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The primary hypothesis of this project was to test whether aberrant temporal CREB1 activation, due to PTEN loss, prior to full luminal cell commitment, promotes a prostate cancer oncogenic program that is associated with poor outcomes in patients. The goals were to 1) determine the role of CREB1 in differentiation and oncogenesis; 2) identify the CREB1 targets necessary for prostate cancer oncogenesis; and 3) define the CREB1 signature in clinical human prostate cancer samples. These studies uniquely revealed that there is a specific set of genes elevated in PCa whose expression is controlled by the transcription factor CREB1. We found that CREB1 suppresses terminal cell differentiation in the luminal tumor cells by suppressing expression of the chromatin binding protein, ING4 required for normal luminal cell differentiation. The mechanisms include transcriptional suppression as well as upregulation of an ING4 E3 ligase, JFK. Loss of CREB1 rescues differentiation and suppresses oncogenesis. Several CREB1 targets, GATA2, Twist1, CAMK2B, and Jag1 were identified and validated, and preliminary data indicate these are in part responsible for the tumor phenotypes mediated by CREB1. Human tissue studies revealed that ING4 loss, a target of CREB1, is negatively correlated with Erg fusion and positively correlated with PTEN loss, providing insight into the subclasses of tumors where CREB1 might be most active.

INTRODUCTION: Being able to determine which prostate cancer patient has indolent disease versus those who will die, unless aggressively treated, remains a major challenge. Despite recent studies that identified several possible PCa subtypes, there was relatively little difference in these subtypes between primary cancer and metastatic cancers. However, six of the PCa subclasses identified in those studies were notable in that they are defined by transcription factors; molecules that can control key genetic programs. These same transcription factors have been linked to differentiation and cell fate determination. Oncogenic events associated with PCa, including Myc overexpression or Pten loss, have also been linked to altered differentiation; however, how these oncogenes relate to the transcriptional programs involved in differentiation and cell fate determination remain unresolved. We propose there will be a specific combination of oncogenic events and specific differentiation alterations that produce an aggressive subtype of PCa. If this signature can be identified, then the ability to distinguish indolent from lethal disease can be achieved. We identified a gene signature that is a target of the transcription factor CREB, which is elevated in tumorigenic cells when PTEN is lost. Of the known oncogenes associated with PCa, PTEN loss is most closely associated with poor outcomes in patients. Virtually nothing was known about the function or nature of this CREB/PTEN signature in PCa.

KEYWORDS: CREB1, ATF1, GATA2, TWIST1, PTEN, ING4, differentiation, oncogenesis, gene expression, biomarker, chromatin, luminal cells, prostate cancer.

ACCOMPLISHMENTS:

GOALS: Our goals were to 1) determine the role of CREB1 in differentiation and oncogenesis; 2) identify the CREB1 targets necessary for prostate cancer oncogenesis; and 3) define the CREB1 signature in clinical human prostate cancer samples.

HYPOTHESIS: Aberrant temporal CREB1 activation, due to PTEN loss, prior to full luminal cell commitment, promotes a prostate cancer oncogenic program that is associated with poor outcomes in patients.

Aim 1: Determine the role of CREB1 in differentiation and oncogenesis

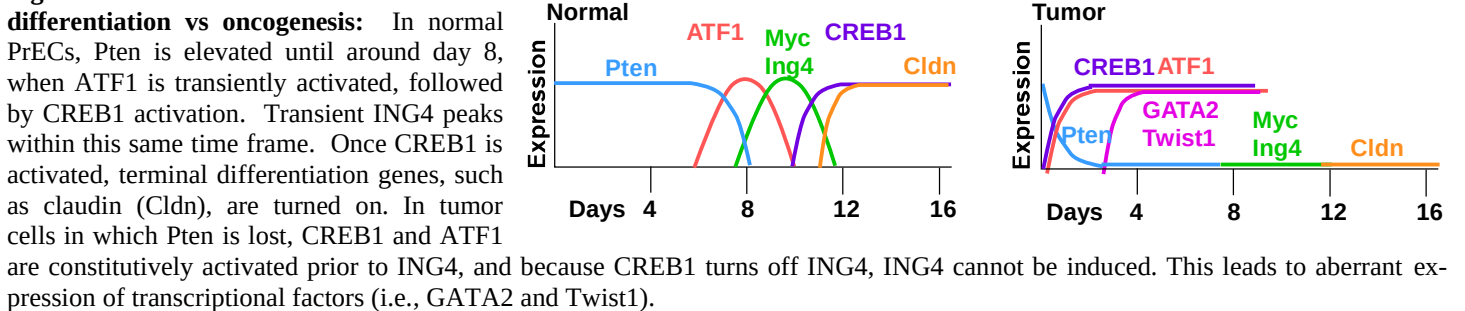
Majority of the work accomplished under this goal was recently published and the publication is in the attached appendix: Watson MJ, Berger PL, Banerjee K, Frank SB, Tang L, Ganguly SS, Hostetter G, Winn M, Miranti CK. Aberrant CREB1 activation in prostate cancer disrupts normal prostate luminal cell differentiation. *Oncogene*. 2021 May;40(18):3260-3272. doi: 10.1038/s41388-021-01772-y. PMID: 33846571.

In these studies, we identified the function of CREB1 in both normal prostate epithelial differentiation and homeostasis and in oncogenesis as detailed below. Using RNA-Seq analysis, we discovered that CREB1 plays a central role in maintaining luminal cell survival and that oncogenesis dramatically changes the CREB1-induced transcriptome. This is the first study to define a molecular mechanism whereby oncogenic loss of PTEN, leading to aberrant CREB1 activation, suppresses ING4 expression causing disruption of luminal cell differentiation.

Normal Prostate: In normal prostate epithelium, CREB1 is active in luminal cells, but not basal cells. We identified ING4 and its E3 ligase, JFK, as CREB1 transcriptional targets in luminal cells. During luminal cell differentiation, transient induction of ING4 expression is followed by a peak in CREB1 activity, while JFK increases concomitantly with CREB1 activation. Transient expression of ING4 is required for luminal cell induction; however, failure to properly down-regulate ING4 leads to luminal cell death. Consequently, blocking CREB1 increased ING4 expression, suppressed JFK, and led to luminal cell death. Thus, CREB1 is responsible for the suppression of ING4 required for luminal cell survival and maintenance. Data supporting these findings are outlined specifically in **Figures 1-4** in the attached manuscript, Watson et al, 2021.

Prostate Cancer: Oncogenic transformation, induced by suppressing PTEN, resulted in constitutive activation of CREB1 in the basal cells. However, these tumorigenic cells could no longer fully differentiate into luminal cells, failed to express ING4, and displayed a unique CREB1 transcriptome. Blocking CREB1 in tumorigenic cells suppressed tumor growth in vivo, rescued ING4 expression, and restored luminal cell formation, but ultimately induced luminal cell death. Data supporting these findings are outlined specifically in **Figures 5 and 7** in the attached manuscript, Watson et al, 2021.

Fig. 8: Model for CREB1/ATF1 action in differentiation vs oncogenesis:

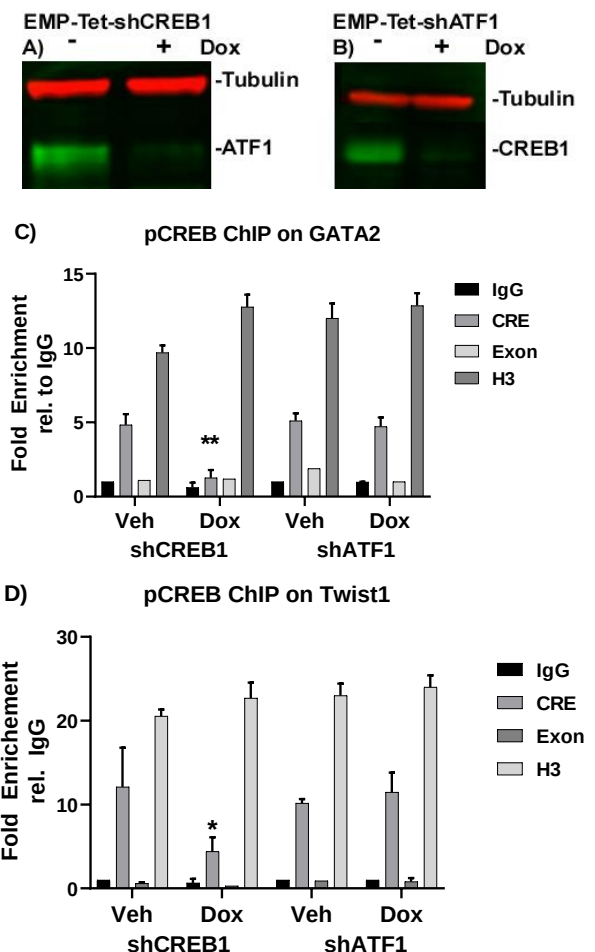


Aim 2: Identify the CREB1/ATF1 targets necessary for prostate cancer oncogenesis

GATA2/Twist1: In addition to the targets identified in Aim 1, i.e., ING4 and JFK, our initial analysis also included identification and focus on two additional CREB targets, GATA2 and Twist1.

Fig. 9: Activated CREB1, but not ATF1, binds the CRE site in the promoters of GATA2 and Twist1. EMP-Tet-shCREB1 and EMP-Tet-shATF1 cells were treated without (Veh) or with doxycycline (Dox) for 5 days to induce shRNA to AFT1 or CREB1. **A,B**) Levels of CREB1 or ATF1 loss were monitored by immunoblotting relative to tubulin. **C,D**) DNA/protein complexes were crosslinked, and chromatin isolated and sheered. Sheered chromatin was subjected to immunoprecipitation with IgG (negative control), p-CREB antibody, or histone 3 (H3) antibody. qPCR was performed on isolated complexes using primers that recognize the CRE site in the proximal promoter or a non-specific site within the gene (exon) of the **C**) GATA2 or **D**) Twist1 genes. Data is expressed as Fold-enrichment of the PCR relative to IgG controls. Error bars are SD, n=3, * $p < 0.05$, ** $p < 0.005$.

We identified 2 full CRE sites in the promoters of GATA2, and 2 CRE $\frac{1}{2}$ sites in the Twist1 promoter. Using a phospho-specific antibody to CREB1, we found that activated CREB1 is bound to both CREs in GATA2 and both $\frac{1}{2}$ sites in Twist1 (**Fig. 9**). We further demonstrated that it is CREB1 and not ATF1, as knock-down of CREB1 with shRNA abolished the ability of the pCREB1 antibody to ChIP these CREs. Knock-down of ATF1 had no effect on the ChIP. Activated CREB was not associated with non-CRE regions of these genes, and Histone H3 ChIP was unaffected by the knock-down of CREB1 or ATF1. Thus, GATA2 and Twist1 are bona-fida targets of CREB1 and not ATF1 in the tumorigenic cells.



We successfully engineered tumorigenic EMP cells where GATA2 and Twist1 are knocked down by Tet-inducible shRNAs (**Fig. 10**). Using these knock-down cell lines we asked whether the loss of Twist1 or GATA2 could restore normal luminal cell differentiation to the tumorigenic EMP cells. Preliminary studies using these cells are suggestive that knock-down of Twist1 or GATA2 partially restores differentiation in tumorigenic EMP cells. However, further studies are needed to unambiguously make this conclusion. It remains to be determined whether loss of Twist1 or GATA2 would similarly reverse the tumorigenic phenotype of the EMP cells.

Additional CREB Targets: We carried out RNA-Seq profiling of tumorigenic EMP cells with CREB1 or ATF1 knock-down versus their controls to further validate CREB1 targets and to identify new ones. We compared Day0 vs Day12 of differentiation with or without Dox-induced knockdown of ATF1 or CREB1. For the shCREB knock-down, we identified a total of 241 significantly differentially expressed genes, 181 were down regulated and 60 were up-regulated. Of these genes 241 genes, 62 have known CREB1 binding sites 1000 bp up or downstream of the coding sequence; 51 were down regulated and 11 were up-regulated. For shATF1, we identified a total of 3303 significantly differentially regulated genes, 1827 were down regulated and 1476 were up regulated. Of these 3303 genes, 435 have ATF1 binding sites 1000 bp up or downstream of the coding sequence; 295 were down regulated and 141 were up regulated. Gene list tables are provided in the **Appendix**.

We were able to detect CREB1 loss of RNA in the RNA seq samples as well as upon revalidation by qRT-PCR (**Fig. 11A**), indicating we had good loss of CREB1 expression in the experiment. However, we did not see a decrease in expression of GATA2 or Twist1 as we expected. Instead, we saw an increase in these between Day0 and Day12, but no loss upon CREB1 knock down with Dox treatment (**Fig. 11F,G**). This was also true for two other genes we validated, GATA3 and PIK3R4 (**Fig. 11H,I**). Interestingly, we also saw a similar 'differentiation'-induced expression of CAMK2B, but in this case, this increase was dependent on CREB1 (**Fig. 11D**). Two targets, Jag1 and Dyrk3, were suppressed upon CREB1 loss, making these true CREB1-dependent targets (**Fig. 11B,C**). Finally, CDH13 went down with differentiation and that was not dependent on CREB1 (**Fig. 11E**). Thus, we have identified both CREB1-dependent and CREB1-independent targets in EMP cells. These data also indicate that other signals, in addition to CREB1, may be important in controlling GATA2 and Twist1 expression in tumorigenic EMP cells. Future work is needed to elucidate this other mechanism.

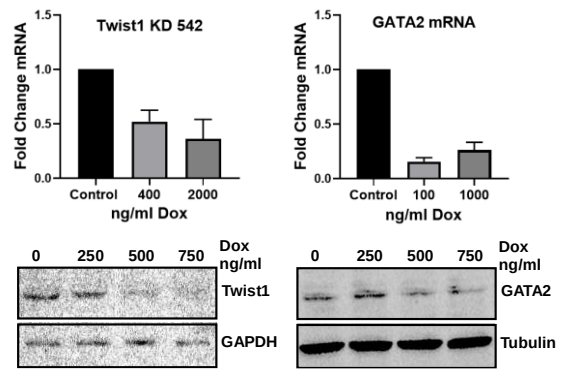


Fig. 10: Tet-inducible GATA2 and Twist1 knock-down in EMP cells. EMP cells were engineered to express Tet-inducible shRNA to target Twist1 and GATA2 respectively. Knock-down was validated by qRT-PCR (top) and immunoblotting (lower) at indicated concentrations of Doxycycline (Dox).

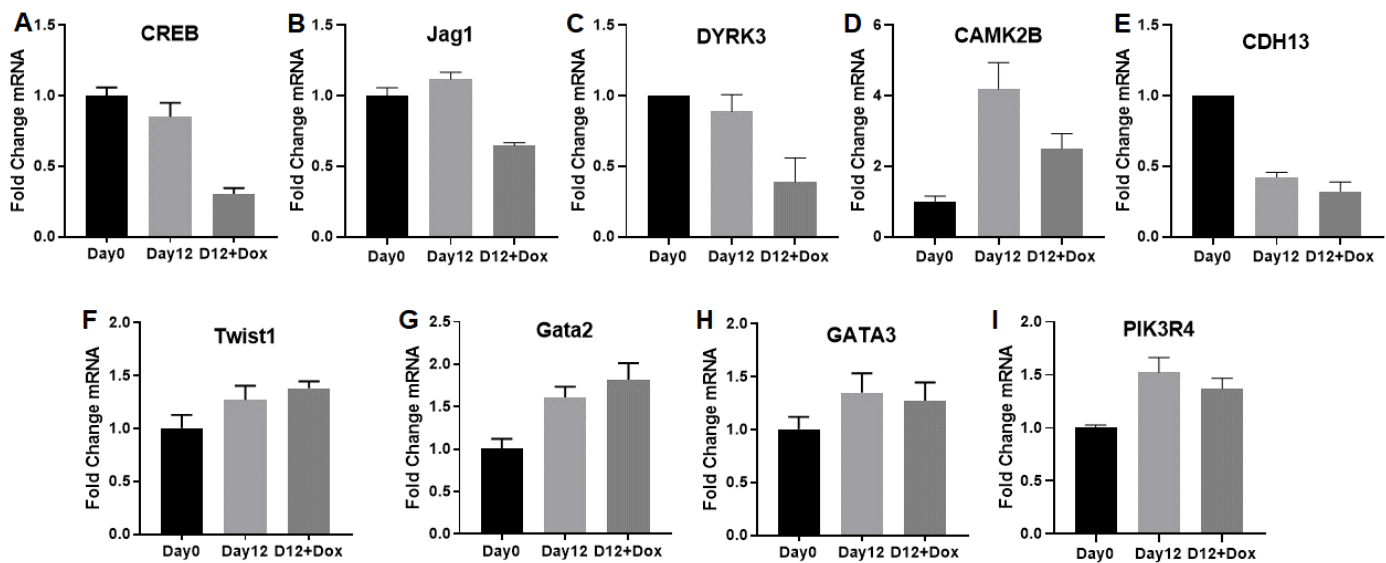


Figure 11: Validation of Targets in shCREB1 EMP cells. EMP cells were differentiated for 0 (Day0) or 12 (Day12) days and CREB1 was knocked down at Day12 by doxycycline (D12+Dox) shCREB1. RNA was collected from biological triplicates and subjected to qRT-PCR to detect different putative CREB1 targets. Genes screened are indicated atop each graph.

Role for ATF1: ATF1 was not the primary focus of this study, and the original intent was to use it as a control. However, we obtained striking data upon ATF1 knockdown (**Fig. 12**). Loss of ATF1 in normal PrECs prevented differentiation (**Fig. 12A**) and blocked expression of ING4 (**Fig 12C**), suggesting ATF1 is crucial for normal differentiation. This is the striking opposite of CREB1 knockdown, suggesting that ATF1 controls induction of ING4, while CREB1 suppresses ING4. Moreover, loss of ATF1 in tumorigenic EMP cells did not reverse differentiation (**Fig. 12B**), indicating ATF1 loss (or inactivation) may be required for tumorigenesis.

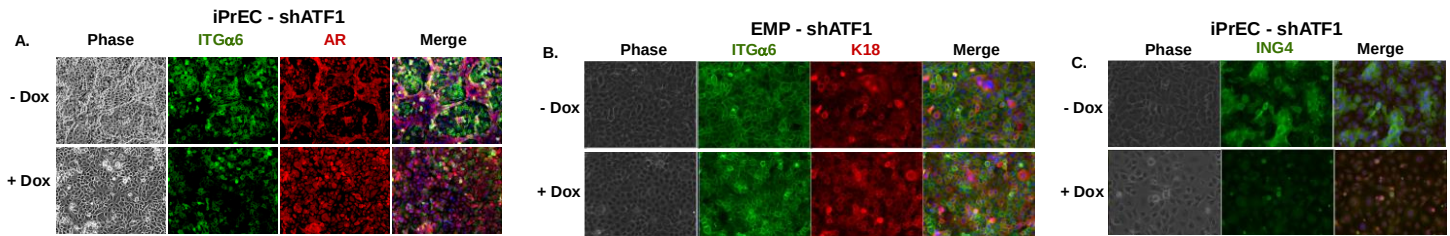
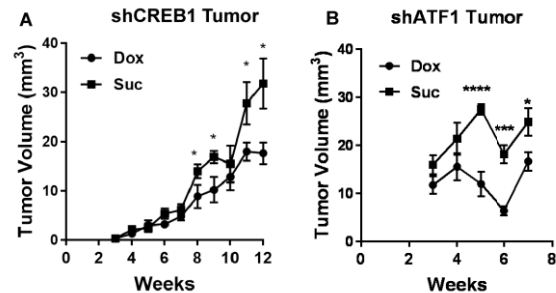


Fig. 12: ATF1 is required for luminal cell differentiation and its loss cannot rescue tumor cells because ING4 cannot be induced. iPrEC-shATF1 or EMP-shATF1 cells were differentiated for 12 days in the presence or absence of doxycycline to induce ATF1 shRNA and immuno-stained for **A**) ITGα6 and AR, **B**) ITGα6 and K18, and **C**) ING4.

In keeping with ATF1 loss as a promotional event for tumorigenesis, ATF1 loss in EMP cells also did not change the rate of tumor growth (**Fig. 13B**). Whereas loss of CREB1 reduced the rate of tumor growth (**Fig. 13A**). We also saw more genes whose expression was impacted by ATF1 loss than CREB1. From the RNA-Seq data we can begin to better understand the differences between how ATF1 and CREB1 each impacts both normal prostate differentiation and prostate cancer development and will be the basis of future studies.

Fig. 13: CREB1 is required for EMP cells to be tumorigenic, whereas loss of ATF1 is require for EMP cell tumorigenesis. A million luciferase-tagged **A**) EMP-Tet-shATF1 **B**) or EMP-Tet-shCREB1 cells were injected into the prostates of 24 male SCID mice respectively. Immediately after injection, half the mice received doxycycline (Dox) in sucrose and the other half only sucrose (Suc). Tumor volumes were recored weekly starting on week 3 post injection. Error bars are SEM, n=12, * $p < 0.05$.



Prostate on Chip Model: We have begun applying the knowledge we are gaining about how human luminal cell differentiation occurs to generate the first human prostate-on-chip model, from which we will ultimately develop an in situ de novo human prostate cancer-on-chip model. This will serve as another model in which to interrogate the role of CREB1/ATF1 and their downstream targets in prostate cancer development. We have established proof-of-principal that using microfluidic-based technology we can 1) co-culture basal epithelial cells with prostate stromal cells, 2) that stimulation of only the stromal cells with androgen is sufficient to induce luminal differentiation of the basal cells, and 3) co-culturing EMP cells or human tumor cells with normal prostate stroma in the chip leads to the generation of cancer-associated fibroblasts and invasion of tumor cells into the stroma (**Fig. 14**). Thus, we have completely recapitulated the human stromal/epithelial interactions and organ architecture as it is seen in both normal and cancerous tissues of human patients. This has resulted in a published manuscript, which is appended to this report: Jiang L, Ivich F, Tahsin S, Tran M, Frank SB, Miranti CK, Zohar Y. Human stroma and epithelium co-culture in a microfluidic model of a human prostate gland. Biomicrofluidics. 2019. 13:064116. PMID: PMC6867939.

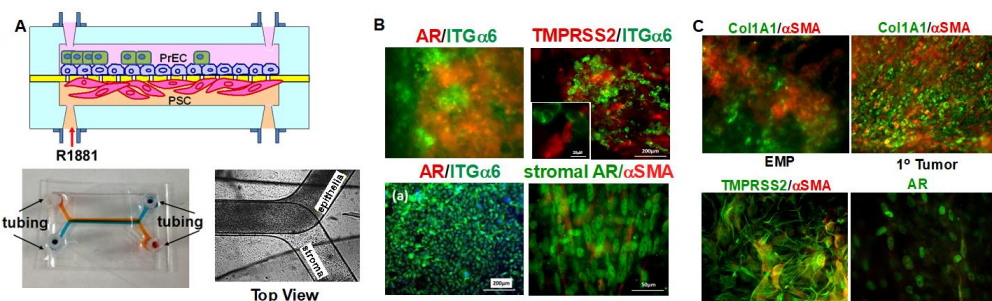


Fig 14: New Prostate on Chip (PoC). **A**) Microfluidic device to coculture PrEC and prostate stroma cells (PSC). **B**) Addition of R1881 to stroma cells induces differentiation of basal PrECs (green) into luminal cells (red). In the absence of R1881, luminal cells do not form (a). AR expression is induced in

the stroma cells by R1881. C) Tumor cells (EMP, C4-2, or primary isolate) induce CAF markers Col1A1 and α SMA. TMPPRS2 positive tumor cells invade α SMA positive stroma cells. Tumor cells cause loss of AR in the stromal compartment.

Aim 3: Define the CREB1 signature in clinical human prostate cancer samples.

ING4/PTEN/ERG Co-expression Status in Human Samples: Using a primary prostate cancer TMA obtained previously from PCBN, we used IHC to measure the expression of ING4. We then obtained the IHC data from Dr. DeMarzo for PTEN and ERG from this same TMA. The TMA consisted of 200 patients, with 4 cores each of normal and primary prostate tumor from each patient. Tumor stage and Gleason grade was provided for all tumor samples. For ING4, IHC staining within the tumor area was scored based on intensity of nuclear staining on a scale of 1 to 4, with 4 being highest, and 1 being null. The amount of nuclear ING4 staining in the normal samples was compared to nuclear ING4 staining in the paired tumor samples. The sample scores in each set were averaged. Of the 184 interpretable matched patient samples, we found that 61.4% had decreased nuclear ING4 expression. For Erg, the tumor cores were scored for the presence (1) or absence (0) of the Erg fusion gene. We found that 52.0% of the tumors had the Erg fusion. For PTEN, the tumor cores were scored for absence (0), decrease (<0.5), or presence (1) of PTEN. We found that only 8.7% of the samples had lost or decreased PTEN expression.

For the statistical analysis, we performed Pearson Chi2 to measure the association between ING4 and presence of the Erg fusion. We found a statistically significant negative association between Erg fusion and ING4 loss (Chi2 = 5.6085, Pr = 0.018; Wilcox Rank-Sum test P=0.008). Thus, tumors that lose ING4 expression are less likely to have the Erg fusion.

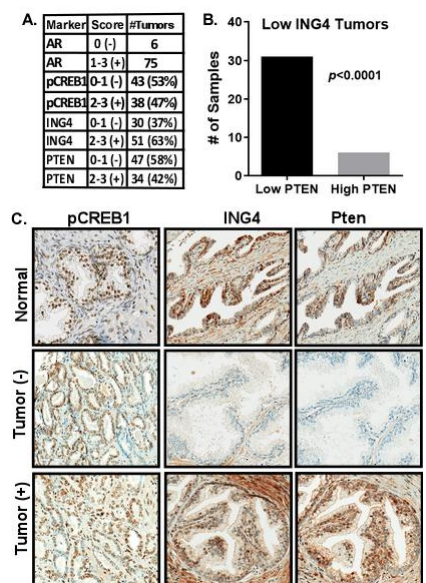
Using the same approach, we measured the association between ING4 loss and PTEN loss. We found there was a trend, that did not quite meet statistical significance, between ING4 and PTEN loss (Chi2 = 2.0651, Pr=0.151; Wilcox Rank-Sum test P=0.056). The failure to reach significance here is most likely due to the unexpected low percentage of PTEN null patients (8.7%) in this cohort of tumors.

Based on our previous studies in another TMA, we previously observed a significant correlation between loss of ING4 and loss of PTEN.

Finally, we correlated ING4 loss, Erg fusion positivity, or PTEN loss to Gleason Grade. There was no correlation between Erg or ING4 status with Gleason grade, while there was a statistically significant increase in Gleason Grade with loss of PTEN (Wilcox Rank-Sum test P=0.008).

ING4/PTEN Correlation: In a separate TMA with a higher number of PTEN negative samples, we used IHC of primary prostate tumors to measure the correlation between loss of ING4 and loss of PTEN. In this study published in the Watson et al 2021 paper, and shown below (**Fig. 15**), we found a very high correlation between ING4 loss and PTEN loss. We found that 80% of the tumors with low ING4 also had low PTEN. Thus, loss of PTEN might be the primary mechanism leading to loss of ING4 as we have proposed, but other mechanism(s) may also exist to account for the remaining tumors with ING4 loss. In this same study we attempted to assess pCREB, but because it is also expressed in normal tissue, we were unable to make a statistically significant difference in expression between tumor and normal tissue. Future studies will be aimed at determining if any of the above CREB1 targets can be correlated with ING4/PTEN loss and patient outcomes.

Fig. 15: Correlation between loss of ING4 and PTEN. A TMA containing 81 tumors and 48 adjacent normal samples was interrogated by IHC for the expression of AR, pCREB1, ING4, and PTEN. **A)** Levels of expression of each indicated marker in the tumor samples. 0-1 scored as negative, 2-3 scored as positive. **B)** Fisher test demonstrating the association between low ING4 and low PTEN. ****p<0.0001. **C)** Representative IHC images.



What opportunities for training and professional development has the project provided?

Nothing to Report

How were the results disseminated to communities of interest?

Nothing to Report

What do you plan to do during the next reporting period to accomplish the goals?

Nothing to Report

IMPACT

What was the impact on the development of the principal discipline(s) of the project?

We have identified a new mechanism for how loss of a specific oncogene, PTEN, leads to prostate cancer. While previous studies have focused on the role of PTEN in controlling the survival of tumors, we demonstrated that PTEN is crucial for oncogenesis. Through dysregulation of CREB1/ATF1 and disruption of differentiation PTEN loss leads to the onset of prostate cancer. We've identified two regulatory mechanisms, i.e., CREB1 and JFK, for how an important differentiation regulatory protein, ING4, is induced and suppressed at the proper time of differentiation to commit the luminal cells to a terminally differentiated state. We further demonstrated how the dysregulation of CREB1, due to PTEN loss, suppresses ING4 to allow for tumor cells to form. We further demonstrated, that CREB1 is responsible for the loss of ING4 protein and ING4 mRNA. These findings fill in the question about why ING4 loss occurs in prostate cancer and how loss of PTEN contributes to ING4 loss. We further validated this relationship in human prostate tumors.

Our newest findings indicate that ING4 loss may identify a distinct subset of primary prostate cancers that is not associated with the Erg fusion event, and more often associated with loss of PTEN. Our future work to assess how GATA2, Twist1, Jag1, and CAMK2B relate to ING4 and PTEN loss, should provide additional insight into the nature of aggressive, lethal prostate cancer.

These are the first studies to ever functionally link PTEN and ING4, to link CREB1/ATF1 with ING4, and to describe a new mechanism for how loss of the tumor suppressor PTEN in prostate cancer promotes tumorigenesis. We have also now unlinked ING4 loss from Erg fusion. What makes these studies even more significant is that they were conducted in a unique human genetic model that mimics many properties of the human prostate gland. Furthermore, we are expanding the way in which we study these interactions, by developing a human prostate-on-chip model that recapitulates the stroma/epithelial interactions observed in the human gland. This model will help us further establish the importance of CREB1 and its downstream targets, GATA2 and Twist1, in prostate cancer oncogenesis.

What was the impact on other disciplines?

Epithelial differentiation occurs in multiple organs and some of the processes involved are likely to be conserved. ING4 and CREB1 expression are also high in liver and kidney, opening the possibility that a similar crosstalk may exist in those tissues.

The unique human prostate luminal epithelial differentiation model employed in these studies serve as a model for developing similar models in other organs. There is a large initiative in the research community to generate 'organs-on-a-chip' based on human tissue to better represent the genetics and physiology of human biology. The goal is to provide better model systems for testing and advancing therapeutic drugs to the clinic. The more we learn about the mechanisms operating in the model, the more we can contribute to defining the authenticity of the 'organs-on-a-chip' and their feasibility for therapy testing.

What was the impact on technology transfer?

Nothing to Report

What was the impact on society beyond science and technology?

Nothing to Report

CHANGES/PROBLEMS:

Changes in approach and reasons for change

The cost to generate a ~500 gene Nanostring panel proved to be prohibitive, and the company was not interested in designing a tissue-specific array. We were not able to negotiate a reasonable price for oligo-based gene expression. Therefore, we took advantage of our shCREB1/shATF1 knock-down cells and used RNA-Seq data to determine which targets are specific to shCREB1 and ATF1.

Actual delays

We were delayed in our analysis of the PTEN signature due to the loss of a CRISPR line we generated. COVID19 and budget constraints have forced us to discontinue this line of enquiry, even though we were successful at regenerating the line.

Changes that had a significant impact on expenditures

COVID19: Salaries still had to be paid, even though work was not allowed and severely impaired.

Significant changes in use or care of human subjects, vertebrate animals, biohazards, and/or select agents

No changes

PRODUCTS:

Publications, conference papers, and presentations

Journal publications – copies are in the appendix

Watson MJ, Berger PL, Banerjee K, Frank SB, Tang L, Ganguly SS, Hostetter G, Winn M, Miranti CK. Aberrant CREB1 activation in prostate cancer disrupts normal prostate luminal cell differentiation. *Oncogene*. 2021 May;40(18):3260-3272. doi: 10.1038/s41388-021-01772-y. PMID: 33846571. Acknowledges DOD support.

Jiang L, Ivich F, Tahsin S, Tran M, Frank SB, Miranti CK, Zohar Y. Human stroma and epithelium co-culture in a microfluidic model of a human prostate gland. *Biomicrofluidics*. 2019. 13:064116. PMCID: PMC6867939. Acknowledges DOD support.

Other publications, conference papers, and presentations – copies are in the appendix

Watson MJ, Berger PL, Frank SB, and **Miranti, CK**. PTEN and CREB Cooperativity during Prostate Luminal Epithelial Differentiation is Disrupted in Prostate Cancer. **11th Prostate Cancer Symposium at Clark Atlanta University**, Atlanta, GA, September 26-28, 2016

Watson MJ, Berger PL, Frank SB, Basile AJ and **Miranti, CK**. Pten Loss Promotes Prostate Cancer Tumorigenesis through Disruption of a CREB-Dependent Differentiation Pathway. **University of Arizona Cancer Center Retreat**, Tucson, AZ, Apr 21, 2017.

Watson MJ, Burger PL, Frank SB, Winn M, and **Miranti, CK**. PTEN Loss Promotes Prostate Cancer Tumorigenesis through Disruption of a CREB-Dependent Differentiation Pathway. **SBUR Annual Meeting: Multiple Genetic and Epigenetic Mechanisms of Urologic Disease**, Tampa, FL, Nov 9-12, 2017.

Watson MJ, Burger PL, Frank SB, Winn M, and **Miranti, CK**. PTEN Loss Disrupts a CREB-Dependent Differentiation Pathway during Prostate Cancer Oncogenesis, **Ventana Medical Systems**, Oro Valley, AZ, Nov 13, 2017.

Watson MJ, Burger PL, Frank SB, Winn M, Tran J, Banerjee K, and **Miranti, CK**. How and Why Integrin $\alpha\beta 1$ Drives Prostate Cancer. **Dana Farber Cancer Institute, Harvard Medical School**, Boston, MA Jun 12, 2018

Watson MJ, Burger P, Frank SB, Winn M, and Miranti CK. CREB1 and ATF1 Differentially Regulate Terminal Prostate Luminal Cell Differentiation by Controlling the Timing of ING4 Expression, while CREB1 Prevents ING4 Expression upon PTEN Loss in Prostate Cancer. **SBUR Annual Meeting: Multiple Genetic and Epigenetic Mechanisms of Urologic Disease**, Tampa, FL, Nov 9-12, 2017.

Abstract Published: *Am J Clin Exp Urol* 2017;5(Suppl 1):1-92 Poster P51, p60. www.ajceu.us

Watson MJ, Burger P, Frank SB, Winn M, and Miranti CK. CREB1 and ATF1 Differentially Regulate Terminal Prostate Luminal Cell Differentiation by Controlling the Timing of ING4 Expression, while CREB1 Prevents ING4 Expression upon PTEN Loss in Prostate Cancer. **AACR Special Conference on Prostate Cancer**, Orlando, FL, Dec 2-5, 2017.

*Watson MJ, Burger P, Frank SB, Winn M, and **Miranti CK**. CREB1 and ATF1 Differentially Regulate Terminal Prostate Luminal Cell Differentiation by Controlling the Timing of ING4 Expression, while CREB1 Prevents ING4 Expression upon PTEN Loss in Prostate Cancer. **SBUR Annual Meeting: Multiple Genetic and Epigenetic Mechanisms of Urologic Disease**, Tampa, FL, Nov 9-12, 2017. *Am J Clin Exp Urol* 2017;5(Suppl 1):1-92. PS51, p60.

Jiang L, Ivich F, Tran M, Frank SB, **Miranti CK** and Zohar Y. Development of a microfluidic-based model of a human prostate gland. **22nd Micro Total Analysis Systems International Conference on Miniaturized Systems for Chemistry and Life Sciences**. Kaohsiung, Taiwan Nov 11-15, 2018.

*Ivich F, Tran M, Tahsin S, Frank SB, Kraft A, **Miranti CK**, Zohar Y, & Jiang L. "Application of a microfluidic-based model of a human prostate gland for cancer research." **Proc. 12th International Conference on Nano/Molecular Medicine and Engineering** (NanoMed 2018), Waikiki, HI, Dec 2-5, 2018, p109-112.

Miranti C, Frank S, Jensen C, Tran J, Berger P, Kim S. Myc Promotes Prostate Epithelial Differentiation through the Induction of ING4, and Loss of ING4 Leads to the Development of PIN Lesions. **SBUR Annual**

Meeting: Precision Medicine in Urology: Molecular Mechanisms, Diagnostics and Therapeutic Targets, Palm Springs, CA, Nov 8-11, 2018, **Am J Clin Exp Urol** 6(Suppl 2):1-138. PS1-08, p15

Tahsin S, Jiang L, Ivich F, Zohar Y, **Miranti C**. Myofibroblasts Promote Prostate Cancer Progression by Causing Aberrant Prostate Epithelial Differentiation. **SBUR Annual Meeting: Precision Medicine in Urology: Molecular Mechanisms, Diagnostics and Therapeutic Targets**. Palm Springs, CA, Nov 8-11, 2018, **Am J Clin Exp Urol** 6(Suppl 2):1-138. PS2-64, p132

Banerjee K, Watson MJ, Berger, PL, and **Miranti CK**. GATA-2 and Twist-1 as targets of CREB-1 in prostate cancer development. SBUR Annual Meeting: Novel Discoveries in Urology, New Orleans, LA, Nov 7-10, 2019. **Am J Clin Exp Urol** 7 (Suppl), p170.

Tahsin S, Jiang L, Zohar Y, and **Miranti CK**. Loss of androgen receptor in prostate cancer stroma inhibits luminal epithelial cell differentiation. SBUR Annual Meeting: Novel Discoveries in Urology, New Orleans, LA, Nov 7-10, 2019. **Am J Clin Exp Urol** 7 (Suppl), p69.

Other Products

Research Materials:

Throughout these studies we generated Tet-inducible shRNA constructs based on our published technique [BMC Biotechnology, 17:24, 2017]. We will make these freely available to whoever asks. We also deposited these at Addgene for everyone to access. In addition, the stable PREC and EMP cell lines which we generate with these constructs will also be available after they are published.

Models:

We have developed the first human prostate-on-chip model, which has the potential to be used for many applications, including basic biology for understanding cancer oncogenesis, drug testing, and personalized medicine.

PARTICIPANTS & OTHER COLLABORATING ORGANIZATIONS

What individuals have worked on the project?

Name:	Cynthia Miranti, PhD
Project Role:	PI
Researcher Identifier (e.g. ORCID ID):	0000-0003-0668-6106
Nearest person month worked:	1.2 months
Contribution to Project:	Supervisor
Funding Support:	DOD/UA

Name:	Kasturi Banerjee, PhD
Project Role:	Assistant Scientific Investigator
Researcher Identifier (e.g. ORCID ID):	
Nearest person month worked:	12 months
Contribution to Project:	ChIP, RNA-Seq, differentiation
Funding Support:	DOD

Name:	Shekha Tahsin
Project Role:	Graduate Student
Researcher Identifier (e.g. ORCID ID):	
Nearest person month worked:	6 months
Contribution to Project:	PrEC differentiation, prostate-on-chip
Funding Support:	DOD/UA

Name:	Lin Tang, PhD
Project Role:	Assistant Scientific Investigator
Researcher Identifier (e.g. ORCID ID):	
Nearest person month worked:	2.4 months
Contribution to Project:	Mouse protocols and surgery
Funding Support:	DOD/UA

Name:	Sander Frank, PhD
Project Role:	Postdoctoral Fellow
Researcher Identifier (e.g. ORCID ID):	
Nearest person month worked:	1 month
Contribution to Project:	ING4 studies,
Funding Support:	DOD W81XWH-14-1-0479

Name:	Jack Tran
Project Role:	Research Specialist
Researcher Identifier (e.g. ORCID ID):	
Nearest person month worked:	3.6 months
Contribution to Project:	iPrEC shCREB/ATF1 differentiation studies
Funding Support:	

Has there been a change in the active other support of the PD/PI(s) or senior/key personnel since the last reporting period?

The following grants were funded:

NIH/NCI R01CA254200 (Miranti/Zohar, MPI) 04/01/2021-03/31/2025
 Bioengineered Prostate-on Chip: Mechanisms of Stromal Dysregulation in Prostate Cancer
 The goal is to continue to develop the prostate-on-chip to identify stromal AR functions

NIH/NCI T32 CA009213 (Cress, PI; Miranti Co-I) 09/14/2020 – 8/31/2025
 Integrative Cancer Scholars

American Cancer Society

134181-MBG-19-225-01-MBG ACS (Miranti, PI)

01/01/2020-05/31/2022

Targeting Bone Metastatic Castration Resistant Prostate Cancer

The goal is preclinical testing of combination therapies that target integrin $\alpha 6\beta 1$ and PI3K in CRPC.

R41CA224497 NIH/NCI

(Hurley, PI; Miranti, Subaward)

09/01/2018-12/31/2021

DNA Quadruplex Control of hTERT Transcription: A New Therapy for Taxotere-Resistant Prostate Cancer

The goal is to identify G-quadruplex stabilizing drugs that suppress hTert expression in drug-resistant prostate cancer.

The following grants were completed and closed:

W81XWH-14-1-0479

(Miranti, PI)

09/23/2014-09/22/2020

DoD Prostate Cancer Research Program

ING4 Loss, Decreased Differentiation, and Prostate Cancer Progression

The goal is to determine if ING4 loss in prostate cancer is associated with decreased prostate differentiation, tumorigenesis, and predictive of poor patient prognosis.

What other organizations were involved as partners?

Nothing to report

SPECIAL REPORTING REQUIREMENTS

Not applicable

APPENDICES:

8 Abstracts

2 Published papers

Gene Expression Tables

Pten and CREB Cooperativity during Prostate Luminal Epithelial Differentiation is Disrupted in Prostate Cancer

Watson M¹, Berger PL¹, Frank SB^{1,2}, and Cindy K. Miranti¹

¹Laboratory of Integrin Signaling and Tumorigenesis, Van Andel Research Institute, Grand Rapids, MI and ²Genetics Graduate Program, Michigan State University, Lansing, MI

Myc is overexpressed in the majority of human prostate cancers (PCa), yet the mechanisms by which Myc drives PCa are not fully understood. Using a novel *in vitro* differentiation model in which human basal prostate epithelial cells (PrECs) are induced to differentiate into luminal cells, we previously demonstrated that Myc is required for transient expression of the chromatin-binding protein ING4, whose transient induction and subsequent down regulation is required for normal luminal cell differentiation. ING4 expression is lost in >60% of primary prostate tumors, loss of ING4 prevented PrEC differentiation, and was necessary for Myc-dependent tumorigenesis *in vivo*. Furthermore, loss of Pten prevented ING4 induction and differentiation (Cancer Res 74:3357-68, 2014). Our objective is to identify the mechanism by which ING4 expression is controlled by Pten. Using RNA-Seq to interrogate genes induced during PrEC differentiation we determined that ~20% of the differentially regulated genes are targets of the transcription factor, CREB. Furthermore, CREB-regulated genes were highly expressed in PrECs transformed by overexpression of Erg, Myc, and shRNA to Pten (EMP cells). However, the CREB genes induced in normal PrECs were completely different from the genes induced in EMP cells, suggesting there is a major genetic switch surrounding CREB-mediated transcription in tumor cells vs normal cells. We found that during normal PrEC differentiation, Pten is elevated until around Day 8-10, then its expression drops and CREB is then activated around Day 12. Loss of Pten results in constitutive activation of CREB indicating that Pten acts to control the timing of CREB activation. ING4 is induced prior to CREB activation and decreases when CREB activity is high, and removal of CREB by shRNA results in constitutive induction of ING4. Thus, CREB is a negative regulator of ING4, downstream of Pten during normal PrEC differentiation. Thus, in the tumor cells when Pten is lost, CREB is constitutively activated and prevents ING4 induction. Furthermore, in this context CREB induces a different set of genes that promote tumorigenesis, rather than differentiation. Defining these differential targets may allow us to identify specific therapeutic targets or biomarkers.

11th Prostate Cancer Symposium at Clark Atlanta University, Atlanta, GA, September 26-28, 2016

Pten Loss Promotes Prostate Cancer Tumorigenesis through Disruption of a CREB-Dependent Differentiation Pathway

McLane J. Watson¹, Penny L. Berger¹, Sander B. Frank², Ashton J. Basile², and **Cindy K. Miranti**^{1,2}

¹Van Andel Research Institute, Grand Rapids, MI and ²Dept of Cellular and Molecular Medicine, University of Arizona, Tucson, AZ.

Background: Genetic drivers of prostate cancer (PCa) development, including Myc overexpression or Pten loss, are linked to prostate epithelial differentiation. But, how these oncogenes alter the differentiation program during PCa development remains unresolved. We previously showed, in normal human prostate epithelium, that Myc induces transient expression of a chromatin-binding protein, ING4, which is required for prostate luminal cell differentiation. However, ING4 expression is lost in >60% of primary tumors and ING4 loss prevents luminal cell differentiation. In fact, ING4 loss is necessary for Myc-overexpressing cells to produce tumors. We further found that Pten loss prevents luminal cell differentiation by blocking ING4 induction and 50% of primary tumors with ING4 loss also lack Pten. We sought to determine how Pten loss suppresses ING4 expression and differentiation.

Methods: We used RNA-Seq to identify gene signatures induced during human luminal cell differentiation and compared them to those induced in tumor cells with combined Myc overexpression and Pten loss (Myc/shPten). Gene signatures were validated by qRT-PCR and immunoblotting. Functional assessment of the role of specific genes on differentiation, ING4 expression, and tumorigenesis was carried out using shRNA knock-down and chromatin immunoprecipitation (ChIP).

Results: During luminal cell differentiation, ~30% of the differentially regulated genes are targets of the transcription factor CREB. We found that late in luminal cell differentiation, ATF1 activation precedes CREB1, at a time when Pten expression drops. CREB-target genes associated with luminal cell differentiation are induced at this time, including ING4 and its E3-ligase JFK. Accordingly, CREB1/ATF1 are bound to the promoters of both ING4 and JFK. Paradoxically, knock-down of CREB1 results in overexpression of ING4 and accelerated differentiation, while knock-down of ATF1 prevents ING4 induction and differentiation. Loss of CREB1 also eventually induces luminal cell death. Surprisingly, a large set of CREB-regulated genes are highly expressed in the Myc/shPten tumor cells; however, this set of genes is distinctly different from those induced in the normal cells. Pten loss, with or without Myc overexpression, is sufficient to constitutively activate CREB1 and ATF1 in normal prostate epithelium. Several CREB targets involved in progenitor cell maintenance, including GATA2 and Twist1, are elevated in the tumor cells. Knock-down of CREB1 in tumor cells restores ING4 expression and rescues differentiation.

Conclusions: Early in prostate luminal cell differentiation, elevated Pten prevents premature activation of ATF1 and CREB1. ATF1 is required for the transcriptional induction of ING4 and initiation of luminal differentiation, while CREB1 limits ING4 expression, possibly through induction of its E3-ligase, and is required for luminal cell survival. However, in the absence of Pten, CREB1 and ATF1 are activated prematurely, preventing ING4 induction and terminal differentiation, leading to maintenance of a progenitor cell-like proliferative population.

Impact: Determining which PCa patients are at risk for lethal disease remains a major challenge. We propose there will be a specific combination of oncogenic events and differentiation alterations that produce an aggressive subtype of PCa. If this signature can be identified, then the ability to distinguish indolent from lethal disease can be achieved.

University of Arizona Cancer Center Retreat, Tucson, AZ, Apr 21, 2017

CREB1 and ATF1 differentially regulate terminal prostate luminal cell differentiation by controlling the timing of ING4 expression, while CREB1 prevents ING4 expression upon PTEN loss in prostate cancer

McLane Watson¹, Penny Burger¹, Sander Frank², Mary Winn¹, and Cindy K. Miranti^{1,2}

¹Van Andel Research Institute, Grand Rapids, MI and ²University of Arizona Cancer Center, Tucson, AZ

We previously demonstrated that transient ING4 expression is required for luminal cell differentiation. Additionally, ING4 is downregulated in ~60% of primary prostate tumors and its loss is correlated with loss of PTEN. We further demonstrated in a primary prostate cancer model overexpressing ERG, MYC, and shPTEN (EMP) that loss of PTEN was responsible for ING4 downregulation, though the mechanism remained elusive. Utilizing RNA-seq and our *in vitro* differentiation model, we identified transcriptional nodes required for luminal differentiation. Of the ~600 differentially regulated genes during differentiation, the largest transcription factor signature (29% of genes) was CREB/ATF. A subset of these targets (Blimp1, Claudin1, Plk2, Chek1) were further validated by qRT-PCR and immunoblotting.

CREB/ATF bind constitutively to open chromatin CRE elements and can be activated by multiple kinases, including AKT. Both CREB1 and ATF1 are inducibly phosphorylated midway through luminal differentiation, with ATF1 preceding CREB1. Knockdown of CREB1 with shRNA increased ING4, accelerated differentiation, and induced premature luminal cell death. Conversely, knockdown of ATF1 blocked ING4 induction and prevented supra-basal layer formation. CREB1/ATF1 ChIP was enriched at the ING4 promoter at mid-differentiation, when ING4 expression peaks. Additionally, CREB1/ATF1 was constitutively bound to the promoter of JFK, an E3-ligase that targets ING4 and whose mRNA levels increase during differentiation. Thus, we propose that ATF1 is required to induce ING4 transcription while CREB1 suppresses ING4 by both transcriptional repression and induction of JFK. We compared the gene signature of differentiated cells to that of the tumorigenic EMPs. Surprisingly, 30% of the differentially expressed genes were CREB/ATF targets but there is less than 10% overlap, indicating CREB/ATF control distinct subsets of genes in differentiated luminal cells versus cancer cells. Some EMP-specific CREB/ATF targets (GATA2, TWIST1, Necdin, PPM1F) were further validated by qRT-PCR and immunoblotting. CREB1 and ATF1 were highly phosphorylated in EMP cells and knockdown of CREB1 restored ING4 expression and supra-basal formation.

Our working model is that AKT activation upon PTEN loss in transiently differentiating luminal cells results in premature and constitutive activation of CREB1/ATF1 bound to genes prior to induction of the ING4 chromatin switch. This prevents ING4 induction and the chromatin rearrangements required for terminal differentiation. In normal PreCs, CREB/ATF1 activation is tightly controlled by as of yet undetermined factors and is only permitted when the proper CRE binding sites are exposed. This model helps to explain how loss of PTEN disrupts luminal cell terminal differentiation to promote prostate cancer oncogenesis.

SBUR Annual Meeting: Multiple Genetic and Epigenetic Mechanisms of Urologic Disease, Tampa, FL, Nov 9-12, 2017. Abstract Published in **Am J Clin Exp Urol** 2017;5(Suppl 1):1-92 Poster P51, p60. www.ajceu.us

CREB1 and ATF1 differentially regulate terminal prostate luminal cell differentiation by controlling the timing of ING4 expression, while CREB1 prevents ING4 expression upon PTEN loss in prostate cancer

McLane Watson¹, Penny Burger¹, Sander Frank², Mary Winn¹, and Cindy K. Miranti^{1,2}

¹Van Andel Research Institute, Grand Rapids, MI and ²University of Arizona Cancer Center, Tucson, AZ

Many genes aberrantly expressed in prostate cancer are involved in normal basal to luminal cell differentiation. We previously demonstrated that transient ING4 expression is required for luminal cell differentiation and is downregulated in ~60% of primary prostate tumors. We further demonstrated in a primary prostate cancer model overexpressing ERG, MYC, and shPTEN (EMP) that loss of PTEN was responsible for ING4 loss. Furthermore, half of the human tumor samples that lose ING4 have also lost PTEN. However, we did not know how PTEN loss inhibits ING4 expression. Utilizing our *in vitro* differentiation model, whereby prostate basal epithelial cells (iPrEC) treated with KGF and androgen induce a supra-basal layer of luminal-like cells, and RNA-seq we identified transcriptional nodes required for luminal differentiation. Differentially expressed genes were analyzed by GeneGo to identify enriched transcription-factor signatures. Of the ~600 differentially regulated genes during differentiation, the largest signature (29% of genes) was CREB/ATF targets. Induction of Blimp1, Claudin1, and Plk2 and inhibition of Chek1 were further validated by qRT-PCR and immunoblotting.

CREB/ATF bind constitutively to open chromatin CRE elements in the promoters of genes and are activated through signaling-induced phosphorylation at Ser133 by kinases, including AKT. We found that both CREB1 and ATF1 are inducibly phosphorylated midway through luminal differentiation, with ATF1 preceding CREB1. Knockdown of CREB1 with shRNA increased ING4, accelerated differentiation, and induced premature luminal cell death. Conversely, knockdown of ATF1 blocked ING4 induction and prevented supra-basal layer formation. CREB1/ATF1 ChIP was enriched at the ING4 promoter at mid-differentiation, when ING4 expression peaks. Additionally, CREB1/ATF1 was constitutively bound to the promoter of JFK, an E3-ligase that targets ING4 and whose mRNA levels increase during differentiation. Thus, we propose that ATF1 is required to induce ING4 transcription, while CREB1 suppresses ING4 and simultaneously activates its E3-ligase to tightly control the timing of ING4 expression. We compared the gene signature of luminal cells to that of the tumorigenic EMP cells and surprisingly found 30% of the differentially expressed genes were also CREB/ATF targets. However, there is less than 10% overlap in these targets, indicating CREB/ATF control distinct subsets of genes in differentiated luminal cells versus cancer cells. Some of EMP-specific CREB/ATF targets included GATA2, TWIST1, Necdin, and PPM1F, which were further validated by qRT-PCR and immunoblotting. CREB1 and ATF1 were highly phosphorylated in EMP cells and knockdown of CREB1 restored ING4 expression and supra-basal formation.

Our working model is that AKT activation upon PTEN loss in transiently differentiating luminal cells results in premature and constitutive activation of CREB1/ATF1 bound to genes prior to induction of the ING4 chromatin switch. This prevents ING4 induction and the chromatin rearrangements required for terminal differentiation. In normal PrECs, CREB/ATF1 activation is tightly controlled by as of yet undetermined factors and is only permitted when the proper CRE binding sites are exposed. This model helps to explain how loss of PTEN disrupts luminal cell terminal differentiation to promote prostate cancer oncogenesis.

AACR Special Conference on Prostate Cancer, Orlando, FL, Dec 2-5, 2017.

PS1-08 Myc Promotes Prostate Epithelial Differentiation through the in induction of ING4, and Loss of ING4 Leads to the Development of PIN lesions

C Miranti¹, S Frank², C Jensen³, J Tran, P Berger, S Kim³

¹University of Arizona College of Medicine; ²Fred Hutchinson Cancer Research Center; ³Collaborator

Introduction & Objective: Inhibitor of Growth Factor 4 (ING4) is a protein that binds to the trimethylated lysine 4 in Histone H3 to recruit the acetyltransferase HBO1. ING4 is recognized as a tumor suppressor gene in the context of breast cancer, which suppresses the oncogenic activities of Myc. Our previous work showed that overexpression of Myc or ING4 accelerates luminal prostate epithelial cell (PrEC) differentiation, and overexpression of Myc increases endogenous ING4 protein. Interestingly, ING4 overexpression does not affect Myc protein levels. Strikingly, by overexpressing ING4 in a tumorigenic cell line, iPEC37-EMP, we are able to rescue PrEC differentiation. We propose that Myc normally promotes PrEC differentiation through chromatin remodeling mediated by ING4, such that loss of ING4 is required for Myc oncogenesis, which leads to aggressive disease through suppression of differentiation. **Methods:** We generated a CRSPR KO ING4 mouse line, which will allow us to interrogate how loss of ING4 impacts Myc-driven prostate cancer develop *in-vivo*. IHC and PCR was used to validate ING4 loss in the mouse tissues. We used IHC to ascertain ING4 status in normal human prostate compared to prostate cancer. **Results:** ING4 expression is reduced or null in prostatic intra-epithelial neoplasia (PIN) lesions when compared to normal human tissue. Genotyping and IHC have validated successful generation of the ING4 KO mouse. We noted that ING KO alone was not sufficient to generate tumors in 1-year old mice. We intend to stain H&E for the collected organs of these mice to further evaluate tissue architecture. Additionally, we plan to cross ING4 KO mice with prostate-specific Myc overexpressing mice. **Conclusions:** Preliminary IHC staining showed low and null expression of ING4 in human disease prostate compared to normal human prostate tissue. We have successfully generated a CRSPR ING4 KO mouse line. Crossing these mice with our prostate-specific overexpressing mice will create a promising model, allowing us to ask *in-vivo* questions regarding the concerted mechanism involving Myc and ING4 observed in our *in-vitro* differentiation model.

**PS2-64 Myofibroblasts Promote Prostate Cancer Progression
by Causing Aberrant Prostate Epithelial Differentiation**

S Tahsin¹, L Jiang¹, F Ivich¹, Y Zohar¹, C Miranti²

¹University of Arizona; ²University of Arizona College of Medicine

Introduction & Objective: Differentiation of the prostate ducts into basal and luminal cell types is driven by the normal underlying stroma. The stroma surrounding the tumor is predominantly made up of myofibroblasts. However, what generates the myofibroblasts and how they are involved tumor development is not well understood. Recently it was shown that the PIM1 serine-threonine protein kinase is elevated in patient tumor-associated fibroblasts. The ability of the normal prostate stroma to support normal basal and luminal cell differentiation is dependent on androgen and AR activation in the stroma. Interestingly, the loss of stromal-expressed AR is directly proportional to the decrease in tumor differentiation (i.e. Gleason grade) and increased progression of prostate cancer. We hypothesize that myofibroblasts generated by PIM1 overexpression promotes prostate cancer progression by disrupting normal basal-luminal differentiation through downregulation of AR signaling in the stroma. **Methods:** Using a microfluidics model, BHPs1 prostate stromal cells, co-cultured with iPREc prostate epithelial cells, were stimulated with androgen, to induce luminal cell differentiation. BHPs1 cells with or without PIM1 kinase were co-cultured for 16-21 days with iPREc or tumorigenic EMP-iPREc respectively to measure the generation of myofibroblasts. Differentiation state of basal and luminal cells and generation of myofibroblasts was monitored by immunostaining of lineage markers. Stromal AR target gene expression (mRNA) was monitored by qRT-PCR. **Results:** we successfully differentiated basal epithelial cells into luminal cells through direct stimulation of stromal cells with androgen. We observed nuclear localization of AR and AR induced gene expression in the stroma. We successfully generated myofibroblasts, with increased expression of α -SMA and Collagen A1, with PIM1 overexpressing BHPs1 stroma. Normal BHPs1 developed into myofibroblasts when co-cultured with tumorigenic EMP-iPREc. **Conclusions:** Studies using this unique bioengineered prostate-on-chip model will ultimately determine how myofibroblasts suppress prostate epithelial differentiation and lead to aggressive prostate cancer. This approach will potentially assist in the subcategorization of prostate tumors based on their differentiation status to provide patients with better prognostic information.

Loss of Androgen Receptor in Prostate Cancer Stroma Inhibits Luminal Epithelial Differentiation

Shekha Tahsin¹, Linan Jiang², Yitshak Zohar^{2,3}, and Cindy K. Miranti^{1,4}

1) Cancer Biology Graduate Program, 2) Aerospace & Mechanical Engineering,
3) Biomedical Engineering, and 4) Cellular and Molecular Medicine.
University of Arizona, Tucson, AZ

Background: Despite the well-known role of AR as an oncogenic driver of prostate cancer (PCa) in the epithelia, AR has a pivotal function within the stroma to drive luminal epithelial differentiation. Stromal AR signaling produces the paracrine factors required for luminal differentiation. However, studies shown that stromal AR expression is decreased in PCa and associated with poor clinical outcomes. Furthermore, stromal AR loss is proportional to higher Gleason scores. The ability of tumor cells to convert the stroma into cancer-associated fibroblasts (CAF) is well documented. But how AR signaling is lost from cancer stroma and how its loss in turn influences epithelial differentiation and oncogenesis unknown. In this study, we set out to determine the mechanism by which tumor cells induce loss of stromal AR.

Method: A new microfluidic-base Prostate-on-Chip model was used to co-culture normal prostate stromal fibroblasts, BHPs1, with either normal basal prostate epithelial cells or two PCa cell lines, C4-2 and EMP. Using cytokine array profiling, we identified a set of secreted proteins shared by two PCa cell lines, C4-2 and 22RV1. Immunofluorescence imaging and immunoblotting was used to monitor CAF markers, and AR. Levels of AR mRNA expression were analyzed by qRT-PCR.

Results: Coculture of BHPs1 cells with tumor cells for 12 days, led to tumor-induced CAF conversion as well as downregulation of AR expression. We identified TNF- α , FGF9, and GDNF as top candidate secreted cytokines shared by two PCa cell lines. Treatment of the BHPs1 with synthetic androgen (R1881) induces the expression and nuclear localization of AR. Treatment of BHPs1 with TNF- α for 5 days in the presence of R1881 resulted in a loss of AR expression and reduced nuclear localization. Loss of AR occurred in the absence of CAF conversion. Loss of AR protein was detectable within 24 hr after TNF- α treatment and was partially overcome by R1881. Examination of AR mRNA revealed that 1) R1881 induction of AR protein is not due to transcription, and 2) loss of AR protein by TNF α is accompanied by a decrease in mRNA, which is not recovered by R1881.

Conclusion: These results show that there are two mechanisms controlling AR expression, a post transcription mechanism induced by R1881 and a transcriptional repression induced by TNF- α .

GATA-2 and Twist-1 as Targets of CREB-1 in Prostate Cancer Development

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¹Department of Cellular and Molecular Medicine, University of Arizona Cancer Center
Tucson, AZ

²Van Andel Research Institute, Grand Rapids, MI

Background: Dysregulation in the normal process of basal to luminal cell differentiation results in prostate cancer development. Although TMPRSS2-ERG oncogenic fusion, loss of NKX3.1, Myc overexpression, and PTEN loss are known genetic abnormalities that drive human prostate cancer, the mechanisms that perturb differentiation at the molecular level still remains unclear. Through RNA seq analysis we unexpectedly identified two distinct pools of CREB target genes, one involved in luminal cell differentiation and the other in tumor induction. GATA-2 and Twist-1 were identified as potential CREB targets that are overexpressed in cancer cells. The current study was undertaken to experimentally validate whether GATA-2 and Twist-1 are targets of activated CREB-1 in tumor cells.

Method: The human tumorigenic cell line EMP (overexpressing Erg, Myc and shPTEN) was engineered to express Tet-inducible shRNA to CREB-1 or ATF-1. Chromatin immunoprecipitation (ChIP) using phospho-CREB primary antibody followed by qPCR was performed to measure the enrichment of CRE-containing promoter regions in the GATA-2 and Twist-1 promoters.

Result: CHIP analysis showed an approximate 8-fold enrichment of the GATA-2 promoter region spanning the TGACGTCA CRE binding site whereas the coding region of GATA-2 had very little to no enrichment. Similarly, the Twist-1 promoter showed a 5-fold enrichment spanning the ½ CRE site, around which the primer was designed, with no enrichment in the Twist-1 coding region. Upon knock-down of CREB-1 with shRNA using doxycycline, the enrichment of GATA-2 and Twist-1 at their respective loci decreased to a minimum level. This finding establishes that the enrichment of GATA-2 and Twist-1 promoter loci is specific to phospho-CREB. Since the phospho-CREB antibody also recognizes another CREB-related transcription factor, ATF-1, ChIP was also performed in EMP cells after knocking down ATF-1 with shRNA using doxycycline. No change in the percentage enrichment in the ATF-1 knock-down condition was observed in both the GATA-2 and Twist-1 promoters. This finding substantiates the prediction that enrichment of GATA-2 and Twist-1 is specific to phospho-CREB-1.

Conclusion: GATA-2 and Twist-1 are targets of activated CREB-1, but not ATF-1, in the tumorigenic EMP cells. This finding supports the novel connection between activation of the CREB-1 transcription factor and prostate cancer development.

Studies were supported by funding from DOD PCRP W81XWH-17-1-0570

Human stroma and epithelium co-culture in a microfluidic model of a human prostate gland

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L. Jiang, F. Ivich, S. Tahsin, M. Tran , S. B. Frank , C. K. Miranti, and Y. Zohar



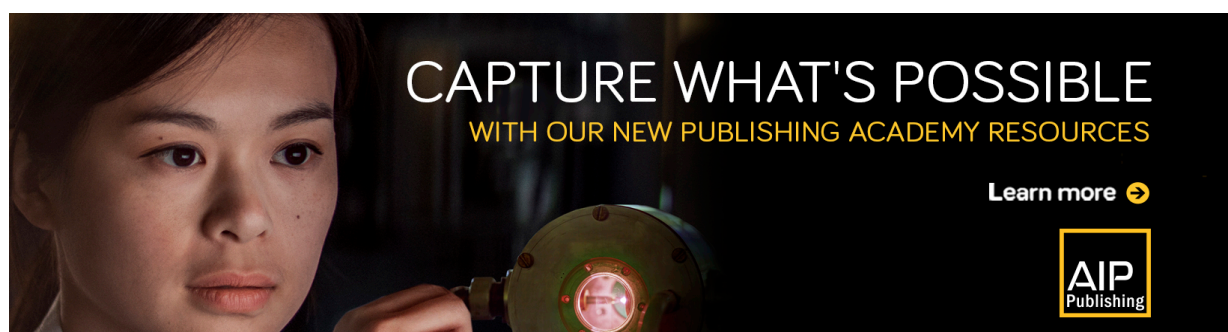
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Human stroma and epithelium co-culture in a microfluidic model of a human prostate gland

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L. Jiang,^{1,a)} F. Ivich,² S. Tahsin,^{3,4} M. Tran,² S. B. Frank,^{3,4} C. K. Miranti,^{3,4} and Y. Zohar^{1,2,4}

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ABSTRACT

The prostate is a walnut-sized gland that surrounds the urethra of males at the base of the bladder comprising a muscular portion, which controls the release of urine, and a glandular portion, which secretes fluids that nourish and protect sperms. Here, we report the development of a microfluidic-based model of a human prostate gland. The polydimethylsiloxane (PDMS) microfluidic device, consisting of two stacked microchannels separated by a polyester porous membrane, enables long-term *in vitro* cocultivation of human epithelial and stromal cells. The porous separation membrane provides an anchoring scaffold for long-term culturing of the two cell types on its opposite surfaces allowing paracrine signaling but not cell crossing between the two channels. The microfluidic device is transparent enabling high resolution bright-field and fluorescence imaging. Within this coculture model of a human epithelium/stroma interface, we simulated the functional development of the *in vivo* human prostate gland. We observed the successful differentiation of basal epithelial cells into luminal secretory cells determined biochemically by immunostaining with known differentiation biomarkers, particularly androgen receptor expression. We also observed morphological changes where glandlike mounds appeared with relatively empty centers reminiscent of prostatic glandular acini structures. This prostate-on-a-chip will facilitate the direct evaluation of paracrine and endocrine cross talk between these two cell types as well as studies associated with normal vs disease-related events such as prostate cancer.

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I. INTRODUCTION

The human prostate is a small organ in males surrounding the urethra just below the bladder. It is a male sex accessory gland that produces and secretes fluids that nourish and protect sperm, and thereby significantly enhance male fertility. A normal prostate contains a system of branching ducts comprising bistratified epithelium surrounded by a fibromuscular stroma with a basement membrane separating the epithelium and stroma.¹ The mature prostate epithelium contains three distinct cell types that differ in their morphology, as shown in Fig. 1. The luminal cells are tall columnar secretory epithelial cells that express cytokeratins (CK8 and CK18) and secrete proteins such as prostate-specific antigens (PSA and TMPRSS2).^{2,3} All luminal cells express high levels of androgen receptor (AR) and AR-regulated proteins.^{4,6} Below the luminal layer are nonsecretory basal cells that line the basement membrane.

The prostate basal cells express certain types of integrin (e.g., $\alpha 6$ and $\beta 1$) and cytokeratins (e.g., CK5 and CK14),^{3,5} and also express low or undetectable levels of the androgen receptor (AR). Within the basal layer are occasional intermediate cells that coexpress luminal and basal markers as well as additional markers such as CK19.^{3,7} Despite considerable speculation, it remains unclear whether intermediate cells represent a functionally distinct cell type. Rare neuroendocrine cells are basally localized expressing secreted neuropeptides and other hormones, and often display a dendriticlike shape that contacts the glandular lumen.⁸ Although several cell populations are present in the epithelium, the basal cell layer appears to be continuous in histological sections of the human prostate.⁹ The stroma compartment of the prostate also contains a number of differentiated cell types. Cells of the embryonic urogenital sinus mesenchyme (UGM) form a layer of smooth muscle, which lines the epithelium and exhibits a contractile

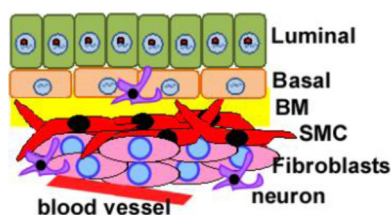


FIG. 1. A schematic of different cell types in an adult prostate. AR-positive luminal cells sit atop AR-negative basal cells, which adhere to a laminin-rich basement membrane (BM). Underlying AR-positive smooth muscle (SMC) and fibroblasts support the epithelial cells. Neurons, endocrine cells, and blood vessels are also present.

characteristic to aid the expulsion of the prostatic fluid into the ejaculate.¹⁰ The adult prostate stroma also contains a population of mature fibroblasts that secrete the extracellular matrix, consisting of fibrillary proteins, glycoproteins, and proteoglycans, form a structural network, and mediate growth factor signaling.¹¹ Other components of the stroma include blood vessels, lymphatics, nerves, and immune cells, which have been implicated in the stem cell regulation as well as tumorigenesis within the prostate.¹ Human prostate ducts are contained within a continuous thick mass of fibromuscular stroma, where stromal and epithelial cells are present in equal numbers.¹²

Similar to other stratified epithelia, prostate basal cells are mitotic and adhere to the basement membrane giving rise to terminally differentiated secretory luminal cells.^{13–15} However, unlike other epithelia, prostate epithelial differentiation is regulated by androgen signaling.^{16–18} The androgen receptor (AR) is a nuclear transcription factor activated in response to the steroid hormone androgen, which is expressed in the differentiated secretory cells but not in the basal cells.¹⁹ In an *in vitro* luminal cell differentiation model, confluent prostate epithelial basal cell cultures were treated with keratinocyte growth factor (KGF) and dihydrotestosterone (DHT) in a long-term culture for 17–21 days.²⁰ While this model suggested that the survival of differentiated prostate epithelial cells is mediated by cell-cell adhesion, the clarification of the stroma's role in prostate epithelial differentiation and survival was hampered by the lack of an *in vitro* human prostate model involving both epithelium and stroma.

Model systems that recapitulate the functional features observed in tissues are of high demand to study morphogenesis as well as disease initiation and progression. However, insight into the underlying biological mechanisms remains limited. One of the major hurdles is the gap between the mechanism-defining *in vitro* single-type monolayered cell culture (MCC) models and the physiology-relevant *in vivo* animal model. Current MCC models, although being extremely useful in delineating intracellular mechanics, have proven to be a poor predictor of physiological responses. The lack of critical communications between different cell types in the MCC models has been the major reason for this failure. Signaling pathways between different cell types have long been implicated in morphogenesis and disease development. Therefore, a model system that recreates the architectural features

to recapitulate the biology and physiology of the human prostate gland *in vivo* is critically needed.

A growing number of 3D cell culture systems are being introduced to provide controlled mechanical, chemical, and biological cues.²¹ Several methods have been proposed with the aim to manipulate the spatial and temporal properties of a cellular microenvironment such as stiffness, shear stress, micropatterns, 3D configuration, and concentration gradients. Endothelial cells cultured within a chamber capable of applying physiological shear stresses are induced to differentiate due to the stimulation of specific integrin/endothelial cell-mediated signaling cascades.²² Also, epithelial cells cultured on soft extracellular matrix gels organize themselves into polarized structures that strongly resemble functional tissue *in vivo*.^{23,24} Lab-on-chip (LOC) systems, incorporating a unique 3D microenvironment with a high spatio-temporal precision, provide physiologically relevant models to study vascular tissues *in vitro*.²⁵

Microfluidic systems have already enabled various biological studies including protein crystallization,²⁶ collection of cellular secretions,²⁷ blood circulation,²⁸ angiogenesis,²⁹ and cellular cocultures.³⁰ Multicompartmental 3D microfluidic cell culture devices, often termed as organs-on-chips (OoC), have been introduced to address the limitations of *in vitro* modeling. So far, numerous OoC devices have been proposed to reproduce various functions of organs and tissues.³¹ Examples of *in vitro* research models representing major organs include lung,³² liver,³³ kidney,³⁴ intestine,³⁵ gut,³⁶ and bone.^{37,38} These models represent robust compartmentalized, heterogeneous cell culture systems to faithfully simulate the physiology and anatomy of human organs, and thus enhance our understanding of *in vivo* mechanisms that are otherwise difficult to study.^{39,40} Interestingly, despite the high prevalence of life-threatening diseases and cancers that affect exocrine glands, there are fewer reports on LOC systems for investigating a prostate.^{41–43} Organ-on-a-chip models have been used to investigate the interaction between different cell types in human lung small airways,⁴⁴ human endometrium,⁴⁵ and breast.⁴⁶ To date, though, an organ-on-a-chip system for *in vitro* modeling of a human prostate gland is yet to be reported. Here, we develop a prostate-on-a-chip (PoC) system to provide a physiologically relevant *in vitro* model to mimic the functional epithelial-stromal interface lining the ductal systems of a human prostate gland.

II. EXPERIMENTAL METHODS

A. Device design

A microfluidic system, PoC, is developed to provide a physiologically relevant *in vitro* model to mimic the functions of a human prostate gland *in vivo*. Clearly, it is not feasible to replicate in every detail, *in vitro*, the adult prostate since it is a highly complex system containing multiple cell types with intricate interactions among them. Rather, the goal is to simplify the biomimetic system to allow the recapitulation of the dominant structural and functional features of the human epithelium-stroma interface, which is the fundamental component of a living prostate. A major obstacle for realizing 3D cocultures of different cell types in dishes and transwells is due

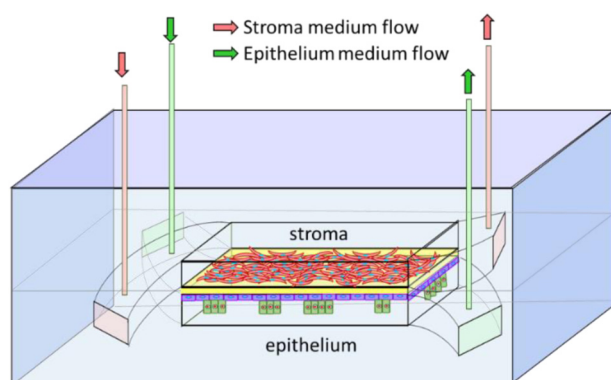


FIG. 2. A conceptual design of a prostate-on-a-chip model featuring two chambers for prostate stroma and epithelium cultured on opposite surfaces of a porous separation membrane (yellow color); the epithelium is composed of basal and luminal cells.

to the mixing of incompatible specific media required for maintaining different types of cells. Our previous attempt to coculture stroma/epithelium in transwells failed since the fully confluent epithelium cells, normally cultured in serum-free medium, deteriorated within three days of the coculture with stromal cells, whose medium containing 5% fetal bovine serum (FBS). Therefore, as sketched in Fig. 2, the model conceptual design features two individual chambers separated by a porous membrane to provide a scaffold for the cocultivation of epithelial and stromal cells, while allowing signaling between the two cultures. Similarly, as cocultures in dishes and transwells, a long-term coculture of two types of cells in the two chambers cannot be maintained under static conditions without flow, since the two media will be fully mixed within a short time due to the diffusion through the membrane pores. Therefore, independent flows of two media, specific for the two cell types,

are utilized that can realize a coculture of two cell types even with incompatible media.

B. Device fabrication

In order to realize the PoC concept, microfluidic devices were fabricated using soft-lithography techniques⁴⁷ as sketched in Fig. 3. Polydimethylsiloxane (PDMS) (Sylgard® 184, Dow Corning Corporation) is used as the structural material resulting in a transparent device, which allows real-time inspection of the cell cultures and high resolution image analysis. A commercially-available polyester membrane was selected with $0.8\mu\text{m}$ -diameter pores, 1% porosity, and a thickness of $23\mu\text{m}$. A 3D Computer-Aided Design (CAD) of a mold for microchannels was first completed including alignment marks to facilitate device assembly alignment and packaging. The mold was fabricated using a computer numerical control (CNC) machine in an aluminum block forming replicas of microchannels about $500\mu\text{m}$ in height, 1 mm in width, and 40 mm in total length. A mixture of the PDMS base and the curing agents, at a ratio of 10:1 weight by weight, was dispensed on the aluminum mold, and air bubbles in the mixture were removed under vacuum. The PDMS was cured in a 55°C oven for 2 h and peeled off the mold with complimentary microchannel grooves, Fig. 3(a). The membrane, after activation in an oxygen-plasma reactor (Harrick Plasma, USA), was treated in 5% 3-Aminopropyltriethoxysilane (APTES, Sigma-Aldrich) solution in water to prepare its surfaces for bonding. After forming inlet/outlet holes for each microchannel, the bonding surfaces of PDMS substrate pair were also oxygen-plasma treated. Each substrate pair was then brought into firm contact with a treated membrane sandwiched between the aligned microchannels, Fig. 3(b). The device fabrication was completed with the assembly of two pairs of custom-made inlet/outlet adapters for connections with the external fluid handling system, Fig. 3(c). A photograph of a fabricated and packaged device is shown in Fig. 3(d), where the length of the overlapping segment of the two microchannels is about 20 mm. The device allows independent control of both the medium-constituents and the flow rate required for maintaining any specific cell culture.

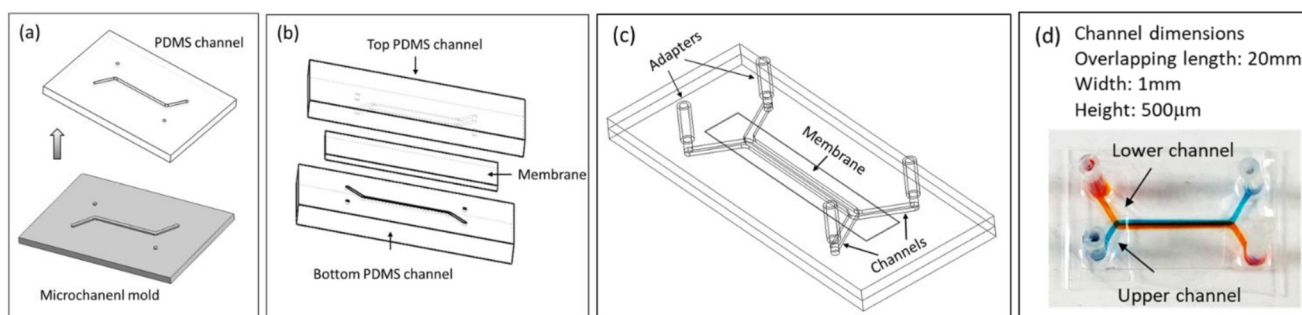


FIG. 3. Microfluidic device fabrication process: (a) dispensing PDMS polymer solution on an aluminum mold followed by peeling off the cured PDMS substrate, (b) bonding two PDMS microchannels with a porous separation membrane sandwiched between them, (c) device assembly with inlet/outlet adapters, and (d) a fabricated and packaged microfluidic device with inlet/outlet tubing adapters. Each microchannel is about $500\mu\text{m}$ in height, 1 mm in width, and 40 mm in total length with a 20 mm overlapping segment between the upper and lower microchannels; red- and blue-color inks fill the lower and upper channels, respectively, demonstrating independent fluid flows along the two channels.

C. Cell cultures

Primary human prostate basal epithelial cells (PrECs), immortalized as previously described,⁴⁸ were used to form the epithelium in the microfluidic model. PrECs were grown in keratinocyte serum-free medium (KSFM, Gibco 17005042) supplemented with bovine pituitary extract (BPE), epidermal growth factor (EGF), and 1% penicillin-streptomycin. Benign human prostate stromal cells (BHPPrS1s), obtained from Simon Hayward,⁴⁹ were used to form the stroma compartment in the microfluidic model. BHPPrS1s were grown in RPMI medium (Gibco) with 5% fetal bovine serum (FBS) and 1% penicillin-streptomycin. Recombinant KGF was purchased from Cell Sciences and Synthetic androgen (R1881) from Perkin Elmer.

Epithelium differentiation of PrEC cells in a culture dish was induced by supplementing the medium with R1881 at a concentration of 5 nM every other day. In the PoC model, epithelium differentiation in a PrEC monoculture was achieved under KSFM flow with 2.5 ng/ml recombinant KGF and R1881 treatment while, in a PrEC/BHPPrS1 coculture, it was achieved under independent epithelial and stromal media flows with the R1881 treatment of the stromal medium only. The R1881 treatment was performed by spiking the medium flow with in-flow injections of R1881 every other day resulting in a periodic spikelike profile of R1881 concentration. In comparison with the R1881 treatment in a culture dish, the cells were exposed to R1881 for a much shorter time of about a couple of hours. It was experimentally determined that the injection of R1881 at a concentration of 50 nM was needed to obtain sufficient epithelium differentiation in all experiments performed in a PoC model; R1881 concentration was initially estimated based on the total medium volume under a 30 $\mu\text{l/h}$ flow rate for two days.

D. Immunofluorescence

Antibodies ITG α 6 (GoH3), AR, and p63 were purchased from Santa Cruz, TMPRSS2 from Abcam, AR from Cell Signaling Technology, and HMWCK from Dako. Cells were fixed in the devices with 4% paraformaldehyde, followed by quenching with 125 mM Glycine at room temperature. The cells were permeabilized using 0.2% Triton and washed 3 times with 1 $\times$ PBS. The culture was blocked using 5% goat serum or 1% BSA for 1 h at room temperature. Cells were then incubated at 4 $^{\circ}\text{C}$ overnight in designated primary antibody solutions diluted in 1% BSA at adequate concentrations. Next, the cells were washed 4 times with 1 $\times$ PBS before incubation at room temperature in secondary antibody solutions for 1 h. The cultures were finally washed thoroughly using 1 $\times$ PBS and followed, when needed, by nucleus staining with 10 $\mu\text{g/ml}$ Hoechst (Sigma-Aldrich) for 10 min. Fluorescence images were recorded using a Nikon Eclipse TE2000-U microscope—under 4 $\times$, 10 $\times$, 20 $\times$, 40 $\times$, and 100 $\times$ oil immersion objectives—to inspect global features along the channels as well as to examine local details in individual cells.

III. RESULTS AND DISCUSSIONS

A. Microfluidic system modeling

The PoC model provides an environment where two types of cells in coculture can communicate via diffusion, due to

concentration gradient, while each cell culture is maintained under a specific medium flow. A proper balance between convection and diffusion mass transport is, therefore, required to minimize media mixing and maximize cell signaling across the separation membrane. The steady-state concentration distribution of the dilute species in a PoC model, $c(x, y, z)$, is governed by the following incompressible convection-diffusion equation:

$$u \frac{\partial c}{\partial x} + v \frac{\partial c}{\partial y} + w \frac{\partial c}{\partial z} = D \left(\frac{\partial^2 c}{\partial x^2} + \frac{\partial^2 c}{\partial y^2} + \frac{\partial^2 c}{\partial z^2} \right), \quad (1)$$

where u , v , and w are the components of the velocity vector in x , y , and z directions of the 3D coordinate system, respectively, and D is the dilute-species diffusion coefficient. Numerical simulations of the convective-diffusive flow field were performed for a pair of microchannels separated by a porous membrane in the absence of cells to compute the steady-state concentration distributions under various conditions. Properties of water at 37 $^{\circ}\text{C}$ were used to approximately represent the culture media,⁵⁰ while a diffusivity coefficient of $10^{-10} \text{ m}^2/\text{s}$ was selected to represent typical biospecies. The initial uniform relative concentrations at the upper and lower channels are one and zero, respectively, and each channel is 500 μm high and 1 mm wide with an overlapping length of 20 mm.

Numerically computed concentration distributions and gradients are summarized in Fig. 4. A sketch of the PoC physical model used in the simulations is illustrated in Fig. 4(a) along with the selected coordinate system; its origin is set at the start of the overlapping channel segment ($x=0$), the channel midspan ($y=0$), and membrane midthickness ($z=0$). Cross stream relative-concentration profiles across and near the membrane, $c(z)$, at the channel midspan ($y=0$) and 3 locations along the channels overlapping segment ($x=5, 10$, and 15 mm), are compared in Fig. 4(b) for a 10–100 $\mu\text{l/h}$ flow rate range. Within the membrane pores, no convection, diffusion due to concentration gradients is the only molecular transport mechanism. Under 30 $\mu\text{l/h}$ flow rate at the channel center ($x=10 \text{ mm}$), the relative concentration at the top channel decreases only to about 0.9, while it increases to just about 0.1 at the lower channel within a short distance away from the membrane. Cross stream concentration gradients, $\partial c/\partial z(z)$ shown in Fig. 4(c), exhibit a pulselike profile. The profile shows that the diffusion of the two media is restrained in proximity of the membrane, whereas bulk of the medium flow in each channel remains unaffected by diffusion. The pulse level across the membrane is constantly increasing with increasing flow rate; namely, the convective mass transport in the bulk flow is enhanced, and the molecular diffusion across the membrane is suppressed. Away from the membrane, convection is the dominant mass transport mechanism, and diffusion is negligible with vanishing concentration gradient. Steady streamwise relative-concentration profiles, $c(x)$, at the channel midspan near the membrane ($y=0, z=-40 \mu\text{m}$), are plotted in Fig. 4(d) for the same flow rate range. As a result of the continuous diffusion along the channel, the relative concentration increases nonlinearly from zero at the channel inlet to a level inversely proportional to the flow rate at the channel

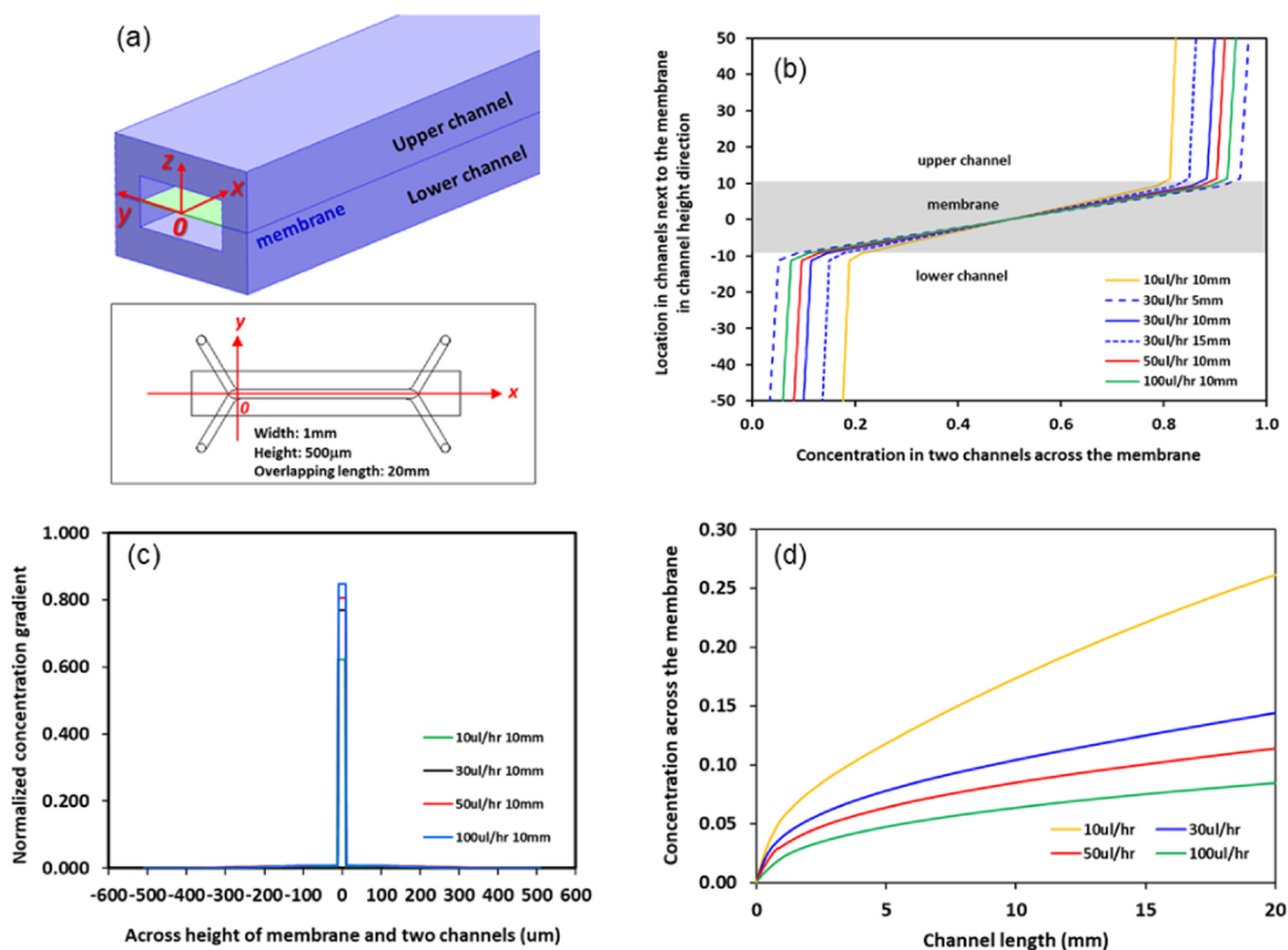


FIG. 4. Numerical simulation results showing: (a) a sketch of the PoC physical model used for the computations, (b) cross stream relative-concentration distributions, $c(z)$, around the membrane at 3 streamwise locations, $x = 5, 10$, and 15 mm, (c) Cross stream concentration-gradient distributions, $\partial c/\partial z(z)$, at the channel center, $x = 10$ mm, under the same flow rates, and (d) streamwise relative-concentration distributions, $c(x)$, at the lower channel near the membrane, $z = -40 \mu\text{m}$; all profiles are computed at the channel mid-span, $y = 0$, under flow rates of $10, 30, 50$, and $100 \mu\text{l/h}$.

outlet; e.g., $c(x = 20 \text{ mm})$ increases from 0.05 to 0.25 as the flow rate decreases from 100 to $10 \mu\text{l/h}$.

The numerical simulations demonstrate that the concentration distribution of biospecies around the membrane can be manipulated by varying the specific medium flow rate at each channel. This flow rate control parameter can be optimized to minimize the mixing of incompatible flowing media, while maximizing diffusion through the membrane. Thus, in the PoC model, flowing the media at an optimal rate will enable long-term maintenance of cocultures by confining each medium type to its proper culture and, simultaneously, allowing cell signaling between the two types of cultures. The results suggest, for example, that each cell culture can be maintained in its specific medium containing less than 15% of the other incompatible cell culture medium under an intermediate flow rate of $30 \mu\text{l/h}$ in both channels.

In a human prostate, blood flow, characterized by the flow rate passing through a unit volume of tissue, is reported about $0.34\text{--}0.97 \text{ ml}/(\text{min cm}^3)$.⁵¹ In our experiments, a volumetric flow rate of medium flow in the range of $10\text{--}100 \mu\text{l/h}$ over a monolayer of cells in a microchannel is estimated to be on the order of $0.1\text{--}1 \text{ ml}/(\text{min cm}^3)$ in terms of the same characterized blood flow in a human prostate. In addition, this flow rate range corresponds to a wall shear stress ranging $5 \times 10^{-4}\text{--}5 \times 10^{-3} \text{ dyn/cm}^2$, thus the flow shear stress effect on the cells is negligible. Therefore, the medium flow rate used in the *in vitro* experiments is comparable with that of *in vivo*. This further demonstrates that the microfluidic human prostate model, which provides a favorable culture environment to each type of cells while allows communication between the two types of cells, closely recapitulates the biology and physiology of the human prostate gland *in vivo*.

B. Cellular cultures in a microfluidic device

Procedures were developed for culturing human prostate epithelial or stromal cells in microfluidic devices. The microchannels were first cleaned by flowing 70% ethanol solution followed by one-hour exposure to UV radiation in a biosafety cabinet. For stroma culture, the channel was coated with a thin layer of 5% fibronectin to enhance cell adherence to the membrane. The microchannels were washed with $1\times$ PBS in the preparation for cell seeding and were filled by suspensions at a density of 1×10^6 – 2×10^6 cells/ml. After seeding, the cells were allowed to attach to the membrane under static (no flow) conditions to establish firm adhesion mediated by laminins secreted by the epithelial cells and to fibronectin by the stromal cells.²⁰ All cultures were maintained in an incubator at 37 °C with 5% CO₂. Confluent epithelial and stromal monolayers were obtained within 24 and 72 h, respectively, while the media were manually refreshed daily. Upon confluency, the devices are connected to a multitrack syringe pump where designated medium supply is provided to each individual channel device at a constant rate of 30 μ l/h for the maintenance of the cell culture over the following 21 days.

The procedures for the cocultivation of stromal/epithelial bilayers in microfluidic devices were similar to those described for monolayer cell cultures; however, the two cell types were seeded sequentially. Stromal cells were typically seeded first in upper channels of devices with adapters facing up. After attachment to the membrane, the cells were cultured under static conditions for 2–3 days until a fully confluent stromal monolayer was developed. Epithelial cells were next seeded in the lower channels followed by device flipping, with adapters facing down, to ensure cell's settlements on the opposite surface of the separation membranes. The adapters of the microfluidic devices were plugged during the ensuing incubation to keep the media from flowing out of the channels. Upon epithelial cells attachment, the devices were flipped back to their upright position with epithelial/stromal cell bilayers established on opposite sides of the separation membranes. The cocultures were maintained for 21 days under independent media flows delivered by a syringe pump in corresponding channels at a constant 30 μ l/h rate. A bright-field image of epithelial/stromal cell bilayer in a microfluidic device is shown in Fig. 5(a),

where closeup views of confluent PrEC and BHPPrS1 monolayers are shown in Figs. 5(b) and 5(c), respectively. The PrEC cells exhibit a typical epithelial cobblestone morphology, whereas the BHPPrS1 cells demonstrate a typical stromal stringy morphology with cells aligned in directional bundles.

Two sets of experiments were conducted to study epithelium differentiation, utilizing the PoC model, as summarized in Table I detailing cell type(s), media, and treatments. Study I experiments were carried out with epithelial cultures only, without stroma, to evaluate cell culture and differentiation characteristics in comparison with similar reports in dish cultures. This evaluation is critically needed to guide the adjustment of certain experimental parameters as well as to demonstrate the viability of the PoC model in duplicating previously published data. Study II experiments were carried out with epithelial/stromal cocultures uniquely enabled by the PoC model. These experiments allow investigating, *in vitro*, the role of stroma in epithelium differentiation in a setting much closer to the *in vivo* microenvironment. All experiments were repeated at least three times to confirm the repeatability and reliability of the results in the PoC model.

C. Prostate epithelial differentiation without stroma (Study I)

KGF has been reported in previous studies to be an important epithelium differentiation factor in many tissues including prostate.^{52–55} Androgen, acting via the androgen receptor, also plays an important role in prostate epithelial cell differentiation.¹⁷ Indeed, an *in vitro* differentiation model of the human prostate luminal epithelium has been established demonstrating that the combination of KGF and androgen is sufficient to induce the differentiation of a stratified epithelium grown in a culture dish.²⁰ In this culture-dish model, human primary basal prostate epithelial cells (PrECs), grown to confluency in monolayer cell cultures, were treated with 10 ng/ml (KGF) and 5–10 nM androgen (dihydrotestosterone, DHT). Culturing the cells for 10–15 days with KGF and DHT resulted in the formation of stratified cell patches consisting of at least two cell layers, resembling the bilayer of basal and secretory luminal cells observed in the prostate epithelium *in vivo*. The suprabasal cell layer was validated to be luminal by assessing

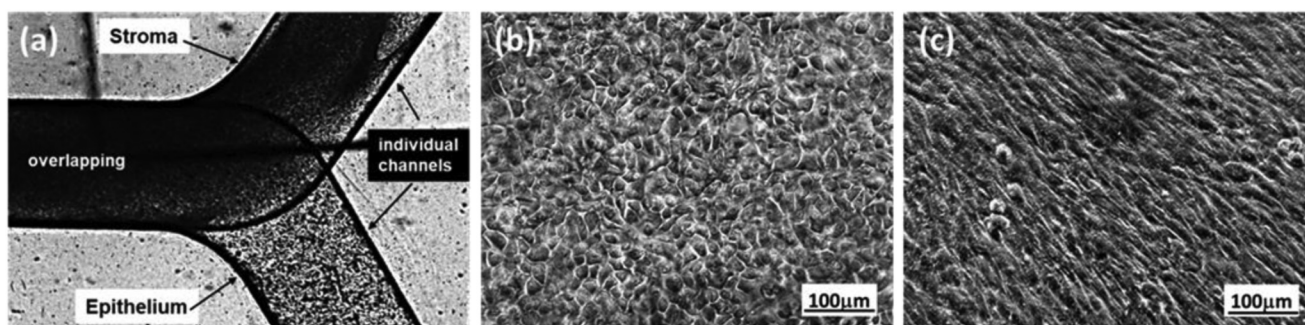
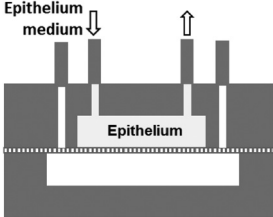
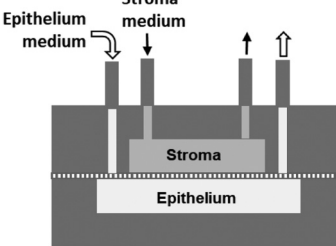


FIG. 5. Bright-field images of epithelium/stroma coculture in a microfluidic device: (a) PrEC and BHPPrS1 in individual channels with an overlapping segment for cocultures; (b) a confluent PrEC monolayer, and (c) a confluent BHPPrS1 monolayer are established in the device for a coculture experiment.

TABLE I. A summary of the prostate epithelium differentiation experiments utilizing the PoC model.

Study	Cell type	Experiment	Medium	Treatment
(I) Epithelium differentiation in the absence of stroma	Epithelium	Differentiation I	Epithelium medium	+KGF&+R1881
		Control I-1		None
		Control I-2		+KGF
		Control I-3		+R1881
				
(II) Epithelium differentiation in coculture with stroma	Stroma epithelium	Differentiation II	Stroma medium	+R1881
	Stroma	Control II-1	Epithelium medium	None
	epithelium		Stroma medium	None
			Epithelium medium	None
				

known basal and luminal markers. The suprabasal cells no longer expressed integrins $\alpha 2$, $\alpha 3$, $\alpha 6$, αv , $\beta 1$ or $\beta 4$, or p63, K5, K14, EGFR, FGFR2IIIb, or Bcl-2, but instead expressed AR and androgen-induced differentiation markers, including K18, K19, TMPRSS2, Nkx3.1, PMSA, KLK2, and secreted prostate-specific antigen (PSA). The differentiated cells possess the important features of terminally differentiated secretory prostate epithelial cells *in vivo*; namely, they do not proliferate, adhere to a basal cell layer but not to the basement membrane, they express AR protein, and they respond to DHT by inducing AR-dependent genes. Differentiated prostate cell survival depended on E-cadherin and PI3K, but not KGF, androgen, AR or MAPK; it is mediated by cell-cell adhesion, and not through androgen activity or prostate stroma-derived KGF.

We first determined whether epithelial cell differentiation could occur in the context of the microfluidic devices. PRECs were cultured in a microchannel under conditions as described for Study I in Table I. The seeded epithelial cells are proliferative; they adhere to the polyester membrane surface via secreted laminins 5 and 10 mediated by integrins $\alpha 6 \beta 4$ and $\alpha 3 \beta 1$. Once the cellular monolayer is confluent, the culture is maintained under a constant flow of KSFM culture medium, at a rate of $30 \mu\text{l/h}$, supplemented by both 10 ng/ml prostate-derived keratinocyte growth factor (KGF) and an in-flow injection of 50 nM synthetic androgen (R1881) every other day. After a 21-day culture in an incubator, epithelium differentiation is examined by immunofluorescence staining using AR and ITG $\alpha 6$ antibodies to monitor the presence of luminal and basal cells, respectively.

As observed in the culture dish differentiation model, some basal cells differentiate into luminal cells in microchannel devices. Figure 6(a) is a bright-field image showing the formation of

stratified luminal cell clusters on the basal cell layer, similar to those observed in the *in vitro* luminal cell differentiation model in culture dishes.²⁰ The differentiation is also detected by losing the expression of basal marker integrin $\alpha 6$ (ITG $\alpha 6$) and gaining the expression of luminal marker AR, as shown in Figs. 6(b) and 6(c). Distinct ITG $\alpha 6$ -expressing basal cells (green) and AR-expressing luminal cells (red) are observed in the epithelium culture treated with KGF and R1881. A close inspection reveals that most of the cells are either red or green, and not overlapping, indicating the successful differentiation of epithelial basal cells into luminal cells. Furthermore, glandlike buds and extensions are observed in the epithelial PoC culture, reminiscent of glandular acini structures in the overall shape but without lumens.⁵⁶ Occasionally, groups of cells appear to form mounds with a relatively hollow center similar to structures observed in the culture-dish model.²⁰

In addition, three control experiments were performed, I-1, I-2, and I-3, to examine the roles of KGF and R1881 in cell differentiation. Epithelial basal cells (PRECs) were cultured in microfluidic devices for 20 days under 3 different conditions: (i) KSFM culture medium with neither KGF addition nor R1881 injection, I-1; (ii) KGF-containing KSFM medium but without R1881 injection, I-2; and (iii) non-KGF containing KSFM medium with R1881 injection, I-3. Fluorescence images recorded at the completion of these control experiments are compared in Figs. 6(d)–6(f). In all cases, the basal cells clearly express ITG $\alpha 6$ (green) but not AR (red) biomarker. The results confirm that both KGF and R1881 are required for successful epithelium differentiation; in the absence of either KGF or R1881 treatment, basal epithelial cells cannot differentiate into luminal cells.

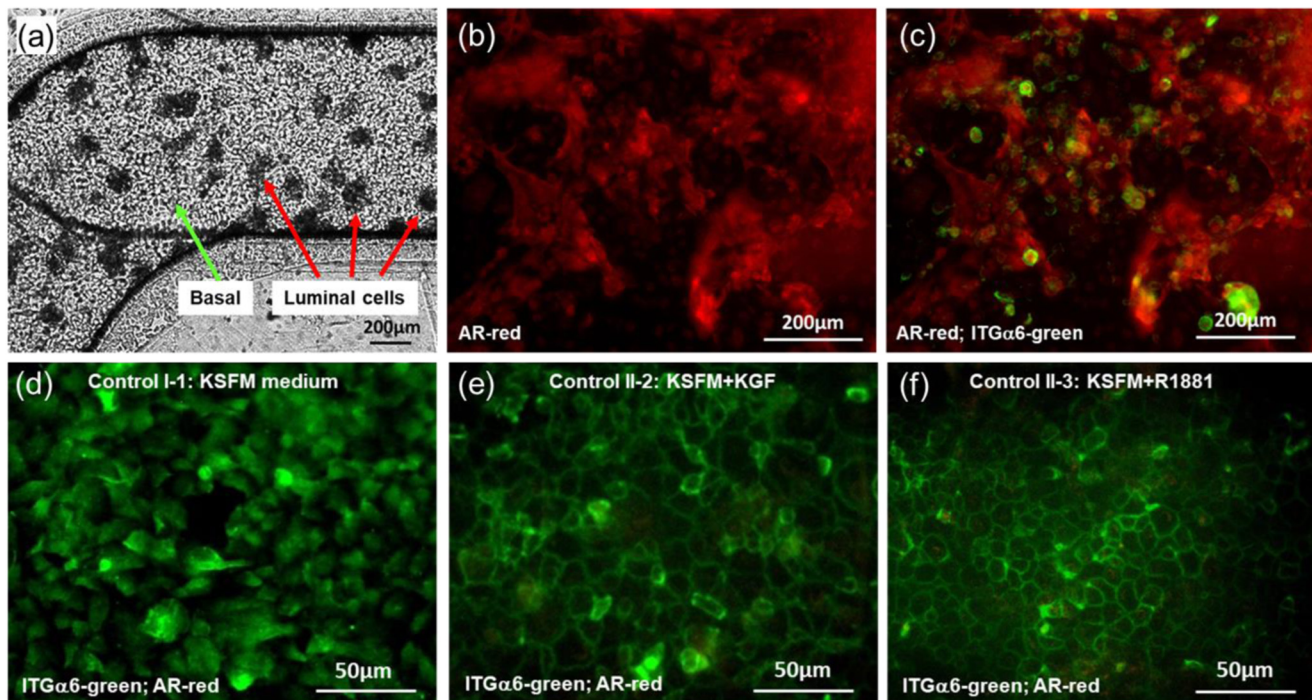


FIG. 6. Bright-field image and fluorescence images of PREC cells from experiments under various medium conditions in a microdevice. Under KGF-containing medium flow with the R1881 treatment, differentiation of PREC cells is realized showing the formation of stratified luminal cell clusters on the basal cell layer (a); the luminal cells are AR positive (b); luminal cells (red) do not express the ITGα6 basal biomarker (green) (c). Under control conditions, (d) KSFM medium alone, (e) KSFM + KGF medium, and (f) KSFM + R1881 treatment, the presence of ITGα6-basal expressing cells (green) and the absence of AR-expressing luminal cells (red) indicate lack of differentiation.

D. Prostate epithelial differentiation with stroma (Study II)

A proper model of a prostate gland requires the presence of both epithelial and stromal cells separated by a basement membrane, and the microfluidic system is ideally suited to recreate such a microenvironment. Thus, epithelial and stromal cells were cocultured on either side of a separation membrane to establish an organ-culture model of a human prostate gland. Stroma BHP1S1 and epithelial PREC cells were sequentially seeded on opposite surfaces of a separation membrane in a microfluidic device. In about 3–5 days, the stroma reached confluency in the upper channel filled with its RPMI culture medium, while the epithelium reached confluency in the lower channel filled with its KSFM culture medium. During this incubation period, the medium in each microchannel was manually replenished every 1–2 days using a pipette. Continuous maintenance of the coculture with no flow in the microfluidic device, after reaching confluency, resulted in severe deterioration of the epithelium over a span of 7 days. Temporal numerical computations predict that two different media separated by a porous membrane, in a PoC model, would diffuse and completely mix together in less than one hour due to concentration gradients. Thus, under the static conditions, the coculture was exposed most of the time to a fully mixed solution of the two media. The incompatible ingredients in the

stroma medium led to the deterioration of the epithelial layer losing confluency, which is a necessary condition for differentiation. Experiments were conducted to maintain confluent epithelial and stromal monolayers in culture dishes under various mixture combinations of the two media. The results confirmed that a confluent epithelial layer could not be sustained under mixtures containing more than 10% stromal medium. Similarly, a confluent stromal layer turned patchy with signs of stress under mixtures containing more than 10% epithelial medium.

A prominent feature of the microfluidic system is the flow of incompatible culture media enabling the cocultivation of different cell types. The flow rate can be fine-tuned, adjusting the proper balance between convection and diffusion mass transport, to minimize mixing of the two media and sustain a coculture. Indeed, based on the numerical simulations for a 30 $\mu\text{l/h}$ flow rate, the concentration of the incompatible medium is approximately 10% in the channel center and less than 15% at the channel outlet. Therefore, confluent layers of both stromal and epithelial cells were maintained under this optimal flow rate for at least 3 weeks. R1881 at a concentration of 50 nM was injected every other day only into the stromal medium flow to enhance BHP1S1 secretion of KGF which, in turn, induces PREC differentiation. After 21-day incubation of the coculture, the cells were fixed in the microfluidic device

and stained for differentiation markers. With R1881 stromal treatment, AR- and TMPRSS2-expressing luminal cells are observed in Figs. 7(a)–7(c) indicating epithelium differentiation. Distinct and separate ITG α 6- and p63-expressing basal cells are also evident in Figs. 7(a)–7(c). High magnification images, Figs. 7(d)–7(f), demonstrate the coexistence of distinct sets of basal and luminal cells following PrEC differentiation. Thus, flow is required to maintain the confluency and integrity of each cell line, and R1881 stimulation of the stroma alone is sufficient to induce differentiation in the juxtaposed epithelium.

A control experiment for the coculture was repeated under the same conditions but in the absence of the R1881 treatment, Table I (II-1), to test the dependency of differentiation on the R1881 treatment of the stroma. Images of epithelial stained for basal and luminal biomarkers are shown in Figs. 7(g)–7(i). While p63- and ITG α 6-expressing PrEC cells (green) are observed throughout of the channels, maintaining their basal phenotype, AR- and TMPRSS2-expressing cells (red) are barely detectable at a very few locations with weak signals. Thus, the absence of cells expressing luminal biomarkers, AR and TMPRSS2, indicates that

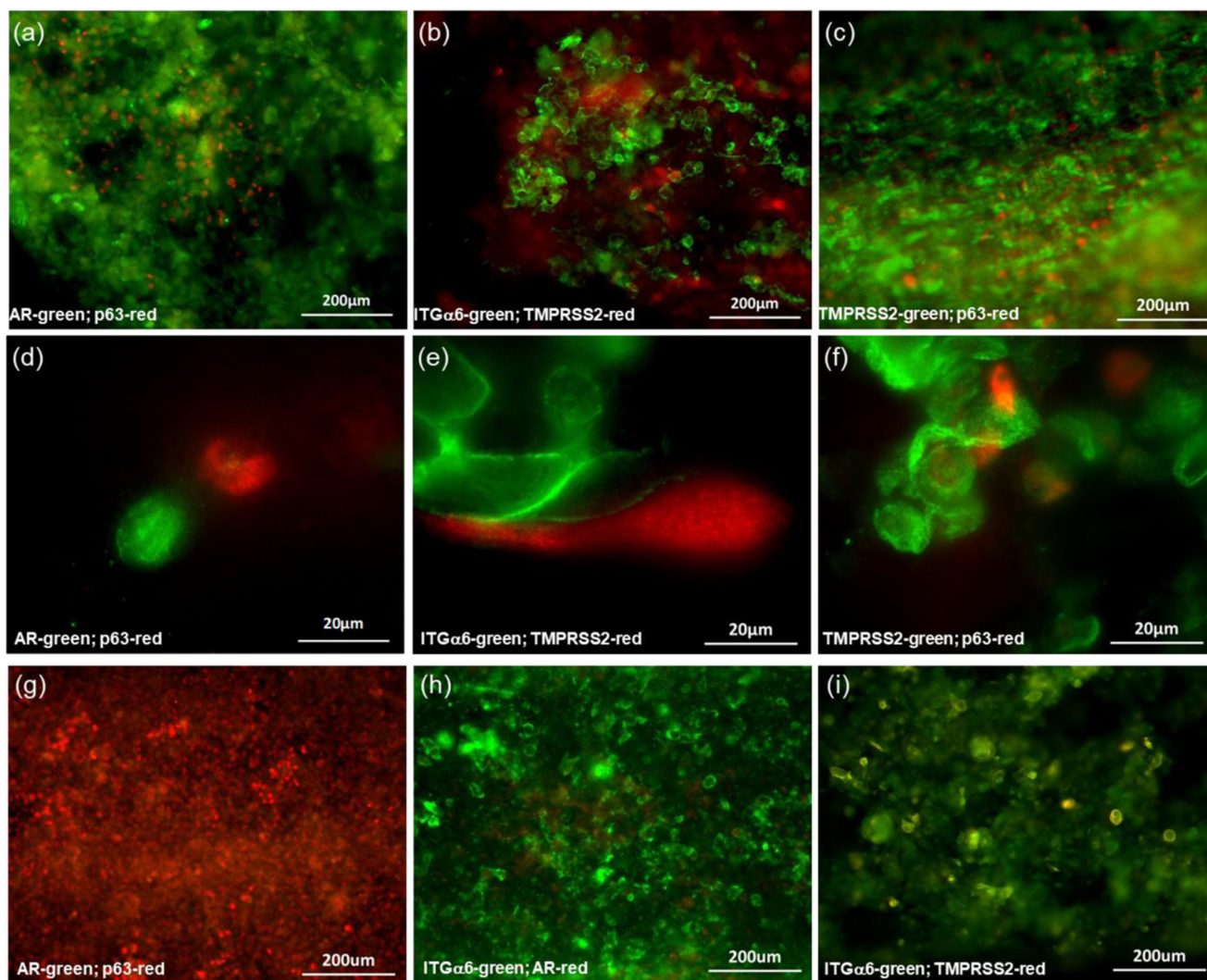


FIG. 7. Fluorescence images of immunostained PrEC epithelium cocultured with BHPs1 stroma for 21 days under corresponding medium flows with [(a)–(c)] and without [(g)–(i)] R1881 stromal treatment. The epithelial cells were stained for AR, p63, ITG α 6, and TMPRSS2 markers. AR-expressing and TMPRSS2-expressing luminal cells as well as p63- and ITG α 6-expressing basal cells are clearly observed for experiments with the R1881 treatment [(a)–(c)]. Higher magnification images (d)–(f) show that AR- and TMPRSS2-expressing luminal cells are distinctly different from the p63- and ITG α 6-expressing basal cells indicating complete differentiation. For control experiment without the R1881 treatment [(g)–(i)], the epithelial cells express p63- and ITG α 6-basal markers but not the AR- and TMPRSS2-luminal biomarkers indicating the absence of luminal cells in the culture.

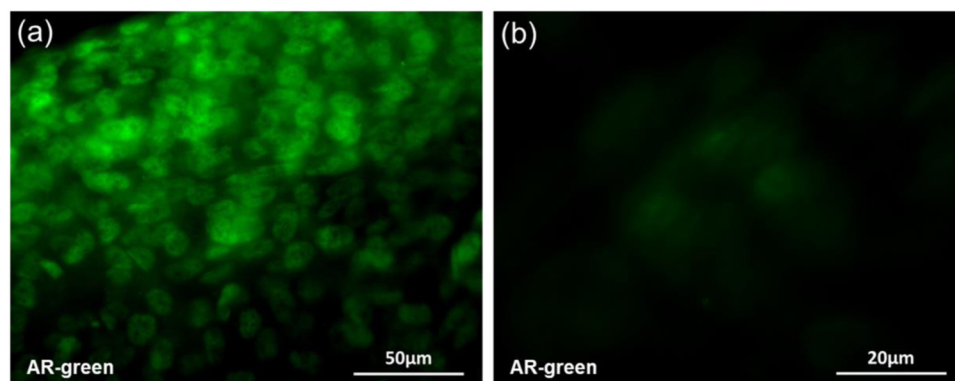


FIG. 8. Fluorescence images of BHPPrS1 stroma, cocultured with PrEC epithelium under corresponding medium flow and immunostained for AR (green): (a) with R1881 stromal treatment; the complete nuclear localization of the AR signal confirm its activation in the BHPPrS1 stromal cells by the R1881 treatment, and (b) without R1881 stromal treatment; the inactive AR signal is barely detectable throughout the cytoplasm of BHPPrS1 stromal cells only under a high magnification.

epithelium differentiation had not been accomplished without the R1881 treatment in the stroma culture.

The presence of distinct AR-expressing luminal cells, within cultures containing distinct p63-expressing basal cells after R1881-treatment of stroma cells, demonstrates that the luminal epithelium differentiation is dependent on androgen acting on AR-expressing stromal cells in the coculture. The ability of androgen (e.g., R1881) to act on the stroma, inducing epithelial differentiation, requires that the AR be activated in the stromal cells. AR translocation into the nucleus is a marker of its activation, and AR nuclear localization in the stromal cells was assessed by immunostaining cocultures with and without the R1881 treatment incubated for 21 days. The stromal treatment with R1881 over the course of 21 days resulted in complete nuclear localization of AR, Fig. 8(a), confirming its activation in the BHPPrS1 stromal cells. However, without the R1881 stromal treatment under the same magnification, the inactive AR signal in the stroma was undetectable. Under a higher magnification, Fig. 8(b), a very dim AR signal is barely detectable throughout the cytoplasm of the BHPPrS1 cells.

We also investigated whether KGF or a related family member, FGF10, might be induced and secreted by the stromal cells in response to the androgen stimulation of the stroma. Upon

qRT-PCR analysis of mRNA collected from androgen-stimulated stromal cells, Fig. 9(a), FGF10 mRNA was found to increase about 4-fold in response to androgen but not KGF mRNA. To determine whether FGF10 was secreted into the medium, FGF10 levels in conditioned medium collected from the stromal chambers of the microfluidic devices were measured using ELISA. The R1881 treatment of the stroma cells in their chamber, Fig. 9(b), resulted in a 100-fold increase in FGF10 secretion. Previous studies demonstrated that FGF10 can substitute for KGF in the tissue culture luminal cell differentiation model.²⁰ Moreover, prior studies in mouse embryonic prostate explant cultures demonstrated the importance of stromal FGF10, and not KGF, in mediating androgen/AR-dependent prostate epithelial differentiation during development.^{57,58} Therefore, it seems that androgen stimulation of stroma cells induces the release of FGF10, which is required for the differentiation of the juxtaposed basal cells into luminal cells.

IV. CONCLUSIONS

A microfluidic system has been developed to model a human prostate gland for a better understanding of the epithelium/stroma interactive role in the human prostate. A long-term coculture of epithelial (PrEC) and stromal (BHPPrS1) cells was established with stromal-dependent R1881-mediated epithelium differentiation of basal cells into luminal cells. Moreover, groups of cells appeared to form glandlike buds of mounds with a relatively hollow center resembling the prostate tissue architecture observed *in vivo*. In addition, androgen-induced secretion of FGF10 in the stroma is likely to be responsible for the androgen-dependency of luminal cell differentiation. Thus, this microfluidic system presents a promising *in vitro* tool to study morphogenesis and carcinogenesis of the human prostate that mimics events known to occur *in vivo*. The presented prostate-on-a-chip model will enable the accurate examination and analysis of morphological and biochemical aspects of the interactive roles of human prostate epithelium and stroma under various well-controlled conditions.

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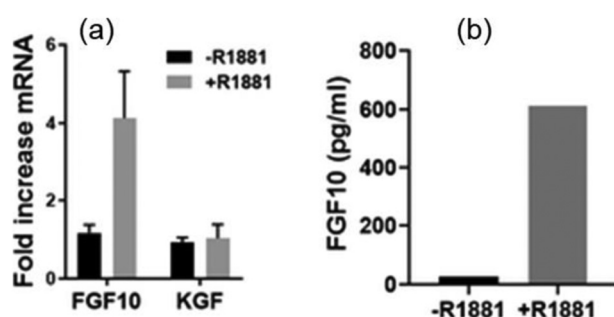


FIG. 9. A comparison between expression levels with or without R1881 stromal treatment of (a) FGF10 and KGF mRNA from BHPPrS1 cells, and (b) FGF10 secreted into the medium in the BHPPrS1 channel after 21 days of PrEC/BHPPrS1 coculture in a microfluidic device.

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Aberrant CREB1 activation in prostate cancer disrupts normal prostate luminal cell differentiation

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Abstract

The molecular mechanisms of luminal cell differentiation are not understood well enough to determine how differentiation goes awry during oncogenesis. Using RNA-Seq analysis, we discovered that CREB1 plays a central role in maintaining new luminal cell survival and that oncogenesis dramatically changes the CREB1-induced transcriptome. CREB1 is active in luminal cells, but not basal cells. We identified ING4 and its E3 ligase, JFK, as CREB1 transcriptional targets in luminal cells. During luminal cell differentiation, transient induction of ING4 expression is followed by a peak in CREB1 activity, while JFK increases concomitantly with CREB1 activation. Transient expression of ING4 is required for luminal cell induction; however, failure to properly down-regulate ING4 leads to luminal cell death. Consequently, blocking CREB1 increased ING4 expression, suppressed JFK, and led to luminal cell death. Thus, CREB1 is responsible for the suppression of ING4 required for luminal cell survival and maintenance. Oncogenic transformation by suppressing PTEN resulted in constitutive activation of CREB1. However, the tumor cells could no longer fully differentiate into luminal cells, failed to express ING4, and displayed a unique CREB1 transcriptome. Blocking CREB1 in tumorigenic cells suppressed tumor growth *in vivo*, rescued ING4 expression, and restored luminal cell formation, but ultimately induced luminal cell death. IHC of primary prostate tumors demonstrated a strong correlation between loss of ING4 and loss of PTEN. This is the first study to define a molecular mechanism whereby oncogenic loss of PTEN, leading to aberrant CREB1 activation, suppresses ING4 expression causing disruption of luminal cell differentiation.

Introduction

The normal prostate gland consists of a series of branched ducts of stratified basal epithelial and suprabasal secretory post-mitotic luminal cells. Well-defined markers distinguish luminal cells from basal cells [1, 2]. It is thought that bi-potential progenitor cells differentiate and give rise to both basal and luminal cells [3, 4]. A hallmark of prostate cancer

is the loss of basal cells and retention of some, but not all, basal markers in luminal-like proliferative cancer cells [5, 6]. These histological anomalies predict that genetic dysregulation of basal and luminal cell differentiation results in prostate cancer development.

Genetic studies in mice have linked prostate cancer development to a defect in differentiation. Knock out of the prostate-specific differentiation gene, Nkx3.1, in mice is a tumor initiating event [7]. About 50% of human primary patient samples contain the TMPRSS2-ERG fusion, which leads to ERG overexpression, a member of the ETS family of transcription factors with known roles in differentiation [8]. Loss of Nkx3.1 cooperates with TMPRSS2-ERG to promote prostate tumor progression in mice [9]. MYC overexpression and PTEN loss are also common genetic abnormalities in human prostate cancer with roles in differentiation [10, 11]. Loss of PTEN in mouse prostates is reportedly accompanied by a decrease in tissue differentiation [12]. Loss of PTEN or overexpression of MYC downregulates Nkx3.1 expression, which is sufficient to

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induce prostate cancer in mice [13]. Although these studies identified specific oncogenic events that drive prostate cancer development and likely dysregulate prostate epithelial cell differentiation, the underlying mechanisms to explain how dysregulated differentiation leads to cancer development is not understood. Moreover, these genetic studies have largely been limited to mouse models and defining of the molecular mechanisms that dysregulate differentiation in human cancer has yet to be achieved.

In an in vitro human prostate epithelial cell differentiation model, transient induction of ING4, via MYC, was required for human prostate luminal cell differentiation and its loss was required for MYC-driven prostate tumorigenesis [14]. Furthermore, ING4 expression is lost in a subset of primary prostate tumors, and that genetic loss of PTEN in the context of MYC overexpression causes loss of ING4 expression and suppresses differentiation. These findings further support the view that prostate cancer arises from defective differentiation [14, 15]. Functionally ING4 is a chromatin reader that binds to tri-methylated histone H3, and recruits HBO1 acetyltransferase to increase histone acetylation [15]. However, the mechanisms regulating the transient expression of ING4 during normal differentiation and how loss of PTEN leads to loss of ING4 are unknown.

CREB1 is primarily known for its role in neurons, but is reportedly involved in the differentiation of several tissue types [16]. CREB1 also reportedly plays a role in some cancers, where it is either overexpressed [17], involved in gene fusions [18], or aberrantly activated [19]. In prostate cancer, CREB1 activation via cAMP signaling is implicated in the switch from adenocarcinoma to neuroendocrine prostate cancer [20]. While no role for CREB1 has been reported for normal prostate differentiation or development, a recent report suggests aberrant CREB1 activation may be associated with prostate cancer recurrence [21].

CREB1 is a bZIP transcription factor that homo- or hetero-dimerizes to activate target genes through cAMP response elements (CRE). CREB1 dimerization with different partners allows selective activation of numerous downstream target genes [16, 22]. CREB1 binds constitutively to CREs in open chromatin and is activated through phosphorylation by numerous kinases, including PKA, AMPK, MAPK, and AKT [16]. CREB1 can also be directly inactivated via PTEN's protein phosphatase activity [23].

We unexpectedly identified CREB1 as a major regulator of human prostate luminal cell differentiation while comparing differentially expressed genes during prostate luminal cell differentiation [24]. In this study, we establish a novel link between CREB1 activation and transient expression of ING4 during normal human prostate luminal cell differentiation and demonstrate that oncogenic loss of PTEN disrupts the induction of ING4 expression via aberrant CREB1 activation.

Results

CREB1 gene signature in differentiating luminal cells

When grown to confluency and treated with KGF plus androgen, basal prostate epithelial cells (PrEC) undergo differentiation such that a suprabasal secretory luminal cell layer forms on top of the basal layer in about 2 weeks [1, 5, 14, 24]. To identify genetic programs associated with luminal cell differentiation, PrECs differentiated for 0–17 days were subjected to RNA sequencing. Over 600 genes were significantly (FDR adjusted $p < 0.05$) differentially expressed over the time course (GSE77460) (Fig. 1A). Pathway analysis indicates enrichment of genes involved in mitosis, epithelial differentiation, translation, cytoskeleton, and cell adhesion (Supplementary Fig. S1, Table S1, S2). Transcription factors predicted to regulate expression of these differentially expressed genes were identified. Majority of the differentially expressed genes at days 8 and 12 are known targets of MYC, p53, AR, SP1, and E2F1 (Fig. 1B). Analysis of isolated suprabasal cells at days 14 (14 L) and 17 (17 L) identified CREB1 as a key transcriptional regulator of ~25% of the differentially expressed genes (Fig. 1B; Supplementary Table S3).

Differential expression of predicted CREB1 targets, *PRDM1*, *PLK2*, *CLDN1*, and *CHEK1* (Fig. 1C), known for their roles in differentiation and cell cycle suppression [25–28], were validated by qRT-PCR (Fig. 1D). BLIMP1 (*PRDM1*), PLK2, and CLDN1 proteins were also upregulated during differentiation, with BLIMP1 transiently peaking between days 8 and 12, while PLK2 and CLDN1 peaked in suprabasal cells at day 14 (Fig. 1E). Nuclear expression of BLIMP1 in suprabasal cells was evident at day 10 (Fig. 1F).

CREB1 is required for luminal cell survival

CREB1 activity, as measured by immunoblotting for Ser133 phosphorylation, was induced after 12 days of differentiation and peaked in the suprabasal cells at day 14, while total CREB1 protein and mRNA were not significantly changed throughout differentiation (Fig. 2A, B). Immunofluorescent staining revealed that CREB1 activity was undetectable until day 12, where it was specifically localized in the suprabasal cells (Fig. 2C). To test the necessity of CREB1 for luminal differentiation, we generated cells expressing Tet-inducible shRNA targeting CREB1 (Fig. 2D, E). Knockdown of CREB1 with Dox did not prevent the induction of suprabasal cells at day 12 as visualized by the presence of AR-positive (luminal marker) integrin $\alpha 6$ -negative (basal marker) suprabasal cells (Fig. 2F). These suprabasal cells express luminal-specific K18

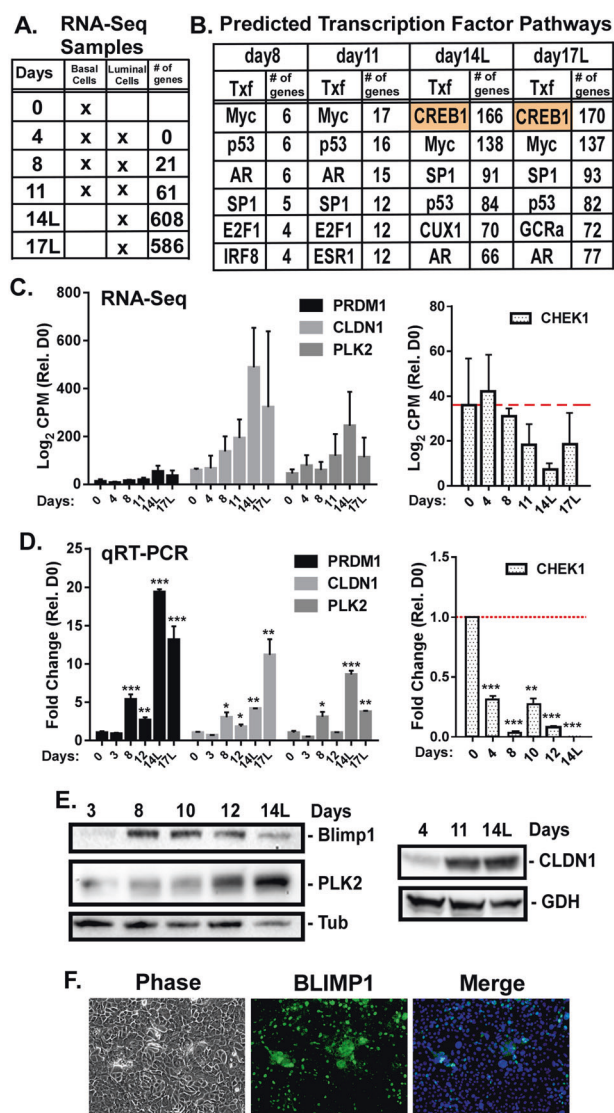


Fig. 1 CREB1 gene signature in differentiating luminal cells. Prostate luminal cell differentiation was initiated by treating basal epithelial cells (PrECs) with 2 ng/mL KGF and 5 nM R1881 for 0–17 days. **A** Isolated poly-A RNA was sequenced from biological triplicates of 0, 4 (no differentiation), 8, 11 (mixed basal and luminal), 14, and 17 (luminal only(L)) day cultures. Differentially expressed genes with $p < 0.05$, relative to basal cells, for each time point were generated. **B** Metacore analysis of transcription factors (Txf) likely involved in regulating the differentially expressed genes during differentiation. Top 6 Txf at each time point and the number of differentially expressed genes regulated by that Txf are indicated. **C** Transcript counts (log₂ CPM) for CREB1-specific target genes *Blimp1*, *CLDN1*, *PLK2*, and *CHEK1* during differentiation. **D** qRT-PCR validation of CREB1-specific target mRNAs. Normalized to 18S rRNA and shown as fold change relative to basal cells. * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$; $n = 3$; error bars SD. **E** BLIMP-1, PLK2, and CLDN1 protein levels were measured by immunoblotting. Tubulin (Tub) and GAPDH (GDH) served as loading controls. **F** BLIMP1 immunostaining of PrECs differentiated for 8 days. Cells were imaged by phase or fluorescence microscopy.

and PSA and lack nuclear p63 (Supplementary Fig. S2). However, the luminal cells displayed increased activation of Caspase 3 and appeared unhealthy (Fig. 2G). Thus, CREB1 is not required for luminal differentiation induction, but is crucial for survival of the new luminal cells.

To test the specificity of CREB1, we monitored activation of a related family member, ATF1, and found it was activated with different kinetics (Fig. 2A), being transiently activated at day 12 and back down by day 14. In contrast to CREB1, knockdown of ATF1 (Supplementary Fig. S3A) blocked suprabasal induction (Supplementary Fig. S3B). Strikingly, the levels of AR were significantly elevated in the shATF1 cells suggesting they may be converting to luminal-like cells in the absence of suprabasal induction. Thus, different CREB family members are likely involved in different aspects of luminal cell differentiation.

CREB1 limits ING4 expression during differentiation

Transient induction of the chromatin remodeling protein ING4 (day 8–10), and its subsequent drop (after day 12), is required for proper luminal cell differentiation [14]. Constitutive ING4 expression initially accelerates suprabasal cell formation, but ultimately induces luminal cell death. Given that loss of CREB1 phenocopies ING4 overexpression (see Fig. 2G), we investigated whether CREB1 is responsible for the normal downregulation of ING4. ING4 protein is transiently elevated between days 8 and 12 of differentiation, and CREB1 activity peaks at the time ING4 declines (Fig. 3A). Knockdown of CREB1 in the PrECs leads to increased levels of ING4 protein (Fig. 3B, C) and mRNA expression (Fig. 3D). Thus, CREB1 is required to limit the duration of ING4 expression to prevent induction of luminal cell death.

PTEN controls CREB1 activation and differentiation

Expression of PTEN, which suppresses CREB1 activity [10] and whose downregulation is required for AKT-dependent survival of the luminal cells [5], is elevated early in differentiation. On the other hand, PTEN drops at day 12 of differentiation, prior to ING4 loss and CREB1 activation, and is lowest in the suprabasal cells at Day 14, when active CREB1 is the highest (Fig. 3A), suggesting PTEN may control CREB1 activity. Indeed, knockdown of PTEN is sufficient to induce robust induction of nuclear-localized activated pCREB1 (Fig. 3G). Moreover, loss of PTEN suppressed PrEC differentiation (Supplementary Fig. S3C). Thus, the loss of PTEN in suprabasal cells may contribute to the timing of CREB1 activation and downregulation of ING4 required for nascent luminal cell survival.

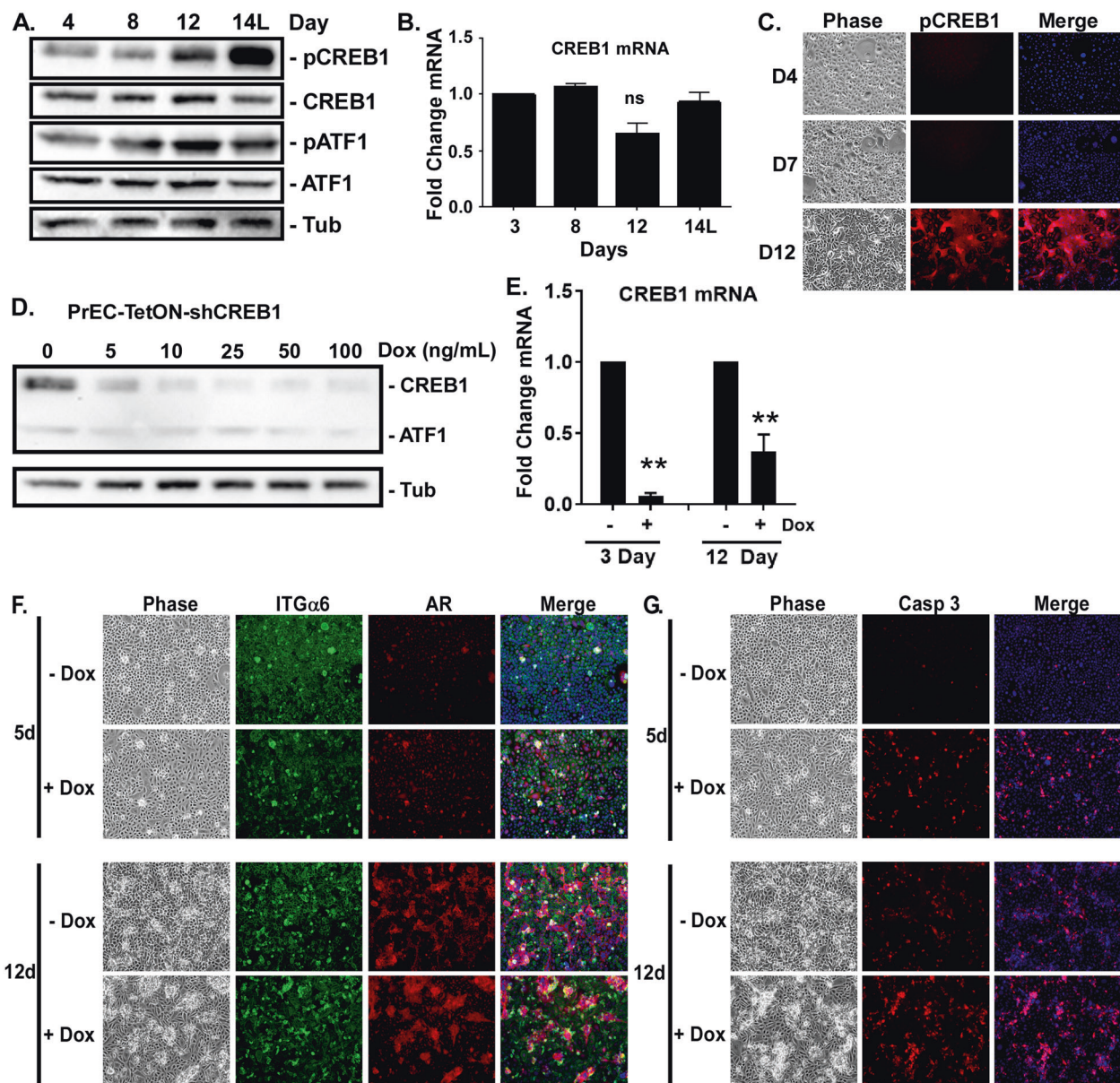


Fig. 2 CREB1 is required for luminal cell survival. Confluent PrECs were induced to differentiate with 2 ng/ml KGF plus 5 nM R1881 for 3–14 days. ‘L’ indicates only the luminal cells were analyzed. **A** Total CREB1, ATF1, and activated levels, i.e., phosphorylation at Ser 133 (pCREB1, pATF1), measured by immunoblotting. Tubulin (Tub) served as loading control. **B** Levels of CREB1 mRNA measured by qRT-PCR. **C** Differentiated cultures immunostained with anti-pCREB (Ser133) antibody and DNA counterstained with Hoescht (Merge) and imaged by phase or fluorescence microscopy. **D, E** Dox concentration required to suppress CREB1 protein and mRNA

expression in PrECs expressing Tet-inducible shRNA (PrEC-TetON-shCREB1) assessed by **(D)** immunoblotting at Day 12 and **(E)** qRT-PCR at Day 3 and 12, $**p < 0.01$; $n = 3$; error bars SD. **F, G** PrEC-TetON-shCREB1 cells induced to differentiate for 5 or 12 days in the absence (-Dox) or presence (+Dox) of 25 ng/ml doxycycline. Cultures immunostained for integrin $\alpha 6$ (ITG $\alpha 6$, basal marker), AR (luminal marker), cleaved caspase 3 (Casp 3), and DNA counterstained with Hoescht (Merge) imaged by phase contrast and fluorescence microscopy.

Chromatin immunoprecipitation (ChIP) at day 3 (low ING4) and at day 10 (high ING4) detected CREB1 constitutively bound to a CRE half site (CRE1) in the ING4 promoter, while CREB1 was inducibly bound to the second full CRE site (CRE2) at day 10 (Fig. 3E). Since CREB1 binding is dictated by open chromatin [29] and ING4 influences chromatin state

[15], we repeated the ChIP in ING4 overexpressing cells. Overexpression of ING4 is sufficient to enrich CREB1 binding to the full CRE at day 3 (Fig. 3F). CREB1 was not enriched at the Histone H3 gene. These data suggest ING4 is required for CREB1 binding to the CRE2 in the ING4 promoter and suppresses its own transcription.

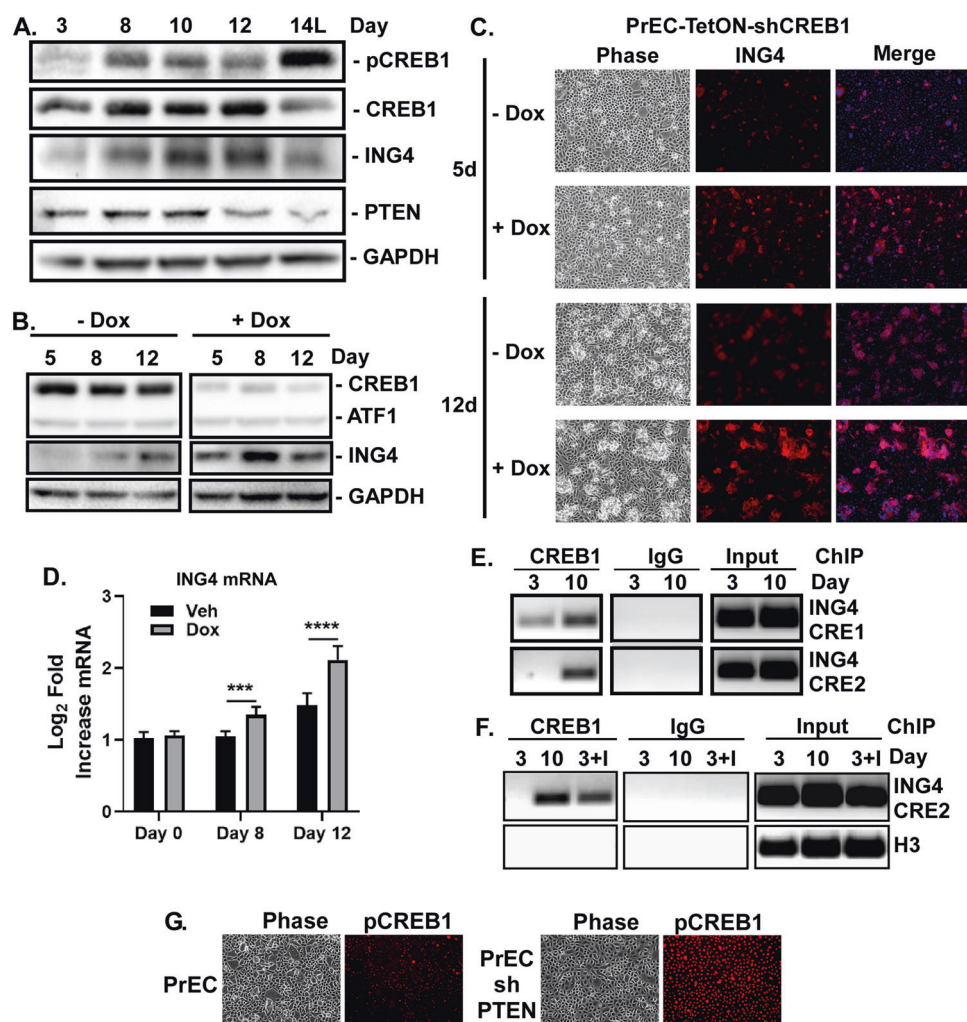


Fig. 3 CREB1 limits ING4 expression during differentiation. Confluent PrECs induced to differentiate with 2 ng/mL KGF and 5 nM R1881 for 3–14 days. ‘L’ indicates only the luminal cells were analyzed. **A** Levels of pCREB1, CREB1, ING4, and PTEN during differentiation measured by immunoblotting. GAPDH served as loading control. **B, C** PrEC-TetON-shCREB1 cells differentiated 5–12 days with (+Dox) or without (-Dox) 25 ng/ml doxycycline. **B** CREB1, ATF1, and ING4 expression measured by immunoblotting. **C** Differentiated cultures immunostained for ING4, nuclei counterstained with

Hoescht (Merge), and imaged by phase and fluorescence microscopy. **D** Log₂-fold expression of ING4 mRNA in PrEC-TetON-shCREB1 cells treated with (Dox) or without (Veh) doxycycline measured by qRT-PCR and normalized to day 0. *** $p < 0.005$; **** $p < 0.001$; $n = 4$; error bars SD. **E** ChIP of CREB1 at day 3 or 10 of differentiation vs. IgG control. Enrichment of CREB1 binding at two CRE elements in the ING4 promoter. **F** ChIP of CREB1 at day 3 or 10 of differentiation or day 3 of differentiation with cells overexpressing ING4 (I). **G** Immunostaining of PrEC and PrEC-shPTEN for pCREB1.

ING4 E3 Ligase JFK is a target of CREB1 and ING4

ING4 protein levels are regulated by ubiquitination via the E3 ligase JFK [30]. We detected increased expression of JFK mRNA during differentiation (Fig. 4A). We found CREB1 to be constitutively associated with the CRE element in the JFK promoter, but not at a non-CRE site (Fig. 4B). In addition, low levels of ING4 were enriched at the JFK transcription initiation site at day 3, and more binding was observed at day 10 when ING4 levels increase. Overexpression of ING4 resulted in more binding at day 3 (Fig. 4C). Finally, knockdown of CREB1 leads to a reduction in JFK mRNA at the time when CREB1 activity peaks

(Fig. 4D). Thus, ING4 and CREB1 appear to work cooperatively to increase JFK expression to coordinate the timing of ING4 destruction during differentiation.

CREB1 targets different genes upon oncogenic transformation

Overexpression of ERG (E), MYC (M), and shPTEN (P) in PrECs (EMP cells) is sufficient to generate tumors when cells are injected orthotopically into mice [14]. EMP cells fail to form a suprabasal layer, fail to fully differentiate into luminal cells, and co-express both basal and luminal markers [14]. EMP cells ‘differentiated’ for 0–17 days were

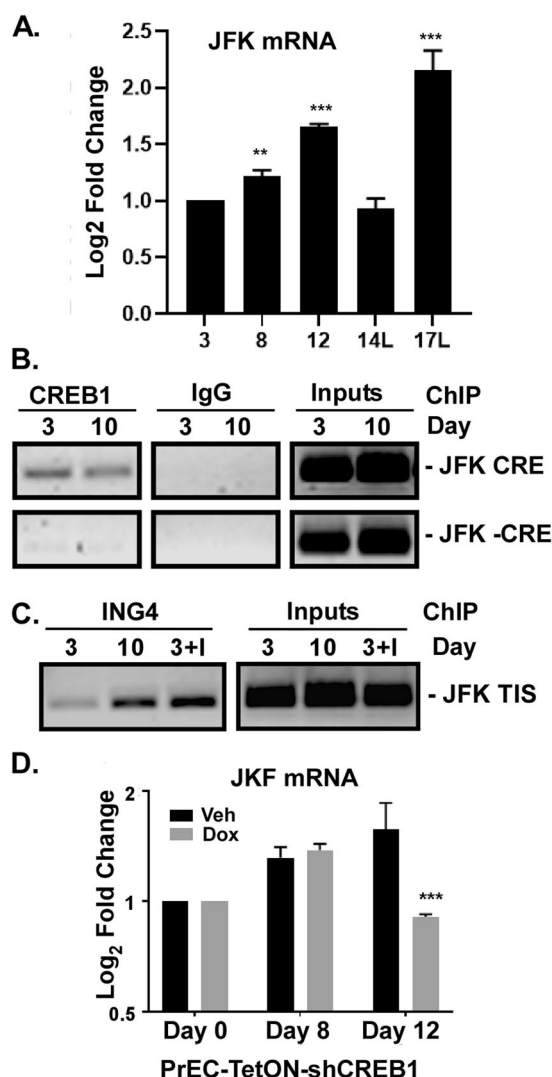


Fig. 4 ING4 E3 Ligase JFK is a target of CREB1 and ING4. **A** JFK mRNA levels during differentiation measured by qRT-PCR. **B** ChIP of CREB1 on the CRE (+CRE) or non-CRE region (–CRE) of the JFK promoter. **C** ChIP of ING4 at the transcriptional initiation site (TIS) of the JFK promoter at day 3 or 10 post differentiation or at day 3 in cells overexpressing ING4 (I). **D** Log₂-fold expression of JFK mRNA in PrEC-TetON-shCREB1 cells treated with (Dox) or without (Veh) doxycycline measured by qRT-PCR and normalized to Day 0. ** $p < 0.01$; *** $p < 0.001$; $n = 4$; error bars SD.

subjected to the same RNA sequencing protocol as normal PrECs. Over 1700 genes were significantly (FDR adjusted $p < 0.05$) differentially expressed compared to normal basal PrECs (GSE77460) (Fig. 5A). Pathway analysis indicates enrichment of genes involved in RNA metabolism, cell death, proliferation, transcription, motility/wounding, and morphogenesis (Supplementary Fig. S1, Table S4, S5). Surprisingly, a CREB1 signature was present in the tumor cells throughout the entire time course (Fig. 5B). CREB1 is predicted to regulate ~25% of the differentially expressed genes (Supplementary Table S6). The CREB1-regulated

genes in PrEC suprabasal cells, when compared with the CREB1-regulated genes in EMP cells, are largely non-overlapping (Fig. 5C, D).

Immunoblot analysis of CREB1 activity in EMPs subjected to the differentiation protocol showed sustained constitutive CREB1 activity throughout compared to PrECs differentiated for 3 or 10 days (Fig. 5E, F). In addition, pCREB was highly elevated in EMP prostate tumor xenografts (Fig. 5G). Differential expression of predicted CREB1 targets *GATA2*, *TWIST1*, *NND* (Necdin, tumor suppressor), and *PPM1F* (CAMK Phosphatase) seen by RNA-Seq (Fig. 5H, I), were validated by qRT-PCR (Fig. 5H, I). Levels of TWIST1 and GATA2 protein were elevated in EMP cells relative to normal PrECs (Fig. 5J). CREB1 targets BLIMP1 and CLDN1, induced during differentiation in PrECs, were not induced in the EMP cells (Fig. 5K).

PTEN loss correlates with ING4 loss

ING4 expression is reduced or lost in a subset of primary prostate tumors and loss of PTEN leads to loss of ING4 in vitro [14]. To assess the relationship between PTEN and ING4 loss and pCREB1, a tissue microarray, consisting of 81 primary tumors and 48 adjacent normal tissues, was scored for pCREB1, ING4, PTEN, and AR expression (Fig. 6A). We found that ~50% of the tumors had higher levels of pCREB1 relative to normal tissue. Over 35% of the tumors in this array had low ING4 expression and 47% had low PTEN. We found that 80% of the tumors with low ING4 also had low PTEN (Fig. 6B), suggesting loss of PTEN contributes to loss of ING4 in primary tumors. We were unable to detect a relationship between activated CREB1 and ING4 or PTEN. We attribute this in part to the high CREB1 activity present in normal tissues (Fig. 6C).

Loss of CREB1 in tumorigenic cells rescues luminal cell differentiation and suppresses tumor growth

To determine if loss of CREB1 in the tumor cells could rescue the defect in EMP differentiation, we induced knockdown of CREB1 in the EMP cells (Fig. 7A). Knockdown of CREB1 did not affect expression of oncogenic ERG, MYC, or shPTEN (Fig. 7B). Untreated EMP cells failed to properly differentiate as seen by the lack of a suprabasal layer compared to normal PrECs (Fig. 7C). Dox-induced suppression of CREB1 lead to re-induction of the suprabasal layer (Fig. 7C). However, as seen in normal PrECs, these suprabasal cells appeared stressed and had elevated caspase activity (Fig. 7D). The induced suprabasal cells are luminal, as indicated by exclusive expression of K18 and PSA and loss of p64, compared to EMP cells, which co-express both luminal and basal markers

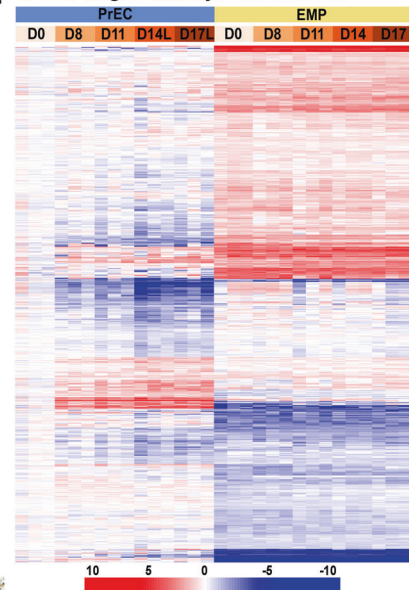
A. RNA-Seq: tumor EMP vs normal PrEC

Days	Tumor Cells	# of genes
0	x	1287
8	x	1526
11	x	1137
14	x	1173
17	x	1708

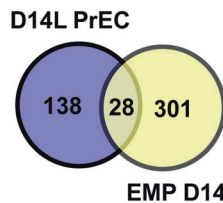
B. Predicted Transcription Factor Pathways

day8		day11		day14		day17	
Txf	# of genes	Txf	# of genes	Txf	# of genes	Txf	# of genes
CREB1	394	CREB1	308	CREB1	329	CREB1	468
Myc	247	Myc	169	Myc	185	Myc	266
SP1	165	SP1	141	SP1	152	SP1	198
p53	153	GCRa	103	p53	105	p53	148
ESR1	146	ESR1	99	ESR1	101	ESR1	148

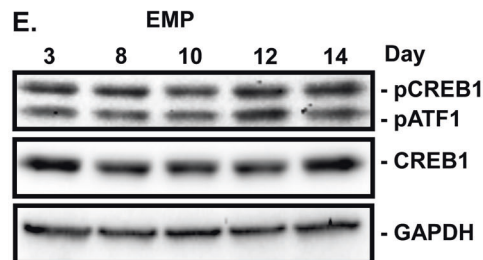
C. CREB1 Target Pathways - PrEC vs EMP



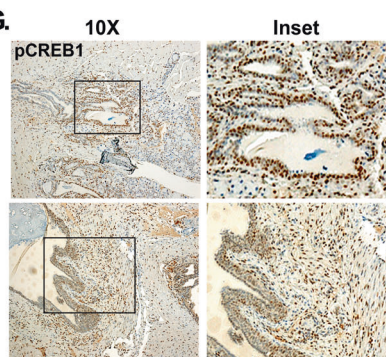
D.



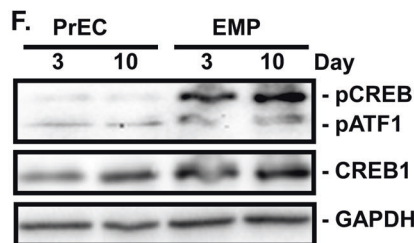
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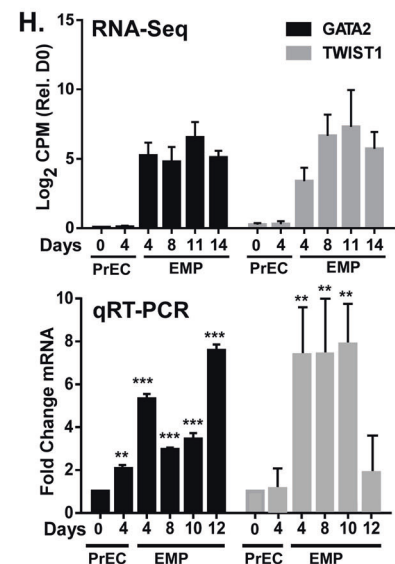
G.



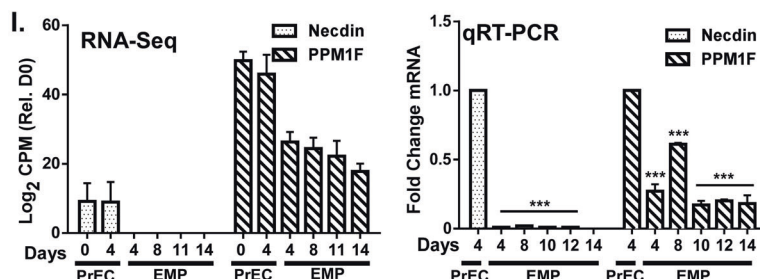
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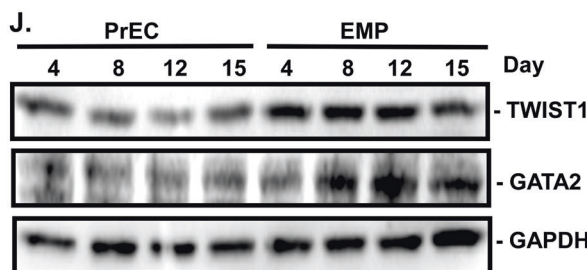
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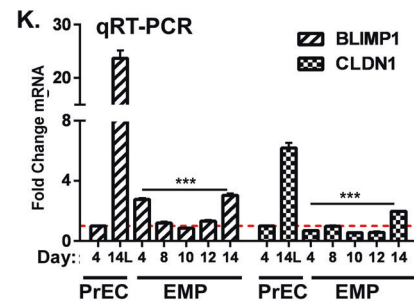
I.



J.



K.



(Supplementary Fig. S4). Thus, inhibiting CREB1 in the tumor cells restores the differentiation phenotype, but since CREB1 is required for luminal cell survival, the luminal cells cannot persist. Inhibiting CREB1 expression in EMP cells also suppressed tumor growth in vivo (Fig. 7E). In

contrast, suppression of ATF1 expression in EMP cells did not rescue suprabasal induction. As seen in normal PrECs (see Fig. S3B), loss of ATF1 in EMP cells also lead to increased AR expression in non-suprabasal cells (Supplementary Fig. S5A, B).

Fig. 5 CREB1 targets different genes upon oncogenic transformation. EMP cells (PrEC overexpressing ERG (E), MYC (M), and shPTEN (P)) subjected to the differentiation protocol for 0–17 days. RNA sequencing was performed on biological triplicates in parallel with PrECs (Fig. 1). Differentially expressed genes with $p < 0.05$ at each time point relative to normal basal cells were identified. **A** Metacore analysis of transcription factors (Tfx) likely involved in regulating differentially expressed genes. **B** Top 5 Tfx shown for each time point and the number of genes regulated by that Tfx are indicated. **C** Heat map comparing CREB1-regulated genes in PrECs vs. EMP cells. **D** Comparison of CREB1-regulated genes from Day 14 luminal (L) PrECs vs. EMP cells. **E, F** Levels of pCREB1 and pATF1 (Ser133), CREB1, and ATF1 measured by immunoblotting during differentiation in (E) EMP or (F) EMP vs. PrEC. GAPDH served as loading control. **G** IHC staining of pCREB1 in two EMP orthotopic xenograft tumors. **H, I** Transcript counts from RNA-seq (log2 CPM) and qRT-PCR mRNA levels (log2 fold change) of EMP CREB1-specific target genes: (H) *GATA2* and *TWIST1*, and (I) *NDN* (Necdin) and *PPM1F*. **J** Levels of *TWIST1* and *GATA2* in differentiating PrEC vs. EMP measured by immunoblotting. **K** Levels of *PMDR1* (BLIMP1) and *CLDN1* mRNA measured by qRT-PCR from differentiating PrEC vs. EMP. ** $p < 0.01$; *** $p < 0.001$; $n = 4$; error bars SD relative to PrEC.

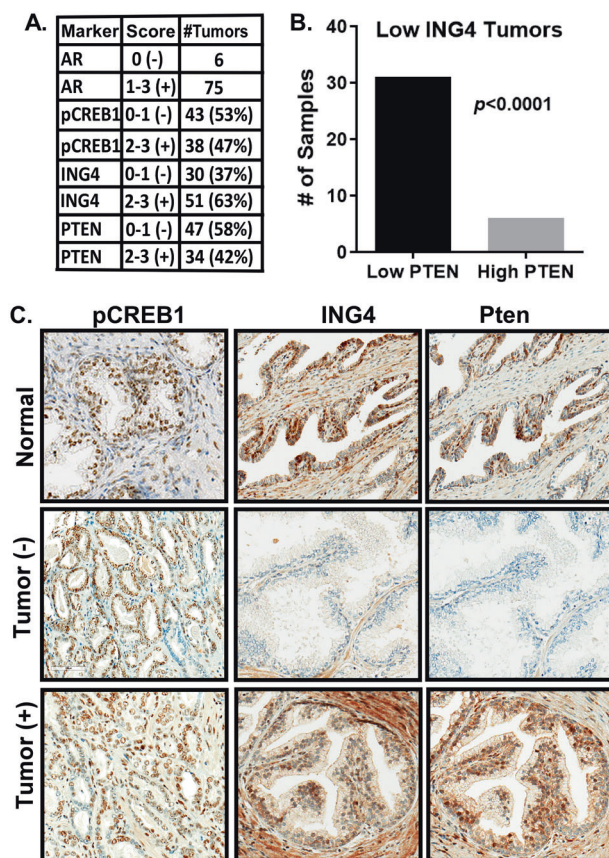


Fig. 6 ING4 loss is associated with PTEN loss. A TMA containing 81 tumors and 48 adjacent normal samples was interrogated by IHC for the expression of AR, pCREB1, ING4, and PTEN. **A** Levels of expression of each indicated marker in the tumor samples. 0–1 scored as negative, 2–3 scored as positive. **B** Fisher test demonstrating the association between low ING4 and low PTEN. *** $p < 0.0001$. **C** Representative IHC images.

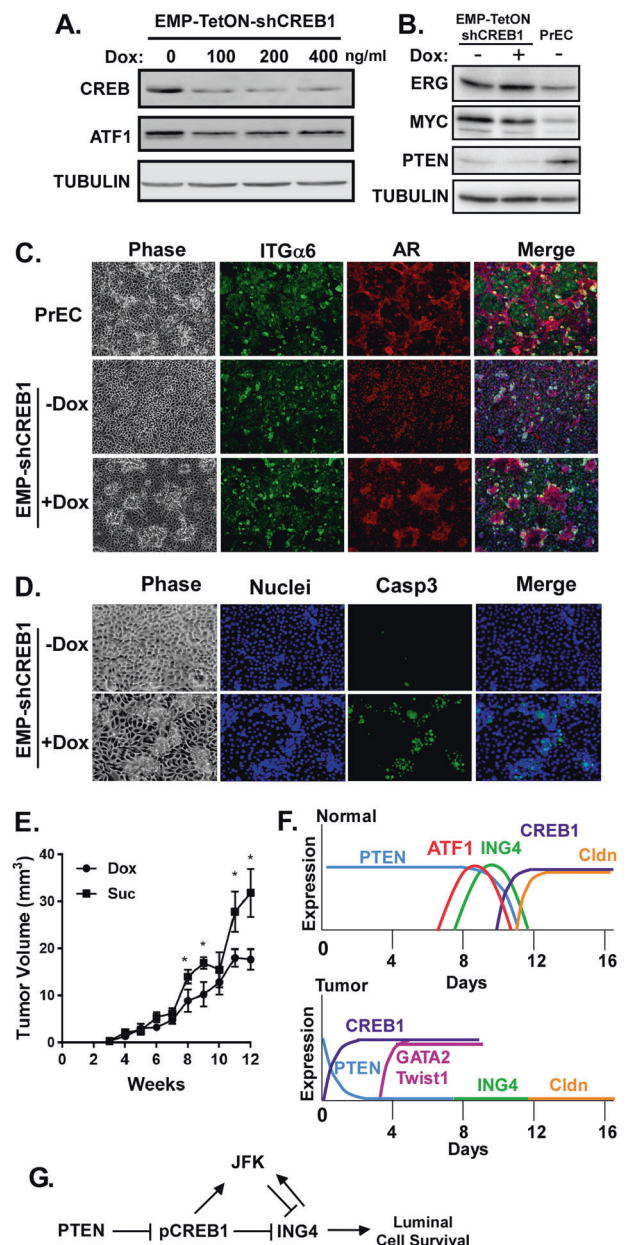


Fig. 7 CREB1 suppresses luminal cell differentiation in tumorigenic EMP cells. **A** Doxycycline concentration required to knock-down CREB1 in EMP-TetON-shCREB1 cells. **B** Validation of ERG, MYC, and PTEN expression in tumorigenic EMP cells relative to normal PrEC by immunoblotting. **C, D** EMP-TetON-shCREB1 cells differentiated for 12 days with (+Dox) or without (–Dox) 100 ng/ml doxycycline. Untreated 12-day differentiated PrECs were included as a control. Cultures were immunostained for (C) integrin $\alpha 6$ (ITG $\alpha 6$, basal marker) and AR (luminal marker) or (D) cleaved caspase 3 (Casp3) and counterstained with Hoechst (Merge), and imaged by phase or fluorescence microscopy. **E** Growth of EMP-TetON-shCREB1 orthotopic tumors in SCID mice treated with (Dox) or without (Suc) doxycycline. * $p < 0.05$; $n = 6$; error bars SD. **F** Models for how PTEN influences CREB1 activation and ING4 expression dynamics in normal (PrEC) vs. tumor (EMP) cells. **G** Pathways by which PTEN and CREB1 control ING4 expression.

Discussion

Previous studies demonstrated the importance of ING4, MYC, Miz1, and p38-MAPK in normal human prostate luminal cell differentiation [1, 14, 24]. Transient induction of ING4 is required for luminal cell differentiation and its loss leads to MYC-driven prostate tumorigenesis [14]. One objective of the current study was to uncover the molecular mechanisms that regulate transient ING4 expression during luminal cell differentiation. Using RNA-Seq analysis, we identified CREB1 as a major transcriptional driver of gene expression in suprabasal luminal cells. CREB1 is activated via phosphorylation late in differentiation. Knockdown of CREB1 does not suppress luminal cell formation, but the new luminal cells cannot survive, indicating CREB1 is required for luminal cell survival and maintenance. Generation of these short-lived luminal cells by CREB1 loss, phenocopies what is seen upon overexpression of ING4 [14]. Correspondingly, we observe an increase in both ING4 protein and mRNA in differentiating cells in which CREB1 is missing, and these cells ultimately die. Thus, the role of activated CREB1 is to limit the duration of ING4 expression (Fig. 7F). CREB1 does this by two mechanisms, through repression of ING4 mRNA transcription and transcriptional induction of the ING4 E3 ligase, JFK (Fig. 7G).

In addition to controlling ING4 expression, we identified a set of genes whose expression is regulated during differentiation and potentially controlled by CREB1. We validated that the CREB1 targets BLIMP1, PLK2, and CLDN1 mRNA and proteins are highly upregulated in suprabasal cells. BLIMP-1 is known to play a fundamental role in embryonic development in many organisms [31]. Epidermal terminal differentiation in the mouse depends on BLIMP1 protein expression in the granular layer of keratinocytes, the most differentiated corneocyte precursors [32]. PLK2 belongs to the polo family of serine/threonine protein kinases involved in normal cell division. In contrast to the role of PLK1 in promoting proliferation, PLK2 activity is associated with loss of proliferation. Recently a study identified PLK2 as a coordinator of early lineage commitment of cardiac progenitor cells [33].

Claudin1, a protein well known for its role in promoting cell-cell adhesion through tight junctions, is expressed in numerous epithelia [34]. Changes in claudin expression are part of a larger program of epithelial differentiation in the gut [34, 35]. There is a threefold increase in E-cadherin expression, another cell-cell adhesion protein, during luminal cell differentiation [5]. Increased cell-cell adhesion is required for survival of the new luminal cells, mediated by E-cadherin-dependent induction of PI3K [5]. The RNA-Seq data also identified cell adhesion molecules as a major set of enriched genes during differentiation. These data suggest that CREB1 not only promotes survival of the

luminal cells by suppressing ING4, but may also enhance expression of cell-cell adhesion proteins required for survival.

CREB1 is crucial for neuronal survival and morphological maturation [36–38]. CREB has also been found to be involved in odontogenic differentiation of dental pulp stem cells [39], osteoclast differentiation [40], and mesoderm-derived embryonic stem cells [41]. In the above reports, a p38-dependent CREB signaling pathway is the most common axis involved. p38-MAPK is required for luminal cell differentiation, where in cooperation with MYC, it induces Notch3 [1]. Further investigation is required to establish whether p38 is also involved in setting up the CREB1 and ING4 interaction.

The most unexpected finding from these studies, is that CREB target genes are also induced upon oncogenic conversion of PrEC. However, the CREB signature in tumor cells is highly distinct from the differentiation signature, and includes genes such as GATA2 and TWIST1, which are associated with prostate cancer progression. While aberrant CREB1 expression has been demonstrated for several cancers, including hematopoietic malignancies [42], non-small cell lung cancer, glioblastoma [43], breast cancer [44], and melanoma [45], very little has been investigated in prostate cancer. A previous report indicated that activated CREB1 is elevated in prostate cancer cell lines [46], and a more recent study identified a CREB1/FoxA1 signature in patient samples associated with pro-survival, cell cycle, and metabolic transcription programs in prostate cancer [21].

Here we demonstrate that the loss of PTEN is sufficient to activate CREB1, a known target of AKT, which is known to phosphorylate and activate CREB1. We found that PTEN is normally elevated in basal cells, which limits AKT activation, but drops during luminal cell differentiation, coincident with the peak in ING4 expression, but prior to CREB1 activation (Fig. 7F). PTEN appears to be responsible for setting the timing for when ING4 expression is suppressed. Once PTEN levels drop, then CREB1 is activated, which in turn suppresses ING4 (Fig. 7G). However, during oncogenic transformation via PTEN loss, CREB1 is activated prematurely, which prevents ING4 induction, because CREB1's normal role is to suppress ING4 expression. Thus, ING4-dependent luminal cell differentiation cannot occur when CREB1 is activated too early in differentiation by high Akt levels due to PTEN loss (Fig. 7F).

ING4 is a tumor suppressor and forms a four-subunit histone acetylation complex containing ING4, HBO1, hEaf6, JADE1/2/3 paralogs [47]. When ING4 associates with HBO1 it prefers acetylation of H4 but also targets H3 to a lesser extent [47, 48]. The transient induction of ING4 during basal to luminal differentiation hints toward a possible role for ING4 in loosening of chromatin structure by

acetylation of H4/H3 residues to allow transcription of genes required for the commitment to terminal differentiation [49, 50]. Interestingly, CREB1 is not activated until after ING4 is induced. CREB1 only binds open chromatin, suggesting that chromatin rearrangements, due in part to ING4, could open new binding sites for CREB1. This is supported by our findings that overexpression of ING4 results in induced CREB1 binding to the CRE site in ING4. This could explain the distinct difference in CREB1 targets activated late in differentiation, vs. those that are activated early under oncogenic conditions. The failure to induce ING4 in the context of PTEN loss might prevent chromatin rearrangement and deny CREB1 access to terminal-differentiation genes. This would prevent permanent exit from mitosis and allow for oncogenesis.

We are the first to demonstrate an association between loss of ING4 and loss of PTEN in primary human prostate cancer. We did not see a correlation with high levels of pCREB1 and low PTEN or low ING4. This is likely due to the high levels of pCREB1 present in the luminal cells of the normal prostate, making it difficult to reliably distinguish normal from cancer tissues based solely on this marker. We would expect to see a better correlation if we were to interrogate some of the cancer-specific CREB1 targets rather than pCREB1 itself. Our ongoing studies are aimed at determining the role of the CREB1 targets in prostate cancer development.

Materials and methods

Cell lines

Primary basal PrEC isolated from clinical prostatectomies, as previously described [51, 52], were immortalized as a pool with retroviruses expressing HPV E6/E7 and hTert [14]. Cultures were routinely tested for Mycoplasma and validated to be derived from prostate basal cells by STR. Oncogenic EMP cells were generated by stably overexpressing Erg (E), MYC (M), and shPTEN (P) as previously described and maintained in 2.0 µg/ml puromycin [14]. Tet-inducible lentiviral shRNAs targeting CREB1 and ATF1 were used to generate PrEC-TetON-shCREB1, PrEC-TetON-shATF1, EMP-TetON-shCREB1, and EMP-TetON-shATF1 cells, which were selected and maintained in 2.0 µg/ml puromycin (PrECs), 200 µg/ml hygromycin (EMP-shCREB1), or 5 µg/ml blasticidin (EMP-shATF1). Non-inducible shRNA targeting PTEN was used to generate PrEC-shPTEN cells, which were selected and maintained in 2.0 µg/ml puromycin. All lines were maintained in Keratinocyte Serum-Free Media (1X)/ (KSFM) (Gibco/Thermo Fisher Scientific) supplemented with bovine pituitary extract and epidermal growth factor as previously described [14, 51, 52].

Differentiation protocol

Each cell line, grown to confluency, were treated in complete growth medium containing 2–5 ng/ml keratinocyte growth factor (KGF) (Cell Sciences) and 5 nM R1881 (PerkinElmer) every other day for up to 17 days. For genetic and biochemical analysis, the differentiated suprabasal layer was separated from the basal layer at days 14 or 17 as previously described [5].

Constructs

pLKO-TetON-shCREB1 and shATF1 vectors were generated by subcloning validated sequences (Supplementary Table S7) from the TRC shRNA library (Broad Institute) into the lentiviral EZ-Tet-pLKO-Puro, EZ-Tet-pLKO-Hygro, or EZ-Tet-pLKO-Blast vectors [53]. pLKO-shPTEN was generated by subcloning sequences complementary to the 3'-UTR of PTEN into a lentiviral vector pLKO.1-puro as previously described [14, 53].

Virus generation and infection

Lentiviral shRNAs were generated by co-transfecting HEK293FT cells with shRNA vector and packaging plasmids as previously described [53]. Virus was harvested 3 days later and immediately used to infect cells.

Antibodies

Immunofluorescence and IHC: AR (C-19) and p63 (BC4A4) were purchased from Santa Cruz. ITGα6 (GoH3) was purchased from BD Pharmingen, ING4 polyclonal antibody was purchased from ProteinTech. K18 (CY-90) came from Sigma and K5/14 (HMW-34βE12/M0630) from DAKO. (pCREB/pATF1-Ser 133(87G3), CREB (D76D11), cleaved Caspase3 (Asp175)(5A1E), PSA (D11E1), and PTEN (138G6) were purchased from Cell Signaling Technology. *Immunoblotting:* ING4 (EP3804) and ATF1 (EPR1590) antibodies were purchased from Abcam. pCREB-Ser 133(87G3), CREB (D76D11) and PTEN (138G6) were purchased from Cell Signaling Technology. Tubulin antibody (DM1A) was purchased from Sigma and GAPDH (6CS) from Millipore. *Chromatin Immunoprecipitations:* ING4 (EP3804) was purchased from Abcam and CREB (D76D11) was purchased from Cell Signaling.

Immunofluorescent microscopy

Differentiated cultures were fixed in 4% paraformaldehyde for 30 min, neutralized with 1 M glycine, and permeabilized with 0.2% Triton-X 100 for 5 min and immunostained as previously described [14]. Coverslips were mounted using

Fluoromount-G (Southern Biotech). Images were acquired on a Nikon Eclipse TE300 fluorescence microscope using OpenLab v5.5.0 image analysis software (Improvision).

Immunohistochemistry

Paraffin-embedded and formalin fixed tissues were processed for IHC staining using automated immunostaining (Ventana Discovery XT). Tissue Microarray (TMA-47) containing 81 tumors and 48 adjacent normal tissues were stained for AR, pCREB, ING4, and PTEN. TMA staining was scored manually by two blinded individuals with IHC assigned to each core as composite scores of 0, 1, 2, or 3 with 0–1 representing complete to major loss of protein, and 2–3 near normal to wild-type levels.

Immunoblotting

Total cell lysates were prepared for immunoblotting as previously described after lysing in RIPA buffer [51]. PVDF membranes were blocked in 5% BSA in TBST overnight at 4 °C then probed with primary antibody, and HRP-conjugated secondary antibodies (Bio-Rad). Signals were visualized by chemiluminescence reagent with a CCD camera in a Bio-Rad Chemi-Doc Imaging System using Quantity One software v4.5.2 (Bio-Rad).

RT-PCR

Total RNA was isolated using Life Technology's RNeasy PureLink Kit. RNA was purified with RNase-free DNase and RNeasy PureLink Mini Kits. For qRT-PCR, 0.5 µg RNA was reversed transcribed using a reverse transcription system (Promega). Synthesized cDNA was amplified for qRT-PCR using SYBR green master mix (Roche) with gene-specific primers and an ABI 7500 RT-PCR system (Applied Biosystems). Gene expression was normalized to 18S rRNA by the 2-ΔΔCt method [54]. Primers for target genes are listed in Supplementary Table S8.

RNA-sequencing

Biological triplicates of PrECs were differentiated for 0, 4, 8, 11, 14, and 17 days. Suprabasal cells on days 14 and 17 were detached from basal cells prior to RNA extraction. Total RNA was isolated using Life Technologies RNeasy kit. RNA was purified using Life Technologies Purelink RNA mini kit. TruSeq mRNA libraries were prepared for sequencing using standard Illumina protocols from PolyA-enriched RNA. Samples were sequenced using Illumina RNAseq as single reads at 50 bp and ~30 M reads per sample. Sequenced reads were mapped to the hg19 whole genome using the Subread aligner (v1.4.3). Reads were

assigned to genes using featureCounts. Raw read counts were voom transformed and differential expression performed using limma. Differentially expressed genes with an FDR adjusted $p < 0.05$ ($n = 3$) and their expression levels were uploaded into the web-based Metacore program. Since samples from Day 4, 8, and 11 are a mixture of basal and luminal cells, we did not set a fold change cut off, as some of these may not be false positives. Gene lists were analyzed using MetaCore's Pathway Enrichment and Transcription Factors one-click analysis and the transcriptional regulation network algorithm. Access to data:

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?token=utahcoigpdubpcj&acc=GSE77460>

Chromatin immunoprecipitation (ChIP)

Cells (3.0×10^6) were fixed in 1% formaldehyde (Thermo Scientific) for 1 min and washed three times with ice cold calcium-magnesium free PBS (CMF-PBS) supplemented with protease inhibitors: pepstatin, aprotinin, leupeptin, and phenylmethylsulfonyl. Cells were scraped and pelleted at 2000 rpm for 8 min at 4 °C. Pellet was resuspended in swelling buffer (5 mM PIPES pH 8.0, 85 mM KCl, 0.5% IGEPAL), and incubated on ice for 30 min. Nuclei were dounce homogenized and then pelleted at 4000 rpm for 10 min, 4 °C. Nuclei were resuspended in sonication buffer (0.1% SDS, 10 mM EDTA, 50 mM Tris-HCl pH 8.1) and incubated on ice for 10 min prior to sonication. Chromatin was sheared at 4 °C using the Covaris E220 Ultra Sonicator following manufacturer's suggested settings of 2% Duty Cycle, 105-Watt Peak Intensity, 200 Cycles/Burst. Chromatin was sonicated for 10 min to achieve 300–500 bp fragments.

Chromatin immunoprecipitations (ChIP) were performed with 1 million cells/IP using magnetic beads (NEB). Chromatin was incubated with 6 mg appropriate antibody overnight at 4 °C with rotation. Following incubation, magnetic beads blocked with 1% BSA supplemented with 10 mg/ml salmon sperm, were added to samples and incubated at 4 °C with rotation for 6 h. Following immunoprecipitations, beads were washed in the following buffers at 4 °C for 10 min with rotation: Triton Wash Buffer (50 mM Tris-HCl pH 7.4, 150 mM NaCl, 1% Triton X-100), followed by Lysis Buffer 500 (0.1% NaDOC, 1 mM EDTA, 50 mM HEPES pH 7.5, 500 mM NaCl, 1% Triton X-100), LiCl Detergent buffer (0.5% NaDOC, 1 mM EDTA, 250 mM LiCl, 0.5% IGEPAL, 10 mM Tris-HCl pH 8.1), and Tris-EDTA pH 8.1. Chromatin was eluted from beads in Elution Buffer (10 mM EDTA, 1% SDS, Tris-HCl pH 8.0) for 30 min at 65 °C. Samples were then treated with 20 mg proteinase K, and 10 mg RNase A, and NaCl (200 mM) was added and incubated at 65 °C overnight to reverse cross-links. DNA was purified using phenol/

chloroform extraction followed by ethanol precipitation. Primers (Supplementary Table S9) were designed referencing the UCSC Genome Browser to determine the transcriptional start sites and locations of CRE sites within ING4 and JFK promoters.

Tumor studies

1×10^6 Tet-inducible EMP-shCREB1 cells were injected orthotopically into male SCID mice at 8 weeks of age. Two days after tumor injection 6 mice each were randomly placed into 2 cohorts; controls were fed 5% glucose in their drinking water, and induced mice were given 2 mg/ml doxycycline in 5% glucose. Tumors growth was blindly measured by palpitation and caliper weekly for 12 weeks. All mouse studies were conducted according to an IACUC approved protocol.

Statistical analyses

TMA analysis: Two-tailed Fishers exact test was used to determine co-occurrence between high pCREB, low PTEN, and low ING4. Power was based on previously published results for ING4 IHC [14]. **Tumor studies:** Tumor volumes for each cohort, $n = 6$, was averaged and 2-way Nova used to calculate statistical significance, which was set at $p < 0.05$. Power was based on previously published results [14]. **qRT-PCR:** Biological triplicates were averaged and statistical significance determined by unpaired student *T* test.

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Compliance with ethical standards

Conflict of interest The authors declare no competing interests.

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translational_gene_name	description	pvalue	FoldChange
SERPINB3	serpin family B member 3 [Source:HGNC Symbol;Acc:HGNC:10569]	2.74E-05	-2.868223232
CREB1	cAMP responsive element binding protein 1 [Source:HGNC Symbol;Acc:HGNC:2345]	1.36E-05	-2.822293039
TMPRSS11E	transmembrane serine protease 11E [Source:HGNC Symbol;Acc:HGNC:24465]	1.17E-08	-2.58064193
MECR	mitochondrial trans-2-enoyl-CoA reductase [Source:HGNC Symbol;Acc:HGNC:19691]	3.67E-38	-2.457434359
SFXN3	sideroflexin 3 [Source:HGNC Symbol;Acc:HGNC:16087]	7.24E-17	-2.302823792
SLC45A1	solute carrier family 45 member 1 [Source:HGNC Symbol;Acc:HGNC:17939]	0.00012	-2.289019408
CAB39	calcium binding protein 39 [Source:HGNC Symbol;Acc:HGNC:20292]	8.73E-36	-2.236193095
SNPH	syntaphilin [Source:HGNC Symbol;Acc:HGNC:15931]	4.69E-15	-2.208820855
CWH43	cell wall biogenesis 43 C-terminal homolog [Source:HGNC Symbol;Acc:HGNC:26133]	4.17E-05	-2.130783044
G3BP1	G3BP stress granule assembly factor 1 [Source:HGNC Symbol;Acc:HGNC:30292]	3.55E-32	-2.126215147
TUBB2A	tubulin beta 2A class IIa [Source:HGNC Symbol;Acc:HGNC:12412]	3.51E-08	-2.071499586
B4GALT6	beta-1,4-galactosyltransferase 6 [Source:HGNC Symbol;Acc:HGNC:929]	1.37E-05	-2.060545974
PSMA1	proteasome 20S subunit alpha 1 [Source:HGNC Symbol;Acc:HGNC:9530]	5.26E-07	-2.011241166
VIM	vimentin [Source:HGNC Symbol;Acc:HGNC:12692]	1.68E-06	-1.982319027
SLC2A10	solute carrier family 2 member 10 [Source:HGNC Symbol;Acc:HGNC:13444]	4.55E-05	-1.959082932
GYS1	glycogen synthase 1 [Source:HGNC Symbol;Acc:HGNC:4706]	0.000177	-1.957742387
CAMK2B	calcium/calmodulin dependent protein kinase II beta [Source:HGNC Symbol;Acc:HGNC:1461]	9.07E-05	-1.948844688
ETV1	ETS variant transcription factor 1 [Source:HGNC Symbol;Acc:HGNC:3490]	9.06E-09	-1.923755153
NUAK1	NUAK family kinase 1 [Source:HGNC Symbol;Acc:HGNC:14311]	0.59E-11	-1.919269565
PCYT1B	phosphate cytidylyltransferase 1, choline, beta [Source:HGNC Symbol;Acc:HGNC:8755]	0.000161	-1.904895138
ATF7	activating transcription factor 7 [Source:HGNC Symbol;Acc:HGNC:792]	1.62E-14	-1.902457514
JAK3	Janus kinase 3 [Source:HGNC Symbol;Acc:HGNC:6193]	5.46E-07	-1.901562797
MAP1B	microtubule associated protein 1B [Source:HGNC Symbol;Acc:HGNC:6836]	2.51E-09	-1.831207875
ARL15	ADP ribosylation factor like GTPase 15 [Source:HGNC Symbol;Acc:HGNC:25945]	7.81E-15	-1.841168777
CEMIP	cell migration inducing hyaluronidase 1 [Source:HGNC Symbol;Acc:HGNC:29213]	6.02E-05	-1.800550981
DEPTOR	DEP domain containing MTOR interacting protein [Source:HGNC Symbol;Acc:HGNC:22953]	1.85E-05	-1.783519994
CYP27B1	cytochrome P450 family 27 subfamily B member 1 [Source:HGNC Symbol;Acc:HGNC:2606]	8.50E-12	-1.777551669
VANGL2	VANGL planar cell polarity protein 2 [Source:HGNC Symbol;Acc:HGNC:15511]	5.10E-06	-1.771561463
FZD10	frizzled class receptor 10 [Source:HGNC Symbol;Acc:HGNC:4039]	8.57E-05	-1.769152802
PUDP	pseudouridine 5'-phosphatase [Source:HGNC Symbol;Acc:HGNC:16818]	1.44E-16	-1.754579894
SLC2A3	solute carrier family 2 member 3 [Source:HGNC Symbol;Acc:HGNC:11007]	1.25E-11	-1.712613183
USP44	ubiquitin specific peptidase 44 [Source:HGNC Symbol;Acc:HGNC:20064]	0.000203	-1.702227745
CCNA2	cyclin A2 [Source:HGNC Symbol;Acc:HGNC:1578]	6.89E-18	-1.68127208
PDSS1	decaprenyl diphosphate synthase subunit 1 [Source:HGNC Symbol;Acc:HGNC:17759]	2.95E-15	-1.661227712
RNRM2B	ribonucleotide reductase regulatory TP53 inducible subunit M2B [Source:HGNC Symbol;Acc:HGNC:1	7.15E-15	-1.658821886
HSBP1	heat shock factor binding protein 1 [Source:HGNC Symbol;Acc:HGNC:5203]	0.000363	-1.633958115
VWDE	von Willebrand factor D and EGF domains [Source:HGNC Symbol;Acc:HGNC:21897]	0.00028	-1.629631427
GPSM1	G protein signaling modulator 1 [Source:HGNC Symbol;Acc:HGNC:17858]	3.93E-05	-1.595918784
TNDC5	thioredoxin domain containing 5 [Source:HGNC Symbol;Acc:HGNC:21073]	0.000253	-1.589502219
RPS6KA2	ribosomal protein S6 kinase A2 [Source:HGNC Symbol;Acc:HGNC:10431]	3.33E-05	-1.58786411
AGK	acylglycerol kinase [Source:HGNC Symbol;Acc:HGNC:21869]	2.52E-06	-1.586291088
NKIRAS1	NFKB inhibitor interacting Ras like 1 [Source:HGNC Symbol;Acc:HGNC:17899]	7.83E-05	-1.58394871
AHR	aryl hydrocarbon receptor [Source:HGNC Symbol;Acc:HGNC:348]	2.75E-05	-1.580778133
RNF38	ring finger protein 38 [Source:HGNC Symbol;Acc:HGNC:18052]	3.86E-10	-1.57318565
ALDH3B2	aldehyde dehydrogenase 3 family member B2 [Source:HGNC Symbol;Acc:HGNC:411]	0.000718	-1.57242624
RASIP1	Ras interacting protein 1 [Source:HGNC Symbol;Acc:HGNC:24716]	2.44E-06	-1.565314561
LYSMD3	LysM domain containing 3 [Source:HGNC Symbol;Acc:HGNC:26969]	4.63E-06	-1.558757132
PANX2	pannexin 2 [Source:HGNC Symbol;Acc:HGNC:8600]	9.25E-06	-1.55098023
KANK1	KN motif and ankyrin repeat domains 1 [Source:HGNC Symbol;Acc:HGNC:19309]	5.51E-11	-1.55000527
JAG1	jagged canonical Notch ligand 1 [Source:HGNC Symbol;Acc:HGNC:6188]	1.06E-13	-1.547283354
ENTPD3	ectonucleoside triphosphate diphosphohydrolase 3 [Source:HGNC Symbol;Acc:HGNC:3365]	0.000674	-1.544415961
HOBX8	homeobox B9 [Source:HGNC Symbol;Acc:HGNC:5120]	1.74E-07	-1.53280339
ERO1A	endoplasmic reticulum oxidoreductase 1 alpha [Source:HGNC Symbol;Acc:HGNC:13280]	8.60E-16	-1.532628385
SNTA1	syntrophin alpha 1 [Source:HGNC Symbol;Acc:HGNC:11167]	5.63E-10	-1.527173594
SGPP1	sphingosine-1-phosphate phosphatase 1 [Source:HGNC Symbol;Acc:HGNC:17720]	4.18E-08	-1.519869591
SEZ6L2	seizure related 6 homolog like 2 [Source:HGNC Symbol;Acc:HGNC:30844]	2.38E-08	-1.514437019
INO80C	INO80 complex subunit C [Source:HGNC Symbol;Acc:HGNC:26994]	0.000872	-1.508121837
SHROOM4	shroom family member 4 [Source:HGNC Symbol;Acc:HGNC:29215]	0.000344	-1.505095414
ADAM9	ADAM metallopeptidase domain 9 [Source:HGNC Symbol;Acc:HGNC:216]	4.06E-05	-1.504893099
MTX3	metaxin 3 [Source:HGNC Symbol;Acc:HGNC:24812]	0.000109	-1.503455955
MAGED1	MAGE family member D1 [Source:HGNC Symbol;Acc:HGNC:6813]	6.50E-08	-1.50283286
SLC16A1	solute carrier family 16 member 1 [Source:HGNC Symbol;Acc:HGNC:10922]	4.04E-17	-1.49881725
RAB3D	RAB3D, member RAS oncogene family [Source:HGNC Symbol;Acc:HGNC:9779]	0.000445	-1.49564684
ERN1	endoplasmic reticulum to nucleus signaling 1 [Source:HGNC Symbol;Acc:HGNC:3449]	6.79E-07	-1.492207803
CSPG4	chondroitin sulfate proteoglycan 4 [Source:HGNC Symbol;Acc:HGNC:2466]	0.000151	-1.486568331
F11R	F11 receptor [Source:HGNC Symbol;Acc:HGNC:14685]	0.000137	-1.486547783
TXNRD1	thioredoxin reductase 1 [Source:HGNC Symbol;Acc:HGNC:12437]	9.02E-05	-1.484933503
SMAD9	SMAD family member 9 [Source:HGNC Symbol;Acc:HGNC:6774]	2.64E-07	-1.481310534
ZNF367	zinc finger protein 367 [Source:HGNC Symbol;Acc:HGNC:18320]	7.41E-09	-1.482148118
CAPZA1	capping actin protein of muscle Z-line subunit alpha 1 [Source:HGNC Symbol;Acc:HGNC:1488]	3.72E-06	-1.478674489
PIK3CD	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit delta [Source:HGNC Symbol;Acc:HGNC:1000514]	0.000514	-1.473677301
ARF3	ADP ribosylation factor 3 [Source:HGNC Symbol;Acc:HGNC:654]	1.34E-05	-1.473130573
BTBD9	BTB domain containing 9 [Source:HGNC Symbol;Acc:HGNC:21228]	4.10E-08	-1.466348009
PRKCH	protein kinase C eta [Source:HGNC Symbol;Acc:HGNC:9403]	3.98E-09	-1.463716744
UGT8	UDP glucosyltransferase 8 [Source:HGNC Symbol;Acc:HGNC:12555]	1.76E-05	-1.462587364
GORASP1	golgi reassembly stacking protein 1 [Source:HGNC Symbol;Acc:HGNC:16769]	2.98E-08	-1.449698011
NOM1	nucleolar protein with MIF4G domain 1 [Source:HGNC Symbol;Acc:HGNC:13244]	8.39E-05	-1.447911577
ZNF793	zinc finger protein 793 [Source:HGNC Symbol;Acc:HGNC:33115]	0.000307	-1.447187011
NEK6	NIMA related kinase 6 [Source:HGNC Symbol;Acc:HGNC:7749]	4.65E-10	-1.444347205
DCHS2	dachsous cadherin-related 2 [Source:HGNC Symbol;Acc:HGNC:23111]	0.000216	-1.43239031
PCED1B	PC-esterase domain containing 1B [Source:HGNC Symbol;Acc:HGNC:28255]	0.00015	-1.431074779
TNXB	tenascin XB [Source:HGNC Symbol;Acc:HGNC:11976]	0.000724	-1.424611408
ARMCX2	armadillo repeat containing X-linked 2 [Source:HGNC Symbol;Acc:HGNC:16869]	3.94E-06	-1.420184345
GALNT2	polypeptide N-acetylgalactosaminyltransferase 2 [Source:HGNC Symbol;Acc:HGNC:4124]	5.14E-05	-1.412626831
LATS1	large tumor suppressor kinase 1 [Source:HGNC Symbol;Acc:HGNC:6514]	1.08E-08	-1.407315401
ATAD2B	ATPase family AAA domain containing 2B [Source:HGNC Symbol;Acc:HGNC:29230]	4.91E-06	-1.403993651
RTL8C	retrotransposon Gag like 8C [Source:HGNC Symbol;Acc:HGNC:2569]	0.000651	-1.402090952
TNC	tenascin C [Source:HGNC Symbol;Acc:HGNC:5318]	0.0001	-1.401315221
THRB	thyroid hormone receptor beta [Source:HGNC Symbol;Acc:HGNC:11799]	0.000525	-1.396711761
NECTIN1	nectin cell adhesion molecule 1 [Source:HGNC Symbol;Acc:HGNC:9706]	0.000168	-1.394130521
SLC27A1	solute carrier family 27 member 1 [Source:HGNC Symbol;Acc:HGNC:10995]	0.000353	-1.393613644
NBR1	NBR1 autophagy cargo receptor [Source:HGNC Symbol;Acc:HGNC:6746]	9.17E-06	-1.392370488
PLPPR2	phospholipid phosphatase related 2 [Source:HGNC Symbol;Acc:HGNC:29566]	0.000364	-1.392164611
PYCR1	pyrroline-5-carboxylate reductase 1 [Source:HGNC Symbol;Acc:HGNC:9721]	1.19E-10	-1.388183894
VGf	VGf nerve growth factor inducible [Source:HGNC Symbol;Acc:HGNC:12684]	0.000507	-1.387960837
WDR44	WD repeat domain 44 [Source:HGNC Symbol;Acc:HGNC:30512]	4.69E-07	-1.386837792
PLIM5	PDZ and LIM domain 5 [Source:HGNC Symbol;Acc:HGNC:17468]	2.74E-08	-1.385660484
LPAR5	lysophosphatidic acid receptor 5 [Source:HGNC Symbol;Acc:HGNC:13307]	0.000522	-1.38286293
RAPH1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1 [Source:HGNC Symbol;Acc:HGNC:106E-07]	1.06E-07	-1.381752541
HDX	highly divergent homeobox [Source:HGNC Symbol;Acc:HGNC:26411]	0.000758	-1.37968453
TMEM164	transmembrane protein 164 [Source:HGNC Symbol;Acc:HGNC:26217]	2.35E-05	-1.376428769
MRC2	mannose receptor C type 2 [Source:HGNC Symbol;Acc:HGNC:16875]	0.000516	-1.372848003
MIA3	MIA SH3 domain ER export factor 3 [Source:HGNC Symbol;Acc:HGNC:24008]	9.90E-16	-1.372597826
USP33	ubiquitin specific peptidase 33 [Source:HGNC Symbol;Acc:HGNC:20059]	9.24E-05	-1.370582519
FAM160A1	family with sequence similarity 160 member A1 [Source:HGNC Symbol;Acc:HGNC:34237]	0.000304	-1.371403214
CDON	cell adhesion associated, oncogene regulated [Source:HGNC Symbol;Acc:HGNC:17104]	6.11E-05	-1.37124539
RHOBTB1	Rho related BTB domain containing 1 [Source:HGNC Symbol;Acc:HGNC:18738]	3.09E-05	-1.367084838
KHLH26	kelch like family member 26 [Source:HGNC Symbol;Acc:HGNC:25623]	3.97E-05	-1.364946681
KDM4B	lysine demethylase 4B [Source:HGNC Symbol;Acc:HGNC:29136]	0.000438	-1.362073783
EEF1AKMT3	EEF1A lysine methyltransferase 3 [Source:HGNC Symbol;Acc:HGNC:24936]	0.000717	-1.359295119
TCEAL3	transcription elongation factor A like 3 [Source:HGNC Symbol;Acc:HGNC:28247]	0.000869	-1.358334211
CDH13	cadherin 13 [Source:HGNC Symbol;Acc:HGNC:1753]	3.65E-06	-1.353843803
CCDC113	coiled-coil domain containing 113 [Source:HGNC Symbol;Acc:HGNC:25002]	0.000477	-1.352951055
ASMTL	acetylserotonin O-methyltransferase like [Source:HGNC Symbol;Acc:HGNC:751]	0.000127	-1.352195225
SEPTIN6	septin 6 [Source:HGNC Symbol;Acc:HGNC:15848]	7.75E-06	-1.352049209
EFNB1	ephrin B1 [Source:HGNC Symbol;Acc:HGNC:3226]	0.000204	-1.351987861
STAT6	signal transducer and activator of transcription 6 [Source:HGNC Symbol;Acc:HGNC:11368]	1.88E-11	-1.348637728
SUMF1	sumfate modifying factor 1 [Source:HGNC Symbol;Acc:HGNC:20376]	6.32E-05	-1.347843056
LRP12	LDL receptor related protein 12 [Source:HGNC Symbol;Acc:HGNC:31708]	0.000121	-1.343533274
SATB2	SATB homeobox 2 [Source:HGNC Symbol;Acc:HGNC:21637]	2.46E-05	-1.342789374
NYFA	nuclear transcription factor Y subunit alpha [Source:HGNC Symbol;Acc:HGNC:7804]	1.29E-05	-1.342692439
DYRK3	dual specificity tyrosine phosphorylation regulated kinase 3 [Source:HGNC Symbol;Acc:HGNC:3094]	0.000217	-1.338811449
CCDC92	coiled-coil domain containing 92 [Source:HGNC Symbol;Acc:HGNC:29563]	0.000529	-1.338700178
ZNF641	zinc finger protein 641 [Source:HGNC Symbol;Acc:HGNC:31834]	0.000109	-1.337666882
GOLGA2	golgin A2 [Source:HGNC Symbol;Acc:HGNC:4425]	4.02E-06	-1.333961719
KLF13	Kruppel like factor 13 [Source:HGNC Symbol;Acc:HGNC:13672]	4.46E-05	-1.333711281
WDR91	WD repeat domain 91 [Source:HGNC Symbol;Acc:HGNC:24997]	5.31E-05	-1.332788118
ETV4	ETS variant transcription factor 4 [Source:HGNC Symbol;Acc:HGNC:3493]	0.000104	-1.33238726
PIK3R4	phosphoinositide-3-kinase regulatory subunit 4 [Source:HGNC Symbol;Acc:HGNC:8982]	0.000587	-1.331798804
USP46	ubiquitin specific peptidase 46 [Source:HGNC Symbol;Acc:HGNC:20075]	2.56E-06	-1.325764137
STX10	syntaxin 10 [Source:HGNC Symbol;Acc:HGNC:11428]	1.10E-05	-1.325739973
MIGA1	mitoguardin 1 [Source:HGNC Symbol;Acc:HGNC:24741]	0.00043	-1.323819746
CALD1	caldesmon 1 [Source:HGNC Symbol;Acc:HGNC:1441]	8.71E-05	-1.322424106
FAR1	fatty acyl-CoA reductase 1 [Source:HGNC Symbol;Acc:HGNC:26222]	5.88E-05	-1.316810441
WDFY3	WD repeat and FYVE domain containing 3 [Source:HGNC Symbol;Acc:HGNC:20751]	0.000136	-1.315485623
FAM171A2	family with sequence similarity 171 member A2 [Source:HGNC Symbol;Acc:HGNC:30480]	0.000774	-1.314197931
SHC1	SHC adaptor protein 1 [Source:HGNC Symbol;Acc:HGNC:10840]	9.00E-07	-1.313479727
SLC13A3	solute carrier family 13 member 3 [Source:HGNC Symbol;Acc:HGNC:14430]	2.07E-09	-1.311986509
TADA3	transcriptional adaptor 3 [Source:HGNC Symbol;Acc:HGNC:19422]	0.000768	-1.307473444
SNX27	sorting nexin 27 [Source:HGNC Symbol;Acc:HGNC:20073]	0.000348	-1.306010138
TXNRD3	thioredoxin reductase 3 [Source:HGNC Symbol;Acc:HGNC:20667]	0.000361	-1.30092377
EPB41L4B	erythrocyte membrane protein band 4.1 like 4B [Source:HGNC Symbol;Acc:HGNC:19818]	0.000456	-1.300052297
BRWD3	bromodomain and WD repeat domain containing 3 [Source:HGNC Symbol;Acc:HGNC:17342]	0.000752	-1.299221196
EDTD10	potassium channel tetramerization domain containing 10 [Source:HGNC Symbol;Acc:HGNC:23236]	4.54E-14	-1.296557609
KDRF1	erythroid differentiation regulatory factor 1 [Source:HGNC Symbol;Acc:HGNC:24640]	0.00059	-1.295698218
TTC3	tetratricopeptide repeat domain 3 [Source:HGNC Symbol;Acc:HGNC:12393]	0.000144	-1.293083972
ZNF391	zinc finger protein 391 [Source:HGNC Symbol;Acc:HGNC:18779]	0.000561	-1.292308094
FKBP1A	FKBP prolyl isomerase 1A [Source:HGNC Symbol;Acc:HGNC:3711]	2.16E-05	-1.289567606
ICAM1	intercellular adhesion molecule 1 [Source:HGNC Symbol;Acc:HGNC:5344]	0.000283	-1.28658072
FBXW11	F-box and WD repeat domain containing 11 [Source:HGNC Symbol;Acc:HGNC:13607]	1.73E-05	-1.28405593
UBQLN2	ubiquilin 2 [Source:HGNC Symbol;Acc:HGNC:12509]	0.00016	-1.282808338
STXBP1	syntaxin binding protein 1 [Source:HGNC Symbol;Acc:HGNC:11444]	2.36E-05	-1.27999572
TLE4	TLE family member 4, transcriptional corepressor [Source:HGNC Symbol;Acc:HGNC:11840]	1.81E-05	-1.274794229
BICD2	BICD cargo adaptor 2 [Source:HGNC Symbol;Acc:HGNC:17208]	9.71E-05	-1.270686951
ZNF197	zinc finger protein 197 [Source:HGNC Symbol;Acc:HGNC:12988]	0.000207	-1.265041682
KLF5	Kruppel like factor 5 [Source:HGNC Symbol;Acc:HGNC:6349]	0.000724	-1.262132961
DNAJB11	DnaJ heat shock protein family (Hsp40) member B11 [Source:HGNC Symbol;Acc:HGNC:14889]	3.42E-05	-1.261168197
PITPNC1	phosphatidylinositol transfer protein cytoplasmic 1 [Source:HGNC Symbol;Acc:HGNC:21045]	0.000873	-1.255876655
LRP10	LDL receptor related protein 10 [Source:HGNC Symbol;Acc:HGNC:14553]	0.000207	-1.255644316
ST6GAL1	ST6 beta-galactoside alpha-2,6-sialyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:10860]	0.000422	-1.250452085
FBXW2	F-box and WD repeat domain containing 2 [Source:HGNC Symbol;Acc:HGNC:13608]	0.000232	-1.249887242
PTER	phosphatidylserine related [Source:HGNC Symbol;Acc:HGNC:9590]	4.47E-05	-1.23890173
STARSD7	STAR related lipid transfer domain containing 7 [Source:HGNC Symbol;Acc:HGNC:18063]	7.65E-06	-1.236179715
FAM120B	family with sequence similarity 120B [Source:HGNC Symbol;Acc:HGNC:21109]	0.000195	-1.233165932
NUMB	NUMB endocytic adaptor protein [Source:HGNC Symbol;Acc:HGNC:8060]	0.000668	-1.225426593
FKBP10	FKBP prolyl isomerase 10 [Source:HGNC Symbol;Acc:HGNC:18169]	1.31E-05	-1.224444385
SNRPD3	small nuclear ribonucleoprotein D3 polypeptide [Source:HGNC Symbol;Acc:HGNC:11160]	5.26E-06	-1.223363662
NFE2L1	nuclear factor, erythroid 2 like 1 [Source:HGNC Symbol;Acc:HGNC:7781]	0.000594	-1.220949613
UBE4A	ubiquitination factor E4A [Source:HGNC Symbol;Acc:HGNC:12499]	0.000736	-1.220393434
HSPA12A	heat shock protein family A (Hsp70) member 12A [Source:HGNC Symbol;Acc:HGNC:19022]	0.00061	-1.220438332
ARMCX3	armadillo repeat containing X-linked 3 [Source:HGNC Symbol;Acc:HGNC:24065]	3.40E-05	-1.219900814
RNPEP	arginyl aminopeptidase [Source:HGNC Symbol;Acc:HGNC:10078]	0.000476	-1.214301183
TF			

ATF targets	description	pvalue	FoldChange
AAAS	aladin WD repeat nucleoporin [Source:HGNC Symbol;Acc:HGNC:21051]	0.003528	-1.32627
AACS	acetoacetyl-CoA synthetase [Source:HGNC Symbol;Acc:HGNC:21052]	0.004883	-1.22448
AADAT	aminoadipate aminotransferase [Source:HGNC Symbol;Acc:HGNC:21053]	0.00884	-1.67989
ABCA13	ATP binding cassette subfamily A member 13 [Source:HGNC Symbol;Acc:HGNC:21054]	0.00679	-2.98596
ABCB8	ATP binding cassette subfamily B member 8 [Source:HGNC Symbol;Acc:HGNC:21055]	1.52E-06	-1.95473
ABCC4	ATP binding cassette subfamily C member 4 [Source:HGNC Symbol;Acc:HGNC:21056]	0.000263	-1.38091
ABCD3	ATP binding cassette subfamily D member 3 [Source:HGNC Symbol;Acc:HGNC:21057]	0.004894	-1.26808
ABCF2	ATP binding cassette subfamily F member 2 [Source:HGNC Symbol;Acc:HGNC:21058]	0.006395	-1.28265
ABCF3	ATP binding cassette subfamily F member 3 [Source:HGNC Symbol;Acc:HGNC:21059]	0.007549	-1.25685
ABCG2	ATP binding cassette subfamily G member 2 (Junior blood group) [Source:HGNC Symbol;Acc:HGNC:21060]	6.16E-07	-1.74546
ABHD17C	abhydrolase domain containing 17C [Source:HGNC Symbol;Acc:HGNC:21061]	0.011572	-1.18333
ABI2	abl interactor 2 [Source:HGNC Symbol;Acc:HGNC:24011]	0.004851	-1.14704
ABL2	ABL proto-oncogene 2, non-receptor tyrosine kinase [Source:HGNC Symbol;Acc:HGNC:24012]	3.00E-05	-1.51382
ABTB2	ankyrin repeat and BTB domain containing 2 [Source:HGNC Symbol;Acc:HGNC:24013]	0.001312	-2.19557
AC092835.1	novel C2H2 type zinc finger protein	0.007079	-1.9144
ACAD9	acyl-CoA dehydrogenase family member 9 [Source:HGNC Symbol;Acc:HGNC:24014]	0.002404	-1.66705
ACD	ACD shelterin complex subunit and telomerase recruitment factor [Source:HGNC Symbol;Acc:HGNC:24015]	0.002291	-1.32502
ACE	angiotensin I converting enzyme [Source:HGNC Symbol;Acc:HGNC:24016]	0.000329	-4.38244
ACIN1	apoptotic chromatin condensation inducer 1 [Source:HGNC Symbol;Acc:HGNC:24017]	0.008328	-1.52319
ACO1	aconitase 1 [Source:HGNC Symbol;Acc:HGNC:117]	2.10E-07	-1.37198
ACOT7	acyl-CoA thioesterase 7 [Source:HGNC Symbol;Acc:HGNC:24157]	0.000542	-1.2189
ACOXL	acyl-CoA oxidase like [Source:HGNC Symbol;Acc:HGNC:25621]	0.003548	-2.03816
ACSL4	acyl-CoA synthetase long chain family member 4 [Source:HGNC Symbol;Acc:HGNC:25622]	1.86E-11	-2.04557
ACTB	actin beta [Source:HGNC Symbol;Acc:HGNC:132]	0.00814	-1.38796
ACTN4	actinin alpha 4 [Source:HGNC Symbol;Acc:HGNC:166]	0.00935	-1.41652
ACTR2	actin related protein 2 [Source:HGNC Symbol;Acc:HGNC:169]	2.77E-07	-1.4936
ADAM10	ADAM metallopeptidase domain 10 [Source:HGNC Symbol;Acc:HGNC:24158]	9.97E-09	-1.719
ADAM11	ADAM metallopeptidase domain 11 [Source:HGNC Symbol;Acc:HGNC:24159]	0.003691	-2.87763
ADAM22	ADAM metallopeptidase domain 22 [Source:HGNC Symbol;Acc:HGNC:24160]	0.003665	-2.01424
ADAMTS12	ADAM metallopeptidase with thrombospondin type 1 motif 12 [Source:HGNC Symbol;Acc:HGNC:24161]	0.000702	-2.98156
ADAMTS6	ADAM metallopeptidase with thrombospondin type 1 motif 6 [Source:HGNC Symbol;Acc:HGNC:24162]	0.01028	-2.16276
ADAR	adenosine deaminase RNA specific [Source:HGNC Symbol;Acc:HGNC:24163]	0.003981	-1.34424
ADAT1	adenosine deaminase tRNA specific 1 [Source:HGNC Symbol;Acc:HGNC:24164]	0.007401	-1.60157
ADD1	adducin 1 [Source:HGNC Symbol;Acc:HGNC:243]	6.49E-05	-1.21612
ADGRB2	adhesion G protein-coupled receptor B2 [Source:HGNC Symbol;Acc:HGNC:24165]	0.008791	-2.11401
ADGRE2	adhesion G protein-coupled receptor E2 [Source:HGNC Symbol;Acc:HGNC:24166]	0.007145	-1.6042
ADGRG6	adhesion G protein-coupled receptor G6 [Source:HGNC Symbol;Acc:HGNC:24167]	0.003765	-1.25803
ADGRV1	adhesion G protein-coupled receptor V1 [Source:HGNC Symbol;Acc:HGNC:24168]	0.000684	-3.21798
ADO	2-aminoethanethiol dioxygenase [Source:HGNC Symbol;Acc:HGNC:24169]	1.89E-05	-1.31086
ADRA1B	adrenoceptor alpha 1B [Source:HGNC Symbol;Acc:HGNC:278]	0.003203	-4.34267
ADSS2	adenylosuccinate synthase 2 [Source:HGNC Symbol;Acc:HGNC:25623]	0.008937	-1.22507
AFAP1L2	actin filament associated protein 1 like 2 [Source:HGNC Symbol;Acc:HGNC:24170]	0.00437	-1.22406
AFG3L2	AFG3 like matrix AAA peptidase subunit 2 [Source:HGNC Symbol;Acc:HGNC:24171]	0.008813	-1.30781
AGAP2	ArfGAP with GTPase domain, ankyrin repeat and PH domain 2 [Source:HGNC Symbol;Acc:HGNC:24172]	0.004243	-2.97219
AGFG1	ArfGAP with FG repeats 1 [Source:HGNC Symbol;Acc:HGNC:5175]	0.000488	-1.17402
AGK	acylglycerol kinase [Source:HGNC Symbol;Acc:HGNC:21869]	0.003066	-1.35519

AGO4	argonaute RISC component 4 [Source:HGNC Symbol;Acc:HGNC:1	0.001526	-1.41666
AGPS	alkylglycerone phosphate synthase [Source:HGNC Symbol;Acc:HGNC:1	2.79E-05	-1.48797
AHCTF1	AT-hook containing transcription factor 1 [Source:HGNC Symbol;Acc:HGNC:1	0.002928	-1.26487
AHCYL1	adenosylhomocysteinase like 1 [Source:HGNC Symbol;Acc:HGNC:1	0.011582	-1.21231
AHI1	Abelson helper integration site 1 [Source:HGNC Symbol;Acc:HGNC:1	8.78E-05	-1.32793
AHR	aryl hydrocarbon receptor [Source:HGNC Symbol;Acc:HGNC:348]	4.72E-08	-1.8286
AIF1L	allograft inflammatory factor 1 like [Source:HGNC Symbol;Acc:HGNC:1	0.000142	-1.78976
AIFM1	apoptosis inducing factor mitochondria associated 1 [Source:HGNC:1	0.006076	-1.35758
AKAP11	A-kinase anchoring protein 11 [Source:HGNC Symbol;Acc:HGNC:3	0.001931	-1.42955
AKAP6	A-kinase anchoring protein 6 [Source:HGNC Symbol;Acc:HGNC:3	0.005354	-1.84494
AKAP7	A-kinase anchoring protein 7 [Source:HGNC Symbol;Acc:HGNC:3	0.008572	-1.39535
ALCAM	activated leukocyte cell adhesion molecule [Source:HGNC Symbo	0.007653	-1.20333
ALDH18A1	aldehyde dehydrogenase 18 family member A1 [Source:HGNC Sy	1.11E-07	-1.37809
ALDH1A3	aldehyde dehydrogenase 1 family member A3 [Source:HGNC Syn	0.00025	-2.83778
ALDH3B1	aldehyde dehydrogenase 3 family member B1 [Source:HGNC Syn	0.002013	-2.1327
ALDH5A1	aldehyde dehydrogenase 5 family member A1 [Source:HGNC Syn	5.60E-07	-2.22793
ALG3	ALG3 alpha-1,3- mannosyltransferase [Source:HGNC Symbol;Acc:	0.001996	-1.28661
ALKBH8	alkB homolog 8, tRNA methyltransferase [Source:HGNC Symbol;A	0.004067	-1.56375
ALMS1	ALMS1 centrosome and basal body associated protein [Source:Ho	3.10E-06	-2.01302
ALOX5AP	arachidonate 5-lipoxygenase activating protein [Source:HGNC Sy	0.002205	-4.77263
ALYREF	Aly/REF export factor [Source:HGNC Symbol;Acc:HGNC:19071]	0.003484	-1.35171
AMOTL2	angiomin like 2 [Source:HGNC Symbol;Acc:HGNC:17812]	0.006473	-1.71469
ANAPC7	anaphase promoting complex subunit 7 [Source:HGNC Symbol;A	6.10E-06	-1.19281
ANGEL1	angel homolog 1 [Source:HGNC Symbol;Acc:HGNC:19961]	0.00086	-1.39625
ANK1	ankyrin 1 [Source:HGNC Symbol;Acc:HGNC:492]	0.006184	-2.74841
ANKH	ANKH inorganic pyrophosphate transport regulator [Source:HGN	0.003118	-1.16995
ANKIB1	ankyrin repeat and IBR domain containing 1 [Source:HGNC Symb	0.004277	-1.21089
ANKRD1	ankyrin repeat domain 1 [Source:HGNC Symbol;Acc:HGNC:15819	0.006895	-3.47197
ANKRD13A	ankyrin repeat domain 13A [Source:HGNC Symbol;Acc:HGNC:212	8.94E-06	-1.56256
ANKRD18A	ankyrin repeat domain 18A [Source:HGNC Symbol;Acc:HGNC:236	0.000343	-1.65924
ANKRD18B	ankyrin repeat domain 18B [Source:HGNC Symbol;Acc:HGNC:236	0.004707	-1.36034
ANKRD26	ankyrin repeat domain 26 [Source:HGNC Symbol;Acc:HGNC:2918	0.007579	-1.8451
ANKRD40	ankyrin repeat domain 40 [Source:HGNC Symbol;Acc:HGNC:2823	2.47E-05	-1.29832
ANKRD42	ankyrin repeat domain 42 [Source:HGNC Symbol;Acc:HGNC:2675	0.000901	-1.48115
ANKS6	ankyrin repeat and sterile alpha motif domain containing 6 [Sour	0.005207	-1.59422
ANLN	anillin actin binding protein [Source:HGNC Symbol;Acc:HGNC:14	2.68E-06	-1.75105
ANP32A	acidic nuclear phosphoprotein 32 family member A [Source:HGN	1.07E-06	-1.42298
ANP32B	acidic nuclear phosphoprotein 32 family member B [Source:HGN	8.49E-11	-1.26271
ANP32E	acidic nuclear phosphoprotein 32 family member E [Source:HGN	0.000421	-1.62082
ANPEP	alanyl aminopeptidase, membrane [Source:HGNC Symbol;Acc:HC	0.000333	-2.57909
ANTXR1	ANTXR cell adhesion molecule 1 [Source:HGNC Symbol;Acc:HGNC	1.14E-05	-1.87886
ANXA10	annexin A10 [Source:HGNC Symbol;Acc:HGNC:534]	0.00327	-4.74359
ANXA11	annexin A11 [Source:HGNC Symbol;Acc:HGNC:535]	0.000939	-1.76137
AP1S3	adaptor related protein complex 1 subunit sigma 3 [Source:HGNC	3.99E-06	-1.40024
AP2B1	adaptor related protein complex 2 subunit beta 1 [Source:HGNC	7.66E-16	-1.57825
AP3B1	adaptor related protein complex 3 subunit beta 1 [Source:HGNC	0.003602	-1.26193
AP3M1	adaptor related protein complex 3 subunit mu 1 [Source:HGNC S	1.06E-05	-1.28448

AP4E1	adaptor related protein complex 4 subunit epsilon 1 [Source:HGNC Symbol;Acc:HGNC:16665]	0.007849	-1.219
APLN	apelin [Source:HGNC Symbol;Acc:HGNC:16665]	0.005796	-1.62266
APLP1	amyloid beta precursor like protein 1 [Source:HGNC Symbol;Acc:HGNC:16665]	0.009362	-1.76111
APLP2	amyloid beta precursor like protein 2 [Source:HGNC Symbol;Acc:HGNC:16665]	6.03E-05	-1.36055
APOBEC3C	apolipoprotein B mRNA editing enzyme catalytic subunit 3C [Source:HGNC Symbol;Acc:HGNC:618]	0.002921	-1.29478
APOL1	apolipoprotein L1 [Source:HGNC Symbol;Acc:HGNC:618]	0.001982	-3.06831
APOL2	apolipoprotein L2 [Source:HGNC Symbol;Acc:HGNC:619]	0.001491	-1.86054
APOL6	apolipoprotein L6 [Source:HGNC Symbol;Acc:HGNC:14870]	0.004862	-1.46866
APP	amyloid beta precursor protein [Source:HGNC Symbol;Acc:HGNC:16665]	0.000509	-1.26023
APPL1	adaptor protein, phosphotyrosine interacting with PH domain and SH2 domain [Source:HGNC Symbol;Acc:HGNC:16665]	2.85E-21	-1.64382
APPL2	adaptor protein, phosphotyrosine interacting with PH domain and SH2 domain [Source:HGNC Symbol;Acc:HGNC:16665]	4.12E-06	-1.4825
AQR	aquarius intron-binding spliceosomal factor [Source:HGNC Symbol;Acc:HGNC:16665]	0.000712	-1.36561
ARFRP1	ADP ribosylation factor related protein 1 [Source:HGNC Symbol;Acc:HGNC:16665]	0.005022	-1.70301
ARGLU1	arginine and glutamate rich 1 [Source:HGNC Symbol;Acc:HGNC:24113]	0.004909	-1.40792
ARHGAP1	Rho GTPase activating protein 1 [Source:HGNC Symbol;Acc:HGNC:24113]	0.001199	-1.40777
ARHGAP10	Rho GTPase activating protein 10 [Source:HGNC Symbol;Acc:HGNC:24113]	0.001785	-1.2683
ARHGAP11A	Rho GTPase activating protein 11A [Source:HGNC Symbol;Acc:HGNC:24113]	3.29E-05	-1.99759
ARHGAP22	Rho GTPase activating protein 22 [Source:HGNC Symbol;Acc:HGNC:24113]	0.006589	-1.32911
ARHGAP26	Rho GTPase activating protein 26 [Source:HGNC Symbol;Acc:HGNC:24113]	0.000114	-3.40266
ARHGAP29	Rho GTPase activating protein 29 [Source:HGNC Symbol;Acc:HGNC:24113]	0.000421	-2.17004
ARHGAP39	Rho GTPase activating protein 39 [Source:HGNC Symbol;Acc:HGNC:24113]	0.003881	-1.75549
ARHGAP44	Rho GTPase activating protein 44 [Source:HGNC Symbol;Acc:HGNC:24113]	0.001199	-1.92934
ARHGAP5	Rho GTPase activating protein 5 [Source:HGNC Symbol;Acc:HGNC:24113]	0.007658	-1.21057
ARHGDIA	Rho GDP dissociation inhibitor alpha [Source:HGNC Symbol;Acc:HGNC:24113]	0.001942	-1.30834
ARHGEF26	Rho guanine nucleotide exchange factor 26 [Source:HGNC Symbol;Acc:HGNC:24113]	0.003656	-1.64256
ARHGEF39	Rho guanine nucleotide exchange factor 39 [Source:HGNC Symbol;Acc:HGNC:24113]	0.006297	-2.06382
ARHGEF40	Rho guanine nucleotide exchange factor 40 [Source:HGNC Symbol;Acc:HGNC:24113]	9.53E-05	-1.74438
ARID4A	AT-rich interaction domain 4A [Source:HGNC Symbol;Acc:HGNC:24113]	0.011705	-1.22733
ARL13B	ADP ribosylation factor like GTPase 13B [Source:HGNC Symbol;Acc:HGNC:24113]	0.001278	-1.24106
ARMC8	armadillo repeat containing 8 [Source:HGNC Symbol;Acc:HGNC:24113]	0.009337	-1.2173
ARMC9	armadillo repeat containing 9 [Source:HGNC Symbol;Acc:HGNC:24113]	0.00173	-1.248
ARNTL2	aryl hydrocarbon receptor nuclear translocator like 2 [Source:HGNC Symbol;Acc:HGNC:24113]	2.90E-05	-1.43298
ARPIN	actin related protein 2/3 complex inhibitor [Source:HGNC Symbol;Acc:HGNC:24113]	0.002036	-1.73852
ARSB	arylsulfatase B [Source:HGNC Symbol;Acc:HGNC:714]	0.006047	-1.69587
ASCC3	activating signal cointegrator 1 complex subunit 3 [Source:HGNC Symbol;Acc:HGNC:24113]	6.53E-05	-1.56806
ASF1B	anti-silencing function 1B histone chaperone [Source:HGNC Symbol;Acc:HGNC:24113]	4.98E-06	-1.88223
ASPH	aspartate beta-hydroxylase [Source:HGNC Symbol;Acc:HGNC:757]	1.59E-06	-1.42982
ASPM	abnormal spindle microtubule assembly [Source:HGNC Symbol;Acc:HGNC:24113]	0.009425	-1.62154
ATAD2	ATPase family AAA domain containing 2 [Source:HGNC Symbol;Acc:HGNC:24113]	4.89E-11	-1.49698
ATAD3A	ATPase family AAA domain containing 3A [Source:HGNC Symbol;Acc:HGNC:24113]	0.00855	-1.57023
ATAD5	ATPase family AAA domain containing 5 [Source:HGNC Symbol;Acc:HGNC:24113]	1.22E-06	-1.45929
ATF1	activating transcription factor 1 [Source:HGNC Symbol;Acc:HGNC:24113]	8.93E-15	-2.3063
ATIC	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase [Source:HGNC Symbol;Acc:HGNC:24113]	0.002343	-1.33159
ATMIN	ATM interactor [Source:HGNC Symbol;Acc:HGNC:29034]	0.002901	-1.14887
ATP11A	ATPase phospholipid transporting 11A [Source:HGNC Symbol;Acc:HGNC:24113]	0.006758	-1.87869
ATP11C	ATPase phospholipid transporting 11C [Source:HGNC Symbol;Acc:HGNC:24113]	0.000138	-1.68978
ATP13A3	ATPase 13A3 [Source:HGNC Symbol;Acc:HGNC:24113]	0.000402	-1.69955

ATP1B1	ATPase Na ⁺ /K ⁺ transporting subunit beta 1 [Source:HGNC Symbol;Acc:HGNC:100]	4.70E-06	-1.63391
ATP2C2	ATPase secretory pathway Ca ²⁺ transporting 2 [Source:HGNC Symbol;Acc:HGNC:100]	0.007664	-1.84708
ATP6V0E2	ATPase H ⁺ transporting V0 subunit e2 [Source:HGNC Symbol;Acc:HGNC:100]	0.002911	-1.59277
ATP7A	ATPase copper transporting alpha [Source:HGNC Symbol;Acc:HGNC:100]	0.001633	-1.46157
ATP8A1	ATPase phospholipid transporting 8A1 [Source:HGNC Symbol;Acc:HGNC:100]	0.000682	-2.04289
ATP9A	ATPase phospholipid transporting 9A (putative) [Source:HGNC Symbol;Acc:HGNC:100]	0.00455	-1.44451
ATR	ATR serine/threonine kinase [Source:HGNC Symbol;Acc:HGNC:88]	0.000373	-1.39062
AURKA	aurora kinase A [Source:HGNC Symbol;Acc:HGNC:11393]	0.001643	-1.28212
AURKB	aurora kinase B [Source:HGNC Symbol;Acc:HGNC:11390]	0.000821	-1.42978
AUTS2	activator of transcription and developmental regulator AUTS2 [Source:HGNC Symbol;Acc:HGNC:100]	0.00017	-1.88869
AVEN	apoptosis and caspase activation inhibitor [Source:HGNC Symbol;Acc:HGNC:100]	5.90E-39	-2.75436
AVL9	AVL9 cell migration associated [Source:HGNC Symbol;Acc:HGNC:100]	0.002263	-1.27561
AXL	AXL receptor tyrosine kinase [Source:HGNC Symbol;Acc:HGNC:90]	0.000649	-2.47588
B3GALNT2	beta-1,3-N-acetylgalactosaminyltransferase 2 [Source:HGNC Symbol;Acc:HGNC:202]	0.002588	-1.28414
B3GLCT	beta 3-glucosyltransferase [Source:HGNC Symbol;Acc:HGNC:202]	0.000103	-1.33695
B3GNT7	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7 [Source:HGNC Symbol;Acc:HGNC:202]	0.001399	-5.43609
B4GALNT1	beta-1,4-N-acetyl-galactosaminyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:202]	0.006975	-2.04433
B4GALT1	beta-1,4-galactosyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:100]	0.002061	-1.32132
B4GALT2	beta-1,4-galactosyltransferase 2 [Source:HGNC Symbol;Acc:HGNC:100]	0.002413	-1.20278
B4GALT5	beta-1,4-galactosyltransferase 5 [Source:HGNC Symbol;Acc:HGNC:100]	3.65E-08	-1.90472
BABAM2	BRISC and BRCA1 A complex member 2 [Source:HGNC Symbol;Acc:HGNC:100]	1.35E-10	-1.84
BACE2	beta-secretase 2 [Source:HGNC Symbol;Acc:HGNC:934]	2.74E-06	-1.27875
BAG3	BCL2 associated athanogene 3 [Source:HGNC Symbol;Acc:HGNC:100]	0.001447	-1.32633
BARD1	BRCA1 associated RING domain 1 [Source:HGNC Symbol;Acc:HGNC:100]	0.000418	-1.28233
BBS5	Bardet-Biedl syndrome 5 [Source:HGNC Symbol;Acc:HGNC:970]	0.001518	-1.6969
BCAR3	BCAR3 adaptor protein, NSP family member [Source:HGNC Symbol;Acc:HGNC:100]	0.000319	-1.46425
BCAT1	branched chain amino acid transaminase 1 [Source:HGNC Symbol;Acc:HGNC:100]	0.008576	-1.71046
BCKDK	branched chain keto acid dehydrogenase kinase [Source:HGNC Symbol;Acc:HGNC:100]	1.80E-05	-2.03751
BCLAF1	BCL2 associated transcription factor 1 [Source:HGNC Symbol;Acc:HGNC:100]	0.005847	-1.34432
BICC1	BicC family RNA binding protein 1 [Source:HGNC Symbol;Acc:HGNC:100]	0.000588	-2.63375
BICD1	BICD cargo adaptor 1 [Source:HGNC Symbol;Acc:HGNC:1049]	0.000287	-1.5113
BLM	BLM RecQ like helicase [Source:HGNC Symbol;Acc:HGNC:1058]	4.43E-05	-2.58031
BLMH	bleomycin hydrolase [Source:HGNC Symbol;Acc:HGNC:1059]	0.004539	-1.14335
BMP2K	BMP2 inducible kinase [Source:HGNC Symbol;Acc:HGNC:18041]	5.87E-06	-1.64707
BMPR2	bone morphogenetic protein receptor type 2 [Source:HGNC Symbol;Acc:HGNC:100]	0.004141	-1.19312
BNC1	basonuclin 1 [Source:HGNC Symbol;Acc:HGNC:1081]	0.008109	-1.29688
BRCA1	BRCA1 DNA repair associated [Source:HGNC Symbol;Acc:HGNC:100]	0.000129	-1.73047
BRCA2	BRCA2 DNA repair associated [Source:HGNC Symbol;Acc:HGNC:100]	0.000768	-1.80122
BRCC3	BRCA1/BRCA2-containing complex subunit 3 [Source:HGNC Symbol;Acc:HGNC:100]	0.000576	-1.57122
BRD7	bromodomain containing 7 [Source:HGNC Symbol;Acc:HGNC:143]	1.78E-05	-1.32273
BRD9	bromodomain containing 9 [Source:HGNC Symbol;Acc:HGNC:258]	0.005883	-1.65444
BRIP1	BRCA1 interacting protein C-terminal helicase 1 [Source:HGNC Symbol;Acc:HGNC:100]	2.11E-05	-2.13326
BRPF3	bromodomain and PHD finger containing 3 [Source:HGNC Symbol;Acc:HGNC:100]	0.007228	-1.43234
BUB1	BUB1 mitotic checkpoint serine/threonine kinase [Source:HGNC Symbol;Acc:HGNC:100]	8.58E-06	-1.4921
BUB1B	BUB1 mitotic checkpoint serine/threonine kinase B [Source:HGNC Symbol;Acc:HGNC:100]	3.96E-05	-1.9169
C1orf198	chromosome 1 open reading frame 198 [Source:HGNC Symbol;Acc:HGNC:100]	2.99E-05	-1.44121
C1orf56	chromosome 1 open reading frame 56 [Source:HGNC Symbol;Acc:HGNC:100]	0.007296	-1.60925

C2CD2	C2 calcium dependent domain containing 2 [Source:HGNC Symbol]	0.004626	-1.52412
C2CD4D	C2 calcium dependent domain containing 4D [Source:HGNC Symbol]	0.005861	-2.61221
C5	complement C5 [Source:HGNC Symbol;Acc:HGNC:1331]	9.49E-05	-1.58388
C9orf116	chromosome 9 open reading frame 116 [Source:HGNC Symbol;Acc:HGNC:1331]	0.001692	-1.86796
CABYR	calcium binding tyrosine phosphorylation regulated [Source:HGNC Symbol]	0.000108	-1.76385
CACHD1	cache domain containing 1 [Source:HGNC Symbol;Acc:HGNC:293]	0.000275	-2.03347
CAD	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, [Source:HGNC Symbol]	7.56E-06	-2.19563
CALD1	caldesmon 1 [Source:HGNC Symbol;Acc:HGNC:1441]	1.96E-05	-1.36361
CALHM2	calcium homeostasis modulator family member 2 [Source:HGNC Symbol]	1.75E-07	-2.01719
CALM3	calmodulin 3 [Source:HGNC Symbol;Acc:HGNC:1449]	0.001641	-1.21854
CALML4	calmodulin like 4 [Source:HGNC Symbol;Acc:HGNC:18445]	0.000993	-1.41687
CAMK2N2	calcium/calmodulin dependent protein kinase II inhibitor 2 [Source:HGNC Symbol]	0.005419	-2.2741
CAMK4	calcium/calmodulin dependent protein kinase IV [Source:HGNC Symbol]	4.05E-05	-1.35822
CAMKK2	calcium/calmodulin dependent protein kinase kinase 2 [Source:HGNC Symbol]	0.000541	-1.25203
CAMSAP2	calmodulin regulated spectrin associated protein family member [Source:HGNC Symbol]	0.000117	-1.32508
CAND1	cullin associated and neddylation dissociated 1 [Source:HGNC Symbol]	0.004617	-1.15692
CANT1	calcium activated nucleotidase 1 [Source:HGNC Symbol;Acc:HGNC:1449]	1.09E-05	-1.66881
CAPN2	calpain 2 [Source:HGNC Symbol;Acc:HGNC:1479]	6.78E-06	-1.27104
CAPNS1	calpain small subunit 1 [Source:HGNC Symbol;Acc:HGNC:1481]	2.99E-10	-1.22958
CAPRIN1	cell cycle associated protein 1 [Source:HGNC Symbol;Acc:HGNC:1449]	0.001205	-1.1602
CARD11	caspase recruitment domain family member 11 [Source:HGNC Symbol]	0.00312	-1.84555
CARD9	caspase recruitment domain family member 9 [Source:HGNC Symbol]	0.004082	-4.12707
CARMIL1	capping protein regulator and myosin 1 linker 1 [Source:HGNC Symbol]	0.010008	-1.27558
CARNMT1	carnosine N-methyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:1449]	0.005443	-1.20739
CASK	calcium/calmodulin dependent serine protein kinase [Source:HGNC Symbol]	0.008983	-1.26076
CASP2	caspase 2 [Source:HGNC Symbol;Acc:HGNC:1503]	0.000934	-1.56116
CASP7	caspase 7 [Source:HGNC Symbol;Acc:HGNC:1508]	0.000994	-1.46918
CASP8AP2	caspase 8 associated protein 2 [Source:HGNC Symbol;Acc:HGNC:1503]	5.04E-05	-1.40638
CAST	calpastatin [Source:HGNC Symbol;Acc:HGNC:1515]	1.12E-05	-1.25192
CAV1	caveolin 1 [Source:HGNC Symbol;Acc:HGNC:1527]	0.00255	-1.14097
CAVIN1	caveolae associated protein 1 [Source:HGNC Symbol;Acc:HGNC:1527]	0.007502	-1.61168
CBFB	core-binding factor subunit beta [Source:HGNC Symbol;Acc:HGNC:1527]	2.28E-10	-1.48865
CBX1	chromobox 1 [Source:HGNC Symbol;Acc:HGNC:1551]	0.000251	-1.2763
CCDC106	coiled-coil domain containing 106 [Source:HGNC Symbol;Acc:HGNC:1551]	0.005321	-1.29659
CCDC15	coiled-coil domain containing 15 [Source:HGNC Symbol;Acc:HGNC:1551]	0.001033	-1.60728
CCDC150	coiled-coil domain containing 150 [Source:HGNC Symbol;Acc:HGNC:1551]	0.000411	-2.47519
CCDC177	coiled-coil domain containing 177 [Source:HGNC Symbol;Acc:HGNC:1551]	0.005422	-3.1015
CCDC18	coiled-coil domain containing 18 [Source:HGNC Symbol;Acc:HGNC:1551]	0.007607	-1.71723
CCDC40	coiled-coil domain containing 40 [Source:HGNC Symbol;Acc:HGNC:1551]	0.002566	-2.30674
CCDC47	coiled-coil domain containing 47 [Source:HGNC Symbol;Acc:HGNC:1551]	9.96E-05	-1.29553
CCDC6	coiled-coil domain containing 6 [Source:HGNC Symbol;Acc:HGNC:1551]	3.14E-05	-1.32315
CCDC68	coiled-coil domain containing 68 [Source:HGNC Symbol;Acc:HGNC:1551]	0.003539	-1.55438
CCDC88A	coiled-coil domain containing 88A [Source:HGNC Symbol;Acc:HGNC:1551]	0.000475	-1.7413
CCDC96	coiled-coil domain containing 96 [Source:HGNC Symbol;Acc:HGNC:1551]	0.005656	-2.8048
CCN2	cellular communication network factor 2 [Source:HGNC Symbol;Acc:HGNC:1551]	0.001698	-2.85599
CCNB3	cyclin B3 [Source:HGNC Symbol;Acc:HGNC:18709]	0.006883	-2.75245
CCND1	cyclin D1 [Source:HGNC Symbol;Acc:HGNC:1582]	4.98E-05	-3.11003

CCNE1	cyclin E1 [Source:HGNC Symbol;Acc:HGNC:1589]	0.004096	-1.83631
CCNJ	cyclin J [Source:HGNC Symbol;Acc:HGNC:23434]	6.03E-05	-1.49098
CCNJL	cyclin J like [Source:HGNC Symbol;Acc:HGNC:25876]	0.005095	-1.8202
CCNK	cyclin K [Source:HGNC Symbol;Acc:HGNC:1596]	6.69E-06	-1.3227
CCNY	cyclin Y [Source:HGNC Symbol;Acc:HGNC:23354]	0.000275	-1.24827
CCP110	centriolar coiled-coil protein 110 [Source:HGNC Symbol;Acc:HGNC:23354]	0.000125	-1.34509
CCS	copper chaperone for superoxide dismutase [Source:HGNC Symbol;Acc:HGNC:23354]	0.00093	-1.25904
CD109	CD109 molecule [Source:HGNC Symbol;Acc:HGNC:21685]	0.001068	-1.26753
CD274	CD274 molecule [Source:HGNC Symbol;Acc:HGNC:17635]	2.06E-05	-3.19742
CD2AP	CD2 associated protein [Source:HGNC Symbol;Acc:HGNC:14258]	0.004347	-1.18848
CD320	CD320 molecule [Source:HGNC Symbol;Acc:HGNC:16692]	0.000266	-1.25465
CD44	CD44 molecule (Indian blood group) [Source:HGNC Symbol;Acc:HGNC:1712]	0.001589	-1.1519
CD83	CD83 molecule [Source:HGNC Symbol;Acc:HGNC:1703]	0.000443	-2.69674
CDA	cytidine deaminase [Source:HGNC Symbol;Acc:HGNC:1712]	0.00691	-1.17941
CDC20	cell division cycle 20 [Source:HGNC Symbol;Acc:HGNC:1723]	0.00125	-1.27658
CDC25A	cell division cycle 25A [Source:HGNC Symbol;Acc:HGNC:1725]	0.007115	-1.44814
CDC27	cell division cycle 27 [Source:HGNC Symbol;Acc:HGNC:1728]	0.001564	-1.21557
CDC37	cell division cycle 37 [Source:HGNC Symbol;Acc:HGNC:1735]	0.006063	-1.18396
CDC42BPA	CDC42 binding protein kinase alpha [Source:HGNC Symbol;Acc:HGNC:1739]	0.000471	-1.56301
CDC45	cell division cycle 45 [Source:HGNC Symbol;Acc:HGNC:1739]	0.00343	-1.4198
CDC5L	cell division cycle 5 like [Source:HGNC Symbol;Acc:HGNC:1743]	0.000187	-1.32087
CDC6	cell division cycle 6 [Source:HGNC Symbol;Acc:HGNC:1744]	7.18E-05	-1.39203
CDCA2	cell division cycle associated 2 [Source:HGNC Symbol;Acc:HGNC:1744]	0.000158	-1.53034
CDCA3	cell division cycle associated 3 [Source:HGNC Symbol;Acc:HGNC:1744]	0.002327	-1.65239
CDCA5	cell division cycle associated 5 [Source:HGNC Symbol;Acc:HGNC:1744]	2.30E-05	-1.6902
CDCA7L	cell division cycle associated 7 like [Source:HGNC Symbol;Acc:HGNC:1744]	1.82E-05	-1.47627
CDCA8	cell division cycle associated 8 [Source:HGNC Symbol;Acc:HGNC:1744]	0.008027	-1.2174
CDCP1	CUB domain containing protein 1 [Source:HGNC Symbol;Acc:HGNC:1744]	0.010675	-1.47438
CDH1	cadherin 1 [Source:HGNC Symbol;Acc:HGNC:1748]	1.03E-07	-1.69717
CDH10	cadherin 10 [Source:HGNC Symbol;Acc:HGNC:1749]	3.30E-05	-6.4142
CDH13	cadherin 13 [Source:HGNC Symbol;Acc:HGNC:1753]	0.00295	-1.22163
CDH24	cadherin 24 [Source:HGNC Symbol;Acc:HGNC:14265]	0.000276	-1.50099
CDK1	cyclin dependent kinase 1 [Source:HGNC Symbol;Acc:HGNC:1722]	0.001276	-1.22969
CDK14	cyclin dependent kinase 14 [Source:HGNC Symbol;Acc:HGNC:888]	1.51E-06	-1.98024
CDK15	cyclin dependent kinase 15 [Source:HGNC Symbol;Acc:HGNC:144]	0.007325	-4.20805
CDK16	cyclin dependent kinase 16 [Source:HGNC Symbol;Acc:HGNC:874]	0.000772	-1.33587
CDK6	cyclin dependent kinase 6 [Source:HGNC Symbol;Acc:HGNC:1777]	0.00439	-1.48952
CDON	cell adhesion associated, oncogene regulated [Source:HGNC Symbol;Acc:HGNC:23354]	0.002033	-1.35399
CDT1	chromatin licensing and DNA replication factor 1 [Source:HGNC Symbol;Acc:HGNC:23354]	1.62E-09	-1.52448
CENPE	centromere protein E [Source:HGNC Symbol;Acc:HGNC:1856]	0.000128	-2.32405
CENPF	centromere protein F [Source:HGNC Symbol;Acc:HGNC:1857]	0.007798	-1.84664
CENPJ	centromere protein J [Source:HGNC Symbol;Acc:HGNC:17272]	4.95E-05	-1.42806
CENPO	centromere protein O [Source:HGNC Symbol;Acc:HGNC:28152]	0.000534	-1.8307
CEP126	centrosomal protein 126 [Source:HGNC Symbol;Acc:HGNC:29264]	0.00018	-1.64586
CEP152	centrosomal protein 152 [Source:HGNC Symbol;Acc:HGNC:29298]	0.008887	-1.27408
CEP162	centrosomal protein 162 [Source:HGNC Symbol;Acc:HGNC:21107]	0.000263	-1.38177
CEP55	centrosomal protein 55 [Source:HGNC Symbol;Acc:HGNC:1161]	0.000424	-1.48129

CEP63	centrosomal protein 63 [Source:HGNC Symbol;Acc:HGNC:25815]	4.10E-05	-1.46648
CEP78	centrosomal protein 78 [Source:HGNC Symbol;Acc:HGNC:25740]	0.00089	-1.5034
CEP83	centrosomal protein 83 [Source:HGNC Symbol;Acc:HGNC:17966]	9.24E-08	-1.49667
CEP85L	centrosomal protein 85 like [Source:HGNC Symbol;Acc:HGNC:216	7.41E-05	-1.69064
CERCAM	cerebral endothelial cell adhesion molecule [Source:HGNC Symb	6.53E-07	-1.38379
CERK	ceramide kinase [Source:HGNC Symbol;Acc:HGNC:19256]	1.39E-09	-1.47574
CERKL	ceramide kinase like [Source:HGNC Symbol;Acc:HGNC:21699]	0.000251	-2.75026
CERS2	ceramide synthase 2 [Source:HGNC Symbol;Acc:HGNC:14076]	0.003168	-1.16641
CFAP157	cilia and flagella associated protein 157 [Source:HGNC Symbol;Ac	0.001912	-3.00163
CFAP69	cilia and flagella associated protein 69 [Source:HGNC Symbol;Acc	0.001359	-1.84593
CGAS	cyclic GMP-AMP synthase [Source:HGNC Symbol;Acc:HGNC:2136	0.001152	-1.27712
CGREF1	cell growth regulator with EF-hand domain 1 [Source:HGNC Sym	0.004902	-1.34604
CHAF1A	chromatin assembly factor 1 subunit A [Source:HGNC Symbol;Acc	0.003572	-1.67223
CHAF1B	chromatin assembly factor 1 subunit B [Source:HGNC Symbol;Acc	3.41E-05	-1.34999
CHAMP1	chromosome alignment maintaining phosphoprotein 1 [Source:H	0.002074	-2.01722
CHD1	chromodomain helicase DNA binding protein 1 [Source:HGNC Sy	0.001538	-1.44834
CHD1L	chromodomain helicase DNA binding protein 1 like [Source:HGNC	0.000362	-1.52223
CHD8	chromodomain helicase DNA binding protein 8 [Source:HGNC Sy	0.01005	-1.20598
CHDH	choline dehydrogenase [Source:HGNC Symbol;Acc:HGNC:24288]	0.009833	-2.17111
CHML	CHM like Rab escort protein [Source:HGNC Symbol;Acc:HGNC:19	3.74E-05	-2.17948
CHMP3	charged multivesicular body protein 3 [Source:HGNC Symbol;Acc	0.000788	-1.18563
CHMP4B	charged multivesicular body protein 4B [Source:HGNC Symbol;Ac	0.000271	-1.47113
CHPT1	choline phosphotransferase 1 [Source:HGNC Symbol;Acc:HGNC:1	7.14E-09	-1.50729
CHRNA5	cholinergic receptor nicotinic alpha 5 subunit [Source:HGNC Sym	0.001052	-1.78845
CHST11	carbohydrate sulfotransferase 11 [Source:HGNC Symbol;Acc:HG	0.000127	-1.41375
CHST15	carbohydrate sulfotransferase 15 [Source:HGNC Symbol;Acc:HG	0.01125	-1.30529
CHUK	component of inhibitor of nuclear factor kappa B kinase complex	8.17E-07	-1.37661
CIP2A	cell proliferation regulating inhibitor of protein phosphatase 2A [	0.00229	-1.79957
CIPC	CLOCK interacting pacemaker [Source:HGNC Symbol;Acc:HGNC:2	0.003711	-1.4832
CIZ1	CDKN1A interacting zinc finger protein 1 [Source:HGNC Symbol;A	0.009705	-1.22387
CKAP2L	cytoskeleton associated protein 2 like [Source:HGNC Symbol;Acc	0.001999	-1.37604
CKAP5	cytoskeleton associated protein 5 [Source:HGNC Symbol;Acc:HGI	0.000832	-1.52409
CLASP2	cytoplasmic linker associated protein 2 [Source:HGNC Symbol;Ac	0.000112	-1.35667
CLCF1	cardiotrophin like cytokine factor 1 [Source:HGNC Symbol;Acc:HC	0.009231	-1.97505
CLDN11	claudin 11 [Source:HGNC Symbol;Acc:HGNC:8514]	0.000936	-2.24026
CLINT1	clathrin interactor 1 [Source:HGNC Symbol;Acc:HGNC:23186]	0.004332	-1.38667
CLN6	CLN6 transmembrane ER protein [Source:HGNC Symbol;Acc:HG	0.00328	-1.99963
CLOCK	clock circadian regulator [Source:HGNC Symbol;Acc:HGNC:2082]	6.10E-05	-1.36588
CLSPN	claspin [Source:HGNC Symbol;Acc:HGNC:19715]	1.15E-05	-2.56956
CLTC	clathrin heavy chain [Source:HGNC Symbol;Acc:HGNC:2092]	1.45E-05	-1.38182
CMTM3	CKLF like MARVEL transmembrane domain containing 3 [Source:l	0.00029	-1.86216
CMTM6	CKLF like MARVEL transmembrane domain containing 6 [Source:l	0.002772	-1.2905
CMTM7	CKLF like MARVEL transmembrane domain containing 7 [Source:l	0.002854	-1.64622
CMTM8	CKLF like MARVEL transmembrane domain containing 8 [Source:l	4.66E-15	-2.18742
CMTR1	cap methyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:21077	0.00892	-1.25976
CNDP2	carnosine dipeptidase 2 [Source:HGNC Symbol;Acc:HGNC:24437]	0.001428	-1.21787
CNIH2	cornichon family AMPA receptor auxiliary protein 2 [Source:HGN	0.003349	-1.64131

CNKS2	connector enhancer of kinase suppressor of Ras 2 [Source:HGNC	0.004321	-2.13749
CNOT1	CCR4-NOT transcription complex subunit 1 [Source:HGNC Symbo	0.011478	-1.28466
CNOT6	CCR4-NOT transcription complex subunit 6 [Source:HGNC Symbo	8.25E-08	-1.5395
CNP	2',3'-cyclic nucleotide 3' phosphodiesterase [Source:HGNC Symb	0.008025	-1.21024
CNTLN	centlein [Source:HGNC Symbol;Acc:HGNC:23432]	4.61E-05	-1.4709
CNTN3	contactin 3 [Source:HGNC Symbol;Acc:HGNC:2173]	0.000285	-1.78374
CNTNAP2	contactin associated protein like 2 [Source:HGNC Symbol;Acc:HG	0.006605	-1.8495
CNTNAP3	contactin associated protein like 3 [Source:HGNC Symbol;Acc:HG	0.003894	-1.66164
CNTROB	centrobin, centriole duplication and spindle assembly protein [So	0.010014	-1.48456
COCH	cochlin [Source:HGNC Symbol;Acc:HGNC:2180]	0.007811	-1.95582
COL12A1	collagen type XII alpha 1 chain [Source:HGNC Symbol;Acc:HGNC:1	7.87E-05	-2.69045
COL13A1	collagen type XIII alpha 1 chain [Source:HGNC Symbol;Acc:HGNC:1	0.004091	-3.06479
COL22A1	collagen type XXII alpha 1 chain [Source:HGNC Symbol;Acc:HGNC:1	0.001142	-1.9149
COL4A2	collagen type IV alpha 2 chain [Source:HGNC Symbol;Acc:HGNC:2	0.001444	-2.2279
COL9A2	collagen type IX alpha 2 chain [Source:HGNC Symbol;Acc:HGNC:2	0.001266	-3.12552
COPZ1	coatamer protein complex subunit zeta 1 [Source:HGNC Symbol;	9.05E-05	-1.59149
COQ8A	coenzyme Q8A [Source:HGNC Symbol;Acc:HGNC:16812]	0.00486	-1.27722
COTL1	coactosin like F-actin binding protein 1 [Source:HGNC Symbol;Acc	0.000857	-1.50657
CPD	carboxypeptidase D [Source:HGNC Symbol;Acc:HGNC:2301]	0.007662	-1.27449
CPLANE1	ciliogenesis and planar polarity effector 1 [Source:HGNC Symbol;	6.57E-07	-1.47444
CPOX	coproporphyrinogen oxidase [Source:HGNC Symbol;Acc:HGNC:23	6.51E-12	-2.16153
CPSF6	cleavage and polyadenylation specific factor 6 [Source:HGNC Syn	4.23E-05	-1.45223
CPSF7	cleavage and polyadenylation specific factor 7 [Source:HGNC Syn	0.009404	-1.26391
CPT1A	carnitine palmitoyltransferase 1A [Source:HGNC Symbol;Acc:HGNC	2.39E-05	-1.25582
CREBZF	CREB/ATF bZIP transcription factor [Source:HGNC Symbol;Acc:HGNC	0.003983	-1.31556
CS	citrate synthase [Source:HGNC Symbol;Acc:HGNC:2422]	1.09E-22	-1.73293
CSE1L	chromosome segregation 1 like [Source:HGNC Symbol;Acc:HGNC:2	4.34E-06	-1.29342
CSF2	colony stimulating factor 2 [Source:HGNC Symbol;Acc:HGNC:243	0.00909	-3.71535
CSGALNACT1	chondroitin sulfate N-acetylgalactosaminyltransferase 1 [Source:	0.009151	-2.58241
CSNK2A2	casein kinase 2 alpha 2 [Source:HGNC Symbol;Acc:HGNC:2459]	0.002198	-1.18323
CSPG5	chondroitin sulfate proteoglycan 5 [Source:HGNC Symbol;Acc:HG	0.005338	-1.9778
CSPP1	centrosome and spindle pole associated protein 1 [Source:HGNC	0.001313	-1.3666
CSTF2	cleavage stimulation factor subunit 2 [Source:HGNC Symbol;Acc:HG	0.009862	-1.38608
CTBP2	C-terminal binding protein 2 [Source:HGNC Symbol;Acc:HGNC:24	0.003558	-1.29331
CTCF	CCCTC-binding factor [Source:HGNC Symbol;Acc:HGNC:13723]	0.003148	-1.36436
CTNNA1	catenin alpha 1 [Source:HGNC Symbol;Acc:HGNC:2509]	0.000178	-1.29192
CTNBL1	catenin beta like 1 [Source:HGNC Symbol;Acc:HGNC:15879]	0.000312	-1.30924
CTPS1	CTP synthase 1 [Source:HGNC Symbol;Acc:HGNC:2519]	0.006086	-1.48175
CTSA	cathepsin A [Source:HGNC Symbol;Acc:HGNC:9251]	0.001308	-1.35336
CTSD	cathepsin D [Source:HGNC Symbol;Acc:HGNC:2529]	0.001292	-1.45037
CTSZ	cathepsin Z [Source:HGNC Symbol;Acc:HGNC:2547]	0.000261	-1.5584
CTTN	cortactin [Source:HGNC Symbol;Acc:HGNC:3338]	1.15E-08	-2.80036
CTTNBP2NL	CTTNBP2 N-terminal like [Source:HGNC Symbol;Acc:HGNC:25330]	4.08E-11	-1.53937
CUL3	cullin 3 [Source:HGNC Symbol;Acc:HGNC:2553]	2.75E-05	-1.35406
CUX1	cut like homeobox 1 [Source:HGNC Symbol;Acc:HGNC:2557]	0.003681	-1.19307
CX3CL1	C-X3-C motif chemokine ligand 1 [Source:HGNC Symbol;Acc:HGNC	0.001605	-1.81574
CXCL16	C-X-C motif chemokine ligand 16 [Source:HGNC Symbol;Acc:HGNC	0.000133	-1.33067

CXXC1	CXXC finger protein 1 [Source:HGNC Symbol;Acc:HGNC:24343]	0.008307	-1.15747
CYP24A1	cytochrome P450 family 24 subfamily A member 1 [Source:HGNC	0.004985	-2.58317
CYP2S1	cytochrome P450 family 2 subfamily S member 1 [Source:HGNC	0.000199	-1.9229
CYP4V2	cytochrome P450 family 4 subfamily V member 2 [Source:HGNC	0.000358	-1.59601
CYTH3	cytohesin 3 [Source:HGNC Symbol;Acc:HGNC:9504]	8.13E-05	-1.31628
DAG1	dystroglycan 1 [Source:HGNC Symbol;Acc:HGNC:2666]	0.000137	-1.61443
DBF4B	DBF4 zinc finger B [Source:HGNC Symbol;Acc:HGNC:17883]	0.010475	-1.59375
DBNDD1	dysbindin domain containing 1 [Source:HGNC Symbol;Acc:HGNC:	1.16E-05	-1.85763
DBNL	drebrin like [Source:HGNC Symbol;Acc:HGNC:2696]	0.000417	-1.4533
DCAF1	DDB1 and CUL4 associated factor 1 [Source:HGNC Symbol;Acc:HG	3.52E-07	-1.34746
DCAF4	DDB1 and CUL4 associated factor 4 [Source:HGNC Symbol;Acc:HG	0.008404	-1.36323
DCBLD2	discoidin, CUB and LCCL domain containing 2 [Source:HGNC Sym	0.000624	-2.63843
DCHS2	dachsous cadherin-related 2 [Source:HGNC Symbol;Acc:HGNC:23	0.002726	-1.73676
DCLK1	doublecortin like kinase 1 [Source:HGNC Symbol;Acc:HGNC:2700	0.00053	-2.993
DCPS	decapping enzyme, scavenger [Source:HGNC Symbol;Acc:HGNC:2	0.000637	-1.36782
DDAH1	dimethylarginine dimethylaminohydrolase 1 [Source:HGNC Symb	5.68E-05	-1.63781
DDB1	damage specific DNA binding protein 1 [Source:HGNC Symbol;Ac	1.72E-19	-1.65006
DDHD1	DDHD domain containing 1 [Source:HGNC Symbol;Acc:HGNC:197	0.000955	-1.44677
DDIAS	DNA damage induced apoptosis suppressor [Source:HGNC Symb	4.95E-05	-1.4284
DDX10	DEAD-box helicase 10 [Source:HGNC Symbol;Acc:HGNC:2735]	0.003089	-1.35449
DDX17	DEAD-box helicase 17 [Source:HGNC Symbol;Acc:HGNC:2740]	0.008375	-1.39561
DDX21	DEAD-box helicase 21 [Source:HGNC Symbol;Acc:HGNC:2744]	0.00958	-1.22398
DDX23	DEAD-box helicase 23 [Source:HGNC Symbol;Acc:HGNC:17347]	3.39E-07	-1.49998
DDX24	DEAD-box helicase 24 [Source:HGNC Symbol;Acc:HGNC:13266]	0.000558	-1.31127
DDX3X	DEAD-box helicase 3 X-linked [Source:HGNC Symbol;Acc:HGNC:2	0.001765	-1.25454
DDX46	DEAD-box helicase 46 [Source:HGNC Symbol;Acc:HGNC:18681]	0.001821	-1.63448
DDX60L	DEAD/H-box 60 like [Source:HGNC Symbol;Acc:HGNC:26429]	0.003719	-1.58106
DEK	DEK proto-oncogene [Source:HGNC Symbol;Acc:HGNC:2768]	1.08E-05	-1.54022
DELE1	DAP3 binding cell death enhancer 1 [Source:HGNC Symbol;Acc:H	0.004013	-1.33055
DEPDC1	DEP domain containing 1 [Source:HGNC Symbol;Acc:HGNC:2294	0.005085	-1.25324
DEPDC1B	DEP domain containing 1B [Source:HGNC Symbol;Acc:HGNC:2490	0.000243	-1.50678
DES11	desumoylating isopeptidase 1 [Source:HGNC Symbol;Acc:HGNC:2	0.008868	-1.26744
DGCR8	DGCR8 microprocessor complex subunit [Source:HGNC Symbol;A	0.006991	-1.84012
DHFR	dihydrofolate reductase [Source:HGNC Symbol;Acc:HGNC:2861]	0.000491	-2.46603
DHTKD1	dehydrogenase E1 and transketolase domain containing 1 [Sourc	8.61E-07	-1.44909
DHX16	DEAH-box helicase 16 [Source:HGNC Symbol;Acc:HGNC:2739]	0.010179	-1.19969
DHX8	DEAH-box helicase 8 [Source:NCBI gene;Acc:1659]	0.000274	-1.29887
DHX9	DEXH-box helicase 9 [Source:HGNC Symbol;Acc:HGNC:2750]	1.33E-05	-1.97752
DIAPH1	diaphanous related formin 1 [Source:HGNC Symbol;Acc:HGNC:28	0.007225	-1.39751
DIAPH3	diaphanous related formin 3 [Source:HGNC Symbol;Acc:HGNC:15	4.19E-06	-2.06704
DIPK2A	divergent protein kinase domain 2A [Source:HGNC Symbol;Acc:H	0.006776	-1.26555
DIS3L	DIS3 like exosome 3'-5' exoribonuclease [Source:HGNC Symbol;A	7.95E-05	-1.47182
DKC1	dyskerin pseudouridine synthase 1 [Source:HGNC Symbol;Acc:HG	1.37E-05	-1.29767
DKK3	dickkopf WNT signaling pathway inhibitor 3 [Source:HGNC Symb	0.00204	-1.33187
DLAT	dihydrolipoamide S-acetyltransferase [Source:HGNC Symbol;Acc:	4.45E-05	-1.2388
DLGAP4	DLG associated protein 4 [Source:HGNC Symbol;Acc:HGNC:2447	0.002636	-1.24859
DLL1	delta like canonical Notch ligand 1 [Source:HGNC Symbol;Acc:HG	0.005884	-1.93793

DNAJA1	DnaJ heat shock protein family (Hsp40) member A1 [Source:HGNC Symbol;Acc:HGNC:2972]	1.93E-05	-1.54019
DNAJC10	DnaJ heat shock protein family (Hsp40) member C10 [Source:HGNC Symbol;Acc:HGNC:2972]	0.007025	-1.28815
DNAJC13	DnaJ heat shock protein family (Hsp40) member C13 [Source:HGNC Symbol;Acc:HGNC:2972]	0.003339	-1.28868
DNAJC2	DnaJ heat shock protein family (Hsp40) member C2 [Source:HGNC Symbol;Acc:HGNC:2972]	0.004325	-1.3525
DNAJC30	DnaJ heat shock protein family (Hsp40) member C30 [Source:HGNC Symbol;Acc:HGNC:2972]	0.003053	-2.69578
DNAJC6	DnaJ heat shock protein family (Hsp40) member C6 [Source:HGNC Symbol;Acc:HGNC:2972]	0.011219	-1.4917
DNAJC7	DnaJ heat shock protein family (Hsp40) member C7 [Source:HGNC Symbol;Acc:HGNC:2972]	0.011425	-1.21757
DNM1	dynamitin 1 [Source:HGNC Symbol;Acc:HGNC:2972]	0.008932	-2.15694
DNMT1	DNA methyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:2976]	0.006689	-1.73526
DOCK1	dedicator of cytokinesis 1 [Source:HGNC Symbol;Acc:HGNC:2987]	2.74E-05	-1.32923
DOCK5	dedicator of cytokinesis 5 [Source:HGNC Symbol;Acc:HGNC:2347]	0.002525	-2.09582
DOCK7	dedicator of cytokinesis 7 [Source:HGNC Symbol;Acc:HGNC:1919]	6.08E-06	-1.48396
DONSON	downstream neighbor of SON [Source:HGNC Symbol;Acc:HGNC:2972]	2.98E-05	-1.56073
DPAGT1	dolichyl-phosphate N-acetylglucosaminylphosphotransferase 1 [Source:HGNC Symbol;Acc:HGNC:2972]	0.000177	-1.32696
DPF1	double PHD fingers 1 [Source:HGNC Symbol;Acc:HGNC:20225]	0.002914	-2.52318
DPF3	double PHD fingers 3 [Source:HGNC Symbol;Acc:HGNC:17427]	0.000122	-3.48865
DPP3	dipeptidyl peptidase 3 [Source:HGNC Symbol;Acc:HGNC:3008]	6.68E-06	-1.55003
DPY19L1	dpy-19 like C-mannosyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:2972]	0.002137	-1.52646
DPYSL2	dihydropyrimidinase like 2 [Source:HGNC Symbol;Acc:HGNC:3014]	6.25E-06	-1.44011
DPYSL3	dihydropyrimidinase like 3 [Source:HGNC Symbol;Acc:HGNC:3014]	5.30E-05	-2.55447
DSE	dermatan sulfate epimerase [Source:HGNC Symbol;Acc:HGNC:2147]	0.003	-1.22772
DSEL	dermatan sulfate epimerase like [Source:HGNC Symbol;Acc:HGNC:2147]	0.000411	-2.5708
DTL	denticless E3 ubiquitin protein ligase homolog [Source:HGNC Symbol;Acc:HGNC:2972]	1.00E-12	-2.13745
DUSP9	dual specificity phosphatase 9 [Source:HGNC Symbol;Acc:HGNC:3113]	1.58E-05	-2.14976
DYRK1A	dual specificity tyrosine phosphorylation regulated kinase 1A [Source:HGNC Symbol;Acc:HGNC:2972]	0.001019	-1.27996
DZIP1	DAZ interacting zinc finger protein 1 [Source:HGNC Symbol;Acc:HGNC:2972]	5.00E-09	-1.58509
E2F1	E2F transcription factor 1 [Source:HGNC Symbol;Acc:HGNC:3113]	3.90E-12	-1.45814
E2F2	E2F transcription factor 2 [Source:HGNC Symbol;Acc:HGNC:3114]	1.22E-05	-2.14485
E2F3	E2F transcription factor 3 [Source:HGNC Symbol;Acc:HGNC:3115]	1.16E-11	-2.23271
E2F7	E2F transcription factor 7 [Source:HGNC Symbol;Acc:HGNC:2382]	5.67E-05	-1.7726
EARS2	glutamyl-tRNA synthetase 2, mitochondrial [Source:HGNC Symbol;Acc:HGNC:2972]	0.005159	-1.33649
ECE1	endothelin converting enzyme 1 [Source:HGNC Symbol;Acc:HGNC:2972]	0.002577	-1.84448
ECPAS	Ecm29 proteasome adaptor and scaffold [Source:HGNC Symbol;Acc:HGNC:2972]	0.006453	-1.45708
EDEM1	ER degradation enhancing alpha-mannosidase like protein 1 [Source:HGNC Symbol;Acc:HGNC:2972]	0.00092	-1.48237
EEF1AKNMT	eEF1A lysine and N-terminal methyltransferase [Source:HGNC Symbol;Acc:HGNC:2972]	0.007785	-1.252
EFCAB11	EF-hand calcium binding domain 11 [Source:HGNC Symbol;Acc:HGNC:2972]	0.000447	-1.3837
EFCAB2	EF-hand calcium binding domain 2 [Source:HGNC Symbol;Acc:HGNC:2972]	0.005444	-1.47894
EFHD1	EF-hand domain family member D1 [Source:HGNC Symbol;Acc:HGNC:2972]	5.97E-07	-1.85366
EFL1	elongation factor like GTPase 1 [Source:HGNC Symbol;Acc:HGNC:2972]	0.001347	-1.2418
EFNB2	ephrin B2 [Source:HGNC Symbol;Acc:HGNC:3227]	0.004223	-1.92146
EFTUD2	elongation factor Tu GTP binding domain containing 2 [Source:HGNC Symbol;Acc:HGNC:2972]	0.002227	-1.43777
EGLN1	egl-9 family hypoxia inducible factor 1 [Source:HGNC Symbol;Acc:HGNC:2972]	4.83E-05	-1.66002
EHBP1	EH domain binding protein 1 [Source:HGNC Symbol;Acc:HGNC:2972]	1.34E-09	-1.50286
EHD1	EH domain containing 1 [Source:HGNC Symbol;Acc:HGNC:3242]	0.004636	-1.87582
EHD2	EH domain containing 2 [Source:HGNC Symbol;Acc:HGNC:3243]	0.00942	-1.43378
EHD3	EH domain containing 3 [Source:HGNC Symbol;Acc:HGNC:3244]	8.50E-06	-3.62428
EHF	ETS homologous factor [Source:HGNC Symbol;Acc:HGNC:3246]	0.000279	-1.39397

EIF2AK2	eukaryotic translation initiation factor 2 alpha kinase 2 [Source:HGNC Symbol;Acc:HGNC:14198]	0.000766	-1.23097
EIF2AK4	eukaryotic translation initiation factor 2 alpha kinase 4 [Source:HGNC Symbol;Acc:HGNC:14199]	1.17E-06	-1.43115
EIF3A	eukaryotic translation initiation factor 3 subunit A [Source:HGNC Symbol;Acc:HGNC:14200]	0.004105	-1.37466
EIF3C	eukaryotic translation initiation factor 3 subunit C [Source:HGNC Symbol;Acc:HGNC:14201]	0.00043	-1.48666
EIF3J	eukaryotic translation initiation factor 3 subunit J [Source:HGNC Symbol;Acc:HGNC:14202]	0.000212	-1.33814
EIF5B	eukaryotic translation initiation factor 5B [Source:HGNC Symbol;Acc:HGNC:14203]	0.000438	-1.46021
ELAC2	elaC ribonuclease Z 2 [Source:HGNC Symbol;Acc:HGNC:14198]	6.68E-05	-1.39265
ELAVL2	ELAV like RNA binding protein 2 [Source:HGNC Symbol;Acc:HGNC:14204]	1.94E-13	-3.03703
ELF3	E74 like ETS transcription factor 3 [Source:HGNC Symbol;Acc:HGNC:14205]	0.000143	-5.08573
ELK3	ETS transcription factor ELK3 [Source:HGNC Symbol;Acc:HGNC:14206]	0.001271	-1.62163
ELOA	elongin A [Source:HGNC Symbol;Acc:HGNC:11620]	0.000446	-1.27475
EMB	embigin [Source:HGNC Symbol;Acc:HGNC:30465]	4.90E-06	-1.48279
EMC1	ER membrane protein complex subunit 1 [Source:HGNC Symbol;Acc:HGNC:14207]	0.007067	-1.23527
EML4	EMAP like 4 [Source:HGNC Symbol;Acc:HGNC:1316]	3.94E-06	-1.9688
ENAH	ENAH actin regulator [Source:HGNC Symbol;Acc:HGNC:18271]	1.45E-07	-1.42507
ENC1	ectodermal-neural cortex 1 [Source:HGNC Symbol;Acc:HGNC:3346]	2.07E-05	-3.9873
ENOSF1	enolase superfamily member 1 [Source:HGNC Symbol;Acc:HGNC:14208]	0.006994	-2.20332
ENPP4	ectonucleotide pyrophosphatase/phosphodiesterase 4 [Source:HGNC Symbol;Acc:HGNC:14209]	0.000706	-2.88429
ENTPD3	ectonucleoside triphosphate diphosphohydrolase 3 [Source:HGNC Symbol;Acc:HGNC:14210]	2.32E-05	-1.73847
ENTPD5	ectonucleoside triphosphate diphosphohydrolase 5 (inactive) [Source:HGNC Symbol;Acc:HGNC:14211]	0.003828	-1.42597
EPAS1	endothelial PAS domain protein 1 [Source:HGNC Symbol;Acc:HGNC:14212]	3.56E-05	-1.74063
EPB41L2	erythrocyte membrane protein band 4.1 like 2 [Source:HGNC Symbol;Acc:HGNC:14213]	0.000753	-1.44439
EPDR1	ependymin related 1 [Source:HGNC Symbol;Acc:HGNC:17572]	0.000951	-1.99683
EPHA2	EPH receptor A2 [Source:HGNC Symbol;Acc:HGNC:3386]	0.002242	-2.33832
EPRS1	glutamyl-prolyl-tRNA synthetase 1 [Source:HGNC Symbol;Acc:HGNC:14214]	4.72E-05	-1.37916
EPS15L1	epidermal growth factor receptor pathway substrate 15 like 1 [Source:HGNC Symbol;Acc:HGNC:14215]	0.008405	-1.20296
EPS8	epidermal growth factor receptor pathway substrate 8 [Source:HGNC Symbol;Acc:HGNC:14216]	0.003596	-1.2376
ERAP1	endoplasmic reticulum aminopeptidase 1 [Source:HGNC Symbol;Acc:HGNC:14217]	0.007575	-1.51133
ERAP2	endoplasmic reticulum aminopeptidase 2 [Source:HGNC Symbol;Acc:HGNC:14218]	4.63E-06	-1.50908
ERBIN	erbb2 interacting protein [Source:HGNC Symbol;Acc:HGNC:1584]	0.000179	-1.40732
ERCC2	ERCC excision repair 2, TFIIH core complex helicase subunit [Source:HGNC Symbol;Acc:HGNC:14219]	0.009306	-1.5429
ERCC6L	ERCC excision repair 6 like, spindle assembly checkpoint helicase [Source:HGNC Symbol;Acc:HGNC:14220]	5.31E-06	-2.33206
ERCC6L2	ERCC excision repair 6 like 2 [Source:HGNC Symbol;Acc:HGNC:2600]	0.006187	-1.3036
EREG	epiregulin [Source:HGNC Symbol;Acc:HGNC:3443]	0.001466	-2.68471
ERI1	exoribonuclease 1 [Source:HGNC Symbol;Acc:HGNC:23994]	1.49E-05	-1.70625
ERMP1	endoplasmic reticulum metalloproteinase 1 [Source:HGNC Symbol;Acc:HGNC:14221]	3.12E-09	-1.60162
ESCO2	establishment of sister chromatid cohesion N-acetyltransferase 2 [Source:HGNC Symbol;Acc:HGNC:14222]	0.000167	-2.53023
ESM1	endothelial cell specific molecule 1 [Source:HGNC Symbol;Acc:HGNC:14223]	0.000345	-4.27236
ESPL1	extra spindle pole bodies like 1, separase [Source:HGNC Symbol;Acc:HGNC:14224]	0.001117	-2.51023
ESX1	ESX homeobox 1 [Source:HGNC Symbol;Acc:HGNC:14865]	0.009689	-2.07657
ESYT1	extended synaptotagmin 1 [Source:HGNC Symbol;Acc:HGNC:295]	0.001378	-1.20478
ESYT2	extended synaptotagmin 2 [Source:HGNC Symbol;Acc:HGNC:222]	0.000771	-1.26824
ETV6	ETS variant transcription factor 6 [Source:HGNC Symbol;Acc:HGNC:14225]	0.000264	-1.74916
EVC2	EvC ciliary complex subunit 2 [Source:HGNC Symbol;Acc:HGNC:14226]	0.001775	-1.52627
EWSR1	EWS RNA binding protein 1 [Source:HGNC Symbol;Acc:HGNC:350]	0.001893	-1.36074
EXO1	exonuclease 1 [Source:HGNC Symbol;Acc:HGNC:3511]	3.32E-07	-2.27496
EXOC7	exocyst complex component 7 [Source:HGNC Symbol;Acc:HGNC:14227]	0.000567	-1.26187

EXOG	exo/endonuclease G [Source:HGNC Symbol;Acc:HGNC:3347]	2.85E-05	-1.74977
EXOSC10	exosome component 10 [Source:HGNC Symbol;Acc:HGNC:9138]	0.001873	-1.24454
EXT1	exostosin glycosyltransferase 1 [Source:HGNC Symbol;Acc:HGNC	0.005007	-1.25436
EXTL1	exostosin like glycosyltransferase 1 [Source:HGNC Symbol;Acc:HG	0.004079	-3.61055
EXTL3	exostosin like glycosyltransferase 3 [Source:HGNC Symbol;Acc:HG	0.000536	-1.30956
EYA1	EYA transcriptional coactivator and phosphatase 1 [Source:HGNC	0.002327	-2.1688
EYA4	EYA transcriptional coactivator and phosphatase 4 [Source:HGNC	0.000456	-1.34855
EZR	ezrin [Source:HGNC Symbol;Acc:HGNC:12691]	0.004485	-1.41361
FADS1	fatty acid desaturase 1 [Source:HGNC Symbol;Acc:HGNC:3574]	0.004329	-1.60529
FADS3	fatty acid desaturase 3 [Source:HGNC Symbol;Acc:HGNC:3576]	0.002641	-1.45133
FAIM	Fas apoptotic inhibitory molecule [Source:HGNC Symbol;Acc:HGNC	0.000252	-1.59083
FAM107B	family with sequence similarity 107 member B [Source:HGNC Sym	0.005823	-1.37622
FAM111A	family with sequence similarity 111 member A [Source:HGNC Sym	0.001784	-2.25272
FAM111B	family with sequence similarity 111 member B [Source:HGNC Sym	5.97E-05	-2.80776
FAM120A	family with sequence similarity 120A [Source:HGNC Symbol;Acc:HG	0.005201	-1.31537
FAM133B	family with sequence similarity 133 member B [Source:HGNC Sym	0.002515	-1.28793
FAM149A	family with sequence similarity 149 member A [Source:HGNC Sym	0.006044	-2.91018
FAM160B1	family with sequence similarity 160 member B1 [Source:HGNC Sy	0.010824	-1.3822
FAM166C	family with sequence similarity 166 member C [Source:HGNC Sym	0.001962	-3.32432
FAM169A	family with sequence similarity 169 member A [Source:HGNC Sym	0.000133	-1.35509
FAM184A	family with sequence similarity 184 member A [Source:HGNC Sym	0.001076	-1.65283
FAM199X	family with sequence similarity 199, X-linked [Source:HGNC Sym	0.001637	-1.38142
FAM214A	family with sequence similarity 214 member A [Source:HGNC Sym	0.001481	-1.61059
FAM222A	family with sequence similarity 222 member A [Source:HGNC Sym	0.002984	-2.40345
FAM234A	family with sequence similarity 234 member A [Source:HGNC Sym	1.28E-06	-1.64807
FAM241A	family with sequence similarity 241 member A [Source:HGNC Sym	0.005824	-1.22154
FAM3C	family with sequence similarity 3 member C [Source:HGNC Symb	0.000905	-2.24742
FAM83D	family with sequence similarity 83 member D [Source:HGNC Sym	4.49E-05	-1.88456
FAM86C1	family with sequence similarity 86 member C1 [Source:HGNC Sym	0.000483	-2.95708
FAM91A1	family with sequence similarity 91 member A1 [Source:HGNC Sym	7.09E-06	-1.3837
FAM98B	family with sequence similarity 98 member B [Source:HGNC Sym	0.00083	-1.71173
FANCA	FA complementation group A [Source:HGNC Symbol;Acc:HGNC:3	0.000243	-1.94165
FANCD2	FA complementation group D2 [Source:HGNC Symbol;Acc:HGNC:	0.007122	-1.48549
FANCG	FA complementation group G [Source:HGNC Symbol;Acc:HGNC:3	2.03E-05	-1.39829
FANCI	FA complementation group I [Source:HGNC Symbol;Acc:HGNC:25	0.000909	-1.50905
FARP1	FERM, ARH/RhoGEF and pleckstrin domain protein 1 [Source:HGI	0.00861	-1.58409
FARP2	FERM, ARH/RhoGEF and pleckstrin domain protein 2 [Source:HGI	0.007299	-1.45052
FASTKD5	FAST kinase domains 5 [Source:HGNC Symbol;Acc:HGNC:25790]	0.000633	-1.2515
FAT4	FAT atypical cadherin 4 [Source:HGNC Symbol;Acc:HGNC:23109]	0.007118	-1.99295
FBXL12	F-box and leucine rich repeat protein 12 [Source:HGNC Symbol;A	0.006363	-1.21887
FBXL14	F-box and leucine rich repeat protein 14 [Source:HGNC Symbol;A	0.009969	-1.45889
FBXL17	F-box and leucine rich repeat protein 17 [Source:HGNC Symbol;A	0.000555	-1.38504
FBXL2	F-box and leucine rich repeat protein 2 [Source:HGNC Symbol;Ac	0.000392	-1.45416
FBXL6	F-box and leucine rich repeat protein 6 [Source:HGNC Symbol;Ac	0.00744	-1.64595
FBXO21	F-box protein 21 [Source:HGNC Symbol;Acc:HGNC:13592]	1.16E-05	-1.4629
FBXO30	F-box protein 30 [Source:HGNC Symbol;Acc:HGNC:15600]	0.001702	-1.17411
FBXO45	F-box protein 45 [Source:HGNC Symbol;Acc:HGNC:29148]	0.00129	-1.28379

FBXO5	F-box protein 5 [Source:HGNC Symbol;Acc:HGNC:13584]	0.004838	-1.32243
FBXW5	F-box and WD repeat domain containing 5 [Source:HGNC Symbol;Acc:HGNC:13585]	0.005157	-1.26106
FEN1	flap structure-specific endonuclease 1 [Source:HGNC Symbol;Acc:HGNC:1587]	5.96E-06	-1.97319
FERMT1	fermitin family member 1 [Source:HGNC Symbol;Acc:HGNC:1588]	0.009048	-1.60536
FERMT2	fermitin family member 2 [Source:HGNC Symbol;Acc:HGNC:1576]	4.33E-11	-2.33326
FEZ2	fasciculation and elongation protein zeta 2 [Source:HGNC Symbol;Acc:HGNC:1589]	0.00508	-1.20335
FGF14	fibroblast growth factor 14 [Source:HGNC Symbol;Acc:HGNC:367]	0.008974	-2.48402
FGF2	fibroblast growth factor 2 [Source:HGNC Symbol;Acc:HGNC:3676]	0.003118	-1.7878
FGFR1	fibroblast growth factor receptor 1 [Source:HGNC Symbol;Acc:HGNC:3677]	0.004313	-2.39818
FGFR1OP	FGFR1 oncogene partner [Source:HGNC Symbol;Acc:HGNC:17012]	2.64E-06	-1.51679
FHDC1	FH2 domain containing 1 [Source:HGNC Symbol;Acc:HGNC:29363]	1.56E-06	-1.47321
FIBP	FGF1 intracellular binding protein [Source:HGNC Symbol;Acc:HGNC:3678]	0.00804	-1.16851
FIG4	FIG4 phosphoinositide 5-phosphatase [Source:HGNC Symbol;Acc:HGNC:3679]	0.001363	-1.30332
FIGN	fidgetin, microtubule severing factor [Source:HGNC Symbol;Acc:HGNC:3680]	0.004498	-1.81396
FILIP1L	filamin A interacting protein 1 like [Source:HGNC Symbol;Acc:HGNC:3681]	0.002721	-1.38139
FKTN	fukutin [Source:HGNC Symbol;Acc:HGNC:3622]	1.50E-05	-1.43685
FLI1	Fli-1 proto-oncogene, ETS transcription factor [Source:HGNC Symbol;Acc:HGNC:3623]	0.003402	-1.83069
FLII	FLII actin remodeling protein [Source:HGNC Symbol;Acc:HGNC:3624]	0.002502	-1.5154
FMNL3	formin like 3 [Source:HGNC Symbol;Acc:HGNC:23698]	0.004376	-1.65048
FMR1	FMRP translational regulator 1 [Source:HGNC Symbol;Acc:HGNC:23699]	0.008848	-1.40448
FN3KRP	fructosamine 3 kinase related protein [Source:HGNC Symbol;Acc:HGNC:23700]	0.006712	-1.25325
FNDC3B	fibronectin type III domain containing 3B [Source:HGNC Symbol;Acc:HGNC:23701]	0.003589	-1.29517
FNDC4	fibronectin type III domain containing 4 [Source:HGNC Symbol;Acc:HGNC:23702]	0.000421	-1.6979
FOXM1	forkhead box M1 [Source:HGNC Symbol;Acc:HGNC:3818]	0.000124	-2.47766
FOXP1	forkhead box P1 [Source:HGNC Symbol;Acc:HGNC:3823]	1.09E-05	-1.39122
FOXP4	forkhead box P4 [Source:HGNC Symbol;Acc:HGNC:20842]	0.00439	-1.54867
FOXRED2	FAD dependent oxidoreductase domain containing 2 [Source:HGNC Symbol;Acc:HGNC:20843]	0.005742	-1.89025
FPGS	folylpolyglutamate synthase [Source:HGNC Symbol;Acc:HGNC:3824]	3.71E-06	-1.36548
FRA10AC1	FRA10A associated CGG repeat 1 [Source:HGNC Symbol;Acc:HGNC:20844]	0.000123	-1.41279
FREM2	FRAS1 related extracellular matrix 2 [Source:HGNC Symbol;Acc:HGNC:20845]	0.000367	-4.6164
FRMD5	FERM domain containing 5 [Source:HGNC Symbol;Acc:HGNC:282]	0.004752	-1.80863
FRYL	FRY like transcription coactivator [Source:HGNC Symbol;Acc:HGNC:20846]	0.005676	-1.22067
FSTL1	follistatin like 1 [Source:HGNC Symbol;Acc:HGNC:3972]	0.002821	-1.76307
FTSJ1	FtsJ RNA 2'-O-methyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:3973]	0.000131	-1.17526
FUCA1	alpha-L-fucosidase 1 [Source:HGNC Symbol;Acc:HGNC:4006]	8.37E-05	-1.48555
FUS	FUS RNA binding protein [Source:HGNC Symbol;Acc:HGNC:4010]	0.000875	-2.03318
FUT11	fucosyltransferase 11 [Source:HGNC Symbol;Acc:HGNC:19233]	0.001337	-1.44326
FUT9	fucosyltransferase 9 [Source:HGNC Symbol;Acc:HGNC:4020]	0.007616	-2.86208
FUZ	fuzzy planar cell polarity protein [Source:HGNC Symbol;Acc:HGNC:4021]	0.004504	-1.63984
FYB1	FYN binding protein 1 [Source:HGNC Symbol;Acc:HGNC:4036]	0.002947	-2.91294
FZD8	frizzled class receptor 8 [Source:HGNC Symbol;Acc:HGNC:4046]	0.006704	-2.0507
G0S2	G0/G1 switch 2 [Source:HGNC Symbol;Acc:HGNC:30229]	5.62E-06	-2.31796
G3BP1	G3BP stress granule assembly factor 1 [Source:HGNC Symbol;Acc:HGNC:30230]	9.01E-05	-1.28574
G6PD	glucose-6-phosphate dehydrogenase [Source:HGNC Symbol;Acc:HGNC:30231]	0.00495	-1.45159
GALNT10	polypeptide N-acetylgalactosaminyltransferase 10 [Source:HGNC Symbol;Acc:HGNC:30232]	0.000302	-2.5368
GALNT12	polypeptide N-acetylgalactosaminyltransferase 12 [Source:HGNC Symbol;Acc:HGNC:30233]	0.003738	-2.26662
GALNT14	polypeptide N-acetylgalactosaminyltransferase 14 [Source:HGNC Symbol;Acc:HGNC:30234]	0.005676	-1.2361

GALNT2	polypeptide N-acetylgalactosaminyltransferase 2 [Source:HGNC	0.000809	-1.33771
GALNT5	polypeptide N-acetylgalactosaminyltransferase 5 [Source:HGNC	0.000508	-1.71276
GAR1	GAR1 ribonucleoprotein [Source:HGNC Symbol;Acc:HGNC:14264	0.008389	-1.28968
GATA3	GATA binding protein 3 [Source:HGNC Symbol;Acc:HGNC:4172]	0.00132	-1.63523
GATA6	GATA binding protein 6 [Source:HGNC Symbol;Acc:HGNC:4174]	0.001566	-2.4217
GATD1	glutamine amidotransferase like class 1 domain containing 1 [Sou	0.007092	-1.43405
GATD3A	glutamine amidotransferase like class 1 domain containing 3A [Sc	0.001879	-1.20516
GCLC	glutamate-cysteine ligase catalytic subunit [Source:HGNC Symbol	0.000795	-1.25784
GCLM	glutamate-cysteine ligase modifier subunit [Source:HGNC Symbo	0.000184	-1.84202
GCNT1	glucosaminyl (N-acetyl) transferase 1 [Source:HGNC Symbol;Acc:	0.000134	-2.30618
GDA	guanine deaminase [Source:HGNC Symbol;Acc:HGNC:4212]	0.009644	-1.80955
GDAP1	ganglioside induced differentiation associated protein 1 [Source:l	0.000723	-2.71398
GDAP2	ganglioside induced differentiation associated protein 2 [Source:l	0.006097	-1.25482
GDF11	growth differentiation factor 11 [Source:HGNC Symbol;Acc:HGNC	0.00073	-1.85963
GEMIN5	gem nuclear organelle associated protein 5 [Source:HGNC Symbo	0.002288	-1.70987
GFM1	G elongation factor mitochondrial 1 [Source:HGNC Symbol;Acc:H	2.64E-06	-1.39444
GINS3	GINS complex subunit 3 [Source:HGNC Symbol;Acc:HGNC:25851]	0.000165	-1.32646
GINS4	GINS complex subunit 4 [Source:HGNC Symbol;Acc:HGNC:28226]	0.00743	-1.7056
GJC1	gap junction protein gamma 1 [Source:HGNC Symbol;Acc:HGNC:4	9.90E-06	-1.78276
GK5	glycerol kinase 5 [Source:HGNC Symbol;Acc:HGNC:28635]	0.006223	-1.28969
GLDC	glycine decarboxylase [Source:HGNC Symbol;Acc:HGNC:4313]	0.002855	-1.70477
GLE1	GLE1 RNA export mediator [Source:HGNC Symbol;Acc:HGNC:431	0.000373	-1.25013
GLIS3	GLIS family zinc finger 3 [Source:HGNC Symbol;Acc:HGNC:28510]	0.002069	-3.20975
GLYATL2	glycine-N-acyltransferase like 2 [Source:HGNC Symbol;Acc:HGNC	0.008399	-2.21262
GLYCK	glycerate kinase [Source:HGNC Symbol;Acc:HGNC:24247]	0.003564	-1.80724
GMDS	GDP-mannose 4,6-dehydratase [Source:HGNC Symbol;Acc:HGNC	0.011572	-1.34211
GMPS	guanine monophosphate synthase [Source:HGNC Symbol;Acc:HG	0.00097	-1.10807
GNAI2	G protein subunit alpha i2 [Source:HGNC Symbol;Acc:HGNC:4385	0.001483	-1.19193
GNAL	G protein subunit alpha L [Source:HGNC Symbol;Acc:HGNC:4388]	0.009008	-1.28291
GNAQ	G protein subunit alpha q [Source:HGNC Symbol;Acc:HGNC:4390]	0.001684	-1.25085
GNAS	GNAS complex locus [Source:HGNC Symbol;Acc:HGNC:4392]	9.28E-05	-1.22041
GNL1	G protein nucleolar 1 (putative) [Source:HGNC Symbol;Acc:HGNC	0.008936	-1.37437
GNPTAB	N-acetylglucosamine-1-phosphate transferase subunits alpha and	4.15E-07	-1.61336
GOLIM4	golgi integral membrane protein 4 [Source:HGNC Symbol;Acc:HG	0.001854	-1.58732
GOLM1	golgi membrane protein 1 [Source:HGNC Symbol;Acc:HGNC:1545	4.03E-11	-2.34149
GOT2	glutamic-oxaloacetic transaminase 2 [Source:HGNC Symbol;Acc:f	0.000103	-1.32963
GPAM	glycerol-3-phosphate acyltransferase, mitochondrial [Source:HGI	0.000204	-1.42895
GPAT3	glycerol-3-phosphate acyltransferase 3 [Source:HGNC Symbol;Ac	0.000312	-1.91464
GPATCH4	G-patch domain containing 4 [Source:HGNC Symbol;Acc:HGNC:2!	0.004995	-1.72045
GPC6	glypican 6 [Source:HGNC Symbol;Acc:HGNC:4454]	0.001239	-1.44533
GPI	glucose-6-phosphate isomerase [Source:HGNC Symbol;Acc:HGNC	0.001022	-1.26335
GPR137C	G protein-coupled receptor 137C [Source:HGNC Symbol;Acc:HGN	0.001451	-2.09063
GPR156	G protein-coupled receptor 156 [Source:HGNC Symbol;Acc:HGNC	4.24E-06	-2.5921
GPR176	G protein-coupled receptor 176 [Source:HGNC Symbol;Acc:HGNC	0.000177	-2.22664
GPR3	G protein-coupled receptor 3 [Source:HGNC Symbol;Acc:HGNC:4	3.46E-08	-2.42919
GPR75	G protein-coupled receptor 75 [Source:HGNC Symbol;Acc:HGNC:	0.002247	-3.11862
GPRC5B	G protein-coupled receptor class C group 5 member B [Source:HC	0.001537	-2.18899

GPSM2	G protein signaling modulator 2 [Source:HGNC Symbol;Acc:HGNC	0.000594	-1.31786
GPSM3	G protein signaling modulator 3 [Source:HGNC Symbol;Acc:HGNC	0.004534	-3.06827
GRIN2D	glutamate ionotropic receptor NMDA type subunit 2D [Source:HGNC Symbol;Acc:HGNC	0.004698	-2.37092
GRK3	G protein-coupled receptor kinase 3 [Source:HGNC Symbol;Acc:HGNC	0.010385	-1.36512
GRK6	G protein-coupled receptor kinase 6 [Source:HGNC Symbol;Acc:HGNC	0.007853	-1.32483
GSK3A	glycogen synthase kinase 3 alpha [Source:HGNC Symbol;Acc:HGNC	0.000244	-1.31624
GTF2F1	general transcription factor IIF subunit 1 [Source:HGNC Symbol;Acc:HGNC	0.001485	-1.3786
GTF3C4	general transcription factor IIIC subunit 4 [Source:HGNC Symbol;Acc:HGNC	0.000697	-1.27331
GTF3C6	general transcription factor IIIC subunit 6 [Source:HGNC Symbol;Acc:HGNC	0.011682	-1.34532
GTPBP2	GTP binding protein 2 [Source:HGNC Symbol;Acc:HGNC:4670]	0.006674	-1.16229
GTSE1	G2 and S-phase expressed 1 [Source:HGNC Symbol;Acc:HGNC:13	0.000716	-2.06664
GUCD1	guanylyl cyclase domain containing 1 [Source:HGNC Symbol;Acc:HGNC	0.006514	-1.18076
GUCY1B1	guanylate cyclase 1 soluble subunit beta 1 [Source:HGNC Symbol;Acc:HGNC	0.000386	-1.23306
GUF1	GUF1 homolog, GTPase [Source:HGNC Symbol;Acc:HGNC:25799]	0.001036	-1.73219
H2AX	H2A.X variant histone [Source:HGNC Symbol;Acc:HGNC:4739]	0.000403	-1.27429
H2AZ2	H2A.Z variant histone 2 [Source:HGNC Symbol;Acc:HGNC:20664]	0.001756	-1.18076
HACE1	HECT domain and ankyrin repeat containing E3 ubiquitin protein ligase 1 [Source:HGNC Symbol;Acc:HGNC:25511]	0.002223	-1.33605
HAPLN3	hyaluronan and proteoglycan link protein 3 [Source:HGNC Symbol;Acc:HGNC:4816]	0.001012	-2.38388
HARS1	histidyl-tRNA synthetase 1 [Source:HGNC Symbol;Acc:HGNC:4816]	0.000296	-1.34076
HARS2	histidyl-tRNA synthetase 2, mitochondrial [Source:HGNC Symbol;Acc:HGNC:4817]	0.001331	-1.31573
HAS2	hyaluronan synthase 2 [Source:HGNC Symbol;Acc:HGNC:4819]	7.09E-05	-6.42956
HAS3	hyaluronan synthase 3 [Source:HGNC Symbol;Acc:HGNC:4820]	0.003444	-1.57051
HDAC2	histone deacetylase 2 [Source:HGNC Symbol;Acc:HGNC:4853]	0.010817	-1.22279
HDGF	heparin binding growth factor [Source:HGNC Symbol;Acc:HGNC:4854]	0.004031	-1.17909
HDGFL2	HDGF like 2 [Source:HGNC Symbol;Acc:HGNC:14680]	0.009415	-1.26163
HEATR1	HEAT repeat containing 1 [Source:HGNC Symbol;Acc:HGNC:25511]	0.010181	-1.28954
HEATR5B	HEAT repeat containing 5B [Source:HGNC Symbol;Acc:HGNC:292]	0.000304	-1.36377
HECTD1	HECT domain E3 ubiquitin protein ligase 1 [Source:HGNC Symbol;Acc:HGNC:25511]	0.000409	-1.45769
HECTD3	HECT domain E3 ubiquitin protein ligase 3 [Source:HGNC Symbol;Acc:HGNC:25511]	2.40E-08	-1.46534
HEG1	heart development protein with EGF like domains 1 [Source:HGNC Symbol;Acc:HGNC:4821]	1.44E-05	-1.817
HELB	DNA helicase B [Source:HGNC Symbol;Acc:HGNC:17196]	0.002194	-1.79635
HELLS	helicase, lymphoid specific [Source:HGNC Symbol;Acc:HGNC:486]	2.26E-05	-2.25667
HERC6	HECT and RLD domain containing E3 ubiquitin protein ligase family 6 [Source:HGNC Symbol;Acc:HGNC:25511]	0.000622	-1.44676
HEXIM1	HEXIM P-TEFb complex subunit 1 [Source:HGNC Symbol;Acc:HGNC:4822]	0.011069	-1.20147
HFE	homeostatic iron regulator [Source:HGNC Symbol;Acc:HGNC:488]	0.006488	-1.24847
HGSNAT	heparan-alpha-glucosaminide N-acetyltransferase [Source:HGNC Symbol;Acc:HGNC:4823]	0.00606	-1.354
HIBCH	3-hydroxyisobutyryl-CoA hydrolase [Source:HGNC Symbol;Acc:HGNC:4824]	0.000369	-1.43868
HIPK3	homeodomain interacting protein kinase 3 [Source:HGNC Symbol;Acc:HGNC:4825]	0.001577	-1.35804
HIRIP3	HIRA interacting protein 3 [Source:HGNC Symbol;Acc:HGNC:4917]	0.003162	-1.5453
HJURP	Holliday junction recognition protein [Source:HGNC Symbol;Acc:HGNC:4826]	0.000507	-1.46385
HLTF	helicase like transcription factor [Source:HGNC Symbol;Acc:HGNC:4827]	0.003211	-1.57234
HM13	histocompatibility minor 13 [Source:HGNC Symbol;Acc:HGNC:164]	0.00026	-1.19951
HMCE5	5-hydroxymethylcytosine binding, ES cell specific [Source:HGNC Symbol;Acc:HGNC:4828]	0.001362	-1.30375
HMG20A	high mobility group 20A [Source:HGNC Symbol;Acc:HGNC:5001]	7.24E-06	-1.56477
HMG1	high mobility group AT-hook 1 [Source:HGNC Symbol;Acc:HGNC:5002]	0.00028	-2.12344
HMG2	high mobility group AT-hook 2 [Source:HGNC Symbol;Acc:HGNC:5003]	0.004878	-1.23174
HMG3	high mobility group AT-hook 3 [Source:HGNC Symbol;Acc:HGNC:5004]	0.001316	-1.73295

HMG5	high mobility group nucleosome binding domain 5 [Source:HGNC	1.42E-05	-2.2603
HNRNPA0	heterogeneous nuclear ribonucleoprotein A0 [Source:HGNC Sym	0.009355	-1.35432
HNRNPA1	heterogeneous nuclear ribonucleoprotein A1 [Source:HGNC Sym	4.95E-06	-1.51302
HNRNPA1L2	heterogeneous nuclear ribonucleoprotein A1 like 2 [Source:HGNC	0.002464	-1.46218
HNRNPA1P48	heterogeneous nuclear ribonucleoprotein A1 pseudogene 48 [So	6.93E-07	-1.8543
HNRNPA2B1	heterogeneous nuclear ribonucleoprotein A2/B1 [Source:HGNC S	0.000111	-1.78167
HNRNPA3	heterogeneous nuclear ribonucleoprotein A3 [Source:HGNC Sym	3.09E-05	-1.70337
HNRNPAB	heterogeneous nuclear ribonucleoprotein A/B [Source:HGNC Syn	7.27E-05	-1.51444
HNRNPD	heterogeneous nuclear ribonucleoprotein D [Source:HGNC Symb	0.002781	-2.03694
HNRNPDL	heterogeneous nuclear ribonucleoprotein D like [Source:HGNC S	0.000136	-1.20606
HNRNPH1	heterogeneous nuclear ribonucleoprotein H1 [Source:HGNC Sym	1.11E-07	-1.2208
HNRNPH2	heterogeneous nuclear ribonucleoprotein H2 [Source:HGNC Sym	0.000249	-1.19622
HNRNPH3	heterogeneous nuclear ribonucleoprotein H3 [Source:HGNC Sym	5.52E-06	-1.54599
HNRNPM	heterogeneous nuclear ribonucleoprotein M [Source:HGNC Sym	0.001114	-1.93299
HNRNPR	heterogeneous nuclear ribonucleoprotein R [Source:HGNC Symb	3.96E-05	-1.78984
HNRNPU	heterogeneous nuclear ribonucleoprotein U [Source:HGNC Symb	0.001078	-2.46224
HNRNPUL1	heterogeneous nuclear ribonucleoprotein U like 1 [Source:HGNC	0.005183	-1.43733
HNRNPUL2	heterogeneous nuclear ribonucleoprotein U like 2 [Source:HGNC	0.001745	-1.65636
HOMER1	homer scaffold protein 1 [Source:HGNC Symbol;Acc:HGNC:17512	0.009598	-1.2102
HOOK3	hook microtubule tethering protein 3 [Source:HGNC Symbol;Acc:	6.49E-05	-1.32818
HOXA1	homeobox A1 [Source:HGNC Symbol;Acc:HGNC:5099]	0.003186	-1.67897
HOXA13	homeobox A13 [Source:HGNC Symbol;Acc:HGNC:5102]	0.000555	-1.31007
HOXA2	homeobox A2 [Source:HGNC Symbol;Acc:HGNC:5103]	0.003676	-2.7725
HOXA3	homeobox A3 [Source:HGNC Symbol;Acc:HGNC:5104]	0.000845	-2.60434
HP1BP3	heterochromatin protein 1 binding protein 3 [Source:HGNC Sym	0.000437	-1.19508
HPS5	HPS5 biogenesis of lysosomal organelles complex 2 subunit 2 [So	0.000558	-1.41774
HS3ST2	heparan sulfate-glucosamine 3-sulfotransferase 2 [Source:HGNC	0.000138	-2.5722
HS6ST2	heparan sulfate 6-O-sulfotransferase 2 [Source:HGNC Symbol;Ac	5.53E-05	-1.37265
HSD17B4	hydroxysteroid 17-beta dehydrogenase 4 [Source:HGNC Symbol;	0.001071	-1.40766
HSP90AA1	heat shock protein 90 alpha family class A member 1 [Source:HG	0.006863	-1.2739
HSPA1B	heat shock protein family A (Hsp70) member 1B [Source:HGNC S	0.003333	-1.1994
HSPH1	heat shock protein family H (Hsp110) member 1 [Source:HGNC S	0.004767	-1.24993
HTATSF1	HIV-1 Tat specific factor 1 [Source:HGNC Symbol;Acc:HGNC:5276	0.003056	-1.4919
HTR1D	5-hydroxytryptamine receptor 1D [Source:HGNC Symbol;Acc:HGI	0.003038	-2.62827
HYDIN	HYDIN axonemal central pair apparatus protein [Source:HGNC Sy	0.000705	-2.98958
IARS1	isoleucyl-tRNA synthetase 1 [Source:HGNC Symbol;Acc:HGNC:53	0.004645	-1.2524
IBA57	iron-sulfur cluster assembly factor IBA57 [Source:HGNC Symbol;A	0.007491	-2.04121
ICE1	interactor of little elongation complex ELL subunit 1 [Source:HG	1.01E-07	-1.58672
ICK	intestinal cell kinase [Source:HGNC Symbol;Acc:HGNC:21219]	0.00035	-1.29483
ICMT	isoprenylcysteine carboxyl methyltransferase [Source:HGNC Sym	0.003855	-1.58396
IFITM10	interferon induced transmembrane protein 10 [Source:HGNC Syr	2.60E-05	-3.62031
IFITM2	interferon induced transmembrane protein 2 [Source:HGNC Sym	0.00556	-1.20831
IFT122	intraflagellar transport 122 [Source:HGNC Symbol;Acc:HGNC:135	0.000353	-1.98129
IFT57	intraflagellar transport 57 [Source:HGNC Symbol;Acc:HGNC:1736	1.48E-05	-1.29924
IFT81	intraflagellar transport 81 [Source:HGNC Symbol;Acc:HGNC:1431	0.000459	-1.58216
IGFBP4	insulin like growth factor binding protein 4 [Source:HGNC Symbo	0.003857	-1.27618
IGFBP6	insulin like growth factor binding protein 6 [Source:HGNC Symbo	0.001136	-1.99041

IKZF3	IKAROS family zinc finger 3 [Source:HGNC Symbol;Acc:HGNC:131	4.22E-05	-1.54995
IL17RD	interleukin 17 receptor D [Source:HGNC Symbol;Acc:HGNC:1761	2.77E-06	-2.10482
IL18R1	interleukin 18 receptor 1 [Source:HGNC Symbol;Acc:HGNC:5988]	0.000988	-1.84117
IL1RAP	interleukin 1 receptor accessory protein [Source:HGNC Symbol;A	0.004288	-1.46753
IL1RL1	interleukin 1 receptor like 1 [Source:HGNC Symbol;Acc:HGNC:59	0.001563	-3.01911
IL27RA	interleukin 27 receptor subunit alpha [Source:HGNC Symbol;Acc:	7.41E-06	-1.45941
IL6	interleukin 6 [Source:HGNC Symbol;Acc:HGNC:6018]	0.011151	-4.22728
IL6ST	interleukin 6 signal transducer [Source:HGNC Symbol;Acc:HGNC:	0.001579	-1.28615
IL7R	interleukin 7 receptor [Source:HGNC Symbol;Acc:HGNC:6024]	0.001663	-3.8111
ILF3	interleukin enhancer binding factor 3 [Source:HGNC Symbol;Acc:	0.008995	-1.41343
IMMT	inner membrane mitochondrial protein [Source:HGNC Symbol;Ac	0.009945	-1.20199
IMPA2	inositol monophosphatase 2 [Source:HGNC Symbol;Acc:HGNC:60	0.000478	-1.28377
IMPAD1	inositol monophosphatase domain containing 1 [Source:HGNC Sy	0.001497	-1.30728
INCENP	inner centromere protein [Source:HGNC Symbol;Acc:HGNC:6058	0.005651	-1.71809
ING2	inhibitor of growth family member 2 [Source:HGNC Symbol;Acc:HGNC:6059]	6.30E-05	-1.2921
INHBA	inhibin subunit beta A [Source:HGNC Symbol;Acc:HGNC:6066]	0.000251	-3.3167
INPP4B	inositol polyphosphate-4-phosphatase type II B [Source:HGNC Sy	0.000227	-1.65216
INPP5A	inositol polyphosphate-5-phosphatase A [Source:HGNC Symbol;A	0.000198	-1.39371
INTS4	integrator complex subunit 4 [Source:HGNC Symbol;Acc:HGNC:21	0.002167	-1.37002
IPO8	importin 8 [Source:HGNC Symbol;Acc:HGNC:9853]	2.18E-06	-1.35917
IPO9	importin 9 [Source:HGNC Symbol;Acc:HGNC:19425]	0.003757	-1.57428
IQCK	IQ motif containing K [Source:HGNC Symbol;Acc:HGNC:28556]	0.000471	-1.82125
IQGAP1	IQ motif containing GTPase activating protein 1 [Source:HGNC Sy	0.000318	-1.24131
IQGAP3	IQ motif containing GTPase activating protein 3 [Source:HGNC Sy	0.000226	-2.58833
IRAK2	interleukin 1 receptor associated kinase 2 [Source:HGNC Symbol;	0.007333	-1.64608
IREB2	iron responsive element binding protein 2 [Source:HGNC Symbol	0.003196	-1.26624
IRF1	interferon regulatory factor 1 [Source:HGNC Symbol;Acc:HGNC:6	0.000944	-1.73814
ISOC1	isochorismatase domain containing 1 [Source:HGNC Symbol;Acc:	0.002207	-1.2623
ITGA1	integrin subunit alpha 1 [Source:HGNC Symbol;Acc:HGNC:6134]	0.005663	-1.81816
ITGA3	integrin subunit alpha 3 [Source:HGNC Symbol;Acc:HGNC:6139]	0.003433	-1.52994
ITGA4	integrin subunit alpha 4 [Source:HGNC Symbol;Acc:HGNC:6140]	0.000173	-2.60043
ITGBL1	integrin subunit beta like 1 [Source:HGNC Symbol;Acc:HGNC:616	0.000242	-2.88
ITM2C	integral membrane protein 2C [Source:HGNC Symbol;Acc:HGNC:	0.003568	-1.38576
ITPKA	inositol-trisphosphate 3-kinase A [Source:HGNC Symbol;Acc:HGNC:	0.0002	-1.80235
ITSN1	intersectin 1 [Source:HGNC Symbol;Acc:HGNC:6183]	2.88E-09	-1.55162
IWS1	interacts with SUPT6H, CTD assembly factor 1 [Source:HGNC Sym	0.001783	-1.17807
JADE1	jade family PHD finger 1 [Source:HGNC Symbol;Acc:HGNC:30027]	0.000907	-1.46597
JAK1	Janus kinase 1 [Source:HGNC Symbol;Acc:HGNC:6190]	0.003848	-1.42362
JAZF1	JAZF zinc finger 1 [Source:HGNC Symbol;Acc:HGNC:28917]	0.006078	-1.61251
JCAD	junctional cadherin 5 associated [Source:HGNC Symbol;Acc:HGNC:	0.000209	-2.65492
JMJD8	jumonji domain containing 8 [Source:HGNC Symbol;Acc:HGNC:14	0.001521	-1.69057
JPT2	Jupiter microtubule associated homolog 2 [Source:HGNC Symbol	5.21E-12	-1.51478
KANK2	KN motif and ankyrin repeat domains 2 [Source:HGNC Symbol;Ac	0.002625	-1.36176
KANSL1	KAT8 regulatory NSL complex subunit 1 [Source:HGNC Symbol;Ac	0.001407	-1.35708
KATNB1	katanin regulatory subunit B1 [Source:HGNC Symbol;Acc:HGNC:6	0.000584	-1.45348
KBTBD11	kelch repeat and BTB domain containing 11 [Source:HGNC Symb	0.001685	-3.0408
KCNIP4	potassium voltage-gated channel interacting protein 4 [Source:HGNC	0.009831	-1.8366

KCNK5	potassium two pore domain channel subfamily K member 5 [Sou	0.00032	-3.00838
KCNMB4	potassium calcium-activated channel subfamily M regulatory bet	0.001168	-1.4569
KCNQ5	potassium voltage-gated channel subfamily Q member 5 [Source	0.000511	-1.61452
KCTD12	potassium channel tetramerization domain containing 12 [Source	0.002652	-1.54829
KCTD17	potassium channel tetramerization domain containing 17 [Source	0.0033	-1.71823
KCTD20	potassium channel tetramerization domain containing 20 [Source	0.011335	-1.22536
KCTD3	potassium channel tetramerization domain containing 3 [Source:	5.17E-06	-1.43056
KDM1A	lysine demethylase 1A [Source:HGNC Symbol;Acc:HGNC:29079]	0.000382	-1.19539
KDM3B	lysine demethylase 3B [Source:HGNC Symbol;Acc:HGNC:1337]	0.000315	-1.33468
KDM5C	lysine demethylase 5C [Source:HGNC Symbol;Acc:HGNC:11114]	1.74E-11	-1.63196
KDM6A	lysine demethylase 6A [Source:HGNC Symbol;Acc:HGNC:12637]	0.008408	-1.16836
KHDRBS1	KH RNA binding domain containing, signal transduction associate	0.006918	-1.60887
KHSRP	KH-type splicing regulatory protein [Source:HGNC Symbol;Acc:HC	0.000178	-1.81459
KIAA0040	KIAA0040 [Source:HGNC Symbol;Acc:HGNC:28950]	0.001633	-1.24288
KIAA0586	KIAA0586 [Source:HGNC Symbol;Acc:HGNC:19960]	2.14E-06	-1.59347
KIAA1549L	KIAA1549 like [Source:HGNC Symbol;Acc:HGNC:24836]	0.003935	-1.85917
KIF11	kinesin family member 11 [Source:HGNC Symbol;Acc:HGNC:6388	7.07E-12	-2.63091
KIF14	kinesin family member 14 [Source:HGNC Symbol;Acc:HGNC:1918	0.000578	-2.13475
KIF15	kinesin family member 15 [Source:HGNC Symbol;Acc:HGNC:1727	2.34E-10	-2.16834
KIF18B	kinesin family member 18B [Source:HGNC Symbol;Acc:HGNC:271	0.006013	-2.03916
KIF20A	kinesin family member 20A [Source:HGNC Symbol;Acc:HGNC:978	2.49E-06	-1.71183
KIF20B	kinesin family member 20B [Source:HGNC Symbol;Acc:HGNC:721	1.02E-06	-1.74277
KIF21A	kinesin family member 21A [Source:HGNC Symbol;Acc:HGNC:193	0.000618	-1.30255
KIF21B	kinesin family member 21B [Source:HGNC Symbol;Acc:HGNC:294	0.011236	-3.03151
KIF22	kinesin family member 22 [Source:HGNC Symbol;Acc:HGNC:6391	0.000251	-1.28714
KIF23	kinesin family member 23 [Source:HGNC Symbol;Acc:HGNC:6392	8.21E-06	-2.18
KIF24	kinesin family member 24 [Source:HGNC Symbol;Acc:HGNC:1991	7.41E-05	-1.73812
KIF2C	kinesin family member 2C [Source:HGNC Symbol;Acc:HGNC:6393	7.10E-06	-1.61817
KIF3A	kinesin family member 3A [Source:HGNC Symbol;Acc:HGNC:6319	0.00045	-1.38507
KIF3B	kinesin family member 3B [Source:HGNC Symbol;Acc:HGNC:6320	0.007547	-1.27452
KIF4A	kinesin family member 4A [Source:HGNC Symbol;Acc:HGNC:1333	6.77E-06	-2.01459
KIF5B	kinesin family member 5B [Source:HGNC Symbol;Acc:HGNC:6324	0.003978	-1.20103
KIFBP	kinesin family binding protein [Source:HGNC Symbol;Acc:HGNC:2	0.006418	-1.30439
KIFC1	kinesin family member C1 [Source:HGNC Symbol;Acc:HGNC:6389	8.52E-06	-1.56592
KITLG	KIT ligand [Source:HGNC Symbol;Acc:HGNC:6343]	1.76E-08	-2.14463
KLHDC4	kelch domain containing 4 [Source:HGNC Symbol;Acc:HGNC:2527	0.002918	-1.52994
KLHL42	kelch like family member 42 [Source:HGNC Symbol;Acc:HGNC:29	7.30E-05	-1.72033
KLHL5	kelch like family member 5 [Source:HGNC Symbol;Acc:HGNC:635	0.000128	-1.24774
KLLN	killin, p53 regulated DNA replication inhibitor [Source:HGNC Sym	0.008101	-2.74415
KMT2E	lysine methyltransferase 2E [Source:HGNC Symbol;Acc:HGNC:189	0.000331	-1.36301
KMT5A	lysine methyltransferase 5A [Source:HGNC Symbol;Acc:HGNC:29	0.008715	-1.27238
KNL1	kinetochore scaffold 1 [Source:HGNC Symbol;Acc:HGNC:24054]	0.001893	-1.7631
KNTC1	kinetochore associated 1 [Source:HGNC Symbol;Acc:HGNC:17259	3.27E-05	-1.37927
KPNA2	karyopherin subunit alpha 2 [Source:HGNC Symbol;Acc:HGNC:63	2.43E-05	-1.49171
KPNB1	karyopherin subunit beta 1 [Source:HGNC Symbol;Acc:HGNC:640	7.40E-06	-1.27933
KRT18	keratin 18 [Source:HGNC Symbol;Acc:HGNC:6430]	0.005381	-1.72666
KRT7	keratin 7 [Source:HGNC Symbol;Acc:HGNC:6445]	0.003468	-1.76978

KRT8	keratin 8 [Source:HGNC Symbol;Acc:HGNC:6446]	0.005503	-1.32877
KRT81	keratin 81 [Source:HGNC Symbol;Acc:HGNC:6458]	0.00065	-3.50212
KRTAP2-3	keratin associated protein 2-3 [Source:HGNC Symbol;Acc:HGNC:1	0.000276	-4.84807
KTN1	kinectin 1 [Source:HGNC Symbol;Acc:HGNC:6467]	2.20E-08	-1.4747
L1CAM	L1 cell adhesion molecule [Source:HGNC Symbol;Acc:HGNC:6470	0.00087	-1.65207
L3MBTL3	L3MBTL histone methyl-lysine binding protein 3 [Source:HGNC Sy	0.000993	-1.27382
LAD1	ladinin 1 [Source:HGNC Symbol;Acc:HGNC:6472]	0.001211	-1.31676
LAMP1	lysosomal associated membrane protein 1 [Source:HGNC Symbol	1.67E-15	-1.64493
LAMP3	lysosomal associated membrane protein 3 [Source:HGNC Symbol	0.000405	-1.70922
LANCL1	LanC like 1 [Source:HGNC Symbol;Acc:HGNC:6508]	0.001329	-1.29041
LAP3	leucine aminopeptidase 3 [Source:HGNC Symbol;Acc:HGNC:1844	0.004466	-1.19221
LARS2	leucyl-tRNA synthetase 2, mitochondrial [Source:HGNC Symbol;A	8.19E-09	-1.58068
LAS1L	LAS1 like ribosome biogenesis factor [Source:HGNC Symbol;Acc:1	0.005032	-1.52635
LATS1	large tumor suppressor kinase 1 [Source:HGNC Symbol;Acc:HGNC	0.009492	-1.17872
LATS2	large tumor suppressor kinase 2 [Source:HGNC Symbol;Acc:HGNC	0.006922	-1.29781
LCA5	lebercilin LCA5 [Source:HGNC Symbol;Acc:HGNC:31923]	0.000316	-1.33573
LCK	LCK proto-oncogene, Src family tyrosine kinase [Source:HGNC Sy	0.003685	-4.55704
LCLAT1	lysocardiolipin acyltransferase 1 [Source:HGNC Symbol;Acc:HGNC	0.000816	-1.48677
LCOR	ligand dependent nuclear receptor corepressor [Source:HGNC Sy	4.36E-09	-1.81679
LCP1	lymphocyte cytosolic protein 1 [Source:HGNC Symbol;Acc:HGNC:	0.000307	-1.29088
LDLR	low density lipoprotein receptor [Source:HGNC Symbol;Acc:HGNC	0.003954	-1.27175
LDLRAD3	low density lipoprotein receptor class A domain containing 3 [Sou	6.82E-05	-1.32394
LEF1	lymphoid enhancer binding factor 1 [Source:HGNC Symbol;Acc:H	0.000418	-1.63435
LEMD3	LEM domain containing 3 [Source:HGNC Symbol;Acc:HGNC:2888	0.007882	-1.32629
LEO1	LEO1 homolog, Paf1/RNA polymerase II complex component [Sou	1.41E-05	-1.30663
LFNG	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase [	0.004034	-2.3305
LHFPL2	LHFPL tetraspan subfamily member 2 [Source:HGNC Symbol;Acc:	1.84E-06	-1.74305
LIMCH1	LIM and calponin homology domains 1 [Source:HGNC Symbol;Acc	0.004447	-1.513
LIPH	lipase H [Source:HGNC Symbol;Acc:HGNC:18483]	2.54E-05	-1.46017
LMBR1	limb development membrane protein 1 [Source:HGNC Symbol;A	0.00441	-1.34228
LMCD1	LIM and cysteine rich domains 1 [Source:HGNC Symbol;Acc:HGNC	1.26E-05	-1.67343
LMF2	lipase maturation factor 2 [Source:HGNC Symbol;Acc:HGNC:2509	0.002488	-1.51661
LMLN	leishmanolysin like peptidase [Source:HGNC Symbol;Acc:HGNC:1	0.007113	-1.34631
LMNB1	lamin B1 [Source:HGNC Symbol;Acc:HGNC:6637]	6.42E-05	-2.33745
LMO7	LIM domain 7 [Source:HGNC Symbol;Acc:HGNC:6646]	0.002072	-1.53325
LNP1	leukemia NUP98 fusion partner 1 [Source:HGNC Symbol;Acc:HGNC	0.010927	-1.43829
LNPEP	leucyl and cystinyl aminopeptidase [Source:HGNC Symbol;Acc:HG	1.54E-05	-1.48829
LOXL1	lysyl oxidase like 1 [Source:HGNC Symbol;Acc:HGNC:6665]	0.00882	-1.40861
LOXL2	lysyl oxidase like 2 [Source:HGNC Symbol;Acc:HGNC:6666]	0.001202	-1.81578
LPAR1	lysophosphatidic acid receptor 1 [Source:HGNC Symbol;Acc:HGNC	5.14E-06	-1.3018
LPCAT2	lysophosphatidylcholine acyltransferase 2 [Source:HGNC Symbol;	1.28E-05	-1.69175
LPCAT3	lysophosphatidylcholine acyltransferase 3 [Source:HGNC Symbol;	2.69E-06	-1.59688
LPGAT1	lysophosphatidylglycerol acyltransferase 1 [Source:HGNC Symbol	0.008492	-1.22563
LPIN2	lipin 2 [Source:HGNC Symbol;Acc:HGNC:14450]	0.005447	-1.36782
LPXN	leupaxin [Source:HGNC Symbol;Acc:HGNC:14061]	0.008689	-2.32158
LRAT	lecithin retinol acyltransferase [Source:HGNC Symbol;Acc:HGNC:	0.003346	-1.89454
LRATD2	LRAT domain containing 2 [Source:HGNC Symbol;Acc:HGNC:2416	0.004326	-2.03409

LRBA	LPS responsive beige-like anchor protein [Source:HGNC Symbol;Acc:HGNC:10410]	8.81E-09	-1.74671
LRIG1	leucine rich repeats and immunoglobulin like domains 1 [Source:HGNC Symbol;Acc:HGNC:10411]	5.17E-05	-2.02969
LRP12	LDL receptor related protein 12 [Source:HGNC Symbol;Acc:HGNC:10412]	2.86E-07	-1.54842
LRRC20	leucine rich repeat containing 20 [Source:HGNC Symbol;Acc:HGNC:10413]	0.001119	-1.28648
LRRC58	leucine rich repeat containing 58 [Source:HGNC Symbol;Acc:HGNC:10414]	3.33E-07	-1.48764
LRRC6	leucine rich repeat containing 6 [Source:HGNC Symbol;Acc:HGNC:10415]	0.007326	-1.56766
LRRC8C	leucine rich repeat containing 8 VRAC subunit C [Source:HGNC Symbol;Acc:HGNC:10416]	3.63E-09	-1.55435
LRRCC1	leucine rich repeat and coiled-coil centrosomal protein 1 [Source:HGNC Symbol;Acc:HGNC:10417]	0.000248	-1.40805
LRRIQ1	leucine rich repeats and IQ motif containing 1 [Source:HGNC Symbol;Acc:HGNC:10418]	0.003222	-1.44839
LTA4H	leukotriene A4 hydrolase [Source:HGNC Symbol;Acc:HGNC:6710]	2.59E-31	-2.10804
LTBP1	latent transforming growth factor beta binding protein 1 [Source:HGNC Symbol;Acc:HGNC:6711]	0.000736	-1.78725
LTBP3	latent transforming growth factor beta binding protein 3 [Source:HGNC Symbol;Acc:HGNC:6712]	0.006955	-2.35163
LUC7L3	LUC7 like 3 pre-mRNA splicing factor [Source:HGNC Symbol;Acc:HGNC:6713]	0.005946	-1.56901
LUZP1	leucine zipper protein 1 [Source:HGNC Symbol;Acc:HGNC:14985]	6.75E-09	-1.76768
LY6E	lymphocyte antigen 6 family member E [Source:HGNC Symbol;Acc:HGNC:6720]	0.00171	-1.28641
LY75	lymphocyte antigen 75 [Source:HGNC Symbol;Acc:HGNC:6729]	0.000123	-1.9974
LZTS1	leucine zipper tumor suppressor 1 [Source:HGNC Symbol;Acc:HGNC:6730]	5.71E-05	-2.74649
MAATS1	MYCBP associated and testis expressed 1 [Source:HGNC Symbol;Acc:HGNC:6731]	0.004374	-1.7964
MACC1	MET transcriptional regulator MACC1 [Source:HGNC Symbol;Acc:HGNC:6732]	0.00237	-1.9075
MAEA	macrophage erythroblast attacher [Source:HGNC Symbol;Acc:HGNC:6733]	0.004835	-1.31635
MAFF	MAF bZIP transcription factor F [Source:HGNC Symbol;Acc:HGNC:6734]	0.003384	-1.33011
MAGEE1	MAGE family member E1 [Source:HGNC Symbol;Acc:HGNC:24934]	0.000497	-1.92245
MALL	mal, T cell differentiation protein like [Source:HGNC Symbol;Acc:HGNC:6735]	0.00572	-1.34596
MAML2	mastermind like transcriptional coactivator 2 [Source:HGNC Symbol;Acc:HGNC:6736]	2.67E-05	-2.62372
MAN1A2	mannosidase alpha class 1A member 2 [Source:HGNC Symbol;Acc:HGNC:6737]	0.004415	-1.27089
MAN2A1	mannosidase alpha class 2A member 1 [Source:HGNC Symbol;Acc:HGNC:6738]	0.001769	-1.50592
MANEAL	mannosidase endo-alpha like [Source:HGNC Symbol;Acc:HGNC:24935]	0.002884	-1.63231
MAP2	microtubule associated protein 2 [Source:HGNC Symbol;Acc:HGNC:6739]	0.000166	-1.54057
MAP2K2	mitogen-activated protein kinase kinase 2 [Source:HGNC Symbol;Acc:HGNC:6740]	0.000212	-1.27151
MAP3K1	mitogen-activated protein kinase kinase kinase 1 [Source:HGNC Symbol;Acc:HGNC:6741]	0.001725	-1.26557
MAP3K21	mitogen-activated protein kinase kinase kinase 21 [Source:HGNC Symbol;Acc:HGNC:6742]	1.45E-05	-1.74126
MAP4K5	mitogen-activated protein kinase kinase kinase kinase 5 [Source:HGNC Symbol;Acc:HGNC:6743]	0.000243	-1.64098
MAP7D1	MAP7 domain containing 1 [Source:HGNC Symbol;Acc:HGNC:255]	0.002882	-1.41829
MAP7D3	MAP7 domain containing 3 [Source:HGNC Symbol;Acc:HGNC:257]	0.000337	-1.50349
MAP9	microtubule associated protein 9 [Source:HGNC Symbol;Acc:HGNC:6744]	0.000182	-1.94212
MAPK1	mitogen-activated protein kinase 1 [Source:HGNC Symbol;Acc:HGNC:6745]	1.44E-07	-1.31656
MAPK1IP1L	mitogen-activated protein kinase 1 interacting protein 1 like [Source:HGNC Symbol;Acc:HGNC:6746]	0.000343	-1.42618
Mar1	mitochondrial amidoxime reducing component 1 [Source:HGNC Symbol;Acc:HGNC:6747]	0.000178	-1.75709
MARCHF4	membrane associated ring-CH-type finger 4 [Source:HGNC Symbol;Acc:HGNC:6748]	0.00836	-3.36006
MASTL	microtubule associated serine/threonine kinase like [Source:HGNC Symbol;Acc:HGNC:6749]	0.002497	-1.34542
MB21D2	Mab-21 domain containing 2 [Source:HGNC Symbol;Acc:HGNC:30]	0.000296	-1.81258
MBNL1	muscleblind like splicing regulator 1 [Source:HGNC Symbol;Acc:HGNC:6750]	9.96E-05	-1.38963
MBOAT1	membrane bound O-acyltransferase domain containing 1 [Source:HGNC Symbol;Acc:HGNC:6751]	0.001469	-1.24223
MBTPS2	membrane bound transcription factor peptidase, site 2 [Source:HGNC Symbol;Acc:HGNC:6752]	0.00041	-1.3374
MCM10	minichromosome maintenance 10 replication initiation factor [Source:HGNC Symbol;Acc:HGNC:6753]	1.48E-17	-2.33774
MCM2	minichromosome maintenance complex component 2 [Source:HGNC Symbol;Acc:HGNC:6754]	2.35E-07	-1.50902
MCM3	minichromosome maintenance complex component 3 [Source:HGNC Symbol;Acc:HGNC:6755]	9.74E-10	-1.87897

MCM4	minichromosome maintenance complex component 4 [Source:HGNC Symbol;Acc:HGNC:2660]	4.48E-05	-1.66077
MCM5	minichromosome maintenance complex component 5 [Source:HGNC Symbol;Acc:HGNC:2661]	7.40E-07	-1.37777
MCM6	minichromosome maintenance complex component 6 [Source:HGNC Symbol;Acc:HGNC:2662]	3.47E-29	-1.53859
MCM7	minichromosome maintenance complex component 7 [Source:HGNC Symbol;Acc:HGNC:2663]	5.41E-05	-1.45424
MCM8	minichromosome maintenance 8 homologous recombination repair protein [Source:HGNC Symbol;Acc:HGNC:2664]	0.002175	-1.42647
MCM9	minichromosome maintenance 9 homologous recombination repair protein [Source:HGNC Symbol;Acc:HGNC:2665]	0.006171	-1.38091
MDFIC	MyoD family inhibitor domain containing [Source:HGNC Symbol;Acc:HGNC:2666]	1.23E-07	-1.48203
MECOM	MDS1 and EVI1 complex locus [Source:HGNC Symbol;Acc:HGNC:2667]	0.002495	-2.13988
MED14	mediator complex subunit 14 [Source:HGNC Symbol;Acc:HGNC:2668]	0.006277	-1.32981
MED22	mediator complex subunit 22 [Source:HGNC Symbol;Acc:HGNC:2669]	0.00591	-1.78525
MELK	maternal embryonic leucine zipper kinase [Source:HGNC Symbol;Acc:HGNC:2670]	2.05E-05	-1.26059
MELTF	melanotransferrin [Source:HGNC Symbol;Acc:HGNC:7037]	0.002599	-2.36889
MET	MET proto-oncogene, receptor tyrosine kinase [Source:HGNC Symbol;Acc:HGNC:2671]	0.000428	-1.86502
METTL15	methyltransferase like 15 [Source:HGNC Symbol;Acc:HGNC:2660]	2.07E-05	-1.47589
METTL7B	methyltransferase like 7B [Source:HGNC Symbol;Acc:HGNC:2827]	0.003341	-3.09853
MFAP1	microfibril associated protein 1 [Source:HGNC Symbol;Acc:HGNC:2672]	1.05E-07	-1.39269
MFSD14B	major facilitator superfamily domain containing 14B [Source:HGNC Symbol;Acc:HGNC:2673]	0.00455	-1.15919
MGAT4A	alpha-1,3-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase 4 [Source:HGNC Symbol;Acc:HGNC:2674]	0.011094	-1.25329
MGLL	monoglyceride lipase [Source:HGNC Symbol;Acc:HGNC:17038]	0.003597	-1.7325
MGRN1	mahogunin ring finger 1 [Source:HGNC Symbol;Acc:HGNC:20254]	2.22E-10	-1.95108
MIA3	MIA SH3 domain ER export factor 3 [Source:HGNC Symbol;Acc:HGNC:2675]	0.008127	-1.13116
MICAL2	microtubule associated monooxygenase, calponin and LIM domain containing 2 [Source:HGNC Symbol;Acc:HGNC:2676]	0.001776	-2.28112
MID1	midline 1 [Source:HGNC Symbol;Acc:HGNC:7095]	0.002905	-1.28548
MIS18BP1	MIS18 binding protein 1 [Source:HGNC Symbol;Acc:HGNC:20190]	0.000275	-1.35126
MITF	melanocyte inducing transcription factor [Source:HGNC Symbol;Acc:HGNC:2677]	0.000719	-2.04596
MLH1	mutL homolog 1 [Source:HGNC Symbol;Acc:HGNC:7127]	0.004945	-1.14674
MMD	monocyte to macrophage differentiation associated [Source:HGNC Symbol;Acc:HGNC:2678]	3.47E-05	-1.64034
MMP14	matrix metalloproteinase 14 [Source:HGNC Symbol;Acc:HGNC:7128]	0.0058	-1.19562
MMP9	matrix metalloproteinase 9 [Source:HGNC Symbol;Acc:HGNC:7129]	0.003905	-3.23975
MMS22L	MMS22 like, DNA repair protein [Source:HGNC Symbol;Acc:HGNC:2679]	4.12E-07	-1.48159
MNS1	meiosis specific nuclear structural 1 [Source:HGNC Symbol;Acc:HGNC:2680]	9.32E-05	-2.21586
MNX1	motor neuron and pancreas homeobox 1 [Source:HGNC Symbol;Acc:HGNC:2681]	0.000115	-1.64367
MOB1B	MOB kinase activator 1B [Source:HGNC Symbol;Acc:HGNC:29801]	0.003963	-1.22986
MOB3B	MOB kinase activator 3B [Source:HGNC Symbol;Acc:HGNC:23825]	0.002431	-1.2638
MOCOS	molybdenum cofactor sulfurase [Source:HGNC Symbol;Acc:HGNC:2682]	0.004467	-1.12973
MOK	MOK protein kinase [Source:HGNC Symbol;Acc:HGNC:9833]	0.009316	-1.82952
MON2	MON2 homolog, regulator of endosome-to-Golgi trafficking [Source:HGNC Symbol;Acc:HGNC:2683]	2.92E-05	-1.51931
MOXD1	monooxygenase DBH like 1 [Source:HGNC Symbol;Acc:HGNC:2100]	0.000105	-1.99861
MPDZ	multiple PDZ domain crumbs cell polarity complex component [Source:HGNC Symbol;Acc:HGNC:2684]	0.003585	-1.72404
MPND	MPN domain containing [Source:HGNC Symbol;Acc:HGNC:25934]	0.00165	-1.75223
MPP2	membrane palmitoylated protein 2 [Source:HGNC Symbol;Acc:HGNC:2685]	0.00811	-1.40522
MPP6	membrane palmitoylated protein 6 [Source:HGNC Symbol;Acc:HGNC:2686]	0.00099	-2.39582
MRE11	MRE11 homolog, double strand break repair nuclease [Source:HGNC Symbol;Acc:HGNC:2687]	0.000642	-1.22874
MRFAP1	Morf4 family associated protein 1 [Source:HGNC Symbol;Acc:HGNC:2688]	1.08E-05	-1.41773
MRTFA	myocardin related transcription factor A [Source:HGNC Symbol;Acc:HGNC:2689]	0.005125	-1.45287
MSH2	mutS homolog 2 [Source:HGNC Symbol;Acc:HGNC:7325]	1.44E-07	-1.61761
MSH3	mutS homolog 3 [Source:HGNC Symbol;Acc:HGNC:7326]	2.06E-05	-1.29812

MSH6	mutS homolog 6 [Source:HGNC Symbol;Acc:HGNC:7329]	2.23E-17	-1.50302
MTA2	metastasis associated 1 family member 2 [Source:HGNC Symbol;Acc:HGNC:7329]	0.002185	-1.24149
MTAP	methylthioadenosine phosphorylase [Source:HGNC Symbol;Acc:HGNC:7329]	0.000294	-1.57019
MTHFD1	methylenetetrahydrofolate dehydrogenase, cyclohydrolase and formyltransferase [Source:HGNC Symbol;Acc:HGNC:7329]	1.56E-12	-1.67422
MTHFD1L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) [Source:HGNC Symbol;Acc:HGNC:7329]	0.001942	-1.24421
MTRNR2L8	MT-RNR2 like 8 [Source:HGNC Symbol;Acc:HGNC:37165]	0.010586	-2.14183
MUTYH	mutY DNA glycosylase [Source:HGNC Symbol;Acc:HGNC:7527]	1.06E-06	-1.77175
MVB12B	multivesicular body subunit 12B [Source:HGNC Symbol;Acc:HGNC:7329]	0.000595	-1.83779
MXD3	MAX dimerization protein 3 [Source:HGNC Symbol;Acc:HGNC:14604]	1.49E-06	-1.66589
MYB	MYB proto-oncogene, transcription factor [Source:HGNC Symbol;Acc:HGNC:754]	3.77E-06	-1.52226
MYBL1	MYB proto-oncogene like 1 [Source:HGNC Symbol;Acc:HGNC:754]	1.48E-07	-1.7766
MYBL2	MYB proto-oncogene like 2 [Source:HGNC Symbol;Acc:HGNC:754]	6.16E-06	-3.43399
MYD88	MYD88 innate immune signal transduction adaptor [Source:HGNC Symbol;Acc:HGNC:754]	2.18E-06	-1.79453
MYEF2	myelin expression factor 2 [Source:HGNC Symbol;Acc:HGNC:1794]	0.000316	-2.41564
MYO1B	myosin IB [Source:HGNC Symbol;Acc:HGNC:7596]	8.42E-08	-1.71564
MYO5C	myosin VC [Source:HGNC Symbol;Acc:HGNC:7604]	0.002475	-1.94798
MYO6	myosin VI [Source:HGNC Symbol;Acc:HGNC:7605]	1.75E-05	-1.44138
MYOF	myoferlin [Source:HGNC Symbol;Acc:HGNC:3656]	0.010156	-1.66402
MYPN	myopalladin [Source:HGNC Symbol;Acc:HGNC:23246]	0.000127	-4.47006
NAA15	N(alpha)-acetyltransferase 15, NatA auxiliary subunit [Source:HGNC Symbol;Acc:HGNC:7604]	0.00864	-1.15234
NAA16	N(alpha)-acetyltransferase 16, NatA auxiliary subunit [Source:HGNC Symbol;Acc:HGNC:7604]	0.000404	-1.36125
NAA40	N(alpha)-acetyltransferase 40, NatD catalytic subunit [Source:HGNC Symbol;Acc:HGNC:7604]	0.000293	-1.95868
NAB1	NGFI-A binding protein 1 [Source:HGNC Symbol;Acc:HGNC:7626]	2.18E-07	-1.47576
NALCN	sodium leak channel, non-selective [Source:HGNC Symbol;Acc:HGNC:7626]	0.001094	-2.44025
NAP1L4	nucleosome assembly protein 1 like 4 [Source:HGNC Symbol;Acc:HGNC:7626]	0.004861	-1.12184
NASP	nuclear autoantigenic sperm protein [Source:HGNC Symbol;Acc:HGNC:7626]	1.03E-06	-1.72057
NAT10	N-acetyltransferase 10 [Source:HGNC Symbol;Acc:HGNC:29830]	0.003107	-1.73834
NAV3	neuron navigator 3 [Source:HGNC Symbol;Acc:HGNC:15998]	0.000133	-3.53807
NBPF3	NBPF member 3 [Source:HGNC Symbol;Acc:HGNC:25076]	0.006826	-1.21205
NCAPD2	non-SMC condensin I complex subunit D2 [Source:HGNC Symbol;Acc:HGNC:7626]	0.000114	-1.75719
NCAPD3	non-SMC condensin II complex subunit D3 [Source:HGNC Symbol;Acc:HGNC:7626]	0.004336	-1.53277
NCAPG	non-SMC condensin I complex subunit G [Source:HGNC Symbol;Acc:HGNC:7626]	6.44E-05	-2.00295
NCAPG2	non-SMC condensin II complex subunit G2 [Source:HGNC Symbol;Acc:HGNC:7626]	0.001181	-1.92781
NCAPH	non-SMC condensin I complex subunit H [Source:HGNC Symbol;Acc:HGNC:7626]	6.05E-05	-2.04376
NCAPH2	non-SMC condensin II complex subunit H2 [Source:HGNC Symbol;Acc:HGNC:7626]	0.001232	-1.3283
NCBP3	nuclear cap binding subunit 3 [Source:HGNC Symbol;Acc:HGNC:25076]	8.40E-09	-1.32582
NCCRP1	NCCRP1, F-box associated domain containing [Source:HGNC Symbol;Acc:HGNC:7626]	0.000724	-3.19056
NCK2	NCK adaptor protein 2 [Source:HGNC Symbol;Acc:HGNC:7665]	0.003454	-1.21966
NCL	nucleolin [Source:HGNC Symbol;Acc:HGNC:7667]	0.000311	-2.01553
NDC1	NDC1 transmembrane nucleoporin [Source:HGNC Symbol;Acc:HGNC:7667]	0.001503	-1.45443
NDC80	NDC80 kinetochore complex component [Source:HGNC Symbol;Acc:HGNC:7667]	3.82E-06	-1.65077
NDRG3	NDRG family member 3 [Source:HGNC Symbol;Acc:HGNC:14462]	6.55E-06	-1.18037
NECTIN3	nectin cell adhesion molecule 3 [Source:HGNC Symbol;Acc:HGNC:7667]	0.008554	-1.34856
NEDD1	NEDD1 gamma-tubulin ring complex targeting factor [Source:HGNC Symbol;Acc:HGNC:7667]	6.77E-06	-1.36684
NEDD4L	NEDD4 like E3 ubiquitin protein ligase [Source:HGNC Symbol;Acc:HGNC:7667]	0.003927	-1.4946
NEDD9	neural precursor cell expressed, developmentally down-regulated [Source:HGNC Symbol;Acc:HGNC:7667]	0.004629	-1.25015
NEMF	nuclear export mediator factor [Source:HGNC Symbol;Acc:HGNC:7667]	0.000776	-1.29036

NEMP2	nuclear envelope integral membrane protein 2 [Source:HGNC Symbol;Acc:HGNC:14600]	0.000148	-1.95565
NET1	neuroepithelial cell transforming 1 [Source:HGNC Symbol;Acc:HGNC:14601]	0.0005	-2.026
NETO2	neuropilin and tolloid like 2 [Source:HGNC Symbol;Acc:HGNC:14602]	0.000986	-2.02604
NEU3	neuraminidase 3 [Source:HGNC Symbol;Acc:HGNC:7760]	0.000392	-1.59603
NEXN	nexilin F-actin binding protein [Source:HGNC Symbol;Acc:HGNC:20000]	0.004493	-2.31468
NFATC2IP	nuclear factor of activated T cells 2 interacting protein [Source:HGNC Symbol;Acc:HGNC:20001]	0.00698	-1.36867
NFIB	nuclear factor I B [Source:HGNC Symbol;Acc:HGNC:7785]	2.68E-09	-2.02411
NFKB1	nuclear factor kappa B subunit 1 [Source:HGNC Symbol;Acc:HGNC:7786]	0.003208	-1.62089
NHLRC3	NHL repeat containing 3 [Source:HGNC Symbol;Acc:HGNC:33751]	2.06E-07	-1.62039
NID1	nidogen 1 [Source:HGNC Symbol;Acc:HGNC:7821]	0.007474	-1.55798
NIN	ninein [Source:HGNC Symbol;Acc:HGNC:14906]	0.003217	-1.21989
NINJ1	ninjurin 1 [Source:HGNC Symbol;Acc:HGNC:7824]	0.008741	-1.34815
NIPAL1	NIPA like domain containing 1 [Source:HGNC Symbol;Acc:HGNC:20002]	1.41E-05	-1.51772
NIPBL	NIPBL cohesin loading factor [Source:HGNC Symbol;Acc:HGNC:20003]	0.003413	-1.27334
NKTR	natural killer cell triggering receptor [Source:HGNC Symbol;Acc:HGNC:20004]	0.003346	-1.38442
NKX1-2	NK1 homeobox 2 [Source:HGNC Symbol;Acc:HGNC:31652]	0.002228	-2.74263
NKX3-1	NK3 homeobox 1 [Source:HGNC Symbol;Acc:HGNC:7838]	0.00148	-2.75549
NLE1	notchless homolog 1 [Source:HGNC Symbol;Acc:HGNC:19889]	0.000567	-1.4551
NLN	neurolysin [Source:HGNC Symbol;Acc:HGNC:16058]	0.002125	-1.25544
NNT	nicotinamide nucleotide transhydrogenase [Source:HGNC Symbol;Acc:HGNC:16059]	1.59E-09	-1.42561
NOC2L	NOC2 like nucleolar associated transcriptional repressor [Source:HGNC Symbol;Acc:HGNC:20005]	0.009124	-1.38618
NOC4L	nucleolar complex associated 4 homolog [Source:HGNC Symbol;Acc:HGNC:20006]	0.000118	-1.39515
NOG	noggin [Source:HGNC Symbol;Acc:HGNC:7866]	0.011375	-2.07204
NOL6	nucleolar protein 6 [Source:HGNC Symbol;Acc:HGNC:19910]	0.000727	-1.63182
NOLC1	nucleolar and coiled-body phosphoprotein 1 [Source:HGNC Symbol;Acc:HGNC:19911]	0.002804	-1.28926
NONO	non-POU domain containing octamer binding [Source:HGNC Symbol;Acc:HGNC:19912]	6.73E-05	-1.51262
NOX1	NADPH oxidase 1 [Source:HGNC Symbol;Acc:HGNC:7889]	0.007371	-2.33974
NPAT	nuclear protein, coactivator of histone transcription [Source:HGNC Symbol;Acc:HGNC:20007]	0.000151	-1.51371
NPBWR1	neuropeptides B and W receptor 1 [Source:HGNC Symbol;Acc:HGNC:20008]	0.003787	-4.30114
NPEPPS	aminopeptidase puromycin sensitive [Source:HGNC Symbol;Acc:HGNC:20009]	0.001339	-1.24011
NPTX1	neuronal pentraxin 1 [Source:HGNC Symbol;Acc:HGNC:7952]	0.001138	-2.15773
NR3C2	nuclear receptor subfamily 3 group C member 2 [Source:HGNC Symbol;Acc:HGNC:8000]	0.001557	-2.34902
NRG1	neuregulin 1 [Source:HGNC Symbol;Acc:HGNC:7997]	0.002292	-1.47532
NRGN	neurogranin [Source:HGNC Symbol;Acc:HGNC:8000]	0.004293	-2.70257
NRIP1	nuclear receptor interacting protein 1 [Source:HGNC Symbol;Acc:HGNC:8001]	0.001713	-1.70063
NRM	nurim [Source:HGNC Symbol;Acc:HGNC:8003]	6.04E-06	-1.51594
NRP1	neuropilin 1 [Source:HGNC Symbol;Acc:HGNC:8004]	0.000215	-2.4436
NRP2	neuropilin 2 [Source:HGNC Symbol;Acc:HGNC:8005]	0.010907	-1.67077
NT5DC2	5'-nucleotidase domain containing 2 [Source:HGNC Symbol;Acc:HGNC:8006]	0.010976	-1.21367
NT5DC3	5'-nucleotidase domain containing 3 [Source:HGNC Symbol;Acc:HGNC:8007]	0.01101	-1.80752
NT5E	5'-nucleotidase ecto [Source:HGNC Symbol;Acc:HGNC:8021]	0.000463	-1.77506
NTN1	netrin 1 [Source:HGNC Symbol;Acc:HGNC:8029]	0.004186	-2.23696
NUDC	nuclear distribution C, dynein complex regulator [Source:HGNC Symbol;Acc:HGNC:8030]	5.07E-07	-1.59085
NUF2	NUF2 component of NDC80 kinetochore complex [Source:HGNC Symbol;Acc:HGNC:8031]	0.00642	-1.24998
NUP133	nucleoporin 133 [Source:HGNC Symbol;Acc:HGNC:18016]	6.84E-06	-1.23063
NUP155	nucleoporin 155 [Source:HGNC Symbol;Acc:HGNC:8063]	0.000145	-1.3671
NUP160	nucleoporin 160 [Source:HGNC Symbol;Acc:HGNC:18017]	1.07E-08	-1.67007

NUP205	nucleoporin 205 [Source:HGNC Symbol;Acc:HGNC:18658]	9.84E-08	-1.38886
NUP62	nucleoporin 62 [Source:HGNC Symbol;Acc:HGNC:8066]	0.001568	-1.43882
NUP93	nucleoporin 93 [Source:HGNC Symbol;Acc:HGNC:28958]	0.002383	-1.14326
NUP98	nucleoporin 98 [Source:HGNC Symbol;Acc:HGNC:8068]	4.65E-05	-1.60727
NUSAP1	nucleolar and spindle associated protein 1 [Source:HGNC Symbol;Acc:HGNC:8078]	0.009081	-1.17772
NXPH4	neurexophilin 4 [Source:HGNC Symbol;Acc:HGNC:8078]	0.000263	-1.65024
OCRL	OCRL inositol polyphosphate-5-phosphatase [Source:HGNC Symbol;Acc:HGNC:8078]	0.000541	-1.22556
OGG1	8-oxoguanine DNA glycosylase [Source:HGNC Symbol;Acc:HGNC:8066]	0.004818	-1.28716
OGT	O-linked N-acetylglucosamine (GlcNAc) transferase [Source:HGNC Symbol;Acc:HGNC:8066]	0.005148	-1.25084
OLFML2B	olfactomedin like 2B [Source:HGNC Symbol;Acc:HGNC:24558]	0.003063	-4.32941
OPA1	OPA1 mitochondrial dynamin like GTPase [Source:HGNC Symbol;Acc:HGNC:8068]	0.000613	-1.26836
ORC1	origin recognition complex subunit 1 [Source:HGNC Symbol;Acc:HGNC:8068]	2.44E-22	-1.64439
OSMR	oncostatin M receptor [Source:HGNC Symbol;Acc:HGNC:8507]	0.010854	-1.32162
OSR1	odd-skipped related transcription factor 1 [Source:HGNC Symbol;Acc:HGNC:8068]	0.011207	-2.76639
OTUD6B	OTU deubiquitinase 6B [Source:HGNC Symbol;Acc:HGNC:24281]	0.00044	-1.61983
OTULIN	OTU deubiquitinase with linear linkage specificity [Source:HGNC Symbol;Acc:HGNC:8068]	0.001005	-1.25016
OXCT1	3-oxoacid CoA-transferase 1 [Source:HGNC Symbol;Acc:HGNC:8507]	0.000466	-1.65546
OXTR	oxytocin receptor [Source:HGNC Symbol;Acc:HGNC:8529]	8.68E-05	-1.45266
PA2G4	proliferation-associated 2G4 [Source:HGNC Symbol;Acc:HGNC:8507]	0.004256	-1.27025
PABPC4L	poly(A) binding protein cytoplasmic 4 like [Source:HGNC Symbol;Acc:HGNC:8068]	6.86E-06	-1.61246
PACS2	phosphofurin acidic cluster sorting protein 2 [Source:HGNC Symbol;Acc:HGNC:8068]	0.00367	-1.44237
PACSL1	protein kinase C and casein kinase substrate in neurons 1 [Source:HGNC Symbol;Acc:HGNC:8068]	0.006953	-1.30134
PAFAH1B2	platelet activating factor acetylhydrolase 1b catalytic subunit 2 [Source:HGNC Symbol;Acc:HGNC:8068]	0.004819	-1.20616
PAK2	p21 (RAC1) activated kinase 2 [Source:HGNC Symbol;Acc:HGNC:8068]	0.000566	-1.31898
PAOX	polyamine oxidase [Source:HGNC Symbol;Acc:HGNC:20837]	0.006014	-2.3158
PAPSS2	3'-phosphoadenosine 5'-phosphosulfate synthase 2 [Source:HGNC Symbol;Acc:HGNC:8068]	2.35E-05	-1.78371
PAQR4	progesterone and adipoQ receptor family member 4 [Source:HGNC Symbol;Acc:HGNC:8068]	0.001506	-1.41672
PAQR8	progesterone and adipoQ receptor family member 8 [Source:HGNC Symbol;Acc:HGNC:8068]	0.001983	-1.85526
PARD3B	par-3 family cell polarity regulator beta [Source:HGNC Symbol;Acc:HGNC:8068]	0.007217	-2.14696
PARP1	poly(ADP-ribose) polymerase 1 [Source:HGNC Symbol;Acc:HGNC:8068]	0.000289	-1.93631
PARP14	poly(ADP-ribose) polymerase family member 14 [Source:HGNC Symbol;Acc:HGNC:8068]	0.001772	-1.48039
PARP4	poly(ADP-ribose) polymerase family member 4 [Source:HGNC Symbol;Acc:HGNC:8068]	2.78E-05	-1.49579
PARVA	parvin alpha [Source:HGNC Symbol;Acc:HGNC:14652]	0.000539	-1.66455
PATL1	PAT1 homolog 1, processing body mRNA decay factor [Source:HGNC Symbol;Acc:HGNC:8068]	0.000561	-1.34049
PAWR	pro-apoptotic WT1 regulator [Source:HGNC Symbol;Acc:HGNC:8068]	0.006967	-1.20957
PAXIP1	PAX interacting protein 1 [Source:HGNC Symbol;Acc:HGNC:8624]	1.91E-05	-1.6287
PBDC1	polysaccharide biosynthesis domain containing 1 [Source:HGNC Symbol;Acc:HGNC:8068]	6.69E-05	-1.47118
PBRM1	polybromo 1 [Source:HGNC Symbol;Acc:HGNC:30064]	0.001347	-1.41321
PCDH7	protocadherin 7 [Source:HGNC Symbol;Acc:HGNC:8659]	0.005221	-1.96842
PCDH9	protocadherin 9 [Source:HGNC Symbol;Acc:HGNC:8661]	0.00169	-2.85641
PCM1	pericentriolar material 1 [Source:HGNC Symbol;Acc:HGNC:8727]	0.000109	-1.37106
PCNX1	pecanex 1 [Source:HGNC Symbol;Acc:HGNC:19740]	0.011574	-1.38912
PCNX4	pecanex 4 [Source:HGNC Symbol;Acc:HGNC:20349]	0.000142	-1.7557
PCSK1N	proprotein convertase subtilisin/kexin type 1 inhibitor [Source:HGNC Symbol;Acc:HGNC:8068]	0.006942	-1.29537
PCSK9	proprotein convertase subtilisin/kexin type 9 [Source:HGNC Symbol;Acc:HGNC:8068]	6.72E-08	-1.35365
PDAP1	PDGFA associated protein 1 [Source:HGNC Symbol;Acc:HGNC:14652]	0.001094	-1.40352
PDCD6IP	programmed cell death 6 interacting protein [Source:HGNC Symbol;Acc:HGNC:8068]	3.40E-06	-1.28834

PDE12	phosphodiesterase 12 [Source:HGNC Symbol;Acc:HGNC:25386]	5.53E-06	-1.47877
PDE5A	phosphodiesterase 5A [Source:HGNC Symbol;Acc:HGNC:8784]	0.001063	-1.38576
PDE8A	phosphodiesterase 8A [Source:HGNC Symbol;Acc:HGNC:8793]	0.002275	-1.43449
PDGFC	platelet derived growth factor C [Source:HGNC Symbol;Acc:HGNC:16501]	1.36E-06	-1.58965
PDLIM4	PDZ and LIM domain 4 [Source:HGNC Symbol;Acc:HGNC:16501]	1.28E-05	-1.30408
PDPN	podoplanin [Source:HGNC Symbol;Acc:HGNC:29602]	0.00014	-1.39879
PDS5A	PDS5 cohesin associated factor A [Source:HGNC Symbol;Acc:HGNC:14005]	0.005045	-1.16281
PDS5B	PDS5 cohesin associated factor B [Source:HGNC Symbol;Acc:HGNC:14005]	0.011332	-1.18658
PEG10	paternally expressed 10 [Source:HGNC Symbol;Acc:HGNC:14005]	0.001171	-1.55793
PFAS	phosphoribosylformylglycinamidine synthase [Source:HGNC Symbol;Acc:HGNC:14005]	0.0044	-2.30206
PFKFB3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 [Source:HGNC Symbol;Acc:HGNC:14005]	0.004042	-1.47168
PFKM	phosphofructokinase, muscle [Source:HGNC Symbol;Acc:HGNC:14005]	5.36E-06	-1.40622
PGBD1	piggyBac transposable element derived 1 [Source:HGNC Symbol;Acc:HGNC:14005]	0.001068	-1.8124
PGP	phosphoglycolate phosphatase [Source:HGNC Symbol;Acc:HGNC:14005]	3.82E-05	-1.38173
PGRMC1	progesterone receptor membrane component 1 [Source:HGNC Symbol;Acc:HGNC:14005]	1.88E-09	-1.38168
PHACTR2	phosphatase and actin regulator 2 [Source:HGNC Symbol;Acc:HGNC:14005]	0.001624	-1.40873
PHACTR4	phosphatase and actin regulator 4 [Source:HGNC Symbol;Acc:HGNC:14005]	0.002265	-1.23427
PHF10	PHD finger protein 10 [Source:HGNC Symbol;Acc:HGNC:18250]	0.003205	-1.30905
PHF13	PHD finger protein 13 [Source:HGNC Symbol;Acc:HGNC:22983]	0.000521	-1.28084
PHF14	PHD finger protein 14 [Source:HGNC Symbol;Acc:HGNC:22203]	0.000187	-1.31966
PHF20L1	PHD finger protein 20 like 1 [Source:HGNC Symbol;Acc:HGNC:24203]	0.002524	-1.2111
PHF3	PHD finger protein 3 [Source:HGNC Symbol;Acc:HGNC:8921]	0.001208	-1.28674
PHKB	phosphorylase kinase regulatory subunit beta [Source:HGNC Symbol;Acc:HGNC:14005]	0.000513	-1.30828
PHLPP1	PH domain and leucine rich repeat protein phosphatase 1 [Source:HGNC Symbol;Acc:HGNC:14005]	7.74E-05	-1.99834
PIANP	PILR alpha associated neural protein [Source:HGNC Symbol;Acc:HGNC:14005]	0.001675	-1.84381
PIF1	PIF1 5'-to-3' DNA helicase [Source:HGNC Symbol;Acc:HGNC:2622]	0.001015	-1.35241
PIGM	phosphatidylinositol glycan anchor biosynthesis class M [Source:HGNC Symbol;Acc:HGNC:14005]	0.00927	-2.18477
PIK3R3	phosphoinositide-3-kinase regulatory subunit 3 [Source:HGNC Symbol;Acc:HGNC:14005]	0.007136	-1.43481
PIK3R4	phosphoinositide-3-kinase regulatory subunit 4 [Source:HGNC Symbol;Acc:HGNC:14005]	0.005772	-1.27875
PIMREG	PICALM interacting mitotic regulator [Source:HGNC Symbol;Acc:HGNC:14005]	0.008216	-1.31718
PINK1	PTEN induced kinase 1 [Source:HGNC Symbol;Acc:HGNC:14581]	0.007873	-1.32791
PITPNA	phosphatidylinositol transfer protein alpha [Source:HGNC Symbol;Acc:HGNC:14005]	0.003417	-1.41242
PITPNM2	phosphatidylinositol transfer protein membrane associated 2 [Source:HGNC Symbol;Acc:HGNC:14005]	0.007808	-1.51843
PITRM1	pitrilysin metalloproteinase 1 [Source:HGNC Symbol;Acc:HGNC:17001]	0.000233	-1.38703
PKIA	cAMP-dependent protein kinase inhibitor alpha [Source:HGNC Symbol;Acc:HGNC:14005]	0.002494	-2.02124
PKMYT1	protein kinase, membrane associated tyrosine/threonine 1 [Source:HGNC Symbol;Acc:HGNC:14005]	6.89E-05	-2.9735
PKP2	plakophilin 2 [Source:HGNC Symbol;Acc:HGNC:9024]	1.46E-07	-1.43771
PKP4	plakophilin 4 [Source:HGNC Symbol;Acc:HGNC:9026]	0.010587	-1.23022
PLAT	plasminogen activator, tissue type [Source:HGNC Symbol;Acc:HGNC:14005]	0.00105	-2.5705
PLCD3	phospholipase C delta 3 [Source:HGNC Symbol;Acc:HGNC:9061]	0.000863	-1.30157
PLCE1	phospholipase C epsilon 1 [Source:HGNC Symbol;Acc:HGNC:1717]	0.000692	-1.88685
PLEKHA5	pleckstrin homology domain containing A5 [Source:HGNC Symbol;Acc:HGNC:14005]	4.27E-08	-1.31735
PLEKHA7	pleckstrin homology domain containing A7 [Source:HGNC Symbol;Acc:HGNC:14005]	0.006541	-1.72791
PLEKHG1	pleckstrin homology and RhoGEF domain containing G1 [Source:HGNC Symbol;Acc:HGNC:14005]	0.004249	-1.48193
PLK1	polo like kinase 1 [Source:HGNC Symbol;Acc:HGNC:9077]	0.000116	-1.64536
PLK4	polo like kinase 4 [Source:HGNC Symbol;Acc:HGNC:11397]	2.50E-05	-1.73119
PLOD1	procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 [Source:HGNC Symbol;Acc:HGNC:14005]	0.007085	-1.46091

PLOD3	procollagen-lysine,2-oxoglutarate 5-dioxygenase 3 [Source:HGNC	0.00321	-1.22076
PLS1	plastin 1 [Source:HGNC Symbol;Acc:HGNC:9090]	2.30E-08	-1.4525
PLXNA1	plexin A1 [Source:HGNC Symbol;Acc:HGNC:9099]	0.011001	-1.92386
PM20D2	peptidase M20 domain containing 2 [Source:HGNC Symbol;Acc:H	0.010892	-1.14101
PNISR	PNN interacting serine and arginine rich protein [Source:HGNC Sy	0.000559	-1.16222
PNKP	polynucleotide kinase 3'-phosphatase [Source:HGNC Symbol;Acc	0.00021	-1.79284
PNN	pinin, desmosome associated protein [Source:HGNC Symbol;Acc:	4.92E-05	-1.57587
PODXL2	podocalyxin like 2 [Source:HGNC Symbol;Acc:HGNC:17936]	0.000416	-1.54114
POFUT1	protein O-fucosyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:	0.009981	-1.44154
POGZ	pogo transposable element derived with ZNF domain [Source:HG	0.004953	-1.4965
POLA1	DNA polymerase alpha 1, catalytic subunit [Source:HGNC Symbol	0.001091	-1.78985
POLD1	DNA polymerase delta 1, catalytic subunit [Source:HGNC Symbol	0.000463	-1.41475
POLH	DNA polymerase eta [Source:HGNC Symbol;Acc:HGNC:9181]	0.001304	-1.3504
POLQ	DNA polymerase theta [Source:HGNC Symbol;Acc:HGNC:9186]	0.000106	-2.53062
POLR2A	RNA polymerase II subunit A [Source:HGNC Symbol;Acc:HGNC:91	0.004573	-1.56439
POLR3A	RNA polymerase III subunit A [Source:HGNC Symbol;Acc:HGNC:31	0.002642	-1.27455
POLR3B	RNA polymerase III subunit B [Source:HGNC Symbol;Acc:HGNC:31	0.004507	-1.75615
POMGNT2	protein O-linked mannose N-acetylglucosaminyltransferase 2 (be	0.004081	-1.43966
PPAT	phosphoribosyl pyrophosphate amidotransferase [Source:HGNC	0.000941	-1.29045
PPM1G	protein phosphatase, Mg2+/Mn2+ dependent 1G [Source:HGNC:	0.00155	-1.50802
PPP1R12A	protein phosphatase 1 regulatory subunit 12A [Source:HGNC Syn	9.47E-05	-1.24635
PPP1R3B	protein phosphatase 1 regulatory subunit 3B [Source:HGNC Sym	0.011482	-1.47168
PPP1R7	protein phosphatase 1 regulatory subunit 7 [Source:HGNC Symbo	6.65E-06	-1.33181
PPP1R9A	protein phosphatase 1 regulatory subunit 9A [Source:HGNC Sym	0.000199	-2.52518
PPP3CA	protein phosphatase 3 catalytic subunit alpha [Source:HGNC Sym	0.011373	-1.38268
PPP4R1	protein phosphatase 4 regulatory subunit 1 [Source:HGNC Symbo	0.002615	-1.26307
PPP5C	protein phosphatase 5 catalytic subunit [Source:HGNC Symbol;Ac	1.19E-06	-1.29082
PPWD1	peptidylprolyl isomerase domain and WD repeat containing 1 [Sc	0.001073	-1.24287
PRC1	protein regulator of cytokinesis 1 [Source:HGNC Symbol;Acc:HGNC	3.48E-05	-1.80918
PREP	prolyl endopeptidase [Source:HGNC Symbol;Acc:HGNC:9358]	0.003427	-1.15642
PREPL	prolyl endopeptidase like [Source:HGNC Symbol;Acc:HGNC:30221	3.39E-15	-1.71011
PREX1	phosphatidylinositol-3,4,5-trisphosphate dependent Rac exchang	0.003608	-2.89326
PRICKLE1	prickle planar cell polarity protein 1 [Source:HGNC Symbol;Acc:H	0.006968	-2.59774
PRKACA	protein kinase cAMP-activated catalytic subunit alpha [Source:HC	0.001241	-1.42649
PRKAR1A	protein kinase cAMP-dependent type I regulatory subunit alpha [	0.005687	-1.20096
PRKAR1B	protein kinase cAMP-dependent type I regulatory subunit beta [S	0.000622	-1.54934
PRKAR2A	protein kinase cAMP-dependent type II regulatory subunit alpha	0.009247	-1.20146
PRKCSH	protein kinase C substrate 80K-H [Source:HGNC Symbol;Acc:HGNC	0.008558	-1.17771
PRKD3	protein kinase D3 [Source:HGNC Symbol;Acc:HGNC:9408]	0.008832	-1.17238
PRKX	protein kinase X-linked [Source:HGNC Symbol;Acc:HGNC:9441]	5.78E-05	-1.24525
PRMT5	protein arginine methyltransferase 5 [Source:HGNC Symbol;Acc:H	2.89E-07	-1.48691
PRMT7	protein arginine methyltransferase 7 [Source:HGNC Symbol;Acc:H	0.002107	-1.38457
PROSER2	proline and serine rich 2 [Source:HGNC Symbol;Acc:HGNC:23728	0.0035	-2.08098
PRPF40A	pre-mRNA processing factor 40 homolog A [Source:HGNC Symbo	0.000868	-1.22169
PRPF6	pre-mRNA processing factor 6 [Source:HGNC Symbol;Acc:HGNC:1	0.006485	-1.45501
PRR11	proline rich 11 [Source:HGNC Symbol;Acc:HGNC:25619]	5.17E-09	-1.61126
PRR5L	proline rich 5 like [Source:HGNC Symbol;Acc:HGNC:25878]	1.34E-05	-1.77334

PRSS12	serine protease 12 [Source:HGNC Symbol;Acc:HGNC:9477]	0.004918	-1.55008
PRSS23	serine protease 23 [Source:HGNC Symbol;Acc:HGNC:14370]	8.75E-05	-1.35629
PRTFDC1	phosphoribosyl transferase domain containing 1 [Source:HGNC S	0.009236	-1.98105
PSIP1	PC4 and SFRS1 interacting protein 1 [Source:HGNC Symbol;Acc:H	1.57E-10	-1.37307
PSMC5	proteasome 26S subunit, ATPase 5 [Source:HGNC Symbol;Acc:HC	0.004328	-1.22711
PSMD1	proteasome 26S subunit, non-ATPase 1 [Source:HGNC Symbol;Ac	3.17E-05	-1.34911
PSMD11	proteasome 26S subunit, non-ATPase 11 [Source:HGNC Symbol;A	0.003376	-1.18426
PSMD12	proteasome 26S subunit, non-ATPase 12 [Source:HGNC Symbol;A	0.000158	-1.39732
PSMD2	proteasome 26S subunit, non-ATPase 2 [Source:HGNC Symbol;Ac	0.000196	-1.61573
PSME4	proteasome activator subunit 4 [Source:HGNC Symbol;Acc:HGNC	0.002051	-1.22244
PSMF1	proteasome inhibitor subunit 1 [Source:HGNC Symbol;Acc:HGNC	0.001796	-1.21798
PSPC1	paraspeckle component 1 [Source:HGNC Symbol;Acc:HGNC:2032	0.000374	-1.49767
PTBP1	polypyrimidine tract binding protein 1 [Source:HGNC Symbol;Acc	0.004542	-1.21562
PTGES2	prostaglandin E synthase 2 [Source:HGNC Symbol;Acc:HGNC:178	0.007749	-1.26613
PTGIS	prostaglandin I2 synthase [Source:HGNC Symbol;Acc:HGNC:9603	0.006234	-3.26898
PTHLH	parathyroid hormone like hormone [Source:HGNC Symbol;Acc:H	0.009728	-1.83021
PTMS	parathymosin [Source:HGNC Symbol;Acc:HGNC:9629]	0.005366	-1.2278
PTP4A2	protein tyrosine phosphatase 4A2 [Source:HGNC Symbol;Acc:HG	3.33E-05	-1.38919
PTPN22	protein tyrosine phosphatase non-receptor type 22 [Source:HGN	0.009166	-2.88509
PTPN6	protein tyrosine phosphatase non-receptor type 6 [Source:HGNC	0.000197	-1.30731
PTPRB	protein tyrosine phosphatase receptor type B [Source:HGNC Sym	0.001233	-2.23258
PTTG1IP	PTTG1 interacting protein [Source:HGNC Symbol;Acc:HGNC:1352	8.42E-05	-1.17584
PUM3	pumilio RNA binding family member 3 [Source:HGNC Symbol;Acc	0.003263	-1.29804
PVR	PVR cell adhesion molecule [Source:HGNC Symbol;Acc:HGNC:97C	0.005579	-1.47226
PXDC1	PX domain containing 1 [Source:HGNC Symbol;Acc:HGNC:21361]	0.007002	-1.2338
PXN	paxillin [Source:HGNC Symbol;Acc:HGNC:9718]	0.006811	-1.7636
PXYLP1	2-phosphoxylose phosphatase 1 [Source:HGNC Symbol;Acc:HGNC	0.000207	-2.29175
PYCR3	pyrroline-5-carboxylate reductase 3 [Source:HGNC Symbol;Acc:H	0.0089	-1.93609
PYGL	glycogen phosphorylase L [Source:HGNC Symbol;Acc:HGNC:9725	1.80E-05	-1.30752
QARS1	glutamyl-tRNA synthetase 1 [Source:HGNC Symbol;Acc:HGNC:S	0.008632	-1.16062
QDPR	quinoid dihydropteridine reductase [Source:HGNC Symbol;Acc:H	4.58E-15	-1.71767
QRFPR	pyroglutamylated RFamide peptide receptor [Source:HGNC Sym	0.000525	-1.30378
QSER1	glutamine and serine rich 1 [Source:HGNC Symbol;Acc:HGNC:261	0.000237	-1.64989
QSOX2	quiescin sulfhydryl oxidase 2 [Source:HGNC Symbol;Acc:HGNC:3C	0.001605	-1.3097
R3HDM1	R3H domain containing 1 [Source:HGNC Symbol;Acc:HGNC:9757]	0.005401	-1.34735
RAB11FIP2	RAB11 family interacting protein 2 [Source:HGNC Symbol;Acc:HG	0.00149	-1.37089
RAB26	RAB26, member RAS oncogene family [Source:HGNC Symbol;Acc	0.003082	-1.61173
RAB27A	RAB27A, member RAS oncogene family [Source:HGNC Symbol;Ac	0.006501	-1.27826
RAB31	RAB31, member RAS oncogene family [Source:HGNC Symbol;Acc	1.60E-05	-1.2564
RAB3GAP1	RAB3 GTPase activating protein catalytic subunit 1 [Source:HGNC	0.002811	-1.28442
RAB7A	RAB7A, member RAS oncogene family [Source:HGNC Symbol;Acc	0.010807	-1.3479
RAB8A	RAB8A, member RAS oncogene family [Source:HGNC Symbol;Acc	0.000511	-1.33503
RAC1	Rac family small GTPase 1 [Source:HGNC Symbol;Acc:HGNC:9801	0.000347	-1.17552
RACGAP1	Rac GTPase activating protein 1 [Source:HGNC Symbol;Acc:HGNC	0.000167	-1.30721
RAD18	RAD18 E3 ubiquitin protein ligase [Source:HGNC Symbol;Acc:HG	4.02E-06	-1.32665
RAD50	RAD50 double strand break repair protein [Source:HGNC Symbol	9.02E-05	-1.48101
RAD51	RAD51 recombinase [Source:HGNC Symbol;Acc:HGNC:9817]	6.28E-05	-1.45346

RAD54L	RAD54 like [Source:HGNC Symbol;Acc:HGNC:9826]	1.20E-05	-2.18283
RALGPS2	Ral GEF with PH domain and SH3 binding motif 2 [Source:HGNC S	0.00046	-1.46802
RANBP17	RAN binding protein 17 [Source:HGNC Symbol;Acc:HGNC:14428]	3.02E-05	-2.03216
RANBP9	RAN binding protein 9 [Source:HGNC Symbol;Acc:HGNC:13727]	5.63E-16	-2.18707
RAPGEF3	Rap guanine nucleotide exchange factor 3 [Source:HGNC Symbol	0.004745	-1.77959
RARA	retinoic acid receptor alpha [Source:HGNC Symbol;Acc:HGNC:986	0.002685	-1.64881
RASAL2	RAS protein activator like 2 [Source:HGNC Symbol;Acc:HGNC:987	0.006461	-1.41894
RAVER1	ribonucleoprotein, PTB binding 1 [Source:HGNC Symbol;Acc:HGN	0.011102	-1.59727
RB1	RB transcriptional corepressor 1 [Source:HGNC Symbol;Acc:HGNC	0.002891	-1.21876
RBFOX2	RNA binding fox-1 homolog 2 [Source:HGNC Symbol;Acc:HGNC:9	0.001291	-1.13341
RBL1	RB transcriptional corepressor like 1 [Source:HGNC Symbol;Acc:H	1.87E-07	-1.63031
RBM12	RNA binding motif protein 12 [Source:HGNC Symbol;Acc:HGNC:9	0.001895	-1.99522
RBM14	RNA binding motif protein 14 [Source:HGNC Symbol;Acc:HGNC:1	6.20E-05	-1.38423
RBM17	RNA binding motif protein 17 [Source:HGNC Symbol;Acc:HGNC:1	0.000112	-1.23221
RBM25	RNA binding motif protein 25 [Source:HGNC Symbol;Acc:HGNC:2	9.69E-07	-1.28591
RBM28	RNA binding motif protein 28 [Source:HGNC Symbol;Acc:HGNC:2	0.003766	-1.55269
RBM38	RNA binding motif protein 38 [Source:HGNC Symbol;Acc:HGNC:1	0.001246	-1.69348
RBMS1	RNA binding motif single stranded interacting protein 1 [Source:f	0.001943	-1.18123
RBMS2	RNA binding motif single stranded interacting protein 2 [Source:f	3.90E-06	-1.74517
RBPM5	RNA binding protein, mRNA processing factor [Source:HGNC Sym	1.83E-07	-2.02659
RCBTB2	RCC1 and BTB domain containing protein 2 [Source:HGNC Symbo	2.13E-08	-2.83806
RCN1	reticulocalbin 1 [Source:HGNC Symbol;Acc:HGNC:9934]	0.001371	-1.55693
RCOR1	REST corepressor 1 [Source:HGNC Symbol;Acc:HGNC:17441]	5.10E-05	-1.36684
RECQL4	RecQ like helicase 4 [Source:HGNC Symbol;Acc:HGNC:9949]	0.008352	-1.82448
REEP2	receptor accessory protein 2 [Source:HGNC Symbol;Acc:HGNC:17	0.001246	-2.13155
REPS2	RALBP1 associated Eps domain containing 2 [Source:HGNC Symb	3.39E-09	-3.0474
RFWD3	ring finger and WD repeat domain 3 [Source:HGNC Symbol;Acc:H	5.70E-08	-1.50081
RFX7	regulatory factor X7 [Source:HGNC Symbol;Acc:HGNC:25777]	0.002439	-1.3052
RFXAP	regulatory factor X associated protein [Source:HGNC Symbol;Acc	6.80E-05	-2.00589
RGCC	regulator of cell cycle [Source:HGNC Symbol;Acc:HGNC:20369]	0.000134	-1.74053
RGL1	ral guanine nucleotide dissociation stimulator like 1 [Source:HGN	0.006471	-1.41544
RGMB	repulsive guidance molecule BMP co-receptor b [Source:HGNC S)	0.002244	-1.41914
RHBDL2	rhomboid like 2 [Source:HGNC Symbol;Acc:HGNC:16083]	0.000968	-1.71327
RHOBTB3	Rho related BTB domain containing 3 [Source:HGNC Symbol;Acc:	0.004907	-1.53904
RHOQ	ras homolog family member Q [Source:HGNC Symbol;Acc:HGNC:	0.001268	-1.20146
RHPN2	rhophilin Rho GTPase binding protein 2 [Source:HGNC Symbol;Ac	1.33E-08	-1.90362
RIBC2	RIB43A domain with coiled-coils 2 [Source:HGNC Symbol;Acc:HG	0.005524	-1.87112
RIF1	replication timing regulatory factor 1 [Source:HGNC Symbol;Acc:l	0.001281	-1.49103
RIMKLB	ribosomal modification protein rimK like family member B [Sourc	0.002904	-1.48722
RIMS2	regulating synaptic membrane exocytosis 2 [Source:HGNC Symbc	0.001339	-2.15032
RMDN3	regulator of microtubule dynamics 3 [Source:HGNC Symbol;Acc:f	3.73E-05	-1.31774
RMI2	RecQ mediated genome instability 2 [Source:HGNC Symbol;Acc:f	0.001541	-1.21964
RNF20	ring finger protein 20 [Source:HGNC Symbol;Acc:HGNC:10062]	7.42E-05	-1.39562
RNF38	ring finger protein 38 [Source:HGNC Symbol;Acc:HGNC:18052]	0.009985	-1.22963
RNPS1	RNA binding protein with serine rich domain 1 [Source:HGNC Syn	0.000673	-1.32153
ROCK1	Rho associated coiled-coil containing protein kinase 1 [Source:HC	0.000379	-1.28125
ROCK2	Rho associated coiled-coil containing protein kinase 2 [Source:HC	1.01E-05	-1.60224

ROGDI	rogdi atypical leucine zipper [Source:HGNC Symbol;Acc:HGNC:29	0.001805	-1.31176
ROR1	receptor tyrosine kinase like orphan receptor 1 [Source:HGNC Sy	4.56E-06	-3.82365
RPA1	replication protein A1 [Source:HGNC Symbol;Acc:HGNC:10289]	0.011466	-1.19852
RPAP3	RNA polymerase II associated protein 3 [Source:HGNC Symbol;Ac	0.000161	-1.39373
RPGR	retinitis pigmentosa GTPase regulator [Source:HGNC Symbol;Acc	0.005377	-1.50936
RPRD1B	regulation of nuclear pre-mRNA domain containing 1B [Source:H	7.88E-08	-1.16887
RPS6KA3	ribosomal protein S6 kinase A3 [Source:HGNC Symbol;Acc:HGNC:	0.000839	-1.42122
RPS6KA4	ribosomal protein S6 kinase A4 [Source:HGNC Symbol;Acc:HGNC:	0.009216	-1.41119
RPS6KB1	ribosomal protein S6 kinase B1 [Source:HGNC Symbol;Acc:HGNC:	0.000118	-1.2603
RPS6KL1	ribosomal protein S6 kinase like 1 [Source:HGNC Symbol;Acc:HGI	0.001351	-3.30202
RRAD	RRAD, Ras related glycolysis inhibitor and calcium channel regula	0.001037	-3.26231
RRM1	ribonucleotide reductase catalytic subunit M1 [Source:HGNC Syn	1.92E-11	-1.38934
RRM2	ribonucleotide reductase regulatory subunit M2 [Source:HGNC S	8.11E-06	-2.65243
RRN3	RRN3 homolog, RNA polymerase I transcription factor [Source:HC	0.002165	-1.26052
RSF1	remodeling and spacing factor 1 [Source:HGNC Symbol;Acc:HGNC	0.010459	-1.18513
RTF1	RTF1 homolog, Paf1/RNA polymerase II complex component [Sou	2.10E-05	-1.31543
RTL8C	retrotransposon Gag like 8C [Source:HGNC Symbol;Acc:HGNC:25	0.011123	-1.29273
RTN3	reticulon 3 [Source:HGNC Symbol;Acc:HGNC:10469]	8.45E-06	-1.24689
RTN4	reticulon 4 [Source:HGNC Symbol;Acc:HGNC:14085]	0.008501	-1.13194
RUNX1	RUNX family transcription factor 1 [Source:HGNC Symbol;Acc:HG	0.002703	-2.18918
RUSC1	RUN and SH3 domain containing 1 [Source:HGNC Symbol;Acc:HG	0.003409	-1.29139
S1PR1	sphingosine-1-phosphate receptor 1 [Source:HGNC Symbol;Acc:f	0.005336	-2.71876
S1PR3	sphingosine-1-phosphate receptor 3 [Source:HGNC Symbol;Acc:f	0.00543	-1.9802
SAA1	serum amyloid A1 [Source:HGNC Symbol;Acc:HGNC:10513]	0.000773	-2.11566
SAE1	SUMO1 activating enzyme subunit 1 [Source:HGNC Symbol;Acc:f	8.54E-07	-1.50812
SALL4	spalt like transcription factor 4 [Source:HGNC Symbol;Acc:HGNC:	0.003148	-2.41003
SAMHD1	SAM and HD domain containing deoxynucleoside triphosphate tr	1.15E-05	-2.74374
SART3	spliceosome associated factor 3, U4/U6 recycling protein [Source	0.001081	-1.28942
SAV1	salvador family WW domain containing protein 1 [Source:HGNC :	5.33E-06	-1.34062
SCAF8	SR-related CTD associated factor 8 [Source:HGNC Symbol;Acc:HG	0.000303	-1.35573
SCARA3	scavenger receptor class A member 3 [Source:HGNC Symbol;Acc:	2.62E-06	-1.5244
SCCPDH	saccharopine dehydrogenase (putative) [Source:HGNC Symbol;Ac	0.00496	-1.36489
SCFD2	sec1 family domain containing 2 [Source:HGNC Symbol;Acc:HGNC	0.002849	-1.26492
SCNN1A	sodium channel epithelial 1 alpha subunit [Source:HGNC Symbol;	0.00897	-1.33509
SCRN2	secernin 2 [Source:HGNC Symbol;Acc:HGNC:30381]	0.008656	-1.18464
SDC3	syndecan 3 [Source:HGNC Symbol;Acc:HGNC:10660]	0.000884	-2.006
SEC23IP	SEC23 interacting protein [Source:HGNC Symbol;Acc:HGNC:1701	0.003055	-1.2321
SEC63	SEC63 homolog, protein translocation regulator [Source:HGNC Sy	0.010999	-1.17359
SECISBP2L	SECIS binding protein 2 like [Source:HGNC Symbol;Acc:HGNC:289	2.93E-08	-1.66677
SECTM1	secreted and transmembrane 1 [Source:HGNC Symbol;Acc:HGNC	0.001162	-1.72393
SEMA3A	semaphorin 3A [Source:HGNC Symbol;Acc:HGNC:10723]	0.00844	-1.70447
SEMA4D	semaphorin 4D [Source:HGNC Symbol;Acc:HGNC:10732]	0.002689	-1.54865
SENP1	SUMO specific peptidase 1 [Source:HGNC Symbol;Acc:HGNC:179	0.001506	-1.19575
SENP6	SUMO specific peptidase 6 [Source:HGNC Symbol;Acc:HGNC:209	0.000576	-1.32858
SEPTIN11	septin 11 [Source:HGNC Symbol;Acc:HGNC:25589]	2.49E-09	-1.44203
SEPTIN6	septin 6 [Source:HGNC Symbol;Acc:HGNC:15848]	7.61E-06	-1.4204
SEPTIN8	septin 8 [Source:HGNC Symbol;Acc:HGNC:16511]	0.007777	-1.17644

SERBP1	SERPINE1 mRNA binding protein 1 [Source:HGNC Symbol;Acc:HGNC:8941]	1.82E-05	-1.44432
SERPINA1	serpin family A member 1 [Source:HGNC Symbol;Acc:HGNC:8941]	4.02E-05	-3.5087
SERTAD2	SERTA domain containing 2 [Source:HGNC Symbol;Acc:HGNC:3071]	7.40E-07	-1.4594
SERTAD4	SERTA domain containing 4 [Source:HGNC Symbol;Acc:HGNC:2522]	5.30E-05	-1.41111
SESN3	sestrin 3 [Source:HGNC Symbol;Acc:HGNC:23060]	0.007166	-1.80459
SESTD1	SEC14 and spectrin domain containing 1 [Source:HGNC Symbol;Acc:HGNC:10733]	0.000131	-1.55937
SET	SET nuclear proto-oncogene [Source:HGNC Symbol;Acc:HGNC:10733]	0.002947	-1.22911
SETBP1	SET binding protein 1 [Source:HGNC Symbol;Acc:HGNC:15573]	0.009342	-1.57473
SETD2	SET domain containing 2, histone lysine methyltransferase [Source:HGNC Symbol;Acc:HGNC:15573]	0.004552	-1.29947
SETD7	SET domain containing 7, histone lysine methyltransferase [Source:HGNC Symbol;Acc:HGNC:15573]	0.00017	-1.35795
SF3A1	splicing factor 3a subunit 1 [Source:HGNC Symbol;Acc:HGNC:10733]	0.000904	-1.37447
SF3A2	splicing factor 3a subunit 2 [Source:HGNC Symbol;Acc:HGNC:10733]	0.00097	-1.37134
SF3A3	splicing factor 3a subunit 3 [Source:HGNC Symbol;Acc:HGNC:10733]	6.04E-05	-1.31267
SF3B3	splicing factor 3b subunit 3 [Source:HGNC Symbol;Acc:HGNC:10733]	7.81E-05	-1.23887
SF3B4	splicing factor 3b subunit 4 [Source:HGNC Symbol;Acc:HGNC:10733]	2.08E-05	-1.65123
SFMBT1	Scm like with four mbt domains 1 [Source:HGNC Symbol;Acc:HGNC:10733]	0.000793	-1.46244
SFMBT2	Scm like with four mbt domains 2 [Source:HGNC Symbol;Acc:HGNC:10733]	0.008476	-1.89794
SFPQ	splicing factor proline and glutamine rich [Source:HGNC Symbol;Acc:HGNC:10733]	0.001265	-2.36643
SFRP1	secreted frizzled related protein 1 [Source:HGNC Symbol;Acc:HGNC:10733]	2.41E-06	-1.36775
SFT2D2	SFT2 domain containing 2 [Source:HGNC Symbol;Acc:HGNC:2514]	0.002081	-1.5136
SFXN2	sideroflexin 2 [Source:HGNC Symbol;Acc:HGNC:16086]	0.000194	-3.4984
SFXN5	sideroflexin 5 [Source:HGNC Symbol;Acc:HGNC:16073]	0.007419	-1.5177
SGMS2	sphingomyelin synthase 2 [Source:HGNC Symbol;Acc:HGNC:2839]	6.56E-09	-1.88528
SGO1	shugoshin 1 [Source:HGNC Symbol;Acc:HGNC:25088]	0.00801	-1.30432
SGO2	shugoshin 2 [Source:HGNC Symbol;Acc:HGNC:30812]	9.21E-06	-1.44458
SH2B3	SH2B adaptor protein 3 [Source:HGNC Symbol;Acc:HGNC:29605]	0.001408	-2.18415
SH3BGR1	SH3 domain binding glutamate rich protein like 1 [Source:HGNC Symbol;Acc:HGNC:10733]	0.000108	-1.30969
SH3BGR2	SH3 domain binding glutamate rich protein like 2 [Source:HGNC Symbol;Acc:HGNC:10733]	0.000108	-1.30969
SH3BP4	SH3 domain binding protein 4 [Source:HGNC Symbol;Acc:HGNC:10733]	3.36E-13	-2.01014
SH3D19	SH3 domain containing 19 [Source:HGNC Symbol;Acc:HGNC:3041]	1.13E-07	-1.36789
SH3KBP1	SH3 domain containing kinase binding protein 1 [Source:HGNC Symbol;Acc:HGNC:10733]	0.000167	-2.14736
SH3RF1	SH3 domain containing ring finger 1 [Source:HGNC Symbol;Acc:HGNC:10733]	0.008654	-1.46606
SHC3	SHC adaptor protein 3 [Source:HGNC Symbol;Acc:HGNC:18181]	0.004009	-2.36367
SHCBP1	SHC binding and spindle associated 1 [Source:HGNC Symbol;Acc:HGNC:10733]	1.38E-05	-2.4339
SHKBP1	SH3KBP1 binding protein 1 [Source:HGNC Symbol;Acc:HGNC:192]	0.007553	-1.28455
SHMT1	serine hydroxymethyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:10733]	0.000361	-1.31067
SHPRH	SNF2 histone linker PHD RING helicase [Source:HGNC Symbol;Acc:HGNC:10733]	0.005661	-1.26977
SHROOM1	shroom family member 1 [Source:HGNC Symbol;Acc:HGNC:2408]	0.002679	-1.93635
SHROOM3	shroom family member 3 [Source:HGNC Symbol;Acc:HGNC:3042]	0.00695	-2.1996
SIAH3	siah E3 ubiquitin protein ligase family member 3 [Source:HGNC Symbol;Acc:HGNC:10733]	0.000202	-3.57985
SIGMAR1	sigma non-opioid intracellular receptor 1 [Source:HGNC Symbol;Acc:HGNC:10733]	0.003616	-1.15796
SIN3A	SIN3 transcription regulator family member A [Source:HGNC Symbol;Acc:HGNC:10733]	0.000161	-1.33312
SIRT1	sirtuin 1 [Source:HGNC Symbol;Acc:HGNC:14929]	0.002833	-1.18298
SIX4	SIX homeobox 4 [Source:HGNC Symbol;Acc:HGNC:10890]	0.000103	-1.41386
SKA1	spindle and kinetochore associated complex subunit 1 [Source:HGNC Symbol;Acc:HGNC:10733]	0.000958	-1.88401
SKP2	S-phase kinase associated protein 2 [Source:HGNC Symbol;Acc:HGNC:10733]	1.02E-05	-1.32885
SLC16A10	solute carrier family 16 member 10 [Source:HGNC Symbol;Acc:HGNC:10733]	0.004883	-1.4792
SLC16A12	solute carrier family 16 member 12 [Source:HGNC Symbol;Acc:HGNC:10733]	0.000802	-2.77213

SLC16A2	solute carrier family 16 member 2 [Source:HGNC Symbol;Acc:HG	0.00478	-1.3237
SLC16A3	solute carrier family 16 member 3 [Source:HGNC Symbol;Acc:HG	0.003989	-1.65279
SLC24A1	solute carrier family 24 member 1 [Source:HGNC Symbol;Acc:HG	0.008152	-1.90864
SLC25A1	solute carrier family 25 member 1 [Source:HGNC Symbol;Acc:HG	4.36E-13	-1.54187
SLC25A10	solute carrier family 25 member 10 [Source:HGNC Symbol;Acc:HG	0.000267	-2.33445
SLC25A13	solute carrier family 25 member 13 [Source:HGNC Symbol;Acc:HG	0.010666	-1.44385
SLC2A13	solute carrier family 2 member 13 [Source:HGNC Symbol;Acc:HG	0.008965	-1.42854
SLC2A3	solute carrier family 2 member 3 [Source:HGNC Symbol;Acc:HG	0.008384	-1.25886
SLC2A6	solute carrier family 2 member 6 [Source:HGNC Symbol;Acc:HG	0.001059	-2.45617
SLC30A4	solute carrier family 30 member 4 [Source:HGNC Symbol;Acc:HG	0.000192	-1.57808
SLC35A3	solute carrier family 35 member A3 [Source:HGNC Symbol;Acc:HG	0.005082	-1.34899
SLC35B2	solute carrier family 35 member B2 [Source:HGNC Symbol;Acc:HG	0.003218	-1.2322
SLC35B4	solute carrier family 35 member B4 [Source:HGNC Symbol;Acc:HG	1.05E-11	-1.85893
SLC35E4	solute carrier family 35 member E4 [Source:HGNC Symbol;Acc:HG	0.003052	-1.43744
SLC35G1	solute carrier family 35 member G1 [Source:HGNC Symbol;Acc:HG	0.000333	-1.8907
SLC37A4	solute carrier family 37 member 4 [Source:HGNC Symbol;Acc:HG	0.000506	-1.327
SLC38A1	solute carrier family 38 member 1 [Source:HGNC Symbol;Acc:HG	3.40E-06	-1.69232
SLC38A7	solute carrier family 38 member 7 [Source:HGNC Symbol;Acc:HG	0.001571	-1.51908
SLC39A1	solute carrier family 39 member 1 [Source:HGNC Symbol;Acc:HG	0.005444	-1.21298
SLC39A8	solute carrier family 39 member 8 [Source:HGNC Symbol;Acc:HG	0.000172	-1.80308
SLC41A2	solute carrier family 41 member 2 [Source:HGNC Symbol;Acc:HG	4.72E-05	-1.94162
SLC45A3	solute carrier family 45 member 3 [Source:HGNC Symbol;Acc:HG	0.00795	-2.3596
SLC45A4	solute carrier family 45 member 4 [Source:HGNC Symbol;Acc:HG	0.004303	-1.63374
SLC4A11	solute carrier family 4 member 11 [Source:HGNC Symbol;Acc:HG	0.005172	-1.90775
SLC4A7	solute carrier family 4 member 7 [Source:HGNC Symbol;Acc:HG	0.000978	-1.22861
SLC5A6	solute carrier family 5 member 6 [Source:HGNC Symbol;Acc:HG	0.002883	-1.4683
SLC66A2	solute carrier family 66 member 2 [Source:HGNC Symbol;Acc:HG	0.004494	-1.33391
SLC6A11	solute carrier family 6 member 11 [Source:HGNC Symbol;Acc:HG	8.71E-05	-1.57253
SLC7A2	solute carrier family 7 member 2 [Source:HGNC Symbol;Acc:HG	0.000777	-2.85187
SLC8A1	solute carrier family 8 member A1 [Source:HGNC Symbol;Acc:HG	0.009251	-2.24998
SLC9A3R2	SLC9A3 regulator 2 [Source:HGNC Symbol;Acc:HGNC:11076]	0.000874	-1.51507
SLC9A7	solute carrier family 9 member A7 [Source:HGNC Symbol;Acc:HG	0.003935	-1.56375
SLCO2A1	solute carrier organic anion transporter family member 2A1 [Sou	0.006079	-3.02457
SLF1	SMC5-SMC6 complex localization factor 1 [Source:HGNC Symbol;	0.000236	-1.35905
SLFN13	schlafen family member 13 [Source:HGNC Symbol;Acc:HGNC:264	0.000175	-1.7339
SLIT2	slit guidance ligand 2 [Source:HGNC Symbol;Acc:HGNC:11086]	0.009883	-2.10889
SLITRK5	SLIT and NTRK like family member 5 [Source:HGNC Symbol;Acc:H	0.000191	-2.3385
SLMAP	sarcolemma associated protein [Source:HGNC Symbol;Acc:HGNC	5.45E-05	-1.23548
SMARCA2	SWI/SNF related, matrix associated, actin dependent regulator of	0.010871	-1.28915
SMARCA5	SWI/SNF related, matrix associated, actin dependent regulator of	8.89E-06	-1.36108
SMARCC1	SWI/SNF related, matrix associated, actin dependent regulator of	0.000733	-1.40858
SMARCC2	SWI/SNF related, matrix associated, actin dependent regulator of	0.008581	-1.60468
SMC1A	structural maintenance of chromosomes 1A [Source:HGNC Symb	6.32E-05	-1.84921
SMC2	structural maintenance of chromosomes 2 [Source:HGNC Symbo	3.29E-07	-1.76542
SMC3	structural maintenance of chromosomes 3 [Source:HGNC Symbo	2.30E-07	-1.64267
SMC4	structural maintenance of chromosomes 4 [Source:HGNC Symbo	6.21E-05	-1.8672
SMC5	structural maintenance of chromosomes 5 [Source:HGNC Symbo	0.000115	-1.44735

SMC6	structural maintenance of chromosomes 6 [Source:HGNC Symbol]	8.83E-08	-1.38647
SMIM15	small integral membrane protein 15 [Source:HGNC Symbol;Acc:HGNC:15862]	0.003476	-1.43919
SMOC1	SPARC related modular calcium binding 1 [Source:HGNC Symbol;Acc:HGNC:15862]	0.000325	-2.86878
SMOX	spermine oxidase [Source:HGNC Symbol;Acc:HGNC:15862]	0.000277	-1.92147
SMPDL3B	sphingomyelin phosphodiesterase acid like 3B [Source:HGNC Symbol;Acc:HGNC:16258]	0.010989	-1.25633
SMYD5	SMYD family member 5 [Source:HGNC Symbol;Acc:HGNC:16258]	0.003627	-1.27089
SNRNP35	small nuclear ribonucleoprotein U11/U12 subunit 35 [Source:HGNC Symbol;Acc:HGNC:16258]	1.02E-05	-1.41897
SNRNP70	small nuclear ribonucleoprotein U1 subunit 70 [Source:HGNC Symbol;Acc:HGNC:16258]	0.001084	-1.32329
SNRPA	small nuclear ribonucleoprotein polypeptide A [Source:HGNC Symbol;Acc:HGNC:16258]	0.000589	-1.39776
SNX12	sorting nexin 12 [Source:HGNC Symbol;Acc:HGNC:14976]	0.006871	-1.13259
SNX18	sorting nexin 18 [Source:HGNC Symbol;Acc:HGNC:19245]	0.000931	-1.31352
SNX29	sorting nexin 29 [Source:HGNC Symbol;Acc:HGNC:30542]	0.003304	-1.22075
SORBS2	sorbin and SH3 domain containing 2 [Source:HGNC Symbol;Acc:HGNC:11186]	0.000353	-2.82812
SORBS3	sorbin and SH3 domain containing 3 [Source:HGNC Symbol;Acc:HGNC:11186]	0.00112	-1.46684
SORT1	sortilin 1 [Source:HGNC Symbol;Acc:HGNC:11186]	0.000293	-1.33382
SOS1	SOS Ras/Rac guanine nucleotide exchange factor 1 [Source:HGNC Symbol;Acc:HGNC:11186]	0.004742	-1.23704
SP4	Sp4 transcription factor [Source:HGNC Symbol;Acc:HGNC:11209]	0.007117	-1.30358
SP6	Sp6 transcription factor [Source:HGNC Symbol;Acc:HGNC:14530]	2.51E-05	-1.65182
SPAG1	sperm associated antigen 1 [Source:HGNC Symbol;Acc:HGNC:11209]	0.000315	-1.58231
SPAG5	sperm associated antigen 5 [Source:HGNC Symbol;Acc:HGNC:13400]	9.60E-05	-1.59817
SPARC	secreted protein acidic and cysteine rich [Source:HGNC Symbol;Acc:HGNC:13400]	1.78E-23	-1.624
SPATA13	spermatogenesis associated 13 [Source:HGNC Symbol;Acc:HGNC:13400]	0.005276	-2.3567
SPATA5	spermatogenesis associated 5 [Source:HGNC Symbol;Acc:HGNC:13400]	1.42E-05	-1.68358
SPATS2L	spermatogenesis associated serine rich 2 like [Source:HGNC Symbol;Acc:HGNC:13400]	8.94E-05	-1.20789
SPC24	SPC24 component of NDC80 kinetochore complex [Source:HGNC Symbol;Acc:HGNC:13400]	1.41E-07	-1.64109
SPC25	SPC25 component of NDC80 kinetochore complex [Source:HGNC Symbol;Acc:HGNC:13400]	0.00175	-1.97295
SPDL1	spindle apparatus coiled-coil protein 1 [Source:HGNC Symbol;Acc:HGNC:13400]	0.011368	-1.50095
SPECC1	sperm antigen with calponin homology and coiled-coil domains 1 [Source:HGNC Symbol;Acc:HGNC:13400]	0.002481	-1.1905
SPG11	SPG11 vesicle trafficking associated, spatacsin [Source:HGNC Symbol;Acc:HGNC:13400]	0.002022	-1.4811
SPOCK1	SPARC (osteonectin), cwcw and kazal like domains proteoglycan 1 [Source:HGNC Symbol;Acc:HGNC:13400]	0.008258	-1.24718
SPRED2	sprouty related EVH1 domain containing 2 [Source:HGNC Symbol;Acc:HGNC:13400]	0.000793	-1.56547
SPRY4	sprouty RTK signaling antagonist 4 [Source:HGNC Symbol;Acc:HGNC:13400]	0.001579	-1.87643
SPTLC2	serine palmitoyltransferase long chain base subunit 2 [Source:HGNC Symbol;Acc:HGNC:13400]	0.002383	-1.33126
SPTLC3	serine palmitoyltransferase long chain base subunit 3 [Source:HGNC Symbol;Acc:HGNC:13400]	2.82E-10	-1.71242
SREK1	splicing regulatory glutamic acid and lysine rich protein 1 [Source:HGNC Symbol;Acc:HGNC:13400]	2.68E-10	-1.51597
SRPK1	SRSF protein kinase 1 [Source:HGNC Symbol;Acc:HGNC:11305]	0.001245	-1.21863
SRPX	sushi repeat containing protein X-linked [Source:HGNC Symbol;Acc:HGNC:11305]	0.000289	-2.29604
SRRT	serrate, RNA effector molecule [Source:HGNC Symbol;Acc:HGNC:11305]	0.003391	-1.53099
SRSF1	serine and arginine rich splicing factor 1 [Source:HGNC Symbol;Acc:HGNC:11305]	0.007617	-1.58703
SRSF10	serine and arginine rich splicing factor 10 [Source:HGNC Symbol;Acc:HGNC:11305]	0.009049	-1.15488
SRSF9	serine and arginine rich splicing factor 9 [Source:HGNC Symbol;Acc:HGNC:11305]	0.005415	-1.12871
SS18	SS18 subunit of BAF chromatin remodeling complex [Source:HGNC Symbol;Acc:HGNC:11305]	0.008956	-1.27047
SSRP1	structure specific recognition protein 1 [Source:HGNC Symbol;Acc:HGNC:11305]	1.03E-05	-1.47801
ST14	suppression of tumorigenicity 14 [Source:HGNC Symbol;Acc:HGNC:11305]	0.00926	-1.28819
ST3GAL1	ST3 beta-galactoside alpha-2,3-sialyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:11305]	0.002709	-1.39799
ST6GALNAC4	ST6 N-acetylgalactosaminide alpha-2,6-sialyltransferase 4 [Source:HGNC Symbol;Acc:HGNC:11305]	0.00335	-1.34877
ST8SIA4	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4 [Source:HGNC Symbol;Acc:HGNC:11305]	0.003668	-2.13072

STAC	SH3 and cysteine rich domain [Source:HGNC Symbol;Acc:HGNC:1	7.37E-07	-1.54438
STAG1	stromal antigen 1 [Source:HGNC Symbol;Acc:HGNC:11354]	2.24E-05	-1.27392
STAM	signal transducing adaptor molecule [Source:HGNC Symbol;Acc:HGNC:1	0.002514	-1.26184
STARD7	StAR related lipid transfer domain containing 7 [Source:HGNC Symbol;Acc:HGNC:1	9.88E-06	-1.2404
STAT3	signal transducer and activator of transcription 3 [Source:HGNC Symbol;Acc:HGNC:1	0.005127	-1.24427
STAT5B	signal transducer and activator of transcription 5B [Source:HGNC Symbol;Acc:HGNC:1	8.17E-05	-1.29335
STAT6	signal transducer and activator of transcription 6 [Source:HGNC Symbol;Acc:HGNC:1	1.12E-10	-1.34133
STAU1	staufen double-stranded RNA binding protein 1 [Source:HGNC Symbol;Acc:HGNC:1	0.004627	-1.28981
STEAP3	STEAP3 metalloredutase [Source:HGNC Symbol;Acc:HGNC:2459	0.004687	-1.31308
STIL	STIL centriolar assembly protein [Source:HGNC Symbol;Acc:HGNC:1	3.88E-06	-2.01908
STIM1	stromal interaction molecule 1 [Source:HGNC Symbol;Acc:HGNC:1	0.00644	-1.26473
STING1	stimulator of interferon response cGAMP interactor 1 [Source:HGNC Symbol;Acc:HGNC:1	0.01021	-1.7718
STK33	serine/threonine kinase 33 [Source:HGNC Symbol;Acc:HGNC:145	0.000128	-2.07739
STK38	serine/threonine kinase 38 [Source:HGNC Symbol;Acc:HGNC:178	7.34E-07	-1.3146
STK4	serine/threonine kinase 4 [Source:HGNC Symbol;Acc:HGNC:1140	1.17E-05	-1.24804
STMN3	stathmin 3 [Source:HGNC Symbol;Acc:HGNC:15926]	0.005241	-2.09523
STRADA	STE20 related adaptor alpha [Source:HGNC Symbol;Acc:HGNC:30	9.88E-05	-2.36384
STRBP	spermatid perinuclear RNA binding protein [Source:HGNC Symbol;Acc:HGNC:1	0.000265	-1.20517
STS	steroid sulfatase [Source:HGNC Symbol;Acc:HGNC:11425]	3.67E-05	-4.00857
STX16	syntaxin 16 [Source:HGNC Symbol;Acc:HGNC:11431]	0.000195	-1.23189
STX4	syntaxin 4 [Source:HGNC Symbol;Acc:HGNC:11439]	0.007631	-1.27997
STYK1	serine/threonine/tyrosine kinase 1 [Source:HGNC Symbol;Acc:HGNC:1	0.00948	-1.50282
SULT4A1	sulfotransferase family 4A member 1 [Source:HGNC Symbol;Acc:HGNC:1	0.002673	-1.67227
SUMF1	sulfatase modifying factor 1 [Source:HGNC Symbol;Acc:HGNC:20	0.011328	-1.21341
SUSD5	sushi domain containing 5 [Source:HGNC Symbol;Acc:HGNC:290	0.001859	-2.14266
SUV39H1	suppressor of variegation 3-9 homolog 1 [Source:HGNC Symbol;Acc:HGNC:1	0.005931	-1.23682
SUZ12	SUZ12 polycomb repressive complex 2 subunit [Source:HGNC Symbol;Acc:HGNC:1	0.002169	-1.21835
SV2A	synaptic vesicle glycoprotein 2A [Source:HGNC Symbol;Acc:HGNC:1	0.000293	-1.56013
SYAP1	synapse associated protein 1 [Source:HGNC Symbol;Acc:HGNC:1	0.00515	-1.17644
SYNCRIP	synaptotagmin binding cytoplasmic RNA interacting protein [Source:HGNC Symbol;Acc:HGNC:1	0.009603	-1.45103
SYPL1	synaptophysin like 1 [Source:HGNC Symbol;Acc:HGNC:11507]	0.007223	-1.20431
TAB3	TGF-beta activated kinase 1 (MAP3K7) binding protein 3 [Source:HGNC Symbol;Acc:HGNC:1	0.008159	-1.1829
TACC1	transforming acidic coiled-coil containing protein 1 [Source:HGNC Symbol;Acc:HGNC:1	6.02E-05	-1.79497
TAF2	TATA-box binding protein associated factor 2 [Source:HGNC Symbol;Acc:HGNC:1	0.003869	-1.23944
TAF3	TATA-box binding protein associated factor 3 [Source:HGNC Symbol;Acc:HGNC:1	1.52E-06	-1.43815
TAF4	TATA-box binding protein associated factor 4 [Source:HGNC Symbol;Acc:HGNC:1	0.002229	-1.65474
TAF4B	TATA-box binding protein associated factor 4b [Source:HGNC Symbol;Acc:HGNC:1	0.001279	-1.54643
TAOK1	TAO kinase 1 [Source:HGNC Symbol;Acc:HGNC:29259]	0.001676	-1.40322
TAOK3	TAO kinase 3 [Source:HGNC Symbol;Acc:HGNC:18133]	6.36E-07	-1.50988
TAP2	transporter 2, ATP binding cassette subfamily B member [Source:HGNC Symbol;Acc:HGNC:1	0.005797	-1.41689
TARDBP	TAR DNA binding protein [Source:HGNC Symbol;Acc:HGNC:11571]	0.000952	-1.23447
TARS1	threonyl-tRNA synthetase 1 [Source:HGNC Symbol;Acc:HGNC:11	0.000624	-1.31625
TARS3	threonyl-tRNA synthetase 3 [Source:HGNC Symbol;Acc:HGNC:24	0.000461	-1.65365
TAS1R3	taste 1 receptor member 3 [Source:HGNC Symbol;Acc:HGNC:156	0.000862	-3.77803
TASOR	transcription activation suppressor [Source:HGNC Symbol;Acc:HGNC:1	5.98E-05	-1.40421
TBC1D1	TBC1 domain family member 1 [Source:HGNC Symbol;Acc:HGNC:1	0.003833	-1.41679
TBC1D31	TBC1 domain family member 31 [Source:HGNC Symbol;Acc:HGNC:1	0.011291	-1.45002

TBX1	T-box transcription factor 1 [Source:HGNC Symbol;Acc:HGNC:115]	0.008193	-1.25196
TCEANC2	transcription elongation factor A N-terminal and central domain	7.84E-05	-1.30958
TCERG1	transcription elongation regulator 1 [Source:HGNC Symbol;Acc:HGNC:11627]	0.006856	-1.1713
TCF15	transcription factor 15 [Source:HGNC Symbol;Acc:HGNC:11627]	0.003588	-3.25463
TCF19	transcription factor 19 [Source:HGNC Symbol;Acc:HGNC:11629]	0.000987	-1.82357
TCF4	transcription factor 4 [Source:HGNC Symbol;Acc:HGNC:11634]	1.58E-08	-1.40773
TCF7	transcription factor 7 [Source:HGNC Symbol;Acc:HGNC:11639]	0.000304	-2.29896
TCF7L2	transcription factor 7 like 2 [Source:HGNC Symbol;Acc:HGNC:11639]	0.009379	-1.58265
TCHP	trichoplein keratin filament binding [Source:HGNC Symbol;Acc:HGNC:11639]	0.008122	-1.76548
TCTA	T cell leukemia translocation altered [Source:HGNC Symbol;Acc:HGNC:11639]	0.000258	-1.45147
TCTN1	tectonic family member 1 [Source:HGNC Symbol;Acc:HGNC:2611]	0.005947	-1.24216
TCTN2	tectonic family member 2 [Source:HGNC Symbol;Acc:HGNC:2577]	9.94E-09	-1.61571
TEAD4	TEA domain transcription factor 4 [Source:HGNC Symbol;Acc:HGNC:11639]	0.010316	-1.27322
TEDC1	tubulin epsilon and delta complex 1 [Source:HGNC Symbol;Acc:HGNC:11639]	0.002645	-2.29757
TELO2	telomere maintenance 2 [Source:HGNC Symbol;Acc:HGNC:29099]	0.004228	-1.91725
TENT4A	terminal nucleotidyltransferase 4A [Source:HGNC Symbol;Acc:HGNC:11639]	0.001349	-1.4531
TEPSIN	TEPSIN adaptor related protein complex 4 accessory protein [Source:HGNC Symbol;Acc:HGNC:11639]	0.008507	-1.70305
TERF1	telomeric repeat binding factor 1 [Source:HGNC Symbol;Acc:HGNC:11639]	0.000195	-1.29124
TET2	tet methylcytosine dioxygenase 2 [Source:HGNC Symbol;Acc:HGNC:11639]	0.00722	-1.31063
TEX10	testis expressed 10 [Source:HGNC Symbol;Acc:HGNC:25988]	0.000426	-1.23486
TEX15	testis expressed 15, meiosis and synapsis associated [Source:HGNC Symbol;Acc:HGNC:25988]	0.010449	-1.67993
TEX2	testis expressed 2 [Source:HGNC Symbol;Acc:HGNC:30884]	0.001368	-1.2214
TFAM	transcription factor A, mitochondrial [Source:HGNC Symbol;Acc:HGNC:11639]	0.007602	-1.33994
TFCP2L1	transcription factor CP2 like 1 [Source:HGNC Symbol;Acc:HGNC:11639]	0.001728	-2.08824
TFDP1	transcription factor Dp-1 [Source:HGNC Symbol;Acc:HGNC:11749]	0.003196	-1.15361
TFG	trafficking from ER to golgi regulator [Source:HGNC Symbol;Acc:HGNC:11639]	0.008957	-1.14581
TGFB111	transforming growth factor beta 1 induced transcript 1 [Source:HGNC Symbol;Acc:HGNC:11639]	0.000327	-1.46177
TGFBI	transforming growth factor beta induced [Source:HGNC Symbol;Acc:HGNC:11639]	6.83E-36	-2.63801
TGFBR1	transforming growth factor beta receptor 1 [Source:HGNC Symbol;Acc:HGNC:11639]	0.007738	-1.27607
TGFBR2	transforming growth factor beta receptor 2 [Source:HGNC Symbol;Acc:HGNC:11639]	0.005198	-1.97659
TGFBRAP1	transforming growth factor beta receptor associated protein 1 [Source:HGNC Symbol;Acc:HGNC:11639]	0.011015	-1.62594
TGM2	transglutaminase 2 [Source:HGNC Symbol;Acc:HGNC:11778]	0.000932	-5.27853
TGS1	trimethylguanosine synthase 1 [Source:HGNC Symbol;Acc:HGNC:11639]	0.009957	-1.2679
THAP12	THAP domain containing 12 [Source:HGNC Symbol;Acc:HGNC:9448]	0.000142	-1.30662
THAP4	THAP domain containing 4 [Source:HGNC Symbol;Acc:HGNC:2318]	2.14E-05	-1.29783
THEM6	thioesterase superfamily member 6 [Source:HGNC Symbol;Acc:HGNC:11639]	0.006175	-1.60283
THOC2	THO complex 2 [Source:HGNC Symbol;Acc:HGNC:19073]	0.003226	-1.31838
THOC5	THO complex 5 [Source:HGNC Symbol;Acc:HGNC:19074]	0.011426	-1.1665
THRAP3	thyroid hormone receptor associated protein 3 [Source:HGNC Symbol;Acc:HGNC:11639]	0.000186	-1.50369
THSD4	thrombospondin type 1 domain containing 4 [Source:HGNC Symbol;Acc:HGNC:11639]	2.48E-21	-2.74808
THTPA	thiamine triphosphatase [Source:HGNC Symbol;Acc:HGNC:18987]	0.007305	-1.85514
TICRR	TOPBP1 interacting checkpoint and replication regulator [Source:HGNC Symbol;Acc:HGNC:11639]	0.00854	-2.09382
TIMELESS	timeless circadian regulator [Source:HGNC Symbol;Acc:HGNC:11639]	0.000423	-1.51474
TIMM17B	translocase of inner mitochondrial membrane 17B [Source:HGNC Symbol;Acc:HGNC:11639]	3.50E-05	-1.49902
TIMP3	TIMP metalloproteinase inhibitor 3 [Source:HGNC Symbol;Acc:HGNC:11639]	0.000457	-1.33554
TINAGL1	tubulointerstitial nephritis antigen like 1 [Source:HGNC Symbol;Acc:HGNC:11639]	0.001024	-2.08467
TJP1	tight junction protein 1 [Source:HGNC Symbol;Acc:HGNC:11827]	0.004423	-1.58392

TK1	thymidine kinase 1 [Source:HGNC Symbol;Acc:HGNC:11830]	8.85E-07	-1.99591
TLCD4	TLC domain containing 4 [Source:HGNC Symbol;Acc:HGNC:26477]	0.000209	-1.48887
TLN2	talin 2 [Source:HGNC Symbol;Acc:HGNC:15447]	0.002873	-1.81119
TM9SF2	transmembrane 9 superfamily member 2 [Source:HGNC Symbol;Acc:HGNC:26477]	0.002946	-1.32346
TMC5	transmembrane channel like 5 [Source:HGNC Symbol;Acc:HGNC:26477]	0.011082	-2.15203
TMCC3	transmembrane and coiled-coil domain family 3 [Source:HGNC Symbol;Acc:HGNC:26477]	0.000578	-1.33279
TMEM123	transmembrane protein 123 [Source:HGNC Symbol;Acc:HGNC:26477]	0.000122	-1.49578
TMEM154	transmembrane protein 154 [Source:HGNC Symbol;Acc:HGNC:26477]	0.006003	-1.23546
TMEM181	transmembrane protein 181 [Source:HGNC Symbol;Acc:HGNC:26477]	0.000137	-1.55123
TMEM184B	transmembrane protein 184B [Source:HGNC Symbol;Acc:HGNC:26477]	0.00186	-1.50463
TMEM185B	transmembrane protein 185B [Source:HGNC Symbol;Acc:HGNC:26477]	0.006903	-1.81634
TMEM200B	transmembrane protein 200B [Source:HGNC Symbol;Acc:HGNC:26477]	0.003862	-1.45336
TMEM241	transmembrane protein 241 [Source:HGNC Symbol;Acc:HGNC:26477]	9.72E-12	-1.47279
TMEM248	transmembrane protein 248 [Source:HGNC Symbol;Acc:HGNC:26477]	0.000213	-1.18984
TMEM260	transmembrane protein 260 [Source:HGNC Symbol;Acc:HGNC:26477]	0.003361	-1.31389
TMEM30B	transmembrane protein 30B [Source:HGNC Symbol;Acc:HGNC:26477]	0.00937	-1.20027
TMEM39B	transmembrane protein 39B [Source:HGNC Symbol;Acc:HGNC:26477]	8.97E-06	-1.43785
TMEM41A	transmembrane protein 41A [Source:HGNC Symbol;Acc:HGNC:26477]	9.62E-16	-1.66655
TMEM97	transmembrane protein 97 [Source:HGNC Symbol;Acc:HGNC:26477]	3.41E-13	-1.61427
TMEM98	transmembrane protein 98 [Source:HGNC Symbol;Acc:HGNC:26477]	0.001414	-1.91098
TMOD3	tropomodulin 3 [Source:HGNC Symbol;Acc:HGNC:11873]	0.00588	-1.27043
TMPO	thymopoietin [Source:HGNC Symbol;Acc:HGNC:11875]	0.000627	-1.43775
TMX3	thioredoxin related transmembrane protein 3 [Source:HGNC Symbol;Acc:HGNC:11875]	0.010051	-1.40304
TNFAIP3	TNF alpha induced protein 3 [Source:HGNC Symbol;Acc:HGNC:11875]	0.001132	-1.8745
TNFRSF10A	TNF receptor superfamily member 10a [Source:HGNC Symbol;Acc:HGNC:11875]	0.007634	-1.20733
TNFRSF8	TNF receptor superfamily member 8 [Source:HGNC Symbol;Acc:HGNC:11875]	0.001088	-2.63558
TNIP1	TNFAIP3 interacting protein 1 [Source:HGNC Symbol;Acc:HGNC:11875]	0.010618	-1.32376
TNS2	tensin 2 [Source:HGNC Symbol;Acc:HGNC:19737]	3.97E-05	-3.41429
TNS3	tensin 3 [Source:HGNC Symbol;Acc:HGNC:21616]	0.000689	-2.39602
TOE1	target of EGR1, exonuclease [Source:HGNC Symbol;Acc:HGNC:15447]	0.006027	-1.70874
TOMM40	translocase of outer mitochondrial membrane 40 [Source:HGNC Symbol;Acc:HGNC:26477]	0.002078	-1.37499
TOP1MT	DNA topoisomerase I mitochondrial [Source:HGNC Symbol;Acc:HGNC:26477]	0.002899	-1.46389
TOP2A	DNA topoisomerase II alpha [Source:HGNC Symbol;Acc:HGNC:11875]	1.18E-07	-1.74315
TOP2B	DNA topoisomerase II beta [Source:HGNC Symbol;Acc:HGNC:11875]	0.010715	-1.542
TOPBP1	DNA topoisomerase II binding protein 1 [Source:HGNC Symbol;Acc:HGNC:11875]	0.004437	-1.18993
TOX2	TOX high mobility group box family member 2 [Source:HGNC Symbol;Acc:HGNC:11875]	0.001873	-2.13417
TP53	tumor protein p53 [Source:HGNC Symbol;Acc:HGNC:11998]	0.010989	-1.51566
TP53BP2	tumor protein p53 binding protein 2 [Source:HGNC Symbol;Acc:HGNC:11998]	0.005822	-1.28751
TP53I11	tumor protein p53 inducible protein 11 [Source:HGNC Symbol;Acc:HGNC:11998]	0.004192	-2.92402
TP53I3	tumor protein p53 inducible protein 3 [Source:HGNC Symbol;Acc:HGNC:11998]	0.004669	-1.5117
TPP1	tripeptidyl peptidase 1 [Source:HGNC Symbol;Acc:HGNC:2073]	0.000156	-1.31339
TPR	translocated promoter region, nuclear basket protein [Source:HGNC Symbol;Acc:HGNC:26477]	0.00521	-1.56303
TPX2	TPX2 microtubule nucleation factor [Source:HGNC Symbol;Acc:HGNC:26477]	1.50E-07	-1.811
TRA2A	transformer 2 alpha homolog [Source:HGNC Symbol;Acc:HGNC:11875]	0.011601	-1.18187
TRABD2A	TraB domain containing 2A [Source:HGNC Symbol;Acc:HGNC:270]	4.56E-05	-1.53282
TRAPPC11	trafficking protein particle complex 11 [Source:HGNC Symbol;Acc:HGNC:26477]	7.01E-05	-1.27168
TRHDE	thyrotropin releasing hormone degrading enzyme [Source:HGNC Symbol;Acc:HGNC:26477]	2.49E-05	-3.62437

TRIM14	tripartite motif containing 14 [Source:HGNC Symbol;Acc:HGNC:10005616]	0.005616	-1.8082
TRIM16L	tripartite motif containing 16 like [Source:HGNC Symbol;Acc:HGNC:10007666]	0.007666	-1.43734
TRIM2	tripartite motif containing 2 [Source:HGNC Symbol;Acc:HGNC:15000699]	0.000699	-1.34232
TRIM44	tripartite motif containing 44 [Source:HGNC Symbol;Acc:HGNC:10003084]	0.003084	-1.66678
TRIM52	tripartite motif containing 52 [Source:HGNC Symbol;Acc:HGNC:10005503]	0.005503	-1.65055
TRIM6	tripartite motif containing 6 [Source:HGNC Symbol;Acc:HGNC:160011443]	0.011443	-1.50675
TRIM68	tripartite motif containing 68 [Source:HGNC Symbol;Acc:HGNC:20000484]	0.000484	-1.38992
TRIP12	thyroid hormone receptor interactor 12 [Source:HGNC Symbol;Acc:HGNC:10009361]	0.009361	-1.28221
TRIP13	thyroid hormone receptor interactor 13 [Source:HGNC Symbol;Acc:HGNC:1000705]	2.07E-05	-1.80654
TRPA1	transient receptor potential cation channel subfamily A member 1 [Source:HGNC Symbol;Acc:HGNC:10005732]	0.005732	-2.42344
TSNARE1	t-SNARE domain containing 1 [Source:HGNC Symbol;Acc:HGNC:20000938]	0.00938	-1.3151
TSPAN14	tetraspanin 14 [Source:HGNC Symbol;Acc:HGNC:23303]	0.003049	-1.21245
TSPAN5	tetraspanin 5 [Source:HGNC Symbol;Acc:HGNC:17753]	0.009586	-1.23542
TSPYL1	TSPY like 1 [Source:HGNC Symbol;Acc:HGNC:12382]	0.00274	-1.40845
TSR1	TSR1 ribosome maturation factor [Source:HGNC Symbol;Acc:HGNC:10000292]	0.000292	-1.32771
TSR2	TSR2 ribosome maturation factor [Source:HGNC Symbol;Acc:HGNC:10004211]	0.004211	-1.18018
TTC22	tetratricopeptide repeat domain 22 [Source:HGNC Symbol;Acc:HGNC:100051E-05]	1.51E-05	-1.59713
TTC26	tetratricopeptide repeat domain 26 [Source:HGNC Symbol;Acc:HGNC:1000359E-06]	3.59E-06	-1.72827
TTC3	tetratricopeptide repeat domain 3 [Source:HGNC Symbol;Acc:HGNC:100020E-06]	1.20E-06	-1.39898
TTC31	tetratricopeptide repeat domain 31 [Source:HGNC Symbol;Acc:HGNC:10000018]	0.0018	-1.64855
TTF2	transcription termination factor 2 [Source:HGNC Symbol;Acc:HGNC:10000659]	0.000659	-1.77919
TTI1	TELO2 interacting protein 1 [Source:HGNC Symbol;Acc:HGNC:290001299]	0.001299	-1.31611
TTLL5	tubulin tyrosine ligase like 5 [Source:HGNC Symbol;Acc:HGNC:190005779]	0.005779	-1.42426
TTLL7	tubulin tyrosine ligase like 7 [Source:HGNC Symbol;Acc:HGNC:260010E-06]	6.10E-06	-1.52874
TTN	titin [Source:HGNC Symbol;Acc:HGNC:12403]	0.001294	-2.12886
TUBB	tubulin beta class I [Source:HGNC Symbol;Acc:HGNC:20778]	0.000188	-1.62376
TUBG1	tubulin gamma 1 [Source:HGNC Symbol;Acc:HGNC:12417]	0.00036	-1.3119
TUBGCP3	tubulin gamma complex associated protein 3 [Source:HGNC Symbol;Acc:HGNC:10000018]	0.00018	-1.30442
TULP3	TUB like protein 3 [Source:HGNC Symbol;Acc:HGNC:12425]	0.010174	-1.19193
TWSG1	twisted gastrulation BMP signaling modulator 1 [Source:HGNC Symbol;Acc:HGNC:10000137]	0.000137	-1.2443
TXNDC16	thioredoxin domain containing 16 [Source:HGNC Symbol;Acc:HGNC:10006037]	0.006037	-1.19604
TXNRD2	thioredoxin reductase 2 [Source:HGNC Symbol;Acc:HGNC:18155]	0.00649	-1.33208
TXNRD3	thioredoxin reductase 3 [Source:HGNC Symbol;Acc:HGNC:20667]	0.009393	-1.25255
TYMS	thymidylate synthetase [Source:HGNC Symbol;Acc:HGNC:12441]	5.13E-05	-1.71346
U2AF1	U2 small nuclear RNA auxiliary factor 1 [Source:HGNC Symbol;Acc:HGNC:10001037]	0.01037	-1.34202
UACA	uveal autoantigen with coiled-coil domains and ankyrin repeats [Source:HGNC Symbol;Acc:HGNC:10000973]	0.000973	-1.74753
UBA1	ubiquitin like modifier activating enzyme 1 [Source:HGNC Symbol;Acc:HGNC:10005049]	0.005049	-1.25086
UBAP2L	ubiquitin associated protein 2 like [Source:HGNC Symbol;Acc:HGNC:10000284]	0.000284	-1.2226
UBASH3B	ubiquitin associated and SH3 domain containing B [Source:HGNC Symbol;Acc:HGNC:10000187]	0.000187	-1.73772
UBE2C	ubiquitin conjugating enzyme E2 C [Source:HGNC Symbol;Acc:HGNC:2014E-05]	2.14E-05	-1.37757
UBE2E3	ubiquitin conjugating enzyme E2 E3 [Source:HGNC Symbol;Acc:HGNC:1000196E-18]	1.96E-18	-1.53726
UBE2K	ubiquitin conjugating enzyme E2 K [Source:HGNC Symbol;Acc:HGNC:10000258]	0.000258	-1.2404
UBE2S	ubiquitin conjugating enzyme E2 S [Source:HGNC Symbol;Acc:HGNC:10000861]	0.000861	-1.29112
UBFD1	ubiquitin family domain containing 1 [Source:HGNC Symbol;Acc:HGNC:10000039]	0.00039	-1.2897
UBL7	ubiquitin like 7 [Source:HGNC Symbol;Acc:HGNC:28221]	0.001835	-1.26908
UBQLN2	ubiquilin 2 [Source:HGNC Symbol;Acc:HGNC:12509]	0.001855	-1.26005
UBR1	ubiquitin protein ligase E3 component n-recognin 1 [Source:HGNC Symbol;Acc:HGNC:10000059]	0.0059	-1.17758

UBR7	ubiquitin protein ligase E3 component n-recognin 7 (putative) [Sc	1.03E-06	-1.26664
UBXN11	UBX domain protein 11 [Source:HGNC Symbol;Acc:HGNC:30600]	0.000765	-2.13356
UBXN2B	UBX domain protein 2B [Source:HGNC Symbol;Acc:HGNC:27035]	0.000494	-1.23575
UCHL5	ubiquitin C-terminal hydrolase L5 [Source:HGNC Symbol;Acc:HGNC:1255]	7.08E-07	-1.42256
UGT8	UDP glycosyltransferase 8 [Source:HGNC Symbol;Acc:HGNC:1255]	0.002143	-1.31975
ULBP3	UL16 binding protein 3 [Source:HGNC Symbol;Acc:HGNC:14895]	0.001158	-1.69469
ULK2	unc-51 like autophagy activating kinase 2 [Source:HGNC Symbol;Acc:HGNC:12579]	0.001265	-1.22776
UNC119B	unc-119 lipid binding chaperone B [Source:HGNC Symbol;Acc:HGNC:12579]	0.00663	-1.20131
UNG	uracil DNA glycosylase [Source:HGNC Symbol;Acc:HGNC:12572]	1.06E-12	-1.5767
UPF2	UPF2 regulator of nonsense mediated mRNA decay [Source:HGNC Symbol;Acc:HGNC:12572]	0.001275	-1.41441
UPF3A	UPF3A regulator of nonsense mediated mRNA decay [Source:HGNC Symbol;Acc:HGNC:12572]	0.007597	-1.27003
UPF3B	UPF3B regulator of nonsense mediated mRNA decay [Source:HGNC Symbol;Acc:HGNC:12572]	7.15E-11	-1.54051
UPK2	uroplakin 2 [Source:HGNC Symbol;Acc:HGNC:12579]	0.003346	-3.07788
UPK3B	uroplakin 3B [Source:HGNC Symbol;Acc:HGNC:21444]	0.0076	-2.4802
URB2	URB2 ribosome biogenesis homolog [Source:HGNC Symbol;Acc:HGNC:12579]	0.008644	-1.75984
URI1	URI1 prefoldin like chaperone [Source:HGNC Symbol;Acc:HGNC:12579]	1.13E-06	-1.25349
UROS	uroporphyrinogen III synthase [Source:HGNC Symbol;Acc:HGNC:12579]	9.91E-05	-1.50742
USP1	ubiquitin specific peptidase 1 [Source:HGNC Symbol;Acc:HGNC:12579]	0.001671	-1.37865
USP13	ubiquitin specific peptidase 13 [Source:HGNC Symbol;Acc:HGNC:12579]	0.000897	-1.44656
USP14	ubiquitin specific peptidase 14 [Source:HGNC Symbol;Acc:HGNC:12579]	0.010293	-1.16658
USP24	ubiquitin specific peptidase 24 [Source:HGNC Symbol;Acc:HGNC:12579]	0.003704	-1.27737
USP37	ubiquitin specific peptidase 37 [Source:HGNC Symbol;Acc:HGNC:12579]	0.00099	-1.56076
USP38	ubiquitin specific peptidase 38 [Source:HGNC Symbol;Acc:HGNC:12579]	0.000124	-1.337
USP5	ubiquitin specific peptidase 5 [Source:HGNC Symbol;Acc:HGNC:12579]	0.001179	-1.22555
USP54	ubiquitin specific peptidase 54 [Source:HGNC Symbol;Acc:HGNC:12579]	0.000158	-1.71304
USP6NL	USP6 N-terminal like [Source:HGNC Symbol;Acc:HGNC:16858]	0.000156	-1.3557
USP7	ubiquitin specific peptidase 7 [Source:HGNC Symbol;Acc:HGNC:12579]	0.00454	-1.46318
UTP14A	UTP14A small subunit processome component [Source:HGNC Symbol;Acc:HGNC:12579]	0.002643	-1.65309
UTP20	UTP20 small subunit processome component [Source:HGNC Symbol;Acc:HGNC:12579]	0.001043	-1.63241
VASP	vasodilator stimulated phosphoprotein [Source:HGNC Symbol;Acc:HGNC:12579]	0.003257	-1.15671
VCAN	versican [Source:HGNC Symbol;Acc:HGNC:2464]	3.49E-05	-3.07939
VCL	vinculin [Source:HGNC Symbol;Acc:HGNC:12665]	0.003419	-1.45156
VCP	valosin containing protein [Source:HGNC Symbol;Acc:HGNC:12665]	0.009221	-1.13445
VEGFC	vascular endothelial growth factor C [Source:HGNC Symbol;Acc:HGNC:12579]	0.008456	-1.65968
VEZF1	vascular endothelial zinc finger 1 [Source:HGNC Symbol;Acc:HGNC:12579]	0.001288	-1.15431
VEZT	vezatin, adherens junctions transmembrane protein [Source:HGNC Symbol;Acc:HGNC:12579]	0.010304	-1.21418
VGLL1	vestigial like family member 1 [Source:HGNC Symbol;Acc:HGNC:12579]	0.000132	-4.7024
VGLL3	vestigial like family member 3 [Source:HGNC Symbol;Acc:HGNC:12579]	0.001003	-1.49816
VGLL4	vestigial like family member 4 [Source:HGNC Symbol;Acc:HGNC:12579]	2.64E-05	-1.3032
VILL	villin like [Source:HGNC Symbol;Acc:HGNC:30906]	0.006176	-2.3957
VOPP1	VOPP1 WW domain binding protein [Source:HGNC Symbol;Acc:HGNC:12579]	0.001757	-1.21565
VPS13A	vacuolar protein sorting 13 homolog A [Source:HGNC Symbol;Acc:HGNC:12579]	0.00204	-1.45571
VPS13C	vacuolar protein sorting 13 homolog C [Source:HGNC Symbol;Acc:HGNC:12579]	0.004609	-1.35151
VPS37B	VPS37B subunit of ESCRT-I [Source:HGNC Symbol;Acc:HGNC:2579]	0.011364	-1.33234
VPS52	VPS52 subunit of GARP complex [Source:HGNC Symbol;Acc:HGNC:12579]	0.005681	-1.17474
VPS54	VPS54 subunit of GARP complex [Source:HGNC Symbol;Acc:HGNC:12579]	0.000156	-1.32672
VWA8	von Willebrand factor A domain containing 8 [Source:HGNC Symbol;Acc:HGNC:12579]	0.003879	-1.27325

VWDE	von Willebrand factor D and EGF domains [Source:HGNC Symbol;Acc:HGNC:23423]	0.003352	-1.54811
WAPL	WAPL cohesin release factor [Source:HGNC Symbol;Acc:HGNC:23423]	0.000936	-1.24347
WASF3	WASP family member 3 [Source:HGNC Symbol;Acc:HGNC:12734]	0.005331	-1.40619
WASHC2C	WASH complex subunit 2C [Source:HGNC Symbol;Acc:HGNC:23423]	0.003466	-1.27093
WASHC5	WASH complex subunit 5 [Source:HGNC Symbol;Acc:HGNC:28984]	0.009587	-1.18721
WBP11	WW domain binding protein 11 [Source:HGNC Symbol;Acc:HGNC:23423]	4.27E-07	-1.3494
WBP2	WW domain binding protein 2 [Source:HGNC Symbol;Acc:HGNC:23423]	1.50E-07	-1.62493
WDCP	WD repeat and coiled coil containing [Source:HGNC Symbol;Acc:HGNC:23423]	0.001688	-2.0914
WDHD1	WD repeat and HMG-box DNA binding protein 1 [Source:HGNC Symbol;Acc:HGNC:23423]	6.16E-05	-1.35964
WDR11	WD repeat domain 11 [Source:HGNC Symbol;Acc:HGNC:13831]	0.00487	-1.2397
WDR13	WD repeat domain 13 [Source:HGNC Symbol;Acc:HGNC:14352]	0.007854	-1.20678
WDR17	WD repeat domain 17 [Source:HGNC Symbol;Acc:HGNC:16661]	0.00025	-2.81548
WDR18	WD repeat domain 18 [Source:HGNC Symbol;Acc:HGNC:17956]	0.005058	-1.37047
WDR34	WD repeat domain 34 [Source:HGNC Symbol;Acc:HGNC:28296]	0.001084	-1.72828
WDR36	WD repeat domain 36 [Source:HGNC Symbol;Acc:HGNC:30696]	0.003226	-1.20401
WDR62	WD repeat domain 62 [Source:HGNC Symbol;Acc:HGNC:24502]	0.005991	-1.63204
WDR7	WD repeat domain 7 [Source:HGNC Symbol;Acc:HGNC:13490]	5.75E-06	-1.57516
WDR76	WD repeat domain 76 [Source:HGNC Symbol;Acc:HGNC:25773]	1.39E-17	-1.47645
WDR77	WD repeat domain 77 [Source:HGNC Symbol;Acc:HGNC:29652]	0.003735	-1.55087
WDR82	WD repeat domain 82 [Source:HGNC Symbol;Acc:HGNC:28826]	0.001737	-1.24988
WIPF1	WAS/WASL interacting protein family member 1 [Source:HGNC Symbol;Acc:HGNC:23423]	9.56E-06	-1.68692
WIPF2	WAS/WASL interacting protein family member 2 [Source:HGNC Symbol;Acc:HGNC:23423]	0.002085	-1.20588
WNT5A	Wnt family member 5A [Source:HGNC Symbol;Acc:HGNC:12784]	0.000192	-2.39824
WNT9A	Wnt family member 9A [Source:HGNC Symbol;Acc:HGNC:12778]	0.000929	-2.31418
WSB2	WD repeat and SOCS box containing 2 [Source:HGNC Symbol;Acc:HGNC:23423]	5.95E-16	-1.49206
WWTR1	WW domain containing transcription regulator 1 [Source:HGNC Symbol;Acc:HGNC:23423]	0.006305	-1.54916
XPO5	exportin 5 [Source:HGNC Symbol;Acc:HGNC:17675]	0.010818	-1.40712
XRCC1	X-ray repair cross complementing 1 [Source:HGNC Symbol;Acc:HGNC:23423]	0.002647	-1.25448
XRCC2	X-ray repair cross complementing 2 [Source:HGNC Symbol;Acc:HGNC:23423]	0.004051	-2.25807
XRCC3	X-ray repair cross complementing 3 [Source:HGNC Symbol;Acc:HGNC:23423]	0.003475	-1.23766
XRCC5	X-ray repair cross complementing 5 [Source:HGNC Symbol;Acc:HGNC:23423]	0.011338	-1.18632
XXYL1	xyloside xylosyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:26126]	0.00826	-1.33889
YAP1	Yes associated protein 1 [Source:HGNC Symbol;Acc:HGNC:16262]	0.010424	-1.16148
YLPM1	YLP motif containing 1 [Source:HGNC Symbol;Acc:HGNC:17798]	0.008352	-1.87179
YTHDC2	YTH domain containing 2 [Source:HGNC Symbol;Acc:HGNC:24721]	0.008395	-1.21663
YWHAH	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activator 1 [Source:HGNC Symbol;Acc:HGNC:23423]	0.003168	-1.3337
YY1	YY1 transcription factor [Source:HGNC Symbol;Acc:HGNC:12856]	0.003386	-1.14646
YY2	YY2 transcription factor [Source:HGNC Symbol;Acc:HGNC:31684]	0.005715	-1.9199
ZBED1	zinc finger BED-type containing 1 [Source:HGNC Symbol;Acc:HGNC:23423]	0.011131	-1.34422
ZBED3	zinc finger BED-type containing 3 [Source:HGNC Symbol;Acc:HGNC:23423]	0.003546	-1.78388
ZBTB12	zinc finger and BTB domain containing 12 [Source:HGNC Symbol;Acc:HGNC:23423]	0.00192	-3.05081
ZBTB18	zinc finger and BTB domain containing 18 [Source:HGNC Symbol;Acc:HGNC:23423]	0.003712	-1.1741
ZBTB2	zinc finger and BTB domain containing 2 [Source:HGNC Symbol;Acc:HGNC:23423]	0.000613	-1.52427
ZC3H11A	zinc finger CCCH-type containing 11A [Source:HGNC Symbol;Acc:HGNC:23423]	0.009793	-1.18217
ZC3H12C	zinc finger CCCH-type containing 12C [Source:HGNC Symbol;Acc:HGNC:23423]	0.000368	-1.39844
ZC3H14	zinc finger CCCH-type containing 14 [Source:HGNC Symbol;Acc:HGNC:23423]	0.007433	-1.19429
ZDHC14	zinc finger DHHC-type containing 14 [Source:HGNC Symbol;Acc:HGNC:23423]	0.001464	-1.67101

ZDHC16	zinc finger DHC-type containing 16 [Source:HGNC Symbol;Acc:HGNC:1002248]	-1.37319
ZDHC23	zinc finger DHC-type containing 23 [Source:HGNC Symbol;Acc:HGNC:1001514]	-1.52041
ZDHC7	zinc finger DHC-type containing 7 [Source:HGNC Symbol;Acc:HGNC:10005129]	-1.23615
ZDHC8	zinc finger DHC-type containing 8 [Source:HGNC Symbol;Acc:HGNC:10008462]	-1.39102
ZFAND4	zinc finger AN1-type containing 4 [Source:HGNC Symbol;Acc:HGNC:10000184]	-2.86044
ZFC3H1	zinc finger C3H1-type containing [Source:HGNC Symbol;Acc:HGNC:10005465]	-1.21778
ZFR2	zinc finger RNA binding protein 2 [Source:HGNC Symbol;Acc:HGNC:10000391]	-1.30246
ZFYVE27	zinc finger FYVE-type containing 27 [Source:HGNC Symbol;Acc:HGNC:10009001]	-1.19399
ZGRF1	zinc finger GRF-type containing 1 [Source:HGNC Symbol;Acc:HGNC:10003665]	-1.54229
ZKSCAN8	zinc finger with KRAB and SCAN domains 8 [Source:HGNC Symbol;Acc:HGNC:100255E-07]	-1.48425
ZMAT3	zinc finger matrin-type 3 [Source:HGNC Symbol;Acc:HGNC:29983]	1.79E-05 -1.34215
ZMYND11	zinc finger MYND-type containing 11 [Source:HGNC Symbol;Acc:HGNC:10000481]	-1.28022
ZNF106	zinc finger protein 106 [Source:HGNC Symbol;Acc:HGNC:12886]	8.63E-06 -1.36891
ZNF112	zinc finger protein 112 [Source:HGNC Symbol;Acc:HGNC:12892]	0.008259 -1.76227
ZNF12	zinc finger protein 12 [Source:HGNC Symbol;Acc:HGNC:12902]	8.19E-07 -1.37466
ZNF131	zinc finger protein 131 [Source:HGNC Symbol;Acc:HGNC:12915]	0.001392 -1.22525
ZNF146	zinc finger protein 146 [Source:HGNC Symbol;Acc:HGNC:12931]	0.010011 -1.29071
ZNF154	zinc finger protein 154 [Source:HGNC Symbol;Acc:HGNC:12939]	0.004665 -3.09642
ZNF280C	zinc finger protein 280C [Source:HGNC Symbol;Acc:HGNC:25955]	2.45E-09 -1.80618
ZNF286A	zinc finger protein 286A [Source:HGNC Symbol;Acc:HGNC:13501]	0.00411 -1.48301
ZNF318	zinc finger protein 318 [Source:HGNC Symbol;Acc:HGNC:13578]	0.006695 -2.0275
ZNF326	zinc finger protein 326 [Source:HGNC Symbol;Acc:HGNC:14104]	2.26E-05 -1.69985
ZNF33B	zinc finger protein 33B [Source:HGNC Symbol;Acc:HGNC:13097]	2.56E-08 -3.35359
ZNF362	zinc finger protein 362 [Source:HGNC Symbol;Acc:HGNC:18079]	0.005128 -1.52671
ZNF367	zinc finger protein 367 [Source:HGNC Symbol;Acc:HGNC:18320]	2.56E-12 -1.68189
ZNF385B	zinc finger protein 385B [Source:HGNC Symbol;Acc:HGNC:26332]	0.000781 -2.3873
ZNF41	zinc finger protein 41 [Source:HGNC Symbol;Acc:HGNC:13107]	0.002616 -1.83105
ZNF512	zinc finger protein 512 [Source:HGNC Symbol;Acc:HGNC:29380]	0.000484 -2.23231
ZNF609	zinc finger protein 609 [Source:HGNC Symbol;Acc:HGNC:29003]	0.007653 -1.48239
ZNF620	zinc finger protein 620 [Source:HGNC Symbol;Acc:HGNC:28742]	0.009161 -2.03744
ZNF664	zinc finger protein 664 [Source:HGNC Symbol;Acc:HGNC:25406]	0.00026 -1.5564
ZNF70	zinc finger protein 70 [Source:HGNC Symbol;Acc:HGNC:13140]	0.0024 -3.47203
ZNF704	zinc finger protein 704 [Source:HGNC Symbol;Acc:HGNC:32291]	0.007617 -1.27164
ZNF804A	zinc finger protein 804A [Source:HGNC Symbol;Acc:HGNC:21711]	0.003613 -3.10835
ZNF878	zinc finger protein 878 [Source:HGNC Symbol;Acc:HGNC:37246]	0.010378 -2.2543
ZNHIT6	zinc finger HIT-type containing 6 [Source:HGNC Symbol;Acc:HGNC:10000311]	-1.67423
ZNRF3	zinc and ring finger 3 [Source:HGNC Symbol;Acc:HGNC:18126]	3.93E-05 -1.63172
ZRANB1	zinc finger RANBP2-type containing 1 [Source:HGNC Symbol;Acc:HGNC:10002038]	-1.23107
ZSWIM4	zinc finger SWIM-type containing 4 [Source:HGNC Symbol;Acc:HGNC:10005311]	-1.84188
ZW10	zw10 kinetochore protein [Source:HGNC Symbol;Acc:HGNC:1319]	5.72E-05 -1.46348
ZWINT	ZW10 interacting kinetochore protein [Source:HGNC Symbol;Acc:HGNC:1002E-05]	-2.06098
ZYX	zyxin [Source:HGNC Symbol;Acc:HGNC:13200]	0.002964 -1.39519

279 yellow = ATF1 targets

ATF1 targets	ensembl_gene_id	pvalue	Fold Change
ABCA12	ATP binding cassette subfamily A member 12 [Source:HGNC Symbol;Acc:HGNC:24210]	0.004052	1.811881
ABHD18	abhydrolase domain containing 18 [Source:HGNC Symbol;Acc:HGNC:24210]	0.02664	1.448135
ABHD3	abhydrolase domain containing 3 [Source:HGNC Symbol;Acc:HGNC:24210]	0.000411	1.538574
ABLIM1	actin binding LIM protein 1 [Source:HGNC Symbol;Acc:HGNC:24210]	0.027476	1.249539
ABRACL	ABRA C-terminal like [Source:HGNC Symbol;Acc:HGNC:21230]	0.001776	1.827098
ABT1	activator of basal transcription 1 [Source:HGNC Symbol;Acc:HGNC:24210]	0.001813	1.524582
AC093012.1	interleukin 1 receptor associated kinase 4 [Source:NCBI gene;Acc:NCBI:24210]	4.26E-05	1.488919
ACADSB	acyl-CoA dehydrogenase short/branched chain [Source:HGNC Symbol;Acc:HGNC:24210]	1.74E-08	1.839578
ACAP1	ArfGAP with coiled-coil, ankyrin repeat and PH domains 1 [Source:HGNC Symbol;Acc:HGNC:24210]	0.008037	2.028714
ACAT1	acetyl-CoA acetyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:24210]	0.021509	1.236002
ACOT13	acyl-CoA thioesterase 13 [Source:HGNC Symbol;Acc:HGNC:20990]	0.000865	1.697869
ACSM1	acyl-CoA synthetase medium chain family member 1 [Source:HGNC Symbol;Acc:HGNC:24210]	0.021543	2.480399
ACSS1	acyl-CoA synthetase short chain family member 1 [Source:HGNC Symbol;Acc:HGNC:24210]	0.035373	1.867174
ACTL6A	actin like 6A [Source:HGNC Symbol;Acc:HGNC:24124]	0.033966	1.338641
ACTR10	actin related protein 10 [Source:HGNC Symbol;Acc:HGNC:17372]	0.003029	1.555871
ACTR6	actin related protein 6 [Source:HGNC Symbol;Acc:HGNC:24025]	0.010391	1.493997
ACYP2	acylphosphatase 2 [Source:HGNC Symbol;Acc:HGNC:180]	0.001417	1.843475
ADPRM	ADP-ribose/CDP-alcohol diphosphatase, manganese dependent [Source:HGNC Symbol;Acc:HGNC:24210]	0.000632	1.872023
ADRB1	adrenoceptor beta 1 [Source:HGNC Symbol;Acc:HGNC:285]	0.026617	1.742934
ADTRP	androgen dependent TFPI regulating protein [Source:HGNC Symbol;Acc:HGNC:24210]	0.01338	1.386155
AFG1L	AFG1 like ATPase [Source:HGNC Symbol;Acc:HGNC:16411]	0.010693	1.503256
AGAP6	ArfGAP with GTPase domain, ankyrin repeat and PH domain 6 [Source:HGNC Symbol;Acc:HGNC:24210]	0.001989	1.507417
AGER	advanced glycosylation end-product specific receptor [Source:HGNC Symbol;Acc:HGNC:24210]	0.002138	1.727996
AHNAK2	AHNAK nucleoprotein 2 [Source:HGNC Symbol;Acc:HGNC:20125]	4.12E-09	1.885915
AK6	adenylate kinase 6 [Source:HGNC Symbol;Acc:HGNC:49151]	3.80E-05	1.599288
AKAP17A	A-kinase anchoring protein 17A [Source:HGNC Symbol;Acc:HGNC:24210]	0.049871	1.305158
AKR1C3	aldo-keto reductase family 1 member C3 [Source:HGNC Symbol;Acc:HGNC:24210]	0.004083	2.758315
AL136454.1	novel protein similar to ribosomal protein S27a RPS27A [Source:NCBI gene;Acc:NCBI:24210]	0.02529	1.824922
ALDH16A1	aldehyde dehydrogenase 16 family member A1 [Source:HGNC Symbol;Acc:HGNC:24210]	0.000878	1.451805
ALG11	ALG11 alpha-1,2-mannosyltransferase [Source:HGNC Symbol;Acc:HGNC:24210]	0.044423	1.361963
ALG5	ALG5 dolichyl-phosphate beta-glucosyltransferase [Source:HGNC Symbol;Acc:HGNC:24210]	0.01249	1.689279
ALKBH2	alkB homolog 2, alpha-ketoglutarate dependent dioxygenase [Source:HGNC Symbol;Acc:HGNC:24210]	0.016577	1.412128
ALKBH3	alkB homolog 3, alpha-ketoglutarate dependent dioxygenase [Source:HGNC Symbol;Acc:HGNC:24210]	0.016017	1.313334
ALS2CL	ALS2 C-terminal like [Source:HGNC Symbol;Acc:HGNC:20605]	0.049704	1.493139
AMN1	antagonist of mitotic exit network 1 homolog [Source:HGNC Symbol;Acc:HGNC:24210]	1.04E-05	1.984233
AMZ2	archaelysin family metalloproteinase 2 [Source:HGNC Symbol;Acc:HGNC:24210]	9.90E-07	1.863539
ANAPC11	anaphase promoting complex subunit 11 [Source:HGNC Symbol;Acc:HGNC:24210]	0.040565	1.66129
ANAPC13	anaphase promoting complex subunit 13 [Source:HGNC Symbol;Acc:HGNC:24210]	0.004503	1.370309
ANAPC16	anaphase promoting complex subunit 16 [Source:HGNC Symbol;Acc:HGNC:24210]	0.002294	1.742359
ANGPTL6	angiopoietin like 6 [Source:HGNC Symbol;Acc:HGNC:23140]	0.045181	1.795507
ANKRA2	ankyrin repeat family A member 2 [Source:HGNC Symbol;Acc:HGNC:24210]	0.014889	1.914638
ANKRD22	ankyrin repeat domain 22 [Source:HGNC Symbol;Acc:HGNC:2830]	3.37E-05	1.827839
ANKRD37	ankyrin repeat domain 37 [Source:HGNC Symbol;Acc:HGNC:2950]	0.001486	2.490594
ANKRD46	ankyrin repeat domain 46 [Source:HGNC Symbol;Acc:HGNC:2720]	0.002214	2.157403
ANKRD49	ankyrin repeat domain 49 [Source:HGNC Symbol;Acc:HGNC:2590]	0.011895	1.781076
ANXA1	annexin A1 [Source:HGNC Symbol;Acc:HGNC:533]	0.031156	1.375899

AP3S1	adaptor related protein complex 3 subunit sigma 1 [Source:HGNC Symbol;Acc:HGNC:1758]	0.000881	1.521469
APIP	APAF1 interacting protein [Source:HGNC Symbol;Acc:HGNC:1758]	0.00047	1.615334
APLF	aprataxin and PNKP like factor [Source:HGNC Symbol;Acc:HGNC:15984]	0.025637	1.422284
APOO	apolipoprotein O [Source:HGNC Symbol;Acc:HGNC:28727]	0.045776	1.331706
APT	aprataxin [Source:HGNC Symbol;Acc:HGNC:15984]	0.019651	1.530757
ARF4	ADP ribosylation factor 4 [Source:HGNC Symbol;Acc:HGNC:655]	0.015819	1.412588
ARG2	arginase 2 [Source:HGNC Symbol;Acc:HGNC:664]	0.021255	1.994039
ARHGEF33	Rho guanine nucleotide exchange factor 33 [Source:HGNC Symbol;Acc:HGNC:24047]	0.003859	1.547472
ARHGEF37	Rho guanine nucleotide exchange factor 37 [Source:HGNC Symbol;Acc:HGNC:24047]	0.032672	1.494775
ARHGEF4	Rho guanine nucleotide exchange factor 4 [Source:HGNC Symbol;Acc:HGNC:655]	0.000291	2.061503
ARIH2OS	ariadne RBR E3 ubiquitin protein ligase 2 opposite strand [Source:HGNC Symbol;Acc:HGNC:24047]	0.037223	1.867051
ARL1	ADP ribosylation factor like GTPase 1 [Source:HGNC Symbol;Acc:HGNC:655]	0.018291	1.494282
ARL16	ADP ribosylation factor like GTPase 16 [Source:HGNC Symbol;Acc:HGNC:655]	0.021034	1.541338
ARL4A	ADP ribosylation factor like GTPase 4A [Source:HGNC Symbol;Acc:HGNC:655]	0.017895	1.392235
ARL6	ADP ribosylation factor like GTPase 6 [Source:HGNC Symbol;Acc:HGNC:655]	0.005245	1.650033
ARL6IP6	ADP ribosylation factor like GTPase 6 interacting protein 6 [Source:HGNC Symbol;Acc:HGNC:24047]	0.022725	1.335715
ARMC1	armadillo repeat containing 1 [Source:HGNC Symbol;Acc:HGNC:24047]	0.00891	1.522795
ARMC10	armadillo repeat containing 10 [Source:HGNC Symbol;Acc:HGNC:24047]	0.01318	1.623577
ARMC12	armadillo repeat containing 12 [Source:HGNC Symbol;Acc:HGNC:24047]	0.02478	2.524746
ARMCX5	armadillo repeat containing X-linked 5 [Source:HGNC Symbol;Acc:HGNC:24047]	0.033966	1.235353
ARPC1A	actin related protein 2/3 complex subunit 1A [Source:HGNC Symbol;Acc:HGNC:24047]	0.00571	1.415342
ARPC3	actin related protein 2/3 complex subunit 3 [Source:HGNC Symbol;Acc:HGNC:24047]	0.020805	1.673124
ARPC5	actin related protein 2/3 complex subunit 5 [Source:HGNC Symbol;Acc:HGNC:24047]	0.000389	1.797481
ARRDC3	arrestin domain containing 3 [Source:HGNC Symbol;Acc:HGNC:24047]	0.027993	1.315235
ARSI	arylsulfatase family member I [Source:HGNC Symbol;Acc:HGNC:24047]	0.010366	1.42404
ARTN	artemin [Source:HGNC Symbol;Acc:HGNC:727]	0.02478	1.311038
ASAH1	N-acylsphingosine amidohydrolase 1 [Source:HGNC Symbol;Acc:HGNC:24047]	0.046012	1.301621
ASB13	ankyrin repeat and SOCS box containing 13 [Source:HGNC Symbol;Acc:HGNC:24047]	0.011435	1.30689
ASCC1	activating signal cointegrator 1 complex subunit 1 [Source:HGNC Symbol;Acc:HGNC:24047]	0.006407	1.393052
ASF1A	anti-silencing function 1A histone chaperone [Source:HGNC Symbol;Acc:HGNC:24047]	0.003209	1.541798
ASIC3	acid sensing ion channel subunit 3 [Source:HGNC Symbol;Acc:HGNC:24047]	0.005924	2.353262
ASNS	asparagine synthetase (glutamine-hydrolyzing) [Source:HGNC Symbol;Acc:HGNC:24047]	0.005004	1.589629
ASNSD1	asparagine synthetase domain containing 1 [Source:HGNC Symbol;Acc:HGNC:24047]	0.012098	1.401035
ATF3	activating transcription factor 3 [Source:HGNC Symbol;Acc:HGNC:24047]	0.001805	2.120073
ATG3	autophagy related 3 [Source:HGNC Symbol;Acc:HGNC:20962]	0.001459	1.330588
ATL2	atlastin GTPase 2 [Source:HGNC Symbol;Acc:HGNC:24047]	0.036921	1.528345
ATOX1	antioxidant 1 copper chaperone [Source:HGNC Symbol;Acc:HGNC:24047]	0.006871	1.366479
ATP5F1C	ATP synthase F1 subunit gamma [Source:HGNC Symbol;Acc:HGNC:24047]	0.021388	1.485086
ATP5F1E	ATP synthase F1 subunit epsilon [Source:HGNC Symbol;Acc:HGNC:24047]	0.005798	1.721134
ATP5IF1	ATP synthase inhibitory factor subunit 1 [Source:HGNC Symbol;Acc:HGNC:24047]	0.013072	1.691883
ATP5MC1	ATP synthase membrane subunit c locus 1 [Source:HGNC Symbol;Acc:HGNC:24047]	0.000448	1.697093
ATP5MD	ATP synthase membrane subunit DAPIT [Source:HGNC Symbol;Acc:HGNC:24047]	0.000582	2.105823
ATP5MF	ATP synthase membrane subunit f [Source:HGNC Symbol;Acc:HGNC:24047]	0.005044	1.79779
ATP5MG	ATP synthase membrane subunit g [Source:HGNC Symbol;Acc:HGNC:24047]	0.022646	1.56203
ATP5MPL	ATP synthase membrane subunit 6.8PL [Source:HGNC Symbol;Acc:HGNC:24047]	0.001113	1.851921
ATP5PB	ATP synthase peripheral stalk-membrane subunit b [Source:HGNC Symbol;Acc:HGNC:24047]	0.017989	1.632474
ATP5PD	ATP synthase peripheral stalk subunit d [Source:HGNC Symbol;Acc:HGNC:24047]	0.003148	1.779333

ATP5PF	ATP synthase peripheral stalk subunit F6 [Source:HGNC Symbol;Acc:HGNC:10548]	0.006569	1.524277
ATP5PO	ATP synthase peripheral stalk subunit OSCP [Source:HGNC Symbol;Acc:HGNC:10549]	0.010315	1.861533
ATP6AP2	ATPase H+ transporting accessory protein 2 [Source:HGNC Symbol;Acc:HGNC:10550]	0.024751	1.459836
ATP6V0E1	ATPase H+ transporting V0 subunit e1 [Source:HGNC Symbol;Acc:HGNC:10551]	0.011812	1.663814
ATP6V1E1	ATPase H+ transporting V1 subunit E1 [Source:HGNC Symbol;Acc:HGNC:10552]	0.037325	1.536709
ATP6V1G1	ATPase H+ transporting V1 subunit G1 [Source:HGNC Symbol;Acc:HGNC:10553]	0.001823	2.137042
ATXN1	ataxin 1 [Source:HGNC Symbol;Acc:HGNC:10548]	0.014015	1.299367
AZIN1	antizyme inhibitor 1 [Source:HGNC Symbol;Acc:HGNC:16432]	0.029561	1.311357
AZIN2	antizyme inhibitor 2 [Source:HGNC Symbol;Acc:HGNC:29957]	0.019428	1.402031
B2M	beta-2-microglobulin [Source:HGNC Symbol;Acc:HGNC:914]	0.004525	2.192743
B3GAT3	beta-1,3-glucuronyltransferase 3 [Source:HGNC Symbol;Acc:HGNC:10554]	0.002897	1.633791
B4GALNT3	beta-1,4-N-acetyl-galactosaminyltransferase 3 [Source:HGNC Symbol;Acc:HGNC:10555]	0.004708	1.669053
B4GAT1	beta-1,4-glucuronyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:10556]	0.019616	1.403807
BANF1	barrier to autointegration factor 1 [Source:HGNC Symbol;Acc:HGNC:10557]	0.023167	1.431746
BBIP1	BBSome interacting protein 1 [Source:HGNC Symbol;Acc:HGNC:26601]	0.000508	1.537912
BBS10	Bardet-Biedl syndrome 10 [Source:HGNC Symbol;Acc:HGNC:26602]	0.001258	1.523372
BBS12	Bardet-Biedl syndrome 12 [Source:HGNC Symbol;Acc:HGNC:26604]	0.013442	1.658425
BCAS2	BCAS2 pre-mRNA processing factor [Source:HGNC Symbol;Acc:HGNC:10558]	0.014853	1.335739
BCDIN3D	BCDIN3 domain containing RNA methyltransferase [Source:HGNC Symbol;Acc:HGNC:10559]	0.035387	1.506526
BCL2L10	BCL2 like 10 [Source:HGNC Symbol;Acc:HGNC:993]	0.010085	2.49721
BCL7B	BAF chromatin remodeling complex subunit BCL7B [Source:HGNC Symbol;Acc:HGNC:10560]	0.042635	1.411766
BDKRB2	bradykinin receptor B2 [Source:HGNC Symbol;Acc:HGNC:1030]	0.020755	1.54718
BET1	Bet1 golgi vesicular membrane trafficking protein [Source:HGNC Symbol;Acc:HGNC:10561]	0.000467	1.782393
BEX2	brain expressed X-linked 2 [Source:HGNC Symbol;Acc:HGNC:309]	0.005433	1.670215
BEX3	brain expressed X-linked 3 [Source:HGNC Symbol;Acc:HGNC:133]	0.000189	1.252801
BFSP1	beaded filament structural protein 1 [Source:HGNC Symbol;Acc:HGNC:10562]	0.029325	1.443246
BICD2	BICD cargo adaptor 2 [Source:HGNC Symbol;Acc:HGNC:17208]	0.028849	1.196236
BLOC1S2	biogenesis of lysosomal organelles complex 1 subunit 2 [Source:HGNC Symbol;Acc:HGNC:10563]	0.040451	1.410175
BLOC1S4	biogenesis of lysosomal organelles complex 1 subunit 4 [Source:HGNC Symbol;Acc:HGNC:10564]	0.005358	1.207724
BLZF1	basic leucine zipper nuclear factor 1 [Source:HGNC Symbol;Acc:HGNC:10565]	0.000182	1.568142
BOLA1	bolA family member 1 [Source:HGNC Symbol;Acc:HGNC:24263]	1.09E-05	1.828693
BOLA3	bolA family member 3 [Source:HGNC Symbol;Acc:HGNC:24415]	0.003447	1.629124
BORCS5	BLOC-1 related complex subunit 5 [Source:HGNC Symbol;Acc:HGNC:10566]	0.04499	1.283603
BRK1	BRICK1 subunit of SCAR/WAVE actin nucleating complex [Source:HGNC Symbol;Acc:HGNC:10567]	0.00438	1.607425
BST2	bone marrow stromal cell antigen 2 [Source:HGNC Symbol;Acc:HGNC:10568]	0.019429	2.018486
BTBD9	BTB domain containing 9 [Source:HGNC Symbol;Acc:HGNC:2122]	0.029063	1.311924
BTF3	basic transcription factor 3 [Source:HGNC Symbol;Acc:HGNC:112]	0.037392	1.26297
BTF3L4	basic transcription factor 3 like 4 [Source:HGNC Symbol;Acc:HGNC:10569]	0.003698	1.735504
C11orf1	chromosome 11 open reading frame 1 [Source:HGNC Symbol;Acc:HGNC:10570]	0.004006	1.407242
C11orf54	chromosome 11 open reading frame 54 [Source:HGNC Symbol;Acc:HGNC:10571]	0.031689	1.449676
C11orf74	chromosome 11 open reading frame 74 [Source:HGNC Symbol;Acc:HGNC:10572]	0.006639	1.458515
C12orf29	chromosome 12 open reading frame 29 [Source:HGNC Symbol;Acc:HGNC:10573]	0.003682	1.651292
C12orf45	chromosome 12 open reading frame 45 [Source:HGNC Symbol;Acc:HGNC:10574]	0.00687	1.549075
C12orf49	chromosome 12 open reading frame 49 [Source:HGNC Symbol;Acc:HGNC:10575]	0.010101	1.272563
C12orf60	chromosome 12 open reading frame 60 [Source:HGNC Symbol;Acc:HGNC:10576]	0.004424	1.821911
C12orf66	chromosome 12 open reading frame 66 [Source:HGNC Symbol;Acc:HGNC:10577]	0.037952	1.341401
C12orf73	chromosome 12 open reading frame 73 [Source:HGNC Symbol;Acc:HGNC:10578]	0.01808	1.675819

C12orf76	chromosome 12 open reading frame 76 [Source:HGNC Symbol;A	0.030118	1.626373
C14orf119	chromosome 14 open reading frame 119 [Source:HGNC Symbol;	0.000882	1.895702
C14orf132	chromosome 14 open reading frame 132 [Source:HGNC Symbol;	0.021625	3.165732
C14orf28	chromosome 14 open reading frame 28 [Source:HGNC Symbol;A	0.020273	1.81051
C15orf40	chromosome 15 open reading frame 40 [Source:HGNC Symbol;A	0.007438	1.572368
C16orf74	chromosome 16 open reading frame 74 [Source:HGNC Symbol;A	0.004347	1.579234
C17orf58	chromosome 17 open reading frame 58 [Source:HGNC Symbol;A	0.029718	1.325587
C17orf75	chromosome 17 open reading frame 75 [Source:HGNC Symbol;A	0.00854	1.521421
C17orf99	chromosome 17 open reading frame 99 [Source:HGNC Symbol;A	0.003889	2.322189
C18orf21	chromosome 18 open reading frame 21 [Source:HGNC Symbol;A	0.01235	1.56575
C19orf38	chromosome 19 open reading frame 38 [Source:HGNC Symbol;A	0.004449	2.603567
C19orf53	chromosome 19 open reading frame 53 [Source:HGNC Symbol;A	0.021034	1.508528
C19orf73	chromosome 19 open reading frame 73 [Source:HGNC Symbol;A	0.008491	2.609793
C1D	C1D nuclear receptor corepressor [Source:HGNC Symbol;Acc:HG	0.000481	2.536758
C1orf109	chromosome 1 open reading frame 109 [Source:HGNC Symbol;A	0.019508	1.346575
C1orf131	chromosome 1 open reading frame 131 [Source:HGNC Symbol;A	0.02442	1.213574
C1orf50	chromosome 1 open reading frame 50 [Source:HGNC Symbol;Ac	0.049855	1.549022
C1orf54	chromosome 1 open reading frame 54 [Source:HGNC Symbol;Ac	0.022381	2.017355
C1QBP	complement C1q binding protein [Source:HGNC Symbol;Acc:HGI	0.002101	1.549602
C2CD4A	C2 calcium dependent domain containing 4A [Source:HGNC Sym	0.018388	2.465835
C2orf49	chromosome 2 open reading frame 49 [Source:HGNC Symbol;Ac	0.018405	1.348509
C2orf76	chromosome 2 open reading frame 76 [Source:HGNC Symbol;Ac	0.001753	2.116605
C3orf62	chromosome 3 open reading frame 62 [Source:HGNC Symbol;Ac	0.005564	1.503512
C3orf67	chromosome 3 open reading frame 67 [Source:HGNC Symbol;Ac	0.033896	1.272293
C4orf3	chromosome 4 open reading frame 3 [Source:HGNC Symbol;Acc	0.041438	1.401886
C4orf33	chromosome 4 open reading frame 33 [Source:HGNC Symbol;Ac	0.033325	1.558957
C4orf36	chromosome 4 open reading frame 36 [Source:HGNC Symbol;Ac	0.023432	1.442602
C4orf47	chromosome 4 open reading frame 47 [Source:HGNC Symbol;Ac	0.04736	1.764132
C5AR1	complement C5a receptor 1 [Source:HGNC Symbol;Acc:HGNC:13	0.013244	1.699609
C5orf30	chromosome 5 open reading frame 30 [Source:HGNC Symbol;Ac	0.011754	1.230922
C6orf226	chromosome 6 open reading frame 226 [Source:HGNC Symbol;A	0.004497	1.835915
C7orf50	chromosome 7 open reading frame 50 [Source:HGNC Symbol;Ac	0.043681	1.287944
C8orf37	chromosome 8 open reading frame 37 [Source:HGNC Symbol;Ac	0.049547	1.299965
C8orf76	chromosome 8 open reading frame 76 [Source:HGNC Symbol;Ac	0.025794	1.910762
C9orf40	chromosome 9 open reading frame 40 [Source:HGNC Symbol;Ac	0.000614	1.292615
C9orf64	chromosome 9 open reading frame 64 [Source:HGNC Symbol;Ac	0.015407	1.112007
C9orf72	C9orf72-SMCR8 complex subunit [Source:HGNC Symbol;Acc:HGI	0.006303	1.688293
CA11	carbonic anhydrase 11 [Source:HGNC Symbol;Acc:HGNC:1370]	0.019651	1.329042
CA14	carbonic anhydrase 14 [Source:HGNC Symbol;Acc:HGNC:1372]	0.030499	1.805646
CACFD1	calcium channel flower domain containing 1 [Source:HGNC Sym]	0.02997	1.463361
CALHM6	calcium homeostasis modulator family member 6 [Source:HGNC	0.010712	1.583679
CALM1	calmodulin 1 [Source:HGNC Symbol;Acc:HGNC:1442]	0.005968	1.362918
CALM2	calmodulin 2 [Source:HGNC Symbol;Acc:HGNC:1445]	0.004254	1.476378
CAMK1D	calcium/calmodulin dependent protein kinase ID [Source:HGNC	0.022052	1.30132
CAMTA1	calmodulin binding transcription activator 1 [Source:HGNC Sym]	0.00454	1.463997
CAPNS2	calpain small subunit 2 [Source:HGNC Symbol;Acc:HGNC:16371]	0.004197	3.533269
CAPZA2	capping actin protein of muscle Z-line subunit alpha 2 [Source:H	0.002454	1.789094

CARD14	caspase recruitment domain family member 14 [Source:HGNC S	0.020044	1.645429
CASC4	cancer susceptibility 4 [Source:HGNC Symbol;Acc:HGNC:24892]	0.030369	1.174662
CASP4	caspase 4 [Source:HGNC Symbol;Acc:HGNC:1505]	0.002302	1.455504
CASP8	caspase 8 [Source:HGNC Symbol;Acc:HGNC:1509]	0.014874	1.287399
CBX3	chromobox 3 [Source:HGNC Symbol;Acc:HGNC:1553]	0.032123	1.291708
CBX8	chromobox 8 [Source:HGNC Symbol;Acc:HGNC:15962]	0.011583	1.299638
CCDC110	coiled-coil domain containing 110 [Source:HGNC Symbol;Acc:HG	0.016953	2.322746
CCDC121	coiled-coil domain containing 121 [Source:HGNC Symbol;Acc:HG	1.83E-06	2.088853
CCDC126	coiled-coil domain containing 126 [Source:HGNC Symbol;Acc:HG	0.035448	1.560099
CCDC138	coiled-coil domain containing 138 [Source:HGNC Symbol;Acc:HG	0.002761	1.576937
CCDC17	coiled-coil domain containing 17 [Source:HGNC Symbol;Acc:HGN	0.038974	1.919316
CCDC51	coiled-coil domain containing 51 [Source:HGNC Symbol;Acc:HGN	0.021146	1.368596
CCDC58	coiled-coil domain containing 58 [Source:HGNC Symbol;Acc:HGN	0.018988	1.371381
CCDC59	coiled-coil domain containing 59 [Source:HGNC Symbol;Acc:HGN	0.003446	1.636116
CCDC62	coiled-coil domain containing 62 [Source:HGNC Symbol;Acc:HGN	0.042792	2.116872
CCDC88B	coiled-coil domain containing 88B [Source:HGNC Symbol;Acc:HG	0.009043	1.429002
CCDC90B	coiled-coil domain containing 90B [Source:HGNC Symbol;Acc:HG	1.08E-05	1.770212
CCNB1IP1	cyclin B1 interacting protein 1 [Source:HGNC Symbol;Acc:HGNC:	0.021146	1.712432
CCNDBP1	cyclin D1 binding protein 1 [Source:HGNC Symbol;Acc:HGNC:158	0.004159	1.595022
CCNH	cyclin H [Source:HGNC Symbol;Acc:HGNC:1594]	0.027672	1.368327
CCNL1	cyclin L1 [Source:HGNC Symbol;Acc:HGNC:20569]	0.033982	1.355324
CCT8	chaperonin containing TCP1 subunit 8 [Source:HGNC Symbol;Acc	0.021034	1.233366
CD46	CD46 molecule [Source:HGNC Symbol;Acc:HGNC:6953]	0.043468	1.408618
CD58	CD58 molecule [Source:HGNC Symbol;Acc:HGNC:1688]	2.40E-05	2.538322
CDC42	cell division cycle 42 [Source:HGNC Symbol;Acc:HGNC:1736]	0.019846	1.629349
CDK7	cyclin dependent kinase 7 [Source:HGNC Symbol;Acc:HGNC:1778	0.016321	1.633593
CDKL3	cyclin dependent kinase like 3 [Source:HGNC Symbol;Acc:HGNC:	0.003619	2.40954
CDKN2AIPNL	CDKN2A interacting protein N-terminal like [Source:HGNC Symb	0.000718	1.534249
CDKN2B	cyclin dependent kinase inhibitor 2B [Source:HGNC Symbol;Acc:l	0.039341	1.218217
CEBPZOS	CEBPZ opposite strand [Source:HGNC Symbol;Acc:HGNC:49288]	0.005077	1.524099
CENPQ	centromere protein Q [Source:HGNC Symbol;Acc:HGNC:21347]	0.026412	1.62196
CEP57L1	centrosomal protein 57 like 1 [Source:HGNC Symbol;Acc:HGNC:2	0.022616	1.536454
CEP76	centrosomal protein 76 [Source:HGNC Symbol;Acc:HGNC:25727]	0.002311	1.454421
CFAP20	cilia and flagella associated protein 20 [Source:HGNC Symbol;Ac	0.040863	1.343186
CFAP300	cilia and flagella associated protein 300 [Source:HGNC Symbol;A	2.75E-05	2.138625
CFL2	cofilin 2 [Source:HGNC Symbol;Acc:HGNC:1875]	8.39E-05	1.683227
CHCHD1	coiled-coil-helix-coiled-coil-helix domain containing 1 [Source:HC	0.010401	1.443671
CHCHD2	coiled-coil-helix-coiled-coil-helix domain containing 2 [Source:HC	0.018207	1.685027
CHCHD5	coiled-coil-helix-coiled-coil-helix domain containing 5 [Source:HC	0.020994	1.492132
CHEK2	checkpoint kinase 2 [Source:HGNC Symbol;Acc:HGNC:16627]	0.030897	1.372422
CHIC2	cysteine rich hydrophobic domain 2 [Source:HGNC Symbol;Acc:f	0.006312	1.410698
CHMP1B	charged multivesicular body protein 1B [Source:HGNC Symbol;A	0.008252	1.648006
CHMP2B	charged multivesicular body protein 2B [Source:HGNC Symbol;A	0.011895	1.454467
CHMP5	charged multivesicular body protein 5 [Source:HGNC Symbol;Acc	0.048664	1.733962
CHST7	carbohydrate sulfotransferase 7 [Source:HGNC Symbol;Acc:HGN	0.011455	1.273884
CIAO2A	cytosolic iron-sulfur assembly component 2A [Source:HGNC Sym	0.000582	1.790058
CIAO3	cytosolic iron-sulfur assembly component 3 [Source:HGNC Symb	0.029175	1.234589

CKLF	chemokine like factor [Source:HGNC Symbol;Acc:HGNC:13253]	0.006957	1.713041
CKS2	CDC28 protein kinase regulatory subunit 2 [Source:HGNC Symbol;Acc:HGNC:13253]	0.00756	1.664054
CLCA4	chloride channel accessory 4 [Source:HGNC Symbol;Acc:HGNC:2046]	0.004162	2.244887
CLDN15	claudin 15 [Source:HGNC Symbol;Acc:HGNC:2036]	0.034994	1.527294
CLDN4	claudin 4 [Source:HGNC Symbol;Acc:HGNC:2046]	0.036383	1.376297
CLDN7	claudin 7 [Source:HGNC Symbol;Acc:HGNC:2049]	0.006299	1.201732
CLEC2D	C-type lectin domain family 2 member D [Source:HGNC Symbol;Acc:HGNC:2049]	0.002238	1.783107
CLEC7A	C-type lectin domain containing 7A [Source:HGNC Symbol;Acc:HGNC:2049]	0.015915	2.753916
CLHC1	clathrin heavy chain linker domain containing 1 [Source:HGNC Symbol;Acc:HGNC:2049]	0.000465	1.611874
CLN8	CLN8 transmembrane ER and ERGIC protein [Source:HGNC Symbol;Acc:HGNC:2049]	0.001313	1.440213
CMC1	C-X9-C motif containing 1 [Source:HGNC Symbol;Acc:HGNC:2878]	0.001187	1.848158
CMC2	C-X9-C motif containing 2 [Source:HGNC Symbol;Acc:HGNC:2444]	0.00047	1.72074
CMYA5	cardiomyopathy associated 5 [Source:HGNC Symbol;Acc:HGNC:13253]	0.012278	1.867725
CNIH1	cornichon family AMPA receptor auxiliary protein 1 [Source:HGNC Symbol;Acc:HGNC:13253]	0.00687	1.613662
CNIH4	cornichon family AMPA receptor auxiliary protein 4 [Source:HGNC Symbol;Acc:HGNC:13253]	0.040469	1.574693
COA1	cytochrome c oxidase assembly factor 1 homolog [Source:HGNC Symbol;Acc:HGNC:13253]	0.006678	1.568471
COA4	cytochrome c oxidase assembly factor 4 homolog [Source:HGNC Symbol;Acc:HGNC:13253]	0.000369	1.614751
COA5	cytochrome c oxidase assembly factor 5 [Source:HGNC Symbol;Acc:HGNC:13253]	0.018554	1.626178
COA6	cytochrome c oxidase assembly factor 6 [Source:HGNC Symbol;Acc:HGNC:13253]	0.002137	1.994444
COA7	cytochrome c oxidase assembly factor 7 (putative) [Source:HGNC Symbol;Acc:HGNC:13253]	0.016309	1.209217
COL1A1	collagen type I alpha 1 chain [Source:HGNC Symbol;Acc:HGNC:2049]	0.00976	1.46055
COL5A3	collagen type V alpha 3 chain [Source:HGNC Symbol;Acc:HGNC:13253]	0.043063	2.187773
COMMD1	copper metabolism domain containing 1 [Source:HGNC Symbol;Acc:HGNC:13253]	0.036766	1.58562
COMMD10	COMM domain containing 10 [Source:HGNC Symbol;Acc:HGNC:13253]	0.017878	1.824605
COMMD5	COMM domain containing 5 [Source:HGNC Symbol;Acc:HGNC:13253]	0.026396	1.396613
COMMD6	COMM domain containing 6 [Source:HGNC Symbol;Acc:HGNC:2049]	0.000452	2.024534
COMMD7	COMM domain containing 7 [Source:HGNC Symbol;Acc:HGNC:13253]	0.036911	1.543176
COMMD8	COMM domain containing 8 [Source:HGNC Symbol;Acc:HGNC:2049]	0.006627	1.8396
COPS3	COP9 signalosome subunit 3 [Source:HGNC Symbol;Acc:HGNC:2049]	0.037055	1.361028
COPS9	COP9 signalosome subunit 9 [Source:HGNC Symbol;Acc:HGNC:2049]	0.00219	1.901073
COQ10B	coenzyme Q10B [Source:HGNC Symbol;Acc:HGNC:25819]	0.009657	1.645055
COQ5	coenzyme Q5, methyltransferase [Source:HGNC Symbol;Acc:HGNC:25819]	0.000175	1.61635
COX14	cytochrome c oxidase assembly factor COX14 [Source:HGNC Symbol;Acc:HGNC:2049]	0.028552	1.927519
COX17	cytochrome c oxidase copper chaperone COX17 [Source:HGNC Symbol;Acc:HGNC:2049]	0.000621	1.663531
COX18	cytochrome c oxidase assembly factor COX18 [Source:HGNC Symbol;Acc:HGNC:2049]	0.026177	1.374567
COX19	cytochrome c oxidase assembly factor COX19 [Source:HGNC Symbol;Acc:HGNC:2049]	0.017257	1.28635
COX5A	cytochrome c oxidase subunit 5A [Source:HGNC Symbol;Acc:HGNC:2049]	0.018569	1.406988
COX5B	cytochrome c oxidase subunit 5B [Source:HGNC Symbol;Acc:HGNC:2049]	0.01373	1.952023
COX6C	cytochrome c oxidase subunit 6C [Source:HGNC Symbol;Acc:HGNC:2049]	0.006769	1.73041
COX7A2	cytochrome c oxidase subunit 7A2 [Source:HGNC Symbol;Acc:HGNC:2049]	0.020002	1.850049
COX7A2L	cytochrome c oxidase subunit 7A2 like [Source:HGNC Symbol;Acc:HGNC:2049]	0.011363	1.804678
COX7B	cytochrome c oxidase subunit 7B [Source:HGNC Symbol;Acc:HGNC:2049]	0.010058	2.093641
COX7C	cytochrome c oxidase subunit 7C [Source:HGNC Symbol;Acc:HGNC:2049]	0.017373	1.419928
CPA6	carboxypeptidase A6 [Source:HGNC Symbol;Acc:HGNC:17245]	0.043897	1.825727
CRABP2	cellular retinoic acid binding protein 2 [Source:HGNC Symbol;Acc:HGNC:13253]	0.027332	1.576041
CRADD	CASP2 and RIPK1 domain containing adaptor with death domain [Source:HGNC Symbol;Acc:HGNC:13253]	0.04499	1.660505
CRB3	crumbs cell polarity complex component 3 [Source:HGNC Symbol;Acc:HGNC:13253]	0.023408	1.439408

CRBN	cereblon [Source:HGNC Symbol;Acc:HGNC:30185]	0.017443	1.605359
CREB1	cAMP responsive element binding protein 1 [Source:HGNC Symt	0.023961	1.215729
CRELD1	cysteine rich with EGF like domains 1 [Source:HGNC Symbol;Acc:	0.02904	1.70062
CREM	cAMP responsive element modulator [Source:HGNC Symbol;Acc	3.14E-14	2.052472
CRIPT	CXXC repeat containing interactor of PDZ3 domain [Source:HGNC	0.002951	1.684731
CRYBG2	crystallin beta-gamma domain containing 2 [Source:HGNC Symb	0.006467	1.53212
CSRP2	cysteine and glycine rich protein 2 [Source:HGNC Symbol;Acc:HC	0.029742	1.445898
CSTA	cystatin A [Source:HGNC Symbol;Acc:HGNC:2481]	0.00848	2.676316
CTBS	chitobiase [Source:HGNC Symbol;Acc:HGNC:2496]	1.90E-05	1.630278
CTH	cystathionine gamma-lyase [Source:HGNC Symbol;Acc:HGNC:25]	0.016558	1.565181
CUTC	cutC copper transporter [Source:HGNC Symbol;Acc:HGNC:24271	0.04746	1.233299
CWC15	CWC15 spliceosome associated protein homolog [Source:HGNC	0.009932	1.550646
CWF19L1	CWF19 like cell cycle control factor 1 [Source:HGNC Symbol;Acc:	0.00874	1.344368
CXorf40A	chromosome X open reading frame 40A [Source:HGNC Symbol;A	0.044999	1.558653
CXorf40B	chromosome X open reading frame 40B [Source:HGNC Symbol;A	0.008276	1.283793
CYB5A	cytochrome b5 type A [Source:HGNC Symbol;Acc:HGNC:2570]	0.002137	1.654215
CYB5R4	cytochrome b5 reductase 4 [Source:HGNC Symbol;Acc:HGNC:20	0.002989	1.469919
CYP2R1	cytochrome P450 family 2 subfamily R member 1 [Source:HGNC	0.000347	1.689648
CYSTM1	cysteine rich transmembrane module containing 1 [Source:HGNC	0.018569	1.854818
CZIB	CXXC motif containing zinc binding protein [Source:HGNC Symbc	8.00E-06	1.496397
DAD1	defender against cell death 1 [Source:HGNC Symbol;Acc:HGNC:2	0.045119	1.424365
DAPK2	death associated protein kinase 2 [Source:HGNC Symbol;Acc:HG	0.039793	1.396774
DAPL1	death associated protein like 1 [Source:HGNC Symbol;Acc:HGNC	0.033227	1.805465
DBF4	DBF4 zinc finger [Source:HGNC Symbol;Acc:HGNC:17364]	0.028518	1.256782
DCK	deoxycytidine kinase [Source:HGNC Symbol;Acc:HGNC:2704]	0.012847	1.520822
DCUN1D5	defective in cullin neddylation 1 domain containing 5 [Source:HC	0.021909	1.21066
DDIT3	DNA damage inducible transcript 3 [Source:HGNC Symbol;Acc:Hi	0.020801	2.291839
DECR1	2,4-dienoyl-CoA reductase 1 [Source:HGNC Symbol;Acc:HGNC:2	0.018308	1.370823
DEF8	differentially expressed in FDCP 8 homolog [Source:HGNC Symb	0.040336	1.231378
DEPDC4	DEP domain containing 4 [Source:HGNC Symbol;Acc:HGNC:2295	0.026506	1.512753
DEPDC7	DEP domain containing 7 [Source:HGNC Symbol;Acc:HGNC:2989	0.006512	1.417691
DERA	deoxyribose-phosphate aldolase [Source:HGNC Symbol;Acc:HGNC	0.039712	1.436606
DGUOK	deoxyguanosine kinase [Source:HGNC Symbol;Acc:HGNC:2858]	0.021034	1.405464
DHRS12	dehydrogenase/reductase 12 [Source:HGNC Symbol;Acc:HGNC:2	0.031689	1.518015
DHRS7B	dehydrogenase/reductase 7B [Source:HGNC Symbol;Acc:HGNC:2	0.033351	1.32789
DIABLO	diablo IAP-binding mitochondrial protein [Source:HGNC Symbol;	0.04369	1.416475
DIMT1	DIMT1 rRNA methyltransferase and ribosome maturation factor	0.035752	1.300177
DIRAS1	DIRAS family GTPase 1 [Source:HGNC Symbol;Acc:HGNC:19127]	0.002843	2.143516
DLX3	distal-less homeobox 3 [Source:HGNC Symbol;Acc:HGNC:2916]	0.022269	1.839753
DLX6	distal-less homeobox 6 [Source:HGNC Symbol;Acc:HGNC:2919]	0.000346	1.568153
DMAC1	distal membrane arm assembly complex 1 [Source:HGNC Symbo	0.021189	1.433031
DMAC2L	distal membrane arm assembly complex 2 like [Source:HGNC Syi	0.026743	1.445915
DNAAF2	dynein axonemal assembly factor 2 [Source:HGNC Symbol;Acc:H	0.000846	1.651068
DNAJB6	DnaJ heat shock protein family (Hsp40) member B6 [Source:HGNC	0.001402	1.535605
DNAJB9	DnaJ heat shock protein family (Hsp40) member B9 [Source:HGNC	0.032585	2.219393
DNAJC12	DnaJ heat shock protein family (Hsp40) member C12 [Source:HG	0.005799	1.485551
DNAJC19	DnaJ heat shock protein family (Hsp40) member C19 [Source:HG	0.003771	1.529684

DNAJC24	DnaJ heat shock protein family (Hsp40) member C24 [Source:HG	0.027993	1.389491
DNAJC25	DnaJ heat shock protein family (Hsp40) member C25 [Source:HG	0.019772	1.261914
DNAL4	dynein axonemal light chain 4 [Source:HGNC Symbol;Acc:HGNC:	0.005155	1.58948
DNHD1	dynein heavy chain domain 1 [Source:HGNC Symbol;Acc:HGNC:2	0.000435	1.619382
DOCK6	dedicator of cytokinesis 6 [Source:HGNC Symbol;Acc:HGNC:1918	0.02723	1.329023
DPH3	diphthamide biosynthesis 3 [Source:HGNC Symbol;Acc:HGNC:27	0.000713	1.63186
DPH5	diphthamide biosynthesis 5 [Source:HGNC Symbol;Acc:HGNC:24	0.022269	1.444083
DPH6	diphthamine biosynthesis 6 [Source:HGNC Symbol;Acc:HGNC:30	0.030184	1.430822
DPM1	dolichyl-phosphate mannosyltransferase subunit 1, catalytic [Soi	0.004254	1.524286
DPY30	dpy-30 histone methyltransferase complex regulatory subunit [S	0.002101	1.779635
DTWD1	DTW domain containing 1 [Source:HGNC Symbol;Acc:HGNC:309	0.010096	1.492179
DTYMK	deoxythymidylate kinase [Source:HGNC Symbol;Acc:HGNC:3061	0.029734	1.251491
DUS2	dihydrouridine synthase 2 [Source:HGNC Symbol;Acc:HGNC:260	0.02561	1.243312
DUS4L	dihydrouridine synthase 4 like [Source:HGNC Symbol;Acc:HGNC:	0.00114	1.361993
DUSP11	dual specificity phosphatase 11 [Source:HGNC Symbol;Acc:HGNC	0.001716	1.895979
DUSP2	dual specificity phosphatase 2 [Source:HGNC Symbol;Acc:HGNC:	0.001877	2.058263
DUSP28	dual specificity phosphatase 28 [Source:HGNC Symbol;Acc:HGNC	0.004757	2.013179
DYNC2LI1	dynein cytoplasmic 2 light intermediate chain 1 [Source:HGNC S	0.000926	1.534576
DYNLL1	dynein light chain LC8-type 1 [Source:HGNC Symbol;Acc:HGNC:1	0.00808	1.667529
DYNLT1	dynein light chain Tctex-type 1 [Source:HGNC Symbol;Acc:HGNC	0.000153	1.937869
DYRK3	dual specificity tyrosine phosphorylation regulated kinase 3 [Sou	0.012114	1.307349
EBF2	ELL associated factor 2 [Source:HGNC Symbol;Acc:HGNC:23115]	1.12E-05	2.137674
EAPP	E2F associated phosphoprotein [Source:HGNC Symbol;Acc:HGNC	0.00172	1.922626
EBAG9	estrogen receptor binding site associated antigen 9 [Source:HGNC	0.014601	1.305025
EBPL	EBP like [Source:HGNC Symbol;Acc:HGNC:18061]	0.000428	1.516315
ECH1	enoyl-CoA hydratase 1 [Source:HGNC Symbol;Acc:HGNC:3149]	0.03243	1.182599
ECHS1	enoyl-CoA hydratase, short chain 1 [Source:HGNC Symbol;Acc:H	0.041616	1.234574
ECI2	enoyl-CoA delta isomerase 2 [Source:HGNC Symbol;Acc:HGNC:1	0.00934	1.408251
EEF1AKMT1	EEF1A lysine methyltransferase 1 [Source:HGNC Symbol;Acc:HGI	0.044835	1.497449
EEF1B2	eukaryotic translation elongation factor 1 beta 2 [Source:HGNC :	0.012494	1.657386
EEF1E1	eukaryotic translation elongation factor 1 epsilon 1 [Source:HGN	0.031891	1.413835
EGR2	early growth response 2 [Source:HGNC Symbol;Acc:HGNC:3239]	6.37E-07	2.631008
EGR4	early growth response 4 [Source:HGNC Symbol;Acc:HGNC:3241]	0.01388	3.049326
EIF1AX	eukaryotic translation initiation factor 1A X-linked [Source:HGNC	0.047119	1.319393
EIF1AY	eukaryotic translation initiation factor 1A Y-linked [Source:HGNC	0.007987	1.326254
EIF2A	eukaryotic translation initiation factor 2A [Source:HGNC Symbol,	0.007831	1.360021
EIF3E	eukaryotic translation initiation factor 3 subunit E [Source:HGNC	0.003449	1.616095
EIF3H	eukaryotic translation initiation factor 3 subunit H [Source:HGNC	0.045365	1.345075
EIF3I	eukaryotic translation initiation factor 3 subunit I [Source:HGNC	0.008335	1.625259
EIF3K	eukaryotic translation initiation factor 3 subunit K [Source:HGNC	0.047381	1.465474
EIF3M	eukaryotic translation initiation factor 3 subunit M [Source:HGN	8.53E-05	1.465625
EIF4E	eukaryotic translation initiation factor 4E [Source:HGNC Symbol;	0.034038	1.269531
EIF5A2	eukaryotic translation initiation factor 5A2 [Source:HGNC Symbo	0.008521	1.413026
ELOB	elongin B [Source:HGNC Symbol;Acc:HGNC:11619]	0.021489	1.626117
ELOC	elongin C [Source:HGNC Symbol;Acc:HGNC:11617]	0.000389	1.648076
ELP5	elongator acetyltransferase complex subunit 5 [Source:HGNC Sy	0.018103	1.474481
EMC3	ER membrane protein complex subunit 3 [Source:HGNC Symbol;	0.015165	1.674983

EMC4	ER membrane protein complex subunit 4 [Source:HGNC Symbol;]	0.016779	1.537752
EMC8	ER membrane protein complex subunit 8 [Source:HGNC Symbol;]	0.023961	1.187966
EMG1	EMG1 N1-specific pseudouridine methyltransferase [Source:HGNC Symbol;]	0.004961	1.528264
ENDOV	endonuclease V [Source:HGNC Symbol;Acc:HGNC:26640]	0.002709	1.746499
ENPP5	ectonucleotide pyrophosphatase/phosphodiesterase family member 5 [Source:HGNC Symbol;]	0.001211	1.961551
ENTPD6	ectonucleoside triphosphate diphosphohydrolase 6 [Source:HGNC Symbol;]	0.003829	1.20531
EPHA4	EPH receptor A4 [Source:HGNC Symbol;Acc:HGNC:3388]	0.005799	1.786697
ERGIC3	ERGIC and golgi 3 [Source:HGNC Symbol;Acc:HGNC:15927]	0.017954	1.439123
ERH	ERH mRNA splicing and mitosis factor [Source:HGNC Symbol;Acc:HGNC:14202]	0.043083	1.4202
ERICH2	glutamate rich 2 [Source:HGNC Symbol;Acc:HGNC:44395]	0.024564	1.894341
ERP44	endoplasmic reticulum protein 44 [Source:HGNC Symbol;Acc:HGNC:1572764]	0.011895	1.572764
ESD	esterase D [Source:HGNC Symbol;Acc:HGNC:3465]	0.01169	1.53486
ETFA	electron transfer flavoprotein subunit alpha [Source:HGNC Symbol;]	0.009657	1.445839
ETFRF1	electron transfer flavoprotein regulatory factor 1 [Source:HGNC Symbol;]	0.000583	1.991439
EVI5L	ecotropic viral integration site 5 like [Source:HGNC Symbol;Acc:HGNC:145679]	0.005271	1.45679
EXD1	exonuclease 3'-5' domain containing 1 [Source:HGNC Symbol;Acc:HGNC:2741272]	7.88E-05	2.741272
EXD3	exonuclease 3'-5' domain containing 3 [Source:HGNC Symbol;Acc:HGNC:1361207]	0.005761	1.361207
EXOC6	exocyst complex component 6 [Source:HGNC Symbol;Acc:HGNC:122911]	0.029768	1.22911
EXOSC8	exosome component 8 [Source:HGNC Symbol;Acc:HGNC:17035]	0.017654	1.270615
FAAP20	FA core complex associated protein 20 [Source:HGNC Symbol;Acc:HGNC:1239378]	0.017797	1.239378
FABP5	fatty acid binding protein 5 [Source:HGNC Symbol;Acc:HGNC:3547913]	0.007868	1.547913
FAM104A	family with sequence similarity 104 member A [Source:HGNC Symbol;]	0.026617	1.194923
FAM104B	family with sequence similarity 104 member B [Source:HGNC Symbol;]	0.000484	1.581175
FAM122A	family with sequence similarity 122A [Source:HGNC Symbol;Acc:HGNC:1229282]	0.016336	1.229282
FAM162A	family with sequence similarity 162 member A [Source:HGNC Symbol;]	0.001106	1.895699
FAM166B	family with sequence similarity 166 member B [Source:HGNC Symbol;]	0.037735	2.083461
FAM174C	family with sequence similarity 174 member C [Source:HGNC Symbol;]	0.037739	1.213509
FAM183A	family with sequence similarity 183 member A [Source:HGNC Symbol;]	0.017915	2.502207
FAM200A	family with sequence similarity 200 member A [Source:HGNC Symbol;]	2.11E-07	1.75945
FAM200B	family with sequence similarity 200 member B [Source:HGNC Symbol;]	0.000405	1.932544
FAM204A	family with sequence similarity 204 member A [Source:HGNC Symbol;]	0.003982	1.71311
FAM210A	family with sequence similarity 210 member A [Source:HGNC Symbol;]	0.019175	1.293965
FAM227B	family with sequence similarity 227 member B [Source:HGNC Symbol;]	0.002907	1.48703
FAM3A	family with sequence similarity 3 member A [Source:HGNC Symbol;]	0.035903	1.287444
FAM49B	family with sequence similarity 49 member B [Source:HGNC Symbol;]	0.000285	1.552859
FAM83F	family with sequence similarity 83 member F [Source:HGNC Symbol;]	0.001191	1.47847
FASTKD2	FAST kinase domains 2 [Source:HGNC Symbol;Acc:HGNC:29160]	0.012876	1.403368
FASTKD3	FAST kinase domains 3 [Source:HGNC Symbol;Acc:HGNC:28758]	0.003447	1.505036
FAT2	FAT atypical cadherin 2 [Source:HGNC Symbol;Acc:HGNC:3596]	0.003343	1.475151
FAU	FAU ubiquitin like and ribosomal protein S30 fusion [Source:HGNC Symbol;]	0.030353	1.701496
FBXO10	F-box protein 10 [Source:HGNC Symbol;Acc:HGNC:13589]	0.012962	1.958832
FBXO16	F-box protein 16 [Source:HGNC Symbol;Acc:HGNC:13618]	0.00419	1.885659
FBXO22	F-box protein 22 [Source:HGNC Symbol;Acc:HGNC:13593]	0.035448	1.371097
FBXO25	F-box protein 25 [Source:HGNC Symbol;Acc:HGNC:13596]	0.018207	1.318996
FBXO31	F-box protein 31 [Source:HGNC Symbol;Acc:HGNC:16510]	0.022675	1.269654
FBXO32	F-box protein 32 [Source:HGNC Symbol;Acc:HGNC:16731]	0.008938	1.275032
FBXO39	F-box protein 39 [Source:HGNC Symbol;Acc:HGNC:28565]	0.023432	1.900953

FBXO4	F-box protein 4 [Source:HGNC Symbol;Acc:HGNC:13583]	0.033317	1.363883
FGFBP1	fibroblast growth factor binding protein 1 [Source:HGNC Symbol	0.041035	1.403569
FGFR1OP2	FGFR1 oncogene partner 2 [Source:HGNC Symbol;Acc:HGNC:23C	0.021255	1.533074
FGGY	FGGY carbohydrate kinase domain containing [Source:HGNC Syn	0.005681	1.660123
FKBP14	FKBP prolyl isomerase 14 [Source:HGNC Symbol;Acc:HGNC:1862	0.017028	1.351819
FLAD1	flavin adenine dinucleotide synthetase 1 [Source:HGNC Symbol;	0.041147	1.265964
FLYWCH2	FLYWCH family member 2 [Source:HGNC Symbol;Acc:HGNC:251	1.90E-05	1.555258
FMO4	flavin containing dimethylaniline monooxygenase 4 [Source:HGNC	0.026483	1.639734
FNTA	farnesyltransferase, CAAX box, alpha [Source:HGNC Symbol;Acc:	0.001945	1.656733
FOPNL	FGFR1OP N-terminal like [Source:HGNC Symbol;Acc:HGNC:2643]	0.01648	1.503646
FOSB	FosB proto-oncogene, AP-1 transcription factor subunit [Source:	0.003771	2.356137
FRG1	FSHD region gene 1 [Source:HGNC Symbol;Acc:HGNC:3954]	0.013927	1.673294
FRMD3	FERM domain containing 3 [Source:HGNC Symbol;Acc:HGNC:241	0.041457	1.861806
FRRS1	ferric chelate reductase 1 [Source:HGNC Symbol;Acc:HGNC:2762	0.013089	1.939143
FUNDC2	FUN14 domain containing 2 [Source:HGNC Symbol;Acc:HGNC:24	0.041215	1.805993
FUT10	fucosyltransferase 10 [Source:HGNC Symbol;Acc:HGNC:19234]	0.031689	1.276928
FXYD3	FXYD domain containing ion transport regulator 3 [Source:HGNC	0.033158	1.963146
FZD10	frizzled class receptor 10 [Source:HGNC Symbol;Acc:HGNC:4039]	0.023029	1.462831
GABARAPL2	GABA type A receptor associated protein like 2 [Source:HGNC Sy	0.008549	1.785479
GCA	grancalcin [Source:HGNC Symbol;Acc:HGNC:15990]	0.000138	1.6255
GCH1	GTP cyclohydrolase 1 [Source:HGNC Symbol;Acc:HGNC:4193]	0.022828	1.429992
GCHFR	GTP cyclohydrolase I feedback regulator [Source:HGNC Symbol;/	1.43E-05	1.838943
GCNA	germ cell nuclear acidic peptidase [Source:HGNC Symbol;Acc:HG	0.007813	2.169804
GEMIN2	gem nuclear organelle associated protein 2 [Source:HGNC Symb	0.000632	1.938833
GEMIN6	gem nuclear organelle associated protein 6 [Source:HGNC Symb	0.003261	1.457549
GEMIN7	gem nuclear organelle associated protein 7 [Source:HGNC Symb	0.00037	2.003307
GGH	gamma-glutamyl hydrolase [Source:HGNC Symbol;Acc:HGNC:42	0.003447	1.752683
GGPS1	geranylgeranyl diphosphate synthase 1 [Source:HGNC Symbol;A	0.00505	1.440513
GHITM	growth hormone inducible transmembrane protein [Source:HGN	0.027642	1.505548
GIN1	gypsy retrotransposon integrase 1 [Source:HGNC Symbol;Acc:HC	0.002699	1.626302
GJB5	gap junction protein beta 5 [Source:HGNC Symbol;Acc:HGNC:42	0.004248	1.291735
GJB6	gap junction protein beta 6 [Source:HGNC Symbol;Acc:HGNC:42	0.038568	1.667931
GLMN	glomulin, FKBP associated protein [Source:HGNC Symbol;Acc:HG	0.048847	1.371896
GLRX	glutaredoxin [Source:HGNC Symbol;Acc:HGNC:4330]	0.021186	1.4269
GLRX2	glutaredoxin 2 [Source:HGNC Symbol;Acc:HGNC:16065]	0.030355	1.277205
GMFB	glia maturation factor beta [Source:HGNC Symbol;Acc:HGNC:43	2.95E-05	1.604268
GMNN	geminin DNA replication inhibitor [Source:HGNC Symbol;Acc:HG	0.031124	1.359617
GNG5	G protein subunit gamma 5 [Source:HGNC Symbol;Acc:HGNC:44	0.001641	1.374638
GNPDA1	glucosamine-6-phosphate deaminase 1 [Source:HGNC Symbol;A	0.03033	1.300925
GNPDA2	glucosamine-6-phosphate deaminase 2 [Source:HGNC Symbol;A	0.005482	1.456775
GOLGA2	golgin A2 [Source:HGNC Symbol;Acc:HGNC:4425]	0.026617	1.203886
GOLGA3	golgin A3 [Source:HGNC Symbol;Acc:HGNC:4426]	0.033272	1.269263
GOLT1B	golgi transport 1B [Source:HGNC Symbol;Acc:HGNC:20175]	0.005295	2.137658
GON7	GON7 subunit of KEOPS complex [Source:HGNC Symbol;Acc:HG	0.001317	1.91087
GORAB	golgin, RAB6 interacting [Source:HGNC Symbol;Acc:HGNC:25676	0.02579	1.402653
GPB1	G protein-coupled estrogen receptor 1 [Source:HGNC Symbol;Ac	0.018455	2.359322
GPN3	GPN-loop GTPase 3 [Source:HGNC Symbol;Acc:HGNC:30186]	0.042972	1.449119

GPR150	G protein-coupled receptor 150 [Source:HGNC Symbol;Acc:HGNC:100222]	0.022229	1.583358
GPR180	G protein-coupled receptor 180 [Source:HGNC Symbol;Acc:HGNC:100327]	0.0327	1.493471
GPR87	G protein-coupled receptor 87 [Source:HGNC Symbol;Acc:HGNC:100203]	0.020319	1.746305
GPX4	glutathione peroxidase 4 [Source:HGNC Symbol;Acc:HGNC:4556]	0.005493	1.273381
GPX8	glutathione peroxidase 8 (putative) [Source:HGNC Symbol;Acc:HGNC:100490]	0.049088	1.502444
GRAMD1C	GRAM domain containing 1C [Source:HGNC Symbol;Acc:HGNC:200178]	0.017887	1.694279
GRAMD4	GRAM domain containing 4 [Source:HGNC Symbol;Acc:HGNC:290087]	0.00874	1.369107
GRHL3	grainyhead like transcription factor 3 [Source:HGNC Symbol;Acc:HGNC:100803]	0.008037	1.508869
GRIP1	glutamate receptor interacting protein 1 [Source:HGNC Symbol;Acc:HGNC:100175]	0.017545	1.389383
GSDMA	gasdermin A [Source:HGNC Symbol;Acc:HGNC:13311]	0.026748	1.600937
GSDMB	gasdermin B [Source:HGNC Symbol;Acc:HGNC:23690]	1.62E-05	2.026226
GSKIP	GSK3B interacting protein [Source:HGNC Symbol;Acc:HGNC:20340]	0.005739	1.833886
GSTA4	glutathione S-transferase alpha 4 [Source:HGNC Symbol;Acc:HGNC:100076]	0.007629	2.050821
GSTCD	glutathione S-transferase C-terminal domain containing [Source:HGNC Symbol;Acc:HGNC:100293]	0.029311	1.329642
GSTM3	glutathione S-transferase mu 3 [Source:HGNC Symbol;Acc:HGNC:646E-05]	6.46E-05	1.933299
GSTO1	glutathione S-transferase omega 1 [Source:HGNC Symbol;Acc:HGNC:100044]	0.004495	1.948056
GSTO2	glutathione S-transferase omega 2 [Source:HGNC Symbol;Acc:HGNC:100001]	0.000151	1.759943
GSTZ1	glutathione S-transferase zeta 1 [Source:HGNC Symbol;Acc:HGNC:100016]	0.001642	1.563509
GTF2A2	general transcription factor IIA subunit 2 [Source:HGNC Symbol;Acc:HGNC:100205]	0.020563	1.414849
GTF2B	general transcription factor IIB [Source:HGNC Symbol;Acc:HGNC:100036]	0.003607	2.013899
GTF2E1	general transcription factor IIE subunit 1 [Source:HGNC Symbol;Acc:HGNC:100033]	0.003329	1.351014
GTF2H1	general transcription factor IIH subunit 1 [Source:HGNC Symbol;Acc:HGNC:100208]	0.020805	1.225462
GTF2H2C	GTF2H2 family member C [Source:HGNC Symbol;Acc:HGNC:31350]	0.015282	1.368313
GTF2H5	general transcription factor IIH subunit 5 [Source:HGNC Symbol;Acc:HGNC:100005]	0.000509	1.775256
GTF3A	general transcription factor IIIA [Source:HGNC Symbol;Acc:HGNC:100166]	0.016616	1.407892
GULP1	GULP PTB domain containing engulfment adaptor 1 [Source:HGNC Symbol;Acc:HGNC:100074]	0.007489	1.661553
H1-2	H1.2 linker histone, cluster member [Source:HGNC Symbol;Acc:HGNC:100114]	0.011405	2.421986
H2AC11	H2A clustered histone 11 [Source:HGNC Symbol;Acc:HGNC:4737]	0.009126	2.262296
H2BC12	H2B clustered histone 12 [Source:HGNC Symbol;Acc:HGNC:1395]	0.026505	1.548118
H2BC15	H2B clustered histone 15 [Source:HGNC Symbol;Acc:HGNC:4749]	0.003483	2.509787
H3-3A	H3.3 histone A [Source:HGNC Symbol;Acc:HGNC:4764]	0.019413	1.40679
H4C8	H4 clustered histone 8 [Source:HGNC Symbol;Acc:HGNC:4788]	0.021109	1.91815
HCAR2	hydroxycarboxylic acid receptor 2 [Source:HGNC Symbol;Acc:HGNC:100133]	0.001332	1.527848
HDDC2	HD domain containing 2 [Source:HGNC Symbol;Acc:HGNC:21078]	0.001742	1.743321
HDHD3	haloacid dehalogenase like hydrolase domain containing 3 [Source:HGNC Symbol;Acc:HGNC:100334]	0.033454	1.236866
HDX	highly divergent homeobox [Source:HGNC Symbol;Acc:HGNC:26042]	0.04247	1.3181
HERC4	HECT and RLD domain containing E3 ubiquitin protein ligase 4 [Source:HGNC Symbol;Acc:HGNC:100484]	0.048491	1.27068
HES2	hes family bHLH transcription factor 2 [Source:HGNC Symbol;Acc:HGNC:100014]	0.001403	1.284808
HEXB	hexosaminidase subunit beta [Source:HGNC Symbol;Acc:HGNC:40316]	0.031608	1.343615
HIGD1A	HIG1 hypoxia inducible domain family member 1A [Source:HGNC Symbol;Acc:HGNC:100018]	0.001848	1.781656
HIKESHI	heat shock protein nuclear import factor hikiishi [Source:HGNC Symbol;Acc:HGNC:1008E-05]	1.08E-05	1.775456
HILPDA	hypoxia inducible lipid droplet associated [Source:HGNC Symbol;Acc:HGNC:100012]	0.001235	2.151842
HINT2	histidine triad nucleotide binding protein 2 [Source:HGNC Symbol;Acc:HGNC:100006]	0.000638	1.679103
HLA-DQB1	major histocompatibility complex, class II, DQ beta 1 [Source:HGNC Symbol;Acc:HGNC:100033]	0.003392	1.32578
HMBS	hydroxymethylbilane synthase [Source:HGNC Symbol;Acc:HGNC:100003]	0.000384	1.229594
HMGCL	3-hydroxy-3-methylglutaryl-CoA lyase [Source:HGNC Symbol;Acc:HGNC:100145]	0.014537	1.535992
HMGN1	high mobility group nucleosome binding domain 1 [Source:HGNC Symbol;Acc:HGNC:100320]	0.032094	1.176308

HMG2	high mobility group nucleosomal binding domain 2 [Source:HGNC Symbol;Acc:HGNC:5132]	0.042289	1.211149
HOXD1	homeobox D1 [Source:HGNC Symbol;Acc:HGNC:5132]	0.032846	1.82601
HOXD8	homeobox D8 [Source:HGNC Symbol;Acc:HGNC:5139]	0.019208	1.542317
HOXD9	homeobox D9 [Source:HGNC Symbol;Acc:HGNC:5140]	0.026505	1.808809
HSBP1	heat shock factor binding protein 1 [Source:HGNC Symbol;Acc:HGNC:5140]	0.028076	1.469061
HSCB	HscB mitochondrial iron-sulfur cluster cochaperone [Source:HGNC Symbol;Acc:HGNC:5140]	0.011952	1.795345
HSD17B7	hydroxysteroid 17-beta dehydrogenase 7 [Source:HGNC Symbol;Acc:HGNC:5140]	0.015909	1.928253
HSPA14	heat shock protein family A (Hsp70) member 14 [Source:HGNC Symbol;Acc:HGNC:5140]	0.001263	1.522329
HSPBAP1	HSPB1 associated protein 1 [Source:HGNC Symbol;Acc:HGNC:16000]	0.049685	1.666109
HTATIP2	HIV-1 Tat interactive protein 2 [Source:HGNC Symbol;Acc:HGNC:16000]	3.45E-05	1.927536
IAH1	isoamyl acetate hydrolyzing esterase 1 (putative) [Source:HGNC Symbol;Acc:HGNC:16000]	0.019444	1.759788
ID1	inhibitor of DNA binding 1, HLH protein [Source:HGNC Symbol;Acc:HGNC:16000]	7.57E-05	1.568644
IER2	immediate early response 2 [Source:HGNC Symbol;Acc:HGNC:28000]	0.025869	1.303714
IER3IP1	immediate early response 3 interacting protein 1 [Source:HGNC Symbol;Acc:HGNC:28000]	0.006157	1.646187
IFI27L2	interferon alpha inducible protein 27 like 2 [Source:HGNC Symbol;Acc:HGNC:28000]	0.018915	1.352157
IFRD1	interferon related developmental regulator 1 [Source:HGNC Symbol;Acc:HGNC:28000]	0.005625	1.67834
IFT52	intraflagellar transport 52 [Source:HGNC Symbol;Acc:HGNC:15900]	0.04511	1.383887
IKBIP	IKKB interacting protein [Source:HGNC Symbol;Acc:HGNC:26430]	0.016195	1.327564
IKZF5	IKAROS family zinc finger 5 [Source:HGNC Symbol;Acc:HGNC:14200]	0.033732	1.486956
IL18	interleukin 18 [Source:HGNC Symbol;Acc:HGNC:5986]	0.019195	1.417622
IL1A	interleukin 1 alpha [Source:HGNC Symbol;Acc:HGNC:5991]	0.00095	1.458434
IL20RA	interleukin 20 receptor subunit alpha [Source:HGNC Symbol;Acc:HGNC:5991]	0.027955	1.55967
IMMP1L	inner mitochondrial membrane peptidase subunit 1 [Source:HGNC Symbol;Acc:HGNC:5991]	0.012494	1.550606
IMMP2L	inner mitochondrial membrane peptidase subunit 2 [Source:HGNC Symbol;Acc:HGNC:5991]	0.028624	1.350836
IMP3	IMP U3 small nucleolar ribonucleoprotein 3 [Source:HGNC Symbol;Acc:HGNC:5991]	0.006407	1.378751
IMPA1	inositol monophosphatase 1 [Source:HGNC Symbol;Acc:HGNC:6147]	0.022456	1.543019
INIP	INTS3 and NABP interacting protein [Source:HGNC Symbol;Acc:HGNC:6147]	0.014031	1.391366
INKA1	inka box actin regulator 1 [Source:HGNC Symbol;Acc:HGNC:3248]	0.017495	2.136179
INO80C	INO80 complex subunit C [Source:HGNC Symbol;Acc:HGNC:2699]	0.037325	1.384033
INTS12	integrator complex subunit 12 [Source:HGNC Symbol;Acc:HGNC:2699]	0.020806	1.349381
IQSEC2	IQ motif and Sec7 domain ArfGEF 2 [Source:HGNC Symbol;Acc:HGNC:2699]	0.009043	1.579625
IRAK1BP1	interleukin 1 receptor associated kinase 1 binding protein 1 [Source:HGNC Symbol;Acc:HGNC:2699]	0.038191	1.361466
IRF2BPL	interferon regulatory factor 2 binding protein like [Source:HGNC Symbol;Acc:HGNC:2699]	0.047526	1.227401
ISCA1	iron-sulfur cluster assembly 1 [Source:HGNC Symbol;Acc:HGNC:2699]	0.012397	1.423585
ISCA2	iron-sulfur cluster assembly 2 [Source:HGNC Symbol;Acc:HGNC:2699]	0.005139	1.685421
ITGAE	integrin subunit alpha E [Source:HGNC Symbol;Acc:HGNC:6147]	0.001333	1.717171
ITGB1BP1	integrin subunit beta 1 binding protein 1 [Source:HGNC Symbol;Acc:HGNC:6147]	0.021036	1.32712
ITGB3BP	integrin subunit beta 3 binding protein [Source:HGNC Symbol;Acc:HGNC:6147]	0.001779	1.77997
ITGB6	integrin subunit beta 6 [Source:HGNC Symbol;Acc:HGNC:6161]	0.011649	1.317537
JAGN1	jagunal homolog 1 [Source:HGNC Symbol;Acc:HGNC:26926]	3.77E-07	1.776221
JKAMP	JNK1/MAPK8 associated membrane protein [Source:HGNC Symbol;Acc:HGNC:26926]	0.000833	1.78788
JTB	jumping translocation breakpoint [Source:HGNC Symbol;Acc:HGNC:26926]	0.005461	1.619694
KATNBL1	katanin regulatory subunit B1 like 1 [Source:HGNC Symbol;Acc:HGNC:26926]	0.003578	1.613158
KBTBD3	kelch repeat and BTB domain containing 3 [Source:HGNC Symbol;Acc:HGNC:26926]	0.015509	2.127452
KCNJ14	potassium inwardly rectifying channel subfamily J member 14 [Source:HGNC Symbol;Acc:HGNC:26926]	0.038825	1.721231
KCTD6	potassium channel tetramerization domain containing 6 [Source:HGNC Symbol;Acc:HGNC:26926]	0.019967	1.743498
KIAA0513	KIAA0513 [Source:HGNC Symbol;Acc:HGNC:29058]	0.004697	1.384861

KIAA1586	KIAA1586 [Source:HGNC Symbol;Acc:HGNC:21360]	0.041875	1.279968
KIN	Kin17 DNA and RNA binding protein [Source:HGNC Symbol;Acc:HGNC:15004]	0.000454	1.400187
KIZ	kizuna centrosomal protein [Source:HGNC Symbol;Acc:HGNC:15006]	0.000635	1.508424
KLHDC2	kelch domain containing 2 [Source:HGNC Symbol;Acc:HGNC:20202]	0.013424	1.531995
KLHL9	kelch like family member 9 [Source:HGNC Symbol;Acc:HGNC:18707]	0.002137	1.352587
KLRG2	killer cell lectin like receptor G2 [Source:HGNC Symbol;Acc:HGNC:20202]	0.005593	1.340066
KPNA3	karyopherin subunit alpha 3 [Source:HGNC Symbol;Acc:HGNC:6203]	0.011476	1.255055
KRBOX4	KRAB box domain containing 4 [Source:HGNC Symbol;Acc:HGNC:20202]	0.016683	1.46091
KRCC1	lysine rich coiled-coil 1 [Source:HGNC Symbol;Acc:HGNC:28039]	0.022981	1.848524
KRT10	keratin 10 [Source:HGNC Symbol;Acc:HGNC:6413]	0.044155	1.663303
KTI12	KTI12 chromatin associated homolog [Source:HGNC Symbol;Acc:HGNC:20202]	0.037648	1.259869
KYAT3	kynurenine aminotransferase 3 [Source:HGNC Symbol;Acc:HGNC:20202]	0.012334	1.413471
L3MBTL1	L3MBTL histone methyl-lysine binding protein 1 [Source:HGNC Symbol;Acc:HGNC:20202]	0.03152	1.627407
LACTB2	lactamase beta 2 [Source:HGNC Symbol;Acc:HGNC:18512]	0.001393	1.693918
LAMTOR3	late endosomal/lysosomal adaptor, MAPK and MTOR activator 3 [Source:HGNC Symbol;Acc:HGNC:20202]	0.006392	1.866364
LAMTOR4	late endosomal/lysosomal adaptor, MAPK and MTOR activator 4 [Source:HGNC Symbol;Acc:HGNC:20202]	0.044968	1.699568
LAMTOR5	late endosomal/lysosomal adaptor, MAPK and MTOR activator 5 [Source:HGNC Symbol;Acc:HGNC:20202]	0.040167	1.702525
LARP6	La ribonucleoprotein 6, translational regulator [Source:HGNC Symbol;Acc:HGNC:20202]	0.023206	1.18016
LCMT1	leucine carboxyl methyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:20202]	0.024564	1.32121
LDAH	lipid droplet associated hydrolase [Source:HGNC Symbol;Acc:HGNC:20202]	0.001268	1.501735
LEPROTL1	leptin receptor overlapping transcript like 1 [Source:HGNC Symbol;Acc:HGNC:20202]	0.000102	1.342494
LIAS	lipoic acid synthetase [Source:HGNC Symbol;Acc:HGNC:16429]	3.45E-05	1.507646
LIG4	DNA ligase 4 [Source:HGNC Symbol;Acc:HGNC:6601]	0.02283	1.243584
LIPA	lipase A, lysosomal acid type [Source:HGNC Symbol;Acc:HGNC:6601]	0.011298	1.430436
LIPT1	lipoyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:29569]	0.002064	2.057886
LMBRD1	LMBR1 domain containing 1 [Source:HGNC Symbol;Acc:HGNC:20202]	0.023961	1.63492
LMO4	LIM domain only 4 [Source:HGNC Symbol;Acc:HGNC:6644]	0.027825	1.37971
LPAR6	lysophosphatidic acid receptor 6 [Source:HGNC Symbol;Acc:HGNC:20202]	0.019164	1.68314
LRIF1	ligand dependent nuclear receptor interacting factor 1 [Source:HGNC Symbol;Acc:HGNC:20202]	0.00012	1.683524
LRP1	LDL receptor related protein 1 [Source:HGNC Symbol;Acc:HGNC:20202]	0.017954	1.512192
LRRC23	leucine rich repeat containing 23 [Source:HGNC Symbol;Acc:HGNC:20202]	0.048847	1.419918
LRRC63	leucine rich repeat containing 63 [Source:HGNC Symbol;Acc:HGNC:20202]	0.000829	2.069816
LRRC9	leucine rich repeat containing 9 [Source:HGNC Symbol;Acc:HGNC:20202]	0.011854	2.205434
LSM1	LSM1 homolog, mRNA degradation associated [Source:HGNC Symbol;Acc:HGNC:20202]	0.011849	1.607412
LSM10	LSM10, U7 small nuclear RNA associated [Source:HGNC Symbol;Acc:HGNC:20202]	0.015671	1.463103
LSM2	LSM2 homolog, U6 small nuclear RNA and mRNA degradation associated [Source:HGNC Symbol;Acc:HGNC:20202]	0.034431	1.649619
LSM3	LSM3 homolog, U6 small nuclear RNA and mRNA degradation associated [Source:HGNC Symbol;Acc:HGNC:20202]	0.006932	1.592558
LSM4	LSM4 homolog, U6 small nuclear RNA and mRNA degradation associated [Source:HGNC Symbol;Acc:HGNC:20202]	0.022882	1.349758
LSM5	LSM5 homolog, U6 small nuclear RNA and mRNA degradation associated [Source:HGNC Symbol;Acc:HGNC:20202]	0.012543	1.411576
LSM6	LSM6 homolog, U6 small nuclear RNA and mRNA degradation associated [Source:HGNC Symbol;Acc:HGNC:20202]	0.024051	1.269759
LSM7	LSM7 homolog, U6 small nuclear RNA and mRNA degradation associated [Source:HGNC Symbol;Acc:HGNC:20202]	0.049396	1.312111
LYPLA1	lysophospholipase 1 [Source:HGNC Symbol;Acc:HGNC:6737]	0.042736	1.413015
LYPLAL1	lysophospholipase like 1 [Source:HGNC Symbol;Acc:HGNC:20440]	0.01855	1.439902
LYRM1	LYR motif containing 1 [Source:HGNC Symbol;Acc:HGNC:25074]	9.58E-06	1.978766
LYRM2	LYR motif containing 2 [Source:HGNC Symbol;Acc:HGNC:25229]	0.008292	1.429278
LZIC	leucine zipper and CTNNBIP1 domain containing [Source:HGNC Symbol;Acc:HGNC:20202]	0.031086	1.298974
MACF1	microtubule actin crosslinking factor 1 [Source:HGNC Symbol;Acc:HGNC:20202]	0.04511	1.341553

MAD2L1	mitotic arrest deficient 2 like 1 [Source:HGNC Symbol;Acc:HGNC:28854]	0.014553	1.327496
MAGT1	magnesium transporter 1 [Source:HGNC Symbol;Acc:HGNC:28855]	0.021945	1.666039
MAIP1	matrix AAA peptidase interacting protein 1 [Source:HGNC Symbol;Acc:HGNC:28856]	0.024625	1.372446
MAL2	mal, T cell differentiation protein 2 (gene/pseudogene) [Source:HGNC Symbol;Acc:HGNC:28857]	0.037615	1.289791
MALSU1	mitochondrial assembly of ribosomal large subunit 1 [Source:HGNC Symbol;Acc:HGNC:28858]	0.000405	1.618072
MANF	mesencephalic astrocyte derived neurotrophic factor [Source:HGNC Symbol;Acc:HGNC:28859]	0.003758	1.565998
MAP1LC3B	microtubule associated protein 1 light chain 3 beta [Source:HGNC Symbol;Acc:HGNC:28860]	0.006692	1.4544
MAP2K4	mitogen-activated protein kinase kinase 4 [Source:HGNC Symbol;Acc:HGNC:28861]	0.010221	1.336802
MAP3K13	mitogen-activated protein kinase kinase kinase 13 [Source:HGNC Symbol;Acc:HGNC:28862]	0.008061	1.634263
MAP3K7CL	MAP3K7 C-terminal like [Source:HGNC Symbol;Acc:HGNC:16457]	3.81E-05	2.639915
MAPKAPK5	MAPK activated protein kinase 5 [Source:HGNC Symbol;Acc:HGNC:28863]	0.008485	1.311412
MARCHF10	membrane associated ring-CH-type finger 10 [Source:HGNC Symbol;Acc:HGNC:28864]	0.002072	4.173639
MARCHF5	membrane associated ring-CH-type finger 5 [Source:HGNC Symbol;Acc:HGNC:28865]	0.012069	1.568157
MARCHF7	membrane associated ring-CH-type finger 7 [Source:HGNC Symbol;Acc:HGNC:28866]	0.028041	1.438067
MAST4	microtubule associated serine/threonine kinase family member 4 [Source:HGNC Symbol;Acc:HGNC:28867]	0.016017	1.229316
MAT2B	methionine adenosyltransferase 2B [Source:HGNC Symbol;Acc:HGNC:28868]	0.004543	1.765482
MCEE	methylmalonyl-CoA epimerase [Source:HGNC Symbol;Acc:HGNC:28869]	0.028167	1.85793
MCRIP1	MAPK regulated corepressor interacting protein 1 [Source:HGNC Symbol;Acc:HGNC:28870]	0.045732	1.730172
MCTS1	MCTS1 re-initiation and release factor [Source:HGNC Symbol;Acc:HGNC:28871]	0.007211	1.48461
MDFI	MyoD family inhibitor [Source:HGNC Symbol;Acc:HGNC:6967]	0.007445	1.219369
MED18	mediator complex subunit 18 [Source:HGNC Symbol;Acc:HGNC:28872]	0.039219	1.546824
MED31	mediator complex subunit 31 [Source:HGNC Symbol;Acc:HGNC:28873]	0.000607	2.108191
MED7	mediator complex subunit 7 [Source:HGNC Symbol;Acc:HGNC:28874]	0.000659	1.729208
MESP1	mesoderm posterior bHLH transcription factor 1 [Source:HGNC Symbol;Acc:HGNC:28875]	0.037153	1.331019
METRNL	meteorin like, glial cell differentiation regulator [Source:HGNC Symbol;Acc:HGNC:28876]	0.021526	1.297295
METTL23	methyltransferase like 23 [Source:HGNC Symbol;Acc:HGNC:2698]	4.01E-05	1.55892
METTL2A	methyltransferase like 2A [Source:HGNC Symbol;Acc:HGNC:2575]	0.016195	1.64893
METTL5	methyltransferase like 5 [Source:HGNC Symbol;Acc:HGNC:2500]	0.041069	1.365383
METTL9	methyltransferase like 9 [Source:HGNC Symbol;Acc:HGNC:2458]	0.029729	1.329529
MFF	mitochondrial fission factor [Source:HGNC Symbol;Acc:HGNC:2459]	0.039003	1.231514
MGST1	microsomal glutathione S-transferase 1 [Source:HGNC Symbol;Acc:HGNC:2460]	0.004303	1.461483
MGST2	microsomal glutathione S-transferase 2 [Source:HGNC Symbol;Acc:HGNC:2461]	0.006312	1.698861
MGST3	microsomal glutathione S-transferase 3 [Source:HGNC Symbol;Acc:HGNC:2462]	0.003178	1.768086
MIB2	mindbomb E3 ubiquitin protein ligase 2 [Source:HGNC Symbol;Acc:HGNC:2463]	0.042264	1.309377
MICOS13	mitochondrial contact site and cristae organizing system subunit 13 [Source:HGNC Symbol;Acc:HGNC:2464]	0.005892	1.516695
MIEN1	migration and invasion enhancer 1 [Source:HGNC Symbol;Acc:HGNC:2465]	0.001088	1.849394
MIS12	MIS12 kinetochore complex component [Source:HGNC Symbol;Acc:HGNC:2466]	0.000796	1.520196
MITD1	microtubule interacting and trafficking domain containing 1 [Source:HGNC Symbol;Acc:HGNC:2467]	0.003632	1.493768
MKKS	McKusick-Kaufman syndrome [Source:HGNC Symbol;Acc:HGNC:2468]	0.013927	1.284916
MLF1	myeloid leukemia factor 1 [Source:HGNC Symbol;Acc:HGNC:712]	0.001742	1.622812
MLX	MAX dimerization protein MLX [Source:HGNC Symbol;Acc:HGNC:2469]	0.011867	1.569939
MMADHC	metabolism of cobalamin associated D [Source:HGNC Symbol;Acc:HGNC:2470]	0.001658	1.579268
MMP1	matrix metalloproteinase 1 [Source:HGNC Symbol;Acc:HGNC:715]	0.010344	2.451694
MMRN2	multimerin 2 [Source:HGNC Symbol;Acc:HGNC:19888]	0.002104	1.776991
MNAT1	MNAT1 component of CDK activating kinase [Source:HGNC Symbol;Acc:HGNC:2471]	0.001846	1.644009
MOB4	MOB family member 4, phocein [Source:HGNC Symbol;Acc:HGNC:2472]	0.046814	1.349983
MOCS2	molybdenum cofactor synthesis 2 [Source:HGNC Symbol;Acc:HGNC:2473]	0.009196	1.41413

MORN2	MORN repeat containing 2 [Source:HGNC Symbol;Acc:HGNC:301	0.044561	1.402941
MOSPD1	motile sperm domain containing 1 [Source:HGNC Symbol;Acc:HGNC:302	0.002369	1.51833
MPC1	mitochondrial pyruvate carrier 1 [Source:HGNC Symbol;Acc:HGNC:303	0.016195	1.408393
MPLKIP	M-phase specific PLK1 interacting protein [Source:HGNC Symbol;Acc:HGNC:304	0.012407	1.364506
MPV17	mitochondrial inner membrane protein MPV17 [Source:HGNC Symbol;Acc:HGNC:305	0.004719	1.368621
MR1	major histocompatibility complex, class I-related [Source:HGNC Symbol;Acc:HGNC:306	0.041906	1.597419
MRC2	mannose receptor C type 2 [Source:HGNC Symbol;Acc:HGNC:307	0.007133	1.375355
MRM3	mitochondrial rRNA methyltransferase 3 [Source:HGNC Symbol;Acc:HGNC:308	0.004703	1.318582
MRPL11	mitochondrial ribosomal protein L11 [Source:HGNC Symbol;Acc:HGNC:309	0.018829	1.516631
MRPL13	mitochondrial ribosomal protein L13 [Source:HGNC Symbol;Acc:HGNC:310	0.009256	1.571476
MRPL14	mitochondrial ribosomal protein L14 [Source:HGNC Symbol;Acc:HGNC:311	0.010994	1.656431
MRPL15	mitochondrial ribosomal protein L15 [Source:HGNC Symbol;Acc:HGNC:312	0.00489	1.501488
MRPL17	mitochondrial ribosomal protein L17 [Source:HGNC Symbol;Acc:HGNC:313	0.015599	1.339332
MRPL18	mitochondrial ribosomal protein L18 [Source:HGNC Symbol;Acc:HGNC:314	0.022568	1.402541
MRPL21	mitochondrial ribosomal protein L21 [Source:HGNC Symbol;Acc:HGNC:315	0.006705	1.432317
MRPL22	mitochondrial ribosomal protein L22 [Source:HGNC Symbol;Acc:HGNC:316	0.026998	1.467551
MRPL23	mitochondrial ribosomal protein L23 [Source:HGNC Symbol;Acc:HGNC:317	0.026016	1.218021
MRPL27	mitochondrial ribosomal protein L27 [Source:HGNC Symbol;Acc:HGNC:318	0.02835	1.477028
MRPL32	mitochondrial ribosomal protein L32 [Source:HGNC Symbol;Acc:HGNC:319	0.011344	1.516877
MRPL33	mitochondrial ribosomal protein L33 [Source:HGNC Symbol;Acc:HGNC:320	0.003751	1.717223
MRPL36	mitochondrial ribosomal protein L36 [Source:HGNC Symbol;Acc:HGNC:321	0.001813	1.532413
MRPL39	mitochondrial ribosomal protein L39 [Source:HGNC Symbol;Acc:HGNC:322	0.002112	1.498117
MRPL42	mitochondrial ribosomal protein L42 [Source:HGNC Symbol;Acc:HGNC:323	0.000525	1.665294
MRPL44	mitochondrial ribosomal protein L44 [Source:HGNC Symbol;Acc:HGNC:324	0.008252	1.471306
MRPL46	mitochondrial ribosomal protein L46 [Source:HGNC Symbol;Acc:HGNC:325	0.042087	1.445468
MRPL48	mitochondrial ribosomal protein L48 [Source:HGNC Symbol;Acc:HGNC:326	0.014282	1.666145
MRPL50	mitochondrial ribosomal protein L50 [Source:HGNC Symbol;Acc:HGNC:327	1.40E-05	1.835038
MRPL51	mitochondrial ribosomal protein L51 [Source:HGNC Symbol;Acc:HGNC:328	0.014714	1.387595
MRPL52	mitochondrial ribosomal protein L52 [Source:HGNC Symbol;Acc:HGNC:329	0.020708	1.481471
MRPL54	mitochondrial ribosomal protein L54 [Source:HGNC Symbol;Acc:HGNC:330	0.008718	1.801166
MRPL57	mitochondrial ribosomal protein L57 [Source:HGNC Symbol;Acc:HGNC:331	0.001455	1.45574
MRPL58	mitochondrial ribosomal protein L58 [Source:HGNC Symbol;Acc:HGNC:332	0.000237	1.758265
MRPL9	mitochondrial ribosomal protein L9 [Source:HGNC Symbol;Acc:HGNC:333	0.007111	1.402185
MRPS11	mitochondrial ribosomal protein S11 [Source:HGNC Symbol;Acc:HGNC:334	0.022286	1.368576
MRPS12	mitochondrial ribosomal protein S12 [Source:HGNC Symbol;Acc:HGNC:335	0.004975	1.469135
MRPS14	mitochondrial ribosomal protein S14 [Source:HGNC Symbol;Acc:HGNC:336	0.003447	1.453782
MRPS15	mitochondrial ribosomal protein S15 [Source:HGNC Symbol;Acc:HGNC:337	0.003889	1.757883
MRPS16	mitochondrial ribosomal protein S16 [Source:HGNC Symbol;Acc:HGNC:338	0.043162	1.213855
MRPS18A	mitochondrial ribosomal protein S18A [Source:HGNC Symbol;Acc:HGNC:339	0.003359	1.296179
MRPS22	mitochondrial ribosomal protein S22 [Source:HGNC Symbol;Acc:HGNC:340	0.039341	1.332571
MRPS23	mitochondrial ribosomal protein S23 [Source:HGNC Symbol;Acc:HGNC:341	0.001403	1.754651
MRPS31	mitochondrial ribosomal protein S31 [Source:HGNC Symbol;Acc:HGNC:342	0.002185	1.342072
MRPS33	mitochondrial ribosomal protein S33 [Source:HGNC Symbol;Acc:HGNC:343	0.001907	1.626403
MRPS35	mitochondrial ribosomal protein S35 [Source:HGNC Symbol;Acc:HGNC:344	0.028483	1.309196
MRPS6	mitochondrial ribosomal protein S6 [Source:HGNC Symbol;Acc:HGNC:345	0.020775	1.43777
MRPS7	mitochondrial ribosomal protein S7 [Source:HGNC Symbol;Acc:HGNC:346	0.003524	1.50212
MRS2	magnesium transporter MRS2 [Source:HGNC Symbol;Acc:HGNC:347	0.026998	1.297742

MSL3	MSL complex subunit 3 [Source:HGNC Symbol;Acc:HGNC:7370]	0.012909	1.312729
MSS51	MSS51 mitochondrial translational activator [Source:HGNC Sym]	0.025794	1.856097
MTERF1	mitochondrial transcription termination factor 1 [Source:HGNC S	0.042635	1.32855
MTERF3	mitochondrial transcription termination factor 3 [Source:HGNC S	0.000632	1.545458
MTHFD2L	methylenetetrahydrofolate dehydrogenase (NADP+ dependent)	0.000466	1.743378
MTLN	mitoregulin [Source:HGNC Symbol;Acc:HGNC:27339]	0.037636	1.703174
MTM1	myotubularin 1 [Source:HGNC Symbol;Acc:HGNC:7448]	0.047551	1.202199
MTMR4	myotubularin related protein 4 [Source:HGNC Symbol;Acc:HGNC	0.014708	1.271737
MTRF1	mitochondrial translation release factor 1 [Source:HGNC Symbol	0.01887	1.483354
MXRA5	matrix remodeling associated 5 [Source:HGNC Symbol;Acc:HGNC	0.046698	1.813716
MYH14	myosin heavy chain 14 [Source:HGNC Symbol;Acc:HGNC:23212]	0.043148	2.03664
MYL12A	myosin light chain 12A [Source:HGNC Symbol;Acc:HGNC:16701]	0.001198	1.51903
MYL12B	myosin light chain 12B [Source:HGNC Symbol;Acc:HGNC:29827]	0.007947	1.814995
MYNN	myoneurin [Source:HGNC Symbol;Acc:HGNC:14955]	0.037099	1.603589
MYOM1	myomesin 1 [Source:HGNC Symbol;Acc:HGNC:7613]	0.003771	2.564576
MZT1	mitotic spindle organizing protein 1 [Source:HGNC Symbol;Acc:H	0.01758	1.412313
NACA	nascent polypeptide associated complex subunit alpha [Source:f	0.001674	1.579371
NADSYN1	NAD synthetase 1 [Source:HGNC Symbol;Acc:HGNC:29832]	0.012656	1.293344
NAGK	N-acetylglucosamine kinase [Source:HGNC Symbol;Acc:HGNC:17	0.018003	1.224886
NANP	N-acetylneuraminic acid phosphatase [Source:HGNC Symbol;Acc	0.022434	1.495485
NAT14	N-acetyltransferase 14 (putative) [Source:HGNC Symbol;Acc:HGI	0.047817	1.220414
NAXD	NAD(P)HX dehydratase [Source:HGNC Symbol;Acc:HGNC:25576]	0.044649	1.200219
NCBP2AS2	NCBP2 antisense 2 (head to head) [Source:HGNC Symbol;Acc:HG	0.032841	1.55652
NDFIP1	Nedd4 family interacting protein 1 [Source:HGNC Symbol;Acc:HC	0.02086	1.516944
NDFIP2	Nedd4 family interacting protein 2 [Source:HGNC Symbol;Acc:HC	0.037037	1.39761
NDUFA1	NADH:ubiquinone oxidoreductase subunit A1 [Source:HGNC Syn	0.03174	1.700104
NDUFA11	NADH:ubiquinone oxidoreductase subunit A11 [Source:HGNC Sy	0.040309	1.471027
NDUFA12	NADH:ubiquinone oxidoreductase subunit A12 [Source:HGNC Sy	0.000713	1.610753
NDUFA2	NADH:ubiquinone oxidoreductase subunit A2 [Source:HGNC Syn	0.025061	1.842098
NDUFA3	NADH:ubiquinone oxidoreductase subunit A3 [Source:HGNC Syn	0.008281	1.421939
NDUFA4	NDUFA4 mitochondrial complex associated [Source:HGNC Symb	0.000967	2.210967
NDUFA7	NADH:ubiquinone oxidoreductase subunit A7 [Source:HGNC Syn	0.041147	1.9751
NDUFA9	NADH:ubiquinone oxidoreductase subunit A9 [Source:HGNC Syn	0.006919	1.45848
NDUFAB1	NADH:ubiquinone oxidoreductase subunit AB1 [Source:HGNC Sy	0.003755	1.766303
NDUFAB2	NADH:ubiquinone oxidoreductase complex assembly factor 2 [S	0.019559	1.561276
NDUFAB4	NADH:ubiquinone oxidoreductase complex assembly factor 4 [S	0.007552	1.483863
NDUFAB5	NADH:ubiquinone oxidoreductase complex assembly factor 5 [S	0.020025	1.522546
NDUFB1	NADH:ubiquinone oxidoreductase subunit B1 [Source:HGNC Syn	0.000196	1.81115
NDUFB11	NADH:ubiquinone oxidoreductase subunit B11 [Source:HGNC Sy	0.017871	1.269087
NDUFB2	NADH:ubiquinone oxidoreductase subunit B2 [Source:HGNC Syn	0.014044	1.503164
NDUFB3	NADH:ubiquinone oxidoreductase subunit B3 [Source:HGNC Syn	0.000204	1.915871
NDUFB4	NADH:ubiquinone oxidoreductase subunit B4 [Source:HGNC Syn	0.020653	1.298553
NDUFB5	NADH:ubiquinone oxidoreductase subunit B5 [Source:HGNC Syn	0.003261	2.081132
NDUFB6	NADH:ubiquinone oxidoreductase subunit B6 [Source:HGNC Syn	0.000305	1.994468
NDUFB9	NADH:ubiquinone oxidoreductase subunit B9 [Source:HGNC Syn	0.00456	1.903047
NDUFC1	NADH:ubiquinone oxidoreductase subunit C1 [Source:HGNC Syn	1.05E-06	1.696728
NDUFS3	NADH:ubiquinone oxidoreductase core subunit S3 [Source:HGNC	0.008831	1.689494

NDUFS4	NADH:ubiquinone oxidoreductase subunit S4 [Source:HGNC Sym	0.010206	1.681678
NDUFS5	NADH:ubiquinone oxidoreductase subunit S5 [Source:HGNC Sym	0.027768	1.390295
NDUFV3	NADH:ubiquinone oxidoreductase subunit V3 [Source:HGNC Sym	0.001516	1.196
NEDD8	NEDD8 ubiquitin like modifier [Source:HGNC Symbol;Acc:HGNC:	0.04186	1.591796
NEPRO	nucleolus and neural progenitor protein [Source:HGNC Symbol;A	0.030718	1.218576
NFU1	NFU1 iron-sulfur cluster scaffold [Source:HGNC Symbol;Acc:HGN	0.001008	1.620209
NGDN	neuroguidin [Source:HGNC Symbol;Acc:HGNC:20271]	0.036234	1.431007
NIF3L1	NGG1 interacting factor 3 like 1 [Source:HGNC Symbol;Acc:HGNC	0.020365	1.520853
NIFK	nucleolar protein interacting with the FHA domain of MKI67 [Sou	0.013607	1.390399
NIPSNAP3A	nipsnap homolog 3A [Source:HGNC Symbol;Acc:HGNC:23619]	0.002406	1.577305
NIT2	nitrilase family member 2 [Source:HGNC Symbol;Acc:HGNC:298	0.001548	1.567627
NLRP1	NLR family pyrin domain containing 1 [Source:HGNC Symbol;Acc	0.007154	1.415431
NMB	neuromedin B [Source:HGNC Symbol;Acc:HGNC:7842]	5.15E-05	1.584309
NMD3	NMD3 ribosome export adaptor [Source:HGNC Symbol;Acc:HGNC	0.005073	1.365559
NME6	NME/NM23 nucleoside diphosphate kinase 6 [Source:HGNC Symr	0.000969	1.519989
NMRK1	nicotinamide riboside kinase 1 [Source:HGNC Symbol;Acc:HGNC	0.000582	1.860384
NOD2	nucleotide binding oligomerization domain containing 2 [Source	0.046529	2.380581
NOP10	NOP10 ribonucleoprotein [Source:HGNC Symbol;Acc:HGNC:143	0.003471	1.70725
NOTCH3	notch receptor 3 [Source:HGNC Symbol;Acc:HGNC:7883]	0.033406	1.297338
NPM1	nucleophosmin 1 [Source:HGNC Symbol;Acc:HGNC:7910]	0.013139	1.408591
NR1H3	nuclear receptor subfamily 1 group H member 3 [Source:HGNC S	0.000572	1.601722
NR4A1	nuclear receptor subfamily 4 group A member 1 [Source:HGNC S	0.000722	2.167639
NR4A2	nuclear receptor subfamily 4 group A member 2 [Source:HGNC S	5.33E-06	2.697571
NRBF2	nuclear receptor binding factor 2 [Source:HGNC Symbol;Acc:HGI	0.016759	1.708179
NRIP3	nuclear receptor interacting protein 3 [Source:HGNC Symbol;Acc	0.002369	1.373239
NSA2	NSA2 ribosome biogenesis factor [Source:HGNC Symbol;Acc:HGI	0.002903	1.603112
NSL1	NSL1 component of MIS12 kinetochore complex [Source:HGNC S	0.006871	1.601346
NSMCE1	NSE1 homolog, SMC5-SMC6 complex component [Source:HGNC	0.035468	1.129211
NSUN3	NOP2/Sun RNA methyltransferase 3 [Source:HGNC Symbol;Acc:H	0.045119	1.308946
NT5C3A	5'-nucleotidase, cytosolic IIIA [Source:HGNC Symbol;Acc:HGNC:1	0.013706	1.213138
NT5DC1	5'-nucleotidase domain containing 1 [Source:HGNC Symbol;Acc:H	0.014354	1.302336
NTPCR	nucleoside-triphosphatase, cancer-related [Source:HGNC Symbo	0.008581	1.83392
NUDT12	nudix hydrolase 12 [Source:HGNC Symbol;Acc:HGNC:18826]	0.000357	1.922014
NUDT13	nudix hydrolase 13 [Source:HGNC Symbol;Acc:HGNC:18827]	0.022413	1.558728
NUDT5	nudix hydrolase 5 [Source:HGNC Symbol;Acc:HGNC:8052]	0.046837	1.246851
NUDT8	nudix hydrolase 8 [Source:HGNC Symbol;Acc:HGNC:8055]	0.007014	1.417357
NUP35	nucleoporin 35 [Source:HGNC Symbol;Acc:HGNC:29797]	0.026211	1.287347
NUP37	nucleoporin 37 [Source:HGNC Symbol;Acc:HGNC:29929]	0.001031	1.524275
NUP42	nucleoporin 42 [Source:HGNC Symbol;Acc:HGNC:17010]	0.019934	1.290538
NUTF2	nuclear transport factor 2 [Source:HGNC Symbol;Acc:HGNC:137	0.022775	1.492606
NXT1	nuclear transport factor 2 like export factor 1 [Source:HGNC Symr	0.04648	1.558249
OAS2	2'-5'-oligoadenylate synthetase 2 [Source:HGNC Symbol;Acc:HGI	0.031261	1.412267
OCIAD1	OCIA domain containing 1 [Source:HGNC Symbol;Acc:HGNC:160	0.007122	1.411897
ODR4	odr-4 GPCR localization factor homolog [Source:HGNC Symbol;A	0.016892	1.59495
OIP5	Opa interacting protein 5 [Source:HGNC Symbol;Acc:HGNC:2030	0.002843	1.474458
OLA1	Obg like ATPase 1 [Source:HGNC Symbol;Acc:HGNC:28833]	0.025794	1.483131
OLR1	oxidized low density lipoprotein receptor 1 [Source:HGNC Symbo	0.001945	1.827088

ORC4	origin recognition complex subunit 4 [Source:HGNC Symbol;Acc:	0.005523	1.587739
ORC5	origin recognition complex subunit 5 [Source:HGNC Symbol;Acc:	0.00249	1.556198
ORMDL2	ORMDL sphingolipid biosynthesis regulator 2 [Source:HGNC Sym	0.005493	1.639353
OSCP1	organic solute carrier partner 1 [Source:HGNC Symbol;Acc:HGNC	0.024404	1.731306
OSER1	oxidative stress responsive serine rich 1 [Source:HGNC Symbol;A	0.005798	1.962639
OSGEPL1	O-sialoglycoprotein endopeptidase like 1 [Source:HGNC Symbol;	0.001601	1.74236
OSGIN1	oxidative stress induced growth inhibitor 1 [Source:HGNC Symbc	0.030327	1.510173
OST4	oligosaccharyltransferase complex subunit 4, non-catalytic [Sou	0.026998	1.626665
OSTC	oligosaccharyltransferase complex non-catalytic subunit [Source	0.00186	2.018432
OXLD1	oxidoreductase like domain containing 1 [Source:HGNC Symbol;	0.000452	1.466888
OXSM	3-oxoacyl-ACP synthase, mitochondrial [Source:HGNC Symbol;A	2.76E-06	2.040077
P2RX4	purinergic receptor P2X 4 [Source:HGNC Symbol;Acc:HGNC:8535	0.04905	1.322904
PAFAH1B1	platelet activating factor acetylhydrolase 1b regulatory subunit 1	0.003423	1.29174
PAIP2	poly(A) binding protein interacting protein 2 [Source:HGNC Symb	0.009851	1.58168
PAK6	p21 (RAC1) activated kinase 6 [Source:HGNC Symbol;Acc:HGNC:	0.001418	1.880125
PANX2	pannexin 2 [Source:HGNC Symbol;Acc:HGNC:8600]	0.000296	1.691286
PARK7	Parkinsonism associated deglycase [Source:HGNC Symbol;Acc:HG	0.015907	1.302553
PARL	presenilin associated rhomboid like [Source:HGNC Symbol;Acc:H	0.046221	1.202939
PARS2	prolyl-tRNA synthetase 2, mitochondrial [Source:HGNC Symbol;/	0.003171	1.400048
PCF11	PCF11 cleavage and polyadenylation factor subunit [Source:HGNC	0.015445	1.29323
PCSK1	proprotein convertase subtilisin/kexin type 1 [Source:HGNC Sym	0.012554	2.129042
PDCD10	programmed cell death 10 [Source:HGNC Symbol;Acc:HGNC:876	0.000865	1.837463
PDCD2	programmed cell death 2 [Source:HGNC Symbol;Acc:HGNC:8762	6.06E-05	1.365933
PDCD2L	programmed cell death 2 like [Source:HGNC Symbol;Acc:HGNC:2	0.028483	1.427851
PDCD6	programmed cell death 6 [Source:HGNC Symbol;Acc:HGNC:8765	0.000722	1.453945
PDE6D	phosphodiesterase 6D [Source:HGNC Symbol;Acc:HGNC:8788]	0.041136	1.401297
PDIA4	protein disulfide isomerase family A member 4 [Source:HGNC Sy	0.016386	1.209562
PDLIM3	PDZ and LIM domain 3 [Source:HGNC Symbol;Acc:HGNC:20767]	0.01464	1.732919
PDLIM5	PDZ and LIM domain 5 [Source:HGNC Symbol;Acc:HGNC:17468]	0.001886	1.260606
PELO	pelota mRNA surveillance and ribosome rescue factor [Source:H	0.038121	1.302262
PEX12	peroxisomal biogenesis factor 12 [Source:HGNC Symbol;Acc:HGI	0.004048	1.508949
PEX2	peroxisomal biogenesis factor 2 [Source:HGNC Symbol;Acc:HGN	0.002821	1.873141
PEX7	peroxisomal biogenesis factor 7 [Source:HGNC Symbol;Acc:HGN	0.00121	1.331616
PFDN4	prefoldin subunit 4 [Source:HGNC Symbol;Acc:HGNC:8868]	0.002918	1.981042
PFN1	profilin 1 [Source:HGNC Symbol;Acc:HGNC:8881]	0.006425	1.259868
PHB	prohibitin [Source:HGNC Symbol;Acc:HGNC:8912]	0.046123	1.311829
PHEX	phosphate regulating endopeptidase homolog X-linked [Source:l	0.000132	1.830985
PHF11	PHD finger protein 11 [Source:HGNC Symbol;Acc:HGNC:17024]	0.003315	1.580614
PHF7	PHD finger protein 7 [Source:HGNC Symbol;Acc:HGNC:18458]	0.039802	1.286419
PHYH	phytanoyl-CoA 2-hydroxylase [Source:HGNC Symbol;Acc:HGNC:8	0.016017	1.646547
PIGC	phosphatidylinositol glycan anchor biosynthesis class C [Source:l	0.0065	1.602526
PIGF	phosphatidylinositol glycan anchor biosynthesis class F [Source:l	0.03033	1.605328
PIGH	phosphatidylinositol glycan anchor biosynthesis class H [Source:l	0.000816	1.942964
PIGL	phosphatidylinositol glycan anchor biosynthesis class L [Source:l	0.039341	1.388659
PIR	pirin [Source:HGNC Symbol;Acc:HGNC:30048]	0.028317	1.782081
PITPNM3	PITPNM family member 3 [Source:HGNC Symbol;Acc:HGNC:2104	0.022767	1.37864
PIWIL2	piwi like RNA-mediated gene silencing 2 [Source:HGNC Symbol;A	0.027945	2.156187

PLA2G4A	phospholipase A2 group IVA [Source:HGNC Symbol;Acc:HGNC:9044]	0.031635	1.272211
PLAC1	placenta enriched 1 [Source:HGNC Symbol;Acc:HGNC:9044]	0.005794	2.4212
PLCG2	phospholipase C gamma 2 [Source:HGNC Symbol;Acc:HGNC:906]	8.00E-06	2.351859
PLCH2	phospholipase C eta 2 [Source:HGNC Symbol;Acc:HGNC:29037]	0.047815	1.430866
PLEKHM2	pleckstrin homology and RUN domain containing M2 [Source:HGNC Symbol;Acc:HGNC:29037]	0.004982	1.415442
PLGRKT	plasminogen receptor with a C-terminal lysine [Source:HGNC Symbol;Acc:HGNC:29037]	9.84E-05	1.840515
PLIN4	perilipin 4 [Source:HGNC Symbol;Acc:HGNC:29393]	0.008274	2.310726
PLPBP	pyridoxal phosphate binding protein [Source:HGNC Symbol;Acc:HGNC:29393]	0.021454	1.422949
PLPP6	phospholipid phosphatase 6 [Source:HGNC Symbol;Acc:HGNC:29393]	0.025119	1.263604
PLRG1	pleiotropic regulator 1 [Source:HGNC Symbol;Acc:HGNC:9089]	0.029045	1.367634
PMS2	PMS1 homolog 2, mismatch repair system component [Source:HGNC Symbol;Acc:HGNC:9089]	0.010452	1.163298
PNO1	partner of NOB1 homolog [Source:HGNC Symbol;Acc:HGNC:3270]	0.000259	1.597568
PNP	purine nucleoside phosphorylase [Source:HGNC Symbol;Acc:HGNC:3270]	0.007542	1.524398
PNPLA4	patatin like phospholipase domain containing 4 [Source:HGNC Symbol;Acc:HGNC:3270]	0.021526	1.547871
PNRC2	proline rich nuclear receptor coactivator 2 [Source:HGNC Symbol;Acc:HGNC:3270]	0.000153	1.526201
POC1B	POC1 centriolar protein B [Source:HGNC Symbol;Acc:HGNC:3085]	0.012627	1.406327
POC5	POC5 centriolar protein [Source:HGNC Symbol;Acc:HGNC:26658]	0.048717	1.433545
POLB	DNA polymerase beta [Source:HGNC Symbol;Acc:HGNC:9174]	0.001596	1.740697
POLD4	DNA polymerase delta 4, accessory subunit [Source:HGNC Symbol;Acc:HGNC:9174]	0.043297	1.490717
POLG2	DNA polymerase gamma 2, accessory subunit [Source:HGNC Symbol;Acc:HGNC:9174]	0.005565	1.348609
POLI	DNA polymerase iota [Source:HGNC Symbol;Acc:HGNC:9182]	1.43E-07	1.511132
POLR1C	RNA polymerase I and III subunit C [Source:HGNC Symbol;Acc:HGNC:9182]	0.014841	1.537244
POLR1D	RNA polymerase I and III subunit D [Source:HGNC Symbol;Acc:HGNC:9182]	0.027476	1.606521
POLR2D	RNA polymerase II subunit D [Source:HGNC Symbol;Acc:HGNC:9182]	0.048792	1.26621
POLR2G	RNA polymerase II subunit G [Source:HGNC Symbol;Acc:HGNC:9182]	0.008881	1.900748
POLR2H	RNA polymerase II subunit H [Source:HGNC Symbol;Acc:HGNC:9182]	0.016049	1.33527
POLR2J	RNA polymerase II subunit J [Source:HGNC Symbol;Acc:HGNC:9182]	0.020878	1.520582
POLR2K	RNA polymerase II subunit K [Source:HGNC Symbol;Acc:HGNC:9182]	0.003607	1.605723
POLR2L	RNA polymerase II subunit L [Source:HGNC Symbol;Acc:HGNC:9182]	0.003819	1.652515
POLR3D	RNA polymerase III subunit D [Source:HGNC Symbol;Acc:HGNC:1024036]	0.024036	1.208197
POLR3K	RNA polymerase III subunit K [Source:HGNC Symbol;Acc:HGNC:1024404]	0.024404	1.266383
POMP	proteasome maturation protein [Source:HGNC Symbol;Acc:HGNC:1024404]	0.001031	1.670134
PON2	paraoxonase 2 [Source:HGNC Symbol;Acc:HGNC:9205]	0.022035	1.276257
POP4	POP4 homolog, ribonuclease P/MRP subunit [Source:HGNC Symbol;Acc:HGNC:9205]	7.88E-05	1.623756
POP5	POP5 homolog, ribonuclease P/MRP subunit [Source:HGNC Symbol;Acc:HGNC:9205]	0.021445	1.333753
POP7	POP7 homolog, ribonuclease P/MRP subunit [Source:HGNC Symbol;Acc:HGNC:9205]	0.03465	1.316983
POT1	protection of telomeres 1 [Source:HGNC Symbol;Acc:HGNC:1728]	0.034042	1.359434
PPA1	inorganic pyrophosphatase 1 [Source:HGNC Symbol;Acc:HGNC:9205]	0.041276	1.449461
PPA2	inorganic pyrophosphatase 2 [Source:HGNC Symbol;Acc:HGNC:2001897]	0.001897	1.467737
PPFIA3	PTPRF interacting protein alpha 3 [Source:HGNC Symbol;Acc:HGNC:9205]	0.008379	1.407232
PIIA	peptidylprolyl isomerase A [Source:HGNC Symbol;Acc:HGNC:925]	0.028516	1.509316
PPIC	peptidylprolyl isomerase C [Source:HGNC Symbol;Acc:HGNC:925]	0.029063	1.604514
PPIL1	peptidylprolyl isomerase like 1 [Source:HGNC Symbol;Acc:HGNC:925]	0.001834	1.681481
PPIL3	peptidylprolyl isomerase like 3 [Source:HGNC Symbol;Acc:HGNC:925]	0.000847	1.763612
PPIL6	peptidylprolyl isomerase like 6 [Source:HGNC Symbol;Acc:HGNC:925]	1.54E-09	1.841045
PPM1N	protein phosphatase, Mg2+/Mn2+ dependent 1N (putative) [Source:HGNC Symbol;Acc:HGNC:925]	0.044561	1.309775
PPP1R1C	protein phosphatase 1 regulatory inhibitor subunit 1C [Source:HGNC Symbol;Acc:HGNC:925]	0.02302	2.332294

PPP1R35	protein phosphatase 1 regulatory subunit 35 [Source:HGNC Sym	0.002128	1.634833
PPP2R3C	protein phosphatase 2 regulatory subunit B'gamma [Source:HGI	0.000448	1.575264
PPP2R5C	protein phosphatase 2 regulatory subunit B'gamma [Source:HGN	0.00153	1.333963
PRDX3	peroxiredoxin 3 [Source:HGNC Symbol;Acc:HGNC:9354]	0.007788	1.469931
PREB	prolactin regulatory element binding [Source:HGNC Symbol;Acc:	0.011017	1.203874
PRELID2	PRELI domain containing 2 [Source:HGNC Symbol;Acc:HGNC:283	0.009942	1.321988
PRELID3B	PRELI domain containing 3B [Source:HGNC Symbol;Acc:HGNC:15	0.011843	1.494991
PRIMPOL	primase and DNA directed polymerase [Source:HGNC Symbol;Ac	0.03449	1.290585
PRKAG1	protein kinase AMP-activated non-catalytic subunit gamma 1 [Sc	0.03494	1.600183
PRKG2	protein kinase cGMP-dependent 2 [Source:HGNC Symbol;Acc:HC	0.026436	1.34917
PRNP	prion protein [Source:HGNC Symbol;Acc:HGNC:9449]	0.011101	1.252165
PRSS16	serine protease 16 [Source:HGNC Symbol;Acc:HGNC:9480]	0.009392	1.426597
PRSS3	serine protease 3 [Source:HGNC Symbol;Acc:HGNC:9486]	0.008549	1.764068
PRSS36	serine protease 36 [Source:HGNC Symbol;Acc:HGNC:26906]	0.001273	2.126977
PSMA1	proteasome 20S subunit alpha 1 [Source:HGNC Symbol;Acc:HGN	0.00687	1.581912
PSMA3	proteasome 20S subunit alpha 3 [Source:HGNC Symbol;Acc:HGN	0.00864	1.478982
PSMA4	proteasome 20S subunit alpha 4 [Source:HGNC Symbol;Acc:HGN	0.00245	1.4938
PSMA5	proteasome 20S subunit alpha 5 [Source:HGNC Symbol;Acc:HGN	0.003549	1.729719
PSMA6	proteasome 20S subunit alpha 6 [Source:HGNC Symbol;Acc:HGN	0.00808	1.733511
PSMB1	proteasome 20S subunit beta 1 [Source:HGNC Symbol;Acc:HGN	0.027478	1.390531
PSMB2	proteasome 20S subunit beta 2 [Source:HGNC Symbol;Acc:HGN	0.015484	1.119106
PSMB7	proteasome 20S subunit beta 7 [Source:HGNC Symbol;Acc:HGN	0.019766	1.316223
PSMC2	proteasome 26S subunit, ATPase 2 [Source:HGNC Symbol;Acc:Hi	0.015172	1.348305
PSMC6	proteasome 26S subunit, ATPase 6 [Source:HGNC Symbol;Acc:Hi	0.031124	1.458117
PSMD13	proteasome 26S subunit, non-ATPase 13 [Source:HGNC Symbol;	0.018038	1.567208
PSME1	proteasome activator subunit 1 [Source:HGNC Symbol;Acc:HGN	0.017629	1.518538
PSME2	proteasome activator subunit 2 [Source:HGNC Symbol;Acc:HGN	0.006942	1.399708
PSME3IP1	proteasome activator subunit 3 interacting protein 1 [Source:HG	0.002476	1.269952
PSMG2	proteasome assembly chaperone 2 [Source:HGNC Symbol;Acc:H	0.017949	1.401277
PSMG3	proteasome assembly chaperone 3 [Source:HGNC Symbol;Acc:H	0.021509	1.524025
PSPH	phosphoserine phosphatase [Source:HGNC Symbol;Acc:HGNC:95	0.01557	1.619802
PSTK	phosphoseryl-tRNA kinase [Source:HGNC Symbol;Acc:HGNC:285	0.000969	1.599417
PSTPIP2	proline-serine-threonine phosphatase interacting protein 2 [Sou	0.046698	1.381187
PTMA	prothymosin alpha [Source:HGNC Symbol;Acc:HGNC:9623]	0.025794	1.29869
PTPRR	protein tyrosine phosphatase receptor type R [Source:HGNC Syn	0.003418	1.796202
PTRH2	peptidyl-tRNA hydrolase 2 [Source:HGNC Symbol;Acc:HGNC:242	1.52E-06	1.714285
PTS	6-pyruvoyltetrahydropterin synthase [Source:HGNC Symbol;Acc:	0.008632	1.639743
PUS10	pseudouridine synthase 10 [Source:HGNC Symbol;Acc:HGNC:265	0.005482	1.835743
PUS7L	pseudouridine synthase 7 like [Source:HGNC Symbol;Acc:HGNC:2	0.028454	1.376147
PYROXD1	pyridine nucleotide-disulphide oxidoreductase domain 1 [Source	0.047156	1.262738
RAB32	RAB32, member RAS oncogene family [Source:HGNC Symbol;Acc:	0.025378	1.680721
RAB33A	RAB33A, member RAS oncogene family [Source:HGNC Symbol;A	0.032872	2.52918
RAB3D	RAB3D, member RAS oncogene family [Source:HGNC Symbol;Ac	0.027935	1.389188
RAB3IP	RAB3A interacting protein [Source:HGNC Symbol;Acc:HGNC:165	0.019651	1.256169
RAB40B	RAB40B, member RAS oncogene family [Source:HGNC Symbol;A	0.049088	1.282421
RAB8B	RAB8B, member RAS oncogene family [Source:HGNC Symbol;Ac	0.018445	1.230199
RAB9A	RAB9A, member RAS oncogene family [Source:HGNC Symbol;Ac	0.021302	1.758792

RABGEF1	RAB guanine nucleotide exchange factor 1 [Source:HGNC Symbol;Acc:HGNC:9797]	0.037154	1.792969
RABGGTB	Rab geranylgeranyltransferase subunit beta [Source:HGNC Symbol;Acc:HGNC:9797]	0.004938	1.678941
RABIF	RAB interacting factor [Source:HGNC Symbol;Acc:HGNC:9797]	0.021885	1.348117
RABL3	RAB, member of RAS oncogene family like 3 [Source:HGNC Symbol;Acc:HGNC:9797]	0.020273	1.20495
RAD52	RAD52 homolog, DNA repair protein [Source:HGNC Symbol;Acc:HGNC:9797]	0.031624	1.217608
RAET1E	retinoic acid early transcript 1E [Source:HGNC Symbol;Acc:HGNC:9797]	0.012128	1.632787
RAMAC	RNA guanine-7 methyltransferase activating subunit [Source:HGNC Symbol;Acc:HGNC:9797]	0.002699	1.664201
RAMACL	RNA guanine-7 methyltransferase activating subunit like (pseudogene) [Source:HGNC Symbol;Acc:HGNC:9797]	0.021526	1.610568
RANBP6	RAN binding protein 6 [Source:HGNC Symbol;Acc:HGNC:9851]	0.005493	1.371392
RAPGEFL1	Rap guanine nucleotide exchange factor like 1 [Source:HGNC Symbol;Acc:HGNC:9851]	0.025427	1.494627
RBBP8NL	RBBP8 N-terminal like [Source:HGNC Symbol;Acc:HGNC:16144]	0.010022	1.828581
RBCK1	RANBP2-type and C3HC4-type zinc finger containing 1 [Source:HGNC Symbol;Acc:HGNC:16144]	0.001219	1.244177
RBIS	ribosomal biogenesis factor [Source:HGNC Symbol;Acc:HGNC:32000]	0.004461	1.737408
RBM7	RNA binding motif protein 7 [Source:HGNC Symbol;Acc:HGNC:9851]	0.011686	1.323917
RBP7	retinol binding protein 7 [Source:HGNC Symbol;Acc:HGNC:30316]	0.017868	1.744137
RBX1	ring-box 1 [Source:HGNC Symbol;Acc:HGNC:9928]	0.003178	1.745874
RCL1	RNA terminal phosphate cyclase like 1 [Source:HGNC Symbol;Acc:HGNC:9928]	0.041354	1.112836
RCSD1	RCSD domain containing 1 [Source:HGNC Symbol;Acc:HGNC:28300]	0.002949	2.845385
REEP4	receptor accessory protein 4 [Source:HGNC Symbol;Acc:HGNC:28300]	0.020691	1.26742
REEP6	receptor accessory protein 6 [Source:HGNC Symbol;Acc:HGNC:30000]	0.007122	1.454599
RER1	retention in endoplasmic reticulum sorting receptor 1 [Source:HGNC Symbol;Acc:HGNC:30000]	0.044561	1.28527
RESF1	retroelement silencing factor 1 [Source:HGNC Symbol;Acc:HGNC:30000]	0.021909	1.494768
RFESD	Rieske Fe-S domain containing [Source:HGNC Symbol;Acc:HGNC:30000]	0.017887	1.669096
RFK	riboflavin kinase [Source:HGNC Symbol;Acc:HGNC:30324]	0.01808	1.381626
RGL2	ral guanine nucleotide dissociation stimulator like 2 [Source:HGNC Symbol;Acc:HGNC:30324]	0.043874	1.177069
RGS10	regulator of G protein signaling 10 [Source:HGNC Symbol;Acc:HGNC:30324]	0.002406	1.963467
RGS14	regulator of G protein signaling 14 [Source:HGNC Symbol;Acc:HGNC:30324]	7.28E-06	1.396521
RGS17	regulator of G protein signaling 17 [Source:HGNC Symbol;Acc:HGNC:30324]	0.012758	1.648716
RGS2	regulator of G protein signaling 2 [Source:HGNC Symbol;Acc:HGNC:30324]	0.013838	2.155069
RGS20	regulator of G protein signaling 20 [Source:HGNC Symbol;Acc:HGNC:30324]	0.019698	1.553643
RHBDL1	rhomboid like 1 [Source:HGNC Symbol;Acc:HGNC:10007]	0.036536	1.819828
RHCE	Rh blood group CcEe antigens [Source:HGNC Symbol;Acc:HGNC:10007]	0.007919	2.028757
RHEB	Ras homolog, mTORC1 binding [Source:HGNC Symbol;Acc:HGNC:10007]	0.003569	1.546642
RHEBL1	RHEB like 1 [Source:HGNC Symbol;Acc:HGNC:21166]	0.006444	1.882058
RHOB	ras homolog family member B [Source:HGNC Symbol;Acc:HGNC:10007]	0.013557	1.504117
RIPPLY2	rippy transcriptional repressor 2 [Source:HGNC Symbol;Acc:HGNC:10007]	0.000574	2.315081
RMDN1	regulator of microtubule dynamics 1 [Source:HGNC Symbol;Acc:HGNC:10007]	0.002434	1.458891
RNAEH2C	ribonuclease H2 subunit C [Source:HGNC Symbol;Acc:HGNC:24100]	0.027021	1.362503
RND1	Rho family GTPase 1 [Source:HGNC Symbol;Acc:HGNC:18314]	0.002668	2.059145
RNF103	ring finger protein 103 [Source:HGNC Symbol;Acc:HGNC:12859]	0.009715	1.278012
RNF114	ring finger protein 114 [Source:HGNC Symbol;Acc:HGNC:13094]	0.033556	1.549018
RNF14	ring finger protein 14 [Source:HGNC Symbol;Acc:HGNC:10058]	0.024338	1.563324
RNF170	ring finger protein 170 [Source:HGNC Symbol;Acc:HGNC:25358]	0.000123	1.372815
RNF34	ring finger protein 34 [Source:HGNC Symbol;Acc:HGNC:17297]	0.037197	1.284485
RNF7	ring finger protein 7 [Source:HGNC Symbol;Acc:HGNC:10070]	0.03997	1.583956
ROMO1	reactive oxygen species modulator 1 [Source:HGNC Symbol;Acc:HGNC:10070]	0.036188	1.746529
RP2	RP2 activator of ARL3 GTPase [Source:HGNC Symbol;Acc:HGNC:10070]	0.011124	1.564822

RPA3	replication protein A3 [Source:HGNC Symbol;Acc:HGNC:10291]	0.005717	1.62732
RPAP2	RNA polymerase II associated protein 2 [Source:HGNC Symbol;Acc:HGNC:10292]	0.019651	1.523864
RPF2	ribosome production factor 2 homolog [Source:HGNC Symbol;Acc:HGNC:10293]	0.000582	1.455488
RPL10A	ribosomal protein L10a [Source:HGNC Symbol;Acc:HGNC:10299]	0.014843	1.731273
RPL12	ribosomal protein L12 [Source:HGNC Symbol;Acc:HGNC:10302]	0.001011	1.819841
RPL13A	ribosomal protein L13a [Source:HGNC Symbol;Acc:HGNC:10304]	0.032883	1.636132
RPL14	ribosomal protein L14 [Source:HGNC Symbol;Acc:HGNC:10305]	0.015361	1.714757
RPL15	ribosomal protein L15 [Source:HGNC Symbol;Acc:HGNC:10306]	0.01925	1.457678
RPL17	ribosomal protein L17 [Source:HGNC Symbol;Acc:HGNC:10307]	0.013055	1.59421
RPL18	ribosomal protein L18 [Source:HGNC Symbol;Acc:HGNC:10310]	0.029742	1.525289
RPL19	ribosomal protein L19 [Source:HGNC Symbol;Acc:HGNC:10312]	0.015083	1.545176
RPL21	ribosomal protein L21 [Source:HGNC Symbol;Acc:HGNC:10313]	0.004726	1.888552
RPL22	ribosomal protein L22 [Source:HGNC Symbol;Acc:HGNC:10315]	0.00587	1.373764
RPL22L1	ribosomal protein L22 like 1 [Source:HGNC Symbol;Acc:HGNC:27000]	0.005482	2.372105
RPL23	ribosomal protein L23 [Source:HGNC Symbol;Acc:HGNC:10316]	0.015299	1.318507
RPL23A	ribosomal protein L23a [Source:HGNC Symbol;Acc:HGNC:10317]	0.008521	1.400594
RPL24	ribosomal protein L24 [Source:HGNC Symbol;Acc:HGNC:10325]	0.014838	1.825814
RPL26	ribosomal protein L26 [Source:HGNC Symbol;Acc:HGNC:10327]	0.006932	1.814988
RPL26L1	ribosomal protein L26 like 1 [Source:HGNC Symbol;Acc:HGNC:17000]	0.00159	1.702744
RPL27	ribosomal protein L27 [Source:HGNC Symbol;Acc:HGNC:10328]	0.003662	2.187319
RPL27A	ribosomal protein L27a [Source:HGNC Symbol;Acc:HGNC:10329]	0.022624	1.869204
RPL30	ribosomal protein L30 [Source:HGNC Symbol;Acc:HGNC:10333]	1.41E-05	1.650081
RPL32	ribosomal protein L32 [Source:HGNC Symbol;Acc:HGNC:10336]	0.042707	1.567903
RPL34	ribosomal protein L34 [Source:HGNC Symbol;Acc:HGNC:10340]	0.004241	1.834415
RPL35A	ribosomal protein L35a [Source:HGNC Symbol;Acc:HGNC:10345]	0.037711	1.659514
RPL36	ribosomal protein L36 [Source:HGNC Symbol;Acc:HGNC:13631]	0.04135	1.686814
RPL37	ribosomal protein L37 [Source:HGNC Symbol;Acc:HGNC:10347]	0.000223	1.510019
RPL37A	ribosomal protein L37a [Source:HGNC Symbol;Acc:HGNC:10348]	0.046062	1.469242
RPL38	ribosomal protein L38 [Source:HGNC Symbol;Acc:HGNC:10349]	0.029486	1.530255
RPL39	ribosomal protein L39 [Source:HGNC Symbol;Acc:HGNC:10350]	0.013558	1.97846
RPL39L	ribosomal protein L39 like [Source:HGNC Symbol;Acc:HGNC:17000]	0.006077	1.554576
RPL5	ribosomal protein L5 [Source:HGNC Symbol;Acc:HGNC:10360]	0.017516	1.693633
RPL7	ribosomal protein L7 [Source:HGNC Symbol;Acc:HGNC:10363]	0.012536	1.323765
RPL7A	ribosomal protein L7a [Source:HGNC Symbol;Acc:HGNC:10364]	0.049683	1.51689
RPL9	ribosomal protein L9 [Source:HGNC Symbol;Acc:HGNC:10369]	0.027399	1.805227
RPP14	ribonuclease P/MRP subunit p14 [Source:HGNC Symbol;Acc:HGNC:10370]	0.006667	1.387835
RPP25L	ribonuclease P/MRP subunit p25 like [Source:HGNC Symbol;Acc:HGNC:10371]	0.002691	1.39568
RPP38	ribonuclease P/MRP subunit p38 [Source:HGNC Symbol;Acc:HGNC:10372]	0.029587	1.23532
RPS11	ribosomal protein S11 [Source:HGNC Symbol;Acc:HGNC:10384]	0.040927	1.587194
RPS13	ribosomal protein S13 [Source:HGNC Symbol;Acc:HGNC:10386]	0.000582	2.094118
RPS14	ribosomal protein S14 [Source:HGNC Symbol;Acc:HGNC:10387]	0.026211	1.857985
RPS15	ribosomal protein S15 [Source:HGNC Symbol;Acc:HGNC:10388]	0.043332	1.486224
RPS15A	ribosomal protein S15a [Source:HGNC Symbol;Acc:HGNC:10389]	0.011686	2.005336
RPS16	ribosomal protein S16 [Source:HGNC Symbol;Acc:HGNC:10396]	0.011691	1.766279
RPS18	ribosomal protein S18 [Source:HGNC Symbol;Acc:HGNC:10401]	0.047961	1.784989
RPS19	ribosomal protein S19 [Source:HGNC Symbol;Acc:HGNC:10402]	0.03033	1.52987
RPS20	ribosomal protein S20 [Source:HGNC Symbol;Acc:HGNC:10405]	0.000241	1.989268

RPS21	ribosomal protein S21 [Source:HGNC Symbol;Acc:HGNC:10409]	0.012876	2.051296
RPS24	ribosomal protein S24 [Source:HGNC Symbol;Acc:HGNC:10411]	0.005271	1.623819
RPS25	ribosomal protein S25 [Source:HGNC Symbol;Acc:HGNC:10413]	0.003447	1.70925
RPS26	ribosomal protein S26 [Source:HGNC Symbol;Acc:HGNC:10414]	0.002112	1.605674
RPS27	ribosomal protein S27 [Source:HGNC Symbol;Acc:HGNC:10416]	0.014561	1.691077
RPS27A	ribosomal protein S27a [Source:HGNC Symbol;Acc:HGNC:10417]	0.00095	2.087011
RPS27L	ribosomal protein S27 like [Source:HGNC Symbol;Acc:HGNC:184]	0.012407	1.600438
RPS28	ribosomal protein S28 [Source:HGNC Symbol;Acc:HGNC:10418]	0.044445	1.389465
RPS29	ribosomal protein S29 [Source:HGNC Symbol;Acc:HGNC:10419]	0.012847	2.079642
RPS3	ribosomal protein S3 [Source:HGNC Symbol;Acc:HGNC:10420]	0.013264	1.891893
RPS3A	ribosomal protein S3A [Source:HGNC Symbol;Acc:HGNC:10421]	0.029895	1.845069
RPS4Y1	ribosomal protein S4 Y-linked 1 [Source:HGNC Symbol;Acc:HGNC:10422]	0.030209	1.346952
RPS6	ribosomal protein S6 [Source:HGNC Symbol;Acc:HGNC:10429]	0.019946	1.785411
RPS7	ribosomal protein S7 [Source:HGNC Symbol;Acc:HGNC:10440]	0.028921	1.795954
RPS8	ribosomal protein S8 [Source:HGNC Symbol;Acc:HGNC:10441]	0.038825	1.587002
RSL24D1	ribosomal L24 domain containing 1 [Source:HGNC Symbol;Acc:HGNC:10442]	0.008169	1.792023
RSPH14	radial spoke head 14 homolog [Source:HGNC Symbol;Acc:HGNC:10443]	0.021445	3.170896
RTCA	RNA 3'-terminal phosphate cyclase [Source:HGNC Symbol;Acc:HGNC:10444]	0.019207	1.326794
RWDD2A	RWD domain containing 2A [Source:HGNC Symbol;Acc:HGNC:10445]	0.001554	2.004594
RWDD2B	RWD domain containing 2B [Source:HGNC Symbol;Acc:HGNC:10446]	0.03918	1.211806
RWDD4	RWD domain containing 4 [Source:HGNC Symbol;Acc:HGNC:10447]	0.003447	1.40749
S100A4	S100 calcium binding protein A4 [Source:HGNC Symbol;Acc:HGNC:10448]	0.040725	2.012957
SAR1B	secretion associated Ras related GTPase 1B [Source:HGNC Symbol;Acc:HGNC:10449]	0.012001	1.528568
SARAF	store-operated calcium entry associated regulatory factor [Source:HGNC Symbol;Acc:HGNC:10450]	0.012221	1.564687
SATL1	spermidine/spermine N1-acetyl transferase like 1 [Source:HGNC Symbol;Acc:HGNC:10451]	0.001049	1.999546
SCFD1	sec1 family domain containing 1 [Source:HGNC Symbol;Acc:HGNC:10452]	0.005493	1.300686
SCML1	Scm polycomb group protein like 1 [Source:HGNC Symbol;Acc:HGNC:10453]	0.01628	1.613916
SCOC	short coiled-coil protein [Source:HGNC Symbol;Acc:HGNC:10454]	0.005327	1.695368
SCRN3	secernin 3 [Source:HGNC Symbol;Acc:HGNC:30382]	0.001232	1.351357
SCYL3	SCY1 like pseudokinase 3 [Source:HGNC Symbol;Acc:HGNC:1928]	0.021992	1.379768
SDCCAG8	serologically defined colon cancer antigen 8 [Source:HGNC Symbol;Acc:HGNC:10455]	0.016195	1.358738
SDF2L1	stromal cell derived factor 2 like 1 [Source:HGNC Symbol;Acc:HGNC:10456]	0.000411	1.463784
SDHAF2	succinate dehydrogenase complex assembly factor 2 [Source:HGNC Symbol;Acc:HGNC:10457]	0.001178	1.613111
SDHAF3	succinate dehydrogenase complex assembly factor 3 [Source:HGNC Symbol;Acc:HGNC:10458]	0.00057	2.045448
SDHAF4	succinate dehydrogenase complex assembly factor 4 [Source:HGNC Symbol;Acc:HGNC:10459]	0.031124	1.747951
SDHB	succinate dehydrogenase complex iron sulfur subunit B [Source:HGNC Symbol;Acc:HGNC:10460]	0.021769	1.467906
SDHC	succinate dehydrogenase complex subunit C [Source:HGNC Symbol;Acc:HGNC:10461]	0.000666	1.777608
SDR16C5	short chain dehydrogenase/reductase family 16C member 5 [Source:HGNC Symbol;Acc:HGNC:10462]	0.018241	2.128874
SEC11A	SEC11 homolog A, signal peptidase complex subunit [Source:HGNC Symbol;Acc:HGNC:10463]	0.021824	1.42775
SEC11C	SEC11 homolog C, signal peptidase complex subunit [Source:HGNC Symbol;Acc:HGNC:10464]	0.000645	1.612132
SEC22A	SEC22 homolog A, vesicle trafficking protein [Source:HGNC Symbol;Acc:HGNC:10465]	0.030118	1.51175
SEC22C	SEC22 homolog C, vesicle trafficking protein [Source:HGNC Symbol;Acc:HGNC:10466]	0.007438	1.495299
SEC61A2	SEC61 translocon alpha 2 subunit [Source:HGNC Symbol;Acc:HGNC:10467]	0.021595	1.296379
SEC61B	SEC61 translocon beta subunit [Source:HGNC Symbol;Acc:HGNC:10468]	0.003038	1.362144
SEC61G	SEC61 translocon gamma subunit [Source:HGNC Symbol;Acc:HGNC:10469]	0.008475	1.628338
SECISBP2	SECIS binding protein 2 [Source:HGNC Symbol;Acc:HGNC:30972]	0.000721	1.364752
SELENOF	selenoprotein F [Source:HGNC Symbol;Acc:HGNC:17705]	0.003607	1.946853

SELENOH	selenoprotein H [Source:HGNC Symbol;Acc:HGNC:18251]	0.022049	1.708407
SELENOK	selenoprotein K [Source:HGNC Symbol;Acc:HGNC:30394]	0.02895	1.78862
SELENOT	selenoprotein T [Source:HGNC Symbol;Acc:HGNC:18136]	0.006696	1.736483
SELENOW	selenoprotein W [Source:HGNC Symbol;Acc:HGNC:10752]	0.009324	1.993013
SEPHS2	selenophosphate synthetase 2 [Source:HGNC Symbol;Acc:HGNC:10752]	0.022483	1.285823
SEPSECS	Sep (O-phosphoserine) tRNA:Sec (selenocysteine) tRNA synthase	0.021625	1.290049
SERPINB5	serpin family B member 5 [Source:HGNC Symbol;Acc:HGNC:8945]	0.033023	1.37441
SERPINI1	serpin family I member 1 [Source:HGNC Symbol;Acc:HGNC:8943]	0.036188	1.484685
SF3B5	splicing factor 3b subunit 5 [Source:HGNC Symbol;Acc:HGNC:2106]	0.002234	1.544467
SF3B6	splicing factor 3b subunit 6 [Source:HGNC Symbol;Acc:HGNC:3006]	0.000717	1.470459
SFR1	SWI5 dependent homologous recombination repair protein 1 [Source:HGNC Symbol;Acc:HGNC:10752]	0.034967	1.596978
SFT2D1	SFT2 domain containing 1 [Source:HGNC Symbol;Acc:HGNC:2110]	0.000194	1.531896
SH3PXD2A	SH3 and PX domains 2A [Source:HGNC Symbol;Acc:HGNC:23664]	0.024294	1.208075
SHLD3	shieldin complex subunit 3 [Source:HGNC Symbol;Acc:HGNC:5388]	0.026243	1.919282
SIRPB2	signal regulatory protein beta 2 [Source:HGNC Symbol;Acc:HGNC:10752]	2.09E-06	2.212678
SIRT7	sirtuin 7 [Source:HGNC Symbol;Acc:HGNC:14935]	0.01784	1.280362
SKP1	S-phase kinase associated protein 1 [Source:HGNC Symbol;Acc:HGNC:10752]	0.003259	1.673878
SLC16A8	solute carrier family 16 member 8 [Source:HGNC Symbol;Acc:HGNC:10752]	0.011681	1.570563
SLC22A23	solute carrier family 22 member 23 [Source:HGNC Symbol;Acc:HGNC:10752]	0.005822	1.661079
SLC25A3	solute carrier family 25 member 3 [Source:HGNC Symbol;Acc:HGNC:10752]	0.020878	1.273714
SLC25A33	solute carrier family 25 member 33 [Source:HGNC Symbol;Acc:HGNC:10752]	0.002272	1.661989
SLC27A5	solute carrier family 27 member 5 [Source:HGNC Symbol;Acc:HGNC:10752]	0.011895	1.400858
SLC28A3	solute carrier family 28 member 3 [Source:HGNC Symbol;Acc:HGNC:10752]	0.046967	2.345093
SLC2A9	solute carrier family 2 member 9 [Source:HGNC Symbol;Acc:HGNC:10752]	0.023929	1.374481
SLC34A1	solute carrier family 34 member 1 [Source:HGNC Symbol;Acc:HGNC:10752]	0.012633	2.641016
SLC35A1	solute carrier family 35 member A1 [Source:HGNC Symbol;Acc:HGNC:10752]	0.029123	1.577077
SLC35A5	solute carrier family 35 member A5 [Source:HGNC Symbol;Acc:HGNC:10752]	0.000979	1.641425
SLC35B1	solute carrier family 35 member B1 [Source:HGNC Symbol;Acc:HGNC:10752]	0.008235	1.250731
SLC35G2	solute carrier family 35 member G2 [Source:HGNC Symbol;Acc:HGNC:10752]	0.001362	2.194004
SLC38A6	solute carrier family 38 member 6 [Source:HGNC Symbol;Acc:HGNC:10752]	0.030139	1.464159
SLC38A9	solute carrier family 38 member 9 [Source:HGNC Symbol;Acc:HGNC:10752]	0.024237	1.372016
SLIRP	SRA stem-loop interacting RNA binding protein [Source:HGNC Symbol;Acc:HGNC:10752]	0.042835	1.286882
SMAD2	SMAD family member 2 [Source:HGNC Symbol;Acc:HGNC:6768]	0.01163	1.290841
SMDT1	single-pass membrane protein with aspartate rich tail 1 [Source:HGNC Symbol;Acc:HGNC:10752]	0.033762	1.597637
SMIM11A	small integral membrane protein 11A [Source:HGNC Symbol;Acc:HGNC:10752]	0.021945	1.436434
SMIM19	small integral membrane protein 19 [Source:HGNC Symbol;Acc:HGNC:10752]	3.80E-05	1.914555
SMIM20	small integral membrane protein 20 [Source:HGNC Symbol;Acc:HGNC:10752]	0.019934	1.577019
SMIM26	small integral membrane protein 26 [Source:HGNC Symbol;Acc:HGNC:10752]	0.022049	1.692323
SMIM27	small integral membrane protein 27 [Source:HGNC Symbol;Acc:HGNC:10752]	0.03918	1.742536
SMIM30	small integral membrane protein 30 [Source:HGNC Symbol;Acc:HGNC:10752]	0.001022	1.871838
SMIM4	small integral membrane protein 4 [Source:HGNC Symbol;Acc:HGNC:10752]	0.005851	1.85283
SMIM7	small integral membrane protein 7 [Source:HGNC Symbol;Acc:HGNC:10752]	0.016195	1.349035
SMIM8	small integral membrane protein 8 [Source:HGNC Symbol;Acc:HGNC:10752]	0.031124	1.531908
SMUG1	single-strand-selective monofunctional uracil-DNA glycosylase 1 [Source:HGNC Symbol;Acc:HGNC:10752]	0.006627	1.386616
SNAPC5	small nuclear RNA activating complex polypeptide 5 [Source:HGNC Symbol;Acc:HGNC:10752]	0.000268	1.503406
SNAPIN	SNAP associated protein [Source:HGNC Symbol;Acc:HGNC:17145]	0.00057	1.685264
SNCG	synuclein gamma [Source:HGNC Symbol;Acc:HGNC:11141]	0.015299	1.282055

SNORC	secondary ossification center associated regulator of chondrocyt	0.006692	1.893415
SNRNP27	small nuclear ribonucleoprotein U4/U6.U5 subunit 27 [Source:HGNC S	0.017878	1.581617
SNRPB2	small nuclear ribonucleoprotein polypeptide B2 [Source:HGNC S	0.000602	1.700648
SNRPC	small nuclear ribonucleoprotein polypeptide C [Source:HGNC Sy	0.000635	1.565516
SNRPD2	small nuclear ribonucleoprotein D2 polypeptide [Source:HGNC S	0.021034	1.699051
SNRPE	small nuclear ribonucleoprotein polypeptide E [Source:HGNC Sy	0.039391	1.264819
SNRPF	small nuclear ribonucleoprotein polypeptide F [Source:HGNC Sy	0.047543	1.204508
SNRPG	small nuclear ribonucleoprotein polypeptide G [Source:HGNC Sy	0.004038	1.79518
SOCS3	suppressor of cytokine signaling 3 [Source:HGNC Symbol;Acc:HG	0.000271	1.784635
SPAG4	sperm associated antigen 4 [Source:HGNC Symbol;Acc:HGNC:11	0.002092	1.578172
SPATA17	spermatogenesis associated 17 [Source:HGNC Symbol;Acc:HGNC	0.039511	1.553438
SPCS2	signal peptidase complex subunit 2 [Source:HGNC Symbol;Acc:H	0.036845	1.283289
SPSB2	splA/ryanodine receptor domain and SOCS box containing 2 [Sol	0.017221	1.534166
SPTSSA	serine palmitoyltransferase small subunit A [Source:HGNC Symb	0.007872	1.546209
SPTSSB	serine palmitoyltransferase small subunit B [Source:HGNC Symb	0.00581	2.381872
SRCAP	Snf2 related CREBBP activator protein [Source:HGNC Symbol;Acc	0.005835	1.419412
SRD5A3	steroid 5 alpha-reductase 3 [Source:HGNC Symbol;Acc:HGNC:25	0.038809	1.346688
SRFBP1	serum response factor binding protein 1 [Source:HGNC Symbol;A	0.031684	1.212433
SS18L2	SS18 like 2 [Source:HGNC Symbol;Acc:HGNC:15593]	0.005523	1.772851
SSR3	signal sequence receptor subunit 3 [Source:HGNC Symbol;Acc:H	0.025795	1.344827
SSR4	signal sequence receptor subunit 4 [Source:HGNC Symbol;Acc:H	0.019899	1.748087
STARD3NL	STARD3 N-terminal like [Source:HGNC Symbol;Acc:HGNC:19169]	0.022391	1.465428
STARD4	StAR related lipid transfer domain containing 4 [Source:HGNC Sy	0.013774	1.582057
STEAP1	STEAP family member 1 [Source:HGNC Symbol;Acc:HGNC:11378	4.43E-05	1.705469
STEAP1B	STEAP family member 1B [Source:HGNC Symbol;Acc:HGNC:4190	0.001754	1.370987
STK17A	serine/threonine kinase 17a [Source:HGNC Symbol;Acc:HGNC:11	0.000481	1.566473
STK19	serine/threonine kinase 19 [Source:HGNC Symbol;Acc:HGNC:11	0.025732	1.47648
STMP1	short transmembrane mitochondrial protein 1 [Source:HGNC Sy	2.65E-05	1.304358
STOML2	stomatin like 2 [Source:HGNC Symbol;Acc:HGNC:14559]	0.033465	1.5236
STX19	syntaxin 19 [Source:HGNC Symbol;Acc:HGNC:19300]	0.008545	2.464715
STX5	syntaxin 5 [Source:HGNC Symbol;Acc:HGNC:11440]	0.02751	1.402668
STX8	syntaxin 8 [Source:HGNC Symbol;Acc:HGNC:11443]	0.046736	1.54505
STYX	serine/threonine/tyrosine interacting protein [Source:HGNC Syn	0.019374	1.335638
STYXL1	serine/threonine/tyrosine interacting like 1 [Source:HGNC Symb	0.001008	1.447864
SUB1	SUB1 regulator of transcription [Source:HGNC Symbol;Acc:HGNC	0.002989	1.69174
SUCLG1	succinate-CoA ligase alpha subunit [Source:HGNC Symbol;Acc:HC	0.030649	1.683882
SUMO2	small ubiquitin like modifier 2 [Source:HGNC Symbol;Acc:HGNC:	0.000717	1.436463
SUMO3	small ubiquitin like modifier 3 [Source:HGNC Symbol;Acc:HGNC:	0.041359	1.358391
SVBP	small vasohibin binding protein [Source:HGNC Symbol;Acc:HGNC	0.024564	1.672143
SVIP	small VCP interacting protein [Source:HGNC Symbol;Acc:HGNC:2	0.037646	1.24269
SWI5	SWI5 homologous recombination repair protein [Source:HGNC S	0.00401	1.421407
SYNE2	spectrin repeat containing nuclear envelope protein 2 [Source:H	0.049088	1.243092
TACC2	transforming acidic coiled-coil containing protein 2 [Source:HGN	0.016147	1.407661
TAF11	TATA-box binding protein associated factor 11 [Source:HGNC Sy	0.019894	1.61417
TAF1D	TATA-box binding protein associated factor, RNA polymerase I si	0.031979	1.326075
TAF7	TATA-box binding protein associated factor 7 [Source:HGNC Sym	0.008549	1.702493
TANK	TRAF family member associated NFKB activator [Source:HGNC S	0.033613	1.612425

TATDN1	TatD DNase domain containing 1 [Source:HGNC Symbol;Acc:HGNC:1157]	0.010405	1.448089
TATDN3	TatD DNase domain containing 3 [Source:HGNC Symbol;Acc:HGNC:1158]	0.002424	1.682987
TBC1D7	TBC1 domain family member 7 [Source:HGNC Symbol;Acc:HGNC:1159]	0.000581	1.605355
TBCA	tubulin folding cofactor A [Source:HGNC Symbol;Acc:HGNC:1157]	0.001356	1.726966
TBCCD1	TBCC domain containing 1 [Source:HGNC Symbol;Acc:HGNC:255]	0.002586	1.32795
TBP	TATA-box binding protein [Source:HGNC Symbol;Acc:HGNC:1158]	0.000239	1.475389
TBPL1	TATA-box binding protein like 1 [Source:HGNC Symbol;Acc:HGNC:1159]	0.038108	1.288477
TCEAL1	transcription elongation factor A like 1 [Source:HGNC Symbol;Acc:HGNC:1160]	0.002066	1.933825
TCEAL9	transcription elongation factor A like 9 [Source:HGNC Symbol;Acc:HGNC:1161]	0.047273	1.364358
TDG	thymine DNA glycosylase [Source:HGNC Symbol;Acc:HGNC:1170]	0.003279	1.476487
TEFM	transcription elongation factor, mitochondrial [Source:HGNC Symbol;Acc:HGNC:1171]	0.008574	1.566658
TENT5A	terminal nucleotidyltransferase 5A [Source:HGNC Symbol;Acc:HGNC:1172]	0.031891	1.350251
TENT5B	terminal nucleotidyltransferase 5B [Source:HGNC Symbol;Acc:HGNC:1173]	0.031086	1.589157
TEX30	testis expressed 30 [Source:HGNC Symbol;Acc:HGNC:25188]	0.002548	1.812649
TFB1M	transcription factor B1, mitochondrial [Source:HGNC Symbol;Acc:HGNC:1174]	4.46E-05	1.873457
TFB2M	transcription factor B2, mitochondrial [Source:HGNC Symbol;Acc:HGNC:1175]	0.001822	1.466333
TGDS	TDP-glucose 4,6-dehydratase [Source:HGNC Symbol;Acc:HGNC:25189]	0.00307	1.674772
TGIF1	TGFB induced factor homeobox 1 [Source:HGNC Symbol;Acc:HGNC:1176]	0.012	1.761986
THAP5	THAP domain containing 5 [Source:HGNC Symbol;Acc:HGNC:231]	0.004449	1.68325
THAP9	THAP domain containing 9 [Source:HGNC Symbol;Acc:HGNC:231]	0.000428	1.529471
THG1L	tRNA-histidine guanylyltransferase 1 like [Source:HGNC Symbol;Acc:HGNC:1177]	0.022406	1.173213
THOC7	THO complex 7 [Source:HGNC Symbol;Acc:HGNC:29874]	0.006992	1.507311
THUMPD3	THUMP domain containing 3 [Source:HGNC Symbol;Acc:HGNC:25190]	0.004449	1.319976
THYN1	thymocyte nuclear protein 1 [Source:HGNC Symbol;Acc:HGNC:25191]	0.039562	1.427151
TIAL1	TIA1 cytotoxic granule associated RNA binding protein like 1 [Source:HGNC Symbol;Acc:HGNC:1178]	0.020847	1.461014
TIFA	TRAF interacting protein with forkhead associated domain [Source:HGNC Symbol;Acc:HGNC:1179]	0.00682	1.308657
TIGD4	tigger transposable element derived 4 [Source:HGNC Symbol;Acc:HGNC:1180]	0.037821	1.521102
TIMM10	translocase of inner mitochondrial membrane 10 [Source:HGNC Symbol;Acc:HGNC:1181]	0.000227	1.60819
TIMM17A	translocase of inner mitochondrial membrane 17A [Source:HGNC Symbol;Acc:HGNC:1182]	0.015004	1.544834
TIMM21	translocase of inner mitochondrial membrane 21 [Source:HGNC Symbol;Acc:HGNC:1183]	0.005959	1.22913
TIMM8B	translocase of inner mitochondrial membrane 8 homolog B [Source:HGNC Symbol;Acc:HGNC:1184]	0.002899	1.815157
TIMM9	translocase of inner mitochondrial membrane 9 [Source:HGNC Symbol;Acc:HGNC:1185]	0.00155	1.635443
TIMMDC1	translocase of inner mitochondrial membrane domain containing 1 [Source:HGNC Symbol;Acc:HGNC:1186]	0.006266	1.393276
TIPRL	TOR signaling pathway regulator [Source:HGNC Symbol;Acc:HGNC:1187]	0.016482	1.498034
TLCD5	TLC domain containing 5 [Source:HGNC Symbol;Acc:HGNC:2828]	0.018445	1.704469
TM2D1	TM2 domain containing 1 [Source:HGNC Symbol;Acc:HGNC:2414]	5.10E-06	2.236574
TM2D2	TM2 domain containing 2 [Source:HGNC Symbol;Acc:HGNC:2415]	0.018704	1.297704
TMA7	translation machinery associated 7 homolog [Source:HGNC Symbol;Acc:HGNC:1188]	0.013052	1.467103
TMC8	transmembrane channel like 8 [Source:HGNC Symbol;Acc:HGNC:1189]	0.01638	1.562834
TMED2	transmembrane p24 trafficking protein 2 [Source:HGNC Symbol;Acc:HGNC:1190]	0.003929	1.61367
TMEM106B	transmembrane protein 106B [Source:HGNC Symbol;Acc:HGNC:25192]	0.02302	1.499879
TMEM106C	transmembrane protein 106C [Source:HGNC Symbol;Acc:HGNC:25193]	0.040119	1.337357
TMEM107	transmembrane protein 107 [Source:HGNC Symbol;Acc:HGNC:25194]	0.01388	1.33318
TMEM116	transmembrane protein 116 [Source:HGNC Symbol;Acc:HGNC:25195]	0.005055	1.477114
TMEM126B	transmembrane protein 126B [Source:HGNC Symbol;Acc:HGNC:25196]	0.000143	2.09117
TMEM128	transmembrane protein 128 [Source:HGNC Symbol;Acc:HGNC:25197]	0.022724	1.520752
TMEM141	transmembrane protein 141 [Source:HGNC Symbol;Acc:HGNC:25198]	0.017534	1.571481

TMEM14A	transmembrane protein 14A [Source:HGNC Symbol;Acc:HGNC:2	0.001235	1.641062
TMEM14B	transmembrane protein 14B [Source:HGNC Symbol;Acc:HGNC:2	0.000856	1.773364
TMEM14C	transmembrane protein 14C [Source:HGNC Symbol;Acc:HGNC:2	0.003551	1.900003
TMEM179B	transmembrane protein 179B [Source:HGNC Symbol;Acc:HGNC:2	0.018139	1.602403
TMEM18	transmembrane protein 18 [Source:HGNC Symbol;Acc:HGNC:25	0.009291	1.425249
TMEM182	transmembrane protein 182 [Source:HGNC Symbol;Acc:HGNC:2	0.022049	1.287228
TMEM186	transmembrane protein 186 [Source:HGNC Symbol;Acc:HGNC:2	0.035903	1.414977
TMEM187	transmembrane protein 187 [Source:HGNC Symbol;Acc:HGNC:1	0.015256	1.519324
TMEM199	transmembrane protein 199 [Source:HGNC Symbol;Acc:HGNC:1	0.000947	1.570879
TMEM203	transmembrane protein 203 [Source:HGNC Symbol;Acc:HGNC:2	0.012168	1.199981
TMEM218	transmembrane protein 218 [Source:HGNC Symbol;Acc:HGNC:2	0.000845	1.52251
TMEM230	transmembrane protein 230 [Source:HGNC Symbol;Acc:HGNC:1	0.001334	1.347396
TMEM251	transmembrane protein 251 [Source:HGNC Symbol;Acc:HGNC:2	0.012835	1.579746
TMEM256	transmembrane protein 256 [Source:HGNC Symbol;Acc:HGNC:2	0.016195	1.686689
TMEM258	transmembrane protein 258 [Source:HGNC Symbol;Acc:HGNC:1	0.008485	1.449992
TMEM267	transmembrane protein 267 [Source:HGNC Symbol;Acc:HGNC:2	0.000148	1.67511
TMEM41B	transmembrane protein 41B [Source:HGNC Symbol;Acc:HGNC:2	0.026713	1.315684
TMEM42	transmembrane protein 42 [Source:HGNC Symbol;Acc:HGNC:28	0.00227	1.866626
TMEM45A	transmembrane protein 45A [Source:HGNC Symbol;Acc:HGNC:2	0.040217	1.482767
TMEM50A	transmembrane protein 50A [Source:HGNC Symbol;Acc:HGNC:3	0.019748	1.641785
TMEM50B	transmembrane protein 50B [Source:HGNC Symbol;Acc:HGNC:1	0.00587	1.607931
TMEM59	transmembrane protein 59 [Source:HGNC Symbol;Acc:HGNC:12	0.035448	1.758179
TMEM60	transmembrane protein 60 [Source:HGNC Symbol;Acc:HGNC:21	0.001333	1.643741
TMEM68	transmembrane protein 68 [Source:HGNC Symbol;Acc:HGNC:26	0.003029	1.862531
TMEM70	transmembrane protein 70 [Source:HGNC Symbol;Acc:HGNC:26	5.85E-05	1.642613
TMEM87B	transmembrane protein 87B [Source:HGNC Symbol;Acc:HGNC:2	0.037099	1.175403
TMPRSS4	transmembrane serine protease 4 [Source:HGNC Symbol;Acc:HG	0.034967	1.189683
TMSB10	thymosin beta 10 [Source:HGNC Symbol;Acc:HGNC:11879]	0.044526	1.670807
TMSB15B	thymosin beta 15B [Source:HGNC Symbol;Acc:HGNC:28612]	0.026396	1.58818
TMSB4X	thymosin beta 4 X-linked [Source:HGNC Symbol;Acc:HGNC:1188	0.003504	1.780691
TNFAIP8	TNF alpha induced protein 8 [Source:HGNC Symbol;Acc:HGNC:1	0.037853	1.302281
TNRC6C	trinucleotide repeat containing adaptor 6C [Source:HGNC Symb	0.036939	2.17209
TNXB	tenascin XB [Source:HGNC Symbol;Acc:HGNC:11976]	0.000722	2.347379
TOB1	transducer of ERBB2, 1 [Source:HGNC Symbol;Acc:HGNC:11979]	0.004105	1.717182
TOM1L1	target of myb1 like 1 membrane trafficking protein [Source:HGN	0.005684	1.370883
TOMM7	translocase of outer mitochondrial membrane 7 [Source:HGNC S	0.002137	1.694825
TOR1A	torsin family 1 member A [Source:HGNC Symbol;Acc:HGNC:3098	0.022167	1.241262
TP53RK	TP53 regulating kinase [Source:HGNC Symbol;Acc:HGNC:16197]	7.56E-05	1.460304
TPD52	tumor protein D52 [Source:HGNC Symbol;Acc:HGNC:12005]	0.005511	1.271982
TPMT	thiopurine S-methyltransferase [Source:HGNC Symbol;Acc:HGNC	0.045165	1.270997
TPRKB	TP53RK binding protein [Source:HGNC Symbol;Acc:HGNC:24259]	0.009045	1.497286
TPT1	tumor protein, translationally-controlled 1 [Source:HGNC Symb	0.007612	1.987421
TRAF3IP3	TRAF3 interacting protein 3 [Source:HGNC Symbol;Acc:HGNC:30	0.008458	1.423162
TRAM1L1	translocation associated membrane protein 1 like 1 [Source:HGM	0.046983	1.414156
TRAPPC13	trafficking protein particle complex 13 [Source:HGNC Symbol;Ac	0.00239	1.8712
TRAPPC2	trafficking protein particle complex 2 [Source:HGNC Symbol;Acc:	0.038036	1.318756
TRAPPC2B	trafficking protein particle complex 2B [Source:HGNC Symbol;Ac	0.000454	1.993285

TRAPPC2L	trafficking protein particle complex 2 like [Source:HGNC Symbol;Acc:HGNC:100296]	0.02966	1.4856
TRIAP1	TP53 regulated inhibitor of apoptosis 1 [Source:HGNC Symbol;Acc:HGNC:100303]	0.03033	1.524217
TRIM13	tripartite motif containing 13 [Source:HGNC Symbol;Acc:HGNC:100238]	0.022381	1.70128
TRIM5	tripartite motif containing 5 [Source:HGNC Symbol;Acc:HGNC:100052]	0.005204	1.228489
TRIM69	tripartite motif containing 69 [Source:HGNC Symbol;Acc:HGNC:100001]	0.000198	1.469155
TRIQK	triple QxxK/R motif containing [Source:HGNC Symbol;Acc:HGNC:100072]	0.007281	1.593798
TRMO	tRNA methyltransferase O [Source:HGNC Symbol;Acc:HGNC:100309]	0.01326	1.367154
TRMT10A	tRNA methyltransferase 10A [Source:HGNC Symbol;Acc:HGNC:100473]	0.047361	1.345372
TRMT10C	tRNA methyltransferase 10C, mitochondrial RNase P subunit [Source:HGNC Symbol;Acc:HGNC:100001]	0.000105	1.641324
TRMT12	tRNA methyltransferase 12 homolog [Source:HGNC Symbol;Acc:HGNC:100014]	0.000147	1.456876
TRMT1L	tRNA methyltransferase 1 like [Source:HGNC Symbol;Acc:HGNC:100036]	0.003619	1.225627
TRMT5	tRNA methyltransferase 5 [Source:HGNC Symbol;Acc:HGNC:100231]	2.58E-05	1.732142
TRMT61B	tRNA methyltransferase 61B [Source:HGNC Symbol;Acc:HGNC:100036]	0.003604	1.316502
TRNAU1AP	tRNA selenocysteine 1 associated protein 1 [Source:HGNC Symbol;Acc:HGNC:100224]	0.022434	1.589733
TRUB2	TruB pseudouridine synthase family member 2 [Source:HGNC Symbol;Acc:HGNC:100117]	0.011708	1.316404
TSG101	tumor susceptibility 101 [Source:HGNC Symbol;Acc:HGNC:100597]	0.012758	1.570584
TSLP	thymic stromal lymphopoietin [Source:HGNC Symbol;Acc:HGNC:100458]	0.045827	1.670046
TSN	translin [Source:HGNC Symbol;Acc:HGNC:100379]	0.041853	1.220021
TSNAX	translin associated factor X [Source:HGNC Symbol;Acc:HGNC:100105]	0.010546	1.451684
TSPAN1	tetraspanin 1 [Source:HGNC Symbol;Acc:HGNC:100657]	0.006023	1.596688
TSPAN10	tetraspanin 10 [Source:HGNC Symbol;Acc:HGNC:100942]	0.02781	2.129837
TSPAN31	tetraspanin 31 [Source:HGNC Symbol;Acc:HGNC:100539]	0.003758	1.771502
TSPAN6	tetraspanin 6 [Source:HGNC Symbol;Acc:HGNC:100858]	0.006003	1.57319
TSSC4	tumor suppressing subtransferable candidate 4 [Source:HGNC Symbol;Acc:HGNC:10071E-05]	7.71E-05	1.47784
TSSK6	testis specific serine kinase 6 [Source:HGNC Symbol;Acc:HGNC:100033]	1.05E-07	1.97483
TST	thiosulfate sulfurtransferase [Source:HGNC Symbol;Acc:HGNC:100131]	0.013139	1.295492
TSTD1	thiosulfate sulfurtransferase like domain containing 1 [Source:HGNC Symbol;Acc:HGNC:100098]	0.009851	1.797986
TTC32	tetratricopeptide repeat domain 32 [Source:HGNC Symbol;Acc:HGNC:100052]	0.005237	1.411729
TTLL1	tubulin tyrosine ligase like 1 [Source:HGNC Symbol;Acc:HGNC:100487]	0.048735	1.350118
TTLL11	tubulin tyrosine ligase like 11 [Source:HGNC Symbol;Acc:HGNC:100040]	0.004053	1.58655
TUBD1	tubulin delta 1 [Source:HGNC Symbol;Acc:HGNC:100681]	0.018619	1.63523
TUSC2	tumor suppressor 2, mitochondrial calcium regulator [Source:HGNC Symbol;Acc:HGNC:100054]	0.005408	1.532943
TVP23B	trans-golgi network vesicle protein 23 homolog B [Source:HGNC Symbol;Acc:HGNC:100255]	0.025558	1.311467
TXN	thioredoxin [Source:HGNC Symbol;Acc:HGNC:100435]	0.001418	1.802323
TXNDC17	thioredoxin domain containing 17 [Source:HGNC Symbol;Acc:HGNC:10089E-05]	3.89E-05	1.862637
TXNDC9	thioredoxin domain containing 9 [Source:HGNC Symbol;Acc:HGNC:100027]	0.02785	1.460743
TXNL1	thioredoxin like 1 [Source:HGNC Symbol;Acc:HGNC:100436]	0.001568	1.661972
TYMP	thymidine phosphorylase [Source:HGNC Symbol;Acc:HGNC:100314]	0.038191	1.459265
TYSND1	trypsin domain containing 1 [Source:HGNC Symbol;Acc:HGNC:100179]	0.017954	1.280337
TYW3	tRNA-yW synthesizing protein 3 homolog [Source:HGNC Symbol;Acc:HGNC:100132]	0.013264	1.389038
TYW5	tRNA-yW synthesizing protein 5 [Source:HGNC Symbol;Acc:HGNC:100118]	0.011895	1.396319
UBA3	ubiquitin like modifier activating enzyme 3 [Source:HGNC Symbol;Acc:HGNC:100044]	0.004432	1.461332
UBE2B	ubiquitin conjugating enzyme E2 B [Source:HGNC Symbol;Acc:HGNC:100095]	0.009561	1.545594
UBE2D2	ubiquitin conjugating enzyme E2 D2 [Source:HGNC Symbol;Acc:HGNC:100135]	0.013571	1.183956
UBE2D3	ubiquitin conjugating enzyme E2 D3 [Source:HGNC Symbol;Acc:HGNC:100228]	0.022828	1.371295
UBE2E1	ubiquitin conjugating enzyme E2 E1 [Source:HGNC Symbol;Acc:HGNC:100496]	0.049648	1.262577
UBE2L6	ubiquitin conjugating enzyme E2 L6 [Source:HGNC Symbol;Acc:HGNC:100488]	0.04882	1.347881

UBE2N	ubiquitin conjugating enzyme E2 N [Source:HGNC Symbol;Acc:HGNC:13736]	0.020682	1.346974
UBE2T	ubiquitin conjugating enzyme E2 T [Source:HGNC Symbol;Acc:HGNC:13736]	0.004154	1.529194
UBE2V2	ubiquitin conjugating enzyme E2 V2 [Source:HGNC Symbol;Acc:HGNC:13736]	0.008516	1.324119
UBE2W	ubiquitin conjugating enzyme E2 W [Source:HGNC Symbol;Acc:HGNC:13736]	0.039544	1.547082
UBE3B	ubiquitin protein ligase E3B [Source:HGNC Symbol;Acc:HGNC:13736]	0.000358	1.503766
UBL5	ubiquitin like 5 [Source:HGNC Symbol;Acc:HGNC:13736]	0.030712	1.708545
UBLCP1	ubiquitin like domain containing CTD phosphatase 1 [Source:HGNC Symbol;Acc:HGNC:13736]	0.003326	1.518503
UBXN8	UBX domain protein 8 [Source:HGNC Symbol;Acc:HGNC:30307]	0.002128	1.523255
UCHL3	ubiquitin C-terminal hydrolase L3 [Source:HGNC Symbol;Acc:HGNC:13736]	0.04135	1.657698
UFM1	ubiquitin fold modifier 1 [Source:HGNC Symbol;Acc:HGNC:20597]	0.04635	1.395622
UFSP2	UFM1 specific peptidase 2 [Source:HGNC Symbol;Acc:HGNC:25600]	0.001363	1.277104
UGP2	UDP-glucose pyrophosphorylase 2 [Source:HGNC Symbol;Acc:HGNC:13736]	0.002001	1.472267
ULBP1	UL16 binding protein 1 [Source:HGNC Symbol;Acc:HGNC:14893]	0.000545	1.607222
UMAD1	UBAP1-MVB12-associated (UMA) domain containing 1 [Source:HGNC Symbol;Acc:HGNC:13736]	0.046059	1.292976
UNC50	unc-50 inner nuclear membrane RNA binding protein [Source:HGNC Symbol;Acc:HGNC:13736]	0.001134	1.773078
UPP1	uridine phosphorylase 1 [Source:HGNC Symbol;Acc:HGNC:12576]	0.017869	1.325304
UQCC2	ubiquinol-cytochrome c reductase complex assembly factor 2 [Source:HGNC Symbol;Acc:HGNC:13736]	0.036607	1.708893
UQCR10	ubiquinol-cytochrome c reductase, complex III subunit X [Source:HGNC Symbol;Acc:HGNC:13736]	0.005155	1.606003
UQCR11	ubiquinol-cytochrome c reductase, complex III subunit XI [Source:HGNC Symbol;Acc:HGNC:13736]	0.044193	1.464005
UQCRB	ubiquinol-cytochrome c reductase binding protein [Source:HGNC Symbol;Acc:HGNC:13736]	0.011561	1.463925
UQCRH	ubiquinol-cytochrome c reductase hinge protein [Source:HGNC Symbol;Acc:HGNC:13736]	0.009657	1.597505
UQCRQ	ubiquinol-cytochrome c reductase complex III subunit VII [Source:HGNC Symbol;Acc:HGNC:13736]	0.017954	1.719968
USE1	unconventional SNARE in the ER 1 [Source:HGNC Symbol;Acc:HGNC:13736]	0.001556	1.490712
USP16	ubiquitin specific peptidase 16 [Source:HGNC Symbol;Acc:HGNC:13736]	0.00249	1.321489
USP44	ubiquitin specific peptidase 44 [Source:HGNC Symbol;Acc:HGNC:13736]	0.021699	1.548914
UTP11	UTP11 small subunit processome component [Source:HGNC Symbol;Acc:HGNC:13736]	0.027363	1.298059
UTY	ubiquitously transcribed tetratricopeptide repeat containing, Y-linked [Source:HGNC Symbol;Acc:HGNC:13736]	0.039543	1.397569
UXT	ubiquitously expressed prefoldin like chaperone [Source:HGNC Symbol;Acc:HGNC:13736]	0.021034	1.609499
VAMP4	vesicle associated membrane protein 4 [Source:HGNC Symbol;Acc:HGNC:13736]	0.03459	1.52371
VAMP8	vesicle associated membrane protein 8 [Source:HGNC Symbol;Acc:HGNC:13736]	0.029265	1.699159
VANGL2	VANGL planar cell polarity protein 2 [Source:HGNC Symbol;Acc:HGNC:13736]	0.03918	1.453775
VBP1	VHL binding protein 1 [Source:HGNC Symbol;Acc:HGNC:12662]	0.003096	1.525798
VCPKMT	valosin containing protein lysine methyltransferase [Source:HGNC Symbol;Acc:HGNC:13736]	0.000351	1.711453
VDAC2	voltage dependent anion channel 2 [Source:HGNC Symbol;Acc:HGNC:13736]	0.022406	1.472067
VDAC3	voltage dependent anion channel 3 [Source:HGNC Symbol;Acc:HGNC:13736]	0.00048	1.580425
VMP1	vacuole membrane protein 1 [Source:HGNC Symbol;Acc:HGNC:20597]	0.000147	1.575968
VPS26A	VPS26, retromer complex component A [Source:HGNC Symbol;Acc:HGNC:13736]	0.004711	1.298371
VPS29	VPS29 retromer complex component [Source:HGNC Symbol;Acc:HGNC:13736]	0.008549	1.530525
VPS33A	VPS33A core subunit of CORVET and HOPS complexes [Source:HGNC Symbol;Acc:HGNC:13736]	0.003771	1.31542
VRK2	VRK serine/threonine kinase 2 [Source:HGNC Symbol;Acc:HGNC:13736]	0.011391	1.256466
VRK3	VRK serine/threonine kinase 3 [Source:HGNC Symbol;Acc:HGNC:13736]	0.033466	1.323829
WASHC3	WASH complex subunit 3 [Source:HGNC Symbol;Acc:HGNC:2425]	0.019934	1.395403
WDR25	WD repeat domain 25 [Source:HGNC Symbol;Acc:HGNC:21064]	0.029147	1.404339
WDR53	WD repeat domain 53 [Source:HGNC Symbol;Acc:HGNC:28786]	0.002209	1.436991
WDR61	WD repeat domain 61 [Source:HGNC Symbol;Acc:HGNC:30300]	0.000545	1.80611
WDR78	WD repeat domain 78 [Source:HGNC Symbol;Acc:HGNC:26252]	0.022226	1.462579
WDSUB1	WD repeat, sterile alpha motif and U-box domain containing 1 [Source:HGNC Symbol;Acc:HGNC:13736]	0.043468	1.586353

WIP1	WD repeat domain, phosphoinositide interacting 1 [Source:HGNC Symbol;Acc:HGNC:25508]	0.01205	1.388087
XKR8	XK related 8 [Source:HGNC Symbol;Acc:HGNC:25508]	0.002199	1.566002
XKR9	XK related 9 [Source:HGNC Symbol;Acc:HGNC:20937]	0.002406	1.587001
YAE1	YAE1 maturation factor of ABCE1 [Source:HGNC Symbol;Acc:HGNC:17363]	0.001217	1.72877
YAF2	YY1 associated factor 2 [Source:HGNC Symbol;Acc:HGNC:17363]	0.013809	1.563339
YBEY	ybeY metalloendoribonuclease [Source:HGNC Symbol;Acc:HGNC:17363]	0.031326	1.53507
YEATS4	YEATS domain containing 4 [Source:HGNC Symbol;Acc:HGNC:24124]	0.010366	1.484272
YIPF4	Yip1 domain family member 4 [Source:HGNC Symbol;Acc:HGNC:24124]	0.046793	1.332587
YIPF6	Yip1 domain family member 6 [Source:HGNC Symbol;Acc:HGNC:24124]	0.005908	1.428348
YPEL5	yippee like 5 [Source:HGNC Symbol;Acc:HGNC:18329]	0.041069	1.803326
ZBED5	zinc finger BED-type containing 5 [Source:HGNC Symbol;Acc:HGNC:18329]	0.008028	1.224188
ZBTB6	zinc finger and BTB domain containing 6 [Source:HGNC Symbol;Acc:HGNC:18329]	2.48E-05	1.597204
ZBTB7B	zinc finger and BTB domain containing 7B [Source:HGNC Symbol;Acc:HGNC:18329]	0.021786	1.272626
ZBTB8OS	zinc finger and BTB domain containing 8 opposite strand [Source:HGNC Symbol;Acc:HGNC:18329]	0.019616	1.377673
ZC3H15	zinc finger CCCH-type containing 15 [Source:HGNC Symbol;Acc:HGNC:18329]	0.021509	1.342366
ZCCHC4	zinc finger CCHC-type containing 4 [Source:HGNC Symbol;Acc:HGNC:18329]	0.007558	1.381864
ZCCHC7	zinc finger CCHC-type containing 7 [Source:HGNC Symbol;Acc:HGNC:18329]	0.042343	1.413485
ZCCHC8	zinc finger CCHC-type containing 8 [Source:HGNC Symbol;Acc:HGNC:18329]	0.002918	1.258111
ZCCHC9	zinc finger CCHC-type containing 9 [Source:HGNC Symbol;Acc:HGNC:18329]	0.003447	1.604323
ZCRB1	zinc finger CCHC-type and RNA binding motif containing 1 [Source:HGNC Symbol;Acc:HGNC:18329]	0.005717	1.601003
ZCWPW1	zinc finger CW-type and PWWP domain containing 1 [Source:HGNC Symbol;Acc:HGNC:18329]	0.005139	1.357712
ZDHC1	zinc finger DHHC-type containing 1 [Source:HGNC Symbol;Acc:HGNC:18329]	0.026617	1.398322
ZDHC13	zinc finger DHHC-type containing 13 [Source:HGNC Symbol;Acc:HGNC:18329]	0.028558	1.342179
ZFAND1	zinc finger AN1-type containing 1 [Source:HGNC Symbol;Acc:HGNC:18329]	0.004397	1.603557
ZFAND2A	zinc finger AN1-type containing 2A [Source:HGNC Symbol;Acc:HGNC:18329]	0.003792	2.216022
ZFAND6	zinc finger AN1-type containing 6 [Source:HGNC Symbol;Acc:HGNC:18329]	0.000189	1.927766
ZFP28	ZFP28 zinc finger protein [Source:HGNC Symbol;Acc:HGNC:1780]	0.004093	1.463262
ZFP37	ZFP37 zinc finger protein [Source:HGNC Symbol;Acc:HGNC:1286]	0.037406	1.713681
ZFP62	ZFP62 zinc finger protein [Source:HGNC Symbol;Acc:HGNC:2324]	0.036696	1.339808
ZFP82	ZFP82 zinc finger protein [Source:HGNC Symbol;Acc:HGNC:2868]	0.010062	1.312468
ZMYM5	zinc finger MYM-type containing 5 [Source:HGNC Symbol;Acc:HGNC:18329]	0.010351	1.316996
ZNF136	zinc finger protein 136 [Source:HGNC Symbol;Acc:HGNC:12920]	0.042585	1.511705
ZNF138	zinc finger protein 138 [Source:HGNC Symbol;Acc:HGNC:12922]	0.039426	1.388289
ZNF14	zinc finger protein 14 [Source:HGNC Symbol;Acc:HGNC:12924]	0.025459	1.535882
ZNF140	zinc finger protein 140 [Source:HGNC Symbol;Acc:HGNC:12925]	0.000705	1.767949
ZNF169	zinc finger protein 169 [Source:HGNC Symbol;Acc:HGNC:12957]	0.013339	1.429797
ZNF181	zinc finger protein 181 [Source:HGNC Symbol;Acc:HGNC:12971]	0.006113	1.297631
ZNF197	zinc finger protein 197 [Source:HGNC Symbol;Acc:HGNC:12988]	0.000109	1.400625
ZNF200	zinc finger protein 200 [Source:HGNC Symbol;Acc:HGNC:12993]	0.008408	1.366204
ZNF222	zinc finger protein 222 [Source:HGNC Symbol;Acc:HGNC:13015]	0.001455	1.831447
ZNF226	zinc finger protein 226 [Source:HGNC Symbol;Acc:HGNC:13019]	0.023372	1.716923
ZNF227	zinc finger protein 227 [Source:HGNC Symbol;Acc:HGNC:13020]	0.033016	1.44221
ZNF251	zinc finger protein 251 [Source:HGNC Symbol;Acc:HGNC:13045]	0.033272	1.223117
ZNF260	zinc finger protein 260 [Source:HGNC Symbol;Acc:HGNC:13499]	0.002137	1.581056
ZNF273	zinc finger protein 273 [Source:HGNC Symbol;Acc:HGNC:13067]	0.047111	1.569071
ZNF277	zinc finger protein 277 [Source:HGNC Symbol;Acc:HGNC:13070]	0.002021	1.771014
ZNF280D	zinc finger protein 280D [Source:HGNC Symbol;Acc:HGNC:25953]	0.021592	1.27594

ZNF285	zinc finger protein 285 [Source:HGNC Symbol;Acc:HGNC:13079]	0.030373	1.415447
ZNF32	zinc finger protein 32 [Source:HGNC Symbol;Acc:HGNC:13095]	0.008018	1.748003
ZNF320	zinc finger protein 320 [Source:HGNC Symbol;Acc:HGNC:13842]	8.84E-05	1.476581
ZNF330	zinc finger protein 330 [Source:HGNC Symbol;Acc:HGNC:15462]	0.029561	1.202578
ZNF333	zinc finger protein 333 [Source:HGNC Symbol;Acc:HGNC:15624]	0.026805	1.344266
ZNF382	zinc finger protein 382 [Source:HGNC Symbol;Acc:HGNC:17409]	0.028929	1.377165
ZNF396	zinc finger protein 396 [Source:HGNC Symbol;Acc:HGNC:18824]	0.032094	1.638382
ZNF419	zinc finger protein 419 [Source:HGNC Symbol;Acc:HGNC:20648]	0.038731	1.445808
ZNF429	zinc finger protein 429 [Source:HGNC Symbol;Acc:HGNC:20817]	6.25E-05	1.827042
ZNF432	zinc finger protein 432 [Source:HGNC Symbol;Acc:HGNC:20810]	2.22E-08	1.641066
ZNF460	zinc finger protein 460 [Source:HGNC Symbol;Acc:HGNC:21628]	0.022275	1.534484
ZNF490	zinc finger protein 490 [Source:HGNC Symbol;Acc:HGNC:23705]	0.022052	1.869938
ZNF501	zinc finger protein 501 [Source:HGNC Symbol;Acc:HGNC:23717]	0.019255	1.449639
ZNF502	zinc finger protein 502 [Source:HGNC Symbol;Acc:HGNC:23718]	0.000909	1.649229
ZNF506	zinc finger protein 506 [Source:HGNC Symbol;Acc:HGNC:23780]	0.000198	1.423128
ZNF528	zinc finger protein 528 [Source:HGNC Symbol;Acc:HGNC:29384]	4.61E-05	1.782511
ZNF555	zinc finger protein 555 [Source:HGNC Symbol;Acc:HGNC:28382]	0.002262	2.020542
ZNF561	zinc finger protein 561 [Source:HGNC Symbol;Acc:HGNC:28684]	1.90E-05	1.56966
ZNF565	zinc finger protein 565 [Source:HGNC Symbol;Acc:HGNC:26726]	0.012375	1.60659
ZNF566	zinc finger protein 566 [Source:HGNC Symbol;Acc:HGNC:25919]	0.005928	1.351855
ZNF570	zinc finger protein 570 [Source:HGNC Symbol;Acc:HGNC:26416]	0.039908	1.555919
ZNF573	zinc finger protein 573 [Source:HGNC Symbol;Acc:HGNC:26420]	0.035149	1.587661
ZNF582	zinc finger protein 582 [Source:HGNC Symbol;Acc:HGNC:26421]	0.001415	1.752117
ZNF596	zinc finger protein 596 [Source:HGNC Symbol;Acc:HGNC:27268]	1.01E-05	2.474479
ZNF600	zinc finger protein 600 [Source:HGNC Symbol;Acc:HGNC:30951]	2.14E-09	1.757477
ZNF606	zinc finger protein 606 [Source:HGNC Symbol;Acc:HGNC:25879]	4.34E-05	1.695857
ZNF613	zinc finger protein 613 [Source:HGNC Symbol;Acc:HGNC:25827]	0.002406	1.470239
ZNF614	zinc finger protein 614 [Source:HGNC Symbol;Acc:HGNC:24722]	3.84E-06	1.661651
ZNF615	zinc finger protein 615 [Source:HGNC Symbol;Acc:HGNC:24740]	0.014838	1.556429
ZNF616	zinc finger protein 616 [Source:HGNC Symbol;Acc:HGNC:28062]	4.20E-12	1.970047
ZNF626	zinc finger protein 626 [Source:HGNC Symbol;Acc:HGNC:30461]	0.011118	1.297376
ZNF627	zinc finger protein 627 [Source:HGNC Symbol;Acc:HGNC:30570]	0.004498	2.019049
ZNF649	zinc finger protein 649 [Source:HGNC Symbol;Acc:HGNC:25741]	0.008262	1.396917
ZNF655	zinc finger protein 655 [Source:HGNC Symbol;Acc:HGNC:30899]	0.024404	1.226955
ZNF66	zinc finger protein 66 [Source:HGNC Symbol;Acc:HGNC:13135]	0.005312	1.974588
ZNF668	zinc finger protein 668 [Source:HGNC Symbol;Acc:HGNC:25821]	0.045421	1.309378
ZNF669	zinc finger protein 669 [Source:HGNC Symbol;Acc:HGNC:25736]	4.80E-09	1.988647
ZNF670-ZNF69	ZNF670-ZNF695 readthrough (NMD candidate) [Source:HGNC Sy	0.001315	1.521482
ZNF675	zinc finger protein 675 [Source:HGNC Symbol;Acc:HGNC:30768]	0.038081	1.486549
ZNF680	zinc finger protein 680 [Source:HGNC Symbol;Acc:HGNC:26897]	0.012127	1.73047
ZNF682	zinc finger protein 682 [Source:HGNC Symbol;Acc:HGNC:28857]	0.001945	1.639552
ZNF684	zinc finger protein 684 [Source:HGNC Symbol;Acc:HGNC:28418]	0.044418	1.569516
ZNF701	zinc finger protein 701 [Source:HGNC Symbol;Acc:HGNC:25597]	1.84E-05	1.684744
ZNF706	zinc finger protein 706 [Source:HGNC Symbol;Acc:HGNC:24992]	0.010892	1.216735
ZNF717	zinc finger protein 717 [Source:HGNC Symbol;Acc:HGNC:29448]	0.011435	1.356683
ZNF738	zinc finger protein 738 [Source:HGNC Symbol;Acc:HGNC:32469]	0.002918	1.409036
ZNF749	zinc finger protein 749 [Source:HGNC Symbol;Acc:HGNC:32783]	0.011437	1.716876

ZNF77	zinc finger protein 77 [Source:HGNC Symbol;Acc:HGNC:13150]	0.029648	1.541643
ZNF773	zinc finger protein 773 [Source:HGNC Symbol;Acc:HGNC:30487]	0.022222	1.438628
ZNF816	zinc finger protein 816 [Source:HGNC Symbol;Acc:HGNC:26995]	0.020691	1.497328
ZNF829	zinc finger protein 829 [Source:HGNC Symbol;Acc:HGNC:34032]	0.004083	1.362283
ZNF83	zinc finger protein 83 [Source:HGNC Symbol;Acc:HGNC:13158]	0.008831	1.341285
ZNF836	zinc finger protein 836 [Source:HGNC Symbol;Acc:HGNC:34333]	5.42E-06	1.863787
ZNF837	zinc finger protein 837 [Source:HGNC Symbol;Acc:HGNC:25164]	0.02249	1.617032
ZNF841	zinc finger protein 841 [Source:HGNC Symbol;Acc:HGNC:27611]	0.003771	1.399731
ZNF844	zinc finger protein 844 [Source:HGNC Symbol;Acc:HGNC:25932]	0.0017	1.604779
ZNF845	zinc finger protein 845 [Source:HGNC Symbol;Acc:HGNC:25112]	6.79E-09	1.770986
ZNF846	zinc finger protein 846 [Source:HGNC Symbol;Acc:HGNC:27260]	0.017096	1.669799
ZNF85	zinc finger protein 85 [Source:HGNC Symbol;Acc:HGNC:13160]	0.032514	1.385911
ZNF880	zinc finger protein 880 [Source:HGNC Symbol;Acc:HGNC:37249]	0.018476	1.560503
ZNF891	zinc finger protein 891 [Source:HGNC Symbol;Acc:HGNC:38709]	0.014934	1.720415
ZNRD1	zinc ribbon domain containing 1 [Source:HGNC Symbol;Acc:HGN	0.019255	1.635954
ZNRD2	zinc ribbon domain containing 2 [Source:HGNC Symbol;Acc:HGN	0.002112	1.45114
ZRANB2	zinc finger RANBP2-type containing 2 [Source:HGNC Symbol;Acc	0.028079	1.339707
ZSCAN18	zinc finger and SCAN domain containing 18 [Source:HGNC Symb	0.021945	1.321089
ZSCAN26	zinc finger and SCAN domain containing 26 [Source:HGNC Symb	0.014553	1.368441
ZSWIM7	zinc finger SWIM-type containing 7 [Source:HGNC Symbol;Acc:H	0.002897	1.499406

125 orange - ATF1 targets

16 blue - 3' ATF1 targets