

Consequences of IRF2BP2 loss of function in mouse development and skeletal muscle regeneration

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ABSTRACT

IRF2BP2 is a corepressor of IRF2, a transcription factor involved in the immune response. IRF2BP2 is also a coactivator of the VGLL4/TEAD4 complex in muscle. Given its functional duality, we asked how IRF2BP2 deletion would affect mouse development and adult muscle regeneration.

Most *Irf2bp2*^{-/-} mice die prior to birth, those that survive develop lymphoma in adulthood. Microarray profiling of *Irf2bp2* knockout liver, heart, and skeletal muscle revealed a shared program of upregulated genes involved in inflammation and immunity. The function of IRF2BP2 in adult skeletal muscle recovery from cardiotoxin-induced injury was evaluated. Compared to WT mice, mice with macrophage-specific ablation of IRF2BP2 (*Irf2bp2*^{flox}/*LysMCre*) or muscle-specific ablation of *Irf2bp2* (*Irf2bp2*^{flox}/*MckCre*) mice showed increased inflammation and impaired muscle regeneration.

Global deletion of *Irf2bp2* in mice results predominantly in embryonic death or lymphoma in adults. *Irf2bp2* suppresses genes that mediate inflammation in mouse liver, heart, and in skeletal muscle, where IRF2BP2 promotes regeneration.

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LIST OF ABBREVIATIONS

AP-1 (activating protein-1)

APA (alternative polyadenylation)

ATF (activating transcription factor)

BCL2A1 (B-cell lymphoma 2-related protein A1)

BH (Benjamini Hochberg)

BMDM (bone marrow-derived macrophage)

CCL (CC chemokine ligand)

CCR (CC chemokine receptor)

CDK (cyclin-dependent kinase)

COX2 (cyclooxygenase-2)

CTX (cardiotoxin)

DAVID (Database for Annotation, Visualization and Integrated Discovery)

DC (dendritic cells)

DD1 (death domain-1)

DIF-1 (DD1-interacting factor-1)

dpc (days post coitum)

EAP1 (enhanced-at-puberty-1)

FASTKD2 (Fas-actiated serine-threonine kinase domain 2)

FDR (false discovery rate)

Flox (flanked by loxP)

Frt (flippase recognition target)

GnRH (gonadotropin-releasing hormone)

H&E (hematoxylin and eosin)

IFN (interferon)

IL (interleukin)

iNOS (inducible nitric oxide synthase)

IRF (interferon regulatory factor)

IRF2BP1 (interferon regulatory factor-2 binding protein-1)

IRF2BP2 (interferon regulatory factor-2 binding protein-2)

IRF2BPL (interferon regulatory factor-2 binding protein-like)

JDP2 (Jun-dimerization protein 2)

KLF2 (Kruppel-like factor-2)

KO (knockout)

Lox (locus of crossing over)

MCK (muscle creatine kinase)

MEF2 (myocyte enhancer factor-2)

MOPS (3-(N-morpholino)propanesulfonic acid)

MT (metallothionein)

Myf (myogenic factor)

NaOAc

NF- κ B (nuclear factor kappa-light-chain-enhancer of activated B cells)

NFAT1 (nuclear factor of activated T-cells 1)

NK (natural killer)

NRIF3 (nuclear receptor interacting factor-3)

PBS (phosphate-buffered saline)

PCR (polymerase chain reaction)

PFA (paraformaldehyde)

PRR (pattern recognition receptors)

RARA (retinoic acid receptor alpha)

RING (Really Interesting New Gene)

RMA (Robust Multi-array Average)

SDS (sodium dodecyl sulfate)

T_H (T-helper)

TA (tibialis anterior)

TEAD (TEA domain family member)

TEF (transcriptional enhancer factor, also **TEAD**)

Th1 (T helper 1 cells)

Th2 (T helper 2 cells)

TGF- β (transforming growth factor beta)

TNF- α (tumor necrosis factor alpha)

UTR (untranslated region)

VCAM-1 (vascular cell adhesion protein-1)

VEGF (vascular endothelial growth factor)

Vg (vestigial)

Vgll1, Vgll2, Vgll3, Vgll4 (Vestigial-like-1, -2, -3, -4)

WT (wildtype)

YAP (Yes-associated protein-1)

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INTRODUCTION

Innate immunity and inflammation

Host defense serves to generate immune responses to invading pathogens and to suppress tumor development, achieved through the action of transcription factors that regulate gene expression (1). The immune response is a characteristic of all living cells, occurring in classical immune tissues such as the liver, spleen, and lungs, as well as non-immune tissues such as cardiac and skeletal muscle (2). Immune cells in tissues, such as macrophages, mast cells, and dendritic cells, as well as circulating monocytes and neutrophils, recognize pathogen invasion or cell damage with pattern recognition receptors (PRRs) (3). The innate immune system is the first line of defense during infection and mediates inflammation (4). This response is activated immediately upon encounter with the pathogen, executed primarily by myeloid cells as well as some lymphocyte subpopulations (5). The inflammatory response must also undergo a series of carefully regulated steps to ensure an efficient return to tissue homeostasis. This process consists of phagocytic cells and antigen-presenting cells such as macrophages and granulocytes that are distributed to affected tissues throughout the organism (7). Thus, inflammation is a highly coordinated process that initially causes damage to the host tissue or organ, but ultimately aims to resolve this damage and return the tissue to a homeostatic environment (4). This balance between damage and resolution is a characteristic of the immune system, which participates in many dual functions – for example, tumor development versus tumor suppression (8). Interestingly, macrophages are known to have two major phenotypes: they can either induce host defense, antitumor immunity, and inflammatory responses, or they can suppress those

functions. Therefore, macrophages have active roles in both the induction and the resolution of immune responses. (9)

Macrophages are multifunctional regulators of the immune system

Macrophages are immune cells with a central role in host protection as the first line of defense against invading foreign pathogens (10). They are involved in the removal of cellular debris generated during tissue remodeling, and they efficiently clear apoptotic cells through the engulfing process of phagocytosis (11). They also produce cytokines, growth factors, and angiogenic factors that are believed to play important roles in regulating fibroproliferation and angiogenesis (12). Macrophages are the mature form of monocytes, which arise from myeloid progenitor cells in the bone marrow (11). The monocytes circulate in the bone marrow, spleen, and bloodstream and can then differentiate into dendritic cells (DCs) or macrophages upon migration into various tissues (12, 13). Macrophages reside in both lymphoid and nonlymphoid tissues and are crucial for maintaining tissue homeostasis. They are highly versatile and multi-functional, having numerous functions related to tissue remodelling, inflammation, immunity and thrombosis, and have the capacity to affect tumor growth and progression. (14). An interesting characteristic of macrophages is their ability to adapt to opposing roles, such as the induction or suppression of immune responses (9), as well as tissue-destructive versus tissue repairing activities (15). For example, macrophages play important roles in skeletal muscle injury and repair (5, 16, 17), propagating an initial “Th1” T-helper cell inflammatory response, then promoting healing and regeneration through the release of anti-inflammatory cytokines (5). Although macrophage polarization has clear implications in tissue damage and repair, it also plays a role in cancer (18). Despite

macrophages being fundamental to innate defense, they are also associated with tumor progression, cell growth, and angiogenesis (14). Macrophages isolated from primary tumors have been found to display an anti-inflammatory M2 phenotype and are thought to be recruited and/or M2 polarized by the tumor cells as a means to prevent their destruction by the immune system (18).

Cross-talk between immune cells and muscle

Skeletal muscles are the most abundant tissue in the body, constituted by stable myofibres and by multipotent myogenic stem cells (termed satellite cells) that differentiate into mature muscle fibres (16). Satellite cells are located underneath the basal lamina that surrounds muscle fibers and contribute to the increase in myonuclei during postnatal muscle growth by proliferating and fusing with existing myofibers (19). Skeletal muscle has an impressive capacity for repair and expresses a variety of proinflammatory cytokines and chemokines following stimuli and injuries, such as damage from physical crushing or necrosis from toxin injections (15, 16). Like most tissues, the muscle contains a stable population of resident macrophages and dendritic cells, but additional immune cells infiltrate after injury or with inflammatory myopathies, and are also detected in disease such as obesity and diabetes (6). After an acute muscle injury, neutrophils are the early invaders followed by phagocytic and nonphagocytic macrophages (20).

Depending on their activation state, macrophages can employ a particular phenotype and function (15), enabling them to further damage muscle cells or promote cell proliferation for healing. In the M1 phenotype, macrophages are said to be “classically” activated and cause tissue damage, propagating the T_H1 response (17). M1 macrophages are

characterized by the expression of iNOS and proinflammatory cytokines such as TNF- α , IL-1 β , IL-6, and IL-12. On the other hand, the M2 phenotype consists of “alternatively” activated macrophages that are characterized by the expression of anti-inflammatory cytokines and growth factors, such as IL-4, IL-10, and TGF- β (17, 18). M2 macrophages are even more diverse and complex, and have been divided into three specialized subcategories designated M2a, M2b, and M2c, each activated by different cytokines (5). M2a macrophages are “alternatively activated” and promote wound healing and tissue repair, especially in the advanced stages in response to IL-4 and IL-13 cytokines (7). M2b macrophages release “Th2” anti-inflammatory cytokines such as IL-10, but they also release some pro-inflammatory cytokines such as IL-1 β and TNF- α . M2c macrophages are capable of promoting satellite cell differentiation and have an anti-inflammatory role by deactivating M1 macrophages (7, 21).

While myeloid cell infiltration is crucial for tissue repair, this process also requires a highly coordinated cross-talk with skeletal muscles (17). Complex interactions between muscle and the immune system are essential in regulating muscle regeneration. The immune response following a skeletal muscle injury coincides with its repair, regeneration, and growth (6), overall consisting of three major stages: proliferation, early differentiation, and terminal differentiation. These stages are regulated by muscle-specific basic helix-loop-helix proteins including MyoD, myogenin, Myf4, and Myf5 (16, 19, 22). Following an acute muscle injury, the invasion of myeloid cell populations occurs alongside a change in expression of myogenic genes and transcription factors (16).

Satellite cell proliferation starts 2 days after muscle injury, and is triggered by multiple cellular signals including sphingosine-1-phosphate synthesis, nitric oxide

production, and activation of matrix metalloproteinases (19). An increase in MyoD expression is followed by elevated myogenin expression at 3 days post-injury (16). At 4 days post-injury, young myotubes with centralized nuclei begin to be identified, indicating muscle regeneration (22). Although the sequence of myogenic gene expression occurs independently of myeloid cells, it can still be greatly influenced by the presence of myeloid cells and release cytokines (16).

The IRFs: Transcriptional control of innate immune responses

The interferon regulatory factors (IRFs) are a family of transcription factors that comprise 9 members in the mammalian family. They all share an N-terminal DNA binding domain as well as a C-terminal “IRF-association” domain (save for IRF6) that interacts with other IRFs, transcription factors, or cofactors (23). There are also regulatory domains only specific to some IRF members, such as repression domains shared by IRF2, -3, -4, and -5 that can become activation domains after certain modification events (24). IRFs were first characterized as transcriptional regulators of type I interferons (IFNs) (i.e. IFN- α and IFN- β) in response to viral infection, as well as regulators of type I and II IFN-inducible genes. However, they also play roles in controlling mechanisms of host defense, through coordinated cellular responses and expression of target genes (1). They are considered important for the differentiation of T-helper (T_H) cells (24), which can develop into Type 1 or Type 2 T-helper cells (T_H1 or T_H2 respectively) that secrete effector cytokines (25). IRFs are now known to be essential in regulating mechanisms of the immune response, cell survival/apoptosis, and oncogenesis (1, 23).

For example, IRF1 and IRF2, among the most studied of the IRFs, both promote T_H1 cell responses and natural killer (NK) cell development, but IRF1 promotes apoptosis while IRF2 promotes oncogenesis by antagonizing IRF1 activity as well as IRF9 activity (1, 24). IRF9 is constitutively expressed in B- and T-cells, but is also induced by IFN- γ and mediates p53 induction (1). IRF3 and IRF7 are similarly structured; both contain inhibitory domains regulated by phosphorylation and induce early type-I IFNs (24). IRF5 interacts with IRF1, -3, and -7. It is required for DNA damage-induced apoptosis and has been shown to be targeted by the p53 tumor suppressor (26), but does not seem to be involved in T_H1 activity (24). Interestingly, IRF6 is involved in the formation of a cleft lip/palate condition (kondo '02) but its role in immune function is unknown. IRF8 promotes apoptosis and inhibits myeloid cell growth through various target genes (1). Thus, with each IRF protein playing unique but related roles, interactions between family members and with other proteins make up an intricate and complex regulatory system.

Role of IRF2 as a repressor and activator

Interferon regulatory factor-2 (IRF2) is a transcription factor that was first described as a DNA binding repressor protein that inhibited IRF1 activity by competing for the same binding sequences (i.e. 5'-AAGTGA-3' repeats) on the IFN- β promoter (27). IRF1 and IRF2 share homology in their N-terminal regions, which bind to the same DNA sequence elements, but differ significantly in their C-terminal regions, in which IRF1 bears its transcriptional activation domain. Thus, IRF2 was shown to negatively regulate type I IFN-induced genes by antagonistically repressing IRF1 binding activity (23). In macrophages *in vitro*, IRF2 represses lipopolysaccharide-induced expression of COX2, an enzyme expressed

at sites of inflammation (28). An early study in IRF-knockout mice showed altered activity of B lymphopoiesis and hematopoiesis following viral infection, indicated by low populations of precursor cells in the bone marrow (29).

A study in mice found that some, but not all, old IRF2 knockout mice developed skin lesions of various severities. Another study of mice with a different genetic background showed IRF2 knockout mice lost fur at 7-10 weeks of age due to a skin disease involving fibrosis and infiltration of inflammatory cells in the dermis (30). More recent mouse studies showed that intrahepatic IRF2 is protective against ischemia/reperfusion injury in the liver, and overexpressing IRF2 decreases IRF1-responsive hepatic inflammation (31). Furthermore, it has been shown that IRF2 regulates B-cell proliferation through IFNAR-mediated signaling and antibody production via activation of Blimp-1 (32). These studies highlight the importance of IRF2, demonstrating that its absence *in vitro* or *in vivo* can result in uncontrolled immune responses and augmented type I IFN signaling (23).

Although it was primarily described as a repressor, IRF2 also contains a latent transcriptional activation domain. When its repression domain was deleted *in vitro*, IRF2 became a transcriptional activator (33). IRF2 was shown to transcriptionally activate the histone H4 gene (34), as well as the gp91^{phox} gene expressed in terminally differentiating myeloid cells (35). Interestingly, the repression domain of IRF2 is not active in muscle cells, where IRF2 activates VCAM-1, a cell adhesion molecule typically expressed on the surface of endothelial cells in response to inflammation (36). VCAM-1 and IRF2 expression are downregulated in adult muscle fibres, and instead are highly expressed on newly forming myotubes and myogenic satellite cells. Following injury or disease, satellite cells proliferate and fuse to regenerate muscle fibres, and VCAM-1 plays a role in recruiting leukocytes to

these sites of myogenic regeneration. Thus, IRF2 appears to function as a transcriptional activator in satellite cells (myogenic stem cells), but as a transcriptional repressor in lymphocytes and other non-muscle cells (36). It is not fully understood why the IRF2 repression domain is not always active, but it may depend on interactions with tissue-specific corepressors or alternatively spliced forms of IRF2 (24).

Novel binding proteins repress IRF2 transcriptional activity

Two novel corepressor molecules were identified in 2003 that interact specifically with IRF2, termed IRF2-binding proteins 1 and 2 (IRF2BP1 and IRF2BP2) (37). IRF2BP2 is comprised of two splicing isoforms IRF2BP2-A and IRF2BP2-B, with the latter lacking 16 amino acids. These nuclear proteins share an N-terminal zinc finger and a C-terminal C₃HC₄ RING finger, inhibiting basal and enhancer-activated transcription through binding to the IRF2 C-terminal repression domain (**Figure 1**), which is highly conserved between species. While all the IRF2BPs sufficiently bind to the C-terminal 58 amino acids, IRF2BP1 is capable of weakly binding to just 18 amino acids in the C-terminal. However, the loss of only two valines (V177 and V178) in IRF2 results in a loss of transcriptional repression by the IRF2BPs, even with its C-terminal repression domain still intact (37).

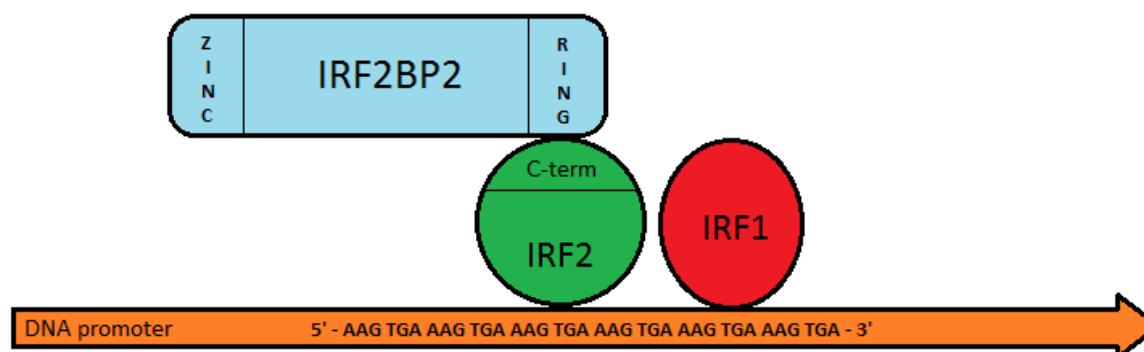


Figure 1. Basic interaction of IRF2BP2 with IRF2 at promoter. RING domain of IRF2BP2 interacts with C-terminal domain of IRF2 to enhance transcriptional repression.

In addition to IRF2BP1 and IRF2BP2, a third homolog initially termed C14orf4 was discovered as a novel intronless gene of unknown function, predominantly expressed in heart tissue and moderately expressed in skeletal muscle (38). The protein has since been renamed to IRF2BPL (IRF2BP-like), or enhanced-at-puberty-1 (EAP1), and shares the conserved C4 zinc finger and C₃HC₄ RING finger domains found in IRF2BP1 and IRF2BP2 (37, 39). EAP1 was found to have increased expression during puberty in the hypothalamus of rodents and nonhuman primates. EAP1 transactivates the transcription of gonadotropin-releasing hormone (*GnRH*), a gene involved in reproductive function, while suppressing the expression of genes that inhibit GnRH neuronal function (39). It is possible that EAP1 binds to the IRF2 C-terminus via its RING finger domain, but their interaction has not been tested (37).

IRF2BP1 also associates with Jun-dimerization protein 2 (JDP2) and enhances its ubiquitination via the RING-finger domain of IRF2BP1 (40). JDP2 is a member of the activating protein-1 (AP-1) transcription factors, which is composed of the Jun, Fos, and activating transcription-factor (ATF) protein subfamilies. AP-1 proteins mediate gene expression in response to stress signals, cytokines and growth factors, infections, and oncogenic stimuli (41). The repression and ubiquitin ligase activities of IRF2BP1 occur independently due to their conflicting functions, as polyubiquitination generally leads to protein degradation (40).

Novel roles of IRF2BP2

Although IRF2BP2 has not been extensively studied, it has been further implicated in various roles since its identification as an IRF2 corepressor. IRF2BP2 was identified as a

novel target gene of p53 (42), a known tumor suppressor that determines how cells respond to stress by promoting cell survival or cell death through various mechanisms (43). However, there was no direct interaction observed between IRF2BP2 and p53, indicating the phenotype could be mediated through IRF2. Many transcriptional targets of p53 are involved in promoting apoptosis, but IRF2BP2 was shown to influence this cellular decision of p53 in the direction of cell growth arrest rather than apoptosis (42). Knockdown of IRF2BP2 after chemotherapeutic treatment in U2OS human osteosarcoma cells led to a faster induction of apoptosis and an upregulation of p21, a cyclin-dependent kinase (CDK) inhibitor that halts the cell cycle in the G₁ phase (43). Thus, IRF2BP2 is suggested to have a role in maintaining cells in a state of growth arrest, possibly allowing them to repair damaged DNA. (42).

IRF2BP2 was identified as a novel partner of NFAT1 (nuclear factor of activated T cells-1) (44). It functions as a transcriptional repressor in Jurkat T lymphocyte cells by binding to the NFAT1 C-terminal domain and inhibiting the expression of NFAT1-regulated genes. The NFAT transcription factors control genes involved in the cell cycle, differentiation, and apoptosis, and NFAT1 showed tumor suppressor activity in NIH/3T3 mouse fibroblast cells by negatively regulating cell proliferation (45). Furthermore, IRF2BP2 was described in a paper under the name DIF1 (DD1 interacting factor-1), as a protein that binds to a region on nuclear receptor interacting-factor 3 (NRIF3) named death domain-1 (DD1) (46). In this study, IRF2BP2 (isoform A) acts as a repressor through the protein deacetylase Sirt1, and this repression is reversed when IRF2BP2 binds to NRIF3/DD1. Interestingly, IRF2BP2 was found to interact with IRF2BP1 and EAP1 in a complex, and this interaction is necessary for repressing FASTKD2 (Fas-activated serine-

threonine kinase domain 2), a pro-apoptotic gene found in breast cancer cells. Indeed, knockdown of IRF2BP2 by siRNA leads to FASTKD2-mediated apoptosis of breast cancer cells. The finding that IRF2BP1 and EAP1 were required for IRF2BP2-mediated repression raised the possibility that the interaction of IRF2BP2 with various proteins in different cell types may determine whether it functioned as a repressor or activator (46).

In addition to its repressive function in breast cancer cell apoptosis, IRF2BP2 has also been implicated in other forms of cancer. In a study investigating translocation events in patients with multiple myeloma, *IRF2BP2* was one of several identified genes located in the chromosomal aberration regions, meaning it could be a potential prognostic marker in the treatment of patients with the *BCL1/JH* t(11;14) translocation (47). However, its expression was not investigated at the mRNA level. Furthermore, a novel fusion was discovered between *IRF2BP2* and *CDX1* (caudal type homeobox 1), a gene encoding a transcription factor, arising after a translocation event in human mesenchymal chondrosarcoma (2012 ref2), which is a rare malignancy of bone or soft tissue (48). More recently, another gene fusion event involving *IRF2BP2* and retinoic acid receptor alpha (*RARA*) was discovered in a patient with acute promyelocytic leukemia (49).

IRF2BP2: Corepressor in myeloid/lymphoid cells, coactivator in skeletal muscle cells

In our lab, IRF2BP2 was identified in a yeast-two hybrid screen as a novel cofactor of the Vestigial-like 4 (Vgll4) transcription factor in muscle cells, linking IRF2BP2 to the TEF1 (transcriptional enhancer factor-1, now called TEAD1) and MEF2 (myocyte enhancer factor 2) transcription factors (50, 51). The *vestigial* (Vg) family was first discovered when the loss of Vgll1 was found to impair wing development in *Drosophila melanogaster*. A

novel human protein, TONDU, was identified in 1999 that specifically interacts with a conserved domain in mammalian TEAD factors, and was able to functionally substitute for Vg during *Drosophila* wing blade formation (52). There are 4 mammalian homologs of vestigial; Vgll2 is skeletal muscle-specific, Vgll3 is placenta-specific, and Vgll4 is expressed in the heart and physically interacts with TEAD1, which regulates cardiac and skeletal muscle genes (51, 53). Vgll2 was suggested to have importance in myogenic activity, as its mRNA levels increased during skeletal myotube formation *in vitro*, and the Vgll2 protein interacted with MEF2, which coactivates muscle gene expression along with MyoD (53, 54, 55).

TEAD proteins (TEA-domain factors, previously named TEF) are required for YAP (Yes-associated protein)-induced cell growth and oncogenic transformation. TEAD4 in particular is expressed in developing skeletal muscle of mouse embryos (56). When complexed with TEAD4 and Vgll4, IRF2BP2 activated the expression of vascular endothelial growth factor-A (VEGFA) in an ischemia-inducible manner in C2C12 muscle cells (51). VEGF is a key regulator of angiogenesis and cell survival, and induces a potent angiogenic response in *in vivo* models (57). Our lab also identified a nuclear localization signal for IRF2BP2, controlling its nucleocytoplasmic location during skeletal muscle differentiation; however, forced nuclear localization did not improve transcriptional activation of IRF2BP2 (58).

More recently, IRF2BP2 was specifically knocked out in the myeloid lineage of mice (i.e. LysMCre/IRF2BP2^{flox} mice), and it was discovered to act as a modulator of macrophage polarization, inhibiting the M1 and promoting the M2 phenotype (59). IRF2BP2 was implicated in the progression of atherosclerosis, as IRF2BP2-deficient

macrophages showed increased propensity for the formation of foam cells, which are lipid-laden macrophages found in atherosclerotic plaques (60). IRF2BP2 was also shown to mediate MEF2-dependent expression of the anti-inflammatory transcription factor, KLF2 (Kruppel-like factor 2), possibly accounting for the impaired phenotype of cholesterol handling in macrophages (59).

Hypothesis

Given the interesting dual function of IRF2BP2 as a corepressor or a coactivator in a skeletal muscle cell line, and its interaction with key regulatory factors in IRF2 and Vgll4, I asked how global deletion of IRF2BP2 from mice will affect gene expression and mouse development. I hypothesized that:

- 1) IRF2BP2 may have a repressor or activator function that is tissue-specific, and
- 2) Ablation of IRF2BP2 in macrophages would have a different effect than ablation of IRF2BP2 in muscle in the process of skeletal muscle regeneration.

To address this hypothesis, IRF2BP2 was knocked out in the germline of mice and the effect of IRF2BP2 ablation on tissue-specific gene expression was ascertained using cDNA microarrays. I report here on the characterization of the first IRF2BP2 knockout mouse that has been studied. Furthermore, as IRF2BP2 has clear implications in the immune system as well as the skeletal muscle system, I asked how tissue-specific deletion of IRF2BP2 in myeloid cells or in muscle cells would impact inflammation-mediated muscle regeneration in a well-established mouse injury model. IRF2BP2 may also have an *in vivo* role in skeletal

muscle angiogenesis due to its ability to upregulate VEGFA *in vitro*. This thesis will present evidence of the importance of IRF2BP2 in mouse embryogenesis, as well as throughout adult development, with a particular focus on skeletal muscle regeneration.

MATERIALS AND METHODS

***Irf2bp2* global knockout mice**

Hemizygous *Irf2bp2*^{+/-} mice were generated by Dr. Siu-Pok Yee (University of Connecticut). Chimeric males were bred with ROSA26-FLPe females to remove the PGK-neo cassette and positive pups were het-floxed. A female Hprt-Cre mouse was also crossed with the chimeric male. The PGKneo cassette is flanked by Frt site and LoxP site (LoxP-exon-Frt-PGKneo-Frt-LoxP). All animal procedures were approved by the University of Ottawa Animal Care Committee in accordance with the Canadian Council on Animal Care guidelines. *Irf2bp2*^{+/-} mice were intercrossed to produce homozygous *Irf2bp2*^{-/-} mice.

***Irf2bp2* tissue-specific knockout mice**

For skeletal muscle regeneration experiments, myeloid cell-specific and muscle tissue-specific IRF2BP2 knockout mice were used. LysMcre mice (Stock #004781, The Jackson Laboratory) were crossed with *Irf2bp2*-floxed mice to produce a conditional deletion in the myeloid cell lineage. MCK-Cre mice (Stock #006475, The Jackson Laboratory) were crossed with *Irf2bp2*-floxed mice to produce a conditional deletion in skeletal and cardiac muscle. For hindlimb ligation experiments, Myf5-Cre mice (a gift from Dr. Michael Rudnicki, University of Ottawa) were crossed with *Irf2bp2*-floxed mice to produce a conditional deletion in skeletal muscle.

Mouse genotyping

PCR genotyping was performed on genomic DNA from mouse tails tips which were digested using 50 µL of alkaline lysis reagent (25 mM NaOH, 0.2 mM EDTA) at 95°C for

30 minutes, then cooled to 4°C, followed by a final addition of 50 µL of neutralization reagent (40 mM Tris-HCl). The PCR parameter used was 33 cycles of 94°C for 30 seconds, 55°C for 30 seconds, and 72°C for 45 seconds, followed by a cool down to 4°C. To genotype the *Irf2bp2* alleles, 5 µL of REDExtract-N-Amp PCR ReadyMix (#R4775, Sigma-Aldrich) was added to 2 µL DNA and 5 µM of primers in a final reaction volume of 10 µL.

Primers “Lox gtR” (5’-CCC TTC ATG TAA GTA TTC TC-3’), “Lox gtF” (5’-GTG CTC CTT AAG TGT TGC AG-3’), and “Frt gtF” (5’-GAC TCT TGG ACA GCC AAG CTC-3’) were used to amplify wildtype (315 bp), deleted (538 bp), and floxed (414 bp) alleles. To genotype the *Cre* recombinase gene driven by the muscle creatine kinase promoter, *Ckmm-cre* (350 bp), primers “MCK Fwd” (5’-ATG TCC AAT TTA CTG ACC G-3’) and “MCK Rev” (5’-CGC CGC ATA ACC AGT GAA AC-3’) were used. Positive control primers used were “Internal ctrl Fwd” (5’-CAA ATG TTG CTT GTC TGG TG-3’) and “Internal ctrl Rev” (5’-GTC AGT CGA GTG CAC AGT TT-3’). For the full mouse targeting vector sequence, see **Appendix 1**.

Timed pregnancies

Timed matings were carried out by intercrossing *Irf2bp2*^{+/-} mice and designating 0.5 dpc to the day of identification of a vaginal plug. Pregnant females were sacrificed by CO₂ euthanization at 11.5, 13.5, 15.5, and 16.5 dpc. The abdominal skin and tissue was cut and opened to expose the abdominal cavity, where the uterine horns were cut free and transferred to ice cold PBS. Using thin and curved forceps, embryos were carefully separated from the placenta and yolk sac, and removed for genotyping as described previously (see **Mouse genotyping**).

RNA isolation

Total RNA was isolated from WT and IRF2BP2^{-/-} mouse heart, skeletal muscle, and liver (n=3 males per genotype) for Northern blot and microarray analysis. After CO₂ euthanization of the mice, approximately 150 mg of each tissue was weighed and collected. Tissues were immediately snap frozen in liquid nitrogen and stored at -80°C until subsequent use. Total RNA was isolated and purified using the RNeasy Midi Kit (#75142, Qiagen). Each tissue sample was placed frozen into a liquid nitrogen-cooled vessel, and disrupted by grinding with a pestle in liquid nitrogen until the tissue was a fine powder. The suspension was decanted into a cooled RNase-free polypropylene tube and the liquid nitrogen was allowed to evaporate. Lysis buffer (Buffer RLT, #79216, Qiagen) containing guanidine isothiocyanate and β-mercaptoethanol was added to the frozen tissue powder. The mixture was homogenized by passing it 10 times through an 18-gauge needle attached to a sterile syringe. The lysate was then diluted with double-distilled H₂O, then digested with Proteinase K (#19131, Qiagen) for 20 minutes at 55°C. Tissue debris was pelleted by centrifugation at 3000 x g for 5 minutes. Ethanol was added to adjust for binding conditions, and the supernatant was further purified by 3 rounds of centrifugation at 3000 x g for 5 minutes each using the provided RNeasy spin columns. The RNA was eluted twice with RNase-free H₂O into a final volume of 300 μL, and stored at -80°C. RNA concentrations and A260/230 purity ratios were measured with the Nanodrop™ 2000 (Model #ND-2000, Thermo Scientific).

Northern blot

All radioactive procedures were approved by the University of Ottawa's Radiation Safety Committee. The RNA samples isolated previously were made into aliquots of 15 µg. RNA was precipitated at -80°C with 1/10 volumes of 3M NaOAc and 2 volumes of 100% ethanol, then samples were centrifuged at 13,000 RPM. The resulting RNA pellets were resuspended in a master mix containing 1X MOPS buffer, formaldehyde, and formamide, then heated at 75°C for 5 minutes and quenched on ice. Total RNA (15 µg/lane) was fractionated on a MOPS/formaldehyde-mix agarose gel at 80V for 3 hours. The gel was washed 4 times in diH₂O, soaked for 15 minutes in water containing 50 µL ethidium bromide (10 mg/mL), then washed again 6 times in diH₂O.

A capillary system was used to transfer the RNA from the agarose gel to a nylon membrane (GeneScreen Plus Hybridization Transfer Membrane, #NEF988, Perkin Elmer). The gel was placed face down on the membrane, atop a wick of blotting paper and Whatman filter paper (#28298020, VWR International) soaked in 10X SSPE solution (1.5 M NaCl, 100 mM NaH₂PO₄, 100 mM Na₂EDTA). The gel was covered with another long piece of Whatman paper, with each end soaked in 10X SSPE buffer. The transfer was carried out overnight. After the overnight transfer, the RNA was immobilized by crosslinking the membrane under UV light for 30 seconds. Meanwhile, ExpressHyb™ Hybridization Solution (#636832, Clontech) was heated at 65°C for 3 hours until clear. The membrane was incubated with 10 mL of the hybridization solution for 1 hour at 65°C in a rotating oven.

The cDNA probe for IRF2BP2 was prepared by releasing the 3'UTR of IRF2BP2 cDNA (clone ID #6476448, Integrated DNA Technologies) using Sali/NotI restriction enzymes (#R0138S and #R0189S, New England Biolabs). 50 pmol of probe was denatured

and randomly primed with Klenow fragment using the Random Primers Labeling Kit (#18187013, Life Technologies Inc), and radioactively labeled with [α - 32 P]dCTP (#BLU013H250UC, Perkin Elmer Health Sciences). The cDNA probe for 18S (control) was radioactively labeled with [γ - 32 P]-ATP (#BLU502Z250UC, Perkin Elmer Health Sciences) in a T4 Polynucleotide Kinase (#M0201S, New England Biolabs) reaction. All labeling reactions were incubated for 1 hour at room temperature. Probes were purified by centrifugation at 1000 x g for 4 minutes with Bio-Spin P30 Gel Columns in Tris Buffer (#7326231, Bio-Rad Laboratories). Radioactivity was quantified in 4 mL liquid scintillation cocktail (#882475, MP Biomedicals) using a liquid scintillation analyzer machine (Model Tri-Carb 2100TR, Packard). The radioactive probe was added to 10 mL of fresh hybridization solution and incubated with the pre-hybridized membrane overnight at 65°C. The next day, the membrane was transferred to a tray and washed 3 times with 0.2% SDS in 2X SSPE buffer. The membrane was then washed 2 times in 0.2% SDS in 0.2X SSPE buffer in a 50°C bath for 15 minutes each. The membrane was covered in plastic wrap and exposed to a film (Storage Phosphor Screen, Amersham Biosciences) overnight in a cassette. The image was developed on the STORM 860 scanner.

Preparation of cDNA for microarray analysis

Microarray analysis was performed using Mouse Gene 1.0 ST Arrays (Affymetrix). Total RNA was isolated and purified from mouse heart, skeletal muscle, and liver as described previously, and samples were sent to the Affymetrix Microarray Facility at StemCore Laboratories (Ottawa Hospital Research Institute). RNA integrity was assessed using the Agilent 2100 Bioanalyzer (#G2943CA, Agilent Technologies), which provides an

RNA integrity number (RIN) from microfluidics analysis. The Ambion Whole-Transcript (WT) Expression kit was used in conjunction with the Affymetrix GeneChip WT Terminal Labeling and Controls Reagent kit to prepare samples for the Mouse Gene 1.0 ST Array.

The Ambion WT Expression Kit (#4411974, Life Technologies) prepared the RNA for microarray analysis by generating sense-strand cDNA for fragmentation and labeling. The first-strand cDNA was synthesized by reverse-transcription from total RNA. The second-strand cDNA was then synthesized using DNA polymerase and RNase H simultaneously to degrade the RNA. Antisense cRNA was synthesized and amplified by *in vitro* transcription of the second-strand cDNA template using T7 RNA polymerase. The cRNA was purified using Nucleic Acid Binding Beads, washed twice with Nucleic Acid Wash Solution, and eluted with 55°C preheated Elution Solution. The cRNA was briefly placed on ice and its yield was assessed by UV absorbance at 260 nm. Next, 10 µg cRNA was mixed with random primers to synthesize 2nd-cycle cDNA by reverse transcription. The cRNA template was degraded with RNase H, and the cDNA was purified to remove enzymes, salts, and unincorporated dNTPs.

Statistical analysis

The Robust Multi-array Average (RMA) algorithm was used to transform and normalize the raw intensity values of the probes using Affymetrix Expression Console™ Software. To identify differential gene expression between wildtype and knockout tissues, a Bayesian t-test analysis was performed (Ragnar Vilmundarson, PhD candidate, Stewart lab) using the Cyber-T analysis package for R. The Benjamini Hochberg (BH) False Discovery Rate (FDR) method was used to correct for multiple testing. The significance threshold for

the BH corrected p-values was set at 0.05, equal to an FDR of 5%. Probes that were not linked to a gene through annotation were excluded from analysis. Gene data was integrated and analyzed using DAVID Bioinformatics Resources.

Skeletal muscle injury

For skeletal muscle regeneration experiments, a well-established *in vivo* injury model was used in which cardiotoxin (CTX) (#C9759, Sigma-Aldrich) is injected into mouse skeletal muscle to induce inflammation. Mice (n=3 per genotype/timepoint) were anesthetized with 3% isoflurane. The tibialis anterior (TA) muscle of one leg from WT, *Irf2bp2flox/LysMCre*, and *Irf2bp2flox/MckCre* mice were injected with 30 μ L of 10 μ M CTX, and 1X PBS (control) injected in the contralateral leg. At 2, 4, and 10 days post-injection, mice were CO₂ euthanized and TA muscles were carefully removed and embedded in Tissue-Tek O.C.T. Compound (#25608930, VWR International) in standard Cryomolds (25mm x 20mm x 5mm, Tissue-Tek #4557). Muscles were immediately frozen in isopentane (#AC126470010, Fisher Scientific), cooled by liquid nitrogen.

Histological staining and analyses

For analysis of skeletal muscles from the CTX regeneration experiment, frozen TA muscles in O.C.T. blocks were removed from -80°C and warmed to -20°C for 1 hour. Muscles were cryosectioned at 8 μ m thickness in a -20°C microtome (Model #CM3050S, Leica) and cross sections were collected on Superfrost® Plus microscope slides (#48311703, VWR International). H&E staining of the samples was performed by XiaoLing Zhao (University of Ottawa Heart Institute). The slides were first dried for 10 minutes at room

temperature, then fixed in 10% formalin for 10 minutes. Slides were then left in hematoxylin solution for 5 minutes, then rinsed under lukewarm tap water for 2 minutes. Slides were dipped 10 times into acid alcohol (1% HCl in 70% ethanol), rinsed under tap water for 2 minutes, washed in PBS for 1 minute, then again under tap water for 1 minute. Slides were left in Eosin Y for 3 minutes. They were then dehydrated through 70%, 80%, and 90% ethanol, followed by 3 changes in 100% ethanol and 3 changes in toluene. Finally, each slide was mounted with a drop of chemical permount mounting medium (#SP15100, Fisher Scientific) and a cover slip was applied.

For analysis of *Irf2bp2*^{-/-} mice, tissues were harvested and immediately fixed in 4% buffered paraformaldehyde (PFA) in PBS for 24-48 hours, then transferred to 70% ethanol. The samples were sent to the University of Ottawa's Department of Pathology and Laboratory Medicine, where they were paraffin-embedded, sectioned at 5 µm thickness, then H&E stained (as described previously) for morphological analyses.

Hindlimb ischemia and Doppler imaging

To assess blood flow recovery, surgical ligation of the femoral artery was performed on WT and *Irf2bp2*^{flox}/*Myf5*^{Cre} mice to induce ischemia in the gastrocnemius muscle. The surgery was performed following a previously described model of hindlimb ischemia (59). Before surgery, mice were anesthetized with 3% isoflurane and injected intraperitoneally with sustained-release buprenorphine (Chiron) at a dosage of 1.2 mg/kg. Fur was removed from the hindlimb with Nair hair removal cream, and the skin was cleaned with a soap solution and chlorhexidine. A longitudinal 1.5 cm skin incision was made along the femoral vessels. Thin Dumont forceps were used to grasp the connective tissue and separate the

femoral artery from the femoral nerve and vein. The artery was occluded with two 6-0 SurgiPro silk (#707G, Ethicon) knots. Skin was re-closed with four interrupted sutures using 6-0 SurgiPro silk. Perfusion recovery was measured at days 1, 3, 5, and 15 post-ligation, as well as preoperatively, using a Laser Doppler imager (moorLDI2, Moor Instruments). Tissue perfusion was quantified in the ligated limb relative to the contralateral non-ligated limb, and displayed as colour-coded images.

RESULTS

Targeted disruption of the mouse *Irf2bp2* gene

Hemizygous *Irf2bp2*^{+/-} mice were generated by Dr. Siu-Pok Yee as described previously, and the structure of the *Irf2bp2* gene (consisting of 2 exons) is shown in **Figure 1**. *Irf2bp2*^{+/-} mice were intercrossed to produce homozygous *Irf2bp2*^{-/-} knockout mice for study and maintain a breeding colony. Their progeny were genotyped by PCR from digested tail DNA, and the representative PCR products in **Figure 2** reveal the WT, hemizygous, and KO alleles, as well as the loxP-flanked *Irf2bp2* alleles for tissue-specific KO mice. To determine the size and number of *Irf2bp2* transcripts and to confirm their loss of expression in tissues, total RNA from the heart, skeletal muscle, and liver was isolated and analyzed by Northern blot, using the 18s rRNA transcript as a control. Indeed, no detectable *Irf2bp2* mRNA was found in the KO tissues, while in the WT tissues, three bands are detected in cardiac and skeletal muscle, and only one band is detected in liver (**Figure 3**).

Loss of IRF2BP2 results in partial embryonic lethality and growth retardation

Mice homozygous for the *Irf2bp2* deletion were not born in accordance to Mendelian ratio. Out of 241 mice, 78 WT, 148 hemizygous, and 15 KO mice were born in a ratio of 1:1.9:0.2. This is significantly ($p < 1E-05$ by Chi squared test) deviated from the expected Mendelian ratio of 1:2:1, and much closer to a classical lethal ratio of 1:2 (**Figure 4**). Furthermore, 5 of those 15 KO mouse pups were found dead within a few days of birth. However, *Irf2bp2*^{+/-} mice were born healthy and viable, showing no discernible phenotype from their WT littermates. The KO mice that survived past birth were significantly smaller than their WT and *Irf2bp2*^{+/-} littermates at the time of weaning (i.e. 21 days), weighing on

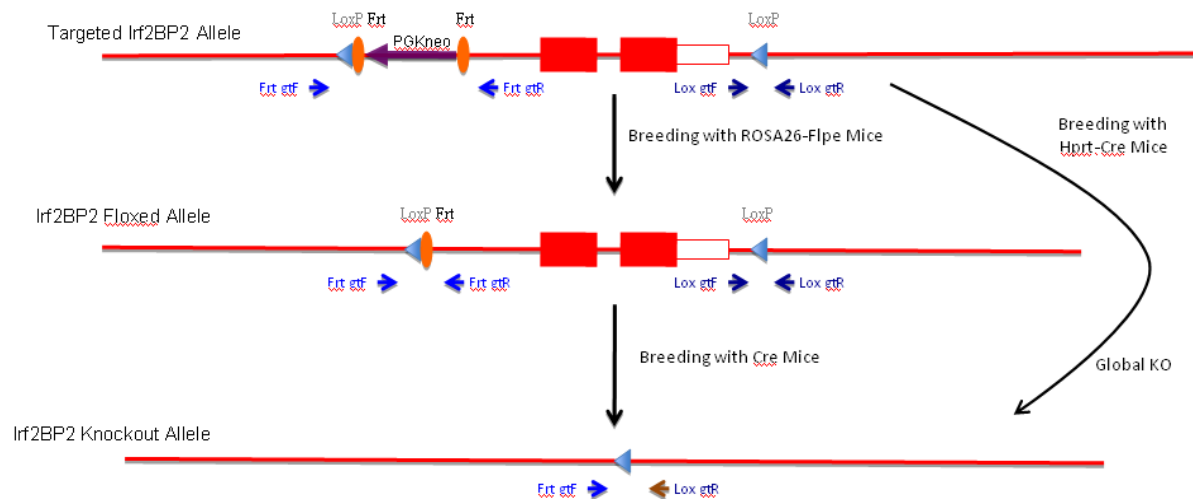


Figure 1. Targeting strategy for generation of *Irf2bp2* knockout mice.

The *Irf2bp2* region is flanked by LoxP sites to create the floxed allele, while the two *Irf2bp2* exons and PGK-neo cassette were ultimately Cre-excised to create the knockout allele. *Irf2bp2*^{+/-} mice were intercrossed to ultimately produce *Irf2bp2*^{-/-} mice for characterization and study.

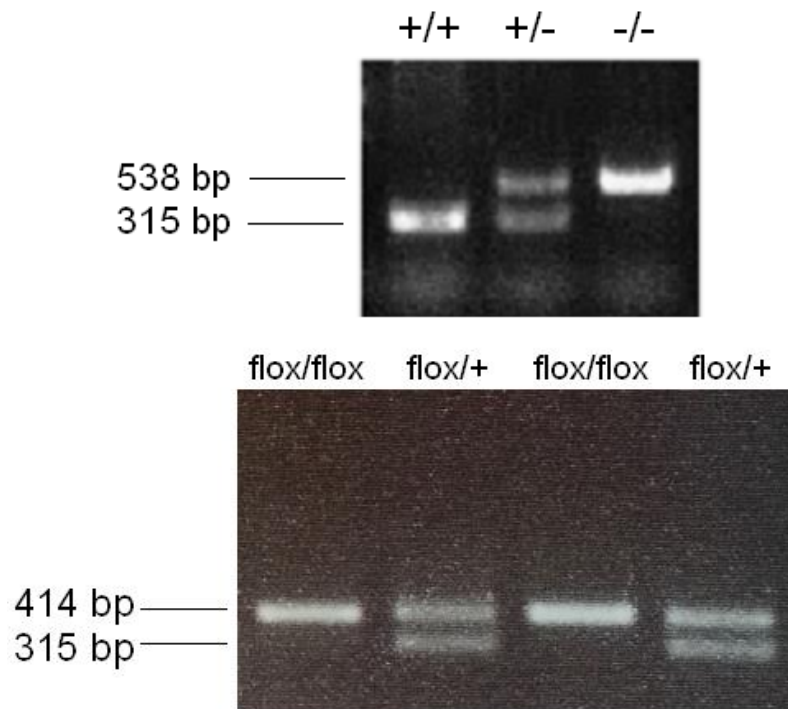


Figure 2. Representative PCR products of genotyped mice.

DNA was extracted from from digested mouse tail tips. Primers “Lox gtR” (5’-CCC TTC ATG TAA GTA TTC TC-3’), “Lox gtF” (5’-GTG CTC CTT AAG TGT TGC AG-3’), and “Frt gtF” (5’-GAC TCT TGG ACA GCC AAG CTC-3’) were used to amplify wild-type (315 bp), deleted (538 bp), and floxed (414 bp) alleles.

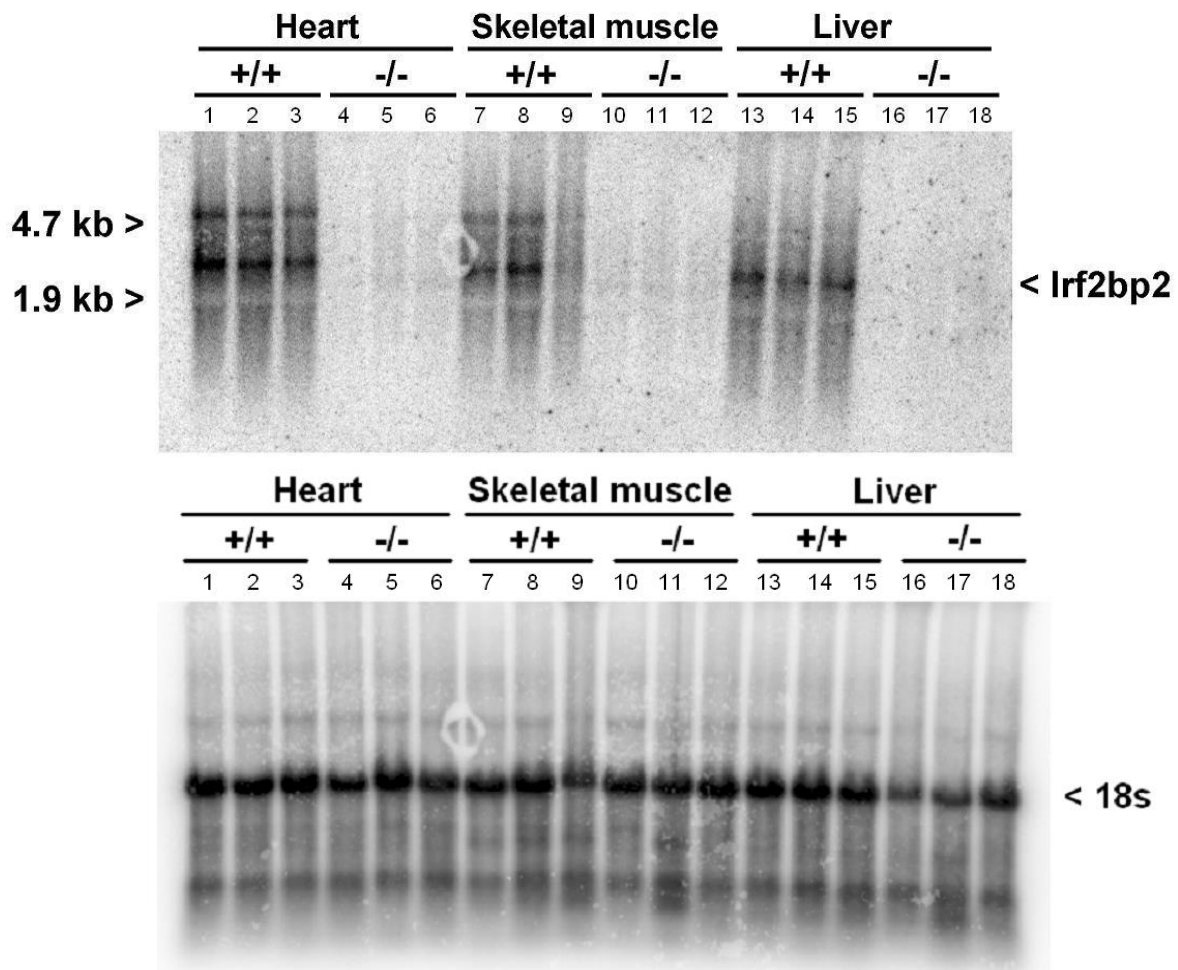


Figure 3. Northern blot analysis of total RNA from WT and *Irf2bp2*^{-/-} mice. RNA was isolated from heart, skeletal muscle, and liver tissues from WT and *Irf2bp2*^{-/-} mice, showing (top panel) *Irf2bp2* expression and (bottom panel) 18s rRNA expression as a control.

	+/+	+/-	-/-	Total
Total mice	78	148	15	241
Actual ratio	0.32	0.61	0.06	
Expected ratio	0.25	0.50	0.25	
KO lethal ratio	0.33	0.66	0.00	

Figure 4. *Irf2bp2*^{-/-} mice are not born in accordance to Mendelian ratio. Out of 241 mice, only 15 KO mice were born, including 5 mouse pups found dead at birth. This ratio is significantly deviated from the expected Mendelian ratio of 1:2:1, and much closer to a lethal ratio of 1:2 ($p < 1E-05$ by Chi squared test).

average less than 8 g compared to more than 12 g for healthy mice (n=6 WT, 19 hemizygous, and 6 KO; p=3.41E-06 by unpaired t-test) (**Figure 5**).

To determine the timing of lethality during embryogenesis, timed matings were performed (n=10 matings) by intercrossing *Irf2bp2*^{+/-} mice. Identification of a vaginal plug on the morning after mating corresponded to dpc 0.5. Pregnant mothers were sacrificed by CO₂ euthanization and embryos were dissected at 11.5, 13.5, 15.5, and 16.5 dpc and were PCR genotyped as described previously. Up to age 15.5 dpc, KO embryos displayed no obvious gross morphological differences compared to their littermates. However, at age 16.5 dpc (Theiler's stage 24) 2 embryos were found undergoing resorption along with 9 normal embryos (**Figure 6**).

Adult IRF2BP2 knockout mice develop murine lymphoma

At approximately 28 weeks of age, *Irf2bp2*^{-/-} mice developed a variety of ailments, including thinning fur, lack of appetite, or general weight loss. These mice were sacrificed for analysis, along with WT and *Irf2bp2*^{+/-} littermates as controls. Gross examination of the KO mice (**Figure 7**) showed enlarged spleen, kidneys, and livers, while control littermates appeared normal. Morphological analysis was performed by H&E staining followed by examination by Dr. Rudolf Mueller (uOttawa Department of Pathology and Laboratory Medicine), revealing a diagnosis of generalized murine lymphoma. Plasma-like cells and a monomorphic lymphoid population infiltrated the liver sinusoids and perivascular regions, as well as having replaced normal follicular structure of the spleen (**Figure 8**).

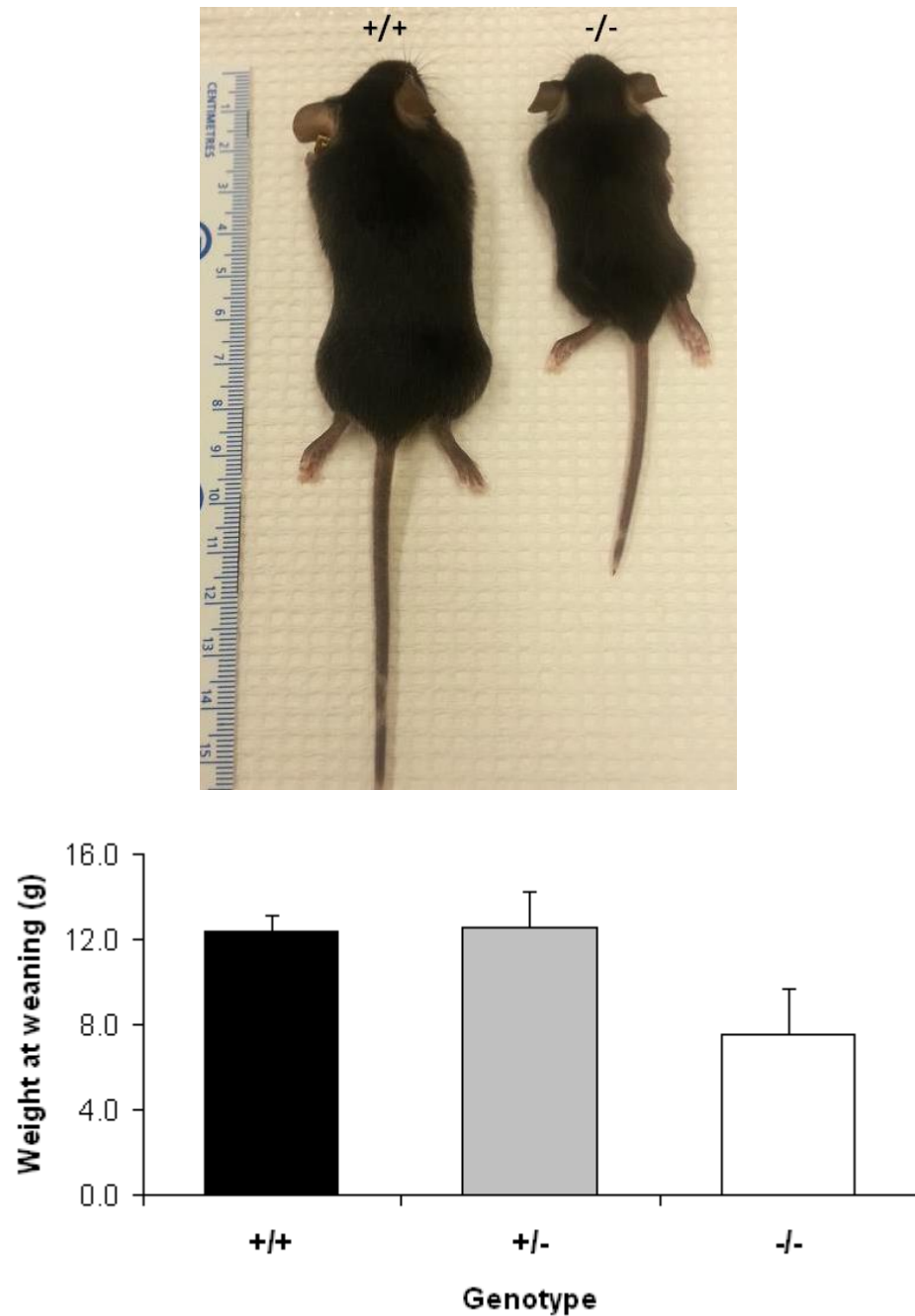


Figure 5. *Irf2bp2*^{-/-} mice display growth retardation at birth and throughout development.

Irf2bp2^{-/-} mice are significantly smaller ($p=3.41E-06$) than their wildtype counterparts at 4 weeks of age (top panel), weighing only ~8 g (KO) compared to ~12 g (WT and *Irf2bp2*^{+/-}) (bottom panel).

Age (dpc)	+/+	+/-	-/- (%)	Total
11.5	9	18	5	32
13.5	7	15	4	26
15.5	9	5	2	16
16.5	3	5	2	10
Weaning	78	148	15	241
	32.37%	61.41%	6.22%	



Figure 6. Timed matings of *Irf2bp2*^{+/-} mice for embryo dissection.

To determine timing of lethality or resorption of KO embryos, timed matings were carried out between *Irf2bp2*^{+/-} mice. Identification of a vaginal plug corresponded to dpc 0.5. The embryos shown (resorbing and healthy) were harvested from the same mother at 16.5 dpc.



Figure 7. Gross examination of WT and *Irf2bp2*^{-/-} mouse organs at 28 weeks old.
Gross examination of sacrificed mice (n=4) showed that the KO mice exhibited enlarged liver (top panel), enlarged spleen (bottom left), and enlarged kidney (bottom right).

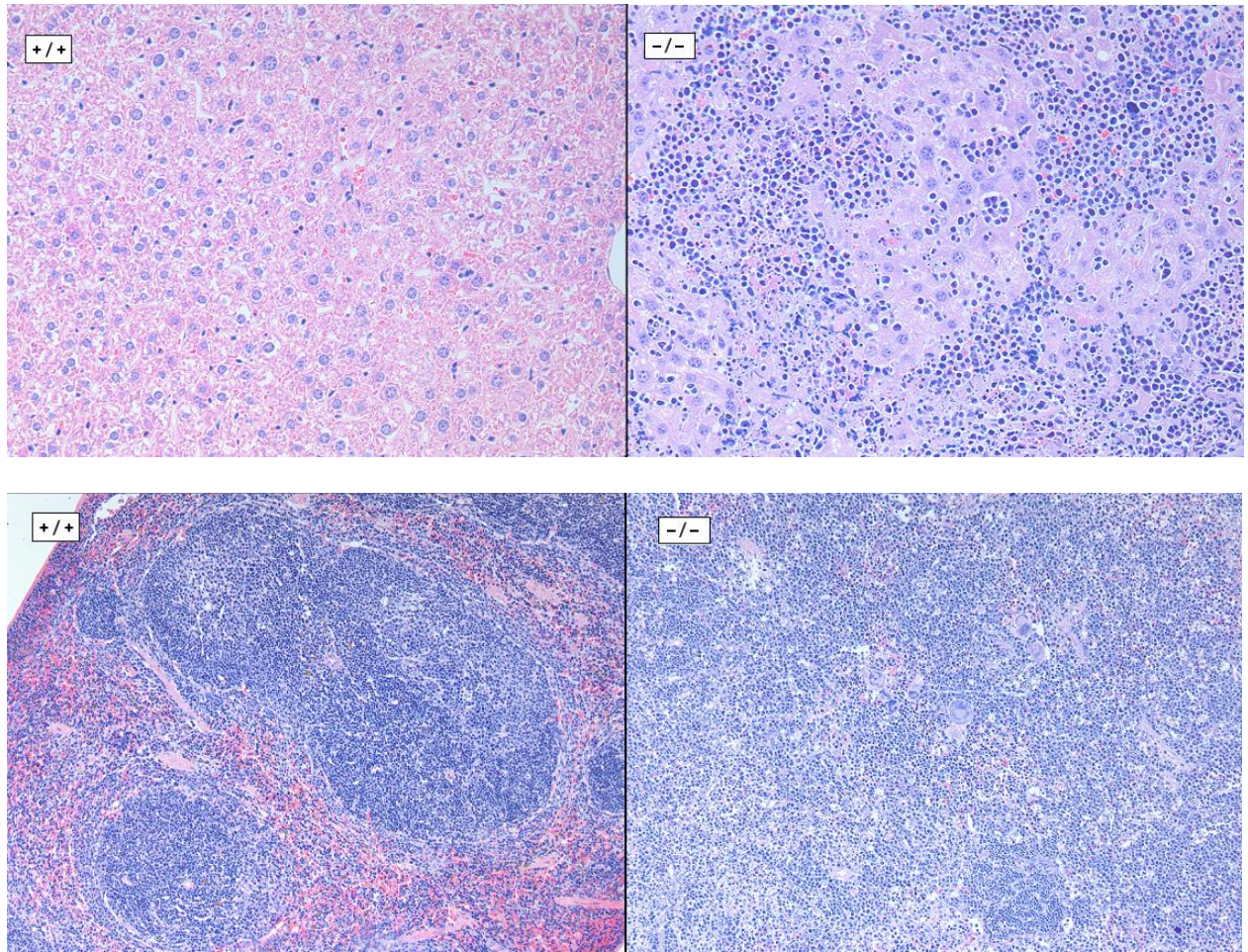


Figure 8. H&E stained sections of WT and *Irf2bp2*^{-/-} liver and spleen.

Irf2bp2^{-/-} mice were diagnosed with generalized murine lymphoma. In the KO liver (top panel), there is dense infiltration of interstitium and sinusoids with a monomorphic population of lymphocytes, compared to a normal WT liver. In the KO spleen (bottom panel), monomorphic lymphoid cells replace the normal follicular structure, while the WT splenic architecture is normal. Magnification 10X.

Microarray analysis of IRF2BP2 knockout tissues

Microarray analysis was performed to identify changes in gene expression in WT and *Irf2bp2*^{-/-} mouse tissues, namely heart, skeletal muscle, and liver (using the same RNA as shown in **Figure 4**). To identify differential gene expression between knockouts and controls, a Bayesian t-test analysis was performed (by Ragnar Vilmundarson) using the Cyber-T analysis package for R. The Benjamini and Hochberg (BH) False Discovery Rate (FDR) method was used to correct for multiple testing. The significance threshold for the BH corrected p-values was set at 0.05, equal to an FDR of 5%. A greater number of significantly upregulated genes were found than downregulated genes in each of the KO tissue genes (ratios of 5.5:1 in heart, 4:1 in skeletal muscle, and 2.4:1 in liver). For upregulated vs. downregulated genes respectively, there were 285 vs. 56 in heart, 147 vs. 44 in skeletal muscle, and 1332 vs. 562 in liver. Furthermore, in male macrophages there were 435 vs. 501, and in female macrophages there were 154 vs. 240 (unpublished data). Using DAVID enrichment analysis to identify significantly affected gene clusters, we found that among skeletal muscle, heart, and liver respectively, there were 4, 8, and 48 upregulated gene clusters compared to 0, 2, and 5 downregulated gene clusters. The top ten most significantly affected genes for each tissue type are listed in **Figure 9**. To visualize the number of differentially expressed genes shared between each of the three tissues, Venn diagrams in **Figure 10** show the overall number of differentially expressed genes shared between each tissue. Of interest, all three tissue types share 49 genes in common that are differentially expressed, and of these, 48 of them are upregulated genes (with the exception being *Irf2bp2*).

Skeletal muscle		
KO/WT	Gene Symbol	Gene Description
0.21625	Irf2bp2	interferon regulatory factor 2 binding protein 2
6.02585	Nr4a3	nuclear receptor subfamily 4, group A, member 3
3.1874	H2-Q6	histocompatibility 2, Q region locus 6
3.28527	H2-Ab1	histocompatibility 2, class II antigen A, beta 1
2.5982	Bcl2a1a	B cell leukemia/lymphoma 2 related protein A1a
2.46139	H2-Q4	histocompatibility 2, Q region locus 4
0.34348	Ostn	osteocrin
6.77352	Mt2	metallothionein 2
2.46712	Bcl2a1d	B cell leukemia/lymphoma 2 related protein A1d
0.44506	C7	complement component 7

Heart		
KO/WT	Gene Symbol	Gene Description
0.11412312	Irf2bp2	interferon regulatory factor 2 binding protein 2
3.74430492	H2-Q6	histocompatibility 2, Q region locus 6
3.68396896	H2-Ab1	histocompatibility 2, class II antigen A, beta 1
3.04379859	Cd74	CD74 antigen
2.43303448	Myot	myotilin
5.69862906	Gm4841	predicted gene 4841
4.04554915	Gm12250	predicted gene 12250
6.68598744	Mt2	metallothionein 2
0.33816955	Pla2g5	phospholipase A2, group V
3.23785895	H2-Eb1	histocompatibility 2, class II antigen E beta

Liver		
KO/WT	Gene Symbol	Gene Description
0.12798	Irf2bp2	interferon regulatory factor 2 binding protein 2
10.5015	Ccl5	chemokine (C-C motif) ligand 5
3.49292	Cd74	CD74 antigen
12.3962	Ccl3	chemokine (C-C motif) ligand 3
3.87326	Fgl2	fibrinogen-like protein 2
7.00565	Nkg7	natural killer cell group 7 sequence
3.60884	H2-Aa	histocompatibility 2, class II antigen A, alpha
5.48375	Lpl	lipoprotein lipase
4.679	Zbp1	Z-DNA binding protein 1
4.27419	Lsp1	lymphocyte specific 1

Figure 9. Top 10 most significantly affected genes by microarray analysis in *Irf2bp2*^{-/-} skeletal muscle, heart, and liver. The top 10 most significantly affected genes in *Irf2bp2*^{-/-} muscle, heart, and liver (compared to WT tissues) were identified by Bayesian t-test analysis. The significance threshold for the Benjamini and Hochberg (BH) corrected p-values was set at 0.05, equal to an FDR of 5%.

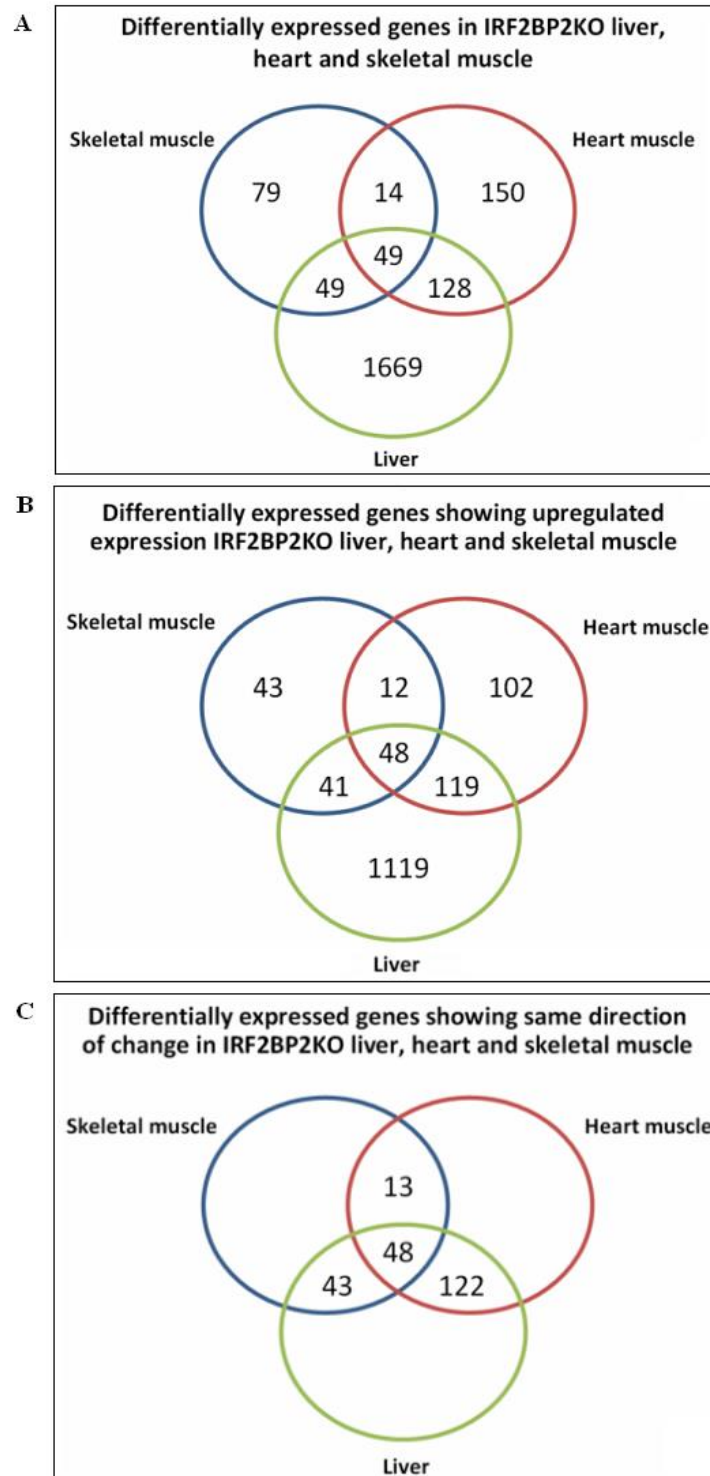


Figure 10. Venn diagrams of differentially expressed genes shared between skeletal muscle, heart muscle, and liver tissues. (A) Overall number of shared differentially expressed genes. **(B)** Shared differentially expressed genes showing upregulation. **(C)** Shared differentially expressed genes showing same direction of change (up- or downregulation).

Skeletal muscle injury and regeneration

To evaluate the role of IRF2BP2 in skeletal muscle regeneration, a well-established *in vivo* injury model was used. TA muscles of one leg were injected with 10 μ m CTX to cause muscle necrosis, while the contralateral muscles received PBS injections as control. *Irf2bp2^{flox}/LysMCre* mice (n=2 per condition) were used for this experiment, which have a conditional knockout of *Irf2bp2* in the myeloid cell lineage, including monocytes, mature macrophages, and granulocytes. The knockout was confirmed by qPCR and immunoblot from bone marrow-derived macrophages (BMDMs), cultured by Kianoosh Keyhanian (Chen lab) (**Figure 11**). At 2 and 4 days post-injection, *Irf2bp2^{flox}/WT* and *Irf2bp2^{flox}/LysMCre* mice developed similar necrotic injuries. After 10 days, muscle fibres with centralized nuclei in both WT and KO tissues revealed the presence of regenerated myofibres, but the KO section had comparatively increased inflammatory cell infiltration (**Figure 12**). To see if IRF2BP2 has a muscle-intrinsic role during skeletal muscle regeneration, the CTX experiment was also performed on *Irf2bp2^{flox}/MckCre* mice (n=2 per condition) which have a conditional deletion of IRF2BP2 in skeletal muscle fibres. The knockout is confirmed by Northern blot (**Figure 13**) from skeletal muscle extracted RNA as described previously. In addition, Western blots were attempted in order to confirm the knockout on the protein level; however, due to difficulties isolating protein from mouse tissues, the resulting Western blots were not satisfactory and these images have not been included. After 10 days, whereas the WT injury is resolved as shown by the widely distributed appearance of centralized nuclei, the *Irf2bp2^{flox}/LysMCre* muscle still consists of inflamed areas among new myofibres (**Figure 14**).

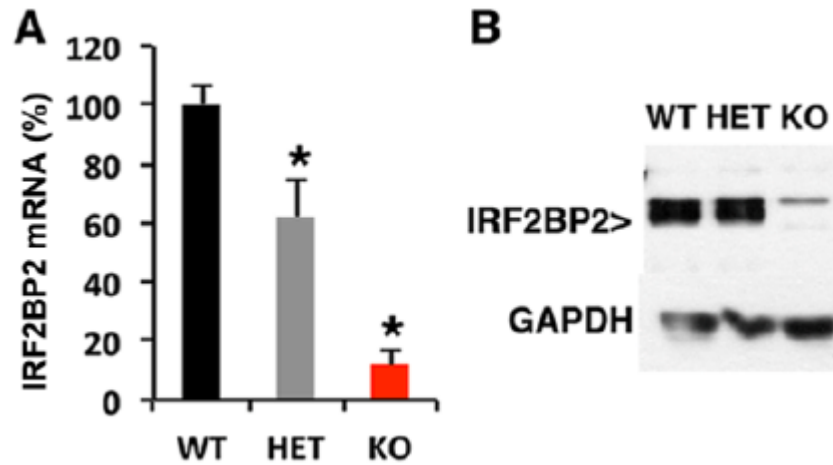
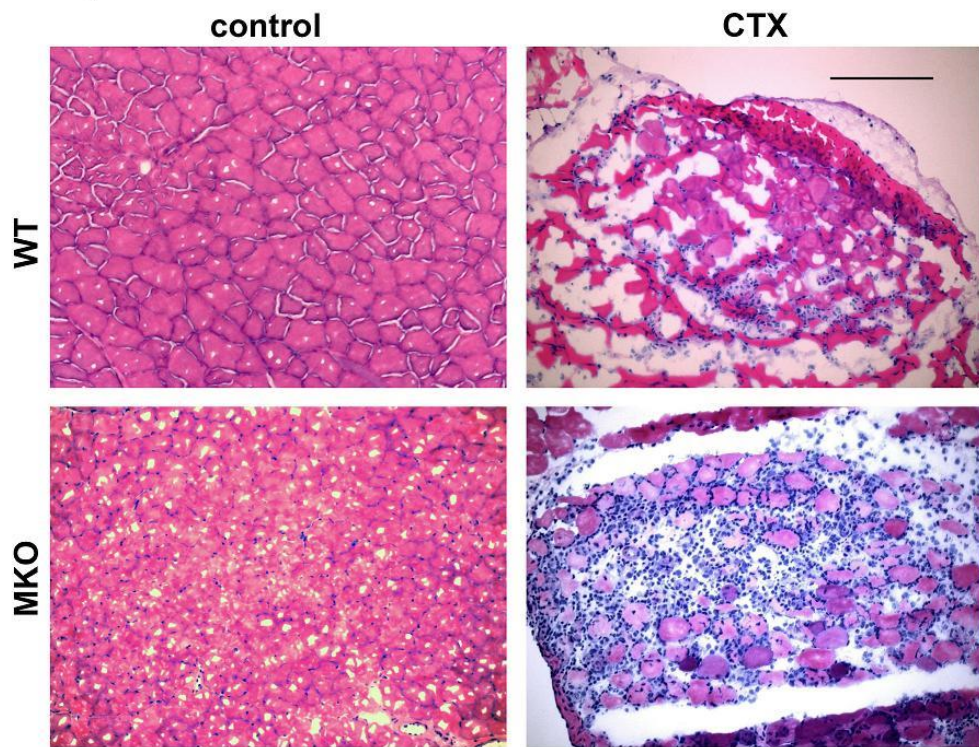


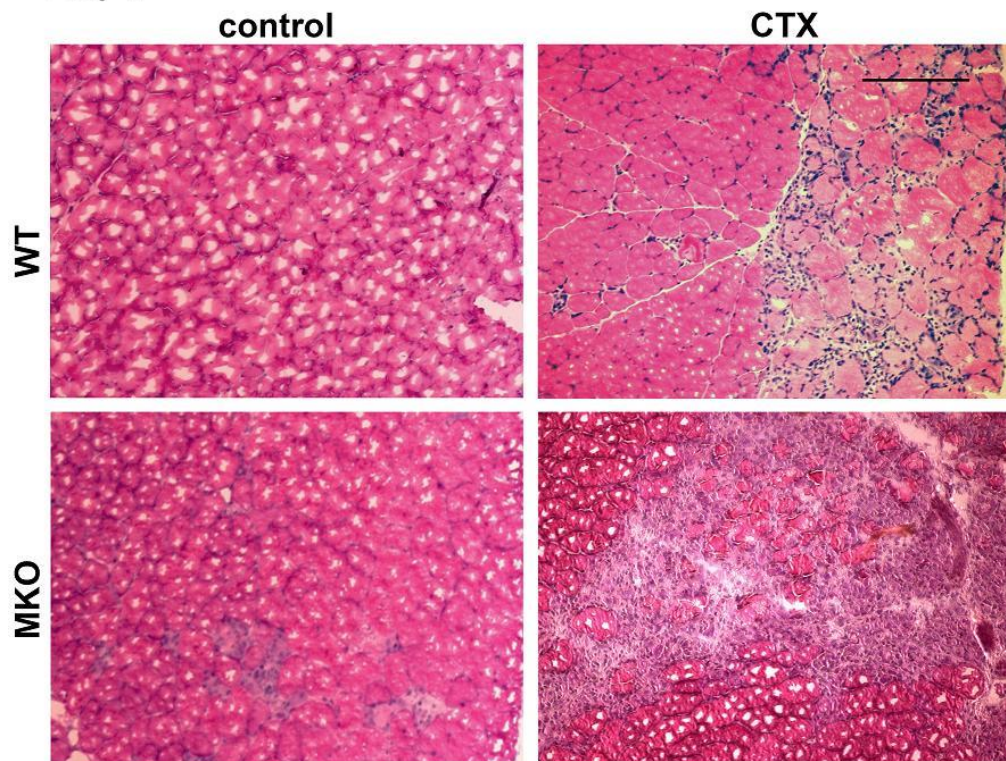
Figure 11. Cultured bone marrow-derived macrophages (BMDM) show reduced mRNA and protein levels in WT, *Irf2bp2*^{+/-}, and *Irf2bp2*^{-/-} mice.

Cultured BMDMs show reduced mRNA levels by qPCR (A) and reduced protein levels in *Irf2bp2*^{-/-} KO mice compared to WT. Experiments were done by Kianoosh Keyhanian (Dr. Chen lab).

A)
Day 2



B)
Day 4



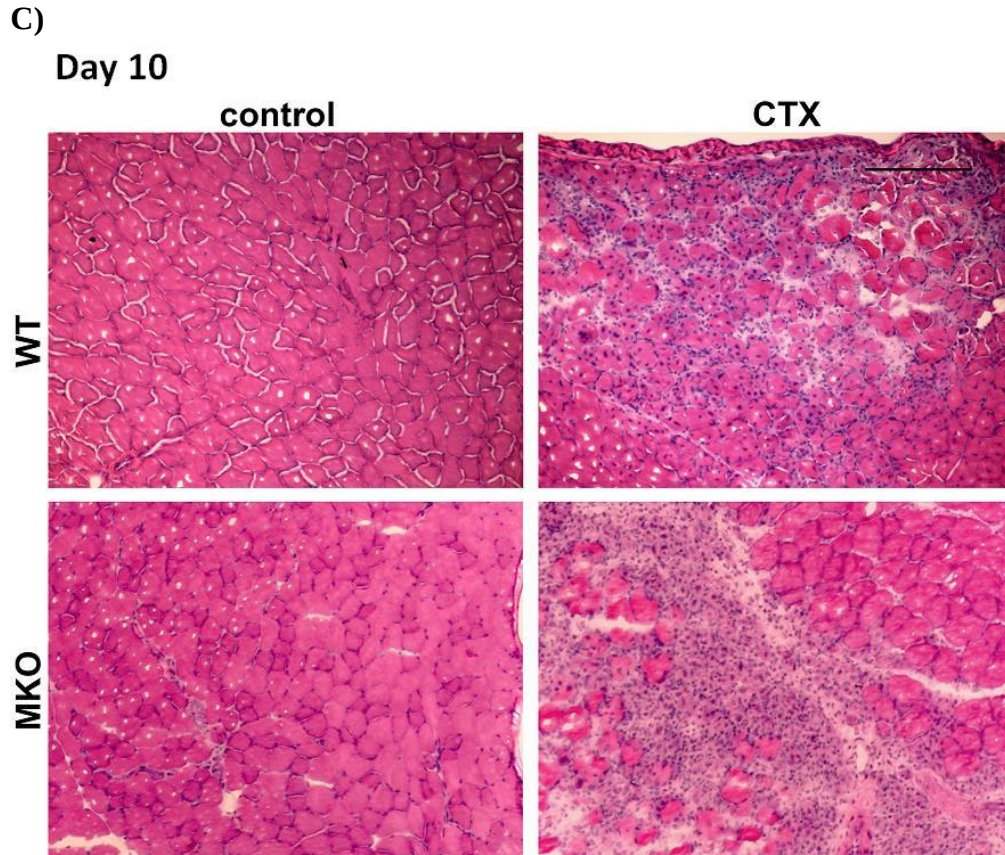


Figure 12. Evaluation of skeletal muscle regeneration after CTX injection in a *Irf2bp2flox/LysMCre* mouse.

CTX was injected into WT and *Irf2bp2flox/LysMCre* mouse hindlimbs to induce necrosis followed by regeneration. Frozen TA muscles were harvested from mice and sections were H&E stained at 2, 4, and 10 days post-injury (panels A, B, C respectively). Interstitial fibrosis is more abundant in *Irf2bp2flox/MckCre* TA muscle.

For day 10 post-injury, n=1 WT mouse and n=1 KO mouse were used. For days 2 and 4 post-injury, n=2 WT and n=2 KO mice were used for each timepoint.

Magnification 10X.

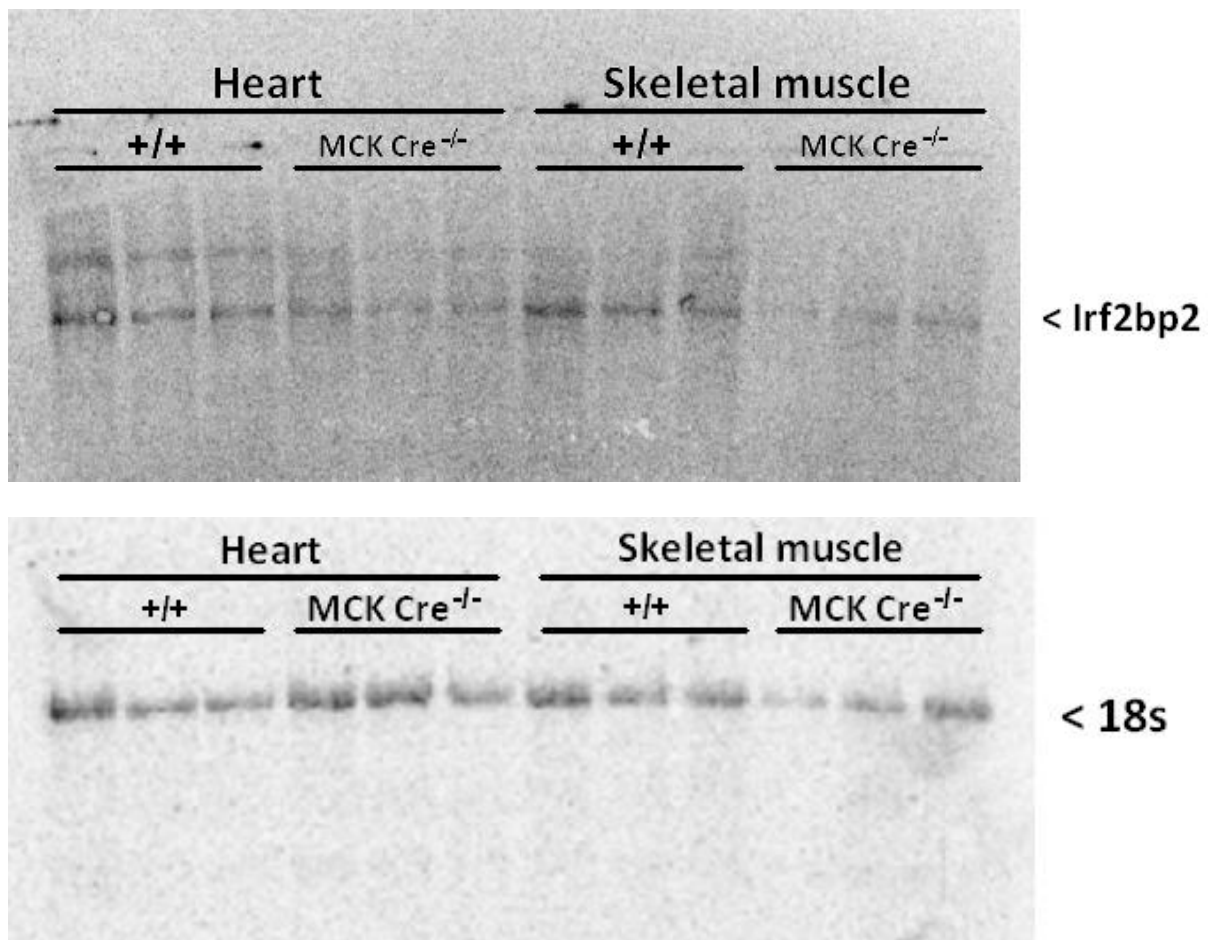


Figure 13 (a). Northern blot analysis of total RNA isolated from heart and skeletal muscle from WT and *Irf2bp2*^{flox}/*MckCre* mice.

RNA was isolated from cardiac and skeletal muscle from WT and *Irf2bp2*^{flox}/*MckCre* mice, showing (top panel) *Irf2bp2* expression and (bottom panel). 18s rRNA expression was used as control.

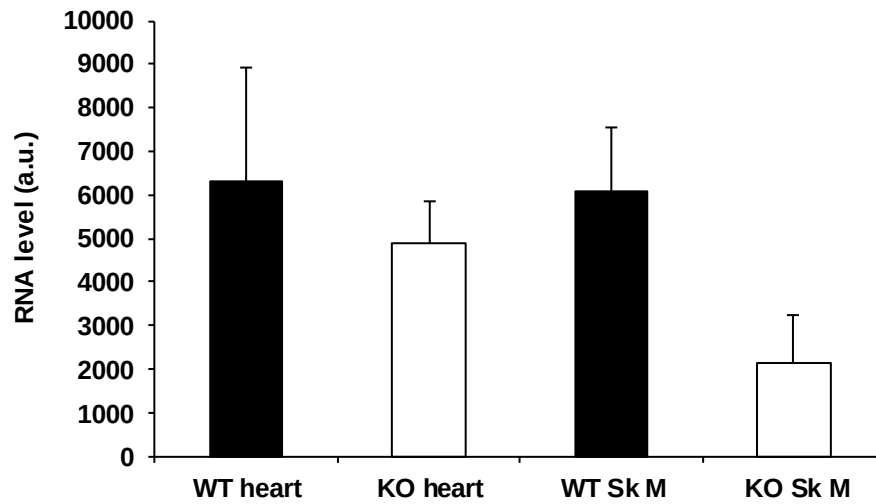
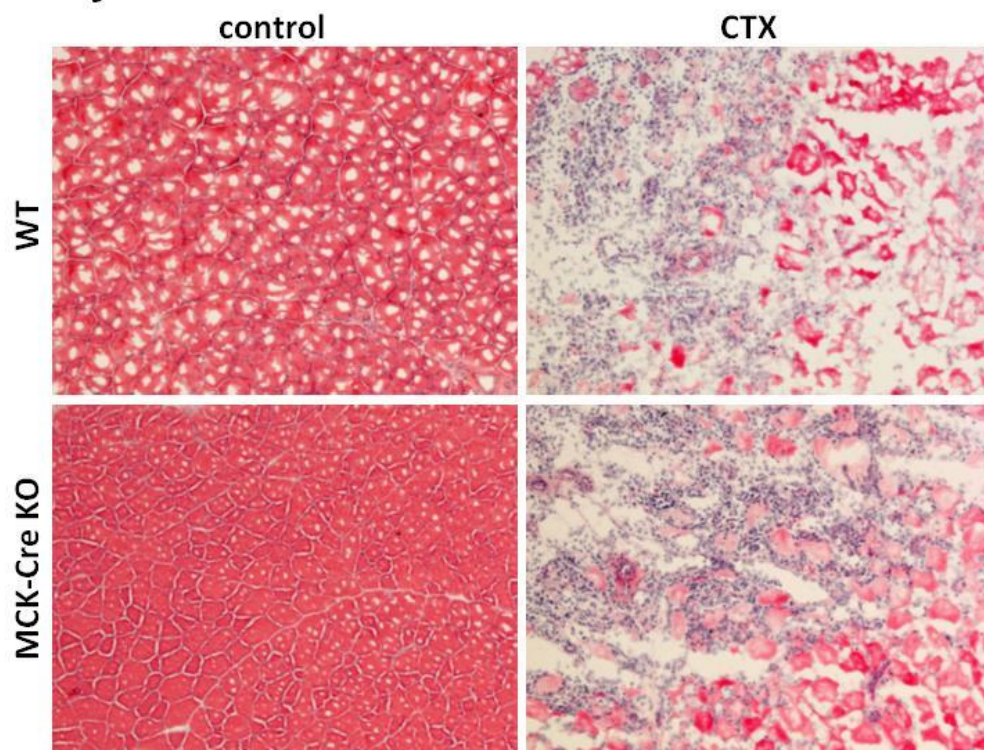


Figure 13 (b). Northern blot analysis of total RNA isolated from heart and skeletal muscle from WT and *Irf2bp2^{flox}/MckCre* mice.

Quantification of RNA levels from Northern blot shown in figure (a). *Irf2bp2* expression is decreased by ~30% in the KO heart, and ~75% in skeletal muscle. Values are not significant ($p=0.1$) due to high standard deviations. A repeated Northern blot with equal loading should give a statistically significant p -value.

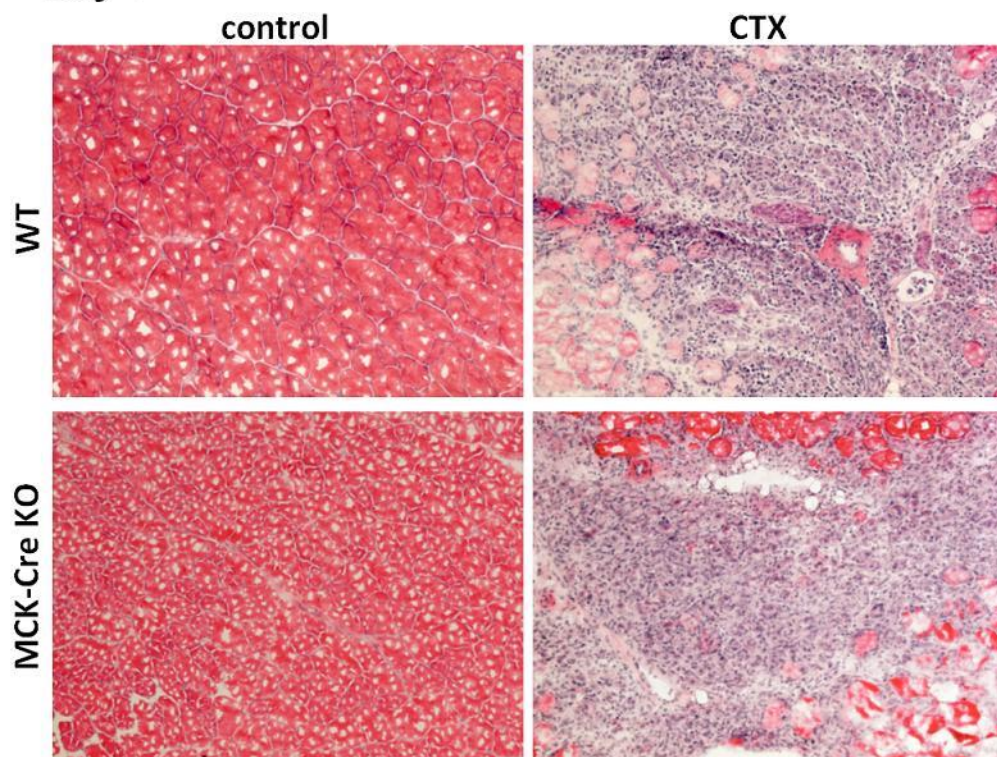
A)

Day 2



B)

Day 4



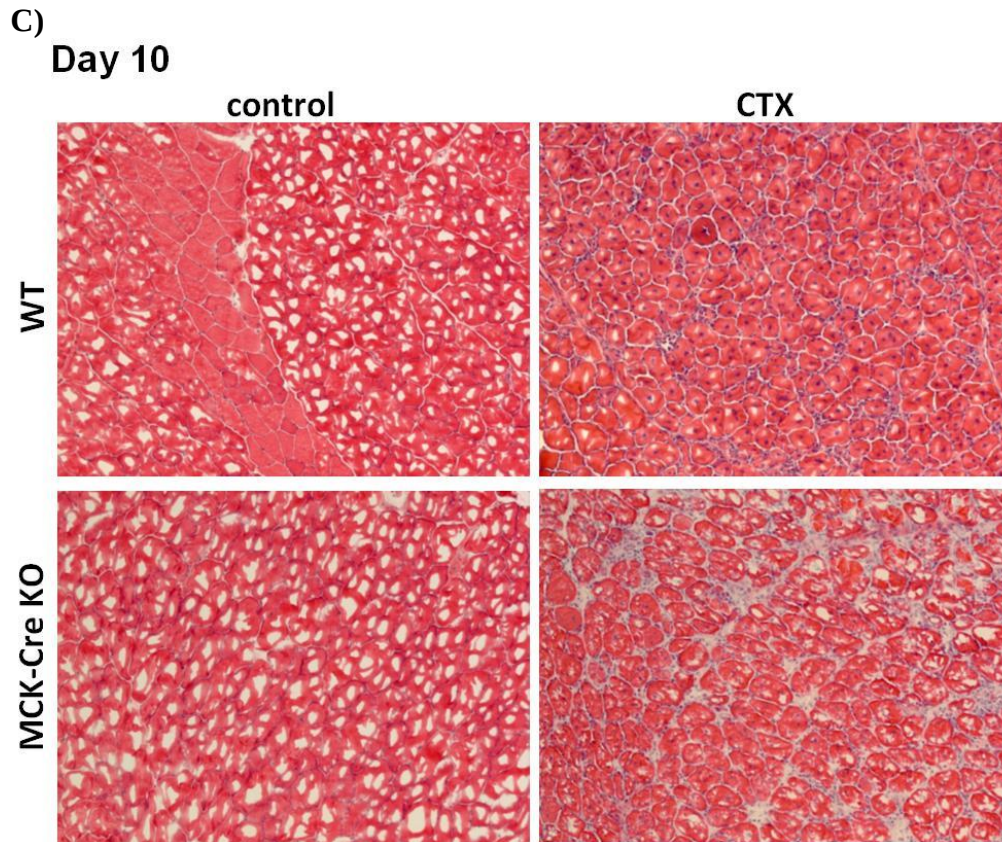


Figure 14. Evaluation of skeletal muscle regeneration after CTX injection in a *Irf2bp2flox/MckCre* mouse.

CTX was injected into WT and *Irf2bp2flox/MckCre* mouse hindlimbs to induce necrosis followed by regeneration. Frozen TA muscles were harvested from mice and sections were H&E stained at 2, 4, and 10 days post-injection (panels A, B, C respectively). Interstitial fibrosis is more abundant in *Irf2bp2flox/MckCre* TA muscle.

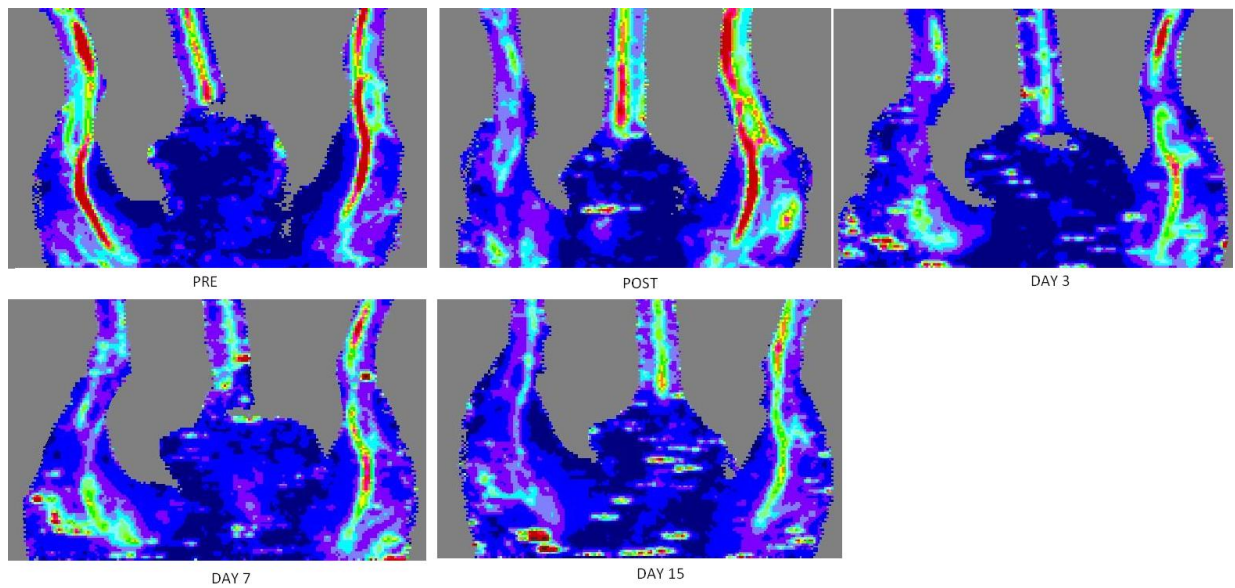
For each timepoint of day 2, 4, and 10 post-injury, n=2 WT and n=2 KO mice were used. Magnification 10X.

Evaluation of hindlimb perfusion recovery

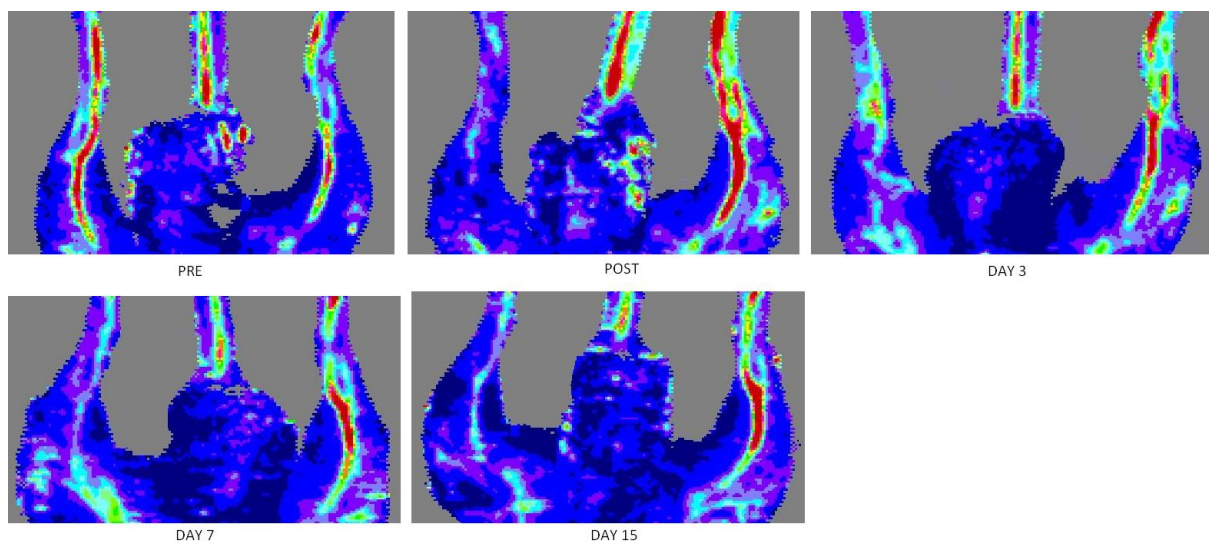
IRF2BP2, a coactivator of the key angiogenic factor VEGFA, is upregulated in ischemic skeletal and cardiac muscle (29). Angiogenic processes increase perfusion of ischemic tissue by sprouting of capillaries (33). To assess if the presence of IRF2BP2 *in vivo* has an effect on blood flow recovery after ischemia, surgical ligation of the femoral artery was performed on WT and *Irf2bp2^{flox}/Myf5^{Cre}* mice to induce ischemia in the gastrocnemius muscle. Number of mice used was n=3 WT and 3 KO mice for each timepoint, which are pre-ligation, immediate post-ligation, 3 days post-ligation, 7 days post-ligation, and 15 days post-ligation. It must be noted that these muscle-specific knockout mice (crossed with Myf5-Cre recombinase mice) are different from the MCK-Cre recombinase floxed mice used in the previous experiment. It is also important to note that downstream studies to confirm the loss of *Irf2bp2* expression in tissues of this mouse were not successful, meaning all mice used in this experiment were essentially WT mice (although this result was not known at the time of surgery).

The surgery was performed following a previously described model of hindlimb ischemia (33). Perfusion recovery was assessed pre-operatively, immediately post-surgery, and at 3, 5, and 15 days post-ligation using Laser Doppler imaging (LDI) of the hindlimbs. No significant difference between WT and *Irf2bp2^{flox}/Myf5^{Cre}* perfusion recovery was found (**Figure 15**).

(A) WT mouse hindlimb recovery



(B) *Irf2bp2^{flox}/Myf5^{Cre}* mouse hindlimb recovery



(C)

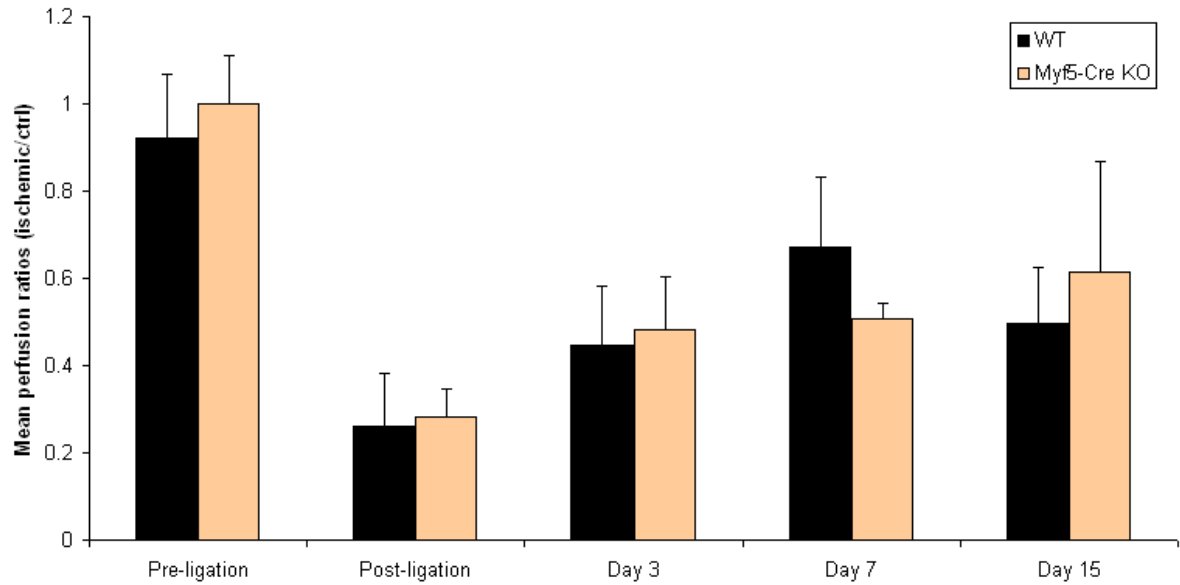


Figure 15. Evaluation of mouse blood perfusion recovery after femoral artery ligation. WT and *Irf2bp2flox/Myf5Cre* mice were subjected to hindlimb ischemia by ligation of the femoral artery. Blood flow recovery was assessed by LDI of the hindlimbs pre-operatively, immediately post-operatively, and at days 3, 7, and 15 after surgery. No significant difference was found between WT (A) and *Irf2bp2flox/Myf5Cre* (B) recovery. The results are expressed as the ratio of ischemic to non-ischemic hindlimb blood flow (C).

DISCUSSION

Here, I show that IRF2BP2 is required for normal mouse embryogenesis, growth, and development, as well as for skeletal muscle regeneration after injury. Global homozygous deletion of the *Irf2bp2* gene from mice resulted in partial embryonic or neonatal death, while mice that survive to adulthood are smaller and display growth retardation throughout their development, ultimately leading to murine lymphoma. Recently, a Dutch group used the gene trapping method to generate an IRF2BP2-deficient mouse model, designated *Irf2bp2*^{trp/trp} mice (62). The *Irf2bp2*^{trp/trp} embryos appeared in normal Mendelian ratios up to day E18.5, but live knockout pups were rarely born. Those *Irf2bp2*^{trp/trp} mice that were born displayed severe growth retardation and did not survive past 4 weeks of age. In contrast with the “gene targeting” method we used to specifically knock out both *Irf2bp2* exons through homologous recombination, the “gene trapping” method that generated the *Irf2bp2*^{trp/trp} mice involved a retrovirally inserted genetrap vector into the first *Irf2bp2* intron, disrupting full-length mRNA production. In general, gene trapping is a more rapid and cost-effective approach that can be used in a high-throughput capacity, while gene targeting can more specifically target a gene of interest that may not be detectable in gene trapping (63). In their study, IRF2BP2 was also identified as a novel component of the LIM-domain-binding protein-1 (LDB1) complex, able to enhance transcriptional repression mediated by eight-twenty-one 2 (ETO2) (62).

In the livers of our *Irf2bp2*^{-/-} mice, Dr. Mueller identified a dense infiltration of the interstitium, sinusoids, and perovascular regions with a monomorphic population of lymphocytes and plasma-like cells. Similar in the *Irf2bp2*^{-/-} spleens, a dense population of

monomorphic lymphoid cells replaced normal follicular structure of the spleen, which normally consists of the white pulp and surrounding red pulp (64). IRF2BP2 is a corepressor of IRF2 (37), which has generally been described as an oncoprotein (65). Although the development of murine lymphoma was an initially unexpected finding, mutations in IRF2BP2 in humans have recently been linked to various cancers including primary central nervous system lymphoma (66), multiple myeloma (47), mesenchymal chondrosarcoma (48), and acute promyelocytic leukemia (49).

While Northern blot analysis confirmed a loss of RNA expression in the *Irf2bp2*^{-/-} KO tissues, analysis of WT tissues revealed one transcript in liver tissue, and three bands in cardiac and skeletal muscle. Northern blotting involves the separation of RNA molecules through a denaturing gel, and remains a valuable analytical method, allowing investigators to determine the molecular weight of the mRNA of interest (67). The different transcript sizes of *Irf2bp2* suggest the presence of alternative polyadenylation (APA) sites, with the multiple bands in cardiac and skeletal muscle corresponding to different polyadenylation sites in the 3'UTR of the *Irf2bp2* transcript. The presence of only one detectable *Irf2bp2* transcript in the liver indicates differential regulation between tissues. Indeed, multiple putative polyadenylation sites, i.e. AAUAAA sequence (68), are found within the 3'UTR of *Irf2bp2*. Like alternative splicing, APA has emerged as a major influence in the regulation of gene expression, allowing one gene to encode multiple mRNA transcripts with different 3'UTR lengths. Tissue-specific APA has been observed at a global level, and can be regulated through mechanisms involving RNA binding proteins, microRNAs, or chromatin structure (69).

For analysis of microarray data, I used DAVID bioinformatics resources, an online biological database and analytic tool that can be used to reduce large gene lists into functionally related gene “clusters” using an “enrichment analysis” algorithm (70). DAVID analysis of data showed that mice deficient for IRF2BP2 are affected by genes associated with cell-mediated immunity, the inflammatory response, cellular differentiation, and cell surface receptor signaling. Among the upregulated genes of interest are *Bcl2a1*, *Ccl* genes, and *Mt1* and *Mt2*, as these were commonly affected across more than one tissue type. All four copies of the *Bcl2a1* gene (i.e. a, b, c, d) were significantly upregulated in KO skeletal muscle and liver. BCL2A1 exerts anti-apoptotic functions and is induced during myeloid differentiation, lymphocyte development, and lymphocyte and macrophage activation. It is a highly regulated NF- κ B target gene and is overexpressed in various cancers, including leukemias and lymphomas (71). Metallothionein (MT) is protein which increases in expression in rapidly proliferating cells, and may have a survival advantage in situations of stress, such as inflammation and infection. Its most widely expressed mammalian isoforms are MT1 and MT2, both of which are induced in the liver by various drugs and inflammatory mediators (72). Here, the *Mt1* and *Mt2* genes are both significantly upregulated in the KO heart, skeletal muscle, and liver. Also of note are the CC chemokine ligands (CCLs), which are small protein ligands that increase cell motility and directional migration after binding to CCR chemokine receptors (73). Significantly upregulated CCL genes in this microarray were *Ccl3*, *Ccl5*, *Ccl6* in liver, *Ccl2*, *Ccl3*, *Ccl6*, *Ccl9* in skeletal muscle, and *Ccl6*, *Ccl8*, *Ccl9* in the heart. Interestingly, *Ccl5* (also named RANTES) is the top significantly differentially expressed gene in the liver microarray (**Appendix 2c**), with a

>10-fold upregulation in the knockout liver. It is responsible for recruiting macrophages and NK cells to sites of inflammation (72). Although there is some overlap between tissues and some standalones, CCL proteins are involved in either inflammatory monocyte trafficking, macrophage and NK-cell migration, or T-cell/dendritic cell interactions. In skeletal muscle, the >3-fold upregulation of *Nr4a3* (also known as *NOR1*) suggests a link to IRF2BP2 in the regulation of cell apoptosis. NR4A3 is a member of an orphan nuclear hormone receptor family that has pro-apoptotic functions in some contexts, and anti-apoptotic functions in other contexts, such as in certain types of cancers (74). The level of *Irf2bp2* gene expression was most significantly decreased in all KO tissues compared to WT counterparts. The full list of differentially expressed genes, ordered by BH corrected p-values, is found in **Appendix 2 (a- skeletal muscle, b- heart, c- liver)**. For upregulated vs. downregulated genes respectively, there were a total of 285 vs. 56 in heart, 147 vs. 44 in skeletal muscle, and 1332 vs. 562 in liver. Venn diagrams were created (**Figure 10**) to visualize how these differentially expressed genes were shared in common by each tissue type. Of interest, 49 differentially expressed genes are shared between skeletal muscle, heart, and liver, and 48 of these are upregulated in the knockout mouse (with the exception being *Irf2bp2*). In the liver, 208 out of 226 “shared” genes have upregulated expression in the KO liver, in the KO heart 179 out of 191 genes are upregulated, and 101 out of 112 genes are upregulated in the KO skeletal muscle. Thus, the affected KO genes showed a higher number of enriched gene clusters among upregulated genes than downregulated genes, strongly suggesting a repressor/corepressor role for IRF2BP2. Heatmaps were created (**Appendix 3a, b, c**) to

further visualize the data, with green showing upregulated gene expression and red showing downregulated gene expression. Related genes are clustered more closely together.

VEGF is a major angiogenic growth factor, important in the regulation of cell survival and angiogenesis, with VEGFA being its most studied isoform (57). Our lab identified IRF2BP2 as an ischemia-induced coactivator of VEGFA expression *in vitro* (50). In addition to stimulating the growth of new blood vessels, VEGF was also shown to modulate skeletal myoblast function by enhancing their migration and survival, while inhibiting ischemia-induced skeletal muscle apoptosis *in vivo* (75). In rats, femoral artery ligation induced a 4-fold increase in IRF2BP2 protein expression in the hindlimb muscle (50), but recovery of blood flow was not assessed. Thus, I followed a previously established murine model of hindlimb ischemia in which ligation of the femoral artery induces ischemia in the gastrocnemius muscle, and the perfusion recovery was assessed over 15 days (61). There appeared to be no significant difference in perfusion recovery between WT and the muscle-specific *Irf2bp2^{flox}/Myf5^{Cre}* mice. Ischemic and hypoxic conditions are known to transcriptionally upregulate VEGF expression, inducing angiogenesis, but the process of arteriogenesis does not rely on hypoxia (76). Arteriogenesis is a key mechanism for enhancing perfusion, and is crucial for rescuing of ischemic tissues (61). Thus, the *in vitro* mechanism of IRF2BP2-induced VEGF upregulation may not translate to an *in vivo* model of ischemic recovery which is primarily regulated by arteriogenic processes.

The resolution of skeletal muscle injury involves a close interaction between the muscle tissue and the immune response, involving cells of the myeloid lineage (18). In the days following an acute muscle injury, there is an influx of myeloid cells along with parallel

changes in myogenic cell population and gene expression (5). At 2 days post-injury, a rise in concentration of phagocytic macrophages coincides with a rise in MyoD and myogenin expression (5). An increase in M2 macrophages coincides with a decline in M1 macrophages up to 4 days post-injury (77), at which point young myotubes begin to form with centralized nuclei indicating skeletal muscle regeneration (22). After 10 days, a skeletal muscle injury from CTX injection is largely resolved in healthy mice (18). Since the global knockout of *Irf2bp2* causes embryonic lethality in mice, we used tissue-specific knockout mice to study skeletal muscle inflammation and regeneration. The experiment was performed in two different mouse models, one being a myeloid cell lineage-specific IRF2BP2 knockout (*Irf2bp2^{flox}/LysMCre*), and the other being a muscle-specific IRF2BP2 knockout (*Irf2bp2^{flox}/MckCre*). I induced skeletal muscle injury by CTX injection into the TA muscles, and allowed the mice to recover for 2, 4, and 10 days, after which I harvested the muscles for analysis. The CTX injections caused comparable local damage in the different genotypes (including WT) after 2 days, indicated by the similar necrotic structure and high infiltration due to initiation of inflammation. Thus, as both *Irf2bp2^{flox}/LysMCre* and *Irf2bp2^{flox}/MckCre* mice show increased inflammation and impaired muscle regeneration, this suggests separate roles for IRF2BP2 in both myeloid cells and muscle cells to coordinate recovery from muscle injury. A higher sample size of mice is required for these muscle injury experiments, to get significant findings (at least n=3 WT and 3 KO mice per injury timepoint). To evaluate whether KO mice have an abnormal complete blood count, Appendix 4 shows hematology values between an *Irf2bp2^{-/-}* mouse compared to a

hemizygous mouse. White blood cell morphology was normal, but the hematocrit value for the KO mouse was low at 39% (76).

In summary, my work shows the importance of IRF2BP2 in embryogenesis and mouse development, and I show that it has implications in tumorigenesis and skeletal muscle regeneration, and affects expression of genes involved in the inflammatory response, cell survival, cell signaling, and immune cell activation. IRF2BP2 has previously been known to have corepressor roles in myeloid cells, as well as coactivator roles in skeletal muscle. My microarray results, visualized in the Venn diagram in Figure 10, show that IRF2BP2 predominantly acts in a repressive role due to the majority of upregulated genes in the IRF2BP2 knockout mouse. Interestingly, IRF2BP2 was shown to have an approximately equal repressive/active role in the skeletal muscle microarray, confirming previous studies. The top most significantly affected genes from the knockout microarray analysis can be individually studied to elucidate their relationship with IRF2BP2. Further experiments can reveal functional interactions between IRF2BP2 and transcriptional factors, and to characterize its mechanism in skeletal muscle regeneration. This work may be applied to cardiac muscle recovery after ischemia with other mouse knockout models. Finally, the role of IRF2BP2 in lymphomas and other cancers must be further elucidated, with future implications for new treatments and therapies in humans.

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APPENDICES

Appendix 1: Irf2bp2 knockout targeting vector sequence

CTGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAGCGTGACCGCTACACTTGCCAGCGCCCT
AGCGCCCGCTCCTTTTCGCTTTCTTCCCTTCTTCGCCACGTTTCGCCGGCTTTCCCGGTCAAGCTCTAAATCGGGGGCTC
CCTTTAGGGTTCGGATTTAGTGCTTTACGGCACCTCGACCCCAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGGCCAT
CGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGTGGACTCTTGTTCCAAACTGGAACAAC
ACTCAACCGTATCTCGGTCTATTTCTTTGATTATAAGGATTTTGGCGATTTCGGCTATTGGTTAAAAATGAGCTGATT
TAACAAAAATTTAACGCGAAATTTTAACAAATATTAACGCTTACAATTTCCATTTCGCATTTCAGGCTCGG

PvuI (500)

CAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGAT

253 seq F (584)

TAAGTTGGGTAACGCCAGGGTTTTCCAGTCACGACGTTGTAAACGACGGCCAGTGAATTGTAATACGACTCACTATAG

ret.5F

NotI (667)

junction marker (681)

SacI (654) SacII (661)

junction marker (673)

[illegible]

ret5r

gcatgtttccagactgtaaaacittattggcagctgtgaatttttttttcgtatttttggtttgtttgtttgaga**caggaatac**
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HindIII

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frt5

junction marker (3383)

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BamHI (4030)

Junction marker

Frt5r

PL451-3'-scr2F (cko)

loxP

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TACCTGACTGATGAAGTTCCTATACTTTCTAGAGAATAGGAAGTTCGAAGGGTTCGCAAGCTCTAGTCGAGCCCCAGCT

PL452-3'-sclF (cko)

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CCCAAGCGG

Neo

CCGGAGAACCTGCGTGCAATCCATCTTGTTCAAATGGCCGATCCCATGGTTTAGTTTCTCACCTTGTCTATTATACTATG

EM7 Promoter

CCGATATACTATGCCGATGATTAATTGTCAACAGGCTGCAGGTTCGAAAGGCCCGAGATGAGGAAGAGGAGAACAGCGC

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CCCCTGAGCCCGCCCGGACCCACCCCTTCCCAGCCTCTGAGCCCAGAAAGCGAAGGAGCAAAGCTGCTATTGGCCGC

TGC

StuI (5528)

SpeI

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TCACGTCTGCACGACGCGAGCTGCGGGGCGGGGGGAAGTTCCTGACTAGGGGAGGAGTAGAAGGTGGCGGAAGGGG

CCACCAAAGAACGGAGCCGTTGGCGCCTACCGGTGGATGTGAATGTGTGCGAGGCCAGAGGCCACTTGTGTAGCGCC

AAG

PGK promoter

TGCCCAGCGGGGCTGCTAAAGCGCATGCTCCAGACTGCCTTGGGAAAAGCGCCTCCCTACCCGGTAGAATTTCGACGA

CCTGCAGCCAAGCTAGCTTGGCTGGACGTAAACTCCTCTTCAGACCTGAAGTTCCTATACTTTCTAGAGAATAGGAAGTTC

Frt3F

Junction marker

EcoRI (5922)

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V S S A A A E H E A R E P S K E K A Q P A H R S P A

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D S L S S A A G A S E L S A E G A G K G R A P G E Q D

TGGGCCAGCAGGCCTAAGACGGTTCGGGACACGCTCTGGCGTGACACCAGCAGCGCCACTCGGGGCCCTTCGAGAGCAA

W A S R P K T V R D T L L A L H Q H G H S G P F E S K

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F K K E P A L T A A G R L L G F E A N G A N G S K A

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exon 2

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L K I P I T P T S S F V S P P P P T A S P H S N R T

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BamHI

SacI XhoI (12093) PL452-loxp-sclR (cko) loxP

(12146) PL452-3'-sc2F (ko) junction marker

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←

lox3F

junction marker

PL452-5'-sc2R (ko)

EcoRI (12185)

PL452scr5R2 (ko/cko)

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SpeI

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SalI

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EcoRI

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ret3F HindIII

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BamHI

BamHI (17232)

ret3R

StuI (17292)

StuI (17363)

AGGCCTGGAATGTTCCACCCAATGTCGAGCAAACCCGCCAGCGTCTTGTCATTGGCGAATTCGAACACGCAGATGCA

Bg1II (17551)

HSV thymidine kinase

M A S Y P G H Q H A S A F D Q A A R S R G H S N

EcoRV (17839)

TCGTCTACGTACCCGAGCCGATGACTTACTGGCGGGTGCTGGGGGCTTCCGAGACAATCGCGAACATCTACACCACACAA

EcoRV (17943)

H R L D Q G E I S A G D A A V V M T S A Q I T M G M P

SacI (18056)

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ApaI (18229)

Q A V L A F V A L I P P T L P G T N I V L G A L P E D

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R H I D R L A K R Q R P G E R L D L A M L A A I R R

PstI (18357)

V Y G L L A N T V R Y L Q G G G S W R E D W G Q L S G

ApaI (18446)

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T A V P P Q G A E P Q S N A G P R P H I G D T L F T L

ApaI (18490)

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F R A P E L L A P N G D L Y N V F A W A L D V L A K

GCCTCCGTCCCATGCACGTCTTTATCCTGGATTACGACCAATCGCCCGCCGGCTGCCGGGACGCCCTGCTGCAACTTACC

R L R P M H V F I L D Y D Q S P A G C R D A L L Q L T

SmaI (18716)

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S G M I Q T H V T T P G S I P T I C D L A R T F A R E

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M G E A N *

AAAACGCACGGGTGTTGGGTCGTTTGTTCATAAACCGCGGGTTCGGTCCCAGGGCTGGCACTCTGTGATACCCACCGAGA
 CCCCATTGGGGCCAATACGCCCGGTTTCTTCCTTTTCCCCACCCACCCCCAAGTTCGGGTGAAGGCCAGGGCTC
 ApaI (19003) NcoI (19027)
 GCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCACGGGCCCCGTGGGTAGGGACGGGGTCCCCATGGGGAATGGT
 NcoI (19112)
 TTATGGTTCGTGGGGTTATTATTTTGGGCGTTGCGTGGGGTCAGTCCACGACTGGACTGAGCAGACAGACCCATGGT'TTTT
 GGATGGCCTGGGCATGGACCGCATGTACTGGCGGCACACGAACACCGGGCGTCTGTGGCTGCCAAACACCCCGACCCCAA
 AAACCACCGCGCGGATTTCTGGCGCCGCCGACGAACATAAACCCTGACTACGGCATCTCTGCCCTTCTTCGCTGGT
 ClaI (19357)
 SacII (19328) NheI (19348)
 ACGAGGAGCGCTTTTGT'TTTGTATTGGTCACCACGGCCGAGTTTCCGCGGGACCCCGGCCAGATCAAGCTAGCTTATCGA
 XhoI (19371) KpnI (19390)
 SalI (19365) ApaI (19384)
 TACCGTCGACCTCGAGGGGGGGCCCGGTACCAGCTTTTGTTCCTTTTAGTGAGGGTTAATTTTCGAGCTTGGCGTAATCATGG
 TCATAGCTGTTTCTGTGTGAAATTGTTATCCGCTCACAAATCCACACAACATACGAGCCGGAAGCATAAAGTGTAAGCCT
 GGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCAGTCGGGAAACCTGTGCTGCCA
 GCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCCTATTGGGCGCTCTTCCGCTTCTCGCTCACTGACTCG
 CTGCGCTCGGTTCGTTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATA
 ACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAG
 GCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAG
 GCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCTTTTCTCCCTT
 CGGGAAGCGTGGCGCTTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTCGCTCCAAGCTGGGCTGTGT
 GCACGAACCCCCGTTAGCCCGACCGCTGCGCCTTATCCGGTAACATATCGTCTTGAGTCCAACCCGTAAGACACGACTTA
 TCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGC
 CTAAGTACGGCTACACTAGAGAAGACAGTATTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAG
 CTCTTGATCCGGCAAAACAAACACCGCTGGTAGCGGTGGTTTTTTTGT'TTGCAAGCAGCAGATTACGCGCAGAAAAAAGGA
 TCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAACGAAACTCACGTTAAGGGATTTTGGTCATGA
 GATTATCAAAAAGGATCTTACCTAGATCCTTTTAAATTAAAAATGAAGTTTAAATCAATCTAAAGTATATATGAGTAAAC
 TTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTTCATCCATAGTTGCCTGA
 CTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCT
 CACCGGCTCCAGATTTATCAGCAATAAACAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCTGCAACTTTATCCGCCTC
 CATCCAGTCTATTAATTGTTGCCGGAAGCTAGAGTAAGTAGTTCCGAGTTAATAGTTTGCAGCAACGTTGTTGCCATTGCT
 ACAGGCATCGTGGTGTACGCTCGTCTGTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGAT
 CCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCC
 PvuI (21046)
 TCCGATCGTTGTGCAAGTAAGTTGGCCGAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCA
 ScaI (21156)
 TGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTG
 CTCTTGCCCGCGCTCAATACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATATTGAAAAAGTTCTTCG
 GGGCGAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGACCCAACTGATCTTCAGCAT
 CTTTACTTTTACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAGGGAATAAGGGCGACACGGAA
 ATGTTGAATACTCATACTCTTCTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGG
 Junction marker
 ATACATATTTGAATGTATTTAGAAAAATAACAAATAGGGGTTCGCGCACATTTCCCCGAAAAGTGCCAC

Appendix 2(a): Skeletal muscle microarray. Microarray analysis of differentially expressed genes in skeletal muscle of KO and WT mice. Pink cells represent downregulated gene expression; green cells represent upregulated gene expression. Ordered by BH.

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT Avg	WTSD	KO Avg	KOSD	KO/WT	BH	Gene
1	4.880	4.813	4.610	2.697	2.150	2.766	27.24	2.61	5.81	1.28	0.213	6.85E-08	Irf2bp2
2	2.190	3.815	3.408	5.695	6.155	5.733	8.80	4.81	58.12	10.86	6.604	1.31E-05	Nr4a3
3	4.960	4.213	4.918	6.468	6.366	6.387	25.94	7.02	84.86	3.19	3.271	3.08E-05	H2-Q6
4	5.707	5.527	6.460	7.925	7.443	7.610	59.64	22.65	202.17	35.31	3.390	1.04E-04	H2-Ab1
5	1.773	1.923	1.976	3.633	3.203	2.876	3.71	0.27	9.43	2.56	2.543	1.96E-04	Bcl2a1a
6	3.241	2.908	3.312	4.503	4.467	4.420	8.90	1.29	22.06	0.63	2.479	1.99E-04	H2-Q4
7	6.365	7.399	7.280	10.589	9.732	8.508	129.32	46.50	781.19	591.11	6.041	1.99E-04	Mt2
8	3.890	3.442	3.502	1.544	2.589	1.919	12.22	2.17	4.05	1.60	0.331	1.99E-04	Ostn
9	2.375	2.534	2.618	4.127	3.752	3.497	5.69	0.48	13.85	3.14	2.433	2.27E-04	Bcl2a1d
10	5.220	5.659	5.599	4.292	4.097	4.582	45.03	7.14	20.03	3.46	0.445	2.38E-04	C7
11	4.903	4.647	5.258	6.745	6.103	6.307	30.62	6.68	83.57	19.92	2.729	2.38E-04	H2-Eb1
12	3.815	4.513	4.090	2.440	2.966	2.977	17.62	4.45	6.94	1.40	0.394	2.38E-04	Nnat
13	2.074	2.241	2.309	3.826	3.474	3.190	4.62	0.38	11.29	2.55	2.443	3.86E-04	Bcl2a1b
14	4.678	5.045	4.560	3.517	3.486	3.705	27.11	4.96	11.87	1.00	0.438	4.02E-04	Kcnq5
15	2.594	2.299	2.803	3.509	4.215	3.743	5.92	1.03	14.14	3.71	2.390	6.99E-04	Tgtp1
16	4.864	5.657	5.467	7.090	6.484	6.709	40.21	10.97	108.46	23.84	2.697	8.96E-04	Sik1
17	3.950	3.776	4.051	2.776	3.040	2.815	15.20	1.45	7.35	0.75	0.483	0.0011	Dkk2
18	4.156	4.954	5.453	6.818	6.532	6.068	28.92	12.99	88.81	22.93	3.071	0.0011	Ifi205
19	5.028	5.551	5.244	6.544	6.312	6.206	38.70	7.20	81.80	10.02	2.114	0.0011	Midn
20	7.137	6.389	7.883	9.044	8.697	8.543	140.69	76.96	433.91	80.18	3.084	0.0016	Cd74
21	1.824	1.781	1.620	3.128	2.648	2.492	3.34	0.25	6.75	1.64	2.020	0.0017	Cd52
22	5.158	5.561	5.889	6.875	6.515	6.620	46.40	11.77	101.84	13.41	2.195	0.0019	Slc7a8
23	6.757	6.505	6.831	7.759	7.487	7.585	103.80	11.98	195.41	18.97	1.883	0.0042	H2-Q7
24	3.787	4.012	4.130	4.920	4.747	5.014	15.74	1.87	29.72	2.76	1.888	0.0042	Slc7a5
25	3.965	3.772	4.249	5.662	5.016	4.829	15.95	2.71	35.98	11.87	2.256	0.0042	Tyrobp
26	5.038	5.333	5.581	6.879	6.468	6.120	39.88	7.51	89.82	24.25	2.252	0.0042	Ucp2
27	4.445	4.710	4.963	3.679	3.851	3.939	26.10	4.70	14.15	1.28	0.542	0.0046	Agbl1
28	5.091	4.611	5.943	7.281	6.317	6.736	37.14	19.25	109.77	38.45	2.956	0.0046	H2-Aa
29	3.212	3.290	3.835	4.728	4.199	4.667	10.89	2.75	23.13	4.42	2.123	0.0046	Mgl2
30	3.963	3.846	3.900	5.201	4.594	4.760	14.96	0.61	28.87	6.61	1.930	0.0046	Pira11
31	3.932	4.683	4.370	6.047	5.135	5.551	20.09	5.21	47.75	15.63	2.377	0.0050	Nfil3
32	3.313	2.967	3.194	4.002	4.518	4.130	8.92	1.07	18.59	3.62	2.083	0.0050	Nlrc5
33	9.075	9.155	9.024	8.111	8.332	7.769	542.92	24.99	268.84	52.26	0.501	0.0050	Zmynd17
34	5.704	6.196	6.319	9.250	7.879	6.980	67.32	14.48	262.53	253.20	3.899	0.0052	Mt1
35	4.076	4.174	5.135	6.828	5.854	5.490	22.04	10.22	66.59	36.49	3.022	0.0056	Al607873
36	3.477	3.817	3.953	5.430	5.201	4.435	13.44	2.22	32.50	11.04	2.417	0.0060	Osmr
37	2.043	2.358	2.315	3.429	2.827	3.206	4.72	0.54	8.90	1.85	1.886	0.0068	Gm10851
38	3.598	3.991	3.957	5.649	5.039	4.496	14.41	2.09	33.39	13.96	2.318	0.0081	Runx1
39	3.873	4.227	4.444	3.333	2.914	3.484	18.15	3.57	9.47	1.87	0.522	0.0081	Lrrn1
40	1.373	1.715	1.724	3.456	2.975	2.108	3.04	0.41	7.19	3.33	2.365	0.0082	Ccl3
41	3.333	3.774	3.519	5.948	4.404	4.716	11.65	1.82	32.51	22.08	2.791	0.0082	Hmox1
42	3.890	3.998	4.081	5.050	5.229	4.601	15.89	1.05	31.13	6.75	1.960	0.0082	Rin3
43	5.405	5.630	5.711	7.012	6.302	6.287	47.90	5.15	92.64	29.18	1.934	0.0085	Laptm5
44	5.565	6.087	6.085	7.242	7.007	6.597	60.23	11.88	123.52	27.39	2.051	0.0090	Gpr56
45	5.668	5.775	5.951	6.768	6.913	6.393	55.64	5.58	103.35	18.64	1.857	0.0090	Arid5b
46	5.158	5.775	6.044	7.918	6.409	6.849	50.51	15.30	133.30	83.21	2.639	0.0090	C1qb

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT Avg	WTSD	KO Avg	KOSD	KOWT	BH	Gene
47	2.563	2.964	2.897	4.722	3.917	3.417	7.00	1.01	16.21	8.10	2.314	0.0090	Csf2rb
48	3.455	2.965	3.504	4.179	4.188	4.215	9.90	1.94	18.30	0.24	1.848	0.0090	Gbp7
49	4.603	2.936	3.039	4.485	6.412	5.513	11.52	9.45	44.32	31.72	3.848	0.0090	Gm3893
50	3.170	2.493	3.178	5.006	4.097	3.749	7.71	1.96	19.48	9.91	2.526	0.0090	Il2rg
51	2.650	3.322	3.145	4.521	4.014	3.763	8.22	1.91	17.14	4.84	2.085	0.0090	Map3k6
52	3.517	3.239	3.973	4.434	4.894	4.397	11.93	3.20	23.84	4.85	1.998	0.0090	Mir692-1
53	9.009	9.482	9.731	10.413	10.218	9.965	678.93	168.37	1174.99	182.07	1.731	0.0090	Pdk4
54	4.431	4.633	4.596	5.347	5.325	5.205	23.48	1.72	39.19	2.05	1.669	0.0090	Sdc3
55	2.731	3.129	2.736	4.293	3.508	3.774	7.29	1.21	14.50	4.24	1.990	0.0090	Sh3pxd2b
56	1.827	2.511	2.268	3.398	3.075	3.025	4.60	1.08	8.98	1.31	1.950	0.0090	Snord116
57	6.682	6.949	6.964	7.871	7.900	7.486	116.55	12.43	215.62	33.17	1.850	0.0090	Srgn
58	5.810	6.641	6.560	7.445	7.583	7.064	80.82	23.81	164.74	29.72	2.038	0.0090	Ucp3
59	4.916	5.377	5.826	6.904	6.448	6.169	41.44	13.33	90.96	24.40	2.195	0.0090	Xdh
60	3.617	3.045	2.779	4.659	4.264	3.817	8.86	2.81	18.98	5.59	2.143	0.0092	Bcl3
61	2.714	2.020	2.799	3.488	3.640	3.195	5.70	1.57	10.86	1.67	1.906	0.0092	Sla
62	7.004	7.745	7.841	8.766	8.492	8.459	184.85	54.52	380.67	46.05	2.059	0.0094	Xirp1
63	6.208	5.844	6.233	7.158	6.767	6.930	68.36	9.90	123.78	17.11	1.811	0.0099	H2-D1
64	7.355	7.891	8.315	9.852	8.866	8.655	231.32	77.35	558.11	284.37	2.413	0.0099	Glul
65	6.076	5.863	6.093	4.838	5.273	5.442	64.48	5.58	36.36	7.58	0.564	0.0106	Osbp16
66	3.542	2.601	2.499	3.576	4.736	4.231	7.36	3.35	18.14	7.37	2.463	0.0107	4933409K07Rik
67	3.115	4.080	3.971	5.323	4.725	4.476	13.20	4.45	28.67	9.30	2.172	0.0107	Ccl9
68	4.245	4.318	4.195	6.223	5.330	4.783	19.06	0.82	43.57	24.40	2.286	0.0107	Il4ra
69	8.224	8.134	7.800	7.451	7.137	7.219	265.48	39.79	154.22	17.84	0.581	0.0107	Aldh1a1
70	3.517	3.479	3.258	4.699	4.480	3.832	10.69	1.01	20.21	6.00	1.891	0.0107	Cyth4
71	3.001	3.328	3.336	4.823	4.399	3.704	9.33	1.19	19.82	7.64	2.124	0.0107	Lilrb3
72	5.484	5.501	5.568	7.441	6.036	6.545	45.82	1.43	102.11	56.19	2.229	0.0107	Rasd2
73	3.455	3.748	3.854	5.430	5.257	4.103	12.86	1.80	30.48	13.78	2.370	0.0108	Egr1
74	2.268	2.647	2.371	0.843	1.866	1.718	5.38	0.75	2.78	0.98	0.517	0.0108	Neto2
75	3.295	3.488	3.130	4.963	4.091	3.900	9.88	1.23	19.95	8.84	2.019	0.0108	Sbno2
76	2.448	2.365	2.665	3.009	3.356	3.690	5.63	0.62	10.21	2.43	1.814	0.0110	Dnase1l3
77	3.779	4.663	4.161	5.874	5.314	4.822	18.39	5.88	40.41	15.34	2.198	0.0110	Serpine1
78	0.493	0.493	0.428	1.100	0.778	1.028	1.39	0.04	1.96	0.22	1.411	0.0119	Vmn1r174
79	1.148	0.891	1.435	2.376	1.827	1.727	2.23	0.43	3.94	1.02	1.764	0.0122	Serpina3k
80	2.441	2.585	3.237	4.153	3.691	3.473	6.75	2.16	13.66	3.46	2.025	0.0124	Pilra
81	3.133	2.822	3.073	3.860	3.735	3.665	8.05	0.90	13.49	0.93	1.675	0.0134	Atoh8
82	2.485	2.538	2.459	3.717	3.528	2.859	5.63	0.16	10.32	3.05	1.832	0.0134	Ccl2
83	3.875	4.058	3.764	4.937	4.629	4.536	14.92	1.56	26.00	3.92	1.743	0.0135	Adams9
84	4.207	4.246	4.601	5.667	5.096	4.934	20.42	3.22	37.59	10.80	1.841	0.0135	Ampd3
85	3.314	3.184	2.996	2.343	2.318	2.603	8.97	0.99	5.36	0.60	0.597	0.0135	Armcx6
86	3.107	3.243	3.023	2.385	2.231	2.631	8.72	0.68	5.34	0.76	0.612	0.0135	Capn6
87	2.511	2.542	3.157	4.241	3.526	3.497	6.67	1.83	13.50	4.33	2.024	0.0135	Fcgr2b
88	4.099	4.900	4.678	6.279	5.293	5.440	23.57	6.48	50.93	21.10	2.161	0.0135	Foxo1
89	3.001	2.312	2.732	3.290	3.776	3.534	6.42	1.52	11.58	1.96	1.805	0.0135	Gm12185
90	4.927	5.113	5.523	6.495	5.904	5.886	36.44	8.05	68.35	17.71	1.876	0.0135	Klf6
91	6.572	6.854	6.966	6.476	4.868	5.113	111.25	15.30	44.82	33.09	0.403	0.0135	Lynx1
92	2.099	2.128	2.034	3.439	2.540	2.921	4.25	0.14	7.82	2.55	1.840	0.0135	Pira2
93	2.606	2.379	2.498	3.531	3.215	3.046	5.64	0.44	9.61	1.69	1.705	0.0135	Ptprc
94	3.802	4.274	4.713	5.843	5.136	4.927	19.20	6.16	39.45	14.42	2.054	0.0135	Ptprj
95	3.145	3.017	2.889	3.796	3.783	3.605	8.09	0.72	13.25	0.96	1.637	0.0135	Rsad2
96	3.725	3.939	4.104	3.045	3.053	3.480	15.16	1.99	9.14	1.66	0.603	0.0135	Slc30a2

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT Avg	WTSD	KO Avg	KOSD	KOWT	BH	Gene
97	5.859	6.166	6.207	7.378	6.648	6.831	67.53	8.61	123.82	34.88	1.834	0.0135	Tgm2
98	8.047	7.981	8.611	7.444	7.196	7.539	296.75	76.77	168.11	20.18	0.567	0.0135	Tnnt1
99	1.005	1.753	1.360	0.777	0.717	0.733	2.59	0.69	1.67	0.04	0.646	0.0135	Vmn2r87
100	3.078	3.765	3.744	4.952	4.574	4.103	11.54	2.92	23.31	6.89	2.020	0.0138	Ifi204
101	4.647	4.605	5.251	5.750	6.076	5.454	28.53	7.74	54.18	11.85	1.899	0.0140	Car4
102	2.882	3.281	3.230	4.145	3.921	3.701	8.76	1.27	15.16	2.34	1.731	0.0140	Fos
103	1.632	1.565	1.447	2.024	2.157	2.356	2.92	0.19	4.53	0.53	1.548	0.0146	Zfp668
104	2.512	3.116	3.053	4.231	3.371	3.894	7.43	1.62	14.24	4.22	1.916	0.0149	Btg2
105	3.502	5.677	4.721	6.066	6.052	6.285	24.82	20.11	70.25	6.51	2.830	0.0151	Atf3
106	3.342	3.329	3.222	4.026	3.957	3.850	9.83	0.44	15.39	0.94	1.565	0.0156	Arrb2
107	4.173	4.295	4.576	5.975	4.866	5.246	20.37	3.01	41.13	17.50	2.020	0.0157	Gm11711
108	2.876	2.594	3.237	4.097	3.475	3.675	7.48	1.71	13.44	3.09	1.798	0.0164	Cdk6
109	0.582	0.622	0.646	1.100	1.085	0.876	1.53	0.03	2.03	0.17	1.323	0.0166	Igfv1
110	2.232	2.178	2.221	3.520	3.023	2.743	4.63	0.09	8.55	2.45	1.847	0.0169	Adam8
111	2.498	2.872	2.841	4.158	3.464	3.339	6.67	0.92	12.59	4.22	1.888	0.0181	Gda
112	2.026	2.086	2.084	3.289	2.727	2.627	4.18	0.10	7.37	1.96	1.760	0.0181	Ms4a6c
113	5.343	5.604	6.212	4.554	5.129	4.849	52.70	17.50	28.72	5.75	0.545	0.0185	Filip1l
114	2.513	2.483	2.408	3.397	3.056	3.014	5.53	0.21	8.91	1.36	1.611	0.0186	Cxcl16
115	3.018	2.894	2.853	1.924	2.043	2.546	7.58	0.46	4.50	1.10	0.594	0.0195	Riiaad1
116	3.628	4.615	4.205	5.357	5.197	4.799	17.75	6.07	34.72	6.71	1.956	0.0203	Irs2
117	5.170	5.271	5.061	4.191	4.057	4.877	35.93	2.61	20.75	6.93	0.577	0.0204	Cbr4
118	2.250	2.815	2.798	1.711	2.141	1.852	6.15	1.29	3.74	0.58	0.607	0.0212	Ccne2
119	1.391	1.547	1.913	1.201	0.847	0.945	3.07	0.59	2.00	0.26	0.651	0.0212	Cd209d
120	2.304	2.270	2.297	2.751	2.980	3.150	4.89	0.06	7.78	1.07	1.591	0.0215	Aim1
121	4.396	4.522	4.330	3.825	3.697	3.906	21.35	1.46	14.02	1.02	0.657	0.0215	Ccdc3
122	4.753	4.988	5.319	6.375	5.555	5.786	32.45	6.54	59.93	18.87	1.847	0.0215	Entpd1
123	3.123	2.537	2.327	4.771	3.450	3.344	6.33	1.95	14.47	9.69	2.286	0.0215	Ifitm1
124	3.190	3.790	3.711	5.326	4.009	4.555	11.82	2.53	24.76	12.29	2.094	0.0216	Ddit4
125	0.662	0.944	0.793	1.464	1.482	1.060	1.74	0.17	2.52	0.40	1.450	0.0218	Bcl2a1c
126	2.517	2.499	3.141	3.909	3.514	3.281	6.58	1.81	11.86	2.71	1.801	0.0218	Fgl2
127	2.591	2.215	2.625	3.160	3.241	3.134	5.57	0.84	9.05	0.35	1.626	0.0218	Igf2bp2
128	3.491	3.066	3.519	4.385	4.223	3.831	10.26	1.72	17.71	3.39	1.726	0.0223	Csf1
129	4.187	4.551	4.932	5.809	5.280	5.210	23.53	6.17	43.20	10.52	1.836	0.0225	Man2a1
130	4.516	4.849	5.072	6.713	5.517	5.412	28.10	5.39	58.92	35.09	2.097	0.0230	Galntl2
131	5.627	5.520	5.219	4.841	4.637	4.765	43.87	6.25	26.87	1.91	0.612	0.0237	Kdr
132	6.017	6.062	6.246	7.491	6.999	6.492	68.99	5.95	127.45	45.12	1.847	0.0248	Tinagl1
133	7.189	6.968	7.335	6.386	6.431	6.619	143.41	18.22	89.18	7.81	0.622	0.0249	Ldhd
134	6.341	6.325	6.339	5.653	5.546	5.840	80.73	0.49	51.26	5.36	0.635	0.0255	H2afv
135	6.736	7.068	6.743	6.277	6.127	6.243	115.30	15.79	74.34	4.01	0.645	0.0256	Atp6v1g1
136	2.637	2.697	2.969	4.507	3.569	3.223	6.81	0.86	13.61	7.12	1.998	0.0262	Sfp1
137	2.619	2.466	2.548	3.845	2.908	3.339	5.83	0.31	10.29	3.46	1.765	0.0262	Tlr9
138	3.913	5.375	5.326	6.878	5.921	5.741	29.27	14.88	72.51	35.16	2.478	0.0266	Ccl6
139	5.843	6.123	7.881	8.274	7.825	8.017	98.09	99.62	262.96	41.70	2.681	0.0269	Chac1
140	0.619	0.685	0.736	1.209	1.341	0.900	1.60	0.07	2.22	0.34	1.385	0.0273	Stap1
141	1.623	1.277	1.185	2.375	2.129	1.657	2.57	0.43	4.15	1.02	1.615	0.0276	Nkg7
142	3.308	3.385	3.546	4.481	3.748	4.463	10.65	0.91	18.78	5.06	1.763	0.0277	Trib1
143	5.170	4.845	5.432	6.063	5.761	5.950	35.48	7.22	60.74	6.36	1.712	0.0278	H2-K1
144	4.183	4.255	4.112	5.324	4.775	4.744	18.16	0.90	30.86	7.50	1.699	0.0294	Lcp1
145	3.801	4.066	3.508	5.541	5.169	4.006	13.85	2.68	29.97	15.48	2.164	0.0294	Rrad
146	8.504	8.820	8.706	7.815	7.917	8.202	409.28	44.92	252.20	36.21	0.616	0.0296	Smpx
147	5.305	5.353	5.179	4.617	4.536	4.852	38.83	2.39	25.42	2.97	0.655	0.0305	Cdon

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT Avg	WTSD	KO Avg	KOSD	KOWT	BH	Gene
148	3.232	2.767	3.154	3.857	3.753	3.752	8.29	1.38	13.81	0.59	1.666	0.0305	Gm111127
149	6.756	6.988	6.831	6.344	5.953	6.382	116.02	9.66	74.87	11.80	0.645	0.0305	Prkcq
150	6.998	6.522	7.053	7.780	7.584	7.381	115.99	22.34	191.58	26.53	1.652	0.0312	Asb15
151	4.126	4.078	4.055	3.164	3.366	3.776	16.99	0.43	10.82	2.44	0.637	0.0312	Rnf128
152	2.773	2.712	2.810	2.048	1.901	2.370	6.80	0.23	4.31	0.74	0.633	0.0335	Bmp5
153	3.558	3.802	3.851	4.490	4.171	4.554	13.33	1.41	21.18	2.92	1.589	0.0340	Aldh1a2
154	1.882	1.947	1.809	4.365	3.387	2.036	3.68	0.18	9.60	8.32	2.609	0.0342	Selp
155	3.447	3.774	3.030	2.286	2.996	2.610	10.68	2.76	6.19	1.56	0.580	0.0348	Cacna2d4
156	3.095	4.113	4.637	5.625	4.926	4.785	15.44	8.17	34.58	11.85	2.240	0.0351	Fam107a
157	0.759	1.020	0.825	1.891	1.258	1.258	1.83	0.18	2.77	0.76	1.517	0.0354	Clec4e
158	1.978	1.763	2.456	3.265	2.652	2.730	4.19	1.09	7.37	1.83	1.761	0.0359	Mpeg1
159	3.437	3.490	3.462	5.208	3.958	4.056	11.03	0.20	21.22	12.07	1.924	0.0369	Cd68
160	3.335	3.417	3.422	5.698	4.267	3.825	10.49	0.35	24.20	20.49	2.306	0.0372	C3ar1
161	3.249	2.883	3.425	3.754	3.907	3.941	9.10	1.70	14.59	0.99	1.604	0.0372	Tap1
162	2.902	2.703	3.246	2.076	2.569	1.980	7.73	1.52	4.62	1.08	0.598	0.0374	Pln
163	4.522	4.708	4.671	5.289	5.479	5.097	24.83	1.67	39.08	5.19	1.574	0.0377	Ceacam1
164	4.871	5.025	4.992	4.146	4.175	4.654	31.18	1.74	20.04	4.21	0.643	0.0379	Ermp1
165	1.814	2.014	1.892	3.859	2.759	2.243	3.75	0.26	7.75	5.16	2.066	0.0379	Lilrb4
166	2.280	2.822	2.510	4.474	3.291	3.058	5.80	1.12	12.19	7.64	2.100	0.0380	C5ar1
167	1.909	2.086	2.415	2.816	2.655	2.741	4.40	0.81	6.67	0.37	1.516	0.0389	H2-DMb2
168	2.619	2.875	2.803	1.780	2.233	2.376	6.80	0.61	4.38	0.91	0.643	0.0389	Kera
169	3.301	3.535	3.303	4.769	3.960	3.926	10.41	1.00	18.62	6.87	1.789	0.0389	Slc39a14
170	4.121	4.033	4.106	5.385	4.484	4.692	16.99	0.55	28.91	10.35	1.702	0.0405	Mamstr
171	3.780	4.477	4.194	5.770	4.807	4.737	17.76	4.27	34.41	15.74	1.938	0.0422	Itga5
172	5.648	5.794	5.655	5.074	4.593	5.312	51.95	3.02	31.84	7.86	0.613	0.0424	Olfml3
173	4.545	4.753	4.479	4.104	3.857	4.087	24.12	2.45	16.18	1.51	0.671	0.0426	Fgfr1op2
174	2.778	2.827	2.685	3.765	3.394	3.132	6.79	0.34	10.78	2.45	1.588	0.0432	Cd44
175	1.554	1.913	1.824	2.484	2.282	2.195	3.40	0.43	5.00	0.52	1.471	0.0432	Gpr64
176	0.704	0.388	0.355	0.929	0.799	0.895	1.40	0.19	1.83	0.09	1.312	0.0433	Tas2r110
177	7.494	7.332	7.467	9.141	7.902	8.132	172.55	10.21	335.93	177.17	1.947	0.0433	Hbb-b1
178	5.295	5.320	5.158	6.092	5.774	5.767	38.26	2.27	58.79	7.89	1.537	0.0435	Efh2
179	2.087	2.102	1.728	1.655	1.036	1.367	3.92	0.55	2.55	0.55	0.651	0.0438	Gm4861
180	3.841	4.091	3.676	2.905	2.842	3.531	14.61	2.15	8.53	2.45	0.584	0.0438	Trim13
181	1.214	1.361	1.372	2.965	1.739	1.836	2.49	0.15	4.53	2.52	1.821	0.0450	Ms4a6d
182	4.327	4.622	4.583	3.784	3.648	4.192	22.79	2.46	14.67	3.02	0.644	0.0450	Nynrin
183	2.907	2.965	3.565	4.871	3.698	3.792	8.85	2.42	17.39	9.16	1.965	0.0466	8430408G22Rik
184	3.519	3.403	3.526	2.359	2.724	3.243	11.18	0.53	6.85	2.21	0.613	0.0474	Cc2d2a
185	1.061	1.047	1.181	1.478	1.674	1.531	2.14	0.11	2.95	0.21	1.381	0.0474	Gbp8
186	5.026	5.141	5.081	4.112	4.288	4.827	33.89	1.35	21.25	5.86	0.627	0.0474	Pkig
187	3.686	3.574	3.494	4.819	3.877	4.398	12.00	0.80	20.60	6.77	1.776	0.0480	BC048679
188	4.080	4.021	3.733	4.617	4.690	4.452	15.40	1.92	24.02	2.01	1.555	0.0484	H2-Q5
189	4.013	3.917	4.129	4.991	4.878	4.303	16.22	1.20	26.42	6.38	1.660	0.0484	Osgin1
190	1.251	1.206	1.077	1.598	1.610	2.263	2.26	0.14	3.54	1.02	1.601	0.0493	BC005685
191	4.316	4.773	4.761	6.007	5.007	5.354	24.53	4.23	43.90	16.64	1.847	0.0497	Srxn1

Appendix 2(b): Heart microarray. Microarray analysis of differentially expressed genes in cardiac muscle of KO and WT mice. Pink cells represent downregulated gene expression; green cells represent upregulated gene expression. Ordered by BH.

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT Avg	WTsd	KO Avg	KOsd	KO/WT	BH	Gene
1	5.577	5.670	5.017	2.339	1.914	2.615	42.86	9.91	4.89	1.18	0.114	1.49E-10	Irf2bp2
2	6.036	5.369	5.653	7.772	7.698	7.345	51.48	12.29	194.68	29.67	3.782	2.86E-07	H2-Q6
3	5.940	5.929	6.230	8.395	7.759	7.442	65.48	8.04	233.17	84.43	3.561	1.75E-06	H2-Ab1
4	7.327	7.494	7.672	9.452	9.092	8.687	180.73	21.75	540.06	144.35	2.988	2.20E-06	Cd74
5	2.866	2.258	2.438	5.681	4.847	4.291	5.74	1.30	30.69	16.33	5.349	2.32E-06	Gm4841
6	6.141	5.934	6.448	7.558	7.324	7.524	72.21	13.25	177.14	15.17	2.453	2.32E-06	Myot
7	2.093	1.969	2.030	4.564	3.484	3.885	4.09	0.18	15.75	6.42	3.856	4.20E-06	Gm12250
8	6.623	7.289	7.191	10.591	9.403	8.851	131.08	30.85	784.25	572.14	5.983	4.22E-06	Mt2
9	5.621	5.591	5.107	3.831	4.022	3.820	43.40	8.24	14.84	1.20	0.342	5.57E-06	Pla2g5
10	4.881	5.068	5.120	7.214	6.538	6.234	32.52	2.79	101.26	38.22	3.114	1.54E-05	H2-Eb1
11	4.555	4.372	4.771	6.935	5.946	6.029	23.68	3.31	78.97	34.05	3.334	2.27E-05	Gbp6
12	4.938	5.060	5.311	6.863	6.443	6.032	34.37	4.63	87.19	25.60	2.537	3.40E-05	Al607873
13	8.477	8.294	8.443	9.870	9.375	9.331	338.92	22.43	736.94	163.08	2.174	3.40E-05	B2m
14	5.698	5.556	5.715	7.615	6.822	6.812	50.43	3.01	135.56	48.13	2.688	4.38E-05	H2-K1
15	4.238	4.161	4.239	5.794	5.579	5.223	18.54	0.57	46.26	9.11	2.495	4.47E-05	H2-Q4
16	5.157	5.486	5.785	7.988	7.053	6.749	44.51	9.73	153.61	78.18	3.451	4.62E-05	H2-Aa
17	2.585	3.111	3.163	4.784	4.178	4.204	7.74	1.62	20.95	5.36	2.705	9.27E-05	Id2
18	4.149	4.141	4.081	5.263	5.225	5.072	17.43	0.45	36.42	2.50	2.089	1.01E-04	Rsad2
19	0.892	1.587	1.432	5.994	3.709	3.319	2.47	0.59	20.26	30.18	8.209	1.07E-04	Fcgr4
20	5.006	5.127	5.251	5.817	6.074	6.159	34.96	2.97	64.74	7.81	1.852	1.17E-04	1810011O10Rik
21	4.337	4.364	4.375	5.888	5.296	5.234	20.51	0.28	44.42	12.02	2.165	1.39E-04	H2-T10
22	2.482	2.764	2.664	4.686	3.550	4.860	6.22	0.61	20.61	9.20	3.314	1.58E-04	Hcn1
23	2.275	2.862	3.364	4.030	4.438	4.957	7.13	2.73	22.24	7.46	3.119	1.91E-04	Ahsg
24	2.128	2.255	2.351	3.244	3.135	3.490	4.74	0.37	9.78	1.26	2.063	1.91E-04	Dnase1l3
25	5.237	5.429	6.059	7.274	6.638	6.826	47.67	15.41	120.49	28.71	2.527	1.91E-04	Ifi205
26	3.605	3.293	3.874	4.821	5.589	4.672	12.05	2.43	32.61	12.35	2.706	1.91E-04	Tgtp1
27	3.509	3.106	3.560	4.637	5.155	4.382	10.49	1.73	26.44	7.64	2.519	2.04E-04	Gm12185
28	7.313	7.177	7.258	8.707	8.268	8.135	152.13	7.20	330.77	72.44	2.174	2.49E-04	H2-Q7
29	3.135	2.864	3.239	4.514	4.881	3.866	8.45	1.11	21.41	7.45	2.533	4.09E-04	Gbp4
30	1.610	2.122	2.080	0.831	1.189	0.884	3.83	0.72	1.96	0.27	0.511	4.71E-04	Gm10635
31	5.108	5.024	5.197	6.766	6.187	5.887	34.53	2.06	77.69	25.64	2.250	6.13E-04	Cdkn1a
32	6.654	6.575	6.766	8.181	7.466	7.421	101.50	6.78	206.37	67.06	2.033	7.08E-04	H2-D1
33	8.525	8.420	8.460	9.780	9.072	9.293	354.15	13.09	667.19	176.86	1.884	7.08E-04	Eef1a1
34	1.624	2.391	2.372	3.988	3.435	3.057	4.37	1.23	11.26	3.84	2.574	7.12E-04	Cyp1b1
35	3.945	3.970	3.753	5.405	4.866	4.659	14.82	1.20	31.48	8.97	2.125	7.38E-04	H2-T22
36	1.841	2.103	1.825	4.371	2.715	3.813	3.79	0.42	12.41	7.07	3.272	7.38E-04	Mmp3
37	5.531	5.522	5.448	3.936	4.680	4.575	45.26	1.41	21.07	5.52	0.465	7.42E-04	Mpped2
38	3.282	2.758	3.159	4.684	4.557	3.849	8.38	1.53	20.58	5.99	2.458	7.42E-04	Nlrc5
39	3.781	3.764	3.968	5.000	4.560	4.762	14.30	1.15	27.37	4.22	1.914	7.46E-04	Gm8995
40	6.887	6.687	6.968	7.503	7.732	7.675	115.15	11.34	199.01	16.19	1.728	8.21E-04	Fuca2
41	4.870	4.502	4.753	3.191	3.757	3.761	26.14	3.34	11.87	2.54	0.454	8.21E-04	Osbpl6
42	4.904	4.935	5.351	6.425	5.858	5.994	33.43	6.11	68.23	14.75	2.041	9.38E-04	Adams1
43	3.866	3.622	4.198	6.792	5.042	5.282	14.88	3.05	52.17	43.33	3.506	0.0010	Ly86
44	4.286	4.438	3.952	2.758	3.561	2.962	18.70	3.15	8.54	2.66	0.456	0.0010	Slc17a7
45	4.587	4.054	4.197	5.817	5.113	5.263	19.42	3.88	42.16	11.62	2.171	0.0010	Gabra3
46	2.416	2.363	2.904	4.060	3.330	4.071	5.90	1.30	14.13	3.86	2.394	0.0011	Cxcl9
47	4.201	4.122	4.287	5.560	5.465	4.746	18.42	1.05	38.24	10.98	2.075	0.0011	H2-Q5
48	2.705	3.289	3.241	7.130	4.604	4.716	8.45	1.79	44.74	66.27	5.297	0.0012	Cd72
49	5.486	5.665	5.229	4.345	4.738	4.442	44.01	6.63	22.76	3.35	0.517	0.0012	Scn4a

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT Avg	WTSD	KO Avg	KOSD	KO/WT	BH	Gene
50	3.491	3.230	3.861	4.467	4.608	4.405	11.53	2.61	22.52	1.65	1.953	0.0012	Shb
51	7.481	7.663	7.883	6.383	7.153	6.595	204.48	28.78	104.73	30.91	0.512	0.0015	Dhrs7c
52	6.066	6.084	6.080	6.806	6.758	6.737	67.51	0.44	108.93	2.67	1.614	0.0016	A530016L24Rik
53	3.733	3.366	3.805	4.821	4.520	4.558	12.42	1.95	24.81	2.91	1.998	0.0016	Mgl2
54	3.859	3.395	3.159	2.606	2.451	2.401	11.09	2.87	5.60	0.42	0.505	0.0017	Gpr22
55	2.486	2.637	2.833	5.733	3.803	3.948	6.29	0.76	22.55	22.24	3.587	0.0017	Sla
56	3.815	4.716	4.953	6.190	5.774	5.431	22.54	8.72	55.66	15.06	2.469	0.0018	Fam107a
57	7.314	7.403	7.559	8.443	8.026	8.040	171.91	14.98	287.93	49.73	1.675	0.0018	S100a10
58	3.861	3.961	3.744	5.672	4.671	4.690	14.47	1.08	32.24	14.64	2.227	0.0018	Tm6sf1
59	2.716	2.795	2.917	5.152	3.660	3.927	7.01	0.50	18.98	12.55	2.708	0.0019	Pilra
60	5.221	5.739	5.406	6.987	6.234	6.214	43.87	8.24	89.15	30.08	2.032	0.0021	Man2a1
61	1.569	1.549	1.426	2.478	2.567	2.080	2.86	0.15	5.19	0.90	1.815	0.0021	Herc6
62	1.692	1.804	1.790	2.407	2.717	2.630	3.39	0.14	6.00	0.65	1.769	0.0022	Tbx15
63	4.296	4.584	4.353	5.391	4.925	5.407	21.27	2.32	37.82	6.83	1.778	0.0023	Mfap4
64	1.035	1.183	0.621	0.397	0.245	0.279	1.93	0.38	1.24	0.07	0.642	0.0026	Olfr172
65	7.113	7.185	6.899	8.409	7.748	7.683	133.92	13.53	246.74	74.97	1.842	0.0026	Pmp22
66	4.817	5.147	5.133	7.369	6.038	5.876	32.73	4.08	86.09	59.65	2.631	0.0027	Acer2
67	4.885	4.908	5.347	6.189	5.721	5.825	33.05	6.30	60.20	10.72	1.821	0.0027	S1pr1
68	4.052	4.744	4.826	6.488	5.547	5.394	23.28	6.40	56.09	26.30	2.410	0.0027	Fkbp5
69	4.724	4.545	4.396	5.882	5.044	5.579	23.50	2.70	45.31	13.03	1.928	0.0027	Apod
70	7.910	8.018	8.003	9.731	8.893	8.521	251.92	10.17	529.39	253.16	2.101	0.0028	Mt1
71	3.699	3.925	3.772	4.751	4.412	4.966	13.91	1.13	26.17	5.00	1.881	0.0029	Irf7
72	4.536	5.287	4.230	3.531	3.784	3.300	25.71	10.67	11.62	1.97	0.452	0.0030	Alox5
73	2.998	2.830	3.660	4.679	4.394	4.033	8.96	2.97	20.66	4.62	2.307	0.0030	Cnksr1
74	4.280	4.072	4.624	5.864	5.282	4.980	20.05	3.99	41.51	13.79	2.071	0.0030	Irgm1
75	3.574	3.138	3.430	4.635	3.932	4.803	10.42	1.57	21.96	6.61	2.108	0.0031	Aldh1l1
76	1.825	2.125	1.459	1.066	0.997	1.173	3.49	0.81	2.11	0.13	0.605	0.0032	Plekhhl1
77	1.257	1.222	1.241	2.102	1.660	2.309	2.36	0.03	4.07	0.91	1.721	0.0032	Gm4951
78	3.062	3.146	3.106	4.800	4.029	3.833	8.60	0.25	18.64	7.33	2.167	0.0033	Upp1
79	2.495	2.585	2.654	3.912	3.306	3.257	5.97	0.33	11.25	3.08	1.884	0.0033	Dock10
80	1.026	0.796	0.973	1.688	1.624	2.739	1.91	0.16	4.05	2.04	2.122	0.0035	Serpina1b
81	3.846	4.053	3.577	6.748	4.579	5.315	14.17	2.33	46.77	44.39	3.300	0.0042	C4b
82	3.587	3.535	3.564	4.972	4.314	4.289	11.81	0.21	23.03	6.74	1.950	0.0043	Gm11127
83	4.472	4.780	4.620	5.894	5.382	5.171	24.66	2.65	44.71	12.22	1.813	0.0043	Osmr
84	3.026	3.055	2.506	1.678	2.259	1.926	7.27	1.47	3.88	0.80	0.533	0.0046	Ano4
85	2.181	2.303	2.112	5.322	3.304	3.273	4.59	0.31	15.63	17.45	3.406	0.0046	Mpeg1
86	1.333	1.551	1.612	2.090	2.418	2.288	2.83	0.28	4.81	0.55	1.702	0.0046	Hist2h2bb
87	4.305	4.512	4.551	6.732	5.060	5.666	21.95	1.97	56.47	38.09	2.573	0.0048	Gm11711
88	1.922	1.975	2.081	3.251	2.717	2.831	3.98	0.23	7.64	1.57	1.919	0.0048	Samd9l
89	3.429	3.718	3.906	4.923	4.817	4.249	12.86	2.12	25.33	6.01	1.970	0.0054	Tap1
90	6.928	7.233	7.526	8.381	7.959	7.780	150.01	31.34	263.20	59.07	1.755	0.0055	Tgm2
91	1.356	1.347	1.302	1.772	2.394	2.338	2.52	0.05	4.49	1.01	1.782	0.0058	Mmp13
92	2.878	2.787	3.237	4.315	3.800	3.659	7.82	1.35	15.19	3.88	1.942	0.0060	Iigp1
93	3.571	3.800	3.318	4.882	4.397	4.223	11.82	1.98	22.64	5.67	1.915	0.0060	Pnp
94	3.085	3.537	3.550	5.835	4.337	4.264	10.49	1.83	28.09	21.59	2.678	0.0062	Ccl9
95	6.726	6.646	7.152	7.437	7.563	7.653	114.68	22.82	187.55	14.05	1.635	0.0062	Ctgf
96	2.995	2.714	3.113	3.780	3.537	3.718	7.68	1.07	12.80	1.10	1.668	0.0062	Ifit3
97	4.697	4.848	4.510	3.521	4.124	3.886	25.73	3.01	14.36	2.98	0.558	0.0065	Asb5
98	2.870	3.358	2.927	3.699	4.042	4.176	8.29	1.62	15.69	2.60	1.892	0.0065	Atp10d
99	5.085	5.522	4.915	6.034	5.857	5.926	36.10	8.24	61.34	3.83	1.699	0.0067	Ifi203
100	8.750	8.888	8.821	9.919	9.237	9.414	451.80	21.67	735.90	191.78	1.629	0.0070	Vim
101	5.494	5.562	5.493	6.138	6.010	6.005	45.78	1.26	66.30	3.51	1.448	0.0080	Rnf213
102	5.783	5.667	5.694	4.459	5.049	5.248	52.51	2.25	30.25	8.20	0.576	0.0080	Ccdc141
103	5.398	5.505	5.336	6.502	5.821	6.259	42.61	2.54	73.21	17.16	1.718	0.0080	Trf

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT Avg	WTSD	KO Avg	KOSD	KO/WT	BH	Gene
104	2.576	2.718	2.718	3.687	3.083	3.704	6.37	0.36	11.25	2.59	1.766	0.0082	Serpinb9
105	0.993	0.802	0.918	2.414	1.757	1.327	1.87	0.12	3.56	1.44	1.903	0.0082	Stap1
106	5.681	5.845	5.991	4.661	5.262	5.267	57.25	6.16	33.43	7.58	0.584	0.0088	Kcnj5
107	0.809	0.554	0.428	0.911	2.688	3.095	1.51	0.21	4.70	3.41	3.105	0.0088	Serpina1c
108	1.464	1.384	1.617	1.964	2.147	2.471	2.81	0.23	4.58	0.84	1.631	0.0088	Pion
109	2.960	3.307	3.109	4.459	4.075	3.659	8.73	1.07	16.73	4.69	1.917	0.0092	Map3k6
110	5.257	5.080	5.531	6.751	5.815	6.011	39.11	6.30	73.12	27.61	1.870	0.0094	H2-T23
111	1.383	1.069	0.965	1.771	1.937	1.767	2.20	0.34	3.54	0.24	1.609	0.0095	Fetub
112	3.916	4.398	3.753	3.034	3.359	3.234	16.25	4.00	9.25	1.04	0.569	0.0096	Cacna1g
113	2.692	3.140	3.148	5.617	3.972	3.774	7.96	1.37	21.92	19.88	2.753	0.0096	Cd53
114	0.708	0.834	0.825	0.436	0.400	0.426	1.73	0.08	1.34	0.02	0.775	0.0098	Olfr704
115	4.808	4.523	4.841	6.883	5.352	5.629	26.43	3.11	62.01	42.27	2.346	0.0099	Lcp1
116	1.635	1.728	1.554	3.940	3.040	2.073	3.11	0.19	8.10	5.64	2.601	0.0100	Gm885
117	3.663	3.856	3.827	4.719	4.411	4.536	13.76	0.98	23.51	2.55	1.709	0.0104	Ifi204
118	8.359	8.561	8.478	10.004	9.065	8.976	353.70	24.77	651.79	293.29	1.843	0.0109	Ly6a
119	1.513	1.611	1.529	3.219	2.157	2.220	2.93	0.11	5.78	2.74	1.974	0.0109	Fyb
120	3.954	3.451	4.324	5.192	4.785	4.525	15.03	4.55	28.52	6.88	1.898	0.0113	Stat1
121	9.254	9.347	9.445	10.331	9.865	9.664	652.02	43.31	991.41	247.70	1.521	0.0113	Ly6c1
122	2.820	2.647	2.562	4.460	3.375	3.378	6.39	0.59	13.34	6.71	2.087	0.0113	Trim12a
123	2.214	2.478	2.324	5.118	3.224	3.189	5.06	0.47	14.36	14.72	2.838	0.0116	Tlr13
124	2.707	3.657	3.679	3.822	4.997	5.119	10.18	3.57	25.04	11.18	2.460	0.0118	2810474O19Rik
125	2.734	2.590	2.541	2.999	4.556	5.682	6.16	0.43	21.30	21.97	3.460	0.0118	Apoa1
126	4.841	4.756	4.402	3.748	3.863	4.097	25.40	3.95	14.96	1.89	0.589	0.0118	Kcnd3
127	5.263	5.435	5.366	6.866	5.950	6.019	40.93	2.45	77.61	30.81	1.896	0.0118	Pnp2
128	3.581	3.583	4.644	4.980	4.841	4.936	15.30	7.52	30.26	1.48	1.977	0.0129	Colec11
129	10.395	10.397	10.343	9.903	10.087	9.993	1330.84	28.23	1019.91	65.17	0.766	0.0130	Acaa2
130	4.867	4.853	5.339	6.221	5.688	5.571	32.44	6.60	56.76	14.60	1.750	0.0130	Sgk1
131	6.182	6.278	6.263	7.489	6.699	6.781	75.62	2.68	127.07	42.06	1.680	0.0131	Emp1
132	6.532	7.293	7.490	8.019	7.638	8.414	137.65	45.22	260.28	71.26	1.891	0.0132	Rbp7
133	3.123	2.585	2.360	3.428	3.749	3.518	6.45	1.87	11.83	1.39	1.835	0.0132	4933409K07Rik
134	3.672	3.593	3.383	4.343	4.047	4.391	11.71	1.19	19.17	2.40	1.637	0.0132	Ifi44
135	8.675	8.573	8.743	9.128	9.182	9.129	405.53	23.96	566.68	12.27	1.397	0.0132	Sparcl1
136	3.696	2.896	2.811	3.833	4.605	4.078	8.78	3.31	18.03	5.23	2.053	0.0141	Gm3893
137	4.483	4.526	4.769	6.617	4.939	5.767	24.12	2.66	54.72	34.23	2.269	0.0146	Col14a1
138	0.732	0.762	0.761	1.249	1.243	1.110	1.68	0.02	2.30	0.12	1.365	0.0146	Pcdhb20
139	4.084	3.680	4.037	4.906	4.956	4.382	15.28	2.25	26.87	5.60	1.758	0.0146	Cd274
140	5.279	5.142	5.551	6.219	5.865	5.898	40.06	5.94	63.72	8.98	1.591	0.0146	Slfn5
141	2.570	2.636	2.759	3.571	3.259	3.309	6.30	0.42	10.41	1.25	1.652	0.0146	Cfhr2
142	5.394	5.552	5.437	7.328	6.077	6.083	44.05	2.53	90.25	53.74	2.049	0.0149	Entpd1
143	4.970	5.002	4.946	6.219	5.375	5.678	31.40	0.62	54.10	16.97	1.723	0.0149	Mgst1
144	3.028	3.386	3.009	2.218	2.350	2.587	8.82	1.36	5.22	0.69	0.592	0.0149	Drd2
145	4.150	4.034	3.995	5.224	4.649	4.602	16.68	0.94	28.35	7.34	1.700	0.0149	Ifi271l
146	3.347	3.538	3.347	4.420	3.977	4.165	10.63	0.83	18.22	2.86	1.713	0.0154	Meox1
147	2.639	2.546	2.509	3.776	3.176	3.303	5.92	0.28	10.69	2.49	1.807	0.0160	Itih4
148	4.579	4.544	4.437	3.724	3.928	3.781	22.94	1.16	14.04	1.04	0.612	0.0163	Gja3
149	3.275	3.575	3.308	4.431	3.951	4.257	10.45	1.23	18.54	3.07	1.774	0.0163	2210010C17Rik
150	7.061	6.580	6.997	7.494	7.389	7.594	117.71	20.39	180.05	12.80	1.530	0.0163	Atpif1
151	4.159	3.610	2.987	1.736	2.805	2.754	12.00	4.98	5.40	2.05	0.450	0.0163	B3galt2
152	6.465	6.630	6.881	7.222	7.583	7.145	101.02	14.96	159.45	27.05	1.578	0.0164	Car4
153	1.556	1.709	1.771	2.877	2.860	1.963	3.20	0.24	5.92	1.97	1.851	0.0168	Gcnt1
154	6.027	6.502	6.837	7.552	7.393	6.885	87.75	24.58	155.06	35.83	1.767	0.0168	Xdh
155	2.089	2.413	2.693	3.023	3.177	3.131	5.27	1.11	8.64	0.47	1.638	0.0168	Gm8979
156	3.191	2.918	2.912	5.342	3.607	3.846	8.04	0.92	19.22	15.78	2.391	0.0171	C1s
157	4.279	4.041	4.224	3.448	3.676	3.525	18.14	1.54	11.71	0.95	0.645	0.0171	Fam65b

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT Avg	WTSD	KO Avg	KOSD	KO/WT	BH	Gene
158	5.814	5.766	6.064	6.541	6.453	6.469	58.95	6.73	89.74	2.95	1.522	0.0171	Sik1
159	4.295	4.271	4.468	3.391	3.858	3.830	20.32	1.54	12.94	2.24	0.637	0.0171	Mrps28
160	2.907	2.846	2.980	2.165	1.991	2.468	7.52	0.35	4.62	0.79	0.614	0.0173	Adams3
161	4.773	5.044	5.059	5.544	5.696	5.515	31.10	3.38	48.00	3.29	1.544	0.0174	Rnf144b
162	4.622	4.793	5.104	5.749	5.374	5.440	28.63	5.00	45.92	6.61	1.604	0.0179	Pparg
163	6.471	6.342	6.038	8.334	6.933	6.945	77.91	11.74	169.34	115.41	2.174	0.0179	Laptm5
164	0.720	0.672	0.941	1.144	1.286	1.550	1.71	0.17	2.51	0.37	1.463	0.0179	Olfr119
165	4.748	4.741	5.037	5.665	5.303	5.390	28.68	3.48	43.79	5.91	1.527	0.0179	Slc39a14
166	4.392	4.457	4.550	5.427	4.833	5.374	22.10	1.22	37.04	7.97	1.676	0.0183	Nnmt
167	1.093	1.232	1.176	1.744	1.795	1.600	2.25	0.11	3.28	0.23	1.460	0.0185	Cep192
168	4.815	4.251	4.698	5.512	5.278	5.145	24.05	4.75	39.71	5.22	1.651	0.0185	Cpxm2
169	8.257	8.270	8.418	9.273	8.854	8.625	318.43	20.21	483.58	114.78	1.519	0.0185	Ly6c2
170	2.849	2.811	2.461	3.845	3.257	3.249	6.53	0.93	10.93	2.79	1.674	0.0185	Trim14
171	2.500	2.696	2.763	3.328	3.408	3.148	6.29	0.59	9.81	0.89	1.560	0.0188	Rtp4
172	2.125	1.948	2.253	2.898	2.500	3.160	4.31	0.46	7.22	1.65	1.675	0.0190	BC028528
173	3.784	3.867	3.917	5.204	4.700	4.773	14.48	0.67	29.70	5.92	2.051	0.0191	Trim30a
174	3.610	3.646	3.548	5.485	4.222	4.268	12.14	0.42	25.25	14.91	2.080	0.0192	Cxcl16
175	1.629	1.921	2.015	4.196	2.789	2.393	3.62	0.49	8.73	7.12	2.413	0.0196	Cd52
176	4.205	4.627	4.380	5.137	4.940	4.946	21.17	3.17	32.17	2.57	1.520	0.0203	Bcl2l1
177	2.057	2.212	2.181	4.284	2.646	3.052	4.44	0.25	10.04	7.12	2.261	0.0203	Casp12
178	3.183	3.147	3.132	4.144	3.694	3.802	8.90	0.16	14.72	2.49	1.654	0.0206	Sp110
179	1.183	1.301	0.953	2.014	1.819	1.544	2.21	0.27	3.46	0.56	1.566	0.0207	Casp1
180	2.751	3.258	3.474	4.177	3.639	4.268	8.94	2.22	16.31	3.64	1.823	0.0209	Carhsp1
181	3.362	2.813	3.116	3.227	5.465	6.172	8.56	1.63	31.01	31.44	3.624	0.0209	Serpina1e
182	1.507	1.182	1.297	1.531	2.962	3.703	2.51	0.29	6.64	5.07	2.646	0.0212	Serpina1a
183	2.257	2.121	2.293	2.937	2.930	2.833	4.67	0.29	7.46	0.30	1.598	0.0214	9330175E14Rik
184	2.704	2.663	2.712	3.477	3.249	3.207	6.47	0.12	9.92	1.03	1.534	0.0217	Cd24a
185	6.730	6.891	6.842	8.044	7.235	7.326	113.06	6.39	185.47	62.77	1.640	0.0217	Bnip3
186	2.656	3.111	3.069	3.858	3.646	3.483	7.70	1.28	12.66	1.67	1.644	0.0217	Slc15a3
187	3.254	3.384	2.829	2.165	2.372	2.619	8.91	1.73	5.22	0.83	0.586	0.0221	Abca4
188	1.392	1.322	1.322	2.760	2.285	1.617	2.54	0.07	4.66	1.85	1.834	0.0221	Gbp8
189	6.454	6.596	6.525	8.093	6.947	7.128	92.09	4.52	167.68	82.09	1.821	0.0221	Ifitm3
190	4.525	4.648	4.367	5.688	4.837	5.332	22.83	2.22	39.00	11.48	1.708	0.0221	Oasl2
191	6.667	6.779	6.630	8.741	7.222	7.308	103.39	5.60	216.28	158.28	2.092	0.0231	C1qb
192	4.644	4.944	5.046	6.243	5.389	5.473	29.40	4.14	52.04	18.84	1.770	0.0231	Clic1
193	3.152	3.742	3.140	2.273	2.962	2.417	10.16	2.61	5.86	1.58	0.577	0.0233	Cicn1
194	3.925	4.153	3.897	5.642	4.700	4.400	15.91	1.59	30.15	15.42	1.895	0.0233	Irak3
195	4.742	5.195	5.303	6.195	5.658	5.627	33.83	6.67	56.76	13.47	1.678	0.0233	Adams9
196	1.030	1.192	1.224	2.136	1.644	1.524	2.22	0.16	3.41	0.82	1.536	0.0233	Gm7609
197	4.529	4.481	4.747	6.371	5.166	5.147	24.01	2.42	47.23	27.21	1.967	0.0233	Ifi30
198	3.400	3.292	3.381	4.072	3.900	4.000	10.25	0.40	15.89	0.95	1.551	0.0233	Tlr3
199	2.693	2.891	2.971	4.907	3.484	3.527	7.22	0.70	15.70	10.77	2.175	0.0233	Lrrc52
200	3.531	3.715	3.898	4.753	4.120	4.462	13.13	1.68	21.78	4.79	1.659	0.0236	Clec1a
201	1.172	0.724	0.650	0.763	6.057	5.594	1.80	0.37	17.60	33.45	9.775	0.0243	Mup19
202	1.011	0.643	0.548	0.636	5.879	5.319	1.66	0.30	15.40	29.20	9.260	0.0247	Mup2
203	0.805	0.774	0.791	0.975	1.942	2.756	1.73	0.02	3.71	2.41	2.145	0.0259	Kng1
204	1.817	1.650	1.562	1.211	1.031	1.249	3.20	0.29	2.24	0.18	0.701	0.0261	Slc1a5
205	7.549	7.536	7.417	6.729	7.151	6.958	181.10	9.01	123.32	18.03	0.681	0.0269	Rrad
206	5.300	5.054	4.712	3.611	4.149	4.528	32.49	6.60	17.10	5.42	0.526	0.0270	Efnb3
207	4.647	4.148	4.061	3.318	3.608	3.739	19.50	4.56	11.75	1.72	0.603	0.0270	Frmd6
208	3.397	3.692	3.782	4.438	4.214	4.159	12.33	1.67	19.30	2.03	1.565	0.0270	Plscr1
209	7.951	7.993	8.024	7.367	7.641	7.481	254.12	6.42	180.57	17.37	0.711	0.0278	Acadvl
210	5.126	5.291	5.346	6.652	5.697	5.698	38.17	2.97	64.69	28.11	1.695	0.0278	Hist2h3c1
211	4.477	4.484	4.707	5.678	5.158	4.910	23.52	2.19	38.02	10.94	1.616	0.0278	Hpcal1

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT Avg	WTSD	KO Avg	KOSD	KO/WT	BH	Gene
212	1.741	1.895	1.776	2.606	2.305	2.253	3.49	0.20	5.23	0.72	1.499	0.0278	Ifit2
213	2.211	2.478	2.385	3.123	2.655	3.493	5.13	0.48	8.52	2.48	1.661	0.0278	Xaf1
214	3.067	3.360	3.182	4.532	3.865	3.655	9.21	0.95	16.19	5.60	1.759	0.0278	Lcp2
215	3.557	3.483	3.357	2.488	2.687	3.155	11.05	0.77	6.85	1.71	0.620	0.0278	Med12l
216	5.795	5.965	6.046	7.341	6.452	6.360	61.19	5.35	105.25	44.70	1.720	0.0281	Hist1h3b
217	2.583	2.623	2.696	2.109	1.972	2.166	6.21	0.25	4.24	0.29	0.682	0.0281	Tox3
218	1.986	2.267	1.929	3.223	2.540	2.598	4.17	0.54	6.90	1.97	1.654	0.0282	Pik3cg
219	7.001	7.298	7.420	8.081	7.909	7.590	151.14	22.08	232.27	39.35	1.537	0.0282	Slc43a3
220	5.791	5.912	6.014	7.298	6.401	6.376	59.95	4.64	103.36	42.47	1.724	0.0283	Hist1h3d
221	5.710	5.874	5.927	7.216	6.286	6.281	57.16	4.41	96.62	40.83	1.690	0.0298	Hist1h3g
222	5.704	5.862	5.571	4.753	5.214	5.267	52.43	5.34	33.77	6.30	0.644	0.0299	Fbp2
223	1.339	0.714	0.664	0.742	6.174	5.606	1.87	0.53	18.05	35.91	9.634	0.0299	Mup11
224	7.702	7.827	7.839	8.512	8.182	8.417	221.20	11.46	330.90	38.15	1.496	0.0299	Tpm4
225	1.643	2.394	2.296	1.200	1.495	1.550	4.32	1.15	2.67	0.34	0.617	0.0301	Cdh20
226	2.832	3.165	3.134	4.232	3.622	3.587	8.25	1.02	14.06	3.83	1.706	0.0301	Gcnt2
227	2.925	3.238	3.004	4.405	3.357	3.843	8.32	0.96	14.61	5.53	1.756	0.0301	Hmox1
228	6.498	6.670	6.344	7.241	6.975	7.015	90.77	10.34	134.99	13.82	1.487	0.0301	Lgals9
229	4.630	4.839	4.967	7.461	5.549	5.431	28.09	3.28	70.86	75.77	2.523	0.0309	Ccl6
230	7.644	7.495	6.974	9.142	7.962	7.924	165.51	38.48	324.61	184.13	1.961	0.0312	Lgals3bp
231	4.026	4.020	4.231	5.208	4.454	4.661	17.06	1.45	27.37	7.90	1.604	0.0315	Acsf5
232	6.009	5.929	6.248	6.792	6.538	6.548	66.82	7.91	98.76	10.16	1.478	0.0317	Cd47
233	3.658	3.695	3.656	3.124	3.181	2.991	12.72	0.19	8.57	0.57	0.673	0.0319	Pla2g4e
234	5.070	4.934	4.581	5.743	5.392	5.461	29.07	4.94	46.27	6.18	1.592	0.0321	Isg20
235	1.537	0.729	0.796	0.801	6.406	5.938	2.03	0.70	20.85	42.82	10.275	0.0324	Gm2083 // Mup7
236	0.501	0.489	0.339	0.837	0.950	0.661	1.36	0.08	1.76	0.18	1.295	0.0325	Olfr471
237	1.547	1.244	1.562	2.636	1.841	2.056	2.73	0.33	4.52	1.38	1.655	0.0331	Ccl3
238	5.094	5.173	5.394	6.083	5.750	5.600	37.28	4.12	56.16	9.96	1.506	0.0344	Galntf2
239	5.417	5.189	5.218	6.420	5.603	5.864	38.71	3.40	62.36	19.22	1.611	0.0349	Gpx1
240	5.596	5.779	5.782	7.142	6.170	6.199	52.68	3.80	90.74	39.54	1.722	0.0349	Hist2h3b
241	6.344	6.374	6.472	7.477	6.862	6.748	84.25	3.96	130.60	38.54	1.550	0.0349	Rhoj
242	1.359	1.781	1.407	3.472	2.278	1.917	2.86	0.48	5.88	3.95	2.056	0.0349	Cysltr1
243	1.267	1.172	1.283	1.410	2.224	2.854	2.36	0.10	4.48	2.29	1.894	0.0351	Ambp
244	5.642	5.210	5.490	6.100	5.879	5.978	43.64	6.52	63.37	4.88	1.452	0.0351	Arrdc3
245	3.723	3.499	4.373	4.688	4.807	4.496	14.57	4.98	25.34	2.73	1.739	0.0351	AW112010
246	2.786	3.006	2.960	3.834	3.383	3.397	7.56	0.60	11.61	2.18	1.537	0.0351	BC013712
247	3.131	3.360	3.233	2.576	2.824	2.560	9.46	0.76	6.29	0.66	0.665	0.0351	Clvs1
248	6.658	6.680	6.845	7.569	7.068	7.194	105.99	7.66	155.10	29.25	1.463	0.0351	Ctsl
249	5.845	5.983	6.044	7.349	6.445	6.336	62.12	4.35	104.67	45.77	1.685	0.0351	Hist1h3c
250	4.247	4.624	4.160	3.304	3.751	3.890	20.31	3.64	12.54	2.56	0.618	0.0351	Inpp5j
251	4.039	4.077	3.930	3.530	3.273	3.519	16.17	0.85	10.86	1.06	0.672	0.0351	Slc16a7
252	3.710	3.388	3.750	5.832	4.351	4.484	12.26	1.63	29.63	20.56	2.417	0.0351	Vcam1
253	4.976	4.783	5.185	5.533	5.445	5.695	31.58	4.43	47.10	4.21	1.491	0.0353	Pdgfd
254	2.158	2.008	2.174	2.786	2.469	2.745	4.33	0.27	6.35	0.74	1.468	0.0354	Pkhd1l1
255	5.011	4.491	5.091	5.651	5.267	5.565	29.13	6.23	45.08	6.12	1.548	0.0370	Aldh1b1
256	4.784	4.404	4.552	5.630	5.267	4.914	23.92	3.23	38.59	9.73	1.614	0.0370	Gm3579
257	0.967	0.820	1.007	2.532	1.256	1.505	1.91	0.13	3.40	1.84	1.782	0.0370	Trim30d
258	0.688	0.872	0.839	2.080	1.285	1.085	1.74	0.12	2.80	1.14	1.606	0.0374	Ptpn22
259	7.530	7.301	7.309	7.942	7.709	7.946	166.57	15.42	233.21	21.35	1.400	0.0375	Emcn
260	3.831	3.587	3.807	3.056	3.254	3.178	13.38	1.22	8.96	0.61	0.669	0.0376	ErbB3
261	4.052	4.187	3.981	4.776	4.657	4.566	16.83	1.24	25.39	1.87	1.509	0.0387	Agt
262	3.822	4.028	3.818	5.571	4.339	4.465	14.82	1.27	27.70	15.25	1.869	0.0391	Unc93b1
263	10.008	9.926	10.369	10.380	10.544	10.476	1098.23	187.71	1415.12	80.60	1.289	0.0391	Ankrd1
264	1.045	0.739	0.884	2.193	1.472	1.166	1.85	0.20	3.05	1.22	1.649	0.0391	Cd3g
265	5.744	5.901	5.954	7.243	6.313	6.301	58.33	4.35	98.28	41.74	1.685	0.0391	Hist1h3h

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT Avg	WTSD	KO Avg	KOSD	KO/WT	BH	Gene
266	5.739	5.929	5.981	7.265	6.332	6.325	59.02	5.11	99.80	42.43	1.691	0.0391	Hist1h3i
267	2.942	2.511	2.576	3.560	3.369	3.185	6.39	1.08	10.35	1.35	1.619	0.0391	Mgat4a
268	7.679	7.760	7.854	8.614	8.201	8.197	217.42	13.24	323.41	56.52	1.487	0.0391	Picalm
269	3.424	3.465	3.263	6.092	3.981	4.126	10.44	0.76	26.60	29.80	2.548	0.0391	Tmem176a
270	1.965	1.574	1.481	2.763	2.186	2.160	3.19	0.60	5.17	1.32	1.620	0.0391	A430084P05Rik
271	3.243	3.618	3.521	5.337	4.220	3.790	11.01	1.45	21.84	14.17	1.984	0.0402	Rassf4
272	2.687	2.557	2.699	3.689	2.921	3.517	6.27	0.34	10.38	2.75	1.657	0.0405	Gsta3
273	4.563	4.887	4.690	6.755	5.362	5.133	26.23	3.01	53.83	40.47	2.052	0.0415	Cybb
274	4.610	4.387	4.388	5.407	5.066	4.838	22.04	2.02	34.38	7.02	1.560	0.0415	Samhd1
275	5.761	5.912	5.957	7.268	6.314	6.321	58.76	4.11	99.37	42.95	1.691	0.0417	Hist1h3a // Hist1h3i // Hist1h3h // Hist1h3g
276	6.240	6.165	5.800	4.680	5.532	5.628	67.10	10.52	38.85	12.93	0.579	0.0417	Mrgprh
277	5.125	4.849	4.953	5.439	5.426	5.490	31.46	3.08	43.77	1.04	1.391	0.0418	Anxa3
278	0.652	0.820	0.739	2.114	0.966	1.332	1.67	0.10	2.77	1.24	1.663	0.0420	Ccr1
279	1.883	2.326	2.107	3.015	2.805	2.450	4.30	0.66	6.76	1.31	1.571	0.0422	Arhgef12
280	2.975	3.825	4.161	4.407	4.601	4.424	12.59	5.07	22.27	1.70	1.770	0.0422	Gm129
281	2.621	2.694	2.875	4.445	3.686	3.002	6.64	0.61	13.10	6.99	1.974	0.0422	Ptpcr
282	9.795	10.070	10.270	10.713	10.275	10.411	1056.44	173.67	1415.04	227.00	1.339	0.0422	Snord49b
283	4.813	4.788	5.013	6.117	5.287	5.386	29.27	2.57	48.38	16.78	1.653	0.0427	Sulf1
284	1.704	1.806	1.499	2.783	2.316	2.134	3.18	0.34	5.32	1.30	1.671	0.0429	Cd180
285	2.161	2.682	2.172	3.204	2.735	3.148	5.06	1.11	8.16	1.39	1.614	0.0430	5430435G22Rik
286	5.903	5.228	5.931	6.678	6.130	6.297	51.53	13.26	82.61	16.79	1.603	0.0430	Erff1
287	5.526	3.915	4.276	2.920	3.541	3.790	23.79	16.80	10.68	3.18	0.449	0.0430	Pla2g2d
288	2.236	2.775	3.018	4.173	3.342	3.174	6.39	1.71	11.82	4.91	1.849	0.0430	Slc41a2
289	1.001	0.998	0.982	3.513	1.508	1.674	1.99	0.01	4.70	4.85	2.359	0.0431	Ccl8
290	7.418	6.861	7.366	6.917	6.400	5.481	148.58	30.00	76.97	38.11	0.518	0.0433	Cyfp2
291	5.991	5.974	5.843	6.690	6.304	6.340	61.21	3.38	87.10	13.43	1.423	0.0440	Sri
292	0.796	0.468	0.525	0.290	5.084	4.390	1.51	0.19	9.54	16.46	6.313	0.0443	Mup16
293	6.373	6.186	6.553	6.801	6.996	6.848	82.74	10.53	117.91	8.44	1.425	0.0443	Ugp2
294	5.086	5.065	5.157	5.306	5.744	5.840	34.37	1.16	49.53	9.36	1.441	0.0447	2810416G20Rik
295	5.209	5.210	5.273	6.935	5.640	5.711	37.55	0.96	68.37	41.15	1.821	0.0447	Ctsc
296	3.985	4.223	4.247	3.832	3.410	3.412	17.77	1.73	11.72	2.08	0.660	0.0447	Gm4947
297	4.330	4.700	4.112	3.717	4.021	3.259	20.83	4.44	12.69	3.33	0.609	0.0447	Hdh3
298	5.750	5.937	6.058	7.318	6.387	6.328	60.34	6.43	102.40	44.83	1.697	0.0447	Hist1h3e
299	0.629	0.587	0.758	0.779	1.229	1.472	1.58	0.10	2.23	0.53	1.416	0.0447	Mug1
300	0.979	0.582	0.467	0.580	2.882	3.312	1.60	0.31	4.78	4.33	2.994	0.0447	Mup20
301	1.472	1.253	1.282	2.704	1.594	1.964	2.52	0.21	4.25	1.82	1.684	0.0447	Olf1396
302	4.110	3.892	3.933	4.774	4.527	4.452	15.76	1.29	23.99	2.89	1.522	0.0447	Sfxn1
303	4.576	4.732	4.718	6.627	5.468	4.983	25.55	1.50	51.71	35.72	2.024	0.0447	Tyrbp
304	5.472	5.525	5.416	6.270	5.792	5.903	44.35	1.67	63.49	11.50	1.431	0.0447	Uck2
305	1.079	0.893	0.919	1.525	1.185	1.753	1.95	0.14	2.80	0.55	1.438	0.0447	Gabrg3
306	4.549	4.280	4.428	4.960	4.913	4.872	21.39	1.99	30.17	0.92	1.410	0.0447	Trim25
307	2.359	2.454	2.091	4.798	3.155	2.685	4.93	0.63	11.68	11.70	2.369	0.0448	Clec4a1
308	4.144	4.288	4.670	5.555	4.883	4.836	20.64	4.06	34.09	10.39	1.652	0.0450	Lyve1
309	0.886	0.751	0.797	1.237	1.304	1.085	1.76	0.08	2.31	0.18	1.317	0.0460	Pilrb2
310	7.224	7.162	7.030	6.393	6.717	6.735	140.91	9.56	98.00	12.62	0.695	0.0462	Neo1
311	4.207	4.280	3.923	3.086	3.621	3.757	17.59	2.24	11.22	2.63	0.638	0.0462	Nkain1
312	2.132	2.286	2.117	3.168	2.561	2.769	4.53	0.30	7.13	1.59	1.574	0.0467	Oas1g
313	4.699	4.784	4.882	6.687	5.238	5.326	27.63	1.76	53.83	37.04	1.948	0.0469	Gfpt2
314	5.670	5.458	5.734	6.016	6.095	6.006	49.21	4.84	65.75	2.24	1.336	0.0475	Nt5c2
315	5.805	5.891	6.242	7.618	6.412	6.419	63.09	10.55	112.69	64.13	1.786	0.0476	Cp
316	2.146	2.002	2.306	3.341	2.982	2.445	4.44	0.47	7.58	2.34	1.707	0.0476	Gbp3

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT Avg	WTSD	KO Avg	KOSD	KO/WT	BH	Gene
317	0.878	0.570	0.508	0.909	1.144	1.374	1.57	0.22	2.21	0.36	1.405	0.0480	Cml2
318	4.219	4.290	4.548	4.990	5.187	4.612	20.43	2.53	30.47	6.04	1.492	0.0480	Fgf18
319	1.156	1.840	1.717	2.469	1.921	3.838	2.97	0.71	6.69	5.63	2.252	0.0482	Serpina3k
320	5.614	5.587	5.649	6.464	5.995	6.032	49.07	1.06	71.69	13.71	1.461	0.0483	Fmo1
321	2.119	2.685	2.627	5.361	3.101	3.194	5.57	1.14	14.78	18.62	2.655	0.0483	Ms4a6c
322	1.191	1.492	1.493	1.014	1.047	0.686	2.62	0.31	1.89	0.25	0.719	0.0484	Avpr1b
323	5.174	5.477	5.470	3.910	4.672	5.053	41.46	4.80	23.34	9.11	0.563	0.0484	Igf2
324	3.706	3.934	3.634	4.765	4.330	4.126	13.53	1.51	21.22	5.03	1.568	0.0486	Acot9
325	3.620	3.143	4.013	4.186	4.269	4.310	12.06	3.66	19.09	0.83	1.584	0.0486	Gbp7
326	4.593	4.619	4.519	6.642	5.124	5.059	23.87	0.85	48.79	37.99	2.044	0.0487	Il4ra
327	5.570	5.666	5.747	7.105	6.051	6.070	50.60	3.10	84.94	40.95	1.679	0.0488	Anxa2
328	7.728	7.581	7.584	6.893	7.246	7.205	198.26	11.77	138.60	17.90	0.699	0.0488	Pink1
329	3.931	3.932	3.859	6.491	4.555	4.455	15.01	0.43	35.93	38.83	2.394	0.0488	Fcer1g
330	4.279	4.624	4.312	3.604	3.997	3.993	21.18	2.91	14.57	2.18	0.688	0.0488	Whrn
331	3.978	4.432	4.222	2.886	3.756	3.745	18.52	2.92	11.02	3.50	0.595	0.0489	Casq1
332	0.670	0.824	0.795	0.775	1.864	2.336	1.70	0.09	3.16	1.68	1.860	0.0489	Fabp1
333	0.875	0.889	1.013	0.581	0.369	0.657	1.90	0.10	1.45	0.15	0.763	0.0489	Olf47
334	2.075	2.458	2.453	3.407	2.875	2.785	5.02	0.73	8.13	2.03	1.618	0.0489	Slc10a6
335	6.689	6.665	6.331	7.428	7.355	6.851	94.46	12.63	148.18	30.63	1.569	0.0489	Tinagl1
336	4.963	4.980	4.717	7.001	5.416	5.322	29.58	2.93	60.25	50.08	2.036	0.0490	Il2rg
337	3.123	2.953	2.966	4.362	3.415	3.465	8.08	0.54	13.43	5.61	1.662	0.0493	Rai14
338	2.634	2.478	2.455	4.074	3.017	3.014	5.74	0.39	10.33	5.06	1.798	0.0494	Il1r1
339	2.401	2.231	2.623	3.924	2.937	2.928	5.35	0.74	9.60	4.36	1.796	0.0495	Coro1a
340	1.841	1.898	1.578	1.639	3.946	4.553	3.42	0.39	10.41	10.25	3.047	0.0496	Mug-ps1
341	5.079	5.525	5.356	4.203	4.871	4.849	39.94	6.15	24.95	6.14	0.625	0.0497	ErbB4

Appendix 2(c): Liver microarray. Microarray analysis of differentially expressed genes in livers of KO and WT mice. Pink cells represent downregulated gene expression; green cells represent upregulated gene expression. Ordered by BH.

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT avg	WTsd	KO avg	KOsd	KO/WT	BH	Gene Symbol
1	6.352	6.109	5.907	9.572	9.751	9.204	70.24	10.89	737.60	137.54	10.502	5.92E-12	Ccl5
2	8.162	8.154	8.248	5.202	5.300	5.163	291.80	10.66	37.35	1.84	0.128	5.92E-12	Irf2bp2
3	9.162	8.970	8.957	10.907	11.075	10.462	523.72	42.66	1829.30	381.33	3.493	8.05E-09	Cd74
4	4.131	4.261	4.257	7.327	8.647	7.027	18.60	0.94	230.63	148.30	12.396	1.55E-08	Ccl3
5	5.020	4.936	4.705	6.697	7.040	6.780	29.71	3.28	115.07	14.61	3.873	1.55E-08	Fgl2
6	4.877	4.941	4.294	7.271	7.986	7.234	26.57	6.06	186.15	58.33	7.006	1.55E-08	Nkg7
7	8.660	8.323	8.770	10.323	10.798	10.141	387.08	60.10	1396.93	341.03	3.609	2.33E-08	H2-Aa
8	5.590	5.530	5.801	7.743	7.894	8.536	50.03	5.04	274.34	84.59	5.484	2.33E-08	Lpl
9	6.095	6.235	5.929	8.422	8.223	7.863	68.20	7.20	291.52	55.49	4.274	2.67E-08	Lsp1
10	5.843	5.964	5.626	7.973	8.231	7.908	56.41	6.58	263.95	32.06	4.679	2.67E-08	Zbp1
11	4.892	4.431	4.708	6.338	6.903	6.658	25.80	4.08	100.50	19.40	3.895	5.75E-08	Ifi205
12	6.674	6.540	6.264	9.063	8.591	8.200	90.68	12.79	404.80	121.50	4.464	5.91E-08	Gm11711
13	8.428	7.981	8.355	10.219	10.794	9.974	308.16	48.78	1324.33	401.43	4.298	5.91E-08	H2-Ab1
14	6.222	6.269	6.313	8.535	8.464	7.892	77.08	2.43	320.56	72.45	4.159	7.84E-08	Cd52
15	7.927	7.160	7.345	9.293	10.282	9.945	183.00	53.22	952.74	310.11	5.206	7.84E-08	Cxcl9
16	6.284	7.298	7.108	4.364	4.928	4.474	124.40	41.42	24.42	5.27	0.196	7.84E-08	Gna14
17	5.622	6.200	5.428	8.705	8.396	7.822	55.26	16.09	326.79	95.87	5.914	7.84E-08	Vcam1
18	9.279	9.632	8.420	11.642	11.295	11.100	585.72	227.53	2634.40	511.70	4.498	9.02E-08	Gm3579
19	5.332	5.661	5.318	7.930	7.756	7.113	43.59	6.07	199.47	54.64	4.576	9.24E-08	Il2rg
20	4.045	3.932	4.029	5.680	6.284	5.761	16.03	0.67	61.13	14.60	3.813	9.26E-08	Slamf7
21	6.827	6.839	6.871	8.829	8.557	8.345	115.02	1.79	385.44	65.26	3.351	1.21E-07	Al607873
22	4.389	4.154	4.203	6.053	6.177	5.744	19.06	1.67	64.10	9.57	3.364	1.27E-07	Bcl2a1a
23	5.564	5.601	5.365	8.611	7.275	8.157	45.68	3.93	277.10	118.28	6.066	1.36E-07	Tuba8
24	5.091	5.401	5.228	8.053	7.505	6.938	37.94	4.11	189.95	71.80	5.007	1.86E-07	Plek
25	8.361	8.040	8.260	9.908	10.431	9.645	299.51	33.36	1047.32	299.76	3.497	1.88E-07	H2-Eb1
26	4.544	4.304	4.601	6.224	6.344	5.872	22.45	2.38	71.52	11.69	3.185	2.23E-07	Bcl2a1b
27	4.996	5.420	5.274	7.515	7.240	6.769	37.80	5.50	147.74	37.06	3.909	2.23E-07	Clec12a
28	7.872	7.564	7.581	10.048	9.463	9.237	204.99	25.41	789.28	238.58	3.850	2.38E-07	Gas6
29	6.133	6.268	6.185	4.168	4.193	5.012	73.31	3.48	22.85	8.17	0.312	2.41E-07	Hsd3b4
30	5.132	5.168	4.814	7.250	7.038	6.414	33.05	4.28	122.97	34.27	3.721	2.56E-07	Itga4
31	5.221	5.223	5.008	7.094	6.778	6.459	35.61	2.98	111.44	24.36	3.129	2.77E-07	Cd7
32	4.714	4.413	4.675	6.249	6.416	5.959	24.37	2.67	74.56	11.66	3.059	2.94E-07	Bcl2a1d
33	3.956	4.108	3.955	5.395	5.597	5.437	16.09	1.00	44.60	3.35	2.772	2.94E-07	Itgax
34	6.692	6.918	6.286	9.082	8.592	8.164	100.78	21.58	404.92	128.72	4.018	3.18E-07	Entpd1
35	8.093	8.101	8.587	10.205	10.196	9.665	310.77	63.98	1054.83	210.72	3.394	3.37E-07	Vim
36	7.205	7.760	7.030	5.488	5.228	5.923	164.97	45.62	47.68	11.84	0.289	3.53E-07	Extl1
37	6.747	6.698	6.648	8.647	9.339	8.220	103.85	3.53	448.88	179.57	4.323	3.54E-07	H2-DMA
38	5.605	5.758	5.746	7.129	7.286	7.053	52.14	3.02	142.98	11.94	2.742	3.54E-07	Ifi204
39	6.087	5.553	5.766	7.673	9.421	8.602	56.45	10.66	426.06	242.80	7.548	4.50E-07	Gm12185
40	5.958	5.655	5.539	7.593	9.503	8.583	53.02	8.16	434.04	269.77	8.186	5.32E-07	Tgtp1
41	4.144	4.420	3.798	6.221	6.078	5.561	17.66	3.75	63.12	14.21	3.573	5.56E-07	Ms4a6b
42	8.093	9.646	7.674	11.800	11.374	11.069	426.12	326.60	2789.60	718.00	6.546	5.86E-07	Mt1
43	5.726	6.013	5.622	8.476	8.027	7.275	55.60	8.01	257.24	100.65	4.627	5.95E-07	Tm6sf1
44	5.380	6.342	6.226	9.158	8.133	8.061	65.88	21.22	372.98	171.83	5.662	6.85E-07	Slc16a5
45	5.306	5.857	5.380	7.922	7.611	6.919	46.39	10.08	186.33	61.27	4.016	7.45E-07	Cd72
46	8.454	8.498	8.724	10.772	10.347	9.705	378.38	38.94	1295.20	457.07	3.423	7.51E-07	Srgn
47	4.780	4.968	4.655	6.039	6.951	6.896	27.99	3.09	102.87	32.23	3.675	7.93E-07	Gm8979
48	4.098	4.282	4.370	5.678	6.490	5.765	19.08	1.80	65.15	21.47	3.414	8.34E-07	Cd3g
49	5.212	5.098	4.977	7.226	6.989	6.351	34.27	2.78	119.46	34.68	3.486	9.30E-07	Myof

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT Avg	WTSD	KO Avg	KOSD	KO/WT	BH	Gene
50	6.217	6.527	5.505	8.124	8.157	7.673	70.67	23.62	256.16	45.20	3.625	9.46E-07	Btg2
51	9.703	9.445	9.261	11.605	10.911	10.622	714.68	110.92	2205.20	806.23	3.086	1.11E-06	Steap4
52	5.807	5.926	5.764	7.394	7.727	7.088	57.04	3.37	172.05	38.01	3.016	1.12E-06	Cd180
53	5.457	4.807	4.693	7.164	6.994	6.408	32.59	9.87	118.59	30.27	3.639	1.12E-06	Gbp1
54	4.862	5.062	4.931	6.649	6.507	6.115	31.01	2.21	86.88	15.92	2.802	1.13E-06	Parvg
55	6.746	6.748	6.443	7.936	8.746	8.622	100.60	11.78	356.13	97.91	3.540	1.16E-06	Gvin1
56	4.761	4.927	4.355	8.201	7.241	6.425	26.00	5.07	177.18	106.61	6.815	1.21E-06	Ms4a6d
57	5.071	5.179	5.259	7.019	7.540	6.573	36.05	2.35	137.00	45.92	3.801	1.22E-06	H2-DMb2
58	5.364	5.394	5.364	7.002	7.020	6.515	41.47	0.49	116.49	21.69	2.809	1.33E-06	Tbc1d9
59	4.976	5.233	4.907	7.801	7.257	6.547	33.03	4.04	156.49	64.85	4.738	1.33E-06	Tlr13
60	5.336	5.277	5.133	6.514	6.935	6.442	38.09	2.72	100.24	19.28	2.632	1.37E-06	Tigit
61	8.054	8.018	8.103	10.424	9.869	9.260	266.67	7.91	974.06	381.74	3.653	1.43E-06	Fxyd5
62	5.176	5.453	5.272	7.291	6.970	6.505	39.53	3.90	124.27	32.90	3.144	1.55E-06	Dock10
63	3.899	3.602	3.405	5.611	5.297	4.987	12.55	2.19	39.96	8.60	3.184	1.55E-06	Ptpn22
64	5.521	5.938	5.503	8.093	7.643	7.034	50.87	9.06	201.35	71.02	3.958	1.55E-06	Ptprc
65	5.279	5.067	4.928	6.558	7.518	6.816	34.27	4.25	130.08	47.04	3.796	1.70E-06	Gbp3
66	2.621	1.730	2.433	9.347	7.776	5.229	4.96	1.47	302.62	315.19	61.060	1.76E-06	Ighm
67	4.862	5.442	5.187	8.135	7.143	6.759	36.33	7.20	176.91	91.71	4.869	1.80E-06	Clec4a3
68	6.220	6.181	5.944	7.598	7.894	7.319	69.54	6.98	197.10	39.15	2.834	1.81E-06	Irf8
69	6.371	6.559	6.482	8.031	8.189	7.524	88.80	5.77	245.77	55.54	2.768	1.81E-06	Naaa
70	9.331	9.056	8.838	10.448	10.208	10.236	544.60	93.72	1261.88	117.29	2.317	1.93E-06	Slc41a2
71	4.325	4.412	4.610	6.608	5.712	6.805	21.92	2.25	87.25	30.99	3.981	2.00E-06	Gldn
72	6.074	6.007	5.630	9.579	8.381	7.645	60.40	9.53	432.82	295.27	7.166	2.07E-06	Fcgr4
73	5.426	5.750	5.247	7.469	7.284	6.905	44.94	8.10	150.99	29.01	3.360	2.08E-06	A430084P05Rik
74	6.955	7.228	6.734	9.588	9.055	8.321	126.80	21.84	540.50	225.08	4.263	2.20E-06	Ctss
75	8.258	8.793	8.295	10.514	10.210	9.602	354.62	77.24	1141.35	344.77	3.219	2.20E-06	Laptn5
76	4.126	4.043	4.431	5.539	6.086	5.513	18.51	2.70	53.36	12.63	2.883	2.23E-06	Gzmk
77	5.504	5.715	5.482	8.375	7.431	7.054	47.52	4.34	212.48	105.40	4.471	2.23E-06	Sla
78	5.038	5.492	5.072	8.414	7.404	6.781	37.16	6.81	206.84	120.00	5.566	2.25E-06	Ms4a6c
79	6.087	6.712	6.335	9.249	8.394	7.908	84.51	18.71	394.96	190.91	4.674	2.26E-06	Ear2
80	5.281	5.325	5.386	6.959	7.598	6.665	40.25	1.48	139.87	48.04	3.475	2.28E-06	Cd274
81	6.051	6.267	5.729	7.982	7.387	7.446	65.46	12.01	198.19	47.49	3.028	2.70E-06	Slc37a1
82	3.408	3.438	3.610	5.407	4.829	4.639	11.22	0.86	31.92	9.26	2.844	2.71E-06	Gzma
83	4.181	4.154	4.243	5.465	5.907	5.541	18.29	0.58	50.25	8.55	2.747	3.15E-06	Havcr2
84	5.313	5.422	4.807	6.924	6.547	6.632	36.88	7.85	104.71	14.75	2.839	3.24E-06	Atp10d
85	3.071	3.324	2.940	4.489	4.569	4.451	8.70	1.20	22.69	0.96	2.609	3.32E-06	Stat4
86	6.602	7.016	6.596	9.410	8.727	8.000	107.78	18.78	453.32	213.72	4.206	3.35E-06	Cd53
87	4.528	4.522	4.129	7.321	6.484	5.832	21.18	3.19	102.14	52.64	4.822	3.35E-06	Clec4a1
88	5.515	5.056	5.262	6.579	7.683	7.284	39.12	6.26	152.32	55.03	3.894	3.45E-06	Gbp8
89	4.930	5.128	4.761	7.165	6.716	6.009	30.86	3.94	104.31	39.55	3.380	3.66E-06	Glipr1
90	6.758	6.850	6.798	8.261	8.086	7.947	111.61	3.56	275.14	30.14	2.465	3.87E-06	Crip1
91	4.502	4.855	4.233	5.978	6.209	5.803	23.46	5.12	64.28	9.15	2.740	4.17E-06	Cd86
92	4.055	4.151	4.138	5.795	5.551	5.032	17.33	0.62	45.05	11.52	2.599	4.36E-06	Dock11
93	5.055	5.601	5.341	7.288	6.879	6.479	40.77	7.65	121.07	33.69	2.969	4.51E-06	Mkl
94	7.080	7.847	7.101	9.858	9.178	8.672	167.60	54.21	638.32	264.92	3.809	4.51E-06	Mpeg1
95	7.273	7.433	7.318	8.914	8.868	8.280	162.36	9.42	420.16	94.90	2.588	4.51E-06	Samhd1
96	5.297	5.187	5.007	6.342	7.019	6.375	35.96	3.60	97.94	27.51	2.723	4.57E-06	Gm8995
97	9.180	9.177	8.987	10.381	10.292	9.962	555.44	41.62	1195.17	175.70	2.152	4.60E-06	AW112010
98	4.832	5.122	4.480	6.033	6.348	6.164	28.54	6.25	72.87	8.05	2.553	4.87E-06	Il2rb
99	5.720	6.314	5.761	8.322	7.839	7.140	62.15	15.08	230.04	89.54	3.701	4.94E-06	BC013712
100	6.308	6.109	6.101	7.415	8.012	7.342	72.29	6.00	197.02	53.09	2.725	5.00E-06	Ccl19
101	6.072	6.228	6.104	8.028	7.557	7.164	70.36	4.07	197.60	59.37	2.809	5.34E-06	Hcls1
102	6.808	7.264	6.763	9.226	8.714	8.104	124.80	25.06	431.34	162.22	3.456	5.36E-06	Slc11a1
103	5.838	6.142	5.749	7.760	7.313	6.995	60.53	8.91	167.77	45.23	2.772	5.46E-06	Inpp5d

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT Avg	WTSD	KO Avg	KOSD	KO/WT	BH	Gene
104	4.899	4.971	4.777	6.015	6.760	6.162	29.54	1.99	81.56	23.51	2.761	5.51E-06	Gbp9
105	5.817	5.753	5.838	7.517	7.119	6.752	55.83	1.70	143.31	37.86	2.567	5.54E-06	Fam49a
106	5.573	5.710	5.169	4.470	4.083	4.171	45.31	8.43	19.04	2.75	0.420	5.56E-06	Slc13a2
107	4.416	4.565	5.511	6.621	7.113	6.340	30.21	13.39	105.95	29.44	3.507	5.77E-06	4933409K07Rik
108	6.376	6.605	6.452	9.069	8.036	7.863	89.30	7.30	344.14	167.77	3.854	6.10E-06	Pilra
109	7.985	8.098	7.964	10.118	9.307	9.130	259.00	13.08	768.32	299.33	2.966	6.15E-06	Fabp7
110	4.378	4.391	4.294	5.749	5.516	5.441	20.46	0.74	47.66	5.44	2.329	6.15E-06	Fam111a
111	5.866	6.253	5.935	8.144	7.772	7.212	65.26	9.65	216.57	67.31	3.319	6.15E-06	Selp1g
112	3.408	3.710	4.058	6.079	5.692	5.000	13.45	3.03	50.44	17.84	3.749	6.15E-06	Timp1
113	5.961	5.782	6.182	7.489	7.555	7.070	63.30	8.83	167.34	28.89	2.643	6.19E-06	Cxcl16
114	5.033	5.290	5.009	6.560	6.741	6.039	34.68	3.85	89.02	21.13	2.567	7.08E-06	Hk3
115	6.611	7.328	6.797	9.493	8.439	8.390	123.21	33.10	467.68	219.10	3.796	7.08E-06	Ly86
116	8.077	8.769	8.329	10.524	9.873	9.581	342.63	85.08	1058.62	368.53	3.090	7.09E-06	C1qc
117	7.226	7.576	6.768	8.867	8.304	8.759	149.85	40.89	405.38	79.14	2.705	7.09E-06	Rbp1
118	7.153	7.600	7.280	9.288	8.709	8.418	163.91	26.92	461.91	146.52	2.818	7.10E-06	Cd68
119	5.834	5.583	5.399	6.928	9.045	8.406	49.05	7.49	329.74	203.43	6.722	7.10E-06	Gbp11
120	4.865	4.948	4.684	5.988	6.163	5.893	28.57	2.62	64.85	6.21	2.270	7.14E-06	Tbxas1
121	9.583	9.801	9.862	10.901	10.522	10.643	863.15	85.61	1660.57	226.67	1.924	7.36E-06	Actg1
122	5.429	5.577	5.756	7.537	7.350	6.580	48.28	5.49	148.15	46.85	3.069	7.59E-06	Tmem173
123	9.075	7.304	7.639	10.275	10.256	9.984	298.90	209.25	1157.98	125.99	3.874	7.83E-06	Igfbp1
124	10.633	10.745	10.740	11.586	11.439	11.245	1671.42	72.15	2760.03	324.11	1.651	7.97E-06	Krt8
125	4.810	5.174	4.372	6.909	6.669	5.992	28.29	7.71	95.21	28.83	3.366	7.98E-06	Clec7a
126	10.495	10.420	10.845	8.976	9.664	9.385	1550.75	252.32	661.04	153.95	0.426	7.98E-06	Pklr
127	6.015	6.199	6.032	8.148	7.725	7.104	67.86	4.88	210.91	72.98	3.108	8.18E-06	Iqgap1
128	5.785	6.079	5.664	7.726	6.986	7.096	57.82	8.76	158.45	46.45	2.740	8.18E-06	Lilra5
129	5.913	5.856	5.861	7.421	7.189	6.755	58.76	1.28	141.78	31.87	2.413	8.50E-06	Plekho2
130	6.068	6.561	5.877	7.448	7.906	7.437	73.42	18.65	195.89	38.07	2.668	8.69E-06	Ppl
131	7.839	8.133	7.879	10.085	9.425	8.972	248.34	28.20	758.73	298.53	3.055	9.01E-06	Ifi30
132	5.307	5.319	5.290	7.053	6.555	6.266	39.54	0.41	101.25	28.62	2.561	9.10E-06	Ly9
133	6.605	7.016	6.455	9.028	8.419	7.851	104.83	21.83	365.03	146.82	3.482	9.10E-06	Pld4
134	6.239	6.504	6.701	4.809	5.447	5.203	90.11	14.27	36.17	7.82	0.401	9.11E-06	Cd59b
135	7.170	7.425	7.160	9.389	8.724	8.289	152.95	16.35	468.57	183.10	3.063	9.17E-06	Tyrobp
136	5.462	5.740	5.369	7.712	7.191	6.740	46.29	6.36	154.27	51.89	3.333	9.28E-06	Fyb
137	6.437	6.419	5.862	7.778	7.464	7.501	76.79	16.13	192.39	23.58	2.505	9.92E-06	Snx10
138	3.503	4.026	3.406	6.261	5.596	4.846	12.75	3.09	51.28	24.11	4.023	1.03E-05	Clec4n
139	5.341	5.573	4.859	7.233	6.738	6.462	39.05	9.38	115.10	31.94	2.947	1.03E-05	Elf4
140	5.282	5.592	5.339	7.560	7.152	6.496	42.55	5.00	140.38	49.23	3.299	1.03E-05	Osmr
141	6.598	6.397	6.436	8.449	7.666	7.661	89.25	6.72	251.67	84.71	2.820	1.03E-05	Rhoc
142	7.680	8.160	7.753	9.801	9.304	8.779	235.61	43.97	654.63	227.21	2.778	1.04E-05	Ucp2
143	7.133	7.060	6.813	8.312	8.494	7.961	128.72	14.53	309.19	56.13	2.402	1.05E-05	Lrrc8c
144	7.335	7.552	7.625	9.689	9.180	8.557	182.19	18.60	594.00	224.72	3.260	1.05E-05	Sh3bgrl3
145	8.276	8.433	8.427	5.043	6.785	6.713	333.29	20.14	82.70	43.16	0.248	1.10E-05	Car1
146	8.609	9.173	8.859	10.922	10.260	9.863	477.41	94.15	1365.85	518.40	2.861	1.11E-05	C1qb
147	6.744	6.751	6.474	8.450	8.129	7.611	101.26	10.72	275.03	77.20	2.716	1.12E-05	Slc15a3
148	7.826	9.432	7.946	3.844	6.396	5.174	388.11	262.44	44.89	35.75	0.116	1.14E-05	Lcn13
149	7.006	7.270	6.862	9.334	8.742	8.083	133.08	19.41	448.22	187.89	3.368	1.17E-05	Rac2
150	4.303	4.743	4.212	5.446	5.653	5.568	21.68	4.46	47.11	3.37	2.173	1.18E-05	Ccna2
151	7.827	8.129	7.937	10.241	9.704	9.003	250.71	26.85	852.33	348.96	3.400	1.22E-05	Fcer1g
152	4.553	4.520	4.843	6.543	6.076	5.531	25.04	3.18	68.98	23.55	2.755	1.23E-05	Pfkp
153	8.334	8.028	8.600	6.863	6.417	7.284	323.93	63.44	119.25	35.29	0.368	1.25E-05	Ppp1r3c
154	2.730	3.043	2.922	4.281	4.341	4.194	7.49	0.81	19.34	0.98	2.583	1.27E-05	Bcl2a1c
155	5.051	5.178	5.482	7.506	6.853	6.292	38.01	5.97	125.21	52.35	3.294	1.27E-05	Fcgr1
156	7.453	7.666	7.425	9.352	8.703	8.550	183.35	17.13	481.69	150.11	2.627	1.27E-05	Rcan1
157	6.626	7.199	6.613	9.033	8.452	8.025	114.50	28.04	378.20	133.88	3.303	1.32E-05	Emr1

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT Avg	WTSD	KO Avg	KOSD	KO/WT	BH	Gene
158	4.780	4.892	4.683	6.572	6.159	5.757	27.62	2.00	73.56	20.63	2.663	1.32E-05	Gpr65
159	5.582	5.760	5.398	7.193	6.926	6.523	48.08	6.01	119.97	27.21	2.495	1.33E-05	Akna
160	6.269	6.402	6.527	7.777	7.554	7.499	84.63	7.53	196.10	20.45	2.317	1.33E-05	Cnn2
161	4.710	5.089	4.589	6.550	6.107	5.907	28.09	5.26	74.21	17.45	2.642	1.40E-05	Arhgap25
162	3.914	3.926	4.033	5.699	5.228	4.863	15.55	0.72	39.52	11.56	2.542	1.43E-05	Casp1
163	6.510	6.967	6.431	8.858	8.319	7.771	100.86	21.16	334.02	123.47	3.312	1.43E-05	Lcp2
164	6.464	6.312	6.779	8.170	8.040	7.499	92.51	15.62	244.04	56.09	2.638	1.44E-05	Ccdc80
165	4.614	4.740	5.556	6.514	7.018	6.223	32.75	12.43	98.58	28.17	3.010	1.44E-05	Gm3893
166	6.887	7.582	6.628	9.077	8.690	8.222	136.27	48.88	417.28	120.78	3.062	1.44E-05	Hmox1
167	5.514	5.154	5.004	6.420	6.722	6.476	37.79	7.06	93.40	10.68	2.472	1.53E-05	Atf3
168	8.555	10.759	8.364	11.908	11.842	11.813	812.70	797.04	3703.28	125.92	4.557	1.53E-05	Mt2
169	4.290	4.064	3.983	5.333	5.401	5.041	17.37	1.95	38.50	4.92	2.217	1.53E-05	Phf11
170	3.542	3.572	3.272	4.978	4.906	4.298	11.07	1.22	27.06	6.44	2.445	1.54E-05	Arhgap15
171	4.927	5.155	5.091	6.509	6.236	5.935	33.38	2.67	75.87	14.94	2.273	1.54E-05	Trpv2
172	7.323	7.540	7.130	8.627	8.585	8.238	162.09	23.13	360.47	51.04	2.224	1.56E-05	Acer2
173	6.040	5.734	5.702	4.318	4.674	4.843	57.03	7.61	24.72	4.43	0.433	1.56E-05	Homer2
174	6.323	6.450	6.164	8.893	7.896	7.440	79.73	7.86	295.80	158.97	3.710	1.56E-05	Siglece
175	6.037	6.678	5.918	3.651	4.215	5.113	76.18	22.87	21.91	11.39	0.288	1.58E-05	Chic1
176	9.238	9.012	9.065	10.786	9.987	10.191	551.87	46.15	1316.52	396.76	2.386	1.63E-05	Abhd2
177	5.137	5.223	5.378	6.110	6.479	6.577	38.04	3.26	84.59	13.79	2.224	1.63E-05	Pnpla3
178	7.972	7.877	8.222	10.401	9.600	9.081	261.56	32.99	890.00	417.27	3.403	1.65E-05	S100a11
179	8.688	9.359	8.672	4.235	6.389	7.025	492.27	142.29	77.63	55.97	0.158	1.71E-05	Susd4
180	5.508	5.901	5.492	8.040	7.538	6.705	50.08	8.37	184.46	79.48	3.683	1.74E-05	Cyth4
181	5.496	5.512	5.999	3.805	4.396	4.695	51.57	10.74	20.31	5.99	0.394	1.74E-05	Ncam2
182	5.898	5.956	6.268	7.038	7.244	7.154	66.26	9.45	141.81	10.10	2.140	1.81E-05	Fscn1
183	5.612	5.607	5.499	7.462	7.153	6.525	47.63	2.09	136.91	42.37	2.874	1.81E-05	Rasgrp1
184	5.892	6.447	5.982	7.551	7.484	7.057	69.96	15.10	166.56	29.28	2.381	1.81E-05	Trim30a
185	4.136	4.670	4.300	6.255	5.728	5.340	20.91	4.07	56.62	18.19	2.708	1.91E-05	Cd48
186	8.607	8.148	8.616	6.729	7.155	7.169	355.34	62.10	130.85	21.45	0.368	1.92E-05	Mcc
187	4.919	4.816	4.879	5.664	6.100	6.400	29.28	1.05	67.92	16.89	2.320	1.94E-05	Ccr7
188	5.765	6.245	5.247	7.546	6.888	7.567	56.06	18.99	164.98	40.35	2.943	1.94E-05	Tmc5
189	6.014	6.581	6.092	8.875	8.074	7.316	76.17	17.01	299.50	157.27	3.932	1.99E-05	Itgb2
190	7.900	7.845	7.886	6.705	6.931	7.041	235.04	4.63	119.35	13.86	0.508	2.00E-05	Rnf43
191	3.843	3.708	3.452	7.058	5.463	5.231	12.79	1.72	71.63	53.43	5.603	2.02E-05	Cytip
192	5.648	5.915	5.448	7.063	7.040	6.770	51.39	8.42	124.80	13.61	2.428	2.08E-05	Prkch
193	6.438	6.448	6.314	7.838	7.434	7.499	84.50	4.31	194.22	30.26	2.299	2.10E-05	Hist1h2ak
194	5.126	5.582	5.231	7.472	6.561	6.491	40.12	6.85	120.65	49.30	3.007	2.14E-05	Fam129a
195	6.103	6.580	5.892	8.529	7.565	7.369	74.59	18.82	241.33	111.47	3.235	2.16E-05	Ear10
196	4.559	4.298	4.439	6.355	6.053	5.401	21.65	1.95	63.49	19.96	2.933	2.16E-05	Parp8
197	5.758	6.249	5.878	8.408	7.629	7.009	62.99	11.56	222.20	107.53	3.528	2.19E-05	Pira2
198	5.268	5.145	5.418	4.220	4.348	4.324	38.89	3.70	19.68	0.92	0.506	2.25E-05	1810034E14Rik
199	3.989	4.294	4.026	5.583	5.307	5.020	17.26	2.05	39.98	7.75	2.317	2.26E-05	Aim2
200	3.627	3.631	3.115	4.634	5.640	4.910	11.13	2.14	34.92	13.21	3.137	2.26E-05	Gbp5
201	5.068	5.125	4.884	6.748	6.214	5.963	32.65	2.80	81.35	23.39	2.491	2.34E-05	Myo1g
202	5.297	5.558	5.008	7.384	6.654	6.440	39.53	7.46	118.19	42.89	2.990	2.37E-05	Dock2
203	4.291	4.565	4.288	6.147	5.908	5.195	20.93	2.37	55.85	17.49	2.668	2.48E-05	F630028O10Rik
204	3.885	4.120	2.933	5.096	5.283	5.247	13.27	5.05	37.05	2.51	2.793	2.48E-05	Gm5431
205	5.453	5.682	5.402	7.214	7.283	6.549	45.81	4.86	132.63	33.95	2.895	2.55E-05	9930111J21Rik2
206	5.301	5.470	5.313	6.717	6.512	6.174	41.16	2.73	89.55	16.57	2.176	2.55E-05	Cyfp2
207	3.816	3.956	3.816	6.116	5.353	4.846	14.56	0.83	46.34	20.85	3.182	2.55E-05	Klra2
208	6.935	9.697	6.268	4.219	3.990	4.241	343.16	422.29	17.80	1.67	0.052	2.55E-05	Moxd1
209	8.760	8.174	8.582	9.673	10.363	9.464	368.59	73.50	946.49	325.28	2.568	2.55E-05	Plk3
210	5.919	6.178	6.151	7.869	7.108	7.260	67.98	6.53	175.02	51.47	2.574	2.55E-05	Slc7a8
211	7.244	7.723	7.542	9.733	9.122	8.674	183.07	30.02	605.51	225.03	3.307	2.65E-05	Cyba

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT Avg	WTSD	KO Avg	KOSD	KO/WT	BH	Gene
212	4.443	4.207	3.899	5.275	5.292	5.030	18.38	3.42	36.85	3.63	2.005	2.81E-05	Cst7
213	7.488	8.295	8.307	6.063	7.067	6.168	270.10	78.46	90.96	37.45	0.337	2.81E-05	Nat8
214	4.531	4.565	4.458	6.225	5.510	5.531	22.92	0.86	55.55	16.70	2.423	2.81E-05	Pak1
215	5.505	6.065	5.822	4.264	4.682	4.895	56.30	10.76	24.88	5.32	0.442	2.81E-05	Rhobtb3
216	4.457	4.618	4.542	6.087	6.039	5.382	23.27	1.30	58.48	14.57	2.513	2.81E-05	Sp110
217	9.257	9.121	9.433	9.986	10.443	10.225	619.95	67.41	1201.11	189.23	1.937	2.81E-05	Sparc
218	3.944	3.818	3.858	5.267	5.573	4.817	14.66	0.66	38.10	9.72	2.599	2.99E-05	Niacr1
219	5.016	4.976	4.746	6.379	6.036	5.747	30.22	2.96	67.52	14.86	2.235	3.08E-05	Slc1a5
220	8.823	8.901	8.844	10.672	10.061	9.609	463.46	13.06	1160.22	432.95	2.503	3.08E-05	Tgm2
221	4.873	5.022	4.997	6.273	6.342	5.809	31.24	1.71	71.50	13.52	2.288	3.13E-05	Sema4d
222	5.640	5.788	5.749	7.439	7.081	6.614	52.97	2.80	135.61	37.76	2.560	3.19E-05	Lpcat2
223	6.689	6.775	6.897	8.594	8.095	7.720	110.62	8.06	290.19	88.92	2.623	3.25E-05	Flna
224	5.651	5.803	5.897	8.533	7.796	6.777	55.23	4.70	234.11	130.79	4.239	3.26E-05	Ly6c1
225	5.624	5.595	5.287	7.158	6.892	6.366	45.56	5.67	114.71	30.36	2.517	3.26E-05	P2ry6
226	5.159	5.310	5.012	6.766	6.446	6.004	35.89	3.70	86.73	22.32	2.417	3.36E-05	Sash3
227	6.578	6.900	6.580	8.209	7.847	7.464	103.54	13.73	234.23	59.74	2.262	3.46E-05	Heg1
228	9.019	9.727	9.256	11.340	10.611	10.208	659.23	169.45	1779.88	729.15	2.700	3.73E-05	Gm11428
229	7.067	7.267	7.380	9.092	8.481	8.113	151.59	16.41	393.31	138.11	2.595	3.73E-05	Msn
230	7.630	7.797	7.396	9.510	8.868	8.532	196.29	27.01	522.17	185.70	2.660	3.77E-05	C1qa
231	4.368	4.329	4.467	5.500	5.568	5.227	20.96	1.04	43.39	5.25	2.070	3.79E-05	Cpxm1
232	4.717	4.494	4.610	5.736	5.510	5.398	24.42	1.88	47.01	5.72	1.925	3.79E-05	Oxct1
233	4.906	4.927	4.845	5.685	6.300	6.581	29.71	0.88	75.32	22.34	2.535	3.95E-05	Spr1a
234	5.632	5.919	5.748	6.877	7.183	6.852	54.61	5.52	126.12	16.66	2.309	3.98E-05	Cd3e
235	5.130	5.108	4.814	5.945	7.922	7.701	32.55	3.84	170.74	96.07	5.245	4.06E-05	Gm12250
236	4.219	4.202	4.169	6.124	5.661	4.951	18.34	0.32	50.42	19.41	2.749	4.12E-05	9130014G24Rik
237	6.064	6.638	5.577	9.218	9.019	7.214	71.42	26.22	420.82	238.97	5.892	4.13E-05	Cdkn1a
238	6.877	6.986	6.861	5.333	6.097	5.698	120.17	5.71	53.57	14.15	0.446	4.13E-05	Fn3k
239	5.133	5.633	4.942	7.466	6.518	6.410	38.48	9.89	117.81	51.15	3.062	4.14E-05	Ear1
240	6.316	6.433	6.432	8.432	7.732	7.241	84.14	3.87	236.41	99.23	2.810	4.29E-05	Pip4k2a
241	6.116	6.727	6.800	5.337	5.488	5.581	95.58	22.87	44.39	3.74	0.464	4.36E-05	C330021F23Rik
242	5.221	5.635	5.330	7.399	7.042	6.354	42.41	6.48	127.42	43.64	3.004	4.36E-05	Cd44
243	5.823	6.597	6.480	7.412	7.748	8.498	80.89	21.36	248.95	100.01	3.078	4.44E-05	Lyve1
244	5.384	5.714	5.441	8.318	7.442	6.464	45.89	5.78	193.77	116.67	4.223	4.46E-05	Csf2rb2
245	5.774	6.416	5.804	8.308	7.805	6.959	65.32	17.37	221.64	96.24	3.393	4.54E-05	Nckap1l
246	6.857	7.134	6.884	9.293	8.301	7.980	124.83	13.56	398.34	200.72	3.191	4.77E-05	Arhgdib
247	4.611	5.267	4.680	6.909	6.727	5.768	29.53	7.80	93.53	34.55	3.167	4.77E-05	Syt12
248	4.887	5.187	4.859	6.741	6.233	5.994	31.68	4.11	81.97	22.37	2.588	4.90E-05	Myo1f
249	6.538	6.506	6.538	7.331	8.424	7.961	92.24	1.18	251.24	91.21	2.724	4.99E-05	Gbp7
250	5.018	5.243	4.773	7.349	6.632	6.037	32.54	5.26	109.30	49.48	3.359	4.99E-05	Vav1
251	8.162	8.235	8.258	6.909	7.309	7.302	297.96	10.23	145.49	21.96	0.488	5.09E-05	Al464131
252	4.979	5.017	4.870	6.514	6.193	5.673	31.05	1.62	71.88	20.23	2.315	5.16E-05	Ikzf1
253	6.145	6.470	5.977	8.308	7.569	7.101	74.12	13.16	214.71	92.36	2.897	5.19E-05	Itgal
254	7.420	7.621	7.431	9.374	8.989	8.299	180.21	14.46	495.61	174.66	2.750	5.25E-05	Sirpa
255	4.785	4.304	4.531	5.406	6.836	6.136	23.48	3.93	75.66	36.22	3.222	5.49E-05	Slamf8
256	5.894	6.008	6.365	7.804	7.400	7.062	68.76	12.11	175.33	45.24	2.550	5.54E-05	Anxa2
257	6.010	6.419	5.848	8.686	7.730	7.113	69.20	14.58	254.24	141.51	3.674	5.73E-05	AB124611
258	6.225	6.354	5.653	4.647	5.258	4.543	68.97	16.52	28.88	8.18	0.419	5.77E-05	Syde2
259	5.826	5.817	5.480	8.551	7.551	6.708	52.58	6.88	222.38	138.57	4.230	5.82E-05	Lilrb3
260	5.348	5.401	5.514	7.504	6.399	6.535	42.89	2.53	119.56	53.84	2.788	5.98E-05	Fabp4
261	4.767	4.838	4.494	6.100	6.137	5.752	26.12	3.18	64.27	9.04	2.461	6.04E-05	Coro2a
262	6.363	6.591	6.157	8.800	7.921	7.349	83.36	12.56	283.75	145.85	3.404	6.06E-05	Sfpi1
263	8.860	9.007	8.849	9.560	9.849	10.055	480.09	29.79	913.67	154.85	1.903	6.14E-05	Apol9b
264	6.078	5.898	5.999	7.466	7.207	6.841	63.72	3.97	146.40	31.12	2.297	6.14E-05	Rab8b
265	8.915	9.271	9.283	8.174	7.815	8.304	574.42	79.48	276.72	46.62	0.482	6.14E-05	Srebf1

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT Avg	WTSD	KO Avg	KOSD	KO/WT	BH	Gene
266	5.406	5.435	4.852	7.961	7.432	6.271	38.19	8.07	166.38	86.16	4.357	6.17E-05	Gp49a
267	8.376	9.024	9.443	10.802	10.359	9.929	516.31	181.92	1357.64	407.11	2.630	6.31E-05	Anxa5
268	3.648	3.877	3.607	4.696	4.936	4.526	13.14	1.36	26.52	3.83	2.019	6.51E-05	Ms4a4c
269	3.644	3.337	3.436	4.498	4.273	4.648	11.14	1.23	22.33	2.87	2.004	6.61E-05	Art2b
270	8.098	7.838	7.734	6.270	7.031	6.854	238.52	31.68	107.87	27.63	0.452	6.69E-05	Mn1
271	4.227	4.464	4.113	5.908	5.805	5.104	19.37	2.44	50.11	13.78	2.587	6.86E-05	Pla2g4a
272	6.870	6.934	6.811	8.710	7.957	7.682	117.18	5.00	290.87	112.78	2.482	7.12E-05	Tnfrsf21
273	7.129	7.461	7.869	8.840	9.379	8.364	183.34	47.29	484.54	169.73	2.643	7.30E-05	Ly6a
274	6.227	6.134	6.364	8.361	7.537	7.201	75.84	6.14	220.57	95.77	2.908	7.30E-05	Tagln2
275	6.006	5.645	6.354	7.047	7.124	7.348	65.38	15.90	144.88	16.03	2.216	7.50E-05	Dhrs9
276	4.188	4.373	4.093	5.068	5.736	5.188	18.67	1.87	41.10	10.67	2.201	7.70E-05	5430435G22Rik
277	4.108	4.110	4.197	5.797	5.074	5.172	17.61	0.63	41.78	12.02	2.372	7.70E-05	Dapp1
278	5.649	5.866	5.566	7.317	7.012	6.384	51.96	5.71	124.01	38.20	2.387	7.77E-05	Atp8a1
279	5.858	5.883	6.036	7.040	6.949	6.645	60.89	4.14	118.42	16.38	1.945	7.88E-05	Akt3
280	7.043	7.488	7.166	8.831	8.361	8.003	151.64	24.85	346.85	100.60	2.287	7.88E-05	Axl
281	5.485	5.872	5.965	4.566	4.669	5.026	55.28	9.29	27.24	4.71	0.493	7.88E-05	Dclk3
282	9.087	9.340	9.164	10.412	10.180	9.803	588.48	53.80	1138.66	235.15	1.935	7.88E-05	Hist1h3b
283	3.964	5.489	5.473	10.933	10.014	6.637	34.98	16.78	1029.40	927.52	29.427	7.88E-05	Igkj1
284	6.707	6.803	7.129	4.862	6.056	5.156	118.71	18.79	43.76	19.99	0.369	7.88E-05	Lgr5
285	5.891	5.835	5.974	7.296	6.893	6.818	59.77	2.92	129.63	24.04	2.169	7.88E-05	Marcks
286	6.204	6.783	6.369	8.518	7.734	7.382	88.83	19.00	248.77	104.60	2.800	7.88E-05	P2ry13
287	5.174	5.549	5.249	7.610	7.093	6.194	40.31	5.71	135.01	61.07	3.349	8.06E-05	Plac8
288	5.273	5.744	5.605	7.992	6.949	6.685	46.98	7.61	160.38	82.30	3.414	8.21E-05	Fpr1
289	5.068	5.028	5.131	6.844	6.337	5.924	33.74	1.22	85.46	27.36	2.533	8.26E-05	Fmn1
290	7.817	7.759	7.617	8.783	8.845	8.444	212.77	14.96	416.21	59.59	1.956	8.27E-05	H2-Q4
291	5.085	5.308	5.119	6.638	6.293	5.951	36.11	3.07	79.94	18.91	2.214	8.27E-05	Ppp1r18
292	5.263	5.093	5.126	6.651	6.096	6.016	35.81	2.27	77.86	19.69	2.174	8.27E-05	Ripk3
293	3.626	3.863	3.478	5.264	4.699	4.401	12.68	1.73	28.51	8.92	2.249	8.30E-05	Mmp27
294	4.904	4.864	5.108	6.430	5.998	5.884	31.19	2.89	69.72	14.47	2.235	8.32E-05	Ggta1
295	6.506	6.718	6.317	8.512	7.832	7.367	91.96	12.81	252.63	102.20	2.747	8.34E-05	Il18bp
296	5.148	5.010	4.633	7.164	6.971	5.831	30.83	5.46	108.59	45.63	3.522	8.36E-05	Ccr5
297	5.947	5.517	6.360	6.974	7.442	7.032	63.21	18.22	143.51	26.42	2.270	8.36E-05	Emp1
298	4.699	5.094	4.898	5.811	6.202	5.882	29.99	4.10	62.92	9.38	2.098	8.36E-05	Lck
299	4.286	4.527	4.481	5.586	5.378	5.206	21.63	1.88	42.18	5.59	1.950	8.56E-05	Lrrc33
300	4.714	4.651	4.507	5.633	5.633	5.656	24.70	1.79	49.88	0.47	2.019	8.59E-05	Cd8a
301	5.263	5.201	5.189	7.353	6.295	6.217	37.23	1.03	105.46	50.30	2.833	8.59E-05	Rassf2
302	6.283	6.101	5.883	7.994	7.259	7.096	68.50	9.42	181.61	64.03	2.651	8.67E-05	Stk17b
303	3.557	3.860	3.743	8.724	6.371	5.300	13.23	1.38	181.73	210.07	13.739	8.74E-05	Igj
304	5.971	6.276	6.293	6.955	7.174	7.437	72.89	8.79	147.26	24.74	2.020	8.86E-05	Ifit3
305	6.277	6.195	6.148	6.932	7.622	8.001	73.90	3.37	191.74	67.17	2.594	8.93E-05	Tubb6
306	5.428	5.515	5.330	7.027	6.749	6.155	42.99	2.75	103.07	29.84	2.397	8.95E-05	Il10ra
307	5.877	6.229	5.784	8.250	7.438	6.868	62.95	10.59	198.21	96.24	3.149	9.26E-05	Hck
308	4.344	4.436	3.984	5.240	5.393	5.167	19.26	3.05	38.58	3.12	2.003	9.26E-05	Sectm1a
309	10.412	10.101	10.534	9.150	9.556	9.403	1314.67	196.76	666.02	92.86	0.507	9.65E-05	Cyp2c37
310	5.456	5.605	5.452	7.893	7.210	6.236	45.45	2.80	153.71	81.32	3.382	9.65E-05	Ly6c2
311	6.127	6.385	6.042	8.239	7.579	6.980	73.13	9.27	206.55	88.93	2.825	9.70E-05	4632428N05Rik
312	6.397	6.768	6.728	4.588	5.034	5.940	99.75	13.49	39.41	19.55	0.395	9.70E-05	Serpine2
313	4.320	4.336	4.027	6.186	5.991	4.893	18.83	2.19	55.37	22.69	2.941	9.79E-05	Gzmb
314	5.029	4.745	5.348	4.166	4.043	4.116	33.39	6.99	17.26	0.73	0.517	9.85E-05	Hhip
315	4.672	5.075	4.799	7.616	6.248	5.969	29.01	4.23	111.61	73.54	3.847	9.85E-05	Rgs2
316	7.940	8.115	8.159	7.013	7.190	7.223	269.59	21.20	141.54	10.86	0.525	9.96E-05	Pde9a
317	7.507	7.430	7.594	9.001	8.581	8.176	182.50	10.38	394.72	112.00	2.163	1.01E-04	Mustn1
318	7.085	7.424	7.127	8.820	8.605	7.887	149.13	19.71	359.32	110.76	2.409	1.02E-04	Lass6
319	3.466	3.934	3.772	5.672	4.956	4.613	13.33	2.13	35.50	13.81	2.663	1.03E-04	Samsn1

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT Avg	WTSD	KO Avg	KOSD	KOWT	BH	Gene
320	8.473	8.458	8.585	9.220	9.452	9.190	363.69	17.78	626.89	63.78	1.724	1.03E-04	Tpm4
321	4.833	5.062	4.862	6.081	6.474	5.767	30.33	2.68	70.36	17.38	2.320	1.05E-04	Ccl2
322	8.790	8.785	8.438	5.655	7.746	6.757	410.18	54.92	124.43	83.36	0.303	1.05E-04	Npr2
323	4.325	4.332	4.139	5.845	5.180	5.114	19.27	1.43	42.78	12.75	2.221	1.05E-04	Zdhhc23
324	4.444	4.525	4.334	6.586	5.355	5.621	21.65	1.43	62.07	29.72	2.867	1.08E-04	Tmem71
325	6.075	6.841	6.305	9.021	8.001	7.434	87.05	24.59	316.22	180.98	3.633	1.10E-04	Igsf6
326	6.424	6.160	5.926	7.951	7.258	7.142	72.73	12.56	180.59	58.19	2.483	1.11E-04	Rasgef1b
327	5.350	5.387	5.238	7.519	6.717	6.123	40.13	2.13	119.44	58.20	2.976	1.12E-04	Coro1a
328	3.872	4.116	4.043	5.332	5.068	4.645	16.15	1.37	32.95	7.65	2.040	1.13E-04	Prdm1
329	5.444	5.629	5.224	7.114	6.515	6.205	43.46	6.06	101.25	33.49	2.330	1.15E-04	Arhgef2
330	5.637	5.807	5.804	5.145	4.750	4.928	53.88	3.56	30.90	4.25	0.574	1.15E-04	Tiam2
331	4.534	4.793	4.343	5.833	5.500	5.429	23.72	3.75	48.45	7.50	2.042	1.16E-04	Cd80
332	6.418	6.737	6.461	8.272	7.828	7.206	93.43	11.52	227.96	80.75	2.440	1.19E-04	Abi3
333	8.034	8.718	8.119	10.139	9.630	9.135	320.39	87.56	827.43	284.49	2.583	1.21E-04	Cd5l
334	5.650	5.644	5.192	8.490	7.090	6.612	45.58	7.82	197.86	141.33	4.341	1.22E-04	Cd300e
335	8.639	8.849	8.920	7.518	8.058	7.920	448.06	44.45	230.63	42.81	0.515	1.22E-04	Fam82a1
336	6.876	7.379	7.148	9.359	8.299	8.101	141.89	24.49	415.40	209.98	2.928	1.26E-04	Trem14
337	7.235	7.778	7.652	6.217	6.642	6.680	190.40	35.63	92.27	15.54	0.485	1.27E-04	Fzd8
338	7.341	7.445	7.284	8.882	8.383	8.063	164.09	9.36	357.72	104.20	2.180	1.27E-04	Itga9
339	3.841	4.344	4.079	4.976	5.071	5.369	17.18	3.00	35.48	5.18	2.065	1.27E-04	Ccnb1
340	5.201	5.366	4.765	6.189	6.296	5.908	35.08	7.18	70.53	9.49	2.011	1.29E-04	Ccnb2
341	5.548	5.537	5.211	7.075	6.738	6.077	43.42	5.53	103.04	33.83	2.373	1.29E-04	Trpm2
342	5.469	5.782	5.477	7.439	6.639	6.410	47.96	6.14	119.43	47.44	2.490	1.31E-04	Stk10
343	4.655	4.388	4.690	5.381	5.673	5.427	23.99	2.66	45.24	5.05	1.886	1.34E-04	Flt3
344	4.027	4.023	3.965	5.349	4.922	4.687	16.06	0.38	32.28	7.69	2.010	1.34E-04	Gls
345	6.275	6.694	6.490	8.473	7.685	7.281	90.29	13.05	238.89	104.01	2.646	1.34E-04	Lgals3
346	11.068	11.405	11.152	12.043	11.738	11.623	2377.71	295.53	3596.12	554.99	1.512	1.34E-04	Ly6e
347	5.063	5.215	5.050	6.399	6.211	5.838	34.56	2.23	71.88	13.71	2.080	1.34E-04	Upp1
348	3.672	4.027	3.831	4.783	4.664	4.769	14.43	1.79	26.72	1.19	1.852	1.36E-04	H2-Eb2
349	4.263	4.161	4.160	6.475	5.260	5.138	18.32	0.76	54.16	30.16	2.956	1.36E-04	Cd300lf
350	8.592	8.455	8.125	9.889	9.357	9.183	338.69	54.40	728.39	193.81	2.151	1.38E-04	Rdh9
351	4.816	6.120	5.312	7.771	6.501	7.014	45.81	21.35	146.08	65.56	3.189	1.40E-04	Nipal1
352	5.650	5.004	5.546	6.609	6.457	6.284	43.01	9.62	87.78	9.83	2.041	1.44E-04	Creb3l1
353	3.387	3.400	3.627	4.667	4.241	5.084	11.12	1.06	26.08	7.53	2.344	1.47E-04	BC005685
354	3.813	3.954	3.477	4.864	5.022	4.575	13.57	2.22	28.49	4.37	2.100	1.55E-04	Nlrp3
355	5.346	5.541	5.765	6.672	6.392	6.390	47.21	6.88	89.94	10.42	1.905	1.56E-04	Uap1l1
356	6.582	6.517	6.736	9.290	8.073	7.547	97.97	7.75	360.77	233.41	3.682	1.56E-04	Nid1
357	8.814	9.079	8.934	10.080	9.869	9.568	493.21	45.49	925.43	161.62	1.876	1.59E-04	Hist2h3c1
358	4.638	4.753	4.160	5.719	5.643	5.585	23.25	4.76	50.21	2.34	2.160	1.61E-04	Mki67
359	10.681	10.639	10.413	11.283	11.193	11.068	1533.05	148.71	2326.40	172.73	1.517	1.63E-04	H2-D1
360	3.950	3.905	3.895	4.943	5.119	4.700	15.11	0.30	30.50	4.38	2.019	1.63E-04	Slamf6
361	3.045	3.447	3.432	9.790	4.925	7.158	9.98	1.50	352.80	464.50	35.333	1.63E-04	Igkv4-91
362	6.822	7.016	6.926	8.354	8.018	7.515	121.38	8.17	256.46	72.22	2.113	1.63E-04	Ano6
363	6.785	7.163	7.297	7.991	8.520	8.212	136.98	24.13	306.08	56.94	2.235	1.64E-04	2010003K11Rik
364	6.083	6.101	6.513	4.847	5.246	5.479	75.93	13.35	37.11	7.95	0.489	1.64E-04	Leap2
365	5.018	5.314	4.793	6.022	6.843	6.130	33.31	6.09	83.26	27.41	2.500	1.64E-04	Thbs1
366	4.414	4.422	4.356	5.390	5.356	5.213	21.08	0.52	39.99	2.55	1.898	1.64E-04	Rnase6
367	9.570	9.604	9.089	8.002	8.694	8.408	694.30	130.10	336.76	78.96	0.485	1.64E-04	1600002H07Rik
368	8.492	7.893	7.816	9.099	9.212	9.340	274.39	74.54	596.41	50.10	2.174	1.65E-04	Apobec1
369	3.561	3.963	3.811	5.882	4.578	4.884	13.81	1.91	37.47	18.85	2.713	1.65E-04	Elovl7
370	5.896	6.426	6.034	7.969	7.292	6.938	70.36	13.84	176.61	66.24	2.510	1.65E-04	Soat1
371	10.543	9.304	9.628	10.957	10.901	11.444	971.61	457.27	2228.65	484.16	2.294	1.65E-04	Alas1
372	5.361	5.312	5.309	7.287	6.398	6.080	40.15	0.82	102.70	47.01	2.558	1.65E-04	Plp2
373	6.447	6.891	6.926	8.517	7.871	7.674	109.18	19.06	268.24	86.37	2.457	1.66E-04	Msr1

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT Avg	WTSD	KO Avg	KOSD	KO/WT	BH	Gene
374	4.941	5.130	4.894	6.394	6.022	5.625	31.82	2.81	66.13	17.39	2.078	1.67E-04	Akr1b10
375	4.790	4.731	4.731	5.704	5.767	5.371	26.93	0.63	49.32	6.98	1.831	1.76E-04	Wdfy4
376	4.756	4.981	4.714	6.815	6.216	5.463	28.28	2.88	76.99	34.31	2.722	1.79E-04	Lair1
377	6.065	6.501	6.024	8.345	7.498	7.038	74.21	14.23	212.45	100.66	2.863	1.81E-04	Fcgr3
378	3.889	3.483	3.822	5.585	4.739	4.571	13.38	1.93	32.82	13.23	2.453	1.81E-04	Gm5068
379	7.378	7.556	7.643	8.750	8.659	8.223	184.81	17.02	377.82	69.62	2.044	1.83E-04	Cmtm3
380	4.274	4.541	4.392	5.199	5.361	5.401	21.21	1.98	40.04	2.91	1.888	1.83E-04	Pdcd1
381	6.613	6.730	6.778	7.906	7.803	7.371	104.59	6.06	209.55	39.05	2.004	1.83E-04	Tgfb1
382	6.080	6.411	6.265	7.736	7.410	7.010	76.53	8.72	170.72	42.19	2.231	1.84E-04	Il10rb
383	5.693	4.889	5.815	6.415	7.499	7.014	45.88	14.26	131.83	47.83	2.873	1.85E-04	Dpt
384	7.073	6.616	6.612	7.556	9.760	9.427	110.18	21.21	581.26	352.02	5.275	1.86E-04	Gbp6
385	4.721	4.718	4.684	5.953	5.653	5.404	26.13	0.37	51.54	9.86	1.972	1.86E-04	I830077J02Rik
386	3.297	3.135	3.344	5.771	5.916	3.992	9.59	0.72	43.64	24.19	4.551	1.86E-04	Mybl1
387	6.796	7.146	8.161	9.237	8.633	8.764	179.64	93.51	478.38	109.85	2.663	1.88E-04	Cd36
388	4.032	4.235	3.768	6.103	5.262	4.803	16.27	2.60	45.01	21.21	2.766	1.89E-04	Gm885
389	6.055	6.539	6.210	9.168	8.155	7.133	77.84	13.66	333.48	221.37	4.284	1.92E-04	Csf2rb
390	4.561	4.850	4.429	6.316	5.615	5.398	24.67	3.77	56.96	19.98	2.309	1.92E-04	Elmo1
391	7.574	7.578	7.297	8.695	8.503	8.156	179.65	19.40	354.14	65.06	1.971	1.92E-04	Psmb10
392	9.035	9.284	9.088	10.345	10.113	9.750	564.02	52.27	1089.77	220.12	1.932	1.97E-04	Hist1h3d
393	4.286	4.211	4.263	5.734	5.170	4.978	19.08	0.51	40.25	11.45	2.110	1.97E-04	Tlr4
394	8.797	8.827	8.755	9.538	9.476	9.568	443.58	10.99	738.16	23.80	1.664	1.98E-04	Fga
395	9.020	9.276	9.080	10.344	10.113	9.737	560.05	53.17	1086.86	224.00	1.941	1.99E-04	Hist1h3c
396	4.278	4.669	4.328	5.429	5.497	5.273	21.64	3.30	42.31	3.33	1.955	2.05E-04	Rbl1
397	4.408	5.224	4.753	6.985	6.372	5.578	28.52	8.19	85.74	39.54	3.006	2.05E-04	C5ar1
398	7.449	7.841	7.551	11.156	9.319	8.752	197.22	28.52	1117.24	1014.09	5.665	2.05E-04	Cybb
399	3.740	3.827	4.703	5.273	5.234	5.253	17.86	7.09	38.14	0.52	2.135	2.10E-04	Themis
400	4.757	5.181	5.032	5.895	6.095	5.663	32.01	4.66	59.51	8.85	1.859	2.10E-04	Acot9
401	8.003	8.062	8.077	8.905	8.869	8.706	264.62	7.12	454.79	32.81	1.719	2.10E-04	Hexa
402	6.111	6.122	6.390	4.119	5.070	5.462	74.22	8.34	31.68	13.45	0.427	2.10E-04	Sult1c2
403	5.280	5.444	5.593	6.393	6.619	6.163	43.55	4.70	84.66	13.31	1.944	2.10E-04	Tlr9
404	5.381	5.252	5.481	6.336	6.414	5.991	41.48	3.28	76.54	11.45	1.845	2.10E-04	Zmynd15
405	6.330	6.020	6.520	4.508	5.242	5.498	79.04	13.48	35.27	11.45	0.446	2.11E-04	Spata22
406	4.255	4.974	4.604	6.676	5.804	5.459	24.95	6.20	67.38	30.79	2.701	2.15E-04	Lrrc25
407	5.616	5.876	5.721	7.446	6.903	6.477	53.50	4.89	127.72	43.23	2.387	2.16E-04	Fermt3
408	4.828	4.696	4.690	5.747	5.807	5.320	26.72	1.47	49.88	8.67	1.867	2.16E-04	Grap2
409	4.450	4.613	4.309	5.459	5.246	5.298	22.05	2.33	40.43	3.17	1.834	2.18E-04	Tagap
410	6.310	6.703	6.588	5.118	5.431	5.884	93.24	12.68	45.65	12.36	0.490	2.18E-04	Slc2a5
411	7.123	7.487	7.559	8.876	8.667	8.073	169.13	26.16	381.86	102.55	2.258	2.19E-04	Csrp1
412	3.321	3.615	3.284	5.492	4.642	4.157	10.66	1.38	29.28	14.09	2.746	2.20E-04	Ap1s2
413	5.254	5.477	5.444	8.027	6.710	6.376	42.07	3.42	149.52	96.99	3.554	2.21E-04	Serpib6b
414	4.958	5.348	4.568	7.134	6.271	5.843	31.85	8.53	91.69	43.36	2.879	2.21E-04	Runx1
415	5.340	5.003	5.039	6.713	6.290	5.844	35.14	4.65	80.20	23.80	2.282	2.22E-04	Slamf9
416	9.018	9.279	9.096	10.329	10.097	9.740	562.20	53.14	1078.75	216.24	1.919	2.22E-04	Hist1h3h
417	3.844	3.664	3.874	4.731	4.993	4.427	13.90	1.07	26.64	5.17	1.917	2.23E-04	Gpnmb
418	5.909	6.817	7.497	4.236	5.718	4.883	117.85	60.47	33.67	17.28	0.286	2.28E-04	Acss3
419	8.615	8.995	8.970	6.665	7.901	7.743	467.93	65.92	184.90	73.34	0.395	2.28E-04	Fam55b
420	5.996	6.252	5.817	9.269	7.833	7.013	65.47	10.03	324.68	257.73	4.959	2.28E-04	Ccl6
421	5.617	5.797	5.547	7.359	6.728	6.393	50.48	4.58	118.07	41.42	2.339	2.39E-04	Tfec
422	9.019	9.274	9.075	10.342	10.091	9.743	559.01	52.89	1081.92	220.98	1.935	2.44E-04	Hist1h3i
423	9.736	10.099	9.977	10.859	10.611	10.537	985.68	123.71	1635.29	195.66	1.659	2.44E-04	Krt18
424	6.639	6.592	6.880	7.804	7.519	7.492	104.63	11.49	195.60	24.15	1.869	2.48E-04	Sod3
425	7.514	7.625	7.705	9.648	8.840	8.348	196.25	12.98	528.87	246.09	2.695	2.50E-04	Cd38
426	4.931	5.114	5.374	4.273	4.265	4.281	35.53	5.54	19.33	0.11	0.544	2.50E-04	Srgap3
427	5.160	5.265	5.225	4.486	4.444	3.928	37.20	1.37	19.80	3.97	0.532	2.51E-04	Rfx4

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT avg	WTsd	KO avg	KOsd	KO/WT	BH	Gene Symbol
428	9.015	9.270	9.112	10.318	10.099	9.735	562.64	50.70	1075.07	212.91	1.911	2.53E-04	Hist2h3b
429	7.773	7.952	7.897	8.528	8.840	8.760	234.89	14.72	420.37	45.98	1.790	2.53E-04	Myadm
430	9.008	9.276	9.114	10.325	10.107	9.737	562.95	53.15	1079.71	215.66	1.918	2.54E-04	Hist1h3g
431	7.043	7.261	7.561	5.290	6.427	6.273	158.03	28.78	67.50	24.95	0.427	2.65E-04	Tmie
432	6.637	6.881	6.368	7.746	7.927	7.311	99.99	17.63	205.65	43.03	2.057	2.69E-04	Psmb8
433	5.377	5.590	5.317	6.563	6.401	6.170	43.20	4.38	83.69	11.31	1.937	2.69E-04	Serpib9
434	4.689	4.988	4.726	7.182	5.639	6.186	28.00	3.26	89.30	49.79	3.189	2.71E-04	Tmprss4
435	9.031	9.267	9.075	10.340	10.108	9.722	559.50	49.67	1081.38	226.84	1.933	2.73E-04	Hist1h3e
436	5.432	5.593	5.686	4.732	4.748	4.965	47.64	4.20	28.23	2.61	0.593	2.76E-04	Map2k6
437	3.435	3.467	3.444	4.564	4.303	4.079	10.92	0.12	20.10	3.39	1.841	2.78E-04	Slc28a2
438	6.060	6.024	6.246	7.497	7.407	6.774	69.23	5.83	153.27	38.34	2.214	2.79E-04	Klf6
439	5.752	5.872	5.140	7.675	7.238	6.323	49.24	12.33	145.11	62.34	2.947	2.81E-04	Lilrb4
440	4.623	4.584	4.781	5.517	5.881	5.516	25.37	1.86	50.16	7.59	1.977	2.83E-04	Capg
441	3.362	3.219	2.991	3.887	4.419	4.498	9.18	1.17	19.60	4.20	2.135	2.85E-04	Pyhin1
442	6.731	6.820	6.812	8.047	7.798	7.431	110.53	3.75	219.88	45.95	1.989	2.87E-04	Clic1
443	6.017	6.096	6.260	7.421	7.165	6.731	69.93	6.09	140.39	32.71	2.008	2.89E-04	Cd93
444	6.227	6.324	6.055	7.542	6.949	6.984	73.83	6.88	145.51	35.40	1.971	2.92E-04	9030625A04Rik
445	5.258	5.378	4.832	7.859	6.525	6.062	36.11	6.81	130.34	89.07	3.610	2.92E-04	Btg3
446	4.097	4.413	4.432	5.073	5.202	5.040	20.00	2.51	34.47	2.08	1.723	2.92E-04	Trim30d
447	6.338	6.622	6.241	8.522	7.683	7.119	85.02	11.97	237.40	117.60	2.792	2.93E-04	Pira11
448	4.372	4.356	4.632	3.786	3.714	3.845	21.99	2.43	13.76	0.62	0.626	3.02E-04	4430402118Rik
449	8.508	8.775	8.386	7.467	7.584	7.932	378.86	53.45	204.32	35.31	0.539	3.06E-04	Hes6
450	6.153	6.780	6.308	7.196	7.508	7.349	86.76	20.44	163.90	17.75	1.889	3.06E-04	Ifi203
451	6.044	6.144	6.204	7.239	7.196	6.806	70.15	3.89	136.53	21.45	1.946	3.12E-04	Fyn
452	4.599	5.192	4.853	4.093	4.125	4.058	29.90	6.22	17.06	0.39	0.570	3.13E-04	Fras1
453	8.563	8.623	8.477	9.145	9.684	9.375	376.28	19.06	684.29	129.58	1.819	3.13E-04	H2-Q6
454	6.119	6.705	5.797	9.305	7.839	7.181	76.49	25.12	335.52	260.57	4.386	3.14E-04	Pla2g7
455	5.905	5.933	5.734	7.355	6.915	6.505	58.08	4.25	125.08	36.65	2.154	3.14E-04	Wipf1
456	4.713	4.668	4.628	6.305	5.628	5.309	25.46	0.75	56.05	20.52	2.202	3.27E-04	Sh3pxd2b
457	5.832	6.045	5.983	7.308	6.914	6.719	62.08	4.65	128.13	27.37	2.064	3.30E-04	Kcnk6
458	4.973	5.049	4.892	6.928	6.411	5.637	31.41	1.70	85.56	36.02	2.724	3.30E-04	Ncf4
459	4.565	4.591	4.627	5.719	5.542	5.105	24.16	0.52	44.57	9.30	1.845	3.30E-04	Ptger4
460	5.578	5.621	5.496	4.727	4.851	5.024	47.36	2.07	29.29	3.05	0.618	3.30E-04	Setdb2
461	5.606	5.782	5.794	6.801	6.743	6.390	53.07	3.80	100.83	14.85	1.900	3.36E-04	Ccdc120
462	4.114	4.465	4.243	5.685	5.264	4.885	19.44	2.42	39.81	11.02	2.048	3.36E-04	Trps1
463	8.672	8.867	8.682	9.397	9.703	9.948	428.58	33.29	831.72	156.73	1.941	3.41E-04	Apol9a
464	6.631	6.971	6.719	8.343	7.902	7.449	109.97	13.76	246.23	75.29	2.239	3.46E-04	Abcg1
465	6.363	5.981	5.799	6.752	8.960	8.080	67.05	13.71	292.19	196.08	4.358	3.47E-04	Cxcl10
466	4.484	4.841	4.490	5.452	5.789	5.376	24.51	3.60	46.86	7.39	1.912	3.51E-04	H2-Oa
467	7.641	7.207	7.657	8.611	8.375	8.255	183.10	30.63	342.81	43.73	1.872	3.51E-04	St5
468	5.853	6.137	5.711	7.385	7.127	6.606	60.18	9.22	134.81	35.14	2.240	3.53E-04	Lfng
469	4.791	4.964	5.175	5.896	6.209	5.570	31.68	4.24	60.35	13.26	1.905	3.55E-04	Gm7609
470	7.523	7.620	7.460	8.936	8.356	8.282	185.59	10.43	376.24	98.72	2.027	3.66E-04	Ifngr1
471	4.566	4.737	4.613	5.842	5.463	5.301	24.94	1.54	46.97	9.31	1.883	3.66E-04	Myo9a
472	3.297	3.413	3.269	4.446	4.695	4.070	10.04	0.54	21.50	4.56	2.141	3.68E-04	Gimap3
473	5.147	5.163	5.029	7.458	6.637	5.886	34.64	1.74	111.47	59.24	3.218	3.77E-04	Tspan13
474	5.188	5.301	5.048	8.754	6.809	6.266	36.33	3.17	206.98	195.51	5.698	3.78E-04	Serpine1
475	7.160	6.952	6.967	8.555	8.131	7.587	130.64	10.77	282.86	91.90	2.165	3.80E-04	Cln6
476	7.280	7.116	7.353	6.202	6.507	6.604	152.53	12.63	87.28	12.24	0.572	3.88E-04	Hsf2
477	4.460	4.590	4.714	7.000	5.668	5.571	24.11	2.12	75.45	45.52	3.129	3.90E-04	Aoah
478	4.441	4.237	4.251	6.340	5.598	5.020	19.87	1.60	53.96	24.74	2.715	3.95E-04	Pqlc3
479	4.688	4.276	4.813	6.370	5.622	5.397	24.42	4.52	58.04	21.67	2.376	4.04E-04	Frzb
480	10.165	10.689	10.132	11.407	10.880	11.093	1307.00	298.40	2261.87	421.23	1.731	4.04E-04	Nnmt
481	4.053	4.349	3.721	5.033	5.168	4.732	16.72	3.60	31.76	4.76	1.899	4.04E-04	Top2a

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT avg	WTsd	KO avg	KOsd	KO/WT	BH	Gene Symbol
482	4.393	4.176	4.521	5.609	5.247	5.014	20.68	2.46	39.70	8.38	1.920	4.09E-04	Far1
483	10.191	10.299	9.965	11.159	10.828	10.568	1142.74	132.24	1874.15	387.98	1.640	4.09E-04	Gm
484	5.003	5.163	4.847	6.236	6.027	5.634	32.22	3.53	63.41	12.93	1.968	4.10E-04	Tifab
485	8.129	7.630	7.706	8.732	8.585	8.787	228.93	44.45	417.02	29.71	1.822	4.15E-04	Nampt
486	4.177	4.326	4.345	6.183	5.166	5.067	19.49	1.22	47.36	21.93	2.430	4.15E-04	Pilrb2
487	4.549	4.504	4.504	5.309	5.315	5.329	22.93	0.41	39.89	0.29	1.740	4.26E-04	Sh2d2a
488	4.044	3.895	3.903	4.760	4.647	4.546	15.44	0.91	25.17	1.87	1.630	4.34E-04	Hpgds
489	4.566	4.638	4.538	5.399	6.022	5.201	23.94	0.86	47.99	14.98	2.005	4.37E-04	H2-Ob
490	9.018	9.274	9.170	10.514	10.043	9.691	571.34	50.53	1114.64	321.87	1.951	4.41E-04	Lgmn
491	7.128	6.910	6.640	8.006	7.977	7.479	119.94	20.05	229.14	44.06	1.910	4.41E-04	Prkx
492	6.951	7.365	6.787	8.611	7.727	7.928	133.00	28.37	282.15	95.67	2.121	4.50E-04	Gm6644
493	4.211	4.204	4.138	5.520	5.186	4.680	18.19	0.50	35.98	10.13	1.978	4.55E-04	Cyp1b1
494	4.325	4.704	4.552	6.405	5.744	5.226	23.19	3.02	58.59	24.05	2.527	4.60E-04	Pik3cg
495	7.740	7.564	7.723	6.838	7.122	6.679	204.79	13.48	118.74	18.78	0.580	4.62E-04	Atoh8
496	7.959	8.476	8.062	9.982	9.274	8.849	290.75	57.39	697.27	283.34	2.398	4.64E-04	Csf1r
497	5.269	5.605	5.096	5.954	7.732	6.893	40.47	7.41	131.13	76.05	3.240	4.64E-04	Gbp4
498	8.223	8.337	8.168	9.884	8.969	8.948	303.31	18.32	646.54	258.12	2.132	4.64E-04	Ppap2c
499	7.834	7.776	6.725	9.078	9.289	8.284	184.42	68.24	492.54	162.23	2.671	4.64E-04	Il1r1
500	8.336	8.220	8.393	7.156	6.935	7.841	319.24	19.30	164.73	56.78	0.516	4.64E-04	Mid1ip1
501	8.730	8.385	8.076	9.460	9.451	9.104	342.94	77.71	651.46	87.51	1.900	4.70E-04	Efh2
502	9.003	9.258	9.116	10.314	10.089	9.715	560.16	49.81	1067.46	216.86	1.906	4.71E-04	Hist1h3a // Hist1h3i // Hist1h3h // Hist1h3g
503	5.576	5.764	5.528	6.639	7.033	6.159	49.39	4.35	100.67	29.74	2.038	4.71E-04	Slc16a6
504	4.103	4.491	4.070	5.314	5.371	4.807	18.82	3.17	36.38	7.31	1.933	4.74E-04	Ikzf3
505	5.189	5.267	5.167	6.702	6.340	5.797	36.97	1.35	80.24	24.28	2.170	4.88E-04	Tmem229b
506	4.702	4.734	5.129	6.498	5.874	5.621	29.21	5.02	66.08	21.56	2.262	4.89E-04	P2ry14
507	5.895	5.992	5.839	7.133	6.850	6.455	60.15	3.24	114.50	26.33	1.904	4.89E-04	Hip1
508	5.901	6.027	5.818	7.664	6.744	6.763	60.47	4.45	139.55	54.78	2.308	4.89E-04	Itgb3
509	2.901	3.133	2.785	3.817	4.075	3.676	7.71	0.96	14.58	2.08	1.890	4.92E-04	Ccl8
510	6.985	7.621	6.574	10.160	9.137	7.914	139.62	52.00	649.33	457.47	4.651	4.96E-04	9030619P08Rik
511	4.258	4.292	4.128	5.861	5.224	4.831	18.74	1.11	41.33	15.22	2.206	4.96E-04	Naip5
512	6.749	7.026	6.903	8.256	7.765	7.550	119.20	11.41	236.88	61.40	1.987	4.96E-04	Sema6d
513	5.275	5.587	5.150	7.173	6.749	6.024	40.75	6.52	105.62	39.63	2.592	5.02E-04	Abr
514	6.113	5.966	5.566	6.941	6.993	6.523	59.69	11.19	114.09	19.30	1.911	5.03E-04	Setd7
515	8.597	8.648	8.544	9.501	9.262	9.103	387.21	14.00	629.33	88.26	1.625	5.09E-04	Myh9
516	5.937	5.975	5.885	7.014	7.242	6.424	61.09	1.91	122.16	33.33	2.000	5.12E-04	Fmn12
517	9.667	9.897	9.468	10.591	10.231	10.297	824.95	123.18	1334.11	182.34	1.617	5.12E-04	Slc3a1
518	5.772	6.005	5.796	7.941	7.133	6.532	58.14	5.29	159.51	78.33	2.743	5.12E-04	Eif4e3
519	10.889	10.941	11.258	11.384	11.591	11.752	2103.73	300.73	3069.05	388.72	1.459	5.12E-04	Apoa4
520	6.595	6.432	6.678	7.897	7.713	7.161	95.13	8.13	197.10	48.90	2.072	5.14E-04	Olfml3
521	6.969	7.865	8.244	5.739	5.577	6.963	220.52	89.64	75.30	42.93	0.341	5.14E-04	Fam13a
522	4.284	4.795	4.756	6.053	5.374	5.426	24.75	4.58	50.27	13.96	2.031	5.19E-04	Gpr137b-ps
523	5.728	5.940	5.407	8.584	7.134	6.509	52.29	9.51	205.10	156.72	3.923	5.25E-04	Alox5ap
524	8.071	8.095	8.098	6.613	7.523	7.126	272.09	2.80	140.48	43.04	0.516	5.27E-04	Mmp15
525	4.170	4.201	4.000	5.068	5.146	4.655	17.47	1.28	31.37	5.44	1.796	5.28E-04	Arhgef6
526	4.351	4.412	4.386	5.026	5.370	5.145	20.87	0.44	36.44	4.47	1.746	5.37E-04	Cd2
527	5.195	5.427	5.065	6.547	6.368	5.750	37.70	4.86	76.63	20.50	2.032	5.40E-04	Arhgap30
528	3.005	3.150	3.135	4.143	3.818	3.759	8.56	0.47	15.10	2.24	1.764	5.50E-04	Klrd1
529	8.467	8.290	8.543	9.794	9.340	9.123	346.64	30.66	697.78	170.73	2.013	5.52E-04	Tgfb1
530	6.068	6.370	6.272	7.662	7.328	6.808	75.70	7.93	158.41	45.31	2.093	5.62E-04	Emp3
531	5.276	5.226	5.079	6.401	5.972	5.915	36.67	2.57	69.19	13.31	1.887	5.63E-04	Stk39
532	7.587	7.305	7.551	8.927	8.479	8.017	179.30	18.53	367.53	114.24	2.050	5.64E-04	Ets2
533	8.821	8.826	8.786	9.670	9.465	9.538	449.24	6.84	754.95	54.78	1.681	5.64E-04	Ube2l6

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT avg	WTsd	KO avg	KOsd	KO/WT	BH	Gene Symbol
534	3.026	3.105	3.086	4.567	4.229	3.596	8.41	0.24	18.18	5.83	2.161	5.72E-04	Ms4a7
535	6.734	7.035	6.487	7.698	7.605	7.684	109.12	20.85	202.66	6.94	1.857	5.75E-04	Aig1
536	5.103	5.076	4.744	6.336	6.023	5.566	31.63	4.19	64.41	16.71	2.036	5.78E-04	Plcb2
537	5.219	5.271	4.851	6.728	6.347	5.747	34.91	5.28	80.37	26.17	2.302	5.79E-04	Apbb1ip
538	4.330	4.136	4.436	5.546	5.227	4.848	19.78	2.05	37.65	8.96	1.904	5.85E-04	Ust
539	5.125	5.284	5.131	6.542	6.149	5.735	36.30	2.32	72.46	20.00	1.996	5.90E-04	Pik3cd
540	5.421	5.582	5.431	6.071	7.571	7.282	44.62	2.84	137.67	63.40	3.085	5.93E-04	Cidec
541	4.094	4.249	4.166	5.092	6.990	5.427	18.01	0.97	68.09	51.34	3.780	5.98E-04	Mmp12
542	6.192	5.976	5.715	7.153	7.050	6.557	62.88	10.30	122.99	25.46	1.956	5.98E-04	Nedd9
543	8.415	8.044	7.722	8.632	9.710	9.967	272.14	65.46	745.18	312.53	2.738	6.01E-04	Ccnd1
544	5.600	6.247	5.819	7.349	6.702	6.631	60.29	14.12	122.09	35.54	2.025	6.02E-04	Ehd4
545	8.066	8.118	8.356	6.881	7.471	7.327	291.19	32.01	151.95	30.69	0.522	6.09E-04	Pdk1
546	4.179	4.337	4.398	4.929	5.174	5.049	19.80	1.52	33.22	2.83	1.678	6.12E-04	Rapgef5
547	9.327	9.166	9.091	10.421	9.850	9.837	587.42	49.69	1069.74	261.25	1.821	6.12E-04	Slc39a14
548	7.696	7.610	7.778	6.670	6.623	7.206	207.39	12.04	115.99	27.42	0.559	6.23E-04	Scnn1a
549	3.940	4.278	4.105	4.956	4.859	5.830	17.32	2.03	38.99	15.54	2.252	6.27E-04	Lysmd2
550	7.147	6.524	6.736	7.777	8.031	7.497	113.45	25.51	220.54	40.48	1.944	6.29E-04	Jun
551	9.149	9.206	8.976	9.947	9.667	9.797	554.02	45.23	896.67	87.24	1.618	6.31E-04	Tspan4
552	9.849	10.057	9.849	7.816	8.735	9.350	970.06	82.67	434.68	213.73	0.448	6.38E-04	Arrdc3
553	5.926	5.682	5.557	7.117	6.797	6.262	53.07	7.02	108.91	31.09	2.052	6.43E-04	Hivep2
554	5.335	5.288	5.491	4.854	4.607	4.692	41.46	3.11	26.38	2.32	0.636	6.53E-04	Pard3b
555	5.684	6.469	5.575	4.378	5.289	4.411	62.56	22.63	27.05	10.43	0.432	6.54E-04	Slc39a2
556	6.959	6.045	6.005	7.316	7.576	7.482	84.89	34.26	176.27	15.86	2.076	6.61E-04	Rassf4
557	5.563	5.771	5.666	6.354	6.643	6.338	50.88	3.67	87.54	10.73	1.721	6.64E-04	Sp100
558	7.865	7.605	7.690	6.532	6.909	7.107	211.42	19.65	116.86	22.84	0.553	6.80E-04	Ak4
559	6.747	7.285	6.992	7.769	8.272	7.701	130.23	24.39	245.12	55.65	1.882	6.90E-04	Psmb9
560	5.166	5.365	5.112	6.826	6.305	5.848	37.23	3.51	83.38	28.20	2.240	6.92E-04	Lpxn
561	4.919	5.088	4.997	5.546	5.945	5.952	32.07	1.88	56.74	8.67	1.769	6.94E-04	Cd83
562	9.362	9.436	9.274	10.154	10.034	9.944	656.67	36.95	1057.77	77.68	1.611	6.94E-04	Stat3
563	4.929	5.203	5.266	6.425	5.836	5.923	35.26	4.24	67.91	15.68	1.926	6.97E-04	Aldh18a1
564	4.235	4.457	4.590	5.780	5.843	4.960	21.62	2.64	47.82	14.52	2.212	6.99E-04	Gpr137b
565	4.990	5.030	4.890	6.847	5.845	5.720	31.36	1.55	75.10	34.74	2.394	7.01E-04	Gngt2
566	6.391	6.318	6.460	7.841	7.244	6.989	83.91	4.14	169.29	53.33	2.017	7.01E-04	Pecam1
567	5.544	6.923	5.926	5.048	4.751	4.956	76.27	39.67	30.35	3.13	0.398	7.08E-04	Capn8
568	4.854	5.285	5.012	6.527	6.113	5.676	33.39	5.13	70.87	20.60	2.122	7.10E-04	Psd4
569	3.247	3.637	3.215	4.665	4.284	4.140	10.41	1.76	20.83	4.04	2.001	7.15E-04	Arhgap11a
570	4.210	4.336	4.080	5.662	5.010	4.782	18.54	1.64	36.80	12.22	1.985	7.19E-04	Btk
571	5.807	5.681	5.812	6.843	6.594	6.310	54.50	2.75	96.89	17.71	1.778	7.19E-04	Ezr
572	4.379	4.905	4.261	7.305	5.829	5.350	23.31	5.81	85.25	63.63	3.656	7.20E-04	Alpk1
573	5.057	5.226	5.011	6.193	6.035	5.693	34.32	2.75	63.49	10.87	1.850	7.27E-04	Gpr35
574	5.455	5.374	5.522	6.414	6.315	6.120	43.76	2.25	78.13	7.96	1.785	7.70E-04	Plekha2
575	5.531	6.076	5.389	4.340	4.676	5.101	51.88	13.68	26.71	7.11	0.515	7.76E-04	Tbc1d30
576	6.292	6.831	6.403	7.838	7.529	7.124	92.27	18.93	184.29	44.64	1.997	7.89E-04	Jak3
577	4.426	4.857	5.063	10.372	6.595	6.615	27.97	6.03	506.76	709.16	18.120	7.91E-04	Iglv1
578	4.928	4.756	4.757	6.075	5.254	5.775	28.17	1.96	53.44	14.66	1.897	7.99E-04	Mbnl3
579	5.236	5.057	5.222	6.696	6.119	5.681	36.11	2.44	74.82	26.58	2.072	8.09E-04	Cd34
580	7.567	7.970	7.246	9.194	8.485	8.245	197.39	49.86	415.86	149.69	2.107	8.09E-04	Fndc3b
581	8.347	7.721	8.854	9.027	9.646	10.007	333.11	126.03	783.91	254.29	2.353	8.19E-04	Gsta1
582	4.486	4.976	4.808	6.132	5.604	5.448	27.30	4.57	54.14	14.08	1.983	8.25E-04	Slc38a1
583	7.976	7.763	7.836	8.779	8.408	8.789	232.55	17.64	407.08	58.30	1.751	8.42E-04	B4galt5
584	4.366	4.389	4.415	7.375	6.112	4.994	20.97	0.35	89.01	69.21	4.245	8.59E-04	Sirpb1b
585	6.089	6.467	6.373	7.713	7.122	6.949	79.80	10.53	157.53	45.93	1.974	8.63E-04	Plekho1
586	3.401	3.591	3.485	4.460	4.436	3.962	11.27	0.75	19.75	3.61	1.752	8.64E-04	Scn7a
587	4.512	4.567	4.228	5.629	5.203	5.071	21.76	2.65	39.98	8.40	1.838	8.82E-04	Clec9a

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT avg	WTsd	KO avg	KOsd	KO/WT	BH	Gene Symbol
588	3.516	4.030	4.322	10.889	6.179	6.164	15.93	4.30	680.04	1052.98	42.701	9.06E-04	Igkv1-133
589	7.750	7.620	7.748	6.625	6.989	7.119	208.96	10.61	121.56	20.68	0.582	9.06E-04	Kank1
590	5.055	5.324	4.904	7.530	6.190	5.910	34.42	5.16	106.02	68.60	3.080	9.10E-04	Sell
591	3.652	3.564	3.662	5.063	4.745	4.181	12.35	0.46	26.13	7.67	2.116	9.46E-04	Tlr1
592	6.747	6.745	6.279	8.061	7.953	7.098	97.43	17.14	217.27	70.14	2.230	0.0010	Icam1
593	4.288	4.239	4.161	6.942	5.435	4.970	18.77	0.82	65.85	49.80	3.508	0.0010	Pglyrp1
594	8.264	7.639	8.735	8.918	9.545	9.869	310.96	113.45	721.99	226.59	2.322	0.0010	Gm3776
595	8.151	8.042	7.961	8.946	8.937	8.557	265.68	17.62	453.34	66.44	1.706	0.0010	Myd88
596	9.158	9.276	9.113	10.879	10.029	9.654	581.68	34.40	1244.36	565.89	2.139	0.0010	Ctsc
597	4.269	4.308	4.592	5.252	5.684	4.989	21.07	2.66	40.43	10.04	1.919	0.0010	Il21r
598	5.258	4.819	5.401	6.430	6.333	5.673	36.24	7.23	72.61	18.92	2.004	0.0010	Lum
599	6.943	6.798	7.027	3.792	5.648	6.044	121.56	9.64	43.32	26.72	0.356	0.0010	Ar
600	4.573	4.703	4.720	5.377	5.722	5.391	25.40	1.40	45.43	6.37	1.789	0.0010	Lat
601	3.896	4.201	3.993	5.633	4.814	4.734	16.40	1.80	34.78	12.86	2.121	0.0010	Ptplad2
602	6.355	6.422	6.292	7.115	7.262	6.909	81.97	3.71	137.41	16.64	1.676	0.0010	Stmn1
603	5.077	5.153	4.347	5.987	5.937	5.848	29.90	8.31	60.76	2.93	2.032	0.0010	Plk1
604	8.895	8.811	9.087	8.224	8.073	8.279	489.65	48.68	293.01	21.33	0.598	0.0010	4933403F05Rik
605	5.513	5.523	5.738	4.052	4.166	5.248	48.35	4.36	24.18	11.98	0.500	0.0010	Gm4956
606	4.431	4.446	4.263	5.310	5.027	5.092	20.85	1.44	35.47	3.72	1.701	0.0010	Ap1s3
607	6.952	6.899	7.149	6.170	6.093	6.485	128.37	11.98	76.63	11.38	0.597	0.0010	Depdc7
608	5.349	5.315	5.210	7.266	6.280	5.933	39.20	1.94	97.56	49.47	2.489	0.0010	Fgr
609	4.172	4.307	3.838	5.272	4.957	4.621	17.37	2.80	31.43	7.02	1.810	0.0010	Lax1
610	4.988	5.509	5.178	6.003	6.178	5.877	37.82	7.05	65.11	6.88	1.721	0.0010	Runx3
611	5.402	5.471	4.915	7.047	6.563	5.773	38.93	7.66	93.83	38.79	2.410	0.0010	Sifn2
612	5.909	6.127	5.634	7.443	6.873	6.445	59.88	10.11	126.11	44.12	2.106	0.0010	Cmklr1
613	4.665	4.835	4.634	9.214	6.253	6.057	26.25	2.00	245.55	301.64	9.356	0.0010	D17H6S56E-5
614	4.193	4.561	4.249	5.026	5.003	5.129	20.30	2.88	33.21	1.57	1.636	0.0010	Klf20a
615	6.728	6.864	6.446	7.358	8.051	7.380	103.20	14.84	198.62	57.75	1.925	0.0010	Nlrc5
616	5.596	5.719	5.653	7.319	6.618	6.207	50.46	2.15	110.58	44.20	2.191	0.0010	Rgs19
617	9.196	9.312	9.085	10.088	9.935	9.576	588.53	46.34	943.51	165.31	1.603	0.0010	Hist1h2ao
618	6.842	7.354	6.746	8.504	7.649	7.764	128.55	30.57	260.40	89.23	2.026	0.0010	Akr1b3
619	4.127	4.337	4.223	5.593	5.489	4.626	18.78	1.37	39.28	12.74	2.091	0.0010	Cd63
620	4.817	4.842	4.785	5.853	5.546	5.337	28.15	0.55	48.30	8.79	1.716	0.0010	Ggt5
621	3.038	3.199	3.142	7.947	5.582	4.042	8.74	0.49	103.70	124.87	11.864	0.0010	Mmp8
622	5.472	5.918	5.239	7.660	6.414	6.429	47.54	11.68	124.55	67.27	2.620	0.0010	Tmem26
623	5.455	5.587	5.556	6.717	6.435	6.072	46.32	2.19	86.35	18.97	1.864	0.0010	Gbgt1
624	5.288	5.106	5.353	4.155	4.518	4.764	38.12	3.32	22.63	4.69	0.594	0.0010	Gm10033
625	5.532	5.199	5.474	6.424	6.583	5.911	42.48	5.06	80.65	18.43	1.899	0.0010	Thbs2
626	4.391	4.236	4.324	5.849	5.102	4.989	19.95	1.07	41.23	14.25	2.067	0.0010	Cysltr1
627	5.572	5.753	5.791	6.902	6.456	6.358	52.28	4.14	96.46	20.21	1.845	0.0011	Fli1
628	6.690	6.563	6.790	5.688	6.080	6.076	102.81	8.04	62.22	9.25	0.605	0.0011	Naaladl2
629	3.540	3.823	3.420	4.709	4.505	4.142	12.16	1.78	22.17	4.28	1.823	0.0011	Gcnt1
630	7.446	8.143	7.657	9.806	8.821	8.564	219.66	56.33	575.30	279.44	2.619	0.0011	Cfp
631	5.060	5.285	5.341	6.191	5.747	6.484	37.63	3.78	72.09	17.91	1.915	0.0011	Tspan15
632	6.462	6.703	6.318	7.724	7.231	7.114	90.70	12.40	166.75	39.14	1.839	0.0011	Adcy4
633	7.802	8.011	7.866	9.463	8.825	8.484	238.18	17.89	505.75	179.68	2.123	0.0011	Cd97
634	4.737	4.841	4.836	7.815	6.171	5.540	27.96	1.12	114.58	96.59	4.098	0.0011	Il1rn
635	5.180	5.333	5.292	6.900	6.115	5.966	38.58	2.09	83.73	31.07	2.171	0.0011	Cyp4f16
636	6.230	6.671	6.440	8.671	7.661	6.997	87.91	13.45	245.91	144.84	2.797	0.0011	Tifa
637	4.394	4.614	4.593	5.074	5.504	5.512	23.22	1.90	41.56	6.83	1.790	0.0011	Cd8b1
638	5.647	5.726	6.012	6.825	6.763	6.248	55.85	7.65	99.33	20.33	1.779	0.0011	Lbh
639	4.845	4.826	4.977	6.215	5.729	5.458	29.54	1.71	57.09	15.56	1.933	0.0011	Apaf1
640	6.312	6.285	6.383	7.940	7.398	6.848	80.30	2.86	176.49	65.52	2.198	0.0011	Fam49b
641	5.052	4.816	4.797	5.862	5.570	5.570	29.71	3.00	51.06	6.17	1.719	0.0011	Itipr12

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT avg	WTsd	KO avg	KOsd	KO/WT	BH	Gene Symbol
642	5.607	5.845	5.467	7.804	6.482	6.527	50.16	6.74	135.06	76.62	2.693	0.0011	Pilrb1
643	7.029	6.959	6.781	8.357	7.810	7.484	121.68	10.57	243.78	76.27	2.003	0.0011	Ptpn1
644	7.927	7.749	8.093	8.539	8.887	8.613	243.84	29.00	412.36	53.89	1.691	0.0012	Col14a1
645	2.849	3.020	2.916	3.686	3.692	3.587	7.62	0.46	12.61	0.51	1.654	0.0012	Al504432
646	5.163	5.337	5.160	6.905	6.036	5.920	37.33	2.66	82.00	32.87	2.197	0.0012	Sh3kbp1
647	9.274	9.540	9.507	7.628	8.483	8.831	696.93	67.91	337.06	130.11	0.484	0.0012	Alas2
648	5.847	6.393	6.166	7.415	7.286	6.598	71.12	13.23	141.22	39.07	1.985	0.0012	C3ar1
649	6.725	7.094	6.425	9.296	8.308	7.297	109.43	25.54	367.58	239.69	3.359	0.0012	Cd300ld
650	5.740	5.835	5.989	6.387	7.094	7.632	58.02	5.10	139.57	57.44	2.406	0.0012	Ifi44
651	4.713	5.557	5.102	5.810	6.047	6.251	35.88	10.51	66.13	10.05	1.843	0.0012	Oas1g
652	7.433	7.411	7.780	6.600	6.991	6.698	187.59	27.93	109.35	15.86	0.583	0.0012	Dlc1
653	5.359	5.811	5.434	7.410	6.624	6.073	46.80	8.17	111.99	52.63	2.393	0.0012	Syk
654	5.647	5.867	5.707	7.269	6.575	6.287	53.57	4.29	109.19	39.92	2.038	0.0012	Serpinb6a
655	5.034	4.951	5.299	6.555	6.341	5.513	34.36	4.44	73.59	25.03	2.142	0.0012	Svep1
656	6.621	6.785	6.615	7.868	7.480	7.229	102.24	6.95	187.43	42.48	1.833	0.0012	Evl
657	4.459	4.270	4.244	4.982	5.515	5.009	20.08	1.67	36.51	7.98	1.818	0.0012	Cd27
658	5.566	6.092	5.678	6.698	6.745	6.594	55.60	11.08	102.58	5.45	1.845	0.0012	Oasl2
659	7.256	7.360	7.252	6.183	6.841	6.442	156.49	6.71	91.40	21.34	0.584	0.0012	Ank
660	5.304	5.283	5.439	6.219	6.606	6.005	40.61	2.42	78.71	16.99	1.938	0.0013	Fbn1
661	4.867	4.806	4.502	6.556	5.885	5.326	26.60	3.47	64.44	27.39	2.422	0.0013	Gdpd1
662	4.758	4.667	4.677	5.734	5.415	5.241	26.02	0.91	44.56	7.87	1.713	0.0013	Cxcr4
663	8.678	8.733	8.519	9.561	9.266	9.056	400.65	30.42	634.38	112.72	1.583	0.0013	Tapbp
664	4.580	4.522	4.486	5.989	5.403	5.135	23.11	0.76	47.00	14.76	2.034	0.0013	Slc25a36
665	4.360	4.369	4.630	4.953	5.106	5.310	21.99	2.40	35.02	4.38	1.593	0.0013	D14Ert668e
666	6.778	7.010	6.761	7.621	7.668	7.568	115.67	11.44	196.66	6.77	1.700	0.0013	Parp14
667	5.307	5.162	5.302	4.657	4.512	4.676	38.29	2.15	24.54	1.50	0.641	0.0013	Zfp354a
668	8.442	8.395	8.436	7.510	7.652	7.483	343.49	6.06	187.45	11.96	0.546	0.0013	Ulk2
669	7.490	7.567	7.743	4.752	6.481	6.861	194.59	17.77	77.50	45.80	0.398	0.0013	Bdh2
670	5.407	5.577	5.890	4.940	4.889	4.972	49.82	8.62	30.57	0.89	0.614	0.0013	Gl28d2
671	10.934	10.749	10.824	2.452	7.629	8.971	1830.01	119.09	235.12	250.29	0.128	0.0013	Hsd3b5
672	7.585	7.691	7.523	9.124	8.301	8.218	194.20	11.45	390.32	145.32	2.010	0.0013	Plscr1
673	5.211	5.450	5.337	7.056	6.283	5.851	40.39	3.33	89.55	39.01	2.217	0.0013	Cd84
674	4.554	4.510	4.274	5.219	5.248	5.088	21.87	2.21	36.42	2.12	1.665	0.0014	Pla2g16
675	3.428	3.484	3.278	4.570	4.283	3.894	10.55	0.77	19.36	4.45	1.835	0.0014	Fpr3
676	4.740	4.820	4.553	6.123	5.522	5.325	26.15	2.43	51.91	15.67	1.985	0.0014	Klf21b
677	7.213	7.697	7.267	6.188	6.796	6.589	169.98	32.63	93.41	19.25	0.550	0.0014	Syt1
678	9.445	9.343	9.544	8.484	8.917	8.779	697.67	48.68	426.82	63.50	0.612	0.0014	Slc19a2
679	4.471	4.675	4.864	6.066	5.361	5.220	25.62	3.47	48.46	16.17	1.892	0.0014	Osbpl3
680	5.932	5.897	5.847	6.756	6.759	6.531	59.40	1.77	102.94	9.08	1.733	0.0014	H2-Q1
681	6.562	6.549	6.244	7.524	7.296	7.042	87.96	10.53	157.67	26.13	1.793	0.0014	Mlxip
682	8.144	8.078	8.282	7.086	7.586	7.440	288.08	20.99	167.23	28.69	0.580	0.0014	Fndc4
683	2.603	2.576	2.697	3.443	3.527	3.248	6.18	0.27	10.64	1.03	1.722	0.0014	Slc7a11
684	3.530	3.602	3.602	2.885	2.404	3.045	11.94	0.34	6.98	1.52	0.584	0.0014	Tex12
685	5.197	5.302	4.798	8.405	6.084	6.336	34.65	6.08	162.51	152.94	4.690	0.0014	Apoec3
686	6.299	6.542	6.191	7.283	7.150	6.868	81.67	10.37	138.20	19.76	1.692	0.0014	Mob3a
687	3.053	2.667	2.752	4.032	3.443	3.642	7.13	1.03	13.24	2.82	1.857	0.0015	Hist1h2ab
688	9.201	9.317	9.086	10.078	9.934	9.578	589.89	47.12	941.05	161.57	1.595	0.0015	Hist1h2af
689	4.919	4.640	4.551	5.834	5.302	5.266	26.21	3.58	45.00	10.45	1.717	0.0015	Tes
690	4.572	4.626	4.267	5.859	5.428	4.988	22.58	2.91	44.27	13.19	1.961	0.0015	Ddx26b
691	3.016	2.994	2.987	3.552	3.677	3.799	7.99	0.08	12.81	1.09	1.603	0.0015	Tlr11
692	7.697	8.182	7.816	9.422	8.786	8.544	241.02	43.63	500.29	164.42	2.076	0.0015	Sdc3
693	5.436	5.621	5.622	6.818	6.502	6.042	47.24	3.43	89.76	23.48	1.900	0.0015	Neurl3
694	3.920	3.925	4.022	3.419	3.319	3.391	15.52	0.63	10.39	0.37	0.669	0.0015	4921506M07Rik
695	7.436	7.655	7.581	7.016	6.900	6.376	188.75	14.40	110.63	24.42	0.586	0.0016	Lrrc16a

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT avg	WTsd	KO avg	KOsd	KO/WT	BH	Gene Symbol
696	4.589	4.589	4.978	5.558	5.958	5.172	26.55	4.30	48.44	13.10	1.824	0.0016	Csprs
697	2.545	2.705	2.933	3.391	3.759	3.528	6.67	0.91	11.86	1.55	1.779	0.0016	Klra17
698	7.434	7.485	7.561	7.915	9.039	8.615	180.32	8.03	386.51	142.45	2.144	0.0016	Stat1
699	3.712	3.509	3.979	8.166	5.545	4.746	13.42	2.21	120.23	144.91	8.958	0.0016	Casp12
700	4.704	4.953	4.560	6.233	5.896	5.152	26.87	3.76	56.76	19.96	2.112	0.0016	Dram1
701	7.556	7.469	7.456	8.890	8.410	7.939	180.34	6.82	353.34	115.12	1.959	0.0016	Pkm
702	4.741	5.096	4.849	6.252	5.726	5.454	29.92	3.85	57.66	16.71	1.927	0.0016	1-Mar
703	4.016	4.082	4.030	4.875	4.471	4.840	16.48	0.40	26.72	3.96	1.621	0.0016	Igf2bp3
704	4.915	4.978	4.733	6.218	5.777	5.289	29.43	2.55	56.11	17.70	1.907	0.0016	Ly75
705	8.807	8.500	8.787	7.140	7.642	8.283	417.20	47.92	217.40	86.58	0.521	0.0016	Klb
706	4.979	4.911	5.050	5.553	5.794	5.761	31.59	1.52	52.21	4.61	1.653	0.0016	Ntf3
707	5.672	5.767	5.642	7.807	6.701	6.311	51.80	2.36	135.79	77.35	2.622	0.0017	Ncf2
708	6.170	6.497	6.254	7.915	7.205	6.811	79.54	9.57	167.07	66.76	2.101	0.0017	Gab2
709	4.124	4.653	4.270	6.239	5.138	5.101	20.63	4.03	48.36	23.55	2.344	0.0017	Spic
710	7.039	6.720	6.892	6.097	6.338	6.083	118.55	13.04	72.37	7.40	0.611	0.0017	Mir22
711	9.774	10.976	8.870	11.418	11.176	11.239	1119.16	801.60	2488.80	220.44	2.224	0.0017	Fgl1
712	3.672	3.561	3.437	4.820	4.624	4.049	11.79	0.96	23.15	5.99	1.964	0.0017	Slfn1
713	10.334	10.490	10.476	9.524	9.845	10.001	1384.41	81.65	893.54	145.97	0.645	0.0017	Pecr
714	4.840	4.759	4.911	5.840	5.550	5.368	28.60	1.50	48.48	8.12	1.695	0.0018	Asf1b
715	6.986	7.099	6.833	8.275	7.891	7.448	125.96	11.57	240.63	67.64	1.910	0.0018	Csf2ra
716	10.691	10.478	10.734	9.483	10.207	10.074	1594.17	147.47	991.68	244.73	0.622	0.0018	Glo1
717	5.501	5.847	5.475	7.120	6.666	6.222	49.11	7.33	105.09	32.40	2.140	0.0018	Ncf1
718	7.542	6.928	8.035	8.069	8.716	8.976	190.17	70.34	397.59	119.23	2.091	0.0018	Gm10639
719	6.354	6.384	6.063	7.590	7.113	6.878	77.37	9.16	149.55	38.71	1.933	0.0018	Pgm1
720	5.582	5.009	5.791	5.981	7.480	6.725	45.16	11.83	115.85	58.37	2.565	0.0018	Sparcl1
721	4.169	4.230	4.444	2.740	3.429	3.731	19.51	1.99	10.24	3.33	0.525	0.0018	Omd
722	3.305	3.622	3.582	4.323	4.324	3.866	11.39	1.31	18.21	3.14	1.598	0.0019	Atp8b4
723	7.598	7.623	7.829	6.468	7.317	6.412	206.06	18.56	111.03	41.93	0.539	0.0019	Stard13
724	6.318	6.337	6.369	7.069	7.551	6.918	81.09	1.45	147.60	35.28	1.820	0.0019	Col1a1
725	7.891	7.837	7.958	6.749	7.287	7.085	238.20	10.00	133.17	24.41	0.559	0.0019	Vwce
726	4.794	4.878	5.136	4.192	4.016	4.460	30.77	3.90	18.82	2.95	0.612	0.0019	Gm11992
727	4.583	4.716	4.613	5.400	5.431	5.246	24.90	1.22	41.11	2.78	1.651	0.0019	Ifit2
728	10.107	9.767	9.293	10.572	10.312	10.378	867.04	237.79	1374.63	130.79	1.585	0.0019	Por
729	7.371	6.794	7.053	7.815	7.895	7.893	136.46	27.45	233.59	7.34	1.712	0.0019	Colec11
730	5.812	5.691	5.786	6.452	6.359	6.718	54.34	2.39	91.64	12.12	1.687	0.0019	Gpc6
731	10.944	11.591	10.883	12.040	11.776	11.560	2314.10	668.29	3579.14	600.06	1.547	0.0019	Lrg1
732	5.865	6.074	5.876	7.514	6.785	6.473	61.47	5.13	127.30	49.24	2.071	0.0019	Slc43a2
733	4.792	5.103	4.838	6.045	5.302	6.096	30.22	3.62	57.96	16.08	1.918	0.0019	Gucy2c
734	3.049	3.177	3.200	5.070	4.024	3.752	8.84	0.49	21.11	10.90	2.390	0.0020	Clec4a2
735	6.792	6.907	7.593	6.423	6.174	5.935	141.30	45.11	73.06	12.32	0.517	0.0020	Gas1
736	4.038	4.206	4.068	4.963	4.835	4.552	17.22	1.09	27.73	3.93	1.611	0.0020	Kif23
737	4.862	4.764	4.523	5.781	5.188	5.590	26.41	3.12	46.55	9.37	1.762	0.0020	Galnt7
738	6.761	6.788	7.100	7.648	7.475	7.628	118.70	16.01	192.09	12.39	1.618	0.0020	Gm8300
739	9.257	9.155	8.872	10.722	9.818	9.629	550.05	73.78	1127.75	489.10	2.050	0.0020	Arpc1b
740	6.578	6.646	6.602	7.612	7.379	7.147	97.63	2.34	167.96	26.98	1.720	0.0020	Slc9a9
741	4.496	5.018	4.770	6.242	5.618	5.310	27.42	4.93	54.82	18.66	2.000	0.0020	Epb4.1i3
742	5.415	5.611	5.757	7.031	6.498	6.112	48.55	5.72	96.79	31.30	1.994	0.0021	Agpat9
743	5.569	5.107	4.541	6.172	6.206	5.734	35.07	12.10	66.38	11.43	1.893	0.0021	Gadd45b
744	7.096	7.140	7.289	6.148	6.520	6.589	144.74	10.27	86.32	13.52	0.596	0.0021	Odz3
745	6.017	6.021	5.989	7.044	6.890	6.472	64.41	0.76	113.14	22.13	1.757	0.0021	Fgd2
746	7.190	7.010	7.406	8.066	8.119	7.663	148.15	20.45	249.57	40.91	1.685	0.0021	Dpysl2
747	8.184	8.095	7.740	9.091	8.535	8.678	259.34	40.45	441.93	91.54	1.704	0.0021	Fam134b
748	5.720	5.874	5.804	7.588	6.996	6.217	55.73	2.97	131.48	59.13	2.359	0.0022	Susd2
749	5.322	5.474	4.560	7.120	6.219	5.754	36.02	10.99	89.20	44.45	2.476	0.0022	Cd24a

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT avg	WTsd	KO avg	KOsd	KO/WT	BH	Gene Symbol
750	4.537	4.683	4.853	5.708	5.731	5.219	25.93	2.85	47.53	8.93	1.833	0.0022	Aif1
751	4.647	4.709	4.514	5.919	5.443	5.105	24.68	1.68	46.14	13.24	1.869	0.0022	Adrbk2
752	6.382	6.172	6.314	5.467	5.674	5.417	78.34	5.74	46.00	4.43	0.587	0.0022	Syt3
753	8.791	8.754	8.682	7.413	8.224	8.028	428.37	16.32	243.47	66.06	0.568	0.0022	Al317395
754	8.619	9.132	8.662	10.079	9.630	9.427	453.14	93.58	854.19	203.67	1.885	0.0022	Clec4f
755	3.011	2.729	2.745	3.600	4.362	3.508	7.13	0.81	14.69	5.10	2.059	0.0022	Ly6i
756	4.659	4.684	4.535	5.430	5.425	5.158	24.72	1.35	40.58	4.24	1.642	0.0022	Stard9
757	6.205	6.622	6.235	7.475	6.840	7.078	82.51	13.84	142.53	32.33	1.727	0.0022	Timd4
758	5.480	5.740	5.449	6.779	6.359	6.032	47.25	5.39	85.78	22.41	1.815	0.0022	Cmtm7
759	7.207	7.373	7.635	8.325	8.246	7.921	170.76	25.84	288.89	41.21	1.692	0.0022	Trp53i11
760	7.932	8.061	8.299	7.333	6.897	7.595	275.39	36.06	157.93	37.21	0.573	0.0022	Apol7a
761	4.765	4.986	4.932	5.804	5.582	5.356	29.81	2.33	48.24	7.46	1.619	0.0022	Gramd1b
762	5.526	5.388	5.573	6.407	6.425	6.023	45.19	2.96	78.59	11.77	1.739	0.0022	Pdgfb
763	4.148	4.307	4.990	3.540	3.869	3.559	23.10	7.59	12.68	1.67	0.549	0.0022	Cml3
764	5.219	5.292	5.327	6.309	6.031	5.767	38.85	1.49	66.39	12.45	1.709	0.0023	Dok2
765	6.229	6.383	6.268	8.001	7.125	6.827	78.52	4.39	169.76	75.98	2.162	0.0023	G6pdx
766	6.032	6.142	6.066	8.478	6.700	7.157	67.70	2.67	201.09	136.12	2.971	0.0023	Scd2
767	5.674	5.531	5.632	6.797	6.181	6.226	48.97	2.46	86.21	21.68	1.761	0.0023	Bcl2
768	7.825	7.795	7.636	8.999	8.269	8.414	215.91	14.85	387.13	109.15	1.793	0.0023	Cpd
769	6.559	7.382	6.362	5.830	5.961	5.523	114.46	45.75	55.05	8.31	0.481	0.0023	Acot11
770	6.176	7.211	7.125	5.803	5.331	6.163	120.03	41.54	55.91	15.69	0.466	0.0023	1810046K07Rik
771	7.157	7.336	6.981	6.120	6.007	6.680	143.53	17.66	78.81	20.72	0.549	0.0023	Fam47e
772	4.757	4.875	4.873	5.419	5.341	5.615	28.56	1.32	44.11	4.39	1.544	0.0023	Ube2c
773	10.812	10.685	10.688	11.164	11.044	11.331	1697.73	86.13	2327.19	233.90	1.371	0.0023	Xbp1
774	5.810	6.234	6.013	4.658	5.477	5.304	65.32	9.61	36.43	10.01	0.558	0.0023	Exph5
775	8.162	7.938	7.951	5.681	7.349	6.935	259.75	23.19	112.21	56.53	0.432	0.0023	Avpr1a
776	8.098	8.150	8.317	7.446	7.241	7.658	292.34	23.51	175.86	25.36	0.602	0.0023	Fam20c
777	5.890	6.042	5.689	7.384	6.733	6.350	58.94	7.16	118.30	43.94	2.007	0.0023	Slc16a9
778	5.048	5.729	4.959	8.219	6.364	6.063	39.08	12.14	149.04	129.13	3.814	0.0023	Prtn3
779	6.753	7.061	7.128	5.657	6.388	6.344	127.10	16.94	71.80	18.54	0.565	0.0023	Snx29
780	5.806	6.792	7.790	3.723	4.840	6.023	129.33	84.21	35.63	26.61	0.275	0.0024	Sucnr1
781	5.245	5.531	5.254	6.179	6.430	5.815	40.77	4.75	71.67	14.98	1.758	0.0024	H2-M3
782	6.242	6.659	6.280	8.049	6.993	7.233	84.81	14.10	180.85	73.58	2.132	0.0024	Hexb
783	8.844	8.897	9.612	6.189	7.981	8.293	573.00	181.77	213.06	125.12	0.372	0.0024	Fabp2
784	7.322	7.632	7.712	6.129	6.466	7.240	189.35	26.08	103.19	42.57	0.545	0.0024	P2ry4
785	8.586	8.988	9.016	8.322	8.167	8.101	469.96	74.34	294.02	23.48	0.626	0.0024	Cited2
786	5.032	4.934	5.060	6.386	5.650	5.560	32.21	1.46	60.34	20.22	1.873	0.0024	Ddr1
787	4.816	5.092	4.567	6.290	5.631	5.315	28.66	5.22	55.87	19.99	1.950	0.0024	Rnasel
788	7.057	7.297	7.031	8.457	7.946	7.501	140.41	14.64	259.68	85.83	1.849	0.0024	Mertk
789	7.582	7.790	7.444	8.804	8.380	8.053	195.63	23.84	348.60	91.60	1.782	0.0024	Unc93b1
790	6.550	6.544	6.393	7.412	6.957	7.473	90.37	5.46	157.40	28.98	1.742	0.0024	Il17rb
791	7.439	7.695	7.756	8.628	8.390	8.082	198.97	22.54	334.04	62.39	1.679	0.0025	Ermp1
792	7.897	7.919	8.442	6.465	7.246	7.379	276.09	62.16	135.56	41.54	0.491	0.0025	Mreg
793	3.016	3.238	2.917	5.337	4.138	3.595	8.36	0.97	23.37	15.02	2.796	0.0025	Ccr2
794	4.404	4.475	4.174	7.982	5.797	5.119	20.49	2.17	114.36	120.30	5.582	0.0025	Casp4
795	4.897	5.897	5.319	4.388	4.738	4.519	43.10	15.15	23.52	2.92	0.546	0.0025	LOC100861572
796	6.062	6.264	6.207	6.763	7.043	7.023	72.52	5.15	123.52	12.97	1.703	0.0025	P4ha1
797	5.923	6.167	5.911	6.734	6.680	6.770	64.24	6.62	106.01	3.31	1.650	0.0025	Ctps2
798	6.755	7.051	6.784	8.222	7.667	7.369	116.94	13.61	222.39	68.62	1.902	0.0026	Gltp
799	3.710	3.892	3.863	6.413	5.213	4.263	14.16	0.94	47.16	34.13	3.330	0.0026	Sirpb1a
800	5.519	5.745	5.235	8.189	6.756	6.158	45.71	7.99	157.10	118.08	3.437	0.0026	Cd33
801	8.361	8.104	8.399	4.128	6.733	7.417	313.88	33.76	98.27	77.06	0.313	0.0026	Mup21
802	5.003	5.247	5.334	6.243	6.114	5.649	36.80	4.26	65.07	13.29	1.768	0.0026	Fblim1
803	6.635	6.891	7.073	5.944	6.172	6.119	117.56	17.67	67.72	5.48	0.576	0.0026	Ccdc141

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT avg	WTsd	KO avg	KOsd	KO/WT	BH	Gene Symbol
804	7.254	7.364	7.330	6.380	6.624	6.903	159.44	6.22	100.54	18.27	0.631	0.0026	Kcnn2
805	3.503	3.648	3.293	5.111	4.414	3.880	11.22	1.37	23.54	10.10	2.097	0.0026	A630033H20Rik
806	6.324	6.612	6.717	5.126	5.557	6.158	94.36	12.87	51.14	18.58	0.542	0.0026	2610528J11Rik
807	5.191	5.374	5.156	6.954	5.921	5.816	37.89	3.14	80.30	37.88	2.120	0.0026	Me2
808	4.498	4.643	4.413	5.503	6.059	4.960	22.96	1.87	47.71	17.89	2.078	0.0027	Irg1
809	9.474	9.505	9.831	8.492	8.832	9.241	782.83	111.01	473.52	123.50	0.605	0.0027	Nit2
810	4.023	4.063	4.100	5.284	4.666	4.549	16.71	0.45	29.25	8.46	1.751	0.0027	Anxa1
811	5.373	4.514	3.901	6.742	5.941	5.320	26.41	13.61	69.46	34.26	2.630	0.0027	Rgs1
812	4.958	5.064	4.871	6.432	5.805	5.543	31.27	2.11	62.96	20.78	2.014	0.0027	Tgfb3
813	6.678	6.066	6.310	5.414	5.705	5.719	82.92	17.98	49.17	5.65	0.593	0.0027	Gatad1
814	4.024	4.214	4.175	4.837	4.959	4.555	17.63	1.21	27.73	3.87	1.573	0.0027	Spata6
815	4.220	4.654	4.225	6.624	5.065	5.269	20.84	3.76	56.88	36.24	2.730	0.0027	Clca1
816	6.226	6.203	6.254	5.643	5.407	5.674	74.96	1.34	47.83	4.70	0.638	0.0028	Gpsm2
817	8.849	8.975	8.786	9.727	9.611	9.236	468.64	31.43	744.21	126.76	1.588	0.0028	Hist1h2ag
818	7.799	8.040	8.027	5.718	7.367	6.942	248.97	22.71	113.56	56.82	0.456	0.0028	Dpy19l3
819	4.552	4.552	4.512	5.418	5.366	4.839	23.24	0.37	37.54	7.76	1.615	0.0028	Klhl6
820	4.330	4.438	4.349	5.124	4.938	4.818	20.72	0.84	31.25	3.36	1.508	0.0028	Hvcn1
821	5.482	5.387	3.806	6.255	6.546	5.884	33.50	16.96	76.29	17.18	2.277	0.0029	Mtmr11
822	9.287	9.419	9.170	10.148	10.016	9.651	628.39	54.36	991.22	169.68	1.577	0.0029	Hist1h2ai
823	7.688	7.836	8.067	7.185	6.760	6.969	234.27	31.38	126.39	18.61	0.540	0.0029	1700001C19Rik
824	10.278	9.795	10.464	7.983	9.502	9.298	1180.81	267.05	535.82	249.56	0.454	0.0029	Ces1d
825	5.679	6.226	5.693	4.980	5.137	5.098	59.28	13.51	33.67	1.89	0.568	0.0029	Cpsf4l
826	7.417	7.091	7.264	6.403	6.543	6.861	153.65	17.29	98.04	16.33	0.638	0.0029	Mtftp1
827	4.829	4.963	5.048	5.803	5.337	5.538	30.90	2.34	47.57	7.76	1.539	0.0029	Chaf1b
828	2.970	3.154	3.374	4.723	3.855	3.659	9.04	1.27	17.84	7.48	1.974	0.0029	Trim30b
829	5.797	5.522	5.845	6.773	6.598	6.131	53.00	6.19	92.12	20.09	1.738	0.0029	Col6a1
830	4.822	4.939	5.242	5.846	5.690	5.649	32.26	4.97	53.11	3.89	1.646	0.0029	Loxl2
831	5.590	5.972	5.898	6.964	6.497	6.377	56.85	7.69	99.42	22.33	1.749	0.0030	A530032D15Rik
832	5.605	5.716	5.440	7.073	6.458	6.143	48.22	4.60	97.74	33.08	2.027	0.0030	Prkcb
833	7.680	7.763	8.014	7.063	6.972	7.036	226.93	27.99	130.18	4.20	0.574	0.0030	Hnf1b
834	9.872	9.774	10.191	10.759	10.738	10.316	993.79	154.92	1572.09	257.47	1.582	0.0030	Igfbp7
835	6.853	6.935	6.773	7.882	7.618	7.362	115.79	6.51	198.97	35.77	1.718	0.0030	Cbl
836	4.130	4.337	4.324	6.019	5.032	4.834	19.25	1.50	42.03	19.87	2.184	0.0030	Synpo
837	7.157	7.243	6.985	8.018	7.721	7.688	140.28	12.60	225.46	29.33	1.607	0.0030	Eif1a
838	5.825	6.359	5.654	7.989	7.187	6.397	63.04	16.78	161.31	85.92	2.559	0.0030	AF251705
839	5.507	5.700	5.910	6.793	6.586	6.154	52.53	7.33	92.74	20.06	1.765	0.0030	Lass5
840	11.334	11.279	11.199	11.603	11.637	11.527	2472.30	115.40	3081.93	119.26	1.247	0.0030	H2-Q7
841	6.369	5.777	5.814	6.925	6.768	6.735	64.58	15.68	112.34	8.06	1.740	0.0030	Mapkapk3
842	7.220	6.808	7.183	8.047	7.595	7.749	135.47	20.39	224.31	36.39	1.656	0.0030	Chka
843	6.179	6.160	5.869	6.669	6.711	6.869	67.47	7.83	107.82	8.02	1.598	0.0030	Bcmo1
844	5.368	5.755	5.553	6.166	6.349	6.159	47.42	6.37	74.92	5.72	1.580	0.0031	Slnf5
845	5.110	5.049	5.096	6.298	5.911	5.412	33.95	0.75	60.49	18.06	1.782	0.0031	Arrdc1
846	4.689	4.645	4.490	5.422	5.276	5.102	24.43	1.74	38.66	4.27	1.582	0.0031	Hist2h2bb
847	6.559	8.114	6.533	8.235	8.556	8.251	154.68	106.04	327.43	42.31	2.117	0.0031	Cxcl1
848	6.678	6.896	6.730	7.611	7.445	7.415	109.23	8.73	180.12	13.41	1.649	0.0031	Tnfrsf14
849	6.546	6.471	6.442	5.259	5.638	6.025	89.71	3.37	51.08	13.47	0.569	0.0032	Gm10658
850	6.517	7.030	6.514	8.355	7.521	7.229	104.54	22.62	220.35	94.18	2.108	0.0032	Siglec1
851	5.942	6.165	5.988	7.485	6.885	6.578	65.57	5.47	130.96	43.24	1.997	0.0032	Rab31
852	7.575	8.125	7.845	6.885	7.233	7.080	233.29	44.39	134.66	16.15	0.577	0.0032	Hdhd3
853	8.832	8.705	8.798	7.295	8.255	8.203	439.31	19.83	252.40	82.76	0.575	0.0032	Ugt2b38
854	5.598	5.691	5.296	6.596	6.736	5.907	46.46	6.43	87.78	24.57	1.889	0.0032	Adcy7
855	4.676	4.560	4.706	5.196	5.564	5.259	25.09	1.32	40.75	5.74	1.624	0.0032	Ptafr
856	4.275	4.406	4.205	4.913	5.046	4.787	19.66	1.40	30.27	2.72	1.539	0.0032	Itk
857	4.437	4.169	4.490	5.103	5.242	4.711	20.71	2.39	32.81	5.98	1.584	0.0032	Endod1

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT avg	WTsd	KO avg	KOsd	KO/WT	BH	Gene Symbol
858	4.467	4.837	4.551	5.910	5.483	5.101	24.71	3.42	46.39	12.99	1.877	0.0032	Napsa
859	3.813	3.922	3.717	4.881	4.458	4.266	14.12	1.00	23.56	5.29	1.668	0.0032	Fcrla
860	5.364	5.205	5.423	6.012	5.997	6.339	40.33	3.10	69.78	9.68	1.730	0.0033	Abi2
861	3.047	3.773	2.986	7.678	5.242	4.015	9.95	3.22	86.27	103.22	8.668	0.0033	Retnlg
862	5.420	4.892	5.312	6.048	5.974	5.652	37.41	6.86	59.77	8.37	1.598	0.0034	Leprel1
863	4.200	4.048	3.984	5.689	4.974	4.428	16.91	1.32	34.84	15.32	2.060	0.0034	Adm
864	6.704	6.788	7.361	6.138	6.387	5.985	126.37	33.05	72.48	10.34	0.574	0.0034	D930015E06Rik
865	8.844	9.015	8.904	9.863	9.611	9.377	485.35	29.33	792.78	133.65	1.633	0.0034	Litaf
866	10.827	10.921	11.041	10.483	10.256	10.618	1954.57	145.88	1408.52	175.37	0.721	0.0034	Insig1
867	7.420	7.435	7.879	6.572	6.918	6.975	193.25	36.54	113.95	16.49	0.590	0.0034	Hdac11
868	3.263	3.626	3.339	4.303	3.929	4.054	10.69	1.46	17.19	2.31	1.609	0.0034	Nusap1
869	3.834	4.263	3.870	5.301	4.874	4.376	16.03	2.75	29.84	9.34	1.861	0.0034	BC028528
870	4.248	4.558	5.184	3.775	3.991	3.861	26.30	9.00	14.71	1.12	0.559	0.0034	Gm11128
871	5.257	5.080	5.043	4.060	4.741	4.537	35.01	2.84	22.21	5.10	0.634	0.0034	Rnase13
872	5.257	5.442	5.567	4.423	4.646	4.983	43.04	4.59	26.04	5.16	0.605	0.0035	Foxp2
873	5.414	5.478	5.095	7.490	6.167	5.994	40.46	5.53	105.11	64.75	2.598	0.0035	Glipr2
874	8.542	9.303	8.902	10.616	9.630	9.485	494.29	130.25	1026.00	472.01	2.076	0.0035	Vsig4
875	3.072	3.189	3.027	3.929	3.863	3.480	8.56	0.50	13.65	2.18	1.594	0.0035	Tlr6
876	9.279	8.795	9.061	5.243	7.504	8.298	533.23	88.49	178.07	138.51	0.334	0.0035	Hsd3b2
877	3.387	3.608	3.292	4.405	4.150	3.905	10.81	1.24	17.97	3.11	1.662	0.0035	2810417H13Rik
878	2.160	2.175	2.230	3.131	2.904	2.675	4.56	0.12	7.54	1.19	1.654	0.0035	A330021E22Rik
879	11.280	11.581	11.724	10.764	11.220	11.011	2977.54	453.71	2062.71	323.59	0.693	0.0035	Aldh1a1
880	6.898	6.961	7.206	6.130	6.346	6.391	130.51	15.10	78.43	7.40	0.601	0.0036	Poc1b
881	5.401	5.548	5.362	6.581	6.415	5.847	43.40	2.99	79.54	19.73	1.833	0.0036	Gng2
882	11.579	11.490	11.675	10.011	10.990	11.223	3067.59	196.92	1818.79	704.34	0.593	0.0036	Cyp2c29
883	5.369	5.592	5.047	6.445	6.078	5.860	40.88	7.60	70.92	14.83	1.735	0.0036	Mfsd7b
884	9.613	9.287	9.409	10.284	9.902	9.981	695.83	80.23	1071.31	153.99	1.540	0.0036	Xdh
885	5.592	5.445	5.383	4.849	5.028	4.804	44.51	3.35	29.79	2.49	0.669	0.0036	Sfmbt1
886	10.665	10.608	10.724	9.431	10.085	10.329	1625.68	65.35	1020.89	303.39	0.628	0.0036	Cyp4f14
887	7.161	7.306	7.537	8.225	7.934	7.857	162.36	21.62	258.54	35.72	1.592	0.0036	Filip1l
888	4.762	4.850	4.648	6.398	5.587	5.197	27.02	1.88	56.36	24.88	2.086	0.0036	Ier3
889	5.959	6.224	6.165	7.650	6.760	6.779	69.57	6.56	139.68	52.96	2.008	0.0036	Pygb
890	11.060	11.082	10.798	11.354	11.290	11.540	2027.36	214.68	2700.03	247.86	1.332	0.0036	Saa4
891	5.067	5.460	5.029	7.321	5.933	5.867	36.73	6.33	93.11	57.83	2.535	0.0037	B4galt6
892	9.581	9.634	9.619	7.864	9.352	8.445	782.30	14.81	411.66	217.26	0.526	0.0037	Pcsk6
893	4.547	4.581	4.606	5.688	5.299	5.065	23.89	0.49	41.46	9.22	1.735	0.0037	Epsti1
894	4.699	4.703	4.661	5.651	5.529	5.079	25.77	0.41	43.41	8.57	1.685	0.0037	Adam8
895	3.888	3.726	3.799	4.579	4.590	4.221	13.99	0.79	22.22	3.09	1.588	0.0038	Rab19
896	12.048	12.172	11.910	12.352	12.217	12.225	4231.81	383.28	4925.16	261.20	1.164	0.0038	Hpx
897	6.898	6.987	7.347	5.434	5.696	6.787	136.29	23.23	68.52	36.58	0.503	0.0038	5033411D12Rik
898	6.661	6.592	6.754	5.744	6.154	6.175	101.87	5.75	65.68	10.50	0.645	0.0038	Dna2
899	7.008	7.135	7.571	8.291	8.012	7.750	153.14	32.57	262.17	49.07	1.712	0.0038	Dab2
900	8.515	8.350	8.267	9.275	9.428	8.745	333.32	29.47	579.12	134.52	1.737	0.0038	Dynlt1a // Dynlt1c // Dynlt1f // Dynlt1b
901	4.858	4.943	4.808	5.594	5.495	5.269	29.26	1.38	43.98	4.97	1.503	0.0038	Abcc4
902	8.968	9.000	9.129	5.970	8.039	8.284	524.21	31.32	212.51	132.01	0.405	0.0038	Cyp2u1
903	7.125	7.144	7.266	6.385	6.599	6.771	144.96	7.79	96.56	12.81	0.666	0.0038	Macrod1
904	5.158	5.233	5.417	5.891	6.376	5.949	38.69	3.64	68.06	13.05	1.759	0.0038	Fstl1
905	5.845	5.859	6.025	6.978	6.703	6.374	60.21	4.27	104.37	21.55	1.733	0.0038	Ppp1r9b
906	7.083	7.367	7.190	5.411	6.482	6.699	148.91	14.93	78.62	32.08	0.528	0.0039	Slc25a21
907	10.346	10.114	10.580	10.958	10.872	10.700	1313.72	211.72	1841.80	165.04	1.402	0.0039	Dcn
908	5.813	5.636	5.725	7.073	6.800	6.066	52.95	3.25	104.36	34.38	1.971	0.0039	Pitpnm1
909	7.006	10.718	6.456	11.960	11.051	9.977	633.67	910.49	2371.19	1503.66	3.742	0.0039	Lcn2
910	7.581	7.405	7.552	6.511	7.080	6.801	182.88	11.81	112.65	22.04	0.616	0.0039	Atrn
911	8.302	8.121	8.101	9.124	9.390	8.538	289.50	22.66	533.66	151.11	1.843	0.0039	Atp1b3

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT avg	WTsd	KO avg	KOsd	KO/WT	BH	Gene Symbol
912	8.873	8.768	9.411	10.245	9.646	9.506	528.54	132.90	914.07	262.19	1.729	0.0039	Pltp
913	6.082	5.863	6.275	6.752	6.840	6.669	67.79	9.63	108.06	6.40	1.594	0.0039	Tmsb10
914	4.188	4.396	4.120	4.825	5.113	4.708	18.89	1.92	29.69	4.39	1.572	0.0039	Prr11
915	9.770	9.814	9.754	8.504	8.950	9.457	878.92	19.15	520.07	171.24	0.592	0.0039	Aadat
916	3.739	3.943	3.998	5.283	4.755	4.261	14.90	1.37	28.37	9.95	1.904	0.0039	Cd244
917	4.882	5.138	4.797	5.826	5.674	5.337	30.84	3.88	49.40	8.28	1.602	0.0039	Fam78a
918	5.408	5.836	5.497	7.199	6.340	6.145	48.25	7.81	99.58	41.36	2.064	0.0040	B430306N03Rik
919	6.753	6.687	6.684	6.048	6.058	6.165	104.59	2.85	68.18	3.10	0.652	0.0040	Lrig3
920	7.334	7.245	7.581	5.779	7.016	6.208	168.14	20.76	86.08	38.72	0.512	0.0040	Plekhh1
921	4.679	4.698	4.477	5.702	5.387	5.013	24.61	2.03	42.07	9.89	1.709	0.0040	Renbp
922	8.273	8.163	8.157	9.378	8.903	8.601	293.80	13.44	510.80	141.42	1.739	0.0040	Lyn
923	3.397	3.636	3.628	4.724	4.233	4.002	11.78	1.08	20.42	5.38	1.733	0.0040	Pdk3
924	7.598	7.585	7.829	6.791	6.900	7.148	204.41	19.97	123.99	16.03	0.607	0.0041	Gli3
925	7.577	7.497	7.831	8.208	8.363	8.287	199.78	24.69	312.38	16.71	1.564	0.0041	Cygb
926	10.488	10.260	10.629	9.290	9.557	10.087	1415.47	179.35	822.32	238.61	0.581	0.0041	Cyp2c54
927	3.947	4.031	4.238	4.685	4.777	4.640	16.88	1.78	26.02	1.27	1.541	0.0041	Gfpt2
928	5.892	5.756	6.148	4.636	5.517	5.042	61.45	8.62	34.54	10.56	0.562	0.0041	Adra1a
929	5.026	5.349	5.178	6.663	5.953	5.741	36.51	4.10	72.26	25.55	1.979	0.0042	Was
930	2.589	2.850	2.614	3.395	3.920	3.326	6.45	0.66	11.90	2.82	1.845	0.0042	Ms4a4b
931	3.494	4.118	3.771	4.897	5.384	4.111	14.10	3.07	29.60	12.23	2.100	0.0042	Glp1r
932	3.995	3.965	3.690	6.294	4.671	4.566	14.82	1.67	42.54	31.13	2.870	0.0042	Slc10a6
933	4.829	5.031	5.202	4.415	4.412	4.359	32.65	4.19	21.05	0.46	0.645	0.0042	Gm5887
934	7.756	8.007	7.746	8.329	8.452	8.603	229.32	24.17	353.56	33.82	1.542	0.0042	Dynll1
935	8.057	7.789	7.900	6.843	7.334	7.362	242.13	22.75	146.87	27.81	0.607	0.0042	Agl
936	4.542	4.431	4.227	5.639	5.044	5.010	21.19	2.31	38.35	9.96	1.809	0.0042	Ctla2b
937	4.929	4.663	4.828	5.349	5.691	5.298	28.07	2.58	43.92	6.74	1.565	0.0042	Prkcq
938	7.980	8.021	8.086	6.906	7.244	7.672	261.34	9.75	158.48	42.42	0.606	0.0043	2510002D24Rik
939	5.959	5.597	5.542	6.280	6.653	6.331	52.40	8.53	86.27	12.50	1.646	0.0043	Rhob
940	7.864	7.780	7.816	8.835	8.355	8.230	226.04	6.67	361.51	83.64	1.599	0.0043	Rhog
941	7.740	7.574	7.894	7.030	7.050	7.295	214.08	23.60	140.06	14.70	0.654	0.0044	Ccl27b
942	6.319	6.297	6.433	5.589	5.822	5.742	81.62	4.17	52.74	4.28	0.646	0.0044	2810055F11Rik
943	6.947	7.053	7.107	6.466	6.213	6.353	131.35	7.35	81.45	7.12	0.620	0.0044	Zfp467
944	8.915	9.015	8.797	9.785	9.643	9.299	481.64	36.39	770.58	128.58	1.600	0.0044	Hist1h2an
945	3.815	3.907	3.818	4.479	4.456	4.358	14.39	0.53	21.58	0.95	1.500	0.0044	I730030J21Rik
946	5.730	5.886	5.550	6.786	6.323	6.258	53.02	6.15	88.98	18.61	1.678	0.0045	Hist1h1b
947	7.544	7.616	7.539	6.632	7.030	7.066	189.62	5.74	121.29	19.23	0.640	0.0045	Hectd3
948	3.516	3.813	3.501	4.606	4.383	4.043	12.27	1.55	20.57	3.94	1.676	0.0045	Il7r
949	8.162	8.059	7.943	7.083	7.609	6.996	266.32	20.16	152.84	36.98	0.574	0.0045	Tbx3
950	9.438	10.488	10.002	10.780	10.837	10.574	1051.78	372.06	1704.10	159.74	1.620	0.0045	Serpina3m
951	7.577	6.889	8.095	8.087	8.670	8.975	194.29	77.46	394.18	116.16	2.029	0.0045	Gsta2
952	7.942	8.079	7.564	9.023	8.554	8.335	235.18	41.66	406.34	102.01	1.728	0.0045	Pros1
953	4.096	3.803	4.059	4.797	4.868	4.283	15.91	1.71	25.49	5.26	1.602	0.0046	Tnf
954	7.705	7.717	7.343	6.189	7.081	7.044	193.82	27.25	113.43	35.11	0.585	0.0046	Spry4
955	5.997	6.240	5.923	7.089	6.642	6.567	66.72	7.85	110.26	22.54	1.653	0.0046	Twf2
956	9.804	9.644	9.958	10.368	10.402	10.248	896.09	97.18	1297.08	71.62	1.447	0.0046	Bgn
957	6.883	7.228	7.350	6.155	6.555	6.298	143.72	23.23	81.32	11.63	0.566	0.0046	Fnip2
958	6.082	7.958	8.255	6.410	5.688	5.411	207.32	124.18	59.72	22.38	0.288	0.0046	Lrtm1
959	6.978	7.033	6.619	8.007	7.734	7.244	118.45	17.61	207.18	53.04	1.749	0.0046	Sbno2
960	3.834	3.933	4.169	4.887	4.693	4.390	15.84	1.92	25.48	4.33	1.609	0.0047	C130026I21Rik
961	6.359	7.558	5.048	9.601	8.502	7.120	101.21	79.43	426.15	323.58	4.211	0.0047	Saa3
962	3.925	3.805	4.176	5.438	4.892	4.298	15.75	2.11	30.91	11.90	1.963	0.0047	Bst1
963	3.989	4.054	3.989	5.592	4.721	4.397	16.12	0.42	31.89	14.40	1.978	0.0048	Shc2
964	2.332	2.376	2.151	3.321	2.914	2.868	4.89	0.39	8.28	1.49	1.693	0.0048	Cd200r4
965	6.133	5.770	5.718	4.108	5.376	5.209	59.13	9.62	31.92	12.91	0.540	0.0048	Pdilt

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT avg	WTsd	KO avg	KOsd	KO/WT	BH	Gene Symbol
966	2.785	2.319	2.637	4.102	3.439	3.153	6.03	0.96	12.30	4.32	2.039	0.0048	Ctla2a
967	5.337	5.391	5.183	6.080	5.825	5.761	39.58	2.91	59.52	7.16	1.504	0.0048	Rnf122
968	7.343	7.634	7.483	6.699	6.955	6.958	179.92	18.15	117.43	11.71	0.653	0.0048	Carhsp1
969	5.943	6.132	6.025	6.814	6.739	6.563	65.59	4.34	104.64	9.18	1.595	0.0048	Dysf
970	4.374	4.154	4.287	4.681	5.242	4.808	19.35	1.48	30.51	6.47	1.576	0.0049	Adams9
971	5.826	6.296	5.956	8.426	6.874	6.624	65.79	11.37	186.65	136.57	2.837	0.0049	Emr4
972	2.392	2.414	2.252	6.532	3.828	3.134	5.11	0.31	38.51	46.87	7.530	0.0049	Ighg3
973	4.793	4.710	4.790	6.189	5.334	5.180	27.19	0.87	49.85	20.12	1.834	0.0049	Atp2a3
974	5.295	5.166	5.252	6.167	7.034	5.643	37.75	1.70	84.29	41.97	2.233	0.0050	Plin4
975	5.446	5.513	6.007	7.267	6.221	6.544	51.20	11.41	107.31	41.53	2.096	0.0050	Postn
976	5.393	5.452	5.401	6.150	6.086	5.988	42.67	0.95	67.46	3.79	1.581	0.0050	Parvb
977	4.863	5.353	4.953	4.417	4.512	4.413	33.65	6.32	21.83	0.85	0.649	0.0050	Ppp1r9a
978	5.540	6.005	5.690	7.400	6.676	6.114	54.12	9.11	113.50	50.77	2.097	0.0051	Cd37
979	8.536	8.326	8.269	9.268	9.415	8.746	333.54	33.26	576.08	131.22	1.727	0.0051	Dynlt1c
980	6.792	6.941	6.985	5.778	6.357	6.321	120.11	8.26	72.27	15.09	0.602	0.0051	Pqlc1
981	6.341	6.352	6.622	5.505	5.785	6.052	87.06	9.89	55.63	10.47	0.639	0.0051	Tfcp2l1
982	5.337	5.698	4.997	5.983	6.181	6.126	41.42	10.02	68.55	4.80	1.655	0.0051	Cdk1
983	4.719	4.536	4.721	5.832	5.041	5.679	25.30	1.82	47.04	12.56	1.859	0.0051	Gprc5b
984	6.641	6.120	6.112	6.660	8.182	7.448	79.52	17.57	188.74	95.47	2.373	0.0051	Gm4841
985	11.143	10.999	11.214	10.302	10.734	10.781	2227.85	167.16	1575.33	272.37	0.707	0.0051	Gsta3
986	6.445	6.341	6.807	5.336	6.215	5.651	93.39	16.36	54.98	17.44	0.589	0.0051	Reck
987	4.499	4.644	4.698	5.702	5.253	5.087	24.53	1.72	41.39	9.46	1.687	0.0051	Gpm6b
988	5.402	5.502	5.476	6.828	6.276	5.868	44.03	1.58	83.16	28.02	1.889	0.0051	Slc25a4
989	4.036	4.040	4.044	4.929	4.653	4.342	16.45	0.05	25.30	5.09	1.538	0.0052	Gdf3
990	9.320	9.238	9.674	8.307	8.670	9.006	686.56	114.39	412.74	98.94	0.601	0.0053	Fermt2
991	5.646	5.548	5.799	6.013	6.603	6.577	50.85	4.50	85.76	18.38	1.687	0.0054	Gabra3
992	2.977	3.374	3.912	3.904	4.335	5.185	11.10	3.65	23.85	11.17	2.149	0.0054	Apol7c
993	6.633	6.556	6.623	7.314	7.397	7.116	97.32	2.79	155.45	15.23	1.597	0.0055	Lrrc32
994	6.117	6.434	6.238	8.061	7.043	6.710	77.10	8.65	167.89	86.97	2.177	0.0055	Slc41a3
995	6.673	6.897	6.886	8.131	7.503	7.312	113.20	9.66	206.88	64.53	1.828	0.0055	Ckb
996	5.383	5.527	5.516	6.881	6.400	5.782	44.53	2.44	85.78	31.43	1.926	0.0055	Pik3r5
997	3.737	3.744	3.726	4.243	4.909	4.350	13.32	0.09	23.12	6.03	1.736	0.0055	Eomes
998	8.313	8.443	8.551	7.691	7.808	7.765	347.05	28.51	216.10	8.82	0.623	0.0055	BC029214
999	9.520	9.183	9.713	8.289	8.984	8.914	718.24	129.73	433.73	105.46	0.604	0.0055	Ugp2
1000	6.081	6.111	6.461	5.103	5.889	5.311	74.98	11.40	44.44	13.11	0.593	0.0055	Mapk15
1001	7.231	7.465	6.898	8.667	8.004	7.556	148.74	28.79	283.74	111.57	1.908	0.0056	Dmpk
1002	3.170	3.715	3.493	10.514	6.151	4.398	11.13	2.07	518.06	817.90	46.558	0.0056	Igk-V28
1003	8.574	8.440	8.536	9.704	9.262	8.780	366.49	17.39	629.23	197.63	1.717	0.0056	App
1004	7.487	7.283	8.009	6.774	6.597	7.138	197.53	53.29	115.69	22.65	0.586	0.0056	Hamp2
1005	4.880	4.893	4.892	5.693	5.785	5.310	29.62	0.15	48.84	8.12	1.649	0.0056	Itgb7
1006	4.234	5.135	5.706	6.699	5.658	8.641	35.38	16.69	184.48	187.75	5.214	0.0057	Atp6v0d2
1007	10.744	11.123	11.185	10.259	10.547	10.654	2091.25	329.07	1444.17	198.02	0.691	0.0057	Fasn
1008	4.998	4.915	4.742	5.630	5.520	5.220	29.62	2.64	44.22	6.29	1.493	0.0058	Ptpre
1009	5.744	5.831	5.609	7.406	6.845	5.968	53.12	4.09	115.72	53.50	2.179	0.0058	Tlr2
1010	9.476	9.347	9.443	8.645	8.866	9.048	686.42	31.54	465.38	64.55	0.678	0.0058	Grb7
1011	7.685	7.592	7.706	8.953	8.427	7.978	202.46	8.44	363.95	122.82	1.798	0.0059	Fam177a // 1700047117Rik2
1012	6.120	6.324	6.298	7.666	7.530	6.502	76.13	5.73	159.52	60.34	2.095	0.0059	Mid1
1013	6.219	6.279	5.770	4.919	5.509	5.443	68.90	12.51	39.76	8.30	0.577	0.0060	Gabrb3
1014	11.365	11.497	11.233	11.895	11.653	11.569	2645.04	242.29	3355.80	401.91	1.269	0.0060	Serpina3n
1015	5.599	5.885	5.642	7.035	6.586	6.070	52.49	5.76	98.12	32.03	1.869	0.0060	Cd300a
1016	4.661	4.938	4.792	6.096	5.387	5.190	27.89	2.68	48.91	17.07	1.754	0.0060	Stambpl1
1017	6.145	6.122	6.311	6.909	7.288	6.573	73.28	5.34	123.88	30.72	1.691	0.0060	Col1a2
1018	6.135	6.376	5.836	6.866	6.804	6.682	70.14	12.96	110.36	7.07	1.573	0.0060	Baspl
1019	4.431	4.425	4.325	5.174	5.063	4.798	21.03	0.86	32.45	4.23	1.543	0.0060	Lrmp

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT avg	WTsd	KO avg	KOsd	KO/WT	BH	Gene Symbol
1020	3.201	2.958	3.256	5.568	4.828	3.302	8.84	0.94	28.57	18.79	3.231	0.0061	Clec4e
1021	5.695	5.851	5.655	4.729	5.241	5.400	53.31	3.88	35.52	8.10	0.666	0.0061	Mtx3
1022	4.898	5.293	4.693	10.028	6.679	5.787	31.63	6.86	400.67	557.89	12.667	0.0061	Cd14
1023	3.760	3.890	3.910	5.662	4.133	4.865	14.47	0.80	32.44	16.79	2.243	0.0061	Esm1
1024	9.702	9.880	9.500	10.335	10.121	10.128	833.02	109.09	1174.51	101.35	1.410	0.0062	Serpina10
1025	10.047	10.084	10.151	9.347	9.534	9.708	1093.49	40.30	742.88	92.70	0.679	0.0062	Adi1
1026	5.930	6.038	6.367	4.964	5.783	5.233	69.74	11.33	41.30	12.36	0.592	0.0062	Tnfrsf19
1027	5.473	5.395	5.529	5.903	6.591	5.997	44.22	2.04	73.36	20.04	1.659	0.0062	Col6a3
1028	5.886	5.497	5.713	4.869	5.251	5.148	52.25	6.99	34.26	4.55	0.656	0.0063	Qpct
1029	7.959	7.900	7.780	7.408	7.329	7.192	235.85	14.81	158.96	11.90	0.674	0.0063	C130074G19Rik
1030	7.075	6.701	6.957	7.735	7.707	7.330	121.05	15.65	194.28	28.96	1.605	0.0063	Dse
1031	5.062	5.288	5.399	7.449	6.245	5.598	38.22	4.46	99.66	66.41	2.607	0.0063	Naip2
1032	4.105	3.893	4.210	4.400	5.481	4.844	16.85	1.85	31.50	12.02	1.869	0.0064	Tnc
1033	6.160	6.450	6.196	7.102	6.733	6.864	77.42	8.73	120.09	15.81	1.551	0.0064	Tpm1
1034	8.102	7.394	7.887	10.039	9.070	8.134	226.57	54.01	623.51	392.67	2.752	0.0064	Sik1
1035	8.693	8.373	8.653	7.764	8.051	7.997	382.65	44.64	246.07	25.32	0.643	0.0064	Rassf8
1036	6.757	6.767	6.357	7.343	7.230	7.200	99.69	15.36	153.17	8.11	1.536	0.0065	Dnajc12
1037	4.821	4.837	4.921	5.450	6.572	5.460	29.05	1.08	60.97	29.61	2.099	0.0065	Ciita
1038	5.883	5.849	6.419	5.429	5.407	5.183	67.40	15.72	40.62	3.73	0.603	0.0065	Fam160a1
1039	4.425	4.276	4.308	4.776	5.051	4.850	20.22	1.11	29.80	2.99	1.474	0.0065	Foxm1
1040	6.019	5.972	6.232	8.978	6.934	6.779	67.59	6.63	245.40	224.18	3.631	0.0065	Gpx3
1041	7.590	7.561	7.547	8.227	8.385	8.063	189.52	2.88	300.46	33.41	1.585	0.0065	Mcart1
1042	8.409	8.140	8.652	6.837	7.565	7.927	341.38	60.13	182.31	64.80	0.534	0.0065	Prkd3
1043	6.405	6.586	6.304	7.853	7.137	6.776	86.59	8.69	160.48	63.13	1.853	0.0065	Tnfaip8l2
1044	8.731	9.168	8.974	7.887	8.132	8.589	501.13	75.22	300.80	76.22	0.600	0.0065	Car5a
1045	7.536	7.785	8.067	7.072	7.047	7.347	224.74	41.40	143.20	17.01	0.637	0.0067	Cks2
1046	4.580	5.156	5.788	9.448	6.877	5.818	38.28	15.82	290.74	354.27	7.596	0.0067	Cxcl13
1047	4.774	4.651	4.606	5.701	6.134	4.958	25.61	1.56	51.11	19.59	1.995	0.0067	Dpep1
1048	7.505	6.428	6.696	8.387	7.584	7.602	123.82	50.88	240.35	81.87	1.941	0.0067	Ctgf
1049	8.474	8.473	8.678	7.257	8.020	7.881	373.49	31.24	216.08	55.94	0.579	0.0067	Grb14
1050	7.415	6.851	6.731	7.786	7.859	7.590	130.76	34.84	215.14	20.32	1.645	0.0067	Tgm1
1051	4.879	5.403	5.069	6.272	5.500	5.812	35.10	6.58	59.57	16.27	1.697	0.0068	Bank1
1052	9.187	9.710	9.238	8.763	8.930	8.583	674.72	141.44	435.21	52.18	0.645	0.0068	Prodh
1053	6.633	6.200	6.637	5.826	5.755	6.058	90.76	14.94	59.11	6.65	0.651	0.0068	Prdm10
1054	5.843	5.946	5.943	6.597	6.532	6.329	60.19	2.43	89.91	8.50	1.494	0.0069	Frmd4a
1055	6.010	5.942	6.054	6.745	6.707	6.472	64.12	2.49	100.19	9.99	1.562	0.0070	Ppic
1056	5.726	5.603	5.755	5.093	5.195	5.121	51.84	2.87	35.19	1.29	0.679	0.0070	Lphn1
1057	5.942	6.136	6.128	7.636	6.912	6.510	67.23	5.00	136.85	55.73	2.036	0.0070	Rgs10
1058	3.502	3.944	3.696	5.260	4.669	3.960	13.23	2.04	26.44	11.41	1.999	0.0071	Tpd52
1059	5.273	5.571	5.597	4.731	5.045	4.950	44.87	5.39	30.16	3.30	0.672	0.0073	Acpl2
1060	5.201	5.268	5.110	6.062	5.871	5.621	36.62	2.00	58.19	8.81	1.589	0.0073	Aurkb
1061	5.320	5.806	5.548	7.033	6.292	5.948	47.56	8.03	90.34	36.15	1.899	0.0073	Cerk
1062	6.589	6.348	6.670	5.147	5.540	6.239	93.18	10.53	52.49	20.69	0.563	0.0073	Txnl4b
1063	7.987	7.907	7.675	8.480	8.547	8.358	232.69	25.41	353.08	23.21	1.517	0.0073	H2-Q5
1064	5.116	4.991	5.025	4.214	4.571	4.625	33.01	1.50	22.34	3.31	0.677	0.0074	Tmem14a
1065	5.953	5.925	6.120	5.553	5.451	5.355	64.09	4.77	43.88	3.01	0.685	0.0074	Bahcc1
1066	5.760	5.709	5.978	6.547	6.722	6.302	56.50	5.72	92.65	13.36	1.640	0.0074	Gimap4
1067	6.267	6.308	6.299	7.057	6.796	6.920	78.33	1.17	121.81	11.03	1.555	0.0074	Mcam
1068	5.113	5.174	4.819	6.476	5.833	5.314	32.98	4.19	61.93	24.97	1.878	0.0074	Tnfaip3
1069	6.817	6.585	7.938	4.814	6.590	5.908	151.33	81.73	61.50	34.12	0.406	0.0074	Slc17a8
1070	6.265	5.360	5.655	8.186	6.475	6.546	56.13	18.59	157.86	115.51	2.812	0.0074	Fmo2
1071	8.198	8.282	8.126	7.064	7.365	7.997	294.75	15.95	184.69	63.21	0.627	0.0074	Tmem25
1072	10.340	10.233	10.192	10.951	10.505	10.695	1223.02	65.39	1696.87	265.70	1.387	0.0074	Aass

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT avg	WTsd	KO avg	KOsd	KO/WT	BH	Gene Symbol
1073	3.388	3.351	3.182	4.570	4.292	3.552	9.92	0.74	18.36	6.10	1.851	0.0074	Mgat4a
1074	8.304	8.261	8.495	4.839	6.909	7.940	327.92	28.85	131.47	108.93	0.401	0.0074	Akr1c19
1075	6.254	6.405	6.620	5.888	5.892	5.666	86.46	11.11	56.46	4.93	0.653	0.0075	Frat1
1076	4.680	4.956	4.608	6.975	5.907	5.010	27.02	3.53	72.68	48.08	2.690	0.0075	Gm5150
1077	4.619	5.013	4.839	6.409	5.395	5.354	28.49	3.86	56.00	25.13	1.965	0.0075	Trim12a
1078	2.472	2.385	2.508	1.848	1.843	1.928	5.49	0.24	3.66	0.12	0.668	0.0075	Amy2b
1079	6.945	6.861	7.006	7.855	7.577	7.355	122.63	6.16	195.38	34.16	1.593	0.0075	Chsy1
1080	5.810	5.838	6.091	6.727	6.627	6.591	60.48	6.66	100.40	4.97	1.660	0.0075	Rtn4
1081	7.442	7.951	7.808	7.175	7.223	6.892	215.14	37.61	137.55	16.45	0.639	0.0076	Dock8
1082	7.019	6.788	6.733	5.088	6.473	6.153	115.52	12.43	64.67	27.98	0.560	0.0076	Notum
1083	6.263	5.859	5.887	6.679	6.690	6.466	64.66	10.52	98.06	8.36	1.517	0.0076	Tnfrsf12a
1084	6.451	6.599	6.749	5.386	5.865	6.232	97.33	10.07	58.44	16.68	0.600	0.0076	Ddo
1085	7.049	7.217	7.530	5.979	6.285	6.985	155.35	26.80	89.25	33.28	0.575	0.0077	Bco2
1086	6.311	6.826	6.733	5.407	6.028	5.985	99.73	17.95	57.00	12.66	0.572	0.0077	Mgmt
1087	6.832	6.703	6.722	7.592	7.479	7.288	107.90	5.25	175.90	18.51	1.630	0.0077	Impact
1088	9.617	9.823	9.416	9.959	10.294	10.251	791.38	111.46	1156.37	140.81	1.461	0.0079	Hspb8
1089	7.690	7.542	7.865	6.371	7.086	7.307	208.69	23.43	125.66	38.78	0.602	0.0079	Fam149a
1090	8.654	8.641	8.630	8.082	8.249	8.066	399.43	3.43	281.10	20.13	0.704	0.0079	Zfyve1
1091	6.892	7.119	7.807	8.014	8.057	8.026	160.57	55.85	261.82	4.10	1.631	0.0079	Pparg
1092	10.133	10.005	10.106	9.159	9.713	9.665	1084.25	50.03	740.92	147.22	0.683	0.0080	Slco1b2
1093	5.248	5.253	5.139	6.729	5.793	5.635	37.13	1.64	70.41	31.03	1.897	0.0080	Rcsd1
1094	2.350	2.377	2.362	3.242	3.268	2.843	5.14	0.05	8.76	1.37	1.702	0.0080	Cd200r1
1095	5.974	5.880	6.023	5.042	5.477	5.483	62.26	3.12	40.73	6.74	0.654	0.0080	Msh3
1096	6.113	6.463	6.496	7.223	7.100	6.829	82.55	11.61	133.43	18.13	1.616	0.0081	Aida
1097	8.976	9.106	8.876	9.837	9.697	9.350	508.21	40.76	799.14	133.76	1.572	0.0081	Hist1h2ao // Hist1h2ai // Hist1h2ab // Hist1h2ap // Hist1h2an // Hist1h2ah // Hist1h2ag // Hist1h2ae // Hist1h2ad // Hist1h2ac
1098	8.513	8.458	8.562	7.680	8.130	8.114	365.02	13.15	254.05	42.43	0.696	0.0081	Nxt2
1099	5.886	5.944	6.022	7.228	6.542	6.352	61.89	2.93	108.27	36.54	1.749	0.0081	Ptpm
1100	5.034	4.870	4.865	5.913	5.485	5.536	30.38	2.06	50.48	8.51	1.662	0.0082	Ptgrn
1101	7.329	7.316	7.283	8.451	8.156	7.552	158.63	2.65	274.32	81.68	1.729	0.0082	Ttyh3
1102	5.562	5.516	5.517	6.175	6.460	5.951	46.27	0.85	74.06	13.19	1.601	0.0082	Hdc
1103	6.318	6.400	6.350	7.389	7.005	6.763	81.92	2.37	134.89	30.08	1.647	0.0082	Cotl1
1104	6.592	6.732	6.553	7.078	7.541	7.124	98.91	6.56	153.62	28.33	1.553	0.0083	Fam38a
1105	5.495	5.709	5.492	6.430	6.119	5.954	47.47	4.18	72.57	12.40	1.529	0.0083	Sh3bp1
1106	6.903	7.038	6.881	8.135	7.789	7.307	123.00	7.37	220.19	61.42	1.790	0.0083	Arrb2
1107	3.334	3.185	2.666	6.474	4.845	3.317	8.51	1.94	42.54	41.25	5.000	0.0083	Cxcr2
1108	6.090	6.217	5.889	5.249	4.967	5.765	67.25	7.62	41.22	11.88	0.613	0.0084	Glr3
1109	6.514	6.758	6.640	8.562	7.503	7.088	99.78	8.41	231.76	128.57	2.323	0.0084	Ifit1
1110	7.132	7.185	7.342	6.659	6.687	6.726	149.33	11.45	103.34	2.42	0.692	0.0084	Peli2
1111	5.844	5.987	5.874	6.448	6.544	6.407	59.83	3.16	88.49	4.36	1.479	0.0084	Col3a1
1112	6.977	6.864	7.051	5.940	6.323	6.642	125.02	8.11	80.44	19.26	0.643	0.0084	Ormdl1
1113	5.952	6.148	6.256	7.049	7.033	6.449	69.77	7.33	116.91	25.58	1.676	0.0084	Hpse
1114	4.542	4.725	4.689	5.565	5.113	5.103	25.18	1.66	38.78	7.41	1.540	0.0085	Hmgb2
1115	10.407	10.343	10.247	9.373	9.881	9.752	1290.40	71.50	822.62	144.05	0.637	0.0085	Nfix
1116	9.697	9.653	9.864	9.139	9.383	9.371	855.46	67.09	631.15	58.40	0.738	0.0086	Ppp2r5a
1117	3.324	3.086	3.024	5.505	4.152	3.492	8.88	1.00	24.81	18.14	2.795	0.0087	Emb
1118	5.373	5.409	5.447	7.580	5.900	6.103	42.51	1.08	106.62	73.56	2.508	0.0087	Npdc1
1119	6.292	6.459	6.570	7.556	7.168	6.669	87.11	8.34	144.61	43.23	1.660	0.0088	Zeb2
1120	8.544	8.078	8.208	5.236	7.186	7.833	313.04	53.68	137.08	95.41	0.438	0.0088	Adh6-ps1
1121	5.428	5.337	5.366	6.123	6.009	5.768	41.57	1.35	62.86	7.71	1.512	0.0088	Abcc1
1122	4.402	4.391	4.264	4.943	4.943	4.895	20.44	1.07	30.42	0.58	1.488	0.0088	Ckap2l

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT avg	WTsd	KO avg	KOsd	KO/WT	BH	Gene Symbol
1123	11.092	11.125	11.037	10.606	10.687	10.756	2172.53	67.29	1645.44	85.40	0.757	0.0089	Cyp2d22
1124	3.941	4.053	3.771	7.248	4.540	4.989	15.20	1.48	69.02	72.02	4.540	0.0089	Lepr
1125	5.607	5.828	5.640	5.303	5.123	5.187	51.81	4.38	36.92	2.35	0.713	0.0089	Bik
1126	3.591	3.913	3.705	5.829	4.613	4.078	13.38	1.53	32.74	21.23	2.446	0.0089	Il1r2
1127	4.605	4.791	4.594	5.578	5.141	5.256	25.39	1.98	40.43	6.53	1.592	0.0089	St6galnac4
1128	6.019	6.134	6.007	7.296	6.688	6.409	66.48	3.28	115.06	37.55	1.731	0.0089	Gdf10
1129	7.040	6.940	7.202	8.206	7.666	7.439	133.86	12.35	223.93	63.50	1.673	0.0089	Adam23
1130	4.924	4.807	4.678	5.433	5.591	5.269	27.98	2.38	43.33	4.82	1.549	0.0089	Gpr132
1131	11.053	10.930	10.914	11.316	11.321	11.185	2001.50	106.88	2478.40	130.45	1.238	0.0090	H2-K1
1132	7.314	7.685	7.540	8.107	8.166	8.037	183.66	23.43	275.17	12.26	1.498	0.0090	Rnf213
1133	5.366	5.404	5.735	4.796	4.878	5.153	45.61	6.64	30.92	4.12	0.678	0.0091	1110034B05Rik
1134	6.525	6.465	6.511	7.420	7.210	6.863	90.54	1.97	145.24	27.57	1.604	0.0091	Prcp
1135	5.152	4.868	5.061	5.455	5.578	5.653	32.72	3.24	47.32	3.25	1.447	0.0091	Gpx8
1136	3.889	3.871	3.838	5.985	4.681	4.222	14.58	0.26	35.89	24.05	2.461	0.0091	Kcnt2
1137	10.857	10.912	10.847	11.403	11.273	11.024	1874.10	45.55	2421.90	316.15	1.292	0.0092	Psap
1138	8.520	8.985	8.699	9.285	9.472	9.186	429.83	70.77	638.88	65.02	1.486	0.0092	H2-T22
1139	5.193	5.120	5.725	6.277	6.103	5.727	41.41	9.98	66.41	12.45	1.604	0.0092	Il1a
1140	6.709	6.301	6.615	5.461	6.022	6.089	93.82	13.39	59.02	13.07	0.629	0.0092	Pde4c
1141	5.125	5.216	5.005	5.921	5.623	5.509	34.72	2.53	51.79	7.84	1.492	0.0093	Tnfrsf11a
1142	8.203	8.046	8.085	7.442	7.577	7.728	276.78	15.84	192.28	19.07	0.695	0.0093	Gnas
1143	8.419	8.528	8.567	7.761	7.906	8.242	363.56	19.15	253.17	44.49	0.696	0.0093	Mccc2
1144	7.573	7.315	7.447	6.575	6.598	6.806	174.73	15.63	101.37	9.14	0.580	0.0093	Ocln
1145	4.827	4.840	4.486	6.234	5.363	5.197	26.48	3.53	51.03	21.10	1.927	0.0093	Pot1b
1146	6.396	6.049	6.306	6.715	7.114	6.797	76.52	9.27	118.25	17.81	1.545	0.0094	Adams2
1147	4.591	4.666	4.594	3.879	4.162	4.279	24.54	0.74	17.34	2.40	0.707	0.0094	9830147E19Rik
1148	7.190	7.358	7.052	6.332	6.710	6.676	147.57	15.72	95.81	13.27	0.649	0.0094	Fn3krp
1149	8.292	7.846	7.783	8.590	8.600	8.552	254.61	51.25	382.90	6.78	1.504	0.0094	B4galt1
1150	9.023	8.952	9.164	7.908	8.350	8.736	529.72	39.97	330.94	93.15	0.625	0.0094	Cml1
1151	9.783	9.503	9.664	8.116	9.030	9.336	805.97	77.83	482.18	187.77	0.598	0.0096	Fbxo21
1152	7.189	7.071	5.313	8.044	7.916	7.403	106.70	58.25	224.88	49.46	2.108	0.0096	Scara5
1153	7.084	6.759	6.940	5.948	6.659	6.113	122.25	13.69	77.33	20.87	0.633	0.0096	Cyr61
1154	5.013	5.244	5.031	6.200	5.702	5.444	34.30	3.12	56.36	15.45	1.643	0.0097	Nfkbie
1155	4.662	4.674	4.681	5.357	5.383	5.036	25.50	0.17	38.50	4.95	1.510	0.0097	Tnfrsf10b
1156	4.575	4.850	4.648	5.550	5.676	5.270	25.92	2.61	45.53	6.37	1.757	0.0097	Fam26f
1157	5.511	5.521	5.766	6.758	6.052	6.089	48.64	4.99	80.88	23.69	1.663	0.0098	Rgs5
1158	6.052	6.214	6.287	7.298	7.075	6.465	72.90	5.99	126.83	35.21	1.740	0.0098	Slc44a2
1159	6.481	6.273	6.718	5.819	5.836	5.862	90.64	14.03	57.24	0.87	0.632	0.0099	Rhpn2
1160	5.100	4.999	4.737	5.935	5.698	5.203	30.98	3.92	49.97	12.28	1.613	0.0099	Arhgap9
1161	5.459	5.608	5.294	6.684	6.055	5.820	44.00	4.76	75.25	24.38	1.710	0.0099	Dennd1c
1162	6.503	6.438	6.111	8.246	7.238	6.678	82.17	11.47	185.66	105.03	2.260	0.0099	Aldh3b1
1163	8.842	8.685	9.026	7.555	8.217	8.559	463.95	55.02	287.60	94.96	0.620	0.0100	Als2
1164	6.499	6.359	6.566	5.592	5.990	5.958	89.09	6.45	57.97	8.46	0.651	0.0100	Dixdc1
1165	7.916	8.056	8.288	7.369	7.637	7.455	273.39	36.01	179.94	17.30	0.658	0.0100	Tbcel
1166	3.202	2.945	2.997	2.322	2.532	2.662	8.30	0.80	5.70	0.67	0.688	0.0100	Ranbp3l
1167	5.378	5.286	5.376	6.106	5.869	5.714	40.71	1.46	59.94	8.31	1.472	0.0100	Rinl
1168	8.577	8.075	8.514	7.179	7.897	7.869	339.06	60.73	205.70	52.72	0.607	0.0100	Gm10768
1169	11.505	11.432	11.320	10.224	11.140	11.046	2742.09	175.94	1856.01	575.86	0.677	0.0101	Cyp1a2
1170	4.560	4.481	4.792	5.276	4.983	5.082	24.54	2.81	34.74	3.64	1.416	0.0102	Mef2c
1171	5.631	6.014	5.553	6.596	6.278	6.218	53.71	9.54	82.92	12.06	1.544	0.0103	Tmc8
1172	9.179	8.814	9.038	6.150	8.126	8.507	518.46	65.10	238.10	150.76	0.459	0.0103	Slc22a30
1173	3.076	3.279	3.090	3.593	3.746	3.799	8.89	0.71	13.13	0.96	1.478	0.0103	Prc1
1174	8.023	7.843	7.548	8.785	8.675	8.027	225.63	36.64	370.29	96.14	1.641	0.0103	Tnfrsf1b
1175	5.322	5.453	5.228	5.995	5.916	5.817	40.44	3.18	60.17	3.72	1.488	0.0103	Limk1
1176	5.377	5.273	5.491	4.894	4.995	4.741	41.74	3.16	29.45	2.58	0.706	0.0104	Chrb2

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT avg	WTsd	KO avg	KOsd	KO/WT	BH	Gene Symbol
1177	6.613	6.547	6.616	5.674	5.873	6.306	96.49	2.61	62.92	14.54	0.652	0.0104	Magix
1178	9.777	9.640	9.589	10.567	10.091	9.955	815.18	55.53	1200.04	279.10	1.472	0.0104	Ptp4a1
1179	9.146	8.770	9.058	9.714	9.461	9.570	512.07	67.44	768.26	67.85	1.500	0.0104	Crip2
1180	7.634	7.754	7.721	7.859	8.849	8.693	208.49	8.88	369.05	120.96	1.770	0.0104	Irgm1
1181	9.360	9.144	9.402	7.960	8.744	8.886	633.22	59.15	383.62	118.67	0.606	0.0106	Car8
1182	4.260	4.598	4.364	5.368	4.865	4.948	21.32	2.61	33.77	6.58	1.584	0.0106	Abcg3
1183	6.345	6.291	6.025	6.620	7.224	7.192	74.90	8.59	131.35	28.60	1.754	0.0106	D5Erd579e
1184	7.162	7.111	7.073	6.098	6.739	6.539	138.71	4.28	89.42	19.41	0.645	0.0106	Pfkm
1185	7.556	7.683	7.711	6.980	7.211	7.169	201.07	11.36	139.43	11.63	0.693	0.0106	Fchsd2
1186	7.935	7.415	8.005	7.323	7.081	5.712	224.14	46.70	115.99	56.43	0.518	0.0107	Pttg1
1187	5.944	6.202	6.159	7.275	6.717	6.477	68.87	6.42	116.39	34.31	1.690	0.0107	Fas
1188	6.332	6.476	6.430	7.420	7.159	6.690	85.27	4.29	139.15	34.18	1.632	0.0107	Nfkb2
1189	7.446	7.630	7.737	8.696	8.122	7.983	195.29	19.65	315.45	86.83	1.615	0.0107	Mrc1
1190	6.043	5.853	5.437	6.819	6.435	6.157	55.69	11.45	90.29	21.02	1.621	0.0107	Skil
1191	5.413	5.576	5.392	6.666	6.102	5.804	44.10	3.14	75.37	23.58	1.709	0.0108	P2rx7
1192	4.428	4.476	4.728	5.431	5.031	4.934	23.43	2.69	35.47	6.74	1.514	0.0108	5330426P16Rik
1193	8.091	8.376	8.382	10.548	9.077	8.695	312.80	34.75	817.36	592.30	2.613	0.0109	Shisa5
1194	8.175	7.905	8.223	7.343	7.506	7.649	275.83	31.66	181.60	19.17	0.658	0.0109	Ccl27a
1195	3.644	3.912	3.972	4.877	3.994	4.840	14.42	1.69	24.66	7.57	1.710	0.0110	Sytl5
1196	7.159	7.301	7.129	8.291	7.837	7.531	146.88	9.49	242.20	65.18	1.649	0.0110	Necap2
1197	5.674	6.045	5.774	5.047	5.365	5.338	57.28	7.80	38.24	4.51	0.668	0.0110	Mras
1198	5.469	5.542	5.753	4.907	5.045	5.049	48.27	5.03	32.04	1.76	0.664	0.0110	1810048J11Rik
1199	4.473	5.059	4.570	5.794	5.380	5.157	26.43	6.03	44.27	10.17	1.675	0.0110	Cd300lb
1200	8.025	7.984	8.395	6.873	7.522	7.707	283.48	46.20	169.98	47.41	0.600	0.0110	Osbpl8
1201	9.748	9.706	9.809	10.646	10.080	10.162	864.09	31.18	1276.65	283.40	1.477	0.0110	Sdc1
1202	7.106	7.171	7.483	6.393	6.993	6.452	153.59	22.10	99.65	24.09	0.649	0.0111	Fzd7
1203	9.895	9.941	9.943	9.237	9.570	9.345	973.25	18.38	671.31	80.45	0.690	0.0111	Npc1
1204	4.454	4.395	4.294	4.830	5.122	4.784	20.86	1.16	30.27	3.98	1.451	0.0111	Tnfrsf4
1205	6.376	6.835	6.753	5.705	6.091	6.211	101.70	16.46	64.80	11.35	0.637	0.0112	Prkcz
1206	6.656	6.778	6.724	5.826	6.384	6.085	105.42	4.45	69.37	13.45	0.658	0.0112	Haus4
1207	4.013	4.460	4.168	4.812	4.711	4.608	18.71	3.00	26.22	1.86	1.401	0.0113	Cxcr6
1208	6.434	6.504	6.374	7.070	7.030	7.039	86.72	3.91	132.18	1.90	1.524	0.0113	Slc36a4
1209	11.565	11.611	11.707	10.924	11.381	11.388	3166.88	160.67	2429.86	422.15	0.767	0.0114	Slc10a1
1210	8.047	8.177	8.390	8.965	8.717	8.635	296.43	35.98	439.39	53.41	1.482	0.0114	Cdh5
1211	9.924	9.821	10.000	8.747	9.394	9.640	966.48	59.81	633.36	187.12	0.655	0.0115	Bbox1
1212	7.444	7.519	5.983	8.670	8.021	7.737	140.29	66.89	293.52	101.30	2.092	0.0115	Fkbp5
1213	7.192	7.500	7.813	6.200	7.116	6.824	184.03	39.37	108.53	32.86	0.590	0.0115	Paqr7
1214	4.932	4.755	5.264	4.301	4.416	4.514	31.98	5.84	21.30	1.56	0.666	0.0115	Slc6a16
1215	8.151	7.747	7.990	7.087	7.416	7.567	251.06	34.78	165.45	27.19	0.659	0.0115	Zranb1
1216	4.727	5.177	4.960	6.712	5.609	5.474	31.26	4.85	66.05	33.69	2.113	0.0115	P2ry12
1217	6.257	6.447	6.475	5.660	6.155	5.278	84.22	6.75	53.53	16.43	0.636	0.0115	Tnfaip8l1
1218	4.600	5.016	4.740	4.939	5.789	5.986	27.77	4.15	49.77	17.03	1.792	0.0115	Xaf1
1219	5.042	5.268	5.197	5.994	5.518	5.974	36.05	2.85	57.48	10.10	1.594	0.0116	Lipo1
1220	9.164	9.121	8.797	8.331	8.694	7.887	525.11	69.97	324.32	88.78	0.618	0.0117	Cpeb2
1221	3.615	4.061	3.702	7.487	5.280	4.142	13.99	2.37	78.62	87.88	5.622	0.0117	S100a8
1222	10.883	10.789	10.891	10.047	10.631	10.394	1852.49	71.80	1329.68	264.10	0.718	0.0117	Dhrs1
1223	4.880	4.868	4.745	5.822	5.393	5.143	28.49	1.45	44.64	10.86	1.567	0.0117	Rhoh
1224	5.977	6.308	6.182	5.434	5.770	5.552	71.61	8.19	48.25	5.78	0.674	0.0118	0610008F07Rik
1225	3.959	4.171	3.853	6.653	5.040	4.342	16.01	1.82	51.27	43.20	3.202	0.0118	Tmc3
1226	6.439	7.201	6.851	6.880	8.729	9.056	116.46	30.23	358.05	214.97	3.074	0.0118	Usp18
1227	9.307	9.485	9.500	10.166	9.856	9.760	691.53	50.35	980.89	148.32	1.418	0.0118	Tpm3
1228	3.590	4.041	3.724	5.404	4.620	4.010	13.91	2.29	27.68	13.39	1.991	0.0118	Naip6
1229	5.405	5.361	5.280	4.685	5.009	4.815	40.78	1.79	28.69	3.27	0.704	0.0118	Cspg5
1230	4.334	4.168	4.057	4.533	4.830	4.861	18.26	1.78	26.88	3.25	1.472	0.0118	Grhl1

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT avg	WTsd	KO avg	KOsd	KO/WT	BH	Gene Symbol
1231	3.841	4.388	4.404	4.826	5.061	4.528	18.81	3.89	28.27	5.15	1.502	0.0119	Fam105a
1232	10.578	10.707	10.402	11.481	10.915	10.842	1517.88	159.57	2208.00	564.99	1.455	0.0119	Tmem176b
1233	6.825	6.765	6.751	7.211	7.516	7.265	109.94	3.00	161.69	18.71	1.471	0.0119	Rnf19b
1234	8.167	8.887	8.682	7.702	8.013	8.021	390.54	94.61	242.08	29.30	0.620	0.0120	Glrx
1235	5.114	5.146	4.924	6.483	5.972	5.322	33.47	2.72	64.08	24.75	1.914	0.0121	Sorl1
1236	3.462	3.184	3.489	3.799	4.670	3.833	10.45	1.18	17.88	6.57	1.711	0.0122	H2-M2
1237	4.273	4.407	4.262	4.998	4.762	4.810	19.91	1.13	29.05	2.57	1.459	0.0122	A630001G21Rik
1238	3.956	3.968	3.855	4.636	4.535	4.340	15.21	0.64	22.76	2.34	1.497	0.0123	Cebpd
1239	8.671	8.247	8.556	5.893	7.855	7.852	362.65	53.21	173.99	99.21	0.480	0.0123	Nox4
1240	1.869	1.849	2.262	2.884	2.587	2.550	4.02	0.68	6.41	0.84	1.597	0.0123	P2ry10
1241	4.819	4.733	4.734	5.331	5.276	5.173	27.14	0.94	38.36	2.11	1.414	0.0123	Rhof
1242	3.935	4.652	3.911	3.253	3.467	3.569	18.49	5.76	10.82	1.19	0.585	0.0123	Tmeff2
1243	5.086	4.760	5.097	4.204	4.380	4.557	31.76	4.04	20.93	2.55	0.659	0.0124	Amy2a5
1244	6.668	6.877	6.707	8.050	7.273	7.161	107.90	8.47	187.58	67.26	1.738	0.0124	Ifi2712b
1245	3.878	3.909	3.603	4.321	4.662	4.225	13.96	1.58	21.34	3.51	1.529	0.0124	Prr5l
1246	3.354	3.452	3.313	5.549	4.320	3.637	10.37	0.52	26.41	18.07	2.547	0.0124	Ubd
1247	5.144	5.340	5.038	7.522	5.852	5.681	36.23	3.90	97.64	74.74	2.695	0.0125	Cd79b
1248	9.207	9.511	9.355	9.979	9.718	9.833	658.52	69.45	921.12	83.66	1.399	0.0125	Cyp3a13
1249	5.520	5.988	5.356	4.029	5.545	4.265	50.10	11.84	27.41	16.76	0.547	0.0125	Erbp4
1250	6.609	6.645	6.470	7.264	7.171	7.024	95.45	6.02	142.62	11.83	1.494	0.0125	Dst
1251	5.625	5.851	5.652	6.287	6.873	6.068	52.45	4.57	87.48	26.35	1.668	0.0128	Thbd
1252	5.978	6.354	6.198	7.442	6.880	6.513	72.73	9.41	127.67	42.16	1.755	0.0129	Agtrp
1253	5.779	5.753	5.619	6.284	6.470	6.241	52.66	3.09	80.74	6.96	1.533	0.0129	Smox
1254	8.733	8.903	8.760	9.943	9.314	9.147	445.90	28.55	729.15	223.67	1.635	0.0129	Ifngr2
1255	5.962	6.670	5.625	8.422	7.539	6.296	71.16	27.31	202.53	133.00	2.846	0.0129	Cxcl14
1256	7.508	7.441	7.548	6.449	7.074	7.116	180.99	6.73	120.27	28.56	0.665	0.0130	Abcb10
1257	5.433	5.705	5.452	6.700	6.066	5.916	46.38	5.02	77.10	23.48	1.662	0.0131	Anxa3
1258	5.833	6.170	6.076	7.016	6.553	6.527	65.47	7.69	105.18	20.99	1.606	0.0132	Tmem98
1259	5.739	5.768	5.623	7.019	6.358	5.959	52.38	2.75	91.30	34.71	1.743	0.0132	Arhgap4
1260	9.634	9.522	9.437	10.205	9.988	9.912	740.92	50.99	1053.04	113.23	1.421	0.0132	Aldoa
1261	7.522	7.619	7.941	7.104	7.339	6.836	208.74	32.67	137.90	23.81	0.661	0.0132	Zfp395
1262	6.462	6.283	6.543	7.551	7.380	6.672	86.43	7.83	152.04	44.58	1.759	0.0133	Cd9
1263	3.097	3.470	3.145	2.566	2.765	2.631	9.50	1.38	6.30	0.45	0.664	0.0135	Olf1249
1264	6.324	6.954	6.554	7.498	6.929	7.547	99.37	22.41	163.23	35.95	1.643	0.0136	Fam25c
1265	4.677	4.295	4.974	5.402	5.154	5.323	25.55	5.90	39.30	3.39	1.538	0.0136	Gnai1
1266	8.072	7.636	7.677	7.252	6.701	7.133	224.21	39.02	132.27	25.18	0.590	0.0136	Ppp1r3b
1267	5.529	5.657	5.393	6.808	6.075	5.867	46.21	4.23	79.27	28.76	1.715	0.0136	Vopp1
1268	10.009	10.003	10.068	8.757	9.431	9.811	1043.46	25.94	673.70	233.22	0.646	0.0136	Ccbl1
1269	7.555	7.800	7.688	8.216	8.232	8.310	205.69	17.36	305.05	10.74	1.483	0.0136	Psme2
1270	7.900	7.543	7.821	6.768	7.104	7.508	217.14	27.33	142.84	36.80	0.658	0.0137	Ccdc101
1271	5.616	5.874	5.641	6.826	6.393	6.028	52.52	5.32	87.56	24.29	1.667	0.0137	Hmha1
1272	8.404	8.207	8.558	7.526	8.054	7.769	337.01	40.70	222.75	40.93	0.661	0.0138	Zfp1
1273	5.668	5.563	5.458	5.004	5.200	5.141	47.35	3.45	34.71	2.39	0.733	0.0138	Mycn
1274	7.281	7.288	7.219	6.756	6.549	6.830	153.58	3.99	105.17	10.37	0.685	0.0139	Ngef
1275	4.703	4.787	4.321	5.512	5.046	5.165	24.55	4.02	38.18	6.61	1.555	0.0139	Ctsw
1276	3.537	3.532	3.433	4.437	4.152	3.703	11.32	0.45	17.49	4.33	1.544	0.0139	Cd69
1277	9.928	10.033	9.942	8.678	9.584	9.308	1001.99	39.82	603.75	180.95	0.603	0.0140	Ugt3a1
1278	6.283	6.723	6.445	5.494	5.811	6.094	90.20	14.14	56.50	11.62	0.626	0.0141	9630013D21Rik
1279	4.915	4.697	4.587	5.567	5.607	5.005	26.71	3.14	42.75	9.24	1.601	0.0141	Hk2
1280	4.316	8.976	4.175	2.606	3.684	2.845	180.52	279.80	8.71	3.63	0.048	0.0142	Ear11
1281	8.759	9.093	8.780	9.482	9.280	9.616	472.95	63.53	707.17	81.69	1.495	0.0142	Sqle
1282	5.453	5.182	5.448	5.991	6.067	5.630	41.25	4.29	60.05	9.29	1.456	0.0144	Arhgap27
1283	7.396	7.675	7.854	5.519	6.480	7.501	201.39	31.58	105.44	69.11	0.524	0.0144	Sult1b1
1284	6.669	6.675	6.809	5.979	6.363	6.164	105.36	5.89	72.37	9.64	0.687	0.0144	Rap2a

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT avg	WTsd	KO avg	KOsd	KO/WT	BH	Gene Symbol
1285	5.469	5.373	5.458	6.420	5.839	6.096	43.23	1.57	70.43	14.30	1.629	0.0145	Jdp2
1286	4.085	4.984	5.347	4.075	3.963	3.978	29.77	11.97	16.07	0.68	0.540	0.0145	Fign
1287	6.995	6.826	6.603	7.816	7.490	7.264	112.74	15.21	186.29	36.26	1.652	0.0145	Il17ra
1288	9.386	9.250	9.378	8.351	8.988	8.961	647.82	33.66	444.16	101.93	0.686	0.0146	0610011F06Rik
1289	5.310	5.531	5.421	6.063	5.826	5.783	42.91	3.29	59.55	6.40	1.388	0.0147	Lpar5
1290	4.400	4.730	4.347	5.036	5.223	4.981	22.66	3.37	33.91	3.03	1.496	0.0147	Racgap1
1291	5.440	5.208	5.236	7.319	5.805	5.794	39.36	3.54	90.35	60.01	2.295	0.0147	Rbbp8
1292	5.832	5.975	5.915	5.458	5.209	5.499	60.07	2.97	42.06	4.45	0.700	0.0147	Al661453
1293	6.734	6.761	6.644	7.842	7.194	7.064	104.98	4.43	169.92	51.96	1.619	0.0147	Hn1
1294	8.378	8.497	8.237	8.039	7.544	7.543	331.83	29.78	212.01	44.11	0.639	0.0147	Kcnk5
1295	3.665	4.002	3.705	4.254	4.281	4.350	13.92	1.83	19.64	0.68	1.411	0.0148	Tpx2
1296	6.413	6.028	6.420	5.468	5.628	5.812	78.69	11.64	49.97	5.97	0.635	0.0148	1110049F12Rik
1297	8.197	8.357	8.171	9.154	8.969	8.516	303.22	21.58	478.88	103.53	1.579	0.0148	Itm2c
1298	7.314	7.471	7.579	8.301	7.942	7.747	175.90	16.05	258.76	51.47	1.471	0.0148	Tle3
1299	8.839	8.837	8.821	9.385	9.156	9.275	455.92	3.14	619.48	49.13	1.359	0.0149	Capza1
1300	10.805	10.838	10.642	9.525	10.442	10.391	1739.20	123.74	1156.79	364.78	0.665	0.0149	Nr1d1
1301	7.111	7.258	7.223	6.004	6.598	6.919	146.92	7.77	94.00	28.52	0.640	0.0149	Nars2
1302	4.931	5.337	4.765	6.761	5.988	5.206	32.70	6.88	69.62	36.18	2.129	0.0151	Csf3r
1303	4.303	4.401	4.530	5.033	4.758	4.905	21.32	1.69	29.92	2.83	1.403	0.0151	Kctd12b
1304	6.327	6.232	6.504	5.487	5.911	5.944	82.08	7.96	55.54	9.27	0.677	0.0151	Orc5
1305	7.737	7.973	7.663	8.730	8.301	8.137	222.42	25.48	340.48	74.75	1.531	0.0152	Zyx
1306	4.829	5.420	5.290	5.781	5.718	5.840	36.79	7.47	54.97	2.32	1.494	0.0152	Samd9l
1307	5.741	5.923	5.907	6.770	6.559	6.173	58.05	3.96	91.86	18.61	1.582	0.0152	Leprot
1308	10.427	10.197	10.285	10.854	10.547	10.729	1266.21	102.55	1681.32	177.85	1.328	0.0153	Tm6sf2
1309	3.615	3.402	4.166	4.467	4.585	4.190	13.59	3.86	21.45	2.93	1.579	0.0153	6720489N17Rik
1310	4.267	5.113	4.576	4.890	5.964	5.752	25.90	7.87	48.65	17.01	1.878	0.0153	Mcm6
1311	5.704	5.677	5.710	6.341	6.344	6.176	51.87	0.61	78.20	5.13	1.508	0.0153	Tspan3
1312	6.087	6.601	6.168	7.117	6.779	6.781	78.99	15.79	119.52	16.70	1.513	0.0153	Isg20
1313	6.482	6.413	6.416	5.524	6.018	6.101	86.66	2.38	59.82	12.11	0.690	0.0153	Epb4.1l4b
1314	6.136	5.978	6.703	7.719	6.569	7.070	79.19	21.97	146.67	58.86	1.852	0.0153	Kcnj8
1315	5.440	5.991	5.943	6.554	6.857	6.040	56.18	11.10	91.89	25.14	1.636	0.0153	Tor3a
1316	6.924	7.060	7.099	6.656	6.047	6.592	130.65	8.18	87.80	18.91	0.672	0.0154	Gm10319
1317	5.772	5.771	6.025	5.035	5.038	5.635	58.13	6.05	38.44	9.74	0.661	0.0154	Polr3g
1318	3.753	4.154	4.219	5.081	4.871	4.216	16.64	2.76	27.23	7.83	1.637	0.0154	Slfn4
1319	4.428	4.762	4.531	6.396	5.299	4.895	23.93	2.89	51.12	29.08	2.137	0.0155	1700112E06Rik
1320	7.667	7.696	7.888	6.924	7.214	7.368	215.82	18.39	145.04	22.09	0.672	0.0155	Aldh5a1
1321	3.549	3.618	3.527	3.979	4.410	3.930	11.84	0.39	17.43	3.34	1.472	0.0155	Traf1
1322	4.332	4.790	4.438	5.213	5.152	4.904	23.16	3.98	34.20	3.77	1.476	0.0155	Haus8
1323	6.643	6.644	6.835	7.408	7.297	7.173	104.71	8.20	157.10	12.75	1.500	0.0156	Pea15a
1324	6.714	6.898	6.710	7.718	7.375	7.211	109.66	8.31	174.90	32.11	1.595	0.0156	Bak1
1325	8.024	7.987	8.071	7.488	7.569	7.679	261.01	7.61	191.47	12.81	0.734	0.0157	Trmt2b
1326	5.280	5.201	5.245	6.091	5.905	5.563	37.86	1.03	58.46	10.51	1.544	0.0157	Cx3cr1
1327	8.943	8.981	8.170	9.264	9.830	9.280	428.40	121.79	715.57	168.46	1.670	0.0157	Bcl3
1328	3.392	3.297	3.382	3.374	4.695	5.500	10.25	0.37	27.17	17.47	2.651	0.0158	Ccr3
1329	6.004	10.179	3.510	11.097	9.728	9.138	411.70	648.19	1200.37	868.49	2.916	0.0158	Saa1
1330	9.666	9.677	9.801	9.189	9.025	9.465	840.90	44.35	603.73	94.42	0.718	0.0158	Suox
1331	9.337	8.940	9.161	8.235	8.450	8.844	570.14	77.84	370.16	81.06	0.649	0.0159	Ern1
1332	5.232	5.801	5.437	5.827	6.295	6.276	45.55	9.29	70.92	12.28	1.557	0.0159	Parp11
1333	6.388	6.594	6.590	6.017	5.917	5.901	92.25	7.35	61.64	2.70	0.668	0.0159	1810020D17Rik
1334	8.620	8.735	8.628	8.024	8.221	8.161	405.03	18.21	281.66	19.43	0.695	0.0159	Adra1b
1335	5.593	5.640	5.459	5.024	5.081	5.255	47.37	3.04	34.86	2.96	0.736	0.0159	Dlg3
1336	4.733	4.864	4.652	4.336	4.360	4.190	26.95	2.01	19.66	1.23	0.730	0.0159	Sec31b
1337	4.867	4.960	5.204	4.284	4.218	4.762	32.40	4.00	21.74	4.69	0.671	0.0160	Pstk
1338	4.911	4.566	4.683	5.530	5.464	5.018	26.49	3.27	40.92	7.44	1.545	0.0160	Slc39a6

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT avg	WTsd	KO avg	KOsd	KO/WT	BH	Gene Symbol
1339	5.532	5.490	5.047	5.814	5.939	5.918	41.42	7.28	59.34	2.72	1.433	0.0160	Etv5
1340	2.831	2.974	3.096	3.751	3.512	3.257	7.84	0.72	11.48	1.95	1.464	0.0160	Plod2
1341	7.752	7.817	7.691	8.650	8.195	8.174	215.88	9.39	327.86	63.96	1.519	0.0160	Snx5
1342	6.827	6.766	6.725	7.715	7.404	7.175	109.37	3.93	174.68	33.16	1.597	0.0161	Kctd12
1343	7.682	11.524	6.031	11.877	11.220	10.559	1071.95	1623.67	2551.11	1135.37	2.380	0.0161	Saa2
1344	3.380	3.348	3.368	3.898	4.422	3.780	10.31	0.12	16.69	4.15	1.620	0.0162	Penk
1345	4.464	4.552	4.866	5.733	5.366	4.878	24.90	3.76	41.27	11.88	1.658	0.0163	Asprv1
1346	3.419	3.811	3.864	5.618	4.387	4.066	13.09	2.10	28.93	17.61	2.210	0.0163	Cd79a
1347	4.153	4.063	4.164	5.066	4.795	4.308	17.48	0.67	27.02	6.87	1.546	0.0163	Smpdl3b
1348	6.301	6.219	6.492	6.926	7.082	6.904	81.10	8.00	125.61	8.64	1.549	0.0163	Esam
1349	7.091	7.056	7.099	8.620	7.981	7.237	135.48	2.10	265.60	121.79	1.960	0.0163	Mvp
1350	8.566	8.585	8.611	9.450	8.996	8.923	384.61	5.98	565.21	117.06	1.470	0.0163	Sdcbp
1351	5.735	5.807	5.680	6.398	6.505	6.020	53.50	2.36	80.03	13.48	1.496	0.0163	Dennd4b
1352	4.692	4.808	4.753	5.422	5.412	5.234	26.94	1.08	41.03	2.94	1.523	0.0165	Rftn1
1353	5.938	6.131	5.705	7.074	6.597	6.179	61.19	8.97	101.33	31.39	1.656	0.0166	Phf15
1354	3.697	4.092	4.030	4.679	4.351	4.358	15.45	2.18	22.18	2.98	1.435	0.0167	Fam164a
1355	5.015	4.680	4.929	5.448	5.342	5.390	29.48	3.46	42.06	1.55	1.427	0.0167	D2Ertd750e
1356	6.142	6.311	6.081	7.629	6.851	6.373	72.57	6.08	132.09	59.31	1.820	0.0167	Fes
1357	3.267	3.523	3.285	4.020	3.721	3.961	10.29	1.05	15.00	1.60	1.457	0.0167	Anln
1358	5.492	5.562	5.331	6.410	6.031	5.706	44.18	3.57	67.55	16.54	1.529	0.0168	C130050O18Rik
1359	5.978	5.939	5.790	6.554	6.456	6.361	59.91	4.05	87.99	5.88	1.469	0.0168	H2-Q2
1360	6.855	7.209	7.255	6.393	6.548	6.585	138.82	20.11	91.19	6.32	0.657	0.0169	Hnmt
1361	7.796	7.873	7.956	7.088	7.451	7.353	235.02	13.03	158.16	19.99	0.673	0.0171	Fgfr1
1362	5.805	6.165	5.624	6.827	6.603	6.259	59.00	11.54	95.77	18.53	1.623	0.0171	Slc7a7
1363	9.369	9.290	9.470	7.856	8.069	9.399	665.38	41.83	391.85	246.06	0.589	0.0171	Agxt21l
1364	5.350	5.307	5.622	4.601	5.162	4.859	43.21	5.27	29.70	5.79	0.687	0.0171	Pgm5
1365	6.661	6.681	6.220	7.289	7.166	7.179	92.77	15.81	148.30	7.07	1.599	0.0171	Kctd17
1366	3.945	3.986	4.483	7.034	4.808	4.755	17.87	3.90	62.03	59.80	3.471	0.0172	Tmem45b
1367	4.725	4.713	4.868	5.760	5.338	5.111	27.29	1.65	43.07	10.08	1.578	0.0172	Pstpip1
1368	4.800	4.791	4.702	5.201	5.491	5.124	27.19	1.01	38.87	5.36	1.430	0.0172	Ccr12
1369	6.438	6.513	6.367	5.895	5.955	5.989	86.84	4.38	61.68	2.02	0.710	0.0172	Tomm40l
1370	10.087	9.906	10.127	9.839	9.303	9.422	1054.95	84.43	744.67	150.99	0.706	0.0173	Pm20d1
1371	10.940	11.106	10.794	11.366	11.202	11.206	1981.17	214.56	2453.10	161.97	1.238	0.0173	C4b
1372	5.104	5.418	5.455	5.684	6.096	5.849	40.33	5.19	59.15	8.58	1.467	0.0175	Tnfsf10
1373	4.567	4.597	4.932	5.660	5.147	5.518	26.14	3.81	43.94	7.75	1.681	0.0175	Galnt2
1374	6.757	6.863	6.856	5.930	6.517	6.261	113.48	4.64	76.41	15.29	0.673	0.0175	Gga2
1375	9.787	9.948	9.531	11.426	10.435	9.916	870.39	124.50	1700.31	933.50	1.953	0.0175	Lbp
1376	6.157	6.109	6.232	8.897	6.975	6.528	71.85	3.10	231.57	212.88	3.223	0.0176	Mfge8
1377	6.776	6.762	6.719	6.139	6.376	5.714	107.85	2.22	68.68	15.37	0.637	0.0176	Plip
1378	7.007	7.429	7.298	7.556	8.623	7.901	152.80	22.22	273.84	107.36	1.792	0.0177	Tap1
1379	5.275	4.819	5.433	5.902	5.752	5.631	36.72	7.69	54.41	5.15	1.482	0.0177	Taf9b
1380	4.701	4.680	4.653	5.063	5.128	5.106	25.60	0.43	34.28	0.78	1.339	0.0177	Atad2
1381	4.795	4.240	4.628	5.468	5.227	4.991	23.79	4.50	37.83	6.23	1.590	0.0177	Cdc14a
1382	10.218	10.433	10.388	10.750	10.777	10.617	1304.61	100.25	1682.49	98.23	1.290	0.0177	Ctsd
1383	8.139	8.433	8.138	9.006	8.736	8.635	303.04	36.84	445.93	60.66	1.472	0.0177	Ppt1
1384	5.440	5.468	5.454	5.046	5.025	4.993	43.84	0.42	32.48	0.60	0.741	0.0177	Rab3a
1385	10.793	10.815	10.863	10.369	10.500	10.556	1812.93	45.36	1425.20	93.78	0.786	0.0178	Aes
1386	7.780	7.747	7.804	7.123	7.299	7.397	219.36	4.34	155.16	14.74	0.707	0.0179	Papd7
1387	5.505	5.660	5.675	6.657	6.087	6.063	49.02	3.15	78.60	19.34	1.603	0.0180	Tbc1d1
1388	3.772	3.496	4.259	3.236	3.186	3.285	14.70	4.03	9.42	0.32	0.641	0.0180	Zfp354b
1389	8.182	7.885	7.877	6.878	7.633	7.508	253.99	31.59	166.03	42.73	0.654	0.0181	Adck5
1390	11.344	11.543	11.442	11.093	10.961	11.236	2788.77	192.14	2196.52	209.63	0.788	0.0181	Cyb5r3
1391	5.468	5.730	5.435	6.823	6.376	5.798	46.87	5.40	83.97	28.81	1.792	0.0182	A830007P12Rik
1392	12.202	12.211	11.989	11.641	12.010	11.933	4505.80	382.04	3742.93	487.96	0.831	0.0182	Gstp1

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT avg	WTsd	KO avg	KOsd	KO/WT	BH	Gene Symbol
1393	4.283	4.103	4.167	4.987	4.781	4.361	18.20	1.16	26.58	5.64	1.460	0.0182	Adams15
1394	5.915	4.815	4.578	7.467	6.445	5.348	37.46	19.94	101.57	69.22	2.711	0.0182	Il1b
1395	7.111	6.860	7.431	8.245	7.694	7.559	142.33	28.40	232.99	61.66	1.637	0.0183	Ednra
1396	8.267	7.975	8.258	7.220	7.607	7.800	288.57	32.07	188.92	37.23	0.655	0.0183	Pgap1
1397	8.397	8.292	8.387	7.382	8.023	7.840	328.46	13.03	218.68	47.51	0.666	0.0184	Traf4
1398	7.773	7.671	7.742	7.073	7.042	7.411	212.18	7.67	145.53	21.37	0.686	0.0184	Acy1
1399	5.042	4.912	4.911	5.456	5.339	5.560	31.05	1.65	43.85	3.35	1.412	0.0184	Ank2
1400	3.607	4.256	4.134	5.329	4.448	4.540	16.29	3.63	28.44	10.22	1.746	0.0184	Tnfrsf23
1401	4.384	4.265	4.585	4.025	3.968	3.921	21.37	2.42	15.69	0.57	0.734	0.0184	Lrp2
1402	6.299	6.382	6.463	5.822	6.029	5.782	83.46	4.73	58.97	5.53	0.707	0.0184	Ror1
1403	10.018	9.662	9.754	10.449	10.402	10.067	903.47	118.67	1274.43	175.96	1.411	0.0184	Tm4sf4
1404	4.973	5.054	5.369	6.100	5.764	5.508	35.31	5.28	56.15	11.66	1.590	0.0184	Cd55
1405	4.406	4.363	4.496	5.304	5.253	4.673	21.45	1.02	34.38	7.71	1.603	0.0184	Tnfsf13b
1406	6.733	6.830	6.584	5.864	6.301	6.201	105.37	8.96	70.22	10.70	0.666	0.0184	1190007I07Rik
1407	7.480	7.154	7.240	7.801	7.705	7.968	157.35	18.80	227.40	21.22	1.445	0.0185	Rock2
1408	6.526	6.715	6.300	7.044	7.510	7.043	92.01	13.13	148.73	29.07	1.616	0.0185	Herc6
1409	5.852	6.187	5.808	7.882	6.515	6.319	62.22	9.27	135.73	86.90	2.181	0.0185	6330416G13Rik
1410	10.872	10.920	10.922	10.171	10.641	10.627	1916.94	37.19	1443.53	252.18	0.753	0.0185	Hsd3b7
1411	5.059	5.003	4.928	5.639	5.271	5.496	31.94	1.46	44.52	5.64	1.394	0.0186	Tmem51
1412	6.966	6.693	6.879	7.539	7.726	7.125	115.40	10.97	179.10	36.54	1.552	0.0186	Chst15
1413	9.045	8.913	9.050	7.627	8.733	8.480	513.44	27.16	326.71	116.84	0.636	0.0186	Mmd
1414	5.112	6.191	5.641	4.917	5.111	4.819	52.51	19.37	31.00	3.24	0.590	0.0186	Slc22a3
1415	4.206	4.360	4.188	4.699	4.741	4.770	19.08	1.27	26.66	0.66	1.398	0.0187	Icosl
1416	10.568	10.529	10.617	10.149	10.228	10.265	1521.84	46.81	1188.45	48.24	0.781	0.0187	Prdx6
1417	9.752	9.617	9.471	8.650	9.435	8.824	785.57	76.28	515.65	154.90	0.656	0.0187	Slc6a9
1418	9.497	9.361	9.497	8.189	8.992	9.129	700.88	37.58	453.63	142.45	0.647	0.0187	Cyp2d13
1419	4.699	4.766	4.787	5.591	5.394	5.058	26.93	0.86	41.19	7.49	1.529	0.0188	Kcnab2
1420	6.474	7.519	5.236	5.572	4.884	5.060	103.34	73.95	36.83	9.51	0.356	0.0188	Slc15a5
1421	6.682	6.855	6.762	6.190	6.283	6.246	109.00	6.53	75.60	2.44	0.694	0.0188	Smcr7
1422	5.135	4.796	4.718	5.826	5.160	5.495	29.74	4.72	45.85	10.51	1.542	0.0188	Tc2n
1423	5.107	5.347	5.283	5.615	5.991	5.908	38.04	3.21	57.55	7.60	1.513	0.0188	Cmpk2
1424	8.704	8.583	8.793	7.302	8.144	8.392	414.68	30.04	258.88	91.44	0.624	0.0188	Ociad2
1425	11.024	11.098	11.015	9.912	10.949	10.497	2114.68	66.79	1461.81	507.43	0.691	0.0188	Glul
1426	6.460	6.560	6.607	7.509	7.168	6.827	93.29	4.82	146.50	34.39	1.570	0.0189	Lmo2
1427	6.357	6.232	7.000	5.598	4.263	6.210	95.03	28.74	47.23	27.44	0.497	0.0189	Slco1a4
1428	6.558	6.628	6.759	5.644	5.908	6.456	100.48	7.16	65.94	19.56	0.656	0.0189	Mblac2
1429	5.358	5.466	5.499	5.886	5.853	5.972	43.48	2.20	59.90	2.58	1.378	0.0189	Fam126a
1430	4.553	4.502	3.919	3.602	3.684	3.916	20.42	4.60	13.37	1.54	0.655	0.0190	Eef1b2
1431	2.328	2.110	2.031	3.224	2.811	2.401	4.47	0.49	7.21	2.04	1.612	0.0190	Gpr141
1432	5.060	5.362	5.275	6.089	6.145	5.552	37.74	3.98	61.92	13.05	1.641	0.0190	Tlr3
1433	10.124	9.816	10.423	7.954	9.501	9.674	1130.30	236.15	596.48	305.29	0.528	0.0192	Retsat
1434	9.616	9.508	10.042	8.375	9.554	8.949	855.72	174.51	525.99	211.62	0.615	0.0194	Me1
1435	5.721	5.562	5.334	6.720	6.104	5.845	46.78	6.22	77.24	25.06	1.651	0.0194	Ankrd44
1436	6.633	6.817	6.691	6.226	6.269	6.196	105.11	6.90	75.09	1.94	0.714	0.0195	Wwox
1437	3.621	3.560	3.633	4.102	4.241	3.895	12.17	0.33	16.99	2.02	1.396	0.0195	Fut4
1438	6.958	6.977	7.026	6.045	6.296	6.750	126.84	3.10	84.07	21.36	0.663	0.0195	Kdm1b
1439	3.968	4.168	4.070	4.685	4.566	4.544	16.81	1.17	24.25	1.29	1.443	0.0195	Bub1b
1440	5.552	5.569	5.521	6.819	6.138	5.788	46.76	0.78	79.53	29.89	1.701	0.0195	Sema6b
1441	10.374	10.301	10.292	9.298	9.880	9.996	1280.83	40.44	864.34	207.30	0.675	0.0195	Slc25a23
1442	7.792	7.450	7.682	6.912	7.289	7.190	200.66	23.76	140.93	18.51	0.702	0.0196	Znrf3
1443	8.046	8.411	7.828	7.419	7.736	7.133	277.24	57.64	174.91	36.58	0.631	0.0196	Bmyc
1444	7.184	7.004	6.984	7.577	7.668	7.641	133.47	10.42	197.98	6.34	1.483	0.0196	Rnf145
1445	7.646	7.587	7.767	6.667	6.765	7.476	203.44	13.05	129.45	42.18	0.636	0.0196	Anks4b
1446	5.416	5.560	5.594	4.682	4.972	5.262	46.06	2.96	31.80	6.36	0.690	0.0196	Fanci

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT avg	WTsd	KO avg	KOsd	KO/WT	BH	Gene Symbol
1447	8.445	8.400	8.612	7.618	7.989	8.151	359.21	28.37	244.94	44.61	0.682	0.0197	Gramd3
1448	5.389	5.725	5.185	7.426	5.976	5.872	43.73	8.41	97.82	64.26	2.237	0.0197	Nfam1
1449	3.933	3.947	4.013	4.048	6.289	5.060	15.62	0.46	42.69	31.87	2.734	0.0199	Mmp13
1450	6.209	6.366	6.483	7.419	7.061	6.631	81.98	7.77	134.59	36.00	1.642	0.0200	Tmem86a
1451	6.591	6.400	6.690	6.084	5.945	6.032	94.70	9.50	64.95	3.14	0.686	0.0201	2310004I24Rik
1452	4.818	4.527	4.748	5.752	5.335	5.377	26.04	2.68	45.28	7.49	1.739	0.0202	6-Sep
1453	3.588	3.275	3.789	4.255	4.124	3.964	11.84	2.08	17.38	1.74	1.468	0.0203	Ctsk
1454	5.238	5.257	5.196	6.056	5.635	5.785	37.54	0.81	57.12	8.59	1.522	0.0204	Orai2
1455	2.558	2.601	2.564	3.304	3.260	3.031	5.96	0.10	9.21	0.91	1.547	0.0205	Nlrc4
1456	8.056	8.041	8.236	7.323	7.655	7.608	276.93	21.24	185.59	22.30	0.670	0.0205	Rassf3
1457	5.047	4.860	5.059	4.509	4.669	4.457	31.82	2.40	23.39	1.82	0.735	0.0205	Dfna5
1458	5.094	5.838	5.731	4.788	4.789	5.192	48.14	12.29	30.60	5.14	0.636	0.0205	Tert
1459	4.598	4.840	4.406	6.093	5.333	4.856	24.68	3.74	45.85	20.22	1.857	0.0206	Pram1
1460	7.682	7.802	7.666	6.949	7.233	7.322	210.53	10.97	144.66	18.90	0.687	0.0206	Tpst1
1461	5.301	5.581	5.245	6.374	6.024	5.609	41.75	5.36	65.61	17.07	1.572	0.0208	Map3k8
1462	4.048	4.497	4.340	4.856	4.939	4.610	19.79	3.05	28.02	3.24	1.416	0.0208	Lxn
1463	9.487	9.468	9.446	10.124	9.860	9.716	707.80	9.96	961.95	140.27	1.359	0.0208	Cap1
1464	7.000	6.774	6.800	6.182	6.210	6.535	116.30	10.18	79.79	11.25	0.686	0.0208	Plekhg3
1465	4.972	5.223	5.030	5.878	5.592	5.416	33.80	3.13	49.91	8.17	1.476	0.0209	Trim12c
1466	6.804	6.827	6.762	7.289	7.573	7.242	111.26	2.51	166.08	21.23	1.493	0.0209	Pcolce
1467	6.766	6.494	6.878	7.422	7.725	6.975	105.51	14.04	169.64	42.88	1.608	0.0211	Pdgfrb
1468	7.423	7.222	7.538	6.668	6.929	7.098	168.91	18.42	120.18	17.69	0.712	0.0211	D2hgdh
1469	5.039	4.978	5.180	5.800	5.513	5.354	33.55	2.43	47.42	7.57	1.414	0.0211	Rap1gap2
1470	6.531	6.417	6.792	7.106	7.456	6.854	96.24	13.08	143.00	30.34	1.486	0.0211	Lhfp
1471	8.105	7.936	8.332	6.954	7.315	7.969	280.82	38.97	177.94	65.38	0.634	0.0213	Chac2
1472	6.713	7.097	6.686	7.982	7.410	7.266	114.94	19.08	192.29	53.06	1.673	0.0213	Rasa3
1473	4.173	4.915	4.847	6.038	5.304	4.966	25.66	6.64	45.49	17.99	1.773	0.0213	Plekhm3
1474	6.618	6.913	6.843	6.066	6.327	6.342	111.18	11.60	76.14	7.91	0.685	0.0214	Mzt2
1475	6.862	6.466	6.408	7.263	7.024	7.054	96.54	17.21	138.89	12.81	1.439	0.0214	Asap3
1476	6.929	7.329	7.265	6.042	6.788	6.699	145.47	20.76	93.42	24.07	0.642	0.0214	BC048355
1477	5.689	5.728	5.999	4.984	5.421	5.388	56.19	6.77	38.78	6.20	0.690	0.0214	Dapk2
1478	6.142	6.120	6.127	5.337	5.450	5.804	70.01	0.57	46.66	8.14	0.666	0.0214	Txnrd3
1479	5.854	5.774	5.862	6.574	6.475	6.143	56.91	1.89	84.96	12.77	1.493	0.0214	E130203B14Rik
1480	6.222	5.851	6.346	5.225	5.651	5.816	71.24	12.18	48.00	9.67	0.674	0.0216	Ppp2r3a
1481	6.050	6.276	6.151	5.642	5.582	5.676	71.60	5.64	49.65	1.63	0.694	0.0218	Prkra
1482	5.119	5.159	5.032	6.077	5.682	5.324	34.39	1.53	52.96	13.80	1.540	0.0219	Gmip
1483	3.852	3.743	4.213	5.100	4.378	4.335	15.46	2.73	25.09	7.98	1.623	0.0219	Ly6f
1484	9.202	9.091	9.256	8.385	8.821	8.825	581.91	33.56	413.36	68.47	0.710	0.0219	Pccb
1485	5.349	6.237	5.175	3.973	4.045	5.549	50.77	21.47	26.34	17.73	0.519	0.0219	Trhde
1486	8.708	9.057	8.794	8.182	8.347	8.553	464.85	60.09	330.55	42.81	0.711	0.0220	Mmp19
1487	4.745	4.261	4.563	3.991	4.117	4.085	23.21	3.84	16.74	0.75	0.721	0.0220	Lrp2bp
1488	6.611	6.716	6.442	7.364	7.249	6.903	96.60	9.14	145.51	23.27	1.506	0.0222	Fosl2
1489	11.897	11.842	11.896	12.039	11.956	12.040	3765.60	80.88	4130.65	136.33	1.097	0.0224	Fgg
1490	4.586	5.064	4.527	5.242	5.239	5.539	26.84	5.74	40.69	5.01	1.516	0.0224	Mcm4
1491	8.648	10.398	8.762	11.373	9.902	10.178	728.34	538.36	1589.02	925.95	2.182	0.0224	Apcs
1492	5.721	5.891	5.470	6.819	6.366	5.941	52.14	7.53	85.60	25.89	1.642	0.0224	Nfkbiz
1493	8.069	7.919	8.140	6.931	7.648	7.576	264.22	20.38	171.14	42.81	0.648	0.0224	Cryl1
1494	10.094	10.051	10.135	9.433	9.890	9.520	1092.83	32.13	791.41	138.15	0.724	0.0225	Khk
1495	6.751	6.510	6.236	7.484	7.376	6.748	91.42	16.19	150.85	38.12	1.650	0.0226	1810011O10Rik
1496	8.865	8.901	8.865	8.071	8.415	8.500	470.25	6.70	324.04	48.89	0.689	0.0227	1300018J18Rik
1497	3.146	3.109	3.637	5.130	4.222	3.455	9.98	2.14	21.55	12.28	2.160	0.0227	Mrgpra2a
1498	4.258	4.916	4.839	6.172	5.106	5.146	25.98	5.98	47.32	21.48	1.821	0.0228	Marco
1499	7.386	7.246	7.594	6.769	7.000	6.223	170.74	20.92	103.92	27.01	0.609	0.0232	Celsr1
1500	6.776	6.823	7.056	7.853	7.463	7.189	118.62	12.67	184.54	43.26	1.556	0.0232	Rgl1

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT avg	WTsd	KO avg	KOsd	KO/WT	BH	Gene Symbol
1501	10.236	9.940	10.291	8.967	9.838	9.771	1147.05	144.59	763.11	228.57	0.665	0.0232	Ugt2b5
1502	4.673	4.607	4.560	5.402	5.269	4.846	24.49	0.97	36.54	7.00	1.492	0.0232	Adams12
1503	9.324	9.566	9.108	10.458	9.754	9.614	650.16	103.34	1017.89	338.80	1.566	0.0232	Tmem176a
1504	7.162	7.182	7.362	6.038	6.710	6.955	150.98	11.71	98.17	29.71	0.650	0.0233	Pdzk1
1505	4.942	4.972	4.853	5.484	5.639	5.325	30.34	1.29	44.90	4.88	1.480	0.0233	Lst1
1506	8.964	9.179	9.073	9.847	9.628	9.388	539.13	40.16	794.01	125.52	1.473	0.0234	Tnfrsf1a
1507	5.717	5.447	5.624	4.825	5.215	5.301	48.51	4.54	34.96	5.85	0.721	0.0234	Alg6
1508	5.967	5.942	6.025	6.628	6.638	6.310	63.05	1.87	92.60	11.49	1.469	0.0235	Acvrl1
1509	6.252	6.263	6.372	5.575	5.691	6.016	78.61	3.65	54.68	8.93	0.696	0.0235	Cdkl5
1510	8.891	8.548	9.520	6.488	7.969	8.710	527.77	185.75	253.03	164.48	0.479	0.0235	Ces1e
1511	7.884	8.044	7.720	8.566	8.228	8.392	236.97	26.57	338.25	39.72	1.427	0.0235	Rhbdd2
1512	8.382	8.235	8.610	7.456	7.903	8.073	341.91	45.26	228.06	47.90	0.667	0.0237	4933439F18Rik
1513	9.483	9.619	9.347	9.973	10.033	9.698	717.76	67.66	961.15	114.89	1.339	0.0238	Hist2h2aa1
1514	3.440	3.743	3.351	5.089	4.039	3.846	11.48	1.68	21.61	10.80	1.882	0.0241	Tmem156
1515	9.598	9.402	9.611	8.470	8.933	9.268	744.42	58.94	486.60	130.99	0.654	0.0241	Il1rap
1516	4.176	4.052	3.878	4.709	4.427	4.447	16.46	1.69	23.16	2.59	1.407	0.0241	Ptger2
1517	7.393	7.431	7.309	6.435	6.962	6.962	166.42	7.12	111.95	22.01	0.673	0.0242	Spnb3
1518	8.349	11.144	7.921	11.988	10.792	10.141	943.87	1143.31	2321.13	1540.75	2.459	0.0242	Orm2
1519	6.266	6.676	6.395	5.526	5.924	6.111	87.78	13.05	58.64	11.67	0.668	0.0242	Tmem144
1520	5.810	6.486	5.293	7.763	6.639	6.258	61.65	25.67	131.15	75.49	2.127	0.0242	Cyb561
1521	10.398	10.221	10.427	8.519	9.708	10.109	1306.49	98.47	769.28	373.47	0.589	0.0243	Akr1c14
1522	3.725	3.777	3.642	4.147	4.304	4.099	13.14	0.62	18.20	1.37	1.385	0.0243	Cd96
1523	6.211	6.071	6.221	6.607	6.720	6.470	71.98	4.10	97.18	8.39	1.350	0.0243	Gpr97
1524	1.746	1.789	1.769	2.232	2.089	2.446	3.41	0.05	4.80	0.60	1.409	0.0243	Mir5117
1525	7.375	7.406	7.294	7.889	7.896	7.916	164.18	6.53	238.92	2.34	1.455	0.0243	Etv6
1526	5.658	5.812	5.855	7.002	6.385	5.948	54.84	3.87	91.16	33.84	1.662	0.0243	Vwf
1527	11.106	11.374	11.266	10.810	11.122	10.785	2440.33	226.01	1929.51	259.81	0.791	0.0244	Alad
1528	5.644	5.730	6.001	6.576	6.425	6.113	55.71	7.38	83.52	13.27	1.499	0.0244	Emilin1
1529	3.358	3.546	3.405	4.614	4.091	3.582	10.84	0.74	17.84	6.30	1.645	0.0244	Clec4d
1530	6.885	7.386	7.415	5.396	6.643	6.904	152.06	29.36	87.28	40.35	0.574	0.0244	Olfml1
1531	7.556	7.359	7.351	6.567	6.894	7.069	171.89	14.15	115.98	19.89	0.675	0.0244	Phf17
1532	10.290	10.314	10.580	9.288	10.006	10.121	1351.85	155.36	922.55	260.97	0.682	0.0246	Acat1
1533	5.355	5.387	5.398	5.979	6.009	5.611	41.65	0.64	58.78	8.59	1.411	0.0246	Hk1
1534	9.910	9.862	9.857	8.383	9.331	9.562	939.96	19.02	577.81	218.64	0.615	0.0246	Hao1
1535	8.604	8.335	8.429	6.935	8.180	7.929	352.25	33.76	218.67	86.57	0.621	0.0248	Hspb6
1536	4.668	4.662	4.939	5.565	5.265	5.107	27.14	3.06	40.09	6.60	1.477	0.0248	Fam102b
1537	6.298	6.347	7.052	5.869	6.162	5.357	97.61	30.43	57.01	15.35	0.584	0.0249	Fam198a
1538	4.333	5.314	4.751	5.643	5.381	5.495	28.96	9.98	45.58	4.16	1.574	0.0249	Ifi27l2a
1539	8.510	8.140	8.458	7.519	7.955	7.964	332.71	44.35	227.10	37.84	0.683	0.0249	Ahctf1
1540	4.372	4.391	4.324	5.148	4.789	4.621	20.57	0.49	29.24	5.61	1.421	0.0251	5031414D18Rik
1541	5.909	6.088	6.836	7.076	6.832	7.082	80.77	29.23	128.09	12.28	1.586	0.0251	Gm13251
1542	6.212	6.082	6.488	6.914	7.003	6.628	77.20	11.32	115.91	15.22	1.501	0.0253	Rhoj
1543	4.975	4.860	4.784	5.368	5.562	5.288	29.34	1.97	42.54	4.23	1.450	0.0253	Card11
1544	10.544	10.616	10.526	8.860	10.025	10.317	1512.16	50.41	927.38	417.50	0.613	0.0253	Ttc39c
1545	8.746	8.996	8.759	9.773	9.128	9.317	457.76	45.93	690.76	164.25	1.509	0.0254	Il13ra1
1546	5.228	5.135	5.431	5.917	5.992	5.541	38.59	4.11	56.88	9.07	1.474	0.0257	Fkbp10
1547	4.645	4.700	4.872	5.501	5.436	4.975	26.77	2.23	40.01	7.49	1.495	0.0257	Tmem119
1548	2.716	2.297	2.364	4.266	3.341	2.573	5.54	0.90	11.77	6.80	2.124	0.0260	Ccr1
1549	2.775	2.909	2.850	3.442	3.449	3.301	7.19	0.33	10.55	0.60	1.468	0.0260	Bub1
1550	6.095	5.979	6.423	6.709	6.804	6.659	72.42	11.89	105.81	5.46	1.461	0.0261	Rcn3
1551	7.549	7.743	6.726	8.124	8.241	7.803	169.08	56.42	268.27	40.73	1.587	0.0261	Tsku
1552	8.887	8.831	9.024	7.699	8.294	8.710	483.21	33.63	313.43	105.46	0.649	0.0261	Acsn3
1553	4.557	4.285	4.338	3.852	3.837	4.068	21.09	2.16	15.17	1.39	0.719	0.0261	Zfp81
1554	3.651	3.521	3.336	4.030	3.923	4.144	11.38	1.24	16.40	1.26	1.441	0.0262	Sgol2

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT avg	WTsd	KO avg	KOsd	KO/WT	BH	Gene Symbol
1555	8.125	8.520	7.034	8.513	8.907	8.805	259.09	119.28	430.85	59.17	1.663	0.0262	Fabp5
1556	4.344	4.584	4.575	4.956	5.018	4.830	22.71	2.08	30.63	2.00	1.349	0.0262	Adap1
1557	5.090	6.431	5.415	7.139	6.114	6.715	54.34	28.02	105.10	35.86	1.934	0.0263	Nrg4
1558	8.834	9.364	8.591	9.833	9.646	9.284	500.19	141.86	779.00	145.74	1.557	0.0263	Slc39a4
1559	7.358	7.179	7.455	6.375	6.712	6.880	161.46	15.45	101.87	17.59	0.631	0.0265	Phlpp1
1560	8.327	8.806	8.652	10.160	9.131	8.836	390.29	64.04	720.61	370.56	1.846	0.0265	Rbm3
1561	5.470	5.635	5.607	6.008	6.166	6.131	47.59	2.86	68.73	3.89	1.444	0.0265	Serpinh1
1562	6.455	6.242	6.048	5.583	5.796	5.526	76.53	10.83	49.85	5.02	0.651	0.0265	Axin2
1563	6.744	6.755	7.040	6.390	6.348	6.213	115.58	13.85	79.84	5.04	0.691	0.0265	Camk2b
1564	4.878	4.940	4.882	5.618	5.222	5.421	29.86	0.73	43.10	5.91	1.443	0.0265	Grb10
1565	6.337	6.328	6.329	7.196	6.950	6.532	80.53	0.27	120.93	27.13	1.502	0.0266	Map3k1
1566	3.092	3.322	3.289	3.635	3.757	3.747	9.43	0.79	13.12	0.61	1.391	0.0266	Casc5
1567	5.917	5.994	6.250	5.034	5.464	5.800	66.74	8.26	44.21	11.47	0.662	0.0266	Dnajc28
1568	7.115	7.181	7.131	7.883	7.623	7.558	141.31	3.38	207.26	25.33	1.467	0.0266	Dusp7
1569	7.347	7.067	7.420	7.492	8.078	8.087	156.05	19.47	240.69	52.56	1.542	0.0266	Timp3
1570	3.459	3.202	3.163	3.866	3.872	3.584	9.72	1.11	13.74	1.51	1.414	0.0266	Ncr1
1571	9.409	9.580	9.289	10.020	9.962	9.656	690.29	70.34	947.58	123.54	1.373	0.0268	Hist2h2ac
1572	5.260	5.468	5.635	6.060	6.039	5.827	44.09	5.68	63.08	5.48	1.431	0.0269	Rab3il1
1573	4.465	4.292	4.063	5.121	4.829	4.496	19.46	2.68	28.60	6.12	1.469	0.0270	Dok1
1574	5.736	5.621	5.665	6.168	6.369	5.987	51.08	2.06	72.66	9.64	1.422	0.0270	Map4k4
1575	5.074	5.075	4.899	4.564	4.506	4.685	32.41	2.23	24.03	1.53	0.742	0.0271	Mnd1
1576	2.848	3.245	3.343	4.118	3.561	3.568	8.94	1.55	13.67	3.19	1.529	0.0272	Lilra6
1577	9.296	8.690	9.017	9.646	9.417	9.486	519.82	107.84	733.80	60.54	1.412	0.0274	Gabbr2
1578	8.667	8.487	8.590	7.908	8.109	8.260	383.63	23.90	274.30	33.18	0.715	0.0275	Stard7
1579	9.782	9.539	9.682	9.118	9.235	9.416	815.31	68.40	613.78	64.44	0.753	0.0276	Sdc2
1580	5.399	5.331	5.251	4.895	4.886	4.837	40.18	2.07	29.30	0.63	0.729	0.0276	Sp5
1581	8.593	8.487	8.645	7.461	7.956	8.450	381.78	21.07	258.06	87.17	0.676	0.0276	Fkbp4
1582	10.500	10.479	10.316	10.979	10.712	10.680	1383.53	94.71	1778.87	208.30	1.286	0.0276	Ctsz
1583	2.504	2.748	3.234	2.073	2.119	2.368	7.26	1.93	4.57	0.52	0.629	0.0277	Olf1537-ps1
1584	5.002	4.968	4.862	7.121	5.623	5.158	30.80	1.54	74.73	56.27	2.426	0.0278	Pou2af1
1585	6.754	7.014	6.891	7.637	7.398	7.208	118.63	10.67	171.86	25.70	1.449	0.0278	Ptpn6
1586	8.227	7.914	8.163	7.453	7.844	7.323	275.85	30.75	188.36	36.62	0.683	0.0279	Slc30a10
1587	4.124	4.271	3.873	4.550	4.487	4.610	17.13	2.34	23.42	0.99	1.367	0.0279	Cdkn3
1588	5.601	5.229	5.645	4.568	4.981	5.220	45.35	6.84	30.85	6.80	0.680	0.0279	Gm6907
1589	4.494	4.573	4.593	5.237	5.231	4.772	23.49	0.85	34.20	5.95	1.456	0.0279	Sgcb
1590	5.226	5.507	5.217	4.935	4.908	4.773	40.03	4.72	29.32	1.74	0.732	0.0279	1110008J03Rik
1591	4.969	4.875	4.879	5.536	5.348	5.285	30.03	1.12	42.05	3.87	1.400	0.0279	Ebi3
1592	5.492	5.519	5.401	5.902	6.068	5.891	44.37	1.88	62.07	4.33	1.399	0.0279	Prkd2
1593	9.518	9.544	9.471	10.217	9.895	9.713	729.81	18.52	993.86	179.03	1.362	0.0280	Gnai2
1594	9.191	9.248	9.128	8.380	8.857	8.836	583.98	24.36	417.89	73.54	0.716	0.0281	Slc46a1
1595	6.245	6.741	6.467	7.850	7.065	6.781	90.43	15.65	158.20	63.93	1.749	0.0283	Ptgs1
1596	5.082	5.233	5.215	5.586	5.995	5.558	36.21	2.04	52.97	9.37	1.463	0.0284	Oas1a
1597	7.630	7.624	7.551	8.415	8.131	7.906	194.33	5.88	287.20	51.10	1.478	0.0284	Adrbk1
1598	5.865	5.785	5.716	5.087	5.515	5.246	55.34	2.87	39.21	5.97	0.709	0.0284	Ggnbp1
1599	3.433	3.305	3.469	4.395	3.940	3.646	10.59	0.62	16.30	4.34	1.540	0.0286	Ccdc88a
1600	10.564	10.725	10.721	10.082	10.228	10.508	1631.19	101.42	1246.31	190.55	0.764	0.0286	Dmgdh
1601	7.349	7.226	7.310	6.654	6.901	6.891	157.16	6.79	112.94	10.62	0.719	0.0286	Hmgn5
1602	4.852	4.225	4.475	5.340	5.327	4.761	23.27	5.16	35.93	7.63	1.544	0.0287	Cdca7l
1603	4.219	4.072	4.219	4.561	4.691	4.816	18.03	1.04	25.87	2.29	1.435	0.0289	Asb4
1604	7.501	7.054	7.691	6.539	6.780	7.086	173.56	37.48	112.91	21.58	0.651	0.0289	Nfib
1605	8.256	8.481	8.441	7.592	7.994	7.988	336.85	27.41	233.89	35.44	0.694	0.0289	Sfxn5
1606	5.537	5.780	5.207	7.379	6.117	5.772	46.11	9.01	96.84	60.74	2.100	0.0289	Slc13a5
1607	10.519	10.476	10.478	9.971	10.053	10.292	1439.44	24.32	1106.51	130.62	0.769	0.0289	Sephs2
1608	4.976	5.252	5.669	3.197	4.188	5.311	40.14	9.86	22.37	15.68	0.557	0.0291	Cyp2c55

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT avg	WTsd	KO avg	KOsd	KO/WT	BH	Gene Symbol
1609	3.498	3.614	3.665	4.019	4.297	3.984	12.08	0.71	17.23	2.11	1.427	0.0291	Kdelr3
1610	10.757	10.640	10.725	10.256	10.389	10.398	1672.75	69.76	1304.41	70.68	0.780	0.0293	Pipox
1611	8.254	8.276	8.343	8.034	7.720	7.709	313.35	10.18	227.37	30.07	0.726	0.0293	Shroom1
1612	8.698	8.623	8.552	8.030	8.272	8.116	394.94	20.00	282.62	24.27	0.716	0.0296	Zkscan1
1613	4.560	4.910	4.643	4.166	4.404	4.162	26.21	3.41	19.01	1.87	0.725	0.0296	4930452B06Rik
1614	8.354	8.341	8.134	7.665	8.065	7.660	310.81	25.95	224.33	37.64	0.722	0.0296	Abca2
1615	7.530	7.485	7.518	6.868	6.966	6.964	182.42	2.89	122.23	4.68	0.670	0.0296	Adcy9
1616	4.692	4.463	4.643	5.248	5.369	4.821	24.29	1.99	35.87	6.79	1.477	0.0296	Cdk14
1617	7.300	7.128	7.169	6.734	6.655	6.674	147.13	9.28	103.12	2.97	0.701	0.0296	Sap30l
1618	6.995	7.523	7.569	6.344	6.662	7.090	167.10	34.41	106.24	27.84	0.636	0.0296	Mmab
1619	10.332	10.163	10.331	9.648	9.932	10.006	1241.31	81.83	935.86	118.31	0.754	0.0297	Galm
1620	4.542	4.999	4.716	3.877	4.240	4.527	27.19	4.41	18.88	4.18	0.694	0.0297	Gm15417
1621	8.740	8.423	8.532	7.214	7.867	8.457	380.23	43.11	244.40	101.87	0.643	0.0297	Klf12
1622	4.470	4.562	4.346	3.962	4.068	4.095	22.04	1.65	16.48	0.79	0.748	0.0298	Rln1
1623	5.542	5.188	5.024	5.915	5.648	5.919	38.52	7.24	57.00	5.93	1.480	0.0298	Aph1b
1624	6.118	6.038	5.867	6.470	6.489	6.554	64.51	5.65	90.81	2.80	1.408	0.0300	Chd7
1625	2.988	3.069	3.155	3.938	3.539	3.387	8.41	0.49	12.47	2.54	1.482	0.0300	Clec5a
1626	3.689	3.670	3.620	4.101	4.080	4.080	12.64	0.31	17.00	0.14	1.345	0.0300	Klhl38
1627	8.649	8.077	8.613	5.405	7.534	8.134	354.39	73.22	169.55	120.08	0.478	0.0300	Abca8a
1628	7.864	7.793	7.896	7.171	7.377	7.534	230.97	8.36	165.23	20.64	0.715	0.0302	Fggy
1629	4.478	4.250	4.102	4.829	4.768	4.730	19.49	2.59	27.40	0.95	1.406	0.0303	Kif11
1630	8.189	8.503	8.118	8.665	8.937	8.670	310.87	45.55	434.53	48.30	1.398	0.0303	H2-T10
1631	7.362	7.260	7.090	7.429	8.264	7.751	151.36	14.21	231.67	68.96	1.531	0.0304	Hspa1a
1632	6.950	6.970	7.128	6.217	6.345	6.815	129.63	8.89	89.40	20.36	0.690	0.0304	Lym5
1633	5.795	5.652	5.628	5.211	5.170	5.379	51.76	3.30	38.21	2.99	0.738	0.0304	Tfap4
1634	7.437	7.217	7.493	6.775	6.945	6.942	167.41	16.46	118.55	7.85	0.708	0.0305	Dyrk2
1635	6.469	6.569	6.478	5.934	5.926	6.250	90.89	3.50	66.03	8.75	0.727	0.0305	Mrps12
1636	11.131	11.154	11.219	10.829	10.782	10.984	2302.05	73.40	1868.34	138.64	0.812	0.0306	Haao
1637	6.452	6.430	6.571	7.016	7.054	6.780	89.59	4.77	124.09	12.40	1.385	0.0306	Ets1
1638	5.270	5.265	5.180	6.048	5.684	5.670	37.76	1.31	56.16	8.66	1.487	0.0306	Snx20
1639	9.860	10.049	10.315	8.912	9.635	9.764	1087.52	174.16	715.26	205.74	0.658	0.0309	Necab1
1640	6.373	6.475	6.453	7.077	6.979	6.643	86.48	3.21	120.39	18.24	1.392	0.0309	Mfsd10
1641	9.632	9.817	9.633	8.832	8.997	9.503	829.96	62.63	564.01	142.54	0.680	0.0309	Ido2
1642	5.125	5.289	4.967	4.759	4.624	4.766	35.09	3.92	26.31	1.43	0.750	0.0310	Tsply4
1643	4.850	5.301	5.208	6.507	5.495	5.534	35.07	5.54	60.79	26.12	1.733	0.0311	Cpne8
1644	4.352	4.265	4.628	5.335	4.697	4.783	21.45	2.89	31.28	7.91	1.458	0.0311	Pycard
1645	8.729	8.774	8.682	8.152	8.402	8.244	424.30	13.52	308.67	27.34	0.727	0.0312	Nelf
1646	3.588	3.466	3.684	3.738	4.637	4.207	11.98	0.90	18.90	5.78	1.578	0.0313	A53009J19Rik
1647	3.774	3.726	3.855	4.801	4.566	3.840	13.79	0.63	21.96	6.94	1.593	0.0313	Donson
1648	4.808	4.565	4.804	5.430	5.078	5.215	26.54	2.48	38.00	4.72	1.432	0.0313	Ssh2
1649	5.497	5.628	5.650	6.265	6.286	5.822	48.27	2.71	70.51	12.10	1.461	0.0314	Sema4c
1650	4.839	4.707	4.503	5.169	5.170	4.952	25.80	2.99	34.31	2.91	1.330	0.0314	Fos
1651	6.530	6.295	6.477	5.889	6.086	5.957	86.68	7.25	63.10	4.42	0.728	0.0315	Zfand4
1652	11.033	11.013	11.020	9.592	10.695	10.768	2079.55	15.03	1391.12	538.33	0.669	0.0315	Akr1c6
1653	4.615	4.461	4.616	4.887	5.359	4.886	23.69	1.44	33.41	6.62	1.410	0.0315	Egr2
1654	6.905	6.951	7.011	7.901	8.070	6.972	124.18	4.57	211.11	75.55	1.700	0.0315	Jam2
1655	5.631	6.302	6.556	6.618	7.613	6.619	74.18	22.63	130.75	56.28	1.763	0.0315	Myc
1656	7.106	7.385	7.385	6.625	6.782	6.944	157.37	17.02	110.62	12.19	0.703	0.0317	Atp7b
1657	9.133	9.292	9.160	8.524	8.724	8.856	586.88	35.23	418.09	47.79	0.712	0.0317	Slc25a17
1658	5.279	5.334	5.263	5.798	5.926	5.617	39.19	1.01	55.17	5.88	1.408	0.0317	Adora2a
1659	11.640	11.523	11.456	11.652	11.877	11.815	2981.15	194.47	3526.86	279.27	1.183	0.0317	Ldha
1660	10.540	10.756	10.605	10.049	10.373	10.341	1591.95	124.26	1227.59	146.50	0.771	0.0317	Lect2
1661	6.605	6.501	6.615	5.690	6.029	6.282	95.30	4.11	64.91	13.08	0.681	0.0318	2700050L05Rik
1662	5.633	5.729	5.543	5.218	5.326	5.051	49.77	3.22	36.83	3.50	0.740	0.0319	Pm20d2

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT avg	WTsd	KO avg	KOsd	KO/WT	BH	Gene Symbol
1663	5.768	5.622	5.982	6.259	6.498	6.148	55.65	7.05	79.31	10.03	1.425	0.0320	Gimap6
1664	7.692	7.726	7.626	8.218	8.356	8.091	205.32	7.21	299.36	27.49	1.458	0.0320	Tmem50b
1665	4.191	4.402	4.343	4.007	3.779	3.849	19.90	1.48	14.74	1.21	0.740	0.0320	Eil3
1666	6.536	6.541	6.405	7.591	7.002	6.711	90.21	4.73	141.93	45.64	1.573	0.0321	Irak4
1667	4.070	4.134	3.952	4.910	4.395	4.349	16.61	1.05	23.83	5.42	1.435	0.0322	Gab3
1668	10.348	10.427	10.478	7.728	9.993	9.867	1368.65	62.01	721.45	443.20	0.527	0.0322	Slc2a2
1669	6.051	6.286	6.212	5.449	5.920	5.667	72.83	5.98	51.67	8.46	0.710	0.0322	Sec22c
1670	6.355	6.390	6.378	7.229	6.975	6.676	82.95	1.02	126.06	23.90	1.520	0.0323	Tmem106a
1671	9.392	9.636	9.632	9.784	10.144	9.942	753.72	70.89	998.95	125.68	1.325	0.0324	Lgals3bp
1672	3.224	3.872	3.568	4.022	4.200	4.050	11.95	2.65	17.07	1.15	1.428	0.0326	Phxr4
1673	4.835	4.764	5.024	5.234	5.532	5.336	29.41	2.78	41.43	4.40	1.409	0.0326	Akap2
1674	8.927	9.037	9.037	8.526	8.628	8.616	512.42	22.32	385.54	14.65	0.752	0.0326	AU022252
1675	8.443	7.794	7.897	4.859	6.656	8.076	269.44	68.62	133.23	123.62	0.494	0.0327	Gpr110
1676	5.903	5.529	6.034	4.576	5.503	5.351	57.18	9.96	36.67	11.33	0.641	0.0327	Snora34
1677	8.704	8.645	8.670	7.445	8.274	8.333	408.16	8.45	268.72	82.03	0.658	0.0327	Abcc6
1678	7.182	7.012	7.043	6.264	6.717	6.814	135.35	8.61	98.18	18.85	0.725	0.0329	Cdc37l1
1679	7.356	7.264	7.948	6.703	6.874	7.163	188.16	51.13	121.59	19.96	0.646	0.0330	Plxna2
1680	5.505	5.485	5.580	4.694	5.197	5.239	46.02	1.60	33.44	6.56	0.727	0.0330	Lama3
1681	10.138	9.989	10.003	9.382	9.795	9.544	1056.56	61.28	767.33	112.10	0.726	0.0330	Pygl
1682	10.106	10.011	10.232	9.498	9.566	9.841	1111.97	85.75	799.58	103.54	0.719	0.0332	Adck3
1683	9.936	9.702	9.777	9.088	9.521	9.419	896.45	75.18	654.54	98.88	0.730	0.0333	Cyp4f13
1684	7.322	6.973	7.003	6.615	6.566	6.553	137.96	19.11	95.57	2.20	0.693	0.0336	Dcaf6
1685	5.188	5.268	5.006	5.713	5.659	5.495	35.70	3.27	49.36	3.81	1.383	0.0336	Rasal3
1686	3.724	3.661	3.634	4.132	4.254	4.037	12.76	0.41	17.68	1.34	1.385	0.0336	Txk
1687	4.193	4.238	4.293	5.005	4.773	4.399	18.93	0.66	26.85	5.52	1.418	0.0336	Prune2
1688	7.969	7.606	7.802	6.948	7.327	7.442	222.80	27.83	152.67	26.14	0.685	0.0337	Sos1
1689	8.797	8.465	8.777	7.612	8.257	8.342	412.24	51.06	275.32	69.64	0.668	0.0338	Rbpms2
1690	5.079	4.861	6.019	4.919	4.493	4.500	42.57	19.43	25.14	4.44	0.591	0.0338	Dsg1a
1691	6.309	6.320	6.176	6.991	6.785	6.532	77.16	4.23	110.01	17.35	1.426	0.0339	Vasp
1692	8.044	7.426	8.109	6.361	7.316	7.504	237.33	56.91	140.99	52.12	0.594	0.0339	Ocel1
1693	8.461	8.250	8.442	7.576	7.896	8.083	334.83	26.43	233.42	40.41	0.697	0.0339	Arl5b
1694	2.553	2.558	2.349	1.919	2.186	1.909	5.62	0.45	4.03	0.45	0.717	0.0339	Stfa3
1695	6.257	6.232	6.142	6.722	6.969	6.468	74.09	3.07	106.43	18.40	1.436	0.0340	Col4a1
1696	3.764	3.558	3.561	4.265	4.197	4.002	12.39	1.04	17.86	1.66	1.442	0.0340	St8sia4
1697	10.616	10.303	10.418	8.035	9.857	10.195	1400.57	155.66	787.49	470.97	0.562	0.0341	Ugt2a3
1698	8.412	8.165	8.467	7.025	7.743	8.192	327.17	35.37	212.33	81.16	0.649	0.0342	Tprkb
1699	9.590	9.707	9.704	9.047	9.161	9.471	813.51	36.97	603.65	94.31	0.742	0.0343	Pdpf
1700	9.052	8.979	9.200	7.260	8.522	8.842	541.24	42.70	326.65	156.88	0.604	0.0343	Agphd1
1701	7.367	6.747	7.422	6.135	6.839	6.575	148.01	35.28	93.35	22.16	0.631	0.0343	Glcc1
1702	5.362	5.755	5.562	6.653	6.488	5.678	47.45	6.44	80.53	26.00	1.697	0.0344	Enc1
1703	9.561	9.777	9.726	10.120	10.082	10.025	826.49	63.63	1079.36	35.80	1.306	0.0344	H3f3b
1704	6.681	6.409	6.449	5.828	6.055	6.130	91.65	9.54	64.43	6.84	0.703	0.0344	Jmy
1705	10.251	10.291	10.475	8.984	9.996	9.969	1298.16	109.81	843.19	291.75	0.650	0.0345	Rgn
1706	4.927	5.143	4.889	5.743	5.390	5.230	31.79	3.09	44.34	8.28	1.395	0.0349	Serpina3h
1707	10.695	10.003	10.302	10.511	10.997	10.930	1315.36	319.32	1818.01	314.39	1.382	0.0349	Hsd17b6
1708	7.697	7.683	7.916	7.236	7.313	7.393	218.19	20.23	159.26	8.68	0.730	0.0349	Abtb2
1709	7.228	8.017	8.100	8.377	8.424	8.349	227.76	67.88	334.01	8.81	1.466	0.0350	Lgals1
1710	5.431	5.069	4.906	4.306	4.762	4.815	35.56	6.80	25.02	4.56	0.704	0.0351	Exd1
1711	6.977	7.149	7.150	7.763	7.820	7.348	136.63	9.21	201.99	34.17	1.478	0.0352	Tap2
1712	6.913	6.916	6.832	5.899	6.177	6.727	118.41	3.86	79.32	23.91	0.670	0.0353	Sox5
1713	3.409	3.306	3.085	4.489	3.863	3.420	9.67	1.08	15.90	5.99	1.645	0.0353	Gm6377
1714	6.369	7.080	6.700	5.581	6.018	6.556	107.30	26.50	68.91	23.37	0.642	0.0355	Prok1
1715	10.929	10.919	10.927	8.391	10.418	10.629	1943.92	7.18	1095.54	666.71	0.564	0.0355	Ugt2b1
1716	7.120	8.225	7.830	5.259	7.283	7.081	222.01	80.22	109.82	62.77	0.495	0.0356	Cml5

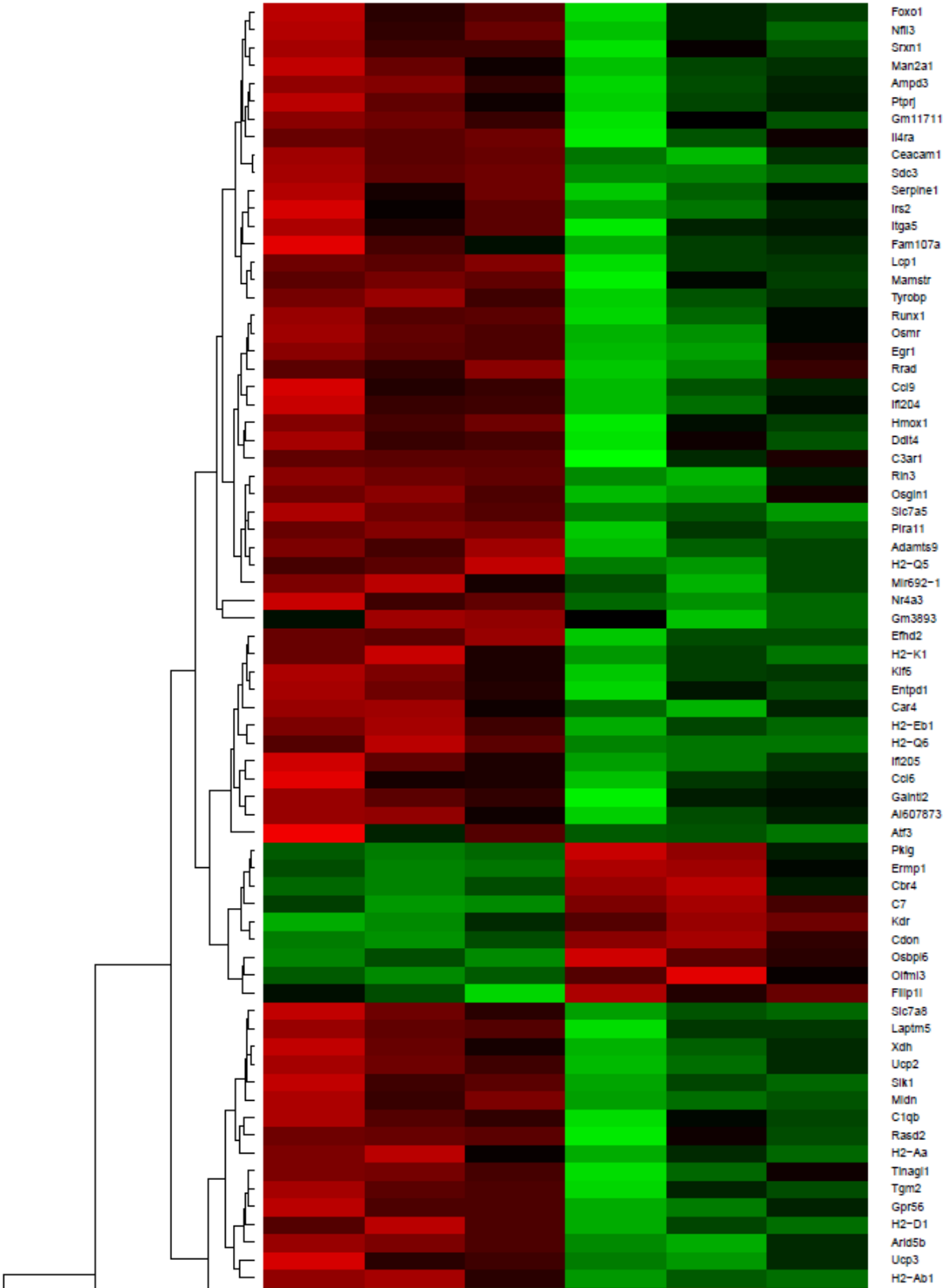
Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT avg	WTsd	KO avg	KOsd	KO/WT	BH	Gene Symbol
1717	4.484	4.664	4.486	4.974	5.103	4.856	23.38	1.71	31.58	2.70	1.351	0.0356	Cxcr3
1718	9.472	9.088	9.343	6.206	8.863	8.734	634.59	84.00	321.81	215.66	0.507	0.0356	Sdr9c7
1719	7.520	7.717	7.785	9.007	8.135	7.921	204.82	19.10	345.95	147.19	1.689	0.0356	Sptlc2
1720	4.333	4.224	4.202	4.503	4.706	4.715	19.08	0.94	25.01	2.03	1.311	0.0356	Vsig10
1721	9.547	9.601	9.652	9.141	9.334	8.918	776.53	28.31	564.57	80.89	0.727	0.0356	Fpgs
1722	7.695	8.014	7.832	7.111	7.461	7.486	231.18	25.80	164.55	22.84	0.712	0.0356	Cln2
1723	4.896	4.647	4.679	5.003	5.271	5.364	26.81	2.58	37.29	4.70	1.391	0.0357	Slc9a7
1724	4.906	4.934	4.860	5.870	5.531	5.034	29.86	0.78	45.83	12.85	1.535	0.0359	Kcnn4
1725	11.512	11.545	11.507	11.103	11.278	11.363	2939.31	42.21	2439.23	220.58	0.830	0.0359	Pah
1726	6.916	7.272	7.116	8.470	7.858	7.222	137.99	16.89	245.28	103.28	1.778	0.0360	Gmfg
1727	6.747	6.856	6.711	6.001	6.249	6.504	109.36	5.79	76.96	13.40	0.704	0.0360	Hemk1
1728	6.062	5.847	5.745	5.563	5.475	5.337	59.32	6.76	44.06	3.45	0.743	0.0362	Ihh
1729	10.090	9.997	10.273	9.429	9.815	9.678	1116.49	110.26	803.14	106.50	0.719	0.0363	Enpp3
1730	7.068	6.953	6.809	7.955	7.727	7.045	123.43	11.02	197.36	59.41	1.599	0.0363	Prkcd
1731	5.452	5.621	5.369	6.590	5.937	5.792	44.78	4.04	71.00	22.15	1.586	0.0364	Scube1
1732	8.917	8.920	9.070	8.287	8.440	8.749	501.71	30.86	363.29	60.50	0.724	0.0367	Ssbp3
1733	6.442	6.326	6.596	5.705	5.932	6.206	87.96	8.32	62.34	10.89	0.709	0.0368	Fam151b
1734	9.236	8.765	9.019	9.744	9.836	9.180	519.01	83.96	783.68	178.57	1.510	0.0368	Trp53inp1
1735	5.557	5.615	6.331	6.583	6.264	6.441	58.87	18.77	86.54	9.53	1.470	0.0368	1700029I01Rik
1736	3.580	3.692	3.859	3.998	4.237	4.306	13.13	1.29	18.20	1.98	1.387	0.0368	Srsf3
1737	7.034	7.175	7.355	6.027	6.719	6.896	146.44	16.41	96.55	27.99	0.659	0.0370	Smyd2
1738	7.033	7.174	7.143	6.470	6.534	6.674	138.87	7.05	94.46	6.90	0.680	0.0371	Scn2
1739	3.699	4.011	3.747	4.979	4.271	4.052	14.18	1.70	22.47	7.96	1.585	0.0373	Slc8a1
1740	4.673	4.530	4.548	5.613	5.064	4.688	24.00	1.31	36.05	11.79	1.502	0.0373	Pfkfb4
1741	9.900	10.113	10.045	8.890	9.761	9.590	1039.77	77.31	704.12	204.69	0.677	0.0373	Srd5a1
1742	6.165	6.365	6.133	7.169	6.789	6.448	74.78	6.66	113.92	28.43	1.523	0.0375	Gpsm3
1743	4.441	4.570	4.210	7.621	4.958	4.867	21.33	2.65	85.70	96.25	4.018	0.0375	Ifitm6
1744	4.727	4.536	4.594	4.907	5.043	5.118	24.61	1.69	32.57	2.39	1.323	0.0380	Slfn9
1745	7.263	7.207	7.102	6.741	6.825	6.749	146.25	8.22	109.27	3.54	0.747	0.0380	Hdac6
1746	9.113	8.795	9.252	8.461	8.752	8.562	535.76	84.17	387.18	40.19	0.723	0.0381	Enpep
1747	8.798	9.084	9.184	7.934	8.427	8.879	523.25	70.34	353.19	113.43	0.675	0.0381	Shmt1
1748	5.704	6.039	5.834	6.454	6.348	6.285	58.32	6.90	82.38	4.93	1.412	0.0382	Ecscr
1749	12.239	12.172	12.268	12.039	12.125	12.150	4792.80	162.68	4406.44	175.67	0.919	0.0384	Apoa2
1750	8.849	8.798	9.006	7.950	8.511	8.639	473.42	36.04	336.95	79.48	0.712	0.0384	Nadkd1
1751	6.884	6.836	7.051	6.296	6.358	6.611	121.65	9.67	86.11	10.20	0.708	0.0384	Txnrd2
1752	6.827	6.976	6.542	6.326	6.345	6.226	110.88	16.54	78.79	3.45	0.711	0.0385	Gba2
1753	4.419	4.572	4.275	4.845	4.970	4.745	21.51	2.21	28.97	2.27	1.346	0.0385	Gpr183
1754	4.720	5.013	4.650	8.264	5.702	5.039	27.92	3.84	130.81	153.32	4.685	0.0387	S100a9
1755	5.283	5.289	5.413	4.779	4.847	5.053	40.21	2.06	29.81	3.00	0.741	0.0387	Polg2
1756	7.775	7.718	7.514	8.130	8.107	8.199	204.09	18.93	283.18	9.44	1.388	0.0388	Smg1
1757	7.857	8.325	8.157	7.201	7.546	7.891	279.33	44.75	190.46	45.17	0.682	0.0389	Rtn4ip1
1758	3.271	3.339	3.270	3.926	3.926	3.566	9.81	0.27	14.08	1.94	1.436	0.0389	Myo5a
1759	7.712	7.622	7.620	6.646	7.197	7.359	201.11	7.47	137.03	33.10	0.681	0.0392	Mettl22
1760	6.343	6.322	6.223	7.876	6.785	6.558	78.64	3.47	146.46	77.01	1.862	0.0392	Ssbp4
1761	5.730	5.652	5.851	6.502	6.154	6.158	53.70	3.77	77.77	11.16	1.448	0.0392	Crtap
1762	11.132	11.076	11.013	9.417	10.504	10.997	2156.53	88.26	1392.81	681.71	0.646	0.0393	Ces3b
1763	5.570	5.383	5.450	4.888	4.950	5.158	44.32	2.95	32.07	3.21	0.724	0.0393	Cep57l1
1764	4.145	4.406	4.157	4.848	4.773	4.471	18.91	1.99	26.10	3.48	1.380	0.0393	Mmp7
1765	6.547	6.163	6.239	6.734	6.984	6.820	80.24	11.66	115.32	10.29	1.437	0.0393	Spred1
1766	6.052	6.073	6.047	6.641	6.667	6.393	66.60	0.62	95.17	9.67	1.429	0.0399	Atp7a
1767	4.348	4.470	4.433	5.153	4.774	4.664	21.37	0.92	29.43	5.43	1.377	0.0399	Galnt6
1768	8.693	8.563	8.487	9.209	8.961	8.979	383.64	27.88	531.63	52.10	1.386	0.0399	Gde1
1769	7.588	7.589	7.405	6.214	6.980	7.366	184.81	13.30	121.81	45.50	0.659	0.0400	Tle1
1770	8.708	8.701	8.881	8.280	8.438	8.369	435.38	31.35	329.36	18.01	0.756	0.0400	H2afv

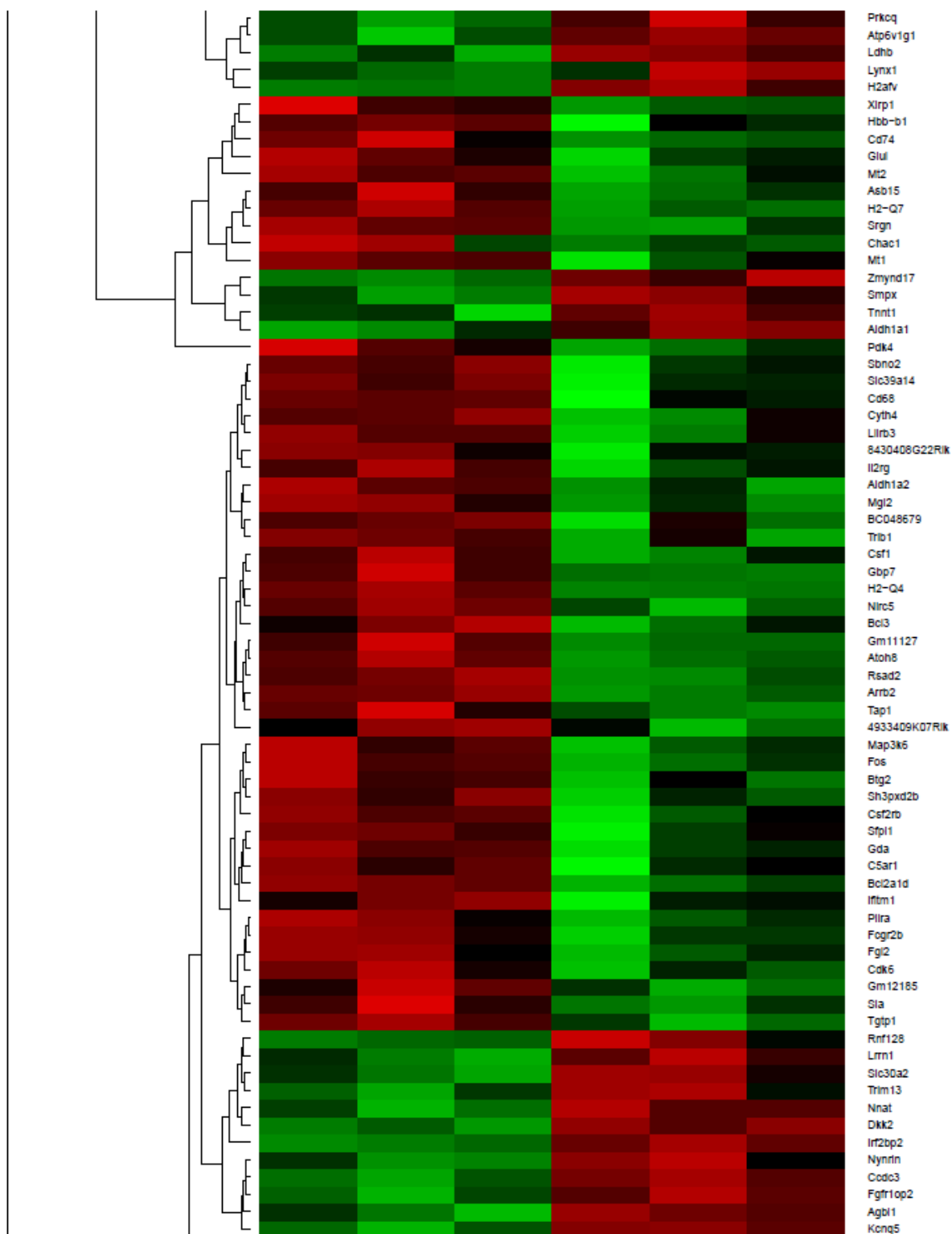
Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT avg	WTsd	KO avg	KOsd	KO/WT	BH	Gene Symbol
1771	5.839	6.035	6.511	4.793	5.637	5.790	71.33	17.68	44.27	14.59	0.621	0.0400	Rnf152
1772	9.208	8.909	9.085	8.448	8.766	8.669	538.45	55.43	397.15	43.89	0.738	0.0400	Wdtdc1
1773	8.833	8.647	8.689	8.119	8.461	8.115	423.27	28.94	302.57	43.17	0.715	0.0401	Coq10a
1774	3.758	3.863	3.428	4.238	4.238	4.117	12.95	1.96	18.36	0.88	1.418	0.0401	Kif22
1775	5.236	5.071	5.179	4.895	4.899	4.351	35.85	2.05	26.66	5.42	0.744	0.0401	Maoa
1776	5.514	5.372	5.322	6.192	5.831	5.645	42.36	2.97	60.03	11.83	1.417	0.0401	Sepn1
1777	4.839	4.961	4.849	4.389	4.588	4.471	29.54	1.41	22.39	1.56	0.758	0.0401	Spr
1778	8.515	8.554	8.508	8.080	8.166	8.140	368.53	6.38	280.00	8.58	0.760	0.0409	Cdk18
1779	4.303	4.098	4.210	2.885	3.124	4.294	18.46	1.31	11.91	6.71	0.645	0.0409	Zfp931
1780	9.099	9.211	9.136	9.476	9.773	9.664	567.85	22.52	799.41	82.26	1.408	0.0410	H2-T23
1781	4.699	4.541	4.723	4.873	5.115	5.294	25.22	1.70	34.40	4.97	1.364	0.0411	Smc2
1782	5.591	5.675	5.316	5.004	5.104	5.175	46.38	5.84	34.21	2.03	0.738	0.0411	Snord15a
1783	8.282	8.262	8.454	7.307	7.976	7.959	322.95	24.08	219.63	53.13	0.680	0.0414	Gpr125
1784	7.106	7.199	7.479	6.314	6.797	7.005	154.40	21.33	106.39	24.79	0.689	0.0414	Elp4
1785	5.211	5.282	5.232	4.557	5.114	4.724	37.85	0.96	28.20	5.75	0.745	0.0415	Pkhd1
1786	2.223	2.246	2.030	3.382	2.883	2.262	4.50	0.36	7.53	2.82	1.674	0.0415	Rgs18
1787	10.648	10.427	10.572	9.644	10.085	10.409	1501.10	115.27	1081.71	279.76	0.721	0.0416	Cyp2c40
1788	7.447	7.349	7.676	6.292	7.185	7.149	180.64	21.38	121.94	37.79	0.675	0.0416	3010026O09Rik
1789	6.002	5.906	6.151	6.501	6.612	6.461	65.03	5.59	92.16	5.05	1.417	0.0416	Epb4.1l2
1790	4.936	5.151	4.868	5.884	5.559	5.174	31.78	3.32	47.43	11.48	1.493	0.0417	Ppm1h
1791	7.027	7.255	6.763	6.476	6.438	6.595	130.59	22.05	90.78	5.20	0.695	0.0419	A930005H10Rik
1792	7.655	7.744	7.958	7.157	7.180	7.321	221.50	24.40	149.21	9.34	0.674	0.0420	9430023L20Rik
1793	4.645	4.987	4.631	5.950	5.256	5.012	27.17	3.94	44.09	15.63	1.623	0.0421	Rab27a
1794	4.387	5.857	5.247	8.275	6.228	5.471	38.96	18.54	143.00	145.17	3.671	0.0421	Smpd3
1795	10.199	10.116	10.344	9.046	9.699	10.102	1194.81	96.37	819.66	285.37	0.686	0.0421	Lactb2
1796	4.219	4.367	4.199	4.782	4.918	4.546	19.21	1.24	27.04	3.47	1.407	0.0421	Gdap10
1797	5.202	5.346	5.055	6.157	5.611	5.509	36.91	3.72	55.25	14.03	1.497	0.0421	Calhm2
1798	4.860	4.742	4.500	5.671	5.492	4.859	26.14	3.25	41.66	11.33	1.594	0.0423	Map3k6
1799	3.203	3.433	3.198	5.358	4.235	3.262	9.73	0.93	23.15	16.15	2.379	0.0425	Il1f9
1800	9.266	9.083	9.235	10.230	9.745	9.305	586.94	39.11	897.22	286.25	1.529	0.0425	Prelp
1801	6.608	6.619	6.557	6.412	5.986	5.370	96.65	2.21	63.29	21.89	0.655	0.0425	Zfp39
1802	6.000	6.352	6.067	6.553	6.699	6.674	70.90	9.45	99.97	5.35	1.410	0.0426	Slc1a4
1803	5.771	5.968	5.844	5.175	5.444	5.532	58.22	4.05	41.98	5.24	0.721	0.0426	Trib3
1804	4.934	4.975	4.852	5.847	5.510	5.192	30.30	1.30	46.56	10.54	1.536	0.0426	Ampd3
1805	5.558	5.599	5.248	4.983	4.839	5.257	44.53	5.70	32.83	4.92	0.737	0.0426	Klf1
1806	7.308	7.255	7.136	7.781	7.688	7.587	150.63	9.07	206.18	13.87	1.369	0.0427	Adam17
1807	5.588	5.565	5.545	6.238	5.805	6.007	47.38	0.72	65.24	9.82	1.377	0.0427	G6pd2
1808	6.328	6.362	6.086	7.039	6.722	6.562	76.85	7.79	110.51	18.99	1.438	0.0428	Nt5c3l
1809	3.181	3.217	3.001	4.195	3.473	3.487	8.79	0.69	13.55	4.14	1.541	0.0428	Scn8a
1810	6.093	6.106	6.080	5.587	5.655	5.644	68.26	0.60	49.49	1.24	0.725	0.0429	Kif1c
1811	4.239	4.364	4.272	3.825	3.761	3.924	19.59	0.89	14.30	0.82	0.730	0.0430	Mkx
1812	7.342	7.421	7.475	6.531	6.983	7.202	170.47	7.86	122.08	27.66	0.716	0.0430	Tom1l1
1813	10.683	10.411	10.567	9.234	10.119	10.450	1507.65	141.43	1037.61	403.30	0.688	0.0430	Cyp2c67
1814	5.818	5.677	5.675	4.910	5.367	5.482	52.89	3.04	38.68	7.65	0.731	0.0435	Psd3
1815	6.682	6.408	6.250	5.860	5.935	6.081	87.89	13.53	62.33	4.91	0.709	0.0435	Ptpn3
1816	10.267	10.272	10.256	9.450	9.942	10.064	1230.42	6.96	917.94	194.04	0.746	0.0436	Dhdh
1817	4.200	3.883	4.185	4.504	5.007	4.479	17.11	2.04	25.72	5.59	1.503	0.0436	Fam26e
1818	5.063	5.163	4.990	5.871	5.636	5.254	33.68	2.03	48.80	10.21	1.449	0.0436	Map4k1
1819	5.055	5.422	5.251	6.124	5.566	5.674	38.07	4.82	56.06	12.01	1.473	0.0440	Sdcbp2
1820	4.304	4.473	4.377	4.854	5.053	4.578	20.91	1.23	28.67	4.67	1.371	0.0441	Nfkbid
1821	6.029	5.517	6.007	6.789	6.919	5.934	58.47	10.98	97.60	32.01	1.669	0.0441	Pdgfra
1822	9.244	8.970	9.234	8.582	8.786	8.680	569.96	59.22	411.63	29.23	0.722	0.0443	Ranbp10
1823	7.602	7.558	7.620	6.751	7.202	7.351	193.13	4.28	139.42	28.59	0.722	0.0445	C030006K11Rik
1824	6.014	5.786	6.038	5.247	5.340	5.768	61.83	5.78	44.32	8.90	0.717	0.0445	Zfp943

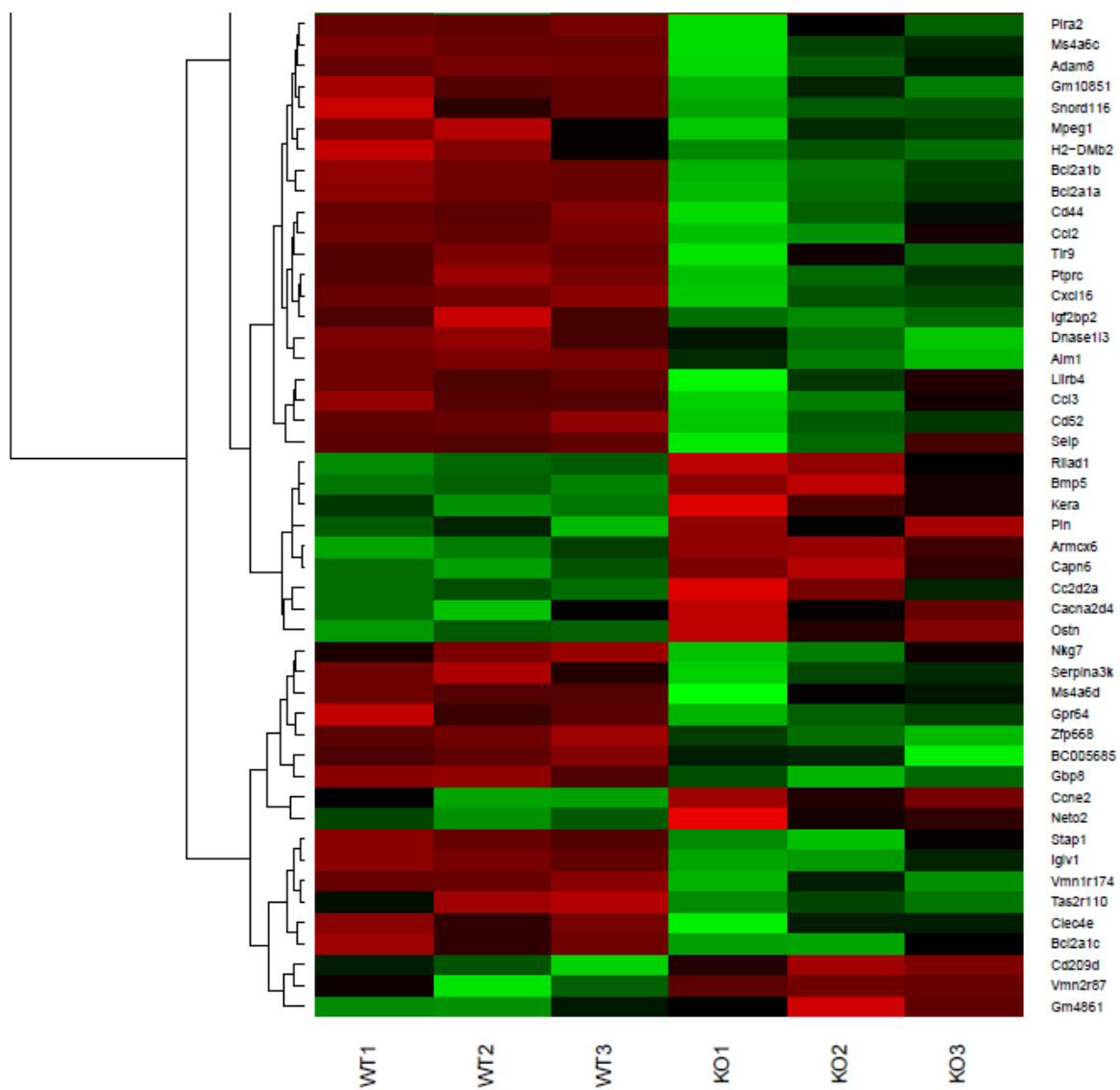
Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT avg	WTsd	KO avg	KOsd	KO/WT	BH	Gene Symbol
1825	4.902	4.900	5.110	5.471	5.443	5.413	31.43	2.69	43.49	0.88	1.384	0.0446	Etv1
1826	6.559	6.709	6.691	7.502	7.016	7.029	100.74	5.64	147.13	29.60	1.460	0.0447	Adck4
1827	5.695	5.656	6.011	4.995	5.202	5.498	55.57	7.74	37.96	6.73	0.683	0.0447	Rpa3
1828	3.664	3.630	3.136	3.942	4.101	3.999	11.28	2.16	16.17	0.91	1.433	0.0448	Gimap7
1829	9.033	8.952	9.198	9.605	9.325	9.501	535.57	47.18	714.89	69.17	1.335	0.0448	Idh2
1830	5.438	5.097	5.346	5.625	5.846	5.764	39.41	4.69	53.74	4.11	1.364	0.0452	Inhbb
1831	5.569	5.584	5.469	6.358	6.052	5.767	46.57	2.00	67.60	13.82	1.452	0.0452	Arid5a
1832	6.551	6.500	6.707	6.155	6.170	6.196	96.27	7.30	72.18	1.03	0.750	0.0452	Prosapip1
1833	5.500	5.737	5.692	6.759	5.975	5.959	50.10	4.28	77.79	26.40	1.553	0.0452	St3gal6
1834	3.264	3.198	3.562	5.043	4.126	3.470	10.20	1.41	20.50	11.26	2.010	0.0455	Mrgpra2b
1835	5.090	5.213	5.141	5.539	5.644	5.729	35.48	1.53	49.86	3.28	1.405	0.0455	Cacnb3
1836	7.008	7.054	7.383	6.349	6.885	6.654	142.86	20.94	100.14	18.33	0.701	0.0457	Shank2
1837	4.473	4.307	4.600	5.125	5.221	4.563	22.08	2.23	31.94	7.29	1.447	0.0457	Ubash3b
1838	6.327	6.492	6.399	5.325	6.018	6.064	84.90	4.89	57.26	14.92	0.674	0.0457	Mettl8
1839	7.984	7.764	8.156	7.488	7.475	7.519	251.91	34.02	180.31	2.83	0.716	0.0457	Samd8
1840	2.147	1.573	2.038	1.357	1.435	1.515	3.84	0.76	2.71	0.15	0.706	0.0458	Olfir1134
1841	7.527	8.085	7.992	7.686	7.149	7.106	236.85	46.14	161.87	38.22	0.683	0.0459	Gnpda1
1842	7.299	6.899	7.431	7.757	7.941	7.567	149.79	27.44	217.22	28.08	1.450	0.0460	Efemp1
1843	4.156	4.171	4.115	5.398	4.572	4.360	17.72	0.35	28.83	11.67	1.627	0.0461	S100a6
1844	3.181	3.430	3.012	4.869	3.417	3.793	9.30	1.37	17.92	9.91	1.926	0.0461	Sh2d1b1
1845	8.228	7.764	7.984	6.488	7.422	7.811	256.75	41.31	161.92	67.91	0.631	0.0461	Gm9992
1846	4.724	5.011	5.425	3.898	4.554	4.804	33.88	8.39	22.11	6.62	0.653	0.0461	Impg2
1847	8.854	9.062	9.082	8.194	8.487	8.816	513.10	43.72	367.47	79.30	0.716	0.0461	Shpk
1848	8.484	8.529	8.539	7.702	8.126	8.227	366.52	7.41	262.40	47.99	0.716	0.0461	Zadh2
1849	5.816	6.412	6.005	5.355	5.706	5.445	68.58	14.90	45.56	5.89	0.664	0.0462	Htra4
1850	5.918	5.835	6.044	6.917	6.349	6.214	61.18	4.50	92.19	25.08	1.507	0.0462	Man1c1
1851	7.254	7.233	7.293	6.754	6.893	6.861	153.31	3.25	114.34	5.71	0.746	0.0463	Pigy
1852	6.737	6.608	6.664	5.915	6.507	6.193	101.89	4.61	74.81	15.36	0.734	0.0463	Atat1
1853	4.193	4.326	4.179	6.851	4.991	4.351	18.82	1.08	55.89	51.91	2.970	0.0464	Itgam
1854	4.593	4.731	4.498	5.063	4.930	5.063	24.43	1.99	32.45	1.70	1.328	0.0466	Pus7l
1855	2.991	2.982	3.387	5.596	3.773	3.319	8.77	1.46	24.01	21.18	2.737	0.0466	Cd28
1856	8.519	8.457	8.687	8.042	8.180	8.157	376.74	31.63	279.66	14.08	0.742	0.0467	Xpot
1857	4.234	4.391	4.138	5.886	4.550	4.603	19.13	1.71	35.62	20.37	1.862	0.0467	Armxc4
1858	4.281	4.286	4.149	5.270	4.553	4.470	18.90	1.00	28.08	9.13	1.486	0.0467	Slc2a3
1859	8.181	7.714	7.966	6.436	7.356	7.791	250.07	40.10	157.32	67.72	0.629	0.0468	Unc93a
1860	4.777	4.779	4.758	5.356	5.099	5.125	27.31	0.22	36.71	3.68	1.344	0.0469	Arl11
1861	4.727	4.797	4.823	4.194	4.368	4.421	27.53	0.94	20.12	1.63	0.731	0.0471	Zfp235
1862	4.976	4.361	4.390	4.540	5.727	5.741	24.33	6.20	43.24	17.30	1.777	0.0471	4930528F23Rik
1863	5.298	5.126	5.526	6.019	5.660	5.811	40.11	5.61	57.19	7.21	1.426	0.0472	Maml2
1864	2.687	2.902	2.853	5.234	3.352	3.150	7.05	0.54	18.91	16.24	2.684	0.0472	I830127L07Rik
1865	5.837	6.432	6.468	5.518	5.828	5.763	77.33	17.51	52.30	5.76	0.676	0.0472	Gypc
1866	6.431	6.428	6.424	5.662	6.053	6.141	86.07	0.20	62.52	10.52	0.726	0.0473	Ccdc58
1867	4.928	5.175	5.098	10.153	5.805	5.673	33.61	2.90	415.20	626.55	12.354	0.0474	Ly6d
1868	8.001	8.041	8.042	7.355	7.623	7.737	261.02	4.27	191.39	25.29	0.733	0.0475	Mrpl14
1869	5.399	5.736	5.416	7.374	5.569	6.228	46.06	6.27	96.09	61.94	2.086	0.0475	Ostb
1870	5.674	5.039	5.560	5.672	6.291	6.043	43.70	9.58	65.07	13.67	1.489	0.0475	Tnxb
1871	6.085	6.406	6.068	6.714	6.688	6.481	73.25	10.00	99.14	8.53	1.353	0.0477	Ralb
1872	7.023	7.188	7.017	7.654	7.643	7.402	135.11	9.23	190.15	18.20	1.407	0.0477	Sema4b
1873	5.921	5.981	6.105	6.612	6.607	6.264	64.20	4.22	90.71	12.01	1.413	0.0479	Tmem2
1874	9.546	9.608	9.473	8.958	9.197	9.223	746.24	34.92	560.48	55.13	0.751	0.0481	Urod
1875	4.424	4.520	4.474	6.056	4.577	5.012	22.21	0.74	40.89	22.61	1.841	0.0484	Ctca2
1876	5.873	5.822	5.159	5.997	6.250	6.294	50.30	12.66	72.82	7.83	1.448	0.0484	Ccne1
1877	7.416	6.879	7.007	5.799	6.634	6.804	139.03	28.05	88.90	29.42	0.639	0.0485	Cecr2
1878	11.293	11.201	11.204	10.773	11.083	10.960	2407.83	87.86	1970.16	209.87	0.818	0.0485	Cyp27a1

Rank	WT1	WT2	WT3	KO1	KO2	KO3	WT avg	WTsd	KO avg	KOsd	KO/WT	BH	Gene Symbol
1879	4.528	4.992	4.746	4.323	4.142	4.391	27.25	4.39	19.55	1.71	0.718	0.0486	Bglap
1880	8.278	8.313	8.262	7.894	7.824	7.846	311.79	5.60	231.51	5.79	0.743	0.0486	Dhtkd1
1881	5.787	5.906	5.770	6.164	6.397	6.356	56.58	2.93	79.29	6.68	1.401	0.0488	Marcksl1
1882	5.146	5.265	5.359	4.659	4.551	5.146	38.31	2.82	28.04	6.46	0.732	0.0488	Stxbp4
1883	6.594	6.921	7.189	6.305	6.563	6.323	121.24	24.67	84.54	8.66	0.697	0.0489	Nav2
1884	5.613	6.063	6.046	5.352	5.192	5.524	60.62	10.12	41.14	4.74	0.679	0.0492	B4galnt3
1885	5.267	5.150	5.036	4.387	4.930	4.828	35.60	2.85	26.61	5.03	0.747	0.0493	4930473A06Rik
1886	3.527	3.464	3.742	3.604	4.846	4.375	11.98	1.24	20.55	8.30	1.715	0.0493	Pydc4
1887	7.010	7.040	7.097	7.770	7.580	7.289	132.48	4.08	188.65	31.06	1.424	0.0493	Arrb1
1888	7.896	7.972	8.007	7.106	7.589	7.596	248.82	9.73	174.57	31.89	0.702	0.0495	Ttc7b
1889	4.153	4.091	4.249	3.748	3.779	3.819	17.95	1.00	13.76	0.34	0.766	0.0495	Olf420
1890	5.222	5.037	5.212	5.460	5.663	5.516	35.74	2.52	46.81	3.46	1.310	0.0497	Unc5b
1891	7.940	7.991	8.083	7.513	7.611	7.626	257.02	13.00	191.90	8.05	0.747	0.0497	Tmem63a
1892	7.229	7.284	7.151	6.463	6.873	6.626	149.31	6.90	101.39	14.70	0.679	0.0497	Fyco1
1893	6.921	7.169	7.116	6.714	6.540	6.359	134.60	11.87	93.38	11.47	0.694	0.0497	Fzd4
1894	1.882	1.832	2.217	1.500	1.504	1.564	3.96	0.60	2.87	0.07	0.725	0.0498	Olf201

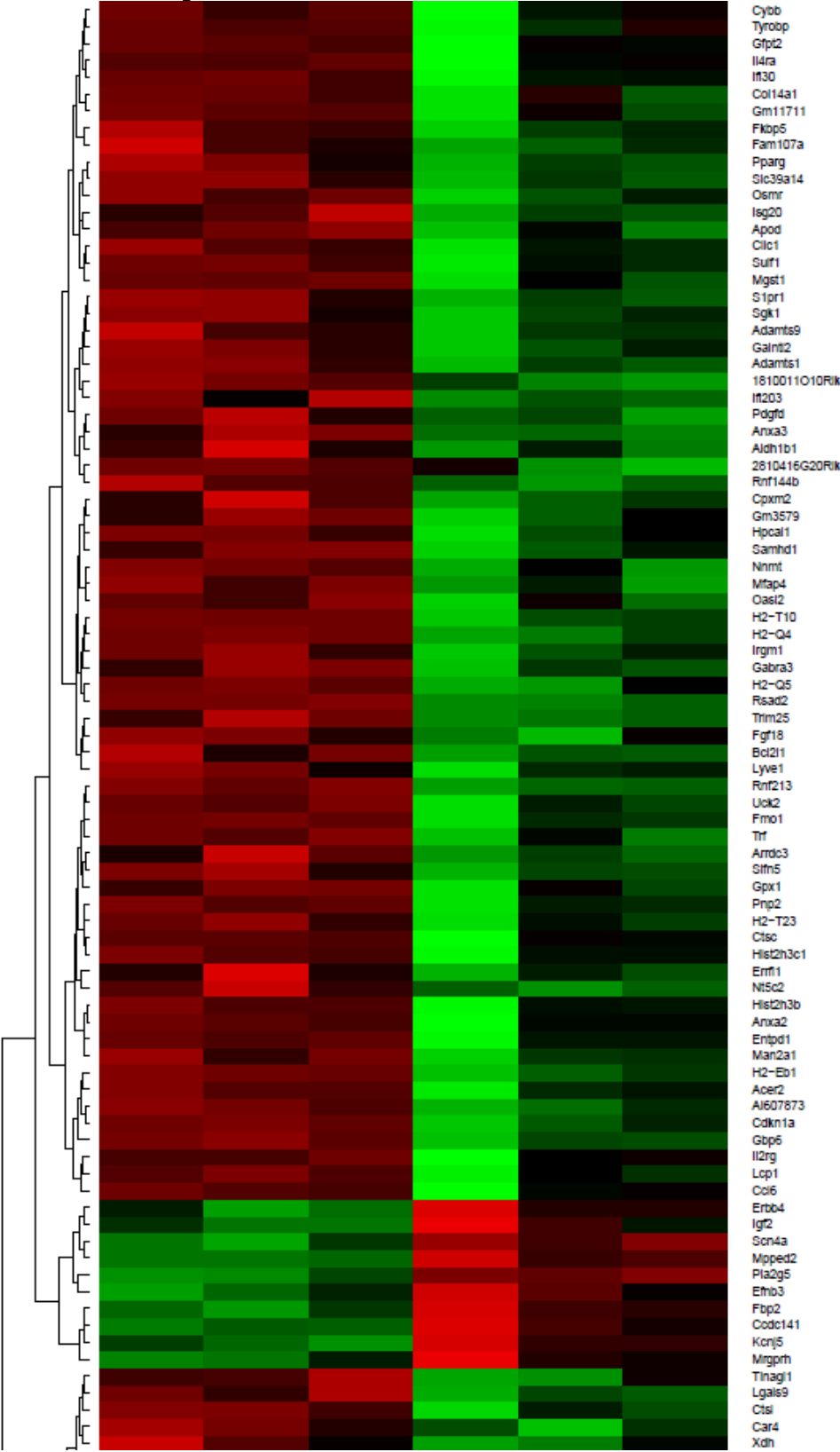
Appendix 3(a): Skeletal muscle heatmap

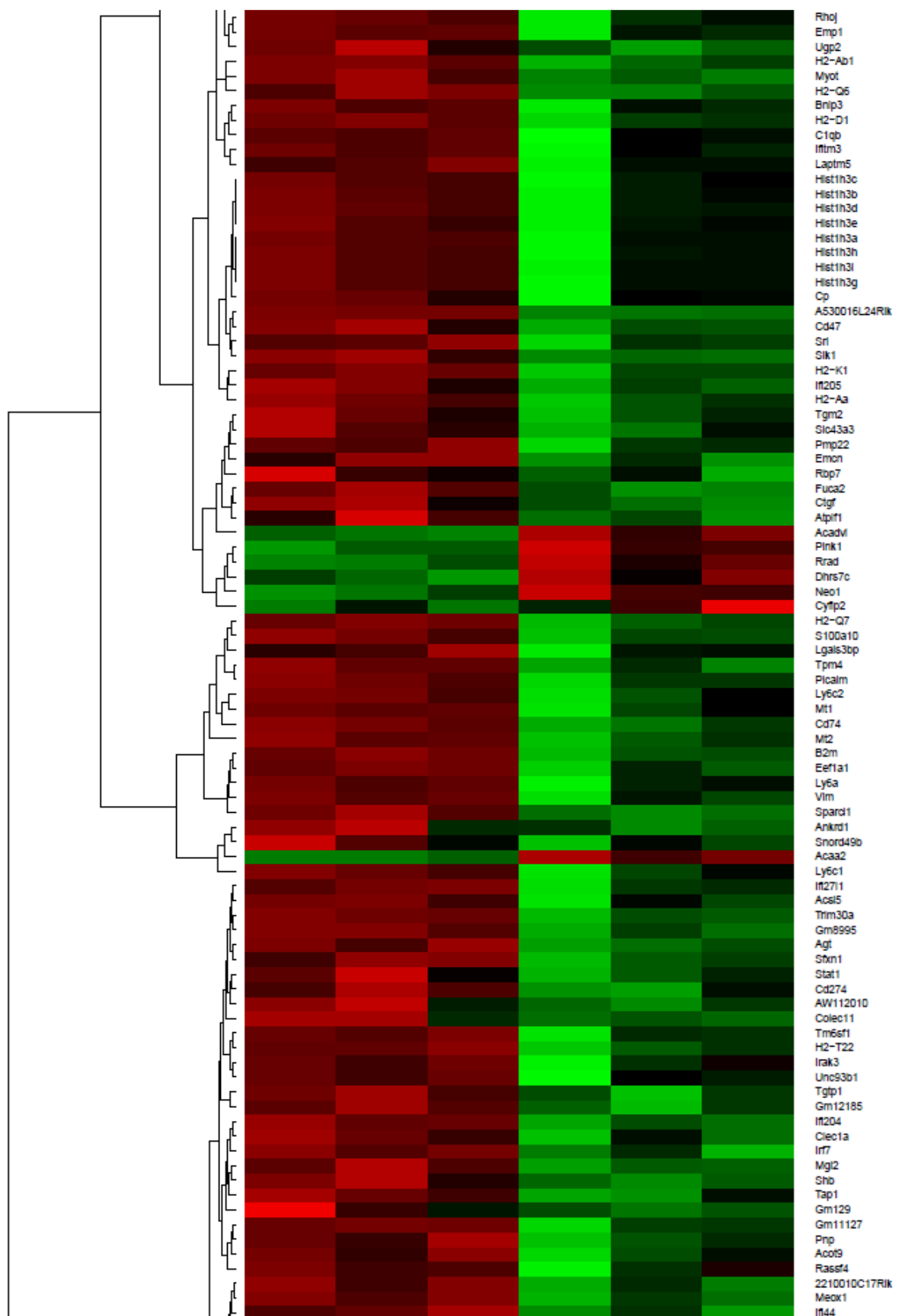


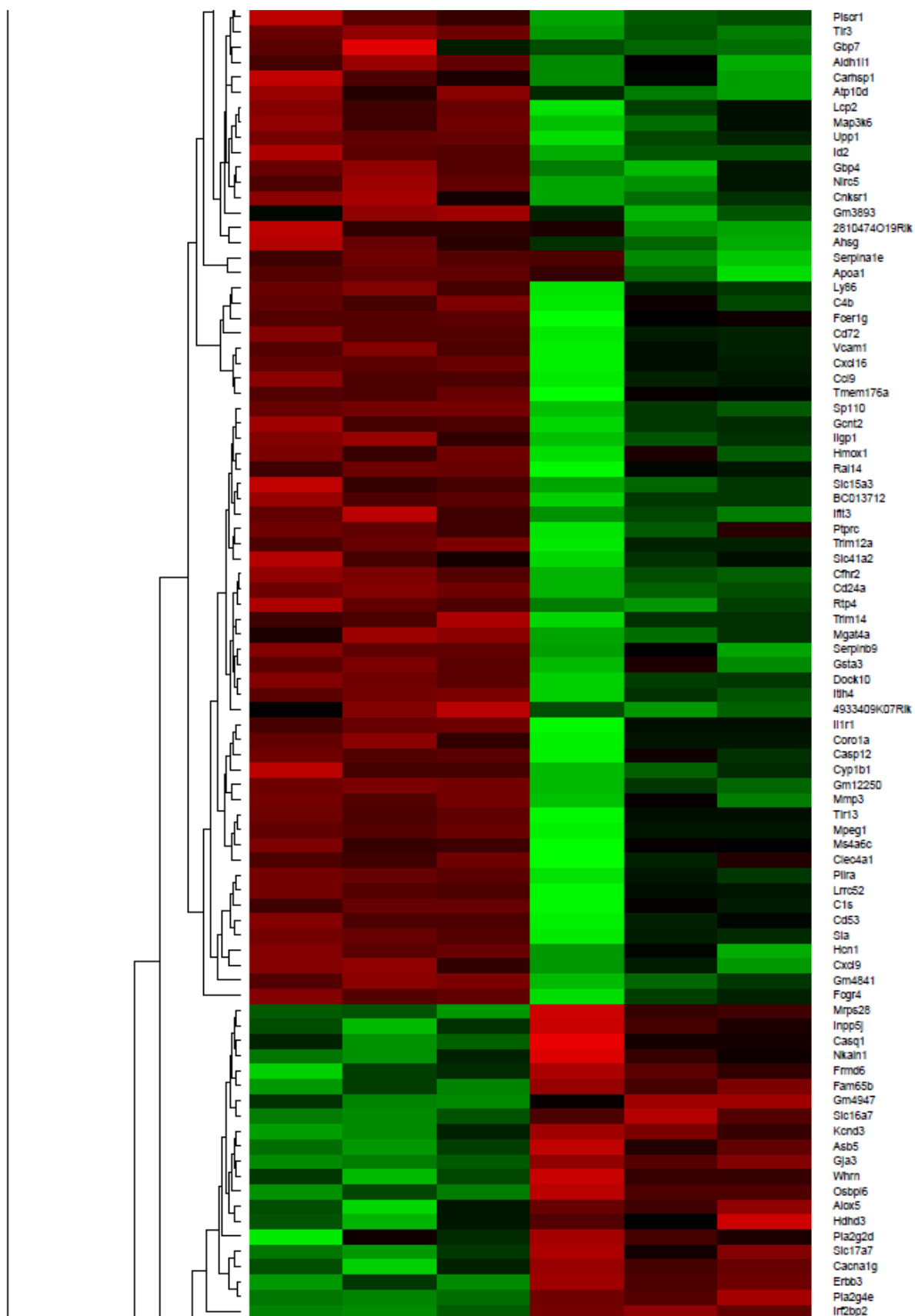


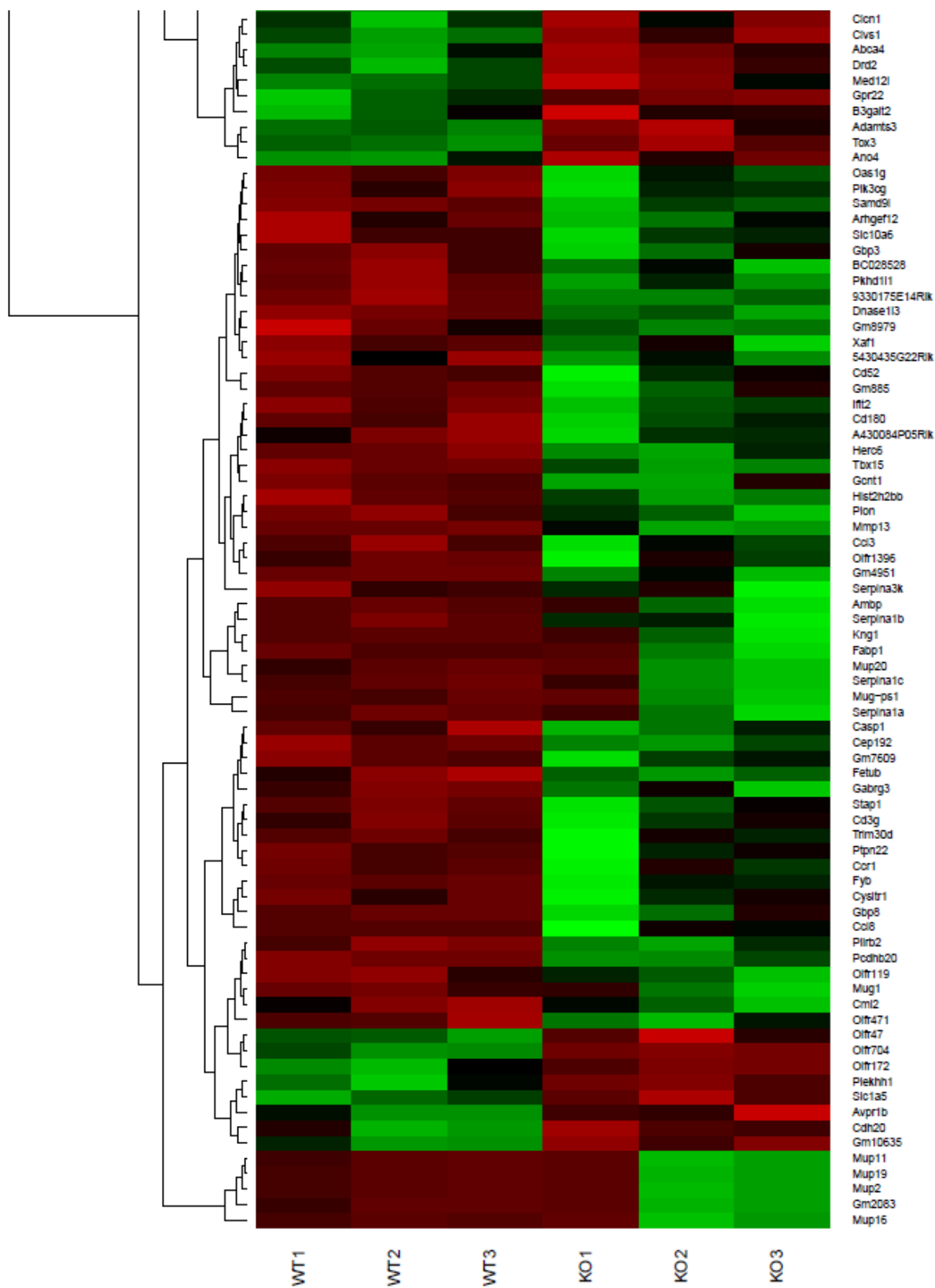


Appendix 3(b): Heart heatmap

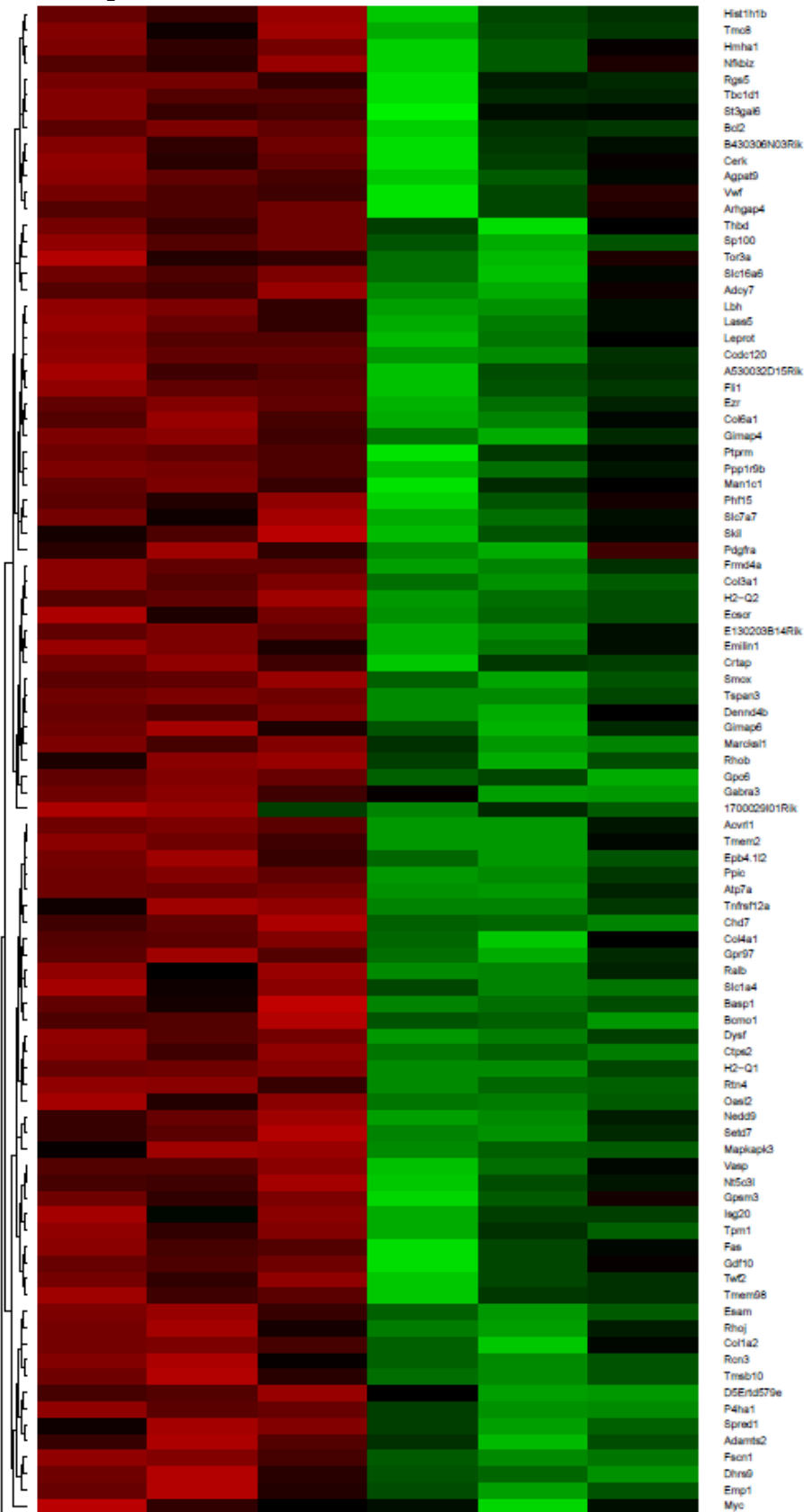


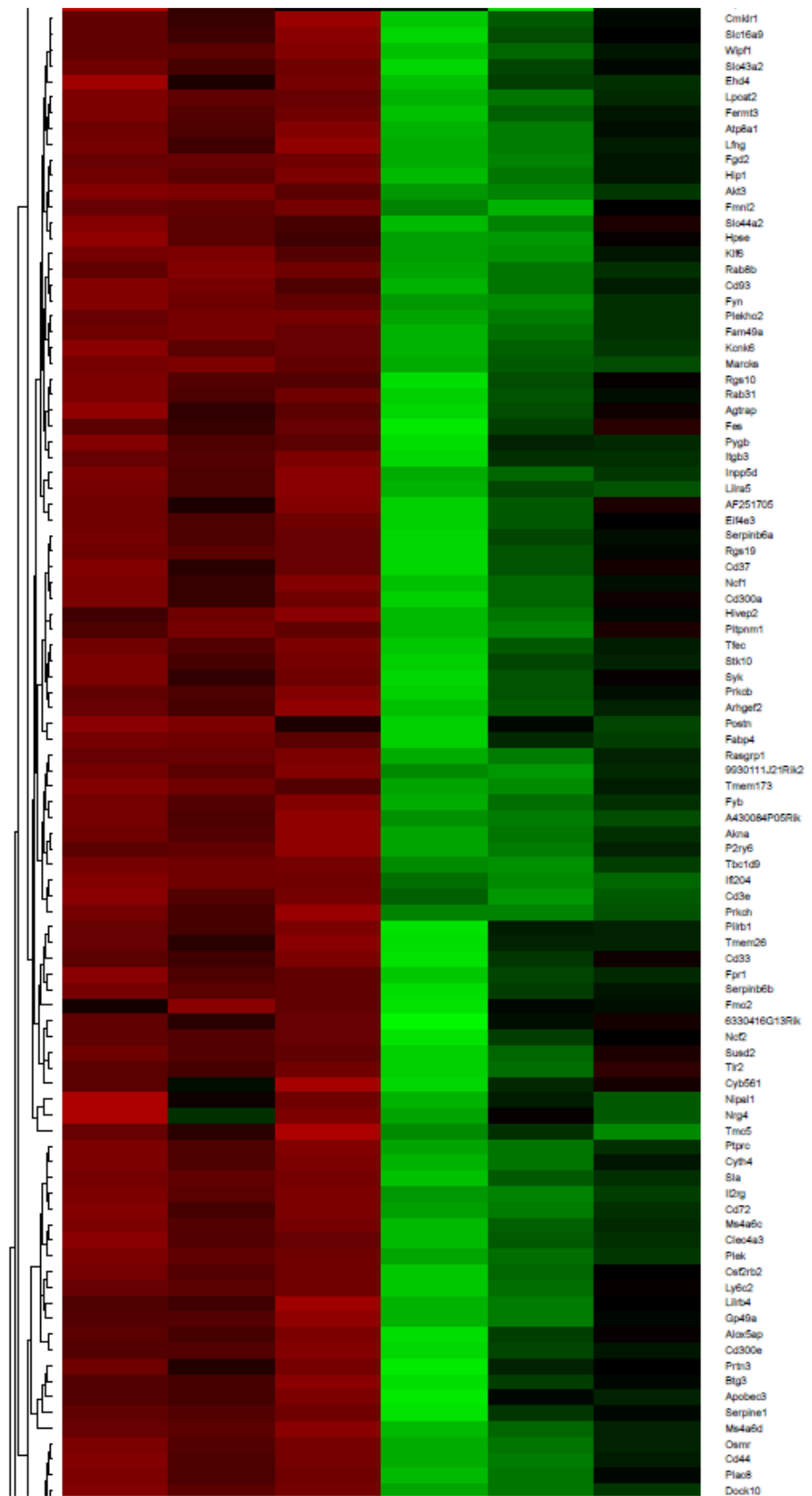


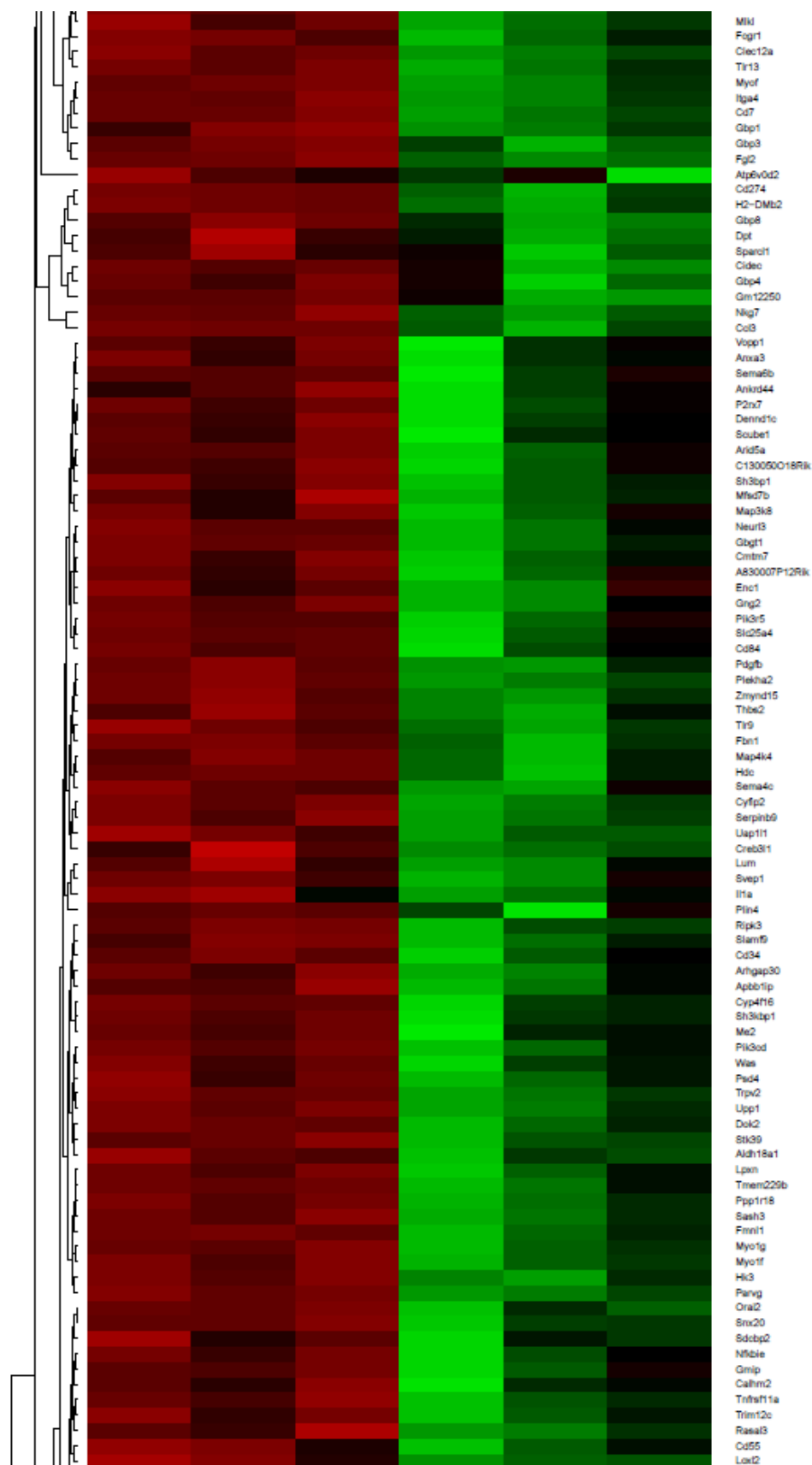


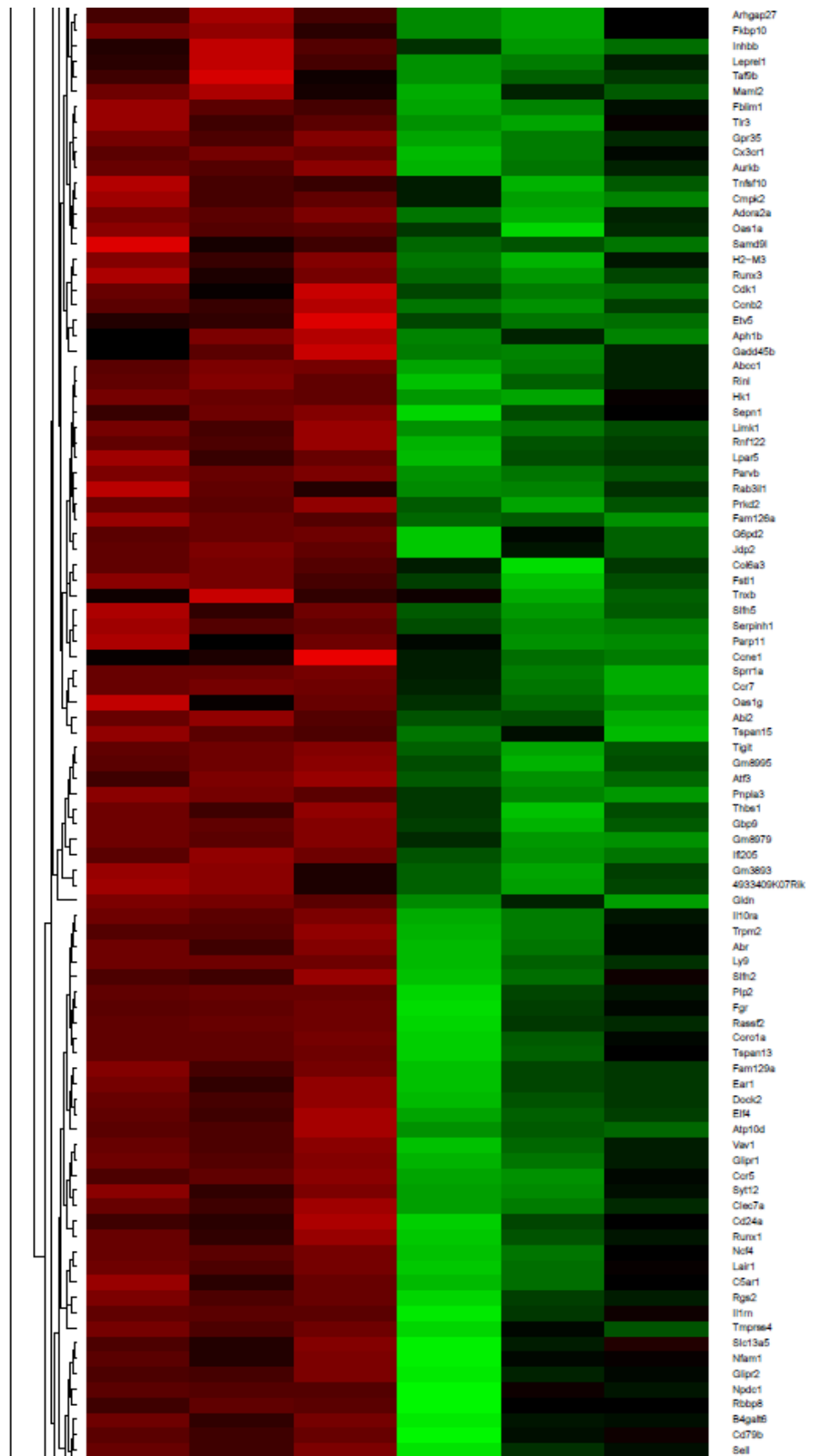


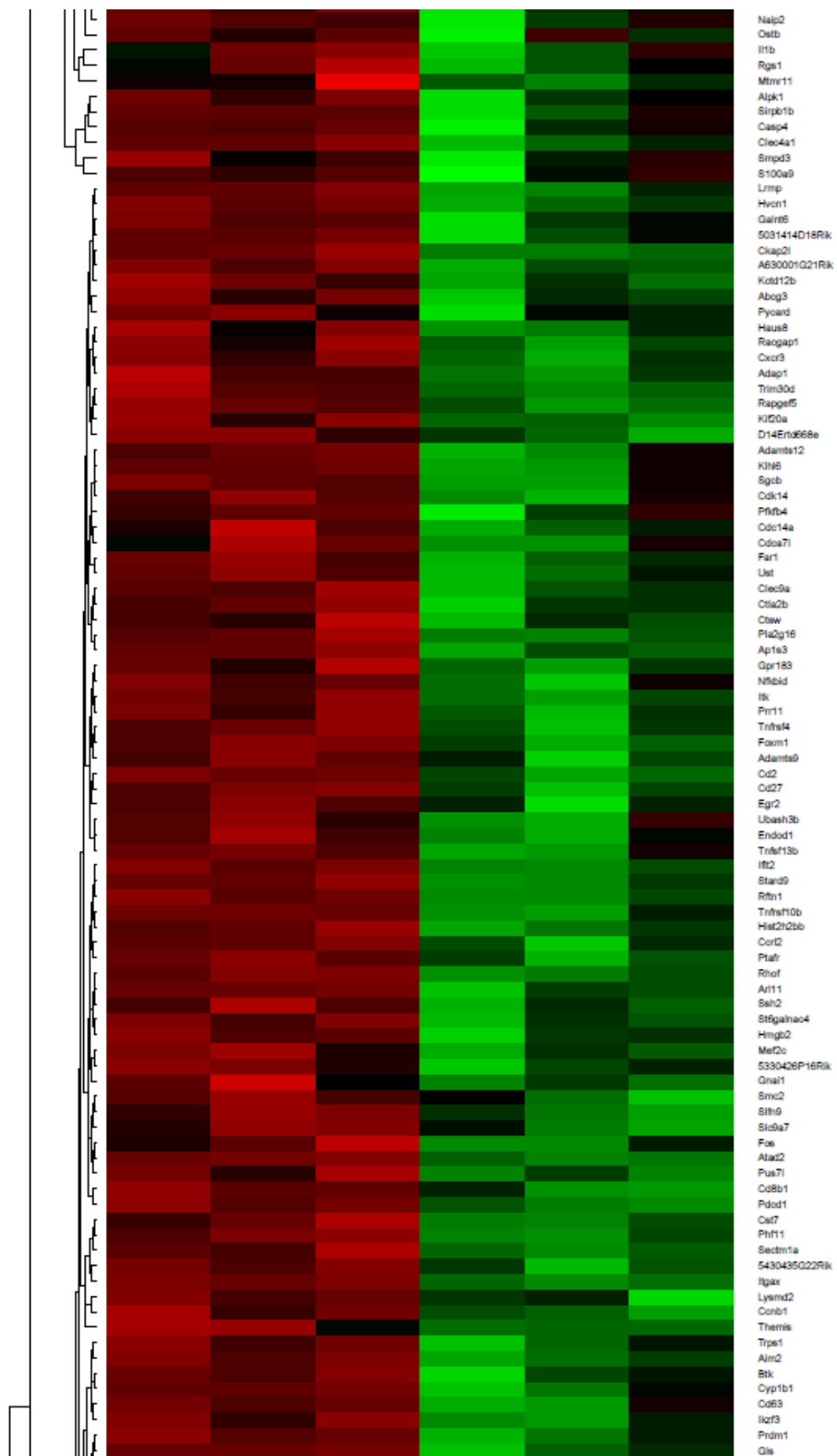
Appendix 3(c): Liver heatmap

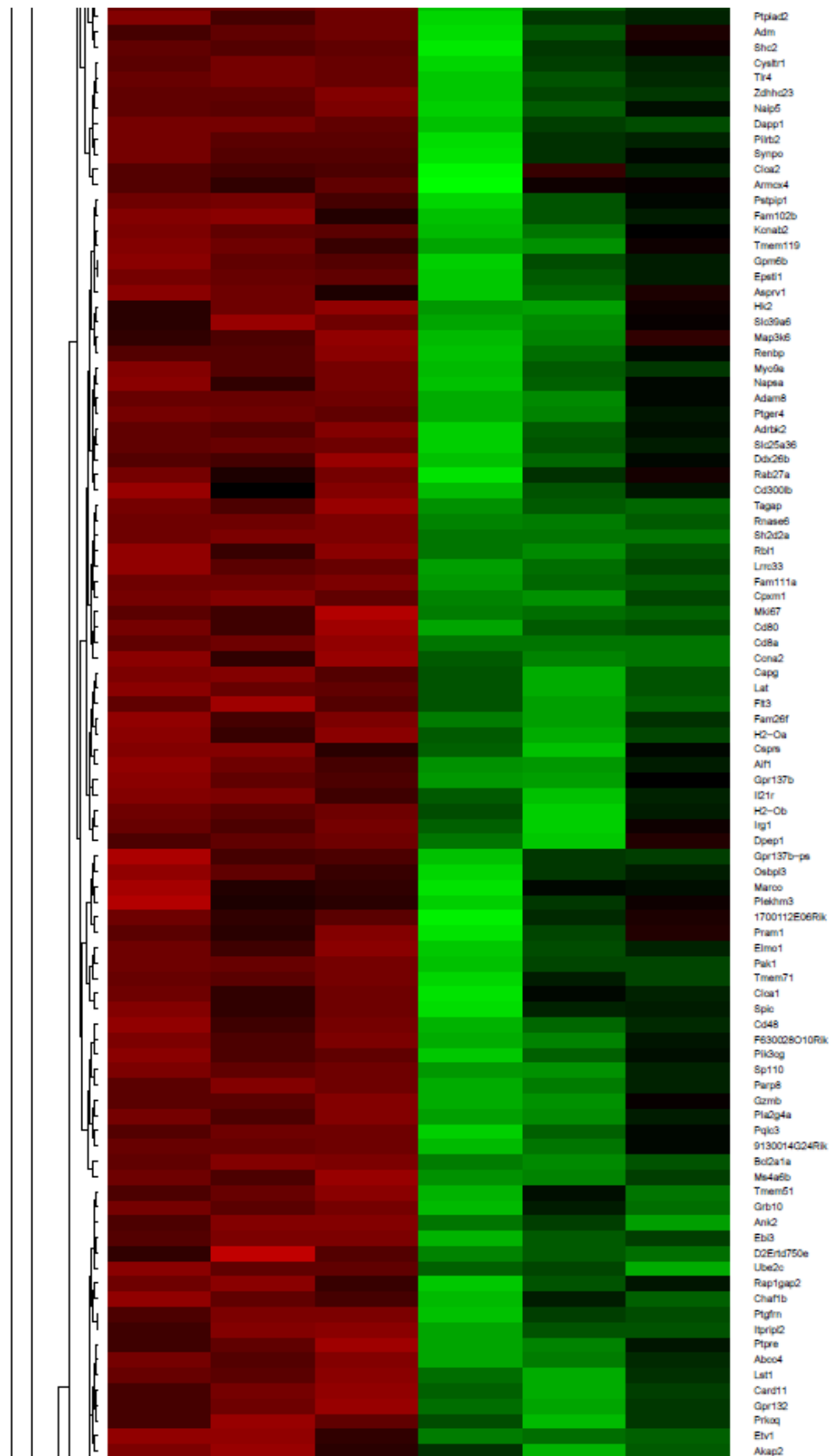


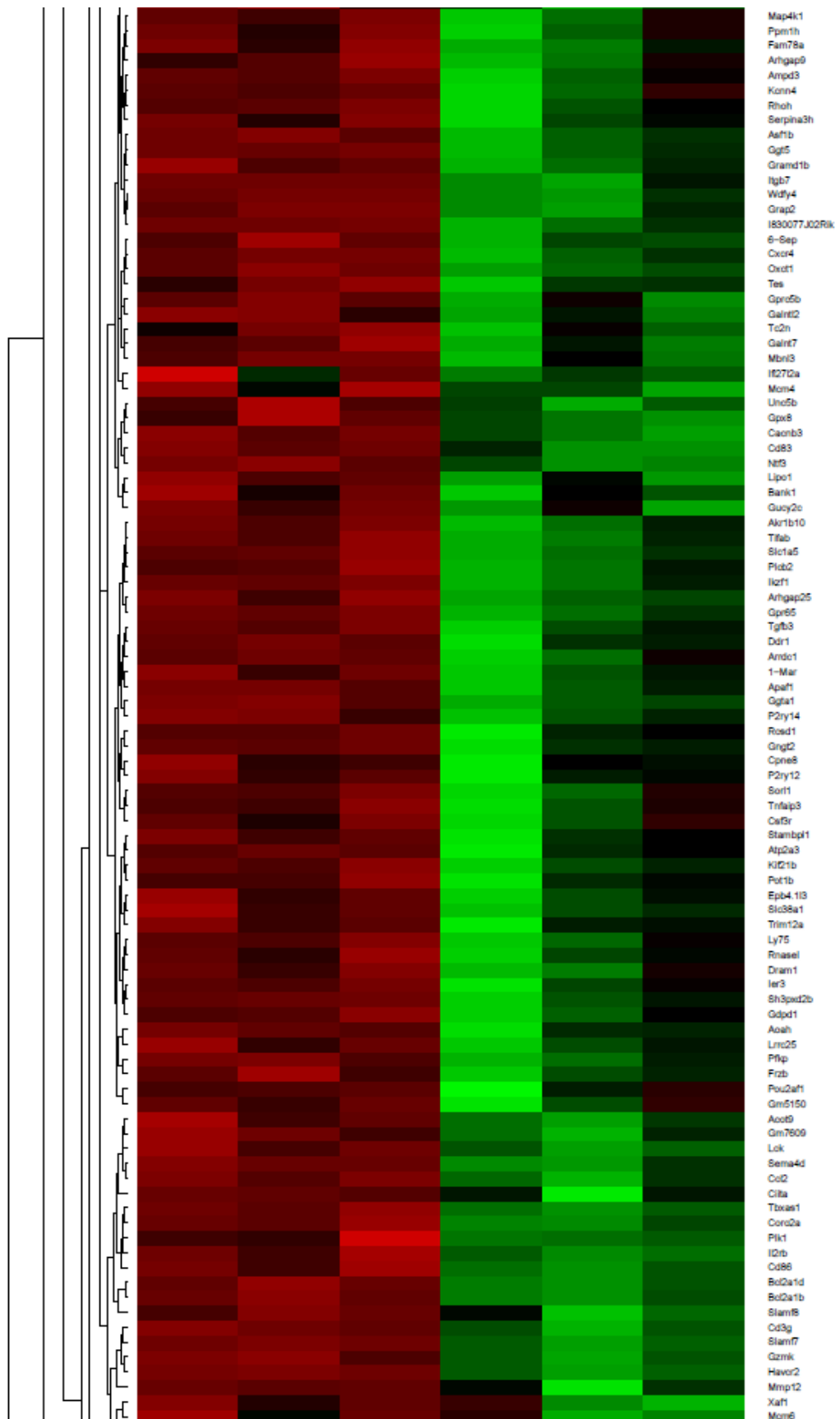


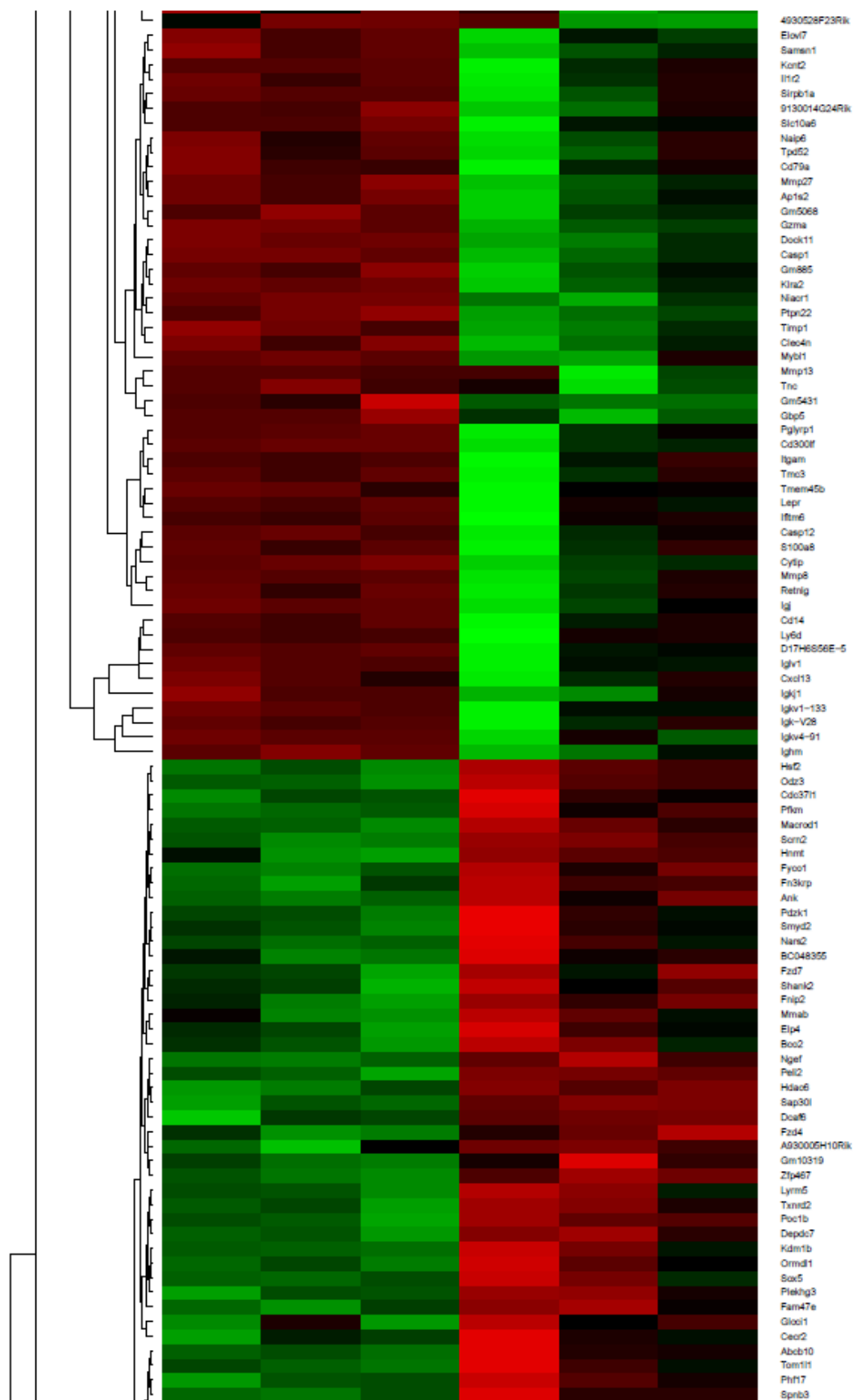


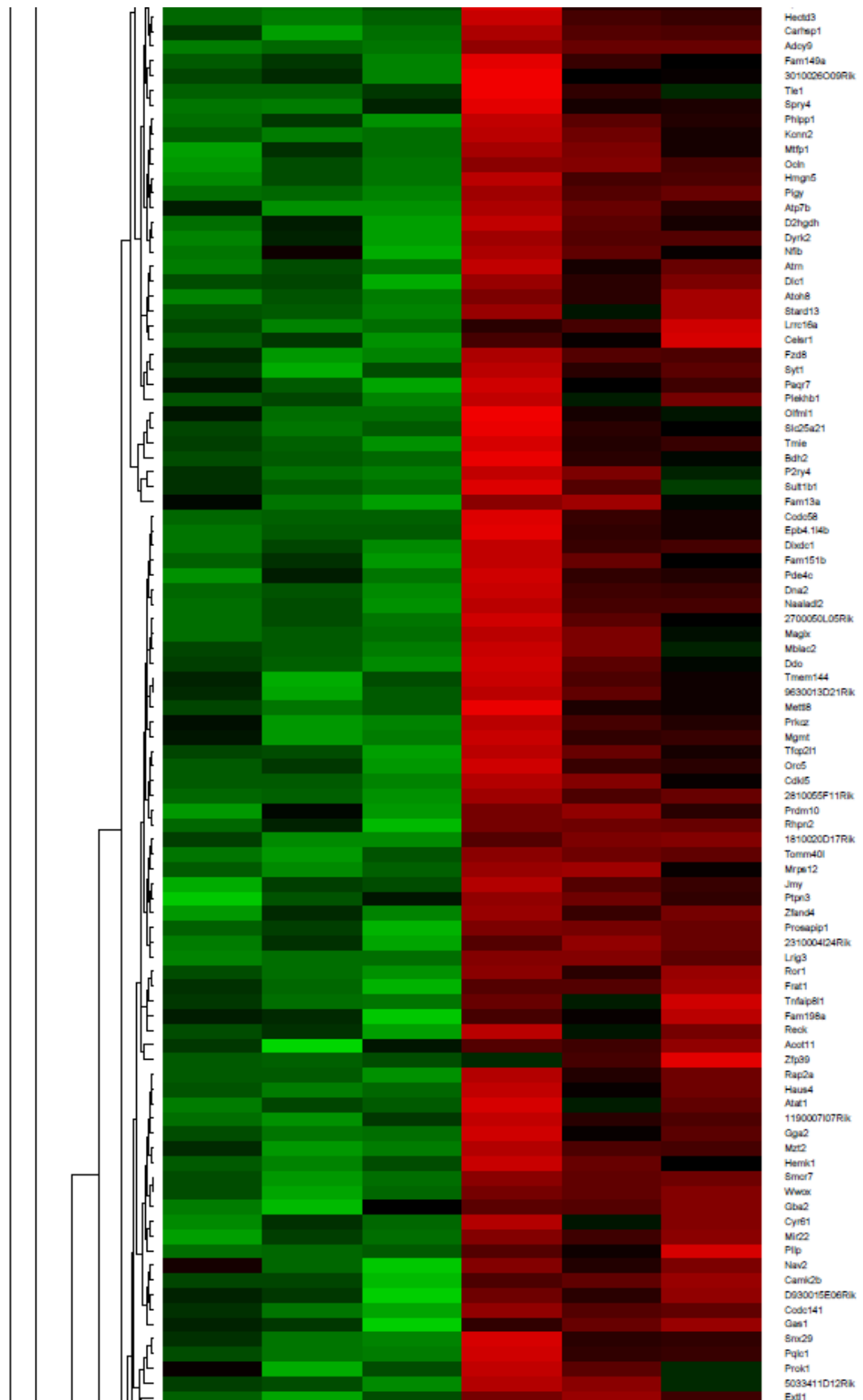


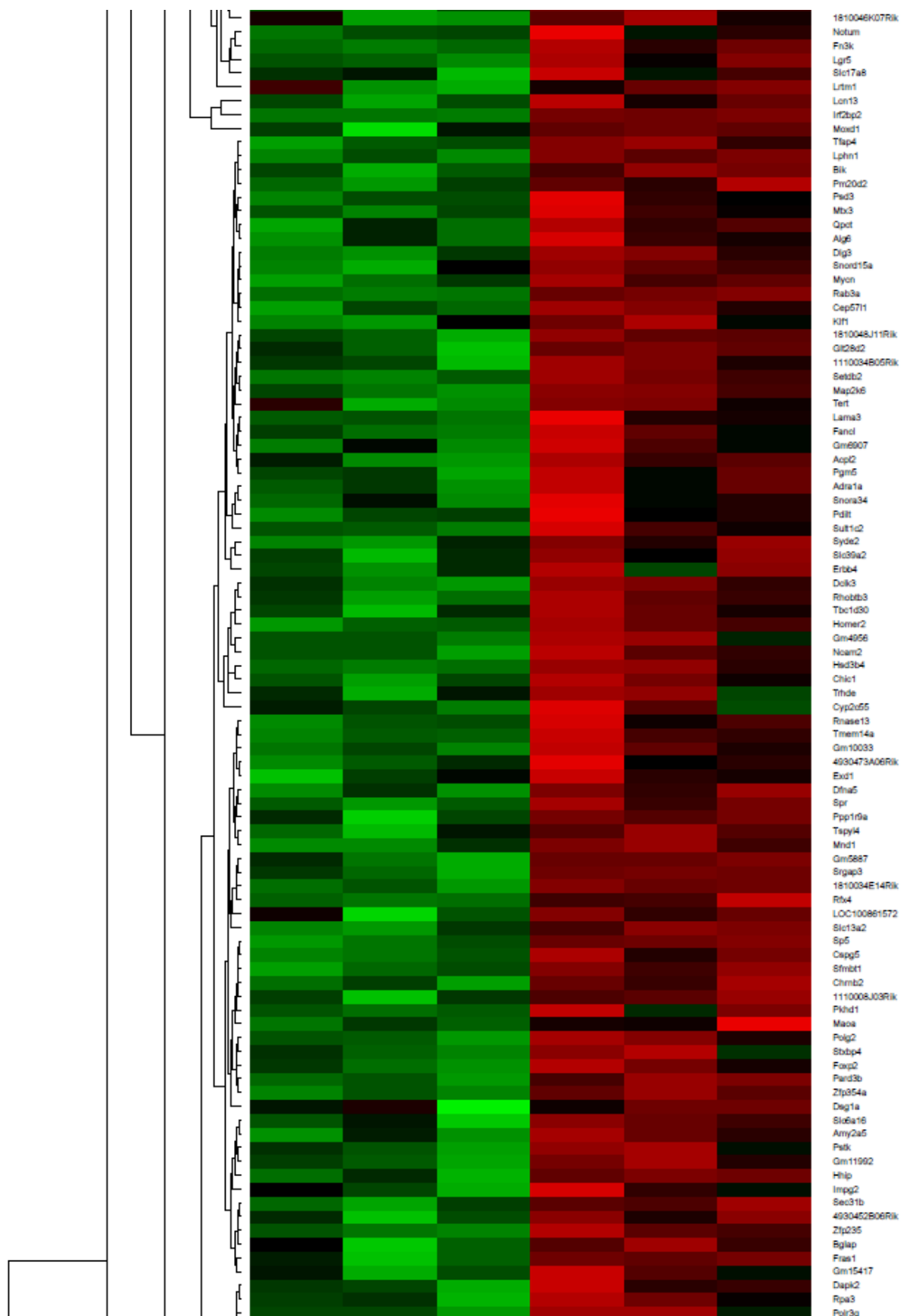


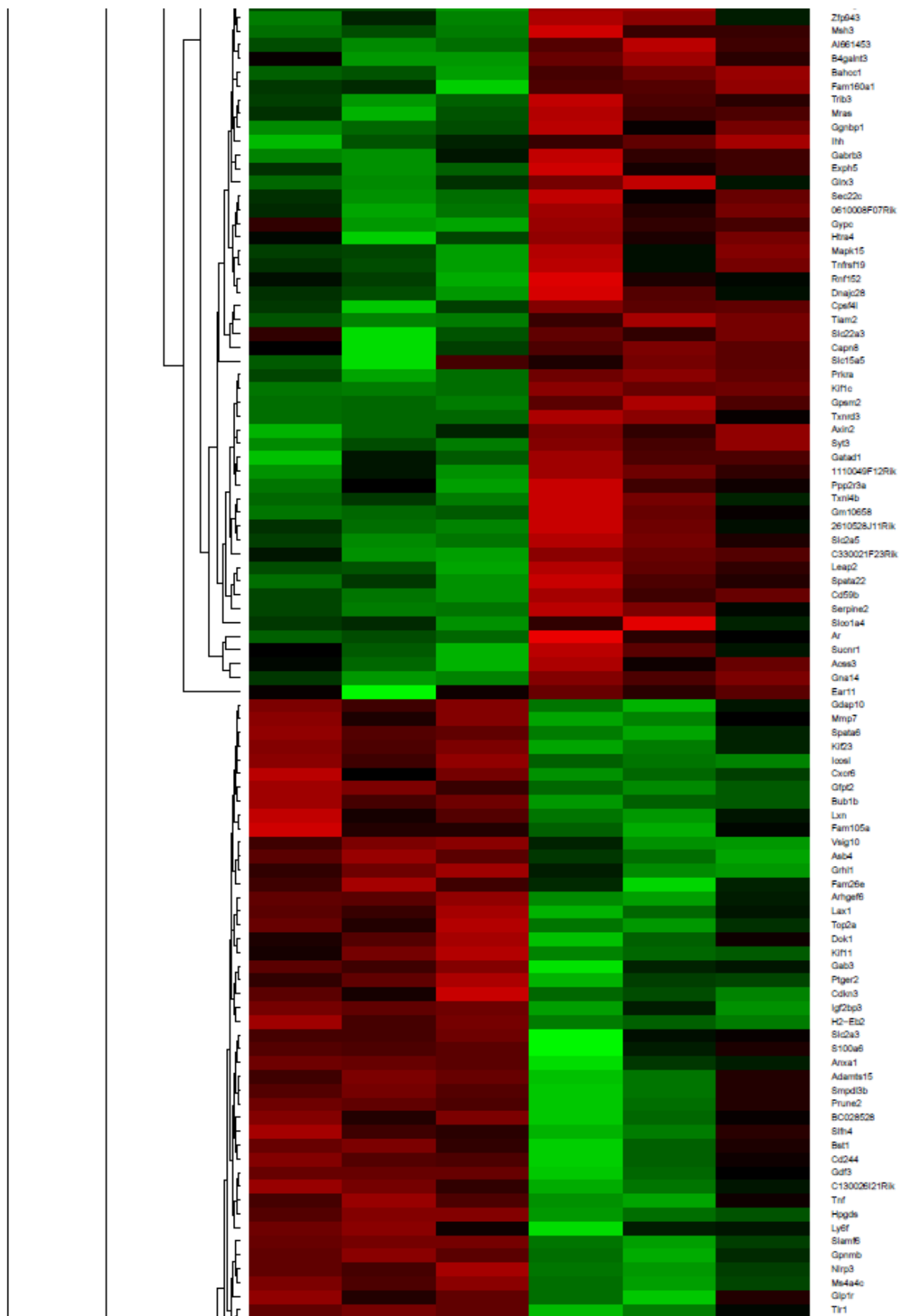


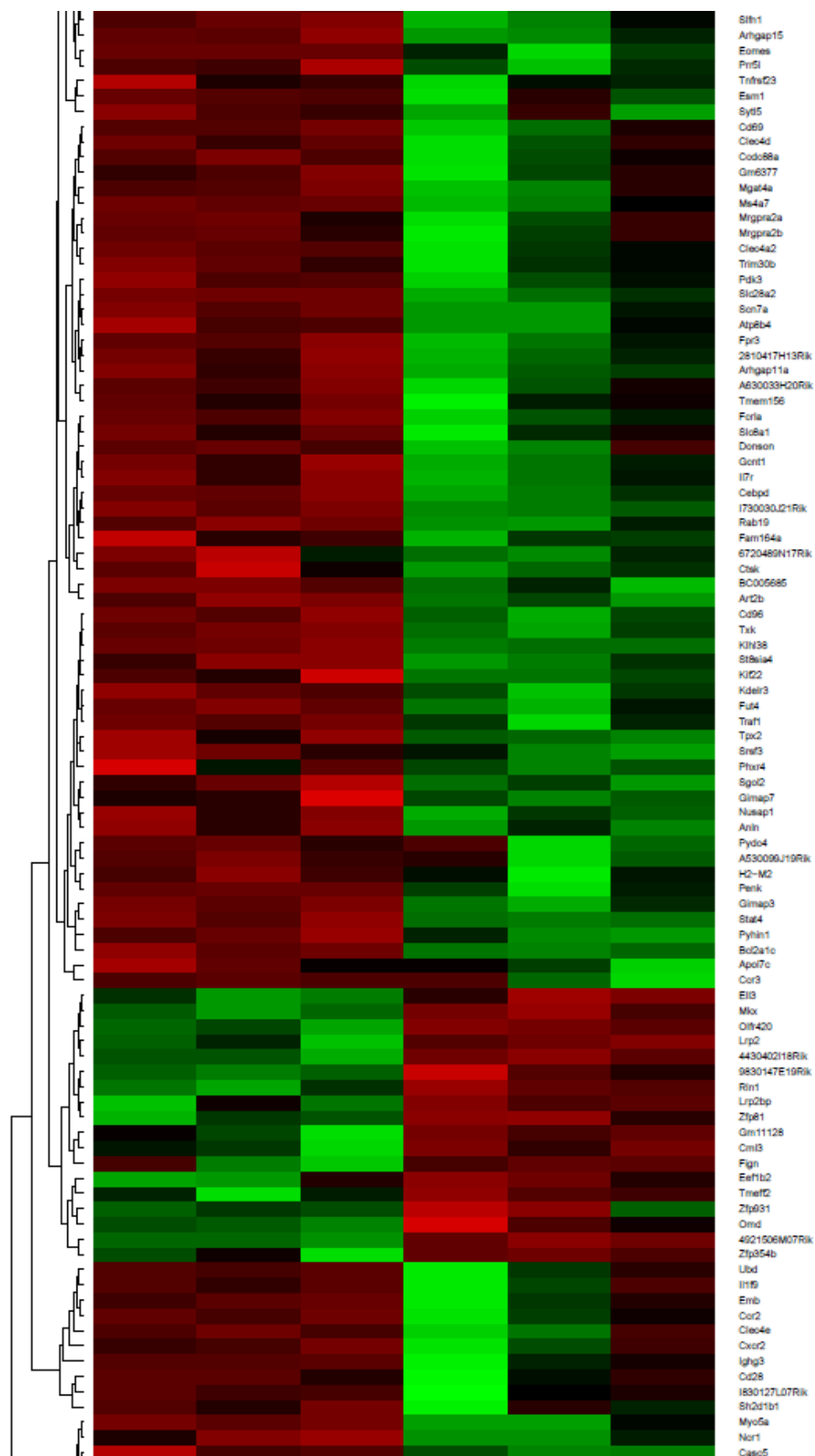


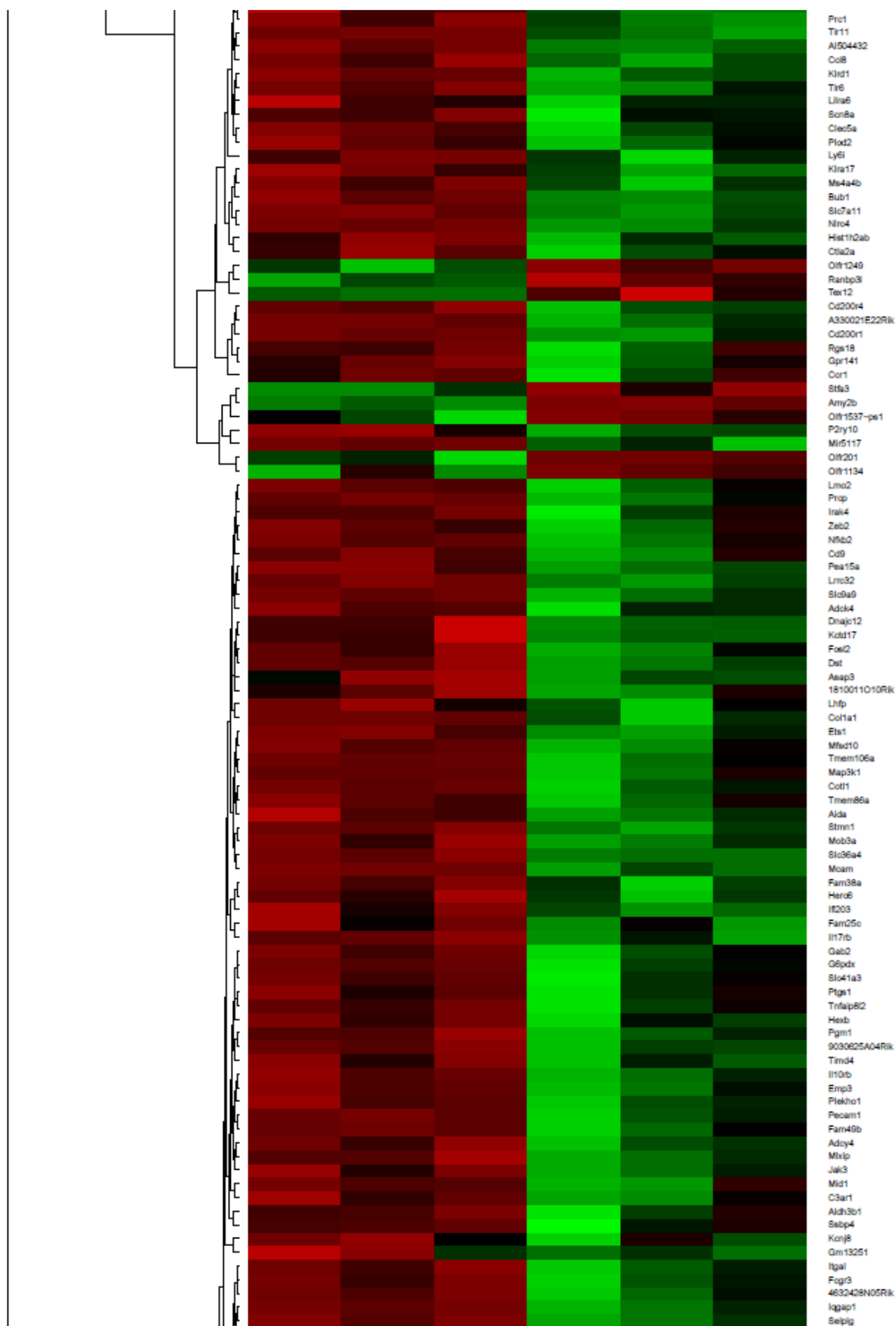


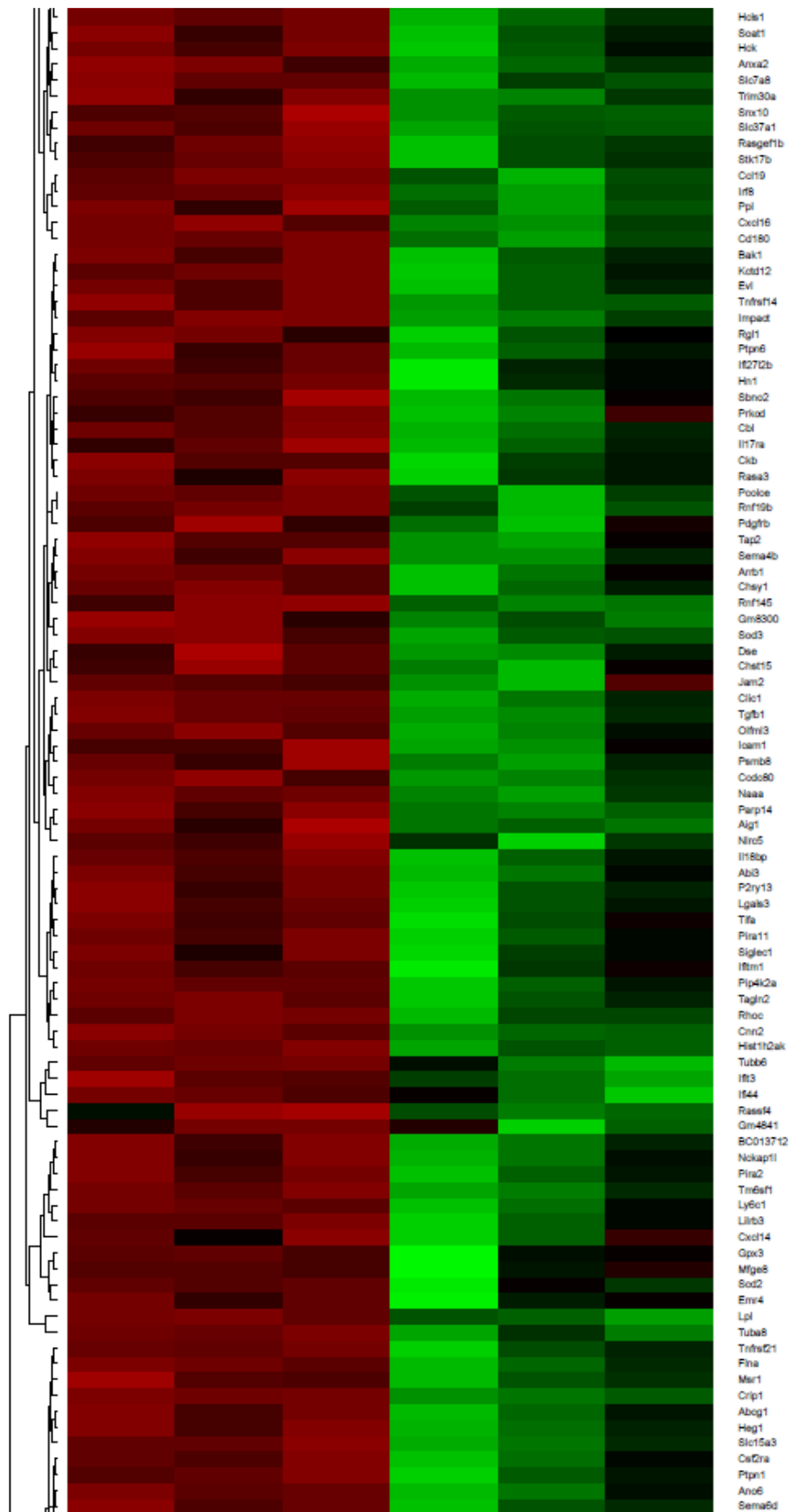


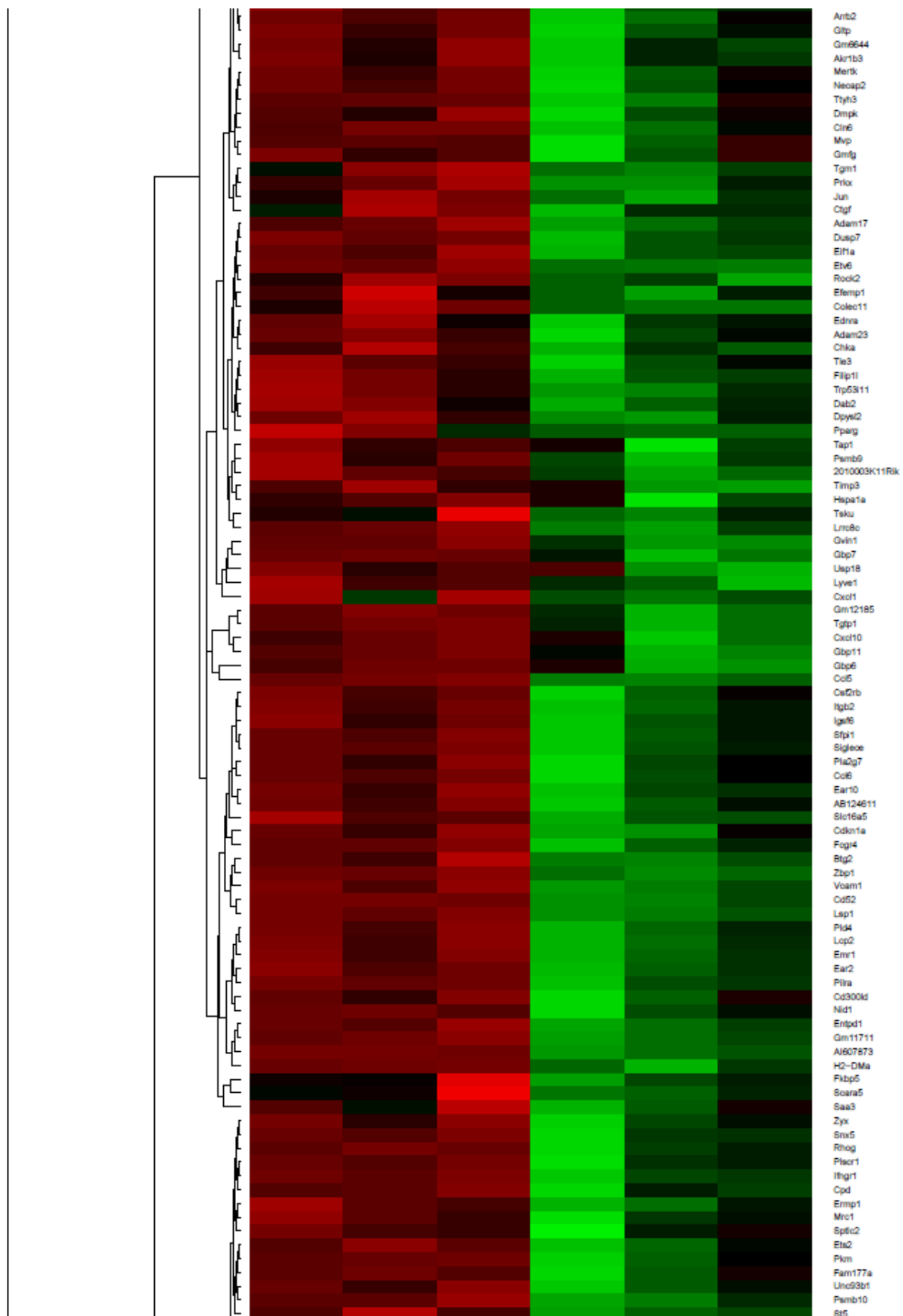


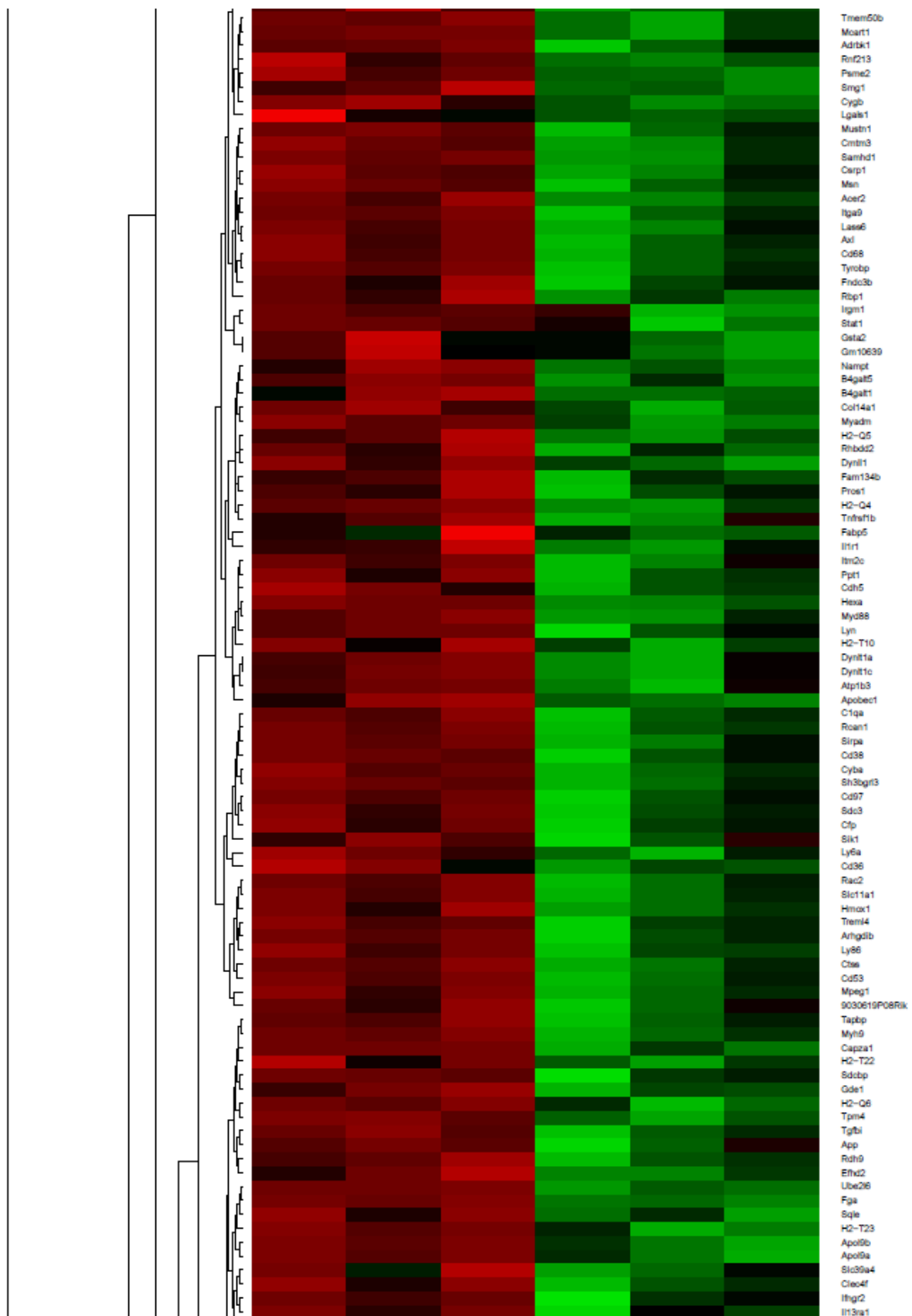


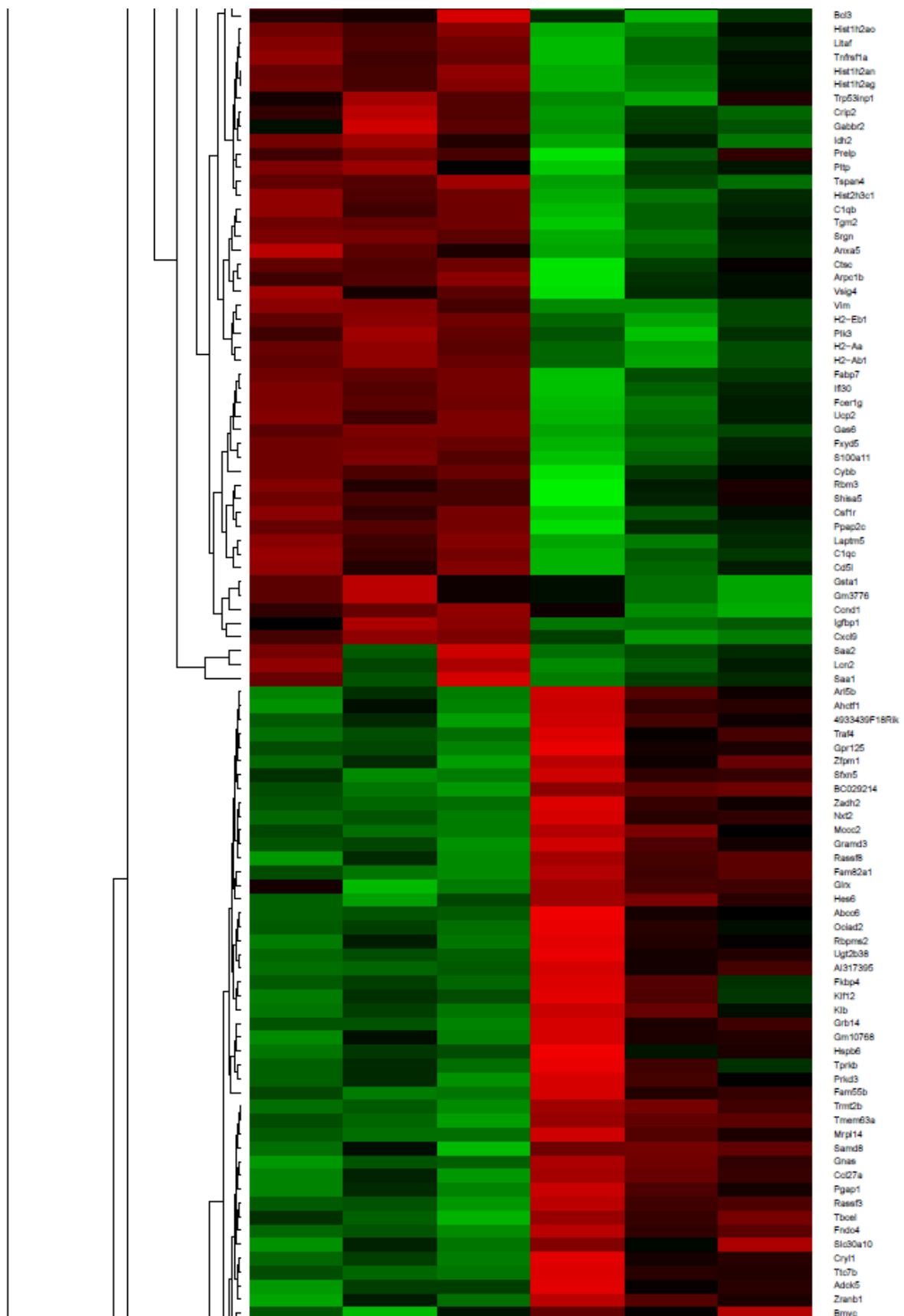


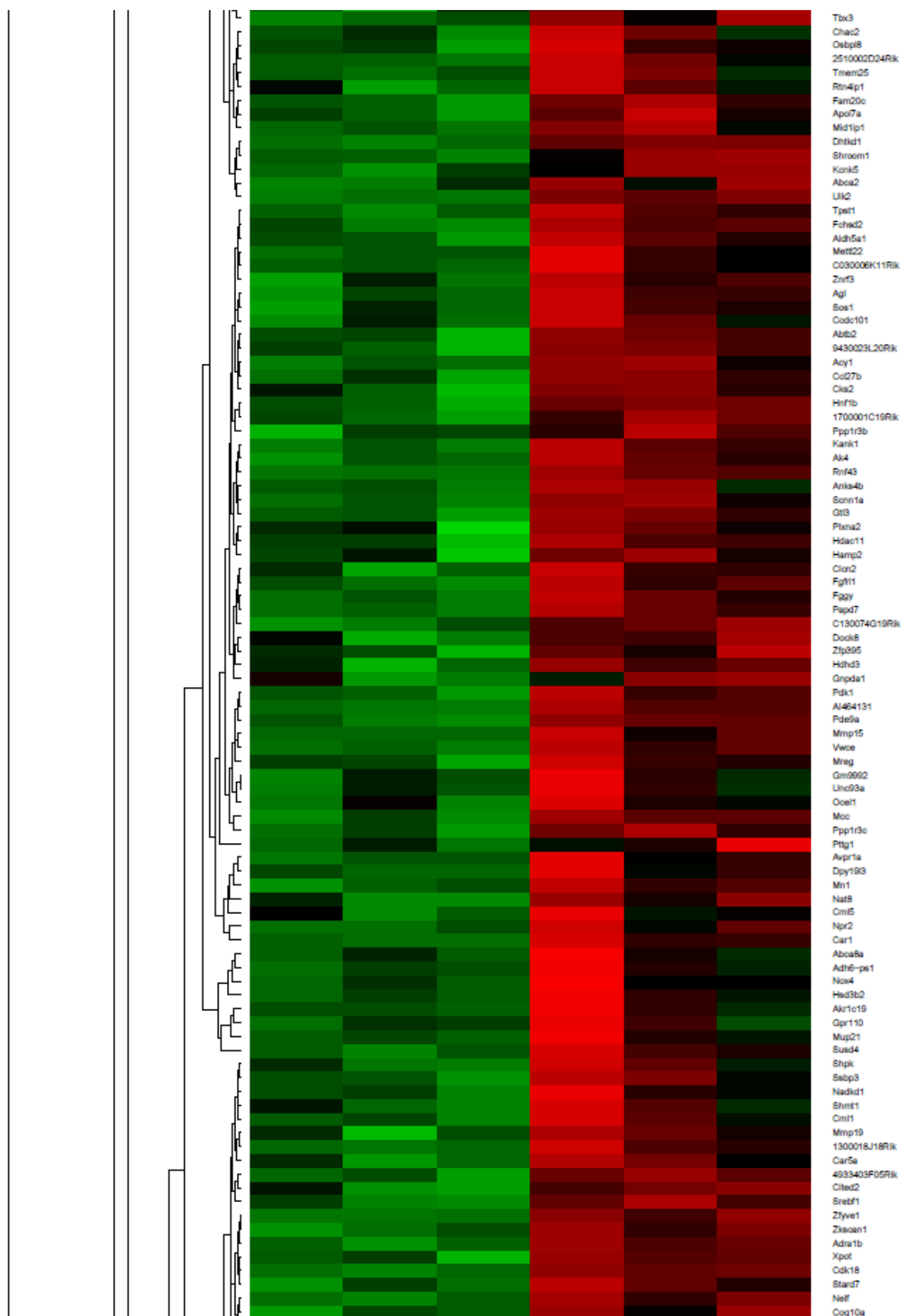


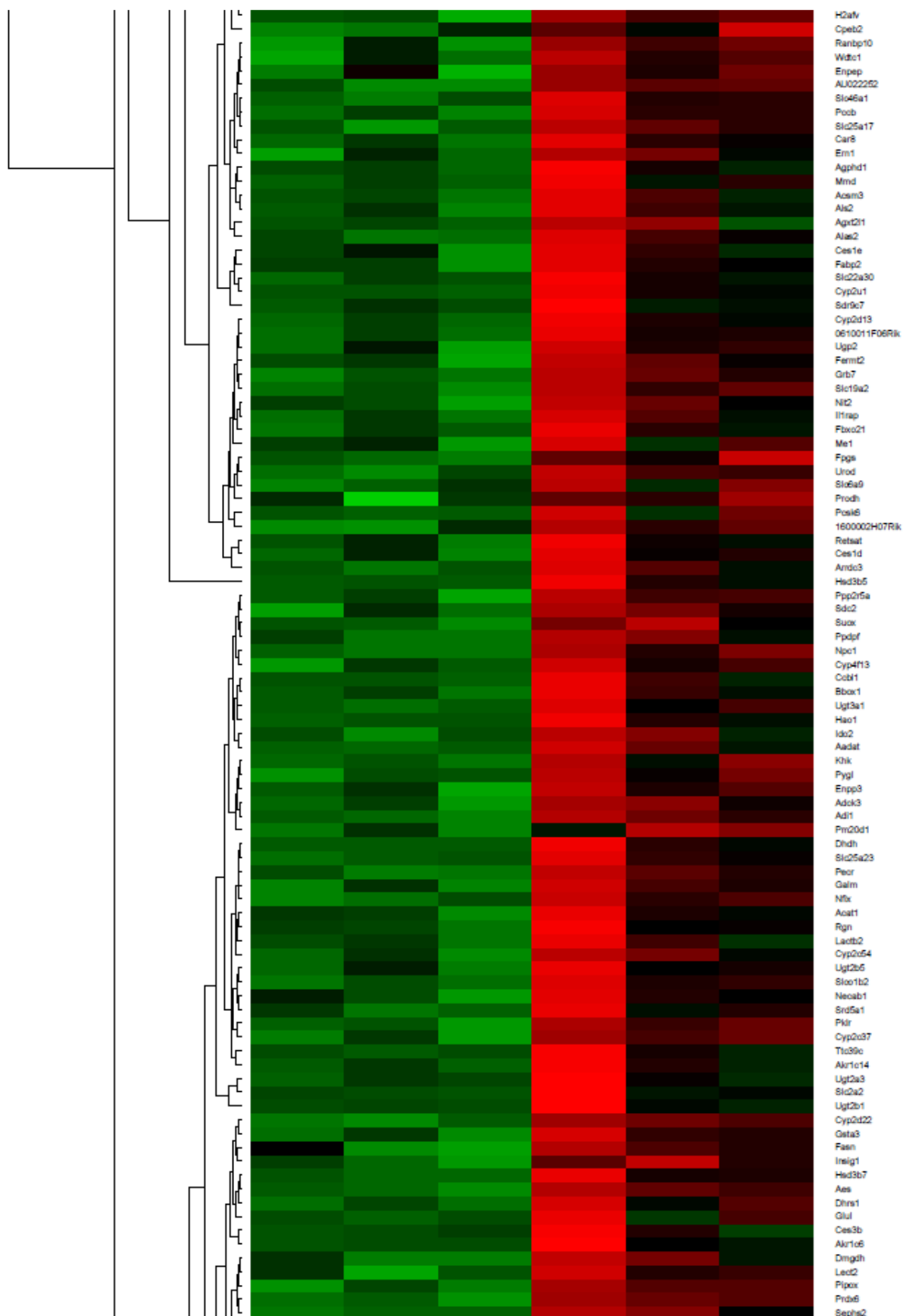


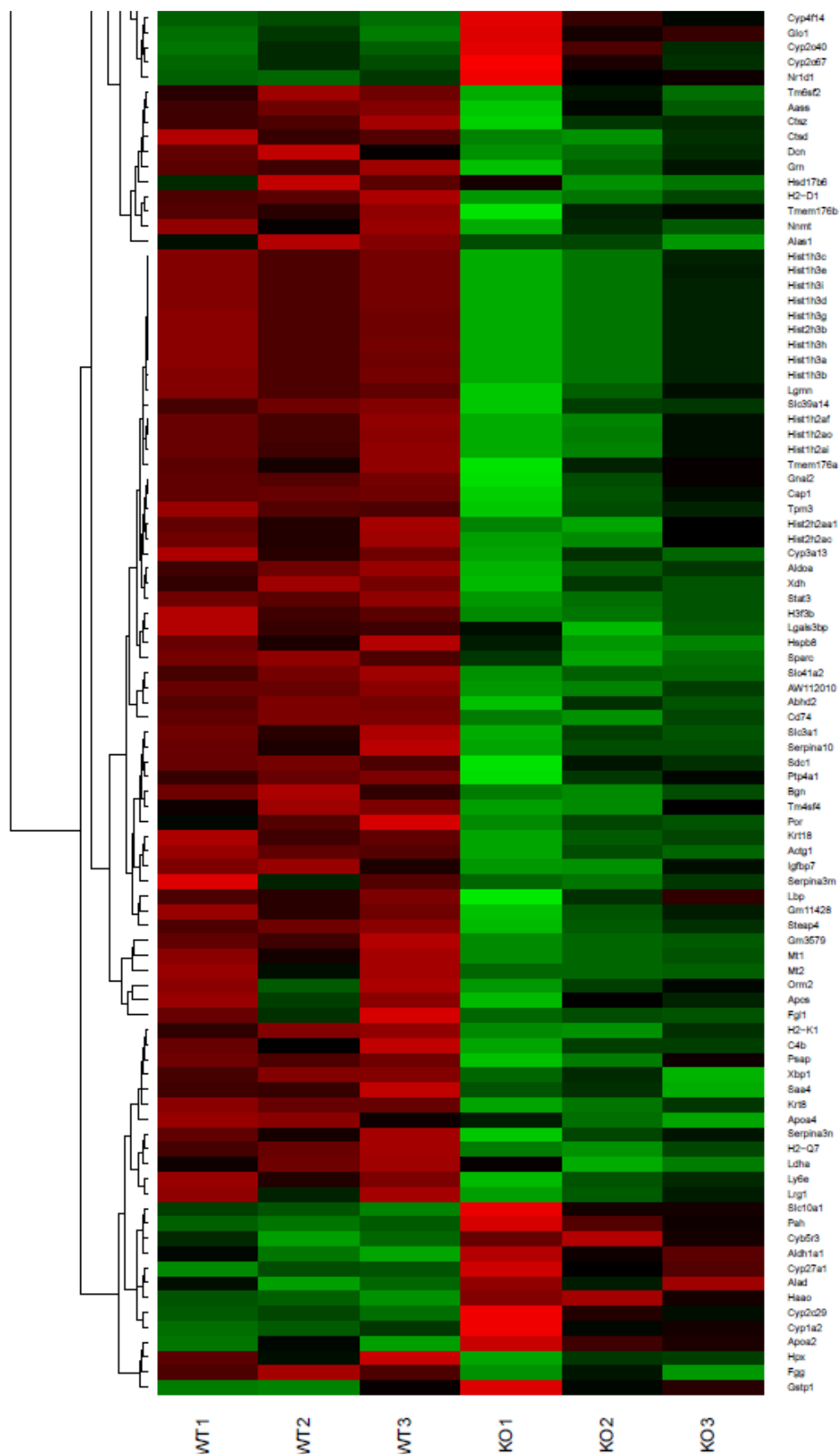












Appendix 4(a): Hematology values of an *Irf2bp2*^{-/-} knockout mouse.

HEMATOLOGY				
Test	Results	Reference	Units	Lab
WBC	1.9	-	x10E9/L	TOR
RBC	7.7	-	x10E12/L	TOR
Hemoglobin	114	-	g/L	TOR
Hematocrit	0.39	-	L/L	TOR
MCV	52	-	fl	TOR
MCH	15	-	pg	TOR
MCHC	289	-	g/L	TOR
Reticulocytes	3.5	-	%	TOR
Platelets	472	-	x10E9/L	TOR

Differential:	%	abs.		
Bands	0.0	0.0	-	x10E9/L
Neutrophils	8.0	0.2	-	x10E9/L
Lymphocytes	84.0	1.6	-	x10E9/L
Monocytes	8.0	0.2	-	x10E9/L
Eosinophils	0.0	0.0	-	x10E9/L
Basophils	0.0	0.0	-	x10E9/L

Morphology:

WBC MORPHOLOGY

Normal

RBC MORPHOLOGY

Polychromasia 2-5 /HPF

PLT MORPHOLOGY

Normal

COMMENTS

Small clot present

Appendix 4(b): Hematology values of an *Irf2bp2*^{+/-} mouse.

HEMATOLOGY				
Test	Results	Reference	Units	Lab
WBC	2.2	-	x10E9/L	TOR
RBC	8.8	-	x10E12/L	TOR
Hemoglobin	131	-	g/L	TOR
Hematocrit	0.49	-	L/L	TOR
MCV	56	-	fl	TOR
MCH	15	-	pg	TOR
MCHC	269	-	g/L	TOR
Reticulocytes	2.6	-	%	TOR
Platelets	834	-	x10E9/L	TOR
Differential:				
	%	abs.		
Bands	0.0	0.0	-	x10E9/L
Neutrophils	17.0	0.4	-	x10E9/L
Lymphocytes	79.0	1.7	-	x10E9/L
Monocytes	2.0	0.0	-	x10E9/L
Eosinophils	2.0	0.0	-	x10E9/L
Basophils	0.0	0.0	-	x10E9/L

Morphology:

WBC MORPHOLOGY

Normal

RBC MORPHOLOGY

Polychromasia 2-5 /HPF

PLT MORPHOLOGY

Normal

COMMENTS

Small clot present