P. m*
Gm11626	Balderrama	*M.m*	Ccr8	Balderrama	*P.l*	Ccna2	Schweizer	*P.m*	Nbeal1	Schweizer	*P. m*
Gm11722	Balderrama	*M.m*	Ccrl2	Balderrama	*P.l*	Cd180	Schweizer	*P.m*	Ncald	Schweizer	*P. m*
Gm11772	Balderrama	*M.m*	Cd14	Balderrama	*P.l*	Cdh16	Schweizer	*P.m*	Ncam1	Schweizer	*P. m*
Gm11795	Balderrama	*M.m*	Cd274	Balderrama	*P.l*	Cdh2	Schweizer	*P.m*	Ncapd3	Schweizer	*P. m*
Gm12065	Balderrama	*M.m*	Cd40	Balderrama	*P.l*	Cdh20	Schweizer	*P.m*	Nceh1	Schweizer	*P. m*
Gm12185	Balderrama	*M.m*	Cd44	Balderrama	*P.l*	Cdh7	Schweizer	*P.m*	Ndn	Schweizer	*P. m*
Gm12253	Balderrama	*M.m*	Cdkn1a	Balderrama	*P.l*	Cdk2	Schweizer	*P.m*	Ndufa4l2	Schweizer	*P. m*
Gm12356	Balderrama	*M.m*	Cebpb	Balderrama	*P.l*	Cdk8	Schweizer	*P.m*	Ndufa5	Schweizer	*P. m*
Gm12480	Balderrama	*M.m*	Cebpd	Balderrama	*P.l*	Cdon	Schweizer	*P.m*	Ndufb5	Schweizer	*P. m*
Gm12505	Balderrama	*M.m*	Cemip2	Balderrama	*P.l*	Cep126	Schweizer	*P.m*	Ndufc1	Schweizer	*P. m*
Gm12534	Balderrama	*M.m*	Cfap161	Balderrama	*P.l*	Cep162	Schweizer	*P.m*	Nectin1	Schweizer	*P. m*
Gm12606	Balderrama	*M.m*	Cfb	Balderrama	*P.l*	Cep57	Schweizer	*P.m*	Nelfcd	Schweizer	*P. m*
Gm12764	Balderrama	*M.m*	Cflar	Balderrama	*P.l*	Ces3	Schweizer	*P.m*	Nemp1	Schweizer	*P. m*
Gm12840	Balderrama	*M.m*	Cgas	Balderrama	*P.l*	Cetn1	Schweizer	*P.m*	Nfatc2	Schweizer	*P. m*
Gm13067	Balderrama	*M.m*	Chi3l1	Balderrama	*P.l*	Cfap43	Schweizer	*P.m*	Nfya	Schweizer	*P. m*
Gm13074	Balderrama	*M.m*	Chp2	Balderrama	*P.l*	Cfap70	Schweizer	*P.m*	Ngef	Schweizer	*P. m*
Gm13264	Balderrama	*M.m*	Chrna2	Balderrama	*P.l*	Chek1	Schweizer	*P.m*	Nhlrc3	Schweizer	*P. m*
Gm13305	Balderrama	*M.m*	Cldn1	Balderrama	*P.l*	Chordc1	Schweizer	*P.m*	Nhsl2	Schweizer	*P. m*
Gm13481	Balderrama	*M.m*	Cldn24	Balderrama	*P.l*	Cirbp	Schweizer	*P.m*	Nid2	Schweizer	*P. m*
Gm13822	Balderrama	*M.m*	Clec4e	Balderrama	*P.l*	Cldn11	Schweizer	*P.m*	Nin	Schweizer	*P. m*

Gm13889	Balderrama	*M.m*	Clstn3	Balderrama	*P.l*	Clec16a	Schweizer	*P.m*	Nipal2	Schweizer	*P. m*
Gm14236	Balderrama	*M.m*	Cmpk2	Balderrama	*P.l*	Clmp	Schweizer	*P.m*	Nlgn1	Schweizer	*P. m*
Gm14280	Balderrama	*M.m*	Cnga1	Balderrama	*P.l*	Clnk	Schweizer	*P.m*	Nlrx1	Schweizer	*P. m*
Gm15056	Balderrama	*M.m*	Cngb3	Balderrama	*P.l*	Clrn1	Schweizer	*P.m*	Nnat	Schweizer	*P. m*
Gm15133	Balderrama	*M.m*	Cntfr	Balderrama	*P.l*	Cmtm4	Schweizer	*P.m*	Noct	Schweizer	*P. m*
Gm15241	Balderrama	*M.m*	Col6a5	Balderrama	*P.l*	Cntn5	Schweizer	*P.m*	Nol3	Schweizer	*P. m*
Gm15283	Balderrama	*M.m*	Crispld2	Balderrama	*P.l*	Col12a1	Schweizer	*P.m*	Nol4	Schweizer	*P. m*
Gm15287	Balderrama	*M.m*	Crnn	Balderrama	*P.l*	Col14a1	Schweizer	*P.m*	Nov	Schweizer	*P. m*
Gm15323	Balderrama	*M.m*	Csf2	Balderrama	*P.l*	Col1a2	Schweizer	*P.m*	Nox4	Schweizer	*P. m*
Gm15340	Balderrama	*M.m*	Csf3	Balderrama	*P.l*	Col5a3	Schweizer	*P.m*	Npepl1	Schweizer	*P. m*
Gm15418	Balderrama	*M.m*	Csrnp1	Balderrama	*P.l*	Col9a1	Schweizer	*P.m*	Nr3c1	Schweizer	*P. m*
Gm15512	Balderrama	*M.m*	Csrp3	Balderrama	*P.l*	Colec10	Schweizer	*P.m*	Nrep	Schweizer	*P. m*
Gm1559	Balderrama	*M.m*	Cst7	Balderrama	*P.l*	Colec12	Schweizer	*P.m*	Nsmaf	Schweizer	*P. m*
Gm15684	Balderrama	*M.m*	CUNH11orf91	Balderrama	*P.l*	Coq10a	Schweizer	*P.m*	Nsmce2	Schweizer	*P. m*
Gm15701	Balderrama	*M.m*	CUNH15orf48	Balderrama	*P.l*	Cpa3	Schweizer	*P.m*	Ntm	Schweizer	*P. m*
Gm15734	Balderrama	*M.m*	CUNH3orf80	Balderrama	*P.l*	Cpa4	Schweizer	*P.m*	Nudt6	Schweizer	*P. m*
Gm15845	Balderrama	*M.m*	CUNH6orf222	Balderrama	*P.l*	Cpb1	Schweizer	*P.m*	Nxf1	Schweizer	*P. m*
Gm15856	Balderrama	*M.m*	CUNH9orf50	Balderrama	*P.l*	Cped1	Schweizer	*P.m*	Nxpe2	Schweizer	*P. m*
Gm15888	Balderrama	*M.m*	Cx3cl1	Balderrama	*P.l*	Cpm	Schweizer	*P.m*	Ocln	Schweizer	*P. m*
Gm15990	Balderrama	*M.m*	Cxcl10	Balderrama	*P.l*	Cpsf6	Schweizer	*P.m*	Odf1	Schweizer	*P. m*
Gm16014	Balderrama	*M.m*	Cxcl11	Balderrama	*P.l*	Cr1l	Schweizer	*P.m*	Olah	Schweizer	*P. m*
Gm16094	Balderrama	*M.m*	Cxcl16	Balderrama	*P.l*	Cramp1	Schweizer	*P.m*	Olfm2	Schweizer	*P. m*
Gm16096	Balderrama	*M.m*	Cxcl5	Balderrama	*P.l*	Crip3	Schweizer	*P.m*	Olfml2a	Schweizer	*P. m*
Gm16098	Balderrama	*M.m*	Cystm1	Balderrama	*P.l*	Crtam	Schweizer	*P.m*	Opcml	Schweizer	*P. m*
Gm16175	Balderrama	*M.m*	Dcbld1	Balderrama	*P.l*	Cs	Schweizer	*P.m*	Oprk1	Schweizer	*P. m*
Gm16325	Balderrama	*M.m*	Ddx43	Balderrama	*P.l*	Csmd3	Schweizer	*P.m*	Orc4	Schweizer	*P. m*
Gm16349	Balderrama	*M.m*	Ddx58	Balderrama	*P.l*	Csn1s1	Schweizer	*P.m*	Ormdl2	Schweizer	*P. m*

Gm16685	Balderrama	*M.m*	Dennd4a	Balderrama	*P.l*	Csn2	Schweizer	*P.m*	Osbpl2	Schweizer	*P. m*
Gm16726	Balderrama	*M.m*	Depp1	Balderrama	*P.l*	Cth	Schweizer	*P.m*	P2ry1	Schweizer	*P. m*
Gm16758	Balderrama	*M.m*	Dgat2	Balderrama	*P.l*	Ctsz	Schweizer	*P.m*	P2ry12	Schweizer	*P. m*
Gm17034	Balderrama	*M.m*	Dgkk	Balderrama	*P.l*	Cul5	Schweizer	*P.m*	P2ry13	Schweizer	*P. m*
Gm17334	Balderrama	*M.m*	Dio2	Balderrama	*P.l*	Cul7	Schweizer	*P.m*	P2ry14	Schweizer	*P. m*
Gm17641	Balderrama	*M.m*	Dio3	Balderrama	*P.l*	Cul9	Schweizer	*P.m*	Pabpc4l	Schweizer	*P. m*
Gm19299	Balderrama	*M.m*	Dmp1	Balderrama	*P.l*	Cwf19l1	Schweizer	*P.m*	Paip2	Schweizer	*P. m*
Gm19412	Balderrama	*M.m*	Dpysl5	Balderrama	*P.l*	Cwf19l2	Schweizer	*P.m*	Pan2	Schweizer	*P. m*
Gm19684	Balderrama	*M.m*	Dram1	Balderrama	*P.l*	Cxcl17	Schweizer	*P.m*	Panx3	Schweizer	*P. m*
Gm19744	Balderrama	*M.m*	Dtx3l	Balderrama	*P.l*	Cxcr5	Schweizer	*P.m*	Pcdh10	Schweizer	*P. m*
Gm19951	Balderrama	*M.m*	Dusp1	Balderrama	*P.l*	Daam2	Schweizer	*P.m*	Pcdh18	Schweizer	*P. m*
Gm20139	Balderrama	*M.m*	Edn1	Balderrama	*P.l*	Dcaf13	Schweizer	*P.m*	Pck1	Schweizer	*P. m*
Gm20186	Balderrama	*M.m*	Eif2ak2	Balderrama	*P.l*	Dclk1	Schweizer	*P.m*	Pcsk1	Schweizer	*P. m*
Gm20412	Balderrama	*M.m*	Epha4	Balderrama	*P.l*	Dctn2	Schweizer	*P.m*	Pdcl	Schweizer	*P. m*
Gm20532	Balderrama	*M.m*	Eppk1	Balderrama	*P.l*	Dcun1d1	Schweizer	*P.m*	Pdk4	Schweizer	*P. m*
Gm20559	Balderrama	*M.m*	Eqtn	Balderrama	*P.l*	Ddit3	Schweizer	*P.m*	Pdzd3	Schweizer	*P. m*
Gm2065	Balderrama	*M.m*	Erfe	Balderrama	*P.l*	Deptor	Schweizer	*P.m*	Peg3	Schweizer	*P. m*
Gm20661	Balderrama	*M.m*	Fam221a	Balderrama	*P.l*	Derl1	Schweizer	*P.m*	Pex1	Schweizer	*P. m*
Gm20705	Balderrama	*M.m*	Fam71a	Balderrama	*P.l*	Dgka	Schweizer	*P.m*	Pex5l	Schweizer	*P. m*
Gm21149	Balderrama	*M.m*	Fbxo27	Balderrama	*P.l*	Dgkd	Schweizer	*P.m*	Pgr	Schweizer	*P. m*
Gm21833	Balderrama	*M.m*	Fbxo39	Balderrama	*P.l*	Dhdh	Schweizer	*P.m*	Pgrmc2	Schweizer	*P. m*
Gm2270	Balderrama	*M.m*	Fgf21	Balderrama	*P.l*	Dhx36	Schweizer	*P.m*	Phc3	Schweizer	*P. m*
Gm2511	Balderrama	*M.m*	Fjx1	Balderrama	*P.l*	Diaph2	Schweizer	*P.m*	Phf14	Schweizer	*P. m*
Gm26535	Balderrama	*M.m*	Fkbp5	Balderrama	*P.l*	Dido1	Schweizer	*P.m*	Phf20	Schweizer	*P. m*
Gm26603	Balderrama	*M.m*	Flrt3	Balderrama	*P.l*	Dlg5	Schweizer	*P.m*	Phf3	Schweizer	*P. m*
Gm26637	Balderrama	*M.m*	Fn1	Balderrama	*P.l*	Dmd	Schweizer	*P.m*	Phldb1	Schweizer	*P. m*
Gm26679	Balderrama	*M.m*	Foxi2	Balderrama	*P.l*	Dnah12	Schweizer	*P.m*	Pid1	Schweizer	*P. m*

Gm26809	Balderrama	*M.m*	Fpr1	Balderrama	*P.l*	Dnajc14	Schweizer	*P.m*	Pik3ca	Schweizer	*P. m*
Gm27019	Balderrama	*M.m*	Fpr2	Balderrama	*P.l*	Dnajc19	Schweizer	*P.m*	Pip4k2c	Schweizer	*P. m*
Gm27167	Balderrama	*M.m*	Frem3	Balderrama	*P.l*	Dnm2	Schweizer	*P.m*	Pkhd1	Schweizer	*P. m*
Gm28055	Balderrama	*M.m*	Fscn1	Balderrama	*P.l*	Dopey2	Schweizer	*P.m*	Pkhd1l1	Schweizer	*P. m*
Gm28177	Balderrama	*M.m*	Fut1	Balderrama	*P.l*	Dpagt1	Schweizer	*P.m*	Pknox2	Schweizer	*P. m*
Gm28347	Balderrama	*M.m*	Gadd45b	Balderrama	*P.l*	Dppa5	Schweizer	*P.m*	Pla2g15	Schweizer	*P. m*
Gm28626	Balderrama	*M.m*	Gem	Balderrama	*P.l*	Dpy19l1	Schweizer	*P.m*	Plch1	Schweizer	*P. m*
Gm29010	Balderrama	*M.m*	Gfpt2	Balderrama	*P.l*	Dpy19l2	Schweizer	*P.m*	Plcl2	Schweizer	*P. m*
Gm29064	Balderrama	*M.m*	Gfra1	Balderrama	*P.l*	Drd2	Schweizer	*P.m*	Pld1	Schweizer	*P. m*
Gm29094	Balderrama	*M.m*	Gjb4	Balderrama	*P.l*	Dsc1	Schweizer	*P.m*	Plekha5	Schweizer	*P. m*
Gm29106	Balderrama	*M.m*	Gpr33	Balderrama	*P.l*	Dsg3	Schweizer	*P.m*	Plk4	Schweizer	*P. m*
Gm29371	Balderrama	*M.m*	Gpr39	Balderrama	*P.l*	Dsg4	Schweizer	*P.m*	Polh	Schweizer	*P. m*
Gm29408	Balderrama	*M.m*	Gramd2a	Balderrama	*P.l*	Dst	Schweizer	*P.m*	Polk	Schweizer	*P. m*
Gm29461	Balderrama	*M.m*	Hcar2	Balderrama	*P.l*	Dtna	Schweizer	*P.m*	Pon1	Schweizer	*P. m*
Gm29686	Balderrama	*M.m*	Helz2	Balderrama	*P.l*	Dtx3	Schweizer	*P.m*	Pon2	Schweizer	*P. m*
Gm30676	Balderrama	*M.m*	Herc6	Balderrama	*P.l*	Dusp13	Schweizer	*P.m*	Postn	Schweizer	*P. m*
Gm31026	Balderrama	*M.m*	Hes3	Balderrama	*P.l*	Dync1h1	Schweizer	*P.m*	Pou2f3	Schweizer	*P. m*
Gm31522	Balderrama	*M.m*	Hhla2	Balderrama	*P.l*	Dync2h1	Schweizer	*P.m*	Ppp1r9a	Schweizer	*P. m*
Gm32089	Balderrama	*M.m*	Hp	Balderrama	*P.l*	Dyrk1a	Schweizer	*P.m*	Ppp3cb	Schweizer	*P. m*
Gm32296	Balderrama	*M.m*	Hpx	Balderrama	*P.l*	Dyrk2	Schweizer	*P.m*	Ppp4r2	Schweizer	*P. m*
Gm32540	Balderrama	*M.m*	Ibsp	Balderrama	*P.l*	Dysf	Schweizer	*P.m*	Prdm10	Schweizer	*P. m*
Gm33056	Balderrama	*M.m*	Ido1	Balderrama	*P.l*	E2f4	Schweizer	*P.m*	Prelid3b	Schweizer	*P. m*
Gm33091	Balderrama	*M.m*	Ido2	Balderrama	*P.l*	E2f5	Schweizer	*P.m*	Prkci	Schweizer	*P. m*
Gm3331	Balderrama	*M.m*	Ier3	Balderrama	*P.l*	Edil3	Schweizer	*P.m*	Proser1	Schweizer	*P. m*
Gm33994	Balderrama	*M.m*	Ifi44	Balderrama	*P.l*	Edn3	Schweizer	*P.m*	Prpf18	Schweizer	*P. m*
Gm34045	Balderrama	*M.m*	Ifih1	Balderrama	*P.l*	Eepd1	Schweizer	*P.m*	Prph2	Schweizer	*P. m*
Gm3411	Balderrama	*M.m*	Ifnb1	Balderrama	*P.l*	Eif2a	Schweizer	*P.m*	Ptbp1	Schweizer	*P. m*

Gm34322	Balderrama	*M.m*	Ifrd1	Balderrama	*P.l*	Eif5a2	Schweizer	*P.m*	Ptk7	Schweizer	*P. m*
Gm34471	Balderrama	*M.m*	Igf2bp1	Balderrama	*P.l*	Elf2	Schweizer	*P.m*	Ptp4a1	Schweizer	*P. m*
Gm34585	Balderrama	*M.m*	Il10	Balderrama	*P.l*	Endod1	Schweizer	*P.m*	Ptprc	Schweizer	*P. m*
Gm35028	Balderrama	*M.m*	Il15	Balderrama	*P.l*	Eno4	Schweizer	*P.m*	Ptprz1	Schweizer	*P. m*
Gm36107	Balderrama	*M.m*	Il15ra	Balderrama	*P.l*	Enpp2	Schweizer	*P.m*	Pura	Schweizer	*P. m*
Gm36186	Balderrama	*M.m*	Il17rb	Balderrama	*P.l*	Epas1	Schweizer	*P.m*	Pus3	Schweizer	*P. m*
Gm37026	Balderrama	*M.m*	Il19	Balderrama	*P.l*	Epb41l4a	Schweizer	*P.m*	R3hdm1	Schweizer	*P. m*
Gm37042	Balderrama	*M.m*	Il1a	Balderrama	*P.l*	Erap1	Schweizer	*P.m*	R3hdm2	Schweizer	*P. m*
Gm37043	Balderrama	*M.m*	Il1b	Balderrama	*P.l*	Erbb3	Schweizer	*P.m*	Rab22a	Schweizer	*P. m*
Gm37347	Balderrama	*M.m*	Il1r2	Balderrama	*P.l*	Erbin	Schweizer	*P.m*	Rab23	Schweizer	*P. m*
Gm37560	Balderrama	*M.m*	Il1rn	Balderrama	*P.l*	Ercc4	Schweizer	*P.m*	Rab33b	Schweizer	*P. m*
Gm37639	Balderrama	*M.m*	Il22	Balderrama	*P.l*	Ercc6l2	Schweizer	*P.m*	Rab39b	Schweizer	*P. m*
Gm37728	Balderrama	*M.m*	Il27	Balderrama	*P.l*	Erg	Schweizer	*P.m*	Rab3d	Schweizer	*P. m*
Gm37795	Balderrama	*M.m*	Il31ra	Balderrama	*P.l*	Erich6	Schweizer	*P.m*	Rab5b	Schweizer	*P. m*
Gm37842	Balderrama	*M.m*	Il6	Balderrama	*P.l*	Esam	Schweizer	*P.m*	Rad17	Schweizer	*P. m*
Gm37881	Balderrama	*M.m*	Irf7	Balderrama	*P.l*	Esyt1	Schweizer	*P.m*	Rap1b	Schweizer	*P. m*
Gm37975	Balderrama	*M.m*	Irf9	Balderrama	*P.l*	Exoc6b	Schweizer	*P.m*	Raver1	Schweizer	*P. m*
Gm38177	Balderrama	*M.m*	Irx3	Balderrama	*P.l*	Exosc8	Schweizer	*P.m*	Rb1cc1	Schweizer	*P. m*
Gm38220	Balderrama	*M.m*	Isg20	Balderrama	*P.l*	F2rl1	Schweizer	*P.m*	Rbm7	Schweizer	*P. m*
Gm38258	Balderrama	*M.m*	Itgb6	Balderrama	*P.l*	Fam118b	Schweizer	*P.m*	Rc3h2	Schweizer	*P. m*
Gm38271	Balderrama	*M.m*	Izumo1	Balderrama	*P.l*	Fam132a	Schweizer	*P.m*	Rcan2	Schweizer	*P. m*
Gm38316	Balderrama	*M.m*	Kcne4	Balderrama	*P.l*	Fam132b	Schweizer	*P.m*	Rfesd	Schweizer	*P. m*
Gm38377	Balderrama	*M.m*	Kcng3	Balderrama	*P.l*	Fam135a	Schweizer	*P.m*	Rftn1	Schweizer	*P. m*
Gm38554	Balderrama	*M.m*	Kif1a	Balderrama	*P.l*	Fam13b	Schweizer	*P.m*	Rfx3	Schweizer	*P. m*
Gm39556	Balderrama	*M.m*	Klf15	Balderrama	*P.l*	Fam149b1	Schweizer	*P.m*	Rhag	Schweizer	*P. m*
Gm40578	Balderrama	*M.m*	Klk9	Balderrama	*P.l*	Fam177a1	Schweizer	*P.m*	Rhpn2	Schweizer	*P. m*
Gm4065	Balderrama	*M.m*	Krt16	Balderrama	*P.l*	Fam19a2	Schweizer	*P.m*	Rims2	Schweizer	*P. m*

Gm40655	Balderrama	*M.m*	Krt8	Balderrama	*P.l*	Fam3c	Schweizer	*P.m*	Riok3	Schweizer	*P. m*
Gm40685	Balderrama	*M.m*	Lcn2	Balderrama	*P.l*	Fam76b	Schweizer	*P.m*	Rlim	Schweizer	*P. m*
Gm4070	Balderrama	*M.m*	Lgals9	Balderrama	*P.l*	Fam84b	Schweizer	*P.m*	Rnf133	Schweizer	*P. m*
Gm42450	Balderrama	*M.m*	Lipg	Balderrama	*P.l*	Fam91a1	Schweizer	*P.m*	Rnf148	Schweizer	*P. m*
Gm42503	Balderrama	*M.m*	Liph	Balderrama	*P.l*	Faxc	Schweizer	*P.m*	Rnf19a	Schweizer	*P. m*
Gm42519	Balderrama	*M.m*	LOC114680639	Balderrama	*P.l*	Fbxo11	Schweizer	*P.m*	Robo4	Schweizer	*P. m*
Gm42726	Balderrama	*M.m*	LOC114680957	Balderrama	*P.l*	Fbxo32	Schweizer	*P.m*	Rock1	Schweizer	*P. m*
Gm42763	Balderrama	*M.m*	LOC114681164	Balderrama	*P.l*	Fer1l6	Schweizer	*P.m*	Rp1	Schweizer	*P. m*
Gm42917	Balderrama	*M.m*	LOC114681165	Balderrama	*P.l*	Fgf2	Schweizer	*P.m*	Rp9	Schweizer	*P. m*
Gm42963	Balderrama	*M.m*	LOC114681329	Balderrama	*P.l*	Fli1	Schweizer	*P.m*	Rprd1a	Schweizer	*P. m*
Gm43068	Balderrama	*M.m*	LOC114681470	Balderrama	*P.l*	Flnb	Schweizer	*P.m*	Rps25	Schweizer	*P. m*
Gm43069	Balderrama	*M.m*	LOC114681565	Balderrama	*P.l*	Flt1	Schweizer	*P.m*	Rps28	Schweizer	*P. m*
Gm43196	Balderrama	*M.m*	LOC114681707	Balderrama	*P.l*	Fmr1	Schweizer	*P.m*	Rrm2b	Schweizer	*P. m*
Gm43198	Balderrama	*M.m*	LOC114681708	Balderrama	*P.l*	Fndc3b	Schweizer	*P.m*	Rsad2	Schweizer	*P. m*
Gm43237	Balderrama	*M.m*	LOC114681711	Balderrama	*P.l*	Foxo1	Schweizer	*P.m*	Rsbn1l	Schweizer	*P. m*
Gm43302	Balderrama	*M.m*	LOC114681715	Balderrama	*P.l*	Foxp2	Schweizer	*P.m*	Rtel1	Schweizer	*P. m*
Gm43399	Balderrama	*M.m*	LOC114681718	Balderrama	*P.l*	Frem2	Schweizer	*P.m*	Rtl1	Schweizer	*P. m*
Gm43464	Balderrama	*M.m*	LOC114681719	Balderrama	*P.l*	Frmd7	Schweizer	*P.m*	S1pr5	Schweizer	*P. m*
Gm43635	Balderrama	*M.m*	LOC114681724	Balderrama	*P.l*	Fry	Schweizer	*P.m*	Samd12	Schweizer	*P. m*
Gm43694	Balderrama	*M.m*	LOC114681726	Balderrama	*P.l*	Fsd1l	Schweizer	*P.m*	Samd9	Schweizer	*P. m*
Gm43814	Balderrama	*M.m*	LOC114681897	Balderrama	*P.l*	Fut11	Schweizer	*P.m*	Satb1	Schweizer	*P. m*
Gm43884	Balderrama	*M.m*	LOC114681904	Balderrama	*P.l*	Fxr1	Schweizer	*P.m*	Sc5d	Schweizer	*P. m*
Gm43900	Balderrama	*M.m*	LOC114681905	Balderrama	*P.l*	Gabra3	Schweizer	*P.m*	Scamp1	Schweizer	*P. m*
Gm44013	Balderrama	*M.m*	LOC114681963	Balderrama	*P.l*	Gabrq	Schweizer	*P.m*	Scgb2a2	Schweizer	*P. m*
Gm44165	Balderrama	*M.m*	LOC114682175	Balderrama	*P.l*	Galnt1	Schweizer	*P.m*	Scn3b	Schweizer	*P. m*
Gm44448	Balderrama	*M.m*	LOC114682671	Balderrama	*P.l*	Gatad1	Schweizer	*P.m*	Sdr9c7	Schweizer	*P. m*
Gm44542	Balderrama	*M.m*	LOC114682933	Balderrama	*P.l*	Gdf11	Schweizer	*P.m*	Sec24c	Schweizer	*P. m*

Gm44672	Balderrama	*M.m*	LOC114683008	Balderrama	*P.l*	Gfm2	Schweizer	*P.m*	Sec62	Schweizer	*P. m*
Gm44696	Balderrama	*M.m*	LOC114683116	Balderrama	*P.l*	Gfpt1	Schweizer	*P.m*	Serp1	Schweizer	*P. m*
Gm44815	Balderrama	*M.m*	LOC114683786	Balderrama	*P.l*	Gfra3	Schweizer	*P.m*	Serpinb8	Schweizer	*P. m*
Gm44867	Balderrama	*M.m*	LOC114683802	Balderrama	*P.l*	Glp2r	Schweizer	*P.m*	Sertm1	Schweizer	*P. m*
Gm45193	Balderrama	*M.m*	LOC114683803	Balderrama	*P.l*	Gls2	Schweizer	*P.m*	Sesn3	Schweizer	*P. m*
Gm45326	Balderrama	*M.m*	LOC114683804	Balderrama	*P.l*	Gltscr1l	Schweizer	*P.m*	Setd7	Schweizer	*P. m*
Gm45418	Balderrama	*M.m*	LOC114683863	Balderrama	*P.l*	Gmcl1	Schweizer	*P.m*	Sgol1	Schweizer	*P. m*
Gm45528	Balderrama	*M.m*	LOC114684563	Balderrama	*P.l*	Gmps	Schweizer	*P.m*	Sh3glb1	Schweizer	*P. m*
Gm45542	Balderrama	*M.m*	LOC114684565	Balderrama	*P.l*	Gnb1	Schweizer	*P.m*	Shisa9	Schweizer	*P. m*
Gm45717	Balderrama	*M.m*	LOC114684566	Balderrama	*P.l*	Gnb4	Schweizer	*P.m*	Shmt2	Schweizer	*P. m*
Gm45774	Balderrama	*M.m*	LOC114684568	Balderrama	*P.l*	Gns	Schweizer	*P.m*	Shoc2	Schweizer	*P. m*
Gm45912	Balderrama	*M.m*	LOC114684569	Balderrama	*P.l*	Golga3	Schweizer	*P.m*	Siae	Schweizer	*P. m*
Gm47034	Balderrama	*M.m*	LOC114684570	Balderrama	*P.l*	Gpn1	Schweizer	*P.m*	Sik3	Schweizer	*P. m*
Gm47043	Balderrama	*M.m*	LOC114684572	Balderrama	*P.l*	Gpr149	Schweizer	*P.m*	Skil	Schweizer	*P. m*
Gm47118	Balderrama	*M.m*	LOC114684574	Balderrama	*P.l*	Gpr182	Schweizer	*P.m*	Slc10a2	Schweizer	*P. m*
Gm47140	Balderrama	*M.m*	LOC114684575	Balderrama	*P.l*	Gpr75	Schweizer	*P.m*	Slc13a1	Schweizer	*P. m*
Gm47214	Balderrama	*M.m*	LOC114684798	Balderrama	*P.l*	Gpr87	Schweizer	*P.m*	Slc13a5	Schweizer	*P. m*
Gm47242	Balderrama	*M.m*	LOC114685183	Balderrama	*P.l*	Gramd1b	Schweizer	*P.m*	Slc16a7	Schweizer	*P. m*
Gm47243	Balderrama	*M.m*	LOC114685334	Balderrama	*P.l*	Greb1l	Schweizer	*P.m*	Slc22a8	Schweizer	*P. m*
Gm47480	Balderrama	*M.m*	LOC114685648	Balderrama	*P.l*	Grhl2	Schweizer	*P.m*	Slc25a27	Schweizer	*P. m*
Gm47571	Balderrama	*M.m*	LOC114685651	Balderrama	*P.l*	Gria4	Schweizer	*P.m*	Slc25a31	Schweizer	*P. m*
Gm47595	Balderrama	*M.m*	LOC114685652	Balderrama	*P.l*	Grik2	Schweizer	*P.m*	Slc25a32	Schweizer	*P. m*
Gm47657	Balderrama	*M.m*	LOC114685662	Balderrama	*P.l*	Grip1	Schweizer	*P.m*	Slc25a46	Schweizer	*P. m*
Gm47735	Balderrama	*M.m*	LOC114685748	Balderrama	*P.l*	Gspt1	Schweizer	*P.m*	Slc29a1	Schweizer	*P. m*
Gm47800	Balderrama	*M.m*	LOC114686303	Balderrama	*P.l*	Gucy1a2	Schweizer	*P.m*	Slc2a2	Schweizer	*P. m*
Gm47822	Balderrama	*M.m*	LOC114686891	Balderrama	*P.l*	Gyg1	Schweizer	*P.m*	Slc2a5	Schweizer	*P. m*
Gm47922	Balderrama	*M.m*	LOC114686894	Balderrama	*P.l*	Has2	Schweizer	*P.m*	Slc30a8	Schweizer	*P. m*

Gm4841	Balderrama	*M.m*	LOC114687018	Balderrama	*P.l*	Helb	Schweizer	*P.m*	Slc33a1	Schweizer	*P. m*
Gm48545	Balderrama	*M.m*	LOC114687407	Balderrama	*P.l*	Hells	Schweizer	*P.m*	Slc35a4	Schweizer	*P. m*
Gm48878	Balderrama	*M.m*	LOC114687526	Balderrama	*P.l*	Hepacam	Schweizer	*P.m*	Slc35e3	Schweizer	*P. m*
Gm48899	Balderrama	*M.m*	LOC114687677	Balderrama	*P.l*	Hepacam2	Schweizer	*P.m*	Slc39a5	Schweizer	*P. m*
Gm48942	Balderrama	*M.m*	LOC114687761	Balderrama	*P.l*	Hinfp	Schweizer	*P.m*	Slc39a6	Schweizer	*P. m*
Gm49339	Balderrama	*M.m*	LOC114688093	Balderrama	*P.l*	Hmbs	Schweizer	*P.m*	Slc44a2	Schweizer	*P. m*
Gm49342	Balderrama	*M.m*	LOC114688145	Balderrama	*P.l*	Hps3	Schweizer	*P.m*	Slc4a9	Schweizer	*P. m*
Gm49420	Balderrama	*M.m*	LOC114688398	Balderrama	*P.l*	Hs6st1	Schweizer	*P.m*	Slc7a1	Schweizer	*P. m*
Gm49442	Balderrama	*M.m*	LOC114688399	Balderrama	*P.l*	Hsd11b1	Schweizer	*P.m*	Slc7a11	Schweizer	*P. m*
Gm49482	Balderrama	*M.m*	LOC114688405	Balderrama	*P.l*	Hsd17b3	Schweizer	*P.m*	Slc7a14	Schweizer	*P. m*
Gm49507	Balderrama	*M.m*	LOC114688407	Balderrama	*P.l*	Hsf4	Schweizer	*P.m*	Slco1a2	Schweizer	*P. m*
Gm4951	Balderrama	*M.m*	LOC114688409	Balderrama	*P.l*	Hspa4l	Schweizer	*P.m*	Slco1b3	Schweizer	*P. m*
Gm49730	Balderrama	*M.m*	LOC114688413	Balderrama	*P.l*	Hspa8	Schweizer	*P.m*	Slco1c1	Schweizer	*P. m*
Gm49751	Balderrama	*M.m*	LOC114688414	Balderrama	*P.l*	Hspa9	Schweizer	*P.m*	Slco4c1	Schweizer	*P. m*
Gm5152	Balderrama	*M.m*	LOC114688415	Balderrama	*P.l*	Hsph1	Schweizer	*P.m*	Slf1	Schweizer	*P. m*
Gm5416	Balderrama	*M.m*	LOC114688611	Balderrama	*P.l*	Htr1b	Schweizer	*P.m*	Slmap	Schweizer	*P. m*
Gm5431	Balderrama	*M.m*	LOC114688826	Balderrama	*P.l*	Htr3a	Schweizer	*P.m*	Sltm	Schweizer	*P. m*
Gm5483	Balderrama	*M.m*	LOC114689091	Balderrama	*P.l*	Hyls1	Schweizer	*P.m*	Smarcc2	Schweizer	*P. m*
Gm5796	Balderrama	*M.m*	LOC114689226	Balderrama	*P.l*	Hyou1	Schweizer	*P.m*	Smpd3	Schweizer	*P. m*
Gm6377	Balderrama	*M.m*	LOC114689273	Balderrama	*P.l*	Icam1	Schweizer	*P.m*	Snap91	Schweizer	*P. m*
Gm6902	Balderrama	*M.m*	LOC114689274	Balderrama	*P.l*	Icam4	Schweizer	*P.m*	Sntb1	Schweizer	*P. m*
Gm6904	Balderrama	*M.m*	LOC114689300	Balderrama	*P.l*	Ifng	Schweizer	*P.m*	Snx14	Schweizer	*P. m*
Gm7598	Balderrama	*M.m*	LOC114689301	Balderrama	*P.l*	Igsf10	Schweizer	*P.m*	Snx19	Schweizer	*P. m*
Gm8098	Balderrama	*M.m*	LOC114689426	Balderrama	*P.l*	Igsf9b	Schweizer	*P.m*	Snx29	Schweizer	*P. m*
Gm8110	Balderrama	*M.m*	LOC114689864	Balderrama	*P.l*	Ikzf4	Schweizer	*P.m*	Sohlh2	Schweizer	*P. m*
Gm9920	Balderrama	*M.m*	LOC114689891	Balderrama	*P.l*	Il18	Schweizer	*P.m*	Sorcs3	Schweizer	*P. m*
Gng4	Balderrama	*M.m*	LOC114690079	Balderrama	*P.l*	Il23a	Schweizer	*P.m*	Sorl1	Schweizer	*P. m*

Gpr12	Balderrama	*M.m*	LOC114690363	Balderrama	*P.l*	Ilf3	Schweizer	*P.m*	Sox18	Schweizer	*P. m*
Gpr171	Balderrama	*M.m*	LOC114690609	Balderrama	*P.l*	Irak3	Schweizer	*P.m*	Sox2	Schweizer	*P. m*
Gpr31b	Balderrama	*M.m*	LOC114690618	Balderrama	*P.l*	Itga7	Schweizer	*P.m*	Spata24	Schweizer	*P. m*
Gpr84	Balderrama	*M.m*	LOC114690676	Balderrama	*P.l*	Itgbl1	Schweizer	*P.m*	Spata5	Schweizer	*P. m*
Gpr85	Balderrama	*M.m*	LOC114690678	Balderrama	*P.l*	Iws1	Schweizer	*P.m*	Spdya	Schweizer	*P. m*
Gprc5a	Balderrama	*M.m*	LOC114690679	Balderrama	*P.l*	Jade1	Schweizer	*P.m*	Spg20	Schweizer	*P. m*
Gucy2c	Balderrama	*M.m*	LOC114690754	Balderrama	*P.l*	Jam3	Schweizer	*P.m*	Spo11	Schweizer	*P. m*
Gzmb	Balderrama	*M.m*	LOC114690782	Balderrama	*P.l*	Kank2	Schweizer	*P.m*	Spryd4	Schweizer	*P. m*
Gzmc	Balderrama	*M.m*	LOC114690951	Balderrama	*P.l*	Kat2b	Schweizer	*P.m*	Srek1	Schweizer	*P. m*
H2-T24	Balderrama	*M.m*	LOC114691127	Balderrama	*P.l*	Kat6b	Schweizer	*P.m*	Srgap1	Schweizer	*P. m*
Hamp	Balderrama	*M.m*	LOC114691422	Balderrama	*P.l*	Kbtbd3	Schweizer	*P.m*	Srpra	Schweizer	*P. m*
Has1	Balderrama	*M.m*	LOC114691549	Balderrama	*P.l*	Kcnh8	Schweizer	*P.m*	Ss18	Schweizer	*P. m*
Hc	Balderrama	*M.m*	LOC114691550	Balderrama	*P.l*	Kcnj1	Schweizer	*P.m*	St14	Schweizer	*P. m*
Hck	Balderrama	*M.m*	LOC114691605	Balderrama	*P.l*	Kcnj5	Schweizer	*P.m*	Stard13	Schweizer	*P. m*
Hcn4	Balderrama	*M.m*	LOC114691641	Balderrama	*P.l*	Kcnj6	Schweizer	*P.m*	Stard4	Schweizer	*P. m*
Hdc	Balderrama	*M.m*	LOC114691764	Balderrama	*P.l*	Kcnma1	Schweizer	*P.m*	Stat6	Schweizer	*P. m*
Hephl1	Balderrama	*M.m*	LOC114691793	Balderrama	*P.l*	Kcnq3	Schweizer	*P.m*	Stk3	Schweizer	*P. m*
Hk2	Balderrama	*M.m*	LOC114691953	Balderrama	*P.l*	Kcnv1	Schweizer	*P.m*	Stk33	Schweizer	*P. m*
Hpcal4	Balderrama	*M.m*	LOC114692262	Balderrama	*P.l*	Kctd1	Schweizer	*P.m*	Strbp	Schweizer	*P. m*
Hsh2d	Balderrama	*M.m*	LOC114692453	Balderrama	*P.l*	Kdm3b	Schweizer	*P.m*	Stt3a	Schweizer	*P. m*
Htr7	Balderrama	*M.m*	LOC114692696	Balderrama	*P.l*	Kdm6a	Schweizer	*P.m*	Stt3b	Schweizer	*P. m*
Htra4	Balderrama	*M.m*	LOC114692731	Balderrama	*P.l*	Kiaa0196	Schweizer	*P.m*	Stx16	Schweizer	*P. m*
Ifi202b	Balderrama	*M.m*	LOC114693504	Balderrama	*P.l*	Kiaa0430	Schweizer	*P.m*	Sucnr1	Schweizer	*P. m*
Ifi203	Balderrama	*M.m*	LOC114694347	Balderrama	*P.l*	Kiaa0895	Schweizer	*P.m*	Suox	Schweizer	*P. m*
Ifi204	Balderrama	*M.m*	LOC114694350	Balderrama	*P.l*	Kiaa1109	Schweizer	*P.m*	Supt20h	Schweizer	*P. m*
Ifi205	Balderrama	*M.m*	LOC114694372	Balderrama	*P.l*	Kiaa1217	Schweizer	*P.m*	Sybu	Schweizer	*P. m*
Ifi206	Balderrama	*M.m*	LOC114694376	Balderrama	*P.l*	Kiaa1328	Schweizer	*P.m*	Synpo2l	Schweizer	*P. m*

Ifi207	Balderrama	*M.m*	LOC114694510	Balderrama	*P.l*	Kiaa2022	Schweizer	*P.m*	Syt4	Schweizer	*P. m*
Ifi208	Balderrama	*M.m*	LOC114694511	Balderrama	*P.l*	Kidins220	Schweizer	*P.m*	Taf2	Schweizer	*P. m*
Ifi209	Balderrama	*M.m*	LOC114694553	Balderrama	*P.l*	Kif24	Schweizer	*P.m*	Taf4b	Schweizer	*P. m*
Ifi211	Balderrama	*M.m*	LOC114695173	Balderrama	*P.l*	Kif5a	Schweizer	*P.m*	Taf8	Schweizer	*P. m*
Ifi213	Balderrama	*M.m*	LOC114695766	Balderrama	*P.l*	Kif6	Schweizer	*P.m*	Tas2r40	Schweizer	*P. m*
Ifi214	Balderrama	*M.m*	LOC114696384	Balderrama	*P.l*	Kl	Schweizer	*P.m*	Tatdn1	Schweizer	*P. m*
Ifi35	Balderrama	*M.m*	LOC114696646	Balderrama	*P.l*	Klc4	Schweizer	*P.m*	Tbc1d30	Schweizer	*P. m*
Ifi44l	Balderrama	*M.m*	LOC114696647	Balderrama	*P.l*	Klf10	Schweizer	*P.m*	Tbc1d31	Schweizer	*P. m*
Ifi47	Balderrama	*M.m*	LOC114697129	Balderrama	*P.l*	Klhdc3	Schweizer	*P.m*	Tbc1d5	Schweizer	*P. m*
Ifit1	Balderrama	*M.m*	LOC114697185	Balderrama	*P.l*	Kmt2a	Schweizer	*P.m*	Tbcel	Schweizer	*P. m*
Ifit1bl1	Balderrama	*M.m*	LOC114697570	Balderrama	*P.l*	Lama3	Schweizer	*P.m*	Tbk1	Schweizer	*P. m*
Ifit1bl2	Balderrama	*M.m*	LOC114697821	Balderrama	*P.l*	Lama5	Schweizer	*P.m*	Tcfl5	Schweizer	*P. m*
Ifit2	Balderrama	*M.m*	LOC114697855	Balderrama	*P.l*	Large	Schweizer	*P.m*	Tecta	Schweizer	*P. m*
Ifit3	Balderrama	*M.m*	LOC114697856	Balderrama	*P.l*	Lhfp	Schweizer	*P.m*	Tfap2b	Schweizer	*P. m*
Ifit3b	Balderrama	*M.m*	LOC114697860	Balderrama	*P.l*	LOC102902765	Schweizer	*P.m*	Tfap2d	Schweizer	*P. m*
Ifitm3	Balderrama	*M.m*	LOC114697861	Balderrama	*P.l*	LOC102902789	Schweizer	*P.m*	Tfpi2	Schweizer	*P. m*
Ifitm5	Balderrama	*M.m*	LOC114698011	Balderrama	*P.l*	LOC102903073	Schweizer	*P.m*	Thy1	Schweizer	*P. m*
Ifna2	Balderrama	*M.m*	LOC114698246	Balderrama	*P.l*	LOC102903383	Schweizer	*P.m*	Thyn1	Schweizer	*P. m*
Ifna4	Balderrama	*M.m*	LOC114698259	Balderrama	*P.l*	LOC102903517	Schweizer	*P.m*	Tjap1	Schweizer	*P. m*
Ifnab	Balderrama	*M.m*	LOC114698852	Balderrama	*P.l*	LOC102903712	Schweizer	*P.m*	Tm4sf4	Schweizer	*P. m*
Ighv2-7	Balderrama	*M.m*	LOC114698905	Balderrama	*P.l*	LOC102903802	Schweizer	*P.m*	Tmed1	Schweizer	*P. m*
Igtp	Balderrama	*M.m*	LOC114699623	Balderrama	*P.l*	LOC102903992	Schweizer	*P.m*	Tmem123	Schweizer	*P. m*
Iigp1	Balderrama	*M.m*	LOC114700187	Balderrama	*P.l*	LOC102903994	Schweizer	*P.m*	Tmem136	Schweizer	*P. m*
Il11ra2	Balderrama	*M.m*	LOC114700341	Balderrama	*P.l*	LOC102904031	Schweizer	*P.m*	Tmem151b	Schweizer	*P. m*
Il12b	Balderrama	*M.m*	LOC114700344	Balderrama	*P.l*	LOC102904307	Schweizer	*P.m*	Tmem161b	Schweizer	*P. m*
Il12rb1	Balderrama	*M.m*	LOC114700346	Balderrama	*P.l*	LOC102904434	Schweizer	*P.m*	Tmem173	Schweizer	*P. m*
Il12rb2	Balderrama	*M.m*	LOC114700347	Balderrama	*P.l*	LOC102904812	Schweizer	*P.m*	Tmem212	Schweizer	*P. m*

Il17a	Balderrama	*M.m*	LOC114700427	Balderrama	*P.l*	LOC102904934	Schweizer	*P.m*	Tmem218	Schweizer	*P. m*
Il17f	Balderrama	*M.m*	LOC114700507	Balderrama	*P.l*	LOC102905396	Schweizer	*P.m*	Tmem241	Schweizer	*P. m*
Il1f6	Balderrama	*M.m*	LOC114700540	Balderrama	*P.l*	LOC102905460	Schweizer	*P.m*	Tmem25	Schweizer	*P. m*
Il1f9	Balderrama	*M.m*	LOC114701096	Balderrama	*P.l*	LOC102905605	Schweizer	*P.m*	Tmem30a	Schweizer	*P. m*
Il2ra	Balderrama	*M.m*	LOC114701399	Balderrama	*P.l*	LOC102905707	Schweizer	*P.m*	Tmprss5	Schweizer	*P. m*
Il33	Balderrama	*M.m*	LOC114701719	Balderrama	*P.l*	LOC102905782	Schweizer	*P.m*	Tnfrsf11b	Schweizer	*P. m*
Ildr1	Balderrama	*M.m*	LOC114701735	Balderrama	*P.l*	LOC102905923	Schweizer	*P.m*	Tnfsf10	Schweizer	*P. m*
Iltifb	Balderrama	*M.m*	LOC114701736	Balderrama	*P.l*	LOC102906152	Schweizer	*P.m*	Tnik	Schweizer	*P. m*
Inhbb	Balderrama	*M.m*	LOC114701896	Balderrama	*P.l*	LOC102906218	Schweizer	*P.m*	Tnks	Schweizer	*P. m*
Iqcf1	Balderrama	*M.m*	LOC114702149	Balderrama	*P.l*	LOC102906541	Schweizer	*P.m*	Tppp3	Schweizer	*P. m*
Irf1	Balderrama	*M.m*	LOC114702286	Balderrama	*P.l*	LOC102906561	Schweizer	*P.m*	Treh	Schweizer	*P. m*
Irgm1	Balderrama	*M.m*	LOC114702542	Balderrama	*P.l*	LOC102906846	Schweizer	*P.m*	Trerf1	Schweizer	*P. m*
Irgm2	Balderrama	*M.m*	LOC114702545	Balderrama	*P.l*	LOC102906935	Schweizer	*P.m*	Trhr	Schweizer	*P. m*
Irx6	Balderrama	*M.m*	LOC114702823	Balderrama	*P.l*	LOC102907006	Schweizer	*P.m*	Trib1	Schweizer	*P. m*
Isg15	Balderrama	*M.m*	LOC114702919	Balderrama	*P.l*	LOC102907220	Schweizer	*P.m*	Trmt12	Schweizer	*P. m*
Itgb8	Balderrama	*M.m*	LOC114703306	Balderrama	*P.l*	LOC102907251	Schweizer	*P.m*	Trpc3	Schweizer	*P. m*
Jaml	Balderrama	*M.m*	LOC114703392	Balderrama	*P.l*	LOC102907276	Schweizer	*P.m*	Trpc4	Schweizer	*P. m*
Jdp2	Balderrama	*M.m*	LOC114703402	Balderrama	*P.l*	LOC102907317	Schweizer	*P.m*	Trps1	Schweizer	*P. m*
Jun	Balderrama	*M.m*	LOC114703403	Balderrama	*P.l*	LOC102907513	Schweizer	*P.m*	Tsc22d2	Schweizer	*P. m*
Junb	Balderrama	*M.m*	LOC114703406	Balderrama	*P.l*	LOC102907544	Schweizer	*P.m*	Ttbk1	Schweizer	*P. m*
Kank4	Balderrama	*M.m*	LOC114703660	Balderrama	*P.l*	LOC102907590	Schweizer	*P.m*	Ttc3	Schweizer	*P. m*
Kcns1	Balderrama	*M.m*	LOC114704347	Balderrama	*P.l*	LOC102907619	Schweizer	*P.m*	Tubb1	Schweizer	*P. m*
Klf14	Balderrama	*M.m*	LOC114704434	Balderrama	*P.l*	LOC102907678	Schweizer	*P.m*	Tyk2	Schweizer	*P. m*
Klk4	Balderrama	*M.m*	LOC114704463	Balderrama	*P.l*	LOC102907711	Schweizer	*P.m*	Tyr	Schweizer	*P. m*
Krt24	Balderrama	*M.m*	LOC114704902	Balderrama	*P.l*	LOC102907993	Schweizer	*P.m*	Ubash3b	Schweizer	*P. m*
Krt81	Balderrama	*M.m*	LOC114705900	Balderrama	*P.l*	LOC102908027	Schweizer	*P.m*	Ube2d2	Schweizer	*P. m*
Lamc2	Balderrama	*M.m*	LOC114706381	Balderrama	*P.l*	LOC102908268	Schweizer	*P.m*	Ubr2	Schweizer	*P. m*

Ldhd	Balderrama	*M.m*	LOC114706384	Balderrama	*P.l*	LOC102908477	Schweizer	*P.m*	Ubr5	Schweizer	*P. m*
Lgals3bp	Balderrama	*M.m*	LOC114706385	Balderrama	*P.l*	LOC102908633	Schweizer	*P.m*	Ubxn2b	Schweizer	*P. m*
Lif	Balderrama	*M.m*	LOC114706392	Balderrama	*P.l*	LOC102908952	Schweizer	*P.m*	Ufm1	Schweizer	*P. m*
Lilr4b	Balderrama	*M.m*	LOC114706400	Balderrama	*P.l*	LOC102909014	Schweizer	*P.m*	Usp12	Schweizer	*P. m*
Lilrb4a	Balderrama	*M.m*	LOC114706607	Balderrama	*P.l*	LOC102909057	Schweizer	*P.m*	Usp13	Schweizer	*P. m*
Lox	Balderrama	*M.m*	LOC114706978	Balderrama	*P.l*	LOC102909107	Schweizer	*P.m*	Usp15	Schweizer	*P. m*
Lrrc6	Balderrama	*M.m*	LOC114707400	Balderrama	*P.l*	LOC102909279	Schweizer	*P.m*	Usp2	Schweizer	*P. m*
Ly6a	Balderrama	*M.m*	LOC114707630	Balderrama	*P.l*	LOC102909369	Schweizer	*P.m*	Usp28	Schweizer	*P. m*
Mab21l3	Balderrama	*M.m*	LOC114707719	Balderrama	*P.l*	LOC102909407	Schweizer	*P.m*	Usp40	Schweizer	*P. m*
Map3k8	Balderrama	*M.m*	LOC114707726	Balderrama	*P.l*	LOC102909417	Schweizer	*P.m*	Usp42	Schweizer	*P. m*
Meig1	Balderrama	*M.m*	LOC114707727	Balderrama	*P.l*	LOC102909592	Schweizer	*P.m*	Usp54	Schweizer	*P. m*
Meikin	Balderrama	*M.m*	LOC114707728	Balderrama	*P.l*	LOC102909690	Schweizer	*P.m*	Uspl1	Schweizer	*P. m*
Mfsd2a	Balderrama	*M.m*	LOC114707732	Balderrama	*P.l*	LOC102909735	Schweizer	*P.m*	Vapb	Schweizer	*P. m*
Mir155hg	Balderrama	*M.m*	LOC114707940	Balderrama	*P.l*	LOC102909864	Schweizer	*P.m*	Vcl	Schweizer	*P. m*
Misp	Balderrama	*M.m*	LOC114708004	Balderrama	*P.l*	LOC102909871	Schweizer	*P.m*	Vps13b	Schweizer	*P. m*
Mlkl	Balderrama	*M.m*	LOC114708095	Balderrama	*P.l*	LOC102909979	Schweizer	*P.m*	Vps26b	Schweizer	*P. m*
Mmp13	Balderrama	*M.m*	LOC114708750	Balderrama	*P.l*	LOC102910012	Schweizer	*P.m*	Vps50	Schweizer	*P. m*
Mmp20	Balderrama	*M.m*	LOC114708899	Balderrama	*P.l*	LOC102910196	Schweizer	*P.m*	Wdr33	Schweizer	*P. m*
Mmp3	Balderrama	*M.m*	LOC114708913	Balderrama	*P.l*	LOC102910510	Schweizer	*P.m*	Wdyhv1	Schweizer	*P. m*
Mndal	Balderrama	*M.m*	LOC114709118	Balderrama	*P.l*	LOC102910758	Schweizer	*P.m*	Wwtr1	Schweizer	*P. m*
Mov10	Balderrama	*M.m*	LOC114709884	Balderrama	*P.l*	LOC102910861	Schweizer	*P.m*	Xpot	Schweizer	*P. m*
Mrgpra2a	Balderrama	*M.m*	LOC114710025	Balderrama	*P.l*	LOC102910947	Schweizer	*P.m*	Ythdc1	Schweizer	*P. m*
Mrgpra2b	Balderrama	*M.m*	LOC114710130	Balderrama	*P.l*	LOC102910975	Schweizer	*P.m*	Zbtb16	Schweizer	*P. m*
Ms4a4a	Balderrama	*M.m*	LOC114710246	Balderrama	*P.l*	LOC102911074	Schweizer	*P.m*	Zbtb39	Schweizer	*P. m*
Ms4a4c	Balderrama	*M.m*	LOC114710254	Balderrama	*P.l*	LOC102911142	Schweizer	*P.m*	Zbtb44	Schweizer	*P. m*
Ms4a4d	Balderrama	*M.m*	LOC114710804	Balderrama	*P.l*	LOC102911167	Schweizer	*P.m*	Zbtb45	Schweizer	*P. m*
Ms4a6d	Balderrama	*M.m*	LOC114710822	Balderrama	*P.l*	LOC102911278	Schweizer	*P.m*	Zbtb6	Schweizer	*P. m*

Msr1	Balderrama	*M.m*	Loxl2	Balderrama	*P.l*	LOC102911575	Schweizer	*P.m*	Zc3h7a	Schweizer	*P. m*
Mt1	Balderrama	*M.m*	Lpo	Balderrama	*P.l*	LOC102911621	Schweizer	*P.m*	Zdbf2	Schweizer	*P. m*
Mt2	Balderrama	*M.m*	Lrg1	Balderrama	*P.l*	LOC102911850	Schweizer	*P.m*	Zdhhc13	Schweizer	*P. m*
Mt4	Balderrama	*M.m*	Lyve1	Balderrama	*P.l*	LOC102912008	Schweizer	*P.m*	Zfpm2	Schweizer	*P. m*
Muc1	Balderrama	*M.m*	Macc1	Balderrama	*P.l*	LOC102912016	Schweizer	*P.m*	Zhx2	Schweizer	*P. m*
Mx1	Balderrama	*M.m*	Maff	Balderrama	*P.l*	LOC102912036	Schweizer	*P.m*	Zmat3	Schweizer	*P. m*
Mx2	Balderrama	*M.m*	Mamstr	Balderrama	*P.l*	LOC102912117	Schweizer	*P.m*	Znf202	Schweizer	*P. m*
Mxd1	Balderrama	*M.m*	Marcksl1	Balderrama	*P.l*	LOC102912198	Schweizer	*P.m*	Znf24	Schweizer	*P. m*
Neb	Balderrama	*M.m*	Mcidas	Balderrama	*P.l*	LOC102912308	Schweizer	*P.m*	Znf317	Schweizer	*P. m*
Nfil3	Balderrama	*M.m*	Medag	Balderrama	*P.l*	LOC102912376	Schweizer	*P.m*	Znf318	Schweizer	*P. m*
Nmi	Balderrama	*M.m*	Mefv	Balderrama	*P.l*	LOC102912415	Schweizer	*P.m*	Znf436	Schweizer	*P. m*
Nod2	Balderrama	*M.m*	Meox1	Balderrama	*P.l*	LOC102912625	Schweizer	*P.m*	Znf451	Schweizer	*P. m*
Nos2	Balderrama	*M.m*	Mgam	Balderrama	*P.l*	LOC102912747	Schweizer	*P.m*	Znf512	Schweizer	*P. m*
Nr4a3	Balderrama	*M.m*	Mitd1	Balderrama	*P.l*	LOC102912792	Schweizer	*P.m*	Znf518b	Schweizer	*P. m*
Nt5c1a	Balderrama	*M.m*	Mlph	Balderrama	*P.l*	LOC102912857	Schweizer	*P.m*	Znf521	Schweizer	*P. m*
Nts	Balderrama	*M.m*	Mmp8	Balderrama	*P.l*	LOC102912934	Schweizer	*P.m*	Znf638	Schweizer	*P. m*
Nudt17	Balderrama	*M.m*	Ms4a3	Balderrama	*P.l*	LOC102912971	Schweizer	*P.m*	Znf706	Schweizer	*P. m*
Nupr1	Balderrama	*M.m*	Mst1r	Balderrama	*P.l*	LOC102913033	Schweizer	*P.m*	Znf831	Schweizer	*P. m*
Oacyl	Balderrama	*M.m*	Musk	Balderrama	*P.l*	LOC102913167	Schweizer	*P.m*	Znfx1	Schweizer	*P. m*
Oas1a	Balderrama	*M.m*	Mymk	Balderrama	*P.l*	LOC102913247	Schweizer	*P.m*	Zscan30	Schweizer	*P. m*
Oas1b	Balderrama	*M.m*	Nampt	Balderrama	*P.l*	LOC102913558	Schweizer	*P.m*	Zw10	Schweizer	*P. m*
Oas1e	Balderrama	*M.m*	Neurl3	Balderrama	*P.l*	LOC102913583	Schweizer	*P.m*			

Supplemental Table 3: Statistical values for body temperature analysis between lowland and highland-ancestry deer mice gathered through the residuals (difference between predicted and actual temperatures) which were generated for each individual for one week. For the first three days, residuals were further divided into active and rest phase temperatures. The residuals were averaged by population, fitted to a linear mixed effect model, and statistical values were calculated through a type 3 ANOVA. Mouse ID was accounted for as a random effect. For all days and phases, the numerator degrees of freedom were 1, and the denominator degrees of freedom was 18.0. Rows with a $P < 0.05$ are bolded.

Day	Hours	F-statistic	P-value
1	0-24	2.39	0.140
	0-12 (active)	**5.90**	**0.026**
	12-24 (rest)	0.286	0.599
2	**24-48**	**7.41**	**0.014**
	24-36 (active)	**9.48**	**0.006**
	36-48 (rest)	3.51	0.077
3	48-72	3.94	0.063
	48-60 (active)	3.69	0.071
	60-72 (rest)	3.00	0.100
4	**72-96**	**4.55**	**0.047**
5	96-120	2.79	0.112
6	120-144	4.14	0.057
7	144-168	0.483	0.496
Overall	**0-240**	**4.65**	**0.045**

Supplemental Table 4: List of the 86 differentially expressed genes (DEGs) that are shared across the three myomorph species (*Peromyscus maniculatus, Peromyscus leucopus,* and *Mus musculus*).

Gene_ID	P. maniculatus logFC	P. maniculatus adj_P.val	P. leucopus logFC	P. leucopus adj_P.val	M. musculus logFC	M. musculus adj_P.val
Cxcl5	-1.617353457	2.041937053	2.98847981	2.17651E-31	5.486739251	1.3163E-95
Fscn1	1.093525996	3.058035499	2.28427019	9.4585E-35	2.578339409	6.26606E-43
Medag	1.548395897	3.457591202	3.34082705	4.26018E-10	2.409435313	1.58773E-22
Maff	1.023390124	2.774317835	2.25994541	5.52573E-64	3.294441462	1.51175E-89
Upp1	0.668565421	2.4399068	2.96257842	1.01305E-73	3.816860763	5.27343E-40
Plat	0.799304079	2.198692107	2.60822651	1.25828E-49	2.530532926	1.40415E-09
Prss23	0.861166834	2.017766183	2.17984187	6.60364E-61	2.08123372	2.97045E-35
Cebpb	0.562413996	2.084012838	2.64156231	1.94851E-93	2.740633024	2.97569E-37
Stat2	0.738146527	1.028172778	2.16408391	6.80441E-79	3.029770361	2.7394E-118
Ccrl2	-0.818400156	0.808319769	3.89685749	1.7641E-175	3.465083026	5.52824E-61
Cebpd	0.684596344	2.640051364	3.50806394	2.4124E-145	2.604437718	9.61762E-30
Ier3	-0.584732619	1.777584312	2.05835826	3.15826E-27	2.766555698	5.7243E-27
Arid5a	0.481868559	2.185116267	2.31409889	1.96067E-56	2.075379569	7.42941E-26
Ccn4	0.292017771	0.920478645	2.39918631	7.68801E-36	2.369986211	5.33834E-11
Il1b	0.819487432	5.211902744	3.47891381	6.86781E-67	3.886037212	3.98205E-62
Cfb	0.659332282	3.336949982	3.57647637	2.7919E-130	2.435368436	3.77839E-37
Fpr1	-0.521002551	2.395711634	3.03847926	3.98398E-42	2.58904077	1.72045E-32
Pfkfb3	0.443102315	2.076923456	2.81011599	5.1486E-234	2.641081646	5.00082E-47
Snx10	-0.326821139	0.900299465	2.63135069	1.51573E-76	2.217383931	8.73499E-47
Trex1	0.407138963	1.130585434	2.31908884	1.4043E-105	2.214132018	6.30748E-24
Mitd1	0.39019835	1.004194746	2.06509421	1.30924E-36	2.216586091	2.92065E-80
Nfkbia	0.400481614	2.188202159	2.82488136	2.0046E-129	2.492067817	1.12349E-77
Gfpt2	0.669684994	2.53459546	2.95564252	1.21637E-16	2.156470366	1.50399E-17
Nlrc5	0.474754819	1.815206259	2.32411437	1.35011E-25	2.529248324	1.28228E-26
Tubb6	0.338235004	2.087962307	2.88374956	9.0861E-48	2.767581017	1.6226E-67
Ppa1	0.288582935	1.538374703	2.18252534	1.73611E-79	2.720643792	9.05432E-39
Samhd1	0.397709003	1.826372409	3.02520909	4.5426E-102	2.312898717	6.0003E-51
Parp12	0.333198769	0.970064745	2.42250357	2.33711E-50	3.821692324	4.6576E-127
Ubd	1.046081907	4.869152488	4.80821652	4.19244E-41	2.145364662	2.95642E-08
Gfra1	0.447431652	1.415484214	2.18446479	3.23611E-19	3.494472278	2.62143E-35
Pml	0.393787036	1.40312096	2.18983044	1.46253E-83	2.371234449	2.53753E-86
Tnfaip3	0.569785165	3.399816975	3.65768961	1.4885E-289	3.294472334	1.84598E-83
Nfkbiz	0.350208836	1.957223255	2.99136522	2.2875E-149	2.855608019	1.8964E-53
Cd274	0.376540221	2.280208411	2.64569027	2.0845E-102	3.432016491	3.00679E-70

Lcn2	-0.739580071	2.549734243	2.79486766	3.38885E-23	2.324722611	0.002872927
Nlrp3	0.319707297	1.118832901	2.01066864	7.11225E-27	2.488294442	1.66061E-44
Vcan	0.681960493	4.762736035	4.12934599	8.52895E-68	4.768366693	1.63357E-43
Rgs1	0.527969381	2.471069823	2.18584171	1.98799E-26	3.445425592	4.69685E-46
Nr4a3	0.40023407	1.870247736	2.14187865	3.09163E-22	3.507400737	1.98108E-46
Il15ra	0.360192014	1.031325588	2.82688832	6.32533E-35	2.624047629	3.80427E-76
Dusp1	-0.305408088	0.778658269	2.20935362	1.60023E-45	3.022861358	5.61751E-65
Timp1	0.549126884	4.563822045	3.56698926	1.0191E-110	4.84623562	8.4358E-63
Helz2	0.333169933	1.862851019	3.04595658	2.40752E-50	2.927164838	1.45001E-43
Nfil3	0.466099693	3.555441145	3.62528199	2.18411E-84	2.735086007	3.60586E-34
Icam1	-0.21744014	1.822059165	3.27576459	2.1201E-214	2.596253225	1.25327E-62
Sdc4	0.309510358	3.555617335	4.40027786	1.4757E-183	3.546101261	4.09956E-75
Sod2	0.326418522	3.847324051	4.43667605	0	2.620764195	2.67388E-85
Xaf1	0.329347419	1.208073275	2.5502077	1.08673E-71	3.364157763	1.90024E-54
Csrnp1	0.33301721	2.127972716	2.56114595	8.39912E-92	2.045976327	1.95279E-46
Kcne4	0.413232397	3.120841111	3.12846113	1.20831E-28	2.663959877	4.8519E-25
Batf	0.595016664	3.550054052	2.98053891	2.3831E-89	2.329925436	1.64493E-28
Slc15a3	0.226291362	1.68484418	2.37663648	1.0943E-214	2.667222416	1.48292E-85
Rtp4	0.497798734	2.697012403	3.09890369	3.68508E-26	3.951827499	5.0765E-101
Socs1	0.603379902	3.908161978	3.72180313	4.2133E-120	3.969491543	2.01483E-59
Edn1	0.422521558	3.202308606	3.49196731	4.98443E-36	3.65051117	1.27987E-75
Ifih1	0.372067949	1.636429155	4.16855466	2.04169E-94	4.106177752	2.80907E-94
Irf7	0.451559483	2.545952164	3.37504701	3.08424E-23	3.952958991	4.32374E-61
Bcl3	0.224525819	2.700713148	2.41973666	7.9387E-106	2.547841558	6.20988E-54
Socs3	0.325686495	4.119584614	3.49289279	7.5457E-238	4.296562797	2.9552E-159
Dhx58	0.360023431	2.444168124	3.45668315	2.72736E-41	3.994586216	4.1438E-112
Ddx58	0.222510972	1.557690651	3.22390932	1.70509E-56	3.043397608	3.78416E-60
Cgas	0.151920356	1.148523148	2.63587511	1.63034E-65	2.42155091	1.73789E-26
Batf2	0.321622507	2.259432491	2.90122653	3.6042E-108	3.639794251	3.80017E-27
Parp9	0.153062568	1.556058438	2.05147275	4.78545E-59	3.214872903	3.1909E-136
Nampt	0.110776363	1.077405237	2.44472812	8.3896E-128	2.843339337	6.12429E-63
Slc2a6	0.192270397	2.925980725	3.54162259	4.7561E-234	2.016724371	2.4626E-34
Gadd45b	0.194819064	2.735275005	2.56792397	6.47643E-66	2.964017283	4.78891E-53
Herc6	-0.305518648	2.218745179	4.66947727	8.77415E-35	3.883040856	2.9532E-102
Cx3cl1	0.3805231	4.352876118	5.47932812	4.6008E-135	2.411068048	4.6802E-21
Nupr1	0.122415117	1.065343291	3.66929785	6.40904E-40	2.801806788	2.24931E-33
Serpine1	0.199902063	5.651710035	4.87174449	2.2491E-101	4.051559844	9.79624E-48
Tnf	-0.105493929	1.611960777	3.56067922	3.53768E-97	3.55009658	1.55341E-64

Marcksl1	0.085702387	2.6360073	3.39542754	6.6782E-109	3.288350011	7.79484E-65
Tlr2	-0.059464547	2.237862624	2.81880546	1.9977E-100	2.055158204	4.1591E-58
Eif2ak2	0.075655446	1.614351884	3.27440936	4.01404E-47	3.738882625	4.405E-105
Dtx3l	0.058730233	1.72116287	2.59635681	2.44093E-79	3.01183212	1.10256E-48
Cxcl10	0.115355369	5.126022613	5.70977535	4.2565E-162	6.242638702	5.80442E-81
Tap1	-0.030709826	1.850467099	2.19226285	4.77435E-89	2.095863988	2.88038E-46
Tnfaip2	0.029996166	3.108087642	3.09482615	2.43031E-86	2.288188242	4.14903E-34
Tnip3	0.042113528	3.009352626	4.71154675	4.32068E-66	5.933984403	1.85477E-43
Usp18	-0.025512697	3.224312942	4.41147382	3.03857E-25	4.850585876	1.66332E-88
Isg15	-0.024881231	2.832850205	3.93094102	1.21773E-18	4.369397241	1.88134E-32
Cdkn1a	0.00988555	2.867853303	3.04843901	6.8554E-105	3.194727737	2.1163E-106
Il1a	0.007881537	1.782777619	2.53332022	1.67496E-18	3.416062531	4.10967E-54
Lgals9	0.007056211	1.356751471	2.4643079	9.87191E-46	2.678090996	2.96975E-53
Uba7	-0.006694929	1.695525082	2.92906763	7.33922E-45	2.00233888	1.74302E-43

Supplemental Table 5: Enriched GO terms from a list of significantly upregulated genes (P < 0.05 and logFC > 0.5) in response to LPS.

Term ID	Term Name	P value	Term Size	Precision	Intersection Size	Query Size
GO:0006952	defense response	6.49E-28	725	0.15186246	212	1396
GO:0042254	ribosome biogenesis	2.71E-27	164	0.05945559	83	1396
GO:0043207	response to external biotic stimulus	3.73E-27	655	0.13968481	195	1396
GO:0051707	response to other organism	3.73E-27	655	0.13968481	195	1396
GO:0009605	response to external stimulus	3.73E-27	1007	0.18767908	262	1396
GO:0009607	response to biotic stimulus	3.73E-27	680	0.14326648	200	1396
GO:0044419	biological process involved in interspecies interaction between organisms	7.10E-25	738	0.14756447	206	1396
GO:0002376	immune system process	7.10E-25	1226	0.21131805	295	1396
GO:1901652	response to peptide	2.61E-23	437	0.1017192	142	1396
GO:0034097	response to cytokine	6.12E-23	436	0.10100287	141	1396
GO:0098542	defense response to other organism	6.17E-22	484	0.10673352	149	1396
GO:0032101	regulation of response to external stimulus	3.95E-21	557	0.11604585	162	1396
GO:0031347	regulation of defense response	4.33E-21	416	0.09527221	133	1396
GO:0022613	ribonucleoprotein complex biogenesis	4.37E-21	234	0.06590258	92	1396
GO:0140546	defense response to symbiont	1.40E-19	426	0.09455587	132	1396
GO:0006955	immune response	1.49E-19	734	0.13753582	192	1396
GO:0071345	cellular response to cytokine stimulus	2.89E-19	396	0.08954155	125	1396
GO:0001816	cytokine production	3.49E-19	397	0.08954155	125	1396
GO:0001817	regulation of cytokine production	1.00E-18	392	0.08810888	123	1396
GO:0002682	regulation of immune system process	1.22E-18	808	0.14541547	203	1396
GO:0045087	innate immune response	2.81E-17	368	0.08237822	115	1396
GO:0051239	regulation of multicellular organismal process	1.85E-16	1390	0.21203438	296	1396
GO:0042221	response to chemical	6.32E-16	1457	0.21848138	305	1396
GO:0006954	inflammatory response	2.81E-15	340	0.0752149	105	1396

GO:0001819	positive regulation of cytokine production	6.39E-15	250	0.06088825	85	1396
GO:0009617	response to bacterium	2.80E-14	274	0.06375358	89	1396
GO:0051240	positive regulation of multicellular organismal process	2.94E-14	766	0.13108883	183	1396
GO:0019221	cytokine-mediated signaling pathway	2.94E-14	211	0.05372493	75	1396
GO:0009615	response to virus	5.78E-14	196	0.0508596	71	1396
GO:0006364	rRNA processing	6.23E-14	93	0.03223496	45	1396
GO:0002831	regulation of response to biotic stimulus	6.25E-14	292	0.06590258	92	1396
GO:0031349	positive regulation of defense response	1.74E-13	268	0.06160458	86	1396
GO:0032103	positive regulation of response to external stimulus	1.99E-13	341	0.07234957	101	1396
GO:0016072	rRNA metabolic process	1.99E-13	114	0.03581662	50	1396
GO:0050727	regulation of inflammatory response	2.01E-13	179	0.04727794	66	1396
GO:0050776	regulation of immune response	5.22E-13	474	0.09025788	126	1396
GO:0080134	regulation of response to stress	6.75E-13	734	0.1239255	173	1396
GO:0006950	response to stress	7.84E-13	1835	0.252149	352	1396
GO:0002684	positive regulation of immune system process	8.91E-13	569	0.10243553	143	1396
GO:0048518	positive regulation of biological process	1.13E-12	3102	0.38610315	539	1396
GO:0045088	regulation of innate immune response	1.33E-12	249	0.05730659	80	1396
GO:0048522	positive regulation of cellular process	4.43E-12	2942	0.36747851	513	1396
GO:0001775	cell activation	8.21E-12	601	0.10458453	146	1396
GO:0002237	response to molecule of bacterial origin	1.13E-11	158	0.04154728	58	1396
GO:0045321	leukocyte activation	1.86E-11	535	0.09527221	133	1396
GO:0010467	gene expression	6.13E-11	3053	0.37464183	523	1396
GO:0010557	positive regulation of macromolecule biosynthetic process	9.11E-11	1266	0.18194842	254	1396
GO:0032501	multicellular organismal process	9.62E-11	2977	0.36604585	511	1396
GO:0042274	ribosomal small subunit biogenesis	1.02E-10	59	0.0222063	31	1396
GO:0032496	response to lipopolysaccharide	1.33E-10	149	0.03868195	54	1396
GO:0009891	positive regulation of biosynthetic process	1.79E-10	1312	0.18624642	260	1396

GO:0010604	positive regulation of macromolecule metabolic process	2.12E-10	1634	0.22206304	310	1396
GO:0050896	response to stimulus	2.84E-10	3841	0.4512894	630	1396
GO:0042981	regulation of apoptotic process	5.04E-10	708	0.11389685	159	1396
GO:0009893	positive regulation of metabolic process	7.69E-10	1795	0.23782235	332	1396
GO:0006915	apoptotic process	1.07E-09	899	0.13610315	190	1396
GO:0009059	macromolecule biosynthetic process	1.07E-09	3287	0.39326648	549	1396
GO:0008219	cell death	1.07E-09	942	0.14111748	197	1396
GO:0012501	programmed cell death	1.07E-09	942	0.14111748	197	1396
GO:0042273	ribosomal large subunit biogenesis	1.17E-09	24	0.01289398	18	1396
GO:0043067	regulation of programmed cell death	1.54E-09	742	0.11676218	163	1396
GO:0007165	signal transduction	2.50E-09	2555	0.31661891	442	1396
GO:0051241	negative regulation of multicellular organismal process	3.03E-09	506	0.08667622	121	1396
GO:0051607	defense response to virus	4.41E-09	144	0.03581662	50	1396
GO:0009058	biosynthetic process	4.41E-09	3764	0.43839542	612	1396
GO:0050778	positive regulation of immune response	4.64E-09	383	0.07020057	98	1396
GO:0007166	cell surface receptor signaling pathway	5.36E-09	1272	0.1769341	247	1396
GO:0048583	regulation of response to stimulus	5.43E-09	1998	0.25644699	358	1396
GO:0002274	myeloid leukocyte activation	7.93E-09	120	0.03151862	44	1396
GO:0042742	defense response to bacterium	7.93E-09	95	0.02722063	38	1396
GO:0048584	positive regulation of response to stimulus	9.66E-09	1172	0.16475645	230	1396
GO:0002833	positive regulation of response to biotic stimulus	1.33E-08	224	0.04727794	66	1396
GO:0071216	cellular response to biotic stimulus	2.12E-08	119	0.03080229	43	1396
GO:0071219	cellular response to molecule of bacterial origin	2.12E-08	102	0.02793696	39	1396
GO:0048869	cellular developmental process	2.26E-08	1827	0.23567335	329	1396
GO:0030154	cell differentiation	2.26E-08	1827	0.23567335	329	1396
GO:0050729	positive regulation of inflammatory response	2.34E-08	63	0.02077364	29	1396
GO:0071222	cellular response to lipopolysaccharide	2.99E-08	99	0.02722063	38	1396

GO:0050793	regulation of developmental process	3.80E-08	1177	0.16332378	228	1396
GO:0050865	regulation of cell activation	3.80E-08	333	0.06160458	86	1396
GO:0032102	negative regulation of response to external stimulus	4.19E-08	186	0.04083095	57	1396
GO:0060255	regulation of macromolecule metabolic process	5.38E-08	2736	0.32951289	460	1396
GO:2000026	regulation of multicellular organismal development	5.95E-08	677	0.10458453	146	1396
GO:0045089	positive regulation of innate immune response	7.05E-08	213	0.04441261	62	1396
GO:0140888	interferon-mediated signaling pathway	7.05E-08	51	0.01790831	25	1396
GO:0002683	negative regulation of immune system process	7.34E-08	269	0.05229226	73	1396
GO:0009889	regulation of biosynthetic process	7.90E-08	2370	0.29083095	406	1396
GO:0034341	response to type II interferon	8.04E-08	66	0.02077364	29	1396
GO:0010468	regulation of gene expression	8.59E-08	2228	0.27578797	385	1396
GO:0010556	regulation of macromolecule biosynthetic process	8.74E-08	2290	0.28223496	394	1396
GO:0023052	signaling	1.11E-07	2730	0.3273639	457	1396
GO:0007154	cell communication	1.16E-07	2731	0.3273639	457	1396
GO:0010628	positive regulation of gene expression	1.24E-07	602	0.09455587	132	1396
GO:0002694	regulation of leukocyte activation	1.72E-07	306	0.05659026	79	1396
GO:0051716	cellular response to stimulus	2.19E-07	3237	0.37750716	527	1396
GO:0046649	lymphocyte activation	2.59E-07	458	0.07593123	106	1396
GO:0050866	negative regulation of cell activation	3.34E-07	116	0.0286533	40	1396
GO:0033993	response to lipid	3.63E-07	338	0.06017192	84	1396
GO:0032502	developmental process	4.83E-07	2829	0.33452722	467	1396
GO:0051246	regulation of protein metabolic process	5.04E-07	902	0.1282235	179	1396
GO:0070887	cellular response to chemical stimulus	6.33E-07	936	0.13180516	184	1396
GO:0048856	anatomical structure development	6.80E-07	2654	0.31590258	441	1396
GO:0045595	regulation of cell differentiation	6.80E-07	727	0.10744986	150	1396
GO:0032606	type I interferon production	7.26E-07	80	0.0222063	31	1396
GO:0032479	regulation of type I interferon production	7.26E-07	80	0.0222063	31	1396

GO:0032649	regulation of type II interferon production	7.42E-07	64	0.01934097	27	1396
GO:0002218	activation of innate immune response	7.44E-07	176	0.03724928	52	1396
GO:0002221	pattern recognition receptor signaling pathway	8.43E-07	162	0.03510029	49	1396
GO:0002695	negative regulation of leukocyte activation	8.70E-07	102	0.02578797	36	1396
GO:0032609	type II interferon production	1.07E-06	65	0.01934097	27	1396
GO:0002758	innate immune response-activating signaling pathway	1.27E-06	164	0.03510029	49	1396
GO:0030097	hemopoiesis	1.31E-06	578	0.08882521	124	1396
GO:0043065	positive regulation of apoptotic process	1.60E-06	257	0.04799427	67	1396
GO:1901700	response to oxygen-containing compound	1.62E-06	640	0.09598854	134	1396
GO:0043068	positive regulation of programmed cell death	1.67E-06	268	0.04942693	69	1396
GO:0008150	biological_process	1.84E-06	8517	0.86461318	1207	1396
GO:0050794	regulation of cellular process	1.98E-06	5150	0.55945559	781	1396
GO:0050789	regulation of biological process	2.09E-06	5325	0.57593123	804	1396
GO:0001818	negative regulation of cytokine production	2.09E-06	152	0.03295129	46	1396
GO:0002252	immune effector process	2.10E-06	313	0.05515759	77	1396
GO:0048646	anatomical structure formation involved in morphogenesis	2.29E-06	590	0.08954155	125	1396
GO:0051249	regulation of lymphocyte activation	2.39E-06	276	0.05014327	70	1396
GO:0002253	activation of immune response	2.68E-06	293	0.05229226	73	1396
GO:0060759	regulation of response to cytokine stimulus	3.14E-06	98	0.0243553	34	1396
GO:0031348	negative regulation of defense response	3.64E-06	126	0.0286533	40	1396
GO:0050777	negative regulation of immune response	3.93E-06	90	0.02292264	32	1396
GO:0042116	macrophage activation	6.13E-06	54	0.01647564	23	1396
GO:0019222	regulation of metabolic process	6.15E-06	3013	0.3474212	485	1396
GO:0065007	biological regulation	7.38E-06	5456	0.58524355	817	1396
GO:0045597	positive regulation of cell differentiation	7.38E-06	396	0.06446991	90	1396
GO:0009966	regulation of signal transduction	7.38E-06	1545	0.19484241	272	1396
GO:0071396	cellular response to lipid	8.02E-06	252	0.04584527	64	1396

GO:0043066	negative regulation of apoptotic process	9.40E-06	427	0.06805158	95	1396
GO:1902570	protein localization to nucleolus	1.00E-05	15	0.00787966	11	1396
GO:0051094	positive regulation of developmental process	1.01E-05	600	0.08882521	124	1396
GO:0002757	immune response-activating signaling pathway	1.02E-05	270	0.04799427	67	1396
GO:0060760	positive regulation of response to cytokine stimulus	1.05E-05	44	0.01432665	20	1396
GO:0043170	macromolecule metabolic process	1.16E-05	4636	0.50573066	706	1396
GO:0050830	defense response to Gram-positive bacterium	1.18E-05	37	0.01289398	18	1396
GO:0051250	negative regulation of lymphocyte activation	1.29E-05	90	0.0222063	31	1396
GO:0009987	cellular process	1.32E-05	8276	0.84025788	1173	1396
GO:0009888	tissue development	1.39E-05	941	0.12750716	178	1396
GO:1901701	cellular response to oxygen-containing compound	1.43E-05	502	0.07664756	107	1396
GO:0042110	T cell activation	1.44E-05	317	0.05372493	75	1396
GO:0050900	leukocyte migration	1.51E-05	193	0.03724928	52	1396
GO:0045824	negative regulation of innate immune response	1.55E-05	45	0.01432665	20	1396
GO:0009967	positive regulation of signal transduction	1.61E-05	804	0.11174785	156	1396
GO:0032481	positive regulation of type I interferon production	1.66E-05	49	0.01504298	21	1396
GO:0071346	cellular response to type II interferon	1.70E-05	53	0.01575931	22	1396
GO:0043069	negative regulation of programmed cell death	1.73E-05	451	0.07020057	98	1396
GO:0001959	regulation of cytokine-mediated signaling pathway	2.09E-05	92	0.0222063	31	1396
GO:0034340	response to type I interferon	2.31E-05	46	0.01432665	20	1396
GO:1903131	mononuclear cell differentiation	2.43E-05	299	0.0508596	71	1396
GO:0002764	immune response-regulating signaling pathway	2.49E-05	277	0.04799427	67	1396
GO:0023051	regulation of signaling	2.53E-05	1704	0.20916905	292	1396
GO:0030099	myeloid cell differentiation	2.82E-05	278	0.04799427	67	1396
GO:2001233	regulation of apoptotic signaling pathway	2.85E-05	229	0.04154728	58	1396
GO:0071706	tumor necrosis factor superfamily cytokine production	3.01E-05	89	0.02148997	30	1396
GO:1903555	regulation of tumor necrosis factor superfamily cytokine production	3.01E-05	89	0.02148997	30	1396

GO:0097529	myeloid leukocyte migration	3.41E-05	108	0.0243553	34	1396
GO:0010646	regulation of cell communication	3.89E-05	1699	0.20773639	290	1396
GO:0002521	leukocyte differentiation	3.95E-05	360	0.05802292	81	1396
GO:0001568	blood vessel development	4.03E-05	395	0.06232092	87	1396
GO:0002250	adaptive immune response	4.52E-05	174	0.03366762	47	1396
GO:0060333	type II interferon-mediated signaling pathway	4.52E-05	14	0.00716332	10	1396
GO:0038061	non-canonical NF-kappaB signal transduction	4.81E-05	73	0.01862464	26	1396
GO:0048519	negative regulation of biological process	4.92E-05	2661	0.30659026	428	1396
GO:0007275	multicellular organism development	4.92E-05	2095	0.24856734	347	1396
GO:0007155	cell adhesion	5.82E-05	634	0.09025788	126	1396
GO:0030595	leukocyte chemotaxis	6.50E-05	111	0.0243553	34	1396
GO:0048514	blood vessel morphogenesis	6.59E-05	336	0.05444126	76	1396
GO:0002460	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	6.89E-05	156	0.03080229	43	1396
GO:0141124	intracellular signaling cassette	9.15E-05	912	0.12106017	169	1396
GO:0060337	type I interferon-mediated signaling pathway	9.62E-05	42	0.01289398	18	1396
GO:0071357	cellular response to type I interferon	9.62E-05	42	0.01289398	18	1396
GO:0019882	antigen processing and presentation	9.62E-05	54	0.01504298	21	1396
GO:0071674	mononuclear cell migration	9.73E-05	113	0.0243553	34	1396
GO:0046631	alpha-beta T cell activation	9.73E-05	113	0.0243553	34	1396
GO:0007249	canonical NF-kappaB signal transduction	0.0001145	159	0.03080229	43	1396
GO:0035456	response to interferon-beta	0.00011818	18	0.00787966	11	1396
GO:0010608	post-transcriptional regulation of gene expression	0.00011877	273	0.04584527	64	1396
GO:0080090	regulation of primary metabolic process	0.00012129	2458	0.28366762	396	1396
GO:0002832	negative regulation of response to biotic stimulus	0.00012129	59	0.01575931	22	1396
GO:0006457	protein folding	0.00012207	95	0.02148997	30	1396
GO:0042330	taxis	0.00013258	197	0.03581662	50	1396
GO:0006935	chemotaxis	0.00013258	197	0.03581662	50	1396

GO:0035036	sperm-egg recognition	0.00013258	10	0.00573066	8	1396
GO:0060326	cell chemotaxis	0.000138	150	0.02936963	41	1396
GO:2001234	negative regulation of apoptotic signaling pathway	0.00014284	140	0.02793696	39	1396
GO:0001944	vasculature development	0.00014285	420	0.06375358	89	1396
GO:0042127	regulation of cell population proliferation	0.00014705	760	0.10315186	144	1396
GO:0043123	positive regulation of canonical NF-kappaB signal transduction	0.00014878	96	0.02148997	30	1396
GO:0001525	angiogenesis	0.000151	281	0.0465616	65	1396
GO:0045765	regulation of angiogenesis	0.00015564	156	0.03008596	42	1396
GO:0002697	regulation of immune effector process	0.00015678	193	0.03510029	49	1396
GO:0032640	tumor necrosis factor production	0.00015971	87	0.02005731	28	1396
GO:0032680	regulation of tumor necrosis factor production	0.00015971	87	0.02005731	28	1396
GO:0042060	wound healing	0.00016325	188	0.03438395	48	1396
GO:0032944	regulation of mononuclear cell proliferation	0.00016797	131	0.0265043	37	1396
GO:0002699	positive regulation of immune effector process	0.00016797	126	0.02578797	36	1396
GO:0001961	positive regulation of cytokine-mediated signaling pathway	0.00018294	40	0.01217765	17	1396
GO:0002224	toll-like receptor signaling pathway	0.00018294	40	0.01217765	17	1396
GO:0003158	endothelium development	0.00018294	83	0.01934097	27	1396
GO:0097530	granulocyte migration	0.00018375	65	0.01647564	23	1396
GO:0043122	regulation of canonical NF-kappaB signal transduction	0.00019161	142	0.02793696	39	1396
GO:0009611	response to wounding	0.00019165	244	0.04154728	58	1396
GO:0098586	cellular response to virus	0.00020043	29	0.01002865	14	1396
GO:0009719	response to endogenous stimulus	0.00021206	596	0.08381089	117	1396
GO:1902680	positive regulation of RNA biosynthetic process	0.00021206	811	0.10816619	151	1396
GO:0016070	RNA metabolic process	0.00021206	2096	0.24498567	342	1396
GO:0060429	epithelium development	0.00022472	572	0.08094556	113	1396
GO:0030098	lymphocyte differentiation	0.00022482	251	0.04226361	59	1396
GO:0002753	cytoplasmic pattern recognition receptor signaling pathway	0.00022893	108	0.02292264	32	1396

GO:0048585	negative regulation of response to stimulus	0.00023934	871	0.11461318	160	1396
GO:0032611	interleukin-1 beta production	0.00025748	41	0.01217765	17	1396
GO:0032651	regulation of interleukin-1 beta production	0.00025748	41	0.01217765	17	1396
GO:0051254	positive regulation of RNA metabolic process	0.0002617	879	0.11532951	161	1396
GO:0031399	regulation of protein modification process	0.00026362	482	0.07020057	98	1396
GO:0016477	cell migration	0.00026639	770	0.10315186	144	1396
GO:0045893	positive regulation of DNA-templated transcription	0.00027294	809	0.10744986	150	1396
GO:1901342	regulation of vasculature development	0.00027294	160	0.03008596	42	1396
GO:0050670	regulation of lymphocyte proliferation	0.00027294	129	0.02578797	36	1396
GO:0035556	intracellular signal transduction	0.00031641	1555	0.18767908	262	1396
GO:0023056	positive regulation of signaling	0.00033006	870	0.11389685	159	1396
GO:0002700	regulation of production of molecular mediator of immune response	0.0003328	115	0.02363897	33	1396
GO:0032612	interleukin-1 production	0.0003477	46	0.01289398	18	1396
GO:0032729	positive regulation of type II interferon production	0.0003477	46	0.01289398	18	1396
GO:2000630	positive regulation of miRNA metabolic process	0.0003477	46	0.01289398	18	1396
GO:0032652	regulation of interleukin-1 production	0.0003477	46	0.01289398	18	1396
GO:0035710	CD4-positive, alpha-beta T cell activation	0.00036925	77	0.01790831	25	1396
GO:0141187	nucleic acid biosynthetic process	0.00036925	2013	0.23495702	328	1396
GO:1903706	regulation of hemopoiesis	0.00037524	222	0.03796562	53	1396
GO:0000165	MAPK cascade	0.00038338	325	0.0508596	71	1396
GO:0097190	apoptotic signaling pathway	0.00041351	367	0.05587393	78	1396
GO:0050730	regulation of peptidyl-tyrosine phosphorylation	0.00041925	87	0.01934097	27	1396
GO:0001562	response to protozoan	0.00041925	17	0.00716332	10	1396
GO:0097398	cellular response to interleukin-17	0.00042102	14	0.00644699	9	1396
GO:1903557	positive regulation of tumor necrosis factor superfamily cytokine production	0.00044181	51	0.01361032	19	1396
GO:0009653	anatomical structure morphogenesis	0.00044241	1252	0.15472779	216	1396
GO:0045935	positive regulation of nucleobase-containing compound metabolic process	0.00046383	994	0.12679083	177	1396

GO:0006909	phagocytosis	0.00046383	107	0.0222063	31	1396
GO:0010647	positive regulation of cell communication	0.00048346	864	0.11246418	157	1396
GO:0046632	alpha-beta T cell differentiation	0.00048625	83	0.01862464	26	1396
GO:0008037	cell recognition	0.00049572	39	0.01146132	16	1396
GO:0002718	regulation of cytokine production involved in immune response	0.00052665	74	0.01719198	24	1396
GO:0002367	cytokine production involved in immune response	0.00052665	74	0.01719198	24	1396
GO:0030155	regulation of cell adhesion	0.00053263	406	0.06017192	84	1396
GO:0008283	cell population proliferation	0.00054045	951	0.1217765	170	1396
GO:0048871	multicellular organismal-level homeostasis	0.00055091	455	0.06590258	92	1396
GO:0008284	positive regulation of cell population proliferation	0.00057668	413	0.06088825	85	1396
GO:0048523	negative regulation of cellular process	0.00058755	2574	0.29083095	406	1396
GO:0070202	regulation of establishment of protein localization to chromosome	0.00058841	9	0.00501433	7	1396
GO:0007339	binding of sperm to zona pellucida	0.00058841	9	0.00501433	7	1396
GO:1904816	positive regulation of protein localization to chromosome, telomeric region	0.00058841	9	0.00501433	7	1396
GO:0032494	response to peptidoglycan	0.00058841	9	0.00501433	7	1396
GO:0042088	T-helper 1 type immune response	0.00059815	28	0.00931232	13	1396
GO:0045766	positive regulation of angiogenesis	0.00060786	89	0.01934097	27	1396
GO:0018108	peptidyl-tyrosine phosphorylation	0.00060786	89	0.01934097	27	1396
GO:0070663	regulation of leukocyte proliferation	0.00067064	140	0.0265043	37	1396
GO:1901698	response to nitrogen compound	0.00067784	397	0.05873926	82	1396
GO:0032946	positive regulation of mononuclear cell proliferation	0.00068595	80	0.01790831	25	1396
GO:0002440	production of molecular mediator of immune response	0.00068906	135	0.02578797	36	1396
GO:1902533	positive regulation of intracellular signal transduction	0.0006895	551	0.07664756	107	1396
GO:0002825	regulation of T-helper 1 type immune response	0.00074222	18	0.00716332	10	1396
GO:0034612	response to tumor necrosis factor	0.00076845	100	0.02077364	29	1396
GO:0070371	ERK1 and ERK2 cascade	0.00077381	141	0.0265043	37	1396
GO:0042832	defense response to protozoan	0.00082049	15	0.00644699	9	1396

GO:0097396	response to interleukin-17	0.00082049	15	0.00644699	9	1396
GO:0002443	leukocyte mediated immunity	0.00082091	179	0.03151862	44	1396
GO:0007159	leukocyte cell-cell adhesion	0.00084074	218	0.03653295	51	1396
GO:0046634	regulation of alpha-beta T cell activation	0.00085312	67	0.01575931	22	1396
GO:0006417	regulation of translation	0.00086781	174	0.03080229	43	1396
GO:0070555	response to interleukin-1	0.00086987	45	0.01217765	17	1396
GO:0002294	CD4-positive, alpha-beta T cell differentiation involved in immune response	0.00086987	45	0.01217765	17	1396
GO:0042093	T-helper cell differentiation	0.00086987	45	0.01217765	17	1396
GO:0032757	positive regulation of interleukin-8 production	0.00088035	29	0.00931232	13	1396
GO:0018212	peptidyl-tyrosine modification	0.00088035	91	0.01934097	27	1396
GO:1904851	positive regulation of establishment of protein localization to telomere	0.00089612	7	0.00429799	6	1396
GO:0032637	interleukin-8 production	0.00090862	41	0.01146132	16	1396
GO:0032677	regulation of interleukin-8 production	0.00090862	41	0.01146132	16	1396
GO:0032722	positive regulation of chemokine production	0.00092603	33	0.01002865	14	1396
GO:0014070	response to organic cyclic compound	0.00094529	294	0.04584527	64	1396
GO:0002720	positive regulation of cytokine production involved in immune response	0.00094761	54	0.01361032	19	1396
GO:0030855	epithelial cell differentiation	0.00095291	300	0.0465616	65	1396
GO:0032943	mononuclear cell proliferation	0.00095942	175	0.03080229	43	1396
GO:0071715	icosanoid transport	0.00098703	22	0.00787966	11	1396
GO:0019538	protein metabolic process	0.00098933	2449	0.2765043	386	1396
GO:0045637	regulation of myeloid cell differentiation	0.00101442	117	0.02292264	32	1396
GO:0032774	RNA biosynthetic process	0.00101657	1951	0.2256447	315	1396
GO:0070665	positive regulation of leukocyte proliferation	0.00101899	87	0.01862464	26	1396
GO:1990266	neutrophil migration	0.0010279	50	0.01289398	18	1396
GO:1904018	positive regulation of vasculature development	0.0010279	92	0.01934097	27	1396
GO:0031620	regulation of fever generation	0.0010279	5	0.00358166	5	1396
GO:0032760	positive regulation of tumor necrosis factor production	0.0010279	50	0.01289398	18	1396

GO:0009451	RNA modification	0.00103529	102	0.02077364	29	1396
GO:0022407	regulation of cell-cell adhesion	0.00105749	249	0.04011461	56	1396
GO:0002287	alpha-beta T cell activation involved in immune response	0.00111294	46	0.01217765	17	1396
GO:0002366	leukocyte activation involved in immune response	0.00111294	160	0.0286533	40	1396
GO:0002293	alpha-beta T cell differentiation involved in immune response	0.00111294	46	0.01217765	17	1396
GO:0034654	nucleobase-containing compound biosynthetic process	0.00111777	2143	0.24498567	342	1396
GO:0046651	lymphocyte proliferation	0.00112118	171	0.03008596	42	1396
GO:0098609	cell-cell adhesion	0.00112118	404	0.05873926	82	1396
GO:0050671	positive regulation of lymphocyte proliferation	0.00113238	78	0.01719198	24	1396
GO:0071887	leukocyte apoptotic process	0.00117195	83	0.01790831	25	1396
GO:0035239	tube morphogenesis	0.00117195	466	0.06590258	92	1396
GO:0032689	negative regulation of type II interferon production	0.00119052	19	0.00716332	10	1396
GO:0040011	locomotion	0.00119431	617	0.08309456	116	1396
GO:0050868	negative regulation of T cell activation	0.00124945	69	0.01575931	22	1396
GO:0002263	cell activation involved in immune response	0.00125033	161	0.0286533	40	1396
GO:0019220	regulation of phosphate metabolic process	0.00130608	406	0.05873926	82	1396
GO:0043367	CD4-positive, alpha-beta T cell differentiation	0.00132141	60	0.01432665	20	1396
GO:0048468	cell development	0.00132307	1278	0.15472779	216	1396
GO:0031401	positive regulation of protein modification process	0.00132307	304	0.0465616	65	1396
GO:0070741	response to interleukin-6	0.00141125	16	0.00644699	9	1396
GO:0002696	positive regulation of leukocyte activation	0.00142454	184	0.03151862	44	1396
GO:0051251	positive regulation of lymphocyte activation	0.00142968	173	0.03008596	42	1396
GO:0006399	tRNA metabolic process	0.00144828	130	0.0243553	34	1396
GO:0070372	regulation of ERK1 and ERK2 cascade	0.00144828	130	0.0243553	34	1396
GO:0030522	intracellular receptor signaling pathway	0.00144965	201	0.03366762	47	1396
GO:0050863	regulation of T cell activation	0.00144965	201	0.03366762	47	1396
GO:0046636	negative regulation of alpha-beta T cell activation	0.00147431	23	0.00787966	11	1396

GO:0070661	leukocyte proliferation	0.00147431	190	0.03223496	45	1396
GO:0050867	positive regulation of cell activation	0.00147431	190	0.03223496	45	1396
GO:0051174	regulation of phosphorus metabolic process	0.00149299	408	0.05873926	82	1396
GO:0140895	cell surface toll-like receptor signaling pathway	0.00154079	43	0.01146132	16	1396
GO:0045944	positive regulation of transcription by RNA polymerase II	0.00154079	615	0.08237822	115	1396
GO:0015908	fatty acid transport	0.00154079	43	0.01146132	16	1396
GO:1902531	regulation of intracellular signal transduction	0.00162532	1001	0.12464183	174	1396
GO:0060284	regulation of cell development	0.00165594	391	0.05659026	79	1396
GO:0035295	tube development	0.00182367	573	0.0773639	108	1396
GO:0002292	T cell differentiation involved in immune response	0.00187614	48	0.01217765	17	1396
GO:0048870	cell motility	0.0018786	832	0.10601719	148	1396
GO:0018193	peptidyl-amino acid modification	0.0018786	255	0.04011461	56	1396
GO:0009988	cell-cell recognition	0.00192141	20	0.00716332	10	1396
GO:0010629	negative regulation of gene expression	0.0019816	568	0.07664756	107	1396
GO:0002752	cell surface pattern recognition receptor signaling pathway	0.00206773	44	0.01146132	16	1396
GO:0045785	positive regulation of cell adhesion	0.00223065	245	0.03868195	54	1396
GO:1901224	positive regulation of non-canonical NF-kappaB signal transduction	0.00223613	40	0.01074499	15	1396
GO:0032648	regulation of interferon-beta production	0.00223613	40	0.01074499	15	1396
GO:2000147	positive regulation of cell motility	0.00223613	304	0.04584527	64	1396
GO:0032608	interferon-beta production	0.00223613	40	0.01074499	15	1396
GO:0008285	negative regulation of cell population proliferation	0.00223613	328	0.0487106	68	1396
GO:0006357	regulation of transcription by RNA polymerase II	0.00232074	975	0.12106017	169	1396
GO:0046330	positive regulation of JNK cascade	0.0023879	49	0.01217765	17	1396
GO:0060339	negative regulation of type I interferon-mediated signaling pathway	0.0023879	17	0.00644699	9	1396
GO:0090594	inflammatory response to wounding	0.0023879	17	0.00644699	9	1396
GO:0030217	T cell differentiation	0.0023879	183	0.03080229	43	1396
GO:0032309	icosanoid secretion	0.0023879	17	0.00644699	9	1396

GO:0032731	positive regulation of interleukin-1 beta production	0.0023879	28	0.00859599	12	1396
GO:0002673	regulation of acute inflammatory response	0.0023879	17	0.00644699	9	1396
GO:0030335	positive regulation of cell migration	0.0023879	299	0.04512894	63	1396
GO:0002526	acute inflammatory response	0.00239921	32	0.00931232	13	1396
GO:0043331	response to dsRNA	0.00239921	32	0.00931232	13	1396
GO:0051247	positive regulation of protein metabolic process	0.00245429	521	0.07091691	99	1396
GO:0070203	regulation of establishment of protein localization to telomere	0.00247436	8	0.00429799	6	1396
GO:0002922	positive regulation of humoral immune response	0.00247436	8	0.00429799	6	1396
GO:0002675	positive regulation of acute inflammatory response	0.00247436	8	0.00429799	6	1396
GO:0009892	negative regulation of metabolic process	0.00248273	1396	0.16547278	231	1396
GO:0048872	homeostasis of number of cells	0.0025135	235	0.03724928	52	1396
GO:0051248	negative regulation of protein metabolic process	0.00258208	318	0.04727794	66	1396
GO:1990823	response to leukemia inhibitory factor	0.0026217	68	0.01504298	21	1396
GO:0015718	monocarboxylic acid transport	0.0026395	54	0.01289398	18	1396
GO:0022603	regulation of anatomical structure morphogenesis	0.00272992	404	0.05730659	80	1396
GO:0043011	myeloid dendritic cell differentiation	0.00274525	14	0.00573066	8	1396
GO:0035872	nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway	0.00274525	14	0.00573066	8	1396
GO:0043408	regulation of MAPK cascade	0.00274525	277	0.04226361	59	1396
GO:0032675	regulation of interleukin-6 production	0.00274984	78	0.01647564	23	1396
GO:0032635	interleukin-6 production	0.00274984	78	0.01647564	23	1396
GO:0002286	T cell activation involved in immune response	0.00286157	59	0.01361032	19	1396
GO:0022409	positive regulation of cell-cell adhesion	0.00287028	157	0.02722063	38	1396
GO:1904814	regulation of protein localization to chromosome, telomeric region	0.00288454	11	0.00501433	7	1396
GO:0098581	detection of external biotic stimulus	0.00288454	11	0.00501433	7	1396
GO:0002827	positive regulation of T-helper 1 type immune response	0.00288454	11	0.00501433	7	1396
GO:0035924	cellular response to vascular endothelial growth factor stimulus	0.00296118	50	0.01217765	17	1396

GO:0071495	cellular response to endogenous stimulus	0.00296118	537	0.07234957	101	1396
GO:0002819	regulation of adaptive immune response	0.00298914	109	0.02077364	29	1396
GO:0002449	lymphocyte mediated immunity	0.00299157	141	0.02507163	35	1396
GO:0071347	cellular response to interleukin-1	0.00305541	37	0.01002865	14	1396
GO:0060338	regulation of type I interferon-mediated signaling pathway	0.00323699	33	0.00931232	13	1396
GO:1903038	negative regulation of leukocyte cell-cell adhesion	0.00323699	74	0.01575931	22	1396
GO:0002702	positive regulation of production of molecular mediator of immune response	0.00329464	84	0.01719198	24	1396
GO:0051093	negative regulation of developmental process	0.00350098	420	0.05873926	82	1396
GO:0001932	regulation of protein phosphorylation	0.00355015	322	0.04727794	66	1396
GO:0040017	positive regulation of locomotion	0.00356579	310	0.04584527	64	1396
GO:0002822	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	0.00373643	100	0.01934097	27	1396
GO:0070199	establishment of protein localization to chromosome	0.0037949	18	0.00644699	9	1396
GO:0010605	negative regulation of macromolecule metabolic process	0.00380712	1284	0.1525788	213	1396
GO:0044238	primary metabolic process	0.00399163	5058	0.52722063	736	1396
GO:0042542	response to hydrogen peroxide	0.00405127	38	0.01002865	14	1396
GO:0006418	tRNA aminoacylation for protein translation	0.00405127	38	0.01002865	14	1396
GO:0001660	fever generation	0.00405127	6	0.00358166	5	1396
GO:0002544	chronic inflammatory response	0.00405127	6	0.00358166	5	1396
GO:0031650	regulation of heat generation	0.00405127	6	0.00358166	5	1396
GO:0097527	necroptotic signaling pathway	0.00405127	6	0.00358166	5	1396
GO:0070427	nucleotide-binding oligomerization domain containing 1 signaling pathway	0.00405127	6	0.00358166	5	1396
GO:0000470	maturation of LSU-rRNA	0.00405127	6	0.00358166	5	1396
GO:1901222	regulation of non-canonical NF-kappaB signal transduction	0.00405127	56	0.01289398	18	1396
GO:0002246	wound healing involved in inflammatory response	0.00405127	6	0.00358166	5	1396
GO:0044085	cellular component biogenesis	0.00421365	1659	0.19126074	267	1396
GO:0002220	innate immune response activating cell surface receptor signaling pathway	0.00423581	47	0.01146132	16	1396

GO:0008152	metabolic process	0.00429857	5687	0.58667622	819	1396
GO:0030198	extracellular matrix organization	0.00432299	144	0.02507163	35	1396
GO:0045229	external encapsulating structure organization	0.00432299	144	0.02507163	35	1396
GO:0043062	extracellular structure organization	0.00432299	144	0.02507163	35	1396
GO:0050878	regulation of body fluid levels	0.00432299	144	0.02507163	35	1396
GO:1990868	response to chemokine	0.00452712	30	0.00859599	12	1396
GO:1990869	cellular response to chemokine	0.00452712	30	0.00859599	12	1396
GO:0097028	dendritic cell differentiation	0.00452754	26	0.00787966	11	1396
GO:0001503	ossification	0.00452754	195	0.03151862	44	1396
GO:0045446	endothelial cell differentiation	0.00452754	71	0.01504298	21	1396
GO:0071356	cellular response to tumor necrosis factor	0.00452754	86	0.01719198	24	1396
GO:0010562	positive regulation of phosphorus metabolic process	0.00457382	230	0.03581662	50	1396
GO:0071354	cellular response to interleukin-6	0.00457382	15	0.00573066	8	1396
GO:0045937	positive regulation of phosphate metabolic process	0.00457382	230	0.03581662	50	1396
GO:0023057	negative regulation of signaling	0.00457382	726	0.09240688	129	1396
GO:0035458	cellular response to interferon-beta	0.00457382	15	0.00573066	8	1396
GO:0002685	regulation of leukocyte migration	0.00499134	118	0.02148997	30	1396
GO:0071224	cellular response to peptidoglycan	0.00534728	4	0.00286533	4	1396
GO:0042592	homeostatic process	0.00534728	841	0.10458453	146	1396
GO:1904874	positive regulation of telomerase RNA localization to Cajal body	0.00534728	4	0.00286533	4	1396
GO:0002502	peptide antigen assembly with MHC class I protein complex	0.00534728	4	0.00286533	4	1396
GO:0002397	MHC class I protein complex assembly	0.00534728	4	0.00286533	4	1396
GO:0031652	positive regulation of heat generation	0.00534728	4	0.00286533	4	1396
GO:0002755	MyD88-dependent toll-like receptor signaling pathway	0.00534728	4	0.00286533	4	1396
GO:0031622	positive regulation of fever generation	0.00534728	4	0.00286533	4	1396
GO:0042554	superoxide anion generation	0.0053509	12	0.00501433	7	1396
GO:0070431	nucleotide-binding oligomerization domain containing 2 signaling pathway	0.0053509	12	0.00501433	7	1396

GO:0060334	regulation of type II interferon-mediated signaling pathway	0.00543969	9	0.00429799	6	1396
GO:0060330	regulation of response to type II interferon	0.00543969	9	0.00429799	6	1396
GO:0051769	regulation of nitric-oxide synthase biosynthetic process	0.00543969	9	0.00429799	6	1396
GO:0051767	nitric-oxide synthase biosynthetic process	0.00543969	9	0.00429799	6	1396
GO:0002474	antigen processing and presentation of peptide antigen via MHC class I	0.00543969	9	0.00429799	6	1396
GO:0002703	regulation of leukocyte mediated immunity	0.00562405	119	0.02148997	30	1396
GO:0050818	regulation of coagulation	0.00563071	35	0.00931232	13	1396
GO:0048513	animal organ development	0.00563071	1316	0.15472779	216	1396
GO:0046686	response to cadmium ion	0.00563071	19	0.00644699	9	1396
GO:0034976	response to endoplasmic reticulum stress	0.00563071	152	0.02578797	36	1396
GO:0001934	positive regulation of protein phosphorylation	0.00563071	209	0.03295129	46	1396
GO:0006396	RNA processing	0.00563071	510	0.06805158	95	1396
GO:0010648	negative regulation of cell communication	0.00566405	724	0.09169054	128	1396
GO:0097191	extrinsic apoptotic signaling pathway	0.00567061	141	0.0243553	34	1396
GO:0009968	negative regulation of signal transduction	0.00571769	698	0.08882521	124	1396
GO:0032602	chemokine production	0.00583914	44	0.01074499	15	1396
GO:0032642	regulation of chemokine production	0.00583914	44	0.01074499	15	1396
GO:2000628	regulation of miRNA metabolic process	0.00589983	58	0.01289398	18	1396
GO:0009725	response to hormone	0.00591607	311	0.04512894	63	1396
GO:0032732	positive regulation of interleukin-1 production	0.00591694	31	0.00859599	12	1396
GO:0032728	positive regulation of interferon-beta production	0.00611214	27	0.00787966	11	1396
GO:0030890	positive regulation of B cell proliferation	0.00611214	27	0.00787966	11	1396
GO:0043330	response to exogenous dsRNA	0.00611214	27	0.00787966	11	1396
GO:0002437	inflammatory response to antigenic stimulus	0.00611214	27	0.00787966	11	1396
GO:0060041	retina development in camera-type eye	0.00620399	68	0.01432665	20	1396
GO:0006366	transcription by RNA polymerase II	0.00703476	1049	0.1260745	176	1396
GO:1903037	regulation of leukocyte cell-cell adhesion	0.00713172	194	0.03080229	43	1396

GO:0007259	cell surface receptor signaling pathway via JAK-STAT	0.00728456	59	0.01289398	18	1396
GO:0097300	programmed necrotic cell death	0.00737997	36	0.00931232	13	1396
GO:0050728	negative regulation of inflammatory response	0.00743381	79	0.01575931	22	1396
GO:0006959	humoral immune response	0.00743381	45	0.01074499	15	1396
GO:0010586	miRNA metabolic process	0.00743381	64	0.01361032	19	1396
GO:0050731	positive regulation of peptidyl-tyrosine phosphorylation	0.00743381	64	0.01361032	19	1396
GO:0030334	regulation of cell migration	0.00744628	502	0.06661891	93	1396
GO:2001243	negative regulation of intrinsic apoptotic signaling pathway	0.00749391	69	0.01432665	20	1396
GO:0042327	positive regulation of phosphorylation	0.00752702	218	0.03366762	47	1396
GO:0072359	circulatory system development	0.00754325	586	0.07593123	106	1396
GO:0042325	regulation of phosphorylation	0.00758554	345	0.0487106	68	1396
GO:0032755	positive regulation of interleukin-6 production	0.00805808	50	0.01146132	16	1396
GO:0002269	leukocyte activation involved in inflammatory response	0.00836333	20	0.00644699	9	1396
GO:0001773	myeloid dendritic cell activation	0.00836333	20	0.00644699	9	1396
GO:0010573	vascular endothelial growth factor production	0.00836333	20	0.00644699	9	1396
GO:0043277	apoptotic cell clearance	0.00836333	20	0.00644699	9	1396
GO:0030212	hyaluronan metabolic process	0.00836333	20	0.00644699	9	1396
GO:0043039	tRNA aminoacylation	0.00841762	41	0.01002865	14	1396
GO:0043410	positive regulation of MAPK cascade	0.00859598	196	0.03080229	43	1396
GO:0070200	establishment of protein localization to telomere	0.00924382	13	0.00501433	7	1396
GO:1901699	cellular response to nitrogen compound	0.00928729	256	0.03796562	53	1396
GO:2000514	regulation of CD4-positive, alpha-beta T cell activation	0.00935417	46	0.01074499	15	1396
GO:0050920	regulation of chemotaxis	0.00975592	107	0.01934097	27	1396
GO:0071621	granulocyte chemotaxis	0.01005151	51	0.01146132	16	1396
GO:0006953	acute-phase response	0.01028437	7	0.00358166	5	1396
GO:1904749	regulation of protein localization to nucleolus	0.01028437	7	0.00358166	5	1396
GO:0016045	detection of bacterium	0.01028437	7	0.00358166	5	1396

GO:2000556	positive regulation of T-helper 1 cell cytokine production	0.01028437	7	0.00358166	5	1396
GO:0071352	cellular response to interleukin-2	0.01028437	7	0.00358166	5	1396
GO:2000554	regulation of T-helper 1 cell cytokine production	0.01028437	7	0.00358166	5	1396
GO:0061041	regulation of wound healing	0.01028437	56	0.01217765	17	1396
GO:0038110	interleukin-2-mediated signaling pathway	0.01028437	7	0.00358166	5	1396
GO:0035744	T-helper 1 cell cytokine production	0.01028437	7	0.00358166	5	1396
GO:0034112	positive regulation of homotypic cell-cell adhesion	0.01028437	7	0.00358166	5	1396
GO:0043414	macromolecule methylation	0.01028437	56	0.01217765	17	1396
GO:0098543	detection of other organism	0.01028437	7	0.00358166	5	1396
GO:0007162	negative regulation of cell adhesion	0.01049275	152	0.02507163	35	1396
GO:0007411	axon guidance	0.01049442	61	0.01289398	18	1396
GO:1990830	cellular response to leukemia inhibitory factor	0.01049442	66	0.01361032	19	1396
GO:0015732	prostaglandin transport	0.01049442	10	0.00429799	6	1396
GO:0030282	bone mineralization	0.01049442	66	0.01361032	19	1396
GO:0045651	positive regulation of macrophage differentiation	0.01049442	10	0.00429799	6	1396
GO:0034134	toll-like receptor 2 signaling pathway	0.01049442	10	0.00429799	6	1396
GO:0043038	amino acid activation	0.01049769	42	0.01002865	14	1396
GO:1902895	positive regulation of miRNA transcription	0.01049769	42	0.01002865	14	1396
GO:0061448	connective tissue development	0.01068973	141	0.02363897	33	1396
GO:0002429	immune response-activating cell surface receptor signaling pathway	0.01069853	158	0.02578797	36	1396
GO:0002230	positive regulation of defense response to virus by host	0.01117384	17	0.00573066	8	1396
GO:0070301	cellular response to hydrogen peroxide	0.01123489	29	0.00787966	11	1396
GO:0032615	interleukin-12 production	0.01123489	29	0.00787966	11	1396
GO:0032655	regulation of interleukin-12 production	0.01123489	29	0.00787966	11	1396
GO:0022408	negative regulation of cell-cell adhesion	0.01142038	103	0.01862464	26	1396
GO:2000145	regulation of cell motility	0.0116544	523	0.06805158	95	1396
GO:0030856	regulation of epithelial cell differentiation	0.01172829	82	0.01575931	22	1396

GO:0043030	regulation of macrophage activation	0.01176525	25	0.00716332	10	1396
GO:0007260	tyrosine phosphorylation of STAT protein	0.01176525	25	0.00716332	10	1396
GO:0010883	regulation of lipid storage	0.01176525	25	0.00716332	10	1396
GO:0042509	regulation of tyrosine phosphorylation of STAT protein	0.01176525	25	0.00716332	10	1396
GO:0061081	positive regulation of myeloid leukocyte cytokine production involved in immune response	0.01176525	25	0.00716332	10	1396
GO:0050819	negative regulation of coagulation	0.01181356	21	0.00644699	9	1396
GO:0061900	glial cell activation	0.01181356	21	0.00644699	9	1396
GO:0006023	aminoglycan biosynthetic process	0.01182097	38	0.00931232	13	1396
GO:1905952	regulation of lipid localization	0.01190033	77	0.01504298	21	1396
GO:0010876	lipid localization	0.01224944	206	0.03151862	44	1396
GO:0097485	neuron projection guidance	0.01224944	62	0.01289398	18	1396
GO:0097696	cell surface receptor signaling pathway via STAT	0.01224944	62	0.01289398	18	1396
GO:0006022	aminoglycan metabolic process	0.01224944	62	0.01289398	18	1396
GO:0032259	methylation	0.01224944	67	0.01361032	19	1396
GO:0000302	response to reactive oxygen species	0.01236613	93	0.01719198	24	1396
GO:0090304	nucleic acid metabolic process	0.01248489	2453	0.26790831	374	1396
GO:0006139	nucleobase-containing compound metabolic process	0.01260801	2712	0.29369628	410	1396
GO:0009890	negative regulation of biosynthetic process	0.01286475	1113	0.13108883	183	1396
GO:0070374	positive regulation of ERK1 and ERK2 cascade	0.01287395	88	0.01647564	23	1396
GO:0007254	JNK cascade	0.01287395	88	0.01647564	23	1396
GO:0048525	negative regulation of viral process	0.01388097	48	0.01074499	15	1396
GO:0031214	biomineral tissue development	0.0139281	78	0.01504298	21	1396
GO:0002573	myeloid leukocyte differentiation	0.01419439	138	0.02292264	32	1396
GO:0035743	CD4-positive, alpha-beta T cell cytokine production	0.01452881	14	0.00501433	7	1396
GO:0141061	disruption of cell in another organism	0.01452881	14	0.00501433	7	1396
GO:0031640	killing of cells of another organism	0.01452881	14	0.00501433	7	1396
GO:2000106	regulation of leukocyte apoptotic process	0.01465721	63	0.01289398	18	1396

GO:0002456	T cell mediated immunity	0.01465721	63	0.01289398	18	1396
GO:0042113	B cell activation	0.01473338	167	0.0265043	37	1396
GO:0006766	vitamin metabolic process	0.01493206	39	0.00931232	13	1396
GO:0001960	negative regulation of cytokine-mediated signaling pathway	0.01493206	39	0.00931232	13	1396
GO:0002262	myeloid cell homeostasis	0.01516645	133	0.0222063	31	1396
GO:0048731	system development	0.01540992	1715	0.19269341	269	1396
GO:0072593	reactive oxygen species metabolic process	0.01567083	111	0.01934097	27	1396
GO:0040012	regulation of locomotion	0.01589496	542	0.06948424	97	1396
GO:0021545	cranial nerve development	0.01589756	26	0.00716332	10	1396
GO:0072594	establishment of protein localization to organelle	0.0159419	239	0.03510029	49	1396
GO:0009595	detection of biotic stimulus	0.01628617	18	0.00573066	8	1396
GO:0060907	positive regulation of macrophage cytokine production	0.01628617	18	0.00573066	8	1396
GO:0001774	microglial cell activation	0.01628617	18	0.00573066	8	1396
GO:0070098	chemokine-mediated signaling pathway	0.01649532	22	0.00644699	9	1396
GO:0050922	negative regulation of chemotaxis	0.01649532	22	0.00644699	9	1396
GO:0048483	autonomic nervous system development	0.01649532	22	0.00644699	9	1396
GO:0062207	regulation of pattern recognition receptor signaling pathway	0.01651742	106	0.01862464	26	1396
GO:0033209	tumor necrosis factor-mediated signaling pathway	0.01681656	49	0.01074499	15	1396
GO:0007338	single fertilization	0.01693836	35	0.00859599	12	1396
GO:0042100	B cell proliferation	0.01724427	54	0.01146132	16	1396
GO:0070227	lymphocyte apoptotic process	0.0172546	64	0.01289398	18	1396
GO:1903320	regulation of protein modification by small protein conjugation or removal	0.01741001	140	0.02292264	32	1396
GO:0002768	immune response-regulating cell surface receptor signaling pathway	0.01741001	163	0.02578797	36	1396
GO:1903039	positive regulation of leukocyte cell-cell adhesion	0.01741001	140	0.02292264	32	1396
GO:1902339	positive regulation of apoptotic process involved in morphogenesis	0.01757167	5	0.00286533	4	1396
GO:0071104	response to interleukin-9	0.01757167	5	0.00286533	4	1396
GO:0030656	regulation of vitamin metabolic process	0.01757167	5	0.00286533	4	1396

GO:1904748	regulation of apoptotic process involved in development	0.01757167	5	0.00286533	4	1396
GO:1904747	positive regulation of apoptotic process involved in development	0.01757167	5	0.00286533	4	1396
GO:1903972	regulation of cellular response to macrophage colony-stimulating factor stimulus	0.01757167	5	0.00286533	4	1396
GO:1903969	regulation of response to macrophage colony-stimulating factor	0.01757167	5	0.00286533	4	1396
GO:0021783	preganglionic parasympathetic fiber development	0.01757167	11	0.00429799	6	1396
GO:0090666	scaRNA localization to Cajal body	0.01757167	5	0.00286533	4	1396
GO:0070943	neutrophil-mediated killing of symbiont cell	0.01757167	5	0.00286533	4	1396
GO:0010888	negative regulation of lipid storage	0.01757167	11	0.00429799	6	1396
GO:0035771	interleukin-4-mediated signaling pathway	0.01757167	5	0.00286533	4	1396
GO:0038113	interleukin-9-mediated signaling pathway	0.01757167	5	0.00286533	4	1396
GO:1902337	regulation of apoptotic process involved in morphogenesis	0.01757167	5	0.00286533	4	1396
GO:0000463	maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	0.01757167	5	0.00286533	4	1396
GO:0042362	fat-soluble vitamin biosynthetic process	0.01757167	5	0.00286533	4	1396
GO:0071355	cellular response to interleukin-9	0.01757167	5	0.00286533	4	1396
GO:0071316	cellular response to nicotine	0.01757167	5	0.00286533	4	1396
GO:0002457	T cell antigen processing and presentation	0.01757167	5	0.00286533	4	1396
GO:0048486	parasympathetic nervous system development	0.01757167	11	0.00429799	6	1396
GO:0048008	platelet-derived growth factor receptor signaling pathway	0.01808639	40	0.00931232	13	1396
GO:0030193	regulation of blood coagulation	0.01848597	31	0.00787966	11	1396
GO:1900046	regulation of hemostasis	0.01848597	31	0.00787966	11	1396
GO:0061077	chaperone-mediated protein folding	0.01848597	31	0.00787966	11	1396
GO:0042129	regulation of T cell proliferation	0.01931662	102	0.01790831	25	1396
GO:0007167	enzyme-linked receptor protein signaling pathway	0.01931662	462	0.06017192	84	1396
GO:0046328	regulation of JNK cascade	0.01931662	70	0.01361032	19	1396
GO:1903900	regulation of viral life cycle	0.01931662	70	0.01361032	19	1396
GO:0002688	regulation of leukocyte chemotaxis	0.01977254	65	0.01289398	18	1396

GO:0002824	positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	0.01977254	65	0.01289398	18	1396
GO:0065008	regulation of biological quality	0.01985709	1174	0.13610315	190	1396
GO:0032310	prostaglandin secretion	0.01989327	8	0.00358166	5	1396
GO:0018216	peptidyl-arginine methylation	0.01989327	8	0.00358166	5	1396
GO:0018195	peptidyl-arginine modification	0.01989327	8	0.00358166	5	1396
GO:0002756	MyD88-independent toll-like receptor signaling pathway	0.01989327	8	0.00358166	5	1396
GO:0000460	maturation of 5.8S rRNA	0.01989327	8	0.00358166	5	1396
GO:0000462	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	0.01989327	8	0.00358166	5	1396
GO:0035094	response to nicotine	0.01989327	8	0.00358166	5	1396
GO:0030203	glycosaminoglycan metabolic process	0.01989327	60	0.01217765	17	1396
GO:0070669	response to interleukin-2	0.01989327	8	0.00358166	5	1396
GO:0140374	antiviral innate immune response	0.02012288	27	0.00716332	10	1396
GO:0090303	positive regulation of wound healing	0.02012288	27	0.00716332	10	1396
GO:0045071	negative regulation of viral genome replication	0.02012288	27	0.00716332	10	1396
GO:2001242	regulation of intrinsic apoptotic signaling pathway	0.02018764	108	0.01862464	26	1396
GO:0061082	myeloid leukocyte cytokine production	0.02045841	36	0.00859599	12	1396
GO:0006024	glycosaminoglycan biosynthetic process	0.02045841	36	0.00859599	12	1396
GO:0010558	negative regulation of macromolecule biosynthetic process	0.02045841	1086	0.12679083	177	1396
GO:0034504	protein localization to nucleus	0.02108013	189	0.0286533	40	1396
GO:0045649	regulation of macrophage differentiation	0.02118903	15	0.00501433	7	1396
GO:2001236	regulation of extrinsic apoptotic signaling pathway	0.02129166	92	0.01647564	23	1396
GO:0045596	negative regulation of cell differentiation	0.02148095	299	0.04154728	58	1396
GO:0051216	cartilage development	0.02148095	103	0.01790831	25	1396
GO:0070198	protein localization to chromosome, telomeric region	0.02154286	23	0.00644699	9	1396
GO:0060761	negative regulation of response to cytokine stimulus	0.02201279	41	0.00931232	13	1396
GO:0030888	regulation of B cell proliferation	0.02201279	41	0.00931232	13	1396

GO:0070498	interleukin-1-mediated signaling pathway	0.02209063	19	0.00573066	8	1396
GO:0032733	positive regulation of interleukin-10 production	0.02209063	19	0.00573066	8	1396
GO:2000515	negative regulation of CD4-positive, alpha-beta T cell activation	0.02209063	19	0.00573066	8	1396
GO:1902105	regulation of leukocyte differentiation	0.02237575	172	0.0265043	37	1396
GO:1901873	regulation of post-translational protein modification	0.02265412	143	0.02292264	32	1396
GO:0045069	regulation of viral genome replication	0.02287707	46	0.01002865	14	1396
GO:0070664	negative regulation of leukocyte proliferation	0.02287707	46	0.01002865	14	1396
GO:0045620	negative regulation of lymphocyte differentiation	0.02326705	32	0.00787966	11	1396
GO:1903707	negative regulation of hemopoiesis	0.02340858	56	0.01146132	16	1396
GO:0034142	toll-like receptor 4 signaling pathway	0.02588436	37	0.00859599	12	1396
GO:0042092	type 2 immune response	0.0264973	28	0.00716332	10	1396
GO:0006897	endocytosis	0.0264973	302	0.04154728	58	1396
GO:0015909	long-chain fatty acid transport	0.0264973	28	0.00716332	10	1396
GO:0045581	negative regulation of T cell differentiation	0.0264973	28	0.00716332	10	1396
GO:0070487	monocyte aggregation	0.02685458	3	0.002149	3	1396
GO:0002676	regulation of chronic inflammatory response	0.02685458	3	0.002149	3	1396
GO:0090402	oncogene-induced cell senescence	0.02685458	3	0.002149	3	1396
GO:0060579	ventral spinal cord interneuron fate commitment	0.02685458	3	0.002149	3	1396
GO:0060581	cell fate commitment involved in pattern specification	0.02685458	3	0.002149	3	1396
GO:0034342	response to type III interferon	0.02685458	3	0.002149	3	1396
GO:2000627	positive regulation of miRNA catabolic process	0.02685458	3	0.002149	3	1396
GO:1902263	apoptotic process involved in embryonic digit morphogenesis	0.02685458	3	0.002149	3	1396
GO:0046637	regulation of alpha-beta T cell differentiation	0.02704311	42	0.00931232	13	1396
GO:0097193	intrinsic apoptotic signaling pathway	0.02715807	192	0.0286533	40	1396
GO:0002275	myeloid cell activation involved in immune response	0.02785013	47	0.01002865	14	1396
GO:0030216	keratinocyte differentiation	0.02791834	52	0.01074499	15	1396
GO:0032695	negative regulation of interleukin-12 production	0.02791834	12	0.00429799	6	1396

GO:0008625	extrinsic apoptotic signaling pathway via death domain receptors	0.02791834	52	0.01074499	15	1396
GO:0060142	regulation of syncytium formation by plasma membrane fusion	0.02791834	12	0.00429799	6	1396
GO:0006775	fat-soluble vitamin metabolic process	0.02791834	12	0.00429799	6	1396
GO:0002920	regulation of humoral immune response	0.02791834	12	0.00429799	6	1396
GO:2000232	regulation of rRNA processing	0.02791834	12	0.00429799	6	1396
GO:0048566	embryonic digestive tract development	0.02791834	12	0.00429799	6	1396
GO:0071675	regulation of mononuclear cell migration	0.02807217	78	0.01432665	20	1396
GO:0008630	intrinsic apoptotic signaling pathway in response to DNA damage	0.02807217	78	0.01432665	20	1396
GO:0050691	regulation of defense response to virus by host	0.02866179	24	0.00644699	9	1396
GO:0050792	regulation of viral process	0.02887703	89	0.01575931	22	1396
GO:0051235	maintenance of location	0.02888611	169	0.02578797	36	1396
GO:0030199	collagen fibril organization	0.02925592	33	0.00787966	11	1396
GO:0150076	neuroinflammatory response	0.02925592	33	0.00787966	11	1396
GO:0045727	positive regulation of translation	0.02934265	73	0.01361032	19	1396
GO:1900017	positive regulation of cytokine production involved in inflammatory response	0.03032788	16	0.00501433	7	1396
GO:0030278	regulation of ossification	0.03032788	68	0.01289398	18	1396
GO:0002726	positive regulation of T cell cytokine production	0.03032788	20	0.00573066	8	1396
GO:0002821	positive regulation of adaptive immune response	0.03032788	68	0.01289398	18	1396
GO:0071353	cellular response to interleukin-4	0.03032788	20	0.00573066	8	1396
GO:0002861	regulation of inflammatory response to antigenic stimulus	0.03032788	16	0.00501433	7	1396
GO:0001523	retinoid metabolic process	0.03032788	20	0.00573066	8	1396
GO:2000377	regulation of reactive oxygen species metabolic process	0.03032788	68	0.01289398	18	1396
GO:0141060	disruption of anatomical structure in another organism	0.03032788	16	0.00501433	7	1396
GO:0032495	response to muramyl dipeptide	0.03032788	16	0.00501433	7	1396
GO:0002507	tolerance induction	0.03032788	16	0.00501433	7	1396
GO:0046639	negative regulation of alpha-beta T cell differentiation	0.03032788	16	0.00501433	7	1396

GO:0045063	T-helper 1 cell differentiation	0.03032788	16	0.00501433	7	1396
GO:0045064	T-helper 2 cell differentiation	0.03032788	16	0.00501433	7	1396
GO:0051604	protein maturation	0.03063758	261	0.03653295	51	1396
GO:0042098	T cell proliferation	0.0309029	129	0.02077364	29	1396
GO:0030593	neutrophil chemotaxis	0.03093947	38	0.00859599	12	1396
GO:0006986	response to unfolded protein	0.03115863	63	0.01217765	17	1396
GO:0032945	negative regulation of mononuclear cell proliferation	0.03219627	43	0.00931232	13	1396
GO:0050672	negative regulation of lymphocyte proliferation	0.03219627	43	0.00931232	13	1396
GO:0002706	regulation of lymphocyte mediated immunity	0.03227962	90	0.01575931	22	1396
GO:1901136	carbohydrate derivative catabolic process	0.03228891	118	0.01934097	27	1396
GO:0002285	lymphocyte activation involved in immune response	0.03228891	118	0.01934097	27	1396
GO:0006351	DNA-templated transcription	0.03240891	1497	0.16762178	234	1396
GO:1903510	mucopolysaccharide metabolic process	0.03250072	48	0.01002865	14	1396
GO:0032870	cellular response to hormone stimulus	0.03271659	262	0.03653295	51	1396
GO:0140253	cell-cell fusion	0.03272717	29	0.00716332	10	1396
GO:2000351	regulation of endothelial cell apoptotic process	0.03272717	29	0.00716332	10	1396
GO:0000768	syncytium formation by plasma membrane fusion	0.03272717	29	0.00716332	10	1396
GO:0006413	translational initiation	0.03313676	74	0.01361032	19	1396
GO:0048771	tissue remodeling	0.03413469	85	0.01504298	21	1396
GO:2000341	regulation of chemokine (C-X-C motif) ligand 2 production	0.03435068	9	0.00358166	5	1396
GO:0031649	heat generation	0.03435068	9	0.00358166	5	1396
GO:0070486	leukocyte aggregation	0.03435068	9	0.00358166	5	1396
GO:0002829	negative regulation of type 2 immune response	0.03435068	9	0.00358166	5	1396
GO:0072567	chemokine (C-X-C motif) ligand 2 production	0.03435068	9	0.00358166	5	1396
GO:0090085	regulation of protein deubiquitination	0.03435068	9	0.00358166	5	1396
GO:1901739	regulation of myoblast fusion	0.03435068	9	0.00358166	5	1396
GO:0002407	dendritic cell chemotaxis	0.03435068	9	0.00358166	5	1396

GO:0030213	hyaluronan biosynthetic process	0.03435068	9	0.00358166	5	1396
GO:1903556	negative regulation of tumor necrosis factor superfamily cytokine production	0.03582465	34	0.00787966	11	1396
GO:0072538	T-helper 17 type immune response	0.03673517	25	0.00644699	9	1396
GO:0002369	T cell cytokine production	0.03673517	25	0.00644699	9	1396
GO:0002724	regulation of T cell cytokine production	0.03673517	25	0.00644699	9	1396
GO:0006721	terpenoid metabolic process	0.03673517	25	0.00644699	9	1396
GO:0016525	negative regulation of angiogenesis	0.03703095	59	0.01146132	16	1396
GO:1901343	negative regulation of vasculature development	0.03703095	59	0.01146132	16	1396
GO:1900182	positive regulation of protein localization to nucleus	0.03703095	59	0.01146132	16	1396
GO:2000181	negative regulation of blood vessel morphogenesis	0.03703095	59	0.01146132	16	1396
GO:0070391	response to lipoteichoic acid	0.03772527	6	0.00286533	4	1396
GO:0002925	positive regulation of humoral immune response mediated by circulating immunoglobulin	0.03772527	6	0.00286533	4	1396
GO:0032306	regulation of prostaglandin secretion	0.03772527	6	0.00286533	4	1396
GO:0060613	fat pad development	0.03772527	6	0.00286533	4	1396
GO:0060335	positive regulation of type II interferon-mediated signaling pathway	0.03772527	6	0.00286533	4	1396
GO:0071223	cellular response to lipoteichoic acid	0.03772527	6	0.00286533	4	1396
GO:0045625	regulation of T-helper 1 cell differentiation	0.03772527	6	0.00286533	4	1396
GO:2000644	regulation of receptor catabolic process	0.03772527	6	0.00286533	4	1396
GO:0050864	regulation of B cell activation	0.03772527	86	0.01504298	21	1396
GO:2000343	positive regulation of chemokine (C-X-C motif) ligand 2 production	0.03772527	6	0.00286533	4	1396
GO:0060332	positive regulation of response to type II interferon	0.03772527	6	0.00286533	4	1396
GO:0002501	peptide antigen assembly with MHC protein complex	0.03772527	6	0.00286533	4	1396
GO:0042026	protein refolding	0.03772527	6	0.00286533	4	1396
GO:0051873	killing by host of symbiont cells	0.03772527	6	0.00286533	4	1396
GO:0002396	MHC protein complex assembly	0.03772527	6	0.00286533	4	1396
GO:0042573	retinoic acid metabolic process	0.03772527	6	0.00286533	4	1396

GO:1900426	positive regulation of defense response to bacterium	0.03772527	6	0.00286533	4	1396
GO:0032308	positive regulation of prostaglandin secretion	0.03772527	6	0.00286533	4	1396
GO:0050829	defense response to Gram-negative bacterium	0.0393285	21	0.00573066	8	1396
GO:0016101	diterpenoid metabolic process	0.0393285	21	0.00573066	8	1396
GO:0070670	response to interleukin-4	0.0393285	21	0.00573066	8	1396
GO:0048002	antigen processing and presentation of peptide antigen	0.0393285	21	0.00573066	8	1396
GO:0044319	wound healing, spreading of cells	0.0393285	21	0.00573066	8	1396
GO:0043372	positive regulation of CD4-positive, alpha-beta T cell differentiation	0.0393285	21	0.00573066	8	1396
GO:0090505	epiboly involved in wound healing	0.0393285	21	0.00573066	8	1396
GO:0007520	myoblast fusion	0.0393285	21	0.00573066	8	1396
GO:0006520	amino acid metabolic process	0.03945248	126	0.02005731	28	1396
GO:0043412	macromolecule modification	0.03945248	1498	0.16690544	233	1396
GO:0045624	positive regulation of T-helper cell differentiation	0.04020276	13	0.00429799	6	1396
GO:0034101	erythrocyte homeostasis	0.04020276	109	0.01790831	25	1396
GO:0036336	dendritic cell migration	0.04020276	13	0.00429799	6	1396
GO:0030194	positive regulation of blood coagulation	0.04020276	13	0.00429799	6	1396
GO:1900048	positive regulation of hemostasis	0.04020276	13	0.00429799	6	1396
GO:0003159	morphogenesis of an endothelium	0.04020276	13	0.00429799	6	1396
GO:0061154	endothelial tube morphogenesis	0.04020276	13	0.00429799	6	1396
GO:0006925	inflammatory cell apoptotic process	0.04020276	13	0.00429799	6	1396
GO:0006949	syncytium formation	0.04020276	30	0.00716332	10	1396
GO:0071363	cellular response to growth factor stimulus	0.04084521	310	0.04154728	58	1396
GO:0042531	positive regulation of tyrosine phosphorylation of STAT protein	0.04086285	17	0.00501433	7	1396
GO:0071276	cellular response to cadmium ion	0.04086285	17	0.00501433	7	1396
GO:0034250	positive regulation of amide metabolic process	0.04086285	17	0.00501433	7	1396
GO:0032735	positive regulation of interleukin-12 production	0.04086285	17	0.00501433	7	1396
GO:0010574	regulation of vascular endothelial growth factor production	0.04086285	17	0.00501433	7	1396

GO:1990000	amyloid fibril formation	0.04086285	17	0.00501433	7	1396
GO:0002705	positive regulation of leukocyte mediated immunity	0.04170976	76	0.01361032	19	1396
GO:0071496	cellular response to external stimulus	0.04263443	35	0.00787966	11	1396
GO:0061028	establishment of endothelial barrier	0.04263443	35	0.00787966	11	1396
GO:0071260	cellular response to mechanical stimulus	0.04263443	35	0.00787966	11	1396
GO:0030218	erythrocyte differentiation	0.04288278	104	0.01719198	24	1396
GO:1902106	negative regulation of leukocyte differentiation	0.04300527	55	0.01074499	15	1396
GO:0051252	regulation of RNA metabolic process	0.04326368	1544	0.17120344	239	1396
GO:0021675	nerve development	0.0438117	40	0.00859599	12	1396
GO:1902893	regulation of miRNA transcription	0.0438117	50	0.01002865	14	1396
GO:0061614	miRNA transcription	0.0438117	50	0.01002865	14	1396
GO:0006720	isoprenoid metabolic process	0.0438117	40	0.00859599	12	1396
GO:0001885	endothelial cell development	0.0438117	40	0.00859599	12	1396
GO:0007169	cell surface receptor protein tyrosine kinase signaling pathway	0.04388246	305	0.04083095	57	1396
GO:0006412	translation	0.04408047	408	0.05229226	73	1396
GO:0046635	positive regulation of alpha-beta T cell activation	0.04408047	45	0.00931232	13	1396
GO:0009628	response to abiotic stimulus	0.0441099	480	0.06017192	84	1396
GO:0051049	regulation of transport	0.04477278	687	0.08237822	115	1396
GO:0032653	regulation of interleukin-10 production	0.04518822	26	0.00644699	9	1396
GO:0032613	interleukin-10 production	0.04518822	26	0.00644699	9	1396
GO:0046640	regulation of alpha-beta T cell proliferation	0.04518822	26	0.00644699	9	1396
GO:0030858	positive regulation of epithelial cell differentiation	0.04518822	26	0.00644699	9	1396
GO:0010720	positive regulation of cell development	0.04713864	206	0.02936963	41	1396
GO:0050870	positive regulation of T cell activation	0.04716567	128	0.02005731	28	1396
GO:1903034	regulation of response to wounding	0.04717179	77	0.01361032	19	1396
GO:0046903	secretion	0.04760761	377	0.0487106	68	1396
GO:0019724	B cell mediated immunity	0.04804611	61	0.01146132	16	1396

GO:0006400	tRNA modification	0.04804611	61	0.01146132	16	1396
GO:0010038	response to metal ion	0.04896712	111	0.01790831	25	1396
GO:0072577	endothelial cell apoptotic process	0.04943767	31	0.00716332	10	1396
GO:0048010	vascular endothelial growth factor receptor signaling pathway	0.04943767	31	0.00716332	10	1396
GO:1903036	positive regulation of response to wounding	0.04943767	31	0.00716332	10	1396
GO:1905517	macrophage migration	0.04943767	31	0.00716332	10	1396
GO:0043370	regulation of CD4-positive, alpha-beta T cell differentiation	0.04943767	31	0.00716332	10	1396
GO:0035966	response to topologically incorrect protein	0.04987376	72	0.01289398	18	1396
GO:0046394	carboxylic acid biosynthetic process	0.04991781	117	0.01862464	26	1396
GO:2001235	positive regulation of apoptotic signaling pathway	0.04992036	83	0.01432665	20	1396
GO:0002040	sprouting angiogenesis	0.04992036	83	0.01432665	20	1396
GO:0005730	nucleolus	1.22E-20	612	0.12320917	172	1396
GO:0030684	preribosome	1.15E-14	57	0.02507163	35	1396
GO:0032040	small-subunit processome	1.60E-12	49	0.02148997	30	1396
GO:0005576	extracellular region	1.60E-12	402	0.07951289	111	1396
GO:0009986	cell surface	1.10E-10	318	0.06446991	90	1396
GO:0005615	extracellular space	1.49E-08	294	0.05730659	80	1396
GO:0009897	external side of plasma membrane	1.49E-08	126	0.03223496	45	1396
GO:0098552	side of membrane	3.43E-07	215	0.04369628	61	1396
GO:0005732	sno(s)RNA-containing ribonucleoprotein complex	9.23E-05	14	0.00716332	10	1396
GO:0030686	90S preribosome	0.00044703	6	0.00429799	6	1396
GO:0110165	cellular anatomical structure	0.00142683	8229	0.8273639	1155	1396
GO:0043020	NADPH oxidase complex	0.00258757	5	0.00358166	5	1396
GO:0042824	MHC class I peptide loading complex	0.00258757	5	0.00358166	5	1396
GO:0005575	cellular_component	0.00315805	8345	0.83524355	1166	1396
GO:0065010	extracellular membrane-bounded organelle	0.00432028	48	0.01217765	17	1396
GO:0043230	extracellular organelle	0.00432028	48	0.01217765	17	1396

GO:0005783	endoplasmic reticulum	0.0063013	754	0.09670487	135	1396
GO:0017101	aminoacyl-tRNA synthetase multienzyme complex	0.00665352	11	0.00501433	7	1396
GO:0101031	protein folding chaperone complex	0.0071229	25	0.00787966	11	1396
GO:0005832	chaperonin-containing T-complex	0.00854661	6	0.00358166	5	1396
GO:0002199	zona pellucida receptor complex	0.00854661	6	0.00358166	5	1396
GO:0090575	RNA polymerase II transcription regulator complex	0.01122222	163	0.02722063	38	1396
GO:0005736	RNA polymerase I complex	0.01122222	12	0.00501433	7	1396
GO:0071944	cell periphery	0.01122222	1941	0.21919771	306	1396
GO:1903561	extracellular vesicle	0.01154332	44	0.01074499	15	1396
GO:0070062	extracellular exosome	0.01274552	40	0.01002865	14	1396
GO:0005886	plasma membrane	0.02378766	1782	0.20057307	280	1396
GO:0001650	fibrillar center	0.03376539	111	0.01934097	27	1396
GO:0000176	nuclear exosome (RNase complex)	0.04573761	8	0.00358166	5	1396
GO:0031234	extrinsic component of cytoplasmic side of plasma membrane	0.04780043	15	0.00501433	7	1396
GO:0004896	cytokine receptor activity	4.45E-09	39	0.01719198	24	1396
GO:0140375	immune receptor activity	3.59E-08	46	0.01790831	25	1396
GO:0038023	signaling receptor activity	4.41E-06	338	0.05945559	83	1396
GO:0060089	molecular transducer activity	4.41E-06	338	0.05945559	83	1396
GO:0140098	catalytic activity, acting on RNA	5.45E-06	260	0.0487106	68	1396
GO:0030515	snoRNA binding	1.32E-05	19	0.00931232	13	1396
GO:0043021	ribonucleoprotein complex binding	1.64E-05	99	0.0243553	34	1396
GO:0000978	RNA polymerase II cis-regulatory region sequence-specific DNA binding	1.85E-05	276	0.04942693	69	1396
GO:0005126	cytokine receptor binding	3.43E-05	104	0.0243553	34	1396
GO:0000987	cis-regulatory region sequence-specific DNA binding	3.43E-05	287	0.05014327	70	1396
GO:0003723	RNA binding	3.43E-05	609	0.08954155	125	1396
GO:0140662	ATP-dependent protein folding chaperone	3.43E-05	24	0.01002865	14	1396
GO:0097159	organic cyclic compound binding	3.43E-05	2775	0.32163324	449	1396

GO:0051082	unfolded protein binding	5.04E-05	42	0.01361032	19	1396
GO:0003676	nucleic acid binding	0.00013966	1605	0.1969914	275	1396
GO:0004888	transmembrane signaling receptor activity	0.00014302	262	0.04512894	63	1396
GO:0003700	DNA-binding transcription factor activity	0.00018729	367	0.05802292	81	1396
GO:0005102	signaling receptor binding	0.00037976	524	0.07593123	106	1396
GO:0000977	RNA polymerase II transcription regulatory region sequence-specific DNA binding	0.00055225	331	0.05229226	73	1396
GO:0000981	DNA-binding transcription factor activity, RNA polymerase II-specific	0.00069117	316	0.05014327	70	1396
GO:0000976	transcription cis-regulatory region binding	0.00073572	400	0.06017192	84	1396
GO:0001067	transcription regulatory region nucleic acid binding	0.00073572	400	0.06017192	84	1396
GO:0044183	protein folding chaperone	0.00108925	35	0.01074499	15	1396
GO:0005125	cytokine activity	0.00108925	35	0.01074499	15	1396
GO:0097367	carbohydrate derivative binding	0.00109407	1208	0.14971347	209	1396
GO:0004950	chemokine receptor activity	0.0012287	9	0.00501433	7	1396
GO:0001637	G protein-coupled chemoattractant receptor activity	0.0012287	9	0.00501433	7	1396
GO:0140101	catalytic activity, acting on a tRNA	0.00130524	99	0.02077364	29	1396
GO:1990275	preribosome binding	0.00230402	5	0.00358166	5	1396
GO:0019955	cytokine binding	0.00230438	59	0.01432665	20	1396
GO:0005488	binding	0.00241693	6736	0.68982808	963	1396
GO:0043565	sequence-specific DNA binding	0.00292126	543	0.07449857	104	1396
GO:0043022	ribosome binding	0.00305061	65	0.01504298	21	1396
GO:0030545	signaling receptor regulator activity	0.00363441	95	0.01934097	27	1396
GO:1990837	sequence-specific double-stranded DNA binding	0.00433635	474	0.06590258	92	1396
GO:0048018	receptor ligand activity	0.0051438	87	0.01790831	25	1396
GO:0003674	molecular_function	0.00580148	8411	0.83882521	1171	1396
GO:0044877	protein-containing complex binding	0.00580148	574	0.07664756	107	1396
GO:0030546	signaling receptor activator activity	0.00580148	93	0.01862464	26	1396
GO:0140110	transcription regulator activity	0.00845741	638	0.08309456	116	1396

GO:0004812	aminoacyl-tRNA ligase activity	0.00845741	38	0.01002865	14	1396
GO:0016875	ligase activity, forming carbon-oxygen bonds	0.00845741	38	0.01002865	14	1396
GO:0044020	histone H4R3 methyltransferase activity	0.01072729	4	0.00286533	4	1396
GO:0140640	catalytic activity, acting on a nucleic acid	0.01072729	433	0.05945559	83	1396
GO:0016176	superoxide-generating NADPH oxidase activator activity	0.01072729	4	0.00286533	4	1396
GO:0016175	superoxide-generating NAD(P)H oxidase activity	0.01072729	4	0.00286533	4	1396
GO:0005178	integrin binding	0.01072729	67	0.01432665	20	1396
GO:0045182	translation regulator activity	0.01282069	78	0.01575931	22	1396
GO:0001217	DNA-binding transcription repressor activity	0.01282069	120	0.02148997	30	1396
GO:0003690	double-stranded DNA binding	0.01481151	521	0.06876791	96	1396
GO:0090079	translation regulator activity, nucleic acid binding	0.01481151	64	0.01361032	19	1396
GO:0001216	DNA-binding transcription activator activity	0.01691822	190	0.03008596	42	1396
GO:0019001	guanyl nucleotide binding	0.0183888	244	0.03653295	51	1396
GO:0001228	DNA-binding transcription activator activity, RNA polymerase II-specific	0.02001646	186	0.02936963	41	1396
GO:0034511	U3 snoRNA binding	0.02018281	7	0.00358166	5	1396
GO:0042379	chemokine receptor binding	0.02214652	17	0.00573066	8	1396
GO:0001227	DNA-binding transcription repressor activity, RNA polymerase II-specific	0.02653332	115	0.02005731	28	1396
GO:0004222	metalloendopeptidase activity	0.02922869	53	0.01146132	16	1396
GO:0003724	RNA helicase activity	0.03299421	44	0.01002865	14	1396
GO:0032561	guanyl ribonucleotide binding	0.03516147	240	0.03510029	49	1396
GO:0019957	C-C chemokine binding	0.0362109	5	0.00286533	4	1396
GO:0097677	STAT family protein binding	0.0362109	5	0.00286533	4	1396
GO:0008186	ATP-dependent activity, acting on RNA	0.03943999	45	0.01002865	14	1396
GO:0008135	translation factor activity, RNA binding	0.04096081	55	0.01146132	16	1396
GO:0042802	identical protein binding	0.04180398	1148	0.13323782	186	1396
GO:0140677	molecular function activator activity	0.04180398	380	0.0508596	71	1396
HP:0002733	Abnormal lymph node morphology	1.31E-06	207	0.04441261	62	1396

HP:0002716	Lymphadenopathy	4.18E-06	196	0.04154728	58	1396
HP:0011111	Abnormal immune serum protein physiology	6.44E-05	37	0.01361032	19	1396
HP:0011112	Abnormal circulating cytokine concentration	0.00018936	36	0.01289398	18	1396
HP:0033331	Acute phase response	0.00020119	140	0.03008596	42	1396
HP:0003565	Elevated erythrocyte sedimentation rate	0.0006156	55	0.01575931	22	1396
HP:0025021	Abnormal erythrocyte sedimentation rate	0.0006156	55	0.01575931	22	1396
HP:0010280	Stomatitis	0.00079553	52	0.01504298	21	1396
HP:0011450	Unusual CNS infection	0.00249921	82	0.01934097	27	1396
HP:0031446	Erosion of oral mucosa	0.0026186	78	0.01862464	26	1396
HP:0001945	Fever	0.00291677	301	0.0487106	68	1396
HP:0002102	Pleuritis	0.00291677	19	0.00787966	11	1396
HP:0011107	Recurrent aphthous stomatitis	0.00297169	33	0.01074499	15	1396
HP:0011830	Abnormal oral mucosa morphology	0.00363067	276	0.04512894	63	1396
HP:0011227	Elevated circulating C-reactive protein concentration	0.00365951	54	0.01432665	20	1396
HP:0011117	Abnormal circulating interleukin concentration	0.00444472	27	0.00931232	13	1396
HP:0032436	Abnormal circulating C-reactive protein concentration	0.00444472	55	0.01432665	20	1396
HP:0032158	Unusual infection by anatomical site	0.00686346	89	0.01934097	27	1396
HP:0010987	Abnormal cellular immune system morphology	0.00772746	496	0.07020057	98	1396
HP:0001881	Abnormal leukocyte morphology	0.00772746	496	0.07020057	98	1396
HP:0001701	Pericarditis	0.00914676	29	0.00931232	13	1396
HP:0032251	Abnormal immune system morphology	0.01685959	513	0.07091691	99	1396
HP:0100614	Myositis	0.01959732	31	0.00931232	13	1396
HP:0011123	Inflammatory abnormality of the skin	0.01973646	362	0.0530086	74	1396
HP:0001287	Meningitis	0.01973646	57	0.01361032	19	1396
HP:0011122	Abnormality of skin physiology	0.02959002	410	0.05802292	81	1396
HP:0001954	Recurrent fever	0.02987322	83	0.01719198	24	1396
HP:0004370	Abnormality of temperature regulation	0.03242252	375	0.05372493	75	1396

HP:0100721	Mediastinal lymphadenopathy	0.03302696	25	0.00787966	11	1396
HP:0010974	Abnormal myeloid leukocyte morphology	0.04163395	273	0.04083095	57	1396
HP:0032154	Aphthous ulcer	0.04163395	6	0.00358166	5	1396
HP:0002740	Recurrent E. coli infections	0.04163395	4	0.00286533	4	1396
HP:0002741	Recurrent Serratia marcescens infections	0.04163395	4	0.00286533	4	1396
HP:0002742	Recurrent Klebsiella infections	0.04163395	4	0.00286533	4	1396
HP:0002840	Lymphadenitis	0.04163395	15	0.00573066	8	1396
HP:0030355	Abnormal circulating interferon-gamma concentration	0.04163395	22	0.00716332	10	1396
HP:0001874	Abnormality of neutrophils	0.04163395	213	0.03366762	47	1396
HP:0010975	Abnormal B cell count	0.04163395	87	0.01719198	24	1396
HP:0011116	Abnormal circulating interferon concentration	0.04163395	22	0.00716332	10	1396
HP:0000988	Skin rash	0.04163395	129	0.02292264	32	1396
HP:0025323	Abnormal arterial physiology	0.04163395	123	0.0222063	31	1396
HP:0011893	Abnormal leukocyte count	0.04163395	399	0.05587393	78	1396
HP:0002846	Abnormal B cell morphology	0.04163395	92	0.01790831	25	1396
HP:0001911	Abnormal granulocyte morphology	0.04346825	250	0.03796562	53	1396
HP:0002024	Malabsorption	0.04556783	158	0.0265043	37	1396
HP:0002039	Anorexia	0.04641895	88	0.01719198	24	1396
HP:0000554	Uveitis	0.04874475	49	0.01146132	16	1396

Supplemental Table 6: Enriched GO processes from a list of significantly downregulated genes (P < 0.05 and logFC < -0.5) from injection of LPS.

Term ID	Term Name	P value	Term Size	Precision	Intersection Size	Query Size
GO:0007389	pattern specification process	0.00111638	180	0.03448276	52	1508
GO:0009653	anatomical structure morphogenesis	0.00111638	1252	0.16047745	242	1508
GO:0035295	tube development	0.0012414	573	0.08289125	125	1508
GO:0006911	phagocytosis, engulfment	0.0012414	21	0.00862069	13	1508
GO:0048731	system development	0.00180589	1715	0.20623342	311	1508
GO:0003002	regionalization	0.00180589	165	0.03116711	47	1508
GO:0035239	tube morphogenesis	0.00180589	466	0.06896552	104	1508
GO:0030030	cell projection organization	0.00206658	700	0.09549072	144	1508
GO:0120036	plasma membrane bounded cell projection organization	0.00206658	693	0.09482759	143	1508
GO:0048646	anatomical structure formation involved in morphogenesis	0.00267517	590	0.08222812	124	1508
GO:0072329	monocarboxylic acid catabolic process	0.00267517	60	0.01525199	23	1508
GO:0044282	small molecule catabolic process	0.00267517	136	0.0265252	40	1508
GO:0003008	system process	0.00331805	603	0.08289125	125	1508
GO:0030198	extracellular matrix organization	0.00331805	144	0.02718833	41	1508
GO:0009887	animal organ morphogenesis	0.00331805	469	0.06763926	102	1508
GO:0035721	intraciliary retrograde transport	0.00331805	10	0.00530504	8	1508
GO:0043062	extracellular structure organization	0.00331805	144	0.02718833	41	1508
GO:0045229	external encapsulating structure organization	0.00331805	144	0.02718833	41	1508
GO:0016042	lipid catabolic process	0.00342013	135	0.02586207	39	1508
GO:0007154	cell communication	0.00556564	2731	0.30503979	460	1508
GO:0048870	cell motility	0.00556564	832	0.10742706	162	1508
GO:0032501	multicellular organismal process	0.00556564	2977	0.3295756	497	1508
GO:0023052	signaling	0.00646667	2730	0.30437666	459	1508
GO:0016054	organic acid catabolic process	0.00748931	93	0.01923077	29	1508

GO:0046395	carboxylic acid catabolic process	0.00748931	93	0.01923077	29	1508
GO:2000145	regulation of cell motility	0.011308	523	0.07161804	108	1508
GO:0001944	vasculature development	0.01170114	420	0.0596817	90	1508
GO:0032787	monocarboxylic acid metabolic process	0.01173378	259	0.04045093	61	1508
GO:0099024	plasma membrane invagination	0.01173378	28	0.00862069	13	1508
GO:0048754	branching morphogenesis of an epithelial tube	0.01283595	87	0.01790451	27	1508
GO:0072359	circulatory system development	0.01340092	586	0.07824934	118	1508
GO:0006909	phagocytosis	0.01532111	107	0.02055703	31	1508
GO:0007610	behavior	0.01550173	263	0.04045093	61	1508
GO:0040012	regulation of locomotion	0.01550173	542	0.0729443	110	1508
GO:0060271	cilium assembly	0.01550173	204	0.0331565	50	1508
GO:0061138	morphogenesis of a branching epithelium	0.01591026	103	0.0198939	30	1508
GO:0010324	membrane invagination	0.01613695	33	0.00928382	14	1508
GO:0002009	morphogenesis of an epithelium	0.01771677	265	0.04045093	61	1508
GO:0007186	G protein-coupled receptor signaling pathway	0.01793589	260	0.0397878	60	1508
GO:0060562	epithelial tube morphogenesis	0.01793589	185	0.03050398	46	1508
GO:0030031	cell projection assembly	0.01915473	323	0.04708223	71	1508
GO:0030334	regulation of cell migration	0.01915473	502	0.06763926	102	1508
GO:0016477	cell migration	0.01915473	770	0.09748011	147	1508
GO:0048598	embryonic morphogenesis	0.01915473	306	0.04509284	68	1508
GO:0007399	nervous system development	0.01915473	974	0.1193634	180	1508
GO:0050877	nervous system process	0.01915473	329	0.04774536	72	1508
GO:0010463	mesenchymal cell proliferation	0.01915473	23	0.00729443	11	1508
GO:0044782	cilium organization	0.01915473	218	0.03448276	52	1508
GO:0043436	oxoacid metabolic process	0.01915473	363	0.05172414	78	1508
GO:0006082	organic acid metabolic process	0.02007429	364	0.05172414	78	1508
GO:0007275	multicellular organism development	0.02021498	2095	0.23541114	355	1508

GO:0044248	cellular catabolic process	0.02039565	126	0.02254642	34	1508
GO:0001568	blood vessel development	0.02256299	395	0.05503979	83	1508
GO:1901890	positive regulation of cell junction assembly	0.02256299	43	0.01061008	16	1508
GO:0001763	morphogenesis of a branching structure	0.02256299	112	0.02055703	31	1508
GO:0060972	left/right pattern formation	0.0240244	65	0.01392573	21	1508
GO:0001822	kidney development	0.02816291	149	0.02519894	38	1508
GO:0007165	signal transduction	0.02837797	2555	0.28050398	423	1508
GO:0009190	cyclic nucleotide biosynthetic process	0.02885663	11	0.00464191	7	1508
GO:0006897	endocytosis	0.02976701	302	0.04376658	66	1508
GO:0001501	skeletal system development	0.0300404	252	0.03779841	57	1508
GO:0048513	animal organ development	0.03083868	1316	0.15384615	232	1508
GO:0120031	plasma membrane bounded cell projection assembly	0.03083868	320	0.04575597	69	1508
GO:0034330	cell junction organization	0.03083868	320	0.04575597	69	1508
GO:0072001	renal system development	0.03200029	156	0.02586207	39	1508
GO:0019752	carboxylic acid metabolic process	0.03201943	355	0.04973475	75	1508
GO:0048699	generation of neurons	0.03261989	573	0.07427056	112	1508
GO:0001658	branching involved in ureteric bud morphogenesis	0.03449101	25	0.00729443	11	1508
GO:0034440	lipid oxidation	0.03521663	54	0.01193634	18	1508
GO:0007368	determination of left/right symmetry	0.03521663	63	0.0132626	20	1508
GO:0007224	smoothened signaling pathway	0.03853893	87	0.01657825	25	1508
GO:0010975	regulation of neuron projection development	0.03970259	169	0.02718833	41	1508
GO:0048014	Tie signaling pathway	0.03970259	4	0.00265252	4	1508
GO:0030209	dermatan sulfate catabolic process	0.03970259	4	0.00265252	4	1508
GO:0048729	tissue morphogenesis	0.03970259	313	0.04442971	67	1508
GO:0005975	carbohydrate metabolic process	0.04321411	280	0.04045093	61	1508
GO:0042474	middle ear morphogenesis	0.04587132	12	0.00464191	7	1508
GO:0010976	positive regulation of neuron projection development	0.04587132	51	0.01127321	17	1508

GO:0048562	embryonic organ morphogenesis	0.04627352	134	0.02254642	34	1508
GO:0040011	locomotion	0.04627352	617	0.07824934	118	1508
GO:0009062	fatty acid catabolic process	0.04892201	47	0.01061008	16	1508
GO:0071944	cell periphery	4.95E-14	1941	0.26525199	400	1508
GO:0005886	plasma membrane	1.82E-10	1782	0.2367374	357	1508
GO:0042995	cell projection	1.65E-06	761	0.11007958	166	1508
GO:0120025	plasma membrane bounded cell projection	3.94E-06	750	0.10742706	162	1508
GO:0043235	receptor complex	7.09E-06	143	0.03050398	46	1508
GO:0031012	extracellular matrix	7.37E-05	122	0.02586207	39	1508
GO:0030312	external encapsulating structure	7.98E-05	123	0.02586207	39	1508
GO:0005775	vacuolar lumen	0.00010318	11	0.00596817	9	1508
GO:0005576	extracellular region	0.00019376	402	0.06100796	92	1508
GO:0005929	cilium	0.0005006	286	0.04575597	69	1508
GO:0005615	extracellular space	0.00058149	294	0.0464191	70	1508
GO:0043202	lysosomal lumen	0.00058149	8	0.00464191	7	1508
GO:0098590	plasma membrane region	0.00294752	387	0.05570292	84	1508
GO:0062023	collagen-containing extracellular matrix	0.0053719	85	0.01724138	26	1508
GO:0016020	membrane	0.00642219	3278	0.35411141	534	1508
GO:0097546	ciliary base	0.0160128	25	0.00729443	11	1508
GO:0097648	G protein-coupled receptor complex	0.0191085	4	0.00265252	4	1508
GO:0016010	dystrophin-associated glycoprotein complex	0.02112077	9	0.00397878	6	1508
GO:0005764	lysosome	0.02555309	278	0.0397878	60	1508
GO:0000323	lytic vacuole	0.02555309	278	0.0397878	60	1508
GO:0036038	MKS complex	0.03846472	10	0.00397878	6	1508
GO:0009986	cell surface	0.03846472	318	0.04376658	66	1508
GO:0005773	vacuole	0.04861896	333	0.04509284	68	1508
GO:0038023	signaling receptor activity	2.58E-07	338	0.06100796	92	1508

GO:0060089	molecular transducer activity	2.58E-07	338	0.06100796	92	1508
GO:0005509	calcium ion binding	4.23E-06	302	0.05371353	81	1508
GO:0004888	transmembrane signaling receptor activity	7.35E-06	262	0.04774536	72	1508
GO:0016849	phosphorus-oxygen lyase activity	0.00605186	14	0.00596817	9	1508
GO:0004930	G protein-coupled receptor activity	0.00605186	111	0.02188329	33	1508
GO:0004713	protein tyrosine kinase activity	0.00605186	74	0.01657825	25	1508
GO:0004714	transmembrane receptor protein tyrosine kinase activity	0.01150996	32	0.00928382	14	1508
GO:0019199	transmembrane receptor protein kinase activity	0.02073222	42	0.01061008	16	1508
GO:0009975	cyclase activity	0.02073222	13	0.00530504	8	1508
GO:0004553	hydrolase activity, hydrolyzing O-glycosyl compounds	0.03044735	52	0.01193634	18	1508
GO:0022857	transmembrane transporter activity	0.0441588	443	0.0596817	90	1508
GO:0050840	extracellular matrix binding	0.04622137	33	0.00862069	13	1508
GO:0004551	dinucleotide phosphatase activity	0.04940625	4	0.00265252	4	1508
HP:0100259	Postaxial polydactyly	0.00041155	118	0.02586207	39	1508
HP:0001162	Postaxial hand polydactyly	0.00041155	76	0.01923077	29	1508
HP:0002612	Congenital hepatic fibrosis	0.00041155	37	0.01259947	19	1508
HP:0001830	Postaxial foot polydactyly	0.00041155	64	0.01724138	26	1508
HP:0010306	Short thorax	0.00323842	36	0.01127321	17	1508
HP:0011534	Abnormal spatial orientation of the cardiac segments	0.01494377	76	0.01657825	25	1508
HP:0001161	Hand polydactyly	0.01494377	137	0.02519894	38	1508
HP:0000090	Nephronophthisis	0.01494377	33	0.00994695	15	1508
HP:0001829	Foot polydactyly	0.01494377	106	0.02122016	32	1508
HP:0010322	Abnormal fifth toe morphology	0.01494377	78	0.01724138	26	1508
HP:0010442	Polydactyly	0.01494377	198	0.0331565	50	1508
HP:0010459	True hermaphroditism	0.01494377	17	0.0066313	10	1508
HP:0000037	Male pseudohermaphroditism	0.01494377	27	0.00862069	13	1508
HP:0000888	Horizontal ribs	0.01494377	14	0.00596817	9	1508

HP:0009136	Duplication involving bones of the feet	0.01494377	110	0.02188329	33	1508
HP:0012622	Chronic kidney disease	0.01881768	139	0.02519894	38	1508
HP:0000691	Microdontia	0.02328947	131	0.02387268	36	1508
HP:0000062	Ambiguous genitalia	0.02328947	74	0.01591512	24	1508
HP:0001696	Situs inversus totalis	0.02733633	75	0.01591512	24	1508
HP:0006703	Aplasia/Hypoplasia of the lungs	0.02733633	108	0.02055703	31	1508
HP:0010979	Abnormality of lipoprotein cholesterol concentration	0.02749396	62	0.01392573	21	1508
HP:0002983	Micromelia	0.03024718	76	0.01591512	24	1508
HP:0011506	Choroidal neovascularization	0.03296249	13	0.00530504	8	1508
HP:0005769	Fifth finger distal phalanx clinodactyly	0.04294388	27	0.00795756	12	1508
HP:0100732	Pancreatic fibrosis	0.04351328	20	0.0066313	10	1508
HP:0002323	Anencephaly	0.04351328	31	0.00862069	13	1508
HP:0010454	Acetabular spurs	0.04502358	8	0.00397878	6	1508
HP:0000068	Urethral atresia	0.0482034	17	0.00596817	9	1508

Supplemental Table 7: Additive genes that are significantly upregulated by population and injection ($P < 0.05$ and logFC > 0.5).

ID	Population logFC	Injection logFC	Population adj_P.Val	Injection adj_P.Val
LOC121824839	1.52907905	0.5954173	8.02E-05	0.02949607
LOC102928772	1.28574554	1.37372685	0.00018957	1.73E-06
Elp6	0.92618406	0.95817746	0.00019064	3.34E-06
LOC121826055	1.54216408	0.93880288	0.00030195	0.00378939
LOC102917115	1.23109688	0.56593419	0.00051322	0.0229894
Irf6	1.03097467	1.16603267	0.00165313	1.12E-05
Cd38	0.99840063	1.5178304	0.00176879	1.64E-07
LOC121826338	1.35751355	0.75848305	0.00176879	0.01078099
LOC102915445	0.99027264	0.83335054	0.00177837	0.00032723
Crtc3	0.70733092	0.50034614	0.00187059	0.00187058
LOC102909396	1.55640659	1.09232848	0.00201784	0.0030791
Hspa1l	1.50442087	0.73503839	0.00234753	0.03376037
Nod1	0.7031276	0.79360831	0.00239246	1.67E-05
LOC102915160	1.38002752	0.84190332	0.00239246	0.0079885
Pnpla2	0.83308949	0.79569026	0.0024497	0.00013466
LOC102906561	1.00895583	0.74046851	0.0024497	0.00232849
LOC102921616	1.06819063	0.5711645	0.00283882	0.02327189
LOC102917419	1.0560375	0.81462837	0.00289995	0.001511
LOC102906108	1.23419729	0.91750633	0.00290937	0.00202485
LOC102912367	0.59144697	0.53525168	0.00307102	0.00050211
Tmed10	0.62605546	0.54218701	0.00307102	0.00050475
LOC121820889	1.10233416	0.9662127	0.00350567	0.0005542
LOC102907829	1.16120835	1.12628228	0.00350567	0.00020081
Ms4a6a	0.9638522	0.57902208	0.0038119	0.01406237
LOC121832753	0.81964702	1.66777778	0.00418381	1.24E-08
LOC102905475	0.87474975	0.7808698	0.00466882	0.00072611
Per1	1.07092572	0.7614784	0.00485797	0.00525343
Zbtb16	2.11236404	1.94319314	0.00501741	0.0006547
Elfn2	1.77171471	1.0736066	0.00504935	0.03017005
LOC107399876	1.24499189	1.54472255	0.00505588	2.27E-05
Slc39a6	1.01811859	1.8478643	0.00532922	1.26E-07
Naxd	0.65060856	0.6493695	0.00546733	0.00035469
Rarres1	2.5777917	3.04929281	0.00567845	4.58E-05
LOC121826573	1.15316293	1.0660614	0.00588825	0.00073745
Fkbp5	1.04450427	1.87002368	0.00594454	1.61E-07

LOC102922462	0.84972744	0.74237738	0.00594454	0.00123919
Tbc1d8	0.8607826	0.78698493	0.00692767	0.00091779
Kcnc3	1.09580291	0.65651898	0.00732936	0.03504152
Plac8	1.26207546	2.45953093	0.00972757	1.48E-07
LOC102927177	1.16320652	1.61000598	0.0103155	1.56E-05
LOC102913947	2.1004864	1.7446632	0.01077068	0.00598957
LOC102904392	1.33767204	1.83928465	0.01122365	2.06E-05
LOC102903947	0.90926581	0.61601231	0.01282547	0.02396722
Nhs	0.92909986	0.71328961	0.01290075	0.01195076
Chd7	0.61529947	0.98966673	0.01399016	4.12E-06
Sema4g	1.31626384	0.97446493	0.01430925	0.01634703
Ggct	0.58078309	0.75857739	0.01463577	7.09E-05
LOC121820976	1.24807153	2.40953622	0.01554763	3.18E-07
Ccdc154	0.66878811	0.76664989	0.01768072	0.00045327
Adora2a	1.29617582	2.59368055	0.01768072	2.29E-07
Comtd1	0.59858588	0.60365253	0.01775337	0.00157412
Tmem100	1.39118356	1.15713946	0.01780654	0.01056607
Ccl19	1.08529591	1.51859273	0.0181385	4.47E-05
LOC121826054	0.85183118	0.65953693	0.01825967	0.01160191
Bicdl1	0.89805715	0.72632064	0.01877355	0.01007601
Ctss	0.5270025	1.09015819	0.01877362	2.16E-07
LOC102914220	0.86981104	0.57247319	0.01939475	0.03345648
Kcnab2	0.72498092	0.67393686	0.01959287	0.00325302
LOC121826272	1.17704345	0.84692103	0.02124859	0.02337115
Arl5c	1.1057694	1.63393444	0.02420941	3.20E-05
Mfsd2a	0.96617754	0.84811724	0.02475096	0.00724717
Arap2	0.63975535	0.71004228	0.02661175	0.00110462
Ldlrad3	0.63755635	1.17191594	0.02764301	2.90E-06
Gpr132	0.9070267	1.45814942	0.0278866	1.89E-05
LOC102926929	0.91542364	1.24109802	0.02894822	0.00017004
Dgkh	0.64426193	0.68840237	0.0301255	0.00196242
Mvd	0.78022863	0.62509246	0.03059562	0.02020525
Glrx	0.74676418	1.66751981	0.03097992	2.78E-07
Vdr	1.06497369	2.08182937	0.03123174	1.58E-06
Oaf	1.19010117	1.44249481	0.03160005	0.0007263
Sez6l	1.34427823	1.05879151	0.03297262	0.02099244
LOC102920505	0.73623698	0.99625442	0.03341877	0.00021726
Spire1	0.60259977	1.30718594	0.03341877	4.60E-07

LOC107400967	0.95803135	0.84691417	0.03424398	0.01055692
Pde3b	0.64295335	0.53744599	0.03464264	0.01679306
Enox1	0.77104074	0.88372446	0.03468218	0.00131736
Nr4a1	0.81102662	1.10310992	0.04033759	0.00033192
LOC102911918	0.94063712	1.90453283	0.04121876	1.39E-06
LOC102922327	0.79069135	1.530969	0.04469908	3.69E-06
Gstcd	0.59780861	0.81922504	0.04480086	0.00043676
Lox	1.49789673	1.94850629	0.04537917	0.00070075
LOC102911182	0.78607536	1.69450374	0.04537917	7.74E-07
Fcgr2b	0.7071093	0.71133122	0.04603278	0.00599367
Slco3a1	0.64005668	0.98284212	0.04656042	0.00012581
LOC102904896	0.74422109	1.38917452	0.04656042	7.71E-06
Satb1	0.66202019	0.94670193	0.04753909	0.0002613
Ptger3	0.75222377	0.62186917	0.04911257	0.02527972
Dis3	0.68938159	0.92667806	0.04929679	0.00059745
Slco4a1	0.76519026	0.80445543	0.04991187	0.00631337

Supplemental Table 8: Additive genes that are significantly downregulated by population and injection ($P < 0.05$ and logFC < -0.5).

ID	Population logFC	Injection logFC	Population adjusted P Value	Injection adjusted P Value
Gpr160	-1.6232124	-0.7870323	4.99E-06	0.00044748
Pkd1l1	-1.0112872	-0.8785578	0.00021287	2.70E-05
LOC102911309	-1.1420722	-1.1418423	0.00045328	9.63E-06
Gstk1	-0.9201216	-0.9016693	0.00122927	4.23E-05
Tmprss9	-1.8201292	-1.0436757	0.00165313	0.00739385
Ccdc125	-1.1283239	-0.9535079	0.00176879	0.0003508
Ctnnal1	-1.0109119	-0.6937477	0.00281634	0.00359001
Dna2	-1.0855499	-0.9687589	0.00350567	0.00051103
Cpz	-1.7846966	-1.5162552	0.00450454	0.0009112
Dtx3	-0.6832655	-1.332509	0.00465765	1.43E-07
C6H4orf3	-0.7098499	-0.5528549	0.00466882	0.00252711
Trmt9b	-0.8534848	-0.9174258	0.00466882	0.00010617
Espn	-1.772505	-3.6002013	0.0048916	2.26E-07
Primpol	-0.7713665	-0.7592695	0.00588825	0.00040091
Bend7	-0.92724	-1.0106865	0.00737131	0.00021304
Fxyd6	-1.4214905	-1.6012785	0.00747167	0.00024378
Ctsd	-0.7882856	-0.7808373	0.00948984	0.00060452

Mthfd2l	-1.1509072	-1.0267514	0.01007952	0.00172461
Unc119	-0.7682408	-0.6115452	0.01036599	0.00542353
Eaf2	-0.8189789	-0.8818446	0.01098942	0.00044597
LOC102918846	-0.9643586	-0.5417192	0.01110488	0.03741948
LOC102916240	-1.0307926	-0.8169306	0.01137985	0.00558925
Stab2	-1.7582829	-1.4965479	0.01189982	0.00337968
LOC102917318	-0.9375674	-1.347463	0.01233726	2.46E-05
Pla2g7	-1.1877154	-0.771554	0.01512288	0.02635684
Stc2	-1.3430831	-1.4551385	0.01564342	0.00085418
Hsdl2	-0.5310165	-0.6198029	0.01592798	0.00036031
Eva1a	-0.8706754	-1.1482344	0.01623468	9.76E-05
C11H1orf112	-0.7220031	-0.5595164	0.01645336	0.00989356
Adamtsl5	-0.8508399	-1.3190227	0.01737072	2.28E-05
LOC121827242	-1.0279136	-0.8388402	0.01768072	0.00722894
Zbtb47	-1.0265832	-1.4533278	0.01780654	4.94E-05
LOC102904682	-1.7510283	-1.0389489	0.01780654	0.03743137
Mpzl1	-0.7532379	-0.9589585	0.01825967	0.00026745
Rsph3	-0.8633276	-0.8627939	0.01927144	0.00166304
Mcoln3	-1.2868454	-1.9368001	0.01959287	2.10E-05
LOC121823710	-0.6305585	-1.2684305	0.02122982	5.48E-07
LOC102919098	-0.5442782	-0.5274768	0.02183756	0.00255103
Hadh	-0.6206209	-1.0915852	0.02754751	1.79E-05
Smpd2	-0.5734312	-0.5174482	0.02894822	0.00828176
Rab6b	-1.1375569	-1.2698243	0.02958011	0.00157501
LOC121828733	-0.7729141	-0.5664962	0.03214996	0.02839099
Wdr86	-1.6424772	-1.3118151	0.03248404	0.0164532
Lyplal1	-0.7524464	-0.6246405	0.03464264	0.01517339
Clcn3	-1.0609587	-0.7444127	0.03619012	0.03972386
Gdf11	-0.5663013	-0.5655457	0.03688327	0.00454087
Manba	-0.5348637	-0.6969697	0.03839228	0.00065359
Chek2	-0.5244626	-0.6551671	0.03848296	0.00099173
LOC121828934	-0.8495113	-0.7366474	0.03848296	0.01308556
Acap3	-0.6936668	-0.7707326	0.03974875	0.00258397
Cep128	-0.8066236	-0.62103	0.04002433	0.02849545
LOC107400912	-0.833512	-0.7914488	0.04537917	0.00891378
Nectin1	-0.8314127	-0.9959641	0.04963126	0.00189369

Supplemental Table 9: List of additive genes found in the Schweizer et al., 2021 *a priori* list. These genes are matched with their respective population and injection logFC as well as their published NCBI function.

Gene Name	Population logFC	Injection logFC	NCBI GO Function (if not found, GO Process provided)
Kbtbd3	1.38	-0.794	Enables protein binding
Rab5b	-0.407	-0.336	Enables GTP binding, enables GTPase activity
Usp28	0.333	-0.259	Enables cysteine-type deubiquitinase activity, enables cysteine-type endopeptidase activity, enables protein binding
LOC102906561 (zinc finger protein 431-like)	1.01	0.740	GO Process: Involved in regulation of DNA-templated transcription
Dtx3	-0.683	-1.33	GO Process: Involved in Notch signaling pathway, involved in protein ubiquitination
Slc39a6	1.02	1.85	Enables zinc ion transmembrane transporter activity
Spdya	0.547	-0.347	Enables protein kinase binding
Gdf11	-0.566	-0.566	Enables cytokine activity, enables growth factor activity
Dyrk1a	-0.255	-0.208	Enables ATP binding, enables protein serine/threonine kinase activity, enables protein serine/threonine/tyrosine kinase activity, enables transcription coactivator activity
Pdcl	0.331	0.216	GO Process: Involved in regulation of G protein-coupled receptor signaling pathway
LOC102926914 (zinc finger protein 431-like)	0.299	0.193	Enables DNA-binding transcription factor activity, RNA polymerase II specific, enables RNA polymerase II cis-regulatory region sequence-specific DNA binding
Sik3	0.377	0.223	Enables ATP binding, enables protein serine/threonine kinase activity, enables tau protein kinase activity
Osbpl2	0.306	-0.249	Enables cholesterol binding
Usp54	0.375	-0.296	Enables cysteine-type deubiquitinase activity
LOC102927177 (von Willebrand factor A domain-containing protein 5A-like)	1.16	1.61	Unknown
Slc29a1	-0.556	-0.397	Enables nucleoside transmembrane transporter activity
Nectin1	-0.831	-0.996	GO Process: Involved in heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules, involved in homophilic cell-cell adhesion via plasma membrane cell adhesion molecules, involved in protein localization to cell junction
Zbtb16	2.11	1.94	Enables protein binding
Nxf1	0.262	0.246	Enables RNA binding, enables protein binding
Satb1	0.662	0.947	Enables DNA-binding transcription factor activity, RNA polymerase II specific, enables RNA polymerase II cis-regulatory region sequence-specific DNA binding

Supplemental Table 10: GO terms that are enriched from the downregulated by highlanders gene set (P < 0.05 and logFC < -0.5).

Term ID	Term Name	P value	Term Size	Precision	Intersection Size	Query Size
GO:0006259	DNA metabolic process	0.00118014	543	0.14736842	28	190
GO:0006261	DNA-templated DNA replication	0.0035236	105	0.05789474	11	190
GO:0005657	replication fork	0.01802037	55	0.03684211	7	190
GO:0140097	catalytic activity, acting on DNA	0.0281194	177	0.06315789	12	190
GO:0017116	single-stranded DNA helicase activity	0.0281194	14	0.02105263	4	190
GO:0031390	Ctf18 RFC-like complex	0.03120301	7	0.01578947	3	190
GO:0003824	catalytic activity	0.04090786	3330	0.44210526	84	190
GO:0008094	ATP-dependent activity, acting on DNA	0.0455523	97	0.04210526	8	190
GO:0003689	DNA clamp loader activity	0.0455523	8	0.01578947	3	190