

# Harnessing powers of genomics to build molecular maps of coronavirus targets in human cells: a guide for existing drug repurposing and experimental studies identifying candidate therapeutics to mitigate the pandemic COVID-19.

Gennadi Glinsky

Submitted date: 01/04/2020 • Posted date: 03/04/2020

Licence: CC BY-NC-ND 4.0

Citation information: Glinsky, Gennadi (2020): Harnessing powers of genomics to build molecular maps of coronavirus targets in human cells: a guide for existing drug repurposing and experimental studies identifying candidate therapeutics to mitigate the pandemic COVID-19.. ChemRxiv. Preprint.

<https://doi.org/10.26434/chemrxiv.12052512.v2>

Coronavirus pandemic COVID-19 caused by the newly emerged SARS-CoV-2 virus is rapidly spreading around the globe and entering the most dangerous acute phase of its evolution in the United States. Recent progress in defining genetic and molecular determinants mediating the SARS-CoV-2 entry into human cells (Walls et al., 2020) should facilitate development of targeted therapeutics and efficient vaccines. Here, human genes required for SARS-CoV-2 entry into human cells, ACE2 and FURIN, were employed as baits to build genomics-guided maps of up-stream regulatory elements, their expression and functions in human body, including pathophysiologically-relevant cell types. Genes acting as repressors and activators of the ACE2 and FURIN genes were identified based on the analyses of gene silencing and overexpression experiments as well as relevant transgenic mouse models. Panels of repressors (VDR; GATA5; SFTPC; HIF1a) and activators (HMGA2; INSIG1) were then employed to identify existing drugs that manifest gene expression signatures of the potential coronavirus infection mitigation agents. Using this strategy, Vitamin D and Quercetin have been identified as putative pandemic mitigation agents. Gene expression profiles of Vitamin D and Quercetin activities and their established safety records as over-the-counter medicinal substances suggest that they may represent viable candidates for further assessment and considerations of their potential utility as coronavirus pandemic mitigation agents. Notably, gene set enrichment analyses and expression profiling experiments identify multiple drugs, smoking, and many disease conditions that appear to act as putative coronavirus infection-promoting agents. Discordant patterns of Testosterone versus Estradiol impacts on SCARS-CoV-2 targets suggest a plausible molecular explanation of the apparently higher male mortality during coronavirus pandemic. Observations reported in this contribution are intended to facilitate follow-up targeted experimental studies and, if warranted, randomized clinical trials to identify and validate therapeutically-viable interventions to combat the pandemic.

## File list (2)

---

- Harnessing powers of genomics to build molecular maps... (673.73 KiB) [view on ChemRxiv](#) • [download file](#)
- 
- Supplemenmtal Figure S1\_S13. ACE2 and FURIN genes.... (3.95 MiB) [view on ChemRxiv](#) • [download file](#)
-

**Harnessing powers of genomics to build molecular maps of coronavirus targets in human cells: a guide for existing drug repurposing and experimental studies identifying candidate therapeutics to mitigate the pandemic COVID-19.**

Gennadi V. Glinsky<sup>1</sup>

<sup>1</sup> Institute of Engineering in Medicine

University of California, San Diego

9500 Gilman Dr. MC 0435

La Jolla, CA 92093-0435, USA

Correspondence: [gglinskii@ucsd.edu](mailto:gglinskii@ucsd.edu)

Web: <http://iem.ucsd.edu/people/profiles/gennadi-v-glinskii.html>

**Running title:** Genomics-guided mitigation maps for coronavirus pandemic

**Key words:** COVID-19; SARS-CoV-2 coronavirus; genomics; mitigation approaches; drugs & medicinal substances repurposing; Vitamin D; Quercetin

## **Abstract**

Coronavirus pandemic COVID-19 caused by the newly emerged SARS-CoV-2 virus is rapidly spreading around the globe and entering the most dangerous acute phase of its evolution in the United States. Recent progress in defining genetic and molecular determinants mediating the SARS-CoV-2 entry into human cells (Walls et al., 2020) should facilitate development of targeted therapeutics and efficient vaccines. Here, human genes required for SARS-CoV-2 entry into human cells, *ACE2* and *FURIN*, were employed as baits to build genomics-guided maps of up-stream regulatory elements, their expression and functions in human body, including pathophysiologically-relevant cell types. Genes acting as repressors and activators of the *ACE2* and *FURIN* genes were identified based on the analyses of gene silencing and overexpression experiments as well as relevant transgenic mouse models. Panels of repressors (*VDR*; *GATA5*; *SFTPC*; *HIF1a*) and activators (*HMGA2*; *INSIG1*) were then employed to identify existing drugs that manifest gene expression signatures of the potential coronavirus infection mitigation agents. Using this strategy, Vitamin D and Quercetin have been identified as putative pandemic mitigation agents. Gene expression profiles of Vitamin D and Quercetin activities and their established safety records as over-the-counter medicinal substances suggest that they may represent viable candidates for further assessment and considerations of their potential utility as coronavirus pandemic mitigation agents. Notably, gene set enrichment analyses and expression profiling experiments identify multiple drugs, smoking, and many disease conditions that appear to act as putative coronavirus infection-promoting agents. Discordant patterns of Testosterone versus Estradiol impacts on SCARS-CoV-2 targets suggest a plausible molecular explanation of the apparently higher male mortality during coronavirus pandemic. Observations reported in this contribution are intended to facilitate follow-up targeted experimental studies and, if warranted, randomized clinical trials to identify and validate therapeutically-viable interventions to combat the pandemic.

## **Introduction**

Coronavirus pandemic COVID-19 caused by the newly emerged SARS-CoV-2 virus is rapidly entering the most dangerous acute phase of its evolution in the United States. Absence of the vaccine and lack of efficient targeted therapeutic approaches emphasizes the urgent need for identification of candidate pandemic mitigation agents among existing drugs and medicinal substances.

SARS-CoV-2 virus was discovered in December 2019 and shortly thereafter it was isolated and sequenced (Zhou et al., 2020; Zhu et al., 2020). Recent analyses of the structure, function, and antigenicity of the SARS-CoV-2 spike glycoprotein revealed the key role of the *ACE2* and *FURIN* genes in facilitating the high-affinity binding of viral particles and their entry into human cells (Walls et al., 2020). The efficient invasion of host cells by the SARS-CoV-2 is further enhanced by the presence of the unexpected furin cleavage site, which is cleaved during the biosynthesis (Walls et al., 2020). This novel feature distinguishes the previously known SARS-CoV and the newly emerged SARS-CoV-2 viruses and possibly contributes to the expansion of the cellular tropism of the SARS-CoV-2 (Walls et al., 2020). The crystal structure and high-resolution cryo-electron microscopy of the SARS-CoV-2 receptor-binding domain (RBD) in complex with human ACE2 revealed specific structural features of the SARS-CoV-2 RBD that appear to enhance its binding affinity to human ACE2 (Shang et al., 2020; Yan et al., 2020). Collectively, these observations firmly established protein products of the human genes *ACE2* and *FURIN* as the high-affinity receptor (*ACE2*) and invasion-promoting protease (*FURIN*) as the principal mediators of the SARS-CoV-2 invasion into human cells.

In this contribution, genomic screens were performed employing the *ACE2* and *FURIN* genes as baits to build genomics-guided human tissues-tailored maps of up-stream regulatory elements, their expression and functions. To identify the high-priority list of potential candidate mitigation agents, the validation analyses were performed using gene silencing and

overexpression experiments as well as relevant transgenic mouse models with the emphasis on pathophysiologically-relevant cell types. Panels of repressors (*VDR*; *GATA5*; *SFTPC*) and activators (*HMGAA2*; *INSIG1*) of the *ACE2* and *FURIN* expression were identified and then employed to identify existing drugs and medicinal substances that could be repurposed to ameliorate the outcomes of the coronavirus infection. Two of the most promising candidate mitigation agents, namely Vitamin D and Quercetin, manifest gene expression-altering activities and have established safety records as over-the-counter medicinal substances that seem sufficient for further assessment and considerations of their potential utility for amelioration of the clinical course of coronavirus pandemic. Unexpectedly, present analyses revealed discordant patterns of Testosterone versus Estradiol impacts on SCARS-CoV-2 targets with the former manifesting the potential coronavirus infection-promoting activities, which is consistent with the apparently higher male mortality across all age groups during the coronavirus pandemic.

## Results and Discussion

### **Gene set enrichment analyses (GSEA) of genomic features associated with the *ACE2* and *FURIN* genes**

One of the goals of this work was to identify human genes implicated in regulatory cross-talks affecting expression and functions of the *ACE2* and *FURIN* genes to build a model of genomic regulatory interactions potentially affecting the SCARS-CoV-2 coronavirus infection. To this end, GSEA were carried out using the *ACE2* and *FURIN* genes as baits applied to a broad spectrum of genomic databases reflecting the current state of knowledge regarding the structural, functional, regulatory, and pathophysiological features that could be statistically linked to these genes. Expression profiling experiments and GSEA revealed ubiquitous patterns of both *ACE2* and *FURIN* genes across human tissues (Supplemental Figure S1) with notable examples of high expression of the *FURIN* gene in the lung (second-ranked tissue in the GTEx database)

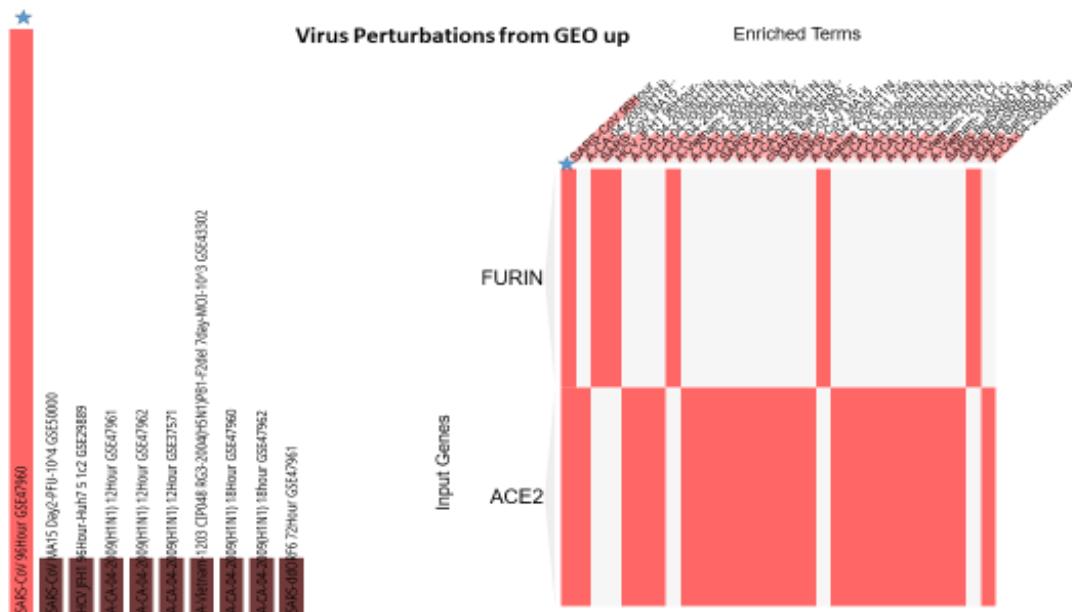
and testis being identified as the top-ranked *ACE2*-expressing tissue. In addition to the human lung tagged by the *ACE2* expression in the ACRHS4 Human Tissues database search, other noteworthy significantly enriched records are the Peripheral Blood Mononuclear Cells (PBMC), Natural Killer Cells and Macrophages tagged by the *FURIN* expression (Supplemental Figure S1).

GSEA of the virus perturbations' data sets among Gene Expression Omnibus (GEO) records of up-regulated genes identified the SARS-CoV challenge at 96 hrs (GSE47960) as the most significantly enriched record (Supplemental Figure S2) tagged by expression of both *ACE2* and *FURIN* in human airway epithelial cells. These observations suggest that coronavirus infection triggers the increased expression of both *ACE2* and *FURIN* genes 4 days after the initial encounter with host cells (Figure 1; Supplemental Figure S2). These findings were corroborated by the increased *FURIN* expression documented in the PBMC of patients with severe acute respiratory syndrome (Figure 1; Supplemental Figure S1; Reghunathan et al., 2005). It would be of interest to investigate whether this potentially infection-promoting effect on expression of the host genes in virus-targeted cells is mediated by the virus-induced release of the biologically-active molecules with the paracrine mode of actions such as interleukins and cytokines.

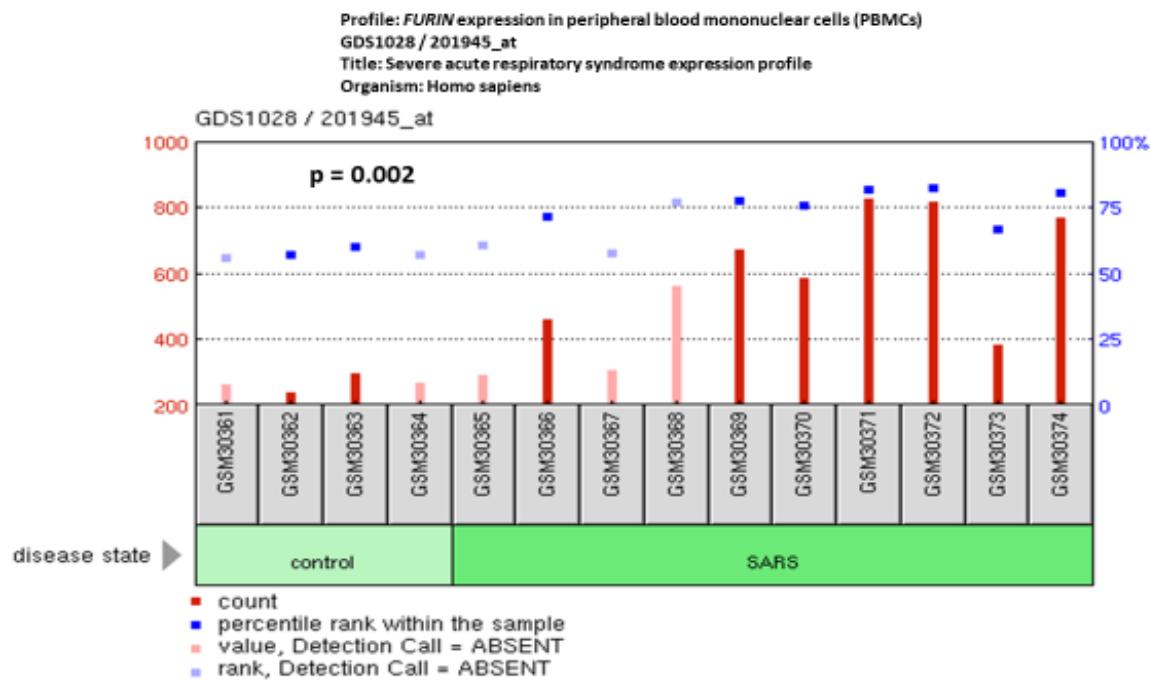
GSEA identified numerous significantly enriched records of common human disorders manifesting up-regulation of either *ACE* or *FURIN* genes (Supplemental Figure S3), which is consistent with the clinical observations that individuals with underlying health conditions are more likely to have clinically severe and lethal coronavirus infection. Similarly, exploration of the DisGeNET database of human disorders highlighted multiple disease states' records manifesting altered expression of either *ACE2* or *FURIN* genes (Supplemental Figure S3). Cigarette smoking appears to significantly increase the *ACE2* expression in human large airway

epithelial cells (Supplemental Figure S3), indicating that cigarette smoking should be considered as a potential coronavirus infection-promoting agent.

A



B



**Figure 1. Effects of viral challenges on expression of the *ACE2* and *FURIN* genes.**

- a. Gene Set Enrichment analyses of the Virus Perturbations from GEO focused on up-regulated genes.
- b. Increased *FURIN* expression in peripheral blood mononuclear cells (PBMC) of patients with Severe Acute Respiratory Syndrome (SARS).

Gene Ontology (GO) analyses revealed that *ACE2* and *FURIN* genes are associated with the largely non-overlapping records of GO Biological Processes, GO Molecular Functions, and GO Cellular Components (Supplemental Figure S4). The common significantly enriched records are Viral Life Cycle (GO Biological Process 2018); Peptidase activity (acting on L-amino acid peptides) and Endopeptidase activity (GO Molecular Function 2018); Membrane raft (GO Cellular Component 2018); Meprin A complex and Retrotransposon nucleocapsid (Jensen Compartments).

#### **Identifications of the enriched records of transcription factor-binding sites affecting the *ACE2* and *FURIN* expression**

GSEA of the enriched records of transcription factors' binding sites (TFBS) using ENCODE TF ChIP-seq 2015 and ChEA 2016 databases revealed predominantly distinct patterns of TFBS associated with the *ACE2* and *FURIN* genes (Supplemental Figure S5). Common TFBS shared by both *ACE2* and *FURIN* genes are *FOS*, *JUND*, *EP300* (ENCODE TF ChIP-seq 2015) and *GATA1*, *GATA2*, *RUNX1*, *FOXA1*, *HNF4A* (ChIP-seq 2015). Consistent with these findings, non-overlapping profiles of significantly enriched records associated with either *ACE2* or *FURIN* genes were observed of pathways (BioPlanet 2019 database), protein-protein interactions (PPI) hub proteins (PPI Hub Proteins database), and drugs affecting *ACE2* and *FURIN* expression (Drug Signatures Database, DSigDB), indicating that regulatory mechanisms governing the expression and activities of the *ACE2* and *FURIN* genes are predominantly discordant (Supplemental Figure S5).

Next, the Gene Expression Omnibus (GEO) database was interrogated to gauge the effects on *ACE2* and *FURIN* expression of transcription factors having TFBS associated with

their promoters. There are multiple relevant GEO records reporting the activation effects of the *JNK1/c-FOS* pathway on *ACE2* and *FURIN* expression as well as the activation effects of *FURIN* depletion on expression of the *Fos*, *Jun*, *Jund*, and *Junb* genes (Supplemental Figure S5). Conversely, *c-Jun* inhibition (effect of the dominant negative *c-Jun*) nor *c-Jun* depletion (*c-Jun* knockout) has resulted in decreased expression of the *FURIN* gene (Supplemental Figure S5). The summary of these observations is reported in the Figure 2.

Similarly, there are several reports indicating that deletion of either *Hnf4a* or *Runx1* in mouse cells and *RUNX1* in human cells decreases the *ACE2* and *FURIN* expression (Supplemental Figure S6). Conversely, *FURIN* depletion enhances expression of the *Runx1* and *Foxa1* genes in murine T cells (Supplemental Figure S6). In contrast, *FURIN* depletion decreases expression of the *Hnf4a* gene, while *Hnf4a* deletion decreases the *FURIN* gene expression (Supplemental Figure S6). The summary of these observations is reported in the Figure 2.

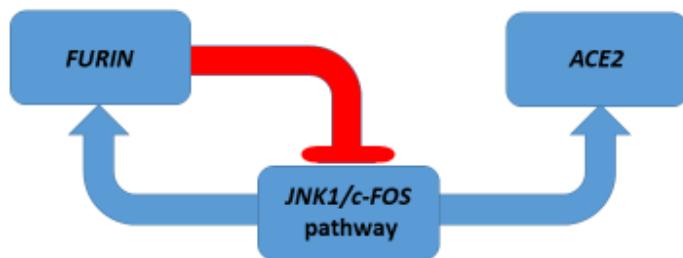
#### **Identification of the *VDR* and *HIF1a* genes as putative repressors of the *ACE2* expression**

Next GSEA of genomic databases were performed to identify the potential activators and repressors of the *ACE2* and *FURIN* genes. Analysis of the ARCHS4 transcription factors' co-expression database identified the *VDR* genes that co-expressed with both *ACE2* and *FURIN* genes in human tissues (Supplemental Figure S7). Other significantly enriched records manifest non-overlapping patterns of co-expression with either *ACE2* or *FURIN* genes. The GTEx expression profile of the *VDR* gene in human tissues revealed the ubiquitous pattern of expression and placed the *VDR* expression in human lungs in the top quartile (Supplemental Figure S7). Analysis of gene expression profiling experiments of wild type and vitamin D receptor (*Vdr*) knockout primary bone marrow-derived macrophages reported by Helming et al. (2005) demonstrate increased expression of the *ACE2* gene in the *VDR* knockout cells (Supplemental Figure S7) implicating the product of the *VDR* gene as the putative repressor of

the *ACE2* expression. Consistent with this hypothesis, Vitamin D appears to inhibit the *ACE2* expression in human bronchial smooth muscle cells (Supplemental Figure S7).

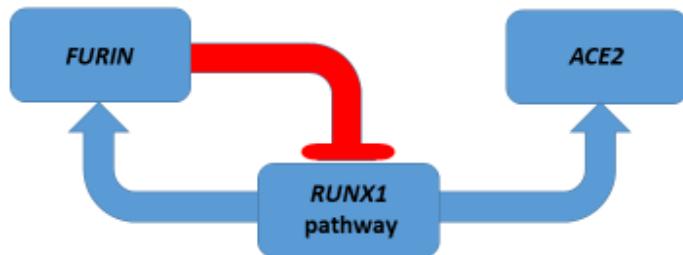
A

*JNK1/c-FOS* pathway-associated activation of the *ACE2* and *FURIN* expression may trigger the auto-regulatory negative feed-back loop of the *FURIN*-mediated repression of the expression of *JUN*, *JUNB*, *JUND*, and *c-FOS* genes



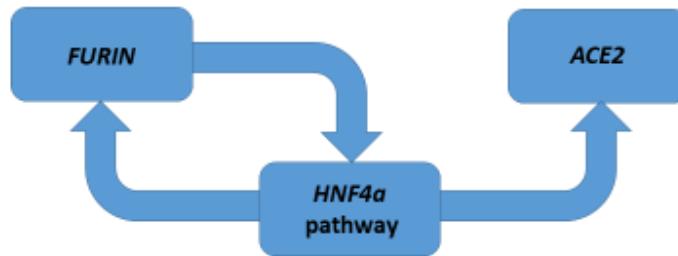
B

*RUNX1* pathway-associated activation of the *ACE2* and *FURIN* expression may trigger the auto-regulatory negative feed-back loop of the *FURIN*-mediated repression of the *RUNX1* gene expression



C

*HNF4a* pathway-associated activation of the *ACE2* and *FURIN* expression may trigger the auto-regulatory positive feed-back loop of the *FURIN*-mediated activation of the *HNF4a* expression



**Figure 2. Pathways and genes affecting the newly emerged SARS-CoV-2 virus-related host targets.**

- a. *JNK1/c-FOS* pathway-associated activation of the *ACE2* and *FURIN* expression may trigger the auto-regulatory negative feed-back loop of the *FURIN*-mediated repression of the expression of *JUN*, *JUNB*, *JUND*, and *c-FOS* genes.
- b. *RUNX1* pathway-associated activation of the *ACE2* and *FURIN* expression may trigger the auto-regulatory negative feed-back loop of the *FURIN*-mediated repression of the *RUNX1* gene expression
- c. *HNF4a* pathway-associated activation of the *ACE2* and *FURIN* expression may trigger the auto-regulatory positive feed-back loop of the *FURIN*-mediated activation of the *HNF4a* expression.

Notably, examinations of direct and reciprocal effects of the *VDR* gene and Vitamin D administration on expression of the *JNK1/c-FOS* pathway genes revealed the expression profiles consistent with the potential therapeutic utility of the Vitamin D administration and activation of the *VDR* gene expression (Supplemental Figure S7). Analyses of direct and reciprocal effects of the *VDR* gene and Vitamin D administration on the *HNF4a* expression revealed that *HNF4a* depletion in human and murine cells inhibits the *VDR* gene expression, while the *Vdr* gene depletion increases the *Hnf4a* expression (Supplemental Figure S7). These

result are consistent with the hypothesis stating that Vitamin D administration and activation of the *VDR* gene expression may have mitigating effects on the coronavirus infection. The summary of these findings is reported in the Figure 3.

GSEA of the Transcription Factor's Perturbations Followed by Expression database and GEO Gene Perturbations database focused on up-regulated genes identified *HIF1a* and *POU5F1* gene products as putative repressors of the *ACE2* and *FURIN* expression (Supplemental Figure S8). These findings were corroborated by observations that *HIF1a* overexpression in human embryonic kidney cells significantly inhibits the *ACE2* expression (Supplemental Figure S8). Notably, Vitamin D significantly increases expression of the *HIF1a* gene in human bronchial smooth muscle cells (Supplemental Figure S8), suggesting that *VDR* and *HIF1A* genes may cooperate as repressors of the *ACE2* expression.

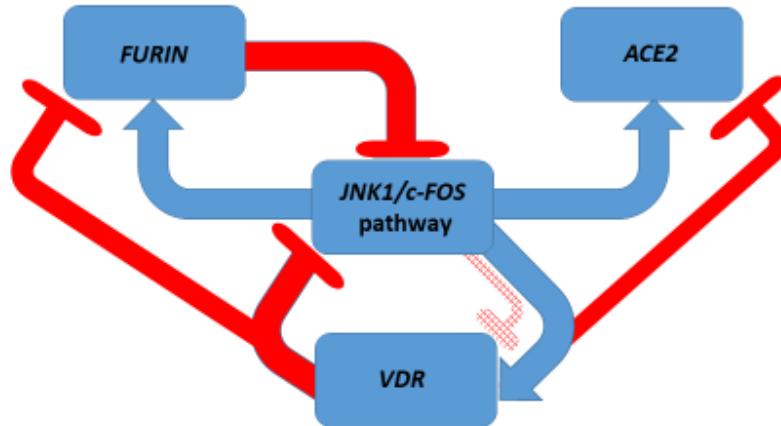
#### **GSEA identify Estradiol and Quercetin as putative candidate coronavirus infection mitigation agents.**

GSEA of the Drug Perturbations from GEO database focused on down-regulated genes identified Estradiol and Quercetin among the top significantly enriched records (Supplemental Figure S9). Estradiol appears to affect both *FURIN* and *ACE2* expression, while Quercetin seems to target the *ACE2* expression. Consistently, GSEA of the Ligand Perturbations from GEO focused on down-regulated genes identified five of Estradiol administration records (50%) among top ten significantly enriched ligand perturbations records (Supplemental Figure S9).

GSEA of the Drug Perturbations from GEO database focused on up-regulated genes indicated that doxorubicin, imatinib, and bleomycin may act as potential coronavirus infection-promoting agents (data not shown). Collectively, these observations provide the initial evidence supporting the hypothesis that both Estradiol and Quercetin may function as potential candidate coronavirus infection mitigation agents.

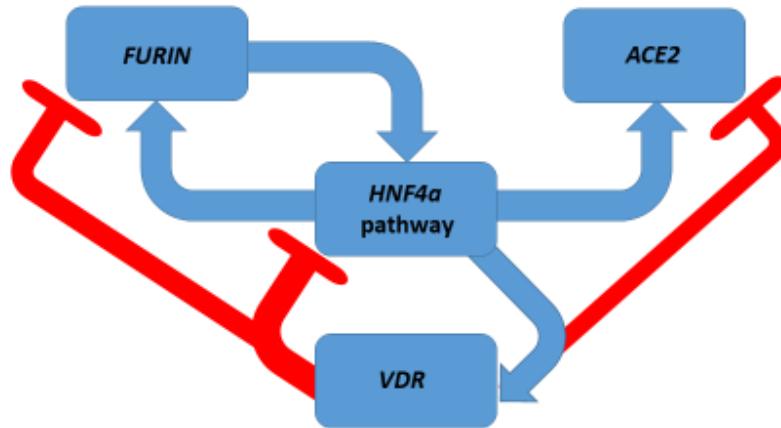
A

JNK1/c-FOS pathway-associated activation of the ACE2 and FURIN expression may trigger the auto-regulatory negative feed-back loop of the FURIN-mediated repression of the expression of JUN, JUNB, JUND, and c-FOS genes



B

HNF4a pathway-associated activation of the ACE2 and FURIN expression may trigger the auto-regulatory positive feed-back loop of the FURIN-mediated activation of the HNF4a expression



**Figure 3. Effects of the VDR gene and Vitamin D on pathways and genes affecting the newly emerged SARS-CoV-2 virus-related host targets.**

- JNK1/c-FOS pathway-associated activation of the ACE2 and FURIN expression may trigger the auto-regulatory negative feed-back loop of the FURIN-mediated repression of the expression of JUN, JUNB, JUND, and c-FOS genes.
- HNF4a pathway-associated activation of the ACE2 and FURIN expression may trigger the auto-regulatory positive feed-back loop of the FURIN-mediated activation of the HNF4a expression.

Consistent with this hypothesis, interrogation of the GEO records revealed that Quercetin appears to inhibit expression of several potential coronavirus infection-promoting genes: *c-FOS* expression in human and rat cells (Supplemental Figure S9); *Runx1* expression in rat cells (Supplemental Figure S9); *HNF4a* expression in human cells (Supplemental Figure S9). However, Quercetin administration appears to increase *c-Fos* expression in cultured rat cardiomyocytes (Supplementary Figure S9).

**Confirmation of the Estradiol and Quercetin activities as potential candidate coronavirus infection mitigation agents.**

Results of GSEA suggest that both Estradiol and Quercetin appear to exhibit biological activities consistent with the activity of medicinal compounds expected to mitigate the coronavirus infection. Next, manual curation of the GEO data sets has been carried out to identify further experimental evidence supporting this hypothesis. Administration of Estradiol appears to inhibit *ACE2* and/or *FURIN* expression in rat, mouse, and human cells (Supplemental Figure S10) and the effects of Estradiol seem to be mediated by the estrogen receptor beta. In agreement with the hypothesis on potential therapeutic utility of the Quercetin, administration of Quercetin has resulted in significantly decreased expression of the *ACE2* gene during differentiation of human intestinal cells (Supplemental Figure S10).

However, Estradiol administration appears to manifest the cell type-specific effects on *c-FOS* expression (Supplemental Figure S10). For example, it decreases the *c-FOS* expression in endometrium of *Macaca mulatta* while it increases *c-FOS* expression in the mouse uterus (Supplemental Figure S10). These observations indicate that any definitive conclusions regarding the potential clinical utility of identified herein potential coronavirus infection mitigating agents should be made only after appropriately designed and carefully executed preclinical studies and randomized clinical trials. In contrast to the Estradiol, which exhibit evidence of both putative coronavirus infection-mitigating actions and coronavirus infection-promoting activities,

administration of Testosterone appears to manifest more clearly-defined patterns of altered gene expression consistent with Testosterone being identified as the potential coronavirus infection-promoting agent (Supplemental Figure S11).

**Potential mechanisms affecting gene expression inferred from transgenic mouse models and observed in pathophysiologically and therapeutically relevant mouse and human cells.**

Taking into considerations that the effects of potential coronavirus infection mitigation agents often manifest cell type-specific patterns of gene expression changes, next the manual curation of the GEO gene expression profiles were carried out to identify the relevant host genetic targets and putative mitigation agents. These analyses identified several candidate repressors (*VDR*; *GATA5*; *SFTC*; *HIF1a*) and activators (*INSIG1*; *HMGA2*) of the *ACE2* and *FURIN* expression (Supplemental Figure S12). Notably, the effects on gene expression of the administration of either Vitamin D or Quercetin appear consistent with their definition as putative coronavirus infection mitigation agents (Supplemental Figure S12). The summary of these observations is presented in the Figure 4. The conclusion regarding the findings of cell type-specific effects on gene expression of putative coronavirus infection mitigating agents remains valid and examples of the potential negative effects of drugs on the *ACE2* expression are reported in the Supplemental Figure S12). For example, the *HIF1a* expression is significantly increased in murine alveolar type I cells deficient in sterol-response element-binding proteins inhibitor *Insig1* (Supplemental Figure S6). These data indicate that the *INSIG1* gene product, which appears to function as activator of the *ACE2* expression, may function as the inhibitor of the *HIF1a* expression, thus interfering with the *HIF1a*-mediated *ACE2* repression in specific cell types. Additional examples of the potential positive and negative effects on gene expression inferred from transgenic mouse models are reported in the Supplemental Figure S13.

## **Is Vitamin D deficiency a potential risk factor for increased disease severity in older adults and elderly individuals?**

Present analyses suggest that Vitamin D and vitamin D receptor (*VDR*) are putative mitigation factors of the coronavirus infection. Conversely, the Vitamin D deficiency could be a potential aggravating factor for the clinical course of pandemic. Multiple lines of evidence suggest that Vitamin D deficiency, particularly in elderly, might be a negative factor affecting the clinical course of the pandemic. In the United States, approximately 30% of whites and 5% of African Americans have sufficient Vitamin D level (Kannel et al., 2010) and the significant increase of the prevalence of individuals with severe Vitamin D deficiency has been reported (Ginde et al., 2009a). Age-associated decline of the human skin function to produce the Vitamin D in response to the sunlight exposure is likely a contributing factor to the Vitamin D deficiency in older individuals, since it has been reported that elderly people produce 75% less of cutaneous Vitamin D3 than young individuals (Lips, 2001). A meta-analysis of randomized controlled clinical trials indicated that intake of ordinary doses of Vitamin D was associated with significant decrease in total mortality rates (Autier and Gandini, 2007). A prospective study of the 3,408 older adults in the United States demonstrated that a group at high risk of all-cause mortality could be defined by the serum 25-hydroxyvitamin D [25(OH)D] level (Ginde et al., 2009b). A significant, independent, inverse association was observed between the serum 25(OH)D level and all-cause and cardiovascular diseases (CVD) mortality (Ginde et al., 2009b). To date, the vast majority of observational studies reported inverse associations between the circulating 25(OH)D concentration and all-cause mortality in generally healthy populations (Heath et al., 2019). In generally healthy adults over 50 years old, significant inverse associations were found between low 25(OH)D levels and all-cause mortality, respiratory and cardiovascular events, as well as markers relating to hip and non-vertebral fractures (Caristia et al., 2019). Therefore, it would be important to determine whether Vitamin D deficiency may be one of the risk factors

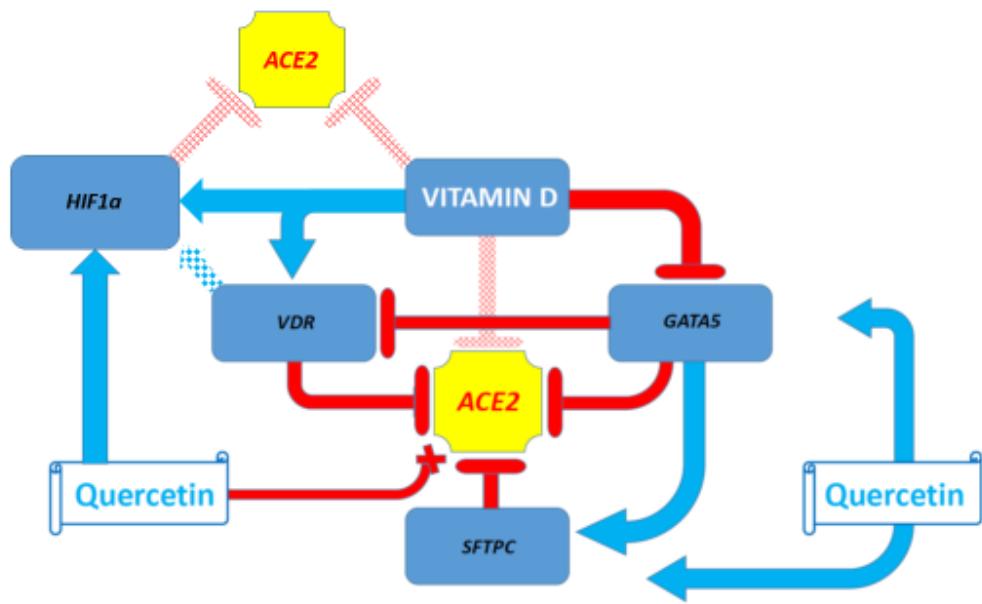
contributing to the increased disease severity in older adults and elderly individuals during coronavirus pandemic.

## Conclusion

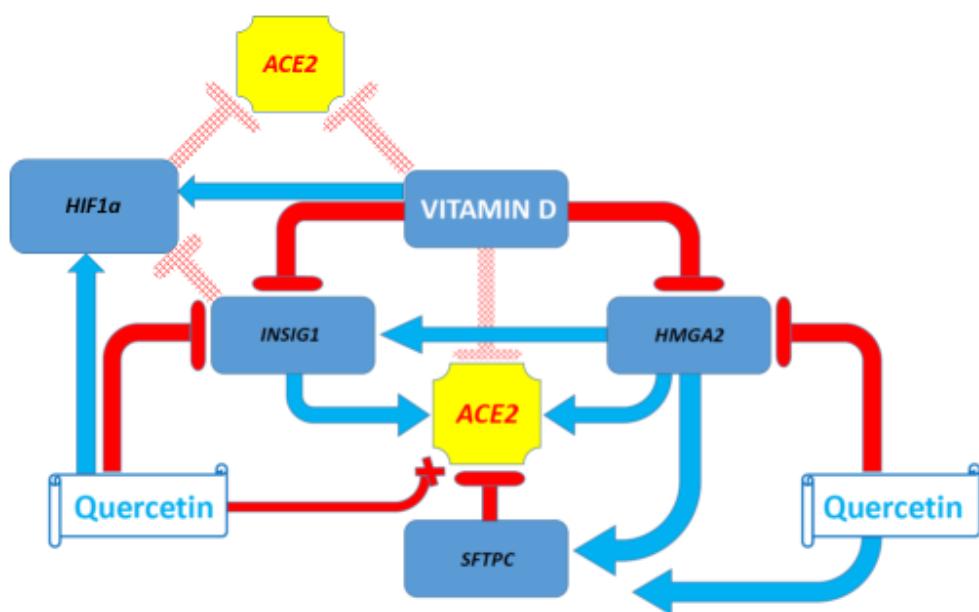
The main motivation of this work was to identify human genes implicated in regulatory cross-talks affecting expression and functions of the *ACE2* and *FURIN* genes to build a model of genomic regulatory interactions potentially affecting the SCARS-CoV-2 coronavirus infection. A panel of genes acting as activators and/or repressor of the *ACE2* and/or *FURIN* expression then could be employed to search for existing drugs and medicinal substances that, based on their mechanisms of activities, could be defined as the candidate coronavirus infection mitigation agents. After experimental and clinical validation, these existing drugs could be utilized to ameliorate the clinical severity of the pandemic. This knowledge could also be exploited in an ongoing effort to discover novel targeted therapeutics tailored to prevent the SCARS-CoV-2 infection and block the virus entry into human cells.

One of the important findings documented herein is that identified medicinal compounds with potential coronavirus infection-mitigating effects also appear to induce cell type-specific patterns of gene expression alterations. Therefore, based on all observations reported in this contribution, it has been concluded that any definitive recommendations regarding the potential clinical utility of identified herein putative coronavirus infection mitigating agents, namely Vitamin D and Quercetin, should be made only after preclinical studies and randomized clinical trials have been appropriately designed, carefully executed, and the desired outcomes have been reached.

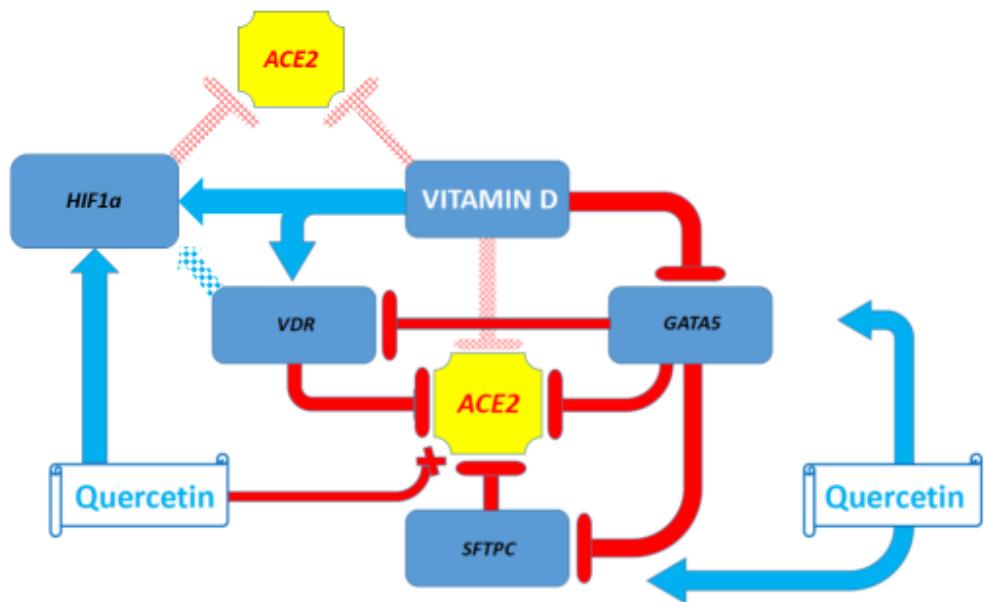
A



B

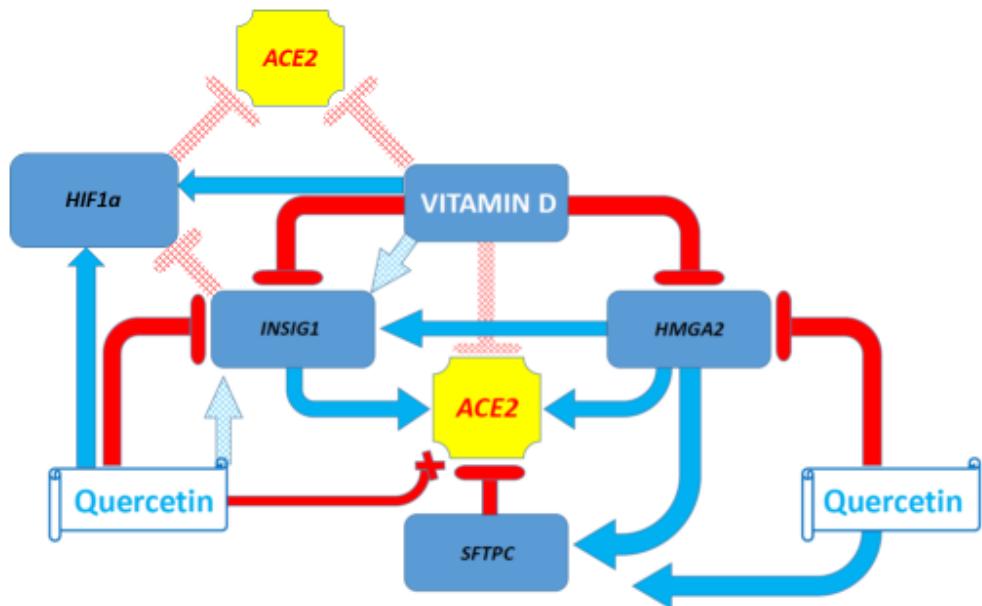


C



*GATA5 inhibits SFTPC expression in the mouse lungs*

D



*Vitamin D enhances INSIG1 expression in human bronchial smooth muscle cells*

*Quercetin enhances INSIG1 expression in human intestinal cells*

**Figure 4. Effects of the *VDR* gene, Vitamin D, and Quercetin on pathways and genes affecting the newly emerged SARS-CoV-2 virus-related host targets.**

- Effects of the *VDR* gene, Vitamin D, and Quercetin on repressors of the *ACE* expression.
- Effects of the *VDR* gene, Vitamin D, and Quercetin on activators of the *ACE* expression.

- c. Effects of the *VDR* gene, Vitamin D, and Quercetin on repressors of the *ACE* expression reflecting *GATA5* inhibitory effects on *SFTPC* expression in the mouse lungs.
- d. Effects of the *VDR* gene, Vitamin D, and Quercetin on activators of the *ACE* expression reflecting the cell type-specific effects of Vitamin D and Quercetin: Vitamin D-induced activation of the *INS/G1* expression in human bronchial smooth muscle cells and Quercetin-induced activation of the *INS/G1* expression in human intestinal cells.

Most recently, a super-computer modeling study using the world's most powerful supercomputer, SUMMIT, identified several candidate small molecule drugs which bind to either the isolated the SCARS-CoV-2 Viral S-protein at its host receptor region or to the S protein-human ACE2 interface (Smith and Smith, 2020). Interestingly, in this study Quercetin was identified among top 5 scoring ligands for viral S-protein-human ACE2 receptor interface. Thus, Quercetin appears also a potentially promising therapeutic molecule that may directly interfere with the binding of the SCARS-CoV-2 virus to human cells. Previously reported experiments demonstrated that Quercetin appears to inhibit the SARS-CoV virus entry into host cells (Yi et al., 2004). Since the SCARS-CoV-2 virus utilizes for the entry in human cells the same receptor (ACE2) and the accessory protease FURIN as the SARS-CoV coronavirus (Wells et al., 2020), these observations suggest that Quercetin may, indeed, possess antiviral activity against the SARS-CoV-2 as well.

It has been observed that administration of Testosterone appears to manifest clearly-defined patterns of altered gene expression consistent with Testosterone being identified as the potential coronavirus infection-promoting agent, particularly in some cell types that may play a role in the virus entry into human body and the respiratory system (Supplemental Figure S11). This is in contrast to Estradiol, which seems to manifest cell type-specific effects on gene expression consistent with either infection-inhibiting or infection-promoting patterns of gene expression changes. It would be of interest to determine whether this discordant effects may contribute to the apparently higher mortality among men with coronavirus infection.

Present analyses highlighted the major uncertainty regarding the outcomes of the current pandemic associated with the potential of the SCARS-CoV-2 virus for the expansion of the cellular tropism (Walls et al., 2020) based on access to genetically vulnerable host cells due to nearly ubiquitous expression of the *ACE2* and *FURIN* genes in the human body. Particularly dangerous seems noted in this contribution the potential ability of the SCARS-CoV-2 virus to infect the immune cells. Taken together with predominantly cell type-specific patterns of expression of genetic repressors and activators of the *ACE2* and *FURIN* expression it may complicate the development of universally effective therapeutics. The availability of many genetically-relevant transgenic mouse models, in particular, the *Furin* null mice, should be regarded as a considerable advantage for preclinical development of drug candidates tailored to target the coronavirus infection. Specifically, the potential therapeutic utility of the highly selective ( $K_i$ , 600 pm) intrinsically-specific FURIN inhibitor (a1-antitrypsin Portland (a1-PDX); Jean et al., 1998) should be tested in the immediate future.

## Methods

### Data source and analytical protocols

All data analyzed in this study were obtained from the publicly available sources. Gene set enrichment analyses (GSEA) were carried-out using the Enrichr bioinformatics platform, which enables the interrogation of nearly 200,000 gene sets from more than 100 gene set libraries. The Enrichr API (January 2020 through March 2020 releases) (Chen et al., 2013; Kuleshov et al., 2016) was used to test genes linked to the *ACE2* and *FURIN* genes (or other genes of interest) for significant enrichment in numerous functional categories. In all tables and plots (unless stated otherwise), in addition to the nominal p values and adjusted p values, the “combined score” calculated by Enrichr is reported, which is a product of the significance estimate and the magnitude of enrichment (combined score  $c = \log(p) * z$ , where  $p$  is the

Fisher's exact test p-value and z is the z-score deviation from the expected rank). Validation of the GSEA findings were carried-out employing the computational retrievals and manual curations of the gene expression profiles of the Gene Expression Omnibus (GEO) database.

### **Statistical Analyses of the Publicly Available Datasets**

All statistical analyses of the publicly available genomic datasets, including error rate estimates, background and technical noise measurements and filtering, feature peak calling, feature selection, assignments of genomic coordinates to the corresponding builds of the reference human genome, and data visualization, were performed exactly as reported in the original publications (Glinsky, 2015-2020; Glinsky and Barakat, 2019; Glinsky et al., 2019; Guffanti et al., 2018) and associated references linked to the corresponding data visualization tracks (<http://genome.ucsc.edu>). Any modifications or new elements of statistical analyses are described in the corresponding sections of the Results. Statistical significance of the Pearson correlation coefficients was determined using GraphPad Prism version 6.00 software. Both nominal and Bonferroni adjusted p values were estimated. The statistical significance between the mean values was estimated using the Student T-test. The significance of the differences in the numbers of events between the groups was calculated using two-sided Fisher's exact and Chi-square test, and the significance of the overlap between the events was determined using the hypergeometric distribution test (Tavazoie et al., 1999).

### **Supplemental Information**

Supplemental information includes Supplemental Figures S1-S13. Supplemental information is available upon request.

### **Author Contributions**

This is a single author contribution. All elements of this work, including the conception of ideas, formulation, and development of concepts, execution of experiments, analysis of data, and writing of the paper, were performed by the author.

## **Acknowledgements**

This work was made possible by the open public access policies of major grant funding agencies and international genomic databases and the willingness of many investigators worldwide to share their primary research data. This work was supported in part by the OncoScar, Inc.

## **References**

- Autier P, Gandini S. Vitamin D supplementation and total mortality: a meta-analysis of randomized controlled trials. *Arch Intern Med.* 2007; 167: 1730-1737.
- Caristia S, Filigheddu N, Barone-Adesi F, Sarro A, Testa T, Magnani C, Aimaretti G, Faggiano F, Marzullo P. Vitamin D as a biomarker of ill health among the over-50s: A systematic review of cohort studies. *Nutrients.* 2019; 11. pii: E2384. doi: 10.3390/nu11102384.
- Chen EY, Tan CM, Kou Y, Duan Q, Wang Z, Meirelles GV, Clark NR, Ma'ayan A. 2013. Enrichr: interactive and collaborative HTML5 gene list enrichment analysis tool. *BMC Bioinformatics* 14, 128. doi: 10.1186/1471-2105-14-128.
- Ginde AA, Liu MC, Camargo CA Jr. Demographic differences and trends of vitamin D insufficiency in the US population, 1988-2004. *Arch Intern Med.* 2009a; 169: 626-632.
- Ginde AA, Scragg R, Schwartz RS, Camargo CA Jr. Prospective study of serum 25-hydroxyvitamin d level, cardiovascular disease mortality, and all-cause mortality in older U.S. Adults. *J Am Geriatr Soc.* 2009b; 57: 1595-1603.
- Glinsky GV. 2015. Transposable elements and DNA methylation create in embryonic stem cells human-specific regulatory sequences associated with distal enhancers and non-coding RNAs. *Genome Biol Evol* 7: 1432-1454.

Glinsky GV. 2016. Mechanistically distinct pathways of divergent regulatory DNA creation contribute to evolution of human-specific genomic regulatory networks driving phenotypic divergence of *Homo sapiens*. *Genome Biol Evol* 8:2774-88.

Glinsky GV. 2016. Activation of endogenous human stem cell-associated retroviruses (SCARs) and therapy-resistant phenotypes of malignant tumors. *Cancer Lett* 376:347-359.

Glinsky GV. 2016. Single cell genomics reveals activation signatures of endogenous SCAR's networks in aneuploid human embryos and clinically intractable malignant tumors. *Cancer Lett* 381:176-93.

Glinsky GV. 2017. Human-specific features of pluripotency regulatory networks link NANOG with fetal and adult brain development. *BioRxiv*.

<https://www.biorxiv.org/content/early/2017/06/19/022913>; doi: <https://doi.org/10.1101/022913>.

Glinsky GV. 2018. Contribution of transposable elements and distal enhancers to evolution of human-specific features of interphase chromatin architecture in embryonic stem cells. *Chromosome Res.* 2018. 26: 61-84.

Glinsky G, Durruthy-Durruthy J, Wossidlo M, Grow EJ, Weirather JL, Au KF, Wysocka J, Sebastian V. 2018. Single cell expression analysis of primate-specific retroviruses-derived HPAT lincRNAs in viable human blastocysts identifies embryonic cells co-expressing genetic markers of multiple lineages. *Helicon* 4: e00667. doi: 10.1016/j.heliyon.2018.e00667. eCollection 2018 Jun. PMID: 30003161.

Glinsky GV, Barakat TS. 2019. The evolution of Great Apes has shaped the functional enhancers' landscape in human embryonic stem cells. 37:101456. PMID: 31100635. DOI: 10.1016/j.scr.2019.101456

Glinsky GV. 2020. A catalogue of 59,732 human-specific regulatory sequences reveals unique to human regulatory patterns associated with virus-interacting proteins, pluripotency and brain development. *DNA and Cell Biology*, 2020; 39: 126-143. doi: 10.1089/dna.2019.4988.

Guffanti G, Bartlett A, Klengel T, Klengel C, Hunter R, Glinsky G, Macciardi F. 2018. Novel bioinformatics approach identifies transcriptional profiles of lineage-specific transposable elements at distinct loci in the human dorsolateral prefrontal cortex. *Mol Biol Evol*. 35: 2435-2453. PMID: 30053206. PMCID: PMC6188555. DOI: 10.1093/molbev/msy143.

Heath, AK, Kim IY, Hodge AM, English DR, and Muller, DC. Vitamin D status and mortality: A systematic review of observational studies. *Int. J. Environ. Res. Public Health* 2019, 16, 383; doi:10.3390/ijerph16030383.

Helming L, Böse J, Ehrchen J, Schiebe S, Frahm T, Geffers R, Probst-Kepper M, Balling R, Lengeling A. 1alpha,25-Dihydroxyvitamin D3 is a potent suppressor of interferon gamma-mediated macrophage activation. *Blood*. 2005; 106: 4351-8.

Kennel KA, Drake MT, Hurley DL. Vitamin D deficiency in adults: when to test and how to treat. *Mayo Clin Proc*. 2010; 85: 752-7.

Kuleshov MV, Jones MR, Rouillard AD, Fernandez NF, Duan Q, Wang Z, Koplev S, Jenkins SL, Jagodnik KM, Lachmann A, McDermott MG, Monteiro CD, Gundersen GW, Ma'ayan A. Enrichr: a comprehensive gene set enrichment analysis web server 2016 update. *Nucleic Acids Research*. 2016; gkw377.

Lips P. Vitamin D deficiency and secondary hyperparathyroidism in the elderly: consequences for bone loss and fractures and therapeutic implications. *Endocr Rev*. 2001; 22: 477-501.

Reghunathan R, Jayapal M, Hsu LY, Chng HH, Tai D, Leung BP, Melendez AJ. Expression profile of immune response genes in patients with Severe Acute Respiratory Syndrome. *BMC Immunol.* 2005; 6:2.

Shang J, Ye G, Shi K, Wan Y, Luo C, Aihara H, Geng Q, Auerbach A, Li F. Structural basis of receptor recognition by SARS-CoV-2. *Nature.* 2020. doi: 10.1038/s41586-020-2179-y. Online ahead of print. PMID: 32225175

Smith M, Smith JC. Repurposing Therapeutics for COVID-19: Supercomputer-Based Docking to the SARS-CoV-2 Viral Spike Protein and Viral Spike Protein-Human ACE2 Interface. *ChemRxiv.* 2020. Preprint. <https://doi.org/10.26434/chemrxiv.11871402.v3>

Tavazoie, S., Hughes, J.D., Campbell, M.J., Cho, R.J., and Church, GM. Systematic determination of genetic network architecture. *Nat Genet* 1999; 22, 281–285.

Walls AC, Park YJ, Tortorici MA, Wall A, McGuire AT, Veesler D. Structure, function, and antigenicity of the SARS-CoV-2 spike glycoprotein. *Cell.* 2020. pii: S0092-8674(20)30262-2. doi: 10.1016/j.cell.2020.02.058. [Epub ahead of print]

Yi L, Li Z, Yuan K, Qu X, Chen J, Wang G, Zhang H, Luo H, Zhu L, Jiang P, Chen L, Shen Y, Luo M, Zuo G, Hu J, Duan D, Nie Y, Shi X, Wang W, Han Y, Li T, Liu Y, Ding M, Deng H, Xu X. Small molecules blocking the entry of severe acute respiratory syndrome coronavirus into host cells. *J Virol.* 2004; 78: 11334-9.

Yan R, Zhang Y, Li Y, Xia L, Guo Y, Zhou Q. Structural basis for the recognition of SARS-CoV-2 by full-length human ACE2. *Science.* 2020; 367: 1444-1448. doi: 10.1126/science.abb2762. Epub 2020 Mar 4. PMID: 32132184

Zhou, P., Yang, X.L., Wang, X.G., Hu, B., Zhang, L., Zhang, W., Si, H.R., Zhu, Y., Li, B., Huang, C.L., et al. (2020). A pneumonia outbreak associated with a new coronavirus of probable bat origin. *Nature*. Published online February 3, 2020. <https://doi.org/10.1038/s41586-020-2012-7>.

Zhu, N., Zhang, D., Wang, W., Li, X., Yang, B., Song, J., Zhao, X., Huang, B., Shi, W., Lu, R., et al. (2020). A Novel Coronavirus from Patients with Pneumonia in China, 2019. *N Engl J Med*. 382, 727–733.

Harnessing powers of genomics to build molecular maps... (673.73 KiB)

[view on ChemRxiv](#)

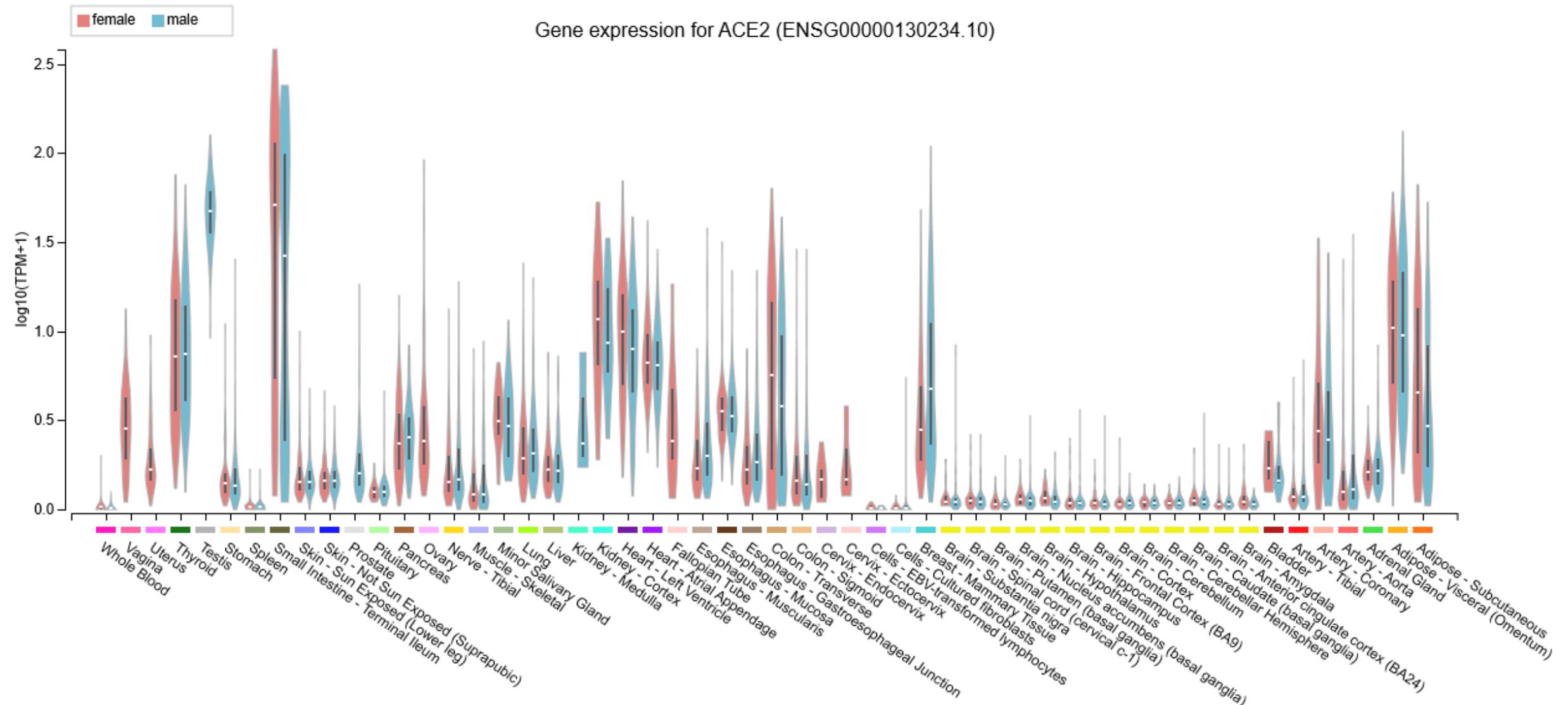
• [download file](#)

---

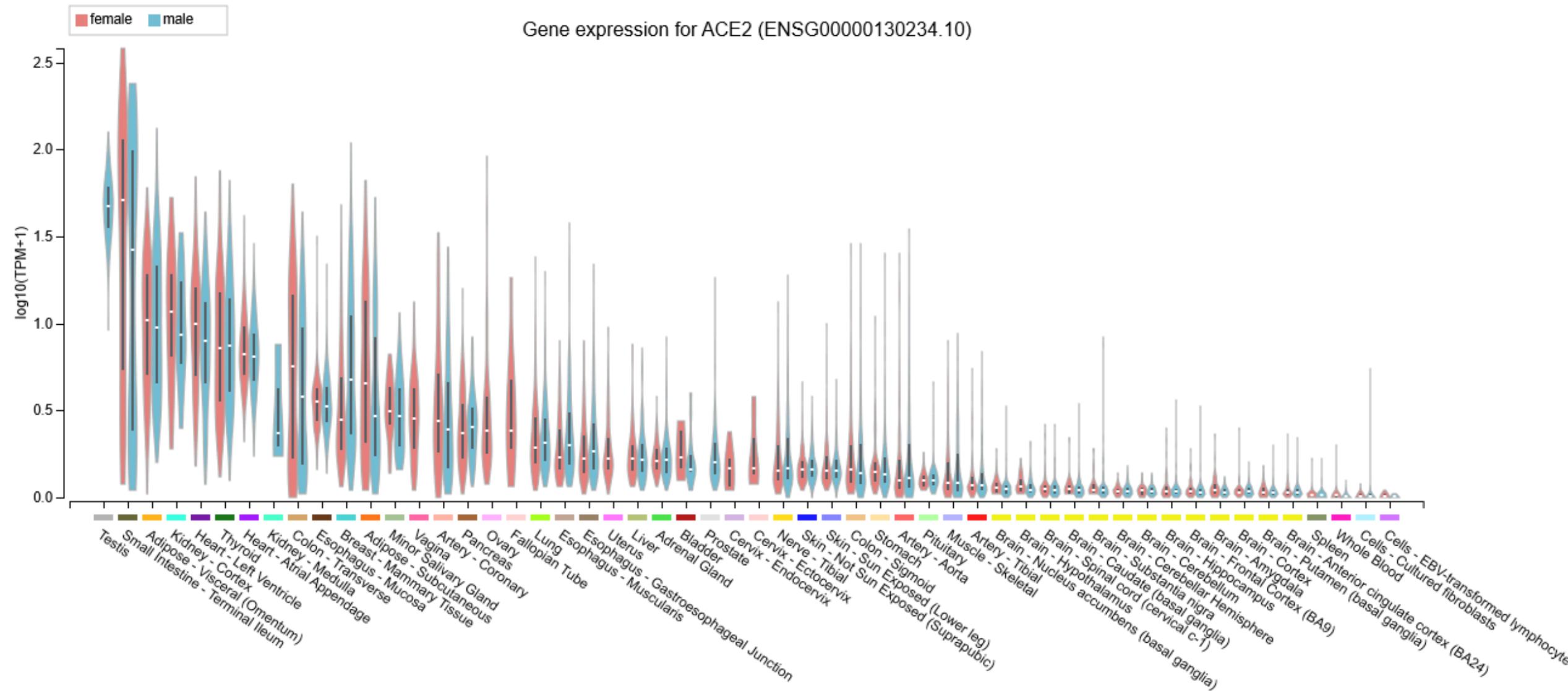
# ACE2 and FURIN

Supplemental Figure S1. Expression in human cells, tissues, and organs

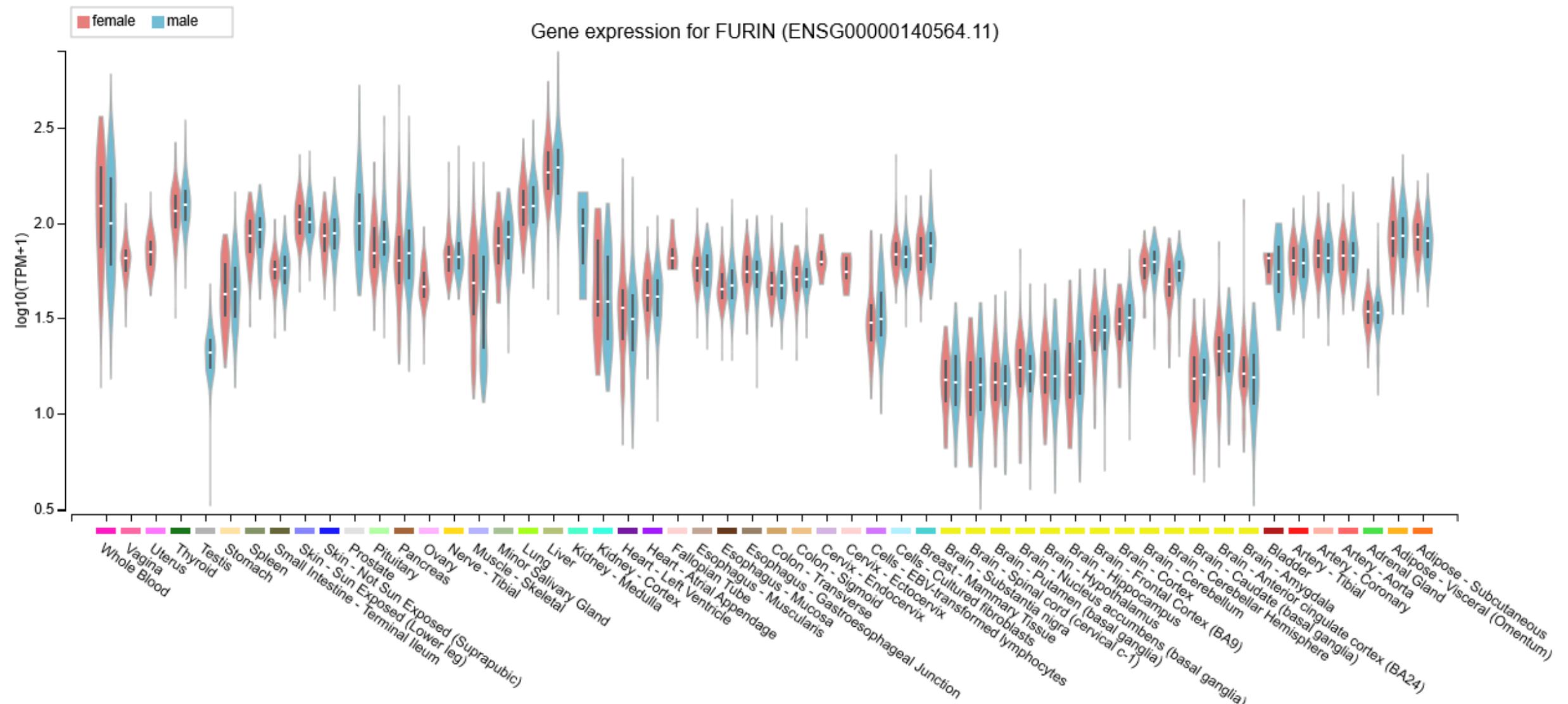
RNA-Seq Expression Data from GTEx (53 Tissues, 570 Donors)



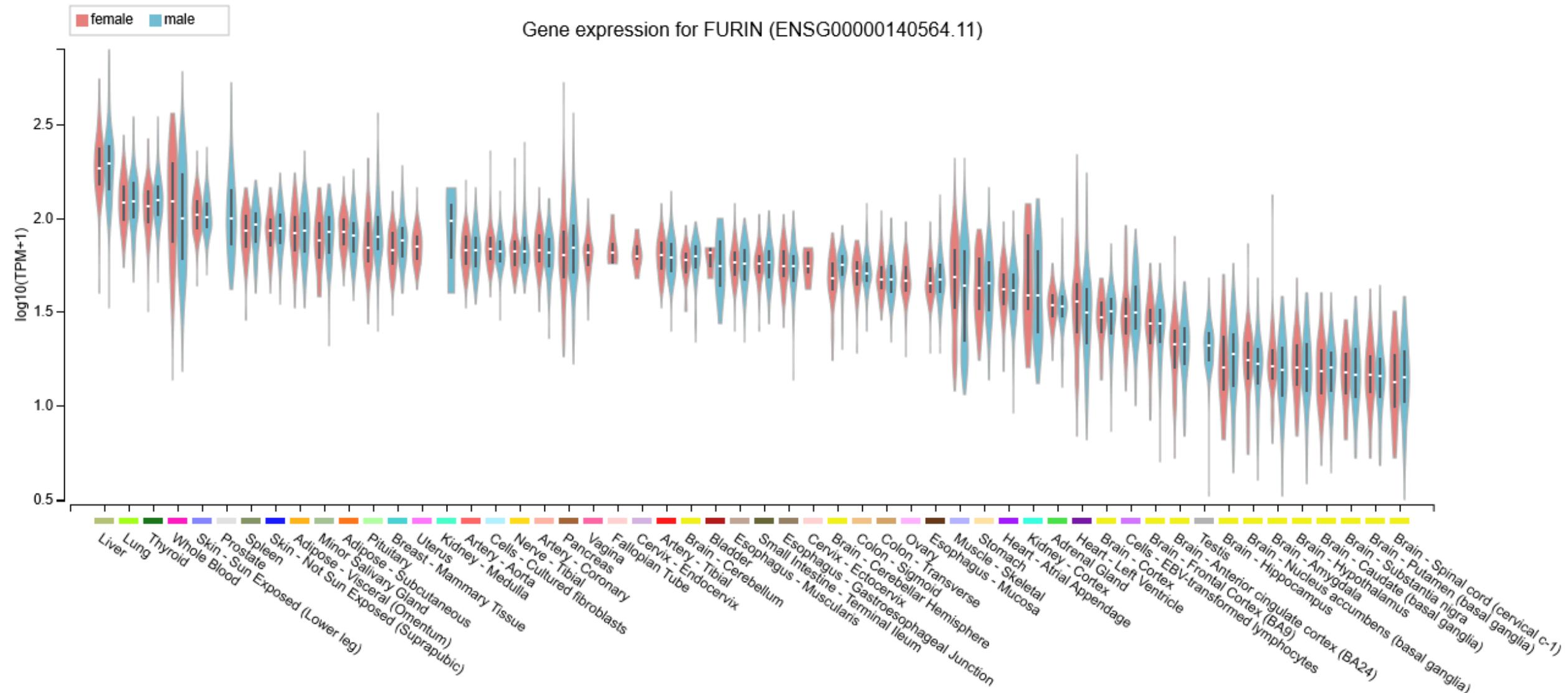
RNA-Seq Expression Data from GTEx (53 Tissues, 570 Donors)

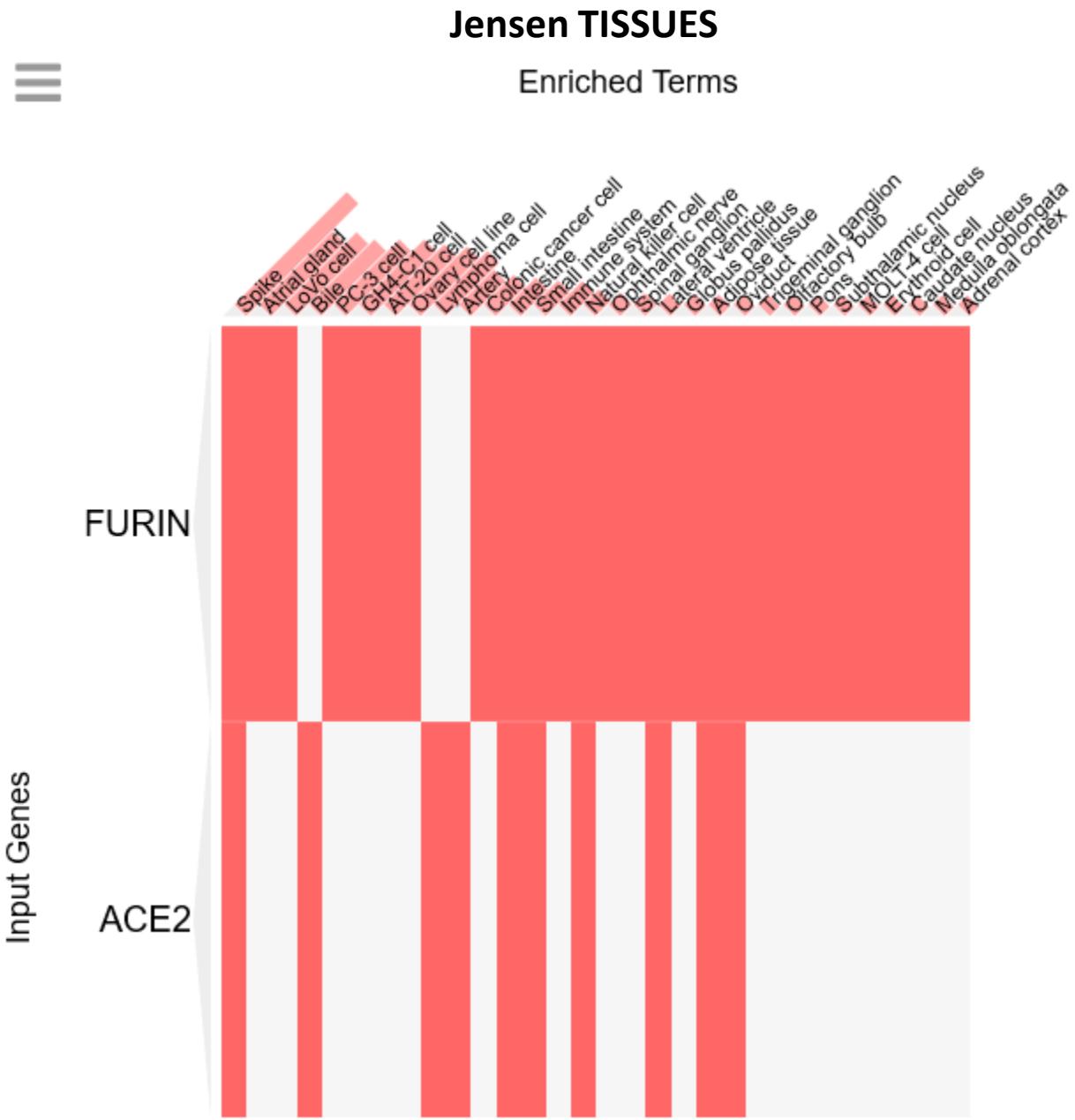


RNA-Seq Expression Data from GTEx (53 Tissues, 570 Donors)



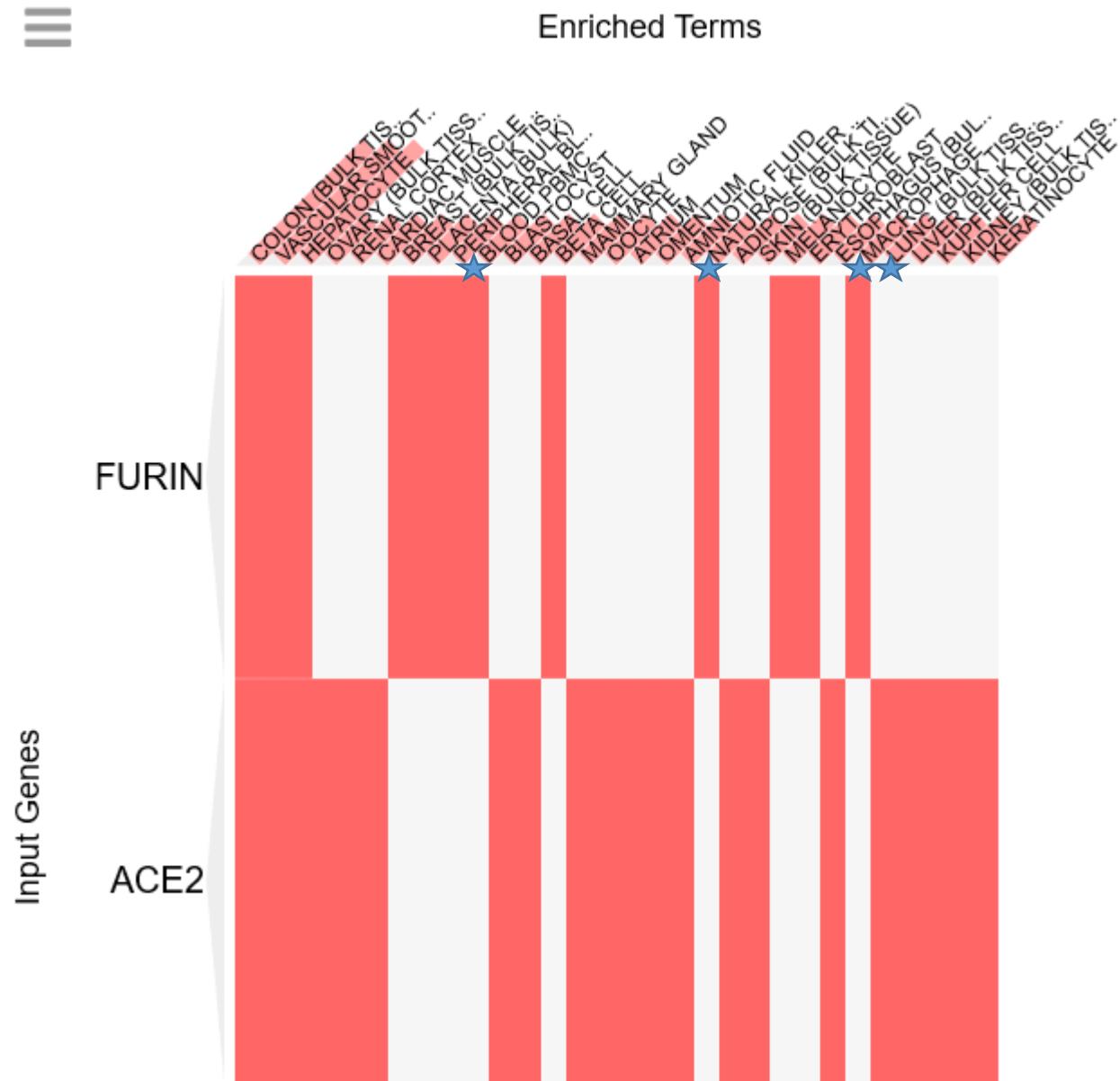
## RNA-Seq Expression Data from GTEx (53 Tissues, 570 Donors)





## ARCHS4 Human Tissues

## Enriched Terms



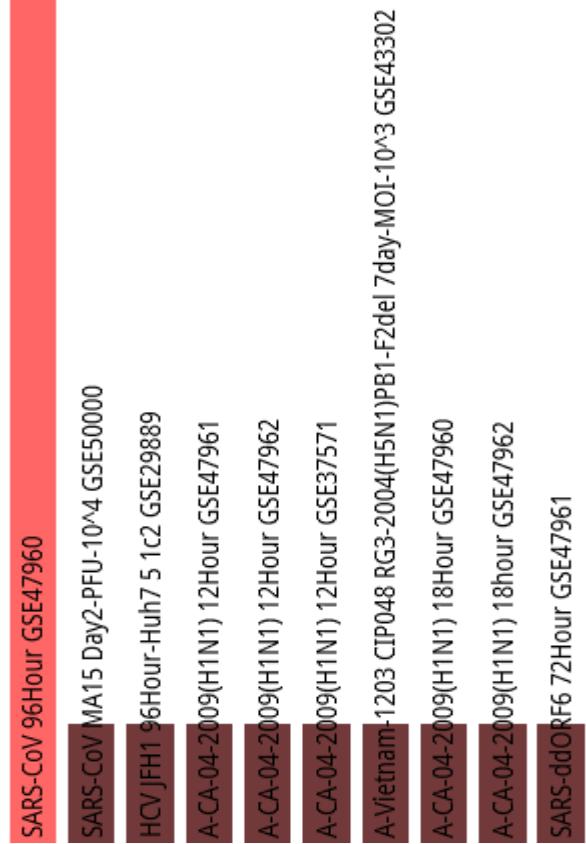
# ACE2 and FURIN

Supplemental Figure S2. Effects of viral challenges on expression

## Virus Perturbations from GEO up

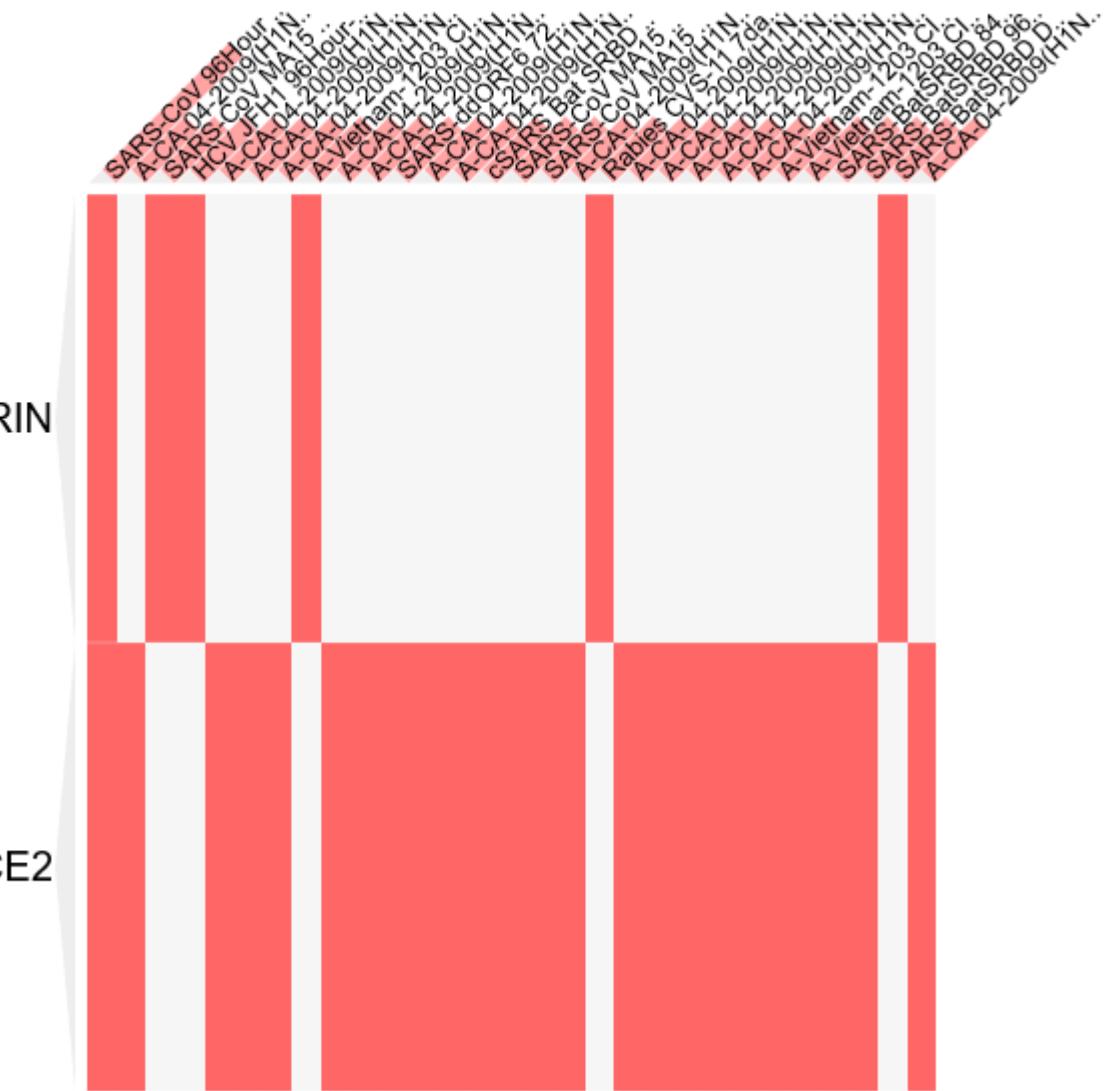


Enriched Terms



Input Genes

FURIN  
ACE2



Profile: *FURIN* expression in peripheral blood mononuclear cells (PBMCs)

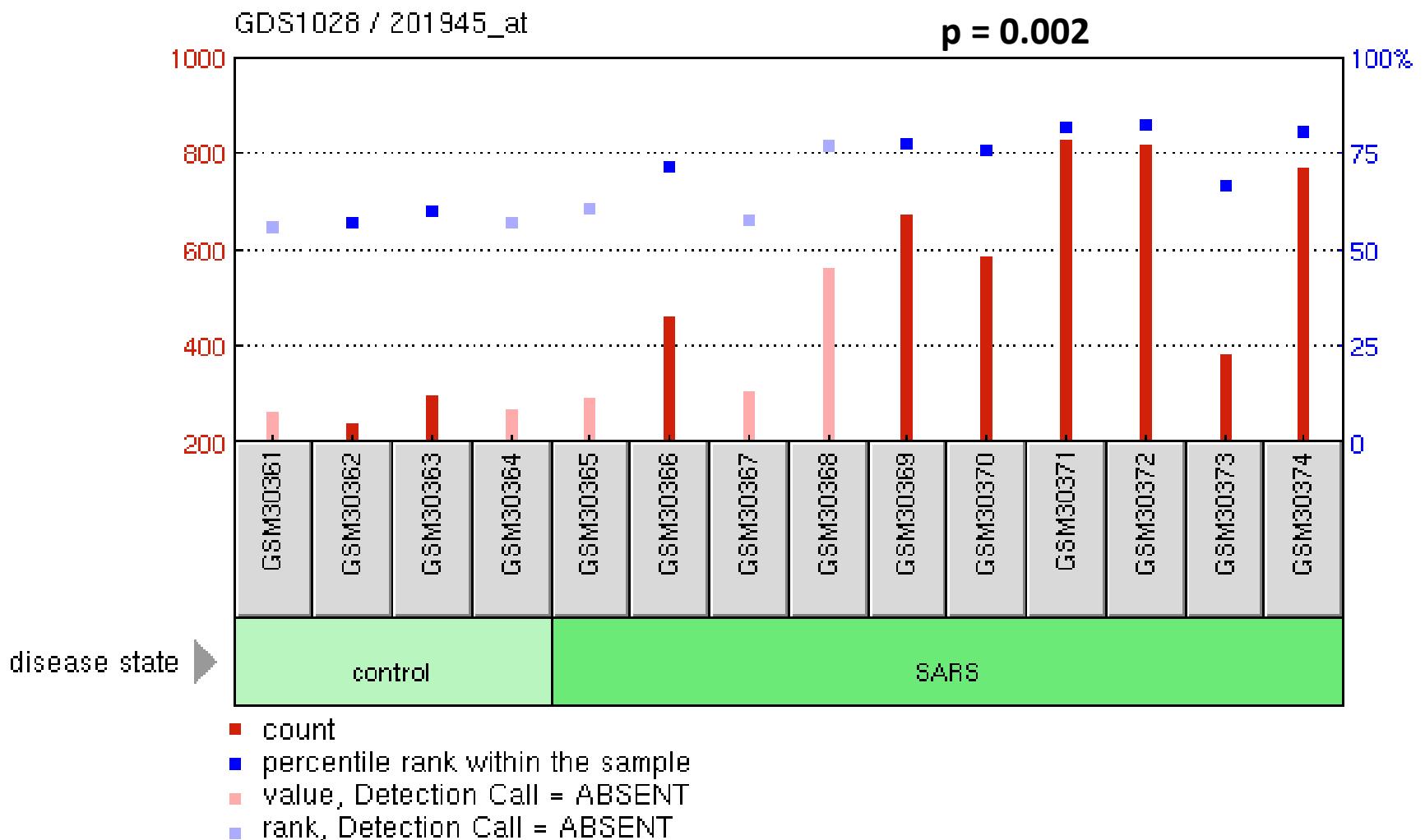
GDS1028 / 201945\_at

Title

Severe acute respiratory syndrome expression profile

Organism

Homo sapiens



***FURIN* expression in peripheral blood mononuclear cells (PBMCs)**

Sample	Title	Value
<a href="#">GSM30361</a>	N1	264.2
<a href="#">GSM30362</a>	N2	241.7
<a href="#">GSM30363</a>	N3	298.1
<a href="#">GSM30364</a>	N4	268.5
<a href="#">GSM30365</a>	S1	295.5
<a href="#">GSM30366</a>	S2	464
<a href="#">GSM30367</a>	S3	309.7
<a href="#">GSM30368</a>	S4	564.1
<a href="#">GSM30369</a>	S5	674.4
<a href="#">GSM30370</a>	S6	588
<a href="#">GSM30371</a>	S7	830.2
<a href="#">GSM30372</a>	S8	818.8
<a href="#">GSM30373</a>	S9	385.1
<a href="#">GSM30374</a>	S10	771.2

# ACE2 and FURIN

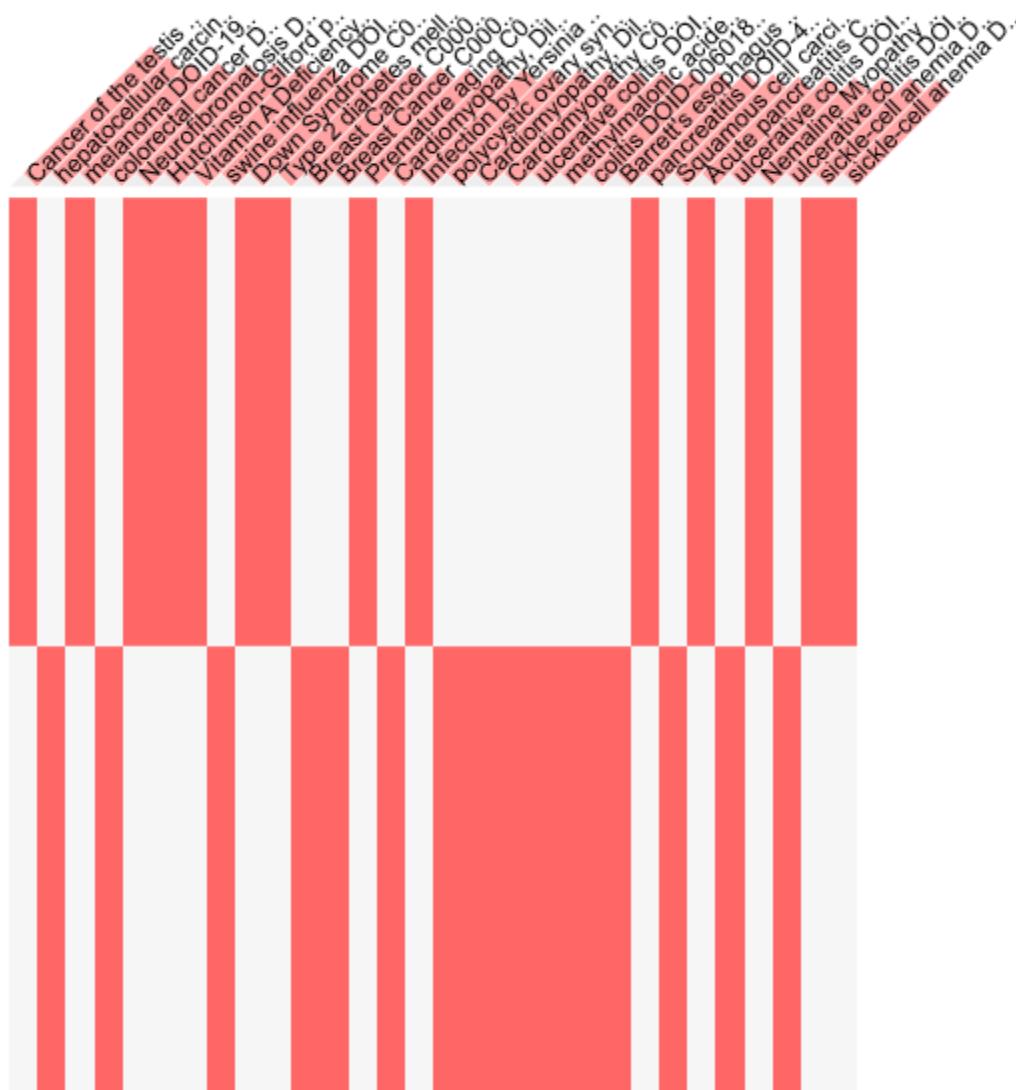
Supplemental Figure S3. Effects of common human diseases on expression changes

## Disease Perturbations from GEO up

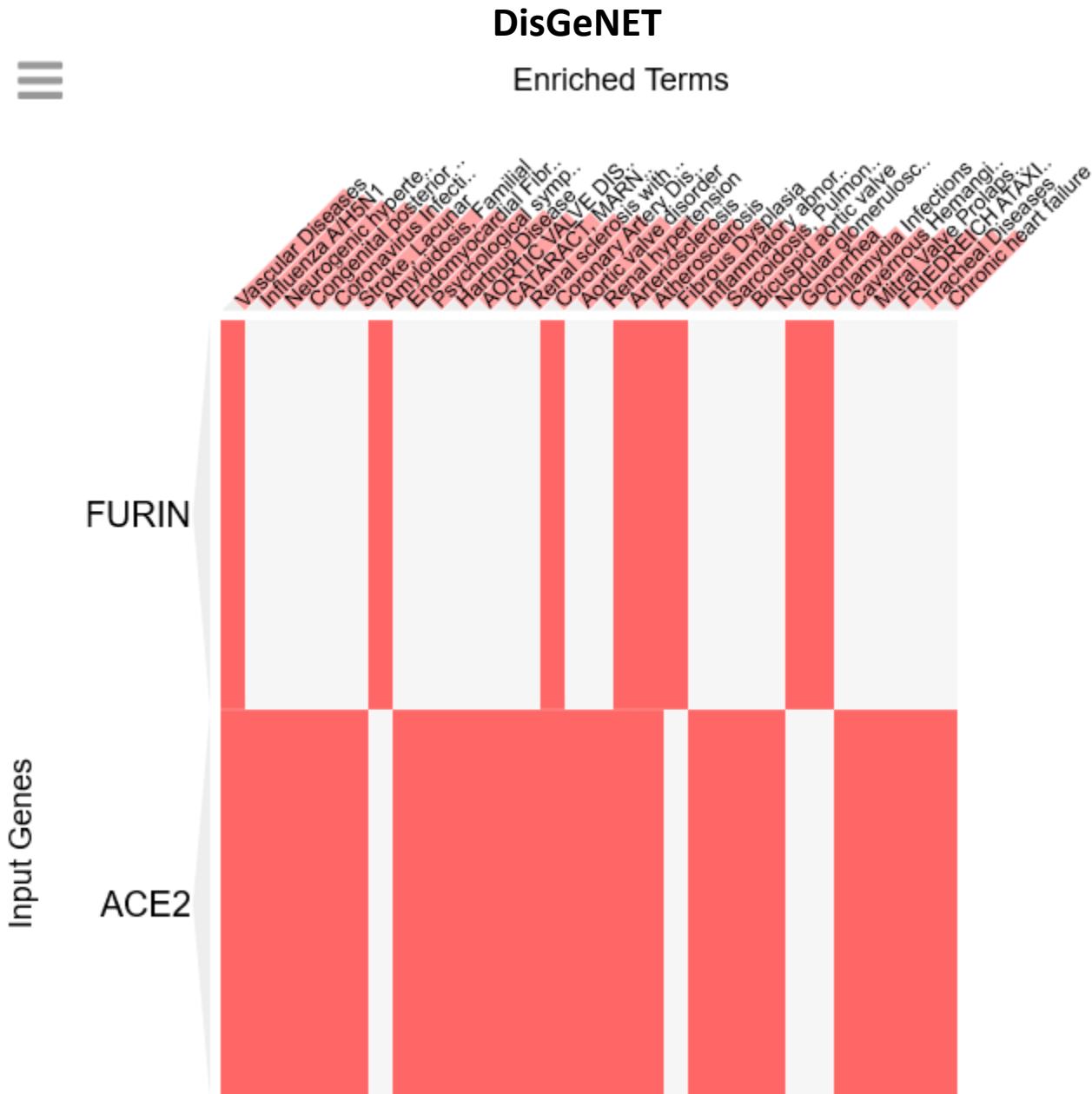


### Enriched Terms

Input Genes  
FURIN  
ACE2



# Distinct patterns of diseases associated with expression changes of the ACE2 and FURIN genes



# Profile: ACE2 expression

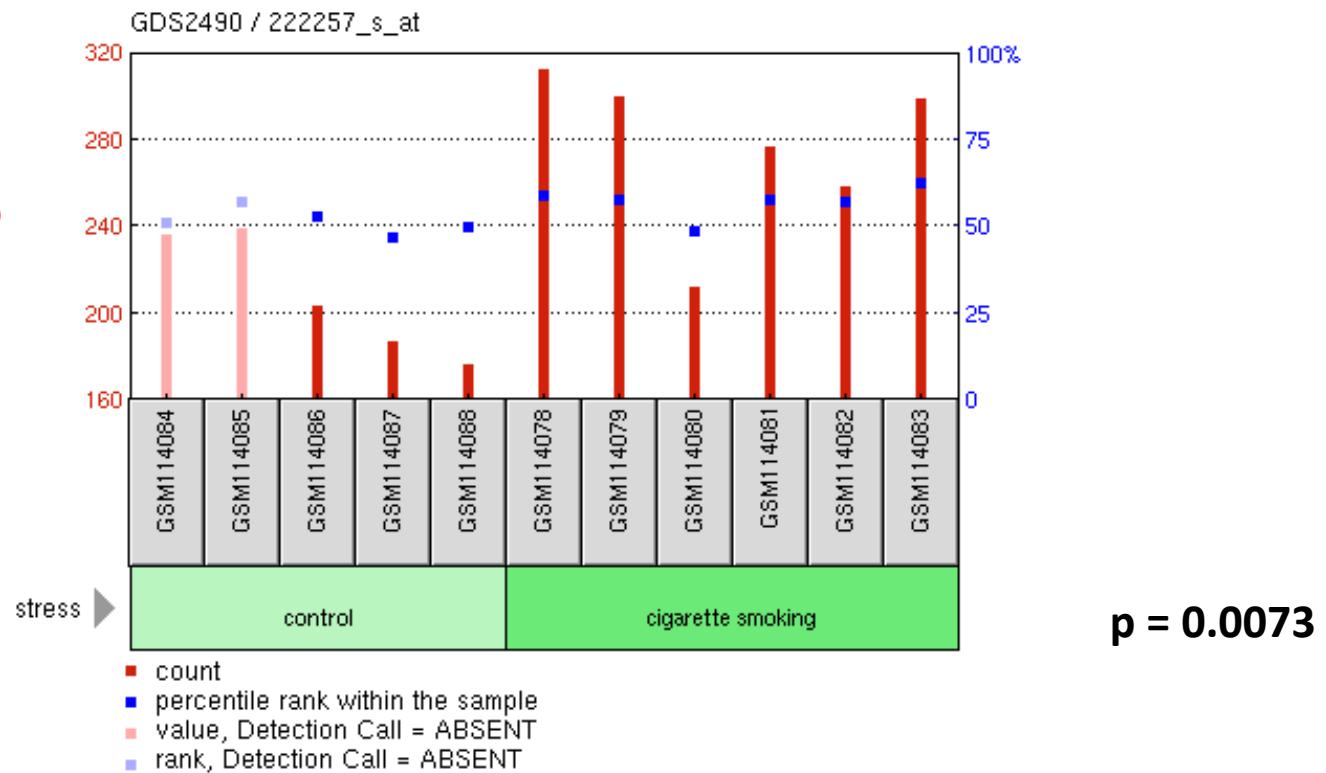
GDS2490 / 222257\_s\_at

## Title

Large airway epithelium response to cigarette smoking (HG-133A)

## Organism

Homo sapiens



Sample	Title	Value
<a href="#">GSM114084</a>	large airways, non-smoker 1, MAS5	236.4
<a href="#">GSM114085</a>	large airways, non-smoker 2, MAS5	239.9
<a href="#">GSM114086</a>	large airways, non-smoker 3, MAS5	203.8
<a href="#">GSM114087</a>	large airways, non-smoker 4, MAS5	187.6
<a href="#">GSM114088</a>	large airways, non-smoker 5, MAS5	176.5
<a href="#">GSM114078</a>	large airways, smoker 1, MAS5	313.1
<a href="#">GSM114079</a>	large airways, smoker 2, MAS5	300.5
<a href="#">GSM114080</a>	large airways, smoker 3, MAS5	212.8
<a href="#">GSM114081</a>	large airways, smoker 4, MAS5	277.3
<a href="#">GSM114082</a>	large airways, smoker 5, MAS5	258.6
<a href="#">GSM114083</a>	large airways, smoker 6, MAS5	299.2

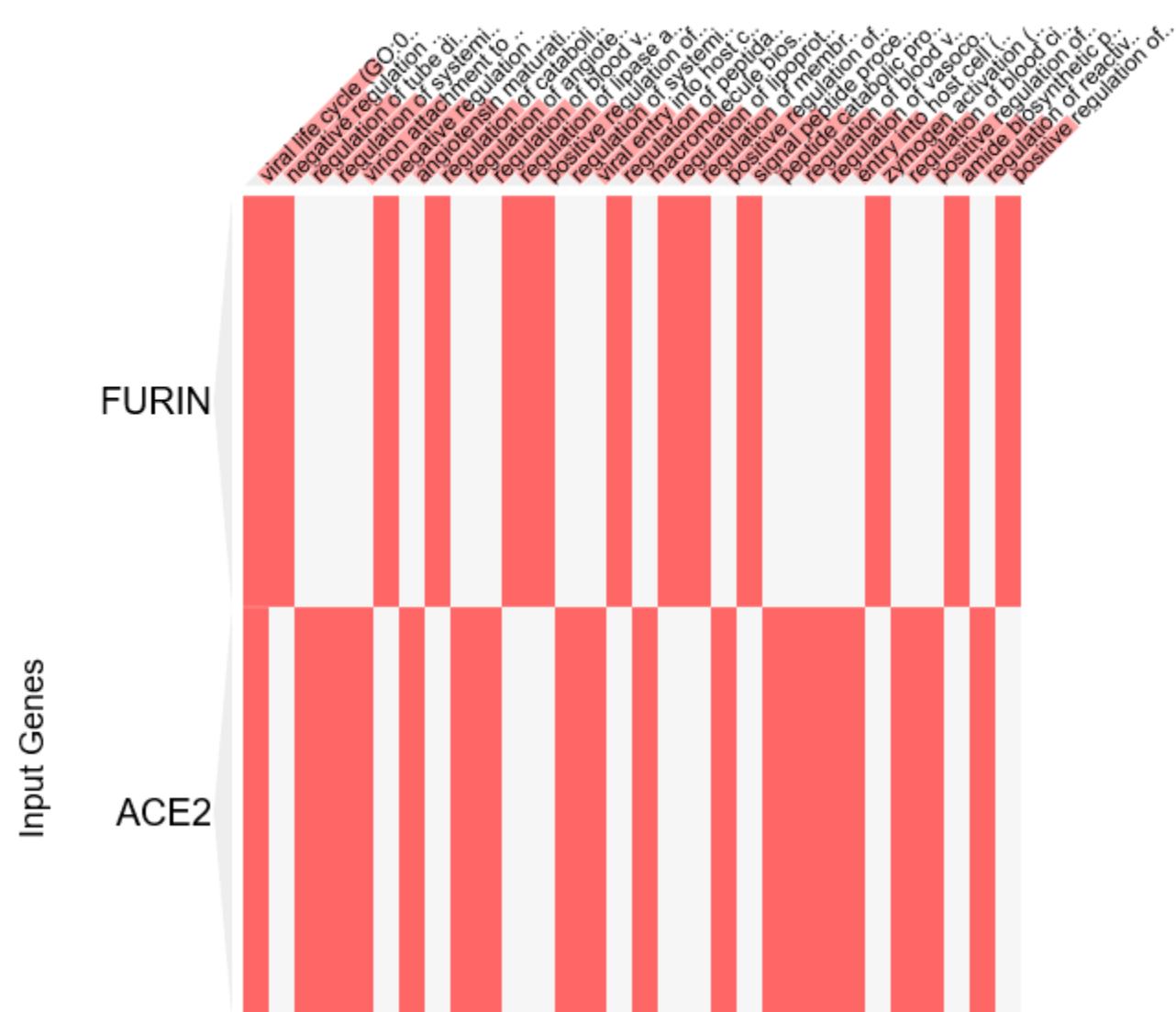
# ACE2 and FURIN

Supplemental Figure S4. Gene ontology (GO) analyses

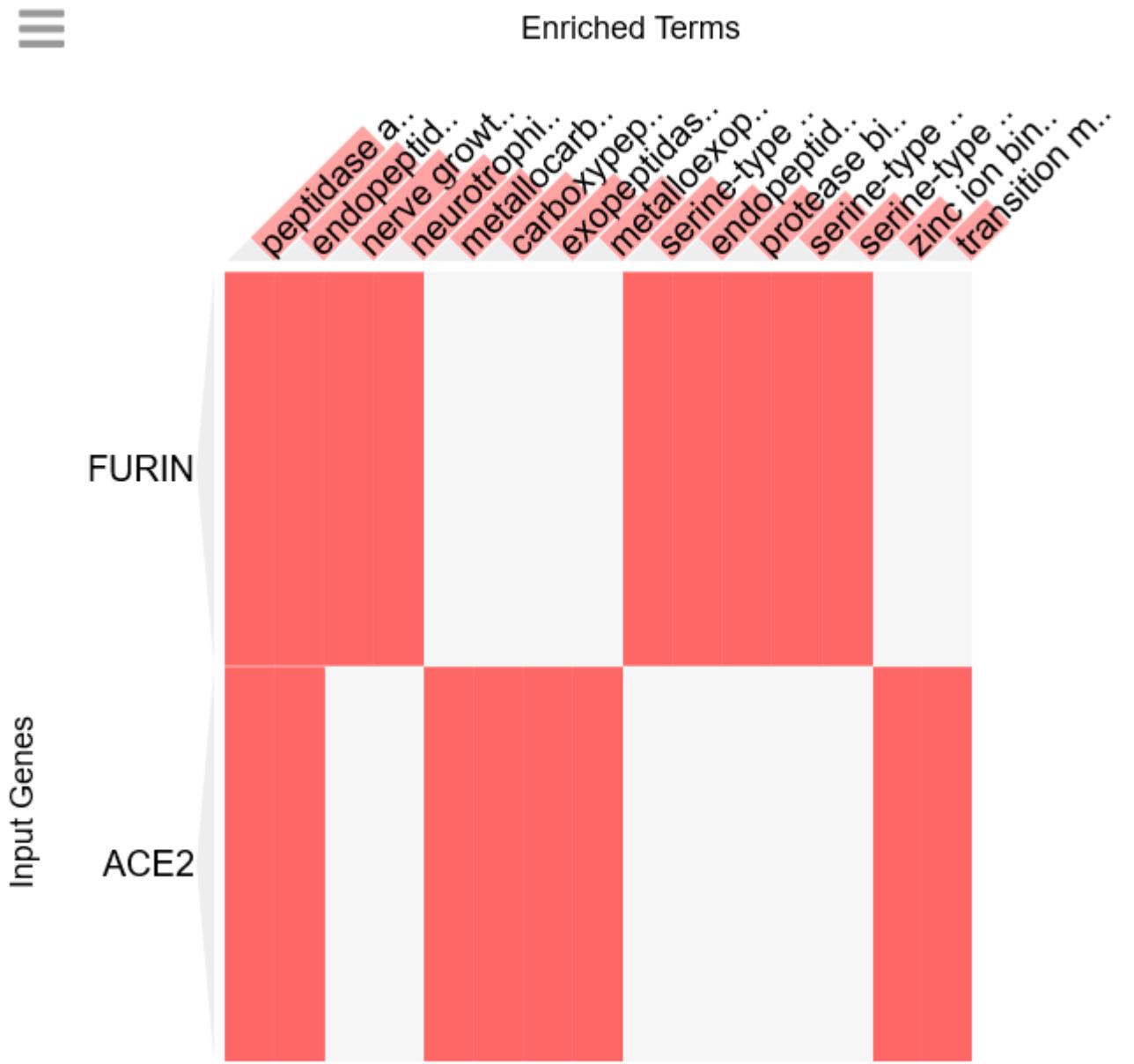
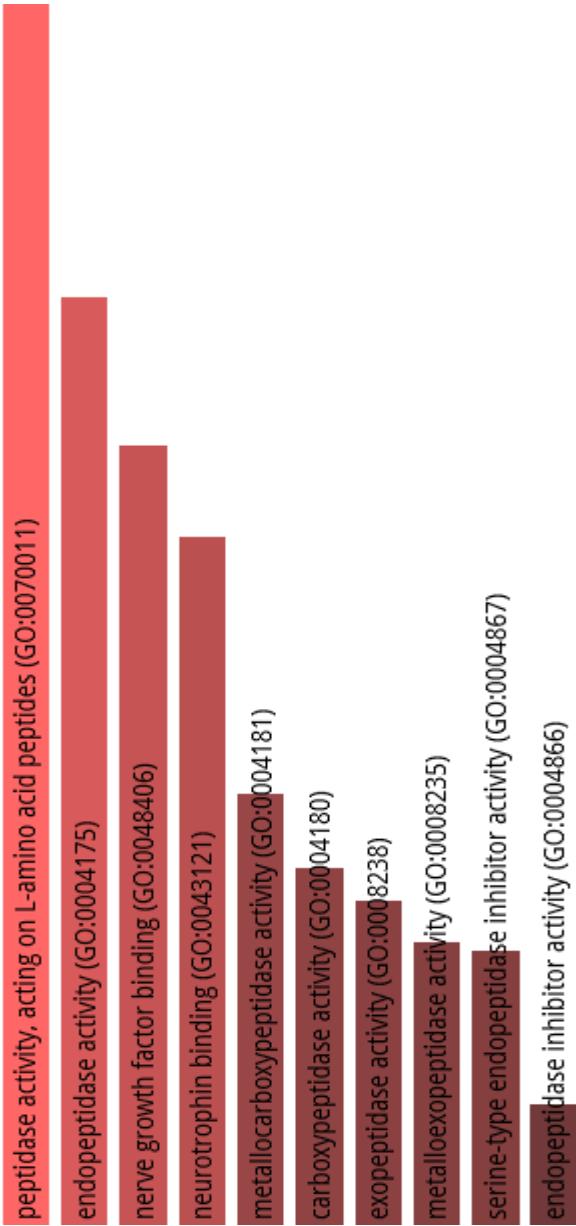
## GO Biological Process 2018



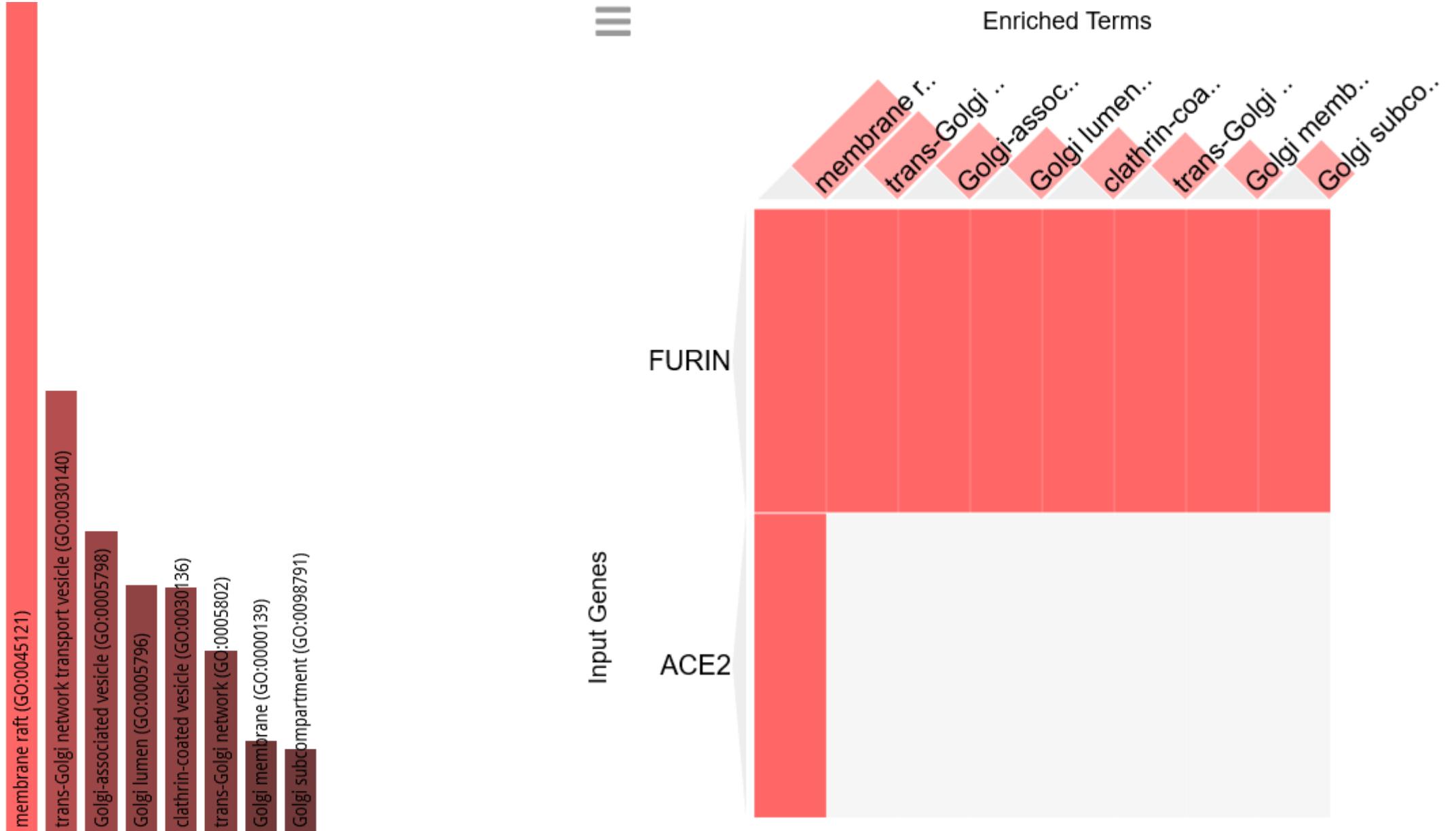
### Enriched Terms



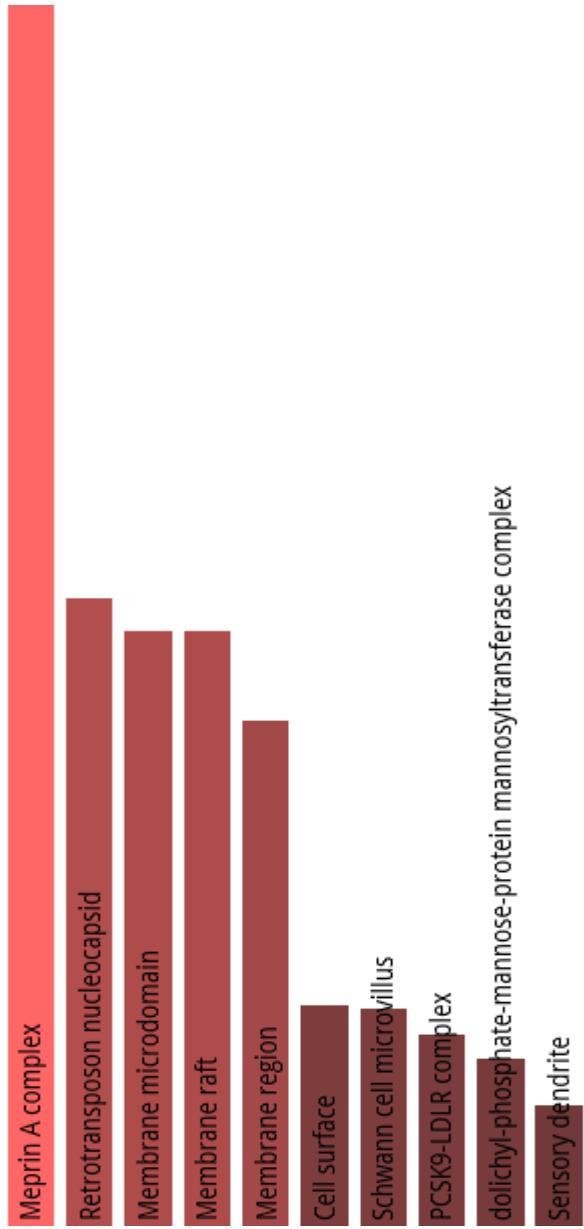
## GO Molecular Function 2018



## GO Cellular Component 2018



# Jensen COMPARTMENTS



## Enriched Terms

Meprin A complex  
Retrotransposon nucleocapsid  
Membrane microdomain  
Membrane raft  
Membrane region  
Schwann cell microvillus  
PCSK9-LDLR complex  
dolichyl-phosphate-mannose-protein mannosyltransferase complex  
Sensory dendrite  
Viral assembly network t.  
RBL2 complex  
Apical complex  
Whole membrane  
Sertoli envelope  
Mating ring envelope  
Amino acid transport.  
F1F0 complex  
Mannosyltransferase  
Weber-Lumen  
EGD coat  
Cortical granule  
Goldberg cisterna  
GARP complex  
Neurofibrillary tangle  
Dendritic branch

FURIN

Input Genes

ACE2

# ACE2 and FURIN

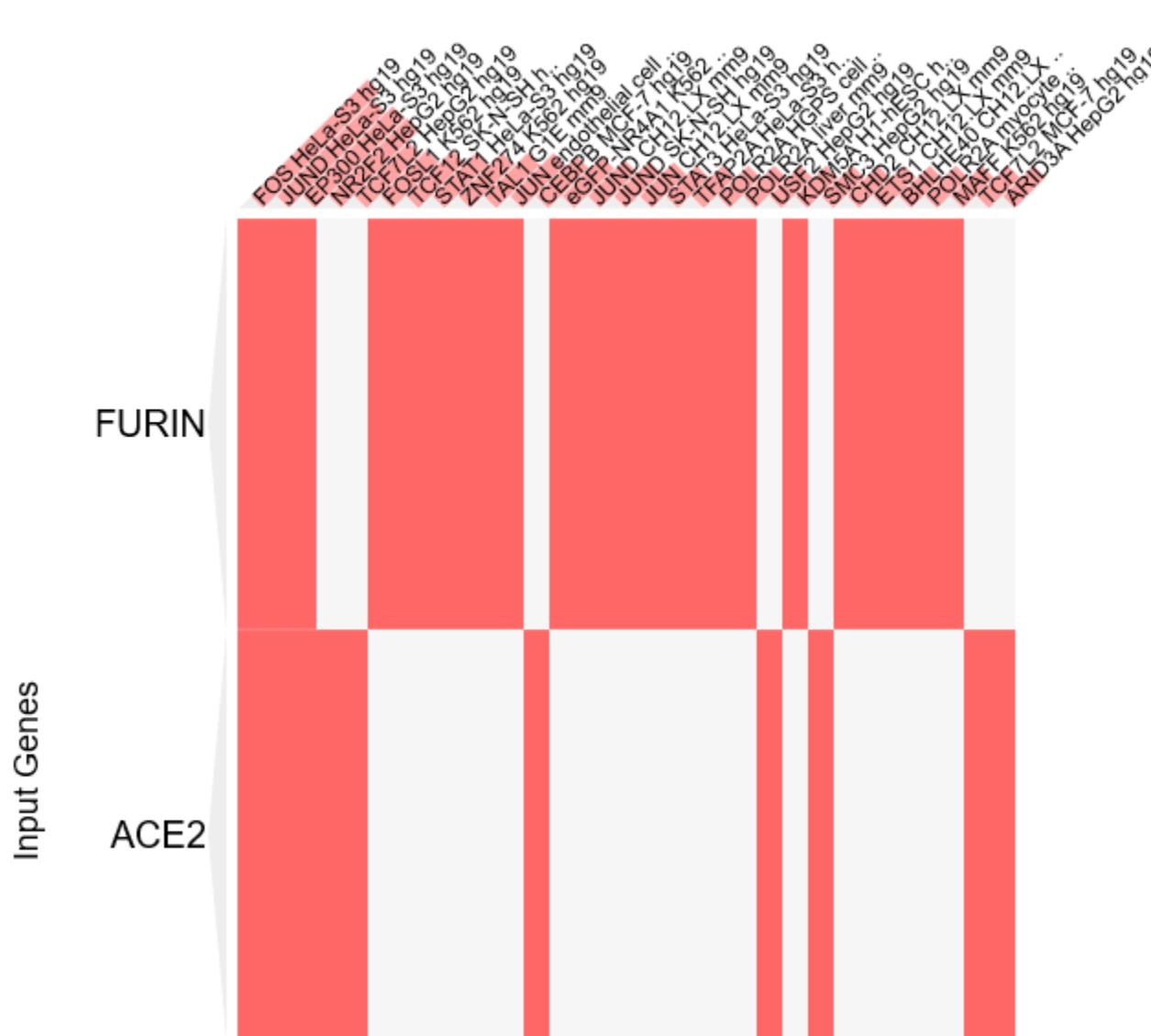
Supplemental Figure S5. Potential mechanisms affecting gene expression: identifications of the enriched records of transcription factor-binding sites

# Predominantly distinct transcription factors make-up chromatin of the ACE2 and FURIN genes

ENCODE TF ChIP-seq 2015



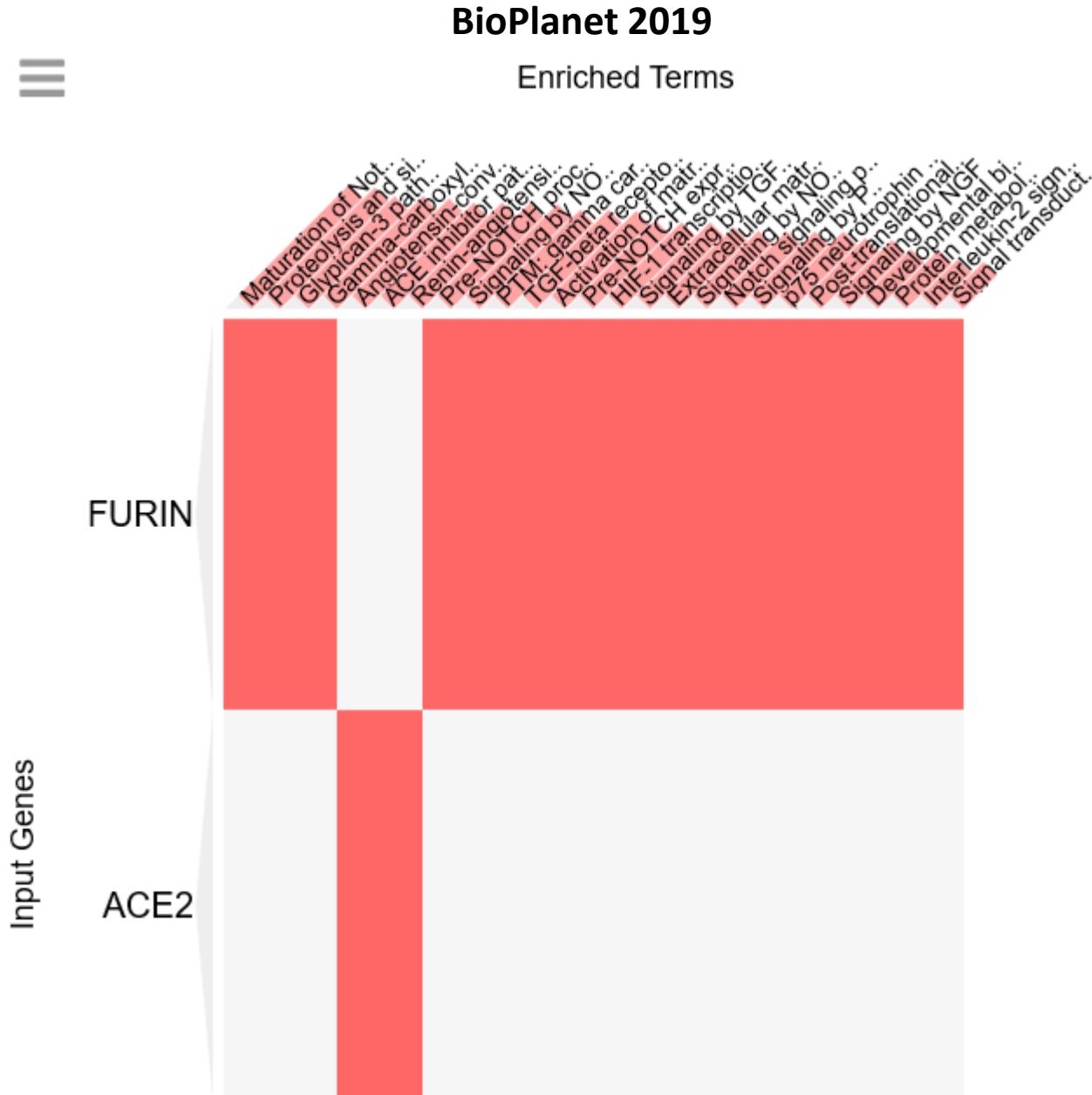
Enriched Terms



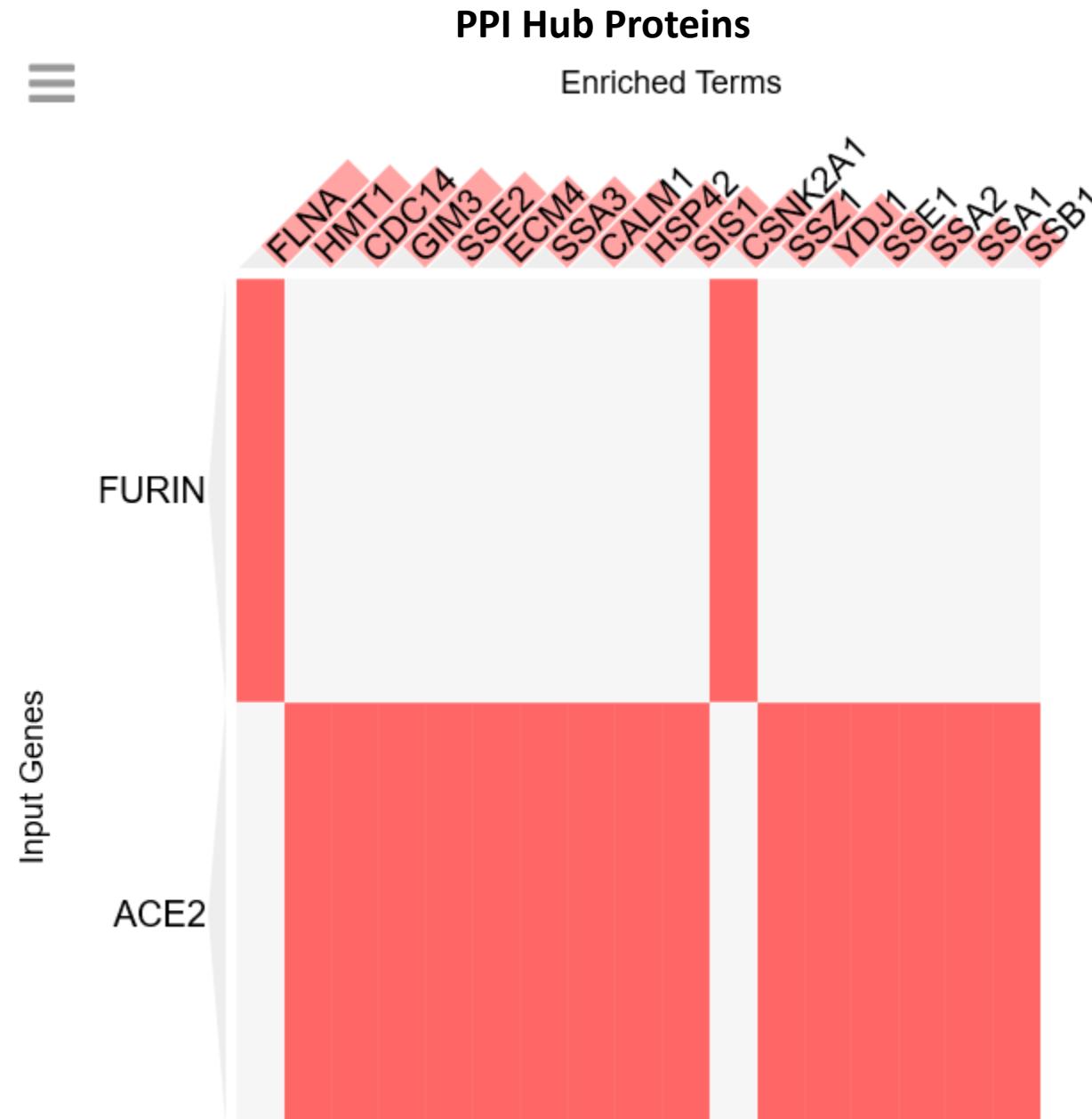
# ACE2 and FURIN

Supplemental Figure S5-1. Potential mechanisms affecting gene expression: identifications of the enriched records of pathways, protein-protein interactions (PPI) hub proteins, and drugs affecting *ACE2* and *FURIN* expression

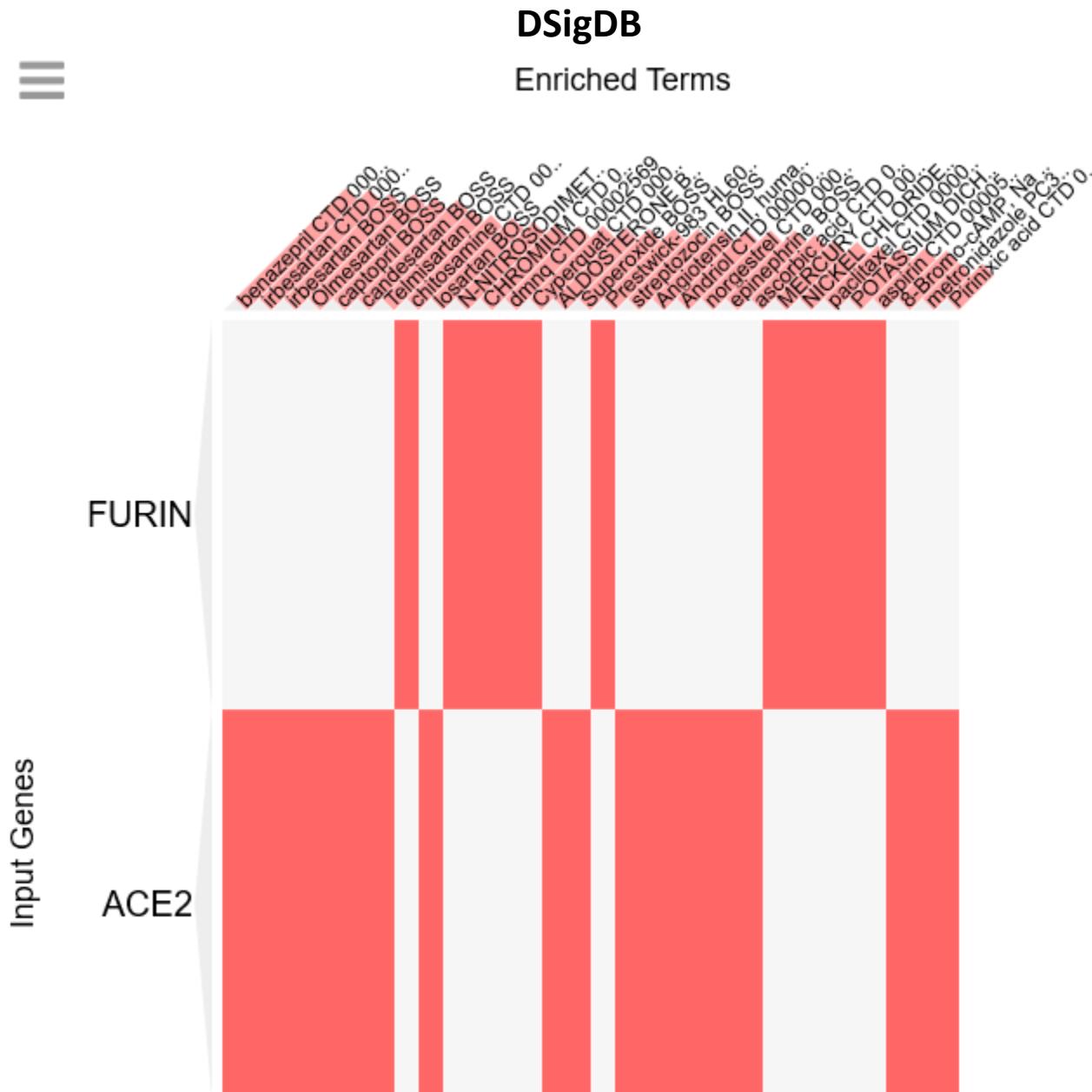
# Distinct patterns of pathways associated with the *ACE2* and *FURIN* genes



# Distinct patterns of protein-protein interactions' (PPI) hub proteins associated with the *ACE2* and *FURIN* gene products



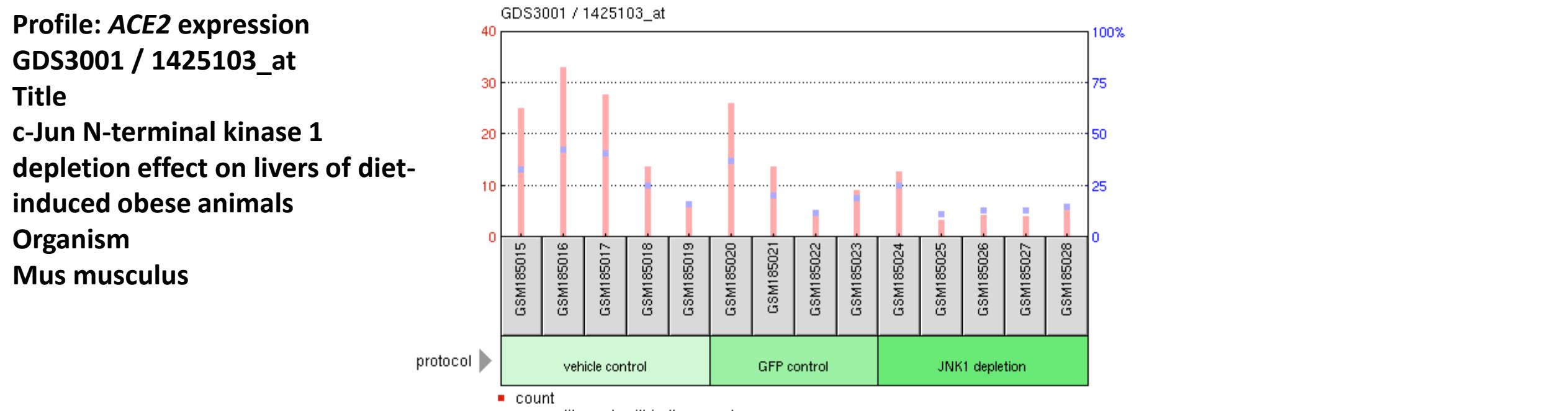
# Distinct patterns of drugs affecting expression of the *ACE2* and *FURIN* genes



Drug Signatures Database  
contains drug/gene associations  
based on quantitative inhibition  
and drug-induced gene expression  
changes

# ACE2 and FURIN

Supplemental Figure S5-2. Potential mechanisms affecting gene expression: identifications of the enriched records of transcription factor-binding sites that affect expression of target genes



### **JNK1 depletion is associated with decreased expression of the ACE2 gene**

Sample	Title	Value
<a href="#">GSM185015</a>	DIO Vehicle 1	25.1364
<a href="#">GSM185016</a>	DIO Vehicle 2	33.1885
<a href="#">GSM185017</a>	DIO Vehicle 3	27.7494
<a href="#">GSM185018</a>	DIO Vehicle 4	13.9459
<a href="#">GSM185019</a>	DIO Vehicle 5	6.24653
<a href="#">GSM185020</a>	GFP Adv-shRNA 1	26.1209
<a href="#">GSM185021</a>	GFP Adv-shRNA 2	13.8813
<a href="#">GSM185022</a>	GFP Adv-shRNA 3	4.77496
<a href="#">GSM185023</a>	GFP Adv-shRNA 5	9.28534
<a href="#">GSM185024</a>	Jnk1 Adv-shRNA 1	12.9219
<a href="#">GSM185025</a>	Jnk1 Adv-shRNA 2	3.46532
<a href="#">GSM185026</a>	Jnk1 Adv-shRNA 3	4.42602
<a href="#">GSM185027</a>	Jnk1 Adv-shRNA 4	4.17173
<a href="#">GSM185028</a>	Jnk1 Adv-shRNA 5	5.42079

# Profile: ACE2 expression

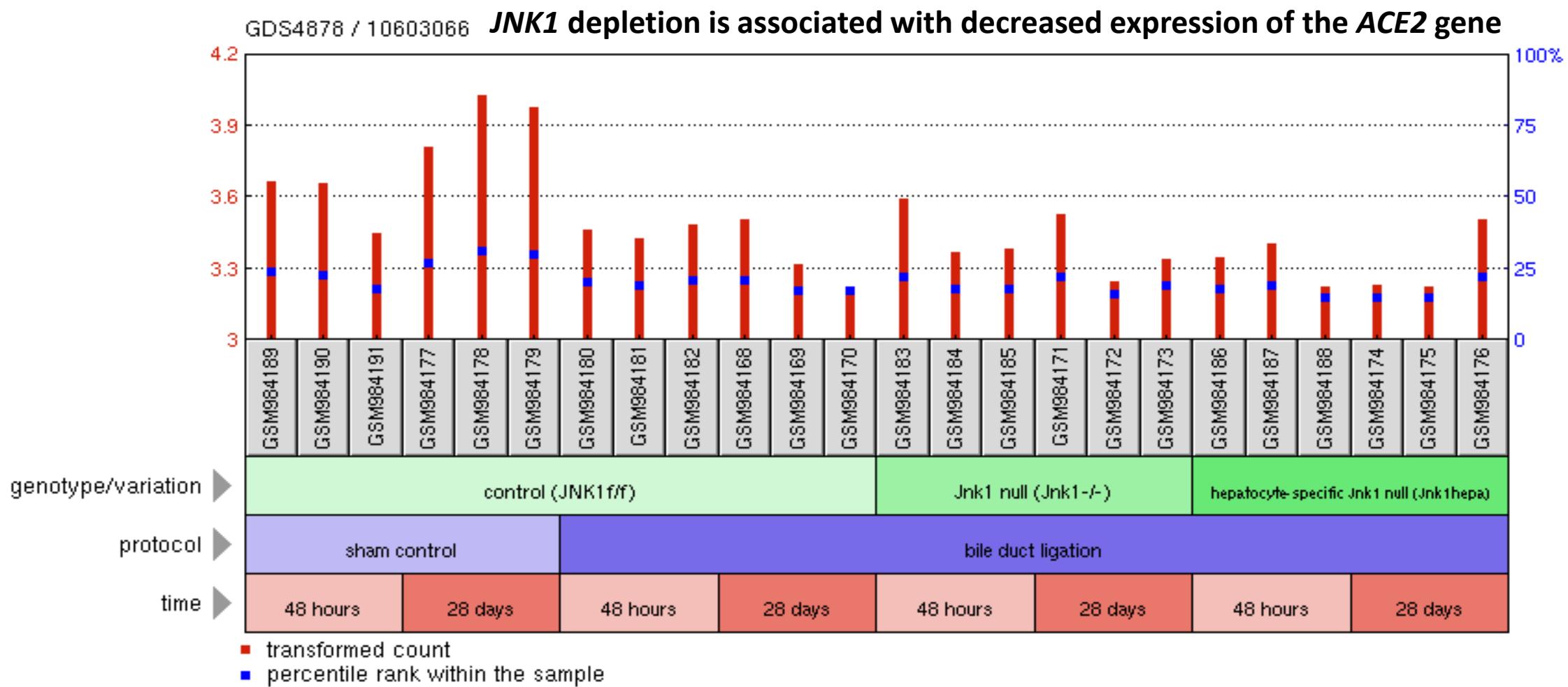
GDS4878 / 10603066

## Title

c-Jun N-terminal kinase-1 deletion effect on bile duct ligation model of liver fibrosis: time course

## Organism

Mus musculus



**Profile: ACE2 expression  
GDS4878 / 10603066**

**Title: c-Jun N-terminal kinase-1 deletion effect on bile duct ligation model of liver fibrosis: time course  
Organism: Mus musculus**

**JNK1 depletion is associated with decreased expression of the ACE2 gene**

Sample	Title	Value
<a href="#">GSM984189</a>	Con sham 48h rep1	3.66522
<a href="#">GSM984190</a>	Con sham 48h rep2	3.65818
<a href="#">GSM984191</a>	Con sham 48h rep3	3.45112
<a href="#">GSM984177</a>	Con sham 28d rep1	3.8128
<a href="#">GSM984178</a>	Con sham 28d rep2	4.03119
<a href="#">GSM984179</a>	Con sham 28d rep3	3.98185
<a href="#">GSM984180</a>	Con BDL 48h rep1	3.46406
<a href="#">GSM984181</a>	Con BDL 48h rep2	3.42924
<a href="#">GSM984182</a>	Con BDL 48h rep3	3.48658
<a href="#">GSM984168</a>	Con BDL 28d rep1	3.50685
<a href="#">GSM984169</a>	Con BDL 28d rep2	3.32075
<a href="#">GSM984170</a>	Con BDL 28d rep3	3.22149
<a href="#">GSM984183</a>	JNK1KO BDL 48h rep1	3.59926
<a href="#">GSM984184</a>	JNK1KO BDL 48h rep2	3.37132
<a href="#">GSM984185</a>	JNK1KO BDL 48h rep3	3.38383
<a href="#">GSM984171</a>	JNK1KO BDL 28d rep1	3.5343
<a href="#">GSM984172</a>	JNK1KO BDL 28d rep2	3.24978
<a href="#">GSM984173</a>	JNK1KO BDL 28d rep3	3.34012
<a href="#">GSM984186</a>	JNK1dhepa BDL 48h rep1	3.34704
<a href="#">GSM984187</a>	JNK1dhepa BDL 48h rep2	3.40698
<a href="#">GSM984188</a>	JNK1dhepa BDL 48h rep3	3.22586
<a href="#">GSM984174</a>	JNK1dhepa BDL 28d rep1	3.23559
<a href="#">GSM984175</a>	JNK1dhepa BDL 28d rep2	3.23042
<a href="#">GSM984176</a>	JNK1dhepa BDL 28d rep3	3.51026

Profile: *Fos* expression

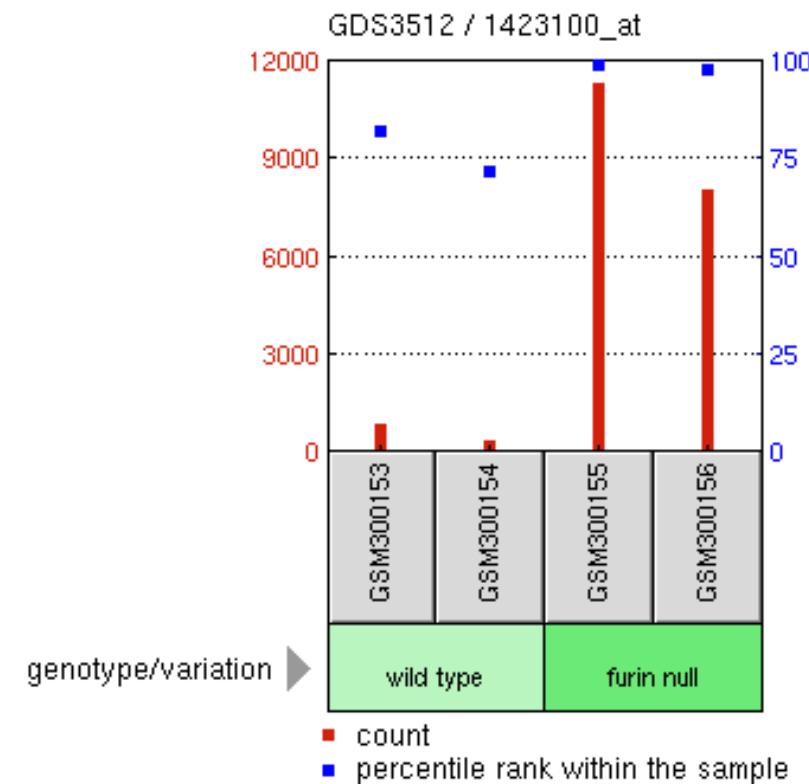
GDS3512 / 1423100\_at

Title

Furin deficiency effect on T-cells

Organism

*Mus musculus*



*Furin* depletion is associated with increased *Fos* expression

Sample	Title	Value
<a href="#">GSM300153</a>	Naive_Furin_Wild-type_1	873.5
<a href="#">GSM300154</a>	Naive_Furin_Wild-type_2	374.2
<a href="#">GSM300155</a>	Naive_Furin_Knockout_1	11333.5
<a href="#">GSM300156</a>	Naive_Furin_Knockout_2	8045.2

Profile: *Jun* expression

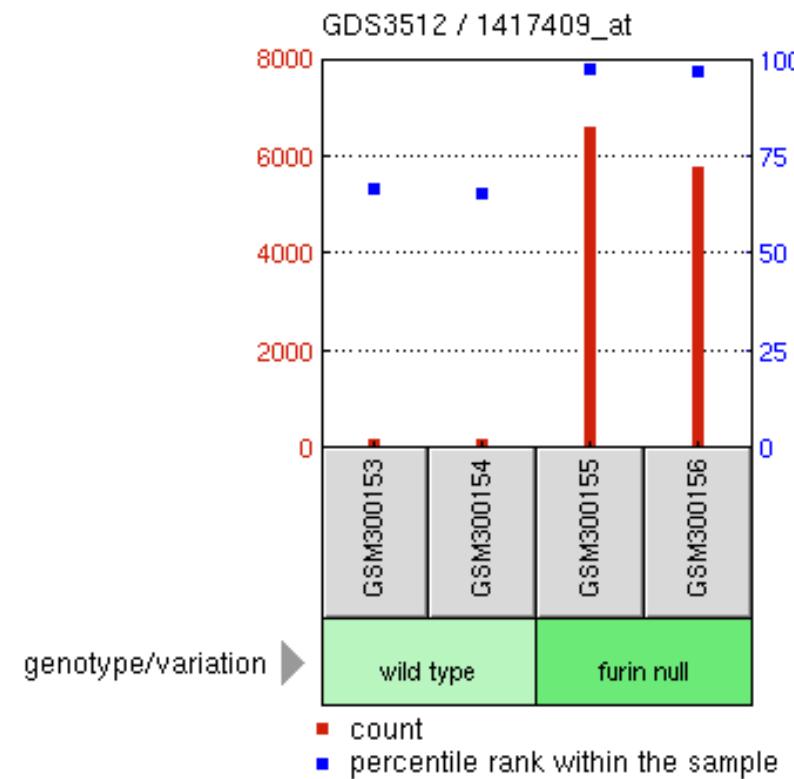
GDS3512 / 1417409\_at

Title

Furin deficiency effect on T-cells

Organism

*Mus musculus*



***Furin* depletion is associated with increased *Jun* expression**

Sample	Title	Value
<a href="#">GSM300153</a>	Naive_Furin_Wild-type_1	232.7
<a href="#">GSM300154</a>	Naive_Furin_Wild-type_2	238.9
<a href="#">GSM300155</a>	Naive_Furin_Knockout_1	6631.6
<a href="#">GSM300156</a>	Naive_Furin_Knockout_2	5795

Profile: *Jund* expression

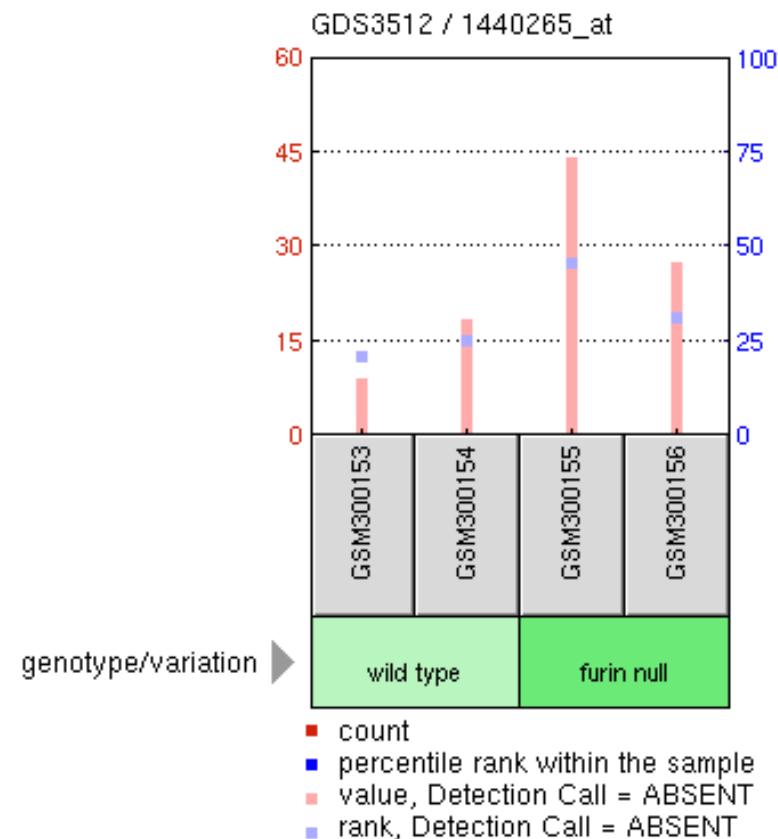
GDS3512 / 1440265\_at

Title

Furin deficiency effect on T-cells

Organism

*Mus musculus*



***Furin* depletion is associated with increased *Jund* expression**

Sample	Title	Value
<a href="#">GSM300153</a>	Naive_Furin_Wild-type_1	9.2
<a href="#">GSM300154</a>	Naive_Furin_Wild-type_2	18.5
<a href="#">GSM300155</a>	Naive_Furin_Knockout_1	44.3
<a href="#">GSM300156</a>	Naive_Furin_Knockout_2	27.6

Profile: *Junb* expression

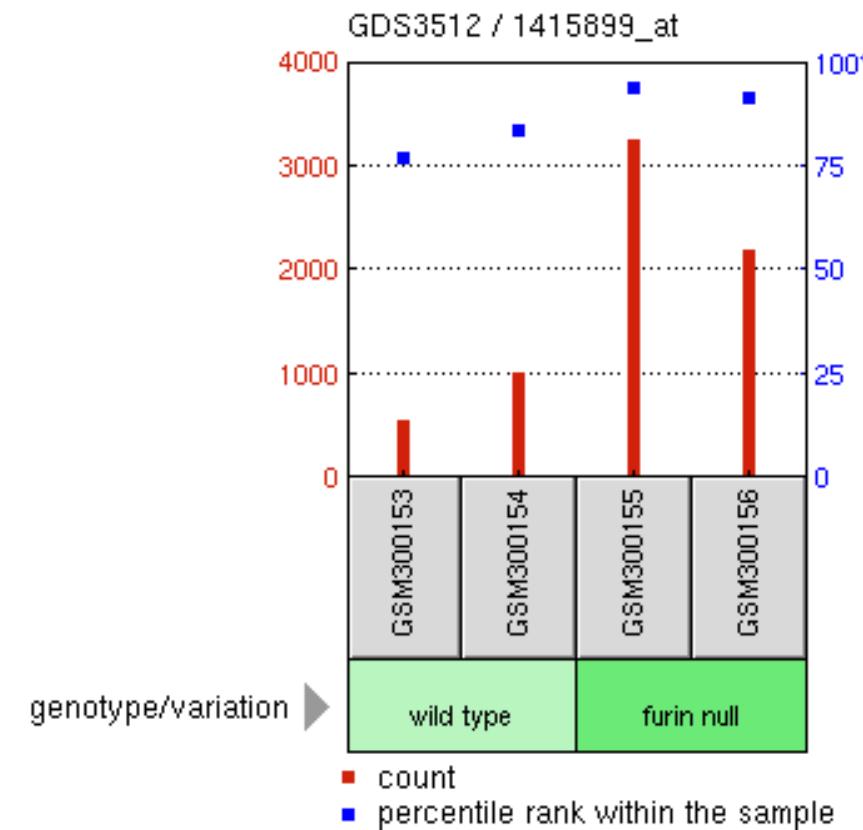
GDS3512 / 1415899\_at

Title

Furin deficiency effect on T-cells

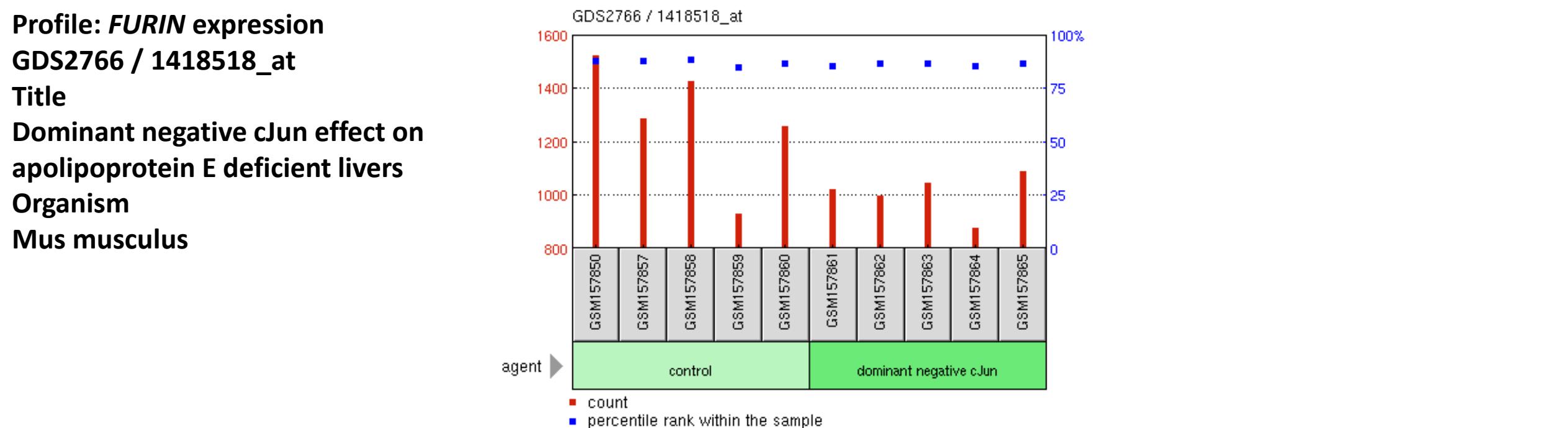
Organism

*Mus musculus*



**Furin depletion is associated with increased *Junb* expression**

Sample	Title	Value
<a href="#">GSM300153</a>	Naive_Furin_Wild-type_1	556
<a href="#">GSM300154</a>	Naive_Furin_Wild-type_2	1032.5
<a href="#">GSM300155</a>	Naive_Furin_Knockout_1	3257.8
<a href="#">GSM300156</a>	Naive_Furin_Knockout_2	2203.1



*cJun inhibition is associated with decreased Furin expression*

Sample	Title	Value
<a href="#">GSM157850</a>	Control VZ11	1526.31
<a href="#">GSM157857</a>	Control VZ12	1290.04
<a href="#">GSM157858</a>	Control VZ13	1426.9
<a href="#">GSM157859</a>	Control VZ14	932.365
<a href="#">GSM157860</a>	Control VZ15	1259.69
<a href="#">GSM157861</a>	Dominant negative cJun VZ16	1026.16
<a href="#">GSM157862</a>	Dominant negative cJun VZ17	1002.07
<a href="#">GSM157863</a>	Dominant negative cJun VZ18	1049.73
<a href="#">GSM157864</a>	Dominant negative cJun VZ19	879.625
<a href="#">GSM157865</a>	Dominant negative cJun VZ20	1093.33

# Profile: *FURIN* expression

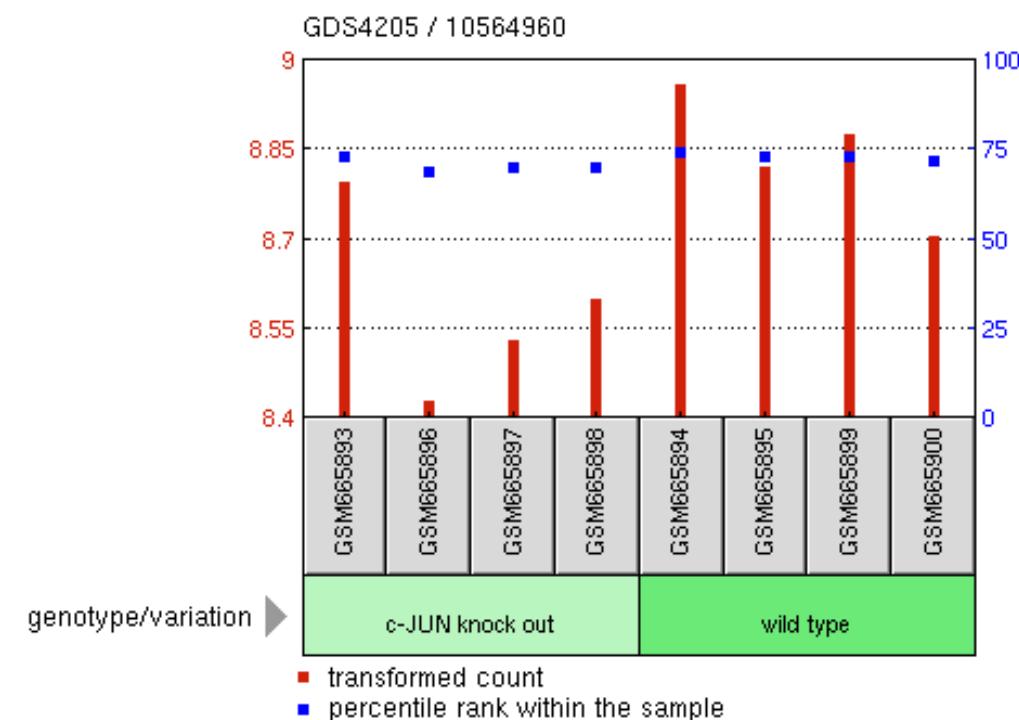
GDS4205 / 10564960

## Title

Transcription factor c-JUN knockout  
effect on B lymphoid cells

## Organism

*Mus musculus*



*cJun* depletion is associated with decreased *Furin* expression

Sample	Title	Value
<a href="#">GSM665893</a>	RO35	8.79585
<a href="#">GSM665896</a>	RO38	8.42939
<a href="#">GSM665897</a>	D1	8.53367
<a href="#">GSM665898</a>	D6	8.60035
<a href="#">GSM665894</a>	RO36	8.96016
<a href="#">GSM665895</a>	RO37	8.82158
<a href="#">GSM665899</a>	F2	8.87409
<a href="#">GSM665900</a>	F4	8.70635

Profile: *FURIN* expression

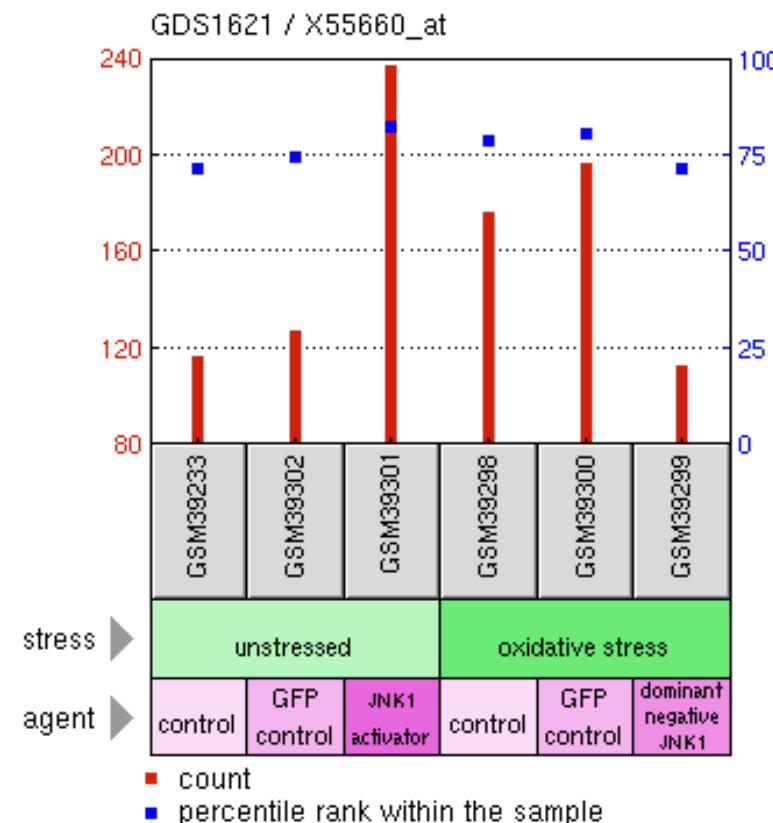
GDS1621 / X55660\_at

Title

c-Jun N-terminal kinase pathway  
activation and suppression effect on  
aortic vascular smooth muscle cells

Organism

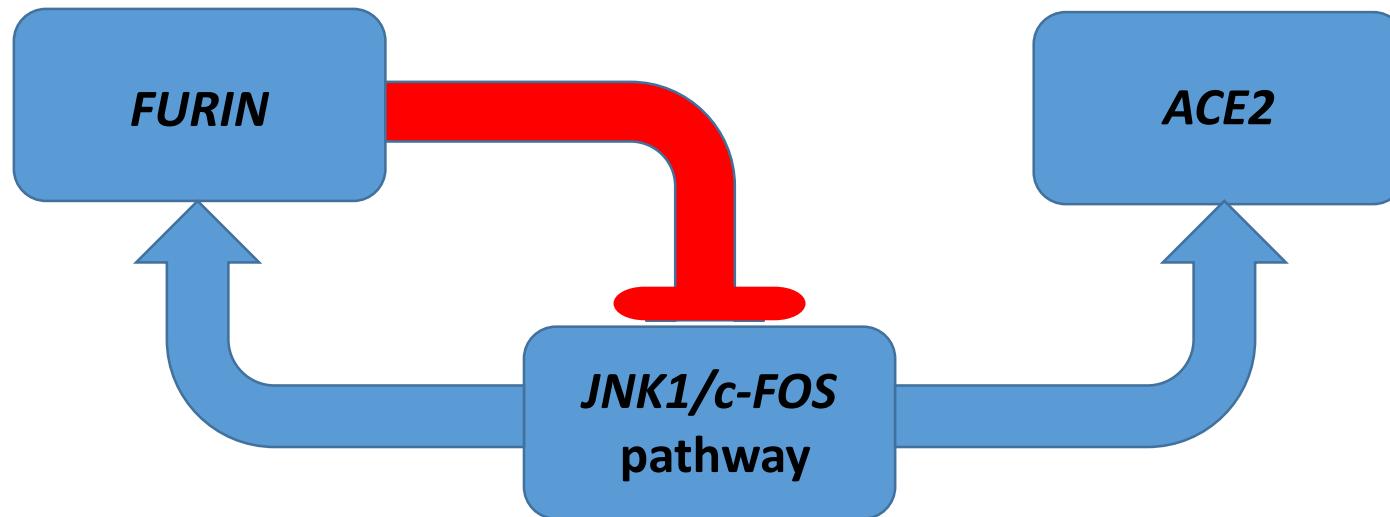
Rattus norvegicus



***JNK1* pathway inhibition is associated with decreased *Furin* expression, while  
*JNK1* activation is associated with increased *Furin* expression**

Sample	Title	Value
<a href="#">GSM39233</a>	rVSMC_control	116.8
<a href="#">GSM39302</a>	rVSMC_nEGFP	128.1
<a href="#">GSM39301</a>	rVSMC_MKK7ED+JNK1WT	237.3
<a href="#">GSM39298</a>	rVSMC_H2O2	177.2
<a href="#">GSM39300</a>	rVSMC_H2O2+nEGFP	197.2
<a href="#">GSM39299</a>	rVSMC_H2O2+APF	113.2

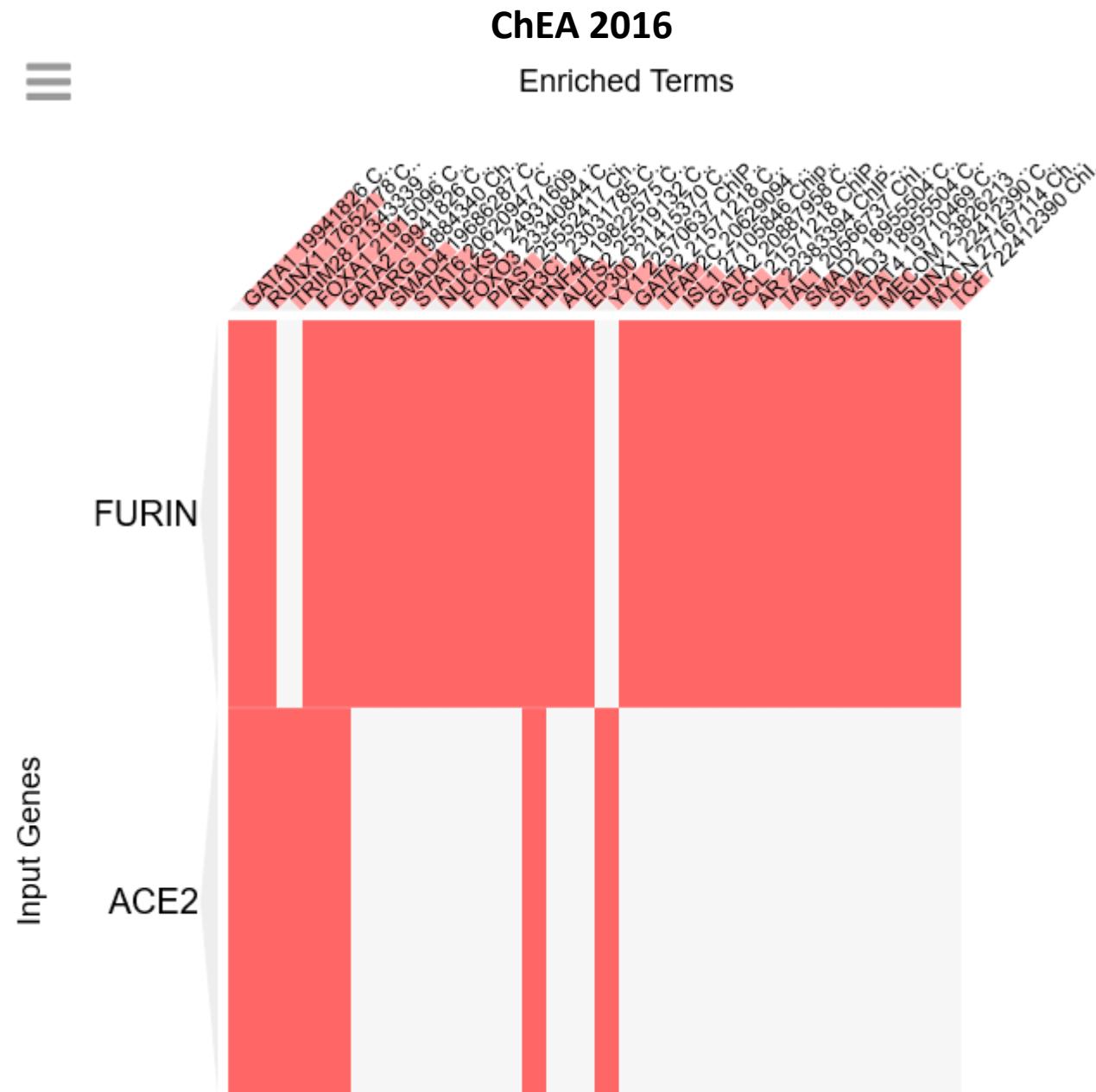
*JNK1/c-FOS* pathway-associated activation of the *ACE2* and *FURIN* expression may trigger the auto-regulatory negative feed-back loop of the *FURIN*-mediated repression of the expression of *JUN*, *JUNB*, *JUND*, and *c-FOS* genes



# ACE2 and FURIN

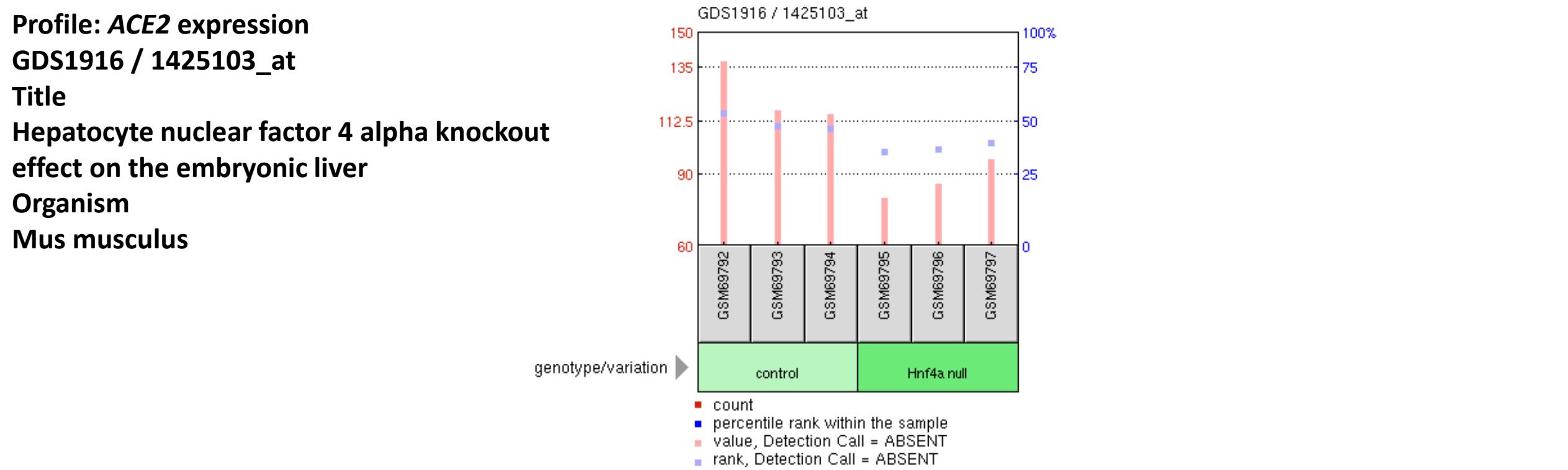
Supplemental Figure S6. Potential mechanisms affecting gene expression: identifications of the enriched records of transcription factor-binding sites

# Predominantly distinct transcription factors make-up chromatin of the ACE2 and FURIN genes



# ACE2 and FURIN

Supplemental Figure S6-1. Potential mechanisms affecting gene expression: identifications of the enriched records of transcription factor-binding sites that affect expression of target genes



***Hnf4a* deficiency decreases ACE2 expression in mouse cells**

Sample	Title	Value
<a href="#">GSM69792</a>	HNF4 Control_8	137.683
<a href="#">GSM69793</a>	HNF4 Control_1192	117.056
<a href="#">GSM69794</a>	HNF4 Control_1193	115.675
<a href="#">GSM69795</a>	HNF4 Null_61	<b>80.4453</b>
<a href="#">GSM69796</a>	HNF4 Null_1191	<b>86.1111</b>
<a href="#">GSM69797</a>	HNF4 Null_1195	<b>96.6528</b>

Profile: ACE2 expression

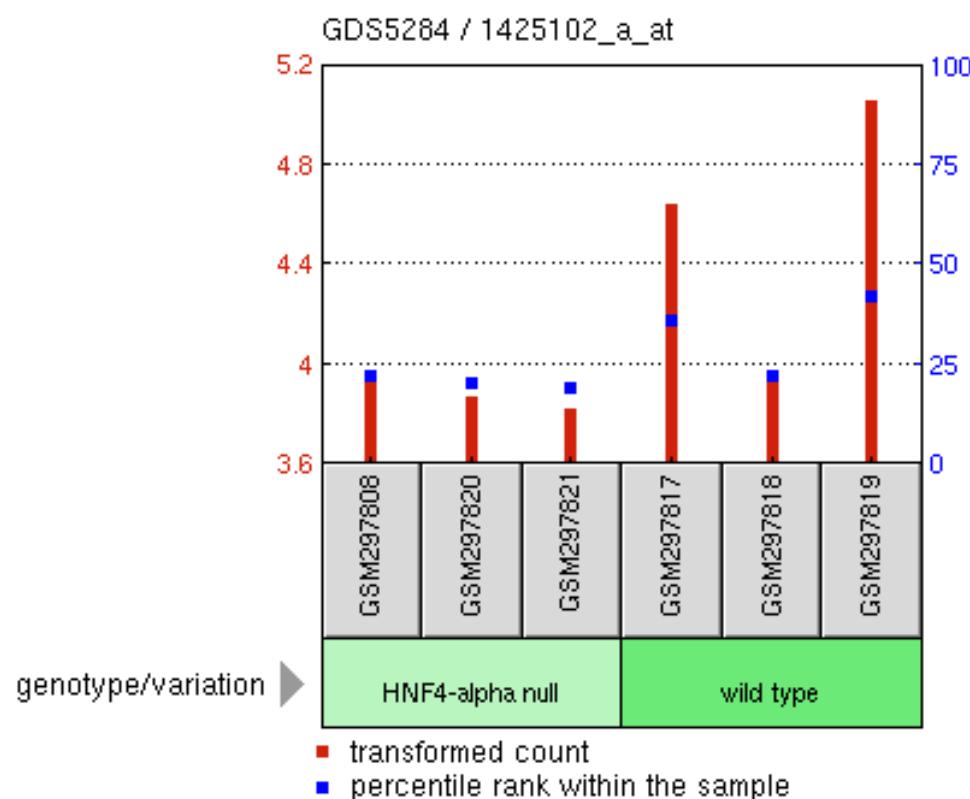
GDS5284 / 1425102\_a\_at

Title

Hepatocyte nuclear factor 4 alpha deficiency effect on the colon

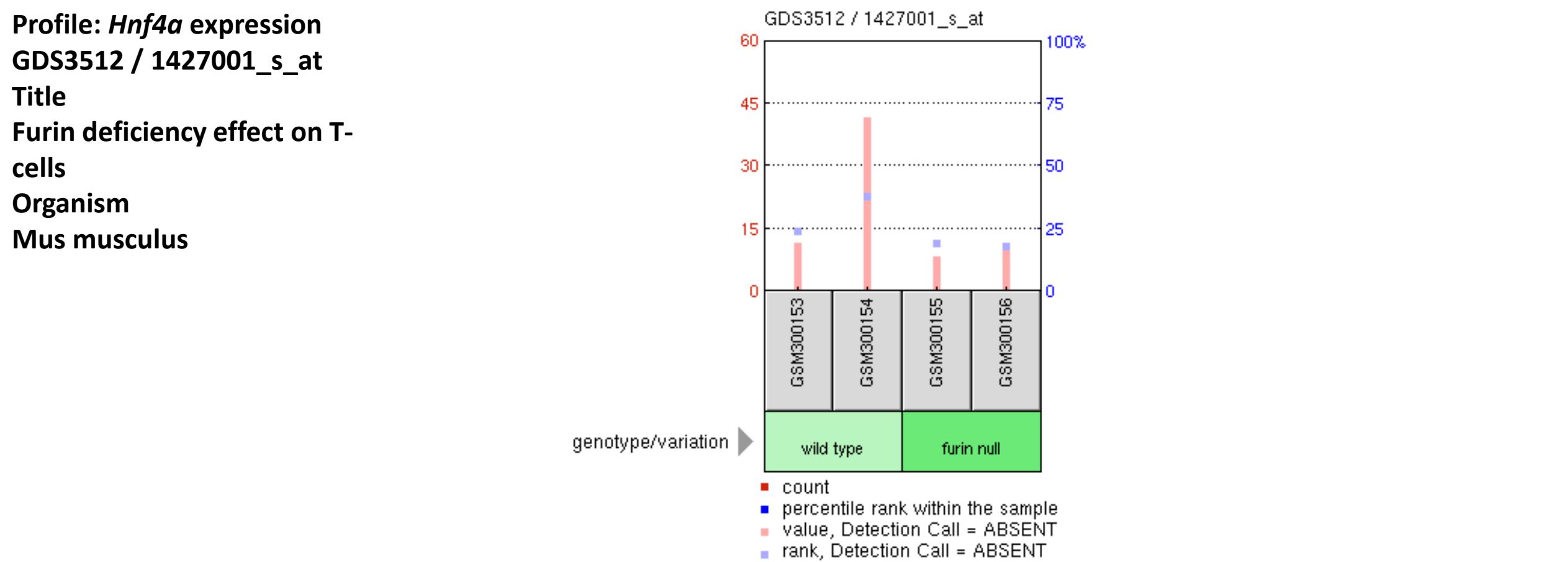
Organism

Mus musculus



***Hnf4a* deficiency decreases ACE2 expression in mouse cells**

Sample	Title	Value
<a href="#">GSM297808</a>	mouse colon_hnf4mutant_rep1	3.94799
<a href="#">GSM297820</a>	mouse colon_hnf4mutant_rep2	3.87791
<a href="#">GSM297821</a>	mouse colon_hnf4mutant_rep3	3.82229
<a href="#">GSM297817</a>	mouse colon_hnf4control_rep1	4.64383
<a href="#">GSM297818</a>	mouse colon_hnf4control_rep2	3.9605
<a href="#">GSM297819</a>	mouse colon_hnf4control_rep3	5.05635



***Furin* deficiency decreases *Hnf4a* expression in murine T-cells**

Sample	Title	Value
<a href="#">GSM300153</a>	Naive_Furin_Wild-type_1	11.6
<a href="#">GSM300154</a>	Naive_Furin_Wild-type_2	41.8
<a href="#">GSM300155</a>	Naive_Furin_Knockout_1	<b>8.4</b>
<a href="#">GSM300156</a>	Naive_Furin_Knockout_2	<b>9.8</b>

Profile: *Furin* expression

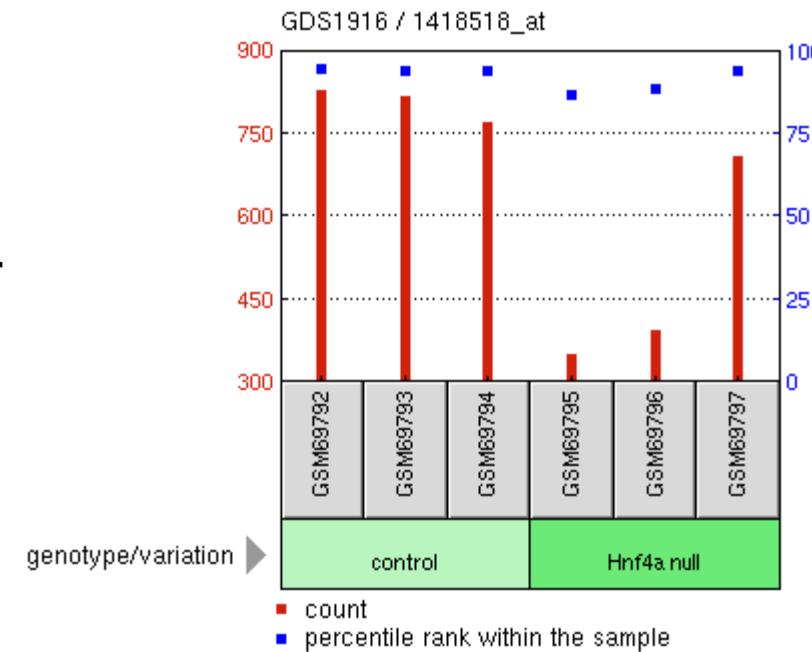
GDS1916 / 1418518\_at

Title

Hepatocyte nuclear factor 4 alpha knockout effect on the embryonic liver

Organism

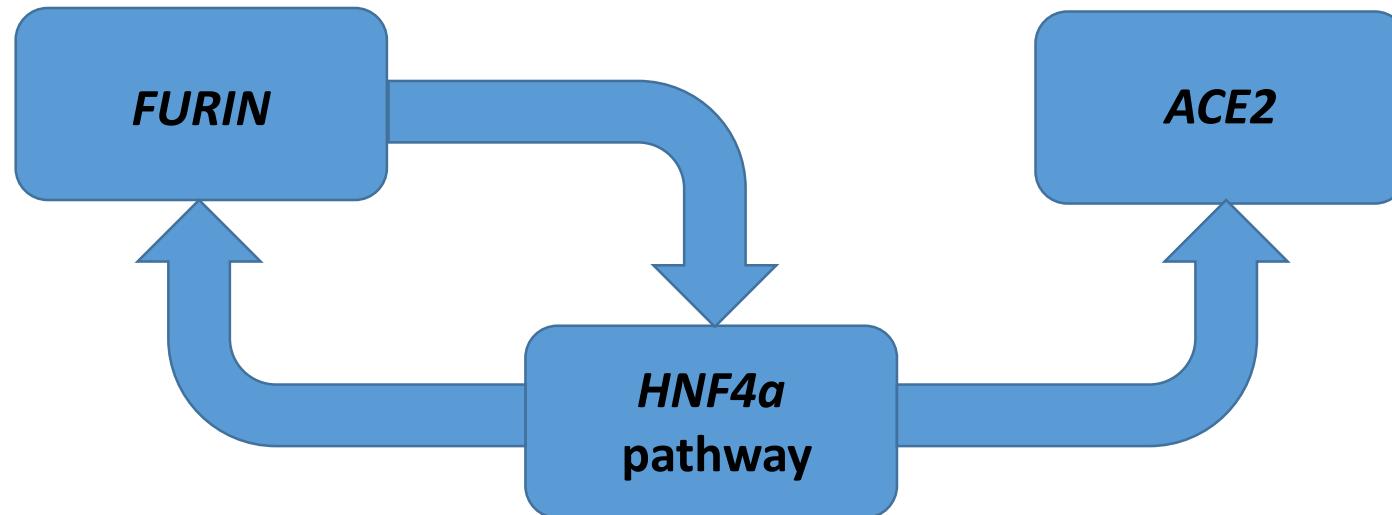
*Mus musculus*



*Hnf4a* deficiency decreases *Furin* expression in murine cells

Sample	Title	Value
<a href="#">GSM69792</a>	HNF4 Control_8	828.42
<a href="#">GSM69793</a>	HNF4 Control_1192	820.313
<a href="#">GSM69794</a>	HNF4 Control_1193	772.082
<a href="#">GSM69795</a>	HNF4 Null_61	354.031
<a href="#">GSM69796</a>	HNF4 Null_1191	396.723
<a href="#">GSM69797</a>	HNF4 Null_1195	708.976

*HNF4a* pathway-associated activation of the *ACE2* and *FURIN* expression may trigger the auto-regulatory positive feed-back loop of the *FURIN*-mediated activation of the *HNF4a* expression



Profile: ACE2 expression

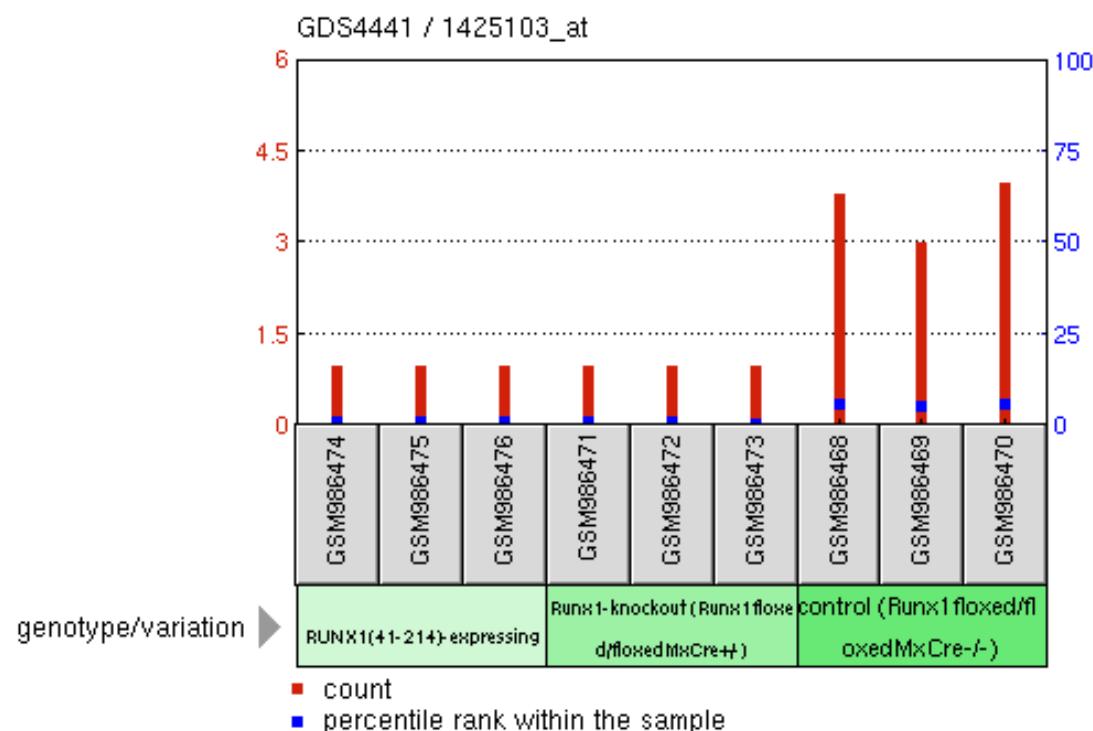
GDS4441 / 1425103\_at

Title

Runt homology domain expression  
effect on hematopoietic stem cells

Organism

Mus musculus



**Runx1 deficiency decreases ACE2 expression in mouse cells**

Sample	Title	Value
<a href="#">GSM986474</a>	RUNX1(41-214), biological replicate 1	1
<a href="#">GSM986475</a>	RUNX1(41-214), biological replicate 2	1
<a href="#">GSM986476</a>	RUNX1(41-214), biological replicate 3	1
<a href="#">GSM986471</a>	Runx1KO, biological replicate 1	1
<a href="#">GSM986472</a>	Runx1KO, biological replicate 2	1
<a href="#">GSM986473</a>	Runx1KO, biological replicate 3	1
<a href="#">GSM986468</a>	Control, biological replicate 1	3.83
<a href="#">GSM986469</a>	Control, biological replicate 2	3
<a href="#">GSM986470</a>	Control, biological replicate 3	4

Profile: *FURIN* expression

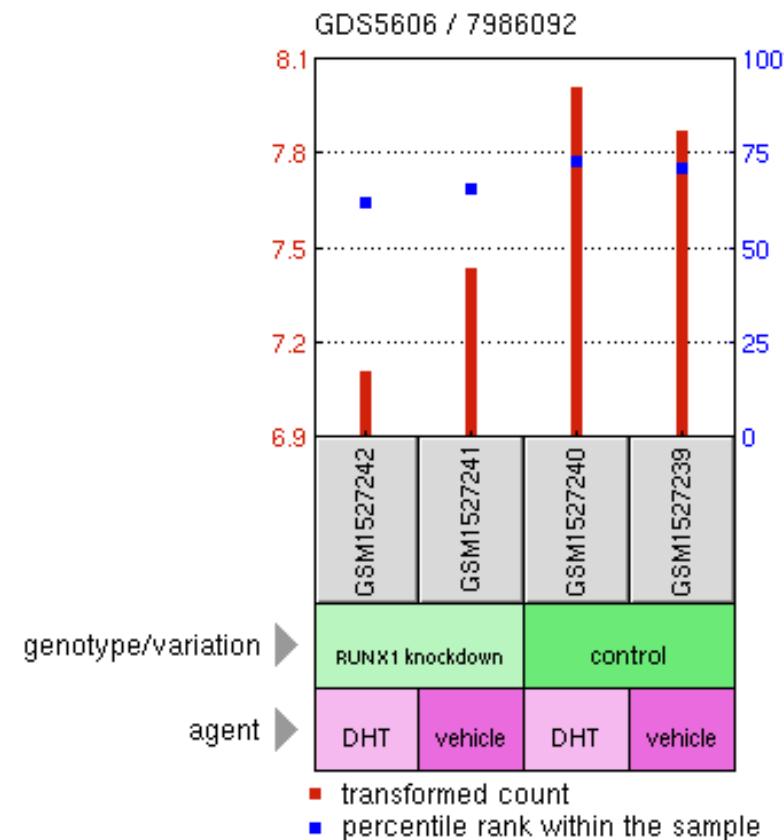
GDS5606 / 7986092

Title

Androgen effect on runt-related transcription factor 1-deficient prostate cancer cell line

Organism

*Homo sapiens*



*RUNX1* deficiency decreases *FURIN* expression in human cells

Sample	Title	Value
<a href="#">GSM1527242</a>	LNCaP_siRUNX1_DHT	<b>7.11175</b>
<a href="#">GSM1527241</a>	LNCaP_siRUNX1_Veh	<b>7.43782</b>
<a href="#">GSM1527240</a>	LNCaP_siControl_DHT	8.00649
<a href="#">GSM1527239</a>	LNCaP_siControl_Veh	7.87368

Profile: *Runx1* expression

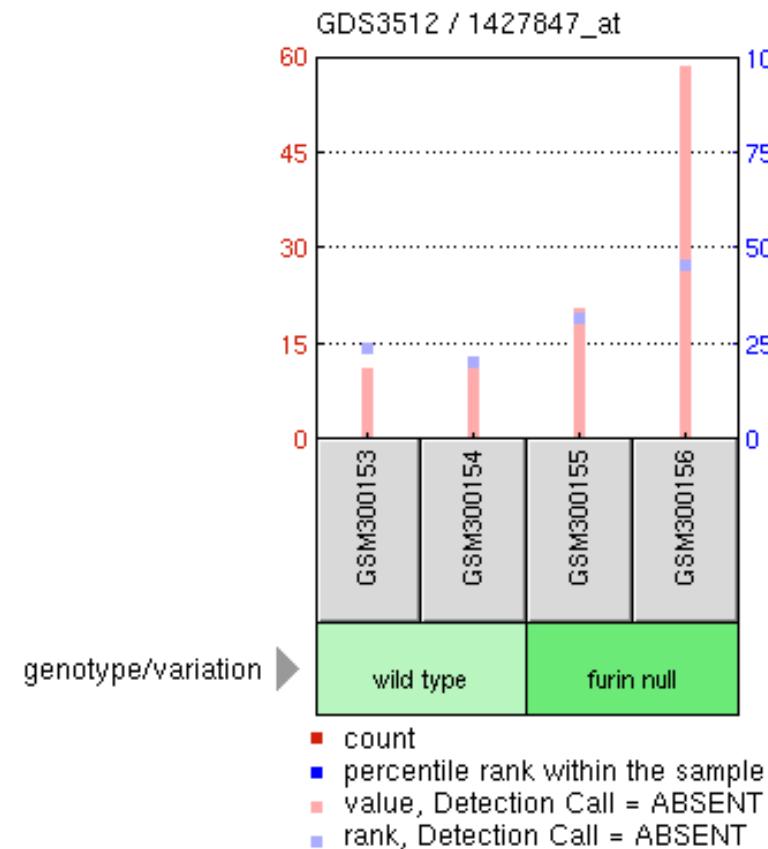
GDS3512 / 1427847\_at

Title

Furin deficiency effect on T-cells

Organism

*Mus musculus*



***Furin* deficiency enhances *Runx1* expression in murine T-cells**

Sample	Title	Value
<a href="#">GSM300153</a>	Naive_Furin_Wild-type_1	11.5
<a href="#">GSM300154</a>	Naive_Furin_Wild-type_2	12.5
<a href="#">GSM300155</a>	Naive_Furin_Knockout_1	20.9
<a href="#">GSM300156</a>	Naive_Furin_Knockout_2	58.7

Profile: *Foxa1* expression

GDS3512 / 1418496\_at

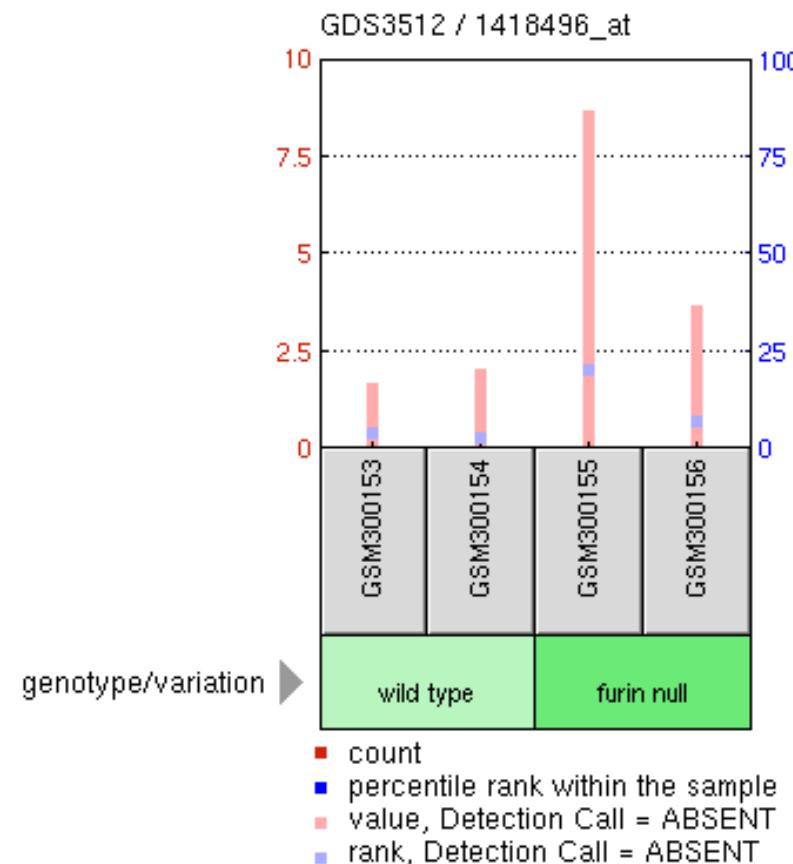
Title

Furin deficiency effect on T-

cells

Organism

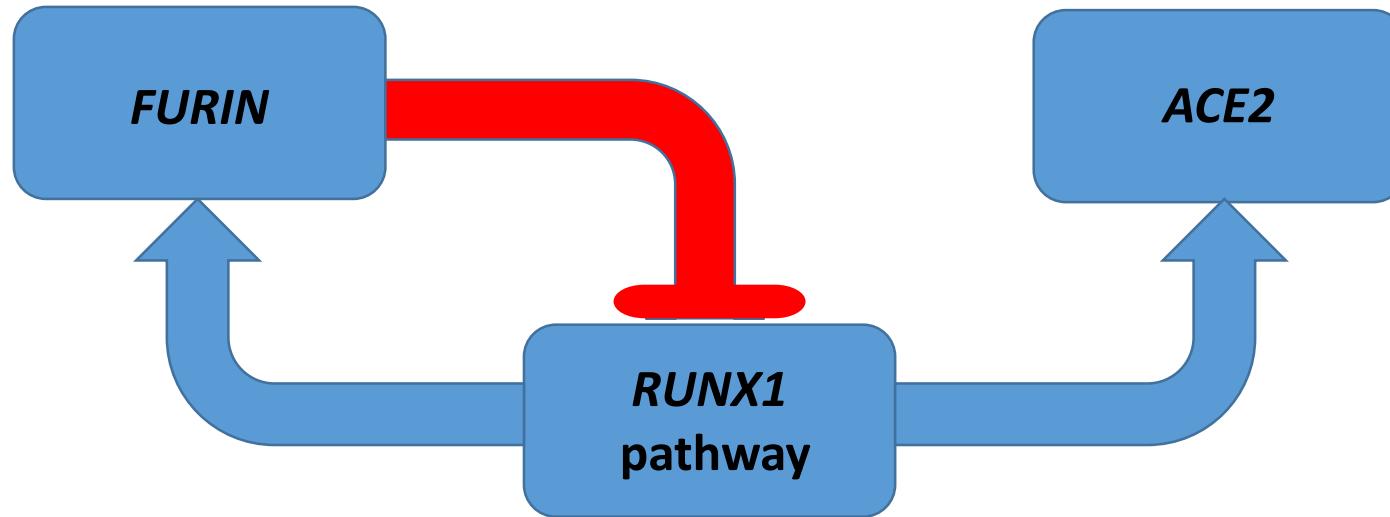
*Mus musculus*



***Furin* deficiency enhances *Foxa1* expression in murine T-cells**

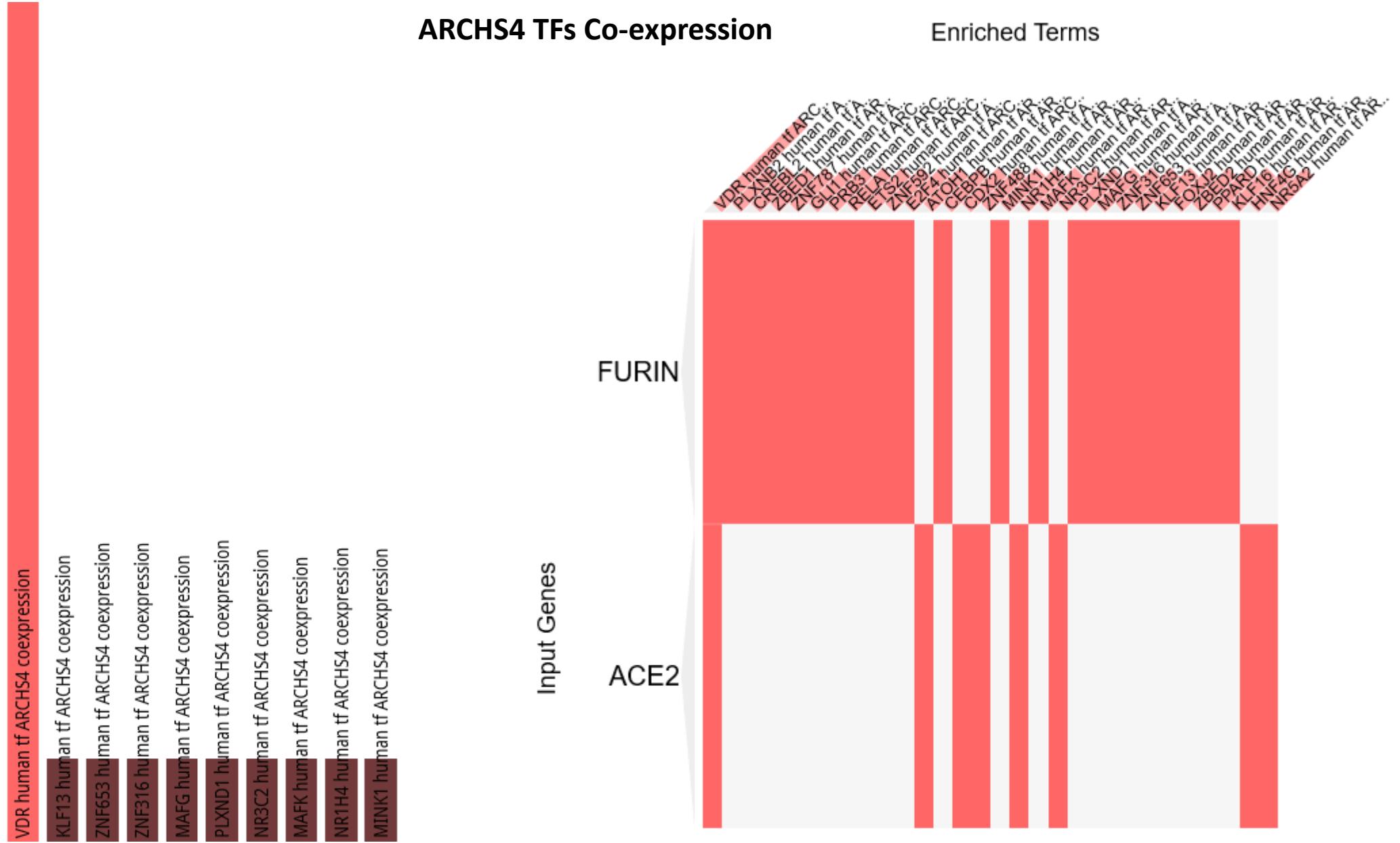
Sample	Title	Value
<a href="#">GSM300153</a>	Naive_Furin_Wild-type_1	1.7
<a href="#">GSM300154</a>	Naive_Furin_Wild-type_2	2.1
<a href="#">GSM300155</a>	Naive_Furin_Knockout_1	8.7
<a href="#">GSM300156</a>	Naive_Furin_Knockout_2	3.7

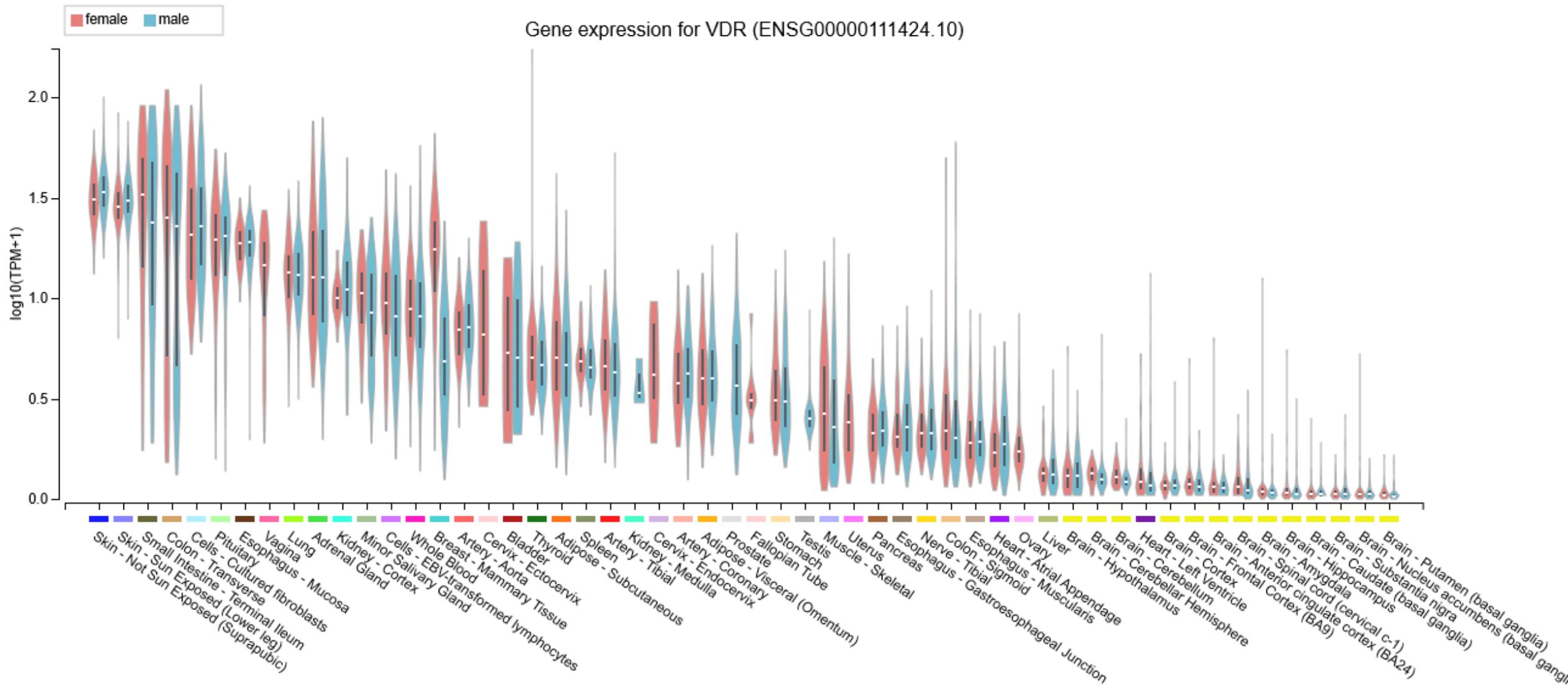
*RUNX1* pathway-associated activation of the *ACE2* and *FURIN* expression may trigger the auto-regulatory negative feed-back loop of the *FURIN*-mediated repression of the *RUNX1* gene expression



# ACE2 and FURIN

Supplemental Figure S7. Potential mechanisms affecting gene expression: Putative inhibitory role of the *VDR* gene and Vitamin D





# ACE2 and FURIN

Supplemental Figure S7-1. Potential mechanisms affecting gene expression: Putative inhibitory role of the *VDR* gene and Vitamin D revealed by gene expression profiles in the GEO data sets

# Profile: ACE2 expression

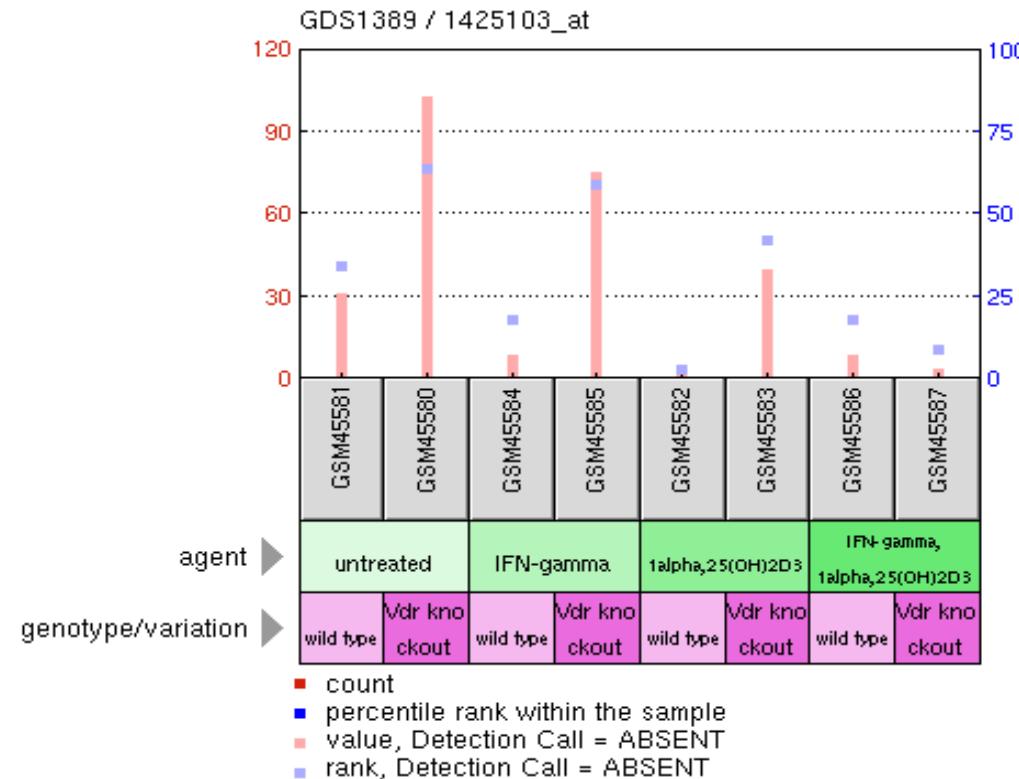
GDS1389 / 1425103\_at

## Title

1alpha,25-dihydroxyvitamin D3  
suppressive effect on IFN-gamma  
activated macrophages

## Organism

Mus musculus



## VDR depletion increases ACE2 expression

Sample	Title	Value
<a href="#">GSM45581</a>	0-WT	31.4
<a href="#">GSM45580</a>	0-KO	102.7
<a href="#">GSM45584</a>	IFN-WT	9.1
<a href="#">GSM45585</a>	IFN-KO	75.7
<a href="#">GSM45582</a>	Vit-WT	3.8
<a href="#">GSM45583</a>	Vit-KO	40.2
<a href="#">GSM45586</a>	IFN/Vit-WT	9
<a href="#">GSM45587</a>	IFN/Vit-KO	4.1

## ***VDR*: a candidate inhibitor of the *ACE2* expression**

GEO profile	GDS1389 / 1452138_a_at	GDS1389 / 1452138_a_at	GDS1389 / 1425103_at	GDS1389 / 1425103_at
Sample	GSM45581	GSM45580	GSM45581	GSM45580
Genotype	VDR-WT	VDR-KO	VDR-WT	VDR-KO
Expression value	27.4	59.8	31.4	102.7

**GEO Profile: *ACE2* expression**  
**GDS1389 / 1425103\_at & 1452138\_a\_at**  
**Title**

**1alpha,25-dihydroxyvitamin D3 suppressive effect on IFN-gamma activated macrophages**

**Organism**

**Mus musculus**

Profile: ACE2 expression

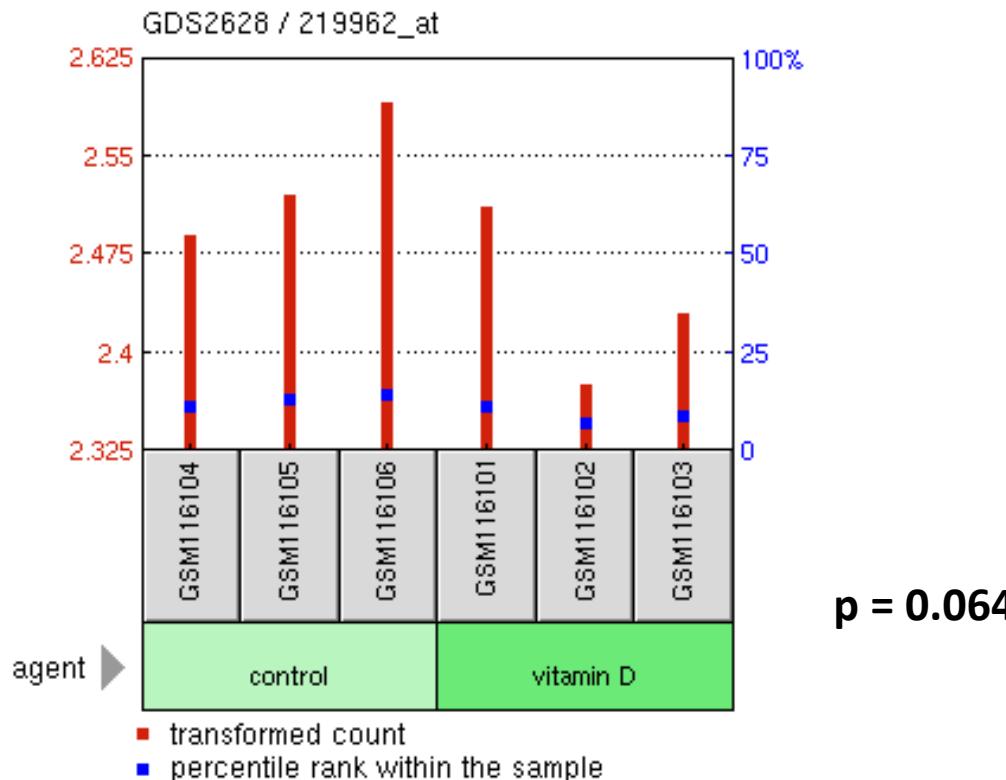
GDS2628 / 219962\_at

Title

Vitamin D effect on bronchial smooth muscle cells

Organism

Homo sapiens



### Vitamin D effect on ACE2 expression

Sample	Title	Value
<a href="#">GSM116104</a>	hBSMC_control_rep1	2.49036
<a href="#">GSM116105</a>	hBSMC_control_rep2	2.52156
<a href="#">GSM116106</a>	hBSMC_control_rep3	2.59211
<a href="#">GSM116101</a>	hBSMC_vitamin D_rep1	2.51261
<a href="#">GSM116102</a>	hBSMC_vitamin D_rep2	2.37673
<a href="#">GSM116103</a>	hBSMC_vitamin D_rep3	2.43005

Direct and reciprocal effects of the *VDR* gene and Vitamin D administration on expression of the *JNK1/c-FOS* pathway genes

Profile: *VDR* expression

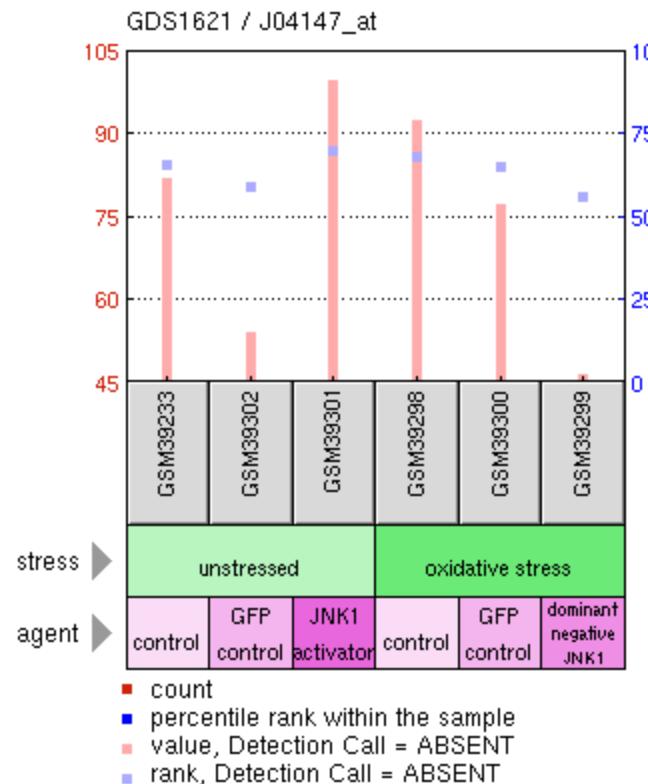
GDS1621 / J04147\_at

Title

c-Jun N-terminal kinase pathway  
activation and suppression effect on  
aortic vascular smooth muscle cells

Organism

Rattus norvegicus



***JNK1* pathway inhibition is associated with decreased *VDR* expression, while  
*JNK1* activation is associated with increased *VDR* expression**

Sample	Title	Value
<a href="#">GSM39233</a>	rVSMC_control	82
<a href="#">GSM39302</a>	rVSMC_nEGFP	54.3
<a href="#">GSM39301</a>	rVSMC_MKK7ED+JNK1WT	99.8
<a href="#">GSM39298</a>	rVSMC_H2O2	92.7
<a href="#">GSM39300</a>	rVSMC_H2O2+nEGFP	77.3
<a href="#">GSM39299</a>	rVSMC_H2O2+APF	45.7

Profile: *c-JUN* expression

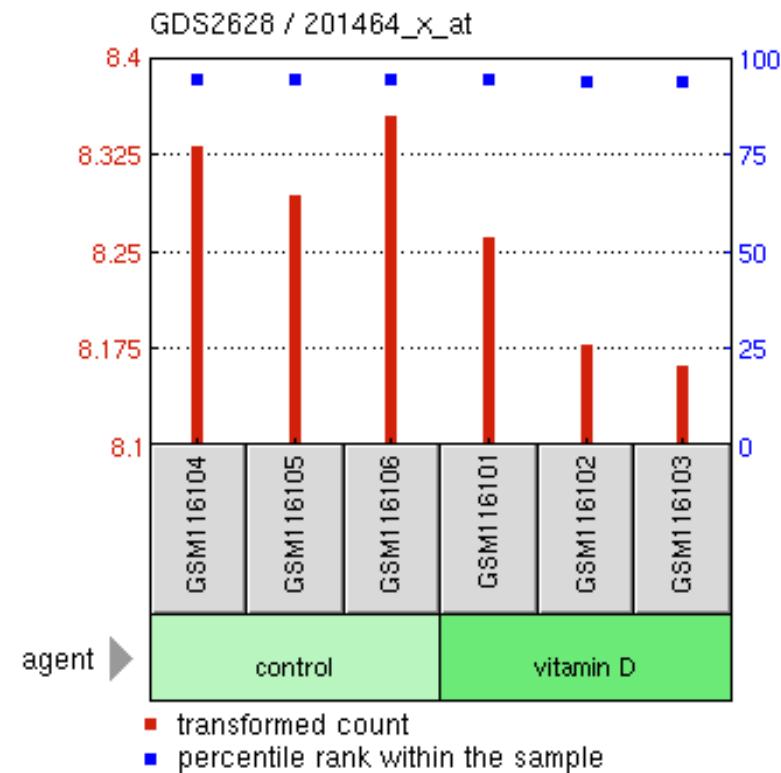
GDS2628 / 201464\_x\_at

Title

Vitamin D effect on bronchial smooth muscle cells

Organism

Homo sapiens



### Vitamin D inhibits *c-JUN* expression

Sample	Title	Value
<a href="#">GSM116104</a>	hBSMC_control_rep1	8.33308
<a href="#">GSM116105</a>	hBSMC_control_rep2	8.29401
<a href="#">GSM116106</a>	hBSMC_control_rep3	8.35545
<a href="#">GSM116101</a>	hBSMC_vitamin D_rep1	8.26197
<a href="#">GSM116102</a>	hBSMC_vitamin D_rep2	8.17801
<a href="#">GSM116103</a>	hBSMC_vitamin D_rep3	8.16188

Profile: *c-FOS* expression

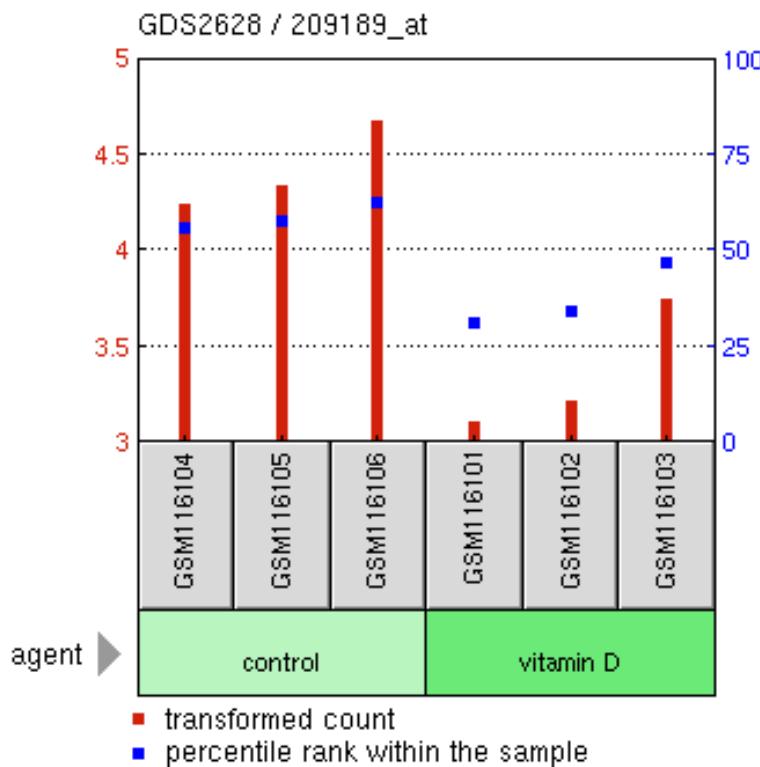
GDS2628 / 209189\_at

Title

Vitamin D effect on bronchial smooth muscle cells

Organism

Homo sapiens



Vitamin D inhibits *c-FOS* expression

Sample	Title	Value
<a href="#">GSM116104</a>	hBSMC_control_rep1	4.24348
<a href="#">GSM116105</a>	hBSMC_control_rep2	4.34194
<a href="#">GSM116106</a>	hBSMC_control_rep3	4.67701
<a href="#">GSM116101</a>	hBSMC_vitamin D_rep1	3.11013
<a href="#">GSM116102</a>	hBSMC_vitamin D_rep2	3.21701
<a href="#">GSM116103</a>	hBSMC_vitamin D_rep3	3.75394

Profile: *VDR* expression

GDS766 / 99964\_at

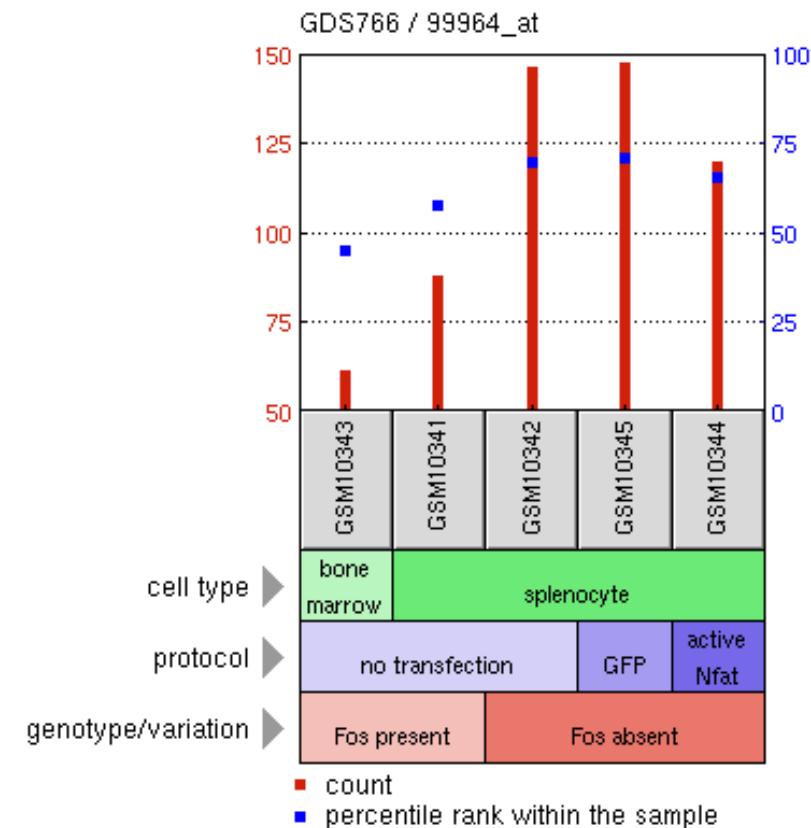
Title

Osteoclastogenesis regulation by c-Fos and

Nfat

Organism

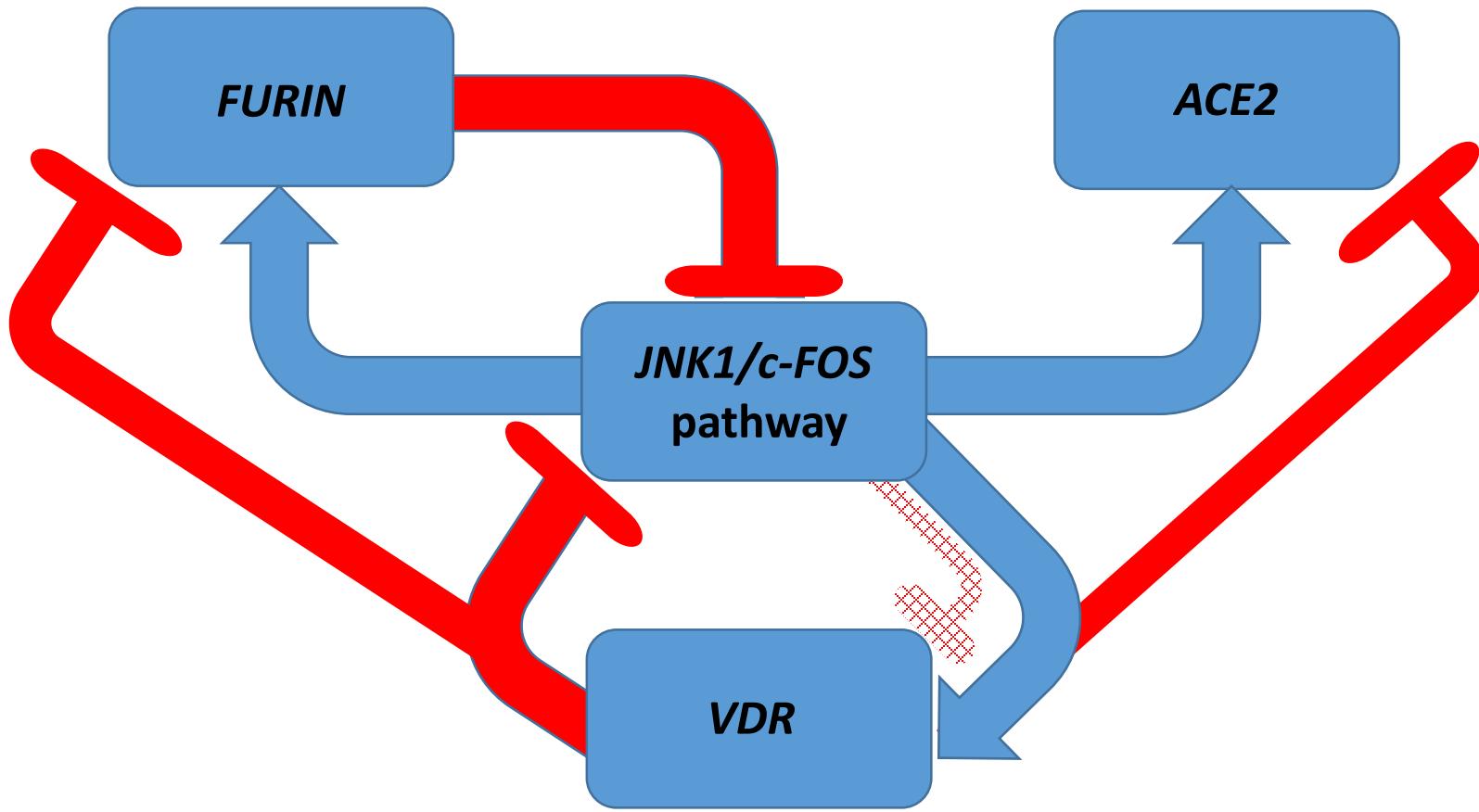
*Mus musculus*



### c-Fos inhibits *Vdr* expression

Sample	Title	Value
<a href="#">GSM10343</a>	Fos+/+ bone-marrow	61.7
<a href="#">GSM10341</a>	Fos+/+ splenocytes	88
<a href="#">GSM10342</a>	Fos-/+ splenocytes	146.8
<a href="#">GSM10345</a>	Fos-/+ splenocytes expressing GFP	147.6
<a href="#">GSM10344</a>	Fos-/+ splenocytes expressing deltaNFAT	120.3

*JNK1/c-FOS* pathway-associated activation of the *ACE2* and *FURIN* expression may trigger the auto-regulatory negative feed-back loop of the *FURIN*-mediated repression of the expression of *JUN*, *JUNB*, *JUND*, and *c-FOS* genes



Direct and reciprocal effects of the *VDR* gene and Vitamin D administration on expression of the *HF4a* gene

Profile: *VDR* expression

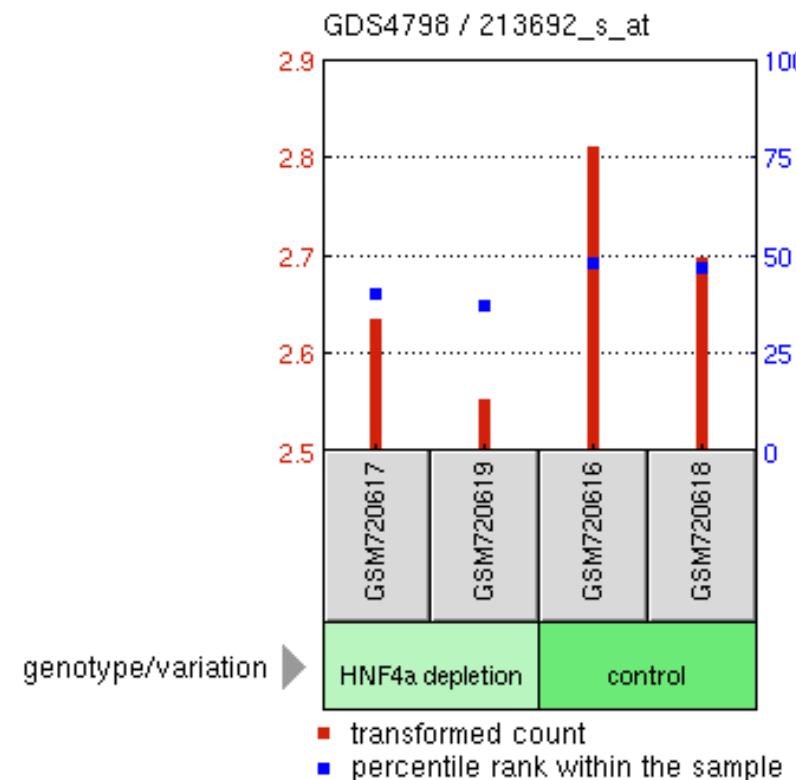
GDS4798 / 213692\_s\_at

Title

Hepatocyte nuclear factor 4 alpha depletion  
effect on hepatocellular carcinoma cell line

Organism

*Homo sapiens*



### *HNF4a* depletion inhibits *VDR* expression

Sample	Title	Value
<a href="#">GSM720617</a>	HepG2 cells, HNF4a RNAi treated, rep1	2.63638
<a href="#">GSM720619</a>	HepG2 cells, HNF4a RNAi treated, rep2	2.5545
<a href="#">GSM720616</a>	HepG2 cells, control, rep1	2.81268
<a href="#">GSM720618</a>	HepG2 cells, control, rep2	2.69839

Profile: *VDR* expression

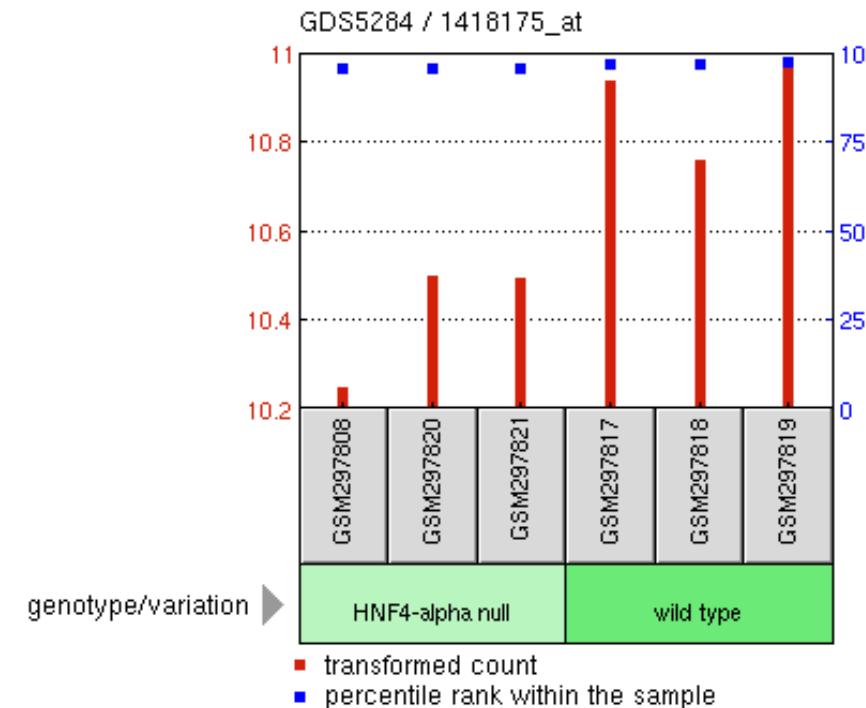
GDS5284 / 1418175\_at

Title

Hepatocyte nuclear factor 4 alpha deficiency effect on the colon

Organism

*Mus musculus*



### *HNF4a* depletion inhibits *VDR* expression

Sample	Title	Value
<a href="#">GSM297808</a>	mouse colon_hnf4mutant_rep1	10.2483
<a href="#">GSM297820</a>	mouse colon_hnf4mutant_rep2	10.4994
<a href="#">GSM297821</a>	mouse colon_hnf4mutant_rep3	10.4987
<a href="#">GSM297817</a>	mouse colon_hnf4control_rep1	10.9398
<a href="#">GSM297818</a>	mouse colon_hnf4control_rep2	10.7599
<a href="#">GSM297819</a>	mouse colon_hnf4control_rep3	10.9741

# Profile: *HNF4a* expression

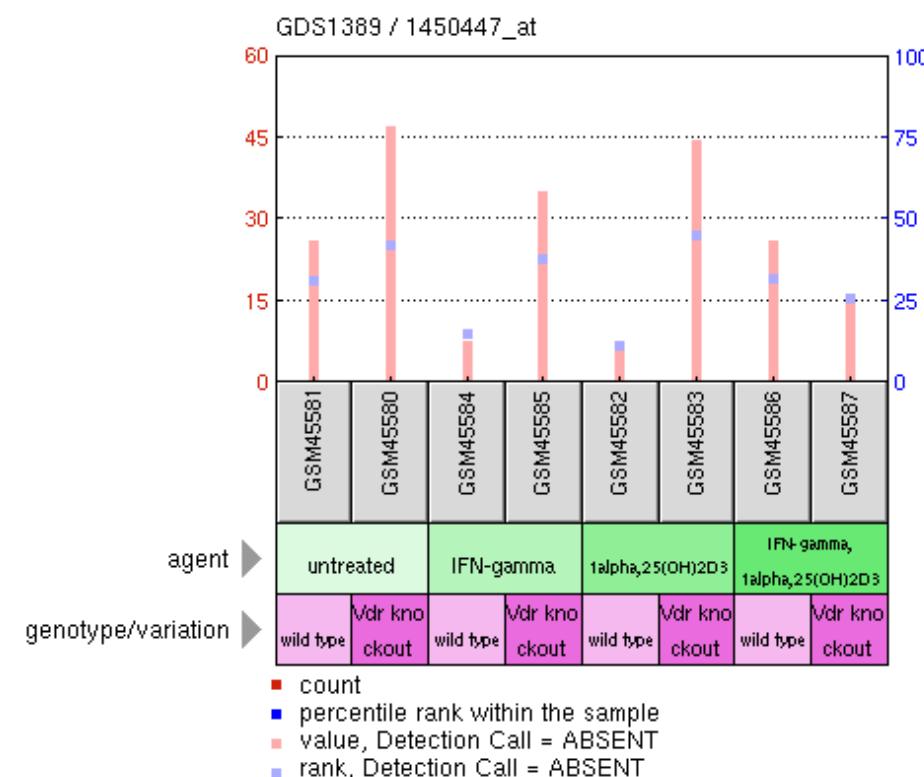
GDS1389 / 1450447\_at

## Title

1alpha,25-dihydroxyvitamin D3  
suppressive effect on IFN-gamma  
activated macrophages

## Organism

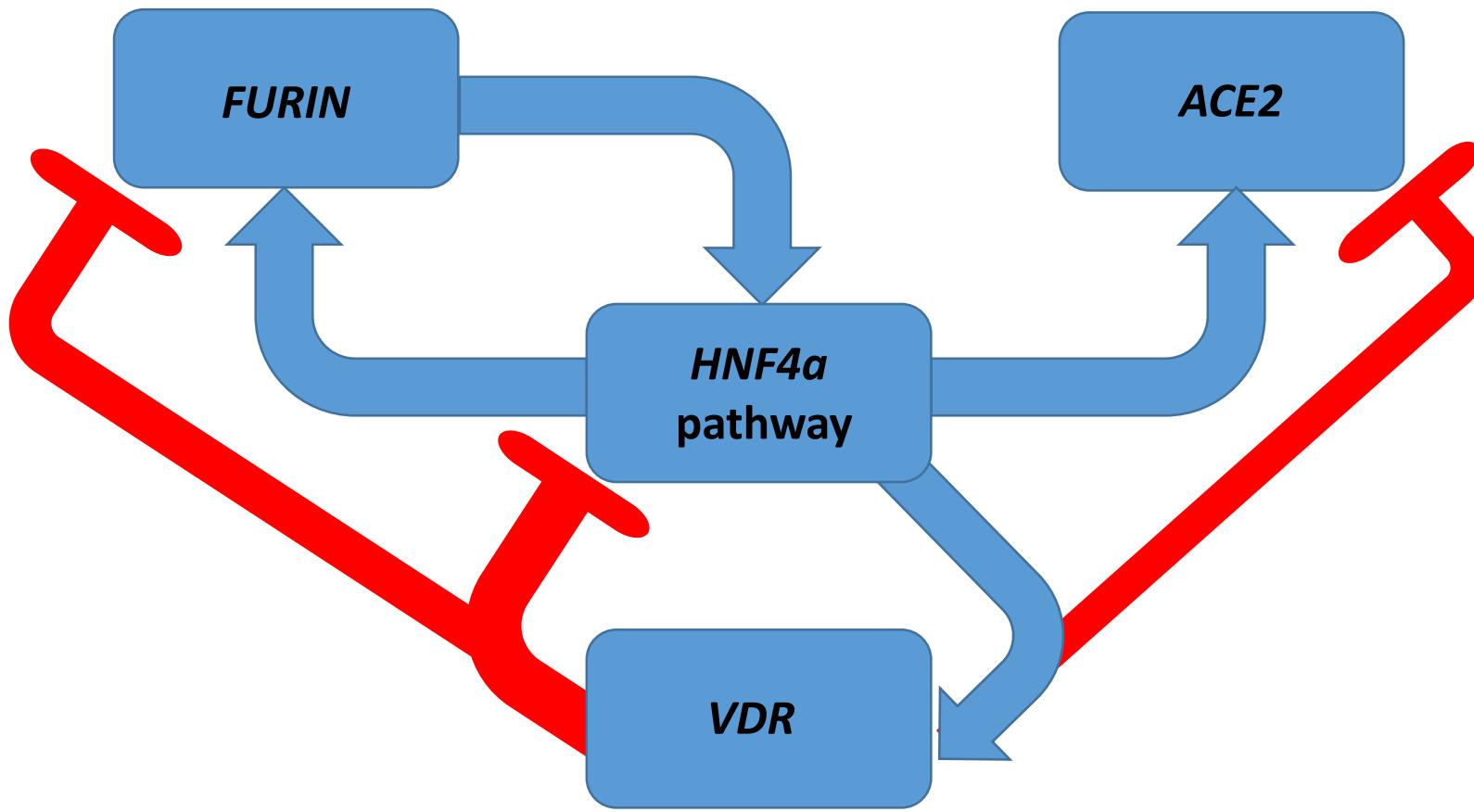
*Mus musculus*



## VDR depletion increases *HNF4a* expression

Sample	Title	Value
<a href="#">GSM45581</a>	0-WT	26.1
<a href="#">GSM45580</a>	0-KO	47.2
<a href="#">GSM45584</a>	IFN-WT	7.8
<a href="#">GSM45585</a>	IFN-KO	35.4
<a href="#">GSM45582</a>	Vit-WT	6.9
<a href="#">GSM45583</a>	Vit-KO	44.6
<a href="#">GSM45586</a>	IFN/Vit-WT	26.2
<a href="#">GSM45587</a>	IFN/Vit-KO	15.1

*HNF4a* pathway-associated activation of the *ACE2* and *FURIN* expression may trigger the auto-regulatory positive feed-back loop of the *FURIN*-mediated activation of the *HNF4a* expression

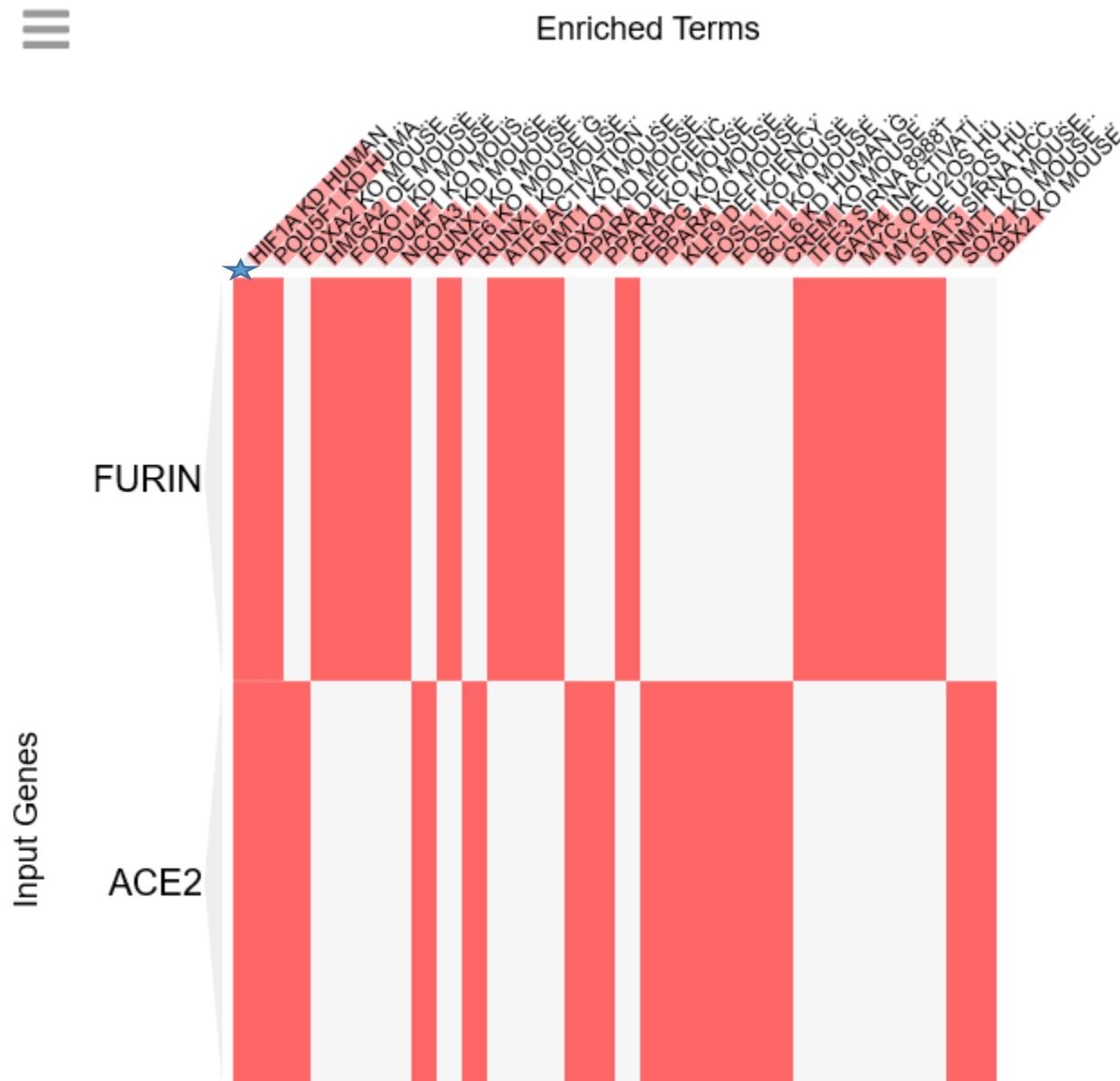


# ACE2 and FURIN

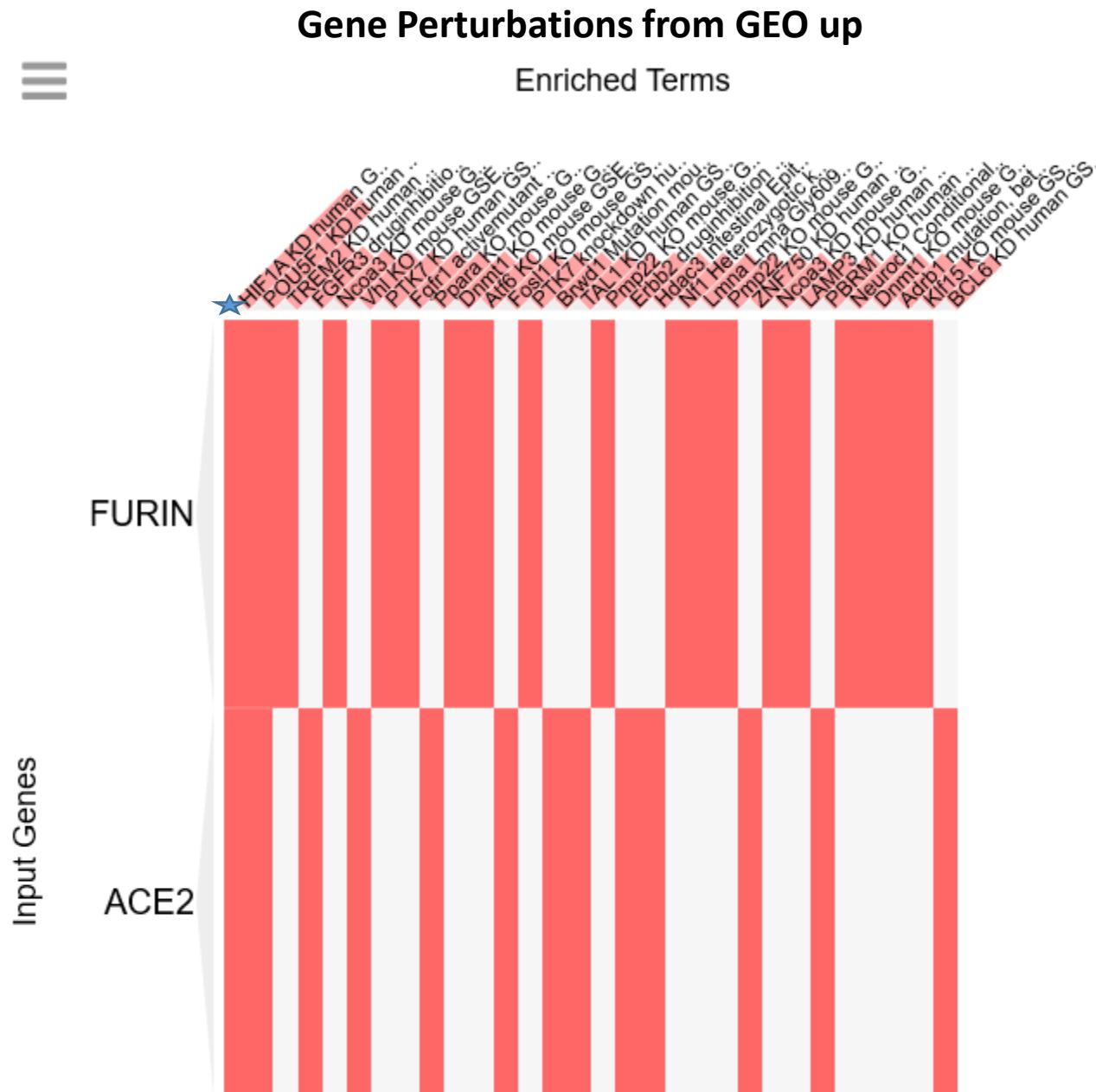
Supplemental Figure S8. Potential mechanisms affecting gene expression:  
*HIF1A* gene product as potential repressor of the *ACE2* expression

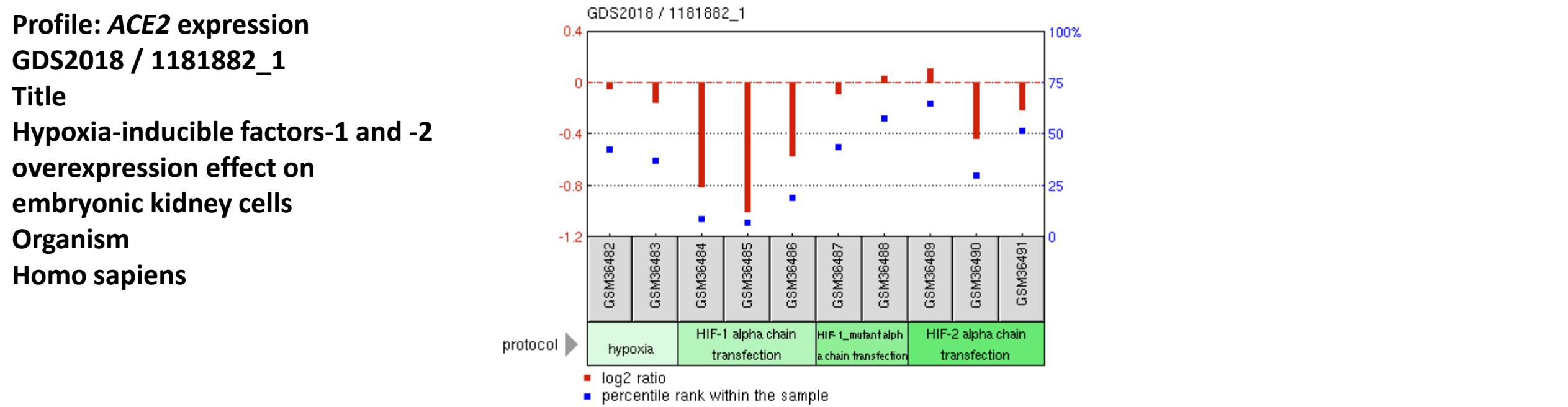
# Predominantly distinct transcription factors affect expression of the ACE2 and FURIN genes

## TF Perturbations Followed by Expression



# *HIF1A* and *POU5F1*: candidate inhibitors of the *ACE2* and *FURIN* expression





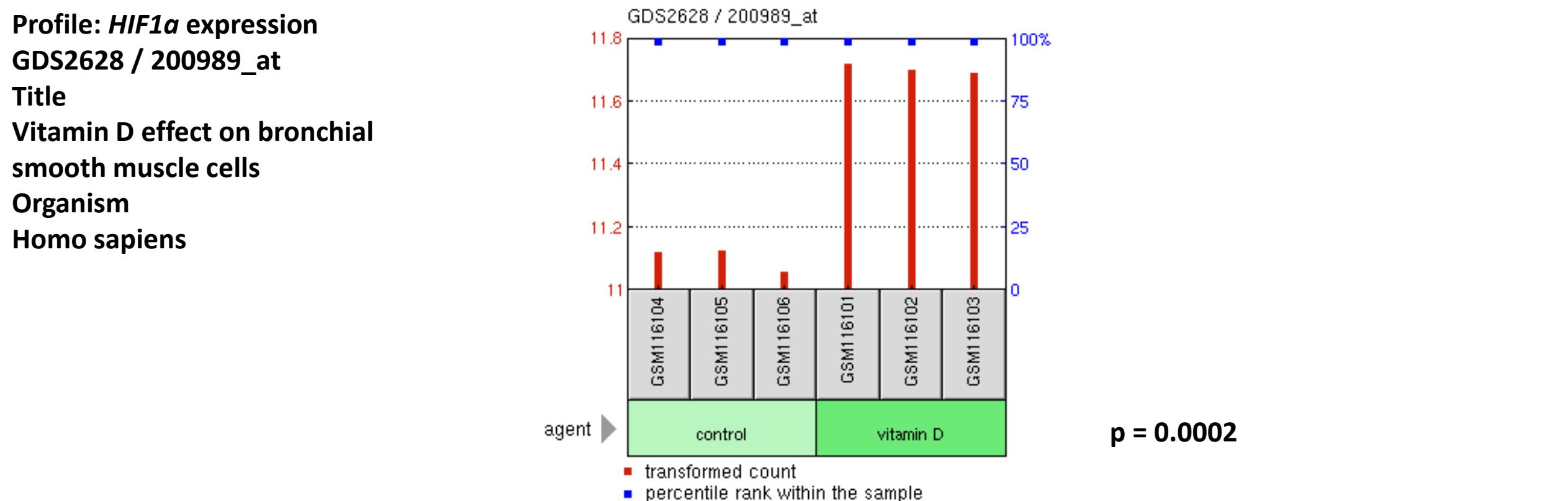
**HIF1a inhibits the ACE2 expression**

Sample	Title	Value
<a href="#">GSM36482</a>	Nor:Hypo rep 1	-0.062
<a href="#">GSM36483</a>	Nor:Hypo rep 2	-0.161
<a href="#">GSM36484</a>	Nor:HIF1a rep 1	<b>-0.821</b>
<a href="#">GSM36485</a>	Nor:HIF1a rep 2	<b>-1.013</b>
<a href="#">GSM36486</a>	Nor:HIF1a rep 3	<b>-0.575</b>
<a href="#">GSM36487</a>	Nor:HIF1amut rep 1	-0.098
<a href="#">GSM36488</a>	Nor:HIF1amut rep 2	0.061
<a href="#">GSM36489</a>	Nor:HIF2a rep 1	<b>0.115</b>
<a href="#">GSM36490</a>	Nor:HIF2a rep 2	<b>-0.44</b>
<a href="#">GSM36491</a>	Nor:HIF2a rep 3	<b>-0.222</b>

p = 0.011

p = 0.007

p = 0.021

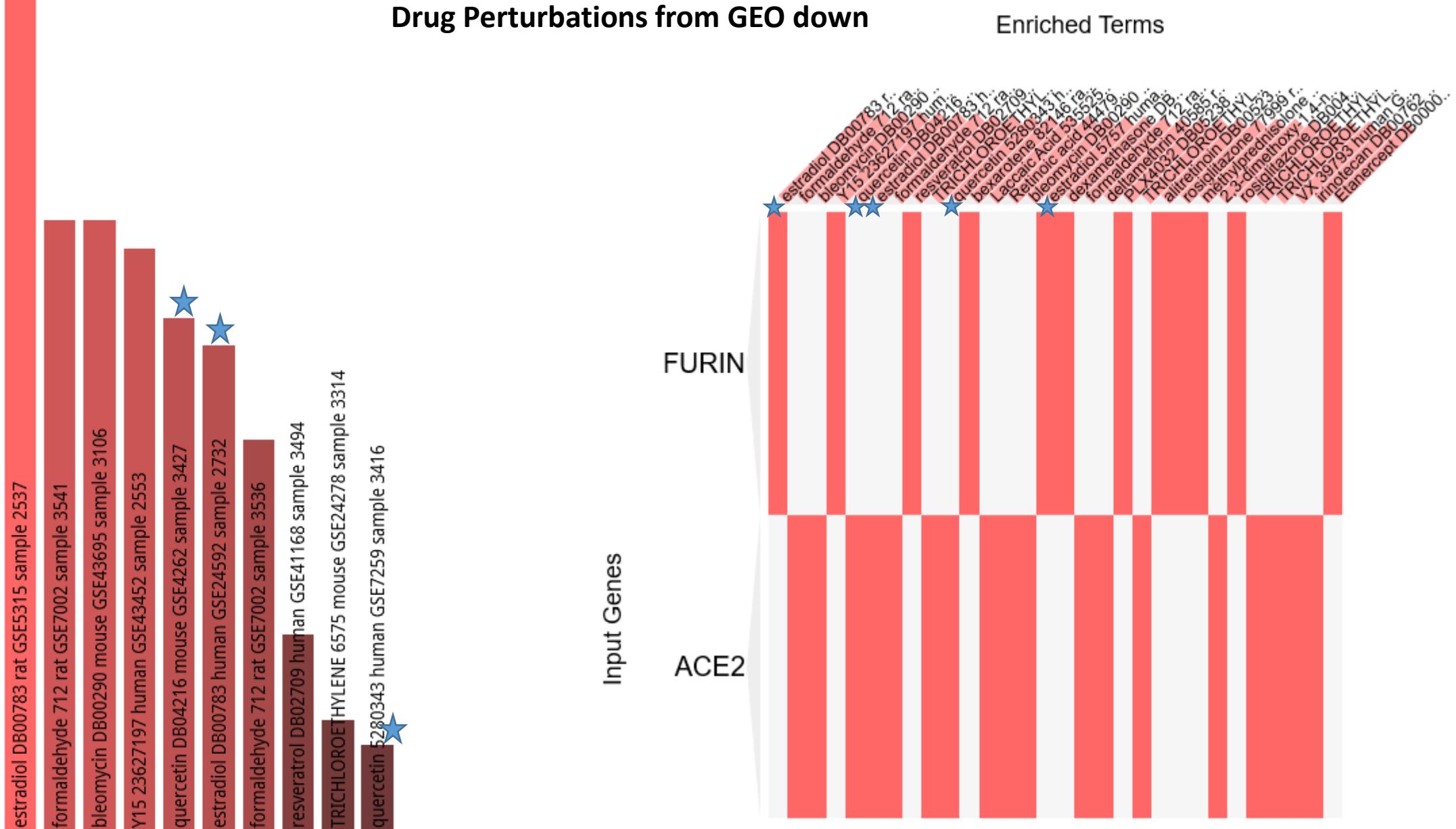


**Vitamin D enhances the *HIF1a* expression**

Sample	Title	Value
<a href="#">GSM116104</a>	hBSMC_control_rep1	11.1243
<a href="#">GSM116105</a>	hBSMC_control_rep2	11.1271
<a href="#">GSM116106</a>	hBSMC_control_rep3	11.0608
<a href="#">GSM116101</a>	hBSMC_vitamin D_rep1	11.7223
<a href="#">GSM116102</a>	hBSMC_vitamin D_rep2	11.7034
<a href="#">GSM116103</a>	hBSMC_vitamin D_rep3	11.6893

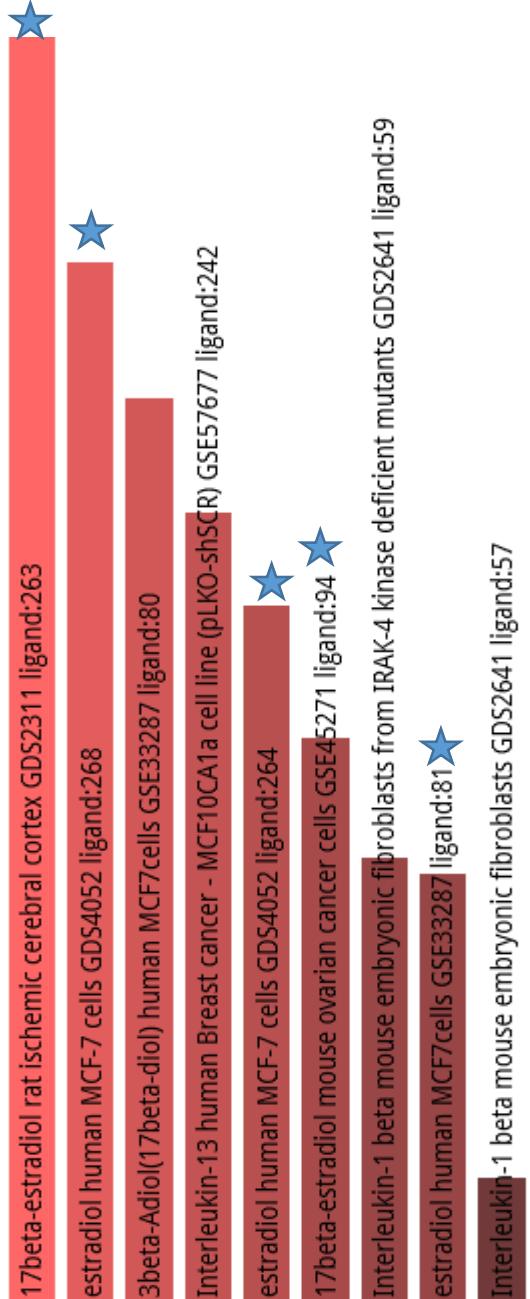
Supplemental Figure S9. GSEA identify Estradiol and Quercetin as potential candidate coronavirus infection mitigation agents

Distinct patterns of drugs down-regulating expression of the *ACE2* and *FURIN* genes:  
**Estradiol and Quercetin emerged as promising candidate coronavirus infection mitigation agents**



# Distinct patterns of ligands down-regulating expression of the *ACE2* and *FURIN* genes

## Ligand Perturbations from GEO down



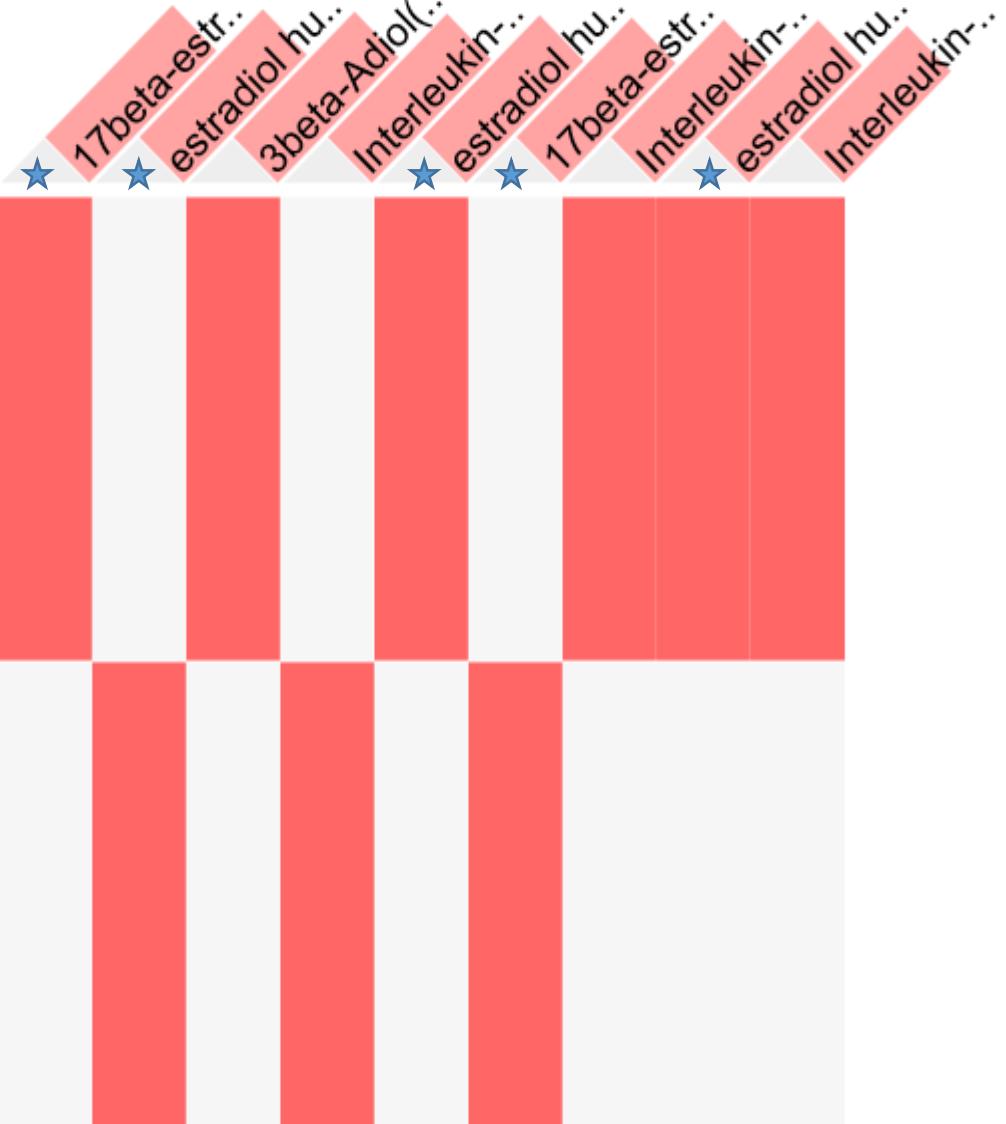
≡

Input Genes

ACE2

FURIN

Enriched Terms



Profile: *c-FOS* expression

GDS3133 / 1375043\_at

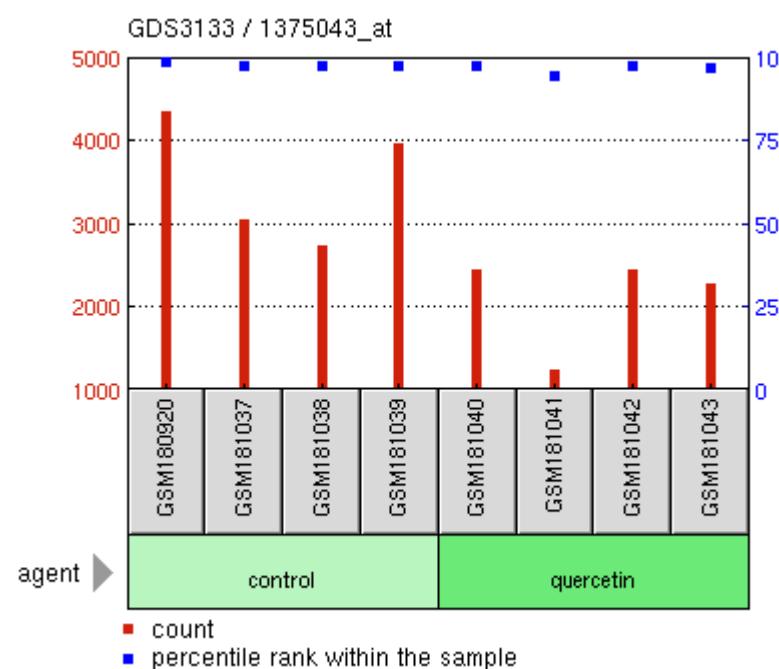
Title

Quercetin effect on the colonic

mucosa

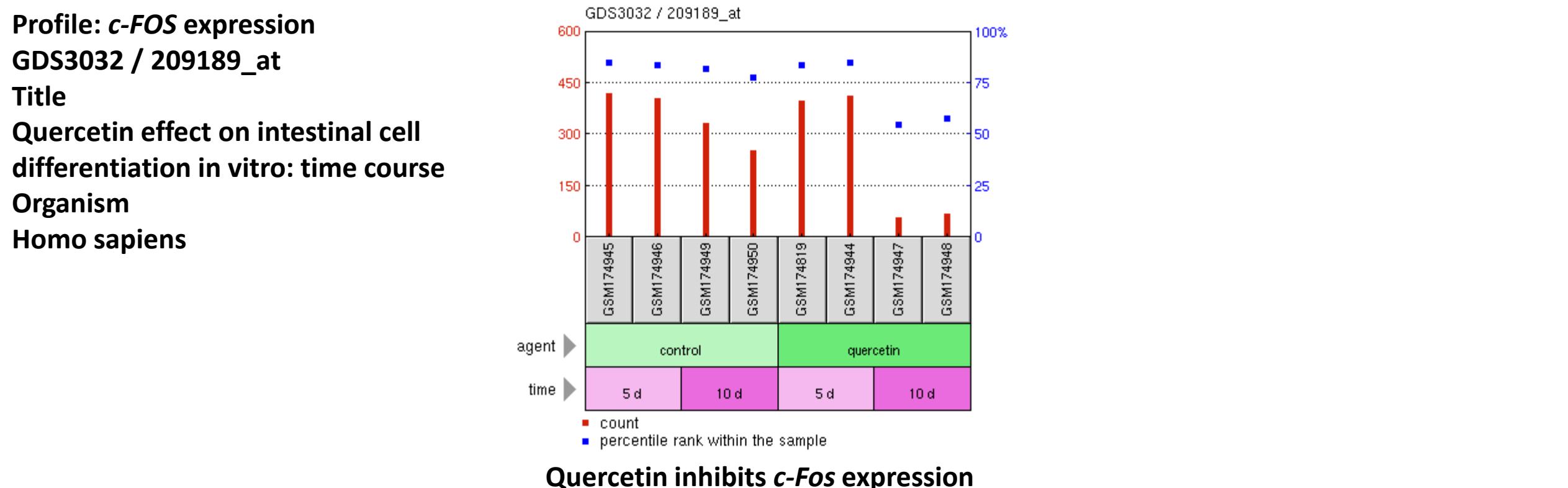
Organism

Rattus norvegicus



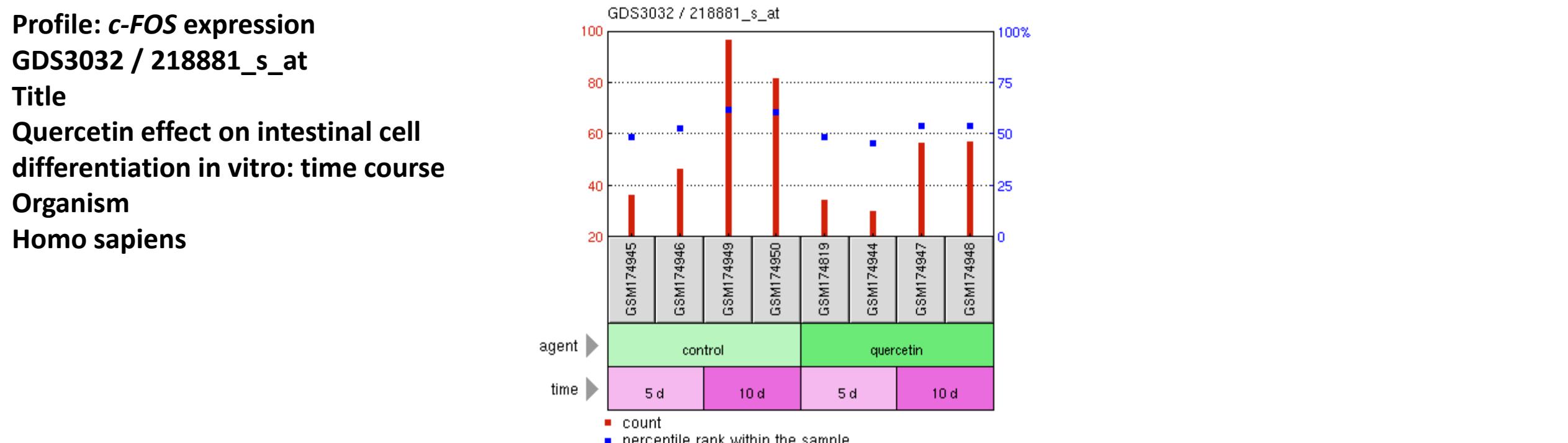
### Quercetin inhibits *c-Fos* expression

Sample	Title	Value
<a href="#">GSM180920</a>	Control, sample 1	4352.72
<a href="#">GSM181037</a>	Control, sample 2	3050.22
<a href="#">GSM181038</a>	Control, sample 3	2743.92
<a href="#">GSM181039</a>	Control, sample 4	3972.13
<a href="#">GSM181040</a>	Quercetin, sample 1	2451.67
<a href="#">GSM181041</a>	Quercetin, sample 2	1258.62
<a href="#">GSM181042</a>	Quercetin, sample 3	2468.64
<a href="#">GSM181043</a>	Quercetin, sample 4	2279.08



### Quercetin inhibits *c-Fos* expression

Sample	Title	Value
<a href="#">GSM174945</a>	Control day 05 sample 1	420.956
<a href="#">GSM174946</a>	Control day 05 sample 2	404.99
<a href="#">GSM174949</a>	Control day 10 sample 1	332.662
<a href="#">GSM174950</a>	Control day 10 sample 2	256.542
<a href="#">GSM174819</a>	Quercetin day 05 sample 1	399.894
<a href="#">GSM174944</a>	Quercetin day 05 sample 2	413.261
<a href="#">GSM174947</a>	Quercetin day 10 sample 1	60.5856
<a href="#">GSM174948</a>	Quercetin day 10 sample 2	71.7716



### Quercetin inhibits *c-Fos* expression

Sample	Title	Value
<a href="#">GSM174945</a>	Control day 05 sample 1	36.7758
<a href="#">GSM174946</a>	Control day 05 sample 2	46.8416
<a href="#">GSM174949</a>	Control day 10 sample 1	96.6905
<a href="#">GSM174950</a>	Control day 10 sample 2	81.9045
<a href="#">GSM174819</a>	Quercetin day 05 sample 1	34.7583
<a href="#">GSM174944</a>	Quercetin day 05 sample 2	30.5511
<a href="#">GSM174947</a>	Quercetin day 10 sample 1	56.9884
<a href="#">GSM174948</a>	Quercetin day 10 sample 2	57.2094

Profile: *Runx1* expression

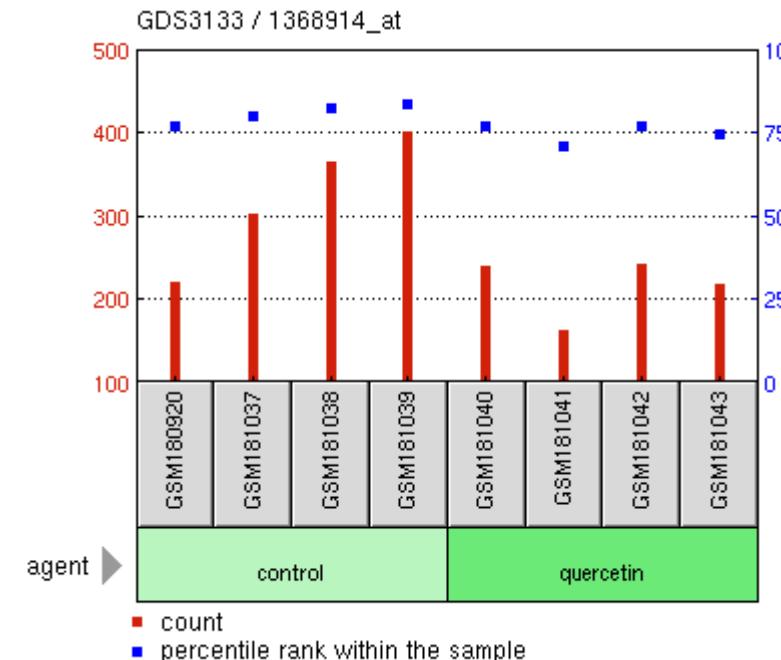
GDS3133 / 1368914\_at

Title

Quercetin effect on the colonic mucosa

Organism

Rattus norvegicus



## Quercetin inhibits *Runx1* expression

Sample	Title	Value
<a href="#">GSM180920</a>	Control, sample 1	222.664
<a href="#">GSM181037</a>	Control, sample 2	302.432
<a href="#">GSM181038</a>	Control, sample 3	366.811
<a href="#">GSM181039</a>	Control, sample 4	402.875
<a href="#">GSM181040</a>	Quercetin, sample 1	241.637
<a href="#">GSM181041</a>	Quercetin, sample 2	163.728
<a href="#">GSM181042</a>	Quercetin, sample 3	243.316
<a href="#">GSM181043</a>	Quercetin, sample 4	218.646

**Profile: Runx1 expression**

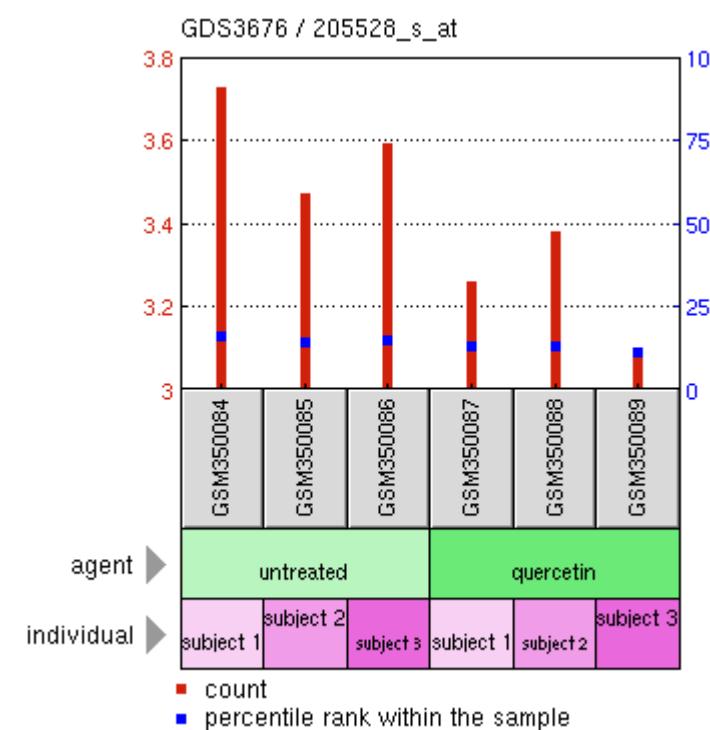
**GDS3676 / 205528\_s\_at**

**Title**

**Quercetin effect on CD14+ monocyte**

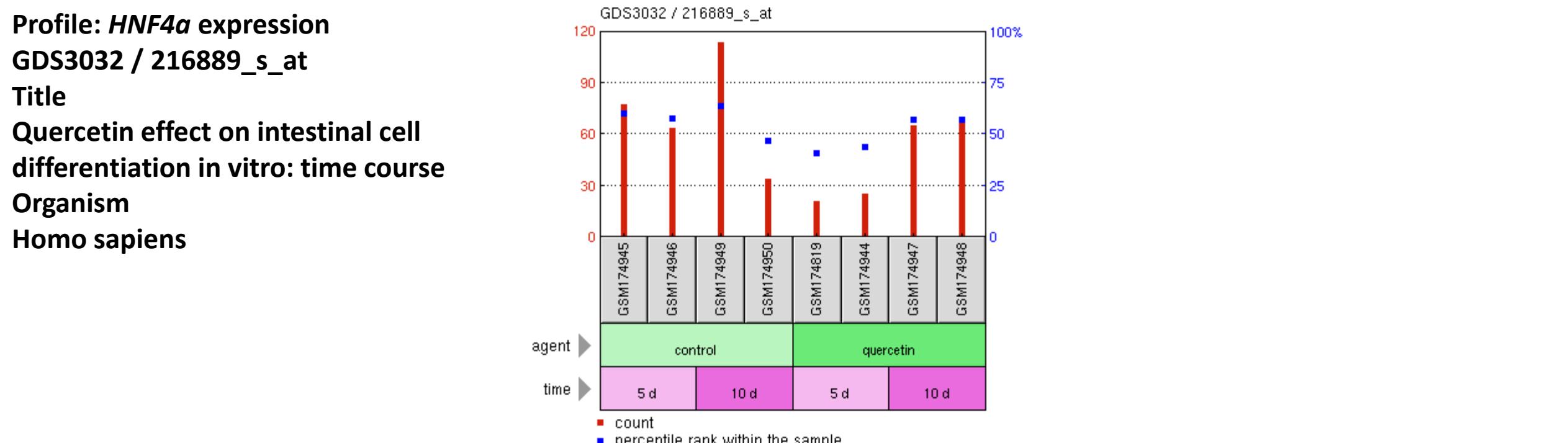
**Organism**

**Homo sapiens**



### Quercetin inhibits *Runx1* expression

Sample	Title	Value
<a href="#">GSM350084</a>	CD14+ at baseline, biological replicate 1	3.72993
<a href="#">GSM350085</a>	CD14+ at baseline, biological replicate 2	3.47495
<a href="#">GSM350086</a>	CD14+ at baseline, biological replicate 3	3.59744
<a href="#">GSM350087</a>	CD14+ after 2 wk quercetin supplementation, biological replicate 1	3.2641
<a href="#">GSM350088</a>	CD14+ after 2 wk quercetin supplementation, biological replicate 2	3.38173
<a href="#">GSM350089</a>	CD14+ after 2 wk quercetin supplementation, biological replicate 3	3.10117



### Quercetin inhibits *HNF4a* expression

Sample	Title	Value
<a href="#">GSM174945</a>	Control day 05 sample 1	<b>77.6175</b>
<a href="#">GSM174946</a>	Control day 05 sample 2	<b>63.792</b>
<a href="#">GSM174949</a>	Control day 10 sample 1	113.821
<a href="#">GSM174950</a>	Control day 10 sample 2	34.1332
<a href="#">GSM174819</a>	Quercetin day 05 sample 1	<b>21.0188</b>
<a href="#">GSM174944</a>	Quercetin day 05 sample 2	<b>25.7496</b>
<a href="#">GSM174947</a>	Quercetin day 10 sample 1	65.2834
<a href="#">GSM174948</a>	Quercetin day 10 sample 2	69.9663

# Profile: *c-FOS* expression

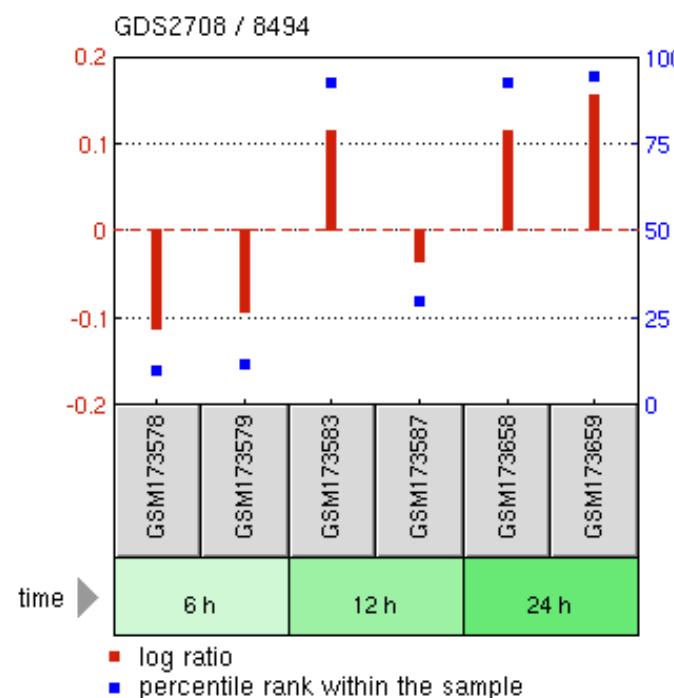
GDS2708 / 8494

## Title

Quercetin effect on cultured cardiomyocytes: time course

## Organism

Rattus norvegicus

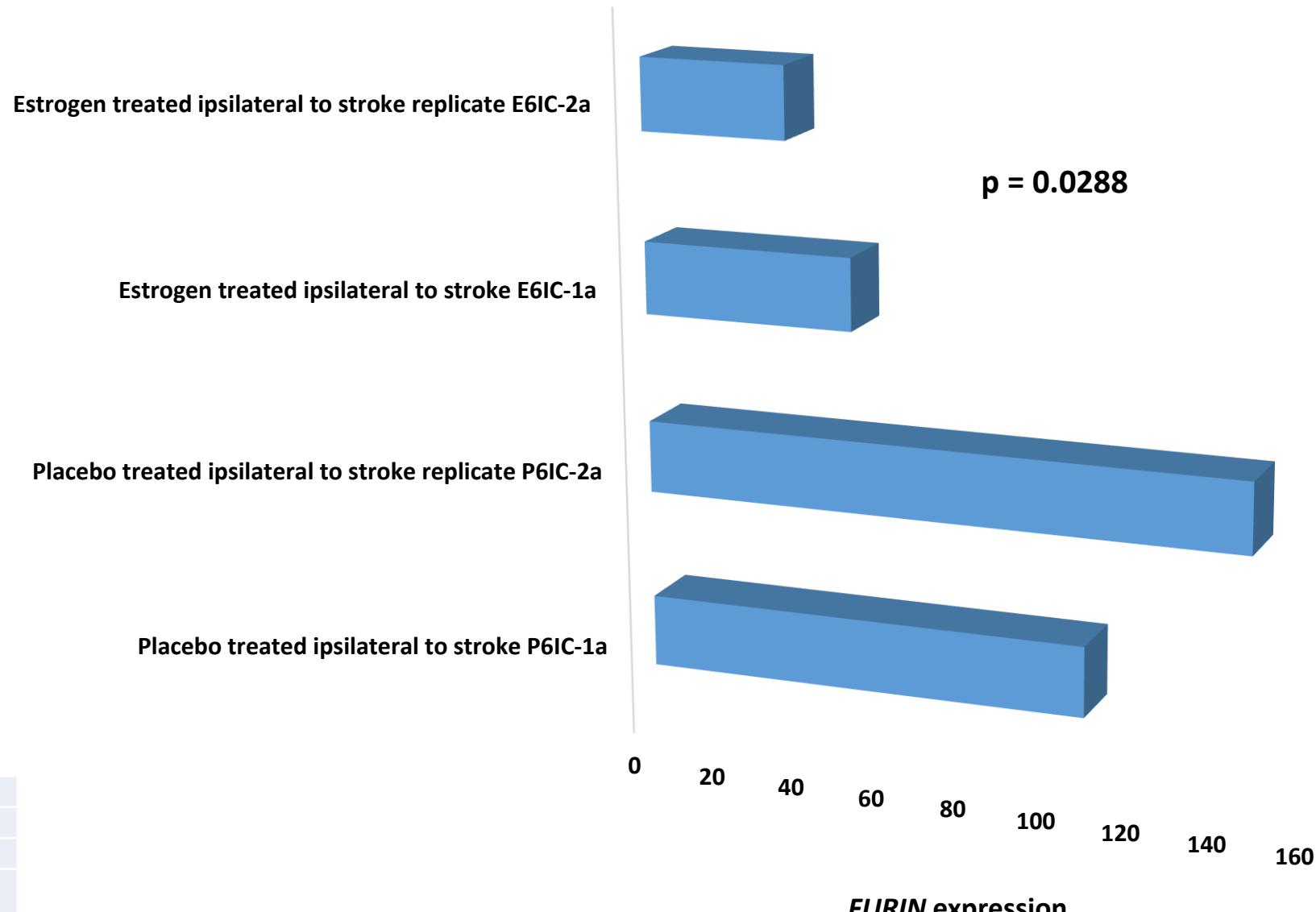


## Quercetin increases *c-Fos* expression

Sample	Title	Value
<a href="#">GSM173578</a>	Quercetin treated cardiomyocytes for 6 hours (Q6-A).	-0.114041
<a href="#">GSM173579</a>	Quercetin treated cardiomyocytes for 6 hours (Q6-B).	-0.0962766
<a href="#">GSM173583</a>	Quercetin treated cardiomyocytes for 12 hours (Q12-A).	0.118043
<a href="#">GSM173587</a>	Quercetin treated cardiomyocytes for 12 hours (Q12-B).	-0.0368638
<a href="#">GSM173658</a>	Quercetin treated cardiomyocytes for 24 hours (Q24-A).	0.118043
<a href="#">GSM173659</a>	Quercetin treated cardiomyocytes for 24 hours (Q24-B).	0.15779

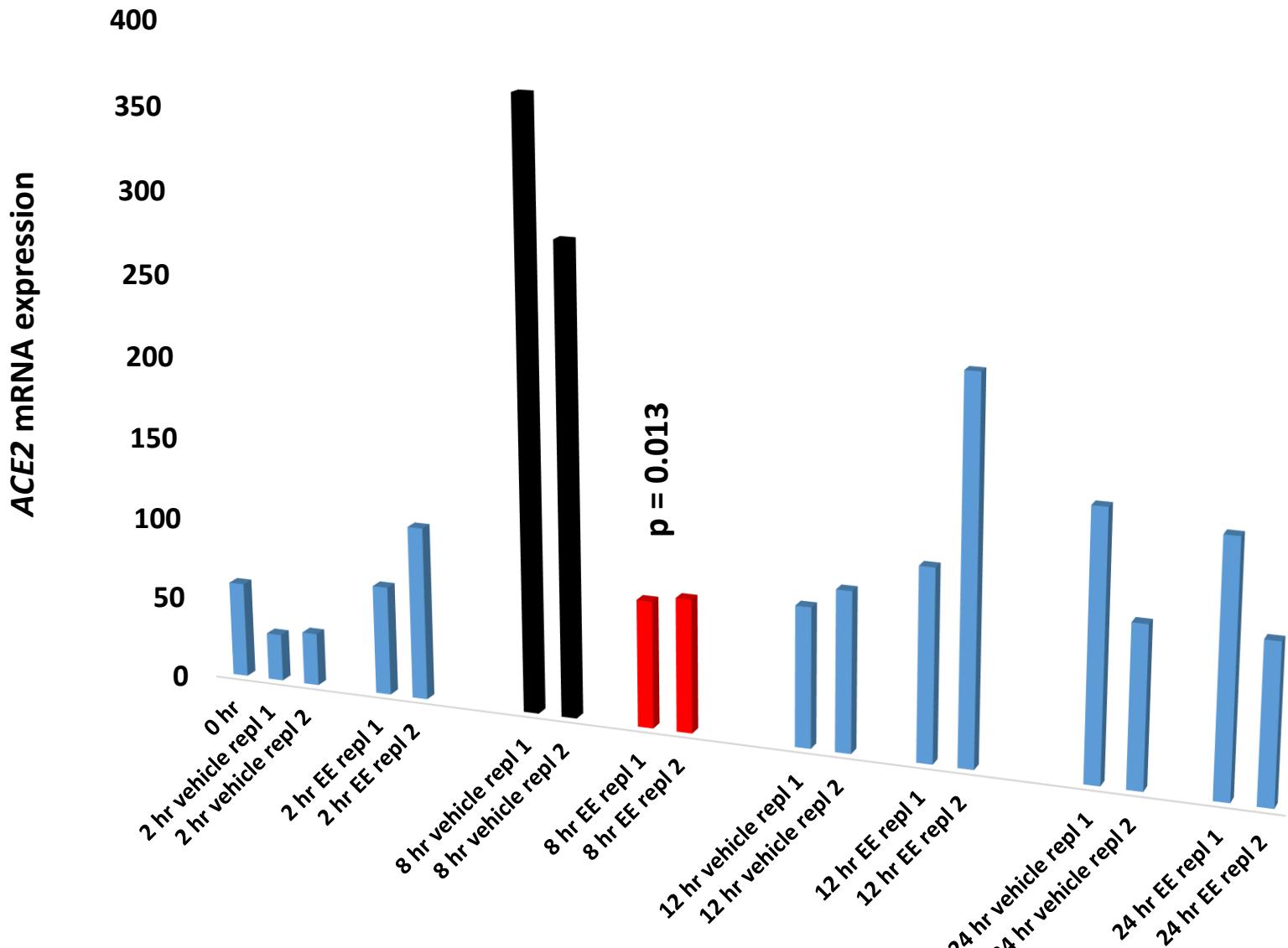
Supplemental Figure S10. Confirmation of the Estradiol and Quercetin activities as potential candidate coronavirus infection mitigation agents

## Estradiol effect on *FURIN* expression in the rat ischemic brain



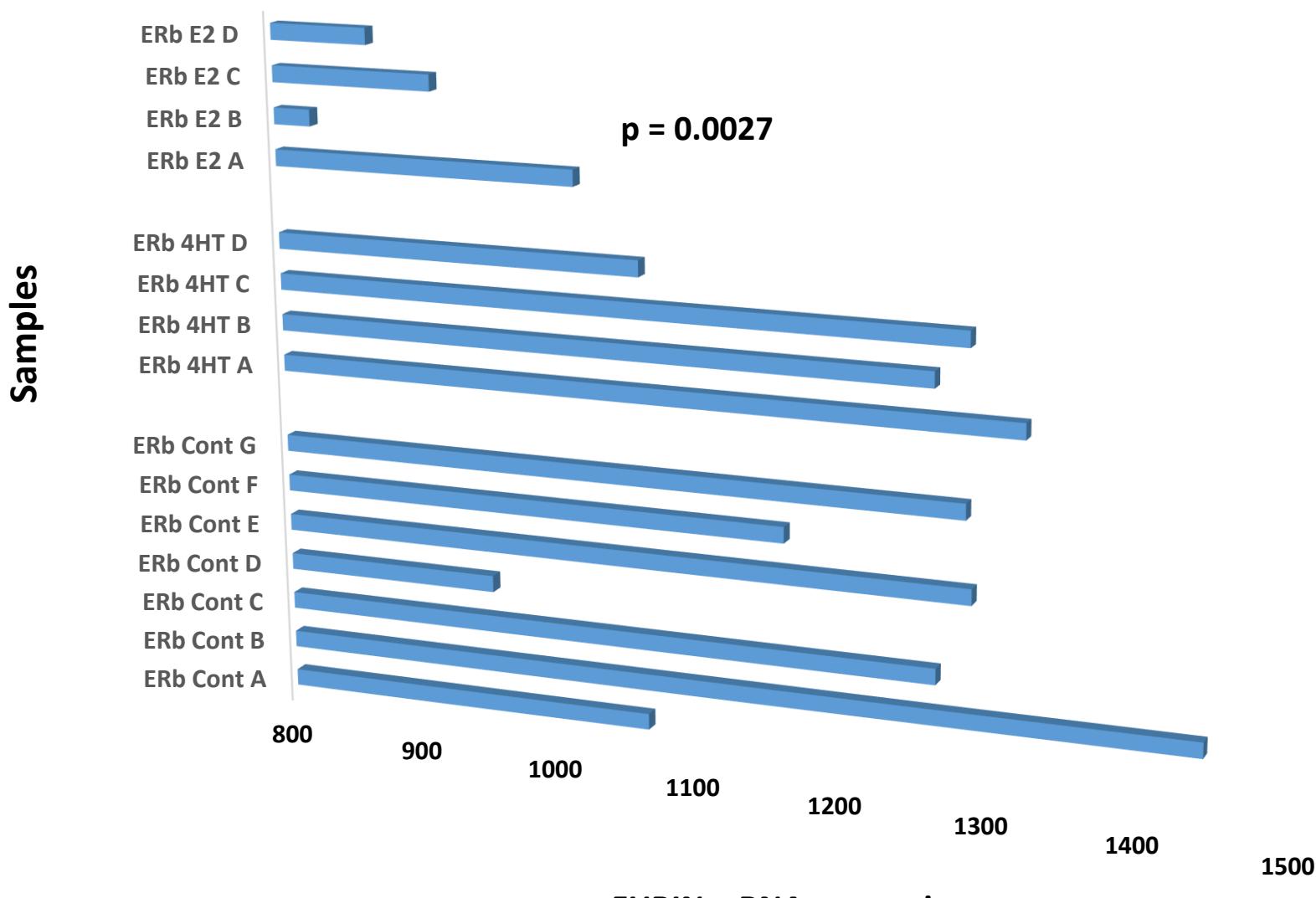
GEO Profile
GDS2311 / X55660_at
Title
Estradiol effect on the ischemic brain
Organism
Rattus norvegicus

## Ethylyn estradiol effects on ACE2 expression in mouse uterus



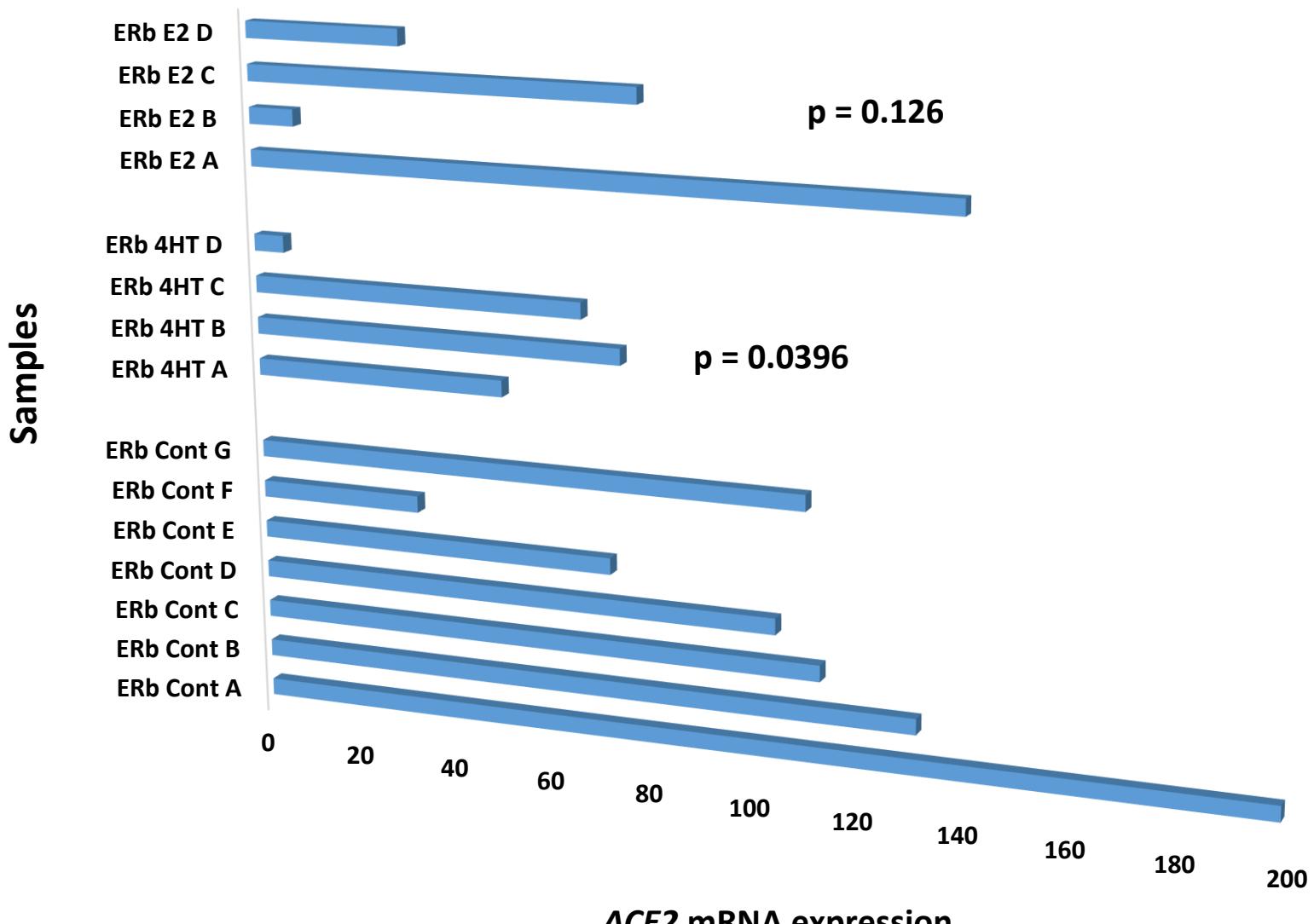
GEO Profile
GDS285 / AA690434_at
Title
Ethylyn estradiol estrogen effect in uterus
Organism
Mus musculus

## Effects of estradiol and tamoxifen on *FURIN* expression mediated by the estrogen receptor beta



GEO Profile
GDS1094 / 201945_at
Title
Estrogen receptor alpha/beta heterodimer action in response to estrogen and tamoxifen
Organism
Homo sapiens

*Effects of estradiol and tamoxifen on ACE2 expression mediated by the estrogen receptor beta*



GEO Profile
GDS1094 / 219962_at
Title
Estrogen receptor alpha/beta heterodimer action in response to estrogen and tamoxifen
Organism
Homo sapiens

Profile: ACE2 expression

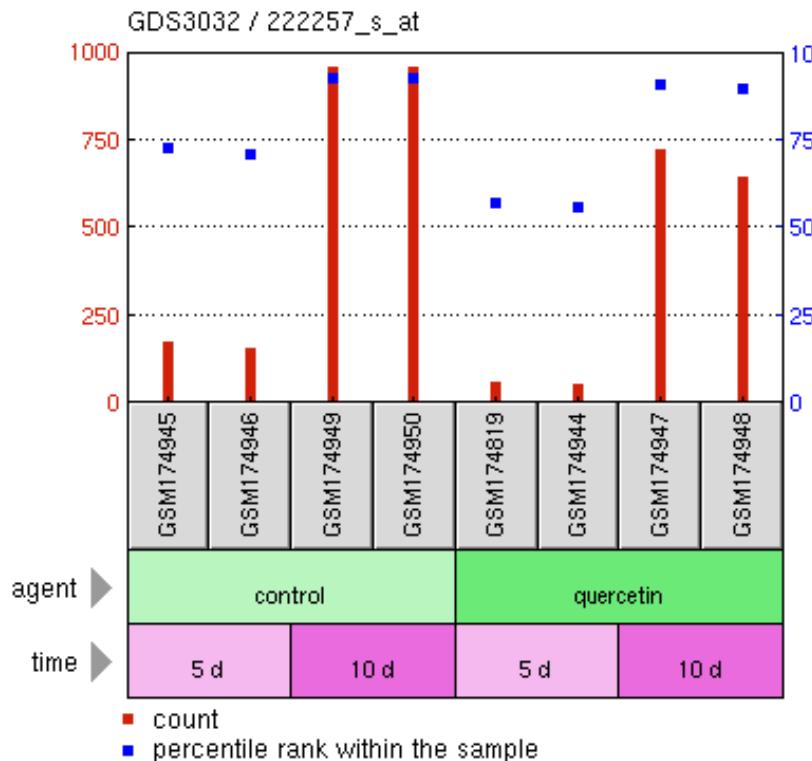
GDS3032 / 222257\_s\_at

Title

Quercetin effect on intestinal cell differentiation in vitro: time course

Organism

Homo sapiens



Day 5  
p = 0.004

Day 10  
p = 0.009

Quercetin inhibits the ACE2 expression

Sample	Title	Value
<a href="#">GSM174945</a>	Control day 05 sample 1	176.763
<a href="#">GSM174946</a>	Control day 05 sample 2	157.459
<a href="#">GSM174949</a>	Control day 10 sample 1	962.644
<a href="#">GSM174950</a>	Control day 10 sample 2	959.364
<a href="#">GSM174819</a>	Quercetin day 05 sample 1	60.6977
<a href="#">GSM174944</a>	Quercetin day 05 sample 2	59.0821
<a href="#">GSM174947</a>	Quercetin day 10 sample 1	725.488
<a href="#">GSM174948</a>	Quercetin day 10 sample 2	649.304

Profile: ACE2 expression

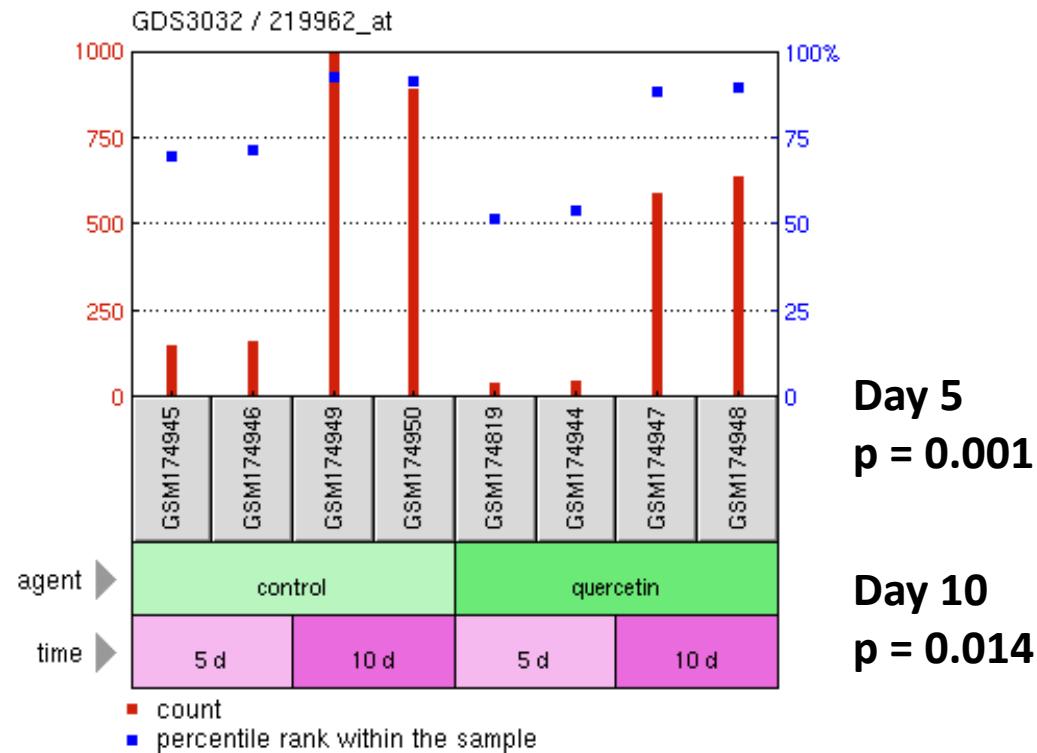
GDS3032 / 219962\_at

Title

Quercetin effect on intestinal cell differentiation in vitro: time course

Organism

Homo sapiens



Quercetin inhibits the ACE2 expression

Sample	Title	Value
<a href="#">GSM174945</a>	Control day 05 sample 1	152.856
<a href="#">GSM174946</a>	Control day 05 sample 2	163.228
<a href="#">GSM174949</a>	Control day 10 sample 1	995.184
<a href="#">GSM174950</a>	Control day 10 sample 2	895.468
<a href="#">GSM174819</a>	Quercetin day 05 sample 1	43.9228
<a href="#">GSM174944</a>	Quercetin day 05 sample 2	49.8735
<a href="#">GSM174947</a>	Quercetin day 10 sample 1	595.486
<a href="#">GSM174948</a>	Quercetin day 10 sample 2	642.974

**Profile: *c-FOS* expression**

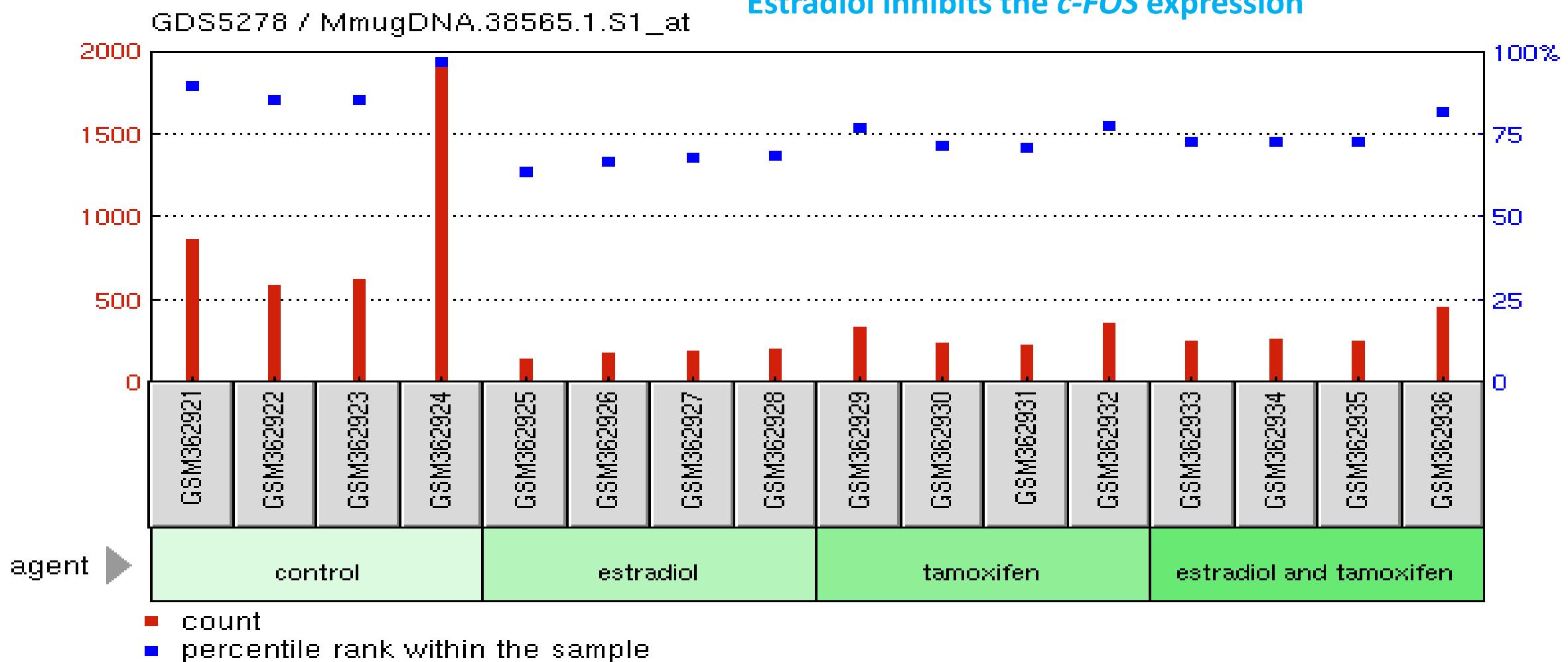
**GDS5278 / MmugDNA.38565.1.S1\_at**

**Title**

**Endometrium response to tamoxifen and low dose estradiol combination therapy**

**Organism: Macaca mulatta**

**Estradiol inhibits the *c-FOS* expression**



**Profile: *c-FOS* expression**

**GDS5278 / MmugDNA.38565.1.S1\_at**

**Title**

**Endometrium response to tamoxifen and low dose estradiol combination therapy**

**Organism: Macaca mulatta**

**Estradiol inhibits the *c-FOS* expression**

Sample	Title	Value
<a href="#">GSM362921</a>	Control 1	868.444
<a href="#">GSM362922</a>	Control 2	596.312
<a href="#">GSM362923</a>	Control 3	633.478
<a href="#">GSM362924</a>	Control 4	1956.61
<a href="#">GSM362925</a>	Estradiol 1	147.047
<a href="#">GSM362926</a>	Estradiol 2	183.666
<a href="#">GSM362927</a>	Estradiol 3	194.779
<a href="#">GSM362928</a>	Estradiol 4	212.397
<a href="#">GSM362929</a>	Tamoxifen 1	347.062
<a href="#">GSM362930</a>	Tamoxifen 2	241.809
<a href="#">GSM362931</a>	Tamoxifen 3	238.437
<a href="#">GSM362932</a>	Tamoxifen 4	363.108
<a href="#">GSM362933</a>	Estradiol and Tamoxifen 1	255.806
<a href="#">GSM362934</a>	Estradiol and Tamoxifen 2	272.225
<a href="#">GSM362935</a>	Estradiol and Tamoxifen 3	264.55
<a href="#">GSM362936</a>	Estradiol and Tamoxifen 4	459.833

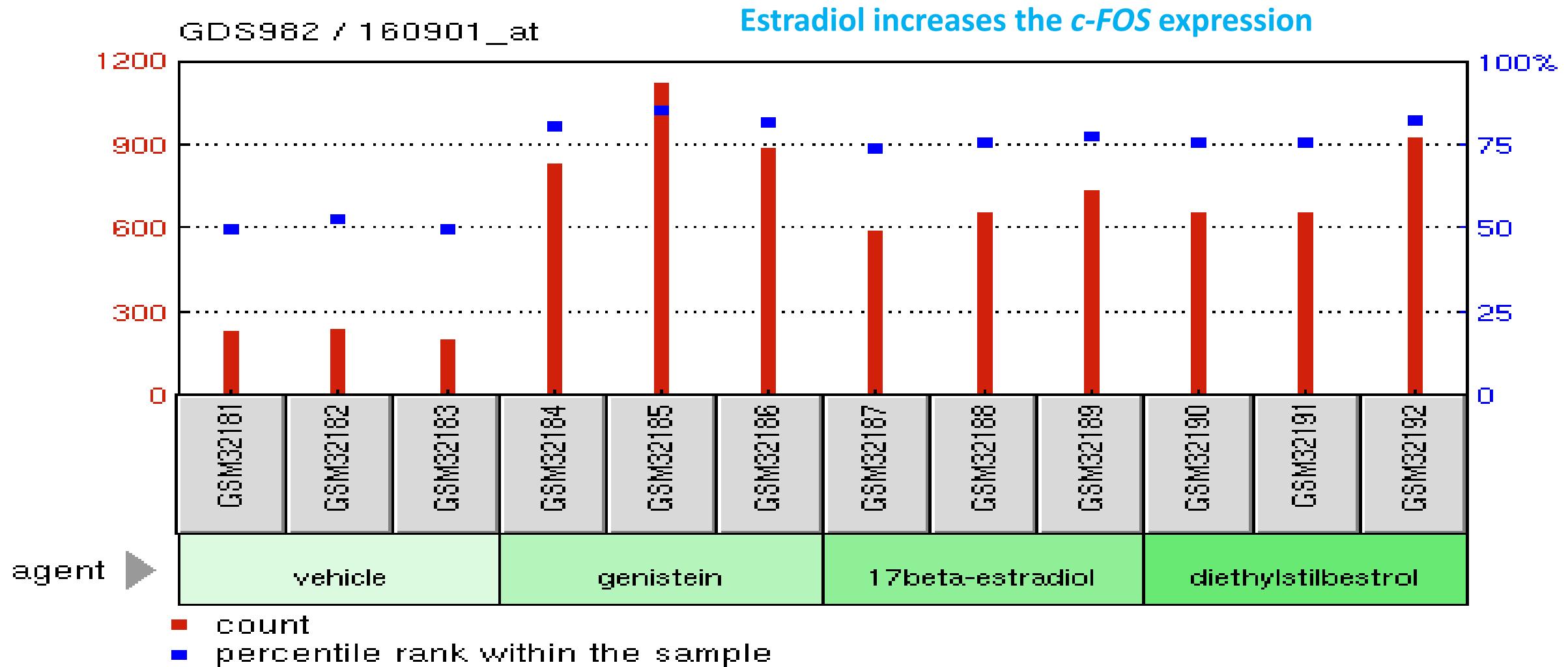
Profile: *c-FOS* expression

GDS982 / 160901\_at

Title

Uterine response to physiologic, plant-derived, and synthetic estrogen

Organism: *Mus musculus*



**Profile: *c-FOS* expression**

**GDS982 / 160901\_at**

**Title**

**Uterine response to physiologic, plant-derived, and synthetic estrogen**

**Organism**

**Mus musculus**

**Estradiol increases the *c-FOS* expression**

Sample	Title	Value
<a href="#"><u>GSM32181</u></a>	AO C1	236.8
<a href="#"><u>GSM32182</u></a>	AO C2	239.8
<a href="#"><u>GSM32183</u></a>	AO C3	208.6
<a href="#"><u>GSM32184</u></a>	GEN G1	834.7
<a href="#"><u>GSM32185</u></a>	GEN G2	1122.6
<a href="#"><u>GSM32186</u></a>	GEN G3	892.9
<a href="#"><u>GSM32187</u></a>	E2 E1	599.6
<a href="#"><u>GSM32188</u></a>	E2 E2	660.6
<a href="#"><u>GSM32189</u></a>	E2 E3	740.3
<a href="#"><u>GSM32190</u></a>	DES D1	659.8
<a href="#"><u>GSM32191</u></a>	DES D2	663.9
<a href="#"><u>GSM32192</u></a>	DES D3	928.8

# Supplemental Figure S11. Testosterone effects on gene expression

An overview of the potential coronavirus-infection promoting activities

**Profile: ACE2 expression**

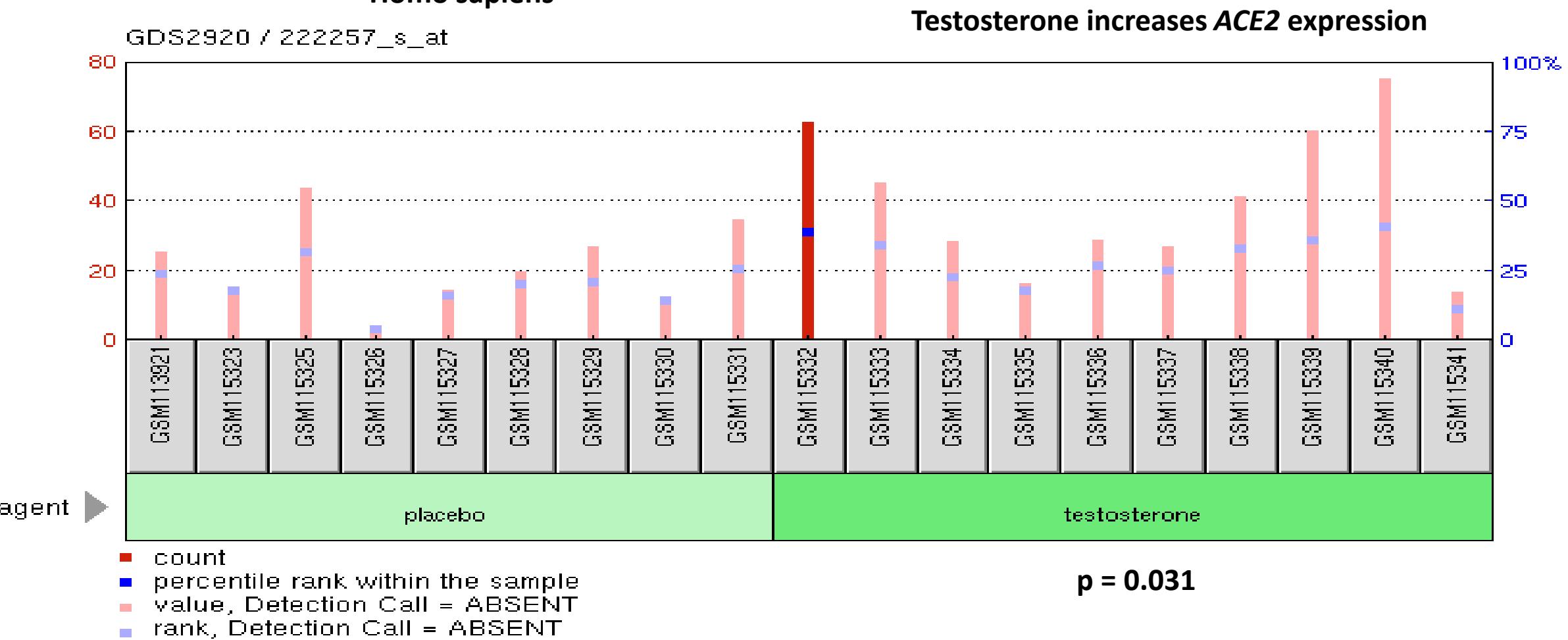
**GDS2920 / 222257\_s\_at**

**Title**

**Testosterone effect on skeletal muscles of HIV-infected males experiencing weight loss**

**Organism**

**Homo sapiens**



**Profile: ACE2 expression****GDS2920 / 222257\_s\_at****Title****Testosterone effect on skeletal muscles of HIV-infected males experiencing weight loss****Organism****Homo sapiens****Testosterone increases ACE2 expression**

Sample	Title	Value
<a href="#">GSM113921</a>	Placebo treated, HIV-1 positive male, day 14 (1)	25.8
<a href="#">GSM115323</a>	Placebo treated, HIV-1 positive male, day 14 (2)	14.3
<a href="#">GSM115325</a>	Placebo treated, HIV-1 positive male, day 14 (3)	44.3
<a href="#">GSM115326</a>	Placebo treated, HIV-1 positive male, day 14 (4)	3.1
<a href="#">GSM115327</a>	Placebo treated, HIV-1 positive male, day 14 (5)	14.8
<a href="#">GSM115328</a>	Placebo treated, HIV-1 positive male, day 14 (6)	20.2
<a href="#">GSM115329</a>	Placebo treated, HIV-1 positive male, day 14 (7)	27
<a href="#">GSM115330</a>	Placebo treated, HIV-1 positive male, day 14 (8)	11.7
<a href="#">GSM115331</a>	Placebo treated, HIV-1 positive male, day 14 (9)	34.9
<a href="#">GSM115332</a>	Testosterone treated, HIV-1 positive male, day 14 (1)	63.1
<a href="#">GSM115333</a>	Testosterone treated, HIV-1 positive male, day 14 (2)	45.6
<a href="#">GSM115334</a>	Testosterone treated, HIV-1 positive male, day 14 (3)	28.8
<a href="#">GSM115335</a>	Testosterone treated, HIV-1 positive male, day 14 (4)	16.8
<a href="#">GSM115336</a>	Testosterone treated, HIV-1 positive male, day 14 (5)	29.2
<a href="#">GSM115337</a>	Testosterone treated, HIV-1 positive male, day 14 (6)	27.3
<a href="#">GSM115338</a>	Testosterone treated, HIV-1 positive male, day 14 (7)	41.7
<a href="#">GSM115339</a>	Testosterone treated, HIV-1 positive male, day 14 (8)	60.3
<a href="#">GSM115340</a>	Testosterone treated, HIV-1 positive male, day 14 (9)	75.5
<a href="#">GSM115341</a>	Testosterone treated, HIV-1 positive male, day 14 (10)	14.1

# Profile: ACE2 expression

GDS1361 / 1598

## Title

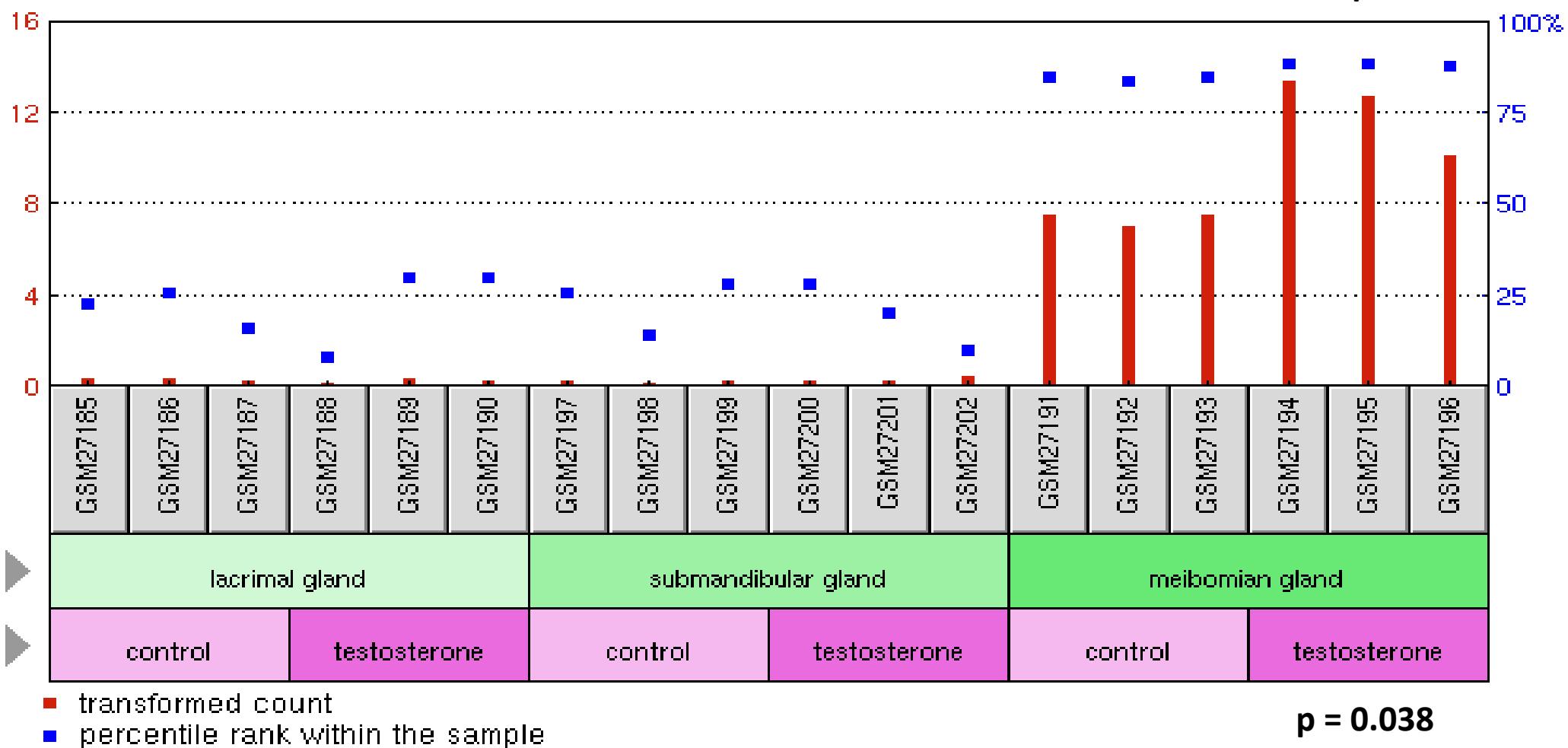
Testosterone effect on meibomian gland

## Organism

Mus musculus

GDS1361 / 1598

Testosterone increases ACE2 expression



# Profile: ACE2 expression

GDS1361 / 1598

## Title

Testosterone effect on meibomian gland

## Organism

Mus musculus

Testosterone increases ACE2 expression

Sample	Title	Value
<a href="#">GSM27185</a>	Male Placebo-Treated Lacrimal Gland Sample A	0.432225
<a href="#">GSM27186</a>	Male Placebo-Treated Lacrimal Gland Sample B	0.457711
<a href="#">GSM27187</a>	Male Placeo-Treated Lacrimal Gland Sample C	0.359507
<a href="#">GSM27188</a>	Male Testosterone-Treated Lacrimal Gland Sample A	0.276599
<a href="#">GSM27189</a>	Male Testosterone-Treated Lacrimal Gland Sample B	0.425166
<a href="#">GSM27190</a>	Male Testosterone-Treated Lacrimal Gland Sample C	0.367615
<a href="#">GSM27197</a>	Male Placebo-Treated Submandibular Gland Sample A	0.343573
<a href="#">GSM27198</a>	Male Placebo-Treated Submandibular Gland Sample B	0.271271
<a href="#">GSM27199</a>	Male Placebo-Treated Submandibular Gland Sample C	0.384337
<a href="#">GSM27200</a>	Male Testosterone-Treated Submandibular Gland Sample A	0.365324
<a href="#">GSM27201</a>	Male Testosterone-Treated Submandibular Gland Sample B	0.308682
<a href="#">GSM27202</a>	Male Testosterone-Treated Submandibular Gland Sample C	0.205059
<a href="#">GSM27191</a>	Male Placebo-Treated Meibomian Gland Sample A	7.61018
<a href="#">GSM27192</a>	Male Placebo-Treated Meibomian Gland Sample B	7.08807
<a href="#">GSM27193</a>	Male Placebo-Treated Meibomian Gland Sample C	7.54525
<a href="#">GSM27194</a>	Male Testosterone-Treated Meibomian Gland Sample A	13.4706
<a href="#">GSM27195</a>	Male Testosterone-Treated Meibomian Gland Sample B	12.7558
<a href="#">GSM27196</a>	Male Testosterone-Treated Meibomian Gland Sample C	10.1925

# Profile: ACE2 expression

GDS1832 / 1598

## Title

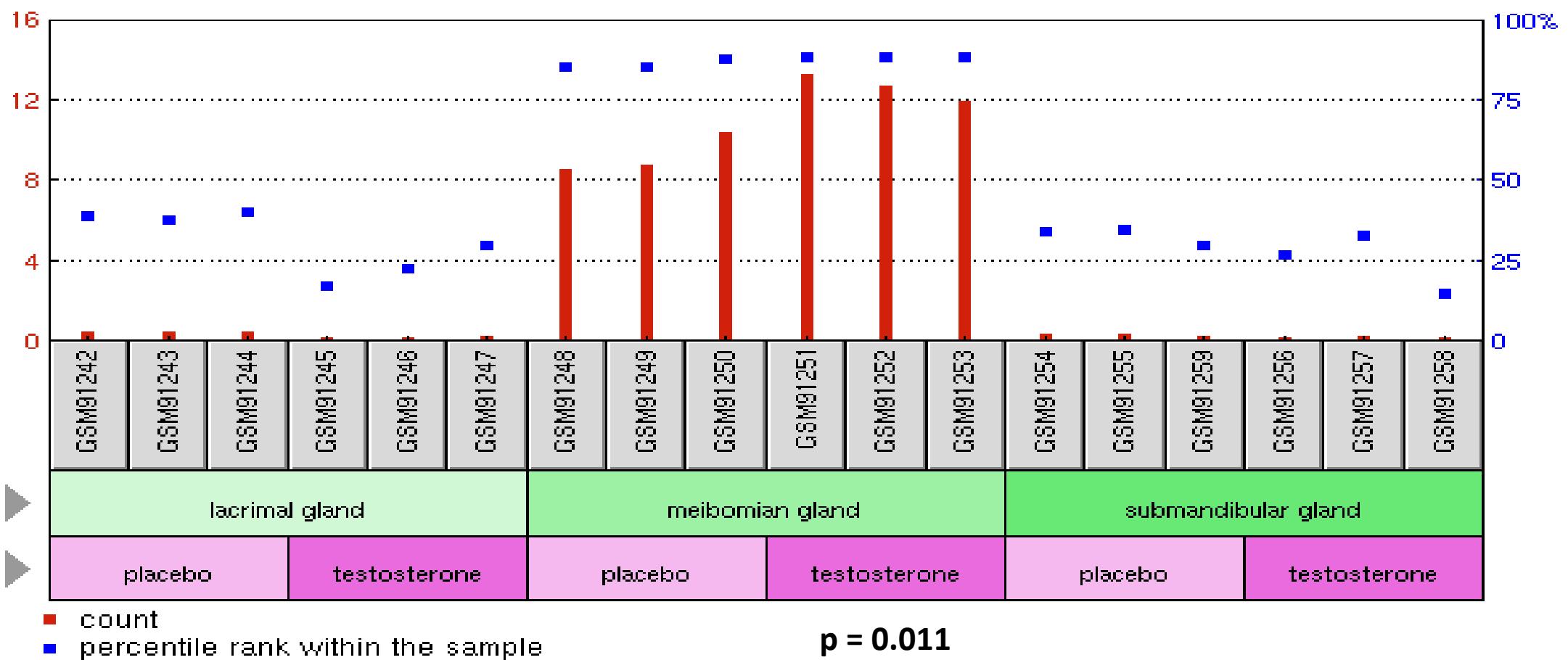
Testosterone effect on female lacrimal, meibomian, and submandibular glands

## Organism

Mus musculus

GDS1832 / 1598

## Testosterone increases ACE2 expression



**Profile: ACE2 expression****GDS1832 / 1598****Title****Testosterone effect on female lacrimal, meibomian, and submandibular glands****Organism*****Mus musculus*****Testosterone increases ACE2 expression**

Sample	Title	Value
<a href="#">GSM91242</a>	Female Placebo-Treated Lacrimal Gland Sample A	0.560279
<a href="#">GSM91243</a>	Female Placebo-Treated Lacrimal Gland Sample B	0.522894 <b>p = 0.024</b>
<a href="#">GSM91244</a>	Female Placebo-Treated Lacrimal Gland Sample C	0.566438
<a href="#">GSM91245</a>	Female Testosterone-Treated Lacrimal Gland Sample A	0.23071
<a href="#">GSM91246</a>	Female Testosterone-Treated Lacrimal Gland Sample B	0.275703
<a href="#">GSM91247</a>	Female Testosterone-Treated Lacrimal Gland Sample C	0.385156
<a href="#">GSM91248</a>	Female Placebo-Treated Meibomian Gland Sample A	8.58739
<a href="#">GSM91249</a>	Female Placebo-Treated Meibomian Gland Sample B	8.79653
<a href="#">GSM91250</a>	Female Placebo-Treated Meibomian Gland Sample C	10.4129
<a href="#">GSM91251</a>	Female Testosterone-Treated Meibomian Gland Sample A	13.3238
<a href="#">GSM91252</a>	Female Testosterone-Treated Meibomian Gland Sample B	12.7645 <b>p = 0.011</b>
<a href="#">GSM91253</a>	Female Testosterone-Treated Meibomian Gland Sample C	11.962
<a href="#">GSM91254</a>	Female Placebo-Treated Submandibular Gland Sample B	0.398068
<a href="#">GSM91255</a>	Female Placebo-Treated Submandibular Gland Sample C	0.403039
<a href="#">GSM91259</a>	Female Placebo-Treated Submandibular Gland Sample A	0.35605
<a href="#">GSM91256</a>	Female Testosterone-Treated Submandibular Gland Sample A	0.238247
<a href="#">GSM91257</a>	Female Testosterone-Treated Submandibular Gland Sample B	0.365064 <b>p = 0.130</b>
<a href="#">GSM91258</a>	Female Testosterone-Treated Submandibular Gland Sample C	0.206147

# Profile: *FURIN* expression

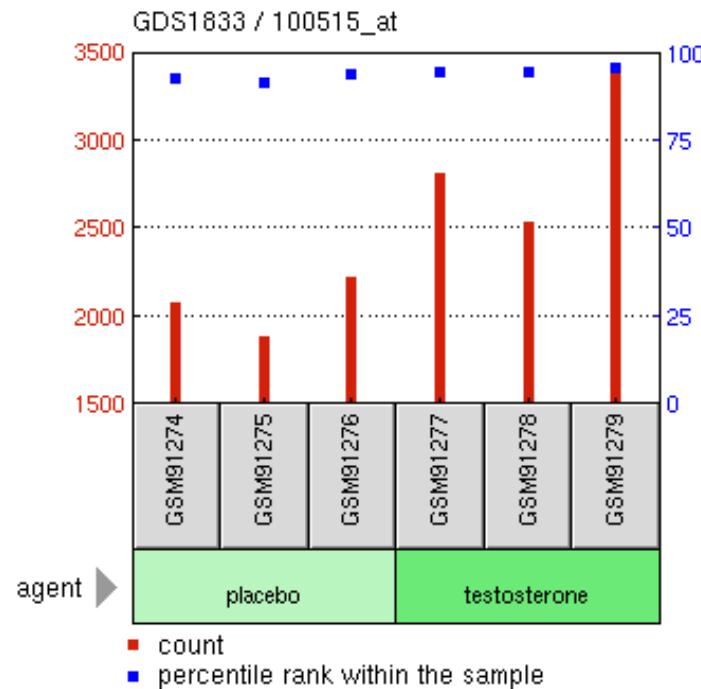
GDS1833 / 100515\_at

## Title

Testosterone effect on the female submandibular gland

## Organism

*Mus musculus*



Testosterone increases *FURIN* expression

Sample	Title	Value
<a href="#">GSM91274</a>	Female Placebo-Treated Submandibular Gland Sample A Technical Replicate	2087.8
<a href="#">GSM91275</a>	Female Placebo-Treated Submandibular Gland Sample B Technical Replicate	1888.3
<a href="#">GSM91276</a>	Female Placebo-Treated Submandibular Gland Sample C Technical Replicate	2230.6
<a href="#">GSM91277</a>	Female Testosterone-Treated Submandibular Gland Sample A Technical Replicate	<b>2822.9</b>
<a href="#">GSM91278</a>	Female Testosterone-Treated Submandibular Gland Sample B Technical Replicate	<b>2536.3</b>
<a href="#">GSM91279</a>	Female Testosterone-Treated Submandibular Gland Sample C Technical Replicate	<b>3392.9</b>

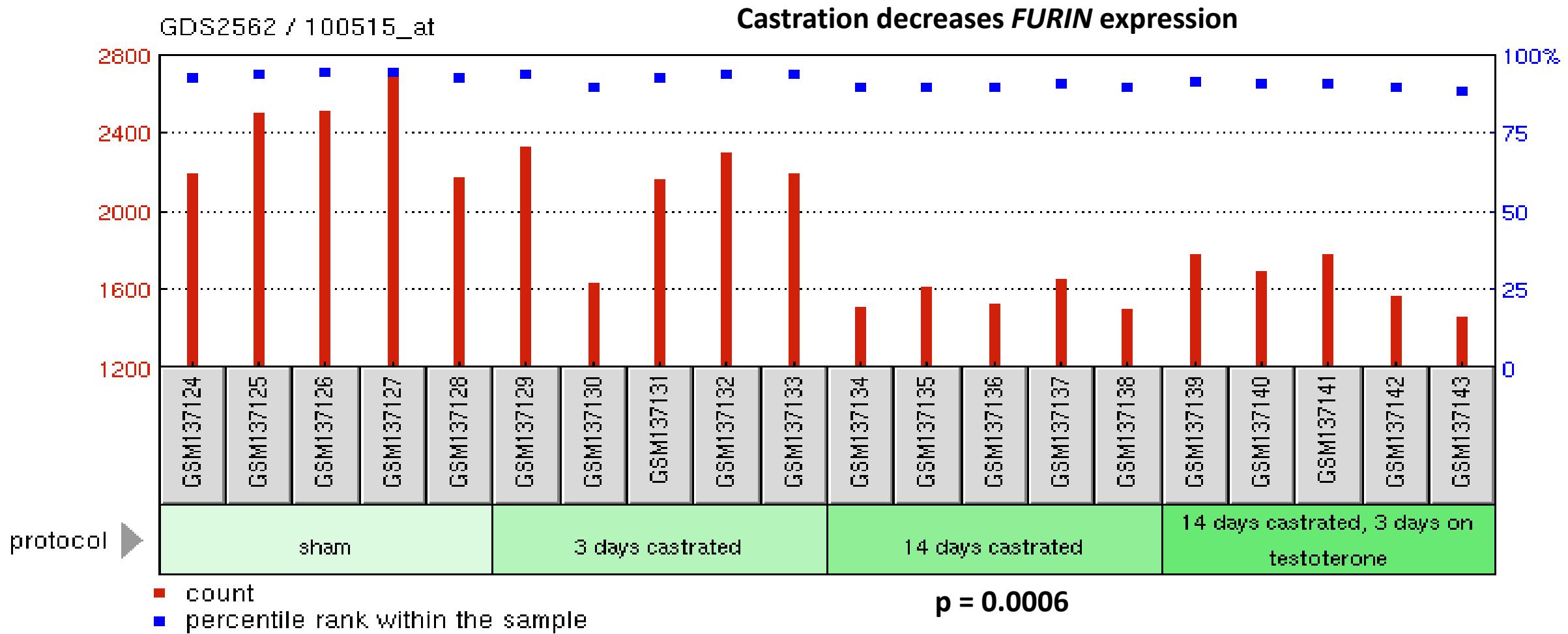
**Profile: *FURIN* expression**

**GDS2562 / 100515\_at**

**Title**

**Prostate response to castration and subsequent hormone replacement**

**Organism: *Mus musculus***



# Profile: *FURIN* expression

GDS2562 / 100515\_at

## Title

Prostate response to castration and subsequent hormone replacement

Organism: *Mus musculus*

Castration decreases *FURIN* expression

Sample	Title	Value
<a href="#">GSM137124</a>	PRB3660 (MG-U74A)	2201.3
<a href="#">GSM137125</a>	PRB3661 (MG-U74A)	2506.4
<a href="#">GSM137126</a>	PRB3662 (MG-U74A)	2519.5
<a href="#">GSM137127</a>	PRB3663 (MG-U74A)	2710.3
<a href="#">GSM137128</a>	PRB3664 (MG-U74A)	2173.5
<a href="#">GSM137129</a>	PRB3665 (MG-U74A)	2332.6
<a href="#">GSM137130</a>	PRB3666 (MG-U74A)	1636.1
<a href="#">GSM137131</a>	PRB3667 (MG-U74A)	2167.8
<a href="#">GSM137132</a>	PRB3668 (MG-U74A)	2305.2
<a href="#">GSM137133</a>	PRB3669 (MG-U74A)	2193.6
<a href="#">GSM137134</a>	PRB3698 (MG-U74A)	1510.4
<a href="#">GSM137135</a>	PRB3699 (MG-U74A)	1619.7
<a href="#">GSM137136</a>	PRB3700 (MG-U74A)	<b>p = 0.0006</b> 1532.1
<a href="#">GSM137137</a>	PRB3701 (MG-U74A)	1654.5
<a href="#">GSM137138</a>	PRB3702 (MG-U74A)	1502.6
<a href="#">GSM137139</a>	PRB3708 (MG-U74A)	1787.8
<a href="#">GSM137140</a>	PRB3709 (MG-U74A)	1695.8
<a href="#">GSM137141</a>	PRB3710 (MG-U74A)	1787.3
<a href="#">GSM137142</a>	PRB3711 (MG-U74A)	1575.8
<a href="#">GSM137143</a>	PRB3712 (MG-U74A)	1467.6

# Profile: *FURIN* expression

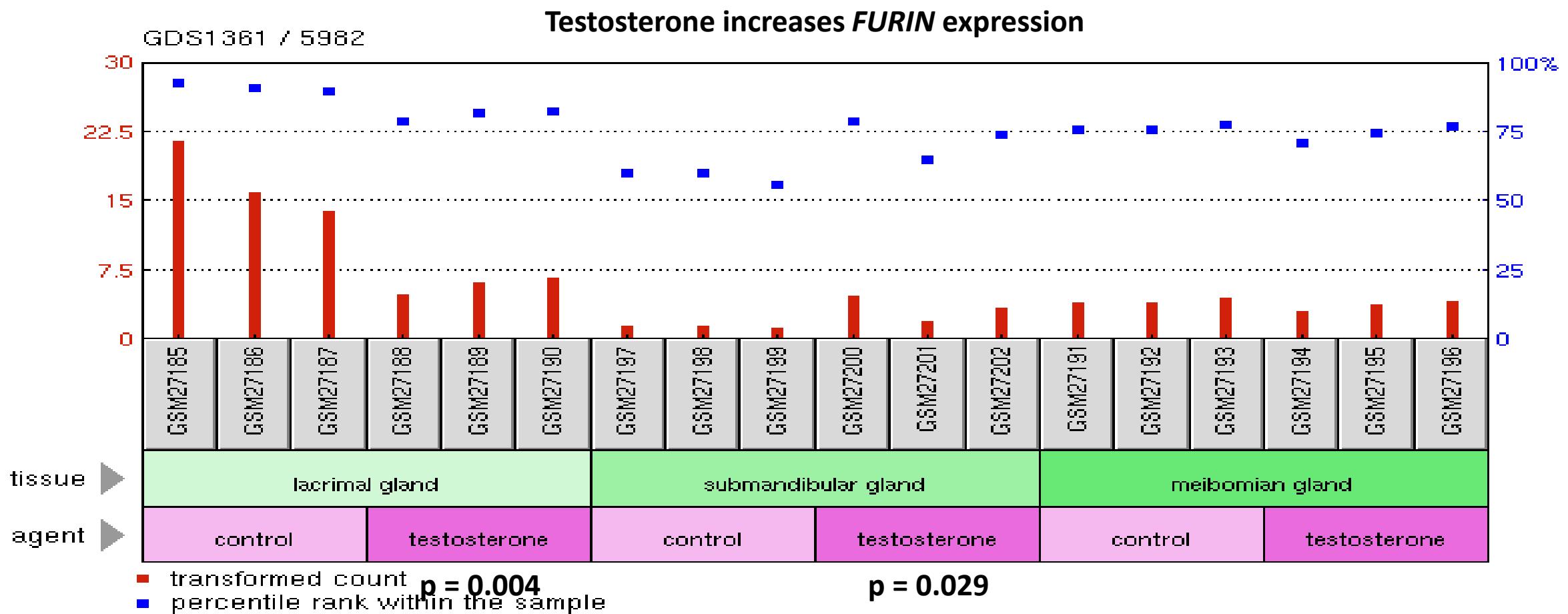
GDS1361 / 5982

## Title

Testosterone effect on meibomian gland

## Organism

*Mus musculus*



# Profile: *FURIN* expression

GDS1361 / 5982

## Title

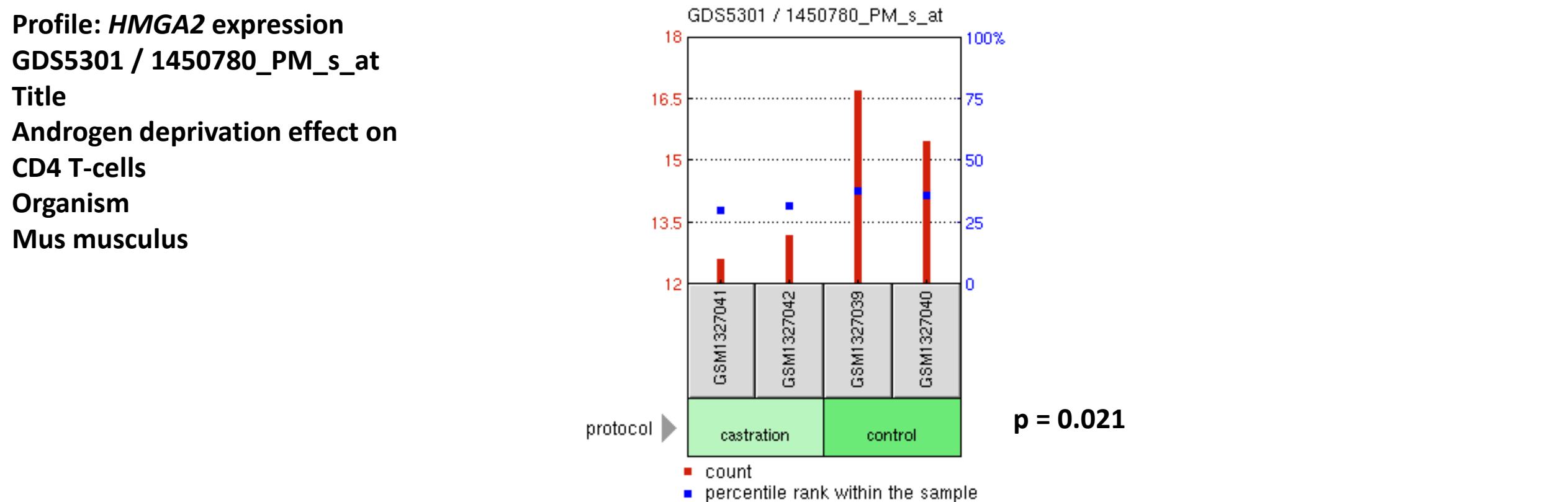
Testosterone effect on meibomian gland

## Organism

*Mus musculus*

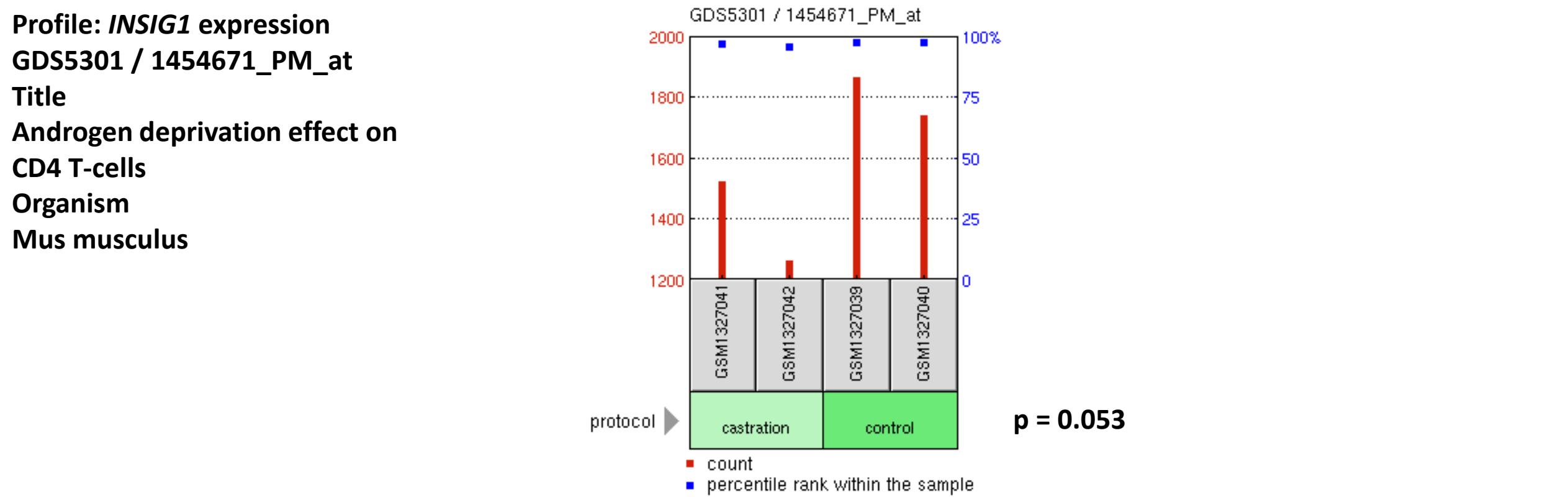
Testosterone increases *FURIN* expression

Sample	Title	Value
<a href="#">GSM27185</a>	Male Placebo-Treated Lacrimal Gland Sample A	21.6254
<a href="#">GSM27186</a>	Male Placebo-Treated Lacrimal Gland Sample B	15.916 <b>p = 0.004</b>
<a href="#">GSM27187</a>	Male Placeo-Treated Lacrimal Gland Sample C	14.0492
<a href="#">GSM27188</a>	Male Testosterone-Treated Lacrimal Gland Sample A	5.04977
<a href="#">GSM27189</a>	Male Testosterone-Treated Lacrimal Gland Sample B	6.27436
<a href="#">GSM27190</a>	Male Testosterone-Treated Lacrimal Gland Sample C	6.81647
<a href="#">GSM27197</a>	Male Placebo-Treated Submandibular Gland Sample A	<b>1.62319</b>
<a href="#">GSM27198</a>	Male Placebo-Treated Submandibular Gland Sample B	<b>1.54446</b> <b>p = 0.029</b>
<a href="#">GSM27199</a>	Male Placebo-Treated Submandibular Gland Sample C	<b>1.27973</b>
<a href="#">GSM27200</a>	Male Testosterone-Treated Submandibular Gland Sample A	<b>4.75181</b>
<a href="#">GSM27201</a>	Male Testosterone-Treated Submandibular Gland Sample B	<b>2.12511</b>
<a href="#">GSM27202</a>	Male Testosterone-Treated Submandibular Gland Sample C	<b>3.60242</b>
<a href="#">GSM27191</a>	Male Placebo-Treated Meibomian Gland Sample A	4.08816
<a href="#">GSM27192</a>	Male Placebo-Treated Meibomian Gland Sample B	4.09734
<a href="#">GSM27193</a>	Male Placebo-Treated Meibomian Gland Sample C	4.58029
<a href="#">GSM27194</a>	Male Testosterone-Treated Meibomian Gland Sample A	3.08708
<a href="#">GSM27195</a>	Male Testosterone-Treated Meibomian Gland Sample B	3.88995
<a href="#">GSM27196</a>	Male Testosterone-Treated Meibomian Gland Sample C	4.22759



Castration decreases *HMGA2* expression

Sample	Title	Value
<a href="#">GSM1327041</a>	Cast_1	12.6312
<a href="#">GSM1327042</a>	Cast_2	13.2155
<a href="#">GSM1327039</a>	Sham_1	16.7133
<a href="#">GSM1327040</a>	Sham_2	15.4878



Castration decreases *INSIG1* expression

Sample	Title	Value
<a href="#">GSM1327041</a>	Cast_1	1525.05
<a href="#">GSM1327042</a>	Cast_2	1265.23
<a href="#">GSM1327039</a>	Sham_1	1866.04
<a href="#">GSM1327040</a>	Sham_2	1741.1

# Profile: GATA5 expression

GDS1361 / 3834

## Title

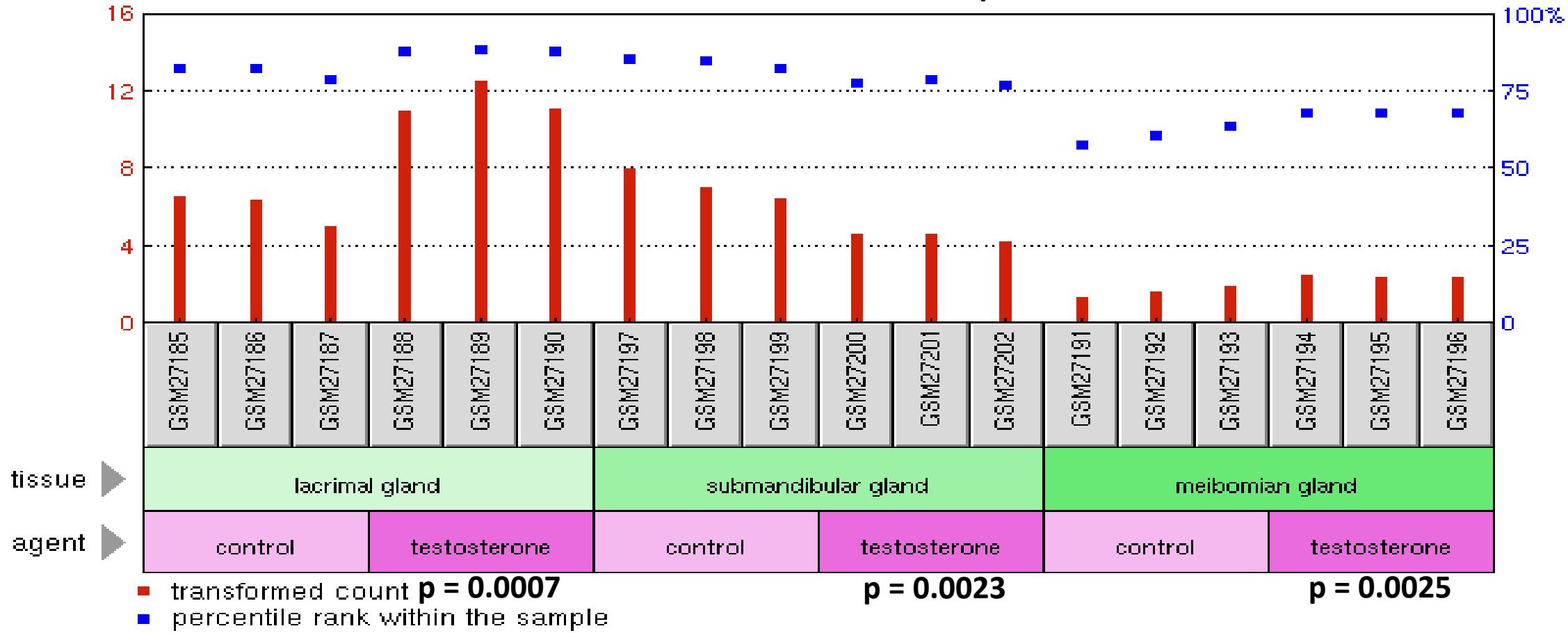
Testosterone effect on meibomian gland

## Organism

Mus musculus

GDS1361 / 3834

## Testosterone decreases GATA5 expression



# Profile: GATA5 expression

GDS1361 / 3834

## Title

Testosterone effect on meibomian gland

## Organism

*Mus musculus*

Testosterone decreases GATA5 expression

Sample	Title	Value
<a href="#">GSM27185</a>	Male Placebo-Treated Lacrimal Gland Sample A	6.64621
<a href="#">GSM27186</a>	Male Placebo-Treated Lacrimal Gland Sample B	6.45423 <b>p = 0.0007</b>
<a href="#">GSM27187</a>	Male Placeo-Treated Lacrimal Gland Sample C	5.10327
<a href="#">GSM27188</a>	Male Testosterone-Treated Lacrimal Gland Sample A	10.9893
<a href="#">GSM27189</a>	Male Testosterone-Treated Lacrimal Gland Sample B	12.5373
<a href="#">GSM27190</a>	Male Testosterone-Treated Lacrimal Gland Sample C	11.1312
<a href="#">GSM27197</a>	Male Placebo-Treated Submandibular Gland Sample A	8.00934
<a href="#">GSM27198</a>	Male Placebo-Treated Submandibular Gland Sample B	7.04778 <b>p = 0.0023</b>
<a href="#">GSM27199</a>	Male Placebo-Treated Submandibular Gland Sample C	6.52222
<a href="#">GSM27200</a>	Male Testosterone-Treated Submandibular Gland Sample A	4.71727
<a href="#">GSM27201</a>	Male Testosterone-Treated Submandibular Gland Sample B	4.67808
<a href="#">GSM27202</a>	Male Testosterone-Treated Submandibular Gland Sample C	4.25649
<a href="#">GSM27191</a>	Male Placebo-Treated Meibomian Gland Sample A	1.42448
<a href="#">GSM27192</a>	Male Placebo-Treated Meibomian Gland Sample B	1.65382 <b>p = 0.0025</b>
<a href="#">GSM27193</a>	Male Placebo-Treated Meibomian Gland Sample C	1.92874
<a href="#">GSM27194</a>	Male Testosterone-Treated Meibomian Gland Sample A	2.54996
<a href="#">GSM27195</a>	Male Testosterone-Treated Meibomian Gland Sample B	2.49176
<a href="#">GSM27196</a>	Male Testosterone-Treated Meibomian Gland Sample C	2.45951

# ACE2 and FURIN

**Supplemental Figure S12. Potential mechanisms affecting gene expression inferred from transgenic mouse models and observed in pathophysiologically & therapeutically relevant mouse and human cells:**

**A knowledge path toward potential therapy-enhancing interventions**

Profile: ACE2 expression

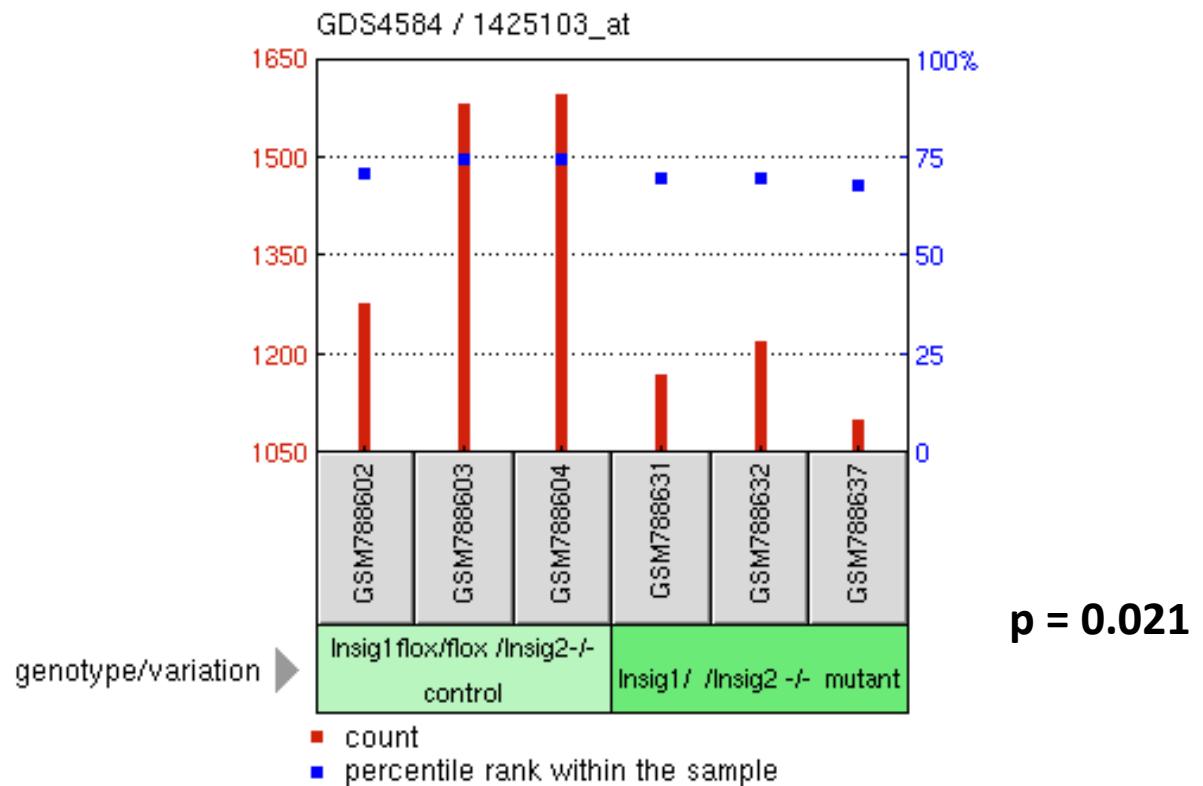
GDS4584 / 1425103\_at

Title

Alveolar type I cells deficient in sterol-response element-binding proteins inhibitor Insig1/2

Organism

Mus musculus



## Insig1: a candidate activator of the ACE2 expression

Sample	Title	Value
<a href="#">GSM788602</a>	Insig1 flox/flox / Insig2 -/- InsigKO_C1	1279.8
<a href="#">GSM788603</a>	Insig1 flox/flox / Insig2 -/- InsigKO_C2	1584.9
<a href="#">GSM788604</a>	Insig1 flox/flox / Insig2 -/- InsigKO_C3	1596
<a href="#">GSM788631</a>	Insig1 Δ/Δ / Insig2 -/- InsigKO_E1	1169.8
<a href="#">GSM788632</a>	Insig1 Δ/Δ / Insig2 -/- InsigKO_E2	1223
<a href="#">GSM788637</a>	Insig1 Δ/Δ / Insig2 -/- InsigKO_E3	1102.8

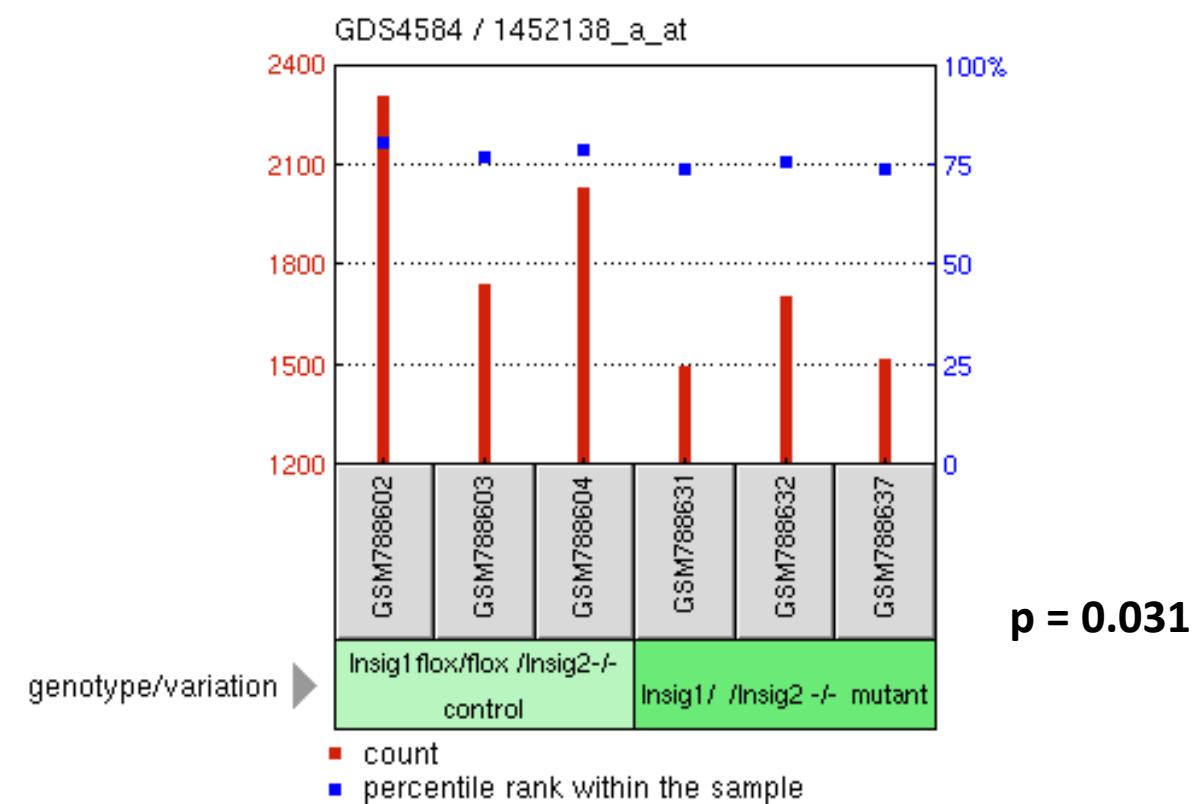
**Profile: ACE2 expression**  
**GDS4584 / 1452138\_a\_at**

**Title**

**Alveolar type I cells deficient in sterol-response element-binding proteins inhibitor Insig1/2**

**Organism**

**Mus musculus**



***Insig1*: a candidate activator of the ACE2 expression**

Sample	Title	Value
<a href="#">GSM788602</a>	Insig1 flox/flox /Insig2 -/- InsigKO_C1	2309.1
<a href="#">GSM788603</a>	Insig1 flox/flox /Insig2 -/- InsigKO_C2	1742.5
<a href="#">GSM788604</a>	Insig1 flox/flox /Insig2 -/- InsigKO_C3	2032.3
<a href="#">GSM788631</a>	Insig1 Δ/Δ /Insig2 -/- InsigKO_E1	1496.5
<a href="#">GSM788632</a>	Insig1 Δ/Δ /Insig2 -/- InsigKO_E2	1706.9
<a href="#">GSM788637</a>	Insig1 Δ/Δ /Insig2 -/- InsigKO_E3	1518.6

Profile: *INSIG1* expression

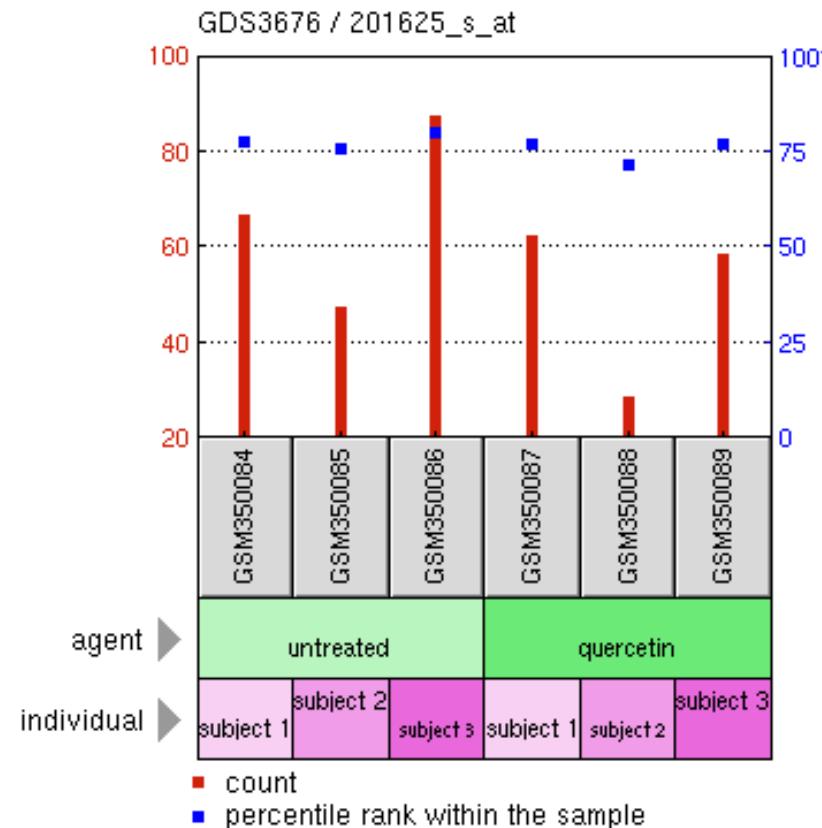
GDS3676 / 201625\_s\_at

Title

Quercetin effect on CD14+ monocyte

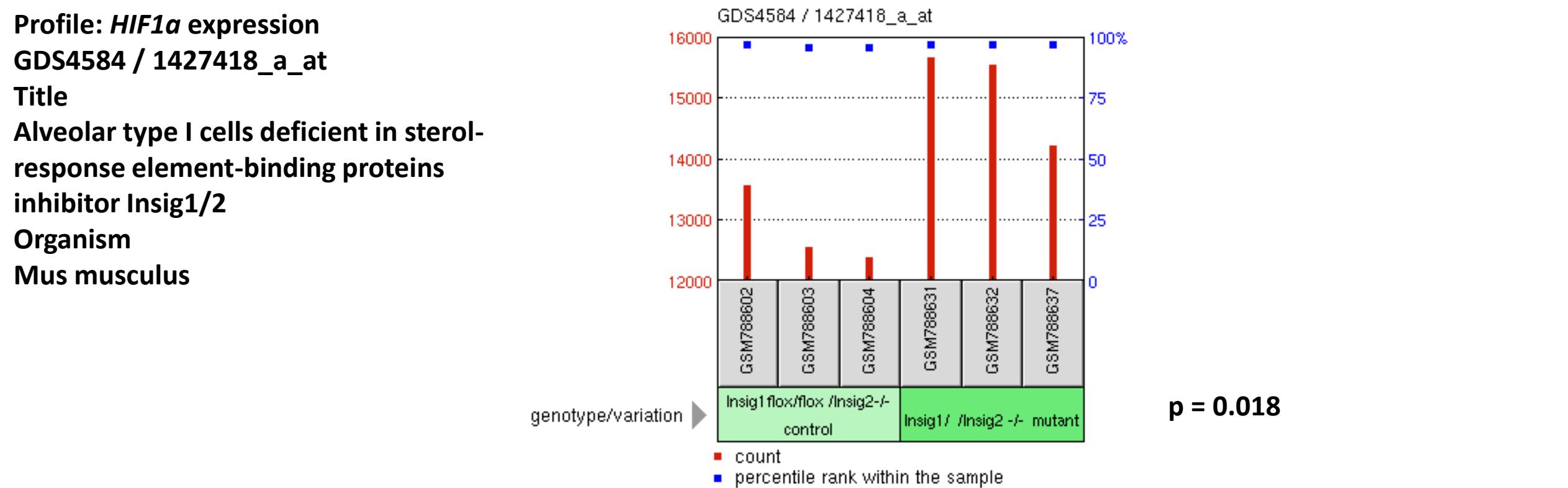
Organism

Homo sapiens



Quercetin inhibits the *INSIG1* expression

Sample	Title	Value	Percent changes
<a href="#">GSM350084</a>	CD14+ at baseline, biological replicate 1	66.9724	
<a href="#">GSM350085</a>	CD14+ at baseline, biological replicate 2	47.9219	
<a href="#">GSM350086</a>	CD14+ at baseline, biological replicate 3	87.5973	
<a href="#">GSM350087</a>	CD14+ after 2 wk quercetin supplementation, biological replicate 1	62.5927	- 7%
<a href="#">GSM350088</a>	CD14+ after 2 wk quercetin supplementation, biological replicate 2	28.8386	- 40%
<a href="#">GSM350089</a>	CD14+ after 2 wk quercetin supplementation, biological replicate 3	58.8768	- 33%



## *Insig1*: a candidate repressor of the *HIF1a* expression

Sample	Title	Value
<a href="#">GSM788602</a>	Insig1 flox/flox /Insig2 -/- InsigKO_C1	13581.9
<a href="#">GSM788603</a>	Insig1 flox/flox /Insig2 -/- InsigKO_C2	12568
<a href="#">GSM788604</a>	Insig1 flox/flox /Insig2 -/- InsigKO_C3	12390.1
<a href="#">GSM788631</a>	Insig1 Δ/Δ /Insig2 -/- InsigKO_E1	15685.4
<a href="#">GSM788632</a>	Insig1 Δ/Δ /Insig2 -/- InsigKO_E2	15544.2
<a href="#">GSM788637</a>	Insig1 Δ/Δ /Insig2 -/- InsigKO_E3	14222.5

Profile: *HIF1a* expression

GDS3676 / 200989\_at

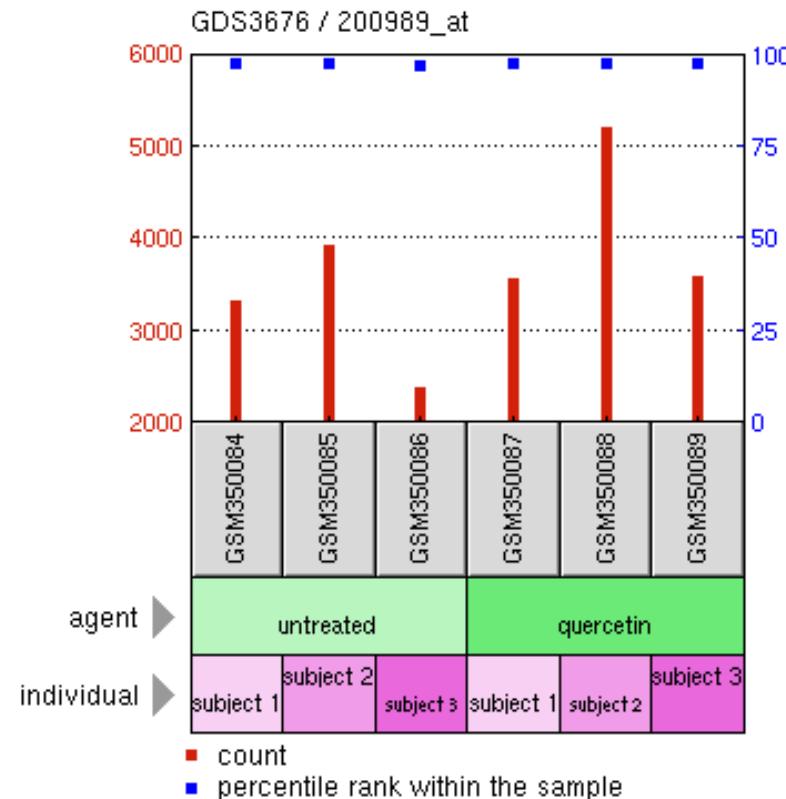
Title

Quercetin effect on CD14+

monocyte

Organism

*Homo sapiens*



## Quercetin activates the *HIF1a* expression

Sample	Title	Value
<a href="#">GSM350084</a>	CD14+ at baseline, biological replicate 1	3338.47
<a href="#">GSM350085</a>	CD14+ at baseline, biological replicate 2	3929.88
<a href="#">GSM350086</a>	CD14+ at baseline, biological replicate 3	2388.45
<a href="#">GSM350087</a>	CD14+ after 2 wk quercetin supplementation, biological replicate 1	3577.94 (+ 7.2%)
<a href="#">GSM350088</a>	CD14+ after 2 wk quercetin supplementation, biological replicate 2	5206.25 (+32.5%)
<a href="#">GSM350089</a>	CD14+ after 2 wk quercetin supplementation, biological replicate 3	3604.21 (+50.9%)

Profile: *HIF1A* expression

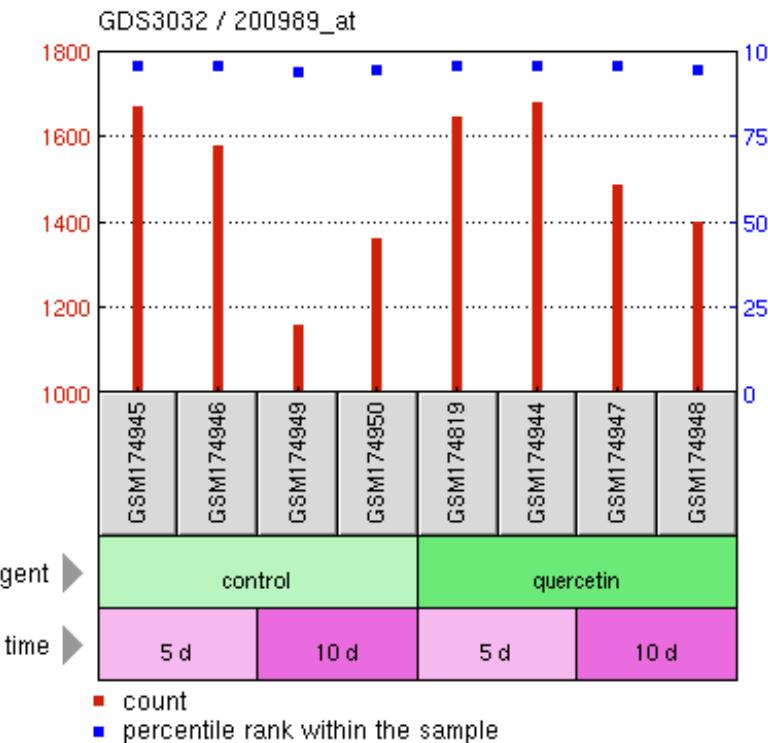
GDS3032 / 200989\_at

Title

Quercetin effect on intestinal cell differentiation in vitro: time course

Organism

*Homo sapiens*



### Quercetin ameliorates decline of the *HIF1a* expression

Sample	Title	Value
<a href="#">GSM174945</a>	Control day 05 sample 1	1673.78
<a href="#">GSM174946</a>	Control day 05 sample 2	1582.51
<a href="#">GSM174949</a>	Control day 10 sample 1	1163.29
<a href="#">GSM174950</a>	Control day 10 sample 2	1364.98
<a href="#">GSM174819</a>	Quercetin day 05 sample 1	1646.59
<a href="#">GSM174944</a>	Quercetin day 05 sample 2	1680.64
<a href="#">GSM174947</a>	Quercetin day 10 sample 1	1491.23
<a href="#">GSM174948</a>	Quercetin day 10 sample 2	1403.56

**Profile: ACE2**

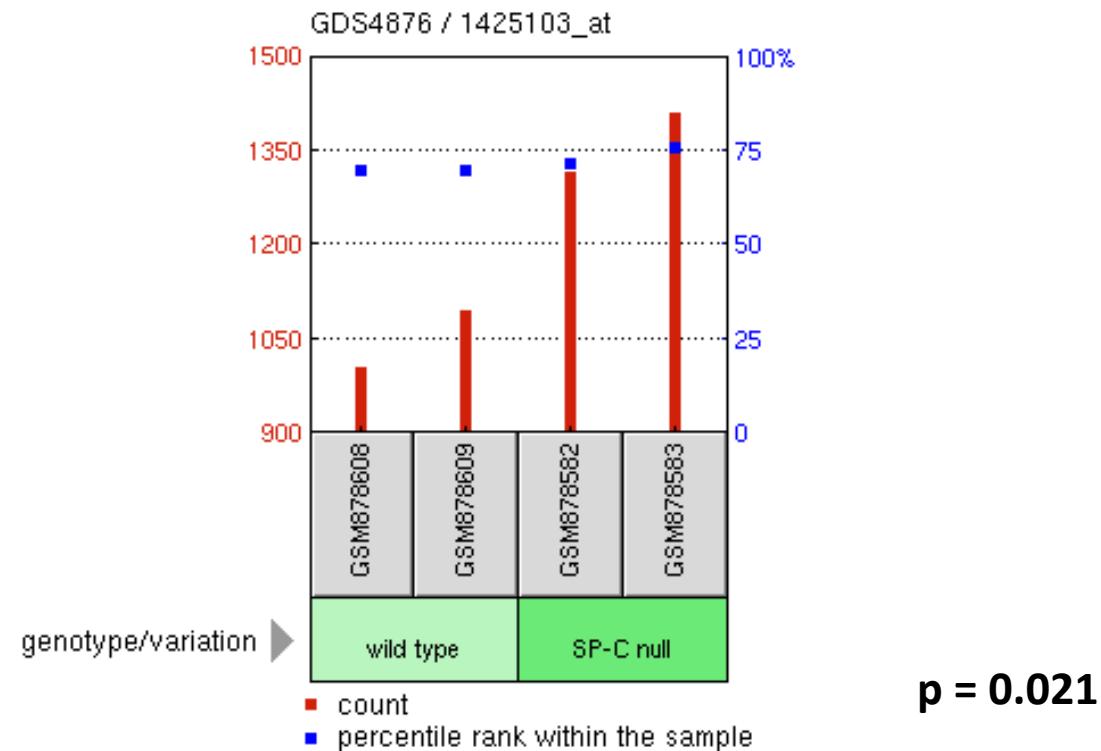
**GDS4876 / 1425103\_at**

**Title**

**Pulmonary surfactant protein-C deficiency effect on alveolar type II epithelial cell**

**Organism**

**Mus musculus**



## ***SP-C (SFTPC): a candidate inhibitor of the ACE2 expression***

Sample	Title	Value
<a href="#">GSM878608</a>	Wild-type Type II 1_8_9_04	1006
<a href="#">GSM878609</a>	Wild-type Type II 9_27_04	1097.9
<a href="#">GSM878582</a>	KO SPC Type II 9_27_04	1317.1
<a href="#">GSM878583</a>	KO SPC Type II 2_8_9_04	1413.2

Profile: FURIN expression

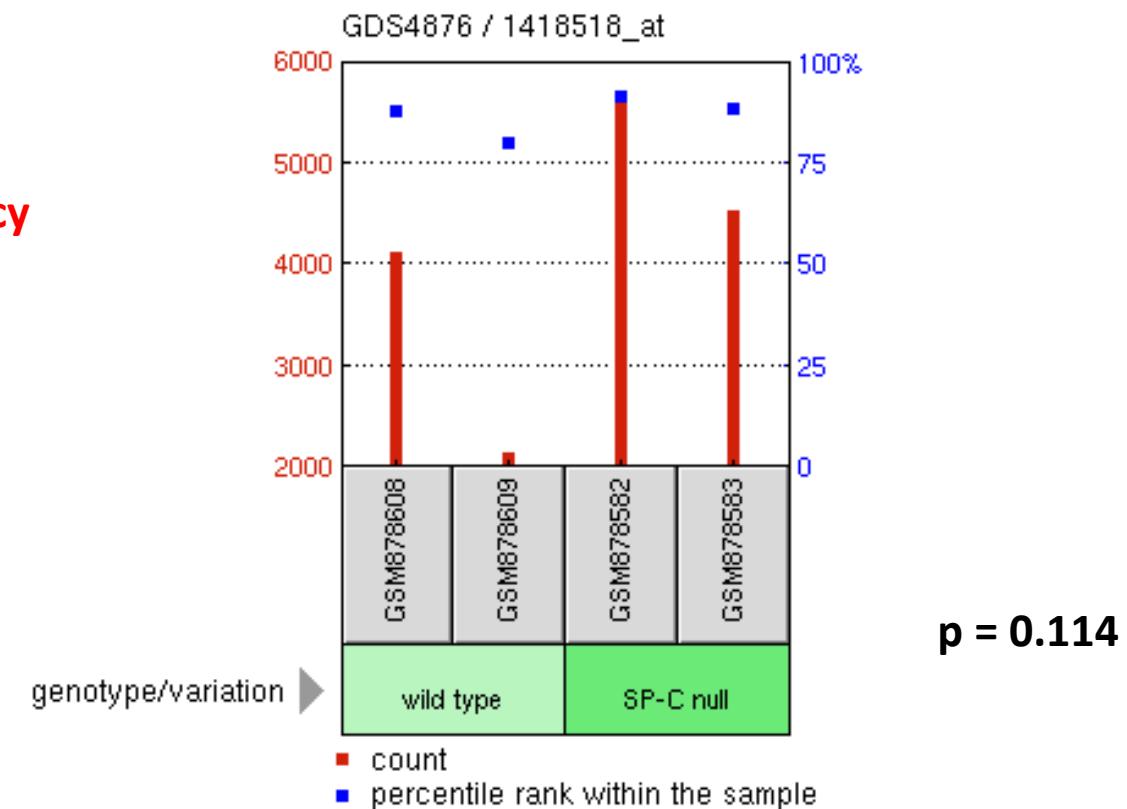
GDS4876 / 1418518\_at

Title

Pulmonary surfactant protein-C deficiency  
effect on alveolar type II epithelial cell

Organism

Mus musculus



***SP-C (SFTPC): a candidate inhibitor of the FURIN expression***

Sample	Title	Value
<a href="#">GSM878608</a>	Wild-type Type II 1_8_9_04	4141.2
<a href="#">GSM878609</a>	Wild-type Type II 9_27_04	2156.1
<a href="#">GSM878582</a>	KO SPC Type II 9_27_04	5733
<a href="#">GSM878583</a>	KO SPC Type II 2_8_9_04	4537.4

# Profile: SP-C (SFTPC) expression

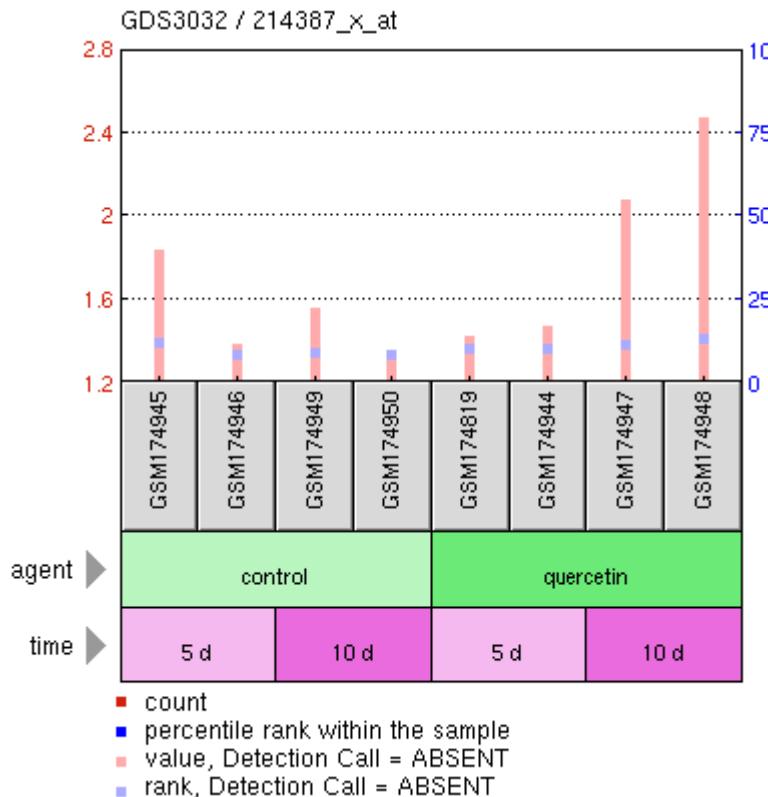
GDS3032 / 214387\_x\_at

## Title

Quercetin effect on intestinal cell differentiation in vitro: time course

## Organism

Homo sapiens



10 days  
p = 0.033

Quercetin enhances the *SP-1 (SFTPC)* expression

Sample	Title	Value
<a href="#">GSM174945</a>	Control day 05 sample 1	1.84127
<a href="#">GSM174946</a>	Control day 05 sample 2	1.38638
<a href="#">GSM174949</a>	Control day 10 sample 1	1.56441
<a href="#">GSM174950</a>	Control day 10 sample 2	1.35256
<a href="#">GSM174819</a>	Quercetin day 05 sample 1	1.42897
<a href="#">GSM174944</a>	Quercetin day 05 sample 2	1.47099
<a href="#">GSM174947</a>	Quercetin day 10 sample 1	2.08499
<a href="#">GSM174948</a>	Quercetin day 10 sample 2	2.47973

# Profile: SP-C (SFTPC) expression

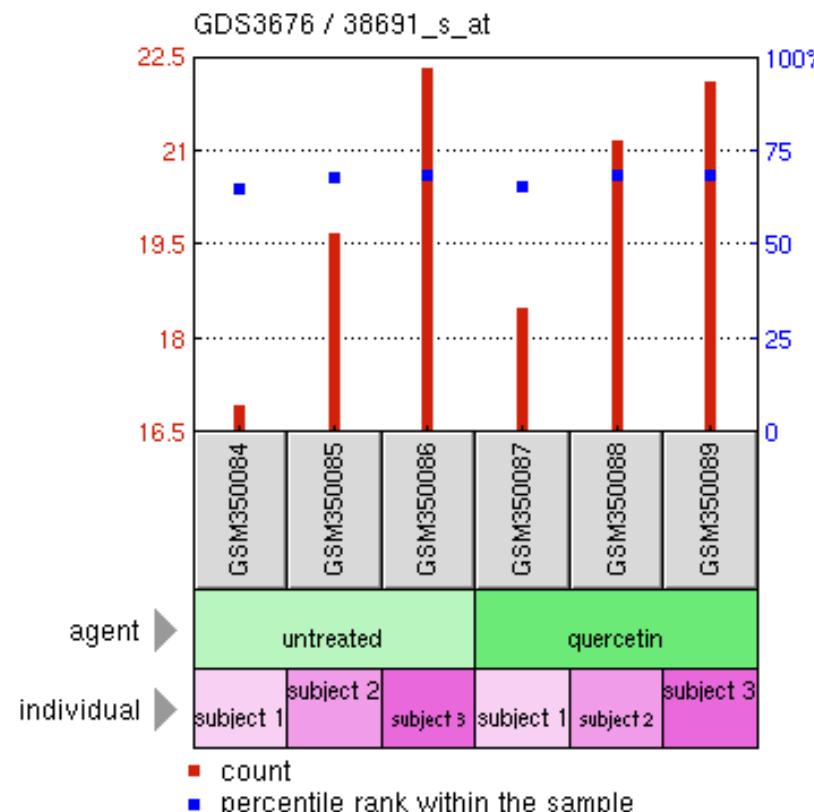
GDS3676 / 38691\_s\_at

## Title

Quercetin effect on CD14+ monocyte

## Organism

Homo sapiens



Quercetin enhances the *SP-1 (SFTPC)* expression

Sample	Title	Value
<a href="#">GSM350084</a>	CD14+ at baseline, biological replicate 1	16.9619
<a href="#">GSM350085</a>	CD14+ at baseline, biological replicate 2	19.6833
<a href="#">GSM350086</a>	CD14+ at baseline, biological replicate 3	22.3292
<a href="#">GSM350087</a>	CD14+ after 2 wk quercetin supplementation, biological replicate 1	18.5089
<a href="#">GSM350088</a>	CD14+ after 2 wk quercetin supplementation, biological replicate 2	21.1853
<a href="#">GSM350089</a>	CD14+ after 2 wk quercetin supplementation, biological replicate 3	22.11

Profile: ACE2 expression

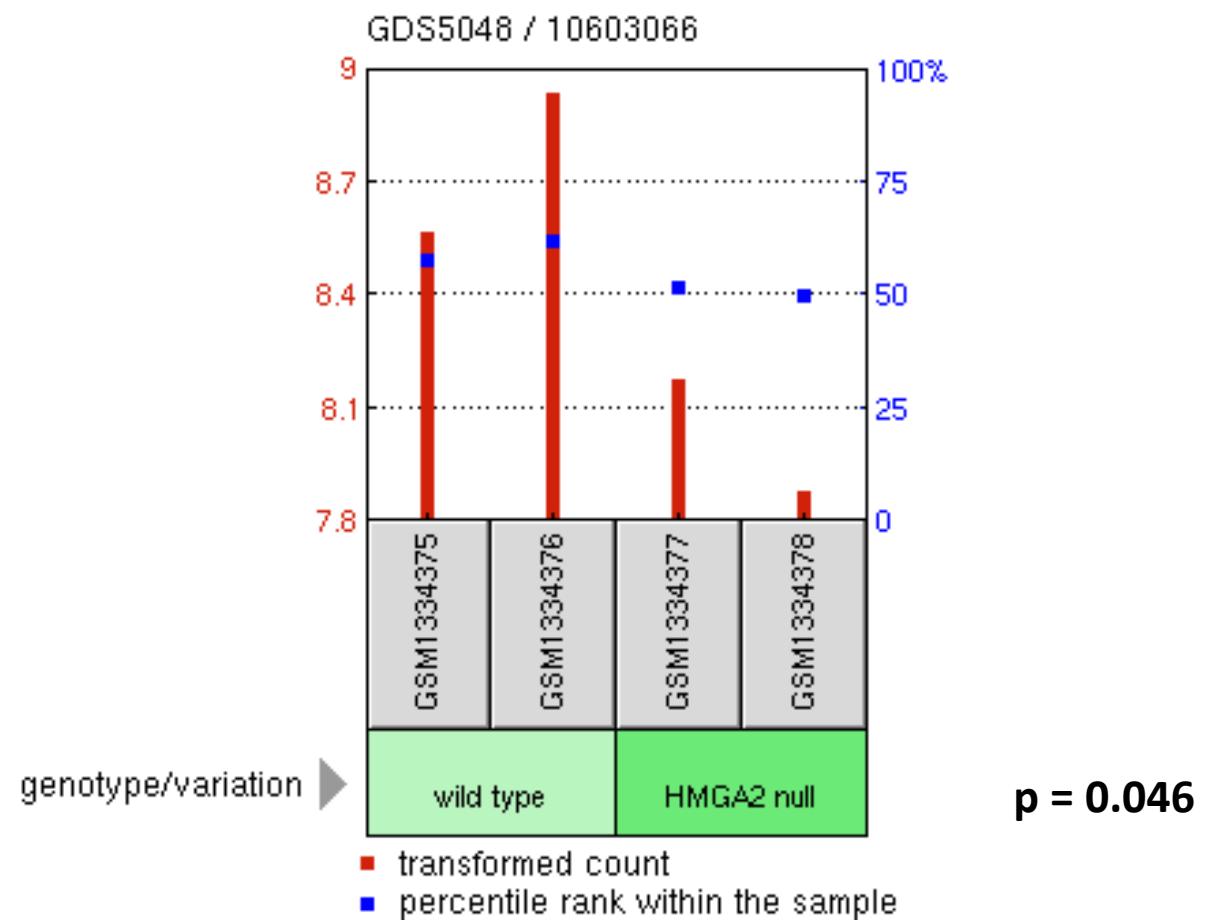
GDS5048 / 10603066

Title

High Mobility Group AT-hook Protein 2 deficiency effect on the embryonic lung

Organism

Mus musculus



## HMGA2: a candidate activator of the ACE2 expression

Sample	Title	Value
<a href="#">GSM1334375</a>	E18.5 lung WT1, biological rep1	8.57131
<a href="#">GSM1334376</a>	E18.5 lung WT1, biological rep2	8.93831
<a href="#">GSM1334377</a>	E18.5 lung KO1, biological rep1	8.18208
<a href="#">GSM1334378</a>	E18.5 lung KO2, biological rep2	7.87966

Profile: *INSIG1* expression

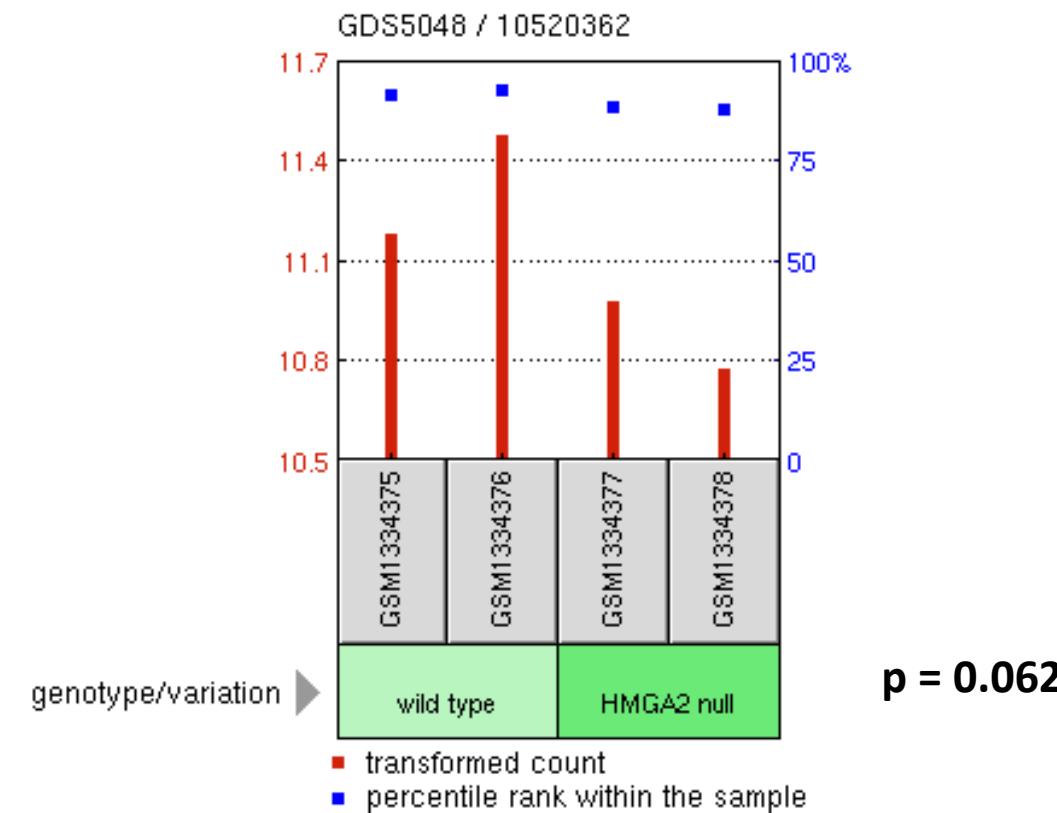
GDS5048 / 10520362

Title

High Mobility Group AT-hook Protein 2 deficiency effect on the embryonic lung

Organism

*Mus musculus*



## ***HMGA2*: a candidate activator of the *INSIG1* expression**

Sample	Title	Value
<a href="#">GSM1334375</a>	E18.5 lung WT1, biological rep1	11.1863
<a href="#">GSM1334376</a>	E18.5 lung WT1, biological rep2	11.4769
<a href="#">GSM1334377</a>	E18.5 lung KO1, biological rep1	10.9789
<a href="#">GSM1334378</a>	E18.5 lung KO2, biological rep2	10.7801

Profile: *SFTPC* expression

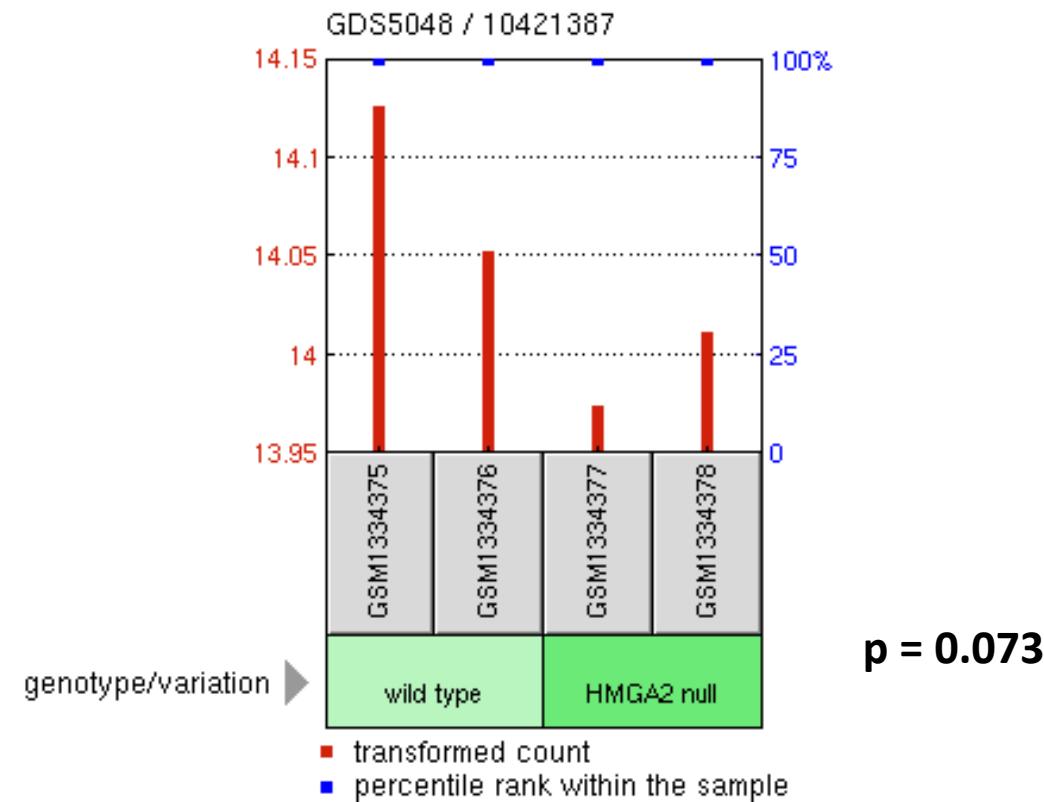
GDS5048 / 10421387

Title

High Mobility Group AT-hook Protein 2 deficiency effect on the embryonic lung

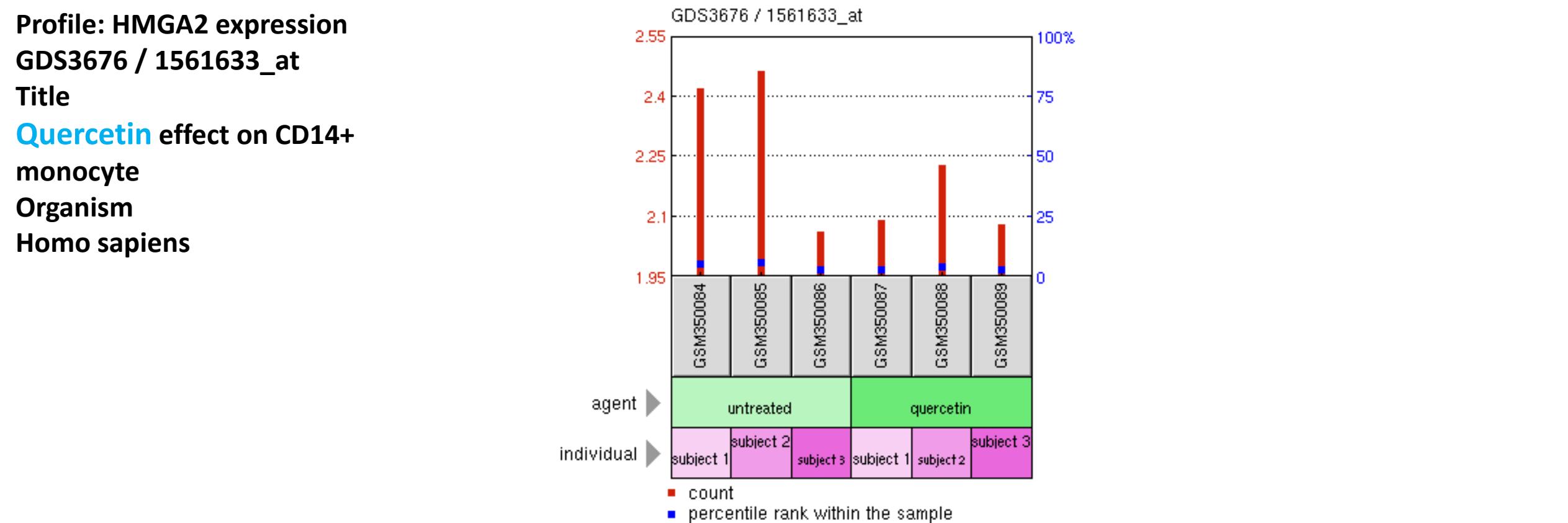
Organism

*Mus musculus*



## *HMGA2*: a candidate activator of the *SFTPC* expression

Sample	Title	Value
<a href="#">GSM1334375</a>	E18.5 lung WT1, biological rep1	14.1269
<a href="#">GSM1334376</a>	E18.5 lung WT1, biological rep2	14.0528
<a href="#">GSM1334377</a>	E18.5 lung KO1, biological rep1	13.975
<a href="#">GSM1334378</a>	E18.5 lung KO2, biological rep2	14.0121



**Quercetin inhibits the *HMGA2* expression**

Sample	Title	Value
<a href="#">GSM350084</a>	CD14+ at baseline, biological replicate 1	2.4219
<a href="#">GSM350085</a>	CD14+ at baseline, biological replicate 2	2.46504
<a href="#">GSM350086</a>	CD14+ at baseline, biological replicate 3	2.06307
<a href="#">GSM350087</a>	CD14+ after 2 wk quercetin supplementation, biological replicate 1	2.09436
<a href="#">GSM350088</a>	CD14+ after 2 wk quercetin supplementation, biological replicate 2	2.22984
<a href="#">GSM350089</a>	CD14+ after 2 wk quercetin supplementation, biological replicate 3	2.0814

# Profile: HMGA2 expression

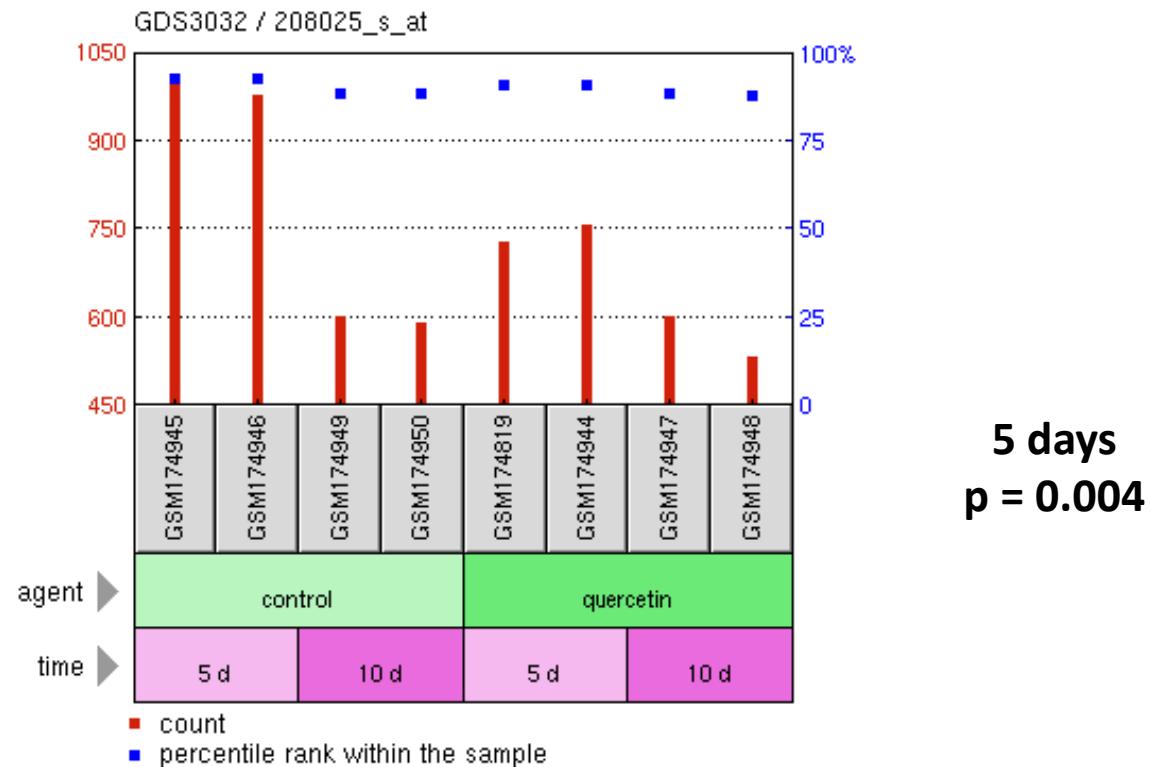
GDS3032 / 208025\_s\_at

## Title

Quercetin effect on intestinal cell differentiation in vitro: time course

## Organism

Homo sapiens



Quercetin inhibits the *HMGA2* expression

Sample	Title	Value
<a href="#">GSM174945</a>	Control day 05 sample 1	1015.28
<a href="#">GSM174946</a>	Control day 05 sample 2	977.764
<a href="#">GSM174949</a>	Control day 10 sample 1	601.884
<a href="#">GSM174950</a>	Control day 10 sample 2	591.613
<a href="#">GSM174819</a>	Quercetin day 05 sample 1	729.032
<a href="#">GSM174944</a>	Quercetin day 05 sample 2	758.127
<a href="#">GSM174947</a>	Quercetin day 10 sample 1	602.964
<a href="#">GSM174948</a>	Quercetin day 10 sample 2	535.877

# Profile: HMGA2 expression

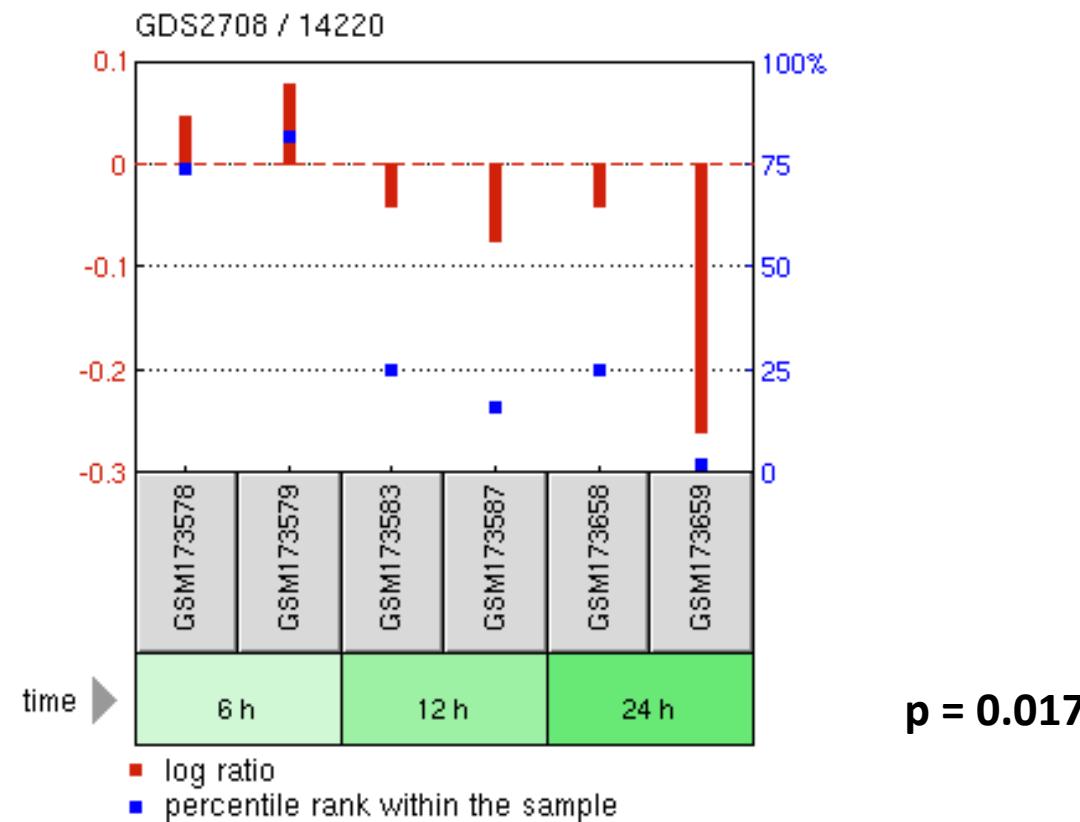
GDS2708 / 14220

## Title

Quercetin effect on cultured cardiomyocytes: time course

## Organism

Rattus norvegicus



Quercetin inhibits the *HMGA2* expression

Sample	Title	Value
<a href="#">GSM173578</a>	Quercetin treated cardiomyocytes for 6 hours (Q6-A).	0.0475828
<a href="#">GSM173579</a>	Quercetin treated cardiomyocytes for 6 hours (Q6-B).	0.0794489
<a href="#">GSM173583</a>	Quercetin treated cardiomyocytes for 12 hours (Q12-A).	-0.0439453
<a href="#">GSM173587</a>	Quercetin treated cardiomyocytes for 12 hours (Q12-B).	-0.078307
<a href="#">GSM173658</a>	Quercetin treated cardiomyocytes for 24 hours (Q24-A).	-0.0439453
<a href="#">GSM173659</a>	Quercetin treated cardiomyocytes for 24 hours (Q24-B).	-0.262591

Profile: *HMGA2* expression

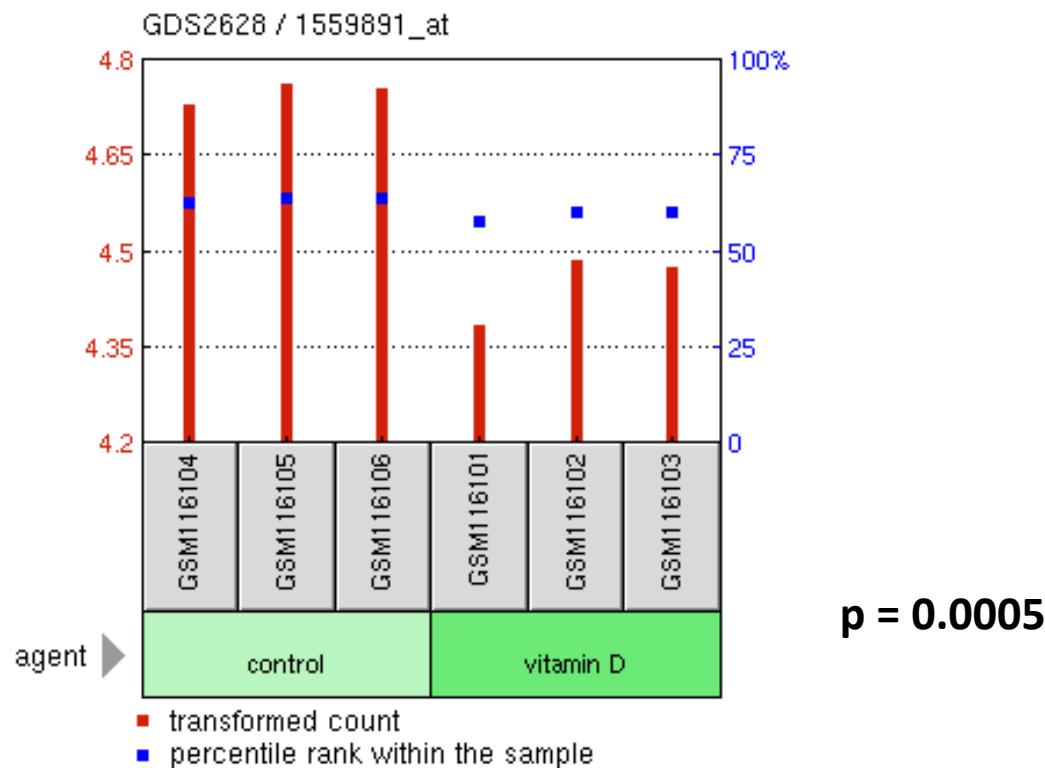
GDS2628 / 1559891\_at

Title

Vitamin D effect on bronchial smooth muscle cells

Organism

*Homo sapiens*



Vitamin D inhibits the *HMGA2* expression

Sample	Title	Value
<a href="#">GSM116104</a>	hBSMC_control_rep1	4.73008
<a href="#">GSM116105</a>	hBSMC_control_rep2	4.7629
<a href="#">GSM116106</a>	hBSMC_control_rep3	4.75495
<a href="#">GSM116101</a>	hBSMC_vitamin D_rep1	4.38522
<a href="#">GSM116102</a>	hBSMC_vitamin D_rep2	4.48749
<a href="#">GSM116103</a>	hBSMC_vitamin D_rep3	4.47664

Profile: *HMGA2* expression

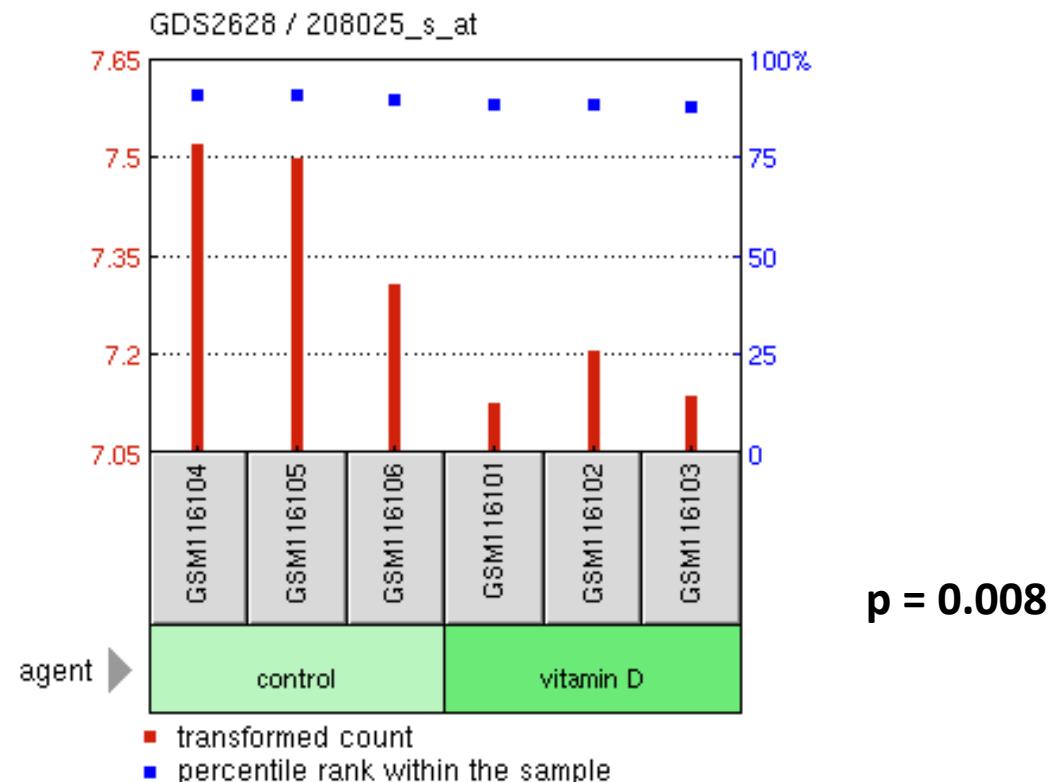
GDS2628 / 208025\_s\_at

Title

Vitamin D effect on bronchial smooth muscle cells

Organism

*Homo sapiens*



Vitamin D inhibits the *HMGA2* expression

Sample	Title	Value
<a href="#">GSM116104</a>	hBSMC_control_rep1	7.52243
<a href="#">GSM116105</a>	hBSMC_control_rep2	7.50027
<a href="#">GSM116106</a>	hBSMC_control_rep3	7.3098
<a href="#">GSM116101</a>	hBSMC_vitamin D_rep1	7.12949
<a href="#">GSM116102</a>	hBSMC_vitamin D_rep2	7.20614
<a href="#">GSM116103</a>	hBSMC_vitamin D_rep3	7.13995

Profile: ACE2 expression

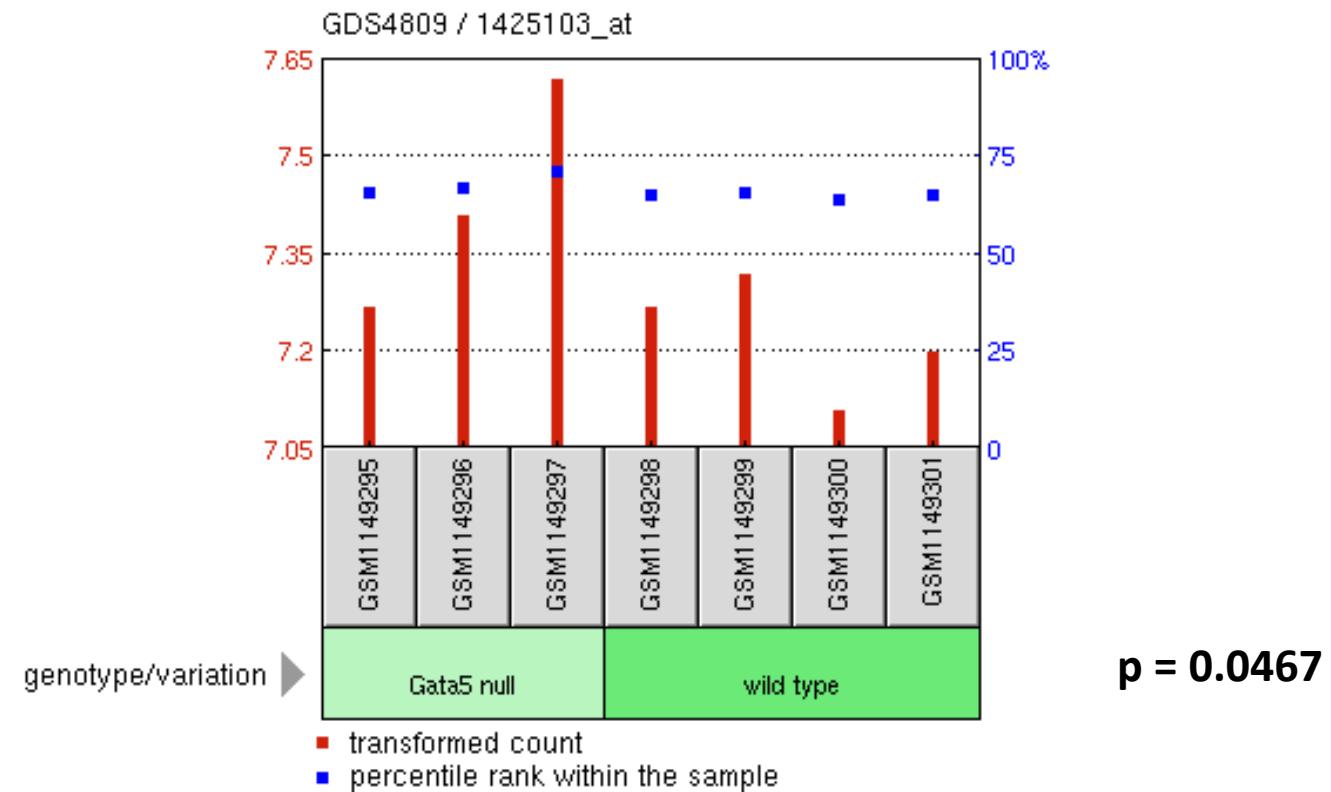
GDS4809 / 1425103\_at

Title

Gata5 deficiency effect on the lung

Organism

Mus musculus



## GATA5: a candidate inhibitor of the ACE2 expression

Sample	Title	Value
<a href="#">GSM1149295</a>	KO618	7.27
<a href="#">GSM1149296</a>	KO621	7.41
<a href="#">GSM1149297</a>	KO624	7.62
<a href="#">GSM1149298</a>	WT619	7.27
<a href="#">GSM1149299</a>	WT623	7.32
<a href="#">GSM1149300</a>	WT648	7.11
<a href="#">GSM1149301</a>	WT659	7.2

Profile: *VDR* expression

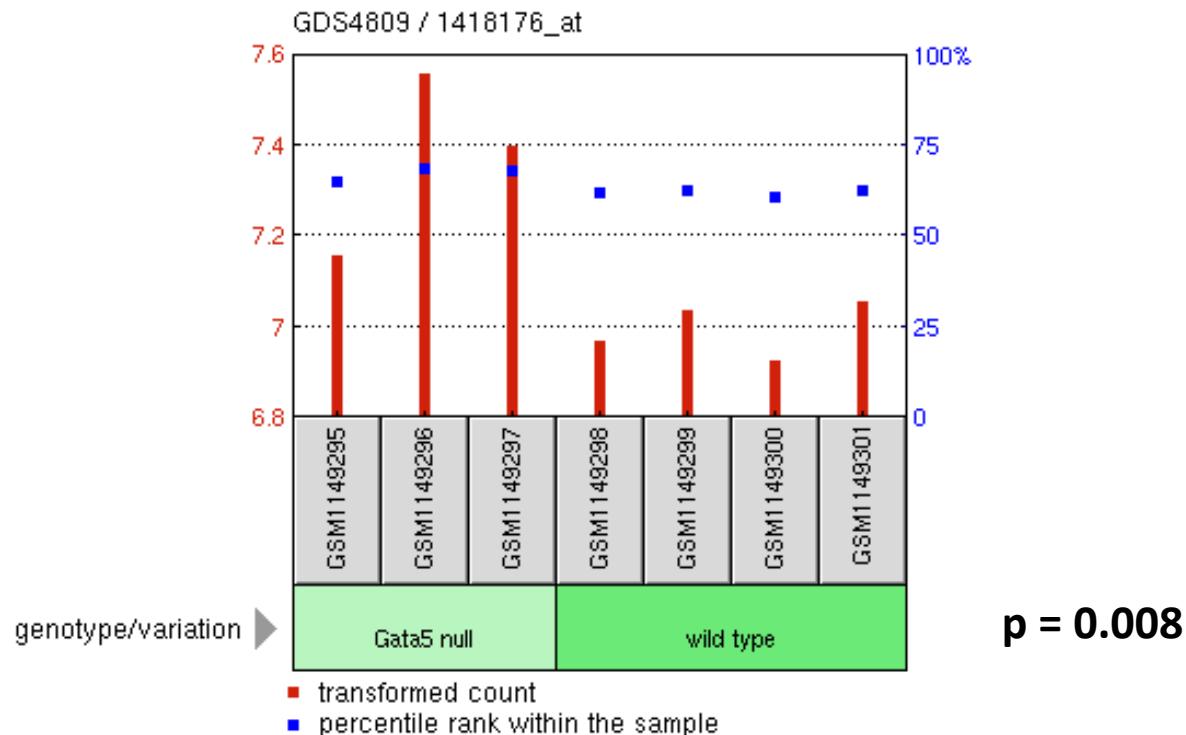
GDS4809 / 1418176\_at

Title

Gata5 deficiency effect on the lung

Organism

*Mus musculus*



## GATA5: a candidate inhibitor of the *VDR* expression

Sample	Title	Value
<a href="#">GSM1149295</a>	KO618	7.16
<a href="#">GSM1149296</a>	KO621	7.56
<a href="#">GSM1149297</a>	KO624	7.4
<a href="#">GSM1149298</a>	WT619	6.97
<a href="#">GSM1149299</a>	WT623	7.04
<a href="#">GSM1149300</a>	WT648	6.93
<a href="#">GSM1149301</a>	WT659	7.06

Profile: *SFTPC* expression

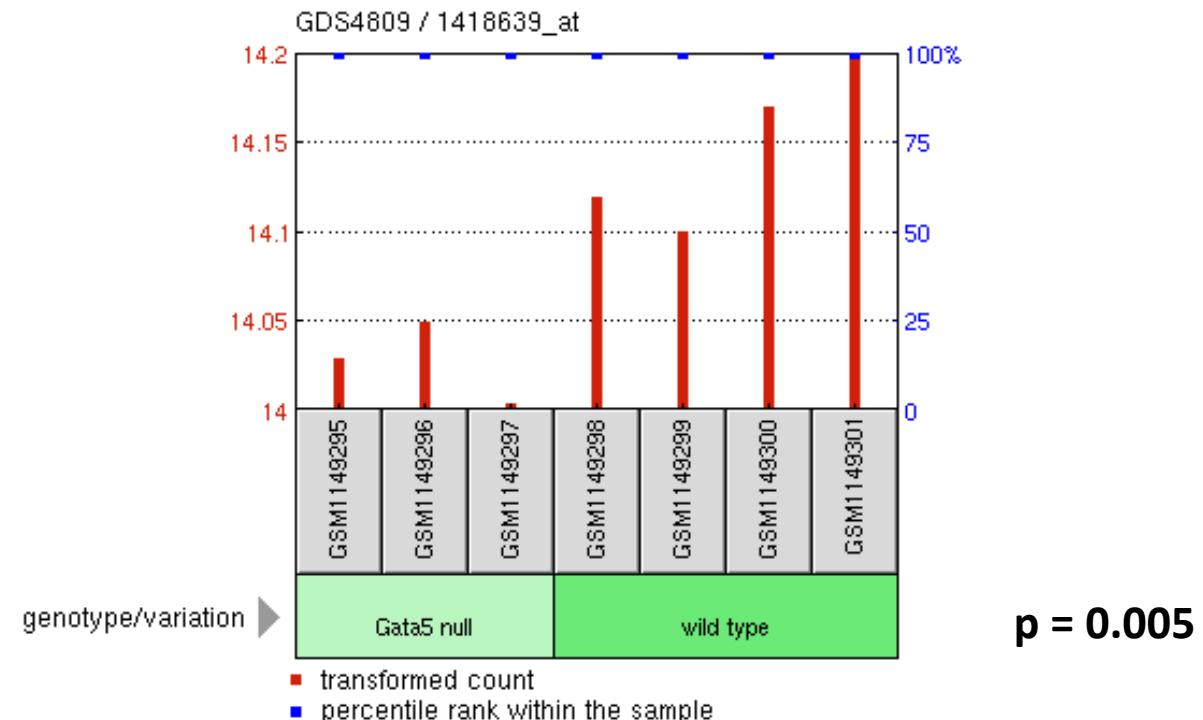
GDS4809 / 1418639\_at

Title

Gata5 deficiency effect on the lung

Organism

*Mus musculus*



**p = 0.005**

## ***GATA5*: a candidate activator of the *SFTPC* expression**

Sample	Title	Value
<a href="#">GSM1149295</a>	KO618	14.03
<a href="#">GSM1149296</a>	KO621	14.05
<a href="#">GSM1149297</a>	KO624	14
<a href="#">GSM1149298</a>	WT619	14.12
<a href="#">GSM1149299</a>	WT623	14.1
<a href="#">GSM1149300</a>	WT648	14.17
<a href="#">GSM1149301</a>	WT659	14.2

# Profile: GATA5 expression

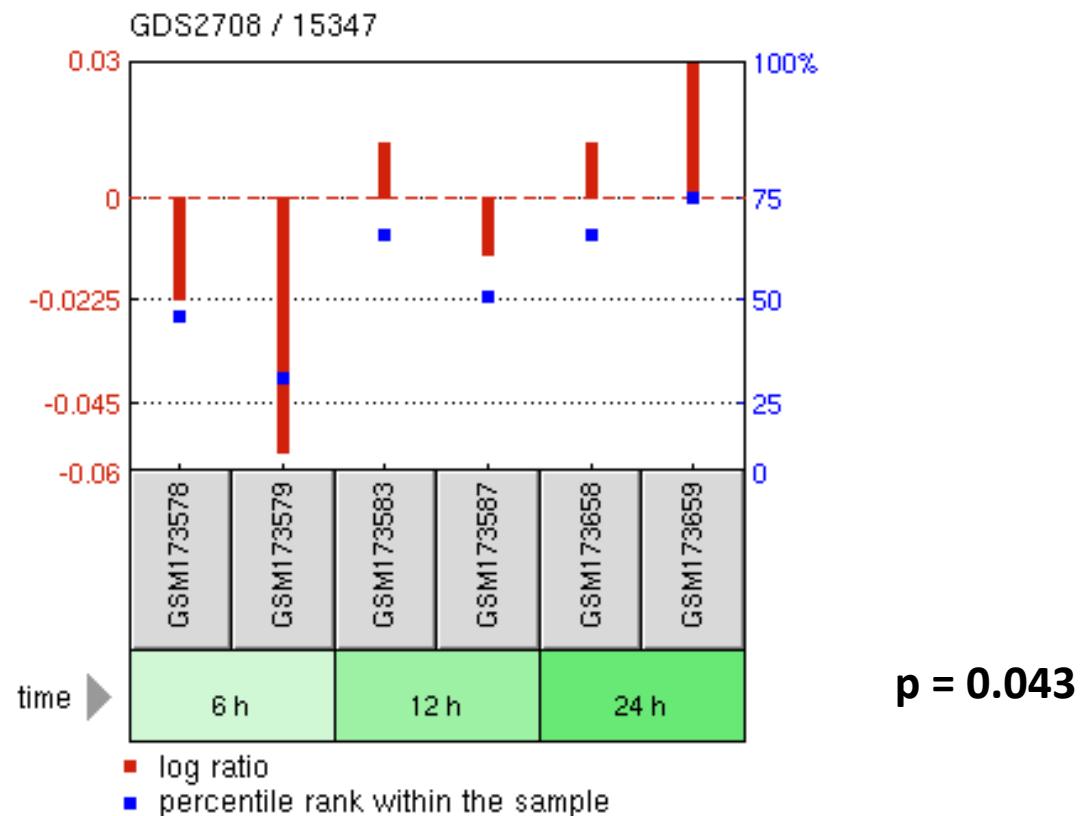
GDS2708 / 15347

## Title

Quercetin effect on cultured cardiomyocytes: time course

## Organism

Rattus norvegicus



Quercetin enhances the *GATA5* expression

Sample	Title	Value
<a href="#">GSM173578</a>	Quercetin treated cardiomyocytes for 6 hours (Q6-A).	-0.0227201
<a href="#">GSM173579</a>	Quercetin treated cardiomyocytes for 6 hours (Q6-B).	-0.0564461
<a href="#">GSM173583</a>	Quercetin treated cardiomyocytes for 12 hours (Q12-A).	0.0121804
<a href="#">GSM173587</a>	Quercetin treated cardiomyocytes for 12 hours (Q12-B).	-0.0128478
<a href="#">GSM173658</a>	Quercetin treated cardiomyocytes for 24 hours (Q24-A).	0.0121804
<a href="#">GSM173659</a>	Quercetin treated cardiomyocytes for 24 hours (Q24-B).	0.0297642

Profile: GATA5 expression

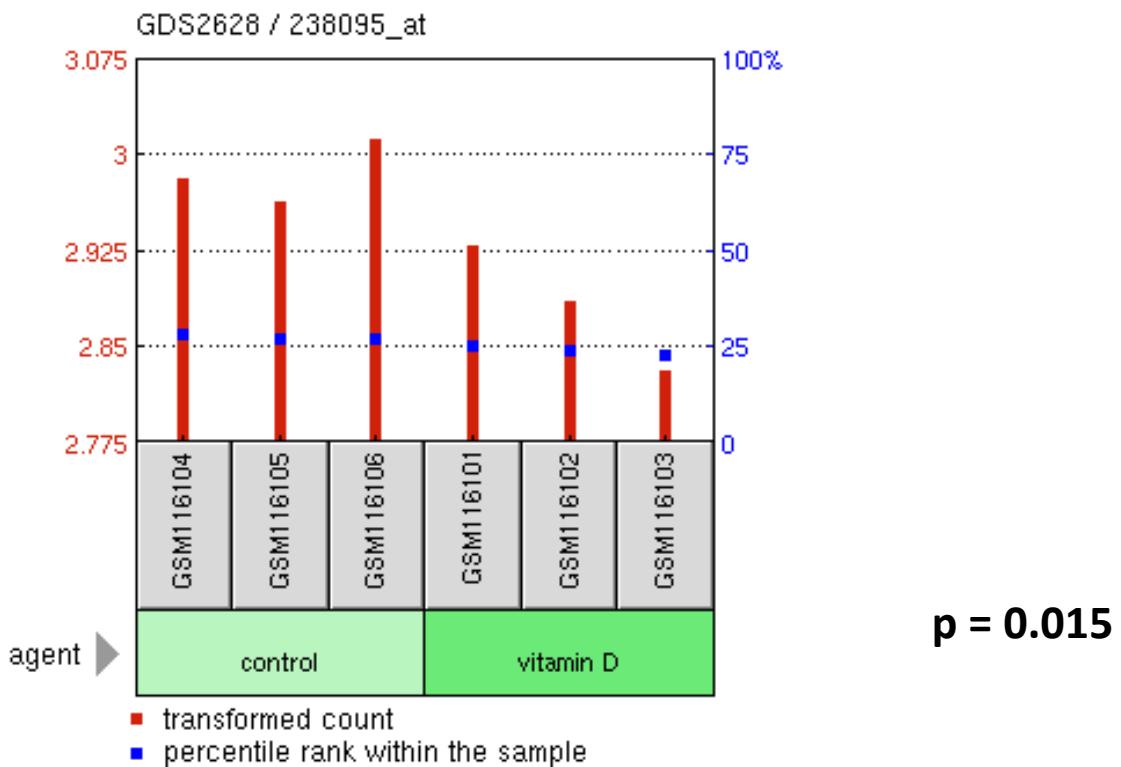
GDS2628 / 238095\_at

Title

Vitamin D effect on bronchial smooth muscle cells

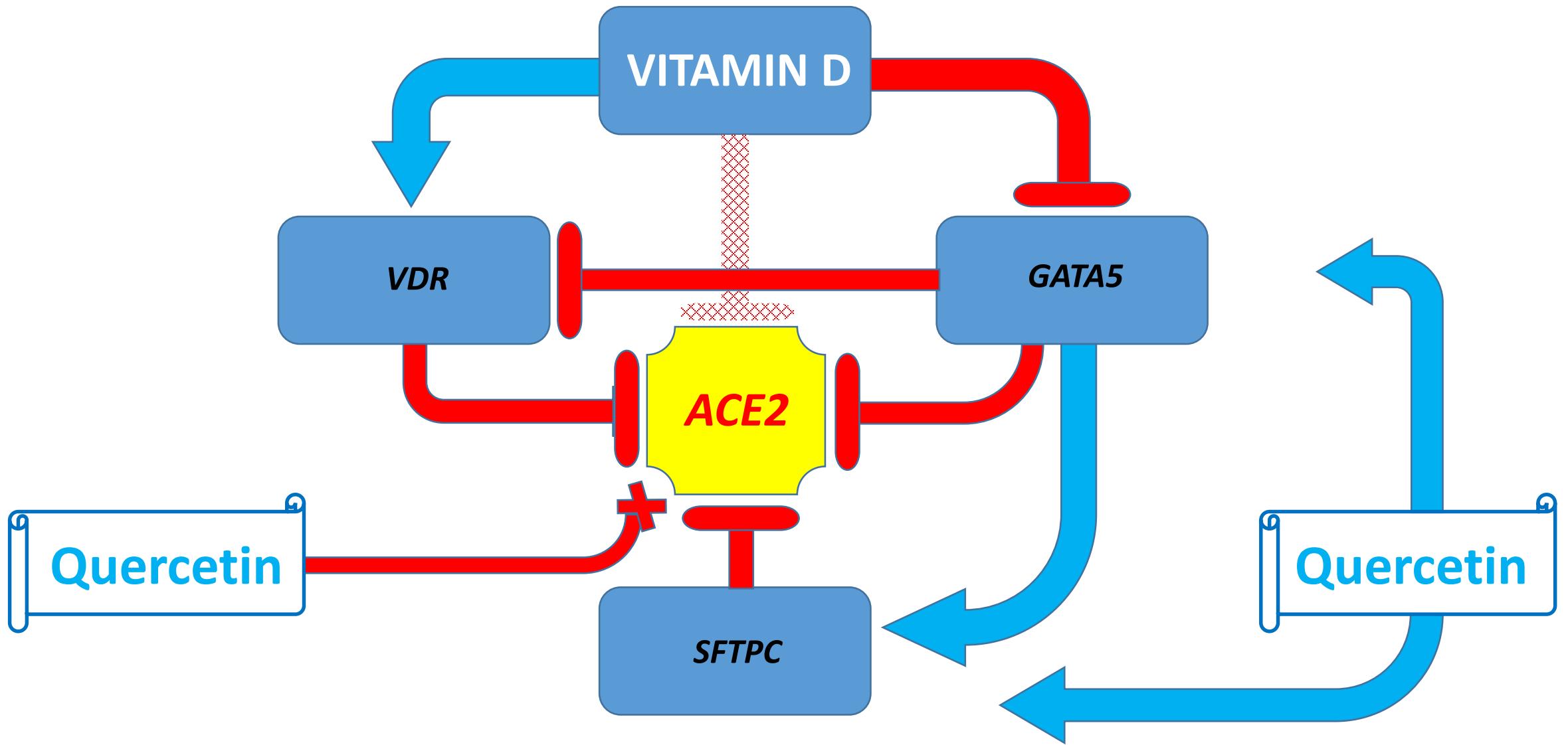
Organism

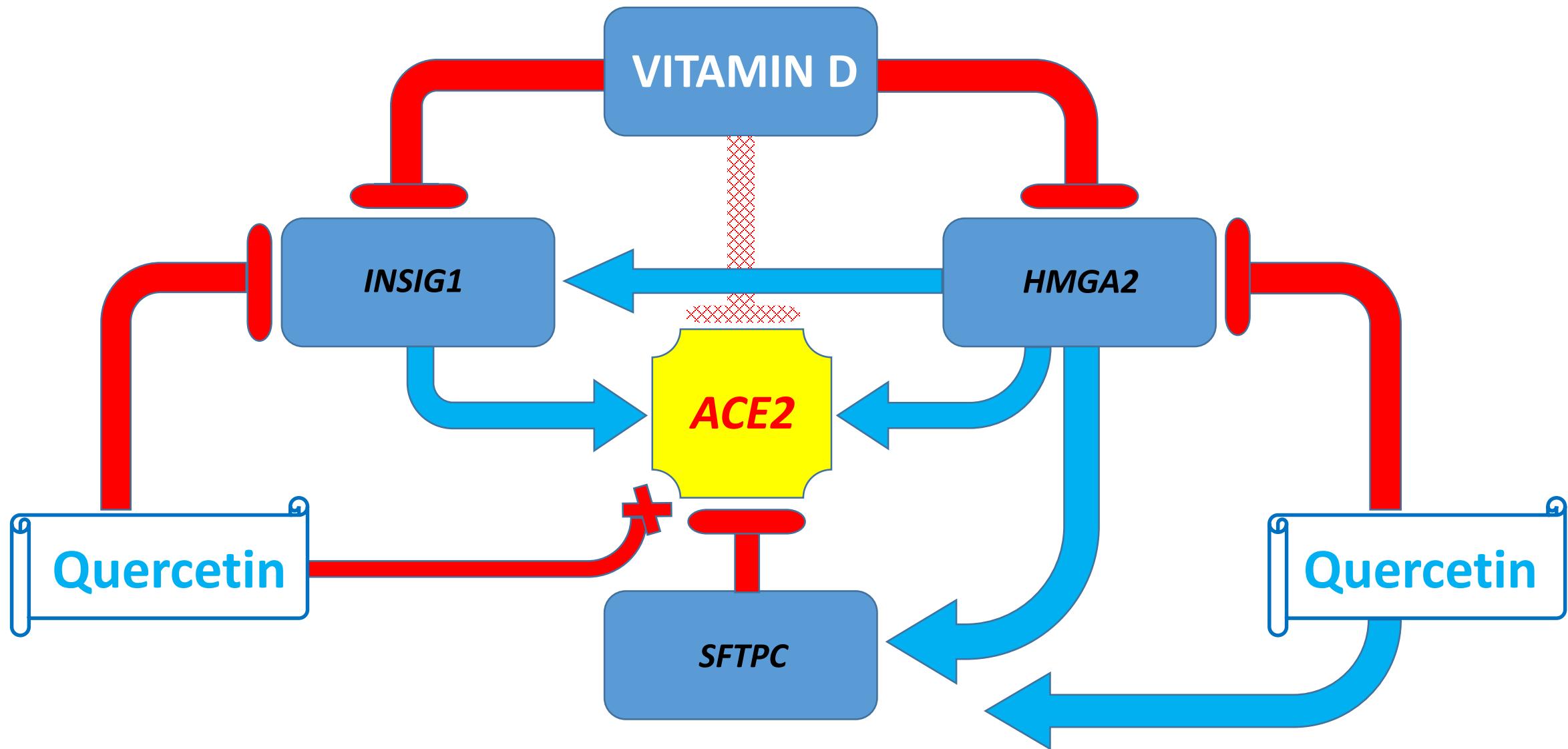
Homo sapiens



Vitamin D inhibits the *GATA5* expression

Sample	Title	Value
<a href="#">GSM116104</a>	hBSMC_control_rep1	2.98202
<a href="#">GSM116105</a>	hBSMC_control_rep2	2.96376
<a href="#">GSM116106</a>	hBSMC_control_rep3	3.01345
<a href="#">GSM116101</a>	hBSMC_vitamin D_rep1	2.92934
<a href="#">GSM116102</a>	hBSMC_vitamin D_rep2	2.88574
<a href="#">GSM116103</a>	hBSMC_vitamin D_rep3	2.83171





Profile: *SFTPC* expression

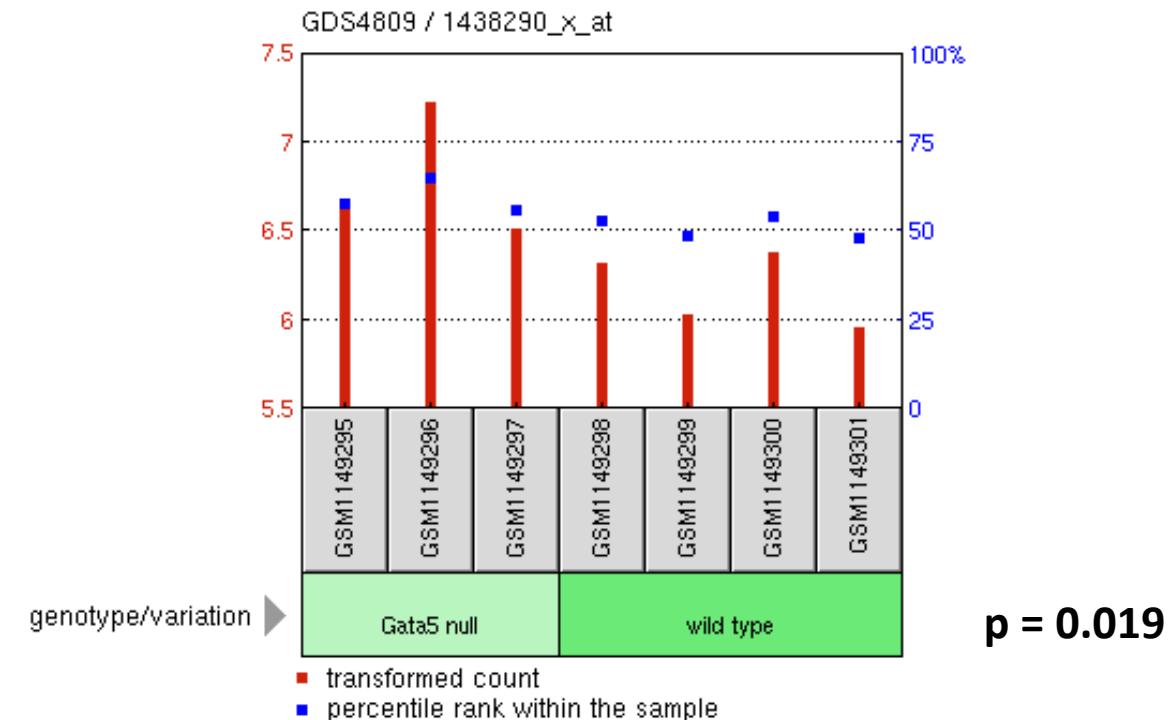
GDS4809 / 1438290\_x\_at

Title

Gata5 deficiency effect on the lung

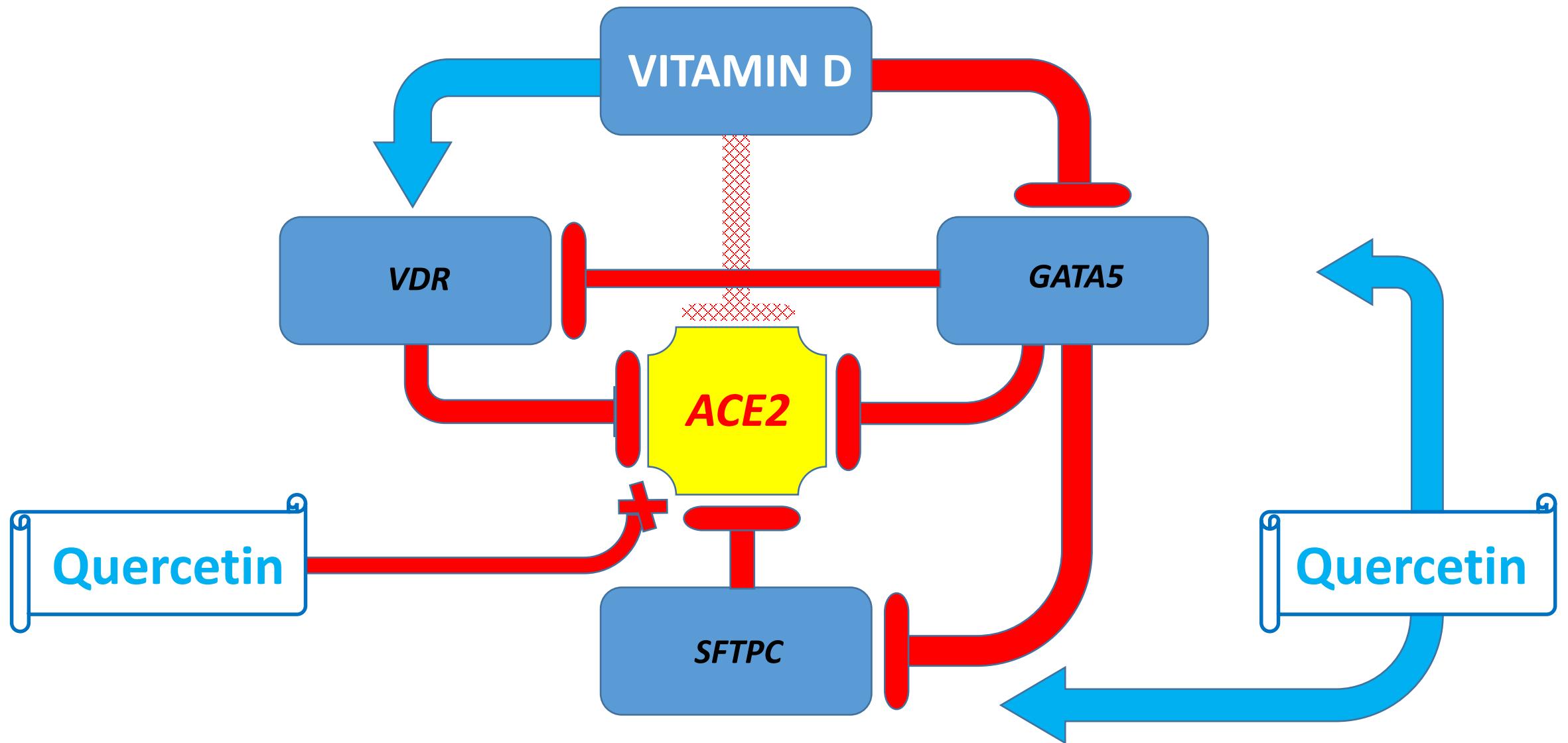
Organism

*Mus musculus*



## ***GATA5*: a candidate inhibitor of the *SFTPC* expression**

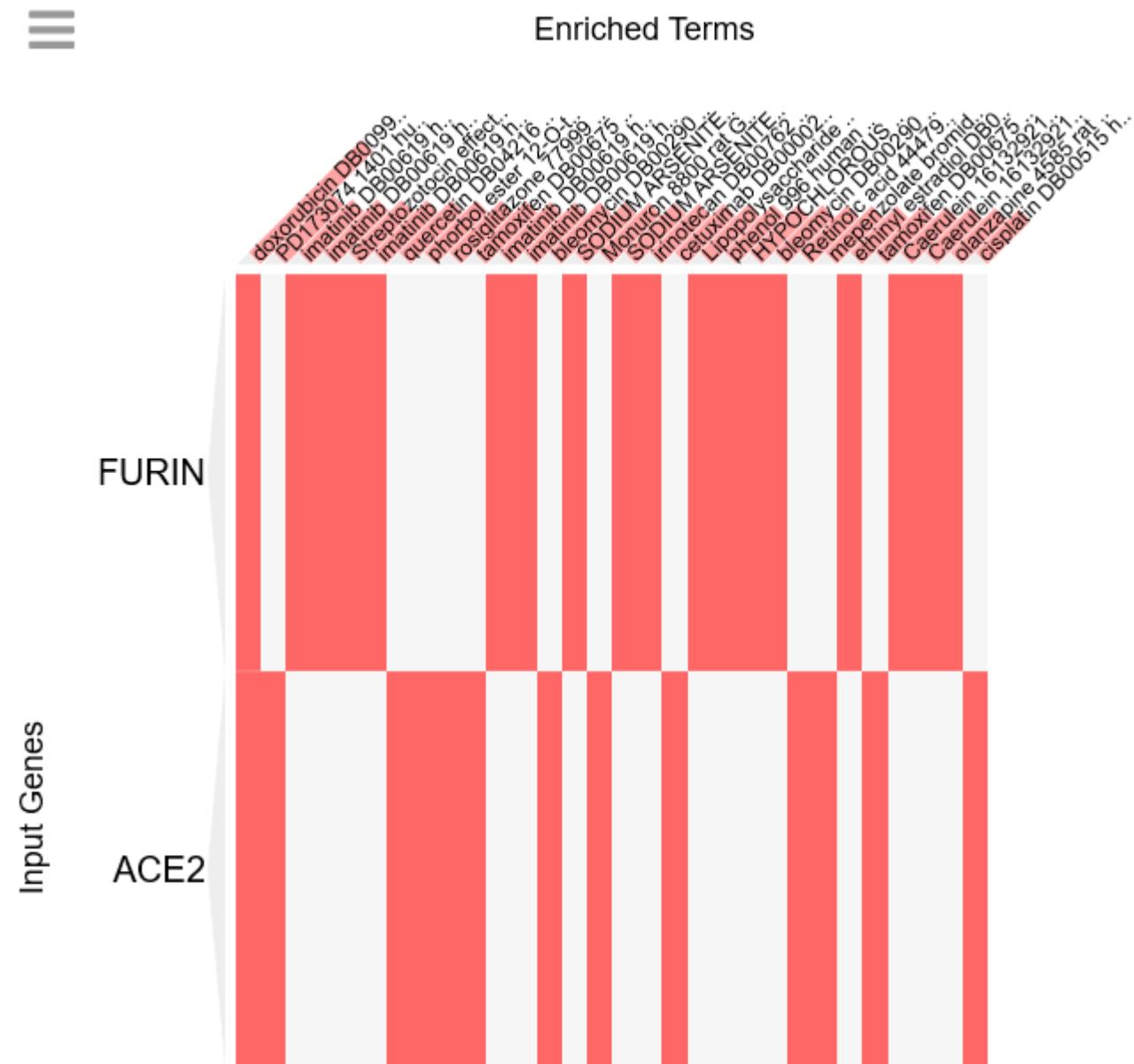
Sample	Title	Value
<a href="#">GSM1149295</a>	KO618	6.65
<a href="#">GSM1149296</a>	KO621	7.23
<a href="#">GSM1149297</a>	KO624	6.52
<a href="#">GSM1149298</a>	WT619	6.32
<a href="#">GSM1149299</a>	WT623	6.04
<a href="#">GSM1149300</a>	WT648	6.39
<a href="#">GSM1149301</a>	WT659	5.96



Examples of the potential negative effects of drugs on the ACE2 expression

## Drug Perturbations from GEO up

## Enriched Terms



# Profile *INSIG1* expression

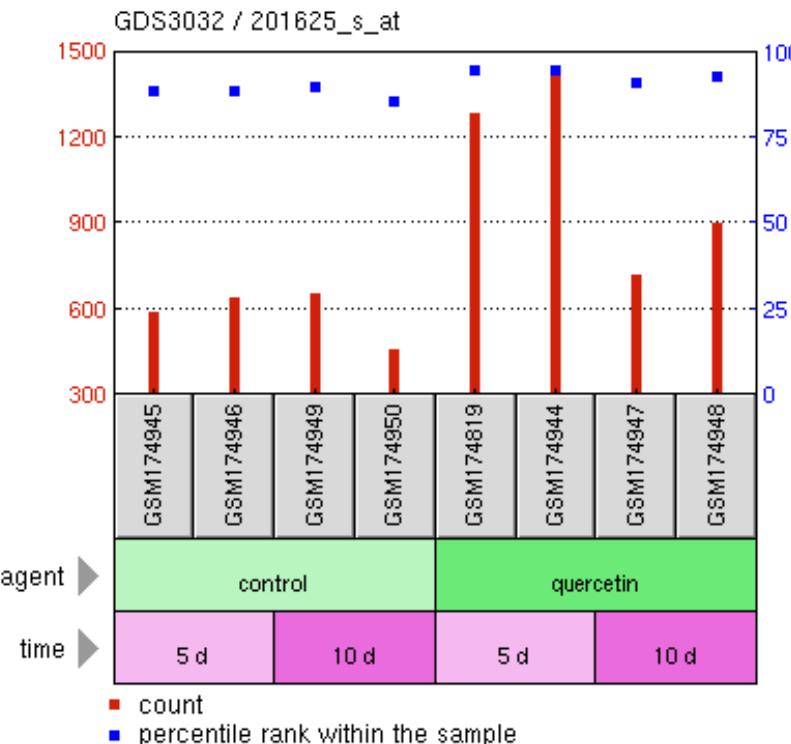
GDS3032 / 201625\_s\_at

## Title

Quercetin effect on intestinal cell differentiation in vitro: time course

## Organism

Homo sapiens



Quercetin enhances the *INSIG1* expression

Sample	Title	Value
<a href="#">GSM174945</a>	Control day 05 sample 1	593.419
<a href="#">GSM174946</a>	Control day 05 sample 2	640.636
<a href="#">GSM174949</a>	Control day 10 sample 1	654.401
<a href="#">GSM174950</a>	Control day 10 sample 2	465.967
<a href="#">GSM174819</a>	Quercetin day 05 sample 1	1286.16
<a href="#">GSM174944</a>	Quercetin day 05 sample 2	1420.46
<a href="#">GSM174947</a>	Quercetin day 10 sample 1	722.644
<a href="#">GSM174948</a>	Quercetin day 10 sample 2	905.527

**Profile: *INSIG1* expression**

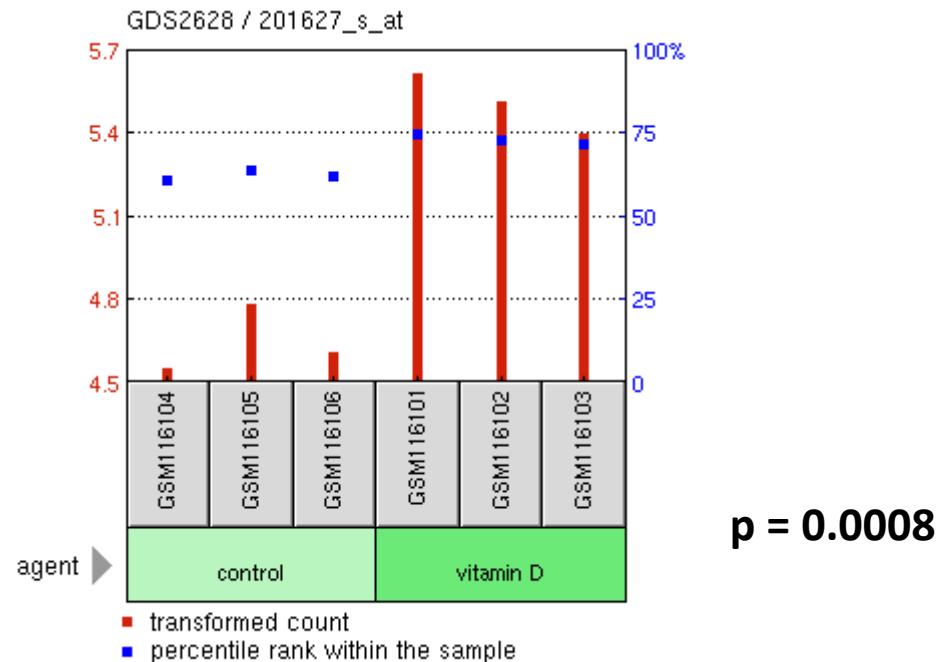
**GDS2628 / 201627\_s\_at**

**Title**

**Vitamin D effect on bronchial smooth muscle cells**

**Organism**

**Homo sapiens**



**Vitamin D enhances the *INSIG1* expression**

Sample	Title	Value
<a href="#">GSM116104</a>	hBSMC_control_rep1	4.5524
<a href="#">GSM116105</a>	hBSMC_control_rep2	4.78368
<a href="#">GSM116106</a>	hBSMC_control_rep3	4.6123
<a href="#">GSM116101</a>	hBSMC_vitamin D_rep1	5.61848
<a href="#">GSM116102</a>	hBSMC_vitamin D_rep2	5.51657
<a href="#">GSM116103</a>	hBSMC_vitamin D_rep3	5.40349

Profile: *INSIG1* expression

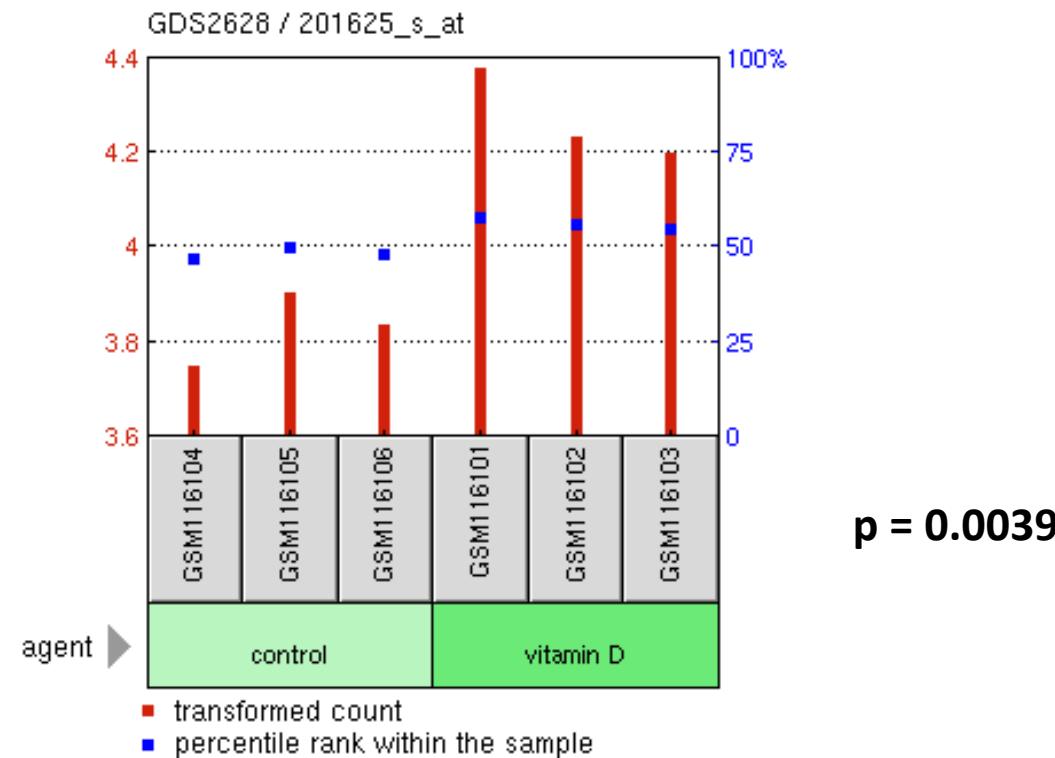
GDS2628 / 201625\_s\_at

Title

Vitamin D effect on  
bronchial smooth muscle  
cells

Organism

*Homo sapiens*



Vitamin D enhances the *INSIG1* expression

Sample	Title	Value
<a href="#">GSM116104</a>	hBSMC_control_rep1	3.75107
<a href="#">GSM116105</a>	hBSMC_control_rep2	3.90763
<a href="#">GSM116106</a>	hBSMC_control_rep3	3.83897
<a href="#">GSM116101</a>	hBSMC_vitamin D_rep1	4.37812
<a href="#">GSM116102</a>	hBSMC_vitamin D_rep2	4.2358
<a href="#">GSM116103</a>	hBSMC_vitamin D_rep3	4.19935

Profile: *INSIG1* expression

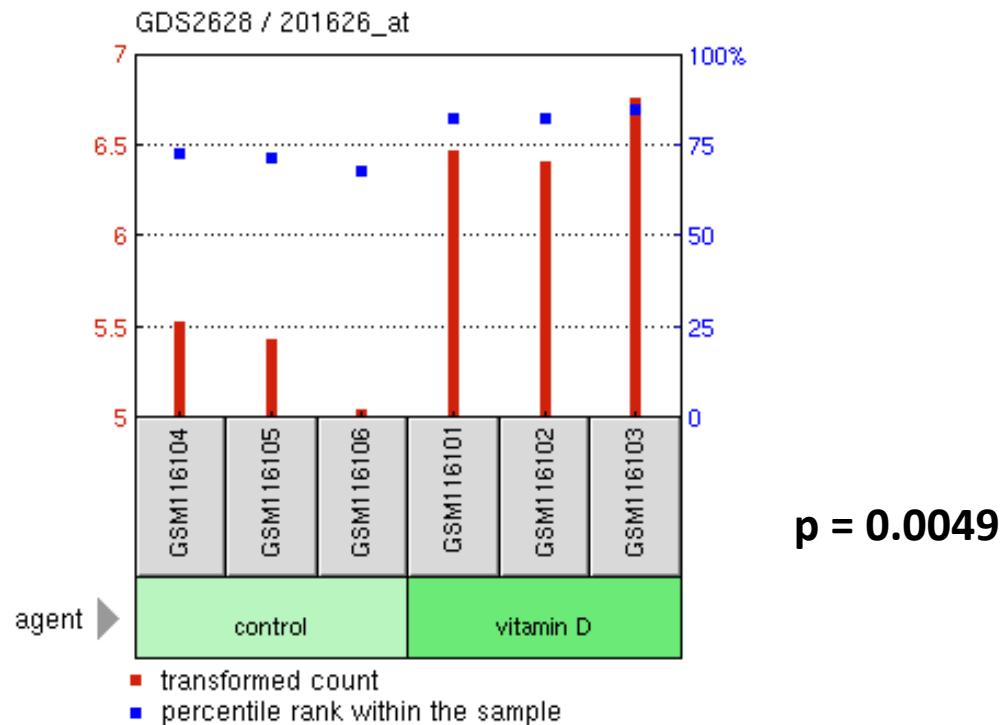
GDS2628 / 201626\_at

Title

Vitamin D effect on  
bronchial smooth muscle  
cells

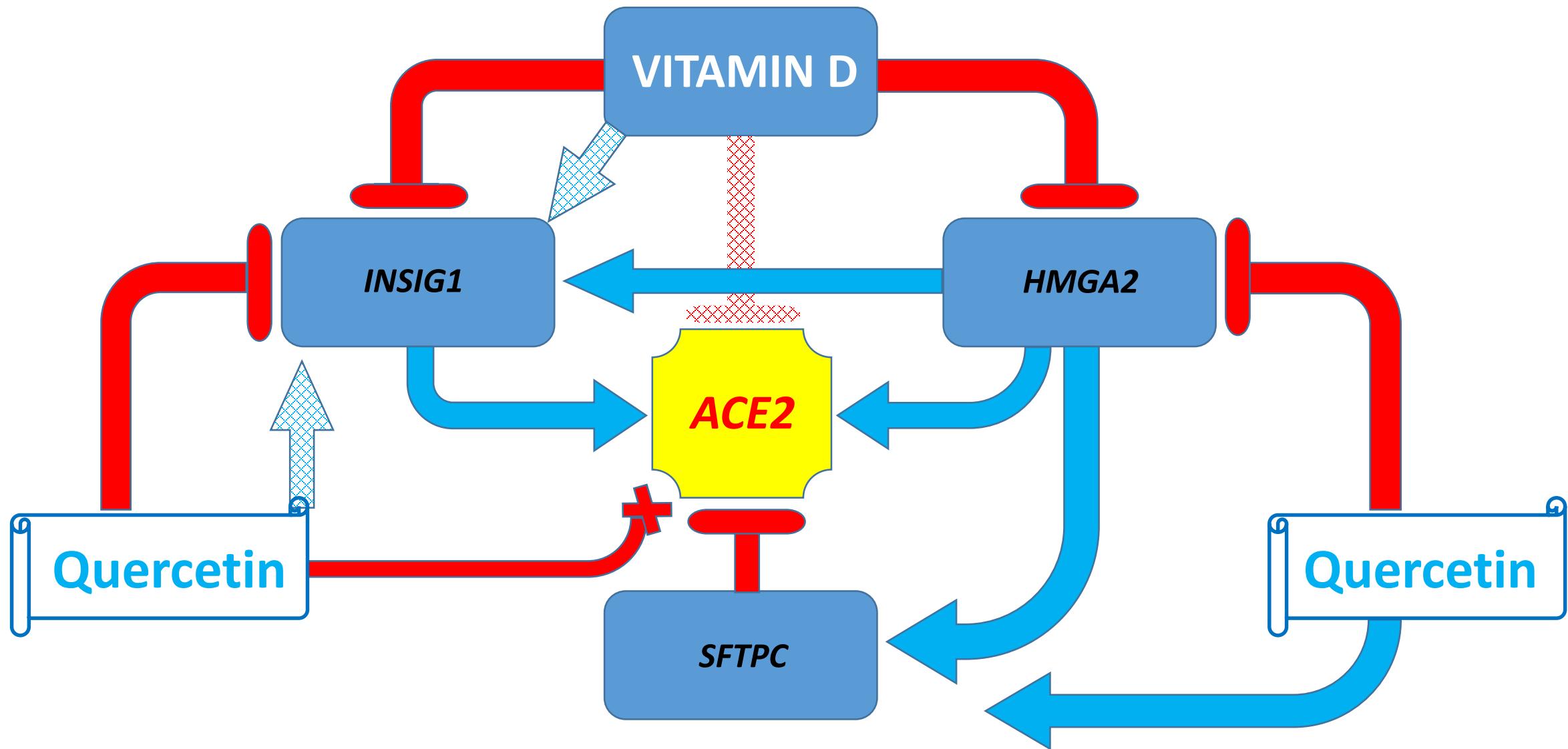
Organism

Homo sapiens



Vitamin D enhances the *INSIG1* expression

Sample	Title	Value
<a href="#">GSM116104</a>	hBSMC_control_rep1	5.53893
<a href="#">GSM116105</a>	hBSMC_control_rep2	5.43847
<a href="#">GSM116106</a>	hBSMC_control_rep3	5.01659
<a href="#">GSM116101</a>	hBSMC_vitamin D_rep1	6.47195
<a href="#">GSM116102</a>	hBSMC_vitamin D_rep2	6.42131
<a href="#">GSM116103</a>	hBSMC_vitamin D_rep3	6.76932



Profile: ACE2 expression

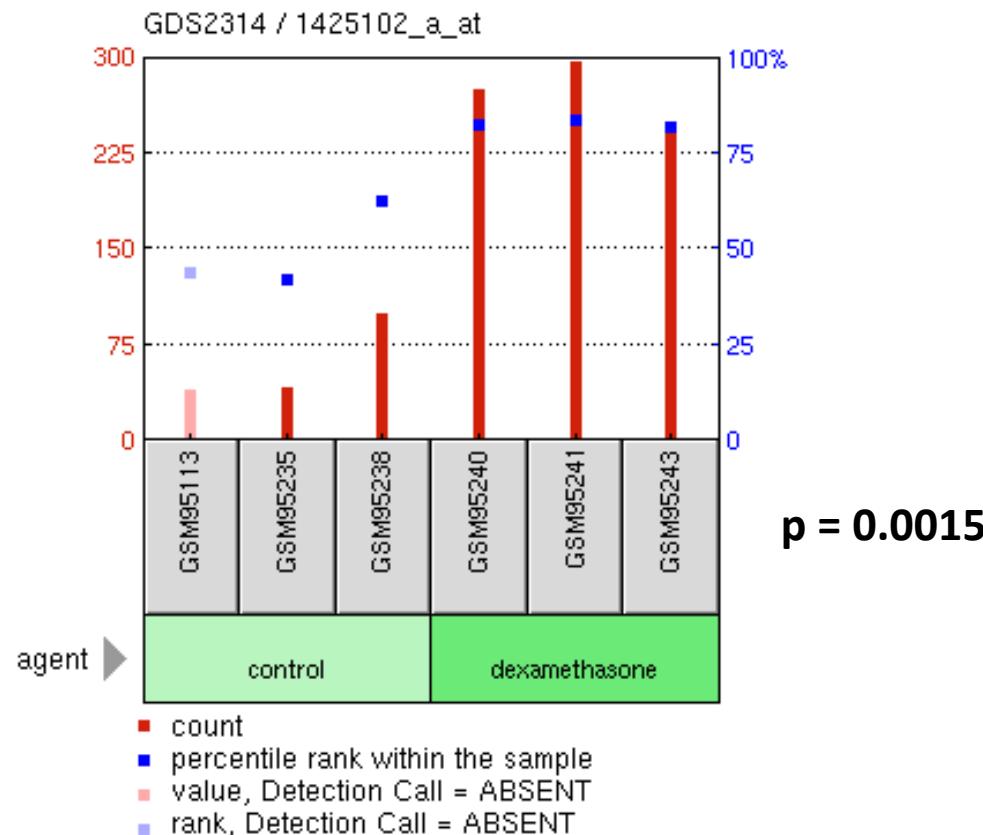
GDS2314 / 1425102\_a\_at

Title

Antenatal steroid effect on the placenta

Organism

Mus musculus



Dexamethasone enhances the ACE2 expression

Sample	Title	Value
<a href="#">GSM95113</a>	Control 1	40.6
<a href="#">GSM95235</a>	Control 2	42
<a href="#">GSM95238</a>	Control 3	100.9
<a href="#">GSM95240</a>	Dexamethasone 1	275.7
<a href="#">GSM95241</a>	Dexamethasone 2	298
<a href="#">GSM95243</a>	Dexamethasone 3	249.5

Profile: ACE2 expression

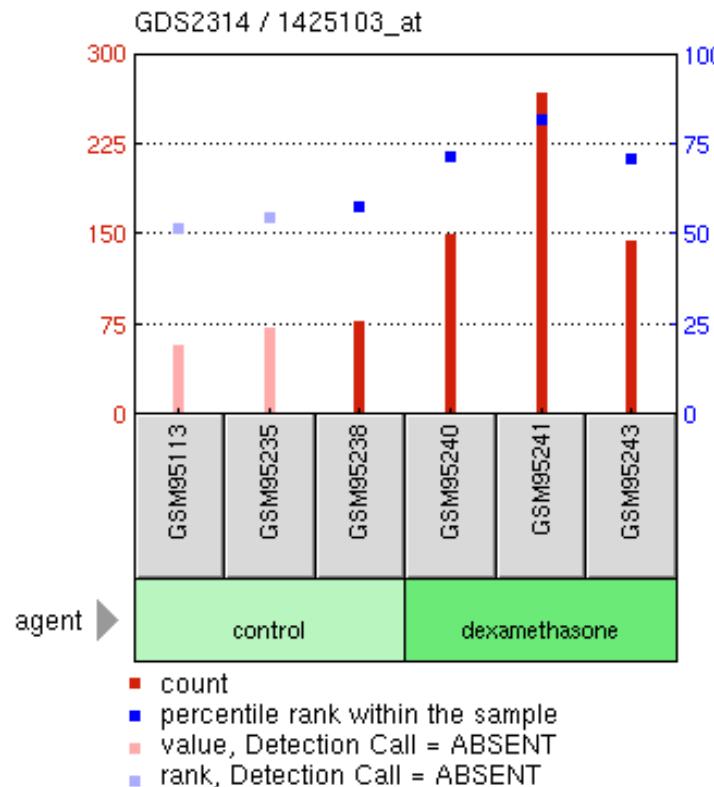
GDS2314 / 1425103\_at

Title

Antenatal steroid effect on the placenta

Organism

Mus musculus



Dexamethasone enhances the *ACE2* expression

Sample	Title	Value	Rank
<a href="#">GSM95113</a>	Control 1	58	52
<a href="#">GSM95235</a>	Control 2	73.3	55
<a href="#">GSM95238</a>	Control 3	79.1	58
<a href="#">GSM95240</a>	Dexamethasone 1	151	72
<a href="#">GSM95241</a>	Dexamethasone 2	268.3	82
<a href="#">GSM95243</a>	Dexamethasone 3	145.8	71

**Profile: ACE2 expression**

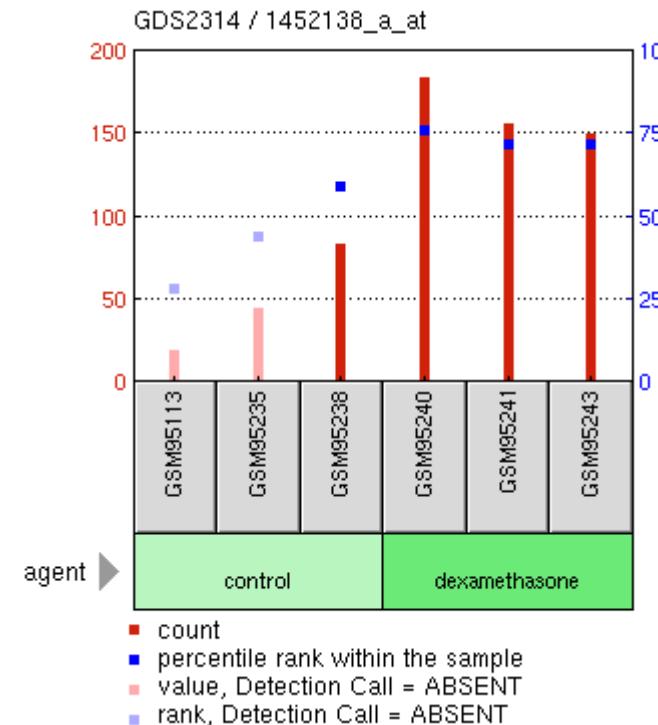
**GDS2314 / 1452138\_a\_at**

**Title**

**Antenatal steroid effect on the placenta**

**Organism**

**Mus musculus**



**Dexamethasone enhances the ACE2 expression**

Sample	Title	Value	Rank
<a href="#">GSM95113</a>	Control 1	19.6	28
<a href="#">GSM95235</a>	Control 2	45.5	44
<a href="#">GSM95238</a>	Control 3	83.4	59
<a href="#">GSM95240</a>	Dexamethasone 1	183.3	76
<a href="#">GSM95241</a>	Dexamethasone 2	155.8	72
<a href="#">GSM95243</a>	Dexamethasone 3	150	72

Supplemental Table S13. Additional examples of the potential activators and repressors of the *ACE2* expression identified using transgenic mouse models

Additional examples of the potential activators of  
the *ACE2* expression identified using transgenic  
mouse models

# Profile: ACE2 expression

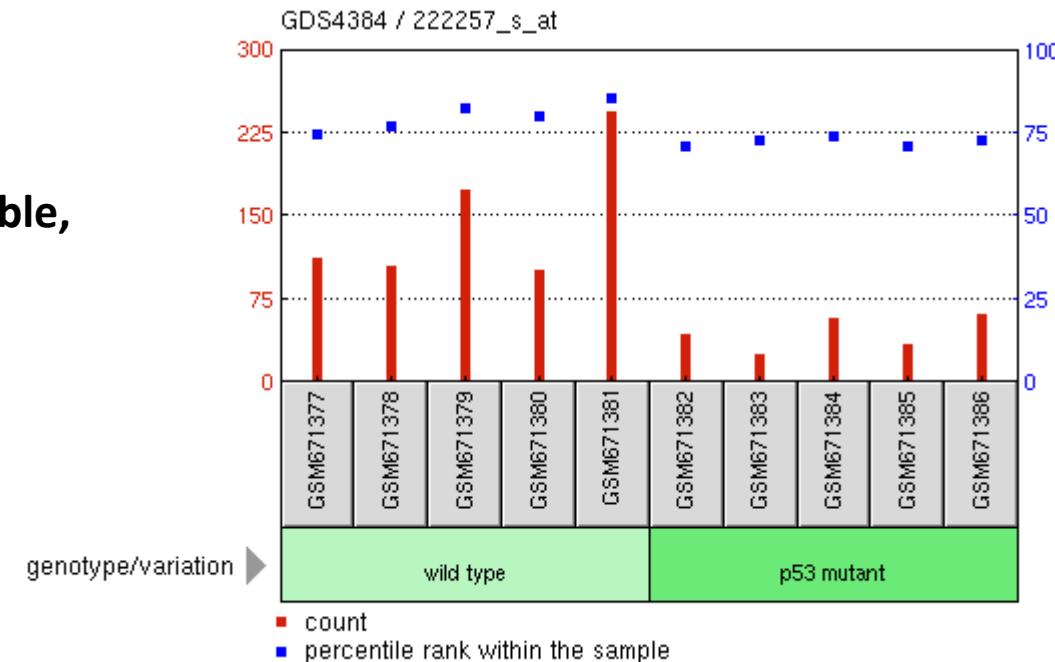
GDS4384 / 222257\_s\_at

## Title

p53 mutations in microsatellite-stable,  
stage III colorectal cancer

## Organism

Homo sapiens



Sample	Title	Value
<a href="#">GSM671377</a>	UM13_Wt_rep1	112.441
<a href="#">GSM671378</a>	UM23_Wt_rep2	105.683
<a href="#">GSM671379</a>	UM30_Wt_rep3	173.535
<a href="#">GSM671380</a>	UM9_Wt_rep4	101.705
<a href="#">GSM671381</a>	UM3_Wt_rep5	244.407
<a href="#">GSM671382</a>	UM1_Mut_rep1	44.3901
<a href="#">GSM671383</a>	UM15_Mtu_rep2	26.5371
<a href="#">GSM671384</a>	UM17_Mtu_rep3	59.3536
<a href="#">GSM671385</a>	UM2_Mtu_rep4	34.4729
<a href="#">GSM671386</a>	UM25_Mtu_rep5	62.1878

# Profile: ACE2 expression

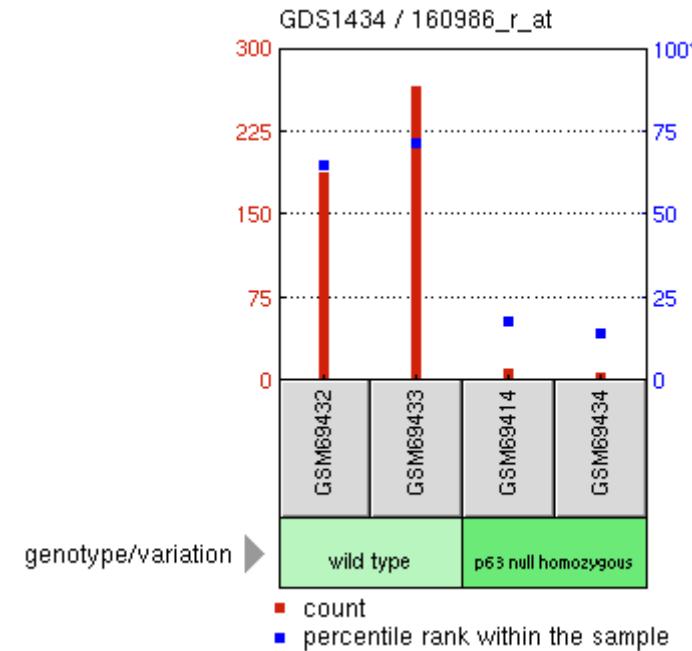
GDS1434 / 160986\_r\_at

Title

Transcription factor p63 null mutation  
effect on skin (MG-U74A)

Organism

Mus musculus



Sample	Title	Value
<a href="#">GSM69432</a>	E18.5 p63 wt skin 1 A-chip	189.3
<a href="#">GSM69433</a>	E18.5 p63 wt skin 2 A-chip	267.1
<a href="#">GSM69414</a>	E18.5 p63 null skin 1 A-chip	11.5
<a href="#">GSM69434</a>	E18.5 p63 null skin 2 A-chip	8.4

## Profile: ACE2 expression

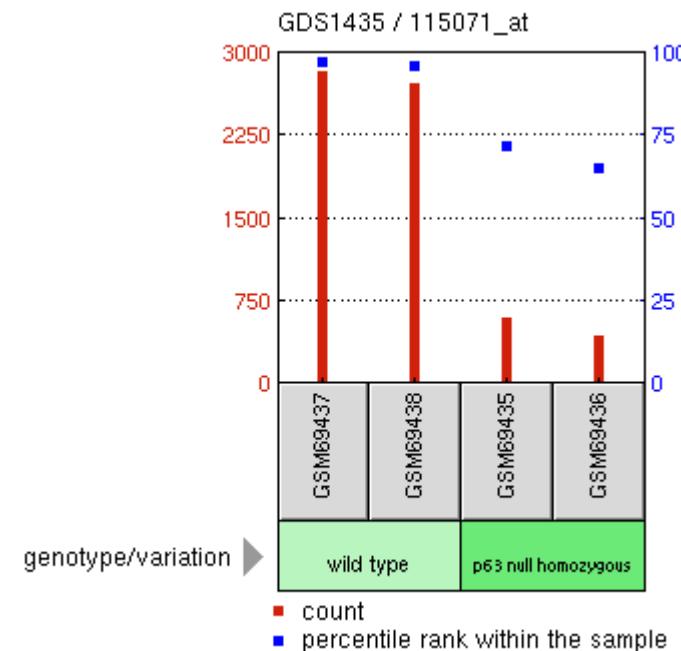
GDS1435 / 115071\_at

### Title

Transcription factor p63 null mutation effect on skin (MG-U74B)

### Organism

Mus musculus



Sample	Title	Value
<a href="#">GSM69437</a>	E18.5 wt skin 1 B-chip	2821.9
<a href="#">GSM69438</a>	E18.5 wt skin 2 B-chip	2718.1
<a href="#">GSM69435</a>	E18.5 p63 null skin 1 B-chip	602.2
<a href="#">GSM69436</a>	E18.5 p63 null skin 2 B-chip	449.1

# Profile: ACE2 expression

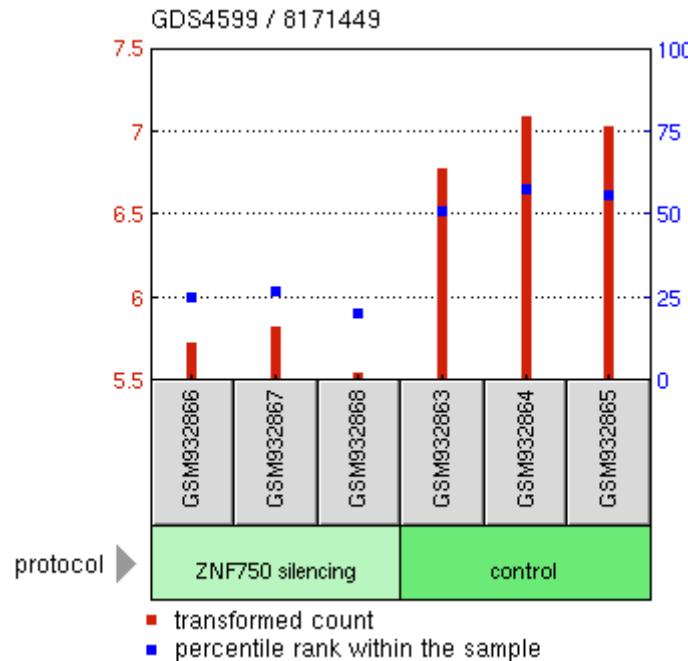
GDS4599 / 8171449

## Title

ZNF750 silencing effect on differentiated keratinocytes

## Organism

Homo sapiens



Sample	Title	Value
<a href="#">GSM932866</a>	HaCaT_ZNF750i_ biological rep1	5.74045
<a href="#">GSM932867</a>	HaCaT_ZNF750i_ biological rep2	5.82679
<a href="#">GSM932868</a>	HaCaT_ZNF750i_ biological rep3	5.52392
<a href="#">GSM932863</a>	HaCaT_Control_ biological rep1	6.78372
<a href="#">GSM932864</a>	HaCaT_Control_ biological rep2	7.09307
<a href="#">GSM932865</a>	HaCaT_Control_ biological rep3	7.03868

# Profile: ACE2 expression

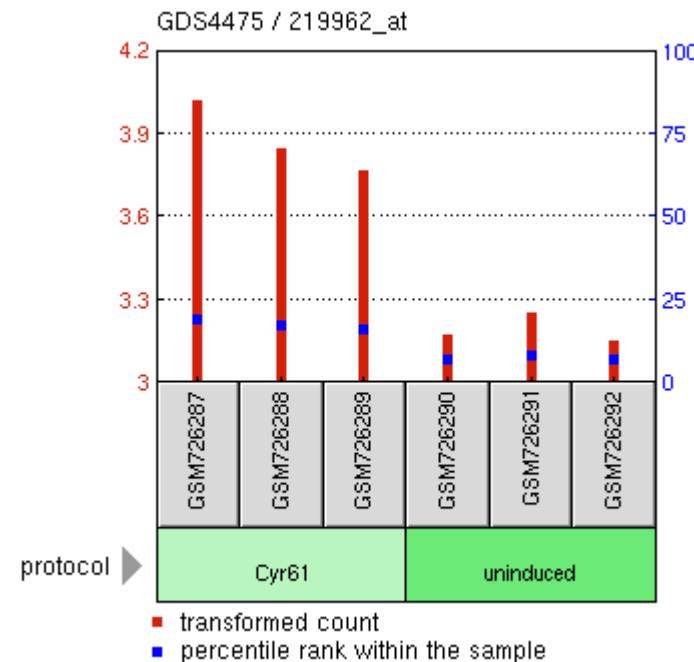
GDS4475 / 219962\_at

## Title

Extracellular matrix protein cysteine rich 61 (CCN1) effect on LN229 glioma cells

## Organism

Homo sapiens



Sample	Title	Value
<a href="#">GSM726287</a>	Tetracycline-inducible glioma cells dox 1	4.02176
<a href="#">GSM726288</a>	Tetracycline-inducible glioma cells dox 2	3.85144
<a href="#">GSM726289</a>	Tetracycline-inducible glioma cells dox 3	3.77096
<a href="#">GSM726290</a>	Tetracycline-inducible glioma cells no dox 1	3.17831
<a href="#">GSM726291</a>	Tetracycline-inducible glioma cells no dox 2	3.25989
<a href="#">GSM726292</a>	Tetracycline-inducible glioma cells no dox 3	3.15658

**Profile: ACE2 expression**

**GDS4061 / 222257\_s\_at**

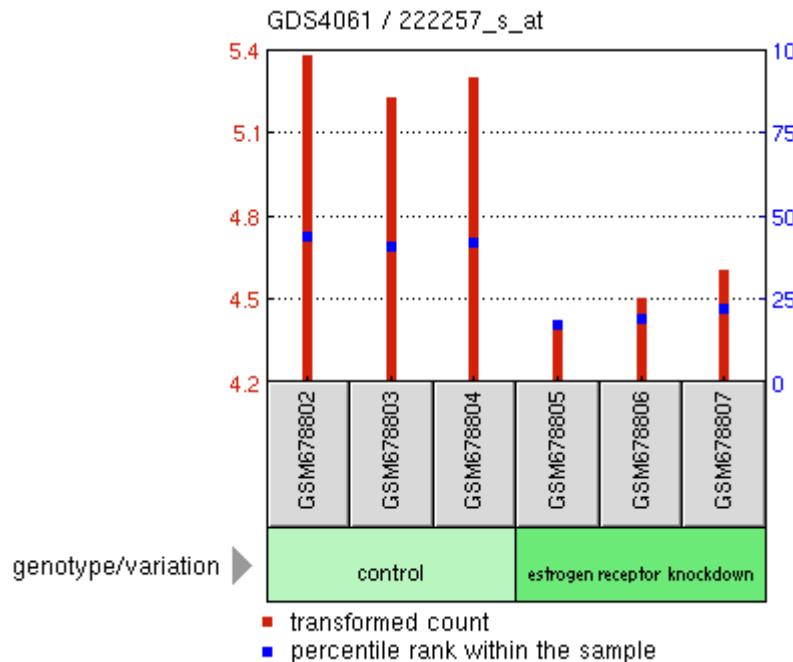
**Title**

**Estrogen receptor alpha-silenced**

**MCF7 breast cancer cells**

**Organism**

**Homo sapiens**



Sample	Title	Value
<a href="#">GSM678802</a>	MCF7, biological rep1	5.37948
<a href="#">GSM678803</a>	MCF7, biological rep2	5.23028
<a href="#">GSM678804</a>	MCF7, biological rep3	5.30543
<a href="#">GSM678805</a>	MCF7 silenced Estrogen receptor, biological rep1	4.40684
<a href="#">GSM678806</a>	MCF7 silenced Estrogen receptor, biological rep2	4.50939
<a href="#">GSM678807</a>	MCF7 silenced Estrogen receptor, biological rep3	4.609

# Profile: ACE2 expression

GDS4061 / 219962\_at

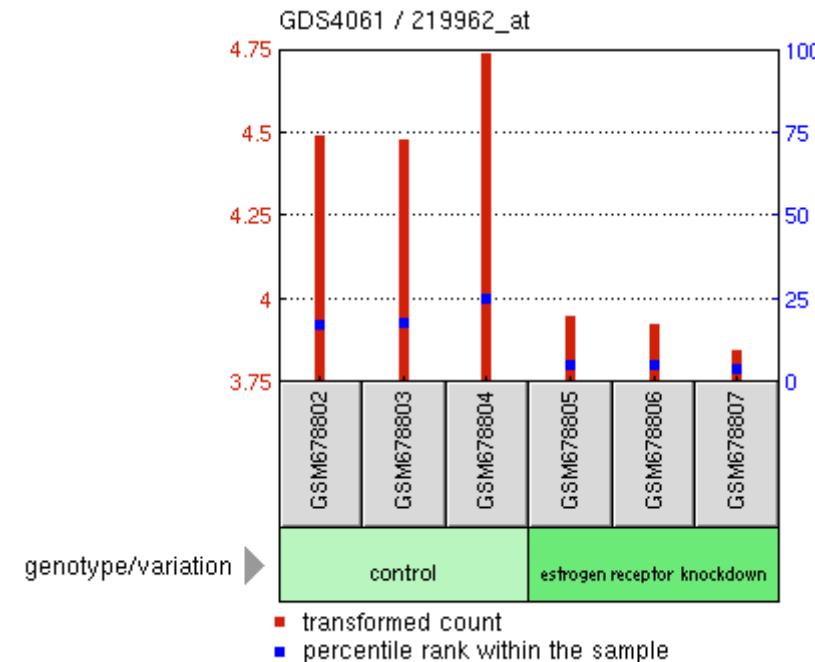
## Title

Estrogen receptor alpha-silenced

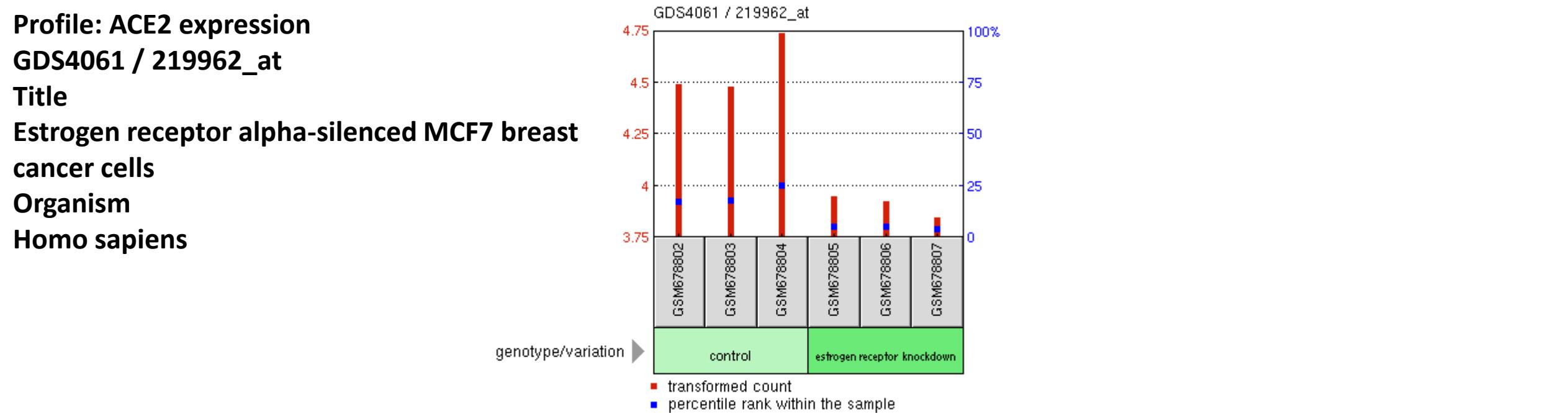
MCF7 breast cancer cells

## Organism

Homo sapiens



Sample	Title	Value
<a href="#">GSM678802</a>	MCF7, biological rep1	4.49106
<a href="#">GSM678803</a>	MCF7, biological rep2	4.48349
<a href="#">GSM678804</a>	MCF7, biological rep3	4.73862
<a href="#">GSM678805</a>	MCF7 silenced Estrogen receptor, biological rep1	3.94941
<a href="#">GSM678806</a>	MCF7 silenced Estrogen receptor, biological rep2	3.9283
<a href="#">GSM678807</a>	MCF7 silenced Estrogen receptor, biological rep3	3.84918



Sample	Title	Value
<a href="#">GSM678802</a>	MCF7, biological rep1	4.49106
<a href="#">GSM678803</a>	MCF7, biological rep2	4.48349
<a href="#">GSM678804</a>	MCF7, biological rep3	4.73862
<a href="#">GSM678805</a>	MCF7 silenced Estrogen receptor, biological rep1	3.94941
<a href="#">GSM678806</a>	MCF7 silenced Estrogen receptor, biological rep2	3.9283
<a href="#">GSM678807</a>	MCF7 silenced Estrogen receptor, biological rep3	3.84918

# Profile: ACE2 expression

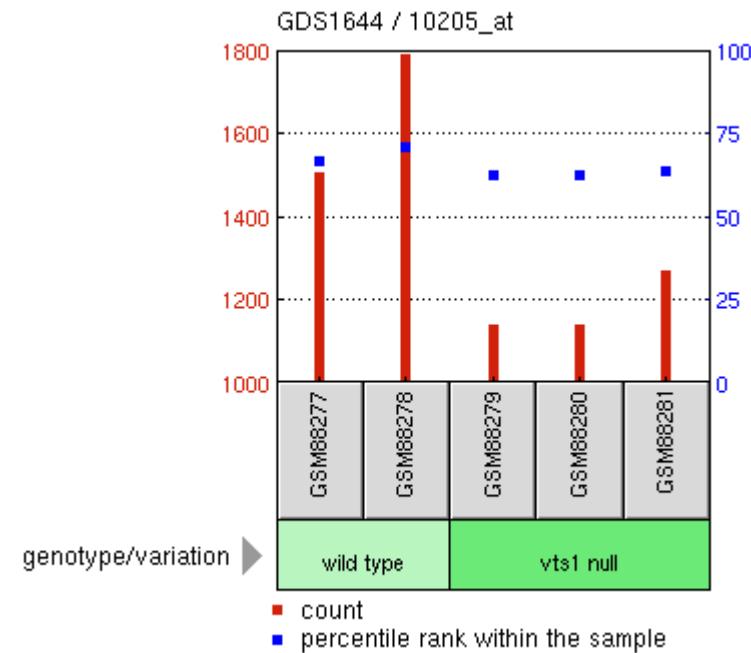
GDS1644 / 10205\_at

Title

VTS1 deletion mutant

Organism

Saccharomyces cerevisiae



Sample	Title	Value
<a href="#">GSM88277</a>	WT1	1506.8
<a href="#">GSM88278</a>	WT2	1791
<a href="#">GSM88279</a>	Exp Pt 1(dvts1-1 VTS1 )	1141.9
<a href="#">GSM88280</a>	Exp Pt 2(dvts1-2 VTS1 )	1143.6
<a href="#">GSM88281</a>	Exp Pt 3(VTS1 )	1271.5

# Profile: ACE2 expression

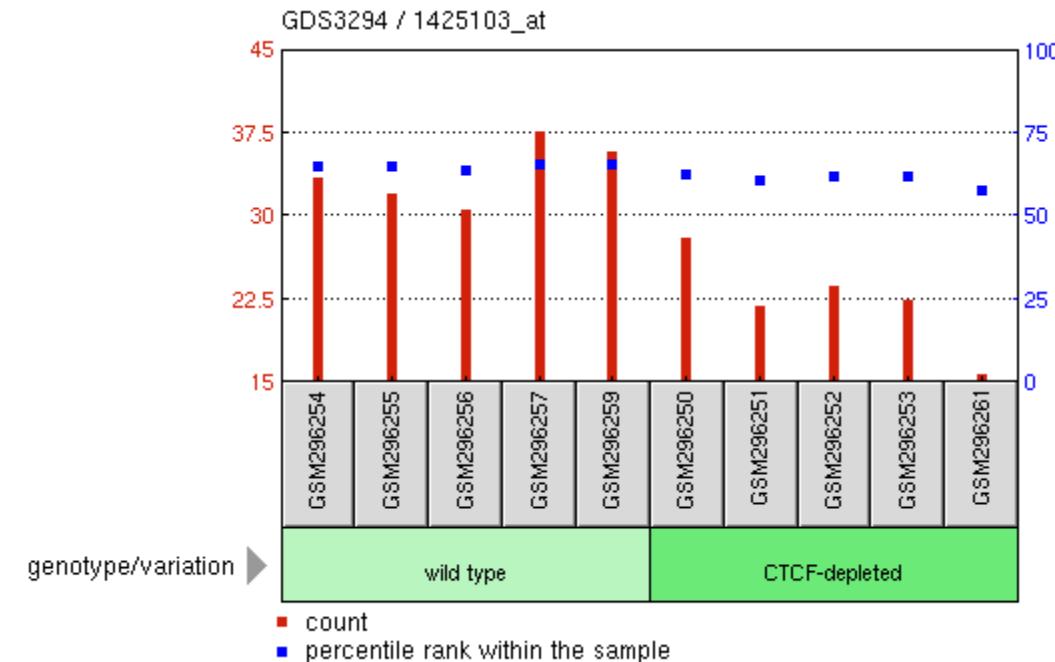
GDS3294 / 1425103\_at

## Title

CTCF depletion effect in oocytes

## Organism

Mus musculus



Sample	Title	Value
<a href="#">GSM296254</a>	gene expression of wild type oocyte, replicate 1	33.5935
<a href="#">GSM296255</a>	gene expression of wild type oocyte, replicate 2	32.1628
<a href="#">GSM296256</a>	gene expression of wild type oocyte, replicate 3	30.5551
<a href="#">GSM296257</a>	gene expression of wild type oocyte, replicate 4	37.7155
<a href="#">GSM296259</a>	gene expression of wild type oocyte, replicate 5	35.8225
<a href="#">GSM296250</a>	gene expression of CTCF-depleted oocyte, replicate 1	28.1471
<a href="#">GSM296251</a>	gene expression of CTCF-depleted oocyte, replicate 3	21.9578
<a href="#">GSM296252</a>	gene expression of CTCF-depleted oocyte, replicate 4	23.7345
<a href="#">GSM296253</a>	gene expression of CTCF-depleted oocyte, replicate 5	22.4628
<a href="#">GSM296261</a>	gene expression of CTCF-depleted oocyte, replicate 2	15.8604

# Profile: ACE2 expression

GDS1555 / 1425103\_at

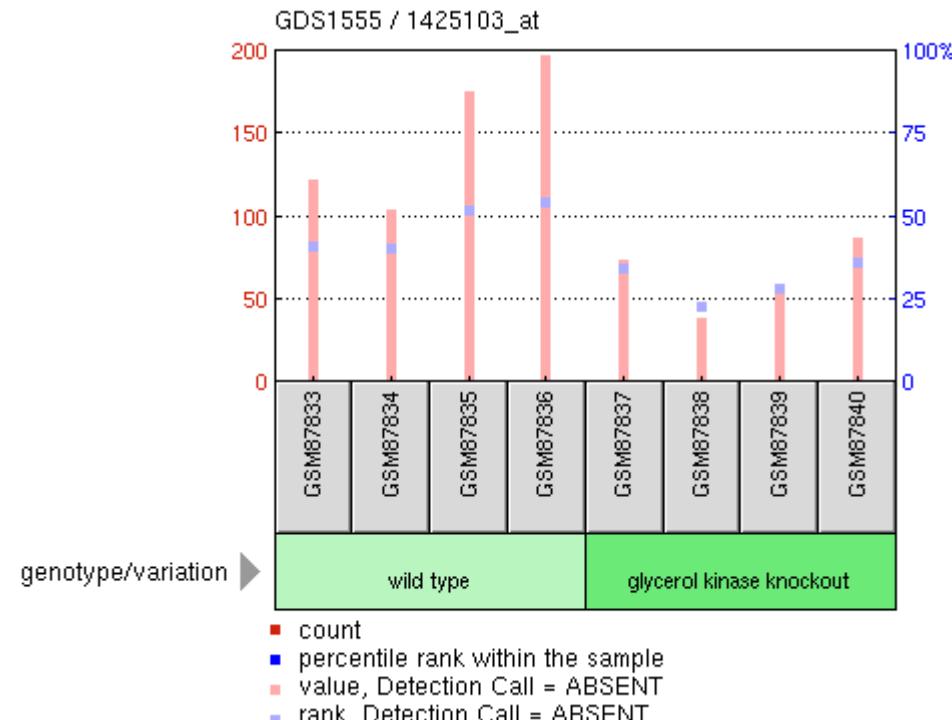
## Title

Glycerol kinase knockout effect on

liver

## Organism

Mus musculus



Sample	Title	Value
<a href="#">GSM87833</a>	Liver_WildType_1	122.1
<a href="#">GSM87834</a>	Liver_WildType_2	104.3
<a href="#">GSM87835</a>	Liver_WildType_3	174.9
<a href="#">GSM87836</a>	Liver_WildType_4	197.4
<a href="#">GSM87837</a>	Liver_KnockOut_1	74
<a href="#">GSM87838</a>	Liver_KnockOut_2	39.3
<a href="#">GSM87839</a>	Liver_KnockOut_3	59.1
<a href="#">GSM87840</a>	Liver_KnockOut_4	87.3

# Profile: ACE2 expression

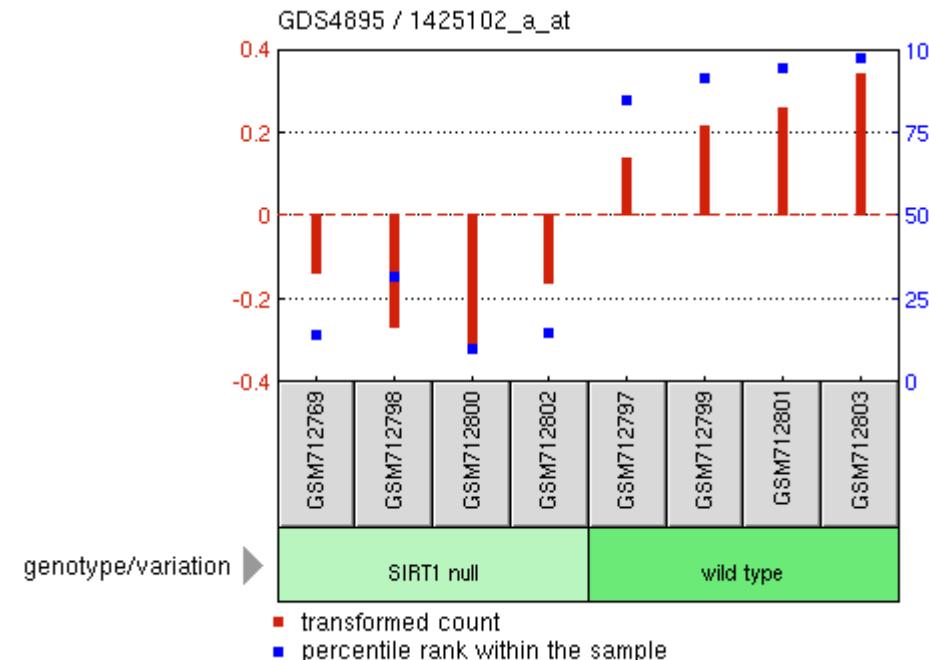
GDS4895 / 1425102\_a\_at

## Title

SIRT1 deficiency effect on the  
brain

## Organism

Mus musculus



Sample	Title	Value
<a href="#">GSM712769</a>	BSKO 1	-0.140546
<a href="#">GSM712798</a>	BSKO 2	-0.27286
<a href="#">GSM712800</a>	BSKO 3	-0.312008
<a href="#">GSM712802</a>	BSKO 4	-0.167778
<a href="#">GSM712797</a>	WT 1	0.140546
<a href="#">GSM712799</a>	WT 2	0.221
<a href="#">GSM712801</a>	WT 3	0.261022
<a href="#">GSM712803</a>	WT 4	0.344256

Additional examples of the potential repressors of  
the *ACE2* expression identified using transgenic  
mouse models

**Profile: ACE2 expression**

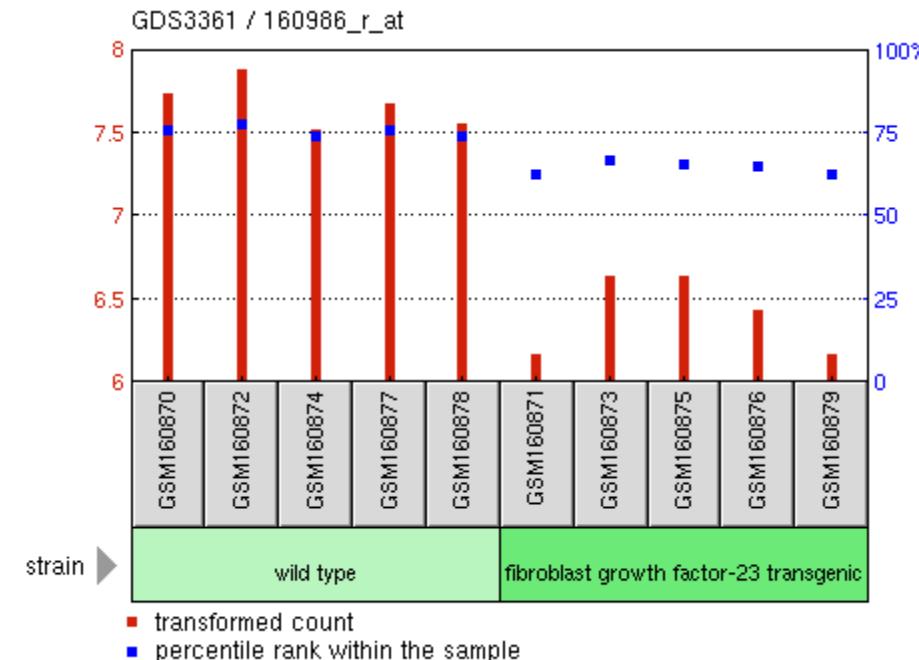
**GDS3361 / 160986\_r\_at**

**Title**

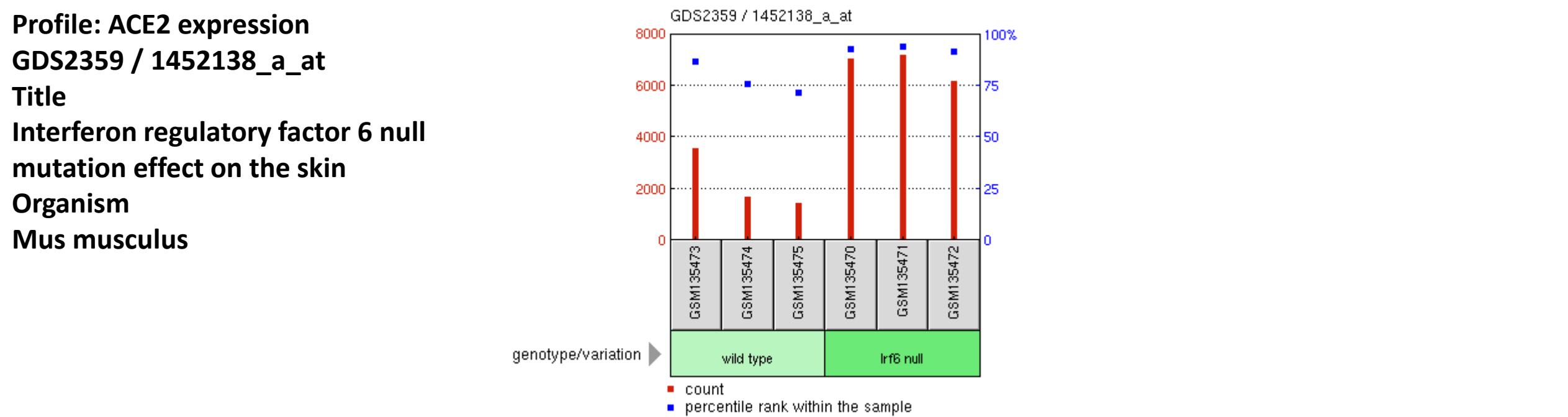
**Fibroblast growth factor-23  
transgenic model**

**Organism**

**Mus musculus**



Sample	Title	Value
<a href="#">GSM160870</a>	Wild Type 612	7.73651
<a href="#">GSM160872</a>	Wild type 618	7.89066
<a href="#">GSM160874</a>	Wild Type 650	7.5183
<a href="#">GSM160877</a>	Wild Type nr 658	7.67757
<a href="#">GSM160878</a>	Wild Type nr 663	7.55491
<a href="#">GSM160871</a>	Transgenic nr 614	6.17722
<a href="#">GSM160873</a>	Transgenic nr 619	6.64023
<a href="#">GSM160875</a>	Transgenic nr 652	6.64915
<a href="#">GSM160876</a>	Transgenic nr 657	6.44524
<a href="#">GSM160879</a>	Transgenic nr 661	6.17914



Sample	Title	Value
<a href="#">GSM135473</a>	IRF6 wt, biological rep1	3607.2
<a href="#">GSM135474</a>	IRF6 wt, biological rep2	1727.4
<a href="#">GSM135475</a>	IRF6 wt, biological rep3	1461.4
<a href="#">GSM135470</a>	IRF6 knockout, biological rep1	7077
<a href="#">GSM135471</a>	IRF6 knockout, biological rep2	7212.6
<a href="#">GSM135472</a>	IRF6 knockout, biological rep3	6184.5

# Profile: ACE2 expression

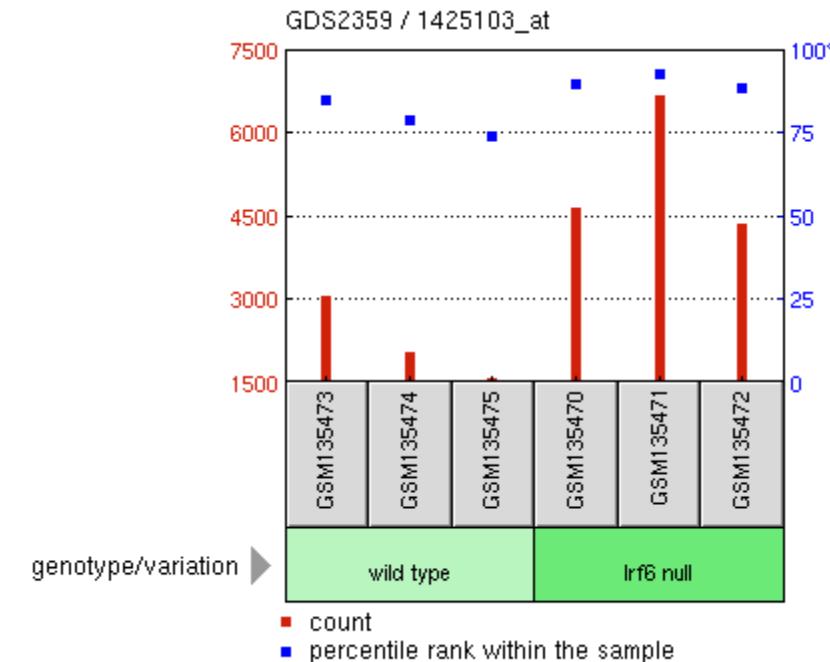
GDS2359 / 1425103\_at

## Title

Interferon regulatory factor 6 null mutation effect on the skin

## Organism

Mus musculus



Sample	Title	Value
<a href="#">GSM135473</a>	IRF6 wt, biological rep1	3067.9
<a href="#">GSM135474</a>	IRF6 wt, biological rep2	2065.9
<a href="#">GSM135475</a>	IRF6 wt, biological rep3	1589.4
<a href="#">GSM135470</a>	IRF6 knockout, biological rep1	4678.8
<a href="#">GSM135471</a>	IRF6 knockout, biological rep2	6695.8
<a href="#">GSM135472</a>	IRF6 knockout, biological rep3	4381.7

## Profile: ACE2 expression

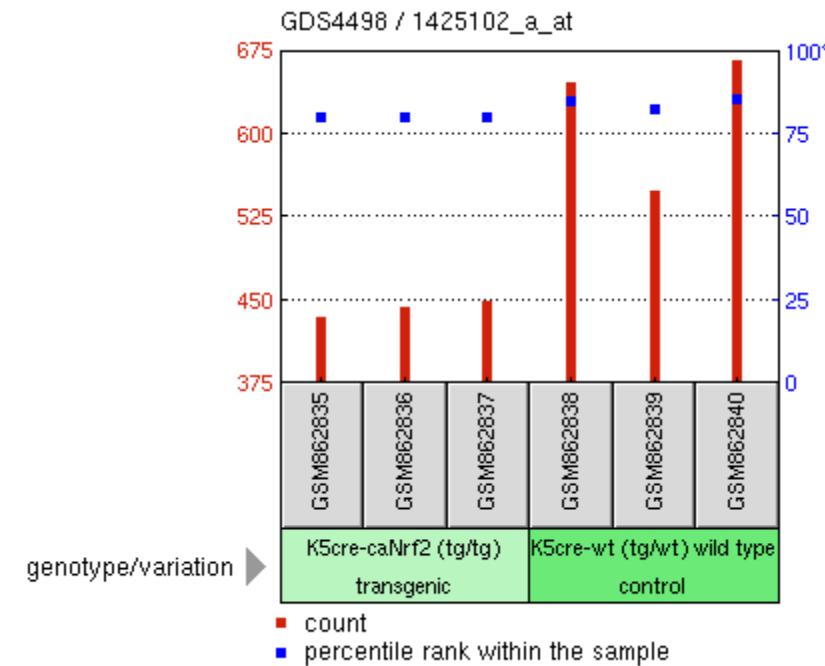
GDS4498 / 1425102\_a\_at

### Title

Transcription factor Nrf2 gain-of-function model: postnatal day 2.5 whole skin

### Organism

Mus musculus



Sample	Title	Value
<a href="#">GSM862835</a>	transgene strong 1	435.03
<a href="#">GSM862836</a>	transgene strong 2	444.737
<a href="#">GSM862837</a>	transgene strong 3	449.601
<a href="#">GSM862838</a>	wildtype strong 1	647.134
<a href="#">GSM862839</a>	wildtype strong 2	548.634
<a href="#">GSM862840</a>	wildtype strong 3	667.753

# Profile: ACE2 expression

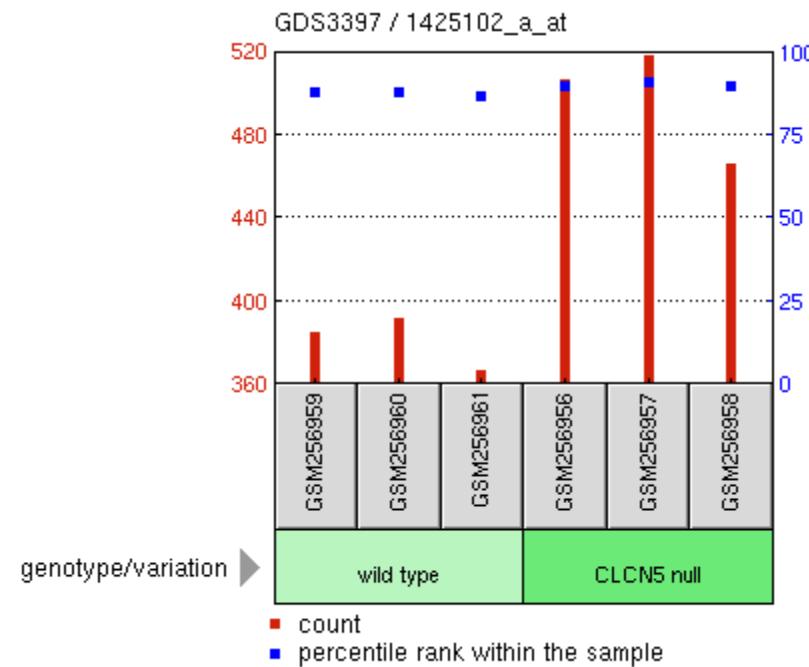
GDS3397 / 1425102\_a\_at

## Title

Dent disease model: renal proximal tubules

## Organism

Mus musculus



Sample	Title	Value
<a href="#">GSM256959</a>	Wild type rep 1	385.878
<a href="#">GSM256960</a>	Wild type rep 2	392.178
<a href="#">GSM256961</a>	Wild type rep 3	367.379
<a href="#">GSM256956</a>	CLC5 ko rep 1	507.455
<a href="#">GSM256957</a>	CLC5 ko rep 2	518.388
<a href="#">GSM256958</a>	CLC5 ko rep 3	466.324

**Profile: ACE2 expression**

**GDS3323 / 1425103\_at**

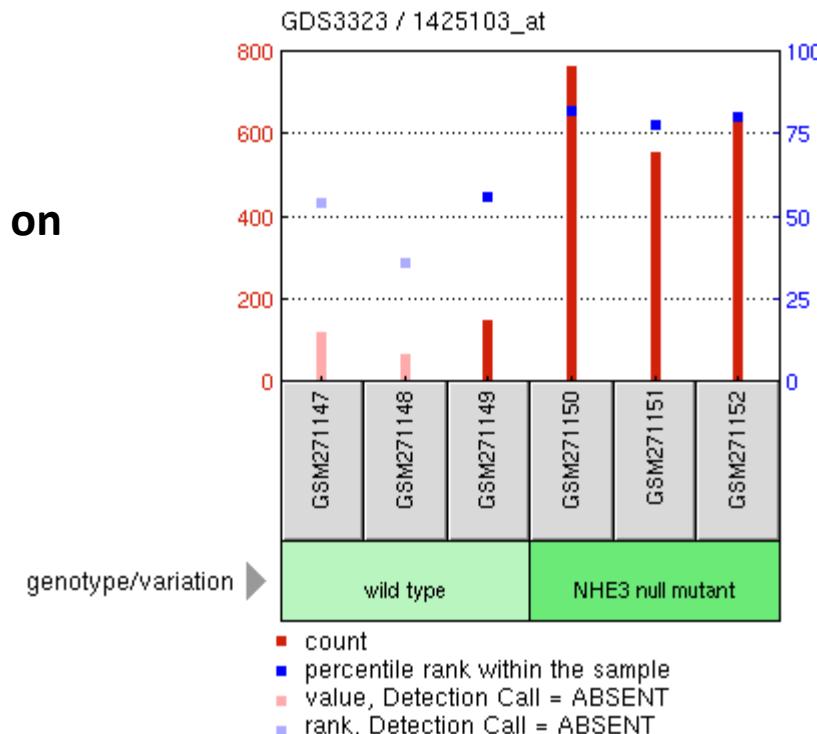
**Title**

**Na<sup>+</sup>/H<sup>+</sup> exchanger 3 deficiency effect on**

**the colon**

**Organism**

**Mus musculus**



Sample	Title	Value
<a href="#">GSM271147</a>	NHE3+/+ replicate 1	122.3
<a href="#">GSM271148</a>	NHE3+/+ replicate 2	68.2
<a href="#">GSM271149</a>	NHE3+/+ replicate 3	150.2
<a href="#">GSM271150</a>	NHE3-/ replicate 1	762.3
<a href="#">GSM271151</a>	NHE3-/ replicate 2	554.9
<a href="#">GSM271152</a>	NHE3-/ replicate 3	634.3

# Profile: ACE2 expression

GDS4910 / 1425103\_at

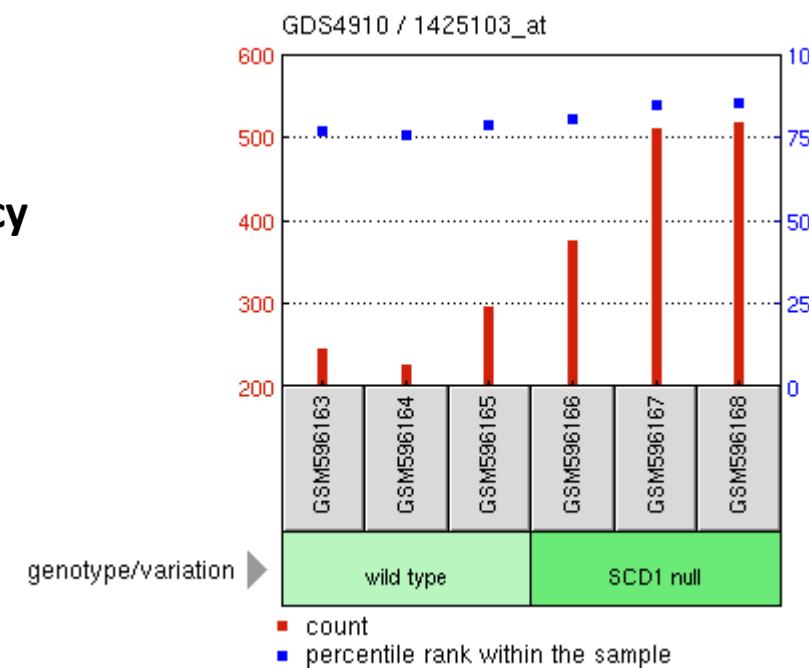
## Title

Stearoyl-CoA desaturase-1 deficiency

effect on the skin

## Organism

Mus musculus



Sample	Title	Value
<a href="#">GSM596163</a>	Skin_Lox_Control_Rep1	246.595
<a href="#">GSM596164</a>	Skin_Lox_Control_Rep2	227.702
<a href="#">GSM596165</a>	Skin_Lox_Control_Rep3	297.552
<a href="#">GSM596166</a>	Skin_SKO_Rep1	377.151
<a href="#">GSM596167</a>	Skin_SKO_Rep2	512
<a href="#">GSM596168</a>	Skin_SKO_Rep3	519.147

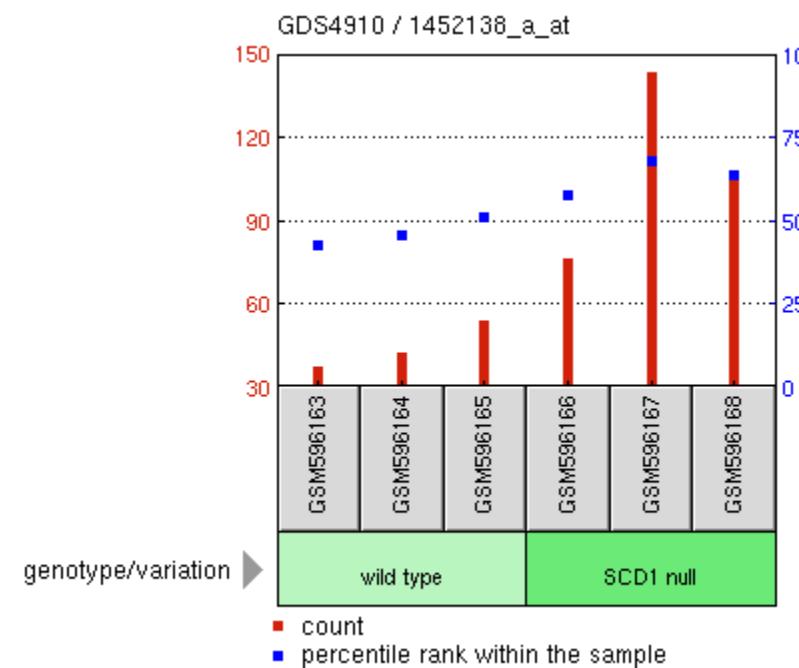
**Profile: ACE2 expression**  
**GDS4910 / 1452138\_a\_at**

**Title**

**Stearoyl-CoA desaturase-1 deficiency**  
**effect on the skin**

**Organism**

**Mus musculus**



Sample	Title	Value
<a href="#">GSM596163</a>	Skin_Lox_Control_Rep1	37.453
<a href="#">GSM596164</a>	Skin_Lox_Control_Rep2	42.992
<a href="#">GSM596165</a>	Skin_Lox_Control_Rep3	53.967
<a href="#">GSM596166</a>	Skin_SKO_Rep1	76.692
<a href="#">GSM596167</a>	Skin_SKO_Rep2	143.908
<a href="#">GSM596168</a>	Skin_SKO_Rep3	105.639

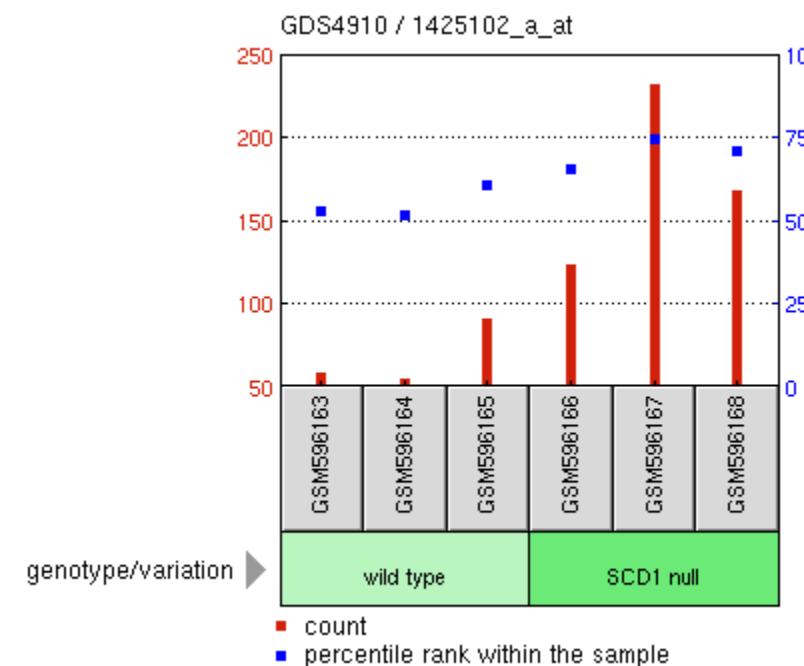
**Profile: ACE2 expression**  
**GDS4910 / 1425102\_a\_at**

**Title**

**Stearoyl-CoA desaturase-1 deficiency  
effect on the skin**

**Organism**

**Mus musculus**



Sample	Title	Value
<a href="#">GSM596163</a>	Skin_Lox_Control_Rep1	59.631
<a href="#">GSM596164</a>	Skin_Lox_Control_Rep2	55.139
<a href="#">GSM596165</a>	Skin_Lox_Control_Rep3	91.71
<a href="#">GSM596166</a>	Skin_SKO_Rep1	123.983
<a href="#">GSM596167</a>	Skin_SKO_Rep2	233.131
<a href="#">GSM596168</a>	Skin_SKO_Rep3	168.429

# Profile: ACE2 expression

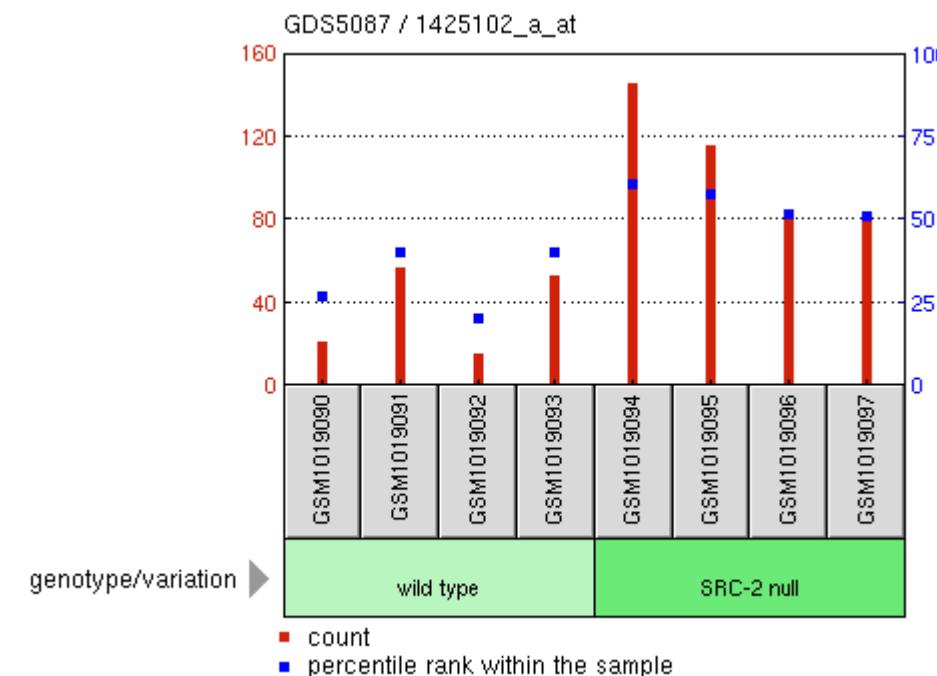
GDS5087 / 1425102\_a\_at

## Title

Transcriptional regulator steroid  
receptor coactivator-2 deficiency  
effect on the heart

## Organism

Mus musculus



Sample	Title	Value
<a href="#">GSM1019090</a>	Heart_WT_1	22.0184
<a href="#">GSM1019091</a>	Heart_WT_2	57.5679
<a href="#">GSM1019092</a>	Heart_WT_3	15.678
<a href="#">GSM1019093</a>	Heart_WT_4	53.6421
<a href="#">GSM1019094</a>	Heart_KO_1	145.776
<a href="#">GSM1019095</a>	Heart_KO_2	116.278
<a href="#">GSM1019096</a>	Heart_KO_3	85.0996
<a href="#">GSM1019097</a>	Heart_KO_4	84.2244

Supplemental Figure S1\_S13. ACE2 and FURIN genes.... (3.95 MiB)

[view on ChemRxiv](#)

• [download file](#)

---